Supplementary table 2

Downregulated transcripts in sarcoid vs control with 1.5-fold change or more and q-value < 5%

Probe Set ID	Gene Symbol	Gene Title	Fold Change	q value (%)
209840_s_at	LRRN3	leucine rich repeat neuronal 3	0.122	0.000
234396_at	---	TCR variable region Va30 subfamily gene (VA30, JA, CA segments), 5' end	0.230	0.000
209841_s_at	LRRN3	leucine rich repeat neuronal 3	0.172	0.000
234013_at	TRA@	T cell receptor alpha locus /// Clone PSA.S.31 T-cell receptor alpha chain	0.412	0.000
231798_at	NOG	Noggin	0.270	0.000
228370_at	---	---	0.414	0.000
205254_x_at	TCF7	transcription factor 7 (T-cell specific, HMG-box)	0.489	0.000
1561363_a_at	---	CDNA FLJ36285 fis, clone THYMU2003470	0.393	0.000
241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	0.446	0.000
204793_at	GPRASP1	G protein-coupled receptor associated sorting protein 1	0.434	0.000
239122_at	---	Transcribed locus	0.523	0.000
216133_at	TRA@	T cell receptor alpha locus	0.481	0.000
238649_at	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	0.579	0.000
214945_at	LOC202134 /// NY-REN-7 /// LOC653316	hypothetical protein LOC202134 /// NY-REN-7 antigen /// hypothetical protein LOC653316	0.328	0.000
221221_s_at	KLHL3	kelch-like 3 (Drosophila)	0.465	0.000
1556402_at	---	CDNA FLJ36234 fis, clone THYMU2001314	0.447	0.000
206150_at	CD27	CD27 molecule /// CD27 molecule	0.542	0.000
209368_at	EPHX2	epoxide hydrolase 2, cytoplasmic	0.399	0.000
203578_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	0.502	0.000
215967_s_at	LY9	lymphocyte antigen 9	0.585	0.000
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	0.493	0.000
242292_at	LOC653687 /// LOC729488	similar to melanoma antigen family B, 18 /// similar to chromosome X open reading frame 50	0.487	0.000
201849_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	0.490	0.116
227449_at	EPHA4	EPH receptor A4	0.447	0.116
1553118_at	THEM4	thioesterase superfamily member 4	0.487	0.116
243735_at	---	CDNA FLJ38461 fis, clone FEBRA2020977	0.543	0.116
212400_at	FAM102A	family with sequence similarity 102, member A	0.532	0.116
210370_s_at	LY9	lymphocyte antigen 9	0.564	0.116
213170_at	GPX7	glutathione peroxidase 7	0.485	0.116
221790_s_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	0.581	0.116
228174_at	GOLGA1	Golgi autoantigen, golgin subfamily a, 1	0.472	0.116
222843_at	FIGNL1	fidgetin-like 1	0.302	0.116
211000_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.443	0.116
204890_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.597	0.116
227686_at	OXNAD1	oxidoreductase NAD-binding domain containing 1	0.522	0.116
200965_s_at	ABLIM1	actin binding LIM protein 1	0.569	0.116
228974_at	ZNF677	Zinc finger protein 677	0.540	0.116

215262_at	OXNAD1	Oxidoreductase NAD-binding domain containing 1	0.386	0.116
221081_s_at	DENND2D	DENN/MADD domain containing 2D	0.629	0.116
230178_s_at	---	CDNA FLJ38461 fis, clone FEBRA2020977	0.624	0.116
225458_at	LOC25845	hypothetical LOC25845	0.570	0.116
221740_x_at	LOC728871 /// LRRC37A2	Hypothetical protein LOC728871 /// Leucine rich repeat containing 37, member A2	0.579	0.116
227796_at	ZFP62 /// LOC643836	zinc finger protein 62 homolog (mouse) /// similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3)	0.512	0.116
202524_s_at	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	0.590	0.116
57082_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	0.591	0.116
223403_s_at	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	0.647	0.116
244798_at	SERTAD4	SERTA domain containing 4	0.251	0.116
203579_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	0.542	0.116
202969_at	---	MRNA; cDNA DKFZp667B0924 (from clone DKFZp667B0924)	0.568	0.116
1554555_a_at	SETD6	SET domain containing 6	0.588	0.116
228046_at	LOC152485	Hypothetical protein LOC152485	0.511	0.116
209504_s_at	PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	0.514	0.116
1569652_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	0.535	0.116
235436_at	---	---	0.608	0.116
207971_s_at	CEP68	centrosomal protein 68kDa	0.561	0.116
218667_at	PJA1	praja 1	0.601	0.116
1552733_at	KLHDC1	kelch domain containing 1	0.527	0.116
225314_at	OCIAD2	OCIA domain containing 2	0.521	0.116
228298_at	FAM113B	family with sequence similarity 113, member B	0.577	0.116
212538_at	DOCK9	dedicator of cytokinesis 9	0.535	0.116
210039_s_at	PRKCQ	protein kinase C, theta	0.575	0.116
226272_at	---	Full length insert cDNA clone ZD79H10	0.518	0.116
235085_at	DKFZp761P0423	homolog of rat pragma of Rnd2	0.608	0.116
226591_at	---	CDNA FLJ33569 fis, clone BRAMY2010317	0.493	0.116
234339_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	0.589	0.116
204863_s_at	IL6ST /// MAGEA4	interleukin 6 signal transducer (gp130, oncostatin M receptor) /// melanoma antigen family A, 4	0.445	0.116
234785_at	---	---	0.537	0.116
230298_at	LOC153364	similar to metallo-beta-lactamase superfamily protein	0.530	0.116
225457_s_at	LOC25845	hypothetical LOC25845	0.577	0.116
229007_at	LOC283788	hypothetical protein LOC283788	0.400	0.116
228109_at	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	0.454	0.116
221757_at	MGC17330	HGFL gene /// HGFL gene	0.589	0.116
221756_at	MGC17330	HGFL gene /// HGFL gene	0.571	0.116
210948_s_at	LEF1	lymphoid enhancer-binding factor 1	0.490	0.116
228423_at	MAP9	microtubule-associated protein 9	0.480	0.116
1555450_a_at	NARG1L	NMDA receptor regulated 1-like	0.523	0.116

211596_s_at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1 /// leucine-rich repeats and immunoglobulin-like domains 1	0.529	0.116
243154_at	---	Transcribed locus	0.589	0.116
218532_s_at	FLJ20152	hypothetical protein FLJ20152	0.541	0.116
222696_at	AXIN2	axin 2 (conductin, axil)	0.457	0.116
242051_at	---	Transcribed locus	0.442	0.116
1569472_s_at	TTC3	tetratricopeptide repeat domain 3	0.395	0.116
206545_at	CD28	CD28 molecule	0.477	0.116
36545_s_at	SFI1	Sfi1 homolog, spindle assembly associated (yeast)	0.593	0.116
218851_s_at	WDR33	WD repeat domain 33	0.631	0.132
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.562	0.132
238524_at	---	---	0.625	0.132
1554007_at	ZNF483	Zinc finger protein 483	0.437	0.132
212677_s_at	CEP68	centrosomal protein 68kDa	0.576	0.132
231817_at	USP53	ubiquitin specific peptidase 53	0.428	0.132
228630_at	ZNF84	Zinc finger protein 84	0.602	0.132
202746_at	ITM2A	integral membrane protein 2A	0.561	0.132
227984_at	LOC650392	Hypothetical protein LOC650392	0.317	0.132
1566448_at	CD6	CD6 molecule	0.527	0.132
238454_at	ZNF540	zinc finger protein 540	0.487	0.132
224518_s_at	ZNF559	zinc finger protein 559 /// zinc finger protein 559	0.597	0.132
1552343_s_at	PDE7A	phosphodiesterase 7A	0.653	0.132
37433_at	PIAS2	protein inhibitor of activated STAT, 2	0.636	0.132
218918_at	MAN1C1	mannosidase, alpha, class 1C, member 1	0.496	0.132
220418_at	IFT52 /// UBASH3A	intraflagellar transport 52 homolog (Chlamydomonas) /// ubiquitin associated and SH3 domain containing, A	0.546	0.132
212675_s_at	---	---	0.589	0.132
1559097_at	C14orf64	chromosome 14 open reading frame 64	0.525	0.132
226388_at	TCEA3	transcription elongation factor A (SII), 3	0.441	0.132
224931_at	SLC41A3	solute carrier family 41, member 3	0.602	0.132
1553132_a_at	MTAC2D1	membrane targeting (tandem) C2 domain containing 1	0.449	0.132
205259_at	NR3C2	nuclear receptor subfamily 3, group C, member 2	0.454	0.132
213049_at	GARNL1	GTPase activating Rap/RanGAP domain-like 1	0.623	0.132
206337_at	CCR7	chemokine (C-C motif) receptor 7 /// chemokine (C-C motif) receptor 7	0.543	0.132
204352_at	TRAF5	TNF receptor-associated factor 5	0.609	0.132
1556061_at	LOC283012	hypothetical protein LOC283012	0.576	0.132
1557733_a_at	CHRM3	Cholinergic receptor, muscarinic 3	0.429	0.132
239487_at	FAM98A	Family with sequence similarity 98, member A	0.565	0.132
204891_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.636	0.132
1559025_at	9-Sep	septin 9	0.528	0.132
232001_at	LOC439949	hypothetical gene supported by AY007155	0.554	0.132
211841_s_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	0.535	0.132
238750_at	---	---	0.551	0.132
244571_s_at	TTC12	Tetratricopeptide repeat domain 12	0.427	0.132
205372_at	PLAG1	pleiomorphic adenoma gene 1	0.603	0.132
241494_at	SERINC5	Serine incorporator 5	0.457	0.132
204749_at	NAP1L3	nucleosome assembly protein 1-like 3	0.418	0.132

212621_at	KIAA0286	KIAA0286 protein	0.620	0.132
225391_at	LOC93622	hypothetical protein BC006130	0.599	0.132
205790_at	SKAP1	src kinase associated phosphoprotein 1	0.629	0.132
210972_x_at	TRA@ /// TRDV2 /// TRAV20 /// TRAJ17 /// TRAC	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant	0.630	0.132
214193_s_at	C1orf107	chromosome 1 open reading frame 107	0.619	0.132
218510_x_at	FLJ20152	hypothetical protein FLJ20152	0.573	0.132
212071_s_at	SPTBN1	spectrin, beta, non-erythrocytic 1	0.640	0.132
230069_at	SFXN1	sideroflexin 1	0.572	0.132
206039_at	RAB33A	RAB33A, member RAS oncogene family	0.595	0.132
222820_at	TNRC6C	trinucleotide repeat containing 6C	0.598	0.132
204977_at	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	0.557	0.132
244878_at	MAGED1	Melanoma antigen family D, 1	0.615	0.132
229029_at	---	---	0.532	0.132
214764_at	KIAA0507	KIAA0507	0.589	0.132
213189_at	MINA	MYC induced nuclear antigen	0.622	0.132
205006_s_at	NMT2	N-myristoyltransferase 2	0.567	0.132
235522_at	CLEC2D	C-type lectin domain family 2, member D	0.605	0.132
226679_at	SLC26A11	solute carrier family 26, member 11	0.603	0.132
215797_at	MGC40069	hypothetical protein MGC40069	0.557	0.132
205878_at	POU6F1	POU domain, class 6, transcription factor 1	0.625	0.132
1556472_s_at	SCML4	sex comb on midleg-like 4 (Drosophila)	0.623	0.132
212655_at	ZCCHC14	zinc finger, CCHC domain containing 14	0.556	0.132
229629_at	---	Transcribed locus	0.544	0.132
227611_at	TARSL2	threonyl-tRNA synthetase-like 2	0.614	0.132
226051_at	SELM	selenoprotein M	0.471	0.132
202780_at	OXCT1	3-oxoacid CoA transferase 1	0.601	0.132
227877_at	AXIIR	similar to annexin II receptor	0.577	0.132
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.601	0.132
210038_at	PRKCQ	protein kinase C, theta	0.626	0.132
233543_s_at	CCDC98	coiled-coil domain containing 98	0.481	0.132
209657_s_at	HSF2	heat shock transcription factor 2	0.589	0.132
232014_at	ZNF30	zinc finger protein 30	0.511	0.132
209670_at	TRAC	T cell receptor alpha constant /// T cell receptor alpha constant	0.636	0.132
223358_s_at	---	CDNA FLJ33024 fis, clone THYMU1000532, moderately similar to HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17)	0.639	0.132
1553219_a_at	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	0.596	0.132
223161_at	KIAA1147	KIAA1147	0.489	0.132
228643_at	COMMD10	CDNA clone IMAGE:5277380 /// COMM domain containing 10	0.525	0.132
224490_s_at	KIAA1267	KIAA1267 /// KIAA1267	0.317	0.132
229544_at	---	CDNA clone IMAGE:4791887 /// MRNA; cDNA DKFZp564C0762 (from clone DKFZp564C0762)	0.572	0.132
215540_at	TRA@	T cell receptor alpha locus	0.519	0.132

204019_s_at	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	0.562	0.132
205456_at	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	0.618	0.132
234970_at	MTAC2D1	membrane targeting (tandem) C2 domain containing 1	0.560	0.132
1566446_at	KLF12	Kruppel-like factor 12	0.648	0.132
203733_at	DEXI	dexamethasone-induced transcript	0.665	0.132
211339_s_at	ITK	IL2-inducible T-cell kinase	0.589	0.132
212894_at	SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)	0.642	0.132
210858_x_at	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	0.666	0.132
239644_at	FLJ37440	Hypothetical protein FLJ37440	0.633	0.132
223477_s_at	FLJ38663	hypothetical protein FLJ38663	0.595	0.132
203386_at	TBC1D4	TBC1 domain family, member 4	0.550	0.132
234377_at	IL23A	interleukin 23, alpha subunit p19	0.582	0.132
209501_at	CDR2	cerebellar degeneration-related protein 2, 62kDa	0.618	0.132
219734_at	SIDT1	SID1 transmembrane family, member 1	0.663	0.132
213262_at	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	0.495	0.132
224580_at	SLC38A1	solute carrier family 38, member 1	0.540	0.132
241365_at	---	CDNA FLJ42259 fis, clone TKIDN2011289	0.582	0.132
227867_at	LOC129293	hypothetical protein LOC129293	0.543	0.132
207826_s_at	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	0.561	0.132
202431_s_at	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	0.617	0.132
209671_x_at	TRA@ /// TRAC	T cell receptor alpha locus /// T cell receptor alpha locus /// T cell receptor alpha constant /// T cell receptor alpha constant	0.663	0.132
228539_at	---	Transcribed locus	0.592	0.132
208744_x_at	HSPH1	heat shock 105kDa/110kDa protein 1	0.663	0.132
219915_s_at	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	0.441	0.132
231979_at	GABPB2	GA binding protein transcription factor, beta subunit 2	0.412	0.132
234819_at	---	TCR alpha variable region (clone XPHER47 I)	0.512	0.132
205356_at	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	0.602	0.132
1563217_at	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0.460	0.132
227093_at	USP36	Ubiquitin specific peptidase 36	0.661	0.132
231919_at	DBT	dihydrolipoamide branched chain transacylase E2	0.607	0.132
205798_at	IL7R	interleukin 7 receptor /// interleukin 7 receptor	0.605	0.132
206042_x_at	SNRPN /// SNURF	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	0.656	0.132
222147_s_at	HBZ	Hemoglobin, zeta	0.599	0.132
218375_at	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	0.658	0.132
219378_at	NARG1L	NMDA receptor regulated 1-like	0.625	0.132
220349_s_at	FLJ21865	endo-beta-N-acetylglucosaminidase	0.620	0.132
221602_s_at	FAIM3	Fas apoptotic inhibitory molecule 3 /// Fas apoptotic inhibitory molecule 3	0.638	0.132
225747_at	ABCD4 /// COQ10A	ATP-binding cassette, sub-family D (ALD), member 4 /// coenzyme Q10 homolog A (S. cerevisiae)	0.627	0.132
218932_at	C1orf181	chromosome 1 open reading frame 181	0.606	0.132

238694_at	---	Transcribed locus	0.560	0.132
208806_at	CHD3	chromodomain helicase DNA binding protein 3	0.615	0.132
225886_at	---	Full-length cDNA clone CS0DF030YM05 of Fetal brain of Homo sapiens (human)	0.618	0.132
224579_at	SLC38A1	solute carrier family 38, member 1	0.617	0.132
214855_s_at	GARNL1	GTPase activating Rap/RanGAP domain-like 1	0.596	0.132
221726_at	RPL22	ribosomal protein L22	0.664	0.132
226604_at	TMTC3	transmembrane and tetratricopeptide repeat containing 3	0.498	0.132
226181_at	TUBE1	tubulin, epsilon 1	0.538	0.132
204700_x_at	C1orf107	chromosome 1 open reading frame 107	0.642	0.132
222557_at	STMN3	stathmin-like 3	0.604	0.132
226483_at	TMEM68	transmembrane protein 68	0.611	0.132
208073_x_at	TTC3	tetratricopeptide repeat domain 3	0.656	0.132
224719_s_at	C12orf57	chromosome 12 open reading frame 57	0.543	0.132
227502_at	RDX	radixin	0.608	0.132
210645_s_at	TTC3	tetratricopeptide repeat domain 3	0.639	0.132
212121_at	C10orf61	chromosome 10 open reading frame 61	0.659	0.132
211902_x_at	TRA@	T cell receptor alpha locus	0.649	0.132
239442_at	CEP68	Centrosomal protein 68kDa	0.632	0.132
208249_s_at	TGDS	TDP-glucose 4,6-dehydratase	0.584	0.132
202931_x_at	BIN1	bridging integrator 1	0.666	0.132
210202_s_at	BIN1	bridging integrator 1	0.654	0.132
230083_at	---	Full length insert cDNA clone YI48C03	0.362	0.132
204918_s_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	0.566	0.132
209798_at	NPAT	nuclear protein, ataxia-telangiectasia locus	0.661	0.132
225158_at	GFM1	G elongation factor, mitochondrial 1	0.642	0.132
234106_s_at	FLYWCH1	FLYWCH-type zinc finger 1	0.566	0.132
212634_at	KIAA0776	KIAA0776	0.598	0.132
235697_at	ZNF544	Zinc finger protein 544	0.545	0.132
227361_at	---	---	0.588	0.132
241299_at	C16orf30	Chromosome 16 open reading frame 30	0.541	0.132
239726_at	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)	0.487	0.132
215030_at	GRSF1	G-rich RNA sequence binding factor 1	0.636	0.132
239794_at	IARS	Isoleucine-tRNA synthetase	0.617	0.132
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.477	0.132
218882_s_at	WDR3	WD repeat domain 3	0.665	0.132
222275_at	---	---	0.649	0.132
218877_s_at	TRMT11	tRNA methyltransferase 11 homolog (S. cerevisiae)	0.532	0.132
226327_at	ZNF507	zinc finger protein 507	0.588	0.132
209068_at	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	0.628	0.132
1560659_at	---	---	0.623	0.132
215440_s_at	BEXL1	brain expressed X-linked-like 1	0.630	0.132
242969_at	---	Transcribed locus	0.662	0.132
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	0.448	0.132
231940_at	ZNF529	zinc finger protein 529	0.627	0.132
219423_x_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	0.572	0.132
204951_at	RHOH	ras homolog gene family, member H	0.610	0.132
226881_at	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	0.570	0.132
229963_at	NGFRAP1L1	NGFRAP1-like 1	0.458	0.132

210847_x_at	TNFRSF25 /// PLEKHG5	tumor necrosis factor receptor superfamily, member 25 /// pleckstrin homology domain containing, family G (with RhoGef domain) member 5	0.557	0.132
203413_at	NELL2	NEL-like 2 (chicken) /// NEL-like 2 (chicken)	0.573	0.132
215211_at	---	Clone 23832 mRNA sequence	0.428	0.132
212672_at	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	0.636	0.132
217412_at	---	Rearranged T-cell receptor alpha chain mRNA, variable region	0.567	0.132
230444_at	MTFR1	Mitochondrial fission regulator 1	0.654	0.132
211874_s_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	0.590	0.132
214439_x_at	BIN1	bridging integrator 1	0.665	0.132
244272_s_at	MTAC2D1	Membrane targeting (tandem) C2 domain containing 1	0.662	0.132
215307_at	ZNF529	Zinc finger protein 529	0.529	0.132
226611_s_at	PRR6	proline rich 6	0.633	0.132
239212_at	LTV1	LTV1 homolog (S. cerevisiae)	0.658	0.132
224162_s_at	FBXO31	F-box protein 31	0.636	0.132
213269_at	ZNF248	zinc finger protein 248	0.590	0.132
216305_s_at	C2orf3	chromosome 2 open reading frame 3	0.621	0.132
1554771_at	---	CDNA clone IMAGE:4300887	0.619	0.132
203263_s_at	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	0.610	0.132
222108_at	AMIGO2	adhesion molecule with Ig-like domain 2	0.561	0.132
220582_at	---	---	0.465	0.132
203387_s_at	TBC1D4	TBC1 domain family, member 4	0.551	0.132
213958_at	CD6	CD6 molecule /// CD6 molecule	0.647	0.183
229141_at	WDR33	WD repeat domain 33	0.660	0.183
217729_s_at	AES	amino-terminal enhancer of split	0.638	0.183
207979_s_at	CD8B	CD8b molecule	0.572	0.183
244267_at	---	---	0.541	0.183
226218_at	IL7R	interleukin 7 receptor	0.579	0.183
202983_at	HLTF	helicase-like transcription factor	0.587	0.183
214820_at	BRWD1	bromodomain and WD repeat domain containing 1	0.580	0.183
203385_at	DGKA /// BCDO2	diacylglycerol kinase, alpha 80kDa /// beta-carotene dioxygenase 2	0.650	0.183
227810_at	ZNF558	zinc finger protein 558	0.611	0.183
203245_s_at	FLJ35348	FLJ35348	0.639	0.183
52940_at	SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	0.664	0.183
226749_at	MRPS9	mitochondrial ribosomal protein S9	0.637	0.183
208442_s_at	ATM /// LOC651610	ataxia telangiectasia mutated (includes complementation groups A, C and D) /// similar to Serine-protein kinase ATM (Ataxia telangiectasia mutated) (A-T, mutated)	0.632	0.183
231449_at	---	Transcribed locus	0.548	0.183
1552315_at	GIMAP1	GTPase, IMAP family member 1	0.642	0.183
228655_at	---	Unknown mRNA sequence	0.579	0.183
218710_at	TTC27	tetratricopeptide repeat domain 27	0.639	0.183
224780_at	RBM17	RNA binding motif protein 17	0.659	0.183
1553719_s_at	ZNF548	zinc finger protein 548	0.539	0.183
215411_s_at	TRAF3IP2	TRAF3 interacting protein 2	0.645	0.183

202968_s_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0.667	0.183
228314_at	---	---	0.650	0.183
231775_at	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	0.635	0.183
204612_at	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0.501	0.183
207623_at	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	0.468	0.183
229725_at	ACSL6	Acyl-CoA synthetase long-chain family member 6	0.486	0.183
210807_s_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	0.577	0.183
235304_at	ZNF573	Zinc finger protein 573	0.627	0.183
211005_at	LAT	linker for activation of T cells	0.647	0.183
212977_at	CXCR7	chemokine (C-X-C motif) receptor 7	0.641	0.183
215177_s_at	ITGA6	integrin, alpha 6	0.562	0.183
218793_s_at	SCML1	sex comb on midleg-like 1 (Drosophila)	0.502	0.183
209421_at	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.611	0.183
217950_at	NOSIP	nitric oxide synthase interacting protein	0.657	0.183
201656_at	ITGA6	integrin, alpha 6	0.643	0.183
219658_at	PTCD2	pentatricopeptide repeat domain 2	0.596	0.183
232584_at	TSHZ2	Teashirt family zinc finger 2	0.354	0.183
221011_s_at	LBH	limb bud and heart development homolog (mouse) /// limb bud and heart development homolog (mouse)	0.659	0.183
233849_s_at	ARHGAP5	Rho GTPase activating protein 5	0.478	0.183
201030_x_at	LDHB	lactate dehydrogenase B	0.624	0.183
212314_at	KIAA0746	KIAA0746 protein	0.616	0.183
228843_at	---	Full length insert cDNA clone YZ38E04	0.565	0.183
229070_at	C6orf105	chromosome 6 open reading frame 105	0.319	0.183
216711_s_at	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	0.586	0.183
225470_at	NUP35	nucleoporin 35kDa	0.588	0.183
225112_at	ABI2	abl interactor 2	0.631	0.183
225903_at	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U	0.641	0.183
236520_at	FKBP1A	FK506 binding protein 1A, 12kDa	0.660	0.183
223506_at	ZC3H8	zinc finger CCCH-type containing 8	0.648	0.183
227600_at	---	Full-length cDNA clone CS0DK012YA15 of HeLa cells Cot 25-normalized of Homo sapiens (human)	0.600	0.183
220755_s_at	C6orf48	chromosome 6 open reading frame 48	0.610	0.183
209871_s_at	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)	0.565	0.183
205376_at	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	0.534	0.183
227900_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	0.633	0.183
235046_at	---	Transcribed locus	0.468	0.183
230489_at	CD5	CD5 molecule	0.649	0.183
230078_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	0.651	0.183
227105_at	CSPP1	centrosome and spindle pole associated protein 1	0.640	0.183
224308_s_at	INTS2	integrator complex subunit 2	0.618	0.183

1569872_a_at	LOC650392	Full-length cDNA clone CS0DF015YK23 of Fetal brain of Homo sapiens (human) /// Hypothetical protein LOC650392	0.364	0.183
243729_at	C14orf161	Chromosome 14 open reading frame 161	0.613	0.183
244663_at	---	Transcribed locus	0.566	0.183
210425_x_at	GOLGA8B	golgi autoantigen, golgin subfamily a, 8B	0.566	0.183
218346_s_at	SESN1	sestrin 1	0.615	0.183
205961_s_at	PSIP1	PC4 and SFRS1 interacting protein 1	0.612	0.183
1553099_at	TIGD1	tigger transposable element derived 1	0.590	0.183
224721_at	WDR75	WD repeat domain 75	0.632	0.183
229202_at	---	Transcribed locus	0.568	0.183
230285_at	DKFZp313A2432	hypothetical protein DKFZp313A2432	0.536	0.183
206966_s_at	KLF12	Kruppel-like factor 12	0.641	0.183
235274_at	GABPB2	GA binding protein transcription factor, beta subunit 2	0.528	0.183
1555882_at	SPIN3	spindlin family, member 3	0.318	0.183
229414_at	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	0.596	0.183
215796_at	---	T-cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AG212	0.485	0.183
218768_at	NUP107	nucleoporin 107kDa	0.635	0.183
1553111_a_at	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	0.642	0.183
1568983_a_at	GABPB2	GA binding protein transcription factor, beta subunit 2	0.468	0.183
1555613_a_at	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	0.657	0.183
229035_s_at	KLHDC4	kelch domain containing 4	0.617	0.183
232171_x_at	KLHDC4	kelch domain containing 4	0.593	0.183
1560089_at	LOC286208	hypothetical protein LOC286208	0.637	0.183
221691_x_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin) /// nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.629	0.183
226039_at	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	0.604	0.183
211272_s_at	DGKA	diacylglycerol kinase, alpha 80kDa	0.584	0.183
237753_at	---	Transcribed locus	0.657	0.183
223300_s_at	CCDC82	coiled-coil domain containing 82	0.498	0.183
208424_s_at	CIAPIN1	cytokine induced apoptosis inhibitor 1	0.660	0.183
1556047_s_at	MAGEE1	melanoma antigen family E, 1	0.638	0.183
238457_at	---	CDNA FLJ33029 fis, clone THYMU2000162	0.638	0.183
231146_at	FAM24B	family with sequence similarity 24, member B	0.511	0.183
1555626_a_at	SLAMF1	signaling lymphocytic activation molecule family member 1	0.589	0.183
212693_at	MDN1	MDN1, midasin homolog (yeast)	0.636	0.183
236401_at	GIMAP5	GTPase, IMAP family member 5	0.658	0.183
232000_at	C9orf52	Chromosome 9 open reading frame 52	0.583	0.183
213564_x_at	LDHB	lactate dehydrogenase B	0.645	0.183
229869_at	---	Transcribed locus	0.641	0.183
234297_at	PDCD6 /// RGS8	Programmed cell death 6 /// Regulator of G-protein signalling 8	0.659	0.183
215314_at	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)	0.520	0.183
201675_at	AKAP1	A kinase (PRKA) anchor protein 1	0.626	0.183
225794_s_at	C22orf32	chromosome 22 open reading frame 32	0.656	0.183

200995_at	IPO7	Importin 7	0.659	0.183
219315_s_at	C16orf30	chromosome 16 open reading frame 30	0.547	0.183
222266_at	C19orf2	Chromosome 19 open reading frame 2	0.662	0.183
212828_at	SYNJ2	synaptojanin 2	0.486	0.183
214551_s_at	CD7	CD7 molecule	0.660	0.183
229317_at	---	---	0.552	0.183
224489_at	KIAA1267	KIAA1267 /// KIAA1267	0.277	0.183
240865_at	---	---	0.519	0.183
243521_at	---	Transcribed locus	0.578	0.183
232589_at	---	CDNA FLJ11489 fis, clone HEMBA1001915	0.627	0.183
212771_at	C10orf38	chromosome 10 open reading frame 38	0.598	0.183
1564154_at	---	---	0.649	0.183
239973_at	---	Full-length cDNA clone CS0DJ013YE21 of T cells (Jurkat cell line) Cot 10-normalized of Homo sapiens (human)	0.641	0.183
218533_s_at	UCKL1	uridine-cytidine kinase 1-like 1	0.593	0.183
227117_at	---	CDNA FLJ40762 fis, clone TRACH2002847	0.630	0.183
226383_at	C11orf46	Chromosome 11 open reading frame 46	0.553	0.183
202516_s_at	DLG1	discs, large homolog 1 (Drosophila)	0.579	0.183
210424_s_at	GOLGA8A /// GOLGA8B	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B	0.533	0.183
213584_s_at	CREBZF	CREB/ATF bZIP transcription factor	0.566	0.183
202514_at	DLG1	discs, large homolog 1 (Drosophila)	0.619	0.183
236293_at	RHOH	Ras homolog gene family, member H	0.586	0.183
244347_at	C10orf61	Chromosome 10 open reading frame 61	0.593	0.183
214093_s_at	FUBP1	far upstream element (FUSE) binding protein 1	0.616	0.183
204773_at	IL11RA	interleukin 11 receptor, alpha	0.571	0.183
210439_at	ICOS	inducible T-cell co-stimulator	0.479	0.183
227415_at	LOC283508	hypothetical protein LOC283508	0.522	0.183
222457_s_at	LIMA1	LIM domain and actin binding 1	0.528	0.183
239278_at	---	CDNA clone IMAGE:5301129	0.563	0.183
228905_at	---	Transcribed locus	0.559	0.183
203410_at	AP3M2	adaptor-related protein complex 3, mu 2 subunit	0.610	0.183
1556471_at	SCML4	sex comb on midleg-like 4 (Drosophila)	0.656	0.183
227805_at	---	Transcribed locus	0.588	0.183
213434_at	STX2	syntaxin 2	0.607	0.183
212690_at	DDHD2	DDHD domain containing 2	0.631	0.183
227077_at	ZNF286	zinc finger protein 286	0.581	0.183
216503_s_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	0.660	0.183
226479_at	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	0.558	0.183
210073_at	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	0.580	0.183
202742_s_at	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	0.542	0.183
222920_s_at	KIAA0748	KIAA0748	0.620	0.183
203774_at	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	0.665	0.183
203678_at	MTMR15	myotubularin related protein 15	0.559	0.183
209337_at	PSIP1	PC4 and SFRS1 interacting protein 1	0.590	0.183
233214_at	KLHL23	Kelch-like 23 (Drosophila)	0.598	0.183
211282_x_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	0.607	0.183

226969_at	LOC149448	hypothetical protein LOC149448	0.637	0.183
213587_s_at	ATP6V0E2	ATPase, H+ transporting V0 subunit e2	0.649	0.183
225553_at	---	CDNA FLJ12874 fis, clone NT2RP2003769	0.636	0.183
241619_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)	0.651	0.183
206761_at	CD96	CD96 molecule	0.660	0.183
55872_at	GM632	KIAA1196 protein	0.645	0.183
212195_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.622	0.183
225048_at	PHF10	PHD finger protein 10	0.571	0.183
202268_s_at	APPBP1	amyloid beta precursor protein binding protein 1	0.618	0.183
227934_at	---	---	0.624	0.183
223486_at	GTPBP8	GTP-binding protein 8 (putative)	0.660	0.183
224870_at	KIAA0114	KIAA0114	0.646	0.183
212413_at	6-Sep	septin 6	0.667	0.183
1558826_at	C20orf174	chromosome 20 open reading frame 174	0.543	0.183
225044_at	NT5C3L	5'-nucleotidase, cytosolic III-like	0.572	0.183
217403_s_at	ZNF227	zinc finger protein 227	0.634	0.183
219029_at	C5orf28	chromosome 5 open reading frame 28	0.562	0.183
224634_at	GPATCH4	G patch domain containing 4	0.645	0.183
217599_s_at	MDFIC	MyoD family inhibitor domain containing	0.638	0.183
1555356_a_at	SCML4	sex comb on midleg-like 4 (Drosophila)	0.655	0.183
228841_at	LYRM7	Lyrm7 homolog (mouse)	0.651	0.183
218689_at	FANCF	Fanconi anemia, complementation group F	0.653	0.183
241925_x_at	---	Transcribed locus	0.602	0.183
229881_at	KLF12	Kruppel-like factor 12	0.596	0.183
231075_x_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	0.656	0.183
222669_s_at	SBDS	Shwachman-Bodian-Diamond syndrome	0.592	0.183
224759_s_at	C12orf23	chromosome 12 open reading frame 23	0.550	0.183
201830_s_at	NET1	neuroepithelial cell transforming gene 1	0.442	0.183
205407_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	0.597	0.183
223774_at	C1orf79	chromosome 1 open reading frame 79	0.603	0.183
226718_at	AMIGO1	adhesion molecule with Ig-like domain 1	0.654	0.183
202950_at	CRYZ	crystallin, zeta (quinone reductase)	0.455	0.183
216863_s_at	MORC2	MORC family CW-type zinc finger 2	0.662	0.183
226800_at	KIAA1799	KIAA1799 protein	0.533	0.183
238653_at	---	CDNA FLJ43454 fis, clone OCBBF2034906	0.647	0.183
211478_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	0.620	0.183
223306_at	EBPL	emopamil binding protein-like	0.607	0.183
225237_s_at	MSI2	musashi homolog 2 (Drosophila)	0.664	0.183
223245_at	STRBP	spermatid perinuclear RNA binding protein	0.579	0.183
227585_at	---	---	0.574	0.183
217895_at	PTCD3	Pentatricopeptide repeat domain 3	0.612	0.183
204327_s_at	ZNF202	zinc finger protein 202	0.652	0.183
220459_at	MCM3APAS	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein antisense	0.611	0.183
243810_at	LOC341333	Similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1)	0.558	0.183
229253_at	THEM4	thioesterase superfamily member 4	0.570	0.183

1559957_a_at	LOC642852	hypothetical LOC642852	0.661	0.183
219342_at	CASD1	CAS1 domain containing 1	0.569	0.183
222931_s_at	THNSL1	threonine synthase-like 1 (bacterial)	0.546	0.183
230003_at	---	Transcribed locus	0.568	0.183
231124_x_at	LY9	lymphocyte antigen 9	0.666	0.183
223227_at	BBS2	Bardet-Biedl syndrome 2	0.659	0.183
221646_s_at	ZDHHC11	zinc finger, DHHC-type containing 11	0.518	0.183
220940_at	KIAA1641	KIAA1641	0.594	0.183
201188_s_at	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	0.635	0.183
227607_at	STAMBPL1	STAM binding protein-like 1	0.618	0.183
1565436_s_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	0.571	0.183
233359_at	---	CDNA clone IMAGE:5262617	0.663	0.183
215766_at	GSTA1	Glutathione S-transferase A1	0.662	0.183
236353_at	---	CDNA FLJ43467 fis, clone OCBBF2036752	0.547	0.183
244534_at	PMPCB	Peptidase (mitochondrial processing) beta	0.615	0.183
239083_at	ZNF786	zinc finger protein 786	0.652	0.183
221648_s_at	---	---	0.587	0.183
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	0.605	0.183
229075_at	---	Transcribed locus	0.645	0.183
235020_at	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	0.622	0.183
221229_s_at	FLJ20628	hypothetical protein FLJ20628 /// hypothetical protein FLJ20628	0.655	0.183
215985_at	HCG8	HLA complex group 8	0.579	0.183
228099_at	ZNF550	zinc finger protein 550	0.609	0.183
229064_s_at	---	---	0.557	0.183
218573_at	MAGEH1	melanoma antigen family H, 1	0.655	0.183
202478_at	TRIB2	tribbles homolog 2 (Drosophila)	0.637	0.183
227037_at	LOC201164	similar to CG12314 gene product	0.601	0.250
220485_s_at	SIRPG	signal-regulatory protein gamma	0.630	0.250
210116_at	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	0.520	0.250
205571_at	LIPT1	lipoyltransferase 1	0.610	0.250
223476_s_at	FLJ38663	hypothetical protein FLJ38663	0.622	0.250
211623_s_at	FBL	fibrillarin /// fibrillarin	0.665	0.250
216902_s_at	RRN3 /// LOC653390 /// LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) /// hypothetical LOC653390 /// hypothetical protein LOC730092	0.606	0.250
224685_at	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	0.421	0.250
235509_at	C8orf38	chromosome 8 open reading frame 38	0.598	0.250
235189_at	NARG2	NMDA receptor regulated 2	0.574	0.250
222448_s_at	CMPK	cytidylate kinase	0.663	0.250
225295_at	SLC39A10	solute carrier family 39 (zinc transporter), member 10	0.640	0.250
212921_at	SMYD2	SET and MYND domain containing 2	0.655	0.250
232489_at	CCDC76	coiled-coil domain containing 76	0.624	0.250
237143_at	---	Transcribed locus	0.563	0.250
231013_at	---	---	0.428	0.250

229728_at	---	---	0.649	0.250
240327_at	6-Sep	Septin 6	0.538	0.250
1558972_s_at	C6orf190	chromosome 6 open reading frame 190	0.560	0.250
217170_at	---	T-cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AA17	0.609	0.250
228020_at	PTCD3	Pentatricopeptide repeat domain 3	0.634	0.250
209302_at	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	0.650	0.250
208939_at	SEPHS1	selenophosphate synthetase 1	0.664	0.250
220147_s_at	FAM60A	family with sequence similarity 60, member A	0.659	0.250
215133_s_at	LOC202134 /// NY-REN-7	hypothetical protein LOC202134 /// NY-REN-7 antigen	0.493	0.250
227485_at	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	0.655	0.250
219864_s_at	DSCR1L2	Down syndrome critical region gene 1-like 2	0.595	0.250
209406_at	BAG2	BCL2-associated athanogene 2	0.452	0.250
201512_s_at	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	0.645	0.250
227261_at	KLF12	Kruppel-like factor 12	0.626	0.250
240102_at	PRSS1	Protease, serine, 1 (trypsin 1)	0.579	0.250
1553987_at	C12orf47	chromosome 12 open reading frame 47	0.649	0.250
229636_at	MPN2	marapsin 2	0.617	0.250
208925_at	CLDND1	claudin domain containing 1	0.626	0.250
205934_at	PLCL1	phospholipase C-like 1	0.564	0.250
236583_at	GIMAP5	GTPase, IMAP family member 5	0.643	0.250
218757_s_at	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	0.652	0.250
231283_at	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	0.654	0.250
214173_x_at	C19orf2	chromosome 19 open reading frame 2	0.667	0.250
203288_at	KIAA0355	KIAA0355	0.643	0.250
229809_at	---	Transcribed locus	0.558	0.250
204791_at	NR2C1	nuclear receptor subfamily 2, group C, member 1	0.644	0.250
202137_s_at	ZMYND11	zinc finger, MYND domain containing 11	0.639	0.250
240339_at	ANKRD23	Ankyrin repeat domain 23	0.659	0.250
219130_at	CCDC76	coiled-coil domain containing 76	0.544	0.250
233302_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.625	0.250
221970_s_at	NOL11	nucleolar protein 11	0.659	0.250
213483_at	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	0.638	0.250
208051_s_at	PAIP1	poly(A) binding protein interacting protein 1	0.609	0.250
221833_at	LONP2	Lon peptidase 2, peroxisomal	0.609	0.250
227471_at	HACE1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	0.605	0.250
213239_at	C13orf24	chromosome 13 open reading frame 24	0.559	0.250
217147_s_at	TRAT1	T cell receptor associated transmembrane adaptor 1	0.473	0.250
206914_at	CRTAM	cytotoxic and regulatory T cell molecule	0.594	0.250
244665_at	ITGA6	Integrin, alpha 6	0.601	0.250
220007_at	METTL8	methyltransferase like 8	0.625	0.250
213703_at	LOC150759	hypothetical protein LOC150759	0.635	0.250
1555989_at	---	Transcribed locus	0.312	0.250
206666_at	GZMK	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	0.546	0.250
238057_at	USP45	ubiquitin specific peptidase 45	0.648	0.250

215731_s_at	MPHOSPH9	M-phase phosphoprotein 9	0.662	0.250
213689_x_at	RPL5	Ribosomal protein L5	0.586	0.250
233005_at	C1orf181	Chromosome 1 open reading frame 181	0.521	0.250
210279_at	GPR18	G protein-coupled receptor 18	0.637	0.250
236032_at	DNM1L	Dynamin 1-like	0.595	0.250
207564_x_at	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	0.659	0.250
225220_at	SNORA24	Small nucleolar RNA, H/ACA box 24	0.532	0.250
206114_at	EPHA4	EPH receptor A4	0.561	0.250
221234_s_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2 /// BTB and CNC homology 1, basic leucine zipper transcription factor 2	0.612	0.250
1562412_at	GPR89A	G protein-coupled receptor 89A	0.648	0.250
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	0.604	0.250
227072_at	RTTN	rotatin	0.657	0.250
204083_s_at	TPM2	tropomyosin 2 (beta)	0.571	0.250
206316_s_at	KNTC1	kinetochore associated 1	0.657	0.250
225792_at	HOOK1	hook homolog 1 (Drosophila)	0.590	0.250
234192_s_at	GKAP1	G kinase anchoring protein 1	0.661	0.250
236198_at	---	Transcribed locus	0.614	0.250
209902_at	ATR /// LOC648152	ataxia telangiectasia and Rad3 related /// similar to ataxia telangiectasia and Rad3 related protein	0.651	0.250
208663_s_at	TTC3	tetratricopeptide repeat domain 3	0.617	0.250
201456_s_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	0.661	0.250
206241_at	KPNA5	karyopherin alpha 5 (importin alpha 6)	0.524	0.250
213093_at	PRKCA	protein kinase C, alpha	0.595	0.250
1554029_a_at	KIAA0372	KIAA0372	0.459	0.250
212215_at	PREPL	prolyl endopeptidase-like	0.635	0.250
203428_s_at	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.610	0.250
222624_s_at	ZNF639	zinc finger protein 639	0.577	0.250
226041_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	0.625	0.250
214723_x_at	KIAA1641	KIAA1641	0.627	0.250
201829_at	NET1	neuroepithelial cell transforming gene 1	0.599	0.250
212731_at	ANKRD46	ankyrin repeat domain 46	0.572	0.250
223671_x_at	DPH5	DPH5 homolog (S. cerevisiae)	0.597	0.250
226352_at	JMY	Junction-mediating and regulatory protein	0.635	0.250
223319_at	GPHN	gephyrin	0.589	0.250
221685_s_at	CCDC99	coiled-coil domain containing 99	0.647	0.250
243016_at	TYMS	Thymidylate synthetase	0.651	0.250
230815_at	LOC389765	similar to KIF27C	0.662	0.250
213623_at	KIF3A	kinesin family member 3A	0.579	0.250
212170_at	RBM12	RNA binding motif protein 12	0.661	0.250
229325_at	ZZZ3	zinc finger, ZZ-type containing 3	0.579	0.250
208661_s_at	TTC3	tetratricopeptide repeat domain 3	0.640	0.250
204143_s_at	ENOSF1	enolase superfamily member 1	0.640	0.250
202747_s_at	ITM2A	integral membrane protein 2A	0.654	0.250
1557684_at	ZNF286	zinc finger protein 286	0.615	0.250

226361_at	TMEM42	transmembrane protein 42	0.644	0.250
232194_at	METTL4	methyltransferase like 4	0.640	0.250
230764_at	C9orf5	Chromosome 9 open reading frame 5	0.663	0.250
212893_at	ZZZ3	zinc finger, ZZ-type containing 3	0.589	0.250
224060_s_at	DPH5	DPH5 homolog (S. cerevisiae)	0.539	0.250
208662_s_at	TTC3	tetratricopeptide repeat domain 3	0.653	0.250
233884_at	---	Homo sapiens, clone IMAGE:5180231, mRNA	0.615	0.250
227409_at	PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 3E	0.611	0.250
212452_x_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	0.638	0.250
205005_s_at	NMT2	N-myristoyltransferase 2	0.611	0.250
213005_s_at	ANKRD15	ankyrin repeat domain 15	0.369	0.250
225409_at	MGC52110	hypothetical protein MGC52110	0.664	0.250
204992_s_at	PFN2	profilin 2	0.618	0.250
243764_at	VSIG1	V-set and immunoglobulin domain containing 1	0.617	0.250
207651_at	GPR171	G protein-coupled receptor 171	0.624	0.250
235912_at	FAM62B	Family with sequence similarity 62 (C2 domain containing) member B	0.657	0.250
209267_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	0.604	0.250
235611_at	---	---	0.661	0.250
243362_s_at	LOC641518	hypothetical protein LOC641518	0.537	0.250
241038_at	CHRM3	Cholinergic receptor, muscarinic 3	0.604	0.250
1557078_at	SLFN5	schlafen family member 5	0.576	0.250
228282_at	MGC33302	Hypothetical protein MGC33302	0.647	0.250
224968_at	CCDC104	coiled-coil domain containing 104	0.599	0.250
222623_s_at	ZNF639	zinc finger protein 639	0.622	0.250
237953_at	DPP4	Dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	0.520	0.250
222736_s_at	TMEM38B	transmembrane protein 38B	0.611	0.250
238907_at	ZNF780A	Zinc finger protein 780A	0.643	0.250
213063_at	ZC3H14	zinc finger CCCH-type containing 14	0.640	0.250
228948_at	EPHA4	EPH receptor A4	0.516	0.250
227722_at	RPS23	ribosomal protein S23	0.565	0.250
244679_at	STK38	Serine/threonine kinase 38	0.648	0.250
217936_at	ARHGAP5	Rho GTPase activating protein 5	0.546	0.250
229327_s_at	---	Transcribed locus	0.558	0.250
228561_at	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	0.548	0.250
214086_s_at	PARP2	poly (ADP-ribose) polymerase family, member 2	0.639	0.250
1562731_s_at	MDS2	myelodysplastic syndrome 2 translocation associated	0.514	0.250
239673_at	NR3C2	Nuclear receptor subfamily 3, group C, member 2	0.618	0.250
209064_x_at	PAIP1	poly(A) binding protein interacting protein 1	0.610	0.250
226444_at	SLC39A10	Solute carrier family 39 (zinc transporter), member 10	0.633	0.250
212196_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.637	0.250
208798_x_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	0.653	0.250
213376_at	ZBTB1	zinc finger and BTB domain containing 1	0.658	0.250
240572_s_at	LOC374443	CLR pseudogene	0.644	0.250
230399_at	---	Transcribed locus	0.659	0.250
227606_s_at	STAMBPL1	STAM binding protein-like 1	0.593	0.250

212637_s_at	WWP1	WW domain containing E3 ubiquitin protein ligase 1	0.638	0.250
205176_s_at	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	0.604	0.250
225619_at	SLAIN1	SLAIN motif family, member 1	0.623	0.250
218948_at	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	0.540	0.250
235414_at	ZNF383	zinc finger protein 383	0.619	0.250
213701_at	C12orf29	chromosome 12 open reading frame 29	0.587	0.250
217911_s_at	BAG3	BCL2-associated athanogene 3	0.566	0.250
221564_at	PRMT2	protein arginine methyltransferase 2	0.636	0.250
234849_at	TRA@	T cell receptor alpha locus	0.610	0.250
240394_at	---	Transcribed locus	0.534	0.250
242539_at	LOC730069 /// LOC731484	similar to nuclear receptor binding factor 2 /// similar to nuclear receptor binding factor 2	0.590	0.250
230075_at	RAB39B	RAB39B, member RAS oncogene family	0.640	0.250
239479_x_at	CHRM3	Cholinergic receptor, muscarinic 3	0.580	0.250
203492_x_at	CEP57	centrosomal protein 57kDa	0.641	0.250
203972_s_at	PEX3	peroxisomal biogenesis factor 3	0.621	0.250
226587_at	---	CDNA FLJ33569 fis, clone BRAMY2010317	0.633	0.250
1565830_at	---	MRNA; cDNA DKFZp686D0673 (from clone DKFZp686D0673)	0.634	0.250
228736_at	HEL308	DNA helicase HEL308	0.658	0.250
228345_at	---	---	0.600	0.250
1558250_s_at	---	CDNA FLJ40891 fis, clone UTERU2001110	0.603	0.250
228334_x_at	KIAA1712	KIAA1712	0.645	0.250
1554089_s_at	SBDS /// SBDSP	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	0.616	0.250
204777_s_at	MAL	mal, T-cell differentiation protein	0.617	0.250
226925_at	ACPL2	acid phosphatase-like 2	0.575	0.250
242761_s_at	ZNF420	zinc finger protein 420	0.615	0.250
216069_at	PRMT2	Protein arginine methyltransferase 2	0.628	0.250
1558971_at	C6orf190	chromosome 6 open reading frame 190	0.568	0.250
212614_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	0.662	0.250
225805_at	HNRPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.655	0.250
243999_at	SLFN5	schlafen family member 5	0.591	0.250
226030_at	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	0.610	0.250
230793_at	LRRC16	leucine rich repeat containing 16	0.543	0.250
225328_at	---	CDNA FLJ39585 fis, clone SKMUS2006633	0.486	0.250
228129_at	SERBP1	SERPINE1 mRNA binding protein 1	0.615	0.250
211861_x_at	CD28	CD28 molecule	0.534	0.250
201872_s_at	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	0.652	0.250
227182_at	SUSD3	sushi domain containing 3	0.630	0.250
212217_at	PREPL	prolyl endopeptidase-like	0.631	0.250
203642_s_at	COBLL1	COBL-like 1	0.657	0.250
1552519_at	ACVR1C	activin A receptor, type IC	0.483	0.250
206181_at	SLAMF1	signaling lymphocytic activation molecule family member 1	0.576	0.250
227022_at	GNPDA2	glucosamine-6-phosphate deaminase 2	0.538	0.250

235048_at	KIAA0888	KIAA0888 protein	0.538	0.250
39248_at	AQP3	aquaporin 3 (Gill blood group)	0.648	0.250
218477_at	TMEM14A	transmembrane protein 14A	0.607	0.250
239591_at	---	Transcribed locus	0.271	0.250
225543_at	GTF3C4	General transcription factor IIIC, polypeptide 4, 90kDa	0.664	0.250
226977_at	LOC492311	similar to bovine IgA regulatory protein	0.606	0.250
219700_at	PLXDC1	plexin domain containing 1	0.622	0.250
225155_at	SNHG5	small nucleolar RNA host gene (non-protein coding) 5	0.600	0.250
1555325_s_at	ZNF26	zinc finger protein 26	0.612	0.250
205758_at	CD8A	CD8a molecule /// CD8a molecule	0.620	0.250
230056_at	BPTF	bromodomain PHD finger transcription factor	0.608	0.250
238695_s_at	RAB39B	RAB39B, member RAS oncogene family	0.609	0.250
229371_at	SLC20A2	Solute carrier family 20 (phosphate transporter), member 2	0.636	0.250
1556451_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	0.619	0.250
202722_s_at	GFPT1	glutamine-fructose-6-phosphate transaminase 1	0.588	0.250
228122_at	CCDC66	coiled-coil domain containing 66	0.622	0.250
1564424_at	FAM62B	Family with sequence similarity 62 (C2 domain containing) member B	0.627	0.250
217777_s_at	PTPLAD1 /// LOC732402	protein tyrosine phosphatase-like A domain containing 1 /// similar to butyrate-induced transcript 1	0.613	0.250
205053_at	PRIM1	primase, polypeptide 1, 49kDa	0.582	0.250
201922_at	TINP1	TGF beta-inducible nuclear protein 1	0.644	0.250
204401_at	KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	0.665	0.250
209434_s_at	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.611	0.250
207904_s_at	LNPEP	leucyl/cystinyl aminopeptidase	0.641	0.250
206958_s_at	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	0.635	0.250
228661_s_at	---	CDNA FLJ11489 fis, clone HEMBA1001915	0.589	0.250
225400_at	C1orf19	chromosome 1 open reading frame 19	0.644	0.250
226605_at	DGKQ	diacylglycerol kinase, theta 110kDa	0.635	0.250
219355_at	CXorf57	chromosome X open reading frame 57	0.551	0.250
212249_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	0.626	0.250
220882_at	---	---	0.632	0.250
226807_at	ZFP1	zinc finger protein 1 homolog (mouse)	0.623	0.250
225698_at	C5orf26	chromosome 5 open reading frame 26	0.660	0.250
211563_s_at	C19orf2	chromosome 19 open reading frame 2	0.631	0.250
227172_at	TMEM116	transmembrane protein 116	0.627	0.250
203427_at	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.625	0.250
1558700_s_at	ZNF260	zinc finger protein 260	0.663	0.250
243176_at	---	CDNA FLJ30090 fis, clone BNGH41000015	0.637	0.341
243602_at	MGC40069	Hypothetical protein MGC40069	0.578	0.341
209849_s_at	RAD51C	RAD51 homolog C (S. cerevisiae)	0.625	0.341
1554667_s_at	METTL8	methyltransferase like 8	0.666	0.341
1569482_at	---	CDNA clone IMAGE:5262617	0.627	0.341

226886_at	---	Clone 114 tumor rejection antigen	0.636	0.341
226528_at	MTX3	metaxin 3	0.643	0.341
205976_at	FASTKD2	FAST kinase domains 2	0.597	0.341
214482_at	ZBTB25	zinc finger and BTB domain containing 25	0.564	0.341
243791_at	---	Transcribed locus	0.606	0.341
226784_at	TWISTNB	TWIST neighbor	0.626	0.341
203367_at	DUSP14	dual specificity phosphatase 14	0.664	0.341
1557555_at	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	0.592	0.341
206255_at	BLK	B lymphoid tyrosine kinase	0.505	0.341
204023_at	RFC4	replication factor C (activator 1) 4, 37kDa	0.585	0.341
1555793_a_at	ZNF545	zinc finger protein 545	0.646	0.341
203543_s_at	KLF9	Kruppel-like factor 9	0.600	0.341
224367_at	BEX2	brain expressed X-linked 2 /// brain expressed X-linked 2	0.528	0.341
209862_s_at	CEP57	centrosomal protein 57kDa	0.597	0.341
236856_x_at	---	CDNA FLJ34374 fis, clone FEBRA2017502	0.609	0.341
200841_s_at	EPRS	glutamyl-prolyl-tRNA synthetase	0.640	0.341
206613_s_at	TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	0.613	0.341
1555964_at	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	0.607	0.341
238451_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	0.610	0.341
215592_at	---	CDNA FLJ12232 fis, clone MAMMA1001206	0.635	0.341
227082_at	---	MRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)	0.614	0.341
225864_at	FAM84B	family with sequence similarity 84, member B	0.559	0.341
219600_s_at	TMEM50B	transmembrane protein 50B	0.629	0.341
1564776_at	LENG10	leukocyte receptor cluster (LRC) member 10	0.442	0.341
229119_s_at	ACTB /// SWS1	actin, beta /// SWIM-domain containing Srs2 interacting protein 1	0.633	0.341
222629_at	REV1	REV1 homolog (S. cerevisiae)	0.667	0.341
206804_at	CD3G	CD3g molecule, gamma (CD3-TCR complex)	0.627	0.341
227291_s_at	BOLA3	bolA homolog 3 (E. coli)	0.659	0.341
243626_at	---	Transcribed locus, moderately similar to XP_944674.2 similar to alpha 3 type VI collagen isoform 1 precursor [Homo sapiens]	0.552	0.341
231530_s_at	C11orf1	chromosome 11 open reading frame 1	0.548	0.341
1565895_at	---	Transcribed locus	0.662	0.341
225359_at	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	0.663	0.341
236301_at	---	Full length insert cDNA clone YY82H04	0.658	0.341
212851_at	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	0.609	0.341
243546_at	SESN3	Sestrin 3	0.579	0.341
217394_at	TRA@	T cell receptor alpha locus	0.649	0.341
213539_at	CD3D	CD3d molecule, delta (CD3-TCR complex)	0.574	0.341
225595_at	CREBZF	CREB/ATF bZIP transcription factor	0.643	0.341
221935_s_at	C3orf64	chromosome 3 open reading frame 64	0.632	0.341
205599_at	TRAF1	TNF receptor-associated factor 1	0.647	0.341
223096_at	NOP5/NOP58	nucleolar protein NOP5/NOP58	0.665	0.341
213983_s_at	SCC-112	SCC-112 protein	0.645	0.341
219133_at	OXSM	3-oxoacyl-ACP synthase, mitochondrial	0.615	0.341

236796_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	0.655	0.341
206734_at	JRKL	jerky homolog-like (mouse)	0.630	0.341
238635_at	C5orf28	chromosome 5 open reading frame 28	0.660	0.341
220797_at	METT10D	methyltransferase 10 domain containing	0.649	0.341
222785_x_at	C11orf1	chromosome 11 open reading frame 1	0.576	0.341
205590_at	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	0.641	0.341
202020_s_at	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	0.647	0.341
227393_at	TMEM16J	transmembrane protein 16J	0.665	0.341
218706_s_at	GRAMD3	GRAM domain containing 3	0.655	0.341
200685_at	SFRS11	splicing factor, arginine/serine-rich 11	0.621	0.341
1558517_s_at	LRRC8C	Leucine rich repeat containing 8 family, member C	0.658	0.341
213534_s_at	PASK	PAS domain containing serine/threonine kinase	0.608	0.341
228909_at	C21orf86	Chromosome 21 open reading frame 86	0.523	0.341
1556462_a_at	LOC730245	Hypothetical protein LOC730245	0.563	0.341
222819_at	CTPS2	CTP synthase II	0.650	0.341
226247_at	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	0.644	0.341
230300_at	---	CDNA FLJ42315 fis, clone TRACH2019661	0.612	0.341
202265_at	BMI1	B lymphoma Mo-MLV insertion region (mouse)	0.631	0.341
223093_at	ANKH	ankylosis, progressive homolog (mouse)	0.631	0.341
215708_s_at	PRIM2A	primase, polypeptide 2A, 58kDa	0.627	0.341
238692_at	BTBD11	BTB (POZ) domain containing 11	0.565	0.341
219869_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	0.621	0.341
214823_at	ZNF204	zinc finger protein 204	0.412	0.341
205041_s_at	ORM1 /// ORM2	orosomucoid 1 /// orosomucoid 2	0.426	0.341
209889_at	SEC31B	SEC31 homolog B (S. cerevisiae)	0.648	0.341
229323_at	LOC387723 /// LOC651940	hypothetical LOC387723 /// hypothetical protein LOC651940	0.625	0.341
221897_at	TRIM52	tripartite motif-containing 52	0.650	0.341
207057_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	0.627	0.341
214662_at	WDR43	WD repeat domain 43	0.652	0.341
243492_at	THEM4	Thioesterase superfamily member 4	0.631	0.341
216044_x_at	FAM69A	family with sequence similarity 69, member A	0.637	0.341
1561181_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	0.625	0.341
228680_at	KIF3A	kinesin family member 3A	0.651	0.341
220121_at	LINS1	lines homolog 1 (Drosophila)	0.634	0.341
220606_s_at	C17orf48	chromosome 17 open reading frame 48	0.641	0.341
228920_at	ZNF260	zinc finger protein 260	0.642	0.341
221618_s_at	TAF9B /// LOC728198	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa /// similar to transcription associated factor 9B	0.516	0.341
211423_s_at	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	0.576	0.341
235172_at	GABPB2	GA binding protein transcription factor, beta subunit 2	0.537	0.341

234427_at	TRA@	T cell receptor alpha locus /// T cell receptor alpha chain (TRCAV2S1-N-AJ41-C) mRNA, anti-melanoma cytotoxic T lymphocyte clone MU-45, -63, -79	0.442	0.341
224365_s_at	TIGD7	tigger transposable element derived 7 /// tigger transposable element derived 7	0.629	0.341
210612_s_at	SYNJ2	synaptojanin 2	0.493	0.341
1569110_x_at	LOC728613	programmed cell death protein 6-like	0.645	0.341
239317_at	---	---	0.615	0.341
1554208_at	RP5-821D11.2	meiosis defective 1	0.633	0.341
239147_at	ARSK	arylsulfatase family, member K	0.617	0.341
239482_x_at	ZNF708	Zinc finger protein 708	0.636	0.341
221973_at	---	CDNA clone IMAGE:5217021, with apparent retained intron	0.656	0.341
203970_s_at	PEX3	peroxisomal biogenesis factor 3	0.610	0.341
215175_at	PCNX	pecanex homolog (Drosophila)	0.632	0.341
222735_at	---	---	0.649	0.341
202979_s_at	CREBZF	CREB/ATF bZIP transcription factor	0.643	0.341
212096_s_at	MTUS1	mitochondrial tumor suppressor 1	0.513	0.341
208602_x_at	CD6	CD6 molecule	0.661	0.341
241699_at	RY1	Putative nucleic acid binding protein RY-1	0.651	0.341
205321_at	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	0.568	0.341
220553_s_at	TAF13 /// PRPF39	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa /// PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	0.632	0.341
203493_s_at	CEP57	centrosomal protein 57kDa	0.626	0.341
220132_s_at	CLEC2D	C-type lectin domain family 2, member D	0.635	0.341
213528_at	C1orf156	chromosome 1 open reading frame 156	0.594	0.341
1568680_s_at	YTHDC2	YTH domain containing 2	0.638	0.341
209602_s_at	GATA3	GATA binding protein 3	0.622	0.341
218984_at	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	0.652	0.341
222579_at	UBE1DC1	ubiquitin-activating enzyme E1-domain containing 1	0.595	0.341
234402_at	TRA@	T cell receptor alpha locus /// T-cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AE212	0.638	0.341
229428_at	PARG	Poly (ADP-ribose) glycohydrolase	0.624	0.341
205288_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.632	0.341
228518_at	IGH@ /// IGHG1 /// IGHM	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu	0.581	0.341
214831_at	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	0.666	0.341
1558956_s_at	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	0.654	0.341
235036_at	LIX1L	Lix1 homolog (mouse)-like	0.639	0.341
203803_at	PCYOX1	prenylcysteine oxidase 1	0.651	0.341
233500_x_at	CLEC2D	C-type lectin domain family 2, member D	0.624	0.341
206059_at	ZNF91	zinc finger protein 91	0.655	0.341
226682_at	LOC283666	hypothetical protein LOC283666	0.656	0.341
225752_at	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	0.631	0.341

233415_at	ERCC5	Excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	0.557	0.341
218545_at	CCDC91	coiled-coil domain containing 91	0.621	0.341
203712_at	KIAA0020	KIAA0020	0.659	0.341
214250_at	NUMA1	nuclear mitotic apparatus protein 1	0.512	0.341
1553380_at	PARP15	poly (ADP-ribose) polymerase family, member 15	0.614	0.341
230020_at	---	Transcribed locus	0.584	0.341
219854_at	ZNF14	zinc finger protein 14	0.633	0.341
1558605_at	---	CDNA clone IMAGE:4819775	0.563	0.341
227559_at	---	---	0.552	0.341
226098_at	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	0.648	0.341
207417_s_at	ZNF177	zinc finger protein 177	0.655	0.341
238940_at	KLF12	Kruppel-like factor 12	0.644	0.341
213677_s_at	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	0.628	0.341
202741_at	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	0.658	0.341
204215_at	C7orf23	chromosome 7 open reading frame 23	0.658	0.341
239709_at	RP11-78J21.1	Heterogeneous nuclear ribonucleoprotein A1-like	0.647	0.341
226989_at	RGMB	RGM domain family, member B	0.363	0.341
244189_at	KIAA1648	KIAA1648 protein	0.485	0.341
204547_at	RAB40B	RAB40B, member RAS oncogene family	0.628	0.341
1567213_at	PNN	pinin, desmosome associated protein	0.620	0.341
1560741_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	0.616	0.341
229252_at	ATG9B	ATG9 autophagy related 9 homolog B (S. cerevisiae)	0.479	0.341
227859_at	RBJ	Ras-associated protein Rap1	0.649	0.341
224860_at	C9orf123	chromosome 9 open reading frame 123	0.593	0.341
226934_at	---	CDNA FLJ41019 fis, clone UTERU2019096	0.572	0.341
219368_at	NAP1L2	nucleosome assembly protein 1-like 2	0.502	0.341
237746_at	SFRS11	Splicing factor, arginine/serine-rich 11	0.488	0.341
243150_at	---	Transcribed locus	0.664	0.341
205047_s_at	ASNS	asparagine synthetase	0.657	0.341
243899_at	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	0.599	0.341
1558512_at	---	CDNA FLJ33400 fis, clone BRACE2009828	0.635	0.341
219595_at	ZNF26	zinc finger protein 26	0.637	0.341
1555004_a_at	RBL1	retinoblastoma-like 1 (p107)	0.643	0.341
244631_at	LOC389834 /// LOC642398 /// LOC727834	hypothetical gene supported by AK123403 /// hypothetical LOC642398 /// hypothetical protein LOC727834	0.333	0.341
212855_at	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	0.650	0.341
210180_s_at	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	0.658	0.341
227385_at	PPAPDC2	phosphatidic acid phosphatase type 2 domain containing 2	0.661	0.341
1557433_at	GPSM2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0.612	0.341
218006_s_at	ZNF22	zinc finger protein 22 (KOX 15)	0.621	0.341

239017_at	---	Transcribed locus, moderately similar to XP_944674.2 similar to alpha 3 type VI collagen isoform 1 precursor [Homo sapiens]	0.633	0.341
232291_at	C13orf25	chromosome 13 open reading frame 25	0.666	0.341
223433_at	C7orf36	chromosome 7 open reading frame 36	0.644	0.341
231022_at	NAIP	similar to Occludin	0.632	0.341
223588_at	THAP2	THAP domain containing, apoptosis associated protein 2	0.620	0.341
244045_at	---	---	0.660	0.341
230187_s_at	---	Full-length cDNA clone CS0DI042YD07 of Placenta Cot 25-normalized of Homo sapiens (human)	0.565	0.341
236935_at	---	CDNA clone IMAGE:4813920	0.625	0.341
214180_at	MAN1C1	mannosidase, alpha, class 1C, member 1	0.641	0.341
238501_at	---	Transcribed locus	0.636	0.341
216945_x_at	PASK	PAS domain containing serine/threonine kinase	0.616	0.341
242509_at	C16orf74	Chromosome 16 open reading frame 74	0.627	0.341
211856_x_at	CD28	CD28 molecule	0.559	0.341
219871_at	FLJ13197 /// LOC727852 /// LOC731366	hypothetical protein FLJ13197 /// hypothetical protein LOC727852 /// hypothetical protein LOC731366	0.628	0.503
1563182_at	---	CDNA clone IMAGE:4796641	0.521	0.503
211675_s_at	MDFIC	MyoD family inhibitor domain containing /// MyoD family inhibitor domain containing	0.641	0.503
213060_s_at	CHI3L2	chitinase 3-like 2 /// chitinase 3-like 2	0.517	0.503
210278_s_at	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	0.644	0.503
228242_at	---	---	0.609	0.503
203893_at	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	0.605	0.503
208664_s_at	TTC3	tetratricopeptide repeat domain 3	0.556	0.503
210718_s_at	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	0.493	0.503
1555543_a_at	CLCC1	chloride channel CLIC-like 1	0.615	0.503
1568836_at	CLK4	CDC-like kinase 4	0.601	0.503
1554878_a_at	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	0.657	0.503
221256_s_at	HDHD3	haloacid dehalogenase-like hydrolase domain containing 3 /// haloacid dehalogenase-like hydrolase domain containing 3	0.638	0.503
218490_s_at	ZNF302	zinc finger protein 302	0.543	0.503
227149_at	TNRC6C	trinucleotide repeat containing 6C	0.647	0.503
235302_at	---	Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)	0.648	0.503
238774_at	KIAA1267	KIAA1267	0.595	0.503
209442_x_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.609	0.503
242523_at	---	Transcribed locus	0.571	0.503
204794_at	DUSP2	dual specificity phosphatase 2	0.660	0.503
242900_at	---	CDNA FLJ41107 fis, clone BLADE2007923	0.655	0.503
222502_s_at	UFM1	ubiquitin-fold modifier 1	0.630	0.503

210034_s_at	RPL5 /// LOC388907 /// LOC642146 /// LOC647436	ribosomal protein L5 /// similar to ribosomal protein L5 /// similar to ribosomal protein L5 /// similar to ribosomal protein L5	0.596	0.503
225358_at	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	0.613	0.503
204148_s_at	ZP3 /// POMZP3 /// MEIS3	zona pellucida glycoprotein 3 (sperm receptor) /// POM (POM121 homolog, rat) and ZP3 fusion /// Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)	0.547	0.503
237009_at	CD69	CD69 molecule	0.566	0.503
218005_at	ZNF22	zinc finger protein 22 (KOX 15)	0.637	0.503
215743_at	NMT2	N-myristoyltransferase 2	0.627	0.503
211209_x_at	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	0.586	0.503
1558093_s_at	MATR3	matrin 3	0.617	0.503
203856_at	VRK1	vaccinia related kinase 1	0.636	0.503
211106_at	SUPT3H	suppressor of Ty 3 homolog (S. cerevisiae)	0.542	0.503
231975_s_at	MIER3	mesoderm induction early response 1, family member 3	0.593	0.503
238174_at	FBXL17	F-box and leucine-rich repeat protein 17	0.666	0.503
210910_s_at	POMZP3	POM (POM121 homolog, rat) and ZP3 fusion	0.486	0.503
235230_at	PLCXD2	Phosphatidylinositol-specific phospholipase C, X domain containing 2	0.639	0.503
230388_s_at	LOC644246	hypothetical protein LOC644246	0.564	0.503
1554609_at	MGC12965	similar to Cytochrome c, somatic	0.574	0.503
224364_s_at	PPIL3	peptidylprolyl isomerase (cyclophilin)-like 3 /// peptidylprolyl isomerase (cyclophilin)-like 3	0.652	0.503
210435_at	LOC641522	ADP-ribosylation factor-like protein	0.407	0.503
232341_x_at	HABP4	hyaluronan binding protein 4	0.659	0.503
228908_s_at	C21orf86	Chromosome 21 open reading frame 86	0.635	0.503
227141_at	TYW3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	0.647	0.503
225455_at	TADA1L	transcriptional adaptor 1 (HFI1 homolog, yeast)-like	0.642	0.503
226290_at	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	0.661	0.503
243179_at	---	CDNA FLJ33993 fis, clone DFNES2007757	0.634	0.503
227375_at	ANKRD13C	ankyrin repeat domain 13C	0.618	0.503
223118_s_at	USP47	ubiquitin specific peptidase 47	0.653	0.503
217850_at	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	0.651	0.503
216166_at	RHOH	Ras homolog gene family, member H	0.577	0.503
219038_at	MORC4	MORC family CW-type zinc finger 4	0.619	0.503
227641_at	FBXL16	F-box and leucine-rich repeat protein 16	0.643	0.503
1555830_s_at	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	0.533	0.503
1555355_a_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.643	0.503
226475_at	FAM118A	family with sequence similarity 118, member A	0.655	0.503
210078_s_at	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	0.610	0.503

209993_at	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.634	0.503
214470_at	KLRB1	killer cell lectin-like receptor subfamily B, member 1 /// killer cell lectin-like receptor subfamily B, member 1	0.521	0.503
224507_s_at	MGC12916	hypothetical protein MGC12916 /// hypothetical protein MGC12916	0.652	0.503
201313_at	ENO2	enolase 2 (gamma, neuronal)	0.653	0.503
205371_s_at	DBT	dihydrolipoamide branched chain transacylase E2	0.652	0.503
213645_at	ENOSF1	enolase superfamily member 1	0.616	0.503
241819_at	---	---	0.659	0.503
222201_s_at	CASP8AP2	CASP8 associated protein 2	0.655	0.503
216683_at	TBCA	Tubulin folding cofactor A	0.584	0.503
1556839_s_at	SPTBN5 /// VEPH1	Homo sapiens, clone IMAGE:4704591 /// Spectrin, beta, non-erythrocytic 5 /// Ventricular zone expressed PH domain homolog 1 (zebrafish)	0.608	0.503
221683_s_at	CEP290	centrosomal protein 290kDa	0.605	0.503
227678_at	XRCC6BP1	XRCC6 binding protein 1	0.572	0.503
1555691_a_at	KLRC4 /// KLRK1	killer cell lectin-like receptor subfamily C, member 4 /// killer cell lectin-like receptor subfamily K, member 1	0.574	0.503
226642_s_at	NUDCD2	NudC domain containing 2	0.658	0.503
235652_at	SCML1	Sex comb on midleg-like 1 (Drosophila)	0.558	0.503
216056_at	CD44	CD44 molecule (Indian blood group)	0.610	0.503
235260_s_at	C4orf28	chromosome 4 open reading frame 28	0.630	0.503
210694_s_at	---	---	0.608	0.503
218859_s_at	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	0.655	0.503
224713_at	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	0.633	0.503
1564435_a_at	KRT72	keratin 72	0.373	0.503
235101_at	FNBP4	formin binding protein 4	0.644	0.503
226350_at	CHML	choroideremia-like (Rab escort protein 2)	0.645	0.503
216850_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	0.604	0.503
223089_at	VEZT	vezatin, adherens junctions transmembrane protein	0.584	0.503
225594_at	CREBZF	CREB/ATF bZIP transcription factor	0.651	0.503
235540_at	---	---	0.623	0.503
236106_at	C17orf67	Chromosome 17 open reading frame 67	0.632	0.503
210676_x_at	RGPD5 /// RGPD8 /// RGPD6	RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 8 /// RANBP2-like and GRIP domain containing 6	0.652	0.503
202843_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.646	0.503
203362_s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.644	0.503
1560171_at	SHPRH	SNF2 histone linker PHD RING helicase	0.641	0.503
231241_at	LOC645744	Similar to PCAF associated factor 65 beta isoform b	0.659	0.503
230149_at	---	Transcribed locus	0.543	0.503
225424_at	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	0.658	0.503
218127_at	NFYB	nuclear transcription factor Y, beta	0.589	0.503
1555890_at	LOC728377	Similar to rho guanine nucleotide exchange factor 5	0.660	0.503
1569040_s_at	FLJ40330	similar to protein immuno-reactive with anti-PTH polyclonal antibodies	0.422	0.503
222580_at	ZNF644	zinc finger protein 644	0.664	0.503

1565811_at	---	CDNA clone IMAGE:5278245	0.638	0.503
227124_at	LOC221710	Hypothetical protein LOC221710	0.647	0.503
244490_at	---	MRNA; cDNA DKFZp686B0610 (from clone DKFZp686B0610)	0.618	0.503
224285_at	GPR174	G protein-coupled receptor 174	0.633	0.503
239385_at	TFG	TRK-fused gene	0.656	0.503
231964_at	---	MRNA; cDNA DKFZp564H1663 (from clone DKFZp564H1663)	0.633	0.503
205250_s_at	CEP290	centrosomal protein 290kDa	0.614	0.503
216050_at	---	CDNA: FLJ20931 fis, clone ADSE01282	0.562	0.503
222805_at	MANEA	mannosidase, endo-alpha	0.638	0.503
213687_s_at	RPL35A	ribosomal protein L35a	0.625	0.503
204917_s_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	0.664	0.503
226764_at	LOC152485	hypothetical protein LOC152485	0.652	0.503
201485_s_at	RCN2	reticulocalbin 2, EF-hand calcium binding domain	0.628	0.503
232063_x_at	FARSLB	phenylalanine-tRNA synthetase-like, beta subunit	0.580	0.679
239063_at	---	CDNA FLJ39803 fis, clone SPLEN2007794	0.644	0.679
235635_at	ARHGAP5	Rho GTPase activating protein 5	0.632	0.679
207583_at	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	0.635	0.679
1558842_at	---	---	0.536	0.679
223079_s_at	GLS	glutaminase	0.622	0.679
222073_at	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	0.455	0.679
217482_at	---	CDNA FLJ11925 fis, clone HEMBB1000354	0.628	0.679
213304_at	KIAA0423	KIAA0423	0.650	0.679
209433_s_at	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.497	0.679
228961_at	MIER3	mesoderm induction early response 1, family member 3	0.653	0.679
204905_s_at	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	0.512	0.679
211709_s_at	CLEC11A	C-type lectin domain family 11, member A /// C-type lectin domain family 11, member A	0.412	0.679
242363_at	---	Full-length cDNA clone CS0DF025YA01 of Fetal brain of Homo sapiens (human)	0.660	0.679
220048_at	EDAR	ectodysplasin A receptor	0.576	0.679
225088_at	C16orf63	chromosome 16 open reading frame 63	0.586	0.679
219049_at	ChGn	chondroitin beta1,4 N-acetylgalactosaminyltransferase	0.636	0.679
1553400_a_at	C17orf69	chromosome 17 open reading frame 69	0.625	0.679
200705_s_at	EEF1B2	eukaryotic translation elongation factor 1 beta 2	0.578	0.679
222128_at	NSUN6	NOL1/NOP2/Sun domain family, member 6	0.651	0.679
240246_at	---	CDNA FLJ44826 fis, clone BRACE3046762	0.531	0.679
235535_x_at	FRG1 /// MGC72104 /// LOC642236 /// LOC730510	FSHD region gene 1 /// similar to FRG1 protein (FSHD region gene 1 protein) /// similar to FRG1 protein (FSHD region gene 1 protein) /// similar to FRG1 protein (FSHD region gene 1 protein)	0.584	0.679
235150_at	---	MRNA; cDNA DKFZp313B1017 (from clone DKFZp313B1017)	0.595	0.679
204559_s_at	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.663	0.679
236316_at	FAM3C	family with sequence similarity 3, member C	0.590	0.679

215339_at	NKTR	natural killer-tumor recognition sequence	0.613	0.679
230305_at	---	Transcribed locus	0.568	0.679
242393_x_at	LOC399761 /// LOC643564 /// CTGLF9P /// CTGLF2	hypothetical protein LOC399761 /// hypothetical protein LOC643564 /// centaurin, gamma-like family, member 9 pseudogene /// centaurin, gamma-like family, member 2	0.647	0.679
202260_s_at	STXBP1	syntaxin binding protein 1	0.607	0.679
235170_at	ZNF92	zinc finger protein 92	0.620	0.679
239266_at	SNHG5	Small nucleolar RNA host gene (non-protein coding) 5	0.661	0.679
221092_at	IKZF3	IKAROS family zinc finger 3 (Aiolos)	0.534	0.679
1555120_at	CD96	CD96 molecule	0.617	0.679
223681_s_at	INADL	InaD-like (Drosophila)	0.649	0.679
233519_at	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	0.558	0.679
227255_at	PDIK1L	PDLIM1 interacting kinase 1 like	0.667	0.679
200002_at	RPL35	ribosomal protein L35 /// ribosomal protein L35	0.663	0.679
1557166_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	0.654	0.679
1555913_at	GON4L	gon-4-like (C. elegans)	0.648	0.679
210690_at	KLRC4	killer cell lectin-like receptor subfamily C, member 4	0.513	0.679
240829_at	PEX3	Peroxisomal biogenesis factor 3	0.642	0.679
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	0.581	0.679
243835_at	ZDHHC21	Zinc finger, DHHC-type containing 21	0.569	0.679
1554606_at	CCDC100	coiled-coil domain containing 100	0.656	0.679
232164_s_at	EPPK1	epiplakin 1	0.454	0.679
1559401_a_at	ZNF609	Zinc finger protein 609	0.645	0.679
226003_at	KIF21A	kinesin family member 21A	0.632	0.679
243319_at	MED31	Mediator of RNA polymerase II transcription, subunit 31 homolog (S. cerevisiae)	0.655	0.679
214251_s_at	NUMA1	nuclear mitotic apparatus protein 1	0.656	0.679
210461_s_at	ABLIM1	actin binding LIM protein 1	0.661	0.679
210639_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	0.662	0.679
235616_at	---	---	0.419	0.679
229028_s_at	LOC641522	ADP-ribosylation factor-like protein	0.586	0.679
1555125_at	C21orf66	chromosome 21 open reading frame 66	0.652	0.679
1554450_s_at	MIER3	mesoderm induction early response 1, family member 3	0.645	0.679
236760_at	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	0.616	0.679
238443_at	---	---	0.633	0.679
242577_at	LOC642398 /// LOC727834	hypothetical LOC642398 /// hypothetical protein LOC727834	0.368	0.679
206497_at	C7orf44	chromosome 7 open reading frame 44	0.665	0.679
243093_at	---	---	0.660	0.679
228529_at	---	Transcribed locus	0.641	0.679
207845_s_at	ANAPC10	anaphase promoting complex subunit 10	0.625	0.679
229437_at	BIC	BIC transcript	0.554	0.679
240070_at	VSIG9	V-set and immunoglobulin domain containing 9	0.653	0.679

244035_at	BCL2	B-cell CLL/lymphoma 2	0.461	0.679
220444_at	ZNF557	zinc finger protein 557	0.563	0.679
202512_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	0.625	0.679
1558279_a_at	---	CDNA FLJ36555 fis, clone TRACH2008716	0.666	0.679
1568658_at	LOC339804	hypothetical gene supported by AK075484; BC014578	0.640	0.679
214567_s_at	XCL1 /// XCL2	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	0.625	0.679
235296_at	EIF5A2	eukaryotic translation initiation factor 5A2	0.636	0.679
204353_s_at	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	0.661	0.679
242134_at	---	Transcribed locus	0.641	0.679
205139_s_at	UST	uronyl-2-sulfotransferase	0.641	0.679
228050_at	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	0.658	0.679
201757_at	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	0.637	0.925
214097_at	RPS21	ribosomal protein S21	0.641	0.925
1555972_s_at	FBXO28	F-box protein 28	0.658	0.925
206157_at	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	0.657	0.925
229187_at	ZNF542 /// MGC72104	Zinc finger protein 542 /// Similar to FRG1 protein (FSHD region gene 1 protein)	0.635	0.925
205040_at	ORM1	orosomucoid 1	0.535	0.925
227993_at	METAP2	methionyl aminopeptidase 2	0.660	0.925
213461_at	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.663	0.925
209662_at	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	0.623	0.925
225014_at	LOC389203	hypothetical gene supported by BC032431	0.613	0.925
223301_s_at	CCDC82	coiled-coil domain containing 82	0.658	0.925
218129_s_at	NFYB	nuclear transcription factor Y, beta	0.540	0.925
223231_at	TATDN1	TatD DNase domain containing 1	0.612	0.925
220961_s_at	TBRG4	transforming growth factor beta regulator 4 /// transforming growth factor beta regulator 4	0.533	0.925
234165_at	PTGDR	prostaglandin D2 receptor (DP)	0.666	0.925
219073_s_at	OSBPL10	oxysterol binding protein-like 10	0.588	0.925
214876_s_at	TUBGCP5	tubulin, gamma complex associated protein 5	0.661	0.925
218100_s_at	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	0.579	0.925
224841_x_at	GAS5	growth arrest-specific 5	0.575	0.925
1553055_a_at	SLFN5	schlafen family member 5	0.613	0.925
236341_at	CTLA4	cytotoxic T-lymphocyte-associated protein 4	0.627	0.925
201812_s_at	TOMM7 /// LOC201725	translocase of outer mitochondrial membrane 7 homolog (yeast) /// hypothetical protein LOC201725	0.588	0.925
229656_s_at	FLJ42562	similar to echinoderm microtubule associated protein like 5	0.575	0.925
212765_at	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	0.596	0.925
213683_at	ACSL6	acyl-CoA synthetase long-chain family member 6	0.629	0.925
237839_at	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)	0.533	0.925
212216_at	PREPL	prolyl endopeptidase-like	0.588	0.925
219109_at	SPAG16	sperm associated antigen 16	0.613	0.925
205230_at	RPH3A	rabphilin 3A homolog (mouse)	0.532	0.925
218698_at	APIP	APAF1 interacting protein	0.567	0.925

220169_at	TMEM156	transmembrane protein 156	0.642	0.925
219313_at	GRAMD1C	GRAM domain containing 1C	0.612	0.925
203303_at	DYNLT3	dynein, light chain, Tctex-type 3	0.642	0.925
226238_at	MCEE	methylmalonyl CoA epimerase	0.659	0.925
239833_at	COMMD1	Copper metabolism (Murr1) domain containing 1	0.658	0.925
228378_at	C12orf29	chromosome 12 open reading frame 29	0.641	0.925
214908_s_at	TRRAP	transformation/transcription domain-associated protein	0.623	0.925
240105_at	C21orf66	Chromosome 21 open reading frame 66	0.666	0.925
214007_s_at	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	0.644	0.925
211210_x_at	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	0.600	0.925
209570_s_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	0.556	0.925
225439_at	NUDCD1	NudC domain containing 1	0.608	0.925
215118_s_at	IGHA1	Immunoglobulin heavy constant alpha 1	0.611	0.925
231950_at	ZNF658	zinc finger protein 658	0.665	0.925
1556889_s_at	---	CDNA FLJ37963 fis, clone CTONG2009689	0.646	0.925
1553725_s_at	ZNF644	zinc finger protein 644	0.651	0.925
241403_at	CLK4	CDC-like kinase 4	0.551	0.925
219714_s_at	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta 3 subunit	0.641	0.925
220917_s_at	WDR19	WD repeat domain 19	0.627	0.925
208978_at	CRIP2	cysteine-rich protein 2	0.467	0.925
226750_at	LARP2	La ribonucleoprotein domain family, member 2	0.653	0.925
224741_x_at	GAS5	growth arrest-specific 5	0.581	0.925
205803_s_at	TRPC1	transient receptor potential cation channel, subfamily C, member 1	0.614	0.925
203939_at	NT5E	5'-nucleotidase, ecto (CD73)	0.615	0.925
243878_at	FOXP1	Forkhead box P1	0.651	0.925
207723_s_at	KLRC3	killer cell lectin-like receptor subfamily C, member 3	0.403	0.925
235078_at	NBEAL1	Neurobeachin-like 1	0.663	0.925
228941_at	---	Transcribed locus	0.657	0.925
203337_x_at	ITGB1BP1	integrin beta 1 binding protein 1	0.631	0.925
208826_x_at	HINT1	histidine triad nucleotide binding protein 1	0.597	1.191
227246_at	---	---	0.645	1.191
1562028_at	CCND3	Cyclin D3	0.579	1.191
235920_at	---	Transcribed locus	0.646	1.191
243049_at	---	---	0.648	1.191
241808_at	C8orf70	Chromosome 8 open reading frame 70	0.666	1.191
228053_s_at	C9orf105	chromosome 9 open reading frame 105	0.611	1.191
224496_s_at	TMEM107	transmembrane protein 107 /// transmembrane protein 107	0.665	1.191
209795_at	CD69	CD69 molecule	0.557	1.191
219147_s_at	C9orf95	chromosome 9 open reading frame 95	0.654	1.191
218311_at	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	0.658	1.191
204864_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.662	1.191
226344_at	ZMAT1	zinc finger, matrin type 1	0.592	1.191
229850_at	---	Full length insert cDNA clone YX81F03	0.648	1.191

225341_at	MTERFD3	MTERF domain containing 3	0.622	1.191
1557624_at	ZNF141	Zinc finger protein 141	0.600	1.191
205619_s_at	MEOX1	mesenchyme homeobox 1	0.579	1.191
226558_at	LOC653071	similar to CG32820-PA, isoform A	0.438	1.191
1569392_at	GPSN2	glycoprotein, synaptic 2	0.638	1.191
236128_at	ZNF91	zinc finger protein 91	0.666	1.191
200962_at	RPL31 /// LOC285260 /// RPL31P4 /// RPL31P10 /// LOC641790 /// LOC646841 /// LOC648737 /// LOC653773 /// LOC727792 /// LOC729646 /// LOC732015	ribosomal protein L31 /// similar to ribosomal protein L31 /// ribosomal protein L31 pseudogene 4 /// ribosomal protein L31 pseudogene 10 /// similar to ribosomal protein L31 /// similar to ribosomal protein L31 /// similar to ribosomal protein L31 /// si	0.665	1.191
213331_s_at	NEK1	NIMA (never in mitosis gene a)-related kinase 1	0.634	1.191
200038_s_at	RPL17	ribosomal protein L17 /// ribosomal protein L17	0.603	1.191
228160_at	LOC400642	hypothetical gene supported by BC041875; BX648984	0.654	1.191
206492_at	FHIT	fragile histidine triad gene	0.421	1.191
213391_at	DPY19L4	dpy-19-like 4 (C. elegans)	0.578	1.191
223341_s_at	SCOC	short coiled-coil protein	0.561	1.191
207721_x_at	HINT1	histidine triad nucleotide binding protein 1	0.613	1.191
214155_s_at	LARP4	La ribonucleoprotein domain family, member 4	0.662	1.191
213174_at	TTC9	tetratricopeptide repeat domain 9	0.646	1.191
219399_at	LIN7C	lin-7 homolog C (C. elegans)	0.655	1.191
235412_at	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	0.619	1.191
226458_at	---	CDNA FLJ30340 fis, clone BRACE2007411	0.637	1.191
238790_at	LOC374443	CLR pseudogene	0.615	1.191
223154_at	MRPL1	mitochondrial ribosomal protein L1	0.609	1.191
204577_s_at	CLUAP1	clusterin associated protein 1	0.627	1.191
218395_at	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	0.643	1.191
220735_s_at	SENP7	SUMO1/sentrin specific peptidase 7	0.662	1.191
212544_at	ZNHIT3	zinc finger, HIT type 3	0.625	1.191
205511_at	FLJ10038	hypothetical protein FLJ10038	0.659	1.191
1559205_s_at	---	Homo sapiens, clone IMAGE:5745627, mRNA	0.625	1.191
237625_s_at	---	Immunoglobulin light chain variable region complementarity determining region (CDR3) mRNA	0.500	1.191
212537_x_at	RPL17	ribosomal protein L17	0.594	1.191
223620_at	GPR34	G protein-coupled receptor 34	0.649	1.191
225036_at	SHB /// C9orf105	Src homology 2 domain containing adaptor protein B /// chromosome 9 open reading frame 105	0.647	1.191

200093_s_at	HINT1	histidine triad nucleotide binding protein 1 /// histidine triad nucleotide binding protein 1	0.618	1.191
206366_x_at	XCL2	chemokine (C motif) ligand 2	0.655	1.191
1556253_s_at	---	CDNA FLJ37989 fis, clone CTONG2011676	0.665	1.191
222848_at	CENPK	centromere protein K	0.361	1.191
226223_at	PAWR	PRKC, apoptosis, WT1, regulator	0.548	2.863
1556054_at	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	0.602	2.863
219278_at	MAP3K6	mitogen-activated protein kinase kinase kinase 6	0.659	2.863
223194_s_at	C6orf85	chromosome 6 open reading frame 85	0.614	2.863
212270_x_at	RPL17	ribosomal protein L17	0.606	2.863
200082_s_at	RPS7 /// LOC644315 /// LOC731257	ribosomal protein S7 /// ribosomal protein S7 /// similar to 40S ribosomal protein S7 (S8) /// similar to 40S ribosomal protein S7 (S8) /// similar to 40S ribosomal protein S7 (S8) /// similar to 40S ribosomal protein S7 (S8)	0.603	2.863
200032_s_at	RPL9	ribosomal protein L9 /// ribosomal protein L9	0.657	2.863
212281_s_at	TMEM97	transmembrane protein 97	0.663	2.863
241762_at	FBXO32	F-box protein 32	0.657	2.863
242770_at	---	CDNA FLJ44826 fis, clone BRACE3046762	0.645	2.863
225525_at	CTA-221G9.4	KIAA1671 protein	0.577	2.863
219629_at	FAM118A	family with sequence similarity 118, member A	0.574	2.863
212578_x_at	RPS17	ribosomal protein S17	0.655	2.863
1557557_at	MATN1	Matrilin 1, cartilage matrix protein	0.664	2.863
202581_at	HSPA1B	heat shock 70kDa protein 1B	0.628	2.863
228381_at	ATF7IP2	Activating transcription factor 7 interacting protein 2	0.654	2.863
209686_at	S100B	S100 calcium binding protein B	0.252	2.863
239292_at	---	Transcribed locus	0.605	2.863
230557_at	XRRA1	X-ray radiation resistance associated 1	0.512	2.863
1558987_at	FLJ40473	hypothetical protein FLJ40473	0.654	2.863
209031_at	IGSF4	Immunoglobulin superfamily, member 4	0.614	2.908
201665_x_at	RPS17	ribosomal protein S17	0.666	2.908
235648_at	ZNF567	zinc finger protein 567	0.653	2.908
200026_at	RPL34 /// LOC342994 /// LOC651249 /// LOC729536 /// LOC731916	ribosomal protein L34 /// ribosomal protein L34 /// similar to ribosomal protein L34 /// similar to ribosomal protein L34 /// similar to ribosomal protein L34 /// similar to ribosomal protein L34 /// hypothetical protein LOC729536 /// hypothetical protein	0.548	2.908
232600_at	ANKRD42	Ankyrin repeat domain 42	0.641	2.908
213941_x_at	RPS7	ribosomal protein S7	0.639	2.908
1555485_s_at	LOC202134	hypothetical protein LOC202134	0.466	2.908
206974_at	CXCR6	chemokine (C-X-C motif) receptor 6	0.644	2.908
211211_x_at	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	0.663	2.908
201406_at	RPL36A /// LOC729362	ribosomal protein L36a /// similar to large subunit ribosomal protein L36a	0.576	2.908
232397_at	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	0.662	2.908
200963_x_at	RPL31	ribosomal protein L31	0.591	2.908

200888_s_at	RPL23	ribosomal protein L23	0.626	2.908
208195_at	TTN	titin	0.622	2.908
236511_at	DUSP16	Dual specificity phosphatase 16	0.629	2.908
221593_s_at	RPL31	ribosomal protein L31	0.641	2.908
229130_at	LOC285535	hypothetical protein LOC285535	0.653	2.908
217915_s_at	C15orf15	chromosome 15 open reading frame 15	0.550	2.908
200099_s_at	RPS3A /// LOC439992	ribosomal protein S3A /// ribosomal protein S3A /// similar to ribosomal protein S3a /// similar to ribosomal protein S3a	0.661	2.908
224786_at	SCOC	short coiled-coil protein	0.606	2.908
236107_at	UBE2Z	ubiquitin-conjugating enzyme E2Z (putative)	0.647	3.003
242432_at	LRRC37A2	Leucine rich repeat containing 37, member A2	0.664	3.003
222229_x_at	LOC392501	similar to 60S ribosomal protein L26	0.662	3.003
1553513_at	VNN3	vanin 3	0.646	3.003
219588_s_at	NCAPG2	non-SMC condensin II complex, subunit G2	0.135	3.003
217753_s_at	RPS26 /// LOC644166 /// LOC644191 /// LOC728937	ribosomal protein S26 /// similar to 40S ribosomal protein S26 /// similar to 40S ribosomal protein S26 /// similar to 40S ribosomal protein S26	0.635	3.003
1565834_a_at	---	---	0.515	3.003
213472_at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	0.631	3.003
1552656_s_at	UHMK1	U2AF homology motif (UHM) kinase 1	0.620	3.003
230110_at	MCOLN2	mucolipin 2	0.664	3.081
228818_at	TPD52	Tumor protein D52	0.641	3.081
218865_at	MOSC1	MOCO sulphurase C-terminal domain containing 1	0.654	3.081
205229_s_at	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	0.611	3.081
244779_at	---	CDNA FLJ34038 fis, clone FCBBF2005645	0.646	3.081
244394_at	BLK	B lymphoid tyrosine kinase	0.649	3.081
225541_at	RPL22L1	ribosomal protein L22-like 1	0.643	3.081
207314_x_at	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	0.638	3.081
232165_at	EPPK1	epiplakin 1	0.665	3.081
240351_at	LOC643749	Hypothetical LOC643749	0.467	3.081
244521_at	---	Transcribed locus	0.433	3.081
209569_x_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	0.576	3.081
200061_s_at	RPS24	ribosomal protein S24 /// ribosomal protein S24	0.665	3.081
220328_at	PHC3	polyhomeotic homolog 3 (Drosophila)	0.613	3.223
202554_s_at	GSTM3	glutathione S-transferase M3 (brain)	0.466	3.223
222465_at	C15orf15 /// LOC284288	chromosome 15 open reading frame 15 /// similar to ribosomal protein L24-like	0.593	3.223
201134_x_at	COX7C	cytochrome c oxidase subunit VIIc	0.639	3.223
238577_s_at	---	Transcribed locus	0.569	3.223
213013_at	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	0.649	3.223
230913_at	---	Full length insert cDNA clone ZE12B03	0.631	3.223
228316_at	FLJ31438	hypothetical protein FLJ31438	0.497	3.223
1558185_at	CLLU1	chronic lymphocytic leukemia up-regulated 1	0.642	3.223

226665_at	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	0.651	3.223
213846_at	COX7C	cytochrome c oxidase subunit VIIc	0.613	3.223
1555194_at	C18orf17	Chromosome 18 open reading frame 17	0.600	3.223
234398_at	---	T-cell receptor alpha, clone PPN82	0.661	3.433
224140_at	NPCDR1	nasopharyngeal carcinoma, down-regulated 1	0.654	3.433
225312_at	COMMD6	COMM domain containing 6	0.650	3.433
202635_s_at	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	0.581	3.433
215891_s_at	GM2A	GM2 ganglioside activator	0.558	3.433
207229_at	KLRA1	killer cell lectin-like receptor subfamily A, member 1	0.574	3.433
1552546_a_at	LETM2	leucine zipper-EF-hand containing transmembrane protein 2	0.593	3.433
1565833_at	---	---	0.508	3.433
235400_at	FCRLA	Fc receptor-like A	0.665	3.631
1554273_a_at	LRAP	leukocyte-derived arginine aminopeptidase	0.664	3.631
206785_s_at	KLRC1 /// KLRC2	killer cell lectin-like receptor subfamily C, member 1 /// killer cell lectin-like receptor subfamily C, member 2	0.642	3.631
231941_s_at	MUC20	mucin 20, cell surface associated	0.653	3.631
206088_at	LRRC37A2	leucine rich repeat containing 37, member A2	0.654	3.913
231996_at	N4BP2	Nedd4 binding protein 2	0.617	3.913
220112_at	ANKRD55	ankyrin repeat domain 55	0.585	3.913
229189_s_at	---	CDNA FLJ90295 fis, clone NT2RP2000240	0.652	3.913
221805_at	NEFL	neurofilament, light polypeptide 68kDa	0.519	3.913
211608_at	---	Rearranged TCR Vbeta 12.3 mRNA for T cell receptor /// Rearranged TCR Vbeta 12.3 mRNA for T cell receptor	0.488	3.913
239287_at	---	Transcribed locus	0.621	4.263
205361_s_at	PFDN4	prefoldin subunit 4	0.654	4.263
234042_at	TAS2R45	taste receptor, type 2, member 45	0.568	4.263
227340_s_at	RGMB	RGM domain family, member B	0.627	4.263
233261_at	EBF1	Early B-cell factor 1	0.622	4.263
208719_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0.651	4.263
206371_at	FOLR3	folate receptor 3 (gamma)	0.580	4.663
206279_at	PRKY	protein kinase, Y-linked	0.507	4.663
232618_at	CYorf15A	chromosome Y open reading frame 15A	0.323	4.663
211469_s_at	CXCR6	chemokine (C-X-C motif) receptor 6	0.648	4.663
229748_x_at	LOC389833	similar to hypothetical protein MGC27019	0.645	4.950