Affymetrix ID	Gene Symbol	Description	log2 (Fold Change)	teststat	Raw p-value	Benjamini-Hochberg
214328_s_at	EIF3S3	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa	0.713576	21.362841	2.63E-10	5.32E-06
224187_x_at	HSPA8	heat shock 70kDa protein 8	2.379127	20.592240	3.91E-10	5.32E-06
210211_s_at	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	0.902148	20.344194	4.45E-10	5.32E-06
208744_x_at	HSPH1	heat shock 105kDa/110kDa protein 1	3.489690	20.296077	4.56E-10	5.32E-06
208687_x_at	HSPA8	heat shock 70kDa protein 8	2.493492	20.175406	4.87E-10	5.32E-06
210338_s_at	HSPA8	heat shock 70kDa protein 8	2.690309	19.772756	6.04E-10	5.50E-06
221891_x_at	HSPA8	heat shock 70kDa protein 8	2.178976	18.416132	1.29E-09	1.01E-05
211969_at	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	2.253354	17.055848	2.93E-09	1.92E-05
200799_at	HSPA1A	heat shock 70kDa protein 1A	1.911737	16.918975	3.19E-09	1.92E-05
224806_at	TRIM25	tripartite motif-containing 25	-2.220000	-16.671099	3.73E-09	1.92E-05
203665_at	HMOX1	heme oxygenase (decycling) 1	5.147491	16.616412	3.86E-09	1.92E-05
209882_at	RIT1	Ras-like without CAAX 1	1.407571	14.891853	1.23E-08	5.60E-05
211968_s_at	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	2.622331	14.569885	1.55E-08	6.09E-05
203810_at	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	3.791099	14.559934	1.56E-08	6.09E-05
239377_at	MGC11102		0.649539	14.440377	1.70E-08	6.19E-05
206976_s_at	HSPH1	heat shock 105kDa/110kDa protein 1	3.593631	13.909715	2.52E-08	8.60E-05
213330_s_at	STIP1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	1.509496	13.818552	2.69E-08	8.67E-05
200800_s_at	HSPA1A	heat shock 70kDa protein 1A	3.359839	13.536778	3.34E-08	9.64E-05
202581_at	HSPA1B	heat shock 70kDa protein 1B	3.516971	13.532665	3.35E-08	9.64E-05
200041_s_at	BAT1	HLA-B associated transcript 1	-0.919782	-13.435815	3.61E-08	9.87E-05
1554241_at	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	0.496340	13.370669	3.80E-08	9.89E-05
1552664_at	FLCN	folliculin	0.795563	13.204005	4.33E-08	0.000107574
204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	1.855945	12.860731	5.69E-08	0.000128752
200627_at	PTGES3	prostaglandin E synthase 3 (cytosolic)	0.814503	12.831463	5.83E-08	0.000128752
201326_at	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	1.271642	12.818525	5.89E-08	0.000128752
228775_at	TMEM111	transmembrane protein 111	1.462819	12.758518	6.18E-08	0.000129967
202059_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	1.175957	12.566972	7.23E-08	0.000138528
209431_s_at	ZNF278	zinc finger protein 278	-2.104674	-12.543550	7.37E-08	0.000138528
234986_at	GCLM	glutamate-cysteine ligase, modifier subunit	3.247132	12.515355	7.54E-08	0.000138528
202912_at	ADM	adrenomedullin	1.787491	12.505879	7.60E-08	0.000138528
221290_s_at	MUM1	melanoma associated antigen (mutated) 1	1.632303	12.240850	9.48E-08	0.00016722
209360_s_at	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1, aml1 oncogene)	-0.914825	-12.099158	1.07E-07	0.000181639
221875_x_at	HLA-F	major histocompatibility complex, class I, F	-0.790801	-12.056972	1.11E-07	0.000181639
201491_at	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	1.744428	11.973440	1.19E-07	0.000181639
201468_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1	2.397648	11.963762	1.20E-07	0.000181639

228519_x_at	CIRBP	cold inducible RNA binding protein	-1.467105	-11.950345	1.21E-07	0.000181639
211296_x_at	UBC	ubiquitin C	1.062867	11.923352	1.24E-07	0.000181639
234005_x_at	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	-0.704830	-11.904852	1.26E-07	0.000181639
218417_s_at	FLJ20489		1.979109	11.786802	1.40E-07	0.000196037
200811_at	CIRBP	cold inducible RNA binding protein	-1.042938	-11.674718	1.54E-07	0.000210799
202939_at	ZMPSTE24	zinc metallopeptidase (STE24 homolog, yeast)	1.166689	11.564525	1.70E-07	0.000226618
210691_s_at	CACYBP	calcyclin binding protein	1.175016	11.382852	2.00E-07	0.000257932
213813_x_at	FTL	ferritin, light polypeptide	1.053770	11.361706	2.04E-07	0.000257932
214696_at	MGC14376		2.370277	11.340221	2.08E-07	0.000257932
229670_at			-2.711321	-11.165782	2.43E-07	0.000293714
212788_x_at	FTL	ferritin, light polypeptide	1.350563	11.129773	2.51E-07	0.000293714
200666_s_at	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	2.547562	11.124220	2.52E-07	0.000293714
200880_at	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	2.092821	11.031222	2.75E-07	0.000307535
225191_at	CIRBP	cold inducible RNA binding protein	-1.952989	-11.028694	2.76E-07	0.000307535
228869_at	SLIC1		-1.770294	-10.974549	2.90E-07	0.000316827
200881_s_at	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	1.923709	10.885837	3.15E-07	0.000337268
226016_at	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	-1.227849	-10.854848	3.24E-07	0.000338132
202636_at	RNF103	ring finger protein 103	0.529587	10.841854	3.28E-07	0.000338132
218366_x_at	FLJ20859		-1.411796	-10.738292	3.61E-07	0.000365732
200047_s_at	YY1	YY1 transcription factor	0.671669	10.711805	3.70E-07	0.000368163
212009_s_at	STIP1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	2.019671	10.688588	3.79E-07	0.000369608
225252_at	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	1.940151	10.643792	3.95E-07	0.000378864
204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	1.919530	10.590784	4.15E-07	0.000386738
232024_at	GIMAP2	GTPase, IMAP family member 2	-2.181120	-10.559078	4.28E-07	0.000386738
213187_x_at	FTL	ferritin, light polypeptide	1.524277	10.540597	4.36E-07	0.000386738
201362_at	IVNS1ABP	influenza virus NS1A binding protein	-1.147069	-10.538096	4.37E-07	0.000386738
209040_s_at	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	-1.638898	-10.533988	4.39E-07	0.000386738
226702_at	LOC129607		-3.034766	-10.477581	4.63E-07	0.000395795
218633_x_at	ABHD10	abhydrolase domain containing 10	-1.405885	-10.476765	4.63E-07	0.000395795
200895_s_at	FKBP4	FK506 binding protein 4, 59kDa	1.756847	10.433491	4.83E-07	0.000397547
219498_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-2.533873	-10.430013	4.85E-07	0.000397547
205133_s_at	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	1.738301	10.421716	4.89E-07	0.000397547
208980_s_at	UBC	ubiquitin C	1.106441	10.409308	4.94E-07	0.000397547
203811_s_at	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	2.493948	10.375352	5.11E-07	0.000404878
200064_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.090934	10.330457	5.34E-07	0.000416878
226743_at	FLJ34922		-1.555100	-10.298692	5.50E-07	0.000423924
226565_at	TMEM99	transmembrane protein 99	0.677681	10.284249	5.58E-07	0.000423969

211628_x_at	FTHP1	ferritin, heavy polypeptide pseudogene 1	1.115844	10.254346	5.75E-07	0.000430567
201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-2.374021	-10.221006	5.94E-07	0.00043486
212560_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-3.035602	-10.216655	5.97E-07	0.00043486
236140_at	GCLM	glutamate-cysteine ligase, modifier subunit	3.281077	10.166387	6.27E-07	0.000450895
224836_at	TP53INP2	tumor protein p53 inducible nuclear protein 2	1.480018	10.148573	6.38E-07	0.000452929
232077_s_at	YPEL3	yippee-like 3 (Drosophila)	-0.945766	-10.063625	6.94E-07	0.000486379
222891_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-1.849530	-10.035498	7.14E-07	0.00049015
1554577_a_at	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0.510416	10.030431	7.17E-07	0.00049015
218566_s_at	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	1.645949	9.994530	7.43E-07	0.000495697
205051_s_at	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	-2.212568	-9.994423	7.43E-07	0.000495697
212714_at	LARP4	La ribonucleoprotein domain family, member 4	1.284338	9.948774	7.78E-07	0.000504874
201266_at	TXNRD1	thioredoxin reductase 1	1.129675	9.947433	7.79E-07	0.000504874
208868_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	0.842676	9.940252	7.85E-07	0.000504874
201009_s_at	TXNIP	thioredoxin interacting protein	-1.795640	-9.898184	8.19E-07	0.000516447
242123_at	PAQR7	progestin and adipoQ receptor family member VII	-1.076242	-9.894608	8.22E-07	0.000516447
238480_at	C18orf17	chromosome 18 open reading frame 17	-2.277150	-9.864401	8.47E-07	0.000526383
236224_at	RIT1	Ras-like without CAAX 1	1.355777	9.845298	8.64E-07	0.00053062
212144_at	UNC84B	unc-84 homolog B (C. elegans)	-0.822789	-9.804295	9.00E-07	0.000546996
205400_at	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	-0.536993	-9.760961	9.41E-07	0.000560683
201994_at	MORF4L2	mortality factor 4 like 2	0.707558	9.758401	9.43E-07	0.000560683
203528_at	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	-1.604594	-9.718233	9.83E-07	0.000577876
225081_s_at	CDCA7L	cell division cycle associated 7-like	-1.392253	-9.697686	1.00E-06	0.000583881
201381_x_at	CACYBP	calcyclin binding protein	1.631961	9.671271	1.03E-06	0.000593601
201471_s_at	SQSTM1	sequestosome 1	0.917402	9.628807	1.08E-06	0.000613644
203445_s_at	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-0.935582	-9.610915	1.10E-06	0.000618626
225917_at			-0.907996	-9.578052	1.14E-06	0.000633466
208667_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	1.194077	9.552740	1.17E-06	0.000643727
226750_at	LARP2	La ribonucleoprotein domain family, member 2	1.437910	9.542048	1.18E-06	0.000644398
204341_at	TRIM16	tripartite motif-containing 16	1.392230	9.504841	1.23E-06	0.00066318
48106_at	FLJ20489		1.255687	9.449364	1.30E-06	0.000695822
235573_at	HSPH1	heat shock 105kDa/110kDa protein 1	2.298647	9.321163	1.49E-06	0.000788536
213005_s_at	ANKRD15	ankyrin repeat domain 15	-2.334785	-9.311457	1.50E-06	0.000789015
218543_s_at	PARP12	poly (ADP-ribose) polymerase family, member 12	-2.183479	-9.244246	1.61E-06	0.000839291
224346_at			1.459265	9.220026	1.65E-06	0.00085311

221952_x_at	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	-0.579579	-9.090627	1.90E-06	0.000970974
204205_at	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	-1.827221	-9.071952	1.94E-06	0.000981574
200996_at	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	0.581828	9.017574	2.06E-06	0.001031562
208786_s_at	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	0.980090	8.980922	2.14E-06	0.001049228
200070_at	C2orf24	chromosome 2 open reading frame 24	0.637644	8.970420	2.16E-06	0.001049228
223528_s_at	FLJ20859		-1.587353	-8.969919	2.17E-06	0.001049228
223988_x_at	FLJ20859		-1.430877	-8.968833	2.17E-06	0.001049228
208706_s_at	EIF5	eukaryotic translation initiation factor 5	0.705113	8.934304	2.25E-06	0.001079977
1570552_at	C18orf50	chromosome 18 open reading frame 50	-1.948226	-8.892708	2.36E-06	0.001099797
221004_s_at	ITM2C	integral membrane protein 2C	-1.200402	-8.885527	2.38E-06	0.001099797
202883_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	1.239607	8.875959	2.40E-06	0.001099797
201010_s_at	TXNIP	thioredoxin interacting protein	-2.003750	-8.867389	2.42E-06	0.001099797
226541_at	FBXO30	F-box protein 30	1.665057	8.866891	2.42E-06	0.001099797
203925_at	GCLM	glutamate-cysteine ligase, modifier subunit	2.287557	8.865071	2.43E-06	0.001099797
210347_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-2.626890	-8.857655	2.45E-06	0.001099797
221688_s_at	IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.219941	-8.855909	2.45E-06	0.001099797
232052_at	LOC440944		0.910454	8.844332	2.49E-06	0.001104855
226757_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	-3.029297	-8.821869	2.55E-06	0.00112344
1567219_at	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	0.565866	8.782879	2.66E-06	0.001159264
210027_s_at	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-1.413045	-8.777091	2.68E-06	0.001159264
229754_at	TMEM44	transmembrane protein 44	-0.661578	-8.771900	2.69E-06	0.001159264
225644_at	FLJ33814		1.127714	8.738012	2.80E-06	0.001194324
229519_at	FXR1	fragile X mental retardation, autosomal homolog 1	1.364556	8.684154	2.97E-06	0.001250503
211761_s_at	CACYBP	calcyclin binding protein	1.444674	8.679479	2.98E-06	0.001250503
214950_at	IL9R	interleukin 9 receptor	-1.723504	-8.676031	3.00E-06	0.001250503
219777_at	GIMAP6	GTPase, IMAP family member 6	-3.393255	-8.668444	3.02E-06	0.001251608
212457_at	TFE3	transcription factor binding to IGHM enhancer 3	1.427368	8.596168	3.28E-06	0.001347203
203037_s_at	MTSS1	metastasis suppressor 1	-1.927279	-8.582141	3.33E-06	0.001358456
225284_at	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	1.020132	8.571843	3.37E-06	0.001364152
213101_s_at	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	0.498459	8.564116	3.40E-06	0.001365988
225670_at	LOC134145		1.729676	8.506865	3.63E-06	0.001444261
225268_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	0.903559	8.502036	3.65E-06	0.001444261
228333_at			-1.503114	-8.461595	3.82E-06	0.001491918

213532_at	ADAM17	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	1.133516	8.460861	3.82E-06	0.001491918
209770_at	BTN3A1	butyrophilin, subfamily 3, member A1	-1.994157	-8.452707	3.86E-06	0.001495177
208021_s_at	RFC1	replication factor C (activator 1) 1, 145kDa	-1.041017	-8.433642	3.94E-06	0.00151732
218802_at	FLJ20647		-0.827663	-8.415105	4.03E-06	0.001537693
202899_s_at	SFRS3	splicing factor, arginine/serine-rich 3	0.911329	8.404410	4.07E-06	0.001537693
204249_s_at	LMO2	LIM domain only 2 (rhombotin-like 1)	-1.572033	-8.403717	4.08E-06	0.001537693
201437_s_at	EIF4E	eukaryotic translation initiation factor 4E	0.286880	8.393486	4.13E-06	0.001545177
228153_at	IBRDC2	IBR domain containing 2	-1.929828	-8.373055	4.22E-06	0.001571087
200810_s_at	CIRBP	cold inducible RNA binding protein	-0.872151	-8.354070	4.32E-06	0.001594915
213895_at	EMP1	epithelial membrane protein 1	1.337966	8.313679	4.52E-06	0.001635212
218284_at	SMAD3	SMAD, mothers against DPP homolog 3 (Drosophila)	-1.623661	-8.304482	4.57E-06	0.001635212
201586_s_at	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	0.569491	8.293045	4.63E-06	0.001635212
227052_at	LOC201895		-1.616678	-8.291772	4.64E-06	0.001635212
216262_s_at	TGIF2	TGFB-induced factor 2 (TALE family homeobox)	-0.882673	-8.284495	4.68E-06	0.001635212
201008_s_at	TXNIP	thioredoxin interacting protein	-2.155261	-8.283849	4.68E-06	0.001635212
209761_s_at	SP110	SP110 nuclear body protein	-1.217201	-8.277150	4.72E-06	0.001635212
219122_s_at	ICF45		-0.682983	-8.275380	4.73E-06	0.001635212
209026_x_at	TUBB	tubulin, beta	-1.096803	-8.274125	4.73E-06	0.001635212
37796_at	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	-0.362550	-8.270586	4.75E-06	0.001635212
214205_x_at	TXNL2	thioredoxin-like 2	0.355600	8.270419	4.76E-06	0.001635212
208290_s_at	EIF5	eukaryotic translation initiation factor 5	1.867168	8.256128	4.83E-06	0.001652164
224415_s_at	HINT2	histidine triad nucleotide binding protein 2	-0.863288	-8.245075	4.90E-06	0.001663123
217980_s_at	MRPL16	mitochondrial ribosomal protein L16	-1.038069	-8.228752	4.99E-06	0.001668344
1555916_at	RPUSD3	RNA pseudouridylate synthase domain containing 3	0.786972	8.227161	5.00E-06	0.001668344
1555847_a_at	LOC284454		1.266218	8.213213	5.08E-06	0.001668344
210519_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1	1.752994	8.212992	5.08E-06	0.001668344
225177_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)	-1.253760	-8.212877	5.08E-06	0.001668344
209921_at	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	3.120008	8.210952	5.10E-06	0.001668344
200789_at	ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	-0.626922	-8.199215	5.17E-06	0.001681275
201310_s_at	C5orf13	chromosome 5 open reading frame 13	-2.015621	-8.192152	5.21E-06	0.001683766
222161_at	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	0.933408	8.187813	5.24E-06	0.001683766
217882_at	TMEM111	transmembrane protein 111	2.264750	8.094817	5.84E-06	0.001866906
210648_x_at	SNX3	sorting nexin 3	0.531289	8.083776	5.92E-06	0.001873047
230741_at			-2.169513	-8.082169	5.93E-06	0.001873047

225267_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	0.815184	8.074943	5.98E-06	0.00187823
201773_at	ADNP	activity-dependent neuroprotector	-0.727924	-8.052110	6.14E-06	0.001904233
222977_at	SURF4	surfeit 4	1.079584	8.050375	6.15E-06	0.001904233
226756_at	FLJ36031		-1.877742	-8.048613	6.17E-06	0.001904233
203879_at	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	-0.863701	-8.044084	6.20E-06	0.001904233
209083_at	CORO1A	coronin, actin binding protein, 1A	-0.819718	-8.028832	6.31E-06	0.001925111
223464_at	OSBPL5	oxysterol binding protein-like 5	-0.720796	-8.025449	6.34E-06	0.001925111
219497_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-2.264249	-8.020712	6.37E-06	0.001925262
230795_at	HIST2H4	histone 2, H4	-1.174741	-8.010417	6.45E-06	0.001938223
218689_at	FANCF	Fanconi anemia, complementation group F	-2.083894	-7.992489	6.59E-06	0.001969139
207168_s_at	H2AFY	H2A histone family, member Y	-0.426183	-7.982239	6.67E-06	0.001982471
228583_at	C14orf46	chromosome 14 open reading frame 46	0.556877	7.975856	6.72E-06	0.001986798
226659_at	DEF6	differentially expressed in FDCP 6 homolog (mouse)	-0.961355	-7.969703	6.77E-06	0.001990657
200651_at	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	-0.476724	-7.946573	6.96E-06	0.002034781
205180_s_at	ADAM8	ADAM metallopeptidase domain 8	-0.850562	-7.942369	7.00E-06	0.002034781
204040_at	RNF144	ring finger protein 144	-2.199367	-7.934117	7.07E-06	0.002044078
209357_at	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	-1.990902	-7.913897	7.24E-06	0.002083127
219209_at	IFIH1	interferon induced with helicase C domain 1	-2.096475	-7.903046	7.33E-06	0.002099345
208708_x_at	EIF5	eukaryotic translation initiation factor 5	1.988537	7.890357	7.45E-06	0.00210943
230142_s_at	CIRBP	cold inducible RNA binding protein	-1.420755	-7.889906	7.45E-06	0.00210943
241418_at	LOC344887		1.961167	7.886067	7.48E-06	0.00210943
216384_x_at	LOC440085		-0.729223	-7.877701	7.56E-06	0.002119811
200748_s_at	FTH1	ferritin, heavy polypeptide 1	1.168571	7.872595	7.61E-06	0.002121983
202950_at	CRYZ	crystallin, zeta (quinone reductase)	1.550771	7.864413	7.68E-06	0.002129989
211015_s_at	HSPA4	heat shock 70kDa protein 4	0.894915	7.861027	7.71E-06	0.002129989
209383_at	DDIT3	DNA-damage-inducible transcript 3	1.619052	7.843176	7.88E-06	0.002165357
200691_s_at	HSPA9B	heat shock 70kDa protein 9B (mortalin-2)	1.159490	7.822986	8.08E-06	0.002207674
200912_s_at	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	-0.508905	-7.811920	8.18E-06	0.002226269
230082_at	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	0.660210	7.799438	8.31E-06	0.002248957
230171_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.361326	7.781244	8.49E-06	0.002287761
243463_s_at	RIT1	Ras-like without CAAX 1	1.629326	7.764711	8.67E-06	0.002322684
200668_s_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.451252	7.755873	8.76E-06	0.002336308
228275_at			-1.555537	-7.743553	8.89E-06	0.002360068
203983_at	TSNAX	translin-associated factor X	-0.893013	-7.738356	8.95E-06	0.002363571
224923_at	TTC7A	tetratricopeptide repeat domain 7A	-0.615909	-7.731705	9.02E-06	0.002371337

226530_at	BMF	Bcl2 modifying factor	-1.624084	-7.721864	9.13E-06	0.002388467
217329_x_at			0.461771	7.667938	9.75E-06	0.00253907
228996_at	RC3H1	ring finger and CCCH-type zinc finger domains 1	1.295621	7.655825	9.90E-06	0.00254767
215963_x_at	RPL3	ribosomal protein L3	-0.326570	-7.654272	9.92E-06	0.00254767
201585_s_at	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	0.496303	7.653614	9.93E-06	0.00254767
200642_at	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	1.560764	7.646234	1.00E-05	0.002552818
208696_at	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	0.856799	7.644356	1.00E-05	0.002552818
223132_s_at	TRIM8	tripartite motif-containing 8	-0.941291	-7.628808	1.02E-05	0.002590025
208666_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	1.257785	7.603985	1.05E-05	0.002653425
230127_at			3.006945	7.601686	1.06E-05	0.002653425
210715_s_at	SPINT2	serine peptidase inhibitor, Kunitz type, 2	-0.474427	-7.596719	1.06E-05	0.002657538
203010_at	STAT5A	signal transducer and activator of transcription 5A	-0.689855	-7.586674	1.08E-05	0.002678459
211686_s_at	RBM13	RNA binding motif protein 13	-1.286709	-7.576692	1.09E-05	0.002699423
224558_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	-1.157176	-7.569750	1.10E-05	0.002703138
240064_at	SELPLG	selectin P ligand	-0.891814	-7.565209	1.11E-05	0.002703138
218259_at	MKL2	MKL/myocardin-like 2	-1.514023	-7.564676	1.11E-05	0.002703138
208549_x_at	LOC440085		-0.712696	-7.548793	1.13E-05	0.002744574
206067_s_at	WT1	Wilms tumor 1	-1.831144	-7.538326	1.14E-05	0.002752853
222988_s_at	TMEM9	transmembrane protein 9	-0.615583	-7.536172	1.15E-05	0.002752853
211509_s_at	RTN4	reticulon 4	0.605525	7.535682	1.15E-05	0.002752853
229390_at	RP1-93H18.5		-1.474251	-7.521321	1.17E-05	0.002790134
222129_at	C2orf17	chromosome 2 open reading frame 17	-0.689500	-7.500154	1.20E-05	0.002827175
200977_s_at	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	0.688179	7.500039	1.20E-05	0.002827175
208985_s_at	EIF3S1	eukaryotic translation initiation factor 3, subunit 1 alpha, 35kDa	0.967209	7.499630	1.20E-05	0.002827175
215313_x_at	HLA-A	major histocompatibility complex, class I, A	-0.531866	-7.494609	1.21E-05	0.002827175
208672_s_at	SFRS3	splicing factor, arginine/serine-rich 3	0.389004	7.493356	1.21E-05	0.002827175
225562_at	RASA3	RAS p21 protein activator 3	-1.357878	-7.473379	1.24E-05	0.002877229
210045_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-0.926205	-7.471932	1.24E-05	0.002877229
208698_s_at	NONO	non-POU domain containing, octamer-binding	-0.620390	-7.469066	1.25E-05	0.002877229
225793_at	LIX1L	Lix1 homolog (mouse) like	-1.201924	-7.461178	1.26E-05	0.002893505
231004_s_at	H1FX	H1 histone family, member X	-1.471258	-7.442212	1.29E-05	0.00295055
202813_at	TARBP1	Tar (HIV-1) RNA binding protein 1	-1.329369	-7.433280	1.30E-05	0.00296957
218684_at	LRRC8D	leucine rich repeat containing 8 family, member D	-0.666012	-7.427497	1.31E-05	0.00296957
223497_at	KIAA1411	KIAA1411	-1.154861	-7.425239	1.32E-05	0.00296957
212723_at	PTDSR	phosphatidylserine receptor	1.472682	7.423832	1.32E-05	0.00296957
235317_at	LOC284454		0.859262	7.407663	1.35E-05	0.003018005
201795_at	LBR	lamin B receptor	0.681728	7.403908	1.35E-05	0.003019897
1554557_at	ATP11B	ATPase, Class VI, type 11B	0.722244	7.398927	1.36E-05	0.003026501

217678_at	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	2.853323	7.381670	1.39E-05	0.003080381
201972_at	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	0.526200	7.369090	1.41E-05	0.003100751
214359_s_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.269671	7.366106	1.42E-05	0.003100751
209543_s_at	CD34	CD34 antigen	-1.378334	-7.364523	1.42E-05	0.003100751
215800_at	DUOX1	dual oxidase 1	0.171109	7.362560	1.43E-05	0.003100751
222985_at	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	0.306360	7.360533	1.43E-05	0.003100751
213385_at	CHN2	chimerin (chimaerin) 2	-1.558444	-7.352743	1.44E-05	0.003118999
225699_at	LOC285958		-1.094899	-7.341184	1.46E-05	0.003143405
209337_at	PSIP1	PC4 and SFRS1 interacting protein 1	-1.626469	-7.340335	1.47E-05	0.003143405
204821_at	BTN3A3	butyrophilin, subfamily 3, member A3	-1.568819	-7.333352	1.48E-05	0.003158885
200087_s_at	TMED2	transmembrane emp24 domain trafficking protein 2	0.343877	7.323571	1.50E-05	0.003185767
204806_x_at	HLA-F	major histocompatibility complex, class I, F	-0.637230	-7.293269	1.56E-05	0.003297662
228762_at	LFNG	lunatic fringe homolog (Drosophila)	-1.219440	-7.274949	1.59E-05	0.003362275
1569003_at	TMEM49	transmembrane protein 49	1.099477	7.261146	1.62E-05	0.003405031
201005_at	CD9	CD9 antigen (p24)	-1.207330	-7.258971	1.63E-05	0.003405031
200940_s_at	RERE	arginine-glutamic acid dipeptide (RE) repeats	-1.117150	-7.231275	1.68E-05	0.003502013
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	-1.022687	-7.230957	1.68E-05	0.003502013
1559530_at	BLOC1S3	biogenesis of lysosome-related organelles complex-1, subunit 3	0.363337	7.224139	1.70E-05	0.003519258
201746_at	TP53	tumor protein p53 (Li-Fraumeni syndrome)	-0.549209	-7.216663	1.72E-05	0.003539636
212295_s_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	0.851962	7.209008	1.73E-05	0.003561019
206649_s_at	TFE3	transcription factor binding to IGHM enhancer 3	0.775786	7.204757	1.74E-05	0.00356703
204236_at	FLI1	Friend leukemia virus integration 1	-1.636723	-7.198369	1.76E-05	0.003582904
218005_at	ZNF22	zinc finger protein 22 (KOX 15)	-0.674694	-7.191187	1.77E-05	0.00360091
209306_s_at	SWAP70		1.200703	7.187243	1.78E-05	0.00360091
212856_at	DIP		-0.814637	-7.185769	1.78E-05	0.00360091
225704_at	KIAA1545		-1.197164	-7.181474	1.79E-05	0.003607486
228490_at	ABHD2	abhydrolase domain containing 2	1.045084	7.169442	1.82E-05	0.003650207
207543_s_at	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	1.030090	7.156721	1.85E-05	0.003696817
212414_s_at	6-Sep	septin 6	-0.969625	-7.150656	1.87E-05	0.00369917
1552585_s_at	ALF		0.189406	7.150571	1.87E-05	0.00369917
219218_at	BAHCC1	BAH domain and coiled-coil containing 1	-0.881645	-7.147649	1.87E-05	0.003699697
223156_at	MRPS23	mitochondrial ribosomal protein S23	-0.894093	-7.132323	1.91E-05	0.003759866
202859_x_at	IL8	interleukin 8	1.918658	7.119395	1.94E-05	0.003809361

209326_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	0.651022	7.099734	1.99E-05	0.003893368
228138_at	ZNF498	zinc finger protein 498	-0.792068	-7.094529	2.01E-05	0.003905707
224990_at	LOC201895		-1.005297	-7.087405	2.03E-05	0.003927854
202477_s_at	TUBGCP2	tubulin, gamma complex associated protein 2	-0.452174	-7.084678	2.03E-05	0.003927854
214629_x_at	RTN4	reticulon 4	0.687133	7.075251	2.06E-05	0.003938174
227144_at	C22orf9	chromosome 22 open reading frame 9	-1.228929	-7.074678	2.06E-05	0.003938174
228394_at	STK10	serine/threonine kinase 10	-1.035618	-7.074509	2.06E-05	0.003938174
224603_at	ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	-0.938752	-7.071197	2.07E-05	0.003941336
201144_s_at	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	0.818817	7.062196	2.09E-05	0.003962695
203349_s_at	ETV5	ets variant gene 5 (ets-related molecule)	0.647650	7.061673	2.09E-05	0.003962695
217758_s_at	SMBP		0.389678	7.051791	2.12E-05	0.004000007
226481_at	VPRBP	Vpr (HIV-1) binding protein	0.597595	7.044695	2.14E-05	0.004023173
208668_x_at	HMGN2	high-mobility group nucleosomal binding domain 2	-0.504991	-7.038543	2.16E-05	0.004041583
221666_s_at	PYCARD	PYD and CARD domain containing	-1.247456	-7.026632	2.19E-05	0.004068031
239843_at	RIT1	Ras-like without CAAX 1	1.954359	7.025894	2.19E-05	0.004068031
200807_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	1.102808	7.025672	2.19E-05	0.004068031
202241_at	TRIB1	tribbles homolog 1 (Drosophila)	-0.451251	-7.016629	2.22E-05	0.00408997
212296_at	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0.966333	7.016354	2.22E-05	0.00408997
222920_s_at	KIAA0748	KIAA0748	-0.634247	-7.008294	2.25E-05	0.004116431
221087_s_at	APOL3	apolipoprotein L, 3	-0.985511	-7.006258	2.25E-05	0.004116431
223501_at	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	-1.501695	-6.999498	2.27E-05	0.004139053
211855_s_at	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	-0.481349	-6.995875	2.28E-05	0.004144855
203217_s_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	-1.466218	-6.984999	2.31E-05	0.004190232
224956_at	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	1.136871	6.981962	2.32E-05	0.004193012
223502_s_at	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	-1.599967	-6.967974	2.37E-05	0.004256391
209606_at	PSCDBP	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	1.426995	6.963186	2.38E-05	0.004269112
227274_at	SYNJ2BP	synaptojanin 2 binding protein	-1.374936	-6.956366	2.40E-05	0.004274407
204574_s_at	MMP19	matrix metallopeptidase 19	-1.272350	-6.956201	2.40E-05	0.004274407
231550_at	XYLT2	xylosyltransferase II	-0.777895	-6.954768	2.41E-05	0.004274407
205011_at	LOH11CR2A	loss of heterozygosity, 11, chromosomal region 2, gene A	-1.192491	-6.945579	2.44E-05	0.004310633
218230_at	ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	-1.352180	-6.943396	2.44E-05	0.004310633
212290_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	1.424611	6.939626	2.46E-05	0.004318079
202947_s_at	GYPC	glycophorin C (Gerbich blood group)	-0.426015	-6.934513	2.47E-05	0.004322767

234672_s_at	TMEM48	transmembrane protein 48	-1.085275	-6.933917	2.47E-05	0.004322767
223474_at	C14orf4	chromosome 14 open reading frame 4	-1.453790	-6.931085	2.48E-05	0.004325056
202135_s_at	ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	-0.787595	-6.928562	2.49E-05	0.004325074
200958_s_at	SDCBP	syndecan binding protein (syntenin)	0.571267	6.926249	2.50E-05	0.004325074
203704_s_at	RREB1	ras responsive element binding protein 1	-1.184710	-6.923556	2.51E-05	0.004326717
34210_at	CD52	CD52 antigen (CAMPATH-1 antigen)	-0.878644	-6.914922	2.54E-05	0.00435747
201350_at	FLOT2	flotillin 2	-0.789650	-6.912220	2.55E-05	0.00435747
225763_at	RCSD1	RCSD domain containing 1	-1.623968	-6.910052	2.55E-05	0.00435747
226681_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	1.163979	6.908639	2.56E-05	0.00435747
216438_s_at	TMSB4X	thymosin, beta 4, X-linked	-1.049788	-6.904286	2.57E-05	0.004368903
201847_at	LIPA	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	-1.119031	-6.898254	2.59E-05	0.004377953
227346_at	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	-2.212259	-6.898014	2.59E-05	0.004377953
202470_s_at	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	0.806190	6.894442	2.61E-05	0.004383584
222401_s_at	TMEM50A	transmembrane protein 50A	0.597654	6.886419	2.63E-05	0.004383584
219067_s_at	C10orf86	chromosome 10 open reading frame 86	-1.082872	-6.882678	2.65E-05	0.004383584
201542_at	SAR1A	SAR1 gene homolog A (S. cerevisiae)	0.505249	6.881248	2.65E-05	0.004383584
212855_at	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	1.035061	6.880456	2.66E-05	0.004383584
200067_x_at	SNX3	sorting nexin 3	0.649476	6.879537	2.66E-05	0.004383584
209014_at	MAGED1	melanoma antigen family D, 1	-0.646552	-6.878349	2.66E-05	0.004383584
212330_at	TFDP1	transcription factor Dp-1	-0.647922	-6.877829	2.66E-05	0.004383584
223361_at	C6orf115	chromosome 6 open reading frame 115	-0.844835	-6.876268	2.67E-05	0.004383584
204923_at	CXorf9	chromosome X open reading frame 9	-1.591539	-6.873808	2.68E-05	0.004384678
202152_x_at	USF2	upstream transcription factor 2, c-fos interacting	-0.582654	-6.870387	2.69E-05	0.004390035
219212_at	HSPA14	heat shock 70kDa protein 14	1.108532	6.868364	2.70E-05	0.004390035
209827_s_at	IL16	interleukin 16 (lymphocyte chemoattractant factor)	-0.799568	-6.856865	2.74E-05	0.004430463
38241_at	BTN3A3	butyrophilin, subfamily 3, member A3	-2.042851	-6.855503	2.74E-05	0.004430463
223711_s_at	THYN1	thymocyte nuclear protein 1	-0.548122	-6.854709	2.75E-05	0.004430463
201327_s_at	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	0.913401	6.833106	2.83E-05	0.004545653
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-0.784750	-6.828798	2.84E-05	0.004552196
223054_at	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	1.005999	6.827599	2.85E-05	0.004552196
227106_at	MMP19	matrix metallopeptidase 19	-1.353400	-6.821299	2.87E-05	0.004577025
228487_s_at	RREB1	ras responsive element binding protein 1	-1.234105	-6.817527	2.89E-05	0.004586633
201051_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.699746	-6.803660	2.94E-05	0.004657305
200664_s_at	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	1.833486	6.801657	2.95E-05	0.004657305
200887_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	-1.742542	-6.795345	2.97E-05	0.004678481

227139_s_at	HPS3	Hermansky-Pudlak syndrome 3	-1.634582	-6.793914	2.98E-05	0.004678481
200633_at	UBB	ubiquitin B	0.902682	6.782502	3.02E-05	0.004736504
202690_s_at	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	-0.493565	-6.779013	3.04E-05	0.004744983
217845_x_at	HIGD1A	HIG1 domain family, member 1A	0.842783	6.775726	3.05E-05	0.004752236
214259_s_at	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	-1.091207	-6.773190	3.06E-05	0.004754489
208815_x_at	HSPA4	heat shock 70kDa protein 4	0.850329	6.771110	3.07E-05	0.004754489
230805_at			-0.515093	-6.765905	3.09E-05	0.00477409
201740_at	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	-0.765344	-6.761300	3.11E-05	0.004789991
203778_at	MANBA	mannosidase, beta A, lysosomal	-1.293467	-6.748312	3.16E-05	0.004855542
218149_s_at	ZNF395	zinc finger protein 395	-1.032774	-6.746920	3.17E-05	0.004855542
204982_at	GIT2	G protein-coupled receptor kinase interactor 2	-1.016720	-6.739033	3.20E-05	0.004893323
209757_s_at	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-3.315542	-6.736302	3.22E-05	0.00489744
212718_at	PAPOLA	poly(A) polymerase alpha	0.724728	6.732528	3.23E-05	0.00489744
201089_at	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	0.841048	6.732168	3.23E-05	0.00489744
219477_s_at	THSD1	thrombospondin, type I, domain containing 1	-1.782578	-6.727846	3.25E-05	0.004912259
208869_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	0.953593	6.725382	3.26E-05	0.004914922
222132_s_at	MULK	multiple substrate lipid kinase	-0.658432	-6.722709	3.27E-05	0.004919
225775_at	TSPAN33	tetraspanin 33	-0.553204	-6.715601	3.31E-05	0.004941261
1568706_s_at	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-0.325181	-6.715253	3.31E-05	0.004941261
218724_s_at	TGIF2	TGFB-induced factor 2 (TALE family homeobox)	-0.761595	-6.713182	3.32E-05	0.004941496
222825_at	OTUD6B	OTU domain containing 6B	1.029650	6.708776	3.34E-05	0.004956206
200910_at	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	1.157814	6.705123	3.35E-05	0.004956206
225048_at	PHF10	PHD finger protein 10	1.192514	6.704899	3.35E-05	0.004956206
232926_x_at	ANKRD19	ankyrin repeat domain 19	-0.387219	-6.701348	3.37E-05	0.004966466
205745_x_at	ADAM17	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	1.038165	6.698687	3.38E-05	0.004970845
209377_s_at	HMGN3	high mobility group nucleosomal binding domain 3	-0.873833	-6.694263	3.40E-05	0.004976189
210688_s_at	CPT1A	carnitine palmitoyltransferase 1A (liver)	-0.445747	-6.693895	3.40E-05	0.004976189
222845_x_at	TMBIM4	transmembrane BAX inhibitor motif containing 4	-0.635782	-6.686804	3.44E-05	0.004998244
229711_s_at	MGC5370		0.334785	6.686126	3.44E-05	0.004998244
225698_at	TIGA1		-1.371055	-6.684662	3.45E-05	0.004998244
202252_at	RAB13	RAB13, member RAS oncogene family	-0.877102	-6.677509	3.48E-05	0.005025208
223513_at	CENPJ	centromere protein J	1.409436	6.676730	3.48E-05	0.005025208
211921_x_at	PTMA	prothymosin, alpha (gene sequence 28)	-0.642513	-6.666622	3.53E-05	0.005029483

227860_at	CPXM	carboxypeptidase X (M14 family)	-0.728240	-6.665734	3.54E-05	0.005029483
201998_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	-1.326676	-6.665635	3.54E-05	0.005029483
213521_at	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	-0.432407	-6.665107	3.54E-05	0.005029483
212632_at	STX7	syntaxin 7	-0.723204	-6.664842	3.54E-05	0.005029483
242984_at	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	0.429875	6.664434	3.54E-05	0.005029483
205668_at	LY75	lymphocyte antigen 75	-1.671470	-6.662381	3.55E-05	0.005030347
229509_at	MGC33302		-0.783779	-6.652337	3.60E-05	0.005074627
202000_at	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	0.812612	6.650170	3.61E-05	0.005074627
208012_x_at	SP110	SP110 nuclear body protein	-1.416582	-6.649509	3.61E-05	0.005074627
202155_s_at	NUP214	nucleoporin 214kDa	-0.797649	-6.648238	3.62E-05	0.005074627
225005_at	PHF13	PHD finger protein 13	1.375230	6.644599	3.64E-05	0.00508424
209020_at	C20orf111	chromosome 20 open reading frame 111	1.275419	6.643046	3.65E-05	0.00508424
1555812_a_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-1.471154	-6.641139	3.65E-05	0.005084379
223305_at	MGC13379		-0.891944	-6.631158	3.70E-05	0.005140327
234573_at	FLJ20859		-0.797002	-6.627360	3.72E-05	0.005153711
204820_s_at	BTN3A3	butyrophilin, subfamily 3, member A3	-2.006064	-6.625151	3.73E-05	0.005156074
219439_at	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	0.827108	6.622292	3.75E-05	0.005163017
208898_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	1.075987	6.613989	3.79E-05	0.005208245
1555197_a_at	C21orf58	chromosome 21 open reading frame 58	-0.346012	-6.605758	3.83E-05	0.005253428
214801_at	TOR1AIP2	torsin A interacting protein 2	0.720121	6.599699	3.87E-05	0.005283508
225546_at	EEF2K	eukaryotic elongation factor-2 kinase	-1.645226	-6.594200	3.89E-05	0.005309782
201636_at	FXR1	fragile X mental retardation, autosomal homolog 1	0.944566	6.587819	3.93E-05	0.005333786
1557910_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.032795	6.587210	3.93E-05	0.005333786
231747_at	CYSLTR1	cysteinyl leukotriene receptor 1	-1.215325	-6.579038	3.98E-05	0.005379951
226915_s_at	ARPC5L	actin related protein 2/3 complex, subunit 5-like	0.587700	6.576882	3.99E-05	0.005382409
222978_at	SURF4	surfeit 4	0.979697	6.572694	4.01E-05	0.005388871
223583_at	TNFAIP8L2	tumor necrosis factor, alpha-induced protein 8-like 2	-1.155868	-6.572375	4.01E-05	0.005388871
219433_at	BCOR	BCL6 co-repressor	-1.889790	-6.570475	4.02E-05	0.005389566
229582_at	C18orf37	chromosome 18 open reading frame 37	-0.821539	-6.567502	4.04E-05	0.005398165
205801_s_at	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	-1.199523	-6.561159	4.07E-05	0.00541242
202257_s_at	CD2BP2	CD2 antigen (cytoplasmic tail) binding protein 2	-0.592539	-6.558142	4.09E-05	0.00541242
203893_at	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	0.971934	6.557710	4.09E-05	0.00541242

214280_x_at	HNRPA1	heterogeneous nuclear ribonucleoprotein A1	-0.724324	-6.556578	4.10E-05	0.00541242
221896_s_at	HIGD1A	HIG1 domain family, member 1A	0.762686	6.555724	4.10E-05	0.00541242
213395_at	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	-0.545233	-6.554862	4.11E-05	0.00541242
224480_s_at	HMFN0839		1.740486	6.543403	4.17E-05	0.005476119
213657_s_at	ZNF710	zinc finger protein 710	-1.060732	-6.542745	4.18E-05	0.005476119
218023_s_at	FAM53C	family with sequence similarity 53, member C	0.972711	6.539497	4.20E-05	0.005487266
225347_at	ARL8A	ADP-ribosylation factor-like 8A	0.258189	6.531729	4.24E-05	0.005532487
222459_at	C1orf108	chromosome 1 open reading frame 108	0.678800	6.524228	4.28E-05	0.00556326
205504_at	BTK	Bruton agammaglobulinemia tyrosine kinase	-0.939381	-6.523019	4.29E-05	0.00556326
230621_at	ADAM17	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	1.090312	6.522440	4.29E-05	0.00556326
202231_at	hfl-B5		-0.536849	-6.517290	4.32E-05	0.005580306
201807_at	VPS26A	vacuolar protein sorting 26 homolog A (yeast)	0.885802	6.516741	4.33E-05	0.005580306
209674_at	CRY1	cryptochrome 1 (photolyase-like)	1.153076	6.511922	4.36E-05	0.005603962
220195_at	MBD5	methyl-CpG binding domain protein 5	0.561617	6.507164	4.38E-05	0.005627307
207666_x_at	SSX3	synovial sarcoma, X breakpoint 3	0.364665	6.504971	4.40E-05	0.005630998
240698_s_at	EXOSC2	exosome component 2	-0.639406	-6.503043	4.41E-05	0.005632682
212954_at	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	-0.576702	-6.500591	4.42E-05	0.005638441
226910_at	COMMD2	COMM domain containing 2	-1.360461	-6.498545	4.44E-05	0.005641108
204868_at	ICT1	immature colon carcinoma transcript 1	-0.558677	-6.487967	4.50E-05	0.005702671
221481_x_at	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-0.384229	-6.485910	4.51E-05	0.005702671
204000_at	GNB5	guanine nucleotide binding protein (G protein), beta 5	-0.771054	-6.484868	4.52E-05	0.005702671
203672_x_at	TPMT	thiopurine S-methyltransferase	0.508375	6.481656	4.54E-05	0.005702671
200053_at	SPAG7	sperm associated antigen 7	-0.397820	-6.481039	4.54E-05	0.005702671
202194_at	TMED5	transmembrane emp24 protein transport domain containing 5	1.550687	6.479253	4.56E-05	0.005702671
203765_at	GCA	grancalcin, EF-hand calcium binding protein	-0.951568	-6.478546	4.56E-05	0.005702671
204970_s_at	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	1.024342	6.477173	4.57E-05	0.005702671
227221_at			-1.534597	-6.470790	4.61E-05	0.005731476
203206_at	FAM53B	family with sequence similarity 53, member B	-0.508288	-6.469191	4.62E-05	0.005731476
212124_at	RAI17	retinoic acid induced 17	-1.576015	-6.468528	4.62E-05	0.005731476
203556_at	ZHX2	zinc fingers and homeoboxes 2	-1.405345	-6.465551	4.64E-05	0.005738454
223777_at	MGC13005		-0.289588	-6.464347	4.65E-05	0.005738454
224516_s_at	CXXC5	CXXC finger 5	-1.674005	-6.462006	4.66E-05	0.005743964
220560_at	C11orf21	chromosome 11 open reading frame 21	-1.002930	-6.459988	4.68E-05	0.005746974

208056_s_at	CBFA2T3	core-binding factor, runt domain, alpha subunit 2, translocated to, 3	-1.219252	-6.452173	4.73E-05	0.005796014
240862_at	RASGRP4	RAS guanyl releasing protein 4	-1.237935	-6.437821	4.82E-05	0.005898393
221691_x_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	-0.344136	-6.433700	4.85E-05	0.005918728
203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-1.623409	-6.428094	4.89E-05	0.005951338
224601_at			-0.851168	-6.426398	4.90E-05	0.005952013
222979_s_at	SURF4	surfeit 4	1.029007	6.423809	4.92E-05	0.005960048
203186_s_at	S100A4	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	-1.323882	-6.421395	4.93E-05	0.005966418
213475_s_at	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1, alpha polypeptide)	-1.300590	-6.419487	4.95E-05	0.005966418
205212_s_at	CENTB1	centaurin, beta 1	-0.894313	-6.418228	4.95E-05	0.005966418
231188_at	ZSCAN2	zinc finger and SCAN domain containing 2	-0.774231	-6.415439	4.97E-05	0.00596812
211458_s_at	GABARAPL3	GABA(A) receptors associated protein like 3	1.862089	6.414522	4.98E-05	0.00596812
230866_at	CYSLTR1	cysteinyl leukotriene receptor 1	-1.350440	-6.413248	4.99E-05	0.00596812
225220_at			-0.953065	-6.398992	5.09E-05	0.00607351
209099_x_at	JAG1	jagged 1 (Alagille syndrome)	-1.337329	-6.394048	5.12E-05	0.006100825
235196_at	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	1.155951	6.392595	5.13E-05	0.006100825
226128_at	C1orf58	chromosome 1 open reading frame 58	0.521008	6.387211	5.17E-05	0.006110669
227344_at	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	-1.922053	-6.386009	5.18E-05	0.006110669
213911_s_at	H2AFZ	H2A histone family, member Z	0.626476	6.384928	5.19E-05	0.006110669
223892_s_at	TMBIM4	transmembrane BAX inhibitor motif containing 4	-0.606997	-6.384558	5.19E-05	0.006110669
200713_s_at	MAPRE1	microtubule-associated protein, RP/EB family, member 1	0.560262	6.383616	5.20E-05	0.006110669
229766_at	ZNF445	zinc finger protein 445	-0.672636	-6.378912	5.23E-05	0.006137398
223773_s_at	C1orf79	chromosome 1 open reading frame 79	-0.601405	-6.369126	5.30E-05	0.006207853
220104_at	ZC3HAV1	zinc finger CCCH-type, antiviral 1	0.587204	6.365868	5.33E-05	0.006218792
221249_s_at	LOC81558		-1.285156	-6.364774	5.33E-05	0.006218792
242007_at			1.192668	6.360332	5.37E-05	0.006243916
225157_at	MLXIP	MLX interacting protein	-1.145211	-6.358526	5.38E-05	0.006246284
226802_s_at	LOC96610		1.121695	6.353496	5.42E-05	0.006276716
200733_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	0.497319	6.350295	5.44E-05	0.006288314
227413_at	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	-0.662918	-6.349122	5.45E-05	0.006288314
243927_x_at	KIAA1429	KIAA1429	0.450590	6.345495	5.48E-05	0.006304875
220885_s_at	CENPJ	centromere protein J	0.997102	6.344197	5.49E-05	0.006304875
217257_at	STMN1	stathmin 1/oncoprotein 18	-1.434986	-6.331098	5.59E-05	0.006404877
225646_at	CTSC	cathepsin C	-1.126399	-6.329863	5.60E-05	0.006404877
90610_at	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	-0.499164	-6.323786	5.65E-05	0.006445794

208778_s_at	TCP1	t-complex 1	1.012490	6.321097	5.67E-05	0.006456497
210044_s_at	LYL1	lymphoblastic leukemia derived sequence 1	-0.529732	-6.316932	5.70E-05	0.006480554
212441_at	KIAA0232		1.148296	6.308593	5.77E-05	0.006537284
219183_s_at	PSCD4	pleckstrin homology, Sec7 and coiled-coil domains 4	-0.923042	-6.307701	5.78E-05	0.006537284
235463_s_at	LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	0.865934	6.301522	5.83E-05	0.006580245
226641_at	ANKRD44	ankyrin repeat domain 44	-1.243788	-6.299019	5.85E-05	0.006589652
201463_s_at	TALDO1	transaldolase 1	0.725643	6.291640	5.91E-05	0.006644184
201263_at	TARS	threonyl-tRNA synthetase	0.761031	6.288664	5.93E-05	0.00665761
208975_s_at	KPNB1	karyopherin (importin) beta 1	0.544238	6.287255	5.94E-05	0.00665761
204972_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	-2.143239	-6.284992	5.96E-05	0.006665029
200953_s_at	CCND2	cyclin D2	-0.587250	-6.280929	5.99E-05	0.006677256
1555500_s_at	SLC2A4RG	SLC2A4 regulator	-1.590086	-6.279743	6.00E-05	0.006677256
219681_s_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)	-1.184671	-6.279305	6.01E-05	0.006677256
224919_at	MRPS6	mitochondrial ribosomal protein S6	1.048378	6.272740	6.06E-05	0.006713206
227677_at	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	-1.209909	-6.272565	6.07E-05	0.006713206
223227_at	BBS2	Bardet-Biedl syndrome 2	-1.180790	-6.267564	6.11E-05	0.006746695
211487_x_at	RPS17	ribosomal protein S17	-0.439568	-6.264776	6.13E-05	0.006759427
227556_at	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-0.941999	-6.255598	6.21E-05	0.006833106
212377_s_at	NOTCH2	Notch homolog 2 (Drosophila)	-0.778926	-6.252757	6.24E-05	0.006842527
222804_x_at	WDR32	WD repeat domain 32	0.652424	6.251750	6.24E-05	0.006842527
215629_s_at	KIAA1799		1.135504	6.248275	6.28E-05	0.006862194
200068_s_at	CANX	calnexin	0.318622	6.244498	6.31E-05	0.00687311
226840_at	H2AFY	H2A histone family, member Y	-0.985105	-6.244295	6.31E-05	0.00687311
201761_at	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	1.125780	6.238435	6.36E-05	0.006909789
212039_x_at	RPL3	ribosomal protein L3	-0.336774	-6.236363	6.38E-05	0.006909789
208692_at	RPS3	ribosomal protein S3	-0.372280	-6.236257	6.38E-05	0.006909789
218962_s_at	FLJ13576		-1.247370	-6.234499	6.40E-05	0.006913176
206687_s_at	PTPN6	protein tyrosine phosphatase, non-receptor type 6	-1.205595	-6.232471	6.42E-05	0.006919221
226219_at	ARHGAP30	Rho GTPase activating protein 30	-1.589523	-6.225059	6.48E-05	0.006976042
238498_at			-0.306275	-6.223372	6.50E-05	0.006976042
1557487_at	SIDT1	SID1 transmembrane family, member 1	0.334776	6.222451	6.51E-05	0.006976042
214316_x_at	CALR	calreticulin	0.262479	6.216936	6.56E-05	0.007004388
1555851_s_at	SEPW1	selenoprotein W, 1	1.146999	6.215127	6.57E-05	0.007004388
202110_at	COX7B	cytochrome c oxidase subunit VIIb	0.464661	6.214838	6.58E-05	0.007004388
203723_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	-1.815186	-6.209903	6.62E-05	0.007004388
212235_at	PLXND1	plexin D1	-0.804563	-6.209699	6.62E-05	0.007004388
242317_at			1.489433	6.209239	6.63E-05	0.007004388
235441_at	ADCY3	adenylate cyclase 3	-0.377895	-6.206261	6.66E-05	0.007004388
207992_s_at	AMPD3	adenosine monophosphate deaminase (isoform E)	-1.234327	-6.205973	6.66E-05	0.007004388
211069_s_at	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	0.467819	6.205502	6.66E-05	0.007004388
225530_at	MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast)	-1.081353	-6.204023	6.68E-05	0.007004388

207559_s_at	ZMYM3	zinc finger, MYM-type 3	-1.125374	-6.203925	6.68E-05	0.007004388
218248_at	FAM111A	family with sequence similarity 111, member A	-1.183026	-6.202166	6.70E-05	0.007004388
216870_x_at	DLEU2	deleted in lymphocytic leukemia, 2	1.072673	6.200702	6.71E-05	0.007004388
201315_x_at	IFITM2	interferon induced transmembrane protein 2 (1-8D)	-1.202019	-6.200327	6.71E-05	0.007004388
233055_at			0.268920	6.194315	6.77E-05	0.007050523
202330_s_at	UNG	uracil-DNA glycosylase	-0.476980	-6.191850	6.79E-05	0.00705094
203236_s_at	LGALS9	lectin, galactoside-binding, soluble, 9 (galectin 9)	-0.608746	-6.190658	6.81E-05	0.00705094
223469_at	MGC10812		-0.916977	-6.189234	6.82E-05	0.00705094
230235_at	C1GALT1C1	C1GALT1-specific chaperone 1	-0.665945	-6.188890	6.82E-05	0.00705094
201300_s_at	PRNP	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	1.829351	6.183952	6.87E-05	0.007073771
204072_s_at	FRY	furry homolog (Drosophila)	-1.216021	-6.183923	6.87E-05	0.007073771
218871_x_at	GALNACT-2		1.002762	6.182222	6.89E-05	0.00707744
225692_at	CAMTA1	calmodulin binding transcription activator 1	1.166092	6.178989	6.92E-05	0.007096471
226765_at	SPTBN1	spectrin, beta, non-erythrocytic 1	-1.226054	-6.176664	6.94E-05	0.007100054
36030_at	HOM-TES-103		-0.866341	-6.175979	6.95E-05	0.007100054
221476_s_at	RPL15	ribosomal protein L15	-0.630313	-6.173024	6.98E-05	0.007116439
218951_s_at	PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1	-1.237092	-6.168216	7.02E-05	0.007151601
202521_at	CTCF	CCCTC-binding factor (zinc finger protein)	-0.903761	-6.164980	7.06E-05	0.007169053
222420_s_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	1.245717	6.162835	7.08E-05	0.007169053
210502_s_at	PPIE	peptidylprolyl isomerase E (cyclophilin E)	-0.507403	-6.162551	7.08E-05	0.007169053
239134_at	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	1.126755	6.158372	7.12E-05	0.007190875
228990_at	C1orf79	chromosome 1 open reading frame 79	-0.715689	-6.157788	7.13E-05	0.007190875
205039_s_at	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	-1.832657	-6.155802	7.15E-05	0.007196233
218089_at	C20orf4	chromosome 20 open reading frame 4	-0.458675	-6.154658	7.16E-05	0.007196233
224572_s_at	IRF2BP2	interferon regulatory factor 2 binding protein 2	-0.891680	-6.151186	7.20E-05	0.007218405
241955_at	HECTD1	HECT domain containing 1	0.381094	6.146459	7.24E-05	0.007253568
203117_s_at	USP52	ubiquitin specific peptidase 52	-0.597455	-6.143269	7.28E-05	0.007273095
234153_at	SYNJ2	synaptojanin 2	0.427706	6.136206	7.35E-05	0.007332847
211714_x_at	TUBB	tubulin, beta	-1.089814	-6.132664	7.39E-05	0.007356337
201324_at	EMP1	epithelial membrane protein 1	0.649192	6.125288	7.46E-05	0.007420188
226238_at	MCEE	methylmalonyl CoA epimerase	-0.737285	-6.122160	7.50E-05	0.007437824
224565_at	TncRNA		0.872043	6.121058	7.51E-05	0.007437824
227395_at	LRRC35	leucine rich repeat containing 35	-0.905226	-6.119190	7.53E-05	0.007444092
207698_at	C6orf123	chromosome 6 open reading frame 123	0.249014	6.114014	7.58E-05	0.007485472
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	-1.477921	-6.112621	7.60E-05	0.007486782
201184_s_at	CHD4	chromodomain helicase DNA binding protein 4	-0.515154	-6.103475	7.70E-05	0.007571108

215091_s_at	GTF3A	general transcription factor IIIA	-1.195689	-6.098380	7.76E-05	0.007592035
229543_at	RP1-93H18.5		-1.506450	-6.097771	7.76E-05	0.007592035
228264_at	PHACS		-0.594415	-6.097751	7.76E-05	0.007592035
229391_s_at	RP1-93H18.5		-1.395080	-6.094586	7.80E-05	0.007596755
205147_x_at	NCF4	neutrophil cytosolic factor 4, 40kDa	-0.776661	-6.093367	7.81E-05	0.007596755
217907_at	MRPL18	mitochondrial ribosomal protein L18	1.038389	6.091260	7.83E-05	0.007596755
AFFX-HUMISGF3A/M97935_3_at	STAT1	signal transducer and activator of transcription 1, 91kDa	-1.921265	-6.091075	7.84E-05	0.007596755
39402_at	IL1B	interleukin 1, beta	-1.115979	-6.090060	7.85E-05	0.007596755
229733_s_at	CBX6	chromobox homolog 6	-0.733497	-6.089813	7.85E-05	0.007596755
219966_x_at	BANP	BTG3 associated nuclear protein	1.005064	6.085236	7.90E-05	0.007632918
211941_s_at	PEBP1	phosphatidylethanolamine binding protein 1	-0.561214	-6.073780	8.03E-05	0.00773365
206019_at	RBM19	RNA binding motif protein 19	-0.520792	-6.073562	8.03E-05	0.00773365
208899_x_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	0.805160	6.069121	8.09E-05	0.007769113
64488_at			0.913146	6.063928	8.15E-05	0.0077897
220346_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	1.678590	6.062151	8.17E-05	0.0077897
201524_x_at	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	0.356250	6.061826	8.17E-05	0.0077897
235829_at			0.699651	6.061568	8.17E-05	0.0077897
38149_at	ARHGAP25	Rho GTPase activating protein 25	-1.121835	-6.061028	8.18E-05	0.0077897
209762_x_at	SP110	SP110 nuclear body protein	-1.186518	-6.059918	8.19E-05	0.0077897
208646_at	RPS14	ribosomal protein S14	-0.493959	-6.055823	8.24E-05	0.007809729
204252_at	CDK2	cyclin-dependent kinase 2	0.583133	6.054916	8.25E-05	0.007809729
205300_s_at	U1SNRNPBP		-0.651605	-6.054476	8.26E-05	0.007809729
201012_at	ANXA1	annexin A1	1.070613	6.052093	8.28E-05	0.007822833
219401_at	XYLT2	xylosyltransferase II	-0.838432	-6.049794	8.31E-05	0.007835051
201346_at	ADIPOR2	adiponectin receptor 2	0.583444	6.039594	8.43E-05	0.007936479
227266_s_at	FYB	FYN binding protein (FYB-120/130)	-1.841954	-6.036675	8.47E-05	0.007956003
202969_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-1.249373	-6.033344	8.51E-05	0.007973257
232300_at	C10orf116	chromosome 10 open reading frame 116	0.358996	6.032101	8.52E-05	0.007973257
200924_s_at	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	0.776312	6.031570	8.53E-05	0.007973257
223329_x_at	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	1.491876	6.029295	8.56E-05	0.007985628
1553708_at	MGC16075		0.252717	6.022806	8.64E-05	0.008046469
217913_at	VPS4A	vacuolar protein sorting 4A (yeast)	0.603416	6.019808	8.68E-05	0.00806737
201829_at	NET1	neuroepithelial cell transforming gene 1	-0.871659	-6.013514	8.75E-05	0.008116869
231932_at	TRAF3IP3	TRAF3 interacting protein 3	-0.993894	-6.012566	8.77E-05	0.008116869
201118_at	PGD	phosphogluconate dehydrogenase	1.390597	6.011993	8.77E-05	0.008116869
216199_s_at	MAP3K4	mitogen-activated protein kinase kinase kinase 4	-0.360580	-6.006472	8.84E-05	0.008167608

212320_at	TUBB	tubulin, beta	-1.299804	-6.004116	8.87E-05	0.008181462
218617_at	TRIT1	tRNA isopentenyltransferase 1	-0.591201	-6.002883	8.89E-05	0.008182152
228152_s_at	FLJ31033		-1.750567	-5.992013	9.03E-05	0.008283676
230997_at	TTC21A	tetratricopeptide repeat domain 21A	-0.370537	-5.991958	9.03E-05	0.008283676
224831_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	1.189023	5.980895	9.17E-05	0.008399682
223236_at	CCDC55	coiled-coil domain containing 55	0.756071	5.978867	9.20E-05	0.008399682
200772_x_at	PTMA	prothymosin, alpha (gene sequence 28)	-0.689887	-5.978797	9.20E-05	0.008399682
205416_s_at	ATXN3	ataxin 3	0.977986	5.972517	9.29E-05	0.008452551
212071_s_at	SPTBN1	spectrin, beta, non-erythrocytic 1	-1.233513	-5.972123	9.29E-05	0.008452551
214453_s_at	IFI44	interferon-induced protein 44	-1.698230	-5.970646	9.31E-05	0.008456467
205304_s_at	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	-0.114246	-5.968550	9.34E-05	0.008467713
218377_s_at	C21orf6	chromosome 21 open reading frame 6	-1.219473	-5.967421	9.35E-05	0.008467713
225217_s_at	BRPF3	bromodomain and PHD finger containing, 3	1.084853	5.960882	9.44E-05	0.008518931
225631_at	KIAA1706		-0.619366	-5.959386	9.46E-05	0.008518931
220633_s_at	HP1BP3	heterochromatin protein 1, binding protein 3	0.252424	5.958789	9.47E-05	0.008518931
54051_at	PKNOX1	PBX/knotted 1 homeobox 1	1.291912	5.958657	9.47E-05	0.008518931
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-0.544216	-5.957281	9.49E-05	0.008521836
217807_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	-0.377098	-5.955908	9.51E-05	0.008524721
218333_at	DERL2	Der1-like domain family, member 2	0.860365	5.951460	9.57E-05	0.00856555
204661_at	CD52	CD52 antigen (CAMPATH-1 antigen)	-0.734851	-5.947548	9.63E-05	0.008584655
207761_s_at	METTL7A	methyltransferase like 7A	-2.347865	-5.946856	9.64E-05	0.008584655
208705_s_at	EIF5	eukaryotic translation initiation factor 5	1.605029	5.945776	9.65E-05	0.008584655
201665_x_at	RPS17	ribosomal protein S17	-0.424760	-5.945395	9.66E-05	0.008584655
218383_at	C14orf94	chromosome 14 open reading frame 94	-0.878614	-5.941887	9.71E-05	0.008606494
238590_x_at	TMEM107	transmembrane protein 107	-0.672908	-5.940182	9.73E-05	0.008606494
229067_at	RP11-343N15.3		0.715559	5.939728	9.74E-05	0.008606494
202691_at	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	-0.576680	-5.939146	9.74E-05	0.008606494
1569352_at	KIAA1450		0.241829	5.933716	9.82E-05	0.008660301
43427_at	ACACB	acetyl-Coenzyme A carboxylase beta	-0.801964	-5.930486	9.87E-05	0.008686812
213507_s_at	KPNB1	karyopherin (importin) beta 1	0.499559	5.929178	9.89E-05	0.008689266
218101_s_at	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	-0.416150	-5.919075	0.000100307	0.008803036
1557116_at			-1.156404	-5.917815	0.00010049	0.008804977
204912_at	IL10RA	interleukin 10 receptor, alpha	-1.300773	-5.915165	0.000100877	0.008819235
238367_s_at	MGC33556		-0.580227	-5.914483	0.000100976	0.008819235
213541_s_at	ERG	v-ets erythroblastosis virus E26 oncogene like (avian)	-1.484639	-5.913384	0.000101137	0.008819235
225655_at	UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	-0.929201	-5.908710	0.000101824	0.008865007
223548_at	C1orf26	chromosome 1 open reading frame 26	0.613695	5.906865	0.000102096	0.008874599
226771_at	ATP8B2	ATPase, Class I, type 8B, member 2	-0.846112	-5.903592	0.000102582	0.008902647

222514_at	RRAGC	Ras-related GTP binding C	0.947090	5.900702	0.000103013	0.008925854
1561666_a_at	KIAA1908		-0.318662	-5.898137	0.000103396	0.008940779
202878_s_at	CD93	CD93 antigen	-1.554405	-5.897225	0.000103533	0.008940779
211578_s_at	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	0.439938	5.896279	0.000103675	0.008940779
204805_s_at	H1FX	H1 histone family, member X	-0.874335	-5.893725	0.00010406	0.008951756
200028_s_at	STARD7	START domain containing 7	-0.484054	-5.893262	0.00010413	0.008951756
1554053_at	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	0.432475	5.890947	0.000104481	0.008954405
210623_at	LOC51035		0.502181	5.889854	0.000104646	0.008954405
208717_at	OXA1L	oxidase (cytochrome c) assembly 1-like	-1.013034	-5.889815	0.000104652	0.008954405
217814_at	CCDC47	coiled-coil domain containing 47	0.697963	5.887416	0.000105017	0.008971595
227002_at	FAM78A	family with sequence similarity 78, member A	-0.896715	-5.884947	0.000105395	0.008989777
222669_s_at	SBDS	Shwachman-Bodian-Diamond syndrome	0.808912	5.874033	0.000107079	0.009094205
38671_at	PLXND1	plexin D1	-0.966379	-5.873500	0.000107162	0.009094205
213359_at	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-0.776032	-5.872886	0.000107258	0.009094205
209710_at	GATA2	GATA binding protein 2	-1.211068	-5.872715	0.000107284	0.009094205
212268_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	-1.172619	-5.857919	0.000109619	0.009266173
236223_s_at	RIT1	Ras-like without CAAX 1	1.888542	5.857710	0.000109652	0.009266173
220755_s_at	C6orf48	chromosome 6 open reading frame 48	-0.615628	-5.853237	0.000110368	0.009305832
201349_at	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	-0.657716	-5.851637	0.000110626	0.009305832
218435_at	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	-0.885160	-5.849233	0.000111014	0.009305832
210968_s_at	RTN4	reticulon 4	0.736582	5.848192	0.000111183	0.009305832
223249_at	CLDN12	claudin 12	-1.366677	-5.847946	0.000111222	0.009305832
237403_at	GFI1B	growth factor independent 1B (potential regulator of CDKN1A, translocated in CML)	-1.631765	-5.846917	0.000111389	0.009305832
200632_s_at	NDRG1	N-myc downstream regulated gene 1	-1.067308	-5.846853	0.0001114	0.009305832
224309_s_at	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	1.634308	5.846341	0.000111483	0.009305832
214394_x_at	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	-0.399053	-5.843461	0.000111952	0.009330738
213036_x_at	ATP2A3	ATPase, Ca++ transporting, ubiquitous	-0.647239	-5.838221	0.00011281	0.009387987
204197_s_at	RUNX3	runt-related transcription factor 3	-1.072947	-5.835999	0.000113177	0.009395737
236798_at			-1.873341	-5.835572	0.000113247	0.009395737
206090_s_at	DISC1	disrupted in schizophrenia 1	-1.650026	-5.832646	0.000113732	0.009421634
224917_at	TMEM49	transmembrane protein 49	1.776330	5.828291	0.000114457	0.009467373
226507_at	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	-0.603505	-5.825713	0.000114889	0.009479555
204798_at	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-1.123200	-5.825083	0.000114994	0.009479555

230627_at	STT3B	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	-0.413302	-5.824309	0.000115124	0.009479555
212340_at	YIPF6	Yip1 domain family, member 6	0.909691	5.817173	0.000116331	0.009558447
211911_x_at	HLA-B	major histocompatibility complex, class I, B	-0.693279	-5.816578	0.000116432	0.009558447
200003_s_at	RPL28	ribosomal protein L28	-0.399957	-5.814676	0.000116756	0.009570677
218113_at	TMEM2	transmembrane protein 2	0.949605	5.811387	0.000117319	0.009590651
231697_s_at	TMEM49	transmembrane protein 49	1.396648	5.810867	0.000117408	0.009590651
203276_at	LMNB1	lamin B1	-1.387063	-5.810181	0.000117526	0.009590651
214155_s_at	LARP4	La ribonucleoprotein domain family, member 4	1.444774	5.801821	0.000118972	0.009688901
201288_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-1.366584	-5.800222	0.000119251	0.009688901
202693_s_at	STK17A	serine/threonine kinase 17a (apoptosis-inducing)	1.520398	5.800161	0.000119262	0.009688901
229354_at	AHRR	aryl-hydrocarbon receptor repressor	-0.805342	-5.798365	0.000119576	0.009700007
232231_at	RUNX2	runt-related transcription factor 2	-1.483114	-5.795187	0.000120133	0.009730801
221883_at	PKNOX1	PBX/knotted 1 homeobox 1	1.208705	5.793171	0.000120489	0.009743964
225390_s_at	KLF13	Kruppel-like factor 13	-0.925659	-5.792245	0.000120652	0.009743964
225407_at	MBP	myelin basic protein	-0.969869	-5.791028	0.000120868	0.00974695
226637_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	1.235818	5.782151	0.00012245	0.00985547
203529_at	PPP6C	protein phosphatase 6, catalytic subunit	0.337742	5.781464	0.000122574	0.00985547
224571_at	IRF2BP2	interferon regulatory factor 2 binding protein 2	-1.494917	-5.779726	0.000122887	0.009866125
203152_at	MRPL40	mitochondrial ribosomal protein L40	-0.740752	-5.778498	0.000123108	0.009869412
217925_s_at	C6orf106	chromosome 6 open reading frame 106	0.644875	5.771659	0.00012435	0.009897797
222996_s_at	CXXC5	CXXC finger 5	-0.596683	-5.771408	0.000124396	0.009897797
218986_s_at	FLJ20035		-1.273476	-5.770670	0.00012453	0.009897797
228415_at	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.551704	5.768903	0.000124854	0.009897797
204549_at	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	-0.385530	-5.768575	0.000124914	0.009897797
221475_s_at	RPL15	ribosomal protein L15	-0.442060	-5.768108	0.000125	0.009897797
240121_x_at	LOC388526		-0.615351	-5.765663	0.000125449	0.009897797
229285_at	RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	-1.296161	-5.764841	0.000125601	0.009897797
216251_s_at	TTLL12	tubulin tyrosine ligase-like family, member 12	-0.378196	-5.764101	0.000125737	0.009897797
218195_at	C6orf211	chromosome 6 open reading frame 211	1.000634	5.763676	0.000125816	0.009897797
216004_s_at	PKNOX1	PBX/knotted 1 homeobox 1	0.972522	5.762633	0.000126009	0.009897797
212543_at	AIM1	absent in melanoma 1	-1.396919	-5.762610	0.000126013	0.009897797
218021_at	DHRS4	dehydrogenase/reductase (SDR family) member 4	-0.233783	-5.762517	0.00012603	0.009897797
216559_x_at	LOC120364		-0.538919	-5.761861	0.000126152	0.009897797
209829_at	C6orf32	chromosome 6 open reading frame 32	-1.249518	-5.761722	0.000126178	0.009897797
228781_at			-0.916565	-5.759726	0.000126548	0.009912648
201319_at	MRCL3		-0.569506	-5.757647	0.000126935	0.009917757
208641_s_at	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	-0.755530	-5.757428	0.000126976	0.009917757

228846_at	MXD1	MAX dimerization protein 1	1.220452	5.754443	0.000127535	0.009947163
203752_s_at	JUND	jun D proto-oncogene	0.450281	5.752348	0.000127928	0.009963637