

Unique id	Gene Symbol	Overlap-Kool et al, 2008-Group:B (SHH)	Gene Description
2796951	PDLIM3	PDLIM3	PDZ and LIM domain
2745899	HHIP		hedgehog interacting
3140037	EYA1		eyes absent homolog
2736224	ATOH1		atonal homolog 1 (Drosophila)
3132782	SFRP1	SFRP1	secreted frizzled-related protein
2759205	PPP2R2C	PPP2R2C	protein phosphatase 2C regulatory subunit gamma
4006280	NDP	NDP	Norrie disease (pseudophakia)
2654454	SOX2	SOX2	SRY (sex determining region Y)-box 2
2740896	NDST3		N-deacetylase/N-sulfotransferase 3
2578028	CXCR4	CXCR4	chemokine (C-X-C motif) receptor 4
2594089	SATB2	SATB2	SATB homeobox 2
3165057	DMRTA1		DMRT-like family A1
3611625	ALDH1A3	ALDH1A3	aldehyde dehydrogenase class 1 family A member 3
3333595	GNG3	GNG3	guanine nucleotide binding protein (G protein)-gamma 3
3347118	GRIA4	GRIA4	glutamate receptor, ionotropic, AMPA 4
3927392	CYYR1	CYYR1	cysteine/tyrosine-rich transcription factor 1
3587495	SCG5	SCG5	secretogranin V (7B2)
2791419	C4orf18	C4orf18	chromosome 4 open reading frame 18
2915571	C6orf117	C6orf117	chromosome 6 open reading frame 117
2853102	PRLR	PRLR	prolactin receptor
2636319	BOC	BOC	Boc homolog (mouse)
3554104	KIF26A		kinesin family member 26A
2918388	POU3F2	POU3F2	POU domain class 3 transcription factor 2
2358092	CA14	CA14	carbonic anhydrase 14
2783596	PDE5A	PDE5A	phosphodiesterase 5A
3234083	ITIH2	ITIH2	inter-alpha (globulin) 2
2872047	SEMA6A	SEMA6A	sema domain, transmembrane 6A
2593796	RFTN2	RFTN2	raftlin family member 2
2703902	BCHE	BCHE	butyrylcholinesterase
3420442	IRAK3		interleukin-1 receptor-associated kinase 3
2859601	ADAMTS6		ADAM metalloproteinase 6
2373564	CRB1	CRB1	crumbs homolog 1 (Drosophila)
2916825	ANKRD6	ANKRD6	ankyrin repeat domain 6
3225855	ANGPTL2	ANGPTL2	angiopoietin-like 2
3359121	IGF2		insulin-like growth factor 2
2739160	HIGD1A		HIG1 domain family, class 1 member 1A
2748198	KIAA0922	KIAA0922	KIAA0922
3440568	NRIP2		nuclear receptor interacting protein 2
2380590	TGFB2		transforming growth factor beta 2
2745547	GAB1	GAB1	GRB2-associated binding protein 1
2321182	PDPN		podoplanin
2363128	VANGL2		vang-like 2 (van Gogh)
3068587	GPR85	GPR85	G protein-coupled receptor class C group 1 member 85
3328600	TSPAN18	TSPAN18	tetraspanin 18
2710599	CLDN1		claudin 1
3775906	ADCYAP1	ADCYAP1	adenylate cyclase activating protein 1
2894573	GCNT2	GCNT2	glucosaminyl (N-acetyl) transferase 2
2406926	GRIK3		glutamate receptor, ionotropic, kainate 3
3445741	MGP		matrix Gla protein
3368054	PAX6		paired box gene 6 (a)
2590582	PDE1A		phosphodiesterase 1A

2584134	IFIH1		interferon induced wi
3214800	OGN	OGN	osteoglycin
2995811	C7orf16	C7orf16	chromosome 7 open
3931495	KCNJ6	KCNJ6	potassium inwardly-r
2449391	KCNT2	KCNT2	potassium channel, ε
3419641	SRGAP1	SRGAP1	SLIT-ROBO Rho GT
2965653	GPR63		G protein-coupled re
3959388	APOL4		apolipoprotein L, 4
2963859	CNR1		cannabinoid receptor
2783978	KIAA1191		KIAA1191
2778440	UNC5C		unc-5 homolog C (C.
2973376	PTPRK	PTPRK	protein tyrosine phos
2855285	SEPP1	SEPP1	selenoprotein P, plas
3128911	STMN4		stathmin-like 4
2339786	PGM1	PGM1	phosphoglucomutas
2569908		39701	septin 10
3797295	L3MBTL4		l(3)mbt-like 4 (Droso
2749380	TMEM144		transmembrane prot
2970607	HS3ST5		heparan sulfate (gluc
2879739	PRELID2		PRELI domain conta
2958232	COL21A1		collagen, type XXI, a
2649824	SCHIP1	SCHIP1	schwannomin interac
2683763	ROBO1	ROBO1	roundabout, axon gu
3128411	EBF2		early B-cell factor 2
4054204	APOD	APOD	apolipoprotein D
2780143	BDH2	BDH2	3-hydroxybutyrate de
3288518	C10orf72		chromosome 10 ope
2918982	GRIK2	GRIK2	glutamate receptor, i
3375396	SYT7		synaptotagmin VII
3108146	SDC2	SDC2	syndecan 2
3465274	DCN	DCN	decorin
3060117	ABCB4	ABCC4	ATP-binding cassette
2649367	PTX3	PTX3	pentraxin-related ger
3019981	MDFIC	MDFIC	MyoD family inhibitor
3924573	PCNT		pericentrin (kendrin)
3020343	MET		met proto-oncogene
3140478	RPESP	RPESP	RPE-spondin
3990727	RAB33A	RAB33A	RAB33A, member R.
3423622	SYT1	SYT1	synaptotagmin I
3407453	PDE3A		phosphodiesterase 3
3679812	GRIN2A	GRIN2A	glutamate receptor, i
2470838	MYCN	MYCN	v-myc myelocytomat
2427619	KCNA3		potassium voltage-g
2859565	ADAMTS6		ADAM metallopeptid
3346412	C11orf70	C11orf70	chromosome 11 ope
3353335	STS-1	STS-1	Cbl-interacting protei
2447324	NMNAT2	NMNAT2	nicotinamide nucleot
3983537	PABPC5		poly(A) binding prote
2898746	LRRC16	LRRC16	leucine rich repeat c
2740507	UGT8	UGT8	UDP glycosyltransfer
2515240	CYBRD1	CYBRD1	cytochrome b reduct
3983324	KLHL4		kelch-like 4 (Drosopl
2834863	ABLIM3	ABLIM3	actin binding LIM prc

3197955	GLDC	GLDC	glycine dehydrogenase
3603436	CHRNA5		cholinergic receptor, alpha 5
3409605	MLSTD1		male sterility domain
2917825	FUT9	FUT9	fucosyltransferase 9
3637818	NTRK3		neurotrophic tyrosine kinase type III class A member 3
3546924	FLRT2		fibronectin leucine rich type 2 repeat domain
2598828	IGFBP5	IGFBP5	insulin-like growth factor binding protein 5
2776670	MAPK10	MAPK10	mitogen-activated protein kinase 10
3130244	TEX15		testis expressed 15
3046444	SFRP4	SFRP4	secreted frizzled-related protein 4
3395464	ASAM	ASAM	adipocyte-specific acyl-CoA oxidase
3653123	PRKCB1		protein kinase C, beta 1
3509677	SOHLH2		spermatogenesis and oogenesis 2
2958172	BMP5		bone morphogenetic protein 5
3883941	TGIF2	TGIF2	TGF-beta-induced factor 2
3126191	PSD3		pleckstrin and Sec7 domain containing 3
3727449	TOM1L1		target of myb1 (chick)
3890109	C20orf108		chromosome 20 open reading frame 108
3998247	NLGN4X	NLGN4X	neuroligin 4, X-linked
3149528	TRPS1	TRPS1	trichorhinophalangeal syndrome 1
2958117	HMGCLL1		3-hydroxymethyl-3-oxoacyl-CoA lyase
3121751	CSMD1		CUB and Sushi multiple domain 1
2822215	PAM	PAM	peptidylglycine alpha-amidohydrolase
3768703	ABCA9		ATP-binding cassette subfamily A member 9
2912416	BAI3		brain-specific angiogenesis inhibitor 3
3189311	PBX3	PBX3	pre-B-cell leukemia transcription factor 3
3837731	EMP3	EMP3	epithelial membrane protein 3
3447694	BCAT1		branched chain aminotransferase 1
3569754	ZFP36L1	ZFP36L1	zinc finger protein 36-like 1
3768627	ABCA8	ABCA8	ATP-binding cassette subfamily A member 8
2652801	NLGN1	NLGN1	neuroligin 1
3662808	GPR56	GPR56	G protein-coupled receptor class C group 5 member 6
2781138	LEF1		lymphoid enhancer factor 1
2781441	COL25A1		collagen, type XXV, alpha 1
2637112	GAP43		growth associated protein 43
2949330	CLIC1	CLIC1	chloride intracellular channel protein 1
3388631	TMEM123	TMEM123	transmembrane protein 123
2604390	ARL4C		ADP-ribosylation factor guanine nucleotide exchange factor 4C
3509645	SOHLH2		spermatogenesis and oogenesis 2
3721452	FKBP10		FK506 binding protein 10
3214845	ASPN	ASPN	asporin
3450775	KIF21A	KIF21A	kinesin family member 21A
4047493	PCDH18	PCDH18	protocadherin 18
3733590	SOX9		SRY (sex determining) box 9
3876645	BTBD3	BTBD3	BTB (POZ) domain containing 3
2648535	SGEF	SGEF	Src homology 3 domain containing protein tyrosine phosphatase SH3 domain binding protein
2498951	SULT1C4		sulfotransferase family 1C member 4
3442854	SLC2A3		solute carrier family 2 member 3
3555300	CCNB1IP1	CCNB1IP1	cyclin B1 interacting protein 1
3214825	OMD		osteomodulin
2870964	EPB41L4A	EPB41L4A	erythrocyte membrane protein 4.1L family class A member 4
2343823	LPHN2	LPHN2	latrophilin 2
4003017	PCYT1B	PCYT1B	phosphate cytidylyltransferase 1B

2777070	HSD17B11	HSD17B11	hydroxysteroid (17-b
2348437	SNX7	SNX7	sorting nexin 7
3661684	MMP2		matrix metallopeptid
3932524	DSCAM		Down syndrome cell
2521574	PLCL1	PLCL1	phospholipase C-like
2335671	ELAVL4		ELAV (embryonic let
2526971	TMEM169		transmembrane prot
3513514	P2RY5	P2RY5	purinergic receptor F
3841134	CACNG7		calcium channel, vol
3143643	C8orf57	C8orf57	chromosome 8 open
2554975	BCL11A	BCL11A	B-cell CLL/lymphoma
2614369	RARB		retinoic acid receptor
3788560	DCC		deleted in colorectal
2354634	PHGDH	PHGDH	phosphoglycerate de
2486178	MEIS1	MEIS1	Meis homeobox 1
3908631	PREX1	PREX1	phosphatidylinositol
2937144	SMOC2	SMOC2	SPARC related mod
2373336	CFH		complement factor H
2770039	NMU		neuromedin U
2882834	C5orf4		chromosome 5 open
2984275	PDE10A		phosphodiesterase 1
3144235	TMEM55A	TMEM55A	transmembrane prot
3426502	PLXNC1		plexin C1
3532935	MIPOL1		mirror-image polydac
2790324	RNF175		ring finger protein 17
3913737	C20orf58		chromosome 20 ope
2489172	MTHFD2	MTHFD2	methylenetetrahydro
2615060	RBMS3	RBMS3	RNA binding motif, s
3833122	DLL3		delta-like 3 (Drosoph
4016193	TMSL8		thymosin-like 8
3559192	PRKD1	PRKD1	protein kinase D1
2880361	JAKMIP2		janus kinase and mic
3974098	MID1IP1		MID1 interacting prot
2462160	NID1	NID1	nidogen 1
3442812	SLC2A14		solute carrier family
2823551	MAN2A1	MAN2A1	mannosidase, alpha,
2954022	---		---
3513549	RCBTB2	RCBTB2	regulator of chromos
3163818	SH3GL2		SH3-domain GRB2-I
2371346	RGL1	RGL1	ral guanine nucleotid
2345286	LMO4	LMO4	LIM domain only 4
2583602	ITGB6		integrin, beta 6
2418078	NEGR1		neuronal growth reg
2863885	LHFPL2	LHFPL2	lipoma HMGIC fusio
2869880	EFNA5		ephrin-A5
3391653	DRD2		dopamine receptor C
3733065	MAP2K6	MAP2K6	mitogen-activated pr
3385769	CTSC	CTSC	cathepsin C
3385951	NOX4		NADPH oxidase 4
3979659	MSN		moesin
2602653	PID1	PID1	phosphotyrosine inte
3041294	FAM126A	FAM126A	family with sequence
2423907	F3	F3	coagulation factor III

3309602	RGS10	RGS10	regulator of G-protein
2523045	FZD7	FZD7	frizzled homolog 7 (L
2580802	RND3	RND3	Rho family GTPase ;
3414885	SLC4A8		solute carrier family ;
3717870	TMEM98		transmembrane prot
3047660	GLI3	GLI3	GLI-Kruppel family m
2364677	PBX1	PBX1	pre-B-cell leukemia t
3683018	RPS15A		ribosomal protein S1
3936167	CECR2	CECR2	cat eye syndrome ch
3962578	A4GALT	AASS	alpha 1,4-galactosylt
2677853	IL17RD		interleukin 17 recept
3447022	ST8SIA1	ST8SIA1	ST8 alpha-N-acetyl-r
3746574	PMP22		peripheral myelin prc
3790704	PMAIP1		phorbol-12-myristate
3298557	GRID1		glutamate receptor, i
3389077	PDGFD	PDGFD	platelet derived grow
2598099	BARD1	BARD1	BRCA1 associated F
2536625	BOK	BOK	BCL2-related ovariar
3817437	FSD1		fibronectin type III ar
2520533	OBFC2A		oligonucleotide/oligo
3811339	BCL2	BCL2	B-cell CLL/lymphoma
2820394	NR2F1	NR2F1	nuclear receptor sub
2776088	CCDC98	CCDC98	coiled-coil domain cc
3507003	LNX2	LNX2	ligand of numb-prote
3424218	FLJ21963		FLJ21963 protein
3801943	ZNF521		zinc finger protein 52
2347625	SLC44A3		solute carrier family ;
3594986	TEX9	TEX9	testis expressed 9
3585905	APBA2		amyloid beta (A4) pr
3442706	CD163		CD163 molecule
3902552	FKHL18		forkhead-like 18 (Drc
3374517	GLYATL2		glycine-N-acyltransfe
2459616	HIST3H2A		histone cluster 3, H2
3944882	LGALS1		lectin, galactoside-bi
3067478	NRCAM	NRCAM	neuronal cell adhesic
3023149	FLNC		filamin C, gamma (a
2431112	NOTCH2	NOTCH2	Notch homolog 2 (Dr
3086206	FDFT1	FDFT1	farnesyl-diphosphate
2903189	HLA-DRA		major histocompatibi
2524653	ADAM23		ADAM metallopeptid
3554818	CRIP2	CRIP2	cysteine-rich protein
3374934	MS4A6A		membrane-spanning
3960110	MFNG		MFNG O-fucosylpep
3323052	NAV2	NAV2	neuron navigator 2
2962383	FAM46A	FAM46A	family with sequence
3806459	ST8SIA5		ST8 alpha-N-acetyl-r
2806091	RAI14	RAI14	retinoic acid induced
2591837	SLC40A1		solute carrier family ;
3361811	STK33		serine/threonine kin
3601511	ISLR		immunoglobulin sup
3376054	BSCL2		Bernardinelli-Seip cc
2502821	DBI		diazepam binding int
3108226	PGCP	PGCP	plasma glutamate ca

2348992	VCAM1	VCAM1	vascular cell adhesic
3540552	FUT8	FUT8	fucosyltransferase 8
2616166	CRTAP	CRTAP	cartilage associated
3988435	DOCK11	DOCK11	dedicator of cytokine
3062082	PDK4	PDK4	pyruvate dehydroger
3302572	CRTAC1		cartilage acidic prote
3257031	STAMBPL1		STAM binding protein
3174816	ANXA1		annexin A1
3735478	SPHK1		sphingosine kinase 1
3376529	HRASLS3		HRAS-like suppresso
3651639	TMEM159		transmembrane prot
3725685	NGFR		nerve growth factor r
3143660	MMP16		matrix metallopeptid
3322958	ZDHHC13	ZDHHC13	zinc finger, DHHC-ty
2756630	CPLX1	CPLX1	complexin 1
3676300	RPS2	RPS2	ribosomal protein S2
2477073	CRIM1	CRIM1	cysteine rich transme
2526759	ATIC	ATIC	5-aminoimidazole-4-
2635998	TAGLN3		transgelin 3
3861786	FBXO17		F-box protein 17
2566848	AFF3		AF4/FMR2 family, m
2509900	KIF5C		kinesin family memb
3875908	PLCB4		phospholipase C, be
2751936	GALNT7		UDP-N-acetyl-alpha-
3154317	NDRG1		N-myc downstream r
3813840	ZNF516	ZNF516	zinc finger protein 51
2977265	HIVEP2		human immunodefici
3463522	PAWR		PRKC, apoptosis, W
3308397	HSPA12A	HSPA12A	heat shock 70kDa pr
3924254	PCBP3		poly(rC) binding prot
3727499	TOM1L1		target of myb1 (chick
2490351	CTNNA2		catenin (cadherin-as
2613880	UBE2E2		ubiquitin-conjugating
2777564	FAM13A1	FAM13A1	family with sequence
2510056	LYPD6	LYPD6	LY6/PLAUR domain
2520429	MYO1B	MYO1B	myosin IB
3866276	SLC1A5		solute carrier family
2698565	TFDP2	TFDP2	transcription factor D
2601414	SERPINE2		serpin peptidase inhi
3181600	GALNT12		UDP-N-acetyl-alpha-
3060300	SRI	SRI	sorcic
3405032	ETV6	ETV6	ets variant gene 6 (T
3569285	C14orf83	C14orf83	chromosome 14 ope
3576749	FBLN5		fibulin 5
3449700	FAM60A		family with sequence
2680819	SUCLG2	SUCLG2	succinate-CoA ligase
2375664	BTG2	BTG2	BTG family, member
2347788	RWDD3	RWDD3	RWD domain contain
3409211	PPFIBP1		PTPRF interacting p
2792800	FLJ20035	FLJ20035	hypothetical protein I
3714177	SPECC1		sperm antigen with c
3066751	SYPL1	SYPL1	synaptophysin-like 1
3984468	SRPX2		sushi-repeat-contain

3446868	LDHB	LDHB	lactate dehydrogenase
2590715	FRZB		frizzled-related protein
2645764	ATP1B3		ATPase, Na ⁺ /K ⁺ translocating
3916527	JAM2	JAM2	junctional adhesion molecule
2780099	NHEDC2	NHEDC2	Na ⁺ /H ⁺ exchanger domain
2358117	C1orf54	C1orf54	chromosome 1 open reading frame
3077273	FAM131B		family with sequence similarity 131B
2617276	CTDSPL	CTDSPL	CTD (carboxy-terminal domain)
2487082	ANTXR1	ANTXR1	anthrax toxin receptor
2379665	PROX1		prospero homeobox domain
2375706	ATP2B4	ATP2B4	ATPase, Ca ⁺⁺ transporting
3940631	YES1		y-yes-1 Yamaguchi sarcoma
2837029	SGCD		sarcoglycan, delta (3 kDa)
2598606	PECR		peroxisomal trans-2-enoyl-CoA
3257670	PCGF5	PCGF5	polycomb group ring finger
3538213	DAAM1	DAAM1	dishevelled associated armadillo
2705164	EIF5A2		eukaryotic translation initiation
4024160	ATP11C	ATP11C	ATPase, Class VI, type I
3042012	C7orf31	C7orf31	chromosome 7 open reading frame
2428079	C1orf183		chromosome 1 open reading frame
3741528	TAX1BP3	TAX1BP3	Tax1 (human T-cell leukemia
3048363	PGAM2		phosphoglycerate mutase
3987228	PAK3	PAK3	p21 (CDKN1A)-activated kinase
3513856	EBPL	EBPL	emopamil binding protein
3002640	EGFR		epidermal growth factor receptor
3908963	B4GALT5	B4GALT5	UDP-Gal:betaGlcNAc 4-epimerase
3583638	CYFIP1	CYFIP1	cytoplasmic FMR1 interacting
3571059	DPF3	DPF3	D4, zinc and double-strand break
3897280	PAK7		p21(CDKN1A)-activated kinase
2376299	CNTN2		contactin 2 (axonal)
2634965	BBX	BBX	bobby sox homolog (Drosophila)
2751066	PALLD	PALLD	palladin, cytoskeletal protein
3419471	RPL14	RPL14	ribosomal protein L14
2950329	HLA-DPA1		major histocompatibility complex
2383356	CABC1		chaperone, ABC1 family
2673873	IMPDH2	IMPDH2	IMP (inosine monophosphate) dehydrogenase
3986730	COL4A5	COL4A5	collagen, type IV, alpha 5 chain
2471978	RHOB		ras homolog gene family B
2373736	NEK7	NEK7	NIMA (never in mitosis) kinase
3165624	---		---
2709778	BCL6		B-cell CLL/lymphoma 6
2645315	SPSB4		splA/ryanodine receptor
3418298	KIF5A		kinesin family member 5A
2781693	CASP6		caspase 6, apoptosis 6
2336439	GPX7	GPX7	glutathione peroxidase 7
3472312	SLC24A6	SLC24A6	solute carrier family 24, member 6
2974935	SLC2A12		solute carrier family 2, member 12
3148582	EIF3S6		eukaryotic translation initiation
3768474	WIP1	WIP1	WD repeat domain, phosphatase
3631397	UACA		uveal autoantigen with
2461037	RPS7	RPS7	ribosomal protein S7
3983962	DIAPH2	DIAPH2	diaphanous homolog 2
2908423	SLC29A1	SLC29A1	solute carrier family 29, member 1

3070183	AASS		aminoadipate-semial
3336094	RAB1B		RAB1B, member RA
3117384	KHDRBS3		KH domain containi
3326400	CAT	CAT	catalase
3808854	TCF4	TCF4	transcription factor 4
3439256	RPS11	RPS11	ribosomal protein S1
2950263	HLA-DMB		major histocompatibi
3216276	SLC35D2	SLC35D2	solute carrier family :
3712098	TRPV2		transient receptor po
3498589	CLYBL		citrate lyase beta like
4027176	FLNA	FLNA	filamin A, alpha (acti
3269939	DOCK1	DOCK1	dedicator of cytokine
2373406	CFHR1		complement factor H
2378325	SERTAD4		SERTA domain conta
3664843	CMTM3	CMTM3	CKLF-like MARVEL t
2766122	FLJ13197		hypothetical FLJ1319
3008220	CLIP2		CAP-GLY domain co
3768791	ABCA6		ATP-binding cassette
2645387	ACPL2		acid phosphatase-lik
2854092	LIFR		leukemia inhibitory fa
2816459	F2R	F2R	coagulation factor II
3862167	DYRK1B		dual-specificity tyrosi
3526544	DCUN1D2		DCN1, defective in c
2700404	WWTR1	WWTR1	WW domain containi
2568687	FHL2	FHL2	four and a half LIM d
3561532	SLC25A21		solute carrier family :
2587961	CHRNA1		cholinergic receptor,
3323413	HTATIP2		HIV-1 Tat interactive
3536706	LGALS3	LGALS3	lectin, galactoside-bi
2520291	GLS	GLS	glutaminase
3403077	ENO2		enolase 2 (gamma, r
3751002	RAB34	RAB34	RAB34, member RA
2477933	GALM	GALM	galactose mutarotas
3971219	CNKSR2		connector enhancer
2657250	LPP	LPP	LIM domain containi
3015911	TRIP6		thyroid hormone rece
3305313	KIAA1754		KIAA1754
3418249	KIF5A		kinesin family memb
3145953	RPL30	RPL30	ribosomal protein L3
3321055	TEAD1	TEAD1	TEA domain family n
3495076	NDFIP2	NDFIP2	Nedd4 family interac
3867796	TEAD2	TEAD2	TEA domain family n
4015397	TSPAN6	TSPAN6	tetraspanin 6
2427720	TMEM77	TMEM77	transmembrane prot
3389529	KIAA1826		KIAA1826
2376922	MAPKAPK2	MAPKAPK2	mitogen-activated pr
2704267	GOLPH4		golgi phosphoprotein
3325820	DEPDC7		DEP domain contain
2371065	LAMC1	LAMC1	laminin, gamma 1 (fc
3278401	FRMD4A		FERM domain conta
2409847	PTCH2		patched homolog 2 (
3444958	DUSP16		dual specificity phos
3610110	NR2F2	NR2F2	nuclear receptor sub

3527662	RNASE6	RNASE6	ribonuclease, RNase
3896034	RASSF2	RASSF2	Ras association (Ral
3420497	HELB		helicase (DNA) B
2971801	MAN1A1	MAN1A1	mannosidase, alpha,
2596514	KLF7		Kruppel-like factor 7
2362089	KIRREL	KIRREL	kin of IRRE like (Dro
3569814	ACTN1	ACTN1	actinin, alpha 1
2404344	FAM77C		family with sequence
3837464	SEPW1		selenoprotein W, 1
2618640	ENTPD3		ectonucleoside triphc
2783316	SEC24D		SEC24 related gene
3587457	ARHGAP11A	ARHGAP11A	Rho GTPase activati
3276337	ITIH5	ITIH5	inter-alpha (globulin)
3934111	SNF1LK	SNF1LK	SNF1-like kinase
2426951	SORT1		sortilin 1
2408351	RIMS3		regulating synaptic n
3414739	METTL7A		methyltransferase lik
2964231	RRAGD	RRAGD	Ras-related GTP bin
2545092	HADHA	HADHA	hydroxyacyl-Coenzym
3928668	TIAM1		T-cell lymphoma inva
3302177	ARHGAP19	ARHGAP19	Rho GTPase activati
2713382	BDH1		3-hydroxybutyrate de
3418120	GLI1		glioma-associated or
3325680	PCID1		PCI domain containi
2340186	RAVER2	RAVER2	ribonucleoprotein, P'
4002173	RPS6KA3	RPS6KA3	ribosomal protein S6
3949722	FAM19A5		family with sequence
2673937	QARS	QARS	glutaminyl-tRNA synt
2635641	PVRL3	PVRL3	poliovirus receptor-re
3313690	TCERG1L	TCERG1L	transcription elongati
2838598	CCNG1	CCNG1	cyclin G1
3019401	ZNF277P		zinc finger protein 27
3817040	HMG20B	HMG20B	high-mobility group 2
3891530	PHACTR3		phosphatase and acti
3863547	ERF	ERF	Ets2 repressor factor
3130872	DUSP26		dual specificity phosp
2583374	PLA2R1		phospholipase A2 re
3943504	TIMP3		TIMP metallopeptida
2451958	RPL21		ribosomal protein L2
2706938	GNB4	GNB4	guanine nucleotide b
3576411	GPR68		G protein-coupled re
2720145	LAP3	LAP3	leucine aminopeptida
2654967	B3GNT5		UDP-GlcNAc:betaGlc
3511031	ELF1	ELF1	E74-like factor 1 (ets
2592005	HIBCH	HIBCH	3-hydroxyisobutyryl-l
3684548	LOC730092		RRN3 RNA polymera
3523881	KDEL1		KDEL (Lys-Asp-Glu-l
3025545	CALD1	CALD1	caldesmon 1
2625907	FLNB	FLNB	filamin B, beta (actin
2884578	CCNJL		cyclin J-like
2452405	NUAK2		NUAK family, SNF1-
2437152	THBS3		thrombospondin 3
2781813	ELOVL6		ELOVL family memb

3320944	TEAD1	TEAD1	TEA domain family n
2938196	EXOC2		exocyst complex con
2820925	RHOBTB3	RHOBTB3	Rho-related BTB dor
3529908	NFATC4	NFATC4	nuclear factor of acti
2716713	STK32B		serine/threonine kin
2460189	PGBD5		piggyBac transposat
3521174	ABCC4		ATP-binding cassette
3595096	TCF12	TCF12	transcription factor 1.
3671935	CRISPLD2		cysteine-rich secreto
3707095	ARRB2	ARRB2	arrestin, beta 2
2910364	TMEM14A		transmembrane prot
3164914	MTAP	MTAP	methylthioadenosine
2463482	OPN3		opsin 3 (encephalop
3452323	SLC38A2	SLC38A2	solute carrier family :
2527196	RPL37A		ribosomal protein L3
3969047	PRPS2		phosphoribosyl pyro
2361154	SYT11	SYT11	synaptotagmin XI
3505319	SACS		spastic ataxia of Che
2991103	BZW2		basic leucine zipper
3168938	POLR1E		polymerase (RNA) I
3130294	PURG		purine-rich element t
3114832	SQLE		squalene epoxidase
2415084	JUN		jun oncogene
2669641	SCN5A		sodium channel, volt
3927226	APP		amyloid beta (A4) pr
3377226	EHD1	EHD1	EH-domain containir
3406493	DERA		2-deoxyribose-5-pho
3501661	ARHGEF7	ARHGEF7	Rho guanine nucleot
2890517	RASGEF1C		RasGEF domain farr
3450899	SLC2A13	SLC2A13	solute carrier family :
2586603	TLK1		tousled-like kinase 1
3413344	PFKM		phosphofructokinase
4001369	SCML2		sex comb on midleg-
2638962	DTX3L		deltex 3-like (Drosop
2580635	C2orf25		chromosome 2 open
2830946	CTNNA1		catenin (cadherin-as
3744800	STX8	STX8	syntaxin 8
2992998	C7orf46		chromosome 7 open
2726072	ATP10D		ATPase, Class V, typ
2971564	C6orf204		chromosome 6 open
2766419	RPL9		ribosomal protein L9
3521372	DZIP1		DAZ interacting prote
2723710	PGM2		phosphoglucomutas
2891052	GNB2L1	GNB2L1	guanine nucleotide b
3316287	EFCAB4A		EF-hand calcium bin
3946351	ADSL	ADSL	adenylosuccinate lya
3442249	C12orf53		chromosome 12 ope
3514849	NEK3	NEK3	NIMA (never in mitos
2470805	MYCN	MYCN	v-myc myelocytomat
2537290	TMEM18	TMEM18	transmembrane prot
3841076	MYADM	MYADM	myeloid-associated c
3464912	WDR51B	WDR51B	WD repeat domain 5
2648873	GMPS	GMPS	guanine monphosph

2784027	ANXA5		annexin A5
2647898	MED12L		mediator of RNA pol
2645690	RNF7		ring finger protein 7
2997907	EPDR1		ependymin related p
2676009	TWF2	TWF2	twinfilin, actin-binding
3613300	NIPA2	NIPA2	non imprinted in Prax
3378281	MRPL11	MRPL11	mitochondrial ribosol
2774971	ANTXR2		anthrax toxin receptc
2779897	MANBA	MANBA	mannosidase, beta A
3587015	KLF13	KLF13	Kruppel-like factor 13
3112713	THRAP6		thyroid hormone rece
2394558	RPL22		ribosomal protein L2
2921402	SLC16A10		solute carrier family
2901620	HLA-E		major histocompatibi
2837479	THG1L	THG1L	tRNA-histidine guany
4004819	DYNLT3		dynein, light chain, T
3241316	ZEB1		zinc finger E-box bin
2489228	WDR54		WD repeat domain 5
3417583	RBMS2		RNA binding motif, s
3368940	ABTB2	ABTB2	ankyrin repeat and B
3128372	KCTD9	KCTD9	potassium channel te
3962678	PACSIN2		protein kinase C and
3482977	POLR1D	POLR1D	polymerase (RNA) I
3456212	MAP3K12		mitogen-activated pr
3867223	RPL18	RPL18	ribosomal protein L1
3868659	C19orf48	C19orf48	chromosome 19 ope
3959631	EIF3S7		eukaryotic translatio
2325192	RPL11	RPL11	ribosomal protein L1
3832616	EIF3S12		eukaryotic translatio
2777487	FAM13A1	FAM13A1	family with sequence
2917767	MANEA	MANEA	mannosidase, endo-
3252170	ADK	ADK	adenosine kinase
2342624	ACADM		acyl-Coenzyme A de
3631498	LARP6		La ribonucleoprotein
3337137	AIP		aryl hydrocarbon rec
3149754	EIF3S3		eukaryotic translatio
2939814	RPP40		ribonuclease P 40kD
3458614	DCTN2		dynactin 2 (p50)
4012299	PHKA1		phosphorylase kinas
3681674	NTAN1	NTAN1	N-terminal asparagir
3475879	ABCB9		ATP-binding cassette
3106310	DECR1	DECR1	2,4-dienoyl CoA red
3302187	ARHGAP19	ARHGAP19	Rho GTPase activati
3680583	RSL1D1	RSL1D1	ribosomal L1 domair
3600212	LRRRC49		leucine rich repeat c
3349293	NCAM1		neural cell adhesion
3976519	RBM3	RBM3	RNA binding motif (F
2890413	RNF130	RNF130	ring finger protein 13
3513096	ESD	ESD	esterase D/formylglu
2738697	CYP2U1	CYP2U1	cytochrome P450, fa
3971877	EIF2S3	EIF2S3	eukaryotic translatio
3090512	DOCK5	DOCK5	dedicator of cytokine
2648378	RAP2B	RAP2B	RAP2B, member of f

3990566	UTP14A	UTP14A	UTP14, U3 small nuclear ribonucleoprotein
3868518	LOC554235		hypothetical protein I
2566645	MITD1		MIT, microtubule interacting domain
3136129	RPS20	RPS20	ribosomal protein S20
3978155	GPR173		G protein-coupled receptor
2707824	MCCC1	MCCC1	methylcrotonoyl-CoA carboxylase
2555630	CCT4	CCT4	chaperonin containing domain class 1 type 4
2464484	LOC284702	LOC284702	hypothetical protein I
2703133	IFT80	IFT80	intraflagellar transport protein 80
2680591	LRIG1		leucine-rich repeats domain containing protein 1
3944620	MPST	MPST	mercaptopyruvate sulfurtransferase
3505781	PARP4	PARP4	poly (ADP-ribose) polymerase 4
4015763	GLA	GLA	galactosidase, alpha-L-galactose 4-epimerase
3130850	RNF122		ring finger protein 122
2550122	COX7A2L	COX7A2L	cytochrome c oxidase subunit 7A2-like
2379009	PPP2R5A	PPP2R5A	protein phosphatase 2A regulatory subunit 5A
2694817	PLXND1	PLXND1	plexin D1
2954025	TRERF1	TRERF1	transcriptional regulator
3375518	C11orf10	C11orf10	chromosome 11 open reading frame 10
2983030	AGPAT4		1-acylglycerol-3-phosphate acyltransferase 4
3325839	TCP11L1		t-complex 11 (mouse)
3386814	SNORA18		small nucleolar RNA 18
3562899	RPL10L	RPL10L	ribosomal protein L10-like
2847264	MED10	MED10	mediator of RNA polymerase II transcription
2952679	GLO1	GLO1	glyoxalase I
2815331	BTF3	BTF3	basic transcription factor 3
3945056	EIF3S6IP		eukaryotic translation initiation factor 3 subunit 6 interacting protein
2341663	CTH		cystathionase (cystathionine gamma-lyase)
2984655	RPS6KA2		ribosomal protein S6 kinase family class A member 2
2955673	ENPP5		ectonucleotide pyrophosphatase 5
3855818	PBX4		pre-B-cell leukemia transcription factor 4
3997780	ARSE		arylsulfatase E (choroideremia)
2492938	RPIA	RPIA	ribose 5-phosphate isomerase
2906872	MDF1		MyoD family inhibitor 1
2434178	MTMR11		myotubularin related protein 11
3944637	KCTD17		potassium channel tetramerization domain containing 17
2619120	TRAK1		trafficking protein, kinase
2699145	ST13		suppression of tumorigenesis 13
2599823	SLC23A3		solute carrier family 23 member 3
3527493	APEX1	APEX1	APEX nuclease (multifunctional)
3850040	EIF3S4		eukaryotic translation initiation factor 3 subunit 4
3838795	BCL2L12	BCL2L12	BCL2-like 12 (proline isomerase)
2898562	THEM2	THEM2	thioesterase superfamily member 2
2527786	PNKD		paroxysmal nonkinetic eye disorder
3332334	MS4A7		membrane-spanning domain 4A family class 7 member 7
2653932	MFN1	MFN1	mitofusin 1
3394068	RPS25	RPS25	ribosomal protein S25
3977590	NUDT10	NUDT10	nudix (nucleoside diphosphate-linked moiety X) motif 10
3438617	EP400	EP400	E1A binding protein 1
3099750	SDCBP		syndecan binding protein
3984840	ARMCX4		armadillo repeat containing protein 4
2603051	SP110	SP110	SP110 nuclear body protein
2325593	CLIC4	CLIC4	chloride intracellular channel protein 4

2614054	UBE2E1		ubiquitin-conjugating
3428671	CHPT1		choline phosphotran:
3951927	BID		BH3 interacting dom
2583631	RBMS1	RBMS1	RNA binding motif, s
3060332	STEAP4		STEAP family memb
2930808	RPS18	RPS18	ribosomal protein S1
2589255	FKBP7		FK506 binding protei
2805786	TARS		threonyl-tRNA synthe
3928070	CCT8	CCT8	chaperonin containin
3415193	GRASP	GRASP	GRP1 (general recep
3869954	ZNF321		zinc finger protein 32
2983138	C6orf59		chromosome 6 open
2878809	CENTD3		centaurin, delta 3
3560711	BAZ1A		bromodomain adjace
2640916	ABTB1		ankyrin repeat and B
2424102	CNN3		calponin 3, acidic
2826343	SNX24	SNX24	sorting nexing 24
2712040	CENTB2	CENTB2	centaurin, beta 2
3642060	CHSY1	CHSY1	carbohydrate (chond
2624074	GNL3		guanine nucleotide b
2560286	LOXL3		lysyl oxidase-like 3
2478928	MTA3		metastasis associate
2485688	CEP68	CEP68	centrosomal protein
3391029	PPP2R1B		protein phosphatase
2595443	WDR12		WD repeat domain 1
3091403	EPHX2		epoxide hydrolase 2,
4011464	PJA1		praja 1
2644128	TMEM22	TMEM22	transmembrane proti
3512527	RCN1		reticulocalbin 1, EF-t
3908934	PTGIS		prostaglandin I2 (pro
2877939	DNAJC18		DnaJ (Hsp40) homol
2515402	MAP1D		methionine aminopep
2700828	SIAH2		seven in absentia ho
2907018	TBN		taube nuss homolog
3945225	MAFF	MAFF	v-maf musculoapone
3442396	SCARNA12		small Cajal body-spe
2360887	RUSC1		RUN and SH3 doma
2905069	KCTD20		potassium channel te
3148796	NUDCD1		NudC domain contai
3960478	CSNK1E		casein kinase 1, eps
2863730	AP3B1	AP3B1	adaptor-related prote
3391816	USP28		ubiquitin specific pep
3838845	CPT1C		carnitine palmitoyltra
2387006	MTR		5-methyltetrahydrofo
2708287	ABCC5		ATP-binding cassette
2902385	NFKBIL1		nuclear factor of kap
3396883	RPUSD4		RNA pseudouridylate
3490251	WDFY2		WD repeat and FYVI
3606034	PDE8A	PDE8A	phosphodiesterase 8
3816333	SF3A2		splicing factor 3a, su
3425108	C12orf29		chromosome 12 ope
3626312	ALDH1A2		aldehyde dehydroge
3899346	SNX5		sorting nexin 5

2550790	LRPPRC	LRPPRC	leucine-rich PPR-mo
2745646	SMARCA5		SWI/SNF related, m
3352485	TMEM136		transmembrane prot
3845365	TCF3		transcription factor 3
2966078	FBXL4	FBXL4	F-box and leucine-ric
3354731	EI24		etoposide induced 2.
3427820	SLC25A3	SLC25A3	solute carrier family ;
3641391	TTC23	TTC23	tetratricopeptide rep
2824354	DCP2		DCP2 decapping en
2656738	EIF4A2		eukaryotic translatio
2607110	HDLBP		high density lipoprote
2561955	SUCLG1		succinate-CoA ligase
3064293	EPHB4	EPHB4	EPH receptor B4
2356300	PIAS3	PIAS3	protein inhibitor of ac
2953435	C6orf130		chromosome 6 open
2776372	WDFY3	WDFY3	WD repeat and FYVI
3831143	TBCB		tubulin folding cofact
3862018	RPS16	RPS16	ribosomal protein S1
2737717	NFKB1		nuclear factor of kap
3299705	PANK1		pantothenate kinase
3449368	CAPRIN2		caprin family membe
2721777	PI4K2B		phosphatidylinositol
3497659	RAP2A		RAP2A, member of f
3200689	RPS6	RPS6	ribosomal protein S6
2568968	UXS1		UDP-glucuronate de
3501471	ING1	ING1	inhibitor of growth fa
3850676	ANKRD25	ANKRD25	ankyrin repeat doma
3464967	GALNT4	GALNT4	UDP-N-acetyl-alpha-
3657193	TGFB111	TGFB111	transforming growth
2618726	ZNF621		zinc finger protein 62
2944491	MBOAT1		membrane bound O-
2500615	TMEM87B		transmembrane prot
2830698	FAM53C		family with sequenc
3459604	PPM1H	PPM1H	protein phosphatase
3709838	NTN1	NTN1	netrin 1
2865050	RPS23	RPS23	ribosomal protein S2
3525679	ANKRD10		ankyrin repeat doma
3840795	ZNF765		zinc finger protein 76
3429754	KIAA1033	KIAA1033	KIAA1033
2586744	RPS26		ribosomal protein S2
3499453	TPP2	TPP2	tripeptidyl peptidase
3358809	HCCA2	HCCA2	HCCA2 protein
3929272	TCP10L		t-complex 10 (mouse
3568184	ESR2		estrogen receptor 2 (
2758978	EVC2	EVC2	Ellis van Creveld syr
2949588	DOM3Z		dom-3 homolog Z (C
2777044	HSD17B13		hydroxysteroid (17-b
2469711	PQLC3		PQ loop repeat cont
3372459	AGBL2		ATP/GTP binding pr
2489440	DOK1		docking protein 1, 62
3825201	UBA52	UBA52	ubiquitin A-52 residu
3815834	DAZAP1	DAZAP1	DAZ associated prot
2878778	FCHSD1		FCH and double SH:

3044072 NOD1
2360728 TRIM46
3089469 SORBS3

SORBS3

nucleotide-binding of
tripartite motif-contai
sorbin and SH3 dom

mRNA Accession	SHH		WNT+GroupC+GroupD	
	GroupA mean	GroupA std.dev.	GroupB mean	GroupB std.dev.
NM_014476	11.384978	1.0542521	6.1415424	0.5520853
NM_022475	9.895174	1.4022031	5.2055955	0.610972
NM_172059	10.203527	1.2710966	5.651108	0.73626447
NM_005172	9.811597	1.4195257	5.6790833	0.45702165
NM_003012	10.0833235	0.8840478	6.0007815	1.0162792
NM_181876	10.63388	1.1193168	6.6616545	1.169267
NM_000266	9.247191	1.1689687	5.438337	0.46930063
NM_003106	12.51783	1.0846337	8.759544	0.88068956
NM_004784	9.159798	1.339129	5.447991	0.8138204
NM_001008540	10.993175	1.1776351	7.312697	1.3108157
NM_015265	9.952387	0.9113761	6.328944	0.92104906
NM_022160	10.280259	2.5804582	6.661782	0.5886649
NM_000693	10.089637	1.3480856	6.4779606	1.382269
NM_012202	10.384539	0.9173079	6.7936463	1.2045612
NM_001077244	9.70136	0.99187475	6.1140347	1.0978295
NM_052954	10.025308	0.5730075	6.4743676	0.754401
NM_003020	9.910113	1.0764272	6.541034	1.441153
NM_016613	10.02513	1.6281036	6.6784053	0.875403
NM_138409	10.009114	0.7962192	6.734468	0.78399265
NM_000949	8.675759	1.3169892	5.411231	0.72400904
NM_033254	9.656323	0.7522589	6.4324536	1.0694278
uc001yos.1	8.668009	1.1571779	5.453084	0.68087035
NM_005604	9.658809	0.5424899	6.517172	1.0749503
NM_012113	9.033576	0.969973	5.929824	1.1579782
NM_001083	9.02854	0.86162716	5.9487576	0.9320875
NM_002216	9.058631	1.6846561	5.996685	1.0137886
NM_020796	10.591843	0.5592175	7.599272	1.152348
NM_144629	9.457992	0.8950967	6.49346	1.0950863
NM_000055	8.103161	0.8404916	5.1626415	0.75711495
NM_007199	8.654664	1.2525715	5.7417326	0.3857196
NM_197941	7.9954762	0.980311	5.2208056	0.5225952
NM_201253	8.447632	0.93290204	5.732919	0.6191033
NM_014942	9.291937	0.89825857	6.59327	0.6670013
NM_012098	10.048753	0.9607553	7.356093	1.1724485
NM_000612	10.550914	1.204325	7.871501	1.4580382
NM_014056	8.452706	0.7734303	5.792071	1.0615147
NM_015196	8.6156645	0.65321666	5.9598536	0.8238138
NM_031474	9.135417	1.255621	6.4846015	0.36278826
NM_003238	9.189094	1.4592638	6.5665545	0.7001849
NM_002039	10.760352	0.88266337	8.173454	0.5463537
NM_001006625	9.632878	1.1352105	7.0493884	0.7834585
NM_020335	9.383052	0.8258907	6.8348904	1.4427781
NM_018970	8.885604	0.8966279	6.365145	0.8194664
NM_001031730	9.667489	0.50106966	7.159966	1.162681
NM_021101	8.27175	1.8107669	5.794206	0.80286664
NM_001117	9.224047	1.1557429	6.752805	1.6397429
NM_145649	7.8855596	0.58952326	5.417865	0.7780397
NM_000831	8.931323	1.1155101	6.4681225	0.9705932
NM_000900	10.944005	1.3522952	8.482257	1.6457801
NM_001604	10.627849	0.75149286	8.172342	1.8860829
NM_001003683	8.121724	1.2186042	5.6778917	0.8593301

NM_022168	8.507733	1.78427	6.077814	1.4606906
NM_024416	8.027622	1.4581753	5.59796	1.1028191
NM_006658	8.315751	1.7181145	5.8931193	0.60691434
NM_002240	8.864758	0.9368106	6.452119	1.2841309
NM_198503	8.393786	0.67091864	5.9941583	0.847272
NM_020762	9.050648	0.55613345	6.6557584	0.8642975
NM_030784	7.7545886	0.5952268	5.37643	0.8272589
NM_030643	9.310837	1.0252647	6.955716	1.7607727
NM_016083	10.142436	0.9273321	7.789745	1.3526702
NM_020444	8.086592	1.4078542	5.752312	0.8269843
NM_003728	8.562368	1.3463213	6.2314396	1.0975718
NM_002844	9.889337	0.7756476	7.562758	1.1364014
NM_005410	9.729283	0.8455409	7.4029784	0.9993304
NM_030795	9.735558	0.78231376	7.4117417	1.5358624
NM_002633	10.016296	1.129388	7.720789	0.68446845
NM_178584	9.202857	0.6304161	6.9213057	0.8487547
NM_173464	9.791342	1.1251302	7.5198007	0.78804934
BC054487	8.024496	1.1908026	5.756291	0.77549565
NM_153612	8.003562	1.2429073	5.7388334	0.49367732
NM_182960	7.900189	0.96432257	5.6705127	1.4647585
NM_030820	8.126391	1.7208053	5.897448	0.3430708
NM_014575	9.709376	0.4127343	7.487043	1.1389582
NM_002941	9.851314	0.5447581	7.6434064	1.5862248
NM_022659	7.637511	1.4509135	5.43359	1.0632427
NM_001647	12.159186	1.1772898	9.957507	1.582144
NM_020139	7.7584386	0.76464504	5.5571046	0.81597215
NM_001031746	9.115014	1.0414886	6.91423	0.8707911
NM_021956	9.672902	1.0644642	7.4856844	1.6424165
NM_004200	9.146382	0.8871025	6.96083	0.8541078
NM_002998	10.338674	0.51945883	8.168441	1.2601999
NM_133503	11.330585	1.1105658	9.16948	1.5831263
NM_000443	7.7161417	0.92086816	5.5602865	0.3679962
NM_002852	7.4702454	0.802157	5.3431726	0.55068403
NM_199072	8.757439	0.8698037	6.6450334	0.8991079
NM_006031	9.346639	1.4396832	7.256022	0.29792157
NM_000245	7.918632	1.4076279	5.8313775	0.6567242
NM_153225	9.207561	1.5753763	7.146539	1.6098976
NM_004794	8.223037	0.45726427	6.16387	0.89418507
NM_005639	10.089493	0.7467577	8.032792	1.5695715
NM_000921	8.395571	1.4907135	6.347349	0.73357564
NM_000833	8.1837225	1.1377282	6.1374564	0.8824751
NM_005378	10.188825	0.8642812	8.163893	1.237482
NM_002232	7.9606595	0.83393544	5.948595	0.76520073
NM_197941	7.585529	0.81490403	5.5851784	0.36734477
BC054869	7.4823675	1.0135969	5.4829187	0.73481184
NM_032873	8.362683	0.8049597	6.3673897	0.83609957
NM_170706	9.385515	0.70770407	7.4001474	1.1114416
NM_080832	7.9182734	0.7076852	5.935839	0.8709596
NM_017640	9.632395	0.86909777	7.673289	1.4937422
NM_003360	8.596388	0.56014824	6.6477013	1.0006977
NM_024843	9.414312	0.61348	7.4684987	0.892621
NM_057162	7.825521	1.1746469	5.8969426	0.9711595
NM_014945	8.893517	0.76931953	6.9685783	0.7605383

NM_000170	7.578402	0.9053856	5.6592913	0.67538315
NM_000745	9.318309	0.9569606	7.401257	1.1862783
NM_018099	8.165406	0.8643006	6.250622	0.70876145
NM_006581	8.799334	0.7780373	6.8860135	1.0165964
NM_001012338	10.578292	1.0024643	8.668691	1.5635618
NM_013231	8.706839	1.0378042	6.7993083	1.1784531
NM_000599	10.112452	0.8613553	8.216561	1.1898818
NM_002753	9.705644	0.6029681	7.8182354	1.2160066
NM_031271	7.123783	1.0319037	5.238099	0.6124988
NM_003014	8.275948	1.1581643	6.398487	1.3828751
NM_024769	7.8505697	0.93664443	5.975422	0.9659502
NM_212535	9.046767	1.316063	7.2014203	1.2897936
BC037403	7.986309	0.91135055	6.1508756	0.89923805
NM_021073	7.073921	1.3531123	5.2402015	0.28443646
NM_021809	8.164559	0.6515995	6.3524427	1.0640094
NM_015310	9.11481	0.6463374	7.303039	0.8299698
NM_005486	7.8246	0.86670536	6.024374	1.0348121
NM_080821	10.885437	0.6648695	9.087049	0.5850828
NM_020742	9.533767	0.6155694	7.738387	1.256047
NM_014112	8.162632	0.8275847	6.3731737	0.7322475
NM_019036	7.5027633	1.2574207	5.715766	0.7932925
NM_033225	7.7740226	0.9582113	5.9947333	0.3886445
NM_138822	9.635013	0.47916293	7.858795	1.1129589
NM_080283	7.5247836	0.79329705	5.749197	0.6468704
NM_001704	9.063834	0.667692	7.28983	1.145579
NM_006195	7.7419596	1.0611137	5.979954	0.8493492
NM_001425	8.262122	1.0514281	6.5045576	0.94773173
NM_005504	8.954047	1.0366005	7.197464	1.1707202
NM_004926	9.592176	0.6310674	7.836204	1.056486
NM_007168	7.4061484	0.94507396	5.6513195	0.59844863
NM_014932	9.170676	0.6151581	7.417367	1.2339889
NM_201524	9.050988	0.6459985	7.303477	1.2141279
NM_016269	8.765269	1.2345746	7.0271525	1.589275
NM_032518	7.9634514	0.813703	6.2268367	0.53278446
NM_002045	11.499579	0.61397547	9.773977	1.5700399
NM_001288	9.021048	0.7142607	7.2975907	0.95168906
NM_052932	10.531839	0.5840412	8.812221	1.374005
NM_005737	8.934985	0.47386444	7.216206	1.1458743
NM_017826	7.3846135	1.0267307	5.670888	0.68383694
NM_021939	8.357738	0.4835063	6.6444564	1.0602548
NM_017680	7.7491612	1.2822031	6.038971	0.88774693
NM_017641	9.673286	0.45934492	7.9662633	0.8758646
NM_019035	8.668816	0.9938261	6.967585	0.70008636
NM_000346	9.0378065	0.7079209	7.337422	1.2671956
NM_014962	10.148607	0.58616	8.450207	0.63222605
NM_015595	7.6511645	0.76246226	5.9544306	0.5344582
NM_006588	7.52541	0.7243306	5.83186	0.6122499
NM_006931	9.216884	0.6333003	7.528846	0.8422825
NM_021178	9.466968	0.55646116	7.7840557	0.74304533
NM_005014	6.7426143	1.22655	5.063979	0.6797932
NM_022140	8.901663	0.83038974	7.225528	0.9203381
NM_012302	9.173663	0.9230963	7.4991593	0.98247457
NM_004845	7.919337	0.6159897	6.249648	0.8632266

NM_016245	10.637113	0.72474366	8.968233	0.82291484
NM_015976	8.342616	0.9363634	6.6774006	0.6874087
NM_004530	8.624273	0.93973327	6.965818	1.7055603
NM_206887	8.42958	0.92072743	6.7757344	1.0978602
NM_006226	7.722507	0.8014766	6.0748205	0.84892434
NM_021952	9.1053505	0.9477139	7.460856	1.9118727
NM_138390	8.396832	0.75129753	6.754643	0.96471477
NM_005767	8.561668	0.75067943	6.9198747	0.8536049
NM_031896	8.191718	1.0802926	6.5535336	0.891952
AL136588	9.110466	0.42191455	7.4736676	1.1650779
NM_022893	8.332893	0.69475037	6.6971555	1.2167273
NM_000965	7.768409	1.1568974	6.13667	0.38495582
NM_005215	10.410209	0.83440727	8.779114	1.5578165
NM_006623	9.1371	1.0416915	7.509801	0.9210638
NM_002398	9.543158	1.0646555	7.9161005	1.400625
NM_020820	9.349815	0.6774921	7.723689	0.800543
NM_022138	7.5150957	0.99796814	5.8930764	0.5005962
NM_000186	8.149568	1.1841521	6.5290794	0.80019814
NM_006681	8.3299465	1.0411433	6.7150836	1.11154
NM_032385	7.8913245	0.7397242	6.2777715	0.48706874
NM_006661	7.4383616	0.8222905	5.832181	0.9754864
NM_018710	8.550128	0.3718983	6.945312	1.0095993
NM_005761	9.682623	0.7448604	8.078732	1.2356058
NM_138731	7.9110537	0.62394637	6.313646	1.1021891
NM_173662	7.3150573	0.8902834	5.719364	1.0342759
NM_152864	8.10087	0.8601817	6.508485	0.6438916
NM_001040409	10.302537	0.6205287	8.722068	1.2515185
NM_001003792	8.007171	0.9794144	6.428033	0.83803076
NM_016941	8.141689	0.97545147	6.563292	0.91635567
NM_021992	10.5441065	0.95628256	8.970208	1.3539146
NM_002742	7.671814	0.55411464	6.0987387	0.42127153
NM_014790	8.392574	0.38365984	6.8289638	1.131974
NM_021242	8.638835	0.89520884	7.083378	0.7853739
NM_002508	8.70021	0.697903	7.149685	0.6460758
NM_153449	7.545075	0.4326419	6.001297	0.6422224
NM_002372	8.695003	0.88799316	7.151624	0.8604228
AF111801	7.8799744	0.5196118	6.336883	0.9846786
NM_001268	9.528845	0.56324	7.9887424	0.7620249
NM_003026	9.66568	1.0398318	8.128594	1.4472103
NM_015149	8.651999	0.56575745	7.11722	1.2529083
NM_006769	10.15122	0.74602854	8.62745	0.7533997
NM_000888	8.74072	0.7834237	7.217163	0.8351912
NM_173808	8.53073	0.8148848	7.0110846	1.1836015
NM_005779	9.422593	0.70953673	7.905208	0.66539013
NM_001962	7.8000946	0.600425	6.2872734	1.1717459
NM_000795	9.593368	1.0403525	8.082361	0.49881706
NM_002758	9.408518	0.7096255	7.897808	0.90667075
NM_001814	8.4208355	0.7408596	6.9102254	0.60316044
NM_016931	8.160278	0.7114501	6.654914	0.76333857
NM_002444	9.832753	0.45086956	8.327852	0.9465735
NM_017933	7.2932916	0.88957936	5.795034	0.73705035
NM_032581	9.474123	0.84864986	7.975987	1.1532259
NM_001993	8.296267	1.1726563	6.799566	0.8880994

NM_001005339	8.472785	0.62110037	6.9806757	0.68770874
NM_003507	9.126753	0.6548865	7.634684	1.4715871
NM_005168	10.842134	0.70074165	9.351159	1.1870105
NM_001039960	8.793828	0.48865688	7.303891	1.0965585
NM_001033504	10.059357	0.70851266	8.570732	1.1838988
NM_000168	7.1024384	0.9114532	5.6195498	0.5559614
NM_002585	9.61037	0.36928996	8.127627	1.0615139
NM_001019	10.224225	0.7037149	8.747042	1.08692
AF336133	8.751489	0.35531145	7.280809	1.294166
NM_017436	7.7205496	0.600721	6.251007	0.24946763
NM_001080973	8.361708	0.4779503	6.9006376	0.9148704
NM_003034	8.35111	0.914129	6.892032	0.8682075
NM_000304	9.475708	0.81596184	8.018705	1.1972563
NM_021127	7.122191	1.0883068	5.665791	1.1493592
NM_017551	8.456051	1.0375011	6.999765	0.66351664
NM_033135	7.231278	1.0159291	5.778461	0.6536076
NM_000465	8.685742	0.7284627	7.2334595	0.74614966
NM_032515	8.989495	0.87423146	7.5407004	0.6148462
NM_024333	8.153986	0.32747805	6.707844	0.6641616
NM_001031716	8.310452	0.6664174	6.866244	0.6614154
NM_000657	8.223514	0.906988	6.782192	0.50585216
NM_005654	9.445321	0.7759743	8.005585	1.1411493
NM_139076	8.318361	0.6988162	6.879379	0.73559296
NM_153371	8.11182	0.5604635	6.681592	0.7791239
NM_024560	7.434195	0.8883788	6.0115285	0.49409974
NM_015461	9.356366	0.6910361	7.9389534	1.4593732
NM_152369	7.0434875	0.8119202	5.626755	0.23984264
NM_198524	8.72306	0.8099059	7.3097486	0.61816126
NM_005503	10.639354	0.566584	9.22654	1.0634038
NM_203416	8.380298	0.9999982	6.9687705	0.93587446
NM_004118	7.53633	0.8667107	6.1396723	0.27117965
NM_145016	6.479744	0.7373187	5.097484	0.27646276
NM_033445	9.605472	0.6421559	8.224368	1.0851072
NM_002305	9.926837	0.77392006	8.550742	0.94061404
NM_001037132	10.230466	0.6356078	8.855556	1.3249482
NM_001458	7.886365	0.71110743	6.5129824	0.5716336
NM_024408	8.366359	0.49410775	6.994745	1.0183045
NM_004462	10.227733	0.45285177	8.857523	0.7338007
NM_019111	9.070075	0.80682504	7.700077	0.93291277
NM_003812	9.025801	0.8889317	7.6606493	0.9864073
NM_001312	10.404307	0.8435992	9.041467	0.699252
NM_152852	8.579494	0.89927983	7.218961	0.81644493
NM_002405	8.001875	0.9906929	6.6497316	1.0849915
NM_145117	8.308391	0.8284137	6.958123	1.0911009
NM_017633	9.245589	0.77975947	7.89834	0.3722642
NM_013305	7.411348	0.8808239	6.0644383	0.57059073
NM_015577	8.439426	0.63639367	7.092752	0.91196203
NM_014585	8.975009	0.7904294	7.63025	0.799113
NM_030906	8.274789	0.4307002	6.9323606	1.2833635
NM_201526	8.1348715	0.8212934	6.7984595	0.97657675
NM_032667	9.900587	0.62150055	8.565371	0.68049437
NM_020548	11.019481	0.6408069	9.685418	0.93659306
NM_016134	7.9580054	0.5461687	6.6241035	0.637381

NM_001078	6.9715686	0.9044694	5.6385837	0.8586713
NM_004480	9.574881	0.62493664	8.24307	0.67772186
NM_006371	9.00184	0.42280963	7.6703916	0.8681362
NM_144658	8.211368	0.5720933	6.8808002	0.8759895
NM_002612	7.7407575	0.64119756	6.4107575	0.72472775
NM_018058	7.856669	1.0339841	6.5312386	0.62449867
NM_020799	7.5885353	0.5605634	6.26447	0.80308527
NM_000700	8.457369	0.919806	7.134803	0.8334445
NM_182965	8.538877	0.7306248	7.2173457	0.17345478
NM_007069	8.102404	0.7751905	6.786136	0.83977616
NM_020422	8.03703	0.9322236	6.7207756	0.7523295
NM_002507	7.5780387	0.789735	6.2626963	0.3210166
NM_005941	8.906111	0.41855645	7.5943627	1.1158602
NM_001001483	9.013339	0.44308254	7.703394	1.1228613
NM_006651	8.5705185	0.6577316	7.2610345	0.30021292
NM_002952	8.218564	0.5983683	6.909894	0.89080065
NM_016441	8.916602	0.45179236	7.610716	0.7651589
NM_004044	9.505967	0.59401137	8.2002735	0.8709344
NM_001008272	10.513299	0.5295415	9.211568	1.4105245
NM_024907	7.561011	0.60620385	6.260552	1.0740914
NM_002285	8.689382	0.5633547	7.390072	1.309431
NM_004522	10.47516	0.49898502	9.178196	1.2764566
NM_000933	8.481533	0.61170495	7.2058477	0.7917025
NM_017423	8.134519	0.4487126	6.8633327	0.9317807
NM_006096	9.183008	0.8457013	7.911948	0.9157439
D86975	7.2852454	0.39763185	6.01792	0.5404182
NM_006734	8.786015	0.73734385	7.522196	0.8408975
NM_002583	7.066851	0.93552643	5.809714	0.26859596
NM_025015	7.962322	0.8999207	6.7112594	0.71296465
NM_020528	8.4483	0.9304835	7.200312	0.96204054
NM_005486	7.069173	0.7272789	5.8221188	0.6682269
NM_004389	8.38715	0.5681065	7.1451015	1.054856
NM_152653	8.143565	0.616733	6.9030495	0.95451134
NM_014883	9.488811	0.5434994	8.2508	1.0826693
NM_194317	8.320002	0.6630233	7.083371	0.54396725
NM_012223	9.265107	0.6354989	8.028684	1.210636
NM_005628	8.571497	0.5971916	7.3406	0.9776491
NM_006286	10.225523	0.6980139	8.996324	0.55171174
NM_006216	8.728061	0.8583562	7.500753	0.8506473
NM_024642	7.6137195	0.7183847	6.389281	1.2801611
NM_003130	10.686655	0.43154994	9.46868	0.6374803
NM_001987	8.350609	0.5585944	7.139063	0.71804893
NM_182526	6.7742095	0.7651334	5.565914	0.41697705
NM_006329	7.924835	0.84662783	6.7168016	0.85680276
NM_021238	9.187645	0.49186692	7.9821568	1.0446521
NM_003848	7.6491723	0.6486629	6.445222	0.8083083
NM_006763	9.333501	0.61871725	8.130927	0.8911165
NM_015485	7.2524233	0.5429725	6.0505805	0.6401886
NM_003622	7.4007735	0.501424	6.2036657	0.5820447
NM_017631	6.733883	0.745583	5.5451317	0.49103534
NM_001033555	8.914403	0.71081984	7.7258687	1.2676011
NM_006754	9.126667	0.5713707	7.945437	0.55868125
NM_014467	7.412018	0.8005106	6.2309523	0.591798

NM_002300	12.419088	0.29588947	11.238311	1.0057095
NM_001463	8.13135	0.74982923	6.9554653	1.1625781
NM_001679	9.350757	0.4622808	8.176549	0.695914
NM_021219	9.045327	0.4386197	7.874097	1.0980394
NM_178833	8.551533	0.3395141	7.381242	0.8568718
NM_024579	7.810574	0.88387364	6.645305	0.53450954
NM_014690	8.018875	0.65439945	6.8581185	0.92737097
NM_001008392	9.134521	0.47851914	7.9743233	0.5399381
NM_018153	9.00394	0.3564586	7.846824	0.7148258
NM_002763	7.79496	0.48496726	6.639087	1.0474073
NM_001001396	9.305223	0.73243004	8.149641	1.1083838
NM_005433	8.949657	0.6412096	7.795988	0.73346406
NM_000337	7.477585	0.78696465	6.324328	1.1490539
NM_018441	7.7180085	0.46640274	6.5678687	0.6233114
NM_032373	7.98597	0.6337049	6.8358884	0.95134753
NM_014992	9.761977	0.5136281	8.613451	0.69846386
NM_020390	7.625275	0.67021877	6.477047	0.5168951
NM_173694	8.607177	0.46246305	7.4603086	0.81023586
NM_138811	7.3767996	0.69769657	6.2321186	0.5008607
NM_019099	7.557461	0.5219407	6.415124	0.32774073
NM_014604	8.646596	0.6795502	7.5067	0.752785
NM_000290	7.6750035	0.78929865	6.5428305	0.6196667
NM_002578	9.498145	0.516902	8.368356	1.2360189
NM_032565	9.877855	0.69913626	8.748487	0.9104918
NM_005228	7.572204	0.72393143	6.4466386	1.0106452
NM_004776	9.743247	0.31389877	8.618826	0.6706356
NM_001033028	9.955636	0.54950947	8.8334055	0.7004687
NM_012074	8.075799	0.8269455	6.956537	0.78247255
NM_020341	7.9329348	0.73030025	6.8160367	0.9648044
NM_005076	7.5175476	0.88776696	6.4042597	0.49741042
NM_020235	8.705244	0.44405615	7.59638	0.65048087
NM_016081	7.952832	0.48824805	6.846048	0.6314667
NM_001034996	9.957974	0.46053883	8.854252	0.7335119
NM_033554	9.68174	0.7959195	8.578036	0.9417466
NM_020247	8.902933	0.5682709	7.799501	0.48768046
NM_000884	10.01	0.6478488	8.907308	0.7939437
NM_033381	8.201233	0.62693375	7.099677	0.783221
NM_004040	10.9779	0.6641689	9.879204	0.74504685
NM_133494	8.282846	0.70564896	7.185331	0.9567064
AK131322	6.4651704	0.7606366	5.3684874	1.003059
NM_138931	8.082956	0.8184741	6.9871407	0.70708835
NM_080862	7.137357	0.813523	6.0431376	0.6697951
NM_004984	9.869797	0.46543863	8.776465	1.282846
NM_001226	8.206337	0.4908026	7.115047	0.5504487
NM_015696	9.231966	0.5356278	8.141223	0.5351644
NM_024959	8.230466	0.6760949	7.1404123	0.5491242
NM_145176	6.9118257	0.78729254	5.8218827	0.5714534
NM_001568	11.172478	0.647276	10.083046	0.7334741
NM_017983	8.519683	0.4724684	7.43122	0.51856375
NM_001008224	8.355036	0.42994192	7.2691746	0.76139563
NM_001011	8.061987	0.2923704	6.9766803	0.66754174
NM_006729	7.0046363	0.55965745	5.9201965	0.9838277
NM_001078175	8.661567	0.63935447	7.578688	0.73021305

NM_005763	8.964077	0.4720817	7.8833575	0.80087364
NM_030981	9.176427	0.67156774	8.096253	1.1440196
NM_006558	9.674757	0.5989092	8.602035	0.9593654
NM_001752	9.132707	0.6406372	8.060235	0.52455497
NM_003199	10.597969	0.5152623	9.529612	0.71511555
NM_001015	9.229837	0.63965034	8.161823	0.8298798
NM_002118	7.9290986	0.70512956	6.86155	0.69096535
NM_007001	8.206804	0.6700746	7.141111	0.410528
NM_016113	11.720634	0.37724602	10.656553	0.893071
NM_138280	7.6250186	0.42934498	6.561685	1.3616725
NM_001456	9.284019	0.6508727	8.221088	0.86065143
NM_001380	7.511933	0.5136393	6.450174	0.7695987
NM_002113	6.1594996	0.7155211	5.098738	0.5043171
NM_019605	7.3846374	0.7080596	6.326151	1.010917
NM_181553	7.990854	0.43738335	6.9334483	0.59744227
AK023259	7.7228317	0.6290397	6.6698866	0.8168048
NM_003388	9.122849	0.52537876	8.070284	0.6997085
NM_080284	6.5239463	0.816581	5.4735475	0.4198093
NM_152282	9.369588	0.5476919	8.320231	0.6144733
NM_002310	8.911181	0.7610269	7.862091	0.80374587
NM_001992	9.238299	0.487263	8.191888	0.7299512
NM_004714	11.205394	0.6508364	10.158989	0.78569114
NM_001014283	9.524499	0.52898115	8.480434	0.6143683
NM_015472	8.724472	0.78016275	7.6808667	0.81306475
NM_201555	8.588332	0.5423072	7.5458946	0.45570058
NM_030631	6.3555875	0.7385162	5.3159685	0.3631944
NM_000079	9.430179	0.5090018	8.391289	1.1280535
NM_006410	7.2951584	0.6050602	6.2567973	0.5044176
NM_002306	8.380201	0.77767533	7.341989	0.80300784
NM_014905	8.880023	0.39285332	7.843333	0.6875269
NM_001975	11.03536	0.44991985	10.001921	0.69090563
NM_031934	8.320944	0.4935864	7.2878385	0.99281883
NM_138801	7.19368	0.42750302	6.160614	0.5344271
NM_014927	8.717821	0.7539513	7.6851945	0.8472697
NM_005578	8.349063	0.51788425	7.317062	0.7157574
NM_003302	8.167158	0.8210828	7.1358795	0.6046417
NM_033397	7.238288	0.61040455	6.2154045	0.8161192
NM_004984	9.4975	0.48322314	8.475431	1.1574566
NM_000989	12.251642	0.4276703	11.230189	0.7823553
NM_021961	9.917633	0.5082377	8.896448	0.98073643
NM_019080	7.841332	0.43273413	6.8210735	0.827112
NM_003598	8.753949	0.50555104	7.735654	0.94596016
NM_003270	9.715388	0.61398906	8.697444	0.5072209
BC091509	9.7273855	0.48888138	8.709792	0.5004874
NM_032424	9.515147	0.47261536	8.497847	0.9543688
NM_004759	8.945657	0.5585067	7.9288154	0.62786573
NM_014498	8.594973	0.42968088	7.5807595	0.9459118
NM_001077242	7.568084	0.45015645	6.55584	0.60157466
NM_002293	8.514883	0.46272552	7.5032163	0.6205704
NM_018027	8.71257	0.63495576	7.7024117	0.8917422
NM_003738	8.104672	0.61965513	7.0970597	0.22965297
NM_030640	8.698046	0.3709434	7.6905904	0.6912282
NM_021005	9.142878	0.3567925	8.139526	1.2391245

NM_005615	7.527736	0.755075	6.5257373	0.64450353
NM_014737	8.788897	0.6434605	7.791653	0.9772327
NM_033647	7.179629	0.43346387	6.183829	0.5058033
NM_005907	7.588336	0.58124673	6.5948744	0.74927974
NM_003709	9.217933	0.36381695	8.227564	0.59723276
NM_018240	7.8802843	0.38309076	6.8921356	0.57594633
NM_001102	8.819077	0.6278168	7.8339505	0.7477639
NM_024522	9.185861	0.63259155	8.202947	0.9843643
NM_003009	9.520429	0.6109347	8.537992	0.60302234
NM_001248	8.870169	0.6686339	7.88789	0.7218014
NM_014822	7.911721	0.60943806	6.930781	0.73875266
NM_014783	9.070978	0.71554595	8.091454	0.8805085
NM_030569	7.720893	0.74903715	6.741921	0.51639926
NM_173354	7.9896083	0.6936199	7.0160203	0.5475981
NM_002959	7.970742	0.45569608	7.0016913	0.42593685
NM_014747	7.9102893	0.6704935	6.941433	0.47209328
NM_014033	8.681398	0.6260624	7.7177896	0.81280404
NM_021244	8.641788	0.54977274	7.67835	1.0924863
NM_000182	10.4919195	0.49131402	9.528631	0.60984814
NM_003253	8.5871525	0.70553917	7.624148	0.77649313
NM_032900	7.4269753	0.6020764	6.468018	0.5470001
NM_203315	7.161315	0.44570664	6.2050347	0.7669476
NM_005269	7.2872963	0.39518073	6.3315196	0.22071283
NM_006360	11.004145	0.39783505	10.050663	0.6954377
NM_018211	8.725695	0.50380224	7.7742705	0.872004
NM_004586	8.035649	0.4045174	7.093256	0.5011269
NM_015381	8.582894	0.5645121	7.6417804	1.0311906
NM_005051	9.892831	0.5366434	8.956183	0.5840661
NM_015480	7.11926	0.72002417	6.1839433	0.646892
NM_174937	8.014209	0.4117138	7.0794935	0.56469905
NM_199246	9.751801	0.5473982	8.818608	0.8037986
NM_021994	8.825733	0.53688765	7.900109	0.63563955
NM_006339	8.623752	0.5141951	7.700178	0.6800166
NM_183244	7.960278	0.5548434	7.0369716	0.6996683
NM_006494	9.081289	0.59982926	8.1585045	0.69014984
NM_024025	8.845401	0.5746687	7.922753	0.6998186
NM_001007267	8.319494	0.54757136	7.400839	0.3576614
NM_000362	9.238769	0.56146693	8.323188	0.87205714
NM_000982	7.965884	0.5809716	7.0516677	0.56198937
NM_021629	8.72233	0.6134129	7.808465	0.64395833
NM_003485	6.406288	0.47869092	5.493657	0.378092
NM_015907	9.732953	0.6266471	8.824299	0.4188668
NM_032047	7.901033	0.64382637	6.994109	0.8299777
NM_172373	8.052484	0.3993925	7.1498547	0.6329988
NM_198047	8.923099	0.63578224	8.020723	0.5563921
AF054994	7.906742	0.54360664	7.007007	0.6948479
NM_024089	7.916616	0.5682541	7.019934	0.70557183
NM_033138	8.92454	0.49462932	8.028039	0.7271674
NM_001457	8.454134	0.6167133	7.559337	0.742323
NM_024565	7.8872094	0.58047515	6.9934607	0.8261937
NM_030952	7.328204	0.5927942	6.4351106	0.32990628
NM_007112	7.6199174	0.5972628	6.7309117	0.5894013
NM_024090	7.8414564	0.49299195	6.9563327	0.6576374

NM_021961	9.018431	0.4332735	8.134744	0.80457264
NM_018303	8.654791	0.47017658	7.77451	0.53202564
NM_014899	10.052907	0.55599535	9.174411	0.90241265
NM_004554	8.080511	0.5560241	7.2030964	0.53541344
NM_018401	6.9425616	0.6644812	6.0681467	0.6292496
NM_024554	8.215435	0.5579484	7.3418326	0.6118915
NM_005845	6.8118844	0.4905826	5.9384227	0.82226855
NM_207038	10.251258	0.41955596	9.377851	0.45124373
NM_031476	6.982235	0.6401352	6.110135	0.49913955
NM_199004	8.761224	0.45702156	7.891596	0.60939014
NM_014051	9.755819	0.4563697	8.88728	0.59472024
NM_002451	8.241369	0.5823919	7.37589	0.48831034
NM_014322	8.615389	0.56749016	7.7527723	0.7945932
NM_018976	10.8938875	0.37425375	10.031516	0.76301026
NM_000998	9.214734	0.63427615	8.35266	0.499362
NM_001039091	8.042552	0.46218777	7.1808796	0.68819445
NM_152280	10.574254	0.35123116	9.714031	0.8565174
NM_014363	9.147245	0.43771082	8.287658	0.9079657
NM_014038	8.678083	0.45989254	7.8257165	0.8001605
NM_022490	8.838584	0.5336521	7.986504	0.4841301
NM_001015508	8.003561	0.37657315	7.154057	0.8969366
NM_003129	9.626801	0.38909194	8.779639	0.5856955
NM_002228	9.685952	0.595817	8.842528	0.7478979
NM_000335	7.1502	0.47464177	6.3094907	0.18824942
NM_000484	11.7745075	0.3600399	10.935395	1.0319606
NM_006795	7.774044	0.37153992	6.936057	0.3310278
NM_015954	8.769726	0.5197942	7.932307	0.7786928
NM_003899	9.739746	0.5184319	8.904429	0.43346715
NM_001031799	7.948367	0.5785691	7.1158834	0.55622596
NM_052885	7.2770905	0.5148318	6.445783	0.429909
NM_012290	8.893229	0.35032675	8.065821	0.8563693
NM_000289	9.936914	0.4721071	9.110345	0.9591687
NM_006089	7.5567994	0.48787767	6.731765	0.48884964
NM_138287	6.9184065	0.63562673	6.096169	0.61125606
NM_015702	10.28786	0.56437325	9.466495	0.66911036
NM_001903	9.043503	0.3816255	8.222241	0.67887086
NM_004853	9.287259	0.5898424	8.466425	0.66468114
BC042034	7.670845	0.47187048	6.854531	0.6212176
NM_020453	7.665485	0.55753136	6.8493643	0.61816025
NM_206921	7.530341	0.467185	6.7152534	0.49891242
NM_000661	9.511201	0.5710008	8.698901	0.64766616
NM_198968	8.781238	0.26667377	7.969636	0.787041
NM_018290	8.273464	0.33623788	7.463571	0.64059514
NM_006098	12.507158	0.26744223	11.697407	0.7050853
NM_173584	8.671651	0.54599464	7.8619256	0.37001973
NM_000026	9.3368025	0.50939906	8.530814	0.5035605
NM_153685	7.4980645	0.4589832	6.6944423	0.66883457
NM_152720	7.6012683	0.49355122	6.7980833	0.5279332
NM_005378	7.5344353	0.59581167	6.731595	0.65925914
NM_152834	9.242401	0.42645857	8.443404	0.49287954
NM_001020819	7.8227735	0.4672029	7.0271673	0.66068053
NM_172240	8.083231	0.5636723	7.287767	0.44759536
NM_003875	10.08082	0.36902007	9.285792	0.41840714

NM_001154	10.885275	0.494398	10.09253	0.79433787
NM_053002	6.875049	0.4255341	6.0833693	0.71890867
NM_014245	8.275228	0.46698868	7.4837065	0.53409916
NM_017549	7.685238	0.5318409	6.8955517	0.77825433
NM_007284	8.769525	0.3763513	7.9800277	0.53934306
NM_030922	9.718177	0.4880512	8.93024	0.52160996
NM_170739	9.052251	0.44095057	8.265451	0.5839047
NM_058172	9.322972	0.49079654	8.536418	0.8452585
NM_005908	7.374429	0.29121655	6.588058	0.41215461
NM_015995	9.318776	0.46224025	8.533639	0.55137295
NM_080651	7.9945908	0.44847715	7.212645	0.46812785
NM_000983	10.623109	0.45897084	9.841897	0.73124284
NM_018593	7.96869	0.5737442	7.1877513	0.6878023
NM_005516	8.46219	0.60669017	7.682307	0.48109195
NM_017872	8.257932	0.5082671	7.479733	0.67931086
NM_006520	9.289831	0.54844487	8.512174	0.7135566
NM_030751	10.40265	0.5202509	9.6268425	0.7413403
NM_032118	8.825155	0.5236476	8.049919	0.549657
NM_002898	8.184982	0.4235643	7.4102497	0.64136046
NM_145804	7.361499	0.59966457	6.588917	0.45137852
NM_017634	7.2248883	0.41443613	6.4539037	0.62956154
NM_007229	8.721855	0.5285113	7.9516115	0.38101003
NM_152705	9.060007	0.4427112	8.291552	0.6460608
NM_006301	7.8132815	0.43631858	7.0462894	0.58185166
NM_000979	12.333174	0.34894592	11.568076	0.8366782
NM_199249	7.836203	0.5496045	7.0727997	0.51520956
NM_003753	10.361235	0.43347192	9.598194	0.4655655
NM_000975	11.954582	0.31378475	11.191604	0.744803
NM_013234	10.6120405	0.49076673	9.849077	0.6416624
NM_014883	7.921313	0.37279478	7.158434	0.67196983
NM_024641	7.7083063	0.55721307	6.946548	0.6027756
NM_006721	8.892004	0.43853256	8.131892	0.46319556
NM_000016	10.030087	0.4855345	9.271636	0.546378
NM_018357	7.873771	0.5387892	7.1154695	0.6538401
NM_003977	8.597608	0.5518831	7.843149	0.6613307
NM_003756	11.631827	0.3357346	10.880519	0.51034456
NM_006638	7.0838313	0.54732716	6.3325295	0.6563082
NM_006400	10.274459	0.37421253	9.524687	0.5303056
NM_002637	6.6064105	0.4988836	5.857002	0.6360092
NM_173474	9.785383	0.36771503	9.036396	0.56368613
NM_203444	7.232722	0.4015462	6.4846997	0.29917055
NM_001359	9.585164	0.5310977	8.83983	0.5663558
NM_032900	8.219224	0.5666621	7.4749165	0.50276166
NM_015659	10.298028	0.45537192	9.554329	0.6212129
NM_017691	9.683099	0.45078745	8.94086	0.70440763
NM_181351	10.950602	0.49683943	10.208752	0.737653
NM_001017430	10.32518	0.37355062	9.588492	0.45517004
NM_018434	10.497115	0.364812	9.760874	0.61172825
NM_001984	10.482709	0.43178588	9.747264	0.56837595
NM_183075	7.7733893	0.27799845	7.0379906	0.5471795
NM_001415	10.601641	0.36784247	9.867187	0.55506337
NM_024940	6.7778344	0.3034302	6.0447116	0.34017995
NM_002886	8.162449	0.26559818	7.4294996	0.501597

NM_006649	8.227538	0.5455621	7.4946632	0.4662041
NM_001024656	7.169535	0.47579432	6.440408	0.23939602
NM_138798	8.521323	0.54914296	7.793086	0.4996957
NM_001023	11.713296	0.32436934	10.985884	0.61179054
NM_018969	7.3674636	0.36606547	6.640722	0.60236377
NM_020166	8.424788	0.33160543	7.6981387	0.48291737
NM_006430	10.538499	0.4704898	9.811883	0.4751278
AK095297	10.575074	0.42588228	9.848592	0.5588556
NM_020800	8.451776	0.47009367	7.7257304	0.50205714
NM_015541	8.511918	0.5063137	7.7875786	0.63340944
NM_001013440	8.04764	0.39669344	7.3233633	0.4881187
NM_006437	8.656678	0.49303478	7.9337096	0.53713316
NM_000169	8.494603	0.49600118	7.772706	0.47635293
NM_024787	8.967174	0.5121893	8.249438	0.6602055
NM_004718	11.193426	0.432952	10.476313	0.48742902
NM_006243	6.7096143	0.4224491	5.9983845	0.5206412
NM_015103	7.796643	0.5225035	7.088229	0.32688993
NM_033502	7.0231895	0.18835992	6.3162975	0.4640215
BC002750	11.031309	0.5190885	10.325212	0.6162873
NM_020133	8.836345	0.25718972	8.130717	0.44258097
NM_018393	8.733237	0.26106977	8.028242	0.5718529
NR_002959	8.633388	0.4797876	7.928597	0.66310084
NM_080746	8.729979	0.29282075	8.027558	0.4929126
NM_032286	8.805705	0.48483166	8.103751	0.39626634
NM_006708	10.078391	0.4611944	9.377781	0.5073065
NM_001037637	10.947951	0.36370462	10.249153	0.6057705
NM_016091	11.623278	0.36354244	10.92784	0.50955415
NM_001902	6.878604	0.48901278	6.1856017	0.47153836
NM_021135	7.293139	0.41392204	6.6025214	0.4461929
NM_021572	6.5242395	0.46551913	5.834348	0.596369
NM_025245	7.72041	0.40991813	7.0322824	0.26194164
NM_000047	6.765518	0.3870515	6.077637	0.7588994
NM_144563	8.527558	0.37736547	7.8399696	0.3546775
NM_005586	7.6555696	0.3901116	6.9700403	0.22719404
NM_181873	6.803254	0.45471144	6.118977	0.5147696
NM_024681	7.76983	0.39979765	7.0871572	0.5428499
NM_001042646	8.795001	0.33932364	8.116495	0.56761575
NM_003932	6.9563584	0.48524034	6.279407	0.41695544
NM_144712	8.207357	0.49695587	7.532326	0.58086014
NM_001641	10.437791	0.3395099	9.765684	0.69013155
NM_003755	9.722015	0.47736686	9.050433	0.57689285
NM_138639	7.21455	0.44478074	6.5437264	0.37875578
NM_018473	7.853947	0.44127432	7.1863956	0.5471778
NM_022572	8.551024	0.499445	7.886279	0.5466448
NM_206938	6.492901	0.52319777	5.828842	0.4151376
NM_033540	9.569611	0.38323084	8.905565	0.5234335
NM_001028	11.820906	0.23618825	11.160155	0.6011695
NM_153183	9.308135	0.38649923	8.650348	0.7490834
NM_015409	8.837652	0.36167383	8.180152	0.3702111
NM_001007070	10.682923	0.3924164	10.028052	0.60825676
BC036206	8.026152	0.40251645	7.372011	0.45963633
NM_004509	6.4688745	0.38905492	5.819396	0.20224291
NM_013943	10.945811	0.38403118	10.296365	0.68010557

NM_182666	9.043415	0.35665536	8.394698	0.60173
NM_020244	8.251511	0.39888558	7.606269	0.46426165
NM_197966	8.445902	0.40335128	7.801816	0.5035749
NM_016839	7.5282226	0.3843332	6.884153	0.38148677
NM_024636	5.861098	0.49085194	5.2220793	0.27588496
NM_022551	9.059675	0.4663048	8.422436	0.4611231
NM_181342	8.143576	0.3560485	7.509067	0.4662052
NM_152295	9.908641	0.35161936	9.275641	0.5107798
NM_006585	9.611435	0.35479647	8.9788475	0.49207306
NM_181711	7.371843	0.36441603	6.7394123	0.40063187
NM_203307	6.2049894	0.4832454	5.5737386	0.47661906
uc003qtu.1	6.8114486	0.43639764	6.183836	0.59120286
NM_022481	7.2921762	0.46866244	6.666106	0.39771476
NM_013448	8.269415	0.36326957	7.6461997	0.6368707
NM_032548	7.751201	0.4365173	7.129689	0.45808977
NM_001839	10.105431	0.40197834	9.485746	0.6029107
NM_014035	7.116515	0.31581032	6.496975	0.49064854
NM_012287	8.73002	0.31833982	8.112117	0.52247715
NM_014918	9.141575	0.35874027	8.526309	0.40250966
NM_206825	9.46105	0.43648472	8.8495455	0.5467927
NM_032603	7.321788	0.36450693	6.7127833	0.41685733
NM_020744	8.628543	0.45085013	8.020885	0.4887452
NM_015147	8.820273	0.28721148	8.215771	0.4513114
NM_181699	8.87431	0.37520978	8.269848	0.48024783
NM_018256	9.308549	0.4428356	8.704231	0.5372574
NM_001979	7.2743325	0.32907897	6.672407	0.57583094
NM_001032396	9.645747	0.37251	9.048022	0.55337936
NM_025246	7.7681584	0.3402716	7.1722383	0.4090696
NM_002901	11.386535	0.39037013	10.790781	0.43996122
NM_000961	6.936888	0.32317334	6.3454943	0.43905994
NM_152686	8.82931	0.3356444	8.23818	0.5850013
NM_199227	7.0847406	0.36488298	6.493737	0.3795176
NM_005067	8.801923	0.2961948	8.213374	0.5088938
NM_138572	7.692509	0.2714644	7.107648	0.5041191
NM_152878	6.686116	0.34958115	6.106278	0.33195388
NR_003010	11.215398	0.3795677	10.636925	0.53607464
NM_014328	8.051729	0.43189728	7.473395	0.38918978
NM_173562	8.679757	0.34565783	8.101627	0.4683035
NM_032869	8.8179455	0.39071545	8.242041	0.4540274
NM_152221	10.754832	0.44548133	10.179443	0.4236158
NM_003664	8.63639	0.39372885	8.061227	0.51520383
NM_020886	7.828031	0.2886717	7.2530937	0.38611844
NM_152359	8.321004	0.35126576	7.7469296	0.6071838
NM_000254	8.400975	0.2962381	7.8289943	0.58922905
NM_005688	8.148298	0.2818031	7.5766587	0.4675787
NM_005007	7.4815087	0.41812447	6.909969	0.35771447
NM_032795	7.7526865	0.3690966	7.1811852	0.44353336
NM_052950	8.270701	0.39717376	7.699884	0.4973682
NM_002605	7.6927958	0.36644745	7.122069	0.61812997
NM_007165	8.894181	0.33319175	8.328863	0.36075622
NM_001009894	7.9687934	0.41793376	7.404702	0.43732247
NM_170696	6.5401926	0.43283537	5.9787655	0.28602055
NM_152227	8.537898	0.40914452	7.9771023	0.4355242

NM_133259	10.092493	0.32601944	9.532243	0.47196522
NM_003601	9.937606	0.2883954	9.377413	0.4156576
NM_174926	7.946385	0.31821457	7.38893	0.5265741
NM_003200	8.62876	0.32888865	8.071526	0.50609
NM_012160	8.774795	0.4133052	8.2213955	0.43429402
NM_004879	10.435064	0.3718033	9.88501	0.5182242
NM_002635	10.5411825	0.31499407	9.992229	0.32338223
NM_001040655	6.9404426	0.38154376	6.4125123	0.46461996
NM_152624	8.944655	0.3604663	8.419218	0.44287708
NM_001967	12.295482	0.26756096	11.772878	0.3705561
NM_203346	10.257624	0.36310416	9.735432	0.48007852
NM_003849	9.752614	0.30200216	9.238881	0.43917188
NM_004444	7.26233	0.1708264	6.7512546	0.29859015
NM_006099	8.22941	0.2812863	7.718631	0.5531759
NM_145063	8.992031	0.3325523	8.481285	0.4586663
NM_014991	9.632494	0.35634992	9.123412	0.43746334
NM_001281	10.978079	0.34479347	10.469706	0.4904521
NM_001020	12.009868	0.2754416	11.502417	0.5107823
NM_003998	7.6168413	0.34423012	7.1112194	0.4566345
NM_148977	8.345059	0.39307263	7.8411436	0.3413246
NM_023925	8.372179	0.3386509	7.868343	0.41622162
NM_018323	7.3600335	0.30358532	6.8592954	0.5486519
NM_021033	10.115828	0.346336	9.624286	0.45729432
NM_001010	12.3604355	0.2133802	11.873388	0.32947278
NM_025076	8.540663	0.33867013	8.063314	0.43631318
NM_005537	8.782858	0.2708552	8.307034	0.26449856
NM_015493	7.21227	0.31031927	6.736466	0.460532
NM_003774	7.667758	0.33693245	7.1950436	0.41574055
NM_015927	7.2954435	0.32199064	6.823491	0.3990927
AK127181	7.900637	0.33006117	7.429569	0.37448645
NM_001080480	6.634675	0.34725073	6.1670046	0.28638136
NM_032824	7.871986	0.30555928	7.4060106	0.3859597
NM_016605	8.138887	0.23853102	7.67478	0.3542305
AK023315	7.9483485	0.34265447	7.486417	0.319168
NM_004822	7.388495	0.32980156	6.926804	0.41315156
NM_001025	11.704135	0.2633647	11.249394	0.397429
NM_017664	10.05985	0.28632888	9.606864	0.4907636
NM_001040185	6.4162383	0.3444716	5.9647007	0.3482736
NM_015275	8.8779955	0.26043683	8.433224	0.488775
NM_001029	7.128448	0.31258214	6.6859193	0.321659
NM_003291	9.5778	0.28499046	9.137077	0.37054774
NM_053005	6.497952	0.32517913	6.0581813	0.27011988
NM_144659	6.2006354	0.28414118	5.769352	0.19412515
NM_001040275	6.762098	0.2958168	6.3323045	0.18769488
NM_147127	6.381265	0.20586525	5.952859	0.22455597
NM_005510	8.1000395	0.24715076	7.683196	0.29566425
NM_178135	5.982944	0.2842025	5.581771	0.28546208
NM_152391	7.472257	0.27280644	7.072159	0.40770018
NM_024783	9.234497	0.2582022	8.854811	0.36875382
NM_001381	6.8008914	0.17759162	6.428041	0.2892261
NM_001033930	13.540339	0.17753352	13.201711	0.34560966
NM_170711	8.60641	0.22534615	8.269566	0.3446437
NM_033449	6.9360876	0.16564101	6.5994945	0.19224301

NM_006092	6.2088118	0.22911125	5.8927646	0.23015302
NM_025058	7.0716395	0.22182338	6.7716866	0.23762567
NM_005775	6.637687	0.1431591	6.4420557	0.16631562

FC-SHH/WNT+Grou	Absolute t value	Degrees of freedom	Raw p value	Adj p value	
	37.88186883	24.825422	33	0	0
	25.80499597	16.983955	31	0	0
	23.46468194	17.660645	35	0	0
	17.53923234	15.056213	29	3.11E-15	5.56E-11
	16.94211403	19.33777	59	0	0
	15.69491706	15.369376	54	0	0
	14.0145547	16.646137	31	0	0
	13.53183889	16.094995	43	0	0
	13.10283419	13.578287	36	8.88E-16	1.59E-11
	12.82136537	13.242645	57	0	0
	12.32437858	17.403654	52	0	0
	12.28202892	7.334384	28	5.50E-08	9.84E-04
	12.22426993	11.673548	53	2.22E-16	3.97E-12
	12.04942753	15.531368	67	0	0
	12.01966931	15.355786	57	0	0
	11.7203228	24.55901	67	0	0
	10.33222457	12.311931	68	0	0
	10.17336255	10.22986	34	6.50E-12	1.16E-07
	9.677577795	18.149055	51	0	0
	9.60994384	12.303682	34	4.49E-14	8.02E-10
	9.342893353	16.396994	72	0	0
	9.285148604	13.671157	35	1.33E-15	2.38E-11
	8.825249099	18.401451	86	0	0
	8.596515511	13.206937	61	0	0
	8.45486899	15.298455	56	0	0
	8.350982837	8.916072	36	1.21E-10	2.17E-06
	7.95891076	16.577734	87	0	0
	7.805721555	13.537325	63	0	0
	7.676876823	15.836955	47	0	0
	7.531469587	12.050384	29	8.18E-13	1.46E-08
	6.84319757	14.099579	34	8.88E-16	1.59E-11
	6.564626818	14.062953	38	2.22E-16	3.97E-12
	6.492018	14.224729	40	0	0
	6.465043154	11.467201	62	0	0
	6.405952053	9.132037	62	4.42E-13	7.90E-09
	6.323112991	13.38059	70	0	0
	6.302005004	16.412266	64	0	0
	6.280221748	10.9663925	29	7.82E-12	1.40E-07
	6.158331376	9.050817	32	2.45E-10	4.39E-06
	6.008054917	14.31886	36	2.22E-16	3.97E-12
	5.993877504	10.924534	39	1.97E-13	3.53E-09
	5.848884906	10.586609	82	0	0
	5.73764616	12.674867	48	0	0
	5.686429221	14.294791	87	0	0
	5.569485269	6.938527	31	8.78E-08	0.001569167
	5.545209627	8.188843	72	6.81E-12	1.22E-07
	5.531591425	16.571156	67	0	0
	5.514386926	10.086625	46	3.09E-13	5.53E-09
	5.508837856	7.4564962	62	3.48E-10	6.21E-06
	5.485058471	8.817863	87	1.06E-13	1.89E-09
	5.440850924	9.58948	39	8.27E-12	1.48E-07

5.388631755	6.3138456	44	1.17E-07	0.002084364
5.387671916	7.859952	41	1.04E-09	1.85E-05
5.36148148	7.2595515	30	4.41E-08	7.88E-04
5.324473964	10.023121	69	4.22E-15	7.54E-11
5.276669777	14.429777	64	0	0
5.25936856	15.759117	77	0	0
5.198727731	15.450599	70	0	0
5.116371421	7.959629	82	8.40E-12	1.50E-07
5.107760927	9.586952	73	1.49E-14	2.66E-10
5.042992221	8.160704	35	1.30E-09	2.32E-05
5.031290182	8.034576	43	4.24E-10	7.57E-06
5.016144818	11.310085	73	0	0
5.01519084	11.400033	61	0	0
5.006548305	9.494535	86	4.88E-15	8.73E-11
4.909264847	9.96066	36	6.90E-12	1.23E-07
4.86200474	14.200787	68	0	0
4.828386953	9.665885	39	6.64E-12	1.19E-07
4.817233982	9.233543	37	3.85E-11	6.89E-07
4.805640075	9.315611	30	2.32E-10	4.15E-06
4.690287311	8.561979	76	9.22E-13	1.65E-08
4.687903915	6.7933354	27	2.69E-07	0.004817608
4.666474461	13.52296	85	0	0
4.620047229	9.759472	84	1.78E-15	3.18E-11
4.607298273	7.2107716	40	9.56E-09	1.71E-04
4.600143926	7.3440623	68	3.39E-10	6.07E-06
4.599043999	12.379479	55	0	0
4.597291035	9.748151	44	1.46E-12	2.61E-08
4.554262979	7.5477023	76	8.05E-11	1.44E-06
4.549008089	10.9453535	50	7.11E-15	1.27E-10
4.5009608	11.558906	87	0	0
4.472572908	7.4356365	72	1.73E-10	3.09E-06
4.456327309	11.964082	30	6.01E-13	1.08E-08
4.368302607	12.740906	38	2.66E-15	4.76E-11
4.324117122	10.554301	53	1.24E-14	2.22E-10
4.259301924	7.6107445	28	2.73E-08	4.88E-04
4.249386297	7.4869666	32	1.60E-08	2.86E-04
4.172818006	5.706621	53	5.28E-07	0.009446332
4.167456094	14.429873	86	0	0
4.160338742	8.420992	87	6.87E-13	1.23E-08
4.135959332	6.9027963	33	6.95E-08	0.00124298
4.130355901	8.439365	42	1.38E-10	2.46E-06
4.069726941	8.933564	72	2.78E-13	4.97E-09
4.033590149	10.867058	48	1.55E-14	2.78E-10
4.000972188	12.4312	32	8.59E-14	1.54E-09
3.998472041	9.3837805	40	1.17E-11	2.09E-07
3.986971521	10.755301	54	4.88E-15	8.73E-11
3.959635416	10.21007	77	6.66E-16	1.19E-11
3.951593104	11.422505	63	0	0
3.888209622	7.80748	82	1.68E-11	3.00E-07
3.860229709	11.781591	83	0	0
3.852548983	12.00011	73	0	0
3.806799007	7.5943284	44	1.55E-09	2.78E-05
3.797207137	11.028146	51	4.22E-15	7.54E-11

3.781898646	10.026838	41	1.36E-12	2.43E-08
3.776505793	8.144487	63	1.99E-11	3.57E-07
3.770573572	10.267061	44	2.94E-13	5.26E-09
3.766750563	9.778114	67	1.58E-14	2.82E-10
3.757051781	6.957977	77	9.98E-10	1.79E-05
3.751664194	7.7319345	58	1.73E-10	3.09E-06
3.721517448	8.535769	70	1.88E-12	3.37E-08
3.699700793	9.834225	87	8.88E-16	1.59E-11
3.695280807	8.981447	35	1.30E-10	2.33E-06
3.674278544	6.6903243	61	7.87E-09	1.41E-04
3.668391716	8.706882	53	8.46E-12	1.51E-07
3.593392931	6.1964297	51	1.01E-07	0.001803428
3.568786016	8.881739	51	6.26E-12	1.12E-07
3.564548869	7.100476	28	1.00E-07	0.00179292
3.511570257	9.911963	79	1.55E-15	2.78E-11
3.510729886	11.229607	65	0	0
3.482747787	8.572569	61	4.58E-12	8.19E-08
3.478313576	12.319789	46	4.44E-16	7.94E-12
3.471068894	9.093696	87	2.89E-14	5.16E-10
3.456850711	9.834452	46	6.90E-13	1.23E-08
3.45095892	6.9235225	37	3.59E-08	6.41E-04
3.432570377	9.479881	31	1.13E-10	2.02E-06
3.425270678	10.581243	87	0	0
3.423771926	10.38643	43	2.70E-13	4.82E-09
3.420018194	9.211556	82	2.73E-14	4.88E-10
3.391693024	7.7382	43	1.12E-09	2.00E-05
3.381268072	7.565511	47	1.14E-09	2.04E-05
3.378968731	7.1425495	58	1.69E-09	3.02E-05
3.377537997	9.781749	81	2.22E-15	3.97E-11
3.374862911	9.040802	37	6.65E-11	1.19E-06
3.371309316	8.98541	87	4.82E-14	8.62E-10
3.35778766	8.885397	85	9.21E-14	1.65E-09
3.335993551	5.6340547	66	3.93E-07	0.0070292
3.332522694	10.336763	37	1.85E-12	3.30E-08
3.307180987	7.47992	86	5.89E-11	1.05E-06
3.302268209	9.512058	68	4.04E-14	7.23E-10
3.293491896	8.328441	87	1.06E-12	1.90E-08
3.291577121	10.058838	87	2.22E-16	3.97E-12
3.280067491	8.061436	38	9.46E-10	1.69E-05
3.279058408	10.528473	87	0	0
3.27203958	6.3990126	39	1.45E-07	0.002587012
3.264863555	12.098079	85	0	0
3.251783032	8.18696	39	5.34E-10	9.55E-06
3.249875611	8.124934	83	3.67E-12	6.56E-08
3.245408316	12.414037	55	0	0
3.241662511	10.652624	39	4.14E-13	7.41E-09
3.234516338	10.757603	45	5.02E-14	8.97E-10
3.222182034	10.516098	68	6.66E-16	1.19E-11
3.21075437	11.910709	68	0	0
3.201249894	6.786423	34	8.36E-08	0.001494272
3.19570669	8.565955	57	7.96E-12	1.42E-07
3.192095247	7.807327	55	1.80E-10	3.22E-06
3.181460038	10.441622	71	4.44E-16	7.94E-12

3.179676515	9.686847	58	9.95E-14	1.78E-09
3.171610045	8.439192	40	2.03E-10	3.62E-06
3.156782799	5.9208817	84	6.77E-08	0.001210783
3.146712996	7.4172664	61	4.44E-10	7.93E-06
3.133307801	8.862456	55	3.51E-12	6.28E-08
3.12638294	5.450459	87	4.62E-07	0.008268734
3.121390811	8.756664	65	1.33E-12	2.38E-08
3.120534799	9.195455	58	6.32E-13	1.13E-08
3.11273854	7.0164633	44	1.08E-08	1.93E-04
3.109749562	9.7381525	85	1.78E-15	3.18E-11
3.107463617	8.066898	83	4.79E-12	8.56E-08
3.098863053	7.2834888	29	5.07E-08	9.07E-04
3.097480071	6.447098	85	6.61E-09	1.18E-04
3.089340735	7.1063457	46	6.31E-09	1.13E-04
3.088823638	6.0585117	67	7.02E-08	0.001254626
3.086829931	9.946276	61	2.20E-14	3.93E-10
3.078055617	8.149803	33	2.08E-09	3.72E-05
3.074791531	6.593299	38	8.78E-08	0.001569316
3.062824919	6.668587	55	1.32E-08	2.35E-04
3.060045278	10.55513	37	1.03E-12	1.84E-08
3.044447849	8.081921	61	3.18E-11	5.69E-07
3.041569563	10.975488	85	0	0
3.039620052	7.608353	80	4.71E-11	8.42E-07
3.025991007	8.72786	83	2.29E-13	4.09E-09
3.022397262	7.475719	60	3.85E-10	6.89E-06
3.015474426	8.750891	41	6.33E-11	1.13E-06
2.990670564	8.001491	87	4.91E-12	8.79E-08
2.987912707	7.396096	45	2.64E-09	4.73E-05
2.986378443	7.240201	49	2.82E-09	5.04E-05
2.977081052	6.3094516	71	2.11E-08	3.77E-04
2.975382818	13.377227	41	2.22E-16	3.97E-12
2.955926097	9.711279	83	2.44E-15	4.37E-11
2.939268186	7.9201493	46	3.88E-10	6.94E-06
2.929237154	9.982055	48	2.69E-13	4.80E-09
2.915570079	13.367481	74	0	0
2.914763844	7.707012	50	4.73E-10	8.46E-06
2.914182846	9.704918	85	2.00E-15	3.57E-11
2.908151846	10.705536	69	2.22E-16	3.97E-12
2.902077405	5.7126517	70	2.50E-07	0.004467924
2.897440429	8.005978	87	4.81E-12	8.61E-08
2.875414619	8.942938	52	4.25E-12	7.61E-08
2.874990124	8.365327	55	2.22E-11	3.97E-07
2.867205679	7.0615554	73	8.01E-10	1.43E-05
2.862716888	9.573623	49	8.38E-13	1.50E-08
2.85367532	8.084021	86	3.58E-12	6.40E-08
2.850089057	7.3150167	32	2.57E-08	4.60E-04
2.849502385	8.546756	65	3.13E-12	5.59E-08
2.849305076	9.465304	43	4.45E-12	7.96E-08
2.838962908	9.081761	55	1.56E-12	2.80E-08
2.838051954	10.213167	87	2.22E-16	3.97E-12
2.825013183	7.786489	44	8.19E-10	1.46E-05
2.824775082	6.8977656	69	2.04E-09	3.64E-05
2.821966771	6.0190153	41	4.07E-07	0.007269226

2.812999507	10.198547	57	1.82E-14	3.26E-10
2.812920931	6.6564107	87	2.41E-09	4.30E-05
2.810788693	7.4305067	81	9.84E-11	1.76E-06
2.808767095	8.916463	87	6.66E-14	1.19E-09
2.806213938	7.3938465	81	1.16E-10	2.07E-06
2.795078109	7.9657416	36	1.86E-09	3.32E-05
2.794796038	9.76738	84	1.78E-15	3.18E-11
2.784045906	7.706531	76	4.01E-11	7.16E-07
2.771524959	8.28335	78	2.66E-12	4.75E-08
2.76934079	12.468159	31	1.29E-13	2.31E-09
2.753125546	9.927945	86	6.66E-16	1.19E-11
2.749326031	7.11942	49	4.33E-09	7.75E-05
2.745374571	6.7279515	74	3.15E-09	5.63E-05
2.744227333	5.7746696	54	3.91E-07	0.0069887
2.744010496	6.823872	37	4.87E-08	8.71E-04
2.737420374	6.9456735	37	3.35E-08	5.99E-04
2.736406382	8.68965	53	9.00E-12	1.61E-07
2.72979876	7.9282727	39	1.18E-09	2.11E-05
2.724784248	13.82318	87	0	0
2.721133995	9.540033	51	6.26E-13	1.12E-08
2.715696018	7.873987	34	3.62E-09	6.46E-05
2.712712208	6.983054	74	1.06E-09	1.89E-05
2.711294826	8.895459	54	3.64E-12	6.50E-08
2.694893014	9.8673	70	6.88E-15	1.23E-10
2.680805404	7.937587	34	3.02E-09	5.40E-05
2.671060401	6.2515864	87	1.46E-08	2.62E-04
2.669801534	9.056498	29	5.95E-10	1.06E-05
2.663478066	8.216094	41	3.35E-10	6.00E-06
2.662559933	8.197418	85	2.27E-12	4.05E-08
2.660186696	6.3226056	49	7.43E-08	0.001329101
2.632909075	8.344508	29	3.38E-09	6.04E-05
2.606764043	9.619356	30	1.12E-10	2.00E-06
2.604676136	7.5212812	81	6.54E-11	1.17E-06
2.595648449	7.2870073	62	6.84E-10	1.22E-05
2.593517312	6.6503263	87	2.47E-09	4.42E-05
2.590772975	8.991507	43	1.96E-11	3.51E-07
2.587598892	8.598781	87	2.98E-13	5.32E-09
2.585081921	10.829416	79	0	0
2.584702078	7.094881	59	1.87E-09	3.34E-05
2.576034116	6.514403	57	2.04E-08	3.65E-04
2.571909717	7.468011	44	2.37E-09	4.24E-05
2.567800287	6.8340383	47	1.46E-08	2.61E-04
2.552911278	5.8165555	56	3.02E-07	0.005393391
2.549594832	6.4583735	67	1.39E-08	2.49E-04
2.5442651	8.705465	32	6.01E-10	1.07E-05
2.543666797	7.418974	37	7.90E-09	1.41E-04
2.54325126	8.065469	72	1.16E-11	2.07E-07
2.539877647	7.4464207	52	9.62E-10	1.72E-05
2.535777917	7.368646	83	1.16E-10	2.07E-06
2.525225107	6.726569	61	6.82E-09	1.22E-04
2.523132552	9.15649	56	1.01E-12	1.80E-08
2.521116874	7.859133	73	2.59E-11	4.63E-07
2.520835366	10.169111	60	1.13E-14	2.02E-10

2.519233592	6.5744257	49	3.03E-08	5.42E-04
2.517184562	9.113395	56	1.18E-12	2.12E-08
2.516551985	9.778334	87	1.11E-15	1.99E-11
2.515016387	8.577045	76	8.63E-13	1.54E-08
2.514026749	8.740391	58	3.56E-12	6.37E-08
2.506076405	6.2850304	36	2.90E-07	0.005178289
2.503706239	9.003934	72	2.05E-13	3.67E-09
2.50110565	6.498525	47	4.72E-08	8.44E-04
2.499312501	9.451569	28	3.29E-10	5.89E-06
2.490211018	7.263884	56	1.27E-09	2.27E-05
2.490187543	6.5676427	43	5.46E-08	9.76E-04
2.488613868	8.5017605	31	1.33E-09	2.38E-05
2.482421849	8.082481	86	3.60E-12	6.44E-08
2.479320879	7.921294	86	7.63E-12	1.36E-07
2.478528761	10.071744	32	1.90E-11	3.40E-07
2.477130715	8.181408	74	5.88E-12	1.05E-07
2.472355152	10.09531	81	4.44E-16	7.94E-12
2.472025285	8.28514	74	3.74E-12	6.69E-08
2.465244947	6.343889	86	1.01E-08	1.80E-04
2.46307234	7.300419	83	1.58E-10	2.82E-06
2.461111466	6.5801897	87	3.39E-09	6.06E-05
2.457112647	6.915585	86	7.77E-10	1.39E-05
2.421137979	8.326396	66	6.90E-12	1.23E-07
2.413599495	8.731715	87	1.59E-13	2.84E-09
2.413388207	6.43059	56	3.00E-08	5.37E-04
2.407148923	12.452716	69	0	0
2.401305569	7.198708	59	1.25E-09	2.23E-05
2.390209376	6.9818234	29	1.12E-07	0.002007792
2.380166668	6.4932556	42	7.75E-08	0.001385559
2.375099577	5.828337	53	3.39E-07	0.006064472
2.373562765	7.7201695	48	5.85E-10	1.05E-05
2.365341516	7.234708	85	1.91E-10	3.42E-06
2.362829452	7.3767986	77	1.60E-10	2.85E-06
2.358731169	7.2133923	86	2.00E-10	3.58E-06
2.35647602	8.642783	44	4.91E-11	8.78E-07
2.3561363	6.3374777	85	1.07E-08	1.92E-04
2.347128779	7.3359804	80	1.59E-10	2.85E-06
2.344367918	8.22943	42	2.68E-10	4.80E-06
2.341297072	6.29725	51	7.00E-08	0.001251654
2.336644893	5.780816	83	1.27E-07	0.002262265
2.326199773	10.598782	74	2.22E-16	3.97E-12
2.315856723	8.6849985	66	1.58E-12	2.83E-08
2.310644798	7.846647	34	3.91E-09	6.98E-05
2.310225053	6.2432766	52	7.93E-08	0.001418472
2.306152951	7.4415617	87	6.65E-11	1.19E-06
2.303695922	7.529784	64	2.18E-10	3.89E-06
2.301499294	7.390183	72	2.10E-10	3.75E-06
2.300333122	9.180098	60	4.92E-13	8.79E-09
2.292795686	9.960819	60	2.49E-14	4.45E-10
2.279553549	7.714884	37	3.23E-09	5.78E-05
2.279210701	5.6685953	83	2.03E-07	0.003632643
2.267700322	9.142352	51	2.50E-12	4.48E-08
2.267442082	6.991722	40	1.93E-08	3.44E-04

2.266988386	8.468645	79	1.06E-12	1.90E-08
2.259313858	5.745946	77	1.74E-07	0.003110942
2.256689609	9.4487	75	2.09E-14	3.73E-10
2.252036172	7.219701	87	1.85E-10	3.31E-06
2.250570877	9.263785	87	1.29E-14	2.30E-10
2.242750293	6.462831	36	1.68E-07	0.003004562
2.235746318	6.796833	71	2.76E-09	4.94E-05
2.234880512	10.222885	58	1.35E-14	2.42E-10
2.230111743	10.235752	87	2.22E-16	3.97E-12
2.228191146	7.1554537	87	2.49E-10	4.45E-06
2.227741752	5.8534846	75	1.19E-07	0.002126174
2.224789745	7.5480895	59	3.19E-10	5.70E-06
2.224154488	5.534924	73	4.63E-07	0.008283205
2.219353994	9.708194	68	1.80E-14	3.22E-10
2.219264464	6.7605104	75	2.60E-09	4.65E-05
2.21687281	8.734481	69	9.09E-13	1.63E-08
2.216414945	8.048684	42	4.79E-10	8.56E-06
2.214327173	8.494922	83	6.69E-13	1.20E-08
2.210972376	7.8191857	40	1.39E-09	2.49E-05
2.207383044	10.670061	36	1.07E-12	1.91E-08
2.203651371	7.1198273	57	2.01E-09	3.59E-05
2.191886356	6.7131233	42	3.74E-08	6.70E-04
2.188267336	6.110682	87	2.72E-08	4.87E-04
2.18762886	6.4322753	66	1.63E-08	2.92E-04
2.181870385	6.000277	71	7.53E-08	0.001346369
2.180140329	10.833256	87	0	0
2.176832649	8.206974	65	1.25E-11	2.24E-07
2.172358187	6.043622	49	2.00E-07	0.003584807
2.168801626	6.051762	67	7.21E-08	0.001289068
2.163381202	6.2100825	34	4.60E-07	0.008229049
2.156757541	9.41646	73	3.09E-14	5.52E-10
2.153650284	9.053395	66	3.50E-13	6.25E-09
2.149084188	8.657536	78	4.99E-13	8.92E-09
2.149057375	5.74338	61	3.14E-07	0.005615354
2.148652238	8.90059	45	1.75E-11	3.13E-07
2.147550415	6.95232	63	2.42E-09	4.33E-05
2.145860067	7.120686	64	1.14E-09	2.04E-05
2.141610326	6.989781	58	3.05E-09	5.45E-05
2.139857906	6.083591	69	5.81E-08	0.001039701
2.138624209	5.7098	67	2.81E-07	0.005030687
2.137338334	6.12684	45	2.02E-07	0.003618091
2.134975331	6.227589	44	1.56E-07	0.002791984
2.133662514	5.9051266	85	7.04E-08	0.001259124
2.13064465	9.395771	58	2.97E-13	5.30E-09
2.129836966	8.946019	52	4.21E-12	7.52E-08
2.128819602	7.4885216	43	2.54E-09	4.55E-05
2.128656261	6.5841236	40	7.15E-08	0.001277828
2.127902429	7.085558	58	2.11E-09	3.76E-05
2.126473682	9.81051	56	9.10E-14	1.63E-09
2.122642485	8.597348	83	4.18E-13	7.47E-09
2.12182651	10.725042	87	0	0
2.12055191	6.6245337	83	3.26E-09	5.82E-05
2.118259002	7.10956	59	1.76E-09	3.16E-05

2.115090655	7.987934	81	7.94E-12	1.42E-07
2.114291065	5.5991874	81	2.86E-07	0.005111922
2.103398205	6.4505706	78	8.57E-09	1.53E-04
2.103033746	7.7609963	44	8.91E-10	1.59E-05
2.097043808	8.023424	70	1.65E-11	2.96E-07
2.096545296	6.6594124	66	6.50E-09	1.16E-04
2.095869079	6.6907682	51	1.68E-08	3.00E-04
2.093175097	7.781896	36	3.18E-09	5.69E-05
2.090837587	7.942942	87	6.46E-12	1.16E-07
2.089754692	5.56657	81	3.27E-07	0.005853113
2.089171604	6.459595	67	1.39E-08	2.48E-04
2.087475116	7.707827	75	4.28E-11	7.66E-07
2.086032449	7.0895925	39	1.62E-08	2.89E-04
2.082745268	5.707938	72	2.38E-07	0.004255963
2.081185701	9.424102	69	5.08E-14	9.09E-10
2.074760919	6.6737566	66	6.14E-09	1.10E-04
2.074214364	7.8993917	68	3.34E-11	5.97E-07
2.071102277	6.433516	33	2.71E-07	0.004843501
2.069607231	8.095228	58	4.24E-11	7.58E-07
2.069224244	5.948479	54	2.06E-07	0.003687814
2.065385381	8.00832	75	1.15E-11	2.06E-07
2.065376792	6.606854	62	1.03E-08	1.83E-04
2.062029539	8.233116	60	1.96E-11	3.51E-07
2.061372599	5.797796	54	3.59E-07	0.006420082
2.059704539	8.856867	44	2.46E-11	4.40E-07
2.055684698	7.072667	33	4.27E-08	7.63E-04
2.054646214	6.020428	87	4.04E-08	7.22E-04
2.053893107	7.9223247	44	5.22E-10	9.33E-06
2.053680852	5.8038197	53	3.71E-07	0.006631626
2.051515423	9.045184	83	5.31E-14	9.49E-10
2.046897699	8.458105	76	1.46E-12	2.61E-08
2.046424583	6.586947	87	3.29E-09	5.88E-05
2.046368554	9.790553	64	2.42E-14	4.33E-10
2.045745247	5.783412	58	3.09E-07	0.005530325
2.044858479	7.726116	70	5.83E-11	1.04E-06
2.043834672	5.9566336	40	5.44E-07	0.009725335
2.031976194	6.5958624	68	7.52E-09	1.35E-04
2.030829328	5.9060774	87	6.64E-08	0.001186632
2.029962393	7.9751215	84	6.80E-12	1.22E-07
2.029585335	6.492545	86	5.20E-09	9.31E-05
2.028282352	7.663988	85	2.67E-11	4.78E-07
2.025523748	6.6340446	85	2.88E-09	5.15E-05
2.025031009	7.670162	44	1.21E-09	2.16E-05
2.024539091	9.074082	53	2.25E-12	4.02E-08
2.024127264	6.7568293	87	1.53E-09	2.73E-05
2.023484222	7.6868925	58	2.05E-10	3.67E-06
2.019801477	6.994538	87	5.19E-10	9.28E-06
2.01704602	8.8527565	68	6.23E-13	1.11E-08
2.016239052	8.593722	68	1.83E-12	3.28E-08
2.014132089	6.1222	71	4.57E-08	8.16E-04
2.010580778	8.349375	30	2.56E-09	4.57E-05
2.010362409	8.967782	85	6.28E-14	1.12E-09
2.004652261	5.8604946	79	1.02E-07	0.001816143

2.002772707	6.0910006	45	2.29E-07	0.004090099
1.99618302	5.739426	76	1.84E-07	0.003294846
1.994186031	9.56581	60	1.12E-13	2.00E-09
1.990956362	6.835846	66	3.17E-09	5.67E-05
1.986693065	9.674109	80	4.22E-15	7.54E-11
1.983637906	9.601551	75	1.07E-14	1.91E-10
1.979486873	6.4822865	61	1.78E-08	3.19E-04
1.976453482	5.682395	77	2.26E-07	0.004043684
1.975800113	7.0910273	51	3.91E-09	6.99E-05
1.97558374	6.2922635	56	5.07E-08	9.06E-04
1.973751004	6.6034026	62	1.04E-08	1.86E-04
1.971814725	5.5822034	63	5.37E-07	0.009610377
1.971060419	6.2750955	39	2.15E-07	0.003842739
1.963718318	6.561102	42	6.19E-08	0.001106859
1.957552093	9.528679	49	9.75E-13	1.74E-08
1.957288335	6.9115076	39	2.84E-08	5.07E-04
1.950181501	6.1370115	66	5.36E-08	9.58E-04
1.949951174	5.558236	86	3.01E-07	0.005374495
1.94974912	7.9668636	63	4.08E-11	7.29E-07
1.949365342	5.806828	57	2.97E-07	0.005317614
1.943904441	7.1933	47	4.16E-09	7.45E-05
1.940300763	7.426193	82	9.46E-11	1.69E-06
1.939623583	11.981768	34	9.39E-14	1.68E-09
1.936540938	8.220543	82	2.55E-12	4.57E-08
1.933781108	6.5145783	82	5.51E-09	9.85E-05
1.921713144	9.474024	63	9.88E-14	1.77E-09
1.920009701	5.5715427	84	2.98E-07	0.005325382
1.914075848	7.4545474	56	6.14E-10	1.10E-05
1.912310379	5.8843527	47	4.03E-07	0.007198542
1.911513647	8.833344	70	5.35E-13	9.56E-09
1.909497459	6.420946	74	1.16E-08	2.07E-04
1.899505646	7.1389422	61	1.34E-09	2.39E-05
1.896808457	7.1041665	67	9.86E-10	1.76E-05
1.896456658	6.7177687	64	5.80E-09	1.04E-04
1.895770732	6.4399543	59	2.38E-08	4.26E-04
1.895591373	6.574669	62	1.16E-08	2.08E-04
1.890352129	8.128859	37	9.41E-10	1.68E-05
1.886328578	5.9694643	77	6.86E-08	0.001227277
1.884545072	6.9812675	50	6.42E-09	1.15E-04
1.884086236	6.441609	54	3.31E-08	5.93E-04
1.882475384	8.910844	42	3.12E-11	5.58E-07
1.877293211	6.9991074	38	2.47E-08	4.41E-04
1.875043415	5.633751	66	3.94E-07	0.007037563
1.869469974	8.185568	78	4.11E-12	7.35E-08
1.869141772	6.4737573	46	5.63E-08	0.001006046
1.865723248	6.643562	65	7.36E-09	1.32E-04
1.86177922	6.4110646	63	2.10E-08	3.75E-04
1.861545656	6.8226004	74	2.10E-09	3.76E-05
1.85934824	5.969134	62	1.26E-07	0.002244566
1.85799768	5.887628	72	1.15E-07	0.00205152
1.857153933	7.466954	34	1.15E-08	2.06E-04
1.851899362	6.5639706	51	2.66E-08	4.75E-04
1.846922974	7.074059	68	1.04E-09	1.87E-05

1.845084641	6.748767	85	1.72E-09	3.08E-05
1.840733794	7.885924	58	9.51E-11	1.70E-06
1.838457722	5.650101	79	2.44E-07	0.00436531
1.837080187	7.010306	50	5.78E-09	1.03E-04
1.833264436	5.874581	49	3.65E-07	0.006526196
1.832232265	6.6695023	56	1.22E-08	2.17E-04
1.832053584	6.2548842	81	1.77E-08	3.17E-04
1.831984123	8.927721	55	2.76E-12	4.93E-08
1.8303252	6.3854303	42	1.11E-07	0.001980234
1.827191697	7.4986835	68	1.78E-10	3.18E-06
1.825812985	7.5760226	66	1.52E-10	2.72E-06
1.821944484	6.8508916	44	1.89E-08	3.38E-04
1.818333339	5.85783	71	1.34E-07	0.00240165
1.818024321	7.1883187	87	2.14E-10	3.82E-06
1.817649463	6.3570113	42	1.22E-07	0.00217574
1.817143558	6.973483	74	1.10E-09	1.97E-05
1.815318886	6.750543	87	1.57E-09	2.81E-05
1.814518794	6.057141	87	3.44E-08	6.15E-04
1.805460053	6.374392	82	1.02E-08	1.82E-04
1.805101548	7.213965	47	3.87E-09	6.93E-05
1.80188133	6.3247566	87	1.06E-08	1.89E-04
1.798958618	8.099572	75	7.71E-12	1.38E-07
1.794303578	5.7254953	64	2.97E-07	0.005309154
1.790930435	9.05641	30	4.37E-10	7.81E-06
1.788949299	5.6823916	84	1.87E-07	0.003340953
1.787554217	10.239567	47	1.48E-13	2.65E-09
1.786850582	6.007746	75	6.27E-08	0.001122003
1.784249045	7.432887	44	2.67E-09	4.77E-05
1.780748284	6.395176	50	5.30E-08	9.48E-04
1.779297191	7.451214	44	2.51E-09	4.48E-05
1.774494374	6.4983845	87	4.89E-09	8.74E-05
1.773462715	5.4742146	87	4.19E-07	0.007484749
1.77157728	7.4224205	52	1.05E-09	1.88E-05
1.768146115	5.7489724	50	5.36E-07	0.009584543
1.767077115	6.0230737	61	1.07E-07	0.001911362
1.76695096	7.3063316	83	1.54E-10	2.75E-06
1.766426842	5.8703957	58	2.23E-07	0.003982416
1.760901242	6.856013	67	2.74E-09	4.90E-05
1.760665323	6.2111845	57	6.47E-08	0.001157008
1.759404979	7.500377	55	5.71E-10	1.02E-05
1.756008709	5.9867225	58	1.43E-07	0.002563094
1.755159328	7.250293	83	1.98E-10	3.54E-06
1.753081417	7.845513	85	1.16E-11	2.07E-07
1.752908876	7.875057	86	9.46E-12	1.69E-07
1.752877771	7.141676	38	1.58E-08	2.83E-04
1.748343304	6.9737997	51	5.99E-09	1.07E-04
1.745478032	6.619406	73	5.25E-09	9.38E-05
1.744949156	6.9921203	55	3.89E-09	6.95E-05
1.744532289	5.7216973	57	4.09E-07	0.007312603
1.739891087	7.8297386	59	1.06E-10	1.90E-06
1.735806582	6.5319104	71	8.37E-09	1.50E-04
1.7356355	6.5881166	43	5.10E-08	9.11E-04
1.735111049	9.067814	58	1.02E-12	1.83E-08

1.732367485	5.7653623	79	1.51E-07	0.002703826
1.731088761	6.5068917	81	5.93E-09	1.06E-04
1.730898947	7.1110764	59	1.75E-09	3.14E-05
1.728698533	5.6020226	73	3.54E-07	0.006322984
1.72847208	7.9953933	72	1.56E-11	2.80E-07
1.726603718	6.9386735	55	4.75E-09	8.50E-05
1.725243503	7.053363	67	1.22E-09	2.17E-05
1.72494935	5.5442758	82	3.50E-07	0.006262697
1.724730561	10.353547	71	8.88E-16	1.59E-11
1.723255954	7.0128508	61	2.20E-09	3.94E-05
1.719448374	7.5530562	54	5.21E-10	9.32E-06
1.718574031	6.147689	78	3.13E-08	5.59E-04
1.7182485	5.608734	61	5.25E-07	0.009392195
1.716991622	6.0029154	42	3.93E-07	0.007034069
1.714988616	6.027439	68	7.61E-08	0.001361437
1.71434444	5.6484327	66	3.72E-07	0.006644344
1.712148101	5.6991158	72	2.47E-07	0.004410397
1.711469995	6.401437	54	3.85E-08	6.88E-04
1.71087256	6.783917	75	2.35E-09	4.21E-05
1.708324448	6.0833344	41	3.29E-07	0.005888128
1.706433981	6.8884892	76	1.42E-09	2.55E-05
1.705557626	6.940176	40	2.27E-08	4.06E-04
1.703444566	6.557721	73	6.81E-09	1.22E-04
1.701718141	6.9271274	68	1.92E-09	3.43E-05
1.699485438	6.117943	87	2.64E-08	4.71E-04
1.697490264	6.218805	49	1.08E-07	0.001923352
1.697064032	7.552774	55	4.69E-10	8.38E-06
1.696989925	6.8342066	87	1.08E-09	1.93E-05
1.69697287	6.179781	67	4.31E-08	7.70E-04
1.696873479	6.893688	84	9.39E-10	1.68E-05
1.695555843	5.8511863	56	2.65E-07	0.004740391
1.6936221	7.479181	54	6.87E-10	1.23E-05
1.691673325	6.592887	58	1.41E-08	2.52E-04
1.691498034	5.7714515	62	2.70E-07	0.004827487
1.686998862	5.634078	61	4.77E-07	0.008527542
1.683318297	8.283458	76	3.15E-12	5.64E-08
1.683311063	5.655724	61	4.39E-07	0.007851657
1.681527065	7.677513	71	6.62E-11	1.18E-06
1.681103443	6.036348	65	8.38E-08	0.001499214
1.680612361	7.5071754	76	9.61E-11	1.72E-06
1.679488946	8.814212	41	5.20E-11	9.30E-07
1.676362321	6.036075	55	1.41E-07	0.002515442
1.675169987	5.9697638	46	3.21E-07	0.005747372
1.674463583	6.3701158	69	1.81E-08	3.23E-04
1.672769892	6.0083995	77	5.83E-08	0.001042474
1.672318916	5.593116	74	3.56E-07	0.006360325
1.666346008	8.073957	62	2.95E-11	5.27E-07
1.665829793	7.0881605	81	4.55E-10	8.14E-06
1.664910933	6.750601	67	4.22E-09	7.55E-05
1.664857502	8.441585	86	6.73E-13	1.20E-08
1.663767683	7.4184594	75	1.51E-10	2.71E-06
1.662233204	10.211159	58	1.42E-14	2.54E-10
1.662033429	9.037449	85	4.53E-14	8.10E-10

1.66194749	6.1641617	45	1.78E-07	0.003184259
1.657635724	7.681675	33	7.61E-09	1.36E-04
1.656613442	5.986623	47	2.82E-07	0.005042565
1.655666384	7.350001	85	1.13E-10	2.02E-06
1.654897198	7.0460734	80	5.79E-10	1.03E-05
1.654791325	8.287048	73	4.07E-12	7.27E-08
1.65475313	6.7619805	52	1.19E-08	2.12E-04
1.654599441	6.7700353	67	3.90E-09	6.97E-05
1.654099018	6.639502	55	1.47E-08	2.62E-04
1.652143958	5.7944245	64	2.27E-07	0.004057998
1.652072157	7.4453926	63	3.33E-10	5.96E-06
1.650574663	6.2607083	56	5.71E-08	0.001020329
1.649349339	6.470784	50	4.04E-08	7.22E-04
1.644599163	5.604675	66	4.41E-07	0.007885268
1.643889128	6.9894633	58	3.05E-09	5.46E-05
1.637199124	6.861069	63	3.49E-09	6.24E-05
1.634006814	6.6135135	36	1.06E-07	0.001896761
1.632283895	10.267523	87	2.22E-16	3.97E-12
1.63138467	5.6264477	61	4.91E-07	0.008779243
1.630854415	9.495966	82	7.33E-15	1.31E-10
1.630139015	8.029661	87	4.31E-12	7.70E-08
1.629908527	5.695425	70	2.68E-07	0.004787024
1.627233178	8.40692	81	1.18E-12	2.11E-08
1.626706528	6.714955	43	3.33E-08	5.96E-04
1.625191811	6.4640613	57	2.47E-08	4.42E-04
1.623151879	6.773603	80	1.93E-09	3.44E-05
1.619375999	7.3683357	71	2.47E-10	4.41E-06
1.616644315	6.2930684	50	7.65E-08	0.00136837
1.613974293	7.1498175	55	2.14E-09	3.83E-05
1.613162194	5.9429326	65	1.21E-07	0.002170091
1.611191079	8.162065	37	8.53E-10	1.53E-05
1.610915701	5.6852612	86	1.76E-07	0.00313985
1.610589016	8.151655	49	1.12E-10	2.00E-06
1.608291928	8.659023	35	3.18E-10	5.69E-06
1.606896491	6.337428	58	3.76E-08	6.73E-04
1.605110701	6.674452	69	5.15E-09	9.21E-05
1.600481499	7.032476	81	5.84E-10	1.04E-05
1.598757803	6.3927994	45	8.14E-08	0.001455347
1.59663108	5.6523905	60	4.64E-07	0.008293441
1.593398365	6.187601	87	1.94E-08	3.47E-04
1.59281863	5.7786965	62	2.63E-07	0.004694392
1.591981532	6.9267	45	1.31E-08	2.34E-04
1.588374825	6.1496153	63	5.90E-08	0.001054764
1.585288045	5.6734157	56	5.13E-07	0.009179269
1.584534421	5.9262743	42	5.07E-07	0.009066608
1.584520143	6.754806	69	3.69E-09	6.60E-05
1.580905355	7.47127	86	6.13E-11	1.10E-06
1.577660738	5.4843273	86	4.10E-07	0.007330726
1.57734692	7.9255466	53	1.47E-10	2.63E-06
1.574475164	6.1154776	77	3.72E-08	6.64E-04
1.573678685	6.8221407	59	5.41E-09	9.67E-05
1.568601081	8.3392935	33	1.24E-09	2.22E-05
1.568565745	5.7566714	83	1.40E-07	0.002505678

1.567773343	6.3664136	81	1.09E-08	1.95E-04
1.564001612	6.7421784	60	6.87E-09	1.23E-04
1.562748914	6.473123	64	1.55E-08	2.77E-04
1.562731149	7.3769665	51	1.38E-09	2.47E-05
1.557269567	6.4443965	34	2.29E-07	0.004101733
1.555349713	6.022608	51	1.89E-07	0.003380317
1.55240932	7.0793824	67	1.09E-09	1.95E-05
1.550786413	6.8164706	73	2.28E-09	4.07E-05
1.55034307	6.901622	70	1.89E-09	3.37E-05
1.55017458	7.386057	57	7.23E-10	1.29E-05
1.548907296	5.761502	51	4.84E-07	0.008648926
1.54500617	5.627293	69	3.63E-07	0.006498186
1.543355271	6.1403947	45	1.93E-07	0.003454101
1.540304198	5.8744154	83	8.50E-08	0.001519998
1.53848673	6.1569405	54	9.54E-08	0.001706464
1.536539654	5.745241	75	1.86E-07	0.003318935
1.53638523	7.180285	77	3.78E-10	6.76E-06
1.53464291	6.8987823	80	1.11E-09	1.98E-05
1.531840407	7.246267	58	1.13E-09	2.02E-05
1.527851683	5.671193	64	3.67E-07	0.006557005
1.525206622	7.0098143	59	2.60E-09	4.66E-05
1.523783565	5.764445	56	3.66E-07	0.006547505
1.520453821	7.6578984	77	4.62E-11	8.27E-07
1.520411666	6.462739	65	1.53E-08	2.73E-04
1.520259916	5.59667	62	5.28E-07	0.009450003
1.517740876	6.270161	83	1.54E-08	2.76E-04
1.513328302	6.008873	74	6.48E-08	0.001158298
1.511436219	7.208504	62	9.36E-10	1.67E-05
1.511262215	6.4374814	58	2.56E-08	4.58E-04
1.506701577	7.1510763	69	7.08E-10	1.27E-05
1.506426203	6.0511093	82	4.12E-08	7.36E-04
1.506294225	7.0247583	54	3.76E-09	6.72E-05
1.503733597	6.883612	82	1.08E-09	1.93E-05
1.499894471	7.12882	85	3.10E-10	5.54E-06
1.494681402	7.398733	49	1.60E-09	2.87E-05
1.493267884	5.8492794	71	1.39E-07	0.002486379
1.493124018	6.0609202	47	2.18E-07	0.003892204
1.492912902	6.5442066	69	8.82E-09	1.58E-04
1.490611712	6.1472244	60	6.97E-08	0.001245451
1.490079185	5.7590775	49	5.49E-07	0.009815811
1.489845781	5.8047757	67	1.93E-07	0.003454069
1.489612723	7.8378844	68	4.32E-11	7.72E-07
1.488722027	5.6420174	82	2.33E-07	0.004167032
1.486563097	6.1203203	86	2.69E-08	4.81E-04
1.486211358	7.16654	80	3.39E-10	6.06E-06
1.486108757	6.270548	45	1.24E-07	0.00221218
1.486069202	6.3743095	62	2.57E-08	4.59E-04
1.485364496	5.818691	64	2.06E-07	0.003690933
1.485271631	5.4519606	81	5.25E-07	0.009395554
1.479713633	7.2596116	56	1.29E-09	2.30E-05
1.478456094	5.8421783	54	3.05E-07	0.005454237
1.475728272	6.27286	38	2.41E-07	0.004302027
1.475082556	5.8988924	55	2.34E-07	0.004187848

1.474524711	6.5177183	73	8.06E-09	1.44E-04
1.474466454	7.383077	72	2.16E-10	3.86E-06
1.471670811	6.1982665	80	2.34E-08	4.19E-04
1.47144539	6.2323275	76	2.36E-08	4.21E-04
1.467539668	5.787581	54	3.73E-07	0.006665352
1.464140498	5.7134495	70	2.49E-07	0.004453667
1.463024065	7.590507	53	5.06E-10	9.06E-06
1.44185921	5.666219	62	4.05E-07	0.007238307
1.439369507	5.947836	63	1.30E-07	0.002327781
1.43654581	7.565671	70	1.15E-10	2.06E-06
1.436135625	5.688757	67	3.06E-07	0.005466398
1.427739723	6.4376903	73	1.13E-08	2.02E-04
1.425112093	10.262222	82	2.22E-16	3.97E-12
1.424819336	5.797828	86	1.09E-07	0.00194219
1.424786745	5.960374	70	9.20E-08	0.001645493
1.423144348	5.8311863	63	2.05E-07	0.003668443
1.422445128	5.639709	72	3.13E-07	0.005604124
1.421536359	6.10121	85	3.02E-08	5.39E-04
1.419735227	5.8017564	67	1.95E-07	0.0034957
1.418056878	5.8590317	46	4.71E-07	0.008418887
1.417978836	6.0698423	63	8.07E-08	0.001443337
1.414937276	5.547782	84	3.29E-07	0.005882255
1.405946795	5.617437	67	4.05E-07	0.007238852
1.401573594	8.381243	76	2.05E-12	3.66E-08
1.392183132	5.6386156	66	3.86E-07	0.006904795
1.390712303	7.771765	51	3.31E-10	5.92E-06
1.390693024	5.7446733	74	1.92E-07	0.003434451
1.387717975	5.714818	63	3.22E-07	0.005761939
1.386985303	5.959425	63	1.24E-07	0.002224673
1.386135218	6.005543	58	1.33E-07	0.002386341
1.38287466	6.2331963	44	1.53E-07	0.002739441
1.381250896	6.1519637	64	5.56E-08	9.94E-04
1.379463228	7.2874427	74	2.85E-10	5.10E-06
1.377384646	6.046556	48	2.13E-07	0.003806188
1.377155052	5.6668425	64	3.73E-07	0.006668689
1.370536737	6.4151416	75	1.13E-08	2.03E-04
1.368870529	5.4881496	82	4.42E-07	0.007903232
1.367496935	5.737197	52	4.99E-07	0.008923896
1.361098523	5.6144595	85	2.43E-07	0.004341252
1.358984216	6.1615005	53	1.00E-07	0.001789492
1.357284354	6.162109	66	4.85E-08	8.67E-04
1.356388728	6.248526	44	1.45E-07	0.002600777
1.348432589	7.2991486	38	9.72E-09	1.74E-04
1.347040755	7.0719867	37	2.27E-08	4.07E-04
1.345745872	8.8811	56	2.81E-12	5.02E-08
1.335003478	6.9555964	61	2.76E-09	4.94E-05
1.320581188	6.1909633	52	9.60E-08	0.001717024
1.319597546	5.4756966	75	5.56E-07	0.009934218
1.301058652	5.613918	72	3.48E-07	0.006216686
1.294908717	7.4936566	79	8.39E-11	1.50E-06
1.264553434	6.129394	86	2.59E-08	4.62E-04
1.262990686	5.515819	76	4.60E-07	0.00821895
1.262771058	8.47872	60	7.51E-12	1.34E-07

1.244914964	6.0498447	52	1.61E-07	0.00287188
1.231104221	5.807021	55	3.29E-07	0.005885037
1.145225183	5.6996655	60	3.88E-07	0.006930264