Landes Bioscience www.landesbioscience.com

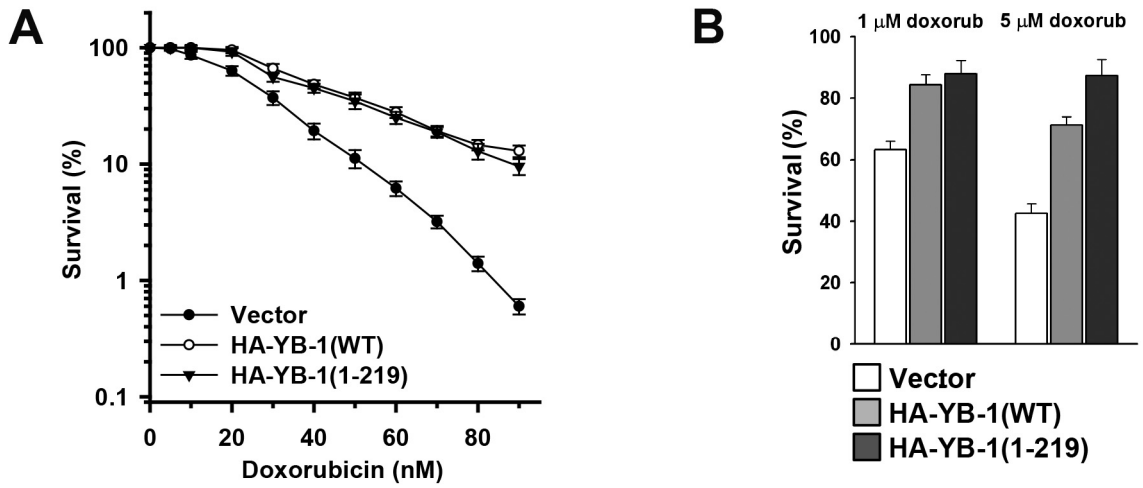
Supplemental Material to:

Ekaterina R Kim, Anastasiia A Selyutina, Ilya A Buldakov, Valentina Evdokimova, Alexey V Sorokin, and Lev P Ovchinnikov

The proteolytic YB-1 fragment interacts with DNA repair machinery and enhances survival during DNA-damaging stress

Cell Cycle 2013; 12(24)
http://dx.doi.org/10.4161/cc.26670

http://www.landesbioscience.com/journals/cc/26670/



Supplementary Figure 1. Effect of full-length and truncated YB-1 proteins on survival of doxorubicin-treated cells. (A) Clonogenic survival assay of NIH3T3 cells stably expressing YB-1 (WT) or YB-1 (1-219) proteins under doxycycline-inducible promoter. Cell lines were treated with increasing concentrations of doxorubicin (0-90 nM) for 14 hours, and the medium was replaced with the regular one. Colonies were left to form for 8 days, fixed in 3.7% paraformaldehyde-PBS, stained with crystal violet, and counted. (B) Cell viability assay was performed as described in Materials and Methods.

Supplementary Table 1. List of common genes whose expression was changed in YB-1 (WT) and YB-1 (1-219) expressing NIH3T3 cells compared to vector control cells (>1.75-fold change).

Gene name	Accession	YB-1 (WT), fold Δ	YB-1 (1-219), fold Δ	Definition	Functional categories
ALOX5AP	NM_009663	-2,24	-2,23	arachidonate 5-lipoxygenase activating protein	Metabolism
CTGF	NM_010217	-1,96	-1,85	Connective tissue growth factor	Protease inhibitor, extracellular matrix, signal transduction, signaling molecule, DNA metabolic process, cell adhesion, cell migration, regulation of cell growth, cellular developmental process
CYBA	NM_007806	-2,08	-1,93	cytochrome b-245, alpha polypeptide	Electron transport
DCN	NM_007833	-4,08	-3,89	decorin	Extracellular matrix, signal transduction, metabolism, immunity, cation transport, electron transport
DLK1	NM_010052	-5,65	-2,16	delta-like 1 homolog (Drosophila)	Cell structure and motility, electron transport
GSTM2	NM_008183	-2,88	-1,96	glutathione S-transferase, mu 2	Metabolism, response to stress
GSTT3	NM_133994	-3,03	-3,00	glutathione S-transferase, theta 3	Metabolism
SDC3	NM_011520	-2,41	-2,06	syndecan 3	Cytoskeletal

					protein, signaling molecule, cell adhesion, cell structure and motility
SPP1	NM_009263	-1,99	-2,99	Secreted phosphoprotein 1	Extracellular matrix, signaling molecule, response to stress, anti-apoptosis, cell adhesion, regulation of cell proliferation, cell migration, cell structure and motility, protease inhibitor, cellular developmental process
AKR1C18	NM_134066	3,17	1,92	aldo-ketoreductase family 1, member C18	Metabolism, cell structure and motility
DHCR24	NM_053272	1,84	1,77	24-dehydrocholesterol reductase	Membrane organization and biogenesis, response to stress, cell cycle arrest, anti-apoptosis, metabolism, translation, cellular developmental process
ILDR2	FJ024494	5,12	2,84	immunoglobulin-like domain containing receptor 2	Unknown
ITGA3	NM_013565	2,14	3,23	Integrin alpha 3	Membrane organization and biogenesis,

					electron transport, cell adhesion, cell migration, cell structure and motility, cellular developmental process
NGEF	NM_001111314	3,83	2,18	neuronal guanine nucleotide exchange factor	Unknown
BLNK	NM_008528	4,88	-2,62	B-cell linker	Signal transduction, signaling molecule
CDH5	NM_009868	1,97	-1,99	cadherin 5	Signal transduction, metabolism, cation transport, cell adhesion, regulation of cell proliferation
PLP1	NM_011123	1,92	-2,43	Proteolipid protein (myelin) 1	Cell structure and motility, metabolism, translation, cation transport, cellular developmental process
S100A7A	NM_199422	-2,51	2,31	S100 calcium binding protein A7A	Unknown

Supplementary Table 2. List of genes whose expression was changed in YB-1 (1-219) expressing NIH3T3 cells compared to vector control cells (>1.75-fold change).

Gene name	Accession	YB-1 (1-219), fold Δ	Definition	Functional categories
ABCG1	NM_009593	2,64	ATP-binding cassette, sub-family G (WHITE), member 1	Metabolism, cation transport, cellular transport
AKR1C12	NM_013777	-3,19	aldo-ketoreductase family 1, member C12	Metabolism
ALDH3A1	NM_007436	-2,69	aldehyde dehydrogenase family 3, subfamily A1	Metabolism
BCL2L1	NM_009743	1,77	Bcl2-like 1	Signaling molecule, anti-apoptosis, metabolism, immunity, cellular developmental process
CCK	NM_031161	2,46	cholecystokinin	Protease inhibitor, signaling molecule, signal transduction, cell migration, translation, cation transport, cellular developmental process
ECM1	NM_007899	-1,78	Extracellular matrix protein 1	Extracellular matrix, signal transduction, immunity
IFITM3	NM_025378	-2,02	Interferon induced transmembrane protein 3	Regulation of cell proliferation
IGFBP4	NM_010517	1,87	insulin-like growth factor binding protein 4	Protease inhibitor, signal transduction, translation, cation transport, regulation of cell growth
LPP	NM_178665	-1,82	LIM domain containing preferred translocation partner in lipoma	Cytoskeletal protein, signal transduction, cell adhesion
MFAP5	NM_015776	2,06	Microfibrillar associated protein 5	Extracellular matrix, cell adhesion, cell

				structure and motility
MSLN	NM_018857	2,54	mesothelin	Extracellular matrix, signal transduction, cell adhesion
PDGFRA	NM_011058	-1,77	platelet derived growth factor receptor, alpha polypeptide	Signal transduction, metabolism
PRELP	NM_054077	-4,55	proline arginine-rich end leucine-rich repeat	Extracellular matrix, signal transduction
RGS16	NM_011267	2,12	regulator of G-protein signaling 16	Signal transduction
SCARA3	NM_172604	-2,37	scavenger receptor class A, member 3	Signal transduction
SCARA5	NM_028903	-2,63	scavenger receptor class A, member 5 (putative)	Cell adhesion, cation transport
SERPINA3N	NM_009252	-8,53	serine (or cysteine) peptidase inhibitor, clade A, member 3N	Protease inhibitor, response to stress
SLURP1	NM_020519	-1,87	secreted Ly6/Plaur domain containing 1	Signaling molecule
SNED1	NM_172463	-2,37	sushi, nidogen and EGF-like domains 1	Signaling molecule, signal transduction, cell adhesion, cell structure and motility, metabolism
SPON2	NM_133903	-2,26	spondin 2, extracellular matrix protein	Extracellular matrix, signal transduction, cell adhesion
TXNIP	NM_023719	-1,95	Thioredoxin interacting protein	Response to stress, metabolism, translation, cellular developmental process

Supplementary Table 3. List of genes whose expression was changed in YB-1 (WT) expressing NIH3T3 cells compared to vector control cells (>1.75-fold change).

Gene name	Accession	YB-1 (WT), fold Δ	Definition	Functional categories
AACS	NM_030210	1,84	acetoacetyl-CoA synthetase	Protease inhibitor, signal transduction, metabolism
ACAT3	NM_153151	1,82	acetyl-Coenzyme A acetyltransferase 3	Metabolism
ACTA2	NM_007392	-7,98	actin, alpha 2, smooth muscle, aorta	Cytoskeletal protein, metabolism, cation transport
ALDH1L2	NM_153543	1,89	aldehyde dehydrogenase 1 family, member L2	Protease inhibitor, metabolism, cation transport
AP1G2	NM_007455	2,65	adaptor protein complex AP-1, gamma 2 subunit	Membrane organization and biogenesis
BHLHB9	NM_001098222	-1,91	basic helix-loop-helix domain containing, class B9	Unknown
BTBD6	NM_201646	-2,39	BTB (POZ) domain containing 6	Extracellular matrix, cation transport
CCL7	NM_013654	-2,26	chemokine (C-C motif) ligand 7	Signaling molecule, signal transduction, response to stress, cation transport
CDSN	NM_001008424	5,25	corneodesmosin	Metabolism
CEACAM2	NM_007543	1,99	CEA-related cell adhesion molecule 2	Signal transduction, immunity, cellular transport
COL1A1	NM_007742	3,87	collagen, type I, alpha 1	Extracellular matrix, signal transduction, cell adhesion, cell structure and motility, metabolism, immunity

CXCL1	NM_008176	-2,15	chemokine (C-X-C motif) ligand 1	Signaling molecule, signal transduction, response to stress, cation transport
CYP51	NM_020010	2,21	cytochrome P450, family 51	Metabolism, electron transport, cellular transport
CYR61	NM_010516	-1,84	Cysteine rich protein 61	Signaling molecule, signal transduction, cell adhesion, regulation of cell growth
DAAM1	NM_172464	-1,88	dishevelled associated activator of morphogenesis 1	Cytoskeletal protein, cell structure and motility
DDIT3	NM_007837	1,80	DNA-damage inducible transcript 3	Signaling molecule, response to stress, cell cycle arrest, cellular developmental process
DDX24	NM_020494	-1,79	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Immunity
EFEMP2	NM_021474	-2,89	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	Extracellular matrix, signaling molecule, signal transduction, response to stress, cell adhesion, cell structure and motility
ENO2	NM_013509	-3,48	enolase 2, gamma neuronal	Metabolism, cation transport
FDPS	NM_134469	1,94	Farnesyl diphosphate synthetase	Metabolism
FGFR2	NM_201601	-1,92	Fibroblast growth factor receptor 2	Regulation of cell proliferation, cellular developmental process
FLT1	NM_010228	1,81	FMS-like tyrosine	Immunity, electron

			kinase 1	transport, cell migration, cellular developmental process
GADD45A	NM_007836	1,83	growth arrest and DNA-damage-inducible 45 alpha	Response to stress, cell cycle arrest
GKN1	NM_025466	1,97	gastrokine 1	Metabolism, translation, cation transport, regulation of cell proliferation
HDAC5	NM_001077696	1,88	histonedeacetylase5	DNA metabolic process
HIST1H2AF	NM_175661	-1,80	Histone cluster 1, H2af	DNA metabolic process, cation transport, protease inhibitor
HIST1H2AH	NM_175659	-2,00	Histone cluster 1, H2ah	DNA metabolic process
HIST1H2AK	NM_178183	-1,84	Histone cluster 1, H2ak	DNA metabolic process, cation transport, protease inhibitor
HIST1H2AN	NM_178184	-1,87	Histone cluster 1, H2an	DNA metabolic process, cation transport, protease inhibitor, translation
HIST2H2AA2	NM_178212	-1,76	Histone cluster 2, H2aa2	DNA metabolic process
HSP90AA1	NM_010480	-1,96	heat shock protein 90, alpha (cytosolic), class A member 1	Response to stress, metabolism, translation, cation transport, cellular developmental process
ITGBL1	NM_145467	1,75	integrin, beta-like 1	Cell adhesion, cellular transport
KPRP	NM_028629	-2,89	Keratinocyte expressed, proline-rich	Unknown
KRT13	NM_010662	2,63	keratin 13	Cytoskeletal protein, cell

				adhesion, cell structure and motility
LBCL1	NM_008487	2,08	rho/rac guanine nucleotide exchange factor	Metabolism, immunity, cation transport, regulation of cell proliferation, cell structure and motility
LIMS2	NM_144862	2,20	LIM and senescent cell antigen like domains 2	Cytoskeletal protein, protease inhibitor, signal transduction
LIP1	NM_021460	-2,25	Lysosomal acid lipase A	Metabolism
LOXL4	NM_053083	-3,51	lysyloxidase-like 4	Signaling molecule, protease inhibitor, cell adhesion
MEF2C	NM_025282	1,92	Myocyte enhancer factor 2C	Immunity, cellular developmental process
MT-ND5	BC055066	1,81	Mitochondrially encoded NADH dehydrogenase 5	Electron transport
NEO1	NM_008684	2,24	neogenin	Membrane organization and biogenesis, signal transduction, cation transport, cell adhesion, cellular developmental process
NNMT	NM_010924	-1,88	nicotinamide N-methyl transferase	Cation transport
OSR1	NM_011859	-1,78	odd-skipped related 1 (Drosophila)	Electron transport
PDLIM2	NM_145978	-2,23	PDZ and LIM domain 2	Cytoskeletal protein, cell structure and motility
RCOR1	NM_198023	-1,95	REST corepressor 1	DNA metabolic process
SDPR	NM_138741	-1,86	Serum deprivation	Metabolism

			response	
SERPINA1B	NM_009244	-4,99	serine (or cysteine) preptidase inhibitor, clade A, member 1b	Protease inhibitor, response to stress, electron transport
SERPINA1D	NM_009246	-2,35	serine (or cysteine) peptidase inhibitor, clade A, member 1d	Protease inhibitor
SLC25A33	NM_027460	1,83	Solute carrier family 25, member 33	Cellular transport
SLC6A9	NM_008135	2,45	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Cellular transport
STARD4	NM_133774	1,75	StAR-related lipid transfer domain containing 4	Metabolism
STOM	NM_013515	2,05	stomatin	Cytoskeletal protein, cell structure and motility, immunity, translation
TINAGL	NM_023476	2,76	Tubulointerstitial nephritis antigen-like	Immunity, cell adhesion
TK1	NM_009387	-1,78	Thymidine kinase 1	Protease inhibitor, cell structure and motility, signal transduction, DNA metabolic process, electron transport
TNNT2	NM_011619	1,92	troponin T2, cardiac	Cytoskeletal protein, cellular developmental process
VLDLR	NM_013703	-3,29	very low density lipoprotein receptor	Membrane organization and biogenesis, metabolism

Supplementary Table 4. List of genes whose expression was changed in YB-1 (WT) expressing NIH3T3 cells compared to vector control cells

Gene Name	Symbol	Fold Change (YB-1 (WT) VS Ctrl.)
expressed sequence AA536749	AA536749	0.803408917
acetoacetyl-CoA synthetase	AACS	1.841224934
alanyl-tRNA synthetase domain containing 1	AARSD1	0.843652261
ATP-binding cassette, sub-family A, member 3	ABCA3	1.394461526
ATP-binding cassette, sub-family D, member 4	ABCD4	0.655626663
abhydrolase domain containing 5	ABHD5	1.398745548
acetyl-Coenzyme A acetyltransferase 2	ACAT2	1.429258295
acetyl-Coenzyme A acetyltransferase 3	ACAT3	1.820257559
acetyl-Coenzyme A acetyltransferase 3	ACAT3	1.369422194
acyl-CoA synthetase short-chain family member 2	ACSS2	1.360615241
actin, alpha 2, smooth muscle, aorta	ACTA2	0.251326512
actin, alpha 2, smooth muscle, aorta	ACTA2	0.12523977
actinin, alpha 1	ACTN1	0.718521202
a disintegrin and metallopeptidase domain 15	ADAM15	1.359479838
a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7	ADAMTS7	1.572671322
ADAMTS-like 5	ADAMTSL5	1.230996139
aarF domain containing kinase 1	ADCK1	0.68784532
adipose differentiation related protein	ADFP	1.30348435
amino-terminal enhancer of split	AES	1.550202939
agrin	AGRN	1.704892239
AT hook containing transcription factor 1	AHCTF1	0.81030777
S-adenosylhomocysteine hydrolase-like 1	AHCYL1	0.700732294
AHNAK nucleoprotein	AHNAK	1.297679496
AHNAK nucleoprotein 2	AHNAK2	0.755459009
AHA1, activator of heat shock protein ATPase homolog 1	AHSA1	0.577909896
expressed sequence AI481316	AI481316	0.701832673
expressed sequence AI846148	AI846148	1.287050628
aryl-hydrocarbon receptor-interacting protein	AIP	1.174241759
aldo-keto reductase family 1, member C12	AKR1C12	1.542663609
aldo-keto reductase family 1, member C18	AKR1C18	3.169006056
aldehyde dehydrogenase 1 family, member L2	ALDH1L2	1.893193272
arachidonate 5-lipoxygenase-activating protein	ALOX5AP	0.447033972
autocrine motility factor receptor	AMFR	1.176444561
AMP deaminase 3	AMPD3	0.79400639
anaphase-promoting complex subunit 5	ANAPC5	1.179496497
anaphase-promoting complex subunit 5	ANAPC5	1.210120182
angel homolog 2	ANGEL2	1.248033686
angiopoietin-like 2	ANGPTL2	1.59289998
angiopoietin-like 4	ANGPTL4	0.607816407
angiopoietin-like 6	ANGPTL6	1.484458716

ankyrin repeat and MYND domain containing 2	ANKMY2	1.171867921
ankyrin repeat domain 13b	ANKRD13B	1.400934587
ankyrin repeat and sterile alpha motif domain containing 3	ANKS3	1.225545296
adaptor protein complex AP-1, gamma 2 subunit	AP1G2	2.653076527
amyloid beta (A4) precursor-like protein 2	APLP2	1.309840541
aquaporin 1	AQP1	1.257566138
ADP-ribosylation factor 6	ARF6	0.686957954
Rho GTPase activating protein 24	ARHGAP24	0.810198762
ariadne homolog 2	ARIH2	1.259320479
ADP-ribosylation factor-like 6 interacting protein 5	ARL6IP5	1.201088058
armadillo repeat containing, X-linked 2	ARMCX2	0.714818974
arrestin domain containing 4	ARRDC4	0.615456438
arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	ASNA1	1.534390728
additional sex combs like 2	ASXL2	1.705454095
activating transcription factor 4	ATF4	1.26254142
activating transcription factor 5	ATF5	1.241217045
ATG2 autophagy related 2 homolog A	ATG2A	1.594932977
ATG2 autophagy related 2 homolog B	ATG2B	0.731839814
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	ATIC	0.81238027
ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	1.290617842
ATPase, H+ transporting, lysosomal accessory protein 1	ATP6AP1	1.250045129
ATPase, H+ transporting, lysosomal V0 subunit B	ATP6V0B	1.550997225
ATPase, H+ transporting, lysosomal V0 subunit D1	ATP6V0D1	1.317289744
ATPase, H+ transporting, lysosomal V0 subunit E2	ATP6V0E2	1.340033215
ATPase, H+ transporting, lysosomal V1 subunit B2	ATP6V1B2	1.258227452
ATPase, H+ transporting, lysosomal V1 subunit C1	ATP6V1C1	1.268771367
VATPase, H+ transporting, lysosomal V1 subunit E1	ATP6V1E1	1.158300742
expressed sequence AU021838	AU021838	1.414645602
expressed sequence AU040320	AU040320	1.355882473
arginine vasopressin-induced 1	AVPI1	1.367789898
axin 1	AXIN1	0.84286294
beta-2 microglobulin	B2M	1.221703343
beta-1,4-N-acetyl-galactosaminyl transferase 1	B4GALNT1	1.506914819
cDNA sequence BC002230	BC002230	0.736947252
cDNA sequence BC008155	BC008155	1.349167579
cDNA sequence BC018399	BC018399	0.786903963
cDNA sequence BC021381	BC021381	1.345057184
cDNA sequence BC021395	BC021395	0.736807512
cDNA sequence BC025076	BC025076	0.746337092
cDNA sequence BC031353	BC031353	1.530660644
cDNA sequence BC031853	BC031853	1.555926337
cDNA sequence BC064033	BC064033	1.686450246
breast carcinoma amplified sequence 3	BCAS3	1.324281302

Bcl2-like 1	BCL2L1	1.37655088
B-cell leukemia/lymphoma 6	BCL6	0.686689145
B-cell CLL/lymphoma 9-like	BCL9L	1.42232857
3-hydroxybutyrate dehydrogenase, type 2	BDH2	0.784672772
biglycan	BGN	0.589355001
basic helix-loop-helix domain containing, class B9	BHLHB9	0.523402225
bladder cancer associated protein homolog (human)	BLCAP	1.291381782
B-cell linker	BLNK	4.876116465
bromodomain containing 2	BRD2	1.187115404
BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	BRF1	0.781193103
BSD domain containing 1	BSDC1	1.240026645
BTB (POZ) domain containing 6	BTBD6	0.419208249
expressed sequence C77080	C77080	1.406917654
calumenin	CALU	1.197175216
adenylate cyclase-associated protein 1	CAP1	1.234842915
capping protein	CAPG	1.213925771
calpain 2	CAPN2	0.822562934
calpain 5	CAPN5	1.499598591
carbonyl reductase 1	CBR1	1.513825299
coiled-coil domain containing 131	CCDC131	1.22311465
coiled-coil domain containing 56	CCDC56	0.828823614
coiled-coil domain containing 85B	CCDC85B	0.725256201
chemokine (C-C motif) ligand 2	CCL2	0.623794877
chemokine (C-C motif) ligand 7	CCL7	0.443079176
cyclin E1	CCNE1	0.59484264
cyclin G1	CCNG1	0.703344918
CD109 antigen	CD109	1.222392249
CD151 antigen	CD151	1.202009664
CD 81 antigen (Cd81).	CD81	1.233097361
CD9 antigen (Cd9).	CD9	1.339976167
Cd99 antigen-like 2 (Cd99l2).	CD99L2	1.323757298
cytidine deaminase (Cda).	CDA	0.666785884
CDC42 effector protein (Rho GTPase binding)	CDC42EP5	0.644479689
CDC42 small effector 1	CDC42SE1	1.199655071
cell division cycle 7	CDC7	0.777575804
cell division cycle associated 4	CDCA4	0.703248746
cadherin 5, type 2 (vascular endothelium)	CDH5	1.967519083
cyclin-dependent kinase inhibitor 3,	CDKN3	0.775899112
cerebellar degeneration-related protein 2-like	CDR2L	1.411136569
corneodesmosin	CDSN	5.250549138
CEA-related cell adhesion molecule 2	CEACAM2	1.993265085
CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	1.146212771
centrosomal protein 170	CEP170	0.708482326

centrosomal protein 63	CEP63	0.807824418
ChaC, cation transport regulator-like 1	CHAC1	1.511855244
choline kinase beta	CHKB	1.254148188
chromatin modifying protein 4B	CHMP4B	1.400766391
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	0.606760658
CAP-GLY domain containing linker protein 1	CLIP1	0.740051422
claspin homolog (Xenopus laevis)	CLSPN	0.628244045
cornichon homolog 4 (Drosophila)	CNIH4	0.840297133
CCR4-NOT transcription complex, subunit 10	CNOT10	1.28914691
cordon-bleu	COBL	1.613363135
collagen, type XVI, alpha 1	COL16A1	1.296505514
collagen, type I, alpha 1	COL1A1	3.865943564
procollagen, type IV, alpha 1	COL4A1	1.446499613
procollagen, type V, alpha 1	COL5A1	0.755098583
procollagen, type VI, alpha 1	COL6A1	1.239542233
procollagen, type VI, alpha 2	COL6A2	1.365543019
procollagen, type VIII, alpha 1	COL8A1	0.636179649
COMM domain containing 10	COMMD10	1.351139479
catechol-O-methyltransferase	COMT	1.183363578
coatomer protein complex, subunit epsilon	COPE	1.156569774
coatomer protein complex, subunit zeta 2	COPZ2	0.734541184
coenzyme Q6 homolog (yeast)	COQ6	0.731241426
cytochrome c oxidase, subunit VI a, polypeptide 2	COX6A2	1.660502717
cytochrome c oxidase, subunit VIc	COX6C	0.69460059
carboxypeptidase E	CPE	1.275793182
cytokine receptor-like factor 1	CRLF1	1.361013911
crystallin, lambda 1	CRYL1	0.586885011
colony stimulating factor 1	CSF1	0.73704922
chondroitin sulfate N-acetylgalactosaminyltransferase 1	CSGALNACT1	0.739252866
chondroitin sulfate proteoglycan 4	CSPG4	1.379000856
CTAGE family, member 5	CTAGE5	1.482201814
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	CTDSP2	1.288864953
connective tissue growth factor	CTGF	0.511201272
catenin (cadherin associated protein), alpha-like 1	CTNNAL1	0.725995678
catenin beta interacting protein 1	CTNNBIP1	1.250010488
cathepsin A	CTSA	1.345308906
cullin 7	CUL7	0.692727581
chemokine (C-X-C motif) ligand 1	CXCL1	0.466175257
CAAX box 1 homolog A (human)	CXX1A	0.834420077
cytochrome b-5	CYB5	0.836893916
cytochrome b-561	CYB561	1.346211171
cytochrome b5 reductase 3	CYB5R3	1.351425238
cytochrome b5 reductase 3	CYB5R3	1.402163808

cytochrome b-245, alpha polypeptide	CYBA	0.481630533
cytochrome P450, family 26, subfamily b, polypeptide 1	CYP26B1	0.75045743
cytochrome P450, family 51	CYP51	2.211898087
cytochrome P450, family 51	CYP51	1.870900329
cysteine rich protein 61	CYR61	0.543137352
D0KIST3	D0KIST3	1.633869386
dishevelled associated activator of morphogenesis 1	DAAM1	0.661582012
aspartyl-tRNA synthetase	DARS	0.783792489
DBF4 homolog (S. cerevisiae)	DBF4	1.422613198
dysbindin (dystrobrevin binding protein 1) domain containing 2	DBNDD2	1.394143451
decorin	DCN	0.511881501
dCMP deaminase	DCTD	0.643338339
dynactin 1	DCTN1	1.339681465
dynactin 2	DCTN2	1.263121785
damage specific DNA binding protein 1	DDB1	1.207867908
DNA-damage inducible transcript 3	DDIT3	1.799001445
DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	DDX24	0.559168279
DEAD (Asp-Glu-Ala-Asp) box polypeptide 26	DDX26	0.781456591
DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	DDX49	1.384887432
DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	DDX6	0.683546445
24-dehydrocholesterol reductase	DHCR24	1.835623581
7-dehydrocholesterol reductase	DHCR7	1.445059645
diablo homolog (Drosophila)	DIABLO	1.357751022
diaphanous homolog 3 (Drosophila)	DIAP3	0.804907104
Dicer1, Dcr-1 homolog (Drosophila)	DICER1	0.655551798
dihydrolipoamide dehydrogenase	DLD	1.214510765
delta-like 1 homolog (Drosophila)	DLK1	0.21174513
dynein, axonemal, heavy chain 11	DNAHC11	0.629897245
dynein, cytoplasmic 1, intermediate chain 2	DNCIC2	0.665752433
dynamin 3, opposite strand (Dnm3os) on chromosome 1	DNM3OS	0.661790045
developmental pluripotency associated 4	DPPA4	1.233537144
dihydropyrimidinase-like 2	DPYSL2	1.150764755
dihydropyrimidinase-like 3	DPYSL3	0.82671628
dystrobrevin alpha	DTNA	0.733374649
deoxythymidylate kinase (thymidylate kinase)	DTYMK	0.71344006
dual specificity phosphatase 1	DUSP1	0.670364654
dynein, cytoplasmic 1 light intermediate chain 2	DYNC1LI2	1.255783558
endothelin converting enzyme 1	ECE1	1.405478256
enoyl Coenzyme A hydratase, short chain, 1	ECHS1	1.385574283
endothelin 1	EDN1	0.597387428
epidermal growth factor-containing fibulin-like extracellular matrix protein 2	EFEMP2	0.346011254
ephrin A1	EFNA1	1.380879182
predicted gene, EG433229, transcript variant 7	EG433229	0.624905601

predicted gene, EG433865	EG433865	1.486097951
predicted gene, EG545886	EG545886	1.245227477
predicted gene, EG633640	EG633640	0.663906133
predicted gene, EG667728	EG667728	0.740672031
predicted gene, EG667728	EG667728	0.739009081
EH domain binding protein 1-like 1	EHBP1L1	1.386437302
EH-domain containing 1	EHD1	1.491406291
eukaryotic translation initiation factor 1B	EIF1B	0.822817135
eukaryotic translation initiation factor 2B, subunit 3 gamma	EIF2B3	0.84502896
ELK3, member of ETS oncogene family	ELK3	0.787319091
elongation of very long chain fatty acids like 1	ELOVL1	1.392565993
ELOVL family member 5, elongation of long chain fatty acids	ELOVL5	1.262388211
ELOVL family member 6, elongation of long chain fatty acids	ELOVL6	1.31832487
EMG1 nucleolar protein homolog (S. cerevisiae)	EMG1	0.811319922
echinoderm microtubule associated protein like 1	EML1	0.613099743
epithelial membrane protein 2	EMP2	1.416890003
ectodermal-neural cortex 1	ENC1	0.614380648
enolase 2, gamma neuronal	ENO2	0.287685496
enolase 3, beta muscle	ENO3	0.621199304
ectonucleoside triphosphate diphosphohydrolase 7	ENTPD7	1.307362506
ERGIC and golgi 3	ERGIC3	1.47757402
ERBB receptor feedback inhibitor 1	ERRFI1	0.716295429
electron transferring flavoprotein, beta polypeptide	ETFB	0.829924288
ets variant gene 4 (E1A enhancer binding protein, E1AF)	ETV4	1.362444779
enhancer of zeste homolog 2 (Drosophila)	EZH2	0.763722294
fatty acid desaturase 2	FADS2	1.296837329
fatty acid desaturase 3	FADS3	1.355009619
fumarylacetoacetate hydrolase	FAH	0.809745979
FERM, RhoGEF and pleckstrin domain protein 2	FARP2	0.685696281
phenylalanine-tRNA synthetase 2 (mitochondrial)	FARS2	1.264051908
F-box and WD-40 domain protein 9	FBXW9	1.374866324
farnesyl diphosphate synthetase	FDPS	1.424903645
fasciculation and elongation protein zeta 1	FEZ1	0.81378431
fibroblast growth factor receptor 2	FGFR2	0.521029275
four and a half LIM domains 2	FHL2	0.720879944
four and a half LIM domains 3	FHL3	1.610120703
FK506 binding protein 10	FKBP10	1.241411496
FK506 binding protein 11	FKBP11	0.669277188
filamin, alpha	FLNA	1.298737046
filamin, beta	FLNB	0.731529521
fibronectin leucine rich transmembrane protein 2	FLRT2	0.63831018
FMS-like tyrosine kinase 1	FLT1	1.807229851
fibronectin 1	FN1	0.741631868

FERM domain containing 6	FRMD6	0.581352984
fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	FSCN1	1.584286723
follistatin-like 1	FSTL1	0.708242451
fat mass and obesity associated	FTO	0.661560551
FXYD domain-containing ion transport regulator 5	FXYD5	1.239627161
frizzled homolog 7 (Drosophila)	FZD7	1.300936685
glucose-6-phosphate dehydrogenase X-linked	G6PDX	1.280389471
gamma-aminobutyric acid receptor-associated protein-like 1	GABARAPL1	1.204749624
growth arrest and DNA-damage-inducible 45 alpha	GADD45A	1.834664878
cyclin G associated kinase	GAK	1.375219321
phosphoribosylglycinamide formyltransferase	GART	0.621293275
GATA zinc finger domain containing 1	GATAD1	1.247479254
glutamate-cysteine ligase, modifier subunit	GCLM	1.326026896
glycerophosphodiester phosphodiesterase domain containing 1	GDPD1	1.532476702
gem (nuclear organelle) associated protein 4	GEMIN4	0.806885013
gap junction membrane channel protein alpha 1	GJA1	0.659878659
gastrokine 1	GKN1	1.97366804
glucuronyl C5-epimerase	GLCE	1.518072205
glutaredoxin 5 homolog (S. cerevisiae)	GLRX5	0.653164345
glycolipid transfer protein	GLTP	1.241084669
gene model 773	GM773	0.179954814
guanine nucleotide binding protein (G protein), alpha inhibiting 2	GNAI2	1.269350909
glucosamine-6-phosphate deaminase 2	GNPDA2	0.649430724
golgi integral membrane protein 4	GOLIM4	1.260382507
golgi membrane protein 1	GOLM1	1.227134382
glycoprotein Ib, beta polypeptide	GP1BB	1.439395159
glypican 1	GPC1	1.282160041
glycoprotein (transmembrane) nmb	GPNMB	1.231130473
G protein-coupled receptor 149	GPR149	0.66768735
glycoprotein, synaptic 2	GPSN2	1.614589645
glutamic pyruvate transaminase 2	GPT2	1.694800733
glutathione peroxidase 1	GPX1	1.503607719
granulin	GRN	1.536576456
germ cell-specific gene 2	GSG2	0.775712338
G1 to S phase transition 1	GSPT1	0.830955972
glutathione S-transferase, mu 2	GSTM2	0.346728724
glutathione S-transferase, theta 3	GSTT3	0.329945005
general transcription factor II I	GTF2I	0.684880944
GTP binding protein 2	GTPBP2	1.689797881
H2-K region expressed gene 6	H2-KE6	0.704878543
histocompatibility 2, T region locus 18	H2-T18	1.26175273
histocompatibility 60a	H60A	0.714067563
hydroxyacyl glutathione hydrolase	HAGH	1.660513532

hyaluronan synthase 2	HAS2	0.665672981
hemoglobin Z, beta-like embryonic chain	HBB-BH1	1.714333687
HMG-box transcription factor 1	HBP1	1.700393865
histone deacetylase 5	HDAC5	1.882436696
hairy and enhancer of split 6	HES6	1.319440439
huntingtin interacting protein 1	HIP1	1.359968271
huntingtin interacting protein 1 related	HIP1R	1.306329418
HIRA interacting protein 3	HIRIP3	0.776175466
histone cluster 1, H2ad	HIST1H2AD	0.61411162
histone cluster 1, H2ae	HIST1H2AE	0.774164999
histone cluster 1, H2af	HIST1H2AF	0.555190635
histone cluster 1, H2ah	HIST1H2AH	0.498760914
histone cluster 1, H2ai	HIST1H2AI	0.647549554
histone cluster 1, H2ak	HIST1H2AK	0.542630049
histone cluster 1, H2an	HIST1H2AN	0.535316629
histone cluster 2, H2aa2	HIST2H2AA2	0.568323149
histone cluster 2, H2ac	HIST2H2AC	0.630053532
heme oxygenase (decycling) 1	HMOX1	0.583778097
hydroxysteroid (17-beta) dehydrogenase 7	HSD17B7	1.508292279
heat shock protein 90, alpha (cytosolic), class A member 1	HSP90AA1	0.509805865
heat shock protein 2	HSPA2	0.767093906
heat shock protein 1	HSPD1	0.766229945
perlecan (heparan sulfate proteoglycan 2)	HSPG2	1.233203449
HtrA serine peptidase 2	HTRA2	0.626394771
HtrA serine peptidase 3	HTRA3	1.747448977
hyaluronoglucosaminidase 2	HYAL2	0.806840403
isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	1.488401693
interferon induced transmembrane protein 3	IFITM3	0.671455329
insulin-like growth factor binding protein 4	IGFBP4	1.497180877
insulin-like growth factor binding protein 6	IGFBP6	1.151003742
interleukin 11 receptor, alpha chain 1	IL11RA1	0.826389622
interleukin 1 receptor-like 1	IL1RL1	0.743319981
ilvB (bacterial acetolactate synthase)-like	ILVBL	1.254094
IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	IMP4	0.808918665
insulin induced gene 1	INSIG1	1.444487417
insulin receptor substrate 1	IRS1	0.63606939
integrin alpha 3	ITGA3	2.141473752
integrin beta 1 binding protein 1	ITGB1BP1	1.334651712
integrin, beta-like 1	ITGBL1	1.448317974
inositol 1,4,5-triphosphate receptor 3	ITPR3	1.477547396
intersectin 2	ITSN2	1.401220148
influenza virus NS1A binding protein	IVNS1ABP	0.760325649
Jun dimerization protein 2	JDP2	0.711696682

jumonji domain containing 2A	JMJD2A	1.615994893
Jun oncogene	JUN	0.642981542
KN motif and ankyrin repeat domains 1	KANK1	1.39338367
potassium voltage-gated channel, shaker-related subfamily, beta member 2	KCNAB2	1.315470027
potassium channel, subfamily K, member 2	KCNK2	0.679305545
potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	KCNN4	1.359611002
potassium channel tetramerisation domain containing 15	KCTD15	1.32781674
KH domain containing, RNA binding, signal transduction associated 1	KHDRBS1	0.791219927
kinesin family member 3C	KIF3C	1.483531925
kinesin light chain 1	KLC1	0.611203694
Kruppel-like factor 13	KLF13	1.278414804
Kruppel-like factor 6	KLF6	0.768274951
kelch domain containing 3	KLHDC3	1.521999636
keratinocyte expressed, proline-rich	KPRP	0.346292766
keratin 13	KRT13	2.632711885
keratin 14	KRT14	1.411234735
laminin, gamma 1	LAMC1	1.174499884
lysosomal-associated membrane protein 1	LAMP1	1.222930506
Lblc1	LBCL1	2.079031169
limb-bud and heart	LBH	1.613622373
low density lipoprotein receptor adaptor protein 1	LDLRAP1	1.316534403
LIM domain and actin binding 1	LIMA1	0.696582251
LIM-domain containing, protein kinase	LIMK1	1.230617896
LIM and senescent cell antigen like domains 2	LIMS2	2.197172981
centromere protein J	LIP1	0.443866181
LPS-induced TN factor	LITAF	1.312856146
hypothetical protein	LOC100038894	1.670473567
similar to SP140 nuclear body protein family member	LOC100039742	0.488036071
similar to reproductive homeobox on X chromosome 2	LOC100040016	0.110794322
similar to Hmgcs1 protein	LOC100040592	1.618352494
similar to KIAA2019 protein	LOC100041194	0.286871964
similar to Translocase of inner mitochondrial membrane 23 homolog (yeast)	LOC100041219	0.839392276
Mus musculus similar to LSM7 homolog, U6 small nuclear RNA associated	LOC100041500	0.847827464
hypothetical protein	LOC100041725	1.337689077
similar to Inosine 5-phosphate dehydrogenase 2	LOC100042069	0.793868715
similar to transmembrane emp24 domain-containing protein 10	LOC100042773	0.581777015
similar to RNA binding motif protein 3	LOC100043257	1.193256277
hypothetical protein LOC100043821	LOC100043821	1.255391351
similar to thioredoxin reductase 2	LOC100044101	0.750505725
hypothetical protein	LOC100044194	0.827485842
similar to euchromatic histone methyltransferase 1	LOC100044324	1.18245652
similar to ribosomal protein L36a	LOC100044425	0.806145665
similar to cyclin N-terminal domain containing 1	LOC100044557	1.187671381

similar to WW domain-containing adapter protein with coiled-coil	LOC100044766	0.719455937
similar to Fibrillarin	LOC100044829	0.776705834
similar to mKIAA1021 protein	LOC100045280	1.195547922
similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1	LOC100045542	1.552756197
similar to purine nucleoside phosphorylase	LOC100045567	1.287850262
similar to synaptotagmin XI	LOC100045981	0.631134504
similar to tripartite motif-containing 41	LOC100046003	1.163226581
similar to histone deacetylase HD1	LOC100046039	1.225667348
similar to OTU domain, ubiquitin aldehyde binding 1	LOC100046081	1.250905615
similar to IKK interacting protein	LOC100046322	0.683460596
similar to aquaporin 5	LOC100046616	1.362172944
similar to Rab6 interacting protein 1	LOC100046953	1.18353463
similar to BCL2-associated athanogene 5	LOC100047042	0.777476565
similar to Small nuclear ribonucleoprotein polypeptide A	LOC100047155	0.751715519
similar to proteasome alpha7/C8 subunit	LOC100047184	0.689388511
hypothetical protein	LOC100047226	1.264174992
similar to spermidine/spermine N1-acetyltransferase	LOC100047261	1.478544106
similar to solute carrier family 7	LOC100047619	1.525709232
hypothetical protein	LOC100047707	1.56855797
similar to Aspartate aminotransferase, cytoplasmic	LOC100047762	1.473513685
similar to Memo1 protein	LOC100047915	0.78563582
similar to ADIR1	LOC100047963	1.375915761
similar to Leucine zipper, putative tumor suppressor 2	LOC100048460	1.227508273
similar to four and a half LIM domains 3	LOC100048796	1.625676417
LOC195286	LOC195286	0.476260263
LOC215098	LOC215098	0.762251594
LOC219049	LOC219049	0.754832478
LOC226017	LOC226017	0.63468471
LOC239727	LOC239727	0.632579
LOC280205	LOC280205	0.800058159
LOC380906	LOC380906	0.704335587
LOC381215	LOC381215	0.800193248
LOC381999	LOC381999	0.8527572
LOC383125	LOC383125	0.686604983
similar to 60S acidic ribosomal protein P0	LOC384710	0.777872224
LOC384710	LOC385615	1.761958704
LOC386135	LOC386135	0.514767162
similar to heterogeneous nuclear ribonucleoprotein A3	LOC621612	0.713194966
similar to ZH10 protein	LOC622491	0.635011804
hypothetical protein	LOC622994	0.85186933
similar to Pyruvate kinase, muscle	LOC631301	1.4383849
similar to ribosomal protein L27a-like	LOC635470	0.784977002
similar to mevalonate kinase	LOC637711	1.5039768

similar to cyclin-dependent kinase 2-interacting protein	LOC640972	0.639953453
similar to cytochrome c	LOC670717	0.75130695
similar to Glutathione S-transferase Mu 2 (GST class-mu 2)	LOC670888	0.390701901
similar to spermine synthase	LOC671878	0.682553439
hypothetical protein	LOC673501	0.556829446
similar to downregulated in ovarian cancer 1 isoform 2	LOC676704	0.650215322
similar to Glucose phosphate isomerase 1	LOC676974	1.274781233
similar to putative protein phosphatase 1 nuclear targeting subunit	LOC677319	0.635933032
lon peptidase 1, mitochondrial	LONP1	1.301555609
lysyl oxidase	LOX	0.690530844
lysyl oxidase-like 1	LOXL1	0.764541794
lysyl oxidase-like 4	LOXL4	0.284584034
lipin 1	LPIN1	1.449745258
LIM domain containing preferred translocation partner in lipoma	LPP	0.763598137
low density lipoprotein receptor-related protein 11	LRP11	1.229556332
leucine rich repeat containing 59	LRRC59	1.377996358
LSM12 homolog (S. cerevisiae)	LSM12	0.79362567
LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM2	1.246244663
LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM6	0.845651728
lanosterol synthase	LSS	1.501851203
latent transforming growth factor beta binding protein 2	LTBP2	0.633833506
latexin	LXN	1.514939958
lymphocyte antigen 6 complex, locus C1	LY6C1	1.356238816
Ly1 antibody reactive clone	LYAR	0.668675367
LYR motif containing 2	LYRM2	0.767070492
melanoma antigen, family D, 1	MAGED1	1.235162049
microtubule-associated protein 1 light chain 3 alpha	MAP1LC3A	1.484785784
mitogen activated protein kinase kinase 3	MAP2K3	1.208839177
mitogen-activated protein kinase kinase kinase 11	MAP3K11	1.257269286
mitogen-activated protein kinase kinase kinase 3	MAP3K3	1.181310712
mitogen-activated protein kinase kinase kinase 8	MAP3K8	1.460241843
mitogen-activated protein kinase kinase kinase 2	MAP4K2	1.300952465
mitogen-activated protein kinase 1	MAPK1	1.266621935
myristoylated alanine rich protein kinase C substrate	MARCKS	0.768863854
microtubule associated serine/threonine kinase family member 4	MAST4	0.8316974
membrane bound C2 domain containing protein	MBC2	1.224907085
methylmalonyl CoA epimerase	MCEE	0.804734307
malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2	1.306015297
mediator complex subunit 16	MED16	0.664772613
mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	MED6	0.671009861
myocyte enhancer factor 2C	MEF2C	1.922007734
milk fat globule-EGF factor 8 protein	MFGE8	1.548532522
mannoside acetylglucosaminyltransferase 4, isoenzyme B	MGAT4B	1.400812767

mindbomb homolog 2 (Drosophila)	MIB2	1.249533796
midline 2	MID2	1.389779829
MAP kinase-interacting serine/threonine kinase 1	MKNK1	1.351534893
matrix metallopeptidase 24	MMP24	0.721823792
meiotic recombination 11 homolog A (S. cerevisiae)	MRE11A	0.72767336
mitochondrial ribosomal protein L38	MRPL38	1.185784141
mitochondrial ribosomal protein L4	MRPL4	1.240209146
mitochondrial ribosomal protein L43	MRPL43	1.194304642
mitochondrial ribosomal protein L51	MRPL51	0.853173848
mitochondrial ribosomal protein S16	MRPS16	0.782990217
mitochondrial ribosomal protein S6	MRPS6	0.772821175
mitochondrial ribosomal protein S9	MRPS9	0.825852723
mutS homolog 6 (E. coli)	MSH6	0.694646616
metastasis-associated gene family, member 2	MTA2	1.182521057
microtubule-associated protein 7 domain containing 1	MTAP7D1	1.225591241
mitochondrial carrier homolog 1 (C. elegans)	MTCH1	1.191974318
mitochondrially encoded NADH dehydrogenase 5	MT-ND5	1.811156025
mammary tumor virus receptor 2	MTVR2	1.210248282
musculoskeletal, embryonic nuclear protein 1	MUSTN1	0.740971809
mevalonate (diphospho) decarboxylase	MVD	1.602075273
mevalonate kinase	MVK	1.656174581
matrix-remodelling associated 8	MXRA8	1.259624562
myeloid-associated differentiation marker	MYADM	1.302177933
myosin XVIIIb	MYO18B	1.957801517
myosin Ixb	MYO9B	1.171040126
myosin IXb	MYO9B	1.174843669
N-6 adenine-specific DNA methyltransferase 1 (putative)	N6AMT1	0.762093628
Ngfi-A binding protein 1	NAB1	1.238031235
nucleosome assembly protein 1-like 1	NAP1L1	0.738467591
nuclear autoantigenic sperm protein (histone-binding)	NASP	0.720328321
neurochondrin	NCDN	1.414199767
N-myc downstream regulated gene 1	NDRG1	1.405912596
NADH dehydrogenase (ubiquinone) flavoprotein 1	NDUFV1	1.233961326
neogenin	NEO1	2.243452254
NeoR	NEOR	0.45136864
nuclear factor, erythroid derived 2,-like 1	NFE2L1	1.651193857
neuronal guanine nucleotide exchange factor	NGEF	3.826907249
nerve growth factor, beta	NGFB	0.598700874
nerve growth factor receptor (TNFRSF16) associated protein 1	NGFRAP1	0.843646873
NHL repeat containing 2	NHLRC2	1.255206221
niban protein	NIBAN	1.652423252
ninjurin 1	NINJ1	1.593606947
NFKB inhibitor interacting Ras-like protein 2	NKIRAS2	1.349787368

non-metastatic cells 4, protein expressed in	NME4	0.735542576
nicotinamide N-methyltransferase	NNMT	0.53329963
nucleolar protein 5A	NOL5A	0.764509368
nucleolar protein family A, member 2	NOLA2	0.849126811
nodal modulator 1	NOMO1	1.20907727
nephronophthisis 1 (juvenile) homolog (human)	NPHP1	0.590437553
nucleoplasmin 3, pseudogene 1	NPM3-PS1	1.216408721
natriuretic peptide precursor type B	NPPB	0.783937184
NAD(P)H dehydrogenase, quinone 2 (Nqo2).	NQO2	1.335825811
nuclear receptor subfamily 2, group F, member 2	NR2F2	0.650250922
nuclear receptor subfamily 2, group F, member 6	NR2F6	1.225071212
neuritin 1	NRN1	1.233346895
NAD(P) dependent steroid dehydrogenase-like	NSDHL	1.238471887
5'-nucleotidase, cytosolic III-like	NT5C3L	0.804002712
5'-nucleotidase domain containing 2	NT5DC2	0.726116226
5'-nucleotidase domain containing 3	NT5DC3	0.802829464
negative regulator of ubiquitin-like proteins 1	NUB1	1.297859703
nuclear distribution gene C homolog (Aspergillus)	NUDC	0.792888405
nudix (nucleoside diphosphate linked moiety X)-type motif 1	NUDT1	0.739830205
nudix (nucleoside diphosphate linked moiety X)-type motif 22	NUDT22	1.258769864
nudix (nucleoside diphosphate linked moiety X)-type motif 5	NUDT5	0.833282791
nuclear protein 1	NUPR1	1.289924273
odd Oz/ten-m homolog 4 (Drosophila)	ODZ4	0.750584159
olfactomedin-like 3	OLFML3	1.321228901
ORAI calcium release-activated calcium modulator 1	ORAI1	1.687211928
ORM1-like 3	ORMDL3	1.472853693
odd-skipped related 1	OSR1	0.561060194
OTU domain containing 1	OTUD1	0.625263013
purinergic receptor P2Y, G-protein coupled 2	P2RY2	1.324202439
prolyl 4-hydroxylase, alpha polypeptide II	P4HA2	1.310336113
prolyl 4-hydroxylase, beta polypeptide	P4HB	1.192562173
phosphofurin acidic cluster sorting protein 2	PACS2	0.761470722
protein kinase C and casein kinase substrate in neurons 3	PACSIN3	1.222946897
poly (A) polymerase alpha	PAPOLA	0.575049106
3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	0.585380401
poly (ADP-ribose) polymerase family, member 3	PARP3	0.818630439
poly(rC) binding protein 2	PCBP2	1.158130873
protocadherin 1	PCDH1	1.174991213
polycomb group ring finger 6	PCGF6	0.740321418
Purkinje cell protein 2	PCP2	0.759346824
phosphate cytidylyltransferase 2, ethanolamine	PCYT2	1.2048178
platelet derived growth factor receptor, alpha polypeptide	PDGFRA	0.693109645
platelet-derived growth factor receptor-like	PDGFRL	1.340598981

PDZ and LIM domain 1	PDLIM1	1.1549359
PDZ and LIM domain 2	PDLIM2	0.642272911
PDZ domain containing 11	PDZD11	0.832624285
peroxisome biogenesis factor 19	PEX19	1.261539756
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	PFKFB4	1.399266441
phosphofructokinase, platelet	PFKP	1.278014724
profilin 2	PFN2	0.742538027
PHD finger protein 10	PHF10	1.246208098
phosphoinositide-3-kinase interacting protein 1	PIK3IP1	1.747774167
phosphatidylinositol-5-phosphate 4-kinase, type II, beta	PIP4K2B	1.176431835
praja 2, RING-H2 motif containing	PJA2	0.82821467
phospholipase A2, activating protein	PLAA	0.753334387
plasminogen activator, tissue	PLAT	1.442542493
phospholipase C, delta 1	PLCD1	1.497950261
pleckstrin homology domain containing, family M (with RUN domain) member 1	PLEKHM1	1.408811165
pleckstrin homology domain containing, family O member 1	PLEKHO1	1.47986083
proteolipid protein (myelin) 1	PLP1	1.916119137
phosphomevalonate kinase	PMVK	1.283183018
patatin-like phospholipase domain containing 2	PNPLA2	1.372878085
podocan-like 1	PODNL1	0.602335331
polymerase (DNA directed), alpha 2	POLA2	1.525438022
polymerase (DNA-directed), delta interacting protein 3	POLDIP3	0.833711028
paraoxonase 2	PON2	1.678253857
phosphatidic acid phosphatase type 2B	PPAP2B	0.574059267
protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2	PPFIBP2	1.516729206
protein phosphatase 1A, magnesium dependent, alpha isoform	PPM1A	0.725920305
protein phosphatase 1, catalytic subunit, alpha isoform	PPP1CA	1.238270439
protein phosphatase 2, regulatory subunit B (B56), beta isoform	PPP2R5B	1.6168081
protein phosphatase 2, regulatory subunit B (B56), gamma isoform	PPP2R5C	0.6442581
protein phosphatase 2, regulatory subunit B (B56), delta isoform	PPP2R5D	1.17963427
putative phosphatase	PPS	1.434201636
proline arginine-rich end leucine-rich repeat	PRELP	0.674879887
protein kinase, cAMP dependent, catalytic, beta	PRKACB	0.800807359
protein kinase C substrate 80K-H	PRKCSH	1.194891288
protein kinase, cGMP-dependent, type II	PRKG2	1.376165355
Prkr interacting protein 1 (IL11 inducible)	PRKRIP1	1.331649266
protein kinase, X-linked	PRKX	1.392950171
protein arginine N-methyltransferase 1	PRMT1	0.82503046
protein arginine N-methyltransferase 6	PRMT6	0.726383847
prion protein	PRNP	1.388609984
proline rich 14	PRR14	1.178472707
presenilin 1	PSEN1	0.72229389
proteasome (prosome, macropain) subunit, beta type 10	PSMB10	0.7363058

proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	PSMD2	0.735456349
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	PSMD7	0.804621868
proteasome (prosome, macropain) 28 subunit, alpha	PSME1	0.742895082
polypyrimidine tract binding protein 1	PTBP1	0.759565871
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	PTPLA	1.310888519
protein tyrosine phosphatase, non-receptor type 21	PTPN21	0.68531007
pentraxin related gene	PTX3	0.674971817
pumilio 2	PUM2	1.30122089
quinoid dihydropteridine reductase	QDPR	1.291169205
RAB11 family interacting protein 5 (class I)	RAB11FIP5	1.232370806
RAB3 GTPase activating protein subunit 1	RAB3GAP1	0.830861246
RAB3 GTPase activating protein subunit 2	RAB3GAP2	1.187666085
RAS-related C3 botulinum substrate 1	RAC1	1.364959091
RAD51-like 1	RAD51L1	0.667794348
hnRNP-associated with lethal yellow	RALY	1.255571477
RAN guanine nucleotide release factor	RANGNRF	0.745027827
RAN guanine nucleotide release factor	RANGRF	0.847648343
RAS related protein 2a	RAP2A	1.399195843
retinoblastoma binding protein 4	RBBP4	1.643711889
RNA binding motif protein 4	RBM4	1.255916546
retinol binding protein 1, cellular	RBP1	1.720072637
regulator of calcineurin 1	RCAN1	1.378348785
RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	RCE1	1.266042087
REST corepressor 1	RCOR1	0.51154413
retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	RDH11	0.818225479
radixin	RDX	0.671819363
receptor accessory protein 4	REEP4	1.452624825
receptor accessory protein 5	REEP5	1.272722777
replication factor C (activator 1) 4	RFC4	0.728105628
RGM domain family, member A	RGMA	0.690834775
regulator of G-protein signaling 16	RGS16	1.340088336
regulator of G-protein signaling 3	RGS3	1.509914296
rhomboid family 1	RHBDF1	1.233489724
Rho-related BTB domain containing 3	RHOBTB3	0.680330757
ras homolog gene family, member D	RHOD	1.198758114
ras homolog gene family, member J	RHOJ	0.759227335
18S RNA	RN18S	0.533320699
ring finger protein 166	RNF166	1.341011561
ring finger protein 167	RNF167	1.315683058
ring finger protein 181	RNF181	1.259436307
similar to histone 2a	RP23-480B19.1	0.564000963
Ribosomal protein L18A	RPL18A	0.752273483
ribosomal protein L30	RPL30	0.743776082

ribosomal protein S19	RPS19	0.763041959
Ras-related GTP binding C	RRAGC	1.285361056
ribosomal RNA processing 1 homolog B (S. cerevisiae)	RRP1B	0.784449056
radial spokehead-like 2A	RSHL2A	0.775614581
RuvB-like protein 1	RUVBL1	0.790716361
retinoid X receptor beta	RXRB	1.215026129
S100 calcium binding protein A3	S100A3	1.575342206
S100 calcium binding protein A7A	S100A7A	0.397807699
plasma membrane associated protein, S3-12	S3-12	1.531224909
sterile alpha motif domain containing 14	SAMD14	1.257108092
SAR1 gene homolog A (S. cerevisiae)	SAR1A	1.309773917
salvador homolog 1 (Drosophila)	SAV1	0.70260065
Shwachman-Bodian-Diamond syndrome homolog (human)	SBDS	1.207390512
SH3-binding kinase 1	SBK1	0.721267807
sterol-C4-methyl oxidase-like	SC4MOL	1.48450073
SR-related CTD-associated factor 1	SCAF1	1.294663423
scavenger receptor class B, member 1	SCARB1	1.3065101
stearoyl-Coenzyme A desaturase 1	SCD1	1.611310023
stearoyl-Coenzyme A desaturase 2	SCD2	1.432758454
SCL0001118.1_0	SCL0001118.1_(	0.701794784
SCL0001849.1_2273	SCL0001849.1_	0.46044733
SCL0002368.1_75	SCL0002368.1_	0.749601591
SCL0015365.1_6	SCL0015365.1_	0.744464442
scotin gene	SCOTIN	1.265638343
sterol carrier protein 2, liver	SCP2	1.322385943
syndecan 3	SDC3	0.414233793
stromal cell derived factor 2	SDF2	1.199385844
serum deprivation response	SDPR	0.536308924
SEC23A	SEC23A	1.409968941
SEC63-like (	SEC63	0.81189794
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEMA3F	1.708875319
SUMO1/sentrin specific peptidase 1	SENP1	0.694007826
SUMO/sentrin specific peptidase 3	SENP3	1.178031541
selenoprotein N, 1	SEPN1	1.23000849
septin 8	SEPT8	1.173685695
selenoprotein W, muscle 1	SEPW1	1.680240487
serine (or cysteine) preptidase inhibitor, clade A, member 1b	SERPINA1B	0.476795522
serine (or cysteine) peptidase inhibitor, clade A, member 1d	SERPINA1D	0.425759286
serine (or cysteine) peptidase inhibitor, clade B, member 6a	SERPINB6A	1.203654842
SEC14 and spectrin domains 1	SESTD1	1.271595505
splicing factor, arginine/serine-rich 5	SFRS5	0.66628071
sideroflexin 1	SFXN1	0.789629222
sideroflexin 3	SFXN3	1.332046466

sphingomyelin synthase 1	SGMS1	0.725621329
SH2 domain containing 6	SH2D6	1.889984598
SH3-domain GRB2-like 3	SH3GL3	0.774677398
serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	1.261745086
SIAT5	SIAT5	0.795597354
silica-induced gene 111	SILG111	1.350394337
signal-induced proliferation-associated 1 like 1	SIPA1L1	0.603524287
SIVA1, apoptosis-inducing factor	SIVA1	0.653164805
S-phase kinase-associated protein 2 (p45)	SKP2	0.708713604
solute carrier family 12, member 6	SLC12A6	1.294292453
solute carrier family 19 (thiamine transporter), member 2	SLC19A2	0.797565724
solute carrier family 1 (neutral amino acid transporter), member 5	SLC1A5	1.387478952
solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	SLC24A6	1.350861113
solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	SLC25A19	1.399493284
solute carrier family 25, member 28	SLC25A28	1.246623666
solute carrier family 25, member 33	SLC25A33	1.82869726
solute carrier family 25, member 39	SLC25A39	1.325637727
solute carrier family 27 (fatty acid transporter), member 1	SLC27A1	1.489840766
solute carrier family 29 (nucleoside transporters), member 1	SLC29A1	1.198780961
solute carrier family 31, member 1 (Slc31a1).	SLC31A1	1.424095138
solute carrier family 38, member 2	SLC38A2	1.235684342
solute carrier family 39 (metal ion transporter), member 11	SLC39A11	1.218702627
solute carrier family 44, member 1	SLC44A1	1.469175131
solute carrier family 4 (anion exchanger), member 2	SLC4A2	1.201382118
solute carrier family 6, member 6	SLC6A6	1.475712824
solute carrier family 6 (neurotransmitter transporter, glycine), member 9	SLC6A9	2.446745004
solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	SLC7A11	1.747569164
solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	SLC9A3R1	1.396262447
slowmo homolog 2 (Drosophila)	SLMO2	0.817131297
secreted Ly6/Plaur domain containing 1	SLURP1	1.382727641
SPARC related modular calcium binding 1	SMOC1	1.513352801
synaptosomal-associated protein 29	SNAP29	0.706838963
small nuclear RNA activating complex, polypeptide 4	SNAPC4	1.29770179
SNW domain containing 1	SNW1	0.711869363
sorting nexin 10	SNX10	1.17780956
sorting nexin 7	SNX7	0.781232724
sterol O-acyltransferase 1	SOAT1	0.76879338
sorbitol dehydrogenase	SORD	1.258403672
SRY (sex determining region Y)-box 9	SOX9	0.814849261
sperm flagellar 1	SPEF1	1.39243009
spectrin beta 2	SPNB2	1.249640034
secreted phosphoprotein 1	SPP1	0.501259662
squalene epoxidase	SQLE	1.548890122

sequestosome 1	SQSTM1	1.35044552
scavenger receptor class B, member 1	SRB1	1.473409909
sterol regulatory element binding factor 2	SREBF2	1.430614375
spermidine synthase	SRM	0.702585017
sushi-repeat-containing protein, X-linked 2	SRPX2	0.7344173
sulfiredoxin 1 homolog (S. cerevisiae)	SRXN1	0.773731455
single-stranded DNA binding protein 3	SSBP3	1.271315283
signal sequence receptor, delta	SSR4	0.835389794
Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	SSSCA1	0.671124805
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	ST3GAL5	1.297051714
StAR-related lipid transfer (START) domain containing 4	STARD4	1.645457869
StAR-related lipid transfer (START) domain containing 5	STARD5	1.437056972
stomatin	STOM	2.047746754
SMT3 suppressor of mif two 3 homolog 3 (yeast)	SUMO3	1.688956281
sulfite oxidase	SUOX	1.60460555
suppressor of Ty 3 homolog (S. cerevisiae)	SUPT3H	0.787750602
synapsin I	SYN1	1.500815282
synaptojanin 2 binding protein	SYNJ2BP	0.671414413
synaptopodin	SYNPO	0.663328186
synaptophysin-like protein	SYPL	1.23808071
synovial apoptosis inhibitor 1	SYVN1	1.469787237
transcription factor 19	TCF19	0.757513414
transcription factor 25 (basic helix-loop-helix)	TCF25	1.326405991
t-complex protein 1	TCP1	0.757324316
Tctex1 domain containing 2	TCTEX1D2	0.754677945
tudor and KH domain containing protein	TDRKH	0.681178225
transferrin receptor	TFRC	1.219194448
TDP-glucose 4,6-dehydratase	TGDS	1.30321036
transforming growth factor, beta 3	TGFB3	1.278668387
transforming growth factor, beta induced	TGFBI	1.723554081
thymus cell antigen 1, theta	THY1	0.583009401
translocase of inner mitochondrial membrane 9 homolog (yeast)	TIMM9	0.740262222
tissue inhibitor of metalloproteinase 3	TIMP3	1.465900912
tubulointerstitial nephritis antigen-like	TINAGL	2.755111161
thymidine kinase 1	TK1	0.561375869
transmembrane channel-like gene family 6	TMC6	1.62816742
transmembrane protein 106C	TMEM106C	0.63849663
transmembrane protein 111	TMEM111	1.201370322
transmembrane protein 43	TMEM43	1.362532702
transmembrane protein 9	TMEM9	1.173820599
thymopoietin	TMPO	0.716641738
thymosin, beta 10	TMSB10	1.674423553
tenascin C	TNC	1.497943128

troponin T2, cardiac	TNNT2	1.920932125
tenascin XB	TNXB	1.246557298
two pore channel 1	TPCN1	1.408551957
Tnf receptor-associated factor 3	TRAF3	0.779861535
Tnf receptor associated factor 4	TRAF4	1.362173188
three prime repair exonuclease 1	TREX1	1.405371817
tribbles homolog 3 (Drosophila)	TRIB3	1.544023726
tripartite motif-containing 27	TRIM27	0.844907408
tripartite motif protein 8	TRIM8	1.349051288
transformation related protein 53	TRP53	1.282617583
transformation related protein 53 inducible nuclear protein 2	TRP53INP2	1.394939192
TSC22 domain family, member 1	TSC22D1	1.344696073
TSC22 domain family 3	TSC22D3	1.618836437
tetraspanin 14	TSPAN14	1.237721149
tumor suppressing subtransferable candidate 1	TSSC1	1.376304134
tetratricopeptide repeat domain 7B	TTC7B	0.651958108
tetratricopeptide repeat domain 8	TTC8	0.662106805
tubby-like protein 2	TULP2	0.632945678
twist gene homolog 1 (Drosophila)	TWIST1	1.269600898
thioredoxin domain containing 5	TXNDC5	1.197072605
thioredoxin interacting protein	TXNIP	0.576618198
thioredoxin-like 4A	TXNL4A	1.27531528
thymidylate synthase	TYMS	0.713161931
uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	1.493109101
ubiquitin-like 3	UBL3	1.185095694
UBX domain containing 1	UBXD1	1.247727138
uridine-cytidine kinase 2	UCK2	0.710451611
ubiquitin-fold modifier conjugating enzyme 1	UFC1	1.219920395
UDP glucuronosyltransferase 1 family, polypeptide A6B	UGT1A6B	1.372294908
ubiquitin-like, containing PHD and RING finger domains 2	UHRF2	0.692511872
uridine monophosphate synthetase	UMPS	0.767284402
unc-84 homolog A (C. elegans)	UNC84A	1.175424297
uridine phosphorylase 1	UPP1	1.288908824
unconventional SNARE in the ER 1 homolog (S. cerevisiae)	USE1	0.75695059
USO1 homolog, vesicle docking protein (yeast)	USO1	1.239565623
ubiquitin specific peptidase 37	USP37	0.625002665
vesicle-associated membrane protein 3	VAMP3	1.242117879
vesicle amine transport protein 1 homolog (T californica)	VAT1	1.327735429
vitamin D receptor	VDR	0.748025227
vestigial like 3	VGLL3	0.629695357
very low density lipoprotein receptor	VLDLR	0.304236402
vacuolar protein sorting 53	VPS53	0.73778934
vaccinia related kinase 1	VRK1	0.579745638

vesicle transport through interaction with t-SNAREs 1B homolog	VTI1B	0.637083388
tryptophanyl-tRNA synthetase	WARS	0.781043121
WD repeat domain 1 (Wdr1).	WDR1	1.224630972
WD repeat domain 36	WDR36	0.781997301
WD repeat domain 45	WDR45	1.473677759
wingless-type MMTV integration site 9A	WNT9A	1.351726792
WT1-interacting protein	WTIP	0.845146905
WW domain containing E3 ubiquitin protein ligase 2	WWP2	1.255092721
X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	XPNPEP1	1.168878022
exportin, tRNA (nuclear export receptor for tRNAs)	XPOT	1.238319703
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	YWHAG	1.62165869
zinc finger and BTB domain containing 12	ZBTB12	0.702027788
zinc finger CCCH type containing 14	ZC3H14	0.724705754
zinc finger E-box binding homeobox 2	ZEB2	0.70937705
zinc finger, AN1-type domain 2A	ZFAND2A	1.305056486
zinc finger, AN1 type domain 2B	ZFAND2B	1.331331319
zinc finger protein 282	ZFP282	1.243102317
zinc finger protein 292	ZFP292	0.755949803
zinc finger protein 639	ZFP639	0.716222932
zinc finger, MIZ-type containing 2	ZMIZ2	1.348206845

Supplementary Table 5.
List of genes whose expression was changed in YB-1 (1-219) expressing NIH3T3 cells compared to vector control cells

Gene Name	Symbol	Fold Change (YB-1 (1-219) VS Ctrl.)
ATP-binding cassette, sub-family F (GCN20), member 2	ABCF2	1.336248197
ATP-binding cassette, sub-family G (WHITE), member 1	ABCG1	2.644996258
acetyl-Coenzyme A acyltransferase 1A	ACAA1A	0.717241269
actin, alpha 2, smooth muscle, aorta	ACTA2	0.774315169
a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	ADAMTS2	0.775645102
ADAMTS-like 5	ADAMTSL5	1.468273565
adiponectin receptor 1	ADIPOR1	1.307085735
amino-terminal enhancer of split	AES	1.539864639
AT hook containing transcription factor 1	AHCTF1	0.75470945
AHNAK nucleoprotein	AHNAK	0.755337591
AI481316	AI481316	0.646866353
adenylate kinase 1	AK1	0.738264186
A kinase (PRKA) anchor protein (yotiao) 9	AKAP9	0.647048001
aldo-keto reductase family 1, member B8	AKR1B8	1.287278439
aldo-keto reductase family 1, member C12	AKR1C12	0.313655767
aldo-keto reductase family 1, member C18	AKR1C18	1.91545248
aldehyde dehydrogenase family 3, subfamily A1	ALDH3A1	0.372051664
arachidonate 5-lipoxygenase-activating protein	ALOX5AP	0.448301136
progressive ankylosis	ANK	0.690161442
ankyrin repeat domain 40	ANKRD40	1.291413144
anthrax toxin receptor 2	ANTXR2	1.446831278
adaptor protein complex AP-2, alpha 2 subunit	AP2A2	1.301184217
acylpeptide hydrolase	APEH	0.776928859
amyloid beta precursor protein (cytoplasmic tail) binding protein 2	APPBP2	0.734982481
adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	APPL2	0.717682045
androgen-induced proliferation inhibitor	APRIN	0.7657142
ADP-ribosylation factor 3	ARF3	1.220871863
Rho GTPase activating protein 17	ARHGAP17	0.78739442
arylsulfatase A	ARSA	0.809673286
arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	ASNA1	1.466702137
ATG9 autophagy related 9 homolog B (S. cerevisiae)	ATG9B	1.64586037
ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	1.192875549
ATPase, H+ transporting, lysosomal V1 subunit B2	ATP6V1B2	1.250830325
ATPase inhibitory factor 1	ATPIF1	0.788130051
expressed sequence AU040320	AU040320	1.22739889
HLA-B associated transcript 2	BAT2	1.270308962
cDNA sequence BC003331	BC003331	0.688404066
cDNA sequence BC017612	BC017612	1.341315208
cDNA sequence BC064033	BC064033	0.688135655
branched chain ketoacid dehydrogenase E1, beta polypeptide	BCKDHB	0.72609317
branched chain ketoacid dehydrogenase kinase	BCKDK	1.249251147
Bcl2-like 1	BCL2L1	1.514138131
B-cell leukemia/lymphoma 6	BCL6	0.697563008
BCS1-like	BCS1L	0.803685272
3-hydroxybutyrate dehydrogenase, type 2	BDH2	0.617435706
biglycan	BGN	0.60514096
bicaudal C homolog 1 (Drosophila)	BICC1	0.803172153
B-cell linker	BLNK	0.381272105
basigin	BSG	1.238225324
bone marrow stromal cell antigen 2	BST2	0.697754335
BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	BTAF1	0.803943057
calcium channel, voltage-dependent, alpha2/delta subunit 1	CACNA2D1	0.692943541
capping protein (actin filament) muscle Z-line, beta	CAPZB	1.315101876
carbonyl reductase 1	CBR1	1.596989185
carbonyl reductase 2	CBR2	0.583255075
carbonyl reductase 3	CBR3	1.33353387
coiled-coil domain containing 131	CCDC131	0.704880422
cholecystokinin	CCK	2.464581834
chemokine (C-C motif) ligand 7	CCL7	0.722341188
chaperonin subunit 8 (theta)	CCT8	1.267018359
CD248 antigen, endosialin	CD248	0.702197917
CDC42 effector protein (Rho GTPase binding) 2	CDC42EP2	1.352940068
cadherin 5, type 2 (vascular endothelium)	CDH5	0.502601823
cyclin-dependent kinase 2	CDK2	1.335008869
ChaC, cation transport regulator-like 1	CHAC1	1.633375442
claudin domain containing 1	CLDND1	1.335227033
chloride intracellular channel 4 (mitochondrial)	CLIC4	1.259262326

CDC-like kinase 1	CLK1	0.765262024
circadian locomoter output cycles kaput	CLOCK	0.781823303
cleft lip and palate associated transmembrane protein 1	CLPTM1	1.286043242
Coenzyme A synthase	COASY	1.482974947
cordon-bleu	COBL	1.40029826
collagen, type I, alpha 1	COL1A1	1.526885393
procollagen, type IV, alpha 1	COL4A1	1.475411381
procollagen, type V, alpha 1	COL5A1	0.683696255
procollagen, type VI, alpha 3	COL6A3	0.814147838
COMM domain containing 3	COMMD3	0.759171736
coatomer protein complex, subunit epsilon	COPE	0.814202856
coatomer protein complex, subunit zeta 2	COPZ2	0.758642134
coenzyme Q10 homolog B (S. cerevisiae)	COQ10B	1.216851477
carnitine acetyltransferase	CRAT	1.346599323
cytokine receptor-like factor 1	CRLF1	0.6474682
crystallin, lambda 1	CRYL1	0.698137879
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	CTDSP1	1.232922938
connective tissue growth factor	CTGF	0.540592089
cytidine 5'-triphosphate synthase	CTPS	1.442466376
CUG triplet repeat, RNA binding protein 1	CUGBP1	1.367477681
CAAX box 1 homolog A (human)	CXX1A	0.716966184
cytochrome b-561	CYB561	0.717508498
cytochrome b5 reductase 3	CYB5R3	1.201001673
cytochrome b-245, alpha polypeptide	CYBA	0.517317298
cytochrome P450, family 26, subfamily b, polypeptide 1	CYP26B1	0.62295764
cytochrome P450, family 2, subfamily d, polypeptide 22	CYP2D22	0.730498244
decorin (Dcn)	DCN	0.25709716
DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	DDX6	0.753086971
24-dehydrocholesterol reductase	DHCR24	1.77421642
delta-like 1 homolog (Drosophila)	DLK1	0.463047046
dystrophia myotonica-containing WD repeat motif	DMWD	1.267936136
dynamin 3, opposite strand (Dnm3os) on chromosome 1	DNM3OS	0.537292844
dual specificity phosphatase 4	DUSP4	1.401135853
extracellular matrix protein 1	ECM1	0.563216732
predicted gene, EG433229	EG433229	0.684416491
predicted gene, EG667135	EG667135	0.399110495
EGR3	EGR3	0.597482832
EH-domain containing 1	EHD1	1.468925176
eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2	0.658038057
argonaute RISC catalytic component 3	EIF2C3	0.600544774
ELK3, member of ETS oncogene family	ELK3	0.797788047
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	ELOVL1	1.283327275
echinoderm microtubule associated protein like 1	EML1	0.666317572
enabled homolog (Drosophila)	ENAH	1.534390077
enolase 2, gamma neuronal	ENO2	0.69326572
predicted gene, ENSMUSG00000053178	ENSMUSG00000053178	0.762646592
epidermal growth factor receptor pathway substrate 8	EPS8	1.401047442
electron transferring flavoprotein, beta polypeptide	ETFB	0.811235565
enhancer trap locus 4	ETL4	0.649559671
ets variant gene 4 (E1A enhancer binding protein, E1AF)	ETV4	1.336689871
fatty acid desaturase 2	FADS2	1.281012441
fumarylacetoacetate hydrolase	FAH	0.76030055
FERM, RhoGEF and pleckstrin domain protein 2	FARP2	0.761976392
phenylalanyl-tRNA synthetase, beta subunit	FARSB	1.211510023
Fas-activated serine/threonine kinase	FASTK	1.383825692
Fc fragment of IgG, receptor, transporter, alpha	FCGRT	0.591505249
fasciculation and elongation protein zeta 2 (zygin II)	FEZ2	1.260207481
four and a half LIM domains 3	FHL3	1.689607612
FK506 binding protein 9	FKBP9	0.804147703
flotillin 1	FLOT1	0.740003382
FMS-like tyrosine kinase 1	FLT1	1.535519234
fibronectin 1	FN1	0.66410919
forkhead box P1	FOXP1	1.409351912
forkhead box S1	FOXS1	0.623071308
fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	FSCN1	1.67953598
follistatin-like 1	FSTL1	0.706535909
glucose-6-phosphate dehydrogenase X-linked	G6PDX	1.371390099
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	0.781070663
alpha glucosidase 2 alpha neutral subunit	GANAB	1.30154027
GTPase activating RANGAP domain-like 3	GARNL3	0.745908093
GTP cyclohydrolase I feedback regulator	GCHFR	1.403499487
glutamate-cysteine ligase , modifier subunit	GCLM	1.348682229

glutamine fructose-6-phosphate transaminase 2	GFPT2	0.672576686
gap junction membrane channel protein alpha 1	GJA1	0.801614749
galactosidase, beta 1	GLB1	0.75163123
glycosyltransferase 8 domain containing 1	GLT8D1	0.771768571
glycine-N-acyltransferase	GLYAT	1.519865128
gene model 773	GM773	0.145740508
glycoprotein Ib, beta polypeptide	GP1BB	1.342068555
GC-rich promoter binding protein 1	GPBP1	0.755772037
glycoprotein (transmembrane) nmb	GPNMB	1.22924837
glycoprotein, synaptic 2	GPSN2	1.252115218
glutathione S-transferase, alpha 4	GSTA4	0.649976454
glutathione S-transferase, mu 2	GSTM2	0.509046203
glutathione S-transferase omega 1	GSTO1	1.28580168
glutathione S-transferase omega 2	GSTO2	1.398543615
glutathione S-transferase, theta 3	GSTT3	0.333837791
general transcription factor II I	GTF2I	0.682484308
H2A histone family, member V	H2AFV	0.773636851
H2A histone family, member X	H2AFX	1.340169299
histocompatibility 2, class II, locus Mb1	H2-DMB1	0.620698421
histocompatibility 2, class II, locus Mb2	H2-DMB2	0.680167802
H2-K region expressed gene 6	H2-KE6	0.724054961
hyaluronan synthase 2	HAS2	0.640926144
hemoglobin Z, beta-like embryonic chain	HBB-BH1	1.558116557
histidine triad nucleotide binding protein 2	HINT2	0.752967832
histone cluster 2, H2aa1	HIST2H2AA1	0.701558085
high mobility group AT-hook 1	HMGA1	1.292306895
heterogeneous nuclear ribonucleoprotein L	HNRPL	1.256032898
inhibitor of apoptosis	IAP	0.702643932
interferon induced transmembrane protein 3	IFITM3	0.500626157
insulin-like growth factor binding protein 4	IGFBP4	1.869043948
insulin-like growth factor binding protein 7	IGFBP7	0.80330239
interleukin 11 receptor, alpha chain 1	IL11RA1	0.735963635
interleukin 1 receptor-like 1	IL1RL1	0.756893547
importin 5	IPO5	1.445704903
IQ motif containing F5	IQCF5	0.65914949
integrin alpha 3	ITGA3	3.225195125
integrin, beta-like 1	ITGBL1	1.287449917
potassium voltage-gated channel, shaker-related subfamily, beta member 2	KCNAB2	1.21639332
KH domain containing, RNA binding, signal transduction associated 1	KHDRBS1	1.272348282
kallikrein related-peptidase 10	KLK10	1.559605935
kinetochore associated 1	KNTC1	0.801067186
laminin, gamma 2	LAMC2	1.298354283
LAG1 homolog, ceramide synthase 2	LASS2	1.219731686
lectin, galactose binding, soluble 9	LGALS9	1.333357503
lipoma HMGIC fusion partner-like 2	LHFPL2	0.812222039
LIM domains containing 1	LIMD1	1.296268983
LIM and senescent cell antigen like domains 2	LIMS2	1.589210626
hypothetical protein LOC100038894	LOC100038894	1.446998459
similar to SP140 nuclear body protein family member	LOC100039742	0.538736562
similar to LSM7 homolog, U6 small nuclear RNA associated	LOC100041500	0.727281781
hypothetical protein LOC100041725	LOC100041725	1.407281493
hypothetical protein LOC100043821	LOC100043821	0.612599446
similar to thioredoxin reductase 2	LOC100044101	0.70183427
hypothetical protein LOC100044177	LOC100044177	1.216920086
hypothetical protein LOC100044194	LOC100044194	0.823809462
hypothetical protein LOC100045737	LOC100045737	1.307379522
similar to histone deacetylase HD1	LOC100046039	1.225151057
similar to Protein phosphatase 2, regulatory subunit B (B56), alpha	LOC100046393	1.26021976
similar to aquaporin 5	LOC100046616	0.55569473
similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	LOC100047619	1.424484835
hypothetical protein LOC100047707	LOC100047707	1.254838619
hypothetical protein LOC100048316	LOC100048316	1.280429844
similar to Myeloid leukemia factor 2	LOC100048413	1.410186002
similar to fibronectin leucine rich transmembrane protein 3, transcript variant 1	LOC100048721	0.755316683
similar to four and a half LIM domains 3	LOC100048796	1.709350286
LOC280487	LOC280487	0.46962632
LOC385068	LOC385068	0.599069041
LOC385615	LOC385615	0.533670614
LOC386135	LOC386135	0.519545438
similar to ZH10 protein	LOC622491	0.811866971
similar to Pyruvate kinase, muscle	LOC631301	1.429010823
similar to Glutathione S-transferase Mu 2 (GST class-mu 2) (Glutathione S-transferase pmGT2)	LOC670888	0.556196287

hypothetical protein LOC673501	LOC673501	0.37749915
similar to Glucose phosphate isomerase 1	LOC676974	1.290089757
LOC98434	LOC98434	0.50225924
lysyl oxidase	LOX	0.616449969
LIM domain containing preferred translocation partner in lipoma	LPP	0.548163774
leucine rich repeat containing 41	LRRC41	1.299605083
LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM2	1.276060053
lanosterol synthase	LSS	1.27301149
latent transforming growth factor beta binding protein 2	LTBP2	0.654115879
lymphocyte antigen 6 complex, locus A	LY6A	0.741213481
lymphocyte antigen 6 complex, locus C1	LY6C1	0.66401449
Ly6/neurotoxin 1	LYNX1	0.674926326
lysophospholipase 3	LYPLA3	0.707520738
melanoma antigen, family D, 1	MAGED1	0.765928325
melanoma antigen, family D, 2	MAGED2	0.799686009
mannosidase, alpha, class 1B, member 1	MAN1B1	1.273365578
mitogen-activated protein kinase 11	MAPK11	1.356030719
MARCKS-like 1	MARCKSL1	1.567474534
microtubule associated serine/threonine kinase 3	MAST3	0.766394901
muscleblind-like 1	MBNL1	0.828778217
membrane bound O-acyltransferase domain containing 1	MBOAT1	1.260147333
mcf.2 transforming sequence-like	MCF2L	0.686763925
mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	MED25	0.768110079
microfibrillar associated protein 5	MFAP5	2.058568425
mannoside acetylglucosaminyltransferase 4, isoenzyme B	MGAT4B	1.486926641
matrix metallopeptidase 14 (membrane-inserted)	MMP14	0.747026629
molybdenum cofactor synthesis 1	MOCS1	0.758298401
mitochondrial ribosomal protein S9	MRPS9	0.75210777
mesothelin	MSLN	2.544207197
mitochondrial carrier homolog 1 (C. elegans)	MTCH1	0.791720372
mitochondrial transcription termination factor.	MTERF	0.76117205
metaxin 1	MTX1	0.798395978
myosin XVIIIb	MYO18B	3.125211946
myosin Ixb	MYO9B	0.806525707
alpha-N-acetylglucosaminidase	NAGLU	0.689715936
neurochondrin	NCDN	1.405265752
N-myc downstream regulated gene 1	NDRG1	1.30858591
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	NDUFA1	0.753811364
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	NDUFA4	0.77647225
neuron derived neurotrophic factor	NENF	0.69528609
NeoR	NEOR	0.560101936
neuronal guanine nucleotide exchange factor	NGEF	2.177744105
nicotinamide N-methyltransferase	NNMT	1.405326152
Notch gene homolog 4 (Drosophila)	NOTCH4	0.796533153
nucleoplasmin 3, pseudogene 1	NPM3-PS1	1.447771073
nuclear receptor binding protein 2	NRBP2	0.682053811
nurim (nuclear envelope membrane protein)	NRM	0.784176336
5'-nucleotidase, cytosolic III-like	NT5C3L	0.790236801
nucleobindin 1	NUCB1	0.611839685
oligonucleotide/oligosaccharide-binding fold containing 2B	OBFC2B	1.645127001
ORAI calcium release-activated calcium modulator 1	ORAI1	1.333327314
poly (ADP-ribose) polymerase family, member 3	PARP3	1.391733994
polybromo 1	PBRM1	0.714353633
poly(rC) binding protein 2	PCBP2	1.230692319
platelet derived growth factor receptor, alpha polypeptide	PDGFRA	0.564011915
PDZ and LIM domain 1 (elfin)	PDLIM1	1.281802249
PDZ and LIM domain 2	PDLIM2	0.692359327
penta-EF hand domain containing 1	PEF1	1.460406865
prefoldin 5	PFDN5	0.80748005
profilin 1	PFN1	1.257668804
phosphatidylinositol 4-kinase type 2 beta	PI4K2B	1.275797751
phosphatidylinositol glycan anchor biosynthesis, class Y-like	PIGYL	0.800354295
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	PLOD2	1.448680729
proteolipid protein (myelin) 1	PLP1	0.410692584
phospholipid scramblase 1	PLSCR1	1.319976416
paraoxonase 2	PON2	1.224026667
phosphatidic acid phosphatase type 2B	PPAP2B	0.624496816
protein phosphatase 1, catalytic subunit, alpha isoform	PPP1CA	1.325941921
protein phosphatase 1, regulatory (inhibitor) subunit 8	PPP1R8	1.224067704
protein phosphatase 1, regulatory subunit 9B	PPP1R9B	1.256617943
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	PPP2R1A	1.258616974
protein phosphatase 2A, regulatory subunit B (PR 53)	PPP2R4	1.249984686

proline arginine-rich end leucine-rich repeat	PRELP	0.219671551
protein kinase, cAMP dependent regulatory, type I, alpha	PRKAR1A	0.790344622
protein kinase, X-linked	PRKX	1.316606046
pleckstrin homology, Sec7 and coiled-coil domains, binding protein	PSCDBP	1.382932135
proteaseome (prosome, macropain) 28 subunit, 3	PSME3	1.231749727
pentraxin related gene	PTX3	0.629769726
poliovirus receptor	PVR	1.512092541
RAB1B, member RAS oncogene family	RAB1B	1.423719023
RAB8B, member RAS oncogene family	RAB8B	0.710384657
RAS-related C3 botulinum substrate 1	RAC1	1.320956175
RAD23a homolog (S. cerevisiae)	RAD23A	1.407241934
hnRNP-associated with lethal yellow	RALY	1.35952281
retinoblastoma binding protein 4	RBBP4	1.726042275
RNA binding motif protein 38	RBM38	1.532850022
retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	RDH11	0.74135948
retinol saturase (all trans retinol 13,14 reductase)	RETSAT	0.758161535
REX1, RNA exonuclease 1 homolog (S. cerevisiae)	REXO1	1.417542089
replication factor C (activator 1) 4	RFC4	0.811632218
RGM domain family, member A	RGMA	0.677915107
regulator of G-protein signaling 16	RGS16	2.124502842
rhomboid domain containing 1	RHBDD1	1.271118833
rhomboid family 1	RHBDF1	0.800800489
ras homolog gene family, member J	RHOJ	0.643352985
18S RNA (Rn18s) on chromosome 17	RN18S	0.380616002
Ras-related GTP binding C	RRAGC	1.315620938
RRP9, small subunit (SSU) processome component, homolog (yeast)	RRP9	1.273462759
S100 calcium binding protein A7A	S100A7A	2.314661744
SAP30-like	SAP30L	1.461875515
suprabasin	SBSN	0.737464611
sterol-C4-methyl oxidase-like	SC4MOL	1.318208525
secretory carrier membrane protein 5	SCAMP5	0.736914486
scavenger receptor class A, member 3	SCARA3	0.421143187
scavenger receptor class A, member 5 (putative)	SCARA5	0.380779176
SCL0001849.1_2273	SCL0001849.1_2273	0.634867947
syndecan 3	SDC3	0.486279528
serum deprivation response	SDPR	1.350954115
SUMO/sentrin specific peptidase 3	SENP3	1.259193182
selenoprotein W, muscle 1	SEPW1	1.517616963
serine (or cysteine) peptidase inhibitor, clade A, member 3N	SERPINA3N	0.117198551
serine (or cysteine) peptidase inhibitor, clade F, member 1	SERPINF1	0.795291026
SET domain containing (lysine methyltransferase) 8	SETD8	1.365194081
splicing factor 1	SF1	1.280495042
splicing factor 3b, subunit 4	SF3B4	1.299054694
SH3-domain GRB2-like 3	SH3GL3	1.424807898
serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	1.321009547
sialic acid binding Ig-like lectin G	SIGLECG	1.718946306
signal-induced proliferation-associated 1 like 1	SIPA1L1	0.775492336
solute carrier family 1 (neutral amino acid transporter), member 5	SLC1A5	1.26498218
solute carrier family 25, member 33	SLC25A33	1.520473794
solute carrier family 25, member 45	SLC25A45	1.57463983
solute carrier family 9 (sodium/hydrogen exchanger), member 1	SLC9A1	0.756636057
secreted Ly6/Plaur domain containing 1	SLURP1	0.536119605
structural maintenance of chromosomes 1A	SMC1A	0.713109717
SMAD specific E3 ubiquitin protein ligase 1	SMURF1	1.389694272
sushi, nidogen and EGF-like domains 1	SNED1	0.421191435
sorting nexin 17	SNX17	0.829081331
sorbitol dehydrogenase	SORD	1.249491887
SPECC1-like	SPECC1L	0.815911413
sphingosine kinase 1	SPHK1	0.601791408
spondin 2, extracellular matrix protein	SPON2	0.442316057
secreted phosphoprotein 1	SPP1	0.334152605
serum response factor	SRF	0.781228421
sushi-repeat-containing protein, X-linked 2	SRPX2	0.671585325
beta galactoside alpha 2,6 sialyltransferase 1	ST6GAL1	0.785958091
stress-induced phosphoprotein 1	STIP1	1.440048247
stomatin	STOM	1.378078235
sulfite oxidase	SUOX	1.304873858
synapsin I	SYN1	1.55420425
synaptopodin	SYNPO	0.431306192
transgelin 2	TAGLN2	1.26546507
transporter 2, ATP-binding cassette, sub-family B	TAP2	0.690490367
tubulin-specific chaperone c	TBCC	0.77313411

TANK-binding kinase 1	TBK1	0.777263836
transforming growth factor beta 1 induced transcript 1	TGFB1I1	0.750393069
transforming growth factor, beta-induced, 68kDa	TGFBI	0.74261492
transforming growth factor, beta receptor associated protein 1	TGFBRAP1	0.772041374
transglutaminase 2, C polypeptide	TGM2	0.66802119
THO complex 7 homolog (Drosophila)	THOC7	0.800640894
thymus cell antigen 1, theta	THY1	0.505043966
translocase of inner mitochondrial membrane 17a	TIMM17A	0.822625595
tubulointerstitial nephritis antigen-like	TINAGL	1.741618798
transmembrane BAX inhibitor motif containing 4	TMBIM4	0.827878554
transmembrane emp24 protein transport domain containing 4	TMED4	1.244137776
transmembrane protein 106C	TMEM106C	0.752335489
transmembrane protein 205	TMEM205	0.686569388
transmembrane protein 43	TMEM43	1.24309307
tenascin C	TNC	1.724978744
troponin T2, cardiac	TNNT2	1.332192226
tensin 1	TNS1	0.619144157
tropomyosin 2, beta	TPM2	0.789141674
translocated promoter region	TPR	0.743019122
Tnf receptor associated factor 4	TRAF4	1.251208791
tribbles homolog 2 (Drosophila)	TRIB2	0.637328764
transformation related protein 53	TRP53	1.349856947
tissue specific transplantation antigen P35B	TSTA3	0.80570229
tweety homolog 2 (Drosophila)	TTYH2	0.655648064
thioredoxin interacting protein	TXNIP	0.512081197
thioredoxin-like 4A	TXNL4A	1.236522838
ubiquitin associated protein 2-like	UBAP2L	1.317177196
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	UBE2M	1.207182997
ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	1.560719143
UDP glycosyltransferase 1 family, polypeptide A10	UGT1A10	0.632451377
ubiquitin-like, containing PHD and RING finger domains 2	UHRF2	1.626143974
unc-5 homolog B (C. elegans)	UNC5B	0.633265806
UPF2 regulator of nonsense transcripts homolog (yeast)	UPF2	0.624685155
uridine phosphorylase 1	UPP1	1.469560797
unconventional SNARE in the ER 1 homolog (S. cerevisiae)	USE1	0.701583061
ubiquitously expressed transcript	UXT	0.805725811
vesicle-associated membrane protein 3	VAMP3	1.270297619
vasohibin 2	VASH2	0.800409134
vesicle amine transport protein 1 homolog (T californica)	VAT1	1.346516997
vascular endothelial zinc finger 1	VEZF1	0.77144934
vacuolar protein sorting 72	VPS72	1.355157171
whirlin	WHRN	0.761505533
Wolf-Hirschhorn syndrome candidate 2	WHSC2	0.770791327
xanthine dehydrogenase	XDH	0.801231532
exportin, tRNA (nuclear export receptor for tRNAs)	XPOT	1.280877034
zinc finger and BTB domain containing 20	ZBTB20	0.689898826
zinc finger homeobox 3	ZFHX3	0.724572271
zinc finger, matrin-like	ZFML	0.791604758
zinc finger protein 148	ZFP148	0.741588149
zinc metallopeptidase, STE24 homolog (S. cerevisiae)	ZMPSTE24	1.30486036
zinc finger, MYND domain containing 11	ZMYND11	1.307665351