Table S1: Primer sequences used in RT-qPCR

Gene	Description	Amplicon Length
CD79A	Hs00998119_m1	118
IGHD	Hs00920518_g1	62
SPIB	Hs00162150_m1	65
TCL1A	Hs00951350_m1	91

RT-qPCR was run with the following conditions: 2 min at 50°C, 10 min at 95°C for 1 cycle and 15 s at 95°C, 1 min at 60°C for 40 cycles.

Table S2: up and down regulated genes following CSC stimulation of cultured PBMCs.

Probe set	Symbol	Description	Fold	P value
202852_s_at	AAGAB	alpha- and gamma-adaptin binding protein	1.15	0.043941
213353_at	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	1.3	0.030279
209993_at	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.43	0.040598
208288_at	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	-1.12	0.026911
203192_at	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	1.72	0.006919
215873_x_at	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	1.13	0.02512
203981_s_at	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	1.37	0.00088
201873_s_at	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	-1.24	0.032693
204567_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	2.04	0.005918
213017_at	ABHD3	abhydrolase domain containing 3	1.14	0.033643
218581_at	ABHD4	abhydrolase domain containing 4	1.24	0.032239
200965_s_at	ABLIM1	actin binding LIM protein 1	1.47	0.012157
204565_at	ACOT13	acyl-CoA thioesterase 13	1.36	0.029471
208636_at	ACTN1	actinin, alpha 1	-1.77	0.02005
222230_s_at	ACTR10	actin-related protein 10 homolog (S. cerevisiae)	1.18	0.008379
213102_at	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	-1.26	0.010611
208219_at	ACVR1B	activin A receptor, type IB	-1.1	0.045692
206833_s_at	ACYP2	acylphosphatase 2, muscle type	1.18	0.027131
213790_at	ADAM12	ADAM metallopeptidase domain 12	-1.13	0.03353
213532_at	ADAM17	ADAM metallopeptidase domain 17	1.77	0.005138
205180_s_at	ADAM8	ADAM metallopeptidase domain 8	-1.25	0.006237
220208_at	ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	-1.05	0.04569
44120_at	ADCK2	aarF domain containing kinase 2	1.22	0.016402
203741_s_at	ADCY7	adenylate cyclase 7	1.38	0.013632
208030_s_at	ADD1	adducin 1 (alpha)	1.2	0.036888
208847_s_at	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	1.14	0.031611
210250_x_at	ADSL	adenylosuccinate lyase	-1.38	0.037356
217939_s_at	AFTPH	aftiphilin	1.36	0.010502
222362_at	AGFG2	ArfGAP with FG repeats 2	-1.13	0.010635
222132_s_at	AGK	acylglycerol kinase	-1.35	0.027575
220602_s_at	AGSK1	golgin subfamily A member 2-like*	1.18	0.021868
220841_s_at	AHI1	Abelson helper integration site 1	-1.31	0.029924
215051_x_at	AIF1	allograft inflammatory factor 1	-1.67	0.046584
220289_s_at	AIM1L	absent in melanoma 1-like	-1.08	0.036502
212173_at	AK2	adenylate kinase 2	-1.4	0.015064

203624_at	AKAP17A	A kinase (PRKA) anchor protein 17A	1.33	0.01779
211653_x_at	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)*	1.12	0.03285
217791_s_at	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	-1.25	0.011136
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	-1.12	0.000394
219374_s_at	ALG9	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)	1.2	0.015494
208211_s_at	ALK	anaplastic lymphoma receptor tyrosine kinase	-1.13	0.033761
206837_at	ALX1	ALX homeobox 1	-1.12	0.025456
209001_s_at	ANAPC13	anaphase promoting complex subunit 13	-1.36	0.021837
204218_at	ANAPC15	anaphase promoting complex subunit 15	-1.42	0.001064
217630_at	ANGEL2	angel homolog 2 (Drosophila)	-1.08	0.045103
212286_at	ANKRD12	ankyrin repeat domain 12	1.62	0.005518
221522_at	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	1.14	0.03053
213035_at	ANKRD28	ankyrin repeat domain 28	-1.2	0.028443
212731_at	ANKRD46	ankyrin repeat domain 46	1.39	0.009446
219069_at	ANKRD49	ankyrin repeat domain 49	1.26	0.014395
218910_at	ANO10	anoctamin 10	1.27	0.030359
201051_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.22	0.010869
221505_at	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-1.3	0.022243
205639_at	AOAH	acyloxyacyl hydrolase (neutrophil)	-1.47	0.049025
203350_at	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	1.25	0.030681
202399_s_at	AP3S2	adaptor-related protein complex 3, sigma 2 subunit*	1.7	0.009902
209871_s_at	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2	-1.14	0.03965
203527_s_at	APC	adenomatous polyposis coli	-1.13	0.010339
211404_s_at	APLP2	amyloid beta (A4) precursor-like protein 2	1.55	0.014741
205108_s_at	APOB	apolipoprotein B (including Ag(x) antigen)	-1.15	0.000618
206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	-1.64	0.033729
221031_s_at	APOLD1	apolipoprotein L domain containing 1	1.36	0.031192
214910_s_at	APOM	apolipoprotein M	-1.18	0.044541
202629_at	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1.2	0.023668
39249_at	AQP3	aquaporin 3 (Gill blood group)	-1.22	0.015313
215955_x_at	ARHGAP26	Rho GTPase activating protein 26	-1.19	0.013591
201288_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-1.28	0.005083
216620_s_at	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	-1.2	0.011484
201333_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	1.15	0.042244
208009_s_at	ARHGEF16	Rho guanine nucleotide exchange factor (GEF) 16	-1.22	0.028834
203264_s_at	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	-1.2	0.010716
202092_s_at	ARL2BP	ADP-ribosylation factor-like 2 binding protein	1.15	0.007476

202207_at	ARL4C	ADP-ribosylation factor-like 4C	1.9	0.023677
203586_s_at	ARL4D	ADP-ribosylation factor-like 4D	-1.07	0.031574
208679_s_at	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	-1.39	0.000044
218832_x_at	ARRB1	arrestin, beta 1	-1.58	0.013006
213702_x_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	1.67	0.021011
205673_s_at	ASB9	ankyrin repeat and SOCS box containing 9	-1.23	0.016353
36553_at	ASMTL	acetylserotonin O-methyltransferase-like	1.2	0.032801
206030_at	ASPA	aspartoacylase	-1.09	0.037977
209135_at	ASPH	aspartate beta-hydroxylase	1.39	0.026443
214993_at	ASPHD1	aspartate beta-hydroxylase domain containing 1	-1.06	0.044282
213197_at	ASTN1	astrotactin 1	-1.07	0.027742
202672_s_at	ATF3	activating transcription factor 3	1.79	0.015017
204568_at	ATG14	autophagy related 14	1.43	0.00433
219164_s_at	ATG2B	autophagy related 2B	1.35	0.014661
208758_at	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	-1.58	0.016583
201854_s_at	ATMIN	ATM interactor	1.57	0.000143
212361_s_at	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.21	0.025016
205410_s_at	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-1.19	0.029124
209934_s_at	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	1.35	0.037467
211755_s_at	ATP5F1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	-1.16	0.026034
210149_s_at	ATP5H	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d	1.07	0.04637
206992_s_at	ATP5S	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (factor B)	-1.3	0.000501
218038_at	ATP5SL	ATP5S-like	1.12	0.028622
207809_s_at	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	1.29	0.039788
205095_s_at	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	1.11	0.049458
201172_x_at	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	1.34	0.005391
208898_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	1.43	0.000961
208832_at	ATXN10	ataxin 10	-1.31	0.023542
205415_s_at	ATXN3	ataxin 3	1.53	0.031136
206251_s_at	AVPR1A	arginine vasopressin receptor 1A	-1.08	0.048016
208108_s_at	AVPR2	arginine vasopressin receptor 2	-1.15	0.028492
203304_at	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	1.17	0.041552
220358_at	BATF3	basic leucine zipper transcription factor, ATF-like 3	-2.71	0.017458
218471_s_at	BBS1	Bardet-Biedl syndrome 1	1.19	0.004954
212744_at	BBS4	Bardet-Biedl syndrome 4	1.21	0.013035
217955_at	BCL2L13	BCL2-like 13 (apoptosis facilitator)	1.48	0.001117
221241_s_at	BCL2L14	BCL2-like 14 (apoptosis facilitator)	-1.2	0.005739

219433_at	BCOR	BCL6 corepressor	1.35	0.029343
219670_at	BEND5	BEN domain containing 5	-1.28	0.02002
218056_at	BFAR	bifunctional apoptosis regulator	1.35	0.046973
207399_at	BFSP2	beaded filament structural protein 2, phakinin	-1.15	0.019505
206119_at	BHMT	betaine--homocysteine S-methyltransferase	-1.19	0.032393
220580_at	BICC1	bicaudal C homolog 1 (Drosophila)	-1.1	0.013374
219191_s_at	BIN2	bridging integrator 2	1.17	0.038095
201032_at	BLCAP	bladder cancer associated protein	1.16	0.028705
202201_at	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	1.65	0.004043
205574_x_at	BMP1	bone morphogenetic protein 1	-1.18	0.007064
221479_s_at	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	1.35	0.044419
216397_s_at	BOP1	block of proliferation 1	-1.24	0.042315
209922_at	BRAP	BRCA1 associated protein	1.2	0.044419
214727_at	BRCA2	breast cancer 2, early onset	-1.35	0.01028
214911_s_at	BRD2	bromodomain containing 2	1.43	0.046173
202227_s_at	BRD8	bromodomain containing 8	1.29	0.00516
212645_x_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.22	0.043862
204481_at	BRPF1	bromodomain and PHD finger containing, 1	1.24	0.033283
222200_s_at	BSDC1	BSD domain containing 1	1.34	0.002537
201236_s_at	BTG2	BTG family, member 2	1.69	0.00183
204821_at	BTN3A3	butyrophilin, subfamily 3, member A3	-1.24	0.045545
217809_at	BZW2	basic leucine zipper and W2 domains 2	-1.4	0.007879
220344_at	C11orf16	chromosome 11 open reading frame 16	-1.09	0.027473
203257_s_at	C11orf49	chromosome 11 open reading frame 49	1.3	0.018458
221599_at	C11orf67	chromosome 11 open reading frame 67	1.68	0.000204
211034_s_at	C12orf51	chromosome 12 open reading frame 51	1.24	0.045051
218820_at	C14orf132	chromosome 14 open reading frame 132	-1.18	0.023405
215087_at	C15orf39	chromosome 15 open reading frame 39	-1.1	0.024971
219784_at	C16orf95	chromosome 16 open reading frame 95	-1.13	0.032509
203830_at	C17orf75	chromosome 17 open reading frame 75	1.18	0.015005
218896_s_at	C17orf85	chromosome 17 open reading frame 85	1.23	0.021779
209574_s_at	C18orf1	chromosome 18 open reading frame 1	1.53	0.013729
214357_at	C1orf105	chromosome 1 open reading frame 105	-1.05	0.047032
218546_at	C1orf115	chromosome 1 open reading frame 115	1.1	0.026889
222281_s_at	C1orf186*	chromosome 1 open reading frame 186*	-1.19	0.0176
207571_x_at	C1orf38	chromosome 1 open reading frame 38	1.34	0.023389
219406_at	C1orf50	chromosome 1 open reading frame 50	1.32	0.000993
205103_at	C1orf61	chromosome 1 open reading frame 61	-1.19	0.016803
203429_s_at	C1orf9	chromosome 1 open reading frame 9	1.42	0.04197
218232_at	C1QA	complement component 1, q subcomponent, A chain	-1.13	0.0141
209020_at	C20orf111	chromosome 20 open reading frame 111	1.43	0.042467
217835_x_at	C20orf24	chromosome 20 open reading frame 24*	1.18	0.044279

206656_s_at	C20orf3	chromosome 20 open reading frame 3	1.27	0.010036
218089_at	C20orf4	chromosome 20 open reading frame 4	1.16	0.021807
207701_at	C22orf24	chromosome 22 open reading frame 24	-1.18	0.00785
209906_at	C3AR1	complement component 3a receptor 1	-1.53	0.002061
219114_at	C3orf18	chromosome 3 open reading frame 18	-1.16	0.019995
201812_s_at	C4orf46	chromosome 4 open reading frame 46*	1.31	0.013369
207698_at	C6orf123	chromosome 6 open reading frame 123	-1.05	0.028163
220659_s_at	C7orf43	chromosome 7 open reading frame 43	-1.12	0.009188
219464_at	CA14	carbonic anhydrase XIV	-1.2	0.022838
221003_s_at	CAB39L	calcium binding protein 39-like	1.21	0.041399
205625_s_at	CALB1	calbindin 1, 28kDa	-1.11	0.01344
205428_s_at	CALB2	calbindin 2	-1.11	0.022112
210817_s_at	CALCOCO2	calcium binding and coiled-coil domain 2	1.32	0.039348
221879_at	CALML4	calmodulin-like 4	-1.24	0.039941
210787_s_at	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-1.13	0.049949
205166_at	CAPN5	calpain 5	-1.1	0.009972
203356_at	CAPN7	calpain 7	1.45	0.010618
201949_x_at	CAPZB	capping protein (actin filament) muscle Z-line, beta	-1.11	0.037916
217940_s_at	CARKD	carbohydrate kinase domain containing	1.29	0.01374
209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase	-1.58	0.013204
207500_at	CASP5	caspase 5, apoptosis-related cysteine peptidase	-1.09	0.042144
208204_s_at	CAV3	caveolin 3	-1.2	0.001558
202370_s_at	CBFB	core-binding factor, beta subunit	-1.17	0.049507
203450_at	CBY1	chibby homolog 1 (Drosophila)	1.24	0.023383
209479_at	CCDC28A	coiled-coil domain containing 28A	1.44	0.009235
218722_s_at	CCDC51	coiled-coil domain containing 51	-1.39	0.043576
218628_at	CCDC53	coiled-coil domain containing 53	1.29	0.002292
212886_at	CCDC69	coiled-coil domain containing 69	1.36	0.033996
219774_at	CCDC93	coiled-coil domain containing 93	1.21	0.004292
206407_s_at	CCL13	chemokine (C-C motif) ligand 13	-1.47	0.017808
214038_at	CCL8	chemokine (C-C motif) ligand 8	-7.06	0.00375
200952_s_at	CCND2	cyclin D2	-2.77	0.017205
204093_at	CCNH	cyclin H	-1.25	0.013392
214151_s_at	CCPG1	cell cycle progression 1*	1.22	0.008642
206337_at	CCR7	chemokine (C-C motif) receptor 7	1.51	0.006646
208059_at	CCR8	chemokine (C-C motif) receptor 8	-1.28	0.01515
207840_at	CD160	CD160 molecule	-1.23	0.027329
217072_at	CD300A	CD300a molecule	-1.13	0.037121
219343_at	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	1.47	0.012159
204126_s_at	CDC45	cell division cycle 45 homolog (S. cerevisiae)	-1.43	0.046221
221436_s_at	CDCA3	cell division cycle associated 3	-1.61	0.046714
218451_at	CDCP1	CUB domain containing protein 1	1.28	0.045826

203256_at	CDH3	cadherin 3, type 1, P-cadherin (placental)	-1.3	0.034566
201253_s_at	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	1.4	0.000901
207318_s_at	CDK13	cyclin-dependent kinase 13	1.42	0.002454
212897_at	CDK19	cyclin-dependent kinase 19	1.41	0.01051
207188_at	CDK3	cyclin-dependent kinase 3*	-1.18	0.026803
219831_at	CDKL3	cyclin-dependent kinase-like 3	1.2	0.026414
210240_s_at	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	-1.28	0.015672
212864_at	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	1.31	0.01367
213554_s_at	CDV3	CDV3 homolog (mouse)	1.29	0.006937
209498_at	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	-1.86	0.002494
217209_at	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	-1.09	0.035561
204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	1.3	0.043979
218741_at	CENPM	centromere protein M	-1.34	0.03286
204075_s_at	CEP104	centrosomal protein 104kDa	1.14	0.004071
206003_at	CEP135	centrosomal protein 135kDa	-1.23	0.034688
221683_s_at	CEP290	centrosomal protein 290kDa	1.12	0.023133
219375_at	CEPT1	choline/ethanolamine phosphotransferase 1	1.2	0.024283
202357_s_at	CFB	complement factor B	-1.12	0.0462
211316_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	1.42	0.01436
217026_at	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	-1.12	0.026495
204605_at	CGRRF1	cell growth regulator with ring finger domain 1	1.53	0.006534
212313_at	CHMP7	charged multivesicular body protein 7	1.47	0.01657
214665_s_at	CHP1	calcineurin-like EF hand protein 1	1.17	0.049118
55093_at	CHPF2	chondroitin polymerizing factor 2	1.53	0.005841
221675_s_at	CHPT1	choline phosphotransferase 1	1.32	0.029685
209763_at	CHRDL1	chordin-like 1	-1.09	0.013522
211772_x_at	CHRNA3	cholinergic receptor, nicotinic, alpha 3 (neuronal)	-1.08	0.024801
205567_at	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-1.15	0.04229
221188_s_at	CIDEB	cell death-inducing DFFA-like effector b	-1.22	0.014066
200999_s_at	CKAP4	cytoskeleton-associated protein 4	1.35	0.018929
207855_s_at	CLCC1	chloride channel CLIC-like 1	1.32	0.018439
201735_s_at	CLCN3	chloride channel, voltage-sensitive 3	1.6	0.001756
221724_s_at	CLEC4A	C-type lectin domain family 4, member A	-1.17	0.036436
207995_s_at	CLEC4M	C-type lectin domain family 4, member M	-1.11	0.012449
201975_at	CLIP1	CAP-GLY domain containing linker protein 1	1.19	0.018697
214683_s_at	CLK1	CDC-like kinase 1	1.56	0.029229
203291_at	CNOT4	CCR4-NOT transcription complex, subunit 4	1.5	0.028046
219302_s_at	CNTNAP2	contactin associated protein-like 2	-1.13	0.032222
219625_s_at	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen)	1.33	0.007125

		binding protein		
206441_s_at	COMMD4	COMM domain containing 4	-1.54	0.033704
213379_at	COQ2	coenzyme Q2 homolog, prenyltransferase (yeast)	-1.4	0.014885
201754_at	COX6C	cytochrome c oxidase subunit VIc	1.15	0.044395
201256_at	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	1.22	0.001014
213846_at	COX7C	cytochrome c oxidase subunit VIIc	1.32	0.030911
201943_s_at	CPD	carboxypeptidase D	1.43	0.015295
202119_s_at	CPNE3	copine III	1.26	0.005956
220479_at	CPS1-IT1	CPS1 intronic transcript 1 (non-protein coding)	-1.08	0.015974
220620_at	CRCT1	cysteine-rich C-terminal 1	-1.08	0.041424
211897_s_at	CRHR1	corticotropin releasing hormone receptor 1	1.1	0.015914
202224_at	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	1.2	0.044508
203807_x_at	CSH2	chorionic somatomammotropin hormone 2	-1.17	0.043894
207951_at	CSN2	casein beta	-1.12	0.019776
203575_at	CSNK2A2	casein kinase 2, alpha prime polypeptide	1.26	0.031838
212901_s_at	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	-1.37	0.002585
211674_x_at	CTAG1A*	cancer/testis antigen 1A*	-1.1	0.032222
200764_s_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	1.72	0.006179
202087_s_at	CTSL1	cathepsin L1	2.77	0.002173
210074_at	CTSL2	cathepsin L2	1.2	0.029021
214450_at	CTSW	cathepsin W	-2.16	0.033548
211122_s_at	CXCL11	chemokine (C-X-C motif) ligand 11	-1.07	0.046307
205242_at	CXCL13	chemokine (C-X-C motif) ligand 13	-3.5	0.032887
217028_at	CXCR4	chemokine (C-X-C motif) receptor 4	1.22	0.037437
212977_at	CXCR7	chemokine (C-X-C motif) receptor 7	-1.13	0.049775
214112_s_at	CXorf40A	chromosome X open reading frame 40A*	1.18	0.033407
207986_x_at	CYB561	cytochrome b-561	-1.1	0.027053
202263_at	CYB5R1	cytochrome b5 reductase 1	1.67	0.001224
221903_s_at	CYLD	cylindromatosis (turban tumor syndrome)	1.24	0.030108
205502_at	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	-1.07	0.047912
205749_at	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	9.16	0.000028
202437_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	5.43	0.000136
208147_s_at	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	1.08	0.032944
214421_x_at	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	-1.11	0.041104
205999_x_at	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	-1.09	0.039162
211231_x_at	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	-1.1	0.049923
206515_at	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	-1.09	0.029283

216060_s_at	DAAM1	dishevelled associated activator of morphogenesis 1	1.23	0.016627
217025_s_at	DBN1	drebrin 1	-1.44	0.027714
218094_s_at	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing 2*	-1.41	0.032348
209383_at	DDIT3	DNA-damage-inducible transcript 3	1.16	0.028113
221081_s_at	DENND2D	DENN/MADD domain containing 2D	-1.28	0.015055
205684_s_at	DENND4C	DENN/MADD domain containing 4C	1.27	0.034953
218333_at	DERL2	derlin 2	1.33	0.032025
214198_s_at	DGCR2	DiGeorge syndrome critical region gene 2	1.21	0.002942
209549_s_at	DGUOK	deoxyguanosine kinase	1.12	0.036967
204800_s_at	DHRS12	dehydrogenase/reductase (SDR family) member 12	-1.14	0.001692
210788_s_at	DHRS7	dehydrogenase/reductase (SDR family) member 7	1.19	0.045127
219799_s_at	DHRS9	dehydrogenase/reductase (SDR family) member 9	-1.16	0.00043
219364_at	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58	-1.3	0.005933
218325_s_at	DIDO1	death inducer-obliterator 1	1.13	0.021872
203700_s_at	DIO2	deiodinase, iodothyronine, type II	-1.1	0.005979
206090_s_at	DISC1	disrupted in schizophrenia 1*	-1.3	0.011156
221126_at	DKK3	dickkopf 3 homolog (Xenopus laevis)	-1.03	0.029827
212727_at	DLG3	discs, large homolog 3 (Drosophila)	-1.18	0.021673
201681_s_at	DLG5	discs, large homolog 5 (Drosophila)	1.18	0.002849
207147_at	DLX2	distal-less homeobox 2	1.1	0.031579
208250_s_at	DMBT1	deleted in malignant brain tumors 1	-1.1	0.034003
203791_at	DMXL1	Dmx-like 1	1.38	0.041102
210345_s_at	DNAH9	dynein, axonemal, heavy chain 9	-1.21	0.044411
200666_s_at	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	1.32	0.028063
202500_at	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	1.56	0.028734
209015_s_at	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	1.73	0.011758
202842_s_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	1.61	0.013024
218409_s_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	1.34	0.007241
212911_at	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	1.14	0.018121
218457_s_at	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	-1.17	0.013637
205744_at	DOC2A	double C2-like domains, alpha	-1.11	0.044072
213482_at	DOCK3	dedicator of cytokinesis 3	-1.21	0.003262
216835_s_at	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	1.3	0.019634
220320_at	DOK3	docking protein 3	-1.12	0.016716
202116_at	DPF2	D4, zinc and double PHD fingers family 2	1.25	0.004268
211624_s_at	DRD2	dopamine receptor D2	-1.15	0.048872
219000_s_at	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	-1.34	0.006289
211325_x_at	DSTNP2	destrin (actin depolymerizing factor) pseudogene 2	1.25	0.033815
210736_x_at	DTNA	dystrobrevin, alpha	-1.15	0.007362
201536_at	DUSP3	dual specificity phosphatase 3	1.29	0.039223
204015_s_at	DUSP4	dual specificity phosphatase 4	1.26	0.033412

208955_at	DUT	deoxyuridine triphosphatase	-1.87	0.005332
211928_at	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	1.36	0.047912
203590_at	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	1.31	0.002882
202968_s_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	1.19	0.013932
221586_s_at	E2F5	E2F transcription factor 5, p130-binding	-1.22	0.048429
203957_at	E2F6	E2F transcription factor 6	1.26	0.01321
219990_at	E2F8	E2F transcription factor 8	-1.35	0.023499
202623_at	EAPP	E2F-associated phosphoprotein	1.31	0.026252
211129_x_at	EDA	ectodysplasin A	1.11	0.046925
219833_s_at	EFHC1	EF-hand domain (C-terminal) containing 1	1.24	0.001396
202669_s_at	EFNB2	ephrin-B2	1.2	0.023058
219454_at	EGFL6	EGF-like-domain, multiple 6	-1.15	0.014818
219232_s_at	EGLN3	egl nine homolog 3 (C. elegans)	-1.11	0.035468
208669_s_at	EID1	EP300 interacting inhibitor of differentiation 1	-1.43	0.006385
211956_s_at	EIF1	eukaryotic translation initiation factor 1	1.22	0.003978
201738_at	EIF1B	eukaryotic translation initiation factor 1B	1.27	0.029695
217736_s_at	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	1.26	0.021086
213294_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	-1.49	0.030812
219426_at	EIF2C3	eukaryotic translation initiation factor 2C, 3	1.53	0.002833
208725_at	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	-1.28	0.026161
208708_x_at	EIF5	eukaryotic translation initiation factor 5	1.37	0.040484
201025_at	EIF5B	eukaryotic translation initiation factor 5B	-1.24	0.044412
210827_s_at	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	-1.15	0.039878
220366_at	ELSPBP1	epididymal sperm binding protein 1	-1.06	0.020971
217882_at	EMC3	ER membrane protein complex subunit 3	1.39	0.004952
217898_at	EMC7	ER membrane protein complex subunit 7	1.21	0.010205
204975_at	EMP2	epithelial membrane protein 2	-1.1	0.015631
219501_at	ENOX1	ecto-NOX disulfide-thiol exchanger 1	-1.18	0.02679
217245_at	EPAG	early lymphoid activation protein	-1.05	0.019958
202017_at	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	1.39	0.042781
37986_at	EPOR	erythropoietin receptor	1.24	0.016896
217887_s_at	EPS15	epidermal growth factor receptor pathway substrate 15	1.28	0.006062
207347_at	ERCC6	excision repair cross-complementing rodent repair deficiency, complementation group 6	1.79	0.000323
219650_at	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	-1.28	0.021094
205767_at	EREG	epiregulin	1.49	0.009974
208959_s_at	ERP44	endoplasmic reticulum protein 44	1.18	0.006959
215552_s_at	ESR1	estrogen receptor 1	-1.1	0.04457
203349_s_at	ETV5	ets variant 5	1.15	0.037842

204503_at	EVPL	envoplakin	-1.03	0.037143
218481_at	EXOSC5	exosome component 5	-1.6	0.041923
203249_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	1.31	0.03946
218080_x_at	FAF1	Fas (TNFRSF6) associated factor 1	1.07	0.02591
212108_at	FAF2	Fas associated factor family member 2	1.2	0.01633
221984_s_at	FAM134A	family with sequence similarity 134, member A	1.24	0.033474
212697_at	FAM134C	family with sequence similarity 134, member C	1.75	0.000706
214889_at	FAM149A	family with sequence similarity 149, member A	-1.15	0.00139
221533_at	FAM162A	family with sequence similarity 162, member A	-1.11	0.023933
213997_at	FAM189A1	family with sequence similarity 189, member A1	-1.08	0.01443
214946_x_at	FAM21A	family with sequence similarity 21, member A*	1.33	0.004183
205775_at	FAM50B	family with sequence similarity 50, member B	1.16	0.003888
218023_s_at	FAM53C	family with sequence similarity 53, member C	1.25	0.020839
220147_s_at	FAM60A	family with sequence similarity 60, member A	-1.15	0.041568
222013_x_at	FAM86A	family with sequence similarity 86, member A	-1.16	0.034769
203678_at	FAN1	FANCD2/FANCI-associated nuclease 1	1.21	0.041813
213008_at	FANCI	Fanconi anemia, complementation group I	-1.49	0.001657
220615_s_at	FAR2	fatty acyl CoA reductase 2	-1.77	0.000395
202159_at	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	-1.36	0.02278
202271_at	FBXO28	F-box protein 28	1.22	0.039524
221945_at	FBXO41	F-box protein 41	-1.07	0.039647
221813_at	FBXO42	F-box protein 42	1.12	0.024476
216950_s_at	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)*	-1.4	0.004739
214511_x_at	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	-1.2	0.0236
204007_at	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	-1.1	0.008208
201275_at	FDPS	farnesyl diphosphate synthase	-1.25	0.018974
212373_at	FEM1B	fem-1 homolog b (C. elegans)	1.12	0.023144
204768_s_at	FEN1	flap structure-specific endonuclease 1	-1.96	0.025438
203656_at	FIG4	FIG4 homolog, SAC1 lipid phosphatase domain containing (S. cerevisiae)	1.25	0.041813
212169_at	FKBP9	FK506 binding protein 9, 63 kDa	1.11	0.038696
203707_at	FLJ39639	uncharacterized protein FLJ39639*	1.22	0.005403
219316_s_at	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	1.29	0.011141
40665_at	FMO3	flavin containing monooxygenase 3	1.03	0.029953
215017_s_at	FNBP1L	formin binding protein 1-like	2.03	0.014711
212232_at	FNBP4	formin binding protein 4	1.49	0.000471
206015_s_at	FOXJ3	forkhead box J3	1.17	0.030271
207683_at	FOXN1	forkhead box N1	-1.15	0.00943
204131_s_at	FOXO3	forkhead box O3	1.7	0.0026
205140_at	FPGT	fucose-1-phosphate guanylyltransferase	1.19	0.04582
213056_at	FRMD4B	FERM domain containing 4B	-1.79	0.022362
214319_at	FRY	furry homolog (Drosophila)	-1.18	0.000198

214211_at	FTH1	ferritin, heavy polypeptide 1	1.67	0.038099
211628_x_at	FTH1P5	ferritin, heavy polypeptide 1 pseudogene 5	1.47	0.006269
212788_x_at	FTL	ferritin, light polypeptide	2.06	0.000717
202838_at	FUCA1	fucosidase, alpha-L- 1, tissue	1.41	0.001525
206109_at	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	-1.13	0.024375
205565_s_at	FXN	frataxin	-1.69	0.038841
205674_x_at	FXYD2	FXYD domain containing ion transport regulator 2	-1.18	0.023932
210105_s_at	FYN	FYN oncogene related to SRC, FGR, YES	1.39	0.038446
211458_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1*	2.89	0.001721
206456_at	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	-1.05	0.012844
216651_s_at	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	-1.13	0.02555
207466_at	GAL	galanin prepropeptide	-1.15	0.003239
219271_at	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	-1.24	0.001225
217787_s_at	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	1.3	0.029329
218912_at	GCC1	GRIP and coiled-coil domain containing 1	1.25	0.00102
204224_s_at	GCH1	GTP cyclohydrolase 1	-1.21	0.020263
202923_s_at	GCLC	glutamate-cysteine ligase, catalytic subunit	1.46	0.017908
203925_at	GCLM	glutamate-cysteine ligase, modifier subunit	1.48	0.031641
213129_s_at	GCSH	glycine cleavage system protein H (aminomethyl carrier)	-1.51	0.043881
220903_at	GFM1	G elongation factor, mitochondrial 1	-1.11	0.017912
213772_s_at	GGA2	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	1.28	0.003494
205582_s_at	GGT5	gamma-glutamyltransferase 5	-1.19	0.017385
214430_at	GLA	galactosidase, alpha	1.62	0.000282
203158_s_at	GLS	glutaminase	2.24	0.000184
218147_s_at	GLT8D1	glycosyltransferase 8 domain containing 1	1.35	0.002252
212737_at	GM2A	GM2 ganglioside activator	1.42	0.027955
214106_s_at	GMDS	GDP-mannose 4,6-dehydratase	-1.33	0.010716
220938_s_at	GMEB1	glucocorticoid modulatory element binding protein 1	-1.22	0.027642
212294_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12	1.13	0.014122
211522_s_at	GNRHR	gonadotropin-releasing hormone receptor	-1.08	0.011951
204384_at	GOLGA2	golgin A2	1.31	0.035988
201057_s_at	GOLGB1	golgin B1	1.52	0.002311
218361_at	GOLPH3L	golgi phosphoprotein 3-like	1.27	0.008261
218873_at	GON4L	gon-4-like (C. elegans)	1.15	0.046341
219818_s_at	GPATCH1	G patch domain containing 1	1.42	0.008014
219078_at	GPATCH2	G patch domain containing 2	1.3	0.013762
217877_s_at	GPBP1L1	GC-rich promoter binding protein 1-like 1	1.14	0.028703
201141_at	GPNMB	glycoprotein (transmembrane) nmb	1.27	0.009211

211979_at	GPR107	G protein-coupled receptor 107	1.18	0.002341
221149_at	GPR77	G protein-coupled receptor 77	-1.19	0.016501
220313_at	GPR88	G protein-coupled receptor 88	1.08	0.016707
219388_at	GRHL2	grainyhead-like 2 (Drosophila)	-1.08	0.039128
208464_at	GRIA4	glutamate receptor, ionotropic, AMPA 4	-1.17	0.037845
205915_x_at	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	-1.1	0.046863
217595_at	GSPT1	G1 to S phase transition 1	-1.15	0.005904
205770_at	GSR	glutathione reductase	1.48	0.012413
215091_s_at	GTF3A	general transcription factor IIIA	-1.28	0.004296
205488_at	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	-2.43	0.046934
214501_s_at	H2AFY	H2A histone family, member Y	-1.22	0.02438
206643_at	HAL	histidine ammonia-lyase	-1.08	0.022825
220138_at	HAND1	heart and neural crest derivatives expressed 1	-1.08	0.035365
209252_at	HARS2	histidyl-tRNA synthetase 2, mitochondrial (putative)	1.27	0.005655
216063_at	HBBP1	hemoglobin, beta pseudogene 1	-1.15	0.024138
209102_s_at	HBP1	HMG-box transcription factor 1	2.03	0.019516
216174_at	HCRP1	hepatocellular carcinoma-related HCRP1	-1.36	0.010087
201209_at	HDAC1	histone deacetylase 1	-1.21	0.037194
46167_at	HEATR8	HEAT repeat containing 8*	1.38	0.022758
218450_at	HEBP1	heme binding protein 1	1.31	0.027811
218603_at	HECA	headcase homolog (Drosophila)	1.35	0.000422
218632_at	HECTD3	HECT domain containing E3 ubiquitin protein ligase 3	1.26	0.04519
220085_at	HELLS	helicase, lymphoid-specific	-1.34	0.013632
206183_s_at	HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3	-1.14	0.010173
211267_at	HESX1	HESX homeobox 1	-1.12	0.013238
201944_at	HEXB	hexosaminidase B (beta polypeptide)	1.23	0.004019
202814_s_at	HEXIM1	hexamethylene bis-acetamide inducible 1	1.21	0.019197
59999_at	HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	1.25	0.005915
200093_s_at	HINT1	histidine triad nucleotide binding protein 1	1.17	0.017542
205426_s_at	HIP1	huntingtin interacting protein 1	1.07	0.014075
209398_at	HIST1H1C	histone cluster 1, H1c	1.37	0.023672
215071_s_at	HIST1H2AC	histone cluster 1, H2ac	1.4	0.026175
209911_x_at	HIST1H2BD	histone cluster 1, H2bd	1.35	0.002836
209806_at	HIST1H2BK	histone cluster 1, H2bk	1.54	0.004939
212641_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	1.35	0.009066
204754_at	HLF	hepatic leukemia factor	-1.12	0.017527
203665_at	HMOX1	heme oxygenase (decycling) 1	3.48	0.00347
216031_x_at	HN1L	hematological and neurological expressed 1-like	-1.17	0.026429
205313_at	HNF1B	HNF1 homeobox B	-1.18	0.043189
211933_s_at	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3*	-1.28	0.010792

209330_s_at	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-1.39	0.016126
209068_at	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	-1.23	0.009142
206194_at	HOXC4	homeobox C4	-1.11	0.019753
206739_at	HOXC5	homeobox C5	-1.19	0.006423
203913_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-1.23	0.039397
204934_s_at	HPN	hepsin	-1.12	0.017462
202854_at	HPRT1	hypoxanthine phosphoribosyltransferase 1	-1.2	0.005226
219984_s_at	HRASLS	HRAS-like suppressor	-1.04	0.032043
205404_at	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	-1.47	0.000017
217989_at	HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	1.56	0.026463
204818_at	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	-1.09	0.041967
214434_at	HSPA12A	heat shock 70kDa protein 12A	-1.17	0.03153
200800_s_at	HSPA1A*	heat shock 70kDa protein 1A*	1.86	0.033259
209448_at	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	1.37	0.012754
207135_at	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	1.08	0.049918
207577_at	HTR4	5-hydroxytryptamine (serotonin) receptor 4, G protein-coupled	-1.12	0.019151
207783_x_at	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase	1.05	0.039046
201193_at	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	1.37	0.010334
202439_s_at	IDS	iduronate 2-sulfatase	1.89	0.000865
218611_at	IER5	immediate early response 5	1.67	0.004057
214022_s_at	IFITM1	interferon induced transmembrane protein 1	-1.55	0.012531
208548_at	IFNA6	interferon, alpha 6	1.09	0.03492
210312_s_at	IFT20	intraflagellar transport 20 homolog (Chlamydomonas)	1.3	0.006419
204703_at	IFT88	intraflagellar transport 88 homolog (Chlamydomonas)	1.22	0.001454
209540_at	IGF1	insulin-like growth factor 1 (somatomedin C)	-1.11	0.032409
202409_at	IGF2	insulin-like growth factor 2 (somatomedin A)*	-1.23	0.027309
201162_at	IGFBP7	insulin-like growth factor binding protein 7	-1.09	0.039342
217198_x_at	IGH	immunoglobulin heavy locus*	-1.14	0.024559
212592_at	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	-1.15	0.018981
211881_x_at	IGLJ3	immunoglobulin lambda joining 3	-1.24	0.02332
217227_x_at	IGLV1-44	immunoglobulin lambda variable 1-44	1.13	0.007344
204549_at	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	-1.15	0.003287
209929_s_at	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	1.21	0.044673
209575_at	IL10RB	interleukin 10 receptor, beta	1.32	0.033428
206618_at	IL18R1	interleukin 18 receptor 1	-1.26	0.017261
207072_at	IL18RAP	interleukin 18 receptor accessory protein	-1.5	0.03396
221271_at	IL21	interleukin 21	-2.8	0.004524
221165_s_at	IL22	interleukin 22	-1.22	0.034491
217326_x_at	IL23A	Interleukin 23, alpha subunit p19*	-1.17	0.022837

221111_at	IL26	interleukin 26	-1.28	0.044212
207902_at	IL5RA	interleukin 5 receptor, alpha	-1.13	0.002636
205945_at	IL6R	interleukin 6 receptor	1.15	0.029984
221688_s_at	IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.61	0.045491
204552_at	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	1.15	0.04934
203607_at	INPP5F	inositol polyphosphate-5-phosphatase F	1.78	0.04747
201625_s_at	INSIG1	insulin induced gene 1	1.38	0.011898
213792_s_at	INSR	insulin receptor	1.43	0.02112
218616_at	INTS12	integrator complex subunit 12	1.33	0.037574
210114_at	INVS	inversin	1.38	0.032102
211953_s_at	IPO5	importin 5	-1.34	0.02057
221974_at	IPW	imprinted in Prader-Willi syndrome (non-protein coding)*	1.3	0.037371
217124_at	IQCE	IQ motif containing E	1.07	0.034198
209184_s_at	IRS2	insulin receptor substrate 2	1.73	0.009374
209075_s_at	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	1.29	0.000252
218893_at	ISOC2	isochorismatase domain containing 2	-1.6	0.029725
200851_s_at	IST1	increased sodium tolerance 1 homolog (yeast)	1.25	0.015139
209744_x_at	ITCH	itchy E3 ubiquitin protein ligase	1.39	0.01121
220590_at	ITFG2	integrin alpha FG-GAP repeat containing 2	-1.09	0.031108
206494_s_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-1.07	0.023231
219829_at	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	-1.1	0.013535
209907_s_at	ITSN2	intersectin 2	1.14	0.007901
212723_at	JMJD6	jumonji domain containing 6	1.22	0.00881
217146_at	JRK	jerky homolog (mouse)	-1.09	0.008118
201464_x_at	JUN	jun proto-oncogene	1.75	0.035639
215046_at	KANSL1L	KAT8 regulatory NSL complex subunit 1-like	1.14	0.004221
206689_x_at	KAT5	K(lysine) acetyltransferase 5	-1.2	0.048858
217938_s_at	KCMF1	potassium channel modulatory factor 1	1.26	0.038734
210179_at	KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	-1.07	0.047086
219564_at	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	-1.05	0.025626
206765_at	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	-1.14	0.006855
215736_at	KCNV1	potassium channel, subfamily V, member 1	-1.04	0.015973
218553_s_at	KCTD15	potassium channel tetramerisation domain containing 15	-1.1	0.014975
212564_at	KCTD2	potassium channel tetramerisation domain containing 2	1.19	0.022741
213474_at	KCTD7	potassium channel tetramerisation domain containing 7*	1.16	0.044902
212689_s_at	KDM3A	lysine (K)-specific demethylase 3A	1.85	0.009199
203205_at	KDM4A	lysine (K)-specific demethylase 4A	1.13	0.00787
203934_at	KDR	kinase insert domain receptor (a type III receptor	-1.04	0.028162

		tyrosine kinase)		
202417_at	KEAP1	kelch-like ECH-associated protein 1	1.29	0.01799
212356_at	KHNYN	KH and NYN domain containing	1.44	0.021645
212735_at	KIAA0226	KIAA0226	1.13	0.04427
212441_at	KIAA0232	KIAA0232	1.49	0.014525
206017_at	KIAA0319	KIAA0319	-1.11	0.042258
203288_at	KIAA0355	KIAA0355	1.65	0.000013
212427_at	KIAA0368	KIAA0368	-1.12	0.039631
204546_at	KIAA0513	KIAA0513	1.4	0.000163
204711_at	KIAA0753	KIAA0753	1.16	0.00227
213316_at	KIAA1462	KIAA1462	-1.06	0.048098
209680_s_at	KIFC1	kinesin family member C1	-1.2	0.026047
213656_s_at	KLC1	kinesin light chain 1	1.24	0.03066
210504_at	KLF1	Kruppel-like factor 1 (erythroid)	-1.14	0.011217
203543_s_at	KLF9	Kruppel-like factor 9	1.2	0.026013
210111_s_at	KLHDC10	kelch domain containing 10	1.36	0.019973
217906_at	KLHDC2	kelch domain containing 2	1.47	0.000687
203068_at	KLHL21	kelch-like 21 (Drosophila)	1.73	0.008519
213610_s_at	KLHL23	kelch-like 23 (Drosophila)*	-1.1	0.041805
221985_at	KLHL24	kelch-like 24 (Drosophila)	2.02	0.004662
213233_s_at	KLHL9	kelch-like 9 (Drosophila)	-1.15	0.028583
211138_s_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-1.86	0.02903
202059_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	1.44	0.030239
220160_s_at	KPTN	kaptin (actin binding protein)	-1.27	0.015422
209351_at	KRT14	keratin 14	-1.04	0.044505
207065_at	KRT75	keratin 75	-1.2	0.01648
204584_at	L1CAM	L1 cell adhesion molecule	1.17	0.040901
206486_at	LAG3	lymphocyte-activation gene 3	-1.68	0.040649
213519_s_at	LAMA2	laminin, alpha 2	-1.22	0.004266
209270_at	LAMB3	laminin, beta 3	-1.08	0.030925
203042_at	LAMP2	lysosomal-associated membrane protein 2	1.52	0.011151
200673_at	LAPTM4A	lysosomal protein transmembrane 4 alpha	1.52	0.017594
207734_at	LAX1	lymphocyte transmembrane adaptor 1	1.36	0.044343
221515_s_at	LCMT1	leucine carboxyl methyltransferase 1	1.13	0.009699
217173_s_at	LDLR	low density lipoprotein receptor	-1.14	0.021961
221557_s_at	LEF1	lymphoid enhancer-binding factor 1	-1.1	0.034354
207092_at	LEP	leptin	-1.12	0.033362
202595_s_at	LEPROTL1	leptin receptor overlapping transcript-like 1	1.16	0.041125
208933_s_at	LGALS8	lectin, galactoside-binding, soluble, 8	1.86	0.036505
203236_s_at	LGALS9	lectin, galactoside-binding, soluble, 9	-1.46	0.007718
205266_at	LIF	leukemia inhibitory factor	-2.48	0.003624
210582_s_at	LIMK2	LIM domain kinase 2	-1.23	0.048473

216935_at	LINC00302	long intergenic non-protein coding RNA 302	1.11	0.032665
220904_at	LINC00574	long intergenic non-protein coding RNA 574	-1.1	0.038648
206606_at	LIPC	lipase, hepatic	-1.18	0.038592
221274_s_at	LMAN2L	lectin, mannose-binding 2-like	1.32	0.002623
218191_s_at	LMBRD1	LMBR1 domain containing 1	1.25	0.002908
211562_s_at	LMOD1	leiomodin 1 (smooth muscle)	-1.04	0.031799
221847_at	LOC100129361	chromosome X open reading frame 69 pseudogene	1.22	0.025703
213893_x_at	LOC100132832	PMS2 postmeiotic segregation increased 2 (S. cerevisiae) pseudogene*	1.21	0.01249
220514_at	LOC100505870	uncharacterized LOC100505870	-1.15	0.007377
213685_at	LOC100506963	uncharacterized LOC100506963	1.29	0.009445
211262_at	LOC100507472	uncharacterized LOC100507472*	-1.13	0.026129
215644_at	LOC100509474	uncharacterized LOC100509474*	-1.07	0.006392
214657_s_at	LOC100653017	uncharacterized LOC100653017*	1.38	0.001333
216659_at	LOC1720	dihydrofolate reductase pseudogene	-1.05	0.029823
219043_s_at	LOC285359	phosducin-like 3 pseudogene*	-1.36	0.011884
214129_at	LOC728802	myomegalin-like*	1.22	0.007927
222001_x_at	LOC728855	uncharacterized LOC728855*	1.4	0.001027
220009_at	LONRF3	LON peptidase N-terminal domain and ring finger 3	-1.17	0.043335
212276_at	LPIN1	lipin 1	1.2	0.023523
216250_s_at	LPXN	leupaxin	1.44	0.001366
207797_s_at	LRP2BP	LRP2 binding protein	-1.07	0.029983
209468_at	LRP5	low density lipoprotein receptor-related protein 5	1.19	0.031544
218550_s_at	LRRC20	leucine rich repeat containing 20	-1.08	0.049102
218364_at	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	1.29	0.001564
204559_s_at	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.28	0.030951
214181_x_at	LST1	leukocyte specific transcript 1	-1.81	0.021303
218437_s_at	LZTFL1	leucine zipper transcription factor-like 1	1.07	0.048087
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.06	0.011732
204970_s_at	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	1.3	0.011651
210437_at	MAGEA9	melanoma antigen family A, 9*	-1.15	0.013205
217920_at	MAN1A2	mannosidase, alpha, class 1A, member 2	1.15	0.039905
220945_x_at	MANSC1	MANSC domain containing 1	-1.11	0.025947
208786_s_at	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	1.43	0.003096
202568_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	1.31	0.002744
212505_s_at	MAU2	MAU2 chromatid cohesion factor homolog (C. elegans)	1.34	0.008942
203353_s_at	MBD1	methyl-CpG binding domain protein 1	1.17	0.03972
218411_s_at	MBIP	MAP3K12 binding inhibitory protein 1	1.08	0.020468

203640_at	MBNL2	muscleblind-like splicing regulator 2	1.3	0.032399
216531_at	MBTPS2	membrane-bound transcription factor peptidase, site 2*	-1.11	0.045876
209623_at	MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)	-1.25	0.031912
201555_at	MCM3	minichromosome maintenance complex component 3	-1.42	0.048293
222036_s_at	MCM4	minichromosome maintenance complex component 4	-1.2	0.043113
210983_s_at	MCM7	minichromosome maintenance complex component 7	-2.07	0.019524
208434_at	MECOM	MDS1 and EVI1 complex locus	-1.14	0.02263
213816_s_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	-1.08	0.031122
219137_s_at	MFF	mitochondrial fission factor	-1.51	0.013441
207098_s_at	MFN1	mitofusin 1	1.44	0.044482
200898_s_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	1.45	0.014082
205904_at	MICA	MHC class I polypeptide-related sequence A	1.46	0.003502
212473_s_at	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	-1.47	0.025697
208384_s_at	MID2	midline 2	1.19	0.003925
214625_s_at	MINK1	misshapen-like kinase 1	-1.13	0.045497
214696_at	MIR22	microRNA 22*	1.91	0.006553
212023_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	-1.42	0.039695
215291_at	MKL1	megakaryoblastic leukemia (translocation) 1	1.13	0.035991
201285_at	MKRN1	makorin ring finger protein 1	1.31	0.010089
218071_s_at	MKRN2	makorin ring finger protein 2	1.3	0.007422
204784_s_at	MLF1	myeloid leukemia factor 1	1.41	0.000274
211071_s_at	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	1.3	0.025833
212508_at	MOAP1	modulator of apoptosis 1	1.29	0.03316
210193_at	MOBP	myelin-associated oligodendrocyte basic protein	-1.08	0.036016
213181_s_at	MOCS1	molybdenum cofactor synthesis 1	-1.21	0.024012
216863_s_at	MORC2	MORC family CW-type zinc finger 2	1.39	0.046833
221965_at	MPHOSPH9	M-phase phosphoprotein 9	-1.33	0.014431
202472_at	MPI	mannose phosphate isomerase	-1.1	0.039415
216825_s_at	MPL	myeloproliferative leukemia virus oncogene	-1.21	0.009008
201874_at	MPZL1	myelin protein zero-like 1	1.34	0.011948
212199_at	MRFAP1L1	Morf4 family associated protein 1-like 1	1.26	0.013169
218202_x_at	MRPL44	mitochondrial ribosomal protein L44	1.08	0.030204
210008_s_at	MRPS12	mitochondrial ribosomal protein S12	-1.22	0.037287
219477_s_at	MRPS31P3	mitochondrial ribosomal protein S31 pseudogene 3*	1.28	0.002335
207496_at	MS4A2	membrane-spanning 4-domains, subfamily A, member 2	-1.13	0.029966
210254_at	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	-1.11	0.044554
209146_at	MSMO1	methylsterol monooxygenase 1	1.25	0.023938
208422_at	MSR1	macrophage scavenger receptor 1	-1.06	0.046523
219281_at	MSRA	methionine sulfoxide reductase A	-1.23	0.007117
205323_s_at	MTF1	metal-regulatory transcription factor 1	1.2	0.039075

202309_at	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	-1.33	0.005282
204673_at	MUC2	mucin 2, oligomeric mucus/gel-forming	-1.12	0.018799
217109_at	MUC4	mucin 4, cell surface associated	-1.11	0.043416
218246_at	MUL1	mitochondrial E3 ubiquitin protein ligase 1	1.06	0.048562
221253_s_at	MUTED-TXNDC5	MUTED-TXNDC5 readthrough (non-protein coding)*	-1.29	0.007421
202364_at	MXI1	MAX interactor 1	1.82	0.012106
214087_s_at	MYBPC1	myosin binding protein C, slow type	-1.1	0.0454
216188_at	MYCNOS	MYCN opposite strand/antisense RNA (non-protein coding)	-1.14	0.035379
216054_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	-1.11	0.033825
220288_at	MYO15A	myosin XVA	-1.15	0.00635
204527_at	MYO5A	myosin VA (heavy chain 12, myoxin)	1.58	0.034316
218966_at	MYO5C	myosin VC	-1.38	0.023573
210155_at	MYOC	myocilin, trabecular meshwork inducible glucocorticoid response	-1.08	0.011037
207148_x_at	MYOZ2	myozenin 2	-1.19	0.03726
221286_s_at	MZB1	marginal zone B and B1 cell-specific protein	-1.5	0.002497
214748_at	N4BP2L2	NEDD4 binding protein 2-like 2	1.12	0.01509
205090_s_at	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	1.19	0.034501
201969_at	NASP	nuclear autoantigenic sperm protein (histone-binding)	-1.3	0.007401
216466_at	NAV3	neuron navigator 3	1.13	0.03923
202907_s_at	NBN	nibrin	-1.61	0.001961
201384_s_at	NBR1	neighbor of BRCA1 gene 1	1.75	0.046276
212789_at	NCAPD3	non-SMC condensin II complex, subunit D3	-1.19	0.00925
212949_at	NCAPH	non-SMC condensin I complex, subunit H	-1.61	0.046345
205147_x_at	NCF4	neutrophil cytosolic factor 4, 40kDa	-1.72	0.002572
212867_at	NCOA2	nuclear receptor coactivator 2	1.37	0.035353
207700_s_at	NCOA3	nuclear receptor coactivator 3	1.15	0.01904
211583_x_at	NCR3	natural cytotoxicity triggering receptor 3	-1.69	0.020138
217800_s_at	NDFIP1	Nedd4 family interacting protein 1	1.48	0.02027
200632_s_at	NDRG1	N-myc downstream regulated 1	1.47	0.002003
202001_s_at	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	1.19	0.044574
204125_at	NDUFAF1	NADH dehydrogenase (ubiquinone) complex I, assembly factor 1	1.32	0.025611
218226_s_at	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	1.13	0.006774
203961_at	NEBL	nebulette	-1.17	0.013886
204634_at	NEK4	NIMA (never in mitosis gene a)-related kinase 4	1.52	0.020256
208926_at	NEU1	sialidase 1 (lysosomal sialidase)	1.32	0.033595
213438_at	NFASC	neurofascin	-1.09	0.024073
214179_s_at	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	1.35	0.008841
218127_at	NFYB	nuclear transcription factor Y, beta	-1.37	0.029846

220742_s_at	NGLY1	N-glycanase 1	1.4	0.038388
217722_s_at	NGRN	neugrin, neurite outgrowth associated	1.19	0.016152
218557_at	NIT2	nitrilase family, member 2	1.29	0.03032
222105_s_at	NKIRAS2	NFKB inhibitor interacting Ras-like 2	1.17	0.045799
221567_at	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	1.16	0.015463
202679_at	NPC1	Niemann-Pick disease, type C1	1.55	0.000876
200701_at	NPC2	Niemann-Pick disease, type C2	1.23	0.028599
213471_at	NPHP4	nephronophthisis 4	1.13	0.009584
205129_at	NPM3	nucleophosmin/nucleoplasmin 3	-1.12	0.013235
221322_at	NPVF	neuropeptide VF precursor	-1.16	0.034982
210519_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1	3.75	0.000005
203814_s_at	NQO2	NAD(P)H dehydrogenase, quinone 2	1.57	0.030638
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	1.88	0.0064
207202_s_at	NR1I2	nuclear receptor subfamily 1, group I, member 2	-1.06	0.033828
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	2.82	0.026147
208709_s_at	NRD1	nardilysin (N-arginine dibasic convertase)	1.16	0.003995
201310_s_at	NREP	neuronal regeneration related protein homolog (rat)	-2.55	0.017882
220248_x_at	NSFL1C	NSFL1 (p97) cofactor (p47)	1.23	0.019776
220194_at	NSUN7	NOP2/Sun domain family, member 7	-1.06	0.022678
209731_at	NTHL1	nth endonuclease III-like 1 (E. coli)	-1.37	0.0297
208605_s_at	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	-1.68	0.044613
215025_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	1.26	0.0389
210575_at	NUDC	nuclear distribution C homolog (A. nidulans)	-1.19	0.011969
219855_at	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	1.23	0.017309
219347_at	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	-1.36	0.037004
208922_s_at	NXF1	nuclear RNA export factor 1	1.21	0.036884
213863_s_at	OAZ3	ornithine decarboxylase antizyme 3	-1.18	0.020273
219277_s_at	OGDHL	oxoglutarate dehydrogenase-like	-1.19	0.008849
202074_s_at	OPTN	optineurin	1.28	0.001917
221465_at	OR6A2	olfactory receptor, family 6, subfamily A, member 2	-1.14	0.002273
201800_s_at	OSBP	oxysterol binding protein	1.12	0.027767
209222_s_at	OSBPL2	oxysterol binding protein-like 2	1.42	0.006248
214637_at	OSM	oncostatin M	-1.9	0.024198
202780_at	OXCT1	3-oxoacid CoA transferase 1	-1.29	0.019666
206880_at	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	-1.16	0.035485
218957_s_at	PAAF1	proteasomal ATPase-associated factor 1	1.15	0.042365
214204_at	PACRG	PARK2 co-regulated	-1.08	0.040353
200815_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	1.32	0.004043
203228_at	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	-1.63	0.016944
201013_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide	-1.43	0.02635

		synthetase		
214620_x_at	PAM	peptidylglycine alpha-amidating monooxygenase	1.12	0.014433
218809_at	PANK2	pantothenate kinase 2	1.22	0.012063
218433_at	PANK3	pantothenate kinase 3	-1.13	0.028087
204715_at	PANX1	pannexin 1	1.38	0.035003
50400_at	PAOX	polyamine oxidase (exo-N4-amino)	-1.18	0.025208
208271_at	PAPOLB	poly(A) polymerase beta (testis specific)	-1.08	0.014404
219639_x_at	PARP6	poly (ADP-ribose) polymerase family, member 6	1.15	0.034323
209494_s_at	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	-1.22	0.013132
202876_s_at	PBX2	pre-B-cell leukemia homeobox 2	-1.19	0.013505
219656_at	PCDH12	protocadherin 12	-1.15	0.035061
201202_at	PCNA	proliferating cell nuclear antigen	-1.18	0.034125
218676_s_at	PCTP	phosphatidylcholine transfer protein	1.23	0.03041
217746_s_at	PDCD6IP	programmed cell death 6 interacting protein	1.28	0.000944
211171_s_at	PDE10A	phosphodiesterase 10A	-1.08	0.013128
205463_s_at	PDGFA	platelet-derived growth factor alpha polypeptide	1.63	0.016105
205226_at	PDGFRL	platelet-derived growth factor receptor-like	-1.25	0.013992
200980_s_at	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	-1.17	0.045466
208911_s_at	PDHB	pyruvate dehydrogenase (lipoamide) beta	-1.16	0.027802
203857_s_at	PDIA5	protein disulfide isomerase family A, member 5	-1.62	0.003271
206348_s_at	PDK3	pyruvate dehydrogenase kinase, isozyme 3	1.17	0.00297
219307_at	PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2	1.18	0.040792
208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule 1	-1.74	0.025072
209243_s_at	PEG3	paternally expressed 3	-1.06	0.030209
218472_s_at	PELO	pelota homolog (Drosophila)	1.48	0.002173
207931_s_at	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-1.09	0.032013
204047_s_at	PHACTR2	phosphatase and actin regulator 2	-1.18	0.02691
205450_at	PHKA1	phosphorylase kinase, alpha 1 (muscle)	-1.26	0.003743
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	3.23	0.043173
210191_s_at	PHTF1	putative homeodomain transcription factor 1	1.26	0.016679
209345_s_at	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	1.45	0.00747
203035_s_at	PIAS3	protein inhibitor of activated STAT, 3	1.29	0.011083
212511_at	PICALM	phosphatidylinositol binding clathrin assembly protein	-1.55	0.026973
218652_s_at	PIGG	phosphatidylinositol glycan anchor biosynthesis, class G	1.27	0.040063
209625_at	PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	1.21	0.046581
220566_at	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	-1.16	0.01017
209019_s_at	PINK1	PTEN induced putative kinase 1	1.71	0.000134
212518_at	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	1.18	0.033397
207469_s_at	PIR	pirin (iron-binding nuclear protein)	5.3	0.000009
214717_at	PKI55	DKFZp434H1419	-1.21	0.014583

63305_at	PKNOX2	PBX/knotted 1 homeobox 2	-1.14	0.016085
204458_at	PLA2G15	phospholipase A2, group XV	1.16	0.011961
219014_at	PLAC8	placenta-specific 8	-1.85	0.023144
214745_at	PLCH1	phospholipase C, eta 1	-1.15	0.033814
217044_s_at	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	-1.25	0.026283
212717_at	PLEKHM1	pleckstrin homology domain containing, family M (with RUN domain) member 1	1.25	0.002659
218992_at	PLGRKT	plasminogen receptor, C-terminal lysine transmembrane protein	-1.1	0.03918
204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	1.14	0.034594
212037_at	PNN	pinin, desmosome associated protein	-1.3	0.019006
209578_s_at	POFUT2	protein O-fucosyltransferase 2	1.31	0.006237
204835_at	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	-1.42	0.039127
219317_at	POLI	polymerase (DNA directed) iota	1.29	0.018224
214263_x_at	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	1.27	0.041088
208554_at	POU4F3	POU class 4 homeobox 3	1.07	0.01727
217848_s_at	PPA1	pyrophosphatase (inorganic) 1	-1.36	0.001598
209147_s_at	PPAP2A	phosphatidic acid phosphatase type 2A	-1.6	0.005325
209434_s_at	PPAT	phosphoribosyl pyrophosphate amidotransferase	-1.39	0.03128
203966_s_at	PPM1A	protein phosphatase, Mg2+/Mn2+ dependent, 1A	1.45	0.039591
202014_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	2.22	0.039873
205643_s_at	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	-1.12	0.03669
202187_s_at	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha	1.15	0.036014
635_s_at	PPP2R5B	protein phosphatase 2, regulatory subunit B', beta	1.15	0.036917
218208_at	PQLC1	PQ loop repeat containing 1	1.22	0.033069
201494_at	PRCP	prolylcarboxypeptidase (angiotensinase C)	1.31	0.003254
203057_s_at	PRDM2	PR domain containing 2, with ZNF domain	1.31	0.0495
201006_at	PRDX2	peroxiredoxin 2	-1.17	0.017884
201619_at	PRDX3	peroxiredoxin 3	-1.44	0.009139
212216_at	PREPL	prolyl endopeptidase-like	1.4	0.009458
210543_s_at	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	-1.4	0.024807
204061_at	PRKX	protein kinase, X-linked	-1.4	0.028729
204304_s_at	PROM1	prominin 1	-1.05	0.041502
208034_s_at	PROZ	protein Z, vitamin K-dependent plasma glycoprotein	-1.19	0.041302
202529_at	PRPSAP1	phosphoribosyl pyrophosphate synthetase-associated protein 1	1.19	0.006484
219383_at	PRR5L	proline rich 5 like	-1.24	0.001497
208165_s_at	PRSS16	protease, serine, 16 (thymus)	-1.19	0.039513
209586_s_at	PRUNE	prune homolog (Drosophila)	1.48	0.000061
200871_s_at	PSAP	prosaposin	1.61	0.009313
203460_s_at	PSEN1	presenilin 1	1.51	0.029925
210195_s_at	PSG1	pregnancy specific beta-1-glycoprotein 1	1.06	0.037149
211746_x_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	1.24	0.010285

214288_s_at	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	1.3	0.011682
200786_at	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	1.29	0.010028
209040_s_at	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	-1.96	0.01525
204279_at	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	-1.48	0.032148
201199_s_at	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	1.33	0.018324
212296_at	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	1.23	0.02257
200830_at	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	1.23	0.002627
200882_s_at	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	1.37	0.002901
201705_at	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.24	0.048482
212219_at	PSME4	proteasome (prosome, macropain) activator subunit 4	1.21	0.0316
219938_s_at	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	-1.56	0.007365
211711_s_at	PTEN	phosphatase and tensin homolog	1.48	0.049421
210831_s_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-1.18	0.008537
208131_s_at	PTGIS	prostaglandin I2 (prostacyclin) synthase	-1.22	0.035208
205911_at	PTH1R	parathyroid hormone 1 receptor	-1.09	0.027187
200773_x_at	PTMA	prothymosin, alpha	-1.18	0.010761
204201_s_at	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	-1.07	0.030143
213136_at	PTPN2	protein tyrosine phosphatase, non-receptor type 2	-1.29	0.036309
1320_at	PTPN21	protein tyrosine phosphatase, non-receptor type 21	-1.13	0.030636
211534_x_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	-1.09	0.027361
200677_at	PTTG1IP	pituitary tumor-transforming 1 interacting protein	1.4	0.005397
201164_s_at	PUM1	pumilio homolog 1 (Drosophila)	1.13	0.042606
216283_s_at	PVR	poliovirus receptor	-1.24	0.033103
219812_at	PVRIG	poliovirus receptor related immunoglobulin domain containing	-1.73	0.02486
212013_at	PXDN	peroxidasin homolog (Drosophila)	-1.2	0.00937
200863_s_at	RAB11A	RAB11A, member RAS oncogene family	1.23	0.016688
219412_at	RAB38	RAB38, member RAS oncogene family	1.73	0.004272
204547_at	RAB40B	RAB40B, member RAS oncogene family	1.24	0.005772
210406_s_at	RAB6A	RAB6A, member RAS oncogene family*	1.28	0.03072
213313_at	RABGAP1	RAB GTPase activating protein 1	1.33	0.002135
203020_at	RABGAP1L	RAB GTPase activating protein 1-like	1.2	0.031155
213970_at	RABL3	RAB, member of RAS oncogene family-like 3	-1.28	0.00068
219828_at	RABL6	RAB, member RAS oncogene family-like 6	-1.13	0.048655
210255_at	RAD51B	RAD51 homolog B (S. cerevisiae)	-1.2	0.006865
204558_at	RAD54L	RAD54-like (S. cerevisiae)	-1.22	0.041756
202845_s_at	RALBP1	ralA binding protein 1	1.31	0.032465

202483_s_at	RANBP1	RAN binding protein 1	-1.94	0.008161
53987_at	RANBP10	RAN binding protein 10	1.09	0.038536
202640_s_at	RANBP3	RAN binding protein 3	1.09	0.045114
217020_at	RARB	retinoic acid receptor, beta	-1.11	0.048633
208534_s_at	RASA4	RAS p21 protein activator 4*	-1.52	0.039811
203185_at	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	-1.19	0.049082
49306_at	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	-1.18	0.002331
219419_at	RBFA	ribosome binding factor A (putative)	-1.33	0.007448
220509_at	RBM26	RNA binding motif protein 26	-1.11	0.042301
221595_at	RBM48	RNA binding motif protein 48	1.17	0.045136
213762_x_at	RBMX	RNA binding motif protein, X-linked*	-1.2	0.024435
210318_at	RBP3	retinol binding protein 3, interstitial	-1.1	0.038232
215253_s_at	RCAN1	regulator of calcineurin 1	-1.08	0.019442
204759_at	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	2.3	0.007148
212397_at	RDX	radixin	1.22	0.009961
204364_s_at	REEP1	receptor accessory protein 1	1.17	0.017798
218777_at	REEP4	receptor accessory protein 4	1.14	0.045673
218194_at	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	1.09	0.040315
208021_s_at	RFC1	replication factor C (activator 1) 1, 145kDa	1.15	0.007143
214409_at	RFPL3-AS1	RFPL3 antisense RNA 1 (non-protein coding)	1.15	0.016084
202988_s_at	RGS1	regulator of G-protein signaling 1	1.46	0.016417
204319_s_at	RGS10	regulator of G-protein signaling 10	1.96	0.013928
220300_at	RGS3	regulator of G-protein signaling 3	1.22	0.004657
204402_at	RHBDD3	rhomboid domain containing 3	1.19	0.020143
207383_s_at	RHBDL1	rhomboid, veinlet-like 1 (Drosophila)	-1.19	0.004039
220282_at	RIC3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	-1.15	0.042841
209882_at	RIT1	Ras-like without CAAX 1	1.84	0.003828
206154_at	RLBP1	retinaldehyde binding protein 1	-1.17	0.00086
212479_s_at	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	1.21	0.005262
202636_at	RNF103	ring finger protein 103	1.4	0.007326
212742_at	RNF115	ring finger protein 115	1.21	0.020762
201780_s_at	RNF13	ring finger protein 13	1.63	0.011265
204040_at	RNF144A	ring finger protein 144A	1.26	0.015747
218426_s_at	RNF216	ring finger protein 216	1.19	0.031322
218528_s_at	RNF38	ring finger protein 38	1.32	0.038531
221909_at	RNFT2	ring finger protein, transmembrane 2	1.15	0.020202
220564_at	RNLS	renalase, FAD-dependent amine oxidase	-1.06	0.028945
202683_s_at	RNMT	RNA (guanine-7-) methyltransferase	1.15	0.044119
213044_at	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	1.34	0.045643
213588_x_at	RPL14	ribosomal protein L14	1.11	0.042429

213084_x_at	RPL23A	ribosomal protein L23a*	1.06	0.047695
201406_at	RPL36A	ribosomal protein L36a*	1.11	0.017958
218836_at	RPP21	ribonuclease P/MRP 21kDa subunit*	1.34	0.019706
213801_x_at	RPSA	ribosomal protein SA*	1.09	0.014939
218088_s_at	RRAGC	Ras-related GTP binding C	1.09	0.047826
208314_at	RRH	retinal pigment epithelium-derived rhodopsin homolog	-1.02	0.027419
202938_x_at	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)*	-1.18	0.010663
213750_at	RSL1D1	ribosomal L1 domain containing 1	1.32	0.040442
211509_s_at	RTN4	reticulon 4	1.26	0.048525
209148_at	RXRB	retinoid X receptor, beta	1.26	0.03721
205485_at	RYR1	ryanodine receptor 1 (skeletal)	1.27	0.000508
219129_s_at	SAP30L	SAP30-like	1.39	0.013958
203408_s_at	SATB1	SATB homeobox 1	-1.36	0.006034
219196_at	SCG3	secretogranin III	-1.07	0.027476
218217_at	SCPEP1	serine carboxypeptidase 1	2.05	0.00001
218427_at	SDCCAG3	serologically defined colon cancer antigen 3	-1.18	0.017993
203090_at	SDF2	stromal cell-derived factor 2	1.24	0.026678
215209_at	SEC24D	SEC24 family, member D (S. cerevisiae)	1.14	0.040992
209889_at	SEC31B	SEC31 homolog B (S. cerevisiae)	-1.36	0.011867
208942_s_at	SEC62	SEC62 homolog (S. cerevisiae)	1.41	0.025335
221931_s_at	SEH1L	SEH1-like (S. cerevisiae)	-1.57	0.04464
212314_at	SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	1.23	0.016622
208671_at	SERINC1	serine incorporator 1	1.74	0.001044
221471_at	SERINC3	serine incorporator 3	1.42	0.000088
211428_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-1.12	0.002989
213572_s_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	-1.79	0.031991
211362_s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	-1.18	0.049298
204614_at	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	5.24	0.028235
205352_at	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	1.55	0.002627
207636_at	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	-1.07	0.031553
202657_s_at	SERTAD2	SERTA domain containing 2	1.49	0.044604
33323_r_at	SFN	stratifin	-1.25	0.006076
210116_at	SH2D1A	SH2 domain containing 1A	-1.49	0.040874
204979_s_at	SH3BGR	SH3 domain binding glutamic acid-rich protein	1.17	0.031554
209091_s_at	SH3GLB1	SH3-domain GRB2-like endophilin B1	1.29	0.024163
202276_at	SHFM1	split hand/foot malformation (ectrodactyly) type 1	1.24	0.014803
217304_at	SHMT1	serine hydroxymethyltransferase 1 (soluble)	1.07	0.016404
220047_at	SIRT4	sirtuin 4	1.13	0.017707

206675_s_at	SKIL	SKI-like oncogene	1.19	0.021301
203626_s_at	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	-1.26	0.008984
208354_s_at	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	-1.11	0.034603
220740_s_at	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	1.16	0.004865
207567_at	SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	-1.19	0.005119
210807_s_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-1.24	0.013224
220455_at	SLC16A8	solute carrier family 16, member 8 (monocarboxylic acid transporter 3)	-1.11	0.034062
221041_s_at	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	1.29	0.01553
211576_s_at	SLC19A1	solute carrier family 19 (folate transporter), member 1	-1.34	0.025766
209610_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.62	0.000289
202744_at	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	-1.05	0.047595
205074_at	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5	1.23	0.028402
57588_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	-1.08	0.001113
203339_at	SLC25A12	solute carrier family 25 (aspartate/glutamate carrier), member 12	-1.39	0.03821
218653_at	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	-1.42	0.003773
214210_at	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	-1.23	0.019187
216712_at	SLC25A30	solute carrier family 25, member 30	-1.11	0.019447
221037_s_at	SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	-1.05	0.041109
220475_at	SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	-1.12	0.049509
201801_s_at	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	-1.66	0.034167
202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	1.53	0.023741
212907_at	SLC30A1	solute carrier family 30 (zinc transporter), member 1	1.23	0.038784
207035_at	SLC30A3	solute carrier family 30 (zinc transporter), member 3	-1.2	0.040592
213083_at	SLC35D2	solute carrier family 35, member D2	1.38	0.009419
218041_x_at	SLC38A2	solute carrier family 38, member 2	1.51	0.004118
218417_s_at	SLC48A1	solute carrier family 48 (heme transporter), member 1	1.49	0.007574
218682_s_at	SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adaptor protein	1.25	0.022794
217678_at	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	2.86	0.019317
216092_s_at	SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8	-1.22	0.019461
215267_s_at	SLC8A2	solute carrier family 8 (sodium/calcium exchanger), member 2	-1.15	0.042656
203909_at	SLC9A6	solute carrier family 9, subfamily A (NHE6, cation	1.33	0.014279

		proton antiporter 6), member 6		
219229_at	SLCO3A1	solute carrier organic anion transporter family, member 3A1	1.38	0.008873
209897_s_at	SLIT2	slit homolog 2 (Drosophila)	-1.1	0.041738
218137_s_at	SMAP1	small ArfGAP 1	1.41	0.006793
203875_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	-1.13	0.0062
201072_s_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	-1.33	0.046858
209420_s_at	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	1.29	0.045355
202043_s_at	SMS	spermine synthase	-1.64	0.003082
212922_s_at	SMYD2	SET and MYND domain containing 2	-1.34	0.029957
220405_at	SNTG1	syntrophin, gamma 1	-1.1	0.040497
202359_s_at	SNX19	sorting nexin 19	1.28	0.01616
203372_s_at	SOCS2	suppressor of cytokine signaling 2	-2.21	0.027473
200642_at	SOD1	superoxide dismutase 1, soluble	1.32	0.001128
201562_s_at	SORD	sorbitol dehydrogenase	-1.19	0.007311
212870_at	SOS2	son of sevenless homolog 2 (Drosophila)	1.66	0.027643
208012_x_at	SP110	SP110 nuclear body protein	-1.37	0.002323
212470_at	SPAG9	sperm associated antigen 9	1.37	0.010317
220299_at	SPATA6	spermatogenesis associated 6	1.07	0.029139
221844_x_at	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	-1.22	0.017975
209436_at	SPON1	spondin 1, extracellular matrix protein	-1.07	0.039766
214026_s_at	SPRED2	Sprouty-related, EVH1 domain containing 2	-1.16	0.021397
46256_at	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	1.43	0.017251
217995_at	SQRDL	sulfide quinone reductase-like (yeast)	1.39	0.012451
201471_s_at	SQSTM1	sequestosome 1	2.35	0.000629
211056_s_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	1.2	0.033153
202401_s_at	SRF	serum response factor (c-fos serum response element-binding transcription factor)	-1.39	0.043122
201859_at	SRGN	serglycin	1.2	0.021349
208920_at	SRI	sorcin	-1.42	0.007687
200685_at	SRSF11	serine/arginine-rich splicing factor 11	-1.42	0.030823
221752_at	SSH1	slingshot homolog 1 (Drosophila)	1.92	0.000306
210871_x_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	-1.18	0.026836
214971_s_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	-1.14	0.040006
207871_s_at	ST7	suppression of tumorigenicity 7*	1.39	0.008129
219753_at	STAG3	stromal antigen 3	-1.83	0.013845
221610_s_at	STAP2	signal transducing adaptor family member 2	-1.34	0.027088
209969_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	1.58	0.016881
207320_x_at	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	1.18	0.048006
201062_at	STOM	stomatin	-1.01	0.048031

209238_at	STX3	syntaxin 3	1.33	0.009806
203457_at	STX7	syntaxin 7	1.12	0.034068
221727_at	SUB1	SUB1 homolog (S. cerevisiae)	-1.46	0.019691
207601_at	SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	-1.23	0.000157
219934_s_at	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	1.05	0.022234
206293_at	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	1.1	0.001415
201484_at	SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	-1.43	0.00184
201836_s_at	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	1.28	0.006273
219389_at	SUSD4	sushi domain containing 4	-1.3	0.002354
205551_at	SV2B	synaptic vesicle glycoprotein 2B	-1.11	0.047294
202553_s_at	SYF2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	1.41	0.005708
217833_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	-1.33	0.036491
213200_at	SYP	synaptophysin	-1.11	0.030883
209198_s_at	SYT11	synaptotagmin XI	1.7	0.004008
221859_at	SYT13	synaptotagmin XIII	-1.15	0.045823
201463_s_at	TALDO1	transaldolase 1	1.26	0.005585
202813_at	TARBP1	TAR (HIV-1) RNA binding protein 1	-1.24	0.042283
221392_at	TAS2R4	taste receptor, type 2, member 4	-1.19	0.006993
221858_at	TBC1D12	TBC1 domain family, member 12	1.24	0.000188
44696_at	TBC1D13	TBC1 domain family, member 13	1.19	0.024362
220260_at	TBC1D19	TBC1 domain family, member 19	1.47	0.003766
215640_at	TBC1D2B	TBC1 domain family, member 2B	-1.14	0.025107
209152_s_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	-1.17	0.018259
219839_x_at	TCL6	T-cell leukemia/lymphoma 6 (non-protein coding)	-1.15	0.021209
205796_at	TCP11L1	t-complex 11 (mouse)-like 1	1.26	0.008328
213361_at	TDRD7	tudor domain containing 7	-1.12	0.022537
201174_s_at	TERF2IP	telomeric repeat binding factor 2, interacting protein	1.31	0.001847
204106_at	TESK1	testis-specific kinase 1	1.2	0.015472
205287_s_at	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	-1.21	0.008629
212457_at	TFE3	transcription factor binding to IGHM enhancer 3	1.35	0.001612
210215_at	TFR2	transferrin receptor 2	-1.22	0.029406
203313_s_at	TGIF1	TGFB-induced factor homeobox 1	1.83	0.00341
206008_at	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	-1.19	0.035659
211003_x_at	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	1.06	0.029542
203834_s_at	TGOLN2	trans-golgi network protein 2	1.15	0.032404
220212_s_at	THADA	thyroid adenoma associated	-1.19	0.027384
219800_s_at	THNSL1	threonine synthase-like 1 (S. cerevisiae)	1.08	0.00085
213869_x_at	THY1	Thy-1 cell surface antigen	-1.34	0.014863

212665_at	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	2.91	1.28E-07
212997_s_at	TLK2	tousled-like kinase 2	1.18	0.033326
221702_s_at	TM2D3	TM2 domain containing 3	1.24	0.00819
217730_at	TMBIM1	transmembrane BAX inhibitor motif containing 1	1.41	0.013055
200803_s_at	TMBIM6	transmembrane BAX inhibitor motif containing 6	1.52	0.028486
43977_at	TMEM161A	transmembrane protein 161A	1.21	0.003054
218345_at	TMEM176A	transmembrane protein 176A	-1.21	0.021634
219074_at	TMEM184C	transmembrane protein 184C	1.27	0.048391
218113_at	TMEM2	transmembrane protein 2	1.25	0.048554
218008_at	TMEM248	transmembrane protein 248	1.25	0.043106
219600_s_at	TMEM50B	transmembrane protein 50B	1.62	0.037533
218562_s_at	TMEM57	transmembrane protein 57	1.36	0.004219
200620_at	TMEM59	transmembrane protein 59	1.37	0.002212
203661_s_at	TMOD1	tropomodulin 1	1.14	0.046431
209754_s_at	TMPO	thymopoietin	-1.15	0.048531
211689_s_at	TMPRSS2	transmembrane protease, serine 2	-1.18	0.022702
218960_at	TMPRSS4	transmembrane protease, serine 4	-1.23	0.028538
210260_s_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	1.49	0.001407
208023_at	TNFRSF4	tumor necrosis factor receptor superfamily, member 4	1.1	0.049347
210643_at	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	-1.6	0.027271
209500_x_at	TNFSF12	tumor necrosis factor (ligand) superfamily, member 12*	-1.33	0.008471
210314_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	-1.24	0.022534
207216_at	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	-1.59	0.020449
204080_at	TOE1	target of EGR1, member 1 (nuclear)	-1.42	0.016616
202807_s_at	TOM1	target of myb1 (chicken)	1.53	0.003119
200662_s_at	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.36	0.02253
203050_at	TP53BP1	tumor protein p53 binding protein 1	1.11	0.044562
209863_s_at	TP63	tumor protein p63	-1.1	0.039171
213616_at	TPGS2	tubulin polyglutamylase complex subunit 2	1.27	0.021833
204140_at	TPST1	tyrosylprotein sulfotransferase 1	1.17	0.018971
204658_at	TRA2A	transformer 2 alpha homolog (Drosophila)	-1.31	0.012081
208315_x_at	TRAF3	TNF receptor-associated factor 3	1.21	0.028105
209751_s_at	TRAPPC2	trafficking protein particle complex 2*	1.28	0.006034
219748_at	TREML2	triggering receptor expressed on myeloid cells-like 2	-1.13	0.012467
202478_at	TRIB2	tribbles homolog 2 (Drosophila)	-1.15	0.04419
204732_s_at	TRIM23	tripartite motif containing 23	1.35	0.0399
212436_at	TRIM33	tripartite motif containing 33	1.26	0.019014
219405_at	TRIM68	tripartite motif containing 68	1.43	0.012244
209778_at	TRIP11	thyroid hormone receptor interactor 11	1.36	0.045916
201546_at	TRIP12	thyroid hormone receptor interactor 12	1.45	0.001461
210882_s_at	TRO	trophinin	1.26	0.033242

209390_at	TSC1	tuberous sclerosis 1	1.27	0.001626
215111_s_at	TSC22D1	TSC22 domain family, member 1	2.63	0.024772
203227_s_at	TSPAN31	tetraspanin 31	1.35	0.012002
209264_s_at	TSPAN4	tetraspanin 4	-1.76	0.006755
205665_at	TSPAN9	tetraspanin 9	-1.05	0.021704
219481_at	TTC13	tetratricopeptide repeat domain 13	1.23	0.004566
215849_x_at	TTC18	tetratricopeptide repeat domain 18	-1.09	0.015983
218442_at	TTC4	tetratricopeptide repeat domain 4	1.26	0.0363
213172_at	TTC9	tetratricopeptide repeat domain 9	-1.16	0.046155
219124_at	TTI2	TELO2 interacting protein 2	1.19	0.019019
205807_s_at	TUFT1	tuftelin 1	1.74	0.02024
205854_at	TULP3	tubby like protein 3	1.51	0.001282
213423_x_at	TUSC3	tumor suppressor candidate 3	-1.12	0.023204
219201_s_at	TWSG1	twisted gastrulation homolog 1 (Drosophila)	1.27	0.034096
208864_s_at	TXN	thioredoxin	1.69	0.006342
201588_at	TXNL1	thioredoxin-like 1	1.15	0.042239
201266_at	TXNRD1	thioredoxin reductase 1	2.31	0.000053
202589_at	TYMS	thymidylate synthetase	-1.29	0.019517
46270_at	UBAP1	ubiquitin associated protein 1	1.25	0.030266
201899_s_at	UBE2A	ubiquitin-conjugating enzyme E2A	1.16	0.000319
202347_s_at	UBE2K	ubiquitin-conjugating enzyme E2K	1.47	0.049361
212751_at	UBE2N	ubiquitin-conjugating enzyme E2N	-1.5	0.011168
218011_at	UBL5	ubiquitin-like 5	1.14	0.046794
212756_s_at	UBR2	ubiquitin protein ligase E3 component n-recognin 2	1.39	0.015452
211950_at	UBR4	ubiquitin protein ligase E3 component n-recognin 4	1.47	0.006463
212007_at	UBXN4	UBX domain protein 4	1.37	0.020971
201387_s_at	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	2.33	0.017151
209103_s_at	UFD1L	ubiquitin fusion degradation 1 like (yeast)	1.33	0.004539
217935_s_at	UQCC	ubiquinol-cytochrome c reductase complex chaperone	1.2	0.041421
210157_at	URI1	URI1, prefoldin-like chaperone	-1.14	0.020739
213327_s_at	USP12	ubiquitin specific peptidase 12	1.31	0.046493
219211_at	USP18	ubiquitin specific peptidase 18	-1.56	0.04248
207211_at	USP2	ubiquitin specific peptidase 2	-1.13	0.027898
203965_at	USP20	ubiquitin specific peptidase 20	1.17	0.039818
221654_s_at	USP3	ubiquitin specific peptidase 3	1.46	0.037349
221518_s_at	USP47	ubiquitin specific peptidase 47	1.35	0.017005
201336_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	1.46	0.03382
208626_s_at	VAT1	vesicle amine transport protein 1 homolog (T. californica)	1.26	0.027777
208649_s_at	VCP	valosin containing protein	1.33	0.036214
217727_x_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	1.13	0.01542
210849_s_at	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	1.12	0.044093
218171_at	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	1.26	0.044345

218022_at	VRK3	vaccinia related kinase 3	1.15	0.044567
217742_s_at	WAC	WW domain containing adaptor with coiled-coil	1.31	0.04802
212264_s_at	WAPAL	wings apart-like homolog (Drosophila)	1.23	0.018206
38964_r_at	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	-1.17	0.037156
202808_at	WBP1L	WW domain binding protein 1-like	1.41	0.005242
220917_s_at	WDR19	WD repeat domain 19	1.99	0.000032
218107_at	WDR26	WD repeat domain 26	1.34	0.005237
217780_at	WDR83OS	WD repeat domain 83 opposite strand	1.31	0.006728
209054_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	-1.14	0.041285
202031_s_at	WIPI2	WD repeat domain, phosphoinositide interacting 2	1.54	0.000271
219077_s_at	WWOX	WW domain containing oxidoreductase	-1.24	0.032831
205672_at	XPA	xeroderma pigmentosum, complementation group A	1.25	0.034913
208643_s_at	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	-1.35	0.017312
217783_s_at	YPEL5	yippee-like 5 (Drosophila)	1.87	0.017105
212455_at	YTHDC1	YTH domain containing 1	1.34	0.029284
201901_s_at	YY1	YY1 transcription factor	1.29	0.031042
208087_s_at	ZBP1	Z-DNA binding protein 1	-1.17	0.025187
203958_s_at	ZBTB40	zinc finger and BTB domain containing 40	1.07	0.034668
204180_s_at	ZBTB43	zinc finger and BTB domain containing 43	1.65	0.032806
203026_at	ZBTB5	zinc finger and BTB domain containing 5	1.26	0.037427
217486_s_at	ZDHHC17	zinc finger, DHHC-type containing 17	1.05	0.041157
218020_s_at	ZFAND3	zinc finger, AN1-type domain 3	1.12	0.031535
210275_s_at	ZFAND5	zinc finger, AN1-type domain 5	1.57	0.013363
218968_s_at	ZFP64	zinc finger protein 64 homolog (mouse)	1.18	0.017919
202050_s_at	ZMYM4	zinc finger, MYM-type 4	-1.08	0.030501
206182_at	ZNF134	zinc finger protein 134	1.13	0.03555
219854_at	ZNF14	zinc finger protein 14	1.4	0.010913
204523_at	ZNF140	zinc finger protein 140	1.29	0.015397
37586_at	ZNF142	zinc finger protein 142	1.21	0.01875
205497_at	ZNF175	zinc finger protein 175	1.13	0.01359
213218_at	ZNF187	zinc finger protein 187	1.34	0.000365
205437_at	ZNF211	zinc finger protein 211	1.38	0.01507
203985_at	ZNF212	zinc finger protein 212	1.12	0.011126
219603_s_at	ZNF226	zinc finger protein 226	1.18	0.049617
220350_at	ZNF235	zinc finger protein 235	1.26	0.000422
207164_s_at	ZNF238	zinc finger protein 238	1.02	0.022441
213858_at	ZNF250	zinc finger protein 250	1.15	0.016228
214686_at	ZNF266	zinc finger protein 266	1.5	0.01765
204937_s_at	ZNF274	zinc finger protein 274	1.57	0.001429
207753_at	ZNF304	zinc finger protein 304	1.33	0.017485
203521_s_at	ZNF318	zinc finger protein 318	1.5	0.041587

209538_at	ZNF32	zinc finger protein 32	1.44	0.014009
219765_at	ZNF329	zinc finger protein 329	1.42	0.022404
206096_at	ZNF35	zinc finger protein 35	1.07	0.048696
219224_x_at	ZNF408	zinc finger protein 408	1.1	0.04247
209944_at	ZNF410	zinc finger protein 410	1.31	0.049951
219826_at	ZNF419	zinc finger protein 419	1.46	0.0019
218937_at	ZNF434	zinc finger protein 434	1.36	0.001636
219968_at	ZNF589	zinc finger protein 589	-1.11	0.018219
212620_at	ZNF609	zinc finger protein 609	-1.12	0.048793
220721_at	ZNF614	zinc finger protein 614	1.16	0.033088
205089_at	ZNF7	zinc finger protein 7	1.36	0.010257
218059_at	ZNF706	zinc finger protein 706	-1.23	0.009736
215570_s_at	ZNF780A	zinc finger protein 780A*	-1.09	0.046788
217541_x_at	ZNF816	zinc finger protein 816*	1.13	0.030445
212544_at	ZNHIT3	zinc finger, HIT-type containing 3	1.2	0.013852
215263_at	ZXDA	zinc finger, X-linked, duplicated A*	1.16	0.001625

Table S3: Selected gene ontology GO categories significantly affected by CSC stimulation.

Group	GO ID	GO categories	GO term	Group P Value	Term P Value	% Associated Genes	Associated Genes Found
1	GO:0021543	BP	pallium development	1.23E-05	4.44E-05	11.1	CNTNAP2, CYP17A1, DLX2, GRIN1, LEF1, PAFAH1B1, PSEN1, PTEN, SLIT2, SRF, TFAP2C, TSC1, ZBTB18
1	GO:0021761	BP	limbic system development	1.23E-05	1.46E-04	11.5	CNTNAP2, CRHR1, CYP17A1, DLX2, LEF1, PAFAH1B1, PTEN, SRF, TSC1, ZBTB18
1	GO:0021766	BP	hippocampus development	1.23E-05	1.86E-04	13.8	CYP17A1, DLX2, LEF1, PAFAH1B1, PTEN, SRF, TSC1, ZBTB18
2	GO:0042503	BP	tyrosine phosphorylation of Stat3 protein	5.02E-05	1.33E-04	18.4	IL21, IL23A, IL6R, LEP, LIF, OSM, PTPN2
2	GO:0042508	BP	tyrosine phosphorylation of Stat1 protein	5.02E-05	1.41E-04	29.4	IL21, IL23A, LIF, OSM, PTPN2
3	GO:0008585	BP	female gonad development	3.30E-05	1.50E-04	10.5	ARRB1, BRCA2, CTNNA1, EREG, ESR1, FOXO3, KDR, LEP, SLIT2, SOD1, TIPARP
3	GO:0001541	BP	ovarian follicle development	3.30E-05	5.54E-04	13.5	ARRB1, CTNNA1, EREG, ESR1, FOXO3, KDR, SOD1
3	GO:0001547	BP	antral ovarian follicle growth	3.30E-05	6.76E-04	50.0	EREG, ESR1, FOXO3
4	GO:0043523	BP	regulation of neuron apoptotic process	1.41E-06	9.59E-06	10.2	DDIT3, FOXO3, GCLC, GCLM, GRIN1, HMOX1, JUN, NQO1, NR4A2, NTRK1, PINK1, PPP2R2B, PRDX2, PSEN1, ROCK1, SOD1, TP63
4	GO:0043524	BP	negative regulation of neuron apoptotic process	1.41E-06	1.14E-04	10.6	GCLC, GCLM, GRIN1, HMOX1, JUN, NR4A2, NTRK1, PINK1,

							PRDX2, PSEN1, ROCK1, SOD1
5	GO:0050772	BP	positive regulation of axonogenesis	2.18E-05	1.12E-04	16.7	FXN, GOLGA2, NTRK3, OPTN, PAFAH1B1, RAB11A, SKIL, SLIT2
5	GO:0045773	BP	positive regulation of axon extension	2.18E-05	5.64E-04	20.8	FXN, NTRK3, OPTN, PAFAH1B1, RAB11A
6	GO:0060443	BP	mammary gland morphogenesis	2.28E-05	1.07E-04	14.3	CAV3, CCNH, ELF3, ESR1, ETV5, LRP5, NCOA3, SLIT2, TFAP2C
6	GO:0061180	BP	mammary gland epithelium development	2.28E-05	1.22E-04	12.3	BRCA2, CAV3, CCNH, ESR1, ETV5, LRP5, NCOA3, SLIT2, TFAP2C, TNFSF11
7	GO:0002685	BP	regulation of leukocyte migration	3.14E-05	1.41E-04	10.7	CCR7, CXCL11, CXCL13, GAL, HMOX1, IL23A, IL6R, MKL1, PAFAH1B1, RPSA, SLIT2
7	GO:0002688	BP	regulation of leukocyte chemotaxis	3.14E-05	1.50E-04	12.7	CCR7, CXCL11, CXCL13, IL23A, IL6R, MKL1, PAFAH1B1, RPSA, SLIT2
7	GO:0090022	BP	regulation of neutrophil chemotaxis	3.14E-05	7.88E-04	19.2	CCR7, IL23A, MKL1, RPSA, SLIT2
8	GO:0030330	BP	DNA damage response, signal transduction by p53 class mediator	9.92E-07	7.54E-06	12.1	BRCA2, FOXO3, KAT5, NBN, NDRG1, PSMA1, PSMB1, PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4, TP63
8	GO:0031397	BP	negative regulation of protein ubiquitination	9.92E-07	4.84E-05	11.2	ARRB1, CHP1, GCLC, PSEN1, PSMA1, PSMB1, PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4
8	GO:0044773	BP	mitotic DNA damage	9.92E-07	1.17E-04	11.7	NBN, PSMA1, PSMB1,

			checkpoint				PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4, TP63
8	GO:0051444	BP	negative regulation of ubiquitin-protein ligase activity	9.92E-07	1.17E-04	12.2	PSEN1, PSMA1, PSMB1, PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4
8	GO:0051437	BP	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	9.92E-07	1.22E-04	12.3	PSMA1, PSMB1, PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4, PTEN
8	GO:2000134	BP	negative regulation of G1/S transition of mitotic cell cycle	9.92E-07	1.45E-04	10.6	PSMA1, PSMB1, PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4, PTEN, TP63
8	GO:0006977	BP	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	9.92E-07	1.91E-04	12.2	PSMA1, PSMB1, PSMB7, PSMB8, PSMB9, PSMD1, PSMD14, PSMD2, PSMD4
9	GO:0006302	BP	double-strand break repair	9.40E-07	9.60E-06	11.7	BRCA2, BRE, FEN1, KAT5, NBN, POLA1, PRKDC, PSMD14, RAD54L, SHFM1, SOD1, TERF2IP, TP53BP1, VCP, XRCC5, YY1
9	GO:0000724	BP	double-strand break repair via homologous recombination	9.40E-07	3.79E-04	12.3	BRCA2, NBN, PSMD14, RAD54L, SHFM1, TERF2IP, TP53BP1, YY1
	GO:0006271	BP	DNA strand elongation involved in DNA replication		4.42E-05	21.1	CDC45, FEN1, MCM3, MCM4, MCM7, PCNA, POLA1, RFC1
	GO:0045682	BP	regulation of epidermis development		1.17E-04	16.0	AQP3, KEAP1, MAFF, MAFG, NCOA3,

					ROCK1, TFAP2C, TP63
GO:0046916	BP	cellular transition metal ion homeostasis	1.22E-04	10.8	APLP2, ATP6V0A1, ATP6V1D, FTH1, FTL, FXN, HELLS, HMOX1, SOD1, SRI, TFR2, TP63
GO:0006289	BP	nucleotide-excision repair	1.88E-04	10.9	ATXN3, BRCA2, CCNH, ERCC6, NTHL1, PCNA, POLA1, POLR2C, RFC1, XPA
GO:0045639	BP	positive regulation of myeloid cell differentiation	1.91E-04	12.2	ACVR1B, FOXO3, HSPA1A, IL23A, JUN, LEF1, LEP, LIF, TNFSF11
GO:0018126	BP	protein hydroxylation	1.97E-04	75.0	ASPH, HIF1AN, JMJD6
GO:0043217	BP	myelin maintenance	2.81E-04	36.4	CXCR4, NDRG1, PTEN, SOD1
GO:0000723	BP	telomere maintenance	3.03E-04	11.3	FEN1, NBN, PCNA, POLA1, PRKDC, PTEN, RFC1, TERF2IP, XRCC5
GO:0004714	MF	transmembrane receptor protein tyrosine kinase activity	8.04E-04	10.8	ALK, CCNH, INSR, KDR, MET, NTRK1, NTRK3, OPTN
GO:1901019	BP	regulation of calcium ion transmembrane transporter activity	9.92E-04	14.3	ASPH, CAV3, CRHR1, MYO5A, PICALM, SRI

Table S4: up and down regulated genes in PBMCs of heavy smokers compared with light smokers.

Probe Set	Symbol	Description	Fold	P value
205434_s_at	AAK1	AP2 associated kinase 1	1.69	0.045538
206527_at	ABAT	4-aminobutyrate aminotransferase	-1.22	0.019255
204567_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	1.23	0.009608
212895_s_at	ABR	active BCR-related	1.19	0.01612
220845_at	ACOXL	acyl-CoA oxidase-like	-1.09	0.030009
201550_x_at	ACTG1	actin, gamma 1	1.12	0.004449
209765_at	ADAM19	ADAM metallopeptidase domain 19	1.25	0.041374
208268_at	ADAM28	ADAM metallopeptidase domain 28	1.54	0.035062
211239_s_at	ADAM7	ADAM metallopeptidase domain 7	-1.07	0.013989
205180_s_at	ADAM8	ADAM metallopeptidase domain 8	1.06	0.048962
220208_at	ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	-1.13	0.019926
214736_s_at	ADD1	adducin 1 (alpha)	1.18	0.03279
208544_at	ADRA2B	adrenoceptor alpha 2B	-1.16	0.047122
212285_s_at	AGRN	agrin	-1.09	0.049947
201782_s_at	AIP	aryl hydrocarbon receptor interacting protein	1.19	0.033903
205633_s_at	ALAS1	aminolevulinate, delta-, synthase 1	1.24	0.010035
209646_x_at	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	-1.11	0.035284
214340_at	ALOX12P2	arachidonate 12-lipoxygenase pseudogene 2	-1.1	0.019988
218093_s_at	ANKRD10	ankyrin repeat domain 10	1.27	0.027256
205678_at	AP3B2	adaptor-related protein complex 3, beta 2 subunit	-1.07	0.038512
220023_at	APOBR	apolipoprotein B receptor	1.35	0.015129
212883_at	APOE	Apolipoprotein E	-1.11	0.023126
211975_at	ARFGAP2	ADP-ribosylation factor GTPase activating protein 2	1.3	0.023669
218076_s_at	ARHGAP17	Rho GTPase activating protein 17	1.22	0.00482
204882_at	ARHGAP25	Rho GTPase activating protein 25	1.09	0.030776
213039_at	ARHGEF18	Rho/Rac guanine nucleotide exchange factor (GEF) 18	1.16	0.043842
205109_s_at	ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	-1.08	0.045059
203263_s_at	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	1.17	0.046553
218694_at	ARMCX1	armadillo repeat containing, X-linked 1	-1.04	0.019523
207220_at	ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	1.1	0.030474
217228_s_at	ASB4	ankyrin repeat and SOCS box containing 4	-1.07	0.013363
214993_at	ASPHD1	aspartate beta-hydroxylase domain containing 1	-1.09	0.014294
203364_s_at	ATG13	autophagy related 13	1.14	0.012994
207367_at	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	-1.14	0.018688
207546_at	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	-1.06	0.023001
202622_s_at	ATXN2	ataxin 2	1.21	0.006493
211107_s_at	AURKC	aurora kinase C	-1.21	0.036706

216231_s_at	B2M	beta-2-microglobulin	-1.12	0.024723
206435_at	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	-1.16	0.028274
211631_x_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	-1.12	0.001691
209364_at	BAD	BCL2-associated agonist of cell death	1.1	0.047134
210208_x_at	BAG6	BCL2-associated athanogene 6	1.19	0.016452
219966_x_at	BANP	BTG3 associated nuclear protein	1.29	0.027637
219497_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	1.51	0.006776
203795_s_at	BCL7A	B-cell CLL/lymphoma 7A	1.16	0.034964
205870_at	BDKRB2	bradykinin receptor B2	-1.07	0.048732
214643_x_at	BIN1	bridging integrator 1	1.15	0.009817
222199_s_at	BIN3	bridging integrator 3	1.14	0.00716
202094_at	BIRC5	baculoviral IAP repeat containing 5	-1.08	0.044568
206255_at	BLK	B lymphoid tyrosine kinase	1.57	0.006269
210462_at	BLZF1	basic leucine zipper nuclear factor 1	-1.05	0.034465
218004_at	BSDC1	BSD domain containing 1	1.18	0.041418
205298_s_at	BTN2A2	butyrophilin, subfamily 2, member A2	1.28	0.026617
209642_at	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-1.09	0.006698
217463_s_at	C11orf9	chromosome 11 open reading frame 9	-1.07	0.013861
219022_at	C12orf43	chromosome 12 open reading frame 43	1.13	0.004396
211034_s_at	C12orf51	chromosome 12 open reading frame 51	1.1	0.014476
218130_at	C17orf62	chromosome 17 open reading frame 62	1.3	0.042792
221048_x_at	C17orf80	chromosome 17 open reading frame 80	-1.11	0.0018
218983_at	C1RL	complement component 1, r subcomponent-like	1.09	0.002485
218089_at	C20orf4	chromosome 20 open reading frame 4	1.12	0.046835
221211_s_at	C21orf7	chromosome 21 open reading frame 7	-1.59	0.028158
219261_at	C7orf26	chromosome 7 open reading frame 26	1.23	0.042438
206208_at	CA4	carbonic anhydrase IV	-1.07	0.017811
213688_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)*	-1.06	0.040881
210349_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	-1.2	0.046824
212763_at	CAMSAP2	calmodulin regulated spectrin-associated protein family, member 2	-1.1	0.043472
212948_at	CAMTA2	calmodulin binding transcription activator 2	1.25	0.020315
208063_s_at	CAPN9	calpain 9	-1.1	0.018169
218153_at	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	1.22	0.046066
206011_at	CASP1	caspase 1, apoptosis-related cysteine peptidase	1.07	0.046561
213373_s_at	CASP8	caspase 8, apoptosis-related cysteine peptidase	1.17	0.040053
208056_s_at	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	1.08	0.036538
212126_at	CBX5	chromobox homolog 5	1.31	0.00853
218026_at	CCDC56	coiled-coil domain containing 56	1.18	0.031604
204606_at	CCL21	chemokine (C-C motif) ligand 21	-1.17	0.041527
206398_s_at	CD19	CD19 molecule	1.42	0.014997
209583_s_at	CD200	CD200 molecule	1.28	0.037472

204581_at	CD22	CD22 molecule	1.38	0.029503
207315_at	CD226	CD226 molecule	-1.31	0.016308
208650_s_at	CD24	CD24 molecule	1.37	0.005202
204192_at	CD37	CD37 molecule	1.47	0.014096
215925_s_at	CD72	CD72 molecule	1.31	0.026785
205049_s_at	CD79A	CD79a molecule, immunoglobulin-associated alpha	1.6	0.00147
205297_s_at	CD79B	CD79b molecule, immunoglobulin-associated beta	1.67	0.013861
200675_at	CD81	CD81 molecule	1.3	0.039221
202910_s_at	CD97	CD97 molecule	1.29	0.022422
204695_at	CDC25A	cell division cycle 25 homolog A (S. pombe)	-1.11	0.017441
201253_s_at	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	1.19	0.038556
209489_at	CELF1	CUGBP, Elav-like family member 1	1.15	0.016439
202157_s_at	CELF2	CUGBP, Elav-like family member 2	1.13	0.033131
219472_at	CENPO	centromere protein O	-1.19	0.023442
204074_s_at	CEP104	centrosomal protein 104kDa	-1.15	0.037093
213644_at	CEP112	centrosomal protein 112kDa	-1.08	0.047107
221378_at	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	-1.21	0.025586
212616_at	CHD9	chromodomain helicase DNA binding protein 9	1.36	0.017644
202230_s_at	CHERP	calcium homeostasis endoplasmic reticulum protein	1.23	0.029935
206079_at	CHML	choroideremia-like (Rab escort protein 2)	-1.14	0.011641
55093_at	CHPF2	chondroitin polymerizing factor 2	1.16	0.049118
216886_at	CHRNA4	cholinergic receptor, nicotinic, alpha 4 (neuronal)	-1.08	0.035225
207274_at	CHRNE	cholinergic receptor, nicotinic, epsilon (muscle)	-1.07	0.04677
221295_at	CIDEA	cell death-inducing DFFA-like effector a	-1.14	0.014976
216708_x_at	CKAP2	Cytoskeleton associated protein 2	-1.14	0.013118
212832_s_at	CKAP5	cytoskeleton associated protein 5	1.15	0.029148
38069_at	CLCN7	chloride channel, voltage-sensitive 7	1.17	0.045131
206908_s_at	CLDN11	claudin 11	-1.04	0.046664
207995_s_at	CLEC4M	C-type lectin domain family 4, member M	-1.06	0.025636
201561_s_at	CLSTN1	calsyntenin 1	1.13	0.043413
210204_s_at	CNOT4	CCR4-NOT transcription complex, subunit 4	-1.14	0.029573
215393_s_at	COBLL1	COBL-like 1	-1.05	0.042944
202312_s_at	COL1A1	collagen, type I, alpha 1	-1.18	0.04668
217404_s_at	COL2A1	collagen, type II, alpha 1	-1.02	0.049192
215076_s_at	COL3A1	collagen, type III, alpha 1	-1.05	0.033972
209132_s_at	COMMD4	COMM domain containing 4	1.07	0.033229
213486_at	COPG2IT1	COPG2 imprinted transcript 1 (non-protein coding)	-1.1	0.034903
209029_at	COPS7A	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	1.24	0.01136
219997_s_at	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	1.1	0.03811
217994_x_at	CPSF3L	cleavage and polyadenylation specific factor 3-like	1.16	0.033242
211897_s_at	CRHR1	corticotropin releasing hormone receptor 1	-1.05	0.030259

210199_at	CRYAA	crystallin, alpha A	-1.16	0.004625
209283_at	CRYAB	crystallin, alpha B	-1.13	0.022911
206843_at	CRYBA4	crystallin, beta A4	-1.17	0.006151
205958_x_at	CSHL1	chorionic somatomammotropin hormone-like 1	-1.13	0.013084
202329_at	CSK	c-src tyrosine kinase	1.25	0.007213
208774_at	CSNK1D	casein kinase 1, delta	1.15	0.041918
217332_at	CTAGE11P	CTAGE family, member 11, pseudogene	-1.08	0.023704
203392_s_at	CTBP1	C-terminal binding protein 1	1.62	0.022717
218058_at	CXXC1	CXXC finger protein 1	1.2	0.021062
215785_s_at	CYFIP2	cytoplasmic FMR1 interacting protein 2	1.16	0.045633
215103_at	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	-1.06	0.009938
215809_at	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	-1.13	0.018437
216720_at	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	-1.04	0.035903
201278_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-1.35	0.048771
212128_s_at	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	-1.19	0.028564
214334_x_at	DAZAP2	DAZ associated protein 2	1.05	0.017854
206450_at	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	-1.18	0.0479
220843_s_at	DCAF13	DDB1 and CUL4 associated factor 13	1	0.046855
91952_at	DCAF15	DDB1 and CUL4 associated factor 15	1.29	0.045833
221744_at	DCAF7	DDB1 and CUL4 associated factor 7	1.25	0.011464
210137_s_at	DCTD	dCMP deaminase	1.14	0.006416
217973_at	DCXR	dicarbonyl/L-xylulose reductase	1.37	0.022995
219111_s_at	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	1.1	0.047008
221885_at	DENND2A	DENN/MADD domain containing 2A	-1.2	0.015192
203695_s_at	DFNA5	deafness, autosomal dominant 5	1.13	0.029246
204383_at	DGCR14	DiGeorge syndrome critical region gene 14*	1.12	0.011305
214079_at	DHRS2	dehydrogenase/reductase (SDR family) member 2	-1.08	0.034733
203694_s_at	DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	1.19	0.008093
216281_at	DICER1	dicer 1, ribonuclease type III	-1.06	0.03859
211150_s_at	DLAT	dihydrolipoamide S-acetyltransferase	-1.25	0.008673
213707_s_at	DLX5	distal-less homeobox 5	-1.14	0.007215
210487_at	DNTT	deoxynucleotidyltransferase, terminal	-1.1	0.005068
205983_at	DPEP1	dipeptidase 1 (renal)	-1.2	0.025419
205493_s_at	DPYSL4	dihydropyrimidinase-like 4	-1.09	0.047259
220154_at	DST	dystonin	-1.08	0.00598
215295_at	DTNB	dystrobrevin, beta	-1.03	0.037989
47105_at	DUS2L	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	1.1	0.047135
205762_s_at	DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	1.03	0.048359
203230_at	DVL1	dishevelled, dsh homolog 1 (Drosophila)	1.12	0.024272
211928_at	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	1.23	0.01802

204557_s_at	DZIP1	DAZ interacting protein 1	-1.06	0.011082
202023_at	EFNA1	ephrin-A1	-1.09	0.014445
202669_s_at	EFNB2	ephrin-B2	-1.14	0.027153
221755_at	EHBP1L1	EH domain binding protein 1-like 1	1.65	0.022281
209039_x_at	EHD1	EH-domain containing 1	1.26	0.004011
203462_x_at	EIF3B	eukaryotic translation initiation factor 3, subunit B	1.25	0.00231
219599_at	EIF4B	eukaryotic translation initiation factor 4B*	-1.46	0.040238
55692_at	ELMO2	engulfment and cell motility 2	1.28	0.033547
217882_at	EMC3	ER membrane protein complex subunit 3	-1.37	0.035817
204399_s_at	EML2	echinoderm microtubule associated protein like 2	-1.13	0.015206
201325_s_at	EMP1	epithelial membrane protein 1	-1.11	0.026671
202221_s_at	EP300	E1A binding protein p300	1.12	0.043843
201719_s_at	EPB41L2	erythrocyte membrane protein band 4.1-like 2	1.08	0.048535
212681_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	1.55	0.041385
215804_at	EPHA1	EPH receptor A1	-1.13	0.019799
203464_s_at	EPN2	epsin 2	-1.08	0.03605
202441_at	ERLIN1	ER lipid raft associated 1	1.19	0.037163
219905_at	ERMAP	erythroblast membrane-associated protein (Scianna blood group)	-1.35	0.000562
221200_at	ERVK3-2	endogenous retrovirus group K3, member 2	-1.08	0.029627
215552_s_at	ESR1	estrogen receptor 1	-1.06	0.048591
212630_at	EXOC3	exocyst complex component 3	1.09	0.013988
206329_at	EXTL1	exostoses (multiple)-like 1	-1.1	0.040648
219429_at	FA2H	fatty acid 2-hydroxylase	-1.07	0.026416
205029_s_at	FABP7	fatty acid binding protein 7, brain	1.02	0.040755
214890_s_at	FAM149A	family with sequence similarity 149, member A	-1.13	0.010875
203206_at	FAM53B	family with sequence similarity 53, member B	1.21	0.014557
209955_s_at	FAP	fibroblast activation protein, alpha	-1.11	0.034062
218938_at	FBXL15	F-box and leucine-rich repeat protein 15	1.08	0.044017
205310_at	FBXO46	F-box protein 46	1.14	0.022156
210638_s_at	FBXO9	F-box protein 9	-1.12	0.049355
214571_at	FGF3	fibroblast growth factor 3	-1.18	0.014523
210310_s_at	FGF5	fibroblast growth factor 5	-1.11	0.027117
31826_at	FKBP15	FK506 binding protein 15, 133kDa	1.2	0.033404
217487_x_at	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1*	-1.22	0.018167
210103_s_at	FOXA2	forkhead box A2	-1.17	0.028019
206307_s_at	FOXD1	forkhead box D1	1.09	0.023818
206912_at	FOXE1	forkhead box E1 (thyroid transcription factor 2)	-1.07	0.010676
221333_at	FOXP3	forkhead box P3	-1.21	0.034673
213056_at	FRMD4B	FERM domain containing 4B	-1.23	0.006893
210398_x_at	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	-1.13	0.027425
217077_s_at	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	-1.11	0.042474
40225_at	GAK	cyclin G associated kinase	1.21	0.042031

205670_at	GAL3ST1	galactose-3-O-sulfotransferase 1	-1.1	0.035373
217788_s_at	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	1.14	0.037033
218131_s_at	GATAD2A	GATA zinc finger domain containing 2A	1.19	0.034059
205164_at	GCAT	glycine C-acetyltransferase	-1.07	0.026413
203500_at	GCDH	glutaryl-CoA dehydrogenase	1.15	0.026631
211545_at	GHRHR	growth hormone releasing hormone receptor	-1.1	0.049915
207899_at	GIP	gastric inhibitory polypeptide	-1.17	0.011989
221415_s_at	GJA9	gap junction protein, alpha 9, 59kDa*	-1.04	0.047228
215243_s_at	GJB3	gap junction protein, beta 3, 31kDa	-1.1	0.00971
221447_s_at	GLT8D2	glycosyltransferase 8 domain containing 2	-1.15	0.035491
212737_at	GM2A	GM2 ganglioside activator	1.32	0.021234
222251_s_at	GMEB2	glucocorticoid modulatory element binding protein 2	1.18	0.036601
201056_at	GOLGB1	golgin B1	1.14	0.01177
218873_at	GON4L	gon-4-like (C. elegans)	1.24	0.002474
211060_x_at	GPAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	1.05	0.047441
211613_s_at	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	-1.07	0.025809
214503_x_at	GPR135	G protein-coupled receptor 135	-1.11	0.043306
214018_at	GRIP1	glutamate receptor interacting protein 1	-1.06	0.030208
210939_s_at	GRM1	glutamate receptor, metabotropic 1	-1.07	0.040253
216256_at	GRM8	glutamate receptor, metabotropic 8	-1.11	0.045971
220190_s_at	GTF2A1L	general transcription factor IIA, 1-like*	-1.12	0.024375
215915_at	GULP1	GULP, engulfment adaptor PTB domain containing 1	-1.09	0.025925
203674_at	HELZ	helicase with zinc finger	1.23	0.024393
203393_at	HES1	hairy and enhancer of split 1, (Drosophila)	-1.08	0.043434
206087_x_at	HFE	hemochromatosis	1.08	0.020891
215071_s_at	HIST1H2AC	histone cluster 1, H2ac	-1.71	0.036986
214455_at	HIST1H2BC	histone cluster 1, H2bc*	-1.43	0.030637
208546_x_at	HIST1H2BH	histone cluster 1, H2bh	-1.74	0.044396
208496_x_at	HIST1H3A	histone cluster 1, H3a*	-1.25	0.010413
215313_x_at	HLA-A	major histocompatibility complex, class I, A	1.23	0.045172
217478_s_at	HLA-DMA	major histocompatibility complex, class II, DM alpha	1.36	0.04878
205671_s_at	HLA-DOB	major histocompatibility complex, class II, DO beta	1.43	0.032739
210747_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	-1.11	0.018458
217456_x_at	HLA-E	major histocompatibility complex, class I, E	1.26	0.014691
221978_at	HLA-F	major histocompatibility complex, class I, F	1.32	0.009504
204753_s_at	HLF	hepatic leukemia factor	-1.11	0.023729
213966_at	HMG20B	High mobility group 20B	-1.09	0.046337
200679_x_at	HMGB1	high mobility group box 1	-1.21	0.049239
208302_at	HMHB1	histocompatibility (minor) HB-1	-1.07	0.039439
216889_s_at	HNF4A	hepatocyte nuclear factor 4, alpha	-1.2	0.026615
204111_at	HNMT	histamine N-methyltransferase	-1.07	0.015065

221411_at	HOXD12	homeobox D12	-1.09	0.009961
207398_at	HOXD13	homeobox D13	-1.15	0.042948
206602_s_at	HOXD3	homeobox D3	-1.07	0.041214
203309_s_at	HPS1	Hermansky-Pudlak syndrome 1	1.15	0.03197
221122_at	HRASLS2	HRAS-like suppressor 2	-1.11	0.015657
205580_s_at	HRH1	histamine receptor H1	-1.18	0.04199
214165_s_at	HS6ST1	Heparan sulfate 6-O-sulfotransferase 1	-1.14	0.037505
204515_at	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	-1.09	0.049596
206638_at	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	-1.07	0.006743
217002_s_at	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A, ionotropic	-1.12	0.00376
202389_s_at	HTT	huntingtin	1.12	0.036144
201611_s_at	ICMT	isoprenylcysteine carboxyl methyltransferase	1.12	0.03044
211198_s_at	ICOSLG	inducible T-cell co-stimulator ligand	-1.12	0.037763
212221_x_at	IDS	iduronate 2-sulfatase	1.18	0.013825
205037_at	IFT27	intraflagellar transport 27 homolog (Chlamydomonas)	1.18	0.039679
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	-1.23	0.015708
219690_at	IGFLR1	IGF-like family receptor 1	1.32	0.006125
217217_at	IGHA1	immunoglobulin heavy constant alpha 1*	-1.07	0.044824
213674_x_at	IGHD	immunoglobulin heavy constant delta	2.3	0.000078
211648_at	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)*	-1.15	0.022996
209374_s_at	IGHM	immunoglobulin heavy constant mu	1.63	0.005332
204912_at	IL10RA	interleukin 10 receptor, alpha	1.21	0.04013
209827_s_at	IL16	interleukin 16	1.17	0.032451
215561_s_at	IL1R1	interleukin 1 receptor, type I	-1.07	0.030226
219971_at	IL21R	interleukin 21 receptor	1.19	0.045679
217328_at	IL23A	Interleukin 23, alpha subunit p19	-1.21	0.000123
217702_at	IL27RA	interleukin 27 receptor, alpha	-1.2	0.042426
217212_s_at	IL9R	interleukin 9 receptor	-1.14	0.028
48825_at	ING4	inhibitor of growth family, member 4	1.14	0.011687
212212_s_at	INTS1	integrator complex subunit 1	1.17	0.045217
211132_at	INTS3	integrator complex subunit 3	-1.1	0.016934
53968_at	INTS5	integrator complex subunit 5	1.18	0.044952
203941_at	INTS9	integrator complex subunit 9	1.15	0.036101
202531_at	IRF1	interferon regulatory factor 1	1.2	0.048961
202621_at	IRF3	interferon regulatory factor 3	1.47	0.019275
220225_at	IRX4	iroquois homeobox 4	-1.16	0.003539
221425_s_at	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-1.24	0.021653
208114_s_at	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	1.16	0.045643
214292_at	ITGB4	integrin, beta 4	-1.09	0.038615
208083_s_at	ITGB6	integrin, beta 6	-1.04	0.035138
205718_at	ITGB7	integrin, beta 7	1.2	0.016232

201188_s_at	ITPR3	inositol 1,4,5-trisphosphate receptor, type 3	1.37	0.03371
210434_x_at	JTB	jumping translocation breakpoint	1.09	0.027065
214258_x_at	KAT5	K(lysine) acetyltransferase 5	1.14	0.024604
221000_s_at	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	-1.14	0.015636
221413_at	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	-1.12	0.042473
208477_at	KCNC1	potassium voltage-gated channel, Shaw-related subfamily, member 1	-1.19	0.027836
205262_at	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	-1.17	0.049346
211046_at	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	-1.05	0.043365
220412_x_at	KCNK7	potassium channel, subfamily K, member 7	-1.15	0.03815
201643_x_at	KDM3B	lysine (K)-specific demethylase 3B	1.2	0.029308
203143_s_at	KIAA0040	KIAA0040	1.26	0.005273
212523_s_at	KIAA0146	KIAA0146	1.1	0.029204
205496_at	KIAA0408	KIAA0408	-1.04	0.023076
212359_s_at	KIAA0913	KIAA0913	1.24	0.048122
215943_at	KIAA1661	KIAA1661 protein	-1.12	0.026168
218355_at	KIF4A	kinesin family member 4A	-1.05	0.029677
208961_s_at	KLF6	Kruppel-like factor 6	1.4	0.010894
210111_s_at	KLHDC10	kelch domain containing 10	1.13	0.037398
221838_at	KLHL22	kelch-like 22 (Drosophila)	1.31	0.017279
220348_at	KLHL29	kelch-like 29 (Drosophila)	-1.04	0.045286
204583_x_at	KLK3	kallikrein-related peptidase 3	-1.1	0.004082
211138_s_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	1.48	0.014277
212101_at	KPNA6	karyopherin alpha 6 (importin alpha 7)*	1.21	0.021362
207509_s_at	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	1.34	0.038649
217173_s_at	LDLR	low density lipoprotein receptor	-1.06	0.045027
204854_at	LEPREL2	leprecan-like 2	-1.14	0.049814
212327_at	LIMCH1	LIM and calponin homology domains 1	-1.09	0.013617
219760_at	LIN7B	lin-7 homolog B (C. elegans)	-1.12	0.015316
215110_at	LOC100288974	BMS1 homolog, ribosome assembly protein (yeast) pseudogene*	-1.09	0.044919
212859_x_at	LOC100505584	metallothionein-2-like*	1.12	0.040994
214857_at	LOC100505761	uncharacterized LOC100505761	-1.22	0.025157
221247_s_at	LOC653375	RCC1-like G exchanging factor-like*	1.1	0.049757
216666_at	LOC93432	maltase-glucoamylase (alpha-glucosidase) pseudogene	-1.16	0.005478
220798_x_at	LPPR3	lipid phosphate phosphatase-related protein type 3	-1.17	0.036993
213496_at	LPPR4	lipid phosphate phosphatase-related protein type 4	1.08	0.028063
221017_s_at	LRRC3	leucine rich repeat containing 3	-1.15	0.045531
212904_at	LRRC47	leucine rich repeat containing 47	1.22	0.021248
204682_at	LTBP2	latent transforming growth factor beta binding protein 2	-1.18	0.037645

210437_at	MAGEA9	melanoma antigen family A, 9*	-1.08	0.037905
217920_at	MAN1A2	mannosidase, alpha, class 1A, member 2	-1.11	0.02788
211083_s_at	MAP3K13	mitogen-activated protein kinase kinase kinase 13	-1.05	0.048247
214219_x_at	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	1.29	0.046927
215471_s_at	MAP7	microtubule-associated protein 7	-1.09	0.024975
212497_at	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	-1.23	0.042471
40016_g_at	MAST4	microtubule associated serine/threonine kinase family member 4	1.29	0.044952
200768_s_at	MAT2A	methionine adenosyltransferase II, alpha	1.37	0.032573
211042_x_at	MCAM	melanoma cell adhesion molecule	1.09	0.023681
210983_s_at	MCM7	minichromosome maintenance complex component 7	1.22	0.038129
213043_s_at	MED24	mediator complex subunit 24	1.17	0.037828
208262_x_at	MEFV	Mediterranean fever	-1.17	0.008804
214077_x_at	MEIS3P1	Meis homeobox 3 pseudogene 1	-1.11	0.030923
221150_at	MEPE	matrix extracellular phosphoglycoprotein	-1.11	0.048749
212945_s_at	MGA	MAX gene associated	1.2	0.049184
220698_at	MGC4294	uncharacterized MGC4294	-1.16	0.01704
55081_at	MICALL1	MICAL-like 1	1.18	0.025707
219332_at	MICALL2	MICAL-like 2	-1.12	0.03484
213166_x_at	MIR4784	microRNA 4784*	1.39	0.038104
212346_s_at	MIR4800	microRNA 4800*	1.15	0.017067
212080_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	1.21	0.035492
203644_s_at	MON1B	MON1 homolog B (yeast)	1.19	0.024257
205123_s_at	MSANTD3-TMEFF1	MSANTD3-TMEFF1 readthrough*	-1.11	0.043924
210297_s_at	MSMB	microseminoprotein, beta-	-1.07	0.009422
205555_s_at	MSX2	msh homeobox 2	-1.07	0.048803
204871_at	MTERF	mitochondrial transcription termination factor	-1.11	0.009949
205323_s_at	MTF1	metal-regulatory transcription factor 1	1.22	0.030284
203208_s_at	MTFR1	mitochondrial fission regulator 1	1.1	0.039388
212767_at	MTG1	mitochondrial GTPase 1 homolog (S. cerevisiae)	1.18	0.014933
222143_s_at	MTMR14	myotubularin related protein 14	1.18	0.043198
217295_at	MUC8	mucin 8	-1.08	0.022792
207727_s_at	MUTYH	mutY homolog (E. coli)	1.13	0.008748
206372_at	MYF6	myogenic factor 6 (herculin)	-1.09	0.019452
201495_x_at	MYH11	myosin, heavy chain 11, smooth muscle	-1.1	0.041454
208208_at	MYH13	myosin, heavy chain 13, skeletal muscle	-1.11	0.028126
212338_at	MYO1D	myosin ID	-1.05	0.049093
45526_g_at	NAA60	N(alpha)-acetyltransferase 60, NatF catalytic subunit	1.23	0.006382
222161_at	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	-1.06	0.021119
210048_at	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	-1.25	0.002205
212443_at	NBEAL2	neurobeachin-like 2	1.29	0.03701

217359_s_at	NCAM1	neural cell adhesion molecule 1	-1.14	0.029052
208979_at	NCOA6	nuclear receptor coactivator 6	1.11	0.048683
200854_at	NCOR1	nuclear receptor corepressor 1	1.13	0.040938
207760_s_at	NCOR2	nuclear receptor corepressor 2	1.34	0.038536
206022_at	NDP	Norrie disease (pseudoglioma)	-1.06	0.046866
209159_s_at	NDRG4	NDRG family member 4	-1.1	0.02286
209223_at	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	-1.09	0.049025
201227_s_at	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	1.18	0.025974
213012_at	NEDD4	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase	-1.16	0.005414
214062_x_at	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	1.17	0.038802
202215_s_at	NFYC	nuclear transcription factor Y, gamma	1.27	0.009526
205204_at	NMB	neuromedin B	-1.12	0.043708
206023_at	NMU	neuromedin U	-1.07	0.047952
216344_at	NPHP4	nephronophthisis 4	-1.11	0.047578
207640_x_at	NTN3	netrin 3	-1.14	0.034913
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	1.27	0.049579
217601_at	NUP188	nucleoporin 188kDa	-1.11	0.028702
207740_s_at	NUP62	nucleoporin 62kDa	1.39	0.012216
213863_s_at	OAZ3	ornithine decarboxylase antizyme 3	-1.12	0.04579
202841_x_at	OGFR	opioid growth factor receptor	1.06	0.041536
222025_s_at	OPLAH	5-oxoprolinase (ATP-hydrolysing)	-1.11	0.043079
219032_x_at	OPN3	opsin 3	1.28	0.03114
207553_at	OPRK1	opioid receptor, kappa 1	-1.02	0.031662
221424_s_at	OR51E2	olfactory receptor, family 51, subfamily E, member 2	-1.1	0.028253
200714_x_at	OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin	1.18	0.03997
220492_s_at	OTOF	otoferlin	-1.07	0.029609
221356_x_at	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	-1.12	0.0111
220779_at	PADI3	peptidyl arginine deiminase, type III	-1.16	0.012627
211413_s_at	PADI4	peptidyl arginine deiminase, type IV	-1.3	0.044449
200906_s_at	PALLD	palladin, cytoskeletal associated protein	-1.09	0.022499
50400_at	PAOX	polyamine oxidase (exo-N4-amino)	1.1	0.043179
206229_x_at	PAX2	paired box 2	-1.11	0.038741
221990_at	PAX8	paired box 8	-1.1	0.022278
204564_at	PCGF3	polycomb group ring finger 3	-1.15	0.002028
203118_at	PCSK7	proprotein convertase subtilisin/kexin type 7	1.17	0.007751
222152_at	PDCD6	Programmed cell death 6	1.09	0.022269
204448_s_at	PDCL	phosducin-like	-1.15	0.022174
206388_at	PDE3A	phosphodiesterase 3A, cGMP-inhibited	-1.15	0.033055
215671_at	PDE4B	phosphodiesterase 4B, cAMP-specific	1.14	0.026621
211093_at	PDE6C	phosphodiesterase 6C, cGMP-specific, cone, alpha prime	1.03	0.035171

218718_at	PDGFC	platelet derived growth factor C	-1.65	0.021985
218019_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	1.28	0.01179
209493_at	PDZD2	PDZ domain containing 2	1.08	0.003498
217923_at	PEF1	penta-EF-hand domain containing 1	1.22	0.023242
213302_at	PFAS	phosphoribosylformylglycinamidine synthase	1.08	0.034692
217009_at	PGK2	phosphoglycerate kinase 2	-1.14	0.001802
212916_at	PHF8	PHD finger protein 8	1.16	0.044179
201397_at	PHGDH	phosphoglycerate dehydrogenase	-1.18	0.024048
207312_at	PHKG1	phosphorylase kinase, gamma 1 (muscle)	-1.14	0.028091
206138_s_at	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	1.23	0.002387
220954_s_at	PILRB	paired immunoglobin-like type 2 receptor beta	1.25	0.042572
201927_s_at	PKP4	plakophilin 4	-1.12	0.002878
215938_s_at	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	1.25	0.03523
210194_at	PLA2R1	phospholipase A2 receptor 1, 180kDa	-1.05	0.049152
207002_s_at	PLAGL1	pleiomorphic adenoma gene-like 1	1.27	0.0114
204613_at	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	1.22	0.042263
217488_x_at	PMS2P3	postmeiotic segregation increased 2 pseudogene 3	-1.09	0.046014
202996_at	POLD4	polymerase (DNA-directed), delta 4, accessory subunit	1.13	0.008284
219066_at	PPCDC	phosphopantothenoylcysteine decarboxylase	1.15	0.019757
206547_s_at	PPEF1	protein phosphatase, EF-hand calcium binding domain 1	-1.14	0.043649
203407_at	PPL	periplakin	-1.07	0.031008
37028_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	1.63	0.033035
208932_at	PPP4C	protein phosphatase 4, catalytic subunit	1.31	0.011052
215705_at	PPP5C	protein phosphatase 5, catalytic subunit	-1.12	0.045951
202791_s_at	PPP6R2	protein phosphatase 6, regulatory subunit 2	1.14	0.010863
209282_at	PRKD2	protein kinase D2	1.19	0.047817
216696_s_at	PRODH2	proline dehydrogenase (oxidase) 2	-1.11	0.018714
216519_s_at	PROSC	proline synthetase co-transcribed homolog (bacterial)	-1.08	0.037476
208880_s_at	PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	1.2	0.020794
213847_at	PRPH	peripherin	-1.14	0.038084
220014_at	PRR16	proline rich 16	1.09	0.018601
205402_x_at	PRSS2	protease, serine, 2 (trypsin 2)	-1.17	0.006865
212806_at	PRUNE2	prune homolog 2 (Drosophila)	-1.09	0.03647
205319_at	PSCA	prostate stem cell antigen	-1.15	0.024194
211270_x_at	PTBP1	polypyrimidine tract binding protein 1	1.12	0.039576
214391_x_at	PTGER1	prostaglandin E receptor 1 (subtype EP1), 42kDa	-1.08	0.042302
203110_at	PTK2B	PTK2B protein tyrosine kinase 2 beta	1.45	0.020221
216915_s_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12	-1.61	0.045535
215172_at	PTPN20A	protein tyrosine phosphatase, non-receptor type 20A*	-1.05	0.033535
206687_s_at	PTPN6	protein tyrosine phosphatase, non-receptor type 6	1.14	0.040602

213799_s_at	PTPRA	protein tyrosine phosphatase, receptor type, A	-1.06	0.042442
205846_at	PTPRB	protein tyrosine phosphatase, receptor type, B	-1.12	0.017948
200635_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	-1.1	0.044636
208300_at	PTPRH	protein tyrosine phosphatase, receptor type, H	-1.06	0.048679
208121_s_at	PTPRO	protein tyrosine phosphatase, receptor type, O	1.26	0.02213
210675_s_at	PTPRR	protein tyrosine phosphatase, receptor type, R	-1.05	0.048043
214443_at	PVR	poliovirus receptor	-1.16	0.031949
212263_at	QKI	QKI, KH domain containing, RNA binding	1.62	0.012186
74694_s_at	RABEP2	rabaptin, RAB GTPase binding effector protein 2	1.25	0.040344
213313_at	RABGAP1	RAB GTPase activating protein 1	1.13	0.04469
220500_s_at	RABL2A	RAB, member of RAS oncogene family-like 2A*	1.15	0.01376
213603_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	1.1	0.047783
204558_at	RAD54L	RAD54-like (S. cerevisiae)	-1.15	0.028583
213205_s_at	RAD54L2	RAD54-like 2 (S. cerevisiae)	1.18	0.040123
212707_s_at	RASA4	RAS p21 protein activator 4*	1.31	0.046441
221440_s_at	RBBP9	retinoblastoma binding protein 9	-1.11	0.044196
221217_s_at	RBFOX1	RNA binding protein, fox-1 homolog (C. elegans) 1	-1.07	0.020293
207207_at	RBMXL2	RNA binding motif protein, X-linked-like 2	-1.05	0.040439
204128_s_at	RFC3	replication factor C (activator 1) 3, 38kDa	-1.24	0.024058
207234_at	RFX3	regulatory factor X, 3 (influences HLA class II expression)	1.06	0.010213
206146_s_at	RHAG	Rh-associated glycoprotein	-1.13	0.037166
219202_at	RHBDF2	rhomboid 5 homolog 2 (Drosophila)	1.19	0.018231
216048_s_at	RHOBTB3	Rho-related BTB domain containing 3	-1.11	0.029971
219446_at	RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	-1.24	0.015703
206137_at	RIMS2	regulating synaptic membrane exocytosis 2	-1.1	0.007445
217984_at	RNASET2	ribonuclease T2	1.13	0.043953
219988_s_at	RNF220	ring finger protein 220	1.06	0.04261
212790_x_at	RPL13A	ribosomal protein L13a*	1.06	0.0417
219762_s_at	RPL36	ribosomal protein L36	1.36	0.016918
210115_at	RPL39L	ribosomal protein L39-like	-1.16	0.029801
200909_s_at	RPLP2	ribosomal protein, large, P2*	1.11	0.008838
212553_at	RPRD2	regulation of nuclear pre-mRNA domain containing 2	1.15	0.036945
213414_s_at	RPS19	ribosomal protein S19	1.09	0.046405
208904_s_at	RPS28	ribosomal protein S28	1.07	0.033354
213481_at	S100A13	S100 calcium binding protein A13	-1.08	0.047298
211322_s_at	SARDH	sarcosine dehydrogenase	-1.26	0.008405
200802_at	SARS	seryl-tRNA synthetase	1.11	0.034117
213236_at	SASH1	SAM and SH3 domain containing 1	1.53	0.04585
218206_x_at	SCAND1	SCAN domain containing 1	1.29	0.029022
212158_at	SDC2	syndecan 2	-1.09	0.026867
221972_s_at	SDF4	stromal cell derived factor 4	1.55	0.023438

218711_s_at	SDPR	serum deprivation response	-1.65	0.047629
202361_at	SEC24C	SEC24 family, member C (S. cerevisiae)	1.3	0.038193
209879_at	SELPLG	selectin P ligand	1.2	0.0376
211362_s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	-1.12	0.022658
205933_at	SETBP1	SET binding protein 1	1.23	0.014508
200687_s_at	SF3B3	splicing factor 3b, subunit 3, 130kDa	1.09	0.019563
217226_s_at	SFXN3	sideroflexin 3	1.11	0.025683
204979_s_at	SH3BGR	SH3 domain binding glutamic acid-rich protein	-1.16	0.007956
220563_s_at	SHANK1	SH3 and multiple ankyrin repeat domains 1	-1.14	0.020941
214096_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	1.25	0.016063
210134_x_at	SHOX2	short stature homeobox 2	-1.17	0.01048
218921_at	SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	1.29	0.022474
204164_at	SIPA1	signal-induced proliferation-associated 1	1.29	0.009453
213600_at	SIPA1L3	signal-induced proliferation-associated 1 like 3	1.23	0.012794
203727_at	SKIV2L	superkiller viralicidic activity 2-like (S. cerevisiae)	1.17	0.014597
211112_at	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	-1.15	0.007413
207074_s_at	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	-1.12	0.041808
219795_at	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	-1.08	0.021609
201349_at	SLC9A3R1	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1	1.14	0.049577
212947_at	SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	1.23	0.033315
206354_at	SLCO1B3	solute carrier organic anion transporter family, member 1B3	-1.05	0.037327
212258_s_at	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	-1.14	0.048716
212167_s_at	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	1.14	0.028131
201321_s_at	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	1.64	0.033009
201827_at	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	1.11	0.034946
208584_at	SNCG	synuclein, gamma (breast cancer-specific protein 1)	-1.11	0.009374
204288_s_at	SORBS2	sorbin and SH3 domain containing 2	-1.09	0.038123
209762_x_at	SP110	SP110 nuclear body protein	1.14	0.040335
216972_at	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	-1.06	0.044527
212480_at	SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1-like	1.17	0.002171
40273_at	SPHK2	sphingosine kinase 2	1.12	0.045658
205861_at	SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	1.48	0.001683
208611_s_at	SPTAN1	spectrin, alpha, non-erythrocytic 1	1.2	0.04472
214145_s_at	SPTB	spectrin, beta, erythrocytic	-1.09	0.03294
213562_s_at	SQLE	squalene epoxidase	-1.07	0.020398

204675_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	1.2	0.037698
202817_s_at	SS18	synovial sarcoma translocation, chromosome 18	1.54	0.038658
221752_at	SSH1	slingshot homolog 1 (Drosophila)	1.2	0.035265
204596_s_at	STC1	stanniocalcin 1	-1.09	0.025824
203439_s_at	STC2	stanniocalcin 2	-1.12	0.030875
40420_at	STK10	serine/threonine kinase 10	1.25	0.013845
217934_x_at	STUB1	STIP1 homology and U-box containing protein 1, E3 ubiquitin protein ligase	1.11	0.041763
207346_at	STX2	syntaxin 2	-1.14	0.006375
213505_s_at	SUGP2	SURP and G patch domain containing 2	1.12	0.032625
212344_at	SULF1	sulfatase 1	-1.14	0.044144
209307_at	SWAP70	SWAP switching B-cell complex 70kDa subunit	1.66	0.048848
207540_s_at	SYK	spleen tyrosine kinase	1.19	0.009162
221914_at	SYN1	synapsin I	-1.08	0.041187
213200_at	SYP	synaptophysin	-1.18	0.015208
217437_s_at	TACC1	transforming, acidic coiled-coil containing protein 1	1.18	0.031063
218308_at	TACC3	transforming, acidic coiled-coil containing protein 3	1.18	0.038762
205966_at	TAF13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	-1.06	0.026231
221324_at	TAS2R1	taste receptor, type 2, member 1	-1.11	0.036522
212350_at	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	1.18	0.035543
201814_at	TBC1D5	TBC1 domain family, member 5	1.17	0.03546
211052_s_at	TBCD	tubulin folding cofactor D	1.31	0.006623
204931_at	TCF21	transcription factor 21	-1.08	0.01558
222146_s_at	TCF4	transcription factor 4	1.34	0.049708
209995_s_at	TCL1A	T-cell leukemia/lymphoma 1A	2.16	0.016979
206438_x_at	TCTN2	tectonic family member 2	-1.23	0.016914
34260_at	TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	1.1	0.039517
214064_at	TF	transferrin	-1.09	0.042101
50221_at	TFEB	transcription factor EB	1.17	0.029798
207334_s_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-1.19	0.045194
212040_at	TGOLN2	trans-golgi network protein 2	1.42	0.031182
218492_s_at	THAP7	THAP domain containing 7	1.26	0.024907
208850_s_at	THY1	Thy-1 cell surface antigen	-1.05	0.034518
201822_at	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	-1.09	0.039332
220052_s_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	1.25	0.003055
214183_s_at	TKTL1	transketolase-like 1	-1.49	0.019995
212770_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	1.19	0.037422
215008_at	TLL2	tolloid-like 2	-1.06	0.030291
210166_at	TLR5	toll-like receptor 5	1.31	0.038007

213349_at	TMCC1	transmembrane and coiled-coil domain family 1	1.22	0.00077
219460_s_at	TMEM127	transmembrane protein 127	1.11	0.02347
218531_at	TMEM134	transmembrane protein 134	1.21	0.02594
218113_at	TMEM2	transmembrane protein 2	1.2	0.011507
222267_at	TMEM209	transmembrane protein 209	-1.18	0.032749
217899_at	TMEM214	transmembrane protein 214	1.17	0.02871
219449_s_at	TMEM70	transmembrane protein 70	-1.7	0.018675
221032_s_at	TMPRSS5	transmembrane protease, serine 5	-1.07	0.02383
207113_s_at	TNF	tumor necrosis factor	2.86	0.044506
214581_x_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	-1.07	0.030206
48531_at	TNIP2	TNFAIP3 interacting protein 2	1.12	0.042731
217121_at	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-1.12	0.033102
209904_at	TNNC1	troponin C type 1 (slow)	-1.08	0.036499
204485_s_at	TOM1L1	target of myb1 (chicken)-like 1	-1.05	0.02927
203050_at	TP53BP1	tumor protein p53 binding protein 1	1.13	0.049225
211834_s_at	TP63	tumor protein p63	-1.1	0.027354
214924_s_at	TRAK1	trafficking protein, kinesin binding 1	1.26	0.042882
213261_at	TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1	1.1	0.024779
210994_x_at	TRIM23	tripartite motif containing 23	-1.37	0.042412
210463_x_at	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae)	1.12	0.03734
205028_at	TRO	trophinin	-1.07	0.049836
220226_at	TRPM8	transient receptor potential cation channel, subfamily M, member 8	-1.19	0.047132
219415_at	TTYH1	tweety homolog 1 (Drosophila)	-1.13	0.037582
218184_at	TULP4	tubby like protein 4	1.13	0.03276
209078_s_at	TXN2	thioredoxin 2	1.22	0.016845
218347_at	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)*	1.13	0.025266
218381_s_at	U2AF2	U2 small nuclear RNA auxiliary factor 2	1.08	0.04085
200964_at	UBA1	ubiquitin-like modifier activating enzyme 1	1.3	0.020264
211950_at	UBR4	ubiquitin protein ligase E3 component n-recognin 4	1.2	0.027953
219172_at	UBTD1	ubiquitin domain containing 1	-1.12	0.030188
201871_s_at	UBXN1	UBX domain protein 1	1.19	0.03571
218533_s_at	UCKL1	uridine-cytidine kinase 1-like 1	1.22	0.004417
215125_s_at	UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1*	-1.08	0.031826
206716_at	UMOD	uromodulin	-1.1	0.018271
211168_s_at	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	1.21	0.018325
206658_at	UPK3B	uroplakin 3B	-1.14	0.018629
208723_at	USP11	ubiquitin specific peptidase 11	1.25	0.022187
205356_at	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	1.12	0.047359
217441_at	USP33	ubiquitin specific peptidase 33	-1.09	0.03309

221098_x_at	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	1.06	0.026733
220068_at	VPREB3	pre-B lymphocyte 3	1.56	0.006654
212326_at	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	1.18	0.035688
221704_s_at	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	1.18	0.028026
202261_at	VPS72	vacuolar protein sorting 72 homolog (S. cerevisiae)	1.21	0.042257
218022_at	VRK3	vaccinia related kinase 3	1.2	0.002414
211383_s_at	WDR37	WD repeat domain 37	1.18	0.049148
219809_at	WDR55	WD repeat domain 55	1.21	0.030831
215711_s_at	WEE1	WEE1 homolog (S. pombe)	-1.14	0.038065
211982_x_at	XPO6	exportin 6	1.18	0.045591
217065_at	YME1L1	YME1-like 1 (S. cerevisiae)	-1.12	0.018968
201369_s_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	1.64	0.019148
203556_at	ZHX2	zinc fingers and homeoboxes 2	1.22	0.032428
214670_at	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	1.32	0.037779
213858_at	ZNF250	zinc finger protein 250	-1.08	0.019944
207753_at	ZNF304	zinc finger protein 304	1.18	0.045855
215767_at	ZNF804A	zinc finger protein 804A	1.1	0.034192
215461_at	ZNRF4	zinc and ring finger 4	-1.16	0.007018
218639_s_at	ZXDC	ZXD family zinc finger C	1.06	0.047562
212601_at	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	1.26	0.01257

Table S5: Selected gene ontology GO categories significantly affected by heavy smokers compared with light smokers.

Group	GO ID	GO categories	GO term	Group P value	Term P value	% Associated Genes	Associated Genes Found
1	GO:0002708	BP	positive regulation of lymphocyte mediated immunity	4.87E-08	1.09E-07	15.0	B2M, CD226, FOXP3, HFE, HLA-A, HLA-E, IL23A, PVR, TNF
1	GO:0001912	BP	positive regulation of leukocyte mediated cytotoxicity	4.87E-08	6.90E-07	17.5	B2M, CD226, HFE, HLA-A, HLA-E, IL23A, PVR
1	GO:0002824	BP	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	4.87E-08	6.34E-08	14.8	B2M, CD226, FOXP3, HFE, HLA-A, HLA-E, IL23A, PVR, TNF
1	GO:0002711	BP	positive regulation of T cell mediated immunity	4.87E-08	6.90E-07	17.5	B2M, FOXP3, HFE, HLA-A, HLA-E, IL23A, PVR
2	GO:0045066	BP	regulatory T cell differentiation	6.03E-06	5.85E-04	25.0	FOXP3, IRF1, NCOR1
2	GO:0031063	BP	regulation of histone deacetylation	6.03E-06	1.26E-04	20.0	CTBP1, FOXP3, NCOR1, PRKD2
	GO:0032770	BP	positive regulation of monooxygenase activity		9.39E-05	22.2	APOE, ESR1, PTK2B, TNF
	GO:0033005	BP	positive regulation of mast cell activation		6.72E-04	23.1	CD226, CRHR1, SYK
	GO:0046006	BP	regulation of activated T cell proliferation		9.46E-05	14.3	FOXP3, ICOSLG, IGFBP2, IL23A, NCOA6
	GO:0016514	CC	SWI/SNF complex		6.42E-05	26.7	SMARCA2, SMARCB1, SMARCC2, SMARCD2

Table S6: Significant genes adjusted for age, race, and gender among smokers

Symbol	*P* value	Symbol	*P* value	Symbol	*P* value
ABAT	0.013812	CD19	0.012946	DVL1	0.015047
ABCG1	0.018317	CD22	0.006198	DYNC1H1	0.016846
ABR	0.038099	CD226	0.033447	DZIP1	0.030158
ACTG1	0.004767	CD24	0.003927	EHBP1L1	0.037899
ADAM28	0.01815	CD72	0.015296	EHD1	0.004701
ADAMTS13	0.03581	CD79A	0.003984	EIF3B	0.002934
ADD1	0.041045	CD79B	0.010824	ELMO2	0.032143
ALOX12P2	0.031775	CD97	0.038437	EML2	0.022202
APOBR	0.040184	CDC25A	0.034124	EMP1	0.030918
ARHGAP17	0.00752	CELF1	0.014182	EPB41L2	0.036477
ARHGAP25	0.034076	CELF2	0.018516	EPHA1	0.030339
ARHGEF9	0.039759	CHERP	0.029433	EPN2	0.037982
ARMCX1	0.016912	CHML	0.030926	ERMAP	0.001913
ASPHD1	0.020469	CIDEA	0.021967	ESR1	0.045689
ATP12A	0.036145	CLEC4M	0.011485	EXOC3	0.022562
AURKC	0.045982	COL2A1	0.043544	FA2H	0.026191
B2M	0.015515	COPS7A	0.031591	FAM53B	0.0248
B4GALNT1	0.010325	CRHR1	0.044699	FAP	0.027327
B4GALT1	0.00225	CRYAA	0.009695	FBXO46	0.023435
BAG6	0.041357	CRYBA4	0.010718	FGF3	0.032265
BANP	0.014584	CSHL1	0.019195	FOXE1	0.022938
BCL11A	0.008311	CSK	0.02214	GAK	0.038101
BCL7A	0.022542	CSNK1D	0.037754	GATAD2A	0.043499
BIN1	0.00932	CTBP1	0.049416	GCDH	0.027358
BIN3	0.005875	CXXC1	0.016449	GHRHR	0.040397
BLK	0.00246	CYP2C18	0.027754	GIP	0.015228
BSDC1	0.02384	CYP2D6	0.025825	GJB3	0.022951
BTN2A2	0.034102	DAG1	0.032422	GLT8D2	0.033068
BUB1	0.012925	DAZAP2	0.033209	GM2A	0.046943
C11orf9	0.021566	DCAF13	0.04604	GMEB2	0.044828
C12orf43	0.011714	DCAF7	0.026779	GOLGB1	0.016543
C12orf51	0.009368	DCXR	0.025495	GON4L	0.003144
C17orf80	0.003859	DENND2A	0.027875	GPD2	0.045856
C1RL	0.006306	DFNA5	0.041489	GULP1	0.048076
CAMSAP2	0.030425	DGCR14	0.026837	HFE	0.026777
CAMTA2	0.028907	DHRS2	0.0138	HIST1H2AC	0.042354
CAPN9	0.015171	DHX16	0.020628	HIST1H2BC	0.030186
CASP8	0.020337	DLAT	0.005526	HIST1H3A	0.026807
CBFA2T3	0.019846	DNTT	0.011368	HLA-DOB	0.017418
CBX5	0.011166	DST	0.017902	HLA-DQB1	0.046151

HLA-F	0.026175
HLF	0.037797
HOXD12	0.013774
HOXD13	0.032693
HRASLS2	0.007005
HTR2B	0.014899
HTR3A	0.00719
IDS	0.016402
IGFBP2	0.023636
IGFLR1	0.012537
IGHD	8.08E-05
IGHM	0.004087
IL16	0.029849
IL21R	0.049877
IL23A	0.000549
ING4	0.028941
INTS1	0.048443
IRF3	0.02538
IRX4	0.006807
ISCA1	0.023463
ITGB7	0.029135
ITPR3	0.03037
KCNAB3	0.039014
KDM3B	0.019774
KIAA0040	0.005965
KIAA0146	0.022127
KIAA0408	0.031432
KIF4A	0.024396
KLHL22	0.036561
KLK3	0.010319
KMO	0.027469
KPNA6	0.021666
LIMCH1	0.014239
LIN7B	0.038171
LPPR3	0.037524
LPPR4	0.046062
LRRC47	0.017243
LTBP2	0.045055
MAP7	0.03615
MAPK1IP1L	0.047836
MAST4	0.029906
MAT2A	0.015817
MCAM	0.004885
MED24	0.026585
MEFV	0.012435
MGA	0.030801
MIR4784	0.047092
MON1B	0.036011
MSANTD3	0.047407
MSX2	0.041907
MTERF	0.021009
MTF1	0.041188
MTG1	0.021365
MUTYH	0.018805
MYF6	0.031706
NAA60	0.01286
NAALAD2	0.049786
NAPG	0.00613
NCAM1	0.023302
NCOR1	0.031761
NDRG4	0.027915
NFYC	0.021429
NUP62	0.027939
OPN3	0.049491
OPRK1	0.040108
OR51E2	0.020218
P2RX2	0.022933
PADI3	0.020437
PALLD	0.026228
PAOX	0.030715
PAX8	0.031345
PCGF3	0.005078
PCSK7	0.010781
PDCD6	0.024399
PDCL	0.01639
PDE3A	0.026318
PDE4B	0.017371
PDE6C	0.031883
PDXK	0.029743
PEF1	0.044794
PFAS	0.021818
PHKG1	0.04743
PI4KB	0.005788
PILRB	0.049759
PKP4	0.00419
PLA2G6	0.047263
PLAGL1	0.017743
PLCG2	0.044096
PMS2P3	0.030162
POLD4	0.022214
PPP1R15A	0.043979
PPP4C	0.018848
PPP6R2	0.017204
PROSC	0.030614
PRPF6	0.026371
PRPH	0.025248
PRSS2	0.012382
PRUNE2	0.049038
PSCA	0.036853
PTK2B	0.049656
PTPRB	0.032258
PVR	0.031656
QKI	0.016045
RABEP2	0.017614
RABGAP1	0.02075
RABL2A	0.032144
RAD54L2	0.049086
RASA4	0.044426
RBFOX1	0.033122
RFC3	0.016791
RHBDF2	0.036393
RIMS2	0.01308
RNASET2	0.041213
RPLP2	0.00897
RPS19	0.037361
S100A13	0.037125
SCAND1	0.038241
SDC2	0.016779
SDF4	0.030569
SEC24C	0.033329

SETBP1	0.035485	TMEM70	0.026456
SF3B3	0.039579	TMPRSS5	0.028334
SFXN3	0.041878	TNF	0.03922
SH3BGR	0.015584	TNFRSF21	0.033036
SHMT2	0.021296	TOM1L1	0.034602
SHOX2	0.020216	TRAK1	0.038974
SIGIRR	0.035148	TRANK1	0.046405
SIPA1	0.023273	TULP4	0.03231
SKIV2L	0.023133	TYW1	0.0352
SLC12A4	0.003349	UBA1	0.043105
SLC6A14	0.049631	UBR4	0.040495
SMARCC2	0.029325	UBTD1	0.021484
SNCG	0.016376	UCKL1	0.011746
SP110	0.034638	UPF1	0.045813
SPAM1	0.039171	UPK3B	0.047508
SPECC1L	0.001083	USP11	0.035534
SPIB	0.004636	USP33	0.038454
SQLE	0.013849	VPREB3	0.003816
SS18	0.030258	VPS13D	0.031442
STC1	0.042317	VPS37B	0.025121
STK10	0.028505	VRK3	0.004152
STX2	0.0197	WDR55	0.027808
SYK	0.0229	ZFP36L2	0.021344
SYP	0.013773	ZHX2	0.019437
TAS2R1	0.04748	ZKSCAN1	0.036963
TBCD	0.009166	ZNF250	0.038896
TCF21	0.031964	ZNRF4	0.012199
TCL1A	0.010359	ZXDC	0.04581
TF	0.032783	ZZEF1	0.022769
TFEB	0.049586		
TGFBR2	0.04557		
TGOLN2	0.04771		
THAP7	0.035754		
TIMM17A	0.045321		
TINF2	0.00552		
TKTL1	0.031103		
TLE3	0.036992		
TMCC1	0.002152		
TMEM134	0.043938		
TMEM2	0.010697		

Table S7: The significant IPA canonical pathways assignment for the set of CSC-stimulated genes

Canonical Pathways	*P* value	Molecules
NRF2-mediated Oxidative Stress Response	7.07946E-05	FTL,NQO2,PIK3R5,GCLC,DNAJB2,MAFG,HMOX1,JUN,KEAP1,VCP,UBE2K,GCLM,DNAJB1,TXN,DNAJC16,SOD1,NQO1,DNAJC1,DNAJB9,MAFF,TXNRD1,GSR,SQSTM1,DNAJB6,FTH1,EPHX1
Inosine-5'-phosphate Biosynthesis II	0.000269153	ADSL,PAICS,ATIC
Role of CHK Proteins in Cell Cycle Checkpoint Control	0.000676083	E2F6,PCNA,PPP2R2B,PPP2R5B,ATMIN,E2F5,SLC19A1,RFC1,TLK2,PPP2R5A,NBN
Purine Nucleotides De Novo Biosynthesis II	0.003981072	ADSL,PAICS,PPAT,ATIC
Protein Ubiquitination Pathway	0.003981072	USP18,USP12,UBE2A,PSMD7,UBR2,UBE2N,USP20,DNAJB2,PSMB8,USP2,USP3,UCHL1,USP47,PSMD14,DNAJB1,DNAJC16,PSMB9,DNAJC1,PSMA1,DNAJB9,SKP2,HSPA12A,PSMB7,PSMD2,PSMB1,PSMD1,PSMD4,DNAJB6
Aryl Hydrocarbon Receptor Signaling	0.005370318	TRIP11,CYP1A1,NQO2,POLA1,NQO1,CYP1B1,NCOA3,TGM2,ALDH1A1,JUN,CCND2,NCOA2,RARB,ALDH18A1,RXRB,ESR1,MCM7
PXR/RXR Activation	0.00676083	ABCB1,ALDH1A1,CYP3A4,NR1I2,FOXO3,ABCB11,CYP2C9,INSR,SULT2A1,CYP2C8
Phosphatidylcholine Biosynthesis I	0.007762471	CEPT1,CHPT1,PHKA1
Choline Biosynthesis III	0.007762471	HMOX1,CEPT1,CHPT1,PHKA1
Dermatan Sulfate Degradation (Metazoa)	0.007762471	MGEA5,IDS,GM2A,HEXB
VDR/RXR Activation	0.01023293	SERPINB1,YY1,TNFSF11,LRP5,NCOA2,PDGFA,RXRB,CALB1,HSD17B2,NCOA3,SULT2A1
PDGF Signaling	0.01023293	CSNK2A2,JUN,INPP5F,PDGFA,SOS2,SRF,PIK3R5,CRK,EIF2AK2,STAT1,CAV3
Glutathione Biosynthesis	0.012022644	GCLC,GCLM
Calcium Transport I	0.016982437	ATP2C1,ATP2A2,ATP2B4
Mismatch Repair in Eukaryotes	0.016982437	PCNA,SLC19A1,FEN1,RFC1
Bupropion Degradation	0.019952623	CYP1A1,CYP3A4,CYP2C9,CYP1B1,CYP2C8
Heme Degradation	0.022908677	HMOX1,BLVRB
α-tocopherol Degradation	0.022908677	CYP4F3,CYP4A11
Cell Cycle Regulation by BTG Family Proteins	0.023442288	E2F6,PPP2R2B,BTG2,PPP2R5B,E2F5,PPP2R5A
Acetone Degradation I (to Methylglyoxal)	0.023442288	CYP1A1,CYP3A4,CYP2C9,CYP1B1,CYP2C8
Epithelial Adherens Junction Signaling	0.023988329	CTNNA1,CRK,TCF3,ACVR1B,CLIP1,APC,PTEN,MET,ACTR3,WAS,ARPC2,KEAP1,MYL4

		,SSX2IP,LEF1,ACTN1
Cyclins and Cell Cycle Regulation	0.02630268	E2F6,CCNH,CDKN2D,CCND2,PPP2R2B,HDAC1,PPP2R5B,E2F5,PPP2R5A,SKP2
Clathrin-mediated Endocytosis Signaling	0.027542287	APOM,APOB,EPS15,PICALM,PDGFA,CHP1,PIK3R5,SH3GLB1,HIP1,MET,CSNK2A2,LDLR,ACTR3,ARRB1,IGF1,PIP5K1C,ARPC2,RAB11A,SERPINA1
Estrogen Biosynthesis	0.030199517	CYP1A1,CYP3A4,CYP2C9,HSD17B2,CYP1B1,CYP2C8
dTMP De Novo Biosynthesis	0.036307805	TYMS,SHMT1
Folate Polyglutamylation	0.036307805	SHMT1,MTHFD1
Fcϒ Receptor-mediated Phagocytosis in Macrophages and Monocytes	0.037153523	MYO5A,HMOX1,FYN,ACTR3,WAS,ARPC2,VAMP3,RAB11A,CRK,FCGR1A,PTEN
Chondroitin Sulfate Degradation (Metazoa)	0.03801894	MGEA5,GM2A,HEXB
Activation of IRF by Cytosolic Pattern Recognition Receptors	0.03801894	DHX58,TRAF3,IKBKG,JUN,ZBP1,IKBKE,STAT1,IFNA6
Small Cell Lung Cancer Signaling	0.038904514	PIAS3,TRAF3,IKBKG,RARB,PIK3R5,IKBKE,RXRB,SKP2,PTEN
Role of PKR in Interferon Induction and Antiviral Response	0.041686938	TRAF3,IKBKG,IKBKE,EIF2AK2,STAT1,FCGR1A
Xenobiotic Metabolism Signaling	0.042657952	ABCB1,CYP1A1,FTL,FMO3,NQO2,PPP2R5B,NQO1,PIK3R5,GCLC,CYP2C9,SULT2A1,PPP2R5A,CYP1B1,CHST1,HMOX1,ALDH1A1,CYP3A4,NR1I2,KEAP1,PPP2R2B,SULT1E1,ALDH18A1,SULT1B1,CYP2C8
AMPK Signaling	0.043651583	TSC1,LEP,PPP2R5B,PIK3R5,CFTR,PFKFB2,PPP2R5A,PPP2R2B,IRS2,PPM1A,INSR,AK2,CHRNA3,PPAT
IGF-1 Signaling	0.047863009	CSNK2A2,JUN,IGF1,SOS2,FOXO3,SOCS2,SRF,PIK3R5,IRS2,IGFBP7,SFN