

Probe	Gene name	Symbol	Location	Unigene	LocusLink	SCZ-CNT IG pval	SCZ-CNT IG ALR
209395_at	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	chr1q32.1	Hs.382202	1116	0.025688	1.44
209396_s_at	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	chr1q32.1	Hs.382202	1116	0.011407	1.38
207574_s_at	growth arrest and DNA-damage-inducible, beta	GADD45B	chr19p13.3	Hs.110571	4616	0.039501	1.37
229259_at	glial fibrillary acidic protein	GFAP	chr17q21	Hs.514227	2670	0.034990	1.33
201613_s_at	adaptor-related protein complex 1, gamma 2 subunit	AP1G2	chr14q11.2	Hs.343244	8906	0.006383	1.33
212203_x_at	interferon induced transmembrane protein 3 (1-8U)	IFITM3	chr11p15.5	Hs.374650	10410	0.005623	1.26
240083_at						0.024525	1.22
1561306_s_at	stereocilin	STRC	chr15q15.3	Hs.550553	161497	0.006986	1.16
235867_at	glutathione S-transferase M3 (brain)	GSTM3	chr1p13.3	Hs.2006	2947	0.010845	1.14
210794_s_at	maternally expressed 3	MEG3	chr14q32	Hs.525589	55384	0.007667	1.11
1552301_a_at	coronin 6	CORO6	chr17q21.2	Hs.143046	84940	0.041185	1.09
219019_at	leucine-rich repeats and death domain containing	LRDD	chr11p15.5	Hs.552597	55367	0.018113	1.07
217911_s_at	BCL2-associated athanogene 3	BAG3	chr10q25.2-q26.2	Hs.523309	9531	0.025526	1.07
231392_at	Hypothetical protein BC008326	LOC89944	chr11q25	Hs.436178	89944	0.016314	1.07
214022_s_at						0.041950	1.07
237870_at	hypothetical protein LOC285771	LOC285771	chr6p25.2	Hs.145597	285771	0.043433	1.04
240048_at	Stereocilin	STRC	chr15q15.3	Hs.550553	161497	0.018828	1.03
230664_at	hypothetical protein MGC39900	MGC39900	chrXq22.2	Hs.496530	286527	0.001994	1.02
225321_s_at	paired immunoglobulin-like type 2 receptor beta	PILRB	chr7q22.1	Hs.530084	29990	0.042260	0.99
1555847_a_at	hypothetical protein LOC284454	LOC284454	chr19p13.13	Hs.436426	284454	0.009724	0.98
230941_at	hypothetical LOC400988	LOC400988	chr2q11.2	Hs.469369	400988	0.007228	0.98
240174_at	Hypothetical LOC388903		chr22q13.1	Hs.474880	388903	0.008394	0.98
226679_at	solute carrier family 26, member 11	SLC26A11	chr17q25.3	Hs.4866	284129	0.002016	0.98
201315_x_at	interferon induced transmembrane protein 2 (1-8D)	IFITM2	chr11p15.5	Hs.174195	10581	0.019868	0.97
243337_at	FRAS1 related extracellular matrix 3	FREM3	chr4q31.21	Hs.252714	166752	0.013947	0.95
201841_s_at	heat shock 27kDa protein 1	HSPB1	chr7q11.23	Hs.520973	3315	0.014354	0.95
202284_s_at	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A	chr6p21.2	Hs.370771	1026	0.032645	0.95
213428_s_at	collagen, type VI, alpha 1	COL6A1	chr21q22.3	Hs.474053	1291	0.031385	0.95
211964_at	collagen, type IV, alpha 2	COL4A2	chr13q34	Hs.508716	1284	0.027987	0.94
240402_at						0.047957	0.93
209304_x_at	growth arrest and DNA-damage-inducible, beta	GADD45B	chr19p13.3	Hs.110571	4616	0.029051	0.93
238333_s_at	GTP binding protein	Sprn	chr10q26.3	Hs.501578	92170	0.049532	0.93
227543_at	AYP1 protein	AYP1	chr11q13.1	Hs.397010	84153	0.003628	0.92
1560089_at	hypothetical protein LOC286208	LOC286208	chr9q34.11	Hs.533252	286208	0.000260	0.91
203973_s_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	chr8p11.2-p11.1	Hs.440829	1052	0.012942	0.91
91617_at	DiGeorge syndrome critical region gene 8	DGCR8	chr22q11.2	Hs.533019	54487	0.020127	0.90
228124_at	chromosome 20 open reading frame 22	C20orf22	chr20p11.21	Hs.441550	26090	0.015525	0.89
1553993_s_at	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	MED25	chr19q13.3	Hs.467128	81857	0.049947	0.88
236677_at	neuroglobin	NGB	chr14q24	Hs.274363	58157	0.034290	0.88
210069_at	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	CHKB /// C	chr22q13.33	Hs.439777	1120 /// 1	0.025336	0.88
230417_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosamin	GALNTL1	chr14q24.1	Hs.21035	57452	0.016818	0.88
212556_at	scribbled homolog (Drosophila)	SCRIB	chr8q24.3	Hs.436329	23513	0.048969	0.87
221501_x_at	hypothetical protein LOC339047	LOC339047	chr16p12.3	Hs.513391	339047	0.004180	0.87
228111_s_at	heat shock regulated 1	XLHSRF-1	chr3p21.31	Hs.9740	25981	0.040957	0.87
204538_x_at	nuclear pore complex interacting protein /// hypothetical protein LOC3	NPIP /// LC	chr16p13-p11 ///	Hs.528782	339047 ///	0.002060	0.87
212185_x_at	metallothionein 2A	MT2A	chr16q13	Hs.418241	4502	0.031322	0.87
204326_x_at	metallothionein 1X	MT1X	chr16q13	Hs.374950	4501	0.021988	0.86
1556762_a_at	Methionine sulfoxide reductase A	MSRA	chr8p23.1	Hs.490981	4482	0.046057	0.86
40569_at	zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	ZNF42	chr19q13.2-q13.4	Hs.399810	7593	0.011935	0.85
214035_x_at	LOC399491 protein	LOC399491	chr16p13.1		399491	0.003100	0.85
214870_x_at	nuclear pore complex interacting protein /// hypothetical protein LOC3	NPIP /// LC	chr16p13-p11 ///	Hs.528782	339047 ///	0.003126	0.85
243061_at	hypothetical gene supported by BX248251	LOC387974	chr14q12	Hs.92556	387978	0.042754	0.85
230418_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosamin	GALNTL1	chr14q24.1	Hs.21035	57452	0.007211	0.85
206204_at	growth factor receptor-bound protein 14	GRB14	chr2q22-q24	Hs.411881	2888	0.031659	0.84
211996_s_at	PI-3-kinase-related kinase SMG-1-like	KIAA0220	chr16p12.3	Hs.528462	283846	0.014660	0.84
209467_s_at	MAP kinase interacting serine/threonine kinase 1	MKINK1	chr1p33	Hs.371594	8569	0.010781	0.84
209381_x_at	splicing factor 3a, subunit 2, 66kDa	SF3A2	chr19p13.3-p13.2	Hs.115232	8175	0.022943	0.84
213900_at	chromosome 9 open reading frame 61	C9orf61	chr9q13-q21	Hs.118003	9413	0.016543	0.84
40020_at	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Dros	CELSR3	chr3p24.1-p21.2	Hs.533070	1951	0.033804	0.83
37462_i_at	splicing factor 3a, subunit 2, 66kDa	SF3A2	chr19p13.3-p13.2	Hs.115232	8175	0.049961	0.82
200840_at	lysyl-tRNA synthetase	KARS	chr16q23-q24	Hs.3100	3735	0.043282	0.82
218552_at	enoyl Coenzyme A hydratase domain containing 2	ECHDC2	chr1p32.3	Hs.476319	55268	0.028020	0.82
205428_s_at	calbindin 2, 29kDa (calretinin)	CALB2	chr16q22.2	Hs.106857	794	0.000149	0.82
225598_at	KIAA1126 protein	KIAA1126	chr8q24.3	Hs.372492	57210	0.034278	0.81
233168_s_at	selenoprotein O	SELO	chr22q13.33	Hs.365405	83642	0.019833	0.81
212732_at	maternally expressed 3	MEG3	chr14q32	Hs.525589	55384	0.029608	0.81
237483_at	Pleckstrin homology domain containing, family A member 5	PLEKHA5	chr12p12	Hs.188614	54477	0.031996	0.81
236229_at	Similar to Hypothetical zinc finger protein KIAA1956		chr19q13.43	Hs.467370	400721	0.010338	0.81
243996_at	Transcribed locus			Hs.151334		0.034990	0.81
244358_at						0.030896	0.80
206461_x_at	metallothionein 1H	MT1H	chr16q13	Hs.438462	4496	0.027586	0.80
212360_at	adenosine monophosphate deaminase 2 (isoform L)	AMPD2	chr1p13.3	Hs.82927	271	0.025468	0.79
208982_at	Platelet/endothelial cell adhesion molecule (CD31 antigen)	PECAM1	chr17q23	Hs.514412	5175	0.000647	0.79

201160_s_at	cold shock domain protein A	CSDA	chr12p13.1	Hs.221889	8531	0.043946	0.79
214241_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFB8	chr10q23.2-q23.3	Hs.523215	4714	0.036464	0.79
37860_at	zinc finger protein 337	ZNF337	chr20p11.21	Hs.213735	26152	0.021584	0.79
207063_at	chromosome Y open reading frame 14	CYorf14	chrYq11.222	Hs.138453	55410	0.046198	0.78
218792_s_at	B-box and SPRY domain containing	BSPRY	chr9q32	Hs.494870	54836	0.008033	0.78
239784_at	MRNA, chromosome 1 specific transcript KIAA0504.			Hs.127406		0.010045	0.78
220349_s_at	endo-beta-N-acetylglucosaminidase	FLJ21865	chr17q25.3	Hs.29288	64772	0.033388	0.78
235205_at	similar to solute carrier family 16 (monocarboxylic acid transporters), member 1	LOC34688	chr8q23.1	Hs.127286	346887	0.026267	0.78
218148_at	hypothetical protein FLJ13111	FLJ13111	chr16q22.1	Hs.288382	80152	0.031946	0.78
1561749_at	Hypothetical protein MGC13098	MGC13098	chr7p13	Hs.549219	84820	0.026898	0.77
201221_s_at	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	SNRP70	chr19q13.3	Hs.467097	6625	0.010586	0.77
215147_at	CUG triplet repeat, RNA binding protein 2	CUGBP2	chr10p13	Hs.309288	10659	0.012478	0.77
235746_s_at	phospholipase A2 receptor 1, 180kDa	PLA2R1	chr2q23-q24	Hs.410477	22925	0.018483	0.77
235418_at	hypothetical protein LOC285014	LOC285014	chr2q11.2	Hs.531247	285014	0.018527	0.77
230932_at	Transcribed locus			Hs.8038		0.002900	0.77
233084_s_at	chromosome 10 open reading frame 94	C10orf94	chr10q26.3	Hs.549231	93426	0.014241	0.76
233393_at	Methionine sulfoxide reductase A	MSRA	chr8p23.1	Hs.490981	4482	0.026175	0.76
229310_at	kelch repeat and BTB (POZ) domain containing 9	KBTD9	chr2p24.1	Hs.130593	114818	0.005392	0.75
214291_at	ribosomal protein L17 /// similar to dj612B15.1 (novel protein similar to	RPL17 /// d	chr18q21 /// chr	Hs.526159	388132 ///	0.015917	0.75
205447_s_at	mitogen-activated protein kinase kinase kinase 12	MAP3K12	chr12q13	Hs.211601	7786	0.018487	0.75
203155_at	SET domain, bifurcated 1	SETDB1	chr1q21	Hs.516278	9869	0.021571	0.75
212723_at	phosphatidylserine receptor	PTDSR	chr17q25	Hs.514505	23210	0.035573	0.75
218507_at	hypoxia-inducible protein 2	HIG2	chr7q32.2	Hs.521171	29923	0.027431	0.75
201601_x_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	chr11p15.5	Hs.458414	8519	0.009302	0.75
1556464_a_at	hypothetical protein LOC257407	LOC257407	chr2q37.1	Hs.526596	257407	0.004497	0.74
1568736_s_at	Discs, large (Drosophila) homolog-associated protein 1	DLGAP1	chr18p11.3	Hs.549086	9229	0.015757	0.74
37996_s_at	dystrophia myotonica-protein kinase	DMPK	chr19q13.3	Hs.546249	1760	0.014468	0.74
244216_at						0.028650	0.74
231635_x_at	Ring finger protein 31	RNF31	chr14q11.2	Hs.375217	55072	0.009657	0.73
242121_at	Ring finger protein 12	RNF12	chrXq13-q21	Hs.122121	51132	0.033101	0.73
235964_x_at	SAM domain and HD domain 1	SAMHD1	chr20pter-q12	Hs.472630	25939	0.039421	0.73
33132_at	cleavage and polyadenylation specific factor 1, 160kDa	CPSF1	chr8q24.23	Hs.493202	29894	0.025462	0.73
205741_s_at	dystrobrevin, alpha	DTNA	chr18q12	Hs.58919	1837	0.015469	0.73
202153_s_at	nucleoporin 62kDa	NUP62	chr19q13.33	Hs.467133	23636	0.047586	0.73
218180_s_at	EPS8-like 2	EPS8L2	chr11p15.5	Hs.55016	64787	0.040438	0.72
211386_at	hypothetical protein MGC12488	MGC12488			84786	0.006225	0.72
47083_at	chromosome 7 open reading frame 26	C7orf26	chr7p22.1	Hs.487511	79034	0.025351	0.72
220331_at	cytochrome P450, family 46, subfamily A, polypeptide 1	CYP46A1	chr14q32.1	Hs.25121	10858	0.038307	0.72
224472_x_at	calcium binding protein Cab45 precursor /// calcium binding protein Cab45	Cab45	chr1p36.33	Hs.42806	51150	0.011107	0.72
204078_at	synaptonemal complex protein SC65	SC65	chr17q21.2	Hs.446459	10609	0.015604	0.72
208581_x_at	metallothionein 1X	MT1X	chr16q13	Hs.374950	4501	0.048516	0.72
222240_s_at	myo-inositol 1-phosphate synthase A1	ISYNA1	chr19p13.11	Hs.405873	51477	0.029867	0.72
1558041_a_at	hypothetical protein LOC283849	LOC283849	chr16q22.1	Hs.444594	283849	0.028450	0.71
218205_s_at	MAP kinase interacting serine/threonine kinase 2	MKMK2	chr19p13.3	Hs.515032	2872	0.034530	0.71
227211_at	PHD finger protein 19	PHF19	chr9q33.2	Hs.460124	26147	0.028612	0.71
235875_at	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 1	SLC1A4	chr2p15-p13	Hs.323878	6509	0.033125	0.71
212975_at	KIAA0870 protein	KIAA0870	chr8q24.3	Hs.18166	22898	0.037298	0.71
226419_s_at	Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing)	SFRS1	chr17q21.3-q22	Hs.68714	6426	0.008737	0.70
233944_at	Homo sapiens, clone IMAGE:5311320, mRNA			Hs.190621		0.006695	0.70
203938_s_at	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 1	TAF1C	chr16q24	Hs.153022	9013	0.016377	0.70
225168_at	FERM domain containing 4A	FRMD4A	chr10p13	Hs.552599	55691	0.017820	0.70
204430_s_at	solute carrier family 2 (facilitated glucose/fructose transporter), member 1	SLC2A5	chr1p36.2	Hs.530003	6518	0.025249	0.70
218175_at	limkain beta 2	FLJ22471	chr12q24.31	Hs.114111	80212	0.039725	0.70
218601_at	up-regulated gene 4	URG4	chr7p13	Hs.520334	55665	0.043947	0.69
219999_at	mannosidase, alpha, class 2A, member 2	MAN2A2	chr15q26.1	Hs.116459	4122	0.003795	0.69
224162_s_at	F-box protein 31	FBXO31	chr16q24.2	Hs.549198	79791	0.010088	0.69
36129_at	RUN and TBC1 domain containing 1	RUTBC1	chr17p13.3	Hs.513861	9905	0.017177	0.69
201680_x_at	arsenate resistance protein ARS2	ARS2	chr7q21	Hs.111801	51593	0.025054	0.69
211724_x_at	hypothetical protein FLJ20323 /// hypothetical protein FLJ20323	FLJ20323	chr7p22-p21	Hs.520215	54468	0.015229	0.69
237937_x_at						0.045989	0.69
235529_x_at	SAM domain and HD domain 1	SAMHD1	chr20pter-q12	Hs.472630	25939	0.038095	0.68
232809_s_at	Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular endothelial cell growth factor receptor tyrosine kinase)	FLT1	chr13q12	Hs.507621	2321	0.005343	0.68
65635_at	endo-beta-N-acetylglucosaminidase	FLJ21865	chr17q25.3	Hs.29288	64772	0.019671	0.68
214428_x_at	complement component 4A /// complement component 4B /// complement component 4C	C4A /// C4B	chr6p21.3	Hs.534847	432395 ///	0.048543	0.68
241654_at	Transcribed locus			Hs.427229		0.049490	0.68
1556103_at	CDNA FLJ30565 fis, clone BRAWH2005008			Hs.323409		0.002762	0.68
1555311_at						0.003828	0.68
221261_x_at	melanoma antigen family D, 4 /// melanoma antigen family D, 4	MAGED4		Hs.522650	81557	0.006403	0.67
200660_at	S100 calcium binding protein A11 (calgizzarin)	S100A11	chr1q21	Hs.417004	6282	0.020369	0.67
1554287_at	tripartite motif-containing 4	TRIM4	chr7q22-q31.1	Hs.50749	89122	0.048969	0.67
1561658_at	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta 1	PPP2R2B	chr5q31-5q32	Hs.193825	5521	0.013079	0.67
229867_at	BTB (POZ) domain containing 9	BTBD9	chr6p21	Hs.116233	114781	0.039744	0.67
223983_s_at	chromosome 19 open reading frame 12	C19orf12	chr19q12	Hs.529094	83636	0.000923	0.67
229871_at	hypothetical protein FLJ10211	FLJ10211	chr19q13.2	Hs.398091	55095	0.029370	0.67

244113_at	Transcribed locus			Hs.436567		0.042804	0.67
217585_at						0.014680	0.66
243249_at	Chromosome 14 open reading frame 119	C14orf119	chr14q11.2	Hs.525238	55017	0.025630	0.66
213165_at	Centrosome-associated protein 350	CAP350	chr1p36.13-q41	Hs.413045	9857	0.046558	0.66
227129_x_at	hypothetical protein LOC284701 /// hypothetical gene supported by AK	LOC284701	chr1p36.33 /// ch	Hs.546653	284701 ///	0.018387	0.66
236484_at	START domain containing 7	STARTD7	chr2q11.2	Hs.469331	56910	0.003308	0.66
221816_s_at	PHD finger protein 11	PHF11	chr13q14.2	Hs.369039	51131	0.021569	0.66
243256_at	MAP kinase interacting serine/threonine kinase 1	MKNK1	chr1p33	Hs.371594	8569	0.011624	0.66
1557814_a_at	Single-stranded DNA binding protein 2	SSBP2	chr5q14.1	Hs.102735	23635	0.045484	0.65
1558748_at	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	NAPE-PLD	chr7q22.1	Hs.324271	222236	0.025084	0.65
235077_at	Maternally expressed 3	MEG3	chr14q32	Hs.525589	55384	0.019848	0.65
228064_at	similar to hypothetical protein LOC192734	LOC388888	chr22q11.23	Hs.113314	388886	0.016729	0.65
204139_x_at	zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	ZNF42	chr19q13.2-q13.4	Hs.399810	7593	0.045674	0.65
1556672_a_at	RNA binding motif protein 6	RBM6	chr3p21.3	Hs.188879	10180	0.014390	0.65
219860_at	lymphocyte antigen 6 complex, locus G5C	LY6G5C	chr6p21.33	Hs.25738	80741	0.033819	0.65
227500_at	F-box and leucine-rich repeat protein 18	FBXL18	chr7p22.1	Hs.487447	80028	0.043961	0.65
1559546_s_at	SNRNP upstream reading frame /// Prader-Willi/Angelman region-1	SNRNP ///	chr15q11.2	Hs.525700	145624 ///	0.025389	0.65
203309_s_at	Hermansky-Pudlak syndrome 1	HPS1	chr10q23.1-q23.3	Hs.404568	3257	0.047252	0.65
206435_at	UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminy)-galactosylgl	GALGT	chr12q13.3	Hs.159481	2583	0.048309	0.65
212359_s_at	KIAA0913	KIAA0913	chr10q22.2	Hs.65135	23053	0.010219	0.65
218697_at	NCK interacting protein with SH3 domain	NCKIPSD	chr3p21	Hs.102929	51517	0.044734	0.65
243526_at	hypothetical protein LOC349136	LOC349136	chr7q36.1	Hs.174373	349136	0.043088	0.64
223192_at	solute carrier family 25, member 28	SLC25A28	chr10q23-q24	Hs.403790	81894	0.015879	0.64
238965_at	Chromosome 21 open reading frame 2	C21orf2	chr21q22.3	Hs.517331	755	0.020472	0.64
213088_s_at	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9	chr10q22.2	Hs.523037	23234	0.043522	0.64
37892_at	collagen, type XI, alpha 1	COL11A1	chr1p21	Hs.523446	1301	0.006354	0.64
239730_at	Testis-specific serine kinase 2	STK22B	chr22q11.21	Hs.505323	23617	0.038494	0.64
221767_x_at	high density lipoprotein binding protein (vigilin)	HDLBP	chr2q37	Hs.471851	3069	0.029695	0.64
210150_s_at	laminin, alpha 5	LAMA5	chr20q13.2-q13.3	Hs.473256	3911	0.030134	0.64
215731_s_at	M-phase phosphoprotein 9	MPHOSPH9	chr12q24.31	Hs.507175	10198	0.021935	0.64
221647_s_at	likely ortholog of mouse synembryn	RIC8	chr11p15.5	Hs.19306	60626	0.031142	0.63
202605_at	glucuronidase, beta	GUSB	chr7q21.11	Hs.255230	2990	0.037929	0.63
234974_at	Galactose mutarotase (aldose 1-epimerase)	GALM	chr2p22.1	Hs.435012	130589	0.032819	0.63
45526_g_at	hypothetical protein FLJ14154	FLJ14154	chr16p13.3	Hs.513296	79903	0.032941	0.63
235580_at	Zinc finger protein 141 (clone pHZ-44)	ZNF141	chr4p16.3	Hs.546311	7700	0.012703	0.63
1558620_at	zinc finger protein 621	ZNF621	chr3p22.1	Hs.19977	285268	0.037889	0.63
220313_at	G-protein coupled receptor 88	GPR88	chr1p21.3	Hs.170053	54112	0.008085	0.63
214080_x_at	protein kinase C substrate 80K-H	PRKCSH	chr19p13.2	Hs.512640	5589	0.023468	0.62
227833_s_at	methyl-CpG binding domain protein 6	MBD6	chr10q25.2	Hs.524523	114785	0.030095	0.62
213105_s_at	hypothetical protein MGC24381	MGC24381	chr16p13.3	Hs.134846	115939	0.011720	0.62
233064_at	hypothetical gene supported by AL365406; BC034005	LOC388499	chr19p13.3	Hs.465612	388494	0.042960	0.62
242610_x_at						0.039034	0.62
222047_s_at	arsenate resistance protein ARS2	ARS2	chr7q21	Hs.111801	51593	0.042557	0.62
201851_at	SH3-domain GRB2-like 1	SH3GL1	chr19p13.3	Hs.97616	6455	0.030410	0.62
227894_at	similar to RIKEN cDNA 3230401M21 [Mus musculus]	LOC197333	chr16p13.3	Hs.511903	197336	0.028514	0.62
48531_at	TNFAIP3 interacting protein 2	TNIP2	chr4p16.3	Hs.368551	79155	0.032076	0.62
213670_x_at	Williams-Beuren Syndrome critical region protein 20 copy B	WBSR20B	chr7q11.23	Hs.549260	155400	0.007835	0.62
1554825_at						0.009887	0.62
241970_at	Poliovirus receptor-related 3	PVRL3	chr3q13	Hs.293917	25945	0.013278	0.61
236904_x_at	Tectorin alpha	TECTA	chr11q22-q24	Hs.248162	7007	0.007372	0.61
242437_at						0.015264	0.61
243003_at	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	MLLT10	chr10p12	Hs.30385	8028	0.013784	0.61
229849_at	Transcribed locus, weakly similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]			Hs.380698		0.006619	0.61
235444_at	forkhead box P1	FOXP1	chr3p14.1	Hs.431498	27086	0.019034	0.61
217807_s_at	glioma tumor suppressor candidate region gene 2	GLTSCR2	chr19q13.3	Hs.421907	29997	0.010142	0.61
208749_x_at	flotillin 1	FLOT1	chr6p21.3	Hs.179986	10211	0.019040	0.61
210142_x_at	flotillin 1	FLOT1	chr6p21.3	Hs.179986	10211	0.027816	0.61
205432_at	oviductal glycoprotein 1, 120kDa (mucin 9, oviductin)	OVGP1	chr1p13	Hs.1154	5016	0.039076	0.61
212735_at	KIAA0226	KIAA0226	chr3q29	Hs.478868	9711	0.038886	0.61
236924_at	Novel protein	RP11-163N11.1	chr1p22.1	Hs.272015	388649	0.009297	0.61
1552634_a_at	zinc finger protein 101	ZNF101	chr19p13.11	Hs.164284	94039	0.002815	0.61
213557_at	CDC2-related protein kinase 7	CRK7	chr17q12	Hs.416108	51755	0.007115	0.61
223727_at	Kv channel interacting protein 2	KCNIP2	chr10q24	Hs.97044	30819	0.039278	0.60
1561642_at	Phosphatase and actin regulator 1	PHACTR1	chr6p24.1	Hs.436996	221692	0.026914	0.60
203940_s_at	KIAA1036	KIAA1036	chr14q24.3	Hs.525479	22846	0.006266	0.60
214096_s_at	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	chr12q12-q14	Hs.75069	6472	0.041589	0.60
230193_at	hypothetical protein MGC33630	MGC33630	chr12q24.31	Hs.507125	144406	0.026493	0.60
221612_at	HTO17 protein	HTO17	chr3p14.3	Hs.552600	57408	0.016956	0.60
1556001_at	hypothetical protein LOC284939	LOC284939	chr22q13.33	Hs.337266	284939	0.030568	0.60
34221_at	KIAA0194	KIAA0194	chr5q33.1	Hs.549664	22993	0.028512	0.59
244859_at	Phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP	chr1q12	Hs.487925	9659	0.005185	0.59
227208_at	similar to DLNB14	DLNB14	chr11q23.3	Hs.534613	338657	0.034317	0.59
236210_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	DDX31	chr9q34.13	Hs.495410	64794	0.036422	0.59
223843_at	scavenger receptor class A, member 3	SCARA3	chr8p21	Hs.128856	51435	0.042767	0.59

243594_x_at	spire homolog 2 (Drosophila)	SPIRE2	chr16q24	Hs.461786	84501	0.017746	0.59
223522_at	chromosome 9 open reading frame 45	C9orf45	chr9q33.3	Hs.21379	81571	0.045707	0.59
242688_at	Thyroid hormone receptor interactor 12	TRIP12	chr2q36.3	Hs.368985	9320	0.024127	0.59
231890_at	CDNA FLJ12742 fis, clone NT2RP2000644			Hs.273830		0.001731	0.59
234946_at	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	ENTPD6	chr20p11.2-p11.2	Hs.500375	955	0.037044	0.59
206402_s_at	neuropeptide FF-amide peptide precursor	NPFF	chr12q13.13	Hs.104555	8620	0.018024	0.59
229100_s_at	translocase of inner mitochondrial membrane 22 homolog (yeast)	TIMM22	chr17p13	Hs.87595	29928	0.042053	0.59
213870_at	collagen, type XI, alpha 2	COL11A2	chr6p21.3	Hs.390171	1302	0.031440	0.58
210580_x_at	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	SULT1A3	chr16p11.2	Hs.460587	6818	0.031892	0.58
59625_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	chr16q21-q23	Hs.513667	8996	0.009000	0.58
214273_x_at	chromosome 16 open reading frame 35	C16orf35	chr16p13.3	Hs.19699	8131	0.021115	0.58
244377_at	Solute carrier family 1 (glutamate/neutral amino acid transporter), mem	SLC1A4	chr2p15-p13	Hs.323878	6509	0.023712	0.58
235302_at	Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)			Hs.169812		0.037836	-0.58
225659_at	hypothetical protein LOC339745	LOC339745	chr2q22.1	Hs.333297	339745	0.005384	-0.58
223470_at	phosphatidylinositol glycan, class M	PIGM	chr1q23.2	Hs.512837	93183	0.026224	-0.58
224975_at	nuclear factor I/A	NFIA	chr1p31.3-p31.2	Hs.191911	4774	0.029832	-0.58
201963_at	acyl-CoA synthetase long-chain family member 1	ACSL1	chr4q34-q35	Hs.406678	2180	0.022260	-0.58
213872_at	Chromosome 6 open reading frame 62	C6orf62	chr6p22.2	Hs.519930	81688	0.039018	-0.58
217883_at	chromosome 2 open reading frame 25	C2orf25	chr2q23.3	Hs.5324	27249	0.004622	-0.58
229167_at	Purine-rich element binding protein A	PURA	chr5q31	Hs.443121	5813	0.000211	-0.58
1557363_a_at	pleckstrin homology domain interacting protein	PHIP	chr6q14	Hs.511817	55023	0.010461	-0.58
232432_s_at	solute carrier family 30 (zinc transporter), member 5	SLC30A5	chr5q12.1	Hs.482363	64924	0.028313	-0.58
1555037_a_at	isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	chr2q33.3	Hs.11223	3417	0.000769	-0.58
202226_s_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	CRK	chr17p13.3	Hs.461896	1398	0.047823	-0.58
219164_s_at	chromosome 14 open reading frame 103	C14orf103	chr14q32.2	Hs.168241	55102	0.041258	-0.58
236308_at	hypothetical protein LOC285878	LOC285878	chr7p11.2	Hs.548149	285878	0.026982	-0.58
222752_s_at	hypothetical protein FLJ10874	FLJ10874	chr1q32.3	Hs.445386	55248	0.009168	-0.58
206770_s_at	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transp	SLC35A3	chr1p21	Hs.448979	23443	0.018265	-0.58
224602_at	HCV F-transactivated protein 1	LOC40115	chr4q26	Hs.173705	401152	0.027418	-0.58
239678_at	AP1 gamma subunit binding protein 1	AP1GBP1	chr17q12	Hs.101480	11276	0.006450	-0.58
208899_x_at	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	ATP6V1D		Hs.272630	51382	0.041395	-0.58
213289_at	Spermidine/spermine N1-acetyl transferase-like 1	SATL1	chrXq21.1	Hs.551594	340562	0.011020	-0.58
219743_at	hairy/enhancer-of-split related with YRPW motif 2	HEY2	chr6q22.2-q22.33	Hs.144287	23493	0.034246	-0.58
232426_at	MRNA full length insert cDNA clone EUROIMAGE 30103			Hs.21754		0.038652	-0.58
202214_s_at	culin 4B	CUL4B	chrXq23	Hs.102914	8450	0.018298	-0.58
227354_at	FLJ37858 protein	FLJ37858	chr8q21.13	Hs.492106	441357	0.004603	-0.58
238494_at	TNF receptor-associated factor 3 interacting protein 1	TRAF3IP1	chr2q37.3	Hs.43086	26146	0.041613	-0.59
227246_at						0.012569	-0.59
222103_at	Activating transcription factor 1	ATF1	chr12q13	Hs.435267	466	0.002317	-0.59
228328_at	CDNA FLJ33653 fis, clone BRAMY2024715			Hs.550906		0.009103	-0.59
218989_x_at	solute carrier family 30 (zinc transporter), member 5	SLC30A5	chr5q12.1	Hs.482363	64924	0.037081	-0.59
218477_at	transmembrane protein 14A	TMEM14A	chr6p12.3	Hs.94896	28978	0.012355	-0.59
227692_at	guanine nucleotide binding protein (G protein), alpha inhibiting activity	GNAI1	chr7q21	Hs.134587	2770	0.001736	-0.59
223006_s_at	chromosome 9 open reading frame 5	C9orf5	chr9q31	Hs.308074	23731	0.047863	-0.59
222679_s_at	RP42 homolog	RP42	chr3q26.3	Hs.104613	54165	0.011011	-0.59
216274_s_at	SEC11-like 1 (S. cerevisiae)	SEC11L1	chr15q25.3	Hs.9534	23478	0.040447	-0.59
221516_s_at	hypothetical protein FLJ20232	FLJ20232	chr22q13	Hs.148677	54471	0.043156	-0.59
219433_at	BCL6 co-repressor	BCOR	chrXp11.4	Hs.186424	54880	0.004624	-0.59
203864_s_at	actinin, alpha 2	ACTN2	chr1q42-q43	Hs.498178	88	0.012860	-0.59
209197_at	synaptotagmin XI	SYT11	chr1q21.2	Hs.32984	23208	0.023593	-0.59
235215_at	Transcribed locus, moderately similar to XP_498452.1 hypothetical gene supported by NM_173697 [H			Hs.513356		0.008341	-0.59
225894_at	synaptopodin 2	SYNPO2	chr4q26	Hs.480615	171024	0.014119	-0.59
213322_at	chromosome 6 open reading frame 130	C6orf130	chr6p21.1	Hs.549281	221443	0.005781	-0.59
224830_at	cleavage and polyadenylation specific factor 5, 25 kDa	CPSF5	chr16q12.2	Hs.528834	11051	0.004455	-0.59
218511_s_at	pyridoxine 5'-phosphate oxidase	PNPO	chr17q21.32	Hs.514278	55163	0.045819	-0.59
226779_at	CDNA FLJ37302 fis, clone BRAMY2016009			Hs.529759		0.009727	-0.59
37512_at	hydroxysteroid (17-beta) dehydrogenase 6	HSD17B6	chr12q13	Hs.524513	8630	0.045654	-0.59
229273_at	sal-like 1 (Drosophila)	SALL1	chr16q12.1	Hs.135787	6299	0.036418	-0.59
242826_at	Transcribed locus			Hs.538962		0.016198	-0.59
226338_at	hypothetical protein DKFZp7620076	DKFZp7620076	chr8q21.3	Hs.202517	55529	0.023788	-0.59
232184_at	amyotrophic lateral sclerosis 2 (juvenile)	ALS2	chr2q33.1	Hs.471096	57679	0.047560	-0.59
201165_s_at	pumilio homolog 1 (Drosophila)	PUM1	chr1p35.2	Hs.281707	9698	0.034896	-0.59
202762_at	Rho-associated, coiled-coil containing protein kinase 2	ROCK2	chr2p24	Hs.58617	9475	0.047312	-0.59
1552370_at	hypothetical protein LOC132321	LOC132321	chr4q28.2	Hs.533190	132321	0.038250	-0.59
222466_s_at	mitochondrial ribosomal protein L42	MRPL42	chr12q22	Hs.199579	28977	0.004477	-0.59
212287_at	suppressor of zeste 12 homolog (Drosophila)	SUZ12	chr17q11.2	Hs.462732	23512	0.019415	-0.59
215422_at	Cri-du-chat region mRNA, clone NIBB11.			Hs.7057		0.038766	-0.59
203310_at	synaptin binding protein 3	STXBP3	chr1p13.3	Hs.530436	6814	0.004549	-0.59
201152_s_at	muscleblind-like (Drosophila)	MBNL1	chr3q25	Hs.478000	4154	0.046094	-0.59
223374_s_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	B3GALT3	chr3q25	Hs.418062	8706	0.002317	-0.59
238344_at	Coatamer protein complex, subunit gamma 2	COPG2	chr7q32	Hs.532231	26958	0.036236	-0.60
221449_s_at	T-cell immunomodulatory protein /// T-cell immunomodulatory protein	CDA08	chr16q12.1	Hs.42217	81533	0.047979	-0.60
201733_at	chloride channel 3	CLCN3	chr4q33	Hs.481186	1182	0.045892	-0.60
1563933_a_at	hypothetical protein FLJ40773	FLJ40773	chr1q43	Hs.498252	200150	0.037454	-0.60



201830_s_at	neuroepithelial cell transforming gene 1	NET1	chr10p15	Hs.25155	10276	0.018720	-0.60
200056_s_at	nuclear DNA-binding protein /// nuclear DNA-binding proteir	C1D	chr2p13-p12	Hs.328883	10438	0.005070	-0.60
225976_at	similar to transcription factor BTF3	MGC23908	chr1p32.3	Hs.429839	91408	0.009429	-0.60
222495_at	protein x 013	AD-020	chr1p13.3	Hs.82933	56900	0.031434	-0.60
244688_at	Transcribed locus			Hs.175610		0.010681	-0.60
223242_s_at	hypothetical protein ET	ET	chr17q25	Hs.464166	79157	0.010072	-0.60
201260_s_at	synaptophysin-like protein	SYPL	chr7q22.3	Hs.80919	6856	0.041432	-0.60
201891_s_at	beta-2-microglobulin	B2M	chr15q21-q22.2	Hs.534255	567	0.007696	-0.60
218268_at	TBC1 domain family, member 15	TBC1D15	chr12q21.1	Hs.284630	64786	0.000401	-0.60
212502_at	chromosome 10 open reading frame 22	C10orf22	chr10q21.3	Hs.99821	84890	0.007960	-0.60
242348_at	family with sequence similarity 19 (chemokine (C-C motif)-like), member 1	FAM19A4	chr3p14.1	Hs.187873	151647	0.005088	-0.60
202898_at	syndecan 3 (N-syndecan)	SDC3	chr1pter-p22.3	Hs.158287	9672	0.046845	-0.60
219132_at	pellino homolog 2 (Drosophila)	PELI2	chr14q21	Hs.105103	57161	0.024703	-0.60
239282_at	NY-REN-58 antigen	NY-REN-58	chr12q22	Hs.279209	51134	0.029587	-0.60
212887_at	Sec23 homolog A (S. cerevisiae)	SEC23A	chr14q21.1	Hs.272927	10484	0.024075	-0.60
224832_at	dual specificity phosphatase 16	DUSP16	chr12p13	Hs.536535	80824	0.018765	-0.60
218521_s_at	hypothetical protein FLJ11011	FLJ11011	chr8q21.11	Hs.492031	55284	0.041840	-0.60
227665_at	Mitochondrial carrier triple repeat 1	MCART1	chr9p13.3-p12	Hs.46791	92014	0.028005	-0.60
223823_at	potassium large conductance calcium-activated channel, subfamily M, member 2	KCNMB2	chr3q26.2-q27.1	Hs.478368	10242	0.000979	-0.60
211933_s_at	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	HNRPA3P1	chr10q11.21 /// chr10q11.21	Hs.524276	10151 /// 10151	0.002225	-0.60
227205_at	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor 1	TAF1	chrXq13.1	Hs.158560	6872	0.009156	-0.60
226161_at	solute carrier family 30 (zinc transporter), member 6	SLC30A6	chr12p22.3	Hs.552598	55676	0.018125	-0.60
209357_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 2	CITED2	chr6q23.3	Hs.82071	10370	0.013875	-0.60
225246_at	stromal interaction molecule 2	STIM2	chr4p15.2	Hs.135763	57620	0.040871	-0.60
212310_at	C219-reactive peptide /// similar to C219-reactive peptide	KIAA0268	chr1p36.33	Hs.508522	348477 /// 348477	0.003864	-0.60
201238_s_at	capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	chr7q31.2-q31.3	Hs.446123	830	0.006289	-0.60
201646_at	scavenger receptor class B, member 2	SCARB2	chr4q21.1	Hs.349656	950	0.014620	-0.60
209025_s_at	synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	chr6q14-q15	Hs.472056	10492	0.031622	-0.60
231763_at	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	POLR3A	chr10q22-q23	Hs.436896	11128	0.017624	-0.61
205705_at	ankyrin repeat domain 26	ANKRD26	chr10pter-q22.1	Hs.361041	22852	0.011185	-0.61
203243_s_at	PDZ and LIM domain 5	PDLIM5	chr4q22	Hs.480311	10611	0.024210	-0.61
224802_at	Nedd4 family interacting protein 2	NDFIP2	chr13q31.1	Hs.525093	54602	0.006858	-0.61
203075_at	SMAD, mothers against DPP homolog 2 (Drosophila)	SMAD2	chr18q21.1	Hs.12253	4087	0.002070	-0.61
226998_at	NMDA receptor regulated 1	NARG1	chr4q31.1	Hs.518994	80155	0.009248	-0.61
206115_at	early growth response 3	EGR3	chr8p23-p21	Hs.534313	1960	0.012442	-0.61
1567219_at						0.009198	-0.61
202089_s_at	solute carrier family 39 (zinc transporter), member 6	SLC39A6	chr18q12.2	Hs.79136	25800	0.007050	-0.61
202055_at	Karyopherin alpha 1 (importin alpha 5)	KPNA1	chr3q21	Hs.161008	3836	0.023377	-0.61
218674_at	hypothetical protein FLJ13611	FLJ13611	chr5q12.3	Hs.482301	80006	0.018418	-0.61
204035_at	secretogranin II (chromogranin C)	SCG2	chr2q35-q36	Hs.516726	7857	0.036762	-0.61
201627_s_at	insulin induced gene 1	INSIG1	chr7q36	Hs.520819	3638	0.004572	-0.61
230068_s_at	Paternally expressed 3	PEG3	chr19q13.4	Hs.201776	5178	0.025675	-0.61
201866_s_at	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	chr5q31	Hs.122926	2908	0.013481	-0.61
209705_at	likely ortholog of mouse metal response element binding transcription factor 1	MTF1	chr1p22.1	Hs.31016	22823	0.020547	-0.61
210471_s_at	potassium voltage-gated channel, shaker-related subfamily, beta member 1	KCNAB1	chr3q26.1	Hs.157818	7881	0.046349	-0.61
201560_at	chloride intracellular channel 4	CLIC4	chr1p36.11	Hs.440544	25932	0.030408	-0.61
222420_s_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	chr7q32	Hs.344165	7328	0.023418	-0.61
209006_s_at	NPD014 protein	NPD014	chr1p36.13-p35.1	Hs.259412	57035	0.041354	-0.61
1558700_s_at	zinc finger protein 260	ZFP260	chr19q13.12	Hs.18103	339324	0.001615	-0.61
204333_s_at	aspartylglucosaminidase	AGA	chr4q32-q33	Hs.207776	175	0.049760	-0.61
225892_at	Iron-responsive element binding protein 2	IREB2	chr15q25.1	Hs.436031	3658	0.014687	-0.61
200059_s_at	ras homolog gene family, member A /// ras homolog gene family, member A	RHOA	chr3p21.3	Hs.247077	387	0.003841	-0.61
218191_s_at	chromosome 6 open reading frame 209	C6orf209	chr6q13	Hs.271643	55788	0.011525	-0.61
242100_at	chondroitin sulfate synthase 3	CSS3	chr5q23.3	Hs.213137	337876	0.011891	-0.61
201067_at	proteasome (prosome, macropain) 26S subunit, ATPase, 2	PSMC2	chr7q22.1-q22.3	Hs.437366	5701	0.029963	-0.61
218128_at	nuclear transcription factor Y, beta	NFYB	chr12q22-q23	Hs.84928	4801	0.039018	-0.61
210537_s_at	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	TADA2L	chr17q12-q21	Hs.500066	6871	0.015331	-0.61
1552617_a_at	ring finger and WD repeat domain 2	RFWD2	chr1q25.1-q25.2	Hs.523744	64326	0.039189	-0.61
225941_at	eukaryotic translation initiation factor 4E member 3	EIF4E3	chr3p14	Hs.476782	317649	0.025950	-0.61
203132_at	retinoblastoma 1 (including osteosarcoma)	RB1	chr13q14.2	Hs.408528	5925	0.026207	-0.61
208840_s_at	Ras-GTPase activating protein SH3 domain-binding protein 2	G3BP2	chr4q21.1	Hs.303676	9908	0.019110	-0.61
233002_at	KIAA1622	KIAA1622	chr14q32.13	Hs.259599	57718	0.017196	-0.61
229240_at	CDNA clone IMAGE:4838003, partial cds			Hs.548738		0.004242	-0.61
221787_at	PHD finger protein 10	PHF10	chr6q27	Hs.435933	55274	0.007057	-0.61
211022_s_at	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog)	ATRAX	chrXq13.1-q21.1	Hs.533526	546	0.027666	-0.61
230958_s_at	Full length insert cDNA clone ZD69D05			Hs.379253		0.040378	-0.61
224630_at	chromosome 2 open reading frame 30	C2orf30	chr2p16.3	Hs.438336	27248	0.004058	-0.61
227033_at	protein disulfide isomerase-associated 3	PDIA3	chr15q15	Hs.308709	2923	0.034061	-0.61
225325_at	FLJ20160 protein	FLJ20160	chr2q32.2	Hs.418581	54842	0.037654	-0.61
212073_at	casein kinase 2, alpha 1 polypeptide	CSNK2A1	chr20p13	Hs.446484	1457	0.048544	-0.61
233546_at	CDNA FLJ13003 fis, clone NT2RP3000418			Hs.301533		0.010952	-0.61
241407_at	CDNA FLJ11682 fis, clone HEMBA1004880			Hs.191828		0.020526	-0.61
217540_at	Transcribed locus, weakly similar to XP_510104.1 similar to hypothetical protein FLJ25224 [Pan troglodytes]			Hs.518129		0.009990	-0.61
225942_at	neurolysin (metallopeptidase M3 family)	NLN	chr5q12.3	Hs.247460	57486	0.007555	-0.61

235072_s_at	Transcribed locus				Hs.94499			0.037769	-0.61
224682_at	ankyrin repeat and IBR domain containing 1	ANKIB1	chr7q21.2	Hs.83293	54467			0.008424	-0.61
238649_at	phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	chr17q24.2	Hs.549130	26207			0.002924	-0.62
225435_at	Signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1	chr6p24.3	Hs.114033	6745			0.043906	-0.62
229097_at	Homo sapiens, Similar to diaphanous homolog 3 (Drosophila), clone IMAGE:5277415, mRNA			Hs.444351				0.022761	-0.62
208945_s_at	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	BECN1	chr17q21	Hs.12272	8678			0.006816	-0.62
200929_at	transmembrane trafficking protein	TMP21	chr14q24.3	Hs.74137	10972			0.009711	-0.62
217819_at	golgi autoantigen, golgin subfamily a, 7	GOLGA7	chr8p11.21	Hs.7953	51125			0.012446	-0.62
221478_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like /// BCL2/adenovir	BNIP3L	chr8p21	Hs.131226	665			0.039810	-0.62
222975_s_at	upstream of NRAS	UNR	chr1p22	Hs.69855	7812			0.026946	-0.62
231921_at	hypothetical protein FLJ13096	FLJ13096	chr2q31.1	Hs.413518	80067			0.010677	-0.62
209257_s_at	chondroitin sulfate proteoglycan 6	CSPG6	chr10q25	Hs.24485	9126			0.035499	-0.62
226770_at	membrane-associated guanylate kinase-related (MAGI-3)	MAGI-3	chr1p12-p11.2	Hs.486189	260425			0.040392	-0.62
212724_at	Rho family GTPase 3	RND3	chr2q23.3	Hs.6838	390			0.007758	-0.62
222731_at	zinc finger, DHHC domain containing 2	ZDHHC2	chr8p21.3-p22	Hs.443852	51201			0.000340	-0.62
225974_at	hypothetical protein DKFZp762C1112	DKFZp762C1112	chr8q21.3	Hs.546514	169200			0.000154	-0.62
222633_at	transducin (beta)-like 1X-linked receptor 1	TBL1XR1	chr3q26.32	Hs.438970	79718			0.009489	-0.62
204525_at	PHD finger protein 14	PHF14	chr7p21.3	Hs.159918	9678			0.025213	-0.62
215073_s_at	nuclear receptor subfamily 2, group F, member 2	NR2F2	chr15q26	Hs.347991	7026			0.002849	-0.62
210843_s_at	microfibrillar-associated protein 3-like	MFAP3L	chr4q32.3	Hs.178121	9848			0.016440	-0.62
218981_at	ACN9 homolog (S. cerevisiae)	ACN9	chr7q21.3	Hs.42785	57001			0.013166	-0.62
208783_s_at	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reacti	MCP	chr1q32	Hs.510402	4179			0.010078	-0.62
204182_s_at	zinc finger protein 297B	ZNF297B	chr9p24.1-q22.32	Hs.355581	23099			0.018473	-0.62
217858_s_at	armadillo repeat containing, X-linked 3	ARMCX3	chrXq21.33-q22.2	Hs.172788	51566			0.004405	-0.62
227018_at	dipeptidylpeptidase 8	DPP8	chr15q22	Hs.458609	54878			0.014598	-0.62
221960_s_at	RAB2, member RAS oncogene family	RAB2	chr8q12.1	Hs.369017	5862			0.023921	-0.62
223760_s_at								0.026938	-0.62
220926_s_at	chromosome 1 open reading frame 22	C1orf22	chr1q24-q25	Hs.523811	80267			0.002461	-0.62
235504_at	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	GREM2	chr1q43	Hs.98206	64388			0.032631	-0.62
224636_at	zinc finger protein 91 homolog (mouse)	ZFP91	chr11q12	Hs.524920	80829			0.012211	-0.62
212217_at	prolyl endopeptidase-like	PREPL	chr2p22.1	Hs.549585	9581			0.015117	-0.62
201604_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	PPP1R12A	chr12q15-q21	Hs.49582	4659			0.026369	-0.62
239486_at	Transcribed locus			Hs.366034				0.000615	-0.62
204675_at	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid d	SRD5A1	chr5p15	Hs.552	6715			0.031496	-0.62
1552658_a_at	neuron navigator 3	NAV3		Hs.306322	89795			0.030266	-0.62
214617_at	perforin 1 (pore forming protein) /// perforin 1 (pore forming protein)	PRF1	chr10q22	Hs.2200	5551			0.011937	-0.63
209576_at	guanine nucleotide binding protein (G protein), alpha inhibiting activit	GNAI1	chr7q21	Hs.134587	2770			0.001824	-0.63
1555246_a_at	sodium channel, voltage-gated, type I, alpha	SCN1A	chr2q24.3	Hs.22654	6323			0.034135	-0.63
208021_s_at	replication factor C (activator 1) 1, 145kDa /// replication factor C (activa	RFC1	chr4p14-p13	Hs.507475	5981			0.040778	-0.63
221761_at	adenylosuccinate synthase	ADSS	chr1cen-q12	Hs.498313	159			0.028319	-0.63
242470_at	hypothetical protein FLJ38944	FLJ38944	chr19q13.2	Hs.135181	126272			0.044746	-0.63
243042_at	FLJ35093 protein	FLJ35093	chr1p31.1	Hs.156625	374986			0.017712	-0.63
217678_at	solute carrier family 7, (cationic amino acid transporter, y+ system) mem	SLC7A11	chr4q28-q32	Hs.6682	23657			0.018375	-0.63
228574_at	Hypothetical protein DKFZp762A217	DKFZp762A217	chr12q21.31	Hs.444240	160335			0.008177	-0.63
226637_at	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	chr7q32	Hs.344165	7328			0.025505	-0.63
223315_at	netrin 4	NTN4	chr12q22-q23	Hs.201034	59277			0.008671	-0.63
222438_at	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	MED4	chr13q14.2	Hs.181112	29079			0.013299	-0.63
220199_s_at	hypothetical protein FLJ12806	FLJ12806	chr1q41	Hs.6236	64853			0.002973	-0.63
224866_at	male sterility domain containing 2	MLSTD2	chr11p15.2	Hs.501991	84188			0.011290	-0.63
202163_s_at	CCR4-NOT transcription complex, subunit 8	CNOT8	chr5q31-q33	Hs.26703	9337			0.013139	-0.63
1558233_s_at	Activating transcription factor 1	ATF1	chr12q13	Hs.435267	466			0.022006	-0.63
224151_s_at	adenylate kinase 3	AK3	chr9p24.1-p24.3	Hs.493362	50808			0.023657	-0.63
227934_at	Karyopherin alpha 5 (importin alpha 6)	KPNA5	chr6q22.1	Hs.182971	3841			0.040212	-0.63
217437_s_at	transforming, acidic coiled-coil containing protein 1	TACC1	chr8p11	Hs.279245	6867			0.048906	-0.63
215143_at	Hypothetical protein FLJ36166	FLJ36166	chr7q22.1	Hs.148768	349152			0.007134	-0.63
210612_s_at	synaptojanin 2	SYNJ2	chr6q25.3	Hs.434494	8871			0.040556	-0.63
208666_s_at	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting p	ST13	chr22q13.2	Hs.546303	6767			0.007776	-0.63
203102_s_at	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransf	MGAT2	chr14q21	Hs.93338	4247			0.010816	-0.63
222602_at	hypothetical protein FLJ10808	FLJ10808	chr4q13.2	Hs.212774	55236			0.008312	-0.63
232305_at	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	HMGCLL1	chr6p12.1	Hs.147054	54511			0.036937	-0.63
227187_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	CBLL1	chr7q31.1	Hs.432792	79872			0.021498	-0.63
230274_s_at	Rabaptin, RAB GTPase binding effector protein 1	RABEP1	chr17p13.2	Hs.551518	9135			0.020547	-0.63
1554433_a_at	zinc finger protein 146	ZNF146	chr19q13.1	Hs.301819	7705			0.013651	-0.63
231532_at	Neural cell adhesion molecule 1	NCAM1	chr11q23.1	Hs.503878	4684			0.039139	-0.63
212829_at	CDNA FLJ13267 fis, clone OVARC1000964 /// CDNA FLJ13267 fis, clone OVARC1000964			Hs.57079				0.035928	-0.63
222631_at	phosphatidylinositol 4-kinase type-II beta	PI4K2B	chr4p15.2	Hs.443733	55300			0.001565	-0.63
201788_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	DDX42	chr17q23.3	Hs.8765	11325			0.040100	-0.63
201051_at	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	ANP32A	chr15q22.3-q23	Hs.458747	8125			0.022909	-0.63
229549_at	Opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	OPN1SW	chr7q31.3-q32	Hs.550465	611			0.019449	-0.63
202842_s_at	DnaJ (Hsp40) homolog, subfamily B, member 9	DNAJB9	chr7q31 14q24.2	Hs.6790	4189			0.008664	-0.63
204235_s_at	GULP, engulfment adaptor PTB domain containing 1	GULP1	chr2q32.3-q33	Hs.470887	51454			0.011080	-0.63
201317_s_at	proteasome (prosome, macropain) subunit, alpha type, 2	PSMA2	chr7p14.1	Hs.333786	5683			0.011730	-0.63
226853_at	BMP2 inducible kinase	BMP2K	chr4q21.21	Hs.146551	55589			0.034064	-0.63
205934_at	phospholipase C-like 1	PLCL1	chr2q33	Hs.153322	5334			0.017911	-0.63

218195_at	chromosome 6 open reading frame 211	C6orf211	chr6q25.1	Hs.15929	79624	0.001503	-0.63
221064_s_at	chromosome 16 open reading frame 28	C16orf28	chr16p13.3	Hs.161279	65259	0.032911	-0.63
225324_at	chromosome 20 open reading frame 155	C20orf155	chr20p13-p12.3	Hs.224764	54675	0.008347	-0.64
226952_at	ELL associated factor 1	EAF1	chr3p25.1	Hs.474479	85403	0.035179	-0.64
226641_at	Hypothetical protein DKFZp434D2328	LOC91526	chr2q33.1	Hs.432706	91526	0.002434	-0.64
225326_at	RNA binding motif protein 27	RBM27	chr5q32	Hs.61441	54439	0.020472	-0.64
209109_s_at	tetraspanin 6	TSPAN6	chrXq22	Hs.43233	7105	0.048406	-0.64
201456_s_at	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	BUB3	chr10q26	Hs.418533	9184	0.037164	-0.64
235762_at	Taste receptor, type 2, member 14	TAS2R14	chr12p13	Hs.552595	50840	0.001433	-0.64
223296_at	mitochondrial carrier protein	MGC4399	chr1p36.22	Hs.443826	84275	0.006839	-0.64
226374_at	Full-length cDNA clone CSODF012YG01 of Fetal brain of Homo sapiens (human)			Hs.7956		0.035237	-0.64
203531_at	Cullin 5	CUL5	chr11q22-q23	Hs.440320	8065	0.000239	-0.64
202422_s_at	acyl-CoA synthetase long-chain family member 4	ACSL4	chrXq22.3-q23	Hs.268785	2182	0.022481	-0.64
230573_at	serum/glucocorticoid regulated kinase 2	SGK2	chr20q32	Hs.472793	10110	0.038180	-0.64
218297_at	chromosome 10 open reading frame 97	C10orf97	chr10p13	Hs.158870	80013	0.000885	-0.64
202165_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	PPP1R2	chr3q29	Hs.184840	5504	0.038999	-0.64
241898_at	Transcribed locus, moderately similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]			Hs.351126		0.033353	-0.64
229298_at	Kelch repeat and BTB (POZ) domain containing 7	KBTD7	chr13q14.11	Hs.63841	84078	0.003588	-0.64
218625_at	neuritin 1	NRN1	chr6p25.1	Hs.103291	51299	0.046021	-0.64
212298_at	neuropilin 1	NRP1	chr10p12	Hs.131704	8829	0.021072	-0.64
239024_at	Zinc finger protein 148 (pHZ-52)	ZNF148	chr3q21	Hs.380334	7707	0.046162	-0.64
204313_s_at	cAMP responsive element binding protein 1	CREB1	chr2q34	Hs.516646	1385	0.032801	-0.64
222562_s_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	TNKS2	chr10q23.3	Hs.329327	80351	0.045780	-0.64
225084_at	SEC10-like 1 (S. cerevisiae)	SEC10L1	chr14q22.3	Hs.365863	10640	0.007475	-0.64
201916_s_at	SEC63-like (S. cerevisiae)	SEC63	chr6q21	Hs.529957	11231	0.019129	-0.64
240095_at	Transcribed locus			Hs.129636		0.037787	-0.64
222614_at	chromosome 21 open reading frame 6	C21orf6	chr21q22.11	Hs.34136	10069	0.039543	-0.64
219232_s_at	egl nine homolog 3 (C. elegans)	EGLN3	chr14q13.1	Hs.135507	112399	0.041717	-0.64
213183_s_at	Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C	chr11p15.5	Hs.106070	1028	0.039015	-0.64
202691_at	small nuclear ribonucleoprotein D1 polypeptide 16kDa	SNRPD1	chr18q11.2	Hs.464734	6632	0.010196	-0.65
1557181_s_at	similar to expressed sequence AI593442	LOC39994	chr11q22.3	Hs.172982	399947	0.024542	-0.65
221778_at	KIAA1718 protein	KIAA1718	chr7q34	Hs.308710	80853	0.039398	-0.65
235698_at	zinc finger protein 90 homolog (mouse)	ZFP90	chr16q22.1	Hs.461074	146198	0.004310	-0.65
235787_at	Cell division cycle 37 homolog (S. cerevisiae)-like 1	CDC37L1		Hs.493361	55664	0.005455	-0.65
203869_at	ubiquitin specific protease 46	USP46	chr4q12	Hs.331478	64854	0.014210	-0.65
1567457_at	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein)	RAC1	chr7p22	Hs.413812	5879	0.009465	-0.65
238497_at	hypothetical protein MGC17839	MGC17839	chr11q23.3	Hs.380228	219902	0.004705	-0.65
206302_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NUDT4	chr12q21	Hs.506325	11163	0.025888	-0.65
1558964_at	FAT tumor suppressor homolog 3 (Drosophila)	FAT3	chr11q21	Hs.98523	120114	0.000482	-0.65
201634_s_at	outer mitochondrial membrane cytochrome b5	CYB5-M	chr16q22.1	Hs.461131	80777	0.027599	-0.65
228480_at	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	VAPA	chr18p11.22	Hs.165195	9218	0.021323	-0.65
223022_s_at	chromosome 6 open reading frame 55	C6orf55	chr6q24.1	Hs.431367	51534	0.014877	-0.65
218252_at	cytoskeleton associated protein 2	CKAP2	chr13q14	Hs.444028	26586	0.002982	-0.65
212286_at	ankyrin repeat domain 12	ANKRD12	chr18p11.22	Hs.464585	23253	0.010755	-0.65
213718_at	RNA binding motif protein 4	RBM4	chr11q13	Hs.533712	5936	0.030657	-0.65
226112_at	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	SGCB	chr4q12	Hs.438953	6443	0.013099	-0.65
225805_at	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor)	HNRPU	chr1q44	Hs.166463	3192	0.003516	-0.65
230194_at	Leucine-rich PPR-motif containing	LRPPRC	chr2p21	Hs.368084	10128	0.016611	-0.65
210675_s_at	protein tyrosine phosphatase, receptor type, R	PTPRR	chr12q15	Hs.506076	5801	0.043762	-0.65
238418_at	solute carrier family 35, member B4	SLC35B4	chr7q33	Hs.490181	84912	0.046062	-0.65
218085_at	chromatin modifying protein 5	CHMP5	chr9p13.3	Hs.415534	51510	0.005035	-0.65
212289_at	ankyrin repeat domain 12	ANKRD12	chr18p11.22	Hs.464585	23253	0.003913	-0.65
223089_at	transmembrane protein vezatin	VEZATIN	chr12q22	Hs.24135	55591	0.007379	-0.65
218090_s_at	WD repeat domain 11	WDR11	chr10q26	Hs.144447	55717	0.034418	-0.65
225640_at	hypothetical gene supported by AK091718	LOC40150	chr9p13.2	Hs.446271	401504	0.017648	-0.65
206381_at	sodium channel, voltage-gated, type II, alpha 2	SCN2A2	chr2q23-q24	Hs.470470	6326	0.038710	-0.65
200040_at	KH domain containing, RNA binding, signal transduction associated 1 ///	KHDRBS1	chr1p32	Hs.445893	10657	0.011866	-0.65
229803_s_at	AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig, mRNA seq			Hs.549673		0.049315	-0.65
236600_at	spastic paraplegia 20, spartin (Troyer syndrome)	SPG20	chr13q13.3	Hs.440414	23111	0.006733	-0.65
1559265_at	FLJ45187 protein	FLJ45187	chr10p12.31	Hs.350848	387640	0.002651	-0.65
214658_at	transmembrane emp24 protein transport domain containing 7	TMED7	chr5q22.3	Hs.508765	51014	0.015508	-0.65
202536_at	chromatin modifying protein 2B	CHMP2B	chr3p12.1	Hs.476930	25978	0.004052	-0.65
1554099_a_at	spindlin family, member 3	SPIN3	chrXp11.1	Hs.522672	169981	0.041192	-0.66
220495_s_at	chromosome 5 open reading frame 14	C5orf14	chr5q31.1	Hs.106534	79770	0.006881	-0.66
225420_at	glycerol-3-phosphate acyltransferase, mitochondrial	GPAM	chr10q25.2	Hs.42586	57678	0.031052	-0.66
209476_at	thioredoxin domain containing	TXNDC	chr14q22.1	Hs.125221	81542	0.009904	-0.66
231804_at						0.022390	-0.66
222726_s_at	SEC10-like 1 (S. cerevisiae)	SEC10L1	chr14q22.3	Hs.365863	10640	0.006225	-0.66
225340_s_at	membrane component, chromosome 11, surface marker 1	M11S1	chr11p13	Hs.471818	4076	0.004353	-0.66
203543_s_at	Kruppel-like factor 9	KLF9	chr9q13	Hs.150557	687	0.027493	-0.66
240974_at	hypothetical LOC153959	LOC153959	chr6q14.1	Hs.435465	153959	0.003599	-0.66
244293_at	Transcribed locus			Hs.160893		0.029977	-0.66
218789_s_at	hypothetical protein FLJ20010	FLJ20010	chr11q14.2-q14.3	Hs.91816	54494	0.001401	-0.66
208689_s_at	ribophorin II	RPN2	chr20q12-q13.1	Hs.370895	6185	0.027956	-0.66

232125_at	CDNA FLJ34585 fis, clone KIDNE2008758				Hs.202577			0.026922	-0.66
212168_at	RNA binding motif protein 12	RBM12	chr20q11.21	Hs.246413	10137			0.039475	-0.66
231927_at	Activating transcription factor 6	ATF6	chr1q22-q23	Hs.492740	22926			0.011081	-0.66
202118_s_at	copine III	CPNE3	chr8q21.3	Hs.191219	8895			0.007346	-0.66
205042_at	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	GNE	chr9p13.2	Hs.5920	10020			0.044741	-0.66
219726_at	neurologin 3	NLGN3	chrXq13.1	Hs.438877	54413			0.022541	-0.66
218230_at	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	ARFIP1	chr4q31.3	Hs.416089	27236			0.014260	-0.66
208643_s_at	X-ray repair complementing defective repair in Chinese hamster cells 5	(XRCC5	chr2q35	Hs.388739	7520			0.012841	-0.66
225821_s_at	KIAA1327 protein	KIAA1327	chr4p16.1	Hs.106204	57219			0.007883	-0.66
203123_s_at	solute carrier family 11 (proton-coupled divalent metal ion transporters)	SLC11A2	chr12q13	Hs.505545	4891			0.040104	-0.66
212224_at	aldehyde dehydrogenase 1 family, member A1	ALDH1A1	chr9q21.13	Hs.76392	216			0.021885	-0.66
201017_at	eukaryotic translation initiation factor 1A, X-linked	EIF1AX	chrXp22.12	Hs.522590	1964			0.038799	-0.66
226073_at	hypothetical protein LOC219854	LOC21985	chr11q24.2	Hs.7626	219854			0.024955	-0.66
212806_at	KIAA0367	KIAA0367	chr9q21.2	Hs.262857	23273			0.015392	-0.66
206806_at	diacylglycerol kinase, iota	DGKI	chr7q32.3-q33	Hs.242947	9162			0.030763	-0.66
221185_s_at	IQ motif containing G	IQCG	chr3q29	Hs.518536	84223			0.018268	-0.66
218251_at	MID1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	MID1IP1	chrXp11.4	Hs.522605	58526			0.028150	-0.67
223530_at	tudor and KH domain containing	TDRKH	chr1q21	Hs.144439	11022			0.034974	-0.67
1560647_at	TSPY-like 1	TSPYL1	chr6q22-q23	Hs.458358	7259			0.004226	-0.67
238661_at	Hypothetical gene supported by BX537900		chr8q12.3	Hs.7023	441351			0.043967	-0.67
228987_at	Family with sequence similarity 49, member B	FAM49B	chr8q24.21	Hs.492869	51571			0.027375	-0.67
232080_at	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	HECW2	chr2q32.3	Hs.314436	57520			0.002557	-0.67
235066_at	microtubule-associated protein 4	MAP4	chr3p21	Hs.517949	4134			0.025427	-0.67
203905_at	poly(A)-specific ribonuclease (deadenylation nuclease)	PARN	chr16p13	Hs.253197	5073			0.011876	-0.67
1552619_a_at	anillin, actin binding protein (scraps homolog, Drosophila)	ANLN	chr7p15-p14	Hs.62180	54443			0.007424	-0.67
210156_s_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase	PCMT1	chr6q24-q25	Hs.279257	5110			0.047643	-0.67
213365_at	similar to RIKEN cDNA 4933424N09 gene	MGC16943	chr16p12.3	Hs.248437	112479			0.039706	-0.67
218578_at	hyperparathyroidism 2 (with jaw tumor)	HRPT2	chr1q25	Hs.378996	79577			0.006950	-0.67
225162_at	SH3 domain protein D19	SH3D19	chr4q31.3	Hs.519018	152503			0.006092	-0.67
235344_at	Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha iso	PPM1A	chr14q23.1	Hs.130036	5494			0.013476	-0.67
219294_at	chromosome 6 open reading frame 139	C6orf139	chr6p12.3	Hs.88663	55166			0.031978	-0.67
218696_at	eukaryotic translation initiation factor 2-alpha kinase 3	EIF2AK3	chr2p12	Hs.434326	9451			0.016791	-0.67
239435_x_at	apical protein 2	APXL2	chr5q23.3	Hs.519574	134549			0.023088	-0.67
202211_at	ADP-ribosylation factor GTPase activating protein 3	ARFGAP3	chr22q13.2-q13.3	Hs.13014	26286			0.018460	-0.67
219979_s_at	hypothetical protein HSPC138	HSPC138	chr11q14.2	Hs.283322	51501			0.019113	-0.67
209633_at	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	PPP2R3A	chr3q22.1	Hs.518155	5523			0.045780	-0.67
212985_at	Full-length cDNA clone CSODC015YK09 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)			Hs.507486				0.029418	-0.67
205121_at	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	SGCB	chr4q12	Hs.438953	6443			0.020270	-0.67
235258_at	DCP2 decapping enzyme homolog (S. cerevisiae)	DCP2	chr5q22.2	Hs.443875	167227			0.006857	-0.67
226742_at	Transcribed locus, moderately similar to XP_512541.1 similar to hypothetical protein [Pan troglodytes]			Hs.432984				0.024623	-0.67
222816_s_at	zinc finger, CCHC domain containing 2	ZCCHC2	chr18q21.33	Hs.114191	54877			0.009062	-0.67
243405_at	Thioredoxin domain containing 5	TXNDC5	chr6p24.3	Hs.150837	81567			0.001517	-0.67
211505_s_at	staufen, RNA binding protein (Drosophila)	STAU	chr20p13.1	Hs.370187	6780			0.036128	-0.67
227942_s_at	postsynaptic protein CRIPT	CRIP1	chr2p21	Hs.534380	9419			0.017850	-0.67
212746_s_at	KARP-1-binding protein	KAB	chr1q44	Hs.533635	9859			0.026724	-0.67
231610_at	Homo sapiens, clone IMAGE:5272626, mRNA			Hs.511837				0.039298	-0.68
224413_s_at	BBP-like protein 1 /// BBP-like protein 1	BLP1	chr8p11.23	Hs.7471	83877			0.005787	-0.68
201133_s_at	praja 2, RING-H2 motif containing	PJA2	chr5q21.3	Hs.483036	9867			0.014848	-0.68
228375_at								0.027233	-0.68
224734_at								0.017909	-0.68
222566_at	suppressor of variegation 4-20 homolog 1 (Drosophila)	SUV420H1	chr11q13.2	Hs.503001	51111			0.035069	-0.68
213047_x_at	SET translocation (myeloid leukemia-associated)	SET	chr9q34	Hs.436687	6418			0.009672	-0.68
230684_at	Hypothetical protein BC004923	LOC85865	chr7q21.13	Hs.489052	85865			0.015245	-0.68
226391_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	NDUFB2	chr7q34	Hs.324250	4708			0.018997	-0.68
225133_at	Kruppel-like factor 3 (basic)	KLF3	chr4p14	Hs.298658	51274			0.011236	-0.68
219696_at	hypothetical protein FLJ20054	FLJ20054	chr1q31.3	Hs.497279	54530			0.016432	-0.68
225835_at	solute carrier family 12 (sodium/potassium/chloride transporters), mem	SLC12A2	chr5q23.3	Hs.162585	6558			0.000011	-0.68
222552_at	golgi transport 1 homolog B (S. cerevisiae)	GOLT1B	chr12p12.1	Hs.62275	51026			0.037509	-0.68
212204_at	DKFZP564G2022 protein	DKFZP564	chr15q15.1	Hs.511138	25963			0.010602	-0.68
225098_at	Abl interactor 2	ABI2	chr2q33	Hs.471156	10152			0.019263	-0.68
220608_s_at								0.028099	-0.68
222603_at	KIAA1815	KIAA1815	chr9p24	Hs.87128	79956			0.020818	-0.68
219279_at	dedicator of cytokinesis 10	DOCK10	chr2q36.3	Hs.46578	55619			0.038103	-0.68
235394_at	Phospholipase A2-activating protein	PLAA	chr9p21	Hs.27182	9373			0.025617	-0.68
235222_x_at	baculoviral IAP repeat-containing 4	BIRC4	chrXq25	Hs.356076	331			0.021977	-0.68
223204_at	hypothetical protein DKFZp434L142	DKFZp434	chr4q32.1	Hs.323583	51313			0.016351	-0.68
222395_s_at	hypothetical protein FLJ13855	FLJ13855	chr17q21.32	Hs.514297	65264			0.040604	-0.68
1555780_a_at	Ras homolog enriched in brain	RHEB	chr7q36	Hs.283521	6009			0.036964	-0.68
221268_s_at	sphingosine-1-phosphate phosphatase 1 /// sphingosine-1-phosphate p	SGPP1	chr14q23.2	Hs.24678	81537			0.014831	-0.68
212306_at	cytoplasmic linker associated protein 2	CLASP2	chr3p23	Hs.108614	23122			0.022659	-0.68
201411_s_at	pleckstrin homology domain containing, family B (evectins) member 2	PLEKHB2	chr2q21.1	Hs.469944	55041			0.016096	-0.68
224605_at	HCV F-transacted protein 1	LOC40115	chr4q26	Hs.173705	401152			0.026622	-0.68
209817_at	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (cal	PPP3CB	chr10q21-q22	Hs.500067	5532			0.000150	-0.68
211563_s_at	chromosome 19 open reading frame 2	C19orf2	chr19q12	Hs.466391	8725			0.020301	-0.68



2028810_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	chr7q36.3	Hs.490745	10049	0.032140	-0.68
224739_at	pim-3 oncogene	PIM3	chr22q13	Hs.530381	415116	0.040496	-0.68
232103_at	3'(2'), 5'-bisphosphate nucleotidase 1	BPNT1	chr1q41	Hs.406134	10380	0.020639	-0.69
215707_s_at	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-S	PRNP	chr20pter-p12	Hs.472010	5621	0.027633	-0.69
204621_s_at	nuclear receptor subfamily 4, group A, member 2	NR4A2	chr2q22-q23	Hs.165258	4929	0.019788	-0.69
213461_at	cleavage and polyadenylation specific factor 5, 25 kDa	CPSF5	chr16q12.2	Hs.528834	11051	0.026782	-0.69
231896_s_at	density-regulated protein	DENR	chr12q24.31	Hs.22393	8562	0.010895	-0.69
218570_at	kelch repeat and BTB (POZ) domain containing 4	KBTD4	chr11p11.2	Hs.440695	55709	0.011223	-0.69
1555274_a_at	selenoprotein I	SELI	chr2p23.3	Hs.189073	85465	0.010546	-0.69
202710_at	BET1 homolog (S. cerevisiae)	BET1	chr7q21.1-q22	Hs.489132	10282	0.029294	-0.69
222525_s_at	hypothetical protein FLJ10853	FLJ10853	chr8p21.1	Hs.445512	55246	0.031674	-0.69
218637_at	hypothetical protein IMPACT	IMPACT	chr18q11.2-q12.1	Hs.515317	55364	0.019894	-0.69
202538_s_at	chromatin modifying protein 2B	CHMP2B	chr3p12.1	Hs.476930	25978	0.010532	-0.69
209425_at						0.007280	-0.69
202820_at	aryl hydrocarbon receptor	AHR	chr7p15	Hs.171189	196	0.000736	-0.69
218276_s_at	salvador homolog 1 (Drosophila)	SAV1	chr14q13-q23	Hs.257341	60485	0.018676	-0.69
209632_at	protein phosphatase 2 (formerly 2A), regulatory subunit B', alpha	PPP2R3A	chr3q22.1	Hs.518155	5523	0.000683	-0.69
243904_at	CDNA clone IMAGE:5287121, partial cds			Hs.375744		0.036069	-0.69
216640_s_at	protein disulfide isomerase-associated 6	PDIA6	chr2p25.1	Hs.212102	10130	0.031136	-0.69
201777_s_at	KIAA0494 gene product	KIAA0494	chr1pter-p22.1	Hs.100874	9813	0.014054	-0.69
226259_at	SEC15-like 1 (S. cerevisiae)	SEC15L1	chr10q23.33	Hs.292097	54536	0.036135	-0.69
201554_x_at	glycogenin	GYG	chr3q24-q25.1	Hs.477892	2992	0.002217	-0.69
235819_at	Similar to transcription factor BTF3	MGC23908	chr1p32.3	Hs.429839	91408	0.022265	-0.69
222587_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosamin	GALNT7	chr4q31.1	Hs.127407	51809	0.013740	-0.69
231213_at	phosphodiesterase 1A, calmodulin-dependent	PDE1A	chr2q32.1	Hs.416061	5136	0.014084	-0.69
236576_at	Transcribed locus			Hs.21375		0.046003	-0.69
204125_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly facto	NDUFAF1	chr15q11.2-q21.1	Hs.106529	51103	0.004412	-0.69
231489_x_at	Transcribed locus, weakly similar to NP_061913.2 elongation protein 4 homolog (S. cerevisiae) [Homc			Hs.13284		0.017848	-0.69
209397_at	malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2	chr6p25-p24 18c	Hs.233119	4200	0.009737	-0.69
212468_at	sperm associated antigen 9	SPAG9	chr17q21.33	Hs.463439	9043	0.023805	-0.69
224812_at	3-hydroxyisobutyrate dehydrogenase	HIBADH	chr7p15.2	Hs.406758	11112	0.001925	-0.70
1558101_at	Full length insert cDNA clone ZD69D05			Hs.379253		0.035179	-0.70
243998_at	Hypothetical protein MGC45562	MGC45562	chr17q21.2	Hs.6920	125113	0.028128	-0.70
226050_at	chromosome 13 open reading frame 11	C13orf11	chr13q34	Hs.317593	55002	0.007017	-0.70
219094_at	armadillo repeat containing 8	ARMC8	chr3q22.3	Hs.266826	25852	0.005243	-0.70
209814_at	zinc finger protein 330	ZNF330		Hs.120766	27309	0.009240	-0.70
222656_at	hypothetical protein FLJ11011	FLJ11011	chr8q21.11	Hs.492031	55284	0.014423	-0.70
226034_at	Homo sapiens, clone IMAGE:3881549, mRNA			Hs.346735		0.029262	-0.70
221727_at	activated RNA polymerase II transcription cofactor 4 /// similar to Activa	PC4 /// LO	chr5p13.3 /// chr	Hs.448070	10923 /// 4	0.014580	-0.70
226370_at	kelch-like 15 (Drosophila)	KLHL15	chrXp22.1-p21	Hs.495854	80311	0.010795	-0.70
225332_at	Keratin associated protein 4-7	KRTAP4-7	chr17q12-q21	Hs.549512	85287	0.021715	-0.70
237983_at						0.038967	-0.70
200927_s_at	RAB14, member RAS oncogene family	RAB14	chr9q32-q34.11	Hs.371563	51552	0.016550	-0.70
227525_at	glucocorticoid induced transcript 1	GLCC1	chr7p21.3	Hs.131673	113263	0.022672	-0.70
225295_at	solute carrier family 39 (zinc transporter), member 10	SLC39A10	chr2q32.3	Hs.413434	57181	0.021915	-0.70
238856_s_at	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	PANK2	chr20p13	Hs.516859	80025	0.001773	-0.70
213882_at	Beta-amyloid binding protein precursor	BBP	chr1p31.3	Hs.276876	83941	0.007701	-0.70
201939_at	polo-like kinase 2 (Drosophila)	PLK2	chr5q12.1-q13.2	Hs.398157	10769	0.048603	-0.70
225619_at	hypothetical protein FLJ30046	FLJ30046	chr13q22.3	Hs.349955	122060	0.026913	-0.70
1561242_at						0.032510	-0.70
221858_at	TBC1 domain family, member 12	TBC1D12	chr10q23.33	Hs.500598	23232	0.000829	-0.70
225416_at	Ring finger protein 12	RNF12	chrXq13-q21	Hs.122121	51132	0.037942	-0.70
223215_s_at	chromosome 14 open reading frame 100	C14orf100	chr14q23.1	Hs.446850	51528	0.002793	-0.70
212373_at	fem-1 homolog b (C. elegans)	FEM1B	chr15q22	Hs.362733	10116	0.021354	-0.70
225048_at	PHD finger protein 10	PHF10	chr6q27	Hs.435933	55274	0.029875	-0.70
211931_s_at	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1 /// heterog	HNRPA3P1	chr10q11.21 /// c	Hs.524276	10151 /// 2	0.015842	-0.70
1552879_a_at	atonal homolog 7 (Drosophila)	ATOH7	chr10q21.3	Hs.175396	220202	0.016309	-0.71
219048_at	phosphatidylinositol glycan, class N	PIGN	chr18q21.33	Hs.157031	23556	0.003767	-0.71
201436_at	eukaryotic translation initiation factor 4E	EIF4E	chr4q21-q25	Hs.249718	1977	0.020066	-0.71
225897_at	Myristoylated alanine-rich protein kinase C substrate	MARCKS	chr6q22.2	Hs.519909	4082	0.033961	-0.71
218967_s_at	phosphotriesterase related	PTER	chr10p12	Hs.444321	9317	0.032377	-0.71
221452_s_at	transmembrane protein 14B /// transmembrane protein 14E	TMEM14B	chr6p25.1-p23	Hs.273077	81853	0.020952	-0.71
209175_at	SEC23 interacting protein	SEC23IP	chr10q25-q26	Hs.435004	11196	0.004645	-0.71
221472_at	tumor differentially expressed 1	TDE1	chr20q13.1-13.3	Hs.272168	10955	0.039999	-0.71
213663_s_at	hypothetical LOC389275	LOC389275	chr5p15.1	Hs.549332	389275	0.024395	-0.71
217821_s_at	WW domain binding protein 11	WBP11	chr12p12.3	Hs.524281	51729	0.015986	-0.71
213549_at	Solute carrier family 18 (vesicular monoamine), member 2	SLC18A2	chr10q25	Hs.369009	6571	0.005651	-0.71
221531_at	recombination protein REC14	REC14	chr15q25.1	Hs.513055	80349	0.026469	-0.71
228731_at	CDNA clone IMAGE:5273964, partial cds			Hs.24321		0.033824	-0.71
212213_x_at	optic atrophy 1 (autosomal dominant)	OPA1	chr3q28-q29 3q2	Hs.478708	4976	0.010605	-0.71
209735_at	ATP-binding cassette, sub-family G (WHITE), member 2	ABCG2	chr4q22	Hs.480218	9429	0.045574	-0.71
217826_s_at	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	chr6q15	Hs.163776	51465	0.027672	-0.71
1553111_a_at	kelch repeat and BTB (POZ) domain containing 6	KBTD6	chr13q14.11	Hs.534040	89890	0.006059	-0.71
200866_s_at	prosaposin (variant Gaucher disease and variant metachromatic leukody	PSAP	chr10q21-q22	Hs.523004	5660	0.029873	-0.71

212751_at	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	UBE2N	chr12q22	Hs.524630	7334	0.012367	-0.71
202373_s_at	rab3 GTPase-activating protein, non-catalytic subunit (150kD)	RAB3-GAP	chr1q41	Hs.549128	25782	0.045061	-0.71
233496_s_at	cofilin 2 (muscle)	CFL2	chr14q12	Hs.180141	1073	0.000352	-0.71
203521_s_at	zinc finger protein 318	ZNF318	chr6pter-p12.1	Hs.509718	24149	0.007214	-0.71
228981_at	hypothetical protein BC008604	LOC92691	chr2q35	Hs.334916	92691	0.003216	-0.71
213224_s_at	hypothetical protein LOC92482	LOC92482	chr10q25.2	Hs.192249	92482	0.007063	-0.71
231174_s_at	Erythrocyte membrane protein band 4.1-like 2	EPB41L2	chr6q23	Hs.486470	2037	0.006169	-0.71
200727_s_at	ARP2 actin-related protein 2 homolog (yeast)	ACTR2	chr2p14	Hs.393201	10097	0.021203	-0.71
218432_at	F-box protein 3	FBXO3	chr11p13	Hs.406787	26273	0.008414	-0.71
212623_at	Transmembrane protein 41B	TMEM41B	chr11p15.3	Hs.501865	23027	0.006403	-0.71
225198_at	VAMP (vesicle-associated membrane protein)-associated protein A, 33k	VAPA	chr18p11.22	Hs.165195	9218	0.011398	-0.71
228390_at	Homo sapiens, clone IMAGE:5259272, mRNA			Hs.184430		0.001560	-0.71
210875_s_at	transcription factor 8 (represses interleukin 2 expression)	TCF8	chr10p11.2	Hs.124503	6935	0.007656	-0.71
202922_at	glutamate-cysteine ligase, catalytic subunit	GCLC	chr6p12	Hs.271264	2729	0.038081	-0.71
1568603_at	Ca2+-dependent secretion activator	CADPS	chr3p14.2	Hs.127013	8618	0.006954	-0.71
218645_at	zinc finger protein 277	ZNF277	chr7q31.1	Hs.489722	11179	0.014590	-0.71
235885_at	purinergic receptor P2Y, G-protein coupled, 12	P2RY12	chr3q24-q25	Hs.532933	64805	0.011685	-0.71
206061_s_at	Dicer1, Dcr-1 homolog (Drosophila)	DICER1	chr14q32.13	Hs.87889	23405	0.025517	-0.71
227708_at	eukaryotic translation elongation factor 1 alpha 1	EEF1A1	chr6q14.1	Hs.439552	1915	0.002729	-0.71
231856_at	KIAA1244	KIAA1244	chr6q23.3	Hs.194408	57221	0.004937	-0.71
203632_s_at	G protein-coupled receptor, family C, group 5, member B	GPRC5B	chr16p12	Hs.148685	51704	0.045317	-0.72
228218_at	Homo sapiens, clone IMAGE:5284125, mRNA			Hs.26409		0.047370	-0.72
202690_s_at	small nuclear ribonucleoprotein D1 polypeptide 16kDa	SNRPD1	chr18q11.2	Hs.464734	6632	0.034706	-0.72
218311_at	mitogen-activated protein kinase kinase kinase 3	MAP4K3	chr2p22.1	Hs.468239	8491	0.034616	-0.72
208852_s_at	calnexin	CANX	chr5q35	Hs.529890	821	0.032075	-0.72
224801_at	Nedd4 family interacting protein 2	NDFIP2	chr13q31.1	Hs.525093	54602	0.034285	-0.72
235775_at	hypothetical protein DKFZp762A217	DKFZp762A217	chr12q21.31	Hs.444240	160335	0.004960	-0.72
212262_at	quaking homolog, KH domain RNA binding (mouse)	QKI	chr6q26-27	Hs.510324	9444	0.011193	-0.72
221568_s_at	lin-7 homolog C (C. elegans)	LIN7C	chr11p14	Hs.91393	55327	0.039308	-0.72
226404_at						0.049365	-0.72
209440_at	phosphoribosyl pyrophosphate synthetase 1	PRPS1	chrXq21-q27	Hs.56	5631	0.021736	-0.72
204160_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	ENPP4	chr6p21.1	Hs.54037	22875	0.010012	-0.72
222437_s_at	vacuolar protein sorting 24 (yeast)	VPS24	chr2p24.3-p24.1	Hs.255015	51652	0.031818	-0.72
228408_s_at						0.041240	-0.72
1554377_a_at	contactin associated protein-like 4	CNTNAP4		Hs.461389	85445	0.023305	-0.72
217862_at	protein inhibitor of activated STAT, 1	PIAS1	chr15q	Hs.162458	8554	0.028621	-0.72
1561055_at	Homo sapiens, clone IMAGE:5303550, mRNA			Hs.407601		0.029663	-0.72
228857_at	hypothetical protein LOC285831	LOC285831	chr6p21.32	Hs.550038	285831	0.019399	-0.72
232001_at	hypothetical gene supported by AY007155	LOC439944	chr10p15.1	Hs.13262	439949	0.020139	-0.72
201915_at	SEC63-like (S. cerevisiae)	SEC63	chr6q21	Hs.529957	11231	0.001146	-0.73
234982_at	zinc finger protein 650	ZNF650	chr2q31.1	Hs.379548	130507	0.002109	-0.73
236117_at	Transcribed locus			Hs.42747		0.023235	-0.73
213229_at	Dicer1, Dcr-1 homolog (Drosophila)	DICER1	chr14q32.13	Hs.87889	23405	0.034619	-0.73
203322_at	KIAA0863 protein	KIAA0863	chr18q23	Hs.131915	22850	0.003015	-0.73
211960_s_at	RAB7, member RAS oncogene family	RAB7	chr3q21.3	Hs.15738	7879	0.006910	-0.73
201880_at	Ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	ARIH1	chr15q24	Hs.268787	25820	0.021358	-0.73
228561_at						0.009221	-0.73
201691_s_at	tumor protein D52	TPD52	chr8q21	Hs.368433	7163	0.006463	-0.73
200604_s_at	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific)	PRKAR1A	chr17q23-q24	Hs.280342	5573	0.038009	-0.73
225433_at	General transcription factor IIA, 1, 19/37kDa	GTF2A1	chr14q31.1	Hs.547415	2957	0.011943	-0.73
225125_at	transmembrane protein 32	TMEM32	chrXq26.3	Hs.110702	93380	0.003000	-0.73
214589_at	fibroblast growth factor 12	FGF12	chr3q28	Hs.185577	2257	0.028789	-0.73
235051_at	chromosome 3 open reading frame 6	C3orf6		Hs.478682	152137	0.005314	-0.73
1556328_at						0.046686	-0.73
219643_at	low density lipoprotein-related protein 1B (deleted in tumors)	LRP1B	chr2q21.2	Hs.470117	53353	0.023936	-0.73
230416_at	Solute carrier family 18 (vesicular monoamine), member 2	SLC18A2	chr10q25	Hs.369009	6571	0.002570	-0.73
212332_at	retinoblastoma-like 2 (p130)	RBL2	chr16q12.2	Hs.513609	5934	0.039081	-0.73
204645_at	cyclin T2	CCNT2	chr2q21.3	Hs.292754	905	0.012936	-0.73
218506_x_at	cytokine-like nuclear factor n-pac	N-PAC	chr16p13.3	Hs.387255	84656	0.005576	-0.73
227961_at	Cathepsin B	CTSB	chr8p22	Hs.520898	1508	0.019335	-0.73
202224_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	CRK	chr17p13.3	Hs.461896	1398	0.038663	-0.73
222393_s_at	Mak3 homolog (S. cerevisiae)	MAK3	chr3q13.2	Hs.269528	80218	0.020315	-0.73
221487_s_at	endosulfine alpha	ENSA	chr1q21.2	Hs.510087	2029	0.016440	-0.73
204161_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	ENPP4	chr6p21.1	Hs.54037	22875	0.001300	-0.73
241734_at	serum response factor binding protein 1	SRFBP1	chr5q23.1	Hs.107622	153443	0.001609	-0.73
235801_at	Tumor suppressor candidate 3	TUSC3	chr8p22	Hs.426324	7991	0.019024	-0.73
219300_s_at	contactin associated protein-like 2	CNTNAP2	chr7q35-q36	Hs.446192	26047	0.003868	-0.74
226721_at	Hypothetical protein LOC286148	LOC286148	chr8q22.1	Hs.546537	286148	0.029766	-0.74
202304_at	fibronectin type III domain containing 3A	FNDC3A	chr13q14.2	Hs.508010	22862	0.014086	-0.74
238035_at	Sp3 transcription factor	SP3	chr2q31	Hs.531587	6670	0.011959	-0.74
202969_at	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	chr12q15	Hs.173135	8445	0.015892	-0.74
238718_at	CDNA FLJ37816 fis, clone BRSSN2003093			Hs.417630		0.009435	-0.74
238546_at	solute carrier family 8 (sodium/calcium exchanger), member 1	SLC8A1	chr2p23-p22	Hs.468274	6546	0.020991	-0.74
228493_at	A kinase (PRKA) anchor protein 14	AKAP14	chrXq24	Hs.184993	158798	0.012554	-0.74

220985_s_at	ring finger protein 170 /// ring finger protein 17C	RNF170	chr8p11.21	Hs.491626	81790	0.002046	-0.74
210363_s_at	sodium channel, voltage-gated, type II, beta	SCN2B	chr11q23	Hs.129783	6327	0.012237	-0.74
1557081_at	RNA binding motif protein 25	RBM25	chr14q24.3	Hs.531106	58517	0.043842	-0.74
224187_x_at	heat shock 70kDa protein 8	HSPA8	chr11q24.1	Hs.180414	3312	0.024661	-0.74
202423_at	MYST histone acetyltransferase (monocytic leukemia) 3	MYST3	chr8p11	Hs.491577	7994	0.025819	-0.74
231964_at	MRNA; cDNA DKFZp564H1663 (from clone DKFZp564H1663)			Hs.137206		0.006879	-0.74
203362_s_at	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	chr4q27	Hs.533185	4085	0.025865	-0.74
226339_at	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	TRUB1	chr10q25.3	Hs.21187	142940	0.001998	-0.74
228189_at	BCL2-associated athanogene 4	BAG4	chr8p12	Hs.194726	9530	0.025277	-0.74
229212_at	Casein kinase 2, alpha 1 polypeptide	CSNK2A1	chr20p13	Hs.446484	1457	0.013157	-0.74
201951_at						0.009496	-0.74
203457_at	syntaxin 7	STX7	chr6q23.1	Hs.520383	8417	0.007686	-0.74
222659_at	importin 11	IPO11	chr5q12.1	Hs.482269	51194	0.027133	-0.75
229414_at	phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	chr17q24.2	Hs.549130	26207	0.025508	-0.75
211769_x_at	tumor differentially expressed 1 /// tumor differentially expressed 1	TDE1	chr20q13.1-13.3	Hs.272168	10955	0.016508	-0.75
223943_s_at						0.024644	-0.75
220994_s_at	syntaxin binding protein 6 (amisyn)	STXBP6	chr14q12	Hs.508958	29091	0.011181	-0.75
241887_at	CDNA FLJ41537 fis, clone BRTHA2017985			Hs.128841		0.010932	-0.75
210292_s_at	protocadherin 11 X-linked /// protocadherin 11 Y-linked	PCDH11X	chrXq21.3 /// chr	Hs.546448	27328 /// 8	0.034755	-0.75
208944_at						0.009691	-0.75
235890_at						0.039240	-0.75
235037_at	transmembrane protein 41A	TMEM41A	chr3q27.2	Hs.549226	90407	0.011455	-0.75
236517_at	MEGF10 protein	MEGF10	chr5q33	Hs.438709	84466	0.032338	-0.75
226399_at	Hypothetical protein FLJ14281	FLJ14281	chr4q23	Hs.512743	79982	0.024881	-0.75
217743_s_at	transmembrane protein 30A	TMEM30A	chr6q14.1	Hs.108530	55754	0.006853	-0.75
205260_s_at	acylphosphatase 1, erythrocyte (common) type	ACYP1	chr14q24.3	Hs.18573	97	0.023872	-0.75
225785_at	chromosome 10 open reading frame 74	C10orf74	chr10q21.3	Hs.499833	221035	0.009623	-0.75
235183_at	Homo sapiens, clone IMAGE:5312689, mRNA			Hs.548069		0.041700	-0.75
228791_at	Hypothetical protein MGC61550	MGC61550	chr15q26.1	Hs.6734	348110	0.045530	-0.75
226347_at						0.034255	-0.75
203253_s_at	KIAA0433 protein	KIAA0433	chr5q21.1	Hs.212046	23262	0.002627	-0.75
226456_at	hypothetical protein MGC24665	MGC24665	chr16p13.13	Hs.347524	116028	0.009320	-0.75
219429_at	fatty acid 2-hydroxylase	FA2H	chr16q23	Hs.461329	79152	0.035608	-0.75
202955_s_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin	ARFGEF1	chr8q13	Hs.411848	10565	0.041277	-0.75
204172_at	coproporphyrinogen oxidase	CPOX	chr3q12	Hs.476982	1371	0.001984	-0.76
201744_s_at	lumican	LUM	chr12q21.3-q22	Hs.406475	4060	0.020713	-0.76
224777_s_at	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kD	PAFAH1B2	chr11q23	Hs.188501	5049	0.041481	-0.76
222442_s_at	ADP-ribosylation factor-like 10C	ARL10C	chr3p26.1	Hs.250009	55207	0.001604	-0.76
227446_s_at						0.014267	-0.76
227256_at	ubiquitin specific protease 31	USP31	chr16p12.1	Hs.183817	57478	0.027129	-0.76
242028_at	hypothetical protein FLJ38281	FLJ38281	chr19p13.2	Hs.306478	163051	0.007344	-0.76
225731_at	KIAA1223 protein	KIAA1223	chr4q28.1	Hs.480694	57182	0.012857	-0.76
224744_at	myo-inositol monophosphatase A3	IMPA3	chr8q12.1	Hs.438689	54928	0.009393	-0.76
221288_at	G protein-coupled receptor 22	GPR22	chr7q22-q31.1	Hs.432557	2845	0.001893	-0.76
1555945_s_at	chromosome 9 open reading frame 10	C9orf10	chr9q22.31	Hs.372003	23196	0.008417	-0.76
201408_at	protein phosphatase 1, catalytic subunit, beta isoform	PPP1CB	chr2p23	Hs.468018	5500	0.043099	-0.76
207142_at	potassium inwardly-rectifying channel, subfamily J, member 3	KCNJ3	chr2q24.1	Hs.199776	3760	0.018154	-0.76
224786_at	short coiled-coil protein	SCOC	chr4q31.1	Hs.480815	60592	0.004076	-0.76
1555334_s_at	solute carrier family 30 (zinc transporter), member 5	SLC30A5	chr5q12.1	Hs.482363	64924	0.013608	-0.76
225872_at	solute carrier family 35, member F5	SLC35F5	chr2q14.1	Hs.292509	80255	0.015576	-0.76
1553106_at	hypothetical protein FLJ37562	FLJ37562	chr5q31.1	Hs.406549	134553	0.003544	-0.76
227316_at	CSRP2 binding protein	CSRP2BP	chr20p11.23	Hs.488051	57325	0.027885	-0.76
206668_s_at	secretory carrier membrane protein 1	SCAMP1	chr5q13.3-q14.1	Hs.482587	9522	0.036014	-0.76
219179_at	dapper homolog 1, antagonist of beta-catenin (xenopus)	DACT1	chr14q23.1	Hs.48950	51339	0.019349	-0.76
220355_s_at	polybromo 1	PB1	chr3p21	Hs.189920	55193	0.002167	-0.76
238521_at	Transcribed locus, weakly similar to XP_376981.1 similar to hypothetical protein (L1H 3 region) - hum			Hs.390250		0.020981	-0.76
208127_s_at	suppressor of cytokine signaling 5	Socs5	chr2p21	Hs.468426	9655	0.002364	-0.76
241966_at	myosin VA (heavy polypeptide 12, myosin)	MYO5A	chr15q21	Hs.21213	4644	0.039750	-0.77
219302_s_at	contactin associated protein-like 2	CNTNAP2	chr7q35-q36	Hs.446192	26047	0.011595	-0.77
226199_at	hypothetical protein MGC23937 similar to CG4798	RP11-311P	chrXq13.3	Hs.91612	139596	0.047320	-0.77
209095_at	dihydroliipoamide dehydrogenase (E3 component of pyruvate dehydrog	DLD	chr7q31-q32	Hs.131711	1738	0.035117	-0.77
219569_s_at	transmembrane protein 22	TMEM22	chr3q22.3	Hs.477692	80723	0.024922	-0.77
202539_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	chr5q13.3-q14	Hs.11899	3156	0.009621	-0.77
227364_at						0.024448	-0.77
242317_at	Transcribed locus			Hs.192124		0.018781	-0.77
230569_at	KIAA1430	KIAA1430	chr4q35.1	Hs.535734	57587	0.017557	-0.77
219421_at	osmosis responsive factor	OSRF	chr5p15.2-p12	Hs.130904	23548	0.008500	-0.77
226077_at	hypothetical protein FLJ31951	FLJ31951	chr5q33.3	Hs.349306	153830	0.037111	-0.77
238850_at	CDNA clone IMAGE:5260726, partial cds			Hs.12827		0.045420	-0.77
224865_at	male sterility domain containing 2	MLSTD2	chr11p15.2	Hs.501991	84188	0.035040	-0.77
226429_at	KIAA1704	KIAA1704	chr13q13-q14	Hs.507922	55425	0.032429	-0.77
239960_x_at	CDNA FLJ32429 fis, clone SKMUS2001014			Hs.508823		0.004194	-0.77
201668_x_at	myristoylated alanine-rich protein kinase C substrate	MARCKS	chr6q22.2	Hs.519909	4082	0.016620	-0.77
212103_at	Karyopherin alpha 6 (importin alpha 7)	KPNA6	chr1p35.1-p34.3	Hs.470588	23633	0.011626	-0.77

1566509_s_at	F-box protein 9	FBXO9	chr6p12.3-p11.2	Hs.216653	26268		<b>0.029702</b>	<b>-0.77</b>
219267_at	glycolipid transfer protein	GLTP	chr12q24.11	Hs.381256	51228		<b>0.000725</b>	<b>-0.77</b>
242206_at	similar to Zinc finger protein 58 (Zfp-58) (Zinc finger protein Mfg-1)	LOC340244	chr7q11.21	Hs.434984	340246		<b>0.011739</b>	<b>-0.77</b>
226887_at	heat shock 70kDa protein 14	HSPA14	chr10p13	Hs.534169	51182		<b>0.008480</b>	<b>-0.78</b>
202932_at	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1	chr18p11.31-p11	Hs.194148	7525		<b>0.003101</b>	<b>-0.78</b>
230265_at	Sel-1 suppressor of lin-12-like (C. elegans)	SEL1L	chr14q24.3-q31	Hs.181300	6400		<b>0.021533</b>	<b>-0.78</b>
219858_s_at	FLJ20160 protein	FLJ20160	chr2q32.2	Hs.418581	54842		<b>0.011393</b>	<b>-0.78</b>
237741_at	Hypothetical protein FLJ10618	FLJ10618	chr3q23	Hs.144130	55186		<b>0.037709</b>	<b>-0.78</b>
203086_at	Kinesin heavy chain member 2	KIF2	chr5q12-q13	Hs.552575	3796		<b>0.013564</b>	<b>-0.78</b>
1554868_s_at	PEST-containing nuclear protein	PCNP	chr3q12.3	Hs.549185	57092		<b>0.043100</b>	<b>-0.78</b>
219109_at	sperm associated antigen 16	SPAG16	chr2q34	Hs.471316	79582		<b>0.032033</b>	<b>-0.78</b>
200638_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation prd	YWHAZ	chr8q23.1	Hs.492407	7534		<b>0.015320</b>	<b>-0.78</b>
201865_x_at	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid recepte	NR3C1	chr5q31	Hs.122926	2908		<b>0.047779</b>	<b>-0.78</b>
210427_s_at	selenoprotein P, plasma, 1	SEPP1	chr5q31	Hs.275775	6414		<b>0.009288</b>	<b>-0.78</b>
208868_s_at	GABA(A) receptor-associated protein like 1	GABARAPL	chr12p13.2	Hs.524250	23710		<b>0.035176</b>	<b>-0.78</b>
204678_s_at	potassium channel, subfamily K, member 1	KCNK1	chr14q2-q43	Hs.208544	3775		<b>0.007349</b>	<b>-0.78</b>
206875_s_at	STE20-like kinase (yeast)	SLK	chr10q25.1	Hs.500972	9748		<b>0.014801</b>	<b>-0.78</b>
227082_at	MRNA; cDNA DKFzP586K1922 (from clone DKFzP586K1922)			Hs.193784			<b>0.033917</b>	<b>-0.78</b>
212908_at	KIAA0962 protein	KIAA0962	chr1p36.1	Hs.549123	23341		<b>0.029391</b>	<b>-0.78</b>
217750_s_at	hypothetical protein FLJ13855	FLJ13855	chr17q21.32	Hs.514297	65264		<b>0.046686</b>	<b>-0.78</b>
235864_at	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	MPP5	chr14q23.3	Hs.509699	64398		<b>0.009474</b>	<b>-0.78</b>
228654_at	hypothetical protein LOC139886	LOC139886	chrXq11.2	Hs.111496	139886		<b>0.033490</b>	<b>-0.78</b>
225575_at	Leukemia inhibitory factor receptor	LIFR	chr5p13-p12	Hs.133421	3977		<b>0.021165</b>	<b>-0.78</b>
212308_at	cytoplasmic linker associated protein 2	CLASP2	chr3p23	Hs.108614	23122		<b>0.027469</b>	<b>-0.78</b>
221830_at	RAP2A, member of RAS oncogene family	RAP2A	chr13q34	Hs.508480	5911		<b>0.046895</b>	<b>-0.79</b>
231862_at	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5	chr12q13.13	Hs.349283	23468		<b>0.011361</b>	<b>-0.79</b>
235164_at	zinc finger protein 25 (KOX 19)	ZNF25	chr10p11.21	Hs.499429	219749		<b>0.034462</b>	<b>-0.79</b>
238792_at	Pecanex homolog (Drosophila)	PCNX	chr14q24.2	Hs.158722	22990		<b>0.012614</b>	<b>-0.79</b>
203789_s_at	sema domain, immunoglobulin domain (Ig), short basic domain, secrete	SEMA3C	chr7q21-q31	Hs.269109	10512		<b>0.000387</b>	<b>-0.79</b>
228214_at	Transcribed locus			Hs.34145			<b>0.002061</b>	<b>-0.79</b>
225388_at	tetraspanin 5	TSPAN5	chr4q23	Hs.118118	10098		<b>0.013469</b>	<b>-0.79</b>
217452_s_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	B3GALT2	chr1q31	Hs.518834	8707		<b>0.018626</b>	<b>-0.79</b>
225626_at	phosphoprotein associated with glycosphingolipid-enriched microdoma	PAG	chr8q21.13	Hs.266175	55824		<b>0.002846</b>	<b>-0.79</b>
228746_s_at	Hypothetical protein H41	H41	chr3q22.1	Hs.518265	55573		<b>0.045162</b>	<b>-0.79</b>
204732_s_at	tripartite motif-containing 23	TRIM23	chr5q12.3	Hs.792	373		<b>0.022236</b>	<b>-0.79</b>
1553247_a_at	hypothetical protein FLJ38281	FLJ38281	chr19p13.2	Hs.306478	163051		<b>0.045118</b>	<b>-0.79</b>
204361_s_at	src family associated phosphoprotein 2	SCAP2	chr7p21-p15	Hs.200770	8935		<b>0.009781</b>	<b>-0.79</b>
201559_s_at	chloride intracellular channel 4	CLIC4	chr1p36.11	Hs.440544	25932		<b>0.000541</b>	<b>-0.79</b>
225219_at	SMAD, mothers against DPP homolog 5 (Drosophila)	SMAD5	chr5q31	Hs.167700	4090		<b>0.016382</b>	<b>-0.79</b>
242762_s_at	KIAA1946	KIAA1946	chr2q32.1	Hs.28872	165215		<b>0.045222</b>	<b>-0.79</b>
231239_at	EPH receptor A5	EPHA5	chr4q13.1	Hs.479853	2044		<b>0.019272</b>	<b>-0.79</b>
230538_at	rai-like protein	RaLP	chr15q21.1-q21.2	Hs.552630	399694		<b>0.017860</b>	<b>-0.79</b>
223661_at							<b>0.039309</b>	<b>-0.79</b>
203883_s_at	RAB11 family interacting protein 2 (class I)	RAB11FIP2	chr10q26.11	Hs.173656	22841		<b>0.018123</b>	<b>-0.79</b>
244334_at	translocation associated membrane protein 1-like 1	TRAM1L1	chr4q26	Hs.154218	133022		<b>0.037515</b>	<b>-0.79</b>
227123_at	RAB3B, member RAS oncogene family	RAB3B	chr1p32-p31	Hs.123072	5865		<b>0.028214</b>	<b>-0.79</b>
223547_at	chromosome 14 open reading frame 100	C14orf100	chr14q23.1	Hs.446850	51528		<b>0.000906</b>	<b>-0.79</b>
203087_s_at	kinesin heavy chain member 2	KIF2	chr5q12-q13	Hs.552575	3796		<b>0.002552</b>	<b>-0.80</b>
202206_at	ADP-ribosylation factor-like 7	ARL7	chr2q37.1	Hs.111554	10123		<b>0.015159</b>	<b>-0.80</b>
233910_at	transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	chr2q32.3	Hs.144513	23671		<b>0.026691</b>	<b>-0.80</b>
201237_at	capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	chr7q31.2-q31.3	Hs.446123	830		<b>0.011359</b>	<b>-0.80</b>
212897_at	cell division cycle 2-like 6 (CDK8-like)	CDC2L6	chr6q21	Hs.193251	23097		<b>0.013763</b>	<b>-0.80</b>
238861_at	MRNA; clone CD 4377			Hs.290856			<b>0.024720</b>	<b>-0.80</b>
205358_at	glutamate receptor, ionotropic, AMPA 2	GRIA2	chr4q32-q33	Hs.32763	2891		<b>0.042270</b>	<b>-0.80</b>
212461_at							<b>0.015618</b>	<b>-0.80</b>
212244_at	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	GRIN1A	chr15q22.1	Hs.437256	81488		<b>0.002648</b>	<b>-0.80</b>
228601_at	hypothetical LOC401022	LOC401022	chr2q31.2	Hs.98661	401022		<b>0.026666</b>	<b>-0.80</b>
227442_at	hypothetical protein FLJ38991	FLJ38991	chr4q13.3	Hs.356697	285521		<b>0.018157</b>	<b>-0.80</b>
207781_s_at	zinc finger protein 6 (CMPX1)	ZNF6	chrXq13-q21.1	Hs.326801	7552		<b>0.027521</b>	<b>-0.80</b>
209243_s_at	paternally expressed 3	PEG3	chr19q13.4	Hs.201776	5178		<b>0.024603</b>	<b>-0.80</b>
202919_at	preimplantation protein 3	PREI3	chr2q33.1	Hs.205173	25843		<b>0.003125</b>	<b>-0.80</b>
204011_at	sprouty homolog 2 (Drosophila)	SPRY2	chr13q31.1	Hs.18676	10253		<b>0.019455</b>	<b>-0.80</b>
230692_at	hypothetical protein LOC157503	LOC157503	chr8q11.23	Hs.103535	157503		<b>0.037472</b>	<b>-0.80</b>
224692_at	protein phosphatase 1, regulatory (inhibitor) subunit 15E	PPP1R15B	chr1q32.1	Hs.304376	84919		<b>0.004442</b>	<b>-0.80</b>
203083_at	thrombospondin 2	THBS2	chr6q27	Hs.371147	7058		<b>0.026602</b>	<b>-0.81</b>
223261_at	polymerase (DNA directed) kappa	POLK	chr5q13	Hs.135756	51426		<b>0.003884</b>	<b>-0.81</b>
227535_at	Chromosome 15 open reading frame 24	C15orf24	chr15q14	Hs.160565	56851		<b>0.037856</b>	<b>-0.81</b>
212335_at	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	GNS	chr12q14	Hs.334534	2799		<b>0.005025</b>	<b>-0.81</b>
208687_x_at	heat shock 70kDa protein 8	HSPA8	chr11q24.1	Hs.180414	3312		<b>0.033309</b>	<b>-0.81</b>
201829_at	neuroepithelial cell transforming gene 1	NET1	chr10p15	Hs.25155	10276		<b>0.035920</b>	<b>-0.81</b>
210729_at	neuropeptide Y receptor Y2	NPY2R	chr4q31	Hs.37125	4887		<b>0.019484</b>	<b>-0.81</b>
200755_s_at	calumenin	CALU	chr7q32	Hs.7753	813		<b>0.004362</b>	<b>-0.81</b>
212572_at	serine/threonine kinase 38 like	STK38L	chr12p11.23	Hs.184523	23012		<b>0.013493</b>	<b>-0.81</b>
209895_at	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome)	PTPN11	chr12q24	Hs.506852	5781		<b>0.012486</b>	<b>-0.81</b>



230779_at	MRNA; cDNA DKFZp761i2317 (from clone DKFZp761i2317)				Hs.442983		0.025558	-0.81
222811_at	hypothetical protein FLJ11171	FLJ11171	chr16q22.2	Hs.72782	55783		0.000015	-0.81
235476_at	tripartite motif-containing 59	TRIM59	chr3q25.33	Hs.212957	286827		0.000419	-0.81
226180_at	WD repeat domain 36	WDR36	chr5q22.1	Hs.533237	134430		0.007475	-0.81
211749_s_at	vesicle-associated membrane protein 3 (cellubrevin) /// vesicle-associat	VAMP3	chr1p36.23	Hs.66708	9341		0.001868	-0.82
225690_at	CDC2-related protein kinase 7	CRK7	chr17q12	Hs.416108	51755		0.015073	-0.82
228129_at	PAI-1 mRNA-binding protein	PAI-RBP1	chr1p31-p22	Hs.530412	26135		0.033104	-0.82
227209_at	Contactin 1	CNTN1	chr12q11-q12	Hs.549027	1272		0.008298	-0.82
227012_at	mitochondrial carrier family protein	MCFP	chr7q21.12	Hs.208414	55972		0.002949	-0.82
225399_at	chromosome 1 open reading frame 19	C1orf19	chr1q25	Hs.440663	116461		0.029873	-0.82
207152_at	neurotrophic tyrosine kinase, receptor, type 2	NTRK2	chr9q22.1	Hs.494312	4915		0.028153	-0.82
214921_at	potassium large conductance calcium-activated channel, subfamily M, a	KCNMA1	chr10q22.3	Hs.144795	3778		0.044464	-0.82
222407_s_at	zinc finger protein 106 homolog (mouse)	ZFP106	chr15q15.1	Hs.511143	64397		0.012684	-0.82
213032_at	Nuclear factor I/B	NFIB	chr9p24.1	Hs.370359	4781		0.019877	-0.82
201083_s_at	BCL2-associated transcription factor 1	BCLAF1	chr6q22-q23	Hs.486542	9774		0.003669	-0.82
211137_s_at	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	chr3q22.1	Hs.546361	27032		0.011749	-0.82
224977_at							0.035918	-0.82
201444_s_at	ATPase, H+ transporting, lysosomal accessory protein 2	ATP6AP2	chrXq21	Hs.495960	10159		0.034105	-0.82
203803_at	prenylcysteine oxidase 1	PCYOX1	chr2p13.3	Hs.551542	51449		0.001167	-0.82
1554133_at	RUN and FYVE domain containing 2	RUFY2	chr10q21.3	Hs.549177	55680		0.014534	-0.82
221905_at	cylindromatosis (turban tumor syndrome)	CYLD	chr16q12-q13 16	Hs.432993	1540		0.038332	-0.82
218458_at	germ cell-less homolog 1 (Drosophila)	GCL	chr2p13.3	Hs.293971	64395		0.007116	-0.82
229115_at	dynein, cytoplasmic, heavy polypeptide 1	DNCH1	chr14q32.3-qter	Hs.7720	1778		0.044525	-0.83
203845_at	p300/CBP-associated factor	PCAF	chr3p24	Hs.533055	8850		0.038929	-0.83
225132_at	F-box and leucine-rich repeat protein 3	FBXL3	chr13q22	Hs.508284	26224		0.006723	-0.83
229138_at	poly (ADP-ribose) polymerase family, member 11	PARP11	chr12p13.3	Hs.504538	57097		0.001291	-0.83
201659_s_at	ADP-ribosylation factor-like 1	ARL1	chr12q23.3	Hs.372616	400		0.006245	-0.83
229074_at	EH-domain containing 4	EHD4	chr15q11.1	Hs.143703	30844		0.010498	-0.83
215303_at	Clones 24632 and 24634 mRNA sequence			Hs.129997			0.007403	-0.83
227481_at	CNKSR family member 3	CNKSR3	chr6q25.2	Hs.16064	154043		0.002104	-0.83
229010_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence	CBL	chr11q23.3	Hs.504096	867		0.040990	-0.83
212678_at	Neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Wats	NF1	chr17q11.2	Hs.435956	4763		0.011618	-0.83
204063_s_at	unc-51-like kinase 2 (C. elegans)	ULK2	chr17p11.2	Hs.168762	9706		0.036779	-0.83
203128_at	serine palmitoyltransferase, long chain base subunit 2	SPTLC2	chr14q24.3-q31	Hs.435661	9517		0.008052	-0.83
219642_s_at	peroxisomal biogenesis factor 5-like	PEX5L	chr3q26.33	Hs.478393	51555		0.034915	-0.83
206075_s_at	casein kinase 2, alpha 1 polypeptide	CSNK2A1	chr20p13	Hs.446484	1457		0.008499	-0.83
200973_s_at	tetraspanin 3	TSPAN3	chr15q24.3	Hs.5062	10099		0.033463	-0.83
212263_at	quaking homolog, KH domain RNA binding (mouse)	QKI	chr6q26-27	Hs.510324	9444		0.008272	-0.84
238929_at	Splicing factor, arginine/serine-rich, 46kD	SRP46	chr11q22	Hs.476680	10929		0.011667	-0.84
219112_at	Rap guanine nucleotide exchange factor (GEF) 6	RAPGEF6	chr5q23.3	Hs.51735	51735		0.035639	-0.84
233437_at	gamma-aminobutyric acid (GABA) A receptor, alpha 4	GABRA4	chr4p12	Hs.248112	2557		0.033427	-0.84
235977_at	CDNA FLJ36725 fis, clone UTERU2012230			Hs.21380			0.019509	-0.84
224614_at	dynein, cytoplasmic, light intermediate polypeptide 2	DNLI2	chr16q22.1	Hs.369068	1783		0.038740	-0.84
221428_s_at	transducin (beta)-like 1X-linked receptor 1 /// transducin (beta)-like 1X-	TBL1XR1	chr3q26.32	Hs.438970	79718		0.031049	-0.84
228734_at	Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	chr8q11.21	Hs.491695	7336		0.001567	-0.84
200864_s_at	RAB11A, member RAS oncogene family	RAB11A	chr15q21.3-q22.3	Hs.321541	8766		0.020181	-0.84
237828_at	KIAA1853 protein	KIAA1853	chr12q24.23	Hs.112577	84530		0.044485	-0.84
208844_at	voltage-dependent anion channel 3	VDAC3	chr8p11.2	Hs.491597	7419		0.045233	-0.85
224908_s_at	tubulin tyrosine ligase	TTL	chr2q13	Hs.358997	150465		0.046800	-0.85
226114_at	zinc finger protein 436	ZNF436	chr1p36	Hs.293798	80818		0.001271	-0.85
211963_s_at	actin related protein 2/3 complex, subunit 5, 16kDa	ARPC5	chr1q25.3	Hs.518609	10092		0.036344	-0.85
214352_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS	chr12p12.1	Hs.505033	3845		0.010152	-0.85
236131_at	Coatomer protein complex, subunit gamma 2	COPG2	chr7q32	Hs.532231	26958		0.039171	-0.85
208615_s_at	protein tyrosine phosphatase type IVA, member 2	PTP4A2	chr1p35	Hs.470477	8073		0.044567	-0.85
227624_at	KIAA1546 protein	KIAA1546	chr4q24	Hs.531250	57667		0.002421	-0.85
217738_at	pre-B-cell colony enhancing factor 1	PBEF1	chr7q22.3	Hs.489615	10135		0.018645	-0.85
223854_at	protocadherin beta 10	PCDHB10	chr5q31	Hs.145256	56126		0.035218	-0.85
201384_s_at	neighbor of BRCA1 gene 1	NBR1	chr17q21.1	Hs.277721	4077		0.017122	-0.85
203962_s_at	nebullette	NEBL	chr10p12	Hs.5025	10529		0.020153	-0.85
238360_s_at	CDNA clone IMAGE:3877454, partial cds			Hs.451488			0.019263	-0.85
225623_at	KIAA1737	KIAA1737	chr14q24.3	Hs.22452	85457		0.047899	-0.85
225086_at	Hypothetical protein FLJ38426	FLJ38426	chr15q14	Hs.6799	283742		0.007893	-0.86
211480_s_at	solute carrier organic anion transporter family, member 1A2	SLCO1A2	chr12p12	Hs.46440	6579		0.000462	-0.86
226819_at	LSM11, U7 small nuclear RNA associated	LSM11	chr5q33.3	Hs.23648	134353		0.030643	-0.86
1557953_at	zinc finger with KRAB and SCAN domains 1	ZKSCAN1	chr7q21.3-q22.1	Hs.423725	7586		0.010631	-0.86
222558_at	hypothetical protein FLJ10656	P15RS	chr18q12.2	Hs.464912	55197		0.030233	-0.86
225850_at	chromosome 6 open reading frame 83	C6orf83	chr6q27	Hs.487143	113402		0.030951	-0.86
212249_at	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	chr5q13.1	Hs.132225	5295		0.012018	-0.86
200605_s_at	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specif	PRKAR1A	chr17q23-q24	Hs.280342	5573		0.031607	-0.86
226276_at	hypothetical protein MGC23909	MGC23909	chr5q14.2	Hs.355606	153339		0.002082	-0.86
214063_s_at	transferrin	TF	chr3q22.1	Hs.518267	7018		0.048555	-0.86
203801_at	mitochondrial ribosomal protein S14	MRPS14	chr1q23-1q25	Hs.247324	63931		0.024782	-0.86
1557481_a_at	Chromosome 21 open reading frame 131	C21orf131	chr21	Hs.547012	387486		0.012318	-0.86
227605_at	Small inducible cytokine subfamily E, member 1 (endothelial monocyte-	SCYE1	chr4q24	Hs.480465	9255		0.023036	-0.86

211671_s_at	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	chr5q31	Hs.122926	2908	0.047499	-0.86
243910_x_at	CDNA FLJ30383 fis, clone BRACE2008102			Hs.505983		0.028778	-0.86
238417_at	phosphoglucomutase 2-like 1	PGM2L1	chr11q13.4	Hs.26612	283209	0.049150	-0.86
202549_at	VAMP (vesicle-associated membrane protein)-associated protein B and	VAPB	chr20q13	Hs.182625	9217	0.020858	-0.86
224581_s_at	Nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	NUCKS	chr1q32.1	Hs.213061	64710	0.018955	-0.86
235103_at						0.000737	-0.87
219683_at	frizzled homolog 3 (Drosophila)	FZD3	chr8p21	Hs.40735	7976	0.016085	-0.87
229428_at	CDNA FLJ40725 fis, clone TKIDN1000001, highly similar to Translocase of inner mitochondrial membrane			Hs.536158		0.013632	-0.87
1553749_at	hypothetical protein MGC33371	MGC33371	chr11q21	Hs.288304	143684	0.036429	-0.87
218158_s_at	adaptor protein containing pH domain, PTB domain and leucine zipper	APPL	chr3p21.1-p14.3	Hs.476415	26060	0.005911	-0.87
213117_at	kelch-like 9 (Drosophila)	KLHL9	chr9p22	Hs.522029	55958	0.002764	-0.87
218185_s_at	armadillo repeat containing 1	ARMC1	chr8q13.1	Hs.269542	55156	0.005674	-0.87
208358_s_at	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	UGT8	chr4q26	Hs.144197	7368	0.000459	-0.87
209574_s_at	chromosome 18 open reading frame 1	C18orf1	chr18p11.2	Hs.464697	753	0.019914	-0.87
1558103_a_at	Transmembrane 6 superfamily member 1	TM6SF1	chr15q24-q26	Hs.513094	53346	0.000428	-0.87
217717_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	YWHAH	chr20q13.1	Hs.279920	7529	0.017438	-0.87
239580_at	Homo sapiens, clone IMAGE:5302158, mRNA			Hs.22247		0.025581	-0.87
1555889_a_at	cartilage associated protein	CRTAP	chr3p22.3	Hs.517888	10491	0.022807	-0.87
235295_at	Pannexin 1	PANX1	chr11q21	Hs.503584	24145	0.008735	-0.87
226649_at	pantothenate kinase 1	PANK1	chr10q23.31	Hs.465933	53354	0.004937	-0.87
1558541_at	hypothetical protein FLJ36980	FLJ36980	chr8p22	Hs.202521	286032	0.039443	-0.88
212812_at	CDNA: FLJ22642 fis, clone HSI06970			Hs.288232		0.023514	-0.88
235465_at	hypothetical protein FLJ25477	FLJ25477	chr13q12.13	Hs.528335	219287	0.013894	-0.88
218469_at	gremlin 1 homolog, cysteine knot superfamily (Xenopus laevis)	GREM1	chr15q13-q15	Hs.40098	26585	0.034668	-0.88
225666_at	hypothetical protein FLJ14624	FLJ14624	chr13q32.3	Hs.190983	84899	0.040173	-0.88
225178_at	tetratricopeptide repeat domain 14	TTC14	chr3q26.33	Hs.43213	151613	0.017465	-0.88
210596_at						0.006356	-0.88
241698_at	chromosome 2 open reading frame 11	C2orf11	chr2q33.1	Hs.350388	130132	0.005942	-0.88
225972_at	Hypothetical protein DKFZp762C1112	DKFZp762C1112	chr8q21.3	Hs.546514	169200	0.008651	-0.88
230207_s_at	Dedicator of cytokinesis 5	DOCK5	chr8p21.2	Hs.195403	80005	0.025808	-0.88
208849_at						0.004652	-0.88
218683_at	polypyrimidine tract binding protein 2	PTBP2	chr1p22.1-p21.3	Hs.269895	58155	0.007454	-0.88
1553101_a_at	hypothetical protein FLJ20308	FLJ20308	chr17p11.2	Hs.462392	54890	0.037496	-0.88
200732_s_at	protein tyrosine phosphatase type IVA, member 1	PTP4A1	chr6q12	Hs.227777	7803	0.012034	-0.89
204036_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor	EDG2	chr9q31.3	Hs.126667	1902	0.034175	-0.89
214579_at	hypothetical protein DJ462023.2	DJ462023.2	chr1p36.12-p35.1	Hs.523442	57185	0.038578	-0.89
1558093_s_at	matrin 3	MATR3	chr5q31.2	Hs.268939	9782	0.034238	-0.89
235067_at	muskelin 1, intracellular mediator containing kelch motifs	MKLN1	chr7q32	Hs.44693	4289	0.035409	-0.89
212397_at	radixin	RDX	chr11q23	Hs.263671	5962	0.018920	-0.89
228486_at	CDW92 antigen	CDW92	chr9q31.2	Hs.494700	23446	0.009542	-0.89
1565601_at	Protocadherin 9	PCDH9	chr13q14.3-q21.1	Hs.407643	5101	0.013231	-0.89
202381_at	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	ADAM9	chr8p11.23	Hs.2442	8754	0.003418	-0.89
221310_at	fibroblast growth factor 14	FGF14	chr13q34	Hs.508616	2259	0.026219	-0.89
212095_s_at	mitochondrial tumor suppressor 1	MTUS1	chr8p22	Hs.7946	57509	0.007200	-0.89
220345_at	leucine rich repeat transmembrane neuronal 4	LRRTM4	chr2p12	Hs.285782	80059	0.003884	-0.89
218738_s_at	ring finger protein 138	RNF138	chr18q12.1	Hs.302408	51444	0.001211	-0.90
205123_s_at	transmembrane protein with EGF-like and two follistatin-like domains 1	TMEFF1	chr9q31	Hs.336224	8577	0.004895	-0.90
227585_at	ATPase family, AAA domain containing 1	ATAD1	chr10q23.31	Hs.435948	84896	0.028666	-0.90
212417_at	secretory carrier membrane protein 1	SCAMP1	chr5q13.3-q14.1	Hs.482587	9522	0.011492	-0.90
225885_at	Early endosome antigen 1, 162kD	EEA1	chr12q22	Hs.506309	8411	0.001025	-0.90
230291_s_at	Nuclear factor I/B	NFIB	chr9p24.1	Hs.370359	4781	0.018317	-0.90
222451_s_at	zinc finger, DHHC domain containing 9	ZDHHC9	chrXq26.1	Hs.193566	51114	0.008873	-0.90
225539_at	zinc finger protein 295	ZNF295	chr21q22.3	Hs.434947	49854	0.042412	-0.90
226533_at						0.010435	-0.90
224410_s_at	chromosome 7 open reading frame 2 /// chromosome 7 open reading frame 2	C7orf2	chr7q36	Hs.549190	64327	0.007296	-0.90
202393_s_at	Kruppel-like factor 10	KLF10	chr8q22.2	Hs.435001	7071	0.001307	-0.90
208703_s_at	amyloid beta (A4) precursor-like protein 2	APLP2	chr11q23-q25.11	Hs.370247	334	0.037745	-0.90
211703_s_at	beta-amyloid binding protein precursor /// beta-amyloid binding protein	BBP	chr1p31.3	Hs.276876	83941	0.013282	-0.90
1565602_at	Protocadherin 9	PCDH9	chr13q14.3-q21.1	Hs.407643	5101	0.004611	-0.90
220462_at	TGF-beta induced apoptosis protein 2	TAIP-2	chr2q24.3	Hs.470479	80034	0.041649	-0.91
242617_at	Transmembrane emp24 domain containing 8	TMED8	chr14q24.3	Hs.547416	283578	0.013864	-0.91
242019_at	LAG1 longevity assurance homolog 6 (S. cerevisiae)	LASS6	chr2q24.3	Hs.506829	253782	0.019654	-0.91
1552752_a_at	immunoglobulin superfamily, member 4D	IGSF4D	chr3p12.1	Hs.333991	253559	0.007062	-0.91
236140_at	glutamate-cysteine ligase, modifier subunit	GCLM	chr1p22.1	Hs.315562	2730	0.007716	-0.91
205618_at	proline rich Gla (G-carboxyglutamic acid) 1	PRRG1	chrXp21.1	Hs.190341	5638	0.005369	-0.91
223020_at	cisplatin resistance related protein CRR9p	CRR9	chr5pter-p15.3	Hs.444673	81037	0.042249	-0.91
224888_at	selenoprotein I	SELI	chr2p23.3	Hs.189073	85465	0.015206	-0.91
227148_at						0.044565	-0.91
224352_s_at	cofilin 2 (muscle) /// cofilin 2 (muscle)	CFL2	chr14q12	Hs.180141	1073	0.015139	-0.92
210968_s_at	reticulin 4	RTN4	chr2p16.3	Hs.429581	57142	0.026179	-0.92
241859_at						0.005137	-0.92
204364_s_at	chromosome 2 open reading frame 23	C2orf23	chr2p11.2	Hs.368884	65055	0.039150	-0.92
235017_s_at	MRNA; cDNA DKFZp564E143 (from clone DKFZp564E143)			Hs.452398		0.035370	-0.92
224949_at	golgi membrane protein SB140	SMAP-5	chr5q31.3	Hs.372050	81555	0.021344	-0.92

225571_at	Leukemia inhibitory factor receptor	LIFR	chr5p13-p12	Hs.133421	3977	0.011908	-0.92
204507_s_at	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha	PPP3R1	chr2p15	Hs.280604	5534	0.046088	-0.92
226837_at	sprouty-related, EVH1 domain containing 1	SPRED1	chr15q14	Hs.525781	161742	0.015565	-0.92
204851_s_at	doublecortin; lissencephaly, X-linked (doublecortin)	DCX	chrXq22.3-q23	Hs.34780	1641	0.046117	-0.92
203998_s_at	synaptotagmin I	SYT1	chr12cen-q21	Hs.310545	6857	0.022789	-0.93
227856_at	hypothetical protein FLJ39370	FLJ39370	chr4q25	Hs.23439	132720	0.001432	-0.93
210561_s_at	WD repeat and SOCS box-containing 1	WSB1	chr17q11.1	Hs.446017	26118	0.010997	-0.93
228483_s_at	CDNA FLJ23869 fis, clone LNG09860			Hs.522836		0.007711	-0.93
212515_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X	chrXp11.3-p11.22	Hs.380774	1654	0.040851	-0.93
212353_at	sulfatase 1	SULF1	chr8q13.2-q13.3	Hs.409602	23213	0.004417	-0.93
233882_s_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (	SEMA6D	chr15q21.1	Hs.511265	80031	0.038267	-0.93
224899_s_at	implantation-associated protein	DKFZp564	chrXq21.1	Hs.323562	84061	0.006369	-0.93
235716_at	Transformer-2 alpha	TRA2A	chr7p15.3	Hs.445652	29896	0.003592	-0.93
205501_at	CDNA FLJ25677 fis, clone TST04054			Hs.348762		0.006515	-0.93
210896_s_at	aspartate beta-hydroxylase	ASPH	chr8q12.1	Hs.332422	444	0.022271	-0.93
203100_s_at	chromodomain protein, Y-like	CDYL	chr6p25.1	Hs.269092	9425	0.006411	-0.94
1552715_a_at	leucine-rich repeat-containing G protein-coupled receptor 7	LGR7	chr4q32.1	Hs.196119	59350	0.022983	-0.94
226106_at	ring finger protein 141	RNF141	chr11p15.4	Hs.44685	50862	0.029479	-0.94
1557137_at	transmembrane protein 17	TMEM17	chr2p15	Hs.308028	200728	0.001328	-0.94
218569_s_at	kelch repeat and BTB (POZ) domain containing 4	KBTD4	chr11p11.2	Hs.440695	55709	0.021380	-0.94
1559256_at	BAI1-associated protein 1	BAIAP1	chr3p14.1	Hs.169441	9223	0.005983	-0.94
230263_s_at	dedicator of cytokinesis 5	DOCK5	chr8p21.2	Hs.195403	80005	0.028438	-0.94
202843_at	Dnaj (Hsp40) homolog, subfamily B, member 9	DNAJB9	chr7q31 14q24.2	Hs.6790	4189	0.002157	-0.94
225097_at	Homeodomain interacting protein kinase 2	HIPK2	chr7q32-q34	Hs.397465	28996	0.040874	-0.95
201986_at	thyroid hormone receptor associated protein 1	THRAP1	chr17q22-q23	Hs.282678	9969	0.027486	-0.95
202164_s_at	CCR4-NOT transcription complex, subunit 8	CNOT8	chr5q31-q33	Hs.26703	9337	0.020079	-0.95
202760_s_at	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 protein	AKAP2 ///	chr9q31-q33	Hs.259461	11217 ///	0.016443	-0.95
208811_s_at	Dnaj (Hsp40) homolog, subfamily B, member 6	DNAJB6	chr7q36.3	Hs.490745	10049	0.044717	-0.95
1552790_a_at	Translocation protein 1	TLOC1	chr3q26.2-q27	Hs.529591	7095	0.007665	-0.95
202589_at	thymidylate synthetase	TYMS	chr18p11.32	Hs.369762	7298	0.025091	-0.95
241403_at	CDC-like kinase 4	CLK4	chr5q35	Hs.406557	57396	0.002324	-0.95
224595_at	CDW92 antigen	CDW92	chr9q31.2	Hs.494700	23446	0.034426	-0.95
201096_s_at	ADP-ribosylation factor 4	ARF4	chr3p21.2-p21.1	Hs.148330	378	0.019187	-0.95
219628_at	p53 target zinc finger protein	WIG1	chr3q26.3-q27	Hs.386299	64393	0.026203	-0.96
201732_s_at	chloride channel 3	CLCN3	chr4q33	Hs.481186	1182	0.005056	-0.96
209301_at	carbonic anhydrase II	CA2	chr8q22	Hs.155097	760	0.004873	-0.96
206434_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)	SPOCK3	chr4q32.3	Hs.481133	50859	0.000557	-0.96
214785_at	vacuolar protein sorting 13A (yeast)	VPS13A	chr9q21	Hs.459790	23230	0.005874	-0.96
202137_s_at	zinc finger, MYND domain containing 11	ZMYND11	chr10p14	Hs.292265	10771	0.016855	-0.96
209966_x_at	estrogen-related receptor gamma	ESRRG	chr1q41	Hs.444225	2104	0.010270	-0.96
223775_at	hedgehog interacting protein	HHIP	chr4q28-q32	Hs.507991	64399	0.003744	-0.96
226596_x_at	Hypothetical gene supported by AK027125		chr7p22.1	Hs.552647	401307	0.004165	-0.96
222880_at	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3	chr14q43-q44	Hs.498292	10000	0.017511	-0.96
231042_s_at	Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	CAMK2D	chr4q26	Hs.144114	817	0.024197	-0.97
229083_at	Heterogeneous nuclear ribonucleoprotein A0	HNRPA0	chr5q31	Hs.96996	10949	0.002071	-0.97
231321_s_at	Phytoceramide, alkaline	PHCA	chr11q13.5	Hs.23862	55331	0.037561	-0.97
201647_s_at	scavenger receptor class B, member 2	SCARB2	chr4q21.1	Hs.349656	950	0.007246	-0.97
203041_s_at	lysosomal-associated membrane protein 2	LAMP2	chrXq24	Hs.496684	3920	0.006118	-0.97
231258_at						0.020039	-0.97
1565939_at	Hypothetical protein FLJ11193	FLJ11193	chr5p13.3	Hs.519246	55322	0.000684	-0.97
1568574_x_at	Secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lyn	SPP1	chr4q21-q25	Hs.313	6696	0.043200	-0.97
201552_at	lysosomal-associated membrane protein 1	LAMP1	chr13q34	Hs.494419	3916	0.018317	-0.97
226907_at	protein phosphatase 1, regulatory (inhibitor) subunit 14C	PPP1R14C	chr6q24.3-q25.3	Hs.486798	81706	0.040415	-0.98
217777_s_at	butyrate-induced transcript 1	HSPC121	chr15q22.2	Hs.512973	51495	0.026875	-0.98
241752_at	solute carrier family 8 (sodium/calcium exchanger), member 1	SLC8A1	chr2p23-p22	Hs.468274	6546	0.024952	-0.98
220238_s_at	kelch-like 7 (Drosophila)	KLHL7	chr7p15.3	Hs.385861	55975	0.007286	-0.98
214817_at	unc-13 homolog A (C. elegans)	UNC13A	chr19p13.11	Hs.164502	23025	0.042404	-0.98
1558373_s_at	CDNA FLJ34038 fis, clone FCBBF2005645			Hs.530150		0.040584	-0.98
202602_s_at	HIV TAT specific factor 1	HTATSF1	chrXq26.1-q27.2	Hs.204475	27336	0.026990	-0.98
203115_at	ferrochelatase (protoporphyrin)	FECH	chr18q21.3	Hs.465221	2235	0.016238	-0.98
238212_at	Clone IMAGE:501887, mRNA sequence			Hs.551985		0.044015	-0.98
231167_at	Transcribed locus			Hs.531813		0.014790	-0.99
225099_at	F-box protein 45	FBXO45	chr3q29	Hs.518526	200933	0.020553	-0.99
200745_s_at	guanine nucleotide binding protein (G protein), beta polypeptide 1	GNB1	chr13q36.33	Hs.430425	2782	0.043185	-0.99
209344_at	tropomyosin 4	TPM4	chr19p13.1	Hs.466088	7171	0.006381	-1.00
225383_at	zinc finger protein 275	ZNF275	chrXq28	Hs.348963	10838	0.003089	-1.00
206794_at	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ERBB4	chr2q33.3-q34	Hs.390729	2066	0.007129	-1.00
238487_at	Hypothetical protein LOC285831	LOC28583	chr6p21.32	Hs.550038	285831	0.045236	-1.00
226636_at	phospholipase D1, phosphatidylcholine-specific	PLD1	chr3q26	Hs.478230	5337	0.012558	-1.01
1559310_at	CDNA FLJ30875 fis, clone FEBRA2004331			Hs.493804		0.029243	-1.01
231873_at	bone morphogenetic protein receptor, type II (serine/threonine kinase)	BMPR2	chr2q33-q34	Hs.471119	659	0.010238	-1.01
223010_s_at	OClA domain containing 1	OClAD1	chr4p11	Hs.518750	54940	0.028489	-1.01
204567_s_at	ATP-binding cassette, sub-family G (WHITE), member 1	ABCG1	chr21q22.3	Hs.124649	9619	0.013915	-1.01
213069_at	HEG homolog 1 (zebrafish)	HEG	chr3q21.2	Hs.477420	57493	0.024820	-1.01

225998_at	GRB2-associated binding protein 1	GAB1	chr4q31.21	Hs.80720	2549	0.011398	-1.01
226005_at	Ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	UBE2G1	chr1q42	Hs.462035	7326	0.002729	-1.01
203354_s_at	pleckstrin and Sec7 domain containing 3	PSD3	chr8pter-p23.3	Hs.434255	23362	0.016623	-1.01
237802_at	KIAA1889 protein	KIAA1889	chr8q12.1	Hs.130197	114786	0.031360	-1.01
203527_s_at	adenomatous polyposis coli	APC	chr5q21-q22	Hs.158932	324	0.006200	-1.02
229642_at	Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	chr13q34	Hs.508738	8874	0.048250	-1.02
229713_at	CDNA FLJ13267 fis, clone OVARC1000964			Hs.57079		0.001103	-1.02
226025_at	CDNA clone IMAGE:3542720			Hs.547037		0.013739	-1.02
219750_at	hypothetical protein FLJ11155	FLJ11155	chr4q32.1	Hs.176227	55314	0.002161	-1.02
240169_at	Full length insert cDNA clone YO64F11			Hs.32118		0.017301	-1.02
203300_x_at	adaptor-related protein complex 1, sigma 2 subunit	AP1S2	chrXp22.2	Hs.121592	8905	0.003935	-1.02
222875_at	DEAH (Asp-Glu-Ala-His) box polypeptide 33	DHX33	chr17p13.2	Hs.250456	56919	0.016961	-1.03
214670_at	zinc finger with KRAB and SCAN domains 1	ZKSCAN1	chr7q21.3-q22.1	Hs.423725	7586	0.002381	-1.03
203638_s_at	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratin)	FGFR2	chr10q26	Hs.533683	2263	0.020262	-1.03
212568_s_at	dihydroliipoamide S-acetyltransferase (E2 component of pyruvate dehyd	DLAT	chr11q23.1	Hs.335551	1737	0.006903	-1.03
227289_at	hypothetical protein LOC144997	LOC144997	chr13q14.3		144997	0.025652	-1.03
223341_s_at	short coiled-coil protein	SCOC	chr4q31.1	Hs.480815	60592	0.001502	-1.04
1558279_a_at	Follicular lymphoma variant translocation 1	FVT1	chr18q21.3	Hs.74050	2531	0.011414	-1.05
230057_at	hypothetical protein LOC285178	LOC285178	chr2q35	Hs.28102	285178	0.022659	-1.05
224778_s_at	CDNA clone IMAGE:5263531, partial cds			Hs.399763		0.025283	-1.06
203758_at	cathepsin O	CTSO	chr4q31-q32	Hs.75262	1519	0.006700	-1.06
234000_s_at	butyrate-induced transcript 1	HSPC121	chr15q22.2	Hs.512973	51495	0.015322	-1.06
231898_x_at	SOX2 overlapping transcript (non-coding RNA)	SOX2OT	chr3q26.3-q27	Hs.546551	347689	0.000798	-1.06
1553194_at	neuronal growth regulator 1	NEGR1	chr1p31.1	Hs.146542	257194	0.010208	-1.06
231866_at	Leucyl/cystinyl aminopeptidase	LNPEP	chr5q15	Hs.551507	4012	0.012553	-1.06
213362_at	Protein tyrosine phosphatase, receptor type, D	PTPRD	chr9p23-p24.3	Hs.446083	5789	0.040375	-1.06
226932_at	Sarcospan (Kras oncogene-associated gene)	SSPN	chr12p11.2	Hs.183428	8082	0.021266	-1.06
201918_at	Hypothetical protein FLJ10618	FLJ10618	chr3q23	Hs.144130	55186	0.022797	-1.06
211967_at	pro-oncosis receptor inducing membrane injury gene	PORIMIN	chr11q22.1	Hs.503709	114908	0.001224	-1.07
227100_at	beta 3-glycosyltransferase-like	B3GTL	chr13q12.3	Hs.13205	145173	0.008237	-1.07
1555226_s_at	chromosome 1 open reading frame 43	C1orf43	chr1q21.2	Hs.287471	25912	0.048212	-1.07
209896_s_at	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome	PTPN11	chr12q24	Hs.506852	5781	0.026819	-1.08
213033_s_at	Nuclear factor I/B	NFIB	chr9p24.1	Hs.370359	4781	0.008588	-1.08
238985_at						0.020371	-1.08
206376_at	solute carrier family 6, member 15	SLC6A15	chr12q21.3	Hs.44424	55117	0.012499	-1.08
211547_s_at	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kD	PAFAH1B1	chr17p13.3	Hs.77318	5048	0.009241	-1.09
219594_at	ninjurin 2	NINJ2	chr12p13	Hs.504422	4815	0.027091	-1.09
230577_at						0.026248	-1.09
213110_s_at	collagen, type IV, alpha 5 (Alport syndrome)	COL4A5	chrXq22	Hs.369089	1287	0.020255	-1.10
223168_at	ras homolog gene family, member U	RHOU	chr1q42.11-q42.3	Hs.435106	58480	0.040109	-1.10
1554462_a_at	DnaJ (Hsp40) homolog, subfamily B, member 9	DNAJB9	chr7q31 14q24.2	Hs.6790	4189	0.002042	-1.10
230360_at	collomin	COLM	chr15q21.2	Hs.526441	342035	0.021472	-1.11
206135_at	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein	ST18	chr8q11.23	Hs.549092	9705	0.010533	-1.11
231193_s_at	CDNA clone IMAGE:5263531, partial cds			Hs.399763		0.017357	-1.11
200821_at	lysosomal-associated membrane protein 2	LAMP2	chrXq24	Hs.496684	3920	0.026712	-1.12
218970_s_at	cutC copper transporter homolog (E.coli)	CUTC	chr10q24.2	Hs.16606	51076	0.037952	-1.13
201485_s_at	reticulocalbin 2, EF-hand calcium binding domain	RCN2	chr15q23	Hs.79088	5955	0.034042	-1.13
222404_x_at	butyrate-induced transcript 1	HSPC121	chr15q22.2	Hs.512973	51495	0.020356	-1.13
221895_at	motile sperm domain containing 2	MOSPD2	chrXp22.2	Hs.190043	158747	0.002532	-1.14
221911_at	ets variant gene 1 /// hypothetical protein LOC22181C	ETV1 /// LOC22181C	chr7p22 /// chr7p22	Hs.22634	2115 /// 2115	0.021642	-1.14
222608_s_at	anillin, actin binding protein (scraps homolog, Drosophila)	ANLN	chr7p15-p14	Hs.62180	54443	0.003379	-1.14
205105_at	mannosidase, alpha, class 2A, member 1	MAN2A1	chr5q21-q22	Hs.432822	4124	0.031997	-1.14
223059_s_at	chromosome 10 open reading frame 45	C10orf45	chr10p13	Hs.446315	83641	0.036392	-1.15
222538_s_at	adaptor protein containing pH domain, PTB domain and leucine zipper n	APPL	chr3p21.1-p14.3	Hs.476415	26060	0.006668	-1.15
222850_s_at	hypothetical protein FLJ14281	FLJ14281	chr4q23	Hs.512743	79982	0.018627	-1.15
202747_s_at	integral membrane protein 2A	ITM2A	chrXq13.3-Xq21.2	Hs.17109	9452	0.025197	-1.15
217721_at	Septin 7	38967	chr7p14.3-p14.1	Hs.191346	989	0.044910	-1.16
212698_s_at	septin 10	38970	chr2q13	Hs.469615	151011	0.002512	-1.17
206849_at	gamma-aminobutyric acid (GABA) A receptor, gamma 2	GABRG2	chr5q31.1-q33.1	Hs.7195	2566	0.012169	-1.17
225308_s_at	TPR domain, ankyrin-repeat and coiled-coil-containing	TANC	chr2q24.2	Hs.61590	85461	0.004410	-1.18
205801_s_at	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	RASGRP3	chr2p25.1-p24.1	Hs.143674	25780	0.000040	-1.18
230135_at	CDNA FLJ42405 fis, clone ASTRO3000474			Hs.548089		0.004112	-1.19
229781_at	LOC442530		chr7	Hs.304253	442530	0.010417	-1.19
201005_at	CD9 antigen (p24)	CD9	chr12p13.3	Hs.114286	928	0.019069	-1.19
212341_at	hypothetical protein MGC21416	MGC21416	chrXq13.1	Hs.82719	286451	0.004826	-1.19
237333_at	Syncoilin, intermediate filament 1	SYNCOILIN	chr1p34.3-p33	Hs.550537	81493	0.012033	-1.20
204484_at	phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	chr1q32	Hs.497487	5287	0.009591	-1.20
216231_s_at	beta-2-microglobulin	B2M	chr15q21-q22.2	Hs.534255	567	0.004945	-1.21
1558028_x_at	HLA complex group 11	HCG11	chr6p21	Hs.272939	493812	0.005646	-1.21
221859_at	synaptotagmin XIII	SYT13	chr11p12-p11	Hs.436643	57586	0.004114	-1.21
217893_s_at	hypothetical protein FLJ12666	FLJ12666	chr1p34.3	Hs.293563	79647	0.021793	-1.22
223243_s_at	chromosome 1 open reading frame 22	C1orf22	chr1q24-q25	Hs.523811	80267	0.003994	-1.22
1558414_at	chromosome 9 open reading frame 4	C9orf4	chr9q31	Hs.347537	23732	0.008975	-1.23
1552789_at	Translocation protein 1	TLOC1	chr3q26.2-q27	Hs.529591	7095	0.008182	-1.23



209535_s_at							<b>0.012348</b>	<b>-1.24</b>
232893_at	hypothetical protein DKFZp434H2226	DKFZp434H2226	chr5p13.2	Hs.294103	92255		<b>0.027878</b>	<b>-1.24</b>
204774_at	ecotropic viral integration site 2A	EVI2A	chr17q11.2	Hs.113874	2123		<b>0.023158</b>	<b>-1.24</b>
207791_s_at	RAB1A, member RAS oncogene family	RAB1A	chr2p14	Hs.310645	5861		<b>0.029154</b>	<b>-1.24</b>
203799_at	CD302 antigen	CD302	chr2q24.2	Hs.130014	9936		<b>0.008175</b>	<b>-1.25</b>
244439_at	sprouty-related, EVH1 domain containing 1	SPRED1	chr15q14	Hs.525781	161742		<b>0.019187</b>	<b>-1.27</b>
1558972_s_at	chromosome 6 open reading frame 190	C6orf190	chr6q22.33	Hs.380210	387357		<b>0.022483</b>	<b>-1.27</b>
208925_at	chromosome 3 open reading frame 4	C3orf4	chr3p11-q11	Hs.107393	56650		<b>0.026537</b>	<b>-1.27</b>
218342_s_at	KIAA1815	KIAA1815	chr9p24	Hs.87128	79956		<b>0.004785</b>	<b>-1.28</b>
210338_s_at	heat shock 70kDa protein 8	HSPA8	chr11q24.1	Hs.180414	3312		<b>0.021407</b>	<b>-1.28</b>
1555882_at	spindlin family, member 3	SPIN3	chrXp11.1	Hs.522672	169981		<b>0.030451</b>	<b>-1.28</b>
228485_s_at	CDW92 antigen	CDW92	chr9q31.2	Hs.494700	23446		<b>0.005506</b>	<b>-1.29</b>
231911_at	KIAA1189	KIAA1189	chr2q24.1	Hs.443894	57471		<b>0.009429</b>	<b>-1.30</b>
219732_at	plasticity related gene 3	PRG-3	chr9q31.1	Hs.382683	54886		<b>0.003302</b>	<b>-1.31</b>
225961_at	kelch domain containing 5	KLHDC5	chr12p11.22	Hs.505104	57542		<b>0.017293</b>	<b>-1.32</b>
226109_at							<b>0.004032</b>	<b>-1.33</b>
209631_s_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37	chr7q31	Hs.406094	2861		<b>0.001127</b>	<b>-1.34</b>
205799_s_at	solute carrier family 3 (cystine, dibasic and neutral amino acid transport)	SLC3A1	chr2p16.3	Hs.112916	6519		<b>0.026598</b>	<b>-1.34</b>
1558971_at	chromosome 6 open reading frame 190	C6orf190	chr6q22.33	Hs.380210	387357		<b>0.008886</b>	<b>-1.35</b>
209392_at	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ENPP2	chr8q24.1	Hs.190977	5168		<b>0.001722</b>	<b>-1.35</b>
1555247_a_at	Rap guanine nucleotide exchange factor (GEF) 6	RAPGEF6	chr5q23.3		51735		<b>0.011516</b>	<b>-1.35</b>
228335_at	claudin 11 (oligodendrocyte transmembrane protein)	CLDN11	chr3q26.2-q26.3	Hs.31595	5010		<b>0.012801</b>	<b>-1.41</b>
210839_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ENPP2	chr8q24.1	Hs.190977	5168		<b>0.006850</b>	<b>-1.43</b>
214724_at	DIX domain containing 1	DIXDC1		Hs.116796	85458		<b>0.008050</b>	<b>-1.44</b>
212040_at	trans-golgi network protein 2	TGOLN2	chr2p11.2	Hs.14894	10618		<b>0.003954</b>	<b>-1.44</b>
222111_at	Hypothetical protein KIAA1164	KIAA1164	chr15q21.3	Hs.368548	54629		<b>0.003145</b>	<b>-1.45</b>
1559129_a_at	hypothetical protein LOC158257	LOC158257	chr9q22.32	Hs.213065	158257		<b>0.030619</b>	<b>-1.46</b>
241685_x_at	Transcribed locus			Hs.200938			<b>0.003678</b>	<b>-1.46</b>
232282_at	WNK lysine deficient protein kinase 3	WNK3	chrXp11.23-p11.2	Hs.92423	65267		<b>0.005867</b>	<b>-1.50</b>
204719_at	ATP-binding cassette, sub-family A (ABC1), member 8	ABCA8	chr17q24	Hs.58351	10351		<b>0.027228</b>	<b>-1.54</b>
207014_at	gamma-aminobutyric acid (GABA) A receptor, alpha 2	GABRA2	chr4p12	Hs.116250	2555		<b>0.011483</b>	<b>-1.58</b>
210198_s_at	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia)	PLP1	chrXq22	Hs.1787	5354		<b>0.010272</b>	<b>-1.59</b>
214586_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37	chr7q31	Hs.406094	2861		<b>0.004829</b>	<b>-1.65</b>
206941_x_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted	SEMA3E	chr7q21.11	Hs.528721	9723		<b>0.001244</b>	<b>-1.68</b>
228624_at	hypothetical protein FLJ11155	FLJ11155	chr4q32.1	Hs.176227	55314		<b>0.021280</b>	<b>-1.76</b>
228956_at	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	UGT8	chr4q26	Hs.144197	7368		<b>0.000562</b>	<b>-1.80</b>
203400_s_at	transferrin	TF	chr3q22.1	Hs.518267	7018		<b>0.033866</b>	<b>-1.90</b>
203348_s_at	ets variant gene 5 (ets-related molecule)	ETV5	chr3q28	Hs.43697	2119		<b>0.004449</b>	<b>-2.00</b>