SUPPLEMENTARY APPENDIX

Immature MEF2C-dysregulated T-cell leukemia patients have an early T-cell precursor acute lymphoblastic leukemia gene signature and typically have non-rearranged T-cell receptors

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Online methods

Immature *MEF2C*-dysregulated T-cell leukemia patients have an early T-cell precursor acute lymphoblastic leukemia gene signature and typically have non-rearranged T-cell receptors

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Fluorescent in-situ hybridization (FISH). FISH analysis was performed on thawed cytospin slide as described before.(1) To identify rearrangements of the *LYL1* locus, we used home-labeled BAC clones RP11-352L7 and RP11-356L15 (BAC/PAC Resource Center, Children's Hospital, Oakland, USA).

Genomic DNA and RNA extraction and ABD status detection by quantitative PCR

Genomic DNA and RNA were isolated from ≥5x10^6 leukemic cells using TRIzol reagent (Invitrogen) according to the manufacturer's protocol, with minor modifications.(2) DNA was stored at 4°C. For RNA isolation, an additional phenol-chloroform extraction was performed as a minor modification of the protocol, and RNA was precipitated with isopropanol together with 1 µl (20 µg/ml) glycogen (Roche, Almere, the Netherlands). After precipitation, the RNA pellets were dissolved in 20 µl RNAse-free TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0), and the concentration was measured spectrophotometrically.(2) The presence of absence of bi-allelic *TRG@* deletions (ABD) was determined using quantitative PCR, targeting the intron between TRGV11 and TRGJP1 as described previously.(3)

In vitro cytotoxicity assay

In vitro cytotoxicities for leukemic cells towards serial dilutions of L-Asparaginase (0.003-10 IU/mL, Paronal, Christiaens, Breda, The Netherlands), prednisolone (0.08-250 µg/mL, BUFA BV, Uitgeest, the Netherlands), vincristine (0.05-50 µg/mL TEVA Pharma BV, Mijdrecht, The Netherlands), daunorubicin hydrochloride (0.002-2.0 µg/mL, Ceubidine, Rhône-Poulenc Rorer, Amstelveen, The Netherlands) or cytarabine (0.002-2.5 µg/mL, Cytosar, Pharmacia & Upjohn, Woerden, the Netherlands) were determined using the MTT assay.(4) Briefly, $1.6x10^5$ leukemic cells (>90% purity as determined by morphological examination of May-Grunwald-Giemsa (Merck, Darmstadt, Germany) stained cytospin slides) were exposed to serial dilutions of chemotherapeutic drugs in duplicate in a final volume of 100 µL culture media (RPMI 1640 (Life Technologies, Breda, The Netherlands) supplemented with 10% fetal calfs serum (Integro, Zaandam, The Netherlands), 5 µg/mL transferrin, 5 ng/mL sodium selenite (ITS media supplement, Sigma-Aldrich, Zwijndrecht, The Netherlands), 100 IU/mL penicellin, 100 µg/mL streptomycin, 0.125 µg/mL fungizone (Life technologies)). Following 4 days of incubation in a humified incubator at 37^oC with 5% CO_2, 5 mg/mL MTT (3-[4,5-dimethyldiazol-2-yl]-2,5-diphenyltetrazoliumbromide, Sigma-Aldrich) was added and incubated for an additional 6 hrs at 37^oC to facilitate reduction of MTT tetrazolium salt into formazan crystals by viable cells. Total formazan production was measured spectrophotometrically at 562 nm. For each patient sample, leukemic cells incubated in the absence of drugs was used as control, whereas the assay performed on pure media containing wells were used for background correction (blank values). Leukemic cells survival following exposure to each drug concentration was calculated for background corrected OD values using the formula: ((OD drug incubated wells / OD control wells) x 100%), and the LC50 drug concentrations, at which 50% of the leukemic cells die, were calculated.

Microarray expression analyses

RNA integrity testing, copy-DNA and copy-copy RNA (ccRNA) syntheses, washing, hybridization to Human Genome U133 plus 2.0 microarrays (Affymetrix, Santa Clara, CA), extraction of probe set intensities from CEL-files and normalization with RMA or VSN methods were performed as previously described.(1)

Geneset enrichment analysis (GSEA; (5)) was performed on our Affymetrix U133 plus 2.0 microarray expression dataset for 117 T-ALL cases(6) using 1000 random permutations . Enrichment scores and nominal p-values were obtained for up- or down-regulated probe sets among the TOP100, 200 or 500 most significantly, differentially expressed probesets for human ETP-ALL compared to other T-ALL cases.(7) Also up- or down-regulated genes or

probesets for C/EBPA-mutated AML(8) and early T-cell (MPP-ETP-DN2A) and commited T-cell (DN2B-and later) subsets(9) were tested.

ETP-ALL patients were identified by Prediction Analysis of Microarrays (PAM) (10) implemented in *R* (11) using the human ETP-ALL probe set signature.(7) The classifier was built on the 100, 200 or 500 most significant probe sets from this ETP-ALL gene signature (**Supplementary Table S1**) (7) using class labels immature cluster (n=15) and non-immature cluster (n-102) in our gene expression cohort comprising 117 T-ALL patient samples. Patients with a cross-validated probability greater than 0.6 for being classified as immature were considered to be ETP-ALL patients. Microarray data are available at the gene expression omnibus (http://www.ncbi.nlm.nih.gov/geo/), accession GSE10609 and GSE26713.

Differentially expressed genes between ETP-ALL cases with or without bi-allelic *TRG@* rearrangements (ABD versus non-ABD ETP-ALL) were obtained by regression analysis using the *limma* package in the R statistical software package.(11) VSN- or RMA-normalized expression values for *MEF2C* (probe set 239966_at), *LMO1* (probe set 206718_at), *LMO2* (probe set 204249_s_at), *LYL1* (probe set 210044_s_at), *ERG1* (probeset 1563392_at) and *BAALC* (probe set 222780_s_at) were used to test for differential expression between the T-ALL groups (representative probe sets were used).

Human hematopoietic progenitor signature genes (probesets) as established by Novershtern and coworkers(12) within the immature cluster gene signature were enriched using the Fisher's exact test. Differentially expressed genes between the immature cluster (n=15) (13) versus other T-ALL cases (n=102) in our T-ALL microarray expression set were analyzed using the Wilcoxon statistical test and corrected for multiple testing error using the false discovery rate procedure as previously described(14) using the Bioconductor package Multitest. A total of 784 probesets with an FDR p-value less than p=0.01 was selected as the immature cluster expression signature gene set (**Supplementary Table S5)**.

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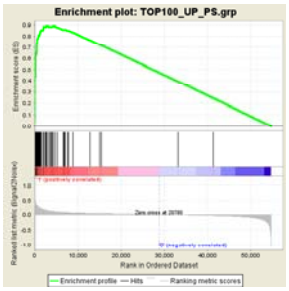
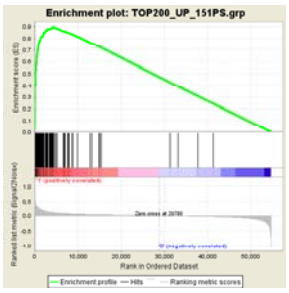
Supplementary Figure S1.

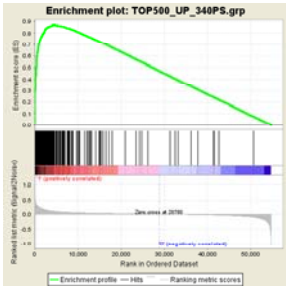
A



1000 permutations
Upregulated in Immature
84 probesets
ES= 0.8906417
NES= 1.7610614
NOM P-value<0.0001
FDR<0.0001

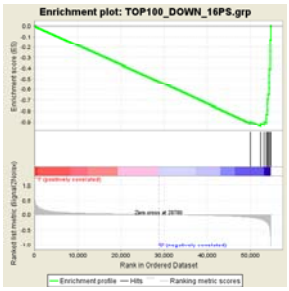


1000 permutations
Upregulated in Immature
151 probesets
ES= 0.8929122
NES= 1.8345773
NOM P-value<0.0001
FDR<0.0001

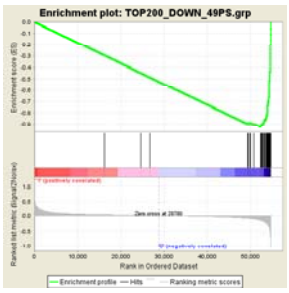


1000 permutations
Upregulated in Immature
340 probesets
ES= 0.8715323
NES= 1.9051393
NOM P-value<0.0001
FDR<0.0001

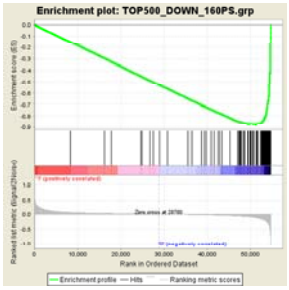
B



1000 permutations
Down regulated in Immature
16 probesets
ES= -0.9412975
NES= -1.5765783
NOM P-value<0.0001
FDR<0.0001

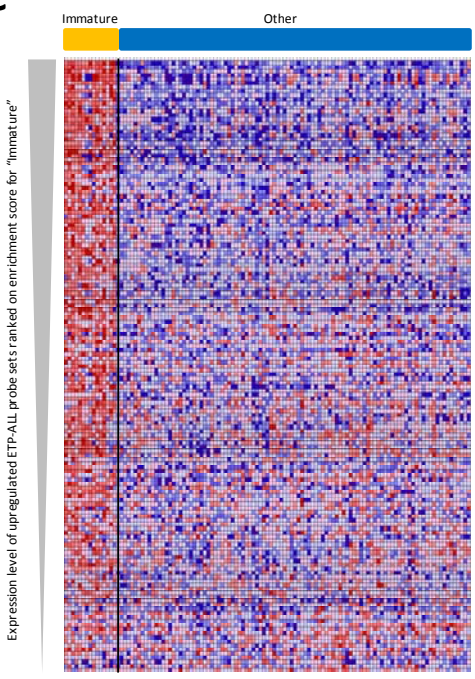


1000 permutations
Down regulated in Immature
49 probesets
ES= -0.9274382
NES= -1.688663
NOM P-value<0.0001
FDR<0.0001

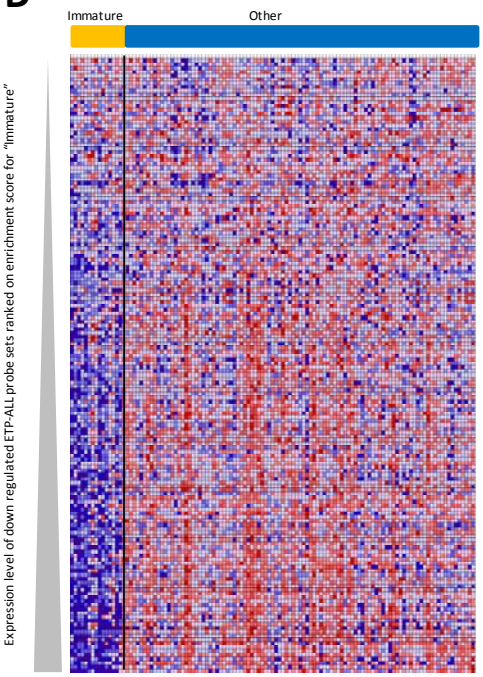


1000 permutations
Down regulated in Immature
160 probesets
ES= -0.8799995
NES= -1.7953509
NOM P-value<0.0001
FDR<0.0001

C

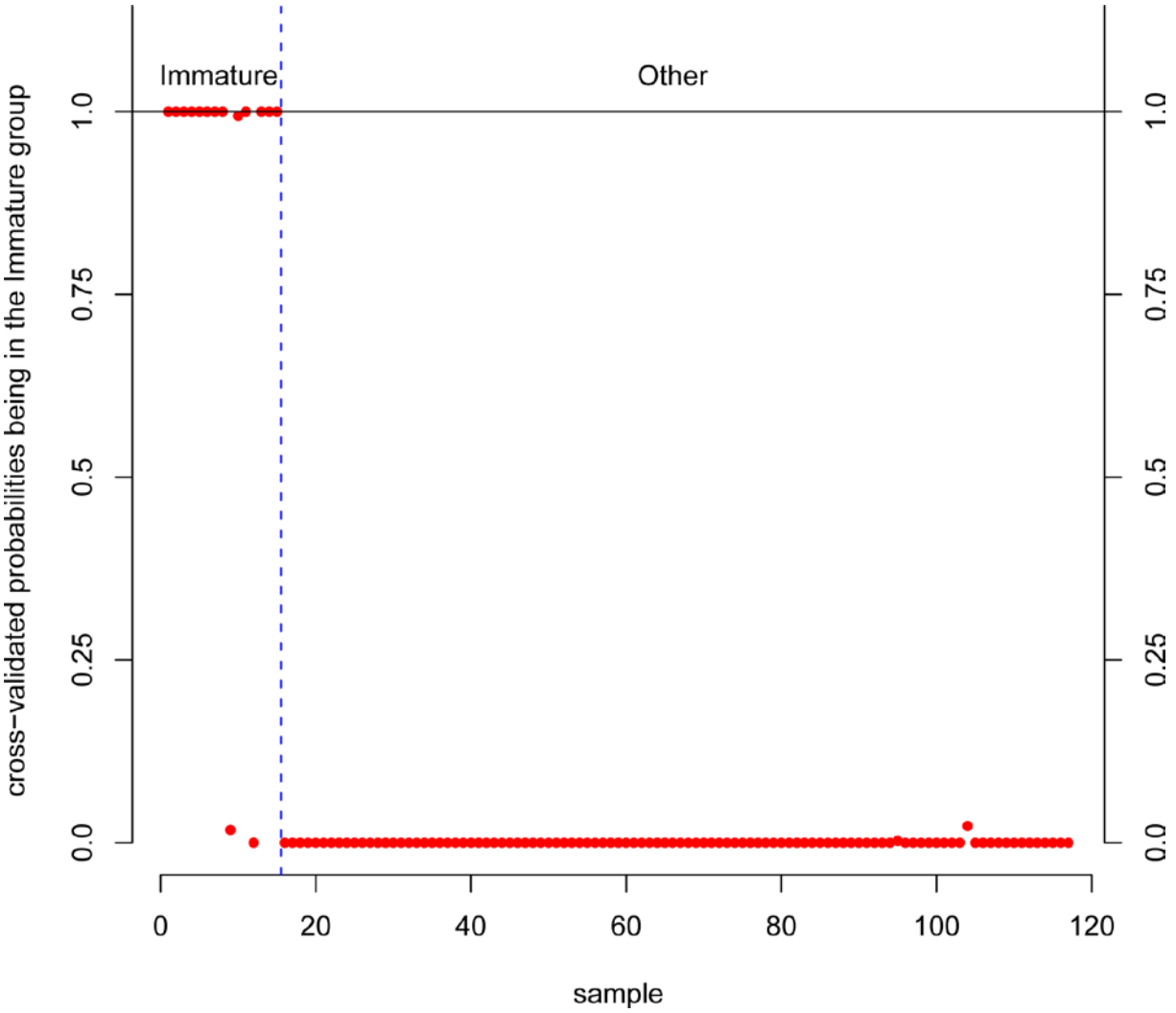


D



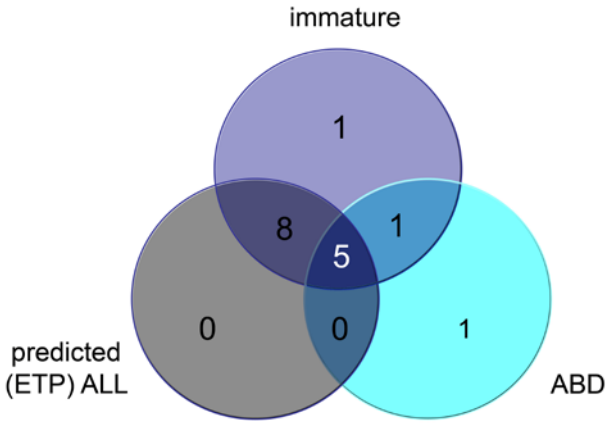
ETP-ALL signatures genes are enriched in the immature T-ALL cluster. Gene set enrichment analysis (GSEA) for **(A)** up- and **(B)** down-regulated probe sets from the top 100, 200 or 500 most significantly differentially expressed probe sets from the human ETP-ALL gene signature (Zhang *et al.*, nature 2012) for immature cluster versus other T-ALL patients. Significance levels for each analysis have been indicated. Heatmaps for **(C)** up- and **(D)** down-regulated probe sets for immature cluster patients versus other T-ALL patients.

Supplementary Figure S2.



PAM prediction of immature cluster cases versus non-immature cluster T-ALL patients based on the TOP100, 200 or 500 most significant probe sets from the human ETP-ALL gene signature (Zhang *et al.*, Nature 2012). Only results for the TOP100 most significant ETP-ALL gene signature probe sets are shown predicting 13 out of 15 immature cluster cases while none of the 102 non-immature cluster cases on this probe selection ($p<0.001$).

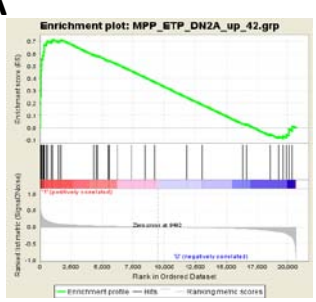
Supplementary Figure S3.



Overlap between the immature cluster, ETP-ALL and ABD characteristics in our pediatric T-ALL cohort. The number of ETP-ALL positive patients in this Venn diagram is depicted by the gray sphere, the number of ABD patients is depicted by blue sphere, and the number of immature cluster patients is depicted by the dark blue sphere. This diagram is based on 117 T-ALL patients for whom gene expression array data is available.

Supplementary Figure S4.

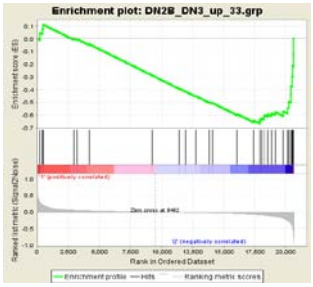
A



Mingueneau et al., Nat. Immunol 2013
"Up-regulated in MPP-ETP-DN2A"

1000 permutations
42 genes
ES= 0.71475744
NES= 1.5796351
NOM P-value=0.007

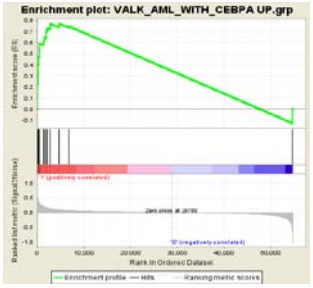
B



Mingueneau et al., Nat. Immunol 2013
"Up-regulated in DN2B-DN3"

1000 permutations
33 genes
ES= -0.66486216
NES= -1.4611057
NOM P-value= 0.045

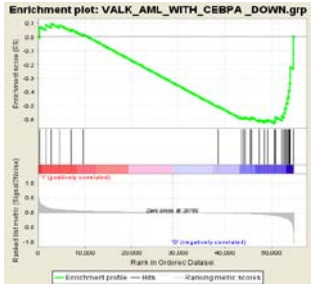
C



Wouters et al., Blood 2007
"ALK_AML_WITH_CEBPA_UP"

1000 permutations
18 probesets
ES=0.77072185
NES=1.3581719
NOM P-value= 0.085

D

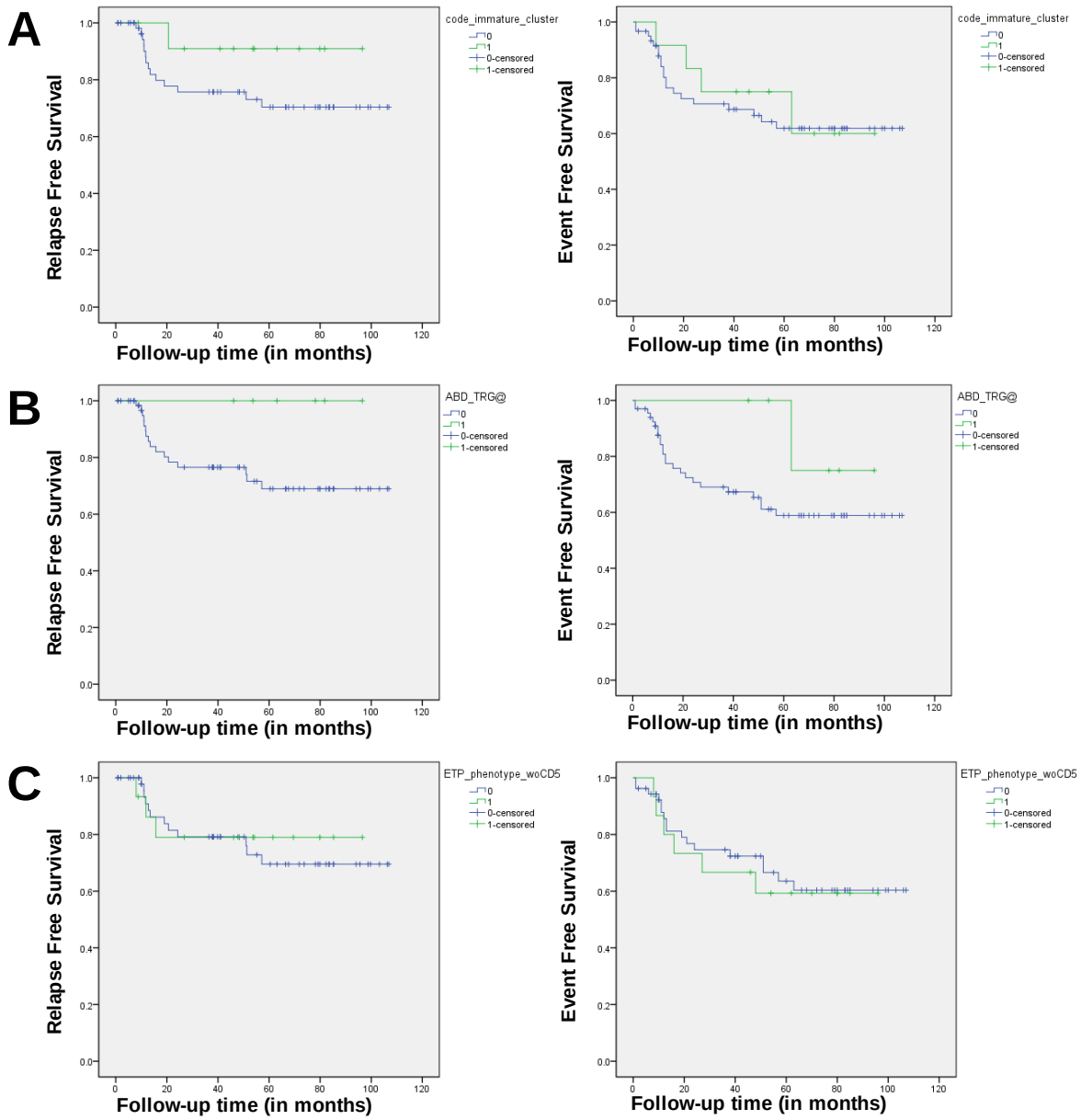


Wouters et al., Blood 2007
"VALK_AML_WITH_CEBPA_Down"

1000 permutations
28 probesets
ES-0.62715673
NES-1.1575706
NOM P-value= 0.26

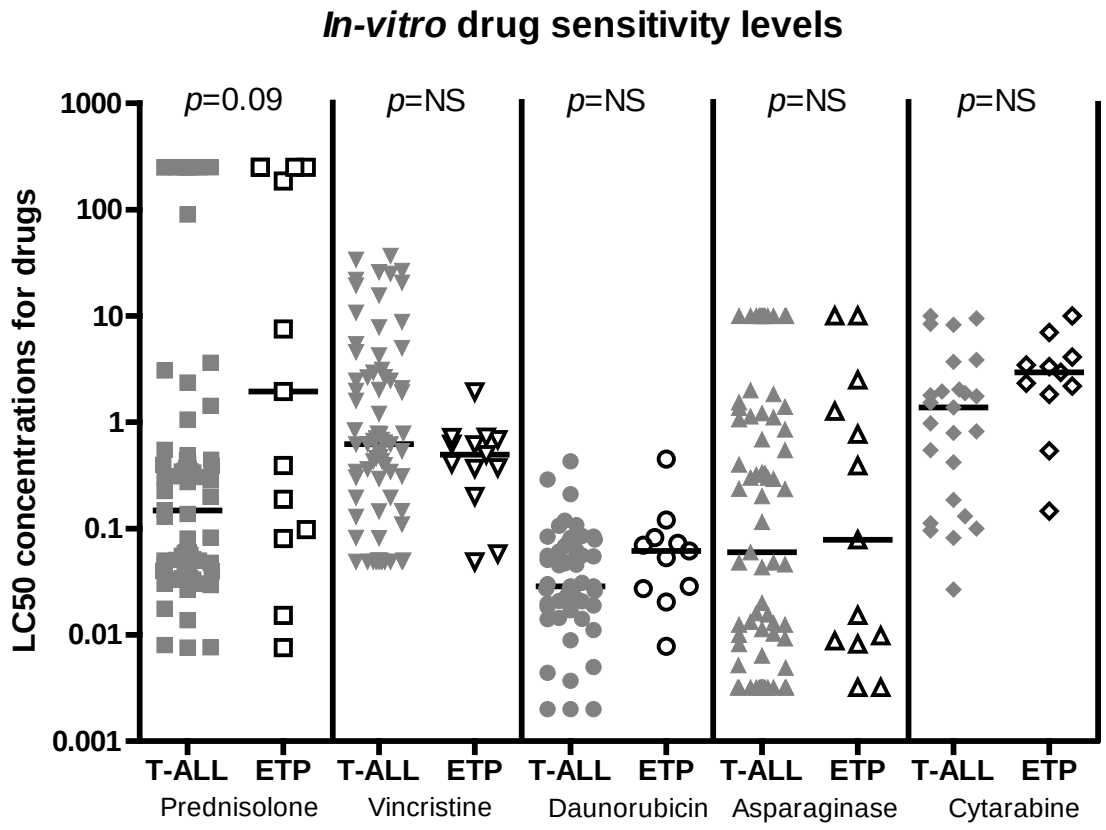
Immature cluster/ETP-ALL cases are enriched for early T-cell development signatures. Enrichment of **(A)** MPP-ETP-DN2A or **(B)** post-DN2A T-cell signatures genes in immature cluster/ETP-ALL T-ALL cases. GSEA for **(C)** up- or **(D)** down-regulated genes of *C/EBPA*-inactivated AML patient samples in immature cluster/ETP-ALL T-ALL cases.

Supplementary Figure S5.



Immature cluster T-ALL, ABD and immunophenotypic ETP-ALL patients treated on the COALL-97 protocol do not predict for poor outcome. Relapse free survival (RFS) and event free survival (EFS) curves for COALL-97 pediatric T-ALL patients. RFS and EFS curves (**A**) for immature cluster T-ALL cases upon unsupervised cluster (green line) versus other T-ALL cases (blue line), **(B)** for ABD T-ALL cases (green line) versus non-ABD cases (blue line), and **(C)** for ETP-ALL cases as identified upon immunophenotypic parameters (green line) compared to other T-ALL cases (blue line). Cases that are lost from further follow-up are represented by vertical tick marks.

Supplementary Figure S6.



In vitro **sensitivity of Immature cluster/ETP-ALLleukemic cells towards chemotherapeutic agents.** *In vitro* drug sensitivity levels towards prednisolone (squares), vincristine (downside-facing triangles), daunorubicin (circles), L-asparaginase (upside-facing triangles) and cytarabine (diamonds) were measured for leukemic cells of Immature cluster/ETP-ALL patients (open symbols) versus other T-ALL cases (closed gray symbols). The sensitivity level for each sample is indicated as the LC50 drug concentration that is lethal for 50 percent of the leukemic cells. Significance levels have been indicated. NS, not significant.

Supplementary Table S1

TOP500 ETP-ALL gene set (Zhang et al., Nature 2012)			Significance level, FDR, ratio and median fold-change for differential expression levels of probesets in immature cluster patients vs other T-ALL patients					
ProbeSet	Genes	Refseq	Wilcoxon pvalues	FDR	Median_Immature	Median_other	ratio	foldchange
1 230127_PM_at	---	---	9.01385E-07	0.000473877	4.194229901	3.594576695	0.599653	1.51535226
2 228188_PM_at	FOSL2	NM_005253	0.00671225	0.100053951	7.50989915	5.734477233	1.775422	3.42338113
3 219054_PM_at	C5orf23	NM_024563	2.45321E-05	0.003529965	7.534769941	6.353576208	1.181194	2.26764332
4 210094_PM_s_at	PARD3	NM_019619	4.65519E-05	0.005152273	7.305311067	8.05188498	-0.74657	-1.67780368
5 209357_PM_at	CITED2	NM_006079	0.213757036	0.582472297	9.004561943	8.731584086	0.272978	1.2082993
6 1558105_PM_a_at	---	---	1.53946E-06	0.000637652	6.078164278	4.740793452	1.337371	2.52690395
7 213638_PM_at	PHACTR1	NM_030948	0.004380388	0.07834404	5.509120343	4.800752024	0.708368	1.63395508
8 221526_PM_x_at	PARD3	NM_019619	3.71537E-06	0.001080611	6.826691301	8.259341722	-1.43265	-2.69942179
9 218109_PM_s_at	MFSD1	NM_022736	0.003206417	0.064955167	8.077145517	7.601927854	0.475218	1.39012794
10 1556950_PM_s_at	SERPINB6	NM_004568	0.001209407	0.036352795	5.55470832	5.340081197	0.214627	1.16040396
11 218618_PM_s_at	FNDC3B	NM_001135095 / NM	0.002697881	0.059239623	5.965123662	5.403995417	0.561128	1.47542261
12 204790_PM_at	SMAD7	NM_005904	0.0038506	0.072397371	7.910114969	6.624478095	1.285637	2.43789649
13 219789_PM_at	NPR3	NM_000908	6.36277E-05	0.006179507	6.058869467	4.690663602	1.368206	2.58149332
14 205330_PM_at	MN1	NM_002430	2.30654E-06	0.000813648	5.764628585	4.361197015	1.403432	2.64530041
15 225032_PM_at	FNDC3B	NM_001135095 / NM	0.033011529	0.243741441	6.254137137	5.546502412	0.707635	1.63312444
16 243830_PM_at	FNDC3B	NM_001135095 / NM	0.951243258	0.986199919	4.764815569	4.741887341	0.022928	1.0160196
17 219183_PM_s_at	CYTH4	NM_013385	1.41877E-06	0.000620571	8.969507312	7.342295209	1.627212	3.08915466
18 222603_PM_at	ERMP1	NM_024896	6.72649E-07	0.000404144	5.428037806	4.447756565	0.980281	1.97284996
19 236126_PM_at	ACVR2B	NM_001106	9.90353E-05	0.007951417	5.878396668	6.456341071	-0.57794	-1.49272086
20 203778_PM_at	MANBA	NM_005908	6.58594E-05	0.006273278	7.034075422	6.593210944	0.440864	1.35741746
21 212658_PM_at	LHFPL2	NM_005779	0.185230461	0.54927191	6.450116274	6.390964099	0.059152	1.04185332
22 205418_PM_at	FES	NM_001143783 / NM	0.006005508	0.094353779	6.108706336	5.623922861	0.484783	1.39937583
23 219812_PM_at	PVRIG	NM_024070	0.280035843	0.646277478	7.793673928	9.053551886	-1.25988	-2.39475482
24 222692_PM_s_at	FNDC3B	NM_001135095 / NM	0.003041337	0.063107445	4.611251544	4.498503114	0.112748	1.0812862
25 233748_PM_x_at	PRKAG2	NM_001040633 / NM	0.000684721	0.025890726	5.593379001	5.178943415	0.414436	1.33277716
26 228831_PM_s_at	GNG7	NM_052847	1.25458E-06	0.000586303	7.116782988	6.236121681	0.880661	1.84121909
27 200696_PM_s_at	GSN	NM_000177 / NM_00	1.46968E-05	0.002583752	7.076339255	6.141363068	0.934976	1.91185908
28 215501_PM_s_at	DUSP10	NM_007207 / NM_14	0.179879322	0.542854885	9.240304215	8.705628686	0.534676	1.44861632
29 211474_PM_s_at	SERPINB6	NM_004568	0.003751901	0.071252244	6.102738137	5.258000042	0.844738	1.79593868
30 244022_PM_at	---	---	0.029193809	0.229236178	4.943574227	4.767581768	0.175992	1.12974131
31 1568943_PM_at	INPP5D	NM_001017915 / NM	5.68214E-07	0.000361263	5.749840345	5.246377653	0.503463	1.41761197
32 209199_PM_s_at	MEF2C	NM_001131005 / NM	6.58641E-10	1.40097E-05	6.868789215	4.335277814	2.533511	5.78979152
33 211037_PM_s_at	MBOAT7	NM_001146056 / NM	0.170791852	0.533296743	6.454058603	6.366910974	0.087148	1.06226788
34 203085_PM_s_at	TGFB1	NM_000660	0.281853708	0.649155776	9.138082867	8.415269073	0.722814	1.65039779
35 200601_PM_at	ACTN4	NM_004924	3.26965E-05	0.004157394	8.773897737	7.736617158	1.037281	2.0523554
36 205254_PM_x_at	TCF7	NM_001134851 / NM	3.5107E-05	0.004352702	6.701599709	7.603760476	-0.90216	-1.86886294
37 225386_PM_s_at	HNRPLL	NM_001142650 / NM	1.46957E-05	0.002583752	7.045757215	8.480916684	-1.43516	-2.70412055
38 213601_PM_at	SLIT1	NM_003061	0.026865225	0.219724185	7.209552649	8.788611643	-1.57906	-2.98774909
39 226397_PM_s_at	---	---	0.001032638	0.033055894	7.059398806	6.386605894	0.672793	1.59415611
40 1554876_PM_a_at	S100Z	NM_130772	1.90176E-05	0.003013985	5.653756715	4.96313965	0.690617	1.61397369
41 206674_PM_at	FLT3	NM_004119	0.376387015	0.722043439	6.271256674	6.335420609	-0.06416	-1.04547889
42 209200_PM_at	MEF2C	NM_001131005 / NM	7.68706E-10	1.40097E-05	6.116013064	4.490358153	1.625655	3.08582214
43 229507_PM_at	C3orf54	NM_203370	0.000794066	0.028394747	7.155011749	6.960729816	0.194282	1.14415454
44 229801_PM_at	C10orf47	NM_153256	4.33981E-05	0.004953631	7.650431301	6.761608437	0.888823	1.85166468
45 229971_PM_at	GPR114	NM_153837	0.005233146	0.086836693	6.037893964	5.662106249	0.375788	1.29754783
46 242903_PM_at	IFNGR1	NM_000416	0.000197864	0.012087373	7.531322726	6.449356587	1.081966	2.1169191
47 236395_PM_at	---	---	7.68539E-10	1.40097E-05	5.610162869	3.734753183	1.87541	3.66905794
48 224925_PM_at	PREX1	NM_020820	0.001974994	0.048927416	7.4327153	6.778418627	0.654297	1.5738485
49 204777_PM_s_at	MAL	NM_002371 / NM_02	0.000625975	0.024554111	8.4973915	11.66184368	-3.16445	-8.96592344
50 228899_PM_at	LOC100132	XR_078381 / XR_0787	0.001336097	0.038775278	4.561113918	4.351226338	0.209888	1.15659805
51 225567_PM_at	---	---	0.001869148	0.047312807	5.652415105	4.875511491	0.776904	1.71344943
52 219383_PM_at	PRR5L	NM_001160167 / NM	8.21248E-06	0.001808973	4.658475409	4.166895418	0.49158	1.40598382
53 221527_PM_s_at	PARD3	NM_019619	5.93885E-05	0.005925306	5.298051358	5.846355409	-0.5483	-1.46236561
54 221563_PM_at	DUSP10	NM_007207 / NM_14	0.302389681	0.664970269	9.678994025	9.191641253	0.487353	1.4018702
55 226550_PM_at	---	---	6.44936E-07	0.000396201	6.74499999	5.165666844	1.579333	2.98831689
56 222693_PM_at	FNDC3B	NM_001135095 / NM	0.051350054	0.305991596	3.303510997	3.221791137	0.08172	1.05827888
57 214152_PM_at	CCPG1	NM_004748 / NM_02	6.81565E-05	0.006392261	3.746400584	3.527983938	0.218417	1.163456
58 224570_PM_s_at	IRF2BP2	NM_001077397 / NM	0.009869916	0.125588262	10.52881118	9.524097606	1.004714	2.00654509
59 1554335_PM_at	CYTH4	NM_013385	5.54143E-05	0.005793068	5.47045646	4.921633665	0.548823	1.46289152
60 243923_PM_at	---	---	0.010842243	0.132354511	4.395867574	4.226607155	0.16926	1.12448188
61 1552386_PM_at	GAPT	NM_152687	6.58573E-05	0.006273278	4.035372554	3.669674939	0.365698	1.28850454
62 225658_PM_at	SPOPL	NM_001001664	0.000408988	0.01909599	5.066057946	4.227591559	0.838466	1.7881483
63 222872_PM_x_at	OBFC2A	NM_001031716 / NR	0.110965651	0.440220587	4.555771626	4.405652909	0.150119	1.10966078
64 205255_PM_x_at	TCF7	NM_001134851 / NM	0.127363737	0.469575669	11.29293642	11.82264856	-0.52971	-1.44364112
65 204891_PM_s_at	LCK	NM_001042771 / NM	0.235527504	0.606099781	10.40306859	11.91755853	-1.51449	-2.85697803
66 242029_PM_at	FNDC3B	NM_001135095 / NM	0.03953561	0.266832422	6.042312703	5.805980541	0.236332	1.17799398
67 219582_PM_at	OGFRL1	NM_024576	2.89049E-08	0.000109046	5.567730337	4.452641525	1.115089	2.16608343
68 202761_PM_s_at	SYNE2	NM_015180 / NM_18	1.08718E-07	0.000163578	5.403168767	7.213025485	-1.80986	-3.50607466
69 221081_PM_s_at	DENND2D	NM_024901	0.00010951	0.008457393	6.41573684	8.385043196	-1.96931	-3.91579803
70 203603_PM_s_at	ZEB2	NM_014795	5.92773E-07	0.000372527	6.132697913	4.247113126	1.885585	3.69502669
71 208759_PM_at	NCSTN	NM_015331	0.221360386	0.591967173	7.471380204	7.523010634	-0.05163	-1.03643557
72 227013_PM_at	LATS2	NM_014572	0.010346205	0.129238917	8.682610965	5.249630104	3.432981	10.8001606
73 243757_PM_at	LOC100129	---	0.008764455	0.117594246	6.301625521	6.768936556	-0.46731	-1.38253024
74 204164_PM_at	SIPA1	NM_006747 / NM_15	1.1754E-05	0.002239205	7.178265991	6.460640609	0.717625	1.64447307
75 36920_PM_at	MTM1	NM_000252	0.245330413	0.615606055	4.033841717	3.887546157	0.146296	1.10672406
76 204890_PM_s_at	LCK	NM_001042771 / NM	0.85445397	0.958324161	9.034704685	10.84364847	-1.80894	-3.50385672

77	224921_PM_at	SCAMP2	NM_005697	0.027431805	0.221803304	7.650939487	7.398761552	0.252178	1.19100373
78	219247_PM_s_at	ZDHHC14	NM_024630 / NM_15	0.138947086	0.486702025	7.656910159	7.58422338	0.072687	1.05167343
79	201163_PM_s_at	IGFBP7	NM_001553	0.58210653	0.843336456	6.247227416	4.373541166	1.873686	3.66467752
80	200736_PM_s_at	GPX1	NM_000581 / NM_20	0.093060716	0.407373472	10.26817087	9.78249188	0.485679	1.40024472
81	220377_PM_at	FAM30A //	NR_026800 / XM_001	1.60345E-06	0.000654244	7.376152453	6.341791097	1.034361	2.04820676
82	241742_PM_at	PRAM1	NM_032152	0.000211038	0.012651882	6.694988049	5.688484512	1.006504	2.00903617
83	206267_PM_s_at	MATK	NM_002378 / NM_13	1.81104E-06	0.000707307	7.52628305	6.523000254	1.003283	2.0045561
84	201162_PM_at	IGFBP7	NM_001553	0.007402298	0.106171746	7.191372738	6.682786188	0.508587	1.4226557
85	203332_PM_s_at	INPP5D	NM_001017915 / NM	0.000626005	0.024554111	8.894413269	7.739214494	1.155199	2.22715007
86	219659_PM_at	ATP8A2	NM_016529	0.000408988	0.01909599	5.609964909	5.912010685	-0.30205	-1.23289144
87	216835_PM_s_at	DOK1	NM_001381	0.116552562	0.450423113	7.631772156	7.474432177	0.15734	1.115229
88	225499_PM_at	C20orf74	NM_020343	0.000645061	0.024995528	6.163590513	5.580492538	0.583098	1.49806267
89	227329_PM_at	ZBTB46	NM_025224	0.010842391	0.132354511	4.313896778	4.110126954	0.20377	1.15170388
90	225262_PM_at	FOSL2	NM_005253	0.674583046	0.887673359	9.765236815	7.469341156	2.295896	4.91058757
91	207857_PM_at	LILRA2	NM_001130917 / NM	0.001374501	0.039469986	5.67188347	4.819547632	0.852336	1.80542168
92	1555486_PM_a_at	PRR5L	NM_001160167 / NM	4.01921E-06	0.00113865	5.438591281	4.847439942	0.591151	1.50644849
93	224569_PM_s_at	IRF2BP2	NM_001077397 / NM	0.004910936	0.084226352	12.67869501	12.20231851	0.476377	1.391245
94	227999_PM_at	PWWP2B	NM_001098637 / NM	3.64628E-08	0.000109046	6.705728735	5.743907412	0.961821	1.94776729
95	230917_PM_at	---	---	4.21929E-07	0.000307602	5.990037062	4.712085528	1.277952	2.42494417
96	224571_PM_at	IRF2BP2	NM_001077397 / NM	0.000165502	0.010941741	8.248554948	7.355452934	0.893102	1.85716502
97	223380_PM_s_at	LATS2	NM_014572	0.905897452	0.973944414	9.512684701	6.366897312	3.145787	8.8506744
98	209321_PM_s_at	ADCY3	NM_004036	0.000589538	0.023718179	6.196818459	5.369274031	0.827544	1.77466219
99	218342_PM_s_at	ERMP1	NM_024896	2.8335E-05	0.003863655	7.072188698	6.689497307	0.382691	1.30377181
100	207980_PM_s_at	CITED2	NM_006079	0.977235764	0.994312293	8.804793591	8.684700536	0.120093	1.08680496
101	227077_PM_at	ZNF286A /,	NM_001130842 / NM	0.000115134	0.008779791	7.144159363	7.975140278	-0.83098	-1.77889445
102	200940_PM_s_at	RERE	NM_001042681 / NM	5.68241E-07	0.000361263	7.937600818	7.117625034	0.819976	1.76537636
103	218909_PM_at	RPS6KC1	NM_001136138 / NM	0.069679889	0.354494083	4.962083268	4.749985027	0.212098	1.15837168
104	222582_PM_at	PRKAG2	NM_001040633 / NM	0.019082324	0.182881395	5.760567854	5.417094152	0.343474	1.26880794
105	209544_PM_at	RIPK2	NM_003821	0.089158414	0.398138011	3.401808435	3.382985275	0.018823	1.01313271
106	202392_PM_s_at	C22orf30 /,	NM_014338 / NM_17	0.004850869	0.08324585	8.185663631	7.827355117	0.358309	1.28192203
107	226685_PM_at	SNTB2	NM_006750	0.012750469	0.144483291	4.002216863	4.156033085	-0.15382	-1.11250839
108	225385_PM_s_at	HNRPLL	NM_001142650 / NM	0.000255669	0.014249828	3.451400393	3.92449979	-0.4731	-1.38808835
109	212257_PM_s_at	SMARCA2	NM_003070 / NM_13	0.001093942	0.034023082	5.065984389	4.814234461	0.25175	1.19065045
110	219148_PM_at	PBK	NM_018492	1.25464E-06	0.000586303	4.801725923	7.116117531	-2.31439	-4.97394863
111	218143_PM_s_at	SCAMP2	NM_005697	0.015636201	0.163591769	8.648616567	8.460881914	0.187735	1.13897387
112	217989_PM_at	HSD17B11	NM_016245	0.056423578	0.320595314	8.688036395	8.176443085	0.511593	1.42562378
113	202546_PM_at	VAMP8	NM_003761	0.204886536	0.572532523	9.782288785	8.98834653	0.793942	1.73380573
114	206478_PM_at	KIAA0125	NR_026800	8.69471E-06	0.00184974	6.012435787	4.967502333	1.044933	2.06327119
115	206631_PM_at	PTGER2	NM_000956	7.27832E-09	7.95884E-05	6.79316302	4.967616945	1.825546	3.54441142
116	211597_PM_s_at	HOPX	NM_001145459 / NM	0.003292042	0.066028016	7.302902205	5.149296906	2.153605	4.44938303
117	1552671_PM_a_at	SLC9A7	NM_032591	0.000121028	0.009003544	5.169851029	4.878945312	0.290906	1.22340809
118	243170_PM_at	---	---	0.001560037	0.042668843	4.01590361	3.873679321	0.142224	1.1036053
119	219660_PM_s_at	ATP8A2	NM_016529	0.000168229	0.011002268	4.985380659	5.56921864	-0.58384	-1.49883127
120	241353_PM_s_at	---	---	0.002522808	0.056786543	8.602912923	7.652840881	0.950072	1.93196913
121	207968_PM_s_at	MEF2C	NM_001131005 / NM	2.40097E-06	0.000820458	6.954339528	6.336123617	0.618216	1.5349758
122	206896_PM_s_at	GNG7	NM_052847	4.51993E-06	0.001205497	6.263040938	5.578537564	0.684503	1.60714865
123	232045_PM_at	PHACTR1	NM_030948	0.024698789	0.209885966	6.338304987	6.264893626	0.073411	1.05220175
124	209545_PM_s_at	RIPK2	NM_003821	0.329930871	0.687120343	7.555789457	7.388917287	0.166872	1.12262195
125	235085_PM_at	PRAGMIN	NM_001080826	0.021270123	0.193923166	5.320567309	5.191379904	0.129187	1.09367752
126	1564378_PM_a_at	---	---	0.465590627	0.778620334	4.603788019	4.552365737	0.051422	1.03628604
127	228606_PM_at	TCTEX1D2	NM_152773	0.004003007	0.074266852	6.807682046	7.428421082	-0.62074	-1.53766266
128	231431_PM_s_at	---	---	0.000748505	0.02730185	7.908344587	7.372959802	0.535385	1.44932866
129	206148_PM_at	IL3RA	NM_002183	0.009192729	0.120791262	6.828958824	6.508172145	0.320787	1.24901143
130	202780_PM_at	OXCT1	NM_000436	1.35853E-07	0.000181165	6.912454672	8.293619635	-1.38116	-2.6047862
131	225883_PM_at	ATG16L2	NM_033388	0.570975213	0.837776609	6.72348089	6.763269529	-0.03979	-1.02796321
132	237491_PM_at	---	---	0.006233363	0.0961651	3.92256851	4.916969785	-0.9944	-1.99225356
133	215206_PM_at	---	---	0.114667573	0.447179	6.610822865	6.764585821	-0.15376	-1.11246732
134	221773_PM_at	ELK3	NM_005230	0.226017013	0.596087028	5.405790456	4.828469786	0.577321	1.49207564
135	205659_PM_at	HDAC9	NM_014707 / NM_05	6.58594E-05	0.006273278	6.612392263	6.227606456	0.384786	1.30566592
136	205317_PM_s_at	SLC15A2	NM_001145998 / NM	0.004789501	0.083001666	4.78915374	4.682246407	0.106907	1.0769172
137	214151_PM_s_at	CCPG1	NM_004748 / NM_02	0.076868985	0.372358622	4.422261468	4.332618699	0.089643	1.06410666
138	202990_PM_at	PYGL	NM_001163940 / NM	0.265772939	0.633551424	4.587550537	4.413658369	0.173892	1.12809782
139	221753_PM_at	SSH1	NM_001161330 / NM	1.05026E-05	0.002080535	8.226131341	7.697909539	0.528222	1.44215057
140	200661_PM_at	CTSA	NM_000308 / NM_00	0.031052345	0.236757351	8.677745302	7.895802665	0.781943	1.7194446
141	223533_PM_at	LRRC8C	NM_032270	4.18968E-05	0.004822707	7.929812727	6.946228429	0.983584	1.97737199
142	221156_PM_x_at	CCPG1	NM_004748 / NM_02	4.34679E-06	0.001205497	3.834329449	3.401994652	0.432335	1.34941565
143	225955_PM_at	METRNL	NM_001004431	0.005502964	0.089574094	9.23786549	7.056476141	2.181389	4.53590162
144	235721_PM_at	DTX3	NM_178502	0.000737505	0.027245332	8.183536801	8.881570424	-0.69803	-1.62229212
145	201792_PM_at	AEBP1	NM_001129	0.001158647	0.035252667	7.580591854	8.721930558	-1.14134	-2.20585614
146	213067_PM_at	MYH10	NM_005964	0.128387883	0.469792974	4.732947305	5.150924663	-0.41798	-1.33605311
147	201845_PM_s_at	RYBP	NM_012234	0.627613656	0.865769563	9.325295045	8.30603454	1.019261	2.02687976
148	244230_PM_at	---	---	9.25835E-05	0.007612266	3.925974092	3.560761942	0.365212	1.28807103
149	225102_PM_at	MGLL	NM_001003794 / NM	0.000462466	0.020523799	7.063611695	6.027488592	1.036123	2.05070945
150	224973_PM_at	FAM46A	NM_017633	1.29953E-07	0.000177639	4.229633478	3.358017061	0.871616	1.82971179
151	209179_PM_s_at	MBOAT7	NM_001146056 / NM	0.041939345	0.274819831	9.654333608	8.887298763	0.767035	1.70176856
152	224837_PM_at	FOXP1	NM_001012505 / NM	0.110056068	0.440023074	9.697203327	9.318980835	0.378222	1.29973949
153	205316_PM_at	SLC15A2	NM_001145998 / NM	0.017866315	0.176582155	5.529219164	5.107476432	0.421743	1.33954471
154	238732_PM_at	COL24A1	NM_152890	0.005785367	0.091791917	4.270885454	3.727493867	0.543392	1.45739464
155	233085_PM_s_at	OBFC2A	NM_001031716 / NR_	0.14335157	0.493659322	4.136702543	3.964017946	0.172685	1.12715397
156	200951_PM_s_at	CCND2	NM_001759	0.112805321	0.443523007	6.214542404	5.12354481	1.090998	2.13021285
157	203181_PM_x_at	SRPK2	NM_182691 / NM_18	0.964234693	0.990279984	7.72179091	7.866774972	-0.14498	-1.10571844

158	220576_PM_at	PGAP1	NM_024989	0.001974956	0.048927416	6.261355533	7.779544292	-1.51819	-2.86431222
159	1553043_PM_a_at	CD300LF	NM_139018	0.11846458	0.453543233	5.464531212	5.241262176	0.223269	1.16737578
160	226438_PM_at	SNTB1	NM_021021	0.010591495	0.130841829	5.978338104	5.821453578	0.156885	1.11487698
161	204554_PM_at	PPP1R3D	NM_006242	0.264024995	0.633500091	3.991938246	4.096941332	-0.105	-1.07549669
162	235048_PM_at	FAM169A	NM_015566	0.003379624	0.066902318	6.483566076	7.847277026	-1.36371	-2.57346284
163	211005_PM_at	LAT /// SPN	NM_001014987 / NM_	0.185230461	0.54927191	8.527250589	10.44959216	-1.92234	-3.79037758
164	224838_PM_at	FOXP1	NM_001012505 / NM_	0.089158414	0.398138011	9.559387911	8.879269748	0.680118	1.60227098
165	239966_PM_at	---	---	2.70673E-06	0.000875682	5.528282785	4.809652361	0.71863	1.64561908
166	210948_PM_s_at	LEF1	NM_001130713 / NM_	0.026865225	0.219724185	7.265122485	8.161715225	-0.89659	-1.86166403
167	212372_PM_at	MYH10	NM_005964	0.001582088	0.042779766	6.392774453	8.397859921	-2.00509	-4.01412479
168	211211_PM_x_at	SH2D1A	NM_001114937 / NM_	0.110056068	0.440023074	7.680970708	8.50239275	-0.82142	-1.76714698
169	220416_PM_at	ATP8B4	NM_024837	0.367652071	0.715633381	3.698386719	3.667619486	0.030767	1.02155525
170	223287_PM_s_at	FOXP1	NM_001012505 / NM_	0.001974917	0.048927416	9.353448186	8.913417473	0.440031	1.35663321
171	1555888_PM_at	UBR5	NM_015902	3.15504E-05	0.004078063	4.700102125	4.227608933	0.472493	1.38750521
172	213395_PM_at	MLC1	NM_015166 / NM_13	5.16928E-05	0.005585584	6.253868577	5.159640406	1.094228	2.13498831
173	211210_PM_x_at	SH2D1A	NM_001114937 / NM_	0.543599046	0.824080238	8.408252255	9.216496572	-0.80824	-1.75107917
174	241833_PM_at	---	---	2.04451E-06	0.000740288	4.152647443	5.43605901	-1.28341	-2.43413902
175	228033_PM_at	E2F7	NM_203394	5.7057E-06	0.001418053	3.989415898	6.279207856	-2.28979	-4.88985592
176	220591_PM_s_at	EFHC2	NM_025184	0.001720119	0.045041908	4.308452638	4.157655423	0.150797	1.11018278
177	215772_PM_x_at	SUCLG2	NM_003848	8.50764E-05	0.007357982	5.174696932	6.928698457	-1.754	-3.37292801
178	1569666_PM_s_at	---	---	0.98373872	0.99601704	4.654351224	4.657780325	-0.00343	-1.0023797
179	230051_PM_at	C10orf47	NM_153256	7.46632E-06	0.001744535	4.902006204	3.867409857	1.034596	2.0485404
180	228155_PM_at	C10orf58	NM_032333 / NR_024	0.000664624	0.025482673	6.459763817	7.686359939	-1.2266	-2.34014207
181	205899_PM_at	CCNA1	NM_001111045 / NM_	0.07755209	0.37243395	4.378356316	4.252896513	0.12546	1.09085535
182	231747_PM_at	CYSLTR1	NM_006639	0.000211038	0.012651882	5.674687908	4.498856837	1.175831	2.25922987
183	225344_PM_at	NCOA7	NM_001122842 / NM_	0.043611616	0.27999825	8.515012383	7.741035911	0.773976	1.70997647
184	220028_PM_at	ACVR2B	NM_001106	4.82091E-05	0.005282229	6.287126186	7.02999719	-0.74287	-1.67350285
185	239798_PM_at	---	---	1.42602E-08	0.000109046	6.236043881	5.001064208	1.23498	2.35378031
186	241756_PM_at	---	---	0.511633664	0.805667193	9.620737562	8.285867294	1.33487	2.52252797
187	205642_PM_at	CEP110	NM_007018	0.772257681	0.928778764	6.392078008	6.525182607	-0.1331	-1.0966511
188	211209_PM_x_at	SH2D1A	NM_001114937 / NM_	0.035787293	0.254744068	7.217280747	7.941347893	-0.72407	-1.65183221
189	49111_PM_at	---	---	0.000919415	0.030839893	7.960818794	7.274033569	0.686785	1.60969262
190	1557961_PM_s_at	LOC100127	XM_001722508 / XM_	4.59226E-08	0.000109166	3.260347806	5.394416873	-2.13407	-4.38953789
191	204613_PM_at	PLCG2	NM_002661	0.000396542	0.018820717	7.662710857	7.159622475	0.503088	1.41724422
192	218346_PM_s_at	SESN1	NM_014454	0.002455718	0.055804814	7.425931797	6.857920917	0.568011	1.48247819
193	212459_PM_x_at	SUCLG2	NM_003848	0.00021793	0.012881448	3.858898242	5.665137122	-1.80624	-3.49729351
194	205504_PM_at	BTK	NM_000061	2.70673E-06	0.000875682	6.843133417	6.013340185	0.829793	1.7774306
195	229029_PM_at	---	---	0.055898967	0.31809962	7.631971895	8.266201878	-0.63423	-1.55210911
196	201853_PM_s_at	CDC25B	NM_004358 / NM_02	0.000748523	0.02730185	8.302389398	9.374231447	-1.07184	-2.10211566
197	212655_PM_at	ZCCHC14	NM_015144	0.00019157	0.01186194	4.903355986	4.561522125	0.341834	1.26736657
198	1552623_PM_at	HSH2D	NM_032855	1.69522E-07	0.000201796	7.678396351	5.776104438	1.902292	3.73806567
199	233265_PM_at	---	---	0.007224175	0.104520185	4.438590448	4.576623424	-0.13803	-1.10040376
200	207705_PM_s_at	NINL	NM_025176	1.2996E-07	0.000177639	5.905185153	7.856852793	-1.95167	-3.86821408
201	202727_PM_s_at	IFNGR1	NM_000416	0.003379624	0.066902318	8.376850382	7.868551833	0.508299	1.42237172
202	206545_PM_at	CD28	NM_006139	0.000142803	0.009959127	4.788600606	8.174084449	-3.38548	-10.4503825
203	205609_PM_at	ANGPT1	NM_001146	0.000705399	0.02632666	4.417390936	3.976295417	0.441096	1.35763486
204	223917_PM_s_at	SLC39A3	NM_144564 / NM_21	0.224457104	0.595275134	7.329551187	7.181161833	0.148389	1.10833142
205	244753_PM_at	---	---	3.26096E-07	0.000254717	7.608369158	5.913153128	1.695216	3.23825373
206	1565706_PM_at	---	---	4.04477E-05	0.004735495	5.509291903	4.615457891	0.893834	1.85810755
207	1556462_PM_a_at	---	---	0.880113135	0.965338342	4.443174494	4.486596906	-0.04342	-1.03055565
208	202934_PM_at	HK2	NM_000189	0.000197864	0.012087373	8.840990611	7.162566093	1.678425	3.20078222
209	201015_PM_s_at	JUP	NM_002230 / NM_02	0.616093292	0.860187357	8.78306427	6.742601356	2.040463	4.11377507
210	226589_PM_at	TMEM192	NM_001100389	0.000408977	0.01909599	5.399863109	5.038307492	0.361556	1.28481053
211	226705_PM_at	FGFR1	NM_015850 / NM_02	6.04383E-08	0.000122388	7.102010008	8.888042505	-1.78603	-3.44865186
212	227552_PM_at	40787	NM_052838	4.18968E-05	0.004822707	6.28863415	7.835677752	-1.54704	-2.92217707
213	241434_PM_at	---	---	0.041940113	0.274819831	4.021085327	4.052099823	-0.03101	-1.02173035
214	219737_PM_s_at	PCDH9	NM_020403 / NM_20	5.00378E-07	0.000337755	5.332925491	6.755988822	-1.42306	-2.68154289
215	223009_PM_at	C11orf59	NM_017907	0.342215578	0.696185674	9.459310201	9.2568493	0.202461	1.15065944
216	205315_PM_s_at	SNTB2	NM_006750	7.75708E-06	0.001774554	5.311910753	5.847781727	-0.53587	-1.44981716
217	37384_PM_at	PPM1F	NM_014634	0.041125087	0.272681892	7.701878329	7.548518301	0.15336	1.11215666
218	228303_PM_at	GALNT6	NM_007210	0.031693059	0.238753154	7.50857065	8.129537994	-0.62097	-1.53790602
219	218928_PM_s_at	SLC37A1	NM_018964	3.30103E-06	0.000997147	7.411931691	6.600527157	0.811405	1.75491911
220	201945_PM_at	FURIN	NM_002569	0.011359927	0.135938721	7.932116632	7.762742526	0.169374	1.1245705
221	232174_PM_at	---	---	0.003469445	0.067941228	4.243291557	4.455452064	-0.21216	-1.15842168
222	233545_PM_at	INPP5D	NM_001017915 / NM_	0.025225703	0.211633466	5.207578686	5.042294325	0.165284	1.12138709
223	213910_PM_at	IGFBP7	NM_001553	0.229156501	0.599283831	3.786157723	3.756408385	0.029749	1.02083474
224	203063_PM_at	PPM1F	NM_014634	0.025762318	0.21390353	7.2840615	7.142305094	0.141756	1.10324744
225	224572_PM_s_at	IRF2BP2	NM_001077397 / NM_	0.011761445	0.139520526	11.24388194	10.75081058	0.493071	1.40743799
226	226287_PM_at	CCDC34	NM_030771 / NM_08	0.000974505	0.031828584	5.621779954	6.603718284	-0.98194	-1.97511729
227	202206_PM_at	ARL4C	NM_005737	0.045777656	0.287861984	10.92506664	10.77065388	0.154413	1.1129685
228	205590_PM_at	RASGRP1	NM_001128602 / NM_	0.000350256	0.017330537	6.697476538	8.889627289	-2.19215	-4.56986248
229	202013_PM_s_at	EXT2	NM_000401 / NM_20	0.925302526	0.978945328	5.67719304	5.720322121	-0.04313	-1.03034614
230	232544_PM_at	---	---	0.005642527	0.090578417	3.990524191	3.878792615	0.111732	1.08052434
231	211796_PM_s_at	TRBC1	---	0.007770063	0.10941693	11.12898707	12.83062131	-1.70163	-3.25269204
232	214438_PM_at	HLX	NM_021958	0.00855683	0.115777829	5.255300082	5.060054911	0.195245	1.14491871
233	202441_PM_at	ERLIN1	NM_001100626 / NM_	0.380801652	0.725194369	7.654936086	7.949763861	-0.29483	-1.22673852
234	211026_PM_s_at	MGLL	NM_001003794 / NM_	0.001093919	0.034023082	7.827272865	6.706301452	1.120971	2.17493368
235	1562550_PM_at	---	---	6.16362E-06	0.001484563	4.297108331	4.583333313	-0.28622	-1.21944525
236	1553635_PM_s_at	TCTEX1D1	NM_152665	0.159620618	0.517140156	4.623935947	4.568284883	0.055651	1.03932803
237	207761_PM_s_at	METTL7A	NM_014033	0.000162826	0.010790936	7.00486286	5.629092976	1.37577	2.59506358
238	215592_PM_at	---	---	0.031693698	0.238753154	8.424413439	9.040824748	-0.61641	-1.53305697

239	218292_PM_s_at	PRKAG2	NM_001040633 / NM	0.116552562	0.450423113	5.796960849	5.58916013	0.207801	1.15492624
240	241074_PM_at	C12orf32	NR_027363 / NR_0273	0.003122883	0.064070053	6.594635136	8.669828444	-2.07519	-4.21400874
241	37152_PM_at	PPARD	NM_006238 / NM_17	0.2019892	0.569383354	5.974090587	6.147418513	-0.17333	-1.1276567
242	232472_PM_at	---	---	0.336036638	0.692297105	4.636060982	4.619196452	0.016865	1.01175819
243	244561_PM_at	---	---	5.48946E-06	0.001395983	4.841984506	4.352538318	0.489446	1.40390585
244	229543_PM_at	FAM26F	NM_001010919	0.000160182	0.010745958	5.264555161	4.757095243	0.50746	1.42154515
245	224833_PM_at	ETS1	NM_001143820 / NM	0.018263233	0.178670582	9.988822688	10.56207485	-0.57325	-1.4878738
246	231780_PM_at	GBGT1	NM_021996	0.145595121	0.496566307	6.826741735	6.659699335	0.167042	1.12275442
247	230664_PM_at	H2BFM ///	NM_001164416 / NR_	0.031052345	0.236757351	6.725302708	7.327081058	-0.60178	-1.51758608
248	222326_PM_at	---	---	1.77151E-07	0.000201796	4.93024641	4.116282496	0.813964	1.75803515
249	204970_PM_s_at	MAFG	NM_002359 / NM_03	0.006233363	0.0961651	6.973643499	6.736197743	0.237446	1.1789036
250	222156_PM_x_at	CCPG1	NM_004748 / NM_02	0.000794066	0.028394747	3.650481678	3.434419361	0.216062	1.1615589
251	233674_PM_at	---	---	0.002326412	0.053942565	5.653894672	5.400318016	0.253577	1.19215899
252	241692_PM_at	---	---	2.04579E-05	0.003160045	6.450926597	8.19435142	-1.74342	-3.34829078
253	227313_PM_at	CNPY4	NM_152755	0.000421787	0.019460945	7.220811615	7.67679524	-0.45598	-1.37171772
254	221752_PM_at	SSH1	NM_001161330 / NM	0.002203369	0.05219636	6.053083991	5.755567246	0.297517	1.22902712
255	215231_PM_at	PRKAG2	NM_001040633 / NM	0.035074552	0.251707207	3.663704339	3.625174867	0.038529	1.02706641
256	205608_PM_s_at	ANGPT1	NM_001146	0.003041392	0.063107445	5.566897866	5.055461689	0.511436	1.42546852
257	220418_PM_at	UBASH3A	NM_001001895 / NM	0.021270365	0.193923166	5.910116322	6.538581093	-0.62846	-1.54591904
258	201432_PM_at	CAT	NM_001752	0.029193809	0.229236178	10.27836521	9.526253643	0.752112	1.68425615
259	1557626_PM_at	---	---	0.030421544	0.234467851	5.562953961	5.041564654	0.521389	1.4353368
260	214860_PM_at	SLC9A7	NM_032591	0.164514979	0.523263508	4.344818172	4.251054377	0.093764	1.06715061
261	230866_PM_at	CYSLTR1	NM_006639	3.90435E-05	0.004630752	4.730999127	3.871144108	0.859855	1.81485592
262	208626_PM_s_at	VAT1	NM_006373	0.00986964	0.125588262	8.980187056	10.50222637	-1.52204	-2.87196728
263	221861_PM_at	---	---	0.000770947	0.027769074	7.981089966	7.403563041	0.577527	1.49228897
264	1569482_PM_at	---	---	0.054861481	0.315377086	5.714159526	5.985475804	-0.27132	-1.20690848
265	206804_PM_at	CD3G	NM_000073	0.159619054	0.517140156	8.907709945	9.34766759	-0.43996	-1.3565645
266	239660_PM_at	C20orf74	NM_020343	0.00023989	0.01363442	5.307233711	4.993909092	0.313325	1.24256784
267	238524_PM_at	---	---	0.048037011	0.2945742	5.065753626	5.268253577	-0.2025	-1.15069058
268	237338_PM_at	B3GNT8	NM_198540	0.095467382	0.410933643	6.34135546	6.167743381	0.173612	1.12787883
269	229389_PM_at	ATG16L2	NM_033388	0.095466762	0.410933643	6.893515117	6.721356961	0.172158	1.12674274
270	221511_PM_x_at	CCPG1	NM_004748 / NM_02	0.001374501	0.039469986	4.946848563	4.65742006	0.289429	1.22215605
271	217901_PM_at	DSG2	NM_001943	8.37042E-06	0.001808973	5.917131512	6.996809278	-1.07968	-2.11356395
272	213954_PM_at	FAM169A	NM_015566	0.006712353	0.100053951	4.793467153	5.60026378	-0.8068	-1.74932291
273	213379_PM_at	COQ2	NM_015697	0.511633664	0.805667193	6.537799525	6.522582213	0.015217	1.01060366
274	230449_PM_x_at	---	---	0.219826143	0.58888004	7.170511417	7.354692859	-0.18418	-1.13617215
275	232784_PM_at	---	---	0.44589102	0.767315186	5.616875078	5.725842449	-0.10897	-1.07845604
276	224333_PM_s_at	MRPS5	NM_031902	0.017094069	0.172057843	8.695582454	8.914733753	-0.21915	-1.1640486
277	206965_PM_at	KLF12	NM_007249	0.686535629	0.892404914	4.836248157	4.805659363	0.030589	1.02142891
278	1566342_PM_at	SOD2	NM_000636 / NM_00	0.054861026	0.315377086	6.482792235	6.074293913	0.408498	1.32730353
279	210055_PM_at	TSHR	NM_000369 / NM_00	6.81586E-05	0.006392261	4.913185516	5.747498131	-0.83431	-1.78300731
280	1569499_PM_at	---	---	0.216778034	0.585879339	6.029239164	5.996918289	0.032321	1.02265596
281	200821_PM_at	LAMP2	NM_001122606 / NM	0.522178744	0.812306109	7.093903031	6.994807327	0.099096	1.07110187
282	238853_PM_at	RAB3IP	NM_001024647 / NM	0.000372732	0.018179435	6.007259426	6.563126233	-0.55587	-1.47005161
283	228250_PM_at	FNIP1	NM_001008738 / NM	0.003561371	0.06919615	6.769719886	5.880569713	0.88915	1.85208482
284	232058_PM_at	---	---	1.88592E-06	0.000721066	8.074427116	6.594208622	1.480218	2.78990983
285	226844_PM_at	MOBKL2B	NM_024761	0.169523136	0.530184044	4.762645828	4.674152355	0.088493	1.0632593
286	219790_PM_s_at	NPR3	NM_000908	0.00010591	0.008296261	5.27337533	4.858316483	0.415059	1.33335306
287	201846_PM_s_at	RYBP	NM_012234	0.006549033	0.098561492	10.79607483	9.551199643	1.244875	2.3699805
288	241435_PM_at	---	---	0.043610828	0.27999825	7.959966076	8.659236201	-0.69927	-1.62368315
289	228573_PM_at	ANTXR2	NM_001145794 / NM	0.00058951	0.023718179	5.554075646	5.025141184	0.528934	1.44286314
290	217794_PM_at	PRR13	NM_001005354 / NM	0.260554697	0.630352942	9.318121728	9.494148847	-0.17603	-1.12976845
291	200974_PM_at	ACTA2	NM_001141945 / NM	0.005102771	0.085661196	7.312431093	7.121724303	0.190707	1.14132272
292	233642_PM_s_at	HEATR5B	NM_019024	0.000589538	0.023718179	6.889083087	6.175808553	0.713275	1.63952117
293	229844_PM_at	---	---	0.00029948	0.015714478	8.103557077	7.582605727	0.520951	1.43490115
294	241871_PM_at	CAMK4	NM_001744	0.212260963	0.582452605	6.214909552	6.654942166	-0.44003	-1.356635
295	232686_PM_at	SIGLECP3	NR_002804	0.058024417	0.323590881	5.593262256	4.97316759	0.620095	1.53697603
296	1554661_PM_s_at	C1orf71	NM_001139459 / NM	0.006549033	0.098561492	8.338803932	7.838175225	0.500629	1.41482999
297	236399_PM_at	---	---	8.65328E-05	0.007357982	4.126041841	3.882016114	0.244026	1.18429273
298	213733_PM_at	MYO1F	NM_012335	1.53939E-06	0.000637652	7.557707917	6.523015206	1.034693	2.04867724
299	201536_PM_at	DUSP3	NM_004090	0.010105562	0.12725226	7.269161616	6.982641443	0.28652	1.21969478
300	213539_PM_at	CD3D	NM_000732 / NM_00	0.501198421	0.798692952	12.44970157	12.98267463	-0.53297	-1.44690787
301	207809_PM_s_at	ATP6AP1	NM_001183	0.621842224	0.863187356	8.634215082	8.597180006	0.037035	1.02600309
302	240159_PM_at	SLC15A2	NM_001145998 / NM	0.179879322	0.542854885	4.423319773	4.373465454	0.049854	1.03516039
303	203927_PM_at	NFKBIE	NM_004556	0.00081779	0.028809717	7.466935863	7.051657663	0.415278	1.33355581
304	236512_PM_at	---	---	0.002734211	0.059370832	5.321084898	5.037362752	0.283722	1.21733155
305	213958_PM_at	CD6	NM_006725	0.14335082	0.493659322	9.672641221	10.11557062	-0.44293	-1.35936172
306	207700_PM_s_at	NCOA3	NM_006534 / NM_18	2.20056E-05	0.003314483	7.235326168	6.501971919	0.733354	1.6624999
307	233177_PM_s_at	PNKD	NM_001077399 / NM	0.892990956	0.969871305	6.711842104	6.719985163	-0.00814	-1.0056603
308	218825_PM_at	EGFL7	NM_016215 / NM_20	0.002662042	0.058499661	6.727373601	6.533190919	0.194183	1.14407583
309	203474_PM_at	IQGAP2	NM_006633	1.88592E-06	0.000721066	8.084974898	6.179624804	1.90535	3.74599791
310	236764_PM_at	---	---	0.333993047	0.68969745	5.019228962	5.001908201	0.017321	1.0120782
311	229693_PM_at	TMEM220	NM_001004313	0.011898958	0.139520526	5.201804322	5.027672272	0.174132	1.1282854
312	206301_PM_at	TEC	NM_003215	0.000138177	0.009760766	6.255165884	5.802441214	0.452725	1.36862259
313	200742_PM_s_at	TPP1	NM_000391	0.219827007	0.58888004	7.116550366	7.059065415	0.057485	1.04065001
314	233176_PM_at	---	---	0.041940497	0.274819831	4.63249044	4.381433793	0.251057	1.19007842
315	233198_PM_at	GOLGA2L1	NM_017600 / NR_024	0.020815861	0.191699554	6.311911729	6.612597295	-0.30069	-1.23172959
316	213689_PM_x_at	FAM69A	NM_001006605	0.222906633	0.591967173	4.656534536	4.746878962	-0.09034	-1.06462432
317	203708_PM_at	PDE4B	NM_001037339 / NM	0.005102854	0.085661196	9.023170987	6.350528414	2.672643	6.37595998
318	210916_PM_s_at	CD44	NM_000610 / NM_00	0.000197858	0.012087373	8.488461008	7.449478406	1.038983	2.0547781
319	202207_PM_at	ARL4C	NM_005737	0.26054666	0.630352942	11.4150005	11.68750131	-0.2725	-1.20789982

320	235112_PM_at	---	---	0.038760079	0.264407648	6.978334426	7.225914188	-0.24758	-1.1872138
321	225591_PM_at	FBXO25	NM_012173 / NM_18	1.73499E-05	0.002892097	7.534160645	8.741113873	-1.20695	-2.30849599
322	207614_PM_s_at	CUL1	NM_003592	0.001768465	0.045740154	6.678799323	6.014605025	0.664194	1.58468303
323	217983_PM_s_at	RNASET2	NM_003730	0.000694988	0.026205852	10.15975206	9.280135532	0.879617	1.83988619
324	228487_PM_s_at	---	---	0.246987062	0.618451142	8.405304505	8.561871009	-0.15657	-1.11463125
325	207434_PM_s_at	FXYD2	NM_001127489 / NM	0.164514979	0.523263508	6.449601817	9.711632216	-3.26203	-9.59332145
326	232950_PM_s_at	PITPNM2	NM_020845	3.17254E-08	0.000109046	7.196672696	8.368055596	-1.17138	-2.25227486
327	225098_PM_at	ABI2	NM_005759	4.01904E-06	0.00113865	7.408507119	8.55606714	-1.14756	-2.21538897
328	224435_PM_at	C10orf58	NM_032333 / NR_024	1.76736E-05	0.002893121	6.464885637	7.603155162	-1.13827	-2.2011684
329	200743_PM_s_at	TPP1	NM_000391	0.647990586	0.876951679	8.509326325	8.550439127	-0.04111	-1.02890715
330	228107_PM_at	LOC100127	XM_001722508 / XM_	4.59226E-08	0.000109166	5.395135938	7.25133546	-1.8562	-3.62052653
331	218601_PM_at	URG4	NM_001077663 / NM	0.065398033	0.345074795	7.908622295	8.321680263	-0.41306	-1.33150511
332	1555355_PM_a_at	ETS1	NM_001143820 / NM	0.838494923	0.953504166	7.751069003	7.945954025	-0.19489	-1.14463293
333	244181_PM_at	---	---	2.8335E-05	0.003863655	6.233661904	4.725715908	1.507946	2.84404836
334	232231_PM_at	RUNX2	NM_001015051 / NM	0.00081779	0.028809717	7.998355295	4.609477036	3.388878	10.4749994
335	228098_PM_s_at	MYLIP	NM_013262	0.747427345	0.918740785	9.323301997	8.391684381	0.931618	1.90741348
336	38398_PM_at	MADD	NM_001135943 / NM	0.102984192	0.427312436	7.771247604	7.643255661	0.127992	1.09277164
337	200808_PM_s_at	ZYX	NM_001010972 / NM	0.025225703	0.211633466	8.082751518	7.606083588	0.476668	1.39152606
338	226745_PM_at	CYP4V2	NM_207352	0.004610043	0.080815162	6.302734763	6.848941256	-0.54621	-1.460241
339	225898_PM_at	WDR54	NM_032118	4.5953E-07	0.000322129	7.990674755	8.931580234	-0.94091	-1.91973274
340	243904_PM_at	---	---	0.00081779	0.028809717	4.59137803	4.453510907	0.137867	1.10027727
341	225112_PM_at	ABI2	NM_005759	6.40493E-06	0.001529334	8.19465041	9.265154952	-1.0705	-2.10016771
342	228314_PM_at	LRRC8C	NM_032270	5.93885E-05	0.005925306	6.306509375	4.977465308	1.329044	2.5123615
343	212408_PM_at	TOR1AIP1	NM_015602	0.532834438	0.818013223	9.681610688	9.387871188	0.29374	1.2258135
344	232939_PM_at	---	---	0.023672982	0.205321842	5.08191326	4.686808638	0.395105	1.31503812
345	216202_PM_s_at	SPTLC2	NM_004863	0.000705415	0.02632666	8.35778664	6.703032368	1.654754	3.14869556
346	229521_PM_at	FLJ36031	NM_175884	0.000919415	0.030839893	8.049883675	7.419128884	0.630755	1.54837486
347	226402_PM_at	CYP2U1	NM_183075	0.16451577	0.523263508	4.268035988	4.427557078	-0.15952	-1.11691631
348	210252_PM_s_at	MADD	NM_001135943 / NM	0.109149736	0.437209298	8.511825129	8.432360571	0.079465	1.05662581
349	221477_PM_s_at	SOD2	NM_000636 / NM_00	0.899440979	0.971799374	8.638125124	8.263026046	0.375099	1.29692862
350	241824_PM_at	---	---	1.88592E-06	0.000721066	5.981270792	4.479341527	1.501929	2.83221201
351	207085_PM_x_at	CSF2RA	NM_001161529 / NM	0.083190806	0.385076234	4.251132517	4.213267535	0.037865	1.02659347
352	228520_PM_s_at	APLP2	NM_001142276 / NM	0.138946346	0.486702025	4.230945621	4.156933579	0.074012	1.05263994
353	1556306_PM_at	---	---	0.193476598	0.560026099	5.254791576	5.397600549	-0.14281	-1.10405265
354	218788_PM_s_at	SMYD3	NM_022743	0.122359486	0.460015463	8.398206745	8.005456507	0.39275	1.31289382
355	233379_PM_at	PRR5L	NM_001160167 / NM	0.010346205	0.129238917	4.183591545	3.889103244	0.294488	1.2264499
356	219642_PM_s_at	PEX5L	NM_016559	0.009639584	0.123777421	4.08700218	4.180137619	-0.09314	-1.06668592
357	206542_PM_s_at	SMARCA2	NM_003070 / NM_13	0.000538492	0.022440568	6.381435158	5.471285548	0.91015	1.87924037
358	201656_PM_at	ITGA6	NM_000210 / NM_00	0.001495814	0.04140942	6.480742087	4.953794235	1.526948	2.88175533
359	222912_PM_at	ARRB1	NM_004041 / NM_02	0.059111832	0.326524492	6.171743865	5.910284405	0.261459	1.19869071
360	232662_PM_x_at	C10orf58	NM_032333 / NR_024	0.000217924	0.012881448	7.441926098	7.797223308	-0.3553	-1.27924909
361	211100_PM_x_at	LILRA2	NM_001130917 / NM	0.004493962	0.079337214	6.694338301	6.371234163	0.323104	1.25101938
362	226810_PM_at	OGFRL1	NM_024576	2.51445E-07	0.000229142	7.502526696	4.285756965	3.21677	9.29702884
363	203331_PM_s_at	INPP5D	NM_001017915 / NM	0.000179533	0.011454507	6.576089398	6.269752818	0.306337	1.23656372
364	205288_PM_at	CDC14A	NM_003672 / NM_03	0.090704187	0.401331346	4.218058473	4.039816951	0.178242	1.13150387
365	221581_PM_s_at	LAT2	NM_014146 / NM_03	0.226017013	0.596087028	10.16080885	7.687787516	2.473021	5.55205298
366	1565852_PM_at	---	---	0.543599046	0.824080238	5.972596728	5.942211306	0.030385	1.02128493
367	222910_PM_s_at	PEX5L	NM_016559	1.30721E-06	0.000590675	5.105959092	6.113695317	-1.00774	-2.01075349
368	222756_PM_s_at	ARRB1	NM_004041 / NM_02	0.145595121	0.496566307	6.527728901	6.315747093	0.211982	1.1582782
369	235421_PM_at	MAP3K8	NM_005204	0.01084254	0.132354511	8.104921119	6.678846564	1.426075	2.68714571
370	209881_PM_s_at	LAT /// SPN	NM_001014987 / NM	0.103849116	0.428169098	8.085867684	9.545364476	-1.4595	-2.75012423
371	209539_PM_at	ARHGEF6	NM_004840	0.300480026	0.664970269	8.07051927	7.847483735	0.223036	1.16718685
372	237782_PM_at	---	---	0.543598291	0.824080238	5.316677762	5.322371407	-0.00569	-1.00395433
373	43511_PM_s_at	---	---	0.001032638	0.033055894	7.860570748	7.103347972	0.757223	1.69023375
374	204490_PM_s_at	CD44	NM_000610 / NM_00	0.001974917	0.048927416	9.013402563	7.935611739	1.077791	2.11080137
375	243286_PM_at	---	---	0.001974956	0.048927416	5.921210135	5.10146755	0.819743	1.76509103
376	212014_PM_x_at	CD44	NM_000610 / NM_00	0.000960432	0.031614451	8.865481947	7.770993182	1.094489	2.13537399
377	215784_PM_at	CD1E	NM_001042583 / NM	0.593338176	0.848523875	4.72985564	9.074496829	-4.34464	-20.317362
378	241613_PM_at	---	---	0.58210653	0.843336456	5.70768321	5.707700383	-1.7E-05	-1.0000119
379	217984_PM_at	RNASET2	NM_003730	0.097921738	0.417263299	10.04501285	9.275884465	0.769128	1.70423984
380	209900_PM_s_at	SLC16A1	NM_003051	0.093857265	0.407696798	5.694568058	6.008771494	-0.3142	-1.24332498
381	227312_PM_at	SNTB2	NM_006750	0.207813972	0.576090297	3.711824913	3.765438366	-0.05361	-1.03786115
382	201896_PM_s_at	PSRC1	NM_001005290 / NM	9.37895E-06	0.001920578	4.982927863	5.533996604	-0.55107	-1.46517068
383	227297_PM_at	ITGA9	NM_002207	0.704611615	0.901013636	3.923361392	3.945975135	-0.02261	-1.01579814
384	219532_PM_at	ELOVL4	NM_022726	0.021732995	0.196083329	5.544322165	8.630048712	-3.08573	-8.48977634
385	226454_PM_at	40611	NM_138396	0.132533886	0.47648145	6.998507862	7.203133289	-0.20463	-1.15238711
386	227627_PM_at	SGK3	NM_001033578 / NM	0.716756391	0.905593559	6.24888443	6.252698743	-0.00381	-1.00264738
387	220712_PM_at	C8orf60	---	0.136780626	0.483022769	6.969420959	6.847956765	0.121464	1.08783835
388	222656_PM_at	UBE2W	NM_001001481 / NM	0.816263651	0.945373986	3.909156811	3.878916611	0.03024	1.02118213
389	235998_PM_at	RHPN1	NM_052924	0.374189798	0.722043439	7.732260956	7.961834612	-0.22957	-1.17248841
390	203523_PM_at	LSP1	NM_001013253 / NM	0.038759714	0.264407648	8.476720703	7.92700336	0.549717	1.46379888
391	219938_PM_s_at	PSTPIP2	NM_024430	2.60076E-06	0.000856644	6.341773838	5.170102341	1.171671	2.25272545
392	218268_PM_at	TBC1D15	NM_001146213 / NM	0.559945527	0.832949582	8.784328893	8.553679781	0.230649	1.17336276
393	241471_PM_at	LOC730236	XM_001133153 / XM_	0.011899117	0.139520526	5.373596348	5.449685508	-0.07609	-1.05415657
394	58780_PM_s_at	FLJ10357	NM_018071	0.317934533	0.677887555	4.376875152	4.276534458	0.100341	1.07202659
395	232914_PM_s_at	SYTL2	NM_001162951 / NM	0.003041282	0.063107445	4.537506656	4.24706062	0.290446	1.22301834
396	224694_PM_at	ANTXR1	NM_018153 / NM_03	2.93096E-06	0.000915715	4.598544782	5.493816106	-0.89527	-1.85995965
397	218076_PM_s_at	ARHGAP17	NM_001006634 / NM	0.044468049	0.282971438	8.038320448	7.801559007	0.236761	1.17834454
398	217603_PM_at	ATP6V0A2	NM_012463	0.000589538	0.023718179	5.768477405	5.435131687	0.333346	1.25993187
399	226782_PM_at	SLC25A30	NM_001010875	0.011359927	0.135938721	6.389021006	6.019026026	0.369995	1.29234833
400	227261_PM_at	KLF12	NM_007249	0.005642527	0.090578417	7.151501995	7.817084904	-0.66558	-1.58620904

401	228174_PM_at	SCAI	NM_001144877 / NM_	5.73688E-05	0.005884877	7.152441584	8.312218575	-1.15978	-2.23422889
402	224884_PM_at	AKAP13	NM_006738 / NM_00	0.540897021	0.824080238	8.691883646	8.004301918	0.687582	1.61058157
403	203127_PM_s_at	SPTLC2	NM_004863	0.090702374	0.401331346	9.230552044	7.768076379	1.462476	2.75580855
404	206471_PM_s_at	PLXNC1	NM_005761	0.028595949	0.227118464	3.948512672	3.723338573	0.225174	1.1689183
405	225659_PM_at	SPOPL	NM_001001664	0.000272425	0.01483551	5.629537956	5.085831288	0.543707	1.45771296
406	226640_PM_at	DAGLB	NM_001142936 / NM_	0.000214447	0.012842131	7.604197614	7.111377161	0.49282	1.40719324
407	224728_PM_at	ATPAF1	NM_001042546 / NM_	7.0538E-05	0.006514642	5.419380637	5.857251954	-0.43787	-1.35460415
408	203182_PM_s_at	SRPK2	NM_182691 / NM_18	0.164514979	0.523263508	6.54300473	7.038985613	-0.49598	-1.41027927
409	212867_PM_at	---	---	0.522177964	0.812306109	7.770699943	7.110707204	0.659993	1.58007467
410	208615_PM_s_at	PTP4A2	NM_080391 / NM_08	0.317931813	0.677887555	10.36167162	10.58309383	-0.22142	-1.16588235
411	205942_PM_s_at	ACSM3	NM_005622 / NM_20	0.130448826	0.473371576	5.162967658	4.930705371	0.232262	1.17467551
412	217523_PM_at	CD44	NM_000610 / NM_00	0.000448516	0.020233189	8.747915167	7.4432235	1.304692	2.47030926
413	224909_PM_s_at	PREX1	NM_020820	0.000506782	0.02180038	7.554609822	6.958024447	0.596585	1.51213335
414	201844_PM_s_at	RYBP	NM_012234	0.162052671	0.520338018	10.32595638	9.223580196	1.102376	2.14708035
415	212560_PM_at	SORL1	NM_003105	0.11096632	0.440220587	8.484958284	8.046479534	0.438479	1.35517461
416	219806_PM_s_at	C11orf75	NM_020179	1.70357E-05	0.002848395	5.261331575	5.846965509	-0.58563	-1.50069827
417	219753_PM_at	STAG3	NM_012447	0.000462454	0.020523799	7.403159909	8.244426815	-0.84127	-1.79162277
418	214835_PM_s_at	SUCLG2	NM_003848	8.95085E-05	0.007494682	3.958475852	5.817767586	-1.85929	-3.62829493
419	236908_PM_at	---	---	6.16362E-06	0.001484563	6.106113465	7.034873015	-0.92876	-1.90363852
420	1558392_PM_at	SYNE2	NM_015180 / NM_18	0.455681765	0.77253955	4.153570864	4.099636523	0.053934	1.03809202
421	242793_PM_at	---	---	0.196283516	0.56320373	6.235077488	6.149132943	0.085945	1.06138241
422	225796_PM_at	PXK	NM_017771	0.061337434	0.332469933	6.554107171	5.822431433	0.731676	1.66056678
423	242346_PM_x_at	---	---	0.000726672	0.026863274	5.969842804	6.570502682	-0.60066	-1.51641
424	1566446_PM_at	---	---	0.656807883	0.879955183	5.954511104	6.027743278	-0.07323	-1.05207108
425	235759_PM_at	---	---	1.03952E-07	0.000162397	5.040674177	6.726823511	-1.68615	-3.21796656
426	1557780_PM_at	---	---	0.728973222	0.911258194	4.642810397	4.60096132	0.041849	1.02943239
427	209835_PM_x_at	CD44	NM_000610 / NM_00	0.73818048	0.916329795	9.277549039	8.168462219	1.109087	2.15709067
428	243841_PM_at	SYNE2	NM_015180 / NM_18	0.002455718	0.055804814	4.777325525	4.949084583	-0.17176	-1.12643109
429	1565868_PM_at	CD44	NM_000610 / NM_00	1.41618E-05	0.002530384	7.425567287	6.221028696	1.204539	2.3046355
430	239761_PM_at	GCNT1	NM_001097633 / NM_	0.11846389	0.453543233	6.322024518	6.025631048	0.296393	1.22807057
431	229202_PM_at	---	---	3.40458E-07	0.000258548	5.847838307	7.33280163	-1.48496	-2.79910057
432	231075_PM_x_at	RAPH1	NM_203365 / NM_21	0.002626541	0.058352763	5.924559539	6.23533864	-0.31078	-1.24037736
433	244838_PM_at	---	---	0.00081779	0.028809717	5.378193961	5.552130583	-0.17394	-1.12813258
434	242794_PM_at	MAML3	NM_018717	0.012460878	0.143129938	4.9865637	4.333476309	0.653087	1.57252984
435	224719_PM_s_at	C12orf57	NM_138425	0.018262798	0.178670582	9.896595622	11.53138175	-1.63479	-3.1054151
436	205484_PM_at	SIT1	NM_014450	0.011228414	0.135521748	7.495441781	8.707407262	-1.21197	-2.31653018
437	209238_PM_at	STX3	NM_004177	0.346375884	0.699235766	5.286250586	5.174249281	0.112001	1.08072638
438	215813_PM_s_at	PTGS1	NM_000962 / NM_08	2.36619E-05	0.003459125	5.863836823	5.129473729	0.734363	1.66366285
439	222803_PM_at	PRTFDC1	NM_020200	4.51993E-06	0.001205497	5.056491412	6.649895507	-1.5934	-3.01760526
440	201719_PM_s_at	EPB41L2	NM_001135554 / NM_	0.003379684	0.066902318	6.579570542	7.319984727	-0.74041	-1.6706554
441	203598_PM_s_at	WBP4	NM_007187	0.3720041	0.718881849	5.944339299	5.940119099	0.00422	1.0029295
442	233031_PM_at	ZEB2	NM_014795	0.308156895	0.670911193	4.382641869	4.325483252	0.057159	1.04041465
443	217848_PM_s_at	PPA1	NM_021129	0.025222695	0.211633466	10.76897354	11.29347591	-0.5245	-1.43843733
444	232867_PM_at	---	---	0.000555031	0.022799633	6.82217735	6.429701072	0.392476	1.31264453
445	203837_PM_at	MAP3K5	NM_005923	0.006233363	0.0961651	4.251512337	3.803338293	0.448174	1.36431241
446	225589_PM_at	SH3RF1	NM_020870	0.002029956	0.049703457	5.372346895	4.429198656	0.943148	1.92271941
447	204319_PM_s_at	RGS10	NM_001005339 / NM_	0.160830032	0.52026704	9.327146075	10.31106803	-0.98392	-1.97783483
448	206966_PM_s_at	KLF12	NM_007249	0.562693063	0.835428293	7.511614715	7.571656282	-0.06004	-1.0424958
449	213902_PM_at	ASAH1	NM_001127505 / NM_	0.008764328	0.117594246	8.216105239	7.836746296	0.379359	1.30076374
450	201397_PM_at	PHGDH	NM_006623	2.30654E-06	0.000813648	6.93795281	8.439716119	-1.50176	-2.83188623
451	212975_PM_at	DENND3	NM_014957	0.005785367	0.091791917	6.889506249	6.394969445	0.494537	1.40886835
452	225590_PM_at	SH3RF1	NM_020870	0.002662042	0.058499661	6.292906841	5.303405789	0.989501	1.9854982
453	200953_PM_s_at	CCND2	NM_001759	0.475618937	0.783646051	9.601046051	6.848300983	2.752745	6.73998354
454	228615_PM_at	---	---	0.078932004	0.375400773	6.100263179	6.257326202	-0.15706	-1.11501493
455	1556728_PM_at	---	---	0.044468049	0.282971438	5.190080857	5.42617113	-0.23609	-1.17779648
456	220911_PM_s_at	KIAA1305	NM_025081	0.31400008	0.674257889	5.42887438	5.325674667	0.1032	1.07415316
457	235483_PM_at	---	---	0.005642617	0.090578417	6.45123554	6.252460283	0.198775	1.14772361
458	223627_PM_at	MEX3B	NM_032246	0.000168229	0.011002268	8.13335779	6.775351775	1.358006	2.56330654
459	223129_PM_x_at	MYLIP	NM_013262	0.051843194	0.306239264	8.49702398	8.001160694	0.495863	1.41016432
460	231013_PM_at	---	---	8.95085E-05	0.007494682	5.746464799	6.237230187	-0.49077	-1.40519017
461	227869_PM_at	FAM104B /	NM_138362 / XR_079	0.014289584	0.154985722	6.35597036	6.605341093	-0.24937	-1.18868853
462	210817_PM_s_at	CALCOCO2	NM_005831	0.506401524	0.801841599	9.523725068	9.066143753	0.457581	1.37323765
463	207643_PM_s_at	TNFRSF1A	NM_001065	0.003751901	0.071252244	7.541434511	7.294503202	0.246931	1.18668029
464	217707_PM_x_at	SMARCA2	NM_003070 / NM_13	0.000197864	0.012087373	6.482136021	5.460961275	1.021175	2.02957091
465	212124_PM_at	ZMIZ1	NM_020338	0.136783567	0.483022769	10.22380821	9.054662604	1.169146	2.2487848
466	202656_PM_s_at	SERTAD2	NM_014755	0.186584811	0.552451515	9.599594899	9.263619666	0.335975	1.26223036
467	224800_PM_at	WDFY1	NM_020830	2.28195E-05	0.003381175	6.94097138	5.844367394	1.096604	2.13850708
468	1559097_PM_at	C14orf64	NR_015430	0.048965093	0.2972369	4.818320859	4.975211073	-0.15689	-1.11488138
469	210221_PM_at	CHRNA3	NM_000743	9.79445E-07	0.000495844	6.089380558	7.414687476	-1.32531	-2.50586192
470	218912_PM_at	GCC1	NM_024523	0.103848468	0.428169098	7.864742636	7.684903391	0.179839	1.13275766
471	205312_PM_at	SPI1	NM_001080547 / NM_	0.042769156	0.277522384	5.0183907	4.914054167	0.104337	1.07499991
472	201200_PM_at	CREG1	NM_003851	0.359044477	0.709207198	7.92745731	7.860099731	0.067358	1.0477958
473	204233_PM_s_at	CHKA	NM_001277 / NM_21	0.000109517	0.008457393	7.477284438	6.439923016	1.037361	2.05247041
474	207677_PM_s_at	NCF4	NM_000631 / NM_01	0.022685353	0.200731781	6.521865644	5.321653222	1.200212	2.297735
475	238050_PM_at	ANTXR2	NM_001145794 / NM_	0.003703291	0.071021025	3.908724443	3.761948373	0.146776	1.10709273
476	220023_PM_at	APOB48R	NM_018690	9.03064E-06	0.001870266	6.985415643	6.26261382	0.722802	1.6503841
477	228391_PM_at	CYP4V2	NM_207352	0.007049803	0.102978351	4.964414314	5.731924416	-0.76751	-1.70232925
478	215223_PM_s_at	SOD2	NM_000636 / NM_00	0.174643928	0.536742932	9.227441594	8.635763547	0.591678	1.50699857
479	201050_PM_at	PLD3	NM_001031696 / NM_	0.565447817	0.835428293	7.384154193	7.517567966	-0.13341	-1.09688614
480	210358_PM_x_at	GATA2	NM_001145661 / NM_	0.44589102	0.767315186	6.769076315	6.710148723	0.058928	1.04169115
481	226452_PM_at	PDK1	NM_002610	1.12315E-08	0.000102347	8.120906402	6.543581736	1.577325	2.98415954

482	1556461_PM_at	---	---	0.91882865	0.977220596	4.125772538	4.077948316	0.047824	1.03370478
483	240765_PM_at	---	---	0.028595949	0.227118464	6.642139437	6.455397762	0.186742	1.13819021
484	228768_PM_at	FNIP1	NM_001008738 / NM_	0.07222766	0.360051723	7.28922146	7.256492113	0.032729	1.02294554
485	218999_PM_at	TMEM140	NM_018295	0.030421855	0.234467851	6.58696476	6.397855417	0.189109	1.14005968
486	225551_PM_at	C1orf71	NM_001139459 / NM_	0.79103701	0.935781481	5.330143948	5.348603262	-0.01846	-1.01287723
487	213241_PM_at	PLXNC1	NM_005761	2.04601E-05	0.003160045	5.795718173	4.917876847	0.877841	1.83762365
488	205505_PM_at	GCNT1	NM_001097633 / NM_	0.639224834	0.871431152	6.913242985	7.112163205	-0.19892	-1.14783894
489	241816_PM_at	C14orf106	NM_018353	0.005642617	0.090578417	7.498696802	6.950447788	0.548249	1.46230983
490	210980_PM_s_at	ASAH1	NM_001127505 / NM_	0.047122935	0.291783289	5.312206999	4.940204737	0.372002	1.29414768
491	219456_PM_s_at	RIN3	NM_024832	0.032347027	0.241245898	6.748192491	6.280217674	0.467975	1.38316649
492	206683_PM_at	ZNF165	NM_003447	8.95112E-05	0.007494682	4.707346103	3.927484665	0.779861	1.71696596
493	232500_PM_at	C20orf74	NM_020343	0.000105913	0.008296261	5.518459793	4.907859957	0.6106	1.52689392
494	1560762_PM_at	LOC285972	---	0.008976182	0.119208112	3.938687315	3.821208209	0.117479	1.08483761
495	204859_PM_s_at	APAF1	NM_001160 / NM_01	0.922064651	0.978945328	4.579414874	4.568712555	0.010702	1.00744587
496	39650_PM_s_at	PCNXL2	NM_014801	5.07968E-06	0.001322584	6.293850992	6.903830552	-0.60998	-1.52623758
497	204849_PM_at	TCFL5	NM_006602	9.03064E-06	0.001870266	6.137567593	7.754904058	-1.61734	-3.06808077
498	229872_PM_s_at	LOC100132	XM_001722799	0.012750469	0.144483291	7.454216424	9.365594943	-1.91138	-3.76168363
499	231395_PM_at	ATP8A2	NM_016529	0.001974994	0.048927416	5.591332664	5.780016425	-0.18868	-1.13972342
500	218900_PM_at	CNNM4	NM_020184	0.002808215	0.060330841	6.667732625	6.353086006	0.314647	1.24370698

Supplementary Table S2. Immunophenotype of the immature cluster, ETP-ALL, and ABD T-ALL patients and patients with an ETP immunophenotype

Patient	unsupervised cluster	ETP-ALL probability PAM top100	ETP-ALL probability PAM top200	ETP-ALL probability PAM top500	ETP-ALL summary PAM	ABD status	simplified ETP-ALL immunophenotype		CD8	CD4	CD1	CD5	CD34	CD13	CD33
	n =15/117	*n* =13/117	*n* =13/117	*n* =13/117		*n* =7/117	including CD5 (≤75%)	excluding CD5 criteria	% positive	% positive	% positive	% positive	% positive	% positive	% positive
9194	**immature**	**1**	**1**	**1**	**ETP-ALL**	**one copy retained**	yes	yes	**1**	1	**1**	**7**	2	NA	**40**
572	**immature**	**1**	**1**	**1**	**ETP-ALL**	**both copies retained**	-	yes	**2**	3	**0**	96	**59**	0	0
1524	**immature**	**1**	**1**	**1**	**ETP-ALL**	**both copies retained**	-	yes	**3**	1	**2**	97	**53**	3	**66**
1964	**immature**	**1**	**1**	**1**	**ETP-ALL**	**both copies retained**	-	yes	**3**	3	**0**	92	**72**	**66**	**86**
10030	**immature**	**1**	**1**	**1**	**ETP-ALL**	**both copies retained**	NA	NA	**1**	1	NA	**56**	1	0	0
167	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	-	yes	**16**	2	**14**	90	**45**	0	0
321	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	-	yes	**6**	5	**6**	97	**35**	2	**60**
491	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	-	-	**3**	1	**23**	95	22	2	15
2130	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	-	yes	**21**	0	**0**	88	**67**	0	5
9577	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	-	-	**15**	9	66	80	0	0	4
2736	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	yes	yes	**1**	1	**0**	**2**	**69**	2	**44**
1509	**immature**	**1**	**1**	**1**	**ETP-ALL**	deleted	yes	yes	**4**	3	**0**	**7**	6	NA	**39**
2703	**immature**	**0.99**	**1**	**1**	**ETP-ALL**	deleted	-	yes	**1**	0	**8**	92	**79**	3	0
2252	**immature**	0.02	0	0	-	deleted	-	-	93	73	90	95	7	2	2
9105	**immature**	0	0	0	-	**one copy retained**	-	-	83	68	7	83	0	0	0
9012	TLX	0	0.36	1	-	deleted	-	-	**3**	13	**10**	96	ND	ND	ND
9226	TAL/LMO	0	0	0	-	deleted	-	-	**3**	2	**6**	96	2	10	10
8639	TLX	0	0	0	-	deleted	-	-	**0**	96	**3**	95	0	0	0
9421	TLX	0.02	0.06	0.28	-	deleted	yes	yes	**17**	10	**7**	**65**	**82**	0	**40**
231	TAL/LMO	0	0	0	-	**one copy retained**	-	-	83	43	60	80	**95**	3	5
2750	TLX	0	0	0	-	deleted	-	yes	**1**	69	**0**	94	0	0	**28**
10111	TAL/LMO	0	0	0	-	deleted	-	yes	**3**	2	**1**	95	**79**	1	4
9858	TLX	0	0	0	-	deleted	-	yes	**4**	68	**2**	97	**67**	NA	4
720	TLX	0	0	0	-	deleted	-	yes	**0**	83	**11**	96	**39**	0	0
2780	TLX	0	0	0	-	deleted	yes	yes	**7**	57	**6**	**70**	7	**28**	**28**
1753	TAL/LMO	0	0	0	-	deleted	-	yes	**6**	6	**4**	90	**49**	0	0
585	TLX	0	0	0	-	deleted	-	yes	**17**	17	**17**	86	**86**	16	20
1032	TAL/LMO	0	0	0	-	deleted	-	yes	**7**	10	**0**	95	**88**	0	0
1632	TAL/LMO	0	0	0	-	deleted	-	yes	**9**	31	**22**	94	**53**	15	5
9963	TAL/LMO	0	0	0	-	deleted	-	yes	**3**	1	**15**	**93**	**83**	14	0

The immature, ETP-ALL and ABD patients are depicted in bold. ETP-ALL, early T-cell precursor ALL; ABD, absence of bi-allelic deletions; Unsupervised subgroups have been published (Homminga *et al*., Cancer Cell 2011). The ETP-ALL immunophenotype for the DCOG and COALL cohorts was based on <25% expression of CD1 and CD8≥25% expression of CD13, CD33 or CD34 with or without ≤75% expression, and are shown in bold.

Supplementary Table S3. Overall clinical, immunophenotypic and molecular cytogenetic characteristics of the immature cluster (MEF2C) versus non-immature cluster T-ALL patients

	Immature Cluster					
	-		+			
	n	(%) or range	n	(%) or range	*p*-value	Bonferroni-Holm alpha
Total	102	(89%)	15	(11%)		
Clinical (*n* =117)						
Gender						-
Male	75		8		0.13	
Female	27		7			
Median age yrs (range)	7.8	(1.5-17.8)	10.1	(3.1-16.4)	0.51*	-
Median WBC x10e9 cells/liter (range)	120	(2-900)	88	(2-435)	0.062*	-
ETP-immunophenotype: CD5 (≤75%) (*n* =111)						
ETP immunophenotype	2	(2%)	3	(20%)	**0.017**	0.0033
non ETP immunophenotype	94	(98%)	12	(80%)		
CD1-, CD4/CD8 DN, CD34/CD33/CD13+ (*n* =111)						
yes	6	(6%)	10	(67%)	**<0.001**	0.0029
no	90	(94%)	5	(33%)		
Chromosomal rearrangements (*n* =117)						
TAL1/2/LYL1 (*n* =27)	27	(26%)	0	(0%)	**0,021**	0.0036
LMO1/2/3 (*n* =14)	14	(14%)	0	(0%)	0.21	
TLX3 (*n* =22)	22	(22%)	0	(0%)	0.07	
TLX1 (*n* =7)	7	(7%)	0	(0%)	0.59	
HOXA (*n* =10)	7	(7%)	3	(20%)	0.12	
MEF2C (*n* =6)	0	(0%)	6	(40%)	**<0.001**	0.0029
NKX2-1/NKX2-2 (*n* =7)	7	(7%)	0	(0%)	0.59	
Unknown (*n* =26)	20	(19%)	6	(40%)	0,097	
NOTCH1/FBXW7 status (*n* =112)						
wild-type (*n* =42)	36	(37%)	6	(40%)	1#	
mutant (*n* =70)	61	(63%)	9	(60%)		
PTEN/AKT status (*n* =113)						
wild-type (*n* =92)	79	(81%)	13	(87%)	0.73	
mutant (*n* =21)	19	(19%)	2	(13%)		
PHF6 status (*n* =41)						
wild-type (*n* =32)	29	(76%)	3	(100%)	1	
mutant (*n* =9)	9	(24%)	0	(0%)		
WT1 status (*n* =115)						
wild-type (*n* =101)	86	(86%)	15	(100%)	0.21	
mutant (*n* =14)	14	(14%)	0	(0%)		

Unsupervised clusters are explained in the legend for Table 3. Significant *p*-values are indicated in bold. The *p*-values were calculated using the Fisher's exact test or the Pearson's Chi-square test (#) instead: *Mann-Whitney *U* test; ^The significance level of immature cluster frequencies for the indicated cytogenetic subtype was compared to all other subtypes. WBC, white blood cell count. Bonferroni-Holm significance level for multiple testing correction is indicated.

Supplementary Table S4. Overall clinical, immunophenotypic and molecular cytogenetic characteristics of ABD versus non-ABD T-ALL patients

	ABD -		ABD +			
	n	**(%) or range**	**n**	**(%) or range**	***p*-value**	**Bonferroni-Holm alpha**
Total	110	(89%)	7	(11%)		
Clinical (*n* =117)						
Gender						-
Male	81		3		0.1	
Female	29		4			
Median age yrs (range)	7.7	(1.5-17.8)	10.8	(5.4-16.1)	0.13*	-
Median WBC x10e9 cells/liter (range)	120	(2-900)	15	(2-248)	**0.002***	0.003
ETP-immunophenotype: CD5 (≤75%) (*n* =111)						
ETP immunophenotype	3	(3%)	1	(14%)	**0,23**	
non ETP immunophenotype	101	(97%)	6	(86%)		
CD1-, CD4/CD8 DN, CD34/CD33/CD13+ (*n* =111)						
yes	12	(12%)	4	(57%)	**0,008**	0.0033
no	92	(88%)	3	(43%)		
Chromosomal rearrangements (*n* =117)						
TAL1/2/LYL1 (*n* =27)	27	(24%)	0	(0%)	0.2	
LMO1/2/3 (*n* =14)	14	(13%)	0	(11%)	0.6	
TLX3 (*n* =22)	22	(20%)	0	(0%)	0.35	
TLX1 (*n* =7)	7	(6%)	0	(0%)	1	
HOXA (*n* =10)	9	(8%)	1	(22%)	0.47	
MEF2C (*n* =6)	3	(2%)	3	(33%)	**0.002**	0.003
NKX2-1/NKX2-2 (*n* =7)	7	(6%)	0	(0%)	1	
Unknown (*n* =26)	23	(21%)	3	(33%)	0.18	
Unsupervised T-ALL clusters (*n* =116)						
TAL/LMO (*n* =53)	52	(48%)	1	(14%)		
Proliferative (*n* =19)	19	(17%)	0	(0%)		
Immature (*n* =15)	9	(8%)	6	(86%)	**<0.001**	0.0028
TLX (*n* =29)	29	(27%)	0	(0%)		
NOTCH1/FBXW7 status (*n* =112)						
wild-type (*n* =42)	39	(37%)	3	(43%)	1	
mutant (*n* =70)	66	(63%)	4	(57%)		
PTEN/AKT status (*n* =113)						
wild-type (*n* =95)	85	(80%)	7	(100%)	0.35	
mutant (*n* =18)	21	(20%)	0	(0%)		
PHF6 status (*n* =41)						
wild-type (*n* =32)	31	(78%)	1	(100%)	1	
mutant (*n* =9)	9	(22%)	0	(0%)		
WT1 status (*n* =115)						
wild-type (*n* =100)	93	(93%)	7	(100%)	0.59	
mutant (*n* =15)	15	(7%)	0	(0%)		

Unsupervised clusters are explained in the legend for Table 3. Significant *p*-values are indicated in bold. The *p*-values were calculated using the Fisher's exact test or the Pearson's Chi-square test (#) instead: * Mann-Whitney *U* test. ^The significance level of ABD frequencies within the indicated cytogenetic subtypes was compared to all other subtypes. ABD, Absence of bi-allelic TCR-gamma deletions; yr, year; WBC, white blood cell count; Bonferroni-Holm significance level for multiple testing correction is indicated.

Supplementary Table S5

Probe ids	Alignments	Gene Title	Gene Symbol	Wilcoxon p	FDR	Median_Immature	Median_other	ratio	foldchange
209199_s_at	chr5:88049813-88214780 (-) // 97.25 // q14.3	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	6.59E-10	1.40E-05	6.868789215	4.335277814	2.533511	5.789792
209200_at	chr5:88049813-88214780 (-) // 97.25 // q14.3	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	7.69E-10	1.40E-05	6.116013064	4.490358153	1.625655	3.085822
236395_at	chr5:88207656-88208193 (-) // 94.29 // q14.3	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	7.69E-10	1.40E-05	5.610162869	3.734753183	1.87541	3.669058
201313_at	chr12:6893874-6903119 (+) // 95.42 // p13.31	enolase 2 (gamma, neuronal)	ENO2	1.49E-09	2.04E-05	5.324463455	7.924160407	-2.5997	-6.06159
206631_at	chr14:51850862-51865062 (+) // 98.61 // q22.1	prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	7.28E-09	7.96E-05	6.79316302	4.967616945	1.825546	3.544411
226452_at	chr2:173287522-173289391 (+) // 92.77 // q31.1	pyruvate dehydrogenase kinase, isoenzyme 1	PDK1	1.12E-08	0.0001023	8.120906402	6.543581736	1.577325	2.98416
1552924_a_at	chr12:121993860-122044081 (-) // 97.99 // q24.31	phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	3.17E-08	0.000109	6.781991031	8.169735032	-1.38774	-2.61669
1554343_a_at	chr4:68253261-68300874 (+) // 85.47 // q13.2	BCR downstream signaling 1	BRDG1	3.65E-08	0.000109	4.925905553	4.379713203	0.546192	1.460227
1568618_a_at	chr18:31488619-31543760 (+) // 94.59 // q12.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1	4.00E-08	0.000109	9.338700411	6.733991156	2.604709	6.082689
201690_s_at	chr8:81110126-81246332 (-) // 97.78 // q21.13	tumor protein D52	TPD52	3.65E-08	0.000109	5.104191689	7.812719481	-2.70853	-6.53654
201704_at	chr20:25124371-25155360 (+) // 97.61 // p11.21	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	ENTPD6	2.18E-08	0.000109	7.062654612	7.747060461	-0.68441	-1.60704
201723_s_at	chr18:31488593-31544206 (+) // 97.94 // q12.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1	4.19E-08	0.000109	8.591210543	7.062579817	1.528631	2.885119
202625_at	---	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog /// v-yes-1 Yamaguchi sarcoma viral rel	LYN	3.03E-08	0.000109	7.936001014	5.193863555	2.742137	6.690609
213423_x_at	chr8:15524959-15666613 (+) // 91.8 // p22	tumor suppressor candidate 3	TUSC3	1.94E-08	0.000109	4.886651584	7.382333319	-2.49568	-5.63995
219582_at	chr6:72062782-72068692 (+) // 98.52 // q13	opioid growth factor receptor-like 1	OGFRL1	2.89E-08	0.000109	5.567730337	4.452641525	1.115089	2.166083
227999_at	chr10:134080775-134081357 (+) // 93.45 // q26.3	PWWP domain containing 2	PWWP2	3.65E-08	0.000109	6.705728735	5.743907412	0.961821	1.947767
230488_s_at	chr9:133549262-133552162 (-) // 86.22 // q34.2	BPR	LOC138948	4.19E-08	0.000109	6.757706708	7.812258569	-1.05455	-2.07707
232950_s_at	chr12:121992907-122010572 (-) // 98.75 // q24.31	phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	3.17E-08	0.000109	7.196672696	8.368055596	-1.17138	-2.25227
235605_x_at	chr9:98973021-98973474 (+) // 59.07 // q22.33	Transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TGFBR1	3.32E-08	0.000109	5.063275383	3.805744129	1.257531	2.390863
239798_at	chr2:173296293-173296989 (+) // 93.53 // q31.1	Transcribed locus	---	1.43E-08	0.000109	6.236043881	5.001064208	1.23498	2.35378
37953_s_at	chr12:48737753-48763663 (+) // 89.7 // q13.12	amiloride-sensitive cation channel 2, neuronal	ACCN2	3.82E-08	0.000109	5.410909037	6.111725754	-0.70082	-1.62542
1557961_s_at	chr8:92039348-92040812 (-) // 92.41 // q21.3	---	---	4.59E-08	0.0001092	3.260347806	5.394416873	-2.13407	-4.38954
228107_at	chr8:92039348-92060059 (-) // 80.27 // q21.3	---	---	4.59E-08	0.0001092	5.395135938	7.25133546	-1.8562	-3.62053
236561_at	chr9:98969496-98970312 (+) // 73.77 // q22.33	Transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TGFBR1	4.81E-08	0.0001095	8.184929139	6.387340262	1.797589	3.476387
210258_at	chr1:189336938-189361044 (+) // 95.09 // q31.2	regulator of G-protein signalling 13	RGS13	5.27E-08	0.0001152	4.727650762	3.379306696	1.348344	2.546197
244413_at	chr12:9766355-9776907 (-) // 100.0 // p13.31	dendritic cell-associated lectin-1	DCAL1	5.52E-08	0.000116	7.233429559	4.053318579	3.180111	9.063768
226705_at	chr8:38387809-38388908 (-) // 86.96 // p12	Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	FGFR1	6.04E-08	0.0001224	7.102010008	8.888042505	-1.78603	-3.44865
226299_at	chr9:128544355-128562749 (+) // 97.95 // q34.11	protein kinase N3	PKN3	6.62E-08	0.0001293	5.961094134	6.448674736	-0.48758	-1.40209
1554628_at	chr19:2851943-2869472 (+) // 98.93 // p13.3	hypothetical protein LOC126295	LOC126295	6.93E-08	0.0001306	5.022959456	7.658666672	-2.63571	-6.2148
209530_at	chr12:47498945-47508991 (+) // 98.58 // q13.12	calcium channel, voltage-dependent, beta 3 subunit	CACNB3	8.30E-08	0.0001513	6.993922479	7.664030001	-0.67011	-1.59119
211772_x_at	chr15:76672451-76700692 (-) // 95.21 // q25.1	cholinergic receptor, nicotinic, alpha polypeptide 3 /// cholinergic receptor, nicotinic, alpha polypept	CHRNA3	8.69E-08	0.0001518	5.219714869	6.643152027	-1.42344	-2.68224
227966_s_at	chr2:132121174-132124971 (+) // 91.48 // q21.1 /// chr2:	hypothetical protein BC016861 /// hypothetical protein DKFZp434E2321	LOC90557 /// DI	8.88E-08	0.0001518	5.740066063	6.468851375	-0.72879	-1.65724
226459_at	chr10:98342787-98344321 (-) // 54.6 // q24.1	phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	9.94E-08	0.0001624	7.416451852	5.978626784	1.437825	2.709121
235759_at	chr8:92038155-92039025 (-) // 84.87 // q21.3	EF-hand calcium binding protein 1	EFCBP1	1.04E-07	0.0001624	5.040674177	6.726823511	-1.68615	-3.21797
34726_at	chr12:47498941-47508991 (+) // 90.66 // q13.12	calcium channel, voltage-dependent, beta 3 subunit	CACNB3	1.04E-07	0.0001624	6.389395248	7.550348485	-1.16095	-2.23605
202761_s_at	chr14:63711436-63761517 (+) // 73.85 // q23.2	spectrin repeat containing, nuclear envelope 2	SYNE2	1.09E-07	0.0001636	5.403168767	7.213025485	-1.80986	-3.50607
218730_s_at	chr9:92226442-92245312 (-) // 99.2 // q22.31	osteoglycin (osteoinductive factor, mimecan)	OGN	1.14E-07	0.0001636	3.968829254	4.804371603	-0.83554	-1.78453
235824_at	chr21:20551070-20551530 (-) // 32.36 // q21.1	Transcribed locus	---	1.14E-07	0.0001636	7.437020733	5.778595783	1.658425	3.156717
207705_s_at	chr20:25381461-25387612 (-) // 99.67 // p11.21	KIAA0980 protein	KIAA0980	1.30E-07	0.0001776	5.905185153	7.856852793	-1.95167	-3.86821
224973_at	chr6:82512165-82519210 (-) // 94.13 // q14.1	family with sequence similarity 46, member A	FAM46A	1.30E-07	0.0001776	4.229633478	3.358017061	0.871616	1.829712
202780_at	chr5:41765925-41906315 (-) // 99.31 // p13.1	3-oxoacid CoA transferase 1	OXCT1	1.36E-07	0.0001812	6.912454672	8.293619635	-1.38116	-2.60479
210239_at	chr16:53523484-53525482 (+) // 95.12 // q12.2	iroquois homeobox protein 5	IRX5	1.42E-07	0.0001849	5.407335231	7.433139316	-2.0258	-4.07219
1552623_at	chr19:16115474-16130351 (+) // 72.66 // p13.11	hematopoietic SH2 domain containing	HSH2D	1.70E-07	0.0002018	7.678396351	5.776104438	1.902292	3.738066
204142_at	chr18:664002-696579 (-) // 96.09 // p11.32	enolase superfamily member 1	ENOSF1	1.70E-07	0.0002018	6.567052152	7.954699403	-1.38765	-2.61652
211302_s_at	chr1:65970884-66551208 (+) // 99.65 // p31.2	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	PDE4B	1.77E-07	0.0002018	7.412061634	5.463405958	1.948656	3.860147
212492_s_at	chr19:5082228-5104609 (+) // 91.47 // p13.3	jumonji domain containing 2B	JMJD2B	1.77E-07	0.0002018	7.795747611	6.571116271	1.224631	2.336957
222326_at	chr1:66534774-66535129 (+) // 62.81 // p31.2	Phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	PDE4B	1.77E-07	0.0002018	4.93024641	4.116282496	0.813964	1.758035
239862_at	chr8:81156921-81157562 (-) // 68.8 // q21.13	Tumor protein D52	TPD52	1.77E-07	0.0002018	4.597275793	5.05721061	-0.45993	-1.37548
201724_s_at	chr18:31488593-31545792 (+) // 98.17 // q12.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1	2.21E-07	0.0002234	8.247398327	6.258683619	1.988715	3.968833
213283_s_at	chr14:21059070-21075077 (-) // 94.97 // q11.2	sal-like 2 (Drosophila)	SALL2	2.21E-07	0.0002234	7.322764459	8.13811775	-0.81535	-1.75973
224793_s_at	chr9:98992082-98995486 (+) // 94.86 // q22.33	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TGFBR1	2.11E-07	0.0002234	8.299110969	6.14415201	2.154959	4.45356
229024_at	chr4:142139931-142140384 (-) // 66.42 // q31.21	CDNA FLJ10151 fis, clone HEMBA1003402	---	2.21E-07	0.0002234	5.82071239	6.639768972	-0.81906	-1.76425
239129_at	chr9:98972277-98973046 (+) // 69.44 // q22.33	---	---	2.11E-07	0.0002234	4.339196484	3.670876446	0.66832	1.589221
242064_at	chr17:68842110-68842543 (-) // 99.54 // q25.1	sidekick homolog 2 (chicken)	SDK2	2.21E-07	0.0002234	6.672171872	5.718510414	0.953661	1.936782
202820_at	chr1:23815267-23831689 (+) // 99.78 // p36.11	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	TCEB3	2.30E-07	0.0002269	8.856042554	6.40161626	2.454426	5.480951
218802_at	chr4:110938953-110966472 (+) // 97.85 // q25	hypothetical protein FLJ20647	FLJ20647	2.41E-07	0.0002269	7.544386516	8.588141749	-1.04376	-2.06159
221766_s_at	chr6:82512165-82519210 (-) // 94.13 // q14.1	family with sequence similarity 46, member A	FAM46A	2.41E-07	0.0002269	8.24516168	5.98920491	2.255957	4.77651
224048_at	chr12:94414016-94447695 (-) // 96.38 // q22	ubiquitin specific peptidase 44	USP44	2.41E-07	0.0002269	5.239789743	5.967285867	-0.7275	-1.65576
221606_s_at	chrX:80175714-80183282 (-) // 63.91 // q21.1	nucleosomal binding protein 1	NSBP1	2.51E-07	0.0002291	4.850969385	6.495404207	-1.64443	-3.12625
226810_at	chr6:72072623-72075482 (+) // 98.51 // q13	MRNA full length insert cDNA clone EUROIMAGE 1509279	---	2.51E-07	0.0002291	7.502526696	4.285756965	3.21677	9.297029
204143_s_at	chr18:664002-696579 (-) // 96.09 // p11.32	enolase superfamily member 1	ENOSF1	2.68E-07	0.000238	6.703252539	8.344436994	-1.64118	-3.11922
208782_at	chr3:121595816-121652515 (-) // 96.42 // q13.33	follistatin-like 1	FSTL1	2.74E-07	0.000238	6.229365578	8.014529363	-1.78516	-3.44658
222722_at	chr9:92225803-92246470 (-) // 98.61 // q22.31	osteoglycin (osteoinductive factor, mimecan)	OGN	2.74E-07	0.000238	4.272888053	5.638636453	-1.36575	-2.5771
1554999_at	chr4:82729226-82750223 (-) // 78.4 // q21.22	RasGEF domain family, member 1B	RASGEF1B	2.86E-07	0.0002409	8.112664942	6.523605051	1.58906	3.008532
201688_s_at	chr8:81110126-81246332 (-) // 97.78 // q21.13	tumor protein D52	TPD52	2.86E-07	0.0002409	4.781398225	6.658599052	-1.8772	-3.67362
201689_s_at	chr8:81110126-81246332 (-) // 97.78 // q21.13	tumor protein D52	TPD52	2.99E-07	0.0002478	4.052231162	6.310890447	-2.25866	-4.78547
218276_s_at	chr14:50170109-50204650 (-) // 86.91 // q22.1	salvador homolog 1 (Drosophila)	SAV1	3.12E-07	0.0002511	5.085159605	5.826904418	-0.74174	-1.6722
224707_at	chr5:139534913-139603556 (+) // 91.87 // q31.2	putative nuclear protein ORF1-FL49	ORF1-FL49	3.12E-07	0.0002511	5.823757245	7.621303839	-1.79755	-3.47629
238865_at	chr4:135475095-135476240 (-) // 98.61 // q28.3	similar to Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PABP 4) (Inducible poly(A)-bir	LOC132430	3.26E-07	0.0002547	5.079303168	6.952752269	-1.87345	-3.66408
244753_at	chr19:43835546-43835936 (+) // 57.4 // q13.2	Actinin, alpha 4	ACTN4	3.26E-07	0.0002547	7.608369158	5.913153128	1.695216	3.238254
213709_at	chrX:101781836-101813994 (+) // 73.38 // q22.1	basic helix-loop-helix domain containing, class B, 9	BHLHB9	3.40E-07	0.0002585	4.79138872	5.377528857	-0.58614	-1.50122
229202_at	chr1:229425916-229426572 (-) // 97.33 // q42.2	Pecanex-like 2 (Drosophila)	PCNXL2	3.40E-07	0.0002585	5.847838307	7.33280163	-1.48496	-2.7991
232191_at	chr21:43210690-43212471 (-) // 39.8 // q22.3	chromosome 21 open reading frame 105	C21orf105	4.04E-07	0.0003028	5.798958178	6.124954016	-0.326	-1.25353
230917_at	chr16:80553341-80553793 (+) // 92.86 // q23.2	CDNA FLJ45450 fis, clone BRSTN2002691	---	4.22E-07	0.0003076	5.990037062	4.712085528	1.277952	2.424944
241788_x_at	chr19:43836375-43837041 (+) // 57.85 // q13.2	Actinin, alpha 4	ACTN4	4.22E-07	0.0003076	6.050700803	5.152523143	0.898178	1.86371
203401_at	chrX:12569213-12601997 (+) // 97.76 // p22.2	phosphoribosyl pyrophosphate synthetase 2	PRPS2	4.60E-07	0.0003221	6.370881474	7.849704257	-1.47882	-2.78721
210063_at	chr9:133558534-133628879 (-) // 99.93 // q34.2	sarcosine dehydrogenase	SARDH	4.60E-07	0.0003221	5.946061104	6.791424529	-0.84536	-1.79672
225898_at	chr2:74560504-74564537 (+) // 93.52 // p13.1	WD repeat domain 54	WDR54	4.60E-07	0.0003221	7.990674755	8.931580234	-0.94091	-1.91973
209228_x_at	chr8:15442162-15666174 (+) // 94.41 // p22	tumor suppressor candidate 3	TUSC3	4.80E-07	0.0003319	5.787234465	7.244521051	-1.45729	-2.74591
213645_at	chr18:662548-702534 (-) // 95.32 // p11.32	enolase superfamily member 1	ENOSF1	5.00E-07	0.0003378	7.030289741	7.995759553	-0.96547	-1.9527
219737_s_at	chr13:65774971-66700691 (-) // 97.01 // q21.32	protocadherin 9	PCDH9	5.00E-07	0.0003378	5.332925491	6.755988822	-1.42306	-2.68154
220307_at	chr1:157613046-157645718 (-) // 99.88 // q23.3	CD244 natural killer cell receptor 2B4	CD244	5.22E-07	0.0003481	7.63435098	6.431229656	1.203121	2.302373
1568943_at	chr2:233750074-233820863 (+) // 40.58 // q37.1	inositol polyphosphate-5-phosphatase, 145kDa	INPP5D	5.68E-07	0.0003613	5.749840345	5.246377653	0.503463	1.417612
1569346_a_at	chr17:3761214-3762372 (-) // 47.49 // p13.2	Purinergic receptor P2X, ligand-gated ion channel, 1	P2RX1	5.68E-07	0.0003613	6.971011173	6.17072501	0.800286	1.741447
200940_s_at	chr1:8346722-8811790 (-) // 95.28 // p36.23	arginine-glutamic acid dipeptide (RE) repeats	RERE	5.68E-07	0.0003613	7.937600818	7.117625034	0.819976	1.765376
211793_s_at	chr2:204018743-204117581 (+) // 93.84 // q33.2	abl interactor 2	ABI2	5.68E-07	0.0003613	6.473026615	7.272202612	-0.79918	-1.74011
203603_s_at	chr2:144979316-145111612 (-) // 99.47 // q22.3	zinc finger homeobox 1b	ZFHX1B	5.93E-07	0.0003725	6.132697913	4.247113126	1.885585	3.695027
226550_at	chrX:46214940-46217749 (-) // 95.81 // p11.3	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	---	6.45E-07	0.0003962	6.74499999	5.165666844	1.579333	2.988317
228073_at	chr20:25542208-25543810 (-) // 81.52 // p11.21	haloacid dehalogenase-like hydrolase domain containing 4	HDHD4	6.45E-07	0.0003962	5.706538573	6.611730166	-0.90519	-1.87279
207169_x_at	chr6:30964148-30975910 (+) // 95.47 // p21.33	discoidin domain receptor family, member 1	DDR1	6.73E-07	0.0004041	6.207036081	6.761197497	-0.55416	-1.46831
222603_at	chr9:5774571-5820977 (-) // 97.33 // p24.1	KIAA1815	KIAA1815	6.73E-07	0.0004041	5.428037806	4.447756565	0.980281	1.97285
238668_at	chr12:53226482-53227550 (+) // 82.84 // q13.2	Transcribed locus, weakly similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens	---	7.01E-07	0.0004169	8.56227637	7.774764674	0.787512	1.726095
228315_at	chr3:180221931-180223454 (-) // 87.92 // q26.32	CDNA FLJ31683 fis, clone NT2RI2005353	---	7.32E-07	0.0004301	8.360188438	6.425197132	1.934991	3.823758
207463_x_at	chr7:141965118-141989076 (+) // 92.69 // q34 /// chr7:14	protease, serine, 3 (mesotrypsin)	PRSS3	7.63E-07	0.0004345	6.491052886	5.708534788	0.782518	1.720131
209053_s_at	chr4:1861739-1951161 (+) // 95.18 // p16.3	Wolf-Hirschhorn syndrome candidate 1	WHSC1	7.63E-07	0.0004345	6.999822401	7.993192694	-0.99337	-1.99083
244035_at	chr18:59132018-59132455 (-) // 93.06 // q21.33	B-cell CLL/lymphoma 2	BCL2	7.63E-07	0.0004345	7.219643557	6.187161478	1.032482	2.04554
219157_at	chr4:166486526-166601898 (+) // 99.83 // q32.3	kelch-like 2, Mayven (Drosophila)	KLHL2	7.95E-07	0.0004393	5.673836399	4.424844635	1.248992	2.376753
241402_at	chr17:71030090-71030644 (+) // 68.77 // q25.1	tRNA splicing endonuclease 54 homolog (SEN54, S. cerevisiae)	TSEN54	7.95E-07	0.0004393	7.860261422	6.935001685	0.92526	1.899026
242946_at	chr1:111151754-111152359 (+) // 99.34 // p13.3	CD53 antigen	CD53	7.95E-07	0.0004393	7.903034863	6.75416936	1.148866	2.217395
1568752_s_at	chr1:189345317-189360649 (+) // 78.08 // q31.2	regulator of G-protein signalling 13	RGS13	8.65E-07	0.0004681	3.883342176	3.516152168	0.36719	1.289838
230005_at	chr11:22798732-22799201 (-) // 79.14 // p14.3	hypothetical protein DKFZp313A2432	DKFZp313A2432	8.65E-07	0.0004681	5.007136272	5.872428536	-0.86529	-1.82171
212592_at	chr4:71886293-71897379 (-) // 95.36 // q13.3	Immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	IGJ	9.01E-07	0.0004739	7.173919199	4.333754843	2.840164	7.161016
219742_at	chr5:176806421-176815889 (+) // 83.79 // q35.3	proline rich 7 (synaptic)	PRR7	9.01E-07	0.0004739	5.59953932	6.719848683	-1.12031	-2.17394
230127_at	chrX:45360893-45361375 (-) // 95.63 // p11.3	Transcribed locus	---	9.01E-07	0.0004739	4.194229901	3.594576695	0.599653	1.515352
217549_at	chr12:53224949-53226410 (+) // 41.14 // q13.2	Transcribed locus, weakly similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens	---	9.40E-07	0.0004847	8.554058666	8.052547163	0.501512	1.415696
224732_at	chr16:67709413-67712053 (-) // 92.98 // q22.1	decreased expression in renal and prostate	DERPC	9.40E-07	0.0004847	8.1787455	8.865088064	-0.68634	-1.6092
1554520_at	chr16:87809120-87811549 (-) // 31.4 // q24.3	hypothetical locus LOC283861	LOC283861	9.79E-07	0.0004958	4.453604065	4.624954839	-0.17135	-1.12611
210221_at	chr15:76674706-76700377 (-) // 78.64 // q25.1	cholinergic receptor, nicotinic, alpha polypeptide 3	CHRNA3	9.79E-07	0.0004958	6.089380558	7.414687476	-1.32531	-2.50586
213378_s_at	chr12:9356889-9357951 (+) // 97.34 // p13.31 /// chr12:3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	DDX11	1.02E-06	0.000512	6.774599107	8.229088155	-1.45449	-2.74059
220059_at	chr4:68253211-68301377 (+) // 99.87 // q13.2	BCR downstream signaling 1	BRDG1	1.06E-06	0.0005289	5.515118487	4.45127296	1.063846	2.090496
202989_at	chr1:189276607-189280728 (+) // 96.74 // q31.2	regulator of G-protein signalling 1	RGS1	1.11E-06	0.0005462	3.767667239	3.539356973	0.22831	1.171462
238581_at	chr1:89436653-89437302 (-) // 91.54 // p22.2	Guanylate binding protein 5	GBP5	1.16E-06	0.0005641	5.301066076	4.023333782	1.277732	2.424576
212230_at	chr1:56672453-56694699 (-) // 95.75 // p32.2	phosphatidic acid phosphatase type 2B	PPAP2B	1.20E-06	0.0005725	4.311091222	4.685040888	-0.37395	-1.2959
218115_at	chr19:14091342-14108429 (-) // 99.82 // p13.12	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	ASF1B	1.20E-06	0.0005725	6.785275868	7.679333774	-0.89406	-1.8584
242672_at	chr3:16525510-16526160 (-) // 62.73 // p24.3	Raft-linking protein	RAFTLIN	1.20E-06	0.0005725	4.973823936	4.161701702	0.812122	1.755792
219148_at	chr8:27723331-27751219 (-) // 98.77 // p21.1	PDZ binding kinase	PBK	1.25E-06	0.0005863	4.801725923	7.116117531	-2.31439	-4.97395
228831_s_at	chr19:2462217-2462894 (-) // 91.49 // p13.3	guanine nucleotide binding protein (G protein), gamma 7	GNG7	1.25E-06	0.0005863	7.116782988	6.236121681	0.880661	1.841219
211587_x_at	chr15:76672448-76700260 (-) // 80.94 // q25.1	cholinergic receptor, nicotinic, alpha polypeptide 3	CHRNA3	1.31E-06	0.0005907	6.620241207	7.620524976	-1.00028	-2.00039
214210_at	chr22:39490133-39539840 (-) // 92.33 // q13.2	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	SLC25A17	1.31E-06	0.0005907	6.19575268	6.557702463	-0.36195	-1.28516
217655_at	chr19:40350337-40350818 (+) // 40.96 // q13.12	FXYD domain containing ion transport regulator 5	FXYD5	1.31E-06	0.0005907	6.420368515	5.404603502	1.015765	2.021975
222910_s_at	chr3:181000751-181237411 (-) // 98.89 // q26.33	peroxisomal biogenesis factor 5-like	PEX5L	1.31E-06	0.0005907	5.105959092	6.113695317	-1.00774	-2.01075
200802_at	chr1:109468581-109492778 (+) // 99.89 // p13.3	seryl-tRNA synthetase	SARS	1.36E-06	0.0006054	7.976478342	8.760856671	-0.78438	-1.72235
224740_at	chr5:60490185-60494044 (-) // 94.53 // q12.1	LOC441075	---	1.36E-06	0.0006054	4.871215928	7.238734354	-2.36752	-5.16053
205830_at	chr4:141667213-141706387 (-) // 98.78 // q31.1	calmegin	CLGN	1.42E-06	0.0006206	4.068055808	4.839685582	-0.77163	-1.7072
219183_s_at	chr22:36002923-36035880 (+) // 86.65 // q13.1	pleckstrin homology, Sec7 and coiled-coil domains 4	PSCD4	1.42E-06	0.0006206	8.969507312	7.342295209	1.627212	3.089155
1554690_a_at	chr8:38719023-38824792 (+) // 84.17 // p11.23	transforming, acidic coiled-coil containing protein 1	TACC1	1.54E-06	0.0006377	6.687366967	6.041966468	0.6454	1.564173
1558105_a_at	chrX:46215156-46218150 (-) // 99.29 // p11.3	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	---	1.54E-06	0.0006377	6.078164278	4.740793452	1.337371	2.526904
203577_at	chr6:30984037-30989858 (+) // 99.76 // p21.33	general transcription factor IIH, polypeptide 4, 52kDa	GTF2H4	1.54E-06	0.0006377	5.91124706	6.589721248	-0.67847	-1.60045
210976_s_at	chr12:46799392-46826154 (+) // 99.25 // q13.11	phosphofructokinase, muscle	PFKM	1.54E-06	0.0006377	5.673706682	7.017177375	-1.34347	-2.53761

213733_at	chr19:8491998-8522947 (-) // 92.71 // p13.2	myosin IF	MYO1F	1.54E-06	0.0006377	7.557707917	6.523015206	1.034693	2.048677
215942_s_at	chr22:45042253-45046871 (+) // 78.42 // q13.31	G-2 and S-phase expressed 1	GTSE1	1.48E-06	0.0006377	5.524562007	6.409450729	-0.88489	-1.84662
225837_at	chr12:2856649-2868952 (+) // 83.12 // p13.33	hypothetical protein MGC13204	MGC13204	1.54E-06	0.0006377	6.827863896	7.498673527	-0.67081	-1.59197
220377_at	chr14:105427024-105459570 (+) // 41.43 // q32.33	chromosome 14 open reading frame 110	C14orf110	1.60E-06	0.0006542	7.376152453	6.341791097	1.034361	2.048207
228333_at	chr2:144975673-144977158 (-) // 99.46 // q22.3	Full length insert cDNA clone YT94E02	---	1.60E-06	0.0006542	4.973879051	4.32035584	0.653523	1.573005
202156_s_at	chr10:11247082-11416363 (+) // 97.04 // p14	CUG triplet repeat, RNA binding protein 2	CUGBP2	1.64E-06	0.0006627	8.814366603	8.081559372	0.732807	1.66187
244887_at	chr1:189341519-189342034 (+) // 67.24 // q31.2	Regulator of G-protein signalling 13	RGS13	1.67E-06	0.0006713	4.033147136	3.402865991	0.630281	1.547867
210973_s_at	chr8:38392667-38434121 (-) // 98.51 // p12	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	FGFR1	1.74E-06	0.0006941	6.574372189	7.855471933	-1.2811	-2.43024
206267_s_at	chr19:3728972-3737280 (-) // 98.14 // p13.3	megakaryocyte-associated tyrosine kinase	MATK	1.81E-06	0.0007073	7.52628305	6.523000254	1.003283	2.004556
217940_s_at	chr13:110066008-110090341 (+) // 99.85 // q34	hypothetical protein FLJ10769	FLJ10769	1.81E-06	0.0007073	7.674276879	8.762738984	-1.08846	-2.12647
233614_at	chr3:106982214-106985705 (-) // 78.12 // q13.11	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	1.81E-06	0.0007073	5.447371831	4.268333616	1.179038	2.264258
203474_at	chr5:75734904-76039711 (+) // 99.29 // q13.3	IQ motif containing GTPase activating protein 2	IQGAP2	1.89E-06	0.0007211	8.084974898	6.179624804	1.90535	3.745998
232058_at	chr19:43847049-43850186 (+) // 91.83 // q13.2	Actinin, alpha 4	ACTN4	1.89E-06	0.0007211	8.074427116	6.594208622	1.480218	2.78991
241824_at	chr2:28531315-28531746 (+) // 81.86 // p23.2	FOS-like antigen 2	FOSL2	1.89E-06	0.0007211	5.981270792	4.479341527	1.501929	2.832212
1007_s_at	chr6:30964144-30975910 (+) // 95.63 // p21.33	discoidin domain receptor family, member 1	DDR1	1.96E-06	0.0007354	6.471633214	6.920316624	-0.44868	-1.36479
208302_at	chr5:143171918-143180475 (+) // 84.38 // q31.3	minor histocompatibility antigen HB-1	HB-1	1.96E-06	0.0007354	5.689616305	6.295120901	-0.6055	-1.52151
228453_at	chr18:41681572-41682532 (-) // 97.1 // q12.3	hypothetical protein LOC284267	LOC284267	1.96E-06	0.0007354	5.401544662	4.893503369	0.508041	1.422118
202119_s_at	chr8:87595813-87642756 (+) // 98.14 // q21.3	copine III	CPNE3	2.04E-06	0.0007403	6.643989519	7.925348315	-1.28136	-2.43068
203270_at	chr2_random:325587-336606 (-) // 98.7 // /// chr2:24233	deoxythymidylate kinase (thymidylate kinase)	DTYMK	2.04E-06	0.0007403	6.391850262	7.337059002	-0.94521	-1.92547
203440_at	chr18:23784931-23845876 (-) // 98.03 // q12.1	cadherin 2, type 1, N-cadherin (neuronal)	CDH2	2.04E-06	0.0007403	5.863937417	7.335702375	-1.47176	-2.77361
223229_at	chr1:199032607-199036581 (-) // 99.85 // q32.1	ubiquitin-conjugating enzyme E2T (putative)	UBE2T	2.04E-06	0.0007403	6.12014888	7.372259262	-1.25211	-2.3819
241833_at	chr3:180995704-180996314 (-) // 100.0 // q26.33	Full length insert cDNA clone YY86C01	---	2.04E-06	0.0007403	4.152647443	5.43605901	-1.28341	-2.43414
210369_at	chr11:9642257-9720061 (+) // 92.15 // p15.4	SWAP-70 protein	SWAP70	2.22E-06	0.0007971	5.725139484	5.272994972	0.452145	1.368072
201397_at	chr1:119975831-119998878 (+) // 66.14 // p12	phosphoglycerate dehydrogenase	PHGDH	2.31E-06	0.0008136	6.93795281	8.439716119	-1.50176	-2.83189
203099_s_at	chr6:4651391-4899490 (+) // 99.25 // p25.1	chromodomain protein, Y-like	CDYL	2.31E-06	0.0008136	7.675707323	6.799666687	0.876041	1.835331
205330_at	chr22:26468819-26522040 (-) // 95.36 // q12.1	meningioma (disrupted in balanced translocation) 1	MN1	2.31E-06	0.0008136	5.764628585	4.361197015	1.403432	2.6453
204793_at	chrX:101712586-101719523 (+) // 99.96 // q22.1	G protein-coupled receptor associated sorting protein 1	GPRASP1	2.40E-06	0.0008205	5.205886282	7.701630568	-2.49574	-5.64019
207968_s_at	chr5:88054071-88155427 (-) // 72.47 // q14.3	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	2.40E-06	0.0008205	6.954339528	6.336123617	0.618216	1.534976
225793_at	chr1:142989738-142990713 (+) // 83.87 // q21.1	Lix1 homolog (mouse) like	LIX1L	2.35E-06	0.0008205	7.691266585	8.464838275	-0.77357	-1.7095
228027_at	chrX:101777794-101778804 (+) // 98.04 // q22.1	G protein-coupled receptor associated sorting protein 2	GPRASP2	2.40E-06	0.0008205	5.559532439	6.937043831	-1.37751	-2.5982
238542_at	chr6:150362013-150362480 (+) // 86.99 // q25.1	UL16 binding protein 2	ULBP2	2.40E-06	0.0008205	4.528278861	5.571349505	-1.04307	-2.06061
1557424_at	chr5:86078390-86081344 (+) // 77.79 // q14.3	CDNA clone IMAGE:5277114	---	2.50E-06	0.0008434	3.829449648	3.568867536	0.260582	1.197962
237317_at	chr12:115922304-115922880 (+) // 40.03 // q24.22	F-box and WD-40 domain protein 8	FBXW8	2.50E-06	0.0008434	5.436186032	4.932521179	0.503665	1.417811
1562529_s_at	chr15:58658577-58660864 (-) // 87.89 // q22.2	RAR-related orphan receptor A	RORA	2.60E-06	0.0008566	5.980412111	5.006593518	0.973819	1.964032
219938_s_at	chr18:41817500-41839497 (-) // 75.72 // q21.1	proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	2.60E-06	0.0008566	6.341773838	5.170102341	1.171671	2.252725
225825_at	chr20:3179230-3269201 (-) // 99.47 // p13	chromosome 20 open reading frame 194	C20orf194	2.60E-06	0.0008566	5.639205426	6.40784774	-0.76864	-1.70367
229874_x_at	chr1:16592487-16593605 (+) // 78.49 // p36.13 /// chr1:1	hypothetical LOC400741	LOC400741	2.60E-06	0.0008566	6.958236226	8.103187476	-1.14495	-2.21139
205504_at	chrX:100410586-100447327 (-) // 99.11 // q22.1	Bruton agammaglobulinemia tyrosine kinase	BTK	2.71E-06	0.0008757	6.843133417	6.013340185	0.829793	1.777431
239966_at	chr5:88156852-88157630 (-) // 97.47 // q14.3	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	2.71E-06	0.0008757	5.528282785	4.809652361	0.71863	1.645619
244592_at	chr11:128093927-128094383 (+) // 70.11 // q24.3	Friend leukemia virus integration 1	FLI1	2.71E-06	0.0008757	6.979220762	6.060494845	0.918726	1.890445
229429_x_at	chr1:146429436-146429859 (+) // 88.84 // q21.1	LOC440669	---	2.76E-06	0.000888	7.046978427	8.192243133	-1.14526	-2.21187
205128_x_at	chr9:122212912-122235123 (+) // 99.84 // q33.2	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	PTGS1	2.82E-06	0.0008902	6.598413537	5.956941319	0.641472	1.55992
236266_at	chr15:58572623-58573181 (-) // 98.94 // q22.2	CDNA FLJ31407 fis, clone NT2NE2000137	---	2.82E-06	0.0008902	6.070169759	5.28463888	0.785531	1.723726
238469_at	chr6:72069029-72070335 (+) // 63.69 // q13	MRNA full length insert cDNA clone EUROIMAGE 1509279	---	2.82E-06	0.0008902	5.132137001	4.27005555	0.862081	1.817659
224694_at	chr2:69216187-69388108 (+) // 91.33 // p13.3	anthrax toxin receptor 1	ANTXR1	2.93E-06	0.0009157	4.598544782	5.493816106	-0.89527	-1.85996
230672_at	chr5:139760283-139760875 (-) // 61.71 // q31.2	CDNA clone IMAGE:4841343	---	2.93E-06	0.0009157	6.450094712	6.842259634	-0.39216	-1.31236
230285_at	chr11:22798915-22799909 (-) // 90.76 // p14.3	hypothetical protein DKFZp313A2432	DKFZp313A2432	3.05E-06	0.000942	5.570472239	6.74975811	-1.17929	-2.26465
236973_at	chr2:95112810-95113327 (-) // 85.33 // q11.1	Mal, T-cell differentiation protein	MAL	3.05E-06	0.000942	4.06291293	4.487999401	-0.42509	-1.34265
207011_s_at	chr6:43152057-43237428 (+) // 98.11 // p21.1	PTK7 protein tyrosine kinase 7	PTK7	3.17E-06	0.0009746	7.038907482	7.58839578	-0.54949	-1.46357
218928_s_at	chr21:42792810-42874593 (+) // 95.93 // q22.3	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	SLC37A1	3.30E-06	0.0009971	7.411931691	6.600527157	0.811405	1.754919
231963_at	chr5:10707586-10710225 (+) // 99.58 // p15.2	Homo sapiens, clone IMAGE:3869276, mRNA	---	3.30E-06	0.0009971	7.177486854	6.547731414	0.629755	1.547303
240546_at	chr2:131998765-131999531 (+) // 97.84 // q21.1	hypothetical gene supported by AK125982; BC042817	LOC389043	3.30E-06	0.0009971	5.521018809	7.065787012	-1.54477	-2.91757
205801_s_at	chr2:33650592-33701323 (+) // 95.72 // p22.3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	RASGRP3	3.43E-06	0.001026	4.61822249	4.108515258	0.509707	1.423761
206726_at	chr4:95577633-95612968 (-) // 100.0 // q22.3	prostaglandin D2 synthase, hematopoietic	PGDS	3.43E-06	0.001026	6.918305041	5.053310815	1.864994	3.642665
222077_s_at	chr12:48669213-48669853 (-) // 94.13 // q13.12	Rac GTPase activating protein 1	RACGAP1	3.57E-06	0.0010615	6.064411907	7.809619665	-1.74521	-3.35243
1570061_at	chr3:130025255-130027144 (+) // 59.85 // q21.3	CDNA clone IMAGE:4555030	---	3.72E-06	0.0010806	5.070112026	4.669846223	0.400266	1.319751
215443_at	chr14:80491756-80645047 (+) // 93.26 // q31.1	thyroid stimulating hormone receptor	TSHR	3.72E-06	0.0010806	4.668519256	6.056956113	-1.38844	-2.61795
221526_x_at	chr10:34438494-35144217 (-) // 95.5 // p11.22	par-3 partitioning defective 3 homolog (C. elegans)	PARD3	3.72E-06	0.0010806	6.826691301	8.259341722	-1.43265	-2.69942
231911_at	chr2:158000633-158009654 (-) // 94.33 // q24.1	KIAA1189	KIAA1189	3.72E-06	0.0010806	4.654005102	4.224186337	0.429819	1.347064
238529_at	chr1:146645921-146646712 (+) // 73.4 // q21.2 /// chr1:1	Histone 2, H4	HIST2H4	3.86E-06	0.001118	3.802592044	4.229569506	-0.42698	-1.34441
1555486_a_at	chr11:36433414-36441799 (+) // 96.81 // p12	hypothetical protein FLJ14213	FLJ14213	4.02E-06	0.0011387	5.438591281	4.847439942	0.591151	1.506448
202713_s_at	chr14:34661492-34816571 (+) // 78.53 // q13.2	KIAA0391	KIAA0391	4.02E-06	0.0011387	8.297605807	9.116933835	-0.81933	-1.76458
209227_at	chr8:15442102-15667225 (+) // 93.38 // p22	tumor suppressor candidate 3	TUSC3	4.02E-06	0.0011387	3.611773434	3.863541762	-0.25177	-1.19067
225098_at	chr2:204120129-204122396 (+) // 96.04 // q33.2	Abl interactor 2	ABI2	4.02E-06	0.0011387	7.408507119	8.55606714	-1.14756	-2.21539
209856_x_at	chr2:204057243-204117671 (+) // 99.68 // q33.2	abl interactor 2	ABI2	4.18E-06	0.001172	6.355562981	6.922291526	-0.56673	-1.48116
212021_s_at	chr10:129784916-129814639 (-) // 97.55 // q26.2	antigen identified by monoclonal antibody Ki-67	MKI67	4.18E-06	0.001172	6.419876125	7.588994794	-1.16912	-2.24874
1556294_at	chr11:117176766-117195344 (-) // 84.7 // q23.3	MRNA; cDNA DKFZp547P0115 (from clone DKFZp547P0115)	---	4.52E-06	0.0012055	4.182034941	4.715937225	-0.5339	-1.44784
206896_s_at	chr19:2465447-2506186 (-) // 92.67 // p13.3	guanine nucleotide binding protein (G protein), gamma 7	GNG7	4.52E-06	0.0012055	6.263040938	5.578537564	0.684503	1.607149
207268_x_at	chr2:204057151-204117757 (+) // 99.79 // q33.2	abl interactor 2	ABI2	4.52E-06	0.0012055	7.749996409	8.21258225	-0.46259	-1.37801
209054_s_at	chr4:1861739-1951161 (+) // 95.35 // p16.3	Wolf-Hirschhorn syndrome candidate 1	WHSC1	4.52E-06	0.0012055	7.89455203	8.495682821	-0.60113	-1.51691
210754_s_at	chr8:57016966-57085241 (+) // 98.75 // q12.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	4.52E-06	0.0012055	8.99519349	6.776812325	2.218381	4.65371
221156_x_at	chr15:53438331-53440128 (-) // 94.88 // q21.3	cell cycle progression 1	CCPG1	4.35E-06	0.0012055	3.834329449	3.401994652	0.432335	1.349416
222803_at	chr10:25177550-25281539 (-) // 99.28 // p12.1	phosphoribosyl transferase domain containing 1	PRTFDC1	4.52E-06	0.0012055	5.056491412	6.649895507	-1.5934	-3.01761
230820_at	chr17:59971836-59972325 (+) // 93.87 // q24.1	SMAD specific E3 ubiquitin protein ligase 2	SMURF2	4.52E-06	0.0012055	7.979957453	6.575591046	1.404366	2.647015
243771_at	chr9:111375634-111376188 (+) // 35.81 // q31.3	zinc finger protein 483	ZNF483	4.35E-06	0.0012055	6.80050135	5.610419869	1.190081	2.281656
38149_at	chr2:68913801-68965606 (+) // 93.02 // p13.3	Rho GTPase activating protein 25	ARHGAP25	4.52E-06	0.0012055	7.937539774	7.138314665	0.799225	1.740166
225810_at	chr15:29018435-29020286 (-) // 98.09 // q13.3	myotubularin related protein 10	MTMR10	4.61E-06	0.0012232	7.225199692	6.614700317	0.610499	1.526788
202158_s_at	chr10:11100075-11416358 (+) // 98.53 // p14	CUG triplet repeat, RNA binding protein 2	CUGBP2	4.70E-06	0.0012413	8.973847699	8.192406617	0.781441	1.718847
244033_at	chr14:80032573-80033023 (-) // 98.9 // q31.1	chromosome 14 open reading frame 145	C14orf145	4.89E-06	0.0012844	4.224910497	6.167384952	-1.94247	-3.84364
201928_at	chr2:159139116-159363850 (+) // 98.73 // q24.1	plakophilin 4	PKP4	5.08E-06	0.0013226	5.269046293	5.778128087	-0.50908	-1.42314
39650_s_at	chr19:11349954-11350001 (-) // 71.21 // p13.2	erythropoietin receptor	EPOR	5.08E-06	0.0013226	6.293850992	6.903830552	-0.60998	-1.52624
1562473_at	chr3:181226644-181229143 (-) // 38.32 // q26.33	Peroxisomal biogenesis factor 5-like	PEX5L	5.49E-06	0.001396	4.634464808	6.136665036	-1.5022	-2.83274
203238_s_at	chr19:15131444-15172792 (-) // 95.54 // p13.12	Notch homolog 3 (Drosophila)	NOTCH3	5.49E-06	0.001396	5.458862941	7.268544266	-1.80968	-3.50565
212886_at	chr5:150540805-150583826 (-) // 76.94 // q33.1	DKFZP434C171 protein	DKFZP434C171	5.49E-06	0.001396	8.145458007	6.939594572	1.205863	2.306753
237849_at	chr6:119544329-119544940 (-) // 53.57 // q22.31	Mannosidase, alpha, class 1A, member 1	MAN1A1	5.49E-06	0.001396	5.909846776	4.233119114	1.676728	3.19702
244561_at	chrX:46218393-46219304 (-) // 89.96 // p11.3	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	---	5.49E-06	0.001396	4.841984506	4.352538318	0.489446	1.403906
212496_s_at	chr19:5082228-5104609 (+) // 91.47 // p13.3	jumonji domain containing 2B	JMJD2B	5.71E-06	0.0014181	8.002265708	6.947975714	1.05429	2.076696
215889_at	chr3:171560112-171562988 (+) // 79.37 // q26.2	SKI-like	SKIL	5.71E-06	0.0014181	4.830564173	4.355236494	0.475328	1.390234
226479_at	chr13:40599706-40602659 (-) // 77.65 // q14.11	kelch repeat and BTB (POZ) domain containing 6	KBTBD6	5.71E-06	0.0014181	4.636027426	5.931790609	-1.29576	-2.45507
228033_at	chr12:75917493-75918997 (-) // 92.9 // q21.2	E2F transcription factor 7	E2F7	5.71E-06	0.0014181	3.989415898	6.279207856	-2.28979	-4.88986
234112_at	chr3:107006836-107008045 (+) // 68.8 // q13.11	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	5.71E-06	0.0014181	4.774968518	3.96479198	0.810177	1.753426
219544_at	chr13:72215688-72227587 (+) // 96.34 // q22.1	FLJ22624 protein	FLJ22624	5.93E-06	0.0014672	5.674508605	6.724326155	-1.04982	-2.07027
1562550_at	chr12:122030934-122033197 (-) // 81.08 // q24.31	Phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	6.16E-06	0.0014846	4.297108331	4.583333313	-0.28622	-1.21945
202971_s_at	chr12:66329020-66340410 (+) // 97.23 // q15	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	6.16E-06	0.0014846	7.016511998	6.072115645	0.944396	1.924384
204214_s_at	chr6:146906693-146917655 (+) // 94.63 // q24.3	RAB32, member RAS oncogene family	RAB32	6.16E-06	0.0014846	7.305894598	9.031607174	-1.72571	-3.30743
217025_s_at	chr5:176816838-176832805 (-) // 94.18 // q35.3	drebrin 1	DBN1	6.16E-06	0.0014846	7.260145865	8.258464561	-0.99832	-1.99767
234107_s_at	chr20:18672743-18692544 (+) // 94.53 // p11.23	histidyl-tRNA synthetase 2	HARS2	6.16E-06	0.0014846	6.46450942	5.432348792	1.032161	2.045085
236908_at	chr3:142466401-142466879 (+) // 27.18 // q23	Acid phosphatase-like 2	ACPL2	6.16E-06	0.0014846	6.106113465	7.034873015	-0.92876	-1.90364
216470_x_at	chr7:141955618-141978749 (+) // 93.56 // q34 /// chr7:14	protease, serine, 1 (trypsin 1) /// protease, serine, 2 (trypsin 2) /// protease, serine, 3 (mesotrypsin)	PRSS1 /// PRSS2	6.41E-06	0.0015293	5.352626072	4.89410382	0.458522	1.374134
225112_at	chr2:204120129-204122396 (+) // 96.04 // q33.2	Abl interactor 2	ABI2	6.40E-06	0.0015293	8.19465041	9.265154952	-1.0705	-2.10017
209061_at	chr20:45564027-45719023 (+) // 93.49 // q13.12	nuclear receptor coactivator 3	NCOA3	6.78E-06	0.0016129	8.131614435	7.478378772	0.653236	1.572691
205789_at	---	CD1D antigen, d polypeptide /// CD1D antigen, d polypeptide	CD1D	7.19E-06	0.0016936	4.499118293	5.316407252	-0.81729	-1.76209
241955_at	chr14:30707390-30712524 (-) // 94.85 // q12	HECT domain containing 1	HECTD1	7.19E-06	0.0016936	6.34201529	5.546806696	0.795209	1.735328
1554256_a_at	chr1:229577492-229700677 (-) // 89.21 // q42.2	pecanex-like 2 (Drosophila)	PCNXL2	7.33E-06	0.0017189	4.792431005	5.376140159	-0.58371	-1.4987
230051_at	chr10:11953524-11954280 (+) // 96.42 // p14	chromosome 10 open reading frame 47	C10orf47	7.47E-06	0.0017445	4.902006204	3.867409857	1.034596	2.04854
1554306_at	chr1:223201631-223233759 (-) // 87.75 // q42.12	inositol 1,4,5-trisphosphate 3-kinase B	ITPKB	7.76E-06	0.0017746	6.408761617	4.996624499	1.412137	2.661311
205315_s_at	chr16:67778550-67892385 (+) // 95.0 // q22.1	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	SNTB2	7.76E-06	0.0017746	5.311910753	5.847781727	-0.53587	-1.44982
207015_s_at	chr15:56034656-56145183 (-) // 99.94 // q21.3	aldehyde dehydrogenase 1 family, member A2	ALDH1A2	7.76E-06	0.0017746	6.257498196	7.151784346	-0.89429	-1.85869
222525_s_at	chr8:27646753-27686089 (-) // 98.65 // p21.1	coiled-coil domain containing 25	CCDC25	7.76E-06	0.0017746	7.058043076	7.851432315	-0.79339	-1.73314
226118_at	chr2:24954291-24957347 (+) // 97.13 // p23.3	hypothetical protein MGC11266	MGC11266	7.76E-06	0.0017746	5.829291677	6.773236141	-0.94394	-1.92378
1570165_at	chr12:103426133-103427710 (+) // 58.89 // q23.3	Carbohydrate (chondroitin 4) sulfotransferase 11	CHST11	8.06E-06	0.001809	8.854070769	7.480140162	1.373931	2.591757
203098_at	chr6:4651391-4900776 (+) // 98.51 // p25.1	chromodomain protein, Y-like	CDYL	8.06E-06	0.001809	7.352063728	6.627037243	0.725026	1.652931
204882_at	chr2:68913770-68965606 (+) // 99.93 // p13.3	Rho GTPase activating protein 25	ARHGAP25	8.06E-06	0.001809	8.100139077	7.079204896	1.020934	2.029233
205786_s_at	---	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrop	ITGAM	8.37E-06	0.001809	7.201343131	5.262923028	1.93842	3.832857
210052_s_at	chr20:29790791-29852956 (+) // 98.58 // q11.21	TPX2, microtubule-associated, homolog (Xenopus laevis)	TPX2	8.37E-06	0.001809	6.427364262	7.987441725	-1.56008	-2.9487
210749_x_at	chr6:30960424-30975910 (+) // 99.68 // p21.33	discoidin domain receptor family, member 1	DDR1	8.37E-06	0.001809	6.286192697	6.730731084	-0.44454	-1.36088
210942_s_at	chr3:99933819-99995495 (+) // 98.91 // q12.1	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	ST3GAL6	8.37E-06	0.001809	3.910169998	4.349314287	-0.43914	-1.3558
211734_s_at	chr1:156085198-156091064 (+) // 93.1 // q23.2	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide /// Fc fragment of IgE, high affinity	FCER1A	8.37E-06	0.001809	4.300626047	3.910403377	0.390223	1.310596
217901_at	chr18:27352198-27382955 (+) // 91.17 // q12.1	Desmoglein 2	DSG2	8.37E-06	0.001809	5.917131512	6.996809278	-1.07968	-2.11356
219383_at	chr11:36354163-36443091 (+) // 99.71 // p13	hypothetical protein FLJ14213	FLJ14213	8.21E-06	0.001809	4.658475409	4.166895418	0.49158	1.405984
223274_at	chr6:31235044-31239534 (+) // 98.48 // p21.33	transcription factor 19 (SC1)	TCF19	8.37E-06	0.001809	6.990843892	7.751775368	-0.76093	-1.69458
223596_at	chr15:32312754-32416337 (-) // 99.32 // q14	solute carrier family 12 (potassium/chloride transporters), member 6	SLC12A6	8.06E-06	0.001809	5.431650839	4.047670356	1.38398	2.609875
225172_at	chr16:1646290-1667910 (+) // 94.18 // p13.3	Crm, cramped-like (Drosophila)	CRAMP1L	8.37E-06	0.001809	7.78024848	6.956081941	0.824167	1.770512
231455_at	chr2:6819897-6820377 (-) // 8.02 // p25.2	FLJ42418 protein	FLJ42418	8.37E-06	0.001809	3.84924241	3.572351158	0.276891	1.211581
206478_at	chr14:105461656-105469545 (+) // 85.86 // q32.33 /// ch	KIAA0125	KIAA0125	8.69E-06	0.0018497	6.012435787	4.967502333	1.044933	2.063271
210401_at	chr17:3746637-3766464 (-) // 86.29 // p13.2	purinergic receptor P2X, ligand-gated ion channel, 1	P2RX1	8.69E-06	0.0018497	9.161173951	8.22578994	0.935384	1.9124
222741_s_at	chr6:39179817-39190922 (-) // 90.77 // p21.2	chromosome 6 open reading frame 64	C6orf64	8.69E-06	0.0018497	6.782139095	7.475257929	-0.69312	-1.61677
223412_at	chr13:40663709-40666619 (-) // 98.43 // q14.11	kelch repeat and BTB (POZ) domain containing 7	KBTBD7	8.69E-06	0.0018497	3.873064244	4.501304446	-0.62824	-1.54568
204849_at	chr20:60942912-60963421 (-) // 91.75 // q13.33	transcription factor-like 5 (basic helix-loop-helix)	TCFL5	9.03E-06	0.0018703	6.137567593	7.754904058	-1.61734	-3.06808
212020_s_at	chr10:129784916-129814639 (-) // 97.55 // q26.2	antigen identified by monoclonal antibody Ki-67	MKI67	9.03E-06	0.0018703	6.055172965	7.113575435	-1.0584	-2.08262
220023_at	chr16:28413493-28417773 (+) // 92.76 // p11.2	apolipoprotein B48 receptor	APOB48R	9.03E-06	0.0018703	6.985415643	6.26261382	0.722802	1.650384
224832_at	chr12:12518160-12565641 (-) // 98.74 // p13.2	dual specificity phosphatase 16	DUSP16	9.03E-06	0.0018703	5.985961099	7.09042218	-1.10446	-2.15019

225303_at	chr1:154879230-154883125 (+) // 92.47 // q23.1	kin of IRRE like (Drosophila)	KIRREL	9.03E-06	0.0018703	4.825215186	5.250068832	-0.42485	-1.34244
227894_at	chr16:656691-657831 (+) // 96.04 // p13.3	similar to RIKEN cDNA 3230401M21 [Mus musculus]	LOC197336	9.03E-06	0.0018703	6.302158679	6.930289138	-0.62813	-1.54556
231990_at	chr12:60940444-61016738 (+) // 84.29 // q14.1	ubiquitin specific peptidase 15	USP15	9.03E-06	0.0018703	9.030548669	7.928213488	1.102335	2.147019
201896_s_at	chr1:109534231-109537789 (-) // 67.23 // p13.3	proline/serine-rich coiled-coil 1	PSRC1	9.38E-06	0.0019206	4.982927863	5.533996604	-0.55107	-1.46517
220740_s_at	chr15:32312957-32398222 (-) // 99.97 // q14	solute carrier family 12 (potassium/chloride transporters), member 6	SLC12A6	9.38E-06	0.0019206	6.591366268	5.532077924	1.059288	2.083903
240594_at	---	Chromodomain protein, Y-like	CDYL	9.38E-06	0.0019206	7.809144534	6.474711746	1.334433	2.521763
216834_at	chr1:189276593-189280809 (+) // 91.99 // q31.2	regulator of G-protein signalling 1	RGS1	9.56E-06	0.0019498	11.37873314	8.291491477	3.087242	8.498697
224906_at	chr12:44103080-44112397 (+) // 98.15 // q12	transmembrane protein 16F	TMEM16F	9.74E-06	0.0019724	6.984590905	7.912846356	-0.92826	-1.90297
243578_at	chr7:16406488-16407089 (-) // 21.8 // p21.1	Ankyrin repeat and MYND domain containing 2	ANKMY2	9.74E-06	0.0019724	4.788346287	4.45531219	0.333034	1.25966
1556209_at	chr12:9896508-9897046 (-) // 15.64 // p13.31	C-type lectin domain family 2, member B	CLEC2B	1.01E-05	0.0020331	7.254867996	5.367857511	1.88701	3.69868
226654_at	chr7:100241363-100255652 (+) // 97.67 // q22.1	mucin 12	MUC12	1.01E-05	0.0020331	5.014462919	5.199398925	-0.18494	-1.13677
1558517_s_at	chr1:89893629-89896223 (+) // 89.22 // p22.2	CDNA FLJ37485 fis, clone BRAWH2014379	---	1.05E-05	0.0020805	5.738382544	4.993806991	0.744576	1.675481
217551_at	chr11:16992459-17030791 (+) // 98.96 // p15.1	similar to olfactory receptor, family 7, subfamily A, member 17	LOC441453	1.05E-05	0.0020805	4.392117499	5.357328432	-0.96521	-1.95235
221753_at	chr12:107678667-107701420 (-) // 92.26 // q24.11	slingshot homolog 1 (Drosophila)	SSH1	1.05E-05	0.0020805	8.226131341	7.697909539	0.528222	1.442151
239427_at	chr1:157390968-157391638 (-) // 96.4 // q23.3	Transcribed locus	---	1.05E-05	0.0020805	5.708896956	6.367202014	-0.65831	-1.57823
202260_s_at	chr9:127454121-127534549 (+) // 99.05 // q34.11	syntaxin binding protein 1	STXBP1	1.09E-05	0.0021143	4.739387515	5.257011008	-0.51762	-1.4316
212226_s_at	chr1:56672453-56694699 (-) // 95.75 // p32.2	phosphatidic acid phosphatase type 2B	PPAP2B	1.09E-05	0.0021143	5.43840511	6.74078354	-1.30238	-2.46635
224911_s_at	chr3:99997505-100000947 (-) // 96.53 // q12.1	discoidin, CUB and LCCL domain containing 2	DCBLD2	1.09E-05	0.0021143	4.099308254	4.288698114	-0.18939	-1.14028
226368_at	chr12:103655759-103658257 (+) // 91.0 // q23.3	Carbohydrate (chondroitin 4) sulfotransferase 11	CHST11	1.09E-05	0.0021143	7.215171749	6.112331169	1.102841	2.147772
229363_at	chr16:64999955-65002925 (+) // 65.19 // q22.1	CDNA FLJ32121 fis, clone PEBLM1000083	---	1.09E-05	0.0021143	5.174660042	5.549602128	-0.37494	-1.29679
242390_at	chr2:224623586-224624042 (-) // 38.0 // q36.1	WD repeat and FYVE domain containing 1	WDFY1	1.09E-05	0.0021143	6.181381944	5.595752997	0.585629	1.500693
222001_x_at	chr1:146389544-146429859 (+) // 84.06 // q21.1 /// chr1:	LOC440669	---	1.13E-05	0.0021797	7.117991583	8.096437931	-0.97845	-1.97034
241893_at	chr2:134738320-134739001 (+) // 75.58 // q21.2	Transcribed locus	---	1.13E-05	0.0021797	4.813992916	4.244228835	0.569764	1.484281
202580_x_at	chr12:2837110-2853954 (-) // 98.68 // p13.33	forkhead box M1	FOXM1	1.18E-05	0.0022392	5.963767929	7.46930594	-1.50554	-2.83931
204164_at	chr11:65164875-65174975 (+) // 96.96 // q13.1	signal-induced proliferation-associated gene 1	SIPA1	1.18E-05	0.0022392	7.178265991	6.460640609	0.717625	1.644473
209464_at	chr17:8048844-8054599 (-) // 96.49 // p13.1	aurora kinase B	AURKB	1.18E-05	0.0022392	6.194651087	7.238352849	-1.0437	-2.06151
1562255_at	chr6:159096758-159101312 (+) // 73.81 // q25.3	synaptotagmin-like 3	SYTL3	1.22E-05	0.0022847	4.999804258	4.186840375	0.812964	1.756817
202806_at	chr16:15950934-16143774 (+) // 97.86 // p13.11	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	ABCC1	1.22E-05	0.0022847	7.185301971	8.800775889	-1.61547	-3.06412
208116_s_at	chr6:119542015-119711788 (-) // 74.71 // q22.31	mannosidase, alpha, class 1A, member 1	MAN1A1	1.22E-05	0.0022847	5.496595339	4.813128202	0.683467	1.605995
209306_s_at	chr11:9642207-9731077 (+) // 91.5 // p15.4	SWAP-70 protein	SWAP70	1.22E-05	0.0022847	6.785966979	5.526577263	1.25939	2.393945
217894_at	chr1:212129279-212183468 (+) // 80.48 // q41	potassium channel tetramerisation domain containing 3	KCTD3	1.22E-05	0.0022847	3.351619069	4.00113964	-0.64952	-1.56865
201910_at	chr13:97592838-97900024 (+) // 98.82 // q32.2	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	FARP1	1.24E-05	0.0023198	6.198008882	6.552595234	-0.35459	-1.27862
204452_s_at	chr7:90538445-90540974 (+) // 97.63 // q21.13	frizzled homolog 1 (Drosophila)	FZD1	1.27E-05	0.0023396	4.1931286	4.639560338	-0.44643	-1.36267
212119_at	chr2:46719789-46723020 (+) // 95.74 // p21 /// chr2:132(	ras homolog gene family, member Q	RHOQ	1.27E-05	0.0023396	8.139066294	7.504457249	0.634609	1.552517
212437_at	chr20:3712497-3715130 (-) // 89.82 // p13	centromere protein B, 80kDa	CENPB	1.27E-05	0.0023396	6.530622505	7.36889232	-0.83827	-1.7879
203839_s_at	chr3:197078545-197124265 (-) // 97.12 // q29	tyrosine kinase, non-receptor, 2	TNK2	1.31E-05	0.0024203	8.536366074	7.914634783	0.621731	1.538721
1560259_at	chr15:58619251-58620709 (-) // 97.0 // q22.2	RAR-related orphan receptor A	RORA	1.36E-05	0.0024704	7.270428123	6.694807236	0.575621	1.490319
207727_s_at	chr1:45464007-45475153 (-) // 99.14 // p34.1	mutY homolog (E. coli)	MUTYH	1.36E-05	0.0024704	7.918613476	8.313950451	-0.39534	-1.31525
221190_s_at	chr18:19338334-19365735 (+) // 97.67 // q11.2	chromosome 18 open reading frame 8	C18orf8	1.36E-05	0.0024704	8.616244191	7.623818504	0.992426	1.989527
224715_at	chr9:128475493-128498612 (-) // 89.46 // q34.11	WD repeat domain 34	WDR34	1.36E-05	0.0024704	7.669303682	8.794858213	-1.12555	-2.18185
234036_x_at	chr15:75316839-75320003 (-) // 78.33 // q24.3	CDNA: FLJ21384 fis, clone COL03354	---	1.36E-05	0.0024704	4.505700418	3.857694421	0.648006	1.567001
1565868_at	chr11:35190672-35192120 (+) // 77.26 // p13	CD44 antigen (homing function and Indian blood group system)	CD44	1.42E-05	0.0025304	7.425567287	6.221028696	1.204539	2.304635
204318_s_at	chr22:45013803-45046942 (+) // 87.84 // q13.31	G-2 and S-phase expressed 1	GTSE1	1.42E-05	0.0025304	5.639639293	7.279670143	-1.64003	-3.11672
216028_at	chr11:43835836-43837270 (+) // 18.7 // p11.2	DKFZP564C152 protein	DKFZP564C152	1.42E-05	0.0025304	5.169559688	5.766845344	-0.59729	-1.51287
241947_at	chr12:45895191-45896394 (-) // 77.19 // q13.11	CDNA FLJ41983 fis, clone SPLEN2011025	---	1.42E-05	0.0025304	4.871544759	4.244541449	0.627003	1.544354
200696_s_at	chr9:121141678-121174674 (+) // 97.19 // q33.2	gelsolin (amyloidosis, Finnish type)	GSN	1.47E-05	0.0025838	7.076339255	6.141363068	0.934976	1.911859
224336_s_at	chr12:12520097-12606512 (-) // 98.44 // p13.2	dual specificity phosphatase 16 /// dual specificity phosphatase 16	DUSP16	1.47E-05	0.0025838	5.301917021	6.205385891	-0.90347	-1.87056
225386_s_at	chr2:38701919-38742133 (-) // 94.31 // p22.1	heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	1.47E-05	0.0025838	7.045757215	8.480916684	-1.43516	-2.70412
227108_at	chr15:40769660-40800471 (+) // 99.32 // q15.2	START domain containing 9	STARD9	1.47E-05	0.0025838	5.519007091	4.888004415	0.631003	1.548641
227713_at	chr13:29674629-29675791 (-) // 97.93 // q12.3	katanin p60 subunit A-like 1	KATNAL1	1.47E-05	0.0025838	6.578334793	7.291902626	-0.71357	-1.63985
203910_at	chr1:94350191-94415142 (-) // 98.43 // p22.1	Rho GTPase activating protein 29	ARHGAP29	1.50E-05	0.0026068	4.47822134	6.441949239	-1.96373	-3.90069
219457_s_at	chr14:92188546-92225091 (+) // 99.22 // q32.12	Ras and Rab interactor 3	RIN3	1.50E-05	0.0026068	7.987856587	7.255751051	0.732106	1.661062
230006_s_at	chr11:22798732-22799201 (-) // 79.14 // p14.3	hypothetical protein DKFZp313A2432	DKFZp313A2432	1.50E-05	0.0026068	6.607153472	7.279210293	-0.67206	-1.59334
202513_s_at	chr6:43065324-43088054 (+) // 91.37 // p21.1	protein phosphatase 2, regulatory subunit B (B56), delta isoform	PPP2R5D	1.53E-05	0.002647	7.58949604	8.098235381	-0.50874	-1.42281
1557098_s_at	chr20:61204004-61206182 (+) // 89.14 // q13.33	CDNA clone IMAGE:4812795	---	1.58E-05	0.002738	5.740756815	6.270637439	-0.52988	-1.44381
205024_s_at	chr15:38774713-38811082 (+) // 98.84 // q15.1	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51	1.64E-05	0.0028055	6.565541232	7.345719611	-0.78018	-1.71734
214992_s_at	chr19:12847803-12853190 (-) // 98.0 // p13.13	deoxyribonuclease II, lysosomal	DNASE2	1.64E-05	0.0028055	5.485091485	5.856544595	-0.37145	-1.29366
225372_at	chr10:73177321-73203283 (-) // 87.3 // q22.1	chromosome 10 open reading frame 54	C10orf54	1.64E-05	0.0028055	7.002031198	6.073083826	0.928947	1.903886
238387_s_at	chr14:105815313-105815961 (+) // 98.9 // q32.33	---	---	1.64E-05	0.0028055	4.41576952	4.697519459	-0.28175	-1.21567
201929_s_at	chr2:159139116-159362848 (+) // 98.5 // q24.1	plakophilin 4	PKP4	1.70E-05	0.0028484	4.393254117	4.76552306	-0.37227	-1.29439
203806_s_at	---	Fanconi anemia, complementation group A /// Fanconi anemia, complementation group A	FANCA	1.70E-05	0.0028484	5.997086094	6.380696791	-0.38361	-1.3046
216203_at	chr14:77071696-77133417 (-) // 85.16 // q24.3	serine palmitoyltransferase, long chain base subunit 2	SPTLC2	1.70E-05	0.0028484	6.612140425	5.169667881	1.442473	2.717863
218175_at	chr12:122945834-122982043 (-) // 96.97 // q24.31	limkain beta 2	FLJ22471	1.70E-05	0.0028484	7.498745451	8.502529171	-1.00378	-2.00525
219806_s_at	chr11:92851288-92916162 (-) // 90.35 // q21	FN5 protein	FN5	1.70E-05	0.0028484	5.261331575	5.846965509	-0.58563	-1.5007
222863_at	chr8:81575064-81598184 (+) // 91.3 // q21.13	zinc finger and BTB domain containing 10	ZBTB10	1.70E-05	0.0028484	6.225319998	6.960727202	-0.73541	-1.66487
241595_at	chr1:8404325-8405236 (-) // 80.22 // p36.23	Arginine-glutamic acid dipeptide (RE) repeats	RERE	1.70E-05	0.0028484	5.525187304	4.998423988	0.526763	1.440693
225591_at	chr8:346832-409575 (+) // 99.56 // p23.3	F-box protein 25	FBXO25	1.73E-05	0.0028921	7.534160645	8.741113873	-1.20695	-2.3085
218552_at	chr1:53073925-53099419 (-) // 99.82 // p32.3	enoyl Coenzyme A hydratase domain containing 2	ECHDC2	1.77E-05	0.0028931	6.560544823	7.1708624	-0.61032	-1.5266
222696_at	chr17:60955146-60985289 (-) // 98.57 // q24.1	axin 2 (conductin, axil)	AXIN2	1.77E-05	0.0028931	4.809844931	5.287875259	-0.47803	-1.39284
224435_at	chr10:82170200-82182371 (+) // 74.49 // q22.3	chromosome 10 open reading frame 58 /// chromosome 10 open reading frame 58	C10orf58	1.77E-05	0.0028931	6.464885637	7.603155162	-1.13827	-2.20117
226335_at	chrX:19927685-19930407 (-) // 97.59 // p22.12	ribosomal protein S6 kinase, 90kDa, polypeptide 3	RPS6KA3	1.77E-05	0.0028931	8.31738062	7.638987853	0.678393	1.600356
229625_at	chr1:89438285-89440424 (-) // 94.41 // p22.2	Guanylate binding protein 5	GBP5	1.77E-05	0.0028931	6.71059058	4.877849606	1.832741	3.562132
237335_at	chr11:60399033-60399736 (+) // 95.01 // q12.2	zona pellucida glycoprotein 1 (sperm receptor)	ZP1	1.77E-05	0.0028931	5.524075761	5.904370134	-0.38029	-1.30161
201365_at	chr15:62766828-62782507 (-) // 98.32 // q22.31	ornithine decarboxylase antizyme 2	OAZ2	1.83E-05	0.0029657	8.489935411	8.092739241	0.397196	1.316946
201580_s_at	chr20:7905999-7948443 (-) // 86.89 // p12.3	thioredoxin domain containing 13	TXNDC13	1.83E-05	0.0029657	8.082367093	7.208731984	0.873635	1.832274
205992_s_at	chr4:142915415-143012003 (+) // 99.5 // q31.21	interleukin 15	IL15	1.83E-05	0.0029657	3.909444972	4.639575131	-0.73013	-1.65879
206274_s_at	chr1:17009501-17044759 (+) // 87.58 // p36.13	ciliary rootlet coiled-coil, rootletin	CROCC	1.83E-05	0.0029657	6.320400334	6.702596615	-0.3822	-1.30332
1554876_a_at	chr5:76181680-76252812 (+) // 87.43 // q13.3	S100 calcium binding protein, zeta	S100Z	1.90E-05	0.003014	5.653756715	4.96313965	0.690617	1.613974
204267_x_at	chr16:2962794-2969851 (-) // 98.46 // p13.3	protein kinase, membrane associated tyrosine/threonine 1	PKMYT1	1.90E-05	0.003014	8.388804991	8.98412751	-0.59532	-1.51081
214933_at	chr19:13178255-13229214 (-) // 96.36 // p13.13	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	CACNA1A	1.90E-05	0.003014	6.45639713	5.724239546	0.732158	1.661121
222164_at	chr8:38411021-38412339 (-) // 77.5 // p12	Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	FGFR1	1.90E-05	0.003014	7.413028389	8.413929766	-1.0009	-2.00125
224582_s_at	chr1:202413977-202417996 (-) // 96.84 // q32.1	Nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS	1.90E-05	0.003014	7.810158628	8.514314099	-0.70416	-1.62919
226607_at	chr20:3177951-3179785 (-) // 97.89 // p13	chromosome 20 open reading frame 194	C20orf194	1.90E-05	0.003014	5.55022077	6.477327918	-0.92711	-1.90146
228442_at	chr20:49436904-49437401 (-) // 94.67 // q13.2	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	NFATC2	1.90E-05	0.003014	7.947949237	6.770694298	1.177255	2.261461
202554_s_at	chr1:109990394-109995683 (-) // 80.03 // p13.3	glutathione S-transferase M3 (brain)	GSTM3	1.97E-05	0.0031082	5.968618218	6.766317723	-0.7977	-1.73833
218520_at	chr12:63132203-63182003 (+) // 100.0 // q14.2	TANK-binding kinase 1	TBK1	1.97E-05	0.0031082	6.727853495	5.946868686	0.780985	1.718303
1560396_at	chr3:184691499-184693930 (-) // 75.97 // q27.1	Kelch-like 6 (Drosophila)	KLHL6	2.05E-05	0.00316	5.856311301	4.903903918	0.952407	1.935099
204880_at	chr10:131224493-131455356 (+) // 96.36 // q26.3	O-6-methylguanine-DNA methyltransferase	MGMT	2.05E-05	0.00316	6.613276406	7.508826215	-0.89555	-1.86032
211519_s_at	chr1:44881177-44901971 (+) // 99.13 // p34.1	kinesin family member 2C	KIF2C	2.05E-05	0.00316	5.077399607	6.117683204	-1.04028	-2.05663
213241_at	chr12:93201709-93203912 (+) // 91.83 // q22	plexin C1	PLXNC1	2.05E-05	0.00316	5.795718173	4.917876847	0.877841	1.837624
227638_at	chr18:41684607-41701711 (-) // 96.0 // q12.3	KIAA1632	KIAA1632	2.05E-05	0.00316	7.990346204	7.31313498	0.677211	1.599046
239555_at	chr8:56993836-56994135 (+) // 28.57 // q12.1	V-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	2.05E-05	0.00316	6.753342259	6.175359595	0.577983	1.49276
241692_at	chr2:38736807-38737278 (-) // 62.94 // p22.1	Heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	2.05E-05	0.00316	6.450926597	8.19435142	-1.74342	-3.34829
229221_at	chr11:35183185-35186287 (+) // 99.04 // p13	CD44 antigen (homing function and Indian blood group system)	CD44	2.12E-05	0.0032498	7.387973128	5.913466455	1.474507	2.778886
239317_at	chr19:46747725-46748472 (+) // 70.76 // q13.2	carcinoembryonic antigen-related cell adhesion molecule 21	CEACAM21	2.12E-05	0.0032498	4.466031504	4.067431089	0.3986	1.318228
240498_at	chr12:11788579-11789111 (+) // 99.81 // p13.2	Ets variant gene 6 (TEL oncogene)	ETV6	2.12E-05	0.0032498	7.376312536	6.012821647	1.363491	2.57307
205300_s_at	chr12:122467586-122475813 (+) // 99.45 // q24.31	U11/U12 snRNP 35K	U1SNRNPBP	2.16E-05	0.0033	7.968389324	7.503316205	0.465073	1.380387
1556323_at	chr10:11403038-11403488 (+) // 96.98 // p14	CUG triplet repeat, RNA binding protein 2	CUGBP2	2.20E-05	0.0033145	7.550797169	6.804511511	0.746286	1.677468
207700_s_at	chr20:45564091-45717893 (+) // 97.68 // q13.12	nuclear receptor coactivator 3	NCOA3	2.20E-05	0.0033145	7.235326168	6.501971919	0.733354	1.6625
214790_at	chr6:76401140-76446302 (+) // 81.66 // q14.1	SUMO1/sentrin specific peptidase 6	SENP6	2.20E-05	0.0033145	7.474565837	6.561116447	0.913449	1.883544
217726_at	chr12:53005177-53031900 (+) // 99.84 // q13.13	coatomer protein complex, subunit zeta 1	COPZ1	2.20E-05	0.0033145	7.827419293	8.655049101	-0.82763	-1.77477
223169_s_at	chr1:225178145-225186464 (+) // 93.9 // q42.13	ras homolog gene family, member U	RHOU	2.20E-05	0.0033145	5.328987955	7.309779468	-1.98079	-3.9471
1554508_at	chr10:98344955-98382988 (-) // 97.35 // q24.1	phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	2.28E-05	0.0033812	4.228492462	3.913210995	0.315281	1.244254
209832_s_at	chr16:87397724-87402418 (+) // 95.01 // q24.3	DNA replication factor	CDT1	2.28E-05	0.0033812	6.343568416	7.977370375	-1.6338	-3.1033
217995_at	chr15:43714547-43770770 (+) // 98.88 // q21.1	sulfide quinone reductase-like (yeast)	SQRDL	2.28E-05	0.0033812	7.072158818	8.321891024	-1.24973	-2.37797
224800_at	chr2:224565570-224635551 (-) // 98.79 // q36.1	WD repeat and FYVE domain containing 1	WDFY1	2.28E-05	0.0033812	6.94097138	5.844367394	1.096604	2.138507
226909_at	chr4:10117785-10124060 (-) // 94.93 // p16.1	KIAA1729 protein	KIAA1729	2.28E-05	0.0033812	5.184331746	6.052467623	-0.86814	-1.8253
232722_at	chr6:167317273-167341090 (-) // 76.91 // q27	ribonuclease T2	RNASET2	2.28E-05	0.0033812	4.92055	4.422441266	0.498109	1.412361
226278_at	chr11:22800072-22807957 (-) // 99.73 // p14.3	hypothetical protein DKFZp313A2432	DKFZp313A2432	2.32E-05	0.0034335	7.779327544	8.757534082	-0.97821	-1.97001
215813_s_at	chr9:122212917-122235011 (+) // 99.91 // q33.2	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	PTGS1	2.37E-05	0.0034591	5.863836823	5.129473729	0.734363	1.663663
219408_at	chr16:66902445-66948663 (+) // 94.31 // q22.1	protein arginine N-methyltransferase 7	PRMT7	2.37E-05	0.0034591	5.695148128	7.011312291	-1.31616	-2.49003
226756_at	chr7:105891163-105892706 (-) // 97.84 // q22.3	Hypothetical protein FLJ36031	FLJ36031	2.37E-05	0.0034591	5.811028385	5.272059923	0.538968	1.452933
237456_at	chr3:72536642-72537125 (-) // 99.79 // p13	RING1 and YY1 binding protein	RYBP	2.37E-05	0.0034591	8.872098937	7.855458793	1.01664	2.023202
1569345_at	chr17:3761214-3762372 (-) // 47.49 // p13.2	Purinergic receptor P2X, ligand-gated ion channel, 1	P2RX1	2.45E-05	0.00353	5.264985988	4.608988035	0.655998	1.575706
210206_s_at	chr12:31118118-31148232 (+) // 99.74 // p11.21 /// chr1:	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	DDX11	2.45E-05	0.00353	5.766737684	6.542080884	-0.77534	-1.7116
213008_at	chr15:87637175-87661958 (+) // 97.74 // q26.1	hypothetical protein FLJ10719	FLJ10719	2.45E-05	0.00353	6.684922721	7.485426657	-0.8005	-1.74171
215442_s_at	chr14:80491756-80645047 (+) // 93.26 // q31.1	thyroid stimulating hormone receptor	TSHR	2.45E-05	0.00353	4.825577799	5.791009809	-0.96543	-1.95265
219054_at	chr5:32824937-32827580 (+) // 99.89 // p13.3	hypothetical protein FLJ14054	FLJ14054	2.45E-05	0.00353	7.534769941	6.353576208	1.181194	2.267643
222746_s_at	chr9:113191375-113213061 (+) // 84.51 // q32	B-box and SPRY domain containing	BSPRY	2.45E-05	0.00353	5.45355092	6.212055699	-0.7585	-1.69174
1555058_a_at	chr1:208311543-208391972 (-) // 95.23 // q32.3	lysophosphatidylglycerol acyltransferase 1	LPGAT1	2.54E-05	0.0035936	5.77390636	5.166300202	0.607606	1.523729
212719_at	chr18:58535289-58798646 (+) // 96.34 // q21.33	PH domain and leucine rich repeat protein phosphatase	PHLPP	2.54E-05	0.0035936	6.413380271	5.034059631	1.379321	2.601458
222774_s_at	chr16:45672943-45735320 (-) // 94.09 // q12.1	neuropilin (NRP) and tolloid (TLL)-like 2	NETO2	2.54E-05	0.0035936	4.431097155	5.204599052	-0.7735	-1.70941
224164_at	chr15:34692954-34693601 (+) // 55.08 // q14 /// chr16:5!	tropomyosin 3	TPM3	2.54E-05	0.0035936	8.937900403	7.875060723	1.06284	2.089039
232635_at	chr14:80033242-80279219 (-) // 95.78 // q31.1	chromosome 14 open reading frame 145	C14orf145	2.54E-05	0.0035936	4.470514525	5.346566015	-0.87605	-1.83535
238509_at	chr7:147865409-147866310 (+) // 59.78 // q36.1	Cullin 1	CUL1	2.54E-05	0.0035936	8.106845323	7.221234169	0.885611	1.847547
242058_at	chr4:160128160-160128558 (+) // 91.85 // q32.1	---	---	2.54E-05	0.0035936	6.48199206	5.923766101	0.558226	1.472457
208456_s_at	chr1:53170888-53171397 (-) // 82.19 // p32.3 /// chr11:1	related RAS viral (r-ras) oncogene homolog 2	RRAS2	2.64E-05	0.003678	4.615329468	6.641027571	-2.0257	-4.07189
227210_at	chr10:7240592-7242111 (-) // 98.89 // p14	Scm-like with four mbt domains 2	SFMBT2	2.64E-05	0.003678	7.113634153	6.138144197	0.97549	1.966309
228471_at	chr2:197678781-197679987 (-) // 93.88 // q33.1	Ankyrin repeat domain 44	LOC91526	2.64E-05	0.003678	5.296531262	4.72046297	0.576068	1.490781
241275_at	chr1:112908402-112908810 (+) // 100.0 // p13.2	Capping protein (actin filament) muscle Z-line, alpha 1	CAPZA1	2.64E-05	0.003678	4.681024646	4.281654071	0.399371	1.318932
243182_at	chr7:91675333-91676031 (+) // 96.53 // q21.2	ankyrin repeat and IBR domain containing 1	ANKIB1	2.64E-05	0.003678	8.21210232	7.027657029	1.184445	2.27276
208779_x_at	chr6:30960319-30975908 (+) // 96.82 // p21.33	discoidin domain receptor family, member 1	DDR1	2.73E-05	0.0037839	6.266857158	6.652069966	-0.38521	-1.30605

213007_at	chr15:87637175-87661958 (+) // 97.74 // q26.1	hypothetical protein FLJ10719	FLJ10719	2.73E-05	0.0037839	5.771155536	6.912251653	-1.1411	-2.20549
221280_s_at	chr10:34440102-35143929 (-) // 97.24 // p11.22	par-3 partitioning defective 3 homolog (C. elegans)	PARD3	2.73E-05	0.0037839	5.16029217	5.517322955	-0.35703	-1.28079
202818_s_at	chr18:21850575-21924540 (-) // 94.96 // q11.2	synovial sarcoma translocation, chromosome 18	SS18	2.83E-05	0.0038637	8.188885189	7.807643675	0.381242	1.302462
205209_at	chr12:50631768-50675740 (+) // 98.7 // q13.13	activin A receptor, type IB	ACVR1B	2.83E-05	0.0038637	7.018653715	6.52144492	0.497209	1.41148
216915_s_at	chr7:76845120-76857618 (+) // 81.13 // q11.23	protein tyrosine phosphatase, non-receptor type 12	PTPN12	2.83E-05	0.0038637	4.989462626	4.22986653	0.759596	1.693017
218342_s_at	chr9:5775192-5795693 (-) // 99.11 // p24.1	KIAA1815	KIAA1815	2.83E-05	0.0038637	7.072188698	6.689497307	0.382691	1.303772
236598_at	chr2:161929263-161929735 (+) // 96.33 // q24.2	CDNA FLJ14635 fis, clone NT2RP2001196	---	2.83E-05	0.0038637	6.41796027	7.3637494	-0.94579	-1.92624
244181_at	chr5:67601026-67601469 (+) // 100.0 // q13.1	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	2.83E-05	0.0038637	6.233661904	4.725715908	1.507946	2.844048
1552611_a_at	chr1:65011955-65144234 (-) // 98.59 // p31.3	Janus kinase 1 (a protein tyrosine kinase)	JAK1	2.94E-05	0.0038884	6.964212443	6.308470587	0.655742	1.575426
1553984_s_at	chr2_random:325544-327470 (-) // 89.52 // /// chr2:2423	deoxythymidylate kinase (thymidylate kinase)	DTYMK	2.94E-05	0.0038884	7.605967889	8.731767928	-1.1258	-2.18223
1559170_at	chr18:14173939-14179153 (+) // 79.59 // p11.21 /// chr2:	Similar to ankyrin repeat domain 20A /// Hypothetical gene supported by NM_032250	---	2.94E-05	0.0038884	5.153948063	5.328020607	-0.17407	-1.12824
1563471_at	chr18:41730522-41736675 (-) // 78.61 // q12.3	KIAA1632	KIAA1632	2.94E-05	0.0038884	6.750938762	6.32561475	0.425324	1.342874
201861_s_at	chr2:238382791-238456078 (+) // 85.89 // q37.3 /// chr3:	leucine rich repeat (in FLII) interacting protein 1	LRRFIP1	2.94E-05	0.0038884	9.351804586	8.572887397	0.778917	1.715843
202183_s_at	chr16:29709558-29724207 (+) // 95.76 // p11.2 /// chr16_	kinesin family member 22	KIF22	2.94E-05	0.0038884	6.863025891	7.728642749	-0.86562	-1.82212
203252_at	chr11:67030544-67032232 (-) // 99.89 // q13.2	CDK2-associated protein 2	CDK2AP2	2.94E-05	0.0038884	7.225562097	8.364048709	-1.13849	-2.2015
204269_at	chrX:48526708-48532531 (-) // 95.4 // p11.23	pim-2 oncogene	PIM2	2.94E-05	0.0038884	8.514098597	7.921347918	0.592751	1.508119
221502_at	chr13:49171444-49264678 (-) // 97.57 // q14.2	karyopherin alpha 3 (importin alpha 4)	KPNA3	2.94E-05	0.0038884	9.158053603	8.45396344	0.70409	1.629117
223037_at	chrX:69289468-69292788 (-) // 97.22 // q13.1	PDZ domain containing 11	PDZK11	2.88E-05	0.0038884	7.000671235	7.861777153	-0.86111	-1.81643
226154_at	chr12:32788836-32789912 (+) // 78.98 // p11.21	Dynamin 1-like /// Tyrosyl-tRNA synthetase 2 (mitochondrial)	DNM1L /// CGI-I	2.94E-05	0.0038884	9.275218186	8.782939024	0.492279	1.406665
236451_at	chr2:161930295-161931067 (+) // 94.66 // q24.2	CDNA FLJ14635 fis, clone NT2RP2001196	---	2.94E-05	0.0038884	5.197730302	5.896884647	-0.69915	-1.62355
203939_at	chr6:86216527-86262215 (+) // 94.31 // q14.3	5'-nucleotidase, ecto (CD73)	NT5E	3.04E-05	0.0040107	5.0871124	4.661950376	0.425162	1.342723
205156_s_at	chr12:48737753-48763660 (+) // 97.07 // q13.12	amiloride-sensitive cation channel 2, neuronal	ACCN2	3.04E-05	0.0040107	6.951660673	7.625191505	-0.67353	-1.59497
201474_s_at	chr17:45488729-45522843 (+) // 98.79 // q21.33	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	ITGA3	3.10E-05	0.0040728	5.832100289	6.165309246	-0.33321	-1.25981
1555888_at	chr8:103325012-103334744 (+) // 77.24 // q22.3	E3 ubiquitin protein ligase, HECT domain containing, 1	EDD	3.16E-05	0.0040781	4.700102125	4.227608933	0.472493	1.387505
207031_at	chr4:13218722-13222307 (-) // 84.48 // p15.33	bagpipe homeobox homolog 1 (Drosophila)	BAPX1	3.16E-05	0.0040781	4.394032233	4.669198347	-0.27517	-1.21013
223821_s_at	chr1:219780030-219908584 (-) // 92.73 // q41 /// chr1_ra	sushi domain containing 4 /// YHGM196	SUSD4 /// LOC3	3.15E-05	0.0040781	4.348614485	4.6947377	-0.34612	-1.27114
235289_at	chr3:172089170-172090568 (-) // 95.6 // q26.2	eukaryotic translation initiation factor 5A2	EIF5A2	3.16E-05	0.0040781	4.340852097	4.908515327	-0.56766	-1.48212
238079_at	chr1:150947114-150947787 (-) // 51.6 // q21.3	Tropomyosin 3	TPM3	3.16E-05	0.0040781	6.962527504	6.124242435	0.838285	1.787924
241027_at	chr3:194863439-194863899 (+) // 98.92 // q29	optic atrophy 1 (autosomal dominant)	OPA1	3.16E-05	0.0040781	5.820274161	4.775662674	1.044611	2.062811
241069_at	chr11:113447227-113447893 (-) // 80.23 // q23.2	Zinc finger and BTB domain containing 16	ZBTB16	3.16E-05	0.0040781	5.789058258	5.505839128	0.283219	1.216907
200601_at	chr19:43829920-43912570 (+) // 97.52 // q13.2	actinin, alpha 4	ACTN4	3.27E-05	0.0041574	8.773897737	7.736617158	1.037281	2.052355
202095_s_at	chr17:73721943-73732372 (+) // 97.65 // q25.3	baculoviral IAP repeat-containing 5 (survivin)	BIRC5	3.27E-05	0.0041574	6.856869629	8.390141761	-1.53327	-2.89442
205891_at	chr17:15788955-15819783 (+) // 100.0 // p12	adenosine A2b receptor	ADORA2B	3.27E-05	0.0041574	5.229989125	5.615681407	-0.38569	-1.30649
212833_at	chr5:110102605-110126383 (+) // 94.81 // q22.1	hypothetical protein BC017169	LOC91137	3.27E-05	0.0041574	7.893332653	8.654598875	-0.76127	-1.69498
218996_at	chr19:59302141-59310848 (-) // 99.07 // q13.42	TCF3 (E2A) fusion partner (in childhood Leukemia)	TFPT	3.27E-05	0.0041574	6.648966044	7.217152674	-0.56819	-1.48266
221503_s_at	chr13:49173404-49264645 (-) // 99.48 // q14.2	karyopherin alpha 3 (importin alpha 4)	KPNA3	3.27E-05	0.0041574	8.280535119	7.700301665	0.580233	1.495091
236975_at	chr13:26637206-26637723 (-) // 83.9 // q12.2	Transcribed locus	---	3.27E-05	0.0041574	7.033966231	5.630320113	1.403646	2.645694
200621_at	chr1:198184316-198207907 (-) // 96.7 // q32.1	cysteine and glycine-rich protein 1	CSRP1	3.33E-05	0.0042222	7.837605635	8.439313315	-0.60171	-1.51751
205689_at	chr1:229426616-229500999 (-) // 93.53 // q42.2	pecanex-like 2 (Drosophila)	PCNXL2	3.39E-05	0.0042586	6.008056565	6.48552025	-0.47746	-1.39229
212538_at	chr13:98243743-98352697 (-) // 99.41 // q32.3	dedicator of cytokinesis 9	DOCK9	3.39E-05	0.0042586	4.027241513	4.892187322	-0.86495	-1.82127
217946_s_at	chr11:122393503-122395528 (+) // 91.1 // q24.1 /// chr1	SUMO-1 activating enzyme subunit 1	SAE1	3.39E-05	0.0042586	7.784155645	8.550279014	-0.76612	-1.70069
231146_at	chr10:124598601-124629111 (-) // 97.64 // q26.13	family with sequence similarity 24, member B	FAM24B	3.39E-05	0.0042586	6.629241779	7.722081336	-1.09284	-2.13293
1558385_at	chr2:239959436-239965208 (-) // 91.31 // q37.3	---	---	3.51E-05	0.0043527	3.966910311	4.506556417	-0.53965	-1.45362
204558_at	chr1:46426006-46456163 (+) // 96.7 // p34.1	RAD54-like (S. cerevisiae)	RAD54L	3.51E-05	0.0043527	6.837791988	7.2629557	-0.42516	-1.34272
204922_at	chr11:66272440-66367369 (+) // 90.96 // q13.2	hypothetical protein FLJ22531	FLJ22531	3.51E-05	0.0043527	6.074381208	6.582191596	-0.50781	-1.42189
205254_x_at	chr5:133479214-133511818 (+) // 89.28 // q31.1	transcription factor 7 (T-cell specific, HMG-box)	TCF7	3.51E-05	0.0043527	6.701599709	7.603760476	-0.90216	-1.86886
213198_at	chr12:50675755-50677128 (+) // 91.03 // q13.13	activin A receptor, type IB	ACVR1B	3.51E-05	0.0043527	8.033695195	7.512106488	0.521589	1.435535
226013_at	chr3:42227294-42229116 (+) // 90.42 // p22.1	OGT(O-Glc-NAc transferase)-interacting protein 106 KDa	OIP106	3.51E-05	0.0043527	6.934768382	6.316861424	0.617907	1.534647
210298_x_at	chrX:134977632-135017704 (+) // 99.82 // q26.3	four and a half LIM domains 1	FHL1	3.64E-05	0.0044395	5.886552089	6.829891671	-0.94334	-1.92297
211569_s_at	chr4:109268473-109313621 (+) // 99.88 // q25	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	HADHSC	3.64E-05	0.0044395	6.66057512	7.727216718	-1.06664	-2.09455
212247_at	chr7:134699933-134790756 (+) // 98.25 // q33	nucleoporin 205kDa	NUP205	3.64E-05	0.0044395	7.317039628	7.673514533	-0.35647	-1.28029
217257_at	---	(clone B3B3E13) Huntington's disease candidate region mRNA fragment	---	3.64E-05	0.0044395	4.121154894	3.853960901	0.267194	1.203465
227197_at	chr3:155457716-155458316 (+) // 79.58 // q25.2	Src homology 3 domain-containing guanine nucleotide exchange factor	SGEF	3.64E-05	0.0044395	4.093351271	4.42843837	-0.33509	-1.26145
235778_s_at	chr2:197789699-197811674 (-) // 96.48 // q33.1	ankyrin repeat domain 44	ANKRD44	3.64E-05	0.0044395	5.793973802	5.412578156	0.381396	1.302601
244025_at	chr10:106059443-106060197 (-) // 68.39 // q25.1	---	---	3.64E-05	0.0044395	7.586818581	6.628653153	0.958165	1.942838
239253_at	chr10:57783412-57784344 (-) // 95.68 // q21.1	Transcribed locus	---	3.70E-05	0.0045086	3.766410718	4.129872173	-0.36346	-1.28651
1561762_s_at	chr10:12101062-12101484 (-) // 21.99 // p14	UPF2 regulator of nonsense transcripts homolog (yeast)	UPF2	3.77E-05	0.0045488	5.593815042	5.252145327	0.34167	1.267222
208576_s_at	chr6:26139856-26140267 (-) // 98.78 // p22.2	histone 1, H3b	HIST1H3B	3.77E-05	0.0045488	5.60523538	6.294512187	-0.68928	-1.61248
213421_x_at	chr9:33740642-33789228 (+) // 96.97 // p13.3	protease, serine, 3 (mesotrypsin)	PRSS3	3.77E-05	0.0045488	7.0427701	6.328946094	0.713824	1.640146
237195_at	chr9:122984587-122985242 (-) // 92.16 // q33.3	Spermatid perinuclear RNA binding protein	STRBP	3.77E-05	0.0045488	4.51887032	4.06148149	0.457389	1.373054
201764_at	chr12:46644257-46648927 (+) // 93.41 // q13.11	hypothetical protein MGC5576	MGC5576	3.90E-05	0.0046308	7.701128681	8.376585252	-0.67546	-1.5971
202510_s_at	chr14:102662416-102673529 (+) // 75.19 // q32.32	tumor necrosis factor, alpha-induced protein 2	TNFAIP2	3.90E-05	0.0046308	6.145305686	7.607000864	-1.4617	-2.75432
202799_at	chr19:6312566-6319912 (+) // 99.9 // p13.3	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	CLPP	3.90E-05	0.0046308	8.522365943	8.894343618	-0.37198	-1.29413
204617_s_at	chr16:66248933-66252214 (-) // 99.95 // q22.1	adrenocortical dysplasia homolog (mouse)	ACD	3.90E-05	0.0046308	7.393587583	7.954601882	-0.56101	-1.47531
221760_at	chr6:119540072-119712625 (-) // 94.18 // q22.31	Mannosidase, alpha, class 1A, member 1	MAN1A1	3.90E-05	0.0046308	6.857373717	4.896393018	1.960981	3.893265
223464_at	chr11:3064921-3106977 (-) // 97.86 // p15.4	oxysterol binding protein-like 5	OSBPL5	3.90E-05	0.0046308	6.428200382	7.023185859	-0.59499	-1.51046
230866_at	chrX:77333115-77333843 (-) // 94.96 // q21.1	---	---	3.90E-05	0.0046308	4.730999127	3.871144108	0.859855	1.814856
241460_at	chrX:19957890-19958344 (-) // 100.0 // p22.12	Ribosomal protein S6 kinase, 90kDa, polypeptide 3	RPS6KA3	3.90E-05	0.0046308	7.262320467	6.957330269	0.30499	1.23541
1557797_a_at	chr2:145073969-145074479 (-) // 75.41 // q22.3	Zinc finger homeobox 1b	ZFHX1B	4.04E-05	0.0047355	5.271534743	4.985554138	0.285981	1.219239
1565706_at	chr3:42060668-42062831 (+) // 59.7 // p22.1	CDNA: FLJ21395 fis, clone COL03557	---	4.04E-05	0.0047355	5.509291903	4.615457891	0.893834	1.858108
203100_s_at	chr6:4651391-4900306 (+) // 98.44 // p25.1	chromodomain protein, Y-like	CDYL	4.04E-05	0.0047355	5.977292813	5.664028452	0.313264	1.242516
219203_at	chr14:23678008-23680634 (-) // 98.69 // q11.2	chromosome 14 open reading frame 122	C14orf122	4.04E-05	0.0047355	6.788759324	7.436115503	-0.64736	-1.5663
222854_s_at	chrX:13786055-13807668 (-) // 89.6 // p22.2	family with sequence similarity 51, member A1	FAM51A1	4.04E-05	0.0047355	5.582513815	6.093518755	-0.511	-1.42504
230452_at	chr2:113118425-113119871 (-) // 83.59 // q13	hypothetical gene supported by AK124342	FLJ42351	4.04E-05	0.0047355	5.529711688	5.933378989	-0.40367	-1.32287
1553015_a_at	chr8:145707621-145713976 (-) // 99.92 // q24.3	RecQ protein-like 4	RECQL4	4.19E-05	0.0048227	6.955368428	7.528330149	-0.57296	-1.48757
1562194_at	chr2:145027239-145027579 (-) // 96.59 // q22.3	Zinc finger homeobox 1b	ZFHX1B	4.19E-05	0.0048227	7.608840812	6.771849561	0.836991	1.786321
1566764_at	chr7:19948925-19952062 (+) // 74.6 // p21.1	MRNA full length insert cDNA clone EUROIMAGE 2344436	---	4.19E-05	0.0048227	3.73341453	3.513978559	0.219436	1.164278
203166_at	chr16:73885115-74024860 (-) // 99.92 // q23.1	craniofacial development protein 1	CFDP1	4.19E-05	0.0048227	7.695485128	8.594936281	-0.89945	-1.86536
223533_at	chr1:89890409-89892734 (+) // 97.57 // p22.2	leucine rich repeat containing 8 family, member C	LRRC8C	4.19E-05	0.0048227	7.929812727	6.946228429	0.983584	1.977372
227552_at	chr16:30296959-30299111 (-) // 82.18 // p11.2	septin 1	Sep-01	4.19E-05	0.0048227	6.28863415	7.835677752	-1.54704	-2.92218
230175_s_at	chr3:99997738-99998586 (+) // 93.52 // q12.1	---	---	4.19E-05	0.0048227	4.221032536	4.455480877	-0.23445	-1.17646
232265_at	chr7:104847873-104858664 (-) // 88.62 // q22.3	ataxin 7-like 1	ATXN7L1	4.19E-05	0.0048227	4.885823972	5.282319924	-0.3965	-1.31631
219306_at	chr3:44778288-44869747 (+) // 99.54 // p21.31	kinesin family member 15	KIF15	4.34E-05	0.0049536	4.534605235	6.227584827	-1.69298	-3.23324
229801_at	chr10:11952035-11952987 (+) // 83.17 // p14	chromosome 10 open reading frame 47	C10orf47	4.34E-05	0.0049536	7.650431301	6.761608437	0.888823	1.851665
229987_at	chr13:26544240-26545036 (-) // 94.28 // q12.13	Ubiquitin specific peptidase 12	USP12	4.34E-05	0.0049536	7.318073001	6.594836725	0.723236	1.650881
239571_at	chr15:98017165-98017616 (+) // 56.37 // q26.3	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	MEF2A	4.34E-05	0.0049536	7.659779136	6.755347515	0.904432	1.871807
219575_s_at	chr16:67920024-67921999 (-) // 98.14 // q22.1	peptide deformylase-like protein /// component of oligomeric golgi complex 8	PDF /// COG8	4.42E-05	0.0050306	6.896785945	7.434693439	-0.53791	-1.45187
207943_x_at	chr6:144303131-144311155 (-) // 80.67 // q24.2	pleiomorphic adenoma gene-like 1	PLAGL1	4.49E-05	0.0050776	5.682773618	4.46130988	1.221464	2.331832
227041_at	chr2:179791926-179793892 (-) // 83.13 // q31.2	CDNA FLJ31513 fis, clone NT2RI1000127	---	4.49E-05	0.0050776	5.053659903	5.924085218	-0.87043	-1.8282
235391_at	chr8:94787468-94809973 (+) // 99.16 // q22.1 /// chr15:3	family with sequence similarity 92, member A1	FAM92A1	4.49E-05	0.0050776	4.437401163	4.996366038	-0.55896	-1.47321
241444_at	chr15:21368411-21368880 (+) // 51.26 // q11.2	---	---	4.49E-05	0.0050776	4.780702191	5.347423571	-0.56672	-1.48115
204266_s_at	chr11:67577021-67645247 (-) // 94.93 // q13.2	choline kinase alpha	CHKA	4.66E-05	0.0051523	7.169572357	6.304653855	0.864919	1.821237
210094_s_at	chr10:34641197-35144217 (-) // 93.05 // p11.21	par-3 partitioning defective 3 homolog (C. elegans)	PARD3	4.66E-05	0.0051523	7.305311067	8.05188498	-0.74657	-1.6778
211700_s_at	chrX:54830269-54840883 (+) // 97.37 // p11.21	trophinin /// trophinin	TRO	4.66E-05	0.0051523	5.768330574	6.575289747	-0.80696	-1.74952
212451_at	chr15:47068132-47125950 (-) // 97.74 // q21.1	KIAA0256 gene product	KIAA0256	4.66E-05	0.0051523	7.729627661	6.87222093	0.857407	1.811779
213652_at	chr9:76037435-76040359 (+) // 95.13 // q21.13	Proprotein convertase subtilisin/kexin type 5	PCSK5	4.65E-05	0.0051523	3.962334738	4.280781531	-0.31845	-1.24699
214949_at	chr8:43103528-43105086 (+) // 3.44 // p11.21	---	---	4.66E-05	0.0051523	5.083677109	6.593649348	-1.50997	-2.84805
218973_at	chr15:80209631-80317754 (-) // 99.89 // q25.2	elongation factor Tu GTP binding domain containing 1	EFTUD1	4.66E-05	0.0051523	6.699258456	7.355925648	-0.65667	-1.57644
221599_at	chr11:77209855-77261045 (+) // 88.87 // q13.5	PTD015 protein	PTD015	4.66E-05	0.0051523	6.835940643	7.489673433	-0.65373	-1.57323
228776_at	chr17:40231342-40235949 (-) // 82.3 // q21.31	gap junction protein, alpha 7, 45kDa (connexin 45)	GJA7	4.66E-05	0.0051523	4.106009534	4.805939665	-0.69993	-1.62443
44120_at	chr7:139827159-139848092 (+) // 89.06 // q34	aarF domain containing kinase 2	ADCK2	4.66E-05	0.0051523	7.089134595	7.525357203	-0.43622	-1.35306
1562745_at	chr3:50682423-50684483 (+) // 88.25 // p21.31	CDNA FLJ36372 fis, clone THYMU2008072	---	4.82E-05	0.0052822	6.174691654	5.809310943	0.365381	1.288222
205673_s_at	chrX:15021767-15047840 (-) // 95.8 // p22.2	ankyrin repeat and SOCS box-containing 9	ASB9	4.82E-05	0.0052822	5.625383375	6.306745316	-0.68136	-1.60365
212651_at	chr10:62299205-62373932 (-) // 97.78 // q21.2	Rho-related BTB domain containing 1	RHOBTB1	4.82E-05	0.0052822	6.420463507	5.246810878	1.173653	2.255821
214948_s_at	chr8:43103528-43105086 (+) // 3.44 // p11.21	TATA element modulatory factor 1	TMF1	4.82E-05	0.0052822	6.804382382	7.733452664	-0.92907	-1.90405
220028_at	chr3:38470813-38499868 (+) // 99.68 // p22.2	activin A receptor, type IIB	ACVR2B	4.82E-05	0.0052822	6.287126186	7.02999719	-0.74287	-1.6735
1556423_at	chr14:76297456-76300103 (+) // 90.45 // q24.3	Vasohibin 1	KIAA1036	4.99E-05	0.0054481	4.500916969	4.190758063	0.310159	1.239844
232375_at	chr2:191662975-191665032 (-) // 82.4 // q32.2	Signal transducer and activator of transcription 1, 91kDa	STAT1	4.99E-05	0.0054481	6.480710786	5.738244179	0.742467	1.673034
225725_at	chr3:180217716-180219965 (-) // 97.2 // q26.32	CDNA FLJ31683 fis, clone NT2RI2005353	---	5.08E-05	0.0055327	7.597931001	7.00138198	0.596549	1.512095
1560284_at	chr16:66152477-66153709 (-) // 65.09 // q22.1	CDNA clone IMAGE:5271145	---	5.17E-05	0.0055856	5.695703364	5.996870486	-0.30117	-1.23214
211548_s_at	chr4:175786341-175818349 (-) // 95.81 // q34.1	hydroxyprostaglandin dehydrogenase 15-(NAD)	HPGD	5.17E-05	0.0055856	6.273740332	4.238869646	2.034871	4.09786
213395_at	chr22:48800280-48826315 (-) // 97.82 // q13.33	megalencephalic leukoencephalopathy with subcortical cysts 1	MLC1	5.17E-05	0.0055856	6.253868577	5.159640406	1.094228	2.134988
226763_at	chr2:179799486-179814791 (-) // 98.98 // q31.2	SEC14 and spectrin domains 1	SESTD1	5.17E-05	0.0055856	4.804036932	7.274282722	-2.47025	-5.54138
210187_at	chr20:1300425-1321673 (-) // 96.22 // p13	FK506 binding protein 1A, 12kDa	FKBP1A	5.35E-05	0.0056494	6.289356372	5.783790836	0.505566	1.41968
216300_x_at	chr17:35741029-35766738 (+) // 85.33 // q21.2	retinoic acid receptor, alpha	RARA	5.35E-05	0.0056494	7.320473013	6.974394028	0.346079	1.271101
218564_at	chr16:73213110-73243514 (-) // 89.69 // q22.3	ring finger and WD repeat domain 3	RFWD3	5.35E-05	0.0056494	5.201054906	6.289718748	-1.08866	-2.12677
219623_at	chr20:36810525-36834226 (+) // 99.95 // q11.23	ARP5 actin-related protein 5 homolog (yeast)	ACTR5	5.35E-05	0.0056494	8.436223164	7.817834352	0.618389	1.53516
223960_s_at	chr16:4501307-4528434 (-) // 99.57 // p13.3	chromosome 16 open reading frame 5	C16orf5	5.35E-05	0.0056494	7.251132239	6.262382367	0.98875	1.984465
226661_at	chr8:25416808-25421307 (+) // 93.31 // p21.2	cell division cycle associated 2	CDCA2	5.35E-05	0.0056494	6.131349227	7.371932974	-1.24058	-2.36294
235134_at	chr11:75832967-75833361 (-) // 52.81 // q13.5	CDNA clone IMAGE:3929520	---	5.35E-05	0.0056494	5.602110904	6.409472354	-0.80736	-1.75001
235567_at	chr15:58573140-58574118 (-) // 92.66 // q22.2	CDNA FLJ31407 fis, clone NT2NE2000137	---	5.35E-05	0.0056494	7.45627344	5.24606019	2.210213	4.627437
235694_at	chr20:60953284-60953932 (-) // 56.17 // q13.33	Transcription factor-like 5 (basic helix-loop-helix)	TCFL5	5.35E-05	0.0056494	5.649454079	6.473946788	-0.82449	-1.77091
237187_at	chr12:115760176-115760644 (-) // 96.88 // q24.22	Transcribed locus, strongly similar to XP_509406.1 PREDICTED: similar to hypothetical protein FLJ14	---	5.35E-05	0.0056494	5.097685994	5.579077044	-0.48139	-1.39609
238669_at	chr9:122236831-122237642 (+) // 23.12 // q33.2	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	PTGS1	5.35E-05	0.0056494	6.05047621	5.642936263	0.40754	1.326422
238919_at	chr13:66673147-66673680 (-) // 93.89 // q21.32	Protocadherin 9	PCDH9	5.26E-05	0.0056494	3.549976152	3.789579941	-0.2396	-1.18067
1554335_at	chr22:36003055-36018888 (+) // 51.5 // q13.1	pleckstrin homology, Sec7 and coiled-coil domains 4	PSCD4	5.54E-05	0.0057931	5.47045646	4.921633665	0.548823	1.462892
218784_s_at	chr6:39179817-39190843 (-) // 90.99 // p21.2	chromosome 6 open reading frame 64	C6orf64	5.54E-05	0.0057931	6.279120819	6.723361974	-0.44424	-1.3606
221436_s_at	chr12:6828467-6830377 (-) // 100.0 // p13.31	cell division cycle associated 3 /// cell division cycle associated 3	CDCA3	5.54E-05	0.0057931	6.252254314	6.785990666	-0.53374	-1.44767
224753_at	chr11:64601500-64608104 (-) // 95.4 // q13.1	cell division cycle associated 5	CDCA5	5.54E-05	0.0057931	7.337576589	8.431578665	-1.094	-2.13465
229715_at	chr11:17359257-17359783 (+) // 80.15 // p15.1	CDNA FLJ41663 fis, clone FEBRA2027297	---	5.54E-05	0.0057931	5.082292801	5.724470736	-0.64218	-1.56068
242874_at	chr14:91294018-91294490 (-) // 25.26 // q32.12	CDNA FLJ37931 fis, clone CTONG2004397	---	5.64E-05	0.0058828	5.305697708	5.050890405	0.254807	1.193176
204560_at	chr6:35651422-35764692 (-) // 100.0 // p21.31	FK506 binding protein 5	FKBP5	5.74E-05	0.0058849	5.081591527	5.644437615	-0.56285	-1.47718

205596_s_at	chr17:59971944-60088648 (-) // 97.63 // q24.1	SMAD specific E3 ubiquitin protein ligase 2	SMURF2	5.74E-05	0.0058849	9.178646434	7.790618867	1.388028	2.617206
205904_at	chr6:31479349-31491069 (+) // 85.49 // p21.33	MHC class I polypeptide-related sequence A	MICA	5.74E-05	0.0058849	5.160111462	5.620747517	-0.46064	-1.37615
212023_s_at	chr10:129784916-129814639 (-) // 97.55 // q26.2	antigen identified by monoclonal antibody Ki-67	MKI67	5.74E-05	0.0058849	5.553446263	6.719679442	-1.16623	-2.24425
218021_at	chr14:23492812-23545450 (+) // 98.36 // q11.2 /// chr14:	dehydrogenase/reductase (SDR family) member 4	DHRS4	5.74E-05	0.0058849	8.103433747	8.605897143	-0.50246	-1.41663
226200_at	chr6:30990039-31002295 (+) // 95.48 // p21.33	valyl-tRNA synthetase like	VARSL	5.74E-05	0.0058849	7.370027502	8.177047335	-0.80702	-1.74959
227286_at	chr16:29923891-29924612 (+) // 95.99 // p11.2	hypothetical protein FLJ90652	FLJ90652	5.74E-05	0.0058849	7.7715037	8.361188317	-0.58968	-1.50492
227476_at	chr1:208305194-208306240 (-) // 71.84 // q32.3	Lysophosphatidylglycerol acyltransferase 1	LPGAT1	5.74E-05	0.0058849	6.697573853	6.350103693	0.34747	1.272328
228174_at	chr9:124784443-124785260 (-) // 95.1 // q33.3	Golgi autoantigen, golgin subfamily a, 1	GOLGA1	5.74E-05	0.0058849	7.152441584	8.312218575	-1.15978	-2.23423
1555790_a_at	chr4:166357176-166391676 (-) // 83.29 // q32.3	zinc finger protein like /// hypothetical protein FLJ38482	ZFPL /// FLJ3848	5.94E-05	0.0059253	5.246741592	4.814772036	0.43197	1.349074
1560869_a_at	chr4:160151510-160151911 (-) // 63.86 // q32.1	Full length insert cDNA clone YQ50C11	---	5.94E-05	0.0059253	5.27880357	4.021153395	1.25765	2.39106
203022_at	chr19:12778438-12785340 (+) // 98.73 // p13.13	ribonuclease H2, large subunit	RNASEH2A	5.94E-05	0.0059253	6.480618881	7.856962434	-1.37634	-2.5961
206114_at	chr2:222116139-222262506 (-) // 100.0 // q36.1	EPH receptor A4	EPHA4	5.94E-05	0.0059253	5.922921022	5.408871608	0.514049	1.428053
210299_s_at	chrX:134977604-135018623 (+) // 97.7 // q26.3	four and a half LIM domains 1	FHL1	5.94E-05	0.0059253	5.634241558	6.726631469	-1.09239	-2.13227
221527_s_at	chr10:34438494-35144217 (-) // 95.9 // p11.22	par-3 partitioning defective 3 homolog (C. elegans)	PARD3	5.94E-05	0.0059253	5.298051358	5.846355409	-0.5483	-1.46237
223095_at	chr10:99463470-99467895 (+) // 91.24 // q24.2	MARVEL domain containing 1	MARVELD1	5.94E-05	0.0059253	6.712109704	7.420845833	-0.70874	-1.63437
223161_at	chr7:140809713-140818304 (-) // 96.12 // q34	LCHN protein	LCHN	5.84E-05	0.0059253	7.748475259	7.143622655	0.604853	1.520823
227527_at	chr12:47698787-47699893 (-) // 97.65 // q13.12	myeloid/lymphoid or mixed-lineage leukemia 2	MLL2	5.94E-05	0.0059253	8.904309389	8.404179592	0.50013	1.414341
227875_at	chrX:116813658-116863787 (-) // 95.15 // q24	kelch-like 13 (Drosophila)	KLHL13	5.94E-05	0.0059253	4.034530213	3.549796856	0.484733	1.399327
228298_at	chr12:45916098-45916710 (+) // 95.03 // q13.11	hypothetical protein MGC16044	MGC16044	5.94E-05	0.0059253	6.203097527	5.759996145	0.443101	1.359524
228314_at	chr1:89896165-89897113 (+) // 98.24 // p22.2	CDNA FLJ37485 fis, clone BRAWH2014379	---	5.94E-05	0.0059253	6.306509375	4.977465308	1.329044	2.512362
235213_at	chr1:223221134-223222449 (-) // 99.54 // q42.12	Inositol 1,4,5-trisphosphate 3-kinase B	ITPKB	5.94E-05	0.0059253	7.718552206	6.046815317	1.671737	3.185979
235582_at	chr1:23578922-23580106 (-) // 72.66 // p36.12	E2F transcription factor 2	E2F2	5.94E-05	0.0059253	5.527461322	5.84998617	-0.32252	-1.25052
33736_at	chr15:72062607-72071676 (-) // 89.95 // q24.1	stomatin (EPB72)-like 1	STOML1	5.94E-05	0.0059253	5.904067698	6.249930979	-0.34586	-1.27091
1559018_at	chr10:129756562-129760911 (+) // 92.14 // q26.2	protein tyrosine phosphatase, receptor type, E	PTPRE	6.15E-05	0.0060344	4.577354041	4.162404597	0.414949	1.333252
201364_s_at	chr15:62767724-62782428 (-) // 98.1 // q22.31	ornithine decarboxylase antizyme 2	OAZ2	6.15E-05	0.0060344	8.516179989	8.015058704	0.501121	1.415313
209219_at	chr6:32027984-32034725 (-) // 88.24 // p21.32	RD RNA binding protein	RDBP	6.15E-05	0.0060344	8.579023035	9.004631072	-0.42561	-1.34314
220297_at	chr14:92829956-92869120 (-) // 55.05 // q32.13	BTB (POZ) domain containing 7	BTBD7	6.15E-05	0.0060344	5.755582121	5.303374072	0.452208	1.368133
220520_s_at	chrX:106172855-106255689 (-) // 88.01 // q22.3	hypothetical protein FLJ20130	FLJ20130	6.15E-05	0.0060344	4.108462057	4.577078001	-0.46862	-1.38378
225836_s_at	chr12:2856649-2868952 (+) // 83.12 // p13.33	hypothetical protein MGC13204	MGC13204	6.15E-05	0.0060344	5.160886602	5.638199115	-0.47731	-1.39215
226149_at	chr20:36508752-36512977 (+) // 92.63 // q11.23	hypothetical gene LOC128439	LOC128439	6.15E-05	0.0060344	6.606317199	7.225336703	-0.61902	-1.53583
232009_at	chr19:14704204-14737384 (-) // 52.21 // p13.12	egf-like module containing, mucin-like, hormone receptor-like 2	EMR2	6.15E-05	0.0060344	5.588478979	5.222303099	0.366176	1.288932
243675_at	chr9:65349828-65351166 (+) // 98.07 // q12 /// chr9:4415	hypothetical LOC401522 /// LOC441423	LOC401522 /// L	6.15E-05	0.0060344	6.614357116	6.338667824	0.275689	1.210572
1569041_at	chr10:64546689-64877339 (-) // 24.63 // q21.3	Hypothetical protein MGC14425	JMJD1C	6.36E-05	0.0061795	6.177107703	7.164107986	-0.987	-1.98206
203110_at	chr8:27238994-27372822 (+) // 95.01 // p21.2	PTK2B protein tyrosine kinase 2 beta	PTK2B	6.36E-05	0.0061795	7.925239544	7.434174639	0.491065	1.405482
219789_at	chr5:32747296-32820747 (+) // 59.84 // p13.3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	NPR3	6.36E-05	0.0061795	6.058869467	4.690663602	1.368206	2.581493
220092_s_at	chr2:69152139-69242215 (+) // 91.36 // p13.3	anthrax toxin receptor 1	ANTXR1	6.36E-05	0.0061795	4.119707648	4.273130948	-0.15342	-1.11221
232512_at	chr2:165769544-165776483 (+) // 98.66 // q24.3	---	---	6.36E-05	0.0061795	4.508099789	5.202781815	-0.69468	-1.61853
232549_at	chr21:14510257-14522024 (+) // 96.45 // q11.2	RNA binding motif protein 11	RBM11	6.36E-05	0.0061795	3.632459234	3.81324534	-0.18079	-1.1335
1552386_at	chr5:57823082-57827943 (+) // 66.01 // q11.2	hypothetical protein FLJ33641	FLJ33641	6.59E-05	0.0062733	4.035372554	3.669674939	0.365698	1.288505
1552726_at	chr15:98329160-98699650 (-) // 91.71 // q26.3	CDNA FLJ27399 fis, clone WMC02922	---	6.59E-05	0.0062733	5.136579014	5.7116964	-0.57512	-1.4898
203778_at	chr4:103909850-104039338 (-) // 98.61 // q24	mannosidase, beta A, lysosomal	MANBA	6.59E-05	0.0062733	7.034075422	6.593210944	0.440864	1.357417
205659_at	chr7:18308608-18481705 (+) // 100.0 // p21.1	histone deacetylase 9	HDAC9	6.59E-05	0.0062733	6.612392263	6.227606456	0.384786	1.305666
205947_s_at	chr7:158322621-158437101 (-) // 99.45 // q36.3	vasoactive intestinal peptide receptor 2	VIPR2	6.59E-05	0.0062733	5.073919235	5.620674509	-0.54676	-1.4608
209060_x_at	chr20:45564027-45719023 (+) // 93.49 // q13.12	nuclear receptor coactivator 3	NCOA3	6.59E-05	0.0062733	6.810380102	6.070795322	0.739585	1.669695
211154_at	chr3:185572474-185576772 (-) // 95.27 // q27.1	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and dev	THPO	6.59E-05	0.0062733	4.034446656	3.889388086	0.145059	1.105776
218881_s_at	chr2:28547441-28549165 (+) // 94.67 // p23.2	FOS-like antigen 2	FOSL2	6.59E-05	0.0062733	7.215460887	6.586220502	0.62924	1.54675
227481_at	chr6:154818435-154819425 (-) // 97.31 // q25.2	CNKSR family member 3	CNKSR3	6.59E-05	0.0062733	3.840451705	3.542587675	0.297864	1.229323
227578_at	chr12:97410455-97412390 (-) // 98.76 // q23.1	Thymopoietin	TMPO	6.59E-05	0.0062733	4.668318046	4.956765934	-0.28845	-1.22133
228806_at	chr1:148591621-148592055 (-) // 90.42 // q21.3	RAR-related orphan receptor C	RORC	6.59E-05	0.0062733	5.886700139	6.544121663	-0.65742	-1.57726
205027_s_at	chr10:30763198-30790767 (+) // 96.92 // p11.23	mitogen-activated protein kinase kinase kinase 8	MAP3K8	6.82E-05	0.0063923	6.815576035	5.178990723	1.636585	3.10929
210055_at	chr14:80491527-80682394 (+) // 98.09 // q31.1	thyroid stimulating hormone receptor	TSHR	6.82E-05	0.0063923	4.913185516	5.747498131	-0.83431	-1.78301
214152_at	chr15:53434331-53435477 (-) // 99.16 // q21.3	cell cycle progression 1	CCPG1	6.82E-05	0.0063923	3.746400584	3.527983938	0.218417	1.163456
215699_x_at	chr22:30323143-30339089 (+) // 95.3 // q12.2	Sfi1 homolog, spindle assembly associated (yeast)	SFI1	6.82E-05	0.0063923	7.061681708	7.382475421	-0.32079	-1.24902
219019_at	chr11:789179-794675 (-) // 98.84 // p15.5	leucine-rich repeats and death domain containing	LRDD	6.82E-05	0.0063923	7.709315169	8.0758777	-0.36656	-1.28928
223401_at	chr17:10548950-10555266 (+) // 94.02 // p13.1	putative protein product of Nbla03831	NBLA03831	6.82E-05	0.0063923	7.294132067	7.757173369	-0.46304	-1.37844
224829_at	chr5:173249274-173320000 (+) // 95.53 // q35.2	cytoplasmic polyadenylation element binding protein 4	CPEB4	6.82E-05	0.0063923	6.329753652	5.201939037	1.127815	2.185275
226925_at	chr3:142488930-142496182 (+) // 87.53 // q23	acid phosphatase-like 2	ACPL2	6.82E-05	0.0063923	6.277754551	7.424142136	-1.14639	-2.21359
38158_at	chr12:51948383-51973692 (+) // 94.06 // q13.13	extra spindle poles like 1 (S. cerevisiae)	ESPL1	6.82E-05	0.0063923	6.883881166	7.620677234	-0.7368	-1.66647
1557684_at	chr17:15545226-15563177 (+) // 72.83 // p12 /// chr17:1	zinc finger protein 286	ZNF286	7.05E-05	0.0065146	5.992841432	6.433073583	-0.44023	-1.35682
200708_at	chr16:57298537-57325641 (-) // 99.4 // q21	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	GOT2	7.05E-05	0.0065146	8.502049438	9.074415153	-0.57237	-1.48696
203894_at	chr17:38064836-38072549 (+) // 96.28 // p21.2	tubulin, gamma 2	TUBG2	7.05E-05	0.0065146	5.500009172	5.749746721	-0.24974	-1.18899
204681_s_at	chr7:21931161-22006574 (-) // 94.37 // p15.3	Rap guanine nucleotide exchange factor (GEF) 5	RAPGEF5	7.05E-05	0.0065146	5.687478963	6.588390555	-0.90091	-1.86725
210783_x_at	chr19:55918455-55920787 (+) // 91.22 // q13.33	C-type lectin domain family 11, member A	CLEC11A	7.05E-05	0.0065146	5.952809476	7.568188798	-1.61538	-3.06392
212192_at	chr13:76352305-76356297 (-) // 96.21 // q22.3	potassium channel tetramerisation domain containing 12	KCTD12	7.05E-05	0.0065146	3.602451255	4.546492167	-0.94404	-1.92391
224728_at	chr1:46810432-46813745 (-) // 72.65 // p33	ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	7.05E-05	0.0065146	5.419380637	5.857251954	-0.43787	-1.3546
224828_at	chr5:173249274-173320000 (+) // 95.53 // q35.2	cytoplasmic polyadenylation element binding protein 4	CPEB4	7.05E-05	0.0065146	5.251522044	4.351450571	0.900071	1.866158
228569_at	chr14:96069782-96070980 (+) // 84.25 // q32.2	poly(A) polymerase alpha	PAPOLA	7.05E-05	0.0065146	7.154632674	6.576688313	0.577944	1.492721
233899_x_at	chr8:81594218-81596849 (+) // 96.79 // q21.13	Zinc finger and BTB domain containing 10	ZBTB10	7.18E-05	0.0066157	6.007521854	7.319004573	-1.31148	-2.48196
244846_at	chr2:101931786-101932222 (+) // 100.0 // q11.2	Mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	7.30E-05	0.0067187	5.072010051	4.391660593	0.680349	1.602528
202900_s_at	chr17:5230145-5263710 (-) // 98.4 // p13.2	nucleoporin 88kDa	NUP88	7.42E-05	0.0068114	8.42327744	7.939700697	0.483577	1.398206
224593_at	chr12:122983358-123024853 (+) // 84.12 // q24.31	zinc finger protein 664	ZNF664	7.42E-05	0.0068114	8.324914524	9.186592116	-0.86168	-1.81715
1569594_a_at	chr14:49365216-49389256 (-) // 96.52 // q21.3	serologically defined colon cancer antigen 1	SDCCAG1	7.55E-05	0.0068258	7.885415205	7.504653472	0.380762	1.302029
202870_s_at	chr12:111807531-111820427 (+) // 88.74 // q24.13	2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	7.55E-05	0.0068258	5.83213321	7.320729565	-1.4886	-2.80616
207002_s_at	chr6:144303126-144327698 (-) // 96.29 // q24.2	pleiomorphic adenoma gene-like 1	PLAGL1	7.55E-05	0.0068258	5.763299718	3.862818462	1.900481	3.733377
215285_s_at	chr1:113960428-113967992 (-) // 97.43 // p13.2	putative homeodomain transcription factor 1	PHTF1	7.55E-05	0.0068258	6.460510349	5.488840888	0.971669	1.961109
224374_s_at	chr18:2837027-2904090 (+) // 98.63 // p11.32	elastin microfibril interfacer 2 /// elastin microfibril interfacer 2	EMILIN2	7.55E-05	0.0068258	6.018901831	7.016767734	-0.99787	-1.99704
225068_at	chr22:19129673-19132081 (+) // 91.46 // q11.21 /// chr1:	kelch-like 12 (Drosophila)	KLHL12	7.55E-05	0.0068258	6.96049239	7.693457067	-0.73296	-1.66205
228910_at	chr11:44597972-44598489 (+) // 91.18 // p11.2	CD82 antigen	KAI1	7.55E-05	0.0068258	8.572189279	7.721843874	0.850345	1.802933
230348_at	chr13:20452171-20452626 (-) // 78.41 // q12.11	LATS, large tumor suppressor, homolog 2 (Drosophila)	LATS2	7.55E-05	0.0068258	7.507588145	5.537080662	1.970507	3.91906
36545_s_at	chr22:30216814-30339087 (+) // 87.01 // q12.2	Sfi1 homolog, spindle assembly associated (yeast)	SFI1	7.55E-05	0.0068258	6.781615538	7.32307972	-0.54146	-1.45545
202131_s_at	---	RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	RIOK3	7.81E-05	0.0069703	7.356406342	6.727013197	0.629393	1.546914
203749_s_at	chr17:35718971-35767421 (+) // 95.06 // q21.2	retinoic acid receptor, alpha	RARA	7.81E-05	0.0069703	7.22199384	6.32220711	0.899787	1.86579
204126_s_at	chr22:17842021-17882677 (+) // 98.98 // q11.21	CDC45 cell division cycle 45-like (S. cerevisiae)	CDC45L	7.81E-05	0.0069703	6.604063774	7.42074736	-0.81668	-1.76135
204315_s_at	chr22:45013794-45048148 (+) // 82.69 // q13.31	G-2 and S-phase expressed 1	GTSE1	7.81E-05	0.0069703	5.113656339	5.584046662	-0.47039	-1.38548
204857_at	chr7:1628674-2043519 (-) // 93.25 // p22.3	MAD1 mitotic arrest deficient-like 1 (yeast)	MAD1L1	7.81E-05	0.0069703	6.319429954	6.992986509	-0.67356	-1.595
205393_s_at	chr11:125001852-125030781 (+) // 99.23 // q24.2	CHK1 checkpoint homolog (S. pombe)	CHEK1	7.81E-05	0.0069703	5.364034293	6.342955422	-0.97892	-1.97099
208101_s_at	chr9:128213193-128232566 (+) // 98.22 // q34.11	chromosome 9 open reading frame 74 /// chromosome 9 open reading frame 74	C9orf74	7.81E-05	0.0069703	8.718623022	9.046209733	-0.32759	-1.25491
228088_at	chr2:179794593-179795898 (-) // 83.92 // q31.2	CDNA FLJ31513 fis, clone NT2RI1000127	---	7.81E-05	0.0069703	4.29815199	5.00528053	-0.70713	-1.63255
201173_x_at	chr2:179144949-179145877 (+) // 66.84 // q31.2 /// chr1:	nuclear distribution gene C homolog (A. nidulans)	NUDC	8.08E-05	0.0070732	8.955738859	9.410494347	-0.45476	-1.37055
204449_at	chr9:122653605-122670464 (-) // 68.11 // q33.2	phosducin-like	PDCL	8.09E-05	0.0070732	6.75158413	6.381845436	0.369739	1.292119
206949_s_at	chr1:152107376-152113976 (+) // 98.74 // q22	RUN and SH3 domain containing 1	RUSC1	8.09E-05	0.0070732	7.316962672	8.011148821	-0.69419	-1.61797
208146_s_at	chr7:28808489-28959343 (-) // 99.63 // p15.1	carboxypeptidase, vitellogenic-like /// carboxypeptidase, vitellogenic-like	CPVL	8.09E-05	0.0070732	6.182284468	7.384937774	-1.20265	-2.30163
212055_at	chr18:32629587-32662985 (-) // 90.47 // q12.2	chromosome 18 open reading frame 10	C18orf10	8.09E-05	0.0070732	8.055190583	8.728446494	-0.67326	-1.59467
218407_x_at	chr1:208994623-209007873 (+) // 93.09 // q32.3	neuron derived neurotrophic factor	NENF	7.95E-05	0.0070732	8.604680451	9.024419483	-0.41974	-1.33769
220865_s_at	chr10:27026593-27075730 (+) // 93.5 // p12.1 /// chr9:50	trans-prenyltransferase	TPRT	8.09E-05	0.0070732	6.07372809	7.514990309	-1.44126	-2.71558
225297_at	chr18:41938314-41962296 (+) // 96.93 // q21.1	coiled-coil domain containing 5 (spindle associated)	CCDC5	8.09E-05	0.0070732	6.903418826	8.029178336	-1.12576	-2.18216
226450_at	chr19:7063265-7064963 (-) // 98.84 // p13.2	Insulin receptor	INSR	8.09E-05	0.0070732	5.975093013	5.611763715	0.363329	1.286391
233813_at	chr20:36901369-36903410 (+) // 37.81 // q11.23	protein phosphatase 1, regulatory (inhibitor) subunit 16B	PPP1R16B	8.09E-05	0.0070732	7.374206541	6.453502764	0.920704	1.893039
236610_at	chr5:58347934-58348455 (-) // 52.76 // q11.2	Phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	PDE4D	8.09E-05	0.0070732	7.135949122	5.931112765	1.204836	2.305111
237146_at	chr11:46894842-46895243 (-) // 96.63 // p11.2	Low density lipoprotein receptor-related protein 4	LRP4	8.09E-05	0.0070732	5.437862792	5.896648074	-0.45879	-1.37438
219312_s_at	chr8:81575064-81596562 (+) // 97.13 // q21.13	zinc finger and BTB domain containing 10	ZBTB10	8.36E-05	0.007271	5.929117296	7.28580128	-1.35668	-2.56096
221643_s_at	chr1:8348418-8417992 (-) // 95.13 // p36.23	arginine-glutamic acid dipeptide (RE) repeats	RERE	8.36E-05	0.007271	5.005467403	4.594764795	0.410703	1.329333
224888_at	chr2:26480642-26530404 (+) // 93.79 // p23.3	selenoprotein I	SELI	8.36E-05	0.007271	6.781896273	7.2921541	-0.51026	-1.4243
240870_at	chr2:239825693-239826260 (-) // 86.41 // q37.3	Histone deacetylase 4	HDAC4	8.36E-05	0.007271	6.877192192	7.425176059	-0.54798	-1.46204
1552923_a_at	chr12:121993860-122044081 (-) // 97.99 // q24.31	phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	8.65E-05	0.007358	5.635641249	6.068660614	-0.43302	-1.35006
204252_at	chr12:54646868-54652805 (+) // 98.92 // q13.2	cyclin-dependent kinase 2	CDK2	8.65E-05	0.007358	7.337280159	8.048874064	-0.71159	-1.63761
205251_at	chr2:238934685-238979092 (-) // 93.39 // q37.3	period homolog 2 (Drosophila)	PER2	8.65E-05	0.007358	8.091846087	6.878020214	1.213826	2.319519
206364_at	chr1:197252963-197321519 (-) // 94.76 // q32.1	kinesin family member 14	KIF14	8.65E-05	0.007358	5.463802686	6.594377245	-1.13057	-2.18946
214052_x_at	chr1:168228608-168233600 (-) // 73.71 // q24.3	BAT2 domain containing 1	XTP2	8.51E-05	0.007358	6.405495371	5.752463621	0.653032	1.572469
214482_at	chr14:64023303-64027004 (-) // 100.0 // q23.3	zinc finger and BTB domain containing 25	ZBTB25	8.51E-05	0.007358	6.559117255	7.002050781	-0.44293	-1.35937
215772_x_at	chr12:93444489-93446793 (+) // 91.81 // q22 /// chr3:675	succinate-CoA ligase, GDP-forming, beta subunit	SUCLG2	8.51E-05	0.007358	5.174696932	6.928698457	-1.754	-3.37293
219158_s_at	chr4:140580259-140640763 (+) // 99.85 // q31.1	NMDA receptor regulated 1	NARG1	8.65E-05	0.007358	8.18910727	7.500608606	0.688499	1.611606
220840_s_at	chr1:166495877-166553884 (+) // 99.45 // q24.2	chromosome 1 open reading frame 112	C1orf112	8.65E-05	0.007358	4.445875584	4.887027239	-0.44115	-1.35769
222820_at	chr17:73613126-73615131 (+) // 80.32 // q25.3	trinucleotide repeat containing 6C	TNRC6C	8.65E-05	0.007358	6.133227856	7.341243639	-1.20802	-2.3102
224818_at	chr1:109564234-109567278 (-) // 96.75 // p13.3	sortilin 1	SORT1	8.65E-05	0.007358	7.319008731	7.942879695	-0.62387	-1.541
236399_at	chr1:231402147-231405581 (-) // 94.33 // q42.3	hypothetical gene supported by BC016972	LOC284527	8.65E-05	0.007358	4.126041841	3.882016114	0.244026	1.184293
242315_at	chr16:17403213-17412581 (-) // 29.59 // p12.3	Transcribed locus	---	8.65E-05	0.007358	5.272857974	4.85401524	0.418843	1.336855
31826_at	chr9:113007347-113063122 (-) // 85.72 // q32	KIAA0674	KIAA0674	8.65E-05	0.007358	7.28539852	7.536749718	-0.25135	-1.19032
214055_x_at	chr1:168228608-168233600 (+) // 73.71 // q24.3	BAT2 domain containing 1	BAT2D1	8.80E-05	0.0074715	9.471185829	8.930326653	0.540859	1.454839
203035_s_at	chr1:143067103-143075590 (+) // 99.22 // q21.1	protein inhibitor of activated STAT, 3	PIAS3	8.95E-05	0.0074947	5.731895838	6.16831944	-0.43642	-1.35325
206683_at	chr6:28156734-28165317 (+) // 96.33 // p22.1	zinc finger protein 165	ZNF165	8.95E-05	0.0074947	4.707346103	3.927484665	0.779861	1.716966
214835_s_at	chr12:93444499-93446793 (+) // 94.32 // q22 /// chr3:675	succinate-CoA ligase, GDP-forming, beta subunit	SUCLG2	8.95E-05	0.0074947	3.958475852	5.817767586	-1.85929	-3.62829
219751_at	chr16:57106927-57111051 (+) // 98.7 // q21	hypothetical protein FLJ21148	FLJ21148	8.95E-05	0.0074947	5.172475721	4.497419612	0.675056	1.596659
221692_s_at	chr19:17277638-17278578 (+) // 69.34 // p13.11	mitochondrial ribosomal protein L34 /// mitochondrial ribosomal protein L34	MRPL34	8.95E-05	0.0074947	7.228214536	7.905279357	-0.67706	-1.59888
226743_at	chr17:30701443-30704119 (-) // 68.21 // q12	likely ortholog of mouse schlafen 8/9	FLJ34922	8.95E-05	0.0074947	4.629655456	5.968252154	-1.3386	-2.52905
230055_at	chr6:74007761-74029616 (-) // 95.2 // q13	chromosome 6 open reading frame 148	C6orf148	8.95E-05	0.0074947	5.791851962	6.305591616	-0.51374	-1.42775
231013_at	chr17_random:2321559-2322138 (+) // 82.59 //	---	---	8.95E-05	0.0074947	5.746464799	6.237230187	-0.49077	-1.40519
239655_at	chr1:13844357-13844835 (+) // 92.53 // p36.21	PR domain containing 2, with ZNF domain	PRDM2	8.95E-05	0.0074947	6.89835278	5.418247348	1.480105	2.789691
202968_s_at	chr12:66329020-66345453 (+) // 96.73 // q15	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	9.10E-05	0.00761	8.446723197	7.76373738	0.682986	1.605459
1555978_s_at	chr18:3237609-3239923 (+) // 86.92 // p11.31	LOC440476	---	9.26E-05	0.0076123	6.357141577	5.624233333	0.732908	1.661986
1570373_at	chr7:148622810-148632472 (-) // 39.45 // q36.1	Hypothetical protein FLJ31413	FLJ31413	9.26E-05	0.0076123	6.12433593	5.327566596	0.796769	1.737207
202848_s_at	chr14:23633388-23643173 (+) // 98.98 // q11.2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	PCK2	9.26E-05	0.0076123	7.22888593	7.979779743	-0.75089	-1.68284

209432_s_at	chr9:35722543-35726834 (+) // 97.45 // p13.3	cAMP responsive element binding protein 3	CREB3	9.26E-05	0.0076123	7.021655548	7.356259193	-0.3346	-1.26103
212590_at	chr1:53169465-53171397 (-) // 91.48 // p32.3 /// chr11:1	related RAS viral (r-ras) oncogene homolog 2	RRAS2	9.26E-05	0.0076123	5.573085949	7.869021283	-2.29594	-4.91072
216056_at	chr11:35188177-35188650 (+) // 55.81 // p13	CD44 antigen (homing function and Indian blood group system)	CD44	9.26E-05	0.0076123	6.080742641	5.591473756	0.489269	1.403733
220040_x_at	chrX:63919282-63979357 (-) // 98.4 // q11.2	KIAA1166	KIAA1166	9.26E-05	0.0076123	6.795359552	7.332542358	-0.53718	-1.45114
220952_s_at	chr12:19366718-19420598 (+) // 97.25 // p12.3	pleckstrin homology domain containing, family A member 5	PLEKHA5	9.26E-05	0.0076123	5.369272664	7.130121837	-1.76085	-3.38898
225619_at	chr13:77170470-77236367 (+) // 96.33 // q22.3	hypothetical protein FLJ30046	FLJ30046	9.26E-05	0.0076123	3.692550316	5.583893245	-1.89134	-3.7098
240146_at	chr7:116143114-116143590 (+) // 89.08 // q31.2	Capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	9.26E-05	0.0076123	6.660383275	5.914978439	0.745405	1.676445
244230_at	chr5:88099007-88099471 (-) // 97.89 // q14.3	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	9.26E-05	0.0076123	3.925974092	3.560761942	0.365212	1.288071
209355_s_at	chr1:56674161-56756716 (-) // 100.0 // p32.2	phosphatidic acid phosphatase type 2B	PPAP2B	9.58E-05	0.0078379	4.44899999	5.153380628	-0.70438	-1.62944
239258_at	chr2:46716369-46717291 (+) // 29.44 // p21	Ras homolog gene family, member Q	RHOQ	9.58E-05	0.0078379	4.890008344	4.526625443	0.363383	1.286439
37996_s_at	chr19:50964814-50978228 (-) // 87.45 // q13.32	dystrophia myotonica-protein kinase	DMPK	9.58E-05	0.0078379	4.950400088	5.39000094	-0.4396	-1.35623
1553105_s_at	chr18:27352198-27381177 (+) // 97.93 // q12.1	desmoglein 2	DSG2	9.90E-05	0.0079514	4.114564107	4.359703932	-0.24514	-1.18521
202726_at	chr19:53310514-53365372 (-) // 99.03 // q13.32	ligase I, DNA, ATP-dependent	LIG1	9.90E-05	0.0079514	7.475497393	8.171025957	-0.69553	-1.61948
204825_at	chr9:36562872-36667678 (+) // 99.96 // p13.2	maternal embryonic leucine zipper kinase	MELK	9.90E-05	0.0079514	6.784946009	7.940116613	-1.15517	-2.22711
207831_x_at	chr19:12647533-12653677 (-) // 97.3 // p13.13	deoxyhypusine synthase	DHPS	9.90E-05	0.0079514	8.275920656	8.678503112	-0.40258	-1.32187
210821_x_at	chr2:26920661-26928413 (+) // 78.91 // p23.3	centromere protein A, 17kDa	CENPA	9.90E-05	0.0079514	5.860607045	6.310888486	-0.45028	-1.36631
210830_s_at	chr7:94679301-94708939 (-) // 99.73 // q21.3	paraoxonase 2	PON2	9.90E-05	0.0079514	4.300114926	5.022880124	-0.72277	-1.65034
211085_s_at	chr20:43043940-43057211 (+) // 95.38 // q13.12	serine/threonine kinase 4 /// serine/threonine kinase 4	STK4	9.90E-05	0.0079514	5.908799794	4.971523861	0.937276	1.914909
226137_at	chr16:71374284-71377719 (-) // 92.73 // q22.2	AT-binding transcription factor 1	ATBF1	9.90E-05	0.0079514	5.404550522	4.740330962	0.66422	1.584711
227268_at	chr17:55384385-55396877 (-) // 98.62 // q23.2	PTD016 protein	LOC51136	9.90E-05	0.0079514	5.094036999	4.281877913	0.812159	1.755837
228273_at	chr17:54636997-54640015 (+) // 48.4 // q23.2	Hypothetical protein FLJ11029	FLJ11029	9.90E-05	0.0079514	5.952364419	7.827158935	-1.87479	-3.66749
235374_at	chr2:63737004-63737699 (+) // 67.08 // p15	Malate dehydrogenase 1, NAD (soluble)	MDH1	9.90E-05	0.0079514	5.550670748	6.353204367	-0.80253	-1.74416
236126_at	chr3:38508959-38509637 (+) // 86.89 // p22.2	Transcribed locus	---	9.90E-05	0.0079514	5.878396668	6.456341071	-0.57794	-1.49272
243364_at	chr4:109454468-109455186 (+) // 94.35 // q25	lymphoid enhancer-binding factor 1	LEF1	9.90E-05	0.0079514	5.350511968	4.516287729	0.834224	1.782898
232010_at	chr4:162662653-163442723 (-) // 99.41 // q32.2	follistatin-like 5	FSTL5	0.0001007	0.0080736	3.928232703	3.791180023	0.137053	1.099656
219688_at	chr4:123106487-123149210 (-) // 99.53 // q27	Bardet-Biedl syndrome 7	BBS7	0.0001024	0.0081394	3.888209781	4.097810321	-0.2096	-1.15637
225784_s_at	chrX:63918702-64037618 (-) // 84.77 // q11.2	KIAA1166	KIAA1166	0.0001024	0.0081394	6.623415614	7.260958255	-0.63754	-1.55568
226363_at	chr3:185184242-185185974 (-) // 95.78 // q27.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	ABCC5	0.0001024	0.0081394	5.486648985	6.707616861	-1.22097	-2.33103
231263_at	chr6:35814151-35824666 (+) // 98.67 // p21.31	chromosome 6 open reading frame 81	C6orf81	0.0001024	0.0081394	4.95715195	5.213171273	-0.25602	-1.19418
239775_at	chr7:17099140-17112221 (-) // 98.17 // p21.1	Aryl hydrocarbon receptor	AHR	0.0001024	0.0081394	5.999242055	5.094238805	0.905003	1.872549
243252_at	chr5:139532401-139532881 (+) // 100.0 // q31.2	Transcribed locus	---	0.0001024	0.0081394	5.132426586	4.775607222	0.356819	1.2806
202970_at	chr12:66329020-66345453 (+) // 96.73 // q15	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	0.0001059	0.0082963	6.223414234	5.931706248	0.291708	1.224089
205794_s_at	chr14:25984929-26136533 (-) // 95.59 // q12	neuro-oncological ventral antigen 1	NOVA1	0.0001059	0.0082963	4.461408362	4.845810538	-0.3844	-1.30532
205934_at	chr2:198773984-198838554 (+) // 94.41 // q33.1	phospholipase C-like 1	PLCL1	0.0001059	0.0082963	4.6780051	5.348553767	-0.67055	-1.59168
217437_s_at	chr8:38797006-38827450 (+) // 93.42 // p11.23	transforming, acidic coiled-coil containing protein 1	TACC1	0.0001059	0.0082963	7.943780043	7.259297927	0.684482	1.607125
219790_s_at	chr5:32747585-32822284 (+) // 97.49 // p13.3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	NPR3	0.0001059	0.0082963	5.27337533	4.858316483	0.415059	1.333353
225922_at	chr4:160184474-160186807 (+) // 99.57 // q32.1	Hypothetical protein FLJ25371	FLJ25371	0.0001059	0.0082963	7.673824175	6.385280758	1.288543	2.442813
227182_at	chr9:92919682-92926975 (+) // 93.43 // q22.31	sushi domain containing 3	SUSD3	0.0001059	0.0082963	5.800505438	6.287649631	-0.48714	-1.40167
232500_at	chr20:20400080-20441244 (-) // 96.57 // p11.23	chromosome 20 open reading frame 74	C20orf74	0.0001059	0.0082963	5.518459793	4.907859957	0.6106	1.526894
235691_at	chr1:95105951-95106794 (+) // 66.86 // p21.3	Hypothetical gene supported by AK094796	---	0.0001059	0.0082963	3.66211459	3.829266485	-0.16715	-1.12284
237305_at	chr18:23912653-23913196 (-) // 96.09 // q12.1	Cadherin 2, type 1, N-cadherin (neuronal)	CDH2	0.0001059	0.0082963	4.034058583	4.431768897	-0.39771	-1.31742
1560397_s_at	chr3:184691499-184693930 (-) // 75.97 // q27.1	kelch-like 6 (Drosophila)	KLHL6	0.0001095	0.0084574	6.095522134	5.593605133	0.501917	1.416094
202718_at	chr2:217323638-217354662 (+) // 90.93 // q35	insulin-like growth factor binding protein 2, 36kDa	IGFBP2	0.0001095	0.0084574	5.838989779	8.630074475	-2.79108	-6.9215
203418_at	chr4:123096158-123102485 (-) // 99.03 // q27	cyclin A2	CCNA2	0.0001095	0.0084574	5.377111566	6.413767179	-1.03666	-2.05147
204233_s_at	chr11:67576901-67645255 (-) // 93.6 // q13.2	choline kinase alpha	CHKA	0.0001095	0.0084574	7.477284438	6.439923016	1.037361	2.05247
204448_s_at	chr9:122661775-122670464 (-) // 99.34 // q33.2	phosducin-like	PDCL	0.0001095	0.0084574	7.365323136	6.759903452	0.60542	1.521421
206102_at	chr20:25336362-25375949 (+) // 42.46 // p11.21	DNA replication complex GINS protein PSF1	PSF1	0.0001095	0.0084574	4.691299448	5.711536467	-1.02024	-2.02825
209682_at	chr3:106859804-107070577 (-) // 99.57 // q13.11	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	0.0001095	0.0084574	7.576255582	6.504767343	1.071488	2.1016
216026_s_at	chr12:131810697-131813255 (-) // 94.17 // q24.33	polymerase (DNA directed), epsilon	POLE	0.0001095	0.0084574	7.760880656	8.177774517	-0.41689	-1.33505
221081_s_at	chr1:111441844-111459073 (-) // 99.0 // p13.3	DENN/MADD domain containing 2D	DENND2D	0.0001095	0.0084574	6.41573684	8.385043196	-1.96931	-3.9158
240544_at	chr6:38084018-38084614 (+) // 77.67 // p21.2	Testis expressed sequence 27	TEX27	0.0001095	0.0084574	4.470807334	4.124500361	0.346307	1.271302
206369_s_at	chr7:106101957-106139884 (+) // 98.39 // q22.3	phosphoinositide-3-kinase, catalytic, gamma polypeptide	PIK3CG	0.0001132	0.0086711	6.283899423	5.330516045	0.953383	1.936409
210993_s_at	chr4:146761561-146836711 (+) // 99.94 // q31.21	SMAD, mothers against DPP homolog 1 (Drosophila)	SMAD1	0.0001132	0.0086711	5.700223066	6.628547064	-0.92832	-1.90306
215982_s_at	chr6:32045632-32047719 (-) // 99.92 // p21.32	dom-3 homolog Z (C. elegans)	DOM3Z	0.0001132	0.0086711	7.369608662	7.779477634	-0.40987	-1.32857
218431_at	chr14:76962775-76993684 (-) // 99.84 // q24.3	chromosome 14 open reading frame 133	C14orf133	0.0001132	0.0086711	6.659330674	7.110215852	-0.45089	-1.36688
235392_at	chr2:227482906-227483712 (-) // 95.82 // q36.3	Insulin receptor substrate 1	IRS1	0.0001132	0.0086711	3.952277802	4.272385938	-0.32011	-1.24842
242325_at	chr22:30666988-30667545 (+) // 99.82 // q12.3	---	---	0.0001132	0.0086711	7.175121161	6.173481719	1.001639	2.002274
227077_at	chr17:15563189-15564823 (+) // 53.39 // p12 /// chr17:1	zinc finger protein 286	ZNF286	0.0001151	0.0087798	7.144159363	7.975140278	-0.83098	-1.77889
227489_at	chr17:59968863-59969926 (-) // 90.52 // q24.1	SMAD specific E3 ubiquitin protein ligase 2	SMURF2	0.0001151	0.0087798	6.792309063	5.866596257	0.925713	1.899623
244054_at	chr3:171584035-171584530 (+) // 97.24 // q26.2	SKI-like	SKIL	0.0001151	0.0087798	6.625615146	6.131547651	0.494067	1.40841
201802_at	chr6:44295370-44309856 (+) // 96.58 // p21.1	solute carrier family 29 (nucleoside transporters), member 1	SLC29A1	0.0001171	0.0088412	6.809917525	7.386864787	-0.57695	-1.49169
203229_s_at	chr1:152045737-152056193 (-) // 100.0 // q22	CDC-like kinase 2	CLK2	0.0001171	0.0088412	8.183148845	8.488597701	-0.30545	-1.2358
212022_s_at	chr10:129784916-129814639 (-) // 97.55 // q26.2	antigen identified by monoclonal antibody Ki-67	MKI67	0.0001171	0.0088412	6.903598246	7.600645001	-0.69705	-1.62118
236613_at	chr14:72637190-72637645 (+) // 100.0 // q24.2	RNA binding motif protein 25	RBM25	0.0001171	0.0088412	5.253724192	4.854929158	0.398795	1.318406
242069_at	chr12:52953879-52960128 (-) // 86.62 // q13.13	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5	0.0001171	0.0088412	6.056871762	6.813426285	-0.75655	-1.68945
242733_at	chr4:175794613-175795070 (-) // 94.53 // q34.1	Hydroxyprostaglandin dehydrogenase 15-(NAD)	HPGD	0.0001171	0.0088412	7.075097223	6.56028343	0.514814	1.42881
244226_s_at	chr17:53808437-53808731 (+) // 91.5 // q23.2	Suppressor of Ty 4 homolog 1 (S. cerevisiae)	SUPT4H1	0.0001171	0.0088412	4.428704041	4.125439306	0.303265	1.233934
205402_x_at	chr7:141985492-141989078 (+) // 99.38 // q34 /// chr7:1	protease, serine, 2 (trypsin 2)	PRSS2	0.000119	0.0089769	5.72058629	5.343047055	0.377539	1.299124
1552671_a_at	chrX:46222344-46374726 (-) // 98.2 // p11.3	solute carrier family 9 (sodium/hydrogen exchanger), member 7	SLC9A7	0.000121	0.0090035	5.169851029	4.878945312	0.290906	1.223408
201801_s_at	chr6:44295449-44309268 (+) // 99.33 // p21.1	solute carrier family 29 (nucleoside transporters), member 1	SLC29A1	0.000121	0.0090035	5.611997078	6.224856158	-0.61286	-1.52929
202000_at	chr22:40806030-40811249 (-) // 86.27 // q13.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	NDUFA6	0.000121	0.0090035	7.794671527	8.105712697	-0.31104	-1.2406
209729_at	chr22:28027598-28033327 (+) // 96.32 // q12.2	growth arrest-specific 2 like 1	GAS2L1	0.000121	0.0090035	5.984317582	6.450337912	-0.46602	-1.38129
218741_at	chr22:40659241-40667615 (-) // 97.07 // q13.2	chromosome 22 open reading frame 18	C22orf18	0.000121	0.0090035	6.692782475	7.639183479	-0.9464	-1.92706
222147_s_at	chr20:36810535-36833873 (+) // 99.94 // q11.23	ARP5 actin-related protein 5 homolog (yeast)	ACTR5	0.000121	0.0090035	6.949174098	6.217557514	0.731617	1.660499
223104_at	chr3:9907327-9910520 (+) // 98.54 // p25.3	jagunal homolog 1 (Drosophila)	JAGN1	0.000121	0.0090035	7.745300563	8.162027016	-0.41673	-1.3349
229854_at	chr1:224854992-224855685 (+) // 95.29 // q42.13	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	OBSCN	0.000121	0.0090035	5.89641468	6.360321844	-0.46391	-1.37927
232676_x_at	chr15:46221284-46231741 (-) // 98.41 // q21.1	myelin expression factor 2	MYEF2	0.000121	0.0090035	7.568561363	8.293419668	-0.72486	-1.65274
239695_at	chr1:65052061-65052564 (-) // 60.83 // p31.3	Janus kinase 1 (a protein tyrosine kinase)	JAK1	0.000121	0.0090035	8.040109665	6.909405067	1.130705	2.189657
201036_s_at	chr4:109268605-109313927 (+) // 98.03 // q25	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	HADHSC	0.0001251	0.0092447	7.300042628	8.438616764	-1.13857	-2.20163
208109_s_at	chr15:75303306-75304801 (-) // 70.64 // q24.3	chromosome 15 open reading frame 5 /// chromosome 15 open reading frame 5	C15orf5	0.0001251	0.0092447	5.037645072	4.294853576	0.742791	1.673411
209603_at	chr10:8136675-8157219 (+) // 95.62 // p14	GATA binding protein 3	GATA3	0.0001251	0.0092447	7.576331642	6.93850855	0.637823	1.55598
211637_x_at	chr15:19974283-19974577 (-) // 66.92 // q11.2	IgH chain VDJ region /// IgH chain VDJ region	---	0.0001251	0.0092447	6.83045473	7.502651077	-0.6722	-1.5935
218355_at	chr5:154373566-154377875 (+) // 93.49 // q33.2 /// chrX:	kinesin family member 4A	KIF4A	0.0001251	0.0092447	5.751119453	6.456026095	-0.70491	-1.63004
223203_at	chrX:52819356-52820604 (+) // 98.81 // p11.22 /// chrX:5	transmembrane protein 29	TMEM29	0.0001272	0.0093857	8.549243328	9.091756795	-0.54251	-1.45651
201384_s_at	chr17:38576770-38719014 (+) // 98.23 // q21.31 /// chr1	neighbor of BRCA1 gene 1	NBR1	0.0001293	0.0094667	7.016597707	7.754352715	-0.73776	-1.66758
204817_at	chr12:51948383-51973686 (+) // 99.91 // q13.13	extra spindle poles like 1 (S. cerevisiae)	ESPL1	0.0001293	0.0094667	7.078245466	7.508772634	-0.43053	-1.34773
206686_at	chr2:173246334-173286337 (+) // 94.01 // q31.1	pyruvate dehydrogenase kinase, isoenzyme 1	PDK1	0.0001293	0.0094667	6.540330058	6.236359053	0.303971	1.234538
212742_at	chr1:143100098-143177993 (+) // 87.52 // q21.1	zinc finger protein 364	ZNF364	0.0001293	0.0094667	8.553437101	8.169047363	0.38439	1.305308
232508_at	chr10:80498816-80647187 (+) // 56.84 // q22.3	Retinoic acid induced 17	RAI17	0.0001293	0.0094667	5.697552568	5.324294702	0.373258	1.295274
235801_at	chr8:15667411-15667865 (+) // 64.58 // p22	Tumor suppressor candidate 3	TUSC3	0.0001293	0.0094667	3.605565775	3.771191209	-0.16563	-1.12165
203279_at	chr3:5204432-5236642 (+) // 96.01 // p26.1	ER degradation enhancer, mannosidase alpha-like 1	EDEM1	0.0001315	0.0096109	8.261764085	8.993617475	-0.73185	-1.66077
1558173_a_at	chr1:23165241-23249607 (-) // 93.72 // p36.12	leucine zipper protein 1	LUZP1	0.0001337	0.0096177	6.298838422	5.806986427	0.491852	1.406249
201691_s_at	chr8:81110303-81246324 (-) // 99.26 // q21.13	tumor protein D52	TPD52	0.0001337	0.0096177	3.71469296	3.871705577	-0.15701	-1.11498
201710_at	chr20:41735858-41778538 (+) // 94.4 // q13.12	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	MYBL2	0.0001337	0.0096177	7.436645667	8.22623137	-0.78959	-1.72858
201906_s_at	chr3:37878128-38000963 (+) // 90.01 // p22.3	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	CTDSPL	0.0001337	0.0096177	5.952785929	6.260027282	-0.30724	-1.23734
201965_s_at	chr9:132168835-132216789 (-) // 99.97 // q34.13	amyotrophic lateral sclerosis 4	ALS4	0.0001337	0.0096177	8.162198196	7.635602324	0.526596	1.440526
203764_at	chr14:54684600-54725528 (-) // 99.89 // q22.3	discs, large homolog 7 (Drosophila)	DLG7	0.0001337	0.0096177	4.877439402	6.084257051	-1.20682	-2.30828
217371_s_at	chr4:143000711-143011619 (+) // 74.49 // q31.21	interleukin 15	IL15	0.0001337	0.0096177	3.75189583	3.956110208	-0.20421	-1.15206
219787_s_at	chr3:174003363-174021959 (+) // 99.9 // q26.31	epithelial cell transforming sequence 2 oncogene	ECT2	0.0001337	0.0096177	4.096905613	6.102069131	-2.00516	-4.01434
222993_at	chr1:54377912-54396070 (+) // 99.3 // p32.3	mitochondrial ribosomal protein L37	MRPL37	0.0001337	0.0096177	8.302743905	8.865320536	-0.56258	-1.4769
225034_at	chr8:134536273-134539258 (-) // 96.0 // q24.22	hypothetical protein LOC286167	LOC286167	0.0001337	0.0096177	6.670356392	6.169335909	0.50102	1.415214
227657_at	chr4:142144329-142412221 (-) // 82.43 // q31.21	ring finger protein 150	RNF150	0.0001337	0.0096177	4.996910502	5.420780661	-0.42387	-1.34152
243992_at	chr3:137289018-137289423 (-) // 89.71 // q22.2	Protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	PPP2R3A	0.0001337	0.0096177	7.886931988	7.452247285	0.434685	1.351615
1562863_at	chr8:119067627-119069146 (-) // 79.43 // q24.11	Exostoses (multiple) 1	EXT1	0.0001359	0.0097519	3.706022557	3.826809805	-0.12079	-1.08733
201445_at	chr1:95074786-95104659 (-) // 98.44 // p21.3	calponin 3, acidic	CNN3	0.0001359	0.0097519	4.50459512	5.329502548	-0.82491	-1.77142
1556239_a_at	chr7:35501907-35503521 (-) // 91.95 // p14.2	Hypothetical protein FLJ22313	FLJ22313	0.0001382	0.0097608	7.742415244	6.906203378	0.836212	1.785356
1560332_at	chr12:103481619-103485574 (+) // 54.33 // q23.3	Carbohydrate (chondroitin 4) sulfotransferase 11	CHST11	0.0001382	0.0097608	9.119802214	7.845903592	1.273899	2.418141
206301_at	chr4:47978728-48071606 (-) // 96.52 // p12	tec protein tyrosine kinase	TEC	0.0001382	0.0097608	6.255165884	5.802441214	0.452725	1.368623
209408_at	chr1:44874643-44902453 (+) // 99.85 // p34.1	kinesin family member 2C	KIF2C	0.0001382	0.0097608	7.22985153	8.159205258	-0.92935	-1.90442
212807_s_at	chr1:109567116-109652593 (-) // 99.47 // p13.3	sortilin 1	SORT1	0.0001382	0.0097608	5.586129265	6.121919755	-0.53579	-1.44974
213329_at	chr1:202945759-203026173 (+) // 90.49 // q32.1	SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	0.0001382	0.0097608	4.971282614	5.362823698	-0.39154	-1.31179
214043_at	chr9:8304246-8304734 (-) // 77.35 // p24.1	Protein tyrosine phosphatase, receptor type, D	PTPRD	0.0001382	0.0097608	4.27503072	4.878329974	-0.6033	-1.51919
218098_at	chr20:46971833-47086636 (+) // 99.46 // q13.13	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	ARFGEF2	0.0001382	0.0097608	8.003314566	7.476859386	0.526455	1.440386
219502_at	chr4:178606176-178659149 (+) // 99.69 // q34.3	nei endonuclease VIII-like 3 (E. coli)	NEIL3	0.0001382	0.0097608	5.115686824	5.703966276	-0.58828	-1.50345
222142_at	chr16:49341374-49379160 (+) // 99.46 // q12.1	cylindromatosis (turban tumor syndrome)	CYLD	0.0001382	0.0097608	7.88186848	6.666846521	1.215022	2.321443
228813_at	chr2:239706123-239706766 (-) // 89.15 // q37.3	histone deacetylase 4	HDAC4	0.0001382	0.0097608	6.228484752	6.990930048	-0.76245	-1.69636
243527_at	chr7:150515857-150516153 (-) // 96.42 // q36.1	hypothetical protein LOC349136	LOC349136	0.0001382	0.0097608	5.678585755	5.225258331	0.453327	1.369195
1553183_at	chr21:42414334-42436174 (+) // 90.8 // q22.3	uromodulin-like 1	UMODL1	0.0001428	0.0099591	6.54351257	4.787827328	1.755685	3.376867
1554903_at	chr11:64910683-64911304 (+) // 86.03 // q13.1	FKSG44 gene /// FKSG43 gene	FKSG44 /// FKSG	0.0001428	0.0099591	8.211060038	7.521169889	0.68989	1.613161
205127_at	chr9:122212852-122236700 (+) // 90.37 // q33.2	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	PTGS1	0.0001428	0.0099591	6.456419999	6.189160956	0.267259	1.203519
205718_at	chr12:51871374-51880498 (-) // 94.1 // q13.13	integrin, beta 7	ITGB7	0.0001428	0.0099591	7.794464447	7.293669078	0.500795	1.414993
206545_at	chr2:204396703-204428062 (+) // 86.09 // q33.2	CD28 antigen (Tp44)	CD28	0.0001428	0.0099591	4.788600606	8.174084449	-3.38548	-10.4504
219429_at	chr16:73304361-73366197 (-) // 98.8 // q22.3	fatty acid 2-hydroxylase	FA2H	0.0001428	0.0099591	4.470181374	4.788633605	-0.31845	-1.24699
221538_s_at	chr3:128237523-128238925 (+) // 98.1 // q21.2	plexin A1	PLXNA1	0.0001428	0.0099591	4.757093335	5.543713497	-0.78662	-1.72503
225729_at	chr6:37002237-37004718 (+) // 88.86 // p21.2	Chromosome 6 open reading frame 89	C6orf89	0.0001428	0.0099591	6.570666103	7.061246881	-0.49058	-1.40501
237104_at	chr1:147534025-147534506 (-) // 11.62 // q21.2	Cathepsin S	CTSS	0.0001428	0.0099591	4.624772672	4.300579114	0.324194	1.251964
57532_at	chr17:7069384-7069969 (-) // 90.56 // p13.1	dishevelled, dsh homolog 2 (Drosophila)	DVL2	0.0001428	0.0099591	7.466479942	7.978000059	-0.51152	-1.42555

Supplementary Table S6. Increased expression of hematopoietic progenitor population signature genes in the immature cluster gene signature.

significance levels for enriched signature gene selections in the Immature cluster signature (784 genes)

Threshold for gene selection	1.00E-09		1.00E-08		1.00E-07		1.00E-06		1.00E-05	
Signatures from Novershtern *et al.*, 2011	**Genes**	***p*-value**	**Genes**	***p*-value**	**Genes**	***p*-value**	**Genes**	***p*-value**	**Genes**	***p*-value**
B-cell down-regulated	44	**0.0015231**	80	**0.00079029**	124	**0.0039393**	214	0.025091	317	0.082069
B-cell up-regulated	540	**0.0019873**	646	**0.00053342**	827	**0.0012076**	1059	**0.0011589**	1286	**0.0003373**
ERY down-regulated	801	0.12107	973	0.23755	1171	0.40063	1414	0.30715	1647	0.34433
ERY up-regulated	830	0.42728	914	0.51118	1007	0.58083	1144	0.45755	1227	0.55181
GMP down-regulated	6	0.030566	7	0.03557	10	0.050427	28	0.13492	58	0.036192
GMP up-regulated	325	1	400	1	484	1	598	0.40081	699	0.29357
HSC down-regulated	3	1	7	1	14	1	35	1	59	1
HSC/ early ERY down-regulated	188	0.62328	252	0.6259	360	0.44348	473	0.55774	586	0.41461
HSC/ early ERY up-regulated	1020	**0.0065799**	1163	**0.0071626**	1310	**0.0077648**	1509	0.011102	1687	0.027455
HSC up-regulated	355	**0.0024999**	452	**0.0091381**	560	**0.0086623**	710	0.031054	872	**0.0055616**
Late ERY down-regulated	1400	0.29717	1603	0.44659	1854	0.24862	2112	0.2002	2334	0.14741
Late ERY up-regulated	947	0.27527	1013	0.39682	1095	0.50064	1181	0.59086	1269	0.51653
NK down-regulated	19	1	33	0.15704	64	0.28216	137	0.15766	249	0.36856
NK up-regulated	41	1	52	1	73	1	105	1	133	0.49837
T-cell down-regulated	314	**0.0058655**	392	0.016251	510	0.016784	658	**0.0071884**	797	**0.00088026**
T-cell up-regulated	1071	0.050717	1236	0.055021	1423	0.11768	1669	0.089891	1868	0.1668