

Probe	Gene name	Symbol	Location	Unigene	LocusLink	SCZ-CNT SG pval	SCZ-CNT SG ALR
211696_x_at	hemoglobin, beta /// hemoglobin, beta	HBB	chr11p15.5	Hs.523443	3043	0.035108	1.62
227697_at	suppressor of cytokine signaling 3	SOCS3	chr17q25.3	Hs.527973	9021	0.023769	1.59
209396_s_at	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	chr1q32.1	Hs.382202	1116	0.038525	1.46
36711_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF	chr22q13.1	Hs.517617	23764	0.039594	1.27
202912_at	adrenomedullin	ADM	chr11p15.4	Hs.441047	133	0.049439	1.26
207574_s_at	growth arrest and DNA-damage-inducible, beta	GADD45B	chr19p13.3	Hs.110571	4616	0.044614	1.21
212203_x_at	interferon induced transmembrane protein 3 (1-8U)	IFITM3	chr11p15.5	Hs.374650	10410	0.019347	1.18
201613_s_at	adaptor-related protein complex 1, gamma 2 subunit	AP1G2	chr14q11.2	Hs.343244	8906	0.002995	1.17
213560_at	Growth arrest and DNA-damage-inducible, beta	GADD45B	chr19p13.3	Hs.110571	4616	0.046790	1.17
202284_s_at	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A	chr6p21.2	Hs.370771	1026	0.009753	1.10
201315_x_at	interferon induced transmembrane protein 2 (1-8D)	IFITM2	chr11p15.5	Hs.174195	10581	0.027505	1.09
236448_at	unc-5 homolog A (C. elegans)	UNC5A	chr5q35.2	Hs.33191	90249	0.014266	1.09
235867_at	glutathione S-transferase M3 (brain)	GSTM3	chr1p13.3	Hs.2006	2947	0.007112	1.08
219019_at	leucine-rich repeats and death domain containing	LRDD	chr11p15.5	Hs.552597	55367	0.001621	1.07
213571_s_at	eukaryotic translation initiation factor 4E member 2	EIF4E2	chr2q37.1	Hs.292026	9470	0.006901	1.07
1553993_s_at	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	MED25	chr19q13.3	Hs.467128	81857	0.002369	1.05
226640_at	KCCR13L	LOC221955	chr7p22.1	Hs.487498	221955	0.009000	1.04
201506_at	transforming growth factor, beta-induced, 68kDa	TGFB1	chr5q31	Hs.369397	7045	0.036300	1.04
201841_s_at	heat shock 27kDa protein 1	HSPB1	chr7q11.23	Hs.520973	3315	0.000410	1.02
230757_at	FLJ44796 protein	FLJ44796	chr5q31.1	Hs.34198	401209	0.045225	1.01
91617_at	DiGeorge syndrome critical region gene 8	DGCR8	chr22q11.2	Hs.533019	54487	0.006566	1.01
217911_s_at	BCL2-associated athanogene 3	BAG3	chr10q25.2-q26.2	Hs.523309	9531	0.031914	1.01
214655_at	G protein-coupled receptor 6	GPR6	chr6q21	Hs.46332	2830	0.032945	1.00
206850_at	RAS-related on chromosome 22	RRP22	chr22q12.2	Hs.73088	10633	0.040728	0.97
205432_at	oviductal glycoprotein 1, 120kDa (mucin 9, oviductin)	OVGP1	chr1p13	Hs.1154	5016	0.007629	0.94
212723_at	phosphatidylserine receptor	PTDSR	chr17q25	Hs.514505	23210	0.010992	0.93
212556_at	scribbled homolog (Drosophila)	SCRIB	chr8q24.3	Hs.436329	23513	0.005086	0.92
226814_at	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motifs	ADAMTS9	chr3p14.3-p14.2	Hs.549184	56999	0.014068	0.92
214097_at	ribosomal protein S21	RPS21	chr20q13.3	Hs.190968	6227	0.011556	0.92
201160_s_at	cold shock domain protein A	CSDA	chr17p13.1	Hs.221889	8531	0.024100	0.92
1561306_s_at	stereocilin	STRC	chr15q15.3	Hs.550553	161497	0.016301	0.91
208982_at	Platelet/endothelial cell adhesion molecule (CD31 antigen)	PECAM1	chr17q23	Hs.514412	5175	0.001551	0.90
227984_at	Homo sapiens, clone IMAGE:5242623, mRNA, partial cds			Hs.371980		0.021200	0.90
214022_s_at						0.043149	0.90
211964_at	collagen, type IV, alpha 2	COL4A2	chr13q34	Hs.508716	1284	0.010290	0.90
201601_x_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	chr11p15.5	Hs.458414	8519	0.007109	0.90
210794_s_at	maternally expressed 3	MEG3	chr14q32	Hs.525589	55384	0.008982	0.89
236045_x_at	LOC441801		chr17p13.3	Hs.113418	441801	0.046585	0.89
201590_x_at	annexin A2	ANXA2	chr15q21-q22	Hs.511605	302	0.028797	0.87
210427_x_at	annexin A2	ANXA2	chr15q21-q22	Hs.511605	302	0.020751	0.87
1569872_a_at	Homo sapiens, clone IMAGE:5246470, mRNA /// Homo sapiens, clone IMAGE:5242623, mRNA, partial cds			Hs.371980 /// Hs.54952		0.039127	0.87
231392_at	Hypothetical protein BC008326	LOC89944	chr11q25	Hs.436178	89944	0.008091	0.86
204326_x_at	metallothionein 1X	MT1X	chr16q13	Hs.374950	4501	0.044621	0.86
242268_at	CUG triplet repeat, RNA binding protein 2	CUGBP2	chr10p13	Hs.309288	10659	0.017305	0.86
223895_s_at	epsin 3	EPN3	chr17q21.33	Hs.165904	55040	0.013197	0.86
204231_s_at	fatty acid amide hydrolase	FAAH	chr1p35-p34	Hs.528334	2166	0.043702	0.86
216950_s_at	Fc fragment of IgG, high affinity Ia, receptor (CD64)	FCGR1A	chr1q21.2-q21.3	Hs.77424	2209	0.034751	0.85
226679_at	solute carrier family 26, member 11	SLC26A11	chr17q25.3	Hs.4866	284129	0.010541	0.85
202039_at	TGFB1-induced anti-apoptotic factor 1 /// myosin XVIIIa	TIAF1 /// MYO18A	chr17q11.2	Hs.462589	399687 ///	0.008373	0.85
217250_s_at	chromodomain helicase DNA binding protein 5	CHD5	chr1p36.31	Hs.522898	26038	0.006974	0.84
64474_g_at	DiGeorge syndrome critical region gene 8	DGCR8	chr22q11.2	Hs.533019	54487	0.000163	0.84
235205_at	similar to solute carrier family 16 (monocarboxylic acid transporters), member 1	LOC346887	chr8q23.1	Hs.127286	346887	0.002054	0.84
209191_at	tubulin, beta 6	TUBB6	chr18p11.21	Hs.193491	84617	0.027490	0.83
221009_s_at	angiopoietin-like 4	ANGPTL4	chr19p13.3	Hs.9613	51129	0.048483	0.83
219911_s_at	solute carrier organic anion transporter family, member 4A1	SLCO4A1	chr20q13.33	Hs.235782	28231	0.030355	0.83
237870_at	hypothetical protein LOC285771	LOC285771	chr6p25.2	Hs.145597	285771	0.041068	0.83
237048_at	Homo sapiens, clone IMAGE:4797878, mRNA, partial cds			Hs.547831		0.008461	0.83
223316_at	coiled-coil domain containing 3	CCDC3	chr10p13	Hs.498720	83643	0.001474	0.82
201221_s_at	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	SNRP70	chr19q13.3	Hs.467097	6625	0.002171	0.82
33132_at	cleavage and polyadenylation specific factor 1, 160kDa	CPSF1	chr8q24.23	Hs.493202	29894	0.004044	0.82
1560060_s_at	vacuolar protein sorting 37C (yeast)	VPS37C	chr11q12.2	Hs.523715	55048	0.023378	0.82
203973_s_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	chr8p11.2-p11.1	Hs.440829	1052	0.001652	0.81
213900_at	chromosome 9 open reading frame 61	C9orf61	chr9q13-q21	Hs.118003	9413	0.039741	0.81
230417_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyl transferase 1	GALNT1	chr14q24.1	Hs.21035	57452	0.003454	0.81
213526_s_at	presenilin enhancer 2 homolog (C. elegans) /// protein F25965	PSENEN ///	chr19q13.12 ///	Hs.534465	55851 ///	0.036517	0.80
224864_at	steroid receptor RNA activator 1	SRA1	chr5q31.3	Hs.32587	10011	0.017098	0.80
59697_at	RAB15, member RAS oncogene family	RAB15	chr14q23.3	Hs.512492	376267	0.018906	0.79
223950_s_at	FLYWCH-type zinc finger 1	FLYWCH1	chr16p13.3	Hs.459715	84256	0.036740	0.79
224447_s_at	chromosome 17 open reading frame 37 /// chromosome 17 open reading frame 37	C17orf37	chr17q12	Hs.333526	84299	0.000864	0.79
226200_at	valyl-tRNA synthetase 2-like	VARS2L		Hs.102910	57176	0.007180	0.79
201695_s_at	nucleoside phosphorylase	NP	chr14q13.1	Hs.75514	4860	0.006782	0.79
218148_at	hypothetical protein FLJ13111	FLJ13111	chr16q22.1	Hs.288382	80152	0.041286	0.79
201680_x_at	arsenate resistance protein ARS2	ARS2	chr7q21	Hs.111801	51593	0.004394	0.79

241035_s_at	CDNA clone IMAGE:4814828, partial cds			Hs.535810			0.049405	0.79
200986_at	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member	SERPING1	chr11q12-q13.1	Hs.384598	710		0.048110	0.79
213485_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	ABCC10	chr6p21.1	Hs.55879	89845		0.049462	0.78
202756_s_at	glypican 1	GPC1	chr2q35-q37	Hs.328232	2817		0.034910	0.78
231478_at	Transcribed locus, strongly similar to NP_000914.1 phosphodiesterase 4C, cAMP-specific (phosphodie			Hs.132584			0.001467	0.78
35666_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted	SEMA3F	chr3p21.3	Hs.32981	6405		0.011114	0.78
1556776_a_at	Zinc finger protein 426	ZNF426	chr19p13.2	Hs.324978	79088		0.043149	0.77
221538_s_at	plexin A1	PLXNA1	chr3q21.3	Hs.432329	5361		0.019334	0.77
203938_s_at	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 1	TAF1C	chr16q24	Hs.153022	9013		0.003640	0.77
228532_at	hypothetical protein MGC24133	MGC24133	chr1p13.2	Hs.288010	128346		0.025756	0.77
228918_at	Solute carrier family 43, member 2	SLC43A2	chr17p13.3	Hs.160550	124935		0.035260	0.77
230418_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyl	GALNTL1	chr14q24.1	Hs.21035	57452		0.004051	0.77
213870_at	collagen, type XI, alpha 2	COL11A2	chr6p21.3	Hs.390171	1302		0.013513	0.77
225899_x_at	hypothetical protein LOC284701 /// hypothetical gene supported by AK1	LOC284701	chr1p36.33 /// ch	Hs.546654	284701 ///		0.024446	0.76
37254_at	zinc finger protein 133 (clone pHZ-13)	ZNF133	chr20p11.23-20p	Hs.472221	7692		0.003661	0.76
203385_at	diacylglycerol kinase, alpha 80kDa	DGKA	chr12q13.3	Hs.524488	1606		0.037461	0.76
224186_s_at	ring finger protein 123	RNF123	chr3p24.3	Hs.551556	63891		0.039047	0.76
237783_at	PLAC8-like 1	PLAC8L1	chr5q32	Hs.162369	153770		0.014717	0.76
227131_at	mitogen-activated protein kinase kinase kinase 3	MAP3K3	chr17q23.3	Hs.29282	4215		0.004176	0.75
1555958_at	cartilage acidic protein 1	CRTAC1	chr10q22	Hs.500741	55118		0.027410	0.75
224162_s_at	F-box protein 31	FBXO31	chr16q24.2	Hs.549198	79791		0.001237	0.75
242931_at	Transcribed locus			Hs.175048			0.045834	0.75
205741_s_at	dystrobrevin, alpha	DTNA	chr18q12	Hs.58919	1837		0.015788	0.75
219627_at	hypothetical protein FLJ12700	FLJ12700	chr7q36.1	Hs.520785	79970		0.033508	0.74
212735_at	KIAA0226	KIAA0226	chr3q29	Hs.478868	9711		0.005899	0.74
208335_s_at	Duffy blood group	FY	chr1q21-q22	Hs.153381	2532		0.014185	0.74
227896_at	BRCA2 and CDKN1A interacting protein	BCCIP	chr10q26.1	Hs.370292	56647		0.000912	0.73
214096_s_at	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	chr12q12-q14	Hs.75069	6472		0.010960	0.73
209785_s_at	phospholipase A2, group IVC (cytosolic, calcium-independent)	PLA2G4C	chr19q13.3	Hs.18858	8605		0.012120	0.73
210069_at	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	CHKB /// C	chr22q13.33	Hs.439777	1120 /// 1		0.028615	0.73
213178_s_at	mitogen-activated protein kinase 8 interacting protein 3	MAPK8IP3	chr16p13.3	Hs.207763	23162		0.011718	0.73
228111_s_at	heat shock regulated 1	XLHRSF-1	chr3p21.31	Hs.9740	25981		0.005760	0.73
205918_at	solute carrier family 4, anion exchanger, member 3	SLC4A3	chr2q36	Hs.1176	6508		0.011747	0.73
1555363_s_at	hypothetical protein MGC39821	MGC39821	chr19p13.11	Hs.351906	284440		0.044671	0.72
209909_s_at	transforming growth factor, beta 2	TGFbeta 2	chr1q41	Hs.133379	7042		0.023798	0.72
216960_s_at	zinc finger protein 133 (clone pHZ-13)	ZNF133	chr20p11.23-20p	Hs.472221	7692		0.014483	0.72
1556464_a_at	hypothetical protein LOC257407	LOC257407	chr2q37.1	Hs.526596	257407		0.009418	0.72
240048_at	Stereocilin	STRC	chr15q15.3	Hs.550553	161497		0.021064	0.72
202953_at	complement component 1, q subcomponent, beta polypeptide	C10B	chr1p36.3-p34.1	Hs.8986	713		0.045149	0.72
209467_s_at	MAP kinase interacting serine/threonine kinase 1	MKNK1	chr1p33	Hs.371594	8569		0.000111	0.72
38157_at	dom-3 homolog Z (C. elegans)	DOM3Z	chr6p21.3	Hs.153299	1797		0.011530	0.71
220027_s_at	Ras interacting protein 1	RASIP1	chr19p13.33	Hs.233955	54922		0.033306	0.71
223843_at	scavenger receptor class A, member 3	SCARA3	chr8p21	Hs.128856	51435		0.009761	0.71
225596_at	kinesin-like 8	KNSL8	chr6p21.1	Hs.408062	89953		0.023026	0.70
214486_x_at	CASP8 and FADD-like apoptosis regulator	CFLAR	chr2q33-q34	Hs.390736	8837		0.021237	0.70
201186_at	low density lipoprotein receptor-related protein associated protein 1	LRPAP1	chr4p16.3	Hs.533136	4043		0.026724	0.70
200710_at	acyl-Coenzyme A dehydrogenase, very long chain	ACADVL	chr17p13-p11	Hs.437178	37		0.012119	0.70
213946_s_at	KIAA0657 protein	KIAA0657	chr2q35	Hs.526594	23363		0.007247	0.70
235964_x_at	SAM domain and HD domain 1	SAMHD1	chr20pter-q12	Hs.472630	25939		0.012588	0.70
227543_at	AYP1 protein	AYP1	chr1q13.1	Hs.397010	84153		0.001214	0.70
225067_at	unc-51-like kinase 3 (C. elegans)	ULK3	chr15q24.1	Hs.513034	25989		0.002394	0.70
244113_at	Transcribed locus			Hs.436567			0.015718	0.69
229100_s_at	translocase of inner mitochondrial membrane 22 homolog (yeast)	TIMM22	chr17p13	Hs.87595	29928		0.025593	0.69
243818_at	Surfactant associated protein F mRNA, partial sequence, mRNA sequence			Hs.31562			0.045689	0.69
238364_x_at	GLI-Kruppel family member GLI4	GLI4	chr8q24.3	Hs.400533	2738		0.011344	0.69
50965_at	RAB26, member RAS oncogene family	RAB26	chr16p13.3	Hs.3797	25837		0.008853	0.69
225306_s_at	solute carrier family 25, member 29	SLC25A29	chr14q32.2	Hs.497598	123096		0.015357	0.69
218205_s_at	MAP kinase interacting serine/threonine kinase 2	MKNK2	chr19p13.3	Hs.515032	2872		0.023387	0.69
203430_at	heme binding protein 2	HEBP2	chr6q24	Hs.486589	23593		0.016628	0.69
205493_s_at	dihydropyrimidinase-like 4	DPYSL4	chr10q26	Hs.100058	10570		0.006240	0.69
222047_s_at	arsenate resistance protein ARS2	ARS2	chr7q21	Hs.111801	51593		0.007634	0.68
236070_at	similar to Retinol dehydrogenase 12	LOC388963	chr2p13.1	Hs.445377	388963		0.013774	0.68
215147_at	CUG triplet repeat, RNA binding protein 2	CUGBP2	chr10p13	Hs.309288	10659		0.027239	0.68
217973_at	dicarbonyl/L-xylulose reductase	DCXR	chr17q25.3	Hs.9857	51181		0.021451	0.68
218103_at	FtsJ homolog 3 (E. coli)	FTSJ3	chr17q23	Hs.463785	117246		0.030629	0.68
203119_at	hypothetical protein MGC2574	MGC2574	chr11q12.2	Hs.4253	79080		0.013058	0.68
221647_s_at	likely ortholog of mouse synembryn	RIC8	chr11p15.5	Hs.19306	60626		0.004798	0.68
221645_s_at	zinc finger protein 83 (HPF1)	ZNF83	chr19q13.3	Hs.467210	55769		0.036978	0.68
235529_x_at	SAM domain and HD domain 1	SAMHD1	chr20pter-q12	Hs.472630	25939		0.018115	0.68
228177_at	CREB binding protein (Rubinstein-Taybi syndrome)	CREBBP	chr16p13.3	Hs.459759	1387		0.019435	0.68
204294_at	aminomethyltransferase (glycine cleavage system protein T)	AMT	chr3p21.2-p21.1	Hs.102	275		0.031621	0.68
203468_at	cyclin-dependent kinase (CDC-like) 10	CDK10	chr16q24	Hs.77313	8558		0.019397	0.67
203911_at	RAP1, GTPase activating protein 1	RAP1GA1	chr1p36.1-p35	Hs.148178	5909		0.046967	0.67
210247_at	synapsin II	SYN2	chr3p25	Hs.445503	6854		0.006844	0.67

225868_at	tripartite motif-containing 47	TRIM47		Hs.293660	91107	0.008911	0.67
230932_at	Transcribed locus			Hs.8038		0.012802	0.67
220661_s_at	hypothetical protein FLJ20531	FLJ20531	chr1q44	Hs.377705	55657	0.004482	0.67
210672_s_at	chromosome 16 open reading frame 35	C16orf35	chr16p13.3	Hs.196999	8131	0.010077	0.67
231171_at	Transcribed locus			Hs.97104		0.016592	0.67
214246_x_at	missshapen-like kinase 1 (zebrafish)	MINK1	chr17p13.2	Hs.443417	50488	0.023888	0.67
207992_s_at	adenosine monophosphate deaminase (isoform E)	AMPD3	chr11p15	Hs.501890	272	0.027470	0.67
219562_at	RAB26, member RAS oncogene family	RAB26	chr16p13.3	Hs.3797	25837	0.011124	0.67
221820_s_at	MYST histone acetyltransferase 1	MYST1	chr16p11.2	Hs.533803	84148	0.017207	0.67
221867_at	Nedd4 binding protein 1	N4BP1	chr16q12.1	Hs.511839	9683	0.036914	0.67
1559946_s_at	RuvB-like 2 (E. coli)	RUVBL2	chr19q13.3	Hs.515846	10856	0.013694	0.67
37860_at	zinc finger protein 337	ZNF337	chr20p11.21	Hs.213735	26152	0.024961	0.67
227325_at	hypothetical protein LOC255783	LOC255783	chr19q13.33	Hs.128690	255783	0.040597	0.66
214961_at	KIAA0774	KIAA0774	chr13q12.3	Hs.507630	23281	0.041798	0.66
223467_at	RAS, dexamethasone-induced 1	RASD1	chr17p11.2	Hs.25829	51655	0.023386	0.66
216336_x_at	Metallothionein 1K	MT1K	chr16q13	Hs.188518	4499	0.048381	0.66
219155_at	phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	chr17q24.2	Hs.549130	26207	0.045039	0.66
227051_at	Homo sapiens, clone IMAGE:4393354, mRNA			Hs.43047		0.022130	0.66
206204_at	growth factor receptor-bound protein 14	GRB14	chr2q22-q24	Hs.411881	2888	0.018319	0.65
238054_at	ADP-ribosylhydrolase like 1	ADPRHL1	chr13q34	Hs.98669	113622	0.017676	0.65
223983_s_at	chromosome 19 open reading frame 12	C19orf12	chr19q12	Hs.529094	83636	0.002492	0.65
209179_s_at	leukocyte receptor cluster (LRC) member 4	LENG4	chr19q13.4	Hs.467279	79143	0.001103	0.65
200840_at	lysyl-tRNA synthetase	KARS	chr16q23-q24	Hs.3100	3735	0.036188	0.65
212559_at	protein kinase, cAMP-dependent, regulatory, type I, beta	PRKAR1B	chr7pter-p22	Hs.534340	5575	0.029343	0.65
231400_s_at	Translocase of inner mitochondrial membrane 22 homolog (yeast)	TIMM22	chr17p13	Hs.87595	29928	0.043161	0.65
230075_at	RAB39B, member RAS oncogene family	RAB39B	chrXq28	Hs.24970	116442	0.034099	0.65
203718_at	neuropathy target esterase	NTE	chr19p13.3-p13.2	Hs.511760	10908	0.019965	0.65
222240_s_at	myo-inositol 1-phosphate synthase A1	ISYNA1	chr19p13.11	Hs.405873	51477	0.028284	0.65
224735_at	cytochrome b, ascorbate dependent 3	CYBASC3	chr11q12.2	Hs.22546	220002	0.005958	0.65
218650_at	DiGeorge syndrome critical region gene 8	DGCR8	chr22q11.2	Hs.533019	54487	0.008720	0.65
218175_at	limkain beta 2	FLJ22471	chr12q24.31	Hs.114111	80212	0.024967	0.65
34868_at	Est1p-like protein B	EST1B	chr1q21.2	Hs.516837	23381	0.012135	0.64
212360_at	adenosine monophosphate deaminase 2 (isoform L)	AMPD2	chr1p13.3	Hs.82927	271	0.027247	0.64
213273_at	odz, odd Oz/ten-m homolog 4 (Drosophila)	ODZ4	chr11q14.1	Hs.213087	26011	0.010804	0.64
40569_at	zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	ZNF42	chr19q13.2-q13.4	Hs.399810	7593	0.004059	0.64
227618_at	TPT1-like protein	FLJ44635	chrXq13.1	Hs.496303	392490	0.026998	0.64
209522_s_at	carnitine acetyltransferase	CRAT	chr9q34.1	Hs.12068	1384	0.031332	0.64
231118_at	ankyrin repeat domain 35	ANKRD35	chr1q21.1	Hs.133081	148741	0.046583	0.64
226610_at	proline rich 6	PRR6	chr17p11.2	Hs.433422	201161	0.012359	0.64
208630_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase	HADHA	chr2p23	Hs.516032	3030	0.036531	0.63
220331_at	cytochrome P450, family 46, subfamily A, polypeptide 1	CYP46A1	chr14q32.1	Hs.25121	10858	0.032352	0.63
229086_at	hypothetical protein BC007899	LOC148898	chr1p36.12	Hs.61884	148898	0.031211	0.63
202255_s_at	signal-induced proliferation-associated 1 like 1	SIPA1L1	chr14q24.2	Hs.208846	26037	0.024649	0.63
222905_s_at	hypothetical protein FLJ10922	FLJ10922	chr19q13.32	Hs.351335	55260	0.013978	0.63
203068_at	kelch-like 21 (Drosophila)	KLHL21	chr1p36.31	Hs.7764	9903	0.000590	0.63
221657_s_at	ankyrin repeat and SOCS box-containing 6	ASB6		Hs.125037	140459	0.009667	0.63
1556938_a_at	CDNA FLJ38433 fis, clone FEBRA2014578			Hs.143746		0.038508	0.63
202440_s_at	suppression of tumorigenicity 5	ST5	chr11p15	Hs.117715	6764	0.010201	0.63
212359_s_at	KIAA0913	KIAA0913	chr10q22.2	Hs.65135	23053	0.009849	0.63
232792_at	ring finger protein 36	RNF36	chr15q14	Hs.169810	140691	0.009628	0.63
57539_at	zinc finger, CCH-type with G patch domain	ZGPAT	chr20q13.3	Hs.11900	84619	0.035192	0.63
204336_s_at	regulator of G-protein signalling 19	RGS19	chr20q13.3	Hs.422336	10287	0.032595	0.63
227129_x_at	hypothetical protein LOC284701 /// hypothetical gene supported by AK1	LOC284701	chr1p36.33 /// ch	Hs.546653	284701 ///	0.020602	0.63
224472_x_at	calcium binding protein Cab45 precursor /// calcium binding protein Cab45	Cab45	chr1p36.33	Hs.42806	51150	0.014246	0.63
209516_at	SMYD family member 5	SMYD5	chr2p13.2	Hs.516095	10322	0.030164	0.63
215235_at	Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	SPTAN1	chr9q33-q34	Hs.372331	6709	0.040879	0.63
227207_x_at	zinc finger protein 213	ZNF213	chr16p13.3	Hs.115284	7760	0.010313	0.62
212674_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	DHX30	chr3p21.31	Hs.517948	22907	0.008292	0.62
213620_s_at						0.049552	0.62
226072_at	fucokinase	FUK	chr16q22.1	Hs.7907	197258	0.007075	0.62
233571_x_at	chromosome 20 open reading frame 149	C20orf149	chr20q13.33	Hs.79625	79144	0.047274	0.62
229867_at	BTB (POZ) domain containing 9	BTBD9	chr6p21	Hs.116233	114781	0.017748	0.62
214511_x_at						0.041274	0.62
215280_s_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), inter	PPFIA3	chr19q13.33	Hs.413748	8541	0.039859	0.62
235420_at	hyaluronan and proteoglycan link protein 4	HAPLN4	chr19p13.1	Hs.367829	404037	0.005621	0.62
210142_x_at	flotillin 1	FLOT1	chr6p21.3	Hs.179986	10211	0.006780	0.62
45526_g_at	hypothetical protein FLJ14154	FLJ14154	chr16p13.3	Hs.513296	79903	0.009637	0.62
218631_at	arginine vasopressin-induced 1	AVP11	chr10q24.2	Hs.23918	60370	0.034818	0.61
218697_at	NCK interacting protein with SH3 domain	NCKIPSD	chr3p21	Hs.102929	51517	0.023000	0.61
210336_x_at	zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	ZNF42	chr19q13.2-q13.4	Hs.399810	7593	0.003071	0.61
201851_at	SH3-domain GRB2-like 1	SH3GL1	chr19p13.3	Hs.97616	6455	0.024574	0.61
229310_at	kelch repeat and BTB (POZ) domain containing 9	KBTBD9	chr2p24.1	Hs.130593	114818	0.035858	0.61
205056_s_at	gene rich cluster, A gene	GRCA	chr12p13	Hs.418105	27239	0.006912	0.61
36030_at	HOM-TES-103 tumor antigen-like	HOM-TES-1	chr12p13.3	Hs.15243	25900	0.016186	0.61

33760_at	peroxisomal biogenesis factor 14	PEX14	chr1p36.22	Hs.149983	5195	0.017942	0.61
201743_at	CD14 antigen /// CD14 antigen	CD14	chr5q22-q32 5q3	Hs.163867	929	0.032139	0.61
1558412_at	hypothetical protein LOC113230	LOC113230	chr19p13.12	Hs.372775	113230	0.021854	0.61
239064_at	CDNA FLJ36582 fis, clone TRACH2013081			Hs.182514		0.024654	0.61
37462_i_at	splicing factor 3a, subunit 2, 66kDa	SF3A2	chr19p13.3-p13.2	Hs.115232	8175	0.033547	0.61
227308_x_at	latent transforming growth factor beta binding protein 3	LTBP3	chr11q12	Hs.289019	4054	0.003061	0.61
225874_at	LOC124402	LOC124402	chr16p13.3	Hs.513313	124402	0.033844	0.61
204169_at	IMP (inosine monophosphate) dehydrogenase 1	IMPDH1	chr7q31.3-q32	Hs.534808	3614	0.027638	0.61
217968_at	tumor suppressing subtransferable candidate 1	TSSC1	chr2p25.2	Hs.4992	7260	0.046970	0.60
221767_x_at	high density lipoprotein binding protein (vigilin)	HDLBP	chr2q37	Hs.471851	3069	0.023349	0.60
231553_s_at	Microtubule associated monooxygenase, calponin and LIM domain containi	MICAL3	chr22q11.21	Hs.528024	57553	0.030928	0.60
233238_s_at	CDNA FLJ10720 fis, clone NT2RP3001116			Hs.549665		0.010415	0.60
227337_at	ankyrin repeat domain 37	ANKRD37	chr4q35.1	Hs.508154	353322	0.030165	0.60
219165_at	PDZ and LIM domain 2 (mystique)	PDLIM2	chr8p21.2	Hs.550527	64236	0.009323	0.60
78495_at	hypothetical protein DKFZp762P2111	DKFZp762P2111	chr7q36.1		55537	0.042627	0.60
232794_at	Hypothetical protein LOC153682	LOC153682	chr5p13.1	Hs.165175	153682	0.026904	0.60
217231_s_at	microtubule associated serine/threonine kinase 1	MAST1	chr19p13.2	Hs.227489	22983	0.027843	0.60
214035_x_at	LOC399491 protein	LOC399491	chr16p13.1		399491	0.010017	0.60
217795_s_at	transmembrane protein 43	TMEM43	chr3p25.1	Hs.517817	79188	0.007279	0.59
209295_at	tumor necrosis factor receptor superfamily, member 10b	TNFRSF10B	chr8p22-p21	Hs.521456	8795	0.016815	0.59
1553612_at						0.041493	0.59
221810_at	RAB15, member RAS oncogene family	RAB15	chr14q23.3	Hs.512492	376267	0.025806	0.59
219188_s_at	LRP16 protein	LRP16	chr11q11	Hs.502814	28992	0.009000	0.59
221708_s_at	smooth muscle cell associated protein-1 /// smooth muscle cell associat	SMAP-1	chr15q26.1	Hs.389461	55898	0.010038	0.59
228124_at	chromosome 20 open reading frame 22	C20orf22	chr20p11.21	Hs.441550	26090	0.018353	0.59
236677_at	neuroglobin	NGB	chr14q24	Hs.274363	58157	0.044436	0.59
222250_s_at	DKFZP434B168 protein	DKFZP434B168	chr1p36.13-q42.3	Hs.369285	25896	0.031361	0.59
226415_at	KIAA1576 protein	KIAA1576	chr16q23.1	Hs.461405	57687	0.005909	0.59
208749_x_at	flotillin 1	FLOT1	chr6p21.3	Hs.179986	10211	0.004379	0.59
224505_s_at	phospholipase C, delta 4 /// phospholipase C, delta 4	PLCD4	chr2q35	Hs.549218	84812	0.013444	0.59
207618_s_at	BCS1-like (yeast)	BCS1L	chr2q33	Hs.471401	617	0.047004	0.59
213191_at	TIR domain containing adaptor inducing interferon-beta	TRIF	chr19p13.3	Hs.29344	148022	0.010253	0.59
238594_x_at	Dual specificity phosphatase 8	DUSP8	chr11p15.5	Hs.41688	1850	0.019954	0.59
206583_at	zinc finger protein 673	ZNF673	chrXp11.3	Hs.444269	55634	0.002318	0.59
226043_at	G-protein signalling modulator 1 (AGS3-like, C. elegans)	GPSM1	chr9q34.3	Hs.239370	26086	0.017787	0.59
228971_at						0.038981	0.59
36129_at	RUN and TBC1 domain containing 1	RUTBC1	chr17p13.3	Hs.513861	9905	0.010976	0.58
232113_at	Hypothetical gene supported by BX647608		chr11q24.1	Hs.411391	399959	0.036249	0.58
230864_at	hypothetical protein MGC42105	MGC42105	chr5p12	Hs.25845	167359	0.031121	0.58
203117_s_at	ubiquitin specific protease 52	USP52	chr12q13.2-q13.3	Hs.273397	9924	0.039026	0.58
243209_at	potassium voltage-gated channel, KQT-like subfamily, member 4	KCNQ4	chr1p34	Hs.473058	9132	0.028960	0.58
209429_x_at	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	EIF2B4	chr2p23.3	Hs.169474	8890	0.034292	0.58
213088_s_at	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9	chr10q22.2	Hs.523037	23234	0.021036	0.58
242972_at	CDNA FLJ42357 fis, clone UTERU2022773			Hs.547723		0.035324	0.58
225598_at	KIAA1126 protein	KIAA1126	chr8q24.3	Hs.372492	57210	0.026984	0.58
209895_at	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome	PTPN11	chr12q24	Hs.506852	5781	0.031578	-0.58
221268_s_at	sphingosine-1-phosphate phosphatase 1 /// sphingosine-1-phosphate ph	SGPP1	chr14q23.2	Hs.24678	81537	0.012990	-0.58
218191_s_at	chromosome 6 open reading frame 209	C6orf209	chr6q13	Hs.271643	55788	0.018143	-0.59
237983_at						0.014164	-0.59
203883_s_at	RAB11 family interacting protein 2 (class I)	RAB11FIP2	chr10q26.11	Hs.173656	22841	0.034932	-0.59
201830_s_at	neuroepithelial cell transforming gene 1	NET1	chr10p15	Hs.25155	10276	0.028566	-0.59
206233_at	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	B4GALT6	chr18q11	Hs.464848	9331	0.022823	-0.59
227624_at	KIAA1546 protein	KIAA1546	chr4q24	Hs.531250	57667	0.034764	-0.59
243401_at	Formin-like 2	FMNL2	chr2q23.3	Hs.149566	114793	0.010828	-0.59
205523_at	hyaluronan and proteoglycan link protein 1	HAPLN1	chr5q14.3	Hs.2799	1404	0.040638	-0.60
235164_at	zinc finger protein 25 (KOX 19)	ZNF25	chr10p11.21	Hs.499429	219749	0.034156	-0.60
223943_s_at						0.025556	-0.60
203100_s_at	chromodomain protein, Y-like	CDYL	chr6p25.1	Hs.269092	9425	0.037659	-0.60
223204_at	hypothetical protein DKFZp434L142	DKFZp434L142	chr4q32.1	Hs.323583	51313	0.045595	-0.60
217717_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pro	YWHAZ	chr20q13.1	Hs.279920	7529	0.044820	-0.60
206941_x_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted	SEMA3E	chr7q21.11	Hs.528721	9723	0.024731	-0.60
241407_at	CDNA FLJ11682 fis, clone HEMBA1004880			Hs.191828		0.015549	-0.60
212908_at	KIAA0962 protein	KIAA0962	chr1p36.1	Hs.549123	23341	0.045626	-0.60
208811_s_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAB6	chr7q36.3	Hs.490745	10049	0.037363	-0.61
215073_s_at	nuclear receptor subfamily 2, group F, member 2	NR2F2	chr15q26	Hs.347991	7026	0.030823	-0.61
212417_at	secretory carrier membrane protein 1	SCAMP1	chr5q13.3-q14.1	Hs.482587	9522	0.024075	-0.61
200638_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pro	YWHAZ	chr8q23.1	Hs.492407	7534	0.043445	-0.61
224786_at	short coiled-coil protein	SCOC	chr4q31.1	Hs.480815	60592	0.027179	-0.61
202206_at	ADP-ribosylation factor-like 7	ARL7	chr2q37.1	Hs.111554	10123	0.029295	-0.61
1552306_at	asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltra	ALG10	chr12p11.1	Hs.102971	84920	0.010242	-0.61
212262_at	quaking homolog, KH domain RNA binding (mouse)	QKI	chr6q26-27	Hs.510324	9444	0.016300	-0.61
212306_at	cytoplasmic linker associated protein 2	CLASP2	chr3p23	Hs.108614	23122	0.010693	-0.62
217322_x_at						0.022654	-0.62
221428_s_at	transducin (beta)-like 1X-linked receptor 1 /// transducin (beta)-like 1X-l	TBL1XR1	chr3q26.32	Hs.438970	79718	0.041726	-0.62



202919_at	preimplantation protein 3	PREI3	chr2q33.1	Hs.205173	25843		0.016497	-0.62
228214_at	Transcribed locus			Hs.34145			0.014167	-0.63
235757_at	Chromosome 10 open reading frame 18	C10orf18	chr10p15.1	Hs.432548	54906		0.016807	-0.63
229083_at	Heterogeneous nuclear ribonucleoprotein A0	HNRPA0	chr5q31	Hs.96996	10949		0.045030	-0.63
206376_at	solute carrier family 6, member 15	SLC6A15	chr12q21.3	Hs.44424	55117		0.045481	-0.63
211703_s_at	beta-amyloid binding protein precursor /// beta-amyloid binding protein	BBP	chr1p31.3	Hs.276876	83941		0.021537	-0.64
224581_s_at	Nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	NUCKS	chr1q32.1	Hs.213061	64710		0.019272	-0.64
232512_at							0.015085	-0.64
203998_s_at	synaptotagmin I	SYT1	chr12cen-q21	Hs.310545	6857		0.046172	-0.64
200607_s_at	RAD21 homolog (S. pombe)	RAD21	chr8q24	Hs.81848	5885		0.046834	-0.64
209071_s_at	regulator of G-protein signalling 5	RG55	chr1q23.1	Hs.24950	8490		0.000981	-0.64
235067_at	muskelin 1, intracellular mediator containing kelch motifs	MKLN1	chr7q32	Hs.44693	4289		0.034494	-0.64
225198_at	VAMP (vesicle-associated membrane protein)-associated protein A, 33kD	VAPA	chr18p11.22	Hs.165195	9218		0.046970	-0.64
204011_at	sprouty homolog 2 (Drosophila)	SPRY2	chr13q31.1	Hs.18676	10253		0.021518	-0.64
215303_at	Clones 24632 and 24634 mRNA sequence			Hs.129997			0.030348	-0.65
225821_s_at	KIAA1327 protein	KIAA1327	chr4p16.1	Hs.106204	57219		0.000511	-0.65
235450_at	F-box and leucine-rich repeat protein 4	FBXL4	chr6q16.1-q16.3	Hs.536850	26235		0.018636	-0.65
201089_s_at	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2	ATP6V1B2	chr8p22-p21	Hs.295917	526		0.049270	-0.65
236700_at	eukaryotic translation initiation factor 3, subunit 8, 110kDa	EIF3S8	chr16p11.2	Hs.192425	8663		0.027351	-0.65
244181_at	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	chr5q13.1	Hs.132225	5295		0.047658	-0.65
222835_at	Hypothetical protein FLJ13710	FLJ13710	chr15q23	Hs.387057	79875		0.020899	-0.65
201238_s_at	capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	chr7q31.2-q31.3	Hs.446123	830		0.046469	-0.65
242134_at	Transcribed locus			Hs.553068			0.026637	-0.65
214499_s_at	BCL2-associated transcription factor 1	BCLAF1	chr6q22-q23	Hs.486542	9774		0.015950	-0.65
1561615_s_at	solute carrier family 8 (sodium/calcium exchanger), member 1	SLC8A1	chr2p23-p22	Hs.468274	6546		0.044271	-0.66
205801_s_at	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	RASGRP3	chr2p25.1-p24.1	Hs.143674	25780		0.011524	-0.66
238494_at	TNF receptor-associated factor 3 interacting protein 1	TRAF3IP1	chr2q37.1	Hs.43086	26146		0.018316	-0.66
229138_at	poly (ADP-ribose) polymerase family, member 11	PARP11	chr12p13.3	Hs.504538	57097		0.001227	-0.66
204182_s_at	zinc finger protein 297B	ZNF297B	chr9p24.1-q22.33	Hs.355581	23099		0.025694	-0.67
207152_at	neurotrophic tyrosine kinase, receptor, type 2	NTRK2	chr9q22.1	Hs.494312	4915		0.030423	-0.67
1562573_at	Cytochrome P450, family 17, subfamily A, polypeptide 1	CYP17A1	chr10q24.3	Hs.438016	1586		0.029114	-0.67
221895_at	motile sperm domain containing 2	MOSPD2	chrXp22.2	Hs.190043	158747		0.019554	-0.68
230291_s_at	Nuclear factor I/B	NFIB	chr9p24.1	Hs.370359	4781		0.032424	-0.69
202137_s_at	zinc finger, MYND domain containing 11	ZMYND11	chr10p14	Hs.292265	10771		0.023652	-0.69
238856_s_at	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	PANK2	chr2p13	Hs.516859	80025		0.000766	-0.69
209243_s_at	paternally expressed 3	PEG3	chr19q13.4	Hs.201776	5178		0.019702	-0.69
242691_at	CDNA FLJ41369 fis, clone BRCAN2006117			Hs.445715			0.030792	-0.69
1565601_at	Protocadherin 9	PCDH9	chr13q14.3-q21.1	Hs.407643	5101		0.032268	-0.69
212244_at	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	GRINL1A	chr15q22.1	Hs.437256	81488		0.008505	-0.69
AFFX-HUMRGE/M10098_5_at							0.042900	-0.69
211931_s_at	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1 /// heteroge	HNRPA3P1	chr10q11.21 /// c	Hs.524276	10151 /// c		0.015313	-0.70
231898_x_at	SOX2 overlapping transcript (non-coding RNA)	SOX2OT	chr3q26.3-q27	Hs.546551	347689		0.021798	-0.70
242968_at							0.028194	-0.70
209301_at	carbonic anhydrase II	CA2	chr8q22	Hs.155097	760		0.001531	-0.71
244331_at	Splicing factor proline/glutamine rich (polypyrimidine tract binding prote	SFPQ	chr1p34.3	Hs.355934	6421		0.015926	-0.71
203527_s_at	adenomatosis polyposis coli	APC	chr5q21-q22	Hs.158932	324		0.017910	-0.71
228909_at	Chromosome 21 open reading frame 86	C21orf86	chr21q22.3	Hs.11637	257103		0.038177	-0.71
237556_at	Similar to BTG3 associated nuclear protein isoform b; BANP homolog; SMAR1 homol	SMAR1	chr16p11.2	Hs.460515	440352		0.004508	-0.71
225666_at	hypothetical protein FLJ14624	FLJ14624	chr13q32.3	Hs.190983	84899		0.015973	-0.72
235222_x_at	baculoviral IAP repeat-containing 4	BIRC4	chrXq25	Hs.356076	331		0.015908	-0.72
1558279_a_at	Follicular lymphoma variant translocation 1	FVT1	chr18q21.3	Hs.74050	2531		0.013121	-0.72
235885_at	purinergic receptor P2Y, G-protein coupled, 12	P2RY12	chr3q24-q25	Hs.532933	64805		0.043782	-0.72
1555247_a_at	Rap guanine nucleotide exchange factor (GEF) 6	RAPGEF6	chr5q23.3		51735		0.016193	-0.73
212461_at							0.046922	-0.73
230135_at	CDNA FLJ42405 fis, clone ASTRO3000474			Hs.548089			0.030251	-0.73
209006_s_at	NPD014 protein	NPD014	chr1p36.13-p35.1	Hs.259412	57035		0.034194	-0.73
242206_at	similar to Zinc finger protein 58 (Zfp-58) (Zinc finger protein Mfg-1)	LOC340246	chr7q11.21	Hs.434984	340246		0.016437	-0.73
225571_at	Leukemia inhibitory factor receptor	LIFR	chr5p13-p12	Hs.133421	3977		0.029754	-0.74
222422_s_at	Nedd4 family interacting protein 1	NDFIP1	chr5q31.3	Hs.9788	80762		0.034349	-0.74
1562686_at	CDNA FLJ20158 fis, clone COL08935			Hs.375659			0.011948	-0.74
227148_at							0.031090	-0.75
223925_s_at							0.010069	-0.75
1558414_at	chromosome 9 open reading frame 4	C9orf4	chr9q31	Hs.347537	23732		0.020893	-0.75
1558372_at	CDNA FLJ34038 fis, clone FCBBF2005645			Hs.530150			0.040078	-0.76
219557_s_at	nuclear receptor interacting protein 3	NRIP3	chr11p15.3	Hs.523467	56675		0.021456	-0.76
238137_at	Pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)	PLRG1	chr4q31.2-q32.1	Hs.249996	5356		0.018375	-0.76
217893_s_at	hypothetical protein FLJ12666	FLJ12666	chr1p34.3	Hs.293563	79647		0.048528	-0.76
225539_at	zinc finger protein 295	ZNF295	chr21q22.3	Hs.434947	49854		0.036119	-0.76
1555889_a_at	cartilage associated protein	CRTAP	chr3p22.3	Hs.517888	10491		0.045547	-0.77
208925_at	chromosome 3 open reading frame 4	C3orf4	chr3p11-q11	Hs.107393	56650		0.033171	-0.77
223242_s_at	hypothetical protein ET	ET	chr17q25	Hs.464166	79157		0.000577	-0.77
219300_s_at	contactin associated protein-like 2	CNTNAP2	chr7q35-q36	Hs.446192	26047		0.023366	-0.77
200605_s_at	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific)	PRKAR1A	chr17q23-q24	Hs.280342	5573		0.027278	-0.77
231167_at	Transcribed locus			Hs.531813			0.021488	-0.78

223661_at							0.043540	-0.78
238929_at	Splicing factor, arginine/serine-rich, 46kD	SRP46	chr11q22	Hs.476680	10929		0.011913	-0.78
210561_s_at	WD repeat and SOCS box-containing 1	WSB1	chr17q11.1	Hs.446017	26118		0.027749	-0.79
233437_at	gamma-aminobutyric acid (GABA) A receptor, alpha 4	GABRA4	chr4p12	Hs.248112	2557		0.037609	-0.80
206794_at	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ERBB4	chr2q33.3-q34	Hs.390729	2066		0.006230	-0.80
1558028_x_at	HLA complex group 11	HCG11	chr6p21	Hs.272939	493812		0.049973	-0.80
220238_s_at	kelch-like 7 (Drosophila)	KLHL7	chr7p15.3	Hs.385861	55975		0.020818	-0.81
1565602_at	Protocadherin 9	PCDH9	chr13q14.3-q21.1	Hs.407643	5101		0.022772	-0.81
238985_at							0.034746	-0.81
203083_at	thrombospondin 2	THBS2	chr6q27	Hs.371147	7058		0.029538	-0.81
206135_at	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ST18	chr8q11.23	Hs.549092	9705		0.017369	-0.82
225308_s_at	TPR domain, ankyrin-repeat and coiled-coil-containing	TANC	chr2q24.2	Hs.61590	85461		0.024029	-0.82
205822_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	chr5p14-p13	Hs.397729	3157		0.043160	-0.82
234000_s_at	butyrate-induced transcript 1	HSPC121	chr15q22.2	Hs.512973	51495		0.019604	-0.82
219732_at	plasticity related gene 3	PRG-3	chr9q31.1	Hs.382683	54886		0.041770	-0.82
237741_at	Hypothetical protein FLJ10618	FLJ10618	chr3q23	Hs.144130	55186		0.010451	-0.83
201668_x_at	myristoylated alanine-rich protein kinase C substrate	MARCKS	chr6q22.2	Hs.519909	4082		0.025983	-0.83
202602_s_at	HIV TAT specific factor 1	HTATSF1	chrXq26.1-q27.2	Hs.204475	27336		0.046456	-0.83
229327_s_at	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF	chr16q22-q23	Hs.134859	4094		0.032536	-0.84
211547_s_at	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kD	PAFAH1B1	chr17p13.3	Hs.77318	5048		0.029163	-0.84
222608_s_at	anillin, actin binding protein (scraps homolog, Drosophila)	ANLN	chr7p15-p14	Hs.62180	54443		0.011042	-0.85
213033_s_at	Nuclear factor I/B	NFIB	chr9p24.1	Hs.370359	4781		0.007599	-0.87
209896_s_at	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome)	PTPN11	chr12q24	Hs.506852	5781		0.027654	-0.87
211480_s_at	solute carrier organic anion transporter family, member 1A2	SLCO1A2	chr12p12	Hs.46440	6579		0.000018	-0.88
209735_at	ATP-binding cassette, sub-family G (WHITE), member 2	ABCG2	chr4q22	Hs.480218	9429		0.011466	-0.88
244439_at	sprouty-related, EVH1 domain containing 1	SPRED1	chr15q14	Hs.525781	161742		0.042872	-0.88
210839_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ENPP2	chr8q24.1	Hs.190977	5168		0.027035	-0.90
222111_at	Hypothetical protein KIAA1164	KIAA1164	chr15q21.3	Hs.368548	54629		0.012408	-0.91
1557953_at	zinc finger with KRAB and SCAN domains 1	ZKSCAN1	chr7q21.3-q22.1	Hs.423725	7586		0.039936	-0.91
213069_at	HEG homolog 1 (zebrafish)	HEG	chr3q21.2	Hs.477420	57493		0.033453	-0.91
222850_s_at	hypothetical protein FLJ14281	FLJ14281	chr4q23	Hs.512743	79982		0.041607	-0.91
228485_s_at	CDW92 antigen	CDW92	chr9q31.2	Hs.494700	23446		0.009019	-0.92
201485_s_at	reticulocalbin 2, EF-hand calcium binding domain	RCN2	chr15q23	Hs.79088	5955		0.049869	-0.92
209631_s_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37	chr7q31	Hs.406094	2861		0.010085	-0.92
217582_at							0.041342	-0.93
241403_at	CDC-like kinase 4	CLK4	chr5q35	Hs.406557	57396		0.006727	-0.94
222404_x_at	butyrate-induced transcript 1	HSPC121	chr15q22.2	Hs.512973	51495		0.019458	-0.95
203758_at	cathepsin O	CTSO	chr4q31-q32	Hs.75262	1519		0.041978	-0.97
203300_x_at	adaptor-related protein complex 1, sigma 2 subunit	AP1S2	chrXp22.2	Hs.121592	8905		0.005445	-0.98
221859_at	synaptotagmin XIII	SYT13	chr11p12-p11	Hs.436643	57586		0.020540	-0.99
214586_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37	chr7q31	Hs.406094	2861		0.030959	-1.03
226533_at							0.008223	-1.08
228956_at	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	UGT8	chr4q26	Hs.144197	7368		0.006779	-1.11
1559129_a_at	hypothetical protein LOC158257	LOC158257	chr9q22.32	Hs.213065	158257		0.017429	-1.14
231911_at	KIAA1189	KIAA1189	chr2q24.1	Hs.443894	57471		0.033621	-1.17
228335_at	claudin 11 (oligodendrocyte transmembrane protein)	CLDN11	chr3q26.2-q26.3	Hs.31595	5010		0.039478	-1.24
241685_x_at	Transcribed locus			Hs.200938			0.046373	-1.24
209392_at	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ENPP2	chr8q24.1	Hs.190977	5168		0.015765	-1.26
203348_s_at	ets variant gene 5 (ets-related molecule)	ETV5	chr3q28	Hs.43697	2119		0.018585	-1.43
210198_s_at	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2)	PLP1	chrXq22	Hs.1787	5354		0.006224	-1.45