Supplementary Materials

Integrative genomic analysis of HIV-specific CD8$^+$ T cells reveals that PD-1 inhibits T cell function by upregulating BATF

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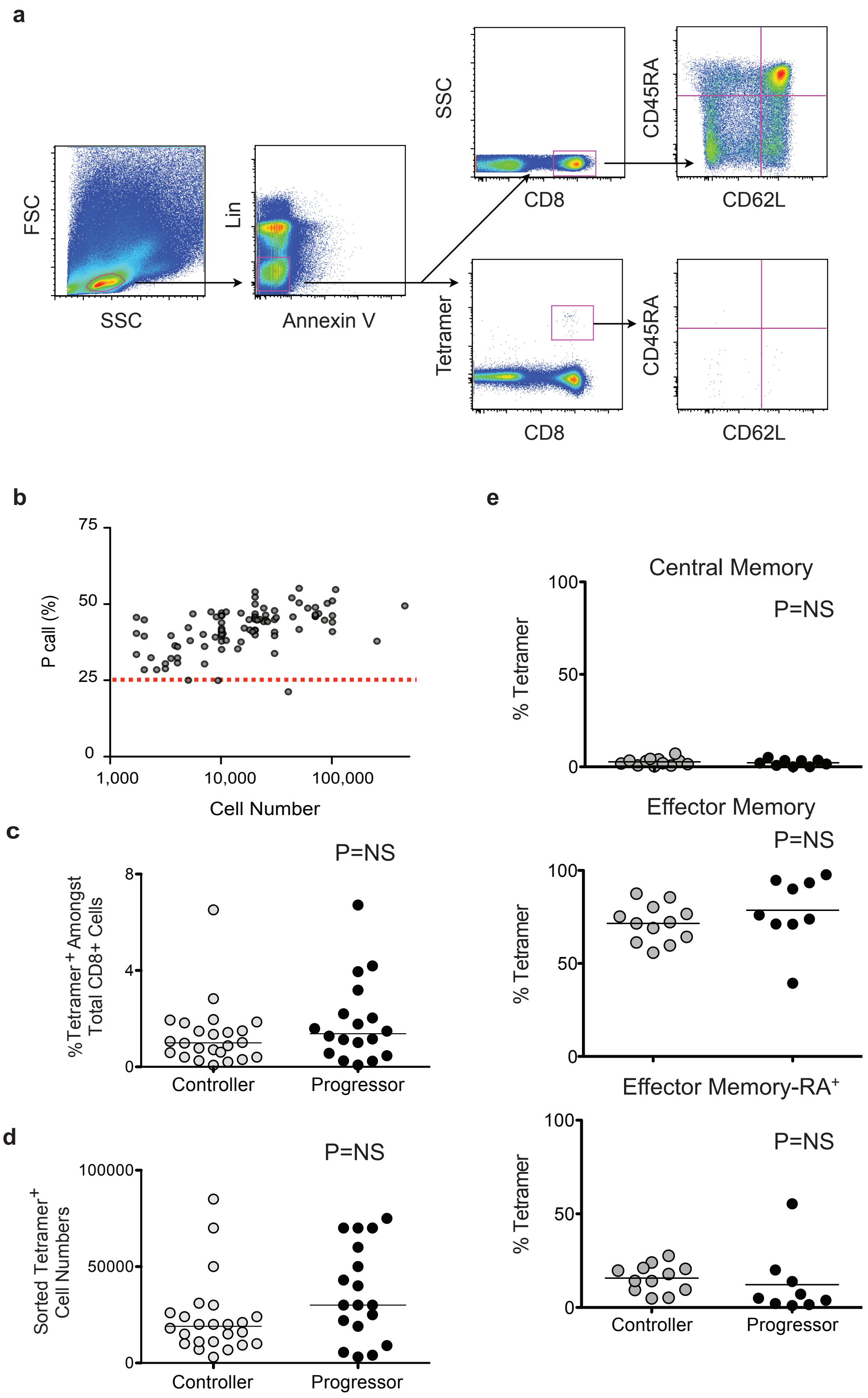
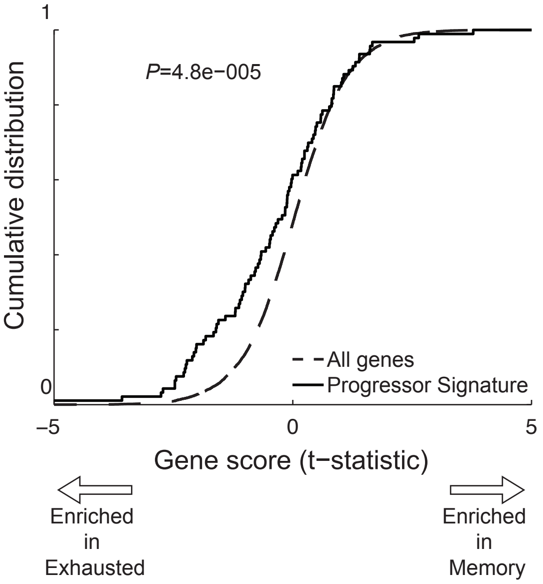
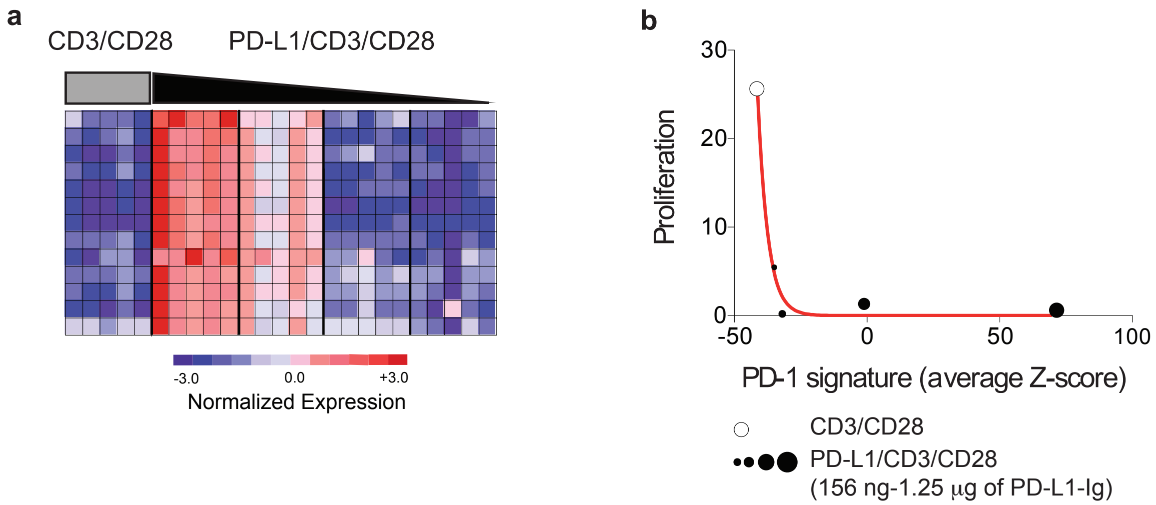


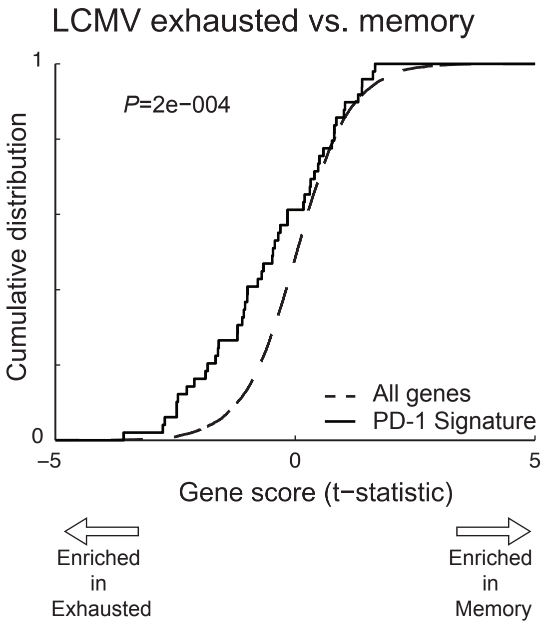
Supplementary Figure 1: Sorting and characterization of HIV-specific CD8+ T cells
(a) Flow cytometry gating strategy for sorting of HIV Gag-tetramer+ CD8+ T cells). (b) Quality of microarray data generated from small numbers of HIV Gag-specific CD8+ T cells as determined by percent P call. (c,d) Percent of tetramer+ cells in total CD8+ T cells (d) and numbers of cells recovered post-sort in controllers (grey circles) and progressors (black circles) cohorts. (e) Fraction of HIV Gag-specific CD8+ T cells with a central memory (upper plot), effector memory (middle plot) or effector memory-RA+ (lower plot) phenotype in controllers (grey circles) and progressors (black circles).



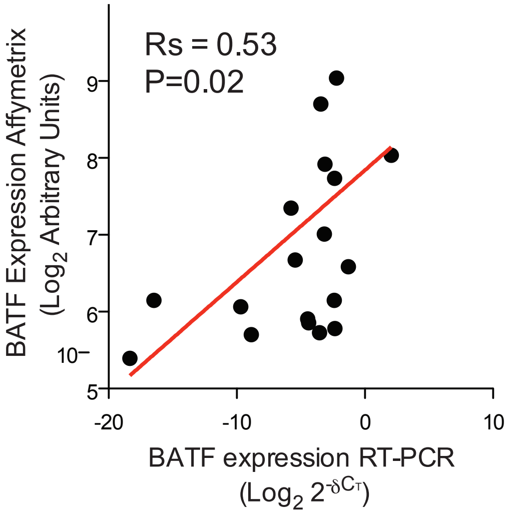
Supplementary Figure 2: Transcriptional profiles of HIV-specific CD8+ T cells from progressors are globally similar to profiles from exhausted CD8+ T cells in the mouse model of chronic LCMV infection.
The top 200 genes in the HIV progressor Gag-specific signature were tested for enrichment in the rank-ordered list of genes differentially expressed in exhausted LCMV-specific vs. functional memory LCMV-specific T cells. X-axis indicates the t-statistic measured for each of the ~11,000 genes mouse genes featured on the array, ranked in order of their differential expression in LCMV-specific CD8+ T cells from clone 13 infection (exhausted) vs. Armstrong (memory). Y-axis indicates the cumulative distribution of all genes (dotted lines) or of the set of 200 HIV-progressor genes (black line). Gene sets that are related to the class distinction on the X-axis would be expected to deviate from the dotted line (i.e. shifted towards the left if enriched in exhausted or shifted towards the right if enriched in memory LCMV-specific CD8+ T cells). A similar analysis using the controller signature show no enriched in CD8+ T cells from mouse model of LCMV Armstrong infection (not shown).



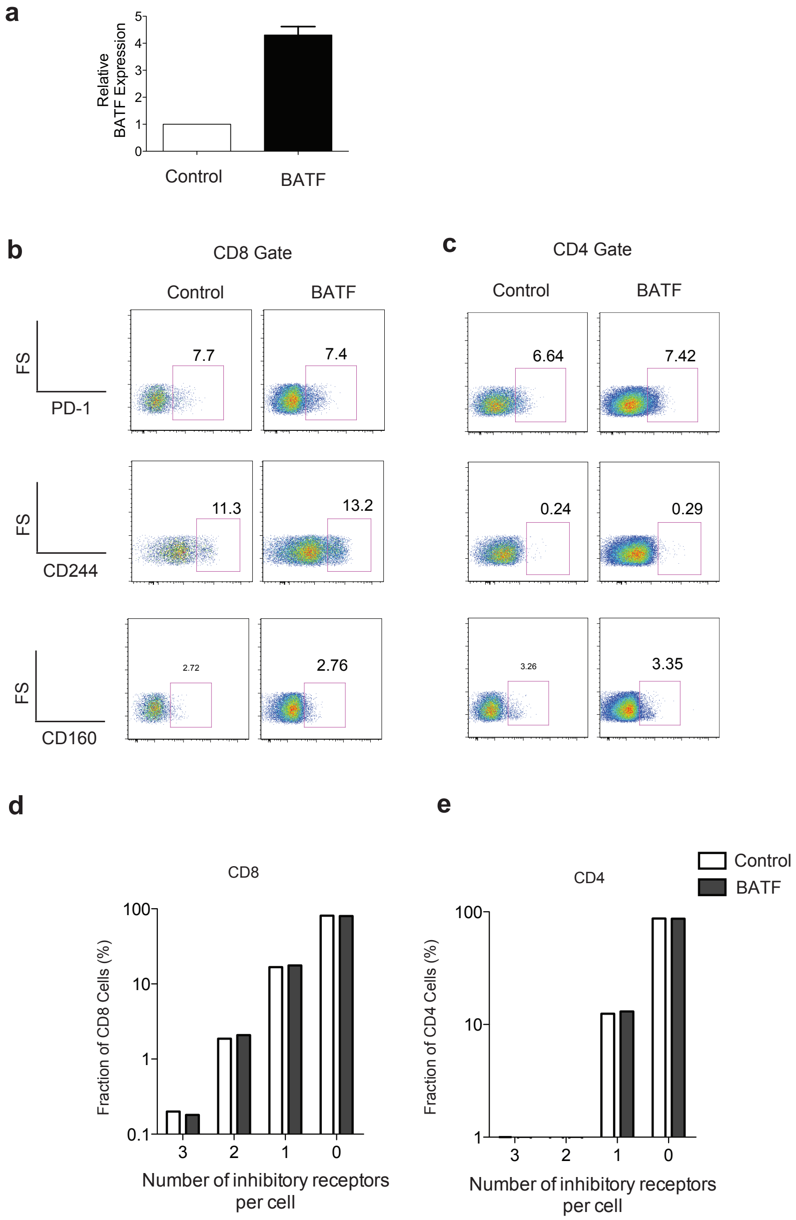
Supplementary Figure 3: PD-1 signature genes are upregulated by PDL1 in primary human T cells.
(a) Dose-dependent induction of the PD-1 signature genes in primary human CD4+ T cells cultured either with CD3/CD28 beads (grey columns) or PDL1/CD3/CD28 beads with a 2-fold decreasing amounts of bead-bound PD-L1-Ig in replicates of five (black columns). (b) Correlation between inhibition of proliferation and upregulated of PD-1 signature genes presented in c. PD-1 signature gene expression summarized by average Z score (x-axis) and extent of proliferation by primary T cells over a four day period of stimulation with the relevant beads (y-axis, $R^2 = 0.98$).



Supplementary Figure 4: PD-1 signature genes are enriched in exhausted CD8+ T cells in the mouse model of chronic LCMV infection.
The top 200 PD-1 signature genes were tested for enrichment in the exhausted vs memory CD8+ T cell profiles from the mouse model of LCMV infection. The enrichment is displayed as a cumulative enrichment plot, with the left-shift of the PD-1 signature (solid black line) indicating enrichment in exhausted T cells.

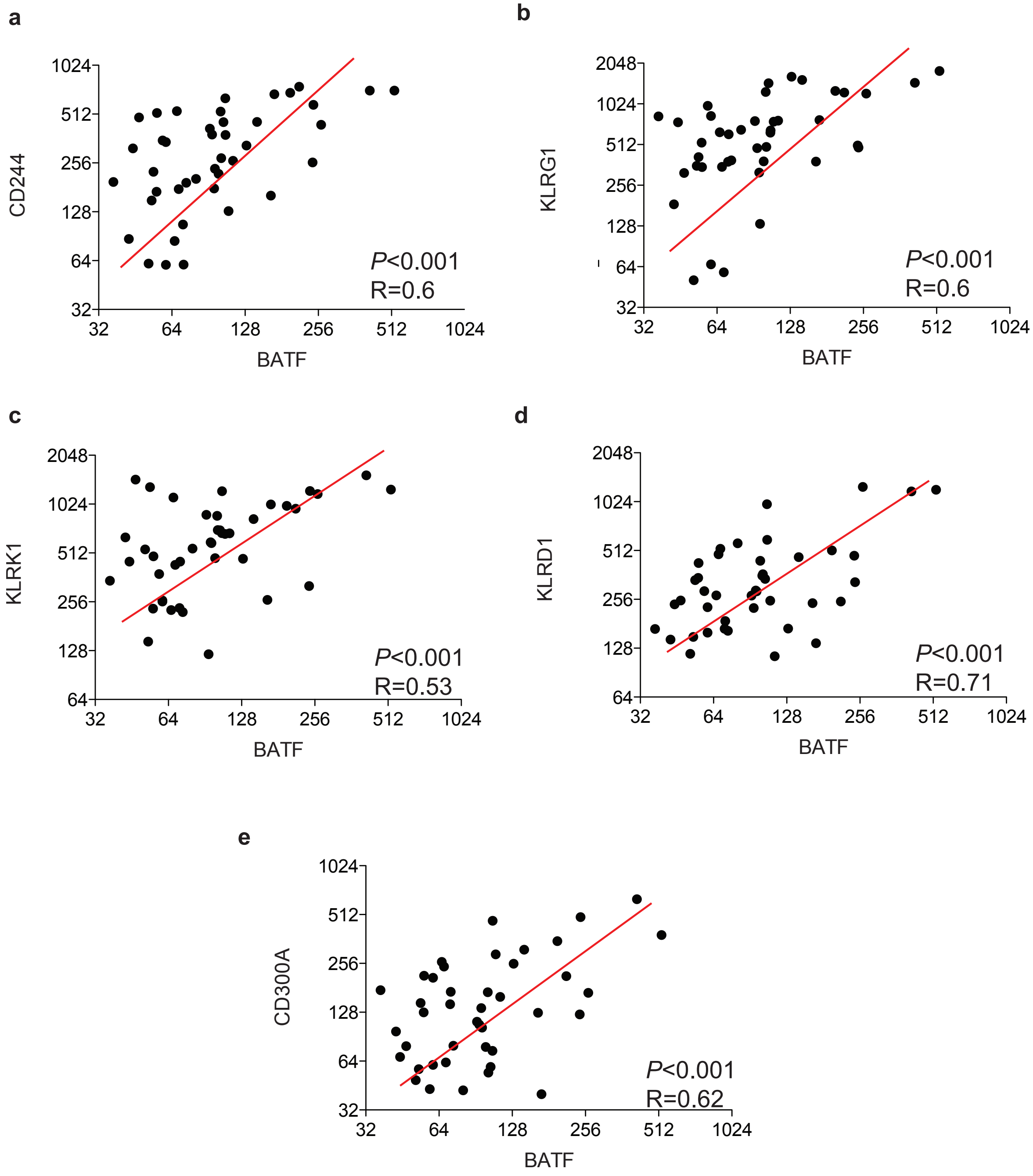


Supplementary Figure 5: Validation of BATF expression in HIV-specific CD8+ T cells. Correlation between BATF expression as quantified by Affymetrix microarray and by quantitative RT-PCR in sorted populations of HIV-specific CD8+ T cells. RNA extracted from each sample underwent a separate linear amplification reaction prior each type of assay. Each point represents an individual patient sample (n=18) from which sufficient RNA was available for both assays. Rs and P value refer to the Spearman correlation coefficient.



Supplementary Figure 6: Inhibitory receptor expression in human T cells over-expressing BATF.

(a) Relative BATF expression by quantitative PCR analysis in primary human T cells transduced with empty vector (white bar) or overexpressing BATF (black bar). (b,c) Multiparameter flow cytometry analysis of human CD8+ (b) and CD4+ T cells (c) for the inhibitory receptors shown two days post transduction with vector or BATF expressing lentivirus. Figures refer to percent of cells expressing the receptor indicated. (d,e) Analysis of the frequency of CD8+ (d) or CD4+ (e) T cells expressing the number of inhibitory receptors shown.



Supplementary Figure 7: BATF expression is correlated with known or putative inhibitory receptors.
A nearest gene neighbor analysis was performed to identify genes whose expression level correlated significantly by Pearson correlation analysis with that of BATF across all samples of HIV-specific CD8+ T cells. Of the top 500 genes, significant correlation was observed for genes with known or putative inhibitory function including CD244 (a); KLRG1 (b); KLRK1 (c); KLRD1 (d) and CD300A (e). Values refer to Affymetrix expression units and are presented in a log2 plot to improve visualization of data.

Supplementary Tables

Supplementary Table 1: Patient characteristics and distribution of class I HLA alleles associated with disease progression

	HIV Controllers	**Chronic Progressors**
Number of subjects	24	18
Gender Male (%)	22 (92)	15 (83)
Female (%)	2 (8)	3 (17)
Race (%) White	19 (79)	10 (56)
Black	3 (13)	1 (6)
Other / Unknown	2 (8)	7 (38)
Plasma HIV RNA, copies/ml median (IQR)	Below detection (49-100)[A]	11,784 (5,035-29,915)
CD4+ cell count, cells/mm^3 median (IQR)	792 (666-945)[A]	468 (358-582)
Duration of HIV diagnosis, years median (IQR)	14 (7-20)	4 (2-10)
HLA B*57 (%)	8 (33)	6 (33)
HLA B*27 (%)	7 (29)	0 (0)
All protective HLA alleles[B]	20 (83)	8 (44)

[A] HIV controllers compared to chronic progressors * *P* <0.0001 *(non-parametric Mann Whitney test)*

[B] Includes HLA B*57, 27, 13, 14, 1503, 51 and 5801

Supplementary Table 2: Transcripts increased in expression in HIV-gag-specific CD8$^+$ T cells from HIV Controllers (t > 2.0; green font), or progressors (t < –2.0; red font).

probeset_id	GeneTitle	GeneSymbol	GeneID	t	q
210621_s_at	RAS p21 protein activator (GTPase activating protein) 1	RASA1	5921	6.102845	0.007526
202524_s_at	sparc/osteonectin. cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	9806	4.358444	0.358674
202677_at	RAS p21 protein activator (GTPase activating protein) 1	RASA1	5921	4.019843	0.421399
205288_at	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	CDC14A	8556	3.954898	0.421399
216668_at	---	---	---	3.938437	0.421399
216042_at	tumor necrosis factor receptor superfamily. member 25	TNFRSF25	8718	3.893672	0.421399
204897_at	prostaglandin E receptor 4 (subtype EP4)	PTGER4	5734	3.878922	0.421399
212594_at	programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	27250	3.870662	0.421399
202643_s_at	tumor necrosis factor. alpha-induced protein 3	TNFAIP3	7128	3.86239	0.421399
203725_at	growth arrest and DNA-damage-inducible. alpha	GADD45A	1647	3.860574	0.421399
216834_at	regulator of G-protein signaling 1	RGS1	5996	3.838977	0.421399
210538_s_at	baculoviral IAP repeat-containing 3	BIRC3	330	3.78425	0.421399
201195_s_at	solute carrier family 7 (cationic amino acid transporter. y+ system). member 5	SLC7A5	8140	3.77992	0.421399
203708_at	phosphodiesterase 4B. cAMP-specific (phosphodiesterase E4 dunce homolog. Drosophila)	PDE4B	5142	3.736681	0.421399
203413_at	NEL-like 2 (chicken)	NELL2	4753	3.736636	0.421399
211426_x_at	guanine nucleotide binding protein (G protein). q polypeptide	GNAQ	2776	3.718252	0.421399
202644_s_at	tumor necrosis factor. alpha-induced protein 3	TNFAIP3	7128	3.699406	0.421399
208744_x_at	heat shock 105kDa/110kDa protein 1	HSPH1	10808	3.685959	0.421399
221618_s_at	TAF9B RNA polymerase II. TATA box binding protein (TBP)-associated factor. 31kDa /// similar to transcriptio	LOC728198 //	51616 /// 728	3.685703	0.421399
202988_s_at	regulator of G-protein signaling 1	RGS1	5996	3.681003	0.421399
218346_s_at	sestrin 1	SESN1	27244	3.675679	0.421399
204093_at	cyclin H	CCNH	902	3.665929	0.421399
202147_s_at	interferon-related developmental regulator 1	IFRD1	3475	3.663846	0.421399
202612_s_at	mediator complex subunit 14	MED14	9282	3.642599	0.428654
219220_x_at	mitochondrial ribosomal protein S22	MRPS22	56945	3.6085	0.433373
217434_at	melanocortin 2 receptor (adrenocorticotropic hormone)	MC2R	4158	3.603807	0.433373
213198_at	activin A receptor. type IB	ACVR1B	91	3.54465	0.471311
215671_at	phosphodiesterase 4B. cAMP-specific (phosphodiesterase E4 dunce homolog. Drosophila)	PDE4B	5142	3.535287	0.4723
212828_at	synaptojanin 2	SYNJ2	8871	3.52019	0.47591
205667_at	Werner syndrome	WRN	7486	3.445721	0.524274
212774_at	zinc finger protein 238	ZNF238	10472	3.429588	0.524274
212652_s_at	sorting nexin 4	SNX4	8723	3.427343	0.524274
210440_s_at	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	CDC14A	8556	3.409686	0.524274
222366_at	Transcribed locus	---	---	3.408979	0.524274
212842_x_at	RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 4 /// RANBP2-like a	RGPD4 /// RG	285190 /// 72	3.404826	0.524274
221756_at	phosphoinositide-3-kinase interacting protein 1	PIK3IP1	113791	3.393236	0.524274
211856_x_at	CD28 molecule	CD28	940	3.377707	0.524274
212723_at	jumonji domain containing 6	JMJD6	23210	3.36603	0.524274
204155_s_at	KIAA0999 protein	KIAA0999	23387	3.360743	0.524274
200911_s_at	transforming. acidic coiled-coil containing protein 1	TACC1	6867	3.359818	0.524274
201260_s_at	synaptophysin-like 1	SYPL1	6856	3.356806	0.524274
213161_at	chromosome 9 open reading frame 97	C9orf97	158427	3.316162	0.562181
208113_x_at	poly(A) binding protein. cytoplasmic 3	PABPC3	5042	3.309036	0.562181
204567_s_at	ATP-binding cassette. sub-family G (WHITE). member 1	ABCG1	9619	3.301306	0.562181
216507_at	transmembrane anterior posterior transformation 1	TAPT1	202018	3.298073	0.562181
217783_s_at	yippee-like 5 (Drosophila)	YPEL5	51646	3.278703	0.569778
222149_x_at	golgi autoantigen. golgin subfamily a. 8G /// golgi autoantigen. golgin subfamily a. 8E /// golgin-like hypothe	FLJ32679 /// (	283768 /// 39	3.261185	0.572938
207785_s_at	recombination signal binding protein for immunoglobulin kappa J region	RBPJ	3516	3.254771	0.572938
206240_s_at	zinc finger protein 136	ZNF136	7695	3.242229	0.578032
211302_s_at	phosphodiesterase 4B. cAMP-specific (phosphodiesterase E4 dunce homolog. Drosophila)	PDE4B	5142	3.240741	0.578032
217936_at	Rho GTPase activating protein 5	ARHGAP5	394	3.238402	0.578032
213097_s_at	zuotin related factor 1	ZRF1	27000	3.230394	0.584702
211956_s_at	eukaryotic translation initiation factor 1	EIF1	10209	3.218113	0.592547
220009_at	LON peptidase N-terminal domain and ring finger 3	LONRF3	79836	3.217957	0.592547
205239_at	amphiregulin (schwannoma-derived growth factor) /// similar to Amphiregulin precursor (AR) (Colorectum ce	AREG /// LOC	374 /// 72773	3.193815	0.620402
203758_at	cathepsin O	CTSO	1519	3.157571	0.65843
207041_at	mannan-binding lectin serine peptidase 2	MASP2	10747	3.152405	0.659793
202027_at	transmembrane protein 184B	TMEM184B	25829	3.149718	0.659793
204015_s_at	dual specificity phosphatase 4	DUSP4	1846	3.133074	0.665781
209267_s_at	solute carrier family 39 (zinc transporter). member 8	SLC39A8	64116	3.132592	0.665781
214081_at	plexin domain containing 1	PLXDC1	57125	3.116051	0.668264
203053_at	breast carcinoma amplified sequence 2	BCAS2	10286	3.114933	0.668264
218311_at	mitogen-activated protein kinase kinase kinase kinase 3	MAP4K3	8491	3.109655	0.668264
217843_s_at	mediator complex subunit 4	MED4	29079	3.107119	0.668264
214700_x_at	RAP1 interacting factor homolog (yeast)	RIF1	55183	3.104424	0.668264
219700_at	plexin domain containing 1	PLXDC1	57125	3.098819	0.668264
219312_s_at	zinc finger and BTB domain containing 10	ZBTB10	65986	3.077987	0.679372
217142_at	similar to Elongation FacTor family member (eft-4)	LOC442215	442215	3.077047	0.679372
204433_s_at	spermatogenesis associated 2	SPATA2	9825	3.074281	0.679372
204995_at	cyclin-dependent kinase 5. regulatory subunit 1 (p35)	CDK5R1	8851	3.062	0.686712
211596_s_at	leucine-rich repeats and immunoglobulin-like domains 1	LRIG1	26018	3.060855	0.686712
212400_at	family with sequence similarity 102. member A	FAM102A	399665	3.020866	0.707388
212561_at	RAB6 interacting protein 1	RAB6IP1	23258	3.016257	0.707388
202866_at	DnaJ (Hsp40) homolog. subfamily B. member 12	DNAJB12	54788	3.01409	0.707388
206621_s_at	eukaryotic translation initiation factor 4H	EIF4H	7458	3.013139	0.707388
216056_at	CD44 molecule (Indian blood group)	CD44	960	3.007286	0.707388
201800_s_at	oxysterol binding protein	OSBP	5007	2.989052	0.707388
222308_x_at	Transcribed locus	---	---	2.988094	0.707388
208881_x_at	isopentenyl-diphosphate delta isomerase 1	IDI1	3422	2.977631	0.707388
216823_at	ribosomal protein S3A /// similar to ribosomal protein S3a /// similar to 40S ribosomal protein S3a (V-fos tra	LOC146053 //	146053 /// 39	2.97665	0.707388
202371_at	transcription elongation factor A (SII)-like 4	TCEAL4	79921	2.968666	0.707388
218149_s_at	zinc finger protein 395	ZNF395	55893	2.968342	0.707388
220657_at	kelch-like 11 (Drosophila)	KLHL11	55175	2.967117	0.707388
209682_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	868	2.965748	0.707388
205798_at	interleukin 7 receptor	IL7R	3575	2.956947	0.710946
221423_s_at	Yip1 domain family. member 5	YIPF5	81555	2.953985	0.710946
214177_s_at	pre-B-cell leukemia homeobox interacting protein 1	PBXIP1	57326	2.952906	0.710946
215915_at	GULP. engulfment adaptor PTB domain containing 1	GULP1	51454	2.937958	0.729414
220671_at	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	CCRN4L	25819	2.934848	0.729414

212439_at	inositol hexaphosphate kinase 1	IHPK1	9807	2.91777	0.744465
214910_s_at	apolipoprotein M	APOM	55937	2.917463	0.744465
209871_s_at	amyloid beta (A4) precursor protein-binding. family A. member 2 (X11-like)	APBA2	321	2.901997	0.74575
56919_at	WD repeat domain 48	WDR48	57599	2.900309	0.74575
212479_s_at	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	RMND5A	64795	2.893239	0.74575
214480_at	ets variant gene 3	ETV3	2117	2.871235	0.763884
210281_s_at	zinc finger. MYM-type 2	ZMYM2	7750	2.865801	0.763884
212098_at	hypothetical protein LOC151162	LOC151162	151162	2.862768	0.763884
213737_x_at	golgi autoantigen. golgin subfamily a. 8G /// golgi autoantigen. golgin subfamily a. 8E /// golgin-like hypothe	FLJ32679 ///	283768 /// 39	2.859986	0.763884
202731_at	programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	27250	2.859792	0.763884
204064_at	THO complex 1	THOC1	9984	2.854056	0.769097
209824_s_at	aryl hydrocarbon receptor nuclear translocator-like	ARNTL	406	2.852889	0.769097
215592_at	CDNA FLJ12232 fis. clone MAMMA1001206	---	---	2.851328	0.769097
221821_s_at	chromosome 12 open reading frame 41	C12orf41	54934	2.840881	0.778228
207113_s_at	tumor necrosis factor (TNF superfamily. member 2)	TNF	7124	2.833033	0.782863
213285_at	transmembrane protein 30B	TMEM30B	161291	2.829208	0.786818
213615_at	Membrane bound O-acyltransferase domain containing 5	MBOAT5	10162	2.809843	0.813
220814_at	---	---	---	2.807338	0.813
207184_at	solute carrier family 6 (neurotransmitter transporter. GABA). member 13	SLC6A13	6540	2.80416	0.813
208122_x_at	killer cell immunoglobulin-like receptor. two domains. short cytoplasmic tail. 3	KIR2DS3	3808	2.803959	0.813
204568_at	KIAA0831	KIAA0831	22863	2.797555	0.814269
208910_s_at	complement component 1. q subcomponent binding protein	C1QBP	708	2.79368	0.818641
208624_s_at	eukaryotic translation initiation factor 4 gamma. 1	EIF4G1	1981	2.786457	0.824301
211449_at	mutS homolog 6 (E. coli)	MSH6	2956	2.783996	0.824301
221127_s_at	regulated in glioma	RIG	10530	2.783884	0.824301
214775_at	Nedd4 binding protein 3	N4BP3	23138	2.77957	0.826033
217191_x_at	---	---	---	2.774094	0.830816
204135_at	filamin A interacting protein 1-like	FILIP1L	11259	2.772083	0.830816
216248_s_at	nuclear receptor subfamily 4. group A. member 2	NR4A2	4929	2.768435	0.83379
204615_x_at	isopentenyl-diphosphate delta isomerase 1	IDI1	3422	2.767244	0.83379
203543_s_at	Kruppel-like factor 9	KLF9	687	2.757837	0.843005
218784_s_at	chromosome 6 open reading frame 64	C6orf64	55776	2.746884	0.848523
218472_s_at	pelota homolog (Drosophila)	PELO	53918	2.739202	0.852106
204992_s_at	profilin 2	PFN2	5217	2.734342	0.852106
203313_s_at	TGFB-induced factor homeobox 1	TGIF1	7050	2.731691	0.852106
214176_s_at	Transcribed locus	---	---	2.728847	0.852106
209181_s_at	Rab geranylgeranyltransferase. beta subunit	RABGGTB	5876	2.718975	0.852106
213547_at	cullin-associated and neddylation-dissociated 2 (putative)	CAND2	23066	2.716758	0.852106
202193_at	LIM domain kinase 2	LIMK2	3985	2.715031	0.852106
213555_at	RWD domain containing 2A	RWDD2A	112611	2.714331	0.852106
214247_s_at	dickkopf homolog 3 (Xenopus laevis)	DKK3	27122	2.71381	0.852106
207735_at	ring finger protein 125	RNF125	54941	2.712912	0.852106
219132_at	pellino homolog 2 (Drosophila)	PELI2	57161	2.712876	0.852106
218399_s_at	cell division cycle associated 4	CDCA4	55038	2.710363	0.852106
213518_at	protein kinase C. iota	PRKCI	5584	2.708574	0.852106
215716_s_at	ATPase. Ca++ transporting. plasma membrane 1	ATP2B1	490	2.703858	0.853874
209535_s_at	---	---	---	2.702875	0.853874
208673_s_at	splicing factor. arginine/serine-rich 3	SFRS3	6428	2.700417	0.853874
202595_s_at	leptin receptor overlapping transcript-like 1	LEPROTL1	23484	2.69904	0.853874
202165_at	protein phosphatase 1. regulatory (inhibitor) subunit 2	PPP1R2	5504	2.69716	0.853874
201259_s_at	synaptophysin-like 1	SYPL1	6856	2.694686	0.853874
220643_s_at	Fas apoptotic inhibitory molecule	FAIM	55179	2.693547	0.853874
212063_at	CD44 molecule (Indian blood group)	CD44	960	2.693352	0.853874
213970_at	RAB. member of RAS oncogene family-like 3 /// similar to RAB. member of RAS oncogene family-like 3	LOC653256 //	285282 /// 65	2.687393	0.853874
217579_x_at	Transcribed locus	---	---	2.678399	0.853874
218577_at	leucine rich repeat containing 40	LRRC40	55631	2.673808	0.853874
207681_at	chemokine (C-X-C motif) receptor 3	CXCR3	2833	2.670851	0.853874
204622_x_at	nuclear receptor subfamily 4. group A. member 2	NR4A2	4929	2.668807	0.853874
214871_x_at	CDNA clone IMAGE:3347954	---	---	2.664172	0.853874
203408_s_at	SATB homeobox 1	SATB1	6304	2.659846	0.853874
205836_s_at	YTH domain containing 2	YTHDC2	64848	2.658214	0.853874
206587_at	chaperonin containing TCP1. subunit 6B (zeta 2)	CCT6B	10693	2.656478	0.853874
218252_at	cytoskeleton associated protein 2	CKAP2	26586	2.655766	0.853874
215157_x_at	poly(A) binding protein. cytoplasmic 1	PABPC1	26986	2.65513	0.853874
217709_at	---	---	---	2.649384	0.859457
202381_at	ADAM metallopeptidase domain 9 (meltrin gamma)	ADAM9	8754	2.645573	0.860415
204334_at	Kruppel-like factor 7 (ubiquitous)	KLF7	8609	2.642512	0.860415
216962_at	RPA interacting protein	RPAIN	84268	2.638828	0.862215
206055_s_at	small nuclear ribonucleoprotein polypeptide A'	SNRPA1	6627	2.629298	0.866649
65591_at	WD repeat domain 48	WDR48	57599	2.629056	0.866649
208144_s_at	---	---	---	2.628945	0.866649
212648_at	DEAH (Asp-Glu-Ala-His) box polypeptide 29	DHX29	54505	2.621064	0.873794
214801_at	CDNA FLJ11392 fis. clone HEMBA1000575	---	---	2.618272	0.874998
210871_x_at	synovial sarcoma. X breakpoint 2 interacting protein	SSX2IP	117178	2.612874	0.880393
219276_x_at	chromosome 9 open reading frame 82	C9orf82	79886	2.606586	0.886545
206910_x_at	complement factor H-related 2	CFHR2	3080	2.605852	0.886545
201181_at	guanine nucleotide binding protein (G protein). alpha inhibiting activity polypeptide 3	GNAI3	2773	2.602662	0.888013
214332_s_at	Ts translation elongation factor. mitochondrial	TSFM	10102	2.601444	0.888013
208989_s_at	F-box and leucine-rich repeat protein 11	FBXL11	22992	2.594543	0.890175
201408_at	protein phosphatase 1. catalytic subunit. beta isoform	PPP1CB	5500	2.59275	0.890891
207877_s_at	nuclear VCP-like	NVL	4931	2.588869	0.892861
200004_at	eukaryotic translation initiation factor 4 gamma. 2	EIF4G2	1982	2.583782	0.900002
203006_at	inositol polyphosphate-5-phosphatase. 40kDa	INPP5A	3632	2.581643	0.902077
209609_s_at	mitochondrial ribosomal protein L9	MRPL9	65005	2.572996	0.913069
209149_s_at	transmembrane 9 superfamily member 1	TM9SF1	10548	2.572861	0.913069
213224_s_at	hypothetical protein LOC92482	LOC92482	92482	2.563975	0.919927
209273_s_at	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	ISCA1	81689	2.563248	0.919927
212177_at	splicing factor. arginine/serine-rich 18	SFRS18	25957	2.554404	0.919927
53987_at	RAN binding protein 10	RANBP10	57610	2.549391	0.919927
218203_at	asparagine-linked glycosylation 5 homolog (S. cerevisiae. dolichyl-phosphate beta-glucosyltransferase)	ALG5	29880	2.543379	0.919927
219117_s_at	FK506 binding protein 11. 19 kDa	FKBP11	51303	2.541763	0.919927
201504_s_at	translin	TSN	7247	2.541723	0.919927

212782_x_at	polymerase (RNA) II (DNA directed) polypeptide J. 13.3kDa	POLR2J	5439	2.541173	0.919927
206147_x_at	sex comb on midleg-like 2 (Drosophila)	SCML2	10389	2.540181	0.919927
216062_at	Transcribed locus	---	---	2.539996	0.919927
208798_x_at	golgi autoantigen. golgin subfamily a. 8A	GOLGA8A	23015	2.534337	0.930224
201070_x_at	splicing factor 3b. subunit 1. 155kDa	SF3B1	23451	2.52693	0.934755
203580_s_at	solute carrier family 7 (cationic amino acid transporter. y+ system). member 6	SLC7A6	9057	2.526793	0.934755
220386_s_at	echinoderm microtubule associated protein like 4	EML4	27436	2.523807	0.934755
209898_x_at	intersectin 2	ITSN2	50618	2.523776	0.934755
218017_s_at	heparan-alpha-glucosaminide N-acetyltransferase	HGSNAT	138050	2.520065	0.934878
212508_at	modulator of apoptosis 1	MOAP1	64112	2.519008	0.934878
217028_at	chemokine (C-X-C motif) receptor 4	CXCR4	7852	2.518981	0.934878
215167_at	mediator complex subunit 14	MED14	9282	2.517989	0.934878
208190_s_at	lipolysis stimulated lipoprotein receptor	LSR	51599	2.51541	0.9383
218587_s_at	KTEL (Lys-Tyr-Glu-Leu) containing 1	KTELC1	56983	2.512075	0.940768
215951_at	TBC1 domain family. member 2B	TBC1D2B	23102	2.509793	0.940768
214446_at	elongation factor. RNA polymerase II. 2	ELL2	22936	2.508233	0.940768
219361_s_at	interferon stimulated exonuclease gene 20kDa-like 1	ISG20L1	64782	2.506478	0.941568
203775_at	solute carrier family 25. member 13 (citrin)	SLC25A13	10165	2.504291	0.944149
221986_s_at	kelch-like 24 (Drosophila)	KLHL24	54800	2.503127	0.944387
214327_x_at	tumor protein. translationally-controlled 1	TPT1	7178	2.494126	0.94564
208968_s_at	cytokine induced apoptosis inhibitor 1	CIAPIN1	57019	2.492988	0.94564
221894_at	aarF domain containing kinase 2	ADCK2	90956	2.492683	0.94564
211955_at	RAN binding protein 5	RANBP5	3843	2.491585	0.94564
204270_at	v-ski sarcoma viral oncogene homolog (avian)	SKI	6497	2.491374	0.94564
203865_s_at	adenosine deaminase. RNA-specific. B1 (RED1 homolog rat)	ADARB1	104	2.48929	0.94564
215053_at	Snf2-related CREBBP activator protein	SRCAP	10847	2.486605	0.94564
202181_at	KIAA0247	KIAA0247	9766	2.485502	0.94564
212284_x_at	tumor protein. translationally-controlled 1	TPT1	7178	2.485277	0.94564
219717_at	chromosome 4 open reading frame 30	C4orf30	54876	2.485262	0.94564
202523_s_at	sparc/osteonectin. cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	9806	2.48326	0.94564
205540_s_at	Ras-related GTP binding B	RRAGB	10325	2.48273	0.94564
201389_at	integrin. alpha 5 (fibronectin receptor. alpha polypeptide)	ITGA5	3678	2.477595	0.945648
202843_at	DnaJ (Hsp40) homolog. subfamily B. member 9	DNAJB9	4189	2.47685	0.945648
218579_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 35	DHX35	60625	2.475459	0.945989
214683_s_at	CDC-like kinase 1	CLK1	1195	2.473706	0.945989
212434_at	GrpE-like 1. mitochondrial (E. coli)	GRPEL1	80273	2.472534	0.945989
211893_x_at	CD6 molecule	CD6	923	2.470514	0.945989
205966_at	TAF13 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 18kDa	TAF13	6884	2.46959	0.945989
207079_s_at	mediator complex subunit 6	MED6	10001	2.464536	0.945989
218386_x_at	ubiquitin specific peptidase 16	USP16	10600	2.46445	0.945989
202146_at	interferon-related developmental regulator 1	IFRD1	3475	2.462514	0.945989
202436_s_at	cytochrome P450. family 1. subfamily B. polypeptide 1	CYP1B1	1545	2.456843	0.953221
203380_x_at	splicing factor. arginine/serine-rich 5	SFRS5	6430	2.455063	0.955096
201417_at	SRY (sex determining region Y)-box 4	SOX4	6659	2.453488	0.955994
200921_s_at	B-cell translocation gene 1. anti-proliferative	BTG1	694	2.451227	0.955994
204790_at	SMAD family member 7	SMAD7	4092	2.4503	0.955994
206976_s_at	heat shock 105kDa/110kDa protein 1	HSPH1	10808	2.446554	0.955994
212722_s_at	jumonji domain containing 6	JMJD6	23210	2.444481	0.955994
210017_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	MALT1	10892	2.443662	0.955994
205259_at	nuclear receptor subfamily 3. group C. member 2	NR3C2	4306	2.440498	0.955994
215823_x_at	poly(A) binding protein. cytoplasmic 3 /// poly(A) binding protein. cytoplasmic 1 /// hypothetical LOC341315	LOC341315 //	26986 /// 341	2.439228	0.955994
212089_at	lamin A/C	LMNA	4000	2.436625	0.956222
212014_x_at	CD44 molecule (Indian blood group)	CD44	960	2.435005	0.95725
208724_s_at	RAB1A. member RAS oncogene family	RAB1A	5861	2.429922	0.963147
200082_s_at	ribosomal protein S7 /// similar to 40S ribosomal protein S7 (S8)	LOC644315 //	6201 /// 6443	2.421208	0.965103
210054_at	chromosome 4 open reading frame 15	C4orf15	79441	2.420858	0.965103
219028_at	homeodomain interacting protein kinase 2	HIPK2	28996	2.415199	0.965103
218218_at	adaptor protein. phosphotyrosine interaction. PH domain and leucine zipper containing 2	APPL2	55198	2.415134	0.965103
213310_at	Eukaryotic translation initiation factor 2C. 2	EIF2C2	27161	2.4133	0.965103
221773_at	ELK3. ETS-domain protein (SRF accessory protein 2)	ELK3	2004	2.413153	0.965103
212447_at	kelch repeat and BTB (POZ) domain containing 2	KBTBD2	25948	2.412631	0.965103
206404_at	fibroblast growth factor 9 (glia-activating factor)	FGF9	2254	2.412065	0.965103
201513_at	translin	TSN	7247	2.410556	0.965103
217998_at	pleckstrin homology-like domain. family A. member 1 /// hypothetical LOC652993	LOC652993 //	22822 /// 652	2.410412	0.965103
214125_s_at	Neuron derived neurotrophic factor	NENF	29937	2.410151	0.965103
209185_s_at	insulin receptor substrate 2	IRS2	8660	2.40643	0.965484
208160_at	hypothetical protein FLJ10232	FLJ10232	55099	2.404512	0.965484
209712_at	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter). member D1	SLC35D1	23169	2.403846	0.965484
216044_x_at	family with sequence similarity 69. member A	FAM69A	388650	2.395344	0.968985
37433_at	protein inhibitor of activated STAT. 2	PIAS2	9063	2.394352	0.968985
209993_at	ATP-binding cassette. sub-family B (MDR/TAP). member 1	ABCB1	5243	2.393495	0.968985
206337_at	chemokine (C-C motif) receptor 7	CCR7	1236	2.391027	0.968985
206114_at	EPH receptor A4	EPHA4	2043	2.390647	0.968985
208804_s_at	splicing factor. arginine/serine-rich 6	SFRS6	6431	2.389085	0.968985
221768_at	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ	6421	2.388672	0.968985
206156_at	gap junction protein. beta 5. 31.1kDa	GJB5	2709	2.387915	0.968985
202565_s_at	supervillin	SVIL	6840	2.387738	0.968985
214879_x_at	upstream transcription factor 2. c-fos interacting	USF2	7392	2.38314	0.973168
214124_x_at	Transcribed locus	---	---	2.382812	0.973168
222326_at	Transcribed locus	---	---	2.382554	0.973168
216945_x_at	PAS domain containing serine/threonine kinase	PASK	23178	2.378087	0.97962
201917_s_at	solute carrier family 25. member 36	SLC25A36	55186	2.376248	0.981949
216282_x_at	polymerase (RNA) II (DNA directed) polypeptide C. 33kDa	POLR2C	5432	2.375281	0.982256
220271_x_at	EF-hand calcium binding domain 6	EFCAB6	64800	2.370658	0.982963
60815_at	polymerase (RNA) II (DNA directed) polypeptide J. 13.3kDa pseudogene	POLR2J4	84820	2.37039	0.982963
214129_at	similar to phosphodiesterase 4D interacting protein isoform 2	LOC727942	727942	2.370315	0.982963
221425_s_at	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	ISCA1	81689	2.368778	0.982963
201690_s_at	tumor protein D52	TPD52	7163	2.365403	0.982963
213538_at	SON DNA binding protein	SON	6651	2.364927	0.982963
219826_at	zinc finger protein 419	ZNF419	79744	2.363416	0.982963
205100_at	glutamine-fructose-6-phosphate transaminase 2	GFPT2	9945	2.362071	0.982963
206618_at	interleukin 18 receptor 1	IL18R1	8809	2.36182	0.982963

202733_at	procollagen-proline. 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase). alpha polypeptide II	P4HA2	8974	2.359704	0.983708
218936_s_at	coiled-coil domain containing 59	CCDC59	29080	2.353506	0.983708
217790_s_at	signal sequence receptor. gamma (translocon-associated protein gamma)	SSR3	6747	2.349436	0.983708
212154_at	syndecan 2	SDC2	6383	2.346603	0.983708
202055_at	karyopherin alpha 1 (importin alpha 5)	KPNA1	3836	2.345873	0.983708
208602_x_at	CD6 molecule	CD6	923	2.344537	0.983708
202673_at	dolichyl-phosphate mannosyltransferase polypeptide 1. catalytic subunit	DPM1	8813	2.344374	0.983708
217798_at	CCR4-NOT transcription complex. subunit 2	CNOT2	4848	2.343613	0.983708
201711_x_at	RAN binding protein 2	RANBP2	5903	2.343207	0.983708
217242_at	zinc finger protein 154	ZNF154	7710	2.339597	0.985797
208313_s_at	splicing factor 1	SF1	7536	2.339157	0.985797
211861_x_at	CD28 molecule	CD28	940	2.338931	0.985797
201300_s_at	prion protein (p27-30) (Creutzfeldt-Jakob disease. Gerstmann-Strausler-Scheinker syndrome. fatal familial ir	PRNP	5621	2.33728	0.985797
218606_at	zinc finger. DHHC-type containing 7	ZDHHC7	55625	2.331543	0.985797
200705_s_at	eukaryotic translation elongation factor 1 beta 2 /// hCG1983058	EEF1B2 /// hC	1933 /// 6448	2.329986	0.985797
203068_at	kelch-like 21 (Drosophila)	KLHL21	9903	2.325087	0.987521
221871_s_at	TRK-fused gene	TFG	10342	2.324693	0.987521
215545_at	---	---	---	2.322949	0.989811
222101_s_at	dachsous 1 (Drosophila)	DCHS1	8642	2.319277	0.990446
203357_s_at	calpain 7	CAPN7	23473	2.318887	0.990446
212521_s_at	phosphodiesterase 8A	PDE8A	5151	2.318399	0.990446
207339_s_at	lymphotoxin beta (TNF superfamily. member 3)	LTB	4050	2.314409	0.990482
210117_at	sperm associated antigen 1	SPAG1	6674	2.312762	0.990482
208632_at	ring finger protein 10	RNF10	9921	2.312234	0.990482
202496_at	enhancer of mRNA decapping 4	EDC4	23644	2.311507	0.990482
212869_x_at	tumor protein. translationally-controlled 1	TPT1	7178	2.308857	0.991589
201257_x_at	ribosomal protein S3A	RPS3A	6189	2.307594	0.991589
216342_x_at	similar to 40S ribosomal protein S4. X isoform	LOC390183 //	390183 /// 44	2.307366	0.991589
209363_s_at	mediator complex subunit 21	MED21	9412	2.30657	0.991744
208263_at	---	---	---	2.304408	0.992138
211113_s_at	ATP-binding cassette. sub-family G (WHITE). member 1	ABCG1	9619	2.301922	0.992432
215889_at	SKI-like oncogene	SKIL	6498	2.300162	0.993134
209674_at	cryptochrome 1 (photolyase-like)	CRY1	1407	2.295257	0.995336
207310_s_at	nitric oxide synthase 1 (neuronal)	NOS1	4842	2.294198	0.995336
207937_x_at	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2. Pfeiffer syndrome)	FGFR1	2260	2.293767	0.995336
204203_at	CCAAT/enhancer binding protein (C/EBP). gamma	CEBPG	1054	2.293108	0.995336
210995_s_at	tripartite motif-containing 23	TRIM23	373	2.292316	0.995336
200719_at	S-phase kinase-associated protein 1	SKP1	6500	2.289812	0.995336
219423_x_at	tumor necrosis factor receptor superfamily. member 25	TNFRSF25	8718	2.287152	0.995336
202160_at	CREB binding protein (Rubinstein-Taybi syndrome)	CREBBP	1387	2.286371	0.995336
221617_at	TAF9B RNA polymerase II. TATA box binding protein (TBP)-associated factor. 31kDa	TAF9B	51616	2.285063	0.995336
217822_at	WW domain binding protein 11	WBP11	51729	2.284145	0.995786
216947_at	desmin	DES	1674	2.28285	0.997165
216297_at	MRNA; cDNA DKFZp564C156 (from clone DKFZp564C156)	---	---	2.280524	0.999842
206545_at	CD28 molecule	CD28	940	2.279083	0.999842
200893_at	splicing factor. arginine/serine-rich 10 (transformer 2 homolog. Drosophila)	SFRS10	6434	2.277612	0.999842
205042_at	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	GNE	10020	2.275836	0.999842
221976_s_at	Hepatoma-derived growth factor. related protein 3	HDGFRP3	50810	2.273036	0.999842
219864_s_at	RCAN family member 3	RCAN3	11123	2.272653	0.999842
205388_at	troponin C type 2 (fast)	TNNC2	7125	2.270959	0.999842
208828_at	polymerase (DNA directed). epsilon 3 (p17 subunit)	POLE3	54107	2.270571	0.999842
209501_at	cerebellar degeneration-related protein 2. 62kDa	CDR2	1039	2.270007	0.999842
202689_at	RNA binding motif protein 15B	RBM15B	29890	2.268699	0.999842
217824_at	ubiquitin-conjugating enzyme E2. J1 (UBC6 homolog. yeast)	UBE2J1	51465	2.267532	0.999842
215737_x_at	upstream transcription factor 2. c-fos interacting	USF2	7392	2.266026	0.999842
204202_at	IQ motif containing E	IQCE	23288	2.265529	0.999842
209994_s_at	ATP-binding cassette. sub-family B (MDR/TAP). member 1 /// ATP-binding cassette. sub-family B (MDR/TAP)	ABCB1 /// AB	5243 /// 5244	2.264393	0.999842
201185_at	HtrA serine peptidase 1	HTRA1	5654	2.262879	0.999842
215640_at	TBC1 domain family. member 2B	TBC1D2B	23102	2.257998	0.999842
221834_at	Seven in absentia homolog 1 (Drosophila)	SIAH1	6477	2.257215	0.999842
221478_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	BNIP3L	665	2.256252	0.999842
212237_at	additional sex combs like 1 (Drosophila)	ASXL1	171023	2.254407	0.999842
222177_s_at	SCAN domain containing 2	SCAND2	54581	2.253338	0.999842
219927_at	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	FCF1	51077	2.252937	0.999842
200738_s_at	phosphoglycerate kinase 1	PGK1	5230	2.252717	0.999842
212309_at	cytoplasmic linker associated protein 2	CLASP2	23122	2.25031	0.999842
220486_x_at	transmembrane protein 164	TMEM164	84187	2.250191	0.999842
216497_at	heterogeneous nuclear ribonucleoprotein A1 /// similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix	hCG_2023776	120364 /// 14	2.247925	0.999842
221847_at	Full-length cDNA clone CS0DE005YD08 of Placenta of Homo sapiens (human)	---	---	2.24739	0.999842
211927_x_at	eukaryotic translation elongation factor 1 gamma /// elongation factor 1 gamma pseudogene	EEF1G /// LO	1937 /// 7299	2.247272	0.999842
209686_at	S100 calcium binding protein B	S100B	6285	2.245669	0.999842
219343_at	cell division cycle 37 homolog (S. cerevisiae)-like 1	CDC37L1	55664	2.2454	0.999842
202930_s_at	succinate-CoA ligase. ADP-forming. beta subunit	SUCLA2	8803	2.236365	0.999842
222309_at	Chromosome 6 open reading frame 62	C6orf62	81688	2.233855	0.999842
206406_at	sperm mitochondria-associated cysteine-rich protein	SMCP	4184	2.233241	0.999842
217682_at	CDNA FLJ37032 fis. clone BRACE2011265	---	---	2.227829	0.999842
212764_at	---	---	---	2.227796	0.999842
201324_at	epithelial membrane protein 1	EMP1	2012	2.227739	0.999842
207515_s_at	polymerase (RNA) I polypeptide C. 30kDa	POLR1C	9533	2.226737	0.999842
215707_s_at	prion protein (p27-30) (Creutzfeldt-Jakob disease. Gerstmann-Strausler-Scheinker syndrome. fatal familial ir	PRNP	5621	2.22629	0.999842
215512_at	membrane-associated ring finger (C3HC4) 6	6-Mar	10299	2.225775	0.999842
206592_s_at	adaptor-related protein complex 3. delta 1 subunit	AP3D1	8943	2.225278	0.999842
211720_x_at	ribosomal protein. large. P0	RPLP0	6175	2.222868	0.999842
204566_at	protein phosphatase 1D magnesium-dependent. delta isoform	PPM1D	8493	2.221209	0.999842
222373_at	---	---	---	2.220988	0.999842
217591_at	Transcribed locus	---	---	2.219113	0.999842
216035_x_at	transcription factor 7-like 2 (T-cell specific. HMG-box)	TCF7L2	6934	2.218585	0.999842
218296_x_at	misato homolog 1 (Drosophila) /// similar to misato	LOC731059 //	55154 /// 731	2.218276	0.999842
218923_at	chitobiase. di-N-acetyl-	CTBS	1486	2.215965	0.999842
37005_at	neuroblastoma. suppression of tumorigenicity 1	NBL1	4681	2.215959	0.999842
201528_at	replication protein A1. 70kDa	RPA1	6117	2.21572	0.999842
222311_s_at	splicing factor. arginine/serine-rich 15	SFRS15	57466	2.214884	0.999842

202611_s_at	mediator complex subunit 14	MED14	9282	2.211491	0.999842
213612_x_at	neuroblastoma breakpoint family. member 15 /// neuroblastoma breakpoint family. member 10 /// neurobla	LOC728980 //	284565 /// 44	2.209781	0.999842
200099_s_at	ribosomal protein S3A /// similar to ribosomal protein S3a	LOC439992 //	439992 /// 61	2.209133	0.999842
218372_at	mediator complex subunit 9	MED9	55090	2.208667	0.999842
210676_x_at	RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 8 /// RANBP2-like a	RGPD5 /// RG	727851 /// 72	2.20714	0.999842
217607_x_at	eukaryotic translation initiation factor 4 gamma. 2	EIF4G2	1982	2.204431	0.999842
219543_at	phenazine biosynthesis-like protein domain containing	PBLD	64081	2.204246	0.999842
200892_s_at	splicing factor. arginine/serine-rich 10 (transformer 2 homolog. Drosophila)	SFRS10	6434	2.203327	0.999842
200668_s_at	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog. yeast)	UBE2D3	7323	2.201794	0.999842
221687_s_at	family with sequence similarity 125. member B	FAM125B	89853	2.19819	0.999842
212391_x_at	ribosomal protein S3A	RPS3A	6189	2.197912	0.999842
213282_at	CDNA FLJ39590 fis. clone SKNMC1000079	---	---	2.19722	0.999842
204023_at	replication factor C (activator 1) 4. 37kDa	RFC4	5984	2.196373	0.999842
218091_at	HIV-1 Rev binding protein	HRB	3267	2.195946	0.999842
202981_x_at	seven in absentia homolog 1 (Drosophila)	SIAH1	6477	2.195529	0.999842
204458_at	lysophospholipase 3 (lysosomal phospholipase A2)	LYPLA3	23659	2.194908	0.999842
222035_s_at	poly(A) polymerase alpha	PAPOLA	10914	2.194582	0.999842
204593_s_at	Smith-Magenis syndrome chromosome region. candidate 7-like	SMCR7L	54471	2.192288	0.999842
209980_s_at	serine hydroxymethyltransferase 1 (soluble)	SHMT1	6470	2.190352	0.999842
211973_at	AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig	---	---	2.190082	0.999842
209406_at	BCL2-associated athanogene 2	BAG2	9532	2.189011	0.999842
209024_s_at	synaptotagmin binding. cytoplasmic RNA interacting protein	SYNCRIP	10492	2.188887	0.999842
204642_at	endothelial differentiation. sphingolipid G-protein-coupled receptor. 1	EDG1	1901	2.18445	0.999842
202537_s_at	chromatin modifying protein 2B	CHMP2B	25978	2.182319	0.999842
213346_at	chromosome 13 open reading frame 27	C13orf27	93081	2.18125	0.999842
212684_at	zinc finger protein 3	ZNF3	7551	2.180188	0.999842
217252_at	sequestosome 1	SQSTM1	8878	2.179627	0.999842
203466_at	MpV17 mitochondrial inner membrane protein	MPV17	4358	2.179359	0.999842
208275_x_at	undifferentiated embryonic cell transcription factor 1	UTF1	8433	2.179327	0.999842
212787_at	YLP motif containing 1	YLPM1	56252	2.178219	0.999842
201033_x_at	ribosomal protein. large. P0	RPLP0	6175	2.178118	0.999842
216479_at	ribosomal protein L21 /// similar to 60S ribosomal protein L21 /// similar to ribosomal protein L21 /// ribosor	LOC387753 //	387753 /// 38	2.176185	0.999842
214553_s_at	cyclic AMP phosphoprotein. 19 kD	ARPP-19	10776	2.174524	0.999842
212933_x_at	ribosomal protein L13	RPL13	6137	2.173498	0.999842
204142_at	enolase superfamily member 1	ENOSF1	55556	2.1705	0.999842
215490_at	chromosome 1 open reading frame 69	C1orf69	200205	2.167572	0.999842
211202_s_at	jumonji. AT rich interactive domain 1B	JARID1B	10765	2.166096	0.999842
217748_at	adiponectin receptor 1	ADIPOR1	51094	2.166035	0.999842
201359_at	coatomer protein complex. subunit beta 1	COPB1	1315	2.165479	0.999842
200949_x_at	ribosomal protein S20	RPS20	6224	2.163448	0.999842
214785_at	vacuolar protein sorting 13 homolog A (S. cerevisiae)	VPS13A	23230	2.158774	0.999842
213227_at	progesterone receptor membrane component 2	PGRMC2	10424	2.158444	0.999842
208868_s_at	GABA(A) receptor-associated protein like 1	GABARAPL1	23710	2.157821	0.999842
213172_at	tetratricopeptide repeat domain 9	TTC9	23508	2.155316	0.999842
202646_s_at	cold shock domain containing E1. RNA-binding	CSDE1	7812	2.155085	0.999842
214305_s_at	splicing factor 3b. subunit 1. 155kDa	SF3B1	23451	2.154989	0.999842
203847_s_at	A kinase (PRKA) anchor protein 8	AKAP8	10270	2.154964	0.999842
211751_at	phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP	9659	2.154377	0.999842
210426_x_at	RAR-related orphan receptor A	RORA	6095	2.153926	0.999842
215233_at	jumonji domain containing 6	JMJD6	23210	2.151668	0.999842
201919_at	solute carrier family 25. member 36	SLC25A36	55186	2.151462	0.999842
221493_at	TSPY-like 1	TSPYL1	7259	2.15084	0.999842
208856_x_at	ribosomal protein. large. P0	RPLP0	6175	2.150626	0.999842
206559_x_at	eukaryotic translation elongation factor 1 alpha 1	EEF1A1	1915	2.150424	0.999842
204080_at	target of EGR1. member 1 (nuclear)	TOE1	114034	2.150146	0.999842
214245_at	ribosomal protein S14	RPS14	6208	2.14823	0.999842
212101_at	karyopherin alpha 6 (importin alpha 7)	KPNA6	23633	2.145419	0.999842
221842_s_at	zinc finger protein 131	ZNF131	7690	2.145166	0.999842
217356_s_at	phosphoglycerate kinase 1	PGK1	5230	2.143442	0.999842
217807_s_at	glioma tumor suppressor candidate region gene 2	GLTSCR2	29997	2.143058	0.999842
209845_at	makorin. ring finger protein. 1	MKRN1	23608	2.142511	0.999842
204856_at	UDP-GlcNAc:betaGal beta-1.3-N-acetylglucosaminyltransferase 3	B3GNT3	10331	2.138608	0.999842
212813_at	junctional adhesion molecule 3	JAM3	83700	2.13849	0.999842
214834_at	small nuclear ribonucleoprotein polypeptide N /// Prader-Willi/Angelman syndrome-5 /// small nucleolar RNA	PAR-SN /// PA	338427 /// 34	2.137113	0.999842
206044_s_at	v-raf murine sarcoma viral oncogene homolog B1	BRAF	673	2.135943	0.999842
200650_s_at	lactate dehydrogenase A	LDHA	3939	2.135006	0.999842
215528_at	MRNA; cDNA DKFZp586O1318 (from clone DKFZp586O1318)	---	---	2.132419	0.999842
221657_s_at	ankyrin repeat and SOCS box-containing 6	ASB6	140459	2.130539	0.999842
214658_at	transmembrane emp24 protein transport domain containing 7	TMED7	51014	2.128668	0.999842
218168_s_at	chaperone. ABC1 activity of bc1 complex homolog (S. pombe)	CABC1	56997	2.128069	0.999842
217850_at	guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	26354	2.127825	0.999842
215575_at	phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP	9659	2.12757	0.999842
218829_s_at	chromodomain helicase DNA binding protein 7	CHD7	55636	2.126938	0.999842
214947_at	CDNA FLJ43660 fis. clone SYNOV4004823	---	---	2.126398	0.999842
211439_at	splicing factor. arginine/serine-rich 7. 35kDa	SFRS7	6432	2.125496	0.999842
202730_s_at	programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	27250	2.124808	0.999842
218478_s_at	zinc finger. CCHC domain containing 8	ZCCHC8	55596	2.124477	0.999842
216350_s_at	zinc finger protein 10	ZNF10	7556	2.122403	0.999842
213864_s_at	nucleosome assembly protein 1-like 1	NAP1L1	4673	2.122277	0.999842
209412_at	transmembrane protein 1	TMEM1	7109	2.121527	0.999842
219449_s_at	transmembrane protein 70	TMEM70	54968	2.121243	0.999842
210671_x_at	mitogen-activated protein kinase 8	MAPK8	5599	2.117429	0.999842
202021_x_at	eukaryotic translation initiation factor 1	EIF1	10209	2.117223	0.999842
204612_at	protein kinase (cAMP-dependent. catalytic) inhibitor alpha	PKIA	5569	2.117206	0.999842
212655_at	zinc finger. CCHC domain containing 14	ZCCHC14	23174	2.11646	0.999842
212635_at	transportin 1	TNPO1	3842	2.115769	0.999842
219359_at	ATH1. acid trehalase-like 1 (yeast)	ATHL1	80162	2.114544	0.999842
209524_at	hepatoma-derived growth factor. related protein 3	HDGFRP3	50810	2.114294	0.999842
209655_s_at	transmembrane protein 47	TMEM47	83604	2.114111	0.999842
211943_x_at	tumor protein. translationally-controlled 1	TPT1	7178	2.113465	0.999842
200061_s_at	ribosomal protein S24	RPS24	6229	2.11251	0.999842
211598_x_at	vasoactive intestinal peptide receptor 2	VIPR2	7434	2.110932	0.999842

218886_at	PAK1 interacting protein 1	PAK1IP1	55003	2.110751	0.999842
210178_x_at	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS-interacting serine-arginine-rich protein 1 (T	FUSIP1 /// LO	10772 /// 727	2.110265	0.999842
212392_s_at	phosphodiesterase 4D interacting protein (myomegalin) /// similar to phosphodiesterase 4D interacting prote	LOC652526 //	652526 /// 72	2.110079	0.999842
215509_s_at	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	699	2.108765	0.999842
210284_s_at	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	MAP3K7IP2	23118	2.107827	0.999842
218852_at	protein phosphatase 2 (formerly 2A). regulatory subunit B''. gamma	PPP2R3C	55012	2.10757	0.999842
204651_at	nuclear respiratory factor 1	NRF1	4899	2.107524	0.999842
211808_s_at	CREB binding protein (Rubinstein-Taybi syndrome)	CREBBP	1387	2.106633	0.999842
201328_at	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	2114	2.10658	0.999842
204817_at	extra spindle pole bodies homolog 1 (S. cerevisiae)	ESPL1	9700	2.106148	0.999842
216430_x_at	isovaleryl Coenzyme A dehydrogenase	IVD	3712	2.102387	0.999842
214280_x_at	heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	3178	2.101729	0.999842
58367_s_at	zinc finger protein 419	ZNF419	79744	2.100589	0.999842
207016_s_at	aldehyde dehydrogenase 1 family. member A2	ALDH1A2	8854	2.098652	0.999842
217576_x_at	son of sevenless homolog 2 (Drosophila)	SOS2	6655	2.096924	0.999842
212515_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3. X-linked	DDX3X	1654	2.095366	0.999842
201548_s_at	jumonji. AT rich interactive domain 1B	JARID1B	10765	2.095061	0.999842
211913_s_at	c-mer proto-oncogene tyrosine kinase	MERTK	10461	2.093882	0.999842
209733_at	hypothetical protein LOC286440	LOC286440	286440	2.093813	0.999842
209841_s_at	leucine rich repeat neuronal 3	LRRN3	54674	2.093564	0.999842
208184_s_at	transmembrane protein 1	TMEM1	7109	2.093338	0.999842
208752_x_at	nucleosome assembly protein 1-like 1	NAP1L1	4673	2.093069	0.999842
209163_at	cytochrome b-561	CYB561	1534	2.092255	0.999842
210047_at	solute carrier family 11 (proton-coupled divalent metal ion transporters). member 2	SLC11A2	4891	2.09167	0.999842
208044_s_at	peroxisome proliferator-activated receptor delta	PPARD	5467	2.091135	0.999842
219471_at	chromosome 13 open reading frame 18	C13orf18	80183	2.091007	0.999842
208274_at	oculomedin	OCLM	10896	2.090496	0.999842
208290_s_at	eukaryotic translation initiation factor 5	EIF5	1983	2.088403	0.999842
201210_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3. X-linked	DDX3X	1654	2.088047	0.999842
208567_s_at	potassium inwardly-rectifying channel. subfamily J. member 12	KCNJ12	3768	2.087219	0.999842
209838_at	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	COPS2	9318	2.086468	0.999842
209870_s_at	amyloid beta (A4) precursor protein-binding. family A. member 2 (X11-like)	APBA2	321	2.082192	0.999842
50277_at	golgi associated. gamma adaptin ear containing. ARF binding protein 1	GGA1	26088	2.081811	0.999842
44146_at	glucocorticoid modulatory element binding protein 2	GMEB2	26205	2.080694	0.999842
218683_at	polypyrimidine tract binding protein 2	PTBP2	58155	2.08031	0.999842
220346_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	MTHFD2L	441024	2.078247	0.999842
203375_s_at	tripeptidyl peptidase II	TPP2	7174	2.077853	0.999842
216347_s_at	protein phosphatase 1. regulatory (inhibitor) subunit 13B	PPP1R13B	23368	2.077437	0.999842
203636_at	midline 1 (Opitz/BBB syndrome)	MID1	4281	2.075067	0.999842
213019_at	RAN binding protein 6	RANBP6	26953	2.074864	0.999842
202352_s_at	proteasome (prosome. macropain) 26S subunit. non-ATPase. 12	PSMD12	5718	2.074244	0.999842
217120_s_at	mediator complex subunit 14	MED14	9282	2.074153	0.999842
214863_at	Full length insert cDNA clone ZC35F11	---	---	2.07363	0.999842
213763_at	homeodomain interacting protein kinase 2	HIPK2	28996	2.073523	0.999842
210778_s_at	MAX dimerization protein 4	MXD4	10608	2.071656	0.999842
221675_s_at	choline phosphotransferase 1	CHPT1	56994	2.070737	0.999842
220576_at	GPI deacylase	PGAP1	80055	2.065053	0.999842
207984_s_at	membrane protein. palmitoylated 2 (MAGUK p55 subfamily member 2)	MPP2	4355	2.064386	0.999842
214354_x_at	surfactant. pulmonary-associated protein B	SFTPB	6439	2.063379	0.999842
221919_at	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical protein LOC728844	HNRNPA1 ///	3178 /// 7288	2.062624	0.999842
210691_s_at	calcyclin binding protein	CACYBP	27101	2.062483	0.999842
216548_x_at	high-mobility group (nonhistone chromosomal) protein 4-like	HMG4L	128872	2.062217	0.999842
219321_at	membrane protein. palmitoylated 5 (MAGUK p55 subfamily member 5)	MPP5	64398	2.062179	0.999842
219248_at	THUMP domain containing 2	THUMPD2	80745	2.061558	0.999842
205198_s_at	ATPase. Cu++ transporting. alpha polypeptide (Menkes syndrome) /// similar to ATPase. Cu++ transporting.	ATP7A /// LOC	538 /// 64473	2.061512	0.999842
210429_at	Rh blood group. D antigen	RHD	6007	2.060246	0.999842
218856_at	tumor necrosis factor receptor superfamily. member 21	TNFRSF21	27242	2.058949	0.999842
217719_at	eukaryotic translation initiation factor 3. subunit E interacting protein	EIF3EIP	51386	2.058583	0.999842
206095_s_at	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS-interacting serine-arginine-rich protein 1 (T	FUSIP1 /// LO	10772 /// 727	2.058476	0.999842
205981_s_at	inhibitor of growth family. member 2	ING2	3622	2.055621	0.999842
215734_at	chromosome 19 open reading frame 36	C19orf36	113177	2.054489	0.999842
214449_s_at	ras homolog gene family. member Q	RHOQ	23433	2.054307	0.999842
51176_at	mediator complex subunit 27	MED27	9442	2.052362	0.999842
208198_x_at	killer cell immunoglobulin-like receptor. two domains. short cytoplasmic tail. 1	KIR2DS1	3806	2.047843	0.999842
212805_at	prune homolog 2 (Drosophila)	PRUNE2	158471	2.047256	0.999842
217367_s_at	zinc fingers and homeoboxes 3	ZHX3	23051	2.044521	0.999842
204621_s_at	nuclear receptor subfamily 4. group A. member 2	NR4A2	4929	2.044483	0.999842
219562_at	RAB26. member RAS oncogene family	RAB26	25837	2.042244	0.999842
215630_at	CDNA FLJ14102 fis. clone MAMMA1000940	---	---	2.041621	0.999842
200737_at	phosphoglycerate kinase 1	PGK1	5230	2.041303	0.999842
214008_at	Twinfilin. actin-binding protein. homolog 1 (Drosophila)	TWF1	5756	2.041221	0.999842
211345_x_at	eukaryotic translation elongation factor 1 gamma /// elongation factor 1 gamma pseudogene	EEF1G /// LOC	1937 /// 7299	2.041174	0.999842
213725_x_at	xylosyltransferase I	XYLT1	64131	2.038204	0.999842
216979_at	nuclear receptor subfamily 4. group A. member 3	NR4A3	8013	2.037575	0.999842
208384_s_at	midline 2	MID2	11043	2.036539	0.999842
212558_at	sprouty homolog 1. antagonist of FGF signaling (Drosophila)	SPRY1	10252	2.035056	0.999842
203321_s_at	ADNP homeobox 2	ADNP2	22850	2.034107	0.999842
217655_at	FXYD domain containing ion transport regulator 5	FXYD5	53827	2.029777	0.999842
89948_at	chromosome 20 open reading frame 67	C20orf67	63935	2.027922	0.999842
212628_at	protein kinase N2	PKN2	5586	2.027843	0.999842
219182_at	hypothetical protein FLJ22167	FLJ22167	79583	2.027446	0.999842
212176_at	splicing factor. arginine/serine-rich 18	SFRS18	25957	2.027393	0.999842
205892_s_at	fatty acid binding protein 1. liver	FABP1	2168	2.027061	0.999842
208410_x_at	amelogenin (amelogenesis imperfecta 1. X-linked)	AMELX	265	2.025715	0.999842
46256_at	splA/ryanodine receptor domain and SOCS box containing 3	SPSB3	90864	2.023653	0.999842
222247_at	putative X-linked retinopathy protein	DXS542	57825	2.023276	0.999842
211555_s_at	guanylate cyclase 1. soluble. beta 3	GUCY1B3	2983	2.021895	0.999842
213281_at	Jun oncogene	JUN	3725	2.020379	0.999842
208051_s_at	poly(A) binding protein interacting protein 1	PAIP1	10605	2.020016	0.999842
207128_s_at	zinc finger protein 223	ZNF223	7766	2.016375	0.999842
221971_x_at	centaurin. gamma-like family. member 2	CTGLF2	729092	2.012843	0.999842
218406_x_at	neuron derived neurotrophic factor	NENF	29937	2.012699	0.999842

220212_s_at	thyroid adenoma associated	THADA	63892	2.010788	0.999842
214016_s_at	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ	6421	2.009902	0.999842
212279_at	transmembrane protein 97	TMEM97	27346	2.008972	0.999842
36711_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF	23764	2.008811	0.999842
213958_at	CD6 molecule	CD6	923	2.00796	0.999842
215135_at	aspartyl aminopeptidase	DNPEP	23549	2.007805	0.999842
210346_s_at	CDC-like kinase 4	CLK4	57396	2.00762	0.999842
211979_at	G protein-coupled receptor 107	GPR107	57720	2.004594	0.999842
212607_at	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B. gamma)	AKT3	10000	2.00203	0.999842
203362_s_at	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	4085	2.001594	0.999842
212017_at	p20	LOC130074	130074	2.001472	0.999842
206799_at	secretoglobin. family 1D. member 2	SCGB1D2	10647	2.000709	0.999842
208713_at	heterogeneous nuclear ribonucleoprotein U-like 1	HNRPUL1	11100	2.000289	0.999842
218739_at	abhydrolase domain containing 5	ABHD5	51099	2.000006	0.999842
201387_s_at	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	UCHL1	7345	-2.000432	0.999842
214123_s_at	chromosome 4 open reading frame 10	C4orf10	317648	-2.000534	0.999842
37424_at	coiled-coil alpha-helical rod protein 1	CCHCR1	54535	-2.00116	0.999842
210427_x_at	annexin A2	ANXA2	302	-2.002025	0.999842
203311_s_at	ADP-ribosylation factor 6	ARF6	382	-2.002828	0.999842
201572_x_at	dCMP deaminase	DCTD	1635	-2.002974	0.999842
202307_s_at	transporter 1. ATP-binding cassette. sub-family B (MDR/TAP)	TAP1	6890	-2.004624	0.999842
216004_s_at	PBX/knotted 1 homeobox 1	PKNOX1	5316	-2.005241	0.999842
222139_at	KIAA1466 gene	KIAA1466	57612	-2.005652	0.999842
222180_at	CDNA FLJ14122 fis. clone MAMMA1002033	---	---	-2.006673	0.999842
203825_at	bromodomain containing 3	BRD3	8019	-2.008574	0.999842
206795_at	coagulation factor II (thrombin) receptor-like 2	F2RL2	2151	-2.011262	0.999842
201762_s_at	proteasome (prosome. macropain) activator subunit 2 (PA28 beta)	PSME2	5721	-2.012016	0.999842
216991_at	zinc finger protein 224	ZNF224	7767	-2.012839	0.999842
221771_s_at	M-phase phosphoprotein 8	MPHOSPH8	54737	-2.012947	0.999842
204279_at	proteasome (prosome. macropain) subunit. beta type. 9 (large multifunctional peptidase 2)	PSMB9	5698	-2.013904	0.999842
202205_at	vasodilator-stimulated phosphoprotein	VASP	7408	-2.014419	0.999842
222225_at	60S ribosomal pseudogene	FLJ45055	644128	-2.014512	0.999842
215193_x_at	major histocompatibility complex. class II. DR beta 1 /// major histocompatibility complex. class II. DR beta	HLA-DRB1 ///	3123 /// 3125	-2.015716	0.999842
208678_at	ATPase. H+ transporting. lysosomal 31kDa. V1 subunit E1	ATP6V1E1	529	-2.01657	0.999842
201633_s_at	cytochrome b5 type B (outer mitochondrial membrane)	CYB5B	80777	-2.0168	0.999842
205231_s_at	epilepsy. progressive myoclonus type 2A. Lafora disease (laforin)	EPM2A	7957	-2.016821	0.999842
203249_at	enhancer of zeste homolog 1 (Drosophila)	EZH1	2145	-2.017039	0.999842
212047_s_at	ring finger protein 167	RNF167	26001	-2.019783	0.999842
219450_at	chromosome 4 open reading frame 19	C4orf19	55286	-2.02243	0.999842
212678_at	neurofibromin 1 (neurofibromatosis. von Recklinghausen disease. Watson disease)	NF1	4763	-2.022693	0.999842
207181_s_at	caspase 7. apoptosis-related cysteine peptidase	CASP7	840	-2.024013	0.999842
208997_s_at	uncoupling protein 2 (mitochondrial. proton carrier)	UCP2	7351	-2.025785	0.999842
201040_at	guanine nucleotide binding protein (G protein). alpha inhibiting activity polypeptide 2	GNAI2	2771	-2.026031	0.999842
219920_s_at	GDP-mannose pyrophosphorylase B	GMPPB	29925	-2.026423	0.999842
215746_at	(clone B3B3E13) chromosome 4p16.3 DNA fragment	---	---	-2.027182	0.999842
201614_s_at	RuvB-like 1 (E. coli)	RUVBL1	8607	-2.027701	0.999842
221080_s_at	DENN/MADD domain containing 1C	DENND1C	79958	-2.028539	0.999842
211644_x_at	immunoglobulin kappa constant /// netrin 2-like (chicken) /// immunoglobulin kappa locus	IGK@ /// IGK(	3514 /// 4917	-2.031678	0.999842
221936_x_at	Mitochondrial ribosomal protein L41	MRPL41	64975	-2.032229	0.999842
201863_at	family with sequence similarity 32. member A	FAM32A	26017	-2.032426	0.999842
201216_at	endoplasmic reticulum protein 29	ERP29	10961	-2.032913	0.999842
218700_s_at	RAB7. member RAS oncogene family-like 1	RAB7L1	8934	-2.034548	0.999842
213062_at	N-terminal asparagine amidase	NTAN1	123803	-2.034967	0.999842
201267_s_at	proteasome (prosome. macropain) 26S subunit. ATPase. 3	PSMC3	5702	-2.034989	0.999842
220085_at	helicase. lymphoid-specific	HELLS	3070	-2.035038	0.999842
201127_s_at	ATP citrate lyase	ACLY	47	-2.038535	0.999842
217381_s_at	T cell receptor gamma variable 5 /// hypothetical protein LOC648852	LOC648852 //	648852 /// 69	-2.038913	0.999842
202577_s_at	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	DDX19A	55308	-2.04079	0.999842
207391_s_at	phosphatidylinositol-4-phosphate 5-kinase. type I. alpha	PIP5K1A	8394	-2.041488	0.999842
214883_at	thyroid hormone receptor. alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog. avian)	THRA	7067	-2.042525	0.999842
218734_at	N-acetyltransferase 11	NAT11	79829	-2.044525	0.999842
214377_s_at	chymotrypsin-like	CTRL	1506	-2.045597	0.999842
221997_s_at	Mitochondrial ribosomal protein L52	MRPL52	122704	-2.046959	0.999842
206150_at	CD27 molecule	CD27	939	-2.051925	0.999842
202270_at	guanylate binding protein 1. interferon-inducible. 67kDa	GBP1	2633	-2.052094	0.999842
219031_s_at	nuclear import 7 homolog (S. cerevisiae)	NIP7	51388	-2.053791	0.999842
205229_s_at	coagulation factor C homolog. cochlin (Limulus polyphemus)	COCH	1690	-2.053924	0.999842
208000_at	GPI anchored molecule like protein	GML	2765	-2.054524	0.999842
215236_s_at	phosphatidylinositol binding clathrin assembly protein	PICALM	8301	-2.05492	0.999842
202323_s_at	acyl-Coenzyme A binding domain containing 3	ACBD3	64746	-2.054985	0.999842
201308_s_at	septin 11	11-Sep	55752	-2.055677	0.999842
212082_s_at	myosin. light chain 6. alkali. smooth muscle and non-muscle	MYL6	4637	-2.055771	0.999842
219807_x_at	RAB4B. member RAS oncogene family	RAB4B	53916	-2.05898	0.999842
214342_at	ataxin 7-like 1	ATXN7L1	222255	-2.060414	0.999842
206441_s_at	COMM domain containing 4	COMMD4	54939	-2.061628	0.999842
215071_s_at	histone cluster 1. H2ac	HIST1H2AC	8334	-2.061937	0.999842
213446_s_at	IQ motif containing GTPase activating protein 1	IQGAP1	8826	-2.062222	0.999842
213280_at	GTPase activating Rap/RanGAP domain-like 4	GARNL4	23108	-2.062227	0.999842
208816_x_at	annexin A2 pseudogene 2	ANXA2P2	304	-2.065256	0.999842
209446_s_at	chromosome 7 open reading frame 44	C7orf44	55744	-2.066757	0.999842
211742_s_at	ecotropic viral integration site 2B	EVI2B	2124	-2.069932	0.999842
210972_x_at	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell re	TRA@ /// TRA	28517 /// 286	-2.071463	0.999842
203160_s_at	ring finger protein 8	RNF8	9025	-2.073032	0.999842
218811_at	ORAI calcium release-activated calcium modulator 2	ORAI2	80228	-2.073336	0.999842
218774_at	decapping enzyme. scavenger	DCPS	28960	-2.073863	0.999842
211139_s_at	NGFI-A binding protein 1 (EGR1 binding protein 1)	NAB1	4664	-2.074392	0.999842
215287_at	ELISC-1	---	---	-2.074413	0.999842
213521_at	protein tyrosine phosphatase. non-receptor type 18 (brain-derived)	PTPN18	26469	-2.07455	0.999842
202269_x_at	guanylate binding protein 1. interferon-inducible. 67kDa	GBP1	2633	-2.074827	0.999842
205572_at	angiopoietin 2	ANGPT2	285	-2.076672	0.999842
209685_s_at	protein kinase C. beta 1	PRKCB1	5579	-2.077604	0.999842
203103_s_at	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	PRPF19	27339	-2.080886	0.999842

200814_at	proteasome (prosome. macropain) activator subunit 1 (PA28 alpha)	PSME1	5720	-2.081854	0.999842
200787_s_at	phosphoprotein enriched in astrocytes 15	PEA15	8682	-2.08508	0.999842
206306_at	ryanodine receptor 3	RYR3	6263	-2.088117	0.999842
213349_at	transmembrane and coiled-coil domain family 1	TMCC1	23023	-2.089437	0.999842
214995_s_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3G /// apolipoprotein B mRNA editing enzy	APOBEC3F ///	200316 /// 60	-2.089937	0.999842
217126_at	Kpni repeat mrna (cdna clone pcd-kpni-8). 3' end	---	---	-2.090014	0.999842
209424_s_at	alpha-methylacyl-CoA racemase	AMACR	23600	-2.090059	0.999842
213730_x_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3	6929	-2.090391	0.999842
220124_at	giant axonal neuropathy (gigaxonin)	GAN	8139	-2.093448	0.999842
214970_s_at	ST6 beta-galactosamide alpha-2.6-sialyltranferase 1	ST6GAL1	6480	-2.095149	0.999842
219308_s_at	adenylate kinase 5	AK5	26289	-2.095852	0.999842
212748_at	megakaryoblastic leukemia (translocation) 1	MKL1	57591	-2.097535	0.999842
204160_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	ENPP4	22875	-2.098283	0.999842
201735_s_at	chloride channel 3	CLCN3	1182	-2.098285	0.999842
205114_s_at	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3	CCL3 /// CCL3	414062 /// 63	-2.098934	0.999842
207419_s_at	ras-related C3 botulinum toxin substrate 2 (rho family. small GTP binding protein Rac2)	RAC2	5880	-2.102638	0.999842
214735_at	phosphoinositide-binding protein PIP3-E	PIP3-E	26034	-2.102814	0.999842
57539_at	zinc finger. CCCH-type with G patch domain	ZGPAT	84619	-2.103581	0.999842
205703_at	---	---	---	-2.106786	0.999842
204226_at	staufen. RNA binding protein. homolog 2 (Drosophila)	STAU2	27067	-2.10817	0.999842
205396_at	SMAD family member 3	SMAD3	4088	-2.108608	0.999842
207870_at	A kinase (PRKA) anchor protein (yotiao) 9	AKAP9	10142	-2.109249	0.999842
212784_at	capicua homolog (Drosophila)	CIC	23152	-2.109293	0.999842
220990_s_at	transmembrane protein 49 /// microRNA 21	MIRN21 /// TN	406991 /// 81	-2.111163	0.999842
215541_s_at	diaphanous homolog 1 (Drosophila)	DIAPH1	1729	-2.111547	0.999842
218409_s_at	DnaJ (Hsp40) homolog. subfamily C. member 1	DNAJC1	64215	-2.111661	0.999842
216528_at	MRNA; cDNA DKFZp564C163 (from clone DKFZp564C163)	---	---	-2.111825	0.999842
203595_s_at	interferon-induced protein with tetratricopeptide repeats 5	IFIT5	24138	-2.11479	0.999842
210807_s_at	solute carrier family 16. member 7 (monocarboxylic acid transporter 2)	SLC16A7	9194	-2.115275	0.999842
201275_at	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase. dimethylallyltranstransferase. geranyltra	FDPS	2224	-2.116677	0.999842
203227_s_at	tetraspanin 31	TSPAN31	6302	-2.118554	0.999842
214137_at	Protein tyrosine phosphatase. receptor type. J	PTPRJ	5795	-2.118709	0.999842
211178_s_at	proline-serine-threonine phosphatase interacting protein 1	PSTPIP1	9051	-2.11889	0.999842
221864_at	ORAI calcium release-activated calcium modulator 3	ORAI3	93129	-2.121945	0.999842
201021_s_at	destrin (actin depolymerizing factor)	DSTN	11034	-2.124301	0.999842
220947_s_at	TBC1 domain family. member 10B	TBC1D10B	26000	-2.125496	0.999842
206484_s_at	X-prolyl aminopeptidase (aminopeptidase P) 2. membrane-bound	XPNPEP2	7512	-2.125971	0.999842
221542_s_at	ER lipid raft associated 2	ERLIN2	11160	-2.12849	0.999842
222217_s_at	solute carrier family 27 (fatty acid transporter). member 3	SLC27A3	11000	-2.129071	0.999842
219994_at	amyloid beta (A4) precursor protein-binding. family B. member 1 interacting protein	APBB1IP	54518	-2.129079	0.999842
215379_x_at	immunoglobulin lambda locus /// immunoglobulin lambda variable 3-25 /// immunoglobulin lambda variable	IGL@ /// IGLJ	28793 /// 288	-2.129778	0.999842
209671_x_at	T cell receptor alpha locus /// T cell receptor alpha constant	TRA@ /// TRA	28755 /// 695	-2.129991	0.999842
208649_s_at	valosin-containing protein	VCP	7415	-2.130846	0.999842
1405_i_at	chemokine (C-C motif) ligand 5	CCL5	6352	-2.130885	0.999842
212116_at	tripartite motif-containing 27	TRIM27	5987	-2.131953	0.999842
205426_s_at	huntingtin interacting protein 1	HIP1	3092	-2.132452	0.999842
212663_at	FK506 binding protein 15. 133kDa	FKBP15	23307	-2.132801	0.999842
210812_at	X-ray repair complementing defective repair in Chinese hamster cells 4	XRCC4	7518	-2.135329	0.999842
209825_s_at	uridine-cytidine kinase 2	UCK2	7371	-2.135386	0.999842
214545_s_at	proline synthetase co-transcribed homolog (bacterial)	PROSC	11212	-2.137106	0.999842
201756_at	replication protein A2. 32kDa	RPA2	6118	-2.137819	0.999842
215843_s_at	tolloid-like 2	TLL2	7093	-2.138123	0.999842
221744_at	WD repeat domain 68	WDR68	10238	-2.140478	0.999842
217770_at	phosphatidylinositol glycan anchor biosynthesis. class T	PIGT	51604	-2.140963	0.999842
35254_at	TRAF-type zinc finger domain containing 1	TRAFD1	10906	-2.141184	0.999842
42361_g_at	coiled-coil alpha-helical rod protein 1	CCHCR1	54535	-2.143308	0.999842
213589_s_at	UDP-GlcNAc:betaGal beta-1.3-N-acetylglucosaminyltransferase-like 1	B3GNTL1	146712	-2.143421	0.999842
209198_s_at	synaptotagmin XI	SYT11	23208	-2.143766	0.999842
203515_s_at	phosphomevalonate kinase	PMVK	10654	-2.14437	0.999842
47069_at	proline rich 5 (renal)	PRR5	55615	-2.145005	0.999842
201700_at	cyclin D3	CCND3	896	-2.145947	0.999842
209762_x_at	SP110 nuclear body protein	SP110	3431	-2.146903	0.999842
216835_s_at	docking protein 1. 62kDa (downstream of tyrosine kinase 1)	DOK1	1796	-2.149075	0.999842
215121_x_at	immunoglobulin lambda locus /// immunoglobulin lambda variable 4-3 /// immunoglobulin lambda variable 3	IGL@ /// IGLV	28786 /// 287	-2.149809	0.999842
205241_at	SCO cytochrome oxidase deficient homolog 2 (yeast)	SCO2	9997	-2.150315	0.999842
209482_at	processing of precursor 7. ribonuclease P/MRP subunit (S. cerevisiae)	POP7	10248	-2.152565	0.999842
218270_at	mitochondrial ribosomal protein L24	MRPL24	79590	-2.152597	0.999842
57163_at	elongation of very long chain fatty acids (FEN1/Elo2. SUR4/Elo3. yeast)-like 1	ELOVL1	64834	-2.153494	0.999842
219193_at	WD repeat domain 70	WDR70	55100	-2.154374	0.999842
219205_at	serine racemase	SRR	63826	-2.15459	0.999842
204882_at	Rho GTPase activating protein 25	ARHGAP25	9938	-2.155266	0.999842
201954_at	actin related protein 2/3 complex. subunit 1B. 41kDa /// similar to Actin-related protein 2/3 complex subunit	ARPC1B /// LC	10095 /// 653	-2.155304	0.999842
209679_s_at	small trans-membrane and glycosylated protein	LOC57228	57228	-2.15685	0.999842
78383_at	Topoisomerase I binding. arginine/serine-rich	TOPORS	10210	-2.158688	0.999842
202121_s_at	chromatin modifying protein 2A	CHMP2A	27243	-2.159458	0.999842
218913_s_at	GEM interacting protein	GMIP	51291	-2.160334	0.999842
209155_s_at	5'-nucleotidase. cytosolic II	NT5C2	22978	-2.170779	0.999842
214340_at	arachidonate 12-lipoxygenase pseudogene 2	ALOX12P2	245	-2.172329	0.999842
213060_s_at	chitinase 3-like 2	CHI3L2	1117	-2.175725	0.999842
213046_at	poly(A) binding protein. nuclear 1	PABPN1	8106	-2.176327	0.999842
206066_s_at	RAD51 homolog C (S. cerevisiae)	RAD51C	5889	-2.178267	0.999842
200996_at	ARP3 actin-related protein 3 homolog (yeast)	ACTR3	10096	-2.181321	0.999842
201194_at	selenoprotein W. 1	SEPW1	6415	-2.181792	0.999842
210892_s_at	general transcription factor II. i	GTF2I	2969	-2.182621	0.999842
210568_s_at	RecQ protein-like (DNA helicase Q1-like)	RECQL	5965	-2.191442	0.999842
219003_s_at	mannosidase. endo-alpha	MANEA	79694	-2.192031	0.999842
209514_s_at	RAB27A. member RAS oncogene family	RAB27A	5873	-2.192759	0.999842
217962_at	nucleolar protein family A. member 3 (H/ACA small nucleolar RNPs)	NOLA3	55505	-2.193999	0.999842
217776_at	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	RDH11	51109	-2.197094	0.999842
203226_s_at	tetraspanin 31	TSPAN31	6302	-2.198671	0.999842
219690_at	transmembrane protein 149	TMEM149	79713	-2.202343	0.999842
207416_s_at	nuclear factor of activated T-cells. cytoplasmic. calcineurin-dependent 3	NFATC3	4775	-2.204823	0.999842

218504_at	fumarylacetoacetate hydrolase domain containing 2A	FAHD2A	51011	-2.205066	0.999842
212252_at	calcium/calmodulin-dependent protein kinase kinase 2. beta	CAMKK2	10645	-2.206291	0.999842
210164_at	granzyme B (granzyme 2. cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	3002	-2.212516	0.999842
203143_s_at	KIAA0040	KIAA0040	9674	-2.213193	0.999842
203405_at	proteasome (prosome. macropain) assembly chaperone 1	PSMG1	8624	-2.213451	0.999842
200982_s_at	annexin A6	ANXA6	309	-2.214011	0.999842
218163_at	malignant T cell amplified sequence 1	MCTS1	28985	-2.214785	0.999842
202747_s_at	integral membrane protein 2A	ITM2A	9452	-2.214827	0.999842
211804_s_at	cyclin-dependent kinase 2	CDK2	1017	-2.21587	0.999842
221374_at	fibroblast growth factor 16	FGF16	8823	-2.217071	0.999842
221804_s_at	family with sequence similarity 45. member B /// family with sequence similarity 45. member A /// similar to	FAM45A /// FA	404636 /// 55	-2.217733	0.999842
209808_x_at	inhibitor of growth family. member 1	ING1	3621	-2.217818	0.999842
219549_s_at	reticulon 3	RTN3	10313	-2.218935	0.999842
213867_x_at	actin. beta	ACTB	60	-2.222052	0.999842
218520_at	TANK-binding kinase 1	TBK1	29110	-2.224399	0.999842
217508_s_at	chromosome 18 open reading frame 25	C18orf25	147339	-2.224458	0.999842
207057_at	solute carrier family 16. member 7 (monocarboxylic acid transporter 2)	SLC16A7	9194	-2.227306	0.999842
215672_s_at	adenosylhomocysteinase 3	KIAA0828	23382	-2.229487	0.999842
209503_s_at	proteasome (prosome. macropain) 26S subunit. ATPase. 5	PSMC5	5705	-2.230395	0.999842
208972_s_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit C1 (subunit 9)	ATP5G1	516	-2.232452	0.999842
200617_at	KIAA0152	KIAA0152	9761	-2.234502	0.999842
217183_at	low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	3949	-2.23891	0.999842
207622_s_at	ATP-binding cassette. sub-family F (GCN20). member 2	ABCF2	10061	-2.238971	0.999842
213293_s_at	tripartite motif-containing 22	TRIM22	10346	-2.244567	0.999842
207795_s_at	killer cell lectin-like receptor subfamily D. member 1	KLRD1	3824	-2.245444	0.999842
222369_at	N-acetyltransferase 11	NAT11	79829	-2.246198	0.999842
217309_s_at	Down syndrome critical region gene 3	DSCR3	10311	-2.247293	0.999842
210951_x_at	RAB27A. member RAS oncogene family	RAB27A	5873	-2.248046	0.999842
214293_at	Septin 11	11-Sep	55752	-2.248806	0.999842
216980_s_at	sialophorin (leukosialin. CD43)	SPN	6693	-2.252631	0.999842
208677_s_at	basigin (Ok blood group)	BSG	682	-2.255795	0.999842
212811_x_at	solute carrier family 1 (glutamate/neutral amino acid transporter). member 4	SLC1A4	6509	-2.257732	0.999842
205484_at	signaling threshold regulating transmembrane adaptor 1	SIT1	27240	-2.260847	0.999842
218388_at	6-phosphogluconolactonase	PGLS	25796	-2.262343	0.999842
211796_s_at	T cell receptor beta variable 19 /// T cell receptor beta variable 7-2 /// T cell receptor beta variable 5-4 /// T	TRBC1 /// TRB	28568 /// 285	-2.262811	0.999842
200913_at	protein phosphatase 1G (formerly 2C). magnesium-dependent. gamma isoform	PPM1G	5496	-2.264556	0.999842
215342_s_at	RAB GTPase activating protein 1-like	RABGAP1L	9910	-2.265079	0.999842
212025_s_at	flightless I homolog (Drosophila)	FLII	2314	-2.265235	0.999842
213596_at	caspase 4. apoptosis-related cysteine peptidase	CASP4	837	-2.266037	0.999842
204128_s_at	replication factor C (activator 1) 3. 38kDa	RFC3	5983	-2.268727	0.999842
203773_x_at	biliverdin reductase A	BLVRA	644	-2.273153	0.999842
209389_x_at	diazepam binding inhibitor (GABA receptor modulator. acyl-Coenzyme A binding protein)	DBI	1622	-2.274519	0.999842
90265_at	centaurin. alpha 1	CENTA1	11033	-2.274589	0.999842
218397_at	Fanconi anemia. complementation group L	FANCL	55120	-2.276529	0.999842
202546_at	vesicle-associated membrane protein 8 (endobrevin)	VAMP8	8673	-2.278573	0.999842
218112_at	mitochondrial ribosomal protein S34	MRPS34	65993	-2.285039	0.995336
202848_s_at	G protein-coupled receptor kinase 6	GRK6	2870	-2.285218	0.995336
213023_at	utrophin	UTRN	7402	-2.285846	0.995336
209933_s_at	CD300a molecule	CD300A	11314	-2.286991	0.995336
202555_s_at	myosin. light chain kinase	MYLK	4638	-2.287423	0.995336
214731_at	CTTNBP2 N-terminal like	CTTNBP2NL	55917	-2.2881	0.995336
202446_s_at	phospholipid scramblase 1	PLSCR1	5359	-2.288756	0.995336
215209_at	SEC24 related gene family. member D (S. cerevisiae)	SEC24D	9871	-2.296886	0.994105
202339_at	symplekin	SYMPK	8189	-2.296936	0.994105
208965_s_at	interferon. gamma-inducible protein 16	IFI16	3428	-2.298739	0.993134
222065_s_at	flightless I homolog (Drosophila)	FLII	2314	-2.298779	0.993134
209127_s_at	squamous cell carcinoma antigen recognized by T cells 3	SART3	9733	-2.300519	0.993134
219821_s_at	glucose-fructose oxidoreductase domain containing 1	GFOD1	54438	-2.302577	0.992432
216748_at	pyrin and HIN domain family. member 1	PYHIN1	149628	-2.303495	0.992138
212517_at	attractin	ATRN	8455	-2.303933	0.992138
203243_s_at	PDZ and LIM domain 5	PDLIM5	10611	-2.305576	0.992138
212136_at	ATPase. Ca++ transporting. plasma membrane 4	ATP2B4	493	-2.307716	0.991589
204003_s_at	nucleoporin like 2	NUPL2	11097	-2.3096	0.991589
31826_at	FK506 binding protein 15. 133kDa	FKBP15	23307	-2.311638	0.990482
220603_s_at	multiple C2 domains. transmembrane 2	MCTP2	55784	-2.313553	0.990482
202645_s_at	multiple endocrine neoplasia I	MEN1	4221	-2.315952	0.990446
202430_s_at	phospholipid scramblase 1	PLSCR1	5359	-2.316283	0.990446
210824_at	---	---	---	-2.317314	0.990446
205642_at	centrosomal protein 110kDa	CEP110	11064	-2.318111	0.990446
205599_at	TNF receptor-associated factor 1	TRAF1	7185	-2.318147	0.990446
221666_s_at	PYD and CARD domain containing	PYCARD	29108	-2.321191	0.990446
211791_s_at	potassium voltage-gated channel. shaker-related subfamily. beta member 2	KCNAB2	8514	-2.326949	0.985797
218294_s_at	nucleoporin 50kDa	NUP50	10762	-2.327504	0.985797
213888_s_at	TRAF3 interacting protein 3	TRAF3IP3	80342	-2.328011	0.985797
201823_s_at	ring finger protein 14	RNF14	9604	-2.328307	0.985797
205345_at	BRCA1 associated RING domain 1	BARD1	580	-2.329218	0.985797
202358_s_at	sorting nexin 19	SNX19	399979	-2.33007	0.985797
209670_at	T cell receptor alpha constant	TRAC	28755	-2.330755	0.985797
208438_s_at	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	FGR	2268	-2.330904	0.985797
204079_at	tyrosylprotein sulfotransferase 2	TPST2	8459	-2.333184	0.985797
203612_at	bystin-like	BYSL	705	-2.333648	0.985797
206332_s_at	interferon. gamma-inducible protein 16	IFI16	3428	-2.334376	0.985797
207332_s_at	transferrin receptor (p90. CD71)	TFRC	7037	-2.334941	0.985797
206486_at	lymphocyte-activation gene 3	LAG3	3902	-2.335934	0.985797
205272_s_at	proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2	PRH1 /// PRH	5554 /// 5555	-2.340475	0.985797
215176_x_at	Netrin 2-like (chicken)	NTN2L	4917	-2.34512	0.983708
209196_at	WD repeat domain 46	WDR46	9277	-2.345284	0.983708
220096_at	ribonuclease T2	RNASET2	8635	-2.345308	0.983708
217103_at	low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	3949	-2.347621	0.983708
218507_at	hypoxia-inducible protein 2	HIG2	29923	-2.34774	0.983708
203030_s_at	protein tyrosine phosphatase. receptor type. N polypeptide 2	PTPRN2	5799	-2.348458	0.983708
213603_s_at	ras-related C3 botulinum toxin substrate 2 (rho family. small GTP binding protein Rac2)	RAC2	5880	-2.349372	0.983708

221669_s_at	acyl-Coenzyme A dehydrogenase family. member 8	ACAD8	27034	-2.350417	0.983708
217223_s_at	breakpoint cluster region	BCR	613	-2.352349	0.983708
201230_s_at	ariadne homolog 2 (Drosophila)	ARIH2	10425	-2.352848	0.983708
205126_at	vaccinia related kinase 2	VRK2	7444	-2.355216	0.983708
209553_at	vacuolar protein sorting 8 homolog (S. cerevisiae)	VPS8	23355	-2.355407	0.983708
214096_s_at	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	6472	-2.357866	0.983708
207629_s_at	rho/rac guanine nucleotide exchange factor (GEF) 2	ARHGEF2	9181	-2.36097	0.983057
215057_at	Hypothetical protein FLJ44451	FLJ44451	100101122	-2.363465	0.982963
210606_x_at	killer cell lectin-like receptor subfamily D. member 1	KLRD1	3824	-2.364968	0.982963
202369_s_at	translocation associated membrane protein 2	TRAM2	9697	-2.365521	0.982963
219861_at	DnaJ (Hsp40) homolog. subfamily C. member 17	DNAJC17	55192	-2.36604	0.982963
213418_at	heat shock 70kDa protein 6 (HSP70B')	HSPA6	3310	-2.366397	0.982963
220558_x_at	tetraspanin 32	TSPAN32	10077	-2.367895	0.982963
204655_at	chemokine (C-C motif) ligand 5	CCL5	6352	-2.368428	0.982963
209473_at	ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1	953	-2.380552	0.975852
218670_at	pseudouridylate synthase 1	PUS1	80324	-2.38687	0.969041
212863_x_at	C-terminal binding protein 1	CTBP1	1487	-2.390791	0.968985
203729_at	epithelial membrane protein 3	EMP3	2014	-2.391383	0.968985
202330_s_at	uracil-DNA glycosylase	UNG	7374	-2.392323	0.968985
213863_s_at	ornithine decarboxylase antizyme 3	OAZ3	51686	-2.396142	0.968985
209890_at	tetraspanin 5	TSPAN5	10098	-2.397432	0.968985
218783_at	integrator complex subunit 7	INTS7	25896	-2.399517	0.968985
212342_at	Yip1 domain family. member 6	YIPF6	286451	-2.401605	0.966636
214677_x_at	immunoglobulin lambda locus /// immunoglobulin lambda variable 4-3 /// immunoglobulin lambda variable 3	IGL@ /// IGLJ	28786 /// 287	-2.402143	0.966636
209734_at	NCK-associated protein 1-like	NCKAP1L	3071	-2.404151	0.965484
205449_at	SAC3 domain containing 1	SAC3D1	29901	-2.404316	0.965484
50374_at	chromosome 17 open reading frame 90	C17orf90	339229	-2.405973	0.965484
219846_at	gon-4-like (C. elegans)	GON4L	54856	-2.406746	0.965484
219843_at	intracisternal A particle-promoted polypeptide	IPP	3652	-2.411438	0.965103
203252_at	CDK2-associated protein 2	CDK2AP2	10263	-2.413337	0.965103
201339_s_at	sterol carrier protein 2	SCP2	6342	-2.414247	0.965103
209611_s_at	solute carrier family 1 (glutamate/neutral amino acid transporter). member 4	SLC1A4	6509	-2.414601	0.965103
218045_x_at	parathymosin	PTMS	5763	-2.420425	0.965103
36004_at	inhibitor of kappa light polypeptide gene enhancer in B-cells. kinase gamma	IKBKG	8517	-2.421728	0.965103
219519_s_at	sialic acid binding Ig-like lectin 1. sialoadhesin	SIGLEC1	6614	-2.42246	0.965103
204747_at	interferon-induced protein with tetratricopeptide repeats 3	IFIT3	3437	-2.422839	0.965103
213045_at	microtubule associated serine/threonine kinase 3	MAST3	23031	-2.423957	0.965103
206558_at	single-minded homolog 2 (Drosophila)	SIM2	6493	-2.425833	0.965103
209403_at	TBC1 domain family. member 3 /// TBC1 domain family. member 3B /// TBC1 domain family. member 3C ///	LOC653380 //	414059 /// 41	-2.43324	0.957631
202101_s_at	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	5899	-2.434327	0.95725
203153_at	interferon-induced protein with tetratricopeptide repeats 1	IFIT1	3434	-2.437652	0.955994
217457_s_at	RAP1. GTP-GDP dissociation stimulator 1	RAP1GDS1	5910	-2.438018	0.955994
203401_at	phosphoribosyl pyrophosphate synthetase 2	PRPS2	5634	-2.43916	0.955994
221797_at	chromosome 17 open reading frame 90	C17orf90	339229	-2.439745	0.955994
220073_s_at	pleckstrin homology domain containing. family G (with RhoGef domain) member 6	PLEKHG6	55200	-2.440486	0.955994
215409_at	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase. eta)	AGPAT7	254531	-2.440614	0.955994
205483_s_at	ISG15 ubiquitin-like modifier	ISG15	9636	-2.44086	0.955994
217755_at	hematological and neurological expressed 1	HN1	51155	-2.442135	0.955994
203016_s_at	synovial sarcoma. X breakpoint 2 interacting protein	SSX2IP	117178	-2.44516	0.955994
57715_at	family with sequence similarity 26. member B	FAM26B	51063	-2.452142	0.955994
202592_at	biogenesis of lysosome-related organelles complex-1. subunit 1	BLOC1S1	2647	-2.460968	0.945989
218543_s_at	poly (ADP-ribose) polymerase family. member 12	PARP12	64761	-2.461486	0.945989
203882_at	interferon regulatory factor 9	IRF9	10379	-2.463635	0.945989
202402_s_at	cysteinyl-tRNA synthetase	CARS	833	-2.463806	0.945989
52159_at	HemK methyltransferase family member 1	HEMK1	51409	-2.467389	0.945989
206687_s_at	protein tyrosine phosphatase. non-receptor type 6	PTPN6	5777	-2.467811	0.945989
208647_at	farnesyl-diphosphate farnesyltransferase 1	FDFT1	2222	-2.46951	0.945989
205081_at	cysteine-rich protein 1 (intestinal)	CRIP1	1396	-2.474319	0.945989
206513_at	absent in melanoma 2	AIM2	9447	-2.478787	0.945648
208659_at	chloride intracellular channel 1	CLIC1	1192	-2.479185	0.945648
200862_at	24-dehydrocholesterol reductase	DHCR24	1718	-2.480873	0.94564
202748_at	guanylate binding protein 2. interferon-inducible	GBP2	2634	-2.48152	0.94564
210007_s_at	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	GPD2	2820	-2.482177	0.94564
201848_s_at	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3	664	-2.487797	0.94564
215999_at	CMT1A duplicated region transcript 1	CDRT1	374286	-2.488423	0.94564
212804_s_at	GTPase activating protein and VPS9 domains 1	GAPVD1	26130	-2.489935	0.94564
204006_s_at	Fc fragment of IgG. low affinity IIIa. receptor (CD16a) /// Fc fragment of IgG. low affinity IIIb. receptor (CD	FCGR3A /// F	2214 /// 2215	-2.494078	0.94564
210140_at	cystatin F (leukocystatin)	CST7	8530	-2.498432	0.94564
220771_at	melanoma antigen	LOC51152	51152	-2.500688	0.94564
210893_at	---	---	---	-2.507891	0.940768
213733_at	myosin IF	MYO1F	4542	-2.509095	0.940768
204252_at	cyclin-dependent kinase 2	CDK2	1017	-2.509392	0.940768
209813_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading fran	TARP /// TRG	445347 /// 69	-2.522398	0.934755
221876_at	zinc finger protein 783	ZNF783	155060	-2.522887	0.934755
37012_at	capping protein (actin filament) muscle Z-line. beta	CAPZB	832	-2.523261	0.934755
204398_s_at	echinoderm microtubule associated protein like 2	EML2	24139	-2.527401	0.934755
202145_at	lymphocyte antigen 6 complex. locus E	LY6E	4061	-2.532151	0.932664
220586_at	chromodomain helicase DNA binding protein 9	CHD9	80205	-2.540493	0.919927
216920_s_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading fran	TARP /// TRG	445347 /// 69	-2.542233	0.919927
218197_s_at	oxidation resistance 1	OXR1	55074	-2.543601	0.919927
206615_s_at	ADAM metallopeptidase domain 22	ADAM22	53616	-2.545701	0.919927
215084_s_at	leucine rich repeat containing 42	LRRC42	115353	-2.545709	0.919927
214657_s_at	Trophoblast-derived noncoding RNA	TncRNA	283131	-2.546708	0.919927
215806_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading fran	TARP /// TRG	445347 /// 69	-2.548486	0.919927
215713_at	CDNA: FLJ23125 fis. clone LNG08217	---	---	-2.549053	0.919927
215797_at	T cell receptor alpha variable 8-3	TRAV8-3	28683	-2.55185	0.919927
209138_x_at	Immunoglobulin lambda locus	IGL@	3535	-2.554937	0.919927
204959_at	myeloid cell nuclear differentiation antigen	MNDA	4332	-2.559718	0.919927
214895_s_at	ADAM metallopeptidase domain 10	ADAM10	102	-2.560982	0.919927
211786_at	tumor necrosis factor receptor superfamily. member 9	TNFRSF9	3604	-2.561003	0.919927
200800_s_at	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	HSPA1A /// H	3303 /// 3304	-2.567499	0.917727
213374_x_at	3-hydroxyisobutyryl-Coenzyme A hydrolase	HIBCH	26275	-2.56778	0.917727

213915_at	natural killer cell group 7 sequence	NKG7	4818	-2.571943	0.913069
221514_at	UTP14. U3 small nucleolar ribonucleoprotein. homolog A (yeast)	UTP14A	10813	-2.574838	0.913069
208670_s_at	EP300 interacting inhibitor of differentiation 1	EID1	23741	-2.588208	0.892861
203169_at	RGP1 retrograde golgi transport homolog (S. cerevisiae)	RGP1	9827	-2.58995	0.892861
215443_at	thyroid stimulating hormone receptor	TSHR	7253	-2.594297	0.890175
202837_at	TRAF-type zinc finger domain containing 1	TRAFD1	10906	-2.595966	0.890175
207667_s_at	mitogen-activated protein kinase kinase 3	MAP2K3	5606	-2.597547	0.890175
215611_at	transcription factor 12 (HTF4. helix-loop-helix transcription factors 4)	TCF12	6938	-2.598297	0.890175
218335_x_at	TNFAIP3 interacting protein 2	TNIP2	79155	-2.60439	0.887011
204441_s_at	polymerase (DNA directed). alpha 2 (70kD subunit)	POLA2	23649	-2.610632	0.881556
212099_at	ras homolog gene family. member B	RHOB	388	-2.612423	0.880393
201233_at	proteasome (prosome. macropain) 26S subunit. non-ATPase. 13	PSMD13	5719	-2.617423	0.874998
213507_s_at	karyopherin (importin) beta 1	KPNB1	3837	-2.620521	0.873794
203814_s_at	NAD(P)H dehydrogenase. quinone 2	NQO2	4835	-2.623466	0.872958
201639_s_at	cleavage and polyadenylation specific factor 1. 160kDa	CPSF1	29894	-2.623673	0.872958
220788_s_at	ring finger protein 31	RNF31	55072	-2.631476	0.866649
200850_s_at	S-adenosylhomocysteine hydrolase-like 1	AHCYL1	10768	-2.633959	0.866649
211070_x_at	diazepam binding inhibitor (GABA receptor modulator. acyl-Coenzyme A binding protein)	DBI	1622	-2.637035	0.863216
220449_at	hypothetical protein MGC5566	MGC5566	79015	-2.638811	0.862215
218681_s_at	stromal cell-derived factor 2-like 1	SDF2L1	23753	-2.642281	0.860415
211504_x_at	Rho-associated. coiled-coil containing protein kinase 2	ROCK2	9475	-2.644899	0.860415
221873_at	zinc finger protein 143	ZNF143	7702	-2.645331	0.860415
217497_at	endothelial cell growth factor 1 (platelet-derived)	ECGF1	1890	-2.653325	0.853874
202760_s_at	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2	AKAP2 /// PAL	11217 /// 445	-2.653912	0.853874
218593_at	RNA binding motif protein 28	RBM28	55131	-2.656287	0.853874
201541_s_at	zinc finger. HIT type 1	ZNHIT1	10467	-2.658826	0.853874
200812_at	chaperonin containing TCP1. subunit 7 (eta)	CCT7	10574	-2.661078	0.853874
217173_s_at	low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	3949	-2.664139	0.853874
208097_s_at	thioredoxin domain containing 1	TXNDC1	81542	-2.664249	0.853874
204162_at	NDC80 homolog. kinetochore complex component (S. cerevisiae)	NDC80	10403	-2.665556	0.853874
219159_s_at	SLAM family member 7	SLAMF7	57823	-2.66699	0.853874
217857_s_at	RNA binding motif protein 8A	RBM8A	9939	-2.667241	0.853874
202086_at	myxovirus (influenza virus) resistance 1. interferon-inducible protein p78 (mouse)	MX1	4599	-2.667578	0.853874
37425_g_at	coiled-coil alpha-helical rod protein 1	CCHCR1	54535	-2.671183	0.853874
206589_at	growth factor independent 1 transcription repressor	GFI1	2672	-2.675827	0.853874
203150_at	Rab9 effector protein with kelch motifs	RABEPK	10244	-2.67629	0.853874
221079_s_at	methyltransferase like 2B /// methyltransferase like 2A	METTL2A ///	339175 /// 55	-2.681647	0.853874
206092_x_at	regulator of telomere elongation helicase 1	RTEL1	51750	-2.68586	0.853874
204661_at	CD52 molecule	CD52	1043	-2.687852	0.853874
217292_at	myotubularin related protein 7	MTMR7	9108	-2.691707	0.853874
202869_at	2'.5'-oligoadenylate synthetase 1. 40/46kDa	OAS1	4938	-2.700101	0.853874
214004_s_at	vestigial like 4 (Drosophila)	VGLL4	9686	-2.708912	0.852106
214059_at	Interferon-induced protein 44	IFI44	10561	-2.709346	0.852106
220307_at	CD244 molecule. natural killer cell receptor 2B4	CD244	51744	-2.711134	0.852106
212567_s_at	microtubule-associated protein 4	MAP4	4134	-2.713028	0.852106
201061_s_at	stomatin	STOM	2040	-2.715958	0.852106
203931_s_at	mitochondrial ribosomal protein L12	MRPL12	6182	-2.723132	0.852106
211144_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading fran	TARP /// TRG	445347 /// 69	-2.724738	0.852106
204340_at	transmembrane protein 187	TMEM187	8269	-2.727179	0.852106
215105_at	hypothetical gene CG030	CG030	116828	-2.731114	0.852106
202198_s_at	myotubularin related protein 3	MTMR3	8897	-2.734718	0.852106
214926_at	spectrin. alpha. non-erythrocytic 1 (alpha-fodrin)	SPTAN1	6709	-2.748293	0.848523
201580_s_at	thioredoxin domain containing 13	TXNDC13	56255	-2.749566	0.848523
202411_at	interferon. alpha-inducible protein 27	IFI27	3429	-2.752903	0.846362
216298_at	hypothetical protein LOC648852	LOC648852	648852	-2.755525	0.844341
33850_at	microtubule-associated protein 4	MAP4	4134	-2.758097	0.843005
203109_at	ubiquitin-conjugating enzyme E2M (UBC12 homolog. yeast)	UBE2M	9040	-2.765071	0.834774
204994_at	myxovirus (influenza virus) resistance 2 (mouse)	MX2	4600	-2.772816	0.830816
218986_s_at	hypothetical protein FLJ20035	FLJ20035	55601	-2.779552	0.826033
200863_s_at	RAB11A. member RAS oncogene family	RAB11A	8766	-2.785379	0.824301
222154_s_at	viral DNA polymerase-transactivated protein 6	LOC26010	26010	-2.799965	0.813
213433_at	ADP-ribosylation factor-like 3	ARL3	403	-2.80017	0.813
221708_s_at	unc-45 homolog A (C. elegans)	UNC45A	55898	-2.801569	0.813
200675_at	CD81 molecule	CD81	975	-2.802487	0.813
204073_s_at	chromosome 11 open reading frame 9	C11orf9	745	-2.81372	0.813
32402_s_at	symplekin	SYMPK	8189	-2.833536	0.782863
200623_s_at	calmodulin 3 (phosphorylase kinase. delta)	CALM3	808	-2.839109	0.778228
201601_x_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	8519	-2.843273	0.777545
202428_x_at	diazepam binding inhibitor (GABA receptor modulator. acyl-Coenzyme A binding protein)	DBI	1622	-2.846548	0.774818
205904_at	MHC class I polypeptide-related sequence A	MICA	4276	-2.862126	0.763884
214836_x_at	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5	IGKC /// IGKV	28299 /// 351	-2.863496	0.763884
44673_at	sialic acid binding Ig-like lectin 1. sialoadhesin	SIGLEC1	6614	-2.864676	0.763884
220631_at	O-sialoglycoprotein endopeptidase-like 1	OSGEPL1	64172	-2.865379	0.763884
218367_x_at	ubiquitin specific peptidase 21	USP21	27005	-2.866218	0.763884
218999_at	transmembrane protein 140	TMEM140	55281	-2.868119	0.763884
216519_s_at	proline synthetase co-transcribed homolog (bacterial)	PROSC	11212	-2.884539	0.758815
202659_at	proteasome (prosome. macropain) subunit. beta type. 10	PSMB10	5699	-2.894005	0.74575
215719_x_at	Fas (TNF receptor superfamily. member 6)	FAS	355	-2.894768	0.74575
219211_at	ubiquitin specific peptidase 18	USP18	11274	-2.895115	0.74575
221513_s_at	UTP14. U3 small nucleolar ribonucleoprotein. homolog C (yeast) /// UTP14. U3 small nucleolar ribonucleoprot	UTP14A /// U	10813 /// 972	-2.896457	0.74575
206746_at	beaded filament structural protein 1. filensin	BFSP1	631	-2.897094	0.74575
213294_at	Full-length cDNA clone CS0DK002YF13 of HeLa cells Cot 25-normalized of Homo sapiens (human)	---	---	-2.8981	0.74575
34210_at	CD52 molecule	CD52	1043	-2.901647	0.74575
117_at	heat shock 70kDa protein 6 (HSP70B')	HSPA6	3310	-2.909103	0.74575
221143_at	replication protein A4. 34kDa	RPA4	29935	-2.921265	0.744465
202604_x_at	ADAM metallopeptidase domain 10	ADAM10	102	-2.931555	0.730023
204853_at	origin recognition complex. subunit 2-like (yeast)	ORC2L	4999	-2.934116	0.729414
214343_s_at	ataxin 7-like 1	ATXN7L1	222255	-2.946185	0.719337
208492_at	regulatory factor X-associated protein	RFXAP	5994	-2.953293	0.710946
210321_at	granzyme H (cathepsin G-like 2. protein h-CCPX)	GZMH	2999	-2.964101	0.707388
212166_at	exportin 7	XPO7	23039	-2.96494	0.707388
200643_at	high density lipoprotein binding protein (vigilin)	HDLBP	3069	-2.965827	0.707388

218620_s_at	HemK methyltransferase family member 1	HEMK1	51409	-2.972887	0.707388
216197_at	activating transcription factor 7 interacting protein	ATF7IP	55729	-2.976676	0.707388
216883_x_at	phosphodiesterase 6D. cGMP-specific. rod. delta	PDE6D	5147	-2.979193	0.707388
216540_at	T cell receptor alpha locus	TRA@	6955	-2.979247	0.707388
207761_s_at	methyltransferase like 7A	METTL7A	25840	-2.981419	0.707388
207492_at	N-glycanase 1	NGLY1	55768	-2.987963	0.707388
217138_x_at	Immunoglobulin lambda locus	IGL@	3535	-2.992135	0.707388
222002_at	Chromosome 7 open reading frame 26	C7orf26	79034	-2.995426	0.707388
201315_x_at	interferon induced transmembrane protein 2 (1-8D)	IFITM2	10581	-3.006596	0.707388
202942_at	electron-transfer-flavoprotein. beta polypeptide	ETFB	2109	-3.021587	0.707388
208003_s_at	nuclear factor of activated T-cells 5. tonicity-responsive	NFAT5	10725	-3.0318	0.704919
202480_s_at	death effector domain containing	DEDD	9191	-3.040346	0.694092
213617_s_at	chromosome 18 open reading frame 10	C18orf10	25941	-3.040592	0.694092
205702_at	putative homeodomain transcription factor 1	PHTF1	10745	-3.041724	0.694092
207509_s_at	leukocyte-associated immunoglobulin-like receptor 2	LAIR2	3904	-3.045286	0.694092
210156_s_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase	PCMT1	5110	-3.054953	0.688018
216565_x_at	interferon induced transmembrane protein pseudogene	LOC391020	391020	-3.058544	0.686712
209732_at	C-type lectin domain family 2. member B	CLEC2B	9976	-3.059706	0.686712
205552_s_at	2'.5'-oligoadenylate synthetase 1. 40/46kDa	OAS1	4938	-3.083134	0.679372
200900_s_at	mannose-6-phosphate receptor (cation dependent)	M6PR	4074	-3.087961	0.6765
216958_s_at	isovaleryl Coenzyme A dehydrogenase	IVD	3712	-3.095566	0.668264
203471_s_at	pleckstrin	PLEK	5341	-3.095829	0.668264
203392_s_at	C-terminal binding protein 1	CTBP1	1487	-3.098844	0.668264
210137_s_at	dCMP deaminase	DCTD	1635	-3.118266	0.668264
216237_s_at	minichromosome maintenance complex component 5	MCM5	4174	-3.125737	0.668264
209044_x_at	splicing factor 3b. subunit 4. 49kDa	SF3B4	10262	-3.133064	0.665781
205718_at	integrin. beta 7	ITGB7	3695	-3.13477	0.665781
221879_at	calmodulin-like 4	CALML4	91860	-3.16149	0.65785
200760_s_at	ADP-ribosylation-like factor 6 interacting protein 5	ARL6IP5	10550	-3.163834	0.65785
205842_s_at	Janus kinase 2 (a protein tyrosine kinase)	JAK2	3717	-3.188324	0.623484
212162_at	kinase D-interacting substrate of 220 kDa	KIDINS220	57498	-3.208084	0.602636
218272_at	hypothetical protein FLJ20699	FLJ20699	55020	-3.253421	0.572938
216252_x_at	Fas (TNF receptor superfamily. member 6)	FAS	355	-3.258874	0.572938
212203_x_at	interferon induced transmembrane protein 3 (1-8U)	IFITM3	10410	-3.258878	0.572938
204103_at	chemokine (C-C motif) ligand 4	CCL4	6351	-3.275972	0.569778
218927_s_at	carbohydrate (chondroitin 4) sulfotransferase 12	CHST12	55501	-3.280979	0.569778
201263_at	threonyl-tRNA synthetase	TARS	6897	-3.293493	0.562471
203941_at	integrator complex subunit 9	INTS9	55756	-3.306854	0.562181
206133_at	XIAP associated factor-1	XAF1	54739	-3.326924	0.5527
209449_at	LSM2 homolog. U6 small nuclear RNA associated (S. cerevisiae)	LSM2	57819	-3.332443	0.551467
64408_s_at	calmodulin-like 4	CALML4	91860	-3.35522	0.524274
209969_s_at	signal transducer and activator of transcription 1. 91kDa	STAT1	6772	-3.367198	0.524274
202305_s_at	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2	9637	-3.378249	0.524274
215864_at	CDNA: FLJ21424 fis. clone COL04157	---	---	-3.392941	0.524274
213403_at	Clone 23908 mRNA sequence	---	---	-3.395549	0.524274
212729_at	discs. large homolog 3 (neuroendocrine-dlg. Drosophila)	DLG3	1741	-3.436891	0.524274
214195_at	tripeptidyl peptidase I	TPP1	1200	-3.45291	0.524274
221651_x_at	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 /// immunoglobulin kappa variable 2-	IGK@ /// IGK	28299 /// 289	-3.46206	0.521169
201886_at	WD repeat domain 23	WDR23	80344	-3.479719	0.504724
201641_at	bone marrow stromal cell antigen 2	BST2	684	-3.484017	0.504724
203470_s_at	pleckstrin	PLEK	5341	-3.49573	0.500671
218400_at	2'-5'-oligoadenylate synthetase 3. 100kDa	OAS3	4940	-3.529733	0.4723
206553_at	2'-5'-oligoadenylate synthetase 2. 69/71kDa	OAS2	4939	-3.547919	0.471311
213797_at	radical S-adenosyl methionine domain containing 2	RSAD2	91543	-3.569007	0.458443
204415_at	interferon. alpha-inducible protein 6	IFI6	2537	-3.586851	0.445071
203790_s_at	heat-responsive protein 12	HRSP12	10247	-3.615157	0.433373
205965_at	basic leucine zipper transcription factor. ATF-like	BATF	10538	-3.630572	0.430313
215345_x_at	T cell receptor gamma variable 7	TRGV7	6981	-3.640388	0.428654
208741_at	Sin3A-associated protein. 18kDa	SAP18	10284	-3.664203	0.421399
221671_x_at	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 /// immunoglobulin kappa variable 2-	IGK@ /// IGK	28299 /// 289	-3.703389	0.421399
202417_at	kelch-like ECH-associated protein 1	KEAP1	9817	-3.712357	0.421399
207229_at	killer cell lectin-like receptor subfamily A. member 1	KLRA1	10748	-3.74285	0.421399
214669_x_at	immunoglobulin kappa locus	IGK@	50802	-3.797643	0.421399
201484_at	suppressor of Ty 4 homolog 1 (S. cerevisiae)	SUPT4H1	6827	-3.81015	0.421399
212070_at	G protein-coupled receptor 56	GPR56	9289	-3.915727	0.421399
201949_x_at	capping protein (actin filament) muscle Z-line. beta	CAPZB	832	-3.983587	0.421399
214617_at	perforin 1 (pore forming protein)	PRF1	5551	-3.994811	0.421399
204968_at	chromosome 6 open reading frame 47	C6orf47	57827	-4.054763	0.421399
202458_at	protease. serine. 23	PRSS23	11098	-4.133224	0.421399
204439_at	interferon-induced protein 44-like	IFI44L	10964	-4.330995	0.358674
206582_s_at	G protein-coupled receptor 56	GPR56	9289	-4.572991	0.253543
209417_s_at	interferon-induced protein 35	IFI35	3430	-5.028481	0.080065
214453_s_at	interferon-induced protein 44	IFI44	10561	-5.110811	0.080065

pZC	dZC	Set	Collection
0.000004	-1	Interferon-mediated_immunity	ABI_Process
0.005124	-1	MHCI-mediated_immunity	ABI_Process
0.007238	-1	Pyrimidine_metabolism	ABI_Process
0.005599	-1	Parkinson_disease	ABI_Pathway
0.000948	-0.96	Cytoskeletal_regulation_by_Rho_GTPase	ABI_Pathway
0.046254	-0.91	Cell_motility	ABI_Process
0.003262	-0.91	Inflammation_mediated_by_chemokine_and_cytokine_signaling_pathway	ABI_Pathway
0.001052	-0.88	Natural_killer_cell_mediated_immunity	ABI_Process
0.027051	-0.84	Immunity_and_defense	ABI_Process
0.003106	-0.8	Cell_adhesion-mediated_signaling	ABI_Process
0.043577	-0.63	Calcium_mediated_signaling	ABI_Process
0.020896	-0.58	Nerve-nerve_synaptic_transmission	ABI_Process
0.039849	-0.58	Apoptosis_signaling_pathway	ABI_Pathway
0.027594	-0.4	Neuronal_activities	ABI_Process
0.012109	-0.39	Apoptosis	ABI_Process
0.032994	-0.34	Other_polysaccharide_metabolism	ABI_Process
0.010968	-0.28	Olfaction	ABI_Process
0.00612	-0.09	Cadherin_signaling_pathway	ABI_Pathway
0.002987	-0.01	Steroid_hormone_metabolism	ABI_Process

Supplementary Table 3: Gene sets significantly increased in expression profiles of HIV-specific T cells from Progressors vs. Controllers. ABI Pathway and Process gene sets were tested for enrichment in expression profiles of Gag-specific CD8 T cells from progressors compared to controllers. Genesets with significant enrichment values shown. pZC indicates the enrichment p-value, as computed by RenderCat (details in Methods); dZC indicates the direction of the enrichment: negative value indicate that the genes are lower-expressed in controllers (higher-expressed in progressors); set is the name of the set; collection is the gene set collection to which the set belongs.

pZC	dZC	Set	Collection
0.000069	0.97	Protein_biosynthesis	ABI_Process
0.00025	0.91	mRNA_splicing	ABI_Process
0.002554	0.92	Protein_targeting_and_localization	ABI_Process
0.005124	1	mRNA_polyadenylation	ABI_Process
0.008909	0.11	Regulation_of_vasoconstriction,_dilation	ABI_Process
0.011298	0.12	Heterotrimeric_G-protein_signaling_pathway-Gi_alpha_and_Gs_alpha_mediated_pathway	ABI_Pathway
0.011872	1	mRNA_end-processing_and_stability	ABI_Process
0.013505	0.3	Synaptic_transmission	ABI_Process
0.016145	0.79	Steroid_metabolism	ABI_Process
0.017479	0.87	Insulin_IGF_pathway-mitogen_activated_protein_kinase_kinase_MAP_kinase_cascade	ABI_Pathway
0.029288	0.46	Skeletal_development	ABI_Process
0.029288	0.69	Anterior_posterior_patterning	ABI_Process
0.032345	1	Circadian_clock_system	ABI_Pathway
0.03644	0.9	Signal_transduction	ABI_Process
0.044012	0.28	Alzheimer_disease-presenilin_pathway	ABI_Pathway

Supplementary Table 4: Gene sets significantly increased in expression profiles of HIV-specific T cells from Controllers vs. Progressors. ABI Pathway and Process gene sets were tested for enrichment in expression profiles of Gag-specific CD8 T cells from controllers compared to progressors. pZC indicates the enrichment p-value, as computed by RenderCat (details in Methods); dZC indicates the direction of the enrichment: positive values indicate that the genes are higher-expressed in elite controllers (lower-expressed in progressors); set is the name of the set; collection is the gene set collection to which the set belongs.

Supplementary Table 5: Transcripts increased in expression in PD-1 Jurkat cells stimulated with PD1/CD3/CD28 beads (t > 2.0), or in those stimulated with CD3/CD28 beads (t < –2.0).

probeset_id	GeneTitle	GeneSymbol	GeneID	t	q
210164_at	granzyme B (granzyme 2. cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	3002	18.227709	0.001874
209969_s_at	signal transducer and activator of transcription 1. 91kDa	STAT1	6772	14.929347	0.00444
202269_x_at	guanylate binding protein 1. interferon-inducible. 67kDa	GBP1	2633	10.838547	0.034349
205066_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENPP1	5167	10.210011	0.040357
200887_s_at	signal transducer and activator of transcription 1. 91kDa	STAT1	6772	9.269462	0.066247
201105_at	lectin. galactoside-binding. soluble. 1 (galectin 1)	LGALS1	3956	8.888005	0.075221
209417_s_at	interferon-induced protein 35	IFI35	3430	8.664381	0.077699
205488_at	granzyme A (granzyme 1. cytotoxic T-lymphocyte-associated serine esterase 3)	GZMA	3001	8.343608	0.089478
202688_at	tumor necrosis factor (ligand) superfamily. member 10	TNFSF10	8743	7.975849	0.105387
217997_at	pleckstrin homology-like domain. family A. member 1	PHLDA1	22822	7.794043	0.106351
201649_at	ubiquitin-conjugating enzyme E2L 6	UBE2L6	9246	7.128327	0.183614
217996_at	pleckstrin homology-like domain. family A. member 1	PHLDA1	22822	6.857691	0.222102
201666_at	TIMP metallopeptidase inhibitor 1	TIMP1	7076	6.69877	0.227814
204279_at	proteasome (prosome. macropain) subunit. beta type. 9 (large multifunctional peptidase 2)	PSMB9	5698	6.66554	0.227814
207351_s_at	SH2 domain protein 2A	SH2D2A	9047	6.547141	0.227814
202307_s_at	transporter 1. ATP-binding cassette. sub-family B (MDR/TAP)	TAP1	6890	6.491677	0.227814
203939_at	5'-nucleotidase. ecto (CD73)	NT5E	4907	6.478622	0.227814
216231_s_at	beta-2-microglobulin	B2M	567	6.466658	0.227814
200905_x_at	major histocompatibility complex. class I. E	HLA-E	3133	6.240698	0.263103
202659_at	proteasome (prosome. macropain) subunit. beta type. 10	PSMB10	5699	6.238794	0.263103
203882_at	interferon regulatory factor 9	IRF9	10379	6.143691	0.278594
202270_at	guanylate binding protein 1. interferon-inducible. 67kDa	GBP1	2633	6.071515	0.288521
202531_at	interferon regulatory factor 1	IRF1	3659	5.737293	0.368172
203695_s_at	deafness. autosomal dominant 5	DFNA5	1687	5.725111	0.368172
204804_at	tripartite motif-containing 21	TRIM21	6737	5.683695	0.368172
202975_s_at	Rho-related BTB domain containing 3	RHOBTB3	22836	5.643445	0.368172
206118_at	signal transducer and activator of transcription 4	STAT4	6775	5.495037	0.368172
210140_at	cystatin F (leukocystatin)	CST7	8530	5.487539	0.368172
210948_s_at	lymphoid enhancer-binding factor 1	LEF1	51176	5.451529	0.368172
201858_s_at	serglycin	SRGN	5552	5.449523	0.368172
203760_s_at	Src-like-adaptor	SLA	6503	5.448234	0.368172
209670_at	T cell receptor alpha constant	TRAC	28755	5.435559	0.368172
209365_s_at	extracellular matrix protein 1	ECM1	1893	5.423926	0.368172
211005_at	linker for activation of T cells	LAT	27040	5.42136	0.368172
204070_at	retinoic acid receptor responder (tazarotene induced) 3	RARRES3	5920	5.385485	0.374415
203729_at	epithelial membrane protein 3	EMP3	2014	5.358671	0.376963
217456_x_at	major histocompatibility complex. class I. E	HLA-E	3133	5.324484	0.383186
204415_at	interferon. alpha-inducible protein 6	IFI6	2537	5.300603	0.384986
205065_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENPP1	5167	5.272298	0.389122
34210_at	CD52 molecule	CD52	1043	5.222255	0.395123
209667_at	carboxylesterase 2 (intestine. liver)	CES2	8824	5.133136	0.42509
209813_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate	TARP /// TRG	445347 /// 69	5.127041	0.42509
208581_x_at	metallothionein 1X	MT1X	4501	5.075682	0.443485
209040_s_at	proteasome (prosome. macropain) subunit. beta type. 8 (large multifunctional peptidase 7)	PSMB8	5696	5.058703	0.443676
33304_at	interferon stimulated exonuclease gene 20kDa	ISG20	3669	4.959533	0.482434
221269_s_at	SH3 domain binding glutamic acid-rich protein like 3	SH3BGRL3	83442	4.920797	0.487407
213193_x_at	T cell receptor beta variable 19 /// T cell receptor beta constant 1	TRBC1 /// TR	28568 /// 286	4.664671	0.623444
204637_at	glycoprotein hormones. alpha polypeptide	CGA	1081	4.647779	0.623444
208899_x_at	ATPase. H+ transporting. lysosomal 34kDa. V1 subunit D	ATP6V1D	51382	4.61805	0.623444
205856_at	solute carrier family 14 (urea transporter). member 1 (Kidd blood group)	SLC14A1	6563	4.617547	0.623444
210397_at	defensin. beta 1	DEFB1	1672	4.597083	0.623444
211165_x_at	EPH receptor B2	EPHB2	2048	4.52819	0.643373
219716_at	apolipoprotein L. 6	APOL6	80830	4.483015	0.658014
213220_at	hypothetical protein LOC92482	LOC92482	92482	4.474231	0.658014
204698_at	interferon stimulated exonuclease gene 20kDa	ISG20	3669	4.460427	0.659838
201762_s_at	proteasome (prosome. macropain) activator subunit 2 (PA28 beta)	PSME2	5721	4.448891	0.659838
204747_at	interferon-induced protein with tetratricopeptide repeats 3	IFIT3	3437	4.400184	0.659838
209140_x_at	major histocompatibility complex. class I. B	HLA-B	3106	4.368345	0.659838
209732_at	C-type lectin domain family 2. member B	CLEC2B	9976	4.357969	0.659838
203761_at	Src-like-adaptor	SLA	6503	4.336402	0.659838
200904_at	major histocompatibility complex. class I. E	HLA-E	3133	4.331984	0.659838
205406_s_at	sperm autoantigenic protein 17	SPA17	53340	4.297531	0.659838
206584_at	lymphocyte antigen 96	LY96	23643	4.269787	0.659838
219326_s_at	UDP-GlcNAc:betaGal beta-1.3-N-acetylglucosaminyltransferase 2	B3GNT2	10678	4.249119	0.659838
205987_at	CD1c molecule	CD1C	911	4.226312	0.659838
200872_at	S100 calcium binding protein A10	S100A10	6281	4.224039	0.659838
203298_s_at	jumonji. AT rich interactive domain 2	JARID2	3720	4.219837	0.659838
210915_x_at	T cell receptor beta variable 19 /// T cell receptor beta constant 1	TRBC1 /// TR	28568 /// 286	4.212395	0.659838
214757_at	CDNA clone IMAGE:3456494	---	---	4.204413	0.659838
202712_s_at	creatine kinase. mitochondrial 1B /// creatine kinase. mitochondrial 1A	CKMT1A /// C	1159 /// 5485	4.160303	0.659838
207288_at	chromosome X and Y open reading frame 2	CXYorf2	80161	4.159694	0.659838
204661_at	CD52 molecule	CD52	1043	4.15591	0.659838
221139_s_at	cysteine sulfinic acid decarboxylase	CSAD	51380	4.128038	0.659838
202687_s_at	tumor necrosis factor (ligand) superfamily. member 10	TNFSF10	8743	4.12724	0.659838
215806_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate	TARP /// TRG	445347 /// 69	4.120661	0.659838
209515_s_at	RAB27A. member RAS oncogene family	RAB27A	5873	4.088021	0.659838
215082_at	ELOVL family member 5. elongation of long chain fatty acids (FEN1/Elo2. SUR4/Elo3-like. yeast)	ELOVL5	60481	4.074971	0.659838
219209_at	interferon induced with helicase C domain 1	IFIH1	64135	4.062895	0.659838
219717_at	chromosome 4 open reading frame 30	C4orf30	54876	4.06228	0.659838
212573_at	endonuclease domain containing 1	ENDOD1	23052	4.045748	0.659838
220021_at	transmembrane channel-like 7	TMC7	79905	4.039762	0.659838
212570_at	endonuclease domain containing 1	ENDOD1	23052	4.031653	0.659838
216920_s_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate	TARP /// TRG	445347 /// 69	4.028937	0.659838

205798_at	interleukin 7 receptor	IL7R	3575	4.010822	0.659838
221419_s_at	---	---	---	3.997943	0.659838
212998_x_at	major histocompatibility complex. class II. DQ beta 1	HLA-DQB1	3119	3.980246	0.659838
214717_at	hypothetical protein DKFZp434H1419	DKFZp434H14	150967	3.958514	0.659838
212249_at	phosphoinositide-3-kinase. regulatory subunit 1 (p85 alpha)	PIK3R1	5295	3.957294	0.659838
220704_at	IKAROS family zinc finger 1 (Ikaros)	IKZF1	10320	3.947866	0.659838
213060_s_at	chitinase 3-like 2	CHI3L2	1117	3.942297	0.659838
220358_at	basic leucine zipper transcription factor. ATF-like 3	BATF3	55509	3.933133	0.659838
210946_at	phosphatidic acid phosphatase type 2A	PPAP2A	8611	3.929366	0.659838
209769_s_at	glycoprotein Ib (platelet). beta polypeptide	GP1BB	2812	3.90943	0.659838
211600_at	---	---	---	3.909174	0.659838
205768_s_at	solute carrier family 27 (fatty acid transporter). member 2	SLC27A2	11001	3.907836	0.659838
202156_s_at	CUG triplet repeat. RNA binding protein 2	CUGBP2	10659	3.893065	0.659838
217773_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex. 4. 9kDa	NDUFA4	4697	3.872607	0.659838
211434_s_at	chemokine (C-C motif) receptor-like 2 /// similar to chemokine (C-C motif) receptor-like 2	CCRL2 /// LOC	727811 /// 90	3.865089	0.659838
208965_s_at	interferon. gamma-inducible protein 16	IFI16	3428	3.859984	0.659838
205891_at	adenosine A2b receptor	ADORA2B	136	3.842007	0.659838
215537_x_at	dimethylarginine dimethylaminohydrolase 2	DDAH2	23564	3.83539	0.659838
201426_s_at	vimentin	VIM	7431	3.830078	0.659838
219296_at	zinc finger. DHHC-type containing 13	ZDHHC13	54503	3.826049	0.659838
201564_s_at	fascin homolog 1. actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	6624	3.802566	0.659838
200848_at	S-adenosylhomocysteine hydrolase-like 1	AHCYL1	10768	3.795461	0.659838
201329_s_at	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	2114	3.775619	0.659838
212185_x_at	metallothionein 2A	MT2A	4502	3.772668	0.659838
215949_x_at	immunoglobulin heavy constant mu	IGHM	3507	3.74507	0.659838
217065_at	T cell receptor alpha locus	TRA@	6955	3.742999	0.659838
202110_at	cytochrome c oxidase subunit VIIb	COX7B	1349	3.735991	0.659838
216538_at	MRNA; cDNA DKFZp566C093 (from clone DKFZp566C093)	---	---	3.718778	0.659838
206248_at	protein kinase C. epsilon	PRKCE	5581	3.704881	0.659838
205267_at	POU class 2 associating factor 1	POU2AF1	5450	3.70105	0.659838
207734_at	lymphocyte transmembrane adaptor 1	LAX1	54900	3.690583	0.659838
204138_s_at	myeloid zinc finger 1	MZF1	7593	3.684846	0.659838
218751_s_at	F-box and WD repeat domain containing 7	FBXW7	55294	3.673787	0.659838
210279_at	G protein-coupled receptor 18	GPR18	2841	3.668422	0.659838
210951_x_at	RAB27A. member RAS oncogene family	RAB27A	5873	3.667693	0.659838
221309_at	RNA binding motif protein 17	RBM17	84991	3.667668	0.659838
217622_at	rhomboid domain containing 3	RHBDD3	25807	3.646813	0.659838
204220_at	glia maturation factor. gamma	GMFG	9535	3.641916	0.659838
205173_x_at	CD58 molecule	CD58	965	3.638125	0.659838
218193_s_at	golgi transport 1 homolog B (S. cerevisiae)	GOLT1B	51026	3.62911	0.659838
213996_at	yippee-like 1 (Drosophila)	YPEL1	29799	3.621062	0.659838
208522_s_at	patched homolog 1 (Drosophila)	PTCH1	5727	3.610641	0.659838
214459_x_at	major histocompatibility complex. class I. C	HLA-C	3107	3.609019	0.659838
217371_s_at	interleukin 15	IL15	3600	3.593537	0.659838
219600_s_at	transmembrane protein 50B	TMEM50B	757	3.59194	0.659838
206458_s_at	wingless-type MMTV integration site family. member 2B	WNT2B	7482	3.579152	0.659838
202262_x_at	dimethylarginine dimethylaminohydrolase 2	DDAH2	23564	3.57425	0.659838
206824_at	carboxylesterase 1 (monocyte/macrophage serine esterase 1) /// carboxylesterase 4-like	CES1 /// CES4	1066 /// 5171	3.574053	0.659838
219070_s_at	motile sperm domain containing 3	MOSPD3	64598	3.568675	0.659838
212956_at	TBC1 domain family. member 9 (with GRAM domain)	TBC1D9	23158	3.565038	0.659838
205966_at	TAF13 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 18kDa	TAF13	6884	3.557187	0.659838
221927_s_at	abhydrolase domain containing 11	ABHD11	83451	3.557071	0.659838
203763_at	dynein. cytoplasmic 2. light intermediate chain 1	DYNC2LI1	51626	3.549701	0.659838
209761_s_at	SP110 nuclear body protein	SP110	3431	3.52679	0.659838
214244_s_at	ATPase. H+ transporting. lysosomal 9kDa. V0 subunit e1	ATP6V0E1	8992	3.518142	0.659838
207191_s_at	immunoglobulin superfamily containing leucine-rich repeat	ISLR	3671	3.517028	0.659838
208791_at	clusterin	CLU	1191	3.516989	0.659838
205992_s_at	interleukin 15	IL15	3600	3.516398	0.659838
218747_s_at	TAP binding protein-like	TAPBPL	55080	3.513271	0.659838
217993_s_at	methionine adenosyltransferase II. beta	MAT2B	27430	3.512097	0.659838
221474_at	myosin regulatory light chain MRLC2	MRLC2	103910	3.510823	0.659838
203297_s_at	jumonji. AT rich interactive domain 2	JARID2	3720	3.505619	0.659838
203002_at	angiomotin like 2	AMOTL2	51421	3.488415	0.659838
207955_at	chemokine (C-C motif) ligand 27	CCL27	10850	3.484061	0.659838
204234_s_at	zinc finger protein 195	ZNF195	7748	3.479671	0.659838
203581_at	RAB4A. member RAS oncogene family	RAB4A	5867	3.453963	0.659838
214329_x_at	tumor necrosis factor (ligand) superfamily. member 10	TNFSF10	8743	3.448907	0.659838
220952_s_at	pleckstrin homology domain containing. family A member 5	PLEKHA5	54477	3.44818	0.659838
203233_at	interleukin 4 receptor	IL4R	3566	3.431601	0.659838
222256_s_at	phospholipase A2. group IVB (cytosolic)	PLA2G4B	8681	3.429655	0.659838
219201_s_at	twisted gastrulation homolog 1 (Drosophila)	TWSG1	57045	3.429153	0.659838
221838_at	kelch-like 22 (Drosophila)	KLHL22	84861	3.419488	0.659838
215669_at	major histocompatibility complex. class II. DR beta 4	HLA-DRB4	3126	3.418962	0.659838
205731_s_at	nuclear receptor coactivator 2	NCOA2	10499	3.417031	0.659838
204035_at	secretogranin II (chromogranin C)	SCG2	7857	3.416442	0.659838
202158_s_at	CUG triplet repeat. RNA binding protein 2	CUGBP2	10659	3.4148	0.659838
212419_at	chromosome 10 open reading frame 56	C10orf56	219654	3.404936	0.659838
204951_at	ras homolog gene family. member H	RHOH	399	3.399886	0.659838
217097_s_at	putative homeodomain transcription factor 2	PHTF2	57157	3.38868	0.659838
220092_s_at	anthrax toxin receptor 1	ANTXR1	84168	3.373963	0.659838
200968_s_at	peptidylprolyl isomerase B (cyclophilin B)	PPIB	5479	3.368793	0.659838
221968_s_at	Zinc finger protein 771	ZNF771	51333	3.361364	0.659838
221577_x_at	growth differentiation factor 15	GDF15	9518	3.358331	0.659838
205750_at	biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	BPHL	670	3.357068	0.659838
215142_at	chromosome X open reading frame 27	CXorf27	25763	3.356985	0.659838
211996_s_at	KIAA0220-like protein /// hypothetical gene LOC283846 /// hypothetical protein LOC440345 /// r	DKFZp547E08	23117 /// 283	3.355306	0.659838

209349_at	RAD50 homolog (S. cerevisiae)	RAD50	10111	3.352697	0.659838
208812_x_at	major histocompatibility complex. class I. C /// similar to major histocompatibility complex. class	HLA-C /// LOC	3107 /// 7320	3.352429	0.659838
204833_at	ATG12 autophagy related 12 homolog (S. cerevisiae)	ATG12	9140	3.349624	0.659838
211211_x_at	SH2 domain protein 1A. Duncan's disease (lymphoproliferative syndrome)	SH2D1A	4068	3.349475	0.659838
203140_at	B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	604	3.347008	0.659838
210325_at	CD1a molecule	CD1A	909	3.341012	0.659838
213303_x_at	zinc finger and BTB domain containing 7A	ZBTB7A	51341	3.338424	0.659838
202499_s_at	solute carrier family 2 (facilitated glucose transporter). member 3	SLC2A3	6515	3.337949	0.659838
213295_at	cylindromatosis (turban tumor syndrome)	CYLD	1540	3.334121	0.659838
211025_x_at	cytochrome c oxidase subunit Vb	COX5B	1329	3.330707	0.659838
204030_s_at	schwannomin interacting protein 1	SCHIP1	29970	3.329693	0.659838
208305_at	progesterone receptor	PGR	5241	3.326261	0.659838
214303_x_at	mucin 5AC. oligomeric mucus/gel-forming	MUC5AC	4586	3.322572	0.659838
201470_at	glutathione S-transferase omega 1	GSTO1	9446	3.321774	0.659838
216526_x_at	major histocompatibility complex. class I. C	HLA-C	3107	3.319907	0.659838
200760_s_at	ADP-ribosylation-like factor 6 interacting protein 5	ARL6IP5	10550	3.319819	0.659838
221750_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	3157	3.318456	0.659838
208729_x_at	major histocompatibility complex. class I. B	HLA-B	3106	3.31338	0.659838
215685_s_at	distal-less homeobox 2	DLX2	1746	3.311145	0.659838
216986_s_at	interferon regulatory factor 4	IRF4	3662	3.310301	0.659838
209514_s_at	RAB27A. member RAS oncogene family	RAB27A	5873	3.284745	0.659838
205069_s_at	Rho GTPase activating protein 26	ARHGAP26	23092	3.280985	0.659838
51200_at	chromosome 19 open reading frame 60	C19orf60	55049	3.280458	0.659838
209575_at	interleukin 10 receptor. beta	IL10RB	3588	3.276532	0.659838
202996_at	polymerase (DNA-directed). delta 4	POLD4	57804	3.274484	0.659838
209381_x_at	splicing factor 3a. subunit 2. 66kDa	SF3A2	8175	3.273434	0.659838
209463_s_at	TAF12 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 20kDa	TAF12	6883	3.273109	0.659838
209331_s_at	MYC associated factor X	MAX	4149	3.272007	0.659838
205379_at	carbonyl reductase 3	CBR3	874	3.269499	0.659838
212451_at	KIAA0256 gene product	KIAA0256	9728	3.266836	0.659838
207742_s_at	nuclear receptor subfamily 6. group A. member 1	NR6A1	2649	3.25911	0.659838
211856_x_at	CD28 molecule	CD28	940	3.252538	0.659838
200814_at	proteasome (prosome. macropain) activator subunit 1 (PA28 alpha)	PSME1	5720	3.242506	0.659838
212613_at	butyrophilin. subfamily 3. member A2	BTN3A2	11118	3.241053	0.659838
217165_x_at	metallothionein 1F	MT1F	4494	3.236414	0.659838
203842_s_at	microtubule-associated protein. RP/EB family. member 3	MAPRE3	22924	3.230593	0.659838
217329_x_at	---	---	---	3.229426	0.659838
215313_x_at	major histocompatibility complex. class I. A	HLA-A	3105	3.228022	0.659838
217422_s_at	CD22 molecule	CD22	933	3.225762	0.659838
211796_s_at	T cell receptor beta variable 19 /// T cell receptor beta variable 7-2 /// T cell receptor beta variab	TRBC1 /// TR	28568 /// 285	3.22505	0.659838
216055_at	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	PDGFB	5155	3.214513	0.659838
202709_at	fibromodulin	FMOD	2331	3.211581	0.659838
202343_x_at	cytochrome c oxidase subunit Vb	COX5B	1329	3.211032	0.659838
212509_s_at	matrix-remodelling associated 7	MXRA7	439921	3.201045	0.659838
210123_s_at	cholinergic receptor. nicotinic. alpha 7 /// CHRNA7 (cholinergic receptor. nicotinic. alpha 7. exons	CHRFAM7A ///	1139 /// 8983	3.200541	0.659838
204571_x_at	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting. 4 (parvulin)	PIN4	5303	3.200525	0.659838
202101_s_at	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	5899	3.195971	0.659838
216448_at	CDNA FLJ12624 fis. clone NT2RM4001754	---	---	3.195322	0.659838
214669_x_at	immunoglobulin kappa locus	IGK@	50802	3.191469	0.659838
208465_at	glutamate receptor. metabotropic 2	GRM2	2912	3.184808	0.659838
215075_s_at	growth factor receptor-bound protein 2	GRB2	2885	3.182688	0.659838
207132_x_at	prefoldin subunit 5	PFDN5	5204	3.175111	0.659838
203831_at	R3H domain containing 2	R3HDM2	22864	3.173792	0.659838
206337_at	chemokine (C-C motif) receptor 7	CCR7	1236	3.172548	0.659838
218922_s_at	LAG1 homolog. ceramide synthase 4	LASS4	79603	3.165543	0.659838
208040_s_at	myosin binding protein C. cardiac	MYBPC3	4607	3.164944	0.659838
208187_s_at	---	---	---	3.163819	0.659838
222294_s_at	CDNA clone IMAGE:5745639	---	---	3.163475	0.659838
219451_at	methionine sulfoxide reductase B2	MSRB2	22921	3.158655	0.659838
202206_at	ADP-ribosylation factor-like 4C	ARL4C	10123	3.145435	0.659838
203758_at	cathepsin O	CTSO	1519	3.145395	0.659838
221912_s_at	coiled-coil domain containing 28B	CCDC28B	79140	3.143915	0.659838
205163_at	fast skeletal myosin light chain 2	MYLPF	29895	3.142725	0.659838
200046_at	defender against cell death 1	DAD1	1603	3.127426	0.659838
218380_at	NLR family. pyrin domain containing 1	NLRP1	22861	3.127069	0.659838
203595_s_at	interferon-induced protein with tetratricopeptide repeats 5	IFIT5	24138	3.125097	0.659838
203313_s_at	TGFB-induced factor homeobox 1	TGIF1	7050	3.123613	0.659838
202822_at	LIM domain containing preferred translocation partner in lipoma	LPP	4026	3.123101	0.659838
214358_at	acetyl-Coenzyme A carboxylase alpha	ACACA	31	3.117105	0.659838
206821_x_at	HIV-1 Rev binding protein-like	HRBL	3268	3.108878	0.659838
215412_x_at	postmeiotic segregation increased 2-like 2	PMS2L2	5380	3.108382	0.659838
200616_s_at	KIAA0152	KIAA0152	9761	3.108375	0.659838
214069_at	acyl-CoA synthetase medium-chain family member 2A /// acyl-CoA synthetase medium-chain fa	ACSM2A /// A	123876 /// 34	3.107276	0.659838
209846_s_at	butyrophilin. subfamily 3. member A2	BTN3A2	11118	3.104637	0.659838
218600_at	LIM domain containing 2	LIMD2	80774	3.103956	0.659838
218589_at	purinergic receptor P2Y. G-protein coupled. 5	P2RY5	10161	3.100489	0.659838
215211_at	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	LOC730092	730092	3.097573	0.659838
208403_x_at	MYC associated factor X	MAX	4149	3.097516	0.659838
204867_at	GTP cyclohydrolase I feedback regulator	GCHFR	2644	3.095074	0.659838
219724_s_at	KIAA0748	KIAA0748	9840	3.092041	0.659838
214054_at	docking protein 2. 56kDa	DOK2	9046	3.088263	0.659838
203964_at	N-myc (and STAT) interactor	NMI	9111	3.078189	0.659838
219759_at	endoplasmic reticulum aminopeptidase 2	ERAP2	64167	3.076226	0.659838
204174_at	arachidonate 5-lipoxygenase-activating protein	ALOX5AP	241	3.074033	0.659838
202296_s_at	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	RER1	11079	3.074005	0.659838
202207_at	ADP-ribosylation factor-like 4C	ARL4C	10123	3.071935	0.659838

213915_at	natural killer cell group 7 sequence	NKG7	4818	3.071858	0.659838
200604_s_at	protein kinase. cAMP-dependent. regulatory. type I. alpha (tissue specific extinguisher 1)	PRKAR1A	5573	3.071435	0.659838
219066_at	phosphopantothenoylcysteine decarboxylase	PPCDC	60490	3.070842	0.659838
212853_at	DCN1. defective in cullin neddylation 1. domain containing 4 (S. cerevisiae)	DCUN1D4	23142	3.065712	0.659838
207677_s_at	neutrophil cytosolic factor 4. 40kDa	NCF4	4689	3.062292	0.659838
218610_s_at	hypothetical protein FLJ11151	FLJ11151	55313	3.059331	0.659838
212452_x_at	MYST histone acetyltransferase (monocytic leukemia) 4	MYST4	23522	3.056358	0.659838
221044_s_at	tripartite motif-containing 34 /// TRIM6-TRIM34	TRIM34 /// TR	445372 /// 53	3.052578	0.659838
49679_s_at	Metallothionein 1 pseudogene 3	MT1P3	140851	3.050689	0.659838
213357_at	general transcription factor IIH. polypeptide 5	GTF2H5	404672	3.050053	0.659838
214512_s_at	SUB1 homolog (S. cerevisiae)	SUB1	10923	3.049781	0.659838
201328_at	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	2114	3.045932	0.659838
209201_x_at	chemokine (C-X-C motif) receptor 4	CXCR4	7852	3.044945	0.659838
218992_at	chromosome 9 open reading frame 46	C9orf46	55848	3.043275	0.659838
218559_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	MAFB	9935	3.039409	0.659838
201045_s_at	RAB6A. member RAS oncogene family /// RAB6C-like	LOC150786 //	150786 /// 58	3.038122	0.659838
217888_s_at	ADP-ribosylation factor GTPase activating protein 1	ARFGAP1	55738	3.035113	0.659838
212954_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	DYRK4	8798	3.035098	0.659838
215173_at	leucine rich repeat containing 50	LRRC50	123872	3.033865	0.659838
202393_s_at	Kruppel-like factor 10	KLF10	7071	3.029521	0.659838
215223_s_at	superoxide dismutase 2. mitochondrial	SOD2	6648	3.026709	0.659838
209147_s_at	phosphatidic acid phosphatase type 2A	PPAP2A	8611	3.024863	0.659838
205910_s_at	carboxyl ester lipase (bile salt-stimulated lipase)	CEL	1056	3.023574	0.659838
214144_at	Polymerase (RNA) II (DNA directed) polypeptide D	POLR2D	5433	3.01744	0.659838
220160_s_at	kaptin (actin binding protein)	KPTN	11133	3.016844	0.659838
211456_x_at	metallothionein 1 pseudogene 2	MT1P2	645745	3.012768	0.659838
217981_s_at	fracture callus 1 homolog (rat)	FXC1	26515	3.010512	0.659838
207179_at	T-cell leukemia homeobox 1	TLX1	3195	3.008433	0.659838
214841_at	cornichon homolog 3 (Drosophila)	CNIH3	149111	3.008379	0.659838
217751_at	glutathione S-transferase kappa 1	GSTK1	373156	3.008181	0.659838
216470_x_at	protease. serine. 1 (trypsin 1) /// protease. serine. 2 (trypsin 2) /// protease. serine. 3 (mesotry	PRSS1 /// PRS	154754 /// 56	3.007066	0.659838
209344_at	tropomyosin 4	TPM4	7171	3.005798	0.659838
220492_s_at	otoferlin	OTOF	9381	3.004706	0.659838
216859_x_at	---	---	---	3.00434	0.659838
221693_s_at	mitochondrial ribosomal protein S18A	MRPS18A	55168	3.003459	0.659838
208012_x_at	SP110 nuclear body protein	SP110	3431	2.991967	0.659838
209292_at	Inhibitor of DNA binding 4. dominant negative helix-loop-helix protein	ID4	3400	2.991604	0.659838
219534_x_at	cyclin-dependent kinase inhibitor 1C (p57. Kip2)	CDKN1C	1028	2.989513	0.659838
218400_at	2'-5'-oligoadenylate synthetase 3. 100kDa	OAS3	4940	2.98878	0.659838
201295_s_at	---	---	---	2.987276	0.659838
218250_s_at	CCR4-NOT transcription complex. subunit 7	CNOT7	29883	2.984043	0.659838
220769_s_at	WD repeat domain 78	WDR78	79819	2.983825	0.659838
221277_s_at	pseudouridylate synthase 3	PUS3	83480	2.978688	0.659838
205198_s_at	ATPase. Cu++ transporting. alpha polypeptide (Menkes syndrome) /// similar to ATPase. Cu++ t	ATP7A /// LOC	538 /// 64473	2.976605	0.659838
200849_s_at	S-adenosylhomocysteine hydrolase-like 1	AHCYL1	10768	2.975782	0.659838
206508_at	CD70 molecule	CD70	970	2.972228	0.659838
221200_at	---	---	---	2.966979	0.659838
212587_s_at	protein tyrosine phosphatase. receptor type. C	PTPRC	5788	2.958381	0.659838
205692_s_at	CD38 molecule	CD38	952	2.957133	0.659838
204326_x_at	metallothionein 1X	MT1X	4501	2.953085	0.659838
207238_s_at	protein tyrosine phosphatase. receptor type. C	PTPRC	5788	2.952252	0.659838
218725_at	solute carrier family 25 (mitochondrial carrier: glutamate). member 22	SLC25A22	79751	2.951625	0.659838
212851_at	DCN1. defective in cullin neddylation 1. domain containing 4 (S. cerevisiae)	DCUN1D4	23142	2.950332	0.659838
207766_at	cyclin-dependent kinase-like 1 (CDC2-related kinase)	CDKL1	8814	2.948535	0.659838
206751_s_at	phosphate cytidylyltransferase 1. choline. beta	PCYT1B	9468	2.940486	0.659838
222275_at	Full-length cDNA clone CS0DK012YA15 of HeLa cells Cot 25-normalized of Homo sapiens (human	---	---	2.937275	0.659838
200878_at	endothelial PAS domain protein 1	EPAS1	2034	2.935505	0.659838
209924_at	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	CCL18	6362	2.933877	0.659838
207694_at	POU class 3 homeobox 4	POU3F4	5456	2.933324	0.659838
201246_s_at	OTU domain. ubiquitin aldehyde binding 1	OTUB1	55611	2.932434	0.659838
210638_s_at	F-box protein 9	FBXO9	26268	2.931394	0.659838
201055_s_at	heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	10949	2.930226	0.659838
202435_s_at	cytochrome P450. family 1. subfamily B. polypeptide 1	CYP1B1	1545	2.927656	0.659838
216137_s_at	Mitogen-activated protein kinase 8 interacting protein 3	MAPK8IP3	23162	2.92755	0.659838
1431_at	cytochrome P450. family 2. subfamily E. polypeptide 1	CYP2E1	1571	2.925226	0.659838
221562_s_at	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	SIRT3	23410	2.915722	0.659838
219506_at	chromosome 1 open reading frame 54	C1orf54	79630	2.9111	0.659838
205784_x_at	armadillo repeat gene deletes in velocardiofacial syndrome	ARVCF	421	2.910897	0.659838
221507_at	transportin 2 (importin 3. karyopherin beta 2b)	TNPO2	30000	2.907218	0.659838
222200_s_at	BSD domain containing 1	BSDC1	55108	2.907084	0.659838
205796_at	t-complex 11 (mouse)-like 1	TCP11L1	55346	2.906775	0.659838
45714_at	host cell factor C1 regulator 1 (XPO1 dependent)	HCFC1R1	54985	2.904465	0.659838
206100_at	carboxypeptidase M	CPM	1368	2.902093	0.659838
206410_at	nuclear receptor subfamily 0. group B. member 2	NR0B2	8431	2.901963	0.659838
203304_at	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	BAMBI	25805	2.898868	0.659838
205116_at	laminin. alpha 2 (merosin. congenital muscular dystrophy)	LAMA2	3908	2.898746	0.659838
212007_at	UBX domain containing 2	UBXD2	23190	2.897988	0.659838
204759_at	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	RCBTB2	1102	2.894497	0.659838
207084_at	POU class 3 homeobox 2	POU3F2	5454	2.888394	0.659838
206804_at	CD3g molecule. gamma (CD3-TCR complex)	CD3G	917	2.8863	0.659838
205852_at	cyclin-dependent kinase 5. regulatory subunit 2 (p39)	CDK5R2	8941	2.886288	0.659838
203005_at	lymphotoxin beta receptor (TNFR superfamily. member 3)	LTBR	4055	2.885604	0.659838
204683_at	intercellular adhesion molecule 2	ICAM2	3384	2.885463	0.659838
220909_at	tripartite motif-containing 46	TRIM46	80128	2.882499	0.659838
213257_at	sterile alpha and TIR motif containing 1	SARM1	23098	2.879932	0.659838
201012_at	annexin A1	ANXA1	301	2.878469	0.659838

220740_s_at	solute carrier family 12 (potassium/chloride transporters). member 6	SLC12A6	9990	2.876374	0.659838
215069_at	N-myristoyltransferase 2	NMT2	9397	2.875929	0.659838
213757_at	Transcribed locus. weakly similar to XP_001478155.1 PREDICTED: hypothetical protein [Mus mus	---	---	2.87568	0.659838
215259_s_at	cell adhesion molecule 4	CADM4	199731	2.874941	0.659838
222041_at	DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor in ovarian cancer 2	DPH1 /// OVC	124641 /// 18	2.872937	0.659838
215863_at	transferrin receptor 2	TFR2	7036	2.871378	0.659838
221243_s_at	---	---	---	2.869943	0.659838
206556_at	clusterin-like 1 (retinal)	CLUL1	27098	2.867342	0.659838
210104_at	mediator complex subunit 6	MED6	10001	2.865525	0.659838
202180_s_at	major vault protein	MVP	9961	2.861996	0.659838
204350_s_at	mediator complex subunit 7	MED7	9443	2.857736	0.659838
216127_at	protein disulfide isomerase family A. member 2	PDIA2	64714	2.856509	0.659838
207090_x_at	zinc finger protein 30 homolog (mouse)	ZFP30	22835	2.85321	0.659838
205224_at	surfeit 2	SURF2	6835	2.851708	0.659838
213931_at	inhibitor of DNA binding 2. dominant negative helix-loop-helix protein /// inhibitor of DNA binding	ID2 /// ID2B	3398 /// 8409	2.850662	0.659838
211753_s_at	relaxin 1	RLN1	6013	2.850191	0.659838
201739_at	serum/glucocorticoid regulated kinase 1	SGK1	6446	2.845651	0.659838
221210_s_at	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NPL	80896	2.845403	0.659838
204257_at	fatty acid desaturase 3	FADS3	3995	2.843792	0.659838
203260_at	HD domain containing 2	HDDC2	51020	2.84045	0.659838
218169_at	Vac14 homolog (S. cerevisiae)	VAC14	55697	2.834142	0.659838
221557_s_at	lymphoid enhancer-binding factor 1	LEF1	51176	2.831736	0.660294
215797_at	T cell receptor alpha variable 8-3	TRAV8-3	28683	2.817516	0.666139
206076_at	leucine rich repeat containing 23	LRRC23	10233	2.815688	0.666139
202011_at	tight junction protein 1 (zona occludens 1)	TJP1	7082	2.813338	0.666139
201194_at	selenoprotein W. 1	SEPW1	6415	2.812785	0.666139
219667_s_at	B-cell scaffold protein with ankyrin repeats 1	BANK1	55024	2.811398	0.666139
209772_s_at	CD24 molecule	CD24	934	2.80833	0.666139
205343_at	sulfotransferase family. cytosolic. 1C. member 2	SULT1C2	6819	2.8079	0.666139
211613_s_at	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	GPD2	2820	2.807271	0.666139
202298_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex. 1. 7.5kDa	NDUFA1	4694	2.804105	0.667653
200605_s_at	protein kinase. cAMP-dependent. regulatory. type I. alpha (tissue specific extinguisher 1)	PRKAR1A	5573	2.801286	0.669687
202929_s_at	D-dopachrome tautomerase	DDT	1652	2.799737	0.670415
202446_s_at	phospholipid scramblase 1	PLSCR1	5359	2.797744	0.670898
201628_s_at	Ras-related GTP binding A	RRAGA	10670	2.796942	0.670898
208104_s_at	TSC22 domain family. member 4	TSC22D4	81628	2.79553	0.670898
209168_at	glycoprotein M6B	GPM6B	2824	2.793972	0.670898
211902_x_at	T cell receptor alpha locus	TRA@	6955	2.791069	0.670898
211986_at	AHNAK nucleoprotein	AHNAK	79026	2.789055	0.670898
212784_at	capicua homolog (Drosophila)	CIC	23152	2.788591	0.670898
218482_at	enhancer of yellow 2 homolog (Drosophila)	ENY2	56943	2.787771	0.670898
207339_s_at	lymphotoxin beta (TNF superfamily. member 3)	LTB	4050	2.782622	0.670898
218815_s_at	transmembrane protein 51	TMEM51	55092	2.779073	0.672775
221185_s_at	IQ motif containing G	IQCG	84223	2.778605	0.672775
211861_x_at	CD28 molecule	CD28	940	2.776363	0.672775
219113_x_at	hydroxysteroid (17-beta) dehydrogenase 14	HSD17B14	51171	2.771317	0.67416
211465_x_at	fucosyltransferase 6 (alpha (1.3) fucosyltransferase)	FUT6	2528	2.761412	0.677651
209671_x_at	T cell receptor alpha locus /// T cell receptor alpha constant	TRA@ /// TRA	28755 /// 695	2.760719	0.677651
205579_at	histamine receptor H1	HRH1	3269	2.753222	0.677769
217332_at	similar to CTAGE family. member 5	LOC647288 //	647288 /// 73	2.750663	0.677769
218376_s_at	microtubule associated monoxygenase. calponin and LIM domain containing 1	MICAL1	64780	2.750547	0.677769
219161_s_at	chemokine-like factor	CKLF	51192	2.749735	0.677769
211911_x_at	major histocompatibility complex. class I. B	HLA-B	3106	2.749108	0.677769
202637_s_at	intercellular adhesion molecule 1 (CD54). human rhinovirus receptor	ICAM1	3383	2.7474	0.677769
221696_s_at	serine/threonine/tyrosine kinase 1	STYK1	55359	2.744325	0.677769
219214_s_at	5'. 3'-nucleotidase. cytosolic	NT5C	30833	2.742564	0.677769
218118_s_at	translocase of inner mitochondrial membrane 23 homolog (yeast)	TIMM23	10431	2.740762	0.677769
218369_s_at	exosome component 1	EXOSC1	51013	2.740281	0.677769
210218_s_at	SP100 nuclear antigen	SP100	6672	2.739249	0.677769
219107_at	brevican	BCAN	63827	2.737701	0.677769
222356_at	Transcribed locus	---	---	2.73657	0.677769
203610_s_at	tripartite motif-containing 38	TRIM38	10475	2.73411	0.677769
209276_s_at	glutaredoxin (thioltransferase)	GLRX	2745	2.732356	0.677769
208659_at	chloride intracellular channel 1	CLIC1	1192	2.73142	0.677769
210693_at	signal peptide peptidase-like 2B	SPPL2B	56928	2.730862	0.677769
211098_x_at	transmembrane and coiled-coil domains 1	TMCO1	54499	2.727776	0.677769
215645_at	Folliculin	FLCN	201163	2.720219	0.677769
203037_s_at	metastasis suppressor 1	MTSS1	9788	2.719512	0.677769
214480_at	ets variant gene 3	ETV3	2117	2.71931	0.677769
202592_at	biogenesis of lysosome-related organelles complex-1. subunit 1	BLOC1S1	2647	2.717615	0.677769
213050_at	cordon-bleu homolog (mouse)	COBL	23242	2.717062	0.677769
215579_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3G	APOBEC3G	60489	2.716052	0.677769
202562_s_at	chromosome 14 open reading frame 1	C14orf1	11161	2.714535	0.677769
211120_x_at	estrogen receptor 2 (ER beta)	ESR2	2100	2.713074	0.677769
207508_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit C3 (subunit 9)	ATP5G3	518	2.711119	0.677769
201514_s_at	GTPase activating protein (SH3 domain) binding protein 1	G3BP1	10146	2.710628	0.677769
220544_at	testis-specific kinase substrate	TSKS	60385	2.706436	0.677769
212087_s_at	Era G-protein-like 1 (E. coli)	ERAL1	26284	2.705626	0.677769
204973_at	gap junction protein. beta 1. 32kDa	GJB1	2705	2.704887	0.677769
217059_at	mucin 7. secreted	MUC7	4589	2.704338	0.677769
218491_s_at	thymocyte nuclear protein 1	THYN1	29087	2.703529	0.677769
201601_x_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	8519	2.702711	0.677769
216598_s_at	chemokine (C-C motif) ligand 2	CCL2	6347	2.702394	0.677769
203485_at	reticulon 1	RTN1	6252	2.697201	0.677769
201590_x_at	annexin A2	ANXA2	302	2.696669	0.677769
203932_at	major histocompatibility complex. class II. DM beta	HLA-DMB	3109	2.694472	0.677769

218282_at	ER degradation enhancer. mannosidase alpha-like 2	EDEM2	55741	2.692505	0.677769
203008_x_at	thioredoxin domain containing 9	TXNDC9	10190	2.690061	0.677769
201891_s_at	beta-2-microglobulin	B2M	567	2.689404	0.677769
221816_s_at	PHD finger protein 11	PHF11	51131	2.684377	0.677769
211031_s_at	CAP-GLY domain containing linker protein 2	CLIP2	7461	2.683228	0.677769
210723_x_at	hypothetical protein MGC4771	MGC4771	84754	2.681853	0.677769
217966_s_at	family with sequence similarity 129. member A	FAM129A	116496	2.679718	0.677769
218117_at	ring-box 1	RBX1	9978	2.679083	0.677769
212303_x_at	---	---	---	2.67643	0.677769
219147_s_at	chromosome 9 open reading frame 95	C9orf95	54981	2.6756	0.677769
212079_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog. Drosophila)	MLL	4297	2.675356	0.677769
218996_at	TCF3 (E2A) fusion partner (in childhood Leukemia)	TFPT	29844	2.674804	0.677769
201641_at	bone marrow stromal cell antigen 2	BST2	684	2.672552	0.677769
220941_s_at	chromosome 21 open reading frame 91	C21orf91	54149	2.672014	0.677769
205179_s_at	ADAM metallopeptidase domain 8	ADAM8	101	2.668417	0.677769
218048_at	COMM domain containing 3	COMMD3	23412	2.666564	0.677769
206484_s_at	X-prolyl aminopeptidase (aminopeptidase P) 2. membrane-bound	XPNPEP2	7512	2.665828	0.677769
214150_x_at	ATPase. H+ transporting. lysosomal 9kDa. V0 subunit e1	ATP6V0E1	8992	2.662168	0.677769
217497_at	endothelial cell growth factor 1 (platelet-derived)	ECGF1	1890	2.660791	0.677769
201631_s_at	immediate early response 3	IER3	8870	2.659463	0.677769
202325_s_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit F6	ATP5J	522	2.658999	0.677769
205345_at	BRCA1 associated RING domain 1	BARD1	580	2.656693	0.677769
201927_s_at	plakophilin 4	PKP4	8502	2.655599	0.677769
202040_s_at	jumonji. AT rich interactive domain 1A	JARID1A	5927	2.654263	0.677769
219475_at	oxidative stress induced growth inhibitor 1	OSGIN1	29948	2.652746	0.677769
207867_at	paired box 4	PAX4	5078	2.652009	0.677769
205098_at	chemokine (C-C motif) receptor 1	CCR1	1230	2.651702	0.677769
202497_x_at	solute carrier family 2 (facilitated glucose transporter). member 3	SLC2A3	6515	2.650363	0.677769
204960_at	protein tyrosine phosphatase. receptor type. C-associated protein	PTPRCAP	5790	2.648818	0.677769
211436_at	Clone FLB4228 PRO1095	---	---	2.647207	0.677769
208249_s_at	TDP-glucose 4.6-dehydratase	TGDS	23483	2.645811	0.677769
202074_s_at	optineurin	OPTN	10133	2.645191	0.677769
205681_at	BCL2-related protein A1	BCL2A1	597	2.642668	0.677769
214200_s_at	Collagen. type VI. alpha 1	COL6A1	1291	2.637952	0.677769
219950_s_at	T-cell lymphoma invasion and metastasis 2	TIAM2	26230	2.637371	0.677769
213875_x_at	chromosome 6 open reading frame 62	C6orf62	81688	2.636735	0.677769
215444_s_at	tripartite motif-containing 31	TRIM31	11074	2.635291	0.677769
212979_s_at	family with sequence similarity 115. member A	FAM115A	9747	2.633892	0.677769
210223_s_at	major histocompatibility complex. class I-related	MR1	3140	2.632832	0.677769
218232_at	complement component 1. q subcomponent. A chain	C1QA	712	2.632177	0.677769
210865_at	Fas ligand (TNF superfamily. member 6)	FASLG	356	2.631157	0.677769
218786_at	5'-nucleotidase domain containing 3	NT5DC3	51559	2.630898	0.677769
205721_at	GDNF family receptor alpha 2	GFRA2	2675	2.628027	0.677769
214534_at	histone cluster 1. H1b	HIST1H1B	3009	2.622854	0.677769
200785_s_at	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	LRP1	4035	2.621803	0.677769
202022_at	aldolase C. fructose-bisphosphate	ALDOC	230	2.61928	0.677769
216780_at	CDNA: FLJ21911 fis. clone HEP03855	---	---	2.618278	0.677769
209789_at	coronin. actin binding protein. 2B	CORO2B	10391	2.616127	0.677769
213346_at	chromosome 13 open reading frame 27	C13orf27	93081	2.615397	0.677769
201585_s_at	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ	6421	2.613151	0.677769
205278_at	glutamate decarboxylase 1 (brain. 67kDa)	GAD1	2571	2.61178	0.677769
208963_x_at	fatty acid desaturase 1	FADS1	3992	2.610965	0.677769
213260_at	forkhead box C1	FOXC1	2296	2.609683	0.677769
201224_s_at	serine/arginine repetitive matrix 1	SRRM1	10250	2.609477	0.677769
203851_at	insulin-like growth factor binding protein 6	IGFBP6	3489	2.608294	0.677769
218251_at	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	MID1IP1	58526	2.607466	0.677769
220291_at	glycerophosphodiester phosphodiesterase domain containing 2	GDPD2	54857	2.605695	0.677769
214909_s_at	dimethylarginine dimethylaminohydrolase 2	DDAH2	23564	2.602671	0.677769
209584_x_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3C	APOBEC3C	27350	2.601623	0.677769
200890_s_at	signal sequence receptor. alpha (translocon-associated protein alpha)	SSR1	6745	2.598212	0.677769
214554_at	histone cluster 1. H2al	HIST1H2AL	8332	2.596813	0.677769
207263_x_at	vezatin. adherens junctions transmembrane protein	VEZT	55591	2.591569	0.677769
209483_s_at	---	---	---	2.591377	0.677769
216971_s_at	plectin 1. intermediate filament binding protein 500kDa	PLEC1	5339	2.589861	0.677769
211304_x_at	potassium inwardly-rectifying channel. subfamily J. member 5	KCNJ5	3762	2.588996	0.677769
213806_at	Purine-rich element binding protein A	PURA	5813	2.588207	0.677769
210042_s_at	cathepsin Z	CTSZ	1522	2.588089	0.677769
203456_at	PRA1 domain family. member 2	PRAF2	11230	2.587603	0.677769
221684_s_at	nyctalopin	NYX	60506	2.586138	0.677769
218742_at	nuclear prelamin A recognition factor-like	NARFL	64428	2.584359	0.677769
204586_at	bassoon (presynaptic cytomatrix protein)	BSN	8927	2.584095	0.677769
208020_s_at	calcium channel. voltage-dependent. L type. alpha 1C subunit	CACNA1C	775	2.582774	0.677769
216628_at	---	---	---	2.581445	0.677769
221597_s_at	HSPC171 protein	HSPC171	29100	2.580699	0.677769
205139_s_at	uronyl-2-sulfotransferase	UST	10090	2.580267	0.677769
212595_s_at	DAZ associated protein 2	DAZAP2	9802	2.578054	0.677955
221617_at	TAF9B RNA polymerase II. TATA box binding protein (TBP)-associated factor. 31kDa	TAF9B	51616	2.576151	0.678698
214177_s_at	pre-B-cell leukemia homeobox interacting protein 1	PBXIP1	57326	2.575209	0.679061
219599_at	eukaryotic translation initiation factor 4B	EIF4B	1975	2.573357	0.679125
220748_s_at	zinc finger protein 580	ZNF580	51157	2.570412	0.680212
217867_x_at	beta-site APP-cleaving enzyme 2	BACE2	25825	2.568516	0.680212
201480_s_at	suppressor of Ty 5 homolog (S. cerevisiae)	SUPT5H	6829	2.567312	0.680212
216649_at	ras responsive element binding protein 1	RREB1	6239	2.567245	0.680212
204565_at	thioesterase superfamily member 2	THEM2	55856	2.566983	0.680212
218805_at	GTPase. IMAP family member 5	GIMAP5	55340	2.565282	0.681388
218685_s_at	single-strand-selective monofunctional uracil-DNA glycosylase 1	SMUG1	23583	2.563839	0.682293

202518_at	B-cell CLL/lymphoma 7B	BCL7B	9275	2.563223	0.68232
204994_at	myxovirus (influenza virus) resistance 2 (mouse)	MX2	4600	2.559994	0.682811
213826_s_at	---	---	---	2.559324	0.682811
221877_at	CDNA FLJ38849 fis. clone MESAN2008936	---	---	2.557714	0.683802
208945_s_at	beclin 1 (coiled-coil. myosin-like BCL2 interacting protein)	BECN1	8678	2.553835	0.684821
209890_at	tetraspanin 5	TSPAN5	10098	2.551888	0.685223
210908_s_at	prefoldin subunit 5	PFDN5	5204	2.551711	0.685223
206344_at	paraoxonase 1	PON1	5444	2.550452	0.685344
221875_x_at	major histocompatibility complex. class I. F	HLA-F	3134	2.549092	0.685344
217811_at	selenoprotein T	SELT	51714	2.547193	0.685344
220989_s_at	amnionless homolog (mouse)	AMN	81693	2.545981	0.685344
39549_at	neuronal PAS domain protein 2	NPAS2	4862	2.540313	0.685344
203349_s_at	ets variant gene 5 (ets-related molecule)	ETV5	2119	2.539169	0.685344
208757_at	transmembrane emp24 protein transport domain containing 9	TMED9	54732	2.536351	0.685344
216964_at	Ubiquitin specific peptidase 22	USP22	23326	2.535836	0.685344
200601_at	actinin. alpha 4	ACTN4	81	2.5348	0.685344
214533_at	chymase 1. mast cell	CMA1	1215	2.533767	0.685344
216611_s_at	solute carrier family 6 (neurotransmitter transporter. noradrenalin). member 2	SLC6A2	6530	2.532548	0.685344
211997_x_at	H3 histone. family 3B (H3.3B)	H3F3B	3021	2.529995	0.685344
216843_x_at	postmeiotic segregation increased 2-like 1 /// similar to postmeiotic segregation increased 2-like	LOC732139 //	5379 /// 7321	2.52914	0.685344
201833_at	histone deacetylase 2	HDAC2	3066	2.528667	0.685344
201983_s_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog. avia	EGFR	1956	2.527836	0.685344
215359_x_at	zinc finger protein 44	ZNF44	51710	2.52717	0.685344
203910_at	Rho GTPase activating protein 29	ARHGAP29	9411	2.525466	0.685344
215088_s_at	succinate dehydrogenase complex. subunit C. integral membrane protein. 15kDa	SDHC	6391	2.524155	0.685344
221350_at	homeobox C8	HOXC8	3224	2.52376	0.685344
212223_at	iduronate 2-sulfatase (Hunter syndrome)	IDS	3423	2.520859	0.685344
211030_s_at	solute carrier family 6 (neurotransmitter transporter. taurine). member 6	SLC6A6	6533	2.518367	0.685344
209359_x_at	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	RUNX1	861	2.517362	0.685344
219533_at	cyclin-dependent kinase inhibitor 1C (p57. Kip2)	CDKN1C	1028	2.514528	0.685344
221479_s_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	BNIP3L	665	2.511276	0.685344
204607_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	HMGCS2	3158	2.51098	0.685344
218357_s_at	translocase of inner mitochondrial membrane 8 homolog B (yeast)	TIMM8B	26521	2.510156	0.685344
218861_at	ring finger protein 25	RNF25	64320	2.508715	0.685344
201275_at	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase. dimethylallyltranstransferase	FDPS	2224	2.507374	0.685344
218634_at	pleckstrin homology-like domain. family A. member 3	PHLDA3	23612	2.504763	0.685344
218031_s_at	forkhead box N3	FOXN3	1112	2.50473	0.685344
209046_s_at	GABA(A) receptor-associated protein-like 2	GABARAPL2	11345	2.504257	0.685344
206754_s_at	cytochrome P450. family 2. subfamily B. polypeptide 7 pseudogene 1	CYP2B7P1	1556	2.502132	0.685344
218007_s_at	ribosomal protein S27-like	RPS27L	51065	2.500566	0.685344
211529_x_at	major histocompatibility complex. class I. G	HLA-G	3135	2.500225	0.685344
217950_at	nitric oxide synthase interacting protein	NOSIP	51070	2.499986	0.685344
200885_at	ras homolog gene family. member C	RHOC	389	2.499244	0.685344
219386_s_at	SLAM family member 8	SLAMF8	56833	2.499004	0.685344
219106_s_at	kelch repeat and BTB (POZ) domain containing 10	KBTBD10	10324	2.496366	0.685344
214298_x_at	septin 6	6-Sep	23157	2.494717	0.685344
219668_at	ganglioside-induced differentiation-associated protein 1-like 1	GDAP1L1	78997	2.490818	0.685344
219871_at	hypothetical FLJ13197	FLJ13197	79667	2.490472	0.685344
201531_at	zinc finger protein 36. C3H type. homolog (mouse)	ZFP36	7538	2.490183	0.685344
202961_s_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit F2	ATP5J2	9551	2.488572	0.685344
209156_s_at	collagen. type VI. alpha 2	COL6A2	1292	2.486827	0.685344
216605_s_at	carcinoembryonic antigen-related cell adhesion molecule 21	CEACAM21	90273	2.486406	0.685344
216122_at	CDNA: FLJ20890 fis. clone ADKA03323	---	---	2.481554	0.685344
219097_x_at	chromosome 19 open reading frame 42	C19orf42	79086	2.48075	0.685344
215526_at	MRNA; cDNA DKFZp586C2020 (from clone DKFZp586C2020)	---	---	2.478739	0.685344
214617_at	perforin 1 (pore forming protein)	PRF1	5551	2.478682	0.685344
221326_s_at	tubulin. delta 1	TUBD1	51174	2.475581	0.685344
207401_at	prospero homeobox 1	PROX1	5629	2.474158	0.685344
218439_s_at	COMM domain containing 10	COMMD10	51397	2.472923	0.685344
210304_at	phosphodiesterase 6B. cGMP-specific. rod. beta (congenital stationary night blindness 3. autosom	PDE6B	5158	2.472216	0.685344
214157_at	GNAS complex locus	GNAS	2778	2.471159	0.685344
204461_x_at	RAD1 homolog (S. pombe)	RAD1	5810	2.470726	0.685344
202747_s_at	integral membrane protein 2A	ITM2A	9452	2.470191	0.685344
209216_at	WD repeat domain 45	WDR45	11152	2.469745	0.685344
202641_at	ADP-ribosylation factor-like 3	ARL3	403	2.469619	0.685344
213846_at	cytochrome c oxidase subunit VIIc	COX7C	1350	2.469423	0.685344
201653_at	cornichon homolog (Drosophila)	CNIH	10175	2.468773	0.685344
217717_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. beta polypeptide	YWHAB	7529	2.46836	0.685344
33736_at	stomatin (EPB72)-like 1	STOML1	9399	2.46806	0.685344
203508_at	tumor necrosis factor receptor superfamily. member 1B	TNFRSF1B	7133	2.468014	0.685344
208792_s_at	clusterin	CLU	1191	2.467382	0.685344
210241_s_at	TP53 activated protein 1	TP53AP1	11257	2.465538	0.685344
212056_at	KIAA0182	KIAA0182	23199	2.465133	0.685344
201331_s_at	signal transducer and activator of transcription 6. interleukin-4 induced	STAT6	6778	2.464769	0.685344
210188_at	GA binding protein transcription factor. alpha subunit 60kDa	GABPA	2551	2.463944	0.685344
213560_at	Growth arrest and DNA-damage-inducible. beta	GADD45B	4616	2.46292	0.685344
203591_s_at	colony stimulating factor 3 receptor (granulocyte)	CSF3R	1441	2.462517	0.685344
211732_x_at	histamine N-methyltransferase	HNMT	3176	2.461607	0.685344
207437_at	neuro-oncological ventral antigen 1	NOVA1	4857	2.460697	0.685344
221599_at	chromosome 11 open reading frame 67	C11orf67	28971	2.458657	0.685344
211799_x_at	major histocompatibility complex. class I. C	HLA-C	3107	2.453284	0.685344
35436_at	golgi autoantigen. golgin subfamily a. 2	GOLGA2	2801	2.452143	0.685344
222165_x_at	chromosome 9 open reading frame 16	C9orf16	79095	2.451037	0.685344
221494_x_at	eukaryotic translation initiation factor 3. subunit K	EIF3K	27335	2.450573	0.685344
211301_at	potassium voltage-gated channel. Shal-related subfamily. member 3	KCND3	3752	2.449972	0.685344
204897_at	prostaglandin E receptor 4 (subtype EP4)	PTGER4	5734	2.446946	0.685344

205081_at	cysteine-rich protein 1 (intestinal)	CRIP1	1396	2.446518	0.685344
207531_at	crystallin. gamma C	CRYGC	1420	2.446422	0.685344
203960_s_at	chromosome 1 open reading frame 41	C1orf41	51668	2.446014	0.685344
207115_x_at	mbt domain containing 1	MBTD1	54799	2.44549	0.685344
220190_s_at	general transcription factor IIA. 1-like /// STON1-GTF2A1L	GTF2A1L /// S	11036 /// 286	2.44526	0.685344
212279_at	transmembrane protein 97	TMEM97	27346	2.444399	0.685344
213676_at	transmembrane protein 151B	TMEM151B	441151	2.444084	0.685344
214475_x_at	calpain 3. (p94)	CAPN3	825	2.443977	0.685344
220798_x_at	plasticity-related gene 2	PRG2	79948	2.443451	0.685344
221563_at	dual specificity phosphatase 10	DUSP10	11221	2.442232	0.685344
203928_x_at	microtubule-associated protein tau	MAPT	4137	2.441271	0.685344
216882_s_at	nebulette	NEBL	10529	2.438473	0.685344
211451_s_at	potassium inwardly-rectifying channel. subfamily J. member 4	KCNJ4	3761	2.43702	0.685344
214526_x_at	postmeiotic segregation increased 2-like 1	PMS2L1	5379	2.434364	0.685365
201541_s_at	zinc finger. HIT type 1	ZNHIT1	10467	2.434071	0.685365
221212_x_at	polybromo 1	PBRM1	55193	2.432558	0.685365
215640_at	TBC1 domain family. member 2B	TBC1D2B	23102	2.432211	0.685365
210734_x_at	MYC associated factor X	MAX	4149	2.431253	0.685365
203451_at	LIM domain binding 1	LDB1	8861	2.431062	0.685365
221198_at	secretin	SCT	6343	2.430977	0.685365
206993_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit s (factor B)	ATP5S	27109	2.429895	0.685365
213169_at	sema domain. seven thrombospondin repeats (type 1 and type 1-like). transmembrane domain (	SEMA5A	9037	2.428232	0.685365
201319_at	myosin regulatory light chain MRCL3 /// similar to myosin regulatory light chain-like	LOC645094 //	10627 /// 645	2.428228	0.685365
215144_at	Transcribed locus	---	---	2.4279	0.685365
214463_x_at	histone cluster 1. H4k /// histone cluster 1. H4j	HIST1H4J ///	8362 /// 8363	2.426872	0.685365
216210_x_at	TRIO and F-actin binding protein	TRIOBP	11078	2.426764	0.685365
212003_at	chromosome 1 open reading frame 144	C1orf144	26099	2.425967	0.685365
215392_at	CDNA FLJ14136 fis. clone MAMMA1002744	---	---	2.421503	0.685365
204530_s_at	thymocyte selection-associated high mobility group box	TOX	9760	2.421259	0.685365
213383_at	SAPS domain family. member 2	SAPS2	9701	2.42032	0.685365
205654_at	complement component 4 binding protein. alpha	C4BPA	722	2.419779	0.685365
203056_s_at	PR domain containing 2. with ZNF domain	PRDM2	7799	2.41818	0.685365
216223_at	carboxypeptidase N. polypeptide 2	CPN2	1370	2.417499	0.685365
220903_at	G elongation factor. mitochondrial 1	GFM1	85476	2.41743	0.685365
219807_x_at	RAB4B. member RAS oncogene family	RAB4B	53916	2.417185	0.685365
204479_at	osteoclast stimulating factor 1	OSTF1	26578	2.415404	0.685365
216516_at	---	---	---	2.414743	0.685365
203709_at	phosphorylase kinase. gamma 2 (testis)	PHKG2	5261	2.413644	0.685365
200836_s_at	microtubule-associated protein 4	MAP4	4134	2.412961	0.685365
209829_at	chromosome 6 open reading frame 32	C6orf32	9750	2.411805	0.685365
221973_at	CDNA clone IMAGE:5217021. with apparent retained intron	---	---	2.411769	0.685365
201720_s_at	lysosomal associated multispanning membrane protein 5	LAPTM5	7805	2.410701	0.685365
206929_s_at	nuclear factor I/C (CCAAT-binding transcription factor)	NFIC	4782	2.410506	0.685365
64488_at	CDNA FLJ38849 fis. clone MESAN2008936	---	---	2.410432	0.685365
207052_at	hepatitis A virus cellular receptor 1	HAVCR1	26762	2.409681	0.685365
204769_s_at	transporter 2. ATP-binding cassette. sub-family B (MDR/TAP)	TAP2	6891	2.409004	0.685365
207127_s_at	heterogeneous nuclear ribonucleoprotein H3 (2H9)	HNRPH3	3189	2.40838	0.685365
208949_s_at	lectin. galactoside-binding. soluble. 3	LGALS3	3958	2.407378	0.685365
219497_s_at	B-cell CLL/lymphoma 11A (zinc finger protein)	BCL11A	53335	2.406401	0.685365
216222_s_at	myosin X	MYO10	4651	2.404643	0.685365
213018_at	GATA zinc finger domain containing 1	GATAD1	57798	2.402838	0.685365
210807_s_at	solute carrier family 16. member 7 (monocarboxylic acid transporter 2)	SLC16A7	9194	2.401928	0.685365
202638_s_at	intercellular adhesion molecule 1 (CD54). human rhinovirus receptor	ICAM1	3383	2.401177	0.685365
201026_at	eukaryotic translation initiation factor 5B	EIF5B	9669	2.399581	0.685365
214398_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells. kinase epsilon	IKBKE	9641	2.398373	0.685365
220557_s_at	phosphofurin acidic cluster sorting protein 1	PACS1	55690	2.397916	0.685365
201341_at	ectodermal-neural cortex (with BTB-like domain)	ENC1	8507	2.396271	0.685365
215625_at	hypothetical protein LOC644450	LOC644450	644450	2.388714	0.685365
208204_s_at	caveolin 3	CAV3	859	2.385785	0.685365
202331_at	branched chain keto acid dehydrogenase E1. alpha polypeptide	BCKDHA	593	2.385376	0.685365
204658_at	transformer-2 alpha	TRA2A	29896	2.383945	0.685365
205746_s_at	ADAM metallopeptidase domain 17 (tumor necrosis factor. alpha. converting enzyme)	ADAM17	6868	2.382838	0.685365
205005_s_at	N-myristoyltransferase 2	NMT2	9397	2.381715	0.685365
222244_s_at	taurine upregulated gene 1	TUG1	55000	2.380933	0.685365
201416_at	SRY (sex determining region Y)-box 4	SOX4	6659	2.379837	0.685365
213717_at	LIM domain binding 3	LDB3	11155	2.379835	0.685365
217419_x_at	agrin	AGRN	375790	2.379116	0.685365
203987_at	frizzled homolog 6 (Drosophila)	FZD6	8323	2.376525	0.685365
208515_at	histone cluster 1. H2bm	HIST1H2BM	8342	2.37339	0.685365
212642_s_at	human immunodeficiency virus type I enhancer binding protein 2	HIVEP2	3097	2.370399	0.685365
205368_at	family with sequence similarity 131. member B	FAM131B	9715	2.367576	0.685365
210990_s_at	laminin. alpha 4	LAMA4	3910	2.366895	0.685365
204205_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3G	APOBEC3G	60489	2.36614	0.685365
215572_at	Similar to Golgin subfamily A member 6 (Golgin linked to PML) (Golgin-like protein)	LOC646934	646934	2.365812	0.685365
216361_s_at	MYST histone acetyltransferase (monocytic leukemia) 3	MYST3	7994	2.364447	0.685365
211833_s_at	BCL2-associated X protein	BAX	581	2.363029	0.685365
206790_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex. 1. 7kDa	NDUFB1	4707	2.360036	0.685365
217249_x_at	---	---	---	2.359444	0.685365
221728_x_at	X (inactive)-specific transcript	XIST	7503	2.359297	0.685365
216033_s_at	FYN oncogene related to SRC. FGR. YES	FYN	2534	2.358959	0.685365
219927_at	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	FCF1	51077	2.357155	0.685365
203792_x_at	polycomb group ring finger 2	PCGF2	7703	2.357119	0.685365
214995_s_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3G /// apolipoprotein B mRNA e	APOBEC3F ///	200316 /// 60	2.356971	0.685365
216449_x_at	heat shock protein 90kDa beta (Grp94). member 1	HSP90B1	7184	2.354796	0.685365
208736_at	actin related protein 2/3 complex. subunit 3. 21kDa	ARPC3	10094	2.353836	0.685365
202595_s_at	leptin receptor overlapping transcript-like 1	LEPROTL1	23484	2.35359	0.685365

206739_at	homeobox C5	HOXC5	3222	2.349507	0.685365
206940_s_at	POU class 4 homeobox 1	POU4F1	5457	2.348675	0.685365
200663_at	CD63 molecule	CD63	967	2.347926	0.685365
214788_x_at	dendrin	DDN	23109	2.347333	0.685365
201859_at	serglycin	SRGN	5552	2.346423	0.685365
217468_at	Cytochrome P450. family 2. subfamily D. polypeptide 6	CYP2D6	1565	2.346057	0.685365
210715_s_at	serine peptidase inhibitor. Kunitz type. 2	SPINT2	10653	2.34257	0.685365
205510_s_at	hypothetical protein FLJ10038	FLJ10038	55056	2.342325	0.685365
218913_s_at	GEM interacting protein	GMIP	51291	2.341721	0.685365
219236_at	progestin and adipoQ receptor family member VI	PAQR6	79957	2.34057	0.685365
217554_at	Transcribed locus	---	---	2.340448	0.685365
218537_at	host cell factor C1 regulator 1 (XPO1 dependent)	HCFC1R1	54985	2.338598	0.685365
212952_at	Transcribed locus	---	---	2.337874	0.685365
207986_x_at	cytochrome b-561	CYB561	1534	2.336603	0.685365
203416_at	CD53 molecule	CD53	963	2.336025	0.685365
207099_s_at	choroideremia (Rab escort protein 1)	CHM	1121	2.33508	0.685365
208042_at	angiogenic factor with G patch and FHA domains 1	AGGF1	55109	2.333987	0.685365
220274_at	IQ motif containing with AAA domain	IQCA	79781	2.333357	0.685365
208076_at	histone cluster 1. H4d	HIST1H4D	8360	2.333251	0.685365
211868_x_at	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m mar	IGHA1 /// IG	28396 /// 349	2.332643	0.685365
216659_at	dihydrofolate reductase pseudogene	LOC1720	1720	2.332572	0.685365
214436_at	F-box and leucine-rich repeat protein 2	FBXL2	25827	2.332083	0.685365
217677_at	pleckstrin homology domain containing. family A (phosphoinositide binding specific) member 2	PLEKHA2	59339	2.331452	0.685365
214324_at	glycoprotein 2 (zymogen granule membrane)	GP2	2813	2.330371	0.685365
220609_at	hypothetical protein LOC202181	LOC202181	202181	2.329875	0.685365
203534_at	LSM1 homolog. U6 small nuclear RNA associated (S. cerevisiae)	LSM1	27257	2.329813	0.685365
204170_s_at	CDC28 protein kinase regulatory subunit 2	CKS2	1164	2.329535	0.685365
203247_s_at	zinc finger protein 24	ZNF24	7572	2.329093	0.685365
216555_at	chromosome 22 open reading frame 30	C22orf30	253143	2.32902	0.685365
211012_s_at	promyelocytic leukemia /// hypothetical protein LOC161527	LOC161527 //	161527 /// 53	2.328721	0.685365
215219_at	dopey family member 2	DOPEY2	9980	2.327902	0.685365
205362_s_at	prefoldin subunit 4	PFDN4	5203	2.326771	0.685365
213736_at	Cytochrome c oxidase subunit Vb	COX5B	1329	2.326611	0.685365
212030_at	RNA binding motif protein 25	RBM25	58517	2.326325	0.685365
210282_at	zinc finger. MYM-type 2	ZMYM2	7750	2.325716	0.685365
221125_s_at	potassium large conductance calcium-activated channel. subfamily M beta member 3	KCNMB3	27094	2.325421	0.685365
214419_s_at	Cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	1559	2.325237	0.685365
202980_s_at	seven in absentia homolog 1 (Drosophila)	SIAH1	6477	2.324244	0.685365
202257_s_at	CD2 (cytoplasmic tail) binding protein 2	CD2BP2	10421	2.323957	0.685365
208439_s_at	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	FCN2	2220	2.32369	0.685365
212991_at	F-box protein 9	FBXO9	26268	2.322894	0.685365
215924_at	CDNA FLJ12040 fis. clone HEMBB1001944	---	---	2.322551	0.685365
210102_at	loss of heterozygosity. 11. chromosomal region 2. gene A	LOH11CR2A	4013	2.322301	0.685365
204175_at	zinc finger protein 593	ZNF593	51042	2.321135	0.685365
206526_at	RIB43A domain with coiled-coils 2	RIBC2	26150	2.317583	0.685365
214940_s_at	Smg-6 homolog. nonsense mediated mRNA decay factor (C. elegans)	SMG6	23293	2.316067	0.685365
221892_at	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	H6PD	9563	2.313815	0.685365
207398_at	homeobox D13	HOXD13	3239	2.31349	0.685365
210605_s_at	milk fat globule-EGF factor 8 protein	MFGE8	4240	2.313454	0.685365
212239_at	phosphoinositide-3-kinase. regulatory subunit 1 (p85 alpha)	PIK3R1	5295	2.311151	0.685365
204671_s_at	ankyrin repeat domain 6	ANKRD6	22881	2.310891	0.685365
220615_s_at	male sterility domain containing 1	MLSTD1	55711	2.310606	0.685365
208664_s_at	tetratricopeptide repeat domain 3	TTC3	7267	2.309084	0.685365
217188_s_at	chromosome 14 open reading frame 1	C14orf1	11161	2.306911	0.685365
203167_at	TIMP metallopeptidase inhibitor 2	TIMP2	7077	2.305578	0.685365
205376_at	inositol polyphosphate-4-phosphatase. type II. 105kDa	INPP4B	8821	2.30436	0.685365
213001_at	angiopoietin-like 2	ANGPTL2	23452	2.303988	0.685365
202785_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex. 7. 14.5kDa	NDUFA7	4701	2.302922	0.685365
217755_at	hematological and neurological expressed 1	HN1	51155	2.302605	0.685365
214695_at	ubiquitin associated protein 2-like	UBAP2L	9898	2.302487	0.685365
220861_at	---	---	---	2.301407	0.685365
209563_x_at	calmodulin 1 (phosphorylase kinase. delta)	CALM1	801	2.301142	0.685365
215027_at	hypothetical protein HSU79275	HSU79275	27105	2.298765	0.685365
205184_at	guanine nucleotide binding protein (G protein). gamma 4	GNG4	2786	2.297879	0.685365
207731_at	---	---	---	2.297251	0.685365
203671_at	thiopurine S-methyltransferase	TPMT	7172	2.296889	0.685365
210383_at	sodium channel. voltage-gated. type I. alpha subunit	SCN1A	6323	2.296578	0.685365
213376_at	zinc finger and BTB domain containing 1	ZBTB1	22890	2.296177	0.685365
201498_at	ubiquitin specific peptidase 7 (herpes virus-associated)	USP7	7874	2.295342	0.685365
214184_at	neuropeptide FF-amide peptide precursor	NPFF	8620	2.295087	0.685365
212865_s_at	collagen. type XIV. alpha 1 (undulin)	COL14A1	7373	2.294995	0.685365
203484_at	Sec61 gamma subunit	SEC61G	23480	2.294769	0.685365
202478_at	tribbles homolog 2 (Drosophila)	TRIB2	28951	2.294619	0.685365
216243_s_at	interleukin 1 receptor antagonist	IL1RN	3557	2.294207	0.685365
220780_at	phospholipase A2. group III	PLA2G3	50487	2.292886	0.685365
219406_at	chromosome 1 open reading frame 50	C1orf50	79078	2.292572	0.685365
209602_s_at	GATA binding protein 3	GATA3	2625	2.292342	0.685365
205075_at	serpin peptidase inhibitor. clade F (alpha-2 antiplasmin. pigment epithelium derived factor). mem	SERPINF2	5345	2.291389	0.685365
220389_at	coiled-coil domain containing 81	CCDC81	60494	2.291318	0.685365
213312_at	chromosome 6 open reading frame 162	C6orf162	57150	2.290579	0.685365
217359_s_at	neural cell adhesion molecule 1	NCAM1	4684	2.288542	0.685365
222088_s_at	solute carrier family 2 (facilitated glucose transporter). member 3	SLC2A3	6515	2.287054	0.685365
202481_at	dehydrogenase/reductase (SDR family) member 3	DHRS3	9249	2.286618	0.685365
214412_at	H2A histone family. member B3 /// H2A histone family. member B1	H2AFB1 /// H	474382 /// 83	2.28626	0.685365
203904_x_at	CD82 molecule	CD82	3732	2.285981	0.685365
222216_s_at	mitochondrial ribosomal protein L17	MRPL17	63875	2.285753	0.685365

219465_at	apolipoprotein A-II	APOA2	336	2.285733	0.685365
217069_at	myeloid/lymphoid or mixed-lineage leukemia 4	MLL4	9757	2.284943	0.685365
215919_s_at	mitochondrial ribosomal protein S11	MRPS11	64963	2.284846	0.685365
216686_at	Similar to protein immuno-reactive with anti-PTH polyclonal antibodies	FLJ40330	645784	2.284382	0.685365
219879_s_at	chromosome 17 open reading frame 53	C17orf53	78995	2.281608	0.685365
209672_s_at	hypothetical protein FLJ20323	FLJ20323	54468	2.279025	0.685365
221954_at	Chromosome 20 open reading frame 111	C20orf111	51526	2.278848	0.685365
214997_at	Golgi autoantigen. golgin subfamily a. 1	GOLGA1	2800	2.278316	0.685365
210352_at	bromodomain containing 8	BRD8	10902	2.277381	0.685365
208673_s_at	splicing factor. arginine/serine-rich 3	SFRS3	6428	2.27637	0.685365
217438_at	MRNA. clone:RES4-16	---	---	2.274527	0.685365
220864_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex. 13	NDUFA13	51079	2.274215	0.685365
206520_x_at	sialic acid binding Ig-like lectin 6	SIGLEC6	946	2.273893	0.685365
218154_at	gasdermin domain containing 1	GSDMDC1	79792	2.273098	0.685365
207663_x_at	G antigen 3	GAGE3	2575	2.272838	0.685365
214740_at	polymerase (RNA) II (DNA directed) polypeptide J. 13.3kDa pseudogene /// DNA directed RNA pc	POLR2J2 /// P	246721 /// 54	2.272776	0.685365
217499_x_at	olfactory receptor. family 7. subfamily E. member 37 pseudogene	OR7E37P	26636	2.272436	0.685365
215279_at	Clone 23676 mRNA sequence	---	---	2.272429	0.685365
218463_s_at	MUS81 endonuclease homolog (S. cerevisiae)	MUS81	80198	2.271188	0.685365
221555_x_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	CDC14B	8555	2.270668	0.685365
215554_at	glycosylphosphatidylinositol specific phospholipase D1	GPLD1	2822	2.270387	0.685365
209762_x_at	SP110 nuclear body protein	SP110	3431	2.269991	0.685365
200622_x_at	calmodulin 3 (phosphorylase kinase. delta)	CALM3	808	2.269867	0.685365
208024_s_at	DiGeorge syndrome critical region gene 6 /// DiGeorge syndrome critical region gene 6-like	DGCR6 /// DG	8214 /// 8535	2.269125	0.685365
217962_at	nucleolar protein family A. member 3 (H/ACA small nucleolar RNPs)	NOLA3	55505	2.267983	0.685365
202289_s_at	transforming. acidic coiled-coil containing protein 2	TACC2	10579	2.267559	0.685365
217992_s_at	EF-hand domain family. member D2	EFHD2	79180	2.26745	0.685365
221409_at	olfactory receptor. family 2. subfamily S. member 2	OR2S2	56656	2.265153	0.685365
210446_at	GATA binding protein 1 (globin transcription factor 1)	GATA1	2623	2.265004	0.685365
221996_s_at	Clathrin. light chain (Lcb)	CLTB	1212	2.264987	0.685365
210790_s_at	SAR1 gene homolog A (S. cerevisiae)	SAR1A	56681	2.264337	0.685368
214715_x_at	zinc finger protein 160	ZNF160	90338	2.264107	0.685368
209531_at	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	GSTZ1	2954	2.263808	0.685368
214004_s_at	vestigial like 4 (Drosophila)	VGLL4	9686	2.262271	0.685408
220309_at	tetratricopeptide repeat domain 22	TTC22	55001	2.261792	0.685408
218291_at	mitogen-activated protein-binding protein-interacting protein	MAPBPIP	28956	2.260532	0.685408
211638_at	Similar to Ig heavy chain V-II region ARH-77 precursor	LOC652128	652128	2.2605	0.685408
202323_s_at	acyl-Coenzyme A binding domain containing 3	ACBD3	64746	2.254929	0.686542
213955_at	myozenin 3	MYOZ3	91977	2.254523	0.686542
201370_s_at	cullin 3	CUL3	8452	2.253869	0.686542
207503_at	t-complex 10 (mouse)	TCP10	6953	2.253314	0.686542
217267_s_at	RAB7A. member RAS oncogene family	RAB7A	7879	2.253126	0.686542
208133_at	replication factor C (activator 1) 1. 145kDa	RFC1	5981	2.251193	0.686542
221701_s_at	stimulated by retinoic acid gene 6 homolog (mouse)	STRA6	64220	2.249169	0.686542
202869_at	2'.5'-oligoadenylate synthetase 1. 40/46kDa	OAS1	4938	2.248862	0.686542
222381_at	Programmed cell death 6 /// CDNA FLJ37304 fis. clone BRAMY2016070	PDCD6	10016	2.248641	0.686542
208604_s_at	homeobox A3	HOXA3	3200	2.248318	0.686542
208032_s_at	glutamate receptor. ionotrophic. AMPA 3	GRIA3	2892	2.247864	0.686542
209696_at	fructose-1.6-bisphosphatase 1	FBP1	2203	2.247086	0.686542
206277_at	purinergic receptor P2Y. G-protein coupled. 2	P2RY2	5029	2.246319	0.686542
213015_at	ARTC1 mRNA. complete sequence	---	---	2.245347	0.686542
206915_at	NK2 homeobox 2	NKX2-2	4821	2.245256	0.686542
204129_at	B-cell CLL/lymphoma 9	BCL9	607	2.24416	0.686542
219358_s_at	centaurin. alpha 2	CENTA2	55803	2.24281	0.686542
200923_at	lectin. galactoside-binding. soluble. 3 binding protein	LGALS3BP	3959	2.241452	0.686542
208333_at	LIM homeobox 5	LHX5	64211	2.240645	0.686542
215377_at	C-terminal binding protein 2	CTBP2	1488	2.238911	0.686542
221566_s_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	8996	2.23834	0.686542
216494_at	similar to insulin-like growth factor 2 mRNA binding protein 3 /// similar to IGF-II mRNA-binding	LOC645468 //	645468 /// 65	2.23657	0.686542
204235_s_at	GULP. engulfment adaptor PTB domain containing 1	GULP1	51454	2.23571	0.686542
216450_x_at	heat shock protein 90kDa beta (Grp94). member 1	HSP90B1	7184	2.23556	0.686542
201028_s_at	CD99 molecule	CD99	4267	2.233166	0.686542
207847_s_at	mucin 1. cell surface associated	MUC1	4582	2.232621	0.686542
211008_s_at	ubiquitin-conjugating enzyme E2I (UBC9 homolog. yeast)	UBE2I	7329	2.231888	0.686542
215961_at	coagulation factor XII (Hageman factor)	F12	2161	2.231611	0.686542
202952_s_at	ADAM metallopeptidase domain 12 (meltrin alpha)	ADAM12	8038	2.231472	0.686542
203486_s_at	armadillo repeat containing 8	ARMC8	25852	2.22897	0.686542
213587_s_at	ATPase. H+ transporting V0 subunit e2	ATP6V0E2	155066	2.228641	0.686542
206542_s_at	SWI/SNF related. matrix associated. actin dependent regulator of chromatin. subfamily a. membe	SMARCA2	6595	2.226959	0.686542
201871_s_at	SAPK substrate protein 1	LOC51035	51035	2.226203	0.686542
218654_s_at	mitochondrial ribosomal protein S33	MRPS33	51650	2.225808	0.686542
212634_at	KIAA0776	KIAA0776	23376	2.225537	0.686542
207279_s_at	nebulette	NEBL	10529	2.224584	0.686542
210756_s_at	Notch homolog 2 (Drosophila)	NOTCH2	4853	2.224404	0.686542
207027_at	HGF activator	HGFAC	3083	2.224334	0.686542
206208_at	carbonic anhydrase IV	CA4	762	2.223236	0.686542
214040_s_at	gelsolin (amyloidosis. Finnish type)	GSN	2934	2.223026	0.686542
201400_at	proteasome (prosome. macropain) subunit. beta type. 3	PSMB3	5691	2.221302	0.686542
218540_at	thiamine triphosphatase	THTPA	79178	2.221296	0.686542
210461_s_at	actin binding LIM protein 1	ABLIM1	3983	2.221034	0.686542
213296_at	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	RER1	11079	2.220332	0.686542
213456_at	sclerostin domain containing 1	SOSTDC1	25928	2.218429	0.686542
219834_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region. candidate 8	ALS2CR8	79800	2.216558	0.686542
205965_at	basic leucine zipper transcription factor. ATF-like	BATF	10538	2.216441	0.686542
203021_at	secretory leukocyte peptidase inhibitor	SLPI	6590	2.21626	0.686542
208810_at	DnaJ (Hsp40) homolog. subfamily B. member 6 /// similar to DnaJ (Hsp40) homolog. subfamily E	DNAJB6 /// LC	10049 /// 387	2.215277	0.686542

209716_at	colony stimulating factor 1 (macrophage)	CSF1	1435	2.21252	0.686542
215224_at	ribosomal protein L23	RPL23	9349	2.21125	0.686542
219910_at	FIC domain containing	FICD	11153	2.210662	0.686542
206281_at	adenylate cyclase activating polypeptide 1 (pituitary)	ADCYAP1	116	2.210606	0.686542
205007_s_at	calcium and integrin binding family member 2	CIB2	10518	2.210098	0.686542
204786_s_at	interferon (alpha. beta and omega) receptor 2	IFNAR2	3455	2.209646	0.686542
201908_at	dishevelled. dsh homolog 3 (Drosophila)	DVL3	1857	2.209346	0.686542
222371_at	MRNA; cDNA DKFZp686B1142 (from clone DKFZp686B1142)	---	---	2.20858	0.686542
202452_at	zer-1 homolog (C. elegans)	ZER1	10444	2.208358	0.686542
222255_at	periaxin	PRX	57716	2.207523	0.686542
206386_at	serpin peptidase inhibitor. clade A (alpha-1 antiproteinase. antitrypsin). member 7	SERPINA7	6906	2.207396	0.686542
202004_x_at	succinate dehydrogenase complex. subunit C. integral membrane protein. 15kDa	SDHC	6391	2.206949	0.686542
204428_s_at	lecithin-cholesterol acyltransferase	LCAT	3931	2.206919	0.686542
202596_at	endosulfine alpha	ENSA	2029	2.206692	0.686542
210138_at	regulator of G-protein signaling 20	RGS20	8601	2.20624	0.686542
203700_s_at	deiodinase. iodothyronine. type II	DIO2	1734	2.205741	0.686542
216960_s_at	zinc finger protein 133	ZNF133	7692	2.2054	0.686542
205006_s_at	N-myristoyltransferase 2	NMT2	9397	2.204788	0.686542
218994_s_at	stromal antigen 3-like 4	STAG3L4	64940	2.201562	0.686542
221484_at	UDP-Gal:betaGlcNAc beta 1.4- galactosyltransferase. polypeptide 5	B4GALT5	9334	2.200931	0.686542
218311_at	mitogen-activated protein kinase kinase kinase kinase 3	MAP4K3	8491	2.199441	0.686542
217484_at	complement component (3b/4b) receptor 1 (Knops blood group)	CR1	1378	2.199143	0.686542
201296_s_at	WD repeat and SOCS box-containing 1	WSB1	26118	2.197079	0.686542
219557_s_at	nuclear receptor interacting protein 3	NRIP3	56675	2.195917	0.686542
200925_at	cytochrome c oxidase subunit VIa polypeptide 1	COX6A1	1337	2.195285	0.686542
213327_s_at	ubiquitin specific peptidase 12	USP12	219333	2.195071	0.686542
210972_x_at	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20	TRA@ /// TRA	28517 /// 286	2.195039	0.686542
218773_s_at	methionine sulfoxide reductase B2	MSRB2	22921	2.194751	0.686542
209441_at	Rho-related BTB domain containing 2	RHOBTB2	23221	2.19239	0.686542
218429_s_at	hypothetical protein FLJ11286	FLJ11286	55337	2.191984	0.686542
208475_at	FERM domain containing 4A	FRMD4A	55691	2.190816	0.686542
221727_at	---	---	---	2.188555	0.686542
204179_at	myoglobin	MB	4151	2.188163	0.686542
213644_at	coiled-coil domain containing 46	CCDC46	201134	2.186955	0.686542
217536_x_at	Transcribed locus	---	---	2.1846	0.686542
221994_at	PDZ and LIM domain 5	PDLIM5	10611	2.184223	0.686542
207574_s_at	growth arrest and DNA-damage-inducible. beta	GADD45B	4616	2.183148	0.686542
210213_s_at	eukaryotic translation initiation factor 6	EIF6	3692	2.182961	0.686542
207643_s_at	tumor necrosis factor receptor superfamily. member 1A	TNFRSF1A	7132	2.182931	0.686542
203254_s_at	talin 1	TLN1	7094	2.182096	0.686542
211769_x_at	serine incorporator 3	SERINC3	10955	2.181857	0.686542
209527_at	exosome component 2	EXOSC2	23404	2.181689	0.686542
200700_s_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDELR2	11014	2.180996	0.686542
208317_at	xylulokinase homolog (H. influenzae)	XYLB	9942	2.179615	0.686542
200921_s_at	B-cell translocation gene 1. anti-proliferative	BTG1	694	2.179412	0.686542
203692_s_at	E2F transcription factor 3	E2F3	1871	2.179221	0.686542
213252_at	SH3 and PX domains 2A	SH3PXD2A	9644	2.179136	0.686542
213547_at	cullin-associated and neddylation-dissociated 2 (putative)	CAND2	23066	2.178278	0.686542
219693_at	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase. delta)	AGPAT4	56895	2.177822	0.686542
213822_s_at	ubiquitin protein ligase E3B	UBE3B	89910	2.17689	0.686542
219616_at	acyl-CoA synthetase short-chain family member 3	ACSS3	79611	2.176475	0.686542
209066_x_at	ubiquinol-cytochrome c reductase binding protein	UQCRB	7381	2.175597	0.686542
203300_x_at	adaptor-related protein complex 1. sigma 2 subunit	AP1S2	8905	2.175503	0.686542
208829_at	TAP binding protein (tapasin)	TAPBP	6892	2.174176	0.686542
218628_at	coiled-coil domain containing 53	CCDC53	51019	2.173592	0.686542
201846_s_at	RING1 and YY1 binding protein	RYBP	23429	2.173463	0.686542
215796_at	T-cell receptor active alpha-chain V-region (V-J-C) mRNA. partial cds. clone AG212	---	---	2.173287	0.686542
206433_s_at	sparc/osteonectin. cwcv and kazal-like domains proteoglycan (testican) 3	SPOCK3	50859	2.173097	0.686542
220982_s_at	sperm acrosome associated 1	SPACA1	81833	2.170379	0.686542
210633_x_at	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	KRT10	3858	2.169077	0.686542
210038_at	protein kinase C. theta	PRKCQ	5588	2.168467	0.686542
220449_at	hypothetical protein MGC5566	MGC5566	79015	2.168114	0.686542
203326_x_at	---	---	---	2.167762	0.686542
202864_s_at	SP100 nuclear antigen	SP100	6672	2.167579	0.686542
217721_at	Full-length cDNA clone CS0DB003YD12 of Neuroblastoma Cot 10-normalized of Homo sapiens (hu	---	---	2.164745	0.686542
203176_s_at	transcription factor A. mitochondrial	TFAM	7019	2.164343	0.686542
203983_at	translin-associated factor X	TSNAX	7257	2.164018	0.686542
207588_at	myelin transcription factor 2	MYT2	8827	2.16357	0.686542
220747_at	HSPC072 protein	HSPC072	29075	2.163561	0.686542
213669_at	FCH domain only 1	FCHO1	23149	2.163116	0.686542
217396_at	MRNA; cDNA DKFZp434M0317 (from clone DKFZp434M0317)	---	---	2.162694	0.686542
202909_at	EPM2A (laforin) interacting protein 1	EPM2AIP1	9852	2.162674	0.686542
201095_at	death-associated protein	DAP	1611	2.159332	0.686542
218288_s_at	coiled-coil domain containing 90B	CCDC90B	60492	2.1586	0.686542
220698_at	hypothetical protein MGC4294	MGC4294	79160	2.15846	0.686542
220565_at	chemokine (C-C motif) receptor 10	CCR10	2826	2.158248	0.686542
214851_at	hepatocyte nuclear factor 4. alpha	HNF4A	3172	2.157853	0.686542
207008_at	interleukin 8 receptor. beta	IL8RB	3579	2.156955	0.686542
218029_at	family with sequence similarity 65. member A	FAM65A	79567	2.156528	0.686542
202000_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex. 6. 14kDa	NDUFA6	4700	2.156429	0.686542
202710_at	blocked early in transport 1 homolog (S. cerevisiae)	BET1	10282	2.155901	0.686542
207100_s_at	vesicle-associated membrane protein 1 (synaptobrevin 1)	VAMP1	6843	2.155753	0.686542
220091_at	solute carrier family 2 (facilitated glucose transporter). member 6	SLC2A6	11182	2.155729	0.686542
221113_s_at	wingless-type MMTV integration site family. member 16	WNT16	51384	2.154654	0.686542
208864_s_at	thioredoxin	TXN	7295	2.154394	0.686542
214980_at	Ubiquitin protein ligase E3A (human papilloma virus E6-associated protein. Angelman syndrome)	UBE3A	7337	2.153301	0.686542

203549_s_at	lipoprotein lipase	LPL	4023	2.152699	0.686542
209788_s_at	endoplasmic reticulum aminopeptidase 1	ERAP1	51752	2.151776	0.686542
210993_s_at	SMAD family member 1	SMAD1	4086	2.151288	0.686542
210874_s_at	N-acetyltransferase 6	NAT6	24142	2.150985	0.686542
208926_at	sialidase 1 (lysosomal sialidase)	NEU1	4758	2.150867	0.686542
220502_s_at	solute carrier family 13 (sodium/sulfate symporters). member 1	SLC13A1	6561	2.150679	0.686542
204771_s_at	transcription termination factor. RNA polymerase I	TTF1	7270	2.150614	0.686542
212188_at	potassium channel tetramerisation domain containing 12	KCTD12	115207	2.15002	0.686542
215784_at	CD1e molecule	CD1E	913	2.149881	0.686542
217502_at	interferon-induced protein with tetratricopeptide repeats 2	IFIT2	3433	2.149733	0.686542
201119_s_at	cytochrome c oxidase subunit 8A (ubiquitous)	COX8A	1351	2.146657	0.686542
213940_s_at	formin binding protein 1	FNBP1	23048	2.145019	0.686542
212082_s_at	myosin. light chain 6. alkali. smooth muscle and non-muscle	MYL6	4637	2.144227	0.686542
205939_at	cytochrome P450. family 3. subfamily A. polypeptide 7	CYP3A7	1551	2.144084	0.686542
208278_s_at	---	---	---	2.144047	0.686542
213114_at	---	---	---	2.142667	0.686542
218010_x_at	chromosome 20 open reading frame 149	C20orf149	79144	2.142565	0.686542
212081_x_at	HLA-B associated transcript 2	BAT2	7916	2.141804	0.686542
220122_at	multiple C2 domains. transmembrane 1	MCTP1	79772	2.140819	0.686542
213620_s_at	intercellular adhesion molecule 2	ICAM2	3384	2.139908	0.686542
216815_at	---	---	---	2.139472	0.686542
217998_at	pleckstrin homology-like domain. family A. member 1 /// hypothetical LOC652993	LOC652993 //	22822 /// 652	2.139247	0.686542
205209_at	activin A receptor. type IB	ACVR1B	91	2.138683	0.686542
204090_at	serine/threonine kinase 19	STK19	8859	2.138364	0.686542
214567_s_at	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	XCL1 /// XCL2	6375 /// 6846	2.136803	0.686542
214984_at	PI-3-kinase-related kinase SMG-1 /// hypothetical gene LOC283846 /// hypothetical protein LOC	DKFZp547E08	23049 /// 283	2.136729	0.686542
221905_at	cylindromatosis (turban tumor syndrome)	CYLD	1540	2.136069	0.686542
220069_at	tubulin. alpha 8	TUBA8	51807	2.135725	0.686542
201758_at	tumor susceptibility gene 101	TSG101	7251	2.134177	0.686542
214637_at	oncostatin M	OSM	5008	2.133991	0.686542
221438_s_at	testis expressed 12	TEX12	56158	2.13269	0.686542
213995_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit s (factor B)	ATP5S	27109	2.131809	0.686542
211377_x_at	v-myc myelocytomatosis viral related oncogene. neuroblastoma derived (avian)	MYCN	4613	2.13178	0.686542
212203_x_at	interferon induced transmembrane protein 3 (1-8U)	IFITM3	10410	2.131392	0.686542
203248_at	zinc finger protein 24	ZNF24	7572	2.131298	0.686542
213241_at	plexin C1	PLXNC1	10154	2.131291	0.686542
221613_s_at	zinc finger. AN1-type domain 6	ZFAND6	54469	2.13113	0.686542
200751_s_at	heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRNPC	3183	2.130673	0.686542
212994_at	THO complex 2	THOC2	57187	2.1305	0.686542
206848_at	homeobox A7	HOXA7	3204	2.130443	0.686542
222214_at	CDNA: FLJ21335 fis. clone COL02546	---	---	2.130439	0.686542
206811_at	adenylate cyclase 8 (brain)	ADCY8	114	2.129184	0.686542
204345_at	collagen. type XVI. alpha 1	COL16A1	1307	2.128767	0.686542
211595_s_at	mitochondrial ribosomal protein S11	MRPS11	64963	2.128085	0.686542
208184_s_at	transmembrane protein 1	TMEM1	7109	2.127982	0.686542
211398_at	fibroblast growth factor receptor 2 (bacteria-expressed kinase. keratinocyte growth factor recept	FGFR2	2263	2.127673	0.686542
219232_s_at	egl nine homolog 3 (C. elegans)	EGLN3	112399	2.126346	0.686542
214723_x_at	KIAA1641	KIAA1641	57730	2.126087	0.686542
209795_at	CD69 molecule	CD69	969	2.12557	0.686542
218921_at	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	SIGIRR	59307	2.125232	0.686542
212961_x_at	chromosome X open reading frame 40B	CXorf40B	541578	2.124805	0.686542
220475_at	solute carrier family 28 (sodium-coupled nucleoside transporter). member 3	SLC28A3	64078	2.124628	0.686542
202423_at	MYST histone acetyltransferase (monocytic leukemia) 3	MYST3	7994	2.124453	0.686542
220444_at	zinc finger protein 557	ZNF557	79230	2.123719	0.686542
210009_s_at	golgi SNAP receptor complex member 2	GOSR2	9570	2.123151	0.686542
219771_at	TBC1 domain family. member 8B (with GRAM domain)	TBC1D8B	54885	2.123065	0.686542
217617_at	Transcribed locus	---	---	2.122411	0.686542
211944_at	BAT2 domain containing 1	BAT2D1	23215	2.121578	0.686542
201825_s_at	saccharopine dehydrogenase (putative)	SCCPDH	51097	2.121248	0.686542
200736_s_at	glutathione peroxidase 1	GPX1	2876	2.121183	0.686542
204285_s_at	phorbol-12-myristate-13-acetate-induced protein 1	PMAIP1	5366	2.120986	0.686542
214238_at	Clone DT1P1B6 mRNA. CAG repeat region	---	---	2.119169	0.686728
210057_at	PI-3-kinase-related kinase SMG-1	SMG1	23049	2.118753	0.686728
215828_at	MRNA; cDNA DKFZp547C126 (from clone DKFZp547C126)	---	---	2.115299	0.686728
200835_s_at	microtubule-associated protein 4	MAP4	4134	2.114987	0.686728
218609_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 2	NUDT2	318	2.114765	0.686728
201324_at	epithelial membrane protein 1	EMP1	2012	2.114244	0.686728
211074_at	folate receptor 1 (adult)	FOLR1	2348	2.112322	0.686728
209020_at	chromosome 20 open reading frame 111	C20orf111	51526	2.111923	0.686728
218410_s_at	hypothetical protein LOC283871	LOC283871	283871	2.111561	0.686728
204499_at	ATP/GTP binding protein 1	AGTPBP1	23287	2.109359	0.686728
217044_s_at	pleckstrin homology domain containing. family G (with RhoGef domain) member 3	PLEKHG3	26030	2.108293	0.686728
221081_s_at	DENN/MADD domain containing 2D	DENND2D	79961	2.107415	0.686728
205418_at	feline sarcoma oncogene	FES	2242	2.106854	0.686728
213031_s_at	WD repeat domain 73	WDR73	84942	2.106808	0.686728
206602_s_at	homeobox D3	HOXD3	3232	2.10626	0.686728
219754_at	RNA binding motif protein 41	RBM41	55285	2.105277	0.686728
204334_at	Kruppel-like factor 7 (ubiquitous)	KLF7	8609	2.10475	0.686728
221353_at	olfactory receptor. family 3. subfamily A. member 1	OR3A1	4994	2.104647	0.686728
202759_s_at	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2	AKAP2 /// PAL	11217 /// 445	2.104181	0.686916
204292_x_at	serine/threonine kinase 11	STK11	6794	2.103761	0.687055
52837_at	KIAA1644 protein	LL22NC03-75	85352	2.101906	0.687862
220706_at	ADAM metallopeptidase with thrombospondin type 1 motif. 7	ADAMTS7	11173	2.101165	0.687862
206151_x_at	elastase 3B. pancreatic	ELA3B	23436	2.099434	0.689206
208749_x_at	flotillin 1	FLOT1	10211	2.09818	0.689932
216338_s_at	Yip1 domain family. member 3	YIPF3	25844	2.097274	0.689975

219672_at	erythroid associated factor	ERAF	51327	2.096058	0.690746
210370_s_at	lymphocyte antigen 9	LY9	4063	2.095188	0.690746
206908_s_at	claudin 11 (oligodendrocyte transmembrane protein)	CLDN11	5010	2.094753	0.690746
214972_at	Meningioma expressed antigen 5 (hyaluronidase)	MGEA5	10724	2.094738	0.690746
217507_at	solute carrier family 11 (proton-coupled divalent metal ion transporters). member 1	SLC11A1	6556	2.093673	0.690746
201456_s_at	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	BUB3	9184	2.093054	0.690746
204246_s_at	dynactin 3 (p22)	DCTN3	11258	2.091968	0.690746
214720_x_at	septin 10	10-Sep	151011	2.091112	0.690746
208244_at	bone morphogenetic protein 3 (osteogenic)	BMP3	651	2.090262	0.690746
213067_at	myosin. heavy chain 10. non-muscle	MYH10	4628	2.08946	0.690746
206327_s_at	cadherin 15. M-cadherin (myotubule)	CDH15	1013	2.089449	0.690746
216161_at	Strawberry notch homolog 1 (Drosophila)	SBNO1	55206	2.089148	0.690746
214998_at	AP2 associated kinase 1	AAK1	22848	2.087479	0.690746
221567_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	8996	2.087247	0.690746
203264_s_at	Cdc42 guanine nucleotide exchange factor (GEF) 9	ARHGEF9	23229	2.086567	0.690746
212925_at	chromosome 19 open reading frame 21	C19orf21	126353	2.08622	0.690746
211144_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate	TARP /// TRG	445347 /// 69	2.085175	0.690746
210610_at	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1	634	2.08344	0.690746
221377_s_at	recombination signal binding protein for immunoglobulin kappa J region-like	RBPJL	11317	2.083155	0.690746
211919_s_at	chemokine (C-X-C motif) receptor 4	CXCR4	7852	2.082936	0.690746
214544_s_at	synaptosomal-associated protein. 23kDa	SNAP23	8773	2.082393	0.690746
221442_at	melanocortin 3 receptor	MC3R	4159	2.081525	0.690746
210553_x_at	proprotein convertase subtilisin/kexin type 6	PCSK6	5046	2.080664	0.690746
216315_x_at	ubiquitin-conjugating enzyme E2 variant 1 /// TMEM189-UBE2V1 /// similar to ubiquitin-conjugat	LOC730052 //	387522 /// 73	2.080554	0.690746
202366_at	acyl-Coenzyme A dehydrogenase. C-2 to C-3 short chain	ACADS	35	2.080237	0.690746
209993_at	ATP-binding cassette. sub-family B (MDR/TAP). member 1	ABCB1	5243	2.079959	0.690746
219881_s_at	---	---	---	2.079153	0.690746
204130_at	hydroxysteroid (11-beta) dehydrogenase 2	HSD11B2	3291	2.07896	0.690746
209405_s_at	family with sequence similarity 3. member A	FAM3A	60343	2.077668	0.690921
217251_x_at	Isovaleryl Coenzyme A dehydrogenase	IVD	3712	2.076359	0.691681
220670_at	---	---	---	2.075213	0.691792
216980_s_at	sialophorin (leukosialin. CD43)	SPN	6693	2.074857	0.691792
219555_s_at	centromere protein N	CENPN	55839	2.073749	0.692639
212486_s_at	FYN oncogene related to SRC. FGR. YES	FYN	2534	2.071921	0.693749
217732_s_at	integral membrane protein 2B	ITM2B	9445	2.07024	0.693852
208927_at	speckle-type POZ protein	SPOP	8405	2.069217	0.693852
217316_at	olfactory receptor. family 7. subfamily A. member 10	OR7A10	390892	2.069101	0.693852
213311_s_at	transcription factor 25 (basic helix-loop-helix)	TCF25	22980	2.068584	0.693852
210221_at	cholinergic receptor. nicotinic. alpha 3	CHRNA3	1136	2.068357	0.693852
205616_at	CDNA FLJ25134 fis. clone CBR06934	---	---	2.067962	0.693852
221998_s_at	vaccinia related kinase 3	VRK3	51231	2.067095	0.694015
208406_s_at	GRB2-related adaptor protein 2	GRAP2	9402	2.064681	0.694181
221014_s_at	RAB33B. member RAS oncogene family	RAB33B	83452	2.064485	0.694181
201264_at	coatomer protein complex. subunit epsilon	COPE	11316	2.062264	0.694215
214011_s_at	hypothetical protein HSPC111	HSPC111	51491	2.06209	0.694215
218136_s_at	solute carrier family 25. member 37	SLC25A37	51312	2.061799	0.694215
221515_s_at	leucine carboxyl methyltransferase 1	LCMT1	51451	2.060269	0.694598
221797_at	chromosome 17 open reading frame 90	C17orf90	339229	2.059472	0.694598
206535_at	solute carrier family 2 (facilitated glucose transporter). member 2	SLC2A2	6514	2.058244	0.694598
212126_at	CDNA clone IMAGE:4842353	---	---	2.057114	0.694598
208799_at	proteasome (prosome. macropain) subunit. beta type. 5	PSMB5	5693	2.05679	0.694598
214556_at	somatostatin receptor 4	SSTR4	6754	2.055841	0.694598
202152_x_at	upstream transcription factor 2. c-fos interacting	USF2	7392	2.055689	0.694598
204713_s_at	coagulation factor V (proaccelerin. labile factor)	F5	2153	2.055032	0.694719
204440_at	CD83 molecule	CD83	9308	2.054483	0.695017
214296_x_at	chromosome 19 open reading frame 36	C19orf36	113177	2.053631	0.695353
222267_at	hypothetical protein FLJ14803	FLJ14803	84928	2.05133	0.696075
205882_x_at	adducin 3 (gamma)	ADD3	120	2.05089	0.696105
216068_at	MRNA; cDNA DKFZp434N021 (from clone DKFZp434N021)	---	---	2.050488	0.696105
65630_at	transmembrane protein 80	TMEM80	283232	2.049535	0.696209
208102_s_at	pleckstrin and Sec7 domain containing	PSD	5662	2.049406	0.696209
208421_at	---	---	---	2.047489	0.696209
208966_x_at	interferon. gamma-inducible protein 16	IFI16	3428	2.047386	0.696209
206420_at	immunoglobulin superfamily. member 6	IGSF6	10261	2.047226	0.696209
221192_x_at	major facilitator superfamily domain containing 11	MFSD11	79157	2.047147	0.696209
37462_i_at	splicing factor 3a. subunit 2. 66kDa	SF3A2	8175	2.046665	0.696438
203018_s_at	synovial sarcoma. X breakpoint 2 interacting protein	SSX2IP	117178	2.046267	0.696577
205293_x_at	BAI1-associated protein 2	BAIAP2	10458	2.04534	0.696807
207972_at	glycine receptor. alpha 1 (startle disease/hyperekplexia)	GLRA1	2741	2.044536	0.696807
209633_at	protein phosphatase 2 (formerly 2A). regulatory subunit B''. alpha	PPP2R3A	5523	2.043908	0.696807
209205_s_at	LIM domain only 4	LMO4	8543	2.043741	0.696807
207266_x_at	RNA binding motif. single stranded interacting protein 1	RBMS1	5937	2.043634	0.696807
213979_s_at	C-terminal binding protein 1	CTBP1	1487	2.042227	0.697458
214699_x_at	WD repeat domain. phosphoinositide interacting 2	WIPI2	26100	2.041927	0.697492
210100_s_at	ATP-binding cassette. sub-family A (ABC1). member 2	ABCA2	20	2.04132	0.697859
219033_at	poly (ADP-ribose) polymerase family. member 8	PARP8	79668	2.040884	0.697915
214804_at	---	---	---	2.039566	0.698889
205503_at	protein tyrosine phosphatase. non-receptor type 14	PTPN14	5784	2.037962	0.700341
215024_at	asparagine synthetase /// chromosome 7 open reading frame 28A /// chromosome 7 open readin	ASNS /// C7or	221960 /// 38	2.035138	0.701657
221957_at	pyruvate dehydrogenase kinase. isozyme 3	PDK3	5165	2.035038	0.701657
202760_s_at	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2	AKAP2 /// PAL	11217 /// 445	2.033722	0.701657
213432_at	mucin 5B. oligomeric mucus/gel-forming	MUC5B	727897	2.033377	0.701657
211744_s_at	CD58 molecule	CD58	965	2.032573	0.701657
206150_at	CD27 molecule	CD27	939	2.032149	0.701657
220606_s_at	chromosome 17 open reading frame 48	C17orf48	56985	2.031601	0.701657
201435_s_at	eukaryotic translation initiation factor 4E	EIF4E	1977	2.030359	0.701657

208478_s_at	BCL2-associated X protein	BAX	581	2.030295	0.701657
218446_s_at	family with sequence similarity 18. member B	FAM18B	51030	2.03009	0.701657
215492_x_at	pre T-cell antigen receptor alpha	PTCRA	171558	2.030015	0.701657
210796_x_at	sialic acid binding Ig-like lectin 6	SIGLEC6	946	2.029813	0.701657
218285_s_at	3-hydroxybutyrate dehydrogenase. type 2	BDH2	56898	2.029157	0.701657
218669_at	RAP2C. member of RAS oncogene family	RAP2C	57826	2.02907	0.701657
201251_at	pyruvate kinase. muscle	PKM2	5315	2.028925	0.701657
221553_at	implantation-associated protein /// similar to implantation-associated protein	LOC728866 //	728866 /// 84	2.027564	0.701657
214906_x_at	hypothetical gene CG018	CG018	90634	2.027534	0.701657
205893_at	neuroligin 1	NLGN1	22871	2.027108	0.701657
207130_at	zinc finger. MYND-type containing 8	ZMYND8	23613	2.027097	0.701657
212241_at	glutamate receptor. ionotropic. N-methyl D-aspartate-like 1A /// GRINL1A combined protein /// s	Gcom1 /// GR	145781 /// 33	2.026624	0.701657
210037_s_at	nitric oxide synthase 2A (inducible. hepatocytes)	NOS2A	4843	2.026548	0.701657
206982_at	crystallin. beta A1	CRYBA1	1411	2.026499	0.701657
219026_s_at	RAS protein activator like 2	RASAL2	9462	2.026072	0.701657
219385_at	SLAM family member 8	SLAMF8	56833	2.02596	0.701657
205857_at	solute carrier family 18 (vesicular monoamine). member 2	SLC18A2	6571	2.025399	0.701657
212631_at	Syntaxin 7	STX7	8417	2.025176	0.701657
212103_at	karyopherin alpha 6 (importin alpha 7)	KPNA6	23633	2.025125	0.701657
219538_at	WD repeat domain 5B	WDR5B	54554	2.024372	0.701657
218831_s_at	Fc fragment of IgG. receptor. transporter. alpha	FCGRT	2217	2.023605	0.701657
216566_at	Ribosomal protein L14	RPL14	9045	2.023178	0.701657
211422_at	transient receptor potential cation channel. subfamily M. member 3	TRPM3	80036	2.022757	0.701657
219981_x_at	zinc finger protein 587	ZNF587	84914	2.022097	0.701657
218240_at	NFKB inhibitor interacting Ras-like 2	NKIRAS2	28511	2.021955	0.701657
216212_s_at	dyskeratosis congenita 1. dyskerin	DKC1	1736	2.021933	0.701657
221145_at	---	---	---	2.018788	0.701821
215199_at	caldesmon 1	CALD1	800	2.018632	0.701821
201205_at	---	---	---	2.018631	0.701821
200001_at	calpain. small subunit 1	CAPNS1	826	2.018556	0.701821
220326_s_at	hypothetical protein FLJ10357	FLJ10357	55701	2.018222	0.701821
201876_at	paraoxonase 2	PON2	5445	2.017604	0.701821
207034_s_at	GLI-Kruppel family member GLI2	GLI2	2736	2.017196	0.701821
218708_at	NTF2-like export factor 1	NXT1	29107	2.01716	0.701821
221234_s_at	BTB and CNC homology 1. basic leucine zipper transcription factor 2	BACH2	60468	2.016732	0.701821
203024_s_at	chromosome 5 open reading frame 15	C5orf15	56951	2.016486	0.701821
203590_at	dynein. cytoplasmic 1. light intermediate chain 2	DYNC1LI2	1783	2.016396	0.701821
218027_at	mitochondrial ribosomal protein L15	MRPL15	29088	2.015465	0.701821
216607_s_at	cytochrome P450. family 51. subfamily A. polypeptide 1	CYP51A1	1595	2.014472	0.701821
217624_at	PDGFA associated protein 1	PDAP1	11333	2.01423	0.701821
217237_at	Cyritestin 2-like mRNA. partial sequence	---	---	2.012285	0.701821
219382_at	SERTA domain containing 3	SERTAD3	29946	2.012211	0.701821
202173_s_at	vascular endothelial zinc finger 1	VEZF1	7716	2.011852	0.701821
220713_at	CDNA FLJ12345 fis. clone MAMMA1002294	---	---	2.011754	0.701821
216495_x_at	Isovaleryl Coenzyme A dehydrogenase	IVD	3712	2.011191	0.701821
201482_at	quiescin Q6 sulfhydryl oxidase 1	QSOX1	5768	2.011111	0.701821
211210_x_at	SH2 domain protein 1A. Duncan's disease (lymphoproliferative syndrome)	SH2D1A	4068	2.010776	0.701821
213639_s_at	zinc finger protein 500	ZNF500	26048	2.009621	0.701821
221896_s_at	HIG1 domain family. member 1A	HIGD1A	25994	2.00925	0.701821
206967_at	cyclin T1	CCNT1	904	2.008741	0.701821
206506_s_at	suppressor of Ty 3 homolog (S. cerevisiae)	SUPT3H	8464	2.008314	0.701821
209404_s_at	transmembrane emp24 protein transport domain containing 7	TMED7	51014	2.008168	0.701821
210427_x_at	annexin A2	ANXA2	302	2.008161	0.701821
213315_x_at	chromosome X open reading frame 40A	CXorf40A	91966	2.008044	0.701821
221790_s_at	low density lipoprotein receptor adaptor protein 1	LDLRAP1	26119	2.007726	0.701821
214034_at	endoplasmic reticulum aminopeptidase 1	ERAP1	51752	2.007357	0.701821
208746_x_at	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit G	ATP5L	10632	2.006394	0.701821
202617_s_at	methyl CpG binding protein 2 (Rett syndrome)	MECP2	4204	2.00608	0.701821
217042_at	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	RDH11	51109	2.005352	0.701821
212868_x_at	chromosome 12 open reading frame 47	C12orf47	51275	2.005119	0.701821
210107_at	chloride channel. calcium activated. family member 1	CLCA1	1179	2.004572	0.701821
210131_x_at	succinate dehydrogenase complex. subunit C. integral membrane protein. 15kDa	SDHC	6391	2.003848	0.701821
207143_at	cyclin-dependent kinase 6	CDK6	1021	2.002531	0.702274
219806_s_at	chromosome 11 open reading frame 75	C11orf75	56935	2.001108	0.703269
219664_s_at	2.4-dienoyl CoA reductase 2. peroxisomal	DECR2	26063	-2.00043	0.703454
209254_at	KIAA0265 protein	KIAA0265	23008	-2.000571	0.703454
219934_s_at	sulfotransferase family 1E. estrogen-preferring. member 1	SULT1E1	6783	-2.001338	0.703269
200064_at	heat shock protein 90kDa alpha (cytosolic). class B member 1	HSP90AB1	3326	-2.002673	0.702274
221101_at	chromosome 14 open reading frame 113	C14orf113	54792	-2.003456	0.701821
204305_at	mitochondrial intermediate peptidase	MIPEP	4285	-2.003511	0.701821
209339_at	seven in absentia homolog 2 (Drosophila)	SIAH2	6478	-2.003799	0.701821
201814_at	TBC1 domain family. member 5	TBC1D5	9779	-2.004175	0.701821
220777_at	kinesin family member 13A	KIF13A	63971	-2.004408	0.701821
209402_s_at	solute carrier family 12 (potassium/chloride transporters). member 4	SLC12A4	6560	-2.004658	0.701821
209942_x_at	melanoma antigen family A. 3	MAGEA3	4102	-2.004926	0.701821
213334_x_at	UCHL5 interacting protein	UCHL5IP	55559	-2.005561	0.701821
205818_at	deleted in bladder cancer 1	DBC1	1620	-2.005688	0.701821
201528_at	replication protein A1. 70kDa	RPA1	6117	-2.006227	0.701821
221923_s_at	nucleophosmin (nucleolar phosphoprotein B23. numatrin)	NPM1	4869	-2.006951	0.701821
211651_s_at	laminin. beta 1	LAMB1	3912	-2.007124	0.701821
207756_at	---	---	---	-2.007216	0.701821
206563_s_at	opiate receptor-like 1	OPRL1	4987	-2.008492	0.701821
202431_s_at	v-myc myelocytomatosis viral oncogene homolog (avian)	MYC	4609	-2.008501	0.701821
65493_at	HEAT repeat containing 6	HEATR6	63897	-2.008826	0.701821
213993_at	spondin 1. extracellular matrix protein	SPON1	10418	-2.009684	0.701821
203493_s_at	centrosomal protein 57kDa	CEP57	9702	-2.009696	0.701821

222077_s_at	Rac GTPase activating protein 1	RACGAP1	29127	-2.011196	0.701821
207357_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-	GALNT10	55568	-2.0116	0.701821
221849_s_at	hypothetical protein BC002926	LOC90379	90379	-2.011694	0.701821
204101_at	myotubularin 1	MTM1	4534	-2.012369	0.701821
213349_at	transmembrane and coiled-coil domain family 1	TMCC1	23023	-2.012496	0.701821
216511_s_at	transcription factor 7-like 2 (T-cell specific. HMG-box)	TCF7L2	6934	-2.012646	0.701821
218052_s_at	ATPase type 13A1	ATP13A1	57130	-2.012863	0.701821
203196_at	ATP-binding cassette. sub-family C (CFTR/MRP). member 4	ABCC4	10257	-2.012868	0.701821
207264_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	KDELR3	11015	-2.014337	0.701821
38707_r_at	E2F transcription factor 4. p107/p130-binding	E2F4	1874	-2.0152	0.701821
213014_at	mitogen-activated protein kinase 8 interacting protein 1	MAPK8IP1	9479	-2.015757	0.701821
218536_at	MRS2-like. magnesium homeostasis factor (S. cerevisiae)	MRS2L	57380	-2.017258	0.701821
210687_at	carnitine palmitoyltransferase 1A (liver)	CPT1A	1374	-2.019357	0.701821
217457_s_at	RAP1. GTP-GDP dissociation stimulator 1	RAP1GDS1	5910	-2.019452	0.701821
65635_at	endo-beta-N-acetylglucosaminidase	FLJ21865	64772	-2.019874	0.701821
206916_x_at	tyrosine aminotransferase	TAT	6898	-2.020475	0.701821
217725_x_at	SERPINE1 mRNA binding protein 1	SERBP1	26135	-2.021433	0.701821
201594_s_at	protein phosphatase 4. regulatory subunit 1	PPP4R1	9989	-2.022356	0.701657
212738_at	Rho GTPase activating protein 19	ARHGAP19	84986	-2.022382	0.701657
202239_at	poly (ADP-ribose) polymerase family. member 4	PARP4	143	-2.022719	0.701657
206780_at	glutamate decarboxylase 2 (pancreatic islets and brain. 65kDa)	GAD2	2572	-2.02274	0.701657
218663_at	non-SMC condensin I complex. subunit G	NCAPG	64151	-2.022795	0.701657
205531_s_at	glutaminase 2 (liver. mitochondrial)	GLS2	27165	-2.022807	0.701657
212379_at	phosphoribosylglycinamide formyltransferase. phosphoribosylglycinamide synthetase. phosphorib	GART	2618	-2.023628	0.701657
208688_x_at	eukaryotic translation initiation factor 3. subunit B	EIF3B	8662	-2.024641	0.701657
217434_at	melanocortin 2 receptor (adrenocorticotropic hormone)	MC2R	4158	-2.02494	0.701657
210541_s_at	tripartite motif-containing 27	TRIM27	5987	-2.025389	0.701657
208454_s_at	plasma glutamate carboxypeptidase	PGCP	10404	-2.029082	0.701657
205489_at	crystallin. mu	CRYM	1428	-2.029929	0.701657
211525_s_at	glycoprotein V (platelet)	GP5	2814	-2.030884	0.701657
203871_at	SUMO1/sentrin/SMT3 specific peptidase 3	SENP3	26168	-2.031191	0.701657
221096_s_at	transmembrane and coiled-coil domains 6	TMCO6	55374	-2.031825	0.701657
218818_at	four and a half LIM domains 3	FHL3	2275	-2.03252	0.701657
206990_at	tenascin R (restrictin. janusin)	TNR	7143	-2.033148	0.701657
211865_s_at	fizzy/cell division cycle 20 related 1 (Drosophila)	FZR1	51343	-2.034789	0.701657
214331_at	Ts translation elongation factor. mitochondrial	TSFM	10102	-2.034896	0.701657
206695_x_at	zinc finger protein 43	ZNF43	7594	-2.035761	0.701657
220413_at	solute carrier family 39 (zinc transporter). member 2	SLC39A2	29986	-2.036782	0.701042
221328_at	claudin 17	CLDN17	26285	-2.037624	0.700417
202720_at	testis derived transcript (3 LIM domains)	TES	26136	-2.040733	0.697915
217370_x_at	fusion (involved in t(12;16) in malignant liposarcoma)	FUS	2521	-2.042745	0.697188
210658_s_at	golgi associated. gamma adaptin ear containing. ARF binding protein 2	GGA2	23062	-2.043191	0.696995
209645_s_at	aldehyde dehydrogenase 1 family. member B1	ALDH1B1	219	-2.044306	0.696807
202386_s_at	KIAA0430	KIAA0430	9665	-2.04456	0.696807
202320_at	general transcription factor IIIC. polypeptide 1. alpha 220kDa	GTF3C1	2975	-2.044952	0.696807
209856_x_at	abl interactor 2	ABI2	10152	-2.045973	0.696604
220842_at	Abelson helper integration site 1	AHI1	54806	-2.047505	0.696209
202396_at	transcription elongation regulator 1	TCERG1	10915	-2.048332	0.696209
210228_at	colony stimulating factor 2 (granulocyte-macrophage)	CSF2	1437	-2.04838	0.696209
219149_x_at	debranching enzyme homolog 1 (S. cerevisiae)	DBR1	51163	-2.048508	0.696209
205990_s_at	wingless-type MMTV integration site family. member 5A	WNT5A	7474	-2.048627	0.696209
208627_s_at	Y box binding protein 1	YBX1	4904	-2.049175	0.696209
218057_x_at	COX4 neighbor	COX4NB	10328	-2.050527	0.696105
201736_s_at	membrane-associated ring finger (C3HC4) 6	6-Mar	10299	-2.051522	0.696075
215955_x_at	Rho GTPase activating protein 26	ARHGAP26	23092	-2.05159	0.696075
215106_at	tetratricopeptide repeat domain 22	TTC22	55001	-2.051656	0.696075
215980_s_at	immunoglobulin mu binding protein 2	IGHMBP2	3508	-2.053084	0.695353
203654_s_at	coilin	COIL	8161	-2.053128	0.695353
217127_at	cystathionase (cystathionine gamma-lyase)	CTH	1491	-2.05326	0.695353
205393_s_at	CHK1 checkpoint homolog (S. pombe)	CHEK1	1111	-2.055081	0.694719
209871_s_at	amyloid beta (A4) precursor protein-binding. family A. member 2 (X11-like)	APBA2	321	-2.056033	0.694598
209650_s_at	TBC1 domain family. member 22A	TBC1D22A	25771	-2.056161	0.694598
219940_s_at	PCI domain containing 2	PCID2	55795	-2.056326	0.694598
212085_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator). member 6	SLC25A6	293	-2.056396	0.694598
212722_s_at	jumonji domain containing 6	JMJD6	23210	-2.057826	0.694598
216354_at	---	---	---	-2.057904	0.694598
205129_at	nucleophosmin/nucleoplasmin. 3	NPM3	10360	-2.05862	0.694598
209138_x_at	Immunoglobulin lambda locus	IGL@	3535	-2.058654	0.694598
209823_x_at	major histocompatibility complex. class II. DQ beta 1	HLA-DQB1	3119	-2.058661	0.694598
214096_s_at	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	6472	-2.059216	0.694598
37943_at	zinc finger. FYVE domain containing 26	ZFYVE26	23503	-2.059572	0.694598
213561_at	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A	25842	-2.060117	0.694598
219084_at	nuclear receptor binding SET domain protein 1	NSD1	64324	-2.060804	0.694598
203145_at	sperm associated antigen 5	SPAG5	10615	-2.061519	0.694215
219847_at	histone deacetylase 11	HDAC11	79885	-2.06153	0.694215
202293_at	stromal antigen 1	STAG1	10274	-2.062926	0.694181
201255_x_at	HLA-B associated transcript 3	BAT3	7917	-2.062969	0.694181
208274_at	oculomedin	OCLM	10896	-2.063432	0.694181
201146_at	nuclear factor (erythroid-derived 2)-like 2	NFE2L2	4780	-2.063551	0.694181
218348_s_at	zinc finger CCCH-type containing 7A	ZC3H7A	29066	-2.063924	0.694181
211953_s_at	RAN binding protein 5	RANBP5	3843	-2.064133	0.694181
203377_s_at	cell division cycle 40 homolog (S. cerevisiae)	CDC40	51362	-2.064164	0.694181
200779_at	activating transcription factor 4 (tax-responsive enhancer element B67)	ATF4	468	-2.064636	0.694181
200749_at	RAN. member RAS oncogene family	RAN	5901	-2.065283	0.694181
200992_at	importin 7	IPO7	10527	-2.066117	0.694015
211019_s_at	lanosterol synthase (2.3-oxidosqualene-lanosterol cyclase)	LSS	4047	-2.066148	0.694015

40020_at	cadherin. EGF LAG seven-pass G-type receptor 3 (flamingo homolog. Drosophila)	CELSR3	1951	-2.066292	0.694015
214407_x_at	glycophorin B (MNS blood group)	GYPB	2994	-2.066496	0.694015
207926_at	glycoprotein V (platelet)	GP5	2814	-2.067526	0.693989
217760_at	tripartite motif-containing 44	TRIM44	54765	-2.06793	0.693852
206037_at	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K. kyneurenine aminotransf	CCBL1	883	-2.068385	0.693852
221666_s_at	PYD and CARD domain containing	PYCARD	29108	-2.068809	0.693852
218878_s_at	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	SIRT1	23411	-2.069412	0.693852
212584_at	aquarius homolog (mouse)	AQR	9716	-2.069802	0.693852
216943_at	---	---	---	-2.070088	0.693852
218948_at	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	QRSL1	55278	-2.070823	0.693852
201790_s_at	7-dehydrocholesterol reductase	DHCR7	1717	-2.07159	0.693806
216784_at	CDNA: FLJ21769 fis. clone COLF7354	---	---	-2.07281	0.693092
209622_at	serine/threonine kinase 16	STK16	8576	-2.07351	0.692639
204423_at	muskelin 1. intracellular mediator containing kelch motifs	MKLN1	4289	-2.074993	0.691792
213234_at	KIAA1467	KIAA1467	57613	-2.075773	0.691708
209109_s_at	tetraspanin 6	TSPAN6	7105	-2.07582	0.691708
216633_s_at	phospholipase C. eta 1	PLCH1	23007	-2.076661	0.691657
206919_at	ELK4. ETS-domain protein (SRF accessory protein 1)	ELK4	2005	-2.077626	0.690921
203863_at	actinin. alpha 2	ACTN2	88	-2.077948	0.690921
209442_x_at	ankyrin 3. node of Ranvier (ankyrin G)	ANK3	288	-2.078631	0.690746
219041_s_at	replication initiator 1	REPIN1	29803	-2.078711	0.690746
203755_at	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	BUB1B	701	-2.078732	0.690746
208463_at	gamma-aminobutyric acid (GABA) A receptor. alpha 4	GABRA4	2557	-2.078739	0.690746
211643_x_at	Major histocompatibility complex. class I. C	HLA-C	3107	-2.078784	0.690746
215071_s_at	histone cluster 1. H2ac	HIST1H2AC	8334	-2.078902	0.690746
221297_at	G protein-coupled receptor. family C. group 5. member D	GPRC5D	55507	-2.07894	0.690746
219224_x_at	zinc finger protein 408	ZNF408	79797	-2.079864	0.690746
203363_s_at	KIAA0652	KIAA0652	9776	-2.079902	0.690746
212469_at	Nipped-B homolog (Drosophila)	NIPBL	25836	-2.081399	0.690746
214306_at	optic atrophy 1 (autosomal dominant)	OPA1	4976	-2.081402	0.690746
214888_at	calpain 2. (m/II) large subunit	CAPN2	824	-2.08157	0.690746
217761_at	acireductone dioxygenase 1	ADI1	55256	-2.081683	0.690746
208045_at	surfactant protein A binding protein	SPAR	9981	-2.082129	0.690746
216945_x_at	PAS domain containing serine/threonine kinase	PASK	23178	-2.082178	0.690746
200859_x_at	filamin A. alpha (actin binding protein 280)	FLNA	2316	-2.082903	0.690746
208340_at	Evolutionarily related interleukin-1beta converting enzyme	---	---	-2.083463	0.690746
211015_s_at	heat shock 70kDa protein 4	HSPA4	3308	-2.083981	0.690746
218080_x_at	Fas (TNFRSF6) associated factor 1	FAF1	11124	-2.084302	0.690746
219916_s_at	ring finger protein 39	RNF39	80352	-2.084744	0.690746
215942_s_at	G-2 and S-phase expressed 1	GTSE1	51512	-2.084968	0.690746
206070_s_at	EPH receptor A3	EPHA3	2042	-2.087681	0.690746
211952_at	RAN binding protein 5	RANBP5	3843	-2.087985	0.690746
218826_at	solute carrier family 35. member F2	SLC35F2	54733	-2.08825	0.690746
207081_s_at	phosphatidylinositol 4-kinase. catalytic. alpha	PI4KA	5297	-2.088335	0.690746
219253_at	transmembrane protein 185B	TMEM185B	79134	-2.088494	0.690746
206439_at	epiphycan	EPYC	1833	-2.088748	0.690746
214908_s_at	transformation/transcription domain-associated protein	TRRAP	8295	-2.088777	0.690746
200917_s_at	signal recognition particle receptor ('docking protein')	SRPR	6734	-2.089363	0.690746
219034_at	poly (ADP-ribose) polymerase family. member 16	PARP16	54956	-2.090203	0.690746
204986_s_at	TAO kinase 2	TAOK2	9344	-2.090474	0.690746
217742_s_at	WW domain containing adaptor with coiled-coil	WAC	51322	-2.09089	0.690746
210988_s_at	prune homolog (Drosophila)	PRUNE	58497	-2.092776	0.690746
202983_at	helicase-like transcription factor	HLTF	6596	-2.095223	0.690746
215962_at	EST clone 22453 mariner transposon Hsmar1 sequence	---	---	-2.095559	0.690746
209894_at	leptin receptor	LEPR	3953	-2.097299	0.689975
206020_at	suppressor of cytokine signaling 6	SOCS6	9306	-2.097476	0.689975
206643_at	histidine ammonia-lyase	HAL	3034	-2.098356	0.689932
210776_x_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3	6929	-2.100978	0.687862
200957_s_at	structure specific recognition protein 1	SSRP1	6749	-2.101388	0.687862
211971_s_at	leucine-rich PPR-motif containing	LRPPRC	10128	-2.101504	0.687862
202128_at	KIAA0317	KIAA0317	9870	-2.101795	0.687862
201073_s_at	SWI/SNF related. matrix associated. actin dependent regulator of chromatin. subfamily c. membe	SMARCC1	6599	-2.101842	0.687862
206295_at	interleukin 18 (interferon-gamma-inducing factor)	IL18	3606	-2.104929	0.686728
218103_at	FtsJ homolog 3 (E. coli)	FTSJ3	117246	-2.105221	0.686728
218819_at	integrator complex subunit 6	INTS6	26512	-2.105946	0.686728
200723_s_at	cell cycle associated protein 1	CAPRIN1	4076	-2.106325	0.686728
221956_at	leucine-rich repeats and calponin homology (CH) domain containing 4	LRCH4	4034	-2.106531	0.686728
203331_s_at	inositol polyphosphate-5-phosphatase. 145kDa	INPP5D	3635	-2.106672	0.686728
209416_s_at	fizzy/cell division cycle 20 related 1 (Drosophila)	FZR1	51343	-2.107804	0.686728
217723_x_at	---	---	---	-2.108104	0.686728
205166_at	calpain 5	CAPN5	726	-2.108491	0.686728
205468_s_at	interferon regulatory factor 5	IRF5	3663	-2.108715	0.686728
201674_s_at	A kinase (PRKA) anchor protein 1	AKAP1	8165	-2.108877	0.686728
213023_at	utrophin	UTRN	7402	-2.10932	0.686728
209144_s_at	core-binding factor. runt domain. alpha subunit 2; translocated to. 2	CBFA2T2	9139	-2.10975	0.686728
218879_s_at	methenyltetrahydrofolate synthetase domain containing	MTHFSD	64779	-2.110068	0.686728
206796_at	WNT1 inducible signaling pathway protein 1	WISP1	8840	-2.110411	0.686728
212360_at	adenosine monophosphate deaminase 2 (isoform L)	AMPD2	271	-2.111929	0.686728
215862_at	CDNA FLJ12301 fis. clone MAMMA1001858	---	---	-2.112094	0.686728
204018_x_at	hemoglobin. alpha 1 /// hemoglobin. alpha 2	HBA1 /// HBA	3039 /// 3040	-2.112173	0.686728
212878_s_at	kinesin light chain 1	KLC1	3831	-2.112648	0.686728
218832_x_at	arrestin. beta 1	ARRB1	408	-2.113476	0.686728
213155_at	WSC domain containing 1	WSCD1	23302	-2.113552	0.686728
202146_at	interferon-related developmental regulator 1	IFRD1	3475	-2.113685	0.686728
220632_s_at	protein-O-mannosyltransferase 2	POMT2	29954	-2.11401	0.686728
211123_at	solute carrier family 5 (sodium iodide symporter). member 5	SLC5A5	6528	-2.114491	0.686728

206438_x_at	tectonic family member 2	TCTN2	79867	-2.114874	0.686728
219508_at	glucosaminyl (N-acetyl) transferase 3. mucin type	GCNT3	9245	-2.11492	0.686728
204812_at	ZW10. kinetochore associated. homolog (Drosophila)	ZW10	9183	-2.116306	0.686728
209560_s_at	delta-like 1 homolog (Drosophila)	DLK1	8788	-2.116453	0.686728
205603_s_at	diaphanous homolog 2 (Drosophila)	DIAPH2	1730	-2.116627	0.686728
203239_s_at	CCR4-NOT transcription complex. subunit 3	CNOT3	4849	-2.117422	0.686728
206222_at	tumor necrosis factor receptor superfamily. member 10c. decoy without an intracellular domain	TNFRSF10C	8794	-2.117558	0.686728
204105_s_at	neuronal cell adhesion molecule	NRCAM	4897	-2.118006	0.686728
218272_at	hypothetical protein FLJ20699	FLJ20699	55020	-2.118028	0.686728
204729_s_at	syntaxin 1A (brain)	STX1A	6804	-2.119262	0.686728
219699_at	leucine-rich repeat LGI family. member 2	LGI2	55203	-2.119283	0.686728
206968_s_at	nuclear factor related to kappaB binding protein	NFRKB	4798	-2.119337	0.686728
209178_at	DEAH (Asp-Glu-Ala-His) box polypeptide 38	DHX38	9785	-2.119756	0.686728
1861_at	BCL2-antagonist of cell death	BAD	572	-2.12153	0.686542
214586_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37	2861	-2.121871	0.686542
218423_x_at	vacuolar protein sorting 54 homolog (S. cerevisiae)	VPS54	51542	-2.121902	0.686542
203004_s_at	myocyte enhancer factor 2D	MEF2D	4209	-2.122219	0.686542
220531_at	hypothetical protein FLJ14126	FLJ14126	79907	-2.122334	0.686542
216999_at	erythropoietin receptor	EPOR	2057	-2.122534	0.686542
218187_s_at	chromosome 8 open reading frame 33	C8orf33	65265	-2.122742	0.686542
212695_at	cryptochrome 2 (photolyase-like)	CRY2	1408	-2.123731	0.686542
219272_at	tripartite motif-containing 62	TRIM62	55223	-2.124852	0.686542
210419_at	BARX homeobox 2	BARX2	8538	-2.125676	0.686542
220872_at	hypothetical protein PRO2964	PRO2964	55415	-2.126031	0.686542
212145_at	mitochondrial ribosomal protein S27	MRPS27	23107	-2.126068	0.686542
204001_at	small nuclear RNA activating complex. polypeptide 3. 50kDa	SNAPC3	6619	-2.126071	0.686542
204800_s_at	dehydrogenase/reductase (SDR family) member 12	DHRS12	79758	-2.130237	0.686542
215108_x_at	TOX high mobility group box family member 3	TOX3	27324	-2.130624	0.686542
202922_at	glutamate-cysteine ligase. catalytic subunit	GCLC	2729	-2.13114	0.686542
218898_at	family with sequence similarity 57. member A	FAM57A	79850	-2.131284	0.686542
213410_at	chromosome 10 open reading frame 137	C10orf137	26098	-2.131417	0.686542
221668_s_at	dynein. axonemal. intermediate chain 2	DNAI2	64446	-2.132977	0.686542
213330_s_at	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1	10963	-2.133426	0.686542
215427_s_at	zinc finger. CCHC domain containing 14	ZCCHC14	23174	-2.133719	0.686542
202719_s_at	testis derived transcript (3 LIM domains)	TES	26136	-2.134118	0.686542
218156_s_at	TSR1. 20S rRNA accumulation. homolog (S. cerevisiae)	TSR1	55720	-2.135615	0.686542
214300_s_at	topoisomerase (DNA) III alpha	TOP3A	7156	-2.135752	0.686542
202557_at	stress 70 protein chaperone. microsome-associated. 60kDa	STCH	6782	-2.135785	0.686542
215707_s_at	prion protein (p27-30) (Creutzfeldt-Jakob disease. Gerstmann-Strausler-Scheinker syndrome. fat	PRNP	5621	-2.136941	0.686542
202062_s_at	sel-1 suppressor of lin-12-like (C. elegans)	SEL1L	6400	-2.136946	0.686542
203334_at	DEAH (Asp-Glu-Ala-His) box polypeptide 8	DHX8	1659	-2.136985	0.686542
206053_at	zinc finger protein 510	ZNF510	22869	-2.137601	0.686542
213329_at	SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	23380	-2.1388	0.686542
209206_at	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	SEC22B	9554	-2.138914	0.686542
203515_s_at	phosphomevalonate kinase	PMVK	10654	-2.139167	0.686542
206523_at	pleckstrin homology. Sec7 and coiled-coil domains 3	PSCD3	9265	-2.140126	0.686542
222094_at	sulfotransferase family. cytosolic. 1A. phenol-preferring. member 3 /// sulfotransferase family. cy	SULT1A3 /// S	445329 /// 68	-2.140386	0.686542
204984_at	glypican 4	GPC4	2239	-2.140567	0.686542
201843_s_at	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	2202	-2.140826	0.686542
211121_s_at	docking protein 1. 62kDa (downstream of tyrosine kinase 1)	DOK1	1796	-2.141491	0.686542
202978_s_at	CREB/ATF bZIP transcription factor	CREBZF	58487	-2.142049	0.686542
210040_at	solute carrier family 12. (potassium-chloride transporter) member 5	SLC12A5	57468	-2.142179	0.686542
210299_s_at	four and a half LIM domains 1	FHL1	2273	-2.142228	0.686542
201555_at	minichromosome maintenance complex component 3	MCM3	4172	-2.143043	0.686542
204366_s_at	general transcription factor IIIC. polypeptide 2. beta 110kDa	GTF3C2	2976	-2.144035	0.686542
202294_at	stromal antigen 1	STAG1	10274	-2.144257	0.686542
215003_at	DiGeorge syndrome critical region gene 9	DGCR9	25787	-2.145093	0.686542
217674_at	Transcribed locus	---	---	-2.145515	0.686542
203734_at	forkhead box J2	FOXJ2	55810	-2.145855	0.686542
208914_at	golgi associated. gamma adaptin ear containing. ARF binding protein 2	GGA2	23062	-2.146197	0.686542
215938_s_at	phospholipase A2. group VI (cytosolic. calcium-independent)	PLA2G6	8398	-2.146673	0.686542
213181_s_at	molybdenum cofactor synthesis 1	MOCS1	4337	-2.147583	0.686542
221806_s_at	SET domain containing 5	SETD5	55209	-2.147709	0.686542
207199_at	telomerase reverse transcriptase	TERT	7015	-2.148831	0.686542
213078_x_at	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase. eta)	AGPAT7	254531	-2.149065	0.686542
203204_s_at	jumonji domain containing 2A	JMJD2A	9682	-2.150122	0.686542
200815_s_at	platelet-activating factor acetylhydrolase. isoform Ib. alpha subunit 45kDa	PAFAH1B1	5048	-2.150662	0.686542
213137_s_at	protein tyrosine phosphatase. non-receptor type 2	PTPN2	5771	-2.150883	0.686542
216071_x_at	mediator complex subunit 12	MED12	9968	-2.151957	0.686542
219545_at	potassium channel tetramerisation domain containing 14	KCTD14	65987	-2.151986	0.686542
202012_s_at	exostoses (multiple) 2	EXT2	2132	-2.152582	0.686542
201803_at	polymerase (RNA) II (DNA directed) polypeptide B. 140kDa	POLR2B	5431	-2.153225	0.686542
218148_at	centromere protein T	CENPT	80152	-2.153251	0.686542
200027_at	asparaginyl-tRNA synthetase	NARS	4677	-2.154465	0.686542
209383_at	DNA-damage-inducible transcript 3	DDIT3	1649	-2.154921	0.686542
215087_at	chromosome 15 open reading frame 39	C15orf39	56905	-2.155535	0.686542
219436_s_at	endomucin	EMCN	51705	-2.155581	0.686542
210811_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	DDX49	54555	-2.155755	0.686542
201614_s_at	RuvB-like 1 (E. coli)	RUVBL1	8607	-2.156781	0.686542
212001_at	splicing factor. arginine/serine-rich 14	SFRS14	10147	-2.157099	0.686542
205714_s_at	zinc finger. MYND-type containing 10	ZMYND10	51364	-2.157685	0.686542
218770_s_at	transmembrane protein 39B	TMEM39B	55116	-2.158253	0.686542
200895_s_at	FK506 binding protein 4. 59kDa	FKBP4	2288	-2.159055	0.686542
207082_at	colony stimulating factor 1 (macrophage)	CSF1	1435	-2.159385	0.686542
206219_s_at	vav 1 guanine nucleotide exchange factor	VAV1	7409	-2.160304	0.686542
207262_at	apolipoprotein F	APOF	319	-2.162416	0.686542

215994_x_at	TBC1 domain family. member 9B (with GRAM domain)	TBC1D9B	23061	-2.162849	0.686542
213567_at	Clone 23728 mRNA sequence	---	---	-2.162979	0.686542
208250_s_at	deleted in malignant brain tumors 1	DMBT1	1755	-2.163094	0.686542
206816_s_at	sperm associated antigen 8	SPAG8	26206	-2.163388	0.686542
200976_s_at	Tax1 (human T-cell leukemia virus type I) binding protein 1	TAX1BP1	8887	-2.163838	0.686542
214759_at	Wilms tumor 1 associated protein	WTAP	9589	-2.16405	0.686542
202585_s_at	nuclear transcription factor. X-box binding 1	NFX1	4799	-2.16434	0.686542
220705_s_at	ADAM metallopeptidase with thrombospondin type 1 motif. 7	ADAMTS7	11173	-2.164575	0.686542
210220_at	frizzled homolog 2 (Drosophila)	FZD2	2535	-2.16495	0.686542
218466_at	TBC1 domain family. member 17	TBC1D17	79735	-2.165674	0.686542
206223_at	lemur tyrosine kinase 2	LMTK2	22853	-2.166302	0.686542
211845_at	poliovirus receptor-related 1 (herpesvirus entry mediator C)	PVRL1	5818	-2.166726	0.686542
213194_at	roundabout. axon guidance receptor. homolog 1 (Drosophila)	ROBO1	6091	-2.167464	0.686542
203117_s_at	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae)	PAN2	9924	-2.167475	0.686542
212227_x_at	eukaryotic translation initiation factor 1	EIF1	10209	-2.168232	0.686542
217806_s_at	polymerase (DNA-directed). delta interacting protein 2	POLDIP2	26073	-2.168344	0.686542
208209_s_at	complement component 4 binding protein. beta	C4BPB	725	-2.168382	0.686542
202193_at	LIM domain kinase 2	LIMK2	3985	-2.169083	0.686542
36612_at	KIAA0280	KIAA0280	23201	-2.170443	0.686542
204633_s_at	ribosomal protein S6 kinase. 90kDa. polypeptide 5	RPS6KA5	9252	-2.170597	0.686542
208251_at	potassium voltage-gated channel. Shaw-related subfamily. member 4	KCNC4	3749	-2.171525	0.686542
209054_s_at	Wolf-Hirschhorn syndrome candidate 1	WHSC1	7468	-2.172839	0.686542
216133_at	T cell receptor V alpha gene segment V-alpha-w23. clone IGRa01	---	---	-2.172954	0.686542
201925_s_at	CD55 molecule. decay accelerating factor for complement (Cromer blood group)	CD55	1604	-2.17338	0.686542
212507_at	transmembrane protein 131	TMEM131	23505	-2.173763	0.686542
222315_at	Transcribed locus	---	---	-2.174098	0.686542
212945_s_at	MAX gene associated	MGA	23269	-2.17413	0.686542
214665_s_at	calcium binding protein P22	CHP	11261	-2.174309	0.686542
201930_at	minichromosome maintenance complex component 6	MCM6	4175	-2.174455	0.686542
204760_s_at	thyroid hormone receptor. alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog. avia	NR1D1 /// THI	7067 /// 9572	-2.174969	0.686542
217791_s_at	aldehyde dehydrogenase 18 family. member A1	ALDH18A1	5832	-2.175986	0.686542
214404_x_at	SAM pointed domain containing ets transcription factor	SPDEF	25803	-2.176221	0.686542
219627_at	zinc finger family member 767	ZNF767	79970	-2.176367	0.686542
219578_s_at	cytoplasmic polyadenylation element binding protein 1	CPEB1	64506	-2.177137	0.686542
207268_x_at	abl interactor 2	ABI2	10152	-2.178838	0.686542
37232_at	KIAA0586	KIAA0586	9786	-2.179151	0.686542
212826_s_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator). member 6	SLC25A6	293	-2.179688	0.686542
207990_x_at	acrosomal vesicle protein 1	ACRV1	56	-2.180286	0.686542
214552_s_at	rabaptin. RAB GTPase binding effector protein 1	RABEP1	9135	-2.180834	0.686542
203841_x_at	microtubule-associated protein. RP/EB family. member 3	MAPRE3	22924	-2.181209	0.686542
218954_s_at	BRF2. subunit of RNA polymerase III transcription initiation factor. BRF1-like	BRF2	55290	-2.181907	0.686542
202444_s_at	ER lipid raft associated 1	ERLIN1	10613	-2.182987	0.686542
210718_s_at	ADP-ribosylation factor-like 17 pseudogene 1	ARL17P1	51326	-2.184163	0.686542
218168_s_at	chaperone. ABC1 activity of bc1 complex homolog (S. pombe)	CABC1	56997	-2.184196	0.686542
214323_s_at	UPF3 regulator of nonsense transcripts homolog A (yeast)	UPF3A	65110	-2.184649	0.686542
201195_s_at	solute carrier family 7 (cationic amino acid transporter. y+ system). member 5	SLC7A5	8140	-2.184749	0.686542
207915_at	---	---	---	-2.184892	0.686542
201651_s_at	protein kinase C and casein kinase substrate in neurons 2	PACSIN2	11252	-2.185535	0.686542
204373_s_at	centrosomal protein 350kDa	CEP350	9857	-2.185897	0.686542
219615_s_at	potassium channel. subfamily K. member 5	KCNK5	8645	-2.188829	0.686542
213378_s_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog. S. cerevisiae) //	DDX11 /// DD	1663 /// 4400	-2.189251	0.686542
203990_s_at	ubiquitously transcribed tetratricopeptide repeat. X chromosome	UTX	7403	-2.189485	0.686542
200806_s_at	heat shock 60kDa protein 1 (chaperonin)	HSPD1	3329	-2.189498	0.686542
204849_at	transcription factor-like 5 (basic helix-loop-helix)	TCFL5	10732	-2.18992	0.686542
208839_s_at	cullin-associated and neddylation-dissociated 1	CAND1	55832	-2.190477	0.686542
218889_at	nucleolar complex associated 3 homolog (S. cerevisiae)	NOC3L	64318	-2.191022	0.686542
204169_at	IMP (inosine monophosphate) dehydrogenase 1	IMPDH1	3614	-2.191228	0.686542
204502_at	SAM domain and HD domain 1	SAMHD1	25939	-2.191747	0.686542
213759_at	ADP-ribosylation factor-like 4C	ARL4C	10123	-2.192081	0.686542
54970_at	zinc finger. MIZ-type containing 2	ZMIZ2	83637	-2.19274	0.686542
213900_at	chromosome 9 open reading frame 61	C9orf61	9413	-2.193065	0.686542
211280_s_at	nuclear respiratory factor 1	NRF1	4899	-2.196489	0.686542
221868_at	poly(A) binding protein interacting protein 2B	PAIP2B	400961	-2.197351	0.686542
201561_s_at	calsyntenin 1	CLSTN1	22883	-2.19793	0.686542
219715_s_at	tyrosyl-DNA phosphodiesterase 1	TDP1	55775	-2.198645	0.686542
202100_at	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	5899	-2.199149	0.686542
205577_at	phosphorylase. glycogen; muscle (McArdle syndrome. glycogen storage disease type V)	PYGM	5837	-2.199636	0.686542
215696_s_at	SEC16 homolog A (S. cerevisiae)	SEC16A	9919	-2.2018	0.686542
208346_at	pro-platelet basic protein-like 2	PPBPL2	10895	-2.202144	0.686542
203623_at	plexin A3	PLXNA3	55558	-2.203018	0.686542
201385_at	DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	1665	-2.203038	0.686542
214934_at	ATPase. class II. type 9B	ATP9B	374868	-2.203082	0.686542
215481_s_at	peroxisomal biogenesis factor 5	PEX5	5830	-2.203987	0.686542
208117_s_at	LAS1-like (S. cerevisiae)	LAS1L	81887	-2.205221	0.686542
216277_at	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	699	-2.20638	0.686542
205080_at	retinoic acid receptor. beta	RARB	5915	-2.207232	0.686542
214484_s_at	opioid receptor. sigma 1	OPRS1	10280	-2.207807	0.686542
215180_at	MRNA full length insert cDNA clone EUROIMAGE 897021	---	---	-2.208227	0.686542
214848_at	Clone 23548 mRNA sequence	---	---	-2.211651	0.686542
200866_s_at	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	PSAP	5660	-2.212461	0.686542
204355_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	DHX30	22907	-2.212603	0.686542
215258_at	cell adhesion molecule 4	CADM4	199731	-2.212824	0.686542
202547_s_at	Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	8874	-2.213502	0.686542
203611_at	telomeric repeat binding factor 2	TERF2	7014	-2.214031	0.686542
210337_s_at	ATP citrate lyase	ACLY	47	-2.214344	0.686542
210812_at	X-ray repair complementing defective repair in Chinese hamster cells 4	XRCC4	7518	-2.214427	0.686542

207711_at	chromosome 20 open reading frame 117	C20orf117	140710	-2.214452	0.686542
203513_at	spastic paraplegia 11 (autosomal recessive)	SPG11	80208	-2.2147	0.686542
221812_at	F-box protein 42	FBXO42	54455	-2.214808	0.686542
221121_at	chromosome X open reading frame 48	CXorf48	54967	-2.215704	0.686542
208368_s_at	breast cancer 2. early onset	BRCA2	675	-2.216422	0.686542
202911_at	mutS homolog 6 (E. coli)	MSH6	2956	-2.216674	0.686542
207529_at	defensin. alpha 5. Paneth cell-specific	DEFA5	1670	-2.217038	0.686542
210958_s_at	microtubule associated serine/threonine kinase family member 4	MAST4	375449	-2.217666	0.686542
213530_at	RAB3 GTPase activating protein subunit 1 (catalytic)	RAB3GAP1	22930	-2.21794	0.686542
218399_s_at	cell division cycle associated 4	CDCA4	55038	-2.218148	0.686542
220435_at	solute carrier family 30. member 10	SLC30A10	55532	-2.218493	0.686542
217678_at	solute carrier family 7. (cationic amino acid transporter. y+ system) member 11	SLC7A11	23657	-2.219935	0.686542
219027_s_at	myosin IXA	MYO9A	4649	-2.220165	0.686542
204584_at	L1 cell adhesion molecule	L1CAM	3897	-2.220599	0.686542
206414_s_at	development and differentiation enhancing factor 2	DDEF2	8853	-2.220922	0.686542
217954_s_at	PHD finger protein 3	PHF3	23469	-2.221766	0.686542
207620_s_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK	8573	-2.221926	0.686542
215832_x_at	phosphatidylinositol binding clathrin assembly protein	PICALM	8301	-2.22245	0.686542
214849_at	potassium channel tetramerisation domain containing 20	KCTD20	222658	-2.223403	0.686542
216491_x_at	immunoglobulin heavy constant mu	IGHM	3507	-2.225147	0.686542
206231_at	potassium intermediate/small conductance calcium-activated channel. subfamily N. member 1	KCNN1	3780	-2.225443	0.686542
203068_at	kelch-like 21 (Drosophila)	KLHL21	9903	-2.225494	0.686542
201713_s_at	RAN binding protein 2	RANBP2	5903	-2.226792	0.686542
218009_s_at	protein regulator of cytokinesis 1	PRC1	9055	-2.227348	0.686542
217295_at	mucin 8	MUC8	4590	-2.227474	0.686542
211671_s_at	nuclear receptor subfamily 3. group C. member 1 (glucocorticoid receptor)	NR3C1	2908	-2.228221	0.686542
220048_at	ectodysplasin A receptor	EDAR	10913	-2.229226	0.686542
212781_at	retinoblastoma binding protein 6	RBBP6	5930	-2.229234	0.686542
206817_x_at	trinucleotide repeat containing 4	TNRC4	11189	-2.234329	0.686542
211938_at	eukaryotic translation initiation factor 4B	EIF4B	1975	-2.234651	0.686542
217715_x_at	---	---	---	-2.234661	0.686542
205437_at	zinc finger protein 211	ZNF211	10520	-2.235113	0.686542
220868_s_at	solute carrier family 7. (neutral amino acid transporter. y+ system) member 10	SLC7A10	56301	-2.236332	0.686542
202807_s_at	target of myb1 (chicken)	TOM1	10043	-2.236589	0.686542
210420_at	solute carrier family 24 (sodium/potassium/calcium exchanger). member 1	SLC24A1	9187	-2.23922	0.686542
201905_s_at	CTD (carboxy-terminal domain. RNA polymerase II. polypeptide A) small phosphatase-like	CTDSPL	10217	-2.23956	0.686542
218636_s_at	mannosidase. alpha. class 1B. member 1	MAN1B1	11253	-2.239969	0.686542
210064_s_at	uroplakin 1B	UPK1B	7348	-2.240195	0.686542
203859_s_at	paralemmin	PALM	5064	-2.241415	0.686542
219832_s_at	homeobox C13	HOXC13	3229	-2.241665	0.686542
200687_s_at	splicing factor 3b. subunit 3. 130kDa	SF3B3	23450	-2.242182	0.686542
209267_s_at	solute carrier family 39 (zinc transporter). member 8	SLC39A8	64116	-2.242247	0.686542
208623_s_at	ezrin	EZR	7430	-2.243041	0.686542
206052_s_at	stem-loop (histone) binding protein	SLBP	7884	-2.243111	0.686542
215039_at	Hypothetical protein LOC339524	LOC339524	339524	-2.243978	0.686542
221939_at	Yip1 domain family. member 2	YIPF2	78992	-2.245067	0.686542
213304_at	KIAA0423	KIAA0423	23116	-2.245211	0.686542
204370_at	CLP1. cleavage and polyadenylation factor I subunit. homolog (S. cerevisiae)	CLP1	10978	-2.245755	0.686542
201583_s_at	Sec23 homolog B (S. cerevisiae)	SEC23B	10483	-2.246997	0.686542
213436_at	cannabinoid receptor 1 (brain)	CNR1	1268	-2.247831	0.686542
219611_s_at	coiled-coil domain containing 21	CCDC21	64793	-2.248277	0.686542
212352_s_at	transmembrane emp24-like trafficking protein 10 (yeast)	TMED10	10972	-2.249222	0.686542
222078_at	Transcribed locus	---	---	-2.250674	0.686542
206260_at	transglutaminase 4 (prostate)	TGM4	7047	-2.251007	0.686542
203338_at	protein phosphatase 2. regulatory subunit B'. epsilon isoform	PPP2R5E	5529	-2.25102	0.686542
209318_x_at	pleiomorphic adenoma gene-like 1	PLAGL1	5325	-2.251729	0.686542
203777_s_at	ribosomal protein S6 kinase. 70kDa. polypeptide 2	RPS6KB2	6199	-2.252934	0.686542
216399_s_at	S phase cyclin A-associated protein in the ER	SCAPER	49855	-2.256001	0.686542
208227_x_at	ADAM metallopeptidase domain 22	ADAM22	53616	-2.256773	0.686542
208160_at	hypothetical protein FLJ10232	FLJ10232	55099	-2.25808	0.685974
207722_s_at	BTB (POZ) domain containing 2	BTBD2	55643	-2.258385	0.685974
203083_at	thrombospondin 2	THBS2	7058	-2.259101	0.685667
207752_x_at	proline-rich protein BstNI subfamily 1	PRB1	5542	-2.259564	0.685566
213323_s_at	zinc finger CCCH-type containing 7B	ZC3H7B	23264	-2.260079	0.685408
219048_at	phosphatidylinositol glycan anchor biosynthesis. class N	PIGN	23556	-2.260154	0.685408
206882_at	solute carrier family 1 (high affinity aspartate/glutamate transporter). member 6	SLC1A6	6511	-2.260321	0.685408
206960_at	G protein-coupled receptor 23	GPR23	2846	-2.260431	0.685408
220939_s_at	dipeptidyl-peptidase 8	DPP8	54878	-2.261081	0.685408
206798_x_at	deleted in lung and esophageal cancer 1	DLEC1	9940	-2.261741	0.685408
206942_s_at	pro-melanin-concentrating hormone	PMCH	5367	-2.264922	0.685365
211815_s_at	golgi associated. gamma adaptin ear containing. ARF binding protein 3	GGA3	23163	-2.26522	0.685365
212674_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	DHX30	22907	-2.265978	0.685365
211207_s_at	acyl-CoA synthetase long-chain family member 6	ACSL6	23305	-2.266437	0.685365
202309_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1. methenyltetrahydrofolate cycl	MTHFD1	4522	-2.266963	0.685365
203636_at	midline 1 (Opitz/BBB syndrome)	MID1	4281	-2.267064	0.685365
222353_at	LIM domains containing 1	LIMD1	8994	-2.268024	0.685365
208225_at	fibroblast growth factor receptor 2 (bacteria-expressed kinase. keratinocyte growth factor recept	FGFR2	2263	-2.268229	0.685365
203077_s_at	SMAD family member 2	SMAD2	4087	-2.268909	0.685365
206419_at	RAR-related orphan receptor C	RORC	6097	-2.270099	0.685365
209291_at	inhibitor of DNA binding 4. dominant negative helix-loop-helix protein	ID4	3400	-2.270506	0.685365
216676_x_at	killer cell immunoglobulin-like receptor. three domains. long cytoplasmic tail. 3	KIR3DL3	115653	-2.271168	0.685365
211185_s_at	splicing factor 3b. subunit 1. 155kDa	SF3B1	23451	-2.271568	0.685365
211599_x_at	met proto-oncogene (hepatocyte growth factor receptor)	MET	4233	-2.271828	0.685365
206412_at	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	FER	2241	-2.272748	0.685365
214387_x_at	surfactant. pulmonary-associated protein C	SFTPC	6440	-2.272893	0.685365
213318_s_at	HLA-B associated transcript 3	BAT3	7917	-2.273493	0.685365

221870_at	EH-domain containing 2	EHD2	30846	-2.273936	0.685365
210157_at	chromosome 19 open reading frame 2	C19orf2	8725	-2.274789	0.685365
214198_s_at	DiGeorge syndrome critical region gene 2	DGCR2	9993	-2.275103	0.685365
216825_s_at	myeloproliferative leukemia virus oncogene	MPL	4352	-2.275909	0.685365
215624_at	tuberous sclerosis 2	TSC2	7249	-2.277161	0.685365
202159_at	phenylalanyl-tRNA synthetase. alpha subunit	FARSA	2193	-2.277216	0.685365
201079_at	synaptogyrin 2	SYNGR2	9144	-2.277694	0.685365
222038_s_at	Non-metastatic cells 1. protein (NM23A) expressed in	NME1	4830	-2.27775	0.685365
206730_at	glutamate receptor. ionotrophic. AMPA 3	GRIA3	2892	-2.27797	0.685365
203902_at	hephaestin	HEPH	9843	-2.27797	0.685365
220206_at	zinc finger. MYM-type 1	ZMYM1	79830	-2.278194	0.685365
201490_s_at	peptidylprolyl isomerase F (cyclophilin F)	PPIF	10105	-2.279127	0.685365
218794_s_at	thioredoxin-like 4B	TXNL4B	54957	-2.279673	0.685365
206748_s_at	sperm associated antigen 9	SPAG9	9043	-2.280403	0.685365
213191_at	toll-like receptor adaptor molecule 1	TICAM1	148022	-2.280527	0.685365
220332_at	claudin 16	CLDN16	10686	-2.280852	0.685365
205282_at	low density lipoprotein receptor-related protein 8. apolipoprotein e receptor	LRP8	7804	-2.280869	0.685365
216155_at	CDNA: FLJ20890 fis. clone ADKA03323	---	---	-2.281237	0.685365
220124_at	giant axonal neuropathy (gigaxonin)	GAN	8139	-2.281394	0.685365
213511_s_at	myotubularin related protein 1	MTMR1	8776	-2.28229	0.685365
209424_s_at	alpha-methylacyl-CoA racemase	AMACR	23600	-2.282733	0.685365
209776_s_at	solute carrier family 19 (folate transporter). member 1	SLC19A1	6573	-2.283009	0.685365
207275_s_at	acyl-CoA synthetase long-chain family member 1	ACSL1	2180	-2.283874	0.685365
217532_x_at	Transcribed locus	---	---	-2.284628	0.685365
200000_s_at	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	PRPF8	10594	-2.285924	0.685365
201386_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	1665	-2.287825	0.685365
211199_s_at	inducible T-cell co-stimulator ligand	ICOSLG	23308	-2.288636	0.685365
205074_at	solute carrier family 22 (organic cation transporter). member 5	SLC22A5	6584	-2.289157	0.685365
200699_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDELR2	11014	-2.290323	0.685365
204077_x_at	ectonucleoside triphosphate diphosphohydrolase 4	ENTPD4	9583	-2.290761	0.685365
209256_s_at	KIAA0265 protein	KIAA0265	23008	-2.29189	0.685365
207865_s_at	bone morphogenetic protein 8b (osteogenic protein 2)	BMP8B	656	-2.292354	0.685365
210194_at	phospholipase A2 receptor 1. 180kDa	PLA2R1	22925	-2.292799	0.685365
218093_s_at	ankyrin repeat domain 10	ANKRD10	55608	-2.294319	0.685365
200860_s_at	CCR4-NOT transcription complex. subunit 1	CNOT1	23019	-2.294494	0.685365
202140_s_at	CDC-like kinase 3	CLK3	1198	-2.295039	0.685365
204374_s_at	galactokinase 1	GALK1	2584	-2.296676	0.685365
212331_at	retinoblastoma-like 2 (p130)	RBL2	5934	-2.296832	0.685365
212098_at	hypothetical protein LOC151162	LOC151162	151162	-2.297328	0.685365
211527_x_at	vascular endothelial growth factor A	VEGFA	7422	-2.297748	0.685365
215913_s_at	GULP. engulfment adaptor PTB domain containing 1	GULP1	51454	-2.298642	0.685365
203721_s_at	UTP18. small subunit (SSU) processome component. homolog (yeast)	UTP18	51096	-2.299919	0.685365
214840_at	target of myb1-like 2 (chicken)	TOM1L2	146691	-2.300746	0.685365
208030_s_at	adducin 1 (alpha)	ADD1	118	-2.301123	0.685365
211160_x_at	actinin. alpha 1	ACTN1	87	-2.303101	0.685365
215954_s_at	chromosome 19 open reading frame 29	C19orf29	58509	-2.303515	0.685365
210475_at	POU class 3 homeobox 1	POU3F1	5453	-2.304302	0.685365
219650_at	excision repair cross-complementing rodent repair deficiency. complementation group 6-like	ERCC6L	54821	-2.30513	0.685365
205935_at	forkhead box F1	FOXF1	2294	-2.306617	0.685365
201380_at	cartilage associated protein	CRTAP	10491	-2.306769	0.685365
209345_s_at	phosphatidylinositol 4-kinase type 2 alpha	PI4K2A	55361	-2.306846	0.685365
202186_x_at	protein phosphatase 2. regulatory subunit B'. alpha isoform	PPP2R5A	5525	-2.306997	0.685365
202407_s_at	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	PRPF31	26121	-2.308361	0.685365
212214_at	optic atrophy 1 (autosomal dominant)	OPA1	4976	-2.309132	0.685365
208918_s_at	NAD kinase	NADK	65220	-2.30924	0.685365
203315_at	NCK adaptor protein 2 /// similar to NCK adaptor protein 2	LOC729030 //	729030 /// 84	-2.309435	0.685365
220911_s_at	KIAA1305	KIAA1305	57523	-2.310209	0.685365
204824_at	endonuclease G	ENDOG	2021	-2.310731	0.685365
221987_s_at	TSR1. 20S rRNA accumulation. homolog (S. cerevisiae)	TSR1	55720	-2.31182	0.685365
211934_x_at	glucosidase. alpha; neutral AB	GANAB	23193	-2.311841	0.685365
205911_at	parathyroid hormone receptor 1	PTHR1	5745	-2.311931	0.685365
203743_s_at	thymine-DNA glycosylase	TDG	6996	-2.312533	0.685365
201516_at	spermidine synthase	SRM	6723	-2.314169	0.685365
200659_s_at	prohibitin	PHB	5245	-2.314251	0.685365
211391_s_at	POZ (BTB) and AT hook containing zinc finger 1	PATZ1	23598	-2.314692	0.685365
211852_s_at	attractin	ATRN	8455	-2.316475	0.685365
215072_x_at	chromosome 10 open reading frame 137	C10orf137	26098	-2.316519	0.685365
205236_x_at	superoxide dismutase 3. extracellular	SOD3	6649	-2.316625	0.685365
222161_at	N-acetylated alpha-linked acidic dipeptidase 2	NAALAD2	10003	-2.318389	0.685365
204119_s_at	adenosine kinase	ADK	132	-2.319495	0.685365
208694_at	protein kinase. DNA-activated. catalytic polypeptide	PRKDC	5591	-2.321562	0.685365
211519_s_at	kinesin family member 2C	KIF2C	11004	-2.32162	0.685365
210789_x_at	carcinoembryonic antigen-related cell adhesion molecule 3	CEACAM3	1084	-2.321977	0.685365
55065_at	MAP/microtubule affinity-regulating kinase 4	MARK4	57787	-2.323205	0.685365
216696_s_at	proline dehydrogenase (oxidase) 2	PRODH2	58510	-2.323785	0.685365
215644_at	zinc finger protein 518A	ZNF518A	9849	-2.324186	0.685365
215261_at	Clone 23578 mRNA sequence	---	---	-2.325709	0.685365
214511_x_at	Fc fragment of IgG. high affinity Ib. receptor (CD64)	FCGR1B	2210	-2.327473	0.685365
202679_at	Niemann-Pick disease. type C1	NPC1	4864	-2.328666	0.685365
210620_s_at	general transcription factor IIIC. polypeptide 2. beta 110kDa	GTF3C2	2976	-2.329217	0.685365
216389_s_at	WD repeat domain 23	WDR23	80344	-2.329373	0.685365
57516_at	zinc finger protein 764	ZNF764	92595	-2.3302	0.685365
211673_s_at	molybdenum cofactor synthesis 1	MOCS1	4337	-2.330765	0.685365
202009_at	twinfilin. actin-binding protein. homolog 2 (Drosophila)	TWF2	11344	-2.330858	0.685365
212739_s_at	non-metastatic cells 4. protein expressed in	NME4	4833	-2.331026	0.685365
215379_x_at	immunoglobulin lambda locus /// immunoglobulin lambda variable 3-25 /// immunoglobulin lamb	IGL@ /// IGLJ	28793 /// 288	-2.333067	0.685365

218137_s_at	stromal membrane-associated protein 1	SMAP1	60682	-2.333254	0.685365
209582_s_at	CD200 molecule	CD200	4345	-2.333521	0.685365
203637_s_at	midline 1 (Opitz/BBB syndrome)	MID1	4281	-2.333611	0.685365
201802_at	solute carrier family 29 (nucleoside transporters). member 1	SLC29A1	2030	-2.334749	0.685365
218813_s_at	SH3-domain GRB2-like endophilin B2	SH3GLB2	56904	-2.334893	0.685365
202571_s_at	discs. large (Drosophila) homolog-associated protein 4	DLGAP4	22839	-2.3351	0.685365
209006_s_at	chromosome 1 open reading frame 63	C1orf63	57035	-2.335214	0.685365
220743_at	---	---	---	-2.33566	0.685365
215113_s_at	SUMO1/sentrin/SMT3 specific peptidase 3	SENP3	26168	-2.336442	0.685365
214550_s_at	transportin 3	TNPO3	23534	-2.338635	0.685365
214614_at	motor neuron and pancreas homeobox 1	MNX1	3110	-2.338754	0.685365
210500_at	---	---	---	-2.338995	0.685365
218639_s_at	ZXD family zinc finger C	ZXDC	79364	-2.339756	0.685365
214738_s_at	NIMA (never in mitosis gene a)- related kinase 9	NEK9	91754	-2.33984	0.685365
207635_s_at	potassium voltage-gated channel. subfamily H (eag-related). member 1	KCNH1	3756	-2.340166	0.685365
221056_x_at	epidermal growth factor receptor pathway substrate 15-like 1	EPS15L1	58513	-2.340366	0.685365
217855_x_at	stromal cell derived factor 4	SDF4	51150	-2.342152	0.685365
201941_at	carboxypeptidase D	CPD	1362	-2.343245	0.685365
203073_at	component of oligomeric golgi complex 2	COG2	22796	-2.344046	0.685365
210962_s_at	A kinase (PRKA) anchor protein (yotiao) 9	AKAP9	10142	-2.34415	0.685365
216052_x_at	artemin	ARTN	9048	-2.345033	0.685365
204043_at	transcobalamin II; macrocytic anemia	TCN2	6948	-2.346284	0.685365
210930_s_at	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2. neuro/glioblastoma derived oncogen	ERBB2	2064	-2.348138	0.685365
218221_at	aryl hydrocarbon receptor nuclear translocator	ARNT	405	-2.348315	0.685365
201421_s_at	WD repeat domain 77	WDR77	79084	-2.349401	0.685365
219202_at	rhomboid 5 homolog 2 (Drosophila)	RHBDF2	79651	-2.349621	0.685365
220232_at	stearoyl-CoA desaturase 5	SCD5	79966	-2.350153	0.685365
221404_at	interleukin 1 family. member 6 (epsilon)	IL1F6	27179	-2.350505	0.685365
206333_at	musashi homolog 1 (Drosophila)	MSI1	4440	-2.350669	0.685365
218645_at	zinc finger protein 277	ZNF277	11179	-2.352026	0.685365
201289_at	cysteine-rich. angiogenic inducer. 61	CYR61	3491	-2.352145	0.685365
221755_at	EH domain binding protein 1-like 1	EHBP1L1	254102	-2.352364	0.685365
219720_s_at	chromosome 14 open reading frame 118	C14orf118	55668	-2.354206	0.685365
202054_s_at	aldehyde dehydrogenase 3 family. member A2	ALDH3A2	224	-2.354724	0.685365
210741_at	Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	23365	-2.355883	0.685365
208625_s_at	eukaryotic translation initiation factor 4 gamma. 1	EIF4G1	1981	-2.357007	0.685365
203620_s_at	FCH and double SH3 domains 2	FCHSD2	9873	-2.357986	0.685365
220060_s_at	chromosome 12 open reading frame 48	C12orf48	55010	-2.359063	0.685365
212310_at	melanoma inhibitory activity family. member 3	MIA3	375056	-2.360437	0.685365
201689_s_at	tumor protein D52	TPD52	7163	-2.360594	0.685365
221314_at	growth differentiation factor 9	GDF9	2661	-2.361871	0.685365
210463_x_at	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	TRMT1	55621	-2.362536	0.685365
219829_at	integrin beta 1 binding protein (melusin) 2	ITGB1BP2	26548	-2.36288	0.685365
211205_x_at	phosphatidylinositol-4-phosphate 5-kinase. type I. alpha	PIP5K1A	8394	-2.363046	0.685365
215217_at	---	---	---	-2.364227	0.685365
202642_s_at	transformation/transcription domain-associated protein	TRRAP	8295	-2.364658	0.685365
215847_at	hypothetical protein LOC283755	LOC283755	283755	-2.365307	0.685365
216860_s_at	growth differentiation factor 11	GDF11	10220	-2.365759	0.685365
207074_s_at	solute carrier family 18 (vesicular monoamine). member 1	SLC18A1	6570	-2.36641	0.685365
212387_at	transcription factor 4	TCF4	6925	-2.366796	0.685365
206209_s_at	carbonic anhydrase IV	CA4	762	-2.368052	0.685365
209729_at	growth arrest-specific 2 like 1	GAS2L1	10634	-2.369159	0.685365
215928_at	CDNA FLJ12130 fis. clone MAMMA1000251	---	---	-2.36917	0.685365
200939_s_at	arginine-glutamic acid dipeptide (RE) repeats	RERE	473	-2.369223	0.685365
203660_s_at	pericentrin (kendrin)	PCNT	5116	-2.370059	0.685365
218412_s_at	GTF2I repeat domain containing 1	GTF2IRD1	9569	-2.371453	0.685365
221490_at	ubiquitin associated protein 1	UBAP1	51271	-2.37163	0.685365
220095_at	chromosome 9 open reading frame 39	C9orf39	54875	-2.373883	0.685365
207205_at	carcinoembryonic antigen-related cell adhesion molecule 4	CEACAM4	1089	-2.374159	0.685365
219481_at	tetratricopeptide repeat domain 13	TTC13	79573	-2.375585	0.685365
213845_at	glutamate receptor. ionotropic. kainate 2	GRIK2	2898	-2.375823	0.685365
212574_x_at	chromosome 19 open reading frame 6	C19orf6	91304	-2.37745	0.685365
201542_at	SAR1 gene homolog A (S. cerevisiae)	SAR1A	56681	-2.378148	0.685365
206470_at	plexin C1	PLXNC1	10154	-2.378448	0.685365
203764_at	discs. large homolog 7 (Drosophila)	DLG7	9787	-2.378796	0.685365
217935_s_at	ubiquinol-cytochrome c reductase complex chaperone. CBP3 homolog (yeast)	UQCC	55245	-2.378985	0.685365
208275_x_at	undifferentiated embryonic cell transcription factor 1	UTF1	8433	-2.379448	0.685365
212065_s_at	ubiquitin specific peptidase 34	USP34	9736	-2.3801	0.685365
221916_at	neurofilament. light polypeptide 68kDa	NEFL	4747	-2.380808	0.685365
211807_x_at	protocadherin gamma subfamily B. 5	PCDHGB5	56101	-2.381777	0.685365
206845_s_at	ring finger protein 40	RNF40	9810	-2.38221	0.685365
212219_at	proteasome (prosome. macropain) activator subunit 4	PSME4	23198	-2.382821	0.685365
209684_at	Ras and Rab interactor 2	RIN2	54453	-2.386389	0.685365
213707_s_at	distal-less homeobox 5	DLX5	1749	-2.386812	0.685365
208619_at	damage-specific DNA binding protein 1. 127kDa	DDB1	1642	-2.3882	0.685365
218252_at	cytoskeleton associated protein 2	CKAP2	26586	-2.388424	0.685365
212846_at	ribosomal RNA processing 1 homolog B (S. cerevisiae)	RRP1B	23076	-2.389091	0.685365
212072_s_at	casein kinase 2. alpha 1 polypeptide	CSNK2A1	1457	-2.389376	0.685365
218596_at	TBC1 domain family. member 13	TBC1D13	54662	-2.390208	0.685365
218918_at	mannosidase. alpha. class 1C. member 1	MAN1C1	57134	-2.39499	0.685365
44146_at	glucocorticoid modulatory element binding protein 2	GMEB2	26205	-2.396197	0.685365
215119_at	myosin XVI	MYO16	23026	-2.397469	0.685365
214721_x_at	CDC42 effector protein (Rho GTPase binding) 4	CDC42EP4	23580	-2.398135	0.685365
202798_at	SEC24 related gene family. member B (S. cerevisiae)	SEC24B	10427	-2.398942	0.685365
218656_s_at	lipoma HMGIC fusion partner	LHFP	10186	-2.399281	0.685365
207575_at	golgin-like protein /// golgi autoantigen. golgin subfamily a. 6 /// similar to Golgin subfamily A m	GOLGA /// GO	342096 /// 55	-2.400009	0.685365

210017_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	MALT1	10892	-2.402101	0.685365
201929_s_at	plakophilin 4	PKP4	8502	-2.402221	0.685365
218803_at	checkpoint with forkhead and ring finger domains	CHFR	55743	-2.403077	0.685365
219378_at	NMDA receptor regulated 1-like	NARG1L	79612	-2.403949	0.685365
209929_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells. kinase gamma	IKBKG	8517	-2.405699	0.685365
214513_s_at	cAMP responsive element binding protein 1	CREB1	1385	-2.406554	0.685365
202787_s_at	mitogen-activated protein kinase-activated protein kinase 3	MAPKAPK3	7867	-2.407131	0.685365
215104_at	nuclear receptor interacting protein 2	NRIP2	83714	-2.407308	0.685365
211555_s_at	guanylate cyclase 1. soluble. beta 3	GUCY1B3	2983	-2.408504	0.685365
207983_s_at	stromal antigen 2	STAG2	10735	-2.409478	0.685365
211711_s_at	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	PTEN	5728	-2.410335	0.685365
221038_at	PRO1942	---	---	-2.41101	0.685365
212556_at	scribbled homolog (Drosophila)	SCRIB	23513	-2.411883	0.685365
209784_s_at	jagged 2	JAG2	3714	-2.412885	0.685365
213682_at	nucleoporin 50kDa	NUP50	10762	-2.413768	0.685365
213099_at	angel homolog 1 (Drosophila)	ANGEL1	23357	-2.414372	0.685365
207020_at	heat shock transcription factor 2 binding protein	HSF2BP	11077	-2.415318	0.685365
200614_at	clathrin. heavy chain (Hc)	CLTC	1213	-2.415906	0.685365
209000_s_at	septin 8	8-Sep	23176	-2.416741	0.685365
210318_at	retinol binding protein 3. interstitial	RBP3	5949	-2.421761	0.685365
211089_s_at	NIMA (never in mitosis gene a)-related kinase 3	NEK3	4752	-2.422279	0.685365
59999_at	hypoxia-inducible factor 1. alpha subunit inhibitor	HIF1AN	55662	-2.423303	0.685365
212563_at	block of proliferation 1 /// similar to block of proliferation 1	BOP1 /// LOC	23246 /// 727	-2.424067	0.685365
209055_s_at	CDC5 cell division cycle 5-like (S. pombe)	CDC5L	988	-2.425212	0.685365
221733_s_at	G patch domain containing 4	GPATCH4	54865	-2.429712	0.685365
204894_s_at	amine oxidase. copper containing 3 (vascular adhesion protein 1)	AOC3	8639	-2.430867	0.685365
220819_at	FERM domain containing 1	FRMD1	79981	-2.432723	0.685365
206110_at	histone cluster 1. H3h	HIST1H3H	8357	-2.432928	0.685365
207317_s_at	calsequestrin 2 (cardiac muscle)	CASQ2	845	-2.43558	0.685365
214429_at	myotubularin related protein 6	MTMR6	9107	-2.437402	0.685344
211913_s_at	c-mer proto-oncogene tyrosine kinase	MERTK	10461	-2.437435	0.685344
218595_s_at	HEAT repeat containing 1	HEATR1	55127	-2.437683	0.685344
201997_s_at	spen homolog. transcriptional regulator (Drosophila)	SPEN	23013	-2.438393	0.685344
203471_s_at	pleckstrin	PLEK	5341	-2.438571	0.685344
219318_x_at	mediator complex subunit 31	MED31	51003	-2.439188	0.685344
207391_s_at	phosphatidylinositol-4-phosphate 5-kinase. type I. alpha	PIP5K1A	8394	-2.439928	0.685344
221195_at	PTD016 protein	LOC51136	51136	-2.440993	0.685344
202314_at	cytochrome P450. family 51. subfamily A. polypeptide 1	CYP51A1	1595	-2.44138	0.685344
211447_s_at	phosphodiesterase 4A. cAMP-specific (phosphodiesterase E2 dunce homolog. Drosophila)	PDE4A	5141	-2.441963	0.685344
220182_at	solute carrier family 25 (mitochondrial carrier; phosphate carrier). member 23	SLC25A23	79085	-2.442225	0.685344
202021_x_at	eukaryotic translation initiation factor 1	EIF1	10209	-2.442766	0.685344
202819_s_at	transcription elongation factor B (SIII). polypeptide 3 (110kDa. elongin A)	TCEB3	6924	-2.44313	0.685344
220325_at	TAF7-like RNA polymerase II. TATA box binding protein (TBP)-associated factor. 50kDa	TAF7L	54457	-2.445122	0.685344
221853_s_at	NODAL modulator 1 /// NODAL modulator 2 /// NODAL modulator 3	NOMO1 /// NC	23420 /// 283	-2.445609	0.685344
1494_f_at	cytochrome P450. family 2. subfamily A. polypeptide 6	CYP2A6	1548	-2.446052	0.685344
211101_x_at	leukocyte immunoglobulin-like receptor. subfamily A (with TM domain). member 2	LILRA2	11027	-2.446908	0.685344
201571_s_at	dCMP deaminase	DCTD	1635	-2.449242	0.685344
204040_at	ring finger protein 144A	RNF144A	9781	-2.449365	0.685344
214994_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3F	APOBEC3F	200316	-2.449632	0.685344
206085_s_at	cystathionase (cystathionine gamma-lyase)	CTH	1491	-2.452718	0.685344
211501_s_at	eukaryotic translation initiation factor 3. subunit B	EIF3B	8662	-2.452858	0.685344
218771_at	pantothenate kinase 4	PANK4	55229	-2.454032	0.685344
215857_at	nicalin homolog (zebrafish)	NCLN	56926	-2.454363	0.685344
210995_s_at	tripartite motif-containing 23	TRIM23	373	-2.455597	0.685344
217424_at	MRNA; cDNA DKFZp434L098 (from clone DKFZp434L098)	---	---	-2.456005	0.685344
201282_at	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	OGDH	4967	-2.45629	0.685344
207254_at	solute carrier family 15 (oligopeptide transporter). member 1	SLC15A1	6564	-2.457005	0.685344
200793_s_at	aconitase 2. mitochondrial	ACO2	50	-2.45721	0.685344
214310_s_at	zinc finger protein-like 1	ZFPL1	7542	-2.457213	0.685344
219904_at	zinc finger and SCAN domain containing 5	ZSCAN5	79149	-2.457399	0.685344
210754_s_at	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	4067	-2.457399	0.685344
208787_at	mitochondrial ribosomal protein L3	MRPL3	11222	-2.458274	0.685344
221418_s_at	mediator complex subunit 16	MED16	10025	-2.45877	0.685344
219610_at	Rho-guanine nucleotide exchange factor	RGNEF	64283	-2.45887	0.685344
218782_s_at	ATPase family. AAA domain containing 2	ATAD2	29028	-2.459308	0.685344
210473_s_at	G protein-coupled receptor 125	GPR125	166647	-2.459875	0.685344
201946_s_at	chaperonin containing TCP1. subunit 2 (beta)	CCT2	10576	-2.45999	0.685344
209247_s_at	ATP-binding cassette. sub-family F (GCN20). member 2	ABCF2	10061	-2.460919	0.685344
218236_s_at	protein kinase D3	PRKD3	23683	-2.461095	0.685344
212306_at	cytoplasmic linker associated protein 2	CLASP2	23122	-2.461105	0.685344
214030_at	hypothetical protein DKFZp667G2110	DKFZp667G21	131544	-2.461612	0.685344
215272_at	transcriptional adaptor 3 (NGG1 homolog. yeast)-like	TADA3L	10474	-2.462776	0.685344
215551_at	estrogen receptor 1	ESR1	2099	-2.462889	0.685344
222006_at	Leucine zipper-EF-hand containing transmembrane protein 1	LETM1	3954	-2.463389	0.685344
212997_s_at	tousled-like kinase 2	TLK2	11011	-2.46341	0.685344
213049_at	GTPase activating Rap/RanGAP domain-like 1	GARNL1	253959	-2.464024	0.685344
208595_s_at	methyl-CpG binding domain protein 1	MBD1	4152	-2.464419	0.685344
201401_s_at	adrenergic. beta. receptor kinase 1	ADRBK1	156	-2.469221	0.685344
209390_at	tuberous sclerosis 1	TSC1	7248	-2.469378	0.685344
214604_at	homeobox D11	HOXD11	3237	-2.469687	0.685344
218189_s_at	N-acetylneuraminic acid synthase (sialic acid synthase)	NANS	54187	-2.47103	0.685344
211256_x_at	butyrophilin. subfamily 2. member A1	BTN2A1	11120	-2.471393	0.685344
213739_at	CDNA clone IMAGE:4801297	---	---	-2.472666	0.685344
203445_s_at	CTD (carboxy-terminal domain. RNA polymerase II. polypeptide A) small phosphatase 2	CTDSP2	10106	-2.473639	0.685344
216251_s_at	tubulin tyrosine ligase-like family. member 12	TTLL12	23170	-2.474117	0.685344
202633_at	topoisomerase (DNA) II binding protein 1	TOPBP1	11073	-2.475946	0.685344

205273_s_at	pitrilysin metallopeptidase 1	PITRM1	10531	-2.47626	0.685344
214657_s_at	Trophoblast-derived noncoding RNA	TncRNA	283131	-2.477821	0.685344
210060_at	phosphodiesterase 6G. cGMP-specific. rod. gamma	PDE6G	5148	-2.478084	0.685344
218781_at	structural maintenance of chromosomes 6	SMC6	79677	-2.479473	0.685344
203789_s_at	sema domain. immunoglobulin domain (Ig). short basic domain. secreted. (semaphorin) 3C	SEMA3C	10512	-2.47991	0.685344
217448_s_at	TOX high mobility group box family member 4 /// similar to Epidermal Langerhans cell protein LC	LOC285412 //	285412 /// 98	-2.483929	0.685344
218131_s_at	GATA zinc finger domain containing 2A	GATAD2A	54815	-2.484529	0.685344
218590_at	chromosome 10 open reading frame 2	C10orf2	56652	-2.484853	0.685344
216300_x_at	retinoic acid receptor. alpha	RARA	5914	-2.48576	0.685344
202521_at	CCCTC-binding factor (zinc finger protein)	CTCF	10664	-2.486121	0.685344
212015_x_at	polypyrimidine tract binding protein 1	PTBP1	5725	-2.486965	0.685344
220824_at	CDNA FLJ20123 fis. clone COL06041	---	---	-2.488086	0.685344
210347_s_at	B-cell CLL/lymphoma 11A (zinc finger protein)	BCL11A	53335	-2.488512	0.685344
204395_s_at	G protein-coupled receptor kinase 5	GRK5	2869	-2.4902	0.685344
203566_s_at	amylo-1. 6-glucosidase. 4-alpha-glucanotransferase (glycogen debranching enzyme. glycogen st	AGL	178	-2.490899	0.685344
206510_at	SIX homeobox 2	SIX2	10736	-2.49148	0.685344
208773_s_at	ankyrin repeat and KH domain containing 1 /// ANKHD1-EIF4EBP3	ANKHD1 /// A	404734 /// 54	-2.493806	0.685344
208309_s_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	MALT1	10892	-2.495158	0.685344
204797_s_at	echinoderm microtubule associated protein like 1	EML1	2009	-2.495162	0.685344
210144_at	TBC1 domain family. member 22A	TBC1D22A	25771	-2.495712	0.685344
207071_s_at	aconitase 1. soluble	ACO1	48	-2.496354	0.685344
202779_s_at	ubiquitin-conjugating enzyme E2S /// similar to Ubiquitin-conjugating enzyme E2S (Ubiquitin-con	LOC731049 //	27338 /// 731	-2.497197	0.685344
211502_s_at	PFTAIRE protein kinase 1	PFTK1	5218	-2.499433	0.685344
208029_s_at	lysosomal associated protein transmembrane 4 beta	LAPTM4B	55353	-2.499919	0.685344
203838_s_at	tyrosine kinase. non-receptor. 2	TNK2	10188	-2.500086	0.685344
217007_s_at	ADAM metallopeptidase domain 15	ADAM15	8751	-2.501117	0.685344
206590_x_at	dopamine receptor D2	DRD2	1813	-2.502495	0.685344
206625_at	peripherin 2 (retinal degeneration. slow)	PRPH2	5961	-2.50253	0.685344
209981_at	cold shock domain containing C2. RNA binding	CSDC2	27254	-2.503751	0.685344
204822_at	TTK protein kinase	TTK	7272	-2.504792	0.685344
205921_s_at	solute carrier family 6 (neurotransmitter transporter. taurine). member 6	SLC6A6	6533	-2.506431	0.685344
202861_at	period homolog 1 (Drosophila)	PER1	5187	-2.50714	0.685344
201104_x_at	neuroblastoma breakpoint family. member 14 /// neuroblastoma breakpoint family. member 11 /	LOC728980 //	200030 /// 25	-2.507143	0.685344
221581_s_at	linker for activation of T cells family. member 2	LAT2	7462	-2.507961	0.685344
219016_at	FAST kinase domains 5	FASTKD5	60493	-2.5085	0.685344
209839_at	dynamin 3	DNM3	26052	-2.510319	0.685344
214220_s_at	Alstrom syndrome 1	ALMS1	7840	-2.510432	0.685344
215178_x_at	N-acylsphingosine amidohydrolase (acid ceramidase)-like	ASAHL	27163	-2.512118	0.685344
209186_at	ATPase. Ca++ transporting. cardiac muscle. slow twitch 2	ATP2A2	488	-2.512233	0.685344
204930_s_at	BCL2/adenovirus E1B 19kDa interacting protein 1	BNIP1	662	-2.51369	0.685344
219749_at	SH2 domain containing 4A	SH2D4A	63898	-2.51425	0.685344
215976_at	CDNA FLJ12040 fis. clone HEMBB1001944	---	---	-2.514425	0.685344
205344_at	chondroitin sulfate proteoglycan 5 (neuroglycan C)	CSPG5	10675	-2.514819	0.685344
210014_x_at	isocitrate dehydrogenase 3 (NAD+) beta	IDH3B	3420	-2.515182	0.685344
209295_at	tumor necrosis factor receptor superfamily. member 10b	TNFRSF10B	8795	-2.515933	0.685344
201883_s_at	UDP-Gal:betaGlcNAc beta 1.4- galactosyltransferase. polypeptide 1	B4GALT1	2683	-2.516366	0.685344
202019_s_at	LanC lantibiotic synthetase component C-like 1 (bacterial)	LANCL1	10314	-2.517284	0.685344
210570_x_at	mitogen-activated protein kinase 9	MAPK9	5601	-2.517319	0.685344
221571_at	TNF receptor-associated factor 3	TRAF3	7187	-2.518109	0.685344
210243_s_at	UDP-Gal:betaGlcNAc beta 1.4- galactosyltransferase. polypeptide 3	B4GALT3	8703	-2.519776	0.685344
212712_at	calmodulin regulated spectrin-associated protein 1	CAMSAP1	157922	-2.528222	0.685344
213552_at	glucuronic acid epimerase	GLCE	26035	-2.528502	0.685344
203048_s_at	KIAA0372	KIAA0372	9652	-2.528676	0.685344
204647_at	homer homolog 3 (Drosophila)	HOMER3	9454	-2.528967	0.685344
210905_x_at	POU class 5 homeobox 1 pseudogene 4	POU5F1P4	645682	-2.530453	0.685344
211133_x_at	leukocyte immunoglobulin-like receptor. subfamily B (with TM and ITIM domains). member 3	LILRB3	11025	-2.531278	0.685344
202111_at	solute carrier family 4. anion exchanger. member 2 (erythrocyte membrane protein band 3-like 1	SLC4A2	6522	-2.531979	0.685344
209380_s_at	ATP-binding cassette. sub-family C (CFTR/MRP). member 5	ABCC5	10057	-2.533885	0.685344
212713_at	microfibrillar-associated protein 4	MFAP4	4239	-2.534089	0.685344
214748_at	phosphonoformate immuno-associated protein 5	RP11-298P3.3	10443	-2.539163	0.685344
221226_s_at	amiloride-sensitive cation channel 4. pituitary	ACCN4	55515	-2.543363	0.685344
219390_at	FK506 binding protein 14. 22 kDa	FKBP14	55033	-2.544849	0.685344
212542_s_at	pleckstrin homology domain interacting protein	PHIP	55023	-2.546445	0.685344
212568_s_at	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	DLAT	1737	-2.547529	0.685344
202661_at	inositol 1.4.5-triphosphate receptor. type 2	ITPR2	3709	-2.548146	0.685344
201013_s_at	phosphoribosylaminoimidazole carboxylase. phosphoribosylaminoimidazole succinocarboxamide s	PAICS	10606	-2.549691	0.685344
221317_x_at	protocadherin beta 6	PCDHB6	56130	-2.550375	0.685344
218277_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 40	DHX40	79665	-2.552392	0.685223
210270_at	regulator of G-protein signaling 6	RGS6	9628	-2.554586	0.684643
54632_at	thyroid adenoma associated	THADA	63892	-2.554923	0.684643
217293_at	---	---	---	-2.555509	0.684643
217564_s_at	carbamoyl-phosphate synthetase 1. mitochondrial	CPS1	1373	-2.556778	0.684175
49111_at	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	---	---	-2.559232	0.682811
218081_at	chromosome 20 open reading frame 27	C20orf27	54976	-2.559438	0.682811
221893_s_at	aarF domain containing kinase 2	ADCK2	90956	-2.559819	0.682811
210542_s_at	solute carrier organic anion transporter family. member 3A1	SLCO3A1	28232	-2.561301	0.682811
214161_at	Oxidative stress induced growth inhibitor family member 2	OSGIN2	734	-2.567061	0.680212
221253_s_at	thioredoxin domain containing 5	TXNDC5	81567	-2.569194	0.680212
203889_at	secretogranin V (7B2 protein)	SCG5	6447	-2.569349	0.680212
205003_at	dedicator of cytokinesis 4	DOCK4	9732	-2.570368	0.680212
217716_s_at	Sec61 alpha 1 subunit (S. cerevisiae)	SEC61A1	29927	-2.573388	0.679125
218768_at	nucleoporin 107kDa	NUP107	57122	-2.573555	0.679125
207174_at	glypican 5	GPC5	2262	-2.576361	0.678698
214626_s_at	glucosidase. alpha; neutral AB	GANAB	23193	-2.578552	0.677955
202715_at	carbamoyl-phosphate synthetase 2. aspartate transcarbamylase. and dihydroorotase	CAD	790	-2.579188	0.677955
219432_at	---	---	---	-2.580033	0.677769

208065_at	ST8 alpha-N-acetyl-neuraminide alpha-2.8-sialyltransferase 3	ST8SIA3	51046	-2.581146	0.677769
213270_at	membrane protein. palmitoylated 2 (MAGUK p55 subfamily member 2)	MPP2	4355	-2.582229	0.677769
212457_at	transcription factor binding to IGHM enhancer 3	TFE3	7030	-2.582827	0.677769
218044_x_at	parathymosin	PTMS	5763	-2.582927	0.677769
204545_at	peroxisomal biogenesis factor 6	PEX6	5190	-2.585253	0.677769
218355_at	kinesin family member 4A /// kinesin family member 4B	KIF4A /// KIF	24137 /// 285	-2.586005	0.677769
211062_s_at	carboxypeptidase Z	CPZ	8532	-2.586752	0.677769
206099_at	protein kinase C. eta	PRKCH	5583	-2.587293	0.677769
203286_at	ring finger protein 44	RNF44	22838	-2.587358	0.677769
210005_at	phosphoribosylglycinamide formyltransferase. phosphoribosylglycinamide synthetase. phosphorib	GART	2618	-2.58878	0.677769
214290_s_at	histone cluster 2. H2aa3 /// histone cluster 2. H2aa4	HIST2H2AA3 /	723790 /// 83	-2.589673	0.677769
216913_s_at	ribosomal RNA processing 12 homolog (S. cerevisiae)	RRP12	23223	-2.590475	0.677769
214056_at	Myeloid cell leukemia sequence 1 (BCL2-related)	MCL1	4170	-2.59162	0.677769
222192_s_at	chromosome 2 open reading frame 43	C2orf43	60526	-2.592113	0.677769
202672_s_at	activating transcription factor 3	ATF3	467	-2.59414	0.677769
222114_x_at	WD repeat domain 55	WDR55	54853	-2.594462	0.677769
219271_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-	GALNT14	79623	-2.596929	0.677769
217635_s_at	polymerase (DNA directed). gamma	POLG	5428	-2.596945	0.677769
211271_x_at	polypyrimidine tract binding protein 1	PTBP1	5725	-2.597433	0.677769
218308_at	transforming. acidic coiled-coil containing protein 3	TACC3	10460	-2.597859	0.677769
219410_at	transmembrane protein 45A	TMEM45A	55076	-2.599313	0.677769
202189_x_at	polypyrimidine tract binding protein 1	PTBP1	5725	-2.599966	0.677769
211851_x_at	breast cancer 1. early onset	BRCA1	672	-2.600013	0.677769
210052_s_at	TPX2. microtubule-associated. homolog (Xenopus laevis)	TPX2	22974	-2.600916	0.677769
220357_s_at	serum/glucocorticoid regulated kinase 2	SGK2	10110	-2.601453	0.677769
213073_at	zinc finger. FYVE domain containing 26	ZFYVE26	23503	-2.602283	0.677769
209822_s_at	very low density lipoprotein receptor	VLDLR	7436	-2.602789	0.677769
203154_s_at	p21(CDKN1A)-activated kinase 4	PAK4	10298	-2.604554	0.677769
217771_at	golgi membrane protein 1	GOLM1	51280	-2.607065	0.677769
203879_at	phosphoinositide-3-kinase. catalytic. delta polypeptide	PIK3CD	5293	-2.60731	0.677769
207000_s_at	protein phosphatase 3 (formerly 2B). catalytic subunit. gamma isoform	PPP3CC	5533	-2.608889	0.677769
202195_s_at	transmembrane emp24 protein transport domain containing 5	TMED5	50999	-2.609134	0.677769
220599_s_at	caspase recruitment domain family. member 14	CARD14	79092	-2.609842	0.677769
204153_s_at	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	MFNG	4242	-2.612307	0.677769
208591_s_at	phosphodiesterase 3B. cGMP-inhibited	PDE3B	5140	-2.612962	0.677769
210269_s_at	splicing factor. arginine/serine-rich 17A	SFRS17A	8227	-2.614108	0.677769
221443_x_at	prolactin releasing hormone	PRLH	51052	-2.614455	0.677769
219126_at	PHD finger protein 10	PHF10	55274	-2.615397	0.677769
206550_s_at	nucleoporin 155kDa	NUP155	9631	-2.615577	0.677769
218783_at	integrator complex subunit 7	INTS7	25896	-2.6159	0.677769
211136_s_at	cleft lip and palate associated transmembrane protein 1	CLPTM1	1209	-2.615969	0.677769
211258_s_at	transforming growth factor. alpha	TGFA	7039	-2.616477	0.677769
213656_s_at	kinesin light chain 1	KLC1	3831	-2.61871	0.677769
218765_at	SID1 transmembrane family. member 2	SIDT2	51092	-2.621293	0.677769
209260_at	stratifin	SFN	2810	-2.623495	0.677769
206471_s_at	plexin C1	PLXNC1	10154	-2.624523	0.677769
215827_x_at	ciliary rootlet coiled-coil. rootletin-like 2	CROCCL2	114819	-2.625228	0.677769
212248_at	CDNA FLJ41088 fis. clone ASTRO2002459 /// Metadherin	MTDH	92140	-2.627065	0.677769
220826_at	chromosome 21 open reading frame 77	C21orf77	55264	-2.62745	0.677769
201344_at	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog. yeast)	UBE2D2	7322	-2.629755	0.677769
216294_s_at	KIAA1109	KIAA1109	84162	-2.630419	0.677769
214364_at	MTERF domain containing 2	MTERFD2	130916	-2.633407	0.677769
219745_at	transmembrane protein 180	TMEM180	79847	-2.633861	0.677769
202184_s_at	nucleoporin 133kDa	NUP133	55746	-2.634026	0.677769
220607_x_at	TH1-like (Drosophila)	TH1L	51497	-2.634134	0.677769
206074_s_at	high mobility group AT-hook 1	HMGA1	3159	-2.634337	0.677769
217305_s_at	testicular soluble adenylyl cyclase	SAC	55811	-2.638782	0.677769
203961_at	nebulette	NEBL	10529	-2.64196	0.677769
218331_s_at	chromosome 10 open reading frame 18	C10orf18	54906	-2.643984	0.677769
201662_s_at	acyl-CoA synthetase long-chain family member 3	ACSL3	2181	-2.644598	0.677769
203701_s_at	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	TRMT1	55621	-2.646432	0.677769
200662_s_at	translocase of outer mitochondrial membrane 20 homolog (yeast)	TOMM20	9804	-2.647788	0.677769
203991_s_at	ubiquitously transcribed tetratricopeptide repeat. X chromosome	UTX	7403	-2.64886	0.677769
209859_at	tripartite motif-containing 9	TRIM9	114088	-2.64996	0.677769
205794_s_at	neuro-oncological ventral antigen 1	NOVA1	4857	-2.650414	0.677769
212074_at	unc-84 homolog A (C. elegans)	UNC84A	23353	-2.653991	0.677769
36545_s_at	Sfi1 homolog. spindle assembly associated (yeast)	SFI1	9814	-2.654315	0.677769
221632_s_at	WD repeat domain 4	WDR4	10785	-2.654646	0.677769
215317_at	CDNA FLJ37610 fis. clone BRCOC2011398	---	---	-2.655751	0.677769
205520_at	striatin. calmodulin binding protein	STRN	6801	-2.656257	0.677769
216332_at	POU class 6 homeobox 1	POU6F1	5463	-2.656899	0.677769
215642_at	Clone HQ0085	---	---	-2.657265	0.677769
205996_s_at	adenylate kinase 2	AK2	204	-2.659454	0.677769
218139_s_at	chromosome 14 open reading frame 108	C14orf108	55745	-2.65994	0.677769
211068_x_at	family with sequence similarity 21. member C /// family with sequence similarity 21. member D	FAM21C /// F	253725 /// 65	-2.662309	0.677769
209824_s_at	aryl hydrocarbon receptor nuclear translocator-like	ARNTL	406	-2.662397	0.677769
212963_at	TM2 domain containing 1	TM2D1	83941	-2.663311	0.677769
202188_at	nucleoporin 93kDa	NUP93	9688	-2.663453	0.677769
219822_at	mitochondrial translational release factor 1	MTRF1	9617	-2.665183	0.677769
200690_at	heat shock 70kDa protein 9 (mortalin)	HSPA9	3313	-2.665411	0.677769
205963_s_at	DnaJ (Hsp40) homolog. subfamily A. member 3	DNAJA3	9093	-2.666504	0.677769
205867_at	protein tyrosine phosphatase. non-receptor type 11 (Noonan syndrome 1)	PTPN11	5781	-2.666885	0.677769
203929_s_at	microtubule-associated protein tau	MAPT	4137	-2.667747	0.677769
204702_s_at	nuclear factor (erythroid-derived 2)-like 3	NFE2L3	9603	-2.667883	0.677769
204473_s_at	zinc finger protein 592	ZNF592	9640	-2.675603	0.677769
204079_at	tyrosylprotein sulfotransferase 2	TPST2	8459	-2.675921	0.677769

218124_at	retinol saturase (all-trans-retinol 13.14-reductase)	RETSAT	54884	-2.677667	0.677769
206720_at	mannosyl (alpha-1.6-)-glycoprotein beta-1.6-N-acetyl-glucosaminyltransferase	MGAT5	4249	-2.680582	0.677769
207046_at	histone cluster 2. H4a /// histone cluster 2. H4b	HIST2H4A ///	554313 /// 83	-2.681133	0.677769
204677_at	cadherin 5. type 2. VE-cadherin (vascular epithelium)	CDH5	1003	-2.681451	0.677769
215099_s_at	retinoid X receptor. beta	RXRB	6257	-2.682345	0.677769
215870_s_at	phospholipase A2. group V	PLA2G5	5322	-2.683809	0.677769
215849_x_at	CDNA FLJ12173 fis. clone MAMMA1000696	---	---	-2.683929	0.677769
202220_at	KIAA0907	KIAA0907	22889	-2.686147	0.677769
217900_at	isoleucyl-tRNA synthetase 2. mitochondrial	IARS2	55699	-2.686714	0.677769
201000_at	alanyl-tRNA synthetase	AARS	16	-2.689408	0.677769
37079_at	YDD19 protein	YDD19	11049	-2.689782	0.677769
212118_at	tripartite motif-containing 27	TRIM27	5987	-2.690117	0.677769
209336_at	PWP2 periodic tryptophan protein homolog (yeast)	PWP2	5822	-2.690979	0.677769
222245_s_at	fer-1-like 4 (C. elegans)	FER1L4	80307	-2.692154	0.677769
204089_x_at	mitogen-activated protein kinase kinase kinase 4	MAP3K4	4216	-2.692314	0.677769
206473_at	membrane-bound transcription factor peptidase. site 2	MBTPS2	51360	-2.69255	0.677769
209615_s_at	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog. yeast)	PAK1	5058	-2.692753	0.677769
217168_s_at	homocysteine-inducible. endoplasmic reticulum stress-inducible. ubiquitin-like domain member 1	HERPUD1	9709	-2.694847	0.677769
217399_s_at	forkhead box O3	FOXO3	2309	-2.695697	0.677769
202491_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells. kinase complex-associated protein	IKBKAP	8518	-2.695956	0.677769
215513_at	hydatidiform mole associated and imprinted	HYMAI	57061	-2.697634	0.677769
208700_s_at	transketolase (Wernicke-Korsakoff syndrome)	TKT	7086	-2.698039	0.677769
206499_s_at	regulator of chromosome condensation 1 /// SNHG3-RCC1	RCC1 /// SNH	1104 /// 7518	-2.698862	0.677769
201697_s_at	DNA (cytosine-5-)-methyltransferase 1	DNMT1	1786	-2.699453	0.677769
212949_at	non-SMC condensin I complex. subunit H	NCAPH	23397	-2.70129	0.677769
212338_at	myosin ID	MYO1D	4642	-2.703924	0.677769
215167_at	mediator complex subunit 14	MED14	9282	-2.704087	0.677769
213092_x_at	DnaJ (Hsp40) homolog. subfamily C. member 9	DNAJC9	23234	-2.704277	0.677769
201973_s_at	chromosome 7 open reading frame 28A	C7orf28A	51622	-2.706342	0.677769
201746_at	tumor protein p53 (Li-Fraumeni syndrome)	TP53	7157	-2.707826	0.677769
218125_s_at	coiled-coil domain containing 25	CCDC25	55246	-2.709459	0.677769
207891_s_at	UCHL5 interacting protein	UCHL5IP	55559	-2.710299	0.677769
222132_s_at	acylglycerol kinase	AGK	55750	-2.71142	0.677769
203223_at	rabaptin. RAB GTPase binding effector protein 1	RABEP1	9135	-2.712777	0.677769
203050_at	tumor protein p53 binding protein 1	TP53BP1	7158	-2.714858	0.677769
210512_s_at	vascular endothelial growth factor A	VEGFA	7422	-2.718555	0.677769
214448_x_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor. beta	NFKBIB	4793	-2.720854	0.677769
202176_at	excision repair cross-complementing rodent repair deficiency. complementation group 3 (xeroder	ERCC3	2071	-2.724266	0.677769
217786_at	protein arginine methyltransferase 5	PRMT5	10419	-2.724482	0.677769
212389_at	SET binding factor 1	SBF1	6305	-2.725384	0.677769
207061_at	endoplasmic reticulum to nucleus signaling 1	ERN1	2081	-2.727189	0.677769
217944_at	protein O-linked mannose beta1.2-N-acetylglucosaminyltransferase	POMGNT1	55624	-2.727284	0.677769
202855_s_at	solute carrier family 16. member 3 (monocarboxylic acid transporter 4)	SLC16A3	9123	-2.730027	0.677769
222235_s_at	chondroitin sulfate GalNAcT-2	GALNACT-2	55454	-2.732504	0.677769
210398_x_at	fucosyltransferase 6 (alpha (1.3) fucosyltransferase)	FUT6	2528	-2.732506	0.677769
204817_at	extra spindle pole bodies homolog 1 (S. cerevisiae)	ESPL1	9700	-2.732787	0.677769
212316_at	nucleoporin 210kDa	NUP210	23225	-2.733436	0.677769
215230_x_at	eukaryotic translation initiation factor 3. subunit C /// eukaryotic translation initiation factor 3. su	EIF3C /// EIF	728689 /// 86	-2.735905	0.677769
219278_at	mitogen-activated protein kinase kinase kinase 6	MAP3K6	9064	-2.737079	0.677769
212025_s_at	flightless I homolog (Drosophila)	FLII	2314	-2.742227	0.677769
203226_s_at	tetraspanin 31	TSPAN31	6302	-2.743346	0.677769
202013_s_at	exostoses (multiple) 2	EXT2	2132	-2.745667	0.677769
208923_at	cytoplasmic FMR1 interacting protein 1	CYFIP1	23191	-2.746498	0.677769
211279_at	nuclear respiratory factor 1	NRF1	4899	-2.74745	0.677769
213199_at	C2 calcium-dependent domain containing 3	C2CD3	26005	-2.748129	0.677769
215332_s_at	CD8b molecule	CD8B	926	-2.748315	0.677769
218973_at	elongation factor Tu GTP binding domain containing 1	EFTUD1	79631	-2.748594	0.677769
207648_at	dystrophin related protein 2	DRP2	1821	-2.748618	0.677769
210076_x_at	SERPINE1 mRNA binding protein 1	SERBP1	26135	-2.754077	0.677769
207387_s_at	glycerol kinase	GK	2710	-2.755004	0.677769
220634_at	T-box 4	TBX4	9496	-2.759779	0.677769
222231_s_at	leucine rich repeat containing 59	LRRC59	55379	-2.761272	0.677651
212667_at	secreted protein. acidic. cysteine-rich (osteonectin)	SPARC	6678	-2.761438	0.677651
215781_s_at	topoisomerase (DNA) III beta	TOP3B	8940	-2.761458	0.677651
219705_at	glutamine and serine rich 1	QSER1	79832	-2.761468	0.677651
206129_s_at	arylsulfatase B	ARSB	411	-2.766572	0.676577
216692_at	MRNA; cDNA DKFZp761N1323 (from clone DKFZp761N1323)	---	---	-2.76672	0.676577
211543_s_at	G protein-coupled receptor kinase 6	GRK6	2870	-2.769131	0.675594
212749_s_at	ring finger and CHY zinc finger domain containing 1	RCHY1	25898	-2.771994	0.67416
215760_s_at	strawberry notch homolog 2 (Drosophila)	SBNO2	22904	-2.772749	0.67416
214130_s_at	phosphodiesterase 4D interacting protein (myomegalin) /// similar to phosphodiesterase 4D inter	LOC727942 //	727942 /// 96	-2.774869	0.673001
207359_at	calcium/calmodulin-dependent protein kinase kinase 2. beta	CAMKK2	10645	-2.775901	0.672775
201819_at	scavenger receptor class B. member 1	SCARB1	949	-2.77658	0.672775
208438_s_at	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	FGR	2268	-2.777808	0.672775
213097_s_at	zuotin related factor 1	ZRF1	27000	-2.782801	0.670898
202395_at	N-ethylmaleimide-sensitive factor	NSF	4905	-2.782939	0.670898
204272_at	lectin. galactoside-binding. soluble. 4 (galectin 4)	LGALS4	3960	-2.782974	0.670898
218594_at	HEAT repeat containing 1	HEATR1	55127	-2.783348	0.670898
219270_at	ChaC. cation transport regulator homolog 1 (E. coli)	CHAC1	79094	-2.783922	0.670898
221156_x_at	cell cycle progression 1	CCPG1	9236	-2.785387	0.670898
217955_at	BCL2-like 13 (apoptosis facilitator)	BCL2L13	23786	-2.788516	0.670898
205222_at	enoyl-Coenzyme A. hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	EHHADH	1962	-2.788582	0.670898
204512_at	human immunodeficiency virus type I enhancer binding protein 1	HIVEP1	3096	-2.789053	0.670898
220806_x_at	guanine nucleotide binding protein (G protein). gamma 13	GNG13	51764	-2.792734	0.670898
208851_s_at	Thy-1 cell surface antigen	THY1	7070	-2.79336	0.670898
207050_at	calcium channel. voltage-dependent. alpha 2/delta subunit 1	CACNA2D1	781	-2.805538	0.66705

216641_s_at	ladinin 1	LAD1	3898	-2.807319	0.666139
206291_at	neurotensin	NTS	4922	-2.808148	0.666139
218228_s_at	tankyrase. TRF1-interacting ankyrin-related ADP-ribose polymerase 2	TNKS2	80351	-2.8123	0.666139
212946_at	KIAA0564	KIAA0564	23078	-2.812606	0.666139
222308_x_at	Transcribed locus	---	---	-2.812773	0.666139
219154_at	Ras homolog gene family. member F (in filopodia)	RHOF	54509	-2.81728	0.666139
211269_s_at	interleukin 2 receptor. alpha	IL2RA	3559	-2.818701	0.666139
211016_x_at	heat shock 70kDa protein 4	HSPA4	3308	-2.819278	0.666139
215756_at	hypothetical protein LOC730227	LOC730227	730227	-2.821346	0.665777
217805_at	interleukin enhancer binding factor 3. 90kDa	ILF3	3609	-2.821995	0.665777
208952_s_at	La ribonucleoprotein domain family. member 5	LARP5	23185	-2.822781	0.665777
217099_s_at	gem (nuclear organelle) associated protein 4	GEMIN4	50628	-2.825648	0.664041
201064_s_at	poly(A) binding protein. cytoplasmic 4 (inducible form)	PABPC4	8761	-2.826461	0.664041
212720_at	poly(A) polymerase alpha	PAPOLA	10914	-2.831068	0.660294
212247_at	nucleoporin 205kDa	NUP205	23165	-2.83174	0.660294
203944_x_at	butyrophilin. subfamily 2. member A1	BTN2A1	11120	-2.834712	0.659838
213363_at	Homo sapiens. clone IMAGE:5244869. mRNA	---	---	-2.834993	0.659838
221329_at	olfactory receptor. family 52. subfamily A. member 1	OR52A1	23538	-2.835532	0.659838
207300_s_at	coagulation factor VII (serum prothrombin conversion accelerator)	F7	2155	-2.837244	0.659838
214359_s_at	heat shock protein 90kDa alpha (cytosolic). class B member 1	HSP90AB1	3326	-2.838452	0.659838
211982_x_at	exportin 6	XPO6	23214	-2.838847	0.659838
202083_s_at	SEC14-like 1 (S. cerevisiae)	SEC14L1	6397	-2.839853	0.659838
201928_at	plakophilin 4	PKP4	8502	-2.841018	0.659838
211365_s_at	protocadherin alpha 2	PCDHA2	56146	-2.842468	0.659838
206766_at	integrin. alpha 10	ITGA10	8515	-2.84248	0.659838
218395_at	ARP6 actin-related protein 6 homolog (yeast)	ACTR6	64431	-2.84267	0.659838
214672_at	tubulin tyrosine ligase-like family. member 5	TTLL5	23093	-2.843454	0.659838
217401_at	---	---	---	-2.843475	0.659838
219369_s_at	OTU domain. ubiquitin aldehyde binding 2	OTUB2	78990	-2.844774	0.659838
206050_s_at	ribonuclease/angiogenin inhibitor 1	RNH1	6050	-2.845847	0.659838
216969_s_at	kinesin family member 22 /// kinesin-like DNA-binding protein pseudogene	KIF22 /// LOC	3835 /// 7280	-2.84965	0.659838
221379_at	---	---	---	-2.85234	0.659838
220547_s_at	family with sequence similarity 35. member A	FAM35A	54537	-2.85405	0.659838
212197_x_at	myosin phosphatase-Rho interacting protein	M-RIP	23164	-2.85566	0.659838
216360_x_at	ribosomal RNA processing 12 homolog (S. cerevisiae)	RRP12	23223	-2.855982	0.659838
201112_s_at	CSE1 chromosome segregation 1-like (yeast)	CSE1L	1434	-2.857241	0.659838
211042_x_at	melanoma cell adhesion molecule	MCAM	4162	-2.860596	0.659838
212105_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9	1660	-2.860912	0.659838
220809_at	hypothetical protein FLJ14327	FLJ14327	79972	-2.862177	0.659838
211270_x_at	polypyrimidine tract binding protein 1	PTBP1	5725	-2.863465	0.659838
202414_at	excision repair cross-complementing rodent repair deficiency. complementation group 5 (xeroder	ERCC5	2073	-2.863683	0.659838
209921_at	solute carrier family 7. (cationic amino acid transporter. y+ system) member 11	SLC7A11	23657	-2.864739	0.659838
222249_at	KIAA1651 protein	---	---	-2.866844	0.659838
218153_at	cysteinyl-tRNA synthetase 2. mitochondrial (putative)	CARS2	79587	-2.867047	0.659838
217632_at	guanine nucleotide binding protein-like 3 (nucleolar)-like	GNL3L	54552	-2.867895	0.659838
219321_at	membrane protein. palmitoylated 5 (MAGUK p55 subfamily member 5)	MPP5	64398	-2.868159	0.659838
203506_s_at	mediator complex subunit 12	MED12	9968	-2.868665	0.659838
215910_s_at	fibronectin type III domain containing 3A	FNDC3A	22862	-2.869086	0.659838
222047_s_at	arsenate resistance protein 2	ARS2	51593	-2.87061	0.659838
218511_s_at	pyridoxamine 5'-phosphate oxidase	PNPO	55163	-2.871684	0.659838
215413_at	exocyst complex component 7	EXOC7	23265	-2.87229	0.659838
202290_at	PDGFA associated protein 1	PDAP1	11333	-2.872778	0.659838
216373_at	transmembrane anterior posterior transformation 1	TAPT1	202018	-2.875988	0.659838
211027_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells. kinase beta	IKBKB	3551	-2.881524	0.659838
200647_x_at	eukaryotic translation initiation factor 3. subunit C /// eukaryotic translation initiation factor 3. su	EIF3C /// EIF3	728689 /// 86	-2.882124	0.659838
221276_s_at	syncoilin. intermediate filament 1	SYNC1	81493	-2.884527	0.659838
209699_x_at	aldo-keto reductase family 1. member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein	AKR1C2	1646	-2.884794	0.659838
201774_s_at	non-SMC condensin I complex. subunit D2	NCAPD2	9918	-2.885752	0.659838
207622_s_at	ATP-binding cassette. sub-family F (GCN20). member 2	ABCF2	10061	-2.88778	0.659838
203935_at	activin A receptor. type I	ACVR1	90	-2.890088	0.659838
201086_x_at	SON DNA binding protein	SON	6651	-2.89182	0.659838
218838_s_at	tetratricopeptide repeat domain 31	TTC31	64427	-2.89251	0.659838
207579_at	melanoma antigen family B. 3	MAGEB3	4114	-2.894599	0.659838
217156_at	---	---	---	-2.895667	0.659838
204157_s_at	KIAA0999 protein	KIAA0999	23387	-2.895754	0.659838
201680_x_at	arsenate resistance protein 2	ARS2	51593	-2.895824	0.659838
202893_at	unc-13 homolog B (C. elegans)	UNC13B	10497	-2.89693	0.659838
202070_s_at	isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A	3419	-2.897518	0.659838
221817_at	dolichyl pyrophosphate phosphatase 1	DOLPP1	57171	-2.899453	0.659838
205748_s_at	ring finger protein 126	RNF126	55658	-2.899626	0.659838
209777_s_at	solute carrier family 19 (folate transporter). member 1	SLC19A1	6573	-2.901126	0.659838
201563_at	sorbitol dehydrogenase	SORD	6652	-2.901571	0.659838
214050_at	---	---	---	-2.90191	0.659838
203550_s_at	chromosome 1 open reading frame 2	C1orf2	10712	-2.903663	0.659838
204536_s_at	---	---	---	-2.904602	0.659838
209320_at	adenylate cyclase 3	ADCY3	109	-2.904722	0.659838
206997_s_at	heparan sulfate 6-O-sulfotransferase 1 /// similar to Heparan-sulfate 6-O-sulfotransferase 1 (HS6	HS6ST1 /// LC	728969 /// 93	-2.905705	0.659838
221626_at	zinc finger protein 506	ZNF506	440515	-2.906564	0.659838
201529_s_at	replication protein A1. 70kDa	RPA1	6117	-2.909241	0.659838
203289_s_at	chromosome 16 open reading frame 35	C16orf35	8131	-2.909359	0.659838
217136_at	peptidylprolyl isomerase A (cyclophilin A)-like 4 /// similar to peptidylprolyl isomerase A (cycloph	LOC653505 //	164022 /// 65	-2.909391	0.659838
202558_s_at	stress 70 protein chaperone. microsome-associated. 60kDa	STCH	6782	-2.913598	0.659838
203443_at	echinoderm microtubule associated protein like 3	EML3	256364	-2.91405	0.659838
216205_s_at	mitofusin 2	MFN2	9927	-2.914629	0.659838
204072_s_at	furry homolog (Drosophila)	FRY	10129	-2.914833	0.659838
202565_s_at	supervillin	SVIL	6840	-2.917728	0.659838

217492_s_at	phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /// phosphatase and	LOC731292 //	11191 /// 572	-2.9189	0.659838
201476_s_at	ribonucleotide reductase M1 polypeptide	RRM1	6240	-2.9221	0.659838
200643_at	high density lipoprotein binding protein (vigilin)	HDLBP	3069	-2.922339	0.659838
207134_x_at	tryptase alpha/beta 1	TPSAB1	7177	-2.922383	0.659838
214336_s_at	coatomer protein complex. subunit alpha	COPA	1314	-2.923415	0.659838
220761_s_at	TAO kinase 3	TAOK3	51347	-2.924593	0.659838
208034_s_at	protein Z. vitamin K-dependent plasma glycoprotein	PROZ	8858	-2.926092	0.659838
217525_at	olfactomedin-like 1	OLFML1	283298	-2.926247	0.659838
208202_s_at	PHD finger protein 15	PHF15	23338	-2.926422	0.659838
201578_at	podocalyxin-like	PODXL	5420	-2.928591	0.659838
217333_at	keratin 18 pseudogene 44	KRT18P44	139748	-2.928839	0.659838
217825_s_at	ubiquitin-conjugating enzyme E2. J1 (UBC6 homolog. yeast)	UBE2J1	51465	-2.931948	0.659838
219884_at	LIM homeobox 6	LHX6	26468	-2.934571	0.659838
214771_x_at	myosin phosphatase-Rho interacting protein	M-RIP	23164	-2.941299	0.659838
218306_s_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domai	HERC1	8925	-2.941586	0.659838
205252_at	zinc finger protein 174	ZNF174	7727	-2.941655	0.659838
212618_at	zinc finger protein 609	ZNF609	23060	-2.942197	0.659838
202636_at	ring finger protein 103	RNF103	7844	-2.942925	0.659838
210256_s_at	phosphatidylinositol-4-phosphate 5-kinase. type I. alpha	PIP5K1A	8394	-2.943648	0.659838
216232_s_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	GCN1L1	10985	-2.947385	0.659838
202107_s_at	minichromosome maintenance complex component 2	MCM2	4171	-2.950055	0.659838
219426_at	eukaryotic translation initiation factor 2C. 3	EIF2C3	192669	-2.951402	0.659838
204243_at	rearranged L-myc fusion	RLF	6018	-2.952424	0.659838
203690_at	tubulin. gamma complex associated protein 3	TUBGCP3	10426	-2.953104	0.659838
203580_s_at	solute carrier family 7 (cationic amino acid transporter. y+ system). member 6	SLC7A6	9057	-2.953437	0.659838
203372_s_at	suppressor of cytokine signaling 2	SOCS2	8835	-2.955747	0.659838
222087_at	Pvt1 oncogene homolog. MYC activator (mouse)	PVT1	5820	-2.955868	0.659838
212575_at	chromosome 19 open reading frame 6	C19orf6	91304	-2.955954	0.659838
203120_at	tumor protein p53 binding protein. 2	TP53BP2	7159	-2.957876	0.659838
207524_at	suppression of tumorigenicity 7	ST7	7982	-2.958305	0.659838
201384_s_at	neighbor of BRCA1 gene 1 /// similar to neighbor of BRCA1 gene 1	LOC727732 //	4077 /// 7277	-2.958683	0.659838
204206_at	MAX binding protein	MNT	4335	-2.95914	0.659838
212110_at	solute carrier family 39 (zinc transporter). member 14	SLC39A14	23516	-2.960955	0.659838
216008_s_at	ariadne homolog 2 (Drosophila)	ARIH2	10425	-2.962294	0.659838
220288_at	myosin XVA	MYO15A	51168	-2.966403	0.659838
203875_at	SWI/SNF related. matrix associated. actin dependent regulator of chromatin. subfamily a. membe	SMARCA1	6594	-2.966509	0.659838
209203_s_at	bicaudal D homolog 2 (Drosophila)	BICD2	23299	-2.967285	0.659838
222021_x_at	succinate dehydrogenase complex. subunit A. flavoprotein pseudogene 1	SDHALP1	255812	-2.968924	0.659838
205839_s_at	benzodiazapine receptor (peripheral) associated protein 1	BZRAP1	9256	-2.971092	0.659838
220840_s_at	chromosome 1 open reading frame 112	C1orf112	55732	-2.971318	0.659838
204444_at	kinesin family member 11	KIF11	3832	-2.973032	0.659838
221879_at	calmodulin-like 4	CALML4	91860	-2.975206	0.659838
216090_x_at	---	---	---	-2.978601	0.659838
203648_at	TatD DNase domain containing 2	TATDN2	9797	-2.982513	0.659838
201266_at	thioredoxin reductase 1	TXNRD1	7296	-2.982972	0.659838
217687_at	adenylate cyclase 2 (brain)	ADCY2	108	-2.985605	0.659838
215170_s_at	centrosomal protein 152kDa	CEP152	22995	-2.986306	0.659838
204240_s_at	structural maintenance of chromosomes 2	SMC2	10592	-2.994212	0.659838
209386_at	transmembrane 4 L six family member 1	TM4SF1	4071	-2.994983	0.659838
204947_at	E2F transcription factor 1	E2F1	1869	-2.99637	0.659838
206854_s_at	mitogen-activated protein kinase kinase kinase 7	MAP3K7	6885	-3.000481	0.659838
209352_s_at	SIN3 homolog B. transcription regulator (yeast)	SIN3B	23309	-3.006793	0.659838
215195_at	protein kinase C. alpha	PRKCA	5578	-3.008978	0.659838
213059_at	cAMP responsive element binding protein 3-like 1	CREB3L1	90993	-3.010615	0.659838
203040_s_at	hydroxymethylbilane synthase	HMBS	3145	-3.01265	0.659838
200028_s_at	StAR-related lipid transfer (START) domain containing 7	STARD7	56910	-3.014835	0.659838
209724_s_at	zinc finger protein 161 homolog (mouse)	ZFP161	7541	-3.019622	0.659838
220276_at	RERG/RAS-like	RERGL	79785	-3.02006	0.659838
211375_s_at	interleukin enhancer binding factor 3. 90kDa	ILF3	3609	-3.022281	0.659838
201598_s_at	inositol polyphosphate phosphatase-like 1	INPPL1	3636	-3.022463	0.659838
210061_at	zinc finger protein 589	ZNF589	51385	-3.027497	0.659838
212159_x_at	adaptor-related protein complex 2. alpha 2 subunit	AP2A2	161	-3.031842	0.659838
203438_at	stanniocalcin 2	STC2	8614	-3.032651	0.659838
220852_at	PRO1768 protein	PRO1768	29018	-3.037981	0.659838
208231_at	neuregulin 1	NRG1	3084	-3.040949	0.659838
212381_at	ubiquitin specific peptidase 24	USP24	23358	-3.043775	0.659838
218269_at	ribonuclease III. nuclear	RNASEN	29102	-3.044677	0.659838
207614_s_at	cullin 1	CUL1	8454	-3.049613	0.659838
201800_s_at	oxysterol binding protein	OSBP	5007	-3.049985	0.659838
212992_at	AHNAK nucleoprotein 2	AHNAK2	113146	-3.05414	0.659838
208258_s_at	growth arrest-specific 2 like 1	GAS2L1	10634	-3.057215	0.659838
211561_x_at	mitogen-activated protein kinase 14	MAPK14	1432	-3.058794	0.659838
201622_at	staphylococcal nuclease and tudor domain containing 1	SND1	27044	-3.064297	0.659838
220363_s_at	engulfment and cell motility 2	ELMO2	63916	-3.065556	0.659838
221972_s_at	stromal cell derived factor 4	SDF4	51150	-3.069527	0.659838
209599_s_at	prune homolog (Drosophila)	PRUNE	58497	-3.06964	0.659838
201729_s_at	KIAA0100	KIAA0100	9703	-3.073301	0.659838
203601_s_at	zinc finger and BTB domain containing 17	ZBTB17	7709	-3.075183	0.659838
204152_s_at	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	MFNG	4242	-3.08229	0.659838
204360_s_at	N-acetylglucosaminidase. alpha- (Sanfilippo disease IIIB)	NAGLU	4669	-3.093124	0.659838
202132_at	WW domain containing transcription regulator 1	WWTR1	25937	-3.09341	0.659838
200990_at	tripartite motif-containing 28	TRIM28	10155	-3.100609	0.659838
202413_s_at	ubiquitin specific peptidase 1	USP1	7398	-3.103641	0.659838
212815_at	activating signal cointegrator 1 complex subunit 3	ASCC3	10973	-3.104893	0.659838
217403_s_at	zinc finger protein 227	ZNF227	7770	-3.107458	0.659838
200828_s_at	zinc finger protein 207	ZNF207	7756	-3.111647	0.659838

34764_at	leucyl-tRNA synthetase 2. mitochondrial	LARS2	23395	-3.11324	0.659838
208431_s_at	tubby homolog (mouse)	TUB	7275	-3.115667	0.659838
211870_s_at	protocadherin alpha 3	PCDHA3	56145	-3.116323	0.659838
213672_at	methionyl-tRNA synthetase	MARS	4141	-3.117677	0.659838
209975_at	cytochrome P450. family 2. subfamily E. polypeptide 1	CYP2E1	1571	-3.119674	0.659838
221215_s_at	receptor-interacting serine-threonine kinase 4	RIPK4	54101	-3.122246	0.659838
218390_s_at	chromosome 10 open reading frame 84	C10orf84	63877	-3.124169	0.659838
218020_s_at	zinc finger. AN1-type domain 3	ZFAND3	60685	-3.12464	0.659838
222014_x_at	mitochondrial translation optimization 1 homolog (S. cerevisiae)	MTO1	25821	-3.125901	0.659838
215995_x_at	CDNA FLJ12226 fis. clone MAMMA1001143	---	---	-3.126418	0.659838
210018_x_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	MALT1	10892	-3.128328	0.659838
212932_at	RAB3 GTPase activating protein subunit 1 (catalytic)	RAB3GAP1	22930	-3.128875	0.659838
212263_at	quaking homolog. KH domain RNA binding (mouse)	QKI	9444	-3.128914	0.659838
211615_s_at	leucine-rich PPR-motif containing	LRPPRC	10128	-3.130975	0.659838
219484_at	host cell factor C2	HCFC2	29915	-3.132682	0.659838
206352_s_at	peroxisome biogenesis factor 10	PEX10	5192	-3.135224	0.659838
208955_at	deoxyuridine triphosphatase	DUT	1854	-3.14338	0.659838
207788_s_at	sorbin and SH3 domain containing 3	SORBS3	10174	-3.147085	0.659838
212370_x_at	family with sequence similarity 21. member B /// family with sequence similarity 21. member A	FAM21A /// FA	387680 /// 55	-3.147427	0.659838
216767_at	CDNA: FLJ21710 fis. clone COL10087	---	---	-3.147823	0.659838
203422_at	polymerase (DNA directed). delta 1. catalytic subunit 125kDa	POLD1	5424	-3.151891	0.659838
220745_at	interleukin 19	IL19	29949	-3.152826	0.659838
203099_s_at	chromodomain protein. Y-like	CDYL	9425	-3.152886	0.659838
202968_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	8445	-3.153709	0.659838
202364_at	MAX interactor 1	MXI1	4601	-3.157846	0.659838
202049_s_at	zinc finger. MYM-type 4	ZMYM4	9202	-3.177339	0.659838
218604_at	LEM domain containing 3	LEMD3	23592	-3.181182	0.659838
207559_s_at	zinc finger. MYM-type 3	ZMYM3	9203	-3.18285	0.659838
201461_s_at	mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2	9261	-3.190135	0.659838
220130_x_at	leukotriene B4 receptor 2	LTB4R2	56413	-3.191735	0.659838
219515_at	PR domain containing 10	PRDM10	56980	-3.192417	0.659838
220349_s_at	endo-beta-N-acetylglucosaminidase	FLJ21865	64772	-3.192798	0.659838
217601_at	nucleoporin 188kDa	NUP188	23511	-3.197626	0.659838
219490_s_at	DNA cross-link repair 1B (PSO2 homolog. S. cerevisiae)	DCLRE1B	64858	-3.19834	0.659838
212439_at	inositol hexaphosphate kinase 1	IHPK1	9807	-3.198576	0.659838
210983_s_at	minichromosome maintenance complex component 7	MCM7	4176	-3.200229	0.659838
212388_at	ubiquitin specific peptidase 24	USP24	23358	-3.209458	0.659838
203809_s_at	v-akt murine thymoma viral oncogene homolog 2	AKT2	208	-3.209949	0.659838
201159_s_at	N-myristoyltransferase 1	NMT1	4836	-3.210127	0.659838
212084_at	testis expressed 261	TEX261	113419	-3.211376	0.659838
206498_at	oculocutaneous albinism II (pink-eye dilution homolog. mouse)	OCA2	4948	-3.211379	0.659838
210455_at	chromosome 10 open reading frame 28	C10orf28	27291	-3.212398	0.659838
38158_at	extra spindle pole bodies homolog 1 (S. cerevisiae)	ESPL1	9700	-3.214741	0.659838
213112_s_at	sequestosome 1	SQSTM1	8878	-3.215406	0.659838
203157_s_at	glutaminase	GLS	2744	-3.218287	0.659838
200722_s_at	cell cycle associated protein 1	CAPRIN1	4076	-3.221415	0.659838
212196_at	Interleukin 6 signal transducer (gp130. oncostatin M receptor)	IL6ST	3572	-3.222908	0.659838
215194_at	protein kinase C. alpha	PRKCA	5578	-3.233247	0.659838
209997_x_at	pericentriolar material 1	PCM1	5108	-3.236244	0.659838
222039_at	hypothetical protein LOC146909	LOC146909	146909	-3.240897	0.659838
218016_s_at	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	POLR3E	55718	-3.249579	0.659838
220768_s_at	casein kinase 1. gamma 3	CSNK1G3	1456	-3.250021	0.659838
214582_at	phosphodiesterase 3B. cGMP-inhibited	PDE3B	5140	-3.251366	0.659838
217735_s_at	eukaryotic translation initiation factor 2-alpha kinase 1	EIF2AK1	27102	-3.253415	0.659838
210787_s_at	calcium/calmodulin-dependent protein kinase kinase 2. beta	CAMKK2	10645	-3.254698	0.659838
215960_at	solute carrier family 5 (low affinity glucose cotransporter). member 4	SLC5A4	6527	-3.255202	0.659838
216599_x_at	solute carrier family 22 (organic anion transporter). member 6	SLC22A6	9356	-3.257306	0.659838
206445_s_at	protein arginine methyltransferase 1	PRMT1	3276	-3.259405	0.659838
204744_s_at	isoleucyl-tRNA synthetase	IARS	3376	-3.260419	0.659838
217895_at	Pentatricopeptide repeat domain 3	PTCD3	55037	-3.271357	0.659838
218343_s_at	general transcription factor IIIC. polypeptide 3. 102kDa	GTF3C3	9330	-3.2729	0.659838
211724_x_at	hypothetical protein FLJ20323	FLJ20323	54468	-3.278673	0.659838
44120_at	aarF domain containing kinase 2	ADCK2	90956	-3.286476	0.659838
210544_s_at	aldehyde dehydrogenase 3 family. member A2	ALDH3A2	224	-3.288576	0.659838
205700_at	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	HSD17B6	8630	-3.289485	0.659838
202477_s_at	tubulin. gamma complex associated protein 2	TUBGCP2	10844	-3.290951	0.659838
210692_s_at	solute carrier family 43. member 3	SLC43A3	29015	-3.293499	0.659838
208979_at	nuclear receptor coactivator 6	NCOA6	23054	-3.298875	0.659838
213807_x_at	met proto-oncogene (hepatocyte growth factor receptor)	MET	4233	-3.299836	0.659838
202653_s_at	membrane-associated ring finger (C3HC4) 7	7-Mar	64844	-3.303499	0.659838
213929_at	CDNA clone IMAGE:4733238	---	---	-3.30791	0.659838
218479_s_at	exportin 4	XPO4	64328	-3.308857	0.659838
202095_s_at	baculoviral IAP repeat-containing 5 (survivin)	BIRC5	332	-3.310453	0.659838
203890_s_at	death-associated protein kinase 3	DAPK3	1613	-3.322887	0.659838
217449_at	MRNA; cDNA DKFZp434D1516 (from clone DKFZp434D1516)	---	---	-3.327842	0.659838
205544_s_at	complement component (3d/Epstein Barr virus) receptor 2	CR2	1380	-3.33664	0.659838
219918_s_at	asp (abnormal spindle) homolog. microcephaly associated (Drosophila)	ASPM	259266	-3.339053	0.659838
202094_at	baculoviral IAP repeat-containing 5 (survivin)	BIRC5	332	-3.33953	0.659838
207890_s_at	matrix metallopeptidase 25	MMP25	64386	-3.341023	0.659838
204651_at	nuclear respiratory factor 1	NRF1	4899	-3.34182	0.659838
201977_s_at	KIAA0141	KIAA0141	9812	-3.341932	0.659838
210206_s_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog. S. cerevisiae)	DDX11	1663	-3.345102	0.659838
215509_s_at	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	699	-3.346864	0.659838
220236_at	pyruvate dehydrogenase phosphatase regulatory subunit	PDPR	55066	-3.348782	0.659838
212689_s_at	jumonji domain containing 1A	JMJD1A	55818	-3.349623	0.659838
215897_at	mediator complex subunit 25	MED25	81857	-3.350978	0.659838

203118_at	proprotein convertase subtilisin/kexin type 7	PCSK7	9159	-3.351132	0.659838
217445_s_at	phosphoribosylglycinamide formyltransferase. phosphoribosylglycinamide synthetase. phosphorib	GART	2618	-3.353902	0.659838
203092_at	translocase of inner mitochondrial membrane 44 homolog (yeast)	TIMM44	10469	-3.355713	0.659838
213209_at	TAF6-like RNA polymerase II. p300/CBP-associated factor (PCAF)-associated factor. 65kDa	TAF6L	10629	-3.356676	0.659838
218575_at	anaphase promoting complex subunit 1	ANAPC1	64682	-3.358109	0.659838
213223_at	ribosomal protein L28	RPL28	6158	-3.360826	0.659838
202226_s_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	CRK	1398	-3.365529	0.659838
207629_s_at	rho/rac guanine nucleotide exchange factor (GEF) 2	ARHGEF2	9181	-3.366402	0.659838
212669_at	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CAMK2G	818	-3.371637	0.659838
203194_s_at	nucleoporin 98kDa	NUP98	4928	-3.382784	0.659838
219566_at	pleckstrin homology domain containing. family F (with FYVE domain) member 1	PLEKHF1	79156	-3.383601	0.659838
211109_at	Janus kinase 3 (a protein tyrosine kinase. leukocyte)	JAK3	3718	-3.387591	0.659838
220212_s_at	thyroid adenoma associated	THADA	63892	-3.387613	0.659838
206425_s_at	transient receptor potential cation channel. subfamily C. member 3	TRPC3	7222	-3.393535	0.659838
209453_at	solute carrier family 9 (sodium/hydrogen exchanger). member 1 (antiporter. Na+/H+. amiloride	SLC9A1	6548	-3.398832	0.659838
210053_at	TAF5 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 100kDa	TAF5	6877	-3.414184	0.659838
219098_at	MYB binding protein (P160) 1a	MYBBP1A	10514	-3.416388	0.659838
210457_x_at	high mobility group AT-hook 1	HMGA1	3159	-3.42584	0.659838
214820_at	bromodomain and WD repeat domain containing 1	BRWD1	54014	-3.426963	0.659838
204736_s_at	chondroitin sulfate proteoglycan 4	CSPG4	1464	-3.438347	0.659838
205667_at	Werner syndrome	WRN	7486	-3.439393	0.659838
217750_s_at	ubiquitin-conjugating enzyme E2Z	UBE2Z	65264	-3.446538	0.659838
208021_s_at	replication factor C (activator 1) 1. 145kDa	RFC1	5981	-3.452363	0.659838
211955_at	RAN binding protein 5	RANBP5	3843	-3.457148	0.659838
210949_s_at	eukaryotic translation initiation factor 3. subunit C /// eukaryotic translation initiation factor 3. su	EIF3C /// EIF3	728689 /// 86	-3.457437	0.659838
213118_at	UHRF1 (ICBP90) binding protein 1-like	UHRF1BP1L	23074	-3.457614	0.659838
203947_at	cleavage stimulation factor. 3' pre-RNA. subunit 3. 77kDa	CSTF3	1479	-3.459899	0.659838
200685_at	splicing factor. arginine/serine-rich 11	SFRS11	9295	-3.46931	0.659838
200656_s_at	procollagen-proline. 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase). beta polypeptide	P4HB	5034	-3.469481	0.659838
212315_s_at	nucleoporin 210kDa	NUP210	23225	-3.473049	0.659838
37860_at	zinc finger protein 337	ZNF337	26152	-3.473772	0.659838
47083_at	chromosome 7 open reading frame 26	C7orf26	79034	-3.481351	0.659838
220275_at	CUB and zona pellucida-like domains 1	CUZD1	50624	-3.486819	0.659838
204190_at	ubiquitin specific peptidase like 1	USPL1	10208	-3.493441	0.659838
203395_s_at	hairy and enhancer of split 1. (Drosophila)	HES1	3280	-3.503021	0.659838
202458_at	protease. serine. 23	PRSS23	11098	-3.513778	0.659838
203630_s_at	component of oligomeric golgi complex 5	COG5	10466	-3.515034	0.659838
207895_at	N-acetylated alpha-linked acidic dipeptidase-like 1	NAALADL1	10004	-3.51824	0.659838
213302_at	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	PFAS	5198	-3.520731	0.659838
205726_at	diaphanous homolog 2 (Drosophila)	DIAPH2	1730	-3.533306	0.659838
201391_at	TNF receptor-associated protein 1	TRAP1	10131	-3.535212	0.659838
204016_at	leucyl-tRNA synthetase 2. mitochondrial	LARS2	23395	-3.538666	0.659838
218755_at	kinesin family member 20A	KIF20A	10112	-3.540792	0.659838
208127_s_at	suppressor of cytokine signaling 5	SOCS5	9655	-3.543413	0.659838
216397_s_at	block of proliferation 1 /// similar to block of proliferation 1	BOP1 /// LOC	23246 /// 727	-3.556269	0.659838
215357_s_at	polymerase (DNA-directed). delta interacting protein 3	POLDIP3	84271	-3.558791	0.659838
212756_s_at	ubiquitin protein ligase E3 component n-recognin 2	UBR2	23304	-3.575786	0.659838
210505_at	alcohol dehydrogenase 7 (class IV). mu or sigma polypeptide	ADH7	131	-3.58159	0.659838
219702_at	placenta-specific 1	PLAC1	10761	-3.581873	0.659838
204835_at	polymerase (DNA directed). alpha 1	POLA1	5422	-3.581904	0.659838
200903_s_at	S-adenosylhomocysteine hydrolase	AHCY	191	-3.585197	0.659838
212471_at	KIAA0241	KIAA0241	23080	-3.588245	0.659838
203106_s_at	vacuolar protein sorting 41 homolog (S. cerevisiae)	VPS41	27072	-3.596842	0.659838
216682_s_at	family with sequence similarity 48. member A	FAM48A	55578	-3.610767	0.659838
221965_at	M-phase phosphoprotein 9	MPHOSPH9	10198	-3.619428	0.659838
213756_s_at	heat shock transcription factor 1	HSF1	3297	-3.619831	0.659838
212016_s_at	polypyrimidine tract binding protein 1	PTBP1	5725	-3.622621	0.659838
201918_at	solute carrier family 25. member 36	SLC25A36	55186	-3.625142	0.659838
212125_at	Ran GTPase activating protein 1	RANGAP1	5905	-3.63484	0.659838
203115_at	ferrochelatase (protoporphyria)	FECH	2235	-3.636278	0.659838
220773_s_at	gephyrin	GPHN	10243	-3.641602	0.659838
212789_at	non-SMC condensin II complex. subunit D3	NCAPD3	23310	-3.652501	0.659838
221147_x_at	WW domain containing oxidoreductase	WWOX	51741	-3.661956	0.659838
205450_at	phosphorylase kinase. alpha 1 (muscle)	PHKA1	5255	-3.678124	0.659838
216021_s_at	glycine receptor. alpha 3	GLRA3	8001	-3.687395	0.659838
202367_at	cut-like homeobox 1	CUX1	1523	-3.692489	0.659838
212896_at	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	SKIV2L2	23517	-3.694827	0.659838
206923_at	protein kinase C. alpha	PRKCA	5578	-3.695092	0.659838
202476_s_at	tubulin. gamma complex associated protein 2	TUBGCP2	10844	-3.696805	0.659838
205884_at	integrin. alpha 4 (antigen CD49D. alpha 4 subunit of VLA-4 receptor)	ITGA4	3676	-3.704958	0.659838
212048_s_at	tyrosyl-tRNA synthetase	YARS	8565	-3.708899	0.659838
216736_at	transmembrane 6 superfamily member 2	TM6SF2	53345	-3.714685	0.659838
212238_at	additional sex combs like 1 (Drosophila)	ASXL1	171023	-3.730621	0.659838
216757_at	CDNA: FLJ21342 fis. clone COL02673	---	---	-3.734329	0.659838
213222_at	phospholipase C. beta 1 (phosphoinositide-specific)	PLCB1	23236	-3.736999	0.659838
203783_x_at	polymerase (RNA) mitochondrial (DNA directed)	POLRMT	5442	-3.737653	0.659838
214158_s_at	PR domain containing 10	PRDM10	56980	-3.741032	0.659838
203195_s_at	nucleoporin 98kDa	NUP98	4928	-3.768153	0.659838
209408_at	kinesin family member 2C	KIF2C	11004	-3.770192	0.659838
205581_s_at	nitric oxide synthase 3 (endothelial cell)	NOS3	4846	-3.789026	0.659838
216199_s_at	mitogen-activated protein kinase kinase kinase 4	MAP3K4	4216	-3.789942	0.659838
211550_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog. avia	EGFR	1956	-3.792789	0.659838
216305_s_at	chromosome 2 open reading frame 3	C2orf3	6936	-3.796848	0.659838
219320_at	myosin XIX	MYO19	80179	-3.810062	0.659838
210114_at	inversin	INVS	27130	-3.826297	0.659838
203100_s_at	chromodomain protein. Y-like	CDYL	9425	-3.82816	0.659838

209229_s_at	SAPS domain family. member 1	SAPS1	22870	-3.829086	0.659838
208597_at	ciliary neurotrophic factor	CNTF	1270	-3.837091	0.659838
203235_at	thimet oligopeptidase 1	THOP1	7064	-3.845062	0.659838
209642_at	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	699	-3.847238	0.659838
219017_at	ethanolamine kinase 1	ETNK1	55500	-3.859679	0.659838
36830_at	mitochondrial intermediate peptidase	MIPEP	4285	-3.861645	0.659838
208699_x_at	transketolase (Wernicke-Korsakoff syndrome)	TKT	7086	-3.862596	0.659838
212272_at	lipin 1	LPIN1	23175	-3.872718	0.659838
219307_at	prenyl (decaprenyl) diphosphate synthase. subunit 2	PDSS2	57107	-3.872858	0.659838
203462_x_at	eukaryotic translation initiation factor 3. subunit B	EIF3B	8662	-3.886074	0.659838
210412_at	glutamate receptor. ionotropic. N-methyl D-aspartate 2B	GRIN2B	2904	-3.920012	0.659838
210625_s_at	A kinase (PRKA) anchor protein 1	AKAP1	8165	-3.936975	0.659838
220988_s_at	C1q and tumor necrosis factor related protein 3	C1QTNF3	114899	-3.954415	0.659838
210555_s_at	nuclear factor of activated T-cells. cytoplasmic. calcineurin-dependent 3	NFATC3	4775	-3.965315	0.659838
212164_at	transmembrane protein 183A	TMEM183A	92703	-3.989355	0.659838
203835_at	leucine rich repeat containing 32	LRRC32	2615	-4.021946	0.659838
203373_at	suppressor of cytokine signaling 2	SOCS2	8835	-4.02917	0.659838
47571_at	zinc finger protein 236	ZNF236	7776	-4.035174	0.659838
202302_s_at	arginine/serine-rich coiled-coil 2	RSRC2	65117	-4.054584	0.659838
211791_s_at	potassium voltage-gated channel. shaker-related subfamily. beta member 2	KCNAB2	8514	-4.086634	0.659838
203578_s_at	solute carrier family 7 (cationic amino acid transporter. y+ system). member 6	SLC7A6	9057	-4.092662	0.659838
215747_s_at	regulator of chromosome condensation 1 /// SNHG3-RCC1	RCC1 /// SNH	1104 /// 7518	-4.093268	0.659838
219608_s_at	F-box protein 38	FBXO38	81545	-4.1201	0.659838
215581_s_at	minichromosome maintenance complex component 3 associated protein	MCM3AP	8888	-4.169899	0.659838
202099_s_at	DiGeorge syndrome critical region gene 2	DGCR2	9993	-4.170982	0.659838
212653_s_at	EH domain binding protein 1	EHBP1	23301	-4.187376	0.659838
202496_at	enhancer of mRNA decapping 4	EDC4	23644	-4.193291	0.659838
201167_x_at	Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	396	-4.196988	0.659838
201479_at	dyskeratosis congenita 1. dyskerin	DKC1	1736	-4.224747	0.659838
204275_at	small optic lobes homolog (Drosophila)	SOLH	6650	-4.232288	0.659838
211337_s_at	tubulin. gamma complex associated protein 4	TUBGCP4	27229	-4.244358	0.659838
212431_at	KIAA0194 protein	KIAA0194	22993	-4.319757	0.659838
216217_at	phospholipase C-like 2	PLCL2	23228	-4.353492	0.659838
218927_s_at	carbohydrate (chondroitin 4) sulfotransferase 12	CHST12	55501	-4.409404	0.659838
201842_s_at	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	2202	-4.47356	0.658014
205895_s_at	nucleolar and coiled-body phosphoprotein 1	NOLC1	9221	-4.523706	0.643373
222113_s_at	epidermal growth factor receptor pathway substrate 15-like 1	EPS15L1	58513	-4.550499	0.640184
202179_at	bleomycin hydrolase	BLMH	642	-4.569564	0.634111
213077_at	YTH domain containing 2	YTHDC2	64848	-4.594537	0.623444
212893_at	zinc finger. ZZ-type containing 3	ZZZ3	26009	-4.634696	0.623444
201796_s_at	valyl-tRNA synthetase	VARS	7407	-4.650356	0.623444
203159_at	glutaminase	GLS	2744	-4.748201	0.585101
218382_s_at	U2 small nuclear RNA auxiliary factor 2	U2AF2	11338	-4.774282	0.576315
205095_s_at	ATPase. H+ transporting. lysosomal V0 subunit a1	ATP6V0A1	535	-4.921941	0.487407
205461_at	RAB35. member RAS oncogene family	RAB35	11021	-4.973428	0.482434
201478_s_at	dyskeratosis congenita 1. dyskerin	DKC1	1736	-5.246881	0.392181
220950_s_at	KIAA1310	KIAA1310	55683	-5.424994	0.368172
203644_s_at	MON1 homolog B (yeast)	MON1B	22879	-5.673282	0.368172
213578_at	bone morphogenetic protein receptor. type IA	BMPR1A	657	-6.010642	0.295814
201638_s_at	cleavage and polyadenylation specific factor 1. 160kDa	CPSF1	29894	-7.908362	0.105387

Supplementary Table 6: List of genes both upregulated by PD-1 stimulation in Jurkat cells (t > 2.0) and in HIV Progressors as compared with Controllers (t < –2.0)

probeset_id	GeneTitle	GeneSymbol	t
210164_at	granzyme B (granzyme 2. cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	21.620876
209969_s_a	**signal transducer and activator of transcription 1. 91kDa**	**STAT1**	**19.349693**
202269_x_at	guanylate binding protein 1. interferon-inducible. 67kDa	GBP1	13.790309
209417_s_at	interferon-induced protein 35	IFI35	13.758327
202659_at	proteasome (prosome. macropain) subunit. beta type. 10	PSMB10	9.567776
204415_at	interferon. alpha-inducible protein 6	IFI6	9.376857
202307_s_at	transporter 1. ATP-binding cassette. sub-family B (MDR/TAP)	TAP1	9.037264
204279_at	proteasome (prosome. macropain) subunit. beta type. 9 (large multifunctional peptidase 2)	PSMB9	8.909184
203882_at	**interferon regulatory factor 9**	**IRF9**	**8.694727**
34210_at	CD52 molecule	CD52	8.48951
209670_at	T cell receptor alpha constant	TRAC	8.145286
203729_at	epithelial membrane protein 3	EMP3	8.119499
210140_at	cystatin F (leukocystatin)	CST7	7.86001
209732_at	C-type lectin domain family 2. member B	CLEC2B	7.856387
209813_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading	TARP /// TRG	7.525085
214669_x_at	immunoglobulin kappa locus	IGK@	7.403741
202270_at	guanylate binding protein 1. interferon-inducible. 67kDa	GBP1	7.219952
204747_at	interferon-induced protein with tetratricopeptide repeats 3	IFIT3	7.204917
204661_at	CD52 molecule	CD52	6.915314
218400_at	2'-5'-oligoadenylate synthetase 3. 100kDa	OAS3	6.903254
201762_s_at	proteasome (prosome. macropain) activator subunit 2 (PA28 beta)	PSME2	6.886636
200760_s_at	ADP-ribosylation-like factor 6 interacting protein 5	ARL6IP5	6.759636
208965_s_at	interferon. gamma-inducible protein 16	IFI16	6.528202
214617_at	perforin 1 (pore forming protein)	PRF1	6.359152
216920_s_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading	TARP /// TRG	6.319274
201641_at	bone marrow stromal cell antigen 2	BST2	6.252856
205965_at	**basic leucine zipper transcription factor. ATF-like**	**BATF**	**6.235932**
215806_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading	TARP /// TRG	6.235368
210951_x_at	RAB27A. member RAS oncogene family	RAB27A	6.18875
213060_s_at	chitinase 3-like 2	CHI3L2	6.050052
213915_at	natural killer cell group 7 sequence	NKG7	6.044779
209514_s_at	RAB27A. member RAS oncogene family	RAB27A	5.824808
211796_s_at	T cell receptor beta variable 19 /// T cell receptor beta variable 7-2 /// T cell receptor beta variable 5-4 /	TRBC1 /// TR	5.664187
202592_at	biogenesis of lysosome-related organelles complex-1. subunit 1	BLOC1S1	5.566296
202101_s_at	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	5.519963
212203_x_at	interferon induced transmembrane protein 3 (1-8U)	IFITM3	5.44233
201541_s_at	zinc finger. HIT type 1	ZNHIT1	5.432486
208659_at	chloride intracellular channel 1	CLIC1	5.430092
214004_s_at	vestigial like 4 (Drosophila)	VGLL4	5.380125
201601_x_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	5.374556
200814_at	proteasome (prosome. macropain) activator subunit 1 (PA28 alpha)	PSME1	5.367468
204994_at	myxovirus (influenza virus) resistance 2 (mouse)	MX2	5.316415
205081_at	cysteine-rich protein 1 (intestinal)	CRIP1	5.314466
209890_at	tetraspanin 5	TSPAN5	5.276698
212784_at	capicua homolog (Drosophila)	CIC	5.269762
209671_x_at	T cell receptor alpha locus /// T cell receptor alpha constant	TRA@ /// TRA	5.267778
201194_at	selenoprotein W. 1	SEPW1	5.245011
211144_x_at	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading	TARP /// TRG	5.228222
220449_at	hypothetical protein MGC5566	MGC5566	5.22753
217497_at	endothelial cell growth factor 1 (platelet-derived)	ECGF1	5.20215
215797_at	T cell receptor alpha variable 8-3	TRAV8-3	5.201479
205345_at	BRCA1 associated RING domain 1	BARD1	5.189021
217755_at	hematological and neurological expressed 1	HN1	5.102404
214343_s_at	ataxin 7-like 1	ATXN7L1	5.058278
208492_at	regulatory factor X-associated protein	RFXAP	5.01901
201275_at	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase. dimethylallyltranstransferase. geran	FDPS	4.992341
202760_s_at	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2	AKAP2 /// PAL	4.98906
216298_at	hypothetical protein LOC648852	LOC648852	4.861568
206484_s_at	X-prolyl aminopeptidase (aminopeptidase P) 2. membrane-bound	XPNPEP2	4.838981
202747_s_at	integral membrane protein 2A	ITM2A	4.823814
206687_s_at	protein tyrosine phosphatase. non-receptor type 6	PTPN6	4.78005
203595_s_at	interferon-induced protein with tetratricopeptide repeats 5	IFIT5	4.732435
202446_s_at	phospholipid scramblase 1	PLSCR1	4.699799
217962_at	nucleolar protein family A. member 3 (H/ACA small nucleolar RNPs)	NOLA3	4.657467
210972_x_at	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T ce	TRA@ /// TRA	4.647777
214995_s_at	apolipoprotein B mRNA editing enzyme. catalytic polypeptide-like 3G /// apolipoprotein B mRNA editing	APOBEC3F ///	4.629687
218913_s_at	GEM interacting protein	GMIP	4.617402
219807_x_at	RAB4B. member RAS oncogene family	RAB4B	4.609035
210807_s_at	solute carrier family 16. member 7 (monocarboxylic acid transporter 2)	SLC16A7	4.535773
202323_s_at	acyl-Coenzyme A binding domain containing 3	ACBD3	4.462806
206150_at	CD27 molecule	CD27	4.462507
209389_x_at	diazepam binding inhibitor (GABA receptor modulator. acyl-Coenzyme A binding protein)	DBI	4.45446

222369_at	N-acetyltransferase 11	NAT11	4.394234
206332_s_at	interferon. gamma-inducible protein 16	IFI16	4.375824
212082_s_at	myosin. light chain 6. alkali. smooth muscle and non-muscle	MYL6	4.21968

Supplementary Methods

Microarray data analysis

Prior to analysis, microarray data were pre-processed and normalized using robust multi-chip averaging, as previously described[1]. Differentially expressed genes between classes were ranked using Smyth's variance-moderated t-test[2].

Gene Set Enrichment Analysis

Traditional strategies for gene expression analysis have focused on identifying individual genes that exhibit differences between two states of interest. Although useful, they may fail to detect biological processes, such as transcriptional programs, that are distributed across an entire network of genes but are hard to distinguish at the level of individual genes. Enrichment Analysis provides a general statistical method to test for the enrichment of a set of related genes in an independent expression dataset.[3,4]

Enrichment analysis considers a priori defined gene sets comprised of biologically related genes (e.g. members of a metabolic pathway, genes at the same genomic locus, or, in this case, genes upregulated in HIV-specific $CD8^+$ T cells from progressors or genes upregulated by PD-1 ligation). Using such a priori defined gene sets one can ask whether that set of genes, as whole, tends to occur towards the top (or bottom) of the rank-ordered set of all genes differentially expressed between two cell types of interest (e.g. exhausted vs. memory T cell samples). Sets of genes that are highly related to one cell-type should be distributed at the top of the rank ordered list; gene sets that are not related would be expected to be randomly distributed throughout the list.

Enrichment analysis estimates the degree of enrichment and assesses significance with a *P* value obtained by permutation testing. Considering groups of related genes, enrichment analysis increases resolution and statistical power, and can detect subtle but consistent changes that are often missed by inspection alone. The methodology of the statstical test has been previously described and used in several recent studies[1,5,6].

Gene set enrichment analysis on groups of samples was performed as previously described using the Zhang statistic as implemented in the program RenderCat[7]. To characterize further the gene expression signatures of CD8$^+$ T cells from controllers and progressors, we tested for enrichment of differentially expressed genes in sets of functionally related genes. We used the Applied Biosystems Panther collection (http://www.pantherdb.org). Gene sets with less than five genes were excluded. To test for enrichments, we used a threshold-free technique based on the Zhang C statistic, implemented in the program RenderCat[7].

Single Sample Enrichment Analysis

A variant of GSEA, termed single sample GSEA was used to identify the relative enrichment of the PD-1 signature genes in individual samples of HIV-specific CD8$^+$ T cells, or of CD8$^+$ T cells analyzed in a previous study [1].

The PD-1 signature was projected across expression profiling data from 42 tetramer-sorted HIV-specific CD8$^+$ T cell samples and from a further 24 samples of CMV-, EBV- or influenza-specific CD8$^+$ T cells generated in our previous study[3]. This was accomplished by a 'single sample' extension of GSEA that allows one to define an enrichment score that represents the degree of absolute enrichment of a gene set in each sample within a given data set[8]. The gene expression values for a given sample were rank-normalized, and an enrichment score was produced using the Empirical Cumulative Distribution Functions (ECDF) of the genes in the signature and the remaining genes. This procedure is similar to that used in a previous implementation of GSEA [4] but the list is ranked by absolute expression (in one sample). The enrichment score is obtained by an integration of the difference between the ECDF. The enrichment score is obtained, not by a weighted Kolmogorov-Smirnov statistic like in GSEA[4], but by an integration of the difference between the ECDFs.

Cell Culture

PD-1 expressing Jurkat cells were generated by transduction with a lentivirus expressing full-length PD-1, and maintained in RPMI 1640 (MediaTech) supplemented with 10% Fetal Bovine Serum (Hyclone), 1% of both pen/strep and L-glutamine, 16.6 ug/ml gentamicin (Gibco/Invitrogen) and 10 ug/ml blasticidin (InvivoGen).

Primary human $CD4^+$ or $CD8^+$ T cells from the peripheral blood of healthy volunteers were isolated via magnetic selection using the respective isolation kits (Miltenyi Biotec), and in most cases were labeled with CFSE according to manufacturer's instructions (Molecular Probes/Invitrogen).

293FT cells used to generate lentivirus particles were maintained in DMEM (MediaTech) supplemented with 10% Fetal Bovine Serum (Hyclone), 1% of both pen/strep and L-glutamine and 16.6 μg/ml gentamicin (Gibco/Invitrogen).

Bead preparation

Beads used for cell stimulation were generated by conjugation of antibodies against CD3 (64 ng, clone UCHT1) and CD28 (80 ng, clone CD28.2) as well as either control IgG1 (1.25 μg clone MOPC-31C) for positive CD3/CD28 beads or either an antibody against human PD-1 (1.25 μg, clone EH12) or PDL1-Ig fusion protein[9] (1.25 μg) for PD1/CD3/CD28 or PDL1/CD3/CD28 beads, respectively, to CELLection Pan Mouse IgG beads (Invitrogen/Dynal). For PDL1-Ig titration experiments, the amount of PDL1-Ig conjugated to the beads was decreased in 2-fold increments while IgG1 was added to maintain equivalent amounts of total protein on the beads (1.394 μg total protein). Binding occurred over a 90 minute incubation period at 4 °C with constant end-over-end rotation. Following incubation, beads were washed twice and stored at 4 °C in the 0.1% FBS-containing PBS prior to use.

RNA Isolation and cDNA conversion

RNA was isolated from cells resuspended in TRIzol and cDNA was generated from a reverse transcription reaction using the ImProm-II Reverse Transcription System (Promega) or, for samples with fewer than 50,000 cells, with the WT-Ovation Pico RNA Amplification system (NuGEN) according to the manufacturer's directions.

Lentiviral vectors and transduction

Lentiviral vectors encoding shRNA hairpin sequences targeting BATF or GFP as control as well as a puromycin resistance cassette in the pLKO.1 backbone were obtained from The RNAi Consortium (TRC, http://broadinstitute.org/rnai/trc) of the Broad Institute (Cambridge, MA). The lentiviral vector used to overexpress BATF was generated by gateway cloning of full-length human BATF cDNA (Open Biosystems) into the pLenti6.2/V5-DEST vector that includes a blasticidin resistance cassette (Invitrogen). Lentivirus-containing supernatant was generated according to TRC protocols (http://www.broadinstitute.org/rnai/trc/lib) via a lipid-based delivery system using TransIT-LT1 transfection reagent (Mirus Bio) and 293FT cells provided by the TRC.

For lentiviral transduction of primary human T cells, following isolation and CFSE labeling, cells were placed at a concentration of 2 x 10^6 cells well^{-1} in 24 well plates previously coated with 2.5 μg/ml of antibodies against CD3 (OKT3 clone, eBiosciences, San Diego, CA) and CD28 (CD28.2 clone, BD Biosciences) antibodies in media comprised of RPMI 1640 supplemented with 10% FBS, 1% of pen/strep, L-glutamine and HEPES and 16.6 μg/ml gentamicin (Gibco/Invitrogen), in the presence of 20 U ml^{-1} recombinant human IL-2 (Roche Diagnostics). Following 2 days of stimulation, cells were counted and placed in wells of a 96 well U-bottom plate at a concentration of 2 x 10^5 cells well^{-1} in media supplemented with 8 μg/ml of polybrene (Sigma, St. Louis, MO) and 20 U ml^{-1} rhIL-2 together with lentivirus-containing supernatant at an MOI of 1. Transduction occurred via a 90 min spin infection at 2250 rpm at 37 °C, after which the lentivirus-containing supernatant was removed and replaced with fresh media supplemented with 20 U ml^{-1} rhIL-2. At day 2 following transduction, media containing selection reagents, (puromycin for shRNA vectors and blasticidin for overexpression vectors), as well as IL-2 was added and selection was allowed to occur for a total of 5 days. All subsequent experiments with lentivirus-transduced T cells were conducted in the absence of IL-2.

Cytokine measurements

IL-2 and IFN-γ production was measured using Quantikine Immunoassays according to manufacturer's direction (R&D Systems). For HIV-specific experiments, cytokines were measured with the Milliplex High sensitivity Kit (Millipore) using the Bio-Plex 200 system (BioRad) according to the manufacturer's instructions

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