Supplementary Table 1

Unigene		Gene symbol		Description	Log2 ratio (A/B)		*P*-value (*t*-test)	
Human	Mouse	Hs.GENE	Mm.Gene		Human	Mouse	Human	Mouse
More Expressed in subclass A								
Hs.155421	Mm.80	AFP	Afp	alpha-fetoprotein	0.97	1.45	1.3E-06	3.2E-07
Hs.75313	Mm.451	AKR1B1	Akr1b3	aldo-keto reductase family 1, member B1 (aldose reductase)	0.72	1.42	0.0011	7E-07
Hs.273415	Mm.275831	ALDOA	Aldo1	aldolase A, fructose-bisphosphate	1.02	1.22	2.8E-07	4.9E-05
Hs.100194	Mm.19844	ALOX5AP	Alox5ap	arachidonate 5-lipoxygenase-activating protein	0.87	1.43	4.4E-05	2.2E-05
Hs.78225	Mm.14860	ANXA1	Anxa1	annexin A1	0.78	0.70	0.00032	0.03648
Hs.1378	Mm.7214	ANXA3	Anxa3	annexin A3	1.13	1.09	7E-09	0.00112
Hs.300711	Mm.1620	ANXA5	Anxa5	annexin A5	1.09	0.91	3.2E-08	0.00419
Hs.83583	Mm.17912	ARPC2	Arpc2	actin related protein 2/3 complex, subunit 2, 34kDa	1.35	0.86	2.9E-13	0.00701
Hs.152759	Mm.22430	ASK	Ask-pendin	activator of S phase kinase	1.15	0.96	8.3E-09	0.00838
Hs.75692	Mm.2942	ASNS	Asns	asparagine synthetase	0.76	1.00	0.00084	0.00136
Hs.194688	Mm.40331	BAZ1B	Baz1b	bromodomain adjacent to zinc finger domain, 1B	0.79	0.92	0.00012	0.00378
Hs.77054	Mm.16596	BTG1	Btg1	B-cell translocation gene 1, anti-proliferative	0.86	1.22	2E-05	5.6E-05
Hs.75462	Mm.239605	BTG2	Btg2	BTG family, member 2	0.71	1.46	0.00057	2.3E-07
Hs.94953	Mm.3453	C1QG	C1qg	complement component 1, q subcomponent, gamma polypeptide	0.81	0.86	6.4E-05	0.00783
Hs.433337	Mm.29763	C20orf16	Smox-penc	chromosome 20 open reading frame 16	0.80	0.82	0.00098	0.01804
Hs.7753	Mm.7515	CALU	Calu	calumenin	0.85	0.73	2.9E-05	0.02427
Hs.75498	Mm.116739	CCL20	Ccl20	chemokine (C-C motif) ligand 20	1.02	1.70	2.7E-07	0.00013
Hs.75703	Mm.1255	CCL4	Ccl4	chemokine (C-C motif) ligand 4	0.84	1.18	3.9E-05	0.00135
Hs.79150	Mm.46781	CCT4	Cct4	chaperonin containing TCP1, subunit 4 (delta)	1.07	0.68	6.3E-08	0.03822
Hs.1600	Mm.1813	CCT5	Cct5	chaperonin containing TCP1, subunit 5 (epsilon)	0.96	1.16	1.5E-06	0.00014
Hs.108809	Mm.914	CCT7	Cct7	chaperonin containing TCP1, subunit 7 (eta)	1.06	0.75	7E-08	0.02015
Hs.375108	Mm.6417	CD24	Cd24a	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	0.99	1.45	8E-07	1.3E-05
Hs.374340	Mm.259329	CD2AP	Cd2ap	CD2-associated protein	0.67	0.72	0.00115	0.02677
Hs.82212	Mm.2692	CD53	Cd53	CD53 antigen	0.87	0.73	1.7E-05	0.02719
Hs.433996	Mm.4426	CD63	Cd63	CD63 antigen (melanoma 1 antigen)	0.84	1.62	3.8E-05	1.2E-09
Hs.246381	Mm.15819	CD68	Cd68	CD68 antigen	0.79	0.86	0.00011	0.00715
Hs.79197	Mm.57175	CD83	Cd83	CD83 antigen (activated B lymphocytes, immunoglobulin superfam	0.62	1.57	0.00467	0.00014
Hs.1634	Mm.29800	CDC25A	Cdc25a	cell division cycle 25A	0.58	1.32	0.00989	2E-05
Hs.28853	Mm.20842	CDC7L1	Cdc7l1	CDC7 cell division cycle 7-like 1 (S. cerevisiae)	0.84	0.95	0.00012	0.0342
Hs.95577	Mm.6839	CDK4	Cdk4	cyclin-dependent kinase 4	1.31	0.93	2.4E-12	0.00319
Hs.20295	Mm.16753	CHEK1	Chek1	CHK1 checkpoint homolog (S. pombe)	1.06	1.23	1.6E-07	0.00251
Hs.414565	Mm.29524	CLIC1	Clic1	chloride intracellular channel 1	1.51	0.68	4.9E-18	0.03685
Hs.81343	Mm.2423	COL2A1	Col2a1	collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiph	0.49	1.34	0.02497	8.9E-05
Hs.119129	Mm.738	COL4A1	Col4a1	collagen, type IV, alpha 1	0.56	1.01	0.00743	0.00123
Hs.5057	Mm.20910	CPD	Cpd	carboxypeptidase D	0.78	0.93	0.00014	0.00635
Hs.198726	Mm.193526	CSDA	Csda	cold shock domain protein A	0.92	0.78	0.00014	0.01616
Hs.90073	Mm.22417	CSE1L	Cse1l	CSE1 chromosome segregation 1-like (yeast)	1.13	0.90	4.9E-09	0.00486
Hs.171391	Mm.226905	CTBP2	Ctbp2	C-terminal binding protein 2	0.80	0.75	7.9E-05	0.04437
Hs.78056	Mm.930	CTSL	Ctsl	cathepsin L	0.70	0.73	0.00067	0.02488
Hs.75562	Mm.5021	DDR1	Ddr1	discoidin domain receptor family, member 1	0.69	1.49	0.00114	4.4E-07
Hs.6790	Mm.27432	DNAJB9	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.70	1.57	0.00067	4E-07
Hs.122579	Mm.2995	ECT2	Ect2	epithelial cell transforming sequence 2 oncogene	1.39	0.98	2.8E-12	0.0099
Hs.119503	Mm.206404	EIF3S6IP	Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting	0.76	0.75	0.0002	0.02354
Hs.183684	Mm.525	EIF4G2	Eif4g2	eukaryotic translation initiation factor 4 gamma, 2	0.92	0.87	5E-06	0.00635
Hs.408061	Mm.741	FABP5	Fabp5	fatty acid binding protein 5 (psoriasis-associated)	1.29	1.30	2.8E-11	1E-05
Hs.750	Mm.735	FBN1	Fbn1	fibrillin 1 (Marfan syndrome)	0.61	1.26	0.0057	0.00098
Hs.351808	Mm.292100	FGL2	Fgl2	fibrinogen-like 2	0.70	1.42	0.00067	1.2E-05
Hs.3849	Mm.3894	FKBP10	Fkbp10	FK506 binding protein 10, 65 kDa	1.02	0.70	4.3E-07	0.03914
Hs.333418	Mm.1870	FXYD5	Fxyd5	FXYD domain containing ion transport regulator 5	0.85	1.03	3.7E-05	0.00099
Hs.114218	Mm.4769	FZD6	Fzd6	frizzled homolog 6 (Drosophila)	0.80	1.10	8.9E-05	0.00206
Hs.80206	Mm.27210	G6PD	G6pdx	glucose-6-phosphate dehydrogenase	0.79	1.38	0.0001	3.7E-06
Hs.111867	Mm.12090	GLI2	Gli2	GLI-Kruppel family member GLI2	0.87	1.08	6.6E-05	0.02525
Hs.215595	Mm.2344	GNB1	Gnb1	guanine nucleotide binding protein (G protein), beta polypeptide	0.84	0.86	0.00045	0.00751
Hs.172654	Mm.9336	GNB4	Gnb4	guanine nucleotide binding protein (G protein), beta polypeptide	0.96	1.32	1.9E-06	0.00047
Hs.122552	Mm.20858	GTSE1	Gtse1	G-2 and S-phase expressed 1	1.01	1.21	3.2E-06	6.1E-05
Hs.75307	Mm.18843	H1FX	Tgm2	H1 histone family, member X	0.57	1.19	0.00617	9.1E-05
Hs.89555	Mm.715	HCK	Hck	hemopoietic cell kinase	0.86	1.21	2.4E-05	0.00099
Hs.1162	Mm.3322	HLA-DMB	H2-DMb1	major histocompatibility complex, class II, DM beta	0.73	1.03	0.00038	0.00613
Hs.251064	Mm.2756	HMGN1	Hmgn1	high-mobility group nucleosome binding domain 1	1.04	0.68	1.4E-07	0.03601
Hs.109706	Mm.1775	HN1	Hn1	hematological and neurological expressed 1	1.16	1.46	1.9E-09	2.1E-06
Hs.376844	Mm.12236	HNRPA1	Zfp207	heterogeneous nuclear ribonucleoprotein A1	1.25	0.98	4.4E-11	0.00193
Hs.110637	Mm.5	HOXA10	Hoxa10	homeo box A10	0.62	1.16	0.00409	0.01575
Hs.171545	Mm.6461	HRB	Hrb	HIV-1 Rev binding protein	1.14	1.48	3.5E-09	1.2E-07
Hs.180414	Mm.197551	HSPA8	Hspa8	heat shock 70kDa protein 8	0.77	1.25	0.00017	3.1E-05
Hs.168383	Mm.25455	ICAM1	Icam1	intercellular adhesion molecule 1 (CD54), human rhinovirus recept	0.71	1.52	0.0006	3.6E-08
Hs.1742	Mm.56685	IQGAP1	Iqgap1	IQ motif containing GTPase activating protein 1	1.14	1.08	4.7E-09	0.00062
Hs.149609	Mm.16234	ITGA5	Itga5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	0.70	0.77	0.0016	0.01743
Hs.77515	Mm.26945	ITPR3	Itpr3	inositol 1,4,5-triphosphate receptor, type 3	0.87	1.36	0.00013	5.2E-06
Hs.91143	Mm.22398	JAG1	Jag1	jagged 1 (Alagille syndrome)	0.59	1.17	0.00822	0.00045

Hs.8878	Mm.42203	KIF11	Kif11	kinesin family member 11	1.28	0.81	1.3E-11	0.02463
Hs.20830	Mm.197684	KIFC1	Kifc1	kinesin family member C1	0.89	0.97	0.00025	0.01451
Hs.180446	Mm.16710	KPNB1	Kpnb1	karyopherin (importin) beta 1	0.98	0.75	9.8E-07	0.0208
Hs.113503	Mm.151329	KPNB3	Kpnb3	karyopherin (importin) beta 3	0.97	0.81	1E-06	0.01176
Hs.2785	Mm.14046	KRT17	Krt1-17	keratin 17	0.70	0.96	0.00233	0.00308
Hs.182265	Mm.1012	KRT19	Krt1-19	keratin 19	1.01	1.10	3.3E-07	0.00035
Hs.432855	Mm.260684	LAMC1	LOC22651	laminin, gamma 1 (formerly LAMB2)	0.75	1.14	0.00245	0.00028
Hs.79356	Mm.4554	LAPTM5	Laptm5	Lysosomal-associated multispanning membrane protein-5	1.02	0.66	2.6E-07	0.04783
Hs.18069	Mm.17185	LGMN	Lgmn	legumain	0.74	1.04	0.00032	0.00116
Hs.279943	Mm.200426	LMCD1	Lmcd1	LIM and cysteine-rich domains 1	0.94	1.30	3.3E-06	0.0003
Hs.15984	Mm.512	LOC51186	Wbp5	pp21 homolog	0.56	1.60	0.00766	2.2E-09
Hs.56729	Mm.2183	LSP1	Lsp1	lymphocyte-specific protein 1	1.08	0.99	3.9E-08	0.0017
Hs.109276	Mm.2632	LXN	Lxn	latexin protein	0.76	1.02	0.00107	0.00703
Hs.425427	Mm.28560	LYAR	Lyar	hypothetical protein FLJ20425	0.68	0.83	0.00092	0.00947
Hs.401150	Mm.15918	MAP3K1	Map3k1	mitogen-activated protein kinase kinase kinase 1	0.53	1.48	0.01239	1.2E-07
Hs.861	Mm.8385	MAPK3	Mapk3	mitogen-activated protein kinase 3	0.85	0.81	3E-05	0.01164
Hs.234279	Mm.259691	MAPRE1	Mapre1	microtubule-associated protein, RP/EB family, member 1	1.36	1.04	1.5E-13	0.00091
Hs.75607	Mm.30059	MARCKS	Marcks	myristoylated alanine-rich protein kinase C substrate	1.33	1.03	8.6E-13	0.001
Hs.179565	Mm.4502	MCM3	Mcmd	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	1.09	1.02	2.1E-08	0.00363
Hs.155462	Mm.4933	MCM6	Mcmd6	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S	1.25	1.34	1.1E-10	0.00021
Hs.1695	Mm.2055	MMP12	Mmp12	matrix metalloproteinase 12 (macrophage elastase)	0.67	0.79	0.00152	0.01451
Hs.2256	Mm.4825	MMP7	Mmp7	matrix metalloproteinase 7 (matrilysin, uterine)	0.69	1.71	0.00091	6.5E-07
Hs.151738	Mm.4406	MMP9	Mmp9	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa	0.83	1.24	0.00019	0.00069
Hs.78934	Mm.4619	MSH2	Msh2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	1.17	0.67	1.5E-09	0.04401
Hs.3248	Mm.18210	MSH6	Msh6	mutS homolog 6 (E. coli)	0.88	1.04	1.3E-05	0.00087
Hs.23643	Mm.46254	MST4	Mst4-pendi	Mst3 and SOK1-related kinase	0.96	1.68	3.5E-06	0.00015
Hs.154672	Mm.443	MTHFD2	Mthfd2	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), me	0.95	0.88	3.7E-06	0.00581
Hs.75789	Mm.4063	NDRG1	Ndr1	N-myc downstream regulated gene 1	0.78	0.94	0.00023	0.00298
Hs.155595	Mm.336	NEDD5	66	neural precursor cell expressed, developmentally down-regulated 5	1.24	0.76	6.3E-11	0.01938
Hs.119908	Mm.10303	NOP5/NOP5	Nol5	nucleolar protein NOP5/NOP58	0.97	0.78	1.4E-06	0.01592
Hs.355719	Mm.6343	NPM1	Npm1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.92	0.72	4.6E-06	0.02577
Hs.172182	Mm.2642	PABPC1	Pabpc1	poly(A) binding protein, cytoplasmic 1	0.62	1.31	0.00307	8.4E-06
Hs.6793	Mm.597	PAFAH1B3	Pafah1b3	platelet-activating factor acetylhydrolase, isoform Ib, gamma sub	0.80	1.14	0.00027	0.00042
Hs.89901	Mm.36865	PDE4A	Pde4a	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dun	0.71	1.09	0.00073	0.00174
Hs.13501	Mm.28659	PES1	Pes1	pescadillo homolog 1, containing BRCT domain (zebrafish)	0.93	0.78	3.1E-06	0.01507
Hs.3343	Mm.16898	PHGDH	Phgdh	phosphoglycerate dehydrogenase	0.63	1.60	0.00292	2.9E-09
Hs.154036	Mm.23697	PHLDA2	Phlda2/Tss	pleckstrin homology-like domain, family A, member 2)	0.86	1.22	0.0001	0.00168
Hs.93837	Mm.1860	PITPNM1	Pitpnm	Nir2; phosphatidylinositol transfer protein, membrane-associated 1	0.64	1.20	0.002	0.00017
Hs.198281	Mm.2635	PKM2	Pkm2	pyruvate kinase, muscle	1.45	0.80	4.4E-16	0.01296
Hs.93304	Mm.9277	PLA2G7	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhyd	0.89	1.16	1.9E-05	0.00015
Hs.77436	Mm.98232	PLEK	Plek	pleckstrin	0.92	1.46	5.1E-06	1.2E-05
Hs.418093	Mm.7999	PTGFRN	Ptgfrn	prostaglandin F2 receptor negative regulator	0.98	0.90	1.8E-06	0.01475
Hs.82643	Mm.38233	PTK9	Ptk9	PTK9 protein tyrosine kinase 9	0.80	1.19	9.7E-05	8.7E-05
Hs.258609	Mm.4715	PTPRO	Ptpro	protein tyrosine phosphatase, receptor type, O	0.57	1.27	0.01364	0.00182
Hs.8036	Mm.260157	RAB3D		RAB3D, member RAS oncogene family	0.91	1.53	8.5E-06	3.3E-08
Hs.241548	Mm.205142	RASA2	Rasa2	RAS p21 protein activator 2	0.63	1.00	0.00306	0.00241
Hs.87	Mm.2994	RBL1	Rbl1	retinoblastoma-like 1 (p107)	0.64	1.15	0.00343	0.00049
Hs.78944	Mm.28262	RGS2	Rgs2	regulator of G-protein signalling 2, 24kDa	1.11	0.80	1.2E-08	0.01522
Hs.425293	Mm.2424	RPL10A	Rpl10a	ribosomal protein L10a	0.93	0.84	1.3E-05	0.00887
Hs.406682	Mm.3229	RPL26	Rpl26	ribosomal protein L26	0.98	0.90	9E-07	0.00481
Hs.182825	Mm.16423	RPL35	Rpl35	ribosomal protein L35	1.04	0.97	1.3E-07	0.00207
Hs.433411	Mm.11376	RPL36	Rpl36	ribosomal protein L36	0.93	0.77	3.5E-06	0.01727
Hs.153	Mm.37835	RPL7	Rpl7	ribosomal protein L7	0.58	1.17	0.00575	0.00018
Hs.178551	Mm.30066	RPL8	Rpl8	ribosomal protein L8	0.73	1.08	0.00042	0.00047
Hs.298262	Mm.103634	RPS19	Rps19	ribosomal protein S19	1.22	0.78	1.4E-10	0.01589
Hs.180450	Mm.16775	RPS24	Rps24	ribosomal protein S24	1.03	0.77	1.8E-07	0.0177
Hs.380843	Mm.1139	RPS6	Rps6	ribosomal protein S6	1.09	0.71	2.5E-08	0.03014
Hs.301547	Mm.5281	RPS7	Rps7	ribosomal protein S7	0.95	0.74	2E-06	0.02157
Hs.2934	Mm.656	RRM1	Rrm1	ribonucleotide reductase M1 polypeptide	0.77	0.72	0.00017	0.02707
Hs.81256	Mm.3925	S100A4	S100a4	S100 calcium binding protein A4 (calcium protein, calvasculin, me	0.96	0.98	1.4E-06	0.0038
Hs.275243	Mm.100144	S100A6	S100a6	S100 calcium binding protein A6 (calcyclin)	1.20	1.20	1.8E-07	0.00012
Hs.145279	Mm.28805	SET	Set	SET translocation (myeloid leukemia-associated)	1.03	0.76	1.7E-07	0.01866
Hs.115232	Mm.262677	SF3A2	Sf3a2	splicing factor 3a, subunit 2, 66kDa	0.71	0.89	0.00066	0.00976
Hs.109051	Mm.22240	SH3BGRL3	Sh3bgrl3	SH3 domain binding glutamic acid-rich protein like 3	0.87	0.84	1.9E-05	0.00909
Hs.75367	Mm.7601	SLA	Sla	Src-like-adaptor	0.75	1.08	0.00025	0.00276
Hs.184601	Mm.27943	SLC7A5	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ syst	0.72	1.21	0.00063	0.00062
Hs.194693	Mm.142455	SLC7A7	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ syst	0.93	1.57	5E-06	7.3E-09
Hs.3068	Mm.3909	SMARCA3	Smarca3	SWI/SNF related, matrix associated, actin dependent regulator of	0.67	0.67	0.00157	0.04082
Hs.172280	Mm.1050	SMARCC1	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of	1.03	0.75	2E-07	0.02042
Hs.332848	Mm.27330	SMARCE1	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of	0.98	0.98	8.8E-07	0.00208
Hs.173255	Mm.243946	SNRPA	Snrpa	small nuclear ribonucleoprotein polypeptide A	0.96	0.92	3.5E-06	0.00378
Hs.82575	Mm.1323	SNRPB2	Snrpb2	small nuclear ribonucleoprotein polypeptide B"	1.00	0.75	4.8E-07	0.01985
Hs.105465	Mm.34095	SNRPF	Snrpf	small nuclear ribonucleoprotein polypeptide F	1.13	1.08	6.4E-09	0.00046

Hs.2316	Mm.46607	SOX9	Sox9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autc	0.58	1.52	0.00559	8E-08
Hs.22065	Mm.28189	SPEC1	Spec1-pen	small protein effector 1 of Cdc42	0.87	0.87	1.9E-05	0.00636
Hs.68061	Mm.20944	SPHK1	Sphk1	sphingosine kinase 1	1.30	1.04	5.5E-12	0.00086
Hs.157441	Mm.1302	SPI1	Sfpi1	spleen focus forming virus (SFFV) proviral integration oncogene s	0.70	1.02	0.00073	0.00244
Hs.199263	Mm.198414	STK39	Stk39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	0.65	1.14	0.00443	0.00607
Hs.166556	Mm.3019	TEAD2	Tead2	TEA domain family member 2	0.81	0.71	9.5E-05	0.04926
Hs.165986	Mm.88645	TES	Tes	testis derived transcript (3 LIM domains)	1.04	1.04	1.8E-07	0.00085
Hs.82961	Mm.4641	TFF3	Tff3	trefoil factor 3 (intestinal)	0.55	1.57	0.00844	7.8E-09
Hs.87409	Mm.4159	THBS1	Thbs1	thrombospondin 1	0.84	1.41	3.8E-05	6.8E-05
Hs.239489	Mm.2291	TIA1	Tia1	TIA1 cytotoxic granule-associated RNA binding protein	0.99	1.14	6.3E-07	0.00028
Hs.12956	Mm.186	TIP-1	1300011C2	Tax interaction protein 1	0.85	0.93	2.5E-05	0.00332
Hs.406660	Mm.124	TMPO	Tmpo	thymopoietin	0.80	0.76	0.00085	0.01885
Hs.115770	Mm.6426	TNFSF11	Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11	0.81	0.85	0.00012	0.03427
Hs.236510	Mm.790	TPARL	Tparl	TPA regulated locus	1.26	1.48	2.7E-11	1.4E-07
Hs.300772	Mm.646	TPM2	Tpm2	tropomyosin 2 (beta)	0.82	1.31	6.4E-05	9.1E-06
Hs.373508	Mm.3399	TRAF2	Traf2	TNF receptor-associated factor 2	0.67	0.78	0.00127	0.01526
Hs.151787	Mm.873	U5-116KD	Snrp116-pe	U5 snRNP-specific protein, 116 kD	0.91	0.74	6.2E-06	0.0215
Hs.93183	Mm.9684	VASP	Vasp	vasodilator-stimulated phosphoprotein	1.33	1.10	9.4E-13	0.00035
Hs.166068	Mm.4010	VIL1	Vil	villin 1	0.77	0.81	0.00016	0.02849
Hs.155191	Mm.4551	VIL2	Vil2	villin 2 (ezrin)	0.96	0.80	1.4E-06	0.01322
Hs.85100	Mm.2654	WDR1	Wdr1	WD repeat domain 1	0.85	1.29	2.7E-05	1.3E-05
Hs.136644	Mm.28489	WSB2	Wsb2-penc	WD repeat and SOCS box containing protein 2	0.76	1.20	0.00022	7.7E-05
Hs.349530	Mm.3308	YWHAH	Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activatio	1.12	0.88	8.4E-09	0.00564
Less Expressed in subclass A								
Hs.184168	Mm.18651	AASS	Aass	aminoadipate-semialdehyde synthase	-1.12	-1.31	1.3E-08	8.6E-06
Hs.21330	Mm.6404	ABCB1	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1	-1.06	-1.07	7.6E-08	0.00054
Hs.73812	Mm.14172	ABCB4	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	-1.23	-0.93	1.1E-10	0.0033
Hs.348900	Mm.18759	ACADS	Acads	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	-0.92	-1.03	4.2E-06	0.00101
Hs.81934	Mm.28430	ACADSB	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	-0.98	-1.28	9E-07	1.8E-05
Hs.82208	Mm.18630	ACADVL	Acadvl	acyl-Coenzyme A dehydrogenase, very long chain	-0.73	-1.15	0.00038	0.00018
Hs.154721	Mm.4927	ACO1	Aco1	aconitase 1, soluble	-1.02	-1.04	3.2E-07	0.00087
Hs.379991	Mm.8403	ACOX1	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	-1.21	-1.22	2.1E-10	5.3E-05
Hs.1219	Mm.25845	ADH4	Adh4	alcohol dehydrogenase 4 (class II), pi polypeptide	-1.09	-1.46	2.8E-08	2.3E-07
Hs.76392	Mm.4514	ALDH1A1	Aldh1a1	aldehyde dehydrogenase 1 family, member A1	-0.96	-1.05	1.7E-06	0.00079
Hs.195432	Mm.2621	ALDH2	Aldh2	aldehyde dehydrogenase 2 family (mitochondrial)	-1.27	-0.92	1.8E-11	0.00388
Hs.159608	Mm.4210	ALDH3A2	Aldh3a2	aldehyde dehydrogenase 3 family, member A2	-1.03	-0.97	1.6E-07	0.00215
Hs.74294	Mm.30250	ALDH7A1	Aldh7a1	aldehyde dehydrogenase 7 family, member A1	-1.24	-1.43	6.6E-11	5.1E-07
Hs.128749	Mm.2787	AMACR	Amacr	alpha-methylacyl-CoA racemase	-1.10	-1.18	1.9E-08	9.7E-05
Hs.332764	Mm.202665	ANG	Ang	angiogenin, ribonuclease, RNase A family, 5	-1.00	-0.69	4.1E-07	0.03371
Hs.283923	Mm.29738	APOA5	Apoa5	apolipoprotein A-V	-1.32	-1.39	1E-12	1.4E-06
Hs.110675	Mm.8239	APOC4	Apoc4	apolipoprotein C-IV	-1.40	-0.73	1.3E-14	0.02691
Hs.75249	Mm.29924	ARL6IP	Arl6ip	ADP-ribosylation factor-like 6 interacting protein	-1.04	-1.23	2.2E-07	4.7E-05
Hs.88251	Mm.620	ARSA	Arsa	arylsulfatase A	-0.99	-1.00	6E-07	0.00138
Hs.153489	Mm.234152	ASB1	Asb1	ankyrin repeat and SOCS box-containing 1	-0.81	-0.77	6.8E-05	0.03783
Hs.12056	Mm.6559	ASGR1	Asgr1	asialoglycoprotein receptor 1	-1.10	-0.91	1.9E-08	0.00407
Hs.71	Mm.30061	AZGP1	Azgp1	alpha-2-glycoprotein 1, zinc	-1.07	-0.84	4.4E-08	0.00848
Hs.159440	Mm.2859	BAAT	Baat	bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-cho	-1.42	-1.14	3.5E-15	0.0002
Hs.433307	Mm.25848	BCKDHA	Bckdha	branched chain keto acid dehydrogenase E1, alpha polypeptide (m	-0.59	-1.22	0.00429	5.4E-05
Hs.76893	Mm.29884	BDH	Bdh	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	-1.38	-1.14	4.4E-14	0.00021
Hs.150557	Mm.19788	BTEB1	Klf9	basic transcription element binding protein 1	-1.13	-1.31	5.9E-09	8.7E-06
Hs.2253	Mm.2081	C2	C2	complement component 2	-1.21	-0.72	2.1E-10	0.02733
Hs.1012	Mm.14087	C4BPA	C4bp	complement component 4 binding protein, alpha	-1.31	-0.75	2.6E-12	0.02048
Hs.155097	Mm.1186	CA2	Car2	carbonic anhydrase II	-0.61	-1.09	0.00312	0.0004
Hs.177446	Mm.116761	CA5A	Car5a	carbonic anhydrase VA, mitochondrial	-1.01	-1.60	3.6E-07	2.9E-09
Hs.395771	Mm.4215	CAT	Cat	catalase	-1.34	-1.16	5.2E-13	0.00015
Hs.5002	Mm.21414	CCS	Ccs	copper chaperone for superoxide dismutase	-0.95	-1.03	1.8E-06	0.00096
Hs.76171	Mm.34537	CEBPA	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	-0.61	-0.97	0.00314	0.002
Hs.118554	Mm.89572	CGI-83	Cgi-83-pen	lactamase, beta 2	-0.75	-1.01	0.00031	0.0012
Hs.211773	Mm.87594	CHES1	Ches1	checkpoint suppressor 1	-0.80	-1.29	9.1E-05	1.2E-05
Hs.107809	Mm.24376	CLSTN3	Clstn3	calsyntenin 3	-0.60	-1.17	0.00399	0.00018
Hs.24697	Mm.8396	CMAH	Cmah	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CM	-0.48	-1.46	0.02823	2.6E-07
Hs.274336	Mm.29499	CPT2	Cpt2	carnitine palmitoyltransferase II	-1.03	-1.22	1.7E-07	5.1E-05
Hs.155566	Mm.17493	CRADD	Cradd	CASP2 and RIPK1 domain containing adaptor with death domain	-0.86	-1.05	2.2E-05	0.00072
Hs.12068	Mm.20396	CRAT	Crat	carnitine acetyltransferase	-1.11	-0.87	1.3E-08	0.00674
Hs.75183	Mm.21758	CYP2E1	Cyp2e1	cytochrome P450, family 2, subfamily E, polypeptide 1	-0.80	-1.11	9.8E-05	0.00032
Hs.403436	Mm.291743	DCI	Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzy	-0.98	-1.46	9.1E-07	2.5E-07
Hs.9857	Mm.29180	DCXR	Dcxr	dicarbonyl/L-xylulose reductase	-1.40	-1.49	1.1E-14	1E-07
Hs.180015	Mm.5731	DDT	Ddt	D-dopachrome tautomerase	-0.76	-0.90	0.00023	0.00478
Hs.15898		DECR2		2,4-dienoyl CoA reductase 2, peroxisomal	-1.38	-1.38	3.8E-14	1.8E-06
Hs.251415	Mm.2774	DIO1	Dio1	deiodinase, iodothyronine, type I	-1.23	-1.10	1.2E-10	0.00035
Hs.88646	Mm.10287	DNASE1L3	Dnase1l3	deoxyribonuclease I-like 3	-0.46	-1.34	0.03119	8.3E-06
Hs.44926	Mm.1151	DPP4	Dpp4	dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing pr	-1.08	-1.13	3.8E-08	0.00022

Hs.10755	Mm.30994	DPYS	Dpys	dihydropyrimidinase	-1.32	-1.05	1.5E-12	0.00078
Hs.433278	Mm.22758	EBRP	Ebrp-pendi	emopamil binding related protein, delta8-delta7 sterol isomerase re	-0.75	-1.20	0.00024	7.1E-05
Hs.76394	Mm.24452	ECHS1	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	-1.06	-0.81	1.7E-07	0.01126
Hs.343911	Mm.4337	EI24	Ei24	etoposide induced 2.4 mRNA	-0.86	-0.96	2E-05	0.00236
Hs.80975	Mm.10211	ENTPD5	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	-1.25	-0.72	4.2E-11	0.0265
Hs.113	Mm.15295	EPHX2	Ephx2	epoxide hydrolase 2, cytoplasmic	-1.17	-1.64	1.3E-09	4E-10
Hs.1321	Mm.42224	F12	F12	coagulation factor XII (Hageman factor)	-1.44	-0.85	1.3E-15	0.00766
Hs.68601	Mm.30105	F13B	F13b	coagulation factor XIII, B polypeptide	-1.46	-1.33	1.9E-16	6.6E-06
Hs.73875	Mm.3798	FAH	Fah	fumarylacetoacetate hydrolase (fumarylacetoacetase)	-1.36	-1.09	1.8E-13	0.0004
Hs.160318	Mm.1491	FXYD1	Fxyd1	FXYD domain containing ion transport regulator 1 (phospholemma	-0.63	-1.28	0.00224	1.7E-05
Hs.432132	Mm.3283	G0S2	G0s2	putative lymphocyte G0/G1 switch gene	-0.54	-1.30	0.00982	1.2E-05
Hs.242	Mm.18064	G6PC	G6pc	glucose-6-phosphatase, catalytic (glycogen storage disease type I,	-1.09	-1.58	2.2E-08	6.2E-09
Hs.75641	Mm.2420	GALT	Galt	galactose-1-phosphate uridylyltransferase	-1.09	-1.47	2.4E-08	1.7E-07
Hs.184141	Mm.2475	GCDH	Gcdh	glutaryl-Coenzyme A dehydrogenase	-1.02	-1.21	2.5E-07	6.2E-05
Hs.208	Mm.22329	GCGR	Gcgr	glucagon receptor	-0.87	-1.03	1.9E-05	0.00098
Hs.78619	Mm.20461	GGH	Ggh	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hy	-0.91	-0.86	7.6E-06	0.00712
Hs.333303	Mm.21198	GJB1	Gjb1	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-T	-1.26	-1.16	2.3E-11	0.00014
Hs.170171	Mm.2338	GLUL	Glul	glutamate-ammonia ligase (glutamine synthase)	-0.76	-0.66	0.00021	0.04256
Hs.5920	Mm.30193	GNE	Uae1	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kin	-1.36	-0.94	1.3E-13	0.00293
Hs.144914	Mm.29395	GNMT	Gnmt	glycine N-methyltransferase	-1.11	-1.17	1.4E-08	0.00012
Hs.170197	Mm.18916	GOT2	Got2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate ami	-1.10	-1.21	1.8E-08	6.2E-05
Hs.13405	Mm.40282	GPHN	Gphn	gephyrin	-0.97	-1.51	1.1E-06	6.3E-08
Hs.108118	Mm.34901	GRTP1	Grtp1	growth hormone regulated TBC protein 1	-0.91	-1.27	1E-05	1.9E-05
Hs.378199	Mm.197422	GSTA2	Gsta2	glutathione S-transferase A2	-1.08	-0.67	3.5E-08	0.04135
Hs.26403	Mm.29652	GSTZ1	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	-0.71	-1.26	0.00061	2.6E-05
Hs.102910	Mm.10182	GTF2H4	Gtf2h4	general transcription factor IIH, polypeptide 4, 52kDa	-0.95	-0.90	2.3E-06	0.00483
Hs.82614	Mm.25781	GYS2	Gys2	glycogen synthase 2 (liver)	-0.83	-1.04	4.2E-05	0.0008
Hs.171280	Mm.6994	HADH2	Hadh2	hydroxyacyl-Coenzyme A dehydrogenase, type II	-1.07	-1.05	4.7E-08	0.00072
Hs.8110	Mm.2491	HADHSC	Hadhsc	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-1.04	-0.90	1.5E-07	0.00472
Hs.1802	Mm.29188	HLA-DOB	H2-Ob	major histocompatibility complex, class II, DO beta	-0.83	-1.42	4.7E-05	1.3E-06
Hs.93564	Mm.228	HOMER2	Homer2	homer homolog 2 (Drosophila)	-1.16	-0.89	1.7E-09	0.00549
Hs.2899	Mm.6584	HPD	Hpd	4-hydroxyphenylpyruvate dioxygenase	-1.22	-1.53	1.8E-10	2.6E-08
Hs.75441	Mm.2108	HSD17B4	Ttr	hydroxysteroid (17-beta) dehydrogenase 4	-1.33	-0.96	9.1E-13	0.00228
Hs.187579	Mm.12882	HSD17B7	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	-0.79	-0.91	0.0001	0.00437
Hs.825	Mm.140811	HSD3B2	Hsd3b1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-is	-0.47	-1.56	0.02586	9.7E-09
Hs.75253	Mm.14825	IDH3G	Idh3g	isocitrate dehydrogenase 3 (NAD+) gamma	-0.92	-1.10	5.2E-06	0.00034
Hs.89560	Mm.3054	IDUA	Idua	iduronidase, alpha-L-	-0.88	-1.43	2E-05	6.2E-07
Hs.20315	Mm.6718	IFIT1	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	-0.83	-0.66	4.3E-05	0.04832
Hs.839	Mm.3135	IGFALS	Igfals	insulin-like growth factor binding protein, acid labile subunit	-0.61	-1.51	0.00488	6.3E-08
Hs.374664	Mm.2594	INHBC	Inhbc	inhibin, beta C	-1.21	-1.46	2.6E-10	2.3E-07
Hs.374536	Mm.29877	IVD	Ubap1	isovaleryl Coenzyme A dehydrogenase	-1.13	-0.91	7.9E-09	0.00424
Hs.12337	Mm.285	KDR	Kdr	kinase insert domain receptor (a type III receptor tyrosine kinase)	-0.78	-0.82	0.00014	0.01107
Hs.81454	Mm.22451	KHK	Khk	ketohexokinase (fructokinase)	-1.24	-0.95	5.3E-11	0.00274
Hs.272215	Mm.41389	KLF15	Klf15	Kruppel-like factor 15	-0.92	-1.50	6.9E-06	7.2E-08
Hs.348401	Mm.1593	LCAT	Lcat	lecithin-cholesterol acyltransferase	-0.84	-1.15	3.8E-05	0.00017
Hs.167877	Mm.16973	LECT2	Lect2	leukocyte cell-derived chemotaxin 2	-0.98	-0.67	1.8E-06	0.03995
Hs.9994	Mm.362	LIPC	Lipc	lipase, hepatic	-0.59	-1.71	0.00472	2E-11
Hs.446467	Mm.7221	LRP1	Lrp1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin rec	-0.84	-1.32	4E-05	1.5E-05
Hs.153863	Mm.27935	MADH6	Madh6	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	-1.18	-0.80	9.2E-10	0.01783
Hs.119983	Mm.260161	MASP2	Masp2	mannan-binding lectin serine protease 2	-1.46	-0.96	3.6E-16	0.0024
Hs.2314	Mm.281805	MBL2	Mbl1	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	-0.81	-0.82	6.7E-05	0.01079
Hs.417710	Mm.34532	MGC15416		hypothetical protein MGC15416	-0.64	-1.25	0.00239	2.9E-05
Hs.172665	Mm.29584	MTHFD1	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), m	-1.13	-0.82	5.8E-09	0.01025
Hs.195799	Mm.2941	MTP	Mttp	microsomal triglyceride transfer protein (large polypeptide, 88kDa)	-1.00	-0.83	2.2E-05	0.00941
Hs.155212	Mm.4299	MUT	Mut	methylmalonyl Coenzyme A mutase	-1.37	-1.38	6.2E-14	1.9E-06
Hs.243960	Mm.26722	NDRG2	Ndr2	NDRG family member 2	-1.15	-1.37	3.2E-09	2.7E-06
Hs.20894	Mm.181862	NDST1	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-0.87	-0.93	1.9E-05	0.00323
Hs.1565	Mm.16553	NEDD4	Nedd4	neural precursor cell expressed, developmentally down-regulated 4	-0.81	-0.75	6.5E-05	0.02094
Hs.33287	Mm.260021	NFIB		nuclear factor I/B	-0.83	-1.29	4.1E-05	1.4E-05
Hs.35841	Mm.9394	NFIX	Nfix	nuclear factor I/X (CCAAT-binding transcription factor)	-0.64	-1.54	0.00223	2.1E-08
Hs.146406	Mm.12915	NIT1	Nit1	nitrilase 1	-1.32	-0.95	1.6E-12	0.0028
Hs.347353	Mm.22690	NR1H3	Nr1h3	nuclear receptor subfamily 1, group H, member 3	-1.28	-0.93	1.1E-11	0.00389
Hs.75485	Mm.13694	OAT	Oat	ornithine aminotransferase (gyrate atrophy)	-0.81	-1.02	7.7E-05	0.00111
Hs.117050	Mm.2611	OTC	Otc	ornithine carbamoyltransferase	-1.52	-0.71	1.7E-13	0.02916
Hs.1870	Mm.2422	PAH	Pah	phenylalanine hydroxylase	-1.37	-0.90	8E-14	0.00459
Hs.1872	Mm.42246	PCK1	Pck1	phosphoenolpyruvate carboxykinase 1 (soluble)	-1.12	-1.12	1E-08	0.0003
Hs.285218	Mm.5062	PCTP	Pctp	phosphatidylcholine transfer protein	-1.10	-0.67	1.5E-08	0.04124
Hs.92261	Mm.29768	PDK2	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	-1.31	-0.81	3.1E-09	0.01215
Hs.12592	Mm.10723	PER3	Per3	period homolog 3 (Drosophila)	-0.83	-0.79	4.4E-05	0.01445
Hs.31034	Mm.20615	PEX11A	Pex11a	peroxisomal biogenesis factor 11A	-0.91	-1.39	1.4E-05	1.4E-06
Hs.90061	Mm.9052	PGRMC1	Pgrmc1	progesterone receptor membrane component 1	-1.17	-0.95	1.1E-09	0.00263
Hs.172887	Mm.27066	PHYH	Phyh	phytanoyl-CoA hydroxylase (Refsum disease)	-1.04	-1.42	1.2E-07	7.5E-07
Hs.271167	Mm.8543	PIPOX	Pso	pipecolic acid oxidase	-1.43	-1.27	2.5E-15	2.1E-05

Hs.1898	Mm.30107	PON1	Pon1	paraoxonase 1	-1.14	-1.18	3.4E-09	9.6E-05
Hs.167246	Mm.3863	POR	Por	P450 (cytochrome) oxidoreductase	-1.24	-1.28	5.8E-11	1.6E-05
Hs.198468	Mm.10707	PPARGC1	Ppargc1	peroxisome proliferative activated receptor, gamma, coactivator 1	-1.13	-1.43	1.2E-08	5.9E-07
Hs.120	Mm.6587	PRDX6	Prdx6	peroxiredoxin 6	-1.18	-0.98	8.7E-10	0.0023
Hs.2351	Mm.2786	PROC	Proc	protein C (inactivator of coagulation factors Va and VIIIa)	-0.94	-0.88	2.6E-06	0.00551
Hs.123641	Mm.37213	PTPRB	Ptprb	protein tyrosine phosphatase, receptor type, B	-0.88	-1.02	3E-05	0.00112
Hs.168670	Mm.144235	PXF	Pxf	peroxisomal farnesylated protein	-1.14	-1.17	5.2E-09	0.00013
Hs.430299	Mm.21853	PXMP2	Pxmp2	peroxisomal membrane protein 2, 22kDa	-0.77	-0.86	0.00017	0.00698
Hs.3210	Mm.220955	REN	Ren1	renin	-0.71	-1.20	0.00055	0.0001
Hs.77854	Mm.2118	RGN	Rgn	regucalcin (senescence marker protein-30)	-1.45	-0.90	3.9E-16	0.00468
Hs.20084	Mm.3470	RXRA	Rxra	retinoid X receptor, alpha	-1.21	-1.13	2.7E-10	0.00022
Hs.75760	Mm.1779	SCP2	Scp2	sterol carrier protein 2	-0.95	-1.42	0.00023	6.6E-07
Hs.334841	Mm.196558	SELENBP1	Selenbp1	selenium binding protein 1	-1.42	-0.82	5.3E-15	0.01051
Hs.166975	Mm.43331	SFRS5	Sfrs5	splicing factor, arginine/serine-rich 5	-0.84	-0.90	8.6E-05	0.00462
Hs.8889	Mm.3379	SHMT1	Shmt1	serine hydroxymethyltransferase 1 (soluble)	-0.91	-0.87	2.1E-05	0.0067
Hs.75317	Mm.5045	SLC16A2	Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), membe	-1.11	-1.29	1.3E-08	1.4E-05
Hs.380	Mm.2861	SLC1A2	Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), mei	-0.65	-0.93	0.00754	0.0032
Hs.117367	Mm.594	SLC22A1	Slc22a1	solute carrier family 22 (organic cation transporter), member 1	-1.00	-0.96	4.2E-07	0.00329
Hs.50868	Mm.15093	SLC22A1L	Slc22a1l	solute carrier family 22 (organic cation transporter), member 1-like	-1.20	-1.00	4.3E-10	0.00141
Hs.77239	Mm.42185	SLC22A4	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	-0.87	-1.22	7.6E-05	0.0002
Hs.11729	Mm.6611	SLC27A2	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	-1.27	-1.02	1.7E-11	0.00145
Hs.305971	Mm.34147	SLC2A10	Slc2a10	solute carrier family 2 (facilitated glucose transporter), member 10	-0.66	-1.34	0.00182	5E-06
Hs.167584	Mm.18443	SLC2A2	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	-1.35	-1.02	2.1E-13	0.00111
Hs.197366	Mm.29279	SMO	Smo	smoothened homolog (Drosophila)	-0.46	-1.42	0.03361	9.4E-07
Hs.108924	Mm.29030	SORBS1	Sorbs1	sorbin and SH3 domain containing 1	-0.64	-1.32	0.00213	7.3E-06
Hs.118725	Mm.20294	SPS2	Sps2	selenophosphate synthetase 2	-0.77	-1.27	0.00016	1.9E-05
Hs.94952	Mm.112	TCEA3	Tcea3	transcription elongation factor A (SII), 3	-0.88	-1.36	1.4E-05	3E-06
Hs.183671	Mm.21545	TDO2	Tdo2	tryptophan 2,3-dioxygenase	-0.90	-1.23	8.2E-06	4.6E-05
Hs.351863	Mm.15312	TST	Tst	thiosulfate sulfurtransferase (rhodanese)	-1.08	-1.02	3.4E-08	0.00118
Hs.427202	Mm.2108	TTR	Ttr	transthyretin (prealbumin, amyloidosis type I)	-1.09	-1.11	2.5E-06	0.00032
Hs.285681	Mm.34213	WBSCR14	Wbscr14	Williams Beuren syndrome chromosome region 14	-1.41	-1.34	6.1E-15	4.6E-06
Hs.108219	Mm.22182	WNT11	Wnt11	wingless-type MMTV integration site family, member 11	-1.12	-1.24	2.9E-08	5.5E-05
Hs.159456	Mm.38250	ZNF288	Zfp288	zinc finger protein 288	-1.07	-1.42	4.9E-08	7.5E-07