Supplementary Table 3. Significantly perturbed genes and proteins following *ex vivo* stimulation of whole blood by LPS or GM+I.

Gene expression significantly perturbed in response to LPS (fold change = LPS/Control)

Probeset ID	Gene Symbol	Gene ID	Gene Name	Fold Change =	q-value (%)
219577_s_at	**ABCA7**	10347	ATP-binding cassette, sub-family A (ABC1), member 7	-4.56	0.22
202804_at	**ABCC1**	4363	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	4.15	0.00
226363_at	**ABCC5**	10057	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-12.76	0.06
200045_at	**ABCF1**	23	ATP-binding cassette, sub-family F (GCN20), member 1	7.79	0.00
211113_s_at	**ABCG1**	9619	ATP-binding cassette, sub-family G (WHITE), member 1	-2.57	0.10
237974_at	**ABHD12B**	145447	abhydrolase domain containing 12B	-9.90	0.13
228490_at	**ABHD2**	11057	abhydrolase domain containing 2	-4.72	0.00
213017_at	**ABHD3**	171586	abhydrolase domain containing 3	-7.99	0.03
218739_at	**ABHD5**	51099	abhydrolase domain containing 5	-4.79	0.00
239579_at	**ABHD7**	253152	abhydrolase domain containing 7	2.79	0.22
227631_at	**ABI2**	10152	Abl interactor 2	2.47	0.37
231907_at	**ABL2**	27	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	2.12	0.37
229164_s_at	**ABTB1**	80325	ankyrin repeat and BTB (POZ) domain containing 1	-7.27	0.00
209608_s_at	**ACAT2**	39	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	4.82	0.58
225317_at	**ACBD6**	84320	acyl-Coenzyme A binding domain containing 6	2.91	0.00
201128_s_at	**ACLY**	47	ATP citrate lyase	-4.01	0.22
216103_at	**ACOT11**	26027	acyl-CoA thioesterase 11	2.15	0.22
221641_s_at	**ACOT9**	23597	acyl-CoA thioesterase 9	2.72	0.00
227962_at	**ACOX1**	51	acyl-Coenzyme A oxidase 1, palmitoyl	-6.34	0.03
215227_x_at	**ACP1**	52	acid phosphatase 1, soluble	-6.62	0.06
222592_s_at	**ACSL5**	51703	acyl-CoA synthetase long-chain family member 5	51.52	0.00
208636_at	**ACTN1**	87	actinin, alpha 1	-2.13	0.00
203861_s_at	**ACTN2**	88	actinin, alpha 2	-2.87	0.10
200601_at	**ACTN4**	81	actinin, alpha 4	-3.03	0.22
205209_at	**ACVR1B**	91	activin A receptor, type IB	2.08	0.37
214895_s_at	**ADAM10**	102	ADAM metallopeptidase domain 10	-2.42	0.37
205745_x_at	**ADAM17**	6868	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	2.04	0.00
209765_at	**ADAM19**	8728	ADAM metallopeptidase domain 19 (meltrin beta)	-16.31	0.00
206134_at	**ADAMDEC1**	27299	ADAM-like, decysin 1	68.83	0.10
219384_s_at	**ADAT1**	23536	adenosine deaminase, tRNA-specific 1	2.41	0.37
235049_at	**ADCY1**	107	adenylate cyclase 1 (brain)	2.14	0.22
206281_at	**ADCYAP1**	116	adenylate cyclase activating polypeptide 1 (pituitary)	3.00	0.10
214736_s_at	**ADD1**	118	adducin 1 (alpha)	-2.38	0.37
201752_s_at	**ADD3**	120	adducin 3 (gamma)	-9.60	0.00
209122_at	**ADFP**	123	adipose differentiation-related protein	9.01	0.22
208848_at	**ADH5**	128	alcohol dehydrogenase 5 (class III), chi polypeptide	2.03	0.22
222400_s_at	**ADI1**	55256	acireductone dioxygenase 1	-3.37	0.37
203322_at	**ADNP2**	22850	ADNP homeobox 2	3.89	0.06
205013_s_at	**ADORA2A**	135	adenosine A2a receptor	14.50	0.00

228042_at	**ADPRH**	141	ADP-ribosylarginine hydrolase	6.18	0.13
206170_at	**ADRB2**	154	adrenergic, beta-2-, receptor, surface	-8.09	0.03
243487_at	**AFF4**	27125	AF4/FMR2 family, member 4	3.61	0.03
217939_s_at	**AFTPH**	54812	aftiphilin	2.21	0.03
224776_at	**AGPAT6**	137964	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	3.04	0.03
204500_s_at	**AGTPBP1**	23287	ATP/GTP binding protein 1	-5.86	0.00
210327_s_at	**AGXT**	189	alanine-glyoxylate aminotransferase	3.25	0.37
214766_s_at	**AHCTF1**	25909	AT hook containing transcription factor 1	-11.55	0.00
215051_x_at	**AIF1**	199	allograft inflammatory factor 1	-2.54	0.00
223136_at	**AIG1**	51390	androgen-induced 1	4.35	0.37
204348_s_at	**AK3L1** /// **AK3L2** /// **LOC645619**	205 /// 387851 /// 645619	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2 /// similar to Adenylate kinase isoenzyme 4, mitochondrial (ATP-AMP transphosphorylase)	33.07	0.13
205045_at	**AKAP10**	11216	A kinase (PRKA) anchor protein 10	-2.48	0.37
222024_s_at	**AKAP13**	11214	A kinase (PRKA) anchor protein 13	-2.02	0.03
202759_s_at	**AKAP2** /// **PALM2-AKAP2**	11217 /// 445815	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 protein	2.44	0.22
225701_at	**AKNA**	80709	AT-hook transcription factor	-2.61	0.00
201900_s_at	**AKR1A1**	10327	aldo-keto reductase family 1, member A1 (aldehyde reductase)	10.42	0.00
207163_s_at	**AKT1**	207	v-akt murine thymoma viral oncogene homolog 1	-15.12	0.37
218373_at	**AKTIP**	64400	AKT interacting protein	-9.94	0.00
201952_at	**ALCAM**	214	activated leukocyte cell adhesion molecule	2.31	0.37
201612_at	**ALDH9A1**	223	aldehyde dehydrogenase 9 family, member A1	-4.62	0.00
208212_s_at	**ALK**	238	anaplastic lymphoma kinase (Ki-1)	3.68	0.58
207381_at	**ALOX12B**	242	arachidonate 12-lipoxygenase, 12R type	2.52	0.22
207328_at	**ALOX15**	246	arachidonate 15-lipoxygenase	-3.44	0.37
204446_s_at	**ALOX5**	240	arachidonate 5-lipoxygenase	-5.18	0.03
215783_s_at	**ALPL**	249	alkaline phosphatase, liver/bone/kidney	-18.17	0.00
204664_at	**ALPP**	250	alkaline phosphatase, placental (Regan isozyme)	6.11	0.22
226431_at	**ALS2CR13**	150864	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13	-17.74	0.58
1553956_at	**ALS2CR4**	65062	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	2.22	0.22
228094_at	**AMICA1**	120425	adhesion molecule, interacts with CXADR antigen 1	-7.77	0.00
204976_s_at	**AMMECR1**	9949	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	-4.58	0.58
224010_at	**ANAPC11**	51529	APC11 anaphase promoting complex subunit 11 homolog (yeast)	3.02	0.06
237316_at	**ANKDD1A**	348094	ankyrin repeat and death domain containing 1A	9.04	0.03
228356_at	**ANKRD11**	29123	ankyrin repeat domain 11	-3.21	0.10
1565832_at	**ANKRD15**	23189	Ankyrin repeat domain 15	3.51	0.10
231423_s_at	**ANKRD16**	54522	ankyrin repeat domain 16	2.64	0.00
238439_at	**ANKRD22**	118932	ankyrin repeat domain 22	6.01	0.00
225731_at	**ANKRD50**	57182	ankyrin repeat domain 50	-3.27	0.00
238626_at	**ANKS6**	203286	ankyrin repeat and sterile alpha motif domain containing 6	-3.03	0.03
218274_s_at	**ANKZF1**	55139	ankyrin repeat and zinc finger domain containing 1	-6.85	0.10

202888_s_at	**ANPEP**	290	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	-2.32	0.22
214783_s_at	**ANXA11**	311	annexin A11	-11.43	0.03
208816_x_at	**ANXA2P2**	304	annexin A2 pseudogene 2	3.99	0.58
209369_at	**ANXA3**	306	annexin A3	-7.17	0.06
200782_at	**ANXA5**	308	annexin A5	6.56	0.00
205639_at	**AOAH**	313	acyloxyacyl hydrolase (neutrophil)	-3.74	0.13
204894_s_at	**AOC3**	8639	amine oxidase, copper containing 3 (vascular adhesion protein 1)	-5.75	0.37
223024_at	**AP1M1**	8907	adaptor-related protein complex 1, mu 1 subunit	-2.49	0.58
208074_s_at	**AP2S1**	1175	adaptor-related protein complex 2, sigma 1 subunit	-2.04	0.37
204859_s_at	**APAF1**	317	apoptotic peptidase activating factor 1	-2.75	0.00
208703_s_at	**APLP2**	334	amyloid beta (A4) precursor-like protein 2	-2.08	0.00
219466_s_at	**APOA2**	336	apolipoprotein A-II	2.93	0.00
220023_at	**APOB48R**	55911	apolipoprotein B48 receptor	-2.12	0.58
207158_at	**APOBEC1**	339	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	2.32	0.00
204205_at	**APOBEC3G**	60489	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	2.69	0.37
1554545_at	**APOBEC4**	403314	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative)	2.61	0.10
204561_x_at	**APOC2** /// **APOC4**	344 /// 346	apolipoprotein C-II /// apolipoprotein C-IV	-2.42	0.03
209546_s_at	**APOL1**	8542	apolipoprotein L, 1	2.11	0.58
221087_s_at	**APOL3**	80833	apolipoprotein L, 3	10.75	0.06
219716_at	**APOL6**	80830	apolipoprotein L, 6	3.62	0.00
201176_s_at	**ARCN1**	372	archain 1	2.93	0.22
201097_s_at	**ARF4**	378	ADP-ribosylation factor 4	2.45	0.00
218870_at	**ARHGAP15**	55843	Rho GTPase activating protein 15	-7.53	0.13
37577_at	**ARHGAP19**	84986	Rho GTPase activating protein 19	-13.62	0.13
226576_at	**ARHGAP26**	23092	Rho GTPase activating protein 26	-4.01	0.03
225618_at	**ARHGAP27**	201176	Rho GTPase activating protein 27	-2.23	0.03
204425_at	**ARHGAP4**	393	Rho GTPase activating protein 4	-7.73	0.06
226906_s_at	**ARHGAP9**	64333	Rho GTPase activating protein 9	-2.30	0.00
201288_at	**ARHGDIB**	397	Rho GDP dissociation inhibitor (GDI) beta	-6.92	0.00
221656_s_at	**ARHGEF10L**	55160	Rho guanine nucleotide exchange factor (GEF) 10-like	6.43	0.06
213039_at	**ARHGEF18**	23370	rho/rac guanine nucleotide exchange factor (GEF) 18	-4.20	0.37
1554783_s_at	**ARHGEF2**	9181	rho/rac guanine nucleotide exchange factor (GEF) 2	3.00	0.00
209539_at	**ARHGEF6**	9459	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-5.35	0.10
218917_s_at	**ARID1A**	8289	AT rich interactive domain 1A (SWI-like)	-4.76	0.06
233339_s_at	**ARID1B**	57492	AT rich interactive domain 1B (SWI1-like)	-3.04	0.58
225181_at	**ARID1B** /// **LOC729446**	57492 /// 729446	AT rich interactive domain 1B (SWI1-like) /// similar to AT rich interactive domain 1B (SWI1-like) isoform 1	-2.00	0.13
205062_x_at	**ARID4A**	5926	AT rich interactive domain 4A (RBP1-like)	-2.86	0.00
213138_at	**ARID5A**	10865	AT rich interactive domain 5A (MRF1-like)	-2.26	0.22
212614_at	**ARID5B**	84159	AT rich interactive domain 5B (MRF1-like)	22.31	0.00
202641_at	**ARL3**	403	ADP-ribosylation factor-like 3	-5.00	0.13
242727_at	**ARL5B**	221079	ADP-ribosylation factor-like 5B	27.21	0.00
225707_at	**ARL6IP6**	151188	ADP-ribosylation-like factor 6 interacting protein 6	-4.56	0.06

222442_s_at	**ARL8B**	55207	ADP-ribosylation factor-like 8B	4.89	0.00
217858_s_at	**ARMCX3**	51566	armadillo repeat containing, X-linked 3	8.38	0.00
214749_s_at	**ARMCX6**	54470	armadillo repeat containing, X-linked 6	6.20	0.22
202655_at	**ARMET**	7873	arginine-rich, mutated in early stage tumors	2.53	0.22
230619_at	**ARNT**	405	aryl hydrocarbon receptor nuclear translocator	-2.14	0.22
209824_s_at	**ARNTL**	406	aryl hydrocarbon receptor nuclear translocator-like	-4.45	0.37
221482_s_at	**ARPP-19**	10776	cyclic AMP phosphoprotein, 19 kD	-2.28	0.13
226055_at	**ARRDC2**	27106	arrestin domain containing 2	5.48	0.03
224797_at	**ARRDC3**	57561	arrestin domain containing 3	-3.26	0.03
204443_at	**ARSA**	410	arylsulfatase A	-2.15	0.22
232197_x_at	**ARSB**	411	arylsulfatase B	5.86	0.00
1552632_a_at	**ARSG**	22901	arylsulfatase G	-4.85	0.13
1570479_at	**ART1**	417	ADP-ribosyltransferase 1	4.60	0.58
227135_at	**ASAHL**	27163	N-acylsphingosine amidohydrolase (acid ceramidase)-like	-15.71	0.00
219996_at	**ASB7**	140460	ankyrin repeat and SOCS box-containing 7	-2.80	0.58
226861_at	**ASB8**	140461	ankyrin repeat and SOCS box-containing 8	-2.10	0.00
1554627_a_at	**ASCC1**	51008	activating signal cointegrator 1 complex subunit 1	2.85	0.58
209988_s_at	**ASCL1**	429	achaete-scute complex homolog 1 (Drosophila)	2.61	0.06
209517_s_at	**ASH2L**	9070	ash2 (absent, small, or homeotic)-like (Drosophila)	-4.50	0.03
217987_at	**ASNSD1**	54529	asparagine synthetase domain containing 1	-2.45	0.22
202672_s_at	**ATF3**	467	activating transcription factor 3	14.57	0.06
204998_s_at	**ATF5**	22809	activating transcription factor 5	15.14	0.00
226941_at	**ATF6**	22926	activating transcription factor 6	-2.75	0.10
229389_at	**ATG16L2**	89849	ATG16 autophagy related 16-like 2 (S. cerevisiae)	-6.15	0.00
219164_s_at	**ATG2B**	55102	ATG2 autophagy related 2 homolog B (S. cerevisiae)	-4.28	0.58
224025_s_at	**ATG7**	10533	ATG7 autophagy related 7 homolog (S. cerevisiae)	5.64	0.00
202492_at	**ATG9A**	79065	ATG9 autophagy related 9 homolog A (S. cerevisiae)	-4.70	0.03
219359_at	**ATHL1**	80162	ATH1, acid trehalase-like 1 (yeast)	-3.65	0.00
212672_at	**ATM**	472	ataxia telangiectasia mutated	-6.10	0.03
208442_s_at	**ATM /// LOC651610**	472 /// 651610	ataxia telangiectasia mutated /// similar to Serine-protein kinase ATM (Ataxia telangiectasia mutated) (A-T, mutated)	-3.71	0.37
228890_at	**ATOH8**	84913	atonal homolog 8 (Drosophila)	13.29	0.10
238811_at	**ATP11B**	23200	ATPase, Class VI, type 11B	-3.09	0.00
219558_at	**ATP13A3**	79572	ATPase type 13A3	11.24	0.00
243585_at	**ATP13A5**	344905	ATPase type 13A5	2.74	0.22
220948_s_at	**ATP1A1**	476	ATPase, Na+/K+ transporting, alpha 1 polypeptide	4.99	0.00
201243_s_at	**ATP1B1**	481	ATPase, Na+/K+ transporting, beta 1 polypeptide	4.21	0.37
208836_at	**ATP1B3**	483	ATPase, Na+/K+ transporting, beta 3 polypeptide	5.62	0.13
209186_at	**ATP2A2**	488	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	2.42	0.06
213036_x_at	**ATP2A3**	489	ATPase, Ca++ transporting, ubiquitous	-5.57	0.00
215716_s_at	**ATP2B1**	490	ATPase, Ca++ transporting, plasma membrane 1	2.53	0.00
212136_at	**ATP2B4**	493	ATPase, Ca++ transporting, plasma membrane 4	-4.04	0.13

209492_x_at	**ATP5I**	521	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	-2.12	0.37
207809_s_at	**ATP6AP1**	537	ATPase, H+ transporting, lysosomal accessory protein 1	2.45	0.37
202874_s_at	**ATP6V1C1**	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	4.68	0.00
208899_x_at	**ATP6V1D**	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	3.68	0.00
201527_at	**ATP6V1F**	9296	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	3.19	0.10
208737_at	**ATP6V1G1**	9550	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	3.98	0.00
221504_s_at	**ATP6V1H**	51606	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	3.03	0.22
218671_s_at	**ATPIF1**	93974	ATPase inhibitory factor 1	-3.23	0.13
205539_at	**AVIL**	10677	advillin	-3.29	0.58
225557_at	**AXUD1**	64651	AXIN1 up-regulated 1	2.40	0.00
227889_at	**AYTL1**	54947	acyltransferase like 1	-2.20	0.37
201818_at	**AYTL2**	79888	acyltransferase like 2	2.67	0.00
201772_at	**AZIN1**	51582	antizyme inhibitor 1	3.68	0.06
1554835_a_at	**B3GNT5**	84002	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	5.71	0.00
212876_at	**B4GALT4**	8702	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	3.62	0.22
203304_at	**BAMBI**	25805	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	2.06	0.06
205965_at	**BATF**	10538	basic leucine zipper transcription factor, ATF-like	12.02	0.00
228439_at	**BATF2**	116071	basic leucine zipper transcription factor, ATF-like 2	18.88	0.00
203080_s_at	**BAZ2B**	29994	bromodomain adjacent to zinc finger domain, 2B	-3.35	0.06
200837_at	**BCAP31**	10134	B-cell receptor-associated protein 31	-3.08	0.10
214452_at	**BCAT1**	586	branched chain aminotransferase 1, cytosolic	41.65	0.13
219498_s_at	**BCL11A**	53335	B-cell CLL/lymphoma 11A (zinc finger protein)	4.14	0.37
225606_at	**BCL2L11**	10018	BCL2-like 11 (apoptosis facilitator)	-4.62	0.06
227616_at	**BCL9L**	283149	B-cell CLL/lymphoma 9-like	8.23	0.00
219433_at	**BCOR**	54880	BCL6 co-repressor	3.21	0.00
201169_s_at	**BHLHB2**	8553	basic helix-loop-helix domain containing, class B, 2	4.73	0.00
229437_at	**BIC**	114614	BIC transcript	10.64	0.10
213154_s_at	**BICD2**	23299	bicaudal D homolog 2 (Drosophila)	-5.52	0.00
211725_s_at	**BID**	637	BH3 interacting domain death agonist	2.04	0.00
219191_s_at	**BIN2**	51411	bridging integrator 2	-2.35	0.00
210538_s_at	**BIRC3**	330	baculoviral IAP repeat-containing 3	6.18	0.10
225858_s_at	**BIRC4**	331	baculoviral IAP repeat-containing 4	2.82	0.13
203840_at	**BLZF1**	8548	basic leucine zipper nuclear factor 1 (JEM-1)	2.08	0.37
226530_at	**BMF**	90427	Bcl2 modifying factor	9.46	0.00
214716_at	**BMP2K**	55589	BMP2 inducible kinase	-5.15	0.13
221478_at	**BNIP3L**	665	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-2.24	0.00
205557_at	**BPI**	671	bactericidal/permeability-increasing protein	-2.32	0.58
229436_x_at	**BRCC3**	79184	BRCA1/BRCA2-containing complex, subunit 3	-5.11	0.58
204520_x_at	**BRD1**	23774	bromodomain containing 1	-2.40	0.13
202227_s_at	**BRD8**	10902	bromodomain containing 8	-9.47	0.58
205715_at	**BST1**	683	bone marrow stromal cell antigen 1	-6.04	0.13
226963_at	**BTF3L4**	91408	basic transcription factor 3-like 4	2.19	0.10
213134_x_at	**BTG3**	10950	BTG family, member 3	57.73	0.10

205504_at	**BTK**	695	Bruton agammaglobulinemia tyrosine kinase	-2.68	0.58
205298_s_at	**BTN2A2**	10385	butyrophilin, subfamily 2, member A2	3.02	0.37
217207_s_at	**BTNL3**	10917	butyrophilin-like 3	-2.44	0.22
225866_at	**BXDC1**	84154	brix domain containing 1	14.34	0.22
228068_at	**C10orf132**	401647	chromosome 10 open reading frame 132	-2.02	0.13
225192_at	**C10orf46**	143384	chromosome 10 open reading frame 46	-3.22	0.00
225373_at	**C10orf54**	64115	chromosome 10 open reading frame 54	-2.39	0.00
1557531_a_at	**C10orf55**	414236	chromosome 10 open reading frame 55	65.19	0.13
236027_at	**C10orf78**	119392	chromosome 10 open reading frame 78	3.37	0.13
222617_s_at	**C10orf84**	63877	chromosome 10 open reading frame 84	-4.40	0.06
218213_s_at	**C11orf10**	746	chromosome 11 open reading frame 10	2.75	0.00
220987_s_at	**C11orf17** /// **NUAK2**	56672 /// 81788	chromosome 11 open reading frame 17 /// NUAK family, SNF1-like kinase, 2	-28.48	0.00
220560_at	**C11orf21**	29125	chromosome 11 open reading frame 21	-18.65	0.37
219012_s_at	**C11orf30**	56946	chromosome 11 open reading frame 30	-2.53	0.06
212560_at	**C11orf32**	442871	chromosome 11 open reading frame 32	-21.50	0.00
229851_s_at	**C11orf54**	28970	chromosome 11 open reading frame 54	-4.32	0.03
219806_s_at	**C11orf75**	56935	chromosome 11 open reading frame 75	8.19	0.00
220060_s_at	**C12orf48**	55010	chromosome 12 open reading frame 48	4.18	0.10
1553142_at	**C13orf31**	144811	chromosome 13 open reading frame 31	14.31	0.00
223215_s_at	**C14orf100**	51528	chromosome 14 open reading frame 100	-2.54	0.03
213246_at	**C14orf109**	26175	chromosome 14 open reading frame 109	3.01	0.00
223239_at	**C14orf129**	51527	chromosome 14 open reading frame 129	-3.50	0.13
218940_at	**C14orf138**	79609	chromosome 14 open reading frame 138	-14.55	0.06
218298_s_at	**C14orf159**	80017	chromosome 14 open reading frame 159	-7.10	0.03
1563524_a_at	**C14orf85**	319085	chromosome 14 open reading frame 85	-13.09	0.37
218383_at	**C14orf94**	54930	chromosome 14 open reading frame 94	-14.57	0.00
1552310_at	**C15orf40**	123207	chromosome 15 open reading frame 40	-2.98	0.13
223484_at	**C15orf48**	84419	chromosome 15 open reading frame 48	450.80	0.00
229908_s_at	**C16orf28**	65259	chromosome 16 open reading frame 28	2.00	0.10
1559584_a_at	**C16orf54** /// **hCG_1644884**	283897 /// 728070	chromosome 16 open reading frame 54 /// similar to chromosome 16 open reading frame 54	-7.14	0.00
218060_s_at	**C16orf57**	79650	chromosome 16 open reading frame 57	-2.04	0.37
218447_at	**C16orf61**	56942	chromosome 16 open reading frame 61	9.94	0.03
228452_at	**C17orf39**	79018	chromosome 17 open reading frame 39	-3.46	0.37
227668_at	**C17orf56**	146705	chromosome 17 open reading frame 56	-3.10	0.13
218130_at	**C17orf62**	79415	chromosome 17 open reading frame 62	-4.63	0.37
218896_s_at	**C17orf85**	55421	chromosome 17 open reading frame 85	-2.64	0.58
227881_s_at	**C18orf17**	125488	Chromosome 18 open reading frame 17	3.08	0.03
1553934_at	**C18orf20**	221241	chromosome 18 open reading frame 20	6.13	0.13
220178_at	**C19orf28**	126321	chromosome 19 open reading frame 28	3.48	0.10
235515_at	**C19orf46**	163183	chromosome 19 open reading frame 46	2.21	0.22
1553162_x_at	**C19orf55**	148137	chromosome 19 open reading frame 55	-2.25	0.58
235568_at	**C19orf59**	199675	chromosome 19 open reading frame 59	2.41	0.00
51200_at	**C19orf60**	55049	chromosome 19 open reading frame 60	-6.43	0.10
221335_x_at	**C19orf61**	56006	chromosome 19 open reading frame 61	2.85	0.00
219283_at	**C1GALT1C1**	29071	C1GALT1-specific chaperone 1	-3.44	0.22
220193_at	**C1orf113**	79729	chromosome 1 open reading frame 113	16.00	0.06
223123_s_at	**C1orf128**	57095	chromosome 1 open reading frame 128	-2.12	0.22
221182_at	**C1orf129**	80133	chromosome 1 open reading frame 129	2.35	0.22
212003_at	**C1orf144**	26099	chromosome 1 open reading frame 144	2.07	0.13
213528_at	**C1orf156**	92342	chromosome 1 open reading frame 156	-2.23	0.58
241809_at	**C1orf183**	55924	chromosome 1 open reading frame 183	-10.73	0.00
1559638_at	**C1orf200**	644997	chromosome 1 open reading frame 200	2.66	0.22

1559376_at	**C1orf203**	84852	chromosome 1 open reading frame 203	4.23	0.00
225638_at	**C1orf31**	388753	chromosome 1 open reading frame 31	7.36	0.00
241908_at	**C1orf58**	148362	Chromosome 1 open reading frame 58	-2.25	0.58
225841_at	**C1orf59**	113802	chromosome 1 open reading frame 59	-5.63	0.22
222301_at	**C1orf61**	10485	Chromosome 1 open reading frame 61	9.05	0.10
1554660_a_at	**C1orf71**	163882	chromosome 1 open reading frame 71	3.67	0.58
225904_at	**C1orf96**	126731	chromosome 1 open reading frame 96	-2.95	0.10
218983_at	**C1RL**	51279	complement component 1, r subcomponent-like	-3.26	0.00
1552687_a_at	**C20orf152**	140894	chromosome 20 open reading frame 152	2.34	0.13
231991_at	**C20orf160**	140706	chromosome 20 open reading frame 160	24.92	0.03
1567035_at	**C20orf181**	140843	chromosome 20 open reading frame 181	3.40	0.10
218586_at	**C20orf20**	55257	chromosome 20 open reading frame 20	3.16	0.13
206656_s_at	**C20orf3**	57136	chromosome 20 open reading frame 3	-4.74	0.00
220888_s_at	**C20orf32**	57091	chromosome 20 open reading frame 32	-31.93	0.22
225890_at	**C20orf72**	92667	chromosome 20 open reading frame 72	-3.05	0.58
223360_at	**C21orf56**	84221	chromosome 21 open reading frame 56	-3.06	0.03
244369_at	**C21orf59**	56683	chromosome 21 open reading frame 59	2.02	0.58
1556072_at	**C22orf37**	200298	chromosome 22 open reading frame 37	3.73	0.03
217118_s_at	**C22orf9**	23313	chromosome 22 open reading frame 9	-3.04	0.37
1552740_at	**C2orf15**	150590	chromosome 2 open reading frame 15	2.00	0.03
200070_at	**C2orf24**	27013	chromosome 2 open reading frame 24	-3.44	0.03
226951_at	**C2orf49**	79074	chromosome 2 open reading frame 49	-2.32	0.37
219065_s_at	**C2orf4P** /// **MEMO1**	51072 /// 728556 /// 7795	Methylation modifier for class I HLA /// mediator of cell motility 1 /// C2orf4 pseudogene	-4.61	0.06
225799_at	**C2orf59** /// **LOC541471**	112597 /// 541471	chromosome 2 open reading frame 59 /// hypothetical LOC541471	-2.71	0.00
209906_at	**C3AR1**	719	complement component 3a receptor 1	8.21	0.00
1553158_at	**C3orf34**	84984	chromosome 3 open reading frame 34	-7.54	0.00
227599_at	**C3orf59**	151963	chromosome 3 open reading frame 59	7.28	0.58
219023_at	**C4orf16**	55435	chromosome 4 open reading frame 16	6.81	0.06
229152_at	**C4orf7**	260436	chromosome 4 open reading frame 7	2.01	0.06
203024_s_at	**C5orf15**	56951	chromosome 5 open reading frame 15	2.32	0.06
1552386_at	**C5orf29**	202309	chromosome 5 open reading frame 29	2.35	0.10
217925_s_at	**C6orf106**	64771	chromosome 6 open reading frame 106	2.16	0.00
232492_at	**C6orf112**	154442	chromosome 6 open reading frame 112	2.31	0.37
223361_at	**C6orf115**	58527	chromosome 6 open reading frame 115	2.94	0.10
212923_s_at	**C6orf145**	221749	chromosome 6 open reading frame 145	10.08	0.06
236178_at	**C6orf162**	57150	chromosome 6 open reading frame 162	-5.52	0.58
220904_at	**C6orf208**	80069	chromosome 6 open reading frame 208	2.31	0.06
225576_at	**C6orf72**	116254	chromosome 6 open reading frame 72	-3.71	0.37
224987_at	**C6orf89**	221477	chromosome 6 open reading frame 89	2.03	0.13
221573_at	**C7orf25**	79020	chromosome 7 open reading frame 25	-5.19	0.37
226385_s_at	**C7orf30**	115416	chromosome 7 open reading frame 30	-2.44	0.22
226018_at	**C7orf41**	222166	chromosome 7 open reading frame 41	-9.58	0.06
220659_s_at	**C7orf43**	55262	chromosome 7 open reading frame 43	-2.41	0.00
206497_at	**C7orf44**	55744	chromosome 7 open reading frame 44	-2.72	0.37
1557866_at	**C9orf117**	286207	chromosome 9 open reading frame 117	2.63	0.00
1559340_at	**C9orf148**	401550	chromosome 9 open reading frame 148	2.00	0.37
225602_at	**C9orf19**	152007	chromosome 9 open reading frame 19	-3.72	0.00
232270_at	**C9orf3**	84909	Chromosome 9 open reading frame 3	2.44	0.22
1553756_at	**C9orf70**	84850	chromosome 9 open reading frame 70	2.46	0.37
223398_at	**C9orf89**	84270	chromosome 9 open reading frame 89	3.47	0.13
221865_at	**C9orf91**	203197	chromosome 9 open reading frame 91	8.11	0.03

203963_at	**CA12**	771	carbonic anhydrase XII	2.80	0.13
209301_at	**CA2**	760	carbonic anhydrase II	2.18	0.13
217873_at	**CAB39**	51719	calcium binding protein 39	-2.00	0.03
218168_s_at	**CABC1**	56997	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	-11.68	0.00
37652_at	**CABIN1**	23523	calcineurin binding protein 1	-5.61	0.13
209563_x_at	**CALM1**	801	calmodulin 1 (phosphorylase kinase, delta)	-2.19	0.03
212953_x_at	**CALR**	811	calreticulin	3.17	0.06
200757_s_at	**CALU**	813	calumenin	3.28	0.03
235626_at	**CAMK1D**	57118	calcium/calmodulin-dependent protein kinase ID	-13.30	0.00
226382_at	**CAMK1D** /// **LOC283070**	283070 /// 57118	calcium/calmodulin-dependent protein kinase ID /// hypothetical protein LOC283070	-12.35	0.37
34846_at	**CAMK2B**	816	Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	-2.04	0.03
212757_s_at	**CAMK2G**	818	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-7.19	0.00
241871_at	**CAMK4**	814	calcium/calmodulin-dependent protein kinase IV	2.57	0.10
210244_at	**CAMP**	820	cathelicidin antimicrobial peptide	-20.38	0.10
221732_at	**CANT1**	124583	calcium activated nucleotidase 1	-2.15	0.13
208852_s_at	**CANX**	821	calnexin	4.57	0.00
213798_s_at	**CAP1**	10487	CAP, adenylate cyclase-associated protein 1 (yeast)	-2.15	0.03
200752_s_at	**CAPN1**	823	calpain 1, (mu/I) large subunit	-2.88	0.13
220599_s_at	**CARD14**	79092	caspase recruitment domain family, member 14	-2.20	0.37
228641_at	**CARD8**	22900	caspase recruitment domain family, member 8	-2.37	0.22
218153_at	**CARS2**	79587	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	-3.13	0.00
224619_at	**CASC4**	113201	cancer susceptibility candidate 4	-4.12	0.00
208050_s_at	**CASP2**	835	caspase 2, apoptosis-related cysteine peptidase (neural precursor cell expressed, developmentally down-regulated 2)	-5.27	0.13
207500_at	**CASP5**	838	caspase 5, apoptosis-related cysteine peptidase	5.90	0.00
207181_s_at	**CASP7**	840	caspase 7, apoptosis-related cysteine peptidase	2.89	0.37
213373_s_at	**CASP8**	841	caspase 8, apoptosis-related cysteine peptidase	-3.74	0.00
207317_s_at	**CASQ2**	845	calsequestrin 2 (cardiac muscle)	3.04	0.06
238363_at	**CAT**	847	Catalase	-11.06	0.00
216903_s_at	**CBARA1**	10367	calcium binding atopy-related autoantigen 1	2.66	0.10
208056_s_at	**CBFA2T3**	863	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	-53.82	0.00
212816_s_at	**CBS**	875	cystathionine-beta-synthase	-3.73	0.00
226193_x_at	**CBWD1**	55871	COBW domain containing 1	-2.87	0.06
201518_at	**CBX1**	10951	chromobox homolog 1 (HP1 beta homolog Drosophila)	-3.22	0.00
200037_s_at	**CBX3** /// **LOC653972**	11335 /// 653972	chromobox homolog 3 (HP1 gamma homolog, Drosophila) /// similar to chromobox homolog 3	-2.10	0.13
212914_at	**CBX7**	23492	chromobox homolog 7	-9.88	0.03
229063_s_at	**CCDC107**	203260	coiled-coil domain containing 107	2.95	0.58
235208_at	**CCDC112**	153733	coiled-coil domain containing 112	-8.96	0.06
229082_at	**CCDC125**	202243	coiled-coil domain containing 125	-7.22	0.06
1554023_s_at	**CCDC13**	152206	coiled-coil domain containing 13	-5.89	0.00
1557366_at	**CCDC144B**	284047	coiled-coil domain containing 144B	-2.61	0.22
220308_at	**CCDC19**	25790	coiled-coil domain containing 19	-3.45	0.10
209479_at	**CCDC28A**	25901	coiled-coil domain containing 28A	-7.16	0.00

218655_s_at	**CCDC49**	54883	coiled-coil domain containing 49	2.14	0.37
212886_at	**CCDC69**	26112	coiled-coil domain containing 69	-2.04	0.10
223301_s_at	**CCDC82**	79780	coiled-coil domain containing 82	2.29	0.58
209689_at	**CCDC93**	54520	coiled-coil domain containing 93	4.67	0.00
210133_at	**CCL11**	6356	chemokine (C-C motif) ligand 11	2.84	0.03
209924_at	**CCL18**	6362	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	16.71	0.10
216598_s_at	**CCL2**	6347	chemokine (C-C motif) ligand 2	67.78	0.00
205476_at	**CCL20**	6364	chemokine (C-C motif) ligand 20	423.34	0.00
210548_at	**CCL23**	6368	chemokine (C-C motif) ligand 23	9.94	0.22
205114_s_at	**CCL3** /// **CCL3L1** /// **CCL3L3** /// **LOC728830** /// **LOC730422**	414062 /// 6348 /// 6349 /// 728830 /// 730422	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3 /// similar to Small inducible cytokine A3-like 1 precursor (Tonsillar lymphocyte LD78 beta protein) (LD78-beta(1-70)) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2) /// similar to chemokine (C-C motif) ligand 3-like 3	8.29	0.00
204103_at	**CCL4**	6351	chemokine (C-C motif) ligand 4	30.32	0.00
204655_at	**CCL5**	6352	chemokine (C-C motif) ligand 5	4.89	0.37
223164_at	**CCM2**	83605	cerebral cavernous malformation 2	-12.96	0.03
201700_at	**CCND3**	896	cyclin D3	-3.99	0.00
223084_s_at	**CCNDBP1**	23582	cyclin D-type binding-protein 1	-5.23	0.00
202769_at	**CCNG2**	901	cyclin G2	-2.69	0.00
219227_at	**CCNJL**	79616	cyclin J-like	-31.82	0.00
204645_at	**CCNT2**	905	cyclin T2	2.20	0.13
224652_at	**CCNY**	219771	cyclin Y	-5.60	0.00
214151_s_at	**CCPG1**	9236	cell cycle progression 1	-14.10	0.00
206991_s_at	**CCR5**	1234	chemokine (C-C motif) receptor 5	23.95	0.00
206337_at	**CCR7**	1236	chemokine (C-C motif) receptor 7	50.58	0.58
211434_s_at	**CCRL2** /// **LOC727811**	727811 /// 9034	chemokine (C-C motif) receptor-like 2 /// similar to chemokine (C-C motif) receptor-like 2	118.66	0.00
227301_at	**CCT6AP1**	643253	chaperonin containing TCP1, subunit 6A (zeta 1) pseudogene 1	-2.67	0.37
200873_s_at	**CCT8**	10694	chaperonin containing TCP1, subunit 8 (theta)	2.13	0.37
215049_x_at	**CD163**	9332	CD163 molecule	8.56	0.22
217422_s_at	**CD22** /// **MAG**	4099 /// 933	CD22 molecule /// myelin associated glycoprotein	36.76	0.00
209771_x_at	**CD24**	934	CD24 molecule	-2.95	0.22
223834_at	**CD274**	29126	CD274 molecule	7.10	0.00
1553043_a_at	**CD300LF**	146722	CD300 molecule-like family member f	-3.03	0.03
203799_at	**CD302**	9936	CD302 molecule	-31.89	0.00
205692_s_at	**CD38**	952	CD38 molecule	2.45	0.22
35150_at	**CD40**	958	CD40 molecule, TNF receptor superfamily member 5	2.10	0.10
210916_s_at	**CD44**	960	CD44 molecule (Indian blood group)	5.15	0.00
207549_x_at	**CD46**	4179	CD46 molecule, complement regulatory protein	-3.97	0.00
237759_at	**CD48**	962	CD48 molecule	16.70	0.00
34210_at	**CD52**	1043	CD52 molecule	-5.52	0.00
222061_at	**CD58**	965	CD58 molecule	2.02	0.10
203507_at	**CD68**	968	CD68 molecule	6.97	0.00
209795_at	**CD69**	969	CD69 molecule	17.88	0.13
1567627_at	**CD74**	972	CD74 molecule, major histocompatibility complex, class II invariant chain	2.72	0.00
1554519_at	**CD80**	941	CD80 molecule	6.48	0.00
203904_x_at	**CD82**	3732	CD82 molecule	4.42	0.06

204440_at	**CD83**	9308	CD83 molecule	60.66	0.00
202878_s_at	**CD93**	22918	CD93 molecule	-2.07	0.13
202910_s_at	**CD97**	976	CD97 molecule	-3.17	0.06
205627_at	**CDA**	978	cytidine deaminase	-14.02	0.22
201725_at	**CDC123**	8872	cell division cycle 123 homolog (S. cerevisiae)	-4.75	0.00
210441_at	**CDC14A**	8556	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	2.09	0.22
212899_at	**CDC2L6**	23097	cell division cycle 2-like 6 (CDK8-like)	-3.59	0.10
212540_at	**CDC34**	997	cell division cycle 34 homolog (S. cerevisiae)	-2.96	0.58
203376_at	**CDC40**	51362	cell division cycle 40 homolog (S. cerevisiae)	-2.11	0.13
203968_s_at	**CDC6**	990	cell division cycle 6 homolog (S. cerevisiae)	3.46	0.00
226056_at	**CDGAP**	57514	Cdc42 GTPase-activating protein	16.03	0.00
203440_at	**CDH2**	1000	cadherin 2, type 1, N-cadherin (neuronal)	-2.70	0.13
201253_s_at	**CDIPT**	10423	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	-4.53	0.00
211804_s_at	**CDK2**	1017	cyclin-dependent kinase 2	2.33	0.37
201938_at	**CDK2AP1**	8099	CDK2-associated protein 1	-6.89	0.00
218740_s_at	**CDK5RAP3**	80279	CDK5 regulatory subunit associated protein 3	-2.68	0.22
202284_s_at	**CDKN1A**	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	42.61	0.00
209112_at	**CDKN1B**	1027	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-4.90	0.00
218929_at	**CDKN2AIP**	55602	CDKN2A interacting protein	-4.06	0.58
209498_at	**CEACAM1**	634	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	2.77	0.03
206676_at	**CEACAM8**	1088	carcinoembryonic antigen-related cell adhesion molecule 8	-3.25	0.22
203973_s_at	**CEBPD**	1052	CCAAT/enhancer binding protein (C/EBP), delta	-2.41	0.00
203341_at	**CEBPZ**	10153	CCAAT/enhancer binding protein zeta	2.54	0.37
231772_x_at	**CENPH**	64946	centromere protein H	2.07	0.58
205212_s_at	**CENTB1**	9744	centaurin, beta 1	-3.30	0.00
213618_at	**CENTD1**	116984	centaurin, delta 1	3.29	0.22
218950_at	**CENTD3**	64411	centaurin, delta 3	-2.20	0.06
225789_at	**CENTG3**	116988	centaurin, gamma 3	5.29	0.00
207719_x_at	**CEP170**	9859	centrosomal protein 170kDa	2.66	0.58
222151_s_at	**CEP63**	80254	centrosomal protein 63kDa	-7.34	0.00
212675_s_at	**CEP68**	23177	centrosomal protein 68kDa	2.11	0.13
1561884_at	**CEPT1**	10390	choline/ethanolamine phosphotransferase 1	3.32	0.58
209194_at	**CETN2**	1069	centrin, EF-hand protein, 2	-2.54	0.13
202357_s_at	**CFB**	629	complement factor B	34.28	0.00
203166_at	**CFDP1**	10428	craniofacial development protein 1	2.80	0.00
224663_s_at	**CFL2**	1073	cofilin 2 (muscle)	5.47	0.37
213375_s_at	**CG018**	90634	hypothetical gene CG018	5.86	0.37
229595_at	**CHCHD4**	131474	coiled-coil-helix-coiled-coil-helix domain containing 4	-7.02	0.58
243751_at	**CHD2**	1106	Chromodomain helicase DNA binding protein 2	-2.64	0.22
219049_at	**ChGn**	55790	chondroitin beta1,4 N-acetylgalactosaminyltransferase	-5.43	0.06
213060_s_at	**CHI3L2**	1117	chitinase 3-like 2	29.64	0.00
210069_at	**CHKB** /// **CPT1B**	1120 /// 1375	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	-2.33	0.37
218178_s_at	**CHMP1B**	57132	chromatin modifying protein 1B	-3.56	0.10
202536_at	**CHMP2B**	25978	chromatin modifying protein 2B	2.29	0.00
239436_at	**CHORDC1**	26973	Cysteine and histidine-rich domain (CHORD)-containing 1	-4.05	0.03
221675_s_at	**CHPT1**	56994	choline phosphotransferase 1	-5.51	0.00

206533_at	**CHRNA5**	1138	cholinergic receptor, nicotinic, alpha 5	2.13	0.37
206756_at	**CHST7**	56548	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	4.10	0.00
203044_at	**CHSY1**	22856	carbohydrate (chondroitin) synthase 1	-3.47	0.00
212784_at	**CIC**	23152	capicua homolog (Drosophila)	-2.88	0.00
230142_s_at	**CIRBP**	1153	cold inducible RNA binding protein	-3.01	0.03
219161_s_at	**CKLF**	51192	chemokine-like factor	-2.79	0.00
206207_at	**CLC**	1178	Charcot-Leyden crystal protein	-5.87	0.03
228335_at	**CLDN11**	5010	claudin 11 (oligodendrocyte transmembrane protein)	6.91	0.58
1552398_a_at	**CLEC12A**	160364	C-type lectin domain family 12, member A	-2.87	0.10
233500_x_at	**CLEC2D**	29121	C-type lectin domain family 2, member D	2.62	0.58
1552552_s_at	**CLEC4C**	170482	C-type lectin domain family 4, member C	-6.30	0.58
222934_s_at	**CLEC4E**	26253	C-type lectin domain family 4, member E	2.13	0.00
219890_at	**CLEC5A**	23601	C-type lectin domain family 5, member A	22.76	0.00
221881_s_at	**CLIC4**	25932	chloride intracellular channel 4	23.82	0.00
1558924_s_at	**CLIP1**	6249	CAP-GLY domain containing linker protein 1	-2.36	0.37
204809_at	**CLPX**	10845	ClpX caseinolytic peptidase X homolog (E. coli)	-5.08	0.13
201561_s_at	**CLSTN1**	22883	calsyntenin 1	-2.17	0.37
200960_x_at	**CLTA**	1211	clathrin, light chain (Lca)	2.08	0.37
206284_x_at	**CLTB**	1212	clathrin, light chain (Lcb)	-2.89	0.13
200614_at	**CLTC**	1213	clathrin, heavy chain (Hc)	2.09	0.10
1555738_at	**CMTM1**	113540	CKLF-like MARVEL transmembrane domain containing 1	-13.70	0.03
229967_at	**CMTM2**	146225	CKLF-like MARVEL transmembrane domain containing 2	-41.63	0.00
217752_s_at	**CNDP2**	55748	CNDP dipeptidase 2 (metallopeptidase M20 family)	2.33	0.37
223993_s_at	**CNIH4**	29097	cornichon homolog 4 (Drosophila)	-2.00	0.06
220739_s_at	**CNNM3**	26505	cyclin M3	-3.26	0.37
226153_s_at	**CNOT6L**	246175	CCR4-NOT transcription complex, subunit 6-like	-3.59	0.58
223796_at	**CNTNAP3 /// CNTNAP3B /// LOC728577**	389734 /// 728577 /// 79937	contactin associated protein-like 3 /// contactin associated protein-like 3B /// similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3)	-23.69	0.13
211809_x_at	**COL13A1**	1305	collagen, type XIII, alpha 1	13.24	0.00
1555953_at	**COL18A1**	80781	collagen, type XVIII, alpha 1	-4.63	0.06
209132_s_at	**COMMD4**	54939	COMM domain containing 4	3.02	0.00
202078_at	**COPS3**	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	-3.72	0.37
209083_at	**CORO1A**	11151	coronin, actin binding protein, 1A	-3.94	0.00
219040_at	**CORO7**	79585	coronin 7	-2.09	0.22
221059_s_at	**COTL1**	23406	coactosin-like 1 (Dictyostelium)	-3.18	0.00
203880_at	**COX17**	10063	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	2.92	0.00
231831_at	**COX19**	90639	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	-5.36	0.58
217451_at	**COX5A**	9377	cytochrome c oxidase subunit Va	4.71	0.58
204662_at	**CP110**	9738	CP110 protein	-2.21	0.37
229600_s_at	**CPD**	1362	Carboxypeptidase D	3.30	0.00
226939_at	**CPEB2**	132864	cytoplasmic polyadenylation element binding protein 2	-4.43	0.06
241706_at	**CPNE8**	144402	copine VIII	2.52	0.03
208488_s_at	**CR1**	1378	complement component (3b/4b) receptor 1 (Knops blood group)	-14.35	0.00

239205_s_at	**CR1** /// **CR1L** /// **LOC653907**	1378 /// 1379 /// 653907	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like /// similar to complement component (3b/4b) receptor 1 isoform F precursor	-16.83	0.13
212345_s_at	**CREB3L2**	64764	cAMP responsive element binding protein 3-like 2	7.52	0.00
205931_s_at	**CREB5**	9586	cAMP responsive element binding protein 5	-7.82	0.00
201200_at	**CREG1**	8804	cellular repressor of E1A-stimulated genes 1	3.43	0.10
209967_s_at	**CREM**	1390	cAMP responsive element modulator	35.14	0.00
221541_at	**CRISPLD2**	83716	cysteine-rich secretory protein LCCL domain containing 2	-26.68	0.00
208303_s_at	**CRLF2**	64109	cytokine receptor-like factor 2	5.32	0.37
205474_at	**CRLF3**	51379	cytokine receptor-like factor 3	-2.55	0.06
226307_at	**CRTC2**	200186	CREB regulated transcription coactivator 2	2.80	0.58
221139_s_at	**CSAD**	51380	cysteine sulfinic acid decarboxylase	-9.21	0.22
211286_x_at	**CSF2RA**	1438	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	-2.21	0.03
207442_at	**CSF3**	1440	colony stimulating factor 3 (granulocyte)	66.07	0.00
203591_s_at	**CSF3R**	1441	colony stimulating factor 3 receptor (granulocyte)	-3.76	0.00
221799_at	**CSGlcA-T**	54480	chondroitin sulfate glucuronyltransferase	-2.02	0.37
201360_at	**CST3**	1471	cystatin C (amyloid angiopathy and cerebral hemorrhage)	-2.96	0.03
210140_at	**CST7**	8530	cystatin F (leukocystatin)	-7.28	0.00
204971_at	**CSTA**	1475	cystatin A (stefin A)	-2.08	0.00
201201_at	**CSTB**	1476	cystatin B (stefin B)	2.00	0.00
229666_s_at	**CSTF3**	1479	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	6.54	0.00
218923_at	**CTBS**	1486	chitobiase, di-N-acetyl-	-2.61	0.00
202521_at	**CTCF**	10664	CCCTC-binding factor (zinc finger protein)	-2.50	0.03
217844_at	**CTDSP1**	58190	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	-2.85	0.03
203445_s_at	**CTDSP2**	10106	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-7.10	0.00
201904_s_at	**CTDSPL**	10217	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	2.52	0.13
1555106_a_at	**CTDSPL2**	51496	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	-4.35	0.37
221850_x_at	**CTGLF1** /// **CTGLF3** /// **CTGLF4** /// **CTGLF5** /// **CTGLF9P** /// **KIAA1975**	119016 /// 119385 /// 414189 /// 653268 /// 728005 /// 728404	centaurin, gamma-like family, member 1 /// KIAA1975 protein similar to MRIP2 /// centaurin, gamma-like family, member 3 /// centaurin, gamma-like family, member 4 /// centaurin, gamma-like family, member 9 pseudogene /// centaurin, gamma-like family, member 5	-3.71	0.58
200839_s_at	**CTSB**	1508	cathepsin B	3.31	0.10
201487_at	**CTSC**	1075	cathepsin C	-3.26	0.37
200766_at	**CTSD**	1509	cathepsin D	2.16	0.03
202295_s_at	**CTSH**	1512	cathepsin H	4.53	0.37
202087_s_at	**CTSL1**	1514	cathepsin L1	62.22	0.00

210074_at	**CTSL2**	1515	cathepsin L2	11.01	0.22
1555467_a_at	**CUGBP1**	10658	CUG triplet repeat, RNA binding protein 1	2.89	0.00
202157_s_at	**CUGBP2**	10659	CUG triplet repeat, RNA binding protein 2	-5.56	0.00
202213_s_at	**CUL4B**	8450	cullin 4B	-4.92	0.03
204470_at	**CXCL1**	2919	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	4.00	0.00
204533_at	**CXCL10**	3627	chemokine (C-X-C motif) ligand 10	28.49	0.10
210163_at	**CXCL11**	6373	chemokine (C-X-C motif) ligand 11	3.31	0.06
223454_at	**CXCL16**	58191	chemokine (C-X-C motif) ligand 16	2.39	0.00
209774_x_at	**CXCL2**	2920	chemokine (C-X-C motif) ligand 2	14.67	0.00
207850_at	**CXCL3**	2921	chemokine (C-X-C motif) ligand 3	185.85	0.22
214974_x_at	**CXCL5**	6374	chemokine (C-X-C motif) ligand 5	78.45	0.37
1553457_at	**CXorf62**	439943	chromosome X open reading frame 62	2.04	0.22
224735_at	**CYBASC3**	220002	cytochrome b, ascorbate dependent 3	4.41	0.03
203922_s_at	**CYBB**	1536	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	3.70	0.03
214272_at	**CYLD**	1540	cylindromatosis (turban tumor syndrome)	4.44	0.00
205676_at	**CYP27B1**	1594	cytochrome P450, family 27, subfamily B, polypeptide 1	6.55	0.22
210452_x_at	**CYP4F2**	8529	cytochrome P450, family 4, subfamily F, polypeptide 2	-7.34	0.00
206514_s_at	**CYP4F2** /// **CYP4F3**	4051 /// 8529	cytochrome P450, family 4, subfamily F, polypeptide 3 /// cytochrome P450, family 4, subfamily F, polypeptide 2	-9.49	0.00
206515_at	**CYP4F3**	4051	cytochrome P450, family 4, subfamily F, polypeptide 3	-7.74	0.00
231747_at	**CYSLTR1**	10800	cysteinyl leukotriene receptor 1	-4.26	0.06
220813_at	**CYSLTR2**	57105	cysteinyl leukotriene receptor 2	-6.11	0.10
200046_at	**DAD1**	1603	defender against cell death 1	2.33	0.00
201095_at	**DAP**	1611	death-associated protein	2.74	0.13
206324_s_at	**DAPK2**	23604	death-associated protein kinase 2	-14.57	0.00
201624_at	**DARS**	1615	aspartyl-tRNA synthetase	3.00	0.58
223001_at	**DC2**	58505	DC2 protein	7.87	0.00
216725_at	**DCLK2**	166614	Doublecortin-like kinase 2	-2.13	0.00
225443_at	**DCP1A**	55802	DCP1 decapping enzyme homolog A (S. cerevisiae)	4.28	0.03
235258_at	**DCP2**	167227	DCP2 decapping enzyme homolog (S. cerevisiae)	-2.46	0.10
239648_at	**DCUN1D3**	123879	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	6.13	0.00
224796_at	**DDEF1**	50807	development and differentiation enhancing factor 1	-2.19	0.00
225970_at	**DDHD1**	80821	DDHD domain containing 1	3.19	0.58
209383_at	**DDIT3**	1649	DNA-damage-inducible transcript 3	2.75	0.00
202887_s_at	**DDIT4**	54541	DNA-damage-inducible transcript 4	15.95	0.00
208897_s_at	**DDX18**	8886	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	3.60	0.03
208152_s_at	**DDX21**	9188	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	4.86	0.00
227485_at	**DDX26B**	203522	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	-4.24	0.03
201584_s_at	**DDX39**	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	4.92	0.37
226659_at	**DEF6**	50619	differentially expressed in FDCP 6 homolog (mouse)	-16.37	0.37
219646_at	**DEF8**	54849	differentially expressed in FDCP 8 homolog (mouse)	-4.56	0.10
205033_s_at	**DEFA1** /// **DEFA3** /// **LOC728358**	1667 /// 1668 /// 728358	defensin, alpha 1 /// defensin, alpha 3, neutrophil-specific	-3.44	0.03
1568377_x_at	**DEFB124**	245937	defensin, beta 124	4.23	0.22

221081_s_at	**DENND2D**	79961	DENN/MADD domain containing 2D	10.43	0.00
212975_at	**DENND3**	22898	DENN/MADD domain containing 3	-4.40	0.03
214787_at	**DENND4A**	10260	DENN/MADD domain containing 4A	8.56	0.13
221509_at	**DENR**	8562	density-regulated protein	-2.16	0.13
222543_at	**DERL1**	79139	Der1-like domain family, member 1	2.29	0.37
214198_s_at	**DGCR2**	9993	DiGeorge syndrome critical region gene 2	-3.86	0.10
208072_s_at	**DGKD**	8527	diacylglycerol kinase, delta 130kDa	-6.82	0.10
207556_s_at	**DGKZ**	8525	diacylglycerol kinase, zeta 104kDa	-6.85	0.37
204800_s_at	**DHRS12**	79758	dehydrogenase/reductase (SDR family) member 12	-4.57	0.06
210788_s_at	**DHRS7**	51635	dehydrogenase/reductase (SDR family) member 7	-2.85	0.00
219799_s_at	**DHRS9**	10170	dehydrogenase/reductase (SDR family) member 9	-9.88	0.00
227094_at	**DHTKD1**	55526	dehydrogenase E1 and transketolase domain containing 1	-13.39	0.10
203694_s_at	**DHX16**	8449	DEAH (Asp-Glu-Ala-His) box polypeptide 16	-2.87	0.37
223138_s_at	**DHX36**	170506	DEAH (Asp-Glu-Ala-His) box polypeptide 36	3.50	0.06
219364_at	**DHX58**	79132	DEXH (Asp-Glu-X-His) box polypeptide 58	4.58	0.37
205603_s_at	**DIAPH2**	1730	diaphanous homolog 2 (Drosophila)	5.66	0.00
206061_s_at	**DICER1**	23405	Dicer1, Dcr-1 homolog (Drosophila)	-2.27	0.00
1559326_at	**DIO3OS**	64150	deiodinase, iodothyronine, type III opposite strand	2.17	0.00
226026_at	**DIRC2**	84925	disrupted in renal carcinoma 2	-4.23	0.06
231886_at	**DKFZP434B2016**	642780	similar to hypothetical protein LOC284701	-5.60	0.00
211050_x_at	**DKFZP434B2016** /// **LOC643313**	642780 /// 643313	similar to hypothetical protein LOC284701	-2.19	0.00
235167_at	**DKFZp547E087**	283846	hypothetical gene LOC283846	-3.49	0.03
211996_s_at	**DKFZp547E087** /// **LOC23117** /// **LOC440345** /// **LOC440353** /// **LOC613037** /// **LOC728888**	23117 /// 283846 /// 440345 /// 440353 /// 613037 /// 728888	KIAA0220-like protein /// hypothetical gene LOC283846 /// hypothetical protein LOC440345 /// nuclear pore complex interacting protein pseudogene /// similar to Protein KIAA0220	2.26	0.22
214984_at	**087** /// **LOC440345** /// **LOC440354** /// **LOC595101** /// **LOC728423** /// **LOC730099** /// **SMG1**	23049 /// 283846 /// 440345 /// 440354 /// 595101 /// 728423 /// 730099	PI-3-kinase-related kinase SMG-1 /// hypothetical gene LOC283846 /// hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 pseudogene /// similar to PI-3-kinase-related kinase SMG-1	4.09	0.13
236079_at	**DKFZp667E0512**	202025	hypothetical protein DKFZp667E0512	-5.13	0.22
224740_at	**DKFZP686E2158**	643155	hypothetical protein LOC643155	2.79	0.13
231412_at	**DKFZp686L14188**	441366	hypothetical gene supported by BX538329	21.10	0.37

224215_s_at	**DLL1**	28514	delta-like 1 (Drosophila)	52.21	0.37
242940_x_at	**DLX6**	1750	distal-less homeobox 6	4.08	0.00
212820_at	**DMXL2**	23312	Dmx-like 2	3.01	0.00
1553470_at	**DNAH17**	8632	dynein, axonemal, heavy chain 17	12.74	0.37
200664_s_at	**DNAJB1**	3337	DnaJ (Hsp40) homolog, subfamily B, member 1	4.89	0.10
223054_at	**DNAJB11**	51726	DnaJ (Hsp40) homolog, subfamily B, member 11	3.24	0.00
202843_at	**DNAJB9**	4189	DnaJ (Hsp40) homolog, subfamily B, member 9	13.81	0.00
222620_s_at	**DNAJC1**	64215	DnaJ (Hsp40) homolog, subfamily C, member 1	2.76	0.13
205545_x_at	**DNAJC8**	22826	DnaJ (Hsp40) homolog, subfamily C, member 8	4.18	0.58
226281_at	**DNER**	92737	delta/notch-like EGF repeat containing	3.05	0.22
202776_at	**DNTTIP2**	30836	deoxynucleotidyltransferase, terminal, interacting protein 2	5.40	0.00
219279_at	**DOCK10**	55619	dedicator of cytokinesis 10	2.32	0.37
226875_at	**DOCK11**	139818	dedicator of cytokinesis 11	-4.24	0.03
213160_at	**DOCK2**	1794	dedicator of cytokinesis 2	-3.03	0.10
244840_x_at	**DOCK4**	9732	dedicator of cytokinesis 4	10.75	0.00
219921_s_at	**DOCK5**	80005	dedicator of cytokinesis 5	-2.74	0.00
232843_s_at	**DOCK8**	81704	dedicator of cytokinesis 8	-2.99	0.00
212538_at	**DOCK9**	23348	dedicator of cytokinesis 9	-3.93	0.58
219452_at	**DPEP2**	64174	dipeptidase 2	-20.91	0.00
225633_at	**DPY19L3**	147991	dpy-19-like 3 (C. elegans)	-4.31	0.37
218627_at	**DRAM**	55332	damage-regulated autophagy modulator	4.59	0.00
218854_at	**DSE**	29940	dermatan sulfate epimerase	3.89	0.00
234107_s_at	**DTD1**	92675	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	-15.28	0.00
223445_at	**DTNBP1**	84062	dystrobrevin binding protein 1	2.44	0.58
215501_s_at	**DUSP10**	11221	dual specificity phosphatase 10	34.26	0.00
224336_s_at	**DUSP16**	80824	dual specificity phosphatase 16	4.20	0.00
204794_at	**DUSP2**	1844	dual specificity phosphatase 2	33.19	0.06
218845_at	**DUSP22**	56940	dual specificity phosphatase 22	-5.83	0.58
223402_at	**DUSP23**	54935	dual specificity phosphatase 23	-4.11	0.22
201537_s_at	**DUSP3**	1845	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	2.67	0.03
209457_at	**DUSP5**	1847	dual specificity phosphatase 5	22.59	0.13
208956_x_at	**DUT**	1854	dUTP pyrophosphatase	-2.98	0.37
217976_s_at	**DYNC1LI1**	51143	dynein, cytoplasmic 1, light intermediate chain 1	-2.74	0.10
210151_s_at	**DYRK3**	8444	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	3.04	0.13
218660_at	**DYSF**	8291	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	-2.90	0.22
226952_at	**EAF1**	85403	ELL associated factor 1	3.96	0.00
202623_at	**EAPP**	55837	E2F-associated phosphoprotein	-4.32	0.22
219424_at	**EBI3**	10148	Epstein-Barr virus induced gene 3	16.95	0.58
219974_x_at	**ECHDC1**	55862	enoyl Coenzyme A hydratase domain containing 1	-2.44	0.22
206437_at	**EDG6**	8698	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 6	-18.49	0.03
222802_at	**EDN1**	1906	endothelin 1	89.15	0.00
225545_at	**EEF2K**	29904	eukaryotic elongation factor-2 kinase	-7.07	0.22
233375_at	**EFCAB2**	84288	EF-hand calcium binding domain 2	-5.22	0.37
220523_at	**EFHC2**	80258	EF-hand domain (C-terminal) containing 2	-4.51	0.10

218973_at	**EFTUD1**	79631	elongation factor Tu GTP binding domain containing 1	2.09	0.22
221497_x_at	**EGLN1**	54583	egl nine homolog 1 (C. elegans)	-14.90	0.00
206115_at	**EGR3**	1960	early growth response 3	15.46	0.03
209037_s_at	**EHD1**	10938	EH-domain containing 1	2.95	0.37
209536_s_at	**EHD4**	30844	EH-domain containing 4	5.17	0.03
201019_s_at	**EIF1AP1 /// EIF1AX**	1964 /// 280661	eukaryotic translation initiation factor 1A, X-linked /// eukaryotic translation initiation factor 1A pseudogene 1	2.16	0.37
237988_at	**EIF1B**	10289	Eukaryotic translation initiation factor 1B	2.66	0.00
227930_at	**EIF2C4**	192670	eukaryotic translation initiation factor 2C, 4	-5.51	0.00
201144_s_at	**EIF2S1**	1965	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	3.34	0.37
208726_s_at	**EIF2S2**	8894	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	2.02	0.03
208756_at	**EIF3I**	8668	eukaryotic translation initiation factor 3, subunit I	2.64	0.37
211787_s_at	**EIF4A1**	1973	eukaryotic translation initiation factor 4A, isoform 1	2.62	0.10
201303_at	**EIF4A3**	9775	eukaryotic translation initiation factor 4A, isoform 3	2.81	0.06
238461_at	**EIF4E3**	317649	eukaryotic translation initiation factor 4E family member 3	-3.63	0.00
208624_s_at	**EIF4G1**	1981	eukaryotic translation initiation factor 4 gamma, 1	2.24	0.22
208708_x_at	**EIF5**	1983	eukaryotic translation initiation factor 5	2.81	0.00
213757_at	**EIF5A**	1984	Eukaryotic translation initiation factor 5A	2.06	0.13
201727_s_at	**ELAVL1**	1994	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	-2.38	0.37
212418_at	**ELF1**	1997	E74-like factor 1 (ets domain transcription factor)	2.04	0.00
210376_x_at	**ELK1**	2002	ELK1, member of ETS oncogene family	3.22	0.22
226099_at	**ELL2**	22936	elongation factor, RNA polymerase II, 2	4.81	0.00
209477_at	**EMD**	2010	emerin (Emery-Dreifuss muscular dystrophy)	2.73	0.00
204398_s_at	**EML2**	24139	echinoderm microtubule associated protein like 2	4.04	0.00
201324_at	**EMP1**	2012	epithelial membrane protein 1	10.96	0.58
207111_at	**EMR1**	2015	egf-like module containing, mucin-like, hormone receptor-like 1	15.85	0.00
210724_at	**EMR3**	84658	egf-like module containing, mucin-like, hormone receptor-like 3	-3.73	0.00
201231_s_at	**ENO1**	2023	enolase 1, (alpha)	2.03	0.37
209473_at	**ENTPD1**	953	ectonucleoside triphosphate diphosphohydrolase 1	-9.89	0.00
217050_at	**EPAG**	10824	early lymphoid activation protein	11.81	0.58
225051_at	**EPB41**	2035	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	-3.00	0.00
211776_s_at	**EPB41L3**	23136	erythrocyte membrane protein band 4.1-like 3	9.86	0.37
202894_at	**EPHB4**	2050	EPH receptor B4	-32.52	0.00
202909_at	**EPM2AIP1**	9852	EPM2A (laforin) interacting protein 1	5.61	0.03
232164_s_at	**EPPK1**	83481	epiplakin 1	2.90	0.10
217886_at	**EPS15**	2060	epidermal growth factor receptor pathway substrate 15	-3.86	0.03
227609_at	**EPSTI1**	94240	epithelial stromal interaction 1 (breast)	5.83	0.00
1563315_s_at	**ERICH1**	157697	glutamate-rich 1	-7.50	0.03
202444_s_at	**ERLIN1**	10613	ER lipid raft associated 1	-3.23	0.03
222646_s_at	**ERO1L**	30001	ERO1-like (S. cerevisiae)	-2.56	0.37
201574_at	**ETF1**	2107	eukaryotic translation termination factor 1	2.69	0.00
219017_at	**ETNK1**	55500	ethanolamine kinase 1	6.47	0.00

241193_at	**ETS2**	2114	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	4.41	0.03
230102_at	**ETV5**	2119	Ets variant gene 5 (ets-related molecule)	31.47	0.00
235056_at	**ETV6**	2120	ets variant gene 6 (TEL oncogene)	-2.78	0.10
221680_s_at	**ETV7**	51513	ets variant gene 7 (TEL2 oncogene)	3.32	0.06
211742_s_at	**EVI2B**	2124	ecotropic viral integration site 2B	-5.39	0.00
208297_s_at	**EVI5**	7813	ecotropic viral integration site 5	-5.92	0.10
210011_s_at	**EWSR1**	2130	Ewing sarcoma breakpoint region 1	2.31	0.00
211825_s_at	**EWSR1** /// **FLI1**	2130 /// 2313	Ewing sarcoma breakpoint region 1 /// Friend leukemia virus integration 1	-11.57	0.00
1553907_a_at	**EXDL1**	161829	exonuclease 3'-5' domain-like 1	2.30	0.22
226259_at	**EXOC6**	54536	exocyst complex component 6	-7.72	0.03
58696_at	**EXOSC4**	54512	exosome component 4	2.51	0.03
209202_s_at	**EXTL3**	2137	exostoses (multiple)-like 3	-2.43	0.06
226170_at	**EYA3**	2140	eyes absent homolog 3 (Drosophila)	2.35	0.00
203249_at	**EZH1**	2145	enhancer of zeste homolog 1 (Drosophila)	-13.09	0.03
204363_at	**F3**	2152	coagulation factor III (thromboplastin, tissue factor)	5.74	0.37
204714_s_at	**F5**	2153	coagulation factor V (proaccelerin, labile factor)	-15.83	0.10
202535_at	**FADD**	8772	Fas (TNFRSF6)-associated via death domain	-6.20	0.03
226905_at	**FAM101B**	359845	family with sequence similarity 101, member B	-10.89	0.00
225436_at	**FAM108C1**	58489	family with sequence similarity 108, member C1	9.96	0.22
227711_at	**FAM112B**	121355	family with sequence similarity 112, member B	2.63	0.37
221249_s_at	**FAM117A**	81558	family with sequence similarity 117, member A	-6.86	0.13
1555948_s_at	**FAM120A**	23196	family with sequence similarity 120A	-3.31	0.00
225395_s_at	**FAM120AOS**	158293	family with sequence similarity 120A opposite strand	-2.11	0.10
226443_at	**FAM122A**	116224	family with sequence similarity 122A	-6.42	0.22
231874_at	**FAM126B**	285172	family with sequence similarity 126, member B	-6.23	0.00
218037_at	**FAM134A**	79137	family with sequence similarity 134, member A	-2.19	0.37
218532_s_at	**FAM134B**	54463	family with sequence similarity 134, member B	6.41	0.00
212697_at	**FAM134C**	162427	family with sequence similarity 134, member C	-2.15	0.06
212370_x_at	**FAM21A** /// **FAM21B**	387680 /// 55747	family with sequence similarity 21, member B /// family with sequence similarity 21, member A	4.37	0.00
214946_x_at	**FAM21A** /// **FAM21B** /// **FAM21C** /// **FAM21D**	253725 /// 387680 /// 55747 /// 653450	family with sequence similarity 21, member B /// family with sequence similarity 21, member C /// family with sequence similarity 21, member A /// family with sequence similarity 21, member D	3.73	0.00
211068_x_at	**FAM21C** /// **FAM21D**	253725 /// 653450	family with sequence similarity 21, member C /// family with sequence similarity 21, member D	3.80	0.03
232899_at	**FAM41C** /// **MGC70863** /// **RPL23AP7**	118433 /// 284593 /// 284942	ribosomal protein L23a pseudogene 7 /// family with sequence similarity 41, member C /// similar to RPL23AP7 protein	-3.00	0.03
227410_at	**FAM43A**	131583	family with sequence similarity 43, member A	-9.87	0.58
225351_at	**FAM45A**	404636	family with sequence similarity 45, member A	-9.27	0.00
221804_s_at	**FAM45A** /// **FAM45B** /// **LOC731832**	404636 /// 55855 /// 731832	family with sequence similarity 45, member B /// family with sequence similarity 45, member A /// similar to family with sequence similarity 45, member A	-10.94	0.00
226330_s_at	**FAM48A**	55578	family with sequence similarity 48, member A	-3.28	0.37
203262_s_at	**FAM50A**	9130	family with sequence similarity 50, member A	2.55	0.37

203206_at	**FAM53B**	9679	family with sequence similarity 53, member B	-13.50	0.03
220147_s_at	**FAM60A**	58516	family with sequence similarity 60, member A	3.16	0.22
208858_s_at	**FAM62A**	23344	family with sequence similarity 62 (C2 domain containing), member A	-2.99	0.58
221856_s_at	**FAM63A**	55793	family with sequence similarity 63, member A	-3.25	0.00
229764_at	**FAM79B**	285386	family with sequence similarity 79, member B	2.11	0.37
229344_x_at	**FAM80B**	57494	family with sequence similarity 80, member B	6.86	0.03
1564204_at	**FAM91A2**	57234	family with sequence similarity 91, member A2	-2.69	0.10
225132_at	**FBXL3**	26224	F-box and leucine-rich repeat protein 3	-2.57	0.03
203255_at	**FBXO11**	80204	F-box protein 11	-5.54	0.58
202272_s_at	**FBXO28**	23219	F-box protein 28	2.80	0.37
227521_at	**FBXO33**	254170	F-box protein 33	-3.47	0.37
224369_s_at	**FBXO38**	81545	F-box protein 38	-2.02	0.58
212987_at	**FBXO9**	26268	F-box protein 9	-3.25	0.13
211307_s_at	**FCAR**	2204	Fc fragment of IgA, receptor for	3.31	0.00
1554899_s_at	**FCER1G**	2207	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	2.52	0.00
216950_s_at	**FCGR1A**	2209	Fc fragment of IgG, high affinity Ia, receptor (CD64)	2.08	0.22
210889_s_at	**FCGR2B** /// **FCGR2C**	2213 /// 9103	Fc fragment of IgG, low affinity IIb, receptor (CD32) /// Fc fragment of IgG, low affinity IIc, receptor for (CD32)	-5.46	0.13
204006_s_at	**FCGR3A** /// **FCGR3B**	2214 /// 2215	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) /// Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	-3.58	0.00
218831_s_at	**FCGRT**	2217	Fc fragment of IgG, receptor, transporter, alpha	-8.45	0.00
228220_at	**FCHO2**	115548	FCH domain only 2	-10.18	0.13
203620_s_at	**FCHSD2**	9873	FCH and double SH3 domains 2	2.78	0.03
205237_at	**FCN1**	2219	ficolin (collagen/fibrinogen domain containing) 1	-27.89	0.00
210950_s_at	**FDFT1**	2222	farnesyl-diphosphate farnesyltransferase 1	-6.93	0.06
227811_at	**FGD3**	89846	FYVE, RhoGEF and PH domain containing 3	-2.27	0.00
208229_at	**FGFR2**	2263	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	4.23	0.00
204834_at	**FGL2**	10875	fibrinogen-like 2	-17.40	0.00
218034_at	**FIS1**	51024	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	-3.36	0.37
31826_at	**FKBP15**	23307	FK506 binding protein 15, 133kDa	2.21	0.37
203391_at	**FKBP2**	2286	FK506 binding protein 2, 13kDa	4.09	0.00
224856_at	**FKBP5**	2289	FK506 binding protein 5	-4.75	0.00
40850_at	**FKBP8**	23770	FK506 binding protein 8, 38kDa	-4.43	0.22
1552664_at	**FLCN**	201163	folliculin	3.05	0.00
210786_s_at	**FLI1**	2313	Friend leukemia virus integration 1	-8.85	0.00
222065_s_at	**FLII**	2314	flightless I homolog (Drosophila)	-3.13	0.10
227302_s_at	**FLII** /// **LLGL1**	2314 /// 3996	flightless I homolog (Drosophila) /// lethal giant larvae homolog 1 (Drosophila)	-2.64	0.37
224318_s_at	**FLJ10081**	55683	hypothetical protein FLJ10081	2.69	0.37
241627_x_at	**FLJ10357**	55701	hypothetical protein FLJ10357	-7.02	0.00
217940_s_at	**FLJ10769**	55739	hypothetical protein FLJ10769	3.64	0.37
222686_s_at	**FLJ11151**	55313	hypothetical protein FLJ11151	-13.55	0.00
202852_s_at	**FLJ11506**	79719	hypothetical protein FLJ11506	4.00	0.06
220912_at	**FLJ11827**	80163	hypothetical protein FLJ11827	2.14	0.13
233210_at	**FLJ12120**	388439	hypothetical LOC388439	3.42	0.37
232664_at	**FLJ12334**	400946	hypothetical gene supported by AK022396; AK097927	-2.16	0.00

220719_at	**FLJ13769**	80079	hypothetical protein FLJ13769	2.04	0.13
1555486_a_at	**FLJ14213**	79899	hypothetical protein FLJ14213	6.58	0.13
218986_s_at	**FLJ20035**	55601	hypothetical protein FLJ20035	8.53	0.03
220137_at	**FLJ20674**	54621	hypothetical protein FLJ20674	-4.88	0.37
220467_at	**FLJ21272**	80100	hypothetical protein FLJ21272	17.43	0.13
218454_at	**FLJ22662**	79887	hypothetical protein FLJ22662	-28.38	0.00
220674_at	**FLJ22814**	79978	hypothetical protein FLJ22814	26.15	0.10
1564157_at	**FLJ33544**	728283	hypothetical protein LOC728283	4.16	0.13
1566760_at	**FLJ34208**	401106	hypothetical gene supported by AK091527	9.37	0.06
1562217_at	**FLJ34521**	646383	hypothetical protein LOC646383	-3.08	0.58
231698_at	**FLJ36848**	647115	hypothetical LOC647115	2.74	0.37
235235_s_at	**FLJ36874**	219988	FLJ36874 protein	2.40	0.00
244065_at	**FLJ37512**	643792	similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3)	-8.79	0.37
227925_at	**FLJ39051**	399972	Hypothetical gene supported by AK096370	-5.01	0.13
226207_at	**FLJ39378**	353116	hypothetical protein FLJ39378	-4.23	0.58
243547_at	**FLJ39639**	283876	hypothetical protein FLJ39639	-5.21	0.00
229559_at	**FLJ40125**	147699	hypothetical protein FLJ40125	2.96	0.37
240411_at	**FLJ40243**	133558	hypothetical protein FLJ40243	2.70	0.22
1556183_at	**FLJ40330**	645784	similar to protein immuno-reactive with anti-PTH polyclonal antibodies	3.69	0.58
200859_x_at	**FLNA**	2316	filamin A, alpha (actin binding protein 280)	5.14	0.22
211299_s_at	**FLOT2**	2319	flotillin 2	-2.50	0.00
242665_at	**FMNL2**	114793	formin-like 2	2.70	0.13
232249_at	**FMNL3**	91010	formin-like 3	70.88	0.00
241611_s_at	**FNDC3A**	22862	fibronectin type III domain containing 3A	2.90	0.13
218618_s_at	**FNDC3B**	64778	fibronectin type III domain containing 3B	4.81	0.00
206371_at	**FOLR3**	2352	folate receptor 3 (gamma)	-12.36	0.00
209189_at	**FOS**	2353	v-fos FBJ murine osteosarcoma viral oncogene homolog	-2.59	0.37
203734_at	**FOXJ2**	55810	forkhead box J2	2.77	0.10
206708_at	**FOXN2**	3344	forkhead box N2	-4.60	0.03
205022_s_at	**FOXN3**	1112	forkhead box N3	-2.50	0.00
202724_s_at	**FOXO1**	2308	forkhead box O1	-16.81	0.00
204132_s_at	**FOXO3**	2309	forkhead box O3	-5.29	0.06
219889_at	**FRAT1**	10023	frequently rearranged in advanced T-cell lymphomas	-28.81	0.00
209864_at	**FRAT2**	23401	frequently rearranged in advanced T-cell lymphomas 2	-17.37	0.00
228233_at	**FREM1**	158326	FRAS1 related extracellular matrix 1	3.58	0.03
204072_s_at	**FRY**	10129	furry homolog (Drosophila)	-10.90	0.00
210933_s_at	**FSCN1**	6624	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	17.00	0.00
208782_at	**FSTL1**	11167	follistatin-like 1	3.55	0.00
214211_at	**FTH1 /// FTHL16**	2495 /// 2508	ferritin, heavy polypeptide 1 /// ferritin, heavy polypeptide-like 16	2.21	0.00
212824_at	**FUBP3**	8939	far upstream element (FUSE) binding protein 3	2.25	0.58
201945_at	**FURIN**	5045	furin (paired basic amino acid cleaving enzyme)	-2.79	0.58
217696_at	**FUT7**	2529	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	-18.88	0.00
217655_at	**FXYD5**	53827	FXYD domain containing ion transport regulator 5	2.99	0.10
224642_at	**FYTTD1**	84248	forty-two-three domain containing 1	3.01	0.00
213524_s_at	**G0S2**	50486	G0/G1switch 2	5.65	0.00
202275_at	**G6PD**	2539	glucose-6-phosphate dehydrogenase	-2.83	0.06
208868_s_at	**GABARAPL1**	23710	GABA(A) receptor-associated protein like 1	-2.10	0.10

213560_at	**GADD45B**	4616	Growth arrest and DNA-damage-inducible, beta	2.96	0.00
239422_at	**GAL3ST4** /// **GPC2**	221914 /// 79690	galactose-3-O-sulfotransferase 4 /// glypican 2	-2.50	0.37
211810_s_at	**GALC**	2581	galactosylceramidase	3.30	0.13
222235_s_at	**GALNACT-2**	55454	chondroitin sulfate GalNAcT-2	2.34	0.03
1568618_a_at	**GALNT1**	2589	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	-2.81	0.00
203397_s_at	**GALNT3**	2591	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	-6.23	0.22
231832_at	**GALNT4**	8693	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	-3.88	0.37
218313_s_at	**GALNT7**	51809	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	-3.75	0.13
213280_at	**GARNL4**	23108	GTPase activating Rap/RanGAP domain-like 4	-22.59	0.00
208693_s_at	**GARS**	2617	glycyl-tRNA synthetase	2.57	0.00
210872_x_at	**GAS7**	8522	growth arrest-specific 7	3.08	0.06
203282_at	**GBE1**	2632	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	5.01	0.00
231577_s_at	**GBP1**	2633	guanylate binding protein 1, interferon-inducible, 67kDa	4.20	0.00
223434_at	**GBP3**	2635	guanylate binding protein 3	30.84	0.00
235574_at	**GBP4**	115361	guanylate binding protein 4	9.90	0.00
238581_at	**GBP5**	115362	guanylate binding protein 5	4.77	0.00
204224_s_at	**GCH1**	2643	GTP cyclohydrolase 1 (dopa-responsive dystonia)	8.08	0.00
203925_at	**GCLM**	2730	glutamate-cysteine ligase, modifier subunit	7.21	0.00
226271_at	**GDAP1**	54332	ganglioside-induced differentiation-associated protein 1	2.02	0.37
219722_s_at	**GDPD3**	79153	glycerophosphodiester phosphodiesterase domain containing 3	-10.52	0.00
213343_s_at	**GDPD5**	81544	glycerophosphodiester phosphodiesterase domain containing 5	2.98	0.58
50277_at	**GGA1**	26088	golgi associated, gamma adaptin ear containing, ARF binding protein 1	5.15	0.06
237647_at	**GHRL**	51738	Ghrelin/obestatin preprohormone	5.31	0.37
219243_at	**GIMAP4**	55303	GTPase, IMAP family member 4	-2.80	0.00
218805_at	**GIMAP5**	55340	GTPase, IMAP family member 5	6.78	0.03
204982_at	**GIT2**	9815	G protein-coupled receptor kinase interactor 2	-2.79	0.13
223278_at	**GJB2**	2706	gap junction protein, beta 2, 26kDa	106.92	0.00
217167_x_at	**GK**	2710	glycerol kinase	2.25	0.00
216316_x_at	**GK** /// **GK3P**	2710 /// 2713	glycerol kinase /// glycerol kinase 3 pseudogene	2.13	0.00
215966_x_at	**GK3P**	2713	glycerol kinase 3 pseudogene	2.59	0.00
1553772_at	**GK5**	256356	glycerol kinase 5 (putative)	2.32	0.06
214430_at	**GLA**	2717	galactosidase, alpha	3.14	0.06
201576_s_at	**GLB1**	2720	galactosidase, beta 1	-3.17	0.37
227525_at	**GLCCI1**	113263	glucocorticoid induced transcript 1	-6.31	0.37
214085_x_at	**GLIPR1**	11010	GLI pathogenesis-related 1 (glioma)	-15.39	0.00
219933_at	**GLRX2**	51022	glutaredoxin 2	-6.16	0.58

203159_at	**GLS**	2744	glutaminase	2.30	0.10
229770_at	**GLT1D1**	144423	glycosyltransferase 1 domain containing 1	-4.48	0.00
209883_at	**GLT25D2**	23127	glycosyltransferase 25 domain containing 2	2.22	0.37
219267_at	**GLTP**	51228	glycolipid transfer protein	3.61	0.13
218458_at	**GMCL1**	64395	germ cell-less homolog 1 (Drosophila)	-6.78	0.13
204220_at	**GMFG**	9535	glia maturation factor, gamma	-2.64	0.00
205349_at	**GNA15**	2769	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	10.15	0.10
201040_at	**GNAI2**	2771	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	-2.88	0.03
224863_at	**GNAQ**	2776	Guanine nucleotide binding protein (G protein), q polypeptide	-6.20	0.00
200981_x_at	**GNAS**	2778	GNAS complex locus	-3.54	0.00
223487_x_at	**GNB4**	59345	guanine nucleotide binding protein (G protein), beta polypeptide 4	-3.95	0.00
1555766_a_at	**GNG2**	54331	guanine nucleotide binding protein (G protein), gamma 2	4.29	0.00
206896_s_at	**GNG7**	2788	guanine nucleotide binding protein (G protein), gamma 7	-5.66	0.37
203307_at	**GNL1**	2794	guanine nucleotide binding protein-like 1	2.91	0.13
201948_at	**GNL2**	29889	guanine nucleotide binding protein-like 2 (nucleolar)	3.47	0.58
217850_at	**GNL3**	26354	guanine nucleotide binding protein-like 3 (nucleolar)	3.24	0.58
222109_at	**GNL3L**	54552	guanine nucleotide binding protein-like 3 (nucleolar)-like	-2.56	0.58
37145_at	**GNLY**	10578	granulysin	8.64	0.37
202382_s_at	**GNPDA1**	10007	glucosamine-6-phosphate deaminase 1	15.05	0.10
224887_at	**GNPTG**	84572	N-acetylglucosamine-1-phosphate transferase, gamma subunit	2.31	0.13
203676_at	**GNS**	2799	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	2.36	0.00
207575_at	**GOLGA /// GOLGA6 /// LOC653641**	342096 /// 55889 /// 653641	golgin-like protein /// golgi autoantigen, golgin subfamily a, 6 /// similar to Golgin subfamily A member 6 (Golgin linked to PML) (Golgin-like protein)	3.43	0.22
207812_s_at	**GORASP2**	26003	golgi reassembly stacking protein 2, 55kDa	2.27	0.13
201141_at	**GPNMB**	10457	glycoprotein (transmembrane) nmb	12.91	0.22
237690_at	**GPR115**	221393	G protein-coupled receptor 115	2.08	0.37
223887_at	**GPR132**	29933	G protein-coupled receptor 132	3.95	0.00
204137_at	**GPR137B**	7107	G protein-coupled receptor 137B	8.14	0.03
208524_at	**GPR15**	2838	G protein-coupled receptor 15	2.06	0.03
239533_at	**GPR155**	151556	G protein-coupled receptor 155	-3.60	0.06
228950_s_at	**GPR177**	79971	G protein-coupled receptor 177	-46.52	0.00
214586_at	**GPR37**	2861	G protein-coupled receptor 37 (endothelin receptor type B-like)	2.36	0.37
223767_at	**GPR84**	53831	G protein-coupled receptor 84	98.94	0.00
214091_s_at	**GPX3**	2878	glutathione peroxidase 3 (plasma)	2.83	0.58
201106_at	**GPX4**	2879	glutathione peroxidase 4 (phospholipid hydroperoxidase)	2.38	0.37
244808_at	**GRAMD1A**	57655	GRAM domain containing 1A	3.67	0.00
219313_at	**GRAMD1C**	54762	GRAM domain containing 1C	-30.36	0.00
212090_at	**GRINA**	2907	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	5.43	0.10
210981_s_at	**GRK6**	2870	G protein-coupled receptor kinase 6	-3.34	0.22
200696_s_at	**GSN**	2934	gelsolin (amyloidosis, Finnish type)	-3.25	0.22
1557915_s_at	**GSTO1**	9446	glutathione S-transferase omega 1	4.47	0.00

202453_s_at	**GTF2H1**	2965	general transcription factor IIH, polypeptide 1, 62kDa	4.68	0.58
223758_s_at	**GTF2H2**	2966	general transcription factor IIH, polypeptide 2, 44kDa	-2.01	0.22
210891_s_at	**GTF2I /// GTF2IP1 /// LOC100093631 /// LOC732437**	100093631 /// 2969 /// 2970 /// 732437	general transcription factor II, i /// general transcription factor II, i, pseudogene 1 /// similar to general transcription factor II, i isoform 1 /// general transcription factor II, i, pseudogene	-2.79	0.00
225083_at	**GTF3C6**	112495	general transcription factor IIIC, polypeptide 6, alpha 35kDa	10.17	0.00
218238_at	**GTPBP4**	23560	GTP binding protein 4	5.40	0.00
213089_at	**GUSBP1**	153561	glucuronidase, beta pseudogene 1	-5.75	0.00
201554_x_at	**GYG1**	2992	glycogenin 1	-3.12	0.03
202487_s_at	**H2AFV**	94239	H2A histone family, member V	-3.73	0.58
212524_x_at	**H2AFX**	3014	H2A histone family, member X	-2.35	0.13
207168_s_at	**H2AFY**	9555	H2A histone family, member Y	-4.81	0.03
200853_at	**H2AFZ**	3015	H2A histone family, member Z	-3.59	0.00
208579_x_at	**H2BFS**	54145	H2B histone family, member S	-3.76	0.03
206643_at	**HAL**	3034	histidine ammonia-lyase	-9.64	0.00
207316_at	**HAS1**	3036	hyaluronan synthase 1	32.13	0.22
235458_at	**HAVCR2**	84868	hepatitis A virus cellular receptor 2	6.03	0.37
201145_at	**HAX1**	10456	HCLS1 associated protein X-1	2.56	0.03
202299_s_at	**HBXIP**	10542	hepatitis B virus x interacting protein	-2.49	0.00
200886_s_at	**hCG_2015138 /// PGAM1**	5223 /// 642969	phosphoglycerate mutase 1 (brain) /// phosphoglycerate mutase 1 pseudogene	-2.98	0.00
214754_at	**hCG_40738**	200424	hypothetical protein MGC22014	3.25	0.00
1559050_at	**HCG27**	253018	HLA complex group 27	-19.18	0.13
206685_at	**HCG4**	54435	HLA complex group 4	2.73	0.37
215974_at	**HCG4P6**	80868	HLA complex group 4 pseudogene 6	10.90	0.22
216174_at	**HCRP1**	387535	hepatocellular carcinoma-related HCRP1	-3.08	0.37
217937_s_at	**HDAC7A**	51564	histone deacetylase 7A	-3.05	0.00
216484_x_at	**HDGF**	3068	Hepatoma-derived growth factor (high-mobility group protein 1-like)	6.53	0.00
209525_at	**HDGFRP3**	50810	Hepatoma-derived growth factor, related protein 3	-6.28	0.22
203430_at	**HEBP2**	23593	heme binding protein 2	-9.09	0.00
225910_at	**HELZ**	9931	helicase with zinc finger	-3.25	0.22
217902_s_at	**HERC2**	8924	hect domain and RLD 2	-3.96	0.00
206183_s_at	**HERC3**	8916	hect domain and RLD 3	-2.21	0.37
219863_at	**HERC5**	51191	hect domain and RLD 5	3.52	0.03
219352_at	**HERC6**	55008	hect domain and RLD 6	6.04	0.37
201765_s_at	**HEXA**	3073	hexosaminidase A (alpha polypeptide)	2.06	0.03
238591_at	**HEXDC**	284004	Hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	-3.75	0.22
214307_at	**HGD**	3081	homogentisate 1,2-dioxygenase (homogentisate oxidase)	2.03	0.58
215933_s_at	**HHEX**	3087	hematopoietically expressed homeobox	-12.00	0.06
225222_at	**HIAT1**	64645	hippocampus abundant transcript 1	3.11	0.00
223073_at	**HIATL1**	84641	hippocampus abundant transcript-like 1	-2.48	0.03
200989_at	**HIF1A**	3091	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	3.26	0.00
218507_at	**HIG2**	29923	hypoxia-inducible protein 2	4.93	0.10
200093_s_at	**HINT1**	3094	histidine triad nucleotide binding protein 1	3.56	0.03
212293_at	**HIPK1**	204851	homeodomain interacting protein kinase 1	-2.10	0.03
207764_s_at	**HIPK3**	10114	homeodomain interacting protein kinase 3	-2.23	0.00

203253_s_at	**HISPPD1**	23262	histidine acid phosphatase domain containing 1	-10.03	0.58
208569_at	**HIST1H2AB**	8335	histone cluster 1, H2ab	-2.35	0.58
215071_s_at	**HIST1H2AC**	8334	histone cluster 1, H2ac	-10.73	0.00
214542_x_at	**HIST1H2AI**	8329	histone cluster 1, H2ai	-3.51	0.00
208583_x_at	**HIST1H2AJ**	8331	histone cluster 1, H2aj	-3.51	0.03
236193_at	**HIST1H2BC**	8347	histone cluster 1, H2bc	-5.72	0.03
214455_at	**HIST1H2BC /// HIST1H2BG**	8339 /// 8347	histone cluster 1, H2bg /// histone cluster 1, H2bc	-3.37	0.10
209911_x_at	**HIST1H2BD**	3017	histone cluster 1, H2bd	-3.73	0.10
208527_x_at	**HIST1H2BE**	8344	histone cluster 1, H2be	-3.94	0.06
208490_x_at	**HIST1H2BF**	8343	histone cluster 1, H2bf	-3.80	0.03
208546_x_at	**HIST1H2BH**	8345	histone cluster 1, H2bh	-3.27	0.13
208523_x_at	**HIST1H2BI**	8346	histone cluster 1, H2bi	-3.17	0.10
214540_at	**HIST1H2BO**	8348	histone cluster 1, H2bo	-2.24	0.37
214522_x_at	**HIST1H3D**	8351	histone cluster 1, H3d	-2.67	0.00
214290_s_at	**HIST2H2AA3 /// HIST2H2AA4**	723790 /// 8337	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	-2.72	0.22
231681_x_at	**HIST3H2A**	92815	Histone cluster 3, H2a	-3.64	0.06
204512_at	**HIVEP1**	3096	human immunodeficiency virus type I enhancer binding protein 1	3.18	0.00
243254_at	**HIVEP2**	3097	human immunodeficiency virus type I enhancer binding protein 2	7.20	0.00
205936_s_at	**HK3**	3101	hexokinase 3 (white cell)	-10.03	0.37
205671_s_at	**HLA-DOB**	3112	major histocompatibility complex, class II, DO beta	2.61	0.58
208894_at	**HLA-DRA**	3122	major histocompatibility complex, class II, DR alpha	4.49	0.00
214438_at	**HLX**	3142	H2.0-like homeobox	-4.16	0.00
224615_x_at	**HM13**	81502	histocompatibility (minor) 13	2.95	0.00
235944_at	**HMCN1**	83872	hemicentin 1	3.27	0.58
212597_s_at	**HMG2L1**	10042	high-mobility group protein 2-like 1	4.60	0.00
206074_s_at	**HMGA1**	3159	high mobility group AT-hook 1	3.10	0.13
224731_at	**HMGB1**	3146	high-mobility group box 1	-2.19	0.00
208808_s_at	**HMGB2**	3148	high-mobility group box 2	-2.88	0.03
212873_at	**HMHA1**	23526	histocompatibility (minor) HA-1	-2.07	0.06
203665_at	**HMOX1**	3162	heme oxygenase (decycling) 1	3.74	0.00
217755_at	**HN1**	51155	hematological and neurological expressed 1	-7.84	0.00
206808_at	**HNRPA3P1**	10151	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	2.34	0.03
201376_s_at	**HNRPF**	3185	heterogeneous nuclear ribonucleoprotein F	3.48	0.03
222264_at	**HNRPUL2**	221092	heterogeneous nuclear ribonucleoprotein U-like 2	-2.64	0.22
213793_s_at	**HOMER1**	9456	homer homolog 1 (Drosophila)	2.57	0.22
36030_at	**HOM-TES-103**	25900	hypothetical protein LOC25900	-5.05	0.58
228642_at	**HOXA2**	3199	Homeobox A2	-4.03	0.13
208224_at	**HOXB1**	3211	homeobox B1	2.01	0.13
206697_s_at	**HP**	3240	haptoglobin	-2.78	0.00
208470_s_at	**HP /// HPR**	3240 /// 3250	haptoglobin /// haptoglobin-related protein	-3.95	0.22
229204_at	**HP1BP3**	50809	Heterochromatin protein 1, binding protein 3	-3.78	0.00
204934_s_at	**HPN**	3249	hepsin (transmembrane protease, serine 1)	8.62	0.37
204544_at	**HPS5**	11234	Hermansky-Pudlak syndrome 5	3.91	0.37
216879_at	**HR44**	27251	Hr44 antigen	3.04	0.10

205579_at	**HRH1**	3269	histamine receptor H1	22.67	0.22
221062_at	**HS3ST3B1**	9953	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	70.12	0.00
217989_at	**HSD17B11**	51170	hydroxysteroid (17-beta) dehydrogenase 11	-4.43	0.00
201413_at	**HSD17B4**	3295	hydroxysteroid (17-beta) dehydrogenase 4	2.15	0.58
209513_s_at	**HSDL2**	84263	hydroxysteroid dehydrogenase like 2	-7.80	0.00
1552623_at	**HSH2D**	84941	hematopoietic SH2 domain containing	-7.49	0.00
211969_at	**HSP90AA1**	3320	heat shock protein 90kDa alpha (cytosolic), class A member 1	2.22	0.00
200064_at	**HSP90AB1**	3326	heat shock protein 90kDa alpha (cytosolic), class B member 1	2.29	0.22
200599_s_at	**HSP90B1**	7184	heat shock protein 90kDa beta (Grp94), member 1	4.83	0.00
202581_at	**HSPA1B**	3304	heat shock 70kDa protein 1B	3.37	0.00
211936_at	**HSPA5**	3309	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	2.40	0.00
213418_at	**HSPA6**	3310	heat shock 70kDa protein 6 (HSP70B')	-2.43	0.00
200690_at	**HSPA9**	3313	heat shock 70kDa protein 9 (mortalin)	6.72	0.03
219998_at	**HSPC159**	29094	galectin-related protein	2.23	0.37
221597_s_at	**HSPC171**	29100	HSPC171 protein	2.98	0.58
205133_s_at	**HSPE1**	3336	heat shock 10kDa protein 1 (chaperonin 10)	2.63	0.37
208744_x_at	**HSPH1**	10808	heat shock 105kDa/110kDa protein 1	3.88	0.22
200825_s_at	**HYOU1**	10525	hypoxia up-regulated 1	2.42	0.37
230621_at	**IAH1**	285148	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	2.75	0.00
207062_at	**IAPP**	3375	islet amyloid polypeptide	2.05	0.37
239012_at	**IBRDC2**	255488	IBR domain containing 2	2.46	0.00
202638_s_at	**ICAM1**	3383	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	16.70	0.00
204949_at	**ICAM3**	3385	intercellular adhesion molecule 3	-3.82	0.00
204569_at	**ICK**	22858	intestinal cell (MAK-like) kinase	-2.62	0.58
201565_s_at	**ID2**	3398	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3.90	0.00
213931_at	**ID2 /// ID2B**	3398 /// 84099	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	3.34	0.03
201193_at	**IDH1**	3417	isocitrate dehydrogenase 1 (NADP+), soluble	-4.48	0.58
210014_x_at	**IDH3B**	3420	isocitrate dehydrogenase 3 (NAD+) beta	-2.20	0.22
208881_x_at	**IDI1**	3422	isopentenyl-diphosphate delta isomerase 1	-2.25	0.58
201631_s_at	**IER3**	8870	immediate early response 3	2.26	0.00
218611_at	**IER5**	51278	immediate early response 5	3.98	0.00
202411_at	**IFI27**	3429	interferon, alpha-inducible protein 27	6.02	0.03
201422_at	**IFI30**	10437	interferon, gamma-inducible protein 30	2.61	0.00
214453_s_at	**IFI44**	10561	interferon-induced protein 44	4.97	0.03
204415_at	**IFI6**	2537	interferon, alpha-inducible protein 6	2.16	0.03
1555464_at	**IFIH1**	64135	interferon induced with helicase C domain 1	6.98	0.00
229450_at	**IFIT3**	3437	interferon-induced protein with tetratricopeptide repeats 3	2.45	0.00
203595_s_at	**IFIT5**	24138	interferon-induced protein with tetratricopeptide repeats 5	3.17	0.00
225661_at	**IFNAR1**	3454	interferon (alpha, beta and omega) receptor 1	-2.30	0.03
204786_s_at	**IFNAR2**	3455	interferon (alpha, beta and omega) receptor 2	-2.37	0.03
210312_s_at	**IFT20**	90410	intraflagellar transport 20 homolog (Chlamydomonas)	-2.25	0.22
218100_s_at	**IFT57**	55081	intraflagellar transport 57 homolog (Chlamydomonas)	19.17	0.06
243358_at	**IGF1R**	3480	insulin-like growth factor 1 receptor	-14.07	0.10

211648_at	**IGHG1**	3500	Immunoglobulin heavy constant gamma 1 (G1m marker)	8.86	0.22
236249_at	**IKIP**	121457	IKK interacting protein	-29.62	0.00
226680_at	**IKZF5**	64376	IKAROS family zinc finger 5 (Pegasus)	-3.11	0.58
207433_at	**IL10**	3586	interleukin 10	41.13	0.10
204912_at	**IL10RA**	3587	interleukin 10 receptor, alpha	6.58	0.00
207901_at	**IL12B**	3593	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	66.38	0.00
201888_s_at	**IL13RA1**	3597	interleukin 13 receptor, alpha 1	-4.35	0.00
207375_s_at	**IL15RA**	3601	interleukin 15 receptor, alpha	36.36	0.03
209827_s_at	**IL16**	3603	interleukin 16 (lymphocyte chemoattractant factor)	-6.99	0.00
205707_at	**IL17RA**	23765	interleukin 17 receptor A	-4.34	0.00
224283_x_at	**IL18BP**	10068	interleukin 18 binding protein	21.89	0.10
210118_s_at	**IL1A**	3552	interleukin 1, alpha	199.11	0.00
205067_at	**IL1B**	3553	interleukin 1, beta	3.69	0.00
220322_at	**IL1F9**	56300	interleukin 1 family, member 9	28.52	0.22
215561_s_at	**IL1R1**	3554	interleukin 1 receptor, type I	4.63	0.37
211372_s_at	**IL1R2**	7850	interleukin 1 receptor, type II	-2.51	0.22
205227_at	**IL1RAP**	3556	interleukin 1 receptor accessory protein	-6.85	0.00
212659_s_at	**IL1RN**	3557	interleukin 1 receptor antagonist	5.53	0.00
220054_at	**IL23A**	51561	interleukin 23, alpha subunit p19	42.37	0.00
206341_at	**IL2RA**	3559	interleukin 2 receptor, alpha	45.50	0.03
204116_at	**IL2RG**	3561	interleukin 2 receptor, gamma (severe combined immunodeficiency)	2.04	0.03
230966_at	**IL4I1**	259307	interleukin 4 induced 1	91.27	0.03
205207_at	**IL6**	3569	interleukin 6 (interferon, beta 2)	145.39	0.00
212196_at	**IL6ST**	3572	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	5.02	0.00
202859_x_at	**IL8**	3576	interleukin 8	5.39	0.00
207094_at	**IL8RA**	3577	interleukin 8 receptor, alpha	-31.73	0.00
207008_at	**IL8RB**	3579	interleukin 8 receptor, beta	-7.72	0.00
208930_s_at	**ILF3**	3609	interleukin enhancer binding factor 3, 90kDa	3.53	0.37
203126_at	**IMPA2**	3613	inositol(myo)-1(or 4)-monophosphatase 2	-31.83	0.00
210029_at	**INDO**	3620	indoleamine-pyrrole 2,3 dioxygenase	38.51	0.00
1568638_a_at	**INDOL1**	169355	indoleamine-pyrrole 2,3 dioxygenase-like 1	100.82	0.03
208415_x_at	**ING1**	3621	inhibitor of growth family, member 1	-4.26	0.06
213544_at	**ING2**	3622	Inhibitor of growth family, member 2	-3.31	0.58
210511_s_at	**INHBA**	3624	inhibin, beta A	14.22	0.22
203332_s_at	**INPP5D**	3635	inositol polyphosphate-5-phosphatase, 145kDa	-3.22	0.13
201627_s_at	**INSIG1**	3638	insulin induced gene 1	10.07	0.00
206502_s_at	**INSM1**	3642	insulinoma-associated 1	5.04	0.58
229632_s_at	**INTS10**	55174	integrator complex subunit 10	-3.00	0.10
235283_at	**INTS6**	26512	integrator complex subunit 6	-6.44	0.03
218905_at	**INTS8**	55656	integrator complex subunit 8	-2.63	0.13
238488_at	**IPO11**	51194	importin 11	26.29	0.00
219092_s_at	**IPPK**	64768	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	2.41	0.22
210840_s_at	**IQGAP1**	8826	IQ motif containing GTPase activating protein 1	-2.41	0.00
203474_at	**IQGAP2**	10788	IQ motif containing GTPase activating protein 2	-7.61	0.00
203907_s_at	**IQSEC1**	9922	IQ motif and Sec7 domain 1	-3.02	0.00
217908_s_at	**IQWD1**	55827	IQ motif and WD repeats 1	-2.40	0.00
231779_at	**IRAK2**	3656	interleukin-1 receptor-associated kinase 2	41.74	0.00
1568830_at	**IRAK3**	11213	Interleukin-1 receptor-associated kinase 3	15.20	0.00
208436_s_at	**IRF7**	3665	interferon regulatory factor 7	4.37	0.58
209274_s_at	**ISCA1**	81689	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-5.95	0.37

205483_s_at	**ISG15**	9636	ISG15 ubiquitin-like modifier	4.22	0.06
203882_at	**ISGF3G**	10379	interferon-stimulated transcription factor 3, gamma 48kDa	2.33	0.06
225632_s_at	**ISY1 /// RAB43**	339122 /// 57461	ISY1 splicing factor homolog (S. cerevisiae) /// RAB43, member RAS oncogene family	-4.40	0.37
206493_at	**ITGA2B**	3674	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-2.02	0.58
201656_at	**ITGA6**	3655	integrin, alpha 6	-17.44	0.37
205786_s_at	**ITGAM**	3684	integrin, alpha M (complement component 3 receptor 3 subunit)	-2.26	0.00
215878_at	**ITGB1**	3688	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	2.78	0.58
1555349_a_at	**ITGB2**	3689	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	-3.91	0.00
205816_at	**ITGB8**	3696	integrin, beta 8	7.87	0.10
210740_s_at	**ITPK1**	3705	inositol 1,3,4-triphosphate 5/6 kinase	-5.43	0.00
203723_at	**ITPKB**	3707	inositol 1,4,5-trisphosphate 3-kinase B	-2.70	0.37
203710_at	**ITPR1**	3708	inositol 1,4,5-triphosphate receptor, type 1	5.11	0.00
35776_at	**ITSN1**	6453	intersectin 1 (SH3 domain protein)	3.22	0.00
244235_at	**IVNS1ABP**	10625	influenza virus NS1A binding protein	4.53	0.00
231183_s_at	**JAG1**	182	Jagged 1 (Alagille syndrome)	37.85	0.00
223104_at	**JAGN1**	84522	jagunal homolog 1 (Drosophila)	3.11	0.10
226371_at	**JARID1A**	5927	jumonji, AT rich interactive domain 1A	-3.54	0.06
203298_s_at	**JARID2**	3720	jumonji, AT rich interactive domain 2	-3.71	0.00
225798_at	**JAZF1**	221895	JAZF zinc finger 1	-7.28	0.00
221778_at	**JHDM1D**	80853	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	-3.05	0.03
203205_at	**JMJD2A**	9682	jumonji domain containing 2A	-4.35	0.58
212496_s_at	**JMJD2B**	23030	jumonji domain containing 2B	-7.46	0.00
212722_s_at	**JMJD6**	23210	jumonji domain containing 6	2.19	0.58
229294_at	**JPH3**	57338	junctophilin 3	3.18	0.13
201464_x_at	**JUN**	3725	jun oncogene	2.96	0.13
200840_at	**KARS**	3735	lysyl-tRNA synthetase	3.02	0.06
223412_at	**KBTBD7**	84078	kelch repeat and BTB (POZ) domain containing 7	-12.96	0.03
243893_at	**KCNC3**	3748	potassium voltage-gated channel, Shaw-related subfamily, member 3	3.50	0.22
207635_s_at	**KCNH1**	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1	3.34	0.22
224099_at	**KCNH7**	90134	potassium voltage-gated channel, subfamily H (eag-related), member 7	-3.12	0.06
221307_at	**KCNIP1**	30820	Kv channel interacting protein 1	2.47	0.06
204487_s_at	**KCNQ1**	3784	potassium voltage-gated channel, KQT-like subfamily, member 1	-17.52	0.58
205737_at	**KCNQ2**	3785	potassium voltage-gated channel, KQT-like subfamily, member 2	2.76	0.00
233234_at	**KCTD16**	57528	potassium channel tetramerisation domain containing 16	3.62	0.13
200698_at	**KDELR2**	11014	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	2.76	0.06
203143_s_at	**KIAA0040**	9674	KIAA0040	-2.80	0.00
212523_s_at	**KIAA0146**	23514	KIAA0146	-3.03	0.10
201985_at	**KIAA0196**	9897	KIAA0196	2.67	0.22
209256_s_at	**KIAA0265**	23008	KIAA0265 protein	-2.08	0.58
222468_at	**KIAA0319L**	79932	KIAA0319-like	-5.90	0.13
1558697_a_at	**KIAA0430**	9665	KIAA0430	-2.47	0.00
204546_at	**KIAA0513**	9764	KIAA0513	-4.14	0.37
212201_at	**KIAA0692**	23141	KIAA0692	3.55	0.37

213118_at	**KIAA0701**	23074	KIAA0701 protein	-3.19	0.13
204157_s_at	**KIAA0999**	23387	KIAA0999 protein	4.10	0.03
212942_s_at	**KIAA1199**	57214	KIAA1199	69.71	0.00
243349_at	**KIAA1324**	57535	KIAA1324	-13.55	0.06
228984_at	**KIAA1394**	57571	KIAA1394 protein	-2.38	0.22
225922_at	**KIAA1450**	57600	KIAA1450 protein	32.20	0.00
225506_at	**KIAA1468**	57614	KIAA1468	-3.12	0.37
233893_s_at	**KIAA1530**	57654	KIAA1530 protein	-4.39	0.00
211433_x_at	**KIAA1539**	80256	KIAA1539	-3.03	0.00
225703_at	**KIAA1545**	57666	KIAA1545 protein	-3.45	0.13
226155_at	**KIAA1600**	57700	KIAA1600	-25.98	0.00
231956_at	**KIAA1618**	57714	KIAA1618	2.50	0.22
234048_s_at	**KIAA1632**	57724	KIAA1632	2.52	0.03
214723_x_at	**KIAA1641**	57730	KIAA1641	3.75	0.58
216848_at	**KIAA1660**	85374	KIAA1660 protein	2.34	0.22
229891_x_at	**KIAA1704**	55425	KIAA1704	2.35	0.58
226599_at	**KIAA1727**	85462	KIAA1727 protein	9.58	0.03
226909_at	**KIAA1729**	85460	KIAA1729 protein	-3.78	0.22
229878_at	**KIAA1731**	85459	KIAA1731	-2.06	0.37
226691_at	**KIAA1856**	84629	KIAA1856 protein	-4.86	0.03
227370_at	**KIAA1946**	165215	KIAA1946	3.19	0.58
224708_at	**KIAA2013**	90231	KIAA2013	-3.51	0.03
242508_at	**KIAA2018**	205717	KIAA2018	2.68	0.58
238490_at	**KIAA2026**	158358	KIAA2026	-2.19	0.13
230990_at	**KIF13A**	63971	Kinesin family member 13A	-3.92	0.10
204411_at	**KIF21B**	23046	kinesin family member 21B	-5.50	0.58
203943_at	**KIF3B**	9371	kinesin family member 3B	5.16	0.13
1557089_at	**KIF5C**	3800	kinesin family member 5C	33.92	0.00
209661_at	**KIFC3**	3801	kinesin family member C3	15.95	0.13
211397_x_at	**KIR2DL1** /// **KIR2DL2** /// **KIR2DL3** /// **KIR2DS1** /// **KIR2DS2** /// **KIR2DS3** /// **KIR2DS4** /// **KIR2DS5** /// **KIR3DL1** /// **KIR3DL2** /// **KIR3DL3** /// **KIR3DS1**	115653 /// 3802 /// 3803 /// 3804 /// 3806 /// 3807 /// 3808 /// 3809 /// 3810 /// 3811 /// 3812 /// 3813	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, three domains, short cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	2.60	0.37
208426_x_at	**KIR2DL4**	3805	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	3.30	0.37
216676_x_at	**KIR3DL3**	115653	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	3.09	0.06
220825_s_at	**KIRREL**	55243	kin of IRRE like (Drosophila)	2.45	0.22

202393_s_at	**KLF10**	7071	Kruppel-like factor 10	8.94	0.00
208467_at	**KLF12**	11278	Kruppel-like factor 12	-2.38	0.13
219878_s_at	**KLF13**	51621	Kruppel-like factor 13	-3.26	0.58
221302_at	**KLF15**	28999	Kruppel-like factor 15	3.10	0.58
219371_s_at	**KLF2**	10365	Kruppel-like factor 2 (lung)	-2.74	0.00
222913_at	**KLF3**	51274	Kruppel-like factor 3 (basic)	-6.12	0.00
209211_at	**KLF5**	688	Kruppel-like factor 5 (intestinal)	6.26	0.10
204334_at	**KLF7**	8609	Kruppel-like factor 7 (ubiquitous)	-8.92	0.00
208784_s_at	**KLHDC3**	116138	kelch domain containing 3	-3.32	0.06
219157_at	**KLHL2**	11275	kelch-like 2, Mayven (Drosophila)	-2.59	0.06
49329_at	**KLHL22**	84861	kelch-like 22 (Drosophila)	-7.48	0.13
204733_at	**KLK6**	5653	kallikrein-related peptidase 6	2.01	0.03
202055_at	**KPNA1**	3836	karyopherin alpha 1 (importin alpha 5)	-3.11	0.37
203202_at	**KRR1**	11103	KRR1, small subunit (SSU) processome component, homolog (yeast)	-5.82	0.00
218963_s_at	**KRT23**	25984	keratin 23 (histone deacetylase inducible)	-2.61	0.00
235252_at	**KSR1**	8844	Kinase suppressor of ras 1	-3.42	0.10
244572_at	**KY**	339855	kyphoscoliosis peptidase	-5.64	0.00
217388_s_at	**KYNU**	8942	kynureninase (L-kynurenine hydrolase)	12.61	0.00
1552486_s_at	**LACTB**	114294	lactamase, beta	4.56	0.00
203287_at	**LAD1**	3898	ladinin 1	2.20	0.06
206486_at	**LAG3**	3902	lymphocyte-activation gene 3	-2.00	0.10
207509_s_at	**LAIR2**	3904	leukocyte-associated immunoglobulin-like receptor 2	31.93	0.13
216264_s_at	**LAMB2**	3913	laminin, beta 2 (laminin S)	-2.44	0.37
209270_at	**LAMB3**	3914	laminin, beta 3	39.03	0.00
205569_at	**LAMP3**	27074	lysosomal-associated membrane protein 3	34.26	0.00
217933_s_at	**LAP3**	51056	leucine aminopeptidase 3	11.40	0.00
215543_s_at	**LARGE**	9215	like-glycosyltransferase	2.41	0.22
222212_s_at	**LASS2**	29956	LAG1 homolog, ceramide synthase 2	-2.99	0.03
221581_s_at	**LAT2**	7462	linker for activation of T cells family, member 2	-2.71	0.00
201795_at	**LBR**	3930	lamin B receptor	-2.22	0.00
212531_at	**LCN2**	3934	lipocalin 2 (oncogene 24p3)	5.72	0.03
235096_at	**LEO1**	123169	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	2.83	0.37
207092_at	**LEP**	3952	leptin (obesity homolog, mouse)	2.55	0.10
202595_s_at	**LEPROTL1**	23484	leptin receptor overlapping transcript-like 1	-6.75	0.03
201105_at	**LGALS1**	3956	lectin, galactoside-binding, soluble, 1 (galectin 1)	3.93	0.13
208949_s_at	**LGALS3**	3958	lectin, galactoside-binding, soluble, 3	25.30	0.00
208934_s_at	**LGALS8**	3964	lectin, galactoside-binding, soluble, 8 (galectin 8)	2.14	0.37
238061_at	**LGI3**	203190	leucine-rich repeat LGI family, member 3	3.02	0.13
201212_at	**LGMN**	5641	legumain	21.43	0.37
205876_at	**LIFR**	3977	leukemia inhibitory factor receptor alpha	2.16	0.13
210660_at	**LILRA1**	11024	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	-10.44	0.00
211102_s_at	**LILRA2**	11027	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	-5.39	0.03
206881_s_at	**LILRA3**	11026	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	2.12	0.37
218600_at	**LIMD2**	80774	LIM domain containing 2	-9.21	0.00
212687_at	**LIMS1**	3987	LIM and senescent cell antigen-like domains 1	14.10	0.00
223800_s_at	**LIMS3**	96626	LIM and senescent cell antigen-like domains 3	17.92	0.22
206440_at	**LIN7A**	8825	lin-7 homolog A (C. elegans)	-10.69	0.00

232593_at	**LINCR**	93082	likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein	48.49	0.00
236163_at	**LIX1**	167410	Lix1 homolog (mouse)	2.80	0.22
218191_s_at	**LMBRD1**	55788	LMBR1 domain containing 1	-4.93	0.00
204249_s_at	**LMO2**	4005	LIM domain only 2 (rhombotin-like 1)	-2.44	0.00
209205_s_at	**LMO4**	8543	LIM domain only 4	-4.31	0.37
228647_at	**LOC100049716**	1E+08	unknown	2.57	0.37
1553974_at	**LOC128977**	128977	hypothetical protein LOC128977	-4.70	0.22
226702_at	**LOC129607**	129607	hypothetical protein LOC129607	4.43	0.00
212017_at	**LOC130074**	130074	p20	3.85	0.13
244289_at	**LOC134466**	134466	hypothetical protein LOC134466	8.94	0.00
238903_at	**LOC137886**	137886	hypothetical protein LOC137886	-2.29	0.00
225493_at	**LOC144438**	144438	hypothetical protein LOC144438	2.67	0.06
226513_at	**LOC145758**	145758	hypothetical protein LOC145758	-8.00	0.22
1558202_at	**LOC145783**	145783	hypothetical protein LOC145783	2.28	0.58
1557049_at	**LOC149478**	149478	Hypothetical protein LOC149478	37.54	0.10
229101_at	**LOC150166**	150166	Hypothetical protein LOC150166	-3.06	0.00
212098_at	**LOC151162**	151162	hypothetical protein LOC151162	-2.84	0.37
1560679_at	**LOC151438**	151438	hypothetical protein LOC151438	-8.71	0.03
231377_at	**LOC158830**	158830	similar to Ab2-183	2.77	0.58
1559651_at	**LOC161635**	161635	similar to casein kinase I alpha	2.37	0.22
227037_at	**LOC201164**	201164	similar to CG12314 gene product	4.91	0.03
235587_at	**LOC202781**	202781	hypothetical protein LOC202781	4.99	0.03
232034_at	**LOC203274**	203274	hypothetical protein LOC203274	-14.01	0.00
1564385_at	**LOC219688**	219688	hypothetical protein LOC219688	3.75	0.22
215123_at	**LOC23117** /// **LOC339047** /// **LOC642778** /// **LOC642799** /// **LOC728888**	23117 /// 339047 /// 642778 /// 642799 /// 728888	KIAA0220-like protein /// hypothetical protein LOC339047 /// similar to nuclear pore complex interacting protein /// similar to Protein KIAA0220	3.10	0.06
239919_at	**LOC255480**	255480	hypothetical protein LOC255480	2.06	0.37
1563745_a_at	**LOC283050**	283050	hypothetical protein LOC283050	16.87	0.06
1557113_at	**LOC283588**	283588	hypothetical protein LOC283588	-15.31	0.22
1564373_a_at	**LOC283887**	283887	hypothetical protein LOC283887	-2.24	0.13
1558525_at	**LOC283901**	283901	hypothetical protein LOC283901	-14.87	0.10
234664_at	**LOC284701**	284701	hypothetical protein LOC284701	-4.18	0.10
227466_at	**LOC285550**	285550	hypothetical protein LOC285550	-4.73	0.22
226159_at	**LOC285636**	285636	hypothetical protein LOC285636	3.95	0.00
1557359_at	**LOC285758**	285758	hypothetical protein LOC285758	64.43	0.13
230937_at	**LOC285835**	285835	hypothetical protein LOC285835	-3.83	0.22
222662_at	**LOC286044**	286044	hypothetical protein LOC286044	-4.50	0.00
241370_at	**LOC286052**	286052	hypothetical protein LOC286052	-8.39	0.37
224158_s_at	**LOC286144**	286144	hypothetical protein LOC286144	-3.36	0.03
238893_at	**LOC338758**	338758	hypothetical protein LOC338758	8.97	0.37
1561723_at	**LOC339894**	339894	hypothetical protein LOC339894	2.15	0.58

1558011_at	**LOC340089 /// LOC441081 /// LOC643367 /// LOC728452 /// LOC728488 /// LOC728499 /// LOC728506 /// LOC728526 /// LOC728540 /// LOC728575 ///**	340089 /// 441081 /// 643367 /// 728452 /// 728488 /// 728499 /// 728506 /// 728526 /// 728540 /// 728575 /// 730392	POM121 membrane glycoprotein (rat) pseudogene /// similar to Nuclear envelope pore membrane protein POM 121 (Pore membrane protein of 121 kDa) (P145)	-4.82	0.06
1558423_at	**LOC349114**	349114	hypothetical LOC349114	-5.86	0.00
244889_at	**LOC388210**	388210	Similar to CG15828-PA, isoform A	4.51	0.03
226608_at	**LOC388272**	388272	similar to RIKEN cDNA 4921524J17	4.09	0.22
221878_at	**LOC388969**	388969	hypothetical LOC388969	-2.51	0.37
224890_s_at	**LOC389541**	389541	similar to CG14977-PA	-4.24	0.00
230815_at	**LOC389765**	389765	similar to KIF27C	-8.38	0.13
217211_at	**LOC390861**	390861	similar to cytoplasmic beta-actin	-2.83	0.00
1558075_at	**LOC399491**	399491	LOC399491 protein	3.16	0.03
1560058_at	**LOC399900**	399900	hypothetical gene supported by AK093779	5.17	0.13
1561514_at	**LOC400655**	400655	hypothetical gene supported by BC013370; BC034583	2.08	0.22
232953_at	**LOC400723**	400723	hypothetical LOC400723	-5.71	0.00
1558882_at	**LOC401233**	401233	similar to HIV TAT specific factor 1; cofactor required for Tat activation of HIV-1 transcription	-3.33	0.37
1558345_a_at	**LOC439911**	439911	hypothetical gene supported by NM_194304	-6.45	0.06
231989_s_at	**LOC440345 /// LOC641298 /// LOC730099**	440345 /// 641298 /// 730099	hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 - like locus /// similar to PI-3-kinase-related kinase SMG-1	2.18	0.00
215090_x_at	**LOC440434**	440434	hypothetical protein FLJ11822	-2.37	0.06
230796_at	**LOC440900**	440900	hypothetical LOC440900	5.60	0.58
238727_at	**LOC440934**	440934	Hypothetical gene supported by BC008048	152.50	0.00
1560128_x_at	**LOC441108**	441108	MRNA; cDNA DKFZp686D10250 (from clone DKFZp686D10250) /// Hypothetical gene supported by AK128882	2.99	0.03
238788_at	**LOC494150**	494150	prohibitin pseudogene	-3.53	0.58
232135_at	**LOC56755**	56755	hypothetical protein LOC56755	-5.23	0.13
244322_at	**LOC641798 /// LOC646329**	641798 /// 646329	hypothetical protein LOC641798 /// hypothetical LOC646329	3.27	0.13
224752_at	**LOC641845 /// LOC647087**	641845 /// 647087	hypothetical protein LOC641845 /// hypothetical LOC647087	-7.98	0.03
238319_at	**LOC641912 /// LOC644090**	641912 /// 644090	hypothetical protein LOC641912 /// hypothetical LOC644090	6.14	0.06
215160_x_at	**LOC642236**	642236	similar to FRG1 protein (FSHD region gene 1 protein)	-4.00	0.06

243656_at	**LOC642852**	642852	hypothetical LOC642852	-2.18	0.13
227223_at	**LOC643167** /// **RBM39**	643167 /// 9584	RNA binding motif protein 39 /// similar to RNA-binding region-containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1)	-2.64	0.58
226808_at	**LOC643641**	643641	hypothetical protein LOC643641	-6.06	0.10
1557055_s_at	**LOC643837**	643837	hypothetical protein LOC643837	11.86	0.10
239117_at	**LOC643950**	643950	hypothetical LOC643950	-17.47	0.03
204970_s_at	**LOC644132** /// **MAFG**	4097 /// 644132	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) /// similar to v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G	6.94	0.00
201874_at	**LOC644387** /// **MPZL1**	644387 /// 9019	myelin protein zero-like 1 /// similar to myelin protein zero-like 1 isoform a	-5.29	0.03
224424_x_at	**LOC644773**	644773	ARP3 actin-related protein 3 homolog B pseudogene	2.04	0.22
226319_s_at	**LOC644811** /// **THOC4**	10189 /// 644811	THO complex 4 /// similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	2.34	0.37
1560007_at	**LOC645984**	645984	hypothetical LOC645984	2.24	0.13
215207_x_at	**LOC646208** /// **LOC654174** /// **LOC729148** /// **YDD19**	11049 /// 646208 /// 654174 /// 729148	YDD19 protein /// hypothetical LOC646208 /// similar to CG4775-PA /// similar to lethal (2) k00619 CG4775-PA	4.68	0.22
230775_s_at	**LOC646871**	646871	hypothetical LOC646871	5.89	0.06
226789_at	**LOC647121**	647121	similar to embigin homolog	-5.72	0.00
214084_x_at	**LOC648998** /// **LOC652625** /// **LOC652699** /// **NCF1** /// **NCF1B** /// **NCF1C**	648998 /// 652625 /// 652699 /// 653361 /// 654816 /// 654817	similar to Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein) (NOXO2) /// neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1) /// neutrophil cytosolic factor 1B pseudogene /// neutrophil cytosolic factor 1C pseudogene	-2.23	0.03
1569871_at	**LOC650392**	650392	Full-length cDNA clone CS0DF015YK23 of Fetal brain of Homo sapiens (human) /// Hypothetical protein LOC650392	3.39	0.10
212392_s_at	**LOC652526** /// **LOC727927** /// **PDE4DIP**	652526 /// 727927 /// 9659	phosphodiesterase 4D interacting protein (myomegalin) /// similar to phosphodiesterase 4D interacting protein isoform 2	13.64	0.00
1562234_a_at	**LOC652725** /// **NAV3**	652725 /// 89795	neuron navigator 3 /// similar to neuron navigator 3	7.08	0.37
217998_at	**LOC652993** /// **PHLDA1**	22822 /// 652993	pleckstrin homology-like domain, family A, member 1 /// hypothetical LOC652993	40.06	0.00
216902_s_at	**LOC653390** /// **LOC730092** /// **RRN3**	54700 /// 653390 /// 730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) /// RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	13.18	0.37
218338_at	**LOC653441** /// **PHC1**	1911 /// 653441	polyhomeotic homolog 1 (Drosophila) /// similar to polyhomeotic 1-like	32.79	0.00
201239_s_at	**LOC653566** /// **SPCS2**	653566 /// 9789	signal peptidase complex subunit 2 homolog (S. cerevisiae) /// signal peptidase complex subunit 2 homolog pseudogene	2.76	0.22
217767_at	**LOC653879**	653879	similar to Complement C3 precursor	77.43	0.00

212390_at	**LOC727893** /// **PDE4DIP**	727893 /// 9659	phosphodiesterase 4D interacting protein (myomegalin) /// similar to phosphodiesterase 4D interacting protein isoform 1	3.34	0.00
214129_at	**LOC727942**	727942	similar to phosphodiesterase 4D interacting protein isoform 2	12.40	0.03
1558794_at	**LOC728190**	728190	Hypothetical protein LOC728190	-2.09	0.06
202018_s_at	**LOC728320** /// **LTF**	4057 /// 728320	lactotransferrin /// similar to lactotransferrin	-2.19	0.03
213605_s_at	**LOC728411**	728411	Similar to Beta-glucuronidase precursor	-7.95	0.37
216380_x_at	**LOC728453** /// **LOC730288**	728453 /// 730288	similar to 40S ribosomal protein S28	3.13	0.13
217122_s_at	**LOC728661** /// **SLC35E2**	728661 /// 9906	solute carrier family 35, member E2 /// similar to solute carrier family 35, member E2	-7.74	0.00
224899_s_at	**LOC728866** /// **RP11-217H1.1**	728866 /// 84061	implantation-associated protein /// similar to implantation-associated protein	3.20	0.03
227710_s_at	**LOC728913**	728913	Similar to Reticulocalbin-1 precursor /// Pp13759	2.74	0.03
203315_at	**LOC729030** /// **NCK2**	729030 /// 8440	NCK adaptor protein 2 /// similar to NCK adaptor protein 2	-2.12	0.03
203837_at	**LOC729144** /// **MAP3K5**	4217 /// 729144	mitogen-activated protein kinase kinase kinase 5 /// hypothetical protein LOC729144	-2.07	0.22
1556180_at	**LOC729678**	729678	hypothetical protein LOC729678	2.71	0.22
216908_x_at	**LOC730092**	730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	31.45	0.00
215756_at	**LOC730227**	730227	hypothetical protein LOC730227	4.59	0.22
240287_at	**LOC730249**	730249	similar to Immune-responsive protein 1	53.16	0.00
216234_s_at	**LOC730418** /// **PRKACA**	5566 /// 730418	protein kinase, cAMP-dependent, catalytic, alpha /// similar to protein kinase, cAMP-dependent, catalytic, gamma	-3.15	0.37
217492_s_at	**LOC731292** /// **PTEN** /// **PTENP1**	11191 /// 5728 /// 731292	phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /// phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1 /// similar to Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (Phosphatase and tensin homolog) (Mutated in multiple advanced cancers 1)	-2.81	0.00
1569095_at	**LOC731424**	731424	hypothetical protein LOC731424	6.27	0.00
226842_at	**LOC90110**	90110	hypothetical protein LOC90110	-9.44	0.13
228993_s_at	**LOC92482**	92482	hypothetical protein LOC92482	-2.42	0.00
214791_at	**LOC93349**	93349	hypothetical protein BC004921	2.51	0.58
226038_at	**LONRF1**	91694	LON peptidase N-terminal domain and ring finger 1	2.96	0.13
202651_at	**LPGAT1**	9926	lysophosphatidylglycerol acyltransferase 1	-3.48	0.00
202459_s_at	**LPIN2**	9663	lipin 2	-4.41	0.00
219759_at	**LRAP**	64167	leukocyte-derived arginine aminopeptidase	4.98	0.10
232486_at	**LRFN1**	57622	leucine rich repeat and fibronectin type III domain containing 1	-2.31	0.22
228648_at	**LRG1**	116844	leucine-rich alpha-2-glycoprotein 1	-2.53	0.37
35974_at	**LRMP**	4033	lymphoid-restricted membrane protein	-19.41	0.00
200784_s_at	**LRP1**	4035	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2.19	0.03
201412_at	**LRP10**	26020	low density lipoprotein receptor-related protein 10	-2.18	0.00
201186_at	**LRPAP1**	4043	low density lipoprotein receptor-related protein associated protein 1	-3.38	0.03
32062_at	**LRRC14**	9684	leucine rich repeat containing 14	-2.19	0.00

203835_at	**LRRC32**	2615	leucine rich repeat containing 32	2.62	0.37
229231_at	**LRRC37B**	114659	leucine rich repeat containing 37B	-2.36	0.22
223552_at	**LRRC4**	64101	leucine rich repeat containing 4	-7.55	0.06
206483_at	**LRRC6**	23639	leucine rich repeat containing 6	-3.05	0.22
229584_at	**LRRK2**	120892	leucine-rich repeat kinase 2	-2.30	0.00
1568667_s_at	**LSDP5**	440503	lipid storage droplet protein 5	3.99	0.00
214181_x_at	**LST1**	7940	leukocyte specific transcript 1	-2.96	0.00
208771_s_at	**LTA4H**	4048	leukotriene A4 hydrolase	-3.39	0.22
207339_s_at	**LTB**	4050	lymphotoxin beta (TNF superfamily, member 3)	-2.39	0.00
243852_at	**LUC7L2**	51631	LUC7-like 2 (S. cerevisiae)	3.08	0.22
202145_at	**LY6E**	4061	lymphocyte antigen 6 complex, locus E	3.46	0.00
205668_at	**LY75**	4065	lymphocyte antigen 75	-5.48	0.22
226996_at	**LYCAT**	253558	lysocardiolipin acyltransferase	-4.74	0.10
226851_at	**LYPLAL1**	127018	lysophospholipase-like 1	-3.54	0.22
239960_x_at	**LYRM7**	90624	Lyrm7 homolog (mouse)	2.80	0.37
203518_at	**LYST**	1130	lysosomal trafficking regulator	-2.63	0.00
1555745_a_at	**LYZ**	4069	lysozyme (renal amyloidosis)	-2.25	0.00
200900_s_at	**M6PR**	4074	mannose-6-phosphate receptor (cation dependent)	7.85	0.00
210252_s_at	**MADD**	8567	MAP-kinase activating death domain	-3.21	0.37
218559_s_at	**MAFB**	9935	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	15.22	0.00
36711_at	**MAFF**	23764	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	23.00	0.00
224480_s_at	**MAG1**	84803	lung cancer metastasis-associated protein	-4.54	0.00
218176_at	**MAGEF1**	64110	melanoma antigen family F, 1	-2.52	0.58
220302_at	**MAK**	4117	male germ cell-associated kinase	-4.16	0.00
235457_at	**MAML2**	84441	mastermind-like 2 (Drosophila)	23.34	0.00
242794_at	**MAML3**	55534	mastermind-like 3 (Drosophila)	-8.63	0.10
208116_s_at	**MAN1A1**	4121	mannosidase, alpha, class 1A, member 1	-5.50	0.00
226538_at	**MAN2A1**	4124	Mannosidase, alpha, class 2A, member 1	-5.62	0.10
202032_s_at	**MAN2A2**	4122	mannosidase, alpha, class 2A, member 2	-3.39	0.00
214703_s_at	**MAN2B2**	23324	mannosidase, alpha, class 2B, member 2	-3.59	0.22
208786_s_at	**MAP1LC3B**	81631	microtubule-associated protein 1 light chain 3 beta	2.03	0.03
202670_at	**MAP2K1**	5604	mitogen-activated protein kinase kinase 1	2.60	0.06
217971_at	**MAP2K1IP1**	8649	mitogen-activated protein kinase kinase 1 interacting protein 1	2.31	0.00
203266_s_at	**MAP2K4**	6416	mitogen-activated protein kinase kinase 4	-19.64	0.00
225927_at	**MAP3K1**	4214	mitogen-activated protein kinase kinase kinase 1	-3.22	0.00
226979_at	**MAP3K2**	10746	mitogen-activated protein kinase kinase kinase 2	-2.31	0.00
203514_at	**MAP3K3**	4215	mitogen-activated protein kinase kinase kinase 3	-12.04	0.00
205027_s_at	**MAP3K8**	1326	mitogen-activated protein kinase kinase kinase 8	10.96	0.00
222547_at	**MAP4K4**	9448	mitogen-activated protein kinase kinase kinase kinase 4	2.75	0.00
202890_at	**MAP7**	9053	microtubule-associated protein 7	-2.09	0.37
229847_at	**MAPK1**	5594	Mitogen-activated protein kinase 1	-3.98	0.00
210449_x_at	**MAPK14**	1432	mitogen-activated protein kinase 14	-6.80	0.00
204708_at	**MAPK4**	5596	mitogen-activated protein kinase 4	-2.01	0.00
207121_s_at	**MAPK6**	5597	mitogen-activated protein kinase 6	11.63	0.00
210075_at	**MARCH2**	51257	membrane-associated ring finger (C3HC4) 2	-3.53	0.22
230112_at	**MARCH4**	57574	membrane-associated ring finger (C3HC4) 4	-2.27	0.37
221824_s_at	**MARCH8**	220972	membrane-associated ring finger (C3HC4) 8	-2.73	0.37

225897_at	**MARCKS**	4082	myristoylated alanine-rich protein kinase C substrate	2.16	0.00
202568_s_at	**MARK3**	4140	MAP/microtubule affinity-regulating kinase 3	2.19	0.03
212064_x_at	**MAZ**	4150	MYC-associated zinc finger protein (purine-binding transcription factor)	-3.49	0.03
209579_s_at	**MBD4**	8930	methyl-CpG binding domain protein 4	-2.88	0.00
233015_at	**MBNL1**	4154	Muscleblind-like (Drosophila)	-2.44	0.22
227379_at	**MBOAT1**	154141	membrane bound O-acyltransferase domain containing 1	-17.40	0.00
226726_at	**MBOAT2**	129642	membrane bound O-acyltransferase domain containing 2	-19.71	0.03
1559427_at	**MCF2L**	23263	MCF.2 cell line derived transforming sequence-like	2.48	0.10
202556_s_at	**MCRS1**	10445	microspherule protein 1	2.23	0.58
220122_at	**MCTP1**	79772	multiple C2 domains, transmembrane 1	2.36	0.00
243109_at	**MCTP2**	55784	multiple C2 domains, transmembrane 2	-8.55	0.03
204059_s_at	**ME1**	4199	malic enzyme 1, NADP(+)-dependent, cytosolic	2.21	0.22
209397_at	**ME2**	4200	malic enzyme 2, NAD(+)-dependent, mitochondrial	-3.01	0.13
202618_s_at	**MECP2**	4204	methyl CpG binding protein 2 (Rett syndrome)	2.14	0.03
212207_at	**MED13L**	23389	mediator complex subunit 13-like	-2.10	0.03
218846_at	**MED23**	9439	mediator complex subunit 23	-2.25	0.58
1553993_s_at	**MED25**	81857	mediator complex subunit 25	-9.15	0.06
218438_s_at	**MED28**	80306	mediator complex subunit 28	2.90	0.10
1553978_at	**MEF2B**	4207	myocyte enhancer factor 2B	-2.88	0.13
212830_at	**MEGF9**	1955	multiple EGF-like-domains 9	-2.25	0.00
206028_s_at	**MERTK**	10461	c-mer proto-oncogene tyrosine kinase	2.05	0.03
211599_x_at	**MET**	4233	met proto-oncogene (hepatocyte growth factor receptor)	2.59	0.13
207761_s_at	**METTL7A**	25840	methyltransferase like 7A	-5.08	0.06
203406_at	**MFAP1**	4236	microfibrillar-associated protein 1	2.74	0.00
204153_s_at	**MFNG**	4242	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-8.53	0.13
243407_at	**MFSD8**	256471	Major facilitator superfamily domain containing 8	2.83	0.22
230848_s_at	**MGA**	23269	MAX gene associated	6.76	0.13
206522_at	**MGAM**	8972	maltase-glucoamylase (alpha-glucosidase)	-5.34	0.00
201126_s_at	**MGAT1**	4245	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	2.43	0.03
211061_s_at	**MGAT2**	4247	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	2.48	0.58
224507_s_at	**MGC12916**	84815	hypothetical protein MGC12916	8.29	0.03
1553747_at	**MGC16025**	85009	hypothetical protein MGC16025	2.37	0.06
236248_x_at	**MGC21874**	93624	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	-3.50	0.10
210484_s_at	**MGC31957 /// TNFRSF10C**	254896 /// 8794	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain /// hypothetical protein MGC31957	-18.15	0.00
220305_at	**MGC3260**	78993	hypothetical protein MGC3260	-5.45	0.10
226657_at	**MGC33894**	256302	transcript expressed during hematopoiesis 2	-12.08	0.00
239186_at	**MGC39372**	221756	hypothetical protein MGC39372	43.88	0.00
227983_at	**MGC7036**	196383	hypothetical protein MGC7036	2.45	0.00
200899_s_at	**MGEA5**	10724	meningioma expressed antigen 5 (hyaluronidase)	-2.29	0.00
211026_s_at	**MGLL**	11343	monoglyceride lipase	24.05	0.06
236475_at	**MICAL2**	9645	Microtubule associated monoxygenase, calponin and LIM domain containing 2	-19.76	0.00

1555862_s_at	**MICALL2**	79778	MICAL-like 2	-2.52	0.58
206247_at	**MICB**	4277	MHC class I polypeptide-related sequence B	2.35	0.06
226214_at	**MIR16**	51573	membrane interacting protein of RGS16	-5.56	0.10
226329_s_at	**MITD1**	129531	MIT, microtubule interacting and transport, domain containing 1	3.58	0.00
222530_s_at	**MKKS**	8195	McKusick-Kaufman syndrome	3.54	0.06
215292_s_at	**MKL1**	57591	megakaryoblastic leukemia (translocation) 1	-4.34	0.00
204423_at	**MKLN1**	4289	muskelin 1, intracellular mediator containing kelch motifs	-3.27	0.58
222510_s_at	**MKRN2**	23609	makorin, ring finger protein, 2	-3.86	0.58
202520_s_at	**MLH1**	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	5.51	0.13
227528_s_at	**MLL2**	8085	myeloid/lymphoid or mixed-lineage leukemia 2	-2.08	0.22
216480_x_at	**MLLT10**	8028	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	-2.22	0.00
224784_at	**MLLT6**	4302	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	9.79	0.03
239108_at	**MLSTD1**	55711	Male sterility domain containing 1	-3.42	0.22
224866_at	**MLSTD2**	84188	male sterility domain containing 2	-2.99	0.03
202519_at	**MLXIP**	22877	MLX interacting protein	-3.02	0.37
239852_at	**MMAA**	166785	methylmalonic aciduria (cobalamin deficiency) cblA type	4.39	0.00
203434_s_at	**MME**	4311	membrane metallo-endopeptidase	-38.72	0.00
202828_s_at	**MMP14**	4323	matrix metallopeptidase 14 (membrane-inserted)	74.59	0.00
207289_at	**MMP25**	64386	matrix metallopeptidase 25	-6.04	0.00
203936_s_at	**MMP9**	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	-3.04	0.10
204959_at	**MNDA**	4332	myeloid cell nuclear differentiation antigen	-7.66	0.00
225530_at	**MOBKL2A**	126308	MOB1, Mps One Binder kinase activator-like 2A (yeast)	-2.10	0.00
227066_at	**MOBKL2C**	148932	MOB1, Mps One Binder kinase activator-like 2C (yeast)	6.97	0.22
201994_at	**MORF4L2**	9643	mortality factor 4 like 2	2.91	0.00
218865_at	**MOSC1**	64757	MOCO sulphurase C-terminal domain containing 1	-11.82	0.00
64883_at	**MOSPD2**	158747	motile sperm domain containing 2	-2.24	0.37
226841_at	**MPEG1**	219972	macrophage expressed gene 1	-3.23	0.00
203949_at	**MPO**	4353	myeloperoxidase	-4.04	0.00
1564308_a_at	**MPP7**	143098	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-5.72	0.00
206764_x_at	**MPPE1**	65258	metallophosphoesterase 1	-12.94	0.00
210594_x_at	**MPZL1**	9019	myelin protein zero-like 1	-4.52	0.13
203780_at	**MPZL2**	10205	myelin protein zero-like 2	-3.75	0.37
227747_at	**MPZL3**	196264	myelin protein zero-like 3	-3.65	0.00
210224_at	**MR1**	3140	major histocompatibility complex, class I-related	7.32	0.00
219648_at	**MREG**	55686	melanoregulin	20.89	0.03
212199_at	**MRFAP1L1**	114932	Morf4 family associated protein 1-like 1	-3.62	0.13
1553293_at	**MRGPRX3**	117195	MAS-related GPR, member X3	2.65	0.06
225201_s_at	**MRPL14**	64928	mitochondrial ribosomal protein L14	7.35	0.00
218270_at	**MRPL24**	79590	mitochondrial ribosomal protein L24	5.93	0.22
225581_s_at	**MRPL50**	54534	mitochondrial ribosomal protein L50	11.33	0.22
226241_s_at	**MRPL52**	122704	mitochondrial ribosomal protein L52	11.49	0.00
226047_at	**MRVI1**	10335	murine retrovirus integration site 1 homolog	-7.94	0.03

219607_s_at	**MS4A4A**	51338	membrane-spanning 4-domains, subfamily A, member 4	20.54	0.37
219666_at	**MS4A6A**	64231	membrane-spanning 4-domains, subfamily A, member 6A	-19.01	0.00
202911_at	**MSH6**	2956	mutS homolog 6 (E. coli)	-3.66	0.03
226720_at	**MST101**	114825	MSTP101	-3.79	0.13
216336_x_at	**MT1A** /// **MT1M** /// **MT1P2**	4489 /// 4499 /// 645745	metallothionein 1A /// metallothionein 1M /// metallothionein 1 pseudogene 2	6.54	0.00
212859_x_at	**MT1E**	4493	metallothionein 1E	18.67	0.10
213629_x_at	**MT1F**	4494	metallothionein 1F	36.13	0.06
204745_x_at	**MT1G**	4495	metallothionein 1G	22.28	0.10
206461_x_at	**MT1H** /// **MT1P2**	4496 /// 645745	metallothionein 1H /// metallothionein 1 pseudogene 2	24.90	0.03
211456_x_at	**MT1P2**	645745	metallothionein 1 pseudogene 2	11.68	0.00
204326_x_at	**MT1X**	4501	metallothionein 1X	19.86	0.00
212185_x_at	**MT2A**	4502	metallothionein 2A	19.85	0.00
217395_at	**MT4**	84560	metallothionein 4	2.80	0.37
205322_s_at	**MTF1**	4520	metal-regulatory transcription factor 1	5.89	0.00
209705_at	**MTF2**	22823	metal response element binding transcription factor 2	-2.82	0.58
201761_at	**MTHFD2**	10797	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	7.98	0.03
223356_s_at	**MTIF3**	219402	mitochondrial translational initiation factor 3	-3.68	0.06
36920_at	**MTM1**	4534	myotubularin 1	-4.82	0.06
225810_at	**MTMR10**	54893	myotubularin related protein 10	-3.44	0.00
225232_at	**MTMR12**	54545	myotubularin related protein 12	-10.48	0.22
231941_s_at	**MUC20**	200958	mucin 20, cell surface associated	2.13	0.22
223348_x_at	**MUM1**	84939	melanoma associated antigen (mutated) 1	2.80	0.13
202086_at	**MX1**	4599	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	3.64	0.00
202364_at	**MXI1**	4601	MAX interactor 1	-5.33	0.37
225673_at	**MYADM**	91663	myeloid-associated differentiation marker	-5.33	0.00
204798_at	**MYB**	4602	v-myb myeloblastosis viral oncogene homolog (avian)	-6.07	0.58
206304_at	**MYBPH**	4608	myosin binding protein H	2.47	0.03
203359_s_at	**MYCBP**	26292	c-myc binding protein	-3.24	0.10
228133_s_at	**MYH11**	4629	myosin, heavy chain 11, smooth muscle	-2.12	0.00
227761_at	**MYO5A**	4644	myosin VA (heavy chain 12, myoxin)	-11.12	0.03
225299_at	**MYO5B**	4645	myosin VB	2.21	0.03
204601_at	**N4BP1**	9683	Nedd4 binding protein 1	2.79	0.03
1557998_at	**NAALADL2**	254827	N-acetylated alpha-linked acidic dipeptidase-like 2	2.05	0.37
209272_at	**NAB1**	4664	NGFI-A binding protein 1 (EGR1 binding protein 1)	2.87	0.00
204860_s_at	**NAIP** /// **NAIP1B**	4671 /// 728519	NLR family, apoptosis inhibitory protein /// neuronal apoptosis inhibitory protein (centromeric)	-7.28	0.00
228063_s_at	**NAP1L5**	266812	nucleosome assembly protein 1-like 5	-6.91	0.13
206491_s_at	**NAPA**	8775	N-ethylmaleimide-sensitive factor attachment protein, alpha	2.45	0.10
219862_s_at	**NARF**	26502	nuclear prelamin A recognition factor	-5.61	0.00
201970_s_at	**NASP**	4678	nuclear autoantigenic sperm protein (histone-binding)	-2.18	0.13
1556606_at	**NAV2**	89797	neuron navigator 2	2.01	0.37
1552658_a_at	**NAV3**	89795	neuron navigator 3	7.68	0.03
217299_s_at	**NBN**	4683	nibrin	11.74	0.00

204961_s_at	**NCF1** /// **NCF1B** /// **NCF1C**	653361 /// 654816 /// 654817	neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1) /// neutrophil cytosolic factor 1B pseudogene /// neutrophil cytosolic factor 1C pseudogene	-2.52	0.10
200610_s_at	**NCL**	4691	nucleolin	2.36	0.00
215857_at	**NCLN**	56926	nicalin homolog (zebrafish)	-25.20	0.00
209106_at	**NCOA1**	8648	nuclear receptor coactivator 1	-5.42	0.03
205731_s_at	**NCOA2**	10499	nuclear receptor coactivator 2	-4.54	0.06
207700_s_at	**NCOA3**	8202	nuclear receptor coactivator 3	-2.13	0.22
208979_at	**NCOA6**	23054	nuclear receptor coactivator 6	-4.00	0.37
204162_at	**NDC80**	10403	NDC80 homolog, kinetochore complex component (S. cerevisiae)	-2.37	0.58
218414_s_at	**NDE1**	54820	nudE nuclear distribution gene E homolog 1 (A. nidulans)	-2.16	0.58
208093_s_at	**NDEL1**	81565	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	-2.52	0.03
217286_s_at	**NDRG3**	57446	NDRG family member 3	-8.13	0.58
209224_s_at	**NDUFA2**	4695	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	-2.38	0.13
228301_x_at	**NDUFB10**	4716	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	-2.43	0.37
203613_s_at	**NDUFB6**	4712	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	-3.75	0.00
202941_at	**NDUFV2**	4729	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	3.27	0.00
209300_s_at	**NECAP1**	25977	NECAP endocytosis associated 1	5.91	0.00
220731_s_at	**NECAP2**	55707	NECAP endocytosis associated 2	2.47	0.06
201840_at	**NEDD8**	4738	neural precursor cell expressed, developmentally down-regulated 8	-2.34	0.37
1564093_at	**NEK1**	4750	NIMA (never in mitosis gene a)-related kinase 1	2.07	0.58
212530_at	**NEK7**	140609	NIMA (never in mitosis gene a)-related kinase 7	-3.18	0.00
218406_x_at	**NENF**	29937	neuron derived neurotrophic factor	2.43	0.58
208926_at	**NEU1**	4758	sialidase 1 (lysosomal sialidase)	4.49	0.00
224984_at	**NFAT5**	10725	nuclear factor of activated T-cells 5, tonicity-responsive	2.51	0.22
209930_s_at	**NFE2**	4778	nuclear factor (erythroid-derived 2), 45kDa	-10.90	0.00
201146_at	**NFE2L2**	4780	nuclear factor (erythroid-derived 2)-like 2	3.47	0.03
206929_s_at	**NFIC**	4782	nuclear factor I/C (CCAAT-binding transcription factor)	-2.74	0.13
209239_at	**NFKB1**	4790	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	8.49	0.03
209636_at	**NFKB2**	4791	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	8.63	0.00
201502_s_at	**NFKBIA**	4792	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	3.05	0.00
203927_at	**NFKBIE**	4794	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	11.43	0.00
223217_s_at	**NFKBIZ**	64332	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	2.79	0.00
218128_at	**NFYB**	4801	nuclear transcription factor Y, beta	-5.13	0.22
242800_at	**NHS**	4810	Nance-Horan syndrome (congenital cataracts and dental anomalies)	-11.44	0.37
202007_at	**NID1**	4811	nidogen 1	2.13	0.10
225921_at	**NIN**	51199	ninein (GSK3B interacting protein)	-4.30	0.00
201708_s_at	**NIPSNAP1**	8508	nipsnap homolog 1 (C. elegans)	-11.64	0.13
213915_at	**NKG7**	4818	natural killer cell group 7 sequence	3.36	0.37
225930_at	**NKIRAS1**	28512	NFKB inhibitor interacting Ras-like 1	10.94	0.13

229306_at	**NLF2**	388125	Nuclear localized factor 2	24.46	0.37
225944_at	**NLN**	57486	neurolysin (metallopeptidase M3 family)	22.83	0.13
226474_at	**NLRC5**	84166	NLR family, CARD domain containing 5	2.26	0.00
210113_s_at	**NLRP1**	22861	NLR family, pyrin domain containing 1	-16.76	0.00
1552531_a_at	**NLRP11**	204801	NLR family, pyrin domain containing 11	2.48	0.10
1554952_s_at	**NLRP12**	91662	NLR family, pyrin domain containing 12	-13.11	0.03
231870_s_at	**NMD3**	51068	NMD3 homolog (S. cerevisiae)	3.20	0.58
219553_at	**NME7**	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	4.63	0.22
210097_s_at	**NOL7**	51406	nucleolar protein 7, 27kDa	2.34	0.03
223096_at	**NOP5/NOP58**	51602	nucleolar protein NOP5/NOP58	3.59	0.06
218902_at	**NOTCH1**	4851	Notch homolog 1, translocation-associated (Drosophila)	-4.98	0.00
204501_at	**NOV**	4856	nephroblastoma overexpressed gene	-3.69	0.13
202679_at	**NPC1**	4864	Niemann-Pick disease, type C1	3.08	0.37
235033_at	**NPEPL1**	79716	Aminopeptidase-like 1	-5.76	0.06
201455_s_at	**NPEPPS**	9520	aminopeptidase puromycin sensitive	-5.67	0.03
213471_at	**NPHP4**	261734	nephronophthisis 4	3.57	0.10
204760_s_at	**NR1D1 /// THRA**	7067 /// 9572	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian) /// nuclear receptor subfamily 1, group D, member 1	14.13	0.22
203920_at	**NR1H3**	10062	nuclear receptor subfamily 1, group H, member 3	7.25	0.22
225477_s_at	**NR2C2**	7182	nuclear receptor subfamily 2, group C, member 2	-2.48	0.37
209959_at	**NR4A3**	8013	nuclear receptor subfamily 4, group A, member 3	10.06	0.06
224985_at	**NRAS**	4893	neuroblastoma RAS viral (v-ras) oncogene homolog	2.09	0.37
223650_s_at	**NRBF2**	29982	nuclear receptor binding factor 2	-2.14	0.10
202599_s_at	**NRIP1**	8204	nuclear receptor interacting protein 1	4.00	0.13
219557_s_at	**NRIP3**	56675	nuclear receptor interacting protein 3	9.64	0.22
217831_s_at	**NSFL1C**	55968	NSFL1 (p97) cofactor (p47)	-4.46	0.00
209484_s_at	**NSL1**	25936	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	-3.28	0.58
203269_at	**NSMAF**	8439	neutral sphingomyelinase (N-SMase) activation associated factor	2.92	0.00
226536_at	**NSMCE2**	286053	non-SMC element 2, MMS21 homolog (S. cerevisiae)	4.81	0.00
223178_s_at	**NT5DC1**	221294	5'-nucleotidase domain containing 1	-3.03	0.22
233072_at	**NTNG2**	84628	netrin G2	-6.70	0.00
235002_at	**NUDT16**	131870	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-5.63	0.03
224477_s_at	**NUDT16L1**	84309	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	-4.65	0.37
212181_s_at	**NUDT4**	11163	nudix (nucleoside diphosphate linked moiety X)-type motif 4	-3.22	0.06
223100_s_at	**NUDT5**	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5	-8.22	0.03
202155_s_at	**NUP214**	8021	nucleoporin 214kDa	-8.13	0.00
213682_at	**NUP50**	10762	nucleoporin 50kDa	-2.48	0.13
207740_s_at	**NUP62**	23636	nucleoporin 62kDa	3.15	0.03
204435_at	**NUPL1**	9818	nucleoporin like 1	3.05	0.22
225071_at	**NUS1**	116150	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	3.89	0.22
218708_at	**NXT1**	29107	NTF2-like export factor 1	4.34	0.58
205552_s_at	**OAS1**	4938	2',5'-oligoadenylate synthetase 1, 40/46kDa	9.31	0.00

204972_at	**OAS2**	4939	2'-5'-oligoadenylate synthetase 2, 69/71kDa	7.09	0.00
218400_at	**OAS3**	4940	2'-5'-oligoadenylate synthetase 3, 100kDa	6.76	0.10
205660_at	**OASL**	8638	2'-5'-oligoadenylate synthetase-like	2.03	0.03
215952_s_at	**OAZ1**	4946	ornithine decarboxylase antizyme 1	-3.44	0.06
201365_at	**OAZ2**	4947	ornithine decarboxylase antizyme 2	-2.37	0.00
219582_at	**OGFRL1**	79627	opioid growth factor receptor-like 1	-2.01	0.03
229787_s_at	**OGT**	8473	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	-6.81	0.03
224525_s_at	**OLA1**	29789	Obg-like ATPase 1	2.13	0.22
212768_s_at	**OLFM4**	10562	olfactomedin 4	2.46	0.22
210004_at	**OLR1**	4973	oxidized low density lipoprotein (lectin-like) receptor 1	11.80	0.58
218812_s_at	**ORAI2**	80228	ORAI calcium release-activated calcium modulator 2	-4.00	0.22
205040_at	**ORM1**	5004	orosomucoid 1	12.44	0.03
205041_s_at	**ORM1** /// **ORM2**	5004 /// 5005	orosomucoid 1 /// orosomucoid 2	10.67	0.00
201800_s_at	**OSBP**	5007	oxysterol binding protein	2.94	0.06
222586_s_at	**OSBPL11**	114885	oxysterol binding protein-like 11	-3.77	0.00
209485_s_at	**OSBPL1A**	114876	oxysterol binding protein-like 1A	-5.96	0.22
218047_at	**OSBPL9**	114883	oxysterol binding protein-like 9	-4.64	0.58
230170_at	**OSM**	5008	oncostatin M	8.79	0.00
204479_at	**OSTF1**	26578	osteoclast stimulating factor 1	-2.27	0.03
218196_at	**OSTM1**	28962	osteopetrosis associated transmembrane protein 1	3.44	0.00
224745_x_at	**OTUD5**	55593	OTU domain containing 5	3.20	0.03
223879_s_at	**OXR1**	55074	oxidation resistance 1	-3.23	0.13
204088_at	**P2RX4**	5025	purinergic receptor P2X, ligand-gated ion channel, 4	25.06	0.00
207091_at	**P2RX7**	5027	purinergic receptor P2X, ligand-gated ion channel, 7	7.37	0.00
214615_at	**P2RY10**	27334	purinergic receptor P2Y, G-protein coupled, 10	-2.83	0.22
220005_at	**P2RY13**	53829	purinergic receptor P2Y, G-protein coupled, 13	-12.96	0.00
206277_at	**P2RY2**	5029	purinergic receptor P2Y, G-protein coupled, 2	7.04	0.00
207543_s_at	**P4HA1**	5033	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	5.36	0.03
200654_at	**P4HB**	5034	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	3.88	0.10
218957_s_at	**PAAF1**	80227	proteasomal ATPase-associated factor 1	-2.31	0.10
224658_x_at	**PACS1**	55690	phosphofurin acidic cluster sorting protein 1	-14.54	0.10
227053_at	**PACSIN1**	29993	protein kinase C and casein kinase substrate in neurons 1	-2.25	0.37
220001_at	**PADI4**	23569	peptidyl arginine deiminase, type IV	-9.03	0.00
225626_at	**PAG1**	55824	phosphoprotein associated with glycosphingolipid microdomains 1	2.19	0.00
206897_at	**PAGE1**	8712	P antigen family, member 1 (prostate associated)	2.35	0.13
226507_at	**PAK1**	5058	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	-6.70	0.00
1557535_at	**PALLD**	23022	Palladin, cytoskeletal associated protein	3.61	0.37
225563_at	**PAN3**	255967	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-2.18	0.00
239067_s_at	**PANX2**	56666	pannexin 2	-14.66	0.00
229043_at	**PAPD5**	64282	PAP associated domain containing 5	-3.50	0.22

218543_s_at	**PARP12**	64761	poly (ADP-ribose) polymerase family, member 12	3.73	0.22
219034_at	**PARP16**	54956	poly (ADP-ribose) polymerase family, member 16	-4.39	0.37
219033_at	**PARP8**	79668	poly (ADP-ribose) polymerase family, member 8	-2.20	0.06
223220_s_at	**PARP9**	83666	poly (ADP-ribose) polymerase family, member 9	2.70	0.00
243468_at	**PATE**	160065	expressed in prostate and testis	2.14	0.37
202876_s_at	**PBX2**	5089	pre-B-cell leukemia homeobox 2	-2.34	0.13
214177_s_at	**PBXIP1**	57326	pre-B-cell leukemia homeobox interacting protein 1	-4.69	0.00
203845_at	**PCAF**	8850	p300/CBP-associated factor	-3.58	0.22
211365_s_at	**PCDHA2**	56146	protocadherin alpha 2	2.31	0.13
211066_x_at	**##########**	26025 /// 5098 /// 56097 /// 56098 /// 56099 /// 56100 /// 56101 /// 56102 /// 56103 /// 56104 /// 56105 /// 56106 /// 56107 /// 56108 /// 56109 /// 56110 /// 56111 /// 56112 /// 56113 /// 56114 /// 8641 /// 9708	protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 5 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 1	2.21	0.22
211876_x_at	**PCDHGA10** /// **PCDHGA11** /// **PCDHGA12** /// **PCDHGA3** /// **PCDHGA5** /// **PCDHGA6**	26025 /// 56105 /// 56106 /// 56109 /// 56110 /// 56112	protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 3	2.04	0.03
209996_x_at	**PCM1**	5108	pericentriolar material 1	-3.53	0.03
212406_s_at	**PCMTD2**	55251	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-12.27	0.00
213173_at	**PCNX**	22990	pecanex homolog (Drosophila)	-2.26	0.22
212422_at	**PDCD11**	22984	programmed cell death 11	2.46	0.06
212593_s_at	**PDCD4**	27250	programmed cell death 4 (neoplastic transformation inhibitor)	-2.29	0.03
204134_at	**PDE2A**	5138	phosphodiesterase 2A, cGMP-stimulated	57.41	0.00
208591_s_at	**PDE3B**	5140	phosphodiesterase 3B, cGMP-inhibited	-12.41	0.22
203708_at	**PDE4B**	5142	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	2.11	0.10
205872_x_at	**PDE4DIP**	9659	phosphodiesterase 4D interacting protein (myomegalin)	12.59	0.00

208911_s_at	**PDHB**	5162	pyruvate dehydrogenase (lipoamide) beta	-3.34	0.00
208612_at	**PDIA3**	2923	protein disulfide isomerase family A, member 3	2.62	0.00
211048_s_at	**PDIA4**	9601	protein disulfide isomerase family A, member 4	3.60	0.58
208639_x_at	**PDIA6**	10130	protein disulfide isomerase family A, member 6	2.40	0.10
226452_at	**PDK1**	5163	pyruvate dehydrogenase kinase, isozyme 1	-3.37	0.00
221957_at	**PDK3**	5165	pyruvate dehydrogenase kinase, isozyme 3	-11.20	0.03
219165_at	**PDLIM2**	64236	PDZ and LIM domain 2 (mystique)	-4.83	0.58
221898_at	**PDPN**	10630	podoplanin	9.33	0.13
207956_x_at	**PDS5B**	23047	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	-4.05	0.03
213549_at	**PDZD8**	118987	PDZ domain containing 8	-7.65	0.13
200788_s_at	**PEA15**	8682	phosphoprotein enriched in astrocytes 15	2.73	0.37
208982_at	**PECAM1**	5175	platelet/endothelial cell adhesion molecule (CD31 antigen)	-6.44	0.00
232304_at	**PELI1**	57162	Pellino homolog 1 (Drosophila)	-3.85	0.10
219132_at	**PELI2**	57161	pellino homolog 2 (Drosophila)	-6.28	0.00
218472_s_at	**PELO**	53918	pelota homolog (Drosophila)	-2.46	0.37
214753_at	**PFAAP5**	10443	Phosphonoformate immuno-associated protein 5	2.25	0.37
218336_at	**PFDN2**	5202	prefoldin subunit 2	3.26	0.37
228499_at	**PFKFB4**	5210	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-12.70	0.13
204604_at	**PFTK1**	5218	PFTAIRE protein kinase 1	-2.12	0.37
201118_at	**PGD**	5226	phosphogluconate dehydrogenase	-2.18	0.00
207384_at	**PGLYRP1**	8993	peptidoglycan recognition protein 1	-8.21	0.10
201968_s_at	**PGM1**	5236	phosphoglucomutase 1	-8.65	0.22
223738_s_at	**PGM2**	55276	phosphoglucomutase 2	-12.47	0.03
1560431_at	**PGM5P1**	653394	phosphoglucomutase 5 pseudogene 1	-2.35	0.22
213638_at	**PHACTR1**	221692	phosphatase and actin regulator 1	17.73	0.00
204048_s_at	**PHACTR2**	9749	phosphatase and actin regulator 2	7.49	0.13
225958_at	**PHC1**	1911	polyhomeotic homolog 1 (Drosophila)	12.55	0.00
200919_at	**PHC2**	1912	polyhomeotic homolog 2 (Drosophila)	-4.35	0.00
234939_s_at	**PHF12**	57649	PHD finger protein 12	-4.18	0.22
225820_at	**PHF17**	79960	PHD finger protein 17	-8.52	0.10
219606_at	**PHF20L1**	51105	PHD finger protein 20-like 1	-2.07	0.37
203278_s_at	**PHF21A**	51317	PHD finger protein 21A	-3.45	0.00
217951_s_at	**PHF3**	23469	PHD finger protein 3	-2.90	0.03
212542_s_at	**PHIP**	55023	pleckstrin homology domain interacting protein	-2.96	0.22
217996_at	**PHLDA1**	22822	pleckstrin homology-like domain, family A, member 1	73.93	0.03
209803_s_at	**PHLDA2**	7262	pleckstrin homology-like domain, family A, member 2	536.48	0.00
212719_at	**PHLPP**	23239	PH domain and leucine rich repeat protein phosphatase	-5.82	0.00
215285_s_at	**PHTF1**	10745	putative homeodomain transcription factor 1	-6.72	0.58
41469_at	**PI3**	5266	peptidase inhibitor 3, skin-derived (SKALP)	5.18	0.00
222631_at	**PI4K2B**	55300	phosphatidylinositol 4-kinase type 2 beta	5.18	0.22
242760_x_at	**PIGB**	9488	phosphatidylinositol glycan anchor biosynthesis, class B	-9.69	0.00
209707_at	**PIGK**	10026	phosphatidylinositol glycan anchor biosynthesis, class K	-4.68	0.03
1552291_at	**PIGX**	54965	phosphatidylinositol glycan anchor biosynthesis, class X	-10.92	0.00
1554508_at	**PIK3AP1**	118788	phosphoinositide-3-kinase adaptor protein 1	5.35	0.00
203879_at	**PIK3CD**	5293	phosphoinositide-3-kinase, catalytic, delta polypeptide	-3.35	0.00
209019_s_at	**PINK1**	65018	PTEN induced putative kinase 1	-7.36	0.00
214735_at	**PIP3-E**	26034	phosphoinositide-binding protein PIP3-E	-6.86	0.06

212829_at	**PIP4K2A**	5305	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	-2.44	0.37
219155_at	**PITPNC1**	26207	phosphatidylinositol transfer protein, cytoplasmic 1	-6.16	0.58
1561849_at	**PKD1L2**	114780	polycystic kidney disease 1-like 2	2.53	0.37
212629_s_at	**PKN2**	5586	protein kinase N2	-6.89	0.00
204196_x_at	**PKNOX1**	5316	PBX/knotted 1 homeobox 1	-4.07	0.58
206214_at	**PLA2G7**	7941	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	29.11	0.00
219014_at	**PLAC8**	51316	placenta-specific 8	15.76	0.00
202925_s_at	**PLAGL2**	5326	pleiomorphic adenoma gene-like 2	18.65	0.00
205479_s_at	**PLAU**	5328	plasminogen activator, urokinase	53.59	0.00
211924_s_at	**PLAUR**	5329	plasminogen activator, urokinase receptor	6.19	0.00
204046_at	**PLCB2**	5330	phospholipase C, beta 2	-9.24	0.58
213309_at	**PLCL2**	23228	phospholipase C-like 2	-6.00	0.37
226636_at	**PLD1**	5337	phospholipase D1, phosphatidylcholine-specific	2.76	0.58
224892_at	**PLDN**	26258	pallidin homolog (mouse)	3.41	0.06
203470_s_at	**PLEK**	5341	pleckstrin	2.68	0.00
201411_s_at	**PLEKHB2**	55041	pleckstrin homology domain containing, family B (evectins) member 2	4.63	0.00
217044_s_at	**PLEKHG3**	26030	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	-3.45	0.03
220073_s_at	**PLEKHG6**	55200	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	-3.12	0.10
218290_at	**PLEKHJ1**	55111	pleckstrin homology domain containing, family J member 1	-2.95	0.22
230120_s_at	**PLGLB1**	5343	plasminogen-like B1	-3.14	0.37
214415_at	**PLGLB1 /// PLGLB2**	5342 /// 5343	plasminogen-like B2 /// plasminogen-like B1	-5.40	0.10
204958_at	**PLK3**	1263	polo-like kinase 3 (Drosophila)	6.87	0.03
201136_at	**PLP2**	5355	proteolipid protein 2 (colonic epithelium-enriched)	-3.03	0.13
202430_s_at	**PLSCR1**	5359	phospholipid scramblase 1	3.80	0.00
227276_at	**PLXDC2**	84898	plexin domain containing 2	-16.40	0.00
207290_at	**PLXNA2**	5362	plexin A2	3.02	0.58
1553139_s_at	**PLXNA3**	55558	plexin A3	4.10	0.37
206470_at	**PLXNC1**	10154	plexin C1	-2.01	0.03
38671_at	**PLXND1**	23129	plexin D1	4.78	0.06
204285_s_at	**PMAIP1**	5366	phorbol-12-myristate-13-acetate-induced protein 1	2.60	0.00
209640_at	**PML**	5371	promyelocytic leukemia	3.66	0.22
210139_s_at	**PMP22**	5376	peripheral myelin protein 22	4.02	0.22
223310_x_at	**PNPLA8**	50640	patatin-like phospholipase domain containing 8	3.10	0.00
204835_at	**POLA1**	5422	polymerase (DNA directed), alpha 1	-2.79	0.06
210910_s_at	**POMZP3**	22932	POM (POM121 homolog, rat) and ZP3 fusion	3.44	0.58
217848_s_at	**PPA1**	5464	pyrophosphatase (inorganic) 1	6.63	0.06
212230_at	**PPAP2B**	8613	phosphatidic acid phosphatase type 2B	153.35	0.00
201490_s_at	**PPIF**	10105	peptidylprolyl isomerase F (cyclophilin F)	11.31	0.00
242154_x_at	**PPIL5**	122769	peptidylprolyl isomerase (cyclophilin)-like 5	-3.66	0.58
231370_at	**PPM1A**	5494	Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	-2.24	0.00
213225_at	**PPM1B**	5495	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	-2.43	0.00
233911_s_at	**PPM1H**	57460	protein phosphatase 1H (PP2C domain containing)	-2.30	0.58
1566301_at	**PPP1R11**	6992	Protein phosphatase 1, regulatory (inhibitor) subunit 11	2.40	0.37

201958_s_at	**PPP1R12B**	4660	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-25.71	0.00
202014_at	**PPP1R15A**	23645	protein phosphatase 1, regulatory (inhibitor) subunit 15A	4.55	0.00
211169_s_at	**PPP1R3A**	5506	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)	2.11	0.13
204554_at	**PPP1R3D**	5509	protein phosphatase 1, regulatory (inhibitor) subunit 3D	-6.08	0.03
202187_s_at	**PPP2R5A**	5525	protein phosphatase 2, regulatory subunit B', alpha isoform	-10.40	0.00
202425_x_at	**PPP3CA**	5530	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	-3.68	0.00
201594_s_at	**PPP4R1**	9989	protein phosphatase 4, regulatory subunit 1	-11.22	0.00
225429_at	**PPP6C**	5537	protein phosphatase 6, catalytic subunit	-2.35	0.58
200975_at	**PPT1**	5538	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	-5.41	0.00
241742_at	**PRAM1**	84106	PML-RARA regulated adaptor molecule 1	-3.61	0.03
201494_at	**PRCP**	5547	prolylcarboxypeptidase (angiotensinase C)	-3.71	0.00
208680_at	**PRDX1**	5052	peroxiredoxin 1	3.61	0.58
201619_at	**PRDX3**	10935	peroxiredoxin 3	-3.67	0.06
211743_s_at	**PRG2**	5553	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	3.27	0.00
226069_at	**PRICKLE1**	144165	prickle homolog 1 (Drosophila)	-2.29	0.10
218292_s_at	**PRKAG2**	51422	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	2.14	0.03
223904_at	**PRKAG3**	53632	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	2.07	0.22
225011_at	**PRKAR2A**	5576	Protein kinase, cAMP-dependent, regulatory, type II, alpha	-2.98	0.22
209685_s_at	**PRKCB1**	5579	protein kinase C, beta 1	-2.34	0.00
206099_at	**PRKCH**	5583	protein kinase C, eta	14.83	0.00
210543_s_at	**PRKDC**	5591	protein kinase, DNA-activated, catalytic polypeptide	-7.79	0.00
231758_at	**PRM3**	58531	protamine 3	2.06	0.37
1564520_s_at	**PRMT5**	10419	protein arginine methyltransferase 5	-4.02	0.58
201300_s_at	**PRNP**	5621	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	8.61	0.37
232629_at	**PROK2**	60675	prokineticin 2	-4.17	0.00
221546_at	**PRPF18**	8559	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	-3.37	0.13
202529_at	**PRPSAP1**	5635	phosphoribosyl pyrophosphate synthetase-associated protein 1	3.11	0.13
238513_at	**PRRG4**	79056	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	-3.33	0.00
209337_at	**PSIP1**	11168	PC4 and SFRS1 interacting protein 1	-4.38	0.37
201676_x_at	**PSMA1**	5682	proteasome (prosome, macropain) subunit, alpha type, 1	2.74	0.03
201532_at	**PSMA3**	5684	proteasome (prosome, macropain) subunit, alpha type, 3	2.93	0.10
201274_at	**PSMA5**	5686	proteasome (prosome, macropain) subunit, alpha type, 5	3.87	0.00
208805_at	**PSMA6**	5687	proteasome (prosome, macropain) subunit, alpha type, 6	5.02	0.00
200786_at	**PSMB7**	5695	proteasome (prosome, macropain) subunit, beta type, 7	-2.18	0.58
201068_s_at	**PSMC2**	5701	proteasome (prosome, macropain) 26S subunit, ATPase, 2	2.61	0.00

203447_at	**PSMD5**	5711	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	4.48	0.03
1555884_at	**PSMD6**	9861	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	-3.53	0.06
200820_at	**PSMD8**	5714	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	2.52	0.58
207805_s_at	**PSMD9**	5715	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	-2.74	0.03
201762_s_at	**PSME2**	5721	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	2.94	0.00
211178_s_at	**PSTPIP1**	9051	proline-serine-threonine phosphatase interacting protein 1	-2.87	0.22
219938_s_at	**PSTPIP2**	9050	proline-serine-threonine phosphatase interacting protein 2	5.64	0.00
204053_x_at	**PTEN**	5728	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-2.69	0.00
217494_s_at	**PTENP1**	11191	phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1	-3.39	0.00
206631_at	**PTGER2**	5732	prostaglandin E receptor 2 (subtype EP2), 53kDa	6.90	0.00
204897_at	**PTGER4**	5734	prostaglandin E receptor 4 (subtype EP4)	3.05	0.00
210367_s_at	**PTGES**	9536	prostaglandin E synthase	13.26	0.00
238669_at	**PTGS1**	5742	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-2.50	0.22
1554997_a_at	**PTGS2**	5743	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	3.31	0.03
206574_s_at	**PTP4A3**	11156	protein tyrosine phosphatase type IVA, member 3	2.39	0.13
244050_at	**PTPLAD2**	401494	protein tyrosine phosphatase-like A domain containing 2	-11.49	0.00
203555_at	**PTPN18**	26469	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	-3.01	0.58
213137_s_at	**PTPN2**	5771	protein tyrosine phosphatase, non-receptor type 2	3.07	0.10
223150_s_at	**PTPN23**	25930	protein tyrosine phosphatase, non-receptor type 23	4.08	0.22
206157_at	**PTX3**	5806	pentraxin-related gene, rapidly induced by IL-1 beta	12.22	0.06
1552274_at	**PXK**	54899	PX domain containing serine/threonine kinase	-3.08	0.22
201087_at	**PXN**	5829	paxillin	-5.52	0.00
221666_s_at	**PYCARD**	29108	PYD and CARD domain containing	-7.31	0.13
202990_at	**PYGL**	5836	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	-29.28	0.00
219681_s_at	**RAB11FIP1**	80223	RAB11 family interacting protein 1 (class I)	-6.60	0.00
202252_at	**RAB13**	5872	RAB13, member RAS oncogene family	3.24	0.00
207791_s_at	**RAB1A**	5861	RAB1A, member RAS oncogene family	2.30	0.00
219622_at	**RAB20**	55647	RAB20, member RAS oncogene family	6.75	0.00
203885_at	**RAB21**	23011	RAB21, member RAS oncogene family	2.55	0.00
217762_s_at	**RAB31**	11031	RAB31, member RAS oncogene family	-2.34	0.00
228113_at	**RAB37**	326624	RAB37, member RAS oncogene family	-12.35	0.00
225001_at	**RAB3D**	9545	RAB3D, member RAS oncogene family	-3.53	0.00
203581_at	**RAB4A**	5867	RAB4A, member RAS oncogene family	-2.85	0.22
203136_at	**RABAC1**	10567	Rab acceptor 1 (prenylated)	-2.59	0.22
203150_at	**RABEPK**	10244	Rab9 effector protein with kelch motifs	-2.86	0.58
203020_at	**RABGAP1L**	9910	RAB GTPase activating protein 1-like	-9.94	0.00
218310_at	**RABGEF1**	27342	RAB guanine nucleotide exchange factor (GEF) 1	3.93	0.06
201046_s_at	**RAD23A**	5886	RAD23 homolog A (S. cerevisiae)	3.93	0.13

201244_s_at	**RAF1**	5894	v-raf-1 murine leukemia viral oncogene homolog 1	-2.48	0.10
202844_s_at	**RALBP1**	10928	ralA binding protein 1	-12.30	0.00
209050_s_at	**RALGDS**	5900	ral guanine nucleotide dissociation stimulator	109.60	0.00
210552_s_at	**RALGPS1**	9649	Ral GEF with PH domain and SH3 binding motif 1	2.67	0.00
232112_at	**RALGPS2**	55103	Ral GEF with PH domain and SH3 binding motif 2	-5.29	0.10
201271_s_at	**RALY**	22913	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))	-3.60	0.58
201713_s_at	**RANBP2**	5903	RAN binding protein 2	5.37	0.00
242712_x_at	**RANBP2** /// **RGPD1** /// **RGPD2** /// **RGPD3** /// **RGPD4** /// **RGPD5** /// **RGPD6** /// **RGPD7** /// **RGPD8**	285190 /// 400966 /// 5903 /// 652919 /// 653489 /// 727851 /// 729540 /// 729857 /// 84220	RAN binding protein 2 /// RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 4 /// RANBP2-like and GRIP domain containing 1 /// RANBP2-like and GRIP domain containing 7 /// RANBP2-like and GRIP domain containing 3 /// RANBP2-like and GRIP domain containing 8 /// RANBP2-like and GRIP domain containing 6 /// RANBP2-like and GRIP domain containing 2	3.12	0.22
218668_s_at	**RAP2C**	57826	RAP2C, member of RAS oncogene family	2.15	0.37
203097_s_at	**RAPGEF2**	9693	Rap guanine nucleotide exchange factor (GEF) 2	-2.36	0.00
203749_s_at	**RARA**	5914	retinoic acid receptor, alpha	-2.45	0.37
204070_at	**RARRES3**	5920	retinoic acid receptor responder (tazarotene induced) 3	3.07	0.00
208206_s_at	**RASGRP2**	10235	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-4.81	0.00
240862_at	**RASGRP4**	115727	RAS guanyl releasing protein 4	-4.79	0.00
204346_s_at	**RASSF1**	11186	Ras association (RalGDS/AF-6) domain family 1	-7.44	0.06
226436_at	**RASSF4**	83937	Ras association (RalGDS/AF-6) domain family 4	5.99	0.06
202034_x_at	**RB1CC1**	9821	RB1-inducible coiled-coil 1	-3.06	0.03
212783_at	**RBBP6**	5930	retinoblastoma binding protein 6	2.05	0.13
232751_at	**RBBP9**	10741	retinoblastoma binding protein 9	2.64	0.13
212331_at	**RBL2**	5934	retinoblastoma-like 2 (p130)	-6.83	0.00
224781_s_at	**RBM17**	84991	RNA binding motif protein 17	2.48	0.03
218593_at	**RBM28**	55131	RNA binding motif protein 28	4.52	0.58
225839_at	**RBM33**	155435	RNA binding motif protein 33	-2.34	0.10
214943_s_at	**RBM34**	23029	RNA binding motif protein 34	3.46	0.03
225139_at	**RBM35B**	80004	RNA binding motif protein 35B	-4.47	0.03
238066_at	**RBP7**	116362	retinol binding protein 7, cellular	-39.76	0.00
207785_s_at	**RBPJ**	3516	recombination signal binding protein for immunoglobulin kappa J region	-3.34	0.00
208370_s_at	**RCAN1**	1827	regulator of calcineurin 1	4.41	0.00
204759_at	**RCBTB2**	1102	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	-12.57	0.00
214281_s_at	**RCHY1**	25898	ring finger and CHY zinc finger domain containing 1	2.83	0.03
61734_at	**RCN3**	57333	reticulocalbin 3, EF-hand calcium binding domain	-2.83	0.10
222605_at	**RCOR3**	55758	REST corepressor 3	-2.06	0.22

205407_at	**RECK**	8434	reversion-inducing-cysteine-rich protein with kazal motifs	5.25	0.58
208873_s_at	**REEP5**	7905	receptor accessory protein 5	-7.15	0.00
206035_at	**REL**	5966	v-rel reticuloendotheliosis viral oncogene homolog (avian)	3.80	0.00
201783_s_at	**RELA**	5970	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	3.68	0.03
227425_at	**REPS2**	9185	RALBP1 associated Eps domain containing 2	-7.64	0.00
200940_s_at	**RERE**	473	arginine-glutamic acid dipeptide (RE) repeats	-3.80	0.00
220570_at	**RETN**	56729	resistin	7.52	0.00
234950_s_at	**RFWD2**	64326	ring finger and WD repeat domain 2	-2.75	0.00
208031_s_at	**RFX2**	5990	regulatory factor X, 2 (influences HLA class II expression)	-2.42	0.37
231877_at	**RG9MTD2**	93587	RNA (guanine-9-) methyltransferase domain containing 2	-2.55	0.37
209568_s_at	**RGL1**	23179	ral guanine nucleotide dissociation stimulator-like 1	23.72	0.00
202988_s_at	**RGS1**	5996	regulator of G-protein signaling 1	4.01	0.58
38290_at	**RGS14**	10636	regulator of G-protein signaling 14	-16.51	0.00
209325_s_at	**RGS16**	6004	regulator of G-protein signaling 16	3.59	0.22
223809_at	**RGS18**	64407	regulator of G-protein signaling 18	-14.00	0.00
202388_at	**RGS2**	5997	regulator of G-protein signaling 2, 24kDa	-2.18	0.00
219202_at	**RHBDF2**	79651	rhomboid 5 homolog 2 (Drosophila)	10.36	0.37
1552502_s_at	**RHBDL2**	54933	rhomboid, veinlet-like 2 (Drosophila)	3.17	0.37
1555780_a_at	**RHEB**	6009	Ras homolog enriched in brain	2.08	0.03
212099_at	**RHOB**	388	ras homolog gene family, member B	-3.36	0.00
200885_at	**RHOC**	389	ras homolog gene family, member C	8.50	0.00
219045_at	**RHOF**	54509	ras homolog gene family, member F (in filopodia)	2.62	0.58
204951_at	**RHOH**	399	ras homolog gene family, member H	13.43	0.06
223168_at	**RHOU**	58480	ras homolog gene family, member U	10.02	0.10
226312_at	**RICTOR**	253260	rapamycin-insensitive companion of mTOR	-2.77	0.00
209684_at	**RIN2**	54453	Ras and Rab interactor 2	5.63	0.37
219457_s_at	**RIN3**	79890	Ras and Rab interactor 3	-12.15	0.58
209544_at	**RIPK2**	8767	receptor-interacting serine-threonine kinase 2	4.75	0.06
204243_at	**RLF**	6018	rearranged L-myc fusion	2.79	0.13
218979_at	**RMI1**	80010	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	-8.40	0.00
212482_at	**RMND5A**	64795	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	-2.11	0.22
206111_at	**RNASE2**	6036	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	-7.92	0.37
217984_at	**RNASET2**	8635	ribonuclease T2	-15.93	0.00
208632_at	**RNF10**	9921	ring finger protein 10	-2.53	0.37
217865_at	**RNF130**	55819	ring finger protein 130	-2.12	0.06
223591_at	**RNF135**	84282	ring finger protein 135	-5.09	0.13
226106_at	**RNF141**	50862	ring finger protein 141	-5.93	0.00
227726_at	**RNF166**	115992	ring finger protein 166	-2.95	0.06
229932_at	**RNF181**	51255	Ring finger protein 181	34.37	0.13
224750_at	**RNF185**	91445	ring finger protein 185	3.14	0.13
225931_s_at	**RNF213**	57674	ring finger protein 213	2.24	0.00
234461_at	**RNF215**	200312	ring finger protein 215	2.22	0.00
210706_s_at	**RNF24**	11237	ring finger protein 24	-4.04	0.00
218528_s_at	**RNF38**	152006	ring finger protein 38	-3.74	0.10
203286_at	**RNF44**	22838	ring finger protein 44	-4.33	0.00
211387_x_at	**RNGTT**	8732	RNA guanylyltransferase and 5'-phosphatase	6.18	0.10

202683_s_at	**RNMT**	8731	RNA (guanine-7-) methyltransferase	4.60	0.37
226975_at	**RNPC3**	55599	RNA-binding region (RNP1, RRM) containing 3	-2.09	0.13
218301_at	**RNPEPL1**	57140	arginyl aminopeptidase (aminopeptidase B)-like 1	-9.04	0.06
202762_at	**ROCK2**	9475	Rho-associated, coiled-coil containing protein kinase 2	-2.54	0.37
214697_s_at	**ROD1**	9991	ROD1 regulator of differentiation 1 (S. pombe)	-2.05	0.00
223609_at	**ROPN1L**	83853	ropporin 1-like	-7.62	0.06
220436_at	**RP11-138L21.1**	389722	similar to cell recognition molecule CASPR3	-9.01	0.58
1559884_at	**RP11-145E5.4**	1E+08	antisense noncoding RNA in the INK4 locus	2.72	0.37
1569932_at	**RP11-262D11.5**	340527	similar to Nance-Horan syndrome protein	-4.20	0.22
214748_at	**RP11-298P3.3**	88523	CG016	3.67	0.06
1553299_at	**RP4-621O15.2**	200107	hypothetical protein FLJ31401	2.53	0.37
224835_at	**RP5-1022P6.2**	56261	hypothetical protein KIAA1434	-3.90	0.13
206608_s_at	**RPGRIP1**	57096	retinitis pigmentosa GTPase regulator interacting protein 1	-2.27	0.37
212973_at	**RPIA**	22934	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	-2.76	0.58
241703_at	**RPIB9**	154661	Rap2-binding protein 9	2.50	0.10
221989_at	**RPL10**	6134	ribosomal protein L10	2.34	0.22
215224_at	**RPL23**	9349	ribosomal protein L23	2.37	0.06
200013_at	**RPL24**	6152	ribosomal protein L24	2.16	0.06
214143_x_at	**RPL24 /// SLC36A2**	153201 /// 6152	ribosomal protein L24 /// solute carrier family 36 (proton/amino acid symporter), member 2	2.04	0.06
226335_at	**RPS6KA3**	6197	ribosomal protein S6 kinase, 90kDa, polypeptide 3	-4.32	0.06
204635_at	**RPS6KA5**	9252	ribosomal protein S6 kinase, 90kDa, polypeptide 5	-8.99	0.10
204803_s_at	**RRAD**	6236	Ras-related associated with diabetes	2.44	0.00
218088_s_at	**RRAGC**	64121	Ras-related GTP binding C	2.17	0.00
213495_s_at	**RRBP1**	6238	Ribosome binding protein 1 homolog 180kDa (dog)	-2.75	0.37
223342_at	**RRM2B**	50484	ribonucleotide reductase M2 B (TP53 inducible)	-5.05	0.06
216913_s_at	**RRP12**	23223	ribosomal RNA processing 12 homolog (S. cerevisiae)	-14.01	0.00
242625_at	**RSAD2**	91543	radical S-adenosyl methionine domain containing 2	10.89	0.00
213694_at	**RSBN1**	54665	round spermatid basic protein 1	-3.27	0.13
226387_at	**RSBN1L**	222194	round spermatid basic protein 1-like	-9.65	0.00
223713_at	**RSPH3**	83861	radial spoke head 3 homolog (Chlamydomonas)	-3.01	0.22
201980_s_at	**RSU1**	6251	Ras suppressor protein 1	-6.88	0.22
219549_s_at	**RTN3**	10313	reticulon 3	-4.00	0.00
219684_at	**RTP4**	64108	receptor (chemosensory) transporter protein 4	6.49	0.58
232231_at	**RUNX2**	860	runt-related transcription factor 2	-12.57	0.10
204197_s_at	**RUNX3**	864	runt-related transcription factor 3	3.17	0.10
205087_at	**RWDD3**	25950	RWD domain containing 3	-3.12	0.37
209148_at	**RXRB**	6257	retinoid X receptor, beta	-4.42	0.00
212440_at	**RY1**	11017	putative nucleic acid binding protein RY-1	2.21	0.10
203186_s_at	**S100A4**	6275	S100 calcium binding protein A4	-13.18	0.00
217728_at	**S100A6**	6277	S100 calcium binding protein A6	-13.31	0.00
204351_at	**S100P**	6286	S100 calcium binding protein P	-2.74	0.00

213635_s_at	**SAFB**	6294	Scaffold attachment factor B	2.13	0.22
1553876_at	**SAMD3**	154075	sterile alpha motif domain containing 3	2.45	0.58
235643_at	**SAMD9L**	219285	sterile alpha motif domain containing 9-like	2.01	0.00
1555638_a_at	**SAMSN1**	64092	SAM domain, SH3 domain and nuclear localization signals 1	13.56	0.00
219129_s_at	**SAP30L**	79685	SAP30-like	-3.28	0.37
218254_s_at	**SAR1B**	51128	SAR1 gene homolog B (S. cerevisiae)	4.00	0.03
200051_at	**SART1**	9092	squamous cell carcinoma antigen recognized by T cells	-2.01	0.22
200069_at	**SART3**	9733	squamous cell carcinoma antigen recognized by T cells 3	3.38	0.22
222669_s_at	**SBDS** /// **SBDSP**	155370 /// 51119	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	2.24	0.37
212417_at	**SCAMP1**	9522	secretory carrier membrane protein 1	-2.73	0.37
212329_at	**SCAP**	22937	SREBF chaperone	-10.61	0.37
209741_x_at	**SCAPER**	49855	S phase cyclin A-associated protein in the ER	2.83	0.58
1554705_at	**SCARA5**	286133	scavenger receptor class A, member 5 (putative)	5.08	0.13
1555021_a_at	**SCARF1**	8578	scavenger receptor class F, member 1	4.37	0.00
201826_s_at	**SCCPDH**	51097	saccharopine dehydrogenase (putative)	3.46	0.22
219196_at	**SCG3**	29106	secretogranin III	8.27	0.03
1569495_at	**SCLT1**	132320	sodium channel and clathrin linker 1	-8.32	0.13
205508_at	**SCN1B**	6324	sodium channel, voltage-gated, type I, beta	49.45	0.22
218217_at	**SCPEP1**	59342	serine carboxypeptidase 1	-2.50	0.37
212154_at	**SDC2**	6383	syndecan 2	5.55	0.58
202071_at	**SDC4**	6385	syndecan 4	4.96	0.06
1555539_at	**SDS**	10993	serine dehydratase	2.05	0.13
214257_s_at	**SEC22B**	9554	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	2.42	0.00
210293_s_at	**SEC23B**	10483	Sec23 homolog B (S. cerevisiae)	5.99	0.03
212900_at	**SEC24A**	10802	SEC24 related gene family, member A (S. cerevisiae)	7.55	0.22
202375_at	**SEC24D**	9871	SEC24 related gene family, member D (S. cerevisiae)	2.42	0.13
200945_s_at	**SEC31A**	22872	SEC31 homolog A (S. cerevisiae)	3.81	0.37
217716_s_at	**SEC61A1**	29927	Sec61 alpha 1 subunit (S. cerevisiae)	2.84	0.37
203484_at	**SEC61G**	23480	Sec61 gamma subunit	2.10	0.06
204563_at	**SELL**	6402	selectin L (lymphocyte adhesion molecule 1)	-8.05	0.00
209879_at	**SELPLG**	6404	selectin P ligand	-13.45	0.00
223209_s_at	**SELS**	55829	selenoprotein S	5.18	0.00
234725_s_at	**SEMA4B**	10509	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-2.03	0.13
223449_at	**SEMA6A**	57556	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	9.84	0.13
57703_at	**SENP5**	205564	SUMO1/sentrin specific peptidase 5	2.19	0.37
202318_s_at	**SENP6**	26054	SUMO1/sentrin specific peptidase 6	-2.90	0.00
220735_s_at	**SENP7**	57337	SUMO1/sentrin specific peptidase 7	-3.10	0.37
213151_s_at	**SEPT7**	989	septin 7	-2.12	0.10
208657_s_at	**SEPT9**	10801	septin 9	-2.39	0.13
208531_at	**SERPINA2**	390502	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 2	2.60	0.58
206034_at	**SERPINB8**	5271	serpin peptidase inhibitor, clade B (ovalbumin), member 8	6.92	0.00
209723_at	**SERPINB9**	5272	serpin peptidase inhibitor, clade B (ovalbumin), member 9	9.16	0.00

200986_at	**SERPING1**	710	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	2.22	0.58
202656_s_at	**SERTAD2**	9792	SERTA domain containing 2	-2.33	0.10
235684_s_at	**SESN3**	143686	sestrin 3	-5.99	0.00
213153_at	**SETD1B**	23067	SET domain containing 1B	-2.80	0.00
235339_at	**SETDB2**	83852	SET domain, bifurcated 2	3.44	0.00
232229_at	**SETX**	23064	senataxin	-2.32	0.22
240709_at	**SEZ6L**	23544	seizure related 6 homolog (mouse)-like	3.24	0.00
227210_at	**SFMBT2**	57713	Scm-like with four mbt domains 2	16.81	0.00
200893_at	**SFRS10**	6434	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	2.91	0.13
214092_x_at	**SFRS14**	10147	splicing factor, arginine/serine-rich 14	-2.11	0.58
225849_s_at	**SFT2D1**	113402	SFT2 domain containing 1	2.01	0.00
214354_x_at	**SFTPB**	6439	surfactant, pulmonary-associated protein B	7.89	0.00
238567_at	**SGPP2**	130367	sphingosine-1-phosphate phosphotase 2	166.20	0.00
232084_at	**SGTB**	54557	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	12.06	0.00
222169_x_at	**SH2D3A**	10045	SH2 domain containing 3A	2.72	0.10
221269_s_at	**SH3BGRL3**	83442	SH3 domain binding glutamic acid-rich protein like 3	-2.56	0.03
223265_at	**SH3BP5L**	80851	SH3-binding domain protein 5-like	-4.91	0.37
1567027_at	**SH3GLP2**	6459	SH3-domain GRB2-like pseudogene 2	2.02	0.13
223082_at	**SH3KBP1**	30011	SH3-domain kinase binding protein 1	-2.80	0.03
209980_s_at	**SHMT1**	6470	serine hydroxymethyltransferase 1 (soluble)	2.23	0.03
218765_at	**SIDT2**	51092	SID1 transmembrane family, member 2	-2.95	0.22
225056_at	**SIPA1L2**	57568	signal-induced proliferation-associated 1 like 2	-2.14	0.37
206934_at	**SIRPB1**	10326	signal-regulatory protein beta 1	-3.90	0.00
1559034_at	**SIRPB2**	284759	signal-regulatory protein beta 2	-6.68	0.06
232891_at	**SIRPD**	128646	signal-regulatory protein delta	-3.49	0.37
204362_at	**SKAP2**	8935	src kinase associated phosphoprotein 2	-2.19	0.00
229265_at	**SKI**	6497	v-ski sarcoma viral oncogene homolog (avian)	-2.67	0.10
232379_at	**SKIL**	6498	SKI-like oncogene	9.75	0.00
206181_at	**SLAMF1**	6504	signaling lymphocytic activation molecule family member 1	29.31	0.37
219159_s_at	**SLAMF7**	57823	SLAM family member 7	82.45	0.00
206052_s_at	**SLBP**	7884	stem-loop (histone) binding protein	-5.82	0.58
203124_s_at	**SLC11A2**	4891	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	103.70	0.00
220371_s_at	**SLC12A9**	56996	solute carrier family 12 (potassium/chloride transporters), member 9	-19.47	0.00
225057_at	**SLC15A4**	121260	solute carrier family 15, member 4	-2.87	0.00
222939_s_at	**SLC16A10**	117247	solute carrier family 16, member 10 (aromatic amino acid transporter)	76.87	0.58
206600_s_at	**SLC16A5**	9121	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	-2.68	0.13
207038_at	**SLC16A6**	9120	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	-2.40	0.13
211576_s_at	**SLC19A1**	6573	solute carrier family 19 (folate transporter), member 1	-8.61	0.10
212811_x_at	**SLC1A4**	6509	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	3.60	0.58
228497_at	**SLC22A15**	55356	solute carrier family 22 (organic cation transporter), member 15	-3.79	0.58
206097_at	**SLC22A18AS**	5003	solute carrier family 22 (organic cation transporter), member 18 antisense	4.86	0.22
205896_at	**SLC22A4**	6583	solute carrier family 22 (organic cation transporter), member 4	-5.11	0.37

211842_s_at	**SLC24A1**	9187	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	18.18	0.37
243969_at	**SLC24A4**	123041	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	-11.74	0.37
203775_at	**SLC25A13**	10165	solute carrier family 25, member 13 (citrin)	49.24	0.00
242335_at	**SLC25A37**	51312	solute carrier family 25, member 37	-2.02	0.00
226679_at	**SLC26A11**	284129	solute carrier family 26, member 11	6.56	0.37
201802_at	**SLC29A1**	2030	solute carrier family 29 (nucleoside transporters), member 1	-5.64	0.13
1555500_s_at	**SLC2A4RG**	56731	SLC2A4 regulator	5.77	0.10
220091_at	**SLC2A6**	11182	solute carrier family 2 (facilitated glucose transporter), member 6	6.41	0.22
207035_at	**SLC30A3**	7781	solute carrier family 30 (zinc transporter), member 3	-5.25	0.13
207362_at	**SLC30A4**	7782	solute carrier family 30 (zinc transporter), member 4	19.15	0.00
209326_at	**SLC35A2**	7355	solute carrier family 35 (UDP-galactose transporter), member A2	3.89	0.00
224716_at	**SLC35B2**	347734	solute carrier family 35, member B2	9.61	0.00
223304_at	**SLC37A3**	84255	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	-11.91	0.00
217778_at	**SLC39A1**	27173	solute carrier family 39 (zinc transporter), member 1	3.13	0.58
1553126_a_at	**SLC39A12**	221074	solute carrier family 39 (zinc transporter), member 12	2.10	0.22
209267_s_at	**SLC39A8**	64116	solute carrier family 39 (zinc transporter), member 8	91.85	0.00
200924_s_at	**SLC3A2**	6520	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	3.74	0.22
223044_at	**SLC40A1**	30061	solute carrier family 40 (iron-regulated transporter), member 1	-21.13	0.00
223798_at	**SLC41A2**	84102	solute carrier family 41, member 2	13.64	0.58
210692_s_at	**SLC43A3**	29015	solute carrier family 43, member 3	190.79	0.00
225175_s_at	**SLC44A2**	57153	solute carrier family 44, member 2	-27.44	0.00
225598_at	**SLC45A4**	57210	solute carrier family 45, member 4	-6.29	0.03
202111_at	**SLC4A2**	6522	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	6.60	0.58
202219_at	**SLC6A8**	6535	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	-5.24	0.58
209921_at	**SLC7A11**	23657	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	16.56	0.00
204588_s_at	**SLC7A7**	9056	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	7.09	0.00
235518_at	**SLC8A1**	6546	solute carrier family 8 (sodium/calcium exchanger), member 1	-2.84	0.37
201349_at	**SLC9A3R1**	9368	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	-6.29	0.22
227367_at	**SLCO3A1**	28232	solute carrier organic anion transporter family, member 3A1	-5.31	0.22
219911_s_at	**SLCO4A1**	28231	solute carrier organic anion transporter family, member 4A1	47.74	0.00
222071_s_at	**SLCO4C1**	353189	solute carrier organic anion transporter family, member 4C1	-8.45	0.03
226743_at	**SLFN11**	91607	schlafen family member 11	2.42	0.13
1553055_a_at	**SLFN5**	162394	schlafen family member 5	34.78	0.00
225243_s_at	**SLMAP**	7871	sarcolemma associated protein	-3.45	0.03
203021_at	**SLPI**	6590	secretory leukocyte peptidase inhibitor	4.66	0.00

238446_at	**SMA4**	11039	Glucuronidase, beta pseudogene	-3.14	0.22
215043_s_at	**SMA4** /// **SMA5**	11039 /// 11042	glucuronidase, beta pseudogene	-3.23	0.10
218284_at	**SMAD3**	4088	SMAD family member 3	15.29	0.00
1565703_at	**SMAD4**	4089	SMAD family member 4	-3.76	0.13
225282_at	**SMAP1L**	64744	stromal membrane-associated protein 1-like	-4.15	0.00
206542_s_at	**SMARCA2**	6595	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	-6.95	0.00
201075_s_at	**SMARCC1**	6599	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	-4.30	0.03
201827_at	**SMARCD2**	6603	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	-2.71	0.03
201589_at	**SMC1A**	8243	structural maintenance of chromosomes 1A	-2.37	0.13
209258_s_at	**SMC3**	9126	structural maintenance of chromosomes 3	-2.39	0.13
212569_at	**SMCHD1**	23347	structural maintenance of chromosomes flexible hinge domain containing 1	-2.35	0.00
235896_s_at	**SMCR7**	125170	Smith-Magenis syndrome chromosome region, candidate 7	-2.16	0.00
1557986_s_at	**SMCR8**	140775	Smith-Magenis syndrome chromosome region, candidate 8	2.27	0.37
205622_at	**SMPD2**	6610	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	2.15	0.03
213624_at	**SMPDL3A**	10924	sphingomyelin phosphodiesterase, acid-like 3A	7.37	0.22
205596_s_at	**SMURF2**	64750	SMAD specific E3 ubiquitin protein ligase 2	-2.56	0.37
226683_at	**SNAG1**	112574	Sorting nexin associated golgi protein 1	-2.58	0.03
205443_at	**SNAPC1**	6617	small nuclear RNA activating complex, polypeptide 1, 43kDa	16.67	0.00
201622_at	**SND1**	27044	staphylococcal nuclease and tudor domain containing 1	6.02	0.22
242790_at	**SNF8**	11267	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	3.01	0.58
1564906_at	**SNHG4**	724102	small nucleolar RNA host gene (non-protein coding) 4	3.39	0.13
209481_at	**SNRK**	54861	SNF related kinase	-2.11	0.03
201221_s_at	**SNRP70**	6625	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	-2.19	0.10
202690_s_at	**SNRPD1**	6632	small nuclear ribonucleoprotein D1 polypeptide 16kDa	2.77	0.22
207438_s_at	**SNUPN**	10073	snurportin 1	-3.64	0.37
214531_s_at	**SNX1**	6642	sorting nexin 1	-2.59	0.22
244661_at	**SOAT1**	6646	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-4.01	0.03
210677_at	**SOAT2**	8435	sterol O-acyltransferase 2	2.14	0.06
213337_s_at	**SOCS1**	8651	suppressor of cytokine signaling 1	11.64	0.06
206359_at	**SOCS3**	9021	suppressor of cytokine signaling 3	3.77	0.00
215078_at	**SOD2**	6648	superoxide dismutase 2, mitochondrial	2.77	0.00
201563_at	**SORD**	6652	sorbitol dehydrogenase	-7.46	0.00
230707_at	**SORL1**	6653	sortilin-related receptor, L(DLR class) A repeats-containing	-16.65	0.00
217644_s_at	**SOS2**	6655	son of sevenless homolog 2 (Drosophila)	-7.53	0.00
213721_at	**SOX2**	6657	SRY (sex determining region Y)-box 2	2.36	0.58
1563454_at	**SOX6**	55553	SRY (sex determining region Y)-box 6	2.09	0.10
224760_at	**SP1**	6667	Sp1 transcription factor	-4.13	0.00
207777_s_at	**SP140**	11262	SP140 nuclear body protein	3.54	0.03
1553579_a_at	**SPAG11B**	10407	sperm associated antigen 11B	2.11	0.58

212470_at	**SPAG9**	9043	sperm associated antigen 9	2.40	0.00
221057_at	**SPATA1**	64173	spermatogenesis associated 1	-3.30	0.13
1556601_a_at	**SPATA13**	221178	Spermatogenesis associated 13	-2.58	0.37
218164_at	**SPATA20**	64847	spermatogenesis associated 20	2.39	0.06
201240_s_at	**SPCS2**	9789	signal peptidase complex subunit 2 homolog (S. cerevisiae)	2.09	0.00
244461_at	**SPECC1**	92521	sperm antigen with calponin homology and coiled-coil domains 1	-7.40	0.00
201997_s_at	**SPEN**	23013	spen homolog, transcriptional regulator (Drosophila)	-4.01	0.58
212526_at	**SPG20**	23111	spastic paraplegia 20 (Troyer syndrome)	5.17	0.00
219257_s_at	**SPHK1**	8877	sphingosine kinase 1	45.36	0.00
206239_s_at	**SPINK1**	6690	serine peptidase inhibitor, Kazal type 1	33.11	0.22
206318_at	**SPINLW1**	57119	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	3.39	0.03
202826_at	**SPINT1**	6692	serine peptidase inhibitor, Kunitz type 1	-2.27	0.06
210715_s_at	**SPINT2**	10653	serine peptidase inhibitor, Kunitz type, 2	4.21	0.00
209875_s_at	**SPP1**	6696	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	8.93	0.00
226353_at	**SPPL2A**	84888	signal peptide peptidase-like 2A	3.66	0.00
46256_at	**SPSB3**	90864	splA/ryanodine receptor domain and SOCS box containing 3	-2.32	0.03
203128_at	**SPTLC2**	9517	serine palmitoyltransferase, long chain base subunit 2	-9.47	0.03
244804_at	**SQSTM1**	8878	Sequestosome 1	11.37	0.00
213324_at	**SRC**	6714	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	21.64	0.03
208095_s_at	**SRP72**	6731	signal recognition particle 72kDa	4.45	0.58
202200_s_at	**SRPK1**	6732	SFRS protein kinase 1	-4.04	0.00
1558254_s_at	**SRPK2**	6733	SFRS protein kinase 2	-14.59	0.00
202591_s_at	**SSBP1**	6742	single-stranded DNA binding protein 1	2.30	0.58
210829_s_at	**SSBP2**	23635	single-stranded DNA binding protein 2	-6.95	0.37
221752_at	**SSH1**	54434	Slingshot homolog 1 (Drosophila)	-3.80	0.22
226080_at	**SSH2**	85464	slingshot homolog 2 (Drosophila)	-5.75	0.00
200652_at	**SSR2**	6746	signal sequence receptor, beta (translocon-associated protein beta)	2.27	0.03
208666_s_at	**ST13**	6767	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	2.37	0.13
203759_at	**ST3GAL4**	6484	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-4.03	0.37
204542_at	**ST6GALNAC2**	10610	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	-9.97	0.00
1559208_at	**ST7OT4**	338069	ST7 overlapping transcript 4 (non-coding RNA)	2.01	0.58
206925_at	**ST8SIA4**	7903	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	-3.67	0.00
213820_s_at	**STARD5**	80765	StAR-related lipid transfer (START) domain containing 5	-9.67	0.22
225636_at	**STAT2**	6773	signal transducer and activator of transcription 2, 113kDa	2.33	0.00
206118_at	**STAT4**	6775	signal transducer and activator of transcription 4	23.98	0.06
212549_at	**STAT5B**	6777	signal transducer and activator of transcription 5B	-2.73	0.00
201331_s_at	**STAT6**	6778	signal transducer and activator of transcription 6, interleukin-4 induced	-3.26	0.00
202557_at	**STCH**	6782	stress 70 protein chaperone, microsome-associated, 60kDa	23.47	0.00
225987_at	**STEAP4**	79689	STEAP family member 4	-2.22	0.00

228394_at	**STK10**	6793	serine/threonine kinase 10	-2.59	0.22
209622_at	**STK16**	8576	serine/threonine kinase 16	-2.71	0.37
205214_at	**STK17B**	9262	serine/threonine kinase 17b	-3.72	0.22
208855_s_at	**STK24**	8428	serine/threonine kinase 24 (STE20 homolog, yeast)	-2.33	0.00
212572_at	**STK38L**	23012	serine/threonine kinase 38 like	-5.45	0.10
201061_s_at	**STOM**	2040	stomatin	4.96	0.00
205520_at	**STRN**	6801	striatin, calmodulin binding protein	-6.31	0.00
202223_at	**STT3A**	3703	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	4.15	0.22
212625_at	**STX10**	8677	syntaxin 10	-5.81	0.37
221500_s_at	**STX16**	8675	syntaxin 16	-2.07	0.03
203530_s_at	**STX4**	6810	syntaxin 4	3.10	0.00
203310_at	**STXBP3**	6814	syntaxin binding protein 3	-2.56	0.10
217874_at	**SUCLG1**	8802	succinate-CoA ligase, GDP-forming, alpha subunit	-3.85	0.13
224724_at	**SULF2**	55959	sulfatase 2	-7.83	0.03
203615_x_at	**SULT1A1**	6817	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	-4.53	0.06
207122_x_at	**SULT1A2**	6799	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	-4.34	0.22
207601_at	**SULT1B1**	27284	sulfotransferase family, cytosolic, 1B, member 1	-8.06	0.22
226850_at	**SUMF1**	285362	sulfatase modifying factor 1	-4.43	0.03
222979_s_at	**SURF4**	6836	surfeit 4	3.10	0.10
222759_at	**SUV420H1**	51111	suppressor of variegation 4-20 homolog 1 (Drosophila)	-2.74	0.13
209307_at	**SWAP70**	23075	SWAP-70 protein	2.02	0.06
226068_at	**SYK**	6850	spleen tyrosine kinase	-2.98	0.00
1558392_at	**SYNE2**	23224	spectrin repeat containing, nuclear envelope 2	-7.19	0.06
212828_at	**SYNJ2**	8871	synaptojanin 2	8.72	0.22
243313_at	**SYNPO2L**	79933	synaptopodin 2-like	2.52	0.13
224669_at	**SYS1**	90196	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	2.34	0.58
1560879_a_at	**SYT15**	83849	synaptotagmin XV	2.02	0.37
238423_at	**SYTL3**	94120	synaptotagmin-like 3	-2.61	0.58
217437_s_at	**TACC1**	6867	transforming, acidic coiled-coil containing protein 1	-2.25	0.13
218308_at	**TACC3**	10460	transforming, acidic coiled-coil containing protein 3	-20.99	0.00
235135_at	**TAF10**	6881	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	-2.31	0.06
205966_at	**TAF13**	6884	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	2.85	0.03
203893_at	**TAF9**	6880	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	5.93	0.00
221617_at	**TAF9B**	51616	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	2.88	0.37
200916_at	**TAGLN2**	8407	transgelin 2	-2.65	0.00
201463_s_at	**TALDO1**	6888	transaldolase 1	-2.06	0.13
207616_s_at	**TANK**	10010	TRAF family member-associated NFKB activator	4.87	0.00
225973_at	**TAP2**	6891	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	2.05	0.13
227407_at	**TAPT1**	202018	transmembrane anterior posterior transformation 1	-2.80	0.37
216920_s_at	**TARP** /// **TRGC2** /// **TRGV9**	445347 /// 6967 /// 6983	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading frame protein	25.76	0.00

221397_at	**TAS2R10**	50839	taste receptor, type 2, member 10	-2.09	0.58
1553556_at	**TAS2R40**	259286	taste receptor, type 2, member 40	-10.98	0.03
228867_at	**TATDN3**	128387	TatD DNase domain containing 3	-4.72	0.58
203977_at	**TAZ**	6901	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	-2.47	0.37
1569566_at	**TBC1D1**	23216	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	-2.70	0.10
228258_at	**TBC1D10C**	374403	TBC1 domain family, member 10C	-9.65	0.13
224622_at	**TBC1D14**	57533	TBC1 domain family, member 14	-4.43	0.22
223461_at	**TBC1D7**	51256	TBC1 domain family, member 7	7.91	0.03
1563272_at	**TBC1D8B**	54885	TBC1 domain family, member 8B (with GRAM domain)	3.05	0.58
201804_x_at	**TBCB**	1155	tubulin folding cofactor B	-2.14	0.58
218520_at	**TBK1**	29110	TANK-binding kinase 1	3.22	0.00
201868_s_at	**TBL1X**	6907	transducin (beta)-like 1X-linked	-3.79	0.00
207689_at	**TBX10**	347853	T-box 10	3.34	0.37
229565_x_at	**TBX3**	6926	T-box 3 (ulnar mammary syndrome)	2.54	0.37
208130_s_at	**TBXAS1**	6916	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	-4.73	0.03
213142_x_at	**tcag7.1314**	54103	hypothetical protein LOC54103	18.00	0.00
238678_at	**tcag7.907**	402483	hypothetical LOC402483	-8.32	0.03
200085_s_at	**TCEB2**	6923	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	-3.16	0.22
212761_at	**TCF7L2**	6934	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.83	0.58
235694_at	**TCFL5**	10732	transcription factor-like 5 (basic helix-loop-helix)	25.00	0.00
223455_at	**TCHP**	84260	trichoplein, keratin filament binding	-2.34	0.03
221624_at	**TCL6**	27004	T-cell leukemia/lymphoma 6	3.85	0.00
222011_s_at	**TCP1**	6950	t-complex 1	6.60	0.00
1553861_at	**TCP11L2**	255394	t-complex 11 (mouse)-like 2	-30.87	0.00
232692_at	**TDRD6**	221400	tudor domain containing 6	15.63	0.10
218104_at	**TEX10**	54881	testis expressed 10	3.90	0.22
203176_s_at	**TFAM**	7019	transcription factor A, mitochondrial	-2.95	0.58
50221_at	**TFEB**	7942	transcription factor EB	-5.63	0.03
232383_at	**TFEC**	22797	transcription factor EC	79.46	0.00
217839_at	**TFG**	10342	TRK-fused gene	2.19	0.10
202750_s_at	**TFIP11**	24144	tuftelin interacting protein 11	2.46	0.10
209278_s_at	**TFPI2**	7980	tissue factor pathway inhibitor 2	8.74	0.37
207332_s_at	**TFRC**	7037	transferrin receptor (p90, CD71)	54.87	0.00
205016_at	**TGFA**	7039	transforming growth factor, alpha	-7.54	0.00
208944_at	**TGFBR2**	7048	transforming growth factor, beta receptor II (70/80kDa)	-6.45	0.00
203313_s_at	**TGIF1**	7050	TGFB-induced factor homeobox 1	9.30	0.00
211003_x_at	**TGM2**	7052	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	12.13	0.00
219231_at	**TGS1**	96764	trimethylguanosine synthase homolog (S. cerevisiae)	2.14	0.00
1566888_at	**THADA**	63892	Thyroid adenoma associated	-2.07	0.03
203887_s_at	**THBD**	7056	thrombomodulin	-4.99	0.00
201110_s_at	**THBS1**	7057	thrombospondin 1	8.31	0.10
223804_s_at	**THUMPD3**	25917	THUMP domain containing 3	2.81	0.58
223711_s_at	**THYN1**	29087	thymocyte nuclear protein 1	-2.25	0.58
213191_at	**TICAM1**	148022	toll-like receptor adaptor molecule 1	18.93	0.37
238858_at	**TIFA**	92610	TRAF-interacting protein with a forkhead-associated domain	6.55	0.00
229789_at	**TIGD3**	220359	tigger transposable element derived 3	-14.97	0.00

218408_at	**TIMM10**	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)	10.70	0.00
201821_s_at	**TIMM17A**	10440	translocase of inner mitochondrial membrane 17 homolog A (yeast)	3.65	0.06
201666_at	**TIMP1**	7076	TIMP metallopeptidase inhibitor 1	5.95	0.10
231579_s_at	**TIMP2**	7077	TIMP metallopeptidase inhibitor 2	-3.86	0.00
47608_at	**TJAP1**	93643	tight junction associated protein 1 (peripheral)	7.23	0.06
208700_s_at	**TKT**	7086	transketolase (Wernicke-Korsakoff syndrome)	-9.57	0.00
216370_s_at	**TKTL1**	8277	transketolase-like 1	3.98	0.00
214688_at	**TLE4**	7091	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	-3.12	0.03
212997_s_at	**TLK2**	11011	tousled-like kinase 2	-2.02	0.10
210176_at	**TLR1**	7096	toll-like receptor 1	-5.16	0.00
223750_s_at	**TLR10**	81793	toll-like receptor 10	-3.33	0.58
210166_at	**TLR5**	7100	toll-like receptor 5	-18.31	0.03
207446_at	**TLR6**	10333	toll-like receptor 6	-8.89	0.03
220832_at	**TLR8**	51311	toll-like receptor 8	-2.67	0.00
212198_s_at	**TM9SF4**	9777	transmembrane 9 superfamily protein member 4	4.38	0.22
213349_at	**TMCC1**	23023	transmembrane and coiled-coil domain family 1	-4.16	0.10
226489_at	**TMCC3**	57458	transmembrane and coiled-coil domain family 3	-7.26	0.00
226050_at	**TMCO3**	55002	transmembrane and coiled-coil domains 3	-3.30	0.22
213550_s_at	**TMCO6**	55374	transmembrane and coiled-coil domains 6	-2.84	0.10
200929_at	**TMED10**	10972	transmembrane emp24-like trafficking protein 10 (yeast)	3.85	0.00
214658_at	**TMED7**	51014	transmembrane emp24 protein transport domain containing 7	2.25	0.06
205812_s_at	**TMED9**	54732	transmembrane emp24 protein transport domain containing 9	2.34	0.10
212682_s_at	**TMEM112B**	91289	transmembrane protein 112B	-3.04	0.37
225588_s_at	**TMEM129**	92305	transmembrane protein 129	-3.59	0.37
223105_s_at	**TMEM14B** /// **TMEM14C**	51522 /// 81853	transmembrane protein 14C /// transmembrane protein 14B	-2.16	0.37
226752_at	**TMEM157**	345757	transmembrane protein 157	-19.99	0.00
213338_at	**TMEM158**	25907	transmembrane protein 158	15.08	0.37
223202_s_at	**TMEM164**	84187	transmembrane protein 164	-4.53	0.00
224906_at	**TMEM16F**	196527	transmembrane protein 16F	3.73	0.22
218113_at	**TMEM2**	23670	transmembrane protein 2	-3.59	0.00
222735_at	**TMEM38B**	55151	transmembrane protein 38B	7.84	0.22
241392_at	**TMEM39A**	55254	Transmembrane protein 39A	9.87	0.03
209796_s_at	**TMEM4**	10330	transmembrane protein 4	3.09	0.06
217795_s_at	**TMEM43**	79188	transmembrane protein 43	-6.46	0.00
202090_s_at	**TMEM54** /// **UQCR**	10975 /// 113452	ubiquinol-cytochrome c reductase, 6.4kDa subunit /// transmembrane protein 54	-4.27	0.10
226338_at	**TMEM55A**	55529	transmembrane protein 55A	-7.16	0.00
225287_s_at	**TMEM55B**	90809	transmembrane protein 55B	2.84	0.06
241342_at	**TMEM65**	157378	transmembrane protein 65	-5.09	0.37
200847_s_at	**TMEM66**	51669	transmembrane protein 66	-2.53	0.00
226483_at	**TMEM68**	137695	transmembrane protein 68	4.09	0.58
238429_at	**TMEM71**	137835	transmembrane protein 71	-22.85	0.00
221882_s_at	**TMEM8**	58986	transmembrane protein 8 (five membrane-spanning domains)	-3.34	0.22
229957_at	**TMEM91**	641649	transmembrane protein 91	-6.81	0.00
222449_at	**TMEPAI**	56937	transmembrane, prostate androgen induced RNA	-2.98	0.06

223659_at	**TMPRSS13**	84000	transmembrane protease, serine 13	2.21	0.37
224397_s_at	**TMTC1**	83857	transmembrane and tetratricopeptide repeat containing 1	-5.60	0.13
207113_s_at	**TNF**	7124	tumor necrosis factor (TNF superfamily, member 2)	9.69	0.00
202643_s_at	**TNFAIP3**	7128	tumor necrosis factor, alpha-induced protein 3	36.15	0.00
206025_s_at	**TNFAIP6**	7130	tumor necrosis factor, alpha-induced protein 6	9.91	0.00
223583_at	**TNFAIP8L2**	79626	tumor necrosis factor, alpha-induced protein 8-like 2	-3.07	0.37
231775_at	**TNFRSF10A**	8797	tumor necrosis factor receptor superfamily, member 10a	2.87	0.22
211163_s_at	**TNFRSF10C**	8794	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	-20.85	0.00
224090_s_at	**TNFRSF19**	55504	tumor necrosis factor receptor superfamily, member 19	2.18	0.00
203508_at	**TNFRSF1B**	7133	tumor necrosis factor receptor superfamily, member 1B	2.19	0.00
214581_x_at	**TNFRSF21**	27242	tumor necrosis factor receptor superfamily, member 21	8.39	0.58
206729_at	**TNFRSF8**	943	tumor necrosis factor receptor superfamily, member 8	3.35	0.13
207536_s_at	**TNFRSF9**	3604	tumor necrosis factor receptor superfamily, member 9	2.35	0.37
202687_s_at	**TNFSF10**	8743	tumor necrosis factor (ligand) superfamily, member 10	-2.96	0.00
209500_x_at	**TNFSF12-TNFSF13** /// **TNFSF13**	407977 /// 8741	tumor necrosis factor (ligand) superfamily, member 13 /// tumor necrosis factor (ligand) superfamily, member 12-member 13	-5.13	0.13
223501_at	**TNFSF13B**	10673	tumor necrosis factor (ligand) superfamily, member 13b	-2.66	0.00
221085_at	**TNFSF15**	9966	tumor necrosis factor (ligand) superfamily, member 15	15.66	0.00
206907_at	**TNFSF9**	8744	tumor necrosis factor (ligand) superfamily, member 9	34.70	0.10
207196_s_at	**TNIP1**	10318	TNFAIP3 interacting protein 1	2.29	0.00
220655_at	**TNIP3**	79931	TNFAIP3 interacting protein 3	120.69	0.00
212635_at	**TNPO1**	3842	transportin 1	-2.43	0.06
217931_at	**TNRC5**	10695	trinucleotide repeat containing 5	-6.88	0.00
240044_x_at	**TNRC6B**	23112	Trinucleotide repeat containing 6B	-6.03	0.00
222820_at	**TNRC6C**	57690	trinucleotide repeat containing 6C	-3.03	0.37
202807_s_at	**TOM1**	10043	target of myb1 (chicken)	4.34	0.00
226198_at	**TOM1L2**	146691	target of myb1-like 2 (chicken)	-5.80	0.06
226059_at	**TOMM40L**	84134	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	7.70	0.22
202633_at	**TOPBP1**	11073	topoisomerase (DNA) II binding protein 1	-4.12	0.37
204071_s_at	**TOPORS**	10210	topoisomerase I binding, arginine/serine-rich	-3.95	0.00
203050_at	**TP53BP1**	7158	tumor protein p53 binding protein 1	3.19	0.03
203421_at	**TP53I11**	9537	tumor protein p53 inducible protein 11	-7.58	0.00
225912_at	**TP53INP1**	94241	tumor protein p53 inducible nuclear protein 1	-3.85	0.00
235194_at	**TPCN2**	219931	two pore segment channel 2	-3.14	0.03
200742_s_at	**TPP1**	1200	tripeptidyl peptidase I	4.38	0.00
201731_s_at	**TPR**	7175	translocated promoter region (to activated MET oncogene)	-2.95	0.00
205599_at	**TRAF1**	7185	TNF receptor-associated factor 1	71.62	0.00
208315_x_at	**TRAF3**	7187	TNF receptor-associated factor 3	7.35	0.00
215411_s_at	**TRAF3IP2**	10758	TRAF3 interacting protein 2	9.72	0.00
205804_s_at	**TRAF3IP3**	80342	TRAF3 interacting protein 3	2.74	0.00
202871_at	**TRAF4**	9618	TNF receptor-associated factor 4	8.05	0.37

201399_s_at	**TRAM1**	23471	translocation associated membrane protein 1	2.66	0.10
203511_s_at	**TRAPPC3**	27095	trafficking protein particle complex 3	3.47	0.22
219748_at	**TREML2**	79865	triggering receptor expressed on myeloid cells-like 2	-2.60	0.03
229016_s_at	**TRERF1**	55809	transcriptional regulating factor 1	-12.42	0.10
218145_at	**TRIB3**	57761	tribbles homolog 3 (Drosophila)	13.59	0.37
210541_s_at	**TRIM27**	5987	tripartite motif-containing 27	-5.96	0.00
211001_at	**TRIM29**	23650	tripartite motif-containing 29	2.01	0.22
221044_s_at	**TRIM34** /// **TRIM6-TRIM34**	445372 /// 53840	tripartite motif-containing 34 /// tripartite motif-containing 6 and tripartite motif-containing 34	-2.71	0.58
219736_at	**TRIM36**	55521	tripartite motif-containing 36	11.10	0.58
1568592_at	**TRIM69**	140691	tripartite motif-containing 69	2.26	0.00
221012_s_at	**TRIM8**	81603	tripartite motif-containing 8	-6.92	0.00
202734_at	**TRIP10**	9322	thyroid hormone receptor interactor 10	39.56	0.00
221952_x_at	**TRMT5**	57570	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	-2.46	0.00
222768_s_at	**TRMT6**	51605	tRNA methyltransferase 6 homolog (S. cerevisiae)	3.58	0.37
205708_s_at	**TRPM2**	7226	transient receptor potential cation channel, subfamily M, member 2	2.30	0.37
240389_at	**TRPM6**	140803	Transient receptor potential cation channel, subfamily M, member 6	-10.64	0.00
223324_s_at	**TRPM7**	54822	transient receptor potential cation channel, subfamily M, member 7	6.96	0.13
1552586_at	**TRPV3**	162514	transient receptor potential cation channel, subfamily V, member 3	2.49	0.37
241606_s_at	**TRUB1**	142940	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	2.29	0.37
204094_s_at	**TSC22D2**	9819	TSC22 domain family, member 2	2.34	0.03
208763_s_at	**TSC22D3**	1831	TSC22 domain family, member 3	-3.16	0.00
218132_s_at	**TSEN34**	79042	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	-5.94	0.00
214331_at	**TSFM**	10102	Ts translation elongation factor, mitochondrial	-3.77	0.37
238973_s_at	**TSNAX**	7257	translin-associated factor X	2.10	0.00
221002_s_at	**TSPAN14**	81619	tetraspanin 14	2.39	0.22
218693_at	**TSPAN15**	23555	tetraspanin 15	2.12	0.37
242179_s_at	**TSPAN16**	26526	tetraspanin 16	-5.47	0.06
227236_at	**TSPAN2**	10100	tetraspanin 2	-14.02	0.10
202242_at	**TSPAN7**	7102	tetraspanin 7	2.05	0.37
201434_at	**TTC1**	7265	tetratricopeptide repeat domain 1	2.43	0.22
1554672_at	**TTC26**	79989	tetratricopeptide repeat domain 26	2.52	0.13
203584_at	**TTC35**	9694	tetratricopeptide repeat domain 35	3.32	0.03
226120_at	**TTC8**	123016	tetratricopeptide repeat domain 8	-2.21	0.22
227386_s_at	**TTMB**	399474	TTMB protein	-3.52	0.00
209118_s_at	**TUBA1A**	7846	tubulin, alpha 1a	-3.36	0.00
212639_x_at	**TUBA1B**	10376	tubulin, alpha 1b	-2.02	0.00
211750_x_at	**TUBA1C**	84790	tubulin, alpha 1c	-3.38	0.00
210527_x_at	**TUBA3C**	7278	tubulin, alpha 3c	-2.40	0.13
212242_at	**TUBA4A**	7277	tubulin, alpha 4a	-2.47	0.00
207490_at	**TUBA4B**	80086	tubulin, alpha 4b (pseudogene)	-3.03	0.00
204141_at	**TUBB2A**	7280	tubulin, beta 2A	17.68	0.37
214876_s_at	**TUBGCP5**	114791	tubulin, gamma complex associated protein 5	3.35	0.37
223325_at	**TXNDC11**	51061	thioredoxin domain containing 11	2.16	0.22
201580_s_at	**TXNDC13**	56255	thioredoxin domain containing 13	-11.88	0.00
201175_at	**TXNDC14**	51075	thioredoxin domain containing 14	4.50	0.22
201008_s_at	**TXNIP**	10628	thioredoxin interacting protein	-3.07	0.00

205546_s_at	**TYK2**	7297	tyrosine kinase 2	-3.72	0.06
209947_at	**UBAP2L**	9898	ubiquitin associated protein 2-like	2.23	0.58
205890_s_at	**UBD**	10537	ubiquitin D	17.02	0.00
203281_s_at	**UBE1L**	7318	ubiquitin-activating enzyme E1-like	-3.67	0.10
214590_s_at	**UBE2D1**	7321	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	-2.91	0.00
212519_at	**UBE2E1**	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	3.15	0.00
210024_s_at	**UBE2E3**	10477	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	-3.73	0.37
209141_at	**UBE2G1**	7326	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	-2.75	0.22
221962_s_at	**UBE2H**	7328	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	2.93	0.58
217823_s_at	**UBE2J1**	51465	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	-2.78	0.06
201649_at	**UBE2L6**	9246	ubiquitin-conjugating enzyme E2L 6	2.16	0.00
217750_s_at	**UBE2Z**	65264	ubiquitin-conjugating enzyme E2Z	6.23	0.00
202317_s_at	**UBE4B**	10277	ubiquitination factor E4B (UFD2 homolog, yeast)	-3.55	0.00
205687_at	**UBFD1**	56061	ubiquitin family domain containing 1	4.97	0.58
207253_s_at	**UBN1**	29855	ubinuclein 1	-2.30	0.00
224513_s_at	**UBQLN4**	56893	ubiquilin 4	7.66	0.58
238528_at	**UBR1**	197131	ubiquitin protein ligase E3 component n-recognin 1	5.90	0.10
212756_s_at	**UBR2**	23304	ubiquitin protein ligase E3 component n-recognin 2	-5.47	0.00
211950_at	**UBR4**	23352	ubiquitin protein ligase E3 component n-recognin 4	3.26	0.37
1555888_at	**UBR5**	51366	Ubiquitin protein ligase E3 component n-recognin 5	-6.04	0.00
224827_at	**UBTD2**	92181	ubiquitin domain containing 2	3.66	0.10
214881_s_at	**UBTF**	7343	upstream binding transcription factor, RNA polymerase I	-3.26	0.37
223012_at	**UBXD1**	80700	UBX domain containing 1	-3.65	0.10
218050_at	**UFM1**	51569	ubiquitin-fold modifier 1	3.01	0.00
224967_at	**UGCG**	7357	UDP-glucose ceramide glucosyltransferase	2.58	0.00
220746_s_at	**UIMC1**	51720	ubiquitin interaction motif containing 1	-3.14	0.03
209333_at	**ULK1**	8408	unc-51-like kinase 1 (C. elegans)	-4.16	0.22
203271_s_at	**UNC119**	9094	unc-119 homolog (C. elegans)	2.25	0.10
206189_at	**UNC5C**	8633	unc-5 homolog C (C. elegans)	3.20	0.37
230210_at	**UNC84A**	23353	unc-84 homolog A (C. elegans)	2.51	0.37
212144_at	**UNC84B**	25777	unc-84 homolog B (C. elegans)	-2.09	0.13
228219_s_at	**UPB1**	51733	ureidopropionase, beta	19.54	0.06
203519_s_at	**UPF2**	26019	UPF2 regulator of nonsense transcripts homolog (yeast)	-2.87	0.00
218757_s_at	**UPF3B**	65109	UPF3 regulator of nonsense transcripts homolog B (yeast)	2.43	0.58
210064_s_at	**UPK1B**	7348	uroplakin 1B	2.12	0.37
218601_at	**URG4**	55665	up-regulated gene 4	5.30	0.13
202152_x_at	**USF2**	7392	upstream transcription factor 2, c-fos interacting	2.04	0.22
209137_s_at	**USP10**	9100	ubiquitin specific peptidase 10	-4.87	0.00
213327_s_at	**USP12**	219333	ubiquitin specific peptidase 12	2.04	0.10
209475_at	**USP15**	9958	ubiquitin specific peptidase 15	-2.40	0.00
212513_s_at	**USP33**	23032	ubiquitin specific peptidase 33	-2.14	0.37
202682_s_at	**USP4**	7375	ubiquitin specific peptidase 4 (proto-oncogene)	-2.05	0.03
220784_s_at	**UTS2**	10911	urotensin 2	2.21	0.13

203241_at	**UVRAG**	7405	UV radiation resistance associated gene	3.28	0.22
208846_s_at	**VDAC3**	7419	voltage-dependent anion channel 3	-2.98	0.00
201831_s_at	**VDP**	8615	vesicle docking protein p115	2.75	0.00
211527_x_at	**VEGFA**	7422	vascular endothelial growth factor A	22.43	0.00
214004_s_at	**VGLL4**	9686	vestigial like 4 (Drosophila)	3.98	0.37
209950_s_at	**VILL**	50853	villin-like	3.69	0.37
218396_at	**VPS13C**	54832	vacuolar protein sorting 13 homolog C (S. cerevisiae)	3.93	0.00
212323_s_at	**VPS13D**	55187	vacuolar protein sorting 13 homolog D (S. cerevisiae)	3.86	0.22
223346_at	**VPS18**	57617	vacuolar protein sorting 18 homolog (S. cerevisiae)	3.88	0.06
222437_s_at	**VPS24**	51652	vacuolar protein sorting 24 homolog (S. cerevisiae)	-2.01	0.22
225483_at	**VPS26B**	112936	vacuolar protein sorting 26 homolog B (S. pombe)	-5.35	0.22
235625_at	**VPS41**	27072	vacuolar protein sorting 41 homolog (S. cerevisiae)	-2.67	0.37
200629_at	**WARS**	7453	tryptophanyl-tRNA synthetase	4.08	0.00
205400_at	**WAS**	7454	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	-2.12	0.06
224563_at	**WASF2**	10163	WAS protein family, member 2	-4.18	0.13
239194_at	**WBSCR18**	84277	Williams Beuren syndrome chromosome region 18	2.04	0.22
233559_s_at	**WDFY1**	57590	WD repeat and FYVE domain containing 1	2.69	0.37
209216_at	**WDR45**	11152	WD repeat domain 45	-3.37	0.13
65591_at	**WDR48**	57599	WD repeat domain 48	3.52	0.22
224076_s_at	**WHSC1L1**	54904	Wolf-Hirschhorn syndrome candidate 1-like 1	-11.34	0.00
213836_s_at	**WIPI1**	55062	WD repeat domain, phosphoinositide interacting 1	-5.18	0.06
204710_s_at	**WIPI2**	26100	WD repeat domain, phosphoinositide interacting 2	-3.50	0.00
210561_s_at	**WSB1**	26118	WD repeat and SOCS box-containing 1	2.04	0.00
214759_at	**WTAP**	9589	Wilms tumor 1 associated protein	4.92	0.00
222738_at	**WWC2**	80014	WW and C2 domain containing 2	2.52	0.06
219520_s_at	**WWC3**	55841	WWC family member 3	-5.50	0.22
228617_at	**XAF1**	54739	XIAP associated factor-1	6.76	0.00
200670_at	**XBP1**	7494	X-box binding protein 1	25.26	0.00
224589_at	**XIST**	7503	X (inactive)-specific transcript	-2.41	0.37
218753_at	**XKR8**	55113	XK, Kell blood group complex subunit-related family, member 8	-4.62	0.37
209375_at	**XPC**	7508	xeroderma pigmentosum, complementation group C	-2.54	0.37
214784_x_at	**XPO6**	23214	exportin 6	-8.65	0.00
205071_x_at	**XRCC4**	7518	X-ray repair complementing defective repair in Chinese hamster cells 4	-5.34	0.37
1570394_at	**XRN1**	54464	5'-3' exoribonuclease 1	3.56	0.22
212341_at	**YIPF6**	286451	Yip1 domain family, member 6	2.05	0.10
216304_x_at	**YME1L1**	10730	YME1-like 1 (S. cerevisiae)	2.00	0.06
232077_s_at	**YPEL3**	83719	yippee-like 3 (Drosophila)	-10.80	0.00
217812_at	**YTHDF2**	51441	YTH domain family, member 2	2.10	0.10
224718_at	**YY1**	7528	YY1 transcription factor	-2.62	0.13
227608_at	**YY1AP1**	55249	YY1 associated protein 1	-2.26	0.06
213376_at	**ZBTB1**	22890	zinc finger and BTB domain containing 1	3.94	0.03
203601_s_at	**ZBTB17**	7709	zinc finger and BTB domain containing 17	2.10	0.22
214482_at	**ZBTB25**	7597	zinc finger and BTB domain containing 25	5.18	0.06
227111_at	**ZBTB34**	403341	zinc finger and BTB domain containing 34	-3.05	0.06
226148_at	**ZBTB44**	29068	zinc finger and BTB domain containing 44	-5.90	0.00

227329_at	**ZBTB46**	140685	zinc finger and BTB domain containing 46	8.81	0.22
218810_at	**ZC3H12A**	80149	zinc finger CCCH-type containing 12A	3.34	0.00
231899_at	**ZC3H12C**	85463	zinc finger CCCH-type containing 12C	42.01	0.03
218348_s_at	**ZC3H7A**	29066	zinc finger CCCH-type containing 7A	2.30	0.10
221193_s_at	**ZCCHC10**	54819	zinc finger, CCHC domain containing 10	4.44	0.00
242776_at	**ZCCHC6**	79670	zinc finger, CCHC domain containing 6	-2.24	0.00
212982_at	**ZDHHC17**	23390	zinc finger, DHHC-type containing 17	-2.88	0.00
222731_at	**ZDHHC2**	51201	zinc finger, DHHC-type containing 2	-4.25	0.10
218606_at	**ZDHHC7**	55625	zinc finger, DHHC-type containing 7	-2.55	0.13
203603_s_at	**ZEB2**	9839	zinc finger E-box binding homeobox 2	3.86	0.00
202456_s_at	**ZER1**	10444	zer-1 homolog (C. elegans)	-6.72	0.10
226168_at	**ZFAND2B**	130617	zinc finger, AN1-type domain 2B	-3.07	0.13
217781_s_at	**ZFP106**	64397	zinc finger protein 106 homolog (mouse)	-2.58	0.13
201368_at	**ZFP36L2**	678	zinc finger protein 36, C3H type-like 2	-4.50	0.00
1555011_at	**ZFYVE16**	9765	zinc finger, FYVE domain containing 16	4.06	0.37
213073_at	**ZFYVE26**	23503	zinc finger, FYVE domain containing 26	7.92	0.00
203556_at	**ZHX2**	22882	zinc fingers and homeoboxes 2	2.62	0.00
224782_at	**ZMAT2**	153527	zinc finger, matrin type 2	-2.23	0.13
212124_at	**ZMIZ1**	57178	zinc finger, MIZ-type containing 1	2.46	0.00
202778_s_at	**ZMYM2**	7750	zinc finger, MYM-type 2	-4.17	0.58
1560854_s_at	**ZNF107**	51427	zinc finger protein 107	-3.11	0.37
204523_at	**ZNF140**	7699	zinc finger protein 140	3.89	0.10
208019_at	**ZNF157**	7712	zinc finger protein 157	2.43	0.00
205252_at	**ZNF174**	7727	zinc finger protein 174	-2.26	0.22
203585_at	**ZNF185**	7739	zinc finger protein 185 (LIM domain)	-13.20	0.00
207513_s_at	**ZNF189**	7743	zinc finger protein 189	3.04	0.37
203739_at	**ZNF217**	7764	zinc finger protein 217	-3.32	0.00
218005_at	**ZNF22**	7570	zinc finger protein 22 (KOX 15)	2.67	0.03
207128_s_at	**ZNF223**	7766	zinc finger protein 223	3.59	0.37
212774_at	**ZNF238**	10472	zinc finger protein 238	-3.71	0.00
203248_at	**ZNF24**	7572	zinc finger protein 24	2.75	0.03
206862_at	**ZNF254**	9534	zinc finger protein 254	-2.95	0.00
204937_s_at	**ZNF274**	10782	zinc finger protein 274	2.12	0.06
218401_s_at	**ZNF281**	23528	zinc finger protein 281	-2.46	0.00
212368_at	**ZNF292**	23036	zinc finger protein 292	2.81	0.03
203521_s_at	**ZNF318**	24149	zinc finger protein 318	8.13	0.37
231864_at	**ZNF33A**	7581	zinc finger protein 33A	-3.39	0.00
215022_x_at	**ZNF33B**	7582	zinc finger protein 33B	-4.55	0.00
207296_at	**ZNF343**	79175	zinc finger protein 343	3.97	0.10
205427_at	**ZNF354A**	6940	zinc finger protein 354A	-3.63	0.06
226468_at	**ZNF364**	27246	zinc finger protein 364	3.99	0.10
229551_x_at	**ZNF367**	195828	zinc finger protein 367	2.77	0.37
235414_at	**ZNF383**	163087	zinc finger protein 383	-14.82	0.22
214714_at	**ZNF394**	84124	zinc finger protein 394	-2.24	0.37
227768_at	**ZNF407**	55628	zinc finger protein 407	2.24	0.37
229743_at	**ZNF438**	220929	zinc finger protein 438	3.09	0.03
241066_at	**ZNF449**	203523	zinc finger protein 449	2.06	0.37
214746_s_at	**ZNF467**	168544	zinc finger protein 467	-14.41	0.00
203604_at	**ZNF516**	9658	zinc finger protein 516	-4.21	0.22
230205_at	**ZNF561**	93134	zinc finger protein 561	-3.31	0.13
219711_at	**ZNF586**	54807	zinc finger protein 586	-5.38	0.03
227507_at	**ZNF592**	9640	zinc finger protein 592	-3.51	0.10
232367_x_at	**ZNF598**	90850	zinc finger protein 598	-4.42	0.10
235179_at	**ZNF641**	121274	zinc finger protein 641	-2.31	0.37
230029_x_at	**ZNF650**	130507	zinc finger protein 650	-4.26	0.22

225266_at	**ZNF652**	22834	zinc finger protein 652	-8.57	0.00
222851_at	**ZNF654**	55279	zinc finger protein 654	3.34	0.37
227445_at	**ZNF689**	115509	zinc finger protein 689	-4.24	0.13
227080_at	**ZNF697**	90874	zinc finger protein 697	6.07	0.00
227132_at	**ZNF706**	51123	zinc finger protein 706	2.14	0.13
39891_at	**ZNF710**	374655	zinc finger protein 710	2.23	0.00
225848_at	**ZNF746**	155061	zinc finger protein 746	-6.30	0.03
221968_s_at	**ZNF771**	51333	Zinc finger protein 771	2.08	0.03
239838_at	**ZNF776**	284309	Zinc finger protein 776	-2.77	0.37
225131_at	**ZRANB1**	54764	zinc finger, RAN-binding domain containing 1	-3.00	0.37
225338_at	**ZYG11B**	79699	zyg-11 homolog B (C. elegans)	-8.22	0.10
200808_s_at	**ZYX**	7791	zyxin	-5.16	0.00
207190_at	**ZZEF1**	23140	zinc finger, ZZ-type with EF-hand domain 1	-2.49	0.37

Gene expression significantly perturbed in response to GM+I (fold change = GM+I/Control)

Gene ID	Gene Symbol	Gene ID	Gene Name	Fold Change	q-value (%)
1554915_a_at	**2'-PDE**	201626	2'-phosphodiesterase	6.83	0.06
205986_at	**AATK**	9625	apoptosis-associated tyrosine kinase	-2.11	0.16
203504_s_at	**ABCA1**	19	ATP-binding cassette, sub-family A (ABC1), member 1	-3.33	0.13
217504_at	**ABCA6**	23460	ATP-binding cassette, sub-family A (ABC1), member 6	2.09	0.06
219577_s_at	**ABCA7**	10347	ATP-binding cassette, sub-family A (ABC1), member 7	-12.01	0.13
202805_s_at	**ABCC1**	4363	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	5.19	0.00
226363_at	**ABCC5**	10057	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-12.13	0.03
201872_s_at	**ABCE1 /// LOC647150**	6059 /// 647150	ATP-binding cassette, sub-family E (OABP), member 1 /// similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I)	8.02	0.13
200045_at	**ABCF1**	23	ATP-binding cassette, sub-family F (GCN20), member 1	11.50	0.02
211113_s_at	**ABCG1**	9619	ATP-binding cassette, sub-family G (WHITE), member 1	-2.64	0.13
237974_at	**ABHD12B**	145447	abhydrolase domain containing 12B	-20.05	0.08
235348_at	**ABHD13**	84945	abhydrolase domain containing 13	-2.91	0.51
225337_at	**ABHD2**	11057	abhydrolase domain containing 2	-2.19	0.00
213017_at	**ABHD3**	171586	abhydrolase domain containing 3	-5.28	0.07
242023_at	**ABHD4**	63874	Abhydrolase domain containing 4	-2.09	0.08
218739_at	**ABHD5**	51099	abhydrolase domain containing 5	-7.14	0.00
227631_at	**ABI2**	10152	Abl interactor 2	2.29	0.34
231907_at	**ABL2**	27	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	6.03	0.08
229164_s_at	**ABTB1**	80325	ankyrin repeat and BTB (POZ) domain containing 1	-10.32	0.00
209608_s_at	**ACAT2**	39	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	3.09	0.02
207561_s_at	**ACCN3**	9311	amiloride-sensitive cation channel 3	-2.73	0.51
218981_at	**ACN9**	57001	ACN9 homolog (S. cerevisiae)	5.87	0.08
216103_at	**ACOT11**	26027	acyl-CoA thioesterase 11	2.09	0.34
221641_s_at	**ACOT9**	23597	acyl-CoA thioesterase 9	2.16	0.06
227962_at	**ACOX1**	51	acyl-Coenzyme A oxidase 1, palmitoyl	-6.83	0.00
215227_x_at	**ACP1**	52	acid phosphatase 1, soluble	-2.14	0.51
237030_at	**ACPP**	55	acid phosphatase, prostate	-3.72	0.34
238825_at	**ACRC**	93953	acidic repeat containing	-4.10	0.13

222592_s_at	**ACSL5**	51703	acyl-CoA synthetase long-chain family member 5	40.39	0.00
208637_x_at	**ACTN1**	87	actinin, alpha 1	-4.98	0.00
203861_s_at	**ACTN2**	88	actinin, alpha 2	-2.75	0.08
200601_at	**ACTN4**	81	actinin, alpha 4	-2.79	0.25
226950_at	**ACVRL1**	94	activin A receptor type II-like 1	10.61	0.00
225421_at	**ACY1L2**	135293	aminoacylase 1-like 2	2.69	0.34
209765_at	**ADAM19**	8728	ADAM metallopeptidase domain 19 (meltrin beta)	-11.07	0.00
205997_at	**ADAM28**	10863	ADAM metallopeptidase domain 28	-3.29	0.79
202381_at	**ADAM9**	8754	ADAM metallopeptidase domain 9 (meltrin gamma)	2.59	0.08
230167_at	**ADAMTS14**	140766	ADAM metallopeptidase with thrombospondin type 1 motif, 14	2.31	0.79
205882_x_at	**ADD3**	120	adducin 3 (gamma)	-6.78	0.00
209122_at	**ADFP**	123	adipose differentiation-related protein	9.74	0.00
208848_at	**ADH5**	128	alcohol dehydrogenase 5 (class III), chi polypeptide	2.12	0.51
203322_at	**ADNP2**	22850	ADNP homeobox 2	2.78	0.13
205013_s_at	**ADORA2A**	135	adenosine A2a receptor	9.36	0.00
228042_at	**ADPRH**	141	ADP-ribosylarginine hydrolase	5.26	0.06
206170_at	**ADRB2**	154	adrenergic, beta-2-, receptor, surface	-5.84	0.03
225229_at	**AFF4**	27125	AF4/FMR2 family, member 4	2.23	0.02
217046_s_at	**AGER**	177	advanced glycosylation end product-specific receptor	-2.71	0.00
224776_at	**AGPAT6**	137964	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	2.05	0.34
204500_s_at	**AGTPBP1**	23287	ATP/GTP binding protein 1	-5.18	0.00
214766_s_at	**AHCTF1**	25909	AT hook containing transcription factor 1	-4.65	0.00
228445_at	**AIFM2**	84883	apoptosis-inducing factor, mitochondrion-associated, 2	2.15	0.34
223136_at	**AIG1**	51390	androgen-induced 1	5.91	0.00
206513_at	**AIM2**	9447	absent in melanoma 2	2.13	0.25
212175_s_at	**AK2**	204	adenylate kinase 2	2.83	0.00
204348_s_at	**AK3L1 /// AK3L2 /// LOC645619**	205 /// 387851 /// 645619	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2 /// similar to Adenylate kinase isoenzyme 4, mitochondrial (ATP-AMP transphosphorylase)	21.76	0.51
225342_at	**AK3L2**	387851	adenylate kinase 3-like 2	6.00	0.00
205045_at	**AKAP10**	11216	A kinase (PRKA) anchor protein 10	-2.44	0.00
202760_s_at	**AKAP2 /// PALM2-AKAP2**	11217 /// 445815	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 protein	9.74	0.02
225701_at	**AKNA**	80709	AT-hook transcription factor	-2.79	0.00
201900_s_at	**AKR1A1**	10327	aldo-keto reductase family 1, member A1 (aldehyde reductase)	30.30	0.02
207163_s_at	**AKT1**	207	v-akt murine thymoma viral oncogene homolog 1	-7.66	0.51
212609_s_at	**AKT3**	10000	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	2.95	0.25
218373_at	**AKTIP**	64400	AKT interacting protein	-5.31	0.03
201952_at	**ALCAM**	214	activated leukocyte cell adhesion molecule	2.91	0.34
207016_s_at	**ALDH1A2**	8854	aldehyde dehydrogenase 1 family, member A2	51.08	0.06
201612_at	**ALDH9A1**	223	aldehyde dehydrogenase 9 family, member A1	-2.04	0.13
207381_at	**ALOX12B**	242	arachidonate 12-lipoxygenase, 12R type	2.41	0.34
207328_at	**ALOX15**	246	arachidonate 15-lipoxygenase	-5.94	0.16
204446_s_at	**ALOX5**	240	arachidonate 5-lipoxygenase	-3.42	0.00
215783_s_at	**ALPL**	249	alkaline phosphatase, liver/bone/kidney	-76.74	0.00

226431_at	**ALS2CR13**	150864	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13	-13.77	0.51
228094_at	**AMICA1**	120425	adhesion molecule, interacts with CXADR antigen 1	-13.48	0.00
212360_at	**AMPD2**	271	adenosine monophosphate deaminase 2 (isoform L)	-4.05	0.00
208498_s_at	**AMY1A** /// **AMY1B** /// **AMY1C** /// **AMY2A** /// **AMY2B** /// **LOC730924**	276 /// 277 /// 278 /// 279 /// 280 /// 730924	amylase, alpha 1A (salivary) /// amylase, alpha 1B (salivary) /// amylase, alpha 1C (salivary) /// amylase, alpha 2A (pancreatic) /// amylase, alpha 2B (pancreatic) /// similar to Pancreatic alpha-amylase precursor (PA) (1,4-alpha-D-glucan glucanohydrolase)	-4.13	0.34
231973_s_at	**ANAPC1**	64682	anaphase promoting complex subunit 1	-7.38	0.34
238642_at	**ANKRD13D**	338692	ankyrin repeat domain 13 family, member D	-7.53	0.79
231423_s_at	**ANKRD16**	54522	ankyrin repeat domain 16	2.24	0.13
238439_at	**ANKRD22**	118932	ankyrin repeat domain 22	34.47	0.00
211717_at	**ANKRD40**	91369	ankyrin repeat domain 40	5.41	0.34
219496_at	**ANKRD57**	65124	ankyrin repeat domain 57	2.12	0.34
238626_at	**ANKS6**	203286	ankyrin repeat and sterile alpha motif domain containing 6	-3.11	0.03
218274_s_at	**ANKZF1**	55139	ankyrin repeat and zinc finger domain containing 1	-2.66	0.34
208103_s_at	**ANP32E**	81611	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	2.46	0.00
202888_s_at	**ANPEP**	290	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	-5.15	0.03
225524_at	**ANTXR2**	118429	anthrax toxin receptor 2	-2.13	0.51
244206_at	**ANUBL1**	93550	AN1, ubiquitin-like, homolog (Xenopus laevis)	2.07	0.25
214783_s_at	**ANXA11**	311	annexin A11	-6.19	0.07
201590_x_at	**ANXA2**	302	annexin A2	4.73	0.06
208816_x_at	**ANXA2P2**	304	annexin A2 pseudogene 2	6.81	0.00
211241_at	**ANXA2P3**	305	annexin A2 pseudogene 3	2.37	0.79
209369_at	**ANXA3**	306	annexin A3	-2.68	0.25
201301_s_at	**ANXA4**	307	annexin A4	3.32	0.08
200782_at	**ANXA5**	308	annexin A5	4.31	0.00
201366_at	**ANXA7**	310	annexin A7	2.94	0.00
205639_at	**AOAH**	313	acyloxyacyl hydrolase (neutrophil)	-3.76	0.08
204894_s_at	**AOC3**	8639	amine oxidase, copper containing 3 (vascular adhesion protein 1)	-5.14	0.25
237159_x_at	**AP1S3**	130340	adaptor-related protein complex 1, sigma 3 subunit	21.83	0.02
204859_s_at	**APAF1**	317	apoptotic peptidase activating factor 1	-2.74	0.00
230925_at	**APBB1IP**	54518	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	-2.14	0.00
204650_s_at	**APBB3**	10307	amyloid beta (A4) precursor protein-binding, family B, member 3	-3.59	0.79
219465_at	**APOA2**	336	apolipoprotein A-II	5.44	0.51
220023_at	**APOB48R**	55911	apolipoprotein B48 receptor	-2.73	0.16
214994_at	**APOBEC3F**	200316	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	4.34	0.06
214995_s_at	**APOBEC3F** /// **APOBEC3G**	200316 /// 60489	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G /// apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	6.77	0.51
204205_at	**APOBEC3G**	60489	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	4.03	0.00
204561_x_at	**APOC2** /// **APOC4**	344 /// 346	apolipoprotein C-II /// apolipoprotein C-IV	-2.16	0.07

209546_s_at	**APOL1**	8542	apolipoprotein L, 1	4.76	0.00
221087_s_at	**APOL3**	80833	apolipoprotein L, 3	22.98	0.00
223801_s_at	**APOL4**	80832	apolipoprotein L, 4	18.41	0.00
219716_at	**APOL6**	80830	apolipoprotein L, 6	4.66	0.00
221620_s_at	**APOO**	79135	apolipoprotein O	9.62	0.51
244187_at	**APOOL**	139322	Apolipoprotein O-like	2.21	0.79
218527_at	**APTX**	54840	aprataxin	3.82	0.08
39248_at	**AQP3**	360	aquaporin 3 (Gill blood group)	19.97	0.34
201176_s_at	**ARCN1**	372	archain 1	2.15	0.34
201096_s_at	**ARF4**	378	ADP-ribosylation factor 4	3.57	0.00
222518_at	**ARFGEF2**	10564	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	5.13	0.00
218230_at	**ARFIP1**	27236	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	2.05	0.00
202109_at	**ARFIP2**	23647	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	2.25	0.16
206177_s_at	**ARG1**	383	arginase, liver	-3.21	0.79
218870_at	**ARHGAP15**	55843	Rho GTPase activating protein 15	-5.37	0.16
225173_at	**ARHGAP18**	93663	Rho GTPase activating protein 18	4.34	0.00
37577_at	**ARHGAP19**	84986	Rho GTPase activating protein 19	-13.06	0.13
205069_s_at	**ARHGAP26**	23092	Rho GTPase activating protein 26	-4.66	0.03
225618_at	**ARHGAP27**	201176	Rho GTPase activating protein 27	-2.16	0.03
204425_at	**ARHGAP4**	393	Rho GTPase activating protein 4	-5.42	0.08
213606_s_at	**ARHGDIA**	396	Rho GDP dissociation inhibitor (GDI) alpha	5.48	0.00
201288_at	**ARHGDIB**	397	Rho GDP dissociation inhibitor (GDI) beta	-2.78	0.00
221656_s_at	**ARHGEF10L**	55160	Rho guanine nucleotide exchange factor (GEF) 10-like	6.94	0.06
238730_at	**ARHGEF11**	9826	Rho guanine nucleotide exchange factor (GEF) 11	2.40	0.13
213039_at	**ARHGEF18**	23370	rho/rac guanine nucleotide exchange factor (GEF) 18	-3.31	0.34
218501_at	**ARHGEF3**	50650	Rho guanine nucleotide exchange factor (GEF) 3	3.69	0.34
209539_at	**ARHGEF6**	9459	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-8.39	0.07
218917_s_at	**ARID1A**	8289	AT rich interactive domain 1A (SWI-like)	-2.76	0.25
233339_s_at	**ARID1B**	57492	AT rich interactive domain 1B (SWI1-like)	-2.87	0.79
205062_x_at	**ARID4A**	5926	AT rich interactive domain 4A (RBP1-like)	-3.13	0.00
224322_at	**ARID4B**	51742	AT rich interactive domain 4B (RBP1-like)	-2.32	0.25
212614_at	**ARID5B**	84159	AT rich interactive domain 5B (MRF1-like)	8.05	0.25
201659_s_at	**ARL1**	400	ADP-ribosylation factor-like 1	2.46	0.13
202564_x_at	**ARL2**	402	ADP-ribosylation factor-like 2	12.12	0.51
202641_at	**ARL3**	403	ADP-ribosylation factor-like 3	-6.33	0.07
205020_s_at	**ARL4A**	10124	ADP-ribosylation factor-like 4A	2.06	0.51
242727_at	**ARL5B**	221079	ADP-ribosylation factor-like 5B	23.77	0.00
225707_at	**ARL6IP6**	151188	ADP-ribosylation-like factor 6 interacting protein 6	-3.05	0.13
222442_s_at	**ARL8B**	55207	ADP-ribosylation factor-like 8B	4.21	0.00
217858_s_at	**ARMCX3**	51566	armadillo repeat containing, X-linked 3	5.07	0.00
214749_s_at	**ARMCX6**	54470	armadillo repeat containing, X-linked 6	9.11	0.34
202655_at	**ARMET**	7873	arginine-rich, mutated in early stage tumors	2.44	0.02
209824_s_at	**ARNTL**	406	aryl hydrocarbon receptor nuclear translocator-like	-3.33	0.51
220658_s_at	**ARNTL2**	56938	aryl hydrocarbon receptor nuclear translocator-like 2	3.77	0.51
226405_s_at	**ARRDC1**	92714	arrestin domain containing 1	-3.18	0.51
226055_at	**ARRDC2**	27106	arrestin domain containing 2	4.12	0.25
224797_at	**ARRDC3**	57561	arrestin domain containing 3	-5.13	0.00

232197_x_at	**ARSB**	411	arylsulfatase B	2.97	0.51
1552632_a_at	**ARSG**	22901	arylsulfatase G	-6.64	0.08
227135_at	**ASAHL**	27163	N-acylsphingosine amidohydrolase (acid ceramidase)-like	-3.15	0.08
226861_at	**ASB8**	140461	ankyrin repeat and SOCS box-containing 8	-2.29	0.00
1554627_a_at	**ASCC1**	51008	activating signal cointegrator 1 complex subunit 1	2.51	0.13
212815_at	**ASCC3**	10973	activating signal cointegrator 1 complex subunit 3	5.33	0.13
209985_s_at	**ASCL1**	429	achaete-scute complex homolog 1 (Drosophila)	2.06	0.25
227014_at	**ASPHD2**	57168	aspartate beta-hydroxylase domain containing 2	10.31	0.00
224850_at	**ATAD1**	84896	ATPase family, AAA domain containing 1	3.68	0.00
1558233_s_at	**ATF1**	466	activating transcription factor 1	2.18	0.34
202672_s_at	**ATF3**	467	activating transcription factor 3	26.33	0.00
204998_s_at	**ATF5**	22809	activating transcription factor 5	21.26	0.00
226941_at	**ATF6**	22926	activating transcription factor 6	-3.20	0.00
229389_at	**ATG16L2**	89849	ATG16 autophagy related 16-like 2 (S. cerevisiae)	-10.15	0.00
202511_s_at	**ATG5**	9474	ATG5 autophagy related 5 homolog (S. cerevisiae)	2.96	0.16
218673_s_at	**ATG7**	10533	ATG7 autophagy related 7 homolog (S. cerevisiae)	5.18	0.06
202492_at	**ATG9A**	79065	ATG9 autophagy related 9 homolog A (S. cerevisiae)	-3.01	0.07
219359_at	**ATHL1**	80162	ATH1, acid trehalase-like 1 (yeast)	-7.45	0.00
208758_at	**ATIC**	471	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	5.14	0.34
212672_at	**ATM**	472	ataxia telangiectasia mutated	-2.81	0.08
208442_s_at	**ATM /// LOC651610**	472 /// 651610	ataxia telangiectasia mutated /// similar to Serine-protein kinase ATM (Ataxia telangiectasia mutated) (A-T, mutated)	-3.04	0.25
203454_s_at	**ATOX1**	475	ATX1 antioxidant protein 1 homolog (yeast)	4.76	0.00
213238_at	**ATP10D**	57205	ATPase, Class V, type 10D	3.26	0.00
1564064_a_at	**ATP11B**	23200	ATPase, Class VI, type 11B	-2.02	0.00
219558_at	**ATP13A3**	79572	ATPase type 13A3	5.67	0.00
220948_s_at	**ATP1A1**	476	ATPase, Na+/K+ transporting, alpha 1 polypeptide	4.55	0.00
201243_s_at	**ATP1B1**	481	ATPase, Na+/K+ transporting, beta 1 polypeptide	28.54	0.02
208836_at	**ATP1B3**	483	ATPase, Na+/K+ transporting, beta 3 polypeptide	10.48	0.00
209186_at	**ATP2A2**	488	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	4.18	0.00
213036_x_at	**ATP2A3**	489	ATPase, Ca++ transporting, ubiquitous	-2.93	0.34
212136_at	**ATP2B4**	493	ATPase, Ca++ transporting, plasma membrane 4	-6.04	0.07
212255_s_at	**ATP2C1**	27032	ATPase, Ca++ transporting, type 2C, member 1	2.25	0.25
207508_at	**ATP5G3**	518	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	2.36	0.06
207809_s_at	**ATP6AP1**	537	ATPase, H+ transporting, lysosomal accessory protein 1	2.60	0.08
201444_s_at	**ATP6AP2**	10159	ATPase, H+ transporting, lysosomal accessory protein 2	2.18	0.25
202872_at	**ATP6V1C1**	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	4.15	0.00

208898_at	**ATP6V1D**	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	2.83	0.00
201527_at	**ATP6V1F**	9296	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	3.30	0.02
208737_at	**ATP6V1G1**	9550	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	4.43	0.00
221504_s_at	**ATP6V1H**	51606	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	3.21	0.16
205197_s_at	**ATP7A**	538	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	-2.27	0.34
204624_at	**ATP7B**	540	ATPase, Cu++ transporting, beta polypeptide	-4.54	0.79
209903_s_at	**ATR**	545	ataxia telangiectasia and Rad3 related	5.46	0.16
1568706_s_at	**AVIL**	10677	Advillin	-6.67	0.79
225557_at	**AXUD1**	64651	AXIN1 up-regulated 1	2.40	0.00
218043_s_at	**AZI2**	64343	5-azacytidine induced 2	3.20	0.79
201772_at	**AZIN1**	51582	antizyme inhibitor 1	3.94	0.00
225612_s_at	**B3GNT5**	84002	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	3.19	0.00
212876_at	**B4GALT4**	8702	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	4.59	0.00
217911_s_at	**BAG3**	9531	BCL2-associated athanogene 3	2.69	0.25
227371_at	**BAIAP2L1**	55971	BAI1-associated protein 2-like 1	2.84	0.25
202391_at	**BASP1**	10409	brain abundant, membrane attached signal protein 1	-3.31	0.00
205965_at	**BATF**	10538	basic leucine zipper transcription factor, ATF-like	6.33	0.08
228439_at	**BATF2**	116071	basic leucine zipper transcription factor, ATF-like 2	31.13	0.00
203080_s_at	**BAZ2B**	29994	bromodomain adjacent to zinc finger domain, 2B	-8.36	0.00
214452_at	**BCAT1**	586	branched chain aminotransferase 1, cytosolic	26.81	0.16
227322_s_at	**BCCIP**	56647	BRCA2 and CDKN1A interacting protein	4.12	0.16
212312_at	**BCL2L1**	598	BCL2-like 1	5.40	0.06
227616_at	**BCL9L**	283149	B-cell CLL/lymphoma 9-like	4.96	0.51
219433_at	**BCOR**	54880	BCL6 co-repressor	2.48	0.02
201170_s_at	**BHLHB2**	8553	basic helix-loop-helix domain containing, class B, 2	10.05	0.00
223185_s_at	**BHLHB3**	79365	basic helix-loop-helix domain containing, class B, 3	10.55	0.00
229437_at	**BIC**	114614	BIC transcript	33.31	0.00
213154_s_at	**BICD2**	23299	bicaudal D homolog 2 (Drosophila)	-2.78	0.00
219191_s_at	**BIN2**	51411	bridging integrator 2	-2.07	0.00
210538_s_at	**BIRC3**	330	baculoviral IAP repeat-containing 3	4.93	0.16
225859_at	**BIRC4**	331	baculoviral IAP repeat-containing 4	2.98	0.00
229109_s_at	**BLVRA**	644	Biliverdin reductase A	4.03	0.06
226530_at	**BMF**	90427	Bcl2 modifying factor	3.88	0.25
226853_at	**BMP2K**	55589	BMP2 inducible kinase	-3.93	0.25
221478_at	**BNIP3L**	665	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-3.14	0.00
209836_x_at	**BOLA2 /// BOLA2B**	552900 /// 654483	bolA homolog 2 (E. coli) /// bolA homolog 2B (E. coli)	4.89	0.06
232909_s_at	**BPTF**	2186	bromodomain PHD finger transcription factor	-2.65	0.25
202427_s_at	**BRP44**	25874	brain protein 44	-4.05	0.79
235156_at	**BRWD3**	254065	bromodomain and WD repeat domain containing 3	-2.45	0.51
201641_at	**BST2**	684	bone marrow stromal cell antigen 2	3.28	0.06
226963_at	**BTF3L4**	91408	basic transcription factor 3-like 4	2.64	0.02
200921_s_at	**BTG1**	694	B-cell translocation gene 1, anti-proliferative	-2.79	0.00

213134_x_at	**BTG3**	10950	BTG family, member 3	55.79	0.16
215493_x_at	**BTN2A1**	11120	butyrophilin, subfamily 2, member A1	2.06	0.79
205298_s_at	**BTN2A2**	10385	butyrophilin, subfamily 2, member A2	4.41	0.13
209846_s_at	**BTN3A2**	11118	butyrophilin, subfamily 3, member A2	2.41	0.06
217207_s_at	**BTNL3**	10917	butyrophilin-like 3	-2.78	0.16
220421_at	**BTNL8 /// LOC653117**	653117 /// 79908	butyrophilin-like 8 /// similar to Butyrophilin-like protein 8 precursor	-4.51	0.51
225866_at	**BXDC1**	84154	brix domain containing 1	23.07	0.00
219177_at	**BXDC2**	55299	brix domain containing 2	3.32	0.34
218462_at	**BXDC5**	80135	brix domain containing 5	2.89	0.13
224664_at	**C10orf104**	119504	chromosome 10 open reading frame 104	2.04	0.06
219844_at	**C10orf118**	55088	chromosome 10 open reading frame 118	-2.71	0.51
218331_s_at	**C10orf18**	54906	chromosome 10 open reading frame 18	2.39	0.51
225192_at	**C10orf46**	143384	chromosome 10 open reading frame 46	-3.31	0.00
225372_at	**C10orf54**	64115	chromosome 10 open reading frame 54	-2.36	0.00
1557531_a_at	**C10orf55**	414236	chromosome 10 open reading frame 55	35.15	0.00
218213_s_at	**C11orf10**	746	chromosome 11 open reading frame 10	2.81	0.06
220987_s_at	**C11orf17 /// NUAK2**	56672 /// 81788	chromosome 11 open reading frame 17 /// NUAK family, SNF1-like kinase, 2	-21.71	0.00
220560_at	**C11orf21**	29125	chromosome 11 open reading frame 21	-9.72	0.51
224677_x_at	**C11orf31**	280636	chromosome 11 open reading frame 31	4.09	0.06
212560_at	**C11orf32**	442871	chromosome 11 open reading frame 32	-16.81	0.00
229851_s_at	**C11orf54**	28970	chromosome 11 open reading frame 54	-2.29	0.13
219806_s_at	**C11orf75**	56935	chromosome 11 open reading frame 75	14.18	0.00
224759_s_at	**C12orf23**	90488	chromosome 12 open reading frame 23	2.98	0.25
218374_s_at	**C12orf4**	57102	chromosome 12 open reading frame 4	8.50	0.00
226349_at	**C12orf45**	121053	chromosome 12 open reading frame 45	4.39	0.25
225772_s_at	**C12orf62**	84987	chromosome 12 open reading frame 62	3.18	0.51
218723_s_at	**C13orf15**	28984	chromosome 13 open reading frame 15	6.78	0.34
44790_s_at	**C13orf18**	80183	chromosome 13 open reading frame 18	-6.61	0.00
228937_at	**C13orf31**	144811	chromosome 13 open reading frame 31	18.74	0.00
225675_at	**C14orf101**	54916	chromosome 14 open reading frame 101	-3.92	0.79
219166_at	**C14orf104**	55172	chromosome 14 open reading frame 104	2.09	0.51
213246_at	**C14orf109**	26175	chromosome 14 open reading frame 109	3.99	0.02
229520_s_at	**C14orf118**	55668	chromosome 14 open reading frame 118	3.99	0.06
223060_at	**C14orf119**	55017	chromosome 14 open reading frame 119	2.27	0.00
218940_at	**C14orf138**	79609	chromosome 14 open reading frame 138	-6.00	0.08
220107_s_at	**C14orf140**	79696	chromosome 14 open reading frame 140	-2.12	0.00
221434_s_at	**C14orf156**	81892	chromosome 14 open reading frame 156	2.65	0.00
218298_s_at	**C14orf159**	80017	chromosome 14 open reading frame 159	-2.51	0.34
217768_at	**C14orf166**	51637	chromosome 14 open reading frame 166	3.41	0.34
52741_at	**C14orf172**	115708	chromosome 14 open reading frame 172	2.04	0.16
225514_at	**C14orf21**	161424	chromosome 14 open reading frame 21	2.21	0.34
212499_s_at	**C14orf32 /// FCF1**	51077 /// 93487	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae) /// chromosome 14 open reading frame 32	2.59	0.51
227544_at	**C14orf83**	161145	chromosome 14 open reading frame 83	2.12	0.34
1563524_a_at	**C14orf85**	319085	chromosome 14 open reading frame 85	-20.80	0.25
218383_at	**C14orf94**	54930	chromosome 14 open reading frame 94	-9.10	0.00
217915_s_at	**C15orf15**	51187	chromosome 15 open reading frame 15	2.13	0.06
242649_x_at	**C15orf21**	283651	chromosome 15 open reading frame 21	4.81	0.79
223484_at	**C15orf48**	84419	chromosome 15 open reading frame 48	351.48	0.00
229908_s_at	**C16orf28**	65259	chromosome 16 open reading frame 28	2.12	0.00
1559584_a_at	**C16orf54 /// hCG_1644884**	283897 /// 728070	chromosome 16 open reading frame 54 /// similar to chromosome 16 open reading frame 54	-5.09	0.00

218447_at	**C16orf61**	56942	chromosome 16 open reading frame 61	15.55	0.00
225088_at	**C16orf63**	123811	chromosome 16 open reading frame 63	3.04	0.06
225374_at	**C17orf32**	147007	chromosome 17 open reading frame 32	2.76	0.13
227668_at	**C17orf56**	146705	chromosome 17 open reading frame 56	-2.51	0.16
218464_s_at	**C17orf63**	55731	chromosome 17 open reading frame 63	2.32	0.34
221621_at	**C17orf86**	654434	chromosome 17 open reading frame 86	2.82	0.34
225967_s_at	**C17orf89**	284184	chromosome 17 open reading frame 89	3.01	0.08
227881_s_at	**C18orf17**	125488	Chromosome 18 open reading frame 17	2.43	0.16
235022_at	**C18orf19**	125228	chromosome 18 open reading frame 19	7.08	0.51
1553934_at	**C18orf20**	221241	chromosome 18 open reading frame 20	2.42	0.51
229582_at	**C18orf37**	125476	chromosome 18 open reading frame 37	2.11	0.25
1570552_at	**C18orf50**	619463	chromosome 18 open reading frame 50	5.80	0.06
221739_at	**C19orf10**	56005	chromosome 19 open reading frame 10	9.48	0.25
223983_s_at	**C19orf12**	83636	chromosome 19 open reading frame 12	5.66	0.34
55705_at	**C19orf22**	91300	chromosome 19 open reading frame 22	-2.67	0.00
220178_at	**C19orf28**	126321	chromosome 19 open reading frame 28	3.79	0.08
228154_at	**C19orf44**	84167	chromosome 19 open reading frame 44	2.85	0.06
204700_x_at	**C1orf107**	27042	chromosome 1 open reading frame 107	12.63	0.16
212004_at	**C1orf144**	26099	chromosome 1 open reading frame 144	3.71	0.13
241809_at	**C1orf183**	55924	chromosome 1 open reading frame 183	-13.72	0.00
1559638_at	**C1orf200**	644997	chromosome 1 open reading frame 200	2.27	0.06
1559376_at	**C1orf203**	84852	chromosome 1 open reading frame 203	4.06	0.00
1556633_at	**C1orf204**	284677	chromosome 1 open reading frame 204	2.27	0.51
225404_at	**C1orf212**	113444	chromosome 1 open reading frame 212	2.11	0.51
212791_at	**C1orf216**	127703	chromosome 1 open reading frame 216	13.68	0.51
225638_at	**C1orf31**	388753	chromosome 1 open reading frame 31	11.89	0.00
1555226_s_at	**C1orf43**	25912	chromosome 1 open reading frame 43	2.20	0.00
219506_at	**C1orf54**	79630	chromosome 1 open reading frame 54	20.40	0.16
244103_at	**C1orf55**	163859	chromosome 1 open reading frame 55	2.20	0.06
221222_s_at	**C1orf56**	54964	chromosome 1 open reading frame 56	-3.83	0.13
225841_at	**C1orf59**	113802	chromosome 1 open reading frame 59	-6.29	0.13
205103_at	**C1orf61**	10485	chromosome 1 open reading frame 61	6.26	0.16
209007_s_at	**C1orf63**	57035	chromosome 1 open reading frame 63	-2.00	0.07
1554660_a_at	**C1orf71**	163882	chromosome 1 open reading frame 71	3.11	0.51
231835_at	**C1orf93**	127281	chromosome 1 open reading frame 93	4.22	0.13
225904_at	**C1orf96**	126731	chromosome 1 open reading frame 96	-2.54	0.03
202953_at	**C1QB**	713	complement component 1, q subcomponent, B chain	9.16	0.51
214214_s_at	**C1QBP**	708	complement component 1, q subcomponent binding protein	3.58	0.25
239349_at	**C1QTNF7**	114905	C1q and tumor necrosis factor related protein 7	4.58	0.25
218983_at	**C1RL**	51279	complement component 1, r subcomponent-like	-2.80	0.00
225224_at	**C20orf112**	140688	chromosome 20 open reading frame 112	-5.20	0.51
233571_x_at	**C20orf149**	79144	chromosome 20 open reading frame 149	3.46	0.16
225313_at	**C20orf177**	63939	chromosome 20 open reading frame 177	-4.86	0.25
1567035_at	**C20orf181**	140843	chromosome 20 open reading frame 181	2.50	0.02
218586_at	**C20orf20**	55257	chromosome 20 open reading frame 20	2.03	0.34
206656_s_at	**C20orf3**	57136	chromosome 20 open reading frame 3	-3.49	0.00
224584_at	**C20orf30**	29058	chromosome 20 open reading frame 30	2.11	0.51
220888_s_at	**C20orf32**	57091	chromosome 20 open reading frame 32	-7.20	0.25
202217_at	**C21orf33**	8209	chromosome 21 open reading frame 33	2.78	0.51
223360_at	**C21orf56**	84221	chromosome 21 open reading frame 56	-2.67	0.03
225794_s_at	**C22orf32**	91689	chromosome 22 open reading frame 32	4.35	0.25
209906_at	**C3AR1**	719	complement component 3a receptor 1	7.98	0.00
1554147_s_at	**C3orf15**	89876	chromosome 3 open reading frame 15	6.51	0.02

225281_at	**C3orf17**	25871	chromosome 3 open reading frame 17	3.22	0.34
1554176_a_at	**C3orf33**	285315	chromosome 3 open reading frame 33	3.77	0.00
1553158_at	**C3orf34**	84984	chromosome 3 open reading frame 34	-7.95	0.00
226524_at	**C3orf38**	285237	chromosome 3 open reading frame 38	4.38	0.08
227599_at	**C3orf59**	151963	chromosome 3 open reading frame 59	5.26	0.00
241817_at	**C3orf62**	375341	chromosome 3 open reading frame 62	-2.06	0.51
219023_at	**C4orf16**	55435	chromosome 4 open reading frame 16	15.19	0.00
218449_at	**C4orf20**	55325	chromosome 4 open reading frame 20	2.34	0.51
227856_at	**C4orf32**	132720	chromosome 4 open reading frame 32	6.33	0.06
220088_at	**C5AR1**	728	complement component 5a receptor 1	-2.36	0.00
203024_s_at	**C5orf15**	56951	chromosome 5 open reading frame 15	3.63	0.00
226306_at	**C6orf1**	221491	chromosome 6 open reading frame 1	2.31	0.06
217924_at	**C6orf106**	64771	chromosome 6 open reading frame 106	7.64	0.00
39817_s_at	**C6orf108**	10591	chromosome 6 open reading frame 108	3.07	0.16
223361_at	**C6orf115**	58527	chromosome 6 open reading frame 115	2.85	0.02
242557_at	**C6orf12**	80862	Chromosome 6 open reading frame 12	4.90	0.34
225723_at	**C6orf129**	154467	chromosome 6 open reading frame 129	5.65	0.06
212923_s_at	**C6orf145**	221749	chromosome 6 open reading frame 145	13.29	0.06
1559051_s_at	**C6orf150**	115004	chromosome 6 open reading frame 150	7.34	0.13
236178_at	**C6orf162**	57150	chromosome 6 open reading frame 162	-5.83	0.34
1564002_a_at	**C6orf199**	221264	chromosome 6 open reading frame 199	2.49	0.34
218195_at	**C6orf211**	79624	chromosome 6 open reading frame 211	2.08	0.00
209829_at	**C6orf32**	9750	chromosome 6 open reading frame 32	-2.17	0.00
218233_s_at	**C6orf49**	29964	chromosome 6 open reading frame 49	5.07	0.00
219006_at	**C6orf66**	29078	chromosome 6 open reading frame 66	4.68	0.34
225576_at	**C6orf72**	116254	chromosome 6 open reading frame 72	-2.93	0.34
224987_at	**C6orf89**	221477	chromosome 6 open reading frame 89	2.32	0.16
215380_s_at	**C7orf24**	79017	chromosome 7 open reading frame 24	8.87	0.02
221573_at	**C7orf25**	79020	chromosome 7 open reading frame 25	-2.69	0.79
231435_at	**C7orf34**	135927	chromosome 7 open reading frame 34	-3.25	0.34
229762_at	**C7orf38**	221786	Chromosome 7 open reading frame 38	2.36	0.34
225699_at	**C7orf40**	285958	chromosome 7 open reading frame 40	3.08	0.51
226018_at	**C7orf41**	222166	chromosome 7 open reading frame 41	-7.69	0.07
220659_s_at	**C7orf43**	55262	chromosome 7 open reading frame 43	-2.41	0.00
206497_at	**C7orf44**	55744	chromosome 7 open reading frame 44	-3.80	0.08
225534_at	**C8orf40**	114926	chromosome 8 open reading frame 40	5.00	0.51
226165_at	**C8orf59**	401466	chromosome 8 open reading frame 59	2.92	0.00
225702_at	**C8orf76**	84933	chromosome 8 open reading frame 76	2.48	0.34
1557866_at	**C9orf117**	286207	chromosome 9 open reading frame 117	2.48	0.00
232270_at	**C9orf3**	84909	Chromosome 9 open reading frame 3	2.05	0.16
223368_s_at	**C9orf32**	28989	chromosome 9 open reading frame 32	3.81	0.08
1553809_a_at	**C9orf71**	169693	chromosome 9 open reading frame 71	-25.13	0.51
219276_x_at	**C9orf82**	79886	chromosome 9 open reading frame 82	2.59	0.16
223398_at	**C9orf89**	84270	chromosome 9 open reading frame 89	2.04	0.51
221865_at	**C9orf91**	203197	chromosome 9 open reading frame 91	9.88	0.06
209301_at	**CA2**	760	carbonic anhydrase II	3.91	0.02
206209_s_at	**CA4**	762	carbonic anhydrase IV	-10.62	0.79
218168_s_at	**CABC1**	56997	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	-13.62	0.00
37652_at	**CABIN1**	23523	calcineurin binding protein 1	-4.36	0.16
201381_x_at	**CACYBP**	27101	calcyclin binding protein	2.34	0.25
209031_at	**CADM1**	23705	cell adhesion molecule 1	2.25	0.06
235076_at	**CALCOCO2**	10241	calcium binding and coiled-coil domain 2	2.37	0.08
212953_x_at	**CALR**	811	calreticulin	4.75	0.00
214845_s_at	**CALU**	813	calumenin	7.60	0.00

220246_at	**CAMK1D**	57118	calcium/calmodulin-dependent protein kinase ID	-4.19	0.00
226382_at	**CAMK1D** /// **LOC283070**	283070 /// 57118	calcium/calmodulin-dependent protein kinase ID /// hypothetical protein LOC283070	-4.92	0.51
215161_at	**CAMK1G**	57172	calcium/calmodulin-dependent protein kinase IG	10.83	0.51
34846_at	**CAMK2B**	816	Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	-3.10	0.00
231042_s_at	**CAMK2D**	817	Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	6.47	0.34
212757_s_at	**CAMK2G**	818	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-6.93	0.00
210244_at	**CAMP**	820	cathelicidin antimicrobial peptide	-31.91	0.07
46323_at	**CANT1**	124583	calcium activated nucleotidase 1	-2.18	0.00
208852_s_at	**CANX**	821	calnexin	4.60	0.00
201850_at	**CAPG**	822	capping protein (actin filament), gelsolin-like	4.18	0.02
200723_s_at	**CAPRIN1**	4076	cell cycle associated protein 1	2.42	0.25
218153_at	**CARS2**	79587	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	-2.49	0.00
224619_at	**CASC4**	113201	cancer susceptibility candidate 4	-3.86	0.00
207181_s_at	**CASP7**	840	caspase 7, apoptosis-related cysteine peptidase	5.87	0.06
207686_s_at	**CASP8**	841	caspase 8, apoptosis-related cysteine peptidase	-4.99	0.00
207317_s_at	**CASQ2**	845	calsequestrin 2 (cardiac muscle)	3.26	0.08
211922_s_at	**CAT**	847	catalase	-12.24	0.00
216903_s_at	**CBARA1**	10367	calcium binding atopy-related autoantigen 1	3.00	0.00
208056_s_at	**CBFA2T3**	863	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	-36.10	0.00
202370_s_at	**CBFB**	865	core-binding factor, beta subunit	2.40	0.06
212816_s_at	**CBS**	875	cystathionine-beta-synthase	-3.34	0.03
201518_at	**CBX1**	10951	chromobox homolog 1 (HP1 beta homolog Drosophila)	-3.12	0.00
209715_at	**CBX5**	23468	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	17.63	0.16
212914_at	**CBX7**	23492	chromobox homolog 7	-9.98	0.03
224737_x_at	**CCAR1**	55749	cell division cycle and apoptosis regulator 1	2.58	0.34
48117_at	**CCDC101**	112869	coiled-coil domain containing 101	2.77	0.34
229063_s_at	**CCDC107**	203260	coiled-coil domain containing 107	3.68	0.25
229082_at	**CCDC125**	202243	coiled-coil domain containing 125	-4.49	0.08
1554023_s_at	**CCDC13**	152206	coiled-coil domain containing 13	-7.29	0.00
232989_s_at	**CCDC136**	64753	coiled-coil domain containing 136	-2.55	0.79
1557366_at	**CCDC144B**	284047	coiled-coil domain containing 144B	-2.79	0.03
220308_at	**CCDC19**	25790	coiled-coil domain containing 19	-2.65	0.16
209479_at	**CCDC28A**	25901	coiled-coil domain containing 28A	-7.29	0.00
225331_at	**CCDC50**	152137	coiled-coil domain containing 50	4.52	0.34
222792_s_at	**CCDC59**	29080	coiled-coil domain containing 59	2.15	0.08
220094_s_at	**CCDC90A**	63933	coiled-coil domain containing 90A	3.52	0.79
218288_s_at	**CCDC90B**	60492	coiled-coil domain containing 90B	3.00	0.51
209688_s_at	**CCDC93**	54520	coiled-coil domain containing 93	3.77	0.00
226521_s_at	**CCDC98**	84142	coiled-coil domain containing 98	2.73	0.34
210133_at	**CCL11**	6356	chemokine (C-C motif) ligand 11	3.67	0.06
216714_at	**CCL13**	6357	chemokine (C-C motif) ligand 13	93.01	0.00
207900_at	**CCL17**	6361	chemokine (C-C motif) ligand 17	7.35	0.16
32128_at	**CCL18**	6362	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	3.10	0.25
216598_s_at	**CCL2**	6347	chemokine (C-C motif) ligand 2	120.52	0.00
205476_at	**CCL20**	6364	chemokine (C-C motif) ligand 20	169.03	0.00

205114_s_at	**CCL3** /// **CCL3L1** /// **CCL3L3** /// **LOC728830** /// **LOC730422**	414062 /// 6348 /// 6349 /// 728830 /// 730422	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3 /// similar to Small inducible cytokine A3-like 1 precursor (Tonsillar lymphocyte LD78 beta protein) (LD78-beta(1-70)) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2) /// similar to chemokine (C-C motif) ligand 3-like 3	7.89	0.00
204103_at	**CCL4**	6351	chemokine (C-C motif) ligand 4	27.47	0.00
1555759_a_at	**CCL5**	6352	chemokine (C-C motif) ligand 5	2.97	0.25
208075_s_at	**CCL7**	6354	chemokine (C-C motif) ligand 7	50.18	0.00
214038_at	**CCL8**	6355	chemokine (C-C motif) ligand 8	91.74	0.00
223164_at	**CCM2**	83605	cerebral cavernous malformation 2	-6.65	0.07
201955_at	**CCNC**	892	cyclin C	2.46	0.51
200953_s_at	**CCND2**	894	cyclin D2	4.47	0.00
201700_at	**CCND3**	896	cyclin D3	-2.14	0.00
223084_s_at	**CCNDBP1**	23582	cyclin D-type binding-protein 1	-3.65	0.00
202769_at	**CCNG2**	901	cyclin G2	-4.38	0.00
204093_at	**CCNH**	902	cyclin H	2.97	0.02
219470_x_at	**CCNJ**	54619	cyclin J	3.94	0.51
219227_at	**CCNJL**	79616	cyclin J-like	-42.14	0.00
206967_at	**CCNT1**	904	cyclin T1	2.53	0.79
224652_at	**CCNY**	219771	cyclin Y	-4.15	0.00
221156_x_at	**CCPG1**	9236	cell cycle progression 1	-9.97	0.00
206991_s_at	**CCR5**	1234	chemokine (C-C motif) receptor 5	29.95	0.00
205271_s_at	**CCRK**	23552	cell cycle related kinase	2.14	0.25
211434_s_at	**CCRL2** /// **LOC727811**	727811 /// 9034	chemokine (C-C motif) receptor-like 2 /// similar to chemokine (C-C motif) receptor-like 2	118.80	0.00
1554283_at	**CCRN4L**	25819	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	12.28	0.02
201947_s_at	**CCT2**	10576	chaperonin containing TCP1, subunit 2 (beta)	5.72	0.00
200910_at	**CCT3**	7203	chaperonin containing TCP1, subunit 3 (gamma)	5.00	0.34
200877_at	**CCT4**	10575	chaperonin containing TCP1, subunit 4 (delta)	4.67	0.06
201327_s_at	**CCT6A**	908	chaperonin containing TCP1, subunit 6A (zeta 1)	3.22	0.06
227301_at	**CCT6AP1**	643253	chaperonin containing TCP1, subunit 6A (zeta 1) pseudogene 1	-2.63	0.34
200873_s_at	**CCT8**	10694	chaperonin containing TCP1, subunit 8 (theta)	5.17	0.02
215049_x_at	**CD163**	9332	CD163 molecule	5.34	0.00
206749_at	**CD1B**	910	CD1b molecule	41.45	0.79
215784_at	**CD1E**	913	CD1e molecule	15.48	0.08
207277_at	**CD209**	30835	CD209 molecule	63.12	0.02
38521_at	**CD22** /// **MAG**	4099 /// 933	CD22 molecule /// myelin associated glycoprotein	10.82	0.00
207315_at	**CD226**	10666	CD226 molecule	3.16	0.08
223834_at	**CD274**	29126	CD274 molecule	7.57	0.00
203799_at	**CD302**	9936	CD302 molecule	-31.97	0.00
206488_s_at	**CD36**	948	CD36 molecule (thrombospondin receptor)	3.22	0.51
205692_s_at	**CD38**	952	CD38 molecule	2.43	0.51
215346_at	**CD40**	958	CD40 molecule, TNF receptor superfamily member 5	37.80	0.00
210916_s_at	**CD44**	960	CD44 molecule (Indian blood group)	4.02	0.00
204118_at	**CD48**	962	CD48 molecule	3.21	0.00
203507_at	**CD68**	968	CD68 molecule	4.92	0.06
209795_at	**CD69**	969	CD69 molecule	43.13	0.00

1567627_at	**CD74**	972	CD74 molecule, major histocompatibility complex, class II invariant chain	18.11	0.00
207176_s_at	**CD80**	941	CD80 molecule	3.23	0.16
200675_at	**CD81**	975	CD81 molecule	4.82	0.02
204440_at	**CD83**	9308	CD83 molecule	64.43	0.00
211190_x_at	**CD84**	8832	CD84 molecule	2.60	0.51
210895_s_at	**CD86**	942	CD86 molecule	5.24	0.08
202878_s_at	**CD93**	22918	CD93 molecule	-2.63	0.00
202910_s_at	**CD97**	976	CD97 molecule	-2.14	0.25
205627_at	**CDA**	978	cytidine deaminase	-14.94	0.16
233564_s_at	**CDADC1**	81602	cytidine and dCMP deaminase domain containing 1	2.44	0.51
201725_at	**CDC123**	8872	cell division cycle 123 homolog (S. cerevisiae)	-2.08	0.03
211348_s_at	**CDC14B**	8555	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	2.34	0.25
212897_at	**CDC2L6**	23097	cell division cycle 2-like 6 (CDK8-like)	-7.91	0.00
203968_s_at	**CDC6**	990	cell division cycle 6 homolog (S. cerevisiae)	2.34	0.00
226056_at	**CDGAP**	57514	Cdc42 GTPase-activating protein	24.44	0.06
203440_at	**CDH2**	1000	cadherin 2, type 1, N-cadherin (neuronal)	-7.11	0.00
233391_at	**CDH26**	60437	cadherin-like 26	2.60	0.00
201938_at	**CDK2AP1**	8099	CDK2-associated protein 1	-4.98	0.00
202246_s_at	**CDK4**	1019	cyclin-dependent kinase 4	8.84	0.08
204995_at	**CDK5R1**	8851	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	-4.60	0.79
202284_s_at	**CDKN1A**	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	56.76	0.00
209112_at	**CDKN1B**	1027	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-7.98	0.00
238412_at	**CDR2**	1039	Cerebellar degeneration-related protein 2, 62kDa	7.71	0.16
206387_at	**CDX2**	1045	caudal type homeobox 2	2.49	0.51
209498_at	**CEACAM1**	634	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	3.15	0.02
207205_at	**CEACAM4**	1089	carcinoembryonic antigen-related cell adhesion molecule 4	-10.36	0.79
206676_at	**CEACAM8**	1088	carcinoembryonic antigen-related cell adhesion molecule 8	-3.03	0.16
203973_s_at	**CEBPD**	1052	CCAAT/enhancer binding protein (C/EBP), delta	-7.11	0.00
203341_at	**CEBPZ**	10153	CCAAT/enhancer binding protein zeta	4.32	0.02
218592_s_at	**CECR5**	27440	cat eye syndrome chromosome region, candidate 5	6.30	0.25
228559_at	**CENPN**	55839	centromere protein N	2.22	0.79
205212_s_at	**CENTB1**	9744	centaurin, beta 1	-2.39	0.34
213618_at	**CENTD1**	116984	centaurin, delta 1	11.84	0.00
218950_at	**CENTD3**	64411	centaurin, delta 3	-3.43	0.00
225789_at	**CENTG3**	116988	centaurin, gamma 3	6.23	0.00
212746_s_at	**CEP170**	9859	centrosomal protein 170kDa	2.31	0.08
1552717_s_at	**CEP170 /// CEP170L**	645455 /// 9859	centrosomal protein 170kDa /// centrosomal protein 170kDa-like	3.16	0.06
229181_s_at	**CEP27**	55142	centrosomal protein 27kDa	2.58	0.08
233650_at	**CEP63**	80254	centrosomal protein 63kDa	-5.07	0.00
1561884_at	**CEPT1**	10390	choline/ethanolamine phosphotransferase 1	2.06	0.34
218421_at	**CERK**	64781	ceramide kinase	-2.24	0.51
202357_s_at	**CFB**	629	complement factor B	14.22	0.00
203166_at	**CFDP1**	10428	craniofacial development protein 1	3.83	0.00
224663_s_at	**CFL2**	1073	cofilin 2 (muscle)	6.54	0.34
206380_s_at	**CFP**	5199	complement factor properdin	-3.21	0.00

213375_s_at	**CG018**	90634	hypothetical gene CG018	10.21	0.00
206932_at	**CH25H**	9023	cholesterol 25-hydroxylase	11.05	0.02
217720_at	**CHCHD2**	51142	coiled-coil-helix-coiled-coil-helix domain containing 2	3.01	0.00
1556988_s_at	**CHD1L**	9557	chromodomain helicase DNA binding protein 1-like	2.45	0.34
218829_s_at	**CHD7**	55636	chromodomain helicase DNA binding protein 7	-3.69	0.07
219049_at	**ChGn**	55790	chondroitin beta1,4 N-acetylgalactosaminyltransferase	-11.86	0.00
213060_s_at	**CHI3L2**	1117	chitinase 3-like 2	17.85	0.00
207099_s_at	**CHM**	1121	choroideremia (Rab escort protein 1)	2.86	0.51
218178_s_at	**CHMP1B**	57132	chromatin modifying protein 1B	-7.07	0.00
202537_s_at	**CHMP2B**	25978	chromatin modifying protein 2B	2.82	0.00
218571_s_at	**CHMP4A**	29082	chromatin modifying protein 4A	2.49	0.13
239436_at	**CHORDC1**	26973	Cysteine and histidine-rich domain (CHORD)-containing 1	-2.76	0.03
207993_s_at	**CHP**	11261	calcium binding protein P22	-2.08	0.16
221675_s_at	**CHPT1**	56994	choline phosphotransferase 1	-4.46	0.00
218927_s_at	**CHST12**	55501	carbohydrate (chondroitin 4) sulfotransferase 12	2.11	0.06
203044_at	**CHSY1**	22856	carbohydrate (chondroitin) synthase 1	-2.20	0.00
212784_at	**CIC**	23152	capicua homolog (Drosophila)	-3.21	0.00
210925_at	**CIITA**	4261	class II, major histocompatibility complex, transactivator	39.28	0.16
1554451_s_at	**CIP29** /// **DNAJC14**	84324 /// 85406	cytokine induced protein 29 kDa /// DnaJ (Hsp40) homolog, subfamily C, member 14	2.09	0.25
230142_s_at	**CIRBP**	1153	cold inducible RNA binding protein	-3.44	0.00
223377_x_at	**CISH**	1154	cytokine inducible SH2-containing protein	6.49	0.00
240757_at	**CLASP1**	23332	Cytoplasmic linker associated protein 1	-2.05	0.08
212306_at	**CLASP2**	23122	cytoplasmic linker associated protein 2	2.30	0.25
206207_at	**CLC**	1178	Charcot-Leyden crystal protein	-2.77	0.03
213628_at	**CLCC1**	23155	chloride channel CLIC-like 1	-13.20	0.51
203950_s_at	**CLCN6**	1185	chloride channel 6	3.70	0.51
209235_at	**CLCN7**	1186	chloride channel 7	7.84	0.08
228707_at	**CLDN23**	137075	claudin 23	2.60	0.16
206682_at	**CLEC10A**	10462	C-type lectin domain family 10, member A	7.50	0.34
219859_at	**CLEC4E**	26253	C-type lectin domain family 4, member E	3.27	0.00
219890_at	**CLEC5A**	23601	C-type lectin domain family 5, member A	25.76	0.00
221881_s_at	**CLIC4**	25932	chloride intracellular channel 4	14.67	0.00
1558924_s_at	**CLIP1**	6249	CAP-GLY domain containing linker protein 1	-2.99	0.16
214683_s_at	**CLK1**	1195	CDC-like kinase 1	-2.39	0.16
241403_at	**CLK4**	57396	CDC-like kinase 4	-2.15	0.25
221845_s_at	**CLPB**	81570	ClpB caseinolytic peptidase B homolog (E. coli)	2.88	0.25
226935_s_at	**CLPTM1L**	81037	CLPTM1-like	2.32	0.79
204809_at	**CLPX**	10845	ClpX caseinolytic peptidase X homolog (E. coli)	-3.07	0.25
200960_x_at	**CLTA**	1211	clathrin, light chain (Lca)	3.09	0.02
1555738_at	**CMTM1**	113540	CKLF-like MARVEL transmembrane domain containing 1	-9.86	0.03
229967_at	**CMTM2**	146225	CKLF-like MARVEL transmembrane domain containing 2	-18.90	0.00
217752_s_at	**CNDP2**	55748	CNDP dipeptidase 2 (metallopeptidase M20 family)	7.45	0.00
201605_x_at	**CNN2**	1265	calponin 2	-2.54	0.00
220739_s_at	**CNNM3**	26505	cyclin M3	-2.56	0.79
226153_s_at	**CNOT6L**	246175	CCR4-NOT transcription complex, subunit 6-like	-2.62	0.79

223796_at	**CNTNAP3 /// CNTNAP3B /// LOC728577**	389734 /// 728577 /// 79937	contactin associated protein-like 3 /// contactin associated protein-like 3B /// similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3)	-44.42	0.08
211343_s_at	**COL13A1**	1305	collagen, type XIII, alpha 1	10.58	0.00
1555953_at	**COL18A1**	80781	collagen, type XVIII, alpha 1	-3.67	0.08
216898_s_at	**COL4A3**	1285	collagen, type IV, alpha 3 (Goodpasture antigen)	2.39	0.51
204724_s_at	**COL9A3**	1299	collagen, type IX, alpha 3	-12.89	0.08
222637_at	**COMMD10**	51397	COMM domain containing 10	4.81	0.13
206441_s_at	**COMMD4**	54939	COMM domain containing 4	4.50	0.00
224387_at	**COMMD5**	28991	COMM domain containing 5	3.03	0.00
208818_s_at	**COMT**	1312	catechol-O-methyltransferase	2.97	0.34
222386_s_at	**COPZ1**	22818	coatomer protein complex, subunit zeta 1	5.62	0.06
209083_at	**CORO1A**	11151	coronin, actin binding protein, 1A	-3.86	0.00
203880_at	**COX17**	10063	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	3.63	0.00
231831_at	**COX19**	90639	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	-3.87	0.51
201597_at	**COX7A2**	1347	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	2.10	0.00
201119_s_at	**COX8A**	1351	cytochrome c oxidase subunit 8A (ubiquitous)	2.02	0.06
235479_at	**CPEB2**	132864	cytoplasmic polyadenylation element binding protein 2	-5.13	0.03
235706_at	**CPM**	1368	carboxypeptidase M	2.69	0.51
202119_s_at	**CPNE3**	8895	copine III	-3.85	0.13
208488_s_at	**CR1**	1378	complement component (3b/4b) receptor 1 (Knops blood group)	-12.67	0.00
239205_s_at	**CR1 /// CR1L /// LOC653907**	1378 /// 1379 /// 653907	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like /// similar to complement component (3b/4b) receptor 1 isoform F precursor	-9.97	0.13
209432_s_at	**CREB3**	10488	cAMP responsive element binding protein 3	3.49	0.02
212345_s_at	**CREB3L2**	64764	cAMP responsive element binding protein 3-like 2	9.16	0.02
205931_s_at	**CREB5**	9586	cAMP responsive element binding protein 5	-5.61	0.00
201200_at	**CREG1**	8804	cellular repressor of E1A-stimulated genes 1	4.85	0.00
209967_s_at	**CREM**	1390	cAMP responsive element modulator	57.40	0.00
208978_at	**CRIP2**	1397	cysteine-rich protein 2	2.31	0.02
221541_at	**CRISPLD2**	83716	cysteine-rich secretory protein LCCL domain containing 2	-4.63	0.00
221139_s_at	**CSAD**	51380	cysteine sulfinic acid decarboxylase	-5.64	0.25
209716_at	**CSF1**	1435	colony stimulating factor 1 (macrophage)	10.75	0.16
211287_x_at	**CSF2RA**	1438	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	-2.86	0.25
1553297_a_at	**CSF3R**	1441	colony stimulating factor 3 receptor (granulocyte)	-4.58	0.00
227767_at	**CSNK1G3**	1456	casein kinase 1, gamma 3	-3.84	0.79
201360_at	**CST3**	1471	cystatin C (amyloid angiopathy and cerebral hemorrhage)	-2.12	0.08
210140_at	**CST7**	8530	cystatin F (leukocystatin)	-10.76	0.00
229666_s_at	**CSTF3**	1479	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	8.96	0.02
202937_x_at	**CTA-126B4.3**	27341	CGI-96 protein	3.14	0.51
218923_at	**CTBS**	1486	chitobiase, di-N-acetyl-	-2.16	0.13
202521_at	**CTCF**	10664	CCCTC-binding factor (zinc finger protein)	-2.32	0.03

216508_x_at	**CTCFL /// HMG1L1 /// HMG1L6 /// HMGB1**	10357 /// 140690 /// 3146 /// 645292	high-mobility group box 1 /// high-mobility group (nonhistone chromosomal) protein 1-like 1 /// CCCTC-binding factor (zinc finger protein)-like /// high-mobility group (nonhistone chromosomal) protein 1-like 6	-2.30	0.16
217844_at	**CTDSP1**	58190	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	-3.03	0.03
208735_s_at	**CTDSP2**	10106	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-5.40	0.00
221850_x_at	**CTGLF1 /// CTGLF3 /// CTGLF4 /// CTGLF5 /// CTGLF9P /// KIAA1975**	119016 /// 119385 /// 414189 /// 653268 /// 728005 /// 728404	centaurin, gamma-like family, member 1 /// KIAA1975 protein similar to MRIP2 /// centaurin, gamma-like family, member 3 /// centaurin, gamma-like family, member 4 /// centaurin, gamma-like family, member 9 pseudogene /// centaurin, gamma-like family, member 5	-3.19	0.79
211240_x_at	**CTNND1**	1500	catenin (cadherin-associated protein), delta 1	3.48	0.00
36566_at	**CTNS**	1497	cystinosis, nephropathic	3.56	0.13
200661_at	**CTSA**	5476	cathepsin A	2.11	0.02
200838_at	**CTSB**	1508	cathepsin B	10.41	0.00
200766_at	**CTSD**	1509	cathepsin D	3.09	0.00
205653_at	**CTSG**	1511	cathepsin G	-8.65	0.79
202295_s_at	**CTSH**	1512	cathepsin H	5.96	0.06
202087_s_at	**CTSL1**	1514	cathepsin L1	59.50	0.00
210074_at	**CTSL2**	1515	cathepsin L2	7.83	0.06
1563445_x_at	**CTSLL3**	1518	cathepsin L-like 3	9.54	0.02
202157_s_at	**CUGBP2**	10659	CUG triplet repeat, RNA binding protein 2	-2.52	0.00
207614_s_at	**CUL1**	8454	cullin 1	3.86	0.16
201423_s_at	**CUL4A**	8451	cullin 4A	3.63	0.13
202213_s_at	**CUL4B**	8450	cullin 4B	-4.56	0.00
203533_s_at	**CUL5**	8065	cullin 5	2.74	0.34
205898_at	**CX3CR1**	1524	chemokine (C-X3-C motif) receptor 1	-9.57	0.00
204470_at	**CXCL1**	2919	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	2.61	0.00
204533_at	**CXCL10**	3627	chemokine (C-X-C motif) ligand 10	190.28	0.00
211122_s_at	**CXCL11**	6373	chemokine (C-X-C motif) ligand 11	55.47	0.00
223454_at	**CXCL16**	58191	chemokine (C-X-C motif) ligand 16	2.27	0.00
209774_x_at	**CXCL2**	2920	chemokine (C-X-C motif) ligand 2	7.95	0.00
207850_at	**CXCL3**	2921	chemokine (C-X-C motif) ligand 3	53.33	0.00
214974_x_at	**CXCL5**	6374	chemokine (C-X-C motif) ligand 5	50.40	0.02
203915_at	**CXCL9**	4283	chemokine (C-X-C motif) ligand 9	13.67	0.06
223294_at	**CXorf26**	51260	chromosome X open reading frame 26	6.95	0.51
214112_s_at	**CXorf40A /// CXorf40B**	541578 /// 91966	chromosome X open reading frame 40A /// chromosome X open reading frame 40B	2.38	0.08
207843_x_at	**CYB5A**	1528	cytochrome b5 type A (microsomal)	2.55	0.13
224735_at	**CYBASC3**	220002	cytochrome b, ascorbate dependent 3	2.84	0.34
203922_s_at	**CYBB**	1536	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	6.39	0.00
208905_at	**CYCS**	54205	cytochrome c, somatic	9.06	0.08
208923_at	**CYFIP1**	23191	cytoplasmic FMR1 interacting protein 1	4.70	0.79
215785_s_at	**CYFIP2**	26999	cytoplasmic FMR1 interacting protein 2	-3.37	0.34

214272_at	**CYLD**	1540	cylindromatosis (turban tumor syndrome)	2.58	0.25
205676_at	**CYP27B1**	1594	cytochrome P450, family 27, subfamily B, polypeptide 1	2.27	0.06
206153_at	**CYP4F11**	57834	cytochrome P450, family 4, subfamily F, polypeptide 11	2.10	0.34
210452_x_at	**CYP4F2**	8529	cytochrome P450, family 4, subfamily F, polypeptide 2	-7.47	0.00
206514_s_at	**CYP4F2** /// **CYP4F3**	4051 /// 8529	cytochrome P450, family 4, subfamily F, polypeptide 3 /// cytochrome P450, family 4, subfamily F, polypeptide 2	-7.73	0.00
206515_at	**CYP4F3**	4051	cytochrome P450, family 4, subfamily F, polypeptide 3	-8.11	0.00
231747_at	**CYSLTR1**	10800	cysteinyl leukotriene receptor 1	-3.72	0.07
220813_at	**CYSLTR2**	57105	cysteinyl leukotriene receptor 2	-4.78	0.16
212527_at	**D15Wsu75e**	27351	DNA segment, Chr 15, Wayne State University 75, expressed	4.66	0.00
216060_s_at	**DAAM1**	23002	dishevelled associated activator of morphogenesis 1	-4.85	0.79
210757_x_at	**DAB2**	1601	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	4.74	0.51
200046_at	**DAD1**	1603	defender against cell death 1	2.40	0.02
212128_s_at	**DAG1**	1605	dystroglycan 1 (dystrophin-associated glycoprotein 1)	2.22	0.51
201095_at	**DAP**	1611	death-associated protein	2.43	0.51
215184_at	**DAPK2**	23604	death-associated protein kinase 2	-12.13	0.00
201623_s_at	**DARS**	1615	aspartyl-tRNA synthetase	6.05	0.02
218443_s_at	**DAZAP1**	26528	DAZ associated protein 1	4.15	0.08
205818_at	**DBC1**	1620	deleted in bladder cancer 1	-2.14	0.34
223001_at	**DC2**	58505	DC2 protein	8.68	0.25
203302_at	**DCK**	1633	deoxycytidine kinase	2.35	0.51
225443_at	**DCP1A**	55802	DCP1 decapping enzyme homolog A (S. cerevisiae)	3.96	0.06
235258_at	**DCP2**	167227	DCP2 decapping enzyme homolog (S. cerevisiae)	-2.95	0.07
242988_at	**DCST2**	127579	DC-STAMP domain containing 2	2.13	0.34
204296_at	**DCTN1**	1639	dynactin 1 (p150, glued homolog, Drosophila)	17.80	0.00
209231_s_at	**DCTN5**	84516	dynactin 5 (p25)	3.07	0.34
203261_at	**DCTN6**	10671	dynactin 6	2.68	0.34
239648_at	**DCUN1D3**	123879	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	18.13	0.00
224796_at	**DDEF1**	50807	development and differentiation enhancing factor 1	-2.22	0.00
243705_at	**DDHD1**	80821	DDHD domain containing 1	2.02	0.13
209383_at	**DDIT3**	1649	DNA-damage-inducible transcript 3	3.02	0.08
202887_s_at	**DDIT4**	54541	DNA-damage-inducible transcript 4	7.37	0.34
222134_at	**DDO**	8528	D-aspartate oxidase	4.87	0.79
230180_at	**DDX17**	10521	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-2.95	0.08
205763_s_at	**DDX18**	8886	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	7.38	0.02
202577_s_at	**DDX19A**	55308	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	2.49	0.34
202576_s_at	**DDX19A** /// **DDX19B**	11269 /// 55308	DEAD (Asp-Glu-Ala-As) box polypeptide 19B /// DEAD (Asp-Glu-Ala-As) box polypeptide 19A	6.49	0.06
208152_s_at	**DDX21**	9188	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	7.36	0.00
200694_s_at	**DDX24**	57062	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	3.89	0.08
221780_s_at	**DDX27**	55661	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	3.04	0.13
201584_s_at	**DDX39**	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	11.72	0.16
220890_s_at	**DDX47**	51202	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	5.17	0.51
221699_s_at	**DDX50**	79009	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	2.86	0.02

210320_s_at	**DDX52**	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	2.40	0.79
225434_at	**DEDD2**	162989	death effector domain containing 2	-2.10	0.51
221293_s_at	**DEF6**	50619	differentially expressed in FDCP 6 homolog (mouse)	-2.86	0.34
225637_at	**DEF8**	54849	differentially expressed in FDCP 8 homolog (mouse)	-9.15	0.03
205033_s_at	**DEFA1** /// **DEFA3** /// **LOC728358**	1667 /// 1668 /// 728358	defensin, alpha 1 /// defensin, alpha 3, neutrophil-specific	-3.71	0.00
1568377_x_at	**DEFB124**	245937	defensin, beta 124	2.80	0.02
233166_at	**DEFB126**	81623	defensin, beta 126	-2.04	0.16
221081_s_at	**DENND2D**	79961	DENN/MADD domain containing 2D	8.80	0.02
212975_at	**DENND3**	22898	DENN/MADD domain containing 3	-3.41	0.03
1554352_s_at	**DENND4A**	10260	DENN/MADD domain containing 4A	11.32	0.25
219402_s_at	**DERL1**	79139	Der1-like domain family, member 1	2.85	0.06
203733_at	**DEXI**	28955	dexamethasone-induced transcript	2.43	0.34
223518_at	**DFFA**	1676	DNA fragmentation factor, 45kDa, alpha polypeptide	5.56	0.34
203669_s_at	**DGAT1**	8694	diacylglycerol O-acyltransferase homolog 1 (mouse)	-6.49	0.79
214198_s_at	**DGCR2**	9993	DiGeorge syndrome critical region gene 2	-3.94	0.00
208024_s_at	**DGCR6** /// **DGCR6L**	8214 /// 85359	DiGeorge syndrome critical region gene 6 /// DiGeorge syndrome critical region gene 6-like	2.32	0.16
208072_s_at	**DGKD**	8527	diacylglycerol kinase, delta 130kDa	-3.86	0.08
1554623_x_at	**DGKE**	8526	diacylglycerol kinase, epsilon 64kDa	2.21	0.06
207556_s_at	**DGKZ**	8525	diacylglycerol kinase, zeta 104kDa	-4.30	0.34
202534_x_at	**DHFR**	1719	dihydrofolate reductase	-2.76	0.51
204800_s_at	**DHRS12**	79758	dehydrogenase/reductase (SDR family) member 12	-2.23	0.51
226121_at	**DHRS13**	147015	dehydrogenase/reductase (SDR family) member 13	-4.60	0.00
213868_s_at	**DHRS7**	51635	Dehydrogenase/reductase (SDR family) member 7	-3.42	0.00
219799_s_at	**DHRS9**	10170	dehydrogenase/reductase (SDR family) member 9	-2.05	0.34
227094_at	**DHTKD1**	55526	dehydrogenase E1 and transketolase domain containing 1	-5.22	0.16
201385_at	**DHX15**	1665	DEAH (Asp-Glu-Ala-His) box polypeptide 15	2.79	0.34
223138_s_at	**DHX36**	170506	DEAH (Asp-Glu-Ala-His) box polypeptide 36	4.87	0.00
219364_at	**DHX58**	79132	DEXH (Asp-Glu-X-His) box polypeptide 58	2.89	0.79
205726_at	**DIAPH2**	1730	diaphanous homolog 2 (Drosophila)	5.05	0.16
206061_s_at	**DICER1**	23405	Dicer1, Dcr-1 homolog (Drosophila)	-3.49	0.00
226026_at	**DIRC2**	84925	disrupted in renal carcinoma 2	-2.69	0.08
222607_s_at	**DIS3**	22894	DIS3 mitotic control homolog (S. cerevisiae)	2.37	0.79
206090_s_at	**DISC1**	27185	disrupted in schizophrenia 1	-3.01	0.51
216212_s_at	**DKC1**	1736	dyskeratosis congenita 1, dyskerin	3.46	0.25
231886_at	**DKFZP434B2016**	642780	similar to hypothetical protein LOC284701	-6.27	0.00
211050_x_at	**DKFZP434B2016** /// **LOC643313**	642780 /// 643313	similar to hypothetical protein LOC284701	-2.20	0.00
235167_at	**DKFZp547E087**	283846	hypothetical gene LOC283846	-3.07	0.07

211996_s_at	**DKFZp547E087** /// **LOC23117** /// **LOC440345** /// **LOC440353** /// **LOC613037** /// **LOC728888**	23117 /// 283846 /// 440345 /// 440353 /// 613037 /// 728888	KIAA0220-like protein /// hypothetical gene LOC283846 /// hypothetical protein LOC440345 /// nuclear pore complex interacting protein pseudogene /// similar to Protein KIAA0220	2.68	0.02
214984_at	**DKFZp547E087** /// **LOC440345** /// **LOC440354** /// **LOC595101** /// **LOC728423** /// **LOC730099** /// **SMG1**	23049 /// 283846 /// 440345 /// 440354 /// 595101 /// 728423 /// 730099	PI-3-kinase-related kinase SMG-1 /// hypothetical gene LOC283846 /// hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 pseudogene /// similar to PI-3-kinase-related kinase SMG-1	4.09	0.13
215953_at	**DKFZP564C196**	284649	DKFZP564C196 protein	3.52	0.79
236079_at	**DKFZp667E0512**	202025	hypothetical protein DKFZp667E0512	-5.33	0.16
1559756_at	**DKFZp667F0711**	399716	hypothetical protein DKFZp667F0711	-6.75	0.08
214030_at	**DKFZp667G2110**	131544	hypothetical protein DKFZp667G2110	4.47	0.08
224740_at	**DKFZP686E2158**	643155	hypothetical protein LOC643155	5.29	0.08
231412_at	**DKFZp686L14188**	441366	hypothetical gene supported by BX538329	22.21	0.51
242854_x_at	**DLEU2**	8847	deleted in lymphocytic leukemia, 2	-9.02	0.03
1562278_at	**DNAH1**	25981	dynein, axonemal, heavy chain 1	4.06	0.06
223054_at	**DNAJB11**	51726	DnaJ (Hsp40) homolog, subfamily B, member 11	2.88	0.02
202500_at	**DNAJB2**	3300	DnaJ (Hsp40) homolog, subfamily B, member 2	2.66	0.25
203811_s_at	**DNAJB4**	11080	DnaJ (Hsp40) homolog, subfamily B, member 4	2.69	0.25
1554462_a_at	**DNAJB9**	4189	DnaJ (Hsp40) homolog, subfamily B, member 9	7.70	0.00
222620_s_at	**DNAJC1**	64215	DnaJ (Hsp40) homolog, subfamily C, member 1	3.87	0.06
221782_at	**DNAJC10**	54431	DnaJ (Hsp40) homolog, subfamily C, member 10	13.52	0.00
218435_at	**DNAJC15**	29103	DnaJ (Hsp40) homolog, subfamily C, member 15	6.17	0.08
223371_s_at	**DNAJC4**	3338	DnaJ (Hsp40) homolog, subfamily C, member 4	-2.18	0.13
205545_x_at	**DNAJC8**	22826	DnaJ (Hsp40) homolog, subfamily C, member 8	4.27	0.02
201697_s_at	**DNMT1**	1786	DNA (cytosine-5-)-methyltransferase 1	10.47	0.25
202776_at	**DNTTIP2**	30836	deoxynucleotidyltransferase, terminal, interacting protein 2	6.81	0.00
219279_at	**DOCK10**	55619	dedicator of cytokinesis 10	3.90	0.02
226875_at	**DOCK11**	139818	dedicator of cytokinesis 11	-2.35	0.03
213160_at	**DOCK2**	1794	dedicator of cytokinesis 2	-2.22	0.34

205003_at	**DOCK4**	9732	dedicator of cytokinesis 4	6.65	0.00
219921_s_at	**DOCK5**	80005	dedicator of cytokinesis 5	-2.36	0.00
212538_at	**DOCK9**	23348	dedicator of cytokinesis 9	-3.57	0.51
208141_s_at	**DOHH**	83475	deoxyhypusine hydroxylase/monooxygenase	4.11	0.51
223553_s_at	**DOK3**	79930	docking protein 3	-4.18	0.00
209691_s_at	**DOK4**	55715	docking protein 4	-18.45	0.51
219452_at	**DPEP2**	64174	dipeptidase 2	-25.63	0.00
220179_at	**DPEP3**	64180	dipeptidase 3	-14.55	0.79
225195_at	**DPH3**	285381	DPH3, KTI11 homolog (S. cerevisiae)	2.25	0.79
225633_at	**DPY19L3**	147991	dpy-19-like 3 (C. elegans)	-2.58	0.79
218627_at	**DRAM**	55332	damage-regulated autophagy modulator	3.53	0.00
203405_at	**DSCR2**	8624	Down syndrome critical region gene 2	3.61	0.06
203635_at	**DSCR3**	10311	Down syndrome critical region gene 3	2.67	0.00
218854_at	**DSE**	29940	dermatan sulfate epimerase	2.60	0.00
234107_s_at	**DTD1**	92675	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	-2.47	0.51
223445_at	**DTNBP1**	84062	dystrobrevin binding protein 1	3.96	0.00
212611_at	**DTX4**	23220	deltex 4 homolog (Drosophila)	-5.30	0.51
201041_s_at	**DUSP1**	1843	dual specificity phosphatase 1	-5.09	0.07
215501_s_at	**DUSP10**	11221	dual specificity phosphatase 10	24.92	0.00
204794_at	**DUSP2**	1844	dual specificity phosphatase 2	9.62	0.06
201537_s_at	**DUSP3**	1845	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	2.85	0.00
209457_at	**DUSP5**	1847	dual specificity phosphatase 5	46.54	0.00
208956_x_at	**DUT**	1854	dUTP pyrophosphatase	-2.29	0.34
57532_at	**DVL2**	1856	dishevelled, dsh homolog 2 (Drosophila)	4.49	0.34
211684_s_at	**DYNC1I2**	1781	dynein, cytoplasmic 1, intermediate chain 2	5.54	0.79
203303_at	**DYNLT3**	6990	dynein, light chain, Tctex-type 3	11.41	0.00
218660_at	**DYSF**	8291	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	-5.12	0.13
241713_s_at	**DYX1C1**	161582	dyslexia susceptibility 1 candidate 1	-7.66	0.79
203957_at	**E2F6**	1876	E2F transcription factor 6	5.46	0.16
226952_at	**EAF1**	85403	ELL associated factor 1	2.87	0.00
202623_at	**EAPP**	55837	E2F-associated phosphoprotein	-2.80	0.25
205419_at	**EBI2**	1880	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	-3.22	0.34
219424_at	**EBI3**	10148	Epstein-Barr virus induced gene 3	5.89	0.00
201323_at	**EBNA1BP2**	10969	EBNA1 binding protein 2	5.03	0.34
201135_at	**ECHS1**	1892	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	3.98	0.51
203279_at	**EDEM1**	9695	ER degradation enhancer, mannosidase alpha-like 1	5.66	0.06
218282_at	**EDEM2**	55741	ER degradation enhancer, mannosidase alpha-like 2	2.41	0.51
209059_s_at	**EDF1**	8721	endothelial differentiation-related factor 1	2.23	0.02
204038_s_at	**EDG2**	1902	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	5.03	0.00
206723_s_at	**EDG4**	9170	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4	-4.49	0.00
227684_at	**EDG5**	9294	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	8.14	0.34
206437_at	**EDG6**	8698	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 6	-21.46	0.03
230464_at	**EDG8**	53637	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	16.61	0.06
222802_at	**EDN1**	1906	endothelin 1	60.51	0.00
204905_s_at	**EEF1E1**	9521	eukaryotic translation elongation factor 1 epsilon 1	2.00	0.34

204102_s_at	**EEF2**	1938	eukaryotic translation elongation factor 2	2.45	0.34
233375_at	**EFCAB2**	84288	EF-hand calcium binding domain 2	3.10	0.02
220523_at	**EFHC2**	80258	EF-hand domain (C-terminal) containing 2	-5.20	0.07
221497_x_at	**EGLN1**	54583	egl nine homolog 1 (C. elegans)	-14.39	0.00
205249_at	**EGR2**	1959	early growth response 2 (Krox-20 homolog, Drosophila)	19.50	0.00
206115_at	**EGR3**	1960	early growth response 3	17.08	0.00
209536_s_at	**EHD4**	30844	EH-domain containing 4	9.37	0.00
216396_s_at	**EI24**	9538	etoposide induced 2.4 mRNA	2.49	0.79
201019_s_at	**EIF1AP1** /// **EIF1AX**	1964 /// 280661	eukaryotic translation initiation factor 1A, X-linked /// eukaryotic translation initiation factor 1A pseudogene 1	4.62	0.06
201738_at	**EIF1B**	10289	eukaryotic translation initiation factor 1B	2.06	0.00
223015_at	**EIF2A**	83939	eukaryotic translation initiation factor 2A, 65kDa	4.80	0.16
212351_at	**EIF2B5**	8893	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	3.77	0.34
213310_at	**EIF2C2**	27161	Eukaryotic translation initiation factor 2C, 2	-5.33	0.08
227930_at	**EIF2C4**	192670	eukaryotic translation initiation factor 2C, 4	-6.84	0.00
201144_s_at	**EIF2S1**	1965	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	7.47	0.00
208726_s_at	**EIF2S2**	8894	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	3.60	0.02
200595_s_at	**EIF3A**	8661	eukaryotic translation initiation factor 3, subunit A	2.14	0.00
208688_x_at	**EIF3B**	8662	eukaryotic translation initiation factor 3, subunit B	4.26	0.34
210949_s_at	**EIF3C** /// **EIF3CL**	728689 /// 8663	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	4.66	0.02
208697_s_at	**EIF3E**	3646	eukaryotic translation initiation factor 3, subunit E	2.92	0.08
201592_at	**EIF3H**	8667	eukaryotic translation initiation factor 3, subunit H	2.41	0.00
208756_at	**EIF3I**	8668	eukaryotic translation initiation factor 3, subunit I	4.71	0.08
208985_s_at	**EIF3J**	8669	eukaryotic translation initiation factor 3, subunit J	7.28	0.02
217364_x_at	**EIF3J** /// **LOC730021**	730021 /// 8669	eukaryotic translation initiation factor 3, subunit J /// hypothetical protein LOC730021	3.88	0.13
202231_at	**EIF3M**	10480	eukaryotic translation initiation factor 3, subunit M	3.09	0.08
201530_x_at	**EIF4A1**	1973	eukaryotic translation initiation factor 4A, isoform 1	4.41	0.00
201303_at	**EIF4A3**	9775	eukaryotic translation initiation factor 4A, isoform 3	4.23	0.06
201437_s_at	**EIF4E**	1977	eukaryotic translation initiation factor 4E	2.33	0.00
213571_s_at	**EIF4E2**	9470	eukaryotic translation initiation factor 4E family member 2	2.22	0.34
208624_s_at	**EIF4G1**	1981	eukaryotic translation initiation factor 4 gamma, 1	3.33	0.00
208708_x_at	**EIF5**	1983	eukaryotic translation initiation factor 5	2.90	0.00
213757_at	**EIF5A**	1984	Eukaryotic translation initiation factor 5A	2.67	0.00
220198_s_at	**EIF5A2**	56648	eukaryotic translation initiation factor 5A2	3.28	0.25
201024_x_at	**EIF5B**	9669	eukaryotic translation initiation factor 5B	4.74	0.00
222869_s_at	**ELAC1**	55520	elaC homolog 1 (E. coli)	2.51	0.16
210376_x_at	**ELK1**	2002	ELK1, member of ETS oncogene family	4.78	0.02
226099_at	**ELL2**	22936	elongation factor, RNA polymerase II, 2	2.30	0.25
219517_at	**ELL3**	80237	elongation factor RNA polymerase II-like 3	2.01	0.79

204513_s_at	**ELMO1**	9844	engulfment and cell motility 1	-3.91	0.79
212670_at	**ELN**	2006	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	2.95	0.06
227075_at	**ELP3**	55140	elongation protein 3 homolog (S. cerevisiae)	2.23	0.25
209477_at	**EMD**	2010	emerin (Emery-Dreifuss muscular dystrophy)	2.44	0.00
209233_at	**EMG1**	10436	EMG1 nucleolar protein homolog (S. cerevisiae)	2.28	0.34
204398_s_at	**EML2**	24139	echinoderm microtubule associated protein like 2	5.13	0.00
220386_s_at	**EML4**	27436	echinoderm microtubule associated protein like 4	2.05	0.00
201324_at	**EMP1**	2012	epithelial membrane protein 1	27.67	0.13
210724_at	**EMR3**	84658	egf-like module containing, mucin-like, hormone receptor-like 3	-6.60	0.00
201231_s_at	**ENO1**	2023	enolase 1, (alpha)	3.88	0.06
204845_s_at	**ENPEP**	2028	glutamyl aminopeptidase (aminopeptidase A)	-3.59	0.34
209473_at	**ENTPD1**	953	ectonucleoside triphosphate diphosphohydrolase 1	-7.36	0.00
211776_s_at	**EPB41L3**	23136	erythrocyte membrane protein band 4.1-like 3	5.61	0.79
202894_at	**EPHB4**	2050	EPH receptor B4	-22.21	0.00
232164_s_at	**EPPK1**	83481	epiplakin 1	2.39	0.34
218180_s_at	**EPS8L2**	64787	EPS8-like 2	-2.00	0.34
227609_at	**EPSTI1**	94240	epithelial stromal interaction 1 (breast)	6.67	0.00
223847_s_at	**ERGIC1**	57222	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	-2.34	0.00
1563315_s_at	**ERICH1**	157697	glutamate-rich 1	-3.30	0.07
202441_at	**ERLIN1**	10613	ER lipid raft associated 1	4.79	0.00
222646_s_at	**ERO1L**	30001	ERO1-like (S. cerevisiae)	-2.04	0.51
218859_s_at	**ESF1**	51575	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	2.80	0.34
201574_at	**ETF1**	2107	eukaryotic translation termination factor 1	2.64	0.00
201931_at	**ETFA**	2108	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	2.17	0.34
33494_at	**ETFDH**	2110	electron-transferring-flavoprotein dehydrogenase	2.71	0.79
219017_at	**ETNK1**	55500	ethanolamine kinase 1	8.03	0.00
201328_at	**ETS2**	2114	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	3.62	0.06
224225_s_at	**ETV7**	51513	ets variant gene 7 (TEL2 oncogene)	17.49	0.00
211742_s_at	**EVI2B**	2124	ecotropic viral integration site 2B	-4.11	0.00
208297_s_at	**EVI5**	7813	ecotropic viral integration site 5	-4.96	0.08
210011_s_at	**EWSR1**	2130	Ewing sarcoma breakpoint region 1	2.01	0.02
211825_s_at	**EWSR1 /// FLI1**	2130 /// 2313	Ewing sarcoma breakpoint region 1 /// Friend leukemia virus integration 1	-4.36	0.07
58696_at	**EXOSC4**	54512	exosome component 4	4.11	0.00
227696_at	**EXOSC6**	118460	Exosome component 6	2.88	0.51
212627_s_at	**EXOSC7**	23016	exosome component 7	4.06	0.16
205061_s_at	**EXOSC9**	5393	exosome component 9	3.15	0.25
209202_s_at	**EXTL3**	2137	exostoses (multiple)-like 3	-2.63	0.03
226170_at	**EYA3**	2140	eyes absent homolog 3 (Drosophila)	3.08	0.06
203249_at	**EZH1**	2145	enhancer of zeste homolog 1 (Drosophila)	-7.82	0.03
203358_s_at	**EZH2**	2146	enhancer of zeste homolog 2 (Drosophila)	15.55	0.00
226482_s_at	**F11R**	50848	F11 receptor	-2.59	0.13
204363_at	**F3**	2152	coagulation factor III (thromboplastin, tissue factor)	36.23	0.00
231029_at	**F5**	2153	coagulation factor V (proaccelerin, labile factor)	-28.44	0.07
203274_at	**F8A1**	8263	coagulation factor VIII-associated (intronic transcript) 1	-2.20	0.51

202345_s_at	**FABP5** /// **LOC728641** /// **LOC729163**	2171 /// 728641 /// 729163	fatty acid binding protein 5 (psoriasis-associated) /// similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	10.46	0.08
202535_at	**FADD**	8772	Fas (TNFRSF6)-associated via death domain	-3.24	0.07
226905_at	**FAM101B**	359845	family with sequence similarity 101, member B	-5.21	0.00
221249_s_at	**FAM117A**	81558	family with sequence similarity 117, member A	-4.45	0.16
226475_at	**FAM118A**	55007	family with sequence similarity 118, member A	-3.39	0.51
1555948_s_at	**FAM120A**	23196	family with sequence similarity 120A	-2.37	0.00
1556643_at	**FAM125A**	93343	Family with sequence similarity 125, member A	2.41	0.13
1554178_a_at	**FAM126B**	285172	family with sequence similarity 126, member B	-2.13	0.00
212697_at	**FAM134C**	162427	family with sequence similarity 134, member C	-2.15	0.07
218446_s_at	**FAM18B**	51030	family with sequence similarity 18, member B	2.91	0.25
212370_x_at	**FAM21A** /// **FAM21B**	387680 /// 55747	family with sequence similarity 21, member B /// family with sequence similarity 21, member A	4.10	0.00
214946_x_at	**FAM21A** /// **FAM21B** /// **FAM21C** /// **FAM21D**	253725 /// 387680 /// 55747 /// 653450	family with sequence similarity 21, member B /// family with sequence similarity 21, member C /// family with sequence similarity 21, member A /// family with sequence similarity 21, member D	3.47	0.02
211068_x_at	**FAM21C** /// **FAM21D**	253725 /// 653450	family with sequence similarity 21, member C /// family with sequence similarity 21, member D	3.43	0.00
228362_s_at	**FAM26F**	441168	Family with sequence similarity 26, member F	8.58	0.00
227194_at	**FAM3B**	54097	family with sequence similarity 3, member B	-2.09	0.07
232899_at	**FAM41C** /// **MGC70863** /// **RPL23AP7**	118433 /// 284593 /// 284942	ribosomal protein L23a pseudogene 7 /// family with sequence similarity 41, member C /// similar to RPL23AP7 protein	-2.84	0.03
235009_at	**FAM44A**	259282	family with sequence similarity 44, member A	-2.12	0.00
225030_at	**FAM44B**	91272	family with sequence similarity 44, member B	5.46	0.08
225351_at	**FAM45A**	404636	family with sequence similarity 45, member A	-5.95	0.00
221804_s_at	**FAM45A** /// **FAM45B** /// **LOC731832**	404636 /// 55855 /// 731832	family with sequence similarity 45, member B /// family with sequence similarity 45, member A /// similar to family with sequence similarity 45, member A	-11.02	0.00
226330_s_at	**FAM48A**	55578	family with sequence similarity 48, member A	-2.91	0.34
209683_at	**FAM49A**	81553	family with sequence similarity 49, member A	-3.62	0.00
203262_s_at	**FAM50A**	9130	family with sequence similarity 50, member A	3.48	0.06
203206_at	**FAM53B**	9679	family with sequence similarity 53, member B	-4.11	0.08
218023_s_at	**FAM53C**	51307	family with sequence similarity 53, member C	-2.51	0.03
220147_s_at	**FAM60A**	58516	family with sequence similarity 60, member A	2.42	0.51
223038_s_at	**FAM60A** /// **LOC650369** /// **LOC728115**	58516 /// 650369 /// 728115	family with sequence similarity 60, member A /// similar to teratocarcinoma expressed, serine rich /// similar to Protein FAM60A (Tera protein)	2.50	0.51
221856_s_at	**FAM63A**	55793	family with sequence similarity 63, member A	-3.93	0.00
1553749_at	**FAM76B**	143684	family with sequence similarity 76, member B	2.40	0.06
229764_at	**FAM79B**	285386	family with sequence similarity 79, member B	2.62	0.51
242870_at	**FAM80B**	57494	Family with sequence similarity 80, member B	8.86	0.00
218126_at	**FAM82C**	55177	family with sequence similarity 82, member C	2.46	0.51
1564204_at	**FAM91A2**	57234	family with sequence similarity 91, member A2	-2.43	0.13
218074_at	**FAM96B**	51647	family with sequence similarity 96, member B	2.59	0.25
236029_at	**FAT3**	120114	FAT tumor suppressor homolog 3 (Drosophila)	2.31	0.51

211623_s_at	**FBL**	2091	fibrillarin	5.28	0.00
215717_s_at	**FBN2**	2201	fibrillin 2 (congenital contractural arachnodactyly)	2.72	0.08
209696_at	**FBP1**	2203	fructose-1,6-bisphosphatase 1	19.58	0.02
226215_s_at	**FBXL10**	84678	F-box and leucine-rich repeat protein 10	2.68	0.79
235089_at	**FBXL20**	84961	F-box and leucine-rich repeat protein 20	-39.94	0.34
225132_at	**FBXL3**	26224	F-box and leucine-rich repeat protein 3	-2.67	0.07
225736_at	**FBXO22**	26263	F-box protein 22	2.71	0.25
227521_at	**FBXO33**	254170	F-box protein 33	-5.04	0.16
212987_at	**FBXO9**	26268	F-box protein 9	-2.34	0.16
1554899_s_at	**FCER1G**	2207	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	2.42	0.00
206759_at	**FCER2**	2208	Fc fragment of IgE, low affinity II, receptor for (CD23)	8.33	0.25
216950_s_at	**FCGR1A**	2209	Fc fragment of IgG, high affinity Ia, receptor (CD64)	4.79	0.00
214511_x_at	**FCGR1B**	2210	Fc fragment of IgG, high affinity Ib, receptor (CD64)	3.82	0.00
211395_x_at	**FCGR2C**	9103	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	-2.29	0.00
204006_s_at	**FCGR3A** /// **FCGR3B**	2214 /// 2215	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) /// Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	-2.85	0.00
218831_s_at	**FCGRT**	2217	Fc fragment of IgG, receptor, transporter, alpha	-3.93	0.00
228220_at	**FCHO2**	115548	FCH domain only 2	-11.67	0.13
203620_s_at	**FCHSD2**	9873	FCH and double SH3 domains 2	2.13	0.06
205237_at	**FCN1**	2219	ficolin (collagen/fibrinogen domain containing) 1	-3.84	0.07
203646_at	**FDX1**	2230	ferredoxin 1	3.79	0.34
201798_s_at	**FER1L3**	26509	fer-1-like 3, myoferlin (C. elegans)	35.63	0.16
203562_at	**FEZ1**	9638	fasciculation and elongation protein zeta 1 (zygin I)	2.44	0.79
1555407_s_at	**FGD3**	89846	FYVE, RhoGEF and PH domain containing 3	-5.54	0.03
230559_x_at	**FGD4**	121512	FYVE, RhoGEF and PH domain containing 4	-2.39	0.79
219901_at	**FGD6**	55785	FYVE, RhoGEF and PH domain containing 6	2.71	0.25
205110_s_at	**FGF13**	2258	fibroblast growth factor 13	13.30	0.16
1556283_s_at	**FGFR1OP2**	26127	FGFR1 oncogene partner 2	5.14	0.02
208229_at	**FGFR2**	2263	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	3.93	0.08
204834_at	**FGL2**	10875	fibrinogen-like 2	-3.03	0.00
203033_x_at	**FH**	2271	fumarate hydratase	3.65	0.06
203391_at	**FKBP2**	2286	FK506 binding protein 2, 13kDa	5.46	0.00
200894_s_at	**FKBP4**	2288	FK506 binding protein 4, 59kDa	5.00	0.00
224856_at	**FKBP5**	2289	FK506 binding protein 5	-4.75	0.00
40850_at	**FKBP8**	23770	FK506 binding protein 8, 38kDa	-5.39	0.16
1552664_at	**FLCN**	201163	folliculin	2.36	0.02
210786_s_at	**FLI1**	2313	Friend leukemia virus integration 1	-3.91	0.00
222065_s_at	**FLII**	2314	flightless I homolog (Drosophila)	-3.38	0.03
227302_s_at	**FLII** /// **LLGL1**	2314 /// 3996	flightless I homolog (Drosophila) /// lethal giant larvae homolog 1 (Drosophila)	-2.31	0.25
224318_s_at	**FLJ10081**	55683	hypothetical protein FLJ10081	2.91	0.13
218038_at	**FLJ10241**	55101	hypothetical protein FLJ10241	2.76	0.51
237954_x_at	**FLJ10357**	55701	Hypothetical protein FLJ10357	-20.85	0.00
1562904_s_at	**FLJ10661**	286042	similar to CG7889-PA	-2.62	0.79
222686_s_at	**FLJ11151**	55313	hypothetical protein FLJ11151	-9.50	0.00

202852_s_at	**FLJ11506**	79719	hypothetical protein FLJ11506	3.69	0.13
1555486_a_at	**FLJ14213**	79899	hypothetical protein FLJ14213	11.20	0.00
218986_s_at	**FLJ20035**	55601	hypothetical protein FLJ20035	6.65	0.00
220467_at	**FLJ21272**	80100	hypothetical protein FLJ21272	6.93	0.00
218454_at	**FLJ22662**	79887	hypothetical protein FLJ22662	-7.21	0.00
220674_at	**FLJ22814**	79978	hypothetical protein FLJ22814	5.50	0.51
230561_s_at	**FLJ23861**	151050	hypothetical protein FLJ23861	2.18	0.51
1553797_a_at	**FLJ30594**	150622	hypothetical locus FLJ30594	-2.55	0.16
1564157_at	**FLJ33544**	728283	hypothetical protein LOC728283	2.73	0.00
1562217_at	**FLJ34521**	646383	hypothetical protein LOC646383	-4.08	0.25
212547_at	**FLJ35348**	266655	FLJ35348	-7.00	0.16
231698_at	**FLJ36848**	647115	hypothetical LOC647115	4.88	0.02
235235_s_at	**FLJ36874**	219988	FLJ36874 protein	2.44	0.06
1565806_at	**FLJ37035**	399821	FLJ37035 protein	2.74	0.34
244065_at	**FLJ37512**	643792	similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3)	-9.01	0.34
230999_at	**FLJ39051**	399972	Hypothetical gene supported by AK096370	-4.77	0.13
243547_at	**FLJ39639**	283876	hypothetical protein FLJ39639	-3.70	0.07
229054_at	**FLJ39779**	400223	FLJ39779 protein	-4.39	0.25
229559_at	**FLJ40125**	147699	hypothetical protein FLJ40125	3.58	0.08
214752_x_at	**FLNA**	2316	filamin A, alpha (actin binding protein 280)	3.09	0.34
211299_s_at	**FLOT2**	2319	flotillin 2	-2.68	0.00
219316_s_at	**FLVCR2**	55640	feline leukemia virus subgroup C cellular receptor family, member 2	2.41	0.13
1569257_at	**FMNL1**	752	formin-like 1	-2.34	0.07
242665_at	**FMNL2**	114793	formin-like 2	4.37	0.08
232249_at	**FMNL3**	91010	formin-like 3	52.19	0.00
216442_x_at	**FN1**	2335	fibronectin 1	5.71	0.00
212232_at	**FNBP4**	23360	formin binding protein 4	2.68	0.25
202304_at	**FNDC3A**	22862	fibronectin type III domain containing 3A	3.87	0.08
218618_s_at	**FNDC3B**	64778	fibronectin type III domain containing 3B	3.16	0.00
206371_at	**FOLR3**	2352	folate receptor 3 (gamma)	-34.03	0.00
209189_at	**FOS**	2353	v-fos FBJ murine osteosarcoma viral oncogene homolog	-6.37	0.07
204420_at	**FOSL1**	8061	FOS-like antigen 1	3.63	0.34
225262_at	**FOSL2**	2355	FOS-like antigen 2	-3.76	0.03
202724_s_at	**FOXO1**	2308	forkhead box O1	-23.26	0.00
204132_s_at	**FOXO3**	2309	forkhead box O3	-5.71	0.03
205451_at	**FOXO4**	4303	forkhead box O4	-3.94	0.03
224838_at	**FOXP1**	27086	forkhead box P1	-3.15	0.25
205118_at	**FPR1**	2357	formyl peptide receptor 1	-7.78	0.08
214560_at	**FPRL2**	2359	formyl peptide receptor-like 2	25.87	0.00
219889_at	**FRAT1**	10023	frequently rearranged in advanced T-cell lymphomas	-24.12	0.00
209864_at	**FRAT2**	23401	frequently rearranged in advanced T-cell lymphomas 2	-11.79	0.00
228233_at	**FREM1**	158326	FRAS1 related extracellular matrix 1	2.95	0.00
230645_at	**FRMD3**	257019	FERM domain containing 3	9.06	0.08
1570207_at	**FRRS1**	391059	ferric-chelate reductase 1	2.55	0.51
204072_s_at	**FRY**	10129	furry homolog (Drosophila)	-44.95	0.00
210933_s_at	**FSCN1**	6624	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	13.16	0.00
204948_s_at	**FST**	10468	follistatin	2.61	0.00
208782_at	**FSTL1**	11167	follistatin-like 1	2.38	0.08
223120_at	**FUCA2**	2519	fucosidase, alpha-L- 2, plasma	6.18	0.06
223042_s_at	**FUNDC2**	65991	FUN14 domain containing 2	6.78	0.00

201945_at	**FURIN**	5045	furin (paired basic amino acid cleaving enzyme)	-2.18	0.34
213594_x_at	**FUSIP1** /// **LOC642558** /// **LOC727922**	10772 /// 642558 /// 727922	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1 /// similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein...	2.77	0.08
204299_at	**FUSIP1** /// **LOC727922**	10772 /// 727922	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein...	2.13	0.13
209893_s_at	**FUT4**	2526	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	2.61	0.34
217696_at	**FUT7**	2529	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	-18.97	0.00
214046_at	**FUT9**	10690	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	-2.40	0.25
202419_at	**FVT1**	2531	follicular lymphoma variant translocation 1	5.90	0.00
217981_s_at	**FXC1**	26515	fracture callus 1 homolog (rat)	4.45	0.25
217655_at	**FXYD5**	53827	FXYD domain containing ion transport regulator 5	2.81	0.13
224642_at	**FYTTD1**	84248	forty-two-three domain containing 1	5.90	0.00
213524_s_at	**G0S2**	50486	G0/G1switch 2	5.86	0.00
201503_at	**G3BP1**	10146	GTPase activating protein (SH3 domain) binding protein 1	2.34	0.06
202275_at	**G6PD**	2539	glucose-6-phosphate dehydrogenase	-2.04	0.16
225998_at	**GAB1**	2549	GRB2-associated binding protein 1	-13.13	0.13
204618_s_at	**GABPB2**	2553	GA binding protein transcription factor, beta subunit 2	4.17	0.00
203725_at	**GADD45A**	1647	growth arrest and DNA-damage-inducible, alpha	-3.51	0.79
213560_at	**GADD45B**	4616	Growth arrest and DNA-damage-inducible, beta	2.94	0.00
239422_at	**GAL3ST4** /// **GPC2**	221914 /// 79690	galactose-3-O-sulfotransferase 4 /// glypican 2	-2.77	0.08
211810_s_at	**GALC**	2581	galactosylceramidase	3.20	0.51
222235_s_at	**GALNACT-2**	55454	chondroitin sulfate GalNAcT-2	2.02	0.08
213280_at	**GARNL4**	23108	GTPase activating Rap/RanGAP domain-like 4	-7.63	0.00
208693_s_at	**GARS**	2617	glycyl-tRNA synthetase	3.55	0.00
238756_at	**GAS2L3**	283431	Growth arrest-specific 2 like 3	19.26	0.51
211067_s_at	**GAS7**	8522	growth arrest-specific 7	2.19	0.34
238076_at	**GATAD2B**	57459	GATA zinc finger domain containing 2B	-5.34	0.16
203282_at	**GBE1**	2632	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	3.13	0.00
231577_s_at	**GBP1**	2633	guanylate binding protein 1, interferon-inducible, 67kDa	4.46	0.00
223434_at	**GBP3**	2635	guanylate binding protein 3	32.60	0.00
235574_at	**GBP4**	115361	guanylate binding protein 4	15.66	0.00
238581_at	**GBP5**	115362	guanylate binding protein 5	7.58	0.00
204224_s_at	**GCH1**	2643	GTP cyclohydrolase 1 (dopa-responsive dystonia)	8.01	0.00
202922_at	**GCLC**	2729	glutamate-cysteine ligase, catalytic subunit	2.11	0.34

203925_at	**GCLM**	2730	glutamate-cysteine ligase, modifier subunit	11.49	0.00
229868_s_at	**GDF15**	9518	Growth differentiation factor 15	8.58	0.51
219722_s_at	**GDPD3**	79153	glycerophosphodiester phosphodiesterase domain containing 3	-9.17	0.00
225161_at	**GFM1**	85476	G elongation factor, mitochondrial 1	5.93	0.13
202722_s_at	**GFPT1**	2673	glutamine-fructose-6-phosphate transaminase 1	6.14	0.13
218114_at	**GGA1**	26088	golgi associated, gamma adaptin ear containing, ARF binding protein 1	6.80	0.08
202322_s_at	**GGPS1**	9453	geranylgeranyl diphosphate synthase 1	2.70	0.08
211508_s_at	**GH2**	2689	growth hormone 2	3.81	0.00
1552318_at	**GIMAP1**	170575	GTPase, IMAP family member 1	2.06	0.25
232024_at	**GIMAP2**	26157	GTPase, IMAP family member 2	3.69	0.13
218805_at	**GIMAP5**	55340	GTPase, IMAP family member 5	17.43	0.00
219777_at	**GIMAP6**	474344	GTPase, IMAP family member 6	3.29	0.51
204982_at	**GIT2**	9815	G protein-coupled receptor kinase interactor 2	-2.25	0.08
215966_x_at	**GK3P**	2713	glycerol kinase 3 pseudogene	2.10	0.00
214430_at	**GLA**	2717	galactosidase, alpha	3.77	0.06
201576_s_at	**GLB1**	2720	galactosidase, beta 1	-2.19	0.51
227525_at	**GLCCI1**	113263	glucocorticoid induced transcript 1	-12.40	0.13
214085_x_at	**GLIPR1**	11010	GLI pathogenesis-related 1 (glioma)	-5.22	0.00
223079_s_at	**GLS**	2744	glutaminase	5.82	0.00
229770_at	**GLT1D1**	144423	glycosyltransferase 1 domain containing 1	-6.00	0.00
218458_at	**GMCL1**	64395	germ cell-less homolog 1 (Drosophila)	-6.83	0.08
202543_s_at	**GMFB**	2764	glia maturation factor, beta	2.31	0.02
204220_at	**GMFG**	9535	glia maturation factor, gamma	-2.13	0.00
218913_s_at	**GMIP**	51291	GEM interacting protein	-2.95	0.07
222710_at	**GMPPB**	29925	GDP-mannose pyrophosphorylase B	3.46	0.25
205349_at	**GNA15**	2769	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	6.17	0.08
201040_at	**GNAI2**	2771	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	-2.37	0.07
224863_at	**GNAQ**	2776	Guanine nucleotide binding protein (G protein), q polypeptide	-4.13	0.00
200981_x_at	**GNAS**	2778	GNAS complex locus	-2.03	0.00
223564_s_at	**GNB1L**	54584	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-2.07	0.34
206896_s_at	**GNG7**	2788	guanine nucleotide binding protein (G protein), gamma 7	-4.53	0.34
201948_at	**GNL2**	29889	guanine nucleotide binding protein-like 2 (nucleolar)	8.24	0.13
217850_at	**GNL3**	26354	guanine nucleotide binding protein-like 3 (nucleolar)	9.21	0.00
205495_s_at	**GNLY**	10578	granulysin	3.57	0.34
202382_s_at	**GNPDA1**	10007	glucosamine-6-phosphate deaminase 1	14.94	0.00
212959_s_at	**GNPTAB**	79158	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	2.38	0.79
224887_at	**GNPTG**	84572	N-acetylglucosamine-1-phosphate transferase, gamma subunit	3.00	0.06
235540_at	**GNRH1**	2796	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	-6.40	0.34
212335_at	**GNS**	2799	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	2.13	0.00
214997_at	**GOLGA1**	2800	Golgi autoantigen, golgin subfamily a, 1	2.17	0.00
218193_s_at	**GOLT1B**	51026	golgi transport 1 homolog B (S. cerevisiae)	5.99	0.06
207812_s_at	**GORASP2**	26003	golgi reassembly stacking protein 2, 55kDa	2.47	0.34
224632_at	**GPATCH4**	54865	G patch domain containing 4	4.44	0.51
201141_at	**GPNMB**	10457	glycoprotein (transmembrane) nmb	29.68	0.06

239533_at	**GPR155**	151556	G protein-coupled receptor 155	-7.57	0.03
228950_s_at	**GPR177**	79971	G protein-coupled receptor 177	-16.54	0.00
212070_at	**GPR56**	9289	G protein-coupled receptor 56	2.55	0.51
214467_at	**GPR65**	8477	G protein-coupled receptor 65	2.17	0.00
223767_at	**GPR84**	53831	G protein-coupled receptor 84	99.80	0.00
1553723_at	**GPR97**	222487	G protein-coupled receptor 97	-2.61	0.07
201106_at	**GPX4**	2879	glutathione peroxidase 4 (phospholipid hydroperoxidase)	4.47	0.08
219313_at	**GRAMD1C**	54762	GRAM domain containing 1C	-9.18	0.03
212090_at	**GRINA**	2907	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	4.79	0.06
210981_s_at	**GRK6**	2870	G protein-coupled receptor kinase 6	-3.92	0.08
201912_s_at	**GSPT1**	2935	G1 to S phase transition 1	4.08	0.13
225609_at	**GSR**	2936	glutathione reductase	2.07	0.00
204149_s_at	**GSTM4**	2948	glutathione S-transferase M4	-4.59	0.13
1557915_s_at	**GSTO1**	9446	glutathione S-transferase omega 1	5.28	0.00
209595_at	**GTF2F2**	2963	general transcription factor IIF, polypeptide 2, 30kDa	2.46	0.79
202453_s_at	**GTF2H1**	2965	general transcription factor IIH, polypeptide 1, 62kDa	4.81	0.06
210891_s_at	**GTF2I** /// **GTF2IP1** /// **LOC100093631** /// **LOC732437**	100093631 /// 2969 /// 2970 /// 732437	general transcription factor II, i /// general transcription factor II, i, pseudogene 1 /// similar to general transcription factor II, i isoform 1 /// general transcription factor II, i, pseudogene	-3.93	0.00
201338_x_at	**GTF3A**	2971	general transcription factor IIIA	2.37	0.08
225083_at	**GTF3C6**	112495	general transcription factor IIIC, polypeptide 6, alpha 35kDa	6.60	0.02
218238_at	**GTPBP4**	23560	GTP binding protein 4	14.04	0.00
242685_at	**GTPBP8**	29083	GTP-binding protein 8 (putative)	4.28	0.25
243909_x_at	**GUSBL2**	375513	glucuronidase, beta-like 2	2.32	0.34
213089_at	**GUSBP1**	153561	glucuronidase, beta pseudogene 1	-4.10	0.00
202947_s_at	**GYPC**	2995	glycophorin C (Gerbich blood group)	3.33	0.16
210164_at	**GZMB**	3002	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	8.85	0.51
208886_at	**H1F0**	3005	H1 histone family, member 0	2.72	0.34
212524_x_at	**H2AFX**	3014	H2A histone family, member X	-2.38	0.13
200853_at	**H2AFZ**	3015	H2A histone family, member Z	-3.03	0.00
208579_x_at	**H2BFS**	54145	H2B histone family, member S	-4.07	0.03
206643_at	**HAL**	3034	histidine ammonia-lyase	-20.77	0.00
227262_at	**HAPLN3**	145864	hyaluronan and proteoglycan link protein 3	2.63	0.06
235458_at	**HAVCR2**	84868	hepatitis A virus cellular receptor 2	7.28	0.00
201145_at	**HAX1**	10456	HCLS1 associated protein X-1	2.79	0.06
214414_x_at	**HBA2**	3040	hemoglobin, alpha 2	-4.38	0.51
38037_at	**HBEGF**	1839	heparin-binding EGF-like growth factor	19.26	0.00
227089_at	**HBP1**	26959	HMG-box transcription factor 1	-2.55	0.00
203746_s_at	**HCCS**	3052	holocytochrome c synthase (cytochrome c heme-lyase)	4.06	0.16
202474_s_at	**HCFC1**	3054	host cell factor C1 (VP16-accessory protein)	12.31	0.06
1559050_at	**HCG27**	253018	HLA complex group 27	-27.53	0.08
206685_at	**HCG4**	54435	HLA complex group 4	2.68	0.06
215974_at	**HCG4P6**	80868	HLA complex group 4 pseudogene 6	7.70	0.00
216174_at	**HCRP1**	387535	hepatocellular carcinoma-related HCRP1	-4.07	0.16
223640_at	**HCST**	10870	hematopoietic cell signal transducer	4.53	0.06
217937_s_at	**HDAC7A**	51564	histone deacetylase 7A	-3.79	0.00
200896_x_at	**HDGF**	3068	hepatoma-derived growth factor (high-mobility group protein 1-like)	4.31	0.00

209525_at	**HDGFRP3**	50810	Hepatoma-derived growth factor, related protein 3	-5.68	0.25
224129_s_at	**HDPY-30**	84661	dpy-30-like protein	-2.71	0.34
218450_at	**HEBP1**	50865	heme binding protein 1	4.21	0.06
203430_at	**HEBP2**	23593	heme binding protein 2	-6.61	0.00
213069_at	**HEG1**	57493	HEG homolog 1 (zebrafish)	7.52	0.06
1552787_at	**HELB**	92797	helicase (DNA) B	3.79	0.06
240486_at	**HELZ**	9931	Helicase with zinc finger	-3.59	0.08
218306_s_at	**HERC1**	8925	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	-2.84	0.51
203393_at	**HES1**	3280	hairy and enhancer of split 1, (Drosophila)	2.86	0.34
201765_s_at	**HEXA**	3073	hexosaminidase A (alpha polypeptide)	2.32	0.00
218839_at	**HEY1**	23462	hairy/enhancer-of-split related with YRPW motif 1	-7.27	0.00
204689_at	**HHEX**	3087	hematopoietically expressed homeobox	-9.35	0.07
225222_at	**HIAT1**	64645	hippocampus abundant transcript 1	3.13	0.00
200989_at	**HIF1A**	3091	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	2.38	0.00
209328_x_at	**HIGD2A**	192286	HIG1 domain family, member 2A	2.72	0.79
207721_x_at	**HINT1**	3094	histidine triad nucleotide binding protein 1	6.41	0.00
228697_at	**HINT3**	135114	histidine triad nucleotide binding protein 3	2.30	0.02
226297_at	**HIPK3**	10114	Homeodomain interacting protein kinase 3	-2.24	0.00
209398_at	**HIST1H1C**	3006	histone cluster 1, H1c	-4.49	0.51
208569_at	**HIST1H2AB**	8335	histone cluster 1, H2ab	-2.39	0.34
215071_s_at	**HIST1H2AC**	8334	histone cluster 1, H2ac	-9.43	0.00
207156_at	**HIST1H2AG**	8969	histone cluster 1, H2ag	-4.18	0.51
214542_x_at	**HIST1H2AI**	8329	histone cluster 1, H2ai	-3.21	0.03
208583_x_at	**HIST1H2AJ**	8331	histone cluster 1, H2aj	-3.16	0.03
236193_at	**HIST1H2BC**	8347	histone cluster 1, H2bc	-7.93	0.03
214455_at	**HIST1H2BC /// HIST1H2BG**	8339 /// 8347	histone cluster 1, H2bg /// histone cluster 1, H2bc	-5.34	0.07
209911_x_at	**HIST1H2BD**	3017	histone cluster 1, H2bd	-4.68	0.00
208527_x_at	**HIST1H2BE**	8344	histone cluster 1, H2be	-4.76	0.03
208490_x_at	**HIST1H2BF**	8343	histone cluster 1, H2bf	-4.57	0.00
208546_x_at	**HIST1H2BH**	8345	histone cluster 1, H2bh	-3.98	0.08
208523_x_at	**HIST1H2BI**	8346	histone cluster 1, H2bi	-4.07	0.07
214540_at	**HIST1H2BO**	8348	histone cluster 1, H2bo	-3.55	0.00
214522_x_at	**HIST1H3D**	8351	histone cluster 1, H3d	-2.73	0.00
206110_at	**HIST1H3H**	8357	histone cluster 1, H3h	-4.94	0.25
214290_s_at	**HIST2H2AA3 /// HIST2H2AA4**	723790 /// 8337	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	-2.30	0.34
202708_s_at	**HIST2H2BE**	8349	histone cluster 2, H2be	-2.38	0.07
231681_x_at	**HIST3H2A**	92815	Histone cluster 3, H2a	-3.98	0.07
212641_at	**HIVEP2**	3097	human immunodeficiency virus type I enhancer binding protein 2	3.82	0.00
205936_s_at	**HK3**	3101	hexokinase 3 (white cell)	-4.92	0.51
217478_s_at	**HLA-DMA**	3108	major histocompatibility complex, class II, DM alpha	4.83	0.02
203932_at	**HLA-DMB**	3109	major histocompatibility complex, class II, DM beta	4.23	0.06
205671_s_at	**HLA-DOB**	3112	major histocompatibility complex, class II, DO beta	4.49	0.16
213537_at	**HLA-DPA1**	3113	major histocompatibility complex, class II, DP alpha 1	16.27	0.00

201137_s_at	**HLA-DPB1**	3115	major histocompatibility complex, class II, DP beta 1	3.92	0.02
213831_at	**HLA-DQA1**	3117	major histocompatibility complex, class II, DQ alpha 1	8.41	0.00
212671_s_at	**HLA-DQA1** /// **HLA-DQA2** /// **LOC731682**	3117 /// 3118 /// 731682	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2 /// similar to HLA class II histocompatibility antigen, DQ(1) alpha chain precursor (DC-4 alpha chain)	14.39	0.00
212998_x_at	**HLA-DQB1**	3119	major histocompatibility complex, class II, DQ beta 1	19.63	0.00
211654_x_at	**HLA-DQB1** /// **LOC650557**	3119 /// 650557	major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DQ(W1.1) beta chain precursor (DQB1*0501)	17.33	0.00
208894_at	**HLA-DRA**	3122	major histocompatibility complex, class II, DR alpha	12.76	0.00
208306_x_at	**HLA-DRB1**	3123	Major histocompatibility complex, class II, DR beta 1	5.32	0.02
215193_x_at	**HLA-DRB1** /// **HLA-DRB3** /// **LOC730415**	3123 /// 3125 /// 730415	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// hypothetical protein LOC730415	12.25	0.00
209312_x_at	**HLA-DRB1** /// **LOC730415**	3123 /// 730415	major histocompatibility complex, class II, DR beta 1 /// hypothetical protein LOC730415	6.45	0.00
209728_at	**HLA-DRB4**	3126	major histocompatibility complex, class II, DR beta 4	8.39	0.13
217362_x_at	**HLA-DRB6**	3128	major histocompatibility complex, class II, DR beta 6 (pseudogene)	4.10	0.00
232209_x_at	**HM13**	81502	histocompatibility (minor) 13	2.24	0.16
212597_s_at	**HMG2L1**	10042	high-mobility group protein 2-like 1	4.94	0.16
206074_s_at	**HMGA1**	3159	high mobility group AT-hook 1	5.91	0.06
208808_s_at	**HMGB2**	3148	high-mobility group box 2	-3.89	0.00
202772_at	**HMGCL**	3155	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	3.05	0.34
221750_at	**HMGCS1**	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	5.31	0.16
203665_at	**HMOX1**	3162	heme oxygenase (decycling) 1	4.04	0.00
217755_at	**HN1**	51155	hematological and neurological expressed 1	-7.06	0.00
204111_at	**HNMT**	3176	histamine N-methyltransferase	2.16	0.00
208766_s_at	**HNRNPR**	10236	heterogeneous nuclear ribonucleoprotein R	3.86	0.00
211932_at	**HNRPA3**	220988	heterogeneous nuclear ribonucleoprotein A3	2.11	0.25
206808_at	**HNRPA3P1**	10151	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	2.13	0.16
201277_s_at	**HNRPAB**	3182	heterogeneous nuclear ribonucleoprotein A/B	2.12	0.13
1554678_s_at	**HNRPDL**	9987	heterogeneous nuclear ribonucleoprotein D-like	2.04	0.00
201376_s_at	**HNRPF**	3185	heterogeneous nuclear ribonucleoprotein F	4.88	0.00
228642_at	**HOXA2**	3199	Homeobox A2	-4.73	0.08
206697_s_at	**HP**	3240	haptoglobin	-3.57	0.00
208470_s_at	**HP** /// **HPR**	3240 /// 3250	haptoglobin /// haptoglobin-related protein	-5.35	0.13
229204_at	**HP1BP3**	50809	Heterochromatin protein 1, binding protein 3	-2.21	0.07
208471_at	**HPR**	3250	haptoglobin-related protein	3.01	0.06
204544_at	**HPS5**	11234	Hermansky-Pudlak syndrome 5	4.68	0.51
216879_at	**HR44**	27251	Hr44 antigen	3.13	0.06
205579_at	**HRH1**	3269	histamine receptor H1	3.25	0.00
220805_at	**HRH2**	3274	histamine receptor H2	-2.69	0.25

227361_at	**HS3ST3B1**	9953	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	15.42	0.00
217989_at	**HSD17B11**	51170	hydroxysteroid (17-beta) dehydrogenase 11	-4.12	0.00
201413_at	**HSD17B4**	3295	hydroxysteroid (17-beta) dehydrogenase 4	2.34	0.25
222817_at	**HSD3B7**	80270	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	14.13	0.79
209513_s_at	**HSDL2**	84263	hydroxysteroid dehydrogenase like 2	-11.21	0.00
1552623_at	**HSH2D**	84941	hematopoietic SH2 domain containing	-12.35	0.00
211969_at	**HSP90AA1**	3320	heat shock protein 90kDa alpha (cytosolic), class A member 1	3.00	0.00
1557910_at	**HSP90AB1**	3326	heat shock protein 90kDa alpha (cytosolic), class B member 1	11.21	0.00
200599_s_at	**HSP90B1**	7184	heat shock protein 90kDa beta (Grp94), member 1	4.40	0.00
200800_s_at	**HSPA1A /// HSPA1B**	3303 /// 3304	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	-2.74	0.00
208815_x_at	**HSPA4**	3308	heat shock 70kDa protein 4	2.88	0.00
211936_at	**HSPA5**	3309	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	2.22	0.00
213418_at	**HSPA6**	3310	heat shock 70kDa protein 6 (HSP70B')	-5.35	0.00
200692_s_at	**HSPA9**	3313	heat shock 70kDa protein 9 (mortalin)	15.30	0.00
203023_at	**HSPC111**	51491	hypothetical protein HSPC111	3.62	0.00
221597_s_at	**HSPC171**	29100	HSPC171 protein	6.18	0.00
205133_s_at	**HSPE1**	3336	heat shock 10kDa protein 1 (chaperonin 10)	7.41	0.00
206976_s_at	**HSPH1**	10808	heat shock 105kDa/110kDa protein 1	18.68	0.00
202602_s_at	**HTATSF1**	27336	HIV-1 Tat specific factor 1	2.71	0.51
217618_x_at	**HUS1**	3364	HUS1 checkpoint homolog (S. pombe)	3.94	0.51
226879_at	**HVCN1**	84329	hydrogen voltage-gated channel 1	-4.09	0.79
233809_at	**HYPK**	25764	Huntingtin interacting protein K	3.69	0.00
230621_at	**IAH1**	285148	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	2.08	0.00
210970_s_at	**IBTK**	25998	inhibitor of Bruton agammaglobulinemia tyrosine kinase	9.07	0.34
202638_s_at	**ICAM1**	3383	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	18.83	0.00
213620_s_at	**ICAM2**	3384	intercellular adhesion molecule 2	10.20	0.34
204949_at	**ICAM3**	3385	intercellular adhesion molecule 3	-3.86	0.00
209291_at	**ID4**	3400	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	3.15	0.16
202070_s_at	**IDH3A**	3419	isocitrate dehydrogenase 3 (NAD+) alpha	3.37	0.25
201631_s_at	**IER3**	8870	immediate early response 3	2.00	0.00
218611_at	**IER5**	51278	immediate early response 5	2.92	0.00
202411_at	**IFI27**	3429	interferon, alpha-inducible protein 27	6.54	0.13
201422_at	**IFI30**	10437	interferon, gamma-inducible protein 30	2.97	0.00
209417_s_at	**IFI35**	3430	interferon-induced protein 35	5.86	0.00
214453_s_at	**IFI44**	10561	interferon-induced protein 44	2.34	0.25
204439_at	**IFI44L**	10964	interferon-induced protein 44-like	5.13	0.79
219209_at	**IFIH1**	64135	interferon induced with helicase C domain 1	4.91	0.00
203153_at	**IFIT1**	3434	interferon-induced protein with tetratricopeptide repeats 1	-5.71	0.03
229450_at	**IFIT3**	3437	interferon-induced protein with tetratricopeptide repeats 3	2.47	0.00
203595_s_at	**IFIT5**	24138	interferon-induced protein with tetratricopeptide repeats 5	2.07	0.34
201315_x_at	**IFITM2**	10581	interferon induced transmembrane protein 2 (1-8D)	-2.14	0.00
225669_at	**IFNAR1**	3454	interferon (alpha, beta and omega) receptor 1	-2.28	0.16
218100_s_at	**IFT57**	55081	intraflagellar transport 57 homolog (Chlamydomonas)	3.18	0.08

243358_at	**IGF1R**	3480	insulin-like growth factor 1 receptor	-15.63	0.08
203820_s_at	**IGF2BP3**	10643	insulin-like growth factor 2 mRNA binding protein 3	5.43	0.51
216557_x_at	**IGHA1** /// **IGHG1** /// **IGHG3** /// **IGHM** /// **IGHV4-31**	28396 /// 3493 /// 3500 /// 3502 /// 3507	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31	-2.01	0.51
235202_x_at	**IKIP**	121457	IKK interacting protein	-11.97	0.00
227344_at	**IKZF1**	10320	IKAROS family zinc finger 1 (Ikaros)	-5.26	0.07
226759_at	**IKZF4**	64375	IKAROS family zinc finger 4 (Eos)	18.30	0.08
204912_at	**IL10RA**	3587	interleukin 10 receptor, alpha	5.76	0.00
239522_at	**IL12RB1**	3594	Interleukin 12 receptor, beta 1	2.17	0.25
201888_s_at	**IL13RA1**	3597	interleukin 13 receptor, alpha 1	-2.84	0.00
207375_s_at	**IL15RA**	3601	interleukin 15 receptor, alpha	43.69	0.08
209827_s_at	**IL16**	3603	interleukin 16 (lymphocyte chemoattractant factor)	-10.35	0.00
205707_at	**IL17RA**	23765	interleukin 17 receptor A	-3.28	0.00
222868_s_at	**IL18BP**	10068	interleukin 18 binding protein	76.38	0.00
207072_at	**IL18RAP**	8807	interleukin 18 receptor accessory protein	-2.16	0.79
210118_s_at	**IL1A**	3552	interleukin 1, alpha	203.33	0.00
205067_at	**IL1B**	3553	interleukin 1, beta	3.38	0.00
205227_at	**IL1RAP**	3556	interleukin 1 receptor accessory protein	-2.80	0.00
212659_s_at	**IL1RN**	3557	interleukin 1 receptor antagonist	4.46	0.00
219971_at	**IL21R**	50615	interleukin 21 receptor	-2.16	0.25
211269_s_at	**IL2RA**	3559	interleukin 2 receptor, alpha	29.96	0.00
203828_s_at	**IL32**	9235	interleukin 32	12.84	0.08
206148_at	**IL3RA**	3563	interleukin 3 receptor, alpha (low affinity)	2.81	0.06
230966_at	**IL4I1**	259307	interleukin 4 induced 1	96.27	0.00
210744_s_at	**IL5RA**	3568	interleukin 5 receptor, alpha	-2.20	0.34
205207_at	**IL6**	3569	interleukin 6 (interferon, beta 2)	38.50	0.00
204863_s_at	**IL6ST**	3572	interleukin 6 signal transducer (gp130, oncostatin M receptor)	5.03	0.00
202859_x_at	**IL8**	3576	interleukin 8	5.14	0.00
207094_at	**IL8RA**	3577	interleukin 8 receptor, alpha	-40.25	0.00
207008_at	**IL8RB**	3579	interleukin 8 receptor, beta	-6.59	0.00
200052_s_at	**ILF2**	3608	interleukin enhancer binding factor 2, 45kDa	7.09	0.08
211375_s_at	**ILF3**	3609	interleukin enhancer binding factor 3, 90kDa	5.29	0.00
221548_s_at	**ILKAP**	80895	integrin-linked kinase-associated serine/threonine phosphatase 2C	2.27	0.34
203126_at	**IMPA2**	3613	inositol(myo)-1(or 4)-monophosphatase 2	-37.62	0.00
224744_at	**IMPAD1**	54928	inositol monophosphatase domain containing 1	2.98	0.51
210029_at	**INDO**	3620	indoleamine-pyrrole 2,3 dioxygenase	50.71	0.00
1568638_a_at	**INDOL1**	169355	indoleamine-pyrrole 2,3 dioxygenase-like 1	39.61	0.34
213544_at	**ING2**	3622	Inhibitor of growth family, member 2	-3.13	0.79
204926_at	**INHBA**	3624	inhibin, beta A	102.19	0.00
225357_s_at	**INOC1**	54617	INO80 complex homolog 1 (S. cerevisiae)	2.73	0.51
1554757_a_at	**INPP5A**	3632	inositol polyphosphate-5-phosphatase, 40kDa	-2.82	0.25
203332_s_at	**INPP5D**	3635	inositol polyphosphate-5-phosphatase, 145kDa	-2.77	0.16
229632_s_at	**INTS10**	55174	integrator complex subunit 10	-2.93	0.13
218819_at	**INTS6**	26512	integrator complex subunit 6	-3.75	0.07
218905_at	**INTS8**	55656	integrator complex subunit 8	-2.32	0.16
239878_at	**IPMK**	253430	inositol polyphosphate multikinase	-3.10	0.16
238488_at	**IPO11**	51194	importin 11	15.37	0.06
200993_at	**IPO7**	10527	importin 7	3.56	0.08
210840_s_at	**IQGAP1**	8826	IQ motif containing GTPase activating protein 1	-2.36	0.00

203474_at	**IQGAP2**	10788	IQ motif containing GTPase activating protein 2	-6.42	0.00
203906_at	**IQSEC1**	9922	IQ motif and Sec7 domain 1	-3.33	0.00
201587_s_at	**IRAK1**	3654	interleukin-1 receptor-associated kinase 1	3.70	0.06
231779_at	**IRAK2**	3656	interleukin-1 receptor-associated kinase 2	33.64	0.00
220034_at	**IRAK3**	11213	interleukin-1 receptor-associated kinase 3	3.03	0.06
205469_s_at	**IRF5**	3663	interferon regulatory factor 5	6.54	0.02
208436_s_at	**IRF7**	3665	interferon regulatory factor 7	4.34	0.25
204057_at	**IRF8**	3394	interferon regulatory factor 8	3.04	0.51
209185_s_at	**IRS2**	8660	insulin receptor substrate 2	-2.49	0.03
209274_s_at	**ISCA1**	81689	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-3.29	0.79
205483_s_at	**ISG15**	9636	ISG15 ubiquitin-like modifier	3.06	0.13
204698_at	**ISG20**	3669	interferon stimulated exonuclease gene 20kDa	2.26	0.00
219361_s_at	**ISG20L1**	64782	interferon stimulated exonuclease gene 20kDa-like 1	6.38	0.34
225632_s_at	**ISY1 /// RAB43**	339122 /// 57461	ISY1 splicing factor homolog (S. cerevisiae) /// RAB43, member RAS oncogene family	-4.57	0.25
201656_at	**ITGA6**	3655	integrin, alpha 6	-6.38	0.51
216331_at	**ITGA7**	3679	integrin, alpha 7	-2.02	0.51
1553530_a_at	**ITGB1**	3688	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	2.36	0.16
210740_s_at	**ITPK1**	3705	inositol 1,3,4-triphosphate 5/6 kinase	-3.53	0.00
203723_at	**ITPKB**	3707	inositol 1,4,5-trisphosphate 3-kinase B	-4.71	0.13
203710_at	**ITPR1**	3708	inositol 1,4,5-triphosphate receptor, type 1	11.98	0.00
35776_at	**ITSN1**	6453	intersectin 1 (SH3 domain protein)	2.98	0.00
240941_at	**ITSN2**	50618	Intersectin 2	-2.03	0.34
244235_at	**IVNS1ABP**	10625	influenza virus NS1A binding protein	3.50	0.00
231183_s_at	**JAG1**	182	Jagged 1 (Alagille syndrome)	31.00	0.00
223104_at	**JAGN1**	84522	jagunal homolog 1 (Drosophila)	2.00	0.79
205888_s_at	**JAKMIP2**	9832	janus kinase and microtubule interacting protein 2	8.99	0.25
226371_at	**JARID1A**	5927	jumonji, AT rich interactive domain 1A	-2.67	0.16
203298_s_at	**JARID2**	3720	jumonji, AT rich interactive domain 2	-3.22	0.00
225798_at	**JAZF1**	221895	JAZF zinc finger 1	-2.94	0.07
226267_at	**JDP2**	122953	jun dimerization protein 2	-3.73	0.13
221778_at	**JHDM1D**	80853	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	-2.83	0.00
210878_s_at	**JMJD1B**	51780	jumonji domain containing 1B	-2.41	0.08
221763_at	**JMJD1C**	221037	jumonji domain containing 1C	-2.82	0.07
212496_s_at	**JMJD2B**	23030	jumonji domain containing 2B	-5.38	0.03
212723_at	**JMJD6**	23210	jumonji domain containing 6	3.05	0.79
229294_at	**JPH3**	57338	junctophilin 3	2.20	0.51
213281_at	**JUN**	3725	Jun oncogene	5.84	0.00
200079_s_at	**KARS**	3735	lysyl-tRNA synthetase	8.70	0.00
223412_at	**KBTBD7**	84078	kelch repeat and BTB (POZ) domain containing 7	-16.28	0.00
242887_at	**KCMF1**	56888	potassium channel modulatory factor 1	-3.41	0.34
243893_at	**KCNC3**	3748	potassium voltage-gated channel, Shaw-related subfamily, member 3	4.68	0.00
227647_at	**KCNE3**	10008	potassium voltage-gated channel, Isk-related family, member 3	-2.58	0.00
224099_at	**KCNH7**	90134	potassium voltage-gated channel, subfamily H (eag-related), member 7	-5.38	0.03
219615_s_at	**KCNK5**	8645	potassium channel, subfamily K, member 5	2.50	0.51
223823_at	**KCNMB2**	10242	potassium large conductance calcium-activated channel, subfamily M, beta member 2	2.43	0.51

204487_s_at	**KCNQ1**	3784	potassium voltage-gated channel, KQT-like subfamily, member 1	-13.37	0.51
205737_at	**KCNQ2**	3785	potassium voltage-gated channel, KQT-like subfamily, member 2	2.19	0.00
233234_at	**KCTD16**	57528	potassium channel tetramerisation domain containing 16	3.81	0.06
205561_at	**KCTD17**	79734	potassium channel tetramerisation domain containing 17	2.94	0.79
200698_at	**KDELR2**	11014	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	2.83	0.00
203712_at	**KIAA0020**	9933	KIAA0020	3.05	0.34
212395_s_at	**KIAA0090**	23065	KIAA0090	9.05	0.13
212150_at	**KIAA0143**	23167	KIAA0143 protein	2.22	0.08
212523_s_at	**KIAA0146**	23514	KIAA0146	-3.76	0.03
201985_at	**KIAA0196**	9897	KIAA0196	2.37	0.79
212441_at	**KIAA0232**	9778	KIAA0232	-4.98	0.25
212621_at	**KIAA0286**	23306	KIAA0286 protein	2.32	0.16
1554989_at	**KIAA0317**	9870	KIAA0317	-2.02	0.03
222468_at	**KIAA0319L**	79932	KIAA0319-like	-5.88	0.08
203171_s_at	**KIAA0409**	23378	KIAA0409	2.16	0.16
209912_s_at	**KIAA0415**	9907	KIAA0415	3.44	0.16
1558697_a_at	**KIAA0430**	9665	KIAA0430	-3.93	0.00
204546_at	**KIAA0513**	9764	KIAA0513	-4.07	0.34
212943_at	**KIAA0528**	9847	KIAA0528	2.20	0.16
203364_s_at	**KIAA0652**	9776	KIAA0652	-3.87	0.51
213118_at	**KIAA0701**	23074	KIAA0701 protein	-2.62	0.13
230028_at	**KIAA0907**	22889	KIAA0907	3.98	0.25
209654_at	**KIAA0947**	23379	KIAA0947 protein	4.34	0.79
214929_s_at	**KIAA1109**	84162	KIAA1109	-2.58	0.51
223162_s_at	**KIAA1147**	57189	KIAA1147	2.38	0.51
227479_at	**KIAA1244**	57221	KIAA1244	2.01	0.51
1554852_a_at	**KIAA1257**	57501	KIAA1257	-6.92	0.79
243349_at	**KIAA1324**	57535	KIAA1324	-14.98	0.07
228984_at	**KIAA1394**	57571	KIAA1394 protein	-2.96	0.13
225922_at	**KIAA1450**	57600	KIAA1450 protein	27.72	0.00
233893_s_at	**KIAA1530**	57654	KIAA1530 protein	-2.01	0.25
211433_x_at	**KIAA1539**	80256	KIAA1539	-3.87	0.00
1569385_s_at	**KIAA1546**	54790	KIAA1546	-3.05	0.00
226155_at	**KIAA1600**	57700	KIAA1600	-11.68	0.00
232155_at	**KIAA1618**	57714	KIAA1618	3.35	0.25
235552_at	**KIAA1627**	57721	KIAA1627 protein	2.29	0.51
227638_at	**KIAA1632**	57724	KIAA1632	6.80	0.06
229891_x_at	**KIAA1704**	55425	KIAA1704	2.67	0.08
226599_at	**KIAA1727**	85462	KIAA1727 protein	5.55	0.08
226909_at	**KIAA1729**	85460	KIAA1729 protein	-3.06	0.16
1565829_at	**KIAA1731**	85459	KIAA1731	-2.43	0.51
226691_at	**KIAA1856**	84629	KIAA1856 protein	-3.28	0.13
224708_at	**KIAA2013**	90231	KIAA2013	-2.27	0.08
209234_at	**KIF1B**	23095	kinesin family member 1B	-2.83	0.13
209244_s_at	**KIF1C**	10749	kinesin family member 1C	2.54	0.79
204411_at	**KIF21B**	23046	kinesin family member 21B	-3.90	0.79
1557089_at	**KIF5C**	3800	kinesin family member 5C	8.92	0.00
202393_s_at	**KLF10**	7071	Kruppel-like factor 10	8.36	0.00
208467_at	**KLF12**	11278	Kruppel-like factor 12	-2.51	0.13
221302_at	**KLF15**	28999	Kruppel-like factor 15	2.21	0.51
219371_s_at	**KLF2**	10365	Kruppel-like factor 2 (lung)	-2.72	0.00

219657_s_at	**KLF3**	51274	Kruppel-like factor 3 (basic)	-5.14	0.00
209211_at	**KLF5**	688	Kruppel-like factor 5 (intestinal)	7.67	0.00
204334_at	**KLF7**	8609	Kruppel-like factor 7 (ubiquitous)	-7.26	0.00
208784_s_at	**KLHDC3**	116138	kelch domain containing 3	-2.15	0.34
242088_at	**KLHL24**	54800	kelch-like 24 (Drosophila)	-2.75	0.25
228167_at	**KLHL6**	89857	kelch-like 6 (Drosophila)	3.62	0.06
214470_at	**KLRB1**	3820	killer cell lectin-like receptor subfamily B, member 1	4.69	0.00
1555691_a_at	**KLRC4** /// **KLRK1**	22914 /// 8302	killer cell lectin-like receptor subfamily C, member 4 /// killer cell lectin-like receptor subfamily K, member 1	6.18	0.51
202055_at	**KPNA1**	3836	karyopherin alpha 1 (importin alpha 5)	-2.27	0.34
201088_at	**KPNA2**	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	-2.10	0.13
203202_at	**KRR1**	11103	KRR1, small subunit (SSU) processome component, homolog (yeast)	-3.30	0.00
230835_at	**KRTDAP**	388533	keratinocyte differentiation-associated protein	3.21	0.16
235252_at	**KSR1**	8844	Kinase suppressor of ras 1	-3.84	0.07
216315_x_at	**Kua-UEV** /// **LOC730052** /// **UBE2V1**	387522 /// 730052 /// 7335	ubiquitin-conjugating enzyme E2 variant 1 /// similar to ubiquitin-conjugating enzyme E2 variant 1 isoform d	2.27	0.34
201001_s_at	**Kua-UEV** /// **UBE2V1**	387522 /// 7335	ubiquitin-conjugating enzyme E2 variant 1	2.25	0.16
244572_at	**KY**	339855	kyphoscoliosis peptidase	-2.93	0.08
217388_s_at	**KYNU**	8942	kynureninase (L-kynurenine hydrolase)	9.32	0.00
1552486_s_at	**LACTB**	114294	lactamase, beta	7.52	0.00
222714_s_at	**LACTB2**	51110	lactamase, beta 2	5.56	0.08
221982_x_at	**LAGE3**	8270	L antigen family, member 3	14.02	0.06
209270_at	**LAMB3**	3914	laminin, beta 3	23.83	0.00
205569_at	**LAMP3**	27074	lysosomal-associated membrane protein 3	27.36	0.16
217933_s_at	**LAP3**	51056	leucine aminopeptidase 3	27.55	0.00
212137_at	**LARP1**	23367	La ribonucleoprotein domain family, member 1	4.74	0.06
238959_at	**LARP4**	113251	La ribonucleoprotein domain family, member 4	2.18	0.25
235463_s_at	**LASS6**	253782	LAG1 homolog, ceramide synthase 6	5.97	0.08
221581_s_at	**LAT2**	7462	linker for activation of T cells family, member 2	-2.02	0.00
213261_at	**LBA1**	9881	lupus brain antigen 1	-2.54	0.25
201795_at	**LBR**	3930	lamin B receptor	-2.33	0.00
212531_at	**LCN2**	3934	lipocalin 2 (oncogene 24p3)	-2.77	0.16
1563899_at	**LCTL**	197021	lactase-like	2.23	0.02
210712_at	**LDHAL6B**	92483	lactate dehydrogenase A-like 6B	2.02	0.51
232018_at	**LENG1**	79165	leukocyte receptor cluster (LRC) member 1	2.11	0.16
235096_at	**LEO1**	123169	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	6.92	0.25
207092_at	**LEP**	3952	leptin (obesity homolog, mouse)	2.39	0.34
201105_at	**LGALS1**	3956	lectin, galactoside-binding, soluble, 1 (galectin 1)	3.81	0.51
208949_s_at	**LGALS3**	3958	lectin, galactoside-binding, soluble, 3	21.91	0.00
208934_s_at	**LGALS8**	3964	lectin, galactoside-binding, soluble, 8 (galectin 8)	3.92	0.08
201212_at	**LGMN**	5641	legumain	33.00	0.00
212658_at	**LHFPL2**	10184	lipoma HMGIC fusion partner-like 2	13.79	0.00
208333_at	**LHX5**	64211	LIM homeobox 5	2.47	0.00
210660_at	**LILRA1**	11024	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	-4.68	0.00
207857_at	**LILRA2**	11027	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	-2.21	0.00

1555643_s_at	**LILRA5**	353514	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	-3.10	0.34
218600_at	**LIMD2**	80774	LIM domain containing 2	-6.71	0.00
212687_at	**LIMS1**	3987	LIM and senescent cell antigen-like domains 1	5.07	0.00
206440_at	**LIN7A**	8825	lin-7 homolog A (C. elegans)	-12.81	0.00
223350_x_at	**LIN7C**	55327	lin-7 homolog C (C. elegans)	3.67	0.00
232593_at	**LINCR**	93082	likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein	5.67	0.06
201847_at	**LIPA**	3988	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	28.46	0.08
224629_at	**LMAN1**	3998	Lectin, mannose-binding, 1	5.22	0.34
218191_s_at	**LMBRD1**	55788	LMBR1 domain containing 1	-4.49	0.00
225808_at	**LOC124512**	124512	hypothetical protein LOC124512	3.26	0.00
217346_at	**##########**	128192 /// 131691 /// 202227 /// 341457 /// 342541 /// 390299 /// 390419 /// 390791 /// 391532 /// 401859 /// 402213 /// 439953 /// 440063 /// 442336 /// 442713 /// 5478 /// 643997 /// 653214 /// 654188 /// 728322 /// 730794	peptidylprolyl isomerase A (cyclophilin A) /// similar to peptidylprolyl isomerase A isoform 1 /// peptidylprolyl isomerase A (cyclophilin A) pseudogene 8 /// similar to peptidylprolyl isomerase A /// peptidylprolyl isomerase A (cyclophilin A)-like 3	-2.67	0.07
226702_at	**LOC129607**	129607	hypothetical protein LOC129607	3.33	0.00
225493_at	**LOC144438**	144438	hypothetical protein LOC144438	2.28	0.16
226513_at	**LOC145758**	145758	hypothetical protein LOC145758	-3.03	0.51
1557049_at	**LOC149478**	149478	Hypothetical protein LOC149478	17.15	0.34
230502_s_at	**LOC149832**	149832	Hypothetical protein LOC149832	-2.37	0.34
229101_at	**LOC150166**	150166	Hypothetical protein LOC150166	-3.03	0.00
1560679_at	**LOC151438**	151438	hypothetical protein LOC151438	-14.51	0.03
1558565_at	**LOC158267**	158267	hypothetical protein LOC158267	-2.90	0.34
227792_at	**LOC162073**	162073	hypothetical protein LOC162073	11.98	0.02
227037_at	**LOC201164**	201164	similar to CG12314 gene product	2.77	0.51
232034_at	**LOC203274**	203274	hypothetical protein LOC203274	-13.56	0.00
1564385_at	**LOC219688**	219688	hypothetical protein LOC219688	3.63	0.16

215123_at	**LOC23117** /// **LOC339047** /// **LOC642778** /// **LOC642799** /// **LOC728888**	23117 /// 339047 /// 642778 /// 642799 /// 728888	KIAA0220-like protein /// hypothetical protein LOC339047 /// similar to nuclear pore complex interacting protein /// similar to Protein KIAA0220	2.71	0.06
222154_s_at	**LOC26010**	26010	viral DNA polymerase-transactivated protein 6	4.70	0.25
237032_x_at	**LOC283567**	283567	hypothetical protein LOC283567	4.68	0.13
1559363_at	**LOC283587**	283587	hypothetical protein LOC283587	12.50	0.25
1557113_at	**LOC283588**	283588	hypothetical protein LOC283588	-8.49	0.25
1564373_a_at	**LOC283887**	283887	hypothetical protein LOC283887	-2.09	0.79
1558525_at	**LOC283901**	283901	hypothetical protein LOC283901	-17.31	0.07
234664_at	**LOC284701**	284701	hypothetical protein LOC284701	-2.98	0.34
242852_at	**LOC285147**	285147	hypothetical protein LOC285147	-3.27	0.51
226159_at	**LOC285636**	285636	hypothetical protein LOC285636	4.23	0.00
1557359_at	**LOC285758**	285758	hypothetical protein LOC285758	17.85	0.34
1560762_at	**LOC285972**	285972	hypothetical protein LOC285972	26.03	0.25
222662_at	**LOC286044**	286044	hypothetical protein LOC286044	-5.03	0.00
241370_at	**LOC286052**	286052	hypothetical protein LOC286052	-10.44	0.34
243304_at	**LOC286109**	286109	hypothetical protein LOC286109	-3.13	0.07
224158_s_at	**LOC286144**	286144	hypothetical protein LOC286144	-3.33	0.03
225659_at	**LOC339745**	339745	hypothetical protein LOC339745	-2.06	0.00
1562638_at	**LOC339874**	339874	hypothetical LOC339874	2.97	0.08
1558011_at	**LOC340089** /// **LOC441081** /// **LOC643367** /// **LOC728452** /// **LOC728488** /// **LOC728499** /// **LOC728506** /// **LOC728526** /// **LOC728540** /// **LOC728575** ///	340089 /// 441081 /// 643367 /// 728452 /// 728488 /// 728499 /// 728506 /// 728526 /// 728540 /// 728575 /// 730392	POM121 membrane glycoprotein (rat) pseudogene /// similar to Nuclear envelope pore membrane protein POM 121 (Pore membrane protein of 121 kDa) (P145)	-5.61	0.00
1558425_x_at	**LOC349114**	349114	hypothetical LOC349114	-6.95	0.00
232801_at	**LOC375748**	375748	RAD26L hypothetical protein	-2.36	0.51
230445_at	**LOC388419**	388419	galectin-3-binding protein-like	-2.03	0.00
241998_at	**LOC389073**	389073	similar to RIKEN cDNA D630023F18	13.72	0.06
1560841_at	**LOC389247**	389247	hypothetical gene supported by BC038563	-2.45	0.00
224890_s_at	**LOC389541**	389541	similar to CG14977-PA	-3.26	0.00
230815_at	**LOC389765**	389765	similar to KIF27C	-10.59	0.13
200869_at	**LOC390354** /// **RPL18A**	390354 /// 6142	ribosomal protein L18a /// similar to ribosomal protein L18a; 60S ribosomal protein L18a	2.10	0.51
216387_x_at	**LOC390411**	390411	similar to nucleophosmin 1 isoform 1	2.68	0.16
1558075_at	**LOC399491**	399491	LOC399491 protein	3.80	0.06

200063_s_at	**LOC399804** /// **NPM1**	399804 /// 4869	nucleophosmin (nucleolar phosphoprotein B23, numatrin) /// similar to nucleophosmin 1 isoform 1	2.48	0.00
236532_at	**LOC399947**	399947	similar to expressed sequence AI593442	2.32	0.25
243957_at	**LOC400464**	400464	similar to FLJ43276 protein	2.93	0.06
232953_at	**LOC400723**	400723	hypothetical LOC400723	-2.40	0.79
1558882_at	**LOC401233**	401233	similar to HIV TAT specific factor 1; cofactor required for Tat activation of HIV-1 transcription	-3.00	0.25
1558345_a_at	**LOC439911**	439911	hypothetical gene supported by NM_194304	-7.56	0.07
231989_s_at	**LOC440345** /// **LOC641298** /// **LOC730099**	440345 /// 641298 /// 730099	hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 - like locus /// similar to PI-3-kinase-related kinase SMG-1	3.03	0.00
238727_at	**LOC440934**	440934	Hypothetical gene supported by BC008048	87.94	0.00
200054_at	**LOC442240** /// **ZNF259**	442240 /// 8882	zinc finger protein 259 /// similar to zinc finger protein 259	12.12	0.00
238788_at	**LOC494150**	494150	prohibitin pseudogene	-3.19	0.51
225029_at	**LOC550643**	550643	hypothetical protein LOC550643	7.71	0.13
232135_at	**LOC56755**	56755	hypothetical protein LOC56755	-5.97	0.13
238449_at	**LOC595101**	595101	PI-3-kinase-related kinase SMG-1 pseudogene	2.63	0.51
1562749_at	**LOC641912** /// **LOC644090**	641912 /// 644090	hypothetical protein LOC641912 /// hypothetical LOC644090	2.35	0.16
243656_at	**LOC642852**	642852	hypothetical LOC642852	-3.55	0.00
228412_at	**LOC643072**	643072	hypothetical LOC643072	-10.49	0.51
229224_x_at	**LOC643085**	643085	hypothetical LOC643085	3.16	0.08
226404_at	**LOC643167** /// **RBM39**	643167 /// 9584	RNA binding motif protein 39 /// similar to RNA-binding region-containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1)	-2.46	0.16
226808_at	**LOC643641**	643641	hypothetical protein LOC643641	-5.37	0.03
1557055_s_at	**LOC643837**	643837	hypothetical protein LOC643837	16.08	0.00
239117_at	**LOC643950**	643950	hypothetical LOC643950	-5.30	0.13
224466_s_at	**LOC644132** /// **MAFG**	4097 /// 644132	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) /// similar to v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G	4.94	0.00
217753_s_at	**LOC644166** /// **LOC644191** /// **LOC728937** /// **RPS26**	6231 /// 644166 /// 644191 /// 728937	ribosomal protein S26 /// similar to 40S ribosomal protein S26	2.98	0.02
201874_at	**LOC644387** /// **MPZL1**	644387 /// 9019	myelin protein zero-like 1 /// similar to myelin protein zero-like 1 isoform a	-15.94	0.00
208904_s_at	**LOC645899** /// **LOC646195** /// **RPS28**	6234 /// 645899 /// 646195	ribosomal protein S28 /// ribosomal protein S28 pseudogene	2.40	0.02
215207_x_at	**LOC646208** /// **LOC654174** /// **LOC729148** /// **YDD19**	11049 /// 646208 /// 654174 /// 729148	YDD19 protein /// hypothetical LOC646208 /// similar to CG4775-PA /// similar to lethal (2) k00619 CG4775-PA	5.82	0.06
231467_at	**LOC646590**	646590	Hypothetical LOC646590	-2.47	0.25
230775_s_at	**LOC646871**	646871	hypothetical LOC646871	7.77	0.00
226789_at	**LOC647121**	647121	similar to embigin homolog	-5.75	0.00

1566473_a_at	**LOC647305**	647305	Similar to all-trans-13,14-dihydroretinol saturase	-2.15	0.34
220200_s_at	**LOC647597** /// **SETD8**	387893 /// 647597	SET domain containing (lysine methyltransferase) 8 /// similar to Histone-lysine N-methyltransferase, H4 lysine-20 specific (Histone H4-K20 methyltransferase) (H4-K20-HMTase) (SET domain-containing protein 8) (PR/SET domain-containing protein 07) (PR/SET07) (PR-Set7)	-3.05	0.51
214084_x_at	**LOC648998** /// **LOC652625** /// **LOC652699** /// **NCF1** /// **NCF1B** /// **NCF1C**	648998 /// 652625 /// 652699 /// 653361 /// 654816 /// 654817	similar to Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein) (NOXO2) /// neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1) /// neutrophil cytosolic factor 1B pseudogene /// neutrophil cytosolic factor 1C pseudogene	-2.18	0.00
1569871_at	**LOC650392**	650392	Full-length cDNA clone CS0DF015YK23 of Fetal brain of Homo sapiens (human) /// Hypothetical protein LOC650392	4.44	0.02
219762_s_at	**LOC651600** /// **RPL36**	25873 /// 651600	ribosomal protein L36 /// similar to ribosomal protein L36	2.41	0.13
216902_s_at	**LOC653390** /// **LOC730092** /// **RRN3**	54700 /// 653390 /// 730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) /// RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	16.14	0.13
218338_at	**LOC653441** /// **PHC1**	1911 /// 653441	polyhomeotic homolog 1 (Drosophila) /// similar to polyhomeotic 1-like	32.06	0.06
225955_at	**LOC653506** /// **METRNL**	284207 /// 653506	meteorin, glial cell differentiation regulator-like /// similar to meteorin, glial cell differentiation regulator-like	2.82	0.51
201239_s_at	**LOC653566** /// **SPCS2**	653566 /// 9789	signal peptidase complex subunit 2 homolog (S. cerevisiae) /// signal peptidase complex subunit 2 homolog pseudogene	2.35	0.25
217767_at	**LOC653879**	653879	similar to Complement C3 precursor	25.46	0.06
1561169_at	**LOC727818**	727818	similar to PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-2.03	0.34
200624_s_at	**LOC727839** /// **MATR3**	727839 /// 9782	matrin 3 /// similar to Matrin-3 (Nuclear scaffold protein P130/MAT3)	2.07	0.02
214129_at	**LOC727942**	727942	similar to phosphodiesterase 4D interacting protein isoform 2	6.89	0.08
230543_at	**LOC728177**	728177	hypothetical protein LOC728177	-2.29	0.51
202018_s_at	**LOC728320** /// **LTF**	4057 /// 728320	lactotransferrin /// similar to lactotransferrin	-2.14	0.08
213605_s_at	**LOC728411**	728411	Similar to Beta-glucuronidase precursor	-5.24	0.51
216380_x_at	**LOC728453** /// **LOC730288**	728453 /// 730288	similar to 40S ribosomal protein S28	4.79	0.00
217122_s_at	**LOC728661** /// **SLC35E2**	728661 /// 9906	solute carrier family 35, member E2 /// similar to solute carrier family 35, member E2	-10.77	0.00
224899_s_at	**LOC728866** /// **RP11-217H1.1**	728866 /// 84061	implantation-associated protein /// similar to implantation-associated protein	3.50	0.02
227710_s_at	**LOC728913**	728913	Similar to Reticulocalbin-1 precursor /// Pp13759	2.12	0.00
203315_at	**LOC729030** /// **NCK2**	729030 /// 8440	NCK adaptor protein 2 /// similar to NCK adaptor protein 2	-2.35	0.07

203837_at	**LOC729144 /// MAP3K5**	4217 /// 729144	mitogen-activated protein kinase kinase kinase 5 /// hypothetical protein LOC729144	-5.40	0.00
1570541_s_at	**LOC729936**	729936	Similar to guanylate binding protein 3	10.08	0.00
216908_x_at	**LOC730092**	730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	18.87	0.00
240287_at	**LOC730249**	730249	similar to Immune-responsive protein 1	16.08	0.00
244743_x_at	**LOC730295 /// LOC731265 /// ZNF138**	730295 /// 731265 /// 7697	zinc finger protein 138 /// similar to Zinc finger protein 431	-2.41	0.25
216234_s_at	**LOC730418 /// PRKACA**	5566 /// 730418	protein kinase, cAMP-dependent, catalytic, alpha /// similar to protein kinase, cAMP-dependent, catalytic, gamma	-4.30	0.13
207922_s_at	**LOC730744 /// MAEA**	10296 /// 730744	macrophage erythroblast attacher /// similar to macrophage erythroblast attacher	-3.15	0.03
235536_at	**LOC731208 /// RNF149**	284996 /// 731208	ring finger protein 149 /// similar to ring finger protein 149	-2.05	0.00
217492_s_at	**LOC731292 /// PTEN /// PTENP1**	11191 /// 5728 /// 731292	phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /// phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1 /// similar to Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (Phosphatase and tensin homolog) (Mutated in multiple advanced cancers 1)	-2.65	0.00
1569095_at	**LOC731424**	731424	hypothetical protein LOC731424	5.60	0.00
204575_s_at	**LOC732415 /// MMP19**	4327 /// 732415	matrix metallopeptidase 19 /// similar to Matrix metalloproteinase-19 precursor (MMP-19) (Matrix metalloproteinase RASI) (MMP-18)	14.50	0.08
226842_at	**LOC90110**	90110	hypothetical protein LOC90110	-12.99	0.08
228993_s_at	**LOC92482**	92482	hypothetical protein LOC92482	-2.47	0.00
214791_at	**LOC93349**	93349	hypothetical protein BC004921	3.78	0.25
205011_at	**LOH11CR2A**	4013	loss of heterozygosity, 11, chromosomal region 2, gene A	4.70	0.13
209017_s_at	**LONP1**	9361	lon peptidase 1, mitochondrial	4.36	0.08
226038_at	**LONRF1**	91694	LON peptidase N-terminal domain and ring finger 1	4.87	0.00
202651_at	**LPGAT1**	9926	lysophosphatidylglycerol acyltransferase 1	-2.69	0.00
202459_s_at	**LPIN2**	9663	lipin 2	-2.47	0.07
218509_at	**LPPR2**	64748	lipid phosphate phosphatase-related protein type 2	-5.04	0.13
216250_s_at	**LPXN**	9404	leupaxin	4.60	0.51
235126_at	**LQK1**	642946	LQK1 hypothetical protein short isoform	-10.00	0.79
1554273_a_at	**LRAP**	64167	leukocyte-derived arginine aminopeptidase	12.54	0.00
214739_at	**LRCH3**	84859	leucine-rich repeats and calponin homology (CH) domain containing 3	4.48	0.25
232486_at	**LRFN1**	57622	leucine rich repeat and fibronectin type III domain containing 1	-2.26	0.34
204674_at	**LRMP**	4033	lymphoid-restricted membrane protein	-19.56	0.00
200784_s_at	**LRP1**	4035	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2.33	0.34
201412_at	**LRP10**	26020	low density lipoprotein receptor-related protein 10	-5.90	0.00
219631_at	**LRP12**	29967	low density lipoprotein-related protein 12	3.74	0.00
1559502_s_at	**LRRC25**	126364	leucine rich repeat containing 25	-3.06	0.34
203835_at	**LRRC32**	2615	leucine rich repeat containing 32	5.83	0.16
229231_at	**LRRC37B**	114659	leucine rich repeat containing 37B	-2.67	0.16
223552_at	**LRRC4**	64101	leucine rich repeat containing 4	-10.07	0.07

222231_s_at	**LRRC59**	55379	leucine rich repeat containing 59	2.88	0.79
206483_at	**LRRC6**	23639	leucine rich repeat containing 6	-4.21	0.07
223533_at	**LRRC8C**	84230	leucine rich repeat containing 8 family, member C	5.32	0.16
226884_at	**LRRN1**	57633	leucine rich repeat neuronal 1	-27.67	0.79
1568667_s_at	**LSDP5**	440503	lipid storage droplet protein 5	2.23	0.06
221536_s_at	**LSG1**	55341	large subunit GTPase 1 homolog (S. cerevisiae)	7.67	0.25
225748_at	**LTV1**	84946	LTV1 homolog (S. cerevisiae)	4.89	0.00
226758_at	**LUC7L2**	51631	LUC7-like 2 (S. cerevisiae)	4.38	0.34
215967_s_at	**LY9**	4063	lymphocyte antigen 9	3.82	0.34
226996_at	**LYCAT**	253558	lysocardiolipin acyltransferase	-2.66	0.79
221311_x_at	**LYRM2**	57226	LYR motif containing 2	6.13	0.13
218561_s_at	**LYRM4**	57128	LYR motif containing 4	5.68	0.06
239960_x_at	**LYRM7**	90624	Lyrm7 homolog (mouse)	3.99	0.34
210943_s_at	**LYST**	1130	lysosomal trafficking regulator	-3.37	0.00
200900_s_at	**M6PR**	4074	mannose-6-phosphate receptor (cation dependent)	9.94	0.00
202122_s_at	**M6PRBP1**	10226	mannose-6-phosphate receptor binding protein 1	-2.27	0.25
210252_s_at	**MADD**	8567	MAP-kinase activating death domain	-2.66	0.51
209348_s_at	**MAF**	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	5.23	0.02
218559_s_at	**MAFB**	9935	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	10.32	0.00
36711_at	**MAFF**	23764	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	24.40	0.00
226206_at	**MAFK**	7975	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	2.59	0.51
224480_s_at	**MAG1**	84803	lung cancer metastasis-associated protein	-2.00	0.07
218176_at	**MAGEF1**	64110	melanoma antigen family F, 1	-3.25	0.34
220302_at	**MAK**	4117	male germ cell-associated kinase	-12.90	0.00
235106_at	**MAML2**	84441	mastermind-like 2 (Drosophila)	7.79	0.00
242794_at	**MAML3**	55534	mastermind-like 3 (Drosophila)	-12.18	0.07
202032_s_at	**MAN2A2**	4122	mannosidase, alpha, class 2A, member 2	-2.66	0.00
214703_s_at	**MAN2B2**	23324	mannosidase, alpha, class 2B, member 2	-2.74	0.25
202670_at	**MAP2K1**	5604	mitogen-activated protein kinase kinase 1	2.36	0.00
217971_at	**MAP2K1IP1**	8649	mitogen-activated protein kinase kinase 1 interacting protein 1	2.07	0.00
203266_s_at	**MAP2K4**	6416	mitogen-activated protein kinase kinase 4	-8.06	0.00
225927_at	**MAP3K1**	4214	mitogen-activated protein kinase kinase kinase 1	-3.10	0.00
227073_at	**MAP3K2**	10746	mitogen-activated protein kinase kinase kinase 2	-2.45	0.00
203514_at	**MAP3K3**	4215	mitogen-activated protein kinase kinase kinase 3	-7.19	0.00
203836_s_at	**MAP3K5**	4217	mitogen-activated protein kinase kinase kinase 5	-4.59	0.25
1558518_at	**MAP3K7IP3**	257397	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	2.38	0.51
202890_at	**MAP7**	9053	microtubule-associated protein 7	-2.28	0.34
229847_at	**MAPK1**	5594	Mitogen-activated protein kinase 1	-3.03	0.00
202530_at	**MAPK14**	1432	mitogen-activated protein kinase 14	-5.09	0.00
204708_at	**MAPK4**	5596	mitogen-activated protein kinase 4	-2.01	0.00
207121_s_at	**MAPK6**	5597	mitogen-activated protein kinase 6	12.41	0.00
1558839_at	**MAPKBP1**	23005	mitogen activated protein kinase binding protein 1	3.65	0.00
210075_at	**MARCH2**	51257	membrane-associated ring finger (C3HC4) 2	-2.46	0.51

230112_at	**MARCH4**	57574	membrane-associated ring finger (C3HC4) 4	-2.07	0.34
221824_s_at	**MARCH8**	220972	membrane-associated ring finger (C3HC4) 8	-3.06	0.25
213045_at	**MAST3**	23031	microtubule associated serine/threonine kinase 3	-3.61	0.07
200768_s_at	**MAT2A**	4144	methionine adenosyltransferase II, alpha	2.67	0.06
209579_s_at	**MBD4**	8930	methyl-CpG binding domain protein 4	-2.22	0.03
227379_at	**MBOAT1**	154141	membrane bound O-acyltransferase domain containing 1	-4.58	0.00
226726_at	**MBOAT2**	129642	membrane bound O-acyltransferase domain containing 2	-18.97	0.03
209624_s_at	**MCCC2**	64087	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	5.04	0.51
212246_at	**MCFD2**	90411	multiple coagulation factor deficiency 2	3.09	0.13
202556_s_at	**MCRS1**	10445	microspherule protein 1	2.13	0.13
220122_at	**MCTP1**	79772	multiple C2 domains, transmembrane 1	2.46	0.00
243109_at	**MCTP2**	55784	multiple C2 domains, transmembrane 2	-15.14	0.00
217599_s_at	**MDFIC**	29969	MyoD family inhibitor domain containing	2.16	0.79
1569484_s_at	**MDN1**	23195	MDN1, midasin homolog (yeast)	2.00	0.13
225456_at	**MED1**	5469	mediator complex subunit 1	2.41	0.16
1553993_s_at	**MED25**	81857	mediator complex subunit 25	-9.71	0.03
218438_s_at	**MED28**	80306	mediator complex subunit 28	3.20	0.00
225641_at	**MEF2D**	4209	myocyte enhancer factor 2D	-2.15	0.34
212830_at	**MEGF9**	1955	multiple EGF-like-domains 9	-7.14	0.00
214077_x_at	**MEIS3P1**	4213	Meis homeobox 3 pseudogene 1	3.55	0.13
224675_at	**MESDC2**	23184	mesoderm development candidate 2	4.59	0.13
220839_at	**METTL5**	29081	methyltransferase like 5	8.73	0.02
1553689_s_at	**METTL6**	131965	methyltransferase like 6	7.89	0.00
207761_s_at	**METTL7A**	25840	methyltransferase like 7A	-10.58	0.03
227055_at	**METTL7B**	196410	methyltransferase like 7B	2.20	0.51
203406_at	**MFAP1**	4236	microfibrillar-associated protein 1	2.69	0.02
243407_at	**MFSD8**	256471	Major facilitator superfamily domain containing 8	2.36	0.51
212945_s_at	**MGA**	23269	MAX gene associated	5.46	0.00
206522_at	**MGAM**	8972	maltase-glucoamylase (alpha-glucosidase)	-11.95	0.00
201126_s_at	**MGAT1**	4245	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	3.17	0.00
211061_s_at	**MGAT2**	4247	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	2.96	0.51
226039_at	**MGAT4A**	11320	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	-2.20	0.79
214696_at	**MGC14376**	84981	hypothetical protein MGC14376	3.23	0.25
236248_x_at	**MGC21874**	93624	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	-2.36	0.51
210484_s_at	**MGC31957 /// TNFRSF10C**	254896 /// 8794	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain /// hypothetical protein MGC31957	-52.17	0.00
220305_at	**MGC3260**	78993	hypothetical protein MGC3260	-4.15	0.13
226657_at	**MGC33894**	256302	transcript expressed during hematopoiesis 2	-11.13	0.00
239186_at	**MGC39372**	221756	hypothetical protein MGC39372	10.72	0.13
239104_at	**MGC42157**	439933	hypothetical locus MGC42157	23.33	0.06
207775_at	**MGC4859**	79150	hypothetical protein MGC4859 similar to HSPA8	2.07	0.79
228283_at	**MGC61571**	152100	hypothetical protein MGC61571	5.76	0.51
227983_at	**MGC7036**	196383	hypothetical protein MGC7036	2.06	0.00
200899_s_at	**MGEA5**	10724	meningioma expressed antigen 5 (hyaluronidase)	-2.74	0.00
211026_s_at	**MGLL**	11343	monoglyceride lipase	15.40	0.00

1569057_s_at	**MIA3**	375056	melanoma inhibitory activity family, member 3	2.17	0.79
224726_at	**MIB1**	57534	mindbomb homolog 1 (Drosophila)	-3.54	0.34
236475_at	**MICAL2**	9645	Microtubule associated monoxygenase, calponin and LIM domain containing 2	-20.57	0.00
206247_at	**MICB**	4277	MHC class I polypeptide-related sequence B	2.90	0.00
218251_at	**MID1IP1**	58526	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	-3.30	0.08
223411_at	**MIF4GD**	57409	MIF4G domain containing	3.76	0.34
213188_s_at	**MINA**	84864	MYC induced nuclear antigen	2.20	0.34
209585_s_at	**MINPP1**	9562	multiple inositol polyphosphate histidine phosphatase, 1	4.44	0.51
226214_at	**MIR16**	51573	membrane interacting protein of RGS16	-4.10	0.00
226329_s_at	**MITD1**	129531	MIT, microtubule interacting and transport, domain containing 1	6.03	0.00
226066_at	**MITF**	4286	microphthalmia-associated transcription factor	4.97	0.13
224714_at	**MKI67IP**	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein	9.22	0.02
222530_s_at	**MKKS**	8195	McKusick-Kaufman syndrome	4.47	0.34
215292_s_at	**MKL1**	57591	megakaryoblastic leukemia (translocation) 1	-4.68	0.00
204423_at	**MKLN1**	4289	muskelin 1, intracellular mediator containing kelch motifs	-3.45	0.51
202520_s_at	**MLH1**	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	4.54	0.25
220546_at	**MLL**	4297	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	-2.31	0.34
216480_x_at	**MLLT10**	8028	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	-2.17	0.00
224784_at	**MLLT6**	4302	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	8.32	0.08
239108_at	**MLSTD1**	55711	Male sterility domain containing 1	-2.12	0.51
203434_s_at	**MME**	4311	membrane metallo-endopeptidase	-119.70	0.00
202828_s_at	**MMP14**	4323	matrix metallopeptidase 14 (membrane-inserted)	7.40	0.34
207289_at	**MMP25**	64386	matrix metallopeptidase 25	-5.97	0.00
204959_at	**MNDA**	4332	myeloid cell nuclear differentiation antigen	-4.26	0.00
225530_at	**MOBKL2A**	126308	MOB1, Mps One Binder kinase activator-like 2A (yeast)	-3.04	0.00
226844_at	**MOBKL2B**	79817	MOB1, Mps One Binder kinase activator-like 2B (yeast)	2.64	0.51
243052_at	**MOBKL2C**	148932	MOB1, Mps One Binder kinase activator-like 2C (yeast)	6.81	0.00
201994_at	**MORF4L2**	9643	mortality factor 4 like 2	2.77	0.00
218865_at	**MOSC1**	64757	MOCO sulphurase C-terminal domain containing 1	-16.95	0.00
233917_s_at	**MOV10**	4343	Mov10, Moloney leukemia virus 10, homolog (mouse)	6.01	0.06
226841_at	**MPEG1**	219972	macrophage expressed gene 1	-2.91	0.00
203740_at	**MPHOSPH6**	10200	M-phase phosphoprotein 6	5.49	0.06
203949_at	**MPO**	4353	myeloperoxidase	-3.63	0.03
1564308_a_at	**MPP7**	143098	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-9.14	0.00
206764_x_at	**MPPE1**	65258	metallophosphoesterase 1	-11.66	0.00
210594_x_at	**MPZL1**	9019	myelin protein zero-like 1	-6.20	0.08
203780_at	**MPZL2**	10205	myelin protein zero-like 2	-6.63	0.08
227747_at	**MPZL3**	196264	myelin protein zero-like 3	-13.07	0.00
210224_at	**MR1**	3140	major histocompatibility complex, class I-related	6.32	0.00

225185_at	**MRAS**	22808	muscle RAS oncogene homolog	15.32	0.08
204438_at	**MRC1** /// **MRC1L1**	414308 /// 4360	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	51.73	0.06
212199_at	**MRFAP1L1**	114932	Morf4 family associated protein 1-like 1	-2.98	0.07
1553293_at	**MRGPRX3**	117195	MAS-related GPR, member X3	2.44	0.16
225201_s_at	**MRPL14**	64928	mitochondrial ribosomal protein L14	10.24	0.00
218027_at	**MRPL15**	29088	mitochondrial ribosomal protein L15	7.67	0.51
217907_at	**MRPL18**	29074	mitochondrial ribosomal protein L18	2.83	0.13
225315_at	**MRPL21**	219927	mitochondrial ribosomal protein L21	5.44	0.25
218339_at	**MRPL22**	29093	mitochondrial ribosomal protein L22	2.48	0.79
218270_at	**MRPL24**	79590	mitochondrial ribosomal protein L24	8.68	0.00
208787_at	**MRPL3**	11222	mitochondrial ribosomal protein L3	6.70	0.34
225260_s_at	**MRPL32**	64983	mitochondrial ribosomal protein L32	12.63	0.00
218558_s_at	**MRPL39**	54148	mitochondrial ribosomal protein L39	4.29	0.13
201717_at	**MRPL49**	740	mitochondrial ribosomal protein L49	2.43	0.34
225581_s_at	**MRPL50**	54534	mitochondrial ribosomal protein L50	13.31	0.06
224334_s_at	**MRPL51**	51258	mitochondrial ribosomal protein L51	2.76	0.00
225797_at	**MRPL54**	116541	mitochondrial ribosomal protein L54	3.46	0.34
213840_s_at	**MRPS12**	6183	Mitochondrial ribosomal protein S12	4.93	0.51
217408_at	**MRPS18B**	28973	mitochondrial ribosomal protein S18B	5.77	0.02
228019_s_at	**MRPS18C**	51023	mitochondrial ribosomal protein S18C	2.89	0.34
223156_at	**MRPS23**	51649	mitochondrial ribosomal protein S23	3.67	0.16
224948_at	**MRPS24**	64951	mitochondrial ribosomal protein S24	5.38	0.08
224873_s_at	**MRPS25**	64432	mitochondrial ribosomal protein S25	-2.08	0.07
217932_at	**MRPS7**	51081	mitochondrial ribosomal protein S7	5.17	0.34
225126_at	**MRRF**	92399	mitochondrial ribosome recycling factor	6.02	0.79
235783_at	**MRTO4**	51154	mRNA turnover 4 homolog (S. cerevisiae)	2.30	0.79
230214_at	**MRVI1**	10335	murine retrovirus integration site 1 homolog	-4.24	0.25
219607_s_at	**MS4A4A**	51338	membrane-spanning 4-domains, subfamily A, member 4	12.41	0.06
219666_at	**MS4A6A**	64231	membrane-spanning 4-domains, subfamily A, member 6A	-8.23	0.03
223344_s_at	**MS4A7**	58475	membrane-spanning 4-domains, subfamily A, member 7	4.56	0.13
202911_at	**MSH6**	2956	mutS homolog 6 (E. coli)	-2.47	0.16
224765_at	**MSL-1**	339287	male-specific lethal-1 homolog	-2.15	0.00
211887_x_at	**MSR1**	4481	macrophage scavenger receptor 1	33.80	0.25
226720_at	**MST101**	114825	MSTP101	-3.85	0.08
223276_at	**MST150**	85027	MSTP150	-4.55	0.34
205556_at	**MSX2**	4488	msh homeobox 2	2.23	0.13
213629_x_at	**MT1F**	4494	metallothionein 1F	2.62	0.51
206461_x_at	**MT1H** /// **MT1P2**	4496 /// 645745	metallothionein 1H /// metallothionein 1 pseudogene 2	2.58	0.34
204326_x_at	**MT1X**	4501	metallothionein 1X	4.29	0.51
212185_x_at	**MT2A**	4502	metallothionein 2A	9.90	0.06
217772_s_at	**MTCH2**	23788	mitochondrial carrier homolog 2 (C. elegans)	4.77	0.00
212250_at	**MTDH**	92140	metadherin	4.81	0.00
227150_at	**MTF1**	4520	metal-regulatory transcription factor 1	2.97	0.06
235689_at	**MTFMT**	123263	mitochondrial methionyl-tRNA formyltransferase	-7.06	0.51
201761_at	**MTHFD2**	10797	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	16.97	0.00
238762_at	**MTHFD2L**	441024	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	8.17	0.08
203433_at	**MTHFS**	10588	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	-2.05	0.07

203095_at	**MTIF2**	4528	mitochondrial translational initiation factor 2	2.91	0.79
36920_at	**MTM1**	4534	myotubularin 1	-6.62	0.00
225810_at	**MTMR10**	54893	myotubularin related protein 10	-3.29	0.00
203211_s_at	**MTMR2**	8898	myotubularin related protein 2	2.92	0.00
202086_at	**MX1**	4599	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	2.17	0.51
210778_s_at	**MXD4**	10608	MAX dimerization protein 4	-2.47	0.03
202364_at	**MXI1**	4601	MAX interactor 1	-6.41	0.25
204798_at	**MYB**	4602	v-myb myeloblastosis viral oncogene homolog (avian)	-3.99	0.34
203359_s_at	**MYCBP**	26292	c-myc binding protein	-2.83	0.08
201495_x_at	**MYH11**	4629	myosin, heavy chain 11, smooth muscle	-4.25	0.00
244654_at	**MYO1G**	64005	myosin IG	-2.70	0.51
227761_at	**MYO5A**	4644	myosin VA (heavy chain 12, myoxin)	-5.27	0.07
225299_at	**MYO5B**	4645	myosin VB	2.17	0.08
226547_at	**MYST3**	7994	MYST histone acetyltransferase (monocytic leukemia) 3	-2.54	0.07
32069_at	**N4BP1**	9683	Nedd4 binding protein 1	2.08	0.02
209272_at	**NAB1**	4664	NGFI-A binding protein 1 (EGR1 binding protein 1)	2.57	0.16
202943_s_at	**NAGA**	4668	N-acetylgalactosaminidase, alpha-	5.01	0.51
204860_s_at	**NAIP** /// **NAIP1B**	4671 /// 728519	NLR family, apoptosis inhibitory protein /// neuronal apoptosis inhibitory protein (centromeric)	-6.70	0.00
228073_at	**NANP**	140838	N-acetylneuraminic acid phosphatase	2.20	0.34
218189_s_at	**NANS**	54187	N-acetylneuraminic acid synthase (sialic acid synthase)	2.34	0.51
228063_s_at	**NAP1L5**	266812	nucleosome assembly protein 1-like 5	-6.42	0.16
206491_s_at	**NAPA**	8775	N-ethylmaleimide-sensitive factor attachment protein, alpha	3.67	0.08
219862_s_at	**NARF**	26502	nuclear prelamin A recognition factor	-6.41	0.00
219158_s_at	**NARG1**	80155	NMDA receptor regulated 1	22.17	0.25
200027_at	**NARS**	4677	asparaginyl-tRNA synthetase	9.10	0.00
217884_at	**NAT10**	55226	N-acetyltransferase 10	5.17	0.34
1552658_a_at	**NAV3**	89795	neuron navigator 3	4.08	0.06
217299_s_at	**NBN**	4683	nibrin	9.95	0.00
201521_s_at	**NCBP2**	22916	nuclear cap binding protein subunit 2, 20kDa	24.46	0.00
204961_s_at	**NCF1** /// **NCF1B** /// **NCF1C**	653361 /// 654816 /// 654817	neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1) /// neutrophil cytosolic factor 1B pseudogene /// neutrophil cytosolic factor 1C pseudogene	-2.47	0.13
205147_x_at	**NCF4**	4689	neutrophil cytosolic factor 4, 40kDa	-2.38	0.00
200610_s_at	**NCL**	4691	nucleolin	3.40	0.00
215857_at	**NCLN**	56926	nicalin homolog (zebrafish)	-19.55	0.00
209106_at	**NCOA1**	8648	nuclear receptor coactivator 1	-3.08	0.25
205731_s_at	**NCOA2**	10499	nuclear receptor coactivator 2	-3.70	0.07
225145_at	**NCOA5**	57727	nuclear receptor coactivator 5	2.83	0.08
225344_at	**NCOA7**	135112	nuclear receptor coactivator 7	15.06	0.00
218414_s_at	**NDE1**	54820	nudE nuclear distribution gene E homolog 1 (A. nidulans)	-4.66	0.13
208093_s_at	**NDEL1**	81565	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	-3.85	0.00
228355_s_at	**NDUFA12L**	91942	NDUFA12-like	2.04	0.00
208969_at	**NDUFA9**	4704	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	5.87	0.02
202077_at	**NDUFAB1**	4706	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	4.21	0.06

218201_at	**NDUFB2**	4708	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	3.83	0.16
203613_s_at	**NDUFB6**	4712	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	-2.46	0.00
201227_s_at	**NDUFB8**	4714	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	2.03	0.16
222992_s_at	**NDUFB9**	4715	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	4.96	0.06
203478_at	**NDUFC1**	4717	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	2.56	0.79
202941_at	**NDUFV2**	4729	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	5.78	0.00
226616_s_at	**NDUFV3**	4731	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	4.78	0.08
209300_s_at	**NECAP1**	25977	NECAP endocytosis associated 1	4.88	0.00
220731_s_at	**NECAP2**	55707	NECAP endocytosis associated 2	3.00	0.00
237761_at	**NEK6**	10783	NIMA (never in mitosis gene a)-related kinase 6	3.15	0.13
212530_at	**NEK7**	140609	NIMA (never in mitosis gene a)-related kinase 7	-3.12	0.00
201829_at	**NET1**	10276	neuroepithelial cell transforming gene 1	2.35	0.51
218888_s_at	**NETO2**	81831	neuropilin (NRP) and tolloid (TLL)-like 2	3.38	0.13
208926_at	**NEU1**	4758	sialidase 1 (lysosomal sialidase)	2.65	0.25
224984_at	**NFAT5**	10725	nuclear factor of activated T-cells 5, tonicity-responsive	2.05	0.34
212809_at	**NFATC2IP**	84901	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	2.54	0.16
209930_s_at	**NFE2**	4778	nuclear factor (erythroid-derived 2), 45kDa	-10.65	0.00
201146_at	**NFE2L2**	4780	nuclear factor (erythroid-derived 2)-like 2	3.42	0.00
204702_s_at	**NFE2L3**	9603	nuclear factor (erythroid-derived 2)-like 3	2.80	0.08
1560527_at	**NF-E4**	58160	transcription factor NF-E4	-2.97	0.00
209239_at	**NFKB1**	4790	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	3.49	0.34
209636_at	**NFKB2**	4791	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	3.89	0.08
231699_at	**NFKBIA**	4792	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	7.12	0.00
214062_x_at	**NFKBIB**	4793	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	2.67	0.00
203927_at	**NFKBIE**	4794	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	7.32	0.00
1553103_at	**NFX1**	4799	nuclear transcription factor, X-box binding 1	5.60	0.08
227220_at	**NFXL1**	152518	nuclear transcription factor, X-box binding-like 1	-5.26	0.03
218129_s_at	**NFYB**	4801	nuclear transcription factor Y, beta	-2.11	0.08
213794_s_at	**NGDN**	25983	neuroguidin, EIF4E binding protein	3.17	0.08
217722_s_at	**NGRN**	51335	neugrin, neurite outgrowth associated	2.14	0.25
201077_s_at	**NHP2L1**	4809	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	5.62	0.06
242800_at	**NHS**	4810	Nance-Horan syndrome (congenital cataracts and dental anomalies)	-14.84	0.34
225921_at	**NIN**	51199	ninein (GSK3B interacting protein)	-3.26	0.00
203045_at	**NINJ1**	4814	ninjurin 1	2.35	0.02
219594_at	**NINJ2**	4815	ninjurin 2	-3.92	0.13
212469_at	**NIPBL**	25836	Nipped-B homolog (Drosophila)	-2.15	0.34
201708_s_at	**NIPSNAP1**	8508	nipsnap homolog 1 (C. elegans)	-6.74	0.25
225930_at	**NKIRAS1**	28512	NFKB inhibitor interacting Ras-like 1	17.64	0.00
205893_at	**NLGN1**	22871	neuroligin 1	-3.04	0.34
225943_at	**NLN**	57486	neurolysin (metallopeptidase M3 family)	12.74	0.16

1552553_a_at	**NLRC4**	58484	NLR family, CARD domain containing 4	-2.17	0.07
226474_at	**NLRC5**	84166	NLR family, CARD domain containing 5	2.73	0.00
210113_s_at	**NLRP1**	22861	NLR family, pyrin domain containing 1	-14.22	0.00
1552531_a_at	**NLRP11**	204801	NLR family, pyrin domain containing 11	2.29	0.25
1554952_s_at	**NLRP12**	91662	NLR family, pyrin domain containing 12	-11.93	0.03
222497_x_at	**NMD3**	51068	NMD3 homolog (S. cerevisiae)	3.97	0.06
201577_at	**NME1**	4830	non-metastatic cells 1, protein (NM23A) expressed in	15.01	0.02
201268_at	**NME1-NME2 /// NME2**	4831 /// 654364	non-metastatic cells 2, protein (NM23B) expressed in /// NM23-LV	6.47	0.25
227556_at	**NME7**	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	15.30	0.06
222684_s_at	**NOL10**	79954	nucleolar protein 10	5.62	0.06
221970_s_at	**NOL11**	25926	nucleolar protein 11	3.10	0.25
200875_s_at	**NOL5A**	10528	nucleolar protein 5A (56kDa with KKE/D repeat)	3.22	0.13
210097_s_at	**NOL7**	51406	nucleolar protein 7, 27kDa	4.18	0.00
218244_at	**NOL8**	55035	nucleolar protein 8	3.18	0.25
219110_at	**NOLA1**	54433	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	4.16	0.06
205895_s_at	**NOLC1**	9221	nucleolar and coiled-body phosphoprotein 1	3.69	0.51
210470_x_at	**NONO**	4841	non-POU domain containing, octamer-binding	2.00	0.51
223096_at	**NOP5/NOP58**	51602	nucleolar protein NOP5/NOP58	7.77	0.02
223508_at	**NOTCH1**	4851	Notch homolog 1, translocation-associated (Drosophila)	-3.06	0.07
204501_at	**NOV**	4856	nephroblastoma overexpressed gene	-3.84	0.16
201695_s_at	**NP**	4860	nucleoside phosphorylase	5.73	0.13
202679_at	**NPC1**	4864	Niemann-Pick disease, type C1	3.40	0.16
200701_at	**NPC2**	10577	Niemann-Pick disease, type C2	2.31	0.00
89476_r_at	**NPEPL1**	79716	aminopeptidase-like 1	-2.19	0.07
201455_s_at	**NPEPPS**	9520	aminopeptidase puromycin sensitive	-3.82	0.07
213471_at	**NPHP4**	261734	nephronophthisis 4	2.42	0.34
221691_x_at	**NPM1**	4869	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	2.42	0.00
31637_s_at	**NR1D1 /// THRA**	7067 /// 9572	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian) /// nuclear receptor subfamily 1, group D, member 1	2.99	0.34
225477_s_at	**NR2C2**	7182	nuclear receptor subfamily 2, group C, member 2	-3.28	0.07
207978_s_at	**NR4A3**	8013	nuclear receptor subfamily 4, group A, member 3	2.17	0.25
202647_s_at	**NRAS**	4893	neuroblastoma RAS viral (v-ras) oncogene homolog	3.17	0.00
221803_s_at	**NRBF2**	29982	nuclear receptor binding factor 2	-2.82	0.03
202599_s_at	**NRIP1**	8204	nuclear receptor interacting protein 1	8.11	0.08
218625_at	**NRN1**	51299	neuritin 1	2.73	0.51
228102_at	**NRP2**	8828	Neuropilin 2	2.29	0.51
1553943_at	**NS3BP**	171391	NS3BP	2.00	0.51
220248_x_at	**NSFL1C**	55968	NSFL1 (p97) cofactor (p47)	-2.09	0.03
232149_s_at	**NSMAF**	8439	neutral sphingomyelinase (N-SMase) activation associated factor	2.01	0.06
226536_at	**NSMCE2**	286053	non-SMC element 2, MMS21 homolog (S. cerevisiae)	5.62	0.02
223076_s_at	**NSUN2**	54888	NOL1/NOP2/Sun domain family, member 2	2.95	0.00
230200_at	**NSUN6**	221078	NOL1/NOP2/Sun domain family, member 6	5.08	0.06

223298_s_at	**NT5C3**	51251	5'-nucleotidase, cytosolic III	-2.57	0.16
223178_s_at	**NT5DC1**	221294	5'-nucleotidase domain containing 1	-3.00	0.25
233072_at	**NTNG2**	84628	netrin G2	-9.58	0.00
234332_at	**NUB1**	51667	negative regulator of ubiquitin-like proteins 1	2.04	0.02
203978_at	**NUBP1**	4682	nucleotide binding protein 1 (MinD homolog, E. coli)	5.79	0.06
229353_s_at	**NUCKS1**	64710	nuclear casein kinase and cyclin-dependent kinase substrate 1	2.36	0.25
225439_at	**NUDCD1**	84955	NudC domain containing 1	4.58	0.51
201270_x_at	**NUDCD3**	23386	NudC domain containing 3	2.60	0.34
219347_at	**NUDT15**	55270	nudix (nucleoside diphosphate linked moiety X)-type motif 15	6.19	0.13
235002_at	**NUDT16**	131870	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-3.19	0.13
224477_s_at	**NUDT16L1**	84309	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	-3.11	0.79
212181_s_at	**NUDT4**	11163	nudix (nucleoside diphosphate linked moiety X)-type motif 4	-2.51	0.25
223100_s_at	**NUDT5**	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5	-3.65	0.08
218375_at	**NUDT9**	53343	nudix (nucleoside diphosphate linked moiety X)-type motif 9	3.26	0.00
235539_at	**NUMA1**	4926	Nuclear mitotic apparatus protein 1	7.52	0.25
209073_s_at	**NUMB**	8650	numb homolog (Drosophila)	-2.10	0.00
212315_s_at	**NUP210**	23225	nucleoporin 210kDa	-2.09	0.07
202155_s_at	**NUP214**	8021	nucleoporin 214kDa	-4.68	0.00
213682_at	**NUP50**	10762	nucleoporin 50kDa	-2.58	0.03
202153_s_at	**NUP62**	23636	nucleoporin 62kDa	8.64	0.00
202188_at	**NUP93**	9688	nucleoporin 93kDa	2.81	0.34
204435_at	**NUPL1**	9818	nucleoporin like 1	2.56	0.34
225071_at	**NUS1**	116150	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	5.09	0.00
202397_at	**NUTF2**	10204	nuclear transport factor 2	2.84	0.02
218708_at	**NXT1**	29107	NTF2-like export factor 1	14.09	0.00
209628_at	**NXT2**	55916	nuclear transport factor 2-like export factor 2	4.99	0.16
205552_s_at	**OAS1**	4938	2',5'-oligoadenylate synthetase 1, 40/46kDa	11.46	0.00
204972_at	**OAS2**	4939	2'-5'-oligoadenylate synthetase 2, 69/71kDa	6.32	0.00
218400_at	**OAS3**	4940	2'-5'-oligoadenylate synthetase 3, 100kDa	5.50	0.00
201599_at	**OAT**	4942	ornithine aminotransferase (gyrate atrophy)	-3.49	0.34
215952_s_at	**OAZ1**	4946	ornithine decarboxylase antizyme 1	-2.61	0.08
201365_at	**OAZ2**	4947	ornithine decarboxylase antizyme 2	-3.63	0.00
220848_x_at	**OBP2A**	29991	odorant binding protein 2A	2.72	0.79
200790_at	**ODC1**	4953	ornithine decarboxylase 1	2.82	0.25
219582_at	**OGFRL1**	79627	opioid growth factor receptor-like 1	-2.26	0.00
229787_s_at	**OGT**	8473	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	-4.60	0.07
219293_s_at	**OLA1**	29789	Obg-like ATPase 1	2.50	0.79
232586_x_at	**olfactory receptor, family 7, subfamily E, member**	---	CDNA FLJ11504 fis, clone HEMBA1002119	4.61	0.79
228170_at	**OLIG1**	116448	oligodendrocyte transcription factor 1	-6.36	0.25
210004_at	**OLR1**	4973	oxidized low density lipoprotein (lectin-like) receptor 1	19.37	0.02
202074_s_at	**OPTN**	10133	optineurin	2.51	0.34

217499_x_at	**OR7E37P**	26636	olfactory receptor, family 7, subfamily E, member 37 pseudogene	3.21	0.79
221864_at	**ORAI3**	93129	ORAI calcium release-activated calcium modulator 3	-2.40	0.51
203352_at	**ORC4L**	5000	origin recognition complex, subunit 4-like (yeast)	2.14	0.25
205040_at	**ORM1**	5004	orosomucoid 1	3.38	0.13
205041_s_at	**ORM1 /// ORM2**	5004 /// 5005	orosomucoid 1 /// orosomucoid 2	2.93	0.34
201800_s_at	**OSBP**	5007	oxysterol binding protein	2.31	0.34
229527_s_at	**OSBPL11**	114885	Oxysterol binding protein-like 11	-2.12	0.00
209485_s_at	**OSBPL1A**	114876	oxysterol binding protein-like 1A	-2.76	0.79
209221_s_at	**OSBPL2**	9885	oxysterol binding protein-like 2	-2.47	0.51
218047_at	**OSBPL9**	114883	oxysterol binding protein-like 9	-3.66	0.79
219475_at	**OSGIN1**	29948	oxidative stress induced growth inhibitor 1	4.08	0.00
230170_at	**OSM**	5008	oncostatin M	6.66	0.00
218196_at	**OSTM1**	28962	osteopetrosis associated transmembrane protein 1	3.91	0.00
203480_s_at	**OTUD4**	54726	OTU domain containing 4	5.61	0.06
224745_x_at	**OTUD5**	55593	OTU domain containing 5	-2.42	0.25
223879_s_at	**OXR1**	55074	oxidation resistance 1	-2.78	0.16
204088_at	**P2RX4**	5025	purinergic receptor P2X, ligand-gated ion channel, 4	22.75	0.00
207091_at	**P2RX7**	5027	purinergic receptor P2X, ligand-gated ion channel, 7	4.40	0.08
214615_at	**P2RY10**	27334	purinergic receptor P2Y, G-protein coupled, 10	-5.31	0.07
220005_at	**P2RY13**	53829	purinergic receptor P2Y, G-protein coupled, 13	-2.37	0.00
206637_at	**P2RY14**	9934	purinergic receptor P2Y, G-protein coupled, 14	5.42	0.00
206277_at	**P2RY2**	5029	purinergic receptor P2Y, G-protein coupled, 2	5.23	0.00
229686_at	**P2RY8**	286530	purinergic receptor P2Y, G-protein coupled, 8	-3.48	0.07
207543_s_at	**P4HA1**	5033	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	5.24	0.00
202733_at	**P4HA2**	8974	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	2.39	0.34
200654_at	**P4HB**	5034	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	2.90	0.16
208676_s_at	**PA2G4**	5036	proliferation-associated 2G4, 38kDa	4.42	0.06
224658_x_at	**PACS1**	55690	phosphofurin acidic cluster sorting protein 1	-8.55	0.08
227053_at	**PACSIN1**	29993	protein kinase C and casein kinase substrate in neurons 1	-2.12	0.25
201651_s_at	**PACSIN2**	11252	protein kinase C and casein kinase substrate in neurons 2	-4.55	0.03
220001_at	**PADI4**	23569	peptidyl arginine deiminase, type IV	-34.82	0.00
225622_at	**PAG1**	55824	phosphoprotein associated with glycosphingolipid microdomains 1	3.99	0.00
206897_at	**PAGE1**	8712	P antigen family, member 1 (prostate associated)	2.05	0.16
222983_s_at	**PAIP2**	51247	poly(A) binding protein interacting protein 2	-2.07	0.00
226507_at	**PAK1**	5058	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	-2.74	0.03
218886_at	**PAK1IP1**	55003	PAK1 interacting protein 1	8.00	0.25
1557535_at	**PALLD**	23022	Palladin, cytoskeletal associated protein	2.98	0.08
202336_s_at	**PAM**	5066	peptidylglycine alpha-amidating monooxygenase	-5.15	0.25
225563_at	**PAN3**	255967	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-2.46	0.00

244471_x_at	**PANX2**	56666	Pannexin 2	-2.60	0.00
229043_at	**PAPD5**	64282	PAP associated domain containing 5	-3.57	0.16
218543_s_at	**PARP12**	64761	poly (ADP-ribose) polymerase family, member 12	6.03	0.00
232610_at	**PARP14**	54625	poly (ADP-ribose) polymerase family, member 14	5.35	0.00
219034_at	**PARP16**	54956	poly (ADP-ribose) polymerase family, member 16	-4.63	0.25
219639_x_at	**PARP6**	56965	poly (ADP-ribose) polymerase family, member 6	2.31	0.51
223220_s_at	**PARP9**	83666	poly (ADP-ribose) polymerase family, member 9	2.06	0.06
202876_s_at	**PBX2**	5089	pre-B-cell leukemia homeobox 2	-3.49	0.03
214176_s_at	**PBXIP1**	57326	Pre-B-cell leukemia homeobox interacting protein 1	-10.77	0.00
229194_at	**PCGF5**	84333	polycomb group ring finger 5	2.62	0.13
212406_s_at	**PCMTD2**	55251	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-7.10	0.00
227759_at	**PCSK9**	255738	proprotein convertase subtilisin/kexin type 9	3.62	0.00
220049_s_at	**PDCD1LG2**	80380	programmed cell death 1 ligand 2	7.15	0.08
212593_s_at	**PDCD4**	27250	programmed cell death 4 (neoplastic transformation inhibitor)	-2.26	0.00
219275_at	**PDCD5**	9141	programmed cell death 5	2.91	0.06
208591_s_at	**PDE3B**	5140	phosphodiesterase 3B, cGMP-inhibited	-6.40	0.25
211302_s_at	**PDE4B**	5142	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	3.47	0.00
205872_x_at	**PDE4DIP**	9659	phosphodiesterase 4D interacting protein (myomegalin)	9.19	0.00
1552343_s_at	**PDE7A**	5150	phosphodiesterase 7A	-2.11	0.25
1555864_s_at	**PDHA1**	5160	pyruvate dehydrogenase (lipoamide) alpha 1	2.66	0.02
227033_at	**PDIA3**	2923	protein disulfide isomerase family A, member 3	6.07	0.00
211048_s_at	**PDIA4**	9601	protein disulfide isomerase family A, member 4	5.88	0.00
208639_x_at	**PDIA6**	10130	protein disulfide isomerase family A, member 6	3.70	0.00
226452_at	**PDK1**	5163	pyruvate dehydrogenase kinase, isozyme 1	-3.48	0.00
221957_at	**PDK3**	5165	pyruvate dehydrogenase kinase, isozyme 3	-5.41	0.07
213983_s_at	**PDS5A**	23244	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	3.07	0.13
207956_x_at	**PDS5B**	23047	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	-2.22	0.13
202671_s_at	**PDXK**	8566	pyridoxal (pyridoxine, vitamin B6) kinase	4.86	0.00
223037_at	**PDZD11**	51248	PDZ domain containing 11	2.26	0.79
213549_at	**PDZD8**	118987	PDZ domain containing 8	-5.62	0.16
200788_s_at	**PEA15**	8682	phosphoprotein enriched in astrocytes 15	5.00	0.06
208982_at	**PECAM1**	5175	platelet/endothelial cell adhesion molecule (CD31 antigen)	-7.49	0.00
232304_at	**PELI1**	57162	Pellino homolog 1 (Drosophila)	-3.32	0.07
219132_at	**PELI2**	57161	pellino homolog 2 (Drosophila)	-13.16	0.00
215354_s_at	**PELP1**	27043	proline, glutamic acid and leucine rich protein 1	3.17	0.34
1558915_a_at	**PEX14**	5195	peroxisomal biogenesis factor 14	2.25	0.16
218336_at	**PFDN2**	5202	prefoldin subunit 2	5.83	0.00
228499_at	**PFKFB4**	5210	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-11.02	0.16
204604_at	**PFTK1**	5218	PFTAIRE protein kinase 1	-2.26	0.51
243815_at	**PGBD4**	161779	piggyBac transposable element derived 4	4.28	0.34
203501_at	**PGCP**	10404	plasma glutamate carboxypeptidase	-4.02	0.51
207384_at	**PGLYRP1**	8993	peptidoglycan recognition protein 1	-6.96	0.08
201968_s_at	**PGM1**	5236	phosphoglucomutase 1	-10.72	0.16

223738_s_at	**PGM2**	55276	phosphoglucomutase 2	-3.59	0.08
213638_at	**PHACTR1**	221692	phosphatase and actin regulator 1	13.84	0.00
204048_s_at	**PHACTR2**	9749	phosphatase and actin regulator 2	12.25	0.02
225958_at	**PHC1**	1911	polyhomeotic homolog 1 (Drosophila)	15.66	0.00
200919_at	**PHC2**	1912	polyhomeotic homolog 2 (Drosophila)	-4.45	0.00
221816_s_at	**PHF11**	51131	PHD finger protein 11	3.12	0.06
234939_s_at	**PHF12**	57649	PHD finger protein 12	-11.20	0.07
225820_at	**PHF17**	79960	PHD finger protein 17	-8.93	0.07
212726_at	**PHF2**	5253	PHD finger protein 2	-2.04	0.00
209423_s_at	**PHF20**	51230	PHD finger protein 20	2.05	0.34
219606_at	**PHF20L1**	51105	PHD finger protein 20-like 1	-2.55	0.03
203278_s_at	**PHF21A**	51317	PHD finger protein 21A	-2.91	0.00
217952_x_at	**PHF3**	23469	PHD finger protein 3	-2.33	0.07
217997_at	**PHLDA1**	22822	pleckstrin homology-like domain, family A, member 1	22.76	0.00
209803_s_at	**PHLDA2**	7262	pleckstrin homology-like domain, family A, member 2	598.23	0.00
212719_at	**PHLPP**	23239	PH domain and leucine rich repeat protein phosphatase	-12.49	0.00
225683_x_at	**PHPT1**	29085	phosphohistidine phosphatase 1	2.41	0.25
41469_at	**PI3**	5266	peptidase inhibitor 3, skin-derived (SKALP)	4.44	0.00
222631_at	**PI4K2B**	55300	phosphatidylinositol 4-kinase type 2 beta	7.26	0.16
1555513_at	**PIAS2**	9063	protein inhibitor of activated STAT, 2	-2.15	0.25
215832_x_at	**PICALM**	8301	phosphatidylinositol binding clathrin assembly protein	-2.08	0.00
242760_x_at	**PIGB**	9488	phosphatidylinositol glycan anchor biosynthesis, class B	-7.08	0.00
205077_s_at	**PIGF**	5281	phosphatidylinositol glycan anchor biosynthesis, class F	2.44	0.00
235168_at	**PIGM**	93183	phosphatidylinositol glycan anchor biosynthesis, class M	2.05	0.79
1552291_at	**PIGX**	54965	phosphatidylinositol glycan anchor biosynthesis, class X	-13.21	0.00
224660_at	**PIGY**	84992	phosphatidylinositol glycan anchor biosynthesis, class Y	2.39	0.08
1554508_at	**PIK3AP1**	118788	phosphoinositide-3-kinase adaptor protein 1	2.99	0.00
203879_at	**PIK3CD**	5293	phosphoinositide-3-kinase, catalytic, delta polypeptide	-4.47	0.00
206369_s_at	**PIK3CG**	5294	phosphoinositide-3-kinase, catalytic, gamma polypeptide	-3.72	0.16
209193_at	**PIM1**	5292	pim-1 oncogene	2.06	0.00
209019_s_at	**PINK1**	65018	PTEN induced putative kinase 1	-15.65	0.00
214735_at	**PIP3-E**	26034	phosphoinositide-binding protein PIP3-E	-6.33	0.07
1553048_a_at	**PIP4K2B**	8396	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	2.11	0.02
207391_s_at	**PIP5K1A**	8394	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	2.21	0.16
201192_s_at	**PITPNA**	5306	phosphatidylinositol transfer protein, alpha	2.26	0.06
1561849_at	**PKD1L2**	114780	polycystic kidney disease 1-like 2	2.13	0.34
201251_at	**PKM2**	5315	pyruvate kinase, muscle	6.34	0.13
212629_s_at	**PKN2**	5586	protein kinase N2	-5.50	0.00
204196_x_at	**PKNOX1**	5316	PBX/knotted 1 homeobox 1	-4.44	0.25
222171_s_at	**PKNOX2**	63876	PBX/knotted 1 homeobox 2	-2.00	0.51
206214_at	**PLA2G7**	7941	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	30.89	0.00
202924_s_at	**PLAGL2**	5326	pleiomorphic adenoma gene-like 2	4.75	0.25
205479_s_at	**PLAU**	5328	plasminogen activator, urokinase	45.20	0.00
214866_at	**PLAUR**	5329	plasminogen activator, urokinase receptor	3.87	0.00

204046_at	**PLCB2**	5330	phospholipase C, beta 2	-5.95	0.51
213309_at	**PLCL2**	23228	phospholipase C-like 2	-4.38	0.34
218951_s_at	**PLCXD1**	55344	phosphatidylinositol-specific phospholipase C, X domain containing 1	2.90	0.06
224892_at	**PLDN**	26258	pallidin homolog (mouse)	3.93	0.00
203470_s_at	**PLEK**	5341	pleckstrin	2.93	0.00
201411_s_at	**PLEKHB2**	55041	pleckstrin homology domain containing, family B (evectins) member 2	6.09	0.00
209210_s_at	**PLEKHC1**	10979	pleckstrin homology domain containing, family C (with FERM domain) member 1	-2.99	0.16
217044_s_at	**PLEKHG3**	26030	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	-3.48	0.03
220073_s_at	**PLEKHG6**	55200	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	-3.17	0.51
218290_at	**PLEKHJ1**	55111	pleckstrin homology domain containing, family J member 1	-2.07	0.25
205871_at	**PLGLA1** /// **PLGLB1** /// **PLGLB2**	285189 /// 5342 /// 5343	plasminogen-like B2 /// plasminogen-like B1 /// plasminogen-like A1	-3.97	0.00
214415_at	**PLGLB1** /// **PLGLB2**	5342 /// 5343	plasminogen-like B2 /// plasminogen-like B1	-5.57	0.08
204958_at	**PLK3**	1263	polo-like kinase 3 (Drosophila)	4.96	0.79
201136_at	**PLP2**	5355	proteolipid protein 2 (colonic epithelium-enriched)	-2.88	0.25
202430_s_at	**PLSCR1**	5359	phospholipid scramblase 1	3.18	0.00
227276_at	**PLXDC2**	84898	plexin domain containing 2	-2.49	0.13
207290_at	**PLXNA2**	5362	plexin A2	2.53	0.13
1553139_s_at	**PLXNA3**	55558	plexin A3	2.46	0.00
213241_at	**PLXNC1**	10154	plexin C1	-2.74	0.00
1563657_at	**PLXND1**	23129	plexin D1	2.31	0.16
204286_s_at	**PMAIP1**	5366	phorbol-12-myristate-13-acetate-induced protein 1	2.02	0.02
217123_x_at	**PMCHL1**	5369	pro-melanin-concentrating hormone-like 1	2.01	0.16
239582_at	**PML**	5371	promyelocytic leukemia	4.79	0.00
210139_s_at	**PMP22**	5376	peripheral myelin protein 22	4.99	0.08
203718_at	**PNPLA6**	10908	patatin-like phospholipase domain containing 6	2.57	0.51
223310_x_at	**PNPLA8**	50640	patatin-like phospholipase domain containing 8	2.53	0.00
218511_s_at	**PNPO**	55163	pyridoxamine 5'-phosphate oxidase	4.29	0.51
218229_s_at	**POGK**	57645	pogo transposable element with KRAB domain	3.92	0.79
1553587_a_at	**POLE4**	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)	2.77	0.34
217635_s_at	**POLG**	5428	polymerase (DNA directed), gamma	3.39	0.34
223261_at	**POLK**	51426	polymerase (DNA directed) kappa	3.86	0.13
223403_s_at	**POLR1B**	84172	polymerase (RNA) I polypeptide B, 128kDa	2.79	0.79
209302_at	**POLR2H**	5437	polymerase (RNA) II (DNA directed) polypeptide H	4.03	0.06
202635_s_at	**POLR2K**	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	4.49	0.02
208361_s_at	**POLR3D**	661	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	5.23	0.34
218016_s_at	**POLR3E**	55718	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	6.26	0.13
206654_s_at	**POLR3G**	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	-2.39	0.34
222402_at	**POMP**	51371	proteasome maturation protein	3.27	0.00
217848_s_at	**PPA1**	5464	pyrophosphatase (inorganic) 1	11.44	0.00
212230_at	**PPAP2B**	8613	phosphatidic acid phosphatase type 2B	50.86	0.16
223569_at	**PPAPDC1B**	84513	phosphatidic acid phosphatase type 2 domain containing 1B	3.86	0.51

214374_s_at	**PPFIBP1**	8496	PTPRF interacting protein, binding protein 1 (liprin beta 1)	4.18	0.00
200967_at	**PPIB**	5479	peptidylprolyl isomerase B (cyclophilin B)	2.10	0.51
201489_at	**PPIF**	10105	peptidylprolyl isomerase F (cyclophilin F)	3.60	0.00
222500_at	**PPIL1**	51645	peptidylprolyl isomerase (cyclophilin)-like 1	7.60	0.08
242154_x_at	**PPIL5**	122769	peptidylprolyl isomerase (cyclophilin)-like 5	-3.33	0.51
231370_at	**PPM1A**	5494	Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	-2.04	0.00
209296_at	**PPM1B**	5495	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	-2.78	0.00
201958_s_at	**PPP1R12B**	4660	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-49.87	0.00
202014_at	**PPP1R15A**	23645	protein phosphatase 1, regulatory (inhibitor) subunit 15A	3.73	0.00
204554_at	**PPP1R3D**	5509	protein phosphatase 1, regulatory (inhibitor) subunit 3D	-2.47	0.13
201375_s_at	**PPP2CB**	5516	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	2.47	0.16
202187_s_at	**PPP2R5A**	5525	protein phosphatase 2, regulatory subunit B', alpha isoform	-9.48	0.00
1554365_a_at	**PPP2R5C**	5527	protein phosphatase 2, regulatory subunit B', gamma isoform	-3.61	0.07
202425_x_at	**PPP3CA**	5530	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	-3.48	0.00
201594_s_at	**PPP4R1**	9989	protein phosphatase 4, regulatory subunit 1	-15.00	0.00
225429_at	**PPP6C**	5537	protein phosphatase 6, catalytic subunit	-2.63	0.51
241742_at	**PRAM1**	84106	PML-RARA regulated adaptor molecule 1	-5.82	0.00
208680_at	**PRDX1**	5052	peroxiredoxin 1	16.23	0.00
224925_at	**PREX1**	57580	phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1	-2.41	0.00
214617_at	**PRF1**	5551	perforin 1 (pore forming protein)	3.45	0.08
201805_at	**PRKAG1**	5571	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	2.62	0.00
218764_at	**PRKCH**	5583	protein kinase C, eta	3.68	0.08
38269_at	**PRKD2**	25865	protein kinase D2	-2.22	0.25
210543_s_at	**PRKDC**	5591	protein kinase, DNA-activated, catalytic polypeptide	-9.85	0.00
204061_at	**PRKX**	5613	protein kinase, X-linked	3.55	0.16
206445_s_at	**PRMT1**	3276	protein arginine methyltransferase 1	4.40	0.16
221564_at	**PRMT2**	3275	protein arginine methyltransferase 2	-2.34	0.51
1564520_s_at	**PRMT5**	10419	protein arginine methyltransferase 5	-2.90	0.51
201300_s_at	**PRNP**	5621	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	11.76	0.34
215837_x_at	**PRO1621**	29007	PRO1621 protein	-2.01	0.51
203650_at	**PROCR**	10544	protein C receptor, endothelial (EPCR)	37.42	0.00
232629_at	**PROK2**	60675	prokineticin 2	-14.97	0.00
209384_at	**PROSC**	11212	proline synthetase co-transcribed homolog (bacterial)	3.37	0.16
221546_at	**PRPF18**	8559	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	-2.72	0.08
203103_s_at	**PRPF19**	27339	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	5.82	0.25
230270_at	**PRPF38B**	55119	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-4.19	0.79
220553_s_at	**PRPF39**	55015	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	3.77	0.16
202529_at	**PRPSAP1**	5635	phosphoribosyl pyrophosphate synthetase-associated protein 1	3.95	0.06
221734_at	**PRRC1**	133619	proline-rich coiled-coil 1	2.55	0.79

223062_s_at	**PSAT1**	29968	phosphoserine aminotransferase 1	4.16	0.13
1554335_at	**PSCD4**	27128	pleckstrin homology, Sec7 and coiled-coil domains 4	-3.90	0.34
215821_x_at	**PSG3**	5671	pregnancy specific beta-1-glycoprotein 3	2.29	0.02
209337_at	**PSIP1**	11168	PC4 and SFRS1 interacting protein 1	-5.25	0.25
201676_x_at	**PSMA1**	5682	proteasome (prosome, macropain) subunit, alpha type, 1	4.01	0.00
201317_s_at	**PSMA2**	5683	proteasome (prosome, macropain) subunit, alpha type, 2	3.59	0.00
201532_at	**PSMA3**	5684	proteasome (prosome, macropain) subunit, alpha type, 3	3.47	0.00
203396_at	**PSMA4**	5685	proteasome (prosome, macropain) subunit, alpha type, 4	2.84	0.00
201274_at	**PSMA5**	5686	proteasome (prosome, macropain) subunit, alpha type, 5	7.07	0.00
208805_at	**PSMA6**	5687	proteasome (prosome, macropain) subunit, alpha type, 6	4.59	0.00
201114_x_at	**PSMA7**	5688	proteasome (prosome, macropain) subunit, alpha type, 7	2.02	0.02
214288_s_at	**PSMB1**	5689	proteasome (prosome, macropain) subunit, beta type, 1	2.04	0.02
200039_s_at	**PSMB2**	5690	proteasome (prosome, macropain) subunit, beta type, 2	2.38	0.00
202243_s_at	**PSMB4**	5692	proteasome (prosome, macropain) subunit, beta type, 4	2.94	0.00
208799_at	**PSMB5**	5693	proteasome (prosome, macropain) subunit, beta type, 5	5.55	0.13
208827_at	**PSMB6**	5694	proteasome (prosome, macropain) subunit, beta type, 6	2.94	0.08
201068_s_at	**PSMC2**	5701	proteasome (prosome, macropain) 26S subunit, ATPase, 2	6.71	0.00
201267_s_at	**PSMC3**	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3	3.38	0.25
209503_s_at	**PSMC5**	5705	proteasome (prosome, macropain) 26S subunit, ATPase, 5	2.94	0.16
201199_s_at	**PSMD1**	5707	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	2.65	0.08
212296_at	**PSMD14**	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	6.86	0.16
200830_at	**PSMD2**	5708	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	2.04	0.79
201388_at	**PSMD3**	5709	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	14.27	0.00
1555884_at	**PSMD6**	9861	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	-2.62	0.13
201705_at	**PSMD7**	5713	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	2.44	0.16
200820_at	**PSMD8**	5714	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	6.17	0.00
201762_s_at	**PSME2**	5721	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	3.85	0.00
209852_x_at	**PSME3**	10197	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	-2.08	0.51
211178_s_at	**PSTPIP1**	9051	proline-serine-threonine phosphatase interacting protein 1	-5.87	0.00
219938_s_at	**PSTPIP2**	9050	proline-serine-threonine phosphatase interacting protein 2	7.52	0.00
211271_x_at	**PTBP1**	5725	polypyrimidine tract binding protein 1	2.01	0.51
201433_s_at	**PTDSS1**	9791	phosphatidylserine synthase 1	4.70	0.08
211711_s_at	**PTEN**	5728	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-2.52	0.00

217494_s_at	**PTENP1**	11191	phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1	-2.53	0.00
211892_s_at	**PTGIS**	5740	prostaglandin I2 (prostacyclin) synthase	-2.03	0.51
234000_s_at	**PTPLAD1**	51495	protein tyrosine phosphatase-like A domain containing 1	5.12	0.02
244050_at	**PTPLAD2**	401494	protein tyrosine phosphatase-like A domain containing 2	-6.31	0.00
203555_at	**PTPN18**	26469	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	-2.10	0.51
213136_at	**PTPN2**	5771	protein tyrosine phosphatase, non-receptor type 2	2.42	0.02
204852_s_at	**PTPN7**	5778	protein tyrosine phosphatase, non-receptor type 7	2.52	0.16
209899_s_at	**PUF60**	22827	poly-U binding splicing factor 60KDa	3.32	0.25
1552274_at	**PXK**	54899	PX domain containing serine/threonine kinase	-3.18	0.07
211823_s_at	**PXN**	5829	paxillin	-6.20	0.00
1552599_at	**PXT1**	222659	peroxisomal, testis specific 1	2.21	0.51
221666_s_at	**PYCARD**	29108	PYD and CARD domain containing	-3.67	0.16
202990_at	**PYGL**	5836	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	-11.19	0.00
219681_s_at	**RAB11FIP1**	80223	RAB11 family interacting protein 1 (class I)	-3.22	0.00
225746_at	**RAB11FIP4**	84440	RAB11 family interacting protein 4 (class II)	-13.95	0.51
235059_at	**RAB12**	201475	RAB12, member RAS oncogene family	5.42	0.00
202252_at	**RAB13**	5872	RAB13, member RAS oncogene family	2.30	0.08
219622_at	**RAB20**	55647	RAB20, member RAS oncogene family	9.38	0.00
209515_s_at	**RAB27A**	5873	RAB27A, member RAS oncogene family	-2.23	0.07
228113_at	**RAB37**	326624	RAB37, member RAS oncogene family	-16.30	0.00
1554800_at	**RAB39**	54734	RAB39, member RAS oncogene family	9.08	0.06
225001_at	**RAB3D**	9545	RAB3D, member RAS oncogene family	-5.44	0.00
203136_at	**RABAC1**	10567	Rab acceptor 1 (prenylated)	-2.35	0.25
203020_at	**RABGAP1L**	9910	RAB GTPase activating protein 1-like	-7.81	0.00
209181_s_at	**RABGGTB**	5876	Rab geranylgeranyltransferase, beta subunit	3.97	0.13
201039_s_at	**RAD23A**	5886	RAD23 homolog A (S. cerevisiae)	8.01	0.00
201244_s_at	**RAF1**	5894	v-raf-1 murine leukemia viral oncogene homolog 1	-2.98	0.00
219125_s_at	**RAG1AP1**	55974	recombination activating gene 1 activating protein 1	2.61	0.25
215117_at	**RAG2**	5897	recombination activating gene 2	2.49	0.16
214435_x_at	**RALA**	5898	v-ral simian leukemia viral oncogene homolog A (ras related)	5.00	0.00
202844_s_at	**RALBP1**	10928	ralA binding protein 1	-4.55	0.00
209050_s_at	**RALGDS**	5900	ral guanine nucleotide dissociation stimulator	93.68	0.00
232112_at	**RALGPS2**	55103	Ral GEF with PH domain and SH3 binding motif 2	-3.81	0.34
201271_s_at	**RALY**	22913	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))	-2.57	0.79
200750_s_at	**RAN**	5901	RAN, member RAS oncogene family	4.00	0.08
221915_s_at	**RANBP1**	5902	RAN binding protein 1	2.19	0.08
201713_s_at	**RANBP2**	5903	RAN binding protein 2	3.15	0.00
236906_x_at	**RANBP5**	3843	RAN binding protein 5	2.09	0.79
218668_s_at	**RAP2C**	57826	RAP2C, member of RAS oncogene family	2.19	0.16
203097_s_at	**RAPGEF2**	9693	Rap guanine nucleotide exchange factor (GEF) 2	-2.61	0.00
203749_s_at	**RARA**	5914	retinoic acid receptor, alpha	-2.35	0.25
204070_at	**RARRES3**	5920	retinoic acid receptor responder (tazarotene induced) 3	12.10	0.00
201330_at	**RARS**	5917	arginyl-tRNA synthetase	3.58	0.34

232902_s_at	**RARS2**	57038	arginyl-tRNA synthetase 2, mitochondrial (putative)	2.03	0.51
208206_s_at	**RASGRP2**	10235	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-3.38	0.00
240862_at	**RASGRP4**	115727	RAS guanyl releasing protein 4	-4.57	0.00
204346_s_at	**RASSF1**	11186	Ras association (RalGDS/AF-6) domain family 1	-3.47	0.16
212870_at	**RASSF3**	283349	Ras association (RalGDS/AF-6) domain family 3	-8.83	0.16
202033_s_at	**RB1CC1**	9821	RB1-inducible coiled-coil 1	-2.57	0.07
210371_s_at	**RBBP4**	5928	retinoblastoma binding protein 4	2.14	0.79
212783_at	**RBBP6**	5930	retinoblastoma binding protein 6	2.06	0.25
203344_s_at	**RBBP8**	5932	retinoblastoma binding protein 8	2.41	0.79
232751_at	**RBBP9**	10741	retinoblastoma binding protein 9	4.43	0.16
221827_at	**RBCK1**	10616	RanBP-type and C3HC4-type zinc finger containing 1	2.75	0.02
212331_at	**RBL2**	5934	retinoblastoma-like 2 (p130)	-6.50	0.00
51228_at	**RBM12B**	389677	RNA binding motif protein 12B	-2.11	0.51
211686_s_at	**RBM13**	84549	RNA binding motif protein 13	9.76	0.08
219286_s_at	**RBM15**	64783	RNA binding motif protein 15	2.13	0.51
224781_s_at	**RBM17**	84991	RNA binding motif protein 17	2.16	0.06
218593_at	**RBM28**	55131	RNA binding motif protein 28	6.39	0.06
208319_s_at	**RBM3**	5935	RNA binding motif (RNP1, RRM) protein 3	2.62	0.00
225839_at	**RBM33**	155435	RNA binding motif protein 33	-4.62	0.00
212591_at	**RBM34**	23029	RNA binding motif protein 34	4.16	0.00
225141_at	**RBM35B**	80004	RNA binding motif protein 35B	-4.18	0.34
218379_at	**RBM7**	10179	RNA binding motif protein 7	2.20	0.34
208307_at	**RBMY1A1** /// **RBMY1B** /// **RBMY1D** /// **RBMY1E** /// **RBMY1F** /// **RBMY1J**	159163 /// 378948 /// 378949 /// 378950 /// 378951 /// 5940	RNA binding motif protein, Y-linked, family 1, member A1 /// RNA binding motif protein, Y-linked, family 1, member F /// RNA binding motif protein, Y-linked, family 1, member B /// RNA binding motif protein, Y-linked, family 1, member D /// RNA binding motif protein, Y-linked, family 1, member E /// RNA binding motif protein, Y-linked, family 1, member J	2.14	0.16
1552952_at	**RBMY2FP**	159162	RNA binding motif protein, Y-linked, family 2, member F pseudogene	3.33	0.00
238066_at	**RBP7**	116362	retinol binding protein 7, cellular	-29.98	0.00
208370_s_at	**RCAN1**	1827	regulator of calcineurin 1	2.42	0.79
204759_at	**RCBTB2**	1102	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	-2.90	0.00
224578_at	**RCC2**	55920	regulator of chromosome condensation 2	2.46	0.79
214281_s_at	**RCHY1**	25898	ring finger and CHY zinc finger domain containing 1	2.63	0.00
201063_at	**RCN1**	5954	reticulocalbin 1, EF-hand calcium binding domain	6.18	0.34
61734_at	**RCN3**	57333	reticulocalbin 3, EF-hand calcium binding domain	-2.48	0.13
212612_at	**RCOR1**	23186	REST corepressor 1	-2.30	0.08
222203_s_at	**RDH14**	57665	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	2.52	0.34
205407_at	**RECK**	8434	reversion-inducing-cysteine-rich protein with kazal motifs	4.47	0.25
208873_s_at	**REEP5**	7905	receptor accessory protein 5	-3.69	0.00
206036_s_at	**REL**	5966	v-rel reticuloendotheliosis viral oncogene homolog (avian)	2.35	0.16

201783_s_at	**RELA**	5970	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	3.54	0.00
205205_at	**RELB**	5971	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)	4.61	0.34
227425_at	**REPS2**	9185	RALBP1 associated Eps domain containing 2	-12.07	0.00
200940_s_at	**RERE**	473	arginine-glutamic acid dipeptide (RE) repeats	-2.16	0.00
226144_at	**REXO1**	57455	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	2.44	0.02
203224_at	**RFK**	55312	riboflavin kinase	3.59	0.00
234950_s_at	**RFWD2**	64326	ring finger and WD repeat domain 2	-2.19	0.00
208031_s_at	**RFX2**	5990	regulatory factor X, 2 (influences HLA class II expression)	-2.34	0.34
202963_at	**RFX5**	5993	regulatory factor X, 5 (influences HLA class II expression)	5.07	0.00
209568_s_at	**RGL1**	23179	ral guanine nucleotide dissociation stimulator-like 1	27.91	0.02
235816_s_at	**Rgr**	266747	Ral-GDS related protein Rgr	-4.14	0.51
204319_s_at	**RGS10**	6001	regulator of G-protein signaling 10	4.53	0.25
38290_at	**RGS14**	10636	regulator of G-protein signaling 14	-13.29	0.00
209325_s_at	**RGS16**	6004	regulator of G-protein signaling 16	2.70	0.79
223809_at	**RGS18**	64407	regulator of G-protein signaling 18	-28.59	0.00
202388_at	**RGS2**	5997	regulator of G-protein signaling 2, 24kDa	-5.08	0.00
227414_at	**RHBDD1**	84236	rhomboid domain containing 1	11.21	0.51
219202_at	**RHBDF2**	79651	rhomboid 5 homolog 2 (Drosophila)	11.64	0.00
1555780_a_at	**RHEB**	6009	Ras homolog enriched in brain	4.02	0.13
212099_at	**RHOB**	388	ras homolog gene family, member B	-3.58	0.00
200885_at	**RHOC**	389	ras homolog gene family, member C	6.22	0.00
203175_at	**RHOG**	391	ras homolog gene family, member G (rho G)	-2.27	0.13
204951_at	**RHOH**	399	ras homolog gene family, member H	26.50	0.00
212117_at	**RHOQ**	23433	ras homolog gene family, member Q	2.20	0.00
223168_at	**RHOU**	58480	ras homolog gene family, member U	3.48	0.34
241990_at	**RHOV**	171177	ras homolog gene family, member V	2.01	0.02
226312_at	**RICTOR**	253260	rapamycin-insensitive companion of mTOR	-2.58	0.00
209684_at	**RIN2**	54453	Ras and Rab interactor 2	4.06	0.16
220439_at	**RIN3**	79890	Ras and Rab interactor 3	-3.31	0.51
209545_s_at	**RIPK2**	8767	receptor-interacting serine-threonine kinase 2	21.40	0.00
204243_at	**RLF**	6018	rearranged L-myc fusion	2.05	0.13
218979_at	**RMI1**	80010	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	-2.66	0.13
212478_at	**RMND5A**	64795	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	-2.95	0.07
206111_at	**RNASE2**	6036	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	-17.71	0.25
213397_x_at	**RNASE4**	6038	ribonuclease, RNase A family, 4	2.02	0.13
203022_at	**RNASEH2A**	10535	ribonuclease H2, subunit A	2.48	0.51
217984_at	**RNASET2**	8635	ribonuclease T2	-10.62	0.00
208632_at	**RNF10**	9921	ring finger protein 10	-2.86	0.25
223591_at	**RNF135**	84282	ring finger protein 135	-3.34	0.34
226106_at	**RNF141**	50862	ring finger protein 141	-4.75	0.00
227726_at	**RNF166**	115992	ring finger protein 166	-2.33	0.07
229932_at	**RNF181**	51255	Ring finger protein 181	7.24	0.16
224750_at	**RNF185**	91445	ring finger protein 185	4.03	0.16
225929_s_at	**RNF213**	57674	ring finger protein 213	2.38	0.00
210706_s_at	**RNF24**	11237	ring finger protein 24	-2.34	0.03

203286_at	**RNF44**	22838	ring finger protein 44	-3.00	0.00
202683_s_at	**RNMT**	8731	RNA (guanine-7-) methyltransferase	4.74	0.06
226975_at	**RNPC3**	55599	RNA-binding region (RNP1, RRM) containing 3	-2.30	0.00
218301_at	**RNPEPL1**	57140	arginyl aminopeptidase (aminopeptidase B)-like 1	-5.99	0.08
213194_at	**ROBO1**	6091	roundabout, axon guidance receptor, homolog 1 (Drosophila)	2.35	0.13
214578_s_at	**ROCK1**	6093	Rho-associated, coiled-coil containing protein kinase 1	-2.22	0.00
211504_x_at	**ROCK2**	9475	Rho-associated, coiled-coil containing protein kinase 2	-2.25	0.79
214697_s_at	**ROD1**	9991	ROD1 regulator of differentiation 1 (S. pombe)	-2.12	0.03
223609_at	**ROPN1L**	83853	ropporin 1-like	-6.26	0.07
220436_at	**RP11-138L21.1**	389722	similar to cell recognition molecule CASPR3	-12.03	0.34
1569932_at	**RP11-262D11.5**	340527	similar to Nance-Horan syndrome protein	-4.54	0.16
214748_at	**RP11-298P3.3**	88523	CG016	3.43	0.79
227040_at	**RP11-50D16.3**	387921	similar to RIKEN cDNA 8030451K01	8.50	0.25
221143_at	**RPA4**	29935	replication protein A4, 34kDa	3.34	0.34
228183_s_at	**RPAIN**	84268	RPA interacting protein	2.35	0.34
218441_s_at	**RPAP1**	26015	RNA polymerase II associated protein 1	2.22	0.34
221770_at	**RPE**	6120	ribulose-5-phosphate-3-epimerase	3.96	0.51
206608_s_at	**RPGRIP1**	57096	retinitis pigmentosa GTPase regulator interacting protein 1	-2.26	0.51
221475_s_at	**RPL15**	6138	ribosomal protein L15	2.78	0.06
200022_at	**RPL18**	6141	ribosomal protein L18	2.41	0.34
200013_at	**RPL24**	6152	ribosomal protein L24	3.23	0.00
214143_x_at	**RPL24 /// SLC36A2**	153201 /// 6152	ribosomal protein L24 /// solute carrier family 36 (proton/amino acid symporter), member 2	2.74	0.00
200002_at	**RPL35**	11224	ribosomal protein L35	2.22	0.34
224738_x_at	**RPL7L1**	285855	ribosomal protein L7-like 1	3.30	0.02
200936_at	**RPL8**	6132	ribosomal protein L8	2.46	0.06
213399_x_at	**RPN2**	6185	ribophorin II	3.04	0.13
226131_s_at	**RPS16**	6217	ribosomal protein S16	2.38	0.08
213414_s_at	**RPS19**	6223	ribosomal protein S19	2.38	0.08
222487_s_at	**RPS27L**	51065	ribosomal protein S27-like	2.30	0.51
204633_s_at	**RPS6KA5**	9252	ribosomal protein S6 kinase, 90kDa, polypeptide 5	-3.99	0.25
220737_at	**RPS6KA6**	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6	-2.79	0.34
225398_at	**RPUSD4**	84881	RNA pseudouridylate synthase domain containing 4	9.21	0.34
222514_at	**RRAGC**	64121	Ras-related GTP binding C	2.66	0.00
223342_at	**RRM2B**	50484	ribonucleotide reductase M2 B (TP53 inducible)	-3.52	0.13
222204_s_at	**RRN3**	54700	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	2.98	0.25
219037_at	**RRP15**	51018	ribosomal RNA processing 15 homolog (S. cerevisiae)	2.70	0.06
213797_at	**RSAD2**	91543	radical S-adenosyl methionine domain containing 2	4.98	0.00
213694_at	**RSBN1**	54665	round spermatid basic protein 1	-2.42	0.51
226387_at	**RSBN1L**	222194	round spermatid basic protein 1-like	-4.84	0.00
212018_s_at	**RSL1D1**	26156	ribosomal L1 domain containing 1	6.48	0.00
223713_at	**RSPH3**	83861	radial spoke head 3 homolog (Chlamydomonas)	-3.39	0.13

34408_at	**RTN2**	6253	reticulon 2	4.25	0.25
219549_s_at	**RTN3**	10313	reticulon 3	-3.67	0.00
219684_at	**RTP4**	64108	receptor (chemosensory) transporter protein 4	7.72	0.08
210251_s_at	**RUFY3**	22902	RUN and FYVE domain containing 3	2.65	0.25
232231_at	**RUNX2**	860	runt-related transcription factor 2	-10.89	0.13
204197_s_at	**RUNX3**	864	runt-related transcription factor 3	3.39	0.06
205087_at	**RWDD3**	25950	RWD domain containing 3	-2.18	0.34
209148_at	**RXRB**	6257	retinoid X receptor, beta	-4.11	0.00
212440_at	**RY1**	11017	putative nucleic acid binding protein RY-1	5.13	0.00
203186_s_at	**S100A4**	6275	S100 calcium binding protein A4	-6.00	0.00
217728_at	**S100A6**	6277	S100 calcium binding protein A6	-3.75	0.03
203535_at	**S100A9**	6280	S100 calcium binding protein A9	-2.06	0.00
204351_at	**S100P**	6286	S100 calcium binding protein P	-3.05	0.00
217946_s_at	**SAE1**	10055	SUMO1 activating enzyme subunit 1	4.97	0.00
201177_s_at	**SAE2**	10054	SUMO1 activating enzyme subunit 2	6.29	0.25
226603_at	**SAMD9L**	219285	sterile alpha motif domain containing 9-like	3.07	0.00
204502_at	**SAMHD1**	25939	SAM domain and HD domain 1	3.28	0.00
1555638_a_at	**SAMSN1**	64092	SAM domain, SH3 domain and nuclear localization signals 1	7.73	0.00
210790_s_at	**SAR1A**	56681	SAR1 gene homolog A (S. cerevisiae)	2.40	0.25
1554482_a_at	**SAR1B**	51128	SAR1 gene homolog B (S. cerevisiae)	5.82	0.00
209486_at	**SAS10**	57050	disrupter of silencing 10	3.79	0.06
225272_at	**SAT2**	112483	spermidine/spermine N1-acetyltransferase 2	3.82	0.08
234491_s_at	**SAV1**	60485	salvador homolog 1 (Drosophila)	3.01	0.02
222669_s_at	**SBDS /// SBDSP**	155370 /// 51119	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	2.98	0.00
209741_x_at	**SCAPER**	49855	S phase cyclin A-associated protein in the ER	2.44	0.25
1554705_at	**SCARA5**	286133	scavenger receptor class A, member 5 (putative)	2.95	0.02
201646_at	**SCARB2**	950	scavenger receptor class B, member 2	9.35	0.13
1555021_a_at	**SCARF1**	8578	scavenger receptor class F, member 1	5.21	0.00
215548_s_at	**SCFD1**	23256	sec1 family domain containing 1	2.09	0.34
219196_at	**SCG3**	29106	secretogranin III	7.87	0.34
1569495_at	**SCLT1**	132320	sodium channel and clathrin linker 1	-4.77	0.34
218793_s_at	**SCML1**	6322	sex comb on midleg-like 1 (Drosophila)	2.82	0.25
232512_at	**SCN3A**	6328	sodium channel, voltage-gated, type III, alpha subunit	2.10	0.51
202541_at	**SCYE1**	9255	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	3.28	0.08
41329_at	**SCYL3**	57147	SCY1-like 3 (S. cerevisiae)	2.08	0.16
212154_at	**SDC2**	6383	syndecan 2	6.64	0.25
202071_at	**SDC4**	6385	syndecan 4	12.00	0.00
1555495_a_at	**SDCCAG10**	10283	serologically defined colon cancer antigen 10	2.30	0.51
227785_at	**SDCCAG8**	10806	serologically defined colon cancer antigen 8	4.77	0.02
218681_s_at	**SDF2L1**	23753	stromal cell-derived factor 2-like 1	4.01	0.06
223299_at	**SEC11C**	90701	SEC11 homolog C (S. cerevisiae)	2.49	0.06
210293_s_at	**SEC23B**	10483	Sec23 homolog B (S. cerevisiae)	4.58	0.06
212900_at	**SEC24A**	10802	SEC24 related gene family, member A (S. cerevisiae)	6.04	0.00
202375_at	**SEC24D**	9871	SEC24 related gene family, member D (S. cerevisiae)	2.03	0.79
200945_s_at	**SEC31A**	22872	SEC31 homolog A (S. cerevisiae)	5.98	0.25
203484_at	**SEC61G**	23480	Sec61 gamma subunit	3.18	0.02
223225_s_at	**SEH1L**	81929	SEH1-like (S. cerevisiae)	14.67	0.02
1555274_a_at	**SELI**	85465	selenoprotein I	10.07	0.51
204563_at	**SELL**	6402	selectin L (lymphocyte adhesion molecule 1)	-7.75	0.00

209879_at	**SELPLG**	6404	selectin P ligand	-4.31	0.00
223209_s_at	**SELS**	55829	selenoprotein S	5.80	0.00
46665_at	**SEMA4C**	54910	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	5.37	0.79
200961_at	**SEPHS2**	22928	selenophosphate synthetase 2	2.52	0.00
208657_s_at	**SEPT9**	10801	septin 9	-2.25	0.16
209669_s_at	**SERBP1**	26135	SERPINE1 mRNA binding protein 1	2.01	0.08
204614_at	**SERPINB2**	5055	serpin peptidase inhibitor, clade B (ovalbumin), member 2	11.59	0.00
211474_s_at	**SERPINB6**	5269	serpin peptidase inhibitor, clade B (ovalbumin), member 6	3.39	0.79
206034_at	**SERPINB8**	5271	serpin peptidase inhibitor, clade B (ovalbumin), member 8	8.09	0.00
209723_at	**SERPINB9**	5272	serpin peptidase inhibitor, clade B (ovalbumin), member 9	7.77	0.00
200986_at	**SERPING1**	710	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	5.46	0.13
235684_s_at	**SESN3**	143686	sestrin 3	-9.42	0.00
213153_at	**SETD1B**	23067	SET domain containing 1B	-2.05	0.03
225118_at	**SETD8**	387893	SET domain containing (lysine methyltransferase) 8	-2.51	0.79
235339_at	**SETDB2**	83852	SET domain, bifurcated 2	3.22	0.00
200687_s_at	**SF3B3**	23450	splicing factor 3b, subunit 3, 130kDa	3.41	0.16
227210_at	**SFMBT2**	57713	Scm-like with four mbt domains 2	7.35	0.06
200893_at	**SFRS10**	6434	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	3.35	0.16
214092_x_at	**SFRS14**	10147	splicing factor, arginine/serine-rich 14	-2.08	0.25
235579_at	**SFRS2IP**	9169	Splicing factor, arginine/serine-rich 2, interacting protein	3.57	0.25
206108_s_at	**SFRS6**	6431	splicing factor, arginine/serine-rich 6	2.68	0.51
214141_x_at	**SFRS7**	6432	splicing factor, arginine/serine-rich 7, 35kDa	3.84	0.02
214838_at	**SFT2D2**	375035	SFT2 domain containing 2	3.56	0.16
214354_x_at	**SFTPB**	6439	surfactant, pulmonary-associated protein B	4.85	0.00
220038_at	**SGK3**	23678	serum/glucocorticoid regulated kinase family, member 3	3.65	0.34
244780_at	**SGPP2**	130367	sphingosine-1-phosphate phosphotase 2	21.70	0.51
228745_at	**SGTB**	54557	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	4.99	0.00
210116_at	**SH2D1A**	4068	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	2.31	0.06
223265_at	**SH3BP5L**	80851	SH3-binding domain protein 5-like	-5.43	0.25
223082_at	**SH3KBP1**	30011	SH3-domain kinase binding protein 1	-4.21	0.00
202276_at	**SHFM1**	7979	split hand/foot malformation (ectrodactyly) type 1	2.95	0.06
224846_at	**SHKBP1**	92799	SH3KBP1 binding protein 1	-3.13	0.07
209980_s_at	**SHMT1**	6470	serine hydroxymethyltransferase 1 (soluble)	2.59	0.02
210135_s_at	**SHOX2**	6474	short stature homeobox 2	23.63	0.02
218765_at	**SIDT2**	51092	SID1 transmembrane family, member 2	2.56	0.25
44673_at	**SIGLEC1**	6614	sialic acid binding Ig-like lectin 1, sialoadhesin	4.85	0.34
1552807_a_at	**SIGLEC10**	89790	sialic acid binding Ig-like lectin 10	-4.06	0.13
1561880_a_at	**SIGLECP16**	400709	sialic acid binding Ig-like lectin, pseudogene 16	3.66	0.51
206934_at	**SIRPB1**	10326	signal-regulatory protein beta 1	-4.50	0.00
1559034_at	**SIRPB2**	284759	signal-regulatory protein beta 2	-5.96	0.07
232891_at	**SIRPD**	128646	signal-regulatory protein delta	-3.05	0.51
233179_x_at	**SIRT6**	51548	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cerevisiae)	4.36	0.79
232379_at	**SKIL**	6498	SKI-like oncogene	4.75	0.00

206181_at	**SLAMF1**	6504	signaling lymphocytic activation molecule family member 1	5.47	0.79
219159_s_at	**SLAMF7**	57823	SLAM family member 7	71.81	0.00
219386_s_at	**SLAMF8**	56833	SLAM family member 8	115.80	0.00
1553769_at	**SLAMF9**	89886	SLAM family member 9	2.26	0.79
203124_s_at	**SLC11A2**	4891	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	45.12	0.00
220371_s_at	**SLC12A9**	56996	solute carrier family 12 (potassium/chloride transporters), member 9	-10.53	0.00
209900_s_at	**SLC16A1**	6566	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	7.68	0.00
206600_s_at	**SLC16A5**	9121	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	-2.50	0.13
211576_s_at	**SLC19A1**	6573	solute carrier family 19 (folate transporter), member 1	-3.69	0.25
209611_s_at	**SLC1A4**	6509	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.53	0.34
208916_at	**SLC1A5**	6510	solute carrier family 1 (neutral amino acid transporter), member 5	3.13	0.00
201920_at	**SLC20A1**	6574	solute carrier family 20 (phosphate transporter), member 1	2.04	0.00
228497_at	**SLC22A15**	55356	solute carrier family 22 (organic cation transporter), member 15	-4.20	0.34
206097_at	**SLC22A18AS**	5003	solute carrier family 22 (organic cation transporter), member 18 antisense	4.90	0.13
205896_at	**SLC22A4**	6583	solute carrier family 22 (organic cation transporter), member 4	-7.53	0.16
243969_at	**SLC24A4**	123041	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	-13.00	0.25
203340_s_at	**SLC25A12**	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	2.84	0.79
203775_at	**SLC25A13**	10165	solute carrier family 25, member 13 (citrin)	29.58	0.00
218725_at	**SLC25A22**	79751	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	2.53	0.51
225212_at	**SLC25A25**	114789	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	2.14	0.51
223192_at	**SLC25A28**	81894	solute carrier family 25, member 28	2.84	0.25
216721_at	**SLC25A30**	253512	Solute carrier family 25, member 30	4.98	0.08
221020_s_at	**SLC25A32**	81034	solute carrier family 25, member 32	6.50	0.51
223296_at	**SLC25A33**	84275	solute carrier family 25, member 33	49.82	0.00
242335_at	**SLC25A37**	51312	solute carrier family 25, member 37	-3.35	0.00
200657_at	**SLC25A5**	292	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	2.96	0.06
212085_at	**SLC25A6**	293	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	3.62	0.06
226679_at	**SLC26A11**	284129	solute carrier family 26, member 11	8.20	0.02
224963_at	**SLC26A2**	1836	solute carrier family 26 (sulfate transporter), member 2	2.24	0.08
201802_at	**SLC29A1**	2030	solute carrier family 29 (nucleoside transporters), member 1	-3.44	0.16
201250_s_at	**SLC2A1**	6513	solute carrier family 2 (facilitated glucose transporter), member 1	-4.65	0.51
1555500_s_at	**SLC2A4RG**	56731	SLC2A4 regulator	5.85	0.25
207035_at	**SLC30A3**	7781	solute carrier family 30 (zinc transporter), member 3	-4.47	0.13
207362_at	**SLC30A4**	7782	solute carrier family 30 (zinc transporter), member 4	3.78	0.00
226601_at	**SLC30A7**	148867	solute carrier family 30 (zinc transporter), member 7	4.58	0.06

203971_at	**SLC31A1**	1317	solute carrier family 31 (copper transporters), member 1	3.28	0.16
202433_at	**SLC35B1**	10237	solute carrier family 35, member B1	3.13	0.13
224716_at	**SLC35B2**	347734	solute carrier family 35, member B2	6.86	0.06
225881_at	**SLC35B4**	84912	solute carrier family 35, member B4	6.71	0.02
225037_at	**SLC35C2**	51006	solute carrier family 35, member C2	2.01	0.25
234978_at	**SLC36A4**	120103	solute carrier family 36 (proton/amino acid symporter), member 4	4.05	0.79
218928_s_at	**SLC37A1**	54020	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	2.49	0.25
223304_at	**SLC37A3**	84255	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	-6.45	0.00
202088_at	**SLC39A6**	25800	solute carrier family 39 (zinc transporter), member 6	2.29	0.13
209267_s_at	**SLC39A8**	64116	solute carrier family 39 (zinc transporter), member 8	25.96	0.00
200924_s_at	**SLC3A2**	6520	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	4.34	0.06
223044_at	**SLC40A1**	30061	solute carrier family 40 (iron-regulated transporter), member 1	-71.53	0.00
223798_at	**SLC41A2**	84102	solute carrier family 41, member 2	18.72	0.16
210692_s_at	**SLC43A3**	29015	solute carrier family 43, member 3	94.83	0.00
228485_s_at	**SLC44A1**	23446	solute carrier family 44, member 1	3.41	0.00
224609_at	**SLC44A2**	57153	solute carrier family 44, member 2	-14.52	0.00
225598_at	**SLC45A4**	57210	solute carrier family 45, member 4	-6.46	0.03
214719_at	**SLC46A3**	283537	solute carrier family 46, member 3	-9.28	0.08
202111_at	**SLC4A2**	6522	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	8.50	0.00
234976_x_at	**SLC4A5**	57835	Solute carrier family 4, sodium bicarbonate cotransporter, member 5	10.15	0.13
210286_s_at	**SLC4A7**	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7	2.84	0.16
213167_s_at	**SLC5A3**	6526	solute carrier family 5 (inositol transporters), member 3	4.74	0.00
212290_at	**SLC7A1**	6541	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	3.49	0.34
209921_at	**SLC7A11**	23657	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	15.73	0.00
201195_s_at	**SLC7A5**	8140	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	3.87	0.25
201349_at	**SLC9A3R1**	9368	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	-7.71	0.16
203473_at	**SLCO2B1**	11309	solute carrier organic anion transporter family, member 2B1	7.60	0.34
210542_s_at	**SLCO3A1**	28232	solute carrier organic anion transporter family, member 3A1	-3.00	0.25
222071_s_at	**SLCO4C1**	353189	solute carrier organic anion transporter family, member 4C1	-4.07	0.07
226743_at	**SLFN11**	91607	schlafen family member 11	6.96	0.00
1553055_a_at	**SLFN5**	162394	schlafen family member 5	7.70	0.00
225243_s_at	**SLMAP**	7871	sarcolemma associated protein	-2.36	0.07
222441_x_at	**SLMO2**	51012	slowmo homolog 2 (Drosophila)	2.24	0.00
203021_at	**SLPI**	6590	secretory leukocyte peptidase inhibitor	4.31	0.00
238446_at	**SMA4**	11039	Glucuronidase, beta pseudogene	-6.46	0.03
215043_s_at	**SMA4** /// **SMA5**	11039 /// 11042	glucuronidase, beta pseudogene	-3.53	0.07
205398_s_at	**SMAD3**	4088	SMAD family member 3	9.12	0.00
202527_s_at	**SMAD4**	4089	SMAD family member 4	-2.96	0.16
225282_at	**SMAP1L**	64744	stromal membrane-associated protein 1-like	-2.85	0.00

206542_s_at	**SMARCA2**	6595	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	-5.08	0.00
208793_x_at	**SMARCA4**	6597	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	3.09	0.02
204240_s_at	**SMC2**	10592	structural maintenance of chromosomes 2	2.44	0.16
1558747_at	**SMCHD1**	23347	structural maintenance of chromosomes flexible hinge domain containing 1	-2.35	0.00
210057_at	**SMG1**	23049	PI-3-kinase-related kinase SMG-1	3.74	0.02
209420_s_at	**SMPD1**	6609	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	3.59	0.00
205622_at	**SMPD2**	6610	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	2.02	0.02
230367_at	**SMTNL1**	219537	smoothelin-like 1	2.99	0.00
227489_at	**SMURF2**	64750	SMAD specific E3 ubiquitin protein ligase 2	-4.92	0.16
226683_at	**SNAG1**	112574	Sorting nexin associated golgi protein 1	-6.58	0.00
205443_at	**SNAPC1**	6617	small nuclear RNA activating complex, polypeptide 1, 43kDa	10.53	0.00
201622_at	**SND1**	27044	staphylococcal nuclease and tudor domain containing 1	8.06	0.06
218391_at	**SNF8**	11267	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	2.37	0.02
220358_at	**SNFT**	55509	Jun dimerization protein p21SNFT	14.20	0.00
1564906_at	**SNHG4**	724102	small nucleolar RNA host gene (non-protein coding) 4	3.23	0.00
225155_at	**SNHG5**	387066	small nucleolar RNA host gene (non-protein coding) 5	2.43	0.34
244669_at	**SNHG5 /// SNORD50A**	26799 /// 387066	small nucleolar RNA, C/D box 50A /// small nucleolar RNA host gene (non-protein coding) 5	2.75	0.51
225220_at	**SNHG8**	1E+08	small nucleolar RNA host gene (non-protein coding) 8	4.46	0.02
206055_s_at	**SNRPA1**	6627	small nuclear ribonucleoprotein polypeptide A'	7.77	0.25
202690_s_at	**SNRPD1**	6632	small nuclear ribonucleoprotein D1 polypeptide 16kDa	5.62	0.00
200826_at	**SNRPD2**	6633	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	4.40	0.08
203832_at	**SNRPF**	6636	small nuclear ribonucleoprotein polypeptide F	5.96	0.08
1559343_at	**SNRPN**	6638	Small nuclear ribonucleoprotein polypeptide N	3.32	0.51
224684_at	**SNX12**	29934	sorting nexin 12	2.34	0.34
229980_s_at	**SNX5**	27131	sorting nexin 5	3.62	0.16
223028_s_at	**SNX9**	51429	sorting nexin 9	5.26	0.02
244661_at	**SOAT1**	6646	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-2.58	0.51
210001_s_at	**SOCS1**	8651	suppressor of cytokine signaling 1	60.61	0.00
201563_at	**SORD**	6652	sorbitol dehydrogenase	-4.30	0.13
230707_at	**SORL1**	6653	sortilin-related receptor, L(DLR class) A repeats-containing	-17.56	0.00
212807_s_at	**SORT1**	6272	sortilin 1	2.68	0.16
217644_s_at	**SOS2**	6655	son of sevenless homolog 2 (Drosophila)	-8.29	0.00
213721_at	**SOX2**	6657	SRY (sex determining region Y)-box 2	2.40	0.13
224760_at	**SP1**	6667	Sp1 transcription factor	-3.11	0.00
207777_s_at	**SP140**	11262	SP140 nuclear body protein	3.01	0.06
236265_at	**SP4**	6671	Sp4 transcription factor	2.20	0.51
210117_at	**SPAG1**	6674	sperm associated antigen 1	-5.56	0.07
1553579_a_at	**SPAG11B**	10407	sperm associated antigen 11B	2.19	0.25
221057_at	**SPATA1**	64173	spermatogenesis associated 1	-4.09	0.13
225564_at	**SPATA13**	221178	spermatogenesis associated 13	-3.32	0.51

218164_at	**SPATA20**	64847	spermatogenesis associated 20	2.34	0.08
220298_s_at	**SPATA6**	54558	spermatogenesis associated 6	-2.22	0.16
238262_at	**SPDYA**	245711	speedy homolog A (Drosophila)	2.42	0.06
244461_at	**SPECC1**	92521	sperm antigen with calponin homology and coiled-coil domains 1	-6.70	0.00
201997_s_at	**SPEN**	23013	spen homolog, transcriptional regulator (Drosophila)	-3.49	0.13
212526_at	**SPG20**	23111	spastic paraplegia 20 (Troyer syndrome)	5.42	0.00
219257_s_at	**SPHK1**	8877	sphingosine kinase 1	49.30	0.06
222431_at	**SPIN1**	10927	spindlin 1	3.98	0.79
206239_s_at	**SPINK1**	6690	serine peptidase inhibitor, Kazal type 1	23.64	0.02
206318_at	**SPINLW1**	57119	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	2.88	0.25
210715_s_at	**SPINT2**	10653	serine peptidase inhibitor, Kunitz type, 2	5.82	0.00
223173_at	**SPNS1**	83985	spinster homolog 1 (Drosophila)	13.12	0.08
209875_s_at	**SPP1**	6696	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	13.15	0.00
226353_at	**SPPL2A**	84888	signal peptide peptidase-like 2A	3.85	0.00
203458_at	**SPR**	6697	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	7.32	0.25
226837_at	**SPRED1**	161742	sprouty-related, EVH1 domain containing 1	42.35	0.79
46256_at	**SPSB3**	90864	splA/ryanodine receptor domain and SOCS box containing 3	-3.63	0.00
202277_at	**SPTLC1**	10558	serine palmitoyltransferase, long chain base subunit 1	2.46	0.51
203128_at	**SPTLC2**	9517	serine palmitoyltransferase, long chain base subunit 2	-4.12	0.03
201471_s_at	**SQSTM1**	8878	sequestosome 1	4.31	0.00
219055_at	**SRBD1**	55133	S1 RNA binding domain 1	2.43	0.16
213324_at	**SRC**	6714	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	14.96	0.08
208095_s_at	**SRP72**	6731	signal recognition particle 72kDa	8.55	0.08
202200_s_at	**SRPK1**	6732	SFRS protein kinase 1	-7.76	0.00
203182_s_at	**SRPK2**	6733	SFRS protein kinase 2	-6.86	0.00
201138_s_at	**SSB**	6741	Sjogren syndrome antigen B (autoantigen La)	4.46	0.00
202591_s_at	**SSBP1**	6742	single-stranded DNA binding protein 1	4.88	0.02
203787_at	**SSBP2**	23635	single-stranded DNA binding protein 2	-3.74	0.79
221752_at	**SSH1**	54434	Slingshot homolog 1 (Drosophila)	-4.13	0.25
226080_at	**SSH2**	85464	slingshot homolog 2 (Drosophila)	-9.30	0.00
200652_at	**SSR2**	6746	signal sequence receptor, beta (translocon-associated protein beta)	2.15	0.06
222411_s_at	**SSR3**	6747	signal sequence receptor, gamma (translocon-associated protein gamma)	2.35	0.25
207040_s_at	**ST13**	6767	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	4.54	0.00
206135_at	**ST18**	9705	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	2.14	0.34
203759_at	**ST3GAL4**	6484	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-3.51	0.51
203217_s_at	**ST3GAL5**	8869	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	7.84	0.00
204542_at	**ST6GALNAC2**	10610	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	-10.47	0.00
206925_at	**ST8SIA4**	7903	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	-3.08	0.00
213820_s_at	**STARD5**	80765	StAR-related lipid transfer (START) domain containing 5	-8.77	0.16

200028_s_at	**STARD7**	56910	StAR-related lipid transfer (START) domain containing 7	2.31	0.06
206868_at	**STARD8**	9754	StAR-related lipid transfer (START) domain containing 8	4.51	0.08
200887_s_at	**STAT1**	6772	signal transducer and activator of transcription 1, 91kDa	2.28	0.00
225636_at	**STAT2**	6773	signal transducer and activator of transcription 2, 113kDa	2.03	0.00
206118_at	**STAT4**	6775	signal transducer and activator of transcription 4	12.58	0.16
205026_at	**STAT5B**	6777	signal transducer and activator of transcription 5B	-7.52	0.00
202557_at	**STCH**	6782	stress 70 protein chaperone, microsome-associated, 60kDa	12.71	0.00
202764_at	**STIM1**	6786	stromal interaction molecule 1	-2.17	0.51
213330_s_at	**STIP1**	10963	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	2.92	0.79
202695_s_at	**STK17A**	9263	serine/threonine kinase 17a	-5.43	0.13
205214_at	**STK17B**	9262	serine/threonine kinase 17b	-4.48	0.00
204068_at	**STK3**	6788	serine/threonine kinase 3 (STE20 homolog, yeast)	3.03	0.00
212572_at	**STK38L**	23012	serine/threonine kinase 38 like	-3.35	0.13
223746_at	**STK4**	6789	serine/threonine kinase 4	-2.91	0.13
201061_s_at	**STOM**	2040	stomatin	6.07	0.00
33736_at	**STOML1**	9399	stomatin (EPB72)-like 1	2.27	0.06
1558002_at	**STRAP**	11171	Serine/threonine kinase receptor associated protein	-4.63	0.03
205520_at	**STRN**	6801	striatin, calmodulin binding protein	-3.61	0.00
202223_at	**STT3A**	3703	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	3.45	0.34
212625_at	**STX10**	8677	syntaxin 10	-4.53	0.25
212112_s_at	**STX12**	23673	syntaxin 12	2.08	0.08
221499_s_at	**STX16**	8675	syntaxin 16	-5.41	0.00
203530_s_at	**STX4**	6810	syntaxin 4	3.17	0.00
230560_at	**STXBP6**	29091	syntaxin binding protein 6 (amisyn)	2.24	0.79
224309_s_at	**SUGT1**	10910	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	2.19	0.16
224724_at	**SULF2**	55959	sulfatase 2	-7.80	0.00
203615_x_at	**SULT1A1**	6817	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	-7.29	0.03
211385_x_at	**SULT1A2**	6799	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	-7.10	0.08
209607_x_at	**SULT1A3 /// SULT1A4**	445329 /// 6818	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	-4.10	0.07
207601_at	**SULT1B1**	27284	sulfotransferase family, cytosolic, 1B, member 1	-9.05	0.16
222979_s_at	**SURF4**	6836	surfeit 4	3.22	0.06
222759_at	**SUV420H1**	51111	suppressor of variegation 4-20 homolog 1 (Drosophila)	-2.06	0.25
202565_s_at	**SVIL**	6840	supervillin	-2.99	0.03
226068_at	**SYK**	6850	spleen tyrosine kinase	-3.15	0.00
217834_s_at	**SYNCRIP**	10492	synaptotagmin binding, cytoplasmic RNA interacting protein	3.27	0.02
209447_at	**SYNE1**	23345	spectrin repeat containing, nuclear envelope 1	-10.12	0.07
1558392_at	**SYNE2**	23224	spectrin repeat containing, nuclear envelope 2	-8.54	0.03
225895_at	**SYNPO2**	171024	synaptopodin 2	3.53	0.16
243313_at	**SYNPO2L**	79933	synaptopodin 2-like	2.10	0.02

224669_at	**SYS1**	90196	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	3.26	0.02
1560879_a_at	**SYT15**	83849	synaptotagmin XV	2.29	0.06
1555053_at	**SYT9**	143425	synaptotagmin IX	-2.18	0.51
238423_at	**SYTL3**	94120	synaptotagmin-like 3	-3.16	0.13
217437_s_at	**TACC1**	6867	transforming, acidic coiled-coil containing protein 1	-2.33	0.13
218308_at	**TACC3**	10460	transforming, acidic coiled-coil containing protein 3	-9.19	0.00
205966_at	**TAF13**	6884	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	3.42	0.00
235154_at	**TAF3**	83860	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	2.48	0.16
213090_s_at	**TAF4**	6874	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	-4.33	0.51
203893_at	**TAF9**	6880	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	10.52	0.00
1555724_s_at	**TAGLN**	6876	transgelin	2.32	0.06
210978_s_at	**TAGLN2**	8407	transgelin 2	-3.39	0.00
225308_s_at	**TANC1**	85461	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	-2.09	0.25
210458_s_at	**TANK**	10010	TRAF family member-associated NFKB activator	2.12	0.00
204770_at	**TAP2**	6891	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	3.27	0.00
221264_s_at	**TARDBP**	23435	TAR DNA binding protein	-3.05	0.03
216920_s_at	**TARP /// TRGC2 /// TRGV9**	445347 /// 6967 /// 6983	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading frame protein	10.42	0.06
201263_at	**TARS**	6897	threonyl-tRNA synthetase	2.95	0.25
221397_at	**TAS2R10**	50839	taste receptor, type 2, member 10	-2.09	0.34
1553556_at	**TAS2R40**	259286	taste receptor, type 2, member 40	-13.58	0.00
203977_at	**TAZ**	6901	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	-2.98	0.16
228258_at	**TBC1D10C**	374403	TBC1 domain family, member 10C	-10.98	0.13
224622_at	**TBC1D14**	57533	TBC1 domain family, member 14	-4.62	0.16
222173_s_at	**TBC1D2**	55357	TBC1 domain family, member 2	3.00	0.34
223375_at	**TBC1D22B**	55633	TBC1 domain family, member 22B	2.73	0.16
201814_at	**TBC1D5**	9779	TBC1 domain family, member 5	-2.07	0.51
223461_at	**TBC1D7**	51256	TBC1 domain family, member 7	6.60	0.02
203667_at	**TBCA**	6902	tubulin folding cofactor A	3.00	0.06
218520_at	**TBK1**	29110	TANK-binding kinase 1	2.65	0.00
201868_s_at	**TBL1X**	6907	transducin (beta)-like 1X-linked	-3.30	0.00
212685_s_at	**TBL2**	26608	transducin (beta)-like 2	15.11	0.25
207689_at	**TBX10**	347853	T-box 10	2.10	0.06
208130_s_at	**TBXAS1**	6916	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	-5.23	0.00
213142_x_at	**tcag7.1314**	54103	hypothetical protein LOC54103	23.72	0.00
238678_at	**tcag7.907**	402483	hypothetical LOC402483	-6.34	0.03
202824_s_at	**TCEB1**	6921	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	2.37	0.00
213604_at	**TCEB3**	6924	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	2.90	0.00
202396_at	**TCERG1**	10915	transcription elongation regulator 1	2.57	0.34
209152_s_at	**TCF3**	6929	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	3.12	0.06
204849_at	**TCFL5**	10732	transcription factor-like 5 (basic helix-loop-helix)	4.18	0.13

221624_at	**TCL6**	27004	T-cell leukemia/lymphoma 6	2.65	0.00
222011_s_at	**TCP1**	6950	t-complex 1	4.64	0.06
1553861_at	**TCP11L2**	255394	t-complex 11 (mouse)-like 2	-40.61	0.00
203743_s_at	**TDG**	6996	thymine-DNA glycosylase	2.31	0.51
232692_at	**TDRD6**	221400	tudor domain containing 6	14.36	0.34
213361_at	**TDRD7**	23424	tudor domain containing 7	2.28	0.16
218104_at	**TEX10**	54881	testis expressed 10	3.68	0.08
212083_at	**TEX261**	113419	testis expressed 261	4.62	0.13
50221_at	**TFEB**	7942	transcription factor EB	-3.47	0.34
232383_at	**TFEC**	22797	transcription factor EC	66.48	0.00
217839_at	**TFG**	10342	TRK-fused gene	3.34	0.00
202750_s_at	**TFIP11**	24144	tuftelin interacting protein 11	2.78	0.34
207332_s_at	**TFRC**	7037	transferrin receptor (p90, CD71)	11.88	0.06
205016_at	**TGFA**	7039	transforming growth factor, alpha	-2.73	0.25
208944_at	**TGFBR2**	7048	transforming growth factor, beta receptor II (70/80kDa)	-4.45	0.00
203313_s_at	**TGIF1**	7050	TGFB-induced factor homeobox 1	6.83	0.00
216262_s_at	**TGIF2**	60436	TGFB-induced factor homeobox 2	6.18	0.08
201042_at	**TGM2**	7052	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	14.23	0.02
225261_x_at	**TH1L**	51497	TH1-like (Drosophila)	3.17	0.16
203887_s_at	**THBD**	7056	thrombomodulin	-3.16	0.07
204565_at	**THEM2**	55856	thioesterase superfamily member 2	2.37	0.16
226320_at	**THOC4**	10189	THO complex 4	3.34	0.02
225730_s_at	**THUMPD3**	25917	THUMP domain containing 3	9.36	0.02
223711_s_at	**THYN1**	29087	thymocyte nuclear protein 1	-2.34	0.34
228234_at	**TICAM2**	353376	toll-like receptor adaptor molecule 2	4.10	0.16
238858_at	**TIFA**	92610	TRAF-interacting protein with a forkhead-associated domain	9.74	0.00
229789_at	**TIGD3**	220359	tigger transposable element derived 3	-21.53	0.00
203046_s_at	**TIMELESS**	8914	timeless homolog (Drosophila)	2.39	0.13
1555764_s_at	**TIMM10**	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)	10.20	0.00
201821_s_at	**TIMM17A**	10440	translocase of inner mitochondrial membrane 17 homolog A (yeast)	5.12	0.00
225535_s_at	**TIMM23**	10431	translocase of inner mitochondrial membrane 23 homolog (yeast)	3.67	0.25
218119_at	**TIMM23 /// TIMM23B**	10431 /// 653252	translocase of inner mitochondrial membrane 23 homolog (yeast) /// translocase of inner mitochondrial membrane 23 homolog B (yeast)	3.43	0.02
231579_s_at	**TIMP2**	7077	TIMP metallopeptidase inhibitor 2	-3.03	0.00
221857_s_at	**TJAP1**	93643	tight junction associated protein 1 (peripheral)	11.08	0.02
208700_s_at	**TKT**	7086	transketolase (Wernicke-Korsakoff syndrome)	-8.50	0.00
204872_at	**TLE4**	7091	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	-2.22	0.03
210176_at	**TLR1**	7096	toll-like receptor 1	-3.28	0.00
223750_s_at	**TLR10**	81793	toll-like receptor 10	-3.60	0.25
210166_at	**TLR5**	7100	toll-like receptor 5	-8.54	0.03
207446_at	**TLR6**	10333	toll-like receptor 6	-6.05	0.03
229560_at	**TLR8**	51311	toll-like receptor 8	-2.30	0.00
213351_s_at	**TMCC1**	23023	transmembrane and coiled-coil domain family 1	-4.35	0.34
226489_at	**TMCC3**	57458	transmembrane and coiled-coil domain family 3	-5.59	0.00
226050_at	**TMCO3**	55002	transmembrane and coiled-coil domains 3	-6.70	0.07
200929_at	**TMED10**	10972	transmembrane emp24-like trafficking protein 10 (yeast)	3.01	0.06

202194_at	**TMED5**	50999	transmembrane emp24 protein transport domain containing 5	2.27	0.16
209404_s_at	**TMED7**	51014	transmembrane emp24 protein transport domain containing 7	2.70	0.02
225343_at	**TMED8**	283578	transmembrane emp24 protein transport domain containing 8	-2.25	0.79
205812_s_at	**TMED9**	54732	transmembrane emp24 protein transport domain containing 9	2.57	0.00
223277_at	**TMEM103**	54859	transmembrane protein 103	2.99	0.79
221622_s_at	**TMEM126B**	55863	transmembrane protein 126B	4.12	0.00
225462_at	**TMEM128**	85013	transmembrane protein 128	2.57	0.79
225588_s_at	**TMEM129**	92305	transmembrane protein 129	-2.55	0.51
219690_at	**TMEM149**	79713	transmembrane protein 149	2.06	0.13
226752_at	**TMEM157**	345757	transmembrane protein 157	-8.26	0.00
213338_at	**TMEM158**	25907	transmembrane protein 158	32.16	0.00
223202_s_at	**TMEM164**	84187	transmembrane protein 164	-2.34	0.00
224906_at	**TMEM16F**	196527	transmembrane protein 16F	2.60	0.06
227586_at	**TMEM170**	124491	transmembrane protein 170	2.32	0.51
220532_s_at	**TMEM176B**	28959	transmembrane protein 176B	6.54	0.13
218113_at	**TMEM2**	23670	transmembrane protein 2	-4.71	0.00
218772_x_at	**TMEM38B**	55151	transmembrane protein 38B	3.41	0.13
241392_at	**TMEM39A**	55254	Transmembrane protein 39A	2.97	0.34
202857_at	**TMEM4**	10330	transmembrane protein 4	8.39	0.00
217795_s_at	**TMEM43**	79188	transmembrane protein 43	-3.03	0.00
217766_s_at	**TMEM50A**	23585	transmembrane protein 50A	-2.27	0.07
226338_at	**TMEM55A**	55529	transmembrane protein 55A	-3.64	0.00
225287_s_at	**TMEM55B**	90809	transmembrane protein 55B	2.18	0.08
223396_at	**TMEM60**	85025	transmembrane protein 60	2.52	0.00
241342_at	**TMEM65**	157378	transmembrane protein 65	-5.09	0.25
238429_at	**TMEM71**	137835	transmembrane protein 71	-36.83	0.00
212204_at	**TMEM87A**	25963	transmembrane protein 87A	2.76	0.00
229957_at	**TMEM91**	641649	transmembrane protein 91	-5.01	0.00
222449_at	**TMEPAI**	56937	transmembrane, prostate androgen induced RNA	-2.65	0.03
219701_at	**TMOD2**	29767	tropomodulin 2 (neuronal)	-2.48	0.79
217733_s_at	**TMSB10**	9168	thymosin, beta 10	2.97	0.00
207113_s_at	**TNF**	7124	tumor necrosis factor (TNF superfamily, member 2)	9.44	0.00
202643_s_at	**TNFAIP3**	7128	tumor necrosis factor, alpha-induced protein 3	24.68	0.00
206025_s_at	**TNFAIP6**	7130	tumor necrosis factor, alpha-induced protein 6	8.24	0.00
231775_at	**TNFRSF10A**	8797	tumor necrosis factor receptor superfamily, member 10a	7.57	0.00
206222_at	**TNFRSF10C**	8794	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	-31.72	0.00
207536_s_at	**TNFRSF9**	3604	tumor necrosis factor receptor superfamily, member 9	2.13	0.34
221085_at	**TNFSF15**	9966	tumor necrosis factor (ligand) superfamily, member 15	15.80	0.00
207216_at	**TNFSF8**	944	tumor necrosis factor (ligand) superfamily, member 8	7.34	0.00
217931_at	**TNRC5**	10695	trinucleotide repeat containing 5	-4.13	0.03
240044_x_at	**TNRC6B**	23112	Trinucleotide repeat containing 6B	-4.89	0.00
228834_at	**TOB1**	10140	transducer of ERBB2, 1	-2.16	0.79
233881_s_at	**TOLLIP**	54472	toll interacting protein	2.60	0.16
202807_s_at	**TOM1**	10043	target of myb1 (chicken)	3.36	0.02
204485_s_at	**TOM1L1**	10040	target of myb1 (chicken)-like 1	2.19	0.25
226198_at	**TOM1L2**	146691	target of myb1-like 2 (chicken)	-9.18	0.00

212773_s_at	**TOMM20**	9804	translocase of outer mitochondrial membrane 20 homolog (yeast)	5.02	0.08
222474_s_at	**TOMM22**	56993	translocase of outer mitochondrial membrane 22 homolog (yeast)	3.54	0.06
226059_at	**TOMM40L**	84134	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	5.91	0.13
201512_s_at	**TOMM70A**	9868	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	6.50	0.13
202633_at	**TOPBP1**	11073	topoisomerase (DNA) II binding protein 1	-2.77	0.79
204071_s_at	**TOPORS**	10210	topoisomerase I binding, arginine/serine-rich	-4.25	0.00
201746_at	**TP53**	7157	tumor protein p53 (Li-Fraumeni syndrome)	3.55	0.25
203050_at	**TP53BP1**	7158	tumor protein p53 binding protein 1	3.52	0.00
203421_at	**TP53I11**	9537	tumor protein p53 inducible protein 11	-4.12	0.00
225912_at	**TP53INP1**	94241	tumor protein p53 inducible nuclear protein 1	-4.48	0.00
235194_at	**TPCN2**	219931	two pore segment channel 2	-3.78	0.03
214365_at	**TPM3**	7170	tropomyosin 3	-5.62	0.13
200742_s_at	**TPP1**	1200	tripeptidyl peptidase I	4.04	0.00
201730_s_at	**TPR**	7175	translocated promoter region (to activated MET oncogene)	-3.15	0.00
204140_at	**TPST1**	8460	tyrosylprotein sulfotransferase 1	-5.91	0.51
1556876_s_at	**TPTEps1**	440140	TPTE pseudogene 1	2.23	0.51
216191_s_at	**TRA@ /// TRD@**	6955 /// 6964	T cell receptor alpha locus /// T cell receptor delta locus	12.84	0.51
226839_at	**TRA16**	126382	TR4 orphan receptor associated protein TRA16	2.50	0.16
235116_at	**TRAF1**	7185	TNF receptor-associated factor 1	38.73	0.02
208315_x_at	**TRAF3**	7187	TNF receptor-associated factor 3	5.07	0.06
213888_s_at	**TRAF3IP3**	80342	TRAF3 interacting protein 3	-6.56	0.07
243196_s_at	**TRAFD1**	10906	TRAF-type zinc finger domain containing 1	2.30	0.00
201399_s_at	**TRAM1**	23471	translocation associated membrane protein 1	2.86	0.00
203511_s_at	**TRAPPC3**	27095	trafficking protein particle complex 3	2.93	0.08
229016_s_at	**TRERF1**	55809	transcriptional regulating factor 1	-17.92	0.07
218145_at	**TRIB3**	57761	tribbles homolog 3 (Drosophila)	12.89	0.08
231934_at	**TRIM14**	9830	tripartite motif-containing 14	2.52	0.34
210994_x_at	**TRIM23**	373	tripartite motif-containing 23	-4.35	0.03
242812_at	**TRIM26**	7726	Tripartite motif-containing 26	3.78	0.16
210705_s_at	**TRIM5**	85363	tripartite motif-containing 5	2.07	0.25
1568592_at	**TRIM69**	140691	tripartite motif-containing 69	2.25	0.00
221012_s_at	**TRIM8**	81603	tripartite motif-containing 8	-4.98	0.00
202734_at	**TRIP10**	9322	thyroid hormone receptor interactor 10	7.34	0.00
218617_at	**TRIT1**	54802	tRNA isopentenyltransferase 1	2.80	0.08
222768_s_at	**TRMT6**	51605	tRNA methyltransferase 6 homolog (S. cerevisiae)	13.31	0.00
240389_at	**TRPM6**	140803	Transient receptor potential cation channel, subfamily M, member 6	-12.35	0.00
223324_s_at	**TRPM7**	54822	transient receptor potential cation channel, subfamily M, member 7	8.34	0.00
215111_s_at	**TSC22D1**	8848	TSC22 domain family, member 1	6.61	0.06
204094_s_at	**TSC22D2**	9819	TSC22 domain family, member 2	2.17	0.06
208763_s_at	**TSC22D3**	1831	TSC22 domain family, member 3	-4.27	0.00
218132_s_at	**TSEN34**	79042	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	-2.76	0.07
214331_at	**TSFM**	10102	Ts translation elongation factor, mitochondrial	-4.31	0.13
233236_at	**TSPAN16**	26526	tetraspanin 16	-8.09	0.03
225235_at	**TSPAN17**	26262	tetraspanin 17	8.69	0.00
227233_at	**TSPAN2**	10100	tetraspanin 2	-9.62	0.07
218156_s_at	**TSR1**	55720	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	3.40	0.16
209605_at	**TST**	7263	thiosulfate sulfurtransferase (rhodanese)	-17.83	0.34

201434_at	**TTC1**	7265	tetratricopeptide repeat domain 1	3.12	0.02
1554672_at	**TTC26**	79989	tetratricopeptide repeat domain 26	2.22	0.06
208663_s_at	**TTC3**	7267	tetratricopeptide repeat domain 3	2.58	0.51
203584_at	**TTC35**	9694	tetratricopeptide repeat domain 35	5.02	0.00
226120_at	**TTC8**	123016	tetratricopeptide repeat domain 8	-2.62	0.25
209118_s_at	**TUBA1A**	7846	tubulin, alpha 1a	-2.31	0.00
207490_at	**TUBA4B**	80086	tubulin, alpha 4b (pseudogene)	-2.88	0.00
204141_at	**TUBB2A**	7280	tubulin, beta 2A	21.28	0.13
209191_at	**TUBB6**	84617	tubulin, beta 6	13.04	0.34
201113_at	**TUFM**	7284	Tu translation elongation factor, mitochondrial	2.24	0.16
201745_at	**TWF1**	5756	twinfilin, actin-binding protein, homolog 1 (Drosophila)	2.25	0.79
225406_at	**TWSG1**	57045	twisted gastrulation homolog 1 (Drosophila)	4.63	0.06
231169_at	**TXLNA**	200081	Taxilin alpha	3.46	0.02
1552822_at	**TXNDC10**	54495	thioredoxin domain containing 10	2.22	0.25
201580_s_at	**TXNDC13**	56255	thioredoxin domain containing 13	-4.80	0.00
201175_at	**TXNDC14**	51075	thioredoxin domain containing 14	8.58	0.08
201008_s_at	**TXNIP**	10628	thioredoxin interacting protein	-2.37	0.00
201588_at	**TXNL1**	9352	thioredoxin-like 1	2.47	0.00
205546_s_at	**TYK2**	7297	tyrosine kinase 2	-2.16	0.08
209340_at	**UAP1**	6675	UDP-N-acteylglucosamine pyrophosphorylase 1	6.31	0.51
205890_s_at	**UBD**	10537	ubiquitin D	77.53	0.00
203281_s_at	**UBE1L**	7318	ubiquitin-activating enzyme E1-like	-2.70	0.08
224118_at	**UBE2B**	7320	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	-2.66	0.79
212519_at	**UBE2E1**	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	3.27	0.00
209041_s_at	**UBE2G2**	7327	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	4.24	0.25
217823_s_at	**UBE2J1**	51465	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	-2.43	0.03
201649_at	**UBE2L6**	9246	ubiquitin-conjugating enzyme E2L 6	2.69	0.00
201524_x_at	**UBE2N**	7334	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	2.08	0.13
209096_at	**UBE2V2**	7336	ubiquitin-conjugating enzyme E2 variant 2	4.23	0.00
217750_s_at	**UBE2Z**	65264	ubiquitin-conjugating enzyme E2Z	5.55	0.06
211285_s_at	**UBE3A**	7337	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	2.50	0.16
202317_s_at	**UBE4B**	10277	ubiquitination factor E4B (UFD2 homolog, yeast)	-3.01	0.00
207253_s_at	**UBN1**	29855	ubinuclein 1	-2.49	0.00
224513_s_at	**UBQLN4**	56893	ubiquilin 4	9.95	0.13
238528_at	**UBR1**	197131	ubiquitin protein ligase E3 component n-recognin 1	8.81	0.00
212756_s_at	**UBR2**	23304	ubiquitin protein ligase E3 component n-recognin 2	-4.45	0.00
1555888_at	**UBR5**	51366	Ubiquitin protein ligase E3 component n-recognin 5	-7.64	0.00
223012_at	**UBXD1**	80700	UBX domain containing 1	-2.08	0.34
215983_s_at	**UBXD6**	7993	UBX domain containing 6	8.18	0.79
204616_at	**UCHL3**	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	3.45	0.51
208998_at	**UCP2**	7351	uncoupling protein 2 (mitochondrial, proton carrier)	4.99	0.51
217797_at	**UFC1**	51506	ubiquitin-fold modifier conjugating enzyme 1	2.92	0.02
218050_at	**UFM1**	51569	ubiquitin-fold modifier 1	3.22	0.00

224967_at	**UGCG**	7357	UDP-glucose ceramide glucosyltransferase	2.01	0.00
205480_s_at	**UGP2**	7360	UDP-glucose pyrophosphorylase 2	2.36	0.02
220746_s_at	**UIMC1**	51720	ubiquitin interaction motif containing 1	-2.80	0.07
209333_at	**ULK1**	8408	unc-51-like kinase 1 (C. elegans)	-4.34	0.16
228219_s_at	**UPB1**	51733	ureidopropionase, beta	7.62	0.06
218757_s_at	**UPF3B**	65109	UPF3 regulator of nonsense transcripts homolog B (yeast)	2.38	0.79
203234_at	**UPP1**	7378	uridine phosphorylase 1	5.13	0.13
217935_s_at	**UQCC**	55245	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)	2.23	0.34
200883_at	**UQCRC2**	7385	ubiquinol-cytochrome c reductase core protein II	2.86	0.13
202233_s_at	**UQCRH**	7388	ubiquinol-cytochrome c reductase hinge protein	2.52	0.00
218601_at	**URG4**	55665	up-regulated gene 4	2.44	0.51
208101_s_at	**URM1**	81605	ubiquitin related modifier 1 homolog (S. cerevisiae)	2.43	0.51
209137_s_at	**USP10**	9100	ubiquitin specific peptidase 10	-3.30	0.00
226567_at	**USP14**	9097	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	5.39	0.16
218386_x_at	**USP16**	10600	ubiquitin specific peptidase 16	2.45	0.25
224978_s_at	**USP36**	57602	ubiquitin specific peptidase 36	7.11	0.25
223289_s_at	**USP38**	84640	ubiquitin specific peptidase 38	-3.59	0.79
202682_s_at	**USP4**	7375	ubiquitin specific peptidase 4 (proto-oncogene)	-2.60	0.00
218235_s_at	**UTP11L**	51118	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	6.89	0.00
228050_at	**UTP15**	84135	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	8.60	0.06
203721_s_at	**UTP18**	51096	UTP18, small subunit (SSU) processome component, homolog (yeast)	8.67	0.02
203241_at	**UVRAG**	7405	UV radiation resistance associated gene	4.17	0.00
225583_at	**UXS1**	80146	UDP-glucuronate decarboxylase 1	10.89	0.02
204929_s_at	**VAMP5**	10791	vesicle-associated membrane protein 5 (myobrevin)	14.16	0.00
202546_at	**VAMP8**	8673	vesicle-associated membrane protein 8 (endobrevin)	6.44	0.00
226063_at	**VAV2**	7410	vav 2 guanine nucleotide exchange factor	2.50	0.79
212038_s_at	**VDAC1**	7416	voltage-dependent anion channel 1	6.10	0.34
211662_s_at	**VDAC2**	7417	voltage-dependent anion channel 2	2.34	0.13
201831_s_at	**VDP**	8615	vesicle docking protein p115	2.72	0.02
211527_x_at	**VEGFA**	7422	vascular endothelial growth factor A	14.01	0.00
209950_s_at	**VILL**	50853	villin-like	4.49	0.25
235751_s_at	**VMO1**	284013	vitelline membrane outer layer 1 homolog (chicken)	5.08	0.00
205922_at	**VNN2**	8875	vanin 2	-3.33	0.00
220528_at	**VNN3**	55350	vanin 3	-8.54	0.00
218396_at	**VPS13C**	54832	vacuolar protein sorting 13 homolog C (S. cerevisiae)	5.87	0.00
223346_at	**VPS18**	57617	vacuolar protein sorting 18 homolog (S. cerevisiae)	3.18	0.13
225483_at	**VPS26B**	112936	vacuolar protein sorting 26 homolog B (S. pombe)	-4.18	0.25
209553_at	**VPS8**	23355	vacuolar protein sorting 8 homolog (S. cerevisiae)	-2.28	0.79
200628_s_at	**WARS**	7453	tryptophanyl-tRNA synthetase	8.32	0.00
38964_r_at	**WAS**	7454	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	-2.05	0.34
224563_at	**WASF2**	10163	WAS protein family, member 2	-2.97	0.25
217975_at	**WBP5**	51186	WW domain binding protein 5	3.64	0.34

233559_s_at	**WDFY1**	57590	WD repeat and FYVE domain containing 1	2.71	0.25
224897_at	**WDR26**	80232	WD repeat domain 26	-2.34	0.00
238677_at	**WDR36**	134430	WD repeat domain 36	6.12	0.08
222503_s_at	**WDR41**	55255	WD repeat domain 41	2.47	0.51
216885_s_at	**WDR42A**	50717	WD repeat domain 42A	-2.49	0.16
65591_at	**WDR48**	57599	WD repeat domain 48	2.63	0.51
226283_at	**WDR51B**	282809	WD repeat domain 51B	-2.55	0.34
201420_s_at	**WDR77**	79084	WD repeat domain 77	4.35	0.25
225676_s_at	**WDSOF1**	25879	WD repeats and SOF1 domain containing	7.78	0.08
224076_s_at	**WHSC1L1**	54904	Wolf-Hirschhorn syndrome candidate 1-like 1	-4.25	0.03
203112_s_at	**WHSC2**	7469	Wolf-Hirschhorn syndrome candidate 2	2.05	0.51
224465_s_at	**WIBG**	84305	within bgcn homolog (Drosophila)	2.98	0.51
213836_s_at	**WIPI1**	55062	WD repeat domain, phosphoinositide interacting 1	-7.65	0.00
204710_s_at	**WIPI2**	26100	WD repeat domain, phosphoinositide interacting 2	-3.41	0.00
224022_x_at	**WNT16**	51384	wingless-type MMTV integration site family, member 16	2.21	0.16
222489_s_at	**WRNIP1**	56897	Werner helicase interacting protein 1	2.03	0.25
203137_at	**WTAP**	9589	Wilms tumor 1 associated protein	2.89	0.00
219520_s_at	**WWC3**	55841	WWC family member 3	-6.29	0.13
210695_s_at	**WWOX**	51741	WW domain containing oxidoreductase	2.11	0.34
228617_at	**XAF1**	54739	XIAP associated factor-1	5.94	0.00
200670_at	**XBP1**	7494	X-box binding protein 1	19.73	0.00
218753_at	**XKR8**	55113	XK, Kell blood group complex subunit-related family, member 8	-4.53	0.34
209375_at	**XPC**	7508	xeroderma pigmentosum, complementation group C	-2.56	0.34
209045_at	**XPNPEP1**	7511	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	12.06	0.13
214784_x_at	**XPO6**	23214	exportin 6	-6.30	0.00
200792_at	**XRCC6**	2547	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)	2.71	0.06
218069_at	**XTP3TPA**	79077	XTP3-transactivated protein A	2.46	0.16
212048_s_at	**YARS**	8565	tyrosyl-tRNA synthetase	4.71	0.51
208628_s_at	**YBX1**	4904	Y box binding protein 1	2.71	0.00
37079_at	**YDD19**	11049	YDD19 protein	4.61	0.51
212341_at	**YIPF6**	286451	Yip1 domain family, member 6	2.30	0.00
227020_at	**YPEL2**	388403	yippee-like 2 (Drosophila)	-9.19	0.13
223179_at	**YPEL3**	83719	yippee-like 3 (Drosophila)	-13.82	0.00
218647_s_at	**YRDC**	79693	yrdC domain containing (E. coli)	5.88	0.34
217812_at	**YTHDF2**	51441	YTH domain family, member 2	2.66	0.00
222985_at	**YWHAG**	7532	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	2.76	0.00
213699_s_at	**YWHAQ**	10971	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	2.27	0.25
224264_x_at	**ZAN**	7455	zonadhesin	2.27	0.51
213376_at	**ZBTB1**	22890	zinc finger and BTB domain containing 1	3.39	0.00
205340_at	**ZBTB24**	9841	zinc finger and BTB domain containing 24	2.98	0.16
227111_at	**ZBTB34**	403341	zinc finger and BTB domain containing 34	-3.06	0.03
226148_at	**ZBTB44**	29068	zinc finger and BTB domain containing 44	-6.41	0.00
227329_at	**ZBTB46**	140685	zinc finger and BTB domain containing 46	9.55	0.25
205853_at	**ZBTB7B**	51043	zinc finger and BTB domain containing 7B	-2.55	0.08
218810_at	**ZC3H12A**	80149	zinc finger CCCH-type containing 12A	2.19	0.08

231899_at	**ZC3H12C**	85463	zinc finger CCCH-type containing 12C	11.20	0.51
201593_s_at	**ZC3H15**	55854	zinc finger CCCH-type containing 15	2.15	0.00
221193_s_at	**ZCCHC10**	54819	zinc finger, CCHC domain containing 10	5.38	0.00
220933_s_at	**ZCCHC6**	79670	zinc finger, CCHC domain containing 6	-2.14	0.00
212982_at	**ZDHHC17**	23390	zinc finger, DHHC-type containing 17	-2.58	0.07
231908_at	**ZDHHC18**	84243	zinc finger, DHHC-type containing 18	-2.90	0.07
222731_at	**ZDHHC2**	51201	zinc finger, DHHC-type containing 2	-2.81	0.16
224858_at	**ZDHHC5**	25921	zinc finger, DHHC-type containing 5	2.15	0.06
203603_s_at	**ZEB2**	9839	zinc finger E-box binding homeobox 2	3.46	0.00
202456_s_at	**ZER1**	10444	zer-1 homolog (C. elegans)	-10.50	0.07
226168_at	**ZFAND2B**	130617	zinc finger, AN1-type domain 2B	-2.20	0.25
217781_s_at	**ZFP106**	64397	zinc finger protein 106 homolog (mouse)	-2.23	0.07
211962_s_at	**ZFP36L1**	677	zinc finger protein 36, C3H type-like 1	-2.36	0.00
201368_at	**ZFP36L2**	678	zinc finger protein 36, C3H type-like 2	-3.92	0.00
231236_at	**ZFP57**	346171	zinc finger protein 57 homolog (mouse)	-2.26	0.00
213073_at	**ZFYVE26**	23503	zinc finger, FYVE domain containing 26	4.61	0.08
226344_at	**ZMAT1**	84460	zinc finger, matrin type 1	2.01	0.79
210281_s_at	**ZMYM2**	7750	zinc finger, MYM-type 2	-2.89	0.13
219924_s_at	**ZMYM6**	9204	zinc finger, MYM-type 6	2.26	0.34
1560854_s_at	**ZNF107**	51427	zinc finger protein 107	-8.51	0.07
204523_at	**ZNF140**	7699	zinc finger protein 140	4.28	0.16
200050_at	**ZNF146**	7705	zinc finger protein 146	2.57	0.02
208019_at	**ZNF157**	7712	zinc finger protein 157	2.19	0.06
226787_at	**ZNF18**	7566	zinc finger protein 18	-6.45	0.51
213452_at	**ZNF184**	7738	zinc finger protein 184	6.01	0.02
203585_at	**ZNF185**	7739	zinc finger protein 185 (LIM domain)	-11.87	0.00
213218_at	**ZNF187**	7741	zinc finger protein 187	-2.37	0.08
207513_s_at	**ZNF189**	7743	zinc finger protein 189	2.23	0.25
203739_at	**ZNF217**	7764	zinc finger protein 217	-5.07	0.00
218005_at	**ZNF22**	7570	zinc finger protein 22 (KOX 15)	2.60	0.79
212774_at	**ZNF238**	10472	zinc finger protein 238	-3.80	0.00
206862_at	**ZNF254**	9534	zinc finger protein 254	-2.85	0.07
203707_at	**ZNF263**	10127	zinc finger protein 263	4.77	0.51
218645_at	**ZNF277P**	11179	zinc finger protein 277 pseudogene	3.59	0.00
218401_s_at	**ZNF281**	23528	zinc finger protein 281	-3.38	0.03
225296_at	**ZNF317**	57693	zinc finger protein 317	2.93	0.00
203521_s_at	**ZNF318**	24149	zinc finger protein 318	4.50	0.51
213760_s_at	**ZNF330**	27309	zinc finger protein 330	2.62	0.16
231864_at	**ZNF33A**	7581	zinc finger protein 33A	-3.82	0.00
215022_x_at	**ZNF33B**	7582	zinc finger protein 33B	-3.23	0.00
207296_at	**ZNF343**	79175	zinc finger protein 343	3.54	0.34
205427_at	**ZNF354A**	6940	zinc finger protein 354A	-2.29	0.16
226468_at	**ZNF364**	27246	zinc finger protein 364	5.84	0.00
229551_x_at	**ZNF367**	195828	zinc finger protein 367	2.71	0.08
228711_at	**ZNF37A**	7587	zinc finger protein 37A	3.72	0.25
214878_at	**ZNF37A /// ZNF37B**	256112 /// 7587	zinc finger protein 37A /// zinc finger protein 37B	4.51	0.34
226111_s_at	**ZNF385**	25946	zinc finger protein 385	2.13	0.79
229743_at	**ZNF438**	220929	zinc finger protein 438	2.28	0.13
214746_s_at	**ZNF467**	168544	zinc finger protein 467	-7.15	0.00
214751_at	**ZNF468**	90333	zinc finger protein 468	3.37	0.51
222283_at	**ZNF480**	147657	zinc finger protein 480	6.53	0.00
203604_at	**ZNF516**	9658	zinc finger protein 516	-3.54	0.25
219711_at	**ZNF586**	54807	zinc finger protein 586	-5.95	0.00
227507_at	**ZNF592**	9640	zinc finger protein 592	-3.79	0.07
204175_at	**ZNF593**	51042	zinc finger protein 593	11.72	0.79

232367_x_at	**ZNF598**	90850	zinc finger protein 598	-4.93	0.07
227045_at	**ZNF614**	80110	zinc finger protein 614	4.47	0.51
1552643_at	**ZNF626**	199777	zinc finger protein 626	-2.56	0.34
226509_at	**ZNF641**	121274	zinc finger protein 641	-3.34	0.13
230029_x_at	**ZNF650**	130507	zinc finger protein 650	-3.15	0.34
225266_at	**ZNF652**	22834	zinc finger protein 652	-8.38	0.00
227445_at	**ZNF689**	115509	zinc finger protein 689	-4.26	0.16
227080_at	**ZNF697**	90874	zinc finger protein 697	4.62	0.08
235997_at	**ZNF74**	7625	zinc finger protein 74	-2.12	0.03
225848_at	**ZNF746**	155061	zinc finger protein 746	-9.52	0.00
239838_at	**ZNF776**	284309	Zinc finger protein 776	-4.96	0.16
215758_x_at	**ZNF93**	81931	zinc finger protein 93	-2.65	0.08
223639_s_at	**ZNRD1**	30834	zinc ribbon domain containing 1	2.50	0.13
225131_at	**ZRANB1**	54764	zinc finger, RAN-binding domain containing 1	-3.20	0.13
213097_s_at	**ZRF1**	27000	zuotin related factor 1	3.56	0.16
225964_at	**ZXDC**	79364	ZXD family zinc finger C	-3.81	0.79
225350_s_at	**ZYG11B**	79699	zyg-11 homolog B (C. elegans)	-8.73	0.07
200808_s_at	**ZYX**	7791	zyxin	-4.31	0.00
207190_at	**ZZEF1**	23140	zinc finger, ZZ-type with EF-hand domain 1	-2.09	0.79
212893_at	**ZZZ3**	26009	zinc finger, ZZ-type containing 3	5.68	0.51

Gene expression significantly perturbed between GM+I and LPS (fold change = GM+I/LPS)

Probeset ID	Gene Symbol	Gene ID	Gene Name	Fold Change	q-value (%)
235435_at	**AASDH**	132949	2-aminoadipic 6-semialdehyde dehydrogenase	2.25	0.40
203504_s_at	**ABCA1**	19	ATP-binding cassette, sub-family A (ABC1), member 1	-6.06	0.00
228490_at	**ABHD2**	11057	abhydrolase domain containing 2	2.09	0.23
231907_at	**ABL2**	27	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	2.85	0.63
201128_s_at	**ACLY**	47	ATP citrate lyase	3.68	0.18
218981_at	**ACN9**	57001	ACN9 homolog (S. cerevisiae)	5.90	0.40
201629_s_at	**ACP1**	52	acid phosphatase 1, soluble	5.50	0.63
206134_at	**ADAMDEC1**	27299	ADAM-like, decysin 1	-21.71	0.44
225440_at	**AGPAT3**	56894	1-acylglycerol-3-phosphate O-acyltransferase 3	7.62	0.63
214766_s_at	**AHCTF1**	25909	AT hook containing transcription factor 1	2.49	0.63
205996_s_at	**AK2**	204	adenylate kinase 2	2.56	0.23
201900_s_at	**AKR1A1**	10327	aldo-keto reductase family 1, member A1 (aldehyde reductase)	2.91	0.44
207016_s_at	**ALDH1A2**	8854	aldehyde dehydrogenase 1 family, member A2	36.67	0.27
201612_at	**ALDH9A1**	223	aldehyde dehydrogenase 9 family, member A1	2.27	0.90
226414_s_at	**ANAPC11 /// LOC728919**	51529 /// 728919	APC11 anaphase promoting complex subunit 11 homolog (yeast) /// similar to APC11 anaphase promoting complex subunit 11 isoform 2	2.06	0.63
238439_at	**ANKRD22**	118932	ankyrin repeat domain 22	5.73	0.00
201301_s_at	**ANXA4**	307	annexin A4	3.73	0.00
210027_s_at	**APEX1**	328	APEX nuclease (multifunctional DNA repair enzyme) 1	4.82	0.27
209546_s_at	**APOL1**	8542	apolipoprotein L, 1	2.25	0.00
221087_s_at	**APOL3**	80833	apolipoprotein L, 3	2.14	0.18
223801_s_at	**APOL4**	80832	apolipoprotein L, 4	5.36	0.27
225173_at	**ARHGAP18**	93663	Rho GTPase activating protein 18	3.24	0.00
201288_at	**ARHGDIB**	397	Rho GDP dissociation inhibitor (GDI) beta	2.49	0.11
212614_at	**ARID5B**	84159	AT rich interactive domain 5B (MRF1-like)	-2.77	0.63
1554480_a_at	**ARMC10**	83787	armadillo repeat containing 10	2.13	0.18

225283_at	**ARRDC4**	91947	arrestin domain containing 4	3.18	0.63
212815_at	**ASCC3**	10973	activating signal cointegrator 1 complex subunit 3	8.53	0.11
227014_at	**ASPHD2**	57168	aspartate beta-hydroxylase domain containing 2	8.75	0.11
208758_at	**ATIC**	471	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	6.98	0.63
212672_at	**ATM**	472	ataxia telangiectasia mutated	2.17	0.90
203454_s_at	**ATOX1**	475	ATX1 antioxidant protein 1 homolog (yeast)	2.68	0.40
201243_s_at	**ATP1B1**	481	ATPase, Na+/K+ transporting, beta 1 polypeptide	6.78	0.23
215716_s_at	**ATP2B1**	490	ATPase, Ca++ transporting, plasma membrane 1	-2.37	0.00
213738_s_at	**ATP5A1**	498	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	2.45	0.63
207507_s_at	**ATP5G3**	518	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	2.97	0.18
209903_s_at	**ATR**	545	ataxia telangiectasia and Rad3 related	14.52	0.27
229791_at	**AYTL1**	54947	Acyltransferase like 1	2.61	0.44
202391_at	**BASP1**	10409	brain abundant, membrane attached signal protein 1	-3.05	0.00
200837_at	**BCAP31**	10134	B-cell receptor-associated protein 31	3.07	0.63
227322_s_at	**BCCIP**	56647	BRCA2 and CDKN1A interacting protein	4.16	0.23
223185_s_at	**BHLHB3**	79365	basic helix-loop-helix domain containing, class B, 3	25.81	0.00
229437_at	**BIC**	114614	BIC transcript	3.13	0.00
226530_at	**BMF**	90427	Bcl2 modifying factor	-2.43	0.15
229436_x_at	**BRCC3**	79184	BRCA1/BRCA2-containing complex, subunit 3	7.74	0.44
217945_at	**BTBD1**	53339	BTB (POZ) domain containing 1	5.10	0.18
205504_at	**BTK**	695	Bruton agammaglobulinemia tyrosine kinase	2.60	0.44
222464_s_at	**C10orf119**	79892	chromosome 10 open reading frame 119	2.39	0.00
228332_s_at	**C11orf31**	280636	chromosome 11 open reading frame 31	3.45	0.11
222613_at	**C12orf4**	57102	chromosome 12 open reading frame 4	4.37	0.00
228193_s_at	**C13orf15**	28984	Chromosome 13 open reading frame 15	6.66	0.44
219471_at	**C13orf18**	80183	chromosome 13 open reading frame 18	-3.58	0.00
221434_s_at	**C14orf156**	81892	chromosome 14 open reading frame 156	2.20	0.11
225980_at	**C14orf43**	91748	chromosome 14 open reading frame 43	3.28	0.40
213105_s_at	**C16orf42**	115939	chromosome 16 open reading frame 42	2.04	0.27
224574_at	**C17orf49 /// MGC71993**	124944 /// 440400	chromosome 17 open reading frame 49 /// similar to DNA segment, Chr 11, Brigham & Womens Genetics 0434 expressed	2.99	0.11
225967_s_at	**C17orf89**	284184	chromosome 17 open reading frame 89	3.16	0.40
221764_at	**C19orf22**	91300	chromosome 19 open reading frame 22	-2.05	0.15
221587_s_at	**C19orf24**	55009	chromosome 19 open reading frame 24	2.00	0.00
235515_at	**C19orf46**	163183	chromosome 19 open reading frame 46	-2.68	0.40
221335_x_at	**C19orf61**	56006	chromosome 19 open reading frame 61	-2.05	0.27
219283_at	**C1GALT1C1**	29071	C1GALT1-specific chaperone 1	3.95	0.00
219875_s_at	**C1orf121**	51029	chromosome 1 open reading frame 121	2.51	0.90
223124_s_at	**C1orf128**	57095	chromosome 1 open reading frame 128	2.12	0.44
207759_s_at	**C1orf136 /// DISC1**	27185 /// 400574	disrupted in schizophrenia 1 /// chromosome 1 open reading frame 136	-2.12	0.40
224867_at	**C1orf151**	440574	chromosome 1 open reading frame 151	2.90	0.11
219506_at	**C1orf54**	79630	chromosome 1 open reading frame 54	15.45	0.90
214214_s_at	**C1QBP**	708	complement component 1, q subcomponent binding protein	5.67	0.40
231991_at	**C20orf160**	140706	chromosome 20 open reading frame 160	-17.83	0.15

219065_s_at	**C2orf4P** /// **MEMO1**	51072 /// 728556 /// 7795	Methylation modifier for class I HLA /// mediator of cell motility 1 /// C2orf4 pseudogene	3.58	0.11
225799_at	**C2orf59** /// **LOC541471**	112597 /// 541471	chromosome 2 open reading frame 59 /// hypothetical LOC541471	2.93	0.00
231010_at	**C4orf16**	55435	Chromosome 4 open reading frame 16	2.07	0.63
227856_at	**C4orf32**	132720	chromosome 4 open reading frame 32	4.29	0.27
218233_s_at	**C6orf49**	29964	chromosome 6 open reading frame 49	4.57	0.00
215380_s_at	**C7orf24**	79017	chromosome 7 open reading frame 24	4.84	0.27
226386_at	**C7orf30**	115416	chromosome 7 open reading frame 30	2.54	0.18
225604_s_at	**C9orf19**	152007	chromosome 9 open reading frame 19	2.83	0.40
203963_at	**CA12**	771	carbonic anhydrase XII	-3.51	0.63
210691_s_at	**CACYBP**	27101	calcyclin binding protein	2.77	0.18
214845_s_at	**CALU**	813	calumenin	2.28	0.11
235626_at	**CAMK1D**	57118	calcium/calmodulin-dependent protein kinase ID	2.94	0.63
207500_at	**CASP5**	838	caspase 5, apoptosis-related cysteine peptidase	-3.54	0.00
206788_s_at	**CBFB**	865	core-binding factor, beta subunit	2.09	0.44
209213_at	**CBR1**	873	carbonyl reductase 1	2.95	0.11
226193_x_at	**CBWD1**	55871	COBW domain containing 1	2.40	0.44
235208_at	**CCDC112**	153733	coiled-coil domain containing 112	8.09	0.11
226011_at	**CCDC12**	151903	coiled-coil domain containing 12	2.68	0.23
216714_at	**CCL13**	6357	chemokine (C-C motif) ligand 13	21.15	0.11
207900_at	**CCL17**	6361	chemokine (C-C motif) ligand 17	5.83	0.63
205476_at	**CCL20**	6364	chemokine (C-C motif) ligand 20	-2.50	0.00
208075_s_at	**CCL7**	6354	chemokine (C-C motif) ligand 7	17.41	0.00
214038_at	**CCL8**	6355	chemokine (C-C motif) ligand 8	7.06	0.11
200953_s_at	**CCND2**	894	cyclin D2	3.15	0.00
201947_s_at	**CCT2**	10576	chaperonin containing TCP1, subunit 2 (beta)	2.64	0.00
200877_at	**CCT4**	10575	chaperonin containing TCP1, subunit 4 (delta)	4.86	0.40
201327_s_at	**CCT6A**	908	chaperonin containing TCP1, subunit 6A (zeta 1)	3.88	0.11
200873_s_at	**CCT8**	10694	chaperonin containing TCP1, subunit 8 (theta)	2.42	0.40
215784_at	**CD1E**	913	CD1e molecule	18.19	0.27
207277_at	**CD209**	30835	CD209 molecule	15.11	0.18
217422_s_at	**CD22** /// **MAG**	4099 /// 933	CD22 molecule /// myelin associated glycoprotein	-3.41	0.00
207315_at	**CD226**	10666	CD226 molecule	5.00	0.00
1553043_a_at	**CD300LF**	146722	CD300 molecule-like family member f	2.47	0.00
206488_s_at	**CD36**	948	CD36 molecule (thrombospondin receptor)	7.15	0.23
208783_s_at	**CD46**	4179	CD46 molecule, complement regulatory protein	2.28	0.00
237759_at	**CD48**	962	CD48 molecule	-4.84	0.00
204661_at	**CD52**	1043	CD52 molecule	12.71	0.00
209795_at	**CD69**	969	CD69 molecule	2.41	0.11
1567627_at	**CD74**	972	CD74 molecule, major histocompatibility complex, class II invariant chain	6.66	0.00
203904_x_at	**CD82**	3732	CD82 molecule	-3.23	0.00
210895_s_at	**CD86**	942	CD86 molecule	3.14	0.27
201725_at	**CDC123**	8872	cell division cycle 123 homolog (S. cerevisiae)	2.28	0.63
201253_s_at	**CDIPT**	10423	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	3.36	0.00
219505_at	**CECR1**	51816	cat eye syndrome chromosome region, candidate 1	4.24	0.27
213618_at	**CENTD1**	116984	centaurin, delta 1	3.60	0.00

212516_at	**CENTD2**	116985	centaurin, delta 2	-2.35	0.44
202357_s_at	**CFB**	629	complement factor B	-2.41	0.23
206932_at	**CH25H**	9023	cholesterol 25-hydroxylase	11.54	0.11
209396_s_at	**CHI3L1**	1116	chitinase 3-like 1 (cartilage glycoprotein-39)	-2.53	0.00
206756_at	**CHST7**	56548	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	-2.76	0.27
211884_s_at	**CIITA**	4261	class II, major histocompatibility complex, transactivator	2.95	0.63
223377_x_at	**CISH**	1154	cytokine inducible SH2-containing protein	4.19	0.00
221058_s_at	**CKLF**	51192	chemokine-like factor	2.32	0.00
217752_s_at	**CNDP2**	55748	CNDP dipeptidase 2 (metallopeptidase M20 family)	3.19	0.00
1552344_s_at	**CNOT7**	29883	CCR4-NOT transcription complex, subunit 7	3.42	0.11
208818_s_at	**COMT**	1312	catechol-O-methyltransferase	3.49	0.90
224583_at	**COTL1**	23406	coactosin-like 1 (Dictyostelium)	2.37	0.44
208146_s_at	**CPVL**	54504	carboxypeptidase, vitellogenic-like	2.47	0.44
207442_at	**CSF3**	1440	colony stimulating factor 3 (granulocyte)	-55.23	0.00
229212_at	**CSNK2A1**	1457	Casein kinase 2, alpha 1 polypeptide	2.72	0.90
213980_s_at	**CTBP1**	1487	C-terminal binding protein 1	2.04	0.44
201487_at	**CTSC**	1075	cathepsin C	5.49	0.00
202157_s_at	**CUGBP2**	10659	CUG triplet repeat, RNA binding protein 2	2.20	0.40
205898_at	**CX3CR1**	1524	chemokine (C-X3-C motif) receptor 1	-5.33	0.44
204533_at	**CXCL10**	3627	chemokine (C-X-C motif) ligand 10	6.68	0.00
211122_s_at	**CXCL11**	6373	chemokine (C-X-C motif) ligand 11	9.06	0.00
203915_at	**CXCL9**	4283	chemokine (C-X-C motif) ligand 9	9.95	0.23
214112_s_at	**CXorf40A /// CXorf40B**	541578 /// 91966	chromosome X open reading frame 40A /// chromosome X open reading frame 40B	3.93	0.44
215785_s_at	**CYFIP2**	26999	cytoplasmic FMR1 interacting protein 2	-2.93	0.63
212527_at	**D15Wsu75e**	27351	DNA segment, Chr 15, Wayne State University 75, expressed	2.15	0.11
226620_x_at	**DAZAP1**	26528	DAZ associated protein 1	2.30	0.23
203302_at	**DCK**	1633	deoxycytidine kinase	2.81	0.90
239648_at	**DCUN1D3**	123879	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	2.96	0.11
202887_s_at	**DDIT4**	54541	DNA-damage-inducible transcript 4	-2.16	0.90
207431_s_at	**DEGS1**	8560	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	2.36	0.63
200934_at	**DEK**	7913	DEK oncogene (DNA binding)	2.11	0.44
226121_at	**DHRS13**	147015	dehydrogenase/reductase (SDR family) member 13	-2.46	0.63
223365_at	**DHX37**	57647	DEAH (Asp-Glu-Ala-His) box polypeptide 37	3.28	0.63
204405_x_at	**DIMT1L**	27292	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	2.40	0.00
216212_s_at	**DKC1**	1736	dyskeratosis congenita 1, dyskerin	4.26	0.11
214030_at	**DKFZp667G2110**	131544	hypothetical protein DKFZp667G2110	4.79	0.44
202516_s_at	**DLG1**	1739	discs, large homolog 1 (Drosophila)	2.82	0.18
202500_at	**DNAJB2**	3300	DnaJ (Hsp40) homolog, subfamily B, member 2	3.70	0.63
225174_at	**DNAJC10**	54431	DnaJ (Hsp40) homolog, subfamily C, member 10	4.43	0.27
218435_at	**DNAJC15**	29103	DnaJ (Hsp40) homolog, subfamily C, member 15	3.65	0.63
202416_at	**DNAJC7**	7266	DnaJ (Hsp40) homolog, subfamily C, member 7	2.59	0.40
223553_s_at	**DOK3**	79930	docking protein 3	-2.99	0.15
224336_s_at	**DUSP16**	80824	dual specificity phosphatase 16	-5.47	0.00

209457_at	**DUSP5**	1847	dual specificity phosphatase 5	2.06	0.40
210151_s_at	**DYRK3**	8444	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	-2.62	0.63
223088_x_at	**ECHDC1**	55862	enoyl Coenzyme A hydratase domain containing 1	2.77	0.00
209059_s_at	**EDF1**	8721	endothelial differentiation-related factor 1	2.00	0.18
204038_s_at	**EDG2**	1902	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	2.99	0.40
200705_s_at	**EEF1B2 /// hCG_19809 /// hCG_1983058**	1933 /// 644820 /// 647030	eukaryotic translation elongation factor 1 beta 2 /// hCG1983058 /// eukaryotic translation elongation factor 1 beta 2-like	2.51	0.00
233375_at	**EFCAB2**	84288	EF-hand calcium binding domain 2	16.19	0.00
205249_at	**EGR2**	1959	early growth response 2 (Krox-20 homolog, Drosophila)	5.03	0.18
201019_s_at	**EIF1AP1 /// EIF1AX**	1964 /// 280661	eukaryotic translation initiation factor 1A, X-linked /// eukaryotic translation initiation factor 1A pseudogene 1	2.14	0.63
217736_s_at	**EIF2AK1**	27102	eukaryotic translation initiation factor 2-alpha kinase 1	4.03	0.00
201143_s_at	**EIF2S1**	1965	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	3.23	0.23
208697_s_at	**EIF3E**	3646	eukaryotic translation initiation factor 3, subunit E	2.44	0.00
221494_x_at	**EIF3K**	27335	eukaryotic translation initiation factor 3, subunit K	2.96	0.11
202232_s_at	**EIF3M**	10480	eukaryotic translation initiation factor 3, subunit M	3.76	0.11
225940_at	**EIF4E3**	317649	eukaryotic translation initiation factor 4E family member 3	2.51	0.00
214313_s_at	**EIF5B**	9669	Eukaryotic translation initiation factor 5B	3.14	0.23
226099_at	**ELL2**	22936	elongation factor, RNA polymerase II, 2	-2.10	0.27
227075_at	**ELP3**	55140	elongation protein 3 homolog (S. cerevisiae)	2.33	0.90
209233_at	**EMG1**	10436	EMG1 nucleolar protein homolog (S. cerevisiae)	4.04	0.11
228673_s_at	**EML4**	27436	Echinoderm microtubule associated protein like 4	2.95	0.00
207111_at	**EMR1**	2015	egf-like module containing, mucin-like, hormone receptor-like 1	-5.76	0.00
202909_at	**EPM2AIP1**	9852	EPM2A (laforin) interacting protein 1	-2.90	0.44
221056_x_at	**EPS15L1**	58513	epidermal growth factor receptor pathway substrate 15-like 1	-6.82	0.90
227017_at	**ERICH1**	157697	glutamate-rich 1	4.56	0.11
202441_at	**ERLIN1**	10613	ER lipid raft associated 1	4.07	0.23
201931_at	**ETFA**	2108	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	2.99	0.63
203349_s_at	**ETV5**	2119	ets variant gene 5 (ets-related molecule)	-11.64	0.00
235056_at	**ETV6**	2120	ets variant gene 6 (TEL oncogene)	2.04	0.63
221680_s_at	**ETV7**	51513	ets variant gene 7 (TEL2 oncogene)	2.55	0.00
226259_at	**EXOC6**	54536	exocyst complex component 6	4.90	0.27
212627_s_at	**EXOSC7**	23016	exosome component 7	3.05	0.90
204363_at	**F3**	2152	coagulation factor III (thromboplastin, tissue factor)	6.31	0.11
202345_s_at	**FABP5 /// LOC728641 /// LOC729163**	2171 /// 728641 /// 729163	fatty acid binding protein 5 (psoriasis-associated) /// similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	3.75	0.90
218532_s_at	**FAM134B**	54463	family with sequence similarity 134, member B	-4.81	0.00

228362_s_at	**FAM26F**	441168	Family with sequence similarity 26, member F	9.10	0.00
224824_at	**FAM36A**	116228	family with sequence similarity 36, member A	2.33	0.11
218126_at	**FAM82C**	55177	family with sequence similarity 82, member C	2.85	0.18
218074_at	**FAM96B**	51647	family with sequence similarity 96, member B	2.85	0.27
204781_s_at	**FAS**	355	Fas (TNF receptor superfamily, member 6)	2.47	0.11
219200_at	**FASTKD3**	79072	FAST kinase domains 3	3.01	0.40
209696_at	**FBP1**	2203	fructose-1,6-bisphosphatase 1	28.89	0.11
235089_at	**FBXL20**	84961	F-box and leucine-rich repeat protein 20	-5.47	0.44
216951_at	**FCGR1A**	2209	Fc fragment of IgG, high affinity Ia, receptor (CD64)	2.60	0.00
214511_x_at	**FCGR1B**	2210	Fc fragment of IgG, high affinity Ib, receptor (CD64)	2.02	0.00
210889_s_at	**FCGR2B /// FCGR2C**	2213 /// 9103	Fc fragment of IgG, low affinity IIb, receptor (CD32) /// Fc fragment of IgG, low affinity IIc, receptor for (CD32)	7.89	0.23
218831_s_at	**FCGRT**	2217	Fc fragment of IgG, receptor, transporter, alpha	2.15	0.23
205237_at	**FCN1**	2219	ficolin (collagen/fibrinogen domain containing) 1	7.26	0.44
201798_s_at	**FER1L3**	26509	fer-1-like 3, myoferlin (C. elegans)	18.18	0.90
1553906_s_at	**FGD2**	221472	FYVE, RhoGEF and PH domain containing 2	4.82	0.40
227265_at	**FGL2**	10875	fibrinogen-like 2	8.49	0.00
200895_s_at	**FKBP4**	2288	FK506 binding protein 4, 59kDa	3.25	0.63
228149_at	**FLJ31818**	154743	hypothetical protein FLJ31818	-3.34	0.44
1566760_at	**FLJ34208**	401106	hypothetical gene supported by AK091527	-8.21	0.27
216442_x_at	**FN1**	2335	fibronectin 1	6.90	0.00
225262_at	**FOSL2**	2355	FOS-like antigen 2	-5.24	0.00
203734_at	**FOXJ2**	55810	forkhead box J2	-3.21	0.18
214560_at	**FPRL2**	2359	formyl peptide receptor-like 2	13.59	0.00
223120_at	**FUCA2**	2519	fucosidase, alpha-L- 2, plasma	7.72	0.18
223042_s_at	**FUNDC2**	65991	FUN14 domain containing 2	5.53	0.27
202419_at	**FVT1**	2531	follicular lymphoma variant translocation 1	5.19	0.00
224641_at	**FYTTD1**	84248	forty-two-three domain containing 1	2.35	0.00
213280_at	**GARNL4**	23108	GTPase activating Rap/RanGAP domain-like 4	2.96	0.44
232024_at	**GIMAP2**	26157	GTPase, IMAP family member 2	2.97	0.63
219243_at	**GIMAP4**	55303	GTPase, IMAP family member 4	2.73	0.00
64064_at	**GIMAP5**	55340	GTPase, IMAP family member 5	2.68	0.00
235306_at	**GIMAP8**	155038	GTPase, IMAP family member 8	3.94	0.18
223278_at	**GJB2**	2706	gap junction protein, beta 2, 26kDa	-50.90	0.00
223079_s_at	**GLS**	2744	glutaminase	2.39	0.63
218473_s_at	**GLT25D1**	79709	glycosyltransferase 25 domain containing 1	2.27	0.11
215794_x_at	**GLUD2**	2747	glutamate dehydrogenase 2	3.25	0.18
223487_x_at	**GNB4**	59345	guanine nucleotide binding protein (G protein), beta polypeptide 4	4.16	0.11
217850_at	**GNL3**	26354	guanine nucleotide binding protein-like 3 (nucleolar)	2.84	0.40
223887_at	**GPR132**	29933	G protein-coupled receptor 132	-2.55	0.15
204137_at	**GPR137B**	7107	G protein-coupled receptor 137B	-5.64	0.23
200736_s_at	**GPX1**	2876	glutathione peroxidase 1	2.28	0.63
216308_x_at	**GRHPR**	9380	glyoxylate reductase/hydroxypyruvate reductase	3.57	0.40
200696_s_at	**GSN**	2934	gelsolin (amyloidosis, Finnish type)	3.43	0.11
201912_s_at	**GSPT1**	2935	G1 to S phase transition 1	4.86	0.27
225609_at	**GSR**	2936	glutathione reductase	2.63	0.00
202678_at	**GTF2A2**	2958	general transcription factor IIA, 2, 12kDa	2.30	0.00
209595_at	**GTF2F2**	2963	general transcription factor IIF, polypeptide 2, 30kDa	2.56	0.23
201338_x_at	**GTF3A**	2971	general transcription factor IIIA	3.60	0.00

218238_at	**GTPBP4**	23560	GTP binding protein 4	2.60	0.00
220577_at	**GVIN1**	387751	GTPase, very large interferon inducible 1	2.96	0.18
202947_s_at	**GYPC**	2995	glycophorin C (Gerbich blood group)	2.55	0.00
206643_at	**HAL**	3034	histidine ammonia-lyase	-2.15	0.63
38037_at	**HBEGF**	1839	heparin-binding EGF-like growth factor	3.88	0.40
209102_s_at	**HBP1**	26959	HMG-box transcription factor 1	-2.01	0.27
202474_s_at	**HCFC1**	3054	host cell factor C1 (VP16-accessory protein)	5.24	0.90
215780_s_at	**hCG_1644608** /// **LOC389168** /// **SET**	389168 /// 6418 /// 642869	SET translocation (myeloid leukemia-associated) /// similar to Protein SET (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I) (HLA-DR-associated protein II) (PHAPII) (Inhibitor of granzyme A-activated DNase) (IGAAD) /// SET translocation (myeloid leukemia-associated) pseudogene	3.15	0.00
221491_x_at	**hCG_1998957** /// **HLA-DRB1** /// **HLA-DRB3** /// **HLA-DRB4** /// **HLA-DRB5** /// **LOC730415**	3123 /// 3125 /// 3126 /// 3127 /// 730415 /// 731247	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// hypothetical protein LOC730415	16.27	0.11
204225_at	**HDAC4**	9759	histone deacetylase 4	2.93	0.63
213069_at	**HEG1**	57493	HEG homolog 1 (zebrafish)	2.75	0.63
206183_s_at	**HERC3**	8916	hect domain and RLD 3	2.13	0.63
219863_at	**HERC5**	51191	hect domain and RLD 5	-3.56	0.15
201944_at	**HEXB**	3074	hexosaminidase B (beta polypeptide)	2.07	0.40
44783_s_at	**HEY1**	23462	hairy/enhancer-of-split related with YRPW motif 1	-25.97	0.18
223073_at	**HIATL1**	84641	hippocampus abundant transcript-like 1	2.01	0.00
218507_at	**HIG2**	29923	hypoxia-inducible protein 2	-3.75	0.90
217845_x_at	**HIGD1A**	25994	HIG1 domain family, member 1A	2.01	0.18
209329_x_at	**HIGD2A**	192286	HIG1 domain family, member 2A	2.82	0.40
217478_s_at	**HLA-DMA**	3108	major histocompatibility complex, class II, DM alpha	9.26	0.00
203932_at	**HLA-DMB**	3109	major histocompatibility complex, class II, DM beta	7.01	0.00
211990_at	**HLA-DPA1**	3113	major histocompatibility complex, class II, DP alpha 1	18.23	0.00
201137_s_at	**HLA-DPB1**	3115	major histocompatibility complex, class II, DP beta 1	11.82	0.00
213831_at	**HLA-DQA1**	3117	major histocompatibility complex, class II, DQ alpha 1	5.82	0.00
212671_s_at	**HLA-DQA1** /// **HLA-DQA2** /// **LOC731682**	3117 /// 3118 /// 731682	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2 /// similar to HLA class II histocompatibility antigen, DQ(1) alpha chain precursor (DC-4 alpha chain)	11.80	0.00
211656_x_at	**HLA-DQB1**	3119	major histocompatibility complex, class II, DQ beta 1	12.68	0.00
211654_x_at	**HLA-DQB1** /// **LOC650557**	3119 /// 650557	major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DQ(W1.1) beta chain precursor (DQB1*0501)	10.77	0.00
208894_at	**HLA-DRA**	3122	major histocompatibility complex, class II, DR alpha	2.84	0.00
208306_x_at	**HLA-DRB1**	3123	Major histocompatibility complex, class II, DR beta 1	4.51	0.11

215193_x_at	**HLA-DRB1 /// HLA-DRB3 /// LOC730415**	3123 /// 3125 /// 730415	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// hypothetical protein LOC730415	8.75	0.00
209312_x_at	**HLA-DRB1 /// LOC730415**	3123 /// 730415	major histocompatibility complex, class II, DR beta 1 /// hypothetical protein LOC730415	5.50	0.00
209728_at	**HLA-DRB4**	3126	major histocompatibility complex, class II, DR beta 4	7.23	0.63
217362_x_at	**HLA-DRB6**	3128	major histocompatibility complex, class II, DR beta 6 (pseudogene)	3.69	0.00
208766_s_at	**HNRNPR**	10236	heterogeneous nuclear ribonucleoprotein R	2.39	0.00
201277_s_at	**HNRPAB**	3182	heterogeneous nuclear ribonucleoprotein A/B	3.38	0.18
227361_at	**HS3ST3B1**	9953	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	-2.20	0.00
1557910_at	**HSP90AB1**	3326	heat shock protein 90kDa alpha (cytosolic), class B member 1	2.99	0.00
200800_s_at	**HSPA1A /// HSPA1B**	3303 /// 3304	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	-2.47	0.44
202581_at	**HSPA1B**	3304	heat shock 70kDa protein 1B	-3.21	0.00
213418_at	**HSPA6**	3310	heat shock 70kDa protein 6 (HSP70B')	-2.20	0.15
200691_s_at	**HSPA9**	3313	heat shock 70kDa protein 9 (mortalin)	3.07	0.00
203023_at	**HSPC111**	51491	hypothetical protein HSPC111	2.37	0.18
221597_s_at	**HSPC171**	29100	HSPC171 protein	2.08	0.18
200806_s_at	**HSPD1**	3329	heat shock 60kDa protein 1 (chaperonin)	2.44	0.11
205133_s_at	**HSPE1**	3336	heat shock 10kDa protein 1 (chaperonin 10)	2.82	0.00
233746_x_at	**HYPK**	25764	Huntingtin interacting protein K	2.24	0.00
239012_at	**IBRDC2**	255488	IBR domain containing 2	-2.87	0.00
201565_s_at	**ID2**	3398	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	-3.86	0.15
213931_at	**ID2 /// ID2B**	3398 /// 84099	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	-2.37	0.00
201193_at	**IDH1**	3417	isocitrate dehydrogenase 1 (NADP+), soluble	4.77	0.44
202070_s_at	**IDH3A**	3419	isocitrate dehydrogenase 3 (NAD+) alpha	6.83	0.44
208881_x_at	**IDI1**	3422	isopentenyl-diphosphate delta isomerase 1	2.72	0.11
214453_s_at	**IFI44**	10561	interferon-induced protein 44	-2.13	0.40
203153_at	**IFIT1**	3434	interferon-induced protein with tetratricopeptide repeats 1	-9.43	0.00
204786_s_at	**IFNAR2**	3455	interferon (alpha, beta and omega) receptor 2	2.02	0.40
218100_s_at	**IFT57**	55081	intraflagellar transport 57 homolog (Chlamydomonas)	-6.03	0.40
226759_at	**IKZF4**	64375	IKAROS family zinc finger 4 (Eos)	9.18	0.40
207433_at	**IL10**	3586	interleukin 10	-76.41	0.40
207901_at	**IL12B**	3593	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	-61.53	0.00
224283_x_at	**IL18BP**	10068	interleukin 18 binding protein	3.08	0.11
205227_at	**IL1RAP**	3556	interleukin 1 receptor accessory protein	2.44	0.27
220054_at	**IL23A**	51561	interleukin 23, alpha subunit p19	-10.70	0.00
222062_at	**IL27RA**	9466	interleukin 27 receptor, alpha	6.45	0.11
203828_s_at	**IL32**	9235	interleukin 32	6.62	0.44
205207_at	**IL6**	3569	interleukin 6 (interferon, beta 2)	-3.78	0.00
200052_s_at	**ILF2**	3608	interleukin enhancer binding factor 2, 45kDa	3.09	0.90
221548_s_at	**ILKAP**	80895	integrin-linked kinase-associated serine/threonine phosphatase 2C	4.06	0.40
200955_at	**IMMT**	10989	inner membrane protein, mitochondrial (mitofilin)	6.09	0.90

222654_at	**IMPAD1**	54928	inositol monophosphatase domain containing 1	4.29	0.27
231863_at	**ING3**	54556	inhibitor of growth family, member 3	2.46	0.63
210511_s_at	**INHBA**	3624	inhibin, beta A	3.61	0.00
201626_at	**INSIG1**	3638	insulin induced gene 1	-5.23	0.00
241393_at	**IPP**	3652	Intracisternal A particle-promoted polypeptide	-2.43	0.18
220034_at	**IRAK3**	11213	interleukin-1 receptor-associated kinase 3	-2.24	0.00
204057_at	**IRF8**	3394	interferon regulatory factor 8	4.15	0.27
239044_at	**ITFG1**	81533	Integrin alpha FG-GAP repeat containing 1	5.39	0.40
1555349_a_at	**ITGB2**	3689	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	2.02	0.44
203710_at	**ITPR1**	3708	inositol 1,4,5-triphosphate receptor, type 1	2.34	0.00
209972_s_at	**JTV1**	7965	JTV1 gene	3.22	0.23
200079_s_at	**KARS**	3735	lysyl-tRNA synthetase	2.78	0.00
219106_s_at	**KBTBD10**	10324	kelch repeat and BTB (POZ) domain containing 10	-2.30	0.63
221307_at	**KCNIP1**	30820	Kv channel interacting protein 1	-2.49	0.23
212188_at	**KCTD12**	115207	potassium channel tetramerisation domain containing 12	2.65	0.00
203712_at	**KIAA0020**	9933	KIAA0020	3.52	0.63
203144_s_at	**KIAA0040**	9674	KIAA0040	2.67	0.63
212621_at	**KIAA0286**	23306	KIAA0286 protein	2.17	0.18
212943_at	**KIAA0528**	9847	KIAA0528	2.07	0.44
204155_s_at	**KIAA0999**	23387	KIAA0999 protein	-3.20	0.18
212942_s_at	**KIAA1199**	57214	KIAA1199	-24.89	0.00
227624_at	**KIAA1546**	54790	KIAA1546	-2.62	0.44
227433_at	**KIAA2018**	205717	KIAA2018	-2.04	0.15
1557089_at	**KIF5C**	3800	kinesin family member 5C	-3.80	0.00
222913_at	**KLF3**	51274	Kruppel-like factor 3 (basic)	2.37	0.44
221841_s_at	**KLF4**	9314	Kruppel-like factor 4 (gut)	3.06	0.63
230835_at	**KRTDAP**	388533	keratinocyte differentiation-associated protein	2.73	0.90
221982_x_at	**LAGE3**	8270	L antigen family, member 3	9.43	0.23
217933_s_at	**LAP3**	51056	leucine aminopeptidase 3	2.42	0.00
212137_at	**LARP1**	23367	La ribonucleoprotein domain family, member 1	3.66	0.40
224951_at	**LASS5**	91012	LAG1 homolog, ceramide synthase 5	2.25	0.00
235463_s_at	**LASS6**	253782	LAG1 homolog, ceramide synthase 6	3.72	0.63
212531_at	**LCN2**	3934	lipocalin 2 (oncogene 24p3)	-15.83	0.15
202595_s_at	**LEPROTL1**	23484	leptin receptor overlapping transcript-like 1	6.16	0.11
212687_at	**LIMS1**	3987	LIM and senescent cell antigen-like domains 1	-2.78	0.00
223350_x_at	**LIN7C**	55327	lin-7 homolog C (C. elegans)	2.55	0.11
232593_at	**LINCR**	93082	likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein	-8.55	0.00
201847_at	**LIPA**	3988	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	27.79	0.27
244289_at	**LOC134466**	134466	hypothetical protein LOC134466	-6.39	0.15
225934_at	**LOC148413**	148413	Hypothetical protein LOC148413	2.76	0.11
227792_at	**LOC162073**	162073	hypothetical protein LOC162073	10.06	0.18
235587_at	**LOC202781**	202781	hypothetical protein LOC202781	-4.23	0.40
227466_at	**LOC285550**	285550	hypothetical protein LOC285550	2.20	0.63
244889_at	**LOC388210**	388210	Similar to CG15828-PA, isoform A	-2.18	0.90
241998_at	**LOC389073**	389073	similar to RIKEN cDNA D630023F18	8.44	0.44
200029_at	**LOC392557** /// **RPL19**	392557 /// 6143	ribosomal protein L19 /// similar to ribosomal protein L19	2.01	0.00
1560058_at	**LOC399900**	399900	hypothetical gene supported by AK093779	-3.72	0.63

200034_s_at	**LOC401725 /// LOC642828 /// LOC645387 /// RPL6**	401725 /// 6128 /// 642828 /// 645387	ribosomal protein L6 /// similar to 60S ribosomal protein L6 (TAX-responsive enhancer element-binding protein 107) (TAXREB107) (Neoplasm-related protein C140)	2.35	0.00
216348_at	**LOC402057 /// RPS17**	402057 /// 6218	ribosomal protein S17 /// similar to 40S ribosomal protein S17	2.91	0.63
200054_at	**LOC442240 /// ZNF259**	442240 /// 8882	zinc finger protein 259 /// similar to zinc finger protein 259	2.92	0.00
215963_x_at	**LOC642741**	642741	similar to ribosomal protein L3 isoform a	2.40	0.23
208856_x_at	**LOC643779 /// RPLP0**	6175 /// 643779	ribosomal protein, large, P0 /// similar to acidic ribosomal phosphoprotein P0	3.38	0.90
200074_s_at	**LOC649821 /// RPL14 /// RPL14L**	144581 /// 649821 /// 9045	ribosomal protein L14 /// ribosomal protein L14-like /// similar to 60S ribosomal protein L14 (CAG-ISL 7)	2.05	0.11
219762_s_at	**LOC651600 /// RPL36**	25873 /// 651600	ribosomal protein L36 /// similar to ribosomal protein L36	2.27	0.40
217998_at	**LOC652993 /// PHLDA1**	22822 /// 652993	pleckstrin homology-like domain, family A, member 1 /// hypothetical LOC652993	-3.70	0.40
217767_at	**LOC653879**	653879	similar to Complement C3 precursor	-3.04	0.00
201406_at	**LOC729362 /// RPL36A**	6173 /// 729362	ribosomal protein L36a /// similar to large subunit ribosomal protein L36a	2.54	0.00
240287_at	**LOC730249**	730249	similar to Immune-responsive protein 1	-3.31	0.00
207922_s_at	**LOC730744 /// MAEA**	10296 /// 730744	macrophage erythroblast attacher /// similar to macrophage erythroblast attacher	-2.57	0.90
217860_at	**LOC732160 /// NDUFA10**	4705 /// 732160	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa /// similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa precursor	2.40	0.23
201412_at	**LRP10**	26020	low density lipoprotein receptor-related protein 10	-2.71	0.00
201862_s_at	**LRRFIP1**	9208	leucine rich repeat (in FLII) interacting protein 1	2.21	0.23
205036_at	**LSM6**	11157	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	3.03	0.00
211581_x_at	**LST1**	7940	leukocyte specific transcript 1	2.20	0.00
208771_s_at	**LTA4H**	4048	leukotriene A4 hydrolase	2.51	0.18
225748_at	**LTV1**	84946	LTV1 homolog (S. cerevisiae)	4.59	0.11
209348_s_at	**MAF**	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	5.51	0.00
235457_at	**MAML2**	84441	mastermind-like 2 (Drosophila)	-2.94	0.15
221760_at	**MAN1A1**	4121	mannosidase, alpha, class 1A, member 1	3.02	0.63
235421_at	**MAP3K8**	1326	Mitogen-activated protein kinase kinase kinase 8 /// CDNA clone IMAGE:4689481	-3.85	0.00
213045_at	**MAST3**	23031	microtubule associated serine/threonine kinase 3	-2.15	0.40
218163_at	**MCTS1**	28985	malignant T cell amplified sequence 1	2.15	0.44
209397_at	**ME2**	4200	malic enzyme 2, NAD(+)-dependent, mitochondrial	2.45	0.44
212830_at	**MEGF9**	1955	multiple EGF-like-domains 9	-3.16	0.00
220839_at	**METTL5**	29081	methyltransferase like 5	6.60	0.27
217868_s_at	**METTL9**	51108	methyltransferase like 9	-2.13	0.15
204153_s_at	**MFNG**	4242	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	4.35	0.90
206522_at	**MGAM**	8972	maltase-glucoamylase (alpha-glucosidase)	-2.24	0.23
239186_at	**MGC39372**	221756	hypothetical protein MGC39372	-4.10	0.15
239104_at	**MGC42157**	439933	hypothetical locus MGC42157	4.36	0.90
218251_at	**MID1IP1**	58526	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	-3.46	0.15

223411_at	**MIF4GD**	57409	MIF4G domain containing	5.58	0.63
213188_s_at	**MINA**	84864	MYC induced nuclear antigen	2.99	0.44
224714_at	**MKI67IP**	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein	4.25	0.23
230122_at	**MLLT10**	8028	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	4.78	0.18
224866_at	**MLSTD2**	84188	male sterility domain containing 2	2.05	0.63
239852_at	**MMAA**	166785	methylmalonic aciduria (cobalamin deficiency) cblA type	-2.22	0.63
202828_s_at	**MMP14**	4323	matrix metallopeptidase 14 (membrane-inserted)	-10.07	0.00
203740_at	**MPHOSPH6**	10200	M-phase phosphoprotein 6	3.41	0.40
227747_at	**MPZL3**	196264	myelin protein zero-like 3	-3.58	0.90
204438_at	**MRC1** /// **MRC1L1**	414308 /// 4360	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	43.08	0.23
225260_s_at	**MRPL32**	64983	mitochondrial ribosomal protein L32	3.87	0.63
218558_s_at	**MRPL39**	54148	mitochondrial ribosomal protein L39	3.97	0.27
221997_s_at	**MRPL52**	122704	Mitochondrial ribosomal protein L52	-4.15	0.00
223156_at	**MRPS23**	51649	mitochondrial ribosomal protein S23	4.82	0.27
216336_x_at	**MT1A** /// **MT1M** /// **MT1P2**	4489 /// 4499 /// 645745	metallothionein 1A /// metallothionein 1M /// metallothionein 1 pseudogene 2	-3.47	0.15
213629_x_at	**MT1F**	4494	metallothionein 1F	-13.78	0.27
204745_x_at	**MT1G**	4495	metallothionein 1G	-8.47	0.44
206461_x_at	**MT1H** /// **MT1P2**	4496 /// 645745	metallothionein 1H /// metallothionein 1 pseudogene 2	-9.65	0.15
211456_x_at	**MT1P2**	645745	metallothionein 1 pseudogene 2	-5.10	0.15
204326_x_at	**MT1X**	4501	metallothionein 1X	-4.63	0.15
212185_x_at	**MT2A**	4502	metallothionein 2A	-2.01	0.63
217772_s_at	**MTCH2**	23788	mitochondrial carrier homolog 2 (C. elegans)	2.10	0.44
212250_at	**MTDH**	92140	metadherin	2.49	0.00
201761_at	**MTHFD2**	10797	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	2.13	0.23
225673_at	**MYADM**	91663	myeloid-associated differentiation marker	3.04	0.11
206304_at	**MYBPH**	4608	myosin binding protein H	-2.67	0.18
238644_at	**MYSM1**	114803	myb-like, SWIRM and MPN domains 1	-2.06	0.63
218840_s_at	**NADSYN1**	55191	NAD synthetase 1	4.29	0.00
200027_at	**NARS**	4677	asparaginyl-tRNA synthetase	5.12	0.00
201970_s_at	**NASP**	4678	nuclear autoantigenic sperm protein (histone-binding)	3.44	0.11
207677_s_at	**NCF4**	4689	neutrophil cytosolic factor 4, 40kDa	-2.48	0.00
220864_s_at	**NDUFA13**	51079	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	3.47	0.90
217773_s_at	**NDUFA4**	4697	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	3.64	0.40
202077_at	**NDUFAB1**	4706	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	6.11	0.11
201227_s_at	**NDUFB8**	4714	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	3.37	0.11
222992_s_at	**NDUFB9**	4715	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	3.34	0.27
201740_at	**NDUFS3**	4722	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	3.07	0.44
201757_at	**NDUFS5**	4725	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	4.24	0.23

203606_at	**NDUFS6**	4726	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	2.03	0.63
237761_at	**NEK6**	10783	NIMA (never in mitosis gene a)-related kinase 6	4.24	0.23
218888_s_at	**NETO2**	81831	neuropilin (NRP) and tolloid (TLL)-like 2	2.92	0.63
212809_at	**NFATC2IP**	84901	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	2.41	0.00
211524_at	**NFKB2**	4791	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	-2.31	0.18
201076_at	**NHP2L1**	4809	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	2.71	0.18
219594_at	**NINJ2**	4815	ninjurin 2	-3.72	0.90
201577_at	**NME1**	4830	non-metastatic cells 1, protein (NM23A) expressed in	28.92	0.11
227556_at	**NME7**	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	7.97	0.40
200875_s_at	**NOL5A**	10528	nucleolar protein 5A (56kDa with KKE/D repeat)	2.91	0.63
209104_s_at	**NOLA2**	55651	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)	5.08	0.90
223096_at	**NOP5/NOP58**	51602	nucleolar protein NOP5/NOP58	2.16	0.63
218625_at	**NRN1**	51299	neuritin 1	8.38	0.27
220248_x_at	**NSFL1C**	55968	NSFL1 (p97) cofactor (p47)	2.35	0.63
223076_s_at	**NSUN2**	54888	NOL1/NOP2/Sun domain family, member 2	2.15	0.11
219347_at	**NUDT15**	55270	nudix (nucleoside diphosphate linked moiety X)-type motif 15	4.47	0.63
221579_s_at	**NUDT3**	11165	nudix (nucleoside diphosphate linked moiety X)-type motif 3	2.13	0.00
218375_at	**NUDT9**	53343	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2.30	0.18
202188_at	**NUP93**	9688	nucleoporin 93kDa	2.92	0.00
202397_at	**NUTF2**	10204	nuclear transport factor 2	2.57	0.00
218708_at	**NXT1**	29107	NTF2-like export factor 1	3.25	0.18
205660_at	**OASL**	8638	2'-5'-oligoadenylate synthetase-like	-2.15	0.15
200790_at	**ODC1**	4953	ornithine decarboxylase 1	3.27	0.11
219293_s_at	**OLA1**	29789	Obg-like ATPase 1	5.12	0.40
228170_at	**OLIG1**	116448	oligodendrocyte transcription factor 1	-5.73	0.63
205040_at	**ORM1**	5004	orosomucoid 1	-3.68	0.27
205041_s_at	**ORM1 /// ORM2**	5004 /// 5005	orosomucoid 1 /// orosomucoid 2	-3.64	0.00
203480_s_at	**OTUD4**	54726	OTU domain containing 4	4.82	0.27
224745_x_at	**OTUD5**	55593	OTU domain containing 5	-7.75	0.00
220005_at	**P2RY13**	53829	purinergic receptor P2Y, G-protein coupled, 13	5.46	0.00
206637_at	**P2RY14**	9934	purinergic receptor P2Y, G-protein coupled, 14	2.73	0.00
220001_at	**PADI4**	23569	peptidyl arginine deiminase, type IV	-3.86	0.63
209063_x_at	**PAIP1**	10605	poly(A) binding protein interacting protein 1	2.60	0.44
226507_at	**PAK1**	5058	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	2.45	0.90
208878_s_at	**PAK2**	5062	p21 (CDKN1A)-activated kinase 2	2.14	0.18
200006_at	**PARK7**	11315	Parkinson disease (autosomal recessive, early onset) 7	2.41	0.40
209431_s_at	**PATZ1**	23598	POZ (BTB) and AT hook containing zinc finger 1	2.45	0.44
227759_at	**PCSK9**	255738	proprotein convertase subtilisin/kexin type 9	2.17	0.00
221898_at	**PDPN**	10630	podoplanin	-10.60	0.44
223037_at	**PDZD11**	51248	PDZ domain containing 11	2.15	0.44
1553140_at	**PELO**	53918	pelota homolog (Drosophila)	2.38	0.44

219180_s_at	**PEX26**	55670	peroxisome biogenesis factor 26	4.31	0.90
202464_s_at	**PFKFB3**	5209	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-2.70	0.00
232045_at	**PHACTR1**	221692	phosphatase and actin regulator 1	-2.20	0.63
200658_s_at	**PHB**	5245	prohibitin	3.22	0.63
232101_s_at	**PIGN**	23556	phosphatidylinositol glycan anchor biosynthesis, class N	2.40	0.63
224660_at	**PIGY**	84992	phosphatidylinositol glycan anchor biosynthesis, class Y	3.08	0.23
206369_s_at	**PIK3CG**	5294	phosphoinositide-3-kinase, catalytic, gamma polypeptide	-2.83	0.63
219014_at	**PLAC8**	51316	placenta-specific 8	-23.62	0.00
202925_s_at	**PLAGL2**	5326	pleiomorphic adenoma gene-like 2	-3.95	0.18
226636_at	**PLD1**	5337	phospholipase D1, phosphatidylcholine-specific	-4.34	0.63
201429_s_at	**PLK1** /// **RPL37A**	5347 /// 6168	polo-like kinase 1 (Drosophila) /// ribosomal protein L37a	2.02	0.23
227276_at	**PLXDC2**	84898	plexin domain containing 2	6.59	0.63
38671_at	**PLXND1**	23129	plexin D1	-3.55	0.27
225844_at	**POLE4**	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)	5.59	0.23
202306_at	**POLR2G**	5436	polymerase (RNA) II (DNA directed) polypeptide G	3.39	0.27
209302_at	**POLR2H**	5437	polymerase (RNA) II (DNA directed) polypeptide H	4.88	0.11
212226_s_at	**PPAP2B**	8613	phosphatidic acid phosphatase type 2B	-4.08	0.00
214146_s_at	**PPBP**	5473	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	4.59	0.11
214374_s_at	**PPFIBP1**	8496	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.86	0.11
211378_x_at	**PPIA**	5478	peptidylprolyl isomerase A (cyclophilin A)	2.24	0.00
222500_at	**PPIL1**	51645	peptidylprolyl isomerase (cyclophilin)-like 1	6.48	0.40
200975_at	**PPT1**	5538	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	3.01	0.11
201494_at	**PRCP**	5547	prolylcarboxypeptidase (angiotensinase C)	2.44	0.00
208680_at	**PRDX1**	5052	peroxiredoxin 1	4.49	0.00
201619_at	**PRDX3**	10935	peroxiredoxin 3	3.49	0.11
211743_s_at	**PRG2**	5553	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	-2.17	0.18
218764_at	**PRKCH**	5583	protein kinase C, eta	-2.87	0.00
203650_at	**PROCR**	10544	protein C receptor, endothelial (EPCR)	3.36	0.44
232629_at	**PROK2**	60675	prokineticin 2	-3.59	0.00
208880_s_at	**PRPF6**	24148	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	2.23	0.40
221734_at	**PRRC1**	133619	proline-rich coiled-coil 1	2.55	0.63
238513_at	**PRRG4**	79056	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	2.85	0.18
201400_at	**PSMB3**	5691	proteasome (prosome, macropain) subunit, beta type, 3	2.08	0.40
208827_at	**PSMB6**	5694	proteasome (prosome, macropain) subunit, beta type, 6	3.83	0.27
201068_s_at	**PSMC2**	5701	proteasome (prosome, macropain) 26S subunit, ATPase, 2	2.57	0.00
209503_s_at	**PSMC5**	5705	proteasome (prosome, macropain) 26S subunit, ATPase, 5	3.72	0.18
203447_at	**PSMD5**	5711	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-4.29	0.00
200820_at	**PSMD8**	5714	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	2.45	0.40

211270_x_at	**PTBP1**	5725	polypyrimidine tract binding protein 1	2.17	0.23
201433_s_at	**PTDSS1**	9791	phosphatidylserine synthase 1	5.94	0.27
210367_s_at	**PTGES**	9536	prostaglandin E synthase	-7.45	0.00
204748_at	**PTGS2**	5743	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-2.09	0.00
203030_s_at	**PTPRN2**	5799	protein tyrosine phosphatase, receptor type, N polypeptide 2	-5.41	0.18
206157_at	**PTX3**	5806	pentraxin-related gene, rapidly induced by IL-1 beta	-5.38	0.44
202990_at	**PYGL**	5836	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	2.62	0.27
1554800_at	**RAB39**	54734	RAB39, member RAS oncogene family	3.34	0.44
201039_s_at	**RAD23A**	5886	RAD23 homolog A (S. cerevisiae)	2.55	0.11
219125_s_at	**RAG1AP1**	55974	recombination activating gene 1 activating protein 1	2.98	0.63
202844_s_at	**RALBP1**	10928	ralA binding protein 1	2.70	0.11
200750_s_at	**RAN**	5901	RAN, member RAS oncogene family	2.43	0.40
204070_at	**RARRES3**	5920	retinoic acid receptor responder (tazarotene induced) 3	3.94	0.00
226436_at	**RASSF4**	83937	Ras association (RalGDS/AF-6) domain family 4	-2.82	0.63
208319_s_at	**RBM3**	5935	RNA binding motif (RNP1, RRM) protein 3	2.92	0.11
211974_x_at	**RBPJ**	3516	recombination signal binding protein for immunoglobulin kappa J region	2.02	0.11
204759_at	**RCBTB2**	1102	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	4.33	0.27
220570_at	**RETN**	56729	resistin	-4.78	0.15
203224_at	**RFK**	55312	riboflavin kinase	4.04	0.00
202963_at	**RFX5**	5993	regulatory factor X, 5 (influences HLA class II expression)	2.97	0.44
202388_at	**RGS2**	5997	regulator of G-protein signaling 2, 24kDa	-2.33	0.23
1553713_a_at	**RHEBL1**	121268	Ras homolog enriched in brain like 1	6.73	0.00
223169_s_at	**RHOU**	58480	ras homolog gene family, member U	-2.92	0.44
227366_at	**RILP**	83547	Rab interacting lysosomal protein	2.20	0.63
218528_s_at	**RNF38**	152006	ring finger protein 38	2.35	0.63
204208_at	**RNGTT**	8732	RNA guanylyltransferase and 5'-phosphatase	-5.41	0.15
212946_at	**RP11-125A7.3**	23078	KIAA0564 protein	7.18	0.40
221770_at	**RPE**	6120	ribulose-5-phosphate-3-epimerase	5.03	0.63
212973_at	**RPIA**	22934	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	4.17	0.90
229563_s_at	**RPL10A**	4736	ribosomal protein L10a	2.51	0.00
212933_x_at	**RPL13**	6137	ribosomal protein L13	2.33	0.11
219138_at	**RPL14**	9045	ribosomal protein L14	2.06	0.18
200022_at	**RPL18**	6141	ribosomal protein L18	2.03	0.27
208768_x_at	**RPL22**	6146	ribosomal protein L22	2.95	0.11
212039_x_at	**RPL3**	6122	ribosomal protein L3	2.48	0.11
213080_x_at	**RPL5**	6125	ribosomal protein L5	2.70	0.00
200936_at	**RPL8**	6132	ribosomal protein L8	2.25	0.00
200763_s_at	**RPLP1**	6176	ribosomal protein, large, P1	2.83	0.18
200908_s_at	**RPLP2**	6181	ribosomal protein, large, P2	2.17	0.00
201258_at	**RPS16**	6217	ribosomal protein S16	2.07	0.18
212578_x_at	**RPS17**	6218	ribosomal protein S17	2.02	0.11
200926_at	**RPS23**	6228	ribosomal protein S23	2.04	0.18
201094_at	**RPS29**	6235	ribosomal protein S29	2.12	0.63
200858_s_at	**RPS8**	6202	ribosomal protein S8	3.15	0.18
228487_s_at	**RREB1**	6239	Ras responsive element binding protein 1	2.68	0.23

219037_at	**RRP15**	51018	ribosomal RNA processing 15 homolog (S. cerevisiae)	3.04	0.18
212018_s_at	**RSL1D1**	26156	ribosomal L1 domain containing 1	3.71	0.11
211620_x_at	**RUNX1**	861	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	2.83	0.11
212440_at	**RY1**	11017	putative nucleic acid binding protein RY-1	2.32	0.00
205863_at	**S100A12**	6283	S100 calcium binding protein A12	-3.60	0.00
217728_at	**S100A6**	6277	S100 calcium binding protein A6	3.55	0.11
209486_at	**SAS10**	57050	disrupter of silencing 10	3.66	0.40
218793_s_at	**SCML1**	6322	sex comb on midleg-like 1 (Drosophila)	3.96	0.63
218217_at	**SCPEP1**	59342	serine carboxypeptidase 1	3.91	0.18
202542_s_at	**SCYE1**	9255	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	3.15	0.27
41329_at	**SCYL3**	57147	SCY1-like 3 (S. cerevisiae)	3.01	0.90
202071_at	**SDC4**	6385	syndecan 4	2.42	0.44
227785_at	**SDCCAG8**	10806	serologically defined colon cancer antigen 8	3.20	0.18
218681_s_at	**SDF2L1**	23753	stromal cell-derived factor 2-like 1	2.69	0.40
213716_s_at	**SECTM1**	6398	secreted and transmembrane 1	2.84	0.00
223225_s_at	**SEH1L**	81929	SEH1-like (S. cerevisiae)	4.82	0.40
223449_at	**SEMA6A**	57556	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	-16.61	0.40
210466_s_at	**SERBP1**	26135	SERPINE1 mRNA binding protein 1	2.92	0.00
242814_at	**SERPINB9**	5272	serpin peptidase inhibitor, clade B (ovalbumin), member 9	-3.30	0.44
227210_at	**SFMBT2**	57713	Scm-like with four mbt domains 2	-2.29	0.15
214141_x_at	**SFRS7**	6432	splicing factor, arginine/serine-rich 7, 35kDa	2.52	0.11
238567_at	**SGPP2**	130367	sphingosine-1-phosphate phosphotase 2	-3.42	0.40
232084_at	**SGTB**	54557	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	-2.26	0.23
221269_s_at	**SH3BGRL3**	83442	SH3 domain binding glutamic acid-rich protein like 3	2.57	0.27
210135_s_at	**SHOX2**	6474	short stature homeobox 2	7.28	0.27
56256_at	**SIDT2**	51092	SID1 transmembrane family, member 2	7.48	0.18
210569_s_at	**SIGLEC9**	27180	sialic acid binding Ig-like lectin 9	-3.46	0.18
1561880_a_at	**SIGLECP16**	400709	sialic acid binding Ig-like lectin, pseudogene 16	4.03	0.63
219386_s_at	**SLAMF8**	56833	SLAM family member 8	10.40	0.00
206052_s_at	**SLBP**	7884	stem-loop (histone) binding protein	3.01	0.63
203123_s_at	**SLC11A2**	4891	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	-2.63	0.00
209900_s_at	**SLC16A1**	6566	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	2.27	0.40
208916_at	**SLC1A5**	6510	solute carrier family 1 (neutral amino acid transporter), member 5	2.21	0.90
216721_at	**SLC25A30**	253512	Solute carrier family 25, member 30	4.13	0.40
226928_x_at	**SLC25A37**	51312	Solute carrier family 25, member 37	-2.01	0.00
200657_at	**SLC25A5**	292	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	3.84	0.18
212826_s_at	**SLC25A6**	293	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	2.71	0.23
207362_at	**SLC30A4**	7782	solute carrier family 30 (zinc transporter), member 4	-5.07	0.15
225881_at	**SLC35B4**	84912	solute carrier family 35, member B4	6.39	0.11
225037_at	**SLC35C2**	51006	solute carrier family 35, member C2	2.33	0.63
202089_s_at	**SLC39A6**	25800	solute carrier family 39 (zinc transporter), member 6	2.89	0.00
209267_s_at	**SLC39A8**	64116	solute carrier family 39 (zinc transporter), member 8	-3.54	0.00
226629_at	**SLC43A2**	124935	solute carrier family 43, member 2	-2.16	0.40

210692_s_at	**SLC43A3**	29015	solute carrier family 43, member 3	-2.01	0.15
204588_s_at	**SLC7A7**	9056	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	-4.13	0.00
219911_s_at	**SLCO4A1**	28231	solute carrier organic anion transporter family, member 4A1	-10.91	0.00
226743_at	**SLFN11**	91607	schlafen family member 11	2.88	0.18
1553055_a_at	**SLFN5**	162394	schlafen family member 5	-4.52	0.00
208794_s_at	**SMARCA4**	6597	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	3.41	0.00
209258_s_at	**SMC3**	9126	structural maintenance of chromosomes 3	2.47	0.44
209420_s_at	**SMPD1**	6609	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	3.19	0.00
213624_at	**SMPDL3A**	10924	sphingomyelin phosphodiesterase, acid-like 3A	-8.64	0.90
202043_s_at	**SMS**	6611	spermine synthase	-2.12	0.00
220358_at	**SNFT**	55509	Jun dimerization protein p21SNFT	4.13	0.00
201342_at	**SNRPC**	6631	small nuclear ribonucleoprotein polypeptide C	4.84	0.63
202690_s_at	**SNRPD1**	6632	small nuclear ribonucleoprotein D1 polypeptide 16kDa	2.03	0.00
203316_s_at	**SNRPE**	6635	small nuclear ribonucleoprotein polypeptide E	2.18	0.00
203832_at	**SNRPF**	6636	small nuclear ribonucleoprotein polypeptide F	4.48	0.63
200991_s_at	**SNX17**	9784	sorting nexin 17	2.95	0.44
213545_x_at	**SNX3**	8724	sorting nexin 3	2.94	0.11
205329_s_at	**SNX4**	8723	sorting nexin 4	3.33	0.63
229980_s_at	**SNX5**	27131	sorting nexin 5	4.08	0.63
213337_s_at	**SOCS1**	8651	suppressor of cytokine signaling 1	2.37	0.11
212807_s_at	**SORT1**	6272	sortilin 1	2.85	0.44
208921_s_at	**SRI**	6717	sorcin	2.33	0.18
222532_at	**SRPRB**	58477	signal recognition particle receptor, B subunit	4.68	0.00
201138_s_at	**SSB**	6741	Sjogren syndrome antigen B (autoantigen La)	3.77	0.00
202591_s_at	**SSBP1**	6742	single-stranded DNA binding protein 1	2.12	0.40
207040_s_at	**ST13**	6767	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	2.28	0.40
203217_s_at	**ST3GAL5**	8869	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	7.62	0.00
205026_at	**STAT5B**	6777	signal transducer and activator of transcription 5B	-3.74	0.00
220187_at	**STEAP4**	79689	STEAP family member 4	2.45	0.00
204068_at	**STK3**	6788	serine/threonine kinase 3 (STE20 homolog, yeast)	2.16	0.00
217874_at	**SUCLG1**	8802	succinate-CoA ligase, GDP-forming, alpha subunit	3.95	0.00
223330_s_at	**SUGT1**	10910	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	2.65	0.90
226850_at	**SUMF1**	285362	sulfatase modifying factor 1	3.62	0.44
32402_s_at	**SYMPK**	8189	symplekin	3.91	0.44
217834_s_at	**SYNCRIP**	10492	synaptotagmin binding, cytoplasmic RNA interacting protein	2.13	0.27
235154_at	**TAF3**	83860	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	3.83	0.00
1552542_s_at	**TAGAP**	117289	T-cell activation GTPase activating protein	2.01	0.00
216920_s_at	**TARP /// TRGC2 /// TRGV9**	445347 /// 6967 /// 6983	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading frame protein	-2.47	0.18
201263_at	**TARS**	6897	threonyl-tRNA synthetase	3.63	0.23
203667_at	**TBCA**	6902	tubulin folding cofactor A	2.59	0.40
213400_s_at	**TBL1X**	6907	transducin (beta)-like 1X-linked	2.35	0.44
203135_at	**TBP**	6908	TATA box binding protein	2.44	0.63

202396_at	**TCERG1**	10915	transcription elongation regulator 1	4.81	0.63
204849_at	**TCFL5**	10732	transcription factor-like 5 (basic helix-loop-helix)	-3.91	0.00
212083_at	**TEX261**	113419	testis expressed 261	3.57	0.63
212330_at	**TFDP1**	7027	transcription factor Dp-1	-2.61	0.00
207332_s_at	**TFRC**	7037	transferrin receptor (p90, CD71)	-4.62	0.00
203085_s_at	**TGFB1**	7040	transforming growth factor, beta 1	2.99	0.90
201506_at	**TGFBI**	7045	transforming growth factor, beta-induced, 68kDa	2.85	0.63
206004_at	**TGM3**	7053	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	-7.20	0.40
201110_s_at	**THBS1**	7057	thrombospondin 1	-8.06	0.27
219122_s_at	**THG1L**	54974	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	2.05	0.63
218118_s_at	**TIMM23**	10431	translocase of inner mitochondrial membrane 23 homolog (yeast)	3.82	0.11
218357_s_at	**TIMM8B**	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)	3.02	0.11
201666_at	**TIMP1**	7076	TIMP metallopeptidase inhibitor 1	-3.75	0.44
201922_at	**TINP1**	10412	TGF beta-inducible nuclear protein 1	3.69	0.23
216370_s_at	**TKTL1**	8277	transketolase-like 1	-2.66	0.15
212769_at	**TLE3**	7090	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	-2.22	0.40
213550_s_at	**TMCO6**	55374	transmembrane and coiled-coil domains 6	2.19	0.63
219690_at	**TMEM149**	79713	transmembrane protein 149	5.12	0.00
1558281_a_at	**TMEM184A**	202915	transmembrane protein 184A	-2.59	0.23
241392_at	**TMEM39A**	55254	Transmembrane protein 39A	-3.32	0.44
217795_s_at	**TMEM43**	79188	transmembrane protein 43	2.13	0.27
226083_at	**TMEM70**	54968	transmembrane protein 70	2.86	0.11
212204_at	**TMEM87A**	25963	transmembrane protein 87A	2.36	0.44
217733_s_at	**TMSB10**	9168	thymosin, beta 10	2.08	0.00
1552648_a_at	**TNFRSF10A**	8797	tumor necrosis factor receptor superfamily, member 10a	2.59	0.40
206729_at	**TNFRSF8**	943	tumor necrosis factor receptor superfamily, member 8	-7.55	0.18
209500_x_at	**TNFSF12-TNFSF13 /// TNFSF13**	407977 /// 8741	tumor necrosis factor (ligand) superfamily, member 13 /// tumor necrosis factor (ligand) superfamily, member 12-member 13	7.83	0.00
229326_at	**TNFSF13**	8741	Tumor necrosis factor (ligand) superfamily, member 13	6.16	0.00
206907_at	**TNFSF9**	8744	tumor necrosis factor (ligand) superfamily, member 9	-20.09	0.40
220655_at	**TNIP3**	79931	TNFAIP3 interacting protein 3	-44.67	0.00
222474_s_at	**TOMM22**	56993	translocase of outer mitochondrial membrane 22 homolog (yeast)	3.68	0.00
201519_at	**TOMM70A**	9868	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	4.00	0.63
215411_s_at	**TRAF3IP2**	10758	TRAF3 interacting protein 2	-26.41	0.00
205804_s_at	**TRAF3IP3**	80342	TRAF3 interacting protein 3	-5.87	0.00
218403_at	**TRIAP1**	51499	TP53 regulated inhibitor of apoptosis 1	6.39	0.00
212118_at	**TRIM27**	5987	tripartite motif-containing 27	2.91	0.44
202734_at	**TRIP10**	9322	thyroid hormone receptor interactor 10	-5.39	0.15
222768_s_at	**TRMT6**	51605	tRNA methyltransferase 6 homolog (S. cerevisiae)	3.72	0.00
225235_at	**TSPAN17**	26262	tetraspanin 17	5.43	0.11
202096_s_at	**TSPO**	706	translocator protein (18kDa)	3.92	0.40
201113_at	**TUFM**	7284	Tu translation elongation factor, mitochondrial	2.42	0.63
225406_at	**TWSG1**	57045	twisted gastrulation homolog 1 (Drosophila)	4.82	0.27
224511_s_at	**TXNDC17**	84817	thioredoxin domain containing 17	2.18	0.63

205890_s_at	**UBD**	10537	ubiquitin D	4.55	0.00
225783_at	**UBE2F**	140739	ubiquitin-conjugating enzyme E2F (putative)	2.36	0.63
209042_s_at	**UBE2G2**	7327	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	3.47	0.00
213536_s_at	**UBE2I**	7329	Ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	2.50	0.44
218082_s_at	**UBP1**	7342	upstream binding protein 1 (LBP-1a)	2.46	0.44
224827_at	**UBTD2**	92181	ubiquitin domain containing 2	-2.16	0.44
203271_s_at	**UNC119**	9094	unc-119 homolog (C. elegans)	-3.39	0.18
212144_at	**UNC84B**	25777	unc-84 homolog B (C. elegans)	2.26	0.23
202233_s_at	**UQCRH**	7388	ubiquinol-cytochrome c reductase hinge protein	2.15	0.00
220419_s_at	**USP25**	29761	ubiquitin specific peptidase 25	2.10	0.00
212513_s_at	**USP33**	23032	ubiquitin specific peptidase 33	2.03	0.63
218235_s_at	**UTP11L**	51118	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	2.94	0.11
203721_s_at	**UTP18**	51096	UTP18, small subunit (SSU) processome component, homolog (yeast)	6.80	0.11
201336_at	**VAMP3**	9341	vesicle-associated membrane protein 3 (cellubrevin)	2.77	0.23
214115_at	**VAMP5**	10791	Vesicle-associated membrane protein 5 (myobrevin)	7.18	0.00
202546_at	**VAMP8**	8673	vesicle-associated membrane protein 8 (endobrevin)	9.20	0.00
208846_s_at	**VDAC3**	7419	voltage-dependent anion channel 3	2.25	0.44
210512_s_at	**VEGFA**	7422	vascular endothelial growth factor A	-2.09	0.00
223675_s_at	**VEZT**	55591	vezatin, adherens junctions transmembrane protein	3.87	0.63
1558549_s_at	**VNN1**	8876	vanin 1	-2.87	0.63
205922_at	**VNN2**	8875	vanin 2	-2.59	0.00
1553514_a_at	**VNN3**	55350	vanin 3	-4.42	0.00
212323_s_at	**VPS13D**	55187	vacuolar protein sorting 13 homolog D (S. cerevisiae)	-4.96	0.18
218882_s_at	**WDR3**	10885	WD repeat domain 3	2.83	0.44
238677_at	**WDR36**	134430	WD repeat domain 36	6.54	0.40
221531_at	**WDR61**	80349	WD repeat domain 61	2.58	0.63
224748_at	**WDR68**	10238	WD repeat domain 68	2.88	0.23
222489_s_at	**WRNIP1**	56897	Werner helicase interacting protein 1	2.14	0.63
231899_at	**ZC3H12C**	85463	zinc finger CCCH-type containing 12C	-3.75	0.63
203556_at	**ZHX2**	22882	zinc fingers and homeoboxes 2	-2.06	0.00
209049_s_at	**ZMYND8**	23613	zinc finger, MYND-type containing 8	-6.28	0.15
205739_x_at	**ZNF107**	51427	zinc finger protein 107	-9.99	0.40
200050_at	**ZNF146**	7705	zinc finger protein 146	2.10	0.40
213452_at	**ZNF184**	7738	zinc finger protein 184	3.51	0.18
212368_at	**ZNF292**	23036	zinc finger protein 292	-2.02	0.90
222283_at	**ZNF480**	147657	zinc finger protein 480	3.77	0.27
39891_at	**ZNF710**	374655	zinc finger protein 710	-2.07	0.00
226261_at	**ZNRF2**	223082	zinc and ring finger 2	-2.15	0.63

Protein abundance significantly changed in response to LPS (fold change = LPS/Control)

IPI	Protein Symbol	Protein Name	Log2 Ratio	Q-value
IPI00022975.1	**ALOX5AP**	ARACHIDONATE 5-LIPOXYGENASE-ACTIVATING PROTEIN.	1.66	0.02
IPI00220390.4	**ANKRD7**	ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 7.	1.31	0.04
IPI00038356.3	**ARG1**	25 KDA PROTEIN.	1.74	0.02

IPI00014256.2	**ARHGEF6**	ISOFORM 1 OF RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 6.	2.23	0.01
IPI00007280.9	**ARPC5**	17 KDA PROTEIN.	2.01	0.01
IPI00296362.6	**ASPM**	ISOFORM 1 OF ABNORMAL SPINDLE-LIKE MICROCEPHALY-ASSOCIATED PROTEIN.	1.97	0.02
IPI00328350.6	**C1orf24**	NIBAN PROTEIN.	-5.27	0.02
IPI00008274.5	**CAP1**	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1.	1.19	0.02
IPI00550587.3	**CEP290**	CDNA FLJ13615 FIS, CLONE PLACE1010896, WEAKLY SIMILAR TO NUF1 PROTEIN.	1.29	0.02
IPI00472901.2	**CHD7**	CHROMODOMAIN HELICASE DNA BINDING PROTEIN 7.	2.41	0.04
IPI00022744.5	**CSE1L**	ISOFORM 1 OF EXPORTIN-2.	1.23	0.03
IPI00029485.2	**DCTN1**	ISOFORM P150 OF DYNACTIN-1.	-1.57	0.03
IPI00396370.5	**EIF3S9**	ISOFORM 1 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9.	1.73	0.01
IPI00006574.1	**FAM49A**	PROTEIN FAM49A.	1.39	0.03
IPI00029625.4	**FLOT2**	FLOTILLIN 2.	-2.91	0.03
IPI00456878.2	**GVIN1**	PREDICTED: GTPASE, VERY LARGE INTERFERON INDUCIBLE 1.	-4.06	0.01
IPI00217468.2	**HIST1H1B**	HISTONE H1.5.	1.71	0.01
IPI00419833.6	**HIST1H2BK**	HISTONE H2B TYPE 1-K.	3.02	0.03
IPI00018534.3	**HIST1H2BL**	HISTONE H2B TYPE 1-L.	1.06	0.03
IPI00216592.2	**HNRPC**	ISOFORM C1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2.	1.86	0.02
IPI00171903.1	**HNRPM**	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M ISOFORM A.	1.32	0.02
IPI00647205.1	**KIAA0408**	HYPOTHETICAL PROTEIN LOC387104.	-6.28	0.01
IPI00299547.4	**LCN2**	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR.	-1.72	0.02
IPI00465431.6	**LGALS3**	GALECTIN-3.	1.19	0.03
IPI00018278.2	**LOC285957**	HISTONE H2AV.	1.17	0.02
IPI00003734.1	**LOC347701**	PUTATIVE S100 CALCIUM-BINDING PROTEIN H_NH0456N16.1.	-1.61	0.04
IPI00383071.1	**LOC388642**	RCTPI1 (FRAGMENT).	1.24	0.03
IPI00419154.1	**LOC388692**	CDNA FLJ41668 FIS, CLONE FEBRA2028477.	1.35	0.04
IPI00374686.3	**LOC647474**	PREDICTED: SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 ISOFORM 1.	1.44	0.04
IPI00401834.2	**LOC648976**	PREDICTED: HYPOTHETICAL PROTEIN XP_934530.	-4.28	0.04
IPI00219871.4	**LSM8**	U6 SNRNA-ASSOCIATED SM-LIKE PROTEIN LSM8.	-1.98	0.03
IPI00013260.3	**LSP1**	LYMPHOCYTE-SPECIFIC PROTEIN 1.	1.15	0.03
IPI00303882.2	**M6PRBP1**	ISOFORM B OF MANNOSE-6-PHOSPHATE RECEPTOR-BINDING PROTEIN 1.	-1.64	0.02
IPI00030919.3	**MAP2K1IP1**	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1-INTERACTING PROTEIN 1.	-2.37	0.03
IPI00457110.1	**MCTP2**	MCTP2.	-2.06	0.03
IPI00027509.3	**MMP9**	MATRIX METALLOPROTEINASE-9 PRECURSOR.	-2.57	0.01
IPI00000105.3	**MVP**	MAJOR VAULT PROTEIN.	-3.69	0.02
IPI00444262.1	**NCL**	CDNA FLJ45706 FIS, CLONE FEBRA2028457, HIGHLY SIMILAR TO NUCLEOLIN.	-4.85	0.01

IPI00299571.4	**PDIA6**	CDNA FLJ45525 FIS, CLONE BRTHA2026311, HIGHLY SIMILAR TO PROTEIN DISULFIDE ISOMERASE A6.	-3.26	0.02
IPI00329185.3	**PLCG2**	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2.	1.41	0.03
IPI00235481.2	**PMFBP1**	PMFBP1 PROTEIN.	-2.75	0.04
IPI00027808.1	**POLR2B**	DNA-DIRECTED RNA POLYMERASE II 140 KDA POLYPEPTIDE.	-4.35	0.02
IPI00168184.7	**PPP2R1A**	CDNA FLJ34068 FIS, CLONE FCBBF3001918, HIGHLY SIMILAR TO SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, ALPHA ISOFORM.	-2.97	0.02
IPI00016169.1	**PRO0471**	PRO0471.	1.43	0.02
IPI00419433.2	**RAB11FIP1**	ISOFORM 1 OF RAB11 FAMILY-INTERACTING PROTEIN 1.	-3.41	0.02
IPI00221325.3	**RANBP2**	RAN-BINDING PROTEIN 2.	-4.67	0.02
IPI00409720.3	**REEP2**	22 KDA PROTEIN.	-1.74	0.01
IPI00028108.1	**RGS19**	REGULATOR OF G-PROTEIN SIGNALING 19.	-1.08	0.01
IPI00027569.1	**RNF187**	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C-LIKE 1.	-3.84	0.03
IPI00162563.5	**RNF40**	ISOFORM 1 OF UBIQUITIN-PROTEIN LIGASE BRE1B.	-4.10	0.02
IPI00453473.5	**RP11-444E17.2**	HISTONE H4.	1.27	0.02
IPI00026627.3	**RP2**	PROTEIN XRP2.	1.43	0.04
IPI00465429.3	**RUFY1**	ISOFORM 2 OF RUN AND FYVE DOMAIN-CONTAINING PROTEIN 1.	-3.21	0.04
IPI00218131.2	**S100A12**	PROTEIN S100-A12.	-1.40	0.02
IPI00305457.5	**SERPINA1**	PRO2275.	1.69	0.02
IPI00010402.2	**SH3BGRL3**	HYPOTHETICAL PROTEIN.	1.00	0.02
IPI00172421.6	**SKP1A**	ISOFORM 2 OF S-PHASE KINASE-ASSOCIATED PROTEIN 1A.	-4.25	0.03
IPI00003527.4	**SLC9A3R1**	EZRIN-RADIXIN-MOESIN-BINDING PHOSPHOPROTEIN 50.	1.63	0.01
IPI00783228.1	**SPTB**	SPECTRIN BETA ISOFORM B.	-2.75	0.02
IPI00297492.1	**STT3A**	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE SUBUNIT STT3A.	1.26	0.02
IPI00291006.1	**STYXL1**	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	-2.49	0.02
IPI00219274.3	**SYT2**	SYNAPTOTAGMIN-2.	-1.11	0.03
IPI00011727.2	**SYT5**	SYNAPTOTAGMIN-5.	-5.70	0.04
IPI00030536.5	**SYTL2**	CDNA FLJ16407 FIS, CLONE UTERU2028734, HIGHLY SIMILAR TO MUS MUSCULUS SLP2-A SYNAPTOTAGMIN-LIKE PROTEIN 2-A DELTA 2S-III.	-4.02	0.02
IPI00019381.4	**TMEM30A**	ISOFORM 1 OF CELL CYCLE CONTROL PROTEIN 50A.	2.14	0.01
IPI00220827.4	**TMSB10**	THYMOSIN BETA-10.	-1.80	0.03
IPI00023761.3	**TTLL3**	TUBULIN TYROSINE LIGASE-LIKE FAMILY, MEMBER 3 ISOFORM 1.	2.47	0.04
IPI00011696.1	**VAV1**	PROTO-ONCOGENE VAV.	1.54	0.01
IPI00031583.2	**VDP**	HYPOTHETICAL PROTEIN DKFZP451D234.	-1.80	0.02
IPI00216318.5	**YWHAB**	TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION PROTEIN, BETA POLYPEPTIDE.	1.45	0.02

Protein abundance significantly changed in response to GM+I (fold change = GM+I/Control)

IPI	Protein Symbol	Protein Name	Log2 Ratio	Q-value
IPI:IPI00465439.4	**ALDOA**	FRUCTOSE-BISPHOSPHATE ALDOLASE A.	1.06	0.03
IPI:IPI00022975.1	**ALOX5AP**	ARACHIDONATE 5-LIPOXYGENASE-ACTIVATING PROTEIN.	1.77	0.01
IPI:IPI00221225.3	**ANXA4**	ANNEXIN IV.	2.00	0.02
IPI:IPI00329801.11	**ANXA5**	ANNEXIN A5.	1.41	0.05
IPI:IPI00038356.3	**ARG1**	25 KDA PROTEIN.	1.84	0.03
IPI:IPI00291560.4	**ARG1**	ISOFORM 1 OF ARGINASE-1.	-4.15	0.02
IPI:IPI00014256.2	**ARHGEF6**	ISOFORM 1 OF RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 6.	2.52	0.03
IPI:IPI00296362.6	**ASPM**	ISOFORM 1 OF ABNORMAL SPINDLE-LIKE MICROCEPHALY-ASSOCIATED PROTEIN.	1.94	0.03
IPI:IPI00008274.5	**CAP1**	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1.	1.11	0.03
IPI:IPI00027341.1	**CAPG**	MACROPHAGE CAPPING PROTEIN.	1.15	0.01
IPI:IPI00550587.3	**CEP290**	CDNA FLJ13615 FIS, CLONE PLACE1010896, WEAKLY SIMILAR TO NUF1 PROTEIN.	1.72	0.01
IPI:IPI00012011.5	**CFL1**	COFILIN-1.	1.02	0.03
IPI:IPI00024067.3	**CLTC**	CLATHRIN HEAVY CHAIN 1.	-2.25	0.04
IPI:IPI00022744.5	**CSE1L**	ISOFORM 1 OF EXPORTIN-2.	1.34	0.03
IPI:IPI00218433.4	**CYBA**	CYTOCHROME B-245 LIGHT CHAIN.	1.08	0.03
IPI:IPI00218646.2	**CYBB**	CYTOCHROME B-245 HEAVY CHAIN.	1.09	0.03
IPI:IPI00025307.1	**CYP27A1**	CYTOCHROME P450 27, MITOCHONDRIAL PRECURSOR.	1.44	0.04
IPI:IPI00292858.4	**ECGF1**	THYMIDINE PHOSPHORYLASE PRECURSOR.	2.28	0.04
IPI:IPI00216164.2	**EHHADH**	PEROXISOMAL BIFUNCTIONAL ENZYME.	2.27	0.04
IPI:IPI00167909.4	**EML3**	ECHINODERM MICROTUBULE ASSOCIATED PROTEIN LIKE 3.	1.04	0.04
IPI:IPI00006574.1	**FAM49A**	PROTEIN FAM49A.	1.45	0.04
IPI:IPI00025494.1	**FAM78A**	FLJ00024 PROTEIN (FRAGMENT).	2.14	0.03
IPI:IPI00029625.4	**FLOT2**	FLOTILLIN 2.	-2.45	0.04
IPI:IPI00221199.1	**GCN5L2**	ISOFORM 2 OF GENERAL CONTROL OF AMINO ACID SYNTHESIS PROTEIN 5-LIKE 2.	1.70	0.03
IPI:IPI00456878.2	**GVIN1**	PREDICTED: GTPASE, VERY LARGE INTERFERON INDUCIBLE 1.	-1.99	0.03
IPI:IPI00473011.2	**HBD**	HEMOGLOBIN SUBUNIT DELTA.	-2.75	0.03
IPI:IPI00217468.2	**HIST1H1B**	HISTONE H1.5.	1.96	0.01
IPI:IPI00217465.4	**HIST1H1C**	HISTONE H1.2.	1.44	0.03
IPI:IPI00220403.2	**HIST1H2BB**	HISTONE H2B TYPE 1-B.	3.23	0.04
IPI:IPI00419833.6	**HIST1H2BK**	HISTONE H2B TYPE 1-K.	2.78	0.04
IPI:IPI00003935.5	**HIST2H2BE**	HISTONE H2B TYPE 2-E.	1.11	0.03
IPI:IPI00216592.2	**HNRPC**	ISOFORM C1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2.	1.63	0.03
IPI:IPI00299517.3	**KIAA0157**	PROTEIN KIAA0157.	-2.44	0.03
IPI:IPI00647205.1	**KIAA0408**	HYPOTHETICAL PROTEIN LOC387104.	-3.11	0.02
IPI:IPI00006746.3	**KIAA1189**	HYPOTHETICAL PROTEIN LOC57471 ISOFORM B.	1.25	0.03
IPI:IPI00739203.1	**KIAA1957**	PREDICTED: SIMILAR TO NUCLEAR LOCALIZED FACTOR 2.	2.57	0.03
IPI:IPI00032328.1	**KNG1**	ISOFORM HMW OF KININOGEN-1 PRECURSOR.	2.54	0.03
IPI:IPI00297169.1	**LCP2**	LYMPHOCYTE CYTOSOLIC PROTEIN 2.	-1.22	0.04
IPI:IPI00465431.6	**LGALS3**	GALECTIN-3.	1.23	0.03
IPI:IPI00183699.3	**LOC151657**	ISOFORM 2 OF HMG BOX TRANSCRIPTION FACTOR BBX.	-2.12	0.04

IPI:IPI00145540.7	**LOC402643**	PREDICTED: SIMILAR TO TROPOMYOSIN 3 ISOFORM 2.	1.04	0.03
IPI:IPI00374686.3	**LOC647474**	PREDICTED: SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 ISOFORM 1.	1.79	0.03
IPI:IPI00401834.2	**LOC648976**	PREDICTED: HYPOTHETICAL PROTEIN XP_934530.	-4.88	0.05
IPI:IPI00013260.3	**LSP1**	LYMPHOCYTE-SPECIFIC PROTEIN 1.	1.35	0.04
IPI:IPI00298793.4	**MANBA**	BETA-MANNOSIDASE PRECURSOR.	1.48	0.04
IPI:IPI00027509.3	**MMP9**	MATRIX METALLOPROTEINASE-9 PRECURSOR.	-1.82	0.01
IPI:IPI00000105.3	**MVP**	MAJOR VAULT PROTEIN.	-3.54	0.02
IPI:IPI00027255.1	**MYL6B**	MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE A ISOFORM.	1.33	0.02
IPI:IPI00444262.1	**NCL**	CDNA FLJ45706 FIS, CLONE FEBRA2028457, HIGHLY SIMILAR TO NUCLEOLIN.	-6.12	0.03
IPI:IPI00008307.1	**PADI4**	PROTEIN-ARGININE DEIMINASE TYPE-4.	1.03	0.03
IPI:IPI00298547.3	**PARK7**	PROTEIN DJ-1.	1.26	0.04
IPI:IPI00018873.1	**PBEF1**	ISOFORM 1 OF NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE.	1.20	0.04
IPI:IPI00218570.5	**PGAM2**	PHOSPHOGLYCERATE MUTASE 2.	1.27	0.03
IPI:IPI00329185.3	**PLCG2**	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2.	1.80	0.03
IPI:IPI00012865.1	**PLD1**	ISOFORM PLD1A OF PHOSPHOLIPASE D1.	1.66	0.04
IPI:IPI00027808.1	**POLR2B**	DNA-DIRECTED RNA POLYMERASE II 140 KDA POLYPEPTIDE.	-3.64	0.03
IPI:IPI00009316.3	**PPIE**	ISOFORM A OF PEPTIDYL-PROLYL CIS-TRANS ISOMERASE E.	-3.83	0.05
IPI:IPI00044891.1	**PRAM1**	ADAPTOR MOLECULE-1.	-3.09	0.04
IPI:IPI00024915.2	**PRDX5**	ISOFORM MITOCHONDRIAL OF PEROXIREDOXIN-5, MITOCHONDRIAL PRECURSOR.	1.37	0.03
IPI:IPI00016169.1	**PRO0471**	PRO0471.	1.36	0.03
IPI:IPI00004358.3	**PYGB**	GLYCOGEN PHOSPHORYLASE, BRAIN FORM.	1.37	0.02
IPI:IPI00221325.3	**RANBP2**	RAN-BINDING PROTEIN 2.	-3.99	0.02
IPI:IPI00016825.1	**RGS18**	REGULATOR OF G-PROTEIN SIGNALING 18.	1.48	0.04
IPI:IPI00017342.1	**RHOG**	RHO-RELATED GTP-BINDING PROTEIN RHOG PRECURSOR.	1.26	0.03
IPI:IPI00162563.5	**RNF40**	ISOFORM 1 OF UBIQUITIN-PROTEIN LIGASE BRE1B.	-3.78	0.04
IPI:IPI00026627.3	**RP2**	PROTEIN XRP2.	2.06	0.03
IPI:IPI00021266.1	**RPL23A**	60S RIBOSOMAL PROTEIN L23A.	3.23	0.04
IPI:IPI00027463.1	**S100A6**	PROTEIN S100-A6.	-1.81	0.03
IPI:IPI00006640.3	**SERPINI2**	SERPIN I2 PRECURSOR.	-1.95	0.03
IPI:IPI00181702.3	**SFRS15**	ISOFORM 1 OF SPLICING FACTOR, ARGININE/SERINE-RICH 15.	1.21	0.03
IPI:IPI00010402.2	**SH3BGRL3**	HYPOTHETICAL PROTEIN.	1.52	0.02
IPI:IPI00172421.6	**SKP1A**	ISOFORM 2 OF S-PHASE KINASE-ASSOCIATED PROTEIN 1A.	-4.27	0.01
IPI:IPI00783228.1	**SPTB**	SPECTRIN BETA ISOFORM B.	-2.65	0.04
IPI:IPI00102936.3	**SRP68**	ISOFORM 2 OF SIGNAL RECOGNITION PARTICLE 68 KDA PROTEIN.	1.35	0.02
IPI:IPI00297492.1	**STT3A**	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE SUBUNIT STT3A.	1.96	0.01
IPI:IPI00291006.1	**STYXL1**	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	-2.12	0.03

IPI:IPI00219274.3	**SYT2**	SYNAPTOTAGMIN-2.	-1.58	0.04
IPI:IPI00030536.5	**SYTL2**	CDNA FLJ16407 FIS, CLONE UTERU2028734, HIGHLY SIMILAR TO MUS MUSCULUS SLP2-A SYNAPTOTAGMIN-LIKE PROTEIN 2-A DELTA 2S-III.	-3.84	0.01
IPI:IPI00002135.1	**TACC3**	TRANSFORMING ACIDIC COILED-COIL-CONTAINING PROTEIN 3.	1.40	0.04
IPI:IPI00217236.3	**TBCA**	TUBULIN-SPECIFIC CHAPERONE A.	1.02	0.03
IPI:IPI00019381.4	**TMEM30A**	ISOFORM 1 OF CELL CYCLE CONTROL PROTEIN 50A.	1.97	0.01
IPI:IPI00027280.2	**TOP2B**	ISOFORM BETA-2 OF DNA TOPOISOMERASE 2-BETA.	1.53	0.02
IPI:IPI00221178.1	**TPD52L2**	ISOFORM 2 OF TUMOR PROTEIN D54.	2.47	0.05
IPI:IPI00178083.2	**TPM3**	29 KDA PROTEIN.	1.46	0.03
IPI:IPI00010779.3	**TPM4**	TROPOMYOSIN 4.	1.13	0.03
IPI:IPI00166768.2	**TUBA6**	TUBA6 PROTEIN.	1.26	0.02
IPI:IPI00011654.2	**TUBB2A**	TUBULIN BETA-2 CHAIN.	1.60	0.01
IPI:IPI00301058.4	**VASP**	VASODILATOR-STIMULATED PHOSPHOPROTEIN.	1.32	0.03
IPI:IPI00156689.3	**VAT1**	SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG.	1.76	0.03
IPI:IPI00011696.1	**VAV1**	PROTO-ONCOGENE VAV.	1.59	0.02
IPI:IPI00031583.2	**VDP**	HYPOTHETICAL PROTEIN DKFZP451D234.	-1.76	0.04
IPI:IPI00216699.1	**ZC3H3**	ISOFORM 2 OF UNC-112-RELATED PROTEIN 2.	1.36	0.03
IPI:IPI00402104.5		15 KDA PROTEIN.	2.00	0.03