

Differentially expressed genes on collagen

probesetID	Name	Symbol	logFC.col	Fold Change	
				Collagen	adj.P.Val
205199_at	carbonic anhydrase IX	CA9	3.299453256	9.845423	0.002990116
219410_at	transmembrane protein 45A N-myc downstream regulated	TMEM45A	2.753742271	6.744644	0.007988424
200632_s_at	gene 1 BCL2/adenovirus E1B 19kDa	NDRG1	2.688283097	6.445459	0.007043637
221478_at	interacting protein 3-like	BNIP3L	2.355828184	5.11888	0.003930777
204595_s_at	stanniocalcin 1	STC1	2.331592801	5.033608	0.004387256
215446_s_at	lysyl oxidase	LOX	2.227402498	4.682901	0.02543191
204597_x_at	stanniocalcin 1 lysyl oxidase-like 2 /// ectonucleoside triphosphate	STC1	2.121759431	4.352244	0.006921301
202998_s_at	diphosphohydrolase 4	ENTPD4	//, 2.118145508	4.341355	0.010789862
202022_at	aldolase C, fructose-bisphosphate	ALDOC	2.083954485	4.239677	0.007308892
	solute carrier family 6 (neurotransmitter transporter,				
202219_at	creatine), member 8	SLC6A8	2.037283638	4.10472	0.007337164
204298_s_at	lysyl oxidase	LOX	2.02909412	4.081485	0.015091187
203729_at	epithelial membrane protein 3 triggering receptor expressed on	EMP3	1.999103197	3.997514	0.027885596
219434_at	myeloid cells 1	TREM1	1.94597187	3.852972	0.005627889
	solute carrier family 6 (neurotransmitter transporter,				
210854_x_at	creatine), member 8	SLC6A8	1.853352748	3.613389	0.007271766
213397_x_at	ribonuclease, RNase A family, 4 BCL2/adenovirus E1B 19kDa	RNASE4	1.83820444	3.575647	0.024017189
201849_at	interacting protein 3	BNIP3	1.808999226	3.503991	0.005627889
	solute carrier family 6 (neurotransmitter transporter,				
213843_x_at	creatine), member 8	SLC6A8	1.758162859	3.382671	0.00887733
203963_at	carbonic anhydrase XII BCL2/adenovirus E1B 19kDa	CA12	1.755610704	3.376692	0.008546266
201848_s_at	interacting protein 3	BNIP3	1.750101671	3.363823	0.003930777
210735_s_at	carbonic anhydrase XII insulin-like growth factor binding	CA12	1.724284151	3.304161	0.006949425
201163_s_at	protein 7	IGFBP7	1.630067563	3.095275	0.014733441
215867_x_at	carbonic anhydrase XII	CA12	1.611997724	3.056748	0.007257672

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	solute carrier family 6 (neurotransmitter transporter, creatine), member 8 /// solute carrier family 6 (neurotransmitter transporter, creatine), member 10 (pseudogene) /// hypothetical				
215812_s_at	LOC653562	LOC653562	1.587810585	3.005928	0.005627889
214164_x_at	carbonic anhydrase XII	CA12	1.576030486	2.981484	0.007610795
201313_at	enolase 2 (gamma, neuronal)	ENO2	1.574055942	2.977406	0.006293525
205158_at	ribonuclease, RNase A family, 4	RNASE4	1.553832302	2.93596	0.02449946
213640_s_at	lysyl oxidase	LOX	1.497766649	2.824052	0.026683706
204508_s_at	carbonic anhydrase XII vascular endothelial growth	CA12	1.479552769	2.788623	0.017071662
210512_s_at	factor A	VEGFA	1.47723116	2.784139	0.020112851
201185_at	HtrA serine peptidase 1 very low density lipoprotein	HTRA1	1.474539838	2.77895	0.016278635
209822_s_at	receptor BCL2-interacting killer (apoptosis-inducing)	VLDLR	1.466523662	2.763552	0.006994923
205780_at		BIK	1.456313137	2.744062	0.001616605
	procollagen-lysine, 2-				
202620_s_at	oxoglutarate 5-dioxygenase 2 protein kinase C, delta binding	PLOD2	1.435060093	2.703934	0.020959453
213010_at	protein	PRKCDBP	1.429329966	2.693216	0.001616605
202364_at	MAX interactor 1 procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha	MXI1	1.425838466	2.686706	0.012932821
207543_s_at	polypeptide I BCL2/adenovirus E1B 19kDa	P4HA1	1.418199538	2.672518	0.018699219
221479_s_at	interacting protein 3-like	BNIP3L	1.401482172	2.641728	0.009110746
219888_at	sperm associated antigen 4 acyl-Coenzyme A oxidase 2,	SPAG4	1.366358041	2.578189	0.004926805
205364_at	branched chain	ACOX2	1.357728182	2.562813	0.004895765
219232_s_at	egl nine homolog 3 (C. elegans) cysteine and glycine-rich protein	EGLN3	1.332916288	2.519114	0.008546266
207030_s_at	2	CSRP2	1.315815549	2.48943	0.005627889
218507_at	hypoxia-inducible protein 2	HIG2	1.295911215	2.45532	0.001616605
	procollagen-lysine, 2-				
202619_s_at	oxoglutarate 5-dioxygenase 2	PLOD2	1.278971216	2.426659	0.026201143

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	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	PTGS1	1.277701242	2.424524	0.006293525
215813_s_at	insulin-like growth factor binding protein 7	IGFBP7	1.267966477	2.408219	0.023195616
201162_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	1.265426572	2.403983	0.009825362
	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	1.262105186	2.398455	0.039958616
210933_s_at	transforming growth factor, beta 1	TGFB1	1.261478857	2.397414	0.015628504
	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	PTGS1	1.253758494	2.384619	0.007257672
221123_x_at	zinc finger protein 395	ZNF395	1.242957854	2.366833	0.022792248
213201_s_at	troponin T type 1 (skeletal, slow) angiogenin, ribonuclease, RNase	TNNT1	1.240175725	2.362273	0.01323345
205141_at	A family, 5	ANG	1.219137479	2.328075	0.012973447
209230_s_at	nuclear protein 1 nuclear factor, interleukin 3	NUPR1	1.189803901	2.281217	0.035341012
203574_at	regulated	NFIL3	1.188370314	2.278952	0.005627889
218149_s_at	zinc finger protein 395 chromosome 10 open reading	ZNF395	1.153308196	2.224233	0.03601083
209183_s_at	frame 10	C10orf10	1.130009521	2.188602	0.030495392
204596_s_at	stanniocalcin 1	STC1	1.117980918	2.17043	0.005646347
202236_s_at	transporter 1	SLC16A1	1.109297398	2.157406	0.020505006
	solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	1.091455997	2.13089	0.022794017
201250_s_at	solute carrier family 16, member 1 (monocarboxylic acid)				
202234_s_at	transporter 1 nucleosome assembly protein 1-	SLC16A1	1.076506669	2.108923	0.022346379
208753_s_at	like 1	NAP1L1	1.071212806	2.101199	0.030495392
209566_at	insulin induced gene 2	INSIG2	1.064253158	2.091087	0.0102878
	solute carrier family 16, member 1 (monocarboxylic acid)				
209900_s_at	transporter 1	SLC16A1	1.063229562	2.089604	0.037121712
203643_at	Ets2 repressor factor	ERF	1.062395991	2.088397	0.00887733

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222238_s_at	polymerase (DNA directed), mu damage-specific DNA binding	POLM	1.06218116	2.088086	0.009110746
203409_at	protein 2, 48kDa transmembrane and coiled-coil	DDB2	1.056348239	2.079661	0.005627889
208716_s_at	domains 1 calcium regulated heat stable	TMCO1	1.053289209	2.075256	0.028694993
218384_at	protein 1, 24kDa	CARHSP1	1.046935815	2.066137	0.030686502
213629_x_at	metallothionein 1F insulin-like growth factor binding	MT1F	1.030803568	2.043162	0.004926805
203851_at	protein 6 cysteine and glycine-rich protein	IGFBP6	1.026105036	2.036519	0.023508348
211126_s_at	2 sushi-repeat-containing protein,	CSRP2	1.025244645	2.035304	0.003930777
204955_at	X-linked	SRPX	1.023912984	2.033427	0.022122228
221497_x_at	egl nine homolog 1 (<i>C. elegans</i>) spectrin repeat containing,	EGLN1	1.014335734	2.019973	0.001616605
202761_s_at	nuclear envelope 2 lysyl oxidase-like 2 /// ectonucleoside triphosphate	SYNE2	1.008012991	2.011139	0.028522438
202997_s_at	diphosphohydrolase 4 transforming growth factor beta	ENTPD4 //, 0.999880743	1.999835	0.022122228	
209651_at	1 induced transcript 1	TGFB1I1	0.992759749	1.989988	0.013967851
218145_at	tribbles homolog 3 (<i>Drosophila</i>) acyl-CoA synthetase long-chain	TRIB3	0.976221875	1.967307	0.013529536
202422_s_at	family member 4	ACSL4	0.974600654	1.965097	0.041260074
210524_x_at	phosphoglycerate dehydrogenase		0.967645307	1.955646	0.0102878
201397_at	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease,	PHGDH	0.966451538	1.954029	0.015364265
203282_at	glycogen storage disease type IV)	GBE1	0.953832119	1.937011	0.013682976
202686_s_at	AXL receptor tyrosine kinase	AXL	0.945469022	1.925815	0.028641503
205676_at	cytochrome P450, family 27, subfamily B, polypeptide 1	CYP27B1	0.941586364	1.920639	0.048665054
202973_x_at	family with sequence similarity 13, member A1	FAM13A1	0.940247431	1.918857	0.031124797
209373_at	mal, T-cell differentiation protein- like	MALL	0.934295333	1.910957	0.02901003
201666_at	TIMP metallopeptidase inhibitor 1	TIMP1	0.918193976	1.889748	0.016850455
211527_x_at	vascular endothelial growth factor A	VEGFA	0.910792186	1.880078	0.030569297

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206686_at	pyruvate dehydrogenase kinase, isozyme 1	PDK1	0.906138634	1.874023	0.005627889
201983_s_at	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	EGFR	0.903019693	1.869976	0.020225356
204326_x_at	metallothionein 1X laminin, gamma 1 (formerly LAMB2)	MT1X	0.896842796	1.861987	0.035308672
200771_at	ADAM metallopeptidase domain 12 (meltrin alpha)	LAMC1	0.885189062	1.847007	0.034949293
202952_s_at	ORAI calcium release-activated calcium modulator 3	ADAM12	0.884018669	1.845509	0.032075577
221864_at	metallothionein 1F amyloid beta (A4) precursor-like protein 2 family with sequence similarity 13, member A1	ORA13	0.879990072	1.840363	0.030816874
217165_x_at	lectin, galactoside-binding, soluble, 7 (galectin 7) /// galectin- 7 /// similar to Galectin-7 (Gal-7) (HKL-14) (PI7) (p53-induced protein 1)	MT1F	0.863670826	1.819662	0.021162931
208703_s_at	vascular endothelial growth factor A	APLP2	0.854780138	1.808483	0.018190072
217047_s_at	smoothelin amyloid beta (A4) precursor-like protein 2 adducin 3 (gamma)	FAM13A1	0.853251233	1.806568	0.025799468
204900_x_at	Sin3A-associated protein, 30kDa lectin, galactoside-binding, soluble, 7 (galectin 7) /// galectin- 7 /// similar to Galectin-7 (Gal-7) (HKL-14) (PI7) (p53-induced protein 1)	SAP30	0.84938113	1.801728	0.017917278
206400_at	vascular endothelial growth factor A	GAL7 /// LC	0.841699101	1.79216	0.049729879
212171_x_at	smoothelin amyloid beta (A4) precursor-like protein 2	VEGFA	0.833348452	1.781816	0.028320515
207390_s_at	adducin 3 (gamma)	SMTN	0.832912649	1.781278	0.048877822
208704_x_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	APLP2	0.817743579	1.762647	0.030883173
201034_at	transmembrane and coiled-coil domains 1	ADD3	0.817223252	1.762011	0.042597818
202833_s_at	RRAS	SERPINA1	0.817206769	1.761991	0.047872736
212647_at	homolog transmembrane and coiled-coil domains 1	TMCO1	0.81249522	1.756246	0.003901445
211098_x_at	phosphoglycerate kinase 1	PGK1	0.809627965	1.752759	0.047825402
200737_at	solute carrier family 27 (fatty acid transporter), member 3	SLC27A3	0.805884717	1.748218	0.018190072
222217_s_at	vascular endothelial growth factor A	VEGFA	0.802907605	1.744614	0.001527096
210513_s_at	factor A	VEGFA	0.794712981	1.734732	0.023163977

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219545_at	potassium channel tetramerisation domain containing 14	KCTD14	0.794257741	1.734185	0.034446605
	dihydrolipoamide S- succinyltransferase (E2 component of 2-oxo-glutarate complex) /// dihydrolipoamide S- succinyltransferase pseudogene (E2 component of 2-oxo-				
215210_s_at	glutarate complex)	DLST /// DI	0.79379654	1.733631	0.009110746
203476_at	trophoblast glycoprotein	TPBG	0.783142293	1.720875	0.009825362
207559_s_at	zinc finger, MYM-type 3 RAB20, member RAS oncogene	ZMYM3	0.776392365	1.712842	0.007106782
219622_at	family non-SMC condensin I complex,	RAB20	0.774065503	1.710082	0.001616605
201774_s_at	subunit D2	NCAPD2	0.770188419	1.705493	0.047706878
209264_s_at	tetraspanin 4 ankyrin repeat and zinc finger	TSPAN4	0.764982197	1.699349	0.025699386
218274_s_at	domain containing 1	ANKZF1	0.759158108	1.692503	0.006765098
201753_s_at	adducin 3 (gamma)	ADD3	0.756328637	1.689187	0.00982943
201125_s_at	integrin, beta 5 lysosomal-associated membrane	ITGB5	0.755452205	1.688161	0.020104218
201551_s_at	protein 1 peptidylglycine alpha-amidating	LAMP1	0.75074257	1.682659	0.022760006
202336_s_at	monooxygenase	PAM	0.748061195	1.679534	0.04562343
210792_x_at	SIVA1, apoptosis-inducing factor	SIVA1	0.747184939	1.678514	0.024625133
209263_x_at	tetraspanin 4	TSPAN4	0.742768905	1.673384	0.009849164
200762_at	dihydropyrimidinase-like 2	DPYSL2	0.740271894	1.670491	0.02597525
205462_s_at	hippocalcin-like 1 vitamin K epoxide reductase	HPCAL1	0.738746695	1.668726	0.010789862
217949_s_at	complex, subunit 1 THO complex 6 homolog	VKORC1	0.738578046	1.66853	0.010582924
218848_at	(Drosophila) procollagen-lysine 1, 2- oxoglutarate 5-dioxygenase 1 /// hypothetical protein	THOC6	0.734780301	1.664144	0.001277571
200827_at	LOC100130069	LOC100130069	0.733941324	1.663177	0.016350607
203510_at	met proto-oncogene (hepatocyte growth factor receptor) fusion (involved in t(12;16) in	MET	0.727898718	1.656225	0.011833306
217370_x_at	malignant liposarcoma)	FUS	0.723232016	1.650876	0.010545841
204243_at	rearranged L-myc fusion	RLF	0.722057226	1.649533	0.003930777

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202331_at	branched chain keto acid dehydrogenase E1, alpha polypeptide	BCKDHA	0.715478569	1.642028	0.014239772
	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	SLC16A1	0.712401783	1.63853	0.020104218
212552_at	hippocalcin-like 1 fatty acid desaturase 1 /// fatty acid desaturase 3	HPCAL1	0.711879544	1.637937	0.010853986
208964_s_at	U2 small nuclear RNA auxiliary factor 2	FADS1 /// I	0.707958876	1.633491	0.036229085
204688_at	sarcoglycan, epsilon	SGCE	0.703542574	1.628499	0.001616605
201968_s_at	phosphoglucomutase 1	PGM1	0.701851445	1.626591	0.004868451
201628_s_at	Ras-related GTP binding A	RRAGA	0.695262433	1.619179	0.004387256
209170_s_at	glycoprotein M6B peptidylglycine alpha-amidating monooxygenase	GPM6B	0.694339479	1.618143	0.015984393
214620_x_at	fatty acid desaturase 1 /// fatty acid desaturase 3	PAM	0.693729258	1.617459	0.041519922
208962_s_at	Sin3A-associated protein, 30kDa	FADS1 /// I	0.691732723	1.615222	0.021637422
218330_s_at	neuron navigator 2 family with sequence similarity 114, member A1	SAP30	0.687010352	1.609944	0.003930777
205899_at	cyclin A1 family with sequence similarity 62 (C2 domain containing),	NAV2	0.686809049	1.609719	0.049639322
208858_s_at	member A	FAM114A1	0.685502228	1.608262	0.008546266
218498_s_at	ERO1-like (S. cerevisiae) pleiomorphic adenoma gene-like	CCNA1	0.68249769	1.604916	0.008103638
209318_x_at	1 peptidylglycine alpha-amidating monooxygenase	PLAGL1	0.675000647	1.596597	0.020646414
212958_x_at	flotillin 2	PAM	0.673292243	1.594708	0.038035106
201350_at	protein phosphatase 1, regulatory (inhibitor) subunit 13	FLOT2	0.672122772	1.593416	0.030495392
218849_s_at	like	PPP1R13L	0.670073844	1.591154	0.046688116
208886_at	H1 histone family, member 0	H1F0	0.669932385	1.590998	0.030228794
212094_at	paternally expressed 10	PEG10	0.669683623	1.590724	0.02449946
201984_s_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) pyruvate dehydrogenase kinase,	EGFR	0.668502275	1.589422	0.011534663
221957_at	isozyome 3	PDK3	0.6672539	1.588047	0.022122228
212689_s_at	jumonji domain containing 1A	JMJD1A	0.664601435	1.58513	0.027374458

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212366_at	zinc finger protein 292 family with sequence similarity	ZNF292	0.664318147	1.584819	0.035341012
222001_x_at	91, member A2 apolipoprotein B mRNA editing enzyme, catalytic polypeptide-	FAM91A2	0.66090354	1.581073	0.009110746
209584_x_at	like 3C	APOBEC3C	0.660803481	1.580963	0.007435414
207717_s_at	plakophilin 2	PKP2	0.660108619	1.580202	0.031729696
	epidermal growth factor receptor (erythroblastic leukemia viral (v-				
210984_x_at	erb-b) oncogene homolog, avian)	EGFR	0.660107665	1.580201	0.010739422
	hypothetical protein LOC100134282 /// hypothetical				
213605_s_at	protein LOC100134401 chromosome 21 open reading	LOC100134401	0.657582852	1.577438	0.039353364
221211_s_at	frame 7	C21orf7	0.65738899	1.577226	0.045510962
209289_at	nuclear factor I/B chromosome 14 open reading	NFIB	0.655526981	1.575191	0.029644613
219203_at	frame 122	C14orf122	0.6491052	1.568195	0.00887733
201260_s_at	synaptophysin-like 1 chromosome 3 open reading	SYPL1	0.648761564	1.567822	0.048665054
209285_s_at	frame 63	C3orf63	0.647830122	1.56681	0.030955214
217356_s_at	phosphoglycerate kinase 1 chromosome 14 open reading	PGK1	0.646844893	1.56574	0.037095131
218383_at	frame 94	C14orf94	0.645898178	1.564713	0.017917278
201953_at	calcium and integrin binding 1 (calmyrin)	CIB1	0.640804297	1.559198	0.020646414
	3-hydroxy-3-methylglutaryl-				
205822_s_at	Coenzyme A synthase 1 (soluble)	HMGCS1	0.640346811	1.558704	0.032839923
203489_at	SIVA1, apoptosis-inducing factor	SIVA1	0.635467364	1.553441	0.012973447
202472_at	mannose phosphate isomerase	MPI	0.632859228	1.550635	0.010192972
202945_at	folylpolyglutamate synthase	FPGS	0.632476481	1.550224	0.01989318
	epidermal growth factor receptor (erythroblastic leukemia viral (v-				
211607_x_at	erb-b) oncogene homolog, avian)	EGFR	0.630835304	1.548461	0.026383236
209167_at	glycoprotein M6B phosphatidylinositol transfer	GPM6B	0.630462663	1.548061	0.020505006
219155_at	protein, cytoplasmic 1	PITPNM1	0.622972581	1.540045	0.013481296
204165_at	WAS protein family, member 1	WASF1	0.619532702	1.536377	0.017917278
205076_s_at	myotubularin related protein 11	MTMR11	0.619389924	1.536225	0.020104218

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201752_s_at	adducin 3 (gamma)	ADD3	0.616054505	1.532678	0.038594859
44702_at	synapse defective 1, Rho GTPase, homolog 1 (<i>C. elegans</i>)	SYDE1	0.61573845	1.532342	0.012978115
210426_x_at	RAR-related orphan receptor A KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein	RORA	0.614368173	1.530887	0.004926805
204017_at	retention receptor 3	KDELR3	0.608131272	1.524284	0.033843707
208796_s_at	cyclin G1 succinate-CoA ligase, GDP-forming, beta subunit	CCNG1	0.60220836	1.518038	0.042324593
214835_s_at	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha	SUCLG2	0.598552347	1.514196	0.045562906
202733_at	polypeptide II	P4HA2	0.589373502	1.504593	0.029641257
215111_s_at	TSC22 domain family, member 1 G protein-coupled estrogen receptor 1	TSC22D1	0.586875656	1.50199	0.016352277
212873_at	histocompatibility (minor) HA-1	HMHA1	0.58346458	1.498443	0.022346379
221958_s_at	G protein-coupled receptor 177	GPR177	0.57615254	1.490868	0.045899526
214268_s_at	myotubularin related protein 4	MTMR4	0.576108479	1.490822	0.032430413
203439_s_at	stanniocalcin 2	STC2	0.575724561	1.490426	0.008601198
218093_s_at	ankyrin repeat domain 10 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	ANKRD10	0.575522323	1.490217	0.026912528
208103_s_at	tensin like C1 domain containing phosphatase (tensin 2)	ANP32E	0.575437006	1.490129	0.036846349
212494_at	acyl-Coenzyme A dehydrogenase, very long chain vascular endothelial growth factor B	TENC1	0.571166206	1.485724	0.015830371
200710_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	ACADVL	0.568746587	1.483234	0.004868451
203683_s_at	heparan-alpha-glucosaminide N-acetyltransferase	VEGFB	0.56832039	1.482796	0.03871616
213664_at		SLC1A1	0.564307776	1.478678	0.013481296
218017_s_at		HGSNAT	0.562520378	1.476847	0.025223999

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	erythrocyte membrane protein band 4.1-like 2	EPB41L2	0.562092261	1.476409	0.033843707
	cat eye syndrome chromosome region, candidate 5	CECR5	0.560968119	1.475259	0.022219699
	6-phosphofructo-2- kinase/fructose-2,6-				
206246_at	biphosphatase 4	PFKFB4	0.560380405	1.474658	0.020059581
203946_s_at	arginase, type II	ARG2	0.560295986	1.474572	0.009825362
206070_s_at	EPH receptor A3	EPHA3	0.556554244	1.470752	0.047825402
	high-mobility group (nonhistone chromosomal) protein 4-like	HMG4L	0.55284773	1.466979	0.027517515
213029_at	nuclear factor I/B	NFIB	0.552367674	1.46649	0.010192972
36829_at	period homolog 1 (Drosophila)	PER1	0.549943424	1.464028	0.022122228
	solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	0.548916746	1.462987	0.018965453
	UDP-GlcNAc:betaGal beta-1,3-N- acetylglucosaminyltransferase 1	B3GNT1	0.546597797	1.460637	0.037676207
205251_at	period homolog 2 (Drosophila)	PER2	0.545027181	1.459048	0.046039246
211299_s_at	flotillin 2	FLOT2	0.539367473	1.453335	0.008601198
201037_at	phosphofructokinase, platelet	PFKP	0.538744175	1.452707	0.022459318
219715_s_at	tyrosyl-DNA phosphodiesterase 1	TDP1	0.538275351	1.452235	0.04110309
205996_s_at	adenylate kinase 2	AK2	0.537724224	1.451681	0.03555525
	poly (ADP-ribose) polymerase family, member 16	PARP16	0.53723599	1.45119	0.009776226
	solute carrier organic anion transporter family, member 1B1				
	/// solute carrier organic anion transporter family, member 1B3				
	/// organic anion transporter LST- 3b	LST-3TM12	0.537030462	1.450983	0.006203774
206354_at	chromosome 20 open reading frame 20	C20orf20	0.535580755	1.449526	0.026406296
	serine hydroxymethyltransferase				
214437_s_at	2 (mitochondrial)	SHMT2	0.534649883	1.448591	0.006293525
40446_at	PHD finger protein 1	PHF1	0.531175185	1.445106	0.033620767
218045_x_at	parathymosin	PTMS	0.530266652	1.444196	0.016520387

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206103_at	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	RAC3	0.529041016	1.44297	0.008191654
214096_s_at	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	0.529036773	1.442965	0.012973447
221911_at	ets variant gene 1	ETV1	0.527843459	1.441772	0.044254012
209015_s_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	0.519431388	1.43339	0.03150325
221565_s_at	family with sequence similarity 26, member B	FAM26B	0.518421296	1.432387	0.010853986
203192_at	ATP-binding cassette, sub-family B (MDR/TAP), member 6	ABCB6	0.517412394	1.431386	0.009825362
212277_at	myotubularin related protein 4	MTMR4	0.517190555	1.431166	0.035726339
218788_s_at	SET and MYND domain containing 3	SMYD3	0.516716153	1.430695	0.021540206
218204_s_at	FYVE and coiled-coil domain containing 1	FYCO1	0.514369358	1.42837	0.029174693
206307_s_at	forkhead box D1	FOXD1	0.514260707	1.428262	0.035444819
58780_s_at	hypothetical protein FLJ10357	FLJ10357	0.513692953	1.4277	0.004926805
202499_s_at	solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A3	0.513187625	1.4272	0.044751829
212345_s_at	cAMP responsive element binding protein 3-like 2	CREB3L2	0.511591366	1.425622	0.033620767
219862_s_at	nuclear prelamin A recognition factor	NARF	0.50912829	1.42319	0.003901445
210347_s_at	B-cell CLL/lymphoma 11A (zinc finger protein)	BCL11A	0.506543616	1.420643	0.022760006
91816_f_at	mex-3 homolog D (C. elegans)	MEX3D	0.503570485	1.417718	0.032075577
221567_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	0.501272191	1.415461	0.015183691
217872_at	PIH1 domain containing 1	PIH1D1	0.496713043	1.410995	0.015924285
212561_at	RAB6 interacting protein 1	RAB6IP1	0.495179961	1.409497	0.046345183
201043_s_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A // hypothetical protein LOC100128146	ANP32A //	0.49478163	1.409107	0.015973524
220255_at	Fanconi anemia, complementation group E	FANCE	0.492696659	1.407072	0.013677352
218529_at	CD320 molecule	CD320	0.489511195	1.403969	0.026584734

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	nudix (nucleoside diphosphate linked moiety X)-type motif 1 family with sequence similarity	NUDT1	0.488520708	1.403006	0.019624023
204766_s_at	26, member B SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	FAM26B	0.488470723	1.402957	0.021384427
203874_s_at	a, member 1 adaptor-related protein complex	SMARCA1	0.48820374	1.402697	0.011534663
203300_x_at	1, sigma 2 subunit	AP1S2	0.487636489	1.402146	0.028076262
	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	0.48401985	1.398635	0.02901003
59625_at	iroquois homeobox 4 SET and MYND domain	IRX4	0.482496488	1.397159	0.033798226
220225_at	containing 2 mevalonate (diphospho)	SMYD2	0.482205325	1.396877	0.040078673
203027_s_at	decarboxylase NCK interacting protein with SH3 domain	MVD	0.480912176	1.395626	0.035263304
218697_at	septin 6 /// cytokine-like nuclear	NCKIPSD	0.478358579	1.393158	0.012241734
212414_s_at	factor n-pac fibronectin type III domain	N-PAC ///	0.478009886	1.392821	0.042282472
202304_at	containing 3A	FNDC3A	0.477980853	1.392793	0.023822395
202920_at	ankyrin 2, neuronal Family with sequence similarity	ANK2	0.476512436	1.391376	0.008601198
222129_at	134, member A	FAM134A	0.475446351	1.390348	0.007610795
207722_s_at	BTB (POZ) domain containing 2	BTBD2	0.475080076	1.389995	0.047825402
396_f_at	erythropoietin receptor solute carrier family 35, member	EPOR	0.474487356	1.389424	0.014679603
218988_at	E3	SLC35E3	0.47356615	1.388538	0.02897476
203492_x_at	centrosomal protein 57kDa	CEP57	0.472478973	1.387492	0.030228794
209680_s_at	kinesin family member C1	KIFC1	0.471784852	1.386824	0.033843707
220725_x_at	Dynein, axonemal, heavy chain 3	DNAH3	0.467596305	1.382804	0.047324525
	protein phosphatase 2 (formerly 2A), regulatory subunit B'', beta /// similar to protein phosphatase 2 (formerly 2A),				
219264_s_at	regulatory subunit B, beta chromosome 16 open reading	LOC100134	0.464426439	1.379769	0.029288928
218945_at	frame 68 emopamil binding protein (sterol isomerase)	C16orf68	0.463567463	1.378947	0.007043637
202735_at		EBP	0.461452735	1.376928	0.027725725

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	solute carrier family 37 (glucose-6-phosphate transporter), member 4	SLC37A4	0.460664225	1.376175	0.022593789
207735_at	ring finger protein 125	RNF125	0.460469643	1.37599	0.01814502
202605_at	glucuronidase, beta	GUSB	0.460234356	1.375765	0.01199649
202685_s_at	AXL receptor tyrosine kinase acid phosphatase 5, tartrate resistant	AXL	0.458812906	1.37441	0.047719364
204638_at	lipin 2	LPIN2	0.455404132	1.371167	0.035342149
217952_x_at	PHD finger protein 3	PHF3	0.455301806	1.37107	0.022760006
	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) pyruvate dehydrogenase kinase, isozyme 3 emopamil binding protein (sterol isomerase)	PTGS1	0.455036917	1.370818	0.04032077
206348_s_at	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	PDK3	0.454347252	1.370163	0.010192972
213787_s_at	solute carrier family 37 (glucose-6-phosphate transporter), member 4	EBP	0.453998019	1.369831	0.047825402
212851_at	integrin-linked kinase	DCUN1D4	0.453531709	1.369388	0.044254012
	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (lirpin), alpha 4	SLC37A4	0.452885687	1.368775	0.0200001
202830_s_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein	ILK	0.450945735	1.366936	0.027725725
214978_s_at	retention receptor 3 sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain,	PPFIA4	0.449579022	1.365642	0.030553407
207265_s_at	(semaphorin) 4C transcription factor 7-like 1 (T-cell specific, HMG-box)	KDELR3	0.449478435	1.365546	0.037178897
46665_at	S100 calcium binding protein A3 F-box and leucine-rich repeat	SEMA4C	0.443555882	1.359952	0.023508348
221016_s_at	protein 12 tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	TCF7L1	0.443317012	1.359727	0.046352483
206027_at	FBXL12	0.443110396	1.359532	0.038386945	
220127_s_at	THG1L	0.442889194	1.359324	0.006949425	
219122_s_at		0.439637957	1.356264	0.01165288	

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205945_at	interleukin 6 receptor	IL6R	0.438177044	1.354891	0.047324525
210479_s_at	RAR-related orphan receptor A protein inhibitor of activated	RORA	0.437188743	1.353963	0.014546584
214442_s_at	STAT, 2 zinc finger, MYND-type	PIAS2	0.435960762	1.352811	0.041932291
207130_at	containing 8 erythrocyte membrane protein	ZMYND8	0.435826943	1.352686	0.011550549
201718_s_at	band 4.1-like 2 FK506 binding protein 1B, 12.6	EPB41L2	0.433098833	1.35013	0.016824371
206857_s_at	kDa diacylglycerol kinase, alpha	FKBP1B	0.431806435	1.348922	0.02144349
211272_s_at	80kDa chromosome 19 open reading	DGKA	0.431084432	1.348247	0.041095513
215734_at	frame 36 chromosome 7 open reading	C19orf36	0.42923365	1.346518	0.015796973
219655_at	frame 10 phosphatidic acid phosphatase	C7orf10	0.428582512	1.345911	0.02597525
209529_at	type 2C limb region 1 homolog (mouse)-	PPAP2C	0.427461627	1.344865	0.009825362
220036_s_at	like hydroxysteroid (17-beta)	LMBR1L	0.426903602	1.344345	0.006949425
220081_x_at	dehydrogenase 7	HSD17B7	0.426360575	1.343839	0.032430413
219745_at	transmembrane protein 180 beaded filament structural	TMEM180	0.418680159	1.336704	0.018190072
206746_at	protein 1, filensin	BFSP1	0.418154256	1.336217	0.005627889
202009_at	twinfilin, actin-binding protein, homolog 2 (Drosophila)	TWF2	0.415046732	1.333342	0.027540443
204416_x_at	apolipoprotein C-I	APOC1	0.412639141	1.331119	0.025799468
220040_x_at	KIAA1166 acyl-CoA thioesterase 2 /// acyl-	KIAA1166	0.412195518	1.330709	0.005746175
202982_s_at	CoA thioesterase 1 junctional adhesion molecule 3 /// hypothetical protein	ACOT1 ///	0.411334565	1.329915	0.015364265
212813_at	LOC100133502 heterogeneous nuclear	JAM3 /// L	0.410874704	1.329492	0.02115951
207127_s_at	ribonucleoprotein H3 (2H9) methyltransferase 11 domain containing 1 /// similar to methyltransferase 11 domain	HNRNPH3	0.410205036	1.328875	0.032075577
218366_x_at	containing 1 isoform 2	LOC731602	0.409485428	1.328212	0.03266687
213471_at	nephronophthisis 4 EH domain binding protein 1-like	NPHP4	0.407116327	1.326033	0.021162931
91703_at	1	EHBP1L1	0.406363261	1.325341	0.025699386
212086_x_at	lamin A/C	LMNA	0.405432514	1.324486	0.049628339

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	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP				
213603_s_at	binding protein Rac2)	RAC2	0.4053476	1.324408	0.020677472
202140_s_at	CDC-like kinase 3 EGFR-coamplified and	CLK3	0.404810217	1.323915	0.010320629
208091_s_at	overexpressed protein	ECOP	0.403293556	1.322524	0.030228794
220310_at	tubulin, alpha-like 3 tubulin, gamma complex	TUBAL3	0.40210133	1.321431	0.01055221
202477_s_at	associated protein 2 NGFI-A binding protein 2 (EGR1	TUBGCP2	0.401915334	1.321261	0.012143749
216017_s_at	binding protein 2)	NAB2	0.399036683	1.318627	0.039944948
	ets variant gene 4 (E1A enhancer				
211603_s_at	binding protein, E1AF)	ETV4	0.394499124	1.314486	0.044831576
206298_at	Rho GTPase activating protein 22	ARHGAP22	0.392928644	1.313056	0.006334784
209862_s_at	centrosomal protein 57kDa	CEP57	0.389598432	1.310029	0.018665191
202587_s_at	adenylate kinase 1	AK1	0.387656355	1.308266	0.013677352
212169_at	FK506 binding protein 9, 63 kDa acetyl-Coenzyme A carboxylase	FKBP9	0.387418634	1.308051	0.03789462
43427_at	beta	ACACB	0.387027059	1.307696	0.022300352
	solute carrier family 2 (facilitated glucose transporter), member 3 /// solute carrier family 2 (facilitated glucose transporter),				
216236_s_at	member 14 branched chain ketoacid	SLC2A14 //	0.385610428	1.306412	0.013829495
202030_at	dehydrogenase kinase	BCKDK	0.378903739	1.300353	0.017095271
218225_at	ECSIT homolog (Drosophila)	ECSIT	0.378293407	1.299803	0.027220355
	fumarylacetoacetate hydrolase				
222056_s_at	domain containing 2A	FAHD2A	0.378176978	1.299698	0.030553407
	solute carrier family 2 (facilitated glucose transporter), member 3				
202497_x_at		SLC2A3	0.377693945	1.299263	0.026683706
203657_s_at	cathepsin F EH domain binding protein 1-like	CTSF	0.375789531	1.297549	0.041932291
221755_at	1	EHBP1L1	0.373236308	1.295255	0.028076262
219379_x_at	zinc finger protein 358	ZNF358	0.372375972	1.294483	0.025464846
204788_s_at	protoporphyrinogen oxidase SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	PPOX	0.371418594	1.293624	0.03789462
203875_at	a, member 1	SMARCA1	0.37082982	1.293096	0.036557389

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212895_s_at	active BCR-related gene	ABR	0.369254127	1.291685	0.039869083
64440_at	interleukin 17 receptor C ADAM metallopeptidase domain	IL17RC	0.365475738	1.288306	0.012241734
205180_s_at	8	ADAM8	0.365380277	1.288221	0.009195803
34206_at	centaurin, delta 2	CENTD2	0.358839164	1.282394	0.027540443
209535_s_at	ADP-ribosylation factor-like 2 ///		0.358036135	1.28168	0.033997175
202564_x_at	sorting nexin 15 echinoderm microtubule	ARL2 // S	0.357155122	1.280898	0.02597525
204399_s_at	associated protein like 2 phosphatidylinositol glycan	EML2	0.355578565	1.279499	0.024839654
51146_at	anchor biosynthesis, class V insulin-like growth factor binding	PIGV	0.35503668	1.279018	0.046901507
202718_at	protein 2, 36kDa DnaJ (Hsp40) homolog, subfamily	IGFBP2	0.354438025	1.278487	0.024905824
212817_at	B, member 5 phosphatidylinositol glycan	DNAJB5	0.353028811	1.277239	0.030545459
219238_at	anchor biosynthesis, class V farnesyltransferase, CAAX box,	PIGV	0.349807807	1.274391	0.017639897
204764_at	beta	FNTB	0.347285202	1.272164	0.015996216
204882_at	Rho GTPase activating protein 25 ARP1 actin-related protein 1 homolog B, centracin beta	ARHGAP25	0.342755826	1.268177	0.01579422
202135_s_at	(yeast) acetyl-Coenzyme A	ACTR1B	0.342490776	1.267944	0.049628339
209608_s_at	acetyltransferase 2	ACAT2	0.340782642	1.266443	0.018190072
210874_s_at	N-acetyltransferase 6	NAT6	0.339951012	1.265714	0.009373565
212942_s_at	KIAA1199	KIAA1199	0.337197767	1.2633	0.0102878
215028_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A lysosomal-associated membrane	SEMA6A	0.337193729	1.263297	0.048786095
213728_at	protein 1 adenosine monophosphate	LAMP1	0.336918756	1.263056	0.048210253
207992_s_at	deaminase (isoform E)	AMPD3	0.335046783	1.261418	0.045867156
205854_at	tubby like protein 3	TULP3	0.334288361	1.260755	0.033997175
204773_at	interleukin 11 receptor, alpha DALR anticodon binding domain containing 3 /// similar to DALR anticodon binding domain	IL11RA	0.333822966	1.260349	0.047363623
221934_s_at	containing 3 ADP-ribosylation factor-like 17	DALRD3 //	0.330068947	1.257073	0.048877822
210718_s_at	pseudogene 1	ARL17P1	0.326856005	1.254277	0.028976133

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	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily					
215294_s_at	a, member 1	SMARCA1	0.32637609	1.25386	0.010872647	
218451_at	CUB domain containing protein 1	CDCP1	0.325345027	1.252964	0.036868007	
220258_s_at	WD repeat domain 79 solute carrier family 39 (zinc	WDR79	0.325256555	1.252887	0.034583198	
202667_s_at	transporter), member 7	SLC39A7	0.324479647	1.252213	0.046039246	
	p21/Cdc42/Rac1-activated kinase					
209615_s_at	1 (STE20 homolog, yeast)	PAK1	0.31722668	1.245933	0.024395723	
	serine hydroxymethyltransferase					
214095_at	2 (mitochondrial)	SHMT2	0.317062755	1.245792	0.028652297	
201380_at	cartilage associated protein	CRTAP	0.31603727	1.244906	0.048270899	
208971_at	uroporphyrinogen decarboxylase solute carrier family 16, member	UROD	0.313043058	1.242325	0.042497739	
	3 (monocarboxylic acid					
217691_x_at	transporter 4) myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	SLC16A3	0.311784715	1.241242	0.041260074	
204918_s_at	translocated to, 3 deleted in malignant brain	MLLT3	0.310736853	1.240341	0.03555525	
208250_s_at	tumors 1	DMBT1	0.308658316	1.238555	0.02543191	
221939_at	Yip1 domain family, member 2 guanine nucleotide binding protein (G protein), alpha 15 (Gq	YIPF2	0.307605011	1.237651	0.045019726	
205349_at	class) farnesyltransferase, CAAX box,	GNA15	0.306257368	1.236496	0.026683706	
1773_at	beta cysteine conjugate-beta lyase,	FNTB	0.305699114	1.236017	0.015820294	
206037_at	cytoplasmic	CCBL1	0.305101295	1.235505	0.025738674	
216326_s_at	histone deacetylase 3	HDAC3	0.304592023	1.235069	0.027878759	
221544_s_at	mediator complex subunit 16 Rap guanine nucleotide exchange	MED16	0.304414086	1.234917	0.046179549	
204543_at	factor (GEF) 1	RAPGEF1	0.302272128	1.233085	0.040987387	
213553_x_at	apolipoprotein C-I	APOC1	0.301961957	1.23282	0.017601515	
220326_s_at	hypothetical protein FLJ10357	FLJ10357	0.298159024	1.229574	0.008880514	
203799_at	CD302 molecule	CD302	0.298043331	1.229476	0.026406296	
204056_s_at	mevalonate kinase dishevelled, dsh homolog 2	MVK	0.295002921	1.226887	0.035726339	
57532_at	(Drosophila)	DVL2	0.294566108	1.226516	0.009194033	

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HemK methyltransferase family					
218620_s_at	member 1	HEMK1	0.29314315	1.225307	0.012522351
218845_at	dual specificity phosphatase 22	DUSP22	0.286954716	1.220062	0.047324525
Transcribed locus, moderately similar to NP_006570.1					
213789_at	emopamil binding protein (sterol isomerase) [Homo sapiens]		0.284694335	1.218152	0.047825402
215608_at	solute carrier family 30 (zinc transporter), member 3	SLC30A3	0.282365202	1.216187	0.030816874
207035_at	lactase hydroxyacyl-Coenzyme A dehydrogenase	LCT	0.280616536	1.214714	0.030553407
201035_s_at	ATPase, Ca++ transporting, type 2C, member 2	HADH	0.274870159	1.209885	0.02897476
206043_s_at	fms-related tyrosine kinase 3 ligand	ATP2C2	0.273248013	1.208526	0.042105187
217310_s_at	forkhead box J3 coiled-coil alpha-helical rod	FLT3LG	0.263272062	1.200198	0.022219699
37425_g_at	protein 1	CCHCR1	0.260971504	1.198285	0.033997465
207727_s_at	mutY homolog (E. coli)	MUTYH	0.259452184	1.197024	0.036846349
219680_at	NLR family member X1	NLRX1	0.258018939	1.195835	0.016199453
217395_at	metallothionein 4	MT4	0.257283142	1.195226	0.04353849
202926_at	neuroblastoma-amplified protein	NAG	0.257209488	1.195165	0.046356918
218818_at	four and a half LIM domains 3	FHL3	0.2561677	1.194302	0.03383209
215855_s_at	TATA element modulatory factor 1	TMF1	0.25194571	1.190812	0.047782169
immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy					
211430_s_at	variable 4-31 mannosidase, alpha, class 1B,	IGH@ // II	0.251083532	1.190101	0.043327649
218636_s_at	member 1	MAN1B1	0.249096819	1.188463	0.048877822
207709_at	protein kinase, AMP-activated, alpha 2 catalytic subunit aryl-hydrocarbon receptor	PRKAA2	0.247863387	1.187447	0.0200001
202986_at	nuclear translocator 2	ARNT2	0.245554615	1.185548	0.023727684

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204294_at	aminomethyltransferase CDNA: FLJ23540 fis, clone	AMT	0.240971263	1.181788	0.018965453
215907_at	LNG08239 calcium channel, voltage-dependent, beta 1 subunit		0.240805308	1.181652	0.045510962
210185_at	apoptotic peptidase activating factor 1	CACNB1	0.236650544	1.178254	0.049444401
211554_s_at	copine VI (neuronal)	APAF1	0.23658016	1.178196	0.038565301
215700_x_at	calcium/calmodulin-dependent protein kinase I	CPNE6	0.235167331	1.177043	0.036557389
204392_at	poly(rC) binding protein 2	CAMK1	0.233778462	1.175911	0.041325032
213264_at	transient receptor potential cation channel, subfamily V, member 4	PCBP2	0.233348405	1.17556	0.040987387
219516_at	member 4	TRPV4	0.232587408	1.17494	0.034616092
218154_at	gasdermin domain containing 1	GSDMDC1	0.226656798	1.17012	0.035263304
47571_at	zinc finger protein 236	ZNF236	0.214145842	1.160017	0.044344292
219371_s_at	Kruppel-like factor 2 (lung) CDNA FLJ25106 fis, clone	KLF2	0.212252517	1.158496	0.041621834
213675_at	CBR01467		0.211293245	1.157726	0.030553407
211731_x_at	synovial sarcoma, X breakpoint 3 leucine-rich repeats and death domain containing	SSX3	0.210576241	1.15715	0.036520037
219019_at	ret finger protein-like 2	LRDD	0.20930005	1.156127	0.037676207
207227_x_at	calcitonin-related polypeptide	RFPL2	0.20839363	1.155401	0.037963867
217495_x_at	alpha	CALCA	0.207753511	1.154888	0.045525685
206520_x_at	sialic acid binding Ig-like lectin 6	SIGLEC6	0.204397442	1.152205	0.037318715
205359_at	A kinase (PRKA) anchor protein 6	AKAP6	0.202665104	1.150822	0.041932291
210586_x_at	Rh blood group, D antigen PTR2 mRNA for repetitive sequence	RHD	0.202654979	1.150814	0.045301166
216704_at	Transcribed locus		0.191787404	1.142178	0.048505724
220008_at	NKF3 kinase family member	SGK269	0.187786834	1.139015	0.039856933
214957_at	actin-like 8	ACTL8	-0.19936894	-1.1482	0.039944948
213196_at	zinc finger protein 629	ZNF629	-0.21420606	-1.16007	0.034446605
221088_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 9A	PPP1R9A	-0.21616243	-1.16164	0.045728765
217749_at	coatomer protein complex, subunit gamma	COPG	-0.23826968	-1.17958	0.02297483
210790_s_at	SAR1 gene homolog A (S. cerevisiae) SUMO1/sentrin/SMT3 specific peptidase 2	SAR1A	-0.24414957	-1.18439	0.026683706
218122_s_at		SENP2	-0.24472679	-1.18487	0.029594023

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212576_at	mahogunin, ring finger 1	MGRN1	-0.24676287	-1.18654	0.046643175
206175_x_at	zinc finger protein 222	ZNF222	-0.24999702	-1.1892	0.025799468
210112_at	Hermansky-Pudlak syndrome 1	HPS1	-0.2516159	-1.19054	0.038057519
221951_at	transmembrane protein 80	TMEM80	-0.25426236	-1.19273	0.039245729
63825_at	abhydrolase domain containing 2 zinc finger and BTB domain	ABHD2	-0.2570825	-1.19506	0.020400033
213303_x_at	containing 7A	ZBTB7A	-0.25825653	-1.19603	0.046269754
	ankyrin repeat and sterile alpha				
212747_at	motif domain containing 1A	ANKS1A	-0.25866066	-1.19637	0.02012995
215130_s_at	IQ motif containing K	IQCK	-0.26117092	-1.19845	0.03669617
218869_at	malonyl-CoA decarboxylase	MLYCD	-0.261792	-1.19897	0.034308379
209395_at	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	-0.26289612	-1.19988	0.016606812
	protein kinase, cAMP-dependent, regulatory, type II, alpha				
204843_s_at	chromosome 2 open reading frame 42	PRKAR2A	-0.26426349	-1.20102	0.020112851
219128_at	C2orf42	-0.2650744	-1.2017	0.038334795	
209818_s_at	hyaluronan binding protein 4	HABP4	-0.26865401	-1.20468	0.010853986
205266_at	leukemia inhibitory factor (cholinergic differentiation factor)	LIF	-0.26978809	-1.20563	0.023727684
	6-phosphofructo-2- kinase/fructose-2,6- biphosphatase 2	PFKFB2	-0.2719328	-1.20742	0.045424984
	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	YOD1	-0.27379049	-1.20898	0.030495392
	GA binding protein transcription factor, alpha subunit 60kDa	GABPA	-0.27493628	-1.20994	0.047011358
	FK506 binding protein 12- rapamycin associated protein 1	FRAP1	-0.28094519	-1.21499	0.020891228
44696_at	TBC1 domain family, member 13	TBC1D13	-0.28205895	-1.21593	0.025338267
	chromosome 9 open reading frame 3	C9orf3	-0.28457753	-1.21805	0.045019726
218329_at	PR domain containing 4	PRDM4	-0.2863203	-1.21953	0.047782169
208184_s_at	transmembrane protein 1	TMEM1	-0.28651149	-1.21969	0.03669617
204350_s_at	mediator complex subunit 7 DEAD (Asp-Glu-Ala-Asp) box	MED7	-0.28722105	-1.22029	0.030883173
221780_s_at	polypeptide 27	DDX27	-0.2876454	-1.22065	0.043867818

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	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	POLR3C	-0.28995188	-1.2226	0.047825402
210573_s_at	zinc finger protein 557	ZNF557	-0.29164872	-1.22404	0.029409314
214077_x_at	Meis homeobox 3 pseudogene 1 chromosome 17 open reading frame 90	MEIS3P1 C17orf90	-0.2936682 -0.29397963	-1.22575 -1.22602	0.04847513 0.037676207
50374_at	chromosome 2 open reading frame 34	C2orf34	-0.2945507	-1.2265	0.015830371
217930_s_at	toll interacting protein neuroepithelial cell transforming gene 1	TOLLIP NET1	-0.29504029 -0.29573555	-1.22692 -1.22751	0.030553407 0.037676207
221002_s_at	tetraspanin 14 chondroitin sulfate	TSPAN14	-0.29734387	-1.22888	0.03669617
221799_at	glucuronyltransferase La ribonucleoprotein domain	CSGlcA-T	-0.29860816	-1.22996	0.045899526
208952_s_at	family, member 5	LARP5	-0.30368797	-1.2343	0.043045162
	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	GBA /// GB	-0.30462259	-1.2351	0.029594023
201686_x_at	apoptosis inhibitor 5 chromosome 1 open reading frame 50	API5 C1orf50	-0.30638807 -0.30710928	-1.23661 -1.23723	0.030553407 0.048110721
203659_s_at	tripartite motif-containing 13 AFG3 ATPase family gene 3-like 2	TRIM13	-0.30764929	-1.23769	0.009110746
202486_at	(yeast)	AFG3L2	-0.3086825	-1.23858	0.016278635
212837_at	KIAA0157	KIAA0157	-0.31217164	-1.24158	0.047363623
205995_x_at	IQ motif containing B1 tryptophanyl tRNA synthetase 2,	IQCB1	-0.31237	-1.24175	0.024778461
218766_s_at	mitochondrial KTEL (Lys-Tyr-Glu-Leu) containing	WARS2	-0.313028	-1.24231	0.022300352
218587_s_at	1	KTELC1	-0.31797937	-1.24658	0.033997175
218596_at	TBC1 domain family, member 13 isovaleryl Coenzyme A	TBC1D13	-0.31806143	-1.24665	0.031032444
203682_s_at	dehydrogenase	IVD	-0.31938487	-1.2478	0.047692556
218113_at	transmembrane protein 2 glutathione peroxidase 2	TMEM2	-0.32006757	-1.24839	0.031921312
202831_at	(gastrointestinal)	GPX2	-0.32121418	-1.24938	0.039944948
209912_s_at	KIAA0415 myosin phosphatase-Rho	KIAA0415	-0.32131329	-1.24947	0.036868007
212197_x_at	interacting protein	M-RIP	-0.32149639	-1.24963	0.030304577
214741_at	zinc finger protein 131	ZNF131	-0.32199987	-1.25006	0.019500168

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213462_at	neuronal PAS domain protein 2 histone cluster 1, H2bg /// histone cluster 1, H2bf /// histone cluster 1, H2be /// histone cluster 1, H2bi ///	NPAS2	-0.32233276	-1.25035	0.009849164
208523_x_at	histone cluster 1, H2bc	HIST1H2BC	-0.32272137	-1.25069	0.04032077
221745_at	WD repeat domain 68 solute carrier family 4 (anion exchanger), member 1, adaptor	WDR68	-0.32334566	-1.25123	0.046352483
218682_s_at	protein C-type lectin domain family 11,	SLC4A1AP	-0.32565857	-1.25324	0.033442044
205131_x_at	member A	CLEC11A	-0.32779409	-1.25509	0.008488821
212474_at	KIAA0241 CDNA FLJ38849 fis, clone	KIAA0241	-0.32872866	-1.25591	0.041548563
221877_at	MESAN2008936		-0.3315332	-1.25835	0.044000439
213126_at	mediator complex subunit 8 cell growth regulator with ring	MED8	-0.33168873	-1.25849	0.035268202
204605_at	finger domain 1	CGRRF1	-0.33207881	-1.25883	0.03669617
210461_s_at	actin binding LIM protein 1	ABLIM1	-0.33245956	-1.25916	0.009825362
202851_at	hypothetical protein FLJ11506 aldehyde dehydrogenase 3	FLJ11506	-0.33271971	-1.25939	0.018190072
211004_s_at	family, member B1 zinc finger, FYVE domain containing 26	ALDH3B1	-0.33371154	-1.26025	0.044259029
37943_at	kinesin light chain 1	ZFYVE26	-0.33380359	-1.26033	0.022122228
212878_s_at	DEAD (Asp-Glu-Ala-Asp) box	KLC1	-0.33416373	-1.26065	0.026406296
212834_at	polypeptide 52	DDX52	-0.33425674	-1.26073	0.031921312
213392_at	IQ motif containing K	IQCK	-0.334467	-1.26091	0.008191654
219710_at	SH3 domain and tetratricopeptide repeats 2	SH3TC2	-0.33625729	-1.26248	0.031851146
205873_at	phosphatidylinositol glycan anchor biosynthesis, class L	PIGL	-0.3369067	-1.26305	0.020331276
204872_at	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4	-0.33878936	-1.26469	0.012241734
212260_at	GRB10 interacting GYF protein 2	GIGYF2	-0.34034263	-1.26606	0.045125221
219603_s_at	zinc finger protein 226 SUMO1/sentrin specific	ZNF226	-0.34244163	-1.2679	0.03394891
213184_at	peptidase 5	SENP5	-0.34278842	-1.26821	0.042570882
202908_at	Wolfram syndrome 1 (wolframin) metal-regulatory transcription	WFS1	-0.34376435	-1.26906	0.045931814
205322_s_at	factor 1	MTF1	-0.34595357	-1.27099	0.040948632

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212290_at	solute carrier family 7 (cationic amino acid transporter, γ+ system), member 1	SLC7A1	-0.34769555	-1.27253	0.042323058
213090_s_at	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	TAF4	-0.34959901	-1.27421	0.047064544
219675_s_at	UDP-glucuronate decarboxylase 1	UXS1	-0.350009	-1.27457	0.049639322
221946_at	chromosome 9 open reading frame 116	C9orf116	-0.35023712	-1.27477	0.02012995
220642_x_at	G protein-coupled receptor 89B /// G protein-coupled receptor 89A /// G protein-coupled receptor 89C	GPR89A //,	-0.35164037	-1.27601	0.03376599
212497_at	mitogen-activated protein kinase 1 interacting protein 1-like transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	MAPK1IP1	-0.35247668	-1.27675	0.025699386
202818_s_at	LIM and calponin homology domains 1	TCEB3	-0.35298667	-1.2772	0.033997175
212325_at	superkiller viralicidic activity 2-	LIMCH1	-0.35299039	-1.27721	0.035341012
212896_at	like 2 (<i>S. cerevisiae</i>) N-ethylmaleimide-sensitive factor attachment protein, gamma	SKIV2L2	-0.35427138	-1.27834	0.041789977
210048_at	zinc finger, CCCH-type with G patch domain	NAPG	-0.35524977	-1.27921	0.023632473
57539_at	peptidase D	ZGPAT	-0.35719089	-1.28093	0.040856338
202108_at	chromosome 19 open reading frame 53	PEPD	-0.35734753	-1.28107	0.03555525
217926_at	PRA1 domain family, member 2	C19orf53	-0.3588749	-1.28243	0.04032077
203456_at	phosphatidylinositol glycan anchor biosynthesis, class L	PRAF2	-0.35945292	-1.28294	0.039944948
213889_at	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	PIGL	-0.36051898	-1.28389	0.045510962
209895_at	translocase of outer mitochondrial membrane 70	PTPN11	-0.36327242	-1.28634	0.012714488
201512_s_at	homolog A (<i>S. cerevisiae</i>)	TOMM70A	-0.36434895	-1.2873	0.046356918

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209799_at	protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1	-0.36459398	-1.28752	0.04220401
221059_s_at	coactosin-like 1 (Dictyostelium) component of oligomeric golgi	COTL1	-0.36461809	-1.28754	0.048210253
203630_s_at	complex 5	COG5	-0.36771676	-1.29031	0.033837739
59437_at	chromosome 9 open reading frame 116	C9orf116	-0.3683767	-1.2909	0.039419532
204210_s_at	phosphate cytidylyltransferase 1, choline, alpha	PCYT1A	-0.36851943	-1.29103	0.038652244
	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-				
213111_at	kinase, type III	PIP5K3	-0.36918585	-1.29162	0.03394891
	telomeric repeat binding factor 2,				
201174_s_at	interacting protein	TERF2IP	-0.36946926	-1.29188	0.033997175
205246_at	peroxisome biogenesis factor 13	PEX13	-0.36991992	-1.29228	0.030703647
205280_at	glycine receptor, beta	GLRB	-0.37102159	-1.29327	0.020225356
212034_s_at	exocyst complex component 7	EXOC7	-0.37166948	-1.29385	0.021969948
	chromosome 11 open reading				
218314_s_at	frame 57	C11orf57	-0.37209663	-1.29423	0.030686502
	vacuolar protein sorting 33				
204590_x_at	homolog A (S. cerevisiae)	VPS33A	-0.37338263	-1.29539	0.022122228
	GTPase activating protein and				
214869_x_at	VPS9 domains 1	GAPVD1	-0.37420031	-1.29612	0.037676207
	NADH dehydrogenase				
	(ubiquinone) Fe-S protein 1,				
	75kDa (NADH-coenzyme Q				
203039_s_at	reductase)	NDUFS1	-0.37476914	-1.29663	0.036078545
	topoisomerase I binding,				
204071_s_at	arginine-serine-rich	TOPORS	-0.37558678	-1.29737	0.026683706
	transcription factor 25 (basic				
213311_s_at	helix-loop-helix)	TCF25	-0.37580624	-1.29756	0.035341012
87100_at	abhydrolase domain containing 2	ABHD2	-0.37617683	-1.2979	0.0200001
	mitochondrial ribosomal protein				
219244_s_at	L46	MRPL46	-0.37767797	-1.29925	0.037739164
214527_s_at	polyglutamine binding protein 1	PQBP1	-0.37783718	-1.29939	0.041519922
212731_at	ankyrin repeat domain 46	ANKRD46	-0.37823845	-1.29975	0.012476914
	vacuolar protein sorting 45				
209268_at	homolog (S. cerevisiae)	VPS45	-0.3792763	-1.30069	0.030675364

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	wingless-type MMTV integration				
217681_at	site family, member 7B chromosome 7 open reading	WNT7B	-0.38060425	-1.30189	0.026683706
209445_x_at	frame 44	C7orf44	-0.3808174	-1.30208	0.039353364
	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				
214946_x_at	21, member D	FAM21A //	-0.38260266	-1.30369	0.034142802
212216_at	prolyl endopeptidase-like	PREPL	-0.38382369	-1.3048	0.035341012
1487_at	estrogen-related receptor alpha	ESRRA	-0.38386404	-1.30483	0.034029487
212211_at	ankyrin repeat domain 17 latent transforming growth factor	ANKRD17	-0.3845323	-1.30544	0.033997175
219922_s_at	beta binding protein 3 suppressor of Ty 7 (<i>S. cerevisiae</i>)-	LTBP3	-0.38488174	-1.30575	0.040856338
201836_s_at	like	SUPT7L	-0.38642165	-1.30715	0.028976133
203212_s_at	myotubularin related protein 2	MTMR2	-0.38676602	-1.30746	0.006921301
	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 /// transient receptor potential cation				
203579_s_at	channel, subfamily V, member 6 DnaJ (Hsp40) homolog, subfamily	SLC7A6 //	-0.38686779	-1.30755	0.029644613
202843_at	B, member 9	DNAJB9	-0.38907619	-1.30955	0.032128563
204075_s_at	KIAA0562 UDP-glucose ceramide	KIAA0562	-0.38976025	-1.31018	0.030553407
221765_at	glucosyltransferase golgi SNAP receptor complex	UGCG	-0.39145228	-1.31171	0.017353002
204630_s_at	member 1 solute carrier family 37 (glycerol- 3-phosphate transporter),	GOSR1	-0.39324308	-1.31334	0.028368833
218928_s_at	member 1 poly(A) binding protein	SLC37A1	-0.39401195	-1.31404	0.028694993
209064_x_at	interacting protein 1	PAIP1	-0.39457141	-1.31455	0.045867156
214791_at	hypothetical protein BC004921	LOC93349	-0.39479896	-1.31476	0.027725725
209412_at	transmembrane protein 1 3-hydroxybutyrate	TMEM1	-0.39635524	-1.31618	0.021311374
218285_s_at	dehydrogenase, type 2	BDH2	-0.3969674	-1.31674	0.048951461

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	cysteine-rich secretory protein				
221541_at	LCCL domain containing 2 zinc finger, CCCH-type with G	CRISPLD2	-0.39780021	-1.3175	0.009849164
221848_at	patch domain follistatin-like 3 (secreted	ZGPAT	-0.39802983	-1.31771	0.01671059
203592_s_at	glycoprotein)	FSTL3	-0.39915566	-1.31874	0.030553407
207510_at	bradykinin receptor B1	BDKRB1	-0.39915631	-1.31874	0.039384241
205541_s_at	G1 to S phase transition 2	GSPT2	-0.39927802	-1.31885	0.029644613
201712_s_at	RAN binding protein 2 rabaptin, RAB GTPase binding effector protein 2 /// similar to	RANBP2	-0.40121481	-1.32062	0.031124797
74694_s_at	RABEP2 protein	LOC10013	-0.40139185	-1.32078	0.030816874
206764_x_at	metallophosphoesterase 1	MPPE1	-0.40239039	-1.3217	0.017771058
	RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 8 /// RANBP2-like and GRIP domain				
210676_x_at	containing 6 motile sperm domain containing	RGPD5 ///	-0.40263532	-1.32192	0.04084065
221895_at	2	MOSPD2	-0.40292436	-1.32219	0.016520387
221884_at	ecotropic viral integration site 1	EVI1	-0.40346235	-1.32268	0.047706878
39549_at	neuronal PAS domain protein 2 olfactory receptor, family 7, subfamily E, member 47	NPAS2	-0.4037616	-1.32295	0.009110746
222304_x_at	pseudogene	OR7E47P	-0.4046627	-1.32378	0.01323345
203487_s_at	armadillo repeat containing 8	ARMC8	-0.40602138	-1.32503	0.026683706
	transforming growth factor, beta				
205210_at	receptor associated protein 1 general transcription factor IIH,	TGFBRAP1	-0.40683667	-1.32578	0.012932821
202453_s_at	polypeptide 1, 62kDa	GTF2H1	-0.40692095	-1.32585	0.030553407
203115_at	ferrochelatase (protoporphyrin)	FECH	-0.40821618	-1.32704	0.010739422
218318_s_at	nemo-like kinase	NLK	-0.40823074	-1.32706	0.030051009
210085_s_at	annexin A9	ANXA9	-0.4086447	-1.32744	0.013533787
	RNA binding motif, single				
203748_x_at	stranded interacting protein 1	RBMS1	-0.40893449	-1.3277	0.045983569
218763_at	syntaxin 18 solute carrier family 24 (sodium/potassium/calcium	STX18	-0.40928378	-1.32803	0.011347725
218749_s_at	exchanger), member 6	SLC24A6	-0.41016751	-1.32884	0.026584734
205279_s_at	glycine receptor, beta	GLRB	-0.4113859	-1.32996	0.014546584

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	nicotinamide nucleotide adenylyltransferase 2 /// hypothetical protein				
209755_at	LOC100131795 putative homeodomain	LOC100131795	-0.41198589	-1.33052	0.022122228
215285_s_at	transcription factor 1 suppressor of Ty 7 (<i>S. cerevisiae</i>)-	PHTF1	-0.41294406	-1.3314	0.007131295
201837_s_at	like	SUPT7L	-0.41367575	-1.33208	0.028652297
217981_s_at	fracture callus 1 homolog (rat) solute carrier family 20 (phosphate transporter),	FXC1	-0.41403996	-1.33241	0.039768489
202744_at	member 2	SLC20A2	-0.41524332	-1.33352	0.033997175
200629_at	tryptophanyl-tRNA synthetase	WARS	-0.41611049	-1.33433	0.017541446
204231_s_at	fatty acid amide hydrolase ubiquitin protein ligase E3A (human papilloma virus E6- associated protein, Angelman	FAAH	-0.41643117	-1.33462	0.045141397
211285_s_at	syndrome)	UBE3A	-0.41679581	-1.33496	0.027517515
218672_at	sodium channel modifier 1 acetylserotonin O-	SCNM1	-0.41844054	-1.33648	0.020891228
209394_at	methyltransferase-like serine palmitoyltransferase, long	ASMTL	-0.41860357	-1.33663	0.006921301
203128_at	chain base subunit 2	SPTLC2	-0.41867544	-1.3367	0.007610795
217811_at	selenoprotein T	SELT	-0.41869689	-1.33672	0.047825402
	LanC lantibiotic synthetase				
218219_s_at	component C-like 2 (bacterial) phospholipase A2-activating	LANCL2	-0.41936588	-1.33734	0.037735868
209533_s_at	protein	PLAA	-0.41944544	-1.33741	0.030767069
60471_at	Ras and Rab interactor 3	RIN3	-0.42025452	-1.33816	0.00601739
	solute carrier organic anion				
219229_at	transporter family, member 3A1 nuclear cap binding protein	SLCO3A1	-0.42073504	-1.33861	0.035134898
201521_s_at	subunit 2, 20kDa	NCBP2	-0.42205416	-1.33983	0.022794017
57540_at	ribokinase DEAD (Asp-Glu-Ala-As) box	RBKS	-0.42264431	-1.34038	0.028884791
202578_s_at	polypeptide 19A isovaleryl Coenzyme A	DDX19A	-0.423098	-1.3408	0.041052549
216958_s_at	dehydrogenase CDNA FLJ38849 fis, clone	IVD	-0.42359937	-1.34127	0.020059581
64488_at	MESAN2008936 La ribonucleoprotein domain		-0.42361903	-1.34129	0.016278635
208953_at	family, member 5	LARP5	-0.42367344	-1.34134	0.020400033
203245_s_at	FLJ35348	FLJ35348	-0.42398049	-1.34162	0.012571055

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	chromosome 2 open reading frame 37	C2orf37	-0.42402698	-1.34167	0.022122228
	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A	-0.42574805	-1.34327	0.026406296
200604_s_at	WD repeat domain 1	WDR1	-0.42579837	-1.34332	0.048665054
209232_s_at	dynactin 5 (p25) phosphatase and actin regulator	DCTN5	-0.42598522	-1.34349	0.008191654
204047_s_at	2 zinc finger protein 259 /// similar	PHACTR2	-0.42604868	-1.34355	0.033843707
217185_s_at	to zinc finger protein 259	LOC442240	-0.4263799	-1.34386	0.039353364
209234_at	kinesin family member 1B	KIF1B	-0.42679604	-1.34424	0.02449946
	general transcription factor IIIC,				
218343_s_at	polypeptide 3, 102kDa	GTF3C3	-0.42744879	-1.34485	0.01672165
	ASF1 anti-silencing function 1				
203427_at	homolog A (S. cerevisiae)	ASF1A	-0.42779332	-1.34517	0.031415364
211801_x_at	mitofusin 1	MFN1	-0.42861631	-1.34594	0.041260074
213127_s_at	mediator complex subunit 8	MED8	-0.42870661	-1.34603	0.016278635
45526_g_at	hypothetical protein FLJ14154	FLJ14154	-0.42944952	-1.34672	0.013677352
	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	RER1	-0.43013604	-1.34736	0.031124797
208580_x_at		Multiple G	-0.43056028	-1.34776	0.028805485
212312_at	BCL2-like 1	BCL2L1	-0.43265477	-1.34971	0.031236577
218344_s_at	REST corepressor 3	RCOR3	-0.433523	-1.35053	0.015020188
211709_s_at	C-type lectin domain family 11, member A	CLEC11A	-0.43401592	-1.35099	0.01323345
	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)	UQCC	-0.43488351	-1.3518	0.026683706
217935_s_at					
213140_s_at	synovial sarcoma translocation gene on chromosome 18-like 1	SS18L1	-0.43497845	-1.35189	0.028076262
212802_s_at	GTPase activating protein and VPS9 domains 1	GAPVD1	-0.43551217	-1.35239	0.039944948
215075_s_at	growth factor receptor-bound protein 2	GRB2	-0.43613524	-1.35298	0.020677472
	histone cluster 1, H2bg ///				
	histone cluster 1, H2bf ///				
	histone cluster 1, H2be ///				
	histone cluster 1, H2bi ///				
208490_x_at	histone cluster 1, H2bc	HIST1H2BC	-0.43668012	-1.35349	0.037044614
216698_x_at		LOC44145	-0.43682244	-1.35362	0.013682976

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221815_at	abhydrolase domain containing 2	ABHD2	-0.43794135	-1.35467	0.025490308
218295_s_at	nucleoporin 50kDa tumor suppressing	NUP50	-0.43833996	-1.35504	0.014546584
218612_s_at	subtransferable candidate 4	TSSC4	-0.43933664	-1.35598	0.033620767
217150_s_at	neurofibromin 2 (merlin) UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast) /// UTP14, U3 small nucleolar ribonucleoprotein,	NF2	-0.43940806	-1.35605	0.040948632
221513_s_at	homolog A (yeast) family with sequence similarity 21, member B /// family with sequence similarity 21, member	UTP14A //,	-0.44189217	-1.35838	0.030835939
212370_x_at	A steroid sulfatase (microsomal),	FAM21A //	-0.4425154	-1.35897	0.020059581
203767_s_at	isozyme S	STS	-0.44284946	-1.35929	0.023378717
201583_s_at	Sec23 homolog B (<i>S. cerevisiae</i>)	SEC23B	-0.44357429	-1.35997	0.006921301
218527_at	aprataxin	APTX	-0.44365592	-1.36005	0.025699386
218283_at	synovial sarcoma translocation gene on chromosome 18-like 2	SS18L2	-0.44405529	-1.36042	0.035834164
210653_s_at	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	BCKDHB	-0.44446936	-1.36081	0.035264267
203616_at	polymerase (DNA directed), beta lipoma HMGIC fusion partner-like	POLB	-0.44564884	-1.36193	0.039944948
212658_at	2 chromosome X open reading	LHFPL2	-0.44598955	-1.36225	0.019886651
213315_x_at	frame 40A	CXorf40A	-0.44626231	-1.36251	0.029066198
219395_at	RNA binding motif protein 35B	RBM35B	-0.44669792	-1.36292	0.016278635
202347_s_at	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast) chromosome X open reading frame 40A /// chromosome X	UBE2K	-0.44727988	-1.36347	0.035726339
212961_x_at	open reading frame 40B ubiquitin-conjugating enzyme	CXorf40A /	-0.44750831	-1.36368	0.022673136
218837_s_at	E2D 4 (putative) Der1-like domain family, member	UBE2D4	-0.44779065	-1.36395	0.015830371
218333_at	2 chromosome 15 open reading	DERL2	-0.44811102	-1.36425	0.037676207
204495_s_at	frame 39	C15orf39	-0.44825603	-1.36439	0.02901003

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	eukaryotic translation initiation				
201632_at	factor 2B, subunit 1 alpha, 26kDa	EIF2B1	-0.44865143	-1.36476	0.019258724
	G protein-coupled receptor 89B				
	/// G protein-coupled receptor				
	89A /// G protein-coupled				
222140_s_at	receptor 89C	GPR89A //,	-0.44871091	-1.36482	0.037178897
	general transcription factor IIE,				
202680_at	polypeptide 2, beta 34kDa	GTF2E2	-0.44907056	-1.36516	0.02325585
221543_s_at	ER lipid raft associated 2	ERLIN2	-0.44984849	-1.3659	0.034485301
	hypothetical protein				
221847_at	LOC100129361	LOC100129361	-0.45100496	-1.36699	0.030553407
	GTPase activating Rap/RanGAP				
214855_s_at	domain-like 1	GARNL1	-0.45132297	-1.36729	0.022300352
202271_at	F-box protein 28	FBXO28	-0.45159189	-1.36755	0.028368833
218304_s_at	oxysterol binding protein-like 11	OSBPL11	-0.45218842	-1.36811	0.022300352
218479_s_at	exportin 4	XPO4	-0.45281744	-1.36871	0.017583366
203116_s_at	ferrochelatase (protoporphyrin)	FECH	-0.45318098	-1.36906	0.010853986
208822_s_at	death associated protein 3	DAP3	-0.45364469	-1.3695	0.030534502
	craniofacial development protein				
203166_at	1	CFDP1	-0.45366377	-1.36951	0.006949425
205588_s_at	FGFR1 oncogene partner	FGFR1OP	-0.45389879	-1.36974	0.049639322
203517_at	metaxin 2	MTX2	-0.45523462	-1.37101	0.035238023
	protein phosphatase 1,				
202165_at	regulatory (inhibitor) subunit 2	PPP1R2	-0.45592796	-1.37166	0.017797984
	eukaryotic translation initiation				
200596_s_at	factor 3, subunit A	EIF3A	-0.45679046	-1.37249	0.015628504
204374_s_at	galactokinase 1	GALK1	-0.45757518	-1.37323	0.00887733
222116_s_at	TBC1 domain family, member 16	TBC1D16	-0.45802708	-1.37366	0.020331276
	FYN binding protein (FYB-				
205285_s_at	120/130)	FYB	-0.45827374	-1.3739	0.022219699
	cell division cycle 37 homolog (S.				
219343_at	cerevisiae)-like 1	CDC37L1	-0.45918799	-1.37477	0.017353002
	nudix (nucleoside diphosphate				
218375_at	linked moiety X)-type motif 9	NUDT9	-0.4598952	-1.37544	0.02597525
	karyopherin alpha 3 (importin				
221503_s_at	alpha 4)	KPNA3	-0.45990592	-1.37545	0.033843707
203556_at	zinc fingers and homeoboxes 2	ZHX2	-0.4617977	-1.37726	0.015183691

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	transcription elongation factor B (SIII), polypeptide 2 (18kDa,				
213877_x_at	elongin B)	TCEB2	-0.46382922	-1.3792	0.013044506
201854_s_at	ATM interactor golgi SNAP receptor complex	ATMIN	-0.46398511	-1.37935	0.016824371
213021_at	member 1 acetylserotonin O-	GOSR1	-0.46404634	-1.37941	0.012749147
36554_at	methyltransferase-like	ASMTL	-0.46412393	-1.37948	0.025501804
219496_at	ankyrin repeat domain 57 SMAD specific E3 ubiquitin	ANKRD57	-0.46429119	-1.37964	0.020112851
212666_at	protein ligase 1	SMURF1	-0.46442117	-1.37976	0.045983569
	proline synthetase co-transcribed				
214545_s_at	homolog (bacterial)	PROSC	-0.4667049	-1.38195	0.016278635
	mitogen-activated protein kinase				
217971_at	kinase 1 interacting protein 1	MAP2K1IP1	-0.46676882	-1.38201	0.040987387
209922_at	BRCA1 associated protein	BRAP	-0.46718582	-1.38241	0.013358527
	DIM1 dimethyladenosine				
210802_s_at	transferase 1-like (S. cerevisiae)	DIMT1L	-0.46763999	-1.38285	0.034249673
	glucose-fructose oxidoreductase				
219821_s_at	domain containing 1	GFOD1	-0.46817039	-1.38335	0.009110746
	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 // transient receptor potential cation				
203578_s_at	channel, subfamily V, member 6	SLC7A6 //	-0.46820771	-1.38339	0.023508348
55093_at	chondroitin sulfate glucuronyltransferase	CSGlcA-T	-0.46834221	-1.38352	0.008103638
	haloacid dehalogenase-like				
203974_at	hydrolase domain containing 1A	HDHD1A	-0.46845141	-1.38362	0.036520037
219499_at	Sec61 alpha 2 subunit (S. cerevisiae)	SEC61A2	-0.46861263	-1.38378	0.020445743
213310_at	Eukaryotic translation initiation factor 2C, 2	EIF2C2	-0.46908074	-1.38423	0.03789462
	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein,				
211754_s_at	34kDa), member 17	SLC25A17	-0.46941503	-1.38455	0.036846349
	acyl-Coenzyme A dehydrogenase				
221669_s_at	family, member 8	ACAD8	-0.46994017	-1.38505	0.028976133

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220318_at	epsin 3	EPN3	-0.47066715	-1.38575	0.0350019
221277_s_at	pseudouridylate synthase 3	PUS3	-0.47128096	-1.38634	0.011149119
	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)				
219340_s_at	leptin receptor overlapping transcript-like 1	CLN8	-0.4725815	-1.38759	0.013677352
202594_at	family with sequence similarity 21, member C /// family with sequence similarity 21, member	LEPROTL1	-0.47271752	-1.38772	0.03601083
211068_x_at	D CAP, adenylate cyclase- associated protein 1 (yeast)	FAM21C //	-0.47296675	-1.38796	0.014546584
213798_s_at	TAO kinase 2	CAP1	-0.47481335	-1.38974	0.046553557
204986_s_at	PHD finger protein 15 CDNA FLJ42849 fis, A-	TAOK2	-0.47594235	-1.39083	0.03216506
212660_at	BRHIP2004902 DnaJ (Hsp40) homolog, subfamily	PHF15	-0.47602558	-1.39091	0.023632473
208810_at	B, member 6	DNAJB6	-0.47850237	-1.3933	0.036846349
218571_s_at	chromatin modifying protein 4A	CHMP4A	-0.47862938	-1.39342	0.023015457
219460_s_at	transmembrane protein 127	TMEM127	-0.47889886	-1.39368	0.017071662
209905_at	homeobox A9	HOXA9	-0.47929291	-1.39406	0.027725725
208685_x_at	bromodomain containing 2	BRD2	-0.47963978	-1.3944	0.017353002
	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)				
209896_s_at	paired-like homeodomain 1	PTPN11	-0.47984001	-1.39459	0.018190072
209587_at	ataxin 10	PITX1	-0.48074253	-1.39546	0.021384427
208832_at	large subunit GTPase 1 homolog (S. cerevisiae)	ATXN10	-0.48164857	-1.39634	0.014672661
221535_at	solute carrier family 33 (acetyl- CoA transporter), member 1	LSG1	-0.48210322	-1.39678	0.035341012
203164_at	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta	SLC33A1	-0.48285715	-1.39751	0.033997175
202884_s_at	isoform	PPP2R1B	-0.48326098	-1.3979	0.008488821
214948_s_at	TATA element modulatory factor	TMF1	-0.48348067	-1.39811	0.008459494
200867_at	zinc finger protein 313 transcription elongation factor B (SIII), polypeptide 3 (110kDa,	ZNF313	-0.48369208	-1.39832	0.032015473
202819_s_at	elongin A)	TCEB3	-0.48451394	-1.39911	0.017238997
212340_at	Yip1 domain family, member 6	YIPF6	-0.48455534	-1.39915	0.009425165

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	mitogen-activated protein kinase				
212644_s_at	1 interacting protein 1-like ARP2 actin-related protein 2	MAPK1IP1I	-0.48470269	-1.3993	0.016988706
200729_s_at	homolog (yeast)	ACTR2	-0.48475327	-1.39935	0.031945762
217882_at	transmembrane protein 111 eukaryotic translation initiation factor 2B, subunit 3 gamma,	TMEM111	-0.48658586	-1.40113	0.040753506
218488_at	58kDa chromosome 7 open reading	EIF2B3	-0.48784116	-1.40234	0.041087454
220659_s_at	frame 43 asparaginyl-tRNA synthetase 2,	C7orf43	-0.48837215	-1.40286	0.006949425
219217_at	mitochondrial (putative) putative homeodomain	NARS2	-0.48930477	-1.40377	0.040897992
210191_s_at	transcription factor 1	PHTF1	-0.49015072	-1.40459	0.020400033
218572_at	chromatin modifying protein 4A	CHMP4A	-0.49070025	-1.40513	0.013481296
221571_at	TNF receptor-associated factor 3 solute carrier family 39 (zinc	TRAF3	-0.49108565	-1.4055	0.043534978
219215_s_at	transporter), member 4 TMEM9 domain family, member	SLC39A4	-0.49128466	-1.4057	0.015364265
218065_s_at	B	TMEM9B	-0.49142566	-1.40583	0.045715027
209858_x_at	metallophosphoesterase 1 small trans-membrane and	MPPE1	-0.49171084	-1.40611	0.015434646
209679_s_at	glycosylated protein DEAD (Asp-Glu-Ala-Asp) box	LOC57228	-0.49208774	-1.40648	0.032801415
31807_at	polypeptide 49 N-acylsphingosine amidohydrolase (acid	DDX49	-0.49308097	-1.40745	0.011534663
213902_at	ceramidase) 1	ASAH1	-0.49345077	-1.40781	0.01814502
220145_at	microtubule-associated protein 9 chromosome 10 open reading	MAP9	-0.49365744	-1.40801	0.016850455
213410_at	frame 137 ubiquitin-fold modifier	C10orf137	-0.49403859	-1.40838	0.020085667
217797_at	conjugating enzyme 1 chromosome 5 open reading	UFC1	-0.49467666	-1.409	0.047706878
203738_at	frame 22 chromosome 18 open reading	C5orf22	-0.49469693	-1.40902	0.045983569
221190_s_at	frame 8 solute carrier family 36 (proton/amino acid symporter),	C18orf8	-0.49501959	-1.40934	0.026599732
213119_at	member 1	SLC36A1	-0.49553932	-1.40985	0.005627889
204067_at	sulfite oxidase chromosome 12 open reading	SUOX	-0.49605756	-1.41035	0.018665191
218374_s_at	frame 4	C12orf4	-0.49669517	-1.41098	0.024461961

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213727_x_at	metallophosphoesterase 1 synaptosomal-associated protein, 29kDa	MPPE1	-0.49713846	-1.41141	0.014664842
218327_s_at	RAN binding protein 2	SNAP29	-0.49906686	-1.4133	0.020059581
201711_x_at	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha- steroid delta 4-dehydrogenase	RANBP2	-0.49926319	-1.41349	0.017236527
210959_s_at	alpha 1) serum/glucocorticoid regulated kinase family, member 3 /// chromosome 8 open reading frame 44	SRD5A1	-0.49943071	-1.41366	0.04032077
220038_at	GTPase activating protein and	C8orf44 ///	-0.499731	-1.41395	0.039856933
212804_s_at	VPS9 domains 1	GAPVD1	-0.50046724	-1.41467	0.04793172
209231_s_at	dynactin 5 (p25)	DCTN5	-0.50050708	-1.41471	0.022300352
205661_s_at	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	FLAD1	-0.50176769	-1.41595	0.047363623
213153_at	SET domain containing 1B	SETD1B	-0.50206803	-1.41624	0.012241734
213571_s_at	eukaryotic translation initiation factor 4E family member 2 ASF1 anti-silencing function 1	EIF4E2	-0.50212916	-1.4163	0.020743425
203428_s_at	homolog A (S. cerevisiae) neugrin, neurite outgrowth	ASF1A	-0.50232517	-1.41649	0.032426062
217722_s_at	associated elongation of very long chain fatty acids (FEN1/Elo2,	NGRN	-0.50265589	-1.41682	0.046356918
218028_at	SUR4/Elo3, yeast)-like 1	ELOVL1	-0.50444125	-1.41857	0.015796973
203580_s_at	solute carrier family 7 (cationic amino acid transporter, γ+ system), member 6 /// transient receptor potential cation	SLC7A6 ///	-0.50538919	-1.41951	0.017797984
218416_s_at	hypothetical protein FLJ20489 trafficking protein particle complex 2 /// spondyloepiphyseal dysplasia, late, pseudogene /// zinc finger	FLJ20489	-0.50602325	-1.42013	0.020891228
209751_s_at	protein 547 karyopherin alpha 6 (importin alpha 7)	SEDLP /// 1	-0.50605597	-1.42016	0.035334764
212101_at	programmed cell death 6	KPNA6	-0.50824223	-1.42232	0.045565067
203415_at		PDCD6	-0.50833068	-1.4224	0.045899526

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T-cell leukemia translocation					
203054_s_at	altered gene	TCTA	-0.508807	-1.42287	0.02597525
221736_at	KIAA1219 general transcription factor IIH, polypeptide 5 CDNA FLJ31919 fis, clone	KIAA1219	-0.50901589	-1.42308	0.049733581
213357_at	NT2RP7004964	GTF2H5	-0.50901783	-1.42308	0.042105187
214949_at			-0.50926507	-1.42332	0.008546266
205809_s_at	Wiskott-Aldrich syndrome-like DEAD (Asp-Glu-Ala-Asp) box	WASL	-0.50933178	-1.42339	0.02897476
210811_s_at	polypeptide 49 eukaryotic translation initiation	DDX49	-0.50933405	-1.42339	0.008191654
201935_s_at	factor 4 gamma, 3 eukaryotic translation initiation	EIF4G3	-0.50964387	-1.4237	0.015797948
214314_s_at	factor 5B	EIF5B	-0.51032422	-1.42437	0.041547223
204179_at	myoglobin RER1 retention in endoplasmic reticulum 1 homolog (S.	MB	-0.51055395	-1.4246	0.047363623
202296_s_at	cerevisiae) large subunit GTPase 1 homolog	RER1	-0.511521	-1.42555	0.019624023
221536_s_at	(S. cerevisiae) activating signal cointegrator 1	LSG1	-0.51160429	-1.42563	0.049628339
215684_s_at	complex subunit 2	ASCC2	-0.5116218	-1.42565	0.037146889
201733_at	chloride channel 3	CLCN3	-0.51199824	-1.42602	0.03149693
220144_s_at	ankyrin repeat domain 5	ANKRD5	-0.51202822	-1.42605	0.018965453
208066_s_at	general transcription factor IIB	GTF2B	-0.51255419	-1.42657	0.020891228
TAF7 RNA polymerase II, TATA box binding protein (TBP)-					
201023_at	associated factor, 55kDa	TAF7	-0.51458447	-1.42858	0.020112851
201776_s_at	KIAA0494	KIAA0494	-0.51476395	-1.42876	0.022760006
212877_at	kinesin light chain 1 chromosome 3 open reading	KLC1	-0.51487927	-1.42887	0.014788456
219474_at	frame 52 zinc finger, ZZ-type with EF-hand	C3orf52	-0.51575052	-1.42974	0.02449946
212601_at	domain 1	ZZEF1	-0.51582444	-1.42981	0.003901445
213478_at	kazrin	RP1-21O18	-0.51675976	-1.43074	0.040987387
203781_at	mitochondrial ribosomal protein	MRPL33	-0.51738334	-1.43136	0.045441388
219909_at	L33	MMP28	-0.51757135	-1.43154	0.034375372
204058_at	matrix metallopeptidase 28 malic enzyme 1, NADP(+)- dependent, cytosolic estrogen receptor binding site	ME1	-0.51794489	-1.43191	0.046968211
204278_s_at	associated, antigen, 9	EBAG9	-0.51814616	-1.43211	0.031032444

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	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NPL	-0.51998674	-1.43394	0.006765098
221210_s_at	histone cluster 3, H2a	HIST3H2A	-0.52003159	-1.43399	0.034142802
	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	MRS2	-0.52022126	-1.43418	0.017027365
218538_s_at	c-myc binding protein	MYCBP	-0.52061296	-1.43456	0.038182423
203360_s_at	tetraspanin 31	TSPAN31	-0.52072798	-1.43468	0.029644613
	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	ELOVL1	-0.52113718	-1.43509	0.019624023
57163_at	proteasome (prosome, macropain) subunit, alpha type, 5 mitogen-activated protein kinase	PSMA5	-0.5211824	-1.43513	0.041095513
201274_at	kinase 4	MAP2K4	-0.52147852	-1.43543	0.015909665
206953_s_at	latrophilin 2	LPHN2	-0.52191777	-1.43586	0.016850455
220761_s_at	TAO kinase 3	TAOK3	-0.5226027	-1.43654	0.02597525
	solute carrier family 31 (copper transporters), member 2	SLC31A2	-0.52299521	-1.43694	0.028312284
204204_at	microseminoprotein, beta-	MSMB	-0.52462392	-1.43856	0.016606812
	BUD31 homolog (S. cerevisiae)	BUD31	-0.52627639	-1.44021	0.015434646
219597_s_at	dual oxidase 1	DUOX1	-0.52723657	-1.44117	0.018372499
	transmembrane and coiled-coil domain family 1	TMCC1	-0.52724027	-1.44117	0.006921301
213351_s_at	ARP2 actin-related protein 2	ACTR2	-0.52783362	-1.44176	0.020400033
200728_at	homolog (yeast)	TMEM50B	-0.52848347	-1.44241	0.032430413
	tRNA-γW synthesizing protein 1 homolog (S. cerevisiae)	TYW1	-0.52851661	-1.44245	0.007083702
	TAF12 RNA polymerase II, TATA box binding protein (TBP)-				
209463_s_at	associated factor, 20kDa	TAF12	-0.52889315	-1.44282	0.015889948
218840_s_at	NAD synthetase 1	NADSYN1	-0.52907016	-1.443	0.012959052
	proline synthetase co-transcribed homolog (bacterial)	PROSC	-0.52907563	-1.443	0.02325585
	haloacid dehalogenase-like hydrolase domain containing 3	HDHD3	-0.52950601	-1.44343	0.038182423
221256_s_at	ER lipid raft associated 2	ERLIN2	-0.52996024	-1.44389	0.044130621

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	isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A	-0.53138714	-1.44532	0.022760006
203272_s_at	tumor suppressor candidate 2 phosphatidylinositol transfer	TUSC2	-0.53327043	-1.44721	0.012973447
201192_s_at	protein, alpha	PITPNA	-0.53401265	-1.44795	0.01323345
215884_s_at	ubiquilin 2	UBQLN2	-0.53480095	-1.44874	0.023195616
218260_at	DET1 and DDB1 associated 1	DDA1	-0.53492087	-1.44886	0.043855347
213637_at	Transcribed locus DnaJ (Hsp40) homolog, subfamily		-0.53517429	-1.44912	0.006765098
209157_at	A, member 2 sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S.	DNAJA2	-0.53520062	-1.44914	0.010060198
211423_s_at	cerevisiae)-like histone cluster 1, H2bg /// histone cluster 1, H2bf /// histone cluster 1, H2be /// histone cluster 1, H2bi ///	SC5DL	-0.53689421	-1.45085	0.022300352
214455_at	histone cluster 1, H2bc	HIST1H2BC	-0.53766649	-1.45162	0.016291216
220414_at	calmodulin-like 5	CALML5	-0.53792339	-1.45188	0.018190072
214911_s_at	bromodomain containing 2	BRD2	-0.53921868	-1.45319	0.0092838
201142_at	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa sirtuin (silent mating type information regulation 2	EIF2S1	-0.54210115	-1.45609	0.019886651
218797_s_at	homolog) 7 (S. cerevisiae) zinc finger, FYVE domain containing 26	SIRT7	-0.54288131	-1.45688	0.027725725
213073_at	dynein, cytoplasmic 2, light	ZFYVE26	-0.5430382	-1.45704	0.011345489
203762_s_at	intermediate chain 1 leptin receptor overlapping	DYNC2LI1	-0.54366546	-1.45767	0.009825362
202595_s_at	transcript-like 1	LEPROTL1	-0.54398596	-1.458	0.006994923
209926_at	myocyte enhancer factor 2B	MEF2B	-0.54557613	-1.4596	0.005627889
208899_x_at	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	ATP6V1D	-0.54664546	-1.46069	0.039353364
209186_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	-0.54761273	-1.46167	0.028368833
211413_s_at	peptidyl arginine deiminase, type IV	PADI4	-0.54765233	-1.46171	0.009110746
201024_x_at	eukaryotic translation initiation factor 5B	EIF5B	-0.54910532	-1.46318	0.026683706
216905_s_at	suppression of tumorigenicity 14 (colon carcinoma)	ST14	-0.54925079	-1.46333	0.042348015

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	NFKB inhibitor interacting Ras-like 2	NKIRAS2	-0.55113687	-1.46524	0.030686502
	mitogen-activated protein kinase				
212643_at	1 interacting protein 1-like	MAPK1IP1	-0.55121814	-1.46532	0.018965453
218135_at	ERGIC and golgi 2	ERGIC2	-0.55144167	-1.46555	0.023431113
	isocitrate dehydrogenase 3				
202069_s_at	(NAD+) alpha	IDH3A	-0.55220253	-1.46632	0.042138914
	ring finger and CCCH-type zinc				
220202_s_at	finger domains 2	RC3H2	-0.55404275	-1.46819	0.036846349
	solute carrier family 38, member				
214830_at	6	SLC38A6	-0.55525584	-1.46943	0.022965983
203159_at	glutaminase	GLS	-0.55580566	-1.46999	0.042323058
214598_at	claudin 8	CLDN8	-0.55689811	-1.4711	0.03539949
212070_at	G protein-coupled receptor 56	GPR56	-0.55855991	-1.4728	0.049628339
	transmembrane and coiled-coil				
213352_at	domain family 1	TMCC1	-0.55995482	-1.47422	0.022048788
204177_s_at	kelch-like 20 (Drosophila)	KLHL20	-0.56559033	-1.47999	0.017702307
219760_at	lin-7 homolog B (C. elegans)	LIN7B	-0.56594757	-1.48036	0.010235373
220998_s_at	unc-93 homolog B1 (C. elegans)	UNC93B1	-0.56629708	-1.48072	0.00887733
	required for meiotic nuclear				
	division 5 homolog B (S.				
218262_at	cerevisiae)	RMND5B	-0.56677166	-1.48121	0.016101691
	interferon stimulated				
208114_s_at	exonuclease gene 20kDa-like 2	ISG20L2	-0.56719846	-1.48164	0.049261748
212451_at	KIAA0256 gene product	KIAA0256	-0.56954452	-1.48405	0.049942643
	ubiquitin associated protein 2-				
214695_at	like	UBAP2L	-0.56963621	-1.48415	0.011300989
	alpha-methylacyl-CoA racemase				
	/// C1q and tumor necrosis factor				
209425_at	related protein 3	AMACR	-0.56973948	-1.48426	0.004895765
218224_at	paraneoplastic antigen MA1	PNMA1	-0.57145034	-1.48602	0.008459494
217794_at	proline rich 13	PRR13	-0.57337567	-1.488	0.011833306
	methyl-CpG binding domain				
209580_s_at	protein 4	MBD4	-0.57501958	-1.4897	0.012448129
219832_s_at	homeobox C13	HOXC13	-0.57547026	-1.49016	0.006994923
208945_s_at	beclin 1, autophagy related	BECN1	-0.57568984	-1.49039	0.047719364
212481_s_at	tropomyosin 4	TPM4	-0.57585961	-1.49057	0.030951478
217751_at	glutathione S-transferase kappa 1	GSTK1	-0.57614132	-1.49086	0.028552561
	chromosome 1 open reading				
	frame 218 /// DENN/MADD				
219696_at	domain containing 1B	C1orf218 /	-0.57614991	-1.49087	0.030816874

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	CDNA FLJ31688 fis, clone				
213448_at	NT2RI2005520	-0.57819121	-1.49298	0.018922783	
	polymerase (RNA) II (DNA directed) polypeptide G	POLR2G	-0.5789937	-1.49381	0.01671059
202306_at	DnaJ (Hsp40) homolog, subfamily				
212908_at	C, member 16	DNAJC16	-0.57905545	-1.49387	0.006921301
213220_at	hypothetical LOC92482	LOC92482	-0.57926935	-1.49409	0.017095271
202128_at	KIAA0317	KIAA0317	-0.57952835	-1.49436	0.017917278
218915_at	neurofibromin 2 (merlin) dihydrouridine synthase 1-like (S. cerevisiae)	NF2	-0.57964541	-1.49448	0.02449946
217912_at		DUS1L	-0.58180719	-1.49672	0.03376599
	ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D	ATP6V1D	-0.58264513	-1.49759	0.042148929
203665_at	heme oxygenase (decycling) 1 translocase of inner mitochondrial membrane 17	HMOX1	-0.58362127	-1.49861	0.047064544
201821_s_at	homolog A (yeast)	TIMM17A	-0.58427814	-1.49929	0.027147145
208546_x_at	histone cluster 1, H2bh	HIST1H2B	-0.58493742	-1.49997	0.012973447
209300_s_at	NECAP endocytosis associated 1	NECAP1	-0.58585706	-1.50093	0.006293525
	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	SLC9A3R1	-0.58717208	-1.5023	0.022122228
201349_at	nuclear receptor subfamily 3, group C, member 2	NR3C2	-0.58742575	-1.50256	0.003901445
206448_at	zinc finger protein 365	ZNF365	-0.59060867	-1.50588	0.017353002
218032_at	stannin	SNN	-0.59189185	-1.50722	0.046269754
	malic enzyme 1, NADP(+-) dependent, cytosolic trafficking protein, kinesin	ME1	-0.59195624	-1.50729	0.033679601
204059_s_at	binding 2	TRAK2	-0.5932626	-1.50865	0.0102878
221122_at	HRAS-like suppressor 2	HRASLS2	-0.59350735	-1.50891	0.010853986
214168_s_at	tight junction protein 1 (zona occludens 1)	TJP1	-0.59744698	-1.51304	0.017797984
218403_at	TP53 regulated inhibitor of apoptosis 1	TRIAP1	-0.59957917	-1.51527	0.016698837
211712_s_at	annexin A9	ANXA9	-0.59972122	-1.51542	0.036557389
	CDC42 effector protein (Rho				
214721_x_at	GTPase binding) 4	CDC42EP4	-0.60010403	-1.51583	0.040783358
	acyl-Coenzyme A oxidase 3,				
204242_s_at	pristanoyl glycosyltransferase-like domain	ACOX3	-0.60060812	-1.51636	0.009555655
219770_at	containing 1	GTDC1	-0.6012403	-1.51702	0.017979101

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coiled-coil-helix-coiled-coil-helix						
220647_s_at	domain containing 8	CHCHD8	-0.60230653	-1.51814	0.032276785	
ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A						
201971_s_at		ATP6V1A	-0.60751396	-1.52363	0.0307204	
alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor						
209424_s_at	related protein 3	AMACR	/// -0.60960808	-1.52584	0.005627889	
proline synthetase co-transcribed homolog (bacterial)						
209385_s_at		PROSC	-0.61005223	-1.52631	0.039944948	
204137_at	G protein-coupled receptor 137B	GPR137B	-0.61051005	-1.5268	0.012522351	
membrane-associated ring finger (C3HC4) 2						
210075_at		2-Mar	-0.61180627	-1.52817	0.015830371	
solute carrier family 35, member D2						
213083_at		SLC35D2	-0.61210995	-1.52849	0.010853986	
translocase of inner mitochondrial membrane 8						
218357_s_at	homolog B (yeast)	TIMM8B	-0.61419201	-1.5307	0.02597525	
201768_s_at	clathrin interactor 1	CLINT1	-0.61433257	-1.53085	0.045510962	
218126_at	family with sequence similarity 82, member C	FAM82C	-0.61458078	-1.53111	0.009825362	
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2						
203123_s_at		SLC11A2	-0.61514321	-1.53171	0.049565682	
201732_s_at	chloride channel 3	CLCN3	-0.61564532	-1.53224	0.008601198	
211676_s_at	interferon gamma receptor 1	IFNGR1	-0.62033344	-1.53723	0.048665054	
200965_s_at	actin binding LIM protein 1	ABLIM1	-0.62188162	-1.53888	0.006765098	
histone cluster 1, H2bg /// histone cluster 1, H2bf /// histone cluster 1, H2be /// histone cluster 1, H2bi ///						
208527_x_at	histone cluster 1, H2bc	HIST1H2BC	-0.6250554	-1.54227	0.011960948	
UTP3, small subunit (SSU) processome component,						
209486_at	homolog (S. cerevisiae)	UTP3	-0.62510619	-1.54232	0.025799468	
solute carrier family 35, member						
213082_s_at	D2	SLC35D2	-0.62737594	-1.54475	0.009152332	
213031_s_at	WD repeat domain 73	WDR73	-0.62869639	-1.54617	0.010739422	
N-ethylmaleimide-sensitive factor						
202395_at		NSF	-0.62936346	-1.54688	0.03150325	
212993_at	BTB (POZ) domain containing 14A	BTBD14A	-0.63189339	-1.5496	0.001616605	

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	phosphatidylinositol-5-phosphate				
218942_at	4-kinase, type II, gamma	PIP4K2C	-0.63309275	-1.55089	0.02597525
	aldehyde dehydrogenase 5				
	family, member A1 (succinate-				
203608_at	semialdehyde dehydrogenase)	ALDH5A1	-0.63339052	-1.55121	0.005627889
	chromosome 20 open reading				
217835_x_at	frame 24	C20orf24	-0.63387964	-1.55173	0.026683706
	histidine acid phosphatase				
203253_s_at	domain containing 1	HISPPD1	-0.63477571	-1.5527	0.019624023
204341_at	tripartite motif-containing 16	TRIM16	-0.63683103	-1.55491	0.037399893
	cytochrome P450, family 1,				
205749_at	subfamily A, polypeptide 1	CYP1A1	-0.63932075	-1.5576	0.010165029
	BMP and activin membrane-				
	bound inhibitor homolog				
203304_at	(Xenopus laevis)	BAMBI	-0.63952756	-1.55782	0.003901445
	ligase IV, DNA, ATP-dependent				
206235_at	phosphatidylinositol transfer	LIG4	-0.64642847	-1.56529	0.012476914
201190_s_at	protein, alpha	PITPNA	-0.64722982	-1.56616	0.00887733
	Rab geranylgeranyltransferase,				
213704_at	beta subunit	RABGGTB	-0.64867158	-1.56772	0.042587712
	TAF13 RNA polymerase II, TATA				
	box binding protein (TBP)-				
205966_at	associated factor, 18kDa	TAF13	-0.64878342	-1.56785	0.036694406
	Rho-related BTB domain				
216048_s_at	containing 3	RHOBTB3	-0.65083626	-1.57008	0.045334327
203158_s_at	glutaminase	GLS	-0.65664122	-1.57641	0.006949425
	interleukin 18 (interferon-gamma-				
206295_at	inducing factor)	IL18	-0.66018018	-1.58028	0.036520037
	DnaJ (Hsp40) homolog, subfamily				
202842_s_at	B, member 9	DNAJB9	-0.66224692	-1.58255	0.006949425
204667_at	forkhead box A1	FOXA1	-0.66372455	-1.58417	0.005627889
	GTP-binding protein 8 (putative)				
221046_s_at	dimethylarginine	GTPBP8	-0.66471266	-1.58525	0.040001317
	dimethylaminohydrolase 1				
209094_at	chromosome 6 open reading	DDAH1	-0.66495681	-1.58552	0.015021093
	frame 120	C6orf120	-0.66616423	-1.58685	0.017163466
205155_s_at	spectrin, beta, non-erythrocytic 2	SPTBN2	-0.66618843	-1.58687	0.023822395
203273_s_at	tumor suppressor candidate 2	TUSC2	-0.66864164	-1.58958	0.002990116

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204241_at	acyl-Coenzyme A oxidase 3, pristanoyl	ACOX3	-0.66925546	-1.59025	0.010853986
206061_s_at	dicer 1, ribonuclease type III	DICER1	-0.66967348	-1.59071	0.033624312
	alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor				
209426_s_at	related protein 3	AMACR	/// -0.67237816	-1.5937	0.004387256
218150_at	ADP-ribosylation factor-like 5A neural precursor cell expressed, developmentally down-regulated	ARL5A	-0.6727616	-1.59412	0.018190072
202149_at	9	NEDD9	-0.6728883	-1.59426	0.016108825
211383_s_at	WD repeat domain 37 chromosome 9 open reading	WDR37	-0.67330097	-1.59472	0.007131295
222165_x_at	frame 16	C9orf16	-0.6761547	-1.59788	0.009825362
	v-yes-1 Yamaguchi sarcoma viral				
202626_s_at	related oncogene homolog	LYN	-0.67827503	-1.60023	0.02897476
214651_s_at	homeobox A9 cytochrome b-561 domain	HOXA9	-0.67927554	-1.60134	0.012522351
209665_at	containing 2	CYB561D2	-0.68132747	-1.60361	0.016278635
205770_at	glutathione reductase peroxisome proliferator-	GSR	-0.68175005	-1.60408	0.010853986
208510_s_at	activated receptor gamma signal transducer and activator of	PPARG	-0.68272318	-1.60517	0.009110746
206118_at	transcription 4	STAT4	-0.68577598	-1.60857	0.047363623
	spen homolog, transcriptional				
201996_s_at	regulator (Drosophila) motile sperm domain containing	SPEN	-0.68703495	-1.60997	0.035860651
218853_s_at	1	MOSPD1	-0.68990711	-1.61318	0.01579422
203869_at	ubiquitin specific peptidase 46 phosphatidylinositol transfer	USP46	-0.69113828	-1.61456	0.006765098
201191_at	protein, alpha UDP-glucose ceramide	PITPNA	-0.6926668	-1.61627	0.027540443
204881_s_at	glucosyltransferase	UGCG	-0.69538564	-1.61932	0.012448129
	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase				
211985_s_at	kinase, delta solute carrier family 46, member	CALM1	/// -0.69623067	-1.62027	0.046356918
214719_at	3 growth arrest and DNA-damage-	SLC46A3	-0.69774285	-1.62197	0.016108825
209304_x_at	inducible, beta	GADD45B	-0.69880838	-1.62316	0.039944948

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CAP-GLY domain containing					
201975_at	linker protein 1	CLIP1	-0.69909929	-1.62349	0.04302319
201735_s_at	chloride channel 3	CLCN3	-0.70265461	-1.6275	0.013481296
203743_s_at	thymine-DNA glycosylase acyl-Coenzyme A oxidase 1,	TDG	-0.70272108	-1.62757	0.022981502
209600_s_at	palmitoyl	ACOX1	-0.7050067	-1.63015	0.022346379
glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid,					
210589_s_at	pseudogene ATPase, H ⁺ transporting, lysosomal 56/58kDa, V1 subunit B1 (Renal tubular acidosis with deafness)	GBA /// GB	-0.70721722	-1.63265	0.006293525
205473_at	translocase of inner mitochondrial membrane 17	ATP6V1B1	-0.70845821	-1.63406	0.009849164
215171_s_at	homolog A (yeast) trafficking protein, kinesin	TIMM17A	-0.70906468	-1.63474	0.035264267
202124_s_at	binding 2 transmembrane 7 superfamily	TRAK2	-0.7108598	-1.63678	0.014664842
210130_s_at	member 2 ATX1 antioxidant protein 1	TM7SF2	-0.71305295	-1.63927	0.024704744
203454_s_at	homolog (yeast) ectodermal-neural cortex (with BTB-like domain)	ATOX1	-0.71447693	-1.64089	0.032430413
201340_s_at	6-pyruvoyltetrahydropterin synthase	ENC1	-0.71989879	-1.64707	0.013044506
209694_at	breast carcinoma amplified sequence 2	PTS	-0.72043398	-1.64768	0.026965005
203053_at	N-terminal EF-hand calcium	BCAS2	-0.72172339	-1.64915	0.009825362
210720_s_at	binding protein 3	NECAB3	-0.724567	-1.6524	0.00887733
small nuclear RNA activating complex, polypeptide 5, 19kDa					
213203_at	spleen tyrosine kinase ras homolog gene family,	SNAPC5	-0.72493986	-1.65283	0.018311616
207540_s_at	member D	SYK	-0.72914669	-1.65766	0.005533101
31846_at	Yip1 domain family, member 1 C2 calcium-dependent domain	RHOD	-0.73000497	-1.65864	0.043925801
214733_s_at	containing 2	YIPF1	-0.73019677	-1.65887	0.022300352
212875_s_at	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	C2CD2	-0.73077704	-1.65953	0.007610795
218536_at	KIAA0232	MRS2	-0.73170135	-1.6606	0.001616605
212441_at		KIAA0232	-0.73285449	-1.66192	0.017818048

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	microfibrillar-associated protein				
205442_at	3-like	MFAP3L	-0.73506289	-1.66447	0.008191654
	serine/threonine kinase 3 (STE20 homolog, yeast)	STK3	-0.74075392	-1.67105	0.047706878
212415_at	septin 6	6-Sep	-0.74180086	-1.67226	0.006293525
	aldehyde dehydrogenase 3				
205640_at	family, member B1	ALDH3B1	-0.7430995	-1.67377	0.018190072
	chromosome 12 open reading frame 5	C12orf5	-0.74389294	-1.67469	0.034142802
218706_s_at	GRAM domain containing 3	GRAMD3	-0.74511873	-1.67611	0.004902615
212624_s_at	chimerin (chimaerin) 1	CHN1	-0.74665525	-1.6779	0.033775564
	N-acylsphingosine amidohydrolase (acid ceramidase) 1	ASAHI	-0.74672501	-1.67798	0.045562906
	phosphatase and actin regulator 2	PHACTR2	-0.74759272	-1.67899	0.007257672
204048_s_at	peptidase inhibitor 3, skin-derived (SKALP)	PI3	-0.74962606	-1.68136	0.040987387
203691_at	RNA terminal phosphate cyclase domain 1	RTCD1	-0.75145627	-1.68349	0.007051473
218417_s_at	hypothetical protein FLJ20489	FLJ20489	-0.75604598	-1.68886	0.014283294
	sulfotransferase family, cytosolic, 1B, member 1	SULT1B1	-0.76648336	-1.70112	0.002990116
221622_s_at	transmembrane protein 126B	TMEM126	-0.77203354	-1.70768	0.015820294
	DnaJ (Hsp40) homolog, subfamily C, member 12	DNAJC12	-0.77849358	-1.71534	0.006293525
205248_at	dopey family member 2	DOPEY2	-0.77887739	-1.7158	0.007257672
202948_at	interleukin 1 receptor, type I	IL1R1	-0.78040188	-1.71761	0.038182423
201079_at	synaptogyrin 2	SYNGR2	-0.78079459	-1.71808	0.022760006
	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid,				
209093_s_at	pseudogene	GBA	-0.78132114	-1.7187	0.005627889
	peroxisomal membrane protein 4, 24kDa	PXMP4	-0.7820371	-1.71956	0.047324525
219428_s_at	cytochrome b5 type A				
207843_x_at	(microsomal)	CYB5A	-0.78377842	-1.72163	0.023195616
210297_s_at	microseminoprotein, beta-	MSMB	-0.7838985	-1.72178	0.004387256
202951_at	serine/threonine kinase 38	STK38	-0.78558143	-1.72379	0.011512478
	FYN binding protein (FYB-120/130)	FYB	-0.78679134	-1.72523	0.011424114
211795_s_at			-0.7868141	-1.72526	0.004895765
212528_at	CDNA clone IMAGE:3878236	NUPL1	-0.79333	-1.73307	0.036078545

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	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	EIF2S1	-0.80118216	-1.74253	0.006293525
201143_s_at	solute carrier family 16, member 5 (monocarboxylic acid transporter 6) /// similar to MCT	LOC100135353	-0.80368683	-1.74556	0.003572379
209180_at	Rab geranylgeranyltransferase, beta subunit heat shock 105kDa/110kDa	RABGGTB	-0.80536408	-1.74759	0.011534663
208744_x_at	protein 1 amiloride binding protein 1 (amine oxidase (copper-containing))	HSPH1	-0.80941382	-1.7525	0.020336612
203559_s_at	chromosome 6 open reading frame 120	ABP1	-0.81263965	-1.75642	0.021823482
221786_at	abhydrolase domain containing 6 chromosome 17 open reading frame 91	C6orf120	-0.81355497	-1.75754	0.016199453
221552_at	abhydrolase domain containing 6 chromosome 17 open reading frame 91	ABHD6	-0.8148179	-1.75908	0.003901445
214696_at	hypothetical protein FLJ20489 caspase 4, apoptosis-related	FLJ20489	-0.81757032	-1.76244	0.006808225
209310_s_at	cysteine peptidase cytochrome b5 type A	CASP4	-0.81985113	-1.76522	0.004387256
209366_x_at	(microsomal)	CYB5A	-0.82529506	-1.7719	0.024228831
45288_at	abhydrolase domain containing 6 N-acylsphingosine amido hydrolase (acid)	ABHD6	-0.82691688	-1.77389	0.004895765
213702_x_at	ceramidase 1 mitogen-activated protein kinase	ASAHI	-0.82793747	-1.77515	0.034446605
207121_s_at	6	MAPK6	-0.82848301	-1.77582	0.040010642
209882_at	Ras-like without CAAX 1 adaptor-related protein complex	RIT1	-0.82852415	-1.77587	0.021384427
65517_at	1, mu 2 subunit adaptor-related protein complex	AP1M2	-0.83061336	-1.77844	0.019984778
218261_at	1, mu 2 subunit olfactory receptor, family 7, subfamily E, member 37	AP1M2	-0.83154677	-1.77959	0.036212513
217499_x_at	pseudogene	OR7E37P	-0.83637865	-1.78556	0.007043637
206059_at	zinc finger protein 91	ZNF91	-0.8372735	-1.78667	0.016606812
209950_s_at	villin-like family with sequence similarity	VILL	-0.83982634	-1.78983	0.003930777
218532_s_at	134, member B	FAM134B	-0.85299911	-1.80625	0.035341012

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	fermitin family homolog 2 (Drosophila)	FERMT2	-0.85454842	-1.80819	0.020336612
	cytochrome b5 type A (microsomal)	CYB5A	-0.85704006	-1.81132	0.030412658
215726_s_at	prenylcysteine oxidase 1 like	PCYOX1L	-0.85772229	-1.81218	0.011833306
206833_s_at	acylphosphatase 2, muscle type	ACYP2	-0.8585975	-1.81327	0.00740596
209155_s_at	5'-nucleotidase, cytosolic II tumor protein p53 inducible	NT5C2	-0.86052889	-1.8157	0.018372499
210609_s_at	protein 3 ras homolog gene family,	TP53I3	-0.87365046	-1.83229	0.044187722
209885_at	member D acyl-Coenzyme A oxidase 1,	RHOD	-0.88119485	-1.8419	0.02784478
213501_at	palmitoyl ectonucleoside triphosphate	ACOX1	-0.88129622	-1.84203	0.005627889
204076_at	diphosphohydrolase 4	ENTPD4	-0.88165913	-1.84249	0.003930777
208579_x_at	H2B histone family, member S	H2BFS	-0.88196031	-1.84288	0.001616605
205807_s_at	tuftelin 1	TUFT1	-0.88262984	-1.84373	0.006334784
221679_s_at	abhydrolase domain containing 6 fermitin family homolog 2	ABHD6	-0.89026256	-1.85351	0.001616605
209209_s_at	(Drosophila)	FERMT2	-0.89075407	-1.85414	0.013348314
210117_at	sperm associated antigen 1 bolA homolog 2 (E. coli) /// bolA	SPAG1	-0.89823687	-1.86379	0.015971168
209836_x_at	homolog 2B (E. coli)	BOLA2 ///	-0.89905396	-1.86484	0.006341619
206115_at	early growth response 3 fermitin family homolog 2	EGR3	-0.89996941	-1.86603	0.004868451
214212_x_at	(Drosophila)	FERMT2	-0.90672272	-1.87478	0.0046331
212111_at	syntaxin 12	STX12	-0.90819985	-1.8767	0.006921301
209083_at	coronin, actin binding protein, 1A TIMP metallopeptidase inhibitor	CORO1A	-0.91414148	-1.88445	0.007083702
203167_at	2	TIMP2	-0.91591583	-1.88677	0.010853986
209806_at	histone cluster 1, H2bk	HIST1H2BK	-0.92039183	-1.89263	0.011512478
216074_x_at	WW and C2 domain containing 1	WWC1	-0.92312744	-1.89622	0.011534663
204544_at	Hermansky-Pudlak syndrome 5	HPS5	-0.92735812	-1.90179	0.005627889
219628_at	zinc finger, matrin type 3 matrix metallopeptidase 7	ZMAT3	-0.92737794	-1.90182	0.014129109
204259_at	(matrilysin, uterine)	MMP7	-0.92763926	-1.90216	0.006949425
202708_s_at	histone cluster 2, H2be	HIST2H2BE	-0.92772625	-1.90228	0.045867156
219403_s_at	heparanase inhibitor of DNA binding 3, dominant negative helix-loop-	HPSE	-0.93099157	-1.90659	0.009110746
207826_s_at	helix protein	ID3	-0.9345611	-1.91131	0.03555525

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	DnaJ (Hsp40) homolog, subfamily				
204720_s_at	C, member 6	DNAJC6	-0.95360941	-1.93671	0.012825789
212724_at	Rho family GTPase 3	RND3	-0.95391827	-1.93713	0.005627889
203870_at	ubiquitin specific peptidase 46	USP46	-0.95801787	-1.94264	0.005627889
41047_at	chromosome 9 open reading frame 16	C9orf16	-0.95974469	-1.94497	0.012228762
	proteasome (prosome, macropain) subunit, beta type,				
202659_at	10	PSMB10	-0.96551134	-1.95276	0.013881707
210397_at	defensin, beta 1	DEFB1	-0.96736044	-1.95526	0.041052549
	pirin (iron-binding nuclear				
207469_s_at	protein)	PIR	-0.97378175	-1.96398	0.028846728
210986_s_at	tropomyosin 1 (alpha)	TPM1	-0.97662063	-1.96785	0.008601198
	ATPase, H ⁺ transporting,				
208737_at	lysosomal 13kDa, V1 subunit G1	ATP6V1G1	-0.97888011	-1.97093	0.006293525
212112_s_at	syntaxin 12	STX12	-0.98102068	-1.97386	0.009110746
206094_x_at		UGT1A1 //	-0.98327707	-1.97695	0.007257672
214639_s_at	homeobox A1	HOXA1	-0.99411563	-1.99186	0.001543625
	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase,				
210540_s_at	polypeptide 4	B4GALT4	-1.00065451	-2.00091	0.034142802
	neural precursor cell expressed, developmentally down-regulated				
212445_s_at	4-like	NEDD4L	-1.00114232	-2.00158	0.022760006
	major facilitator superfamily				
218109_s_at	domain containing 1	MFSD1	-1.03468417	-2.04867	0.017238997
206117_at	tropomyosin 1 (alpha)	TPM1	-1.04303878	-2.06056	0.01254069
	hydroxyprostaglandin				
211548_s_at	dehydrogenase 15-(NAD)	HPGD	-1.05386965	-2.07609	0.030133423
210987_x_at	tropomyosin 1 (alpha)	TPM1	-1.05728705	-2.08101	0.008601198
	cysteine-rich, angiogenic inducer,				
201289_at	61	CYR61	-1.06386645	-2.09053	0.037146313
	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase,				
221484_at	polypeptide 5	B4GALT5	-1.06398638	-2.0907	0.026683706
219858_s_at	FLJ20160 protein	FLJ20160	-1.06584641	-2.0934	0.030553407
	glutamate-cysteine ligase,				
203925_at	modifier subunit	GCLM	-1.06898817	-2.09796	0.005533101
	coenzyme Q10 homolog B (S. cerevisiae)				
219397_at		COQ10B	-1.07493195	-2.10662	0.006334784
201058_s_at	myosin, light chain 9, regulatory	MYL9	-1.088787	-2.12695	0.022219699
219014_at	placenta-specific 8	PLAC8	-1.09942948	-2.1427	0.022346379
213085_s_at	WW and C2 domain containing 1	WWC1	-1.10094711	-2.14495	0.009825362

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	chromosome 9 open reading frame 16	C9orf16	-1.10207216	-2.14663	0.003901445
204480_s_at	peptidyl arginine deiminase, type IV	PADI4	-1.10607101	-2.15259	0.006341619
	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	NME5	-1.10714739	-2.15419	0.003101146
206197_at	olfactomedin-like 3	OLFML3	-1.10992217	-2.15834	0.004895765
	Rho-related BTB domain containing 3	RHOBTB3	-1.1111758	-2.16022	0.045289649
219995_s_at	zinc finger protein 750	ZNF750	-1.11493714	-2.16586	0.016486948
213680_at	keratin 6B	KRT6B	-1.12665012	-2.18351	0.005627889
209398_at	histone cluster 1, H1c	HIST1H1C	-1.14265898	-2.20788	0.004895765
206116_s_at	tropomyosin 1 (alpha)	TPM1	-1.1535387	-2.22459	0.003901445
202545_at	protein kinase C, delta	PRKCD	-1.16436395	-2.24134	0.013677352
203914_x_at	hydroxyprostaglandin dehydrogenase 15-(NAD)	HPGD	-1.1702437	-2.2505	0.047363623
	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	PTPLB	-1.18069463	-2.26686	0.046159827
212640_at	thioredoxin reductase 1	TXNRD1	-1.18863455	-2.27937	0.00887733
	similar to olfactory receptor, family 7, subfamily A, member 17	LOC44145	-1.18909008	-2.28009	0.003901445
217551_at	histone cluster 2, H2aa3 ///				
218280_x_at	histone cluster 2, H2aa4	HIST2H2AA	-1.20433753	-2.30431	0.007257672
	aldehyde dehydrogenase 3				
205623_at	family, memberA1	ALDH3A1	-1.20497321	-2.30533	0.015796973
	NAD(P)H dehydrogenase,				
201468_s_at	quinone 1	NQO1	-1.22404496	-2.33601	0.010853986
	Rho-related BTB domain				
202975_s_at	containing 3	RHOBTB3	-1.24385788	-2.36831	0.014546584
	keratin 10 (epidermolytic hyperkeratosis; keratosis				
210633_x_at	palmaris et plantaris)	KRT10	-1.24466881	-2.36964	0.004868451
	calcium/calmodulin-dependent protein kinase (CaM kinase) II				
212669_at	gamma histone cluster 2, H2aa3 ///	CAMK2G	-1.24815124	-2.37537	0.015225077
214290_s_at	histone cluster 2, H2aa4	HIST2H2AA	-1.25085744	-2.37983	0.018190072
211597_s_at	HOP homeobox	HOPX	-1.2511356	-2.38029	0.035362626
207126_x_at	keratin 10 (epidermolytic hyperkeratosis; keratosis	UGT1A1 //	-1.29133003	-2.44754	0.003901445
	palmaris et plantaris)	KRT10	-1.29892663	-2.46046	0.006293525

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	solute carrier family 22 (organic cation/carnitine transporter),				
205074_at	member 5	SLC22A5	-1.29999165	-2.46227	0.008191654
204532_x_at		UGT1A1 //,	-1.30194215	-2.46561	0.005627889
201939_at	polo-like kinase 2 (Drosophila)	PLK2	-1.3048292	-2.47054	0.016824371
218231_at	N-acetylglucosamine kinase receptor-interacting serine-	NAGK	-1.31415632	-2.48657	0.003901445
221215_s_at	threonine kinase 4 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase,	RIPK4	-1.35927642	-2.56556	0.047324525
221485_at	polypeptide 5	B4GALT5	-1.39040879	-2.62153	0.020085667
	solute carrier family 16, member 5 (monocarboxylic acid)				
206600_s_at	transporter 6) /// similar to MCT serine threonine kinase 39	LOC100133	-1.39268865	-2.62568	0.003572379
202786_at	(STE20/SPS1 homolog, yeast)	STK39	-1.39449198	-2.62896	0.006054254
208539_x_at	small proline-rich protein 2B	SPRR2B	-1.41153065	-2.66019	0.035726339
203962_s_at	nebulette	NEBL	-1.42063854	-2.67704	0.048325018
203961_at	nebulette keratin 10 (epidermolytic hyperkeratosis; keratosis	NEBL	-1.4343218	-2.70255	0.028368833
207023_x_at	palmaris et plantaris) dickkopf homolog 1 (Xenopus laevis)	KRT10	-1.444271	-2.72125	0.006334784
204602_at	distal-less homeobox 2	DKK1	-1.45021124	-2.73248	0.005879063
207147_at		DLX2	-1.45941253	-2.74996	0.03244829
208596_s_at		UGT1A1 //,	-1.4847415	-2.79867	0.008103638
208711_s_at	cyclin D1	CCND1	-1.48845248	-2.80588	0.003901445
	solute carrier family 16, member 5 (monocarboxylic acid)				
213590_at	transporter 6) /// similar to MCT	LOC100133	-1.49136409	-2.81155	0.001421337
203002_at	angiotonin like 2	AMOTL2	-1.50015332	-2.82873	0.004838106
215125_s_at		UGT1A1 //,	-1.50816041	-2.84447	0.005943342
	calcium/calmodulin-dependent protein kinase (CaM kinase) II				
212757_s_at	gamma solute carrier family 29 (nucleoside transporters),	CAMK2G	-1.51225669	-2.85256	0.012635523
219344_at	member 3	SLC29A3	-1.5171564	-2.86226	0.003901445
201743_at	CD14 molecule	CD14	-1.53291369	-2.8937	0.003901445
218729_at	latexin peptidyl arginine deiminase, type	LXN	-1.54795291	-2.92402	0.015434646
209791_at	II	PADI2	-1.57640184	-2.98225	0.005627889
208651_x_at	CD24 molecule	CD24	-1.64007177	-3.11681	0.037399893
216379_x_at	CD24 molecule	CD24	-1.64374643	-3.12476	0.020290376

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209771_x_at	CD24 molecule sulfotransferase family, cytosolic,	CD24	-1.65086903	-3.14023	0.019186611
205759_s_at	2B, member 1	SULT2B1	-1.67309381	-3.18898	0.003930777
266_s_at	CD24 molecule	CD24	-1.68268061	-3.21024	0.027725725
208650_s_at	CD24 molecule	CD24	-1.72700286	-3.31039	0.022122228
219934_s_at	sulfotransferase family 1E, estrogen-preferring, member 1 inhibitor of DNA binding 2, dominant negative helix-loop-	SULT1E1	-1.8038756	-3.49157	0.001277571
201565_s_at	helix protein	ID2	-1.81546541	-3.51973	0.035341012
214599_at	involutrin	IVL	-1.82087945	-3.53296	0.004868451
210096_at	cytochrome P450, family 4, subfamily B, polypeptide 1	CYP4B1	-1.86813986	-3.65062	0.026995831
CD36 molecule (thrombospondin)					
206488_s_at	receptor)	CD36	-1.89815377	-3.72736	0.03149693
208712_at	cyclin D1	CCND1	-1.90322488	-3.74048	0.003672628
hydroxysteroid (11-beta)					
204130_at	dehydrogenase 2	HSD11B2	-2.03911021	-4.10992	0.018188987
cytochrome P450, family 1,					
202435_s_at	subfamily B, polypeptide 1	CYP1B1	-2.05457216	-4.1542	0.016108825
keratin 23 (histone deacetylase					
218963_s_at	inducible)	KRT23	-2.07004603	-4.199	0.003901445
glycerophosphodiester					
phosphodiesterase domain					
219722_s_at	containing 3	GDPD3	-2.08062197	-4.2299	0.00887733
209772_s_at	CD24 molecule	CD24	-2.11400124	-4.3289	0.023579078
cytochrome P450, family 1,					
202437_s_at	subfamily B, polypeptide 1	CYP1B1	-2.1295861	-4.37592	0.009110746
serum amyloid A1 /// serum					
214456_x_at	amyloid A2	SAA1 /// Sf	-2.17926596	-4.52923	0.016278635
serum amyloid A1 /// serum					
208607_s_at	amyloid A2	SAA1 /// Sf	-2.25229174	-4.76439	0.019822177
chloride intracellular channel 3					
219529_at	aldehyde dehydrogenase 1	CLIC3	-2.39940208	-5.27584	0.016698837
203180_at	family, member A3	ALDH1A3	-2.44128472	-5.43125	0.00245319
cytochrome P450, family 1,					
202436_s_at	subfamily B, polypeptide 1	CYP1B1	-2.47847581	-5.57308	0.006334784
206884_s_at	sciellin	SCEL	-2.50815335	-5.68891	0.029594023
205319_at	prostate stem cell antigen	PSCA	-2.729491	-6.63222	0.009825362
S100 calcium binding protein P					
204351_at		S100P	-2.87697166	-7.34607	0.012973447
small proline-rich protein 1A		SPRR1A	-3.05933374	-8.33588	0.004926805
retinoic acid receptor responder					
206392_s_at	(tazarotene induced) 1	RARRES1	-3.15718048	-8.92085	0.027885596

Differentially expressed genes on collagen

	small proline-rich protein 1B (cornifin)	SPRR1B	-3.19705171	-9.17083	0.006765098
205064_at	retinoic acid receptor responder (tazarotene induced) 1	RARRES1	-3.35181061	-10.2093	0.026584734
213796_at	small proline-rich protein 1A	SPRR1A	-4.11411186	-17.3169	0.003930777