Supplementary Table 6. Probesets with average differential expression change > 2 between microfluidic isolation and Ficoll-dextran isolation. Blue (red) genes are down (up) regulated in microfluidic isolated neutrophils compared to Ficoll-Dextran isolated neutrophils.

				Mean $\log_2$ Expression for subjects 1-5		
Probe Set	**Gene Symbol**	**Gene Title**	**qvalue(FDR)**	*Microfluidic*	*Ficoll-Dextran*	$\log_2$(MF)-$\log_2$(Bulk)
1558365_at	---	---	0.275	4.14153	6.4055	-2.26397
1562529_s_at	---	---	0.275	3.30936	5.31073	-2.00137
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.330	4.60635	7.92852	-3.32217
232307_at	---	---	0.330	5.5337	7.42977	-1.89607
228180_at	---	---	0.330	5.08012	6.6711	-1.59098
1569482_at	---	---	0.330	3.24714	4.78804	-1.5409
237456_at	---	---	0.330	6.98356	8.42898	-1.44542
207185_at	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family	0.330	6.20477	7.64562	-1.44085
1563473_at	---	---	0.330	2.5875	3.83581	-1.24831
242337_at	---	---	0.330	7.7319	8.97068	-1.23878
1567440_at	PSEN1	Presenilin 1	0.330	9.90476	11.0148	-1.11004
243817_at	---	---	0.330	4.58218	5.67799	-1.09581
1567443_x_at	PSEN1	presenilin 1	0.330	9.65895	10.7501	-1.09115
224752_at	PL-5283	PL-5283 protein	0.330	8.54108	7.5166	1.02448
200661_at	CTSA	cathepsin A	0.330	9.30509	8.22141	1.08368
228249_at	C11orf74	chromosome 11 open reading frame 74	0.330	5.5524	4.24077	1.31163
223922_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.330	8.74472	7.31818	1.42654
215958_at	---	---	0.363	5.13968	7.3136	-2.17392
1557915_s_at	GSTO1	glutathione S-transferase omega 1	0.406	9.44098	8.28257	1.15841
210479_s_at	RORA	RAR-related orphan receptor A	0.421	4.40175	6.9338	-2.53205
244719_at	---	---	0.421	4.20246	6.66533	-2.46287
223092_at	ANKH	ankylosis, progressive homolog (mouse)	0.421	4.29977	6.31356	-2.01379
227868_at	LOC154761	hypothetical LOC154761	0.421	5.83873	7.56276	-1.72403
1560342_at	---	---	0.421	4.2838	6.00382	-1.72002
239661_at	---	---	0.421	5.33401	6.99868	-1.66467
209670_at	TRAC	T cell receptor alpha constant	0.421	6.16675	7.74425	-1.5775
243329_at	---	---	0.421	4.31709	5.88297	-1.56588
238988_at	---	---	0.421	4.47696	5.9482	-1.47124
235324_at	SFRS3	splicing factor, arginine/serine-rich 3	0.421	4.84979	6.27572	-1.42593
236645_at	HBP1	HMG-box transcription factor 1	0.421	6.20006	7.57818	-1.37812
236595_at	---	---	0.421	5.09603	6.4299	-1.33387
233852_at	POLH	polymerase (DNA directed), eta	0.421	4.82765	6.09041	-1.26276
216478_at	---	---	0.421	3.39694	4.58287	-1.18593
241906_at	---	---	0.421	3.62346	4.80541	-1.18195
1556277_a_at	PAPD4	PAP associated domain containing 4	0.421	6.11186	7.27447	-1.16261
209696_at	FBP1	fructose-1,6-bisphosphatase 1	0.421	6.68583	5.66691	1.01892
231396_s_at	FAM126A	family with sequence similarity 126, member A	0.421	7.92663	6.80498	1.12165
224918_x_at	MGST1	microsomal glutathione S-transferase 1	0.421	5.66114	4.53236	1.12878
201360_at	CST3	cystatin C	0.421	9.1742	7.8076	1.3666
223280_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.421	8.90328	7.51589	1.38739
224102_at	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	0.421	5.55918	4.053	1.50618
209357_at	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carbox	0.421	6.84902	5.1823	1.66672
228486_at	SLC44A1	solute carrier family 44, member 1	0.421	7.24596	5.22098	2.02498
213539_at	CD3D	CD3d molecule, delta (CD3-TCR complex)	0.424	5.73088	8.07502	-2.34414
206666_at	GZMK	granzyme K (granzyme 3; tryptase II)	0.424	4.08414	6.33835	-2.25421
211339_s_at	ITK	IL2-inducible T-cell kinase	0.424	3.88213	6.0764	-2.19427
202206_at	ARL4C	ADP-ribosylation factor-like 4C	0.424	5.40562	7.10115	-1.69553
204890_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.424	4.73564	6.41139	-1.67575
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.424	4.49719	6.16869	-1.6715
1562619_at	TXNDC6	thioredoxin domain containing 6	0.424	3.33038	4.60699	-1.27661
241740_at	---	---	0.424	3.12739	4.39385	-1.26646
238156_at	---	---	0.424	5.02315	6.28185	-1.2587
215261_at	---	---	0.424	5.52148	6.75771	-1.23623
235680_at	---	---	0.424	7.13744	8.32559	-1.18815
224766_at	RPL37	Ribosomal protein L37	0.424	5.46441	6.62595	-1.16154
227119_at	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	0.424	6.51515	7.56896	-1.05381
217452_s_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypepti	0.424	2.69169	3.70759	-1.0159

224356_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.424	8.90559	7.43717	1.46842
210116_at	SH2D1A	SH2 domain protein 1A	0.427	5.35275	7.71739	-2.36464
207979_s_at	CD8B	CD8b molecule	0.430	5.6602	6.8351	-1.1749
203932_at	HLA-DMB	major histocompatibility complex, class II, DM beta	0.430	7.42606	6.11469	1.31137
205456_at	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	0.451	4.64514	6.63142	-1.98628
237626_at	---	---	0.452	6.79303	8.36796	-1.57493
205758_at	CD8A	CD8a molecule	0.454	4.85774	7.71533	-2.85759
1565666_s_at	LOC100133432 /// LOC100	similar to Mucin-6 precursor (Gastric mucin-6) /// similar to M	0.454	2.82795	5.52981	-2.70186
1558691_a_at	DOCK4	dedicator of cytokinesis 4	0.454	5.27116	7.84946	-2.5783
210426_x_at	RORA	RAR-related orphan receptor A	0.454	4.72869	7.09176	-2.36307
210972_x_at	TRA@ /// TRAC /// TRAJ17	T cell receptor alpha locus /// T cell receptor alpha constant //	0.454	6.33212	8.51505	-2.18293
206804_at	CD3G	CD3g molecule, gamma (CD3-TCR complex)	0.454	5.32531	7.4536	-2.12829
230464_at	S1PR5	sphingosine-1-phosphate receptor 5	0.454	5.86957	7.97631	-2.10674
236510_at	---	---	0.454	5.2783	7.36919	-2.09089
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	0.454	4.87602	6.9663	-2.09028
1562528_at	---	---	0.454	2.01136	4.05345	-2.04209
206545_at	CD28	CD28 molecule	0.454	3.54209	5.49255	-1.95046
244061_at	---	---	0.454	4.76363	6.69714	-1.93351
234778_at	---	---	0.454	5.23201	7.15215	-1.92014
1565588_at	SP140	SP140 nuclear body protein	0.454	4.03991	5.8446	-1.80469
1569477_at	---	---	0.454	6.42708	8.21056	-1.78348
229483_at	---	---	0.454	4.54721	6.33031	-1.7831
209671_x_at	TRA@ /// TRAC	T cell receptor alpha locus /// T cell receptor alpha constant	0.454	6.36478	8.13996	-1.77518
233289_at	---	---	0.454	5.22032	6.8642	-1.64388
211902_x_at	TRA@	T cell receptor alpha locus	0.454	6.51035	8.14226	-1.63191
223527_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	0.454	5.6803	7.31002	-1.62972
240344_x_at	LYRM7	Lyrm7 homolog (mouse)	0.454	6.36197	7.98024	-1.61827
1569077_x_at	ZNF836	zinc finger protein 836	0.454	4.78537	6.37591	-1.59054
227686_at	OXNAD1	oxidoreductase NAD-binding domain containing 1	0.454	6.12246	7.69895	-1.57649
232344_at	---	---	0.454	7.04172	8.59902	-1.5573
1556607_at	EHD4	EH-domain containing 4	0.454	5.21393	6.74767	-1.53374
239655_at	---	---	0.454	3.93822	5.45632	-1.5181
228433_at	NFYA	nuclear transcription factor Y, alpha	0.454	5.75103	7.24994	-1.49891
225187_at	KIAA1967	KIAA1967	0.454	5.65861	7.10882	-1.45021
228211_at	C9orf102	chromosome 9 open reading frame 102	0.454	4.55952	5.95735	-1.39783
236341_at	CTLA4	cytotoxic T-lymphocyte-associated protein 4	0.454	3.43824	4.83029	-1.39205
239829_at	---	---	0.454	4.65366	6.02145	-1.36779
213019_at	RANBP6	RAN binding protein 6	0.454	6.38535	7.73414	-1.34879
226116_at	---	---	0.454	3.83316	5.17606	-1.3429
239861_at	---	---	0.454	7.15376	8.47552	-1.32176
237746_at	SFRS11	Splicing factor, arginine/serine-rich 11	0.454	5.66732	6.98402	-1.3167
243561_at	---	---	0.454	4.76075	6.05437	-1.29362
240652_at	---	---	0.454	5.63074	6.91022	-1.27948
211435_at	---	---	0.454	5.02694	6.30392	-1.27698
226981_at	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homo	0.454	3.94961	5.22376	-1.27415
239571_at	---	---	0.454	5.8535	7.11971	-1.26621
214323_s_at	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	0.454	5.47538	6.74138	-1.266
1557801_x_at	C11orf31	chromosome 11 open reading frame 31	0.454	5.90196	7.16522	-1.26326
239504_at	---	---	0.454	4.8312	6.08311	-1.25191
212604_at	MRPS31	mitochondrial ribosomal protein S31	0.454	6.58557	7.82236	-1.23679
37943_at	ZFYVE26	zinc finger, FYVE domain containing 26	0.454	4.39818	5.62619	-1.22801
229686_at	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	0.454	8.81334	10.0095	-1.19616
213073_at	ZFYVE26	zinc finger, FYVE domain containing 26	0.454	5.63015	6.81836	-1.18821
236338_at	---	---	0.454	5.6839	6.8617	-1.1778
210621_s_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.454	5.32955	6.49458	-1.16503
238438_at	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	0.454	4.99417	6.15017	-1.156
204157_s_at	KIAA0999	KIAA0999 protein	0.454	7.11468	8.25484	-1.14016
232354_at	---	---	0.454	5.02031	6.15472	-1.13441
241865_at	---	---	0.454	8.03896	9.17252	-1.13356
209315_at	HBS1L	HBS1-like (S. cerevisiae)	0.454	5.30182	6.43284	-1.13102
224763_at	RPL37	Ribosomal protein L37	0.454	5.40426	6.53287	-1.12861
226037_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-ass	0.454	6.29182	7.41484	-1.12302
232304_at	PELI1	Pellino homolog 1 (Drosophila)	0.454	8.82955	9.92746	-1.09791
212926_at	SMC5	structural maintenance of chromosomes 5	0.454	4.2384	5.32244	-1.08404
210223_s_at	MR1	major histocompatibility complex, class I-related	0.454	7.89143	8.9719	-1.08047

219269_at	HMBOX1	homeobox containing 1	0.454	4.58186	5.65967	-1.07781
230489_at	CD5	CD5 molecule	0.454	5.42017	6.47902	-1.05885
231470_at	---	---	0.454	3.96809	5.01709	-1.049
240165_at	---	---	0.454	8.62817	9.67472	-1.04655
239401_at	S1PR1	Sphingosine-1-phosphate receptor 1	0.454	3.94138	4.986	-1.04462
228917_at	---	---	0.454	3.57059	4.60993	-1.03934
242946_at	CD53	CD53 molecule	0.454	8.92099	9.95532	-1.03433
244312_at	---	---	0.454	4.14778	5.16383	-1.01605
1555889_a_at	CRTAP	cartilage associated protein	0.454	7.75975	6.74337	1.01638
209500_x_at	TNFSF12-TNFSF13 /// TNFS	TNFSF12-TNFSF13 readthrough transcript /// tumor necrosis f	0.454	7.60369	6.57791	1.02578
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	0.454	7.27507	6.20573	1.06934
1565162_s_at	MGST1	microsomal glutathione S-transferase 1	0.454	3.94188	2.86476	1.07712
223276_at	MST150	MSTP150	0.454	8.04639	6.96852	1.07787
210347_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.454	5.90607	4.80915	1.09692
210314_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	0.454	7.63162	6.52704	1.10458
1555123_at	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	0.454	3.84706	2.73051	1.11655
1554464_a_at	CRTAP	cartilage associated protein	0.454	5.3152	4.15887	1.15633
221765_at	UGCG	UDP-glucose ceramide glucosyltransferase	0.454	5.52702	4.34279	1.18423
231211_s_at	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	0.454	6.62752	5.4232	1.20432
202944_at	NAGA	N-acetylgalactosaminidase, alpha-	0.454	6.85959	5.64832	1.21127
218117_at	RBX1	ring-box 1	0.454	8.19849	6.94416	1.25433
214469_at	HIST1H2AE	histone cluster 1, H2ae	0.454	9.86686	8.56143	1.30543
222552_at	GOLT1B	golgi transport 1 homolog B (S. cerevisiae)	0.454	6.41208	5.08969	1.32239
209499_x_at	TNFSF12-TNFSF13 /// TNFS	TNFSF12-TNFSF13 readthrough transcript /// tumor necrosis f	0.454	7.0333	5.70759	1.32571
210987_x_at	TPM1	tropomyosin 1 (alpha)	0.454	7.32378	5.98711	1.33667
200824_at	GSTP1	glutathione S-transferase pi 1	0.454	8.26694	6.91943	1.34751
220570_at	RETN	resistin	0.454	7.19783	5.82361	1.37422
242038_at	LRRC8B	leucine rich repeat containing 8 family, member B	0.454	7.93507	6.55675	1.37832
219506_at	C1orf54	chromosome 1 open reading frame 54	0.454	6.0764	4.60096	1.47544
210843_s_at	MFAP3L	microfibrillar-associated protein 3-like	0.454	6.90331	5.37311	1.5302
213258_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagul	0.454	4.32018	2.66736	1.65282
210986_s_at	TPM1	tropomyosin 1 (alpha)	0.454	6.52527	4.79766	1.72761
226018_at	C7orf41	chromosome 7 open reading frame 41	0.454	7.73111	5.89093	1.84018
210895_s_at	CD86	CD86 molecule	0.454	5.21563	3.36138	1.85425
204112_s_at	HNMT	histamine N-methyltransferase	0.454	5.40026	3.48177	1.91849
201506_at	TGFBI	transforming growth factor, beta-induced, 68kDa	0.454	8.33708	6.38512	1.95196
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	0.454	7.89658	5.88312	2.01346
216834_at	RGS1	regulator of G-protein signaling 1	0.455	4.10969	6.05967	-1.94998
200736_s_at	GPX1	glutathione peroxidase 1	0.455	8.96884	7.75941	1.20943
229541_at	---	---	0.456	5.41261	6.48867	-1.07606
39248_at	AQP3	aquaporin 3 (Gill blood group)	0.459	6.62173	9.82725	-3.20552
202988_s_at	RGS1	regulator of G-protein signaling 1	0.459	6.16323	8.07935	-1.91612
236266_at	RORA	RAR-related orphan receptor A	0.463	4.99456	6.98257	-1.98801
234044_at	---	---	0.463	7.05028	8.79184	-1.74156
237330_at	---	---	0.463	7.06725	8.24877	-1.18152
201464_x_at	JUN	jun oncogene	0.463	8.86217	9.87624	-1.01407
228376_at	GGTA1	glycoprotein, alpha-galactosyltransferase 1	0.463	6.36979	4.95019	1.4196
243141_at	SGMS2	sphingomyelin synthase 2	0.463	5.76655	4.28815	1.4784
224637_at	LOC100128731	dolichyl-diphosphooligosaccharide--protein glycosyltransferas	0.464	10.5362	9.34466	1.19154
207651_at	GPR171	G protein-coupled receptor 171	0.464	4.17282	6.45171	-2.27889
203828_s_at	IL32	interleukin 32	0.464	7.02434	8.80073	-1.77639
228097_at	MYLIP	myosin regulatory light chain interacting protein	0.464	4.59682	6.13408	-1.53726
204891_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.464	4.4674	5.72097	-1.25357
223818_s_at	RSF1	remodeling and spacing factor 1	0.464	6.96936	8.1714	-1.20204
243659_at	---	---	0.464	4.40296	5.56982	-1.16686
242659_at	---	---	0.464	6.00705	7.13792	-1.13087
239757_at	ZFAND6	Zinc finger, AN1-type domain 6	0.467	4.79426	6.44155	-1.64729
229914_at	FLJ38717	FLJ38717 protein	0.467	6.55714	7.65205	-1.09491
227961_at	CTSB	cathepsin B	0.470	4.51236	3.33116	1.1812
219318_x_at	MED31	mediator complex subunit 31	0.480	5.0929	6.82164	-1.72874
206363_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (	0.480	4.89363	6.5578	-1.66417
208078_s_at	SIK1	salt-inducible kinase 1	0.480	7.01045	8.60103	-1.59058
242960_at	EPC2	Enhancer of polycomb homolog 2 (Drosophila)	0.480	5.87135	7.43599	-1.56464
1554615_at	---	---	0.480	4.80168	6.27272	-1.47104
229064_s_at	RCAN3	RCAN family member 3	0.480	5.36328	6.76155	-1.39827

244423_at	---	---	0.480	7.08983	8.46958	-1.37975
232356_at	---	---	0.480	5.54931	6.92136	-1.37205
1559006_at	---	---	0.480	4.53057	5.90078	-1.37021
1557551_at	---	---	0.480	4.91219	6.28085	-1.36866
232789_at	---	---	0.480	4.94909	6.30352	-1.35443
235159_at	---	---	0.480	5.38635	6.72865	-1.3423
230036_at	SAMD9L	sterile alpha motif domain containing 9-like	0.480	6.60582	7.89236	-1.28654
244537_at	---	---	0.480	3.44565	4.72701	-1.28136
234849_at	TRA@	T cell receptor alpha locus	0.480	2.50689	3.77913	-1.27224
1560297_at	---	---	0.480	7.07249	8.33463	-1.26214
1556735_at	---	---	0.480	4.74338	5.99679	-1.25341
240148_at	MSH6	MutS homolog 6 (E. coli)	0.480	4.93612	6.1798	-1.24368
212781_at	RBBP6	retinoblastoma binding protein 6	0.480	6.52599	7.71419	-1.1882
213958_at	CD6	CD6 molecule	0.480	5.56878	6.74556	-1.17678
213653_at	METTL3	methyltransferase like 3	0.480	6.33565	7.50988	-1.17423
213657_s_at	---	---	0.480	4.89539	6.06474	-1.16935
205254_x_at	TCF7	transcription factor 7 (T-cell specific, HMG-box)	0.480	5.35988	6.4692	-1.10932
230099_at	---	---	0.480	5.44779	6.54232	-1.09453
238243_at	---	---	0.480	5.59165	6.68518	-1.09353
236295_s_at	NLRC3	NLR family, CARD domain containing 3	0.480	3.44031	4.51007	-1.06976
1558787_a_at	---	---	0.480	3.32744	4.39495	-1.06751
215796_at	---	---	0.480	2.7095	3.76297	-1.05347
228531_at	SAMD9	sterile alpha motif domain containing 9	0.480	9.91032	10.9625	-1.05218
239266_at	---	---	0.480	5.10743	6.15512	-1.04769
212677_s_at	CEP68	centrosomal protein 68kDa	0.480	5.96675	7.01275	-1.046
231127_at	---	---	0.480	7.02748	8.05968	-1.0322
208453_s_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.480	4.8967	3.88761	1.00909
210075_at	2-Mar	membrane-associated ring finger (C3HC4) 2	0.480	6.86954	5.85366	1.01588
225693_s_at	CAMTA1	calmodulin binding transcription activator 1	0.480	8.88899	7.86681	1.02218
235237_at	VMA21	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)	0.480	6.97744	5.93263	1.04481
224331_s_at	MRPL36	mitochondrial ribosomal protein L36	0.480	8.42491	7.25867	1.16624
213908_at	WHAMML1 /// WHAMML	WAS protein homolog associated with actin, golgi membranes	0.480	4.4641	3.15816	1.30594
203645_s_at	CD163	CD163 molecule	0.480	7.78417	6.28021	1.50396
227461_at	STON2	stonin 2	0.480	5.32954	3.77803	1.55151
230550_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.480	7.54257	5.97003	1.57254
210254_at	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hem	0.480	9.77658	7.88846	1.88812
223754_at	C2orf88	chromosome 2 open reading frame 88	0.480	7.12366	5.16655	1.95711
227268_at	RNFT1	ring finger protein, transmembrane 1	0.481	5.13101	4.11041	1.0206
240721_at	---	---	0.481	4.80302	6.95864	-2.15562
1558052_at	TMED4	transmembrane emp24 protein transport domain containing	0.481	2.84781	4.93298	-2.08517
226682_at	RORA	RAR-related orphan receptor A	0.481	3.30982	5.12977	-1.81995
210031_at	CD247	CD247 molecule	0.481	6.02887	7.79639	-1.76752
212289_at	ANKRD12	ankyrin repeat domain 12	0.481	7.59621	9.31898	-1.72277
210439_at	ICOS	inducible T-cell co-stimulator	0.481	4.43665	6.15621	-1.71956
234033_at	---	---	0.481	3.56252	5.20709	-1.64457
242320_at	---	---	0.481	6.46564	8.05511	-1.58947
209604_s_at	GATA3	GATA binding protein 3	0.481	4.0684	5.65061	-1.58221
230048_at	---	---	0.481	7.03291	8.60081	-1.5679
239152_at	---	---	0.481	9.13585	10.6798	-1.54395
235739_at	---	---	0.481	5.85927	7.40171	-1.54244
202207_at	ARL4C	ADP-ribosylation factor-like 4C	0.481	5.76392	7.30256	-1.53864
204642_at	S1PR1	sphingosine-1-phosphate receptor 1	0.481	6.49906	8.01203	-1.51297
242898_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	0.481	6.03734	7.54304	-1.5057
231875_at	KIF21A	kinesin family member 21A	0.481	4.59662	6.06259	-1.46597
1556608_a_at	EHD4	EH-domain containing 4	0.481	5.55451	6.99718	-1.44267
244840_x_at	DOCK4	dedicator of cytokinesis 4	0.481	5.6373	7.04209	-1.40479
208467_at	KLF12	Kruppel-like factor 12	0.481	4.48113	5.87745	-1.39632
1553118_at	THEM4	thioesterase superfamily member 4	0.481	4.16512	5.55257	-1.38745
233647_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	0.481	6.17475	7.55392	-1.37917
229844_at	---	---	0.481	5.20356	6.58078	-1.37722
234196_at	---	---	0.481	5.8462	7.21734	-1.37114
227261_at	KLF12	Kruppel-like factor 12	0.481	4.06982	5.42577	-1.35595
1559410_at	---	---	0.481	4.15012	5.45309	-1.30297
204197_s_at	RUNX3	runt-related transcription factor 3	0.481	6.13293	7.42497	-1.29204
226991_at	NFATC2	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-de	0.481	6.26627	7.55749	-1.29122

239045_at	---	---	0.481	7.59703	8.85179	-1.25476
1563259_at	---	---	0.481	5.11778	6.35405	-1.23627
229470_at	---	---	0.481	5.82124	7.05111	-1.22987
243182_at	---	---	0.481	6.45715	7.68312	-1.22597
202479_s_at	TRIB2	tribbles homolog 2 (Drosophila)	0.481	5.51418	6.7284	-1.21422
1554250_s_at	TRIM73	tripartite motif-containing 73	0.481	2.60226	3.8	-1.19774
202524_s_at	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan	0.481	6.91344	8.11024	-1.1968
222667_s_at	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	0.481	6.34638	7.54087	-1.19449
226124_at	ZFP90	zinc finger protein 90 homolog (mouse)	0.481	3.26766	4.3818	-1.11414
1568665_at	RNF103	ring finger protein 103	0.481	4.47391	5.57813	-1.10422
204156_at	KIAA0999	KIAA0999 protein	0.481	8.08311	9.17933	-1.09622
37590_g_at	---	---	0.481	5.9834	7.06345	-1.08005
212368_at	ZNF292	zinc finger protein 292	0.481	7.23764	8.30527	-1.06763
1557370_s_at	MYCBP2	MYC binding protein 2	0.481	6.184	7.23157	-1.04757
214686_at	ZNF266	zinc finger protein 266	0.481	5.96535	6.9999	-1.03455
239923_at	---	---	0.481	6.96814	7.98569	-1.01755
235813_at	---	---	0.481	2.6526	3.66881	-1.01621
202201_at	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.481	7.22483	6.21622	1.00861
212192_at	KCTD12	potassium channel tetramerisation domain containing 12	0.481	8.84778	7.82149	1.02629
223649_s_at	SLC25A39	solute carrier family 25, member 39	0.481	5.90113	4.87427	1.02686
225651_at	UBE2E2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	0.481	5.6007	4.55762	1.04308
235885_at	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	0.481	3.71898	2.65788	1.0611
201125_s_at	ITGB5	integrin, beta 5	0.481	6.03581	4.96494	1.07087
212188_at	KCTD12	potassium channel tetramerisation domain containing 12	0.481	9.80269	8.66702	1.13567
1562007_at	---	---	0.481	7.70999	6.55832	1.15167
205967_at	HIST1H4C	histone cluster 1, H4c	0.481	8.7901	7.60105	1.18905
203432_at	TMPO	thymopoietin	0.481	5.11566	3.86967	1.24599
229830_at	---	---	0.481	6.28005	5.02468	1.25537
211732_x_at	HNMT	histamine N-methyltransferase	0.481	7.0013	5.72886	1.27244
213792_s_at	INSR	insulin receptor	0.481	7.15155	5.83231	1.31924
209772_s_at	CD24	CD24 molecule	0.481	7.60746	6.27996	1.3275
224598_at	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosam	0.481	6.00075	4.67062	1.33013
208553_at	HIST1H1E	histone cluster 1, H1e	0.481	8.97644	7.58137	1.39507
205557_at	BPI	bactericidal/permeability-increasing protein	0.481	7.48709	5.98459	1.5025
215049_x_at	CD163	CD163 molecule	0.481	7.86059	6.28755	1.57304
204838_s_at	MLH3	mutL homolog 3 (E. coli)	0.481	7.68486	5.96791	1.71695
205859_at	LY86	lymphocyte antigen 86	0.481	5.7691	4.03583	1.73327
1554892_a_at	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hem	0.481	6.10458	4.22435	1.88023
205653_at	CTSG	cathepsin G	0.481	8.24895	6.10518	2.14377
235102_x_at	---	---	0.483	9.17045	7.36513	1.80532
243857_at	MORF4L2	Mortality factor 4 like 2	0.483	3.67383	5.10558	-1.43175
205934_at	PLCL1	phospholipase C-like 1	0.483	4.31198	5.33937	-1.02739
205987_at	CD1C	CD1c molecule	0.484	6.03808	4.64374	1.39434
242143_at	---	---	0.487	3.37474	4.6914	-1.31666
203716_s_at	DPP4	dipeptidyl-peptidase 4	0.489	4.62117	6.15573	-1.53456
239555_at	---	---	0.489	7.44463	8.45092	-1.00629
204777_s_at	MAL	mal, T-cell differentiation protein	0.489	4.92148	6.43858	-1.5171
214771_x_at	MPRIP	myosin phosphatase Rho interacting protein	0.490	5.81751	6.88402	-1.06651
240144_at	DNASE1	deoxyribonuclease I	0.490	5.36241	6.40529	-1.04288
202768_at	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	0.491	9.28446	11.1907	-1.90624
239453_at	---	---	0.491	5.81663	7.39482	-1.57819
205831_at	CD2	CD2 molecule	0.491	4.81721	6.29959	-1.48238
230383_x_at	---	---	0.491	5.22792	6.6665	-1.43858
1558972_s_at	TSEPA	thymocyte selection pathway associated	0.491	2.58246	3.96665	-1.38419
213294_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	0.491	5.36309	6.74044	-1.37735
226272_at	RCAN3	RCAN family member 3	0.491	4.09517	5.399	-1.30383
239131_at	---	---	0.491	4.23124	5.51857	-1.28733
1557799_at	C11orf31	chromosome 11 open reading frame 31	0.491	5.81864	7.10361	-1.28497
236293_at	---	---	0.491	4.35455	5.6279	-1.27335
222326_at	---	---	0.491	7.50495	8.77574	-1.27079
1562962_at	---	---	0.491	4.5036	5.7569	-1.2533
238430_x_at	SLFN5	schlafen family member 5	0.491	7.7927	9.01606	-1.22336
231495_at	---	---	0.491	3.49964	4.72119	-1.22155
1556698_a_at	GPRIN3	GPRIN family member 3	0.491	3.95144	5.1664	-1.21496
231292_at	EID3	EP300 interacting inhibitor of differentiation 3	0.491	4.69311	5.89579	-1.20268

209570_s_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequ	0.491	5.32042	6.52008	-1.19966
212079_s_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homo	0.491	4.80294	5.96969	-1.16675
244796_at	---	---	0.491	6.4823	7.58173	-1.09943
205171_at	PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakary	0.491	4.14905	5.23961	-1.09056
221618_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-ass	0.491	7.36832	8.44639	-1.07807
238076_at	GATAD2B	GATA zinc finger domain containing 2B	0.491	4.57916	5.64276	-1.0636
230888_at	WDR91	WD repeat domain 91	0.491	4.52613	5.54967	-1.02354
200703_at	DYNLL1	dynein, light chain, LC8-type 1	0.491	8.20256	7.17468	1.02788
48031_r_at	C5orf4	chromosome 5 open reading frame 4	0.491	4.39247	3.18913	1.20334
206655_s_at	GP1BB /// SEPT5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	0.491	7.64763	6.23731	1.41032
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	0.491	8.71709	6.74836	1.96873
209348_s_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (	0.491	4.37681	6.38655	-2.00974
217591_at	SKIL	SKI-like oncogene	0.491	7.75997	9.17926	-1.41929
216550_x_at	ANKRD12	ankyrin repeat domain 12	0.491	8.65198	10.0382	-1.38622
216361_s_at	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	0.491	8.20203	9.55636	-1.35433
230505_at	LOC145474	hypothetical protein LOC145474	0.491	4.07414	5.39715	-1.32301
1552634_a_at	ZNF101	zinc finger protein 101	0.491	5.94659	7.25742	-1.31083
234645_at	---	---	0.491	3.59044	4.79756	-1.20712
240768_x_at	---	---	0.491	4.96098	6.11782	-1.15684
214748_at	N4BP2L2	NEDD4 binding protein 2-like 2	0.491	4.6408	5.72659	-1.08579
229434_at	---	---	0.491	6.05631	7.1407	-1.08439
242875_at	---	---	0.491	7.76054	8.82743	-1.06689
213281_at	JUN	Jun oncogene	0.491	7.8208	8.84482	-1.02402
235263_at	LOC100134711 /// STAG3L	hypothetical protein LOC100134711 /// stromal antigen 3-like	0.491	6.39412	7.40214	-1.00802
225129_at	CPNE2	copine II	0.491	7.54823	6.52839	1.01984
219099_at	C12orf5	chromosome 12 open reading frame 5	0.491	6.15832	5.04158	1.11674
224496_s_at	TMEM107	transmembrane protein 107	0.491	4.75146	3.55438	1.19708
221260_s_at	CSRNP2	cysteine-serine-rich nuclear protein 2	0.491	5.12377	3.89212	1.23165
215047_at	TRIM58	tripartite motif-containing 58	0.491	3.6895	2.42068	1.26882
208601_s_at	TUBB1	tubulin, beta 1	0.491	7.89438	6.60077	1.29361
219872_at	C4orf18	chromosome 4 open reading frame 18	0.491	5.88527	4.44688	1.43839
200602_at	APP	amyloid beta (A4) precursor protein	0.491	8.03809	6.57952	1.45857
205076_s_at	MTMR11	myotubularin related protein 11	0.491	6.64816	4.91162	1.73654
219607_s_at	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	0.491	4.40373	2.42243	1.9813
1553280_at	PUS10	pseudouridylate synthase 10	0.492	5.46915	6.49849	-1.02934
233694_at	HSPA1L	Heat shock 70kDa protein 1-like	0.492	6.40318	5.33521	1.06797
231199_at	---	---	0.493	3.41429	4.62528	-1.21099
219321_at	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily m	0.493	5.00381	6.39324	-1.38943
1559121_s_at	ARIH2	Ariadne homolog 2 (Drosophila)	0.493	3.63414	4.88618	-1.25204
210321_at	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	0.494	6.20239	7.85702	-1.65463
215889_at	SKIL	SKI-like oncogene	0.494	8.15089	9.59404	-1.44315
241020_at	---	---	0.494	4.86912	6.23297	-1.36385
204731_at	TGFBR3	transforming growth factor, beta receptor III	0.494	4.08643	5.40501	-1.31858
209189_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	0.494	9.70754	10.9043	-1.19676
239960_x_at	LYRM7	Lyrm7 homolog (mouse)	0.494	5.47813	6.62746	-1.14933
207351_s_at	SH2D2A	SH2 domain protein 2A	0.494	4.56821	5.67828	-1.11007
233564_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	0.494	6.62989	7.71681	-1.08692
243842_at	---	---	0.494	4.93739	6.01302	-1.07563
225314_at	OCIAD2	OCIA domain containing 2	0.494	5.33281	6.38542	-1.05261
239163_at	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.494	7.67614	8.6963	-1.02016
226480_at	---	---	0.494	4.25927	5.26551	-1.00624
1569238_a_at	---	---	0.494	4.19252	5.19295	-1.00043
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	0.494	4.23463	3.20948	1.02515
231672_at	CES4	Carboxylesterase 4-like	0.494	6.05612	5.02061	1.03551
230740_at	---	---	0.494	6.96488	5.90246	1.06242
37966_at	PARVB	parvin, beta	0.494	5.5679	4.41834	1.14956
207808_s_at	PROS1	protein S (alpha)	0.494	6.3089	5.11185	1.19705
208690_s_at	PDLIM1	PDZ and LIM domain 1	0.494	7.55483	6.35426	1.20057
204081_at	NRGN	neurogranin (protein kinase C substrate, RC3)	0.494	7.49808	6.22423	1.27385
204110_at	HNMT	histamine N-methyltransferase	0.494	5.39108	4.03474	1.35634
201163_s_at	IGFBP7	insulin-like growth factor binding protein 7	0.494	7.10961	5.75029	1.35932
212460_at	C14orf147	chromosome 14 open reading frame 147	0.494	4.93751	3.56304	1.37447
205307_s_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.494	5.39981	3.7909	1.60891
203949_at	MPO	myeloperoxidase	0.494	7.58669	5.95688	1.62981
207269_at	DEFA4	defensin, alpha 4, corticostatin	0.494	8.76718	6.53813	2.22905

241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	0.494	2.29982	3.30113	-1.00131
205291_at	IL2RB	interleukin 2 receptor, beta	0.495	5.79676	7.52367	-1.72691
201103_x_at	NBPF10 /// NBPF12 /// NB	neuroblastoma breakpoint family, member 10 /// neuroblastc	0.495	8.88519	9.96016	-1.07497
211842_s_at	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchange	0.496	5.15633	7.12972	-1.97339
234326_at	---	---	0.496	7.29181	8.91696	-1.62515
235500_at	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	0.496	4.43199	5.88765	-1.45566
203589_s_at	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	0.496	4.39219	5.80182	-1.40963
202933_s_at	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	0.496	5.00068	6.40783	-1.40715
214923_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	0.496	5.7608	7.13131	-1.37051
1558877_at	---	---	0.496	4.93543	6.24192	-1.30649
235567_at	RORA	RAR-related orphan receptor A	0.496	6.04251	7.27481	-1.2323
1557519_at	---	---	0.496	6.19744	7.35322	-1.15578
213376_at	ZBTB1	zinc finger and BTB domain containing 1	0.496	6.95128	8.06789	-1.11661
232174_at	---	---	0.496	4.76616	5.87507	-1.10891
222122_s_at	THOC2	THO complex 2	0.496	5.59547	6.67786	-1.08239
237488_at	---	---	0.496	6.73592	7.81282	-1.0769
1565888_at	---	---	0.496	5.48354	6.53416	-1.05062
239296_at	---	---	0.496	5.63042	6.66422	-1.0338
232943_at	---	---	0.496	4.01996	5.03121	-1.01125
220254_at	LRP12	low density lipoprotein-related protein 12	0.496	4.65111	3.63804	1.01307
201004_at	SSR4	signal sequence receptor, delta (translocon-associated protei	0.496	8.16422	7.15101	1.01321
213705_at	---	---	0.496	8.81624	7.61848	1.19776
201105_at	LGALS1	lectin, galactoside-binding, soluble, 1	0.496	8.46497	7.21583	1.24914
201058_s_at	MYL9	myosin, light chain 9, regulatory	0.496	8.12437	6.82082	1.30355
210244_at	CAMP	cathelicidin antimicrobial peptide	0.496	9.64942	8.3086	1.34082
228195_at	C2orf88	chromosome 2 open reading frame 88	0.496	6.4496	5.04159	1.40801
229778_at	C12orf39	chromosome 12 open reading frame 39	0.496	5.39544	3.65311	1.74233
202436_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.496	7.38651	5.57042	1.81609
1555829_at	FAM62B	family with sequence similarity 62 (C2 domain containing) me	0.496	3.36953	5.12718	-1.75765
228370_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	0.497	4.09631	5.66978	-1.57347
212599_at	AUTS2	autism susceptibility candidate 2	0.498	3.86801	5.64851	-1.7805
240013_at	---	---	0.498	6.18737	7.71919	-1.53182
233284_at	---	---	0.498	5.63184	6.9621	-1.33026
1565889_at	---	---	0.498	5.12816	6.37062	-1.24246
229447_x_at	NBPF10 /// NBPF11 /// NB	neuroblastoma breakpoint family, member 10 /// neuroblastc	0.498	7.1552	8.29199	-1.13679
1567303_at	---	---	0.498	4.93429	6.01823	-1.08394
235716_at	---	---	0.498	6.02495	7.06379	-1.03884
232001_at	LOC439949	hypothetical protein LOC439949	0.499	5.01352	7.17608	-2.16256
213193_x_at	TRBC1	T cell receptor beta constant 1	0.499	6.49036	8.60504	-2.11468
212402_at	ZC3H13	zinc finger CCCH-type containing 13	0.499	5.55511	7.04508	-1.48997
1556783_a_at	---	---	0.499	3.92094	5.33659	-1.41565
1554036_at	ZBTB24	zinc finger and BTB domain containing 24	0.499	6.10896	7.47002	-1.36106
201027_s_at	EIF5B	eukaryotic translation initiation factor 5B	0.499	5.55644	6.85349	-1.29705
1567304_at	---	---	0.499	4.72483	5.95019	-1.22536
201104_x_at	NBPF10 /// NBPF11 /// NB	neuroblastoma breakpoint family, member 10 /// neuroblastc	0.499	6.87961	8.07847	-1.19886
213612_x_at	NBPF10 /// NBPF12 /// NB	neuroblastoma breakpoint family, member 10 /// neuroblastc	0.499	8.77707	9.91725	-1.14018
205376_at	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	0.499	2.87866	4.01796	-1.1393
215378_at	---	---	0.499	6.48095	7.59921	-1.11826
224833_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.499	8.20578	9.31993	-1.11415
1560706_at	---	---	0.499	6.6898	7.80214	-1.11234
216563_at	ANKRD12	Ankyrin repeat domain 12	0.499	10.1577	11.2488	-1.0911
204835_at	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	0.499	4.10421	5.1805	-1.07629
1555355_a_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.499	7.83225	8.90031	-1.06806
232835_at	---	---	0.499	7.05397	8.11107	-1.0571
1570021_at	---	---	0.499	3.32692	4.37707	-1.05015
241289_at	---	---	0.499	3.65044	4.70001	-1.04957
238987_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypept	0.499	6.05027	7.08873	-1.03846
218554_s_at	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	0.499	7.72869	8.76292	-1.03423
1554287_at	TRIM4	tripartite motif-containing 4	0.499	6.6579	7.68103	-1.02313
1557718_at	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	0.499	4.82274	5.83334	-1.0106
215524_x_at	TRA@ /// TRAC /// TRAJ17	T cell receptor alpha locus /// T cell receptor alpha constant //	0.499	4.29834	5.30524	-1.0069
235959_at	---	---	0.499	4.42055	5.42413	-1.00358
215000_s_at	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	0.499	8.6003	7.58368	1.01662
229618_at	SNX16	sorting nexin 16	0.499	5.66257	4.63701	1.02556
226936_at	C6orf173	chromosome 6 open reading frame 173	0.499	5.35187	4.25727	1.0946

204069_at	MEIS1	Meis homeobox 1	0.499	3.93143	2.82295	1.10848
207156_at	HIST1H2AG	histone cluster 1, H2ag	0.499	5.2865	4.12826	1.15824
224374_s_at	EMILIN2	elastin microfibril interfacer 2	0.499	8.68176	7.51269	1.16907
204037_at	LPAR1	lysophosphatidic acid receptor 1	0.499	8.00269	6.81781	1.18488
206871_at	ELANE	elastase, neutrophil expressed	0.499	4.53052	3.31291	1.21761
208576_s_at	HIST1H3B	histone cluster 1, H3b	0.499	6.12636	4.90273	1.22363
208791_at	CLU	clusterin	0.499	7.37414	6.14418	1.22996
214516_at	HIST1H4B	histone cluster 1, H4b	0.499	8.07614	6.79632	1.27982
227432_s_at	---	---	0.499	7.041	5.70413	1.33687
204364_s_at	REEP1	receptor accessory protein 1	0.499	4.01187	2.6702	1.34167
1555680_a_at	SMOX	spermine oxidase	0.499	6.73894	5.36692	1.37202
202437_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.499	5.5241	3.8707	1.6534
204620_s_at	VCAN	versican	0.499	7.18302	5.42046	1.76256
211745_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.499	11.431	9.57573	1.85527
204018_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.499	11.0736	9.20617	1.86743
217414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.499	11.0402	9.07442	1.96578
218986_s_at	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0.499	5.52518	6.57773	-1.05255
209458_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.499	11.3504	9.41893	1.93147
211324_s_at	RGPD5 /// RGPD7	RANBP2-like and GRIP domain containing 5 /// RANBP2-like ar	0.500	4.18482	5.20391	-1.01909
206390_x_at	PF4	platelet factor 4	0.500	10.0466	8.51672	1.52988
201853_s_at	CDC25B	cell division cycle 25 homolog B (S. pombe)	0.500	5.95218	7.05965	-1.10747
1564052_at	TREML4	triggering receptor expressed on myeloid cells-like 4	0.501	6.91496	8.30516	-1.3902
224685_at	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homo	0.501	4.77748	5.90177	-1.12429
223625_at	FAM126A	family with sequence similarity 126, member A	0.501	4.82643	3.78453	1.0419
1557071_s_at	NUB1	negative regulator of ubiquitin-like proteins 1	0.502	6.12725	7.6056	-1.47835
203717_at	DPP4	dipeptidyl-peptidase 4	0.502	3.23602	4.50413	-1.26811
211699_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.502	11.0232	9.07795	1.94525
201084_s_at	BCLAF1	BCL2-associated transcription factor 1	0.503	7.31042	8.34374	-1.03332
201731_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.503	7.40454	8.76856	-1.36402
240499_at	---	---	0.503	3.93889	5.06186	-1.12297
219208_at	FBXO11	F-box protein 11	0.503	5.10942	6.11212	-1.0027
231721_at	JAM3	junctional adhesion molecule 3	0.503	5.29509	3.98365	1.31144
203680_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	0.503	5.50274	4.03395	1.46879
234255_at	---	---	0.505	7.04699	8.51497	-1.46798
232125_at	---	---	0.505	4.89043	5.93753	-1.0471
203485_at	RTN1	reticulon 1	0.505	7.72189	6.20979	1.5121
217394_at	---	---	0.505	3.30544	5.04924	-1.7438
210985_s_at	SP100	SP100 nuclear antigen	0.505	6.77837	8.38482	-1.60645
1559507_at	LOC100130357	similar to hCG2038897	0.505	6.53343	8.11591	-1.58248
217147_s_at	TRAT1	T cell receptor associated transmembrane adaptor 1	0.505	2.42388	3.81311	-1.38923
205590_at	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	0.505	6.50456	7.78108	-1.27652
231644_at	---	---	0.505	5.59585	6.74882	-1.15297
238659_at	KIAA0141	KIAA0141	0.505	6.27309	7.28239	-1.0093
213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	0.505	8.87663	7.81941	1.05722
234985_at	LDLRAD3	low density lipoprotein receptor class A domain containing 3	0.505	5.85408	4.58086	1.27322
74694_s_at	LOC100133585 /// RABEP2	similar to RABEP2 protein /// rabaptin, RAB GTPase binding ef	0.505	5.34592	4.28937	1.05655
241652_x_at	---	---	0.505	7.35481	6.09841	1.2564
244415_at	---	---	0.505	6.22579	7.59946	-1.37367
219691_at	SAMD9	sterile alpha motif domain containing 9	0.505	6.70694	7.89461	-1.18767
1555068_at	WNK1	WNK lysine deficient protein kinase 1	0.506	4.03319	5.14247	-1.10928
222794_x_at	MTPAP	mitochondrial poly(A) polymerase	0.506	5.45857	4.4345	1.02407
219505_at	CECR1	cat eye syndrome chromosome region, candidate 1	0.506	8.91324	7.58255	1.33069
243759_at	SFRS15	Splicing factor, arginine/serine-rich 15	0.507	3.81906	5.21629	-1.39723
210915_x_at	TRBC1	T cell receptor beta constant 1	0.507	6.80407	8.64169	-1.83762
1568845_at	---	---	0.507	4.62017	6.00052	-1.38035
244578_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukoc	0.507	6.08765	7.25851	-1.17086
211734_s_at	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypept	0.507	7.49975	5.90068	1.59907
200768_s_at	MAT2A	methionine adenosyltransferase II, alpha	0.508	8.96248	7.93856	1.02392
242405_at	---	---	0.508	5.89838	7.57409	-1.67571
223725_at	C3orf42	chromosome 3 open reading frame 42	0.508	6.70832	8.07749	-1.36917
232784_at	---	---	0.508	4.31439	5.59656	-1.28217
239886_at	---	---	0.508	6.87001	8.14025	-1.27024
206081_at	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchange	0.508	4.45704	5.70457	-1.24753
230023_at	NSUN4	NOL1/NOP2/Sun domain family, member 4	0.508	4.70129	5.90958	-1.20829
231801_at	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-de	0.508	4.85209	6.00164	-1.14955

225221_at	---	---	0.508	6.40137	7.54138	-1.14001
224227_s_at	BDP1	B double prime 1, subunit of RNA polymerase III transcription	0.508	6.38506	7.42354	-1.03848
218354_at	TRAPPC2L	trafficking protein particle complex 2-like	0.508	6.14748	5.14249	1.00499
201416_at	SOX4	SRY (sex determining region Y)-box 4	0.508	6.13355	4.88038	1.25317
203715_at	TBCE	tubulin folding cofactor E	0.508	7.3342	5.84777	1.48643
1556055_at	---	---	0.510	5.82333	7.33639	-1.51306
239245_at	---	---	0.510	4.47556	5.61386	-1.1383
222366_at	---	---	0.510	3.89943	4.99928	-1.09985
225579_at	PQLC3	PQ loop repeat containing 3	0.510	7.11758	5.95697	1.16061
229091_s_at	CCNJ	cyclin J	0.510	6.25391	4.76907	1.48484
223111_x_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	0.511	8.42621	9.7558	-1.32959
220577_at	GVIN1	GTPase, very large interferon inducible 1	0.511	5.25868	6.647	-1.38832
1556352_at	---	---	0.511	5.79964	7.15767	-1.35803
201529_s_at	RPA1	replication protein A1, 70kDa	0.511	6.85073	5.84878	1.00195
206932_at	CH25H	cholesterol 25-hydroxylase	0.511	4.76904	3.09635	1.67269
227038_at	SGMS2	sphingomyelin synthase 2	0.512	3.98284	2.72081	1.26203
221092_at	IKZF3	IKAROS family zinc finger 3 (Aiolos)	0.512	4.26074	5.95847	-1.69773
233496_s_at	CFL2	cofilin 2 (muscle)	0.512	3.84933	5.23116	-1.38183
232587_at	EML4	echinoderm microtubule associated protein like 4	0.512	4.32429	5.6998	-1.37551
230086_at	FNBP1	formin binding protein 1	0.512	6.49924	7.83125	-1.33201
224663_s_at	CFL2	cofilin 2 (muscle)	0.512	3.84099	5.03518	-1.19419
239758_at	---	---	0.512	4.27742	5.42651	-1.14909
234492_at	---	---	0.512	3.94316	5.06027	-1.11711
212980_at	USP34	ubiquitin specific peptidase 34	0.512	5.05674	6.1435	-1.08676
212820_at	DMXL2	Dmx-like 2	0.512	7.40617	8.46114	-1.05497
228613_at	RAB11FIP3	RAB11 family interacting protein 3 (class II)	0.512	3.85381	4.90677	-1.05296
214442_s_at	PIAS2	protein inhibitor of activated STAT, 2	0.512	4.26258	5.30315	-1.04057
201083_s_at	BCLAF1	BCL2-associated transcription factor 1	0.512	6.45869	7.47028	-1.01159
1561211_at	---	---	0.512	4.82319	3.70587	1.11732
224983_at	SCARB2	scavenger receptor class B, member 2	0.512	6.69704	5.52047	1.17657
219498_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.512	5.46937	4.23651	1.23286
201890_at	RRM2	ribonucleotide reductase M2 polypeptide	0.512	5.79168	4.49338	1.2983
206110_at	---	---	0.512	8.20484	6.60289	1.60195
214525_x_at	MLH3	mutL homolog 3 (E. coli)	0.512	8.1631	6.51794	1.64516
243361_at	SFRS12	splicing factor, arginine/serine-rich 12	0.512	3.8498	4.98178	-1.13198
231695_at	---	---	0.512	3.832	4.92341	-1.09141
1562468_at	---	---	0.512	7.13269	8.66827	-1.53558
216042_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	0.512	3.67796	4.90933	-1.23137
235597_s_at	RGPD1 /// RGPD2	RANBP2-like and GRIP domain containing 1 /// RANBP2-like ar	0.512	5.77826	6.98059	-1.20233
209839_at	DNM3	dynamin 3	0.512	6.16001	4.98374	1.17627
230014_at	---	---	0.513	7.67351	8.88787	-1.21436
226625_at	TGFBR3	transforming growth factor, beta receptor III	0.513	6.39595	7.56414	-1.16819
234013_at	TRD@	T cell receptor delta locus	0.513	3.96229	5.10703	-1.14474
205790_at	SKAP1	src kinase associated phosphoprotein 1	0.513	5.13192	6.23749	-1.10557
234149_at	---	---	0.513	2.44302	3.54516	-1.10214
223204_at	C4orf18	chromosome 4 open reading frame 18	0.513	5.12354	3.59207	1.53147
235575_at	---	---	0.513	3.74439	4.85452	-1.11013
228617_at	XAF1	XIAP associated factor 1	0.513	6.7428	8.40578	-1.66298
1566446_at	---	---	0.513	2.82189	4.22472	-1.40283
211005_at	LAT /// SPNS1	linker for activation of T cells /// spinster homolog 1 (Drosoph	0.513	7.1684	8.50116	-1.33276
1555225_at	C1orf43	chromosome 1 open reading frame 43	0.513	6.99158	8.17681	-1.18523
228766_at	CD36	CD36 molecule (thrombospondin receptor)	0.513	4.78649	3.26028	1.52621
238183_at	---	---	0.513	7.77556	6.21636	1.5592
1564718_at	---	---	0.514	3.50266	5.01039	-1.50773
229963_at	BEX5	brain expressed, X-linked 5	0.514	3.94573	5.27776	-1.33203
1561129_at	---	---	0.514	2.80238	4.06588	-1.2635
229367_s_at	GIMAP6	GTPase, IMAP family member 6	0.514	4.71646	5.92912	-1.21266
211488_s_at	ITGB8	integrin, beta 8	0.514	4.93057	3.46032	1.47025
212286_at	ANKRD12	ankyrin repeat domain 12	0.514	7.67797	9.20968	-1.53171
205178_s_at	RBBP6	retinoblastoma binding protein 6	0.514	7.29779	8.60938	-1.31159
242029_at	FNDC3B	Fibronectin type III domain containing 3B	0.514	7.26332	8.42186	-1.15854
1570394_at	XRN1	5'-3' exoribonuclease 1	0.514	7.44824	8.54132	-1.09308
204198_s_at	RUNX3	runt-related transcription factor 3	0.514	7.51946	8.59084	-1.07138
223236_at	CCDC55	coiled-coil domain containing 55	0.514	6.50747	7.57399	-1.06652
242182_x_at	---	---	0.514	5.66575	6.72735	-1.0616

202784_s_at	NNT	nicotinamide nucleotide transhydrogenase	0.514	6.8179	5.79942	1.01848
209045_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.514	6.16539	5.0944	1.07099
214509_at	HIST1H3I	histone cluster 1, H3i	0.514	6.96754	5.59169	1.37585
233621_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	0.514	6.3268	4.65337	1.67343
223809_at	RGS18	regulator of G-protein signaling 18	0.514	10.2057	9.18417	1.02153
205033_s_at	DEFA1 /// DEFA3 /// LOC72	defensin, alpha 1 /// defensin, alpha 3, neutrophil-specific ///	0.514	13.0044	11.7449	1.2595
208994_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	0.514	8.73686	9.78769	-1.05083
225775_at	TSPAN33	tetraspanin 33	0.515	8.7802	7.62796	1.15224
225694_at	CRKRS	Cdc2-related kinase, arginine/serine-rich	0.515	7.03812	8.09833	-1.06021
214470_at	KLRB1	killer cell lectin-like receptor subfamily B, member 1	0.517	5.12956	6.68874	-1.55918
205288_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.517	4.59893	5.64361	-1.04468
223106_at	TMEM14C	transmembrane protein 14C	0.517	7.20469	6.18735	1.01734
209778_at	TRIP11	thyroid hormone receptor interactor 11	0.518	5.43859	6.45147	-1.01288
1557049_at	LOC149478	Hypothetical protein LOC149478	0.518	5.73286	7.10359	-1.37073
238480_at	TTC39C	tetratricopeptide repeat domain 39C	0.519	4.71749	6.30441	-1.58692
244433_at	---	---	0.519	4.79493	6.09384	-1.29891
236935_at	---	---	0.520	5.11198	6.19906	-1.08708
205095_s_at	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	0.520	7.28737	6.17526	1.11211
1557450_s_at	WHAMML2	WAS protein homolog associated with actin, golgi membranes	0.520	4.4967	3.27363	1.22307
203413_at	NELL2	NEL-like 2 (chicken)	0.521	3.50805	4.69758	-1.18953
1557797_a_at	---	---	0.521	7.6344	8.89661	-1.26221
1556107_at	---	---	0.521	4.9535	6.07229	-1.11879
242853_at	---	---	0.521	7.06127	8.23662	-1.17535
223117_s_at	USP47	ubiquitin specific peptidase 47	0.521	5.78308	6.91053	-1.12745
1561705_at	---	---	0.521	5.53301	6.63255	-1.09954
229935_s_at	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homo	0.521	4.99699	6.07276	-1.07577
226740_x_at	NBPF1	Neuroblastoma breakpoint family, member 1	0.521	8.8283	9.86751	-1.03921
244299_at	---	---	0.521	7.09056	8.0965	-1.00594
1552277_a_at	C9orf30	chromosome 9 open reading frame 30	0.522	5.64902	4.53578	1.11324
218166_s_at	RSF1	remodeling and spacing factor 1	0.523	5.27838	6.40966	-1.13128
1561813_at	---	---	0.523	4.32377	5.422	-1.09823
217614_at	---	---	0.523	5.59964	6.61566	-1.01602
243969_at	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchange	0.523	5.25897	4.13701	1.12196
211571_s_at	VCAN	versican	0.523	8.50202	7.09297	1.40905
238604_at	---	---	0.523	4.59393	6.14987	-1.55594
208792_s_at	CLU	clusterin	0.523	7.7652	6.70578	1.05942
226603_at	SAMD9L	sterile alpha motif domain containing 9-like	0.523	7.05167	8.1673	-1.11563
235457_at	MAML2	mastermind-like 2 (Drosophila)	0.523	4.56795	5.62854	-1.06059
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	0.523	5.75518	4.3357	1.41948
211796_s_at	TRBC1 /// TRBC2	T cell receptor beta constant 1 /// T cell receptor beta consta	0.524	7.8627	9.72647	-1.86377
224367_at	BEX2	brain expressed X-linked 2	0.524	4.52041	5.86968	-1.34927
205821_at	KLRK1	killer cell lectin-like receptor subfamily K, member 1	0.524	4.95917	6.21813	-1.25896
214059_at	IFI44	Interferon-induced protein 44	0.524	3.50131	4.7368	-1.23549
214670_at	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	0.524	5.09767	6.29324	-1.19557
212672_at	ATM	ataxia telangiectasia mutated	0.524	6.12784	7.29479	-1.16695
1559362_at	---	---	0.524	3.66564	4.8147	-1.14906
1556597_a_at	LOC284513	hypothetical protein LOC284513	0.524	5.27771	6.42259	-1.14488
1554037_a_at	ZBTB24	zinc finger and BTB domain containing 24	0.524	6.05146	7.16418	-1.11272
225522_at	AAK1	AP2 associated kinase 1	0.524	7.7506	8.85113	-1.10053
239668_at	---	---	0.524	6.43419	7.53276	-1.09857
209815_at	PTCH1	patched homolog 1 (Drosophila)	0.524	3.38858	4.449	-1.06042
244811_at	PHIP	pleckstrin homology domain interacting protein	0.524	4.76929	5.82949	-1.0602
1557384_at	ZNF131	Zinc finger protein 131	0.524	5.25006	6.27358	-1.02352
238490_at	KIAA2026	KIAA2026	0.524	5.46531	6.48833	-1.02302
229871_at	SAMD4B	sterile alpha motif domain containing 4B	0.524	3.68706	4.70915	-1.02209
238774_at	---	---	0.524	2.98887	3.99345	-1.00458
226662_at	STX17	syntaxin 17	0.524	5.30786	6.30845	-1.00059
209266_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	0.524	5.55967	4.53131	1.02836
201251_at	PKM2	pyruvate kinase, muscle	0.524	8.8268	7.77037	1.05643
1566472_s_at	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.524	5.13087	4.03383	1.09704
228042_at	ADPRH	ADP-ribosylarginine hydrolase	0.524	7.85049	6.67868	1.17181
1553702_at	ZNF697	zinc finger protein 697	0.524	7.20664	5.81861	1.38803
206851_at	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	0.524	7.23765	5.77682	1.46083
235295_at	---	---	0.524	5.57965	4.06088	1.51877
217216_x_at	MLH3	mutL homolog 3 (E. coli)	0.524	8.00407	6.35791	1.64616

208450_at	LGALS2	lectin, galactoside-binding, soluble, 2	0.524	8.46087	6.7893	1.67157
223343_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	0.524	6.3596	4.10843	2.25117
228495_at	CCDC75	coiled-coil domain containing 75	0.524	4.46162	5.68542	-1.2238
218666_s_at	STX17	syntaxin 17	0.524	5.79647	6.95194	-1.15547
215435_at	---	---	0.524	4.42659	5.57682	-1.15023
1557811_a_at	---	---	0.524	4.44791	5.50819	-1.06028
237949_at	---	---	0.524	6.31397	7.37113	-1.05716
240052_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	0.524	3.3886	4.40065	-1.01205
218332_at	BEX1	brain expressed, X-linked 1	0.524	7.26715	5.95698	1.31017
207017_at	RAB27B	RAB27B, member RAS oncogene family	0.524	7.98247	6.65503	1.32744
204619_s_at	VCAN	versican	0.524	5.77991	4.43407	1.34584
207815_at	PF4V1	platelet factor 4 variant 1	0.524	6.35767	4.65142	1.70625
1553626_a_at	C17orf57	chromosome 17 open reading frame 57	0.525	8.1193	6.40445	1.71485
224579_at	SLC38A1	solute carrier family 38, member 1	0.525	6.74177	8.02588	-1.28411
64064_at	GIMAP5	GTPase, IMAP family member 5	0.525	6.75367	7.84957	-1.0959
243469_at	---	---	0.525	5.86486	6.90444	-1.03958
235376_at	---	---	0.525	8.04421	9.07947	-1.03526
215193_x_at	HLA-DRB1 /// HLA-DRB3 //	major histocompatibility complex, class II, DR beta 1 /// major	0.525	9.9209	8.63976	1.28114
213957_s_at	CEP350	centrosomal protein 350kDa	0.526	5.36524	6.67364	-1.3084
235777_at	ANKRD44	ankyrin repeat domain 44	0.526	5.37947	6.64655	-1.26708
228611_s_at	---	---	0.526	5.38941	6.44435	-1.05494
209555_s_at	CD36	CD36 molecule (thrombospondin receptor)	0.526	7.00412	5.09412	1.91
240928_at	FCF1	FCF1 small subunit (SSU) processome component homolog (S.	0.527	4.28683	5.32095	-1.03412
223548_at	C1orf26	chromosome 1 open reading frame 26	0.527	5.97205	7.02557	-1.05352
234574_at	---	---	0.528	5.68799	7.02654	-1.33855
211828_s_at	TNIK	TRAF2 and NCK interacting kinase	0.528	3.8448	4.94404	-1.09924
1560758_at	---	---	0.528	4.90814	3.63959	1.26855
223777_at	MGC13005	hypothetical LOC84771	0.528	5.74113	4.44904	1.29209
1555689_at	CD80	CD80 molecule	0.528	3.87485	2.4274	1.44745
202820_at	AHR	aryl hydrocarbon receptor	0.528	6.72153	5.54133	1.1802
212783_at	RBBP6	retinoblastoma binding protein 6	0.528	6.96938	8.14737	-1.17799
243954_at	LOC285286	hypothetical protein LOC285286	0.528	3.93153	4.94433	-1.0128
219864_s_at	RCAN3	RCAN family member 3	0.529	5.94692	7.78423	-1.83731
243499_at	---	---	0.529	3.66354	4.81915	-1.15561
214560_at	FPR3	formyl peptide receptor 3	0.529	5.24372	4.19128	1.05244
217478_s_at	HLA-DMA	major histocompatibility complex, class II, DM alpha	0.529	7.26118	6.07727	1.18391
221731_x_at	VCAN	versican	0.529	7.17464	5.45627	1.71837
241786_at	---	---	0.529	5.71838	7.14362	-1.42524
203582_s_at	RAB4A	RAB4A, member RAS oncogene family	0.530	7.30739	6.21648	1.09091
209301_at	CA2	carbonic anhydrase II	0.530	7.21073	6.19473	1.016
231791_at	ASAH2B	N-acylsphingosine amidohydrolase (non-lysosomal ceramidas	0.531	3.43224	5.00699	-1.57475
218027_at	MRPL15	mitochondrial ribosomal protein L15	0.531	4.89414	3.68665	1.20749
242904_x_at	---	---	0.532	7.78267	9.02989	-1.24722
31874_at	GAS2L1	growth arrest-specific 2 like 1	0.532	5.61568	4.46212	1.15356
214808_at	---	---	0.532	7.52948	8.81459	-1.28511
242106_at	---	---	0.532	4.24799	5.47756	-1.22957
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.532	6.30955	7.52165	-1.2121
214673_s_at	HUWE1	HECT, UBA and WWE domain containing 1	0.532	6.57854	7.67756	-1.09902
1558515_at	---	---	0.532	5.21542	6.29844	-1.08302
209312_x_at	HLA-DRB1 /// HLA-DRB4 //	major histocompatibility complex, class II, DR beta 1 /// major	0.532	10.7393	9.52391	1.21539
201121_s_at	PGRMC1	progesterone receptor membrane component 1	0.533	9.68218	8.6043	1.07788
1555691_a_at	KLRK1	killer cell lectin-like receptor subfamily K, member 1	0.534	6.85612	8.65509	-1.79897
223717_s_at	ACRBP	acrosin binding protein	0.534	8.85827	7.59167	1.2666
207802_at	CRISP3	cysteine-rich secretory protein 3	0.535	7.25529	6.2214	1.03389
239835_at	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0.535	5.46891	4.37918	1.08973
200762_at	DPYSL2	dihydropyrimidinase-like 2	0.535	8.36305	7.18611	1.17694
203685_at	BCL2	B-cell CLL/lymphoma 2	0.536	4.37623	5.98387	-1.60764
219777_at	GIMAP6	GTPase, IMAP family member 6	0.536	5.14668	6.27776	-1.13108
210948_s_at	LEF1	lymphoid enhancer-binding factor 1	0.536	3.4338	4.45411	-1.02031
244235_at	IVNS1ABP	influenza virus NS1A binding protein	0.536	8.29274	9.49448	-1.20174
218370_s_at	S100PBP	S100P binding protein	0.536	4.55263	5.62406	-1.07143
202478_at	TRIB2	tribbles homolog 2 (Drosophila)	0.538	5.48698	6.51942	-1.03244
1570552_at	C18orf50	chromosome 18 open reading frame 50	0.539	5.67316	7.06056	-1.3874
205488_at	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated s	0.539	7.5568	8.93701	-1.38021
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.539	5.10163	6.35976	-1.25813

208073_x_at	TTC3	tetratricopeptide repeat domain 3	0.539	5.46064	6.70238	-1.24174
216226_at	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-ass	0.539	3.78724	4.9701	-1.18286
1562056_at	---	---	0.539	5.38955	6.52282	-1.13327
1562865_at	---	---	0.539	5.67027	6.70405	-1.03378
216022_at	---	---	0.539	4.3276	5.33098	-1.00338
1563327_a_at	CXorf31	chromosome X open reading frame 31	0.539	5.17931	6.18253	-1.00322
1555409_a_at	BAGE2 /// BAGE3 /// BAGE	B melanoma antigen family, member 2 /// B melanoma antige	0.539	5.35684	6.35771	-1.00087
230833_at	ACRBP	acrosin binding protein	0.539	7.5419	6.442	1.0999
213566_at	RNASE6	ribonuclease, RNase A family, k6	0.539	9.42561	8.3123	1.11331
234759_at	---	---	0.540	4.12391	5.16902	-1.04511
220657_at	KLHL11	kelch-like 11 (Drosophila)	0.540	5.1778	6.18943	-1.01163
200965_s_at	ABLIM1	actin binding LIM protein 1	0.540	6.1511	7.54814	-1.39704
227565_at	---	---	0.540	5.65907	6.99986	-1.34079
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.540	6.32582	7.63591	-1.31009
203948_s_at	MPO	myeloperoxidase	0.542	4.96599	3.7671	1.19889
213524_s_at	G0S2	G0/G1switch 2	0.542	11.663	12.9464	-1.2834
228962_at	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3	0.542	4.69905	6.06073	-1.36168
226040_at	---	---	0.542	5.43029	6.80731	-1.37702
1565656_x_at	---	---	0.542	4.2834	5.42338	-1.13998
1553681_a_at	PRF1	perforin 1 (pore forming protein)	0.542	5.65095	6.78193	-1.13098
201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.543	9.44692	7.98653	1.46039
235957_at	GRIP1	glutamate receptor interacting protein 1	0.543	5.20115	6.21153	-1.01038
215621_s_at	IGHD	immunoglobulin heavy constant delta	0.544	5.27468	4.10558	1.1691
211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.544	8.35458	6.96091	1.39367
212998_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.544	9.60504	8.36446	1.24058
209795_at	CD69	CD69 molecule	0.545	8.04224	10.2548	-2.21256
1564932_at	---	---	0.546	5.373	6.37568	-1.00268
211654_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.546	8.35218	7.33964	1.01254
238762_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ depender	0.546	6.01281	4.76003	1.25278
1556003_a_at	---	---	0.548	4.25162	5.3471	-1.09548
1558569_at	UNQ6228	Hypothetical LOC100131541	0.548	6.37265	7.81698	-1.44433
233393_at	---	---	0.548	4.95349	5.96825	-1.01476
222451_s_at	ZDHHC9	zinc finger, DHHC-type containing 9	0.548	4.34845	5.3537	-1.00525
226725_at	---	---	0.549	5.52892	7.02651	-1.49759
240951_at	RORA	RAR-related orphan receptor A	0.549	3.69895	4.95112	-1.25217
1552318_at	GIMAP1	GTPase, IMAP family member 1	0.550	4.53267	5.93185	-1.39918
215886_x_at	USP12	ubiquitin specific peptidase 12	0.550	7.84633	6.76809	1.07824
241133_at	TRBV27	T cell receptor beta variable 27	0.550	5.94907	4.76942	1.17965
226218_at	IL7R	interleukin 7 receptor	0.551	7.26983	8.82544	-1.55561
202724_s_at	FOXO1	forkhead box O1	0.551	8.11613	9.23752	-1.12139
233078_at	API5	apoptosis inhibitor 5	0.551	4.21439	5.32497	-1.11058
242475_at	---	---	0.551	7.53323	8.56412	-1.03089
214349_at	---	---	0.551	8.99986	7.65476	1.3451
240481_at	---	---	0.551	4.82731	5.95623	-1.12892
224681_at	GNA12	guanine nucleotide binding protein (G protein) alpha 12	0.553	6.09817	4.84593	1.25224
203157_s_at	GLS	glutaminase	0.553	5.96205	6.98772	-1.02567
1570567_at	---	---	0.553	3.16671	4.30437	-1.13766
241855_s_at	---	---	0.553	4.49357	5.50407	-1.0105
222877_at	---	---	0.553	4.52855	3.50482	1.02373
203305_at	F13A1	coagulation factor XIII, A1 polypeptide	0.554	7.80995	6.64341	1.16654
1557675_at	RAF1	V-raf-1 murine leukemia viral oncogene homolog 1	0.554	6.38059	7.389	-1.00841
205249_at	EGR2	early growth response 2	0.555	7.67289	8.90611	-1.23322
240231_at	---	---	0.556	4.07886	5.30154	-1.22268
209337_at	PSIP1	PC4 and SFRS1 interacting protein 1	0.556	6.29536	7.38917	-1.09381
206331_at	CALCRL	calcitonin receptor-like	0.556	3.66659	2.63954	1.02705
211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	0.557	5.98523	4.62243	1.3628
242607_at	---	---	0.559	6.51471	5.50617	1.00854
223344_s_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	0.559	7.05747	5.32841	1.72906
203893_at	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-asso	0.559	7.83904	6.71194	1.1271
243841_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.559	6.13891	7.50561	-1.3667
1557418_at	---	---	0.559	6.24486	7.48933	-1.24447
228062_at	NAP1L5	nucleosome assembly protein 1-like 5	0.559	3.23929	4.47057	-1.23128
1569020_at	NEDD9	neural precursor cell expressed, developmentally down-regul	0.559	6.45175	7.57169	-1.11994
204373_s_at	CEP350	centrosomal protein 350kDa	0.559	6.22699	7.31351	-1.08652
204466_s_at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	0.559	7.09114	5.84116	1.24998

202710_at	BET1	blocked early in transport 1 homolog (S. cerevisiae)	0.561	6.80705	5.75417	1.05288
202435_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.561	5.42212	4.33226	1.08986
202887_s_at	DDIT4	DNA-damage-inducible transcript 4	0.561	10.6306	12.2272	-1.5966
1554786_at	CASS4	Cas scaffolding protein family member 4	0.562	5.99524	7.36467	-1.36943
203757_s_at	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (n	0.562	5.22844	4.09565	1.13279
241191_at	---	---	0.563	5.69362	6.92477	-1.23115
213534_s_at	PASK	PAS domain containing serine/threonine kinase	0.564	4.65518	5.89937	-1.24419
241462_at	---	---	0.564	6.80032	5.52153	1.27879
213275_x_at	CTSB	cathepsin B	0.565	8.34312	7.33005	1.01307
235009_at	BOD1L	biorientation of chromosomes in cell division 1-like	0.567	9.95491	11.138	-1.18309
237119_at	---	---	0.567	4.92691	6.18822	-1.26131
229155_at	---	---	0.567	6.7646	7.94249	-1.17789
223836_at	FGFBP2	fibroblast growth factor binding protein 2	0.567	5.8412	6.90956	-1.06836
1556332_at	---	---	0.567	6.37559	7.44236	-1.06677
239742_at	TULP4	Tubby like protein 4	0.567	4.90158	5.90337	-1.00179
239223_s_at	FBXL20	F-box and leucine-rich repeat protein 20	0.567	7.83316	6.76306	1.0701
218711_s_at	SDPR	serum deprivation response (phosphatidylserine binding prote	0.568	8.64513	7.58639	1.05874
204115_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	0.568	8.42162	7.16461	1.25701
240695_at	---	---	0.568	6.21092	7.21817	-1.00725
237241_at	ECT2	Epithelial cell transforming sequence 2 oncogene	0.568	5.1097	4.05972	1.04998
214414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.568	13.2229	12.0235	1.1994
211323_s_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	0.568	6.41967	7.43776	-1.01809
222062_at	IL27RA	interleukin 27 receptor, alpha	0.570	4.50389	5.53079	-1.0269
33323_r_at	SFN	stratifin	0.570	6.42863	7.97905	-1.55042
218805_at	GIMAP5	GTPase, IMAP family member 5	0.571	6.81712	7.91184	-1.09472
215646_s_at	VCAN	versican	0.571	7.99608	6.38543	1.61065
217232_x_at	HBB	hemoglobin, beta	0.571	13.0313	11.9055	1.1258
226436_at	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	0.571	5.87806	4.74272	1.13534
1552787_at	HELB	helicase (DNA) B	0.572	5.62341	7.06975	-1.44634
209813_x_at	TARP	TCR gamma alternate reading frame protein	0.572	4.79821	5.85658	-1.05837
211597_s_at	HOPX	HOP homeobox	0.572	4.18507	5.25444	-1.06937
1558561_at	HM13	histocompatibility (minor) 13	0.572	4.86852	5.92891	-1.06039
241956_at	---	---	0.573	6.07103	7.08279	-1.01176
228151_at	---	---	0.573	7.20214	6.16752	1.03462
224358_s_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	0.573	7.257	5.43931	1.81769
1559990_at	---	---	0.574	9.03057	10.0328	-1.00223
205686_s_at	CD86	CD86 molecule	0.575	4.81775	3.78021	1.03754
211696_x_at	HBB	hemoglobin, beta	0.575	13.3005	12.2556	1.0449
216191_s_at	TRA@ /// TRD@	T cell receptor alpha locus /// T cell receptor delta locus	0.576	5.60014	7.31019	-1.71005
226254_s_at	KIAA1430	KIAA1430	0.576	4.7232	5.92548	-1.20228
206295_at	IL18	interleukin 18 (interferon-gamma-inducing factor)	0.576	6.29227	5.09081	1.20146
208173_at	IFNB1	interferon, beta 1, fibroblast	0.576	5.24072	3.79549	1.44523
216493_s_at	IGF2BP3 /// LOC645468	insulin-like growth factor 2 mRNA binding protein 3 /// similar	0.576	6.21246	5.16753	1.04493
1568126_at	ANXA2	annexin A2	0.576	4.5728	3.44435	1.12845
213537_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.579	5.82102	4.54553	1.27549
230535_s_at	---	---	0.580	8.22507	7.03068	1.19439
200869_at	RPL18A /// RPL18AP3	ribosomal protein L18a /// ribosomal protein L18a pseudogen	0.581	9.88993	8.83683	1.0531
1554929_at	KIAA0999	KIAA0999 protein	0.582	4.93941	5.95543	-1.01602
1562348_at	LOC400680	hypothetical gene supported by AK097381; BC040866	0.582	4.29482	5.40683	-1.11201
209116_x_at	HBB	hemoglobin, beta	0.582	13.2845	12.2385	1.046
227954_at	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	0.583	6.22338	5.03878	1.1846
1560485_at	HIVEP1	human immunodeficiency virus type I enhancer binding protei	0.583	5.1814	6.40308	-1.22168
219844_at	C10orf118	chromosome 10 open reading frame 118	0.583	6.402	7.482	-1.08
206676_at	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	0.583	8.78688	7.60611	1.18077
228528_at	---	---	0.584	6.14017	7.31371	-1.17354
200790_at	ODC1	ornithine decarboxylase 1	0.584	8.3779	7.33914	1.03876
212768_s_at	OLFM4	olfactomedin 4	0.584	8.26261	6.90867	1.35394
231270_at	CA13	carbonic anhydrase XIII	0.584	5.11158	4.04377	1.06781
205816_at	ITGB8	integrin, beta 8	0.584	4.44953	3.07189	1.37764
244860_at	---	---	0.585	6.03851	7.21865	-1.18014
1552381_at	SRrp35	serine-arginine repressor protein (35 kDa)	0.585	4.30651	5.30818	-1.00167
208775_at	XPO1	exportin 1 (CRM1 homolog, yeast)	0.586	6.22924	7.26111	-1.03187
1563975_at	RNF130	Ring finger protein 130	0.586	5.79527	6.89095	-1.09568
204057_at	IRF8	interferon regulatory factor 8	0.586	8.04219	6.62327	1.41892
230690_at	TUBB1	tubulin, beta 1	0.587	9.09573	8.00261	1.09312

201730_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.588	7.6846	8.85912	-1.17452
1569607_s_at	ANKRD20A1 /// ANKRD20A	ankyrin repeat domain 20 family, member A1 /// ankyrin repe	0.588	3.26035	4.34543	-1.08508
244414_at	---	---	0.588	5.75654	6.83893	-1.08239
243096_at	---	---	0.588	7.7554	8.78905	-1.03365
212651_at	RHOBTB1	Rho-related BTB domain containing 1	0.588	4.4914	3.27662	1.21478
214146_s_at	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	0.588	11.3032	9.98947	1.31373
204926_at	INHBA	inhibin, beta A	0.588	5.48386	3.84492	1.63894
242471_at	---	---	0.588	4.05238	5.27341	-1.22103
239379_at	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	0.588	6.25842	7.35154	-1.09312
215806_x_at	TARP /// TRGC2	TCR gamma alternate reading frame protein /// T cell recepto	0.589	5.67197	6.69934	-1.02737
227195_at	ZNF503	zinc finger protein 503	0.589	6.96961	5.507	1.46261
213515_x_at	HBG1 /// HBG2	hemoglobin, gamma A /// hemoglobin, gamma G	0.589	9.13104	7.99837	1.13267
203810_at	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	0.590	4.41815	3.19758	1.22057
1552694_at	SLC2A13	solute carrier family 2 (facilitated glucose transporter), memb	0.590	4.8214	3.34849	1.47291
215220_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.592	8.2719	9.31924	-1.04734
239288_at	TNIK	TRAF2 and NCK interacting kinase	0.595	6.01974	7.19856	-1.17882
202761_s_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.596	5.33604	6.73535	-1.39931
212531_at	LCN2	lipocalin 2	0.596	9.26844	7.82236	1.44608
215009_s_at	SEC31A	SEC31 homolog A (S. cerevisiae)	0.598	7.52846	8.64824	-1.11978
201939_at	PLK2	polo-like kinase 2 (Drosophila)	0.598	4.66153	5.80213	-1.1406
225327_at	KIAA1370	KIAA1370	0.598	4.98311	6.06859	-1.08548
222392_x_at	PERP	PERP, TP53 apoptosis effector	0.598	4.40203	5.5644	-1.16237
205495_s_at	GNLY	granulysin	0.599	7.41015	8.60404	-1.19389
232379_at	SKIL	SKI-like oncogene	0.599	8.42986	9.6603	-1.23044
234640_x_at	---	---	0.600	5.99473	7.36482	-1.37009
223027_at	SNX9	sorting nexin 9	0.600	5.28852	4.18399	1.10453
214617_at	PRF1	perforin 1 (pore forming protein)	0.601	7.57992	9.07668	-1.49676
212382_at	TCF4	transcription factor 4	0.602	6.60346	5.45949	1.14397
1560109_s_at	---	---	0.602	6.96877	8.09569	-1.12692
1554283_at	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	0.604	7.55667	6.2452	1.31147
233020_at	---	---	0.605	6.01283	7.2786	-1.26577
230970_at	---	---	0.605	4.90519	5.97821	-1.07302
202018_s_at	LTF	lactotransferrin	0.605	10.5535	9.33816	1.21534
231925_at	---	---	0.606	5.38671	4.32959	1.05712
227180_at	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (	0.606	5.39726	4.16046	1.2368
209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.606	3.93427	4.95302	-1.01875
206111_at	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neur	0.606	9.41214	8.28247	1.12967
221211_s_at	C21orf7	chromosome 21 open reading frame 7	0.606	8.80756	7.33315	1.47441
230741_at	---	---	0.607	5.62718	3.9902	1.63698
220646_s_at	KLRF1	killer cell lectin-like receptor subfamily F, member 1	0.608	3.76586	4.83867	-1.07281
231862_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	0.608	6.06057	7.34182	-1.28125
201063_at	RCN1	reticulocalbin 1, EF-hand calcium binding domain	0.609	6.87721	5.83746	1.03975
207018_s_at	RAB27B	RAB27B, member RAS oncogene family	0.609	6.84396	5.70091	1.14305
208146_s_at	CPVL	carboxypeptidase, vitellogenic-like	0.609	8.30459	6.93786	1.36673
219666_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.609	7.10895	5.83586	1.27309
203414_at	MMD	monocyte to macrophage differentiation-associated	0.610	10.2281	9.13402	1.09408
212828_at	SYNJ2	synaptojanin 2	0.611	5.79185	6.80926	-1.01741
37145_at	GNLY	granulysin	0.611	7.34719	8.56363	-1.21644
227792_at	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	0.614	7.10105	5.98763	1.11342
219956_at	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgal	0.615	4.75605	5.77756	-1.02151
228913_at	LOC100190939	hypothetical LOC100190939	0.616	5.1192	3.97336	1.14584
201024_x_at	EIF5B	eukaryotic translation initiation factor 5B	0.619	7.95701	9.1455	-1.18849
231418_at	---	---	0.619	6.40473	5.3934	1.01133
1557261_at	WHAMML1 /// WHAMML	WAS protein homolog associated with actin, golgi membranes	0.619	5.81633	4.73349	1.08284
212671_s_at	HLA-DQA1 /// HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// majo	0.621	9.21944	7.78691	1.43253
243999_at	SLFN5	schlafen family member 5	0.622	6.12012	7.15788	-1.03776
222717_at	SDPR	serum deprivation response (phosphatidylserine binding prot	0.625	7.34929	6.12292	1.22637
215111_s_at	TSC22D1	TSC22 domain family, member 1	0.626	8.12501	7.053	1.07201
211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.626	9.34192	7.96629	1.37563
204626_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.628	8.8836	7.86533	1.01827
230590_at	---	---	0.629	7.1581	8.21002	-1.05192
221802_s_at	KIAA1598	KIAA1598	0.629	5.8271	4.80975	1.01735
206115_at	EGR3	early growth response 3	0.631	8.14794	9.89041	-1.74247
234632_x_at	---	---	0.632	5.74583	7.30876	-1.56293
1561738_at	---	---	0.632	4.97848	6.08048	-1.102

205798_at	IL7R	interleukin 7 receptor	0.632	6.44862	7.75185	-1.30323
217963_s_at	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	0.633	7.88906	6.88498	1.00408
209191_at	TUBB6	tubulin, beta 6	0.633	6.83519	5.49291	1.34228
1557706_at	ZHX2	zinc fingers and homeoboxes 2	0.633	5.17205	6.59868	-1.42663
207630_s_at	CREM	cAMP responsive element modulator	0.633	7.53042	8.66176	-1.13134
233011_at	ANXA1	Annexin A1	0.633	5.07482	4.04985	1.02497
235086_at	THBS1	Thrombospondin 1	0.636	5.43518	6.45509	-1.01991
231688_at	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	0.637	6.95116	5.89947	1.05169
204512_at	HIVEP1	human immunodeficiency virus type I enhancer binding protei	0.638	7.2298	8.38729	-1.15749
207362_at	SLC30A4	solute carrier family 30 (zinc transporter), member 4	0.638	3.45592	4.46603	-1.01011
1568619_s_at	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	0.638	6.40456	5.3653	1.03926
220695_at	---	---	0.638	7.24572	6.04333	1.20239
222449_at	PMEPA1	prostate transmembrane protein, androgen induced 1	0.640	5.41796	6.47172	-1.05376
1558392_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.640	6.18997	7.19694	-1.00697
202704_at	TOB1	transducer of ERBB2, 1	0.642	6.6246	7.64569	-1.02109
1559413_at	TCP11L2	t-complex 11 (mouse)-like 2	0.642	7.67225	8.70099	-1.02874
203023_at	NOP16	NOP16 nucleolar protein homolog (yeast)	0.648	5.03974	4.03445	1.00529
1560636_a_at	---	---	0.648	6.46517	7.47407	-1.0089
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	0.649	6.82397	5.25537	1.5686
210427_x_at	ANXA2	annexin A2	0.651	9.33	8.25886	1.07114
227193_at	---	---	0.652	4.42969	5.5165	-1.08681
231899_at	ZC3H12C	zinc finger CCCH-type containing 12C	0.656	5.14066	3.97541	1.16525
214073_at	CTTN	cortactin	0.657	7.1694	5.87436	1.29504
1552316_a_at	GIMAP1	GTPase, IMAP family member 1	0.658	6.45221	7.55461	-1.1024
213503_x_at	ANXA2	annexin A2	0.662	9.21252	8.20335	1.00917
230499_at	---	---	0.663	7.10145	8.14087	-1.03942
206214_at	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylh	0.666	7.4812	6.21061	1.27059
1553266_at	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	0.666	4.6773	5.71946	-1.04216
235242_at	---	---	0.673	8.22046	9.28139	-1.06093
1568830_at	IRAK3	interleukin-1 receptor-associated kinase 3	0.680	7.30202	8.34095	-1.03893
216020_at	IFIH1	Interferon induced with helicase C domain 1	0.683	6.87649	7.99309	-1.1166
211138_s_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.683	6.32541	4.78262	1.54279
227844_at	FMNL3	formin-like 3	0.683	4.68823	5.69173	-1.0035
234418_x_at	CD44	CD44 molecule (Indian blood group)	0.688	5.55459	6.75826	-1.20367
204385_at	KYNU	kynureninase (L-kynurenine hydrolase)	0.688	7.38849	6.30931	1.07918
210164_at	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated s	0.688	6.17953	7.44289	-1.26336
1569203_at	CXCL2	chemokine (C-X-C motif) ligand 2	0.689	5.62627	4.54138	1.08489
1553055_a_at	SLFN5	schlafen family member 5	0.694	6.28447	7.354	-1.06953
216056_at	CD44	CD44 molecule (Indian blood group)	0.696	7.54872	8.63525	-1.08653
205306_x_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.709	6.85317	5.53343	1.31974
229437_at	MIRHG2	microRNA host gene 2 (non-protein coding)	0.709	4.77885	3.63738	1.14147
204440_at	CD83	CD83 molecule	0.712	8.68549	10.011	-1.32551
227140_at	---	---	0.712	7.39059	6.27168	1.11891
210662_at	KYNU	kynureninase (L-kynurenine hydrolase)	0.715	5.28775	4.27613	1.01162
211122_s_at	CXCL11	chemokine (C-X-C motif) ligand 11	0.718	4.85918	3.6605	1.19868
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	0.726	9.15382	10.2229	-1.06908
214038_at	CCL8	chemokine (C-C motif) ligand 8	0.731	6.05597	4.99083	1.06514
1563118_at	---	---	0.740	7.28538	8.38768	-1.1023
209684_at	RIN2	Ras and Rab interactor 2	0.752	8.2729	7.20286	1.07004