Symbol	**Accession number**	Name	**Difference**	**p-value**	**Frequency**
ABCB7	NM_004299.3	ATP-binding cassette, sub-family B (MDR/TAP), member 7	0.327	0.0043	96.1
ACCS	NM_004299	1-aminocyclopropane-1-carboxylate synthase homologue	-0.159	0.0053	81
ACE	NM_000789.2	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	-0.137	0.0046	92.2
ACOT9	NM_012332.1	acyl-CoA thioesterase 9	0.348	0.0045	92.1
ACTR3	NM_005721.3	ARP3 actin-related protein 3 homolog (yeast)	0.303	0.0050	73.9
AGA	NM_000027.2	Aspartylglucosaminidase	0.285	0.0053	76.8
AHI1	NM_017651.3	Abelson helper integration site 1	0.383	0.0045	73.9
ALDH3A2	NM_000382.1	Aldehyde dehydrogenase 3 family, member A2	0.268	0.0050	100
AMAC1L1	NM_054028	acyl-malonyl condensing enzyme 1-like 1	-0.326	0.0034	82.7
ANKRD13A	NM_033121.1	Ankyrin repeat domain 13A	0.416	0.0046	88.8
ARIH1	NM_005744.2	Ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1	0.436	0.0048	100
ATP6V0B	NM_004047.2	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	0.337	0.0046	92.2
ATP6V1B2	NM_001693.2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	0.142	0.0053	73.4
BCR	BC066122.1	Breakpoint cluster region	-0.092	0.0042	80.6
BNIP3	NM_004052.2	BCL2/adenovirus E1B 19kDa interacting protein 3	0.746	0.0042	100
BRCTD1	XM_376413.2	BRCT domain containing 1	-0.135	0.0049	76.9
C14orf109	XM_058628.8	Chromosome 14 open reading frame 109	0.503	0.0070	75.8
C20orf85	NM_178456.2	Chromosome 20 open reading frame 85	-0.281	0.0034	100
C5orf42	NM_018691.1	Chromosome 5 open reading frame 42	-0.232	0.0048	74.2
C6orf62	NM_030939.3	Chromosome 6 open reading frame 62	0.273	0.0045	100
CCDC120	AK001937.1	cDNA FLJ11075 fis	0.132	0.0055	80.9
CCDC33	BC009178.2	Coiled-coil domain containing 33	0.163	0.0044	80.9
CEP55	BC008947.2	Centrosomal protein 55kDa	0.758	0.0030	100
CHCHD3	NM_017812.1	Coiled-coil-helix-coiled-coil-helix domain containing 3	0.269	0.0034	96.1
CKAP2	NM_018204.2	Cytoskeleton associated protein 2	0.532	0.0047	77.2
CLEC1A	NM_016511.2	C-type lectin domain family 1, member A	-0.239	0.0046	95.9
CLPX	NM_006660.3	ClpX caseinolytic peptidase X homolog (E. coli)	0.476	0.0038	84.6
CNOT7	NM_013354.4	CCR4-NOT transcription complex, subunit 7	0.103	0.0055	77.1
CRY2	NM_021117.1	Cryptochrome 2 (photolyase-like)	-0.433	0.0044	96.1
CRYAA	X14789.1	Crystallin, alpha A	-0.210	0.0043	100
CSDA	NM_003651.3	Cold shock domain protein A	-0.204	0.0049	78.4
CTNNB1	NM_001904.2	Catenin (cadherin-associated protein), beta 1, 88kDa	0.387	0.0046	76.8
CTTNBP2NL	NM_018704.1	CTTNBP2 N-terminal like	-0.095	0.0045	96.1
CYB5R2	AL133582.1	Cytochrome b5 reductase 2	-0.173	0.0052	84.8
DDX10	NM_004398.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	0.463	0.0042	88.8

DIAPH1	NM_005219.2	Diaphanous homolog 1 (Drosophila)	0.370	0.0048	96.1
DNAJA1	NM_001539.2	DnaJ (Hsp40) homolog, subfamily A, member 1	0.254	0.0053	92.6
DNAJC3	NM_006260.2	DnaJ (Hsp40) homolog, subfamily C, member 3	0.141	0.0056	92.6
DTX2	AB040961.1	Deltex homolog 2 (Drosophila)	-0.099	0.0046	88.2
EFG1	AK022724.1	EFG1 Elongation Factor G, Mitochondrial 1	0.299	0.0046	100
EIF4E	NM_001968.2	Eukaryotic translation initiation factor 4E	0.377	0.0051	92.1
EMX2	NM_004098.2	Empty spiracles homeobox 2	-0.255	0.0049	100
EPB41	NM_004437.2	Erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	-0.274	0.0036	76.8
ERI1	NM_153332.2	exoribonuclease 1	0.137	0.0044	88.6
FAIM	NM_018147.2	Fas apoptotic inhibitory molecule 3	0.428	0.0048	100
FAM40B	NM_020704.1	Family with sequence similarity 40, member B	-0.362	0.0048	88.4
FAM46C	NM_017709.2	Family with sequence similarity 46, member C	-0.075	0.0055	73.5
FAM65A	NM_024519.2	Family with sequence similarity 65, member A	-0.244	0.0046	84.9
GABBR2	NM_005458	gamma aminobutyric acid (GABA) B receptor 2	-0.171	0.0051	77.6
GLTP	NM.016433.3	glycolipid transfert protein	-0.110	0.0038	80.9
GNAS	AJ224868.1	GNAS1 gene	-0.138	0.0038	88.2
GNG12	NM_018841.3	Guanine nucleotide binding protein (G protein), gamma 12	0.163	0.0050	77.1
GSTM5	NM_000851.2	Glutathione S-transferase mu 5	0.030	0.0057	73.9
HGF	X16323.1	hepatocyte growth factor (hepapoietin A; scatter factor)	-0.306	0.0051	80.8
HOXB5	NM_002147.2	Homeobox B5	0.147	0.0043	92.6
HPCA	NM_002143.2	Hippocalcin	-0.326	0.0051	73.5
IGDCC4	NM_020962	immunoglobulin superfamily DCC subclass member 4	-0.120	0.0050	81
IKBKE	NM_014002.2	Inhibitor of kappa light polypeptide gene enhancer, kinase epsilon	-0.064	0.0055	100
IL16	NM_004513.3	Interleukin 16 (lymphocyte chemoattractant factor)	-0.079	0.0055	81.1
ITGA11	NM_012211.3	Integrin alpha 11	-0.247	0.0051	84.6
KCTD17	BC009961.2	potassium channel tetramerization domain containing 17	-0.143	0.0052	84.8
KIAA1704	NM_018559.2	KIAA1704	0.316	0.0044	84.6
LRRC37A	NM_014834.2	Leucine rich repeat containing 37A	-0.228	0.0047	81.1
LRRFIP2	NM_017724.1	Leucine rich repeat (in FLII) interacting protein 2	0.043	0.0055	100
MAGED4	AL136582.1	Melanoma antigen family D, 4	0.333	0.0037	100
MLLT6	BC007859.2	Myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6	-0.206	0.0029	81.1
MRPS18C	NM_016067.1	Mitochondrial ribosomal protein S18C	0.468	0.0042	88.8
MRS2L	NM_020662.1	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	0.571	0.0048	77.2
MTCH2	NM_014342.2	Mitochondrial carrier homolog 2 (C. elegans)	0.241	0.0050	88.6
MTHFD2	NM_006636.2	Mitochondrial carrier homolog 2 (C. elegans)	0.500	0.0047	92.1
MYCN	AJ242956.1	myc myelocytomatosis viral related oncogene	-0.148	0.0047	100
MYL12B	NM_033546	myosin liht chain 12B regultory	0.252	0.0040	74.5

N4BP2	NM_018177.2	NEDD4 binding protein 2	-0.293	0.0046	92.2
NDUFAF2	NM_174889.2	NADH dehydrogenase 1 alpha subcomplex, assembly factor 2	0.342	0.0052	84.6
NOX1	NM_007052.3	NADPH oxidase 1	-0.297	0.0049	84.4
NRBP1	NM_013392.2	nuclear receptor binding protein 1	-0.180	0.0044	100
OCIAD1	NM_017830.1	ovarian cancer immuno-reactive antigen domain containing 1	0.378	0.0045	100
OCRL	NM_013341.3	Inositol polyphosphate 5-phosphatase OCRL-1	-0.218	0.0043	91
OLA1	NM_013341	Obg-like ATPase 1	0.577	0.0041	81
ORAI2	NM_032831	ORAI calcium release-activated calcium modulator 2	0.307	0.0053	86.2
OTOP2	NM_178160.1	otopetrin 2	-0.187	0.0046	84.8
PAPOLA	NM_032632.3	Poly(A) polymerase alpha	0.573	0.0036	76.6
PARP4	NM_006437.2	Poly (ADP-ribose) polymerase family, member 4	0.011	0.0059	73.5
PBOV1	NM_021635.1	Prostate and breast cancer overexpressed 1	-0.272	0.0045	73.4
PCNXL2	NM_014801.2	Pecanex-like 2 (Drosophila)	-0.430	0.0042	96.1
PCTK3	BC040529.1	PCTAIRE protein kinase 3	-0.257	0.0043	92.6
PHF10	NM_018288.2	PHD finger protein 10	0.264	0.0044	96.1
PHKB	NM_000293.1	Phosphorylase kinase, beta	-0.277	0.0050	73.9
PIGL	NM_004278.2	phosphatidylinositol glycan anchor biosynthesis. class L	-0.340	0.0049	81.1
PIK4CB	NM_002651.1	Phosphatidylinositol 4-kinase, catalytic, beta	-0.340	0.0049	100
PLAC2	BC036545.1	Placenta-specific 2 (non-protein coding)	-0.095	0.0054	71.5
PNPT1	NM_033109.2	polyribonucleotide nucleotidyltransferase 1	0.449	0.0044	88.5
PODNL1	NM_024825.2	Podocan-like 1	0.154	0.0050	92.2
POLR2B	NM_000938.1	Polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	0.239	0.0040	76.8
PPAT	NM_002703.3	Phosphoribosyl pyrophosphate amidotransferase	0.337	0.0046	80
PPIL3	BC007693.2	Peptidylprolyl isomerase (cyclophilin)-like 3	0.298	0.0048	88.2
PPM1J	NM_005167.5	Protein phosphatase, Mg2+/Mn2+ dependent, 1J	-0.025	0.0056	80.8
PSAP	NM_002778.1	Prosaposin	-0.236	0.0051	75.2
PSMD14	NM_005805.2	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0.409	0.0049	92.1
PSMD2	NM_002808.3	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	0.306	0.0050	100
RBM38	NM_017495.4	RNA binding motif protein 38	-0.298	0.0045	79
RBPJ	BC020780.1	recombination signal binding protein immunoglobulin kappa J region	-0.449	0.0047	92.2
RLIM	NM_016120.2	Ring finger protein, LIM domain interacting	0.412	0.0035	82.7
SALL2	NM_005407.1	Sal-like 2 (Drosophila)	-0.040	0.0056	75
SDC4	NM_002999.2	Syndecan 4	-0.009	0.0058	86.8
SEC24B	NM_006323.1	SEC24 family, member B (S. cerevisiae)	0.295	0.0047	70.8
SEPTIN	AY679521.1	Septin 6	-0.304	0.0047	80.9
SERPINB6	NM_004568.4	Serpin peptidase inhibitor, clade B (ovalbumin), member 6	0.202	0.0055	74.1
SERPINB8	NM_002640.3	Serpin peptidase inhibitor, clade B (ovalbumin), member 8	0.219	0.0054	77.1

SLC38A2	NM_018976.3	Solute carrier family 38, member 2	0.322	0.0048	84.4
SMARCD3	NM_003078.3	SWI/SNF related,matrix associated, regulator of chromatin, member d3	-0.354	0.0045	72.7
SNX25	NM_031953.2	Sorting nexin 25	0.379	0.0041	84.8
SOLH	NM_005632.2	Small optic lobes homolog (Drosophila)	-0.303	0.0040	70.2
SP100	NM_003113.2	SP100 nuclear antigen	0.326	0.0037	82.9
SP4	NM_003112	Sp4 transcription factor	-0.220	0.0049	100
SS18L2	NM_016305.1	Synovial sarcoma translocation gene on chromosome 18-like 2	0.410	0.0045	75
STX5	NM_003164.2	Syntaxin 5	-0.359	0.0047	84.8
SUPT5H	NM_003169.2	Suppressor of Ty 5 homolog (S. cerevisiae)	-0.356	0.0030	92.6
TAOK3	NM_016281.2	TAO kinase 3	-0.422	0.0048	80.8
TM9SF2	NM_004800.1	Transmembrane 9 superfamily member 2	0.142	0.0052	86.8
TMED7	NM_181836.3	Toll-like receptor adaptor molecule 2	-0.031	0.0055	72.9
TMEM33	NM_018126.1	Transmembrane protein 33	0.423	0.0046	100
TRAPPC3	NM_014408.3	Trafficking protein particle complex 3	0.175	0.0058	78.4
UBE2V2	NM_003350.2	Ubiquitin-conjugating enzyme E2 variant 2	0.554	0.0037	81.4
UCHL3	NM_006002.3	Ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	0.530	0.0035	77.4
UNC5C	NM_003728.2	Unc-5 homolog C (C. elegans)	0.410	0.0044	96.1
USP33	BC016663.1	Ubiquitin specific peptidase 33	0.228	0.0052	92.2
UTF1	NM_003577.1	Undifferentiated embryonic cell transcription factor 1	-0.062	0.0047	77.2
VPS41	NM_014396.2	Vacuolar protein sorting 41 homolog (S. cerevisiae)	-0.173	0.0052	82.9
VPS45A	NM_007259.2	Vacuolar protein sorting 45 homolog (S. cerevisiae)	-0.114	0.0051	74.6
WDR48	NM_020839.2	WD repeat domain 48	0.180	0.0048	100
WRNIP1	NM_020135.2	Werner helicase interacting protein 1	0.350	0.0048	77.6
ZNF26	NM_019591.2	Zinc finger protein 26	0.350	0.0050	76.3
ZNF3	NM_032924.2	Zinc finger protein 3	-0.276	0.0047	71
ZNF574	NM_022752.3	Zinc finger protein 574	-0.113	0.0053	78.2
ABI1	NM_005470.1	Abl-interactor 1	-0.074	0.0046	66.3
ACAT1	NM_000019.2	Acetyl-Coenzyme A acetyltransferase 1	0.264	0.0050	59
ADC	NM_052998.2	Arginine decarboxylase	-0.177	0.0052	32.9
ADCY6	NM_020983.2	Adenylate cyclase 6	0.533	0.0037	40.2
ADORA1	NM_000674.1	Adenosine A1 receptor	-0.257	0.0031	44.2
AGT	S78530.1	angiotensinogen	-0.285	0.0040	62.5
AGTRAP	NM_020350.3	Angiotensin II receptor-associated protein	0.150	0.0046	44.1
ALB	S69192.1	albumin	-0.238	0.0048	59.2
ALG10	NM_032834.2	Asparagine-linked glycosylation 10	0.391	0.0046	32.9
AMH	NM_000479.2	Anti-Mullerian hormone	-0.042	0.0044	44.1

AMHR2	NM_020547.1	Anti-Mullerian hormone receptor, type II	-0.049	0.0051	51.4
ASPM	NM_018136.2	Asp (abnormal spindle) homolog, microcephaly associated	0.299	0.0052	63
ATG2A	NM_015104.1	autophagy related 2 homolog A	-0.209	0.0059	48.3
ATP2B4	NM_001001396.1	ATPase, Ca++ transporting, plasma membrane 4	-0.131	0.0055	51.5
ATP8B2	NM_020452.2	ATPase, class I, type 8B, member 2	0.078	0.0053	32.9
AVEN	NM_020371.2	Apoptosis, caspase activation inhibitor	0.075	0.0051	32.6
B4GALT2	NM_003780.3	betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	-0.038	0.0051	36.4
BCAS2	NM_005872.2	Breast carcinoma amplified sequence 2	0.325	0.0051	40.2
BCCIP	NM_016567.2	BRCA2 and CDKN1A interacting protein	0.259	0.0052	55
BCHE	NM_000055.1	Butyrylcholinesterase	-0.022	0.0058	58.3
BCL2L2	NM_004050.2	BCL2-like 2	0.115	0.0052	51.4
BCL7B	BC000956.2	B-cell CLL/lymphoma 7B	-0.272	0.0037	67.8
BLVRB	NM_000713.1	Biliverdin reductase B (flavin reductase (NADPH))	0.337	0.0047	54.8
C12orf22	NM_030809.1	chromosome 12 open reading frame 22	0.460	0.0076	66.7
C13orf1	NM_020456.1	Chromosome 13 open reading frame 1	0.306	0.0032	48
C14orf10	NM_017917.2	Chromosome 14 open reading frame 10	0.467	0.0044	54.8
C14orf138	NM_024558.1	Chromosome 14 open reading frame 138	-0.079	0.0065	44.4
C14orf166	NM_016039.1	Chromosome 14 open reading frame 166	0.437	0.0039	48
C19orf6	AK090400.1	Chromosome 19 open reading frame 6	-0.046	0.0054	44.1
C1orf21	NM_030806.3	Chromosome 1 open reading frame 21	-0.233	0.0052	48.1
C20orf111	NM_016470.6	Chromosome 20 open reading frame 111	0.167	0.0066	32.2
C20orf23	AB046810.2	Chromosome 20 open reading frame231	0.447	0.0045	48.5
C20orf26	NM_015585.2	Chromosome 20 open reading frame 26	-0.207	0.0053	32.6
C2orf47	NM_015955.2	Chromosome 2 open reading frame 47	0.275	0.0046	36.8
C3orf26	NM_032359.2	Chromosome 3 open reading frame 26	0.399	0.0049	40.6
C6orf139	NM_018132.3	Chromosome 6 open reading frame 139	0.063	0.0045	36.8
C8orf17	NM_020237.1	Chromosome 8 open reading frame 17	0.042	0.0054	40.4
C9orf127	NM_016446.2	Chromosome 9 open reading frame 127	0.254	0.0070	36.1
C9orf156	NM_016481.2	Chromosome 9 open reading frame 156	0.033	0.0049	54.8
C9orf32	NM_014064.2	Chromosome 9 open reading frame 12	-0.028	0.0053	51.8
CA4	NM_000717.2	Carbonic anhydrase IV	-0.136	0.0068	36.8
CACNA1A	NM_023035.1	calcium channel, voltage-dependent, P/Q type, alpha 1A	0.194	0.0046	62.5
CAMSAP1L1	NM_203459.1	Calmodulin regulated spectrin-associated protein 1-like 1	-0.049	0.0036	47.8
CART	NM_004291.2	CART prepropeptide	-0.136	0.0042	44.1
CASZ1	AK022285.1	Castor zinc finger 1	0.030	0.0035	69.8
CCDC104	NM_080667.3	Coiled-coil domain containing 104	-0.302	0.0060	58.7
CCDC82	AK027171.1	Coiled-coil domain containing 82	0.008	0.0055	36.4

CCNC	NM_005190.2	Cyclin C	0.841	0.0034	52
CD209	NM_021155.2	CD209 molecule	0.186	0.0045	54.8
CDADC1	NM_030911.1	Cytidine and dCMP deaminase domain containing 1	0.351	0.0053	33.1
CDC25C	BC019089.2	Cell division cycle 25 homolog C (S. pombe)	0.453	0.0044	62.7
CDC42	BC003682.1	Cell division cycle 42 (GTP binding protein, 25kDa)	0.147	0.0049	36.8
CDC42BPA	NM_014826.3	CDC42 binding protein kinase alpha (DMPK-like)	-0.222	0.0043	59
Cep290	NM_025114.2	Centrosomal protein 290kDa	0.106	0.0053	43.8
CHD6	NM_032221	Chromodomain helicase DNA binding protein 6	-0.263	0.0052	59
CHMP4C	NM_152284.3	Chromatin modifying protein 4C	0.040	0.0038	32.4
CLIC1	NM_001288.4	Chloride intracellular channel 1	0.202	0.0044	40.4
COL4A6	D63562.2	gene for a6(IV) collagen	-0.264	0.0046	66.5
CPNE6	NM_006032.2	Copine VI (neuronal)	-0.087	0.0058	58.8
CTDSP2	NM_005730.2	RNA polymerase II, polypeptide A small phosphatase 2	-0.286	0.0050	40.2
CTNNBIP1	NM_020248.1	Catenin, beta interacting protein 1	-0.170	0.0054	44.4
DBI	NM_020548.4	Diazepam binding inhibitor	0.220	0.0057	48.3
DCHS1	NM_003737.1	Dachsous 1 (Drosophila)	-0.055	0.0054	36.6
DDX18	NM_006773.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	0.238	0.0047	44.5
DKFZP761H	NM_031297.2	hypothetical protein DKFZp761H1710	0.009	0.0070	40.6
DLL3	NM_016941.2	Delta-like 3 (Drosophila)	-0.156	0.0039	50.9
DNAJA2	NM_005880.2	DnaJ (Hsp40) homolog, subfamily A, member 2	0.202	0.0056	51.4
DNAJC15	NM_013238.1	DnaJ (Hsp40) homolog, subfamily C, member 15	0.247	0.0047	54.8
DOK6	NM_152721.2	Docking protein 6	-0.139	0.0053	51.9
DPH5	NM_015958.1	DPH5 homolog (S. cerevisiae)	0.226	0.0054	40.2
DPM1	NM_003859.1	Dolichyl-phosphate mannosyltransferase polypeptide 1	0.336	0.0041	51.8
DPP3	NM_005700.2	Dipeptidyl-peptidase 3	0.089	0.0071	47.8
EAN57	Y11142.1	EAN57 gene	-0.320	0.0040	40.2
EIF2S1	NM_004094.3	Eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	0.505	0.0046	44.4
EPHX1	NM_000120.2	Epoxide hydrolase 1, microsomal (xenobiotic)	-0.411	0.0047	54.8
EVL	NM_016337.2	Enah/Vasp-like	-0.224	0.0044	44.6
EXOC1	NM_018261.2	Exocyst complex component 1	0.083	0.0055	44.1
EXOC3L2	NM_138568.2	exocyst complex component 3-like 2	-0.279	0.0620	63.9
FAIM3	NM_005449.3	Fas apoptotic inhibitory molecule	-0.051	0.0050	40.6
FAM39CP	NG_003159.1	family with sequence similarity 39, member C	-0.071	0.0025	66
FAM89A	NM_198552.1	Family with sequence similarity 89, member A	0.044	0.0053	54.8
FBXO4	NM_033484.1	F-box protein 4	-0.051	0.0045	36.4
FLJ11235	AK002097.1	Hypothetical FLJ11235	-0.162	0.0027	32.9
FOLH1	AF107214.1	Folate hydrolase 1	-0.152	0.0044	40.2

FOXL2	NM_023067.2	Forkhead box L2	0.006	0.0055	32.9
G3BP1	NM_005754.2	GTPase activating protein (SH3 domain) binding protein 1	0.214	0.0087	48
GABARAPL1	AF287012.1	GABA(A) receptor-associated protein like 1	-0.225	0.0047	63.9
GABARAPL2	NM_007285.6	GABA(A) receptor-associated protein-like 2	0.223	0.0090	62.3
GADD45G	NM_006705.2	Growth arrest and DNA-damage-inducible, gamma	-0.209	0.0038	32.6
GAPDHS	NM_014364.3	Glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	0.038	0.0058	40.6
GAS2L1	BC001782.1	Growth arrest-specific 2 like 1	0.419	0.0048	44.6
GBA2	AK057610.1	Glucosidase, beta (bile acid) 2	-0.238	0.0046	62.5
GEC1	AF287012.1	early estrogen-regulated protein	-0.296	0.0085	63.9
GFI1	NM_005263.2	elongation factor G, mitochondrial1	-0.015	0.0052	48.1
GLDC	NM_000170.1	Glycine dehydrogenase (decarboxylating)	0.224	0.0045	44.1
GLTP	NM_016433.3	Nuclear receptor binding protein 1	0.175	0.0042	33.1
GMIP	NM_016573.1	GEM interacting protein	-0.037	0.0059	36.8
GPR51	NM_005458.5	Golgin A5	0.151	0.0037	68.8
GRINA	U44954.1	receptor glutamate-binding chain	-0.233	0.0072	62.3
HCCS	NM_005333.1	Holocytochrome c synthase (cytochrome c heme-lyase)	0.446	0.0039	63
HHLA3	NM_001031693.1	dolichyl-phosphate mannosyltransferase polypeptide 1	-0.154	0.0055	51.8
HKR3	NM_005341.1	HERV-H LTR-associating 3	0.000	0.0091	36.4
HOXB9	NM_024017.3	Homeobox B9	-0.126	0.0048	55
HPRT1	NM_000194.1	Hypoxanthine phosphoribosyltransferase 1	0.452	0.0046	60.2
HTRA2	NM_013247.3	HtrA serine peptidase 2	0.189	0.0050	36.8
INSR	NM_000208.1	Insulin receptor	-0.090	0.0056	32.9
ISOC1	BC014105.2	Isochorismatase domain containing 1	-0.207	0.0050	66.4
ITFG2	NM_018463.2	integrin alpha FG-GAP repeat containing 2	-0.143	0.0043	69.8
ITM2C	BC098563.1	Integral membrane protein 2C	-0.210	0.0051	36.4
ITPKB	NM_002221.2	Inositol 1,4,5-trisphosphate 3-kinase B	0.022	0.0044	62.8
JUB	BC034968.2	Jub, ajuba homolog (Xenopus laevis)	-0.040	0.0057	44.1
KATNB1	NM_005886.1	Katanin p80 (WD repeat containing) subunit B 1	0.317	0.0055	32.9
KIAA0513	NM_014732.2	KIAA0513	-0.271	0.0031	40.6
KIAA1442	XM_044921.5	KIAA1442	0.440	0.0078	44.5
KIAA1843	AK027583.1	KIAA1843	0.396	0.0058	36.8
KLK8	NM_144505.1	Kallikrein-related peptidase 8	-0.236	0.0046	44.1
KLRC2	NM_002260.2	Killer cell lectin-like receptor subfamily C, member 2	0.263	0.0049	44.2
KRTHA1	NM_002277.2	Keratin 31	-0.058	0.0043	62.5
KRTHA4	NM_021013.3	Keratin 34	0.271	0.0051	59.2
LEPROTL1	NM_015344.1	Leptin receptor overlapping transcript-like 1	0.422	0.0044	62.8
LILRP2	NM_024317	leukocyte immunoglobulin-like receptor pseudogene 2	-0.183	0.0056	51.4

LOC57228	NM_020467.2	small trans-membrane and glycosylated protein	0.152	0.0064	48
LOC81691	NM_030941.1	Exonuclease NEF-sp	0.206	0.0051	36.2
LRRC46	AK027206.1	Leucine rich repeat containing 46	-0.077	0.0051	40.6
LSM2	NM_021177.3	LSM2 homolog, U6 small nuclear RNA associated	0.197	0.0055	36.8
LTA	NM_000595.2	Lymphotoxin alpha (TNF superfamily, member 1)	0.052	0.0049	48
LTBR	NM_002342.1	Lymphotoxin beta receptor (TNFR superfamily, member 3)	-0.025	0.0051	32.6
MAGED2	U92544.1	Melanoma antigen family D, 2	-0.355	0.0041	36.8
MAPK10	BC022492.1	mitogen-activated protein kinase 10	-0.263	0.0070	51.5
MDM1	NM_017440.2	Mdm1 nuclear protein homolog (mouse)	-0.292	0.0059	40.4
MED28	NM_025205.3	Mediator complex subunit 28	0.260	0.0039	32.9
MGST1	NM_020300.3	Microsomal glutathione S-transferase 1	0.037	0.0039	36.8
MOCS1	AY423726.1	Molybdenum cofactor synthesis 1	-0.190	0.0042	66.5
MOG	BC035938.1	Homo sapiens myelin oligodendrocyte glycoprotein	-0.075	0.0039	54.5
MORF4L1	NM_006791.2	Mortality factor 4 like 1	0.142	0.0055	36.8
MRLC2	NM_033546.2	myosin regulatory light chain	-0.217	0.0072	68.6
MRPL14	NM_032111.2	Mitochondrial ribosomal protein L14	0.266	0.0044	59
MRPL18	NM_014161.2	Mitochondrial ribosomal protein L18	0.168	0.0050	62.5
MRPL43	NM_032112.2	Mitochondrial ribosomal protein L43	0.098	0.0056	40.2
MRPL44	NM_022915.2	Mitochondrial ribosomal protein L44	0.308	0.0036	59
MST1	NM_020998.2	Macrophage stimulating 1 (hepatocyte growth factor-like)	-0.249	0.0039	44.5
MTMR2	BC052990.1	Methylenetetrahydrofolate dehydrogenase 2	0.396	0.0041	44.5
MTX2	NM_006554.3	Metaxin	0.345	0.0055	32.6
MUC1	Z17325.1	Mucin 1, cell surface associated	0.007	0.0051	63
MUC4	AF058803.1	Mucin 4, cell surface associated	0.144	0.0044	40.2
MYCBP2	AF083244.1	MYC binding protein 2	0.117	0.0041	32.2
MYO10	AB018342.2	Myosin X	-0.139	0.0057	36.8
MYOT	NM_006790.1	myotilin	0.219	0.0056	40.6
NCOR2	NM_006312.2	Nuclear receptor co-repressor 2	-0.086	0.0064	36.4
NDUFS8	NM_002496.1	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0.013	0.0052	32.9
NFIL3	NM_005384.2	Nuclear factor, interleukin 3 regulated	0.725	0.0044	60
NHLH2	AK056621.1	nescient helix loop helix 2	0.021	0.0062	51.8
NIF3L1	NM_021824.2	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	0.339	0.0052	66.8
NONO	NM_007363.3	non-POU domain containing, octamer-binding	0.219	0.0085	48.5
NRXN3	AJ493127.1	Homo sapiens partial mRNA for neurexin 3-beta (NRXN3 gene)	-0.275	0.0048	63
NUBPL	NM_025152.1	nucleotide binding protein-like	0.187	0.0062	44.1
OAS1	NM_002534.1	Nucleotide binding protein-like	0.037	0.0038	69.2
PAAF1	NM_025155.1	proteasomal ATPase-associated factor 1	0.291	0.0074	47.1

PAMCI	NM_005447.2	peptidylglycine alpha-amidating monooxygenase interactor	0.108	0.0052	54.8
PANK2	NM_024960.3	Pantothenate kinase 2	0.203	0.0055	51.8
PDCD10	NM_007217.3	Programmed cell death 10	0.528	0.0049	60
PDCD7	NM_005707.1	Programmed cell death 7	-0.324	0.0062	40.2
PDE4C	NM_000923.1	Phosphodiesterase 4C, cAMP-specific	-0.117	0.0046	32.4
PDHA1	NM_000284.1	pyruvate dehydrogenase alpha 1, variant 1	0.204	0.0071	36.8
PHACS	NM_032592.1	1-aminocyclopropane-1-carboxylate synthase	0.243	0.0042	32.9
PKNOX2	BC045626.1	PBX/knotted 1 homeobox 2	-0.218	0.0051	51.1
PLD2	NM_002663.2	Phospholipase D2	-0.204	0.0050	62.6
PLP2	NM_002668.1	Proteolipid protein 2 (colonic epithelium-enriched)	0.052	0.0058	66.5
PLSCR1	NM_021105.1	Phospholipid scramblase 1	-0.159	0.0053	51.9
POU2F1	NM_002697.2	POU class 2 homeobox 1	-0.223	0.0037	44.9
PRAM1	NM_032152.3	PML-RARA regulated adaptor molecule 1	-0.142	0.0050	60.6
PRPF4B	NM_003913.3	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.203	0.0050	51.4
PTS	NM_000317.1	6-pyruvoyltetrahydropterin synthase	0.314	0.0054	48.6
PVRIG	NM_024070.3	poliovirus receptor related immunoglobulin domain containing	0.177	0.0080	54.8
RAB11FIP1	AK124422.1	RAB11 family interacting protein 1	0.307	0.0053	54.8
RAB32	NM_006834.2	RAB32, member RAS oncogene family	0.308	0.0047	58.8
RERG	NM_032918.1	RAS-like, estrogen-regulated, growth inhibitor	0.200	0.0057	50
RFX5	NM_000449.2	Regulatory factor X, 5 (influences HLA class II expression)	-0.017	0.0065	32.9
RGS3	NM_017790.2	Regulator of G-protein signaling 3	-0.059	0.0044	36.4
RHBG	NM_020407.1	Rh family, B glycoprotein (gene/pseudogene)	-0.045	0.0045	54.8
RHEB	NM_005614.2	Ras homolog enriched in brain	0.294	0.0049	40.6
RNASEH2A	NM_006397.2	Ribonuclease H2, subunit A	0.615	0.0057	40.6
RPS3	NM_001005.2	ribosomal protein S3	0.102	0.0044	48.3
RSAFD1	NM_018264.2	tRNA-yW synthesizing protein 1 homolog	-0.109	0.0084	48.5
SAC3D1	NM_013299.2	SAC3 domain containing 1	0.426	0.0036	32.6
SCRN3	NM_024583.2	Secernin 3	0.087	0.0054	67.1
SDF4	NM_016176.2	Stromal cell derived factor 4	-0.326	0.0051	60.6
SEC22	NM_004206.2	vesicle trafficking protein homolog C transcript variant 2	0.321	0.0082	44.1
SERAC1	NM_032861.2	Serine active site containing 1	-0.124	0.0093	56.9
SF3B1	NM_012433.2	splicing factor 3b, subunit 1	0.347	0.0075	44.5
SF3B14	NM_016047.3	Splicing factor 3B, 14 kDa subunit	0.365	0.0046	44.5
SH3BP2	NM.003023	SH3-domain binding protein 2	-0.179	0.0055	62.5
SH3GL1	NM_003025.2	SH3-domain GRB2-like 1	-0.108	0.0057	54.8
SKP2	NM_032637.2	S-phase kinase-associated protein 2 (p45)	0.236	0.0045	36.4
SLAMF7	NM_021181.3	SLAM family member 7	-0.087	0.0054	51.4

SLC19A1	S78996.1	Solute carrier family 19 (folate transporter), member 1	-0.163	0.0039	59
SLC20A1	NM_005415.3	Solute carrier family 20 (phosphate transporter), member 1	0.391	0.0052	40.6
SLC25A36	NM_018155.1	Solute carrier family 25, member 36	0.298	0.0058	48
SLC43A3	AL157431.1	Solute carrier family 43, member 3	-0.313	0.0037	55
SMS	NM_004595.2	Spermine synthase	0.237	0.0048	40.9
SNAPC1	NM_003082.2	Small nuclear RNA activating complex, polypeptide 1, 43kDa	0.440	0.0050	58.7
SOD3	NM_003102.1	Superoxide dismutase 3, extracellular	-0.437	0.0040	61.2
SOX4	NM_003107.2	SRY (sex determining region Y)-box 4	-0.175	0.0030	58.6
SPI1	NM_003120.1	Spleen focus forming virus proviral integration oncogene	0.317	0.0052	62.4
SPOP	NM_003563.3	Speckle-type POZ protein	-0.220	0.0045	62.8
SPP2	NM_006944.2	Secreted phosphoprotein 2, 24kDa	0.194	0.0048	66.8
SRPRB	NM_021203.2	Signal recognition particle receptor, B subunit	0.058	0.0055	48.3
STAG2	NM_006603.3	Stromal antigen 2	0.418	0.0034	37
STAT5A	NM_003152.2	Signal transducer and activator of transcription 5A	-0.250	0.0052	48
STOM	NM_004099.4	Stomatin	-0.201	0.0054	36.4
SURF5	BC024225.2	Surfeit 5	-0.471	0.0063	58.8
SYNE1	NM_015293.1	Spectrin repeat containing, nuclear envelope 1	-0.200	0.0053	36.6
TANC2	NM_015623	putative ankyrin-repeat containing protein	0.286	0.0045	40.2
TCP1	X52882.1	t-complex polypeptide 1	0.358	0.0053	49
TFB2M	NM_022366.1	Transcription factor B2, mitochondrial	0.230	0.0052	44.4
TIMM9	NM_012460.2	Translocase of inner mitochondrial membrane 9 homolog	0.309	0.0047	48
TMED5	NM_016040.3	Transmembrane emp24 protein transport domain containing 5	0.265	0.0047	55.9
TMEM14B	NM_030969.2	Transmembrane protein 14B	0.612	0.0490	37.2
TMEM159	NM_020422.3	transmembrane protein 159	0.267	0.0052	63.4
TMEM59	NM_004872.3	Transmembrane protein 59	0.194	0.0055	32.9
TMEM87B	U60873.1	transmembrane protein 87B	-0.036	0.0048	62.8
TNEM111	NM_018447.1	transmembrane protein 111	0.031	0.0048	36.8
TNFRSF11A	NM_003839.2	Tumor necrosis factor receptor superfamily, member 11a	-0.329	0.0052	66
TNPO1	NM_002270.2	Transportin 1	0.329	0.0038	58.7
TOPORS	NM_005802.2	Topoisomerase I binding, arginine/serine-rich	0.385	0.0048	51.8
TOR1A	NM_000113.2	Torsin family 1, member A (torsin A)	0.264	0.0031	62.2
TOR3A	AJ299441.1	Torsin family 3, member A	-0.236	0.0056	55.2
TPSG1	NM_012467.1	Tryptase gamma 1	-0.204	0.0053	58.3
TXNDC12	NM_015913.2	Thioredoxin domain containing 12 (endoplasmic reticulum)	0.110	0.0062	40.6
UBA52	NM_003333.2	Ubiquitin A-52 residue ribosomal protein fusion product 1	-0.196	0.0033	67.1
UCK2	NM_012474.3	Uridine-cytidine kinase 2	0.277	0.0049	44.9
USP25	NM_013396.3	Ubiquitin specific peptidase 25	0.055	0.0050	32.6

USP5	BC005139.2	Ubiquitin specific peptidase 5 (isopeptidase T)	-0.124	0.0044	58.7
VAMP3	NM_004781.3	Homo sapiens vesicle-associated membrane protein 3	0.312	0.0049	58.8
VDAC2	NM_003375.2	Voltage-dependent anion channel 2	0.380	0.0041	66.8
VPS13A	AJ608769.1	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	0.018	0.0055	62.5
VPS16	NM_022575.2	Protein tyrosine phosphatase, receptor type, A	0.119	0.0062	51.4
VPS18	NM_020857.2	Vacuolar protein sorting 18 homolog (S. cerevisiae)	-0.126	0.0037	66.3
WDR5B	NM_019069.3	WD repeat domain 5B	0.164	0.0050	54.8
WDR74	NM_018093.1	WD repeat domain 74	0.150	0.0059	36.8
WHSC1	AB029013.1	Wolf-Hirschhorn syndrome candidate 1	-0.100	0.0042	51.4
WHSC1L1	NM_023034.1	Wolf-Hirschhorn syndrome candidate 1-like 1	0.180	0.0034	44.5
WIPI2	BC021068.1	WD repeat domain, phosphoinositide interacting 2	-0.196	0.0040	48
WNK3	AY352048.1	WNK lysine deficient protein kinase 3	-0.221	0.0051	62.5
WWOX	AY256821.1	WW domain containing oxidoreductase	-0.098	0.0053	32.9
XIAP	NM_001167.2	X-linked inhibitor of apoptosis	0.076	0.0048	51.5
XYLT2	NM_022167.1	Xylosyltransferase II	0.090	0.0035	40.2
YWHAB	AF107406.1	Tyrosine 3-/tryptophan 5-monooxygenase activation protein	-0.031	0.0050	32.9
ZBTB4	NM_020899.2	Zinc finger and BTB domain containing 4	-0.057	0.0037	69.8
ZCWPW1	NM_017984.2	Zinc finger, CW type with PWWP domain 1	-0.246	0.0050	50.9
ZDHHC17	AB023163.1	Zinc finger, DHHC-type containing 17	-0.313	0.0045	36.4
ZMYM2	BC036372.1	Zinc finger, MYM-type 2	-0.550	0.0040	63
ZNF34	NM_030580.2	Zinc finger protein 34	-0.024	0.0060	66.1
ZNF587	NM_017961	Zinc finger protein 587	0.175	0.0049	32.9
	AK025047.1		0.331	0.0068	62.3
	AK021678.1		0.134	0.0093	58.3
	AL136582.1	DKFZp761N1924	-0.536	0.0080	55.2
	X74025.1		-0.620	0.0073	55
	LOC63426		-0.145	0.0103	54.8
	AC012543.4		0.638	0.0064	51.8
	BC018638.2		-0.316	0.0090	51.4
	AC037459.16		-0.177	0.0069	51.4
	AC016757.10		-0.589	0.0069	48.3
	AC016757.10		0.497	0.0079	48.1
	AL365410.1		-0.26	0.0075	44.4
	Z99916.1		-0.317	0.0069	43.8
	BK001591.1		-0.315	0.0073	43.8
	AL360271.12		-0.175	0.0085	40.6
	AF336885.1		-0.224	0.0082	40.6

NM_014732.2	KIAA0513	-0.338	0.0067	40.6
AC015908.10		-0.146	0.0055	40.2
AC015804.14		0.125	0.0070	39.9
AL121761.5		0.240	0.0055	39.9
BC052779.1		-0.191	0.0086	36.8
AK027583.1		-0.396	0.0058	36.8
AK027583.1		0.06	0.0091	36.8
AC092057.2		-0.24	0.0077	36.8
AC009153.10		-0.064	0.0091	36.8
AF130063.1		-0.51	0.0059	36.8
AF130066.1		-0.275	0.0074	36.8
AK027198.1		0.096	0.0076	36.4
AC025270.6		-0.32	0.0074	32.6

Supp Table 4