Probe set	Description	Gene symbol	Fold-change: TKD/WT	*P*-value
205844_at	vanin 1	*VNN1*	8.73	< 1e-07
219434_at	triggering receptor expressed on myeloid cells 1	*TREM1*	4.87	0.0005145
228083_at	calcium channel, voltage-dependent, alpha 2/delta subunit 4	*CACNA2D4*	4.64	3.22E-05
205366_s_at	homeobox B6	*HOXB6*	4.34	0.000659
211776_s_at	erythrocyte membrane protein band 4.1-like 3	*EPB41L3*	3.76	0.0007795
205922_at	vanin 2	*VNN2*	3.67	0.0002261
1558549_s_at	vanin 1	*VNN1*	3.64	< 1e-07
209906_at	complement component 3a receptor 1	*C3AR1*	3.62	9.80E-06
1552690_a_at	calcium channel, voltage-dependent, alpha 2/delta subunit 4	*CACNA2D4*	3.58	1.32E-05
209446_s_at	chromosome 7 open reading frame 44	*C7orf44*	3.44	0.0006603
205180_s_at	ADAM metallopeptidase domain 8	*ADAM8*	3.13	1.62E-05
212681_at	erythrocyte membrane protein band 4.1-like 3	*EPB41L3*	3.11	0.0005601
225372_at	chromosome 10 open reading frame 54	*C10orf54*	3.05	0.0005507
204774_at	ecotropic viral integration site 2A	*EVI2A*	3.02	0.0003385
212335_at	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	*GNS*	2.97	0.0005325
213700_s_at	Pyruvate kinase, muscle	*PKM2*	2.95	0.0002389
1554503_a_at	osteoclast-associated receptor	*OSCAR*	2.92	0.0004036
210184_at	integrin, alpha X (complement component 3 receptor 4 subunit)	*ITGAX*	2.91	0.000192
202877_s_at	CD93 molecule	*CD93*	2.87	0.0006775
220507_s_at	ureidopropionase, beta	*UPB1*	2.81	0.0003778
210423_s_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	*SLC11A1*	2.71	0.0009943
202856_s_at	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	*SLC16A3*	2.68	0.0001484
212334_at	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	*GNS*	2.68	0.0002227
225373_at	chromosome 10 open reading frame 54	*C10orf54*	2.55	0.0004141
1554175_at	CD300 molecule-like family member b	*CD300LB*	2.45	0.0004258
244654_at	myosin IG	*MYO1G*	2.43	0.0001465
1554285_at	hepatitis A virus cellular receptor 2	*HAVCR2*	2.40	0.0009532
202855_s_at	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	*SLC16A3*	2.33	0.0005781
218501_at	Rho guanine nucleotide exchange factor (GEF) 3	*ARHGEF3*	2.32	0.0001439
205179_s_at	ADAM metallopeptidase domain 8	*ADAM8*	2.32	0.0001575
241464_s_at	FLJ27365 protein	*FLJ27365*	2.32	0.0007656
217507_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	*SLC11A1*	2.32	0.0005676
209933_s_at	CD300a molecule	*CD300A*	2.31	0.0004433
204575_s_at	matrix metallopeptidase 19 /// similar to Matrix metalloproteinase-19 precursor (MMP-19) (Matrix metalloproteinase RASI) (MMP-18)	*MMP19 /// LOC652543*	2.29	0.0007976
206687_s_at	protein tyrosine phosphatase, non-receptor type 6	*PTPN6*	2.26	5.92E-05
240392_at	Caspase recruitment domain family, member 14	*CARD14*	2.23	0.0005708
204158_s_at	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	*TCIRG1*	2.22	0.0002756
217078_s_at	CD300a molecule	*CD300A*	2.18	0.000213
207270_x_at	CD300c molecule	*CD300C*	2.12	0.0005495
202422_s_at	acyl-CoA synthetase long-chain family member 4	*ACSL4*	2.11	0.0001539
228762_at	lunatic fringe homolog (Drosophila)	*LFNG*	2.09	0.0001027
200766_at	cathepsin D (lysosomal aspartyl peptidase)	*CTSD*	2.09	0.0007615
211286_x_at	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	*CSF2RA*	2.08	0.0007478
207643_s_at	tumor necrosis factor receptor superfamily, member 1A	*TNFRSF1A*	2.05	0.0002626
230261_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	*ST8SIA4*	2.05	0.0009507

230462_at	numb homolog (Drosophila)	*NUMB*	2.04	0.000566
205774_at	coagulation factor XII (Hageman factor)	*F12*	2.03	8.66E-05
1555116_s_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	*SLC11A1*	2.02	0.0005499
1560011_at	prostate stem cell antigen	*PSCA*	2.01	0.0006732
240265_at	TRAF3 interacting protein 3	*TRAF3IP3*	2.00	0.000548
222173_s_at	TBC1 domain family, member 2	*TBC1D2*	1.96	0.0003099
238063_at	transmembrane protein 154	*TMEM154*	1.92	0.0007689
223592_s_at	ring finger protein 135	*RNF135*	1.91	0.000598
218700_s_at	RAB7, member RAS oncogene family-like 1	*RAB7L1*	1.91	0.0009128
205746_s_at	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	*ADAM17*	1.90	0.0001422
216176_at	hepatocellular carcinoma-related HCRP1	*HCRP1*	1.90	0.0004144
209919_x_at	gamma-glutamyltransferase 1	*GGT1*	1.90	0.000392
201389_at	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	*ITGA5*	1.90	0.0006319
228923_at	S100 calcium binding protein A6 (calcyclin)	*S100A6*	1.88	0.0009979
210422_x_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	*SLC11A1*	1.87	0.0005206
207131_x_at	gamma-glutamyltransferase 1	*GGT1*	1.87	0.0006231
1555317_at	polymerase (DNA directed) kappa	*POLK*	1.87	0.0003153
203460_s_at	presenilin 1 (Alzheimer disease 3)	*PSEN1*	1.86	0.0002723
227766_at	ligase IV, DNA, ATP-dependent	*LIG4*	1.86	0.0001341
223686_at	thiamin pyrophosphokinase 1	*TPK1*	1.85	0.000653
223591_at	ring finger protein 135	*RNF135*	1.84	0.0009946
222483_at	EF-hand domain family, member D2	*EFHD2*	1.84	0.0005818
212120_at	hypothetical LOC284988	*LOC284988*	1.84	0.0002808
205601_s_at	homeobox B5	*HOXB5*	1.83	0.0009693
202625_at	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	*LYN*	1.82	0.0006747
242521_at	Homo sapiens, Similar to neuronal thread protein, clone IMAGE:4106635, mRNA		1.81	0.0002627
222442_s_at	ADP-ribosylation factor-like 8B	*ARL8B*	1.80	0.0004824
212587_s_at	protein tyrosine phosphatase, receptor type, C	*PTPRC*	1.79	7.57E-05
233122_at	Keratinocyte associated protein 2 /// MRNA; cDNA DKFZp686L09144 (from clone DKFZp686L09144)	*KRTCAP2*	1.79	0.000337
34206_at	centaurin, delta 2	*CENTD2*	1.77	0.0001001
211417_x_at	gamma-glutamyltransferase 1	*GGT1*	1.76	0.0002583
221041_s_at	solute carrier family 17 (anion/sugar transporter), member 5	*SLC17A5*	1.76	0.0003402
217852_s_at	ADP-ribosylation factor-like 8B	*ARL8B*	1.76	0.0001793
208284_x_at	gamma-glutamyltransferase 1	*GGT1*	1.75	0.0005215
240481_at	TRAF3 interacting protein 3	*TRAF3IP3*	1.75	1.27E-05
217473_x_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	*SLC11A1*	1.75	0.0002989
216322_at	CD58 molecule	*CD58*	1.73	0.0004905
230361_at	hypothetical protein KIAA1833	*KIAA1833*	1.72	0.00026
206600_s_at	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	*SLC16A5*	1.72	0.0004105
207545_s_at	numb homolog (Drosophila)	*NUMB*	1.72	0.0002913
243969_at	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	*SLC24A4*	1.70	0.0006546
202626_s_at	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	*LYN*	1.69	0.0008566
1556747_a_at	CDNA FLJ39784 fis, clone SPLEN2002314		1.69	0.0003754
209370_s_at	SH3-domain binding protein 2	*SH3BP2*	1.68	0.0002566
212685_s_at	transducin (beta)-like 2	*TBL2*	1.68	0.0008339
231099_at	Solute carrier family 31 (copper transporters), member 2	*SLC31A2*	1.68	0.0003979
1569004_at	Homo sapiens, Similar to neuronal thread protein, clone IMAGE:4106635,		1.68	6.15E-05

	mRNA			
215151_at	dedicator of cytokinesis 10	*DOCK10*	1.68	0.0001527
226074_at	protein phosphatase 1M (PP2C domain containing)	*PPM1M*	1.67	0.0003848
212119_at	ras homolog gene family, member Q	*RHOQ*	1.67	0.0004581
213375_s_at	hypothetical gene CG018	*CG018*	1.67	3.34E-05
211250_s_at	SH3-domain binding protein 2	*SH3BP2*	1.66	0.0005319
201126_s_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	*MGAT1*	1.66	0.0008469
200761_s_at	ADP-ribosylation-like factor 6 interacting protein 5	*ARL6IP5*	1.66	0.0008792
205277_at	PR domain containing 2, with ZNF domain	*PRDM2*	1.66	3.35E-05
221641_s_at	acyl-CoA thioesterase 9	*ACOT9*	1.65	0.0003189
214449_s_at	ras homolog gene family, member Q	*RHOQ*	1.64	0.0008107
234942_s_at	deoxynucleotidyltransferase, terminal, interacting protein 1	*DNTTIP1*	1.64	0.0007521
204043_at	transcobalamin II; macrocytic anemia	*TCN2*	1.64	0.0002417
206482_at	PTK6 protein tyrosine kinase 6	*PTK6*	1.63	3.30E-05
228341_at	CDNA FLJ34034 fis, clone FCBBF2004671		1.63	0.0009001
1562608_at	Transmembrane protein 144	*TMEM144*	1.62	0.0006184
213590_at	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	*SLC16A5*	1.62	0.0002214
1568623_a_at	solute carrier family 35, member E4	*SLC35E4*	1.61	6.92E-05
217197_x_at	hypothetical gene CG018	*CG018*	1.60	1.44E-05
206868_at	START domain containing 8	*STARD8*	1.59	5.40E-06
238816_at	CDNA FLJ36867 fis, clone ASTRO2016491		1.59	0.0007242
212117_at	ras homolog gene family, member Q	*RHOQ*	1.58	0.000237
205745_x_at	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	*ADAM17*	1.58	9.47E-05
218821_at	aminopeptidase-like 1	*NPEPL1*	1.58	0.000476
206235_at	ligase IV, DNA, ATP-dependent	*LIG4*	1.58	0.000236
212948_at	calmodulin binding transcription activator 2	*CAMTA2*	1.57	0.0007642
214195_at	tripeptidyl peptidase I	*TPP1*	1.57	0.0002931
1567559_s_at	triggering receptor expressed on myeloid cells-like 4 /// triggering receptor expressed on myeloid cells-like 3	*TREML4 /// TREML3*	1.57	0.0004198
214681_at	glycerol kinase	*GK*	1.57	0.0002659
215603_x_at	gamma-glutamyltransferase 1 /// gamma-glutamyltransferase 2 /// gamma-glutamyltransferase-like 4 /// similar to gamma-glutamyltransferase 2 /// similar to Gamma-glutamyltranspeptidase 1 precursor (Gamma-glutamyltransferase 1) (CD224 antigen)	*GGT1 /// GGT2 /// GGTL4 /// LOC643009 /// LOC653257*	1.56	0.0002188
227098_at	dual specificity phosphatase 18	*DUSP18*	1.56	4.93E-05
219104_at	ring finger protein 141	*RNF141*	1.56	0.0006636
1562321_at	pyruvate dehydrogenase kinase, isozyme 4	*PDK4*	1.55	0.0001894
226577_at	CDNA FLJ36867 fis, clone ASTRO2016491		1.55	0.000362
224846_at	SH3KBP1 binding protein 1	*SHKBP1*	1.55	0.0004526
212516_at	centaurin, delta 2	*CENTD2*	1.51	0.0005174
219620_x_at	hypothetical protein FLJ20245	*FLJ20245*	1.51	0.0007415
213798_s_at	CAP, adenylate cyclase-associated protein 1 (yeast)	*CAP1*	1.51	0.0001402
205781_at	chromosome 16 open reading frame 7	*C16orf7*	1.50	8.49E-05
217416_x_at			1.50	0.0005004
200625_s_at	CAP, adenylate cyclase-associated protein 1 (yeast)	*CAP1*	1.50	0.0006223
217909_s_at	MAX-like protein X	*MLX*	1.50	0.0009422
227352_at	chromosome 19 open reading frame 39	*C19orf39*	1.49	0.0006523
211416_x_at	gamma-glutamyltransferase-like activity 4	*GGTLA4*	1.49	6.90E-05
242956_at	Isocitrate dehydrogenase 1 (NADP+), soluble	*IDH1*	1.49	0.0002917
227954_at	hypothetical protein LOC162073	*LOC162073*	1.49	0.000566

237264_at	Ring finger protein 13	*RNF13*	1.47	0.0001027
226306_at	chromosome 6 open reading frame 1	*C6orf1*	1.46	0.000522
222127_s_at	exocyst complex component 1	*EXOC1*	1.46	0.000836
214906_x_at	hypothetical gene CG018	*CG018*	1.45	0.0001053
223261_at	polymerase (DNA directed) kappa	*POLK*	1.45	0.0003003
228968_at	zinc finger protein 449	*ZNF449*	1.43	0.0006003
203912_s_at	deoxyribonuclease I-like 1	*DNASE1L1*	1.43	0.0005296
222799_at	HSPC049 protein	*HSPC049*	1.43	0.0004919
203278_s_at	PHD finger protein 21A	*PHF21A*	1.43	0.0005486
214121_x_at	PDZ and LIM domain 7 (enigma)	*PDLIM7*	1.43	0.0004867
224825_at	deoxynucleotidyltransferase, terminal, interacting protein 1	*DNTTIP1*	1.41	0.0003835
224065_at	homeodomain interacting protein kinase 2	*HIPK2*	1.40	0.0008998
217910_x_at	MAX-like protein X	*MLX*	1.40	0.0004169
206341_at	interleukin 2 receptor, alpha	*IL2RA*	1.39	0.0001002
210128_s_at	leukotriene B4 receptor	*LTB4R*	1.39	0.0006351
210205_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	*B3GALT4*	1.39	0.0001877
202357_s_at	complement factor B	*CFB*	1.38	0.0004686
242871_at	progestin and adipoQ receptor family member V	*PAQR5*	1.38	0.0007483
207122_x_at	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	*SULT1A2*	1.37	0.0006894
47083_at	chromosome 7 open reading frame 26	*C7orf26*	0.74	0.0002948
217804_s_at	interleukin enhancer binding factor 3, 90kDa	*ILF3*	0.73	0.0006928
201919_at	Solute carrier family 25, member 36	*SLC25A36*	0.73	0.0009325
202268_s_at	amyloid beta precursor protein binding protein 1	*APPBP1*	0.72	0.0007942
209056_s_at	CDC5 cell division cycle 5-like (S. pombe)	*CDC5L*	0.72	0.0008106
223742_at	mitochondrial ribosomal protein L4	*MRPL4*	0.72	0.000961
218954_s_at	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	*BRF2*	0.72	0.0003707
221940_at	RNA pseudouridylate synthase domain containing 2	*RPUSD2*	0.72	0.0005868
209139_s_at	protein kinase, interferon-inducible double stranded RNA dependent activator	*PRKRA*	0.72	0.0006977
202919_at	preimplantation protein 3	*PREI3*	0.72	0.0008599
226572_at	Suppressor of cytokine signaling 7	*SOCS7*	0.72	0.0003692
202230_s_at	calcium homeostasis endoplasmic reticulum protein	*CHERP*	0.71	0.0005509
221749_at	YTH domain family, member 3	*YTHDF3*	0.71	0.0009749
213794_s_at	neuroguidin, EIF4E binding protein	*NGDN*	0.71	0.0001023
1558942_at	zinc finger protein 765	*ZNF765*	0.71	7.00E-04
202396_at	transcription elongation regulator 1	*TCERG1*	0.70	0.0001595
225906_at	CDNA FLJ38264 fis, clone FCBBF3001657		0.70	0.0002669
220607_x_at	TH1-like (Drosophila)	*TH1L*	0.70	0.0005249
225006_x_at	TH1-like (Drosophila)	*TH1L*	0.70	0.0008865
225261_x_at	TH1-like (Drosophila)	*TH1L*	0.70	0.0009768
211375_s_at	interleukin enhancer binding factor 3, 90kDa	*ILF3*	0.70	0.0007373
230588_s_at	hypothetical protein LOC285074 /// similar to anaphase promoting complex subunit 1	*LOC285074 /// LOC653663*	0.70	0.0005761
204847_at	zinc finger and BTB domain containing 11	*ZBTB11*	0.70	0.0006209
202560_s_at	chromosome 1 open reading frame 77	*C1orf77*	0.70	0.0008555
223005_s_at	chromosome 9 open reading frame 5	*C9orf5*	0.69	0.0007256
217830_s_at	NSFL1 (p97) cofactor (p47)	*NSFL1C*	0.69	0.0007806
200052_s_at	interleukin enhancer binding factor 2, 45kDa	*ILF2*	0.69	0.0002613
206095_s_at	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1	*FUSIP1 /// LOC642558*	0.69	2.05E-05
212348_s_at	amine oxidase (flavin containing) domain 2	*AOF2*	0.69	0.0003289
215773_x_at	poly (ADP-ribose) polymerase family, member 2	*PARP2*	0.69	0.0009797

207941_s_at	RNA binding motif protein 39	*RBM39*	0.69	0.0001652
212060_at	U2-associated SR140 protein	*SR140*	0.69	0.000347
207112_s_at	GRB2-associated binding protein 1	*GAB1*	0.69	0.0003457
221158_at	chromosome 21 open reading frame 66	*C21orf66*	0.69	0.0004498
225865_x_at	TH1-like (Drosophila)	*TH1L*	0.69	0.0004849
202968_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	*DYRK2*	0.68	0.0001992
240222_at	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	*COPS8*	0.68	0.0007812
244092_at	zinc finger, RAN-binding domain containing 3	*ZRANB3*	0.68	0.0005096
222430_s_at	YTH domain family, member 2	*YTHDF2*	0.68	0.000199
204752_x_at	poly (ADP-ribose) polymerase family, member 2	*PARP2*	0.68	0.0003664
222703_s_at	yrdC domain containing (E. coli)	*YRDC*	0.68	0.000678
202078_at	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	*COPS3*	0.68	1.38E-05
225157_at	MLX interacting protein	*MLXIP*	0.68	0.0009909
243176_at	CDNA FLJ30090 fis, clone BNGH41000015		0.68	0.0009659
218478_s_at	zinc finger, CCHC domain containing 8	*ZCCHC8*	0.68	0.0002553
201178_at	F-box protein 7	*FBXO7*	0.67	0.0004501
219198_at	general transcription factor IIIC, polypeptide 4, 90kDa	*GTF3C4*	0.67	0.0004279
228380_at	Transcribed locus, moderately similar to NP_689672.2 hypothetical protein MGC45438 [Homo sapiens]		0.67	0.0006192
229428_at	Poly (ADP-ribose) glycohydrolase	*PARG*	0.66	0.0008192
213730_x_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	*TCF3*	0.66	0.000233
212973_at	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	*RPIA*	0.66	0.00053
65591_at	WD repeat domain 48	*WDR48*	0.66	0.000705
235037_at	transmembrane protein 41A	*TMEM41A*	0.65	0.0005426
208811_s_at	DnaJ (Hsp40) homolog, subfamily B, member 6	*DNAJB6*	0.65	2.98E-05
212030_at	RNA binding motif protein 25	*RBM25*	0.65	0.0001225
226990_at	GPI-anchored membrane protein 1	*GPIAP1*	0.65	0.0006658
236477_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	*PRPF40A*	0.65	0.0008693
200993_at	importin 7	*IPO7*	0.65	0.0003838
1554423_a_at	F-box protein 7	*FBXO7*	0.65	0.0001647
1557954_at	chromosome X open reading frame 15	*CXorf15*	0.64	0.000483
211081_s_at	mitogen-activated protein kinase kinase kinase kinase 5	*MAP4K5*	0.64	0.0001311
213811_x_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	*TCF3*	0.64	0.0005413
208810_at	DnaJ (Hsp40) homolog, subfamily B, member 6	*DNAJB6*	0.64	0.0002651
205284_at	KIAA0133	*KIAA0133*	0.64	0.0005368
208115_x_at	chromosome 10 open reading frame 137	*C10orf137*	0.64	0.0007839
227617_at	hypothetical protein LOC199953	*RP13-15M17.2*	0.64	0.0002004
207515_s_at	polymerase (RNA) I polypeptide C, 30kDa	*POLR1C*	0.63	0.0002622
202969_at	MRNA; cDNA DKFZp667B0924 (from clone DKFZp667B0924)		0.63	0.0007744
204568_at	KIAA0831	*KIAA0831*	0.63	0.0004058
202883_s_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	*PPP2R1B*	0.63	7.72E-05
218128_at	nuclear transcription factor Y, beta	*NFYB*	0.63	0.0004935
230274_s_at	Nucleoporin 88kDa	*NUP88*	0.63	0.0008833
219212_at	heat shock 70kDa protein 14	*HSPA14*	0.62	5.40E-06
237299_at	Transcribed locus		0.62	0.0003018
225455_at	transcriptional adaptor 1 (HFI1 homolog, yeast)-like	*TADA1L*	0.62	0.0004717
223297_at	hypothetical protein MGC4268	*MGC4268*	0.62	0.0005147
218544_s_at	RNA terminal phosphate cyclase-like 1	*RCL1*	0.62	0.0009185
227520_at	chromosome X open reading frame 15	*CXorf15*	0.62	0.0006187
225998_at	GRB2-associated binding protein 1	*GAB1*	0.62	0.0008424

1554251_at	heterochromatin protein 1, binding protein 3	*HP1BP3*	0.62	0.0003535
218127_at	nuclear transcription factor Y, beta	*NFYB*	0.62	0.0001648
65588_at	hypothetical LOC388796	*LOC388796*	0.61	5.00E-06
204244_s_at	DBF4 homolog (S. cerevisiae)	*DBF4*	0.61	0.0001619
201947_s_at	chaperonin containing TCP1, subunit 2 (beta)	*CCT2*	0.61	0.0002139
210776_x_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	*TCF3*	0.61	0.0002228
225857_s_at	hypothetical LOC388796	*LOC388796*	0.61	7.80E-06
229594_at	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	*SPTY2D1*	0.61	0.0001053
226687_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	*PRPF40A*	0.60	4.45E-05
203358_s_at	enhancer of zeste homolog 2 (Drosophila)	*EZH2*	0.60	0.0001735
222405_at	similar to butyrate-induced transcript 1	*LOC652500*	0.60	0.0005045
236379_at	Erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	*EPB41*	0.60	0.0008447
209317_at	polymerase (RNA) I polypeptide C, 30kDa	*POLR1C*	0.59	0.0001252
201946_s_at	chaperonin containing TCP1, subunit 2 (beta)	*CCT2*	0.59	0.0001335
244103_at	chromosome 1 open reading frame 55	*C1orf55*	0.59	0.0005025
212739_s_at	non-metastatic cells 4, protein expressed in	*NME4*	0.59	0.0004408
239794_at	Isoleucine-tRNA synthetase	*IARS*	0.59	0.0004463
227993_at	methionyl aminopeptidase 2	*METAP2*	0.59	0.0001066
244304_at	hypothetical protein MGC42174	*MGC42174*	0.58	0.0001755
222623_s_at	zinc finger protein 639	*ZNF639*	0.58	0.0003901
209273_s_at	HESB like domain containing 2	*HBLD2*	0.58	0.0007163
218192_at	inositol hexaphosphate kinase 2	*IHPK2*	0.58	1.16E-05
53987_at	RAN binding protein 10	*RANBP10*	0.58	5.80E-05
205135_s_at	nuclear fragile X mental retardation protein interacting protein 1	*NUFIP1*	0.58	0.0001658
216226_at	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	*TAF4B*	0.58	0.0002697
207332_s_at	transferrin receptor (p90, CD71)	*TFRC*	0.58	0.0005208
230479_at	Transcribed locus		0.57	0.0001006
228378_at	chromosome 12 open reading frame 29	*C12orf29*	0.57	0.0003924
202353_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	*PSMD12*	0.57	0.0008792
221735_at	WD repeat domain 48	*WDR48*	0.57	0.0003617
1556060_a_at	KIAA1702 protein	*KIAA1702*	0.57	0.0007966
226370_at	kelch-like 15 (Drosophila)	*KLHL15*	0.57	9.36E-05
221821_s_at	chromosome 12 open reading frame 41	*C12orf41*	0.57	2.00E-06
221809_at	RAN binding protein 10	*RANBP10*	0.57	5.03E-05
210054_at	chromosome 4 open reading frame 15	*C4orf15*	0.57	2.61E-05
213899_at	methionyl aminopeptidase 2	*METAP2*	0.56	7.05E-05
222157_s_at	WD repeat domain 48	*WDR48*	0.56	0.0002384
219037_at	CGI-115 protein	*CGI-115*	0.56	0.0003837
212061_at	U2-associated SR140 protein	*SR140*	0.56	0.0006201
209711_at	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	*SLC35D1*	0.56	0.0009729
217961_at	hypothetical protein FLJ20551	*FLJ20551*	0.56	6.02E-05
235170_at	zinc finger protein 92	*ZNF92*	0.55	0.0001342
221517_s_at	cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa	*CRSP6*	0.55	2.04E-05
225051_at	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	*EPB41*	0.55	0.0004301
212665_at	TCDD-inducible poly(ADP-ribose) polymerase	*TIPARP*	0.54	0.0004431
222404_x_at	protein tyrosine phosphatase-like A domain containing 1	*PTPLAD1*	0.54	0.0007638
200995_at	Importin 7	*IPO7*	0.54	0.0001826
222624_s_at	zinc finger protein 639	*ZNF639*	0.54	0.0008422
209274_s_at	HESB like domain containing 2	*HBLD2*	0.53	0.0006372
221932_s_at	glutaredoxin 5 homolog (S. cerevisiae)	*GLRX5*	0.53	0.0007867

235061_at	protein phosphatase 1K (PP2C domain containing)	*PPM1K*	0.53	0.0009434
230129_at	chromosome 10 open reading frame 89	*C10orf89*	0.53	0.0003209
217777_s_at	protein tyrosine phosphatase-like A domain containing 1	*PTPLAD1*	0.52	0.0002906
222666_s_at	RNA terminal phosphate cyclase-like 1	*RCL1*	0.52	4.50E-06
228605_at	CDNA FLJ30010 fis, clone 3NB692000154		0.52	0.0001339
222565_s_at	protein kinase D3	*PRKD3*	0.52	0.0005269
237215_s_at	transferrin receptor (p90, CD71)	*TFRC*	0.51	0.0001339
203795_s_at	B-cell CLL/lymphoma 7A	*BCL7A*	0.51	8.16E-05
237194_at	Tetraspanin 5	*TSPAN5*	0.48	0.0005925
209826_at	EGF-like-domain, multiple 8 /// similar to palmitoyl-protein thioesterase 2	*EGFL8 /// LOC653870*	0.48	0.0002465
218756_s_at	short-chain dehydrogenase/reductase	*MGC4172*	0.48	0.0003988
229256_at	phosphoglucomutase 2-like 1	*PGM2L1*	0.48	0.0009557
218883_s_at	MLF1 interacting protein	*MLF1IP*	0.46	0.0004019
235020_at	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	*TAF4B*	0.45	4.89E-05
209064_x_at	poly(A) binding protein interacting protein 1	*PAIP1*	0.45	5.68E-05
208051_s_at	poly(A) binding protein interacting protein 1	*PAIP1*	0.44	5.86E-05
220306_at	family with sequence similarity 46, member C	*FAM46C*	0.43	0.0008025
203116_s_at	ferrochelatase (protoporphyria)	*FECH*	0.41	0.0004223
211658_at	peroxiredoxin 2	*PRDX2*	0.41	0.000567
218236_s_at	protein kinase D3	*PRKD3*	0.39	0.0003232
203502_at	2,3-bisphosphoglycerate mutase	*BPGM*	0.37	0.0002845
204917_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	*MLLT3*	0.37	0.0007285
206077_at	Kell blood group, metalloendopeptidase	*KEL*	0.36	0.000947
204951_at	ras homolog gene family, member H	*RHOH*	0.36	0.0004224
208501_at	growth factor independent 1B (potential regulator of CDKN1A, translocated in CML)	*GFI1B*	0.36	0.0002145
210473_s_at	G protein-coupled receptor 125	*GPR125*	0.33	0.0001269
210504_at	Kruppel-like factor 1 (erythroid)	*KLF1*	0.32	0.0007895
239142_at	LOC317671	*LOC317671*	0.32	0.0008714
204018_x_at	hemoglobin, alpha 1 /// hemoglobin, alpha 2	*HBA1 /// HBA2*	0.30	0.000691
202947_s_at	glycophorin C (Gerbich blood group)	*GYPC*	0.30	0.0002459
205632_s_at	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	*PIP5K1B*	0.30	0.0002694
205268_s_at	adducin 2 (beta)	*ADD2*	0.30	0.0002185
211745_x_at	hemoglobin, alpha 1	*HBA1*	0.30	0.0007297
217414_x_at	hemoglobin, alpha 1 /// hemoglobin, alpha 2	*HBA1 /// HBA2*	0.30	0.0009184
209458_x_at	hemoglobin, alpha 1 /// hemoglobin, alpha 2	*HBA1 /// HBA2*	0.29	0.000579
223708_at	C1q and tumor necrosis factor related protein 4	*C1QTNF4*	0.27	0.0009032
1569652_at	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	*MLLT3*	0.26	0.0006042
211699_x_at	hemoglobin, alpha 1 /// hemoglobin, alpha 2	*HBA1 /// HBA2*	0.25	0.0005855
210746_s_at	erythrocyte membrane protein band 4.2	*EPB42*	0.23	0.0004986
211560_s_at	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	*ALAS2*	0.20	0.0007296
203949_at	myeloperoxidase	*MPO*	0.20	0.0002837
205592_at	interleukin 8	*IL8*	0.19	0.0008662
206698_at	X-linked Kx blood group (McLeod syndrome)	*XK*	0.19	0.0003189
223670_s_at	hemogen	*HEMGN*	0.19	0.0005897

203948_s_at	myeloperoxidase	*MPO*	0.18	0.000286
219672_at	erythroid associated factor	*ERAF*	0.18	0.0007403
211820_x_at	glycophorin A (MNS blood group)	*GYPA*	0.17	0.0006763
39729_at	peroxiredoxin 2	*PRDX2*	0.15	0.0001049