

Supplementary Table S3. shRNA constructs with Olaparib Drug Effect Z scores >1.96

shRNA clone name	Openbiosystems Plate Name	Openbiosystems Plate Row	Openbiosystems Plate Column	Viral Pool
V2LHS_77082_6	172_0517	G	7	6
V2LHS_77440_2	172_0145	G	7	6
V2LHS_24063_6	172_0574	G	2	4
V2LHS_74254_3	172_0251	A	5	6
V2LHS_271756_2	172_0116	D	9	4
V2LHS_96284_5	172_0437	B	11	6
V2LHS_185015_2	172_0108	A	7	3
V2LHS_171732_4	172_0335	G	10	2
V2LHS_107148_2	172_0149	B	10	1
V2LHS_66842_6	172_0549	C	1	6
V2LHS_214664_3	172_0201	D	7	3
V2LHS_262796_3	172_0288	C	7	4
V2LHS_271587_6	172_0555	H	5	4
V2LHS_1008_1	172_0055	D	4	1
V2LHS_33380_4	172_0354	H	6	5
V2LHS_70351_3	172_0203	F	9	6
V2LHS_246970_3	172_0258	B	9	4
V2LHS_78805_6	172_0586	C	11	6
V2LHS_55312_1	172_0006	H	2	5
V2LHS_216335_4	172_0345	G	2	3
V2LHS_53664_2	172_0141	D	6	5
V2LHS_26248_3	172_0206	E	10	4
V2LHS_65108_2	172_0128	D	9	6
V2LHS_122792_4	172_0304	G	5	1
V2LHS_262054_1	172_0088	A	12	4
V2LHS_89888_4	172_0308	E	3	6
V2LHS_26159_2	172_0135	G	7	4
V2LHS_175334_6	172_0551	E	5	2
V2LHS_265946_1	172_0099	C	8	4
V2LHS_67704_3	172_0238	F	12	6
V2LHS_96495_6	172_0558	E	12	6
V2LHS_83855_6	172_0548	D	4	6
V2LHS_90639_6	172_0573	G	10	6
V2LHS_90640_1	172_0059	F	10	6
V2LHS_104270_6	172_0501	B	9	1
V2LHS_227445_6	172_0532	D	5	4
V2LHS_271860_5	172_0402	F	2	4
V2LHS_58912_2	172_0150	C	5	5
V2LHS_23948_5	172_0408	F	12	4
V2LHS_65060_4	172_0341	G	8	6
V2LHS_171702_5	172_0496	C	8	2
V2LHS_108984_6	172_0600	H	12	1
V2LHS_12583_5	172_0470	E	12	1

V2LHS_78291_1	172_0017	E	4	6
V2LHS_89636_1	172_0019	D	5	6
V2LHS_261864_1	172_0092	G	10	4
V2LHS_74501_2	172_0154	B	4	6
V2LHS_75930_4	172_0358	D	3	6
V2LHS_194282_2	172_0179	F	11	3
V2LHS_73495_5	172_0485	D	5	6
V2LHS_46109_2	172_0158	E	8	5
V2LHS_86673_5	172_0469	E	2	6
V2LHS_81116_6	172_0574	D	7	6
V2LHS_99446_4	172_0339	E	6	6
V2LHS_90493_5	172_0484	A	7	6
V2LHS_90495_2	172_0162	B	12	6
V2LHS_55972_6	172_0565	G	4	5
V2LHS_92826_3	172_0287	B	11	6
V2LHS_29377_5	172_0470	B	1	5
V2LHS_29368_5	172_0488	G	10	5
V2LHS_251919_4	172_0340	G	3	4
V2LHS_26304_4	172_0386	G	10	4
V2LHS_55089_1	172_0099	C	3	5
V2LHS_91998_2	172_0137	H	2	6
V2LHS_39522_1	172_0052	E	2	5
V2LHS_264642_1	172_0089	B	1	4
V2LHS_86135_3	172_0290	D	2	6
V2LHS_79585_1	172_0084	D	1	6
V2LHS_64568_1	172_0009	B	8	6
V2LHS_145479_1	172_0002	D	9	2
V2LHS_252883_4	172_0345	F	8	4
V2LHS_39821_6	172_0534	G	10	5
V2LHS_85141_4	172_0386	C	3	6
V2LHS_95918_6	172_0501	D	2	6
V2LHS_96990_3	172_0201	G	5	6
V2LHS_273407_5	172_0442	E	6	4
V2LHS_63544_1	172_0004	E	2	6
V2LHS_10256_1	172_0064	D	2	1
V2LHS_83265_3	172_0230	F	10	6
V2LHS_96010_4	172_0335	D	5	6
V2LHS_265454_6	172_0580	B	12	4
V2LHS_92504_5	172_0457	H	10	6
V2LHS_225737_2	172_0172	D	6	4
V2LHS_225736_1	172_0049	D	5	4
V2LHS_198492_3	172_0282	C	4	3
V2LHS_124863_1	172_0047	E	4	1
V2LHS_89120_4	172_0304	A	5	6
V2LHS_89135_6	172_0534	E	9	6
V2LHS_258813_6	172_0545	G	5	4
V2LHS_30512_1	172_0055	D	3	5
V2LHS_192661_6	172_0581	E	11	3
V2LHS_192666_4	172_0314	D	4	3
V2LHS_78209_1	172_0018	B	10	6

V2LHS_245216_1	172_0094	F	9	4
V2LHS_13157_1	172_0091	E	7	1
V2LHS_81918_5	172_0466	A	3	6
V2LHS_276072_2	172_0122	H	6	4
V2LHS_84108_6	172_0577	E	4	6
V2LHS_188627_3	172_0277	A	12	3
V2LHS_151334_3	172_0204	A	7	2
V2LHS_225776_5	172_0405	A	5	4
V2LHS_254510_2	172_0146	E	8	4
V2LHS_104213_2	172_0155	A	1	1
V2LHS_108369_2	172_0140	G	7	1
V2LHS_102944_4	172_0324	E	11	1
V2LHS_102946_3	172_0234	C	5	1
V2LHS_66640_2	172_0152	E	2	6
V2LHS_106544_6	172_0592	D	11	1
V2LHS_99599_4	172_0301	C	2	6
V2LHS_121234_6	172_0595	B	6	1
V2LHS_67709_1	172_0053	D	10	6
V2LHS_108900_5	172_0416	H	1	1
V2LHS_102954_2	172_0167	C	10	1
V2LHS_80538_4	172_0364	D	10	6
V2LHS_72148_3	172_0217	H	12	6
V2LHS_7215_1	172_0058	C	6	6
V2LHS_136670_2	172_0172	C	8	1
V2LHS_136673_3	172_0258	C	4	1
V2LHS_255250_5	172_0409	A	5	4
V2LHS_86275_2	172_0118	E	11	6
V2LHS_73238_4	172_0393	C	1	6
V2LHS_63951_1	172_0001	C	11	6
V2LHS_80476_6	172_0538	H	5	6
V2LHS_81441_6	172_0515	B	2	6
V2LHS_242495_1	172_0060	F	8	4
V2LHS_163166_3	172_0266	G	4	2
V2LHS_271548_6	172_0576	A	10	4
V2LHS_96214_6	172_0524	F	7	6
V2LHS_96980_6	172_0539	A	9	6
V2LHS_96979_4	172_0394	G	8	6
V2LHS_100195_4	172_0322	A	1	1
V2LHS_100181_6	172_0580	G	6	1
V2LHS_67015_6	172_0600	B	4	6
V2LHS_67012_6	172_0519	H	9	6
V2LHS_76904_6	172_0585	F	3	6
V2LHS_76589_6	172_0556	E	5	6
V2LHS_90151_2	172_0121	F	5	6
V2LHS_262414_2	172_0101	B	10	4
V2LHS_67043_3	172_0284	A	2	6
V2LHS_6705_1	172_0009	E	6	6
V2LHS_202406_5	172_0408	E	3	3
V2LHS_113893_3	172_0284	G	2	1
V2LHS_39269_4	172_0324	D	8	5

V2LHS_242033_3	172_0299	E	8	4
V2LHS_118925_3	172_0242	H	3	1
V2LHS_36305_4	172_0341	D	9	5
V2LHS_76141_4	172_0379	D	6	6
V2LHS_12566_2	172_0107	D	5	1
V2LHS_286849_3	172_0229	E	8	5
V2LHS_76089_2	172_0120	F	7	6
V2LHS_248895_6	172_0581	G	1	4
V2LHS_202658_2	172_0173	B	11	3
V2LHS_86393_6	172_0539	B	10	6
V2LHS_86388_5	172_0457	G	2	6
V2LHS_167287_3	172_0249	E	7	2
V2LHS_107705_6	172_0542	G	7	1
V2LHS_230774_5	172_0468	F	3	4
V2LHS_81491_5	172_0456	H	4	6
V2LHS_53303_4	172_0355	G	4	5
V2LHS_84304_5	172_0490	A	5	6
V2LHS_69167_4	172_0330	C	5	6
V2LHS_111780_1	172_0077	G	8	1
V2LHS_18836_1	172_0018	D	8	3
V2LHS_84168_4	172_0392	A	6	6
V2LHS_270666_6	172_0560	B	5	4
V2LHS_95862_5	172_0416	C	9	6
V2LHS_32227_6	172_0582	D	9	5
V2LHS_69250_3	172_0297	D	10	6
V2LHS_38656_6	172_0569	E	6	5
V2LHS_204822_4	172_0331	D	10	3
V2LHS_108055_6	172_0587	D	2	1
V2LHS_23105_1	172_0054	H	4	4
V2LHS_94824_6	172_0595	D	4	6
V2LHS_227404_5	172_0476	A	10	4
V2LHS_85139_1	172_0018	H	9	6
V2LHS_143220_1	172_0072	C	5	1
V2LHS_244612_3	172_0294	A	2	4
V2LHS_247523_3	172_0249	F	8	4
V2LHS_17689_4	172_0346	H	4	2
V2LHS_93185_5	172_0453	C	4	6
V2LHS_117489_1	172_0004	B	10	1
V2LHS_169860_4	172_0357	A	10	2
V2LHS_111913_5	172_0444	F	5	1
V2LHS_185273_3	172_0271	C	7	3
V2LHS_116662_1	172_0034	E	12	1
V2LHS_167638_2	172_0160	B	10	2
V2LHS_140491_2	172_0140	F	7	1
V2LHS_179308_2	172_0187	E	9	2
V2LHS_85925_4	172_0305	H	3	6
V2LHS_30218_2	172_0144	F	7	5
V2LHS_227661_4	172_0363	E	1	4
V2LHS_80550_5	172_0429	E	7	6
V2LHS_223494_6	172_0547	H	12	4

V2LHS_203111_3	172_0263	B	10	3
V2LHS_39473_2	172_0163	F	6	5
V2LHS_40399_2	172_0193	D	3	5
V2LHS_252155_2	172_0191	E	1	4
V2LHS_87970_1	172_0015	E	8	6
V2LHS_92217_1	172_0004	H	7	6
V2LHS_92221_3	172_0218	G	6	6
V2LHS_35192_4	172_0320	A	5	5
V2LHS_12421_1	172_0045	D	11	1
V2LHS_136139_6	172_0524	B	3	1
V2LHS_84279_1	172_0059	D	3	6
V2LHS_82032_5	172_0425	E	12	6
V2LHS_23539_1	172_0071	B	10	4
V2LHS_41523_3	172_0247	G	8	5
V2LHS_247509_1	172_0087	B	4	4
V2LHS_67391_6	172_0561	A	8	6
V2LHS_108225_2	172_0102	H	11	1
V2LHS_44276_3	172_0216	E	8	5
V2LHS_76814_2	172_0157	A	4	6
V2LHS_113304_6	172_0590	E	7	1
V2LHS_113303_1	172_0096	E	5	1
V2LHS_48949_4	172_0372	F	5	5
V2LHS_103716_1	172_0016	B	6	1
V2LHS_26110_2	172_0197	G	10	4
V2LHS_261086_1	172_0099	C	11	4
V2LHS_92148_3	172_0261	D	11	6
V2LHS_135199_1	172_0060	A	8	1
V2LHS_105952_6	172_0548	F	9	1
V2LHS_138568_4	172_0391	E	5	1
V2LHS_232447_4	172_0362	H	11	4
V2LHS_232450_5	172_0488	G	11	4
V2LHS_183064_4	172_0344	D	4	3
V2LHS_104055_1	172_0052	G	12	1
V2LHS_106994_2	172_0192	D	7	1
V2LHS_66610_5	172_0450	E	1	6
V2LHS_230306_2	172_0189	E	11	4
V2LHS_29098_2	172_0122	F	7	5
V2LHS_268023_3	172_0250	E	7	4
V2LHS_219075_4	172_0342	D	7	3
V2LHS_103404_4	172_0310	E	12	1
V2LHS_103411_4	172_0373	A	11	1
V2LHS_72349_5	172_0459	D	8	6
V2LHS_72348_1	172_0077	F	8	6
V2LHS_222655_5	172_0492	F	4	3
V2LHS_141921_4	172_0373	A	12	1
V2LHS_98941_6	172_0599	F	7	6
V2LHS_85357_2	172_0166	D	3	6
V2LHS_139604_3	172_0237	A	11	1
V2LHS_234356_5	172_0434	A	6	4
V2LHS_96916_6	172_0565	C	4	6

V2LHS_236493_3	172_0231	F	3	4
V2LHS_244923_5	172_0489	E	6	4
V2LHS_76115_5	172_0424	G	2	6
V2LHS_74989_4	172_0349	G	12	6
V2LHS_255507_4	172_0356	G	4	4
V2LHS_36566_1	172_0007	C	11	5
V2LHS_72619_3	172_0299	C	1	6
V2LHS_264582_5	172_0427	C	7	4
V2LHS_91997_5	172_0408	B	1	6
V2LHS_254937_1	172_0083	B	8	4
V2LHS_185689_6	172_0576	F	3	3
V2LHS_70639_4	172_0329	D	1	6
V2LHS_33898_4	172_0379	E	3	5
V2LHS_230802_1	172_0031	D	3	4
V2LHS_97593_1	172_0023	B	3	6
V2LHS_84302_2	172_0163	E	11	6
V2LHS_43710_1	172_0039	H	2	5
V2LHS_76694_2	172_0103	G	11	6
V2LHS_104782_5	172_0500	D	4	1
V2LHS_136523_6	172_0597	F	10	1
V2LHS_95310_1	172_0036	H	8	6
V2LHS_151944_6	172_0524	G	10	2
V2LHS_33479_1	172_0069	G	11	5
V2LHS_204727_3	172_0238	F	1	3
V2LHS_123869_6	172_0535	A	12	1
V2LHS_263074_2	172_0145	H	5	4
V2LHS_133836_5	172_0486	H	3	1
V2LHS_97776_2	172_0178	B	2	6
V2LHS_224073_6	172_0545	C	6	4
V2LHS_119874_6	172_0579	F	6	1
V2LHS_164425_4	172_0312	A	5	2
V2LHS_176062_5	172_0438	G	8	2
V2LHS_263142_6	172_0503	A	9	4
V2LHS_99665_3	172_0205	G	5	6
V2LHS_99661_3	172_0220	D	11	6
V2LHS_27043_5	172_0405	D	4	4
V2LHS_270443_5	172_0460	F	9	4
V2LHS_137752_6	172_0593	E	7	1
V2LHS_137748_5	172_0476	D	9	1
V2LHS_84833_6	172_0527	F	3	6
V2LHS_76819_1	172_0059	H	4	6
V2LHS_80785_5	172_0445	H	7	6
V2LHS_276189_2	172_0200	C	3	4
V2LHS_276345_4	172_0357	A	1	4
V2LHS_92864_1	172_0035	B	5	6
V2LHS_76415_6	172_0589	D	9	6
V2LHS_140048_5	172_0481	B	10	1
V2LHS_91963_6	172_0548	F	11	6
V2LHS_189302_5	172_0420	E	2	3
V2LHS_126962_1	172_0093	C	6	1

V2LHS_284831_3	172_0240	G	9	5
V2LHS_91653_4	172_0381	G	12	6
V2LHS_195870_2	172_0197	C	12	3
V2LHS_96735_3	172_0203	D	12	6
V2LHS_120447_5	172_0418	F	3	1
V2LHS_22786_3	172_0280	B	2	4
V2LHS_26535_4	172_0330	B	5	4
V2LHS_36423_3	172_0221	A	10	5
V2LHS_64978_4	172_0311	D	10	6
V2LHS_285953_5	172_0447	H	6	5
V2LHS_113958_5	172_0403	F	12	1
V2LHS_232338_2	172_0182	D	7	4
V2LHS_204411_1	172_0083	E	4	3
V2LHS_24079_5	172_0478	D	12	4
V2LHS_143748_2	172_0157	E	8	2
V2LHS_71203_1	172_0027	G	11	6
V2LHS_264472_4	172_0369	A	2	4
V2LHS_63387_4	172_0304	C	5	6
V2LHS_67074_4	172_0333	C	4	6
V2LHS_162591_5	172_0444	F	8	2
V2LHS_86535_4	172_0344	A	12	6
V2LHS_6995_1	172_0081	B	8	6
V2LHS_277615_5	172_0496	C	4	4
V2LHS_270144_2	172_0152	A	6	4
V2LHS_93064_4	172_0339	F	5	6
V2LHS_70432_1	172_0039	H	4	6
V2LHS_65493_5	172_0465	G	2	6
V2LHS_72187_1	172_0050	D	6	6
V2LHS_62474_5	172_0494	E	5	6
V2LHS_275770_2	172_0174	E	1	4
V2LHS_70472_2	172_0140	A	10	6
V2LHS_226699_1	172_0028	D	9	4
V2LHS_193766_6	172_0532	E	7	3
V2LHS_80060_1	172_0015	E	10	6
V2LHS_75502_2	172_0176	F	10	6
V2LHS_25681_5	172_0404	C	10	4
V2LHS_239269_6	172_0506	G	6	4
V2LHS_92683_1	172_0025	F	11	6
V2LHS_63983_6	172_0578	D	7	6
V2LHS_286051_3	172_0231	A	10	5
V2LHS_228193_4	172_0382	E	12	4
V2LHS_75357_2	172_0110	H	8	6
V2LHS_65277_2	172_0197	E	9	6
V2LHS_124526_2	172_0155	A	10	1
V2LHS_224570_6	172_0585	E	8	4
V2LHS_84938_4	172_0372	G	10	6
V2LHS_7242_1	172_0062	E	1	6
V2LHS_95836_1	172_0013	H	7	6
V2LHS_98075_6	172_0561	G	7	6
V2LHS_93056_2	172_0141	H	8	6

V2LHS_64088_5	172_0428	D	12	6
V2LHS_242796_2	172_0146	B	11	4
V2LHS_33256_4	172_0344	E	6	5
V2LHS_75449_1	172_0097	A	12	6
V2LHS_141991_4	172_0398	D	6	1
V2LHS_47380_3	172_0295	E	7	5
V2LHS_90914_1	172_0072	C	3	6
V2LHS_93510_6	172_0554	C	3	6
V2LHS_136929_4	172_0345	D	11	1
V2LHS_5499_1	172_0042	E	7	5
V2LHS_10235_2	172_0123	H	11	1
V2LHS_45269_3	172_0289	E	9	5
V2LHS_73182_5	172_0421	C	1	6
V2LHS_60769_5	172_0419	D	3	5
V2LHS_98995_1	172_0086	F	7	6
V2LHS_10399_1	172_0031	C	1	1
V2LHS_44427_4	172_0393	B	4	5
V2LHS_84387_4	172_0366	E	8	6
V2LHS_39981_6	172_0574	G	11	5
V2LHS_45413_3	172_0251	C	8	5
V2LHS_85664_4	172_0397	A	7	6
V2LHS_249417_1	172_0093	C	6	4
V2LHS_232486_1	172_0048	F	6	4
V2LHS_95393_5	172_0441	D	8	6
V2LHS_26635_6	172_0550	C	8	4
V2LHS_72600_6	172_0564	A	10	6
V2LHS_206161_1	172_0031	G	6	3
V2LHS_250440_2	172_0157	F	6	4
V2LHS_44245_4	172_0365	D	7	5
V2LHS_264689_1	172_0095	B	3	4
V2LHS_213099_4	172_0333	E	10	3
V2LHS_80222_4	172_0326	F	1	6
V2LHS_93499_6	172_0558	H	2	6
V2LHS_179686_2	172_0147	G	8	2
V2LHS_47483_1	172_0034	A	11	5
V2LHS_90993_6	172_0533	E	5	6
V2LHS_39484_6	172_0580	A	9	5
V2LHS_88777_4	172_0334	G	7	6
V2LHS_98065_1	172_0058	C	4	6
V2LHS_134853_5	172_0469	B	3	1
V2LHS_58336_2	172_0192	H	3	5
V2LHS_32810_5	172_0472	E	9	5
V2LHS_46274_5	172_0466	A	4	5
V2LHS_67543_5	172_0492	C	7	6
V2LHS_75959_3	172_0226	H	10	6
V2LHS_234803_5	172_0478	A	6	4
V2LHS_42042_4	172_0391	D	6	5
V2LHS_109738_5	172_0496	A	10	1
V2LHS_52988_1	172_0018	H	7	5
V2LHS_27935_3	172_0265	D	9	5

V2LHS_79753_6	172_0557	H	8	6
V2LHS_25934_3	172_0225	G	12	4
V2LHS_19361_5	172_0463	F	12	3
V2LHS_83493_5	172_0441	E	12	6
V2LHS_51691_6	172_0598	E	11	5
V2LHS_276697_2	172_0109	A	6	4
V2LHS_147108_1	172_0007	C	5	2
V2LHS_77414_5	172_0462	E	8	6
V2LHS_85835_3	172_0279	A	8	6
V2LHS_96221_4	172_0390	B	2	6
V2LHS_137711_2	172_0128	F	8	1
V2LHS_97749_2	172_0199	F	11	6
V2LHS_69603_3	172_0269	H	9	6
V2LHS_186222_2	172_0178	E	7	3
V2LHS_81308_5	172_0421	F	9	6
V2LHS_44369_5	172_0433	D	1	5
V2LHS_211745_5	172_0473	C	1	3
V2LHS_58018_4	172_0351	F	11	5
V2LHS_75206_6	172_0577	D	2	6
V2LHS_64590_6	172_0557	D	11	6
V2LHS_39721_2	172_0138	H	6	5
V2LHS_97402_6	172_0543	E	5	6
V2LHS_90513_6	172_0503	G	8	6
V2LHS_254535_5	172_0476	H	6	4
V2LHS_50059_6	172_0516	F	4	5
V2LHS_275187_5	172_0444	E	12	4
V2LHS_98688_6	172_0575	G	4	6
V2LHS_128073_5	172_0419	H	9	1
V2LHS_170101_1	172_0069	G	8	2
V2LHS_108599_6	172_0586	A	2	1
V2LHS_76803_4	172_0361	D	5	6
V2LHS_66951_1	172_0030	C	8	6
V2LHS_12233_1	172_0089	F	1	1
V2LHS_36585_1	172_0048	E	7	5
V2LHS_188392_5	172_0468	B	3	3
V2LHS_132916_5	172_0485	C	1	1
V2LHS_239163_6	172_0506	F	10	4
V2LHS_29810_6	172_0564	H	9	5
V2LHS_140956_3	172_0208	C	4	1
V2LHS_67393_1	172_0025	B	5	6
V2LHS_254600_2	172_0159	G	5	4
V2LHS_118650_6	172_0572	H	10	1
V2LHS_102427_6	172_0588	A	5	1
V2LHS_66960_5	172_0462	D	11	6
V2LHS_95019_4	172_0310	D	7	6
V2LHS_192429_2	172_0109	H	4	3
V2LHS_52539_3	172_0288	A	5	5
V2LHS_188086_4	172_0375	A	3	3
V2LHS_92041_5	172_0402	H	4	6
V2LHS_85905_1	172_0088	E	7	6

V2LHS_137415_5	172_0416	H	4	1
V2LHS_137633_5	172_0448	H	11	1
V2LHS_27928_1	172_0009	C	9	5
V2LHS_69530_5	172_0421	A	12	6
V2LHS_63408_2	172_0128	F	3	6
V2LHS_27177_6	172_0531	H	12	4
V2LHS_80456_1	172_0089	G	6	6
V2LHS_138134_6	172_0524	E	6	1
V2LHS_86930_4	172_0392	C	1	6
V2LHS_39795_1	172_0045	B	7	5
V2LHS_56556_6	172_0533	E	6	5
V2LHS_116443_6	172_0585	C	7	1
V2LHS_13501_1	172_0064	C	6	1
V2LHS_235586_4	172_0340	D	3	4
V2LHS_20095_4	172_0383	E	9	3
V2LHS_72517_2	172_0145	C	9	6
V2LHS_242490_5	172_0493	A	3	4
V2LHS_95660_5	172_0444	A	7	6
V2LHS_83928_2	172_0102	B	9	6
V2LHS_171284_1	172_0067	B	10	2
V2LHS_276729_2	172_0194	E	6	4
V2LHS_226217_1	172_0042	D	2	4
V2LHS_275025_2	172_0154	D	7	4
V2LHS_6355_1	172_0025	G	12	6
V2LHS_284645_3	172_0295	C	12	5
V2LHS_151804_6	172_0542	E	8	2
V2LHS_137860_3	172_0260	C	11	1
V2LHS_17782_5	172_0499	C	8	2
V2LHS_277411_3	172_0210	B	2	4
V2LHS_62172_4	172_0309	A	9	6
V2LHS_95899_4	172_0309	H	1	6
V2LHS_87880_2	172_0200	G	10	6
V2LHS_70564_1	172_0010	B	4	6
V2LHS_113843_1	172_0083	F	2	1
V2LHS_52000_4	172_0339	A	1	5
V2LHS_94229_4	172_0317	E	9	6
V2LHS_125607_6	172_0570	D	5	1
V2LHS_139145_2	172_0176	C	1	1
V2LHS_81010_4	172_0365	G	8	6
V2LHS_92190_5	172_0402	C	4	6
V2LHS_92330_5	172_0475	B	12	6
V2LHS_65032_1	172_0012	G	11	6
V2LHS_36679_1	172_0002	A	4	5
V2LHS_72206_1	172_0035	D	9	6
V2LHS_120164_5	172_0496	D	1	1
V2LHS_193629_2	172_0196	D	4	3
V2LHS_95096_6	172_0534	C	8	6
V2LHS_112540_5	172_0496	G	10	1
V2LHS_173591_4	172_0379	F	5	2
V2LHS_113928_5	172_0500	D	10	1

V2LHS_246262_1	172_0096	E	4	4
V2LHS_142681_2	172_0128	F	3	1
V2LHS_90086_4	172_0335	G	6	6
V2LHS_103967_6	172_0528	C	8	1
V2LHS_70184_4	172_0351	B	9	6
V2LHS_285379_2	172_0170	E	1	5
V2LHS_248744_3	172_0247	E	1	4
V2LHS_223340_3	172_0260	G	9	3
V2LHS_86590_3	172_0234	F	12	6
V2LHS_82571_5	172_0446	C	11	6
V2LHS_211930_6	172_0508	C	2	3
V2LHS_47974_3	172_0289	G	5	5
V2LHS_239006_4	172_0400	E	11	4
V2LHS_173365_4	172_0364	H	8	2
V2LHS_64332_1	172_0069	A	9	6
V2LHS_252882_6	172_0532	D	5	4
V2LHS_79601_6	172_0529	C	1	6
V2LHS_55037_1	172_0047	H	7	5
V2LHS_72237_4	172_0355	E	6	6
V2LHS_266786_5	172_0437	E	11	4
V2LHS_99674_6	172_0526	E	9	6
V2LHS_89800_3	172_0262	D	5	6
V2LHS_96497_1	172_0014	D	3	6
V2LHS_261293_1	172_0091	G	7	4
V2LHS_37729_1	172_0044	E	3	5
V2LHS_62145_4	172_0325	F	11	6
V2LHS_211184_2	172_0153	D	5	3
V2LHS_112227_5	172_0408	B	4	1
V2LHS_192695_4	172_0327	C	10	3
V2LHS_88055_4	172_0350	G	9	6
V2LHS_5212_1	172_0054	E	12	5
V2LHS_75066_4	172_0400	D	3	6
V2LHS_62317_5	172_0492	C	8	6
V2LHS_67565_4	172_0335	F	6	6
V2LHS_54883_6	172_0563	F	12	5
V2LHS_62181_1	172_0025	D	4	6
V2LHS_138371_1	172_0006	A	6	1
V2LHS_73107_5	172_0463	D	9	6
V2LHS_88090_5	172_0413	E	9	6
V2LHS_176081_3	172_0250	D	5	2
V2LHS_73003_4	172_0382	H	5	6
V2LHS_176070_2	172_0111	H	12	2
V2LHS_65654_2	172_0182	G	8	6
V2LHS_86452_4	172_0329	H	7	6
V2LHS_133563_6	172_0600	F	7	1
V2LHS_108706_6	172_0518	E	6	1
V2LHS_239389_1	172_0055	H	3	4
V2LHS_135386_1	172_0065	B	9	1
V2LHS_241507_3	172_0243	G	11	4
V2LHS_26931_5	172_0420	E	9	4

V2LHS_151562_6	172_0595	A	1	2
V2LHS_73125_1	172_0082	D	9	6
V2LHS_78847_4	172_0366	C	11	6
V2LHS_88866_4	172_0374	B	12	6
V2LHS_47254_5	172_0482	G	12	5
V2LHS_80648_3	172_0276	D	2	6
V2LHS_67669_4	172_0383	E	4	6
V2LHS_29824_3	172_0265	D	10	5
V2LHS_108330_3	172_0229	D	4	1
V2LHS_96541_6	172_0505	B	3	6
V2LHS_86736_3	172_0275	A	8	6
V2LHS_78858_6	172_0549	B	1	6
V2LHS_77230_3	172_0257	G	8	6
V2LHS_36329_1	172_0021	B	3	5
V2LHS_112518_1	172_0047	F	4	1
V2LHS_97938_1	172_0090	C	2	6
V2LHS_81527_5	172_0450	D	6	6
V2LHS_227147_1	172_0092	F	12	4
V2LHS_104285_3	172_0246	B	12	1
V2LHS_236770_5	172_0484	D	6	4
V2LHS_64994_1	172_0055	A	11	6
V2LHS_136882_2	172_0111	D	1	1
V2LHS_64715_5	172_0480	A	11	6
V2LHS_33679_1	172_0081	B	7	5
V2LHS_33999_5	172_0484	H	9	5
V2LHS_73229_2	172_0156	E	6	6
V2LHS_123375_6	172_0513	C	6	1
V2LHS_227929_1	172_0092	D	2	4
V2LHS_70689_1	172_0029	C	4	6
V2LHS_137664_4	172_0380	G	7	1
V2LHS_67664_5	172_0436	C	1	6
V2LHS_63568_2	172_0188	H	11	6
V2LHS_121041_5	172_0435	F	9	1
V2LHS_96239_3	172_0291	G	8	6
V2LHS_75921_2	172_0157	F	2	6
V2LHS_79126_2	172_0131	A	8	6
V2LHS_90480_3	172_0296	B	9	6
V2LHS_69010_3	172_0241	E	8	6
V2LHS_233687_4	172_0315	D	2	4
V2LHS_82061_2	172_0164	E	9	6
V2LHS_84652_6	172_0544	G	1	6
V2LHS_75122_1	172_0095	A	6	6
V2LHS_73472_2	172_0165	C	4	6
V2LHS_108945_4	172_0320	C	6	1
V2LHS_141219_2	172_0128	A	8	1
V2LHS_251727_3	172_0238	E	12	4
V2LHS_63583_6	172_0559	B	6	6
V2LHS_63591_1	172_0023	H	6	6
V2LHS_73061_5	172_0443	D	7	6
V2LHS_68912_6	172_0564	B	5	6

V2LHS_13284_1	172_0099	C	11	1
V2LHS_49753_6	172_0561	F	1	5
V2LHS_118889_1	172_0023	C	5	1
V2LHS_216231_1	172_0012	E	3	3
V2LHS_115081_4	172_0370	F	6	1
V2LHS_70552_5	172_0438	D	9	6
V2LHS_14774_5	172_0439	C	5	2
V2LHS_258392_2	172_0102	A	9	4
V2LHS_241193_2	172_0147	F	8	4
V2LHS_32992_6	172_0529	F	9	5
V2LHS_108372_4	172_0386	B	1	1
V2LHS_94612_3	172_0294	B	8	6
V2LHS_130704_6	172_0583	G	4	1
V2LHS_52615_5	172_0498	C	8	5
V2LHS_245601_4	172_0354	H	7	4
V2LHS_112305_3	172_0286	E	4	1
V2LHS_277852_2	172_0147	G	8	4
V2LHS_249016_3	172_0255	B	1	4
V2LHS_132818_5	172_0427	F	7	1
V2LHS_18252_3	172_0297	G	11	3
V2LHS_95808_2	172_0174	D	10	6
V2LHS_187254_2	172_0184	F	5	3
V2LHS_67270_3	172_0216	F	11	6
V2LHS_213701_3	172_0284	B	2	3
V2LHS_94739_2	172_0142	B	11	6
V2LHS_27490_4	172_0328	A	2	4
V2LHS_60032_4	172_0302	E	11	5
V2LHS_11179_1	172_0093	G	4	1
V2LHS_247359_6	172_0507	G	3	4
V2LHS_97011_4	172_0376	C	4	6
V2LHS_102621_6	172_0523	E	12	1
V2LHS_68945_3	172_0268	D	7	6
V2LHS_41869_5	172_0491	B	11	5
V2LHS_71990_6	172_0533	G	8	6
V2LHS_38835_4	172_0318	F	1	5
V2LHS_68703_5	172_0424	C	4	6
V2LHS_68949_2	172_0192	C	10	6
V2LHS_245372_3	172_0256	F	2	4
V2LHS_63661_4	172_0358	G	10	6
V2LHS_26195_5	172_0433	E	1	4
V2LHS_239492_3	172_0261	A	1	4
V2LHS_75052_6	172_0527	A	3	6
V2LHS_31931_4	172_0302	C	8	5
V2LHS_273422_2	172_0147	B	3	4
V2LHS_130581_1	172_0064	G	6	1
V2LHS_23196_6	172_0512	E	7	4
V2LHS_16774_4	172_0317	G	1	2
V2LHS_64043_1	172_0037	C	2	6
V2LHS_118695_1	172_0009	B	3	1
V2LHS_80649_2	172_0168	E	3	6

V2LHS_83600_3	172_0227	C	7	6
V2LHS_142302_5	172_0445	B	4	1
V2LHS_27445_6	172_0503	G	11	4
V2LHS_141183_1	172_0065	E	4	1
V2LHS_56477_3	172_0233	F	3	5
V2LHS_67831_6	172_0561	E	4	6
V2LHS_115418_1	172_0073	F	1	1
V2LHS_115416_5	172_0435	E	6	1
V2LHS_241843_3	172_0248	C	2	4
V2LHS_122057_5	172_0487	E	4	1
V2LHS_256136_1	172_0093	B	10	4
V2LHS_198204_2	172_0142	E	9	3
V2LHS_182478_5	172_0403	H	4	3
V2LHS_125124_3	172_0290	E	8	1
V2LHS_120482_1	172_0091	H	1	1
V2LHS_125613_1	172_0096	F	12	1
V2LHS_255190_5	172_0424	G	4	4
V2LHS_201836_1	172_0067	A	11	3
V2LHS_97621_2	172_0140	B	4	6
V2LHS_129344_1	172_0023	G	8	1
V2LHS_97933_6	172_0577	E	8	6
V2LHS_219398_2	172_0172	F	10	3
V2LHS_61621_3	172_0201	B	7	6
V2LHS_68660_3	172_0257	A	4	6
V2LHS_83455_6	172_0541	E	7	6
V2LHS_33143_3	172_0290	C	11	5
V2LHS_102670_1	172_0022	E	5	1
V2LHS_86197_4	172_0376	E	6	6
V2LHS_7705_1	172_0027	C	6	6
V2LHS_88347_2	172_0125	B	5	6
V2LHS_53909_3	172_0207	D	12	5
V2LHS_72158_6	172_0504	E	3	6
V2LHS_88115_6	172_0583	C	5	6
V2LHS_42033_5	172_0435	B	2	5
V2LHS_141105_1	172_0065	E	6	1
V2LHS_138017_1	172_0067	A	3	1
V2LHS_192651_2	172_0160	F	5	3
V2LHS_16773_5	172_0435	B	3	2
V2LHS_99459_1	172_0086	A	4	6
V2LHS_95810_3	172_0293	D	3	6
V2LHS_107862_4	172_0314	D	1	1
V2LHS_78376_5	172_0498	D	10	6
V2LHS_94347_1	172_0045	D	1	6
V2LHS_147701_5	172_0432	E	8	2
V2LHS_225567_4	172_0329	A	1	4
V2LHS_87398_4	172_0316	F	7	6
V2LHS_105136_6	172_0513	C	5	1
V2LHS_76052_1	172_0019	E	7	6
V2LHS_111440_1	172_0099	G	12	1
V2LHS_113814_5	172_0410	A	8	1

V2LHS_136588_5	172_0405	H	5	1
V2LHS_169668_2	172_0127	E	4	2
V2LHS_63761_1	172_0038	B	12	6
V2LHS_122308_5	172_0424	B	7	1
V2LHS_131849_1	172_0047	G	7	1
V2LHS_118220_2	172_0169	H	12	1
V2LHS_254998_2	172_0200	H	6	4
V2LHS_85056_2	172_0154	A	12	6
V2LHS_131808_4	172_0373	F	8	1
V2LHS_84643_4	172_0376	C	4	6
V2LHS_32053_3	172_0297	D	6	5
V2LHS_82263_6	172_0519	C	12	6
V2LHS_215479_1	172_0049	E	11	3
V2LHS_114651_4	172_0322	H	7	1
V2LHS_85439_4	172_0346	G	4	6
V2LHS_127074_2	172_0190	G	12	1
V2LHS_94784_2	172_0142	G	3	6
V2LHS_230293_6	172_0576	A	10	4
V2LHS_64201_3	172_0237	G	10	6
V2LHS_81292_6	172_0570	E	7	6
V2LHS_17531_4	172_0336	D	9	2
V2LHS_111699_6	172_0592	F	9	1
V2LHS_111706_3	172_0252	C	3	1
V2LHS_87169_5	172_0480	H	8	6
V2LHS_87192_6	172_0507	E	6	6
V2LHS_22643_4	172_0380	E	5	4
V2LHS_63784_3	172_0230	H	3	6
V2LHS_85815_4	172_0333	C	11	6
V2LHS_86942_6	172_0599	D	1	6
V2LHS_130837_4	172_0393	H	12	1
V2LHS_64083_1	172_0050	F	9	6
V2LHS_85622_2	172_0118	F	9	6
V2LHS_63793_3	172_0279	A	4	6
V2LHS_182486_3	172_0265	F	6	3
V2LHS_63540_1	172_0009	G	10	6
V2LHS_182479_3	172_0274	F	3	3
V2LHS_77275_6	172_0539	E	8	6
V2LHS_95276_1	172_0069	B	10	6
V2LHS_124418_2	172_0138	A	7	1
V2LHS_176849_6	172_0538	A	1	2
V2LHS_8219_1	172_0078	C	2	6
V2LHS_84252_4	172_0354	E	7	6
V2LHS_97088_3	172_0225	B	12	6
V2LHS_263532_1	172_0089	B	5	4
V2LHS_84404_5	172_0424	H	9	6
V2LHS_249116_2	172_0179	E	7	4
V2LHS_103266_1	172_0099	C	9	1
V2LHS_87855_3	172_0201	G	5	6
V2LHS_5284_2	172_0111	C	6	5
V2LHS_64328_4	172_0331	B	8	6

V2LHS_73290_6	172_0547	D	3	6
V2LHS_275710_3	172_0222	D	7	4
V2LHS_200209_4	172_0312	B	3	3
V2LHS_273128_2	172_0192	E	6	4
V2LHS_116872_1	172_0026	D	8	1
V2LHS_80984_4	172_0356	G	2	6
V2LHS_12381_4	172_0325	E	7	1
V2LHS_89306_6	172_0533	D	1	6
V2LHS_235350_3	172_0231	D	6	4
V2LHS_120189_4	172_0331	H	10	1
V2LHS_108140_5	172_0413	B	2	1
V2LHS_235246_3	172_0231	B	1	4
V2LHS_99362_1	172_0009	E	2	6
V2LHS_222938_2	172_0111	D	12	3
V2LHS_63802_6	172_0558	C	5	6
V2LHS_87766_1	172_0014	F	5	6
V2LHS_95005_1	172_0045	G	1	6
V2LHS_143265_1	172_0009	H	1	1
V2LHS_79697_3	172_0235	D	5	6
V2LHS_245851_6	172_0514	E	8	4
V2LHS_137821_6	172_0593	A	5	1
V2LHS_34903_3	172_0298	C	1	5
V2LHS_81744_4	172_0371	H	5	6
V2LHS_206820_3	172_0229	D	9	3
V2LHS_44127_2	172_0131	G	5	5
V2LHS_87786_1	172_0014	E	4	6
V2LHS_62188_5	172_0411	F	4	6
V2LHS_254445_5	172_0463	C	1	4
V2LHS_15516_4	172_0359	A	6	2
V2LHS_113436_1	172_0089	E	6	1
V2LHS_64522_1	172_0028	E	1	6
V2LHS_216705_3	172_0291	C	2	3
V2LHS_195795_1	172_0080	F	12	3
V2LHS_11233_1	172_0090	B	6	1
V2LHS_28479_1	172_0009	D	7	5
V2LHS_93320_1	172_0056	E	9	6
V2LHS_83947_4	172_0380	A	1	6
V2LHS_212687_1	172_0024	E	9	3
V2LHS_269098_1	172_0085	E	8	4
V2LHS_201052_4	172_0304	D	10	3
V2LHS_114750_2	172_0138	C	1	1
V2LHS_80900_3	172_0277	G	4	6
V2LHS_284634_5	172_0437	C	12	5
V2LHS_38565_5	172_0495	H	12	5
V2LHS_85106_4	172_0302	D	8	6
V2LHS_31849_4	172_0306	E	7	5
V2LHS_212744_3	172_0291	F	8	3
V2LHS_109776_5	172_0488	F	8	1
V2LHS_112973_5	172_0442	D	5	1
V2LHS_69107_1	172_0066	D	8	6

V2LHS_84105_2	172_0131	E	6	6
V2LHS_70945_5	172_0485	C	7	6
V2LHS_99460_1	172_0032	C	4	6
V2LHS_188478_2	172_0170	H	7	3
V2LHS_61208_6	172_0572	G	12	5
V2LHS_83074_6	172_0558	E	11	6
V2LHS_47320_5	172_0490	C	2	5
V2LHS_21152_5	172_0459	A	8	3
V2LHS_102819_1	172_0013	H	1	1
V2LHS_188207_3	172_0232	E	12	3
V2LHS_2257_2	172_0121	A	3	4
V2LHS_83926_4	172_0398	H	8	6
V2LHS_69117_1	172_0008	C	12	6
V2LHS_96790_1	172_0036	A	4	6
V2LHS_86212_5	172_0446	B	7	6
V2LHS_81162_3	172_0261	G	9	6
V2LHS_6799_1	172_0006	A	9	6
V2LHS_88212_4	172_0391	G	8	6
V2LHS_10285_1	172_0014	G	9	1
V2LHS_73400_4	172_0353	A	11	6
V2LHS_98057_1	172_0009	G	7	6
V2LHS_61490_6	172_0530	H	12	5
V2LHS_118548_4	172_0370	A	2	1
V2LHS_111728_6	172_0555	F	6	1
V2LHS_205604_1	172_0097	E	12	3
V2LHS_26545_6	172_0589	F	3	4
V2LHS_80535_5	172_0415	H	10	6
V2LHS_45615_2	172_0128	D	4	5
V2LHS_123622_6	172_0597	E	11	1
V2LHS_11649_1	172_0084	E	6	1
V2LHS_284808_2	172_0185	D	1	5
V2LHS_267281_5	172_0436	E	11	4
V2LHS_19249_5	172_0429	D	5	3
V2LHS_37541_6	172_0551	C	8	5
V2LHS_64755_6	172_0569	D	7	6
V2LHS_73281_3	172_0206	A	6	6
V2LHS_67609_3	172_0204	B	1	6
V2LHS_52129_3	172_0250	A	12	5
V2LHS_231610_2	172_0123	D	11	4
V2LHS_20481_3	172_0291	F	1	3
V2LHS_93725_2	172_0170	A	4	6
V2LHS_84649_4	172_0345	G	1	6
V2LHS_92022_2	172_0195	A	1	6
V2LHS_84576_6	172_0510	G	11	6
V2LHS_50695_1	172_0044	D	2	5
V2LHS_243116_4	172_0343	G	4	4
V2LHS_64667_1	172_0049	A	1	6
V2LHS_100079_4	172_0366	A	8	1
V2LHS_36975_2	172_0114	G	7	5
V2LHS_4899_1	172_0037	A	4	5

V2LHS_120915_2	172_0196	H	11	1
V2LHS_92406_5	172_0422	D	2	6
V2LHS_239090_4	172_0316	F	6	4
V2LHS_68292_1	172_0027	F	10	6
V2LHS_131700_4	172_0400	G	10	1
V2LHS_179838_2	172_0126	C	1	2
V2LHS_138302_1	172_0074	H	1	1
V2LHS_189807_2	172_0155	E	10	3
V2LHS_90715_6	172_0589	D	8	6
V2LHS_96759_6	172_0578	E	8	6
V2LHS_150259_3	172_0233	H	6	2
V2LHS_188360_1	172_0020	A	6	3
V2LHS_75848_5	172_0470	G	7	6
V2LHS_238788_1	172_0054	B	6	4
V2LHS_78811_6	172_0581	D	4	6
V2LHS_172146_4	172_0356	D	10	2
V2LHS_99376_5	172_0409	C	1	6
V2LHS_252745_2	172_0184	B	1	4
V2LHS_121288_5	172_0492	E	11	1
V2LHS_110428_4	172_0336	H	8	1
V2LHS_154942_6	172_0580	B	2	2
V2LHS_69156_4	172_0362	E	11	6
V2LHS_272750_6	172_0589	C	11	4
V2LHS_231032_2	172_0136	E	3	4
V2LHS_141545_2	172_0125	B	8	1
V2LHS_114214_4	172_0316	E	4	1
V2LHS_277269_2	172_0177	A	1	4
V2LHS_257584_4	172_0386	D	3	4
V2LHS_181601_2	172_0126	C	3	3
V2LHS_37039_6	172_0586	A	5	5
V2LHS_241955_3	172_0237	C	12	4
V2LHS_41653_2	172_0130	C	5	5
V2LHS_30261_1	172_0001	E	4	5
V2LHS_244577_5	172_0412	H	12	4
V2LHS_28841_4	172_0347	F	12	5
V2LHS_99341_5	172_0480	C	3	6
V2LHS_272858_4	172_0397	B	12	4
V2LHS_10468_1	172_0043	C	9	1
V2LHS_67590_3	172_0209	F	2	6
V2LHS_185252_5	172_0436	G	9	3
V2LHS_182964_2	172_0196	G	7	3
V2LHS_81000_2	172_0113	G	3	6
V2LHS_123404_6	172_0575	E	8	1
V2LHS_92290_6	172_0573	F	6	6
V2LHS_91982_1	172_0030	A	9	6
V2LHS_72545_5	172_0456	H	12	6
V2LHS_52304_3	172_0280	C	11	5
V2LHS_67319_1	172_0040	G	11	6
V2LHS_32720_6	172_0577	E	1	5
V2LHS_76522_6	172_0599	E	8	6

V2LHS_173570_1	172_0019	B	9	2
V2LHS_89052_1	172_0067	E	8	6
V2LHS_142862_5	172_0482	H	9	1
V2LHS_81717_5	172_0449	D	8	6
V2LHS_24225_5	172_0412	E	10	4
V2LHS_205798_6	172_0578	F	2	3
V2LHS_76614_1	172_0088	E	3	6
V2LHS_53236_6	172_0564	F	7	5
V2LHS_109213_4	172_0315	A	9	1
V2LHS_84345_4	172_0392	A	11	6
V2LHS_245564_2	172_0148	C	12	4
V2LHS_70565_5	172_0403	C	8	6
V2LHS_144877_2	172_0137	C	6	2
V2LHS_192494_6	172_0532	G	5	3
V2LHS_235844_3	172_0227	F	4	4
V2LHS_135820_2	172_0195	E	2	1
V2LHS_72105_1	172_0001	H	2	6
V2LHS_108442_2	172_0129	D	5	1
V2LHS_76550_5	172_0418	H	2	6
V2LHS_67315_6	172_0548	E	8	6
V2LHS_102938_5	172_0469	F	10	1
V2LHS_260622_1	172_0097	A	12	4
V2LHS_131661_4	172_0366	D	3	1
V2LHS_71294_1	172_0037	C	3	6
V2LHS_112605_5	172_0412	D	7	1
V2LHS_70492_6	172_0553	H	1	6
V2LHS_77622_5	172_0457	F	9	6
V2LHS_63877_5	172_0499	G	6	6
V2LHS_1044_1	172_0044	D	4	1
V2LHS_85777_3	172_0267	D	3	6
V2LHS_94634_6	172_0549	G	10	6
V2LHS_96694_2	172_0168	G	8	6
V2LHS_189694_6	172_0544	B	3	3
V2LHS_63879_6	172_0568	E	12	6
V2LHS_42556_6	172_0555	B	3	5
V2LHS_112013_4	172_0352	B	11	1
V2LHS_76028_4	172_0321	H	7	6
V2LHS_106563_4	172_0338	C	1	1
V2LHS_197470_4	172_0333	D	3	3
V2LHS_102947_5	172_0410	E	9	1
V2LHS_109375_4	172_0314	E	7	1
V2LHS_107055_6	172_0542	C	4	1
V2LHS_96660_1	172_0073	E	8	6
V2LHS_70611_5	172_0413	H	10	6
V2LHS_89090_6	172_0594	B	5	6
V2LHS_96642_1	172_0035	D	7	6
V2LHS_25749_4	172_0308	D	10	4
V2LHS_192496_2	172_0175	D	9	3
V2LHS_179071_6	172_0527	D	4	2
V2LHS_86009_5	172_0500	C	1	6

V2LHS_184339_2	172_0123	E	10	3
V2LHS_35267_5	172_0465	B	5	5
V2LHS_135283_1	172_0058	F	7	1
V2LHS_60699_2	172_0138	F	12	5
V2LHS_203184_3	172_0282	F	7	3
V2LHS_65291_3	172_0229	G	7	6
V2LHS_52572_6	172_0542	E	5	5
V2LHS_43530_6	172_0525	A	8	5
V2LHS_85727_5	172_0424	G	4	6
V2LHS_191640_6	172_0590	B	11	3
V2LHS_59254_1	172_0079	C	4	5
V2LHS_92028_3	172_0239	C	10	6
V2LHS_66836_2	172_0187	C	7	6
V2LHS_78223_2	172_0101	E	4	6
V2LHS_258964_2	172_0105	B	3	4
V2LHS_85085_6	172_0582	H	7	6
V2LHS_138337_1	172_0028	F	7	1
V2LHS_249040_2	172_0112	F	6	4
V2LHS_238403_1	172_0049	E	10	4
V2LHS_64070_3	172_0228	C	11	6
V2LHS_100473_5	172_0406	F	7	1
V2LHS_254587_3	172_0281	F	2	4
V2LHS_57043_5	172_0402	B	4	5
V2LHS_67371_5	172_0491	H	10	6
V2LHS_284921_2	172_0193	D	6	5
V2LHS_63938_6	172_0587	F	9	6
V2LHS_262525_1	172_0088	G	2	4
V2LHS_184775_6	172_0586	B	3	3
V2LHS_189949_6	172_0525	G	11	3
V2LHS_218456_2	172_0116	C	1	3
V2LHS_237406_1	172_0064	C	5	4
V2LHS_102999_2	172_0170	C	8	1
V2LHS_59842_3	172_0228	E	10	5
V2LHS_252935_5	172_0472	D	7	4
V2LHS_245120_5	172_0439	E	6	4
V2LHS_156114_1	172_0093	D	11	2
V2LHS_175929_1	172_0079	A	5	2
V2LHS_83738_3	172_0205	A	2	6
V2LHS_112988_3	172_0258	H	8	1
V2LHS_67512_5	172_0500	G	7	6
V2LHS_136627_3	172_0249	A	5	1
V2LHS_97241_6	172_0531	F	7	6
V2LHS_93599_6	172_0574	E	11	6
V2LHS_117180_6	172_0595	A	5	1
V2LHS_13521_4	172_0372	E	6	1
V2LHS_284938_2	172_0183	B	9	5
V2LHS_78918_4	172_0377	D	2	6
V2LHS_49752_5	172_0493	A	6	5
V2LHS_188682_5	172_0469	D	7	3
V2LHS_84904_4	172_0347	G	1	6

V2LHS_66686_1	172_0045	E	7	6
V2LHS_190304_3	172_0294	G	8	3
V2LHS_226084_1	172_0047	F	7	4
V2LHS_55815_4	172_0324	C	2	5
V2LHS_131948_5	172_0498	A	3	1
V2LHS_88063_5	172_0418	F	4	6
V2LHS_244476_2	172_0104	E	2	4
V2LHS_66997_2	172_0152	G	11	6
V2LHS_246107_2	172_0158	A	7	4
V2LHS_244043_3	172_0219	H	1	4
V2LHS_54199_1	172_0033	C	9	5
V2LHS_251189_2	172_0175	A	3	4
V2LHS_112945_6	172_0547	E	11	1
V2LHS_112298_3	172_0267	D	1	1
V2LHS_109078_2	172_0182	H	4	1
V2LHS_146917_5	172_0451	D	6	2
V2LHS_276972_2	172_0192	E	7	4
V2LHS_99479_1	172_0051	G	12	6
V2LHS_262034_1	172_0091	A	12	4
V2LHS_198301_3	172_0221	B	2	3
V2LHS_64160_1	172_0024	G	9	6
V2LHS_108998_2	172_0121	D	5	1
V2LHS_27639_1	172_0003	A	7	4
V2LHS_76325_1	172_0057	E	1	6
V2LHS_85493_6	172_0588	G	11	6
V2LHS_51739_5	172_0418	C	12	5
V2LHS_78361_5	172_0459	F	2	6
V2LHS_265011_6	172_0582	C	9	4
V2LHS_136062_5	172_0405	C	4	1
V2LHS_124156_6	172_0516	C	8	1
V2LHS_61599_6	172_0582	B	10	6
V2LHS_43170_3	172_0291	A	5	5
V2LHS_138552_1	172_0049	A	5	1
V2LHS_115851_4	172_0381	H	9	1
V2LHS_71968_4	172_0378	G	11	6
V2LHS_40258_2	172_0139	C	8	5
V2LHS_95428_1	172_0097	H	7	6
V2LHS_230136_3	172_0206	C	7	4
V2LHS_107504_2	172_0186	H	12	1
V2LHS_93123_6	172_0582	A	3	6
V2LHS_50031_5	172_0464	E	7	5
V2LHS_81387_5	172_0476	D	3	6
V2LHS_140612_2	172_0196	B	8	1
V2LHS_277826_3	172_0265	B	8	4
V2LHS_226767_5	172_0419	E	5	4
V2LHS_24237_5	172_0408	G	7	4
V2LHS_157852_2	172_0189	A	4	2
V2LHS_96523_3	172_0239	B	6	6
V2LHS_80412_1	172_0094	H	2	6
V2LHS_120330_5	172_0435	G	9	1

V2LHS_104424_4	172_0355	F	5	1
V2LHS_75830_6	172_0535	D	4	6
V2LHS_39617_5	172_0492	C	4	5
V2LHS_66164_6	172_0559	F	10	6
V2LHS_235121_2	172_0191	G	1	4
V2LHS_166235_2	172_0158	D	10	2
V2LHS_66704_5	172_0411	G	7	6
V2LHS_106472_4	172_0393	G	2	1
V2LHS_124779_4	172_0364	A	6	1
V2LHS_107557_1	172_0084	H	7	1
V2LHS_262313_6	172_0585	B	3	4
V2LHS_277409_3	172_0250	F	7	4
V2LHS_171776_2	172_0198	H	3	2
V2LHS_123541_1	172_0049	E	2	1
V2LHS_37538_5	172_0463	H	8	5
V2LHS_102282_1	172_0005	H	3	1
V2LHS_59688_3	172_0209	A	1	5
V2LHS_64937_5	172_0430	D	10	6
V2LHS_268167_6	172_0525	B	8	4
V2LHS_71163_5	172_0440	F	4	6
V2LHS_56328_4	172_0353	B	9	5
V2LHS_18240_4	172_0366	E	12	3
V2LHS_184226_2	172_0171	A	1	3
V2LHS_63430_2	172_0200	C	6	6
V2LHS_59481_3	172_0210	G	8	5
V2LHS_238900_2	172_0141	A	4	4
V2LHS_80371_6	172_0529	D	6	6
V2LHS_81763_5	172_0418	G	12	6
V2LHS_98511_6	172_0565	G	10	6
V2LHS_91717_5	172_0423	B	6	6
V2LHS_21403_6	172_0584	G	12	3
V2LHS_102078_5	172_0499	E	11	1
V2LHS_82567_6	172_0580	H	9	6
V2LHS_83390_6	172_0569	A	6	6
V2LHS_85359_2	172_0131	B	3	6
V2LHS_125485_2	172_0130	E	4	1
V2LHS_27318_5	172_0484	B	4	4
V2LHS_126502_3	172_0288	E	3	1
V2LHS_150894_4	172_0310	E	11	2
V2LHS_243156_5	172_0403	F	7	4
V2LHS_81855_5	172_0415	B	4	6
V2LHS_83228_6	172_0571	C	12	6
V2LHS_57684_3	172_0228	H	12	5
V2LHS_18454_5	172_0422	G	7	3
V2LHS_197853_6	172_0527	F	3	3
V2LHS_91884_1	172_0042	G	11	6
V2LHS_95657_3	172_0269	F	9	6
V2LHS_123074_4	172_0378	F	6	1
V2LHS_117210_6	172_0595	C	12	1
V2LHS_87656_6	172_0590	B	6	6

V2LHS_50315_3	172_0293	D	5	5
V2LHS_136303_3	172_0272	H	9	1
V2LHS_67087_1	172_0057	H	4	6
V2LHS_21710_3	172_0238	F	6	3
V2LHS_52084_6	172_0591	A	3	5
V2LHS_258988_2	172_0105	F	6	4
V2LHS_124132_4	172_0301	F	11	1
V2LHS_81591_6	172_0585	D	9	6
V2LHS_53905_5	172_0402	F	2	5
V2LHS_103822_5	172_0432	C	6	1
V2LHS_11046_2	172_0114	F	7	1
V2LHS_267534_4	172_0389	G	1	4
V2LHS_241090_3	172_0250	G	5	4
V2LHS_235733_6	172_0537	E	7	4
V2LHS_50778_3	172_0280	E	6	5
V2LHS_55751_1	172_0078	A	11	5
V2LHS_221748_1	172_0077	F	2	3
V2LHS_20165_5	172_0421	F	5	3
V2LHS_46640_3	172_0281	C	1	5
V2LHS_33347_3	172_0239	C	1	5
V2LHS_177101_1	172_0081	G	10	2
V2LHS_56101_6	172_0531	E	11	5
V2LHS_29797_5	172_0478	H	7	5
V2LHS_99256_2	172_0200	F	6	6
V2LHS_109220_4	172_0326	A	3	1
V2LHS_75329_5	172_0483	D	4	6
V2LHS_223588_1	172_0046	F	4	4
V2LHS_199505_5	172_0410	C	6	3
V2LHS_73038_6	172_0549	F	3	6
V2LHS_38419_3	172_0300	D	9	5
V2LHS_26220_5	172_0476	B	3	4
V2LHS_76636_6	172_0563	A	6	6
V2LHS_116410_1	172_0091	G	3	1
V2LHS_274798_2	172_0189	H	5	4
V2LHS_117231_2	172_0144	D	10	1
V2LHS_843_1	172_0022	G	4	6
V2LHS_97502_3	172_0267	D	4	6
V2LHS_39019_1	172_0007	A	11	5
V2LHS_13928_1	172_0081	E	5	1
V2LHS_91553_4	172_0340	G	1	6
V2LHS_66022_3	172_0288	C	3	6
V2LHS_54787_2	172_0196	B	12	5
V2LHS_246680_2	172_0145	D	10	4
V2LHS_198630_5	172_0457	D	5	3
V2LHS_88444_6	172_0595	H	8	6
V2LHS_122988_2	172_0139	E	10	1
V2LHS_138702_5	172_0470	D	3	1
V2LHS_72852_5	172_0417	F	12	6
V2LHS_164643_3	172_0254	E	3	2
V2LHS_83891_2	172_0134	G	6	6

V2LHS_29397_1	172_0005	G	6	5
V2LHS_136676_3	172_0247	D	3	1
V2LHS_239397_1	172_0064	A	9	4
V2LHS_67579_6	172_0530	E	11	6
V2LHS_74614_2	172_0131	D	3	6
V2LHS_232114_5	172_0475	E	8	4
V2LHS_56056_2	172_0170	B	9	5
V2LHS_20528_3	172_0294	F	11	3
V2LHS_67133_6	172_0501	F	10	6
V2LHS_6089_2	172_0121	G	1	5
V2LHS_98477_5	172_0413	A	8	6
V2LHS_89058_6	172_0522	E	12	6
V2LHS_64134_6	172_0541	A	8	6
V2LHS_104171_1	172_0012	F	8	1
V2LHS_79146_6	172_0544	B	1	6
V2LHS_83962_4	172_0340	B	6	6
V2LHS_87711_4	172_0386	E	7	6
V2LHS_184670_5	172_0471	C	9	3
V2LHS_230733_2	172_0162	B	1	4
V2LHS_64191_6	172_0505	E	5	6
V2LHS_76086_3	172_0217	E	7	6
V2LHS_235230_2	172_0199	F	9	4
V2LHS_129667_3	172_0299	A	1	1
V2LHS_90172_2	172_0134	C	4	6
V2LHS_69247_3	172_0237	F	7	6
V2LHS_82136_2	172_0157	H	9	6
V2LHS_96364_2	172_0139	F	2	6
V2LHS_269920_6	172_0547	E	9	4
V2LHS_82240_4	172_0341	A	6	6
V2LHS_230740_3	172_0231	D	10	4
V2LHS_64818_5	172_0493	A	7	6
V2LHS_67150_5	172_0459	F	4	6
V2LHS_50057_5	172_0443	H	5	5
V2LHS_117307_5	172_0402	A	1	1
V2LHS_64302_4	172_0357	A	8	6
V2LHS_235024_6	172_0529	H	3	4
V2LHS_98820_1	172_0045	B	8	6
V2LHS_90485_2	172_0198	D	6	6
V2LHS_260590_3	172_0219	H	1	4
V2LHS_142638_2	172_0140	H	10	1
V2LHS_264526_5	172_0499	D	2	4
V2LHS_125828_3	172_0294	F	9	1
V2LHS_53805_1	172_0030	A	10	5
V2LHS_106788_3	172_0219	A	1	1
V2LHS_64619_1	172_0068	C	2	6
V2LHS_130482_5	172_0451	E	9	1
V2LHS_64866_4	172_0369	A	12	6
V2LHS_96891_6	172_0552	H	12	6
V2LHS_73396_4	172_0355	G	5	6
V2LHS_64111_3	172_0244	A	5	6

V2LHS_103942_5	172_0468	F	7	1
V2LHS_26974_6	172_0577	D	8	4
V2LHS_75858_1	172_0082	D	2	6
V2LHS_95571_6	172_0562	C	12	6
V2LHS_247977_2	172_0184	H	11	4
V2LHS_116990_2	172_0145	E	7	1
V2LHS_7607_2	172_0110	E	1	6
V2LHS_137076_2	172_0138	D	8	1
V2LHS_140724_3	172_0204	C	12	1
V2LHS_175763_2	172_0172	F	7	2
V2LHS_35415_5	172_0450	E	9	5
V2LHS_92332_2	172_0140	G	10	6
V2LHS_67154_4	172_0347	E	8	6
V2LHS_85676_6	172_0565	H	10	6
V2LHS_36337_1	172_0030	F	2	5
V2LHS_150279_3	172_0300	F	10	2
V2LHS_205683_4	172_0385	D	9	3
V2LHS_134670_2	172_0178	B	2	1
V2LHS_91724_6	172_0596	B	10	6
V2LHS_94927_5	172_0431	H	8	6
V2LHS_13967_1	172_0057	F	8	1
V2LHS_257632_5	172_0442	F	8	4
V2LHS_92606_3	172_0289	F	1	6
V2LHS_263119_5	172_0416	D	7	4
V2LHS_137724_4	172_0357	C	12	1
V2LHS_67716_3	172_0224	G	2	6
V2LHS_276922_5	172_0473	F	10	4
V2LHS_274485_4	172_0374	B	12	4
V2LHS_242616_3	172_0214	B	11	4
V2LHS_206972_5	172_0445	G	2	3
V2LHS_205284_6	172_0506	F	1	3
V2LHS_65688_3	172_0246	A	9	6
V2LHS_90418_4	172_0337	D	8	6
V2LHS_32196_5	172_0434	A	9	5
V2LHS_79112_6	172_0580	B	10	6
V2LHS_265828_6	172_0546	G	6	4
V2LHS_93501_3	172_0216	D	5	6
V2LHS_77878_6	172_0524	B	1	6
V2LHS_76387_6	172_0590	A	10	6
V2LHS_107829_6	172_0502	C	10	1
V2LHS_75690_5	172_0481	H	2	6
V2LHS_10925_1	172_0032	B	7	1
V2LHS_89958_3	172_0272	B	9	6
V2LHS_234100_6	172_0542	F	9	4
V2LHS_187522_2	172_0111	E	12	3
V2LHS_70206_1	172_0051	F	2	6
V2LHS_72331_6	172_0584	E	7	6
V2LHS_45083_1	172_0024	F	8	5
V2LHS_124967_2	172_0137	C	5	1
V2LHS_172768_6	172_0562	H	12	2

V2LHS_69096_3	172_0253	G	12	6
V2LHS_85210_2	172_0132	A	6	6
V2LHS_125164_6	172_0561	C	7	1
V2LHS_92770_4	172_0332	F	3	6
V2LHS_4464_1	172_0099	G	1	5
V2LHS_231652_1	172_0024	C	7	4
V2LHS_80307_1	172_0018	E	2	6
V2LHS_198563_6	172_0566	A	11	3
V2LHS_81315_4	172_0381	D	8	6
V2LHS_184726_2	172_0148	C	6	3
V2LHS_42476_4	172_0364	E	7	5
V2LHS_45068_4	172_0310	E	9	5
V2LHS_42778_1	172_0092	F	1	5
V2LHS_249998_1	172_0091	F	5	4
V2LHS_64604_2	172_0128	H	10	6
V2LHS_96125_5	172_0401	E	2	6
V2LHS_118860_3	172_0294	C	6	1
V2LHS_94974_3	172_0264	D	6	6
V2LHS_32236_4	172_0334	C	6	5
V2LHS_225078_3	172_0247	D	3	4
V2LHS_97990_4	172_0381	E	12	6
V2LHS_61396_5	172_0496	E	7	5
V2LHS_69273_5	172_0432	A	12	6
V2LHS_89893_4	172_0390	D	6	6
V2LHS_88703_4	172_0379	F	12	6
V2LHS_55836_6	172_0545	F	6	5
V2LHS_173412_5	172_0447	H	4	2
V2LHS_211696_4	172_0303	E	6	3
V2LHS_132151_1	172_0041	D	4	1
V2LHS_50152_6	172_0519	C	12	5
V2LHS_187547_5	172_0467	C	1	3
V2LHS_77204_6	172_0551	F	7	6
V2LHS_46161_5	172_0431	C	5	5
V2LHS_142097_1	172_0068	A	7	1
V2LHS_97427_1	172_0056	C	6	6
V2LHS_81583_3	172_0238	A	6	6
V2LHS_96680_6	172_0553	A	4	6
V2LHS_110000_5	172_0475	A	9	1
V2LHS_231280_3	172_0278	B	11	4
V2LHS_30007_1	172_0007	G	5	5
V2LHS_98390_5	172_0469	G	11	6
V2LHS_92085_4	172_0332	H	5	6
V2LHS_133991_5	172_0446	F	6	1
V2LHS_181125_2	172_0152	E	7	2
V2LHS_245415_4	172_0354	A	10	4
V2LHS_147058_1	172_0043	D	3	2
V2LHS_87677_5	172_0473	D	1	6
V2LHS_89936_2	172_0107	B	1	6
V2LHS_77294_2	172_0178	A	2	6
V2LHS_94071_4	172_0350	D	2	6

V2LHS_79732_5	172_0419	H	8	6
V2LHS_26641_3	172_0258	B	1	4
V2LHS_24258_6	172_0546	H	12	4
V2LHS_23512_5	172_0426	G	1	4
V2LHS_275582_2	172_0188	G	11	4
V2LHS_136677_6	172_0512	A	6	1
V2LHS_111898_6	172_0589	A	7	1
V2LHS_266690_2	172_0102	A	2	4
V2LHS_76512_1	172_0059	H	6	6
V2LHS_82838_4	172_0315	D	6	6
V2LHS_179524_3	172_0274	E	9	2
V2LHS_128643_1	172_0031	E	5	1
V2LHS_218946_3	172_0239	C	6	3
V2LHS_85466_4	172_0377	A	11	6
V2LHS_168072_5	172_0471	D	12	2
V2LHS_46565_5	172_0486	G	4	5
V2LHS_115972_1	172_0045	D	11	1
V2LHS_87424_4	172_0394	B	3	6
V2LHS_187585_2	172_0194	F	12	3
V2LHS_89773_6	172_0567	D	1	6
V2LHS_96104_2	172_0130	E	4	6
V2LHS_84520_5	172_0449	H	6	6
V2LHS_116528_6	172_0580	E	9	1
V2LHS_53698_4	172_0320	B	10	5
V2LHS_81995_4	172_0393	D	10	6
V2LHS_8758_1	172_0057	B	11	6
V2LHS_204644_2	172_0138	H	10	3
V2LHS_176860_6	172_0583	G	6	2
V2LHS_69344_3	172_0288	C	3	6
V2LHS_139956_1	172_0004	G	12	1
V2LHS_248440_4	172_0307	A	6	4
V2LHS_69786_4	172_0385	D	1	6
V2LHS_243479_3	172_0220	E	1	4
V2LHS_67287_1	172_0044	A	11	6
V2LHS_150348_4	172_0400	H	4	2
V2LHS_181269_6	172_0503	F	7	3
V2LHS_64543_2	172_0136	C	10	6
V2LHS_82047_1	172_0018	H	5	6
V2LHS_90233_5	172_0477	H	4	6
V2LHS_128637_2	172_0151	D	2	1
V2LHS_126711_6	172_0591	F	4	1
V2LHS_111926_3	172_0295	D	8	1
V2LHS_90647_4	172_0362	E	5	6
V2LHS_269831_6	172_0590	B	6	4
V2LHS_84859_4	172_0363	H	5	6
V2LHS_72249_1	172_0085	A	10	6
V2LHS_235050_2	172_0112	G	1	4
V2LHS_99310_6	172_0595	F	11	6
V2LHS_12782_2	172_0177	C	12	1
V2LHS_51176_5	172_0474	F	8	5

V2LHS_51041_3	172_0283	A	3	5
V2LHS_163727_5	172_0453	C	7	2
V2LHS_46602_6	172_0582	G	12	5
V2LHS_264165_1	172_0082	A	2	4
V2LHS_82176_2	172_0114	A	11	6
V2LHS_56970_3	172_0266	F	4	5
V2LHS_65177_4	172_0313	D	12	6
V2LHS_91195_3	172_0247	F	6	6
V2LHS_104920_3	172_0256	G	10	1
V2LHS_91061_2	172_0136	F	3	6
V2LHS_104455_3	172_0275	D	12	1
V2LHS_134263_1	172_0036	G	8	1
V2LHS_146032_3	172_0255	C	3	2
V2LHS_185744_3	172_0281	D	2	3
V2LHS_139796_3	172_0221	H	9	1
V2LHS_85837_4	172_0377	E	11	6
V2LHS_135651_4	172_0348	B	5	1
V2LHS_65121_1	172_0002	G	10	6
V2LHS_65390_4	172_0330	H	6	6
V2LHS_85846_6	172_0525	B	9	6
V2LHS_84783_6	172_0576	F	9	6
V2LHS_99300_6	172_0584	F	10	6
V2LHS_80770_5	172_0451	B	6	6
V2LHS_106829_5	172_0464	C	2	1
V2LHS_130051_1	172_0073	H	6	1
V2LHS_251471_5	172_0468	H	12	4
V2LHS_38845_5	172_0425	H	11	5
V2LHS_78358_5	172_0433	A	7	6
V2LHS_49834_1	172_0034	E	11	5
V2LHS_69380_1	172_0007	H	9	6
V2LHS_76467_3	172_0226	B	2	6
V2LHS_70048_5	172_0476	C	2	6
V2LHS_61549_4	172_0385	C	6	5
V2LHS_44120_3	172_0226	A	4	5
V2LHS_189428_4	172_0356	E	8	3
V2LHS_78265_5	172_0468	D	5	6
V2LHS_10232_1	172_0074	D	10	1
V2LHS_131045_4	172_0351	E	5	1
V2LHS_77108_6	172_0513	B	11	6
V2LHS_75945_5	172_0425	C	2	6
V2LHS_243261_5	172_0479	A	12	4
V2LHS_64561_3	172_0280	E	10	6
V2LHS_147845_3	172_0254	G	6	2
V2LHS_72556_2	172_0142	B	7	6
V2LHS_64668_1	172_0025	H	7	6
V2LHS_95381_1	172_0058	D	5	6
V2LHS_141851_6	172_0552	D	7	1
V2LHS_3012_2	172_0110	E	2	5
V2LHS_67700_5	172_0479	B	2	6
V2LHS_235081_2	172_0120	C	12	4

V2LHS_46884_1	172_0003	C	10	5
V2LHS_116874_2	172_0107	F	9	1
V2LHS_77606_3	172_0268	A	1	6
V2LHS_77698_5	172_0407	D	4	6
V2LHS_26483_4	172_0366	F	10	4
V2LHS_161372_2	172_0117	D	7	2
V2LHS_35189_4	172_0373	H	10	5
V2LHS_102741_4	172_0320	H	8	1
V2LHS_49472_4	172_0398	G	10	5
V2LHS_76135_4	172_0333	D	5	6
V2LHS_35190_2	172_0162	F	3	5
V2LHS_103352_5	172_0431	B	4	1
V2LHS_83105_4	172_0334	E	1	6
V2LHS_89539_5	172_0445	B	12	6
V2LHS_40272_6	172_0543	C	9	5
V2LHS_76264_6	172_0526	D	9	6
V2LHS_161165_2	172_0175	E	6	2
V2LHS_71507_5	172_0464	A	4	6
V2LHS_114665_6	172_0525	C	9	1
V2LHS_87834_5	172_0439	B	3	6
V2LHS_95363_2	172_0113	E	10	6
V2LHS_275797_2	172_0124	C	1	4
V2LHS_71509_5	172_0500	G	7	6
V2LHS_55189_6	172_0509	A	1	5
V2LHS_58071_3	172_0257	G	3	5
V2LHS_95677_3	172_0207	H	8	6
V2LHS_88768_5	172_0469	A	2	6
V2LHS_71511_3	172_0244	B	10	6
V2LHS_104979_4	172_0358	G	1	1
V2LHS_71531_3	172_0281	A	3	6
V2LHS_113161_1	172_0035	H	1	1
V2LHS_122479_5	172_0427	C	2	1
V2LHS_59775_3	172_0272	A	2	5
V2LHS_58054_1	172_0051	A	10	5
V2LHS_121959_2	172_0143	E	4	1
V2LHS_21906_1	172_0070	D	1	3
V2LHS_116312_1	172_0026	F	9	1
V2LHS_237741_5	172_0464	E	1	4
V2LHS_127678_6	172_0581	H	2	1
V2LHS_146994_5	172_0408	G	11	2
V2LHS_114734_1	172_0033	F	8	1
V2LHS_63411_4	172_0398	B	6	6
V2LHS_30209_6	172_0513	F	1	5
V2LHS_72040_3	172_0261	E	6	6
V2LHS_68177_6	172_0547	C	5	6
V2LHS_64923_1	172_0050	E	6	6
V2LHS_56747_5	172_0476	F	1	5
V2LHS_35319_2	172_0101	E	7	5
V2LHS_251303_3	172_0224	E	11	4
V2LHS_66755_5	172_0463	G	5	6

V2LHS_54021_4	172_0379	E	11	5
V2LHS_81098_5	172_0434	F	12	6
V2LHS_69970_6	172_0512	G	1	6
V2LHS_141057_5	172_0480	E	8	1
V2LHS_191835_2	172_0111	F	6	3
V2LHS_76303_3	172_0292	B	1	6
V2LHS_142826_4	172_0393	A	5	1
V2LHS_230846_6	172_0531	D	5	4
V2LHS_94265_4	172_0348	G	3	6
V2LHS_35353_1	172_0013	F	4	5
V2LHS_91983_4	172_0321	B	4	6
V2LHS_94374_4	172_0325	D	6	6
V2LHS_83900_5	172_0472	D	5	6
V2LHS_60657_5	172_0483	G	6	5
V2LHS_73261_6	172_0517	C	8	6
V2LHS_97453_6	172_0540	H	10	6
V2LHS_277161_2	172_0195	F	3	4
V2LHS_262045_5	172_0426	F	1	4
V2LHS_82430_2	172_0166	A	3	6
V2LHS_144430_1	172_0069	F	8	2
V2LHS_177542_4	172_0381	D	7	2
V2LHS_275494_3	172_0266	F	7	4
V2LHS_66773_3	172_0235	C	11	6
V2LHS_119221_4	172_0311	C	12	1
V2LHS_174438_1	172_0076	G	4	2
V2LHS_264482_4	172_0341	F	10	4
V2LHS_151862_5	172_0459	A	9	2
V2LHS_91893_5	172_0402	H	11	6
V2LHS_191884_4	172_0304	G	9	3
V2LHS_124466_1	172_0040	C	1	1
V2LHS_255129_5	172_0454	G	12	4
V2LHS_60814_6	172_0504	E	3	5
V2LHS_257690_5	172_0462	D	1	4
V2LHS_55578_5	172_0404	E	7	5
V2LHS_25491_6	172_0556	F	2	4
V2LHS_131379_1	172_0010	A	4	1
V2LHS_103017_4	172_0363	A	9	1
V2LHS_119655_6	172_0540	H	12	1
V2LHS_238957_6	172_0547	E	10	4
V2LHS_108069_2	172_0145	H	2	1
V2LHS_197999_2	172_0139	E	7	3
V2LHS_118414_3	172_0231	D	9	1
V2LHS_33645_2	172_0128	C	7	5
V2LHS_89554_2	172_0143	H	12	6
V2LHS_93687_5	172_0407	G	1	6
V2LHS_154395_6	172_0587	G	11	2
V2LHS_93723_1	172_0099	C	11	6
V2LHS_70462_5	172_0477	E	7	6
V2LHS_191920_2	172_0113	E	6	3
V2LHS_71627_5	172_0461	E	4	6

V2LHS_35453_3	172_0211	D	11	5
V2LHS_71628_1	172_0003	C	2	6
V2LHS_39578_3	172_0266	C	6	5
V2LHS_35474_4	172_0304	H	5	5
V2LHS_71650_4	172_0320	F	6	6
V2LHS_135299_1	172_0060	G	3	1
V2LHS_81480_6	172_0544	D	5	6
V2LHS_109325_4	172_0339	F	7	1
V2LHS_64365_4	172_0329	F	3	6
V2LHS_4882_1	172_0007	A	5	5
V2LHS_113279_6	172_0593	H	2	1
V2LHS_134771_4	172_0387	A	6	1
V2LHS_82876_6	172_0558	C	6	6
V2LHS_81245_3	172_0266	F	3	6
V2LHS_36573_3	172_0299	A	11	5
V2LHS_188904_2	172_0153	H	3	3
V2LHS_239843_2	172_0106	G	11	4
V2LHS_70160_5	172_0499	C	10	6
V2LHS_81133_2	172_0176	D	7	6
V2LHS_17662_4	172_0383	D	6	2
V2LHS_91338_1	172_0088	H	12	6
V2LHS_67587_5	172_0424	G	10	6
V2LHS_26455_4	172_0396	A	8	4
V2LHS_253273_5	172_0441	A	3	4
V2LHS_139394_2	172_0178	A	8	1
V2LHS_186137_2	172_0181	D	3	3
V2LHS_87924_1	172_0090	D	3	6
V2LHS_86311_6	172_0561	E	2	6
V2LHS_257592_6	172_0545	F	7	4
V2LHS_71728_3	172_0220	A	2	6
V2LHS_207080_6	172_0571	C	11	3
V2LHS_49884_2	172_0134	F	6	5
V2LHS_12133_3	172_0262	E	7	1
V2LHS_13004_1	172_0068	F	8	1
V2LHS_255477_2	172_0101	E	1	4
V2LHS_21857_3	172_0270	D	11	3
V2LHS_93598_6	172_0585	D	5	6
V2LHS_259099_4	172_0384	C	11	4
V2LHS_112556_4	172_0327	G	1	1
V2LHS_137525_1	172_0061	G	5	1
V2LHS_24615_5	172_0407	E	8	4
V2LHS_138710_1	172_0037	F	7	1
V2LHS_64606_3	172_0273	G	6	6
V2LHS_77830_6	172_0507	G	9	6
V2LHS_62307_6	172_0511	E	7	6
V2LHS_69864_4	172_0361	G	10	6
V2LHS_249028_4	172_0310	B	3	4
V2LHS_79225_3	172_0238	A	2	6
V2LHS_15449_4	172_0315	D	9	2
V2LHS_119835_1	172_0090	C	9	1

V2LHS_225532_3	172_0247	A	2	4
V2LHS_132480_2	172_0161	C	8	1
V2LHS_176436_3	172_0244	B	8	2
V2LHS_82762_1	172_0084	A	10	6
V2LHS_231019_5	172_0460	D	10	4
V2LHS_194028_5	172_0489	D	7	3
V2LHS_163889_5	172_0441	F	7	2
V2LHS_103214_3	172_0217	F	7	1
V2LHS_8725_1	172_0016	C	5	6
V2LHS_59628_6	172_0539	G	6	5
V2LHS_209440_2	172_0157	E	9	3
V2LHS_87197_6	172_0555	F	7	6
V2LHS_49178_6	172_0509	A	5	5
V2LHS_71327_4	172_0391	A	2	6
V2LHS_102851_1	172_0035	C	6	1
V2LHS_67635_4	172_0342	D	6	6
V2LHS_51859_5	172_0405	C	6	5
V2LHS_257672_3	172_0287	F	11	4
V2LHS_238795_6	172_0516	B	11	4
V2LHS_92526_1	172_0005	H	4	6
V2LHS_108301_1	172_0049	E	5	1
V2LHS_262630_5	172_0437	C	4	4
V2LHS_71372_3	172_0252	E	10	6
V2LHS_92154_2	172_0184	E	6	6
V2LHS_46517_1	172_0035	C	3	5
V2LHS_94753_1	172_0063	F	6	6
V2LHS_91516_4	172_0307	A	3	6
V2LHS_104918_1	172_0037	H	8	1
V2LHS_151443_4	172_0392	E	8	2
V2LHS_98025_2	172_0184	H	2	6
V2LHS_78668_2	172_0150	A	11	6
V2LHS_86087_4	172_0321	G	7	6
V2LHS_230013_2	172_0108	G	10	4
V2LHS_221493_3	172_0218	E	1	3
V2LHS_166718_3	172_0269	G	4	2
V2LHS_72643_5	172_0458	D	3	6
V2LHS_231244_5	172_0448	B	9	4
V2LHS_98761_5	172_0442	D	6	6
V2LHS_48096_5	172_0493	C	2	5
V2LHS_69757_5	172_0483	F	11	6
V2LHS_74615_1	172_0085	C	5	6
V2LHS_91772_6	172_0537	B	10	6
V2LHS_109415_5	172_0481	D	4	1
V2LHS_181099_2	172_0161	B	1	2
V2LHS_83423_1	172_0014	C	12	6
V2LHS_276461_2	172_0187	B	1	4
V2LHS_195833_4	172_0375	D	4	3
V2LHS_90636_4	172_0398	F	1	6
V2LHS_98766_2	172_0200	D	8	6
V2LHS_70612_5	172_0414	H	9	6

V2LHS_175426_2	172_0175	A	11	2
V2LHS_109340_4	172_0362	D	7	1
V2LHS_99114_4	172_0314	E	12	6
V2LHS_106995_2	172_0182	E	5	1
V2LHS_83450_4	172_0393	E	2	6
V2LHS_44861_5	172_0464	F	10	5
V2LHS_85575_4	172_0345	E	9	6
V2LHS_166685_1	172_0019	F	6	2
V2LHS_213716_2	172_0144	C	10	3
V2LHS_171561_5	172_0497	A	9	2
V2LHS_79035_2	172_0104	D	5	6
V2LHS_210754_2	172_0158	G	2	3
V2LHS_121611_1	172_0025	G	2	1
V2LHS_254705_3	172_0206	F	6	4
V2LHS_87987_3	172_0262	D	3	6
V2LHS_222459_1	172_0053	G	5	3
V2LHS_31043_1	172_0004	G	12	5
V2LHS_83108_6	172_0534	B	4	6
V2LHS_88200_5	172_0415	H	3	6
V2LHS_93747_4	172_0392	A	7	6
V2LHS_82904_5	172_0404	G	4	6
V2LHS_25696_1	172_0015	D	11	4
V2LHS_60830_1	172_0036	F	11	5
V2LHS_222653_6	172_0588	C	2	3
V2LHS_54780_4	172_0323	D	6	5
V2LHS_205192_2	172_0196	C	8	3
V2LHS_50982_6	172_0502	G	7	5
V2LHS_139732_1	172_0042	G	6	1
V2LHS_262120_6	172_0569	D	9	4
V2LHS_107746_2	172_0171	E	5	1
V2LHS_96012_3	172_0287	H	9	6
V2LHS_141866_1	172_0063	C	3	1
V2LHS_174028_6	172_0550	D	4	2
V2LHS_237319_6	172_0528	E	2	4
V2LHS_95933_5	172_0485	G	12	6
V2LHS_142729_5	172_0486	D	8	1
V2LHS_161025_2	172_0182	C	11	2
V2LHS_64101_6	172_0525	H	8	6
V2LHS_14265_1	172_0083	F	9	1
V2LHS_73698_3	172_0219	F	3	6
V2LHS_96939_5	172_0426	B	11	6
V2LHS_133987_1	172_0029	B	5	1
V2LHS_117168_1	172_0008	B	7	1
V2LHS_53636_6	172_0509	B	3	5
V2LHS_228395_4	172_0343	H	7	4
V2LHS_81954_6	172_0575	D	9	6
V2LHS_256738_6	172_0585	A	9	4
V2LHS_91702_6	172_0570	D	5	6
V2LHS_150395_1	172_0063	B	8	2
V2LHS_61953_3	172_0240	E	12	6

V2LHS_84701_5	172_0464	C	12	6
V2LHS_200696_1	172_0027	H	10	3
V2LHS_206809_6	172_0526	C	9	3
V2LHS_226243_2	172_0167	B	9	4
V2LHS_90629_5	172_0432	G	6	6
V2LHS_226914_6	172_0567	B	2	4
V2LHS_273967_6	172_0547	D	6	4
V2LHS_48479_1	172_0043	A	8	5
V2LHS_66184_1	172_0042	H	8	6
V2LHS_61332_3	172_0261	C	8	5
V2LHS_84454_4	172_0348	D	5	6
V2LHS_64563_3	172_0203	F	9	6
V2LHS_73670_3	172_0245	E	6	6
V2LHS_32614_6	172_0526	F	5	5
V2LHS_93173_5	172_0407	B	1	6
V2LHS_69410_2	172_0130	F	5	6
V2LHS_127253_2	172_0153	H	5	1
V2LHS_261994_6	172_0549	E	10	4
V2LHS_95576_4	172_0385	G	6	6
V2LHS_108577_6	172_0583	A	4	1
V2LHS_97807_1	172_0004	A	10	6
V2LHS_262041_6	172_0511	C	7	4
V2LHS_262061_1	172_0098	H	9	4
V2LHS_221027_1	172_0062	C	2	3
V2LHS_166296_2	172_0170	B	1	2
V2LHS_83665_4	172_0377	C	6	6
V2LHS_116944_3	172_0280	A	7	1
V2LHS_49505_4	172_0324	A	3	5
V2LHS_45255_1	172_0013	G	8	5
V2LHS_74321_6	172_0584	F	5	6
V2LHS_76444_6	172_0587	G	11	6
V2LHS_197574_6	172_0520	F	2	3
V2LHS_98410_5	172_0402	C	1	6
V2LHS_275284_5	172_0454	E	6	4
V2LHS_130425_1	172_0010	B	12	1
V2LHS_100600_2	172_0105	E	1	1
V2LHS_36498_2	172_0177	B	1	5
V2LHS_206142_4	172_0305	C	7	3
V2LHS_72507_1	172_0084	E	12	6
V2LHS_234317_1	172_0074	C	9	4
V2LHS_142838_3	172_0225	H	9	1
V2LHS_112015_4	172_0368	A	2	1
V2LHS_134823_2	172_0184	C	1	1
V2LHS_88358_6	172_0531	H	8	6
V2LHS_239126_6	172_0576	H	6	4
V2LHS_53195_6	172_0504	D	12	5
V2LHS_75608_2	172_0199	C	12	6
V2LHS_79899_3	172_0290	F	11	6
V2LHS_36354_2	172_0105	B	9	5
V2LHS_28538_2	172_0198	A	7	5

V2LHS_70210_3	172_0264	A	11	6
V2LHS_75893_6	172_0563	E	7	6
V2LHS_86260_2	172_0103	F	9	6
V2LHS_141242_1	172_0042	E	7	1
V2LHS_203641_3	172_0288	G	7	3
V2LHS_244870_3	172_0285	A	5	4
V2LHS_211053_1	172_0097	C	6	3
V2LHS_136777_1	172_0044	A	12	1
V2LHS_177205_1	172_0071	G	9	2
V2LHS_138480_6	172_0534	F	7	1
V2LHS_87414_5	172_0436	D	9	6
V2LHS_100310_4	172_0325	E	3	1
V2LHS_91636_1	172_0090	H	6	6
V2LHS_244490_3	172_0250	H	10	4
V2LHS_183196_6	172_0508	G	11	3
V2LHS_7559_1	172_0067	F	10	6
V2LHS_247170_5	172_0460	A	1	4
V2LHS_265370_1	172_0084	E	7	4
V2LHS_94112_6	172_0540	E	1	6
V2LHS_198117_2	172_0138	G	12	3
V2LHS_76312_3	172_0300	A	10	6
V2LHS_243563_2	172_0102	G	6	4
V2LHS_221881_2	172_0179	D	1	3
V2LHS_180589_3	172_0270	C	4	2
V2LHS_234349_2	172_0141	F	12	4
V2LHS_24257_4	172_0372	E	1	4
V2LHS_127008_5	172_0481	F	5	1
V2LHS_160452_5	172_0441	C	11	2
V2LHS_82536_1	172_0088	B	3	6
V2LHS_82125_5	172_0437	E	8	6
V2LHS_136934_3	172_0202	C	12	1
V2LHS_266524_6	172_0558	F	9	4
V2LHS_265196_6	172_0539	G	10	4
V2LHS_256952_6	172_0529	E	12	4
V2LHS_263942_4	172_0385	C	11	4
V2LHS_150474_6	172_0536	C	5	2
V2LHS_140808_4	172_0355	E	3	1
V2LHS_102915_2	172_0155	A	4	1
V2LHS_37110_3	172_0300	D	2	5
V2LHS_25222_1	172_0020	F	7	4
V2LHS_267872_2	172_0146	C	7	4
V2LHS_69472_5	172_0459	G	12	6
V2LHS_89696_1	172_0086	F	4	6
V2LHS_82314_2	172_0101	A	3	6
V2LHS_73509_1	172_0018	E	9	6
V2LHS_155564_2	172_0148	C	11	2
V2LHS_267728_6	172_0521	E	8	4
V2LHS_69489_5	172_0447	A	10	6
V2LHS_239028_1	172_0060	C	10	4
V2LHS_247634_6	172_0557	A	2	4

V2LHS_89213_4	172_0307	F	2	6
V2LHS_17006_5	172_0409	F	9	2
V2LHS_253057_3	172_0272	A	7	4
V2LHS_143709_2	172_0128	H	7	2
V2LHS_98267_4	172_0350	H	10	6
V2LHS_135415_3	172_0260	E	5	1
V2LHS_234402_3	172_0246	F	12	4
V2LHS_81320_6	172_0537	H	4	6
V2LHS_116392_4	172_0301	B	3	1
V2LHS_60727_5	172_0491	F	5	5
V2LHS_136244_2	172_0198	H	10	1
V2LHS_192983_4	172_0349	H	9	3
V2LHS_3943_1	172_0064	A	5	5
V2LHS_75812_1	172_0087	E	2	6
V2LHS_32515_1	172_0001	H	6	5
V2LHS_70156_3	172_0217	D	6	6
V2LHS_36398_1	172_0038	D	1	5
V2LHS_141497_1	172_0079	A	3	1
V2LHS_20682_2	172_0153	B	9	3
V2LHS_240567_5	172_0465	A	10	4
V2LHS_73283_2	172_0193	D	12	6
V2LHS_69628_1	172_0011	C	2	6
V2LHS_20974_3	172_0289	D	6	3
V2LHS_150257_2	172_0183	B	3	2
V2LHS_134964_6	172_0580	F	2	1
V2LHS_75609_5	172_0449	A	12	6
V2LHS_61267_1	172_0068	C	3	5
V2LHS_97116_4	172_0376	H	2	6
V2LHS_88020_5	172_0472	D	9	6
V2LHS_83474_2	172_0169	G	9	6
V2LHS_114493_4	172_0304	H	11	1
V2LHS_94852_6	172_0589	H	3	6
V2LHS_69552_6	172_0524	D	1	6
V2LHS_69556_4	172_0387	F	3	6
V2LHS_27132_1	172_0008	D	7	4
V2LHS_180147_2	172_0178	A	2	2
V2LHS_73535_3	172_0260	G	10	6
V2LHS_15756_5	172_0475	G	10	2
V2LHS_86643_1	172_0024	C	6	6
V2LHS_193804_6	172_0550	F	1	3
V2LHS_97581_1	172_0030	B	2	6
V2LHS_91574_4	172_0386	G	10	6
V2LHS_64152_3	172_0240	A	6	6
V2LHS_54652_1	172_0039	E	2	5
V2LHS_97065_1	172_0038	D	3	6
V2LHS_231123_1	172_0031	B	11	4
V2LHS_67362_5	172_0470	H	1	6
V2LHS_247853_3	172_0276	B	8	4
V2LHS_64612_6	172_0533	B	1	6
V2LHS_73920_5	172_0462	B	1	6

V2LHS_72375_4	172_0308	G	1	6
V2LHS_222171_2	172_0189	C	11	3
V2LHS_94017_3	172_0241	B	12	6
V2LHS_234553_1	172_0037	E	4	4
V2LHS_223780_4	172_0329	D	4	4
V2LHS_118050_6	172_0507	D	4	1
V2LHS_181173_1	172_0061	F	6	2
V2LHS_87184_2	172_0177	A	5	6
V2LHS_103646_5	172_0434	A	12	1
V2LHS_32547_1	172_0002	C	6	5
V2LHS_209302_2	172_0141	F	7	3
V2LHS_76667_4	172_0342	E	2	6
V2LHS_121633_6	172_0509	C	2	1
V2LHS_73653_2	172_0112	B	1	6
V2LHS_76582_2	172_0116	F	1	6
V2LHS_99891_5	172_0431	G	8	6
V2LHS_91092_2	172_0150	D	2	6
V2LHS_139749_6	172_0528	E	3	1
V2LHS_5959_5	172_0425	D	10	5
V2LHS_116356_2	172_0102	A	8	1
V2LHS_26654_1	172_0074	E	5	4
V2LHS_78289_4	172_0370	F	1	6
V2LHS_71202_2	172_0200	B	12	6
V2LHS_118115_3	172_0217	B	6	1
V2LHS_105574_3	172_0212	E	4	1
V2LHS_98294_5	172_0436	B	2	6
V2LHS_137645_6	172_0566	H	9	1
V2LHS_73862_5	172_0455	C	11	6
V2LHS_12494_5	172_0500	G	4	1
V2LHS_71745_2	172_0158	B	1	6
V2LHS_151470_2	172_0165	B	8	2
V2LHS_64422_3	172_0292	F	6	6
V2LHS_90755_4	172_0371	A	5	6
V2LHS_77969_4	172_0312	F	7	6
V2LHS_26368_5	172_0494	A	12	4
V2LHS_93390_3	172_0211	G	4	6
V2LHS_188901_2	172_0168	B	7	3
V2LHS_39748_5	172_0422	D	4	5
V2LHS_238667_3	172_0222	B	8	4
V2LHS_254683_3	172_0225	B	2	4
V2LHS_142813_6	172_0596	E	10	1
V2LHS_206568_5	172_0465	G	9	3
V2LHS_67620_6	172_0562	G	3	6
V2LHS_91146_6	172_0566	D	3	6
V2LHS_68034_4	172_0325	B	9	6
V2LHS_70122_6	172_0530	E	9	6
V2LHS_72391_4	172_0394	D	1	6
V2LHS_92327_2	172_0137	B	5	6
V2LHS_114113_6	172_0534	C	4	1
V2LHS_87831_6	172_0571	G	6	6

V2LHS_94579_4	172_0369	A	10	6
V2LHS_71903_4	172_0342	F	2	6
V2LHS_70133_1	172_0070	B	11	6
V2LHS_128781_3	172_0273	D	1	1
V2LHS_174223_5	172_0478	B	1	2
V2LHS_83963_2	172_0131	B	4	6
V2LHS_125656_4	172_0322	C	3	1
V2LHS_26475_6	172_0589	A	11	4
V2LHS_124506_3	172_0219	D	3	1
V2LHS_226513_3	172_0229	E	12	4
V2LHS_73376_1	172_0082	D	8	6
V2LHS_88337_4	172_0337	A	2	6
V2LHS_241295_1	172_0068	G	9	4
V2LHS_24135_3	172_0219	D	9	4
V2LHS_35616_4	172_0361	F	1	5
V2LHS_83374_4	172_0328	G	1	6
V2LHS_36785_2	172_0175	H	10	5
V2LHS_36563_6	172_0599	B	4	5
V2LHS_102280_6	172_0574	F	8	1
V2LHS_7127_1	172_0054	E	7	6
V2LHS_237166_4	172_0343	B	11	4
V2LHS_124163_4	172_0317	E	1	1
V2LHS_255352_5	172_0488	E	4	4
V2LHS_71809_5	172_0433	G	11	6
V2LHS_9415_2	172_0125	B	3	6
V2LHS_83809_1	172_0014	B	3	6
V2LHS_93923_4	172_0372	D	12	6
V2LHS_104239_4	172_0358	G	7	1
V2LHS_113922_1	172_0096	F	4	1
V2LHS_46987_4	172_0314	H	7	5
V2LHS_152148_4	172_0382	G	10	2
V2LHS_98310_3	172_0256	C	7	6
V2LHS_40409_5	172_0480	A	12	5
V2LHS_76681_4	172_0374	A	3	6
V2LHS_107534_5	172_0459	F	7	1
V2LHS_78919_6	172_0519	E	6	6
V2LHS_26797_3	172_0210	C	4	4
V2LHS_77787_5	172_0431	B	1	6
V2LHS_188011_2	172_0171	C	6	3
V2LHS_75062_4	172_0339	F	6	6
V2LHS_89040_3	172_0280	H	3	6
V2LHS_238009_4	172_0341	F	7	4
V2LHS_63991_2	172_0170	E	9	6
V2LHS_140914_3	172_0265	C	9	1
V2LHS_116439_1	172_0095	E	3	1
V2LHS_53405_3	172_0279	A	12	5
V2LHS_19256_1	172_0092	D	4	3
V2LHS_255911_2	172_0187	B	2	4
V2LHS_262302_4	172_0327	B	9	4
V2LHS_261736_4	172_0312	A	6	4

V2LHS_85536_6	172_0551	E	5	6
V2LHS_138458_4	172_0385	B	8	1
V2LHS_9794_1	172_0071	F	11	6
V2LHS_24321_6	172_0544	D	1	4
V2LHS_140388_5	172_0474	B	11	1
V2LHS_84190_3	172_0220	D	2	6
V2LHS_266123_2	172_0144	E	2	4
V2LHS_81036_5	172_0406	F	9	6
V2LHS_70633_3	172_0244	B	11	6
V2LHS_89713_4	172_0335	B	2	6
V2LHS_238057_3	172_0205	E	9	4
V2LHS_48621_6	172_0579	C	10	5
V2LHS_50142_3	172_0242	G	5	5
V2LHS_238111_3	172_0260	D	11	4
V2LHS_127207_4	172_0356	B	3	1
V2LHS_46038_3	172_0279	A	12	5
V2LHS_76490_6	172_0571	E	7	6
V2LHS_176403_1	172_0018	G	12	2
V2LHS_4662_1	172_0035	H	3	5
V2LHS_116967_1	172_0002	H	10	1
V2LHS_226802_5	172_0497	A	2	4
V2LHS_238139_2	172_0172	A	8	4
V2LHS_92345_6	172_0540	F	10	6
V2LHS_111447_4	172_0352	D	8	1
V2LHS_90592_4	172_0365	G	6	6
V2LHS_82965_1	172_0042	H	3	6
V2LHS_59124_4	172_0375	F	4	5
V2LHS_96896_3	172_0218	G	12	6
V2LHS_91608_5	172_0439	F	10	6
V2LHS_248226_2	172_0148	C	9	4
V2LHS_131378_5	172_0477	D	9	1
V2LHS_6721_1	172_0086	G	4	6
V2LHS_21267_5	172_0469	D	5	3
V2LHS_99372_5	172_0462	G	5	6
V2LHS_97398_2	172_0120	C	12	6
V2LHS_72511_5	172_0433	H	9	6
V2LHS_77528_2	172_0143	F	7	6
V2LHS_87687_1	172_0017	D	5	6
V2LHS_44776_3	172_0282	C	2	5
V2LHS_238152_4	172_0311	H	11	4
V2LHS_259867_5	172_0434	F	5	4
V2LHS_85243_3	172_0236	G	11	6
V2LHS_67780_5	172_0487	D	12	6
V2LHS_126373_5	172_0406	E	6	1
V2LHS_58690_3	172_0271	A	1	5
V2LHS_52617_5	172_0451	A	1	5
V2LHS_58788_3	172_0216	B	5	5
V2LHS_81558_3	172_0221	E	9	6
V2LHS_95021_6	172_0553	D	12	6
V2LHS_70248_4	172_0359	G	2	6

V2LHS_238187_2	172_0141	G	6	4
V2LHS_136646_3	172_0212	A	10	1
V2LHS_91797_3	172_0275	D	11	6
V2LHS_119558_6	172_0555	G	8	1
V2LHS_81933_6	172_0582	F	3	6
V2LHS_253827_1	172_0088	D	8	4
V2LHS_75814_5	172_0489	C	4	6
V2LHS_37113_6	172_0562	A	8	5
V2LHS_86953_5	172_0417	H	11	6
V2LHS_253250_1	172_0098	E	11	4
V2LHS_205237_4	172_0324	D	5	3
V2LHS_92914_6	172_0547	H	4	6
V2LHS_98036_4	172_0318	H	4	6
V2LHS_118197_4	172_0314	D	2	1
V2LHS_107057_3	172_0289	D	8	1
V2LHS_97677_6	172_0571	C	7	6
V2LHS_129169_1	172_0083	C	12	1
V2LHS_29530_5	172_0443	G	9	5
V2LHS_36932_4	172_0321	D	3	5
V2LHS_83837_4	172_0392	B	2	6
V2LHS_161380_3	172_0207	H	7	2
V2LHS_222934_2	172_0173	F	6	3
V2LHS_231143_6	172_0569	H	2	4
V2LHS_40198_5	172_0423	G	9	5
V2LHS_242663_5	172_0492	D	7	4
V2LHS_10481_1	172_0089	F	11	1
V2LHS_83875_5	172_0439	A	8	6
V2LHS_61741_3	172_0211	G	12	6
V2LHS_204072_1	172_0096	H	10	3
V2LHS_177981_6	172_0581	E	8	2
V2LHS_253420_2	172_0158	B	9	4
V2LHS_67903_4	172_0326	D	9	6
V2LHS_84020_2	172_0117	B	8	6
V2LHS_249182_2	172_0119	C	6	4
V2LHS_82797_3	172_0288	C	7	6
V2LHS_125763_6	172_0553	H	10	1
V2LHS_70468_4	172_0374	C	3	6
V2LHS_96663_5	172_0407	F	4	6
V2LHS_53501_1	172_0027	B	1	5
V2LHS_113606_1	172_0059	F	6	1
V2LHS_24835_4	172_0365	A	7	4
V2LHS_227485_6	172_0563	D	8	4
V2LHS_7749_1	172_0063	H	2	6
V2LHS_54708_6	172_0505	B	5	5
V2LHS_252406_2	172_0148	C	7	4
V2LHS_47603_5	172_0413	E	7	5
V2LHS_248634_1	172_0083	C	4	4
V2LHS_37136_6	172_0568	C	8	5
V2LHS_136660_2	172_0185	C	4	1
V2LHS_255713_6	172_0530	F	5	4

V2LHS_69826_3	172_0234	E	8	6
V2LHS_238936_1	172_0068	C	8	4
V2LHS_40216_1	172_0048	B	1	5
V2LHS_160585_2	172_0195	F	10	2
V2LHS_196831_2	172_0166	F	2	3
V2LHS_127258_5	172_0404	B	2	1
V2LHS_74777_6	172_0518	F	11	6
V2LHS_114778_5	172_0401	G	10	1
V2LHS_93030_1	172_0004	E	11	6
V2LHS_72005_3	172_0207	H	1	6
V2LHS_238237_1	172_0023	E	11	4
V2LHS_99305_1	172_0052	B	5	6
V2LHS_254931_1	172_0090	E	7	4
V2LHS_236000_3	172_0269	C	1	4
V2LHS_245065_5	172_0456	E	6	4
V2LHS_86692_5	172_0473	G	4	6
V2LHS_270527_6	172_0546	G	8	4
V2LHS_24631_1	172_0019	F	3	4
V2LHS_30235_1	172_0020	D	4	5
V2LHS_130728_1	172_0055	F	5	1
V2LHS_72792_6	172_0583	B	12	6
V2LHS_67383_3	172_0264	D	6	6
V2LHS_22810_2	172_0179	B	11	4
V2LHS_171470_1	172_0073	H	4	2
V2LHS_71746_1	172_0025	D	5	6
V2LHS_197144_4	172_0374	H	11	3
V2LHS_126622_3	172_0265	C	6	1
V2LHS_151546_3	172_0248	E	8	2
V2LHS_254620_1	172_0091	H	10	4
V2LHS_81770_1	172_0091	E	8	6
V2LHS_65519_4	172_0350	D	3	6
V2LHS_194870_5	172_0494	H	12	3
V2LHS_275825_2	172_0172	D	7	4
V2LHS_84936_1	172_0098	E	7	6
V2LHS_270653_6	172_0594	F	2	4
V2LHS_61012_4	172_0373	G	9	5
V2LHS_156511_4	172_0341	A	3	2
V2LHS_151489_6	172_0526	E	4	2
V2LHS_151545_1	172_0016	F	7	2
V2LHS_131037_4	172_0346	B	12	1
V2LHS_70477_5	172_0433	B	1	6
V2LHS_235801_1	172_0047	C	7	4
V2LHS_196646_5	172_0467	E	2	3
V2LHS_92486_2	172_0164	E	4	6
V2LHS_74891_1	172_0086	B	4	6
V2LHS_64005_2	172_0130	D	12	6
V2LHS_196824_4	172_0387	C	5	3
V2LHS_72870_1	172_0097	D	11	6
V2LHS_123371_4	172_0306	C	6	1
V2LHS_168895_4	172_0324	D	1	2

Sense Sequence of shRNA target sequence	Ensembl Gene ID	Gene Symbol	Median Drug Effect Z Score	shRNAs per gene in this list
CCTAGTATAGGGAAAGGAT	ENSG00000138018	AC010896.1	2.264922214	2
CTGTTTAATTTCTTATATA	ENSG00000138018	AC010896.1	5.152936137	2
GACACATAGCCCTCGATTA	ENSG00000114331	ACAP2	1.969126313	2
GAGAGGAAATTTGTGGATA	ENSG00000114331	ACAP2	2.372071729	2
CAGCCACACCTAAGCATTT	ENSG00000130234	ACE2	1.966773622	2
GGTTGAACACAATTCTAAA	ENSG00000130234	ACE2	2.21270039	2
GTCAAACGTAGTCGGAAA	ENSG00000173157	ADAMTS20	2.072843245	2
GAATTTGCCATTAACCTCAA	ENSG00000173157	ADAMTS20	2.073602797	2
CGCAATATCCTGAACTAAA	ENSG00000226219	AL049543.3	2.256564017	2
CAGGAGATAACAAAGAGAT	ENSG00000226219	AL049543.3	3.187224532	2
CACCTGATGGCTAATGGAT	ENSG00000185046	ANKS1B	2.074771814	2
GGCTAACTGTCAGAAAGTCT	ENSG00000185046	ANKS1B	2.751654672	2
CTGTCCATGTTCTTTCCAA	ENSG00000120318	ARAP3	1.97157167	2
CACATATTATCCCTGAACA	ENSG00000120318	ARAP3	2.145471126	2
CCCTCTATGCCTTTACTTA	ENSG00000123329	ARHGAP9	2.599949478	2
CTCTCTCAGATACAAGAAT	ENSG00000123329	ARHGAP9	3.389169807	2
CCTACATTATTTAACCCTAA	ENSG00000145782	ATG12	2.105275294	2
GTACATTTCTTATATGTA	ENSG00000145782	ATG12	2.596863218	2
CAATTTATCCCTGAGATGA	ENSG00000105929	ATP6V0A4	2.287725224	2
GTCAGCCTGTGGATTTGAT	ENSG00000105929	ATP6V0A4	3.104411953	2
GAGTTGATCTTGGCAGAGT	ENSG00000009954	BAZ1B	3.699226314	2
CAGTGAGTGCCATACAGAA	ENSG00000009954	BAZ1B	3.800237987	2
CTGTAACCTAAATAGCTCT	ENSG00000122870	BICC1	2.522910959	2
CACCTTATCTCTGAACACT	ENSG00000122870	BICC1	2.753725788	2
AGAACTCTATGAATATTGT	ENSG00000106245	BUD31	2.069403448	2
ACTCTATGAATATTGTATT	ENSG00000106245	BUD31	2.274672984	2
GCAGTTGAGTTTATGAATA	ENSG00000127720	C12orf26	2.161063027	2
GTGCTGTTCTTCAGGATAT	ENSG00000127720	C12orf26	3.282033436	2
CTGGCATCCTGCTATTTGA	ENSG00000126214	C14orf153	2.212125201	2
CGTTTCCTGTGTTTCGAAT	ENSG00000126214	C14orf153	2.432507309	2
GTGATTATGGATTGAGATG	ENSG00000059145	C16orf28	2.126170143	2
CTAAATATATTAGATTTC	ENSG00000059145	C16orf28	5.108893526	2
CACAGTTTGTTATTAAGTA	ENSG00000042304	C2orf83	2.9475548	2
CCCTGACGTTTGGAATTAA	ENSG00000042304	C2orf83	3.938476374	2
CAGATGATATGTCACACAA	ENSG00000174899	C3orf55	2.025634671	2
CTGTTATGTGGCAGTTTGT	ENSG00000174899	C3orf55	3.64281844	2
GGCTTTAACTGAAGTAGAA	ENSG00000163946	C3orf63	2.089951143	2
GCCATATTCACAAGAGAAA	ENSG00000163946	C3orf63	2.492881941	2
GTCGCCACTATCAGAAAGA	ENSG00000163689	C3orf67	2.020766849	2
GAGCAAATAGATAGAAATA	ENSG00000163689	C3orf67	2.809955307	2
GCAGTAGTGTCTTAGATTA	ENSG00000187461	C6orf114	2.454982444	2
GCTACAATGTGTAAGGAAA	ENSG00000187461	C6orf114	3.131513599	2
CTCCTAACACTTCTTTAAA	ENSG00000153790	C7orf31	2.12874407	2
AGAGGAATTTCTTTAAGTA	ENSG00000153790	C7orf31	4.806605859	2
ATTGTTATTCCGTTGAATA	ENSG00000155621	C9orf85	2.103661938	2
CAGAATACGTTTAGCTTCA	ENSG00000155621	C9orf85	2.174109332	2

CTTTCTAATCTACAAGTTA	ENSG00000169239	CA5B	2.684825698	2
GCTGTACATAGTATATAA	ENSG00000169239	CA5B	3.374071919	2
GCTTCACTTTCTTCTGTA	ENSG00000141668	CBLN2	2.048363493	2
GTCTTAAGGAGAAATGAAA	ENSG00000141668	CBLN2	2.887934487	2
GAGAGAAGAGAGCTGAAAT	ENSG00000229140	CCDC26	2.237001291	2
CTGGAAATGATAGACAATA	ENSG00000229140	CCDC26	2.306486212	2
CCTAAAGAATGTAAAGGTA	ENSG00000173588	CCDC41	2.461764305	2
CAAAGAAGAAGGTTATCAA	ENSG00000173588	CCDC41	2.906771709	2
AAGTATCAGTTATTGATAT	ENSG00000163249	CCNYL1	2.142384356	2
CATTTCTTGTGAACTATAA	ENSG00000163249	CCNYL1	2.238156435	2
GACTGCACTTGCTCGAATA	ENSG00000134061	CD180	2.178330231	2
ACCATTAATTTAAGTCATA	ENSG00000134061	CD180	3.425573364	2
CTCTTCAACTTGATCTTCT	ENSG00000085117	CD82	2.176619182	2
CTGTATCAAAGTCACCAAA	ENSG00000085117	CD82	2.218751808	2
CTGTATATTTGAACTGCT	ENSG00000176749	CDK5R1	2.419288612	2
CAAAGTGTGGGTATTGTTA	ENSG00000176749	CDK5R1	3.353921605	2
AGCATAGGTTGCATTCTTA	ENSG00000113240	CLK4	1.989485551	2
GTTGCATTCTTATTGAATA	ENSG00000113240	CLK4	2.762727011	2
CAGAAGAATTGGTCCAGTT	ENSG00000100528	CNIH	2.031761943	2
GGCTTACACTGGGTCTCAA	ENSG00000100528	CNIH	5.3832691	2
GTTCTTCCCTCTTTCCAAT	ENSG00000137449	CPEB2	2.391123703	2
AATGTTAATTATTTAGATA	ENSG00000137449	CPEB2	4.152011678	2
GATAGTAAAGCTAAAGTTA	ENSG00000121005	CRISPLD1	1.983559366	2
CTGGCTGTTTGGATAGTAA	ENSG00000121005	CRISPLD1	3.860286243	2
CCATGCCACAAATATTTAT	ENSG00000144677	CTDSPL	2.113991125	2
CTGTGCCTATGCTCAGAAT	ENSG00000144677	CTDSPL	3.390583584	2
CTTTCGGAGATTTCTTCTA	ENSG00000215883	CYB5RL	2.624806607	2
AGGATACTTTGAAGTGTTA	ENSG00000215883	CYB5RL	2.680387521	2
CTCAAAGCATTATGAATA	ENSG00000147202	DIAPH2	2.063745055	2
CAAATTGAACATTCAAATA	ENSG00000147202	DIAPH2	2.176854902	2
CAATCAAGACAAATTGTTA	ENSG00000211452	DIO1	3.177900291	2
CAGTAAACTAATAACAGAA	ENSG00000211452	DIO1	6.518629961	2
GTGTGATTTACATTTATA	ENSG00000198919	DZIP3	2.175994152	2
CATACTTACTGTTCCCTCAA	ENSG00000198919	DZIP3	4.191511634	2
CATGATTCTTCTTAGTGAA	ENSG00000134001	EIF2S1	2.49449237	2
GGATATATTGATTTGTCAA	ENSG00000134001	EIF2S1	3.047187704	2
CAAGTACCTATATATGTAT	ENSG00000164778	EN2	2.145708187	2
CGCGCTAAACAATGCAATA	ENSG00000164778	EN2	2.818593398	2
GGCAGTATGTGTCTGTAAA	ENSG00000145242	EPHA5	2.058066116	2
GGCAGTATGTGTCTGTAAA	ENSG00000145242	EPHA5	3.174414178	2
CTTATCAAGTGAATATCAT	ENSG00000117036	ETV3	2.35518273	2
GATAGATTTCTTTGGTTTA	ENSG00000117036	ETV3	3.49680841	2
CTCTAAATGTGTGTGAATA	ENSG00000154124	FAM105B	1.962739264	2
CAGAAGTACTTGAGCTTAA	ENSG00000154124	FAM105B	2.658516635	2
CAGTGTCTACCCAGCTTTA	ENSG00000184083	FAM120C	2.100703715	2
CGCTACCTCCCTATGAATA	ENSG00000184083	FAM120C	2.296823088	2
GCAGAAATCTCCTACAGTA	ENSG00000165323	FAT3	2.434322505	2
GGAGTTATTTCATATGACT	ENSG00000165323	FAT3	2.72731806	2
GCATGTTGATCTTTCCATA	ENSG00000141665	FBXO15	1.982457154	2
CCCTCAGAATATTTGGTTT	ENSG00000141665	FBXO15	2.361225013	2

GACAGTTATTTAGAAGGAA	ENSG00000118496	FBXO30	2.064126915	2
CTAGTATAATTTCTTTGTA	ENSG00000118496	FBXO30	5.491906084	2
CTGTCATTCATGTGATTGA	ENSG00000100225	FBXO7	2.359008643	2
CCCAGTCTGGTGTTTGGAA	ENSG00000100225	FBXO7	2.39833343	2
CATGGGACCTCTCTCACCT	ENSG00000189283	FHIT	2.032276124	2
GTCCTTCGCTCTTGTGAAT	ENSG00000189283	FHIT	2.129660176	2
GCAGCAAATTTAGAAGAAA	ENSG00000092140	G2E3	1.963213756	2
CCTTGTTTATGGACCAGAA	ENSG00000092140	G2E3	8.962982329	2
GATCCAGAACGAAGTTTAT	ENSG00000154727	GABPA	2.025484965	2
GACACTGTTGAGGTTGTTA	ENSG00000154727	GABPA	3.471272876	2
CCCTGTCTCAGATACAGAT	ENSG00000151834	GABRA2	2.200520633	2
GCTTACAGTTCAAGCTGAA	ENSG00000151834	GABRA2	3.096323225	2
CCTCTATCTTTCTCTAGCT	ENSG00000102287	GABRE	2.764862546	2
CGACCTCTCTTTAGCTCAA	ENSG00000102287	GABRE	3.675414221	2
GTTATAGAGTCAATCTAAT	ENSG00000164347	GFM2	2.895925506	2
GAGAAAGAGGCATTACTAT	ENSG00000164347	GFM2	3.674460937	2
GTCTTTCTATCCATCGAAT	ENSG00000198380	GFPT1	2.031320976	2
CATTTAATTGGAGTATCTA	ENSG00000198380	GFPT1	2.065545154	2
GTCTGAATGTCTATAAGTT	ENSG00000179399	GPC5	2.251755263	2
CAGTATTTCTTAAAGTATT	ENSG00000179399	GPC5	4.944963683	2
GCCAATACCTGATGGAATT	ENSG00000183150	GPR19	1.987658918	2
CGAAGCAATGCCTATACTA	ENSG00000183150	GPR19	3.289388204	2
CATACTTTCTGTGTCTACA	ENSG00000140030	GPR65	1.983028096	2
AAGTTTAAGTTATGCATTA	ENSG00000140030	GPR65	2.038871299	2
CCATGAATCTGCTTATTAA	ENSG00000132463	GRSF1	1.964204818	2
GTTCTTATAAGGGAAAGAA	ENSG00000132463	GRSF1	4.896029219	2
CTGCCAGCTTGGAATTAAA	ENSG00000075218	GTSE1	2.03320168	2
CCATTCCCTTTATTTAGAA	ENSG00000075218	GTSE1	2.151883764	2
CACCCAGTATCCTAAATAA	ENSG00000099783	HNRNPM	2.020537855	2
CAAGCTATATCTATGTTCA	ENSG00000099783	HNRNPM	2.238392061	2
GACATCACCTGTACCTATA	ENSG00000172987	HPSE2	2.104601467	2
CAGCTTATATGGCCCTAAT	ENSG00000172987	HPSE2	2.886477609	2
CTCTTTCTTTAGAGCCTAA	ENSG00000197915	HRNR	3.18121013	2
GAAATATATTGAGGAGTTA	ENSG00000197915	HRNR	4.111953985	2
CACCTTAAGCACTGATAAA	ENSG00000176160	HSF5	2.412090507	2
CCTAGGAATATGAACTAA	ENSG00000176160	HSF5	3.187685981	2
CTTCCTAATTATCATTTGA	ENSG00000126550	HTN1	3.37132946	2
CAAATTATCTATATGACAA	ENSG00000126550	HTN1	4.02890941	2
CCTACAAATTAATGACACA	ENSG00000115267	IFIH1	2.242650634	2
GAGAGAAGATGATGTATAA	ENSG00000115267	IFIH1	2.754932918	2
CCCATGATTACAGAGATAA	ENSG00000162594	IL23R	2.512559457	2
CTGTGTCATTTATGAATAT	ENSG00000162594	IL23R	4.35036834	2
CACACGATTAGCTTTATTA	ENSG00000173404	INSM1	2.232100556	2
CTATTTATAGAAAGCTTCA	ENSG00000173404	INSM1	2.516081119	2
GAGGACATTGTGAATGATA	ENSG00000164941	INTS8	2.118644101	2
CTGTGGCAATCACAGTGAA	ENSG00000164941	INTS8	3.755652158	2
CAGTTCTTCTTGTGAAGAA	ENSG00000090376	IRAK3	2.512085537	2
ATCGGTATATTAATAGGAA	ENSG00000090376	IRAK3	2.51696776	2
GACATGGCAGGGAAATTAA	ENSG00000163166	IWS1	2.076389221	2
CCAGGCCAGTGATTCGGAA	ENSG00000163166	IWS1	2.378596325	2

CCGGACCTCTTCATCTTAT	ENSG00000197584	KCNMB2	3.727709367	2
GACCAGATTTCTAATTAA	ENSG00000197584	KCNMB2	5.81558614	2
CCCAGAGAAAGATAAGTAA	ENSG00000164794	KCNV1	1.995801824	2
CTTGCCTATTGCTATTATT	ENSG00000164794	KCNV1	2.557672024	2
CTGTTCTTAATGAAGAAAT	ENSG00000164627	KIF6	4.442398939	2
GAGTGGCACTCATAAAGAA	ENSG00000164627	KIF6	6.833704662	2
CTCATCCTTGATTTAATT	ENSG00000129911	KLF16	4.058089409	2
CCTCATCCTTGATTTAAT	ENSG00000129911	KLF16	4.271532682	2
GCCTTATCGCTGCATCTAT	ENSG00000167613	LAIR1	2.18153744	2
CAGGTGGTCCCTTCTACAA	ENSG00000167613	LAIR1	5.571014587	2
GTCCTGAAAGTAACTCATA	ENSG00000164109	MAD2L1	2.157242661	2
GTTGTAGTTATCTCAAATA	ENSG00000164109	MAD2L1	2.814347597	2
CTGGGAAACACGGTATTTA	ENSG00000168067	MAP4K2	2.482396704	2
GTATTTAAGAGAGAACTAT	ENSG00000168067	MAP4K2	3.103384379	2
GAATGCAAGTAATCCTAAT	ENSG00000075413	MARK3	4.205190869	2
CTCTTCAGAGAAGTAAGAA	ENSG00000075413	MARK3	5.52135967	2
CGAAGTTTCTCCTGCTTGA	ENSG00000069020	MAST4	2.377418502	2
CCTTGGAATATTTACATAA	ENSG00000069020	MAST4	2.633247151	2
CATTTACTCGTTTATTTAA	ENSG00000213190	MLLT11	2.35479917	2
ACCATTTACTCGTTTATTT	ENSG00000213190	MLLT11	3.216249119	2
CACTGCAGATAGAGACATA	ENSG00000020426	MNAT1	2.046060237	2
CAGTTAACCATTTATAAGA	ENSG00000020426	MNAT1	4.921312415	2
CCCTTCATCTGGGAATCAT	ENSG00000142961	MOBK2C	3.291293786	2
CGCTATATGGCATTGCTCA	ENSG00000142961	MOBK2C	3.660485439	2
CTGATCAGATAGAAGTTGT	ENSG00000112996	MRPS30	3.088603019	2
CACATATTTGTTGGCTCAA	ENSG00000112996	MRPS30	3.358799143	2
GAGATATATTTCAGCTTCA	ENSG00000100330	MTMR3	2.331705173	2
GCTAGTCTCCAGCAAATTA	ENSG00000100330	MTMR3	2.436374153	2
GCTGTTGTGCTAATAGTGT	ENSG00000139597	N4BP2L1	2.976277982	2
GTCATACAGGGATATATAA	ENSG00000139597	N4BP2L1	3.268937838	2
ATCTGAATATGTTCTTTAA	ENSG00000125814	NAPB	1.978063033	2
CTCTGAATATTTATAGTTA	ENSG00000125814	NAPB	2.033669961	2
GCTCCAATCTGTACATAA	ENSG00000167034	NKX3-1	2.108010864	2
CTGTTTCTATCCTGTTTAA	ENSG00000167034	NKX3-1	2.200388248	2
CAGAGAAGCTCCTGTTTAT	ENSG00000173572	NLRP13	2.009260112	2
CTAATGCCCTCAGCCATAA	ENSG00000173572	NLRP13	2.803401377	2
GAATTTCCAATTATGAAT	ENSG00000170485	NPAS2	2.131614949	2
GACTCAAAGCAAAGCACAA	ENSG00000170485	NPAS2	3.066119198	2
CAGAGGATGCTGATGAGAA	ENSG00000031544	NR2E3	2.027083919	2
CTCCTCCCGTCTTTGAGGT	ENSG00000031544	NR2E3	2.202096154	2
GATACAAATTGATAGTCAA	ENSG00000157168	NRG1	2.031491255	2
ATGTGTTATTTGTCACAAA	ENSG00000157168	NRG1	2.241284736	2
CTGAAGATGTATTTAGCAA	ENSG00000155561	NUP205	2.26807543	2
CTAATGATTTCTTCAGCTA	ENSG00000155561	NUP205	2.320006454	2
CATACTCTGTTCTGACACA	ENSG00000150261	OR8K1	2.493771834	2
CTAAGGAACAAAGAAGTAA	ENSG00000150261	OR8K1	2.878857488	2
CATACTTTGTTGCAGGTAT	ENSG00000163982	OTOP1	2.549770166	2
CTTCTTGTTCCCTCTGCAAT	ENSG00000163982	OTOP1	11.86510592	2
GACCTGATCTGGAACATCA	ENSG00000143799	PARP1	2.008142815	2
GAAGTCATCGATATCTTTA	ENSG00000143799	PARP1	3.401732188	2

GTTTAATAGAAATCCTTAA	ENSG00000105185	PDCD5	2.907899614	2
GCAGTAGAGAATTACCTTA	ENSG00000105185	PDCD5	3.410220679	2
CTCTATCCTTCCAAATGAA	ENSG00000134853	PDGFRA	2.175914981	2
CATTTAATGTTTATGCTTT	ENSG00000134853	PDGFRA	3.960922533	2
CAACGCCTGTGATGGATAA	ENSG00000004799	PDK4	3.05765147	2
CAACGCCTGTGATGGATAA	ENSG00000004799	PDK4	3.414810488	2
CACAATAACTTGTTATCTA	ENSG00000138814	PPP3CA	1.977138221	2
CCTGTTATATTAAATAATA	ENSG00000138814	PPP3CA	6.307732761	2
CTGAATGATGGATACATTA	ENSG00000162976	PQLC3	2.043412867	2
CCACTTAAATTCTTGTTTA	ENSG00000162976	PQLC3	2.829703621	2
GCAGCTGTGATGCATGATA	ENSG00000174231	PRPF8	2.057689967	2
CCCTGTATGTGTTACGTGA	ENSG00000174231	PRPF8	2.166942456	2
GGTTTAAATGTCAGATTTA	ENSG00000152229	PSTPIP2	2.639363832	2
CTCACCAGATGATCCCAAT	ENSG00000152229	PSTPIP2	6.382841871	2
CTTTCACCTCGTGGTGAATA	ENSG00000158079	PTPDC1	2.319467778	2
GTGAATATTTCAGACCTAA	ENSG00000158079	PTPDC1	2.538233891	2
CAGATGATCTTCCAAAGAA	ENSG00000081237	PTPRC	2.89958129	2
CAGATTACATCATTCAAGAA	ENSG00000081237	PTPRC	4.100495289	2
GTCTGTGTTGACACAGAAA	ENSG00000110060	PUS3	2.001373092	2
CAGACTGAGAAGCTCCTAA	ENSG00000110060	PUS3	2.019828275	2
GAAGGAATCATATTCCTTT	ENSG00000197275	RAD54B	1.980665578	2
GAATCATATTCCTTTATGA	ENSG00000197275	RAD54B	2.546117587	2
CTTTGGAAATTTAATGTTA	ENSG00000150681	RGS18	2.624067289	2
CATGCATTAGGCTTTGGAA	ENSG00000150681	RGS18	2.781766887	2
CATGTTATCTGCTAAAGCA	ENSG00000117016	RIMS3	3.495671308	2
CTGAGCCTCTATTCTTATA	ENSG00000117016	RIMS3	5.355518097	2
ACATACTAGTTATGTTAAA	ENSG00000146083	RNF44	2.191659756	2
CAGTATACACATATATATA	ENSG00000146083	RNF44	3.079177329	2
CAGCCAGAGTCAGAAGGTA	ENSG00000183638	RP1L1	2.150153805	2
GCCCAGAAGGCAGAAGGTA	ENSG00000183638	RP1L1	4.277533864	2
CGGATCAACTTCGACAAAT	ENSG00000166441	RPL27A	2.376211287	2
CACTTTACGTTGTTTCAAA	ENSG00000166441	RPL27A	2.8875349	2
CACAGAAATGGTATCAAGA	ENSG00000162244	RPL29	2.190866643	2
GTCCTCCTGTGCTATTTGT	ENSG00000162244	RPL29	2.375688521	2
GAGCTTGAATCTTTGCAGA	ENSG00000136603	SKIL	2.124265104	2
CTGTACTTCTGTTCCCTGAA	ENSG00000136603	SKIL	2.805645413	2
GTTATGGATCCTTTCCCAT	ENSG00000145740	SLC30A5	1.986737246	2
GGCCTGATCTCGGATGGAT	ENSG00000145740	SLC30A5	2.536478163	2
CATGATAGACTCTAACTTA	ENSG00000152683	SLC30A6	2.507611454	2
GGAGCTCTCTTTATATTAA	ENSG00000152683	SLC30A6	3.465262384	2
CGAAATGGATGCATTTCAA	ENSG00000108576	SLC6A4	2.165899209	2
GACATTTAAAGAGCGTATT	ENSG00000108576	SLC6A4	3.555598341	2
GTAGGGAAATTGTTGTTTA	ENSG00000116698	SMG7	2.465881693	2
CAAATAATAGTATGTTCAA	ENSG00000116698	SMG7	2.568080276	2
CAGACATGTCCAAGGAATA	ENSG00000143977	SNRPG	2.429807291	2
GACAAGAAGTTATCATTGA	ENSG00000143977	SNRPG	2.919939332	2
GGCTTACTATTCACTATGA	ENSG00000168807	SNTB2	2.068209769	2
CAGTATTTGTGTTCCCTAAT	ENSG00000168807	SNTB2	3.891946764	2
GCCGAGCTGTTATTATTTA	ENSG00000114850	SSR3	2.594232822	2
CTTCTAAATTTAATGTGAA	ENSG00000114850	SSR3	4.340268383	2

CACTTCACAATTTATCATT	ENSG00000106610	STAG3L4	1.997394681	2
GTATCAATTAACTATATTA	ENSG00000106610	STAG3L4	2.560214567	2
CAGCAAACCTTGATAGTGCT	ENSG00000143183	TMCO1	2.589072674	2
CATTTAGAGATTTAGAAGA	ENSG00000143183	TMCO1	3.571407204	2
CCACTGAAATCATAAGCTA	ENSG00000147003	TMEM27	2.218159367	2
AATTCTATTTGTTGACCAT	ENSG00000147003	TMEM27	3.460876371	2
GTGTCATTGATGTACTGTA	ENSG00000164983	TMEM65	2.012115175	2
CTGTCACAACATTTAGGAA	ENSG00000164983	TMEM65	2.178002036	2
CCCAGAAGATGCTCAAGAA	ENSG00000185361	TNFAIP8L1	2.212163042	2
CACCTTTCACCCGTTTGTA	ENSG00000185361	TNFAIP8L1	2.73085297	2
GCTCAAGTAGTTTAGATAA	ENSG00000197323	TRIM33	1.997060389	2
AGATGAAATCTACTCTTTA	ENSG00000197323	TRIM33	2.401356268	2
CACTTAATTCAGAAGCTAA	ENSG00000033178	UBA6	2.454523767	2
CAGATGCCCTCTTGAATAT	ENSG00000033178	UBA6	5.071607768	2
GGAATACTCAAGCAAAGAA	ENSG00000114062	UBE3A	2.398220444	2
GACAGCAGTTGAATCCATA	ENSG00000114062	UBE3A	3.175897346	2
CAGTGAATGTAGATTCCAA	ENSG00000104517	UBR5	2.050355506	2
GGTGTGCATTCTTTAATAA	ENSG00000104517	UBR5	2.56389944	2
CTGCTCTTGACAGGGAAT	ENSG00000135093	USP30	2.384808663	2
CTAGTCAACACAACCCTAA	ENSG00000135093	USP30	2.919321767	2
GTCATTGGCTTTGCTAAGA	ENSG00000111424	VDR	2.686769666	2
CACGTTCCCTACTGCAGAA	ENSG00000111424	VDR	2.914628037	2
CCTACACACACAGCCTATA	ENSG00000064205	WISP2	2.389057599	2
GGGACAAGCAGTCCCTTAA	ENSG00000064205	WISP2	6.721630983	2
CATATTCCTTTAATTCTAA	ENSG00000162664	ZNF326	2.940308697	2
CTTTACATTTGCGTTCTAA	ENSG00000162664	ZNF326	3.664491379	2
CTTTCCATTTCTAGGTAA	ENSG00000169981	ZNF35	3.004038474	2
GTTGAACCGTGTATTCTAA	ENSG00000169981	ZNF35	3.266623664	2
CCTGGAACTCCTACTGGA	ENSG00000188033	ZNF490	2.221604064	2
CTTCTTAAATGTAAGCAAT	ENSG00000188033	ZNF490	2.329182626	2
CACCTTGTAAGTTCTAAAT	ENSG00000105732	ZNF574	2.293883517	2
GTCAGAGTACCCACCTGAA	ENSG00000105732	ZNF574	2.506921707	2
CAATGTACTCCCTATGAAA	ENSG00000197782	ZNF780A	2.160122213	2
ACTTTACCCTTTATTTAAT	ENSG00000197782	ZNF780A	2.222202435	2
GCCAGAAGATCAGAGTGTA	ENSG00000132485	ZRANB2	2.938326954	2
GTAAGTATATCAAAGGAAA	ENSG00000132485	ZRANB2	4.267178301	2
GTATTAGACTTAAAGATTA	ENSG00000109576	AADAT	2.87495925	1
CAAAGAGATGTAAAGTTTA	ENSG00000181409	AATK	2.805455821	1
CTCTTAAATATATCAGCAA	ENSG00000144452	ABCA12	3.55541358	1
CCTGTAGTGGTGTACATCTA	ENSG00000198691	ABCA4	2.554950672	1
CATATGTGATCTTTGATAT	ENSG00000005471	ABCB4	2.688660872	1
GTCGATCAATCGCATTCAT	ENSG00000160179	ABCG1	3.589920406	1
GGATTTACCCATTATTAA	ENSG00000172350	ABCG4	2.64107762	1
GCACCTACAACGTTGCTAA	ENSG00000143921	ABCG8	5.46091243	1
CACTGATAAGAATCTATTA	ENSG00000163686	ABHD6	2.418868622	1
GCCCTTGCCTAGCCCTGAA	ENSG00000114626	ABTB1	2.442866367	1
CTTAATGATGTCACCATTT	ENSG00000188073	AC004878.1	4.868586117	1
CTCATTAACCTGGCCAAGA	ENSG00000105202	AC005393.1	1.997646611	1
GCAAATAAGCTTAGAACAA	ENSG00000224840	AC005702.2	3.08385257	1
CAGCCATGGTCTACGATTA	ENSG00000139088	AC006432.2	2.314133252	1

CTGACAAGAAGAGTTTGAA	ENSG00000242155	AC007379.5	3.415038324	1
GACTTTAAGAAAGAGGCAT	ENSG00000166329	AC007431.1	2.098495802	1
CCACCATTGTCAGTATCCA	ENSG00000223690	AC008040.8	3.262886171	1
GTTATAAATTATTTAGGAA	ENSG00000180747	AC008740.1	3.093287455	1
CGTGGTTTCTCATGCCAAT	ENSG00000103472	AC009093.1	2.047950544	1
CTGTGGAAGTCATTTCTTA	ENSG00000205084	AC009163.1	2.930506006	1
CTTCACAGATGGTGTGAGA	ENSG00000214163	AC009729.1	2.049802413	1
CACTGTAACAGCTTTATAT	ENSG00000213758	AC010326.1	2.055895928	1
CCCTGTATTTACAGATCTT	ENSG00000235364	AC010635.1	2.192068118	1
CAGCAGCTGCTTCCTGTAA	ENSG00000205271	AC010724.1	2.173408785	1
GTGTCTGTTGAGTGATTAA	ENSG00000145832	AC011427.1	2.025454327	1
CAGAGCAACACTCCTCTTT	ENSG00000188666	AC011487.2	5.03002507	1
CTTATTTCTCTGTACACAA	ENSG00000212974	AC012360.3	2.907086242	1
ATCACAAAGTAGTGTTTA	ENSG00000236338	AC015987.1	1.991759214	1
CAGAATTAACAGAATTTAA	ENSG00000225197	AC018445.1	4.328422368	1
CTGTTTGCTGCTAGAGTTA	ENSG00000235978	AC018816.4	2.359191396	1
GACTTGCCCTTTGTGAAATT	ENSG00000141854	AC022098.1	2.121796318	1
GGCTATAAATTACAAACAA	ENSG00000188933	AC022596.6	3.238241996	1
GATCTAAATACTGTGTAA	ENSG00000232521	AC023424.3	4.846272696	1
CAAACCCCTTCTGTTATTTA	ENSG00000105520	AC024575.2	1.968148504	1
CCTGGTAAAGAGGGAGAGA	ENSG00000178412	AC068473.1	5.008282626	1
CCTGAAAGAAGCAGAAGAA	ENSG00000230561	AC068658.1	2.653557338	1
CCATTTCAGAGCATAAGAA	ENSG00000217702	AC073263.3	2.372930992	1
CCTTCTGGAATGAAGAAAT	ENSG00000197041	AC078819.2	2.184852511	1
CTGATAAAGATAAAGGCAT	ENSG00000147642	AC079061.1	4.490590217	1
CATGGATACAGAAACCGAT	ENSG00000227593	AC079322.1	2.459882845	1
ATGTTACTCTTATTTAATA	ENSG00000231228	AC091874.3	2.105536596	1
GGGAGGATTTCCATTATAA	ENSG00000091490	AC092436.3	3.072551928	1
CTGGTTATCCCATATATTA	ENSG00000238222	AC092474.2	1.990869036	1
CAGGCCTCCTGTGTATGAA	ENSG00000180712	AC103540.1	1.964228891	1
GCATCCCTTCATAAGAAT	ENSG00000233726	AC103749.1	2.079793473	1
CAGTGCCTACGCAATTTA	ENSG00000235353	AC104530.1	2.346510925	1
GTCCTCAGCCCTCACAGCA	ENSG00000233362	AC104841.1	2.897087743	1
GCTACATTGTTTATCATT	ENSG00000184115	AC108938.1	2.027365867	1
AGAATTGTTTCCTAAAGAA	ENSG00000157576	AC109993.1	2.689959138	1
CCTTTAATATCTGTTGGGA	ENSG00000176276	AC113404.1	5.325011677	1
GTTTATAGGTGTCCAATAT	ENSG00000232425	AC135983.3	2.902423315	1
GTACTCTAGGCAGACATTA	ENSG00000185520	AC136428.1	2.059992192	1
GCCTCTAATTTGTTTATCT	ENSG00000238035	AC138035.1	3.505785037	1
GCATCAACATCATCAAGAA	ENSG00000167433	AC140658.4	2.297416571	1
GAAGGATACGGACCTCTTA	ENSG00000205918	AC141586.2	19.00432492	1
CAGAGAAGGAGCTGAACCA	ENSG00000244459	AC147067.1	5.454935722	1
CACATGACCTTAAGATTAT	ENSG00000132142	ACACA	2.132755207	1
CTTAGTTCATTTCAGTTTA	ENSG00000078124	ACER3	2.953946122	1
ATGGCTCTGGCTTATTATA	ENSG00000119673	ACOT2	2.335736631	1
CACCAAAGCTTTATTTATA	ENSG00000097021	ACOT7	2.269393741	1
AGATTTGTCCTTTACAGAA	ENSG00000103740	ACSBG1	2.321723749	1
CCCTGCTTGGGATATAGAA	ENSG00000197142	ACSL5	2.486055234	1
CAACCTATCTCAGAAGTTG	ENSG00000115091	ACTR3	2.030466494	1
GTCTTTGGAAGATGTGGAA	ENSG00000101442	ACTR5	2.287529267	1

CAATCTCTATGTTATGTTT	ENSG00000123612	ACVR1C	2.208025447	1
GTCAGTATGGAATCCTTT	ENSG00000137845	ADAM10	11.98892194	1
CCGAATGGAATTTGAAGAA	ENSG00000168594	ADAM29	2.304804703	1
CTAATATGATTTGTAGGAA	ENSG00000196115	ADAM5P	2.576156871	1
GCCACTCCCTCTACTTCAA	ENSG00000138316	ADAMTS14	2.00571928	1
GCCAGATGGAGAACACAAA	ENSG00000078295	ADCY2	3.774899098	1
GGTGCTATCTCCTTCTTCA	ENSG00000129467	ADCY4	2.25082192	1
GGCACTCTCCCTGGTCATA	ENSG00000120907	ADRA1A	3.770663818	1
CCATGAAGTGCCTGGACAA	ENSG00000173020	ADRBK1	2.533849323	1
CTAACATAACCATTCTTAA	ENSG00000198763	AF347015.27	2.994142729	1
GAGAAGAAGAATTACAGAA	ENSG00000081051	AFP	2.917360106	1
CATATTATCCCAGACATGT	ENSG00000157985	AGAP1	3.357116648	1
CACAGTTTACCCTGTTGCT	ENSG00000158669	AGPAT6	2.179684934	1
CCCTCAAGTTCGCAATTAA	ENSG00000153207	AHCTF1	2.724209699	1
CTTTACACTAAGAAATGTA	ENSG00000147853	AK3	4.164974565	1
CTGTTGATTCCGTGGTAAT	ENSG00000127914	AKAP9	2.454973924	1
GTAATTCGATGATGAATTT	ENSG00000105221	AKT2	2.498964844	1
GAAAGTAGAAATATTCTAA	ENSG00000228936	AL021937.2	3.449300944	1
CCGTCTTGGAAGTAAGAT	ENSG00000197657	AL021997.1	2.11229096	1
CTTGAAACTCAGAAGGAT	ENSG00000205562	AL049775.1	2.391589728	1
ACTGTTTAGTCATCAATTA	ENSG00000235194	AL049829.1	2.256740989	1
GAGGAGTAATCTGTTGGAA	ENSG00000215277	AL049829.5	2.033909166	1
CTGTTGGTTGAAATCATAA	ENSG00000233520	AL139812.2	2.415560186	1
GTCAATGGCTGGTAAGCAA	ENSG00000236368	AL159191.1	2.44334144	1
GCTAAACCAGGAATCAGTA	ENSG00000229665	AL353652.1	2.883132355	1
GCAGGATATTCCAAAGTAT	ENSG00000203973	AL356155.1	2.253121021	1
CAATTATAGTCAGATTCTA	ENSG00000228096	AL365202.2	2.662372331	1
AACTGATGGACACAAGCTT	ENSG00000229888	AL590326.1	2.015582354	1
CAAATTAACCTTAGAAGA	ENSG00000137124	ALDH1B1	3.338835779	1
CAGTGTCTCTTAATTCTTA	ENSG00000088035	ALG6	5.00256974	1
GCCTTGCCAGGTACTCATA	ENSG00000116127	ALMS1	2.588138396	1
CCGGCCACCGGCTATAAAT	ENSG00000136383	ALPK3	2.61101087	1
CTCTTAGCATGTTTGATT	ENSG00000166025	AMOTL1	2.295383655	1
CACCCACATGTGTTACCAA	ENSG00000187689	AMTN	1.969575774	1
CAATTTAAATGACACAGAA	ENSG00000116194	ANGPTL1	4.250299249	1
CTGAGAAGAACTACATATA	ENSG00000132855	ANGPTL3	3.095461273	1
CACATAAACCCAGCAAATA	ENSG00000131503	ANKHD1	2.922585568	1
CTATTCATGCCATTTGAAA	ENSG00000183831	ANKRD45	2.857010621	1
GCTGACAAATCAACACGTA	ENSG00000163516	ANKZF1	2.622586715	1
CTCATCCCATCTTCTGTAA	ENSG00000047617	ANO2	2.113676386	1
GCCTCTCATACTTAATGAA	ENSG00000143401	ANP32E	2.094470622	1
ACTATCTAATCAGCAATTA	ENSG00000109511	ANXA10	2.124760495	1
CCAGGATTGTGAGGACTAT	ENSG00000104537	ANXA13	2.452612767	1
CCTCCAAACAGAGCAACAA	ENSG00000240112	AP000346.2	2.101420838	1
GTCTGCATGGAGAGGATCA	ENSG00000212712	AP002414.3	2.77181311	1
GCTAATGTCTCTAACTGAT	ENSG00000196763	AP002490.2	2.010963323	1
GAGAAGAATGCCATGCTCA	ENSG00000230586	AP002985.1	2.924086491	1
CTGTTAATAACGCAATTAT	ENSG00000180543	AP003115.1	3.817674206	1
ACGTATTGGTTCTTTATTA	ENSG00000204449	AP004607.1	2.014973311	1
CTCATCACACTGGAGCTGA	ENSG00000106367	AP1S1	1.998593662	1

CATATGAAGATGATTATTA	ENSG00000081014	AP4E1	3.191065228	1
CACAGCGACGCCTATGTCA	ENSG00000221838	AP4M1	3.714951368	1
CACCTCTGCTGTATTGATA	ENSG00000166313	APBB1	2.982026025	1
CTCATCAGGTATTGCTGAA	ENSG00000132703	APCS	2.461266915	1
GTGCCTTTACTATTAGAAA	ENSG00000138613	APH1B	4.904889128	1
CTAAACGTAATTATTATTT	ENSG00000149089	APIP	3.731690916	1
CTGCCTAAATATTATATAT	ENSG00000239713	APOBEC3G	6.436077766	1
CCGCATCAAACAGAGTGAA	ENSG00000130208	APOC1	2.394721269	1
CAAGCCAGATGATTTACCA	ENSG00000091583	APOH	2.144594632	1
GTTCTTCTATTTACTTTGT	ENSG00000101246	ARFRP1	5.062677388	1
GCATAAAGAACGTACTTCT	ENSG00000186103	ARGFX	2.313696291	1
CTGCTTATACAATTTCTGA	ENSG00000137727	ARHGAP20	1.973479273	1
GACAGCAAGCTCAATTATA	ENSG00000111348	ARHGDIB	2.452095514	1
CCACCGATCACAAGCCTT	ENSG00000076928	ARHGEF1	2.357329056	1
CCATGTTTATCATCAGTGT	ENSG00000104880	ARHGEF18	1.966336811	1
CTCAGATTCTGAAAGTCAT	ENSG00000102606	ARHGEF7	2.157264527	1
CTCATTTTCATGGAGATGAA	ENSG00000049618	ARID1B	2.129257356	1
CCTTGTGGAAGATGAGTAA	ENSG00000122644	ARL4A	3.49447658	1
GTATATCTGTCCCTATTAA	ENSG00000170540	ARL6IP1	2.296872259	1
GTATTAAGATACAGATTAA	ENSG00000177917	ARL6IP6	2.490070731	1
GCTGTTAGATTATATAGAA	ENSG00000118690	ARMC2	2.331885537	1
GGACTCAGCATTTCTGATA	ENSG00000105643	ARRDC2	2.569351483	1
GCGTGTCAACCTGGAACAA	ENSG00000157399	ARSE	2.155720134	1
CAGATAATGCATTTGATGA	ENSG00000156219	ART3	2.291957423	1
CCAGGTAAGCGCTCATAAT	ENSG00000173409	ARV1	2.043774918	1
GGCTACAGTAGCTCTGAAA	ENSG00000177981	ASB8	2.02025101	1
CAGAGCAGGTGATCAACAA	ENSG00000100325	ASCC2	2.645573119	1
GACTTGAAC TTATTGAGAA	ENSG00000112249	ASCC3	2.656871943	1
CACCTCTCCTTTAATTTAT	ENSG00000141505	ASGR1	2.715612911	1
CCAGAAATTTCCCTTCAAT	ENSG00000070669	ASNS	4.513928546	1
CAAATGAAGCCAAACTGTA	ENSG00000138381	ASNSD1	2.918358599	1
CGGACTCCATTCTGGTTAA	ENSG00000143970	ASXL2	2.254436952	1
CGAACTACACCTTCAGCTA	ENSG00000123268	ATF1	3.402480989	1
CAGTATTTCAAATTGTGAA	ENSG00000166669	ATF7IP2	2.016662346	1
CAGAGAACAGGAGAGGGAT	ENSG00000142102	ATHL1	2.409223424	1
CTGCATATAGGGTATGGAA	ENSG00000119787	ATL2	2.002854851	1
CTTATACGTTTCCATTGAA	ENSG00000206190	ATP10A	4.980972937	1
GGTACAAACTGCTTCATAT	ENSG00000058063	ATP11B	2.123330002	1
CTGACGATAGGGACATCAA	ENSG00000159363	ATP13A2	3.372134319	1
CTTGATGAAC TTCATCGTA	ENSG00000163399	ATP1A1	2.151585971	1
GTGCTATTTACTACTTTAA	ENSG00000174437	ATP2A2	2.090737638	1
CCGACTGGGACAACGAGAA	ENSG00000067842	ATP2B3	1.990299116	1
GCTGTTCCATGGGAGAGTA	ENSG00000152234	ATP5A1	2.951764259	1
CAGCTCTTCTCCTATGCCA	ENSG00000159199	ATP5G1	2.028781006	1
GCCAGATAAGTATGGCCAT	ENSG00000105341	ATP5SL	4.005664033	1
GGGCTAATATGGATACTAA	ENSG00000182220	ATP6AP2	4.686395762	1
CTTTGCAGGAAATATTTAA	ENSG00000114573	ATP6V1A	2.443111021	1
CTTAGCACAGCTCTAGTTA	ENSG00000136888	ATP6V1G1	2.164023842	1
CAGTGAATGTAGGAGATGA	ENSG00000171953	ATPAF2	2.904066984	1
CGCTGCCTCATGGAGGGAA	ENSG00000172508	ATPGD1	2.670951791	1

CCACCTCATTGTCTTTAT	ENSG00000105146	AURKC	4.019043342	1
CCCTGATTATTTGGTTT	ENSG00000105778	AVL9	2.041423134	1
GTTTCAATATTTAAGATTT	ENSG00000163512	AZI2	2.525490709	1
GATCTGGTGTTAAGATAAT	ENSG00000155096	AZIN1	2.46343551	1
ACATGTTCAATCAATGTTGA	ENSG00000183778	B3GALT5	3.290260347	1
GTATTTAATTTGCTTTCAA	ENSG00000109956	B3GAT1	5.264949161	1
CCTGTACCTACAGGCCATA	ENSG00000027847	B4GALT7	3.135762006	1
GCTTTGGAAGTGAAGTGA	ENSG00000130723	BAT2L	2.065768685	1
CTGATGATGTGAGAAGAGT	ENSG00000156127	BATF	3.189203459	1
GCAATGGCACTCTTTCAA	ENSG00000198604	BAZ1A	2.55603047	1
GTTACAATTGCATATTGAA	ENSG00000163093	BBS5	2.022476542	1
GAACCAATGTCAGATGAAA	ENSG00000122507	BBS9	3.839574299	1
CAATGTAGAGAAGAATGAA	ENSG00000145734	BDP1	2.048816852	1
CAGTGTATTTGTTTATGGA	ENSG00000105829	BET1	2.405581048	1
CGAATTAATAACACAGTAA	ENSG00000173626	BET3L	2.793591919	1
CTGCTTTCTAAATTCGCAT	ENSG00000184515	BEX5	2.133371887	1
CAGGAGTTCCTATAGGCTA	ENSG00000198908	BHLHB9	2.294824192	1
CATCAGATGATTTGTCATT	ENSG00000110330	BIRC2	2.637415329	1
CAGTAGCCTTGATAGATTA	ENSG00000115760	BIRC6	1.999114522	1
CTTCCTATGATATTGATAA	ENSG00000197299	BLM	3.602567672	1
GGAGATTCTTCTTTAATTT	ENSG00000125845	BMP2	4.588520544	1
CCGTCTTGCTCATTCTGTT	ENSG00000204217	BMPR2	2.248829077	1
CTCATCCTCATACAACCAT	ENSG00000176720	BOK	2.527409933	1
GAGTTATTAACCAGCCATA	ENSG00000162813	BPNT1	2.153623834	1
CGCTATCCTGCCAACTCTA	ENSG00000164713	BRI3	2.259109808	1
CTGAGTCACAGATTTTATT	ENSG00000060762	BRP44L	2.213371103	1
CATGTAGAACTGAATGTTA	ENSG00000189195	BTBD8	2.477182945	1
GAGCGTATGTAAGTTATTT	ENSG00000154640	BTG3	2.11990218	1
ATGGTGGATTTATTACTAT	ENSG00000154473	BUB3	3.84541738	1
CACAATATTGGATACGGAA	ENSG00000183346	C10orf107	2.30695959	1
CCCAGCAGCGGCAACATGA	ENSG00000166272	C10orf26	2.046037705	1
AAGCTCAAGTCCTCCAGAT	ENSG00000166220	C10orf27	2.194006795	1
CAGCTTCATTCCTCAGAGT	ENSG00000166024	C10orf28	2.297536995	1
CTCTGCCAATTCAGTTTAT	ENSG00000151893	C10orf46	7.972960082	1
GTGTGGCATTCTTACTTAA	ENSG00000178645	C10orf53	4.048080219	1
GAAATTACAGACTTTAATA	ENSG00000182645	C10orf96	2.645356359	1
CACTGTATGATTCTCTTAA	ENSG00000166452	C11orf17	4.59269948	1
CGCTTAGTCTTTGTATTAA	ENSG00000110696	C11orf58	2.030643063	1
CTCCTTACAAGTACCTGAA	ENSG00000166268	C12orf28	1.999162322	1
GTATCCTCCCGGATTGATA	ENSG00000111300	C12orf30	3.366749788	1
GTTGTATATTGATCAGTTT	ENSG00000139620	C12orf41	3.00586845	1
GCAGCACAGTGCTAATCTA	ENSG00000165685	C12orf59	2.476201547	1
GGATTGTGAAGCTTTATAA	ENSG00000165899	C12orf64	2.508259383	1
CAGATATCTTAGCTAAGAA	ENSG00000102445	C13orf18	3.000752566	1
CCTATTCAGGCTAGTGCAA	ENSG00000136122	C13orf34	7.132481632	1
CTGTATTCTTACTGAGAAA	ENSG00000197595	C13orf35	2.046824575	1
CCATGACTCTCTACAATGA	ENSG00000179933	C14orf119	2.104836758	1
ACTCCGGAGTCAACGTTTA	ENSG00000100629	C14orf145	3.178164937	1
CTGGTAATGCTTAAGGCAA	ENSG00000087302	C14orf166	2.001613597	1
CTTAGTCTATTTATACTAA	ENSG00000176438	C14orf49	2.910214152	1

CCCTAAGTAACCTGGTACA	ENSG00000165807	C14orf50	2.159405039	1
GTTATTTTCCTTAAGTCTTT	ENSG00000134152	C15orf29	2.528173152	1
GTCTCATAGATTTAAACAA	ENSG00000138614	C15orf44	1.973774529	1
AGCTAAACGTTAAGATGTA	ENSG00000167523	C16orf55	1.993581621	1
CAGTTCATCCTCAAGGGTA	ENSG00000167861	C17orf28	2.571811867	1
GCTATTATTTGAATGTAA	ENSG00000212719	C17orf51	1.960152874	1
GATATATTGACAATTCCTA	ENSG00000178852	C17orf57	2.302323028	1
GCCACTCTGGGCTGGGTTA	ENSG00000205544	C17orf61	2.099376955	1
CACAACTCATTTGACCTTT	ENSG00000170291	C17orf81	2.084576167	1
GGGAGAAGAAATCAGGTAA	ENSG00000074356	C17orf85	2.396963074	1
CCAAAGGTGGACTTCAGAA	ENSG00000141428	C18orf21	2.405884582	1
CTTCCTGTATAGACACTAA	ENSG00000214046	C19orf42	2.380611429	1
CTCAATGTCTCCAGAAGA	ENSG00000105393	C19orf62	6.867178018	1
CTCCCTGTAAGTCTATTTA	ENSG00000161671	C19orf63	3.069533419	1
ATGATGACATCCCAACAGA	ENSG00000180999	C1orf105	2.696998395	1
CGTTATCCATCTACCAGAT	ENSG00000116922	C1orf109	2.963334917	1
GAAGTAAGGAGATATATTA	ENSG00000117477	C1orf114	1.999289763	1
GTAAGAGTGTTTAGTAAT	ENSG00000163875	C1orf149	2.17674036	1
CCTTTATCTTCCTCATCAT	ENSG00000143110	C1orf162	2.186271843	1
CCCTCTGACTTACATAATC	ENSG00000162377	C1orf163	4.395743212	1
GGGACCCTTTCTATTCTAA	ENSG00000162398	C1orf177	2.251417468	1
CAGTCAAATGGTAAGATGT	ENSG00000197852	C1orf183	3.048919791	1
CATTTTCATTAGAAGAGGGT	ENSG00000204006	C1orf185	2.90509276	1
CTCCACCTCCCATAACCAG	ENSG00000239887	C1orf226	2.248277836	1
CTATATGACTGACTCATGT	ENSG00000198520	C1orf228	2.624784926	1
CACATGAGGAGATGTCAGT	ENSG00000143443	C1orf56	3.633135482	1
CTCAAGTTCTTCTTACATA	ENSG00000162641	C1orf62	3.396566227	1
CGAATGGAGCTGTTAGAAA	ENSG00000117616	C1orf63	2.546840132	1
CTCAGTAAATGATCATCTC	ENSG00000162757	C1orf74	2.195526274	1
GAGATGAAGTCTATATCAA	ENSG00000165985	C1QL1	2.191979815	1
CTCTTTGAAACTAAGTAAA	ENSG00000082196	C1QTNF3	2.883741179	1
CCCACTATAGACATCGAAA	ENSG00000184471	C1QTNF8	2.981951383	1
CTCGTAATGACCCTGAAGA	ENSG00000197183	C20orf112	2.222078917	1
CTCAAACCTGACCATACTAA	ENSG00000101331	C20orf160	2.353654014	1
CAATTTAATGCATTGCTGA	ENSG00000176659	C20orf197	2.665086433	1
GCCAGTATTTCCCATAGTA	ENSG00000174403	C20orf200	4.873750152	1
CTAATTAGGACAAGCTCTA	ENSG00000089063	C20orf30	2.420598301	1
CTGAGTAATTGAATCATGA	ENSG00000101276	C20orf54	2.043274306	1
AGTGTTCAATCCTCTCTAA	ENSG00000188559	C20orf74	2.278130816	1
CACATAAGAAAGTTAACAA	ENSG00000180777	C21orf110	4.177937506	1
GCTCTAGTATAACAATGAT	ENSG00000232560	C21orf37	2.825289692	1
GTCTTGAAAGCATTACAAA	ENSG00000159055	C21orf45	2.801868689	1
CTCATCAACACCTACGGAA	ENSG00000160284	C21orf56	3.687720026	1
CTGTTATATATAGCATATT	ENSG00000242259	C22orf39	2.342773281	1
GGGAGTCCTTACTGAATAT	ENSG00000144406	C2orf21	2.643268548	1
GGGATAGTAACACATTCAA	ENSG00000197927	C2orf27A	2.685866157	1
CTCATGCTTTCATCACCCA	ENSG00000118961	C2orf43	2.533818218	1
CTCTCCATGTGGTGCATGT	ENSG00000172478	C2orf54	3.169296064	1
CAAAGAGTGAAATATGTAA	ENSG00000174928	C3orf33	3.442447582	1
GTTCTTAATTACTAACATG	ENSG00000214097	C3orf43	2.148843321	1

CTATGTCTGATTTGCAAAT	ENSG00000198284	C3orf46	6.560398938	1
CCCACAGTCTATATATGA	ENSG00000187068	C3orf70	2.444826571	1
CCATGGGCATTATAAACAA	ENSG00000123838	C4BPA	3.504064481	1
GTGAGGAAGAAGAAAGGAA	ENSG00000084092	C4orf14	3.93927456	1
CTGAACATCTGTGGAATAA	ENSG00000164074	C4orf29	3.250497045	1
CAATGTCTAGGACCAGATA	ENSG00000173376	C4orf31	2.966990794	1
CATTTATCATCAACACAGT	ENSG00000204709	C6orf100	2.833256759	1
CTGTGTAATTTAACTTGTA	ENSG00000204564	C6orf136	2.579620935	1
ATATTACTTTGTGAAATTT	ENSG00000164430	C6orf150	3.409071552	1
CCCTTTAGTAAAGACATTA	ENSG00000203871	C6orf164	2.459680141	1
CAGTCTTTCCTGACCAATA	ENSG00000112167	C6orf64	3.587939334	1
GCAGTCAGATATGAACAAT	ENSG00000175600	C7orf10	2.185572035	1
CAGATACTCTAAATGTGAA	ENSG00000106341	C7orf16	4.064784054	1
CACAGCTTTATTTACTGTA	ENSG00000239857	C7orf20	2.051466458	1
CCTCTGCAGACCAGAATCA	ENSG00000165131	C7orf34	3.778337274	1
CCCTACATCAGGAATTTCA	ENSG00000164898	C7orf55	1.97150396	1
CAAATAAAGTCACAGATAT	ENSG00000164746	C7orf57	2.002639912	1
GAAATGGGAAATTAAGGAA	ENSG00000205174	C7orf66	2.395805368	1
CATCCAGAAGCATGTGATA	ENSG00000135245	C7orf68	1.998336003	1
GAATTTGAGAAAGCATCTA	ENSG00000165084	C8orf34	1.991564993	1
CCTACAGCTAATGGTGTTA	ENSG00000177459	C8orf47	2.236356711	1
CATACTAGATTCTAAATGT	ENSG00000148057	C9orf103	2.047511945	1
CAATTATTATAAAGATATA	ENSG00000120160	C9orf11	4.708760687	1
GATCCTGAGAGAGAAATTT	ENSG00000158122	C9orf21	2.629062331	1
CAGTGATTAAGGAATCCAT	ENSG00000204173	C9orf29	3.772699328	1
GATTCTCTTCAGACAAGAA	ENSG00000136805	C9orf4	2.997472676	1
CAGGGATCTTCATTCCAAA	ENSG00000135063	C9orf61	4.593376952	1
GAGGTTATAGGAAATTGAT	ENSG00000165118	C9orf64	3.075233202	1
CATTATAACTCAGACCTTT	ENSG00000074410	CA12	2.419763959	1
CTGGATATGTTGAAGGGTA	ENSG00000135932	CAB39	2.142092245	1
CACCGACTTTGATACTGTC	ENSG00000100314	CABP7	2.096776843	1
GACTAAATCTACAAGTGAT	ENSG00000006116	CACNG3	2.91608746	1
GACATTATATGTGACTTAA	ENSG00000116161	CACYBP	2.166764106	1
AGCACAATGTTATAAGGAA	ENSG00000175161	CADM2	2.051291036	1
CATGTATATTATCACTATA	ENSG00000122786	CALD1	4.411968335	1
CATGCAACCCAATAGCATA	ENSG00000164615	CAMLG	2.168543368	1
GGCTCTGAGAAATAAACTA	ENSG00000164047	CAMP	2.150826295	1
GAAATTGCAGCTTATTTAA	ENSG00000171735	CAMTA1	2.375516179	1
CAGATCTTCTTTATAACTA	ENSG00000142330	CAPN10	3.962426756	1
GAATTTATGAAAGGGTTAA	ENSG00000152611	CAPSL	3.598971954	1
CTGCGTCAGTGTAAGGTCA	ENSG00000198286	CARD11	3.198094536	1
CCAACTCTGACATTTGGAT	ENSG00000105483	CARD8	2.370958225	1
CTCATCAAATGTTTACCCA	ENSG00000137757	CASP5	1.982788225	1
GATATTTACTGCTCTTTAT	ENSG00000165806	CASP7	2.272636705	1
CACTCTCTCTAATCCTGTA	ENSG00000143318	CASQ1	2.713384148	1
GGAATAAGCTTGAAAGAAA	ENSG00000078699	CBFA2T2	3.367889436	1
CTGACAAAGTTTACAGTTA	ENSG00000067955	CBFB	2.398478237	1
CGTACTATCTTGTCAGAT	ENSG00000110395	CBL	2.713989257	1
GTGCTTCTGTTATTCAGAA	ENSG00000145439	CBR4	2.471347198	1
CAGATGCCATTCTCATTA	ENSG00000172785	CBWD1	6.087630441	1

GTGAGCTTGGCATAGTGAT	ENSG00000141570	CBX8	2.846926729	1
CTCCCTCCACCATGTGCCT	ENSG00000181378	CCDC108	6.837367807	1
GAGAGAATTAAGAATCTGT	ENSG00000159873	CCDC117	2.801637087	1
CTCCAGATATGCAGAACAA	ENSG00000176714	CCDC121	3.306973943	1
GACACAAGTTCATTAGCTG	ENSG00000151773	CCDC122	2.478495969	1
GGAATAGAAATTTTCATTAA	ENSG00000159214	CCDC24	2.643111164	1
CTGAATGAATGATCTGTAA	ENSG00000147419	CCDC25	2.039368258	1
GAGACATAATCAGCCTATA	ENSG00000186409	CCDC30	2.460189842	1
CTCCAAGTCTGCAAATCTA	ENSG00000109881	CCDC34	3.092399023	1
GTACCAGACCTCATAGTTA	ENSG00000141325	CCDC45	3.097691002	1
GACTTCTAATGGCTGAAGA	ENSG00000152492	CCDC50	4.691076823	1
CAGAATTTACTCTTAATAA	ENSG00000165325	CCDC67	2.004258783	1
CTTCAAGACAGACCCTGAA	ENSG00000105248	CCDC94	2.149247168	1
CAGTCTATCATTTGGTCAT	ENSG00000142039	CCDC97	2.369341636	1
CAAAGTGTCAAGAAATAA	ENSG00000110148	CCKBR	2.22151566	1
GAATTTGGAGTAGTTTCAA	ENSG00000112237	CCNC	4.567577553	1
GTTCCATTTGCCATGGTTA	ENSG00000105173	CCNE1	3.4496786	1
GGATGTTCTCATCTGAAA	ENSG00000118816	CCNI	4.41458501	1
CTACCTCAACCAATGCCAA	ENSG00000126353	CCR7	2.177520585	1
CAGTCAACAGATTATTATT	ENSG00000129048	CCRL1	2.329718893	1
CCTGCCAGCTGATGAGACA	ENSG00000121797	CCRL2	2.846599289	1
GTAATACAATGAACCTTTA	ENSG00000186074	CD300LF	2.009313105	1
CCCAGTCAATCAAAGGAAA	ENSG00000160654	CD3G	1.968555582	1
CTGTTAACTGCCTATTTAT	ENSG00000102245	CD40LG	3.040163279	1
GATTTATTGTGGTGACAAT	ENSG00000117335	CD46	2.565676613	1
CTCCCTATTCTGTTATTTT	ENSG00000073754	CD5L	2.966604246	1
CTCTTGAGAATTAAAGGAA	ENSG00000013725	CD6	2.012484912	1
CTCTCCGAGTCCTAGCCCA	ENSG00000129226	CD68	2.08015481	1
CTCATTAAAGAGTTTGTTA	ENSG00000164045	CDC25A	3.658816914	1
CTGCCACTCTGGACCTAAT	ENSG00000128283	CDC42EP1	3.778781507	1
CAGATCAAATTACTCATTA	ENSG00000093009	CDC45L	3.047152056	1
CATCAAGTCTGGAGAAAGA	ENSG00000163814	CDCP1	2.298312544	1
CTGTTGGTGTCTTTATTAT	ENSG00000039068	CDH1	4.638708455	1
CAGATCTATTTACTTGATA	ENSG00000170558	CDH2	2.676449351	1
CCTTCAATATCCTGGTTAT	ENSG00000107736	CDH23	2.714939891	1
CCTGAACATTCAACATTAA	ENSG00000132964	CDK8	3.479471608	1
ATTATGATGTGTTTAGGTA	ENSG00000138769	CDKL2	2.144842179	1
CCAATATTGCAGAACAGTA	ENSG00000205111	CDKL4	2.382766601	1
CTGTGTACATAACTCTGTA	ENSG00000111276	CDKN1B	2.368456751	1
CACGTGCTATCCAGTAATA	ENSG00000129596	CDO1	5.076058014	1
CTCTGAGTTCAAAGCCAAA	ENSG00000109089	CDR2L	2.057738134	1
CTGATTAGAGCCTTGACTA	ENSG00000101290	CDS2	2.462792434	1
GAGTGTATCTGCTATTCCCT	ENSG00000213822	CEACAM18	2.510504307	1
CAAATAATAACGGGACCTA	ENSG00000105388	CEACAM5	2.220826529	1
CCGTCAAGTGTCTCTAAGAT	ENSG00000215704	CELA2B	2.036227822	1
CTCACCGGCCCATCATTAA	ENSG00000075275	CELSR1	2.098844116	1
CTATTAGAGCTAAATAAAT	ENSG00000153044	CENPH	6.896267112	1
CTGATAGTTCACTAAATAA	ENSG00000198707	CEP290	1.974368315	1
GTGAACCTTTGGTTTCTTA	ENSG00000135837	CEP350	3.092359924	1
GGCAATTTAAGAAAGATAT	ENSG00000011523	CEP68	2.136636694	1

CTGAGCACCTGCTGGTGGA	ENSG00000087237	CETP	3.029734006	1
ACCTTGACTTCATTGTCTA	ENSG00000070748	CHAT	4.255487257	1
CCAATAAACCTCTCATTCT	ENSG00000172586	CHCHD1	2.816900235	1
GTCTTGACATCTTGACATA	ENSG00000163528	CHCHD4	6.418948526	1
GCAGTATTCTCGATATCCT	ENSG00000171316	CHD7	3.183923211	1
CCATAAAGATCATCAGCAA	ENSG00000183765	CHEK2	3.197257245	1
CCAGATTGTGGTTTAGGAA	ENSG00000188419	CHM	4.145483361	1
GCTTTATAATTATATTGAA	ENSG00000164695	CHMP4C	2.347299251	1
CAGAACAGAGCTTGAAGAT	ENSG00000101938	CHRD1	2.798845204	1
CTGATAAGGACACTTCCAA	ENSG00000180720	CHRM4	2.252937779	1
CTGATTCTGGTTTGATAT	ENSG00000184984	CHRM5	2.181596248	1
CGTCCGTGGTCAAGGACAA	ENSG00000101204	CHRNA4	3.690741441	1
CTCCTCATGAGGCCCATTA	ENSG00000127586	CHTF18	3.433229132	1
CAGCTTCAACTGTACTTCA	ENSG00000138615	CILP	1.983341966	1
GCGAGATTATGGAGTATGA	ENSG00000141076	CIRH1A	2.006581198	1
CTTTAACTCATACTGAA	ENSG00000171365	CLCN5	2.473939117	1
CCAATATAATCATCAGAGA	ENSG00000156282	CLDN17	3.771403422	1
CTTCTTGTCTAGATGCAAT	ENSG00000038532	CLEC16A	4.094710662	1
GGCTGTATTTGTTGAGTAT	ENSG00000090269	CLEC5A	4.616889462	1
CATCTCAATTTACTTATCA	ENSG00000184293	CLECL1	2.298177893	1
CTGATGATTTGATTCTGGA	ENSG00000153132	CLGN	2.213318236	1
CTCTCTATTCTAGTTGATA	ENSG00000169504	CLIC4	2.031460631	1
CACGTAGAAAGTTCACTAT	ENSG00000165959	CLMN	1.982865959	1
CTGTTTAGGATCTTCATCA	ENSG00000104853	CLPTM1	2.958021217	1
CAGTAATTTATTTATATTA	ENSG00000134326	CMPK2	5.963867025	1
GATCTCTTCTTCTACTAAA	ENSG00000164309	CMYA5	5.393185393	1
GTCAGTATTTAATGTATTT	ENSG00000119946	CNNM1	3.416322006	1
CAGTCCAATATTGTAGATA	ENSG00000158158	CNNM4	2.156970234	1
GTCAGATTTAGAGGAAATA	ENSG00000044459	CNTLN	2.166967206	1
GTAATATTGTTGTTCAAGT	ENSG00000144619	CNTN4	3.128023224	1
GATAGTAATTGTTGAGGAA	ENSG00000149972	CNTN5	4.045934753	1
CCAGCAAGAGCACCAGCTT	ENSG00000170037	CNTROB	4.248171636	1
CCAAGCACCTGGGCGTCAA	ENSG00000142156	COL6A1	2.238218792	1
CTTATCCTGTGTACCAAGA	ENSG00000169019	COMMD8	1.993272134	1
CTATGCTGTTTCATGGCAAT	ENSG00000122218	COPA	2.182696748	1
CAAGATTCTTTATCTCATA	ENSG00000181789	COPG	2.034237351	1
CAACCTTATAAACATGATA	ENSG00000168090	COPS6	2.614489119	1
CTGTGCCTTGGGATATGAT	ENSG00000119723	COQ6	2.89513602	1
GGCAATGACTTATATTCAA	ENSG00000110880	CORO1C	2.423666495	1
CGGAATAGATTTATTAGAA	ENSG00000103647	CORO2B	2.756769164	1
CCGCACCTGCCTTGGATGT	ENSG00000103426	CORO7	2.724606574	1
CTTTGAGGGTCTTTATACA	ENSG00000006695	COX10	2.000488892	1
CAGTTACTTGCTTATTTAA	ENSG00000163626	COX18	5.231150177	1
CATGCAGACGGTTAAATGA	ENSG00000178741	COX5A	2.019167303	1
CAGAAGAGACGCAGTTATA	ENSG00000178773	CPNE7	4.738078482	1
CAATCTCAAGCAGTGCTAT	ENSG00000111605	CPSF6	3.583245713	1
CCCTAAAGCATTTGATACA	ENSG00000169372	CRADD	2.138858445	1
AGACCACTTCTGCAAATGA	ENSG00000130545	CRB3	2.564373885	1
GGAGTGACTTCCAGAAATA	ENSG00000143578	CREB3L4	4.93873082	1
CAAATATTTAGCTTCCAAA	ENSG00000111269	CREBL2	2.267157821	1

CCGGACTTACCCTTTAAAT	ENSG00000184164	CRELD2	3.954269921	1
GATATCGTGGGTATCAGTA	ENSG00000108255	CRYBA1	2.258474427	1
CTACCAAGGTCAACAATAC	ENSG00000163254	CRYGC	1.984841723	1
ATGTTTACTGTTATTCTTT	ENSG00000060138	CSDAP1	1.963564559	1
GAATGTCTTTAATGAAACA	ENSG00000184371	CSF1	3.098090672	1
GCGTTGATGTTAACTTTGA	ENSG00000182578	CSF1R	4.064295903	1
CATGTATTTATCTCTATTT	ENSG00000108342	CSF3	4.323605628	1
CAGAATTTGCGATGTACTT	ENSG00000113712	CSNK1A1	2.764201982	1
AAGTTATTCACATTATAGA	ENSG00000151292	CSNK1G3	3.06351221	1
CTCATCTTCTGGTGAGTTC	ENSG00000178662	CSRNP3	2.244460452	1
GGAATTGTAACACATATCA	ENSG00000224089	CT47A11	1.999966488	1
CAGAATTATATAGATCAGT	ENSG00000212710	CTAGE1	5.024356192	1
CTGAACACCCTGCTCTACA	ENSG00000175029	CTBP2	2.310305648	1
CCCATGATATTTCTAATAA	ENSG00000124092	CTCFL	6.068337511	1
CTCACAAATTGGTGTTCTA	ENSG00000235552	CTD-2124B20.1	2.165121133	1
GAACTATATAAAGGACTT	ENSG00000137770	CTDSPL2	2.4378952	1
GCTTATTAATCATAAAGAT	ENSG00000119326	CTNNAL1	3.038971198	1
CCAAGTGCGCTTTGCAATA	ENSG00000178585	CTNNBIP1	5.361197617	1
GAACCTCAAGTGTTGTTA	ENSG00000171793	CTPS	3.0100379	1
CCATTCTGTTGCTATTGA	ENSG00000135047	CTSL1	3.795926638	1
GTTATTAACCTTTTGTTTC	ENSG00000108094	CUL2	2.80212479	1
CTGAATATCTACATCATGT	ENSG00000158290	CUL4B	3.489617816	1
CAGATGACCCTCTAACAGA	ENSG00000150316	CWC15	2.007565274	1
CTTTCATGTAGTTTGTA	ENSG00000168329	CX3CR1	2.266891689	1
GTCCTATTATATTCATTCT	ENSG00000163739	CXCL1	4.596433511	1
GACTGCTAGTTTATATAGA	ENSG00000163735	CXCL5	5.117429896	1
CATGCAAGATTATGTACAA	ENSG00000165182	CXorf58	2.390364896	1
CGGACCATGTCTTAGGGCT	ENSG00000166394	CYB5R2	5.765450525	1
CTCAAATAATGCTAATTGA	ENSG00000165168	CYBB	2.791013389	1
CATAGAATTACAAGCTGTA	ENSG00000155833	CYLC2	2.433904041	1
GAACAGTGCTCATGCTAAA	ENSG00000019186	CYP24A1	2.410766366	1
CAGCTTATCTAACATGTCA	ENSG00000095596	CYP26A1	2.869438715	1
GTACCATGATCCTGACCAA	ENSG00000134716	CYP2J2	2.282004724	1
AGCTAGATCTGTTTCTATA	ENSG00000186377	CYP4X1	2.964295463	1
CAGTTTATCTCTGAACTA	ENSG00000126733	DACH2	2.852964854	1
CCACGAGTATCCACACCAA	ENSG00000173402	DAG1	2.734214673	1
GCCTGGCACACAAGGGTAT	ENSG00000164535	DAGLB	2.815825997	1
CCTTACATTTCCATATTTA	ENSG00000112977	DAP	3.677619315	1
GAGTTGAATTTAAGAATAT	ENSG00000035664	DAPK2	3.215418096	1
GTAATTGTTTCCTGAGAAT	ENSG00000006634	DBF4	2.137275788	1
GGAGGAAGCTGGGAAATAA	ENSG00000109851	DBX1	2.558471245	1
GAAAGTTATTTGAGTTAAA	ENSG00000119599	DCAF4	3.537129045	1
GTTCTTAAGTGTTACACA	ENSG00000182308	DCAF4L1	1.996530256	1
CAAATAGTGATGAAGGCAT	ENSG00000146038	DCDC2	5.081553846	1
GCTACAATAACAGAACGAT	ENSG00000133083	DCLK1	3.720352739	1
GTCTTAAAGTTCTTTGGTC	ENSG00000172795	DCP2	1.981275152	1
GTGTTTCCCTGTTGTACCT	ENSG00000179958	DCTPP1	2.133648658	1
GTTGAGAATTTCTTCTGTA	ENSG00000100523	DDHD1	2.206616356	1
CACCTACTGTCAGACTATT	ENSG00000085788	DDHD2	2.149093283	1
GGAAGCATATGCCCATTA	ENSG00000181418	DDN	2.281620348	1

GGAAGAATATTTAATTACT	ENSG00000088205	DDX18	2.539196351	1
CAGGACCGGTTTGAAGTTA	ENSG00000123136	DDX39	1.987911024	1
CCATCTTGAGTCAGATTTA	ENSG00000215301	DDX3X	2.418623341	1
CAGCGCATAGAACACTTAA	ENSG00000213782	DDX47	8.669230288	1
CAAGGCAGATGAGAAATTT	ENSG00000111364	DDX55	2.014868077	1
CTGGCAGATTACACGACAA	ENSG00000119522	DENND1A	3.520572096	1
CCCACCCTCTCGAAAGAAT	ENSG00000172893	DHCR7	2.566189258	1
GGCACATCATTAACATCAA	ENSG00000108272	DHRS11	2.920474613	1
CAGGTTGCATGGTCAATAA	ENSG00000102796	DHRS12	2.800731559	1
CCTAGAGAATGGCAATTTA	ENSG00000100612	DHRS7	2.156717117	1
CAGCTGAATCCAGAGAGTA	ENSG00000132153	DHX30	2.300834096	1
CAGAGACTTTGTAACTAT	ENSG00000135829	DHX9	2.183001422	1
CACTGCACCCTGTTTAACA	ENSG00000184047	DIABLO	2.640917353	1
CCAAGGAGCTTAATTATAA	ENSG00000139734	DIAPH3	3.227673318	1
GACAGGATGCCAATTGTTA	ENSG00000166938	DIS3L	2.361626682	1
GAATTTACCTGCAATTAAA	ENSG00000154309	DISP1	2.435557681	1
GAAACTCTCTGATGTCAGT	ENSG00000150764	DIXDC1	3.350861347	1
CGGTGATGAAGCTAGAAAT	ENSG00000164741	DLC1	2.940720924	1
CACATGCTGCGGAAGAAGA	ENSG00000185559	DLK1	2.20369976	1
CTCACACCAGAAATATTAT	ENSG00000171462	DLK2	3.348916648	1
CGCTTCAATGGCAAGGGAA	ENSG00000144355	DLX1	3.366676243	1
GCCATAAATCTCTTTAAAT	ENSG00000197653	DNAH10	3.975836918	1
CATGTTATTTAATAGTGAA	ENSG00000185842	DNAH14	3.536971908	1
GTGGAGAAAGTTACAAATA	ENSG00000116138	DNAJC16	2.087059864	1
GAAAGAGCATGGTATGATA	ENSG00000168724	DNAJC21	5.79786396	1
CTGATAAAGGCTACAGTGA	ENSG00000177692	DNAJC28	2.378691161	1
CTTGATGACACTTACATAA	ENSG00000168259	DNAJC7	2.303661547	1
GATATTATCTTTAGGAAGA	ENSG00000119661	DNAL1	2.162818432	1
CTTACCATGTCTACAATAT	ENSG00000137976	DNASE2B	2.814473508	1
GTCATGCTTCTCATCGATA	ENSG00000106976	DNM1	2.595478205	1
CTGGTGCATGGATTACAAA	ENSG00000107951	DNM1P17	8.973897537	1
GAGTCTGGCTTTGAGAGTT	ENSG00000130816	DNMT1	2.535282163	1
GTCATACTGTGAAGAA	ENSG00000142182	DNMT3L	2.078859647	1
CATTCTTTGTCAAAGAATA	ENSG00000128512	DOCK4	2.23737348	1
CCGTATGTCTGTGATAAGT	ENSG00000011332	DPF1	3.062972054	1
CCCATGAGAGCATATTTAA	ENSG00000154813	DPH3	2.685120868	1
CGCGGCTGCTGAAAGCCAT	ENSG00000203909	DPPA5	2.363732274	1
CACTGAAATGGGACTTTAT	ENSG00000177990	DPY19L2	4.680664679	1
GAGGAAACCTTATAAATTA	ENSG00000092964	DPYSL2	2.493484459	1
CAGACCATGCCCAATGGCA	ENSG00000149295	DRD2	2.309180546	1
CCTCTTCTGTTTGGCTTTA	ENSG00000151577	DRD3	2.608038073	1
CATTAACTGCATTAAGAA	ENSG00000169676	DRD5	2.351917122	1
CAAGAGGAATCAGTTTATA	ENSG00000151914	DST	3.059057388	1
GCACCATTGTGATTACTTA	ENSG00000163840	DTX3L	2.244119614	1
CCCTCATCTCCCTCATCTA	ENSG00000110042	DTX4	2.506463637	1
CCATGTCATTTATGATGTA	ENSG00000188542	DUSP28	3.25897078	1
CCATTTATAGAGATAAGAT	ENSG00000128951	DUT	3.052297394	1
CATTACATCTGGATCGTCT	ENSG00000004975	DVL2	2.202550085	1
CAAATGGAGTTAACATTTA	ENSG00000230524	DVWA	4.779400678	1
GATGATCAAACAAGATGTA	ENSG00000144635	DYNC1LI1	2.874597109	1

CTCTGTGGCGTACTTATTA	ENSG00000187240	DYNC2H1	1.987051418	1
CCATGTAGACAAAGTGATA	ENSG00000138036	DYNC2LI1	2.727705195	1
GGCTTATGAAATGTAATTA	ENSG00000165169	DYNLT3	2.083904396	1
CAGACCATAGTAAATTTAA	ENSG00000165891	E2F7	2.431945717	1
CTGTCTGTTGGTTCCAATA	ENSG00000108001	EBF3	2.398094008	1
GTTTGAATATGGATGGAAA	ENSG00000106823	ECM2	2.169010146	1
CAGTTGATGACTTTAGAAA	ENSG00000114346	ECT2	2.010750378	1
CAGAAGATCGCCGTCAAGA	ENSG00000158813	EDA	2.98932167	1
CAATTGATCAGATTACTAA	ENSG00000131080	EDA2R	2.496895236	1
CTGTCTGTATATACTTAT	ENSG00000127129	EDN2	3.148056653	1
CACACCATATGGATTCTAT	ENSG00000136160	EDNRB	2.578535052	1
GATCTTAATTCATATCTTG	ENSG00000124802	EEF1E1	2.317993569	1
CTGATAAAGGAGCCTGTCA	ENSG00000203666	EFCAB2	2.276334527	1
CATTTGGAAGGACAGTTTA	ENSG00000214360	EFCAB9	2.399455202	1
CTCATAAATTTATTGCATA	ENSG00000165487	EFHA1	5.053575374	1
CCGACCAACGAGACCCTGT	ENSG00000099617	EFNA2	2.919499098	1
CACGGTAATTAATGTCTTA	ENSG00000090776	EFNB1	2.042634535	1
GAGACTCTCTGGTCCTTCT	ENSG00000084710	EFR3B	1.977692476	1
GCGCTCTGAAGCAGGAGAT	ENSG00000239974	EGFL8	2.119243759	1
GCCAGTGACTGATGATTAA	ENSG00000135766	EGLN1	2.766160592	1
CGTACTCTCACATGTGGCA	ENSG00000120738	EGR1	4.906967187	1
GACAGCAGAACTGAGATA	ENSG00000173442	EHBP1L1	2.231144776	1
CCAAATTTAGGTTAAGCAA	ENSG00000055332	EIF2AK2	1.968984526	1
CTACTTAAC TGATGAAAGA	ENSG00000111361	EIF2B1	2.875315936	1
GGGCTATTCTCCTTGCTTA	ENSG00000107581	EIF3A	3.132717737	1
GACTCAGAAGTGAAGGAGA	ENSG00000175390	EIF3F	2.968735807	1
CAGTGTATTGCAGCCTTAT	ENSG00000149100	EIF3M	3.673093295	1
CCGTGTGTTTGATATGCTT	ENSG00000161960	EIF4A1	2.318042388	1
GACATTATTTCAATATGGA	ENSG00000135930	EIF4E2	2.430061033	1
GGCCTAACACCATTCATAT	ENSG00000148730	EIF4EBP2	2.149782572	1
GCCACCATCCTGCGTGAAT	ENSG00000066044	ELAVL1	2.473116006	1
CTGATATTCTCAATAGTTA	ENSG00000120690	ELF1	2.42306228	1
CTCCCTAATTTATGTGCTA	ENSG00000163435	ELF3	2.628270365	1
GGAATTATGAAGCTAAGAA	ENSG00000105656	ELL	2.363300504	1
CTCCCAGCCTCTTAGCTGA	ENSG00000155849	ELMO1	1.976042191	1
GAGATGAATGGAGGCTTAA	ENSG00000115459	ELMOD3	3.191554001	1
GGTCCTAAGAGCTGATTAT	ENSG00000119915	ELOVL3	2.038429242	1
GCATTAATAGCAAGGTGTA	ENSG00000165521	EML5	2.737447456	1
CTATATAATTGTGAAGTAT	ENSG00000134531	EMP1	3.588288175	1
CCCTTAACCCTGTCTGTTA	ENSG00000127507	EMR2	2.752748206	1
GACCTTGTATATATTTAAT	ENSG00000163064	EN1	11.01324699	1
GTGCCTTCTTGCTACTCTA	ENSG00000151023	ENKUR	3.277293366	1
CGGATCAGAAGTGGCTATA	ENSG00000154269	ENPP3	2.480550501	1
GTTGGGATTACTTATATAA	ENSG00000112796	ENPP5	3.505583815	1
CTGTTATGGTGCTGGTAAT	ENSG00000182156	ENPP7	2.260671507	1
CCAAGTGCAGGACCAGACA	ENSG00000143420	ENSA	2.068064279	1
CTGGTAGAAGAGAAATTTA	ENSG00000159023	EPB41	3.48247665	1
CCTTTGCAATTTGAAATTA	ENSG00000135999	EPC2	2.60363883	1
CTGTCCCTCGCGTTATTTA	ENSG00000127527	EPS15L1	2.343297454	1
CATTGACAGAGATGTGCAA	ENSG00000151491	EPS8	2.11568478	1

CCCGAGATGAGTCAATTAA	ENSG00000187672	ERC2	3.11429132	1
GCTTGAAGTGAAGATTTA	ENSG00000175595	ERCC4	2.355364124	1
CAGACAATCTTATTACACA	ENSG00000049167	ERCC8	2.334231145	1
CTGAACATCAGTTTACCCA	ENSG00000113719	ERGIC1	2.371894514	1
CTCTTAAGGGACTCTAATA	ENSG00000136541	ERMN	8.665716518	1
CTATTTAAAGCTTATTATA	ENSG00000116285	ERRFI1	3.356133692	1
CACCTTATATAGTATAATA	ENSG00000091831	ESR1	5.235051858	1
GTTTCCTTCTGATTTGGAA	ENSG00000139083	ETV6	2.773536088	1
CCGAATCTCCTGGAGACTA	ENSG00000081177	EXD2	2.032223031	1
CTAAAGGTCTCCAGGGACA	ENSG00000187609	EXD3	3.01094135	1
CCTGGTATCTTATAGAGAA	ENSG00000112685	EXOC2	2.531630296	1
CAACTCTCTGCAGAATGTA	ENSG00000144036	EXOC6B	1.969322164	1
CTTATCAATATGAACTAAA	ENSG00000171824	EXOSC10	2.051147157	1
GTGTGAATGTATGTATTAT	ENSG00000107371	EXOSC3	3.342905512	1
CTCTATCGGATATTTAACA	ENSG00000075914	EXOSC7	2.315069347	1
GTTATGTGTCTGCCACATT	ENSG00000104313	EYA1	1.973554597	1
CGAGGATATTGATCCACAT	ENSG00000188107	EYS	2.002320614	1
CCATCATCCGGACACTTAA	ENSG00000164220	F2RL2	2.687482371	1
CTGTTATTACCATTAGCAT	ENSG00000117525	F3	2.447575909	1
GGAAATAAACTTATTGGAA	ENSG00000145384	FABP2	3.088541826	1
CTATTACATTGCTTGAACA	ENSG00000185104	FAF1	2.677420168	1
CCCATCATCTTCAGCAAGT	ENSG00000115042	FAHD2A	2.105491143	1
GCCTTTAAGAGCACAAAGA	ENSG00000145569	FAM105A	3.142268472	1
GGTACTATGTATTCCATTA	ENSG00000107362	FAM108B1	3.620462489	1
GGTTTGTCTCATAATCTA	ENSG00000155744	FAM126B	2.166709872	1
GAGACTCTGCTTCACGAGT	ENSG00000184163	FAM132A	2.180907886	1
GACAGGAGTTTACAGCATA	ENSG00000179083	FAM133A	2.321777575	1
GATATTAAAGGACTCAGCA	ENSG00000234545	FAM133B	3.252007941	1
CAGACAATGGCACATTCAA	ENSG00000141699	FAM134C	3.03836951	1
CCAGTTTATGCAGAAATGA	ENSG00000147724	FAM135B	1.967473502	1
GTTATAGATTGTATCCTAG	ENSG00000138286	FAM149B1	2.086162613	1
GTCTAGGGACCATTTCTGGA	ENSG00000158863	FAM160B2	2.218939773	1
CATCTAATTGGAGAAGGAA	ENSG00000104427	FAM164A	2.107238587	1
CTGAGTATGTAGGCGTGTT	ENSG00000054965	FAM168A	2.283702169	1
CAGATGGTGCTTCTAGAAT	ENSG00000185087	FAM169B	3.174630374	1
CTGATTAGAACAAATCAGA	ENSG00000165660	FAM175B	2.197147671	1
GAAATGAGAGGTAAGGATT	ENSG00000115363	FAM176A	2.70018717	1
CTGGCCCTCTTTGCAGATA	ENSG00000135436	FAM186B	2.003417125	1
CTCAGTCTCAAATTTATAA	ENSG00000198673	FAM19A2	4.306935349	1
CTTGCTGTTGTGACATAAA	ENSG00000203795	FAM24A	7.62596307	1
ATGGAAAGTTTCTAAGTTT	ENSG00000105058	FAM32A	2.461846094	1
GAGATTATTGTAAAGAGTA	ENSG00000128578	FAM40B	2.73665329	1
CTCTTTCCTTAGTAAGGAT	ENSG00000119979	FAM45B	2.406092251	1
CGGAGGAGAACATCATGAA	ENSG00000071859	FAM50A	2.073988654	1
GTGTTTAGCATTTAATAGT	ENSG00000120709	FAM53C	2.886549695	1
GATCTGCATGAATCTGGAA	ENSG00000137634	FAM55D	2.178343922	1
GAAATGAAAGCAGAAGTTA	ENSG00000157470	FAM81A	2.882037984	1
CTGTCAAGGAGAACACTCT	ENSG00000101447	FAM83D	2.262894033	1
GTTACATACACAGTCAATT	ENSG00000187268	FAM9C	2.722121226	1
CTGATAGTGATTGCCTTGA	ENSG00000183161	FANCF	2.069380371	1

GTAATACTTTGGAAATGCA	ENSG00000196159	FAT4	3.107636398	1
CTGATCACAGATGATGGAA	ENSG00000108306	FBXL20	2.305552002	1
CGTGCTGTATGAATCTAGA	ENSG00000183580	FBXL7	4.195775856	1
CCAATAATATGCTTCTTAA	ENSG00000147364	FBXO25	5.10383522	1
CCGTCATTCTGAGGTCAAA	ENSG00000153832	FBXO36	2.051760789	1
GAAATGAAGGTGCACTTAT	ENSG00000163013	FBXO41	4.1152736	1
CGTAGTTGTTCTAATATTA	ENSG00000174989	FBXW8	2.755354848	1
GCAATCATGTAAGTCTATA	ENSG00000143226	FCGR2A	2.075309907	1
GTCAAAGTGTAATTATTCA	ENSG00000162746	FCRLB	2.446353369	1
CCAGCAGTGTTCTTGCAAT	ENSG00000160752	FDPS	3.369526779	1
CTGAGTTGAGACTTTGGAA	ENSG00000168496	FEN1	2.542478247	1
CGATTTAAATGGGCTGAGT	ENSG00000146192	FGD2	3.647590249	1
CAGTTAAACTGATTAGTAT	ENSG00000113578	FGF1	2.518249057	1
CTATGAAATTCAAGTGCTT	ENSG00000138675	FGF5	2.849525652	1
GGCCATCCACCTTATGCAA	ENSG00000134775	FHOD3	2.302390035	1
CCAGGAAACAGATAGTAAT	ENSG00000132436	FIGNL1	3.398866428	1
CTTGGTAGATGGACGTATT	ENSG00000134285	FKBP11	2.013077197	1
GCTCTTAAGTTCTTCCCAA	ENSG00000122176	FMOD	2.897423409	1
AGCATTGTTTGCTTATTGT	ENSG00000170345	FOS	2.001982981	1
GTCATCAAGCCCATCAGCA	ENSG00000075426	FOSL2	3.211027919	1
CTCCGTATATTACATAAC	ENSG00000129514	FOXA1	3.407363845	1
GACAGTGGATGAAGTAGAA	ENSG00000114861	FOXP1	4.290407796	1
CAGGCTTCGTCTTATTCT	ENSG00000164379	FOXQ1	2.627627082	1
CCCTGGATAGCAAGTGAAT	ENSG00000107130	FREQ	2.161995806	1
CAGAGAAACAACATTATA	ENSG00000111816	FRK	3.02117197	1
CGACTTACGGTGTCCATTA	ENSG00000114541	FRMD4B	5.307546767	1
CTTTGTATGGCAAAGAAAT	ENSG00000165694	FRMD7	2.246762652	1
GATGTATTCTGTTTATATT	ENSG00000169933	FRMPD4	2.608208637	1
GCGATAATAATAATTTAGA	ENSG00000170820	FSHR	4.125390263	1
CGGAGCTAAGGAGATCTTA	ENSG00000196968	FUT11	2.340031172	1
CATTTAATCAAGTCCCAA	ENSG00000196371	FUT4	2.230639962	1
ACAGATAACTGCTTTGCAA	ENSG00000111432	FZD10	2.245382521	1
ATCGATGTCTGTACTGTAA	ENSG00000174804	FZD4	2.388472637	1
ATGTTTCATTCAATTGGAAT	ENSG00000145907	G3BP1	2.18577235	1
GCACGCTTGCCCTCTGAAA	ENSG00000186297	GABRA5	2.025824487	1
ACAATCTCGCCATCTTTAA	ENSG00000094755	GABRP	8.741754409	1
GAGACACTTACTGGTTTAA	ENSG00000146276	GABRR1	2.871283949	1
GTTTCCTCTTGACACTCAA	ENSG00000183185	GABRR3	2.426334986	1
GAAACCTTGAGTGACTGAA	ENSG00000205777	GAGE1	2.484825254	1
ACAACAATTTGCCACCTTT	ENSG00000054983	GALC	2.379710642	1
CTGGTTAAGACTTATTAAG	ENSG00000136542	GALNT5	3.070943404	1
CTTTCTCTATTTGTTAAGA	ENSG00000141448	GATA6	3.906030817	1
CACGGAGTCTAAGAATTTA	ENSG00000114480	GBE1	2.298078469	1
CTCAGTGAGTTATTGAGAA	ENSG00000107862	GBF1	2.067137577	1
CAAATCATTGGAGCCAATA	ENSG00000162645	GBP2	2.224942961	1
CACGTCCCATGTGCATGGA	ENSG00000215644	GCGR	1.994814303	1
GAGATATTAAGCTGGGATA	ENSG00000137270	GCM1	9.102524592	1
GCCACTATGTACATGGTAT	ENSG00000111846	GCNT2	2.389999329	1
CTCTGCTCTCGGTGCGTAA	ENSG00000140905	GCSH	3.772732207	1
CCGTCACCAGCTATTCATT	ENSG00000184344	GDF3	2.622506925	1

CTGTTAGACTGTTAGATTT	ENSG00000125965	GDF5	2.382774897	1
CAGAGGAAAGAGAGCTTAT	ENSG00000143869	GDF7	2.777433232	1
CCTTTAAAGGAACGAATAT	ENSG00000178295	GEN1	3.563781349	1
GCCCAGTTCATACATTTAT	ENSG00000127554	GFER	2.063397839	1
CTGTCATTGTCGAGTATAT	ENSG00000145990	GFOD1	2.000857801	1
CGAAGTTATCTGATGACAA	ENSG00000006625	GGCT	2.048427427	1
GAGTTCATAACATCTGCTA	ENSG00000204136	GGTA1	12.01966068	1
GAGAGTAAGCAGAAATGAAA	ENSG00000121742	GJB6	1.96017877	1
GTCAATCTATGAGATTCGT	ENSG00000159248	GJD2	2.815139229	1
CAGTCCCTCTCGTTGATAT	ENSG00000119392	GLE1	2.24451364	1
GATGAAATGGGAGAATTTA	ENSG00000090863	GLG1	2.866596589	1
GCCATTACGGCTTGGTATA	ENSG00000173401	GLIPR1L1	3.089441705	1
CAAGTTAGTGCATTATATA	ENSG00000101958	GLRA2	2.687828707	1
CCAGTGGCCTGACTCATAT	ENSG00000172986	GLT8D4	3.758237188	1
GCACCAAATTTGAGACAAA	ENSG00000135821	GLUL	3.108656606	1
CCTTTGATTTGTTAGCTTT	ENSG00000197045	GMFB	2.383136029	1
CCATGTATATGAAATGCAT	ENSG00000112312	GMNN	2.702933895	1
GTCAGTTGTTTCATGGTGTA	ENSG00000146535	GNA12	2.212372669	1
CAAATTTAATTAAAGCCTT	ENSG00000087460	GNAS	2.053803197	1
CAGCTTAAGTGTGAGTTTA	ENSG00000113552	GNPDA1	2.591216796	1
CATAAGTCCTGCATATTTA	ENSG00000111670	GNPTAB	2.020855836	1
CAGAAGATCCAAGAACCAA	ENSG00000135677	GNS	3.349277351	1
CCTCTAAATTTATTATCCA	ENSG00000136935	GOLGA1	2.712230735	1
CTGATAACATTCGAAATCA	ENSG00000066455	GOLGA5	2.06142783	1
CAAATAACTGGCCACATCA	ENSG00000135052	GOLM1	3.770717788	1
CTGAGCAACTGACGTCAAA	ENSG00000174567	GOLT1A	2.223453276	1
GAGACAATGGCGATTGAGA	ENSG00000108587	GOSR1	2.02682231	1
GAGAGAGAGCCCTTGGGTA	ENSG00000178732	GP5	2.190138268	1
CTGCTGCTGCCTGATGACT	ENSG00000063660	GPC1	2.749267487	1
GACTCTGCGAGTTATCTAT	ENSG00000152642	GPD1L	2.000984786	1
GACTTTCATTCCTGACAGA	ENSG00000164393	GPR111	1.960217885	1
GCCATAGTTTCAGAGAATC	ENSG00000159618	GPR114	2.057337591	1
CTATAACAGTGGGAGTTAT	ENSG00000144820	GPR128	2.566869489	1
CAGAGCATGTTATTTATAT	ENSG00000152749	GPR180	2.584169132	1
CTGGGTCTATAGATGTAAT	ENSG00000198932	GPRASP1	2.575552336	1
CTTGCAAGTTGAAACATTA	ENSG00000115290	GRB14	2.158609456	1
CTATGTACTTAATCCTTTA	ENSG00000177885	GRB2	3.201972368	1
GTCAGTGCCTGAATCTTTA	ENSG00000166923	GREM1	2.932199173	1
GAGAAATCCATATACCATT	ENSG00000134317	GRHL1	3.787642149	1
CAGATTTGCTCAAGAAGAA	ENSG00000158055	GRHL3	2.516996096	1
GATACAATTTCAACACCTA	ENSG00000155974	GRIP1	2.538519479	1
GACAGGTGCTGTTCCCTATA	ENSG00000114124	GRK7	2.534910737	1
CTGTTACCATTACAAATAA	ENSG00000134443	GRP	2.089035021	1
ATATTAATGTCAATCATTT	ENSG00000164284	GRPEL2	3.677536774	1
GCTGTATGTTGTTGTCTCT	ENSG00000073605	GSDMB	2.414286627	1
CACTGACCATGCTGAGTGA	ENSG00000104518	GSDMD	2.247549192	1
CTAATTGTGCTAATTAATA	ENSG00000103342	GSPT1	2.088303165	1
GACGCTCAAGGATGGTGAT	ENSG00000099984	GSTT2	4.001303814	1
CGCGAGTTCGCTTCTAATA	ENSG00000169840	GSX1	2.347596084	1
CAAATCTTATTTACAGGAA	ENSG00000165417	GTF2A1	3.565648082	1

GTCCACATTCTCCTGAA	ENSG00000070019	GUCY2C	2.299578059	1
CTGTAAGTGGGACAGAAGA	ENSG000000105968	H2AFV	2.034239209	1
CCTATGAAAGGATGCAATA	ENSG000000132475	H3F3B	9.495588554	1
GAGAGACTTGTGAAGTATT	ENSG000000085382	HACE1	1.981291395	1
CATGGATTGAAACCAGTTA	ENSG000000084110	HAL	2.192828308	1
CTGTGTATAGTCAACCTCA	ENSG000000113249	HAVCR1	3.71371135	1
CTCACCGATGGATCCTACT	ENSG000000143630	HCN3	2.117560353	1
CACCTAGTGTCCAGATTCA	ENSG000000171720	HDAC3	4.47829753	1
CACAAGATGCAAAGGATGA	ENSG000000048052	HDAC9	6.0449232	1
GCCAGCTTATAGTCATATA	ENSG000000143321	HDGF	2.183180404	1
CACTCCAGAGCTATTTCTA	ENSG000000119285	HEATR1	5.473497674	1
CAGAAGCTGTCAGTGGATA	ENSG000000008869	HEATR5B	3.142665428	1
CTCCGCAATTTCTACAGAA	ENSG000000002746	HECW1	6.180233501	1
CAAAGTCAATGCTGTTTAT	ENSG000000198265	HELZ	4.964804897	1
CAAGTTCAGTAAATGTCTA	ENSG000000114735	HEMK1	2.680499374	1
CGCAGAAGTGGGTACAAAT	ENSG000000103657	HERC1	7.272268784	1
GAGCTGATCGCTTTAAATA	ENSG000000138641	HERC3	2.507939387	1
GGTTTCATTTAGTGGAGAA	ENSG000000138646	HERC5	2.465632003	1
CCATCATTGGAAGATTTAA	ENSG000000138642	HERC6	2.037709756	1
CTGGACATCGTCTCTTCTT	ENSG000000213614	HEXA	3.059396441	1
CTGCTTAGGTTCTTGAGTA	ENSG000000186834	HEXIM1	2.086419612	1
CATATACTTTAATAAATGT	ENSG00000010704	HFE	4.04647191	1
CCCACAGCGGGCTACCAGA	ENSG000000185359	HGS	2.602551921	1
GCTTTATTCCAGTAAACAA	ENSG000000165102	HGSNAT	2.053894412	1
CATGGTATATGTATTGTTA	ENSG000000181061	HIGD1A	1.975735434	1
AGCAGCAACTCATCATTAT	ENSG000000111911	HINT3	3.008638812	1
CTCAAGTCGTTGGACCAGA	ENSG000000160396	HIPK4	2.382020524	1
CGTAAGGAGAGTTATTCTA	ENSG000000146047	HIST1H2BA	3.309589819	1
GGACAATATCCAAGGCATT	ENSG000000197837	HIST4H4	5.320792378	1
CACAGACTCTCCAGAAAGAT	ENSG000000239457	HLA-DOB	2.072427165	1
CTCCCTCTCTGGTTTCCTA	ENSG000000137309	HMGA1	2.107077501	1
CAACTCTTCTATTTATGGA	ENSG000000149948	HMGA2	2.592452369	1
GGACAAGACCCATTATGAA	ENSG000000124097	HMGB1L1	3.706447938	1
CCCTTCAGATGGGAATTAA	ENSG000000146151	HMGCLL1	2.116403401	1
GATGCATAGCCATCCTGTA	ENSG000000113161	HMGCR	5.412190319	1
CCTGATATGCTATCTGAAT	ENSG000000112972	HMGCS1	2.533061838	1
GTGTTAGAACTTTATTATT	ENSG000000134240	HMGCS2	2.680425596	1
CTATTTCTGCTGAAAGTA	ENSG000000182952	HMGN4	2.131491056	1
GTTATTCTATTTGATAAT	ENSG000000221887	HMSD	2.573637722	1
CCTGAAATTTGGAAGCATA	ENSG000000177733	HNRNPA0	2.459707965	1
GAAATTATGGAAGTGGAAA	ENSG000000122566	HNRNPA2B1	2.674202964	1
CAGTGAAGAAGATAATGGA	ENSG000000138668	HNRNPD	2.305816161	1
CTGTTGATATTTTCATCAAG	ENSG000000105323	HNRNPUL1	4.30704122	1
CTGTTTACAGTTCTGTGT	ENSG000000168172	HOOK3	1.983800844	1
CAGGTTATGACCTTGATTT	ENSG000000165704	HPRT1	2.639203334	1
CTATGAATTTGCTAAACTT	ENSG000000198189	HSD17B11	2.631962118	1
CCACCCATCTGCAGTTAAT	ENSG000000165868	HSPA12A	1.985777386	1
GGAAACAGATCCAACAGTA	ENSG000000170606	HSPA4	2.645385452	1
GATTAAATCAGACACTTAA	ENSG000000164070	HSPA4L	2.949694326	1
GCCCAAGGTCCAAGTAGAA	ENSG000000109971	HSPA8	2.187406676	1

CTATCTAAGTGGAAGTAAT	ENSG00000173641	HSPB7	3.392607019	1
CATTCCAAGTTCTGGGCTT	ENSG00000169087	HSPBAP1	2.593839446	1
CTTGGCTACTCCAAGTCT	ENSG00000157219	HTR5A	3.568190832	1
CTCAGAAATGTAAATGATGA	ENSG00000148680	HTR7	3.090293187	1
CACCTCAGCTACTTCAAGT	ENSG00000086758	HUWE1	3.156404597	1
CAGTGAAATTGACACAATA	ENSG00000112144	ICK	3.693256657	1
GAAATTGCTTTGTATTGTA	ENSG00000125968	ID1	3.108111097	1
ATCATTAAATTTATCATTAA	ENSG00000067064	IDI1	2.797648506	1
GGAATTAAATCACAGCTAA	ENSG00000134049	IER3IP1	2.506799946	1
CTTTCTCTCCCAATGAAGA	ENSG00000162783	IER5	2.002317011	1
CCTCTAGTACTGATGATCT	ENSG00000114446	IFT57	2.052073399	1
CTGTTCTGAATCAAAGCA	ENSG00000159217	IGF2BP1	2.033682024	1
CTGCCAACTGCAACAAGA	ENSG00000146678	IGFBP1	2.033995334	1
CACGTCACCTGGTTCAAGA	ENSG00000163395	IGFN1	3.326428687	1
GTTCTAAATATCTTATGA	ENSG00000183067	IGSF5	5.093748102	1
GTGTATTTATTGTTATTTA	ENSG00000124391	IL17C	2.318254961	1
CTATTTATGGGAACTTCTT	ENSG00000115604	IL18R1	2.200387843	1
GACACCTTCCCAATGTCA	ENSG00000142224	IL19	3.375369661	1
CTGGGCATTCTTGTTTCAA	ENSG00000115008	IL1A	2.354867989	1
CTCATCACAGTGCTTAATA	ENSG00000115594	IL1R1	2.579492079	1
CTACCTATTGTAAGTATTA	ENSG00000109471	IL2	3.425129801	1
CTGGCGCTCAGATTACGAA	ENSG00000103522	IL21R	2.007605098	1
CATGTTAGGTGATTCAGAA	ENSG00000111536	IL26	3.687570796	1
CTACTCCTTCCTTAATTTA	ENSG00000182393	IL29	5.243416419	1
GTTAAGAATTTGGTAAATT	ENSG00000113525	IL5	2.625536966	1
CAGAATCACTGAAAGCAAA	ENSG00000091181	IL5RA	2.094048713	1
CTTAGATTCTGAGAATCAA	ENSG00000145103	ILDR1	2.789069608	1
CACTCAATAGCCGTAGTGT	ENSG00000166333	ILK	2.338540608	1
CAGCCATTACCCAGCTAAA	ENSG00000148798	INA	4.387720882	1
GAGGTAGATTAATAAAGTA	ENSG00000149503	INCENP	3.214805309	1
CTGATTCTGATGATAATAA	ENSG00000203485	INF2	3.040515698	1
CAGATAATGTTATTCATTT	ENSG00000125629	INSIG2	2.797645217	1
CCTTCCCAGAATAATACAA	ENSG00000108506	INTS2	2.349179062	1
AGCTATGTTTGTTATTTAA	ENSG00000074706	IPCEF1	2.024256343	1
CCATGTGCTGTGGCAGATA	ENSG00000117408	IPO13	2.32844647	1
CAGTGACAGCCCTAGTGAA	ENSG00000198700	IPO9	2.035980413	1
GCAGTATGCACCTAGAAAT	ENSG00000197429	IPP	2.015595346	1
CTTGATAATAAATGTATT	ENSG00000146243	IRAK1BP1	3.456368145	1
GGAGAAATATCCTATTTAA	ENSG00000134070	IRAK2	3.843722659	1
CACTGAATTGCCATTATTA	ENSG00000136381	IREB2	1.973235834	1
CACACTGGCGGAAGAGGAA	ENSG00000168310	IRF2	2.607773051	1
CTATTCAGAAAGTTTATAGT	ENSG00000176842	IRX5	2.059498425	1
CGTAAGTTATTGTTATTTA	ENSG00000159556	ISL2	3.784139269	1
CTGTGATTAATATTCAGAA	ENSG00000091409	ITGA6	4.315001635	1
CCTGGAAGTGAAACCAATA	ENSG00000077943	ITGA8	3.822606931	1
CTGTGCATCACATTTCTTA	ENSG00000142856	ITGB3BP	2.236458992	1
CTCAGAATATCCTTAACAA	ENSG00000198542	ITGBL1	2.575897389	1
GGCTGTACTCTTGTTCTAT	ENSG00000158764	ITLN2	2.316631715	1
CCCACAAAGGGAGAAGTAT	ENSG00000163207	IVL	2.020465408	1
CATGGAAATGTGTGTACTA	ENSG00000162434	JAK1	2.413044452	1

GTACAGATTTGCGAGATTT	ENSG00000096968	JAK2	5.183740992	1
GTCCTGTATCGCTCAGTAA	ENSG00000140044	JDP2	2.785724872	1
GCAACTATGATGTCAATGT	ENSG00000161677	JOSD2	2.058049725	1
GACTTTGATGTTGAAGATA	ENSG00000183340	JRKL	3.032235229	1
GATTCATATTGAATATAAT	ENSG00000171223	JUNB	4.284966245	1
CATAGAATCCTTGAAGGAA	ENSG00000107104	KANK1	2.053637867	1
CAGGAATTATTGGAGGAAT	ENSG00000102781	KATNAL1	2.09028858	1
CAGTAACTGTACACTGTA	ENSG00000182359	KBTBD3	2.208162131	1
ATGATAAATTTATGTAATA	ENSG00000175538	KCNE3	3.064823101	1
CAGCTCAAGGCTGCACCA	ENSG00000026559	KCNG1	2.241011451	1
GACCATCCATTAAAGACAA	ENSG00000184611	KCNH7	3.789493618	1
GGCATTTAAAGACCTCAAA	ENSG00000153822	KCNJ16	2.178789615	1
CCCAGAACTCAACCATCA	ENSG00000162728	KCNJ9	2.156905425	1
GGGTCAAGATCTTAGCTGT	ENSG00000135643	KCNMB4	4.507302976	1
CTGCTCTTGTGGAGGTACA	ENSG00000198553	KCNRG	3.771902249	1
GCTGGAACTTCTATTTAA	ENSG00000107147	KCNT1	3.412272373	1
CCAAGATTTGGTAAAGAGA	ENSG00000110906	KCTD10	2.565865591	1
GGAAGGTGCTATTCAAGTA	ENSG00000147050	KDM6A	2.094285916	1
CTCCGAATCATCCTGGATA	ENSG00000102763	KIAA0564	1.962875911	1
CAGGCTCCCTCACAGCCAT	ENSG00000205978	KIAA1305	4.929274392	1
CAATAACTTTGGTCTTTA	ENSG00000164944	KIAA1429	2.81021117	1
CTTATCAACTCCAGACATT	ENSG00000164323	KIAA1430	2.684926362	1
AATTGGAATTGAGACACCA	ENSG00000197816	KIAA1529	2.172688352	1
CTTCTTCGTGATCAATTTA	ENSG00000164118	KIAA1712	2.828604445	1
ACGGTTGAGTCAGGAACAA	ENSG00000166004	KIAA1731	2.120291083	1
GGTAGAAATTTATTTAGCA	ENSG00000198894	KIAA1737	3.235285885	1
CATCTTCCAACATAGGGAT	ENSG00000146112	KIAA1949	2.82747569	1
CGTTCTGGAGCTGTTGATA	ENSG00000138160	KIF11	2.516670292	1
GCTGAGAAGTTTCAGATAT	ENSG00000089177	KIF16B	2.131340919	1
CAGTGCAAAGCAGAGCTAA	ENSG00000112984	KIF20A	2.71292725	1
GGCTGTTATTCTCATTTAT	ENSG00000138182	KIF20B	3.459201796	1
GAAATGAGGAGATTAGTAA	ENSG00000139116	KIF21A	3.040043805	1
CAACCTTCTTTGAAATTTA	ENSG00000068796	KIF2A	2.694561497	1
AGCATTGATATTCACTTAA	ENSG00000088727	KIF9	3.132604881	1
CATGTACATAAGAACTTCCA	ENSG00000215764	KIR2DL2	2.029501623	1
CATGATAAACACTACAGTA	ENSG00000157404	KIT	2.835729448	1
GAGTTTGTATTATTACAAA	ENSG00000155090	KLF10	3.537165642	1
GGAATTAACCTTTCGGTTA	ENSG00000118922	KLF12	2.16063756	1
ATCGTTGTGTGGCAGATAA	ENSG00000128607	KLHDC10	2.150966851	1
GACATATGAATATTATTAA	ENSG00000087448	KLHDC5	2.517284791	1
CCTGCAAGATGCACAATAA	ENSG00000076321	KLHL20	2.464786598	1
ATAAGGATTTCTTATGTTA	ENSG00000172578	KLHL6	3.18119227	1
GTAAGTGTGCAATGCTACA	ENSG00000205810	KLRC3	1.986893771	1
CATTTGCAGTGCATCAGAT	ENSG00000134545	KLRK1	2.004154607	1
GTTTGAACACCTTTAATAA	ENSG00000186432	KPNA4	1.989365056	1
GTGTGTCCTGCAAATTGAT	ENSG00000171431	KRT20	2.135894613	1
GCAATTAATTTGAGATGCA	ENSG00000204897	KRT25	2.328397825	1
CTGGACCTGGACAGCATTA	ENSG00000170477	KRT4	2.823678445	1
CAGAGGATCCGCTCAGAGA	ENSG00000170486	KRT72	2.457815024	1
CTGTCAAAGTCACCATTCT	ENSG00000170484	KRT74	3.627740745	1

CTGAAATATTTCAACAGTT	ENSG00000188581	KRTAP1-1	2.731910757	1
CTATGAAAGAGGAATAATA	ENSG00000221880	KRTAP1-3	4.048991005	1
CATGCTGAAGTGTGCAATA	ENSG00000053747	LAMA3	2.411271765	1
GCTCTAAATTGGCTCCATA	ENSG00000185896	LAMP1	4.405766651	1
CTATTTGTTCTCTGGAAGTA	ENSG00000172292	LASS6	4.935180778	1
CCAATGGCTTCTCTAATTA	ENSG00000143815	LBR	2.443645735	1
GCAGTTCGGTGGTTGAATA	ENSG00000168806	LCMT2	2.407331267	1
CAGCGAAGATGCGAAGATA	ENSG00000130164	LDLR	4.777386837	1
GGGACTATTTATATGTGTA	ENSG00000179241	LDLRAD3	5.037618745	1
CAGGCTAAATATTATGAAT	ENSG00000138795	LEF1	3.462836607	1
CTGTTTGGTTAAGTAATTT	ENSG00000186007	LEMD1	3.556849332	1
GATTGCATCTGATTCAGAA	ENSG00000166477	LEO1	2.368694146	1
CCCTTCCAATATACAACAA	ENSG00000104660	LEPROTL1	2.659844387	1
CTTGATCTATCCGTAGTAA	ENSG00000213921	LEUTX	2.516354118	1
CACTGTTCTGCGCAGATAT	ENSG00000128342	LIF	3.668296435	1
GGATGATCATAAAGGATTT	ENSG00000174405	LIG4	2.515058509	1
CTGCTTCCGTTGCTCCTAT	ENSG00000050405	LIMA1	2.578180675	1
CTTTGTATCCTAAGATAAA	ENSG00000144791	LIMD1	3.858599629	1
CATGCTCTGTCCAAATGCA	ENSG00000131914	LIN28	2.669208583	1
CAGATGGACAGAAGTTAAT	ENSG00000189308	LIN54	2.373385157	1
GACAATGATTTGTTTTATA	ENSG00000174482	LINGO2	2.927044247	1
CTGATAAGGGTATTTGTAA	ENSG00000163380	LMOD3	2.056927396	1
CTATGTATTCCTGATGTTT	ENSG00000171517	LPAR3	2.258893314	1
CCTTTGGACTCATGTATAT	ENSG00000150471	LPHN3	2.807732155	1
CCTTTCTAATCACAAATGT	ENSG00000156564	LRFN2	2.084256659	1
GGCACTACTTAAATTTAAT	ENSG00000165379	LRFN5	4.533798444	1
CCGCGAGGACTACATTGAA	ENSG00000123384	LRP1	2.269178841	1
CATCAATAGCGCTAACAAA	ENSG00000134569	LRP4	2.490594214	1
CTAACTATTGATTATGCTA	ENSG00000070018	LRP6	2.125520158	1
GTGATTTACTGCAAATTAT	ENSG00000138095	LRPPRC	2.129051306	1
GCAACTTTATACTTTCAAA	ENSG00000079691	LRRC16A	2.259219207	1
CATTCTTTCAGTTACATCT	ENSG00000184434	LRRC19	2.769067564	1
CAGCTCTTGTCTAAAGTGA	ENSG00000172731	LRRC20	2.90037897	1
CTTCTCCAGAGAAATGAAA	ENSG00000010626	LRRC23	2.424303141	1
CTTAAGATTTCAATTTGATA	ENSG00000241994	LRRC51	3.863164379	1
CATATTATTCCTGGGATAA	ENSG00000129295	LRRC6	2.118365692	1
CCTCCCCTTTAAGAAGAA	ENSG00000146006	LRRTM2	3.159963269	1
CCAACAATTCCTTTCAAA	ENSG00000144771	LRTM1	3.335321051	1
CGGAATATTCCAATGCTCT	ENSG00000170860	LSM3	3.015237146	1
CGGAAATGATCACTTAGAA	ENSG00000106355	LSM5	2.427796625	1
CTTATGGTGGCATGGAGAA	ENSG00000111144	LTA4H	3.531112068	1
CTCTAAATTCCTTAAGAAA	ENSG00000119681	LTBP2	4.968243653	1
AAGTTACTGTGGCTACTAT	ENSG00000102897	LYRM1	2.0610454	1
GGCATTATTTCTAATTGT	ENSG00000176018	LYSMD3	2.414584931	1
CTGATCTAGACTTATATGA	ENSG00000099949	LZTR1	2.210629394	1
CCCTGTAGATGAGAAAGTA	ENSG00000177689	MAGEB10	2.129841916	1
GAAATACCTTCTCCCTTAT	ENSG00000046774	MAGEC2	2.766093438	1
GGTCTTATTTCTGTAGAAA	ENSG00000177383	MAGEF1	3.673782045	1
CAGGCAAAGTCATTAATAA	ENSG00000081026	MAGI3	3.484358441	1
CTGAATCAGTCATCAGAAA	ENSG00000111837	MAK	4.098381734	1

CTAATTAATTTTCAGTAAGA	ENSG00000189221	MAOA	5.082410214	1
CTATTTGTGTGTATGCTGA	ENSG00000169032	MAP2K1	2.463915851	1
CTTACTGTTGTTTAAGCAT	ENSG00000143674	MAP3K19	3.112929127	1
GAGGTATGTTTATTTGTTA	ENSG00000169967	MAP3K2	2.515732119	1
GACCATGTGTCAAGACAGT	ENSG00000107968	MAP3K8	4.384851579	1
CATATGTGGTGACACGTTA	ENSG00000109339	MAPK10	2.245144558	1
CTGCAAACCTTATCCTCTA	ENSG00000008735	MAPK8IP2	2.70278385	1
CAAAGTATCCTGGAATCAA	ENSG00000050748	MAPK9	1.989759471	1
GACATCATTGCATGGGTTA	ENSG00000166974	MAPRE2	2.472343947	1
CATCTCAAATCATTCTGTT	ENSG00000155130	MARCKS	2.65657289	1
CAATGTTAATTTAGTGGA	ENSG00000151224	MAT1A	2.601546242	1
CTCCTCAGTTCTCTACCTA	ENSG00000204406	MBD5	2.329952705	1
CAGAGCGTCCGACTATAAA	ENSG00000197971	MBP	2.375851138	1
GCTATCCTGTCATGATTAA	ENSG00000078070	MCCC1	2.911408797	1
CAGACCAACTCCAGAGGAA	ENSG00000206447	MCCD1	2.446668464	1
CAGATTGTAATTTGGTTTA	ENSG00000180398	MCFD2	2.652583968	1
GAAATTCTTTCAC TTCATT	ENSG00000143384	MCL1	6.51129748	1
GAGCCTTAATGGTACTCAA	ENSG00000137337	MDC1	2.453985019	1
GGGAGAATTAATTACATAT	ENSG00000139915	MDGA2	2.044435928	1
CACAAATAATGAGTGTGTA	ENSG00000244102	MDS1	2.086182144	1
GAAATTATCCATATACATA	ENSG00000136146	MED4	2.883160951	1
AGGCTAACATTAGAACACT	ENSG00000133997	MED6	2.348819505	1
CCTGAGCTTTATTTGTTTA	ENSG00000145794	MEGF10	3.309694748	1
CTGAAAGAACTCCAATTA	ENSG00000165304	MELK	2.032378704	1
CTTGCAATATGAATGTTAA	ENSG00000164024	METAP1	1.977596285	1
CAAGTGAAGAGATTTGGAA	ENSG00000111142	METAP2	2.407519174	1
CAACTACAATGCAGAAACA	ENSG00000145388	METTL14	2.011972263	1
CAGAGTCTGTGGATGTTGT	ENSG00000206562	METTL6	2.101457041	1
CAGTTTATTTCTAAGGTAT	ENSG00000037749	MFAP3	2.022851193	1
CAGATCTTGACCTTATTCA	ENSG00000168958	MFF	2.371145636	1
CAGCATCTGGTTCTGTACA	ENSG00000100060	MFNG	2.337849176	1
CTTTCTTAATCAACA ACTA	ENSG00000174197	MGA	3.497006804	1
GTATGAGAAACCTATATTT	ENSG00000008394	MGST1	2.114382397	1
CTCGGTTCCCTTAACGTTTA	ENSG00000100139	MICALL1	2.684583378	1
GTATTTATAGACTATTAAT	ENSG00000167470	MIDN	3.951397894	1
GTGTATATACCTCTATATT	ENSG00000196588	MKL1	3.335512726	1
CCAGGAAAGTTTGAAGATA	ENSG00000079277	MKNK1	5.463488315	1
GAGATAAGATCAAGAAGAA	ENSG00000118058	MLL	2.703945164	1
CCAAGCAGATACAGAGAAA	ENSG00000055609	MLL3	2.414970668	1
CTGTTACAATATTAGGTGA	ENSG00000171843	MLLT3	2.083611967	1
CAAATTATCCCAAGAGCAT	ENSG00000110347	MMP12	2.079238389	1
GCTCTTAATGGTTATGACA	ENSG00000137745	MMP13	2.240866434	1
GTCCAAAGATGATATATAA	ENSG00000120162	MOBK12B	3.17483068	1
GTGCCAATATTATTATCAA	ENSG00000075643	MOCOS	3.830834295	1
CGTTAAAGGAGATGTCCAA	ENSG00000061987	MON2	2.188150844	1
CTCAGTGTTGTGTGGATAT	ENSG00000101928	MOSPD1	2.624745911	1
CTGGTGGAAGTAACATCCT	ENSG00000008382	MPND	3.765478473	1
CTCAGAATTTAAACCCTAT	ENSG00000161647	MPP3	4.23877907	1
CACAGTATCAATATTT CAT	ENSG00000160588	MPZL3	2.372746298	1
GACTGAAGGCTCATAAATA	ENSG00000135324	MRAP2	2.795805796	1

CCCATTAAGTGGTAGTAAT	ENSG00000020922	MRE11A	3.622922061	1
CTGGATTGGAAAGTCTTAT	ENSG000000179826	MRGPRX3	2.745139635	1
CCCGCGACCTGGCTGATGT	ENSG00000037757	MRI1	4.058195942	1
CCATCAAGGGACAGAAGAA	ENSG000000180992	MRPL14	2.756869682	1
GACATTGTATGCAAACCTG	ENSG000000137547	MRPL15	2.555696065	1
CTCTGAAATTTCAAATAGA	ENSG000000115364	MRPL19	4.040322349	1
GAGTATCCAACGTTGATCA	ENSG000000112651	MRPL2	2.239201692	1
GGTGCGTTATGGATACATA	ENSG000000082515	MRPL22	2.173843784	1
AGCTAATTCCTATTGAAGA	ENSG000000185608	MRPL40	3.125304123	1
ATGAGAGGCTACGTATTAA	ENSG000000120333	MRPS14	2.304042839	1
CTGCTTATAAAGTAAATTT	ENSG000000181610	MRPS23	3.043431822	1
CATAGTCTCTCATCTGCTA	ENSG000000062582	MRPS24	2.167778156	1
GGATGCATGTTAGTCTTTA	ENSG000000131368	MRPS25	3.050609415	1
AGCATAGTAGGCAGTCATA	ENSG000000148187	MRRF	2.67002279	1
GGAATCCTCACCAATAGAA	ENSG000000156738	MS4A1	2.082543401	1
CTCTTTGGCTGCCATCATA	ENSG000000113318	MSH3	3.330583627	1
GTAGAAAGAATACTTAAGA	ENSG000000186715	MSTP9	2.157776723	1
ACTTTAACTTCATTGTAA	ENSG000000065911	MTHFD2	1.963982341	1
GGTCTCAATTCTTCTCAGA	ENSG000000103248	MTHFSD	2.644499332	1
CTGATCCTGAGAAAGTGAA	ENSG000000085760	MTIF2	2.128044206	1
GCCAAAGATGTAACCTATA	ENSG000000087053	MTMR2	2.102983683	1
GGCTACACATCTATTATTT	ENSG000000139505	MTMR6	2.235784889	1
CCTATTCTGAAGGCATTAA	ENSG000000198793	MTOR	2.480912608	1
CTGTTGGAAGGATGTATAA	ENSG000000188428	MUTED	2.683174657	1
CTGCTCTAGGGTTTCCAAA	ENSG000000204053	MYCL2	3.861241081	1
ACTGGAAGTTCATACCTAA	ENSG000000134323	MYCN	2.061285824	1
CTGCTGAGGCACTAAGGAA	ENSG000000141048	MYH4	3.550287549	1
CAGAGGCTGTAAAGGTTT	ENSG000000133020	MYH8	4.010286615	1
GTCTATACAGAGTCAATAT	ENSG000000101608	MYL12A	2.124006317	1
CAGCTTTATTGACAAGAAT	ENSG000000166866	MYO1A	2.012713851	1
CGCAAAGCCTTCAAGACAA	ENSG000000066933	MYO9A	2.757171893	1
GCTGTAACATTATTTAATA	ENSG000000162601	MYSM1	3.061338354	1
CATATCCTATATAGAATCT	ENSG000000148411	NACC2	2.175261566	1
GCAAATCAGTCGGTTGAAA	ENSG000000008130	NADK	2.463763791	1
CCACTTACTGGCCAGGGCT	ENSG000000187556	NANOS3	2.368728133	1
CAATTACACCCAGAAGATT	ENSG000000172766	NARG1L	2.685105462	1
GGGAACACCAGAATCACAT	ENSG000000142794	NBPF3	2.43257116	1
CTATTACTTGTTTGTAAGA	ENSG000000116701	NCF2	2.965104653	1
CATCCTATCTTATCGACAA	ENSG000000061676	NCKAP1	2.323221779	1
CACTGTCATTACCCCAATA	ENSG000000204475	NCR3	2.898997004	1
CACCTATTTCCCTGGATAT	ENSG000000131507	NDFIP1	2.246312462	1
AATAGTAATTGTTTATATT	ENSG000000185115	NDNL2	2.12674505	1
GCTTCGCCCTCATCATCTA	ENSG000000070614	NDST1	2.196204559	1
CGACTGGGATTATATACAT	ENSG000000164100	NDST3	2.118179863	1
GTTTGGAGAACATTGATTA	ENSG000000125356	NDUFA1	2.024792957	1
GTGACCTAATTTATGACAA	ENSG000000167774	NDUFA7	2.468055787	1
GGCTTCATGATAAACGGAA	ENSG000000178057	NDUFAF3	2.088213883	1
AGAATATTAGTAAGATTTA	ENSG000000119013	NDUFB3	3.413863188	1
CTCATAATGAGGCATCATA	ENSG000000129559	NEDD8	3.135939202	1
CAGATGATCAAGTACTTTA	ENSG000000119408	NEK6	2.005191532	1

GCTAGTCCCTGCCTGAATA	ENSG00000132688	NES	4.531398513	1
CTACTGAAGTCTACAGATA	ENSG00000162139	NEU3	2.101674643	1
CCAAAGAAGTTAAGGATTT	ENSG00000124257	NEURL2	2.335397531	1
CCAACATACCCCTTCTTTAA	ENSG00000162992	NEUROD1	3.430977064	1
CCTATAGACATGTCCTATG	ENSG00000123307	NEUROD4	2.383784179	1
CTGTATAAGTTACTAGAAA	ENSG00000109320	NFKB1	2.880667398	1
CCTTGGAATCAATGAAATA	ENSG00000170322	NFRKB	2.536171251	1
CAAGCCCTCTGGGTTAGTA	ENSG00000204131	NHSL2	2.128326675	1
GAATGGGTCCCAACATCTA	ENSG00000184117	NIPSNAP1	2.648020158	1
CGTCAAGAGAGTTTGTAAT	ENSG00000101198	NKAIN4	5.143583997	1
GTGTCTTATATACAGAATA	ENSG00000189134	NKAPL	1.967308054	1
GCCTCAATCCCTACGGTTA	ENSG00000183072	NKX2-5	2.526059799	1
GTGACTACTCCACTGAATT	ENSG00000196338	NLGN3	2.28852948	1
GAGATTATTCCACCGAATT	ENSG00000146938	NLGN4X	7.839471827	1
CTGTTACTCCATTACTGTG	ENSG00000197696	NMB	2.251858455	1
CGCCTCGTGGCCATGAAGT	ENSG00000011052	NME1-NME2	2.939809559	1
CACATCATTGTCATTACTG	ENSG00000140939	NOL3	2.109374524	1
GTGACCAAAGACATGTTTA	ENSG00000116218	NPHS2	1.968600685	1
CAAAGATATCCTGATTAAT	ENSG00000135838	NPL	3.455686047	1
CCCATCAACTGTATCTGAT	ENSG00000221890	NPTXR	6.375544454	1
CAGGGAATCCTGCATTCTA	ENSG00000012504	NR1H4	2.306638354	1
CATTGAAGTATCACGAGAA	ENSG00000120798	NR2C1	2.489768606	1
CTAGTTCTTGAATTGTTA	ENSG00000185551	NR2F2	3.189866423	1
CCTCCACATTACCAATATA	ENSG00000148200	NR6A1	2.498761788	1
CAACCTCCTTCATGCGAAA	ENSG00000197893	NRAP	2.088594695	1
CTAGCTTACTGATAAACCT	ENSG00000213281	NRAS	2.258760336	1
GGATTCAAGTGACATAGAA	ENSG00000165671	NSD1	2.089907711	1
CTGTTCAATCTACAATAAA	ENSG00000156831	NSMCE2	2.873875961	1
CTGTTAGTATTAATGAAGA	ENSG00000107672	NSMCE4A	3.869043572	1
GGCTGGATGTCTTGATCAA	ENSG00000185013	NT5C1B	2.40239735	1
CAGGGTAATTTATATGAAT	ENSG00000111696	NT5DC3	3.811695795	1
GCCATCGATTCCCAAGATA	ENSG00000103274	NUBP1	1.982571187	1
CCATTTAGTTTGTCTAGAT	ENSG00000196368	NUDT11	2.835549067	1
GCTATAAGAGATTATGTTT	ENSG00000112874	NUDT12	3.364727686	1
CGTTTGAAATTGAACTTTA	ENSG00000133961	NUMB	2.635346238	1
CTTAGGATTGGAGATAAA	ENSG00000124789	NUP153	3.105771067	1
CTCTTAGTCTCAAGATTGT	ENSG00000113569	NUP155	2.855954916	1
GCGGCAAATTTATATCTAT	ENSG00000102900	NUP93	2.545893924	1
CACTGGATGCAGATGTAAA	ENSG00000143748	NVL	2.573787021	1
GACTTTCATTCCAACATTA	ENSG00000144227	NXPH2	2.336466847	1
GCTGGCTGTTGATTATGAA	ENSG00000065154	OAT	2.014258357	1
GAGTTATAAAGTTATGATA	ENSG00000173559	OBFC2A	2.883136864	1
CTAGTATCATTAATCAAT	ENSG00000109205	ODAM	3.714022379	1
CTACTTATCTGGACATGGA	ENSG00000087263	OGFOD1	2.464666215	1
GGACCTTAGTGAATATAAA	ENSG00000198836	OPA1	3.882773503	1
GTCTGCATTGAGCTGATAA	ENSG00000174970	OR10AG1	2.271665895	1
CCCTCGGCCTCTAAGAAAT	ENSG00000182880	OR1D4	1.970810797	1
CCCTAAGTGCCCTAATATA	ENSG00000170803	OR2AG1	2.042908529	1
CCTTCAGACTCCCATGTAT	ENSG00000179615	OR2AP1	2.325419685	1
GGCAAATTTATTTCTCTCT	ENSG00000177535	OR2B11	2.060181073	1

ACATGTTTGTACATATATT	ENSG00000196071	OR2L13	1.966530632	1
CTTGCTTATCTTCAGTATA	ENSG00000184022	OR2T10	2.771398858	1
CCCATCCTGTTTGTCTTTA	ENSG00000174339	OR2Y1	2.0064763	1
CCATCTTTCTTATCTTAAT	ENSG00000181903	OR4C6	6.343537559	1
CCCTATTATTTACAGTGTA	ENSG00000176925	OR51F2	2.753655414	1
GCCTAGACATCATGCTTAT	ENSG00000187747	OR52B6	2.647420831	1
CAGCCACTTTAAATCCCAT	ENSG00000232268	OR52I1	2.872623895	1
CACTCAATCCTCTTGTCTA	ENSG00000180923	OR52L2P	2.345368813	1
GCTCTGATCTTATCCTTAT	ENSG00000183389	OR56A4	4.243235442	1
CTCTTTGCATTGTTTCTGT	ENSG00000172464	OR5AP2	2.312343966	1
GTTCTCACCTCATTGCCAT	ENSG00000197786	OR5B17	2.550252868	1
CAGAGTCTGCATACAACTA	ENSG00000179626	OR6C4	2.714474367	1
CTGTATCTTTATGTATATT	ENSG00000188324	OR6C6	3.005054071	1
CACCTCATGGCTGTAACATA	ENSG00000172154	OR8I2	2.011055177	1
GAATTTCTTGTACAAACAA	ENSG00000172199	OR8U8	4.041956317	1
GATCATTGTTGTTTATGTA	ENSG00000172457	OR9G4	2.406573122	1
CTCAGGAAGTGGTGATTAT	ENSG00000186513	OR9Q2	2.453276057	1
GTGATCTATAATTTAATAA	ENSG00000128699	ORMDL1	4.042328087	1
CGGTTCTTGGAGAAACATA	ENSG00000070882	OSBPL3	1.979512842	1
GCAGGTATCTCTGAAACAA	ENSG00000183378	OVCH2	2.173759221	1
CCTATACAGAAGCAGATTA	ENSG00000122884	P4HA1	2.325526353	1
GCGGTACTTTGAGCAGTTA	ENSG00000072682	P4HA2	2.352225155	1
GCCTCCATATTATACACCT	ENSG00000090621	PABPC4	1.967129165	1
CGCACCGTTCCACAGTATA	ENSG00000070756	PABPCP5	3.18221315	1
GTCTCAGTGTCTATCTGTA	ENSG00000100266	PACSIN2	2.438873855	1
CAGTGAAACTAACAAGAGA	ENSG00000076641	PAG1	2.16210212	1
CCAAGAAAGAGCTGATTAT	ENSG00000149269	PAK1	3.431589447	1
CTCGGACATCCATTCTTAA	ENSG00000101349	PAK7	2.263382759	1
GTATTTATATGGTACTGCT	ENSG00000157881	PANK4	2.62772007	1
GAGACCATGTCATGCAGAA	ENSG00000073150	PANX2	2.082058734	1
CCGAAGAGTCAAAGAGCTA	ENSG00000154143	PANX3	2.289077351	1
CTAATCATGTGCTTCAGAA	ENSG00000090060	PAPOLA	4.6842539	1
CATCTTATGTGCTTAATTA	ENSG00000163291	PAQR3	2.510354728	1
CAAGGCTTCTGTCTACTAA	ENSG00000170915	PAQR8	3.716489054	1
CGGGAGCTATGTGAATTTA	ENSG00000111224	PARP11	2.155748476	1
CTCAGTGCCTTAAATTATA	ENSG00000173193	PARP14	2.374694924	1
GGACTIONTATTAATCTTA	ENSG00000102699	PARP4	4.153386891	1
GCCTTTAACCTAAGAAGA	ENSG00000137817	PARP6	2.757531706	1
CATTGTAAGTATTCTGAAT	ENSG00000138496	PARP9	4.359147279	1
CCCAGCAACTTCTGCAGTA	ENSG00000100105	PATZ1	2.662961671	1
GCTGTAACTGTAACATTA	ENSG00000168078	PBK	2.197487977	1
CCCAGAATGGTTCAATGTA	ENSG00000132570	PCBD2	2.209440816	1
CTAAGAAAGCAGAGTTAA	ENSG00000175198	PCCA	3.638336536	1
CCCAATTATGCCAAGAACA	ENSG00000114054	PCCB	3.259632105	1
GAGACTTCATCATCAATAA	ENSG00000150275	PCDH15	2.192388637	1
CAAATAAGGCCATTGTCTA	ENSG00000180628	PCGF5	2.517696479	1
GATTCAGTATCCAGAGTTT	ENSG00000203880	PCMTD2	2.244084349	1
CCCAGTCTACCTATTTCAA	ENSG00000099139	PCSK5	2.554384183	1
GTGCTAACTGGTACCGCA	ENSG00000188389	PDCD1	2.21769925	1
GATATAGTCTGTTAGAATT	ENSG00000150593	PDCD4	2.44749573	1

CTAACTTCCTTGTGTGTTG	ENSG00000090470	PDCD7	2.187849856	1
GGAAGAAGAAGCCATCAAA	ENSG00000095464	PDE6C	2.458759413	1
GCTTTGAAATGTGCTGATA	ENSG00000205268	PDE7A	2.748019322	1
GCTGTAGTATTTAAGCCCA	ENSG00000197461	PDGFA	2.2478744	1
AGGTCTGCCTGACTTTATA	ENSG00000131828	PDHA1	2.146314813	1
CGGCCCATTTGTGAATTTA	ENSG00000168291	PDHB	2.12397632	1
GATGAAATTTGCTCTGCTA	ENSG00000143870	PDIA6	4.818191203	1
CTCATTCTCCACCCATCA	ENSG00000005882	PKD2	2.171691349	1
CTCCTAGCCTCTCTCCCAA	ENSG00000120509	PDZD11	1.963067229	1
CCTAATTTCTGTGAAATAA	ENSG00000162366	PDZK1IP1	2.745463717	1
CTTATTTGAACTGTATTTG	ENSG00000121440	PDZRN3	3.020201365	1
CTGCCAAATTTGCTGTTTA	ENSG00000242265	PEG10	2.595006234	1
GTGGTTTGATCAACAAGAA	ENSG00000108518	PFN1	2.645443956	1
CAGTAGTTCTTATGAGTCA	ENSG00000170950	PGK2	2.784125999	1
GGCTGTACATCGATAGCTA	ENSG00000079739	PGM1	3.156521737	1
GGGACGTTACCACTGGATA	ENSG00000165434	PGM2L1	2.962655884	1
AGATGAATCTTCAACTTTA	ENSG00000197724	PHF2	2.194143204	1
CTCACAATAGTATAGAAGA	ENSG00000010318	PHF7	2.802534225	1
CTGACCCTGTAGTACAGCA	ENSG00000092621	PHGDH	2.531621004	1
GCAACTGGATGAATGATTA	ENSG00000067177	PHKA1	2.34825026	1
CACAGGACTTCTATGAGAA	ENSG00000164776	PHKG1	2.08791574	1
GAGTTTGCGGTGAAGATTA	ENSG00000156873	PHKG2	2.70800238	1
CTCGATACACTCTACAAAT	ENSG00000040199	PHLPP2	2.538309973	1
CCAAATAGTCTATGTATAA	ENSG00000078043	PIAS2	3.660075214	1
CCGAGCCCGAGCTGGTTTA	ENSG00000162896	PIGR	3.830195686	1
CAGATGTATTGCTTGGTAA	ENSG00000121879	PIK3CA	3.012349919	1
CAAGTTATTTCACTTA	ENSG00000105851	PIK3CG	2.80837199	1
GACAGTGCTTGATACAGGA	ENSG00000137193	PIM1	2.119012431	1
GTATGTGCCTTGAAGTAA	ENSG00000158828	PINK1	3.882716579	1
GGCAAGACCTATTTATAAT	ENSG00000186111	PIP5K1C	2.232591533	1
CTTTAAAGCTGATCCGATA	ENSG00000118762	PKD2	4.099974227	1
CCGTCATGTTCTTCATTGT	ENSG00000107593	PKD2L1	2.360014537	1
CTGTAATTCTGTCTGCATA	ENSG00000130943	PKDREJ	2.219005773	1
GCTAACTGTCATTGTGCA	ENSG00000168734	PKIG	2.909668935	1
CCCGGACCACGGGTGACAT	ENSG00000123143	PKN1	2.173601649	1
CTGACTACCTTGACTTGAA	ENSG00000069764	PLA2G10	2.665285618	1
CTCAGTCTTTCTCGAAGCT	ENSG00000127472	PLA2G5	4.436917749	1
GGATGAATTACATCTGGGA	ENSG00000149507	PLAC1L	4.531008552	1
CAAATATTGCGAAGATCTA	ENSG00000101333	PLCB4	2.262064191	1
CTAGTCCTTGCAAATCCAA	ENSG00000114805	PLCH1	1.962837159	1
CCCTTTGTGCTCTGAGAAA	ENSG00000173846	PLK3	1.961429876	1
CAGTATAAGTGGTAGTTTA	ENSG00000142731	PLK4	1.993969558	1
CCAGTATTGTTATCAGTCA	ENSG00000221866	PLXNA4	3.705211257	1
CAGATTGTCTCTGACAGAA	ENSG00000004399	PLXND1	3.98040921	1
CATCCAAGTCCATAAGAAA	ENSG00000183395	PMCH	4.164831824	1
GTGTTTGATCACTATGGGA	ENSG00000078319	PMS2L1	2.467999779	1
CCAAATTTGTGGATGTAAT	ENSG00000175535	PNLIP	2.230095562	1
CAGATCGATTCTGATTTCA	ENSG00000115946	PNO1	1.991521141	1
CTAGATCTGTATGTTAATA	ENSG00000006757	PNPLA4	2.84552696	1
GGGAGTATCTGAGAAAGAA	ENSG00000108439	PNPO	4.725510841	1

CCGAATGTCTGAATGTTGA	ENSG00000143442	POGZ	3.85782164	1
GACCCACAGGCATGAATTA	ENSG00000100479	POLE2	2.140551867	1
CATTTCTTGAGAACGTATT	ENSG00000136480	POLG2	2.388187662	1
GAGTCACCAAGATACATTT	ENSG00000122008	POLK	2.427775756	1
GAGAACTGTCCTGTAGGAT	ENSG00000186184	POLR1D	4.693143487	1
ATTTCAAGGTGTTTATACT	ENSG00000144231	POLR2D	2.256172599	1
CAGACCCTGGAGGAGTTCA	ENSG00000099817	POLR2E	2.362367117	1
GATCTAATCTTAGATGTAA	ENSG00000163882	POLR2H	3.410407091	1
GAATGTGGTTACAGAATAA	ENSG00000224510	POLR2K	1.978486061	1
GCCTTAACTTGAGTTCTGT	ENSG00000183169	POM121L1P	4.538844124	1
CACATTCACAGATGAAGAT	ENSG00000005421	PON1	4.264133478	1
CACTGTGGAGATATTTAAA	ENSG00000105852	PON3	3.798540571	1
GTCTGAAATTTATAAGTAT	ENSG00000132429	POPDC3	4.477226141	1
GAACAAGTTTAATAGTGTA	ENSG00000128513	POT1	2.152375842	1
CACCCGTGTTCAAGTTTAA	ENSG00000151615	POU4F2	2.271260301	1
CTTTCAAAGGGTTAAATGT	ENSG00000162407	PPAP2B	1.965051253	1
CCGATGTTTGTTATTGCAT	ENSG00000147535	PPAPDC1B	2.076078117	1
CCAACACTCAGCTAAGTTA	ENSG00000109819	PPARGC1A	2.590487573	1
CTAAGAGAAACATAGGGAA	ENSG00000233097	PPBPL2	2.263271179	1
GAGAGAAAGGATATGGATA	ENSG00000168938	PPIC	2.129335749	1
CGCTATGTCAACAAGGATA	ENSG00000118898	PPL	2.680332498	1
AGGAGCACCTTCTGTGGAA	ENSG00000100614	PPM1A	1.976684251	1
GTGTTTGATTGCTCTGCTA	ENSG00000163590	PPM1L	2.304608653	1
GACAAGCTCCTGGACAAGA	ENSG00000108819	PPP1R9B	2.114559394	1
CTCTGTATTCTGGAACAA	ENSG00000068971	PPP2R5B	2.364103551	1
CGCTAGACCTGGACAAGTA	ENSG00000119414	PPP6C	2.493046177	1
CAGGTGAAATGCCTGAATA	ENSG00000137509	PRCP	2.417752963	1
CTTCAATATTAATTATCGA	ENSG00000186652	PRG2	2.70685853	1
GAGCTTACATGCTAATGTA	ENSG00000121031	PRKDC	2.596163171	1
ATGTTAAGCAGCTATGAAA	ENSG00000111218	PRMT8	4.773236114	1
CCTGTTGGCTCTTATTTCA	ENSG00000171199	PROL1	3.188140496	1
ATCAATAACGGATATTATT	ENSG00000165630	PRPF18	2.345275979	1
GAGCTAAAGGAAGGAGATA	ENSG00000117360	PRPF3	3.528934401	1
GCCAAGCTATGGGATAGTA	ENSG00000105618	PRPF31	2.820568051	1
CAATGCATTTGCAACAGAA	ENSG00000185246	PRPF39	2.084308342	1
GAATTTAGTGGCAAATACA	ENSG00000205352	PRR13	2.214783719	1
GCCAATACCAAGAAGTTTA	ENSG00000184838	PRR16	2.10440446	1
GCTACAACGCGGTTCCGAT	ENSG00000167371	PRRT2	2.035048556	1
GGCACTTTCCCGCCTCTTT	ENSG00000112812	PRSS16	2.364187626	1
CCAGCCGGCTGGAACCTCA	ENSG00000178226	PRSS36	2.612126548	1
CTATTAATAGATTCCCAT	ENSG00000099256	PRTFDC1	2.793928548	1
CATACTTTATATATGTTTA	ENSG00000135069	PSAT1	5.283142801	1
CCGTGAAGTCATTTCTGTA	ENSG00000204941	PSG5	2.657672317	1
CAATCAAATGCATCATCTG	ENSG00000164985	PSIP1	2.316811094	1
CTCTTGGTGTGATCACATA	ENSG00000147613	PSKH2	2.930446881	1
CTGTCCATCTGCTAACTAT	ENSG00000129084	PSMA1	2.5277998	1
GACAAGAGCTGCGAGAAGA	ENSG00000205220	PSMB10	2.376084887	1
CTGAACCTGTATGAGTTGA	ENSG00000108294	PSMB3	2.441464204	1
GGACCCACATATTTAAGAT	ENSG00000161057	PSMC2	6.838666397	1
GATTGGTTTCTTCAATAAA	ENSG00000013275	PSMC4	2.348545226	1

GCTCTGAACTGGTACAGAA	ENSG00000087191	PSMC5	2.521306574	1
CTATCAAACCTTCGATTAAT	ENSG000000197170	PSMD12	2.128443222	1
AAGGTGGTGTCTCAATAT	ENSG000000204538	PSORS1C2	2.475829571	1
CCTGTACCCTTGCAAGAAA	ENSG000000169403	PTAFR	10.96311671	1
CTGAACAGAGATGAATTGA	ENSG000000188647	PTAR1	2.57994975	1
CATTTAGATTATCCGAAT	ENSG000000165983	PTER	2.873568625	1
CTGAGCATAGTGGGCTGTA	ENSG000000112655	PTK7	3.524523306	1
CCATTTGTGCCATAGATTA	ENSG000000127947	PTPN12	2.102275235	1
GCATTTATGTGAAAGCTGT	ENSG000000163629	PTPN13	3.347958876	1
CCTGGACTTAAATTATTTA	ENSG000000152104	PTPN14	3.752671946	1
CCATTTAACACAACATATA	ENSG000000139304	PTPRQ	2.629752809	1
CAAAGCTATGTGTGGAATA	ENSG000000091127	PUS7	2.012033241	1
GTAACAGCTTCTCCTGTTA	ENSG000000121350	PYROXD1	2.222261671	1
CTATTCCAAACCTTTACAT	ENSG000000060749	QSER1	2.732654422	1
CTGTTGATTTGAGAAGAAA	ENSG000000151576	QTRTD1	2.242006017	1
GGAAATGAAGTATAAATCA	ENSG000000084733	RAB10	2.443169398	1
GCCTGTTTGTCTGTGAGTT	ENSG000000135631	RAB11FIP5	2.029340086	1
AGAAGATCCTTATTGGGAA	ENSG000000139998	RAB15	3.376314887	1
CGAATATGACTACCTGTTT	ENSG000000174903	RAB1B	2.923361511	1
ACATTAATATTATAACAAA	ENSG000000124209	RAB22A	2.765730341	1
CTCAGGATTTGGTAAGGCT	ENSG000000118508	RAB32	3.731004879	1
AGTTTCGTGCCGTTATTTA	ENSG000000111737	RAB35	2.682747626	1
CTTTCTCTGCCTCATTTGA	ENSG000000147127	RAB41	4.984628273	1
GCAATTGAGAAATCGTTTA	ENSG000000167461	RAB8A	2.859950111	1
CTAATAACGTTTCTTTAAT	ENSG000000123595	RAB9A	4.845440764	1
ACAGTTTGCTGATAACCAA	ENSG000000144840	RABL3	2.970684937	1
CTGGAGACTTATTTAATTT	ENSG000000152942	RAD17	2.087685955	1
CTTTCCAGTAGCAGGTCAA	ENSG000000119318	RAD23B	2.213141334	1
GGCATCCTCCTTGAAGTAT	ENSG000000182185	RAD51L1	2.066223007	1
CCCATGTTCCCTGAAATTAT	ENSG000000166349	RAG1	3.162853463	1
CATGTTTCACTGTTGATCA	ENSG000000184672	RALYL	7.837926587	1
CATTAATTGTAAATCTAAT	ENSG000000137040	RANBP6	1.972649126	1
GTCATTGGCTGTTGTGTTA	ENSG00000010017	RANBP9	7.125352252	1
CAATATATGTCTTGTCTTT	ENSG000000123728	RAP2C	2.393323729	1
CTCATTGACCACAACGAAA	ENSG000000107263	RAPGEF1	2.01753843	1
CAATTACTGAGCATGCTAT	ENSG000000173166	RAPH1	2.907250065	1
CTACTTAAGTGGAAGTAAA	ENSG000000075391	RASAL2	2.421335936	1
GGAACCCTGTGGGACAGAA	ENSG000000068831	RASGRP2	2.727369742	1
CTTACTTCCTGAGAGCTAA	ENSG000000152689	RASGRP3	2.117507758	1
CTCAGTACATTAAGTTTGA	ENSG000000107551	RASSF4	2.194068739	1
CCCAGATTCTATGTCTGA	ENSG000000169435	RASSF6	6.740510696	1
CCATTGACCAGAAAGACAA	ENSG000000203867	RBM20	4.009398326	1
CAGTAAATCTTGGAATAAA	ENSG000000086589	RBM22	3.820439653	1
GTATCTATTTTCAAGTCAT	ENSG000000112183	RBM24	2.280410956	1
CTGTGTTTCATTAGTATTA	ENSG000000139746	RBM26	3.256910118	1
CAGACTTGACCGAGCAATA	ENSG000000173933	RBM4	3.273950782	1
GTGACCCAGCTAACTTAAA	ENSG000000056586	RC3H2	3.554409425	1
CCTGTCATATCTCTACTAA	ENSG000000136161	RCBTB2	3.130029959	1
CCATTTGTTTGACAAAGAT	ENSG000000163743	RCHY1	2.859559567	1
GTCATAGTCCCAGAGGATA	ENSG000000142552	RCN3	2.058818525	1

CATTATCATTCCTTATGAA	ENSG00000187456	RDM1	3.156704545	1
CTTGCTGAAGCCCATAGCA	ENSG00000132563	REEP2	2.186240918	1
CTGTCAAGAAGCACAGGAT	ENSG00000143954	REG3G	3.438737478	1
GCCCGTCTATGACAAGAAA	ENSG00000104856	RELB	2.063018188	1
CATAAGTGCTTGTGAGGTA	ENSG00000135945	REV1	2.884851949	1
CTCATCTTCTGCTAAGATT	ENSG00000009413	REV3L	3.759981689	1
CTCTTATGGTCAACAGAAA	ENSG00000242732	RGAG4	3.175208903	1
GACTTTCTGGGAAAGGAGT	ENSG00000076344	RGS11	2.418793673	1
GAGATTATTTAAGTGATT	ENSG00000143333	RGS16	2.486292157	1
CCAAGAGTTTGGATTGCAA	ENSG00000186479	RGS7BP	3.166818964	1
ACATTTACATGCTCATGAA	ENSG00000108370	RGS9	2.899564215	1
CAAATGCTGATCATGACAA	ENSG00000112077	RHAG	2.292948455	1
GGATAAATACTGGACTTAT	ENSG00000144468	RHBDD1	3.712383013	1
CGCTACCTGACATACATCT	ENSG00000141314	RHBDL3	2.663557824	1
ACGCCCATCCTTGAATCAA	ENSG00000132677	RHBG	2.052318636	1
CTATCTAGGCTATTCAATA	ENSG00000126858	RHOT1	2.547724584	1
GCCACCATTATAATTTATA	ENSG00000116574	RHOU	3.008452184	1
GGCACATTCCCAAAGACAT	ENSG00000166405	RIC3	3.36006195	1
GAATCAGTTTCGCAGATTT	ENSG00000132669	RIN2	2.090100218	1
GGATGAAAGGTATATATAA	ENSG00000101782	RIOK3	3.428004535	1
CTCCTCTGGACAAGAAGTA	ENSG00000147223	RIPPLY1	3.659226164	1
GAAACCGACTTATTCATGT	ENSG00000146352	RLBP1L2	2.203551959	1
GAGTATATCTTTGAAGGAT	ENSG00000113360	RNASEN	4.426755519	1
GACATATAATTCTCTATTA	ENSG00000239305	RNF103	3.928229478	1
CGACCAAGCAGACCAGGTA	ENSG00000139797	RNF113B	1.999444031	1
CAGAACATTGGGATTCTAT	ENSG00000133874	RNF122	1.961778881	1
GAATATACTTCATTCACTA	ENSG00000082996	RNF13	2.970983176	1
CAGTATTATTGAATTTATA	ENSG00000170881	RNF139	3.293425273	1
ACTACAGCTTGAGAACGTA	ENSG00000013561	RNF14	2.006749197	1
CGAACATGTCCAATGTGTA	ENSG00000163162	RNF149	2.281977916	1
GGAAGAGTTCCAGAATGGT	ENSG00000141576	RNF157	2.81062829	1
CCATTTGCCTGGATGAATA	ENSG00000108523	RNF167	1.98297678	1
CTGCTGGCCTTGCTCATT	ENSG00000178828	RNF186	5.049751913	1
CACTCAAACCATCTCAGAA	ENSG00000152193	RNF219	2.735254643	1
CTCCTTTAATACAAATTCA	ENSG00000183574	RNF5	4.144099251	1
GTCATCACGGAATACCAGA	ENSG00000154134	ROBO3	2.968610556	1
CAGTTTCTCTACACGTATA	ENSG00000065371	ROPN1	2.854107641	1
CAGCCCTTGTTCTCATCAA	ENSG00000143365	RORC	3.167165667	1
CAAAGAATCTGATATTGAA	ENSG00000104237	RP1	3.492423291	1
CCACAGCACTCTAACCGAA	ENSG00000241450	RP11-247M1.1	4.429624012	1
GAGTAAGTGCTTGTTCCCA	ENSG00000139656	RP11-478K15.1	2.300070634	1
GGCTTACATCATTTCAAAT	ENSG00000203796	RP11-564D11.1	2.149117475	1
CACCTGCTATGTTCAATAT	ENSG00000234797	RP11-568G20.1	2.061311322	1
CACAAGGTACTCTGTGGAT	ENSG00000213867	RP11-829H16.1	1.99951883	1
CAATTCACACATTTGATTA	ENSG00000167046	RP11-93B14.1	2.422704136	1
GTGATTACACTATTGCAAA	ENSG00000102218	RP2	6.08677372	1
GGGACAATGTAGAAATGAT	ENSG00000103494	RPGRIP1L	6.878402378	1
GCATAAGTGGCAATCATAA	ENSG00000188846	RPL14	2.937463689	1
GACTGGCTCCTGATTATGA	ENSG00000223508	RPL23AP53	2.918445055	1
GCCCTCAAATTTATCAAGA	ENSG00000130255	RPL36	3.084897389	1

CACACTGATTGGAAGTGT	ENSG00000172809	RPL38	5.26771115	1
CATTGTTTGTGTTAATAAA	ENSG00000163125	RPRD2	3.803082766	1
CACAGAAAGCCTTATCATA	ENSG00000185088	RPS27L	2.54459813	1
CTCTCTAAAGACCTTTAAT	ENSG00000149273	RPS3P3	2.353203719	1
GCAAACCTTCGTACTTTCTA	ENSG00000137154	RPS6	2.782908871	1
CTGCTGATGTGCAGAGACA	ENSG00000175634	RPS6KB2	5.610066037	1
CATAGGCTCTTAAGCAGCA	ENSG00000168028	RPSA	2.649086379	1
CTGTGGATATGCAATCTTA	ENSG00000116954	RRAGC	3.087660094	1
CTGGCAGACATCCAGCAAA	ENSG00000124782	RREB1	1.98029994	1
GAGAGAGTAAGAGAAATAA	ENSG00000171848	RRM2	2.906077142	1
CCTATGATAATACCATTA	ENSG00000048392	RRM2B	1.998115164	1
CTCTTATCCTCCTTATTTA	ENSG00000114767	RRP9	3.386580331	1
GAGATGGACAGGGCTATAT	ENSG00000102104	RS1	2.033645778	1
CACGTCAGTCCTCTAGGAT	ENSG00000111834	RSHL1	2.654679739	1
CTTTCTCTATCTACAACTT	ENSG00000101282	RSPO4	2.363594176	1
CCATGTGTAACAAAGAGAA	ENSG00000148484	RSU1	2.807021886	1
ATGTAACTTTATTACAAT	ENSG00000139970	RTN1	3.508100023	1
CTCTTCTTCCAAATATATA	ENSG00000160753	RUSC1	3.090116807	1
CTCCTTATTTCTGTACTA	ENSG00000186350	RXRA	2.359349456	1
CTGTGGAGAGGATTCTAGA	ENSG00000143171	RXRG	2.031699691	1
CAGACTACATGGAGTCAAA	ENSG00000198626	RXR2	2.734860855	1
AAGAGCATCTGGAGGGAAT	ENSG00000163221	S100A12	3.428361698	1
GGAATGTGACTACAACAAA	ENSG00000188015	S100A3	2.030887325	1
GTGACCACGTTTCAACAAAT	ENSG00000196420	S100A5	2.146555789	1
CAAATCCAGTGGTGGGTAA	ENSG00000197956	S100A6	3.435241513	1
GGACTAAAGACATGTGGAA	ENSG00000166787	SAA3P	3.334384392	1
CCAGGGATGTCATAGTTAA	ENSG00000142230	SAE1	3.47991915	1
GCCAATCATTAAAGATGAA	ENSG00000130254	SAFB2	2.818874238	1
GAGTTATGCTGCGTATGAA	ENSG00000130561	SAG	2.462748518	1
CTGCCTATGTGTTTACAAA	ENSG00000181433	SAGE1	2.579618214	1
CTGGTATGGTTCTTTGATA	ENSG00000164576	SAP30L	2.239489854	1
CAGACTCTCTGTGACATAG	ENSG00000100239	SAPS2	2.043614743	1
GAAAGGCTGTTAGAGTCAA	ENSG00000152700	SAR1B	1.964041625	1
GCCATACAGAGCAGGAATA	ENSG00000004139	SARM1	2.01428844	1
CAGTCTATTTATGACAAGA	ENSG00000168077	SCARA3	2.57063203	1
CCATGACTCTTCTAAGTGA	ENSG00000143653	SCCPDH	3.00814153	1
CCTTGTTTCAGATATACATA	ENSG00000205209	SCGBL	2.280479588	1
CACTTTGAATGATACATTA	ENSG00000047634	SCML1	2.178171588	1
CTGTTGATTCCACAGAGAA	ENSG00000168356	SCN11A	2.045689958	1
CCGCTATCATTCAGCGTAA	ENSG00000153253	SCN3A	3.705914909	1
CCCGCTACGTCCAGGACTT	ENSG00000130489	SCO2	2.112948402	1
CTCTCTCCCGCCATGTCT	ENSG00000215397	SCRT2	3.869337625	1
CTGATATGATCCCAGAAAT	ENSG00000000457	SCYL3	2.593681349	1
ACGGGAATCTCTGTGGTAT	ENSG00000124145	SDC4	3.056331045	1
ATTTGACTCTTAAGATTAT	ENSG00000137575	SDCBP	4.18604185	1
GAAATGCTGATAGCTCATA	ENSG00000204370	SDHD	2.153099708	1
GGAGCACTCCTGCAAAGAA	ENSG00000146555	SDK1	2.266810881	1
GAAGTAAAGAAGATCAACA	ENSG00000157020	SEC13	2.183321475	1
CTGTGTGTCACTCAATTCT	ENSG00000100934	SEC23A	2.154561434	1
GCTTCTTTGTGAAATTGAT	ENSG00000132432	SEC61G	1.999435092	1

CTTATGACACTAACACTAT	ENSG00000198843	SELT	2.35367944	1
CACATTTCTTGTAACTACT	ENSG00000010319	SEMA3G	3.10731174	1
GAGTGTCGAACTTCGTAA	ENSG00000167680	SEMA6B	2.79805326	1
GACTIONCATGGGTGGGATAA	ENSG00000079387	SENP1	2.838083359	1
GCTTTAGTAGGTACTTATA	ENSG00000111897	SERINC1	2.070670059	1
CTTTGTATTTTCATGTGTAA	ENSG00000120742	SERP1	3.107416586	1
CTCCACCTTTGACAAGAAT	ENSG00000140093	SERPINA10	2.428437282	1
CATTTAATGATTGATTATA	ENSG00000188488	SERPINA5	3.281264551	1
GGGCCAAGCTCGGAATTAA	ENSG00000130766	SESN2	2.370288655	1
CCAGGTCTAATAAACACTA	ENSG00000152217	SETBP1	2.440204262	1
GTCTAATGCTCTTCCGAAT	ENSG00000185917	SETD4	3.011395572	1
AGCTTATTCTGATACAAGA	ENSG00000153914	SFRS12	2.101838021	1
CTCAGTTGGCAAACCTTCAT	ENSG00000161547	SFRS2	2.315012715	1
CTCCCGATTGTTCACCTA	ENSG00000124193	SFRS6	3.164337222	1
GCCTCTGCCTACTTTAGAA	ENSG00000061936	SFRS8	2.277139993	1
GACAGAATTTTCAGTTTAAT	ENSG00000229415	SFTA3	4.061364448	1
CAGAAGAGCTCCATACACA	ENSG00000107819	SFXN3	2.031552808	1
GAGTAAGGACATTCAGAAT	ENSG00000108823	SGCA	2.339179346	1
CCCATAACATTTAATACAA	ENSG00000127990	SGCE	2.001022974	1
CTGATGGCCTGCAAAGCAT	ENSG00000166224	SGPL1	2.533291483	1
CGTCCTCTGGCTTGGGTTA	ENSG00000181523	SGSH	6.176586299	1
CCAGGGTTCTCTATGATTA	ENSG00000097033	SH3GLB1	2.517049231	1
CTGTTATTGTATTTAACTA	ENSG00000107957	SH3PXD2A	2.647766267	1
CAAGCTCCAGGATTTCAAA	ENSG00000182199	SHMT2	3.068190322	1
CCCATTTCTTGATTGAAA	ENSG00000146950	SHROOM2	4.598921113	1
CTGCCTTGCTAAAGAGAAA	ENSG00000158352	SHROOM4	2.023470777	1
CACAGATTGTTAGAGAGTA	ENSG00000112246	SIM1	3.007204697	1
GTGATGAAATTATCACTAA	ENSG00000096717	SIRT1	2.867702251	1
GGAGCTCTATGCCTCAGTA	ENSG00000137078	SIT1	2.090576378	1
GTTCTTAAACCGTAACTAT	ENSG00000125255	SLC10A2	2.977396084	1
GTGCTTTAGCTTTAAATAT	ENSG00000165449	SLC16A9	2.862657338	1
CGACTTACTTCTATGAGTA	ENSG00000124568	SLC17A1	1.978140323	1
GGTGGTTGATAATCACCAA	ENSG00000184999	SLC22A10	2.000743525	1
CAGACCCTGCGTGTGGTCT	ENSG00000168065	SLC22A11	2.11062743	1
GCTAGTAGCCCTCACCTTT	ENSG00000144671	SLC22A14	2.806526436	1
CTGCCTTTAACATTGTTTA	ENSG00000163393	SLC22A15	2.161610314	1
CAGAATGTATGTCAAGAAT	ENSG00000112499	SLC22A2	3.000926927	1
GGAAATACCTCTCATCAAA	ENSG00000146477	SLC22A3	2.062498087	1
CTGTTTCAGGACTCGGAATA	ENSG00000197208	SLC22A4	4.374666123	1
CATCCTAGGCGGTCATTTA	ENSG00000149742	SLC22A9	2.08878881	1
AGAACTCTCTTAGATTTAA	ENSG00000155886	SLC24A2	2.183933173	1
CGGGTATCTTCTAATACCA	ENSG00000089060	SLC24A6	1.961726151	1
CATCATATGGCACCATTAA	ENSG00000102078	SLC25A14	2.101217374	1
GGATTTATCAGAACCTTTA	ENSG00000102743	SLC25A15	2.397905156	1
GGATTCTCAGTTACACTTA	ENSG00000075415	SLC25A3	2.4644839	1
CAGTGTTTCGCCCTAGAGTT	ENSG00000198246	SLC29A3	1.988691217	1
CTGCTTATGTGGTCCCTCA	ENSG00000133460	SLC2A11	2.193189041	1
CCCATATATTCTATCTAGA	ENSG00000146411	SLC2A12	3.063788777	1
GACCAAATGTTACAAGAAA	ENSG00000014824	SLC30A9	4.851992617	1
CATATAATCATCTTTGTTA	ENSG00000136868	SLC31A1	2.190714266	1

AGCAAATGGTGCATACGTA	ENSG00000116704	SLC35D1	2.489969696	1
GTCATCCTTGCGCAACTA	ENSG00000139209	SLC38A4	3.667310413	1
CTTTATGACTGACAATTAA	ENSG00000138821	SLC39A8	2.754444203	1
CTCACACTCATCTTCATCA	ENSG00000133065	SLC41A1	2.830233235	1
CTGTGAATGCCATCACATA	ENSG00000180638	SLC47A2	5.050693269	1
CGTTTCACTGAAGAAGCAT	ENSG00000050438	SLC4A8	2.197942441	1
GCCATCTTCTAAGACTGAA	ENSG00000183023	SLC8A1	2.760835928	1
ACAATTATCTCAGAGACAA	ENSG00000066230	SLC9A3	2.087499402	1
CTCAGTCAGCTCAAAGTAA	ENSG00000180251	SLC9A4	2.884779888	1
CTGTACATCTCCATCTTAT	ENSG00000174640	SLCO2A1	2.479197874	1
GAACCTTACGAATTAAGAA	ENSG00000172716	SLFN11	2.034861677	1
GGTTTACTCTGTTATCATA	ENSG00000163681	SLMAP	2.112829237	1
CTATTTTCATCTGTATCTTA	ENSG00000170365	SMAD1	3.233437606	1
GGCTATATTGGTTTATGTA	ENSG00000166949	SMAD3	2.039060792	1
CAGATTTACTCAATGTCAA	ENSG00000136824	SMC2	2.568971331	1
CACTTAGTATTAAGTTGAA	ENSG00000113810	SMC4	2.229649822	1
CCTAATATCCCAAGTTGCT	ENSG00000196787	SMCHD1	2.225048266	1
ACGATAATTTCCCTGTATA	ENSG00000119953	SMNDC1	2.921003265	1
CCAAGAACCTTGCAAAGAA	ENSG00000198742	SMURF1	3.03224471	1
CATGGCCTATCGTTTGATA	ENSG00000143740	SNAP47	2.377765145	1
CTCTTATCTGTGGATGCAT	ENSG00000065609	SNAP91	2.411841182	1
CATTGGCTATGGACCAGAA	ENSG00000164975	SNAPC3	2.614469281	1
CTTGCAGAGGCCAAGTATA	ENSG00000159210	SNF8	2.327402151	1
CGCATTGCAGACATTCCAA	ENSG00000163877	SNIP1	2.610853808	1
CTATTAACCTTGCCAGTTGT	ENSG00000184209	SNRNP35	3.948124962	1
CTCATTTAATTCTGGATAA	ENSG00000172164	SNTB1	2.481762452	1
CCGATGAAGAAGCTATTAA	ENSG00000100603	SNW1	3.456100391	1
GGTGGTTACTTATTACTTA	ENSG00000086300	SNX10	2.680352405	1
CTACCTATCTTCAAGCTAA	ENSG00000147164	SNX12	2.395425873	1
GTCACTAGTGGATTATGAA	ENSG00000129515	SNX6	2.860681398	1
GAGTGCTCATTGTGAAGAA	ENSG00000134243	SORT1	5.368349648	1
CTCACTCTGTGGTTTGAGA	ENSG00000115904	SOS1	2.326402639	1
CCGAGAATCCATGTATATA	ENSG00000181449	SOX2	2.374990424	1
CAAGACCTCTGATGGCAAA	ENSG00000134532	SOX5	1.989886025	1
CAGTTAACCTTCAAGACAT	ENSG00000125398	SOX9	2.653888161	1
CAGATCTGCAGTCCATTAA	ENSG00000185591	SP1	2.591653893	1
CTAATCCTCCAAGAATATA	ENSG00000079263	SP140	2.713702807	1
CAATGATAATGATAATTTA	ENSG00000170374	SP7	2.095304567	1
CCTAATAATGCCTATGAAT	ENSG00000104450	SPAG1	3.030347488	1
CCAAATAAATCAGAGATAA	ENSG00000008294	SPAG9	2.368333498	1
GGCTTAACATCTAATAATA	ENSG00000163071	SPATA18	2.027141085	1
CTAGTATTGGATGTATTTT	ENSG00000150628	SPATA4	3.199124466	1
GACTGCCCTTTGGATGTTT	ENSG00000042317	SPATA7	1.977186287	1
CCAATCCTATCAGTGAAGA	ENSG00000175374	SPESP1	2.908979014	1
CTCTGGGATTTCTTTGTCA	ENSG00000142539	SPIB	2.221759862	1
GCCACTGAGGAAGGAGGAA	ENSG00000147059	SPIN2A	2.287376016	1
GGGCTCACATATACGAATG	ENSG00000122711	SPINK4	2.431381362	1
GTCTTACTCCATTAATTCA	ENSG00000054796	SPO11	2.013634105	1
GTGACCCATGTATTGCATA	ENSG00000136158	SPRY2	2.164906572	1
CTGTTAACATTCAACCTTA	ENSG00000168939	SPRY3	1.961717289	1

CCCACCAAGGTGGCCTTGA	ENSG00000176422	SPRYD4	2.362559804	1
CAGACGACGAGCTGGATAA	ENSG00000070182	SPTB	1.985345134	1
CCCGTAGTGACATTAAGTT	ENSG00000090054	SPTLC1	2.161917924	1
CAAATCATGCTGAACTTAT	ENSG00000104549	SQLE	2.909026388	1
GATAAATTCTACATCTTCA	ENSG00000185739	SRL	2.845742664	1
CCATTGTCCAGCTCATTGA	ENSG00000184343	SRPK3	6.429866671	1
CCACTGCTCTCAAGAGCAA	ENSG00000132671	SSTR4	3.081655809	1
AACTCACTATGGATACATA	ENSG00000184005	ST6GALNAC3	2.416847905	1
GCGAAATCCACTAAATTTA	ENSG00000004866	ST7	2.683766261	1
CTGACGTTATCTTCGACTA	ENSG00000140557	ST8SIA2	3.225187938	1
CTTCTAATTTCTCTCTAAT	ENSG00000124356	STAMPB	2.908545547	1
GTCGTGTTTCCAAAGAGAA	ENSG00000138378	STAT4	2.395082784	1
CATGTAATTCTTCCTCTAT	ENSG00000127954	STEAP4	7.127435211	1
CTACATGGCTCCAGAAGTA	ENSG00000152953	STK32B	2.981493106	1
CCCACCAAGTATTTCTTTT	ENSG00000112079	STK38	4.041249762	1
CACCATCTCCTATCTCAGA	ENSG00000104435	STMN2	2.029378124	1
GGCCTCATATTTACACTAT	ENSG00000133115	STOML3	2.132803981	1
CTGACTGATTGGGAAAGAA	ENSG00000125695	STRADA	2.179335554	1
CACTGAAGAACGTCCAGAA	ENSG00000168818	STX18	1.979560091	1
CTGAGAGACACCTACATGA	ENSG00000178750	STX19	2.31892717	1
CAGCTAGTTTGTGCTAATT	ENSG00000111450	STX2	2.161889362	1
CATTGATAAGGATTTATA	ENSG00000145087	STXBP5L	2.084839205	1
CAATTGAATTTATTGGGAA	ENSG00000168952	STXBP6	2.7104955	1
CTTGAGATTCCATCACAA	ENSG00000127952	STYXL1	4.473212066	1
GGAGAAATCTTTAATGGTA	ENSG00000165416	SUGT1	3.229139258	1
CTAGGTCAGTTTATATATA	ENSG00000164744	SUNC1	4.274328146	1
GAAGTTTCAATATTTCAAT	ENSG00000106868	SUSD1	2.804615605	1
GCATCATTGACAAGACAAT	ENSG00000169895	SYAP1	2.018611157	1
GGATCTGACAGAGAAATTA	ENSG00000161860	SYCE2	2.910128073	1
CTAATAACGTGAAACTTAT	ENSG00000198765	SYCP1	2.57296327	1
CTTTGAGGATTTGAAGGAA	ENSG00000165025	SYK	3.525176756	1
GGCCTTATTGGAAGGAGAA	ENSG00000182253	SYNM	3.095879642	1
GAGGTACCACTGGTGGTTT	ENSG00000171992	SYNPO	2.589392589	1
CTGTTTATTTGTAAAGCTA	ENSG00000163630	SYNPR	2.508994934	1
CTCTTCCCTTGCTGTCCCA	ENSG00000143028	SYPL2	1.988640328	1
GAATTTATGTCTTACCACA	ENSG00000132718	SYT11	2.509677153	1
GTCACAGTGGTAGCATTTA	ENSG00000146383	TAAR6	3.067796545	1
CTGAGAAATTTATCACTAT	ENSG00000152382	TADA1L	4.094050192	1
ATGTCAGTGTTTATATGAA	ENSG00000120656	TAF12	3.021642785	1
GATATTAAAGCAGGAAATA	ENSG00000135090	TAOK3	2.750829352	1
CAGATTCACTGATGTTCCCT	ENSG00000059588	TARBP1	3.129163593	1
CAGTTCATCTCATTTCAAA	ENSG00000120948	TARDBP	2.643648118	1
GAAAGTAATGTCTATTCTA	ENSG00000121377	TAS2R7	2.016597834	1
CATTTATTGTGCTCACTGAT	ENSG00000121314	TAS2R8	2.007601996	1
GATCTAATCTAAATCTGTT	ENSG00000089123	TASP1	2.289602815	1
CCAATACACTATATAACAA	ENSG00000147687	TATDN1	3.371491892	1
CAGAGTCTTTAGAAAGTAT	ENSG00000065882	TBC1D1	3.207292477	1
GAATGAAATCACTAGTAAA	ENSG00000036054	TBC1D23	2.820056485	1
CGCCAGCTTTGGTGTTTCAT	ENSG00000162065	TBC1D24	2.509914868	1
CAAACCTTGCTGTAATATA	ENSG00000028839	TBPL1	2.34899286	1

CAACAGATTACGAAACTAA	ENSG00000122145	TBX22	2.446550394	1
CCATGACTACCTTTGTCTT	ENSG00000204219	TCEA3	2.641411642	1
CTAACAAAGGGCATGGAATT	ENSG00000100207	TCF20	2.326775038	1
CAGCACACTTGTCTAATAA	ENSG00000152284	TCF7L1	2.647487007	1
CTCTGTTATCTTGACATAA	ENSG00000182898	TCHHL1	2.143014712	1
GGACAATACAGATCATCAA	ENSG00000083544	TDRD3	2.064239104	1
CCCGAGAAGTACATGATGA	ENSG00000007866	TEAD3	3.584452777	1
GTGGACATCCGCCAAATCT	ENSG00000197905	TEAD4	2.036340675	1
CTAATTTTCATTCTTTGTGA	ENSG00000132604	TERF2	3.023262227	1
GCCATTTTCAGGCAGCATAA	ENSG00000166848	TERF2IP	2.2268119	1
GATGTGTTCTCTTATGGTA	ENSG00000070759	TESK2	2.138658376	1
CTTCGATAATTAAGATCAA	ENSG00000138336	TET1	3.326812924	1
CAAATATAATGAAGCTGTT	ENSG00000133863	TEX15	2.527141615	1
CGCAGAGAGGCATTCCTTT	ENSG00000091513	TF	8.698896455	1
CACACACTTAGCCATTGAA	ENSG00000087510	TFAP2C	2.259009912	1
GGCTTCAGCTCTTGTTAA	ENSG00000115112	TFCP2L1	3.132655617	1
GAGTCCAAATCCACTTAAA	ENSG00000105967	TFEC	2.325466262	1
CCATCAGGTGCAGAGGATA	ENSG00000105619	TFPT	2.835454074	1
CATAGAATTTAAATGTCAA	ENSG00000088451	TGDS	4.358940208	1
CTCATTCTCTGTTCTTTAA	ENSG00000135966	TGFBRAP1	2.056075332	1
GACCAGAAGTCCTAACAGA	ENSG00000152291	TGOLN2	2.58078726	1
CAGGCTTTCTCTTCAGTTA	ENSG00000169231	THBS3	3.185629269	1
CATACACTATCCACAGATA	ENSG00000100234	TIMP3	2.988455531	1
CTTCACGAAGGAGACATAA	ENSG00000119139	TJP2	2.652157576	1
AATTATATCCGTTCTGTGA	ENSG00000196781	TLE1	2.046856077	1
CCGACTGTGCTGGTATGAT	ENSG00000095587	TLL2	2.147276222	1
CATATATAATTCATGCCTA	ENSG00000164342	TLR3	3.152959879	1
CTTATCCACTTCTCAGTAT	ENSG00000168955	TM4SF20	2.356262451	1
CATGATTCTTCCTTTAATA	ENSG00000164935	TM7SF4	2.158732372	1
AGGACAAATAGTTTATTTA	ENSG00000077147	TM9SF3	3.498279415	1
CACTGCCTTCTTTGTAATA	ENSG00000135926	TMBIM1	2.552696373	1
CGTATTTATTCTTGCAATTA	ENSG00000165091	TMC1	2.0602152	1
CTTGCTAATGAAGAGACAA	ENSG00000149488	TMC2	2.318167366	1
GCGTATTTGTTAAGCACAA	ENSG00000170537	TMC7	2.506808029	1
CTGTTTCTGCTGCTCCAGT	ENSG00000167895	TMC8	3.796550521	1
CCTTTATCTTCTTAATGTT	ENSG00000150403	TMCO3	2.047043412	1
CCAAATTTGTCCTGTAGTA	ENSG00000241697	TMEFF1	2.19319119	1
CTTCTGATGGGAAATCTTA	ENSG00000144339	TMEFF2	2.225560924	1
CTGCTCTCCAGTTGGGTAT	ENSG00000126062	TMEM115	2.01999304	1
GCATGGAGAATCAAGACAA	ENSG00000139173	TMEM117	2.32144558	1
CTATGTCTATGAGAAAGAA	ENSG00000139364	TMEM132B	4.398016871	1
CAAAGGACTTGATTGGAGT	ENSG00000151952	TMEM132D	3.388462296	1
GAACCAATAAGAATTTCTA	ENSG00000161558	TMEM143	2.398747357	1
GTATCTTCATGTTTAAGGA	ENSG00000164124	TMEM144	2.521503381	1
CCTCTAATATGAACATTAG	ENSG00000096092	TMEM14A	1.973144065	1
GCTGCCATATCAGTTATTA	ENSG00000134851	TMEM165	2.987183162	1
GAGAATTTATATATAGATA	ENSG00000163449	TMEM169	6.035540338	1
GCGATGAAGTGGAGATTAT	ENSG00000151353	TMEM18	2.036895457	1
CTGCTTGATTTATTATTAA	ENSG00000146433	TMEM181	4.610374338	1
CATTAATTGCTATTACAA	ENSG00000139291	TMEM19	3.436939552	1

GCCTGATTAAGATGGTCCA	ENSG00000105518	TMEM205	2.65615434	1
GTGTGGATTATCAATTTAA	ENSG00000198398	TMEM207	2.008904428	1
CATATAATTCGATGTAAGA	ENSG00000187824	TMEM220	3.518929623	1
GGCTACTATTGAAGTGTA	ENSG00000126950	TMEM35	4.63464607	1
GGTACTTTCTTATTAGAAA	ENSG00000151715	TMEM45B	2.250451663	1
CAAAGAATACCAGGAAACA	ENSG00000167904	TMEM68	3.503496532	1
GAGTAGCATTCCACCTTGA	ENSG00000159596	TMEM69	2.128557334	1
CCCAGACCAGCGTTATGTA	ENSG00000165071	TMEM71	2.828847032	1
CTGATTCATTCATTAGTTG	ENSG00000151117	TMEM86A	2.937702949	1
CCCTTCCTCAAGTATTCTT	ENSG00000167920	TMEM99	2.232050453	1
CAGGGTCTCTCCTAGACCA	ENSG00000167664	TMIGD2	3.338171967	1
CATGCACACGCTCATGAGT	ENSG00000136842	TMOD1	2.565763422	1
CACATAACTAATAATTTAA	ENSG00000128872	TMOD2	4.70463993	1
CTTTATTCTCAAGGCAAT	ENSG00000125247	TMTC4	2.063669853	1
GACACAGATGGAGGTTATA	ENSG00000166479	TMX3	2.246492694	1
CTTAGAACTTTAAGCAACA	ENSG00000204490	TNF	5.184424241	1
GACATAATATATGGGTGAT	ENSG00000104689	TNFRSF10A	5.33331105	1
GGGAGAAATTTATATCAGA	ENSG00000173530	TNFRSF10D	2.038279207	1
GGAAGTTCAAGGAAGAATA	ENSG00000141655	TNFRSF11A	9.706500279	1
CAAAGTATTGTAAATTATA	ENSG00000120659	TNFSF11	2.167872119	1
GTAATACGTGAGGAATTTA	ENSG00000125657	TNFSF9	2.046764985	1
ATTAGACATTCAGAAATAGA	ENSG00000141198	TOM1L1	2.103938014	1
CGCCTATTTATGAAATAAT	ENSG00000198846	TOX	2.292477868	1
GAGTTAATCTTATTCTAGA	ENSG00000115129	TP53I3	2.602188693	1
CACCGTGTATGAATGCAGT	ENSG00000078804	TP53INP2	5.475433821	1
CACACAACGGGAGATGAA	ENSG00000186815	TPCN1	2.634460038	1
GAGCTCCTGTTTCAGGGATA	ENSG00000162341	TPCN2	3.722974865	1
GTGTCAACATGGTTCATAT	ENSG00000139287	TPH2	2.256438439	1
CTGTTTATTATGAAAGGTT	ENSG00000137364	TPMT	3.201693704	1
GGATTACTATGACAGAGGA	ENSG00000136527	TRA2B	2.797144222	1
GAGGCATTGATATCATTAA	ENSG00000056972	TRAF3IP2	1.981612977	1
CACAGCAGTGCAATGGAAT	ENSG00000175104	TRAF6	4.733762962	1
CTGTTAATATCTGGTTAAA	ENSG00000115993	TRAK2	3.287423116	1
AAGAGATGCTTGACATTA	ENSG00000132274	TRIM22	2.509348439	1
CACCTAAATTTAGAGCTTT	ENSG00000119401	TRIM32	2.6710588	1
CCATCTCCATTGAGATGAT	ENSG00000043514	TRIT1	1.982677895	1
GAGTCAATCTGAAAGAAAT	ENSG00000067445	TRO	2.98095063	1
CCATATAACTGTGATGAAA	ENSG00000116747	TROVE2	2.17755295	1
CAGTTTACATGGACTGAAA	ENSG00000138741	TRPC3	2.565642131	1
CTCCTCACCGATATGTACA	ENSG00000167112	TRUB2	2.296101351	1
CCAACGTCTTGAAGCAGAA	ENSG00000126467	TSKS	3.302282625	1
CTTGTCAAACCTAAGCATA	ENSG00000106537	TSPAN13	3.276891236	1
CAACGAGTTTGATACAGTT	ENSG00000158526	TSR2	2.414903082	1
GACATCAGCCAATTACAAA	ENSG00000018699	TTC27	3.782045399	1
GAAATTATGACTTTGGTAT	ENSG00000196659	TTC30B	2.484099185	1
CATTTACTCTGGAGATAGA	ENSG00000113638	TTC33	2.700656406	1
CACATATCTGAATGGGTAA	ENSG00000168234	TTC39C	3.681935786	1
CAAAGTTTACTATTTATCA	ENSG00000139865	TTC6	2.124119549	1
AGCCTACGGTCATTGATGA	ENSG00000127824	TUBA1	2.216531545	1
ATGATGAACTGAAATCTAA	ENSG00000130640	TUBGCP2	2.6738829	1

GGCTCAATCCTTTATCCTA	ENSG00000137822	TUBGCP4	2.636171577	1
CCAGGGATATGAATGGATA	ENSG00000151239	TWF1	3.054870778	1
CAATTAAAGTTGAACAAAT	ENSG00000198431	TXNRD1	4.878149293	1
GGCATTTCTGCAATGCAAA	ENSG00000184470	TXNRD2	2.525220553	1
CCAGTTCCTTCCATAATAA	ENSG00000176890	TYMS	5.128958282	1
CTGCTTAATAAATCAAAGA	ENSG00000162623	TYW3	4.83735207	1
CATAGGCTATTTCTTGATA	ENSG00000144744	UBA3	2.252557972	1
CATAGCATATCTGTGGCAA	ENSG00000077721	UBE2A	2.410943891	1
CAGACTATAATATTCATAT	ENSG00000186591	UBE2H	2.115115504	1
GCCTCAGACTGTGAAGTAT	ENSG00000156587	UBE2L6	2.072631157	1
CTTTCATGTGTGTTAAGAA	ENSG00000177889	UBE2N	2.643381457	1
CAGACTGATAGCTGCACAT	ENSG00000140367	UBE2Q2	2.848596584	1
CAGCCAGAATACTGGTTAA	ENSG00000177414	UBE2U	2.090562232	1
CTTCGTAAATTCATCATAT	ENSG00000151148	UBE3B	2.184824279	1
GCTGTTTACTGCAAATCCT	ENSG00000188021	UBQLN2	2.941737122	1
CACACTGGCCTTTGTAAAT	ENSG00000160803	UBQLN4	2.293008579	1
CCAAAGAGTTCAACTTGTA	ENSG00000024048	UBR2	2.282227179	1
GCCTTGAAAGGACAGTACA	ENSG00000130717	UCK1	2.281408415	1
CCATCCAGGAGCGACAGAA	ENSG00000175564	UCP3	2.737657963	1
CAGACACATTTATTGGATA	ENSG00000115446	UNC50	3.327103947	1
GTGATGTCATGGTGTTATA	ENSG00000182168	UNC5C	2.520169259	1
CTGGCAGTGTTCTTCGTAT	ENSG00000112494	UNC93A	2.326771509	1
CTGTGAGCTTTATCAGATA	ENSG00000076248	UNG	2.435933354	1
GTGAGGACTTCATCACATA	ENSG00000125351	UPF3B	2.399113856	1
GAACTAAGTCCCTATAATA	ENSG00000110375	UPK2	2.478900756	1
CATAGGCATACTTAAGTAA	ENSG00000156467	UQCRB	2.710480815	1
GAAACCTTTCCAACACAGA	ENSG00000140740	UQCRC2	2.51805128	1
CTGTGTACTTCACTGGAAA	ENSG00000058056	USP13	2.926845322	1
CAAAGTTAACAAACACATA	ENSG00000156256	USP16	3.668865547	1
CACCAGACCTCATCAGATT	ENSG00000124486	USP9X	1.96898546	1
GGTTTGTAACCATAACTAA	ENSG00000183520	UTP11L	4.190039862	1
GAGATATGAGTTTAAGTGA	ENSG00000120800	UTP20	2.705309453	1
GCGAACATAAGAGAATATT	ENSG00000108651	UTP6	2.577204916	1
CTAACAACTGGAAGAACT	ENSG00000188958	UTS2D	7.842377984	1
CTTAGAACCTGCTATATTA	ENSG00000049245	VAMP3	3.232622599	1
GCCTAGAGGCCGTTAGTAT	ENSG00000071246	VASH1	2.717926985	1
GGGCCACTGTGATGCTTTA	ENSG00000125753	VASP	2.424866714	1
CTGAGCAGCAACTAAGTTT	ENSG00000129862	VCY	2.60529342	1
GTTTATCTTCATTCATTAA	ENSG00000206538	VGLL3	3.286916137	1
CTGGCCAAATTGATAAATT	ENSG00000129003	VPS13C	2.561929626	1
CTCCTCCACTATAAGTCTA	ENSG00000155659	VSIG4	3.769171196	1
CCTATAGGCTGTTATTTCA	ENSG00000110002	VWA5A	2.520491069	1
GTATTTGGTGAAACTACA	ENSG00000132471	WBP2	2.099363464	1
CGGAAGAAGAAGCCATATA	ENSG00000185274	WBSCR17	3.557321547	1
GATCTAAACTATTGGATAA	ENSG00000162923	WDR26	2.407710059	1
GTCTTTCAGTTATGTATAT	ENSG00000198889	WDR40B	4.271576042	1
CTTATAAGCTTATCAATAA	ENSG00000162643	WDR63	2.881144965	1
CTGCTAAGAGAATTACAAT	ENSG00000166483	WEE1	3.644964378	1
CAGCCTAACTATATCTAT	ENSG00000180305	WFDC10A	2.465556479	1
GTAAAGAGGGTATAGAGA	ENSG00000168703	WFDC12	2.150782832	1

GCTGCAGGATGATAAGAAT	ENSG00000156232	WHAMM	2.261654007	1
CTTATAATTTCTACACCAA	ENSG00000147548	WHSC1L1	4.005413668	1
CTTATGAAGATATTCAGAT	ENSG00000171475	WIPF2	2.011757331	1
GAAAGTGCACGATCCTGAA	ENSG00000165238	WNK2	4.743227843	1
GCTCTCAAATGGTTTCTAA	ENSG00000196632	WNK3	2.409793991	1
CTCACTACCTTATTAGGAT	ENSG00000143184	XCL1	5.031186639	1
CCCAGATAAGTATGAATTA	ENSG00000173578	XCR1	1.991888693	1
GAGACTTCATGCAACAATA	ENSG00000163092	XIRP2	2.705021764	1
GTGATAATGATATTGGTAT	ENSG00000172967	XKR3	2.39072844	1
GTTATTATATTGTTAGGGT	ENSG00000221947	XKR9	2.38784616	1
CACCAGAAATGCTAGCCAA	ENSG00000124571	XPO5	2.575062551	1
GTCTTACAGGAGCTGGATA	ENSG00000196419	XRCC6	10.85071678	1
CCAAGTAAATCAACATCAT	ENSG00000114127	XRN1	2.274770965	1
GGCTTTGGATGAAGAGTAT	ENSG00000134684	YARS	1.967517168	1
GCCAGCAGCCTACCACAGA	ENSG00000006047	YBX2	1.967843743	1
GCCGCTGTTACAGAAACAA	ENSG00000167645	YIF1B	2.356114137	1
CTGTTTCATCACCTATAATA	ENSG00000137207	YIPF3	4.429126212	1
CTCACCAAGATGCATTTAA	ENSG00000136758	YME1L1	1.994639932	1
GGACAATCATTACCAGATA	ENSG00000126804	ZBTB1	4.901004619	1
CACCTAATAATGAAACGAA	ENSG00000205189	ZBTB10	2.556305698	1
CTGTCCTGAACCTTAAGAAA	ENSG00000171448	ZBTB26	2.54135445	1
CCAGATATGGCATTCCCTT	ENSG00000011590	ZBTB32	5.667797929	1
CAGCTACTCTGGCCATATA	ENSG00000114853	ZBTB47	3.915151925	1
CAATCTTTGTTTCTTATAT	ENSG00000186130	ZBTB6	5.549858031	1
GAGTCCATCATTAATTA	ENSG00000149289	ZC3H12C	2.494733337	1
CCATCCAAGCTACCTTATA	ENSG00000147905	ZCCHC7	2.551849748	1
CAGATATCATGTTTAGGTA	ENSG00000186908	ZDHHHC17	2.80759637	1
GCTATAAAGTAATAGAAGA	ENSG00000023041	ZDHHHC6	2.354207341	1
GTAATTCAGAAACACAGTA	ENSG00000066827	ZFAT	2.035927952	1
CATTATAACTGTTGTAGAA	ENSG00000020256	ZFP64	2.824794055	1
GTTGCATTTATTTAGTTA	ENSG00000165861	ZFYVE1	2.232681096	1
CATCCAAATGGCTCAATAA	ENSG00000174992	ZG16	2.319221064	1
GAGCACTTTAGATGGCTAT	ENSG00000174306	ZHX3	2.47145467	1
CCTATTTATTCAGTATGAA	ENSG00000139800	ZIC5	2.767188874	1
CATTTAGTATGAGAACCTA	ENSG00000166432	ZMAT1	2.993610324	1
CAGTTGATTGCATATCCTT	ENSG00000146007	ZMAT2	3.582752617	1
GCAACCTTCGGATTCCCTA	ENSG00000125846	ZNF133	3.214511032	1
CAATTAGAAGGGATTATTA	ENSG00000123870	ZNF137	2.264519564	1
GAAATCATACTGGTAAGAA	ENSG00000197008	ZNF138	4.025072555	1
CCTCATTAAGGATTATAAA	ENSG00000105497	ZNF175	3.524860603	1
GTCTGTCACTCCTATCATT	ENSG00000198315	ZNF192	2.20007355	1
CTCTACTCGACTCCAGGA	ENSG00000137185	ZNF193	2.836822688	1
CATACAAGATGCATTCCCA	ENSG00000005801	ZNF195	2.096535171	1
CTTACATTGCTATTTGTAA	ENSG00000010244	ZNF207	2.542029726	1
CCTGCTCCATCGGCACTAA	ENSG00000085644	ZNF213	3.528663041	1
GGCTTCAACAGTAAGTTTA	ENSG00000159882	ZNF225	2.472105984	1
GTATGGCTTCCGTTATTGT	ENSG00000169548	ZNF280A	4.661013712	1
GCCTAGATTTCATCTTGTA	ENSG00000056277	ZNF280C	2.904581972	1
GATTATATAGGAGAGCAAA	ENSG00000089335	ZNF302	2.910936078	1
CCCTTTGACTGCAGTCAGT	ENSG00000130803	ZNF317	1.992285196	1

CACACAGGATAATGCCAAT	ENSG00000171467	ZNF318	2.448179779	1
GAGAGAAGCCCTACAAATA	ENSG00000181894	ZNF329	6.074221672	1
CTGCTGAATGTCATTGAGA	ENSG00000131061	ZNF341	6.274226578	1
CCCTGTAAATACGCTGTTA	ENSG00000160094	ZNF362	3.735381213	1
CGTCAGAAGTCAGCCCTAA	ENSG00000075407	ZNF37A	2.521816261	1
ACATTTATGGGATATCTTA	ENSG00000186496	ZNF396	1.965729661	1
CTGATTATTTGAGATCACT	ENSG00000197050	ZNF420	2.563108149	1
CTGGAGCTCTCATCTTCAA	ENSG00000124459	ZNF45	3.85826774	1
CTCTTATACTGATGAGAAT	ENSG00000112200	ZNF451	2.36248754	1
CTATGACCTTGAATGTTCA	ENSG00000197016	ZNF470	1.968898044	1
CATTCTGTGTGGCAACAGT	ENSG00000173258	ZNF483	3.01785461	1
GAGAGAATCCCTTTATATG	ENSG00000127081	ZNF484	2.172687451	1
CTCAAGATCTTCATTTAAA	ENSG00000186446	ZNF501	4.187515014	1
CCATTCATATCTAGCAGAA	ENSG00000167555	ZNF528	2.516459646	1
CCCTATGAATACAAGGAAT	ENSG00000186020	ZNF529	2.112102364	1
CCACATCTTTCTTCTTAGT	ENSG00000178229	ZNF543	3.711130647	1
GTGCTTCTGTGAACGTGAA	ENSG00000204519	ZNF551	3.154131337	1
CTGTGCAAATTAATTCACA	ENSG00000172000	ZNF556	3.043389244	1
CATTTAAAGCCAAAGGGTT	ENSG00000130544	ZNF557	3.911252351	1
GGGAGAGAAACCCTACAAA	ENSG00000180938	ZNF572	2.850240662	1
CTTCCAAAGGGAGGAGCAT	ENSG00000213015	ZNF580	2.240328586	1
CCTTTATCCTAAGTCTGAA	ENSG00000018869	ZNF582	2.896346066	1
CCCTGATTGGGAGTATGTA	ENSG00000198440	ZNF583	2.202266025	1
GCATATCTCTCTCCAGGAT	ENSG00000168916	ZNF608	2.772601326	1
CTCAGAGAGTCATAGCTTA	ENSG00000176024	ZNF613	3.280413665	1
GTGTTATGAAATTAATATA	ENSG00000197619	ZNF615	2.539605897	1
CAAGGTCATTGGATAATTA	ENSG00000177842	ZNF620	2.968123001	1
GTGAGAGAAATTTCAAGAA	ENSG00000197566	ZNF624	3.417028268	1
CTTTGACCATGAAGAGAAA	ENSG00000188171	ZNF626	2.014607951	1
GACATTCTATTCGTTGTAA	ENSG00000075292	ZNF638	3.272568752	1
GGATTTATTTATGTCAATA	ENSG00000121864	ZNF639	4.967657249	1
GCAAGTCAGGTATAACAAA	ENSG00000167395	ZNF646	2.351752147	1
CGCATGCAGATTTGTGATA	ENSG00000198740	ZNF652	2.384202888	1
GGTATAGTTCACAGCTTAT	ENSG00000144792	ZNF660	2.023370764	1
GAGAACATTTCTACTGGAT	ENSG00000188295	ZNF669	3.024696437	1
CTTCACATTGCTCATGATA	ENSG00000083814	ZNF671	2.769656664	1
CCTTCTCCTCAACTCTTAA	ENSG00000197123	ZNF679	9.397215771	1
CTCACATCTTAATGAACAT	ENSG00000197124	ZNF682	2.640030873	1
ATATGAATTTCAGTGATAT	ENSG00000117010	ZNF684	2.312824803	1
CCAATTCATTTCAAAGACA	ENSG00000198429	ZNF69	4.164052245	1
GTTTGATATTCAGAAAGAA	ENSG00000197951	ZNF71	4.044283829	1
CAATGTATTTCACTAGT	ENSG00000172687	ZNF738	4.508987341	1
CTGTTAATTTCTTGACAA	ENSG00000196453	ZNF777	2.46975004	1
GAGAGAAACCCTATAAGGA	ENSG00000223547	ZNF844	2.04571085	1
GCCTCAGCTATGTAATTAA	ENSG00000130182	ZSCAN10	2.795504124	1
CTCGGCAAAGAATATCTTA	ENSG00000197213	ZSCAN5B	2.86807814	1
CCCTGCGTTCCCATGGTTA	ENSG00000162415	ZSWIM5	2.397170835	1