Table S4. Rat Kidney Medullary Thick Ascending Limb Transcriptome

Gene Title	Gene Symbol	Signal
1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (predicted)	Agpat2_predicted	4.83±0.59
1-acylglycerol-3-phosphate O-acyltransferase 3 (predicted)	Agpat3_predicted	2.57±0.34
1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (predicted)	Agpat5_predicted	1.73±0.32
1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Agpat6	5.21±1.04
1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	Accs / LOC690470	1.4±0.31
2 ' -5 ' oligoadenylate synthetase 1I	Oas1i	0.25±0.26
2,3-bisphosphoglycerate mutase	Bpgm	2.13±0.78
2',3'-cyclic nucleotide 3' phosphodiesterase	Cnp	1±0.06
2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	4.64±1.18
24-dehydrocholesterol reductase	Dhcr24	7.6±2.36
2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	1.11±0.16
2'-5' oligoadenylate synthetase 1A	Oas1a	0.48±0.11
2'-5' oligoadenylate synthetase-like 1	Oasl1	0.69±0.18
2-hydroxyacyl-CoA lyase 1	Hacl1	1.31±0.14
2-oxoglutarate and iron-dependent oxygenase domain containing 1	Ogfod1	0.36±0.21
3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	2.64±0.08
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	2.66±1.69
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	6.71±5.14
3-hydroxybutyrate dehydrogenase, type 1	Bdh1	6.78±2.29
3-hydroxybutyrate dehydrogenase, type 2 (predicted)	Bdh2_predicted	2.65±0.27
3-hydroxyisobutyrate dehydrogenase	Hibadh	28.82±4.7
3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	6.12±0.13
3-ketodihydrosphingosine reductase	Kdsr	0.51±0.01
3-oxoacyl-ACP synthase, mitochondrial	Oxsm	1.3±0.45
3'-phosphoadenosine 5'-phosphosulfate synthase 1 (predicted)	Papss1_predicted	11.58±0.92
3'-phosphoadenosine 5'-phosphosulfate synthase 2 (predicted)	Papss2_predicted	5.2±0.17
3-phosphoinositide dependent protein kinase-1	Pdpk1	1.83±0.36
4-hydroxyphenylpyruvate dioxygenase-like	Hpdl	0.92±0.43
4-hydroxyphenylpyruvic acid dioxygenase	Hpd	4.94±2.58
4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	2.57±0.32
5, 10-methenyltetrahydrofolate synthetase	Mthfs	1.33±0.63
5',3'-nucleotidase, mitochondrial (predicted)	Nt5m_predicted	0.86±0.06
5'-3' exoribonuclease 1 (predicted)	Xrn1_predicted	0.2±0.03
5'-3' exoribonuclease 2 (predicted)	Xrn2_predicted	1.89±1.05
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Atic	2.09±0.49
5-azacytidine induced gene 2	Azi2	1.18±0.4
5-methyltetrahydrofolate-homocysteine methyltransferase	Mtr	0.21±0.07
5-methyltetrahydrofolate-homocysteine methyltransferase reductase	Mtrr	1.64±0.23
5'-nucleotidase domain containing 1 (predicted)	Nt5dc1_predicted	1.12±0.68
5'-nucleotidase, cytosolic III (predicted)	Nt5c3_predicted	2.34±0.64
5'-nucleotidase, cytosolic III-like	Nt5c3l	4.42±1.16
5-oxoprolinase (ATP-hydrolysing)	Oplah	8.87±1.72
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Pfkfb2	0.26±0.12
6-phosphogluconolactonase (predicted)	Pgls_predicted	1.44±0.26
6-pyruvoyl-tetrahydropterin synthase	Pts	5.48±0.16
7-dehydrocholesterol reductase	Dhcr7	1.23±0.2
92Aa-Protein	LOC494529	3.24±0.45
a disintegrin and metallopeptidase domain 10	Adam10	1±0.21
a disintegrin and metallopeptidase domain 17	Adam17	1.11±0.5
a disintegrin and metallopeptidase domain 1a	Adam1a	0.21±0.11
a disintegrin and metallopeptidase domain 9 (meltrin gamma)	Adam9	0.98±0.33
A kinase (PRKA) anchor protein (yotiao) 9	Akap9	3.16±0.64
A kinase (PRKA) anchor protein 1	Akap1	3.78±0.08
A kinase (PRKA) anchor protein 10 (predicted)	Akap10_predicted	0.9±0.05
A kinase (PRKA) anchor protein 11	Akap11	1.14±0.04
A kinase (PRKA) anchor protein 7	Akap7	1.59±0.13
A kinase (PRKA) anchor protein 8	Akap8	3.07±0.57
A kinase (PRKA) anchor protein 8-like	Akap8l	1.04±0.21
aarF domain containing kinase 1 (predicted)	Adck1_predicted	0.37±0.03
aarF domain containing kinase 2 (predicted)	Adck2_predicted	0.66±0.27
aarF domain containing kinase 4	Adck4	1.59±0.25
aarF domain containing kinase 5	Adck5	0.96±0.08
Abelson helper integration site 1	Ahi1	0.47±0.16
abhydrolase domain containing 1	Abhd1	0.53±0.06
abhydrolase domain containing 10	Abhd10	0.48±0.13
abhydrolase domain containing 11 /// similar to abhydrolase domain containing 11	Abhd11 /// LOC686139	1.98±0.04
abhydrolase domain containing 12	Abhd12	1.19±0.45
abhydrolase domain containing 13	Abhd13	1.7±0.03
abhydrolase domain containing 14b	Abhd14b	13.59±0.47
abhydrolase domain containing 3 (predicted)	Abhd3_predicted	2.21±0.27
abhydrolase domain containing 4 (predicted)	Abhd4_predicted	7.09±0.83
abhydrolase domain containing 6	Abhd6	2.98±0.68
abhydrolase domain containing 8 (predicted)	Abhd8_predicted	1.34±0.09
abl-interactor 1	Abi1	1.36±0.64
abl-interactor 2	Abi2	3.39±0.02
ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	Abo	1.59±0.37
Ac1254	LOC362901	8.33±1.05
acetoacetyl-CoA synthetase	Aacs	0.47±0.11
acetyl-coenzyme A acetyltransferase 1	Acat1	33.36±3.13
acetyl-Coenzyme A acetyltransferase 2	Acat2	2.34±0.01
acetyl-Coenzyme A acyltransferase 1 /// similar to 3-ketoacyl-CoA thiolase B, peroxisomal precursor (Beta-ketothiolase B) (predicted)	Acaa1 /// RGD1562373	3.66±0.43
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	14.84±1.13
acetyl-coenzyme A carboxylase alpha	Acaca	2.8±0.24
acetyl-Coenzyme A carboxylase beta	Acacb	1±0.04
acetylserotonin O-methyltransferase-like (predicted)	Asmtl_predicted	2.91±0.23

acid phosphatase 1, soluble	Acp1	2.75±0.1
acid phosphatase 2, lysosomal	Acp2	2.19±0.24
acid phosphatase 5, tartrate resistant	Acp5	4.05±0.4
acid phosphatase 6, lysophosphatidic	Acp6	2.03±0.05
acid phosphatase-like 2	Acpl2	0.62±0.08
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	6.4±2.06
Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	Anp32e	2.97±1.05
acidic nuclear phosphoprotein 32 family, member B	Anp32b	4.64±0.4
acidic ribosomal phosphoprotein P0	Arbp	33.9±0.71
acireductone dioxygenase 1	Adi1	12.75±1.46
ACN9 homolog (S. cerevisiae)	Acn9	3.41±1.03
aconitase 1	Aco1	5.26±0.14
aconitase 2, mitochondrial	Aco2	34.96±3.19
actin filament associated protein 1-like 1	Afap1l1	0.86±0.09
actin related protein 2/3 complex, subunit 1A	Arpc1a	4.95±0.45
actin related protein 2/3 complex, subunit 1B	Arpc1b	0.76±0.11
actin related protein 2/3 complex, subunit 2 (predicted)	Arpc2_predicted	19.82±2.52
actin related protein 2/3 complex, subunit 3 (predicted)	Arpc3_predicted	7.78±0.81
actin related protein 2/3 complex, subunit 4 (predicted)	Arpc4_predicted	3.88±0.48
actin related protein 2/3 complex, subunit 5	Arpc5	6.51±0.49
actin related protein 2/3 complex, subunit 5-like /// similar to actin related protein 2/3 complex, subunit 5-like (predicted)	Arpc5l /// RGD1560362	3.53±0.21
actin, beta	Actb	27.78±3.54
actin, gamma, cytoplasmic 1	Actg1 /// LOC295810 //	0.24±0.32
actin, gamma, cytoplasmic 1 /// similar to Actin, cytoplasmic 2 (Gamma-actin)	Actg1 /// LOC295810	52.52±7.67
actinin alpha 4	Actn4	8.04±0.96
actinin, alpha 1	Actn1	0.48±0.76
actin-like 6A	Actl6a	2.28±0.42
activated leukocyte cell adhesion molecule	Alcam	2.8±0.58
activating signal cointegrator 1 complex subunit 1	Ascc1	0.95±0.18
activating signal cointegrator 1 complex subunit 2	Ascc2	0.55±0.06
activating signal cointegrator 1 complex subunit 3 (predicted)	Ascc3_predicted	1.5±0.66
activating signal cointegrator 1 complex subunit 3-like 1	Ascc3l1	2.39±0.15
activating transcription factor 1	Atf1	5.98±0.29
activating transcription factor 4	Atf4	13.66±2.54
activating transcription factor 5	Atf5	1.42±0.23
Activating transcription factor 6 (predicted)	Atf6_predicted	2.38±0.09
activating transcription factor 7 interacting protein (predicted)	Atf7ip_predicted	1.15±0.19
activator of basal transcription 1	Abt1	1.11±0.21
active BCR-related gene (predicted)	Abr_predicted	0.52±0.17
activin receptor IIA	Acvr2a	0.49±0.1
activin receptor IIB	Acvr2b	0.54±0.28
activity-dependent neuroprotective protein	Adnp	7.08±0.32
acyl-CoA synthetase family member 2	Acsf2	0.54±0.01
acyl-CoA synthetase family member 3	Acsf3	2.77±0.83
acyl-CoA synthetase long-chain family member 1	Acsl1	22.68±0.64
acyl-CoA synthetase long-chain family member 3	Acsl3	1.67±0.3
acyl-CoA synthetase long-chain family member 4	Acsl4	4.86±1.93
acyl-CoA synthetase long-chain family member 5	Acsl5	5.99±0.3
acyl-CoA synthetase short-chain family member 1 (predicted)	Acss1_predicted	18.72±0.3
acyl-CoA synthetase short-chain family member 2 (predicted)	Acss2_predicted	4.72±1.49
acyl-CoA thioesterase 2	Acot2	1.36±0.75
acyl-CoA thioesterase 3 /// acyl-CoA thioesterase 4	Acot3 /// Acot4	0.28±0.06
acyl-CoA thioesterase 7	Acot7	0.32±0.04
acyl-CoA thioesterase 8	Acot8	4.74±1.1
acyl-Coenzyme A binding domain containing 3	Acbd3	1.46±0.22
Acyl-Coenzyme A binding domain containing 5	Acbd5	5.58±0.83
acyl-Coenzyme A binding domain containing 6	Acbd6	1.48±0.1
acyl-Coenzyme A dehydrogenase family, member 11 (predicted)	Acad11_predicted	1.2±0.05
acyl-Coenzyme A dehydrogenase family, member 9	Acad9	4.34±1.03
acyl-Coenzyme A dehydrogenase, long-chain	Acadl	14.86±1.84
acyl-Coenzyme A dehydrogenase, medium chain	Acadm	34.57±3.38
acyl-Coenzyme A dehydrogenase, short chain	Acads	1.95±0.25
acyl-Coenzyme A dehydrogenase, short/branched chain	Acadsb	2.13±0.8
acyl-Coenzyme A dehydrogenase, very long chain	Acadvl	7.45±1.26
acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	8.97±1.42
acylglycerol kinase	Agk	0.97±0.17
acylpeptide hydrolase	Apeh	3.99±0.3
acylphosphatase 1, erythrocyte (common) type (predicted)	Acyp1_predicted	3.08±0.15
ADAMTS-like 2	Adamtsl2	0.48±0.01
ADAMTS-like 5 (predicted)	Adamtsl5_predicted	0.35±0.01
adaptor protein complex AP-1, beta 1 subunit	Ap1b1	2.51±0.91
adaptor protein complex AP-1, sigma 1 (predicted)	Ap1s1_predicted	5.2±0.94
adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	2.17±0.57
adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	Appl2	3.42±0.71
adaptor-related protein complex 1, gamma 1 subunit	Ap1g1	1.66±0.1
adaptor-related protein complex 2, beta 1 subunit	Ap2b1	5.94±0.78
adaptor-related protein complex 2, mu 1 subunit	Ap2m1	20.2±2.47
adaptor-related protein complex 2, sigma 1 subunit	Ap2s1	4.3±0.33
adaptor-related protein complex 3, beta 1 subunit (predicted)	Ap3b1_predicted	2.71±1.16
adaptor-related protein complex 3, delta 1 subunit	Ap3d1	12.26±0.03
adaptor-related protein complex 3, mu 1 subunit	Ap3m1	3.72±0.48
adaptor-related protein complex 3, mu 2 subunit	Ap3m2	0.32±0.14
adaptor-related protein complex 3, sigma 1 subunit (predicted)	Ap3s1_predicted	2.44±0.52
adaptor-related protein complex AP-1, mu subunit 1	Ap1m1	1.5±0.1
adaptor-related protein complex AP-4, beta 1 (predicted)	Ap4b1_predicted	1.34±0.11
adducin 1 (alpha)	Add1	10.12±1.48
adducin 3 (gamma)	Add3	1.14±0.43

adenine phosphoribosyl transferase (predicted)	Aprt_predicted	11.54±0.84
adenosine deaminase, RNA-specific	Adar	0.26±0.21
adenosine kinase	Adk	4.77±1.05
adenosine monophosphate deaminase 2 (isoform L)	Ampd2	1±0.05
adenosine monophosphate deaminase 3	Ampd3	10.3±1.37
adenylate cyclase 6	Adcy6	0.59±0.06
adenylate kinase 1	Ak1	1.67±0.57
adenylate kinase 2	Ak2	5.75±0.04
adenylate kinase 3	Ak3	11.78±2.52
adenylosuccinate lyase	Adsl	1.99±0.35
adenylosuccinate synthetase, non muscle (predicted)	Adss_predicted	9.54±1.42
adhesion molecule with Ig like domain 1	Amigo1	0.7±0.22
adhesion regulating molecule 1	Adrm1	2.14±0.42
adiponectin receptor 1	Adipor1	14.47±0.14
adiponectin receptor 2	Adipor2	2.27±0.52
adipose differentiation related protein	Adfp	1.85±0.45
ADNP homeobox 2	Adnp2	0.9±0.1
ADP-dependent glucokinase	Adpgk	0.29±0.14
ADP-ribosylarginine hydrolase	Adprh	1.3±0.25
ADP-ribosylation factor 1	Arf1	23.44±0.39
ADP-ribosylation factor 2	Arf2	0.36±0.1
ADP-ribosylation factor 3	Arf3	7.62±0.6
ADP-ribosylation factor 4	Arf4	10.42±0.48
ADP-ribosylation factor 4-like (predicted)	Arf4l_predicted	4.86±2.12
ADP-ribosylation factor 5	Arf5	3.87±0.18
ADP-ribosylation factor 6	Arf6	2.43±0.37
ADP-ribosylation factor GTPase activating protein 1	Arfgap1	0.96±0.47
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited) (predicted)	Arfgef1_predicted	2.81±0.62
ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	Arfgef2	1.15±0.05
ADP-ribosylation factor interacting protein 2	Arfip2	2.74±0.69
ADP-ribosylation factor related protein 1	Arfrp1	1.13±0.17
ADP-ribosylation factor-like 1	Arl1	3.96±0.41
ADP-ribosylation factor-like 13B	Arl13b	1.31±0.31
ADP-ribosylation factor-like 2	Arl2	1.02±0.15
ADP-ribosylation factor-like 2 binding protein	Arl2bp	4.44±0.41
ADP-ribosylation factor-like 3	Arl3	3.31±0.55
ADP-ribosylation factor-like 4A	Arl4a	0.52±0.37
ADP-ribosylation factor-like 4C	Arl4c	0.46±0.01
ADP-ribosylation factor-like 5A	Arl5a	0.9±0.38
ADP-ribosylation factor-like 6 (predicted)	Arl6_predicted	3.42±1.47
ADP-ribosylation factor-like 6 interacting protein 1	Arl6ip1	4.74±0.5
ADP-ribosylation factor-like 6 interacting protein 2	Arl6ip2	1.9±0.09
ADP-ribosylation factor-like 6 interacting protein 4	Arl6ip4	1.76±0.72
ADP-ribosylation factor-like 6 interacting protein 5	Arl6ip5	7.91±0.23
ADP-ribosylation factor-like 8A	Arl8a	2.43±0.24
ADP-ribosylation factor-like 8B	Arl8b	4.49±0.93
ADP-ribosylhydrolase like 2 (predicted)	Adprhl2_predicted	1.07±0.35
adrenergic receptor kinase, beta 1	Adrbk1	0.37±0.07
adrenocortical dysplasia	Acd	1.42±0.09
advanced glycosylation end product-specific receptor	Ager /// Agpat1 /// Btnl7	3.34±0.66
AF4/FMR2 family, member 3 (predicted)	Aff3_predicted	0.21±0.01
AF4/FMR2 family, member 4 (predicted)	Aff4_predicted	4.19±1.11
AFG3(ATPase family gene 3)-like 1 (yeast) (predicted)	Afg3l1_predicted	0.73±0.03
AFG3(ATPase family gene 3)-like 2 (yeast)	Afg3l2	3.91±1.33
aftiphilin	Aftph	2.9±0.59
agrin	Agrn	2.76±0.92
AHNAK nucleoprotein (desmoyokin)	Ahnak	8.91±3.82
ajuba	Jub	5.45±2.56
AKT1 substrate 1 (proline-rich) (predicted)	Akt1s1_predicted	1.49±0.2
alanyl-tRNA synthetase	Aars	4.34±0.29
alanyl-tRNA synthetase 2, mitochondrial (putative)	Aars2	0.43±0.11
alanyl-tRNA synthetase domain containing 1	Aarsd1	1.29±0.01
alcohol dehydrogenase 4 (class II), pi polypeptide /// alcohol dehydrogenase 5	Adh4 /// Adh5	5.26±0.36
alcohol dehydrogenase, iron containing, 1	Adhfe1	11.52±0.35
aldehyde dehydrogenase 1 family, member A1	Aldh1a1	39.7±4.82
aldehyde dehydrogenase 1 family, member L1	Aldh1l1	11.64±0.17
aldehyde dehydrogenase 16 family, member A1	Aldh16a1	2.47±0.29
aldehyde dehydrogenase 9 family, member A1	Aldh9a1	3.74±1.22
aldehyde dehydrogenase family 1, subfamily A2	Aldh1a2	4.41±0.79
aldehyde dehydrogenase family 1, subfamily A7	Aldh1a7	0.32±0.06
aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	4.47±0.25
aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	10.8±0.77
aldehyde dehydrogenase family 7, member A1	Aldh7a1	16.14±3.34
aldo-keto reductase family 1, member A1 (aldehyde reductase)	Akr1a1	15.05±0.85
aldo-keto reductase family 1, member B1 (aldose reductase)	Akr1b1	1.13±1.81
aldo-keto reductase family 1, member E1	Akr1e1	3.78±0.73
aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	Akr7a2	3.14±2.3
aldolase A	Aldoa	60.73±1.36
aldolase B	Aldob	12.01±8.31
alkB, alkylation repair homolog (E. coli) (predicted)	Alkbh_predicted	2.11±0.66
alkB, alkylation repair homolog 2 (E. coli) (predicted)	Alkbh2_predicted	1.5±0.22
alkB, alkylation repair homolog 3 (E. coli)	Alkbh3	2.21±0.24
alkB, alkylation repair homolog 5 (E. coli) (predicted)	Alkbh5_predicted	1.21±0.17
alkB, alkylation repair homolog 6 (E. coli)	Alkbh6	1.03±0.47
alkB, alkylation repair homolog 7 (E. coli)	Alkbh7	2.79±0.3
alpha globin regulatory element containing gene	Mare	0.98±0.27
alpha glucosidase 2 alpha neutral subunit (predicted)	Ganab_predicted	2.7±0.4

alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	5.32±0.5
alpha-2-glycoprotein 1, zinc	Azgp1	0.59±0.1
alpha-kinase 2	Alpk2	0.31±0.42
alpha-spectrin 2	Spna2	14.4±3.75
amine oxidase (flavin containing) domain 2	Aof2	1.84±0.07
amine oxidase, flavin containing 1 (predicted)	Aof1_predicted	0.77±0.18
aminoadipate-semialdehyde dehydrogenase	Aasdh	0.9±0.15
aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (predicted)	Aasdhppt_predicted	2.87±0.68
aminolevulinate, delta-, dehydratase	Alad	2.04±0.1
aminolevulinic acid synthase 1	Alas1	8.22±2.36
aminomethyltransferase (glycine cleavage system protein T)	Amt	1.45±0
aminopeptidase puromycin sensitive	Npepps	3.54±0.96
aminopeptidase-like 1 (predicted)	Npepl1_predicted	1.8±0.06
amino-terminal enhancer of split	Aes	9.56±0.78
AMME chromosomal region gene 1-like	Ammecr1l	4.36±1.03
amphiphysin	Amph	1.22±0.52
amplified in osteosarcoma	Os9	1.03±0.96
amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Agl	3.36±0
amyloid beta (A4) precursor protein	App	34.55±4.08
amyloid beta (A4) precursor protein-binding, family A, member 3	Apba3	1.91±0.24
amyloid beta (A4) precursor protein-binding, family B, member 1	Apbb1	1.24±0.03
amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	2±0.12
amyloid beta (A4) precursor protein-binding, family B, member 3	Apbb3	0.2±0.25
amyloid beta (A4) precursor-like protein 2	Aplp2	15.29±0.24
Amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Appbp2	2.43±0.74
amyloid beta precursor protein binding protein 1	Appbp1	1.56±0.57
amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	Als2cr2	4.51±0.09
Amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	Als2	1.22±0.47
anaphase promoting complex subunit 1 (predicted)	Anapc1_predicted	0.57±0.1
anaphase promoting complex subunit 10 (predicted)	Anapc10_predicted	0.64±0.12
anaphase promoting complex subunit 11 homolog (yeast)	Anapc11	3.94±0.26
anaphase promoting complex subunit 2	Anapc2	3.96±1.08
anaphase promoting complex subunit 4	Anapc4	2.64±0.18
anaphase promoting complex subunit 7 (predicted)	Anapc7_predicted	0.8±0.05
anaphase-promoting complex subunit 5 (predicted)	Anapc5_predicted	17.58±1.82
ancient ubiquitous protein 1	Aup1	1.66±0.36
androgen-induced 1	Aig1	1.03±0.28
angel homolog 2 (Drosophila) (predicted)	Angel2_predicted	0.65±0.07
angio-associated migratory protein (predicted)	Aamp_predicted	4.79±0.35
angiogenic factor with G patch and FHA domains 1	Aggf1	1.08±0.13
angiopoietin-like 4	Angptl4	3.45±2.93
angiotensin II receptor, type 1a	Agtr1a	3.15±1.29
angiotensin II, type I receptor-associated protein	Agtrap	0.41±0.37
anillin, actin binding protein (scraps homolog, Drosophila)	Anln	0.46±0.02
ankrin repeat domain 50	Ankrd50	1.87±0.47
ankyrin 2, neuronal	Ank2	1.68±0.02
ankyrin 3, epithelial	Ank3	6.98±0.6
ankyrin repeat and BTB (POZ) domain containing 1	Abtb1	1.63±0.09
ankyrin repeat and FYVE domain containing 1 (predicted)	Ankfy1_predicted	2.98±0.51
ankyrin repeat and IBR domain containing 1	Ankib1	1.87±0.59
ankyrin repeat and LEM domain containing 2	Ankle2	1.07±0.04
ankyrin repeat and MYND domain containing 2 (predicted)	Ankmy2_predicted	3.15±1.32
ankyrin repeat and SAM domain containing 1 (predicted)	Anks1_predicted	13.5±0.31
ankyrin repeat and SOCS box-containing protein 1 (predicted)	Asb1_predicted	0.32±0.06
Ankyrin repeat and SOCS box-containing protein 3 (predicted)	Asb3_predicted	0.99±0.66
ankyrin repeat and SOCS box-containing protein 6	Asb6	0.78±0.29
ankyrin repeat and SOCS box-containing protein 8 (predicted)	Asb8_predicted	4.54±0.67
ankyrin repeat and SOCS box-containing protein 9 (predicted)	Asb9_predicted	3.38±0.8
ankyrin repeat and sterile alpha motif domain containing 3	Anks3	0.81±0.34
ankyrin repeat and zinc finger domain containing 1	Ankzf1	0.57±0.25
ankyrin repeat domain 1 (cardiac muscle)	Ankrd1	0.28±0.22
ankyrin repeat domain 10	Ankrd10	7.64±0.32
ankyrin repeat domain 11 (predicted)	Ankrd11_predicted	0.36±0.18
ankyrin repeat domain 12 (predicted)	Ankrd12_predicted	0.32±0.12
ankyrin repeat domain 13a	Ankrd13a	17.7±3.51
ankyrin repeat domain 13C	Ankrd13c	9.26±0.57
ankyrin repeat domain 15	Ankrd15	6.58±1.15
ankyrin repeat domain 17	Ankrd17	5.25±0.12
ankyrin repeat domain 24 (predicted)	Ankrd24_predicted	1.01±0.25
ankyrin repeat domain 26	Ankrd26	0.2±0.01
ankyrin repeat domain 28	Ankrd28	1.51±0.28
ankyrin repeat domain 46	Ankrd46	5.65±1.03
ankyrin repeat domain 49 (predicted)	Ankrd49_predicted	0.83±0.37
ankyrin repeat domain 52 (predicted)	Ankrd52_predicted	1.4±0.15
ankyrin repeat domain 54	Ankrd54	0.86±0.26
ankyrin repeat domain 6	Ankrd6	0.31±0.12
ankyrin repeat, family A (RFXANK-like), 2	Ankra2	0.56±0.44
annexin A1	Anxa1	1.21±0.29
annexin A11	Anxa11	16.17±1.37
annexin A2	Anxa2	12.43±0.31
annexin A4	Anxa4	1.06±0.21
annexin A5	Anxa5	21.96±5.77
annexin A6	Anxa6	10.74±0.73
annexin A7	Anxa7	2.88±0.02
anterior pharynx defective 1a homolog (C. elegans)	Aph1a	6.31±2.06
anterior pharynx defective 1b homolog (C. elegans)	Aph1b	3.23±2.28
antigen identified by monoclonal antibody Ki-67 (predicted)	Mki67_predicted	1.32±0.6

antigenic determinant of rec-A protein	Kin	0.85±0.64
anti-Mullerian hormone type 2 receptor	Amhr2	0.27±0.17
Antisense paternally expressed gene 3	Apeg3	1.77±0.23
antizyme inhibitor 1	Azin1	3.86±0.51
AP1 gamma subunit binding protein 1	Ap1gbp1	1.9±0.29
APAF1 interacting protein (predicted)	Apip_predicted	0.86±0.01
apolipoprotein A-I binding protein (predicted)	Apoa1bp_predicted	9.23±0.81
apolipoprotein O-like	Apool	3.73±0.85
apoptosis antagonizing transcription factor	Aatf	0.31±0.05
Apoptosis inhibitor 5 (predicted)	Api5_predicted	5.15±0.54
apoptosis-inducing factor, mitochondrion-associated 1	Aifm1	17.84±5.57
apoptosis-inducing factor, mitochondrion-associated 2	Aifm2	0.42±0.01
apoptotic chromatin condensation inducer 1	Acin1	3.63±0.36
apoptotic peptidase activating factor 1	Apaf1	0.26±0.19
aprataxin	Aptx	0.29±0.3
apurinic/apyrimidinic endonuclease 1	Apex1	1.24±0.06
aquarius (predicted)	Aqr_predicted	1.71±0.32
archaelysin family metallopeptidase 2	Amz2	0.9±0.17
archain 1	Arcn1	5.39±1.08
Arg/Abl-interacting protein ArgBP2	Argbp2	1.07±0.48
arginine vasopressin receptor 2	Avpr2	2.25±1.13
arginine vasopressin-induced 1	Avpi1	3.35±0.68
arginine/serine-rich coiled-coil 1	Rsrc1	1.26±0.02
arginine-glutamic acid dipeptide (RE) repeats	Rere	2.41±0.12
arginine-rich, mutated in early stage tumors (predicted)	Armet_predicted	3.16±0.39
arginine-tRNA-protein transferase 1 (predicted)	Ate1_predicted	1.14±1.01
argininosuccinate lyase	Asl	1.69±0.87
arginyl aminopeptidase (aminopeptidase B)	Rnpep	11.27±0.35
arginyl-tRNA synthetase (predicted)	Rars_predicted	2.13±0.43
arginyl-tRNA synthetase 2, mitochondrial	Rars2	1.49±0.11
ariadne homolog 2 (Drosophila) (predicted)	Arih2_predicted	1.2±0.11
Ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	Arih1	0.87±0.25
armadillo repeat containing 1 (predicted)	Armc1_predicted	1.74±0.38
armadillo repeat containing 10	Armc10	1.33±0.01
armadillo repeat containing 5	Armc5	0.77±0.27
armadillo repeat containing 8 (predicted)	Armc8_predicted	1.28±0.28
armadillo repeat containing 9 (predicted)	Armc9_predicted	1.28±0.23
armadillo repeat containing, X-linked 1	Armcx1	0.77±0.03
armadillo repeat containing, X-linked 2	Armcx2	0.29±0.03
armadillo repeat containing, X-linked 3	Armcx3	1.29±0.12
armadillo repeat containing, X-linked 6	Armcx6	0.21±0.14
ARP1 actin-related protein 1 homolog A (yeast) (predicted)	Actr1a_predicted	3.78±0.38
ARP1 actin-related protein 1 homolog B (yeast)	Actr1b	2.75±0.05
ARP10 actin-related protein 10 homolog (S. cerevisiae)	Actr10	5.87±1.78
ARP2 actin-related protein 2 homolog (yeast)	Actr2	11.89±2.24
ARP2 actin-related protein 2 homolog (yeast) /// similar to ARP2 actin-related protein 2 homolog (yeast) (predicted)	Actr2 /// LOC301861	0.23±0.07
ARP3 actin-related protein 3 homolog (yeast)	Actr3	5.51±0.87
ARP5 actin-related protein 5 homolog (yeast) (predicted)	Actr5_predicted	0.37±0.01
ARP6 actin-related protein 6 homolog (yeast) (predicted)	Actr6_predicted	2.86±1.56
ARP8 actin-related protein 8 homolog (S. cerevisiae) (predicted)	Actr8_predicted	2.24±0.08
arrestin domain containing 1	Arrdc1	1.87±0.31
arrestin domain containing 2	Arrdc2	1.39±0.7
arrestin, beta 2	Arrb2	0.37±0.35
arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	Asna1	3.55±1.02
arsenic (+3 oxidation state) methyltransferase	As3mt	0.76±0.34
ARV1 homolog (yeast) (predicted)	Arv1_predicted	1.34±0.06
aryl hydrocarbon receptor nuclear translocator 2	Arnt2	10±0.16
aryl hydrocarbon receptor nuclear translocator-like	Arntl	0.97±0.17
aryl-hydrocarbon receptor-interacting protein	Aip	2.08±0.18
arylsulfatase A	Arsa	3.82±0.68
arylsulfatase B	Arsb	1.61±0.31
arylsulfatase E (chondrodysplasia punctata 1)	Arse	1.1±0.26
arylsulfatase K	Arsk	0.78±0.34
ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (predicted)	Asf1a_predicted	2.14±0.76
ASF1 anti-silencing function 1 homolog B (S. cerevisiae) (predicted)	Asf1b_predicted	0.23±0
ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	3.05±0.4
ash2 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash2l_predicted	1.96±0.46
asp (abnormal spindle)-like, microcephaly associated (Drosophila) (predicted)	Aspm_predicted	0.36±0.03
asparaginase like 1	Asrgl1	1.38±0
asparagine synthetase	Asns	0.8±0.21
asparagine synthetase domain containing 1	Asnsd1	2.22±0.53
asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase) (predicted)	Alg1_predicted	0.4±0.09
asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	Alg10b	1.37±0.24
asparagine-linked glycosylation 11 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)	Alg11	1.39±0.52
asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase) (predicted)	Alg12_predicted	0.59±0
asparagine-linked glycosylation 13 homolog (S. cerevisiae)	Alg13	1.8±0.19
asparagine-linked glycosylation 14 homolog (S. cerevisiae)	Alg14	1.64±0.01
asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg2	3.47±0.22
asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg3	1.13±0.13
asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	Alg5	3.76±0.78
asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	Alg8	1.68±0.29
asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase) (predicted)	Alg9_predicted	0.74±0.02
asparaginyl-tRNA synthetase	Nars	2.55±0.44
asparaginyl-tRNA synthetase 2, mitochondrial	Nars2	0.54±0.01
aspartate-beta-hydroxylase (predicted)	Asph_predicted	0.56±0.08
aspartyl aminopeptidase	Dnpep	11.15±1.24
aspartylglucosaminidase	Aga	3.03±0.08

aspartyl-tRNA synthetase	Dars	5.98±2.64
aspartyl-tRNA synthetase 2 (mitochondrial)	Dars2	1.29±0.3
AT hook containing transcription factor 1 (predicted)	Ahctf1_predicted	1.14±0.34
AT hook, DNA binding motif, containing 1 (predicted)	Ahdc1_predicted	1.13±0.12
AT rich interactive domain 1A (Swi1 like) (predicted)	Arid1a_predicted	5.69±0.27
AT rich interactive domain 1B (Swi1 like)	Arid1b	0.32±0.44
AT rich interactive domain 2 (Arid-rfx like) (predicted)	Arid2_predicted	2.12±0.5
AT rich interactive domain 3A (Bright like) (predicted)	Arid3a_predicted	0.56±0.24
AT rich interactive domain 4A (Rbp1 like) (predicted)	Arid4a_predicted	1.16±0.32
AT rich interactive domain 4B (Rbp1 like)	Arid4b	2.12±0.21
AT rich interactive domain 5B (Mrf1 like) (predicted)	Arid5b_predicted	0.48±0.91
ataxin 10	Atxn10	7.23±0.05
ataxin 2 (predicted)	Atxn2_predicted	3.04±0.98
ataxin 2-like (predicted)	Atxn2l_predicted	0.91±0.34
ATG16 autophagy related 16-like 2 (S. cerevisiae) (predicted)	Atg16l2_predicted	0.36±0.06
ATG2 autophagy related 2 homolog A (S. cerevisiae)	Atg2a	0.96±0.16
ATH1, acid trehalase-like 1 (yeast) (predicted)	Athl1_predicted	0.72±0.02
ATP binding domain 1 family, member B (predicted)	Atpbd1b_predicted	0.49±0
ATP binding domain 1 family, member C	Atpbd1c	1.3±0.21
ATP binding domain 4	Atpbd4	2.83±0.83
ATP citrate lyase	Acly	3.23±0.71
ATP synthase mitochondrial F1 complex assembly factor 1 (predicted)	Atpaf1_predicted	3.9±0.54
ATP synthase mitochondrial F1 complex assembly factor 2 (predicted)	Atpaf2_predicted	3.7±0.9
ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	Atp5b	58.52±1.84
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	49.16±1.78
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	Atp5g3	57.76±0.77
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Atp5g1	47.41±3.52
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	Atp5g2	33.27±2.89
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h	43.49±4.15
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	Atp5i	29.03±5.51
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Atp5j	38.41±3.63
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	Atp5s	2.26±0.41
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1	50.66±2.94
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Atp5d	34±3.54
ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	Atp5e	44.08±3.02
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	55.88±4.45
ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	45.22±4.41
ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted	1.64±0.29
ATP5S-like	Atp5sl	3.25±0.42
ATPase family, AAA domain containing 1	Atad1	8.23±1.09
ATPase family, AAA domain containing 2 (predicted)	Atad2_predicted	1.06±0.62
ATPase family, AAA domain containing 3A	Atad3a	0.93±0.05
ATPase family, AAA domain containing 5	Atad5	0.22±0.11
ATPase inhibitory factor 1	Atpif1	9.98±0.98
ATPase type 13A1 (predicted)	Atp13a1_predicted	1.78±0.03
ATPase type 13A2 (predicted)	Atp13a2_predicted	0.68±0.23
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	10.1±0.18
ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	1.49±0.73
ATPase, Ca++ transporting, plasma membrane 2	Atp2b2	0.41±0.05
ATPase, Ca++ transporting, plasma membrane 3	Atp2b3	1.59±0.16
ATPase, Ca++ transporting, type 2C, member 2	Atp2c2	0.23±0.02
ATPase, Ca++-sequestering	Atp2c1	0.99±0.16
ATPase, Class I, type 8B, member 1 (predicted)	Atp8b1_predicted	2.75±0.13
ATPase, class II, type 9B	Atp9b	1.08±0.08
ATPase, class VI, type 11B	Atp11b	2.24±0.25
Atpase, class VI, type 11C (predicted)	Atp11c_predicted	0.46±0.24
ATPase, Cu++ transporting, beta polypeptide	Atp7b	0.24±0.09
ATPase, H transporting, lysosomal V0 subunit c	Atp6v0c	18.03±0.05
ATPase, H transporting, lysosomal V1 subunit B2	Atp6v1b2	5.82±1.19
ATPase, H transporting, lysosomal V1 subunit F	Atp6v1f	11.32±0.82
ATPase, H transporting, lysosomal V1 subunit G1 (predicted)	Atp6v1g1_predicted	3.19±0.22
ATPase, H+ transporting, lysosomal accessory protein 1	Atp6ap1	6.26±0.12
ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	12.69±1.06
ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	0.63±1.14
ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	0.72±0.11
ATPase, H+ transporting, lysosomal V0 subunit A4	Atp6v0a4	9.83±0.1
ATPase, H+ transporting, lysosomal V0 subunit B	Atp6v0b	5.27±0.08
ATPase, H+ transporting, lysosomal V0 subunit D1	Atp6v0d1	9.92±0.19
ATPase, H+ transporting, lysosomal V0 subunit E1	Atp6v0e	14.18±3.51
ATPase, H+ transporting, lysosomal V0 subunit E2	Atp6v0e2	4.69±0.75
ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	11.46±0.19
ATPase, H+ transporting, lysosomal V1 subunit C1	Atp6v1c1	5.66±0.78
ATPase, H+ transporting, lysosomal V1 subunit D	Atp6v1d	12.35±2.54
ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	5.21±0.37
ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	55.14±1.85
ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	64.21±7.61
ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	8.55±0.16
ATP-binding cassette, sub-family A (ABC1), member 2	Abca2	6.26±1.4
ATP-binding cassette, sub-family A (ABC1), member 3	Abca3	1.55±0.04
ATP-binding cassette, sub-family A (ABC1), member 4 (predicted)	Abca4_predicted	2.95±0.13
ATP-binding cassette, sub-family A (ABC1), member 5	Abca5	0.3±0.27
ATP-binding cassette, sub-family B (MDR/TAP), member 10	Abcb10	6.4±0.87
ATP-binding cassette, sub-family B (MDR/TAP), member 6	Abcb6	1.46±0.36
ATP-binding cassette, sub-family B (MDR/TAP), member 8	Abcb8	2.5±0.41
ATP-binding cassette, sub-family B (MDR/TAP), member 9	Abcb9	0.44±0.03
ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	1.17±0.17
ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	2.49±0.44

ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	0.29±0.11
ATP-binding cassette, sub-family D (ALD), member 3	Abcd3	2.98±0.44
ATP-binding cassette, sub-family E (OABP), member 1	Abce1	3.04±0.62
ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	3.59±0.49
ATP-binding cassette, sub-family F (GCN20), member 2 (predicted)	Abcf2_predicted	1.94±0.55
ATP-binding cassette, sub-family F (GCN20), member 3	Abcf3	2.11±0.44
ATP-binding cassette, sub-family G (WHITE), member 1	Abcg1	3.2±1.25
ATR interacting protein	Atrip	0.54±0.03
atrophin 1	Atn1	2.3±0.17
attractin	Atrn	2.08±0.08
attractin like 1	Atrnl1	3.48±0.22
ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	4.26±0.36
AU RNA binding protein/enoyl-coenzyme A hydratase (predicted)	Auh_predicted	10.57±0.42
aurora kinase A	Aurka	0.39±0.11
aurora kinase A interacting protein 1	Aurkaip1	5.64±1.12
aurora kinase B	Aurkb	0.35±0.2
aurora kinase C (predicted)	Aurkc_predicted	0.5±0.17
autocrine motility factor receptor (predicted)	Amfr_predicted	1.91±0.83
autophagy-related 10 (S. cerevisiae)	Atg10	0.63±0.11
autophagy-related 12 (yeast)	Atg12	2.54±0.07
autophagy-related 16-like 1 (yeast)	Atg16l1	1.01±0.08
autophagy-related 3 (yeast)	Atg3	2.47±0.15
autophagy-related 4B (yeast)	Atg4b	1.19±0.37
Autophagy-related 7 (yeast)	Atg7	0.55±0.15
autophagy-related 9A (yeast)	Atg9a	2.03±0.19
axin 1	Axin1	1.59±0.22
AXIN1 up-regulated 1 (predicted)	Axud1_predicted	0.2±0.44
B9 protein domain 1	B9d1	3.44±0.02
baculoviral IAP repeat-containing 2	Birc2	1.53±0.05
baculoviral IAP repeat-containing 4	Birc4	0.21±0.06
baculoviral IAP repeat-containing 5	Birc5	0.5±0.15
Bardet-Biedl syndrome 2 homolog (human)	Bbs2	1.46±0.43
Bardet-Biedl syndrome 4 homolog (human) (predicted)	Bbs4_predicted	1.13±0.11
Bardet-Biedl syndrome 5	Bbs5	0.43±0.01
Bardet-Biedl syndrome 9	Bbs9	1.26±0.41
barrier to autointegration factor 1	Banf1	7.77±1.15
Bartter syndrome, infantile, with sensorineural deafness (Barttin)	Bsnd	8.03±0.12
basic helix-loop-helix domain containing, class B, 9	Bhlhb9	0.24±0.02
basic helix-loop-helix domain containing, class B2	Bhlhb2	2.5±1.17
basic leucine zipper and W2 domains 1	Bzw1	5.81±0.58
basic leucine zipper and W2 domains 2	Bzw2	1.55±0.3
basic leucine zipper nuclear factor 1	Blzf1	0.44±0.12
basic transcription factor 3	Btf3	12.77±1.4
basic transcription factor 3-like 4	Btf3l4	5.76±1.28
basigin	Bsg	32.58±0.56
basophilic leukemia expressed protein BLES03	Bles03	2.12±0.08
BAT2 domain containing 1	Bat2d	0.63±0.52
B-box and SPRY domain containing	Bspry	2.69±0.78
BCDIN3 domain containing	Bcdin3d	0.94±0.27
B-cell CLL/lymphoma 7B	Bcl7b	2.09±0.19
B-cell CLL/lymphoma 7C (predicted)	Bcl7c_predicted	0.77±0.3
B-cell CLL/lymphoma 9 (predicted)	Bcl9_predicted	0.36±0.17
B-cell CLL/lymphoma 9-like (predicted)	Bcl9l_predicted	3.45±0.53
B-cell leukemia/lymphoma 10	Bcl10	3.69±0.78
B-cell leukemia/lymphoma 6 (predicted)	Bcl6_predicted	3.68±1.47
B-cell linker	Blnk	1.48±1.09
B-cell receptor-associated protein 29	Bcap29	4.07±0.14
B-cell receptor-associated protein 31	Bcap31	12.33±1.77
B-cell translocation gene 1, anti-proliferative	Btg1	30.83±3.27
B-cell translocation gene 2, anti-proliferative	Btg2	3.26±8.42
B-cell translocation gene 3	Btg3	1.48±0.49
Bcl-2 binding component 3	Bbc3	0.64±0.49
BCL2/adenovirus E1B 19 kDa-interacting protein 3	Bnip3	6.57±0.43
BCL2/adenovirus E1B 19kDa-interacting protein 1	Bnip1	2.07±0.05
BCL2/adenovirus E1B interacting protein 2	Bnip2	0.53±0.17
BCL2/adenovirus E1B interacting protein 3-like	Bnip3l	5.49±0.37
BCL2-antagonist/killer 1	Bak1	0.6±0.14
Bcl2-associated athanogene 1 (predicted)	Bag1_predicted	6.11±1.46
Bcl2-associated athanogene 3	Bag3	0.8±1.63
BCL2-associated athanogene 4	Bag4	1.34±0.01
BCL2-associated athanogene 5	Bag5	1.59±0.7
bcl2-associated death promoter	Bad	2.06±0.63
BCL2-associated transcription factor 1	Bclaf1	7.02±0.78
Bcl2-associated X protein	Bax	0.82±0.22
Bcl2-like 1	Bcl2l1	1.63±0.67
BCL2-like 13 (apoptosis facilitator) (predicted)	Bcl2l13_predicted	1.03±0.02
Bcl2-like 14 (apoptosis facilitator)	Bcl2l14	0.76±0.04
Bcl2-like 2	Bcl2l2	1.05±0.07
Bcl2-like 2 /// poly(A) binding protein, nuclear 1	Bcl2l2 /// Pabpn1	5.89±1.49
Bcl6 interacting corepressor (predicted)	Bcor_predicted	0.83±0.23
BCS1-like (yeast)	Bcs1l	1.14±0.29
beclin 1, autophagy related	Becn1	3.7±0.8
Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	3.28±0.53
beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	2.53±1.41
beta-1,4-N-acetyl-galactosaminyl transferase 1	B4galnt1	3.47±1.8
beta-2 microglobulin	B2m	7.84±12.3
beta-transducin repeat containing	Btrc	0.36±0.19

BH3 interacting domain death agonist	Bid	0.3±0.1
bicaudal D homolog 2 (Drosophila)	Bicd2	1.32±0.3
bifunctional apoptosis regulator	Bfar	0.79±0.33
biliverdin reductase A	Blvra	0.43±0.5
biliverdin reductase B (flavin reductase (NADPH)) (predicted) /// similar to biliverdin reductase B (flavin reductase (NADPH))	Blvrb_predicted /// LOC	0.52±0.12
biogenesis of lysosome-related organelles complex-1, subunit 1 (predicted)	Bloc1s1_predicted	5.4±0.33
biogenesis of lysosome-related organelles complex-1, subunit 2	Bloc1s2	1.49±0.2
biotinidase	Btd	1.4±0.45
biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	5.2±1.23
bisphosphate 3'-nucleotidase 1	Bpnt1	6.89±0.5
bladder cancer associated protein homolog (human)	Blcap	3.9±0.38
bleomycin hydrolase	Blmh	1.92±0.08
block of proliferation 1	Bop1	0.38±0.07
blocked early in transport 1 homolog (S. cerevisiae)	Bet1	3.74±0.4
blocked early in transport 1 homolog (S. cerevisiae) like	Bet1l	1.1±0.12
Bloom syndrome homolog (human) (predicted)	Blm_predicted	0.36±0.03
Bm403207	LOC498525	0.89±0.06
BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	Bambi	2.35±1.04
BMS1 homolog, ribosome assembly protein (yeast)	Bms1	0.89±0.61
bobby sox homolog (Drosophila) (predicted)	Bbx_predicted	1.88±0.83
bolA homolog 3 (E. coli)	Bola3	4.58±2.06
bolA-like 1 (E. coli) (predicted)	Bola1_predicted	4.3±1
bone marrow stromal cell antigen 2	Bst2	0.69±1.59
bone morphogenetic protein 1	Bmp1	0.61±0.12
bone morphogenetic protein 4	Bmp4	6.07±0.64
bone morphogenetic protein 7	Bmp7	4.35±0.24
bone morphogenetic protein receptor, type 1A	Bmpr1a	2.59±0.09
bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	1.46±1
bradykinin receptor, beta 2 /// similar to RIKEN cDNA 4933433P14 gene	Bdkrb2 /// RGD130847	0.25±0.22
brain and acute leukemia, cytoplasmic	Baalc	0.77±0.13
brain and reproductive organ-expressed protein	Bre	1.61±0.43
brain expressed gene 1	Bex1	0.5±0.88
brain expressed gene 4	Bex4	0.87±0.98
brain expressed myelocytomatosis oncogene	Bmyc	0.35±0.12
brain expressed X-linked 2 /// brain expressed gene 1	Bex1 /// Bex2	0.33±0.08
brain glycogen phosphorylase	Pygb	7.86±1.59
brain protein 16	Brp16	0.7±0.17
brain protein 44-like	Brp44l	46.52±1.18
brain protein I3	Bri3	6.38±0.05
brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	0.2±0.28
branched chain aminotransferase 2, mitochondrial	Bcat2	10.65±1.54
branched chain keto acid dehydrogenase E1, beta polypeptide	Bckdhb	11.92±0.06
branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	8.1±0.19
branched chain ketoacid dehydrogenase kinase	Bckdk	4.6±0.33
Brca1 associated protein 1 (predicted)	Bap1_predicted	5.22±1.09
BRCA1/BRCA2-containing complex, subunit 3	Brcc3	6.11±1.3
BRCA2 and CDKN1A interacting protein (predicted)	Bccip_predicted	1.22±0.42
breakpoint cluster region homolog (predicted)	Bcr_predicted	0.77±0.44
breast cancer 2	Brca2	0.37±0.13
breast cancer anti-estrogen resistance 1	Bcar1	0.69±0.31
breast cancer anti-estrogen resistance 3 (predicted)	Bcar3_predicted	1.8±0.3
breast cancer metastasis-suppressor 1	Brms1	2.18±0.64
breast cancer metastasis-suppressor 1-like (predicted)	Brms1l_predicted	2.3±0.47
breast carcinoma amplified sequence 2 (predicted)	Bcas2_predicted	2.02±0.34
breast carcinoma amplified sequence 3	Bcas3	0.24±0.04
BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae) (predicted)	Brf1_predicted	0.89±0.01
BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	Brf2	0.27±0.07
bridging integrator 3	Bin3	1.46±0.3
brix domain containing 1 (predicted)	Bxdc1_predicted	0.24±0.02
brix domain containing 2	Bxdc2	1.15±0.13
bromo adjacent homology domain containing 1	Bahd1	0.76±0.26
bromodomain adjacent to zinc finger domain, 1B	Baz1b	2.79±0.25
bromodomain adjacent to zinc finger domain, 2A (predicted)	Baz2a_predicted	0.71±0.38
bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted	1.44±0.09
bromodomain and PHD finger containing, 1	Brpf1	0.7±0.03
bromodomain and WD repeat domain containing 2	Brwd2	2.07±0.23
bromodomain containing 1 (predicted)	Brd1_predicted	0.77±0.09
bromodomain containing 2	Brd2	1.81±0.22
bromodomain containing 3 (predicted)	Brd3_predicted	1.36±0.16
bromodomain containing 4	Brd4	2.31±0.63
bromodomain containing 7 (predicted)	Brd7_predicted	2.7±0.56
bromodomain containing 8	Brd8	0.98±0.14
bromodomain containing 9 (predicted)	Brd9_predicted	1.88±0.24
BSD domain containing 1	Bsdc1	1.37±0.06
BTB (POZ) domain containing 1	Btbd1	10.26±1.24
BTB (POZ) domain containing 10	Btbd10	0.93±0.03
BTB (POZ) domain containing 11 (predicted)	Btbd11_predicted	0.61±0.34
BTB (POZ) domain containing 12	Btbd12	0.61±0.06
BTB (POZ) domain containing 14A	Btbd14a	1.33±0.2
BTB (POZ) domain containing 2	Btbd2	1.62±0.45
BTB (POZ) domain containing 3 (predicted)	Btbd3_predicted	0.99±0.12
BTB (POZ) domain containing 6	Btbd6	3.73±0.61
BTB (POZ) domain containing 9	Btbd9	0.52±0.18
BUD13 homolog (yeast)	Bud13	0.69±0.1
budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted)	Bub1_predicted	0.33±0.05
budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	Bub3	5.44±0.93
Bwk1 leukemia-related gene	Bwk1	1.65±0.45

bystin-like	Bysl	0.64±0.42
C1GALT1-specific chaperone 1	C1galt1c1	4.83±0.38
c-abl oncogene 1, receptor tyrosine kinase	Abl1	0.68±0.1
cadherin 1	Cdh1	9.32±2.89
cadherin 15	Cdh15	0.24±0.1
cadherin 16	Cdh16	32.97±2.19
cadherin 3, type 1, P-cadherin (placental)	Cdh3	1.06±0.08
Cadherin 5 (predicted)	Cdh5_predicted	0.47±0.55
cadherin EGF LAG seven-pass G-type receptor 1	Celsr1	0.46±0.01
cadherin EGF LAG seven-pass G-type receptor 2	Celsr2	3.45±0.29
calcineurin binding protein 1	Cabin1	1.13±0.04
calcitonin gene-related peptide-receptor component protein	Crcp	1.56±0.15
calcitonin receptor	Calcr	0.82±0.23
calcium activated nucleotidase 1	Cant1	0.37±0.11
calcium and integrin binding 1 (calmyrin)	Cib1	5.08±0.23
calcium binding and coiled coil domain 1	Calcoco1	3.46±0.32
calcium binding atopy-related autoantigen 1	Cbara1	0.42±0.05
calcium binding protein 1	Cabp1	1.2±0.49
calcium binding protein 39 (predicted)	Cab39_predicted	4.41±1.19
calcium binding protein 39-like	Cab39l	2.42±1
calcium binding protein p22	Chp	2.86±0.16
calcium binding protein p22 /// similar to calcium binding protein P22 (predicted)	Chp /// RGD1565588_p	1.27±0.3
calcium homeostasis endoplasmic reticulum protein (predicted)	Cherp_predicted	1.16±0.17
calcium modulating ligand	Camlg	0.62±0.15
calcium regulated heat stable protein 1	Carhsp1	1.67±0.74
calcium/calmodulin-dependent protein kinase I	Camk1	1.31±0.15
calcium/calmodulin-dependent protein kinase II gamma	Camk2g	0.41±0.15
Calcium/calmodulin-dependent protein kinase II inhibitor 1	Camk2n1	0.23±0.05
calcium/calmodulin-dependent protein kinase II, delta	Camk2d	2.93±0.16
calcium/calmodulin-dependent protein kinase kinase 1, alpha	Camkk1	0.77±0.07
calcium/calmodulin-dependent protein kinase kinase 2, beta	Camkk2	0.3±0.24
calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Cask	0.79±0.32
calcium-sensing receptor	Casr	9.96±0.69
calcyclin binding protein	Cacybp	2.25±2.16
calmodulin 1	Calm1	11.52±1.12
calmodulin 2	Calm2	26.55±5.18
calmodulin 3	Calm3	2.01±0.5
calmodulin binding transcription activator 2 (predicted)	Camta2_predicted	1.18±0.15
calmodulin regulated spectrin-associated protein 1	Camsap1	0.82±0
calnexin	Canx	21.47±2.6
calpain 1	Capn1	9.48±1.35
calpain 10	Capn10	0.44±0.08
calpain 2	Capn2	7.92±0.96
calpain 7	Capn7	2.97±0.24
calpain, small subunit 1	Capns1	9.07±0.01
calpastatin	Cast	2.85±0.9
calreticulin	Calr	7.87±1.93
calreticulin 3	Calr3	0.58±0.21
calsyntenin 1	Clstn1	4.67±2.24
calumenin	Calu	4.2±0.04
camello-like 5	Cml5	3.55±2.07
cAMP responsive element binding protein 3	Creb3	1±0
cAMP responsive element binding protein 3-like 1	Creb3l1	0.35±0.16
cAMP responsive element binding protein 3-like 2	Creb3l2	0.67±0.36
cAMP responsive element binding protein-like 2	Crebl2	1.06±0.05
cAMP-regulated phosphoprotein 19	Arpp19	4.49±1.16
Cancer susceptibility candidate 3	Casc3	0.93±0.04
cannabinoid receptor 1 (brain)	Cnr1	3.8±1.32
canopy 3 homolog (zebrafish)	Cnpy3	1.23±0.09
canopy 4 homolog (zebrafish)	Cnpy4	0.45±0.23
CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	5.19±0.78
CAP-GLY domain containing linker protein 1	Clip1	0.55±0.05
CAP-GLY domain containing linker protein 2	Clip2	1.63±0
capicua homolog (Drosophila) (predicted)	Cic_predicted	4.49±1.21
capping protein (actin filament) muscle Z-line, alpha 2	Capza2	5.48±2.7
capping protein (actin filament) muscle Z-line, beta	Capzb	8.7±1.45
cappuccino	Cno	1.67±0.28
carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Cad	1.19±0.28
carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	Chst14	0.21±0.21
carbonic anhydrase 11	Car11	1.62±0.45
carbonic anhydrase 2	Ca2	16.64±3.63
carbonic anhydrase 4	Ca4	11.21±1.55
carbonic anhydrase VB, mitochondrial	Ca5b	1.04±0.34
carbonyl reductase 1	Cbr1	3.76±0.09
carbonyl reductase 3 (predicted)	Cbr3_predicted	0.26±0.01
carbonyl reductase 4	Cbr4	3.5±0.33
carboxylesterase 2 (intestine, liver)	Ces2	0.66±0.7
carboxylesterase 3	Ces3	0.76±0.35
carboxymethylenebutenolidase homolog (Pseudomonas)	Cmbl	1.1±1.12
carboxypeptidase A4	Cpa4	0.29±0.06
carboxypeptidase D	Cpd	3.73±1.13
carboxypeptidase M (predicted)	Cpm_predicted	0.85±0.29
carcinoembryonic antigen gene family 4	Cgm4	0.21±0.04
cardiolipin synthase 1	Crls1	1.69±0.32
cardiotrophin 1	Ctf1	0.99±0.47
carnitine acetyltransferase	Crat	6.13±2
carnitine O-octanoyltransferase	Crot	3.87±1.94

carnitine palmitoyltransferase 1a, liver	Cpt1a	17.39±1.64
carnitine palmitoyltransferase 1b, muscle	Cpt1b	12.75±1.34
carnitine palmitoyltransferase 2	Cpt2	2.89±0.45
cartilage associated protein	Crtap	3.66±0.11
casein kinase 1, alpha 1	Csnk1a1	6.91±0.98
casein kinase 1, delta	Csnk1d	3.99±0.16
casein kinase 1, epsilon	Csnk1e	0.42±0.04
casein kinase 1, gamma 2	Csnk1g2	1.32±0.1
casein kinase 1, gamma 3	Csnk1g3	0.96±0.13
casein kinase 2, alpha 1 polypeptide	Csnk2a1	0.79±0.24
casein kinase 2, alpha prime polypeptide	Csnk2a2	1.65±0.21
casein kinase 2, beta subunit	Csnk2b	11.25±1.96
caseinolytic peptidase X (E.coli)	Clpx	5.4±0.65
caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	Clpp	2.43±0.17
Casitas B-lineage lymphoma	Cbl	0.39±0.19
Casitas B-lineage lymphoma b	Cblb	0.45±0.2
Casitas B-lineage lymphoma-like 1 (predicted)	Cbll1_predicted	1.26±0.1
cask-interacting protein 2 (predicted)	Caskin2_predicted	2.65±0.51
CASP2 and RIPK1 domain containing adaptor with death domain (predicted)	Cradd_predicted	0.41±0.04
CASP8 and FADD-like apoptosis regulator	Cflar	0.41±0.3
caspase 2	Casp2	2.5±0.62
caspase 3, apoptosis related cysteine protease	Casp3	0.93±0.4
caspase 6	Casp6	2.04±0.33
caspase 7	Casp7	1.16±0.16
caspase 8 associated protein 2 (predicted)	Casp8ap2_predicted	0.34±0.05
caspase 9	Casp9	0.92±0.01
castration induced prostatic apoptosis-related protein 1	Cipar1	0.84±0.41
catalase	Cat	12.84±3.52
catechol-O-methyltransferase domain containing 1 (predicted)	Comtd1_predicted	8.98±1.69
catenin (cadherin associated protein), alpha 1	Ctnna1	20.97±0.31
Catenin (cadherin associated protein), beta 1	Ctnnb1	36.46±1.4
catenin (cadherin associated protein), delta 1 (predicted)	Ctnnd1_predicted	0.86±0.15
catenin, beta like 1	Ctnnbl1	1.98±0.29
catenin, beta-interacting protein 1	Ctnnbip1	1.77±0.61
cathepsin B	Ctsb	16.62±0.65
cathepsin C	Ctsc	7.04±1.53
cathepsin D	Ctsd	5.84±1.54
cathepsin L	Ctsl	4.69±19.13
caudal type homeo box 2	Cdx2	0.29±0.18
CBF1 interacting corepressor	Cir	1.35±0.09
Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	Cited1	4.9±3.84
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	4.95±1.9
CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	1.81±2.86
CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	0.86±1.78
CCAAT/enhancer binding protein zeta (predicted)	Cebpz_predicted	2.3±0.73
CCCTC-binding factor	Ctcf	2.45±0.63
CCR4-NOT transcription complex, subunit 10	Cnot10	1.42±0.46
CCR4-NOT transcription complex, subunit 2	Cnot2	3.78±0.32
CCR4-NOT transcription complex, subunit 4	Cnot4	2.13±0.38
CCR4-NOT transcription complex, subunit 6	Cnot6	2.12±0.05
CCR4-NOT transcription complex, subunit 7 (predicted)	Cnot7_predicted	2.08±0.76
CCR4-NOT transcription complex, subunit 8	Cnot8	0.75±0.21
CD 81 antigen	Cd81	17.97±1.72
CD151 antigen (Raph blood group)	Cd151	5.24±2.36
CD164 antigen	Cd164	19.53±1.52
CD1d1 antigen	Cd1d1	1.02±0.09
CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)	Cd2bp2_predicted	4.05±1.15
CD24 antigen	Cd24	43.92±1.31
CD276 antigen	Cd276	0.9±0.05
CD320 antigen	Cd320	6.93±1.11
cd36 antigen	Cd36	0.95±0.28
CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Cd47	2.21±0.09
CD59 antigen	Cd59	18.71±1.4
CD63 antigen	Cd63	38.38±1.98
CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	27.81±0.21
CD82 antigen	Cd82	7.14±0.78
CD9 antigen	Cd9	9.43±0.56
CD99 antigen	Cd99	9.17±0.38
Cd99 antigen-like 2	Cd99l2	1.6±0.46
CDC like kinase 4	Clk4	3.35±0.76
CDC16 cell division cycle 16 homolog (S. cerevisiae)	Cdc16	2.24±0.03
CDC23 (cell division cycle 23, yeast, homolog)	Cdc23	1.27±0.24
CDC28 protein kinase regulatory subunit 2	Cks2	2.56±0.69
Cdc2-related kinase, arginine/serine-rich	Crkrs	1.01±0.01
CDC42 binding protein kinase alpha	Cdc42bpa	0.25±0.09
Cdc42 binding protein kinase beta	Cdc42bpb	1.03±0.2
CDC42 effector protein (Rho GTPase binding) 1 (predicted)	Cdc42ep1_predicted	0.34±0.49
CDC42 effector protein (Rho GTPase binding) 2	Cdc42ep2	2.42±0.31
CDC42 effector protein (Rho GTPase binding) 4 (predicted)	Cdc42ep4_predicted	1.04±0.22
CDC42 effector protein (Rho GTPase binding) 5 (predicted)	Cdc42ep5_predicted	0.66±0.01
CDC42 small effector 1	Cdc42se1	3.56±1.15
CDC42 small effector 2	Cdc42se2	1.51±0.45
CDC42 small effector 2 /// hypothetical protein LOC691031	Cdc42se2 /// LOC6910	0.32±0.04
CDC91 cell division cycle 91-like 1 (S. cerevisiae)	Cdc91l1	1.5±0.25
CDC-like kinase 1	Clk1	7.91±1.95
CDC-like kinase 2	Clk2	0.82±0.57
CDC-like kinase 3	Clk3	1.09±0.23

CDGSH iron sulfur domain 1	Cisd1	34.2±1.65
CDGSH iron sulfur domain 2	Cisd2	2.83±0.62
CDK105 protein	Cdk105	5.75±0.13
CDK2 (cyclin-dependent kinase 2)-associated protein 1 (predicted) /// similar to CDK2 (cyclin-dependent kinase 2)-associated protein 1	Cdk2ap1_predicted ///	4.8±0.38
Cdk5 and Abl enzyme substrate 1 (predicted)	Cables1_predicted	1.51±0.29
CDK5 regulatory subunit associated protein 1-like 1 (predicted)	Cdkal1_predicted	0.63±0.16
CDK5 regulatory subunit associated protein 2	Cdk5rap2	1.02±0.27
CDKN1A interacting zinc finger protein 1 (predicted)	Ciz1_predicted	1.75±0.55
CDKN2A interacting protein	Cdkn2aip	0.65±0.46
CDKN2A interacting protein N-terminal like	Cdkn2aipnl	1.25±0.09
CDNA BC060737 (predicted)	BC060737_predicted	0.37±0.18
CDP-diacylglycerol synthase 1	Cds1	3.89±0.18
CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Cdipt	7.83±0.31
CDW92 antigen	Cdw92	4.88±0.63
cell adhesion molecule 1	Cadm1	1.12±0.01
cell adhesion molecule JCAM	LOC304000	6.26±0.13
cell cycle associated protein 1	Caprin1	7.78±2.69
cell cycle progression 1 (predicted)	Ccpg1_predicted	1.87±0.38
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (predicted)	Cidea_predicted	1.73±1.05
cell division cycle 123 homolog (S. cerevisiae)	Cdc123	2.03±0.4
cell division cycle 2 homolog (S.pombe)-like 1	Cdc2l1	0.27±0
cell division cycle 2 homolog (S.pombe)-like 1 /// similar to cell division cycle 2-like 1 (predicted)	Cdc2l1 /// RGD156635	2.06±0.16
cell division cycle 2 homolog A (S. pombe)	Cdc2a	1.22±0.02
cell division cycle 20 homolog (S. cerevisiae)	Cdc20	0.92±0.01
cell division cycle 25 homolog A (S. pombe)	Cdc25a	0.26±0.02
cell division cycle 26	Cdc26	1.07±0.04
cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	1.36±0.46
cell division cycle 2-like 6 (CDK8-like) (predicted)	Cdc2l6_predicted	2.64±0.59
cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted	2.9±0.53
cell division cycle 37 homolog (S. cerevisiae)	Cdc37	6.64±0.12
cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	1.79±0.23
cell division cycle 40 homolog (yeast) (predicted)	Cdc40_predicted	0.85±0.22
cell division cycle 42 homolog (S. cerevisiae)	Cdc42	17.09±1.58
cell division cycle 45 homolog (S. cerevisiae)-like	Cdc45l	0.34±0.31
cell division cycle 5-like (S. pombe)	Cdc5l	3.28±0.53
cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Cdc73	3.7±0.36
cell division cycle and apoptosis regulator 1	Ccar1	3.18±0.32
cell division cycle associated 3	Cdca3	1.55±0.53
cell division cycle associated 4	Cdca4	1.71±0.49
cell division cycle associated 7 like	Cdca7l	0.72±0.14
cell growth regulator with ring finger domain 1	Cgrrf1	2.42±0.18
cellular nucleic acid binding protein	Cnbp	12.42±1.29
cellular repressor of E1A-stimulated genes 1	Creg1	13.58±6.82
centaurin, alpha 1	Centa1	1.37±0.24
centaurin, beta 5 (predicted)	Centb5_predicted	0.58±0.02
centaurin, delta 1 (predicted)	Centd1_predicted	0.21±0.2
centaurin, delta 2	Centd2	1.04±0.16
centaurin, gamma 2 (predicted)	Centg2_predicted	2.82±0.47
centrin 2	Cetn2	9.26±0.98
centrin 3	Cetn3	3.55±0.16
centrin 4	Cetn4	0.26±0.06
centrobin, centrosomal BRCA2 interacting protein (predicted)	Cntrob_predicted	0.28±0.08
centromere protein B	Cenpb	2.32±0.32
centromere protein I	Cenpi	0.29±0
centromere protein J (predicted)	Cenpj_predicted	0.36±0.08
centromere protein K	Cenpk	0.32±0.01
centromere protein L	Cenpl	0.83±0.17
centromere protein N	Cenpn	0.49±0.13
centromere protein Q	Cenpq	0.25±0.02
centrosomal protein 110	Cep110	0.77±0
centrosomal protein 152 (predicted)	Cep152_predicted	0.28±0.1
centrosomal protein 250	Cep250	0.59±0.05
centrosomal protein 27 (predicted)	Cep27_predicted	1.02±0.2
centrosomal protein 27 (predicted) /// similar to Centrosomal protein of 27 kDa (Cep27 protein)	Cep27_predicted /// LO	0.84±0.13
centrosomal protein 57	Cep57	0.9±0.19
centrosomal protein 68 (predicted)	Cep68_predicted	1.32±0.48
centrosomal protein 70	Cep70	1.91±0.46
cereblon	Crbn	1.45±0.09
ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Cln3	2.74±0.43
ceroid-lipofuscinosis, neuronal 5 (predicted)	Cln5_predicted	0.3±0.04
ceroid-lipofuscinosis, neuronal 8	Cln8	0.69±0.09
CGG triplet repeat binding protein 1 (predicted)	Cggbp1_predicted	2.95±0.42
CGI-96 protein	Cgi-96	0.35±0.09
ChaC, cation transport regulator homolog 2 (E. coli)	Chac2	1.1±0.43
ChaC, cation transport regulator-like 1 (E. coli) (predicted)	Chac1_predicted	0.43±0.15
chaperonin containing TCP1, subunit 2 (beta)	Cct2	6.69±0.79
chaperonin subunit 3 (gamma)	Cct3	7.99±1.37
chaperonin subunit 4 (delta)	Cct4	10.75±1.42
chaperonin subunit 5 (epsilon)	Cct5	12.43±2.53
chaperonin subunit 6a (zeta) /// similar to chaperonin subunit 6a (zeta)	Cct6a /// LOC316484 //	2.55±0.25
chaperonin subunit 7 (eta) (predicted)	Cct7_predicted	8.52±0.41
chaperonin subunit 8 (theta) (predicted)	Cct8_predicted	4.81±1.21
checkpoint kinase 1 homolog (S. pombe)	Chek1	0.39±0.1
Checkpoint suppressor 1 (predicted)	Ches1_predicted	1.01±0.2
checkpoint with forkhead and ring finger domains	Chfr	1.31±0.33
chemokine (C-C motif) ligand 27 (predicted)	Ccl27_predicted	0.54±0.14
chemokine (C-X3-C motif) ligand 1	Cx3cl1	0.73±0.81

chemokine (C-X-C motif) ligand 11	Cxcl11	0.9±1.2
chemokine (C-X-C motif) ligand 12	Cxcl12	9.4±0.78
chemokine (C-X-C motif) ligand 16	Cxcl16	2.95±0.75
chibby homolog 1 (Drosophila)	Cby1	2.49±0.7
chimerin (chimaerin) 1	Chn1	0.28±0.13
chitinase domain containing 1	Chid1	0.82±0.2
chitobiase, di-N-acetyl-	Ctbs	1.38±0.06
chloride channel 2	Clcn2	0.22±0.11
chloride channel 3	Clcn3	5.92±0.01
chloride channel 4-2	Clcn4-2	8.75±2.97
Chloride channel 6 (predicted)	Clcn6_predicted	0.59±0.4
chloride channel 7	Clcn7	0.28±0.05
chloride channel calcium activated 5	Clca5	0.34±0.13
chloride channel CLIC-like 1	Clcc1	0.95±0.08
chloride channel Ka	Clcnka	15.78±4.17
chloride channel Kb	Clcnkb	15.84±0.49
chloride channel, nucleotide-sensitive, 1A	Clns1a	2.67±0.58
chloride intracellular channel 1	Clic1	16.8±1.28
CHMP family, member 7 (predicted)	Chmp7_predicted	2.21±0.45
cholecystokinin	Cck	0.23±0.19
choline kinase alpha	Chka	1.96±1.17
choline kinase beta	Chkb	4.53±0.16
choline phosphotransferase 1	Chpt1	7.34±2.21
choline/ethanolamine phosphotransferase 1	Cept1	3.81±0.01
chondroitin sulfate N-acetylgalactosaminyltransferase 2	Csgalnact2	0.87±0.16
chondroitin sulfate proteoglycan 4	Cspg4	1.34±0.21
choroidermia	Chm	0.48±0.23
chromatin accessibility complex 1 (predicted)	Chrac1_predicted	3±0.47
chromatin assembly factor 1, subunit B (p60)	Chaf1b	0.42±0.13
chromatin licensing and DNA replication factor 1	Cdt1	0.62±0.26
chromatin modifying protein 1A	Chmp1a	2.24±0.07
chromatin modifying protein 1B	Chmp1b	1.51±0.3
chromatin modifying protein 2B	Chmp2b	2.63±0.56
chromatin modifying protein 4C	Chmp4c	0.68±0.8
chromatin modifying protein 5	Chmp5	16.66±2.15
chromatin modifying protein 6 (predicted)	Chmp6_predicted	2.01±0.56
chromobox homolog 1 (Drosophila HP1 beta) (predicted)	Cbx1_predicted	3.4±2.13
chromobox homolog 2 (Drosophila Pc class)	Cbx2	0.44±0.01
chromobox homolog 3 (HP1 gamma homolog, Drosophila)	Cbx3	8.48±1.25
chromobox homolog 5 (Drosophila HP1a) (predicted)	Cbx5_predicted	1.12±0.59
chromobox homolog 6	Cbx6	4.57±1.62
chromobox homolog 7	Cbx7	1.72±0.21
chromodomain helicase DNA binding protein 1 (predicted)	Chd1_predicted	1.86±0.29
Chromodomain helicase DNA binding protein 2 (predicted)	Chd2_predicted	2.27±0.04
Chromodomain helicase DNA binding protein 3	Chd3	0.67±0.41
chromodomain helicase DNA binding protein 4	Chd4	5.04±0.25
chromodomain helicase DNA binding protein 6 (predicted)	Chd6_predicted	0.42±0.02
chromodomain helicase DNA binding protein 7 (predicted)	Chd7_predicted	0.92±0.07
chromodomain helicase DNA binding protein 8	Chd8	2.18±0.18
chromosome segregation 1-like (S. cerevisiae) (predicted)	Cse1l_predicted	2.41±1.12
chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	Ctf8	1.5±0.16
churchill domain containing 1 (predicted)	Churc1_predicted	7.08±1.69
ciliary rootlet coiled-coil, rootletin (predicted)	Crocc_predicted	1.13±0.22
cingulin (predicted)	Cgn_predicted	1.78±0.17
cingulin-like 1	Cgnl1	35.96±1.95
cirrhosis, autosomal recessive 1A (human)	Cirh1a	1.12±0.06
cisplatin resistance-associated overexpressed protein	Crop	8.32±0.7
citrate lyase beta like	Clybl	2.18±1.19
Citrate synthase	Cs	26.63±3.33
Citron	Cit	1.92±0.25
CKLF-like MARVEL transmembrane domain containing 6	Cmtm6	3.63±0.89
CKLF-like MARVEL transmembrane domain containing 7	Cmtm7	0.97±0.08
CKLF-like MARVEL transmembrane domain containing 8	Cmtm8	0.29±0.26
clathrin, heavy polypeptide (Hc)	Cltc	14.8±1.68
clathrin, light polypeptide (Lca)	Clta	17.11±0.05
clathrin, light polypeptide (Lcb)	Cltb	2.75±0.49
claudin 10 (predicted)	Cldn10_predicted	46.93±2.56
claudin 12	Cldn12	1.07±0.22
claudin 16	Cldn16	8.91±0.01
claudin 19	Cldn19	14.28±2.39
claudin 3	Cldn3	1.62±0.96
claudin 5	Cldn5	0.66±2.44
claudin 6 (predicted)	Cldn6_predicted	0.32±0.08
claudin 7	Cldn7	2.52±0.16
claudin 8	Cldn8	4.23±0.18
claudin domain containing 1	Cldnd1	3.21±0.29
cleavage and polyadenylation factor subunit homolog (S. cerevisiae) (predicted)	Pcf11_predicted	1.18±0.28
cleavage and polyadenylation specific factor 1	Cpsf1	0.46±0.39
cleavage and polyadenylation specific factor 2 (predicted)	Cpsf2_predicted	2.4±0.34
cleavage and polyadenylation specific factor 3-like	Cpsf3l	1.24±0.3
cleavage and polyadenylation specific factor 5	Cpsf5	3.5±0.49
cleavage and polyadenylation specific factor 6	Cpsf6	4.68±0.1
cleavage and polyadenylation specificity factor 3	Cpsf3	2.41±0.54
cleavage stimulation factor, 3' pre-RNA subunit 2, tau (predicted)	Cstf2t_predicted	7.66±2.4
cleavage stimulation factor, 3' pre-RNA, subunit 1	Cstf1	0.64±0.05
cleft lip and palate associated transmembrane protein 1 (predicted)	Clptm1_predicted	4.45±0.94
CLIP associating protein 2	Clasp2	1.24±0.02

CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	Clp1	0.49±0.08
ClpB caseinolytic peptidase B homolog (E. coli)	Clpb	2.98±0.31
CLPTM1-like	Clptm1l	8.96±0.55
clusterin associated protein 1	Cluap1	1.88±0.44
c-Maf-inducing protein	Cmip	0.95±0.51
Cnksr family member 3	Cnksr3	0.71±0.7
coagulation factor II (thrombin) receptor	F2r	18.56±1.08
coagulation factor II (thrombin) receptor-like 1	F2rl1	1.16±0.38
coagulation factor III	F3	1.04±0.79
coagulation factor V	F5	4.04±6.57
coatomer protein complex subunit alpha	Copa	10.52±0.96
coatomer protein complex, subunit beta 1	Copb1	5.57±1.15
coatomer protein complex, subunit beta 2 (beta prime)	Copb2	9.09±2.16
coatomer protein complex, subunit epsilon (predicted)	Cope_predicted	5.73±1.02
coatomer protein complex, subunit gamma	Copg	4.49±1.76
coatomer protein complex, subunit zeta 1 (predicted)	Copz1_predicted	8.8±0.56
coatomer protein complex, subunit zeta 2 (predicted)	Copz2_predicted	1.65±0.36
Cobl-like 1 (predicted)	Cobll1_predicted	11.4±1.52
COBW domain containing 1	Cbwd1	0.47±0.05
Coenzyme A synthase	Coasy	1.2±0.05
coenzyme Q10 homolog A (yeast) (predicted)	Coq10a_predicted	1.36±0.1
coenzyme Q10 homolog B (S. cerevisiae)	Coq10b	3.22±0.61
coenzyme Q2 homolog, prenyltransferase (yeast)	Coq2	0.82±0.07
coenzyme Q3 homolog, methyltransferase (yeast)	Coq3	2.49±0.4
coenzyme Q4 homolog (yeast)	Coq4	0.69±0.02
coenzyme Q5 homolog, methyltransferase (yeast)	Coq5	0.96±0.3
Coenzyme Q6 homolog (yeast)	Coq6	0.49±1.4
cofactor of BRCA1	Cobra1	2.21±0.51
cofilin 1, non-muscle	Cfl1	6.01±0.12
cofilin 1, non-muscle	Cfl1 /// LOC502589 /// L	0.63±0.02
cofilin 2, muscle (predicted)	Cfl2_predicted	8.42±1.95
Cohen syndrome homolog 1 (predicted)	Cohh1_predicted	2.84±0.67
coiled-coil and C2 domain containing 1A	Cc2d1a	0.86±0.26
coiled-coil and C2 domain containing 1B	Cc2d1b	1.31±0.07
coiled-coil domain containing 100	Ccdc100	1.25±0.3
coiled-coil domain containing 101	Ccdc101	0.69±0.11
coiled-coil domain containing 104	Ccdc104	1.6±0.81
coiled-coil domain containing 107	Ccdc107	0.9±0.11
coiled-coil domain containing 113	Ccdc113	0.3±0.01
coiled-coil domain containing 115	Ccdc115	0.37±0.04
coiled-coil domain containing 117	Ccdc117	3±0.56
coiled-coil domain containing 12 (predicted)	Ccdc12_predicted	1.17±0.07
coiled-coil domain containing 124	Ccdc124	3±0.43
coiled-coil domain containing 125	Ccdc125	1.59±0.39
coiled-coil domain containing 126	Ccdc126	1.63±0.32
coiled-coil domain containing 127	Ccdc127	0.79±0.34
coiled-coil domain containing 130	Ccdc130	0.6±0.05
coiled-coil domain containing 132	Ccdc132	1.85±0.34
coiled-coil domain containing 16	Ccdc16	1.05±0.17
coiled-coil domain containing 17	Ccdc17	1.04±0.12
coiled-coil domain containing 21	Ccdc21	1.49±0.35
coiled-coil domain containing 22 (predicted)	Ccdc22_predicted	1.86±0.18
coiled-coil domain containing 23	Ccdc23	1.62±0.42
coiled-coil domain containing 28A	Ccdc28a	1±0.11
coiled-coil domain containing 34	Ccdc34	0.27±0.04
coiled-coil domain containing 41	Ccdc41	0.96±0.12
coiled-coil domain containing 43	Ccdc43	1.23±0.11
coiled-coil domain containing 45	Ccdc45	0.61±0.29
coiled-coil domain containing 49 (predicted)	Ccdc49_predicted	0.42±0.09
coiled-coil domain containing 5	Ccdc5	0.37±0.02
coiled-coil domain containing 51	Ccdc51	1.01±0.07
coiled-coil domain containing 52	Ccdc52	0.28±0
coiled-coil domain containing 53 (predicted)	Ccdc53_predicted	9.51±0.46
coiled-coil domain containing 55	Ccdc55	0.32±0.07
coiled-coil domain containing 56	Ccdc56	13.07±1.9
coiled-coil domain containing 58 (predicted)	Ccdc58_predicted	2.26±0.33
coiled-coil domain containing 59 (predicted)	Ccdc59_predicted	0.36±0.24
coiled-coil domain containing 64	Ccdc64	5.49±0.28
coiled-coil domain containing 65	Ccdc65	0.52±0.15
coiled-coil domain containing 68	Ccdc68	0.39±0.01
coiled-coil domain containing 72 /// hypothetical protein LOC685117	Ccdc72 /// LOC685117	15.95±2.78
coiled-coil domain containing 84	Ccdc84	0.77±0.1
coiled-coil domain containing 86	Ccdc86	0.49±0.09
coiled-coil domain containing 90B	Ccdc90b	2.27±0.04
coiled-coil domain containing 91	Ccdc91	0.82±0.02
coiled-coil domain containing 92	Ccdc92	1.02±0.25
coiled-coil domain containing 93	Ccdc93	0.48±0.1
coiled-coil domain containing 97	Ccdc97	1.15±0.19
coiled-coil domain containing 98	Ccdc98	0.28±0.05
coiled-coil-helix-coiled-coil-helix domain containing 1 (predicted)	Chchd1_predicted	5.4±0.1
coiled-coil-helix-coiled-coil-helix domain containing 2	Chchd2	24.51±1.59
coiled-coil-helix-coiled-coil-helix domain containing 3 (predicted)	Chchd3_predicted	17.25±4.35
coiled-coil-helix-coiled-coil-helix domain containing 4	Chchd4	1±0.28
coiled-coil-helix-coiled-coil-helix domain containing 5 (predicted)	Chchd5_predicted	1.68±0.16
coiled-coil-helix-coiled-coil-helix domain containing 6 (predicted)	Chchd6_predicted	1.81±0.6
coiled-coil-helix-coiled-coil-helix domain containing 8	Chchd8	0.78±0.38
cold inducible RNA binding protein	Cirbp	1.23±0.37

cold shock domain containing E1, RNA binding	Csde1	12.78±2.43
cold shock domain protein A	Csda	2.32±0.27
collagen, type IV, alpha 5	Col4a5	9.92±1.93
colony stimulating factor 1 (macrophage)	Csf1	1.74±0.07
COMM domain containing 10	Commd10	3.84±0.67
COMM domain containing 2	Commd2	1.95±0.05
COMM domain containing 3	Commd3	12.51±0.51
COMM domain containing 4 (predicted)	Commd4_predicted	2.14±0.04
COMM domain containing 5	Commd5	1.21±0.17
COMM domain containing 6	Commd6	2.31±0.33
COMM domain containing 7	Commd7	0.88±0.1
COMM domain containing 8 (predicted)	Commd8_predicted	4.91±0.84
COMM domain containing 9	Commd9	4.54±0.68
complement component (3b/4b) receptor 1-like	Cr1l	3.15±0.03
complement component 1, q subcomponent binding protein	C1qbp	13.48±0.96
complement component 2	Bat4 /// C2 /// C4a /// Cf	2.18±0.52
complement component 5	C5	4.54±0.79
complement component 8, gamma subunit	C8g	0.41±0.01
component of oligomeric golgi complex 1 (predicted)	Cog1_predicted	1.69±0.23
component of oligomeric golgi complex 3	Cog3	1.29±0.26
component of oligomeric golgi complex 4 (predicted)	Cog4_predicted	1.78±0
component of oligomeric golgi complex 6	Cog6	1.86±0.37
component of oligomeric golgi complex 7	Cog7	1.25±0.05
connector enhancer of kinase suppressor of Ras 1	Cnksr1	0.97±0.38
conserved helix-loop-helix ubiquitous kinase (predicted)	Chuk_predicted	5.48±0.29
conserved nuclear protein Nhn1	Nhn1	0.54±0.4
COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	Cops2	5.47±0.41
COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	Cops3	5.19±1.25
COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	Cops4	7.26±1.37
COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	Cops5	4.5±0.83
COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) (predicted)	Cops6_predicted	9.89±0.08
COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (predicted)	Cops7a_predicted	3.27±0.81
COP9 (constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana) (predicted)	Cops7b_predicted	0.86±0.02
COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)	Cops8	4.17±0.57
Copine III (predicted)	Cpne3_predicted	5.48±0.22
copper chaperone for superoxide dismutase	Ccs	1.69±0.12
copper metabolism (Murr1) domain containing 1 (predicted)	Commd1_predicted	4.59±1.32
coproporphyrinogen oxidase	Cpox	3.63±0.66
cordon-bleu (predicted)	Cobl_predicted	3.34±0.02
core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	C1galt1	0.73±0.14
core binding factor beta	Cbfb	2.85±0.26
cornichon homolog (Drosophila) (predicted)	Cnih_predicted	4.53±1.56
cornichon homolog 4 (Drosophila)	Cnih4	1.65±0.06
coronin 7	Coro7	0.43±0.04
coronin, actin binding protein 6	Coro6	1.39±0.17
coronin, actin-binding protein, 1B	Coro1b	2.1±0.1
cortactin	Cttn	1.54±0.33
cortistatin /// kinesin family member 1B	Cort /// Kif1b	0.5±0.01
cortistatin /// phosphogluconate dehydrogenase	Cort /// Pgd	3.22±0.38
COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	2.98±0.37
COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	Cox18	1.83±0.05
COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	Cox19	2.78±0.09
COX4 neighbor	Cox4nb	1.93±0.3
COXII /// cytochrome c oxidase subunit 3	COX2 /// COX3	83.38±17.95
CP110 protein	Cp110	0.51±0.02
craniofacial development protein 1	Cfdp1	3.03±0.52
creatine kinase, brain	Ckb	19.7±4.61
creatine kinase, mitochondrial 1, ubiquitous	Ckmt1	16.54±3.29
CREB binding protein	Crebbp	1.81±0.03
CREB regulated transcription coactivator 2	Crtc2	0.59±0.27
Crn, crooked neck-like 1 (Drosophila)	Crnkl1	0.87±0.26
crumbs homolog 3 (Drosophila)	Crb3	3.52±0.37
cryptochrome 1 (photolyase-like)	Cry1	0.43±0.19
crystallin, alpha B	Cryab	4.02±20.49
crystallin, mu	Crym	6.45±0.8
crystallin, zeta	Cryz	1.35±2.01
crystallin, zeta (quinone reductase)-like 1	Cryzl1	1.32±0.17
c-src tyrosine kinase	Csk	1.69±0.64
CTAGE family, member 5	Ctage5	5.56±0.23
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (predicted)	Ctdp1_predicted	1.34±0.34
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	Ctdsp1	6.13±0.08
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (predicted)	Ctdspl_predicted	5.13±2.03
CTD-binding SR-like protein rA9	LOC245925	1.45±0.21
C-terminal binding protein 1	Ctbp1	5.6±0.27
C-terminal binding protein 2	Ctbp2	3.11±1.66
Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Ctr9	1.05±0.1
CTTNBP2 N-terminal like (predicted)	Cttnbp2nl_predicted	2.8±0.19
C-type lectin domain family 11, member a	Clec11a	0.31±0.09
C-type lectin domain family 16, member A	Clec16a	2.17±0.65
CUB domain containing protein 1 (predicted)	Cdcp1_predicted	1.1±0.1
CUE domain containing 1	Cuedc1	0.67±0.05
CUE domain containing 2 (predicted)	Cuedc2_predicted	1.13±0.17
CUG triplet repeat, RNA binding protein 1	Cugbp1	2±0.46
CUG triplet repeat, RNA binding protein 2	Cugbp2	0.2±0.23
cullin 1 (predicted)	Cul1_predicted	4.05±0.11
cullin 2 (predicted)	Cul2_predicted	0.46±0.05
cullin 3 (predicted)	Cul3_predicted	8.77±0.84

Cullin 4B (predicted)	Cul4b_predicted	2.24±0.18
cullin 5	Cul5	0.24±0.04
cullin associated and neddylation disassociated 1	Cand1	4.75±0.83
cullin-associated and neddylation-dissociated 2 (putative)	Cand2	1.24±0.17
cutA divalent cation tolerance homolog (E. coli)	Cuta	10.12±2.4
cutC copper transporter homolog (E.coli) (predicted)	Cutc_predicted	0.84±0.13
cut-like homeobox 1	Cux1	1.75±0.28
CWC15 homolog (S. cerevisiae)	Cwc15	4.47±0.35
CXXC finger 1 (PHD domain)	Cxxc1	1.63±0.93
CXXC finger 5	Cxxc5	11.7±0.03
cyclin A2	Ccna2	0.62±0.14
cyclin B1	Ccnb1	0.82±0.13
cyclin B2	Ccnb2	1.46±0.38
cyclin C	Ccnc	2.68±0.55
cyclin D binding myb-like transcription factor 1 /// hypothetical gene supported by AF352170 (predicted)	Dmtf1 /// RGD1562889	2.33±0.5
cyclin D1	Ccnd1	7.71±3.57
cyclin D3	Ccnd3	2.52±0.26
cyclin dependent kinase 2	Cdk2	1.03±0.02
cyclin D-type binding-protein 1	Ccndbp1	2.47±0.03
cyclin E1	Ccne1	0.34±0.15
cyclin G associated kinase	Gak	3.08±0.64
cyclin G1	Ccng1	5.12±2.09
cyclin G2 (predicted)	Ccng2_predicted	1.21±0.63
cyclin H	Ccnh	2.88±0.2
cyclin I (predicted)	Ccni_predicted	15.92±2.02
cyclin J (predicted)	Ccnj_predicted	0.23±0.05
cyclin K	Ccnk	1.38±0.06
cyclin L1	Ccnl1	0.87±2.58
cyclin L2	Ccnl2	2.48±1.36
Cyclin M1 (predicted)	Cnnm1_predicted	0.25±0.14
cyclin M2	Cnnm2	0.71±0.13
cyclin M3 (predicted)	Cnnm3_predicted	5.14±0.25
cyclin T2 (predicted)	Ccnt2_predicted	0.49±0.22
cyclin Y	Ccny	4.14±0.05
cyclin Y-like 1	Ccnyl1	0.41±0.26
cyclin-dependent kinase (CDC2-like) 10	Cdk10	0.81±0.06
cyclin-dependent kinase 2B-inhibitor-related protein	P15rs	0.43±0.2
cyclin-dependent kinase 2-interacting protein	Cinp	1.29±0.2
cyclin-dependent kinase 4	Cdk4	3.57±0.21
cyclin-dependent kinase 5	Cdk5	1.18±0.23
cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	Cdk7	1.67±0.15
cyclin-dependent kinase 9 (CDC2-related kinase)	Cdk9	3.39±0.25
cyclin-dependent kinase inhibitor 1A	Cdkn1a	2.65±2
cyclin-dependent kinase inhibitor 1B	Cdkn1b	4.78±0.85
cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	Cdkn2c	1.57±0.1
cyclin-dependent kinase inhibitor 3 (predicted)	Cdkn3_predicted	1.45±0.39
cylindromatosis (turban tumor syndrome)	Cyld	1.52±0.55
cystathionase (cystathionine gamma-lyase)	Cth	2.59±1.22
cystathionine beta synthase	Cbs	5.52±0.17
cystatin B	Cstb	20.39±1.49
cystatin C	Cst3	16.38±0.58
cysteine and glycine-rich protein 1	Csrp1	2.63±2.06
cysteine and glycine-rich protein 2	Csrp2	3.07±0.25
cysteine and glycine-rich protein 2 binding protein (predicted)	Csrp2bp_predicted	3.43±0.12
cysteine and histidine rich 1	Cyhr1	1.26±0.25
cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 (predicted)	Chordc1_predicted	3.2±0.67
cysteine conjugate-beta lyase 1	Ccbl1	2.41±0.44
cysteine dioxygenase 1, cytosolic	Cdo1	3.92±3.13
cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	1.22±0.6
cysteine sulfinic acid decarboxylase	Csad	2.49±0.15
cysteine-rich hydrophobic domain 2 (predicted)	Chic2_predicted	0.24±0.03
cysteine-rich PDZ-binding protein	Cript	3.33±0.58
cysteine-rich protein 2	Crip2	14.63±0.22
cysteine-rich secretory protein LCCL domain containing 2	Crispld2	1.09±0.06
cysteine-rich with EGF-like domains 2	Creld2	0.35±0.16
cysteine-serine-rich nuclear protein 2	Csnrp2	0.78±0.02
cysteinyl-tRNA synthetase (predicted)	Cars_predicted	0.35±0.02
cytidine 5'-triphosphate synthase (predicted)	Ctps_predicted	0.21±0.3
cytidine 5'-triphosphate synthase 2	Ctps2	1.92±0.32
cytidine and dCMP deaminase domain containing 1	Cdadc1	2.61±0.01
cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	Cmpk1	30.43±5.14
cytidine monophospho-N-acetylneuraminic acid hydroxylase	Cmah	1.06±0.15
cytidine monophospho-N-acetylneuraminic acid synthetase	Cmas	3.19±0.05
Cytidine triphosphate synthase II	Ctps2	1.72±0.42
cytochrome b /// cytochrome c oxidase subunit 3	COX3 /// CYTB	81.6±8.51
cytochrome b, ascorbate dependent 3	Cybasc3	1.27±0.01
cytochrome b-5	Cyb5	6.73±1.04
cytochrome b5 reductase 3	Cyb5r3	1.27±0.69
cytochrome b5 reductase 4	Cyb5r4	3.62±0.12
cytochrome b5 type B	Cyb5b	9.62±1.58
cytochrome b-561 (predicted)	Cyb561_predicted	4.83±0.38
cytochrome b-561 domain containing 1 (predicted)	Cyb561d1_predicted	0.31±0.09
cytochrome b-561 domain containing 2	Cyb561d2	1.93±0.68
cytochrome c oxidase subunit IV isoform 1	Cox4i1	50.09±3.79
cytochrome c oxidase subunit Vb	Cox5b	48.3±2.59
cytochrome c oxidase subunit VIIa polypeptide 2 like (predicted)	Cox7a2l_predicted	9.2±0.76
cytochrome c oxidase subunit VIIb	Cox7b	56.87±1.44

cytochrome c oxidase, subunit Va	Cox5a	47.57±3.34
cytochrome c oxidase, subunit VIa, polypeptide 1	Cox6a1	46.55±3.19
cytochrome c oxidase, subunit VIb polypeptide 1	Cox6b1	43.78±4.79
cytochrome c oxidase, subunit VIc	Cox6c	51.63±2.68
cytochrome c oxidase, subunit VIIa 2	Cox7a2	51.17±1.55
cytochrome c oxidase, subunit VIIIa	Cox8a	58.35±0.33
cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	Cox17	7.25±2.34
cytochrome c, somatic	Cycs	39.56±0.12
cytochrome c-1 (predicted)	Cyc1_predicted	36.6±1.26
cytochrome P450 4F6	Cyp4f6	2.17±0.05
cytochrome P450, family 2, subfamily s, polypeptide 1	Cyp2s1	2.4±0.62
cytochrome P450, family 2, subfamily u, polypeptide 1	Cyp2u1	1.11±0.05
cytochrome P450, family 20, subfamily A, polypeptide 1	Cyp20a1	3.05±0.58
cytochrome P450, family 27, subfamily a, polypeptide 1	Cyp27a1	2.05±0.2
cytochrome P450, family 4, subfamily f, polypeptide 17 (predicted)	Cyp4f17_predicted	0.31±0.06
cytochrome P450, family 4, subfamily v, polypeptide 3	Cyp4v3	6.14±2.86
cytochrome P450, subfamily 51	Cyp51	5.1±1.36
cytokine induced apoptosis inhibitor 1	Ciapin1	5.65±0.52
cytokine induced protein 29 kDa	Cip29	4.37±0.93
cytokine inducible SH2-containing protein	Cish	0.94±0.4
cytoplasmic FMR1 interacting protein 1 (predicted)	Cyfip1_predicted	6.12±1.77
cytoplasmic FMR1 interacting protein 2 (predicted)	Cyfip2_predicted	18.25±2.72
cytoplasmic linker associated protein 1	Clasp1	2.75±0.38
cytoplasmic polyadenylation element binding protein 2 (predicted)	Cpeb2_predicted	4.76±1.39
cytoplasmic polyadenylation element binding protein 4 (predicted)	Cpeb4_predicted	3.2±1.33
cytoskeleton associated protein 2 (predicted)	Ckap2_predicted	0.32±0.18
cytoskeleton associated protein 5	Ckap5	1.58±0.73
cytoskeleton-associated protein 4 (predicted)	Ckap4_predicted	0.38±0.16
cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	Ciao1	1.81±0.39
cytotoxic granule-associated RNA binding protein 1	Tia1	0.32±0.09
cytotoxic T lymphocyte-associated protein 2 alpha	Ctla2a	1.46±0.58
D site albumin promoter binding protein	Dbp	0.79±0.39
D-2-hydroxyglutarate dehydrogenase	D2hgdh	0.83±0.06
D4, zinc and double PHD fingers family 2 (predicted)	Dpf2_predicted	1.96±0.09
damage-specific DNA binding protein 1	Ddb1	4.99±0.23
dapper homolog 2, antagonist of beta-catenin (xenopus) (predicted)	Dact2_predicted	0.73±0.1
DAZ associated protein 1	Dazap1	2.08±0.53
DAZ associated protein 2	Dazap2	11.01±1.68
DAZ interacting protein 1-like	Dzip1l	1.98±0.26
DC2 protein	Dc2	5.39±0.6
dCMP deaminase	Dctd	0.43±0.1
DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae) (predicted)	Dcun1d1_predicted	1.36±0.42
DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae) (predicted)	Dcun1d4_predicted	3.02±0.78
DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	Dcun1d5	0.72±0.85
DCP1 decapping enzyme homolog A (S. cerevisiae)	Dcp1a	0.68±0.35
DCP1 decapping enzyme homolog b (S. cerevisiae)	Dcp1b	0.87±0.01
DDHD domain containing 1	Ddhd1	0.65±0.5
D-dopachrome tautomerase	Ddt	15.24±0.56
DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	5.39±0.9
DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (predicted)	Ddx10_predicted	0.97±0.17
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	Ddx17	2.25±0.74
DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Ddx18	0.79±0.07
DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	Ddx19	2.25±0.1
DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	Ddx20	0.55±0.1
DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	Ddx21	0.46±0.07
DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 (predicted)	Ddx23_predicted	2.54±0.18
DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	2.63±0.11
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	0.89±0.19
DEAD (Asp-Glu-Ala-Asp) box polypeptide 28 (predicted)	Ddx28_predicted	0.29±0.03
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	Ddx39	0.94±0.16
DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 (predicted)	Ddx41_predicted	1.96±0.13
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (predicted)	Ddx42_predicted	2.65±0.03
DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	2.12±0.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	Ddx47	2.23±0.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (predicted)	Ddx49_predicted	0.84±0.06
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	17.18±2.28
DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	Ddx50	1.3±0.67
DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (predicted)	Ddx51_predicted	1.47±0.26
DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	0.37±0.12
DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	0.87±0.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)	Ddx58_predicted	1.31±0.85
DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	Ddx59	0.61±0.01
dead end homolog 1 (zebrafish)	Dnd1	0.62±0.17
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (predicted)	Ddx11_predicted	0.38±0.03
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	13.71±0.58
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 (predicted)	Ddx31_predicted	0.91±0.06
DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	Dhx57	1.12±0.04
DEAH (Asp-Glu-Ala-His) box polypeptide 15 (predicted)	Dhx15_predicted	6.47±1.09
DEAH (Asp-Glu-Ala-His) box polypeptide 30	Dhx30	1.6±0.35
DEAH (Asp-Glu-Ala-His) box polypeptide 35 (predicted)	Dhx35_predicted	0.63±0.18
DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted	2.28±0.37
DEAH (Asp-Glu-Ala-His) box polypeptide 37 (predicted)	Dhx37_predicted	0.44±0.03
DEAH (Asp-Glu-Ala-His) box polypeptide 38 (predicted)	Dhx38_predicted	0.44±0.05
DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	1.43±0.11
DEAH (Asp-Glu-Ala-His) box polypeptide 8	Dhx8	0.6±0.05
DEAH (Asp-Glu-Ala-His) box polypeptide 9 (predicted)	Dhx9_predicted	1.87±0.91
death associated protein 3	Dap3	2.9±0.44

death associated protein kinase 1 (predicted)	Dapk1_predicted	4.14±1.27
death associated protein-like 1	Dapl1	5.05±0.52
Death effector domain-containing	Dedd	4.32±0.04
death inducer-obliterator 1	Dido1	0.58±0.12
death-associated protein	Dap	2.19±0.34
death-associated protein kinase 3	Dapk3	1.6±0.55
debranching enzyme homolog 1 (S. cerevisiae)	Dbr1	0.4±0.05
decapping enzyme, scavenger	Dcps	1.16±0.2
dedicator of cytokinesis 11	Dock11	1.85±0.52
dedicator of cytokinesis 7	Dock7	1.12±0.53
dedicator of cytokinesis 8	Dock8	2.38±0.78
dedicator of cytokinesis 9	Dock9	1.57±2.35
de-etiolated homolog 1 (Arabidopsis)	Det1	0.5±0.35
defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	Dscc1	0.37±0.26
defender against cell death 1	Dad1	14.41±0.79
deformed epidermal autoregulatory factor 1 (Drosophila)	Deaf1	1.08±0.21
degenerative spermatocyte homolog 1 (Drosophila)	Degs1	12.17±0.42
degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	Degs2	0.74±2.2
dehydrodolichyl diphosphate synthase	Dhdds	0.6±0.1
dehydrogenase E1 and transketolase domain containing 1	Dhtkd1	2.48±0.54
dehydrogenase/reductase (SDR family) member 1	Dhrs1	2.93±0.15
dehydrogenase/reductase (SDR family) member 3	Dhrs3	4.96±1.36
dehydrogenase/reductase (SDR family) member 4	Dhrs4	6.05±0.54
dehydrogenase/reductase (SDR family) member 7B	Dhrs7b	2.3±0.08
dehydrogenase/reductase (SDR family) X chromosome	Dhrsx	2.29±0.11
DEK oncogene (DNA binding)	Dek	9.11±1.59
deltex 2 homolog (Drosophila)	Dtx2	0.37±0.17
deltex 3 homolog (Drosophila)	Dtx3	2.78±0.49
deltex 3-like (Drosophila)	Dtx3l	0.45±0.3
demethyl-Q 7	Coq7	6.24±0.55
DENN/MADD domain containing 1A	Dennd1a	1.33±0.03
DENN/MADD domain containing 2D (predicted)	Dennd2d_predicted	2.14±1.07
DENN/MADD domain containing 3	Dennd3	0.92±0.52
DENN/MADD domain containing 4B	Dennd4b	0.54±0.1
deoxyguanosine kinase (predicted)	Dguok_predicted	1.59±0.12
deoxyhypusine hydroxylase/monooxygenase	Dohh	1.41±0.19
deoxyhypusine synthase	Dhps	1.79±0.73
deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	3.05±0.04
deoxynucleotidyltransferase, terminal, interacting protein 2 (predicted)	Dnttip2_predicted	0.89±0.64
deoxyribonuclease I	Dnase1	41.07±6.97
deoxythymidylate kinase (predicted)	Dtymk_predicted	5.08±0.59
deoxyuridine triphosphatase	Dut	4.7±0.38
DEP domain containing 5 (predicted)	Depdc5_predicted	0.47±0.13
dephospho-CoA kinase domain containing	Dcakd	7.02±0.94
Der1-like domain family, member 1	Derl1	4.33±0.12
Dermal papilla derived protein 6	DERP6	0.27±0.06
desmoplakin	Dsp	12.29±0.55
destrin	Dstn	13.29±1.96
DET1 and DDB1 associated 1	Dda1	1.25±0.18
development and differentiation enhancing (predicted)	Ddef1_predicted	0.73±0.31
development and differentiation enhancing factor 2 (predicted)	Ddef2_predicted	1.82±0.42
developmentally regulated GTP binding protein 1	Drg1	1.93±0.05
developmentally regulated GTP binding protein 2	Drg2	1.78±0.64
developmentally regulated protein TPO1	Tpo1	1.62±0.1
dexamethasone-induced transcript	Dexi	2.35±0.26
diablo homolog (Drosophila)	Diablo	4.99±0.88
diacylglycerol kinase zeta	Dgkz	3.23±0.98
diacylglycerol lipase, beta	Daglb	0.43±0.13
diacylglycerol O-acyltransferase 1	Dgat1	2.49±0.31
diacylglycerol O-acyltransferase 2	Dgat2	5.26±1.6
Diaphanous homolog 1 (Drosophila) (predicted)	Diap1_predicted	1.59±0.37
diazepam binding inhibitor	Dbi	41.05±5.91
dicarbonyl L-xylulose reductase	Dcxr	4.88±0.33
Dicer1, Dcr-1 homolog (Drosophila)	Dicer1	0.32±0.22
differentially expressed in FDCP 8	Def8	1.44±0.33
DiGeorge syndrome critical region gene 14	Dgcr14	0.38±0.1
DiGeorge syndrome critical region gene 2	Dgcr2	4.13±0.39
DiGeorge syndrome critical region gene 6 (predicted)	Dgcr6_predicted	2.34±0.01
DiGeorge syndrome critical region gene 8 (predicted)	Dgcr8_predicted	1.58±0.26
dihydrofolate reductase	Dhfr	0.78±0.13
dihydrolipoamide branched chain transacylase E2	Dbt	7.1±0.92
dihydrolipoamide dehydrogenase	Dld	15.18±2.63
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Dlat	4.32±1.66
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst	12.66±2.46
dihydropyrimidinase-like 2	Dpysl2	2.97±1.41
dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	Dus2l	0.59±0.05
dihydrouridine synthase 3-like (S. cerevisiae)	Dus3l	0.85±0.03
dihydroxyacetone kinase 2 homolog (yeast)	Dak	0.34±0.72
DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	Dimt1	0.46±0.29
dimethylarginine dimethylaminohydrolase 2	Ddah2	2.34±0.09
dipeptidyl peptidase 9	Dpp9	0.83±0.32
dipeptidylpeptidase 3	Dpp3 /// LOC678760	2.09±0.62
dipeptidylpeptidase 7	Dpp7	10.61±1.31
dipeptidylpeptidase 8 (predicted)	Dpp8_predicted	2.86±0.19
DIS3 mitotic control homolog (S. cerevisiae)-like	Dis3l	3.17±0.59
DIS3 mitotic control homolog (S. cerevisiae)-like 2	Dis3l2	1.57±0.87
disabled homolog 2 (Drosophila) interacting protein	Dab2ip	0.35±0.21

disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	Dab2	1.59±1.64
Discs, large homolog 1 (Drosophila)	Dlgh1	2.82±0.01
discs, large homolog 3 (Drosophila)	Dlg3	0.25±0.1
discs, large homolog 5 (Drosophila) (predicted)	Dlg5_predicted	2.07±0.22
discs, large homolog-associated protein 4 (Drosophila)	Dlgap4	0.68±0.38
dishevelled associated activator of morphogenesis 1 (predicted)	Daam1_predicted	2.25±0.01
dishevelled, dsh homolog 1 (Drosophila)	Dvl1	2.25±0.61
disrupted in renal carcinoma 2	Dirc2	2.73±0.27
distrobrevin binding protein 1	Dtnbp1	3.15±0.01
DIX domain containing 1	Dixdc1	1.29±0.4
Dmx-like 1 (predicted)	Dmxl1_predicted	0.38±0.22
DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae) (predicted)	Dclre1a_predicted	1.53±0.11
DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	Dclre1b	0.68±0.12
DNA fragmentation factor, alpha subunit	Dffa	1.45±0.04
DNA helicase HEL308	Hel308	0.43±0.11
DNA methyltransferase (cytosine-5) 1	Dnmt1	0.76±0.13
DNA methyltransferase 1-associated protein 1	Dmap1	1.09±0.47
DNA methyltransferase 3A	Dnmt3a	0.73±0.16
DNA primase, p49 subunit	Prim1	3.35±0.07
DNA primase, p58 subunit	Prim2	0.3±0.02
DNA topoisomerase 1, mitochondrial	Top1mt	0.49±0.13
DNA-damage inducible transcript 3	Ddit3	1.09±0.28
DNA-damage-inducible transcript 4	Ddit4	3.14±0.19
DNA-damage-inducible transcript 4-like	Ddit4l	0.68±0.38
DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	9.34±5.45
DnaJ (Hsp40) homolog, subfamily A, member 2	Dnaja2	7.74±0.65
DnaJ (Hsp40) homolog, subfamily A, member 3	Dnaja3	2.22±0.08
DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	0.35±0.15
DnaJ (Hsp40) homolog, subfamily B, member 1 (predicted)	Dnajb1_predicted	30.78±0.74
DnaJ (Hsp40) homolog, subfamily B, member 11	Dnajb11	2.62±0.47
DnaJ (Hsp40) homolog, subfamily B, member 12	Dnajb12	0.62±0.06
DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	0.3±0
DnaJ (Hsp40) homolog, subfamily B, member 9	Dnajb9	1.95±1.09
DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	4.61±0.06
DnaJ (Hsp40) homolog, subfamily C, member 11 (predicted)	Dnajc11_predicted	0.28±0.23
DnaJ (Hsp40) homolog, subfamily C, member 13 (predicted)	Dnajc13_predicted	2.67±0.28
DnaJ (Hsp40) homolog, subfamily C, member 14	Dnajc14	0.86±0.04
DnaJ (Hsp40) homolog, subfamily C, member 15 (predicted)	Dnajc15_predicted	12.33±2.87
DnaJ (Hsp40) homolog, subfamily C, member 17 (predicted)	Dnajc17_predicted	0.43±0.1
DnaJ (Hsp40) homolog, subfamily C, member 18	Dnajc18	0.61±0.17
DnaJ (Hsp40) homolog, subfamily C, member 2	Dnajc2	1.09±0.15
DnaJ (Hsp40) homolog, subfamily C, member 21	Dnajc21	0.71±0.07
DnaJ (Hsp40) homolog, subfamily C, member 3	Dnajc3	3.27±0.13
DnaJ (Hsp40) homolog, subfamily C, member 4	Dnajc4	1.34±0.23
DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	0.43±0.11
DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	4.06±0.17
DnaJ (Hsp40) homolog, subfamily C, member 8	Dnajc8	2.65±0.2
DnaJ (Hsp40) homolog, subfamily C, member 9 (predicted)	Dnajc9_predicted	3.2±0.02
DnaJ homolog subfamily C member 12	Dnajc12	2.58±0.47
dnaj-like protein	LOC56764	0.31±0.01
docking protein 4 (predicted)	Dok4_predicted	0.86±0.05
dodecenoyl-coenzyme A delta isomerase	Dci	7.25±0.02
dolichol kinase	Dolk	3.72±1.46
dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	6.57±0.14
dolichol-phosphate (beta-D) mannosyltransferase 2	Dpm2	1.85±0.31
dolichyl-di-phosphooligosaccharide-protein glycotransferase (predicted)	Ddost_predicted	7.86±0.05
dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	Dpagt1	1.71±0.23
dopey family member 2 (predicted)	Dopey2_predicted	0.68±0.25
DOT1-like, histone H3 methyltransferase (S. cerevisiae) (predicted)	Dot1l_predicted	0.96±0.03
doublecortin domain containing 2	Dcdc2	1.2±0.68
doublecortin-like kinase 1	Dclk1	0.21±0.01
Down syndrome critical region gene 3 (predicted)	Dscr3_predicted	1.67±0.05
Down syndrome critical region homolog 2 (human) (predicted)	Dscr2_predicted	7.56±1.37
down-regulator of transcription 1	Dr1	1.89±0.09
downstream of Stk11 (predicted)	Dos_predicted	0.32±0.75
DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor in ovarian cancer 2	Dph1 /// Ovca2	2.87±0.46
DPH2 homolog (S. cerevisiae)	Dph2	0.5±0.18
DPH3, KTI11 homolog (S. cerevisiae)	Dph3	5.64±0.64
DPH4 homolog (JJJ3, S. cerevisiae)	Dph4	0.53±0.33
DPH5 homolog (S. cerevisiae)	Dph5	0.24±0.09
Dpy-19-like 1 (C. elegans) (predicted)	Dpy19l1_predicted	1.5±0.16
dpy-30 homolog (C. elegans)	Dpy30	5.47±0.37
Dr1 associated protein 1 (negative cofactor 2 alpha) (predicted)	Drap1_predicted	2.92±0.6
drebrin 1	Dbn1	1.85±0.09
drebrin-like	Dbnl	2.45±0.2
D-serine modulator-1	Dsm-1	2.02±0.98
DTW domain containing 1	Dtwd1	0.37±0.01
D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	Dtd1	5.24±0.42
dual specificity phosphatase 1	Dusp1	3.37±5.46
dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	Dusp11	1.27±0.14
dual specificity phosphatase 12	Dusp12	0.2±0.08
dual specificity phosphatase 14 (predicted)	Dusp14_predicted / LO	2.82±1.24
dual specificity phosphatase 18	Dusp18	0.42±0.07
dual specificity phosphatase 19 (predicted)	Dusp19_predicted	0.48±0.07
dual specificity phosphatase 22 (predicted)	Dusp22_predicted	0.35±0.19
dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Dusp3	1.26±0.69
Dual specificity phosphatase 6	Dusp6	1.37±1.7

dual specificity phosphatase 9	Dusp9	0.31±0.07
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	Dyrk1a	1.14±0.35
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (predicted)	Dyrk2_predicted	1.15±0.21
Dullard homolog (Xenopus laevis)	Dullard	0.6±0.29
dymeclin (predicted)	Dym_predicted	2.48±0.06
dynactin 1	Dctn1	3.31±0.05
dynactin 2	Dctn2	3.02±0.16
dynactin 3 (predicted)	Dctn3_predicted	4.98±0.21
dynactin 4	Dctn4	0.52±0.02
dynactin 5	Dctn5	2.74±0.5
dynactin 6 (predicted)	Dctn6_predicted	14.07±3.78
dynamin 1	Dnm1	5.14±1.78
dynamin 1-like	Dnm1l	1.66±0.14
dynamin binding protein	Dnmbp	3.76±0.38
dynein cytoplasmic 1 heavy chain 1	Dync1h1	7.53±0.72
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	5.75±0.76
Dynein cytoplasmic 1 light intermediate chain 1	Dync1li1	4.21±0.8
dynein cytoplasmic 2 heavy chain 1	Dync2h1	0.6±0.02
dynein cytoplasmic 2 light intermediate chain 1	Dync2li1	1.97±0.04
dynein light chain LC8-type 1	Dynll1	14.92±1.31
dynein light chain LC8-type 2	Dynll2	12.96±1.49
dynein light chain roadblock-type 1	Dynlrb1	12.79±0.67
dynein light chain Tctex-type 1	Dynlt1	1.69±0.22
dynein light chain Tctex-type 3	Dynlt3	6.93±1.52
dynein, axonemal, light chain 4	Dnalc4	1.57±0.11
dynein, cytoplasmic 1 light intermediate chain 2	Dync1li2	2.86±0.43
dyskeratosis congenita 1, dyskerin	Dkc1	1.19±0.28
dystonia 1	Dyt1	1.27±0.08
dystonin (predicted)	Dst_predicted	15.94±1.35
dystrobrevin alpha (predicted)	Dtna_predicted	1.3±0.31
dystrobrevin, beta	Dtnb	2.49±0.25
dystroglycan 1	Dag1	6.9±2.25
dystrophia myotonica-protein kinase (predicted)	Dmpk_predicted	2.4±0.35
E030032D13Rik gene	E030032D13Rik	0.37±0.42
E1A binding protein p300	Ep300	4.37±0.52
E1A binding protein p400	Ep400	1.13±0.11
E2F transcription factor 1	E2f1	0.71±0.09
E2F transcription factor 5	E2f5	0.94±0.36
E2F1-inducible gene	LOC303566	0.24±0.11
E2F-associated phosphoprotein	Eapp	3.96±0.36
E74-like factor 1	Elf1	0.58±0.06
E74-like factor 2	Elf2	2.73±0.35
E74-like factor 3	Elf3	4.25±0.37
early endosome antigen 1 (predicted)	Eea1_predicted	1.12±0.14
early growth response 1	Egr1	17.64±7.54
early growth response 2	Egr2	1.68±1.18
EBNA1 binding protein 2	Ebna1bp2	2±0.37
echinoderm microtubule associated protein like 2	Eml2	1.2±0.07
ecotropic viral integration site 1 (predicted)	Evi1_predicted	2.9±0.3
ECSIT homolog (Drosophila)	Ecsit	3.32±1.16
ect2 oncogene (predicted)	Ect2_predicted	0.82±0.13
ectonucleoside triphosphate diphosphohydrolase 2	Entpd2	4.42±0.71
ectonucleoside triphosphate diphosphohydrolase 4 (predicted)	Entpd4_predicted	1.54±0.96
ectonucleoside triphosphate diphosphohydrolase 6	Entpd6	0.43±0.19
ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	1.83±0.52
Ectonucleotide pyrophosphatase/phosphodiesterase 4 (predicted)	Enpp4_predicted	1.26±0.69
EF hand domain containing 1	Efhd1	26.12±4.49
EF hand domain containing 2	Efhd2	0.23±0.45
EF hand domain family A1	Efha1	2.71±0.28
EF hand domain family, member A2	Efha2	1.13±0.18
EF-hand calcium binding domain 2 (predicted)	Efcab2_predicted	0.59±0.27
EF-hand calcium binding domain 7	Efcab7	0.27±0.16
EFR3 homolog A (S. cerevisiae)	Efr3a	6.61±1.9
EGF-containing fibulin-like extracellular matrix protein 2	Efemp2	0.4±0.06
EGF-like domain 8	Egfl8	2.64±0.29
EGL nine homolog 1 (C. elegans)	Egln1	3.11±0.48
EGL nine homolog 2 (C. elegans)	Egln2	2.72±0
EGL nine homolog 3 (C. elegans)	Egln3	1.69±0.18
EH domain binding protein 1 (predicted)	Ehbp1_predicted	0.54±0.39
EH-domain containing 1	Ehd1	0.89±0.07
EH-domain containing 2	Ehd2	0.43±0.84
EH-domain containing 4	Ehd4	0.65±0.87
elaC homolog 2 (E. coli)	Elac2	0.88±0.01
elastase 1, pancreatic	Ela1	0.82±0.33
ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	5.21±0.9
electron transferring flavoprotein, alpha polypeptide	Etfa	14.81±3.93
electron transferring flavoprotein, beta polypeptide	Etfb	24.78±5.97
electron-transferring-flavoprotein dehydrogenase	Etfdh	4.79±0.25
ELK4, member of ETS oncogene family (predicted)	Elk4_predicted	0.83±0.37
ELL associated factor 1 (predicted)	Eaf1_predicted	0.48±0.4
ELMO domain containing 2	Elmod2	0.52±0.2
elongation factor 1 homolog (S. cerevisiae)	Elof1	6.41±0.46
elongation factor RNA polymerase II (predicted)	Ell_predicted	1.02±0.31
elongation factor RNA polymerase II 2	Ell2	0.86±0.04
Elongation factor RNA polymerase II-like 3	Ell3	0.62±0.18
elongation factor Tu GTP binding domain containing 2	Eftud2	3.02±0.59
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (predicted)	Elovl2_predicted	0.39±0.12

elongation protein 2 homolog (S. cerevisiae)	Elp2	2.65±0.02
ELOVL family member 6, elongation of long chain fatty acids (yeast)	Elovl6	4.96±1.04
embigin	Emb	13.23±2.16
embryonic ectoderm development (predicted)	Eed_predicted	1.66±0.35
emerin	Emd	0.44±0.28
empty spiracles homeobox 2	Emx2	2.2±1.38
enabled homolog (Drosophila)	Enah	0.8±0.11
Ena-vasodilator stimulated phosphoprotein	Evl	1.88±0.38
endonuclease G	Endog	1.57±0.1
endonuclease G-like 1 (predicted)	Endogl1_predicted	0.4±0.21
endonuclease/exonuclease/phosphatase family domain containing 1	Eepd1	1.01±0.06
endoplasmic reticulum (ER) to nucleus signalling 1	Ern1	1.42±0.24
endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	Sil1	1.88±0.17
endoplasmic reticulum metallopeptidase 1	Ermp1	2.3±0.51
endoplasmic reticulum protein 29	Erp29	3.88±0.21
endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	Ergic1	2.24±0.32
endosulfine alpha	Ensa	3.15±0.01
endothelial cell adhesion molecule	Esam	5.39±0.8
endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	Edg5	0.5±0.32
endothelial differentiation-related factor 1 (predicted)	Edf1_predicted	15.03±2.05
endothelin converting enzyme 1	Ece1	2.22±0.3
engulfment and cell motility 2, ced-12 homolog (C. elegans)	Elmo2	0.77±0.06
engulfment and cell motility 3, ced-12 homolog (C. elegans)	Elmo3	1.69±0.13
enhancer of polycomb homolog 1 (Drosophila) (predicted)	Epc1_predicted	2.11±0.19
enhancer of polycomb homolog 2 (Drosophila) (predicted)	Epc2_predicted	0.44±0.08
enhancer of rudimentary homolog (Drosophila)	Erh	5.11±0.43
enhancer of zeste homolog 1 (Drosophila) (predicted)	Ezh1_predicted	3.74±0.58
enhancer of zeste homolog 2 (Drosophila)	Ezh2	0.52±0.16
enolase 1, alpha non-neuron	Eno1	37.43±2.13
enolase-phosphatase 1	Enoph1	1.65±0.13
enoyl coenzyme A hydratase 1, peroxisomal	Ech1	8.31±2.67
enoyl Coenzyme A hydratase domain containing 1	Echdc1	5.97±1.08
enoyl Coenzyme A hydratase domain containing 2 (predicted)	Echdc2_predicted	0.38±0.65
enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Echs1	11.77±1.26
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	0.96±0.1
enthoprotin	Enth	17.01±1.9
EP300 interacting inhibitor of differentiation 1	Eid1	8.34±0.67
Eph receptor A4	Epha4	0.3±0.06
Eph receptor B2 (predicted)	Ephb2_predicted	3.36±0.27
Eph receptor B3 (predicted)	Ephb3_predicted	1.01±0.07
ephrin A1	Efna1	0.46±0.46
ephrin A4 (predicted)	Efna4_predicted	0.44±0.06
ephrin B1	Efnb1	0.25±0.11
epidermal growth factor	Egf	39.82±1.43
epidermal growth factor receptor /// peptidase D	Egfr /// Pepd	1.69±0.66
epidermal growth factor receptor pathway substrate 15	Eps15	0.89±0.42
epidermal growth factor receptor pathway substrate 15-like 1	Eps15l1	0.94±0.35
epidermal growth factor receptor pathway substrate 8 (predicted)	Eps8_predicted	0.66±0.19
epidermal growth factor-containing fibulin-like extracellular matrix protein 1	Efemp1	3.89±0.72
EPM2A (laforin) interacting protein 1 (predicted)	Epm2aip1_predicted	8.22±0.89
epoxide hydrolase 1, microsomal	Ephx1	1.62±0.64
epoxide hydrolase 2, cytoplasmic	Ephx2	4.36±0.88
EPS8-like 2 (predicted)	Eps8l2_predicted	11.22±3.01
epsilon-tubulin 1	Tube1	0.2±0.1
Epsin 1	Epn1	1.03±0.13
epsin 2	Epn2	0.82±0.4
epsin 3	Epn3	1.91±0.37
ER degradation enhancer, mannosidase alpha-like 1	Edem1	3.29±0.58
ER degradation enhancer, mannosidase alpha-like 2	Edem2	0.98±0.3
ER lipid raft associated 1	Erlin1	1.47±0.29
ER lipid raft associated 2	Erlin2	7.59±0.61
ERBB receptor feedback inhibitor 1	Errfi1	6.27±7.36
ERGIC and golgi 3 (predicted)	Ergic3_predicted	2.58±0.05
ERO1-like (S. cerevisiae)	Ero1l	2.41±0.15
erythrocyte membrane protein band 4.1	Epb4.1	2.53±0.17
erythrocyte membrane protein band 4.1-like 2	Epb4.1l2	0.39±0.11
erythrocyte protein band 4.1-like 1	Epb4.1l1	3.47±0.47
erythrocyte protein band 4.1-like 4a (predicted)	Epb4.1l4a_predicted	1.95±0.21
erythrocyte protein band 4.1-like 5	Epb4.1l5	2.37±0.23
erythrocyte protein band 4.9 (predicted)	Epb4.9_predicted	10.51±1.93
ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	Esf1	0.45±0.07
establishment of cohesion 1 homolog 1 (S. cerevisiae)	Esco1	3.94±0.07
esterase D/formylglutathione hydrolase	Esd	6.44±0.1
estrogen receptor-binding fragment-associated gene 9	Ebag9	1.88±0.6
estrogen related receptor, alpha	Esrra	4.22±1.81
Ethanolamine kinase 1 (predicted)	Etnk1_predicted	22.78±5.07
ethylmalonic encephalopathy 1 (predicted)	Ethe1_predicted	1.71±0.56
etoposide induced 2.4 mRNA	Ei24	7.16±0.15
Ets2 repressor factor (predicted)	Erf_predicted	2.08±0.65
euchromatic histone methyltransferase 1 (predicted)	Ehmt1_predicted	1.51±0.05
eukaryotic elongation factor, selenocysteine-tRNA-specific	Eefsec	0.5±0.04
eukaryotic elongation factor-2 kinase	Eef2k	0.44±0.25
eukaryotic translation elongation factor 1 alpha 1	Eef1a1	31.52±2.2
eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1 (predicted)	Eef1a1 /// RGD156634	35.76±4.16
eukaryotic translation elongation factor 1 beta 2 (predicted)	Eef1b2_predicted	14.91±2.58
eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d	5.86±0.02
eukaryotic translation elongation factor 1 epsilon 1 (predicted)	Eef1e1_predicted	3.37±0.73

eukaryotic translation elongation factor 1 gamma	Eef1g	20.16±0.38
eukaryotic translation elongation factor 2	Eef2	17.31±2.51
eukaryotic translation initiation factor 1	Eif1	16.97±4.4
eukaryotic translation initiation factor 1A	Eif1a	1.09±0.55
eukaryotic translation initiation factor 1A domain containing	Eif1ad	1.9±0.57
eukaryotic translation initiation factor 1A, Y-linked	Eif1ay	6.27±1.4
eukaryotic translation initiation factor 1B (predicted)	Eif1b_predicted	2.47±0.7
eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	2.99±0.05
eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	1.24±0.02
eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	3.68±1.29
eukaryotic translation initiation factor 2, subunit 1 alpha /// hypothetical gene supported by NM_019356	Eif2s1 /// LOC364604 /	0.98±0.08
eukaryotic translation initiation factor 2, subunit 2 (beta)	Eif2s2	5.55±0.55
eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	6.58±2.72
eukaryotic translation initiation factor 2A	Eif2a	1.21±0.14
eukaryotic translation initiation factor 2-alpha kinase 2	Eif2ak2	0.73±0.76
eukaryotic translation initiation factor 2B, subunit 1 alpha	Eif2b1	1.7±0.13
eukaryotic translation initiation factor 2B, subunit 2 beta	Eif2b2	1.76±0.19
eukaryotic translation initiation factor 2B, subunit 3	Eif2b3	0.55±0.02
eukaryotic translation initiation factor 2B, subunit 4 delta	Eif2b4	3.83±1.41
eukaryotic translation initiation factor 2B, subunit 5 epsilon	Eif2b5	1.57±0.06
eukaryotic translation initiation factor 2C, 1 (predicted)	Eif2c1_predicted	2.77±0.2
eukaryotic translation initiation factor 2C, 2	Eif2c2	0.41±0.21
eukaryotic translation initiation factor 3, subunit 1 alpha (predicted)	Eif3s1_predicted	5.24±0.59
eukaryotic translation initiation factor 3, subunit 10 (theta)	Eif3s10	5.53±0.1
eukaryotic translation initiation factor 3, subunit 6 interacting protein	Eif3s6ip	11.16±0.64
eukaryotic translation initiation factor 3, subunit 9 (eta)	Eif3s9	5.83±0.82
eukaryotic translation initiation factor 3, subunit C	Eif3c	7.75±1.18
eukaryotic translation initiation factor 3, subunit D	Eif3d	3.64±0.04
eukaryotic translation initiation factor 3, subunit E	Eif3e	8.2±0.78
eukaryotic translation initiation factor 3, subunit F	Eif3f	8.96±0.11
eukaryotic translation initiation factor 3, subunit G	Eif3g	10±0.49
eukaryotic translation initiation factor 3, subunit H	Eif3h	11.39±0.33
eukaryotic translation initiation factor 3, subunit K	Eif3k	5.22±0.12
eukaryotic translation initiation factor 4 gamma, 1	Eif4g1	4.48±1
eukaryotic translation initiation factor 4 gamma, 1 /// similar to eukaryotic translation initiation factor 4, gamma 1 isoform a	Eif4g1 /// LOC683907	0.28±0.04
eukaryotic translation initiation factor 4 gamma, 3 (predicted)	Eif4g3_predicted	2.39±0.18
eukaryotic translation initiation factor 4, gamma 2 (predicted)	Eif4g2_predicted	20.93±1.74
eukaryotic translation initiation factor 4A1	Eif4a1	5.44±0.76
eukaryotic translation initiation factor 4A2	Eif4a2	26.87±3.76
eukaryotic translation initiation factor 4B	Eif4b	4.11±0.65
eukaryotic translation initiation factor 4E	Eif4e	7.56±1.41
eukaryotic translation initiation factor 4E binding protein 1	Eif4ebp1	1.19±0.14
eukaryotic translation initiation factor 4E binding protein 2	Eif4ebp2	4.15±0.67
eukaryotic translation initiation factor 4E member 2 (predicted)	Eif4e2_predicted	3.13±0.03
eukaryotic translation initiation factor 4E member 3	Eif4e3	0.3±0.22
eukaryotic translation initiation factor 4E nuclear import factor 1	Eif4enif1	1.33±0.2
eukaryotic translation initiation factor 4H	Eif4h	12.28±0.78
eukaryotic translation initiation factor 5	Eif5	2.47±1.2
eukaryotic translation initiation factor 5A	Eif5a	6.49±0.67
eukaryotic translation initiation factor 5B	Eif5b	1.7±0.34
eukaryotic translation initiation factor 6	Eif6	5.17±0.15
Eukaryotic translation termination factor 1	Etf1	3.7±0.19
Ewing sarcoma breakpoint region 1	Ewsr1	2.76±0.06
Ewing's tumor-associated antigen 1	Etaa1	0.78±0.1
excision repair cross-complementing rodent repair deficiency, complementation group 1 (predicted)	Ercc1_predicted	2.27±0.49
excision repair cross-complementing rodent repair deficiency, complementation group 3	Ercc3	1.01±0.29
excision repair cross-complementing rodent repair deficiency, complementation group 4	Ercc4	0.63±0.3
excision repair cross-complementing rodent repair deficiency, complementation group 5	Ercc5	0.6±0.08
excision repair cross-complementing rodent repair deficiency, complementation group 6 (predicted)	Ercc6_predicted	0.53±0.11
excision repaiross-complementing rodent repair deficiency, complementation group 8	Ercc8	0.32±0.14
exocyst complex component 2	Exoc2	1.97±0.37
exocyst complex component 3	Exoc3	3.21±0.51
Exocyst complex component 4	Exoc4	0.85±0.02
exocyst complex component 5	Exoc5	0.55±0.41
exocyst complex component 6	Exoc6	0.75±0.1
exocyst complex component 7	Exoc7	1.01±0.38
exonuclease 3''-5'' domain-like 2 (predicted)	Exdl2_predicted	1.43±0.14
exosome component 3 (predicted)	Exosc3_predicted	1.71±0.32
Exosome component 4 (predicted)	Exosc4_predicted	1.14±0.36
exosome component 5 (predicted)	Exosc5_predicted	1.19±0.15
exosome component 7	Exosc7	1.36±0.23
exosome component 8 (predicted)	Exosc8_predicted	0.61±0.2
exosome component 9	Exosc9	0.39±0.09
exostoses (multiple) 1	Ext1	2.31±0.02
exostoses (multiple) 2 (predicted)	Ext2 predicted	2.47±0.35
exportin 1, CRM1 homolog (yeast)	Xpo1	3.77±0.35
exportin 4 (predicted)	Xpo4_predicted	0.35±0.15
exportin 5 (predicted)	Xpo5_predicted	0.61±0.22
exportin 6	Xpo6	2.49±0.4
exportin 7	Xpo7	5.42±0.5
Exportin, tRNA (nuclear export receptor for tRNAs) (predicted)	Xpot_predicted	1.52±0.13
expressed in non-metastatic cells 1	Nme1	2.15±0.88
expressed in non-metastatic cells 2	Nme2	21.73±6.65
expressed in non-metastatic cells 4	Nme4	0.22±0.07
Eyes absent 3 homolog (Drosophila) (predicted)	Eya3_predicted	1.45±0.11
F11 receptor	F11r	1.32±1.2
factor 8-associated gene A	F8a	3.64±0.13

family with sequence similarity 100, member A	Fam100a	0.38±0.77
family with sequence similarity 103, member A1	Fam103a1	2.36±0.54
family with sequence similarity 107, member B	Fam107b	5.82±1.21
family with sequence similarity 108, member A1	Fam108a1	2.99±0.74
family with sequence similarity 108, member C1	Fam108c1	11.29±1.64
family with sequence similarity 110, member B	Fam110b	0.22±0.17
family with sequence similarity 110, member C	Fam110c	0.28±0.15
family with sequence similarity 111, member A	Fam111a	3.71±4.12
family with sequence similarity 113, member A	Fam113a	0.34±0.14
family with sequence similarity 116, member A	Fam116a	1.72±0.09
family with sequence similarity 117, member A	Fam117a	0.57±0.58
family with sequence similarity 118, member A	Fam118a	0.22±0.04
family with sequence similarity 120A /// similar to Protein CXorf17 homolog /// hypothetical protein LOC683420	Fam120a /// LOC67948	14.79±0.42
family with sequence similarity 120B	Fam120b	1.18±0.73
family with sequence similarity 120C	FAM120C	1.13±0.33
family with sequence similarity 122A	Fam122a	0.95±0.25
family with sequence similarity 125, member A	Fam125a	5.57±0.1
family with sequence similarity 126, member B	Fam126b	1.82±0.07
family with sequence similarity 128, member B	Fam128b	1.01±0.26
family with sequence similarity 129, member B	Fam129b	1.83±1.05
family with sequence similarity 133, member B	Fam133b	2.56±0.21
family with sequence similarity 134, member A	Fam134a	3.4±0.43
family with sequence similarity 134, member B	Fam134b	5.08±0.76
family with sequence similarity 134, member C	Fam134c	3.11±1.02
family with sequence similarity 149, member B1	Fam149b1	3.35±0.14
family with sequence similarity 151, member B	Fam151b	1.55±0.48
family with sequence similarity 152, member A	Fam152a	3.36±0.11
family with sequence similarity 152, member B	Fam152b	1.21±0.01
family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	Fam19a5	0.7±0.09
family with sequence similarity 20, member B	Fam20b	3.95±0.52
family with sequence similarity 20, member C	Fam20c	3.07±0.44
family with sequence similarity 21, member C	Fam21c	5.99±0.1
family with sequence similarity 3, member A	Fam3a	2.44±0.25
family with sequence similarity 32, member A	Fam32a	3.54±0.62
family with sequence similarity 35, member A	Fam35a	0.76±0.09
family with sequence similarity 40, member A	Fam40a	1.26±0.21
family with sequence similarity 43, member A	Fam43a	7.54±2.69
family with sequence similarity 44, member B	Fam44b	1.68±0.01
family with sequence similarity 45, member A	Fam45a	1.47±0.14
family with sequence similarity 48, member A	Fam48a	2.6±0.15
family with sequence similarity 49, member B	Fam49b	1.2±0.26
family with sequence similarity 50, member A	FAM50A	2.78±0.63
family with sequence similarity 53, member A	Fam53a	0.8±0.04
family with sequence similarity 54, member B	Fam54b	7.04±1.51
family with sequence similarity 55, member C /// hypothetical protein LOC682630	Fam55c /// LOC682630	0.28±0.13
family with sequence similarity 58, member B	Fam58b	2.58±0.63
family with sequence similarity 63, member A	Fam63a	8.36±0.4
family with sequence similarity 73, member B	Fam73b	3.95±1.32
family with sequence similarity 76, member A	Fam76a	0.45±0.36
family with sequence similarity 80, member B	Fam80b	1.32±0.31
family with sequence similarity 81, member A	Fam81a	2.77±0.58
family with sequence similarity 82, member C	Fam82c	1.22±0.35
family with sequence similarity 84, member A	Fam84a	5.39±0.29
family with sequence similarity 92, member A1	Fam92a1	7.27±1.23
family with sequence similarity 96, member A	Fam96a	7.56±2.04
family with sequence similarity 96, member B	Fam96b	2.01±0.6
family with sequence similarity 98, member A	Fam98a	1.98±0.67
family with sequence similarity 98, member B	Fam98b	1.2±0.38
Fanconi anemia, complementation group C	Fancc	0.2±0.02
Fanconi anemia, complementation group E	Fance	0.55±0.2
Fanconi anemia, complementation group L (predicted)	Fancl_predicted	0.58±0.07
far upstream element (FUSE) binding protein 1	Fubp1	2.31±0.68
farnesyl diphosphate farnesyl transferase 1	Fdft1	5.27±2.19
farnesyl diphosphate synthetase	Fdps	4.62±1.85
farnesyltransferase, CAAX box, alpha	Fnta	3.59±0.44
Fas (TNFRSF6) binding factor 1 (predicted)	Fbf1_predicted	0.39±0.19
Fas (TNFRSF6)-associated via death domain	Fadd	0.47±0.17
Fas apoptotic inhibitory molecule	Faim	1.93±0.4
Fas death domain-associated protein	Daxx	0.64±0.42
Fas-activated serine/threonine kinase	Fastk	1.83±0.36
Fas-associated factor 1	Faf1	3.32±0.52
fasciculation and elongation protein zeta 2 (zygin II)	Fez2	4.44±0.77
FAST kinase domains 2	Fastkd2	1.45±0.58
FAST kinase domains 3	Fastkd3	1.25±0.15
FAT tumor suppressor homolog 1 (Drosophila)	Fat1	11.57±2.32
fatty acid amide hydrolase	Faah	2.18±0.81
fatty acid binding protein 3, muscle and heart	Fabp3	40.86±4.22
fatty acid synthase	Fasn	3.95±2.05
FBJ osteosarcoma oncogene	Fos	22.42±0.82
F-box and leucine-rich repeat protein 10	Fbxl10	3.36±0.38
F-box and leucine-rich repeat protein 11 (predicted)	Fbxl11_predicted	1.52±0.28
F-box and leucine-rich repeat protein 12	Fbxl12	0.75±0.37
F-box and leucine-rich repeat protein 14 (predicted)	Fbxl14_predicted	0.98±0.15
F-box and leucine-rich repeat protein 19 (predicted)	Fbxl19_predicted	0.24±0.04
F-box and leucine-rich repeat protein 20	Fbxl20	0.67±0.22
F-box and leucine-rich repeat protein 3	Fbxl3	1.72±0.1
F-box and leucine-rich repeat protein 4 (predicted)	Fbxl4_predicted	2.05±0.12

F-box and leucine-rich repeat protein 5 (predicted)	Fbxl5_predicted	2.63±0.38
F-box and leucine-rich repeat protein 6	Fbxl6	0.66±0.05
F-box and leucine-rich repeat protein 8	Fbxl8	0.23±0.05
F-box and WD-40 domain protein 11 (predicted)	Fbxw11_predicted	5.35±0.84
F-box and WD-40 domain protein 2 (predicted)	Fbxw2_predicted	2.34±0.35
F-box and WD-40 domain protein 4 (predicted)	Fbxw4_predicted	0.96±0.02
F-box and WD-40 domain protein 5	Fbxw5	4.97±0.35
F-box and WD-40 domain protein 8 (predicted)	Fbxw8_predicted	1.48±0.45
F-box and WD-40 domain protein 9	Fbxw9	1.06±0.11
F-box only protein 18 (predicted)	Fbxo18_predicted	4.12±0.2
F-box protein 11	Fbxo11	1.67±0.08
F-box protein 16	Fbxo16	0.46±0.38
F-box protein 21	Fbxo21	1.13±0.13
F-box protein 22	Fbxo22	1.55±0.66
F-box protein 25	Fbxo25	0.25±0.03
F-box protein 28 (predicted)	Fbxo28_predicted	1.09±0.01
F-box protein 3	Fbxo3	10.38±1.93
F-box protein 33	Fbxo33	1.49±0.17
F-box protein 34	Fbxo34	0.54±0.11
F-box protein 38 (predicted)	Fbxo38_predicted	1.31±0.01
F-box protein 4	Fbxo4	0.85±0.11
F-box protein 44	Fbxo44	1.94±0.9
F-box protein 46	Fbxo46	0.4±0.04
F-box protein 6	Fbxo6	2.17±0.04
F-box protein 7	Fbxo7	3.27±0.5
F-box protein 8	Fbxo8	1.95±0.74
f-box protein 9	Fbxo9	3.34±0.43
Fc receptor, IgG, alpha chain transporter	Fcgrt	3.95±0.92
FCH domain only 2 (predicted)	Fcho2_predicted	4.1±0.63
fem-1 homolog c (C.elegans) (predicted)	Fem1c_predicted	2.71±0.33
feminization 1 homolog a (C. elegans)	Fem1a	3.35±0.24
fer (fms/fps related) protein kinase, testis specific 2	Fert2	0.33±0.04
fer-1-like 3, myoferlin (C. elegans)	Fer1l3	2.01±0.35
FERM domain containing 8	Frmd8	2.55±0.24
FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) (predicted)	Farp1_predicted	5.31±0.57
FERM, RhoGEF and pleckstrin domain protein 2 (predicted)	Farp2_predicted	0.48±0.16
ferredoxin 1	Fdx1	11.23±1.71
ferredoxin 1-like	Fdx1l	1.82±0.42
ferredoxin reductase	Fdxr	0.99±0.02
ferric-chelate reductase 1	Frrs1	0.57±0.12
ferritin heavy chain 1	Fth1	61.5±2.05
ferritin light chain 1	Ftl1	16.49±2.32
ferrochelatase (predicted)	Fech_predicted	2.3±0.46
fetal Alzheimer antigen (predicted)	Falz_predicted	0.7±0.05
FGF receptor activating protein 1	Frag1	1.63±0.52
FGFR1 oncogene partner 2	Fgfr1op2	1.48±0.04
FH2 domain containing 1	Fhdc1	1.36±0.55
fibrillarin	Fbl	2.16±0.38
fibroblast growth factor (acidic) intracellular binding protein	Fibp	1.83±0.41
fibroblast growth factor 9	Fgf9	6.34±0.81
fibroblast growth factor binding protein 3	Fgfbp3	1.49±0
Fibroblast growth factor receptor 1	Fgfr1	2.3±0.43
fibroblast growth factor receptor 2	Fgfr2	1.73±0.22
fibroblast growth factor receptor 4	Fgfr4	0.6±0.02
fibroblast growth factor receptor substrate 2 (predicted)	Frs2_predicted	2.28±0.5
fibroblast growth factor receptor substrate 3	Frs3	0.24±0.04
fibronectin type III domain containing 3a (predicted)	Fndc3a_predicted	0.8±0.52
fibronectin type III domain containing 3B (predicted)	Fndc3b_predicted	5.83±0.72
FIG4 homolog (S. cerevisiae)	Fig4	1.01±0.02
filamin, beta (predicted)	Flnb_predicted	0.64±0.49
Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) protein	Fau /// LOC687439 /// L	33.42±0.9
FIP1 like 1 (S. cerevisiae)	Fip1l1	0.81±0.22
fission 1 (mitochondrial outer membrane) homolog (yeast)	Fis1	6.16±0.5
fizzy/cell division cycle 20 related 1 (Drosophila) (predicted)	Fzr1_predicted	2.03±0.39
FK506 binding protein 12-rapamycin associated protein 1	Frap1	1.84±0.16
FK506 binding protein 15	Fkbp15	1.05±0.2
FK506 binding protein 1a	Fkbp1a	5.45±0.27
FK506 binding protein 2 (predicted)	Fkbp2_predicted	5.32±0.14
FK506 binding protein 3 (predicted)	Fkbp3_predicted	4.12±1.04
FK506 binding protein 4	Fkbp4	4.23±0.98
FK506 binding protein 5	Fkbp5	0.49±0.38
FK506 binding protein 7 (predicted)	Fkbp7_predicted	0.29±0.13
FK506 binding protein 8	Fkbp8	5.04±0.2
FK506 binding protein 9	Fkbp9	13.61±1.76
FK506 binding protein-like	Fkbpl	0.59±0.52
flavin adenine dinucleotide synthetase	Flad1	2.06±0.56
flavin containing monooxygenase 5	Fmo5	2.48±0.28
flightless I homolog (Drosophila)	Flii	2.6±0.79
flotillin 1	Flot1	1.41±1.23
flotillin 2	Flot2	3.56±0.18
FLT3-interacting zinc finger 1	Fiz1	1.99±0.04
FLYWCH-type zinc finger 1	Flywch1	3.7±0.09
folate receptor 1 (adult)	Folr1	5.73±0.33
folliculin	Flcn	2.19±0.46
follistatin	Fst	0.53±7.13
follistatin-like 1	Fstl1	0.92±1.35
follistatin-like 3	Fstl3	1.05±0.07

forkhead box J2	Foxj2	1.17±0.35
forkhead box J3 (predicted)	Foxj3_predicted	2.21±0.33
forkhead box K2 (predicted)	Foxk2_predicted	1.14±0.04
forkhead box N3	Foxn3	1.54±0.3
forkhead box O1	Foxo1	1.11±0.29
forkhead box O4	Foxo4	1.24±0.02
forkhead box P1	Foxp1	1.16±0.48
forkhead box Q1	Foxq1	1.08±0.42
formin binding protein 1	Fnbp1	0.21±0.01
formin binding protein 4	Fnbp4	3.49±0.46
formin homology 2 domain containing 1	Fhod1	0.61±0.14
Forty-two-three domain containing 1	Fyttd1	1.31±1.07
four jointed box 1 (Drosophila) (predicted)	Fjx1_predicted	0.43±0.13
fractured callus expressed transcript 1	Fxc1	1.58±0.15
fragile histidine triad gene	Fhit	0.91±0.07
fragile X mental retardation syndrome 1 homolog	Fmr1	0.84±0.56
fragile X mental retardation, autosomal homolog 1	Fxr1	0.75±0.14
fragile X mental retardation, autosomal homolog 2	Fxr2	1.68±0.1
frataxin (predicted)	Fxn_predicted	1.88±0.3
frizzled homolog 3 (Drosophila)	Fzd3	0.31±0.03
frizzled homolog 4 (Drosophila)	Fzd4	1.5±0.96
frizzled homolog 7 (Drosophila) (predicted)	Fzd7_predicted	0.26±0.06
frizzled homolog 8 (Drosophila)	Fzd8	0.54±0.19
fructosamine 3 kinase	Fn3k	0.86±0.05
FSHD region gene 1 (predicted)	Frg1_predicted	1.68±0.45
Ftsj homolog 1 (E. coli) (predicted)	Ftsj1_predicted	0.31±0.18
FtsJ homolog 3 (E. coli)	Ftsj3	0.64±0.1
fucokinase (predicted)	Fuk_predicted	0.6±0.01
fucosidase, alpha-L- 1, tissue	Fuca1	7.36±0.03
fucosidase, alpha-L- 2, plasma	Fuca2	3.92±1.01
fukutin related protein	Fkrp	0.48±0.14
Fukuyama type congenital muscular dystrophy homolog (human) (predicted)	Fcmd_predicted	2.18±0.19
fumarate hydratase 1	Fh1	24.2±3.93
fumarylacetoacetate hydrolase domain containing 1	Fahd1	7.7±0.85
fumarylacetoacetate hydrolase domain containing 2A (predicted)	Fahd2a_predicted	6.19±0.85
FUN14 domain containing 1	Fundc1	1.45±0.76
furin (paired basic amino acid cleaving enzyme)	Furin	1.08±0.12
FUS interacting protein (serine-arginine rich) 1	Fusip1	0.25±0.13
fused toes	Fts	8.42±2.24
fusion, derived from t(12;16) malignant liposarcoma (human)	Fus	8.03±0.76
FXYD domain-containing ion transport regulator 2	Fxyd2	49.83±3.07
FXYD domain-containing ion transport regulator 6	Fxyd6	20.33±1.2
FYVE and coiled-coil domain containing 1 (predicted)	Fyco1_predicted	4.16±0.25
FYVE, RhoGEF and PH domain containing 1	Fgd1	0.81±0.05
G elongation factor, mitochondrial 1	Gfm1	5.61±1.27
G elongation factor, mitochondrial 2	Gfm2	0.98±0.61
G kinase anchoring protein 1	Gkap1	1.47±0.07
G patch domain and KOW motifs	Gpkow	1.91±0.42
G patch domain containing 1	Gpatch1	0.22±0
G protein beta subunit-like	Gbl	0.97±0.19
G protein pathway suppressor 1	Gps1	6.71±0.71
G protein pathway suppressor 2	Gps2	1.25±0.1
G protein pathway suppressor 2 (predicted)	Gps2_predicted	0.86±0.17
G protein-coupled receptor 107 (predicted)	Gpr107_predicted	1.05±0.24
G protein-coupled receptor 108	Gpr108	1.09±0.27
G protein-coupled receptor 114 (predicted)	Gpr114_predicted	0.25±0.02
G protein-coupled receptor 125 (predicted)	Gpr125_predicted	0.78±0.41
G protein-coupled receptor 137	Gpr137	0.82±0.34
G protein-coupled receptor 137B (predicted)	Gpr137b_predicted	3.71±0.16
G protein-coupled receptor 146	Gpr146	0.31±0.34
G protein-coupled receptor 162 (predicted)	Gpr162_predicted	0.59±0.01
G protein-coupled receptor 172B	Gpr172b	0.68±0.04
G protein-coupled receptor 175	Gpr175	1.8±0.29
G protein-coupled receptor 177	Gpr177	2.5±1.52
G protein-coupled receptor 180	Gpr180	0.59±0.02
G protein-coupled receptor 19	Gpr19	0.4±0.11
G protein-coupled receptor 56	Gpr56	9.41±2.12
G protein-coupled receptor 89 (predicted)	Gpr89_predicted	3.13±0.06
G protein-coupled receptor associated sorting protein 1	Gprasp1	0.92±0.11
G protein-coupled receptor associated sorting protein 2	Gprasp2	0.9±0
G protein-coupled receptor kinase 4	Grk4	0.63±0.23
G protein-coupled receptor kinase 6	Grk6	2.96±0.13
G protein-coupled receptor kinase interactor 1	Git1	1.87±0.1
G protein-coupled receptor kinase-interactor 2	Git2	0.71±0
G protein-coupled receptor, family C, group 5, member C	Gprc5c	3.7±0.72
G1 to S phase transition 1	Gspt1	6.22±0.57
G1 to S phase transition 2	Gspt2	0.74±0.22
G7c protein	G7c	0.3±0.02
GA repeat binding protein, alpha (predicted)	Gabpa_predicted	1.56±0.21
GA repeat binding protein, beta 1 /// similar to GA binding protein transcription factor, beta subunit 2 (GABPB2) (predicted)	Gabpb1 /// RGD156039	0.77±0.21
GABA(A) receptor-associated protein like 2	Gabarapl2	21.15±0.93
galactokinase 1	Galk1	1.54±0.04
galactokinase 2	Galk2	3.3±0.68
galactose mutarotase	Galm	19.22±4.93
galactose-1-phosphate uridyl transferase	Galt	4.9±1.16
galactosidase, beta 1 (predicted)	Glb1_predicted	6±0.74
galactosidase, beta 1-like 2	Glb1l2	2.1±0.08

galectin-related protein	Hspc159	2±0.55
gametogenetin	Ggn	0.27±0.07
gametogenetin binding protein 2	Ggnbp2	4.45±1.4
gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1 (predicted)	Gabarapl1_predicted //	1.15±1.24
gamma-aminobutyric acid receptor associated protein	Gabarap	21.63±1.56
gamma-glutamyl carboxylase	Ggcx	1.62±0.27
gamma-glutamyl hydrolase	Ggh	2.22±3.91
ganglioside-induced differentiation-associated-protein 2	Gdap2	1.16±0.32
gap junction membrane channel protein alpha 4	Gja4	0.44±1.18
GATA zinc finger domain containing 1	Gatad1	1.52±0.21
GATA zinc finger domain containing 2A	Gatad2a	0.96±0.14
GATA zinc finger domain containing 2B	Gatad2b	0.32±0.16
GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)	Gcn1l1_predicted	1.04±0.04
GCN5 general control of amino acid synthesis-like 2 (yeast) (predicted)	Gcn5l2_predicted	0.54±0.26
GC-rich promoter binding protein 1	Gpbp1	5.24±0.28
GDNF-inducible zinc finger protein 1	Gzf1	1.18±0.03
GDP dissociation inhibitor 2	Gdi2	15.25±0.06
GDP-mannose 4, 6-dehydratase	Gmds	0.9±0.02
GDP-mannose pyrophosphorylase A	Gmppa	1.72±0.36
GDP-mannose pyrophosphorylase B (predicted)	Gmppb_predicted	0.26±0.2
gelsolin	Gsn	4.1±0.18
gem (nuclear organelle) associated protein 4	Gemin4	0.48±0.3
gem (nuclear organelle) associated protein 6	Gemin6	0.43±0.18
gem (nuclear organelle) associated protein 8	Gemin8	1.34±0.42
general transcription factor II E, polypeptide 2 (beta subunit) (predicted)	Gtf2e2_predicted	1.87±0.5
general transcription factor II H, polypeptide 1 (predicted)	Gtf2h1_predicted	0.91±0.22
general transcription factor II H, polypeptide 2 (predicted)	Gtf2h2_predicted	0.26±0.73
general transcription factor II I	Gtf2i	3.84±0.03
general transcription factor II I repeat domain-containing 1	Gtf2ird1	2.73±0.25
general transcription factor IIa 2	Gtf2a2	7.42±0.72
general transcription factor IIB	Gtf2b	2.71±0.65
general transcription factor IIF, polypeptide 1	Gtf2f1	1.81±0.04
general transcription factor IIF, polypeptide 2	Gtf2f2	0.65±0.2
general transcription factor IIH, polypeptide 3	Gtf2h3	0.59±0.09
general transcription factor IIH, polypeptide 5	Gtf2h5	9.27±2
general transcription factor III A	Gtf3a	0.88±0.18
general transcription factor III C 1	Gtf3c1	2.07±0.14
general transcription factor IIIC, polypeptide 2, beta	Gtf3c2	2.78±0.46
general transcription factor IIIC, polypeptide 3	Gtf3c3	1.17±0.87
general transcription factor IIIC, polypeptide 4	Gtf3c4	1.01±0.24
general transcription factor IIIC, polypeptide 5 (predicted)	Gtf3c5_predicted	0.54±0.13
general transcription factor IIIC, polypeptide 6, alpha	Gtf3c6	1.54±0.1
genetic suppressor element 1	Gse1	0.37±0.25
gephyrin	Gphn	3.5±0.73
geranylgeranyl diphosphate synthase 1	Ggps1	0.33±0.12
germ cell-less homolog 1 (Drosophila)	Gmcl1	4.03±0.39
GH3 domain containing	Ghdc	0.63±0.23
GINS complex subunit 3 (Psf3 homolog)	Gins3	0.33±0.26
GINS complex subunit 4 (Sld5 homolog)	Gins4	0.7±0.3
GIPC PDZ domain containing family, member 1	Gipc1	1.29±0.22
GIY-YIG domain containing 2	Giyd2	0.59±0.3
GLE1 RNA export mediator (yeast)	Gle1	0.52±0.07
GLE1 RNA export mediator-like (yeast)	Gle1l	1.7±0.1
glial cell line derived neurotrophic factor family receptor alpha 2	Gfra2	0.2±0.07
glial cell line derived neurotrophic factor family receptor alpha 3	Gfra3	10.24±0.04
GLI-Kruppel family member HKR3	Hkr3	0.52±0.07
glioblastoma amplified sequence	Gbas	2.03±0.09
glioma tumor suppressor candidate region gene 2	Gltscr2	4.28±0.56
GLIS family zinc finger 2 (predicted)	Glis2_predicted	5.67±2.49
glomulin, FKBP associated protein	Glmn	0.31±0.15
glucagon receptor	Gcgr	6.93±0.13
glucan (1,4-alpha-), branching enzyme 1	Gbe1	14.66±1.64
glucocorticoid modulatory element binding protein 2	Gmeb2	0.59±0.28
glucosamine	Gne	0.75±0.17
glucosamine (N-acetyl)-6-sulfatase	Gns	5.88±0.44
glucosamine-phosphate N-acetyltransferase 1	Gnpnat1	5.5±0.12
glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	1.22±0.08
glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	Gcnt2	8.76±2.15
glucose 6 phosphatase, catalytic, 3	G6pc3	5.6±1.09
glucose phosphate isomerase	Gpi	23.25±5.18
glucose-6-phosphatase, catalytic	G6pc	2.7±1.15
glucose-6-phosphate dehydrogenase X-linked	G6pdx	4.16±0.11
glucosidase 1	Gcs1	1.85±0.67
glucosidase, alpha, acid	Gaa	2.36±0.57
glucuronidase, beta	Gusb	1.21±0.05
glucuronyl C5-epimerase	Glce	1.28±0.11
glutamate dehydrogenase 1	Glud1	9.95±1.88
glutamate oxaloacetate transaminase 1, soluble	Got1	12.84±2.53
glutamate oxaloacetate transaminase 2, mitochondrial	Got2	25.46±3.55
glutamate oxaloacetate transaminase 2, mitochondrial	Got2 / LOC297793 / LC	0.34±0.29
glutamate receptor, ionotropic, kainate 2	Grik2	0.43±0.04
glutamate receptor, ionotropic, kainate 5	Grik5	0.2±0.08
glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	Grina	9.51±0.45
glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Grinl1a	13.32±1.36
glutamate-rich WD repeat containing 1	Grwd1	0.53±0.2
glutamic pyruvic transaminase 1, soluble	Gpt1	0.3±0.27
glutaminase	Gls	7.25±0.39

Glutamine and serine rich 1 (predicted)	Qser1_predicted	0.34±1.21
glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	Qrsl1	1.82±0.53
glutaminyl-tRNA synthetase /// similar to glutaminyl-tRNA synthetase (predicted)	Qars /// RGD1562301_	7.33±1.03
glutamyl-prolyl-tRNA synthetase	Eprs	5.34±0.25
glutamyl-tRNA synthetase 2 mitochondrial (putative)	Ears2	0.43±0.1
glutaredoxin 2 (thioltransferase)	Glrx2	5.94±1.15
glutaredoxin 3	Glrx3	5.31±1.36
glutaredoxin 5 homolog (S. cerevisiae) (predicted)	Glrx5_predicted	19.48±2.78
glutaryl-Coenzyme A dehydrogenase (predicted)	Gcdh_predicted	9.1±0.31
glutathione peroxidase 1	Gpx1	2.1±4.47
glutathione peroxidase 2	Gpx2	0.42±0.49
glutathione peroxidase 4	Gpx4	18.17±0.01
glutathione reductase	Gsr	2.34±0.29
glutathione S-transferase A3 /// glutathione-S-transferase, alpha type2 /// glutathione S-transferase Yc2 subunit	Gsta2 /// Gsta3 /// Yc2	6.99±1.28
glutathione S-transferase kappa 1	Gstk1	5.64±1.07
glutathione S-transferase omega 1	Gsto1	3.94±0.23
glutathione S-transferase omega 2	Gsto2	0.32±0.09
glutathione S-transferase theta 1	Gstt1	0.29±0.38
glutathione S-transferase theta 1 /// glutathione S-transferase, theta 3	Gstt1 /// Gstt3	3.75±6.02
glutathione S-transferase, alpha 4	Gsta4	14.83±1.14
glutathione S-transferase, mu 1	Gstm1	2.1±0.02
glutathione S-transferase, mu 2	Gstm2	7.22±0.31
glutathione S-transferase, mu 5	Gstm5	0.2±0.23
glutathione S-transferase, mu type 3	Gstm3	0.7±0.15
glutathione S-transferase, theta 2	Gstt2	1.22±0.46
glutathione synthetase	Gss	2.11±0.98
glutathione-S-transferase, pi 1	Gstp1	16.81±1.81
glyceraldehyde-3-phosphate dehydrogenase	Gapdh	51.97±1.5
glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyde-3-phosphate dehydrogenase	Gapdh /// LOC686275 /	50.83±2.78
glycerol kinase	Gyk	1.41±0.09
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	1.51±0.17
glycerol-3-phosphate dehydrogenase 2, mitochondrial	Gpd2	0.78±0.11
glyceronephosphate O-acyltransferase	Gnpat	2.2±0.57
glycerophosphodiester phosphodiesterase 1	Gde1	7.68±1.44
glycerophosphodiester phosphodiesterase domain containing 1 (predicted)	Gdpd1_predicted	0.96±0.04
glycerophosphodiester phosphodiesterase domain containing 5	Gdpd5	0.5±0.13
glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	Gcat	2.78±0.36
glycine cleavage system protein H (aminomethyl carrier)	Gcsh	7.06±0.68
glycine N-methyltransferase	Gnmt	6.18±0.16
glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein	LOC246295	0.4±0.36
glycogen synthase kinase 3 alpha	Gsk3a	0.55±0.3
glycogen synthase kinase 3 beta	Gsk3b	0.79±0.24
glycogenin 1	Gyg1	4.47±0.57
glycolipid transfer protein (predicted)	Gltp_predicted	5.37±0.26
glycolipid transfer protein domain containing 1	Gltpd1	2.33±0.51
glycoprotein 2 (zymogen granule membrane)	Gp2	3.11±1
glycoprotein Ib, beta polypeptide /// septin 5	Gp1bb /// Sept5	0.64±0.11
glycoprotein, synaptic 2	Gpsn2	15.97±4.09
glycosylation dependent cell adhesion molecule 1	Glycam1	0.36±0.13
glycosylphosphatidylinositol specific phospholipase D1	Gpld1	0.89±0.32
glycosyltransferase 25 domain containing 1 (predicted)	Glt25d1_predicted	0.58±0.03
glycosyltransferase 8 domain containing 1	Glt8d1	1.43±0.4
glycosyltransferase-like 1B	Gyltl1b	2.07±0.06
glycosyltransferase-like domain containing 1	Gtdc1	0.68±0.2
glycyl-tRNA synthetase	Gars	5.6±1.62
glyoxalase 1	Glo1	8.6±0.17
glyoxalase domain containing 4	Glod4	3.97±0.43
glyoxalase domain containing 5	Glod5	0.53±0
glyoxylate reductase/hydroxypyruvate reductase (predicted)	Grhpr_predicted	2.44±0.89
glypican 1	Gpc1	1.33±0.41
glypican 4	Gpc4	11.21±0.99
GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	Gnas	28.4±0.32
golgi apparatus protein 1	Glg1	1.33±0.04
golgi associated PDZ and coiled-coil motif containing (predicted)	Gopc_predicted	1.74±0.29
golgi associated, gamma adaptin ear containing, ARF binding protein 1	Gga1	1.06±0.22
golgi associated, gamma adaptin ear containing, ARF binding protein 2	Gga2	8.74±1.99
golgi associated, gamma adaptin ear containing, ARF binding protein 3 (predicted)	Gga3_predicted	0.58±0.03
golgi autoantigen, golgin subfamily a, 2	Golga2	1.33±0.22
golgi autoantigen, golgin subfamily a, 3 (predicted)	Golga3_predicted	0.59±0.08
golgi autoantigen, golgin subfamily a, 4	Golga4	3.04±0.66
golgi autoantigen, golgin subfamily a, 5	Golga5	2.08±0.59
golgi autoantigen, golgin subfamily a, 7	Golga7	8.12±0.05
golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	3.98±0.33
golgi integral membrane protein 4	Golim4	0.61±0.19
golgi phosphoprotein 3	Golph3	3.25±0.12
golgi phosphoprotein 3-like	Golph3l	1.93±0.41
golgi reassembly stacking protein 1	Gorasp1	1.29±0.24
golgi reassembly stacking protein 2	Gorasp2	1.97±0.89
Golgi SNAP receptor complex member 1	Gosr1	2.45±0.87
golgi SNAP receptor complex member 2	Gosr2	2.11±0.23
golgi transport 1 homolog B (S. cerevisiae) (predicted)	Golt1b_predicted	0.41±0.12
golgi-specific brefeldin A-resistance factor 1	Gbf1	1.77±0.42
goliath	LOC652955	10.87±0.95
gonadotropin inducible ovarian transcription factor 1	Giot1	0.29±0.43
GPI-anchored membrane protein 1	Gpiap1	9.17±0.46
G-protein signalling modulator 3 (AGS3-like, C. elegans)	Gpsm3	0.69±0.31
GRAM domain containing 3	Gramd3	4.42±1.21

grancalcin (predicted)	Gca_predicted	6.93±0.6
granule cell antiserum positive 14	Gcap14	0.37±0.36
granulin	Grn	19.01±0.51
Granulocyte-macrophage colony stimulating receptor alpha	Csf2ra	0.28±0.18
GRB10 interacting GYF protein 1	Gigyf1	0.76±0.19
G-rich RNA sequence binding factor 1	Grsf1	16.69±2.22
GRINL1A combined protein	Gcom1	0.58±0.05
GRIP and coiled-coil domain containing 2	Gcc2	1.61±0.02
GRIP1 associated protein 1	Gripap1	0.88±0.03
growth arrest and DNA-damage-inducible 45 alpha	Gadd45a	11.52±1.19
growth arrest and DNA-damage-inducible 45 beta	Gadd45b	1.45±3.35
growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	14.88±1.87
growth arrest and DNA-damage-inducible, gamma interacting protein 1	Gadd45gip1	3.68±0.89
growth arrest specific 5	Gas5	1.42±0.22
growth arrest specific 6	Gas6	10.62±1.57
growth arrest-specific 2 like 1 (predicted)	Gas2l1_predicted	1.27±0.25
Growth differentiation factor 11	Gdf11	0.44±0.21
growth factor receptor bound protein 2	Grb2	3.64±0.28
growth factor receptor bound protein 2-associated protein 1 (predicted)	Gab1_predicted	1.85±0.54
growth factor receptor bound protein 7	Grb7	1.1±0.46
growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	Gfer	0.57±0.1
growth hormone inducible transmembrane protein	Ghitm	12.07±1.43
growth hormone receptor	Ghr	0.33±0.28
GrpE-like 1, mitochondrial	Grpel1	8.02±0.06
GrpE-like 2, mitochondrial	Grpel2	0.42±0.04
GSG1-like /// similar to germ cell associated 1 (predicted)	Gsg1l /// LOC687697	0.28±0.01
GTP binding protein 1 (predicted)	Gtpbp1_predicted	0.88±0.24
GTP binding protein 2	Gtpbp2	4.24±0.14
GTP binding protein 3 (mitochondrial)	Gtpbp3	0.65±0.17
GTP binding protein 4	Gtpbp4 /// LOC689842	0.66±0.11
GTP binding protein 5	Gtpbp5	2.01±0.18
GTP binding protein 6 (putative) (predicted)	Gtpbp6_predicted	1.1±0.05
GTP cyclohydrolase I feedback regulator	Gchfr	0.41±0.15
GTPase activating protein and VPS9 domains 1 (predicted)	Gapvd1_predicted	1.75±0.57
GTPase activating RANGAP domain-like 1	Garnl1	0.68±0.35
GTPase activating RANGAP domain-like 4 (predicted)	Garnl4_predicted	5.54±0.43
GTP-binding protein 10 (putative)	Gtpbp10	1.26±0.26
guanine monphosphate synthetase	Gmps	3.03±0.89
guanine nucleotide binding protein (G protein), beta 5	Gnb5	2.17±0.47
guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	Gnb2l1	20.42±2.88
guanine nucleotide binding protein (G protein), gamma 10	Gng10	3.4±0.71
guanine nucleotide binding protein (G protein), gamma 12	Gng12	5.5±1.44
guanine nucleotide binding protein (G protein), gamma 5	Gng5	21.03±0.95
guanine nucleotide binding protein, alpha 11	Gna11	0.84±0.25
guanine nucleotide binding protein, alpha 12	Gna12	0.33±0.14
guanine nucleotide binding protein, alpha 14	Gna14	1.74±0.4
guanine nucleotide binding protein, alpha inhibiting 1	Gnai1	1.69±0.26
guanine nucleotide binding protein, alpha inhibiting 2	Gnai2	0.75±0.1
guanine nucleotide binding protein, alpha inhibiting 3	Gnai3	6.47±1.53
guanine nucleotide binding protein, alpha stimulating, olfactory type	Gnal	0.59±0.1
guanine nucleotide binding protein, beta 1	Gnb1	4.79±0.59
guanine nucleotide binding protein, beta 2	Gnb2	5.15±0.14
guanine nucleotide binding protein-like 1	Gnl1	1.79±0.33
guanine nucleotide binding protein-like 2 (nucleolar)	Gnl2	0.34±0.04
guanine nucleotide binding protein-like 3 (nucleolar)	Gnl3	1.15±0.14
guanosine diphosphate dissociation inhibitor 1	Gdi1	4.62±0.81
guanosine monophosphate reductase	Gmpr	2.7±0.22
guanosine monophosphate reductase 2	Gmpr2	1.98±0.52
guanylate cyclase 2g	Gucy2g	0.25±0.15
guanylate kinase 1	Guk1	6.38±1.23
GULP, engulfment adaptor PTB domain containing 1	Gulp1	3.9±1.41
gypsy retrotransposon integrase 1	Gin1	0.56±0.25
H1 histone family, member 0	H1f0	21.75±0.17
H1 histone family, member X	H1fx	2.25±0.44
H2A histone family, member J	H2afj	3.71±1.09
H2A histone family, member V (predicted)	H2afv_predicted /// LO	8.21±0.38
H2A histone family, member X	H2afx	0.94±0.03
H2A histone family, member Y	H2afy	6.21±0.29
H2A histone family, member Z	H2afz	20.7±1.68
H3 histone, family 3B	H3f3b	26.66±0.91
hairy and enhancer of split 1 (Drosophila)	Hes1	1.75±1.94
hairy and enhancer of split 6 (Drosophila)	Hes6	9.65±2.41
Hairy/enhancer-of-split related with YRPW motif 1	Hey1	0.32±0.29
haloacid dehalogenase-like hydrolase domain containing 2	Hdhd2	2.48±0.14
Harvey rat sarcoma virus oncogene	Hras	4.57±0.63
Hbs1-like (S. cerevisiae)	Hbs1l	2.12±0.04
HCCA2 protein	Hcca2	0.87±0.25
HCR (a-helix coiled-coil rod homolog)	Hcr	0.88±0.17
HD domain containing 2 (predicted)	Hddc2_predicted	0.85±0.09
HD domain containing 3 (predicted)	Hddc3_predicted	7.9±3.22
headcase homolog (Drosophila) (predicted)	Heca_predicted	2.02±0.56
HEAT repeat containing 1 (predicted)	Heatr1_predicted	0.25±0.11
HEAT repeat containing 2	Heatr2	1.22±0.56
HEAT repeat containing 5A	Heatr5a	1.41±0.39
HEAT repeat containing 5B	Heatr5b	0.49±0.25
HEAT repeat containing 6	Heatr6	0.25±0.09
heat shock 10 kDa protein 1 (chaperonin 10)	Hspe1	22.99±1.42

heat shock 105kDa/110kDa protein 1	Hsph1	16.05±1.8
heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	Hspa1a /// Hspa1b	46.48±12.15
heat shock 70kD protein 1B (mapped)	Hspa1b	45.88±8.62
heat shock 70kDa protein 12A (predicted)	Hspa12a_predicted	0.42±0.42
heat shock factor 2	Hsf2	1.01±0.12
heat shock factor binding protein 1	Hsbp1	5.84±0.66
heat shock protein 1	Hspb1	5.2±9.4
heat shock protein 1 (chaperonin)	Hspd1	33.23±0.74
heat shock protein 14	Hspa14	2.35±0.73
heat shock protein 2	Hspa2	0.63±0.06
heat shock protein 4	Hspa4	3.59±0.65
heat shock protein 5	Hspa5	8.31±1.14
heat shock protein 8	Hspa8	51.9±11.4
heat shock protein 9	Hspa9	18.33±3.61
heat shock protein 90, alpha (cytosolic), class A member 1	Hsp90aa1	33.5±4.55
heat shock protein 90kDa alpha (cytosolic), class B member 1	Hsp90ab1	24.84±0.15
heat shock protein, alpha-crystallin-related, B6	Hspb6	5.11±0.76
heat shock transcription factor 1	Hsf1	0.61±0.06
heat-responsive protein 12	Hrsp12	4.46±2.9
hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	Herc1_predicted	2.25±0.18
hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 (predicted)	Herc2_predicted	1.6±0.12
HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (predicted)	Hace1_predicted	1.2±0.04
hect domain and RLD 3 (predicted)	Herc3_predicted	2.45±1.04
hect domain and RLD 4	Herc4	2.08±0.57
HECT domain containing 1	Hectd1	8.14±1.27
hedgehog interacting protein-like 1	Hhipl1	0.23±0.07
helicase with zinc finger domain (predicted)	Helz_predicted	0.78±0.06
helicase-like transcription factor	Hltf	1.6±0.26
hematological and neurological expressed 1-like	Hn1l	2.9±0.86
hematological and neurological expressed sequence 1	Hn1	1.38±0.2
heme binding protein 1 (predicted)	Hebp1_predicted	2.85±0.76
heme oxygenase (decycling) 1	Hmox1	0.4±1.09
heme oxygenase (decycling) 2	Hmox2	2.51±0.64
HemK methyltransferase family member 1 (predicted)	Hemk1_predicted	0.67±0.19
heparan sulfate 2-O-sulfotransferase 1	Hs2st1	2.06±0.17
heparan sulfate 6-O-sulfotransferase 1 (predicted)	Hs6st1_predicted	0.99±0.05
hepatitis B virus x interacting protein (predicted)	Hbxip_predicted	11.22±1.33
hepatocyte growth factor activator	Hgfac	0.4±0.18
hepatoma-derived growth factor	Hdgf	1.73±0.17
hepatoma-derived growth factor, related protein 2	Hdgfrp2	0.62±0.11
hepatoma-derived growth factor, related protein 3	Hdgfrp3	0.33±0.08
hepsin	Hpn	8.35±1.28
Hermansky-Pudlak syndrome 1 homolog (human)	Hps1	4.6±0.13
Hermansky-Pudlak syndrome 3 homolog (human) (predicted)	Hps3_predicted	0.74±0.15
Hermansky-Pudlak syndrome 4 homolog (human) (predicted)	Hps4_predicted	0.41±0.1
HERPUD family member 2	Herpud2	3.35±0.14
heterochromatin protein 1, binding protein 3	Hp1bp3	7.22±0.55
heterogeneous nuclear ribonucleoprotein A/B	Hnrpab	11.25±0.8
heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	2.32±0.21
heterogeneous nuclear ribonucleoprotein A2/B1 /// similar to heterogeneous nuclear ribonucleoprotein A2/B1 (predicted)	Hnrnpa2b1 /// RGD156	3.1±0.87
heterogeneous nuclear ribonucleoprotein A3	Hnrpa3	9.77±1.45
heterogeneous nuclear ribonucleoprotein C	Hnrnpc	7.06±1.23
heterogeneous nuclear ribonucleoprotein D	Hnrpd	1.99±0.27
heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	5.21±1.6
heterogeneous nuclear ribonucleoprotein F	Hnrpf	2.92±0.22
heterogeneous nuclear ribonucleoprotein H1	Hnrph1	15.55±2.2
heterogeneous nuclear ribonucleoprotein H3	Hnrph3	3.58±0.53
heterogeneous nuclear ribonucleoprotein K	Hnrpk	16.81±2.33
heterogeneous nuclear ribonucleoprotein L	Hnrnpl	15.32±0.56
heterogeneous nuclear ribonucleoprotein L-like (predicted)	Hnrpll_predicted	2.39±0.69
heterogeneous nuclear ribonucleoprotein M	Hnrpm	1.34±0.07
heterogeneous nuclear ribonucleoprotein R	Hnrnpr	5.07±0.44
heterogeneous nuclear ribonucleoprotein U	Hnrnpu	9.16±0.9
heterogeneous nuclear ribonucleoprotein U-like 1 (predicted)	Hnrpul1_predicted	1.42±0.04
hexamethylene bis-acetamide inducible 1	Hexim1	4.07±1.6
hexamthylene bis-acetamide inducible 2 (predicted)	Hexim2_predicted	0.24±0.29
hexokinase 1	Hk1	11.86±2.99
hexosaminidase A	Hexa	5.99±0.78
hexosaminidase B	Hexb	9.72±1.47
hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (predicted)	H6pd_predicted	0.25±0.06
HGF-regulated tyrosine kinase substrate	Hgs	3.37±0.03
HIG1 domain family, member 1A	Higd1a	11.07±0.25
HIG1 domain family, member 2A (predicted)	Higd2a_predicted	9.93±1.21
high density lipoprotein binding protein	Hdlbp	4.96±0.65
high mobility group 20 B (predicted)	Hmg20b_predicted	1.9±0.43
high mobility group 20A (predicted)	Hmg20a_predicted	1.89±0.35
high mobility group AT-hook 1	Hmga1	0.68±0.2
high mobility group box 1	Hmgb1	10.51±0.48
high mobility group box 1	Hmgb1 /// LOC678705	12.69±0.72
high mobility group box 2	Hmgb2	4.35±1.23
high mobility group box 2-like 1 (predicted)	Hmgb2l1_predicted	0.6±0.24
high mobility group box 3	Hmgb3	2.76±0.08
high mobility group box transcription factor 1	Hbp1	2.89±0.23
high mobility group nucleosomal binding domain 1	Hmgn1	22.08±3.68
high mobility group nucleosomal binding domain 2	Hmgn2	11.77±2.34
high mobility group nucleosomal binding domain 3	Hmgn3	9.77±1.68
hippocalcin-like 1	Hpcal1	4.08±0.76

hippocampus abundant gene transcript 1 (predicted)	Hiat1_predicted	4.85±1.04
hippocampus abundant transcript-like 1	Hiatl1	4.65±0.71
HIRA interacting protein 3	Hirip3	1.45±0.58
histidine acid phosphatase domain containing 2A	Hisppd2a	1.83±0.28
histidine triad nucleotide binding protein 2 (predicted)	Hint2_predicted	9.59±0.48
histidine triad nucleotide binding protein 3	Hint3	1.86±0.62
histocompatibility 13 (predicted)	H13_predicted	4.66±0.27
histone aminotransferase 1	Hat1	6.73±1.11
histone cluster 1, H1d	Hist1h1d	1.68±0.16
histone cluster 1, H2bl /// histone cluster 1, H2bh /// histone cluster 1, H2bc /// similar to Histone H2B 291B	Hist1h2bc /// Hist1h2bh	1.41±1.92
histone cluster 1, H3f	Hist1h3f	0.3±0.1
histone cluster 1, H4b	Hist1h4b	3.28±1.34
histone cluster 3, H2a	Hist3h2a	0.33±0.6
histone cluster 3, H2ba (predicted)	Hist3h2ba_predicted	0.53±0.45
histone deacetylase 1 (predicted)	Hdac1_predicted	1.1±0.01
histone deacetylase 1 /// histone deacetylase 1 (predicted)	Hdac1 /// Hdac1_predic	1.55±0.09
histone deacetylase 11 (predicted)	Hdac11_predicted	4.69±0.26
histone deacetylase 2	Hdac2	5.05±1.05
histone deacetylase 3	Hdac3	1.72±0.15
histone deacetylase 5	Hdac5	1.8±0.12
histone deacetylase 8 (predicted)	Hdac8_predicted	0.39±0.13
histone H4 variant H4-v.1 (predicted)	RGD1562378_predicte	0.21±0.11
HIV TAT specific factor 1 (predicted)	Htatsf1_predicted	3.14±0.41
HIV-1 Rev binding protein 2 (predicted)	Hrb2_predicted	0.69±0.35
HIV-1 Rev binding protein-like (predicted)	Hrbl_predicted	0.3±0.17
HIV-1 tat interactive protein, homolog (human)	Htatip	1.98±0.39
HLA-B associated transcript 2	Bat2	2.96±0.17
HLA-B associated transcript 5	Bat5	6.4±2.98
HLA-B-associated transcript 1A	Bat1a	5.89±0.96
HLA-B-associated transcript 3	Bat3	1.83±0.21
HNF1 homeobox B	Hnf1b	3.49±1.21
hnRNP-associated with lethal yellow	Raly	2.4±0.53
holocarboxylase synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	Hlcs	0.23±0.02
holocytochrome c synthetase (predicted)	Hccs_predicted	3.46±0.92
homeo box A10	Hoxa10	8.05±3.25
homeo box A2	Hoxa2	0.58±0.21
homeo box A4	Hoxa4	1.65±0.25
homeo box A5	Hoxa5	9.42±0.83
homeo box A9 (predicted)	Hoxa9_predicted	4.84±1.71
homeo box B3 (predicted)	Hoxb3_predicted	1.17±0.58
homeo box B4	Hoxb4	1.7±0.12
homeo box B5	Hoxb5	0.72±0.01
homeo box B6	Hoxb6	9.72±1.61
homeo box B7	Hoxb7	1.86±0.06
homeo box B8	Hoxb8	0.35±0.12
homeo box C10	Hoxc10	3.91±0.77
homeo box C4	Hoxc4	0.35±0.12
homeo box C5 (predicted)	Hoxc5_predicted	0.67±0.36
homeo box D10 (predicted)	Hoxd10_predicted	13.09±1.72
homeobox A9	Hoxa9	3.15±0.47
homeobox C9	Hoxc9	1.04±0.26
homeodomain interacting protein kinase 1 (predicted)	Hipk1_predicted	4±0.29
Homeodomain interacting protein kinase 2 (predicted)	Hipk2_predicted	4.31±0.69
homeodomain interacting protein kinase 3	Hipk3	0.48±0.15
homer homolog 1 (Drosophila)	Homer1	3.81±0.3
Homer homolog 3 (Drosophila)	Homer3	0.43±0.14
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Herpud1	12.39±4.43
homolog of zebrafish ES1	RGD1303003	10.92±0.35
hook homolog 1 (Drosophila) (predicted)	Hook1_predicted	1.75±0.23
hook homolog 2 (Drosophila)	Hook2	0.6±0.11
hook homolog 3 (Drosophila)	Hook3	0.95±0.23
hormone-regulated proliferation associated protein 20	Hrpap20	3.59±1.59
host cell factor C1 (predicted)	Hcfc1_predicted	2.65±0.09
host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	8.63±0.66
host cell factor C2	Hcfc2	0.9±0.08
HpaII tiny fragments locus 9c	Htf9c	0.87±0.01
HRAS like suppressor 3	Hrasls3	4.46±0.63
HscB iron-sulfur cluster co-chaperone homolog (E. coli)	Hscb	0.96±0.18
hsp70-interacting protein	Hspbp1	1.9±0.23
Hspb associated protein 1	Hspbap1	0.23±0.07
HtrA serine peptidase 2	Htra2	2.35±0.31
human immunodeficiency virus type I enhancer binding protein 1	Hivep1	1.1±0.33
human immunodeficiency virus type I enhancer binding protein 2	Hivep2	0.78±0.28
huntingtin	Htt	0.56±0.13
Huntingtin interacting protein 1	Hip1	2.68±0.57
huntingtin interacting protein 1 related	Hip1r	0.33±0.08
huntingtin interacting protein 2 (predicted)	Hip2_predicted	7.82±1.75
Huntingtin interacting protein K	Hypk	7.95±1.06
HUS1 checkpoint homolog (S. pombe)	Hus1	1.3±0.18
hyaluronan mediated motility receptor (RHAMM)	Hmmr	0.58±0.18
hyaluronic acid binding protein 4 (predicted)	Habp4_predicted	2.74±0.14
hyaluronoglucosaminidase 2	Hyal2	1.34±0.02
hyaluronoglucosaminidase 3	Hyal3	2.88±0.68
hydroxyacyl glutathione hydrolase	Hagh	3.35±1.41
hydroxyacyl-Coenzyme A dehydrogenase	Hadh	16.64±3.56
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha sul	Hadha	15.9±2.13
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta sub	Hadhb	29.15±8.55

hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Hsd3b7	0.88±0.07
hydroxymethylbilane synthase	Hmbs	2.3±0.46
hydroxyprostaglandin dehydrogenase 15 (NAD)	Hpgd	1.78±0.96
hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	22.14±2.26
hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	5.72±0.95
hydroxysteroid (17-beta) dehydrogenase 12	Hsd17b12	2.66±0.68
hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	5.88±0.29
hydroxysteroid (17-beta) dehydrogenase 8	Hsd17b8	4.83±0.6
hydroxysteroid dehydrogenase like 2	Hsdl2	14.77±3.68
hypermethylated in cancer 2 (predicted)	Hic2_predicted	0.4±0.17
hyperpolarization activated cyclic nucleotide-gated potassium channel 2	Hcn2	1.47±0.19
hypothetical gene supported by NM_172157	LOC497729	2.68±0.67
hypothetical LOC100125371	LOC100125371	1.86±0.78
hypothetical LOC287306 (predicted)	RGD1307036_predicte	1.15±0.16
hypothetical LOC287388 (predicted)	RGD1310324_predicte	0.55±0.11
hypothetical LOC288978	LOC288978	1.83±0.67
hypothetical LOC290577	LOC290577	2.27±0.35
hypothetical LOC291982 (predicted) /// similar to autoantigen	LOC361399 /// RGD13	1.54±0.08
hypothetical LOC294030	RGD1305481	6.18±0.44
hypothetical LOC298018	LOC298018	0.2±0.09
hypothetical LOC300207 (predicted)	RGD1305928_predicte	2.22±0.87
hypothetical LOC301124	LOC301124	16.54±1.38
hypothetical LOC302495	LOC302495	0.29±0.23
hypothetical LOC303211	RGD1311260	2.45±0.47
hypothetical LOC304650 (predicted)	RGD1310262_predicte	0.63±0.42
hypothetical LOC304654 (predicted)	RGD1306072_predicte	0.39±0.06
hypothetical LOC305452 (predicted)	RGD1309634_predicte	1.26±0.02
hypothetical LOC306766	LOC306766	6.71±2.7
hypothetical LOC308765 (predicted) /// hypothetical protein LOC685841	LOC685841 /// RGD13	1.9±0.15
hypothetical LOC308869	MGC72560	4.91±1.4
hypothetical LOC311134	LOC311134	0.52±0.16
hypothetical LOC316091	RGD1304827	0.59±0.11
hypothetical LOC316976	MGC72974	1±0.03
hypothetical LOC361153	LOC361153	0.87±0.13
hypothetical LOC362564	LOC362564	1.23±0.13
hypothetical LOC366300	LOC366300	9.15±0.46
hypothetical LOC500532	LOC500532	1.19±0
hypothetical protein Dd25	Dd25	0.97±0
hypothetical protein LOC100125364	rCG_22919	0.91±0.08
hypothetical protein LOC100125365	LOC100125365	1.62±0.61
hypothetical protein LOC292764	RGD1303117	1.1±0.48
hypothetical protein LOC303332	LOC303332	1.37±0.21
hypothetical protein LOC307347	LOC307347	4.38±0.64
Hypothetical protein LOC311254	LOC311254	1.34±0.09
hypothetical protein LOC361335	LOC361335	0.9±0.2
hypothetical protein LOC498606	LOC498606	1.26±0.23
hypothetical protein LOC499120	LOC499120	2.03±0.12
hypothetical protein LOC499339	LOC499339	0.7±0.38
hypothetical protein LOC499602	LOC499602	0.45±0.09
hypothetical protein LOC500251	LOC500251	1.05±0.24
hypothetical protein LOC500956	LOC500956	1.56±0.59
hypothetical protein LOC501546	LOC501546	2.88±0.37
hypothetical protein LOC502374	LOC502374	8.67±2.26
hypothetical protein LOC595134	LOC595134	1.19±0.47
hypothetical protein LOC606294	LOC606294	5.61±0.64
Hypothetical protein LOC619558	LOC619558	0.72±0.11
hypothetical protein LOC619574	LOC619574	1.47±0.23
hypothetical protein LOC654482	LOC654482	0.59±0
hypothetical protein LOC678810 /// Purkinje cell protein 4-like 1	LOC678810 /// Pcp4l1	0.25±0.12
hypothetical protein LOC678970	LOC678970	0.22±0.03
hypothetical protein LOC679880	LOC679880	6.04±0.19
hypothetical protein LOC680039	LOC680039	2.38±0.57
Hypothetical protein LOC680080	LOC680080	4.84±1.68
Hypothetical protein LOC680259	LOC680259	12.84±0.87
hypothetical protein LOC680262	LOC680262	0.49±0.01
Hypothetical protein LOC680422	LOC680422	0.57±0
hypothetical protein LOC680687	LOC680687	0.45±0.07
Hypothetical protein LOC680817	LOC296884	0.51±0.59
hypothetical protein LOC681219	LOC681219	17.2±1.26
hypothetical protein LOC681292	LOC681292	0.22±0.16
hypothetical protein LOC681367	LOC681367	3.22±1.07
hypothetical protein LOC682679	LOC682679	3.05±0.47
hypothetical protein LOC682709	LOC682709	7.62±0.13
hypothetical protein LOC682888	LOC682888	4.86±0.27
hypothetical protein LOC683034	LOC683034	1.4±0.23
Hypothetical protein LOC683140	Ak1	5.3±1.34
hypothetical protein LOC683460	LOC683460	3.79±2.36
hypothetical protein LOC683948	LOC683948	0.37±0.12
hypothetical protein LOC684055	LOC684055	3.39±0.23
hypothetical protein LOC684830	LOC684830	0.65±0.1
hypothetical protein LOC684993	LOC684993	1.92±0.23
hypothetical protein LOC685203	LOC685203	0.86±0.1
hypothetical protein LOC685233 /// hypothetical protein LOC688211	LOC685233 /// LOC688	0.98±0.05
hypothetical protein LOC685326	LOC685326	0.6±0.21
hypothetical protein LOC685545	LOC685545	8.61±1.76
hypothetical protein LOC685548	LOC685548	5.01±1.65
hypothetical protein LOC685634	LOC685634	1.78±0.24

hypothetical protein LOC685888	LOC685888	3.09±0.47
hypothetical protein LOC686179	MGC125239	0.23±0.25
hypothetical protein LOC686506	LOC686506	0.2±0.04
hypothetical protein LOC687090	LOC687090	5.24±0.88
hypothetical protein LOC687361	LOC687361	1.27±0.11
hypothetical protein LOC687408	LOC687408	0.28±0.02
hypothetical protein LOC687693	LOC687693	2.08±1.01
hypothetical protein LOC688211	LOC688211	0.58±0.36
hypothetical protein LOC688257	LOC688257	5.04±0.72
hypothetical protein LOC688300	LOC688300	2.63±0.61
Hypothetical protein LOC688495	LOC688495	6.72±0.96
hypothetical protein LOC688765	LOC688765	0.2±0.01
Hypothetical protein LOC689165	LOC689165	0.73±0.1
hypothetical protein LOC689399	LOC689399	0.42±0.1
hypothetical protein LOC689574	LOC689574	4.77±0.14
hypothetical protein LOC689621	LOC689621	0.41±0.09
hypothetical protein LOC689748	LOC689748	8.85±1.07
hypothetical protein LOC689755	LOC689755	0.32±0.03
hypothetical protein LOC689836	LOC689836	0.4±0.04
hypothetical protein LOC689959	LOC689959	1.83±0.54
hypothetical protein LOC690243	LOC690243	3.41±1.24
hypothetical protein LOC690274	LOC690274	0.69±0.08
hypothetical protein LOC690349	LOC690349	1.99±0.11
hypothetical protein LOC690422	LOC690422	0.37±0.35
hypothetical protein LOC690806	LOC690806	0.53±0.05
hypothetical protein LOC691543	LOC691543	0.73±0.29
hypothetical protein LOC691750	LOC691750	0.89±0.12
hypothetical protein LOC691807	rCG_28701	13.29±1.27
hypothetical protein LOC691849	LOC691849	1.36±0.09
hypothetical protein LOC692032	LOC692032	0.7±0.13
hypothetical protein MGC:15854	RGD1302996	7.4±0.86
hypothetical protein MGC:72616	RGD735175	1.14±0.37
hypothetical RNA binding protein RGD1359713	RGD1359713	12.26±1.38
hypoxanthine guanine phosphoribosyl transferase 1	Hprt1	2.83±0.01
hypoxia inducible factor 1, alpha subunit	Hif1a	5.17±1.82
hypoxia up-regulated 1	Hyou1	2.48±0.01
hypoxia-inducible factor prolyl 4-hydroxylase	Ph-4	0.35±0.06
iduronate 2-sulfatase	Ids	4.86±0.22
IK cytokine /// WD repeat domain 55	Ik /// Wdr55	2.71±0.62
IKAROS family zinc finger 5	Ikzf5	0.35±0.23
ilvB (bacterial acetolactate synthase)-like (predicted)	Ilvbl_predicted	1.5±0.39
immature colon carcinoma transcript 1 (predicted)	Ict1_predicted	5.73±0.83
immediate early response 2	Ier2	4.11±0.49
immediate early response 5-like	Ier5l	1.96±0.29
immunoglobulin (CD79A) binding protein 1	Igbp1	3.94±0.07
immunoglobulin mu binding protein 2	Ighmbp2	0.63±0.29
immunoglobulin superfamily, member 3 (predicted)	Igsf3_predicted	0.5±0.03
IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (predicted)	Imp3_predicted	1.96±0.71
IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp4	3.1±0.41
importin 11 (predicted)	Ipo11_predicted	1.7±0.12
importin 13	Ipo13	0.54±0.15
importin 4 (predicted)	Ipo4_predicted	1.37±0
importin 7 (predicted)	Ipo7_predicted	3.64±1.03
Importin 9 (predicted)	Ipo9_predicted	2.12±0.75
influenza virus NS1A binding protein (predicted)	Ivns1abp_predicted	27.39±1.91
ing finger protein 5 pseudogene	rCG_38334	2.63±0.67
Inhibin beta-B	Inhbb	0.84±0.03
inhibitor of Bruton agammaglobulinemia tyrosine kinase (predicted)	Ibtk_predicted	0.82±0.33
inhibitor of DNA binding 2	Id2	3.35±0.2
inhibitor of growth family, member 1	Ing1	2.64±0.02
inhibitor of growth family, member 2	Ing2	1.04±0.22
inhibitor of growth family, member 3	Ing3	1.18±0.37
inhibitor of growth family, member 4	Ing4	0.91±0.07
inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	Ikbkap	1.24±0.08
inhibitor of kappaB kinase beta	Ikbkb	1.09±0.1
inner centromere protein (predicted)	Incenp_predicted	0.37±0.23
inner membrane protein, mitochondrial	Immt	25.77±5.07
INO80 complex homolog 1 (S. cerevisiae)	Inoc1	0.45±0.17
inosine 5'-phosphate dehydrogenase 2	Impdh2	2.98±0.77
inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Itpa	2.84±0.66
Inositol (myo)-1(or 4)-monophosphatase 1	Impa1	1.65±0.2
inositol (myo)-1(or 4)-monophosphatase 2	Impa2	2.67±0.69
inositol 1,4,5-triphosphate receptor 1	Itpr1	6.51±0.16
inositol 1,4,5-triphosphate receptor 3	Itpr3	0.73±0.48
inositol 1,4,5-trisphosphate 3-kinase C	Itpkc	0.66±0.04
inositol hexaphosphate kinase 1	Ihpk1	4.08±0.27
inositol hexaphosphate kinase 2	Ihpk2	2.57±0.68
inositol monophosphatase domain containing 1	Impad1	1.34±0.07
inositol polyphosphate multikinase	Ipmk	7.89±0.48
inositol polyphosphate phosphatase-like 1	Inppl1	2.57±0.7
inositol polyphosphate-1-phosphatase	Inpp1	2.79±1.14
inositol polyphosphate-4-phosphatase, type 1	Inpp4a	0.25±0.06
inositol polyphosphate-5-phosphatase A (predicted)	Inpp5a_predicted	0.84±0.36
inositol polyphosphate-5-phosphatase B	Inpp5b	2.59±0.17
insulin degrading enzyme	Ide	1.23±0.29
insulin induced gene 2	Insig2	1.58±0.68
insulin receptor substrate 1	Irs1	0.53±0.25

insulin receptor substrate 2	Irs2	0.65±0.15
insulin-like growth factor 1	Igf1	21.57±7.44
insulin-like growth factor 1 receptor	Igf1r	4.34±0.76
insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	1.16±0.72
insulin-like growth factor 2 receptor	Igf2r	1.9±1.32
insulin-like growth factor binding protein 1	Igfbp1	22.31±15.79
insulin-like growth factor binding protein 5	Igfbp5	1.88±6.64
insulin-like growth factor binding protein 7	Igfbp7	50.16±4.61
integral membrane protein 2B	Itm2b	64.14±2.37
integral membrane protein 2C	Itm2c	29.05±3.05
integrator complex subunit 10	Ints10	1.6±0.62
integrator complex subunit 3	Ints3	0.67±0.27
integrator complex subunit 4	Ints4	4.08±0.85
integrator complex subunit 5 (predicted)	Ints5_predicted	0.86±0.3
integrator complex subunit 6	Ints6	4.87±0.7
integrator complex subunit 7	Ints7	0.72±0.23
integrin alpha 1	Itga1	2.43±0.74
Integrin alpha 3 (predicted)	Itga3_predicted	0.66±0.12
integrin alpha FG-GAP repeat containing 1	Itfg1	4.3±0.44
integrin alpha FG-GAP repeat containing 2	Itfg2	0.47±0.05
integrin alpha FG-GAP repeat containing 3	Itfg3	7.29±1.64
integrin alpha V (predicted)	Itgav_predicted	0.7±0.01
integrin beta 1 (fibronectin receptor beta)	Itgb1	13.7±1.47
integrin beta 1 binding protein 1 (predicted)	Itgb1bp1_predicted	1.87±0.09
integrin beta 3 binding protein (beta3-endonexin)	Itgb3bp	1.75±0.28
integrin beta 4	Itgb4	0.88±0.18
integrin linked kinase	Ilk	5.96±0.19
integrin, alpha E, epithelial-associated	Itgae	1.58±0.4
integrin, beta 5	Itgb5	7.65±1.16
integrin, beta 6	Itgb6	2.03±1.76
integrin-linked kinase-associated serine/threonine phosphatase 2C	Ilkap	1.66±0.26
inter-alpha trypsin inhibitor, heavy chain 1 (predicted)	Itih1_predicted	1.12±0.01
interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted	2.24±0.46
interferon gamma induced GTPase	Igtp	1.27±0.43
interferon gamma inducible protein 30	Ifi30	9.31±1.43
interferon gamma receptor 1	Ifngr1	0.61±0.36
interferon gamma receptor 2 (predicted)	Ifngr2_predicted	0.76±0.72
interferon induced transmembrane protein 2	Ifitm2	23.94±6.76
interferon regulatory factor 1	Irf1	0.67±5.32
interferon regulatory factor 2 binding protein 1 (predicted)	Irf2bp1_predicted	1.45±0.21
interferon regulatory factor 6 (predicted)	Irf6_predicted	4.48±0.98
interferon regulatory factor 7	Irf7	1.17±0.15
interferon regulatory factor 9	Irf9	0.88±0.49
interferon stimulated exonuclease gene 20-like 1 (predicted)	Isg20l1_predicted	0.32±0.07
interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted	1.29±0.31
interferon-induced protein 35	Ifi35	1.04±0.04
interferon-induced protein 44	Ifi44	0.7±0.4
interferon-related developmental regulator 2 (predicted)	Ifrd2_predicted	1.11±0.1
interleukin 10 receptor, beta	Il10rb	0.49±0.29
interleukin 11 receptor, alpha chain 1	Il11ra1	2.65±0.6
interleukin 13 receptor, alpha 1	Il13ra1	4.69±0.2
interleukin 15	Il15	0.39±0.13
interleukin 17 receptor A	Il17ra	0.64±0.22
interleukin 18 binding protein	Il18bp	0.48±0.01
interleukin 6 signal transducer	Il6st	2.66±1.75
interleukin 7	Il7	0.58±0.19
interleukin enhancer binding factor 2	Ilf2	2.98±1.73
interleukin enhancer binding factor 3	Ilf3	0.48±0.4
interleukin-1 receptor-associated kinase 1 (predicted)	Irak1_predicted	4.69±0.31
interleukin-1 receptor-associated kinase 1 binding protein 1 (predicted)	Irak1bp1_predicted	1.12±0.12
interleukin-1 receptor-associated kinase 2	Irak2	1.16±0.12
intersectin 1	Itsn1	0.28±0.15
intersectin 2	Itsn2	1.21±0.43
intestinal cell kinase	Ick	1.54±0.2
intraflagellar transport 172 homolog (Chlamydomonas)	Ift172	1.05±0.16
intraflagellar transport 20 homolog (Chlamydomonas)	Ift20	3.8±0.45
intraflagellar transport 57 homolog (Chlamydomonas) (predicted)	Ift57_predicted	1.4±0.31
intraflagellar transport 74 homolog (Chlamydomonas)	Ift74	0.54±0.03
intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	0.29±0.2
intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	1.11±0.12
intraflagellar transport 88 homolog (Chlamydomonas) (predicted)	Ift88_predicted	0.54±0.14
invasion inhibitory protein 45	Iip45	0.63±0.09
inversin	Invs	0.35±0.07
IQ calmodulin-binding motif containing 1 (predicted)	Iqcb1_predicted	0.33±0.16
IQ motif and ubiquitin domain containing	Iqub	0.82±0.26
IQ motif and WD repeats 1	Iqwd1	0.53±0.31
IQ motif containing GTPase activating protein 1 (predicted)	Iqgap1_predicted	2.58±0.19
Iron responsive element binding protein 2	Ireb2	2.26±0.6
iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	Isca1	9.7±1.01
Iroquois related homeobox 1 (Drosophila) (predicted)	Irx1_predicted	9.54±1.16
Iroquois related homeobox 2 (Drosophila)	Irx2	3.31±0.34
ischemia related factor NYW-1	Nyw1	1.23±0.28
IscU iron-sulfur cluster scaffold homolog (E. coli)	Iscu	12.51±3.52
isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	Iah1	2.4±0.83
isochorismatase domain containing 1	Isoc1	13.89±1.34
isochorismatase domain containing 2b	Isoc2b	6.59±1.65
isocitrate dehydrogenase 1 (NADP+), soluble	Idh1	4.08±0.44

isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	64.58±0.75
isocitrate dehydrogenase 3 (NAD), gamma	Idh3g	29.76±1.56
isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	10.96±3.29
isocitrate dehydrogenase 3 (NAD+) beta	Idh3B	25.47±4.17
isoleucine-tRNA synthetase (predicted)	Iars_predicted	1.85±0.71
isoleucine-tRNA synthetase 2, mitochondrial (predicted)	Iars2_predicted	3.43±0.97
isopentenyl-diphosphate delta isomerase	Idi1	4.59±3.05
isoprenylcysteine carboxyl methyltransferase	Icmt	0.26±0.02
isovaleryl coenzyme A dehydrogenase	Ivd	6.6±0.51
ISY1 splicing factor homolog (S. cerevisiae)	Isy1	1.71±0.3
IWS1 homolog (S. cerevisiae)	Iws1	2.06±0.17
jagunal homolog 1 (Drosophila)	Jagn1	1.43±0.22
Janus kinase 1	Jak1	10.12±0.01
Janus kinase 2	Jak2	1.88±0.12
Janus kinase 3	Jak3	1.72±0.85
Josephin domain containing 1	Josd1	1.87±0.4
Josephin domain containing 2 (predicted)	Josd2_predicted	0.61±0.18
Josephin domain containing 3	Josd3	0.57±0.5
JTV1 gene	Jtv1	2.95±0.3
jumonji domain containing 1A	Jmjd1a	2.25±0.43
jumonji domain containing 1C	Jmjd1c	2.86±1.5
jumonji domain containing 3 (predicted)	Jmjd3_predicted	0.84±0.96
jumonji domain containing 5	Jmjd5	0.93±0.05
jumonji domain containing 6	Jmjd6	1.11±0.12
jumonji, AT rich interactive domain 1B (Rbp2 like)	Jarid1b	2.04±0.13
jumping translocation breakpoint	Jtb	3.1±0.87
Jun D proto-oncogene	Jund	10.3±2.7
Jun dimerization protein 2	Jundm2	0.52±0.28
Jun dimerization protein 2	Jundp2	2.5±0.12
Jun oncogene	Jun	11.81±0.04
Jun-B oncogene	Junb	3.53±1.44
junction plakoglobin	Jup	3.56±1.23
kalirin, RhoGEF kinase	Kalrn	0.24±0.01
kaptin	Kptn	1.58±0.15
Karyopherin (importin) alpha 1	Kpna1	1.8±0.02
karyopherin (importin) alpha 2	Kpna2	2.54±0.62
Karyopherin (importin) alpha 3	Kpna3	2.04±0.02
karyopherin (importin) alpha 6	Kpna6	0.49±0.14
karyopherin (importin) beta 1	Kpnb1	0.45±0.04
katanin p60 (ATPase-containing) subunit A1	Katna1	1.03±0.24
katanin p80 (WD40-containing) subunit B 1	Katnb1	0.88±0.1
KDEL (Lys-Asp-Glu-Leu) containing 1	Kdelc1	0.53±0.21
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	Kdelr1	8.97±0.16
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Kdelr2	6.47±0.21
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted)	Kdelr3_predicted	16.31±2.64
kelch domain containing 1 (predicted)	Klhdc1_predicted	0.58±0.09
kelch domain containing 2	Klhdc2	4.8±0.09
kelch domain containing 3	Klhdc3	2.7±0.34
kelch domain containing 5	Klhdc5	0.56±0.12
kelch domain containing 8A	Klhdc8a	7.63±1.61
kelch repeat and BTB (POZ) domain containing 2 (predicted)	Kbtbd2_predicted	1.74±0.26
kelch repeat and BTB (POZ) domain containing 3 (predicted)	Kbtbd3_predicted	0.54±0.2
kelch repeat and BTB (POZ) domain containing 4 (predicted)	Kbtbd4_predicted	1.07±0.35
kelch-like 14 (Drosophila)	Klhl14	1.32±0.26
kelch-like 2, Mayven (Drosophila) (predicted)	Klhl2_predicted	0.51±0.15
kelch-like 21 (Drosophila) (predicted)	Klhl21_predicted	0.69±0
kelch-like 22 (Drosophila) (predicted)	Klhl22_predicted	0.4±0.14
kelch-like 23 (Drosophila) (predicted)	Klhl23_predicted	0.71±0.19
kelch-like 24 (Drosophila)	Klhl24	2.97±2.41
kelch-like 25 (Drosophila)	Klhl25	0.32±0.08
kelch-like 26 (Drosophila) (predicted)	Klhl26_predicted	0.52±0.16
kelch-like 30 (Drosophila)	Klhl30	0.38±0.14
kelch-like 5 (Drosophila)	Klhl5	0.76±0.04
kelch-like 7 (Drosophila)	Klhl7	5.82±1.93
kelch-like 8 (Drosophila) (predicted)	Klhl8_predicted	0.4±0.03
kelch-like 9 (Drosophila) (predicted)	Klhl9_predicted	7.77±2.19
Kelch-like ECH-associated protein 1	Keap1	1.36±0.2
keratin 10	Krt10	1.31±0.12
keratin 19	Krt19	0.91±0.87
keratin 7	Krt7	15.31±0.46
keratin 8	Krt8	1.02±1.79
keratinocyte associated protein 2 (predicted)	Krtcap2_predicted	6.98±0.87
KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	5.41±0.08
KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	1.27±0.06
KH-type splicing regulatory protein	Khsrp	5.41±0.61
kidney predominant protein NCU-G1	RGD1303130	4.13±0.24
kin of IRRE like 3 (Drosophila) (predicted)	Kirrel3_predicted	0.66±0.06
kinase D-interacting substrate of 220 kDa	Kidins220	7.58±0.52
kinectin 1 (predicted)	Ktn1_predicted	2.67±0.46
kinesin family member 11	Kif11	0.43±0.07
kinesin family member 12	Kif12	0.68±0
kinesin family member 13A (predicted)	Kif13a_predicted	0.79±0.13
kinesin family member 15	Kif15	0.51±0.04
kinesin family member 16B (predicted)	Kif16b_predicted	0.5±0.11
kinesin family member 20A (predicted)	Kif20a_predicted	0.51±0.14
kinesin family member 21A (predicted)	Kif21a_predicted	1.38±0.04
kinesin family member 22	Kif22	0.58±0.07

kinesin family member 23 (predicted)	Kif23_predicted	0.33±0.08
kinesin family member 2A	Kif2a	1.1±0.16
kinesin family member 3a	Kif3a	0.36±0.16
kinesin family member 3B (predicted)	Kif3b_predicted	1.64±0.14
kinesin family member 3C	Kif3c	0.71±0.27
kinesin family member 5B	Kif5b	0.46±0.18
kinesin family member C3	Kifc3	4.93±1.52
Kinesin heavy chain family, member 2	Kif2	0.86±0.16
kinesin light chain 1	Klc1	1.9±0.68
kinesin light chain 2 (predicted)	Klc2_predicted	2.07±0.18
kinesin light chain 4	Klc4	3.81±0.29
kinesin-associated protein 3 (predicted)	Kifap3_predicted	3.67±0.25
kinetochore associated 1 (predicted)	Kntc1_predicted	0.45±0.14
Klotho	Kl	0.41±0.23
KRAB-A domain containing 1	Krba1	0.59±0.29
KRIT1, ankyrin repeat containing (predicted)	Krit1_predicted	1.11±0.15
Kruppel-like factor 10	Klf10	3.55±0.8
Kruppel-like factor 13	Klf13	0.68±0.22
Kruppel-like factor 15	Klf15	6.2±1.4
Kruppel-like factor 2 (lung) (predicted)	Klf2_predicted	0.59±0.41
Kruppel-like factor 3 (basic)	Klf3	0.87±0.62
Kruppel-like factor 4 (gut)	Klf4	0.2±1.24
Kruppel-like factor 6	Klf6	1.6±3.5
Kruppel-like factor 9	Klf9	10.21±5.14
KTEL (Lys-Tyr-Glu-Leu) containing 1	Ktelc1	1.63±0.28
KTI12 homolog, chromatin associated (S. cerevisiae)	Kti12	1.56±0.05
Kv channel interacting protein 4	Kcnip4	0.44±0.03
kynurenine aminotransferase III	Kat3	3.27±0.24
L antigen family, member 3	Lage3	5.92±0.15
l(3)mbt-like 2 (Drosophila)	L3mbtl2	0.84±0.1
l(3)mbt-like 3 (Drosophila) (predicted)	L3mbtl3_predicted	0.21±0.14
L1 cell adhesion molecule	L1cam	0.39±1
L-2-hydroxyglutarate dehydrogenase (predicted)	L2hgdh_predicted	1.14±0.1
La ribonucleoprotein domain family, member 1 (predicted)	Larp1_predicted	5.8±0.53
La ribonucleoprotein domain family, member 5 (predicted)	Larp5_predicted	4.92±0.58
lactamase, beta (predicted)	Lactb_predicted	0.53±0.2
Lactamase, beta 2	Lactb2	3.77±0.48
lactate dehydrogenase A	Ldha	6.87±4.08
lactate dehydrogenase B	Ldhb	59.29±2
lactate dehydrogenase D	Ldhd	1.75±0.16
lactation elevated 1	Lace1	1.84±0.81
ladinin (predicted)	Lad1_predicted	3.1±0.32
LAG1 homolog, ceramide synthase 1 /// growth differentiation factor 1 (predicted)	Gdf1_predicted /// Lass	5.43±0.16
LAG1 homolog, ceramide synthase 4	Lass4	0.22±0.1
LAG1 homolog, ceramide synthase 5	Lass5	1.36±0.28
lamin B receptor	Lbr	0.3±0.08
Lamin B1	Lmnb1	1.63±0.16
laminin, alpha 1	Lama1	1.2±0.14
laminin, alpha 5	Lama5	1.01±1.26
laminin, beta 1	Lamb1	8.04±0.32
laminin, beta 2	Lamb2	7.58±2.9
laminin, gamma 1	Lamc1	0.32±0.46
lanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	3.76±1.27
LanC (bacterial lantibiotic synthetase component C)-like 2 (predicted)	Lancl2_predicted	1.3±0.76
Lanosterol synthase	Lss	1.24±0.46
large subunit GTPase 1 homolog (S. cerevisiae)	Lsg1	0.46±0.05
large subunit ribosomal protein L36a	LOC685642 /// LOC687	11.05±0.66
large subunit ribosomal protein L36a	LOC687717 /// LOC691	12.64±2.72
large tumor suppressor 2 (predicted)	Lats2_predicted	4.94±2.29
LAS1-like (S. cerevisiae) (predicted)	Las1l_predicted	0.78±0.06
latent transforming growth factor beta binding protein 3	Ltbp3	1.82±0.02
latrophilin 2	Lphn2	3.33±0.59
LEA_4 domain containing protein RGD1359600	RGD1359600	4.56±1.21
lectin, galactose binding, soluble 1	Lgals1	3.44±1.18
lectin, galactose binding, soluble 8	Lgals8	2.21±0.02
lectin, mannose-binding 2 (predicted)	Lman2_predicted	3.66±0.48
Lectin, mannose-binding 2-like (predicted)	Lman2l_predicted	3.07±0.4
lectin, mannose-binding, 1	Lman1	0.94±0.11
LEM domain containing 2	Lemd2	0.62±0.01
LEM domain containing 3	Lemd3	0.96±0.14
Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Leo1	0.83±0.29
leprecan 1	Lepre1	0.89±0.2
leprecan-like 2 (predicted)	Leprel2_predicted	0.98±0.37
leptin receptor overlapping transcript	Leprot	4.44±0.34
leptin receptor overlapping transcript-like 1	Leprotl1	1.59±0.53
lethal giant larvae homolog 1 (Drosophila)	Llgl1	0.58±0.22
leucine aminopeptidase 3	Lap3	1.19±0.48
leucine carboxyl methyltransferase 1	Lcmt1	2.71±0.22
leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	0.58±0.37
leucine rich repeat (in FLII) interacting protein 2	Lrrfip2	0.97±0.13
leucine rich repeat and sterile alpha motif containing 1	Lrsam1	0.57±0.09
leucine rich repeat containing 14	Lrrc14	1.37±0.35
leucine rich repeat containing 16	Lrrc16	2.46±0.47
leucine rich repeat containing 28 (predicted)	Lrrc28_predicted	0.46±0.09
leucine rich repeat containing 40	Lrrc40	1.77±0.37
leucine rich repeat containing 41	Lrrc41	1.37±0.33
leucine rich repeat containing 42	Lrrc42	1.16±0.39

leucine rich repeat containing 48	Lrrc48	0.32±0.04
leucine rich repeat containing 57	Lrrc57	0.94±0.11
leucine rich repeat containing 59	Lrrc59	3.8±0.53
leucine rich repeat containing 61	Lrrc61	0.43±0.15
leucine rich repeat containing 8 family, member B	Lrrc8b	1.01±0.37
leucine rich repeat containing 8 family, member E	Lrrc8e	0.59±0.23
leucine rich repeat containing 8A	Lrrc8a	0.48±0.36
leucine rich repeat containing 8D	Lrrc8d	2.57±1.48
leucine zipper and CTNNBIP1 domain containing	Lzic	0.67±0.04
leucine zipper protein 1	Luzp1	1.24±0.39
leucine zipper transcription factor-like 1	Lztfl1	1.35±0.17
leucine zipper, putative tumor suppressor 2	Lzts2	1.45±0.18
leucine zipper-EF-hand containing transmembrane protein 1	Letm1	2.92±1.25
leucine-rich PPR-motif containing	Lrpprc	7.5±2.13
leucine-rich repeat kinase 1 (predicted)	Lrrk1_predicted	0.89±0.18
leucine-rich repeat-containing G protein-coupled receptor 4	Lgr4	2.13±0.8
leucine-rich repeats and calponin homology (CH) domain containing 1	Lrch1	0.34±0.12
leucine-rich repeats and immunoglobulin-like domains 3	Lrig3	0.36±0.14
leucine-rich repeats and transmembrane domains 2	Lrtm2	0.6±0.2
leucine-zipper-like transcriptional regulator, 1 (predicted)	Lztr1_predicted	1.26±0.18
leucyl-tRNA synthetase	Lars	1.63±0.16
leukemia inhibitory factor receptor	Lifr	0.52±0.06
leukocyte receptor cluster (LRC) member 1 (predicted)	Leng1_predicted	0.33±0.23
leukocyte receptor cluster (LRC) member 4 (predicted)	Leng4_predicted	2.19±0.09
leukocyte receptor cluster (LRC) member 8	Leng8	0.25±0.25
leukotriene A4 hydrolase	Lta4h	4.59±1.5
leukotriene B4 12-hydroxydehydrogenase	Ltb4dh	1.79±0.25
leupaxin	Lpxn	0.25±0.11
ligand of numb-protein X 1 (predicted)	Lnx1_predicted	1.45±0.3
ligand of numb-protein X 2 (predicted)	Lnx2_predicted	0.79±0
ligase I, DNA, ATP-dependent	Lig1	1.24±0.28
ligase III, DNA, ATP-dependent	Lig3	0.2±0.2
LIM and SH3 protein 1	Lasp1	5.68±2.88
LIM domain binding 1 (predicted)	Ldb1_predicted	3.22±0.64
LIM domain binding 3	Ldb3	0.21±0.03
LIM domain only 4	Lmo4	4.96±1.01
LIM domain only 7	Lmo7	7.62±0.07
LIM domain only protein 7	LMO7	15.23±1.34
LIM domains containing 1 (predicted)	Limd1_predicted	2.03±0.26
LIM motif-containing protein kinase 2	Limk2	1.12±0.71
limb region 1-like homolog (mouse)	Lmbr1l	0.23±0.2
limkain b1	Lkap	2.39±0.27
lin-37 homolog (C. elegans)	Lin37	1.65±0.55
lipase maturation factor 1	Lmf1	0.67±0.21
lipase, endothelial	Lipg	1.55±0.27
lipin 3	Lpin3	0.84±0.14
lipoic acid synthetase	Lias	6.74±1.11
lipolysis stimulated lipoprotein receptor	Lsr	2.56±1.08
lipoma HMGIC fusion partner-like 2 (predicted)	Lhfpl2_predicted	1.08±0.28
lipoprotein lipase	Lpl	0.48±2.84
LMBR1 domain containing 1	Lmbrd1	10.54±1.22
LOC360664 (predicted)	RGD1311078_predicte	0.88±0.24
LOC360807	LOC360807	5.19±0.98
LOC361485 /// similar to chromosome 6 open reading frame 70 (predicted)	RGD1309374 /// RGD1	2.1±0.08
LOC361614 (predicted)	RGD1308929_predicte	2.28±0.22
LOC361719 (predicted)	RGD1308106_predicte	0.42±0.11
LOC361774 (predicted)	RGD1306116_predicte	1.69±0.14
LOC362424 (predicted)	RGD1308850_predicte	3.08±0.74
LOC362678 (predicted)	RGD1308923_predicte	0.81±0.09
LOC363015 (predicted)	RGD1310444_predicte	2.27±0.61
LOC363020 (predicted)	RGD1309410_predicte	1.71±0.14
LOC500651	MGC112883	3.56±0
lon peptidase 1, mitochondrial	Lonp1	5.7±1.16
lon peptidase 2, peroxisomal	Lonp2	4.8±1.03
Longevity assurance homolog 2 (S. cerevisiae)	Lass2	7.64±2.08
low density lipoprotein receptor-related protein 11 (predicted)	Lrp11_predicted	1.49±0.17
low density lipoprotein receptor-related protein 5 (predicted)	Lrp5_predicted	2.46±0.27
low density lipoprotein receptor-related protein 6 (predicted)	Lrp6_predicted	0.97±0.43
low density lipoprotein receptor-related protein associated protein 1	Lrpap1	2.13±0.41
low density lipoprotein-related protein 12 (predicted)	Lrp12_predicted	0.49±0.17
low-density lipoprotein receptor-related protein 10	Lrp10	9.85±3.48
LPS-induced TN factor	Litaf	13.91±1.51
LPS-responsive beige-like anchor (predicted)	Lrba_predicted	6.43±1.43
LRRGT00141	LOC499235	8.01±0.41
LSM domain containing 1	Lsmd1	10.12±0.63
LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm1_predicted	1.85±1
LSM12 homolog (S. cerevisiae)	Lsm12	4.3±0.78
LSM14 homolog A (SCD6, S. cerevisiae) (predicted)	Lsm14a_predicted	6.79±0.2
LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm3_predicted	3.98±0.34
LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm4_predicted	1.85±0.33
LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm5_predicted	2.53±0.74
LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm6	6.68±0.34
LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm7_predicted	1.1±0.07
LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm8_predicted	1.15±0.15
LTV1 homolog (S. cerevisiae)	Ltv1	1.47±0.27
LUC7-like (S. cerevisiae)	Luc7l	1.11±0.2
LUC7-like 2 (S. cerevisiae) (predicted)	Luc7l2_predicted	4.17±0.61

luteinizing hormone beta	Lhb	0.52±0.2
Ly1 antibody reactive clone	Lyar	0.56±0.12
Ly6/neurotoxin 1 (predicted)	Lynx1_predicted	1.16±0.19
Ly6/Plaur domain containing 3	Lypd3	0.26±0.09
Ly6-C antigen	LOC300024 / Ly6a_pre	1.07±0.53
lymphocyte antigen 6 complex, locus B	Ly6b	6.46±3.57
lymphotoxin B receptor	Ltbr	3.63±0.19
LYR motif containing 1	Lyrm1	0.42±0.29
lysine-rich coiled-coil 1	Krcc1	4.74±1.1
LysM, putative peptidoglycan-binding, domain containing 1	Lysmd1	0.67±0.25
LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	1.46±0.17
lysophosphatidylcholine acyltransferase 1	Lpcat1	0.41±0.19
lysophospholipase 1	Lypla1	4.81±0.59
lysophospholipase 2	Lypla2	1.6±0.18
lysophospholipase 3	Lypla3	0.77±0
lysophospholipase-like 1 (predicted)	Lyplal1_predicted	3.04±0.81
lysosomal acid lipase A	Lipa	2.23±0.35
lysosomal membrane glycoprotein 1	Lamp1	5.09±1.2
lysosomal membrane glycoprotein 2	Lamp2	12.28±0
lysosomal-associated protein transmembrane 4A	Laptm4a	21.14±3.36
lysosomal-associated protein transmembrane 4B	Laptm4b	6.11±1
lysosomal-associated protein transmembrane 5	Laptm5	0.8±0.26
lysyl-tRNA synthetase	Kars	6.01±1.3
MACRO domain containing 1	Macrod1	1.98±0.08
macrophage erythroblast attacher	Maea	7.72±0.22
macrophage migration inhibitory factor	Mif	14.21±2.09
MAD homolog 1 (Drosophila)	Smad1	4.01±0.83
MAD homolog 2 (Drosophila)	Smad2	1.25±0.2
MAD homolog 4 (Drosophila)	Smad4	3.65±0.86
MAD homolog 5 (Drosophila)	Smad5	0.35±0.3
MAD homolog 6 (Drosophila) (predicted)	Smad6_predicted	0.51±0.02
MAD homolog 7 (Drosophila)	Smad7	1.26±0.42
MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (predicted)	Mad2l1_predicted	0.32±0.11
MAD2 mitotic arrest deficient-like 2 (yeast)	Mad2l2	0.47±0.1
MAD2L1 binding protein	Mad2l1bp	0.78±0.31
MAF1 homolog (S. cerevisiae)	Maf1	3.99±0.75
MAGI family member, X-linked	Magix	1.16±0.2
magnesium transporter 1	Magt1	2.53±0.26
magnesium-dependent phosphatase 1	Mdp1	0.92±0.22
mago-nashi homolog, proliferation-associated (Drosophila) (predicted)	Magoh_predicted	4.2±1.34
major facilitator superfamily domain containing 1 (predicted)	Mfsd1_predicted	1.71±0.65
major facilitator superfamily domain containing 3	Mfsd3	0.6±0.12
major facilitator superfamily domain containing 9	Mfsd9	1±0.12
major histocompatibility complex, class II, DM alpha	Hla-dma	1.9±0.59
major histocompatibility complex, class II, DM beta	Hla-dmb	7.54±0.08
major vault protein	Mvp	3.27±1.02
MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	Mak10	2.95±0.1
makorin, ring finger protein, 2	Mkrn2	1.75±0.12
mal, T-cell differentiation protein 2	Mal2	11.26±5.85
malate dehydrogenase 1, NAD (soluble)	Mdh1	44.06±3.97
malate dehydrogenase 2, NAD (mitochondrial)	Mdh2	20.82±3.54
male-enhanced antigen 1	Mea1	11.39±5.2
male-specific lethal 2-like 1 (Drosophila) (predicted)	Msl2l1_predicted	1.94±0.46
male-specific lethal-3 homolog 1 (Drosophila)	Msl31	3.98±0.48
malic enzyme 2, NAD(+)-dependent, mitochondrial (predicted)	Me2_predicted	1.72±0
malic enzyme 3, NADP(+)-dependent, mitochondrial (predicted)	Me3_predicted	3.94±0.71
malignant fibrous histiocytoma amplified sequence 1 (predicted)	Mfhas1_predicted	0.79±0.16
malignant T cell amplified sequence 1	Mcts1	5.11±1.13
malignant T cell amplified sequence 2	Mcts2	1.95±0.6
malonyl-CoA decarboxylase	Mlycd	2.18±0.15
MAM domain containing 2	Mamdc2	0.59±0.02
mammary tumor virus receptor 2	Mtvr2	3.72±0.41
mannose phosphate isomerase (mapped)	Mpi	3.11±1.17
mannose-6-phosphate protein p76	P76	3.72±0.39
mannose-6-phosphate receptor binding protein 1	M6prbp1	10.18±3.02
mannose-6-phosphate receptor, cation dependent	M6pr	6.04±0.37
mannose-P-dolichol utilization defect 1	Mpdu1	2.04±0.51
mannosidase 2, alpha 1	Man2a1	0.45±0.23
Mannosidase 2, alpha 2 (predicted)	Man2a2_predicted	0.45±0.13
mannosidase 2, alpha B1	Man2b1	2.76±0.46
mannosidase, alpha, class 1A, member 2 (predicted)	Man1a2_predicted	0.28±0.15
mannosidase, alpha, class 1B, member 1	Man1b1	2.69±0.44
mannosidase, alpha, class 1C, member 1 (predicted)	Man1c1_predicted	4.04±0.89
mannosidase, alpha, class 2C, member 1	Man2c1	2.52±0.14
mannosidase, beta A, lysosomal	Manba	3.31±0.73
mannosidase, beta A, lysosomal-like	Manbal	2.73±0.43
mannoside acetylglucosaminyltransferase 1	Mgat1	0.49±0.28
mannoside acetylglucosaminyltransferase 2	Mgat2	1.78±1.37
mannoside acetylglucosaminyltransferase 4, isoenzyme B	Mgat4b	1.96±0.03
MANSC domain containing 1	Mansc1	0.82±0.2
MAP kinase-activated protein kinase 2	Mapkapk2	2.16±1.41
MAP kinase-activated protein kinase 5	Mapkapk5	1.02±0.22
MAP kinase-interacting serine/threonine kinase 1	Mknk1	0.52±0.11
MAP kinase-interacting serine/threonine kinase 2	Mknk2	3.96±0.61
MAP/microtubule affinity-regulating kinase 2	Mark2	1.72±0
MAP/microtubule affinity-regulating kinase 3	Mark3	2.79±1.17
MAP3K12 binding inhibitory protein 1 (predicted)	Mbip_predicted	0.29±0.08

MAP-kinase activating death domain	Madd	0.67±0.07
mastermind like 1 (Drosophila) (predicted)	Maml1_predicted	0.67±0.09
maternal embryonic leucine zipper kinase (predicted)	Melk_predicted	0.34±0.28
maternal G10 transcript	G10	3.32±0.16
matrilin 1, cartilage matrix protein	Matn1	2.89±0
matrin 3	Matr3	12.36±0.7
matrix metallopeptidase 14 (membrane-inserted)	Mmp14	4.96±0.87
matrix metallopeptidase 15 (predicted)	Mmp15_predicted	3.59±0.28
max binding protein (predicted)	Mnt_predicted	1.36±0.21
Max dimerization protein 4 (predicted)	Mxd4_predicted	1.88±1.01
Max interacting protein 1	Mxi1	15.96±4.18
Max protein	Max	3.72±0.55
MAX-like protein X	Mlx	2.63±0.53
MBD2-interacting zinc finger (predicted)	Mizf_predicted	0.68±0.21
MCF.2 cell line derived transforming sequence-like	Mcf2l	0.27±0.22
McKusick-Kaufman syndrome protein	Mkks	5.81±0.11
Meckel syndrome, type 1	Mks1	0.27±0.02
mediator complex subunit 1	Med1	1.4±0
mediator complex subunit 13-like	Med13l	2.33±0.29
mediator complex subunit 14	Med14	3.32±1.1
mediator complex subunit 15	Med15	1.28±0.31
mediator complex subunit 16	Med16	2.39±0.25
mediator complex subunit 17	Med17	0.75±0.16
mediator complex subunit 20 /// similar to ubiquitin specific protease 49 (predicted)	LOC501098 /// Med20	1.95±0.46
mediator complex subunit 21	Med21	1.62±0.06
mediator complex subunit 22	Med22	1.21±0.41
mediator complex subunit 23	Med23	2.46±0.53
mediator complex subunit 24	Med24	2.37±0.38
mediator complex subunit 27	Med27	0.85±0.1
mediator complex subunit 29	Med29	2.29±0.34
mediator complex subunit 30 (predicted)	Med30_predicted	1.79±0.69
mediator of cell motility 1	Memo1	2.39±0.58
mediator of DNA damage checkpoint 1	Mdc1	0.95±0.45
mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae)	Med10	1.64±0.36
mediator of RNA polymerase II transcription, subunit 11 homolog (S. cerevisiae)	Med11	1.91±0.32
mediator of RNA polymerase II transcription, subunit 19 homolog (yeast) (predicted)	Med19_predicted	0.59±0.03
mediator of RNA polymerase II transcription, subunit 25 homolog (yeast) (predicted)	Med25_predicted	1.69±0.19
mediator of RNA polymerase II transcription, subunit 28 homolog (yeast) (predicted)	Med28_predicted	2.95±0.18
mediator of RNA polymerase II transcription, subunit 31 homolog (yeast) (predicted)	Med31_predicted	3.17±0.66
mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	Med4	0.77±0.07
mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (predicted)	Med6_predicted	2.66±0.72
mediator of RNA polymerase II transcription, subunit 8 homolog (yeast) (predicted)	Med8_predicted	0.63±0.07
megakaryoblastic leukemia (translocation) 1	Mkl1	0.76±0.21
melanocyte proliferating gene 1	Myg1	1.6±0.12
melanoma antigen, family D, 1	Maged1	4.93±1.36
melanoma antigen, family D, 2	Maged2	2.78±0.11
melanoma antigen, family H, 1	Mageh1	2.33±0.27
melanoma inhibitory activity 1	Mia1	0.21±0.13
melanoma nuclear protein 13 /// similar to CG3420-PA	LOC688169 /// Mel13	1.41±0.47
membralin	Mbrl	1.27±0.82
membrane associated guanylate kinase, WW and PDZ domain containing 1	Magi1	1.46±0
membrane associated guanylate kinase, WW and PDZ domain containing 3	Magi3	2.54±0.76
membrane bound C2 domain containing protein	Mbc2	0.52±0.64
membrane bound O-acyltransferase domain containing 2	Mboat2	1.51±0.26
membrane bound O-acyltransferase domain containing 5	Mboat5	4.66±0.2
membrane metallo endopeptidase	Mme	9.99±0.23
membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	2.29±0.26
membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (predicted)	Mpp6_predicted	1.06±0.33
Membrane-associated DHHC1 zinc finger protein	LOC291967	0.84±0.24
membrane-associated ring finger (C3HC4) 2	March2	5.31±0.91
membrane-associated ring finger (C3HC4) 3	March3	0.56±0
membrane-associated ring finger (C3HC4) 5 (predicted)	March5_predicted	3.26±0.47
Membrane-associated ring finger (C3HC4) 7	March7	1.93±0.21
membrane-associated ring finger (C3HC4) 8 (predicted)	March8_predicted	2.65±0.31
membrane-bound transcription factor peptidase, site 1	Mbtps1	2.95±0.02
menage a trois 1	Mnat1	2.35±0.3
Meningioma expressed antigen 5 (hyaluronidase)	Mgea5	3.25±1.64
mercaptopyruvate sulfurtransferase	Mpst	4.2±0.12
mesoderm development candidate 1	Mesdc1	0.95±0.59
mesoderm development candidate 2	Mesdc2	5.56±1.19
mesoderm induction early response 1 homolog (Xenopus laevis)	Mier1	6.03±0.57
mesoderm induction early response 1, family member 3	Mier3	1.17±0.18
met proto-oncogene	Asz1 /// Cav1 /// Cav2 /	0.97±0.04
metadherin	Mtdh	1.26±0.52
metal response element binding transcription factor 1 (predicted)	Mtf1_predicted	1.38±0.05
metal response element binding transcription factor 2	Mtf2	1.28±0.01
metallophosphoesterase 1 (predicted)	Mppe1_predicted	3.42±0.91
metallothionein 1a	Mt1a	35.89±21.05
metallothionein 2A	Mt2A	31.77±19.14
metastasis associated 1	Mta1	0.67±0.25
metastasis suppressor 1 (predicted)	Mtss1_predicted	10.64±0.59
metastasis-associated gene family, member 2	Mta2	1.26±0.08
metaxin 2	Mtx2	6.83±2.2
meteorin, glial cell differentiation regulator-like	Metrnl	4.08±0.02
methionine adenosyltransferase II, alpha	Mat2a	8.95±3.18
methionine aminopeptidase 2	Metap2	5.69±1.33
methionine aminopeptidase-like 1 (predicted)	Metapl1_predicted	0.55±0.08

methionine sulfoxide reductase A	Msra	0.58±0.43
methionine sulfoxide reductase B2	Msrb2	2.21±0.24
methionine-tRNA synthetase 2 (mitochondrial) (predicted)	Mars2_predicted	0.94±0.24
methionyl aminopeptidase 1 (predicted)	Metap1_predicted	2.2±0.19
methyl-CpG binding domain protein 1	Mbd1	2.01±0.63
methyl-CpG binding domain protein 2	Mbd2	9.87±1.34
methyl-CpG binding domain protein 3 (predicted)	Mbd3_predicted	4.45±0.73
methyl-CpG binding domain protein 6 (predicted)	Mbd6_predicted	0.6±0.3
methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mccc1	6.28±0.38
methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mccc2	13.4±0.97
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like (predicted)	Mthfd2l_predicted	0.62±0.33
methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthas	Mthfd1	7.66±0.19
methylmalonic aciduria (cobalamin deficiency) cblA type	Mmaa	0.9±0.25
methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	Mmachc	2.95±1.13
methylmalonyl CoA epimerase (predicted)	Mcee_predicted	7.22±0.8
methylmalonyl-Coenzyme A mutase	Mut	6.19±2.77
methylphosphate capping enzyme	Mepce	2.5±0.27
Methylthioadenosine phosphorylase (predicted)	Mtap_predicted	0.84±0.27
methyltransferase 10 domain containing	Mett10d	1.14±0.07
methyltransferase like 10	Mettl10	0.52±0.06
methyltransferase like 2 (predicted)	Mettl2_predicted	0.76±0.23
methyltransferase like 5	Mettl5	2.66±0.73
methyltransferase like 6	Mettl6	0.49±0.28
methyltransferase like 7A	Mettl7a	1.97±0.65
methyltransferase-like 3	Mettl3	1.76±0.56
mevalonate kinase	Mvk	0.81±0.06
MICAL-like 2	Micall2	0.57±0.25
microfibrillar-associated protein 3	Mfap3	1.23±0.13
microfibrillar-associated protein 3-like	Mfap3l	0.68±0.09
microphthalmia-associated transcription factor	Mitf	4.17±0.14
microrchidia 2A	Morc2a	0.94±0
microrchidia 3 (predicted)	Morc3_predicted	1.48±0.32
microrchidia 4	Morc4	0.34±0.03
microsomal glutathione S-transferase 1	Mgst1	15.57±3.8
microsomal glutathione S-transferase 2 (predicted)	Mgst2_predicted	0.21±0.01
microsomal glutathione S-transferase 3 (predicted)	Mgst3_predicted	16.14±3.65
microspherule protein 1	Mcrs1	2.77±0.04
Microtubule associated monoxygenase, calponin and LIM domain containing 3	Mical3	0.86±0.2
microtubule associated serine/threonine kinase 2 (predicted)	Mast2_predicted	0.8±0.21
microtubule associated serine/threonine kinase family member 4	Mast4	1.45±0.12
microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	1.92±0.08
microtubule-associated protein 1 light chain 3 beta	Map1lc3b	3.9±0.16
microtubule-associated protein 2	Mtap2	1.28±0.3
microtubule-associated protein 4	Mtap4	0.7±0.28
microtubule-associated protein 7 (predicted)	Mtap7_predicted	1.99±0.6
microtubule-associated protein 7 domain containing 1	Mtap7d1	0.21±0.4
microtubule-associated protein tau	Mapt	1.4±0.09
microtubule-associated protein, RP/EB family, member 1	Mapre1	3.6±0.32
microtubule-associated protein, RP/EB family, member 3	Mapre3	0.58±0.04
MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	Mid1ip1	7.06±1.2
midasin homolog (yeast)	Mdn1	0.59±0.19
midasin homolog (yeast) /// LYR motif containing 2	Lyrm2 /// Mdn1	3.41±0.71
midnolin (predicted)	Midn_predicted	5.33±0.43
MIF4G domain containing	Mif4gd	2.44±0.6
minichromosome maintenance deficient 2 mitotin (S. cerevisiae) (predicted)	Mcm2_predicted	1.97±0.05
minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (predicted)	Mcm3ap_predicted	0.93±0.19
minichromosome maintenance deficient 4 homolog (S. cerevisiae)	Mcm4	1.05±0.16
minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (predicted)	Mcm5_predicted	0.59±0.03
minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	Mcm6	1.26±0.18
minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	2.28±0.52
minichromosome maintenance deficient 8 (S. cerevisiae) (predicted)	Mcm8_predicted	0.24±0.04
misato homolog 1 (Drosophila) (predicted)	Msto1_predicted	0.4±0.12
MIT, microtubule interacting and transport, domain containing 1	Mitd1	0.27±0.13
mitchondrial ribosomal protein S7	Mrps7	3.67±0.08
Mitochondrial acyl-CoA thioesterase 1	Mte1	1.07±0.19
mitochondrial carrier homolog 1 (C. elegans)	Mtch1	12.5±0.91
mitochondrial carrier homolog 2 (C. elegans) (predicted)	Mtch2_predicted	12.69±4.17
mitochondrial carrier triple repeat 1	Mcart1	7.6±1.15
Mitochondrial fission regulator 1 (predicted)	Mtfr1_predicted	4.64±0.8
mitochondrial intermediate peptidase	Mipep	6.53±1.7
mitochondrial methionyl-tRNA formyltransferase	Mtfmt	0.76±0.18
mitochondrial protein 18 kDa	Mtp18	2.4±0.78
mitochondrial ribosomal protein 63	Mrp63	3.86±0.33
mitochondrial ribosomal protein L1 (predicted)	Mrpl1_predicted	2.85±1.08
mitochondrial ribosomal protein L10 (predicted) /// similar to mitochondrial ribosomal protein L10	LOC688165 /// LOC691	2.06±0.18
mitochondrial ribosomal protein L11	mrpl11	6.46±1.09
mitochondrial ribosomal protein L12	Mrpl12	16.17±4.04
mitochondrial ribosomal protein L13	Mrpl13	8.16±1.63
mitochondrial ribosomal protein L14 (predicted)	Mrpl14_predicted	2.81±0.45
mitochondrial ribosomal protein L15 (predicted)	Mrpl15_predicted	15.04±1
mitochondrial ribosomal protein L16	Mrpl16	7.94±1.77
mitochondrial ribosomal protein L17	Mrpl17	12.3±0.12
mitochondrial ribosomal protein L18 (predicted)	Mrpl18_predicted	7.73±1.2
mitochondrial ribosomal protein L19	Mrpl19	2.79±1.03
mitochondrial ribosomal protein L2	Mrpl2	4±0.9
mitochondrial ribosomal protein L20	Mrpl20	4.51±1.1
mitochondrial ribosomal protein L21 (predicted)	Mrpl21_predicted	2.31±0.18

mitochondrial ribosomal protein L22 (predicted)	Mrpl22_predicted	7.86±0.94
mitochondrial ribosomal protein L23	Mrpl23	4.4±0.35
mitochondrial ribosomal protein L24	mrpl24	6.39±0.37
mitochondrial ribosomal protein L27 (predicted)	Mrpl27_predicted	8.41±1.66
mitochondrial ribosomal protein L28	Mrpl28	4.61±1.13
mitochondrial ribosomal protein L3 (predicted)	Mrpl3_predicted	8.12±2.46
mitochondrial ribosomal protein L30 (predicted)	Mrpl30_predicted	3.66±0.29
mitochondrial ribosomal protein L32 (predicted)	Mrpl32_predicted	6.79±1.19
mitochondrial ribosomal protein L34	Mrpl34	3.68±0.2
mitochondrial ribosomal protein L35 (predicted)	Mrpl35_predicted	4.21±0.02
mitochondrial ribosomal protein L36 (predicted)	Mrpl36_predicted	8.59±1.89
mitochondrial ribosomal protein L37	Mrpl37	6.08±1
mitochondrial ribosomal protein L38	Mrpl38	1.93±0.72
mitochondrial ribosomal protein L4 (predicted)	Mrpl4_predicted	3.62±0.83
mitochondrial ribosomal protein L40	Mrpl40	3.87±0.7
mitochondrial ribosomal protein L41	Mrpl41	15.27±2.79
mitochondrial ribosomal protein L42 (predicted)	Mrpl42_predicted	9.76±3.28
mitochondrial ribosomal protein L43 (predicted)	Mrpl43_predicted	5.88±1.45
mitochondrial ribosomal protein L44	Mrpl44	3.24±0.69
mitochondrial ribosomal protein L45 (predicted)	Mrpl45_predicted	4.58±0.74
mitochondrial ribosomal protein L46	Mrpl46	2.22±0.6
mitochondrial ribosomal protein L47	Mrpl47	1.96±0.6
mitochondrial ribosomal protein L48 (predicted)	Mrpl48_predicted	5±1.34
Mitochondrial ribosomal protein L49	Mrpl49	2.38±1.11
mitochondrial ribosomal protein L50 (predicted)	Mrpl50_predicted	5.53±1.37
mitochondrial ribosomal protein L51 (predicted)	Mrpl51_predicted	5.64±1.09
mitochondrial ribosomal protein L52 (predicted)	Mrpl52_predicted	3.31±0.01
mitochondrial ribosomal protein L53 (predicted)	Mrpl53_predicted	8.99±0.47
mitochondrial ribosomal protein L54 (predicted)	Mrpl54_predicted	11.29±1.18
mitochondrial ribosomal protein L55 (predicted)	Mrpl55_predicted	5.18±1.09
mitochondrial ribosomal protein L9	mrpl9	4.14±0.1
mitochondrial ribosomal protein S11	Mrps11	3.88±0.23
mitochondrial ribosomal protein S12 (predicted)	Mrps12_predicted	4.74±0.73
mitochondrial ribosomal protein S14 (predicted)	Mrps14_predicted	5.61±0.6
mitochondrial ribosomal protein S15	Mrps15	5.51±1.77
mitochondrial ribosomal protein S16	Mrps16	10.87±2.65
mitochondrial ribosomal protein S17 (predicted)	Mrps17_predicted	9.82±1.16
mitochondrial ribosomal protein S18A	Mrps18a	6.66±0.94
mitochondrial ribosomal protein S18C (predicted)	Mrps18c_predicted	1.79±1.65
mitochondrial ribosomal protein S2 (predicted)	Mrps2_predicted	2.14±0.32
mitochondrial ribosomal protein S21	Mrps21	6.56±0.03
mitochondrial ribosomal protein S23 (predicted)	Mrps23_predicted	12.66±2.67
mitochondrial ribosomal protein S24 (predicted)	Mrps24_predicted	7.33±1.2
mitochondrial ribosomal protein S25	Mrps25	5.79±1.24
mitochondrial ribosomal protein S26 (predicted)	Mrps26_predicted	6.44±0.7
mitochondrial ribosomal protein S27 (predicted)	Mrps27_predicted	1.36±0.15
mitochondrial ribosomal protein S30 (predicted)	Mrps30_predicted	6.27±1.5
mitochondrial ribosomal protein S31 (predicted)	Mrps31_predicted	2.49±0.86
mitochondrial ribosomal protein S33 (predicted)	Mrps33_predicted	7.29±1.28
mitochondrial ribosomal protein S34 (predicted)	Mrps34_predicted	3.15±0.8
mitochondrial ribosomal protein S35 (predicted)	Mrps35_predicted	4.03±0.63
mitochondrial ribosomal protein S36 (predicted)	Mrps36_predicted	15.17±2.45
mitochondrial ribosomal protein S5 (predicted)	Mrps5_predicted	2.85±0.79
mitochondrial ribosomal protein S9	Mrps9	2.44±0.2
mitochondrial ribosome recycling factor	Mrrf	1.08±0.25
mitochondrial trans-2-enoyl-CoA reductase	Mecr	1.97±0.47
mitochondrial transcription termination factor	Mterf	2.97±0.85
mitochondrial translation optimization 1 homolog (S. cerevisiae) (predicted)	Mto1_predicted	1.5±0.29
mitochondrial translational initiation factor 2	Mtif2	2.34±2.46
mitochondrial translational release factor 1-like	Mtrf1l	0.87±0.05
mitochondrial ubiquitin ligase activator of NFKB 1	Mul1	0.93±0.14
mitofusin 1	Mfn1	3.77±0.21
mitofusin 2	Mfn2	10.67±1.8
Mitogen activated protein kinase 1	Mapk1	1.49±0.53
mitogen activated protein kinase 13	Mapk13	1.52±0
mitogen activated protein kinase 14	Mapk14	4.6±0.61
mitogen activated protein kinase 3	Mapk3	1.45±0.43
mitogen activated protein kinase kinase 1	Map2k1	2.31±0.52
mitogen activated protein kinase kinase 2	Map2k2	3.9±0.13
mitogen activated protein kinase kinase 3	Map2k3	3.81±0.75
mitogen activated protein kinase kinase 4	Map2k4	0.74±0.04
mitogen activated protein kinase kinase 5	Map2k5	1.02±0.18
mitogen activated protein kinase kinase 7	Map2k7	0.94±0.05
mitogen activated protein kinase kinase kinase 1	Map3k1	5.27±0.12
mitogen activated protein kinase kinase kinase 12	Map3k12	2.23±0.07
mitogen activated protein kinase kinase kinase 3 (predicted)	Map3k3_predicted	0.62±0.16
mitogen activated protein kinase kinase kinase 4 (predicted)	Map3k4_predicted	0.99±0.24
Mitogen activated protein kinase kinase kinase 7 (predicted)	Map3k7_predicted	2.88±0.74
mitogen activated protein kinase kinase kinase kinase 2 (predicted)	Map4k2_predicted	0.5±0.12
mitogen-activated protein binding protein interacting protein	Mapbpip	11.72±2.12
mitogen-activated protein kinase 1 interacting protein 1	Mapk1ip1	1.53±0.17
mitogen-activated protein kinase 6	Mapk6	0.27±0.61
mitogen-activated protein kinase 8	Mapk8	0.66±0.15
mitogen-activated protein kinase 8 interacting protein 1	Mapk8ip1	6.26±0.79
mitogen-activated protein kinase 8 interacting protein 3	Mapk8ip3	0.52±0.05
mitogen-activated protein kinase 9	Mapk9	0.43±0.06
mitogen-activated protein kinase associated protein 1	Mapkap1	1.6±0.08

mitogen-activated protein kinase kinase 1 interacting protein 1	Map2k1ip1	3.22±0.31
mitogen-activated protein kinase kinase 6	Map2k6	1.22±0.27
mitogen-activated protein kinase kinase kinase 11	Map3k11	0.57±0.25
mitogen-activated protein kinase kinase kinase 14 (predicted)	Map3k14_predicted	0.92±0.2
mitogen-activated protein kinase kinase kinase 7 interacting protein 1 (predicted)	Map3k7ip1_predicted	1.94±0.22
mitogen-activated protein kinase kinase kinase 7 interacting protein 2	Map3k7ip2	3.08±0.2
mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	4.96±0.55
mitogen-activated protein kinase kinase kinase kinase 4 (predicted)	Map4k4_predicted	0.33±0.17
mitogen-activated protein kinase kinase kinase kinase 5	Map4k5	0.55±0.08
Mki67 (FHA domain) interacting nucleolar phosphoprotein	Mki67ip	2.12±0.66
MMR_HSR1 domain containing protein RGD1359460	RGD1359460	0.35±0.28
MOB1, Mps One Binder kinase activator-like 1A (yeast) (predicted)	Mobkl1a_predicted	0.73±0.1
MOB1, Mps One Binder kinase activator-like 1B (yeast)	Mobkl1b	2.99±0.37
MOB1, Mps One Binder kinase activator-like 2A (yeast)	Mobkl2a	0.94±0.22
MOB1, Mps One Binder kinase activator-like 3 (yeast)	Mobkl3	1.61±0.68
MOCO sulphurase C-terminal domain containing 2	Mosc2	10.04±2.65
molybdenum cofactor synthesis 1 (predicted)	Mocs1_predicted	0.7±0.06
molybdenum cofactor synthesis 2	Mocs2	3.04±0.61
MON1 homolog A (yeast) (predicted)	Mon1a_predicted	0.98±0.25
monoamine oxidase A	Maoa	1.05±0.04
monocyte to macrophage differentiation-associated	Mmd	5.91±0.44
Monoglyceride lipase	Mgll	5.04±2.18
Morf4 family associated protein 1	Mrfap1	13.3±2.56
MORN repeat containing 1	Morn1	0.34±0.04
mortality factor 4 like 1	Morf4l1	12.41±0.31
mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b	LOC309220 /// Morf4l1	13.53±0.99
mortality factor 4 like 2	Morf4l2	14.74±1.22
motile sperm domain containing 1 /// similar to motile sperm domain containing 1	LOC686087 /// Mospd1	2±0.18
motile sperm domain containing 3	Mospd3	1.81±0.14
M-phase phosphoprotein 1 (predicted)	Mphosph1_predicted	0.51±0.19
M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted)	Mphosph10_predicted	0.55±0.21
M-phase phosphoprotein 8	Mphosph8	3.22±0.4
M-phase phosphoprotein 8 /// poly (ADP-ribose) polymerase family, member 4	Mphosph8 /// Parp4	0.61±0.34
Mpv17 transgene, kidney disease mutant-like (predicted)	Mpv17l_predicted	4.35±0.39
MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	Mrs2	0.98±0.59
MRT4, mRNA turnover 4, homolog (S. cerevisiae)	Mrto4	0.88±0.07
MTERF domain containing 1	Mterfd1	4.49±0.3
MTERF domain containing 2	Mterfd2	2.63±0.37
MTERF domain containing 3	Mterfd3	1.51±0
mucin 1, transmembrane	Muc1	10.06±2.14
mucin and cadherin like	Mucdhl	4.57±0.09
mucolipin 1 (predicted)	Mcoln1_predicted	2.12±0.09
multiple coagulation factor deficiency 2	Mcfd2	4.15±0.67
multiple EGF-like-domains 8	Megf8	0.45±0.26
multiple endocrine neoplasia 1	Men1	1.74±0.29
multiple inositol polyphosphate histidine phosphatase 1	Minpp1	7.86±0.16
multiple PDZ domain protein	Mpdz	0.89±0.01
Musashi homolog 2 (Drosophila)	Msi2	19.42±3.12
muscle and microspikes RAS	Mras	0.71±0.37
muscle glycogen phosphorylase	Pygm	0.2±0.08
muskelin 1, intracellular mediator containing kelch motifs	Mkln1	2.62±0.16
muted	Muted	2.33±0.4
mutL homolog 1 (E. coli)	Mlh1	1.16±0.19
mutS homolog 2 (E. coli)	Msh2	1.56±0.13
MYB binding protein (P160) 1a	Mybbp1a	1.54±0.61
Myb protein P42POP	P42pop	0.38±0.23
myb-like, SWIRM and MPN domains 1 (predicted)	Mysm1_predicted	0.56±0.06
MYC binding protein 2	Mycbp2	3.4±1.3
myc induced nuclear antigen	Mina	0.31±0.09
myelin and lymphocyte protein, T-cell differentiation protein	Mal	26.12±2.05
myelin basic protein expression factor 2, repressor	Myef2	4.79±1.09
myelin protein zero-like 1	Mpzl1	1.93±1.29
myelin-associated glycoprotein	Mag	0.22±0.12
myeloid cell leukemia sequence 1	Mcl1	5.63±0.56
myeloid differentiation primary response gene 116	Myd116	2.17±4.26
myeloid differentiation primary response gene 88	Myd88	3.2±0.92
myeloid leukemia factor 2 (predicted)	Mlf2_predicted	5.71±0.35
myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosophila)	Mllt10	1.26±0.61
myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosophila)	Mllt3	2.22±0.21
myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog (Drosophila) (predicted)	Mllt6_predicted	4.24±1.19
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	Mllt1	0.92±0.3
myeloid/lymphoid or mixed-lineage leukemia 1	Mll1	1.98±0.57
myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	5.88±0.84
myeloid-associated differentiation marker	Myadm	2.19±0.51
myeloma overexpressed 2	Myeov2	12.86±0.9
Myocyte enhancer factor 2D	Mef2d	0.32±0.09
MyoD family inhibitor domain containing (predicted)	Mdfic_predicted	0.25±0.2
myo-inositol 1-phosphate synthase A1	Isyna1	5.54±0.74
myosin 5B	Myo5b	2.28±0.28
myosin binding protein C, fast-type (predicted)	Mybpc2_predicted	0.22±0.02
myosin IC	Myo1c	2.23±0.04
myosin IC /// similar to unconventional myosin Myr2 I heavy chain	LOC686250 /// Myo1c	8.92±0.43
myosin ID	Myo1d	3.82±0.74
myosin IE	Myo1e	1.76±0.45
myosin IG	Myo1g	0.68±0.04
myosin IXb	Myo9b	0.58±0.09
myosin light chain kinase 2, skeletal muscle	Mylk2	0.7±0.78

myosin light chain, regulatory B	Mrlcb	9.7±3.05
myosin phosphatase-Rho interacting protein	M-rip	7.42±1.09
myosin regulatory light chain interacting protein (predicted)	Mylip_predicted	0.87±0.68
myosin VC (predicted)	Myo5c_predicted	0.5±0.15
myosin VI	Myo6	3.47±0.78
myosin X (predicted)	Myo10_predicted	1.62±0.28
Myosin, heavy polypeptide 9, non-muscle	Myh9	6.75±1.13
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (predicted)	LOC684520 /// Myl6 ///	24.21±1.24
myosin, light polypeptide kinase (predicted)	Mylk_predicted	8.62±0.49
myotrophin	Mtpn	8.76±0.98
myotubularin related protein 1 (predicted)	Mtmr1_predicted	0.22±0.04
myotubularin related protein 10	Mtmr10	2.61±0.97
myotubularin related protein 14	Mtmr14	1.2±0.19
myotubularin related protein 2 (predicted)	Mtmr2_predicted	4.71±0.48
myotubularin related protein 3	Mtmr3	3.41±0.7
myotubularin related protein 4 (predicted)	Mtmr4_predicted	2.2±1.11
myotubularin related protein 6 (predicted)	Mtmr6_predicted	2±0.81
myotubularin related protein 7 (predicted)	Mtmr7_predicted	4.7±0.71
myotubularin related protein 9	Mtmr9	1.19±0.13
MYST histone acetyltransferase 2	Myst2	1.42±0.36
myxovirus (influenza virus) resistance 2	Mx2	0.39±0.21
N-6 adenine-specific DNA methyltransferase 1 (putative)	N6amt1	1.59±0.46
N-6 adenine-specific DNA methyltransferase 2 (putative)	N6amt2	1.76±0.43
N-acetyl galactosaminidase, alpha	Naga	1.3±0.1
N-acetylglucosamine kinase	Nagk	0.62±0.16
N-acetylglucosamine-1-phosphotransferase, gamma subunit	Gnptg	1.85±0.37
N-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	Nans_predicted	6.05±1.64
N-acetyltransferase 1 (arylamine N-acetyltransferase)	Nat1	0.7±0.43
N-acetyltransferase 11	Nat11	1.67±0.4
N-acetyltransferase 13	Nat13	1.5±0.03
N-acetyltransferase 14	Nat14	0.94±0.16
N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (predicted)	Nat5_predicted	5.81±0.69
N-acetyltransferase ARD1 homolog (S. cerevisiae) (predicted)	Ard1_predicted	0.55±0.08
N-acylsphingosine amidohydrolase 1	Asah1	3.53±1.01
NAD kinase	Nadk	3.47±0.59
NAD(P) dependent steroid dehydrogenase-like	Nsdhl	1.68±0.42
NAD(P) dependent steroid dehydrogenase-like	Hspc105	0.27±0.06
NAD(P)H dehydrogenase, quinone 1	Nqo1	2.17±0.88
NAD(P)H dehydrogenase, quinone 2	Nqo2	2.46±0.23
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10-like 1 /// NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10 /// Ndufa10l1	12.11±3.24
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	Ndufa11	18.3±5.39
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	Ndufa5	7.12±0.48
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (predicted)	Ndufa1_predicted	48.68±1.98
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)	Ndufa12_predicted	29.47±7.77
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 (predicted)	Ndufa13_predicted	21.13±3.57
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (predicted)	Ndufa2_predicted	22.23±2.93
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	Ndufa4	39.78±4.06
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) (predicted)	Ndufa6_predicted	18.7±1.28
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)	Ndufa7_predicted	15.7±2.62
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	15.98±2.27
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	23.2±1.47
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (predicted)	Ndufaf1_predicted	0.55±0.04
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 (predicted)	Ndufb3_predicted	31.6±4.03
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	Ndufb4	43.34±3.32
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11 (predicted)	Ndufb11_predicted	31.97±0.24
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (predicted)	Ndufb2_predicted	18.65±2.49
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (predicted)	Ndufb5_predicted	39.9±9.7
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (predicted)	Ndufb6_predicted	24.14±5.96
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (predicted)	Ndufb7_predicted	20.76±3.95
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (predicted)	Ndufb9_predicted	58.85±2.57
NADH dehydrogenase (ubiquinone) 1, alpha	LOC683884 /// Ndufab1	25.94±4.5
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	Ndufc1	20.45±5.64
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	Ndufc2	28.05±5.36
NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	24.8±5.35
NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	27.01±3.83
NADH dehydrogenase (ubiquinone) Fe-S protein 3 (predicted)	Ndufs3_predicted	24.64±3.84
NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	4.15±0.8
NADH dehydrogenase (ubiquinone) Fe-S protein 5	Ndufs5	30.21±3.33
NADH dehydrogenase (ubiquinone) Fe-S protein 6	LOC679739 /// LOC692	32.69±2.19
NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	15.11±0.57
NADH dehydrogenase (ubiquinone) Fe-S protein 8 (predicted)	Ndufs8_predicted	20.32±3.76
NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	24.46±4.38
NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	37.86±0.37
NADH dehydrogenase (ubiquinone) flavoprotein 3-like	LOC682566 /// Ndufv3l	12.75±1.76
NADH dehydrogenase subunit 1	ND1	80.95±11.21
NADH dehydrogenase subunit 2	ND2	98.79±11.92
NADH dehydrogenase subunit 3	ND3	62.8±6.7
nardilysin, N-arginine dibasic convertase, NRD convertase 1	Nrd1	2.83±0.1
nasal embryonic LHRH factor	Nelf	0.37±0.16
nascent-polypeptide-associated complex alpha polypeptide (predicted)	Naca_predicted	19.18±0.38
NAT9	Nat9	0.84±0.31
NCK interacting protein with SH3 domain (predicted)	Nckipsd_predicted	0.5±0.15
NCK-associated protein 1	Nckap1	16.04±4.07
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	Ndst1	2.08±0.24
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (predicted)	Ndst2_predicted	1.08±0.47
NECAP endocytosis associated 1	Necap1	1.34±0.09
NECAP endocytosis associated 2	Necap2	3.72±0.5

necdin-like 2	Ndnl2	0.65±0.26
Nedd4 binding protein 1	N4bp1	0.31±0.08
NEDD4 binding protein 2-like 2	N4bp2l2	3.42±0.37
Nedd4 family interacting protein 1	Ndfip1	13.2±0.3
Nedd4 family interacting protein 2 (predicted)	Ndfip2_predicted	6.25±4.82
NEDD8 ultimate buster-1	Nub1	2.6±0.6
NEFA-interacting nuclear protein NIP30	Nip30	2.51±0.26
nei endonuclease VIII-like 1 (E. coli)	Neil1	0.99±0.19
neighbor of Brca1 gene 1	Nbr1	4.16±0.97
neighbor of Brca1 gene 1 /// similar to neighbor of Brca1 gene 1	LOC498369 /// Nbr1	0.65±0.2
nemo like kinase	Nlk	0.97±0.01
neogenin	Neo1	0.93±0.74
nephronophthisis 1 (juvenile) homolog (human) (predicted)	Nphp1_predicted	3.31±0.41
nerve growth factor receptor (TNFRSF16) associated protein 1	Ngfrap1	15.5±2.46
N-ethylmaleimide sensitive fusion protein	Nsf	0.48±0.08
N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	4.06±0.37
N-ethylmaleimide sensitive fusion protein attachment protein gamma	Napg	3.8±1.37
neural precursor cell expressed, developmentally down-regulated gene 1 (predicted)	Nedd1_predicted	0.28±0.21
neural precursor cell expressed, developmentally down-regulated gene 4	Nedd4	9.71±0.66
neural precursor cell expressed, developmentally down-regulated gene 4-like	Nedd4l	2.25±0.35
neural precursor cell expressed, developmentally down-regulated gene 8	Nedd8	14.13±2.54
neural precursor cell expressed, developmentally down-regulated gene 9	Nedd9	2.61±0.82
neural proliferation, differentiation and control, 1	Npdc1	4.13±0.4
neuraminidase 1	Neu1	0.58±0.03
neuraminidase 3	Neu3	0.26±0.14
neuregulin 1	Nrg1	0.44±0.2
neurobeachin-like 2 (predicted)	Nbeal2_predicted	0.22±0.09
neuroblastoma ras oncogene	Nras	0.83±0.42
neuroblastoma, suppression of tumorigenicity 1	Nbl1	0.82±0.22
neurocalcin delta	Ncald	0.92±0.09
neurochondrin	Ncdn	0.38±0.16
neuroepithelial cell transforming gene 1	Net1	1.59±0.41
neurofibromatosis 2	Nf2	3.92±0.04
neuroguidin, EIF4E binding protein	Ngdn	1.39±0.05
neurolysin (metallopeptidase M3 family)	Nln	0.38±0.03
neuromedin B (predicted)	Nmb_predicted	0.65±0.1
neuronal PAS domain protein 2 (predicted)	Npas2_predicted	0.38±0.15
neuronal pentraxin 1	Nptx1	0.33±0.18
Neuronal regeneration related protein	Nrep	11.97±3.53
neuropilin (NRP) and tolloid (TLL)-like 2 (predicted)	Neto2_predicted	7.65±0.86
Neuropilin 1	Nrp1	6.07±1.73
neuroplastin	Nptn	20.34±0.65
neurotrophin receptor associated death domain	Nradd	0.42±0.22
neurturin	Nrtn	2.59±0.39
neutral sphingomyelinase (N-SMase) activation associated factor	Nsmaf	1.26±0.04
NFKB inhibitor interacting Ras-like protein 1 (predicted)	Nkiras1_predicted	0.49±0.05
NFKB inhibitor interacting Ras-like protein 2 (predicted)	Nkiras2_predicted	1.23±0.03
NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	Nfu1	2.07±0.54
Ngfi-A binding protein 1	Nab1	3.3±0.46
Ngfi-A binding protein 2	Nab2	1.2±0.11
Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	1.56±0.18
N-glycanase 1	Ngly1	4.44±2.06
NHL repeat containing 3	Nhlrc3	1.56±0.09
nibrin	Nbn	2.09±0.06
nicalin homolog (zebrafish)	Ncln	1.8±0.91
nicastrin	Ncstn	2.05±0.39
nicolin 1	Nicn1	1.97±0.48
nicotinamide nucleotide adenylyltransferase 1	Nmnat1	1.1±0.23
nicotinamide nucleotide adenylyltransferase 3	Nmnat3	0.99±0.24
nicotinamide nucleotide transhydrogenase	Nnt	38.42±0.29
nicotinate phosphoribosyltransferase domain containing 1	Naprt1	2.45±0.05
Nidogen 1	Nid1	15.88±0.8
Niemann Pick type C2	Npc2	8.61±1.66
NIK and IKK{beta} binding protein	Nibp	0.67±0.01
NIMA (never in mitosis gene a)- related kinase 9 (predicted)	Nek9_predicted	5.63±0.6
NIMA (never in mitosis gene a)-related expressed kinase 1 (predicted)	Nek1_predicted	0.62±0.17
NIMA (never in mitosis gene a)-related expressed kinase 3 (predicted)	Nek3_predicted	1.79±0.62
NIMA (never in mitosis gene a)-related expressed kinase 4	Nek4	0.27±0.09
NIMA (never in mitosis gene a)-related expressed kinase 7	Nek7	10.08±0.84
NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	Nob1	1.29±0.09
ninein (predicted)	Nin_predicted	0.32±0.1
ninein-like	Nlp	4.43±0.14
ninjurin 1	Ninj1	15.37±5.33
NIPA-like domain containing 2	Npal2	5.39±0.59
Nipped-B homolog (Drosophila)	NIPBL	1.77±0.63
nischarin	Nisch	4.67±0.61
nitric oxide synthase 1 (neuronal) adaptor protein	Nos1ap	0.64±0.44
nitric oxide synthase interacting protein (predicted)	Nosip_predicted	1.66±0.02
nitrilase 1	Nit1	4.78±0.83
nitrilase family, member 2	Nit2	9.22±0.43
nitrogen fixation gene 1 (S. cerevisiae)	Nfs1	4.44±0.64
NLR family member X1	Nlrx1	1.12±0.37
NMD3 homolog (S. cerevisiae) (predicted)	Nmd3_predicted	2.34±0.59
NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted	3.35±0.97
N-methylpurine-DNA glycosylase	Mpg	0.73±0.1
NmrA-like family domain containing 1	Nmral1	0.57±0.02
N-myc (and STAT) interactor	Nmi	0.5±0.31

N-myc downstream regulated gene 2	Ndrg2	14.62±1.19
N-myc downstream regulated gene 3	Ndrg3	5.59±1.31
N-myc downstream regulated gene 4	Ndrg4	17.25±1.51
N-myristoyltransferase 1	Nmt1	2.04±0.2
nodal modulator 1	Nomo1	1.73±0.14
NOL1/NOP2/Sun domain family, member 2	Nsun2	1.47±0.05
NOL1/NOP2/Sun domain family, member 4 (predicted)	Nsun4_predicted	1.48±0.15
NOL1/NOP2/Sun domain family, member 5 (predicted)	Nsun5_predicted	1.22±0
non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) (predicted)	Nipa2_predicted	2.66±0.69
non-catalytic region of tyrosine kinase adaptor protein 1 (predicted)	Nck1_predicted	2.77±0.67
non-catalytic region of tyrosine kinase adaptor protein 2 (predicted)	Nck2_predicted	1.72±0.18
non-metastatic cells 3, protein expressed in	Nme3	1.69±0.37
non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	Nme6	0.63±0.02
non-POU-domain-containing, octamer-binding protein	Nono	8.75±0.62
non-SMC condensin I complex, subunit D2	Ncapd2	0.64±0.16
non-SMC condensin I complex, subunit H	Ncaph	0.9±0.05
non-SMC condensin II complex, subunit D3	Ncapd3	0.76±0
non-SMC condensin II complex, subunit H2	Ncaph2	1.16±0.15
non-SMC element 1 homolog (S. cerevisiae)	Nsmce1	2.45±0.08
non-SMC element 2, MMS21 homolog (S. cerevisiae)	Nsmce2	1.53±0.39
non-SMC element 4 homolog A (S. cerevisiae)	Nsmce4a	4.26±0.5
Notch gene homolog 1 (Drosophila)	Notch1	0.48±0.2
Notch gene homolog 2 (Drosophila)	Notch2	4.19±0.54
Notch gene homolog 3 (Drosophila)	Notch3	0.31±0.22
notch1-induced protein	LOC493574	1.15±0.56
notchless homolog 1 (Drosophila) (predicted)	Nle1_predicted	0.41±0.11
NS5A (hepatitis C virus) transactivated protein 9	Ns5atp9	0.98±0.07
NSFL1 (p97) cofactor (p47)	Nsfl1c	2.89±0.02
N-terminal asparagine amidase	Ntan1	5.01±0.06
NTF2-related export protein 1 (predicted)	Nxt1_predicted	1.84±0.09
nth (endonuclease III)-like 1 (E.coli) (predicted)	Nthl1_predicted	0.63±0
NUAK family, SNF1-like kinase, 2	Nuak2	10.13±4.62
nuclear autoantigenic sperm protein (histone-binding)	Nasp	0.9±0.37
nuclear cap binding protein subunit 1, 80kDa	Ncbp1	1.57±0.14
nuclear casein kinase and cyclin-dependent kinase substrate 1	Nucks1	1.97±0.22
nuclear distribution gene C homolog (Aspergillus)	Nudc	3.19±0.3
nuclear distribution gene E homolog 1 (A nidulans)	Nde1	1.52±0.23
nuclear distribution gene E-like homolog 1 (A. nidulans)	Ndel1	0.37±0.3
nuclear factor I/A	Nfia	1.85±0.59
nuclear factor I/B	Nfib	3.82±0.44
Nuclear factor I/C	Nfic	2.11±0.03
nuclear factor I/X	Nfix	1.9±0.24
nuclear factor of activated T-cells 5 (predicted)	Nfat5_predicted	5.06±4.97
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (predicted)	Nfatc3_predicted	1.67±0.42
nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Nfkbib	0.93±0.12
nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	Nfkb1	2.28±0.72
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	Nfkbil1	0.67±0.11
nuclear factor related to kappa B binding protein (predicted)	Nfrkb_predicted	1.16±0.27
nuclear factor, erythroid derived 2, like 2	Nfe2l2	4.17±0.67
nuclear factor, erythroid derived 2,-like 1 (predicted)	Nfe2l1 predicted	4.72±1.07
nuclear factor, interleukin 3 regulated	Nfil3	2.13±0.39
nuclear fragile X mental retardation protein interacting protein 1	Nufip1	2.52±0.57
nuclear import 7 homolog (S. cerevisiae)	Nip7	0.74±0.32
nuclear mitotic apparatus protein 1	Numa1	2.32±0.57
nuclear pore associated protein	Npap60	0.29±0.01
nuclear pore membrane protein 121	Pom121	0.96±0.15
nuclear prelamin A recognition factor	Narf	2.16±0.78
nuclear prelamin A recognition factor-like	Narfl	1.86±0.51
nuclear protein 1	Nupr1	10.5±2.29
nuclear protein E3-3	RGD708545	3.35±0.65
nuclear protein in the AT region (predicted)	Npat_predicted	0.49±0.21
nuclear protein localization 4 homolog (S. cerevisiae)	Nploc4	1.11±0.16
nuclear receptor binding factor 2	Nrbf2	1.32±0.03
nuclear receptor binding protein	Nrbp	0.76±0.32
Nuclear receptor binding SET domain protein 1 (predicted)	Nsd1_predicted	2.61±0.19
nuclear receptor coactivator 1 (predicted)	Ncoa1_predicted	4.53±1.08
nuclear receptor coactivator 3	Ncoa3	0.47±0.08
nuclear receptor coactivator 4 (predicted)	Ncoa4_predicted	11.21±1.51
nuclear receptor coactivator 5 (predicted)	Ncoa5_predicted	0.85±0.18
nuclear receptor coactivator 6	Ncoa6	1.53±0.3
nuclear receptor coactivator 7	Ncoa7	4.35±0.12
nuclear receptor co-repressor 1	Ncor1	5.88±0.43
nuclear receptor co-repressor 2 (predicted)	Ncor2_predicted	3.12±0.85
nuclear receptor subfamily 0, group B, member 2	Nr0b2	4.21±1.02
nuclear receptor subfamily 1, group D, member 1	Nr1d1	0.42±0.96
nuclear receptor subfamily 1, group D, member 2	Nr1d2	1.29±1.08
nuclear receptor subfamily 1, group H, member 2	Nr1h2	2±0.43
nuclear receptor subfamily 1, group H, member 3	Nr1h3	0.4±0.15
nuclear receptor subfamily 1, group H, member 4	Nr1h4	2.07±0.37
nuclear receptor subfamily 2, group F, member 2	Nr2f2	4.97±0.06
nuclear receptor subfamily 2, group F, member 6	Nr2f6	4.52±0.06
nuclear receptor subfamily 2, group F, member 6 /// similar to Orphan nuclear receptor EAR-2 (V-erbA-related protein EAR-2)	LOC688367 /// Nr2f6	1.03±0.49
nuclear receptor subfamily 3, group C, member 1	Nr3c1	2.44±0.76
nuclear receptor subfamily 3, group C, member 2	Nr3c2	2.26±0.66
nuclear receptor subfamily 4, group A, member 2	Nr4a2	0.29±0.2
nuclear RNA export factor 1	Nxf1	4.66±0.85
nuclear transcription factor, X-box binding 1	Nfx1	0.62±0.35

nuclear transcription factor-Y beta	Nfyb	1.26±0.27
nuclear transcription factor-Y gamma	Nfyc	9.37±1.11
nuclear transport factor 2	Nutf2	4.29±1.48
nuclear transport factor 2-like export factor 2 (predicted)	Nxt2_predicted	0.65±0.01
nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	Nus1	1.22±0.29
nuclear VCP-like (predicted)	Nvl_predicted	0.53±0.32
nucleobindin 1	Nucb1	7.39±0.12
nucleolar and coiled-body phosphoprotein 1	Nolc1	0.7±0.06
nucleolar and spindle associated protein 1 (predicted)	Nusap1_predicted	1.18±0.02
nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	0.94±0.17
nucleolar protein 1 (predicted)	Nol1_predicted	0.9±0.11
nucleolar protein 10	Nol10	0.79±0.02
nucleolar protein 14	Nol14	0.77±0.4
nucleolar protein 5	Nol5	1.83±0.07
nucleolar protein 5A	Nol5a	0.89±0.26
nucleolar protein 7	Nol7	3.15±1.04
nucleolar protein 8 (predicted)	Nol8_predicted	0.29±0.11
nucleolar protein 9	Nol9	0.77±0.29
nucleolar protein family 6 (RNA-associated) (predicted)	Nol6_predicted	0.98±0.11
nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	Nola1	1.07±0.27
nucleolar protein family A, member 2 (predicted)	Nola2_predicted	2.03±0.35
nucleolar protein family A, member 3	Nola3	14.12±3.15
nucleolin	Ncl	9.16±0.15
nucleophosmin 1	Npm1	8.52±0.52
nucleophosmin 1 /// similar to Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)	LOC300303 /// Npm1	0.64±0.21
nucleoporin 133 (predicted)	Nup133_predicted	0.29±0.13
nucleoporin 153	Nup153	2.87±0.74
nucleoporin 155	Nup155	1±0.14
nucleoporin 160 (predicted)	Nup160_predicted	0.91±0.01
nucleoporin 188	Nup188	0.41±0.17
nucleoporin 205	Nup205	0.94±0.4
nucleoporin 210	Nup210	0.42±0.18
nucleoporin 214	Nup214	0.72±0.3
nucleoporin 35	Nup35	1.19±0.42
nucleoporin 37 (predicted)	Nup37_predicted	2.1±0.32
nucleoporin 54	Nup54	0.86±0.15
nucleoporin 62	Nup62	1.33±0.26
nucleoporin 85	Nup85	0.39±0.02
nucleoporin 88	Nup88	1.75±0.42
nucleoporin 93	Nup93	3.15±0.68
nucleoporin 98	Nup98	1.28±0.06
nucleoporin like 1	Nupl1	0.96±0.03
nucleoporin like 2	Nupl2	0.45±0.11
nucleoredoxin (predicted)	Nxn_predicted	0.56±0.15
nucleoside phosphorylase	Np	6.86±1.05
Nucleosome assembly protein 1-like 1	Nap1l1	1.83±0.95
nucleosome assembly protein 1-like 3	Nap1l3	0.76±0.41
nucleosome assembly protein 1-like 4	Nap1l4	3.32±0.87
nucleotide binding protein 1	Nubp1	5.17±0.57
nucleotide binding protein 2	Nubp2	3.64±0.49
nucleotide binding protein-like (predicted)	Nubpl_predicted	0.58±0.2
nucleotide-binding oligomerization domain containing 1	Nod1	0.81±0.01
NudC domain containing 1 (predicted)	Nudcd1_predicted	0.57±0.27
NudC domain containing 2	Nudcd2	0.87±0.37
nudix (nucleoside diphosphate linked moiety X)-type motif 1	Nudt1	0.49±0.17
nudix (nucleoside diphosphate linked moiety X)-type motif 12 (predicted)	Nudt12_predicted	0.29±0.1
nudix (nucleoside diphosphate linked moiety X)-type motif 14 (predicted)	Nudt14_predicted	1.48±0.91
nudix (nucleoside diphosphate linked moiety X)-type motif 16 (predicted)	Nudt16_predicted	1.72±0.17
nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	Nudt16l1	2.06±0.04
nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	1.98±0.53
nudix (nucleoside diphosphate linked moiety X)-type motif 2	Nudt2	4.65±0.45
nudix (nucleoside diphosphate linked moiety X)-type motif 22	Nudt22	0.88±0.15
nudix (nucleoside diphosphate linked moiety X)-type motif 4	Nudt4	24.57±0.15
nudix (nucleoside diphosphate linked moiety X)-type motif 5	Nudt5	0.72±0.2
nudix (nucleoside diphosphate linked moiety X)-type motif 6	Nudt6	0.71±0.2
nudix (nucleoside diphosphate linked moiety X)-type motif 7 (predicted)	Nudt7_predicted	8.12±2.25
nudix (nucleoside diphosphate linked moiety X)-type motif 9	Nudt9	1.55±0.45
nudix (nucleotide diphosphate linked moiety X)-type motif 3	Nudt3	4.28±0.22
NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Nuf2	0.61±0.02
Numb gene homolog (Drosophila)	Numb	3.67±0.23
Nur77 downstream gene 2	Ndg2	51.62±2.76
nurim (nuclear envelope membrane protein)	Nrm	0.43±0.03
O-6-methylguanine-DNA methyltransferase	Mgmt	0.43±0.09
OAF homolog (Drosophila)	Oaf	1.29±0.65
Obg-like ATPase 1	Ola1	7.56±2.42
obscurin-like 1	Obsl1	0.8±0.15
occludin /// thiopurine methyltransferase	Ocln /// Tpmt	23.9±5.4
OCIA domain containing 1	Ociad1	13.1±0.82
oculocerebrorenal syndrome of Lowe	Ocrl	0.63±0.13
oligonucleotide/oligosaccharide-binding fold containing 1	Obfc1	1.12±0.03
oligonucleotide/oligosaccharide-binding fold containing 2A	Obfc2a	0.36±0.16
oligonucleotide/oligosaccharide-binding fold containing 2B	Obfc2b	1.9±0.26
oligophrenin 1 (predicted)	Ophn1_predicted	1.37±0.21
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Ogt	8.84±1.45
OMA1 homolog, zinc metallopeptidase (S. cerevisiae) (predicted)	Oma1_predicted	1.73±0.27
open reading frame 19	ORF19	1.59±0.08
opioid growth factor receptor	Ogfr	1.43±0.02

opioid receptor, sigma 1	Oprs1	1.06±0.27
opsin 3	Opn3	1.21±0.25
optic atrophy 1 homolog (human)	Opa1	1.53±0.49
optic atrophy 3	Opa3	0.53±0.3
optineurin	Optn	4.12±0.2
ORAI calcium release-activated calcium modulator 1	Orai1	1.42±0.06
ORAI calcium release-activated calcium modulator 3	Orai3	0.65±0.29
ORAI calcium release-activated calcium modulator 3 /// similar to KIAA0339 protein	Orai3 /// RGD1311624	0.54±0.05
oral cancer overexpressed 1 (predicted)	Oraov1_predicted	0.58±0.14
oral-facial-digital syndrome 1 gene homolog (human)	Ofd1	0.43±0.05
origin recognition complex, subunit 2-like (S. cerevisiae)	Orc2l	1.51±0.01
origin recognition complex, subunit 3-like (S. cerevisiae)	Orc3l	0.29±0.04
origin recognition complex, subunit 4	Orc4	3±0.26
origin recognition complex, subunit 4-like (S. cerevisiae)	Orc4l	1.01±0.51
origin recognition complex, subunit 5-like (S. cerevisiae)	Orc5l	1.45±0.13
origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	0.23±0.04
ORM1-like 2 (S. cerevisiae) (predicted)	Ormdl2_predicted	3.77±0.5
ORM1-like 3 (S. cerevisiae)	Ormdl3	3.15±0.2
ornithine decarboxylase 1	Odc1	1.25±3.36
ornithine decarboxylase antizyme 1	Oaz1	22.16±1.06
O-sialoglycoprotein endopeptidase	Osgep	0.6±0.19
O-sialoglycoprotein endopeptidase-like 1	Osgepl1	0.8±0.19
osteoclast stimulating factor 1	Ostf1	4.28±0.02
osteopetrosis associated transmembrane protein 1	Ostm1	2.51±0.57
OTU domain containing 1	Otud1	2.19±0.28
OTU domain containing 5	Otud5	2.79±0.55
OTU domain containing 7B	Otud7b	0.38±0.18
OTU domain containing 7B /// myotubularin related protein 11	Mtmr11 /// Otud7b	1.34±0.1
OTU domain, ubiquitin aldehyde binding 1 (predicted)	Otub1_predicted	3.91±1.25
OTU domain, ubiquitin aldehyde binding 2 (predicted)	Otub2_predicted	0.42±0.26
outer dense fiber of sperm tails 2	Odf2	0.23±0.09
outer dense fiber of sperm tails 2-like	Odf2l	0.97±0.22
oxidase assembly 1-like	Oxa1l	9.68±0.88
oxidation resistance 1	Oxr1	5.25±0.23
oxidative stress responsive gene	RGD1303142	1.23±0.52
oxidative-stress responsive 1 (predicted)	Oxsr1_predicted	1.78±0.03
oxidoreductase NAD-binding domain containing 1 (predicted)	Oxnad1_predicted	2.66±0.3
oxoglutarate dehydrogenase (lipoamide)	Ogdh	27.73±4.32
oxysterol binding protein (predicted)	Osbp_predicted	7.32±2.1
oxysterol binding protein-like 11 (predicted)	Osbpl11_predicted	0.86±0.15
oxysterol binding protein-like 1A	Osbpl1a	4.09±0.9
oxysterol binding protein-like 2	Osbpl2	4.49±0.13
oxysterol binding protein-like 3	Osbpl3	2.26±0.4
oxysterol binding protein-like 6 (predicted)	Osbpl6_predicted	0.42±0.06
oxysterol binding protein-like 7 (predicted)	Osbpl7_predicted	0.5±0.02
oxysterol binding protein-like 9 (predicted)	Osbpl9_predicted	9.34±2.15
P18SRP protein	P18srp	1.64±0.43
P21 (CDKN1A)-activated kinase 1	Pak1	1.19±0.09
p21 (CDKN1A)-activated kinase 4 (predicted)	Pak4_predicted	2.9±0.37
p300/CBP-associated factor	Pcaf	4.18±0.15
p34 protein	P34	0.95±0.16
P450 (cytochrome) oxidoreductase	Por	1.14±0.6
p53 and DNA damage regulated 1	Pdrg1	0.85±0.06
P55	LOC362855	4.33±0.88
p55 protein	LOC652956	4.9±0.53
Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	Paf1	1.97±0.37
paired box gene 8	Pax8	5.75±1.73
PAK1 interacting protein 1	Pak1ip1	0.41±0.09
pallidin	Pldn	0.99±0.04
palmitoyl-protein thioesterase 1	Ppt1	3.76±0.75
PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	Pan3	3±0.52
Pannexin 1	Panx1	0.2±0.03
pantothenate kinase 1 (predicted)	Pank1_predicted	5.52±0.13
pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	0.65±0.09
pantothenate kinase 4	Pank4	1.91±0.15
PAP associated domain containing 1 (predicted)	Papd1_predicted	1.63±0.06
PAP associated domain containing 5 (predicted)	Papd5_predicted	1.79±0.44
papillary renal cell carcinoma (translocation-associated) (predicted)	Prcc_predicted	1.04±0.22
par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	0.58±0.1
par-6 (partitioning defective 6) homolog beta (C. elegans) (predicted)	Pard6b_predicted	6.04±0.01
par-6 (partitioning defective 6,) homolog alpha (C. elegans)	Pard6a	0.39±0.24
paralemmin	Palm	3.25±0.65
paraoxonase 2	Pon2	2.81±0.3
paraoxonase 3	Pon3	0.99±0.57
paraspeckle protein 1	Pspc1	0.97±0.31
parathymosin	Ptms	7.5±0.84
parathyroid hormone receptor 1	Pthr1	1.36±1.33
Parkinson disease (autosomal recessive, early onset) 7	Park7	16.14±3.67
partner of NOB1 homolog (S. cerevisiae)	Pno1	0.67±0.46
parvin, alpha	Parva	1.02±0.36
patatin-like phospholipase domain containing 2 (predicted)	Pnpla2_predicted	2.98±1.56
patatin-like phospholipase domain containing 7	Pnpla7	1.19±0.28
patatin-like phospholipase domain containing 8	Pnpla8	0.79±0.74
PAX interacting (with transcription-activation domain) protein 1 (predicted)	Paxip1_predicted	0.65±0.2
paxillin	Pxn	3.3±1.23
PC4 and SFRS1 interacting protein 1	Psip1	0.84±0.02
PCTAIRE-motif protein kinase 1	Pctk1	2.35±0.21

PCTAIRE-motif protein kinase 2	Pctk2	0.72±0.46
PDGFA associated protein 1	Pdap1	6.41±0.88
PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	Pds5a	2.3±0.39
PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	Pds5b	0.87±0.16
PDZ and LIM domain 2	Pdlim2	0.43±0.08
PDZ and LIM domain 5	Pdlim5	0.36±0.16
PDZ and LIM domain 7	Pdlim7	0.32±0.12
PDZ binding kinase (predicted)	Pbk_predicted	0.54±0.23
PDZ domain containing 11 (predicted)	Pdzd11_predicted	2.9±0.16
PDZ domain containing 8	Pdzd8	2.11±0.02
PDZK1 interacting protein 1	Pdzk1ip1	5.31±2.62
pecanex homolog (Drosophila)	Pcnx	2.48±0.12
pecanex-like 3 (Drosophila)	Pcnxl3	2.05±0.04
pellino homolog 1 (Drosophila) /// similar to pellino protein (predicted)	Peli1 /// RGD1564594_	1.01±0.74
pelota homolog (Drosophila)	Pelo	2.69±0.54
penta-EF hand domain containing 1	Pef1	2.65±0.08
pentatricopeptide repeat domain 1 (predicted)	Ptcd1_predicted	1.74±0.49
pentatricopeptide repeat domain 2 (predicted)	Ptcd2_predicted	1.27±0.41
Pentatricopeptide repeat domain 3	Ptcd3	4.77±1.19
peptidase (mitochondrial processing) alpha	Pmpca	2.69±0.52
peptidase (mitochondrial processing) beta	Pmpcb	7.46±2.29
peptidylglycine alpha-amidating monooxygenase	Pam	0.3±1.57
peptidylprolyl isomerase (cyclophilin)-like 1	Ppil1	0.76±0.25
peptidylprolyl isomerase (cyclophilin)-like 2	Ppil2	1.22±0.06
peptidylprolyl isomerase (cyclophilin)-like 3	Ppil3	1.29±0.5
peptidylprolyl isomerase (cyclophilin)-like 4 (predicted)	Ppil4_predicted	1.29±0.33
peptidylprolyl isomerase A	Ppia	46.66±3.48
peptidylprolyl isomerase B	Ppib	19.15±1.1
peptidylprolyl isomerase D (cyclophilin D)	Ppid	2.98±0.09
peptidylprolyl isomerase domain and WD repeat containing 1 (predicted)	Ppwd1_predicted	0.34±0.22
peptidylprolyl isomerase E (cyclophilin E)	Ppie	1.41±0.39
peptidylprolyl isomerase F (cyclophilin F)	Ppif	4.97±2
peptidylprolyl isomerase G	Ppig	0.6±0.16
peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae) (predicted)	Ptrh1_predicted	0.53±0.25
Peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae) (predicted)	Tor2a	0.56±0.03
peptidyl-tRNA hydrolase 2	Ptrh2	1.11±0.51
pericentriolar material 1	Pcm1	1.78±0.13
period homolog 1 (Drosophila)	Per1	2.18±0.98
period homolog 3 (Drosophila)	Per3	0.58±0.39
periphilin 1 (predicted)	Pphln1_predicted	1.38±0.06
peroxiredoxin 1	Prdx1	12.61±2.14
peroxiredoxin 2	Prdx2	30.62±2.49
peroxiredoxin 3	Prdx3	12.71±1.74
peroxiredoxin 4	Prdx4	3.16±0.57
peroxiredoxin 5	Prdx5	38.21±2.99
peroxiredoxin 6	Prdx6	5.33±0.72
peroxisomal biogenesis factor 11A	Pex11a	0.47±0.27
peroxisomal biogenesis factor 11b	Pex11b	3.01±0.34
peroxisomal biogenesis factor 12	Pex12	1.85±0.35
peroxisomal biogenesis factor 13 (predicted)	Pex13_predicted	3.7±0.27
peroxisomal biogenesis factor 14	Pex14	1.01±0.18
peroxisomal biogenesis factor 3	Pex3	1.1±0.25
peroxisomal biogenesis factor 6	Pex6	0.56±0.07
peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	Peci	6.25±0.86
peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase /// similar to RIKEN cDNA 1810022C23	Peci /// RGD1310224	1.54±0.17
peroxisomal membrane protein 2	Pxmp2	3.13±0.14
peroxisomal membrane protein 4	Pxmp4	0.47±0.06
peroxisomal trans-2-enoyl-CoA reductase	Pecr	12.95±0.24
peroxisome biogenesis factor 1	Pex1	1.42±0.2
peroxisome biogenesis factor 10	Pex10	0.32±0.24
peroxisome biogenesis factor 16	Pex16	1.13±0
peroxisome biogenesis factor 19	Pex19	1.5±0.55
peroxisome biogenesis factor 19 /// similar to Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxisomal farnesylated protein)	LOC679129 /// Pex19	3.26±0.53
peroxisome biogenesis factor 2	Pex2	1.73±0.44
peroxisome biogenesis factor 26	Pex26	1.49±0.37
peroxisome biogenesis factor 5 (predicted)	Pex5_predicted	2.39±0.05
peroxisome biogenesis factor 7	Pex7	2.48±0.12
peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	3.63±0.35
peroxisome proliferative activated receptor, gamma, coactivator 1 beta	Ppargc1b	1.54±0.23
PEST proteolytic signal containing nuclear protein	Pcnp	6.18±1.17
PET112-like (yeast) (predicted)	Pet112l_predicted	0.63±0.29
peter pan homolog (Drosophila)	Ppan	0.74±0.34
PFTAIRE protein kinase 1 (predicted)	Pftk1_predicted	0.72±0.17
PH domain and leucine rich repeat protein phosphatase	Phlpp	0.42±0.18
PHD finger protein 12	Phf12	1.16±0.19
PHD finger protein 13 (predicted)	Phf13_predicted	0.51±0.18
PHD finger protein 14	Phf14	0.53±0.32
PHD finger protein 17 (predicted)	Phf17_predicted	5.61±0.31
PHD finger protein 2 (predicted)	Phf2_predicted	1.28±0.09
PHD finger protein 20-like 1	Phf20l1	3.08±0.14
PHD finger protein 3 (predicted)	Phf3_predicted	1.5±0.27
PHD finger protein 5A	Phf5a	2.92±0.63
PHD finger protein 7	Phf7	0.21±0.15
phenazine biosynthesis-like protein domain containing	Pbld	9.05±1.5
phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	0.94±0.26
Phenylalanine-tRNA synthetase-like, alpha subunit	Farsla	0.43±0.08
phenylalanyl-tRNA synthetase, beta subunit	Farsb	1.91±0.28

phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Ebp	3.05±0.27
phosducin-like	Pdcl	1.68±0.01
phosducin-like 3	Pdcl3	0.99±0.76
phosphatase and tensin homolog	Pten	1.31±0.08
phosphatase, orphan 2	Phospho2	1.75±0.56
phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	0.91±0.35
phosphate cytidylyltransferase 2, ethanolamine	Pcyt2	5.61±1.35
phosphatidic acid phosphatase 2a	Ppap2a	9.45±1.49
phosphatidic acid phosphatase type 2 domain containing 1B	Ppapdc1b	1.87±0.09
phosphatidic acid phosphatase type 2 domain containing 2	Ppapdc2	1.62±0.54
phosphatidic acid phosphatase type 2 domain containing 3	Ppapdc3	0.9±0.28
phosphatidic acid phosphatase type 2B	Ppap2b	6.32±3.54
phosphatidic acid phosphatase type 2c	Ppap2c	8.35±1.36
phosphatidylcholine transfer protein	Pctp	1.16±0.33
phosphatidylethanolamine binding protein 1	Pebp1	42.03±4.82
phosphatidylglycerophosphate synthase 1	Pgs1	1.09±0.29
phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	Pib5pa	2.47±0.03
phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	Pik3r3	1.05±0.32
phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide (predicted)	Pik3c2a_predicted	1.97±0.12
Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	2.98±0.38
phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	LOC685590 /// Pik3ca	0.32±0.01
phosphatidylinositol 3-kinase, catalytic, beta polypeptide	Pik3cb	0.32±0.05
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	Pik3r1	1.48±1.17
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	Pik3r2	0.73±0.32
phosphatidylinositol 4-kinase type 2 alpha	Pi4k2a	0.34±0.21
phosphatidylinositol 4-kinase type 2 beta	Pi4k2b	0.56±0.3
phosphatidylinositol 4-kinase, catalytic, alpha	Pi4ka	2.28±0.42
phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pi4kb	2.99±0.56
Phosphatidylinositol binding clathrin assembly protein	Picalm	5.62±2.34
phosphatidylinositol glycan anchor biosynthesis, class C	Pigc	2.36±0.59
phosphatidylinositol glycan anchor biosynthesis, class H	Pigh	0.64±0.26
phosphatidylinositol glycan anchor biosynthesis, class L	Pigl	1.27±0.49
phosphatidylinositol glycan anchor biosynthesis, class M	Pigm	0.26±0.12
phosphatidylinositol glycan anchor biosynthesis, class O	Pigo	1.14±0.28
phosphatidylinositol glycan anchor biosynthesis, class P	Pigp	16.84±0.93
phosphatidylinositol glycan anchor biosynthesis, class Q	Pigq	5.19±1.83
phosphatidylinositol glycan anchor biosynthesis, class S	Pigs	1.71±0.06
phosphatidylinositol glycan anchor biosynthesis, class T	Pigt	4.45±1.4
phosphatidylinositol glycan anchor biosynthesis, class V	Pigv	0.36±0.13
phosphatidylinositol glycan anchor biosynthesis, class X	Pigx	3.87±0.3
phosphatidylinositol glycan anchor biosynthesis, class Y	Pigy	8.85±1.51
phosphatidylinositol glycan, class K /// ubiquitin specific peptidase 33	Pigk /// Usp33	3.13±0.16
phosphatidylinositol transfer protein, alpha	Pitpna	2.98±0.46
phosphatidylinositol transfer protein, beta	Pitpnb	3.6±0.87
phosphatidylinositol transfer protein, membrane-associated 1	Pitpnm1	2.04±0.27
phosphatidylinositol transfer protein, membrane-associated 2 (predicted)	Pitpnm2_predicted	1.24±0.24
phosphatidylinositol-4-phosphate 5-kinase, type 1, alpha (predicted)	Pip5k1a_predicted	0.98±0.44
phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	Pip5k1c	2.28±0.18
phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	Pip4k2c	3.29±0.66
phosphatidylserine decarboxylase	Pisd	1.22±0.21
phosphatidylserine synthase 1	Ptdss1	2.88±0.2
phosphatidylserine synthase 2 (predicted)	Ptdss2_predicted	2.03±0.31
phosphodiesterase 1A, calmodulin-dependent	Pde1a	2.77±0.95
phosphodiesterase 1C	Pde1c	0.6±0.03
Phosphodiesterase 4A, cAMP specific	Pde4a	1.87±0.16
phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	0.23±0.04
phosphodiesterase 6D, cGMP-specific, rod, delta (predicted)	Pde6d_predicted	2.49±0.61
phosphodiesterase 7A	Pde7a	0.33±0.05
Phosphodiesterase 8A	Pde8a	1.62±0.42
phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted	2.12±0.12
phosphofructokinase, liver, B-type	Pfkl	1.71±0.27
phosphofructokinase, muscle	Pfkm	6.58±1.08
phosphofructokinase, platelet	Pfkp	16.82±4.4
phosphofurin acidic cluster sorting protein 1	Pacs1	1.32±0.64
phosphoglucomutase 1	Pgm1	2.38±0.27
phosphoglucomutase 2	Pgm2	1.34±0.95
phosphoglucomutase 3 (predicted)	Pgm3_predicted	0.37±0.1
phosphoglycerate dehydrogenase like 1	Phgdhl1	2.13±0.37
phosphoglycerate kinase 1	Pgk1	35.5±1.58
phosphoglycerate mutase 1	Pgam1	24.71±5.11
phosphoglycerate mutase family member 5	Pgam5	1.82±0.54
phosphohistidine phosphatase 1 (predicted)	Phpt1_predicted	6.98±0.34
Phosphoinositide-3-kinase adaptor protein 1 (predicted)	Pik3ap1_predicted	0.53±0.15
phosphoinositide-3-kinase interacting protein 1	Pik3ip1	0.73±0.35
phosphoinositide-3-kinase, class 3	Pik3c3	1.18±0.24
phosphoinositide-3-kinase, regulatory subunit 4, p150 (predicted)	Pik3r4_predicted	1.48±0.39
phospholipase A2, activating protein	Plaa	1.63±0.34
phospholipase A2, group IVA (cytosolic, calcium-dependent)	Pla2g4a	0.29±0.44
phospholipase A2, group VI	Pla2g6	0.51±0.12
phospholipase A2, group XIIA (predicted)	Pla2g12a_predicted	2.71±0.5
phospholipase C, beta 1	Plcb1	1.74±0.09
phospholipase C, delta 1	Plcd1	0.26±0.21
phospholipase C, epsilon 1	Plce1	1.14±0.14
phospholipase C, eta 1	Plch1	0.33±0.41
phospholipase C, gamma 1	Plcg1	1.63±1.02
phospholipase D family, member 3	Pld3	0.55±0.08
phospholipase D1	Pld1	0.36±0.22

phospholipid scramblase 1	Plscr1	2.05±0.41
phospholipid scramblase 2	Plscr2	0.91±0.36
phospholipid scramblase 3	Plscr3	0.37±0.15
phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Lhpp	0.57±0.12
phosphomannomutase 1	Pmm1	4.92±0.3
phosphomannomutase 2 (predicted)	Pmm2_predicted	3.09±0.69
phosphomevalonate kinase	Pmvk	1.94±0.15
phosphopantothenoylcysteine decarboxylase (predicted)	Ppcdc_predicted	0.41±0.07
phosphopantothenoylcysteine synthetase	Ppcs	1±0.28
phosphoribosyl pyrophosphate amidotransferase	Ppat	3.25±0.18
phosphoribosyl pyrophosphate synthetase 1	Prps1	4.14±1.13
phosphoribosyl pyrophosphate synthetase 2	Prps2	9.5±4.23
phosphoribosyl pyrophosphate synthetase-associated protein 1	Prpsap1	3.45±0
phosphoribosyl pyrophosphate synthetase-associated protein 2	Prpsap2	0.96±0.59
phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	Paics	14.72±1.31
phosphoribosylformylglycinamidine synthase (FGAR amidotransferase) (predicted)	Pfas_predicted	2.29±0.5
phosphoribosylglycinamide formyltransferase	Gart	1.5±0.29
Phosphorylase kinase alpha 1	Phka1	0.85±0.17
phosphorylase kinase, gamma 2 (testis)	Phkg2	3.17±0.43
phosphoserine aminotransferase 1	Psat1	0.43±0.76
Phytanoyl-CoA hydroxylase	Phyh	38.34±12.08
Phytn_dehydro and Pyr_redox domain containing protein RGD1303232	RGD1303232	10.79±0.23
phytoceramidase, alkaline	Phca	1.8±0.08
PIH1 domain containing 1	Pih1d1	0.78±0.09
PIN2-interacting protein 1	Pinx1	0.29±0.22
pinin	Pnn	2.17±0.33
pitrilysin metallepetidase 1 (predicted)	Pitrm1_predicted	3.16±0.53
pituitary tumor-transforming 1	Pttg1	0.91±0.32
pituitary tumor-transforming 1 interacting protein	Pttg1ip	8.11±3.29
plakophilin 2	Pkp2	2.59±0.7
plakophilin 3 (predicted)	Pkp3_predicted	1.11±0.29
plakophilin 4 (predicted)	Pkp4_predicted	16.73±1.93
plasma glutamate carboxypeptidase	Pgcp	7.02±1.64
plasminogen activator, urokinase	Plau	46.6±7.64
plastin 3 (T-isoform)	Pls3	13.6±6.79
platelet derived growth factor, alpha	Pdgfa	9.46±0.33
platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	Pafah1b3	0.73±0.32
platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	1.68±0.49
platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	Pafah1b1	2.13±0.11
platelet-derived growth factor, C polypeptide	Pdgfc	1.68±0.01
pleckstrin and Sec7 domain containing 4	Psd4	0.27±0.11
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	Plekha1	2.34±0.2
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	Plekha8	0.62±0.09
Pleckstrin homology domain containing, family A member 5	Plekha5	1.38±0.12
pleckstrin homology domain containing, family A member 6 (predicted)	Plekha6_predicted	5.34±0.75
pleckstrin homology domain containing, family B (evectins) member 2 (predicted)	Plekhb2_predicted	9.05±1.74
pleckstrin homology domain containing, family C (with FERM domain) member 1	Plekhc1	6.35±1.65
pleckstrin homology domain containing, family F (with FYVE domain) member 1	Plekhf1	1.72±0.32
pleckstrin homology domain containing, family F (with FYVE domain) member 2 (predicted)	Plekhf2_predicted	0.4±0.72
pleckstrin homology domain containing, family G (with RhoGef domain) member 3	Plekhg3	5.28±0.68
pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)	Plekhh1_predicted	1.58±0.42
pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	Plekhh3	0.57±0.14
pleckstrin homology domain containing, family J member 1	Plekhj1	1.84±0.78
pleckstrin homology domain containing, family M (with RUN domain) member 1	Plekhm1	0.23±0.16
pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	Plekha3	3.03±0.52
pleckstrin homology, Sec7 and coiled-coil domains 1	Pscd1	0.3±0.02
pleckstrin homology, Sec7 and coiled-coil domains 2	Pscd2	1.65±0.24
pleckstrin homology-like domain, family B, member 2	Phldb2	5.82±0.29
plectin 1	Plec1	3.77±0.45
pleiomorphic adenoma gene-like 1	Plagl1	6.58±1.84
pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	Plrg1	2.82±0.53
plexin A3	Plxna3	0.51±0.12
plexin B1 (predicted)	Plxnb1_predicted	3.23±0.27
plexin B2	Plxnb2	5.8±2.05
plexin domain containing 2 (predicted)	Plxdc2_predicted	2.61±0.01
PMF32 protein	Pmf31	0.62±0.08
pogo transposable element with KRAB domain (predicted)	Pogk_predicted	0.77±0
pogo transposable element with ZNF domain (predicted)	Pogz_predicted	0.75±0.09
poliovirus receptor-related 2	Pvrl2	0.61±0.56
Poliovirus receptor-related 3 (predicted)	Pvrl3_predicted	2.31±0.37
polo-like kinase 4 (Drosophila) (predicted)	Plk4_predicted	0.22±0.07
poly (A) polymerase alpha (predicted)	Papola_predicted	1.48±0.64
poly (ADP-ribose) glycohydrolase	Parg	1.48±0.02
poly (ADP-ribose) polymerase family, member 1	Parp1	1.94±0.25
poly (ADP-ribose) polymerase family, member 12 (predicted)	Parp12_predicted	0.65±0.06
poly (ADP-ribose) polymerase family, member 16	Parp16	0.63±0.01
poly (ADP-ribose) polymerase family, member 2 (predicted)	Parp2_predicted	0.84±0.12
poly (ADP-ribose) polymerase family, member 6	Parp6	1.51±0.07
poly (ADP-ribose) polymerase family, member 8	Parp8	0.3±0.13
poly (ADP-ribose) polymerase family, member 9 (predicted)	Parp9_predicted	1.02±0.02
poly A binding protein, cytoplasmic 4	Pabpc4	9.48±0.55
poly(A) binding protein, cytoplasmic 1	Pabpc1	16.38±3.06
poly(A) polymerase gamma (predicted)	Papolg_predicted	0.42±0.23
poly(A)-specific ribonuclease (deadenylation nuclease)	Parn	0.93±0.04
poly(rC) binding protein 1	Pcbp1	10.84±2.07
poly(rC) binding protein 2	Pcbp2	13.42±0.55
poly(rC) binding protein 3	Pcbp3	0.38±0.06

poly(rC) binding protein 4 (predicted)	Pcbp4_predicted	0.67±0.24
polyadenylate binding protein-interacting protein 1 (predicted)	Paip1_predicted	7.2±0.66
polyadenylate-binding protein interacting protein 2	Paip2	14±1.4
polyamine-modulated factor 1	Pmf1	0.71±0.22
polybromo 1	Pbrm1	0.55±0.18
polycomb group ring finger 1	Pcgf1	1.18±0.03
polycomb group ring finger 2 (predicted)	Pcgf2_predicted	0.56±0.1
polycomb group ring finger 3	Pcgf3	0.34±0.02
Polycomb group ring finger 4 (predicted)	Pcgf4_predicted	4.73±0.45
polycomb group ring finger 5 /// similar to polycomb group ring finger 5	LOC687730 /// Pcgf5	2.6±0.49
polycomb group ring finger 6	Pcgf6	0.88±0.16
polyglutamine binding protein 1	Pqbp1	1.81±0.18
polyhomeotic-like 1 (Drosophila) (predicted)	Phc1_predicted	0.92±0.07
polyhomeotic-like 2 (Drosophila)	Phc2	2.6±0.23
polymerase (DNA directed) sigma (predicted)	Pols_predicted	1.22±0.06
polymerase (DNA directed), alpha 2	Pola2	1.09±0.07
polymerase (DNA directed), beta	Polb	1.46±0.09
polymerase (DNA directed), delta 2, regulatory subunit	Pold2	1.2±0.21
polymerase (DNA directed), epsilon 3 (p17 subunit)	Pole3	2.16±0.19
polymerase (DNA directed), eta (RAD 30 related) (predicted)	Polh_predicted	0.2±0.02
polymerase (DNA directed), gamma	Polg	1.04±0.09
polymerase (DNA directed), gamma 2, accessory subunit (predicted)	Polg2_predicted	1.61±0.01
polymerase (DNA directed), lambda	Poll	0.69±0.31
polymerase (DNA directed), mu	Polm	0.4±0.03
polymerase (DNA-directed), delta 3, accessory subunit	Pold3	0.4±0.05
polymerase (DNA-directed), delta 4	Pold4	2.37±0.37
polymerase (DNA-directed), delta interacting protein 2 (predicted)	Poldip2_predicted	8.21±1.15
polymerase (DNA-directed), delta interacting protein 3 (predicted)	Poldip3_predicted	0.83±0.24
polymerase (DNA-directed), epsilon 4 (p12 subunit) (predicted)	Pole4_predicted	14.77±0.56
polymerase (RNA) I polypeptide E	Polr1e	0.43±0.03
polymerase (RNA) II (DNA directed) polypeptide A	Polr2a	1.59±0.66
polymerase (RNA) II (DNA directed) polypeptide B (predicted)	Polr2b_predicted	2.87±1.07
polymerase (RNA) II (DNA directed) polypeptide C	Polr2c	1.99±0.15
polymerase (RNA) II (DNA directed) polypeptide C /// similar to RIKEN cDNA 2310005O14	LOC498909 /// Polr2c	15.51±1.74
polymerase (RNA) II (DNA directed) polypeptide D (predicted)	Polr2d_predicted	3.32±0.7
polymerase (RNA) II (DNA directed) polypeptide E	Polr2e	8.39±1.2
polymerase (RNA) II (DNA directed) polypeptide F	Polr2f	4.08±1.21
polymerase (RNA) II (DNA directed) polypeptide G	Polr2g	4.37±0.26
polymerase (RNA) II (DNA directed) polypeptide H (predicted)	Polr2h /// Polr2h_predic	1.26±0.29
polymerase (RNA) II (DNA directed) polypeptide I (predicted)	Polr2i_predicted	2.81±0.21
polymerase (RNA) II (DNA directed) polypeptide J (predicted)	Polr2j_predicted	6.23±0.54
polymerase (RNA) III (DNA directed) polypeptide A	Polr3a	1.06±0.34
polymerase (RNA) III (DNA directed) polypeptide C	Polr3c	1.15±0.28
polymerase (RNA) III (DNA directed) polypeptide D	Polr3d	2.02±0.48
polymerase (RNA) III (DNA directed) polypeptide E (predicted)	Polr3e_predicted	0.66±0.11
polymerase (RNA) III (DNA directed) polypeptide F (predicted)	Polr3f_predicted	0.71±0.04
polymerase (RNA) III (DNA directed) polypeptide G	Polr3g	0.75±0.07
polymerase (RNA) III (DNA directed) polypeptide H (predicted)	Polr3h_predicted	0.51±0.1
polymerase (RNA) III (DNA directed) polypeptide K	Polr3k	2.86±0.54
polymerase (RNA) mitochondrial (DNA directed) (predicted)	Polrmt_predicted	1.09±0.24
polynucleotide kinase 3'-phosphatase	Pnkp	1.19±0.32
polypyrimidine tract binding protein 1	Ptbp1	7.08±0.54
polyribonucleotide nucleotidyltransferase 1	Pnpt1	2.61±0.27
popeye domain containing 2	Popdc2	0.34±0.01
postmeiotic segregation increased 1 (S. cerevisiae)	Pms1	1.37±0.54
postmeiotic segregation increased 2 (S. cerevisiae) (predicted)	Pms2_predicted	0.74±0.04
potassium channel tetramerisation domain containing 1	Kctd1	3.27±0.01
potassium channel tetramerisation domain containing 13	Kctd13	0.38±0.13
potassium channel tetramerisation domain containing 14 (predicted)	Kctd14_predicted	1.37±0.36
potassium channel tetramerisation domain containing 15	Kctd15	5.15±0.37
potassium channel tetramerisation domain containing 2	Kctd2	2.22±0.22
potassium channel tetramerisation domain containing 3	Kctd3	1.11±0.02
potassium channel tetramerisation domain containing 5 (predicted)	Kctd5_predicted	0.55±0.03
potassium channel tetramerisation domain containing 6 (predicted)	Kctd6_predicted	1.61±0.52
potassium channel tetramerisation domain containing 9 (predicted)	Kctd9_predicted	0.72±0.13
potassium channel tetramerization domain containing 10	Kctd10	1.01±0.22
potassium channel, subfamily K, member 1	Kcnk1	1.44±0.51
potassium channel, subfamily T, member 1	Kcnt1	4.84±0.16
potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	Kcnn1	0.88±0.07
potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	Kcnn2	0.41±0.14
potassium inwardly-rectifying channel, subfamily J, member 1	Kcnj1	26.6±9.62
potassium inwardly-rectifying channel, subfamily J, member 16	Kcnj16	10.37±0.24
potassium inwardly-rectifying channel, subfamily J, member 4	Kcnj4	0.4±0.07
potassium inwardly-rectifying channel, subfamily J, member 5	Kcnj5	1.14±0.43
potassium voltage-gated channel, subfamily Q, member 1	Kcnq1	1.79±0.05
POU domain, class 2, transcription factor 1	Pou2f1	0.47±0.31
POU domain, class 3, transcription factor 3	Pou3f3	8.96±4.3
POU domain, class 6, transcription factor 1	Pou6f1	0.3±0.15
PP3111 protein	Pp3111	1.87±0.37
PQ loop repeat containing 1	Pqlc1	0.78±1.26
PR domain containing 15 (predicted)	Prdm15_predicted	0.75±0.2
PR domain containing 2, with ZNF domain	Prdm2	0.52±0.24
PR domain containing 4	Prdm4	0.43±0.11
PRA1 domain family 2 (predicted)	Praf2_predicted	2.69±0.63
praja 2, RING-H2 motif containing	Pja2	4.04±0.83
pre B-cell leukemia transcription factor 3 (predicted)	Pbx3_predicted	1.27±0.65
pre-B-cell colony enhancing factor 1	Pbef1	3.67±0.91

pre-B-cell leukemia transcription factor 2	Pbx2	1.88±0.06
pre-B-cell leukemia transcription factor interacting protein 1	Pbxip1	3.71±0.1
prefoldin 1 (predicted)	Pfdn1_predicted	4.14±1.13
prefoldin 2	Pfdn2	2.92±0.01
prefoldin 5 (predicted)	Pfdn5_predicted	6.14±0.5
pregnancy specific beta-1-glycoprotein 4	Psg4	0.38±0.05
PRELI domain containing 1	Prelid1	4.55±0.75
PRELI domain containing 2 /// hypothetical protein LOC683855	LOC683855 /// Prelid2	0.98±0.16
pre-mRNA processing factor 8	Prpf8	5.36±0.21
prenyl (solanesyl) diphosphate synthase, subunit 2	Pdss2	1.3±0.16
Prenylated SNARE protein	Ykt6	1.79±0.28
prenylcysteine oxidase 1	Pcyox1	1.78±0.74
presenilin 1	Psen1	3.23±0.8
presenilin 2	Psen2	0.45±0.09
presenilin 2 /// chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1 /// Psen2	4.21±0.96
presenilin associated, rhomboid-like	Parl	3.06±0.92
presenilin enhancer 2 homolog (C. elegans)	Psenen	9.01±1.22
prickle homolog 3 (Drosophila)	Prickle3	1.54±0.27
prickle homolog 4 (Drosophila)	Prickle4	7.02±0.63
prickle-like 1 (Drosophila)	Prickle1	0.63±0.14
prion protein	Prnp	3.48±0.01
prion protein interacting protein 1	Prnpip1	1.11±0.46
PRKC, apoptosis, WT1, regulator	Pawr	2.64±0.37
Prkr interacting protein 1 (IL11 inducible)	Prkrip1	0.48±0.25
processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae) (predicted)	Pop1_predicted	0.38±0.12
processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	Pop4	1.47±0.15
processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (predicted)	Pop5_predicted	1.48±0.12
processing of precursor 7, ribonuclease P family, (S. cerevisiae) (predicted)	Pop7_predicted	1.66±0.85
procollagen C-endopeptidase enhancer protein	Pcolce	1.87±0.13
procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	Plod2	10.6±2.32
procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein (predicted)	Col4a3bp_predicted	3.46±0.34
procollagen, type IV, alpha 4	Col4a4	1.02±0.36
procollagen, type XVI, alpha 1	Col16a1	0.27±0.06
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	Plod1	0.24±0.06
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	Plod3	1.63±0.31
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	P4ha1	0.39±0.54
profilin 1	Pfn1	6.86±1.53
profilin 2	Pfn2	6.03±1.55
progesterone receptor membrane component 1	Pgrmc1	5.18±3.45
progesterone receptor membrane component 2	Pgrmc2	4.01±0.26
progestin and adipoQ receptor family member V	Paqr5	17.49±3.38
progestin induced protein	Dd5	5.44±0.14
programmed cell death 10	Pdcd10	5.34±0.9
programmed cell death 2	Pdcd2	0.81±0.09
programmed cell death 4	Pdcd4	1.52±3.14
programmed cell death 5 (predicted)	Pdcd5_predicted	7.89±2.42
programmed cell death 6 (predicted)	Pdcd6_predicted	8.93±0.69
programmed cell death 6 interacting protein	Pdcd6ip	2.73±0.32
programmed cell death protein 11 (predicted)	Pdcd11_predicted	1.13±0.24
programmed cell death protein 7 (predicted)	Pdcd7_predicted	1.03±0.1
progressive external ophthalmoplegia 1 (human)	Peo1	0.9±0.23
prohibitin	Phb	12.9±1.44
prohibitin 2	Phb2	14.21±2.72
prolactin regulatory element binding	Preb	1.04±0.31
proliferating cell nuclear antigen	Pcna	8.52±0.49
proliferation-associated 2G4	Pa2g4	2.14±0.24
proline rich 12	Prr12	0.84±0.16
proline rich 13	Prr13	3.43±0.44
proline rich 14	Prr14	1.8±0.03
proline synthetase co-transcribed (predicted)	Prosc_predicted	3.01±0.75
proline, glutamic acid and leucine rich protein 1	Pelp1	0.61±0.11
proline/serine-rich coiled-coil 1	Psrc1	0.27±0.1
proline/serine-rich coiled-coil 2	Psrc2	1.58±0.16
proline-rich nuclear receptor coactivator 1	Pnrc1	4.07±3.31
proline-rich nuclear receptor coactivator 2	Pnrc2	6.46±1.45
proline-rich polypeptide 3	Prr3	0.77±0.23
proline-rich polypeptide 6	Prr6	0.8±0.04
proline-serine-threonine phosphatase-interacting protein 1 (predicted)	Pstpip1_predicted	0.2±0.16
prolyl 4-hydroxylase, beta polypeptide	P4hb	29.6±4.73
prolyl endopeptidase	Prep	1.53±0.12
prolyl endopeptidase-like	Prepl	0.61±0.38
promethin	LOC378467	0.79±0.23
prominin 1	Prom1	5.78±0.26
prominin 2	Prom2	8.4±1.34
propionyl coenzyme A carboxylase, beta polypeptide	Pccb	22.17±0.99
propionyl-coenzyme A carboxylase, alpha polypeptide	Pcca	8.84±1.32
proprotein convertase subtilisin/kexin type 6	Pcsk6	14.4±2.6
proprotein convertase subtilisin/kexin type 7	Pcsk7	1.51±0.11
prosaposin	Psap	10.08±1.32
prostaglandin D2 synthase (brain)	Ptgds	4.45±1.28
Prostaglandin E receptor 3 (subtype EP3)	Ptger3	20.54±3.55
prostaglandin E synthase 2 (predicted)	Ptges2_predicted	6.03±1.24
prostaglandin E synthase 3 (cytosolic) (predicted)	Ptges3_predicted	13.85±0.44
prostaglandin F2 receptor negative regulator	Ptgfrn	1.44±0.14
prostate tumor over expressed gene 1	Ptov1	3.67±0.34
protease (prosome, macropain) 26S subunit, ATPase 1	Psmc1	4.75±0.85
protease (prosome, macropain) 26S subunit, ATPase 5	Psmc5	4.01±1.23

protease, serine, 23	Prss23	18.62±0.21
protease, serine, 36	Prss36	0.26±0.07
protease, serine, 8 (prostasin)	Prss8	4.2±0.09
proteaseome (prosome, macropain) 28 subunit, 3	Psme3	4.19±1.19
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2	12.05±2.19
proteasome (prosome, macropain) 26S subunit, ATPase 3	Psmc3	8.57±1.79
proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	Psmc3ip	1.04±0.66
proteasome (prosome, macropain) 26S subunit, ATPase, 4	Psmc4	3.69±0.88
proteasome (prosome, macropain) 26S subunit, ATPase, 6	Psmc6	1.88±1.31
proteasome (prosome, macropain) 26S subunit, ATPase, 6 /// similar to Psmc6 protein (predicted)	Psmc6 /// RGD155964	1.21±0.23
proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	Psmd1	1.94±0.29
proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmd11_predicted	4.19±0.41
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	Psmd12	4.43±1.76
proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (predicted)	Psmd13_predicted	1.43±0.5
proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Psmd14	3.12±1.31
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Psmd2	6.83±0.89
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	Psmd3	1.35±0.18
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	Psmd4	3.59±0.44
proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (predicted)	Psmd5_predicted	3.41±1.11
proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	Psmd6	7.68±0.4
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (predicted)	Psmd7_predicted	4.76±0.59
proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	Psmd8	5.16±0.43
proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Psmd9	1.01±0.3
proteasome (prosome, macropain) 28 subunit, alpha	Psme1	20.02±4.21
proteasome (prosome, macropain) 28 subunit, beta	Psme2	5.61±0.6
proteasome (prosome, macropain) activator subunit 4	Psme4	4.16±0.01
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	6.15±1.44
proteasome (prosome, macropain) subunit, alpha type 2	Psma2	11.85±1.04
proteasome (prosome, macropain) subunit, alpha type 3 /// proteasome subunit alpha type 3-like	Psma3 /// Psma3l	9.51±0.61
proteasome (prosome, macropain) subunit, alpha type 4	Psma4	5.65±1.29
proteasome (prosome, macropain) subunit, alpha type 5	Psma5	6.81±1.07
proteasome (prosome, macropain) subunit, alpha type 6	Psma6	17.8±0.63
proteasome (prosome, macropain) subunit, alpha type 7	Psma7	17.07±3.75
proteasome (prosome, macropain) subunit, beta type 1	Psmb1	14.66±2.5
proteasome (prosome, macropain) subunit, beta type 10	Psmb10	0.35±0.29
proteasome (prosome, macropain) subunit, beta type 2	Psmb2	7.74±1.31
proteasome (prosome, macropain) subunit, beta type 3	Psmb3	7.39±1.18
proteasome (prosome, macropain) subunit, beta type 4	Psmb4	16.4±0.62
proteasome (prosome, macropain) subunit, beta type 5	Psmb5	15.12±1.52
proteasome (prosome, macropain) subunit, beta type 6	Psmb6	4.93±0.77
proteasome (prosome, macropain) subunit, beta type 7	Psmb7	8.7±1.48
proteasome maturation protein	Pomp	18.88±2.85
protective protein for beta-galactosidase	Ppgb	13.2±0.51
protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (predicted)	Pin1_predicted	3.71±0.24
protein arginine N-methyltransferase 1	Prmt1	2.67±0.96
protein arginine N-methyltransferase 2	Prmt2	2.05±0.27
protein arginine N-methyltransferase 3	Prmt3	0.27±0.16
protein arginine N-methyltransferase 4	Prmt4	1.17±0.14
protein arginine N-methyltransferase 5 (predicted)	Prmt5_predicted	1.7±0.02
protein arginine N-methyltransferase 6 (predicted)	Prmt6_predicted	0.38±0.01
protein associated with topoisomerase II homolog 1 (yeast)	Patl1	1.01±0.11
protein disulfide isomerase associated 3	Pdia3	11.37±2.51
protein disulfide isomerase associated 4	Pdia4	1.29±0.25
protein disulfide isomerase associated 6	Pdia6	8.19±0.97
protein inhibitor of activated STAT 1 (predicted)	Pias1_predicted	1.22±0.05
protein inhibitor of activated STAT 2	Pias2	2.01±0.26
protein inhibitor of activated STAT 3	Pias3	1.37±0.23
protein inhibitor of activated STAT, 4	Pias4	0.68±0.02
protein interacting with C kinase 1	Pick1	1.48±0.41
protein kinase C and casein kinase substrate in neurons 2	Pacsin2	6.34±1.12
protein kinase C and casein kinase substrate in neurons 3	Pacsin3	1.04±0.25
protein kinase C binding protein 1	Prkcbp1	2.64±0
protein kinase C substrate 80K-H (predicted)	Prkcsh_predicted	4.66±1.08
protein kinase C, delta	Prkcd	4.09±0.16
protein kinase C, epsilon	Prkce	0.53±0.09
protein kinase C, iota	Prkci	2.17±1.58
protein kinase C, theta	Prkcq	5.44±0.59
protein kinase C, zeta	Prkcz	2.85±0.29
protein kinase D2	Prkd2	0.45±0.24
protein kinase D3	Prkd3	1.35±0.15
protein kinase inhibitor, gamma	Pkig	5.62±0.22
protein kinase LYK5	Lyk5	1.3±0.17
protein kinase N1	Pkn1	1.18±0.32
protein kinase N2	Pkn2	3.4±0.31
protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	2.31±0.34
protein kinase, AMP-activated, beta 1 non-catalytic subunit	Prkab1	6.35±0.48
protein kinase, AMP-activated, gamma 1 non-catalytic subunit	Prkag1	3.16±0.15
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Prkag2	0.54±0.27
Protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	11.08±1.25
protein kinase, cAMP dependent regulatory, type I, beta	Prkar1b	5.03±0.03
protein kinase, cAMP dependent regulatory, type II beta	Prkar2b	0.58±0.48
protein kinase, cAMP dependent, catalytic, beta	Prkacb	5.38±0.43
protein kinase, cAMP-dependent, catalytic, alpha	Prkaca	2.59±0.16
protein kinase, cAMP-dependent, catalytic, alpha /// similar to CG2662-PA (predicted)	Prkaca /// RGD130509	1.55±0.12
protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	0.3±0.03
protein kinase, DNA activated, catalytic polypeptide (predicted)	Prkdc_predicted	0.88±0.5
protein kinase, interferon inducible double stranded RNA dependent activator	Prkra	5.88±0.71

Protein kinase, lysine deficient 1	Prkwnk1	5.33±0.8
protein kinase, X-linked	Prkx	2.78±0.17
protein O-fucosyltransferase 2 (predicted)	Pofut2_predicted	1.35±0.12
protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	Pomgnt1	2.02±0.22
protein phosphatase 1 (formerly 2C)-like (predicted)	Ppm1l_predicted	1.43±0.36
protein phosphatase 1, catalytic subunit, alpha isoform	Ppp1ca	16.25±1.35
protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	15.11±3.85
protein phosphatase 1, catalytic subunit, gamma isoform	Ppp1cc	20.36±0.69
protein phosphatase 1, regulatory (inhibitor) subunit 11	Ppp1r11	4.15±0.11
protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	1.1±0.86
Protein phosphatase 1, regulatory (inhibitor) subunit 12B (predicted)	Ppp1r12b_predicted	0.98±0.2
protein phosphatase 1, regulatory (inhibitor) subunit 12C	Ppp1r12c	0.49±0.19
protein phosphatase 1, regulatory (inhibitor) subunit 13B (predicted)	Ppp1r13b_predicted	1.03±0.36
protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	8.26±1.11
protein phosphatase 1, regulatory (inhibitor) subunit 15b (predicted)	Ppp1r15b_predicted	2.18±0.21
protein phosphatase 1, regulatory (inhibitor) subunit 16A (predicted)	Ppp1r16a_predicted	0.31±0.14
protein phosphatase 1, regulatory (inhibitor) subunit 1A	Ppp1r1a	24.42±3.25
protein phosphatase 1, regulatory (inhibitor) subunit 1B	Ppp1r1b	17.71±4.82
protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	9.38±1.11
protein phosphatase 1, regulatory (inhibitor) subunit 3B	Ppp1r3b	0.21±0.18
protein phosphatase 1, regulatory (inhibitor) subunit 7	Ppp1r7	1.6±0.01
protein phosphatase 1, regulatory (inhibitor) subunit 8 (predicted)	Ppp1r8_predicted	2.35±0.55
protein phosphatase 1, regulatory subunit 10	Ppp1r10	0.38±0.04
protein phosphatase 1, regulatory subunit 3D	Ppp1r3d	0.61±0.18
protein phosphatase 1, regulatory subunit 9B	Ppp1r9b	0.23±0.04
protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	1.24±0.16
protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	5.98±1.56
protein phosphatase 1D magnesium-dependent, delta isoform (predicted)	Ppm1d_predicted	2.27±0.24
protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	Ppm1g	3.73±0.12
protein phosphatase 1H (PP2C domain containing)	Ppm1h	0.87±0.03
protein phosphatase 1K (PP2C domain containing) (predicted)	Ppm1k_predicted	0.29±0.01
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Ppp2ca	13.35±0.32
protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Ppp2cb	15.89±1.2
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a	5.77±0.04
protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Ppp2r2a	2.97±0.26
protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Ppp2r2b	1.04±0.34
protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	Ppp2r3a	14.59±6.03
protein phosphatase 2, regulatory subunit B (B56), alpha isoform (predicted)	Ppp2r5a_predicted	18.21±3.13
protein phosphatase 2, regulatory subunit B (B56), beta isoform	Ppp2r5b	0.72±0.46
protein phosphatase 2, regulatory subunit B (B56), delta isoform	Ppp2r5d	1.53±0.39
protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (predicted)	Ppp2r5e_predicted	4.06±0.21
protein phosphatase 2, regulatory subunit B' gamma isoform	Ppp2r5c	0.82±0.41
protein phosphatase 2, regulatory subunit B, delta isoform	Ppp2r2d	4.41±0.71
protein phosphatase 2, regulatory subunit B'', gamma	Ppp2r3c	0.81±0.07
protein phosphatase 2A, regulatory subunit B (PR 53) (predicted)	Ppp2r4_predicted	3.14±0.76
protein phosphatase 2C, magnesium dependent, catalytic subunit	Ppm2c	0.63±0.31
protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	3.69±0.33
protein phosphatase 3, catalytic subunit, beta isoform	Ppp3cb	2.92±0.45
protein phosphatase 3, catalytic subunit, gamma isoform	Ppp3cc	1±0.21
protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	Ppp3r1	2.95±0.34
protein phosphatase 4, catalytic subunit	Ppp4c	1.29±0.29
protein phosphatase 4, regulatory subunit 1	Ppp4r1	2.16±0.22
protein phosphatase 4, regulatory subunit 1-like	Ppp4r1l	0.39±0.26
protein phosphatase 4, regulatory subunit 2 (predicted)	Ppp4r2_predicted	6.69±0.15
protein phosphatase 5, catalytic subunit	Ppp5c	1.65±0.13
protein phosphatase 6, catalytic subunit	Ppp6c	2.12±0.15
protein phosphatase methylesterase 1	Ppme1	3.04±0.56
protein regulator of cytokinesis 1 (predicted)	Prc1_predicted	1.53±0.1
protein serine kinase H1 (predicted)	Pskh1_predicted	1.05±0.04
protein tyrosine kinase 2 beta	Ptk2b	0.22±0.02
protein tyrosine phosphatase 4a1	Ptp4a1	5.46±2.16
protein tyrosine phosphatase 4a2	Ptp4a2	9.94±0.42
protein tyrosine phosphatase, mitochondrial 1	Ptpmt1	10.31±2.3
protein tyrosine phosphatase, non-receptor type 1	Ptpn1	0.62±0.25
Protein tyrosine phosphatase, non-receptor type 11	Ptpn11	4.34±0.86
protein tyrosine phosphatase, non-receptor type 12	Ptpn12	4.31±0.41
protein tyrosine phosphatase, non-receptor type 13	Ptpn13	2.96±0.06
Protein tyrosine phosphatase, non-receptor type 14 (predicted)	Ptpn14_predicted	0.98±1.15
protein tyrosine phosphatase, non-receptor type 18	Ptpn18	13.74±2.88
protein tyrosine phosphatase, non-receptor type 2	Ptpn2	1.99±0.46
protein tyrosine phosphatase, non-receptor type 21	Ptpn21	0.55±0.11
protein tyrosine phosphatase, non-receptor type 23	Ptpn23	0.82±0.46
protein tyrosine phosphatase, non-receptor type 3	Ptpn3	3.18±1.16
protein tyrosine phosphatase, non-receptor type 6	Ptpn6	0.36±0.03
protein tyrosine phosphatase, receptor type, A	Ptpra	1.47±0.11
protein tyrosine phosphatase, receptor type, F	Ptprf	2.77±2.56
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1 (predicted)	Ppfia1_predicted	0.93±0.51
protein tyrosine phosphatase, receptor type, J	Ptprj	1.06±0.38
protein tyrosine phosphatase, receptor type, K, extracellular region	Ptprk	1.67±0.72
Protein tyrosine phosphatase, receptor type, M	Ptprm	1.37±0.55
protein tyrosine phosphatase, receptor type, R	Ptprr	5.88±0.9
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b (predicted)	LOC690040 /// Ptplb_p	2.28±0.24
protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) (predicted)	Prkrir_predicted	1.4±0.04
protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	1.77±0.56
protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)	Pcmtd2_predicted	7.45±1.17
protein-O-mannosyltransferase 1	Pomt1	0.68±0.23
protein-O-mannosyltransferase 2	Pomt2	3.43±0.75

proteolipid protein (myelin) 1	Plp1	0.34±0.01
proteolipid protein 2	Plp2	3.3±2.04
prothymosin alpha	Ptma	19.5±1.45
Protocadherin 1 (cadherin-like 1) (predicted)	Pcdh1_predicted	1.02±0.45
protocadherin 19 (predicted)	Pcdh19_predicted	0.87±0.2
protocadherin 3	Pcdh3	0.42±0.11
protocadherin alpha 4	Pcdha1 /// Pcdha10 ///	0.38±0.05
protocadherin beta 13	Pcdhb13	0.26±0
protocadherin gamma subfamily C, 3	Pcdhga1 /// Pcdhga10	1.67±0.15
protoporphyrinogen oxidase (predicted)	Ppox_predicted	0.89±0.12
proviral integration site 3	Pim3	12.68±2.88
PRP18 pre-mRNA processing factor 18 homolog (yeast)	Prpf18	1.88±0.24
PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	2.39±0.09
PRP3 pre-mRNA processing factor 3 homolog (yeast) (predicted)	Prpf3_predicted	1.62±0.06
PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (predicted)	Prpf38a_predicted	1.03±0.39
PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	Prpf38b	0.45±0.01
PRP39 pre-mRNA processing factor 39 homolog (yeast) (predicted)	Prpf39_predicted	2.66±0.14
PRP4 pre-mRNA processing factor 4 homolog (yeast)	Prpf4	1.09±0.23
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	2.71±0.77
PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	Prpf40a	0.63±0.11
PRP6 pre-mRNA splicing factor 6 homolog (S. cerevisiae)	Prpf6	1.8±0.19
pseudouridine synthase 1	Pus1	1.41±0.46
PTC7 protein phosphatase homolog (S. cerevisiae)	Pptc7	4.11±0.49
PTEN induced putative kinase 1 (predicted)	Pink1_predicted	10.4±0.25
pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	8.41±0.19
PTK2 protein tyrosine kinase 2	Ptk2	1.69±0.28
PTK7 protein tyrosine kinase 7 (predicted)	Ptk7_predicted	0.93±0.62
PTPRF interacting protein, binding protein 1 (liprin beta 1) (predicted)	Ppfibp1_predicted	8.07±0.43
Pumilio 1 (Drosophila) (predicted)	Pum1_predicted	3.2±0.89
pumilio 2 (Drosophila)	Pum2	7.43±1.55
purine rich element binding protein A (predicted)	Pura_predicted	6.35±0.85
purine rich element binding protein B	Purb	1.37±0.36
purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	1.04±0.07
purinergic receptor P2X, ligand-gated ion channel, 3	P2rx3	0.22±0.12
purine-rich element binding protein G (predicted)	Purg_predicted	1.46±0.02
putative GTP-binding protein	LOC293589	2.44±0.03
putative homeodomain transcription factor 1	Phtf1	1.82±0.02
putative homeodomain transcription factor 2 (predicted)	Phtf2_predicted	1.3±0.19
putative nucleic acid binding protein RY-1	Ry1	7.38±0.18
putative scaffolding protein POSH	Sh3md2	0.39±0.05
putative small membrane protein NID67	Nid67	1.06±1.07
putative UA20 protein	Ua20	8.73±1.17
PWWP domain containing 2 (predicted)	Pwwp2_predicted	0.64±0.41
PX domain containing serine/threonine kinase	Pxk	3.7±0.51
pygopus 2	Pygo2	0.82±0.27
pyridoxine 5'-phosphate oxidase	Pnpo	3.28±0.33
pyroglutamyl-peptidase I	Pgpep1	5.35±1.48
pyrophosphatase (inorganic) 1	Ppa1	2.48±0.85
pyrophosphatase (inorganic) 2 (predicted)	Ppa2_predicted	6.46±0.89
pyrroline-5-carboxylate reductase family, member 2	Pycr2	0.9±0.5
pyrroline-5-carboxylate reductase-like	Pycrl	4.16±0.25
pyruvate carboxylase	Pcx	0.68±0.02
pyruvate dehydrogenase (lipoamide) beta	Pdhb	18.78±3.09
pyruvate dehydrogenase complex, component X	Pdhx	2.65±0.8
pyruvate dehydrogenase E1 alpha 1	Pdha1	29.38±1.16
pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	0.38±0.04
pyruvate dehydrogenase kinase, isoenzyme 2	Pdk2	10.77±1.2
pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	2.57±0.77
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	1.1±1.07
pyruvate dehydrogenase phosphatase isoenzyme 2	Pdp2	1.18±0.12
pyruvate kinase, muscle	Pkm2	16.41±3.48
quaking	Qk	5.51±0.77
quaking homolog, KH domain RNA binding (mouse) /// quaking	Qk /// Qki	2.61±0.06
quiescin Q6 sulfhydryl oxidase 2	Qsox2	0.67±0.08
quinoid dihydropteridine reductase	Qdpr	2.42±1.34
R3H domain 1 (binds single-stranded nucleic acids)	R3hdm1	2.92±0.03
R3H domain and coiled-coil containing 1 (predicted)	R3hcc1_predicted	1.94±0.23
R3H domain containing 2	R3hdm2	0.37±0.13
Rab acceptor 1 (prenylated)	Rabac1	11.6±1.77
Rab geranylgeranyl transferase, a subunit	Rabggta	0.66±0.06
RAB geranylgeranyl transferase, b subunit	Rabggtb	8.28±2.75
RAB GTPase activating protein 1	Rabgap1	2.02±0.39
RAB GTPase activating protein 1-like	Rabgap1l	0.47±0.07
RAB guanine nucleotide exchange factor (GEF) 1 (predicted)	Rabgef1_predicted	0.59±0.37
RAB interacting factor	Rabif	0.91±0.17
Rab interacting lysosomal protein-like 2	Rilpl2	3.13±0.08
RAB, member of RAS oncogene family-like 2A	Rabl2a	3.19±1.39
RAB, member of RAS oncogene family-like 3 (predicted)	Rabl3_predicted	0.47±0.04
RAB, member of RAS oncogene family-like 4 (predicted)	Rabl4_predicted	0.73±0.48
RAB, member of RAS oncogene family-like 5	Rabl5	0.36±0.02
RAB1, member RAS oncogene family	Rab1	22.82±4.98
RAB10, member RAS oncogene family	Rab10	8.63±1.22
RAB11 family interacting protein 4 (class II) (predicted)	Rab11fip4_predicted	2.42±0.29
RAB11a, member RAS oncogene family	Rab11a	5.67±1.26
RAB11B, member RAS oncogene family	Rab11b	8.85±0.21
RAB12, member RAS oncogene family	Rab12	6.63±0.37
RAB13, member RAS oncogene family	Rab13	0.9±0.18

RAB14, member RAS oncogene family	Rab14	6.03±0.55
RAB17, member RAS oncogene family	Rab17	6.33±1.95
RAB18, member RAS oncogene family	Rab18	2.79±0.28
RAB2, member RAS oncogene family	Rab2	18.72±1.15
RAB20, member RAS oncogene family	Rab20	0.75±1.06
RAB21, member RAS oncogene family	Rab21	3.45±1.47
RAB22A, member RAS oncogene family (predicted)	Rab22a_predicted	1.85±0.06
RAB23, member RAS oncogene family (predicted)	Rab23_predicted	1.38±0.24
RAB24, member RAS oncogene family	Rab24	1.39±0.36
RAB25, member RAS oncogene family (predicted)	Rab25_predicted	2.42±0.44
RAB26, member RAS oncogene family	Rab26	0.58±0.13
RAB28, member RAS oncogene family	Rab28	8.34±0.27
RAB2B, member RAS oncogene family	Rab2b	1.89±0.02
RAB3 GTPase activating protein subunit 2	Rab3gap2	1.42±0.12
RAB31, member RAS oncogene family	Rab31	0.51±0.29
RAB32, member RAS oncogene family	Rab32	0.98±0.17
RAB33B, member of RAS oncogene family (predicted)	Rab33b_predicted	0.97±0.65
RAB34, member of RAS oncogene family	Rab34	2.66±0.38
RAB35, member RAS oncogene family	Rab35	2.57±0.15
RAB3A interacting protein	Rab3ip	2.82±0.03
RAB3A, member RAS oncogene family	Rab3a	0.63±0.16
RAB3D, member RAS oncogene family	Rab3d	0.6±0.48
Rab40b, member RAS oncogene family (predicted)	Rab40b_predicted	0.57±0.28
Rab40c, member RAS oncogene family	Rab40c	1.04±0.29
RAB4A, member RAS oncogene family	Rab4a	2.59±0.03
RAB4B, member RAS oncogene family	Rab4b	1.1±0.05
RAB5A, member RAS oncogene family	Rab5a	7.06±2.23
RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted	7.35±0.98
RAB5C, member RAS oncogene family (predicted)	Rab5c_predicted	2.94±0.66
RAB6A, member RAS oncogene family	Rab6a	5.95±0.35
RAB7, member RAS oncogene family	Rab7	11.16±2.49
RAB7, member RAS oncogene family-like 1	Rab7l1	3.54±2.93
RAB8A, member RAS oncogene family	Rab8a	4.14±0.56
RAB8B, member RAS oncogene family	Rab8b	0.43±0.22
Rab9 effector protein with kelch motifs	Rabepk	1.09±0.1
RAB9, member RAS oncogene family	Rab9	5.82±3.26
rabaptin, RAB GTPase binding effector protein 1	Rabep1	0.89±0.12
rabaptin, RAB GTPase binding effector protein 2	Rabep2	0.38±0
Rac GTPase-activating protein 1 (predicted)	Racgap1_predicted	0.46±0
RAD1 homolog (S. pombe) (predicted)	Rad1_predicted	0.54±0.19
RAD17 homolog (S. pombe)	Rad17	1.21±0.26
RAD21 homolog (S. pombe)	Rad21	12.67±0.46
RAD23a homolog (S. cerevisiae)	Rad23a	0.66±0.36
RAD23b homolog (S. cerevisiae)	Rad23b	5.62±0.6
RAD50 homolog (S. cerevisiae)	Rad50	1.25±0.21
RAD51 homolog (S. cerevisiae)	Rad51	0.77±0.17
Rad51 homolog c (S. cerevisiae)	Rad51c	0.78±0.19
RAD52 homolog (S. cerevisiae) (predicted)	Rad52_predicted	0.26±0.24
RAD52 motif 1 (predicted)	Rdm1_predicted	0.88±0.11
radial spoke head 1 homolog (Chlamydomonas)	Rsph1	0.67±0.14
radical fringe gene homolog (Drosophila)	Rfng	1.8±0.2
radixin	Rdx	4.27±0.79
RAE1 RNA export 1 homolog (S. pombe)	Rae1	1.21±0.33
ralA binding protein 1	Ralbp1	3.37±0.58
RalBP1 associated Eps domain containing protein (predicted)	Reps1_predicted	1.12±0.25
RAN binding protein 10 (predicted)	Ranbp10_predicted	1.25±0.23
RAN binding protein 2	Ranbp2	2.14±1.12
RAN binding protein 3	Ranbp3	2.02±0.16
RAN binding protein 5 (predicted)	Ranbp5_predicted	1.59±0.18
RAN binding protein 6 (predicted)	Ranbp6_predicted	1.18±0.15
RAN GTPase activating protein 1	Rangap1	1.19±0.3
RAN guanine nucleotide release factor	Rangrf	4.97±1.16
RAN, member RAS oncogene family	Ran	11.55±1.39
RanBP-type and C3HC4-type zinc finger containing 1	Rbck1	2.26±0.67
Rap guanine nucleotide exchange factor (GEF) 2 (predicted)	Rapgef2_predicted	1.41±1.35
Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	0.23±0.11
Rap guanine nucleotide exchange factor (GEF)-like 1	Rapgefl1	0.98±0.32
Rap1 GTPase-activating protein	Rap1gap	15.46±0.45
Rap1 interacting factor 1 homolog (yeast)	Rif1	0.59±0
RAP1, GTP-GDP dissociation stimulator 1 (predicted)	Rap1gds1_predicted	1.11±0.17
Rap2 interacting protein	Rap2ip	0.51±0.08
RAR-related orphan receptor alpha (predicted)	Rora_predicted	1.01±0.53
RAR-related orphan receptor C /// leucine rich repeat and Ig domain containing 4	Lingo4 /// Rorc	0.58±0.05
Ras and Rab interactor 2 (predicted)	Rin2_predicted	4.91±1.69
Ras association (RalGDS/AF-6) domain family 1	Rassf1	1.72±1.82
Ras association (RalGDS/AF-6) domain family 3 (predicted)	Rassf3_predicted	4.29±0.03
Ras association (RalGDS/AF-6) domain family 5	Rassf5	0.52±0.16
Ras association (RalGDS/AF-6) domain family 7 (predicted)	Rassf7_predicted	4.17±0.66
Ras association (RalGDS/AF-6) domain family member 6	Rassf6	5.92±0.48
RAS guanyl releasing protein 1	Rasgrp1	0.39±0.26
Ras homolog enriched in brain	Rheb	14.53±2.05
ras homolog gene family, member A	Rhoa	11.77±1.76
ras homolog gene family, member B	Rhob	11.35±5.67
ras homolog gene family, member D (predicted)	Rhod_predicted	4.96±0.5
Ras homolog gene family, member G	Rhog	1.31±0.02
ras homolog gene family, member Q	Rhoq	2.18±0.08
ras homolog gene family, member T2	Rhot2	2.34±0.67

RAS p21 protein activator 1	Rasa1	0.37±0.39
RAS related protein 1b	Rap1b	3.36±0.14
ras responsive element binding protein 1 (predicted)	Rreb1_predicted	1.82±0.56
RAS, dexamethasone-induced 1	Rasd1	1.82±1.08
RAS, guanyl releasing protein 2	Rasgrp2	0.53±0.04
Ras-GTPase-activating protein SH3-domain binding protein 1	G3bp1	3.41±0.28
Ras-like without CAAX 1 (predicted)	Rit1_predicted	0.23±0.1
Ras-related C3 botulinum toxin substrate 1	Rac1	7.92±0.37
Ras-related GTP binding A	Rraga	5.63±1.6
Ras-related GTP binding B	RragB	0.26±0.26
Ras-related GTP binding C (predicted)	Rragc_predicted	4.38±0.44
Ras-related GTP binding D (predicted)	Rragd_predicted	3.19±0.05
RAS-related protein 1a	Rap1a	4.92±0.65
RB1-inducible coiled-coil 1 (predicted)	Rb1cc1_predicted	3.1±0.22
RBSC-skeletrophin	LOC474147	0.6±0.01
rcd1 (required for cell differentiation) homolog 1 (S. pombe)	Rqcd1	0.49±0.09
RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	Rce1	1.98±0.02
rearranged L-myc fusion sequence (predicted)	Rlf_predicted	0.42±0.14
receptor (TNFRSF)-interacting serine-threonine kinase 1 (predicted)	Ripk1_predicted	1.48±0.22
receptor accessory protein 4	Reep4	1.19±0.3
receptor accessory protein 5 (predicted)	Reep5_predicted	5.63±1.04
receptor accessory protein 6	Reep6	0.69±0.24
receptor interacting protein kinase 5	Ripk5	1.16±0.2
receptor-associated protein of the synapse (predicted)	Rapsn_predicted	1.85±0.37
receptor-interacting serine-threonine kinase 4 (predicted)	Ripk4_predicted	2.76±0.04
receptor-like tyrosine kinase	Ryk	1.5±0.51
recombination activating gene 1 activating protein 1 (predicted)	Rag1ap1_predicted	2.64±0.06
recombining binding protein suppressor of hairless (Drosophila) (predicted)	LOC679028 /// Rbpsuh	0.66±0.02
RecQ protein-like	Recql	2.55±0.06
RecQ protein-like 5 (predicted)	Recql5_predicted	0.47±0.07
regulator of calcineurin 1	Rcan1	0.68±1.15
regulator of calcineurin 2	Rcan2	1.63±0.09
regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	Rcbtb1	0.48±0.17
regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	Rcbtb2	1.24±0.16
regulator of chromosome condensation 2 (predicted)	Rcc2_predicted	1.32±0.06
regulator of G-protein signaling 3	Rgs3	1.06±0.28
regulator of telomere elongation helicase 1	Rtel1	0.88±0.25
regulatory factor X domain containing 2 homolog (human)	Rfxdc2	2.02±0.14
regulatory factor X, 1 (influences HLA class II expression) (predicted)	Rfx1_predicted	1.33±0.16
regulatory factor X, 5 (influences HLA class II expression) (predicted)	Rfx5_predicted	0.67±0.07
regulatory factor X-associated protein	Rfxap	0.9±0.34
related RAS viral (r-ras) oncogene homolog 2	Rras2	6.64±0.58
remodeling and spacing factor 1	Rsf1	0.82±0.32
renal tumor antigen	Rage	1.08±0.29
replication factor C (activator 1) 1	Rfc1	0.85±0.08
replication factor C (activator 1) 2	Rfc2	0.92±0.13
replication factor C (activator 1) 3	Rfc3	0.69±0.02
replication factor C (activator 1) 4 (predicted)	Rfc4_predicted	1.25±0.19
replication factor C (activator 1) 5 (predicted)	Rfc5_predicted	0.23±0.06
Replication factor C 1	Recc1	0.9±0.03
Replication protein A1	Rpa1	7.54±0.99
replication protein A2	Rpa2	0.87±0.06
replication protein A3 (predicted)	Rpa3_predicted	2.04±0.3
required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Rmnd5a	5.34±0.27
RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	Rer1	6.14±0.01
resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	1.62±0.48
REST corepressor 1 (predicted)	Rcor1_predicted	1.23±0.36
reticulocalbin 2	Rcn2	1.96±0.55
reticulon 3	Rtn3	13.71±2.13
reticulon 4	Rtn4	10.46±5.86
reticulon 4 interacting protein 1	Rtn4ip1	2.22±0.03
reticulon 4 receptor	Rtn4r	0.58±0.18
reticulon 4 receptor-like 1	Rtn4rl1	1.6±0.37
retinitis pigmentosa 2 homolog (human) (predicted)	Rp2h_predicted	0.33±0.21
Retinitis pigmentosa 9 homolog (human) (predicted)	Rp9h_predicted	1.88±0.68
retinoblastoma 1	Rb1	2.28±0.74
retinoblastoma binding protein 4	Rbbp4	4.79±0.22
retinoblastoma binding protein 5 (predicted)	Rbbp5_predicted	1.12±0.07
retinoblastoma binding protein 6	Rbbp6	1.95±0.92
retinoblastoma binding protein 7	Rbbp7	11.2±1.91
retinoblastoma binding protein 9	Rbbp9	1.78±0.89
retinoblastoma-like 2	Rbl2	2.95±0.17
retinoic acid induced 1 (predicted)	Rai1_predicted	1.65±0.31
retinoic acid induced 12	Rai12	1.93±0.36
retinoic acid receptor, beta	Rarb	1.38±0.21
Retinoid X receptor alpha	Rxra	1.16±0.52
retinoid X receptor beta	Rxrb	0.87±0.01
Retinol dehydrogenase 10 (all-trans)	Rdh10	0.35±0.03
retinol dehydrogenase 11	Rdh11	1.68±0.36
Retinol dehydrogenase 13 (all-trans and 9-cis) (predicted)	Rdh13_predicted	2.34±0.61
retinol saturase (all trans retinol 13,14 reductase)	Retsat	7.13±0.7
REV1 homolog (S. cerevisiae)	Rev1	1.01±0.7
REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	1.89±0.1
reversion-inducing-cysteine-rich protein with kazal motifs (predicted)	Reck_predicted	0.29±1.56
REX1, RNA exonuclease 1 homolog (S. cerevisiae)	Rexo1	0.23±0.15
REX2, RNA exonuclease 2 homolog (S. cerevisiae)	Rexo2	4.13±1.13
REX4, RNA exonuclease 4 homolog (S. cerevisiae)	Rexo4	1.74±0.13

RFT1 homolog (S. cerevisiae) (predicted)	Rft1_predicted	1.82±0.42
RGD1559909 (predicted)	RGD1559909_predicte	1.57±0.25
RGD1560398 (predicted)	RGD1560398_predicte	1.69±0.54
RGD1560566 (predicted)	RGD1560566_predicte	1.94±0.18
RGD1561796 (predicted)	RGD1561796_predicte	0.64±0.08
RGD1561797 (predicted)	RGD1561797_predicte	0.93±0.25
RGD1562012 (predicted)	RGD1562012_predicte	2.03±0.48
RGD1562114 (predicted)	RGD1562114_predicte	1.31±0.51
RGD1562339 (predicted)	RGD1562339_predicte	0.42±0
RGD1563547 (predicted)	RGD1563547_predicte	6.99±0.35
RGD1563912 (predicted)	RGD1563912_predicte	6.34±0.49
RGD1564379 (predicted)	RGD1564379_predicte	2.61±0.12
RGD1564450 (predicted)	RGD1564450_predicte	0.55±0.15
RGD1564491 (predicted)	RGD1564491_predicte	0.24±0.05
RGD1564792 (predicted)	RGD1564792_predicte	0.66±0.08
RGD1564859 (predicted)	RGD1564859_predicte	3.58±1.26
RGD1564982 (predicted)	RGD1564982_predicte	1.38±0.5
RGD1565210 (predicted)	RGD1565210_predicte	2.47±1.08
RGD1565616 (predicted)	RGD1565616_predicte	2.82±0.42
RGD1565641 (predicted)	RGD1565641_predicte	2.97±1.47
RGD1565784 (predicted)	RGD1565784_predicte	1.57±0.44
RGD1566118 (predicted)	RGD1566118_predicte	1.75±1.17
RGD1566320 (predicted)	RGD1566320_predicte	2.08±0.61
RGM domain family, member A (predicted)	Rgma_predicted	0.53±0.08
Rho family GTPase 3	Rnd3	0.23±0.79
Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	5.89±0.89
Rho GTPase activating protein 10	Arhgap10	1.21±0.09
Rho GTPase activating protein 11A	Arhgap11a	1.05±0.24
Rho GTPase activating protein 12 (predicted)	Arhgap12_predicted	0.95±0.52
Rho GTPase activating protein 17	Arhgap17	0.89±1.15
Rho GTPase activating protein 18 (predicted)	Arhgap18_predicted	3.03±0.46
Rho GTPase activating protein 21 (predicted)	Arhgap21_predicted	1.13±0.6
Rho GTPase activating protein 22 (predicted)	Arhgap22_predicted	3.18±0.99
Rho GTPase activating protein 24	Arhgap24	24.21±10.8
Rho GTPase activating protein 27	Arhgap27	0.76±0.1
Rho GTPase activating protein 5	Arhgap5	2.61±0.11
Rho GTPase activating protein 8	Arhgap8	0.28±0.17
Rho GTPase-activating protein	Grit	0.93±0.11
Rho guanine nucleotide exchange factor (GEF) 1	Arhgef1	1.62±0.04
Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	0.58±0.42
Rho guanine nucleotide exchange factor (GEF) 17 (predicted)	Arhgef17_predicted	0.88±0.31
Rho guanine nucleotide exchange factor (GEF) 19 (predicted)	Arhgef19_predicted	0.76±0.08
Rho guanine nucleotide exchange factor (GEF) 3 (predicted)	Arhgef3_predicted	1.68±0.18
Rho guanine nucleotide exchange factor (GEF) 5	Arhgef5	0.74±0.1
Rho guanine nucleotide exchange factor 7	Arhgef7	1.52±0.46
rho/rac guanine nucleotide exchange factor (GEF) 18 (predicted)	Arhgef18_predicted	7.53±1.35
rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	1.45±0.03
Rho-associated coiled-coil forming kinase 2	Rock2	0.26±0.16
Rho-guanine nucleotide exchange factor (predicted)	Rgnef_predicted	1.98±0.72
rhomboid 5 homolog 2 (Drosophila)	Rhbdf2	0.4±0.1
rhomboid domain containing 2	Rhbdd2	1.36±0.38
rhomboid domain containing 3	Rhbdd3	0.41±0.11
rhomboid family 1 (Drosophila)	Rhbdf1	0.55±0.71
rhophilin, Rho GTPase binding protein 2 (predicted)	Rhpn2_predicted	1.44±0
rhotekin	Rtkn	1.63±0.03
riboflavin kinase /// similar to riboflavin kinase (predicted)	Rfk /// RGD1563242_pr	8.48±1.94
ribokinase (predicted)	Rbks_predicted	0.91±0.11
ribonuclease H1	Rnaseh1	0.52±0.23
ribonuclease H2, large subunit	Rnaseh2a	5.12±0.75
ribonuclease H2, subunit B	Rnaseh2b	0.82±0.05
ribonuclease III, nuclear	Rnasen	1.86±0.32
Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	Rnasel	1.19±0.08
ribonuclease P 14 subunit (human)	Rpp14	2.58±0.36
ribonuclease P 21 subunit (human) /// RT1 class I, M10, gene 1	Rpp21 /// RT1-M10-1	2.9±0.69
ribonuclease P 40 subunit (human)	Rpp40	0.5±0.14
ribonuclease P/MRP 30 /// similar to Ribonuclease P protein subunit p30 (RNaseP protein p30) (RNase P subunit 2)	LOC687772 /// Rpp30	0.25±0.04
ribonuclease T2 (predicted)	Rnaset2_predicted	9.06±0.95
ribonuclease, RNase K	Rnasek	10.92±1.03
ribonuclease/angiogenin inhibitor 1	Rnh1	4.46±0.15
ribonucleic acid binding protein S1	Rnps1	3.93±0.02
ribonucleoprotein, PTB-binding 1	Raver1	1.2±0.04
ribonucleoprotein, PTB-binding 2	Raver2	0.93±0.19
ribonucleotide reductase M1	Rrm1	3.16±0.96
ribonucleotide reductase M2	Rrm2	2.73±0.07
ribophorin I	Rpn1	9.23±0.51
ribophorin II	Rpn2	7.99±1.01
ribose 5-phosphate isomerase A (predicted)	Rpia_predicted	2.32±1.09
ribose-phosphate pyrophosphokinase I -like	LOC314140	1.68±0.71
ribosomal L1 domain containing 1	Rsl1d1	1.89±0.65
ribosomal protein L10	Rpl10	22.36±4.39
ribosomal protein L10A	Rpl10a	18.11±0.99
ribosomal protein L11	Rpl11	34.11±1.95
ribosomal protein L12 (predicted) /// similar to 60S ribosomal protein L12 /// similar to similar to 60S ribosomal protein L12	LOC499782 /// LOC685	24.98±2.87
ribosomal protein L13	Rpl13	18.04±1.91
ribosomal protein L13A	Rpl13a	14.81±3.87
ribosomal protein L14	Rpl14	15.01±0.24
ribosomal protein L15	Rpl15	14.63±3.25

ribosomal protein L17	Rpl17	33.48±6.7
ribosomal protein L18	Rpl18	26.34±0.78
ribosomal protein L18A	Rpl18a	27.23±3.45
ribosomal protein L19	Rpl19	28.05±9.71
ribosomal protein L21 /// similar to ribosomal protein L21	LOC679852 /// LOC69	15.3±0.81
ribosomal protein L22	Rpl22	23.41±2.07
ribosomal protein L22 like 1 (predicted)	Rpl22l1_predicted	15.9±2.03
ribosomal protein L23	Rpl23	27.11±2.82
ribosomal protein L23a	Rpl23a	27.29±0
ribosomal protein L24	Rpl24	19.14±0.17
ribosomal protein L26	Rpl26	42.11±0.55
ribosomal protein L27	Rpl27	28.25±0.56
ribosomal protein L27a (predicted)	Rpl27a_predicted	34±1.24
ribosomal protein L28	Rpl28	30.18±2.5
ribosomal protein L29	Rpl29	21.69±0.22
ribosomal protein L3	Rpl3	39.44±4.89
ribosomal protein L3 /// similar to 60S ribosomal protein L3 (L4)	LOC499207 /// Rpl3	0.47±1.37
ribosomal protein L30	Rpl30	25.61±1.19
ribosomal protein L31	Rpl31	34.79±1.02
ribosomal protein L32	Rpl32	40.55±0.26
ribosomal protein L34 (predicted)	Rpl34_predicted	26.91±0.93
ribosomal protein L35	Rpl35	20.27±1.11
ribosomal protein L35a	Rpl35a	30.17±2.33
ribosomal protein L36	LOC364105 /// RGD15	1.9±0.21
ribosomal protein L37	Rpl37	30.7±0.31
ribosomal protein L37a /// similar to 60S ribosomal protein L37a	LOC679823 /// LOC68	32.56±2.35
ribosomal protein L39	Rpl39	0.39±0.09
ribosomal protein L4	Rpl4	15.97±0.44
ribosomal protein L41	Rpl41	29.4±1.22
ribosomal protein L5	Rpl5	26.49±4.8
ribosomal protein L6 /// similar to 60S ribosomal protein L6 (Neoplasm-related protein C140) (predicted)	RGD1563476_predicte	25.37±0.87
ribosomal protein L7	Rpl7	25.03±3.93
ribosomal protein L7a (predicted)	Rpl7a_predicted	53.11±2.86
ribosomal protein L7-like 1	Rpl7l1	3.01±0.26
ribosomal protein L8	Rpl8	18.56±0.25
ribosomal protein L8 /// similar to 60S ribosomal protein L8 /// similar to 60S ribosomal protein L8 (predicted)	LOC365370 /// RGD15	1.97±0.67
ribosomal protein L9 /// EH-domain containing 2	Ehd2 /// Rpl9	38.28±3
ribosomal protein S10	Rps10	19.31±0.53
ribosomal protein S11	Rps11	18.85±0.9
ribosomal protein S12	Rps12	43.36±0.22
ribosomal protein S13 /// similar to ribosomal protein S13	LOC684988 /// Rps13	24.81±1.29
ribosomal protein S14	Rps14	36.26±4.37
ribosomal protein S15	Rps15	22.24±0.77
ribosomal protein S15a	Rps15a	24.32±4.89
ribosomal protein S16	Rps16	30.87±1.54
ribosomal protein S17	Rps17	43.58±2.49
ribosomal protein S18	Rps18	32.39±2.5
ribosomal protein S19	Rps19	24.23±4.18
ribosomal protein S2	Rps2	34.72±0.23
ribosomal protein S2 /// similar to ribosomal protein S2 (predicted) /// similar to 40S ribosomal protein S2	LOC688473 /// RGD15	39.24±4.52
ribosomal protein S20	Rps20	23.73±0.78
ribosomal protein S21	Rps21	29.71±2.34
ribosomal protein S23	Rps23	41.09±4.36
ribosomal protein S24	Rps24	33.64±0.34
ribosomal protein s25	Rps25	8.73±1.06
ribosomal protein S26	Rps26	18.5±2.18
ribosomal protein S27	Rps27	34.06±0.53
ribosomal protein S27a	Rps27a	22.26±1.69
ribosomal protein S28 /// similar to 40S ribosomal protein S28	LOC684733 /// Rps28	20.62±0.15
ribosomal protein S29	Rps29	56.01±1.55
ribosomal protein S3	Rps3	21.36±3.28
ribosomal protein S3a	Rps3a	39.56±0.79
ribosomal protein S4, X-linked	Rps4x	52.16±14.34
ribosomal protein S4, Y-linked 2	Rps4y2	0.73±0.11
ribosomal protein S5	Rps5	20.34±0.17
ribosomal protein S6	Rps6	21.67±0.39
ribosomal protein S6 kinase polypeptide 1	Rps6ka1	0.3±0.01
ribosomal protein S6 kinase polypeptide 6 (predicted)	Rps6ka6_predicted	0.97±0.57
ribosomal protein S6 kinase, 70kDa, polypeptide 1	Rps6kb1	0.85±0.36
ribosomal protein S6 kinase, polypeptide 1	Rps6kc1	0.23±0.01
ribosomal protein S6 kinase, polypeptide 4	Rps6ka4	1.33±0.5
ribosomal protein S6 kinase, polypeptide 5 (predicted)	Rps6ka5_predicted	0.21±0.04
ribosomal protein S7 /// similar to ribosomal protein S7	LOC497813 /// Rps7	19.18±0.41
ribosomal protein S8	Rps8	30.88±0.85
ribosomal protein S9	Rps9	25.98±1.35
ribosomal protein SA	Rpsa	24.18±0.73
ribosomal protein SA	LOC367035 /// LOC68	4.98±2.15
ribosomal protein, large P2 /// hypothetical gene supported by X15098 /// similar to 60S acidic ribosomal protein P2	LOC363929 /// LOC49	26.58±1.4
ribosomal protein, large, P1	Rplp1	37.69±5.32
ribosomal RNA processing 1 homolog (S. cerevisiae)	Rrp1	0.88±0.17
ribosomal RNA processing 1 homolog B (S. cerevisiae)	Rrp1b	0.71±0.16
ribosomal RNA processing 15 homolog (S. cerevisiae)	Rrp15	1.15±0.58
ribosome binding protein 1	Rrbp1	0.42±0.07
ribulose-5-phosphate-3-epimerase	Rpe	1.23±0.56
ring finger (C3HC4 type) and KH domain containing 1 (predicted)	Rkhd1_predicted	0.58±0.16
ring finger 111	Rnf111	1.12±0.2
ring finger and CHY zinc finger domain containing 1	Rchy1	9.87±2.46

ring finger and KH domain containing 2 (predicted)	Rkhd2_predicted	3.1±0.75
ring finger and WD repeat domain 3 /// similar to mixed lineage kinase domain-like	LOC690743 /// Rfwd3	0.52±0.14
ring finger protein (C3H2C3 type) 6 (predicted)	Rnf6_predicted	1.18±0.05
ring finger protein 1	Ring1	0.98±0.49
ring finger protein 10	Rnf10	6.01±0.55
ring finger protein 103	Rnf103	2.83±0.32
ring finger protein 11 (predicted)	Rnf11_predicted	0.34±0.05
ring finger protein 11 (predicted) /// similar to RING finger protein 11 (NEDD4 WW domain-binding protein 2) (Sid 1669)	LOC683844 /// Rnf11_	5.78±0.21
ring finger protein 113A2	Rnf113a2	0.95±0.37
ring finger protein 121 (predicted)	Rnf121_predicted	0.47±0.02
ring finger protein 126	Rnf126	0.64±0.15
ring finger protein 128 /// hypothetical protein LOC680663	LOC680663 /// Rnf128	8.71±1.4
ring finger protein 135 /// ras homolog gene family, member T1 (predicted)	Rhot1_predicted /// Rnf	3.17±0.32
ring finger protein 138	Rnf138	1.34±0.02
ring finger protein 139 (predicted)	Rnf139_predicted	3.21±1.24
ring finger protein 14	Rnf14	7.32±0.07
ring finger protein 141	rnf141	0.27±0.23
ring finger protein 145	Rnf145	1.74±0.69
ring finger protein 146	Rnf146	4.45±0.5
ring finger protein 149	Rnf149	3.66±0.57
ring finger protein 150	Rnf150	0.71±0.18
ring finger protein 152 (predicted)	Rnf152_predicted	0.49±0.1
ring finger protein 166	Rnf166	1.17±0.03
ring finger protein 167	Rnf167	3.47±0.43
ring finger protein 181	Rnf181	2.08±0.1
ring finger protein 185	Rnf185	0.73±0.19
ring finger protein 187 (predicted)	Rnf187_predicted	3.97±0.9
ring finger protein 19A	Rnf19a	6.07±0.9
ring finger protein 2	Rnf2	0.88±0.2
ring finger protein 20 (predicted)	Rnf20_predicted	0.84±0.09
ring finger protein 207	Rnf207	0.65±0.1
ring finger protein 208	Rnf208	2.19±0.57
ring finger protein 215	Rnf215	1.91±0.48
ring finger protein 216	Rnf216	2.01±0.14
ring finger protein 217	Rnf217	0.48±0.16
ring finger protein 219	Rnf219	0.44±0.09
ring finger protein 25	Rnf25	0.94±0.04
ring finger protein 26 (predicted)	Rnf26_predicted	3.19±0.26
ring finger protein 31 (predicted)	Rnf31_predicted	0.9±0.02
ring finger protein 34	Rnf34	2.46±0.04
ring finger protein 4	Rnf4	1.96±0.29
ring finger protein 41	Rnf41	0.74±0.01
Ring finger protein 44	Rnf44	3±0.31
ring finger protein 7 (predicted)	Rnf7_predicted	4.61±0.4
ring finger protein 8	Rnf8	0.68±0.02
RING1 and YY1 binding protein (predicted)	Rybp_predicted	8.79±1.04
ring-box 1	Rbx1	5.11±1.35
RIO kinase 1 (yeast)	Riok1	0.37±0.11
RIO kinase 2 (yeast)	Riok2	0.36±0.16
RIO kinase 3 (yeast) (predicted)	Riok3_predicted	2.91±0.19
RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	Rmi1	1.53±0.64
RNA (guanine-7-) methyltransferase	Rnmt	0.79±0.09
RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1	1.01±0.36
RNA (guanine-9-) methyltransferase domain containing 3	Rg9mtd3	0.89±0.5
RNA binding motif protein 10	Rbm10	1.44±0.12
RNA binding motif protein 12	Rbm12	0.59±0
RNA binding motif protein 12B	Rbm12b	1.17±0.77
RNA binding motif protein 13	Rbm13	0.5±0.08
RNA binding motif protein 15B (predicted)	Rbm15b_predicted	0.24±0.07
RNA binding motif protein 16	Rbm16	2.65±0.06
RNA binding motif protein 17	Rbm17	4.07±1.12
RNA binding motif protein 18 (predicted)	Rbm18_predicted	2.92±0.14
RNA binding motif protein 19 (predicted)	Rbm19_predicted	0.4±0.06
RNA binding motif protein 20 (predicted)	Rbm20_predicted	0.66±0.1
RNA binding motif protein 22	Rbm22	1.14±0.01
RNA binding motif protein 25 (predicted)	Rbm25_predicted	1.78±0
RNA binding motif protein 25 (predicted) /// similar to RNA binding motif protein 25 (predicted)	Rbm25_predicted /// R	1.92±0.53
RNA binding motif protein 27 (predicted)	Rbm27_predicted	0.99±0.12
RNA binding motif protein 3	Rbm3	1.47±0.3
RNA binding motif protein 34	Rbm34	0.82±0.22
RNA binding motif protein 38	Rbm38	0.33±0.06
RNA binding motif protein 39	Rbm39	10.06±1.54
RNA binding motif protein 42	Rbm42	4.11±0.76
RNA binding motif protein 45	Rbm45	3.9±0.66
RNA binding motif protein 4B	Rbm4b	3.92±0.15
RNA binding motif protein 5	Rbm5	5.8±0.75
RNA binding motif protein 6	Rbm6	0.72±0.24
RNA binding motif protein 8 (predicted)	Rbm8_predicted	4.9±0.34
RNA binding motif protein 9 (predicted)	Rbm9_predicted	0.33±0.07
RNA binding motif protein, X chromosome	Rbmx	1.65±0.3
RNA binding motif protein, X chromosome retrogene (predicted)	Rbmxrt_predicted	1.94±0.03
RNA binding motif, single stranded interacting protein 1	Rbms1	0.36±1.4
RNA binding motif, single stranded interacting protein 2	Rbms2	1.07±0.17
RNA guanylyltransferase and 5'-phosphatase (predicted)	Rngtt_predicted	0.59±0
RNA polymerase 1-1	Rpo1-1	4.98±1.1
RNA polymerase II associated protein 2	Rpap2	0.85±0.23
RNA polymerase II associated protein 3	Rpap3	2.06±0.17

RNA pseudouridylate synthase domain containing 4	Rpusd4	0.65±0.17
RNA terminal phosphate cyclase domain 1	Rtcd1	6.26±1.37
RNA terminal phosphate cyclase-like 1	Rcl1	0.66±0.07
RNA U, small nuclear RNA export adaptor	Rnuxa	2.45±0.36
rogdi homolog (Drosophila)	Rogdi	3.23±0.91
rosbin, round spermatid basic protein 1 (predicted)	Rsbn1_predicted	1.41±0.09
round spermatid basic protein 1-like (predicted)	Rsbn1l_predicted	0.3±0.09
Rous sarcoma oncogene	Src	0.7±0.11
RPE-spondin	Rpesp	9.31±1.2
RRN3 RNA polymerase I transcription factor homolog (yeast)	Rrn3	0.21±0.3
rRNA promoter binding protein	LOC257642	9.55±4.56
RRP9, small subunit (SSU) processome component, homolog (yeast)	Rrp9	0.64±0.03
RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (predicted)	Rrs1_predicted	1.01±0.13
RT1 class I, CE12	RT1-CE12	0.72±0.96
RT1 class Ib gene, H2-TL-like, grc region (N3)	Dhx16 /// Ier3 /// Mrps1	2.38±0.82
RT1 class Ib, locus Aw2	RT1-Aw2	1.16±8.53
RT1 class Ib, locus Aw2	Atp6v1g2 /// B3galt4 ///	6.34±0.87
RT1 class Ib, locus Aw2	Atp6v1g2 / B3galt4 / C	1.23±3.3
RT1 class II, locus Ba	RT1-Ba	5.14±2.67
RT1 class II, locus Db1	RT1-Db1	0.92±0.82
Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (predicted)	Rtf1_predicted	0.82±0.25
RUN and FYVE domain containing 1	Rufy1	3.18±1.2
RUN domain containing 1 (predicted)	Rundc1_predicted	1.42±0.15
RuvB-like protein 1	Ruvbl1	0.73±0.01
RuvB-like protein 2	Ruvbl2	1.31±0.36
RWD domain containing 2B	Rwdd2b	0.33±0.08
RWD domain containing 3	Rwdd3	0.2±0.02
RWD domain containing 4A	Rwdd4a	4.62±0.67
S1 RNA binding domain 1	Srbd1	1.07±0.03
S100 calcium binding protein A10 (calpactin)	S100a10	19.12±1.75
S100 calcium binding protein A11 (calizzarin)	S100a11	24.89±6.31
S100 calcium binding protein A13 (predicted)	S100a13_predicted	0.23±0.05
S100 calcium binding protein A16 (predicted)	S100a16_predicted	3.7±0.41
SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	Sacm1l	6.25±0.37
saccharopine dehydrogenase (putative)	Sccpdh	5.44±0.64
S-adenosylhomocysteine hydrolase	Ahcy	0.78±1.01
S-adenosylhomocysteine hydrolase-like 1 (predicted)	Ahcyl1_predicted	13.2±1.36
S-adenosylhomocysteine hydrolase-like 2	Ahcyl2	9.42±2.04
S-adenosylmethionine decarboxylase 1	Amd1	5.15±1.78
Sal-like 1 (Drosophila) (predicted)	Sall1_predicted	8±3.83
salvador homolog 1 (Drosophila) (predicted)	Sav1_predicted	2.24±0.17
SAP30 binding protein (predicted)	Sap30bp_predicted	0.4±0.04
SAP30-like	Sap30l	2.41±0.38
SAPS domain family, member 1 (predicted)	Saps1_predicted	2.13±0.16
SAPS domain family, member 2	Saps2	0.64±0.11
SAPS domain family, member 3 (predicted)	Saps3_predicted	2.89±0.05
SAR1 gene homolog A (S. cerevisiae)	Sar1a	2.97±0.36
SAR1 gene homolog B (S. cerevisiae)	Sar1b	5.83±0.4
sarcoglycan, epsilon	Sgce	2.86±0.73
sarcoma antigen NY-SAR-48	Ny-sar-48	0.33±0.2
sarcosine dehydrogenase	Sardh	0.48±0.4
sarcospan	Sspn	0.21±0.27
scaffold attachment factor B	Safb	1.06±0.15
SCAN domain-containing 1 (predicted)	Scand1_predicted	7.95±0.87
scavenger receptor class F, member 1 (predicted)	Scarf1_predicted	0.31±0.02
scavenger receptor cysteine rich domain containing, group B (4 domains) (predicted)	Srcrb4d_predicted	1.47±0.05
SCF apoptosis response protein 1	LOC499941	1.07±0.97
schwannomin interacting protein 1	Schip1	2.67±1.11
Scinderin	Scin	16.18±3.85
sclerostin domain containing 1	Sostdc1	47.96±8.03
Scm-like with four mbt domains 1	Sfmbt1	0.55±0.02
scotin	MGC94600	2.14±0.37
scribbled homolog (Drosophila)	Scrib	1.64±0.14
SCY1-like 1 (S. cerevisiae)	Scyl1	2.53±0.7
SCY1-like 1 binding protein 1	Scyl1bp1	1.46±0.71
SCY1-like 2 (S. cerevisiae) (predicted)	Scyl2_predicted	4.67±0.35
SCY1-like 3 (S. cerevisiae)	Scyl3	0.32±0.01
sec1 family domain containing 1	Scfd1	3.53±0.46
SEC11 homolog A (S. cerevisiae)	Sec11a	4.54±0.62
SEC11 homolog C (S. cerevisiae)	Sec11c	2.34±0.61
SEC13 homolog (S. cerevisiae)	Sec13	3.91±1.11
SEC14 and spectrin domains 1	Sestd1	2.87±0.23
SEC14-like 1 (S. cerevisiae)	Sec14l1	3.02±0.51
SEC16 homolog A (S. cerevisiae)	Sec16a	2.78±0.19
SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	Sec22a	1.45±0.19
SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	Sec22b	2.52±0.08
SEC23 interacting protein	Sec23ip	0.94±0.24
SEC23A (S. cerevisiae) (predicted)	Sec23a_predicted	0.79±0.08
SEC23B (S. cerevisiae) (predicted)	Sec23b_predicted	3.35±0.52
SEC24 related gene family, member A (S. cerevisiae) (predicted)	Sec24a_predicted	1.62±0.75
SEC24 related gene family, member B (S. cerevisiae) (predicted)	Sec24b_predicted	0.92±0.21
SEC24 related gene family, member D (S. cerevisiae) (predicted)	Sec24d_predicted	4.9±0.28
SEC31 homolog A (S. cerevisiae)	Sec31a	2.38±0
SEC3-like 1 (S. cerevisiae)	Sec3l1	1.98±0.25
Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	4.35±0.31
Sec61 beta subunit (predicted)	Sec61b_predicted	7.62±0.34
Sec61, alpha subunit 2 (S. cerevisiae) (predicted)	Sec61a2_predicted	1.46±0.02

SEC63-like (S. cerevisiae) (predicted)	Sec63_predicted	2.07±0.29
secernin 2	Scrn2	0.91±0.06
SECIS binding protein 2	Secisbp2	1.42±0.2
secreted phosphoprotein 1	Spp1	11.22±33.12
secretin	Sct	0.29±0.06
secretion regulating guanine nucleotide exchange factor	Sergef	2.38±0.5
secretogranin V	Scg5	0.78±0.12
secretory carrier membrane protein 1	Scamp1	4.02±0.3
secretory carrier membrane protein 2	Scamp2	6.89±2.39
secretory carrier membrane protein 3	Scamp3	4.18±0.02
secretory carrier membrane protein 4	Scamp4	1.85±0.42
sedlin-like	LOC287274	9.29±0.85
sedoheptulokinase	Shpk	0.67±0.14
Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	Sel1h	2.56±0.14
SEL1 domain containing protein RGD735029	RGD735029	2.2±0.86
sel-1 suppressor of lin-12-like (C. elegans)	Sel1l	0.49±0.18
selenium binding protein 1	Selenbp1	9.34±0.13
selenocysteine lyase	Scly	3.22±0.01
selenophosphate synthetase 1	Sephs1	2.48±0.38
selenophosphate synthetase 2	Sephs2	3.16±0.87
selenoprotein	Sept15	10.86±1.04
selenoprotein K	Selk	8.39±0.83
selenoprotein P, plasma, 1	Sepp1	32.13±1.22
selenoprotein S	SELS	5.56±0.12
selenoprotein T	Selt	1.95±0.43
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B (predicted)	Sema3b_predicted	3.19±0.24
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Sema4a	5.08±1.39
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Sema4b	3.56±0.01
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	Sema4f	0.79±0.08
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted)	Sema4g_predicted	1.26±0.12
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (predicted)	Sema6d_predicted	5.27±1.12
sepiapterin reductase	Spr	0.7±0.23
septin 1	Sept1	0.64±0.08
septin 11	Sept11	1.45±0.06
septin 14	Sept14	0.24±0.1
septin 2	Sept2	5.96±0.64
septin 4	Sept4	15.06±2.62
septin 7	sept7	5.67±0.36
septin 8 (predicted)	Sept8_predicted	0.61±0.39
septin 9	Sept9	1.99±0.25
sequestosome 1	Sqstm1	11.06±4.31
serine (or cysteine) peptidase inhibitor, clade B, member 6a	Serpinb6a	4.1±0.24
serine (or cysteine) peptidase inhibitor, clade H, member 1	Serpinh1	6.21±1.46
serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpinb1a	1.52±0.3
serine carboxypeptidase 1	Scpep1	1.01±1.84
serine hydroxymethyltransferase 1 (soluble)	Shmt1	3.94±0.23
serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	0.86±0.16
serine incorporator 1	Serinc1	7±1.18
serine incorporator 3	Serinc3	7.55±2.75
serine palmitoyltransferase, long chain base subunit 1 (predicted)	Sptlc1_predicted	7±1.83
serine peptidase inhibitor, Kazal type 8	Spink8	0.23±0.11
serine protease inhibitor, Kunitz type 1	Spint1	2.92±0.46
serine protease inhibitor, Kunitz type 2	Spint2	30.33±0.51
serine racemase	Srr	1.32±0.07
serine/arginine repetitive matrix 1 (predicted)	Srrm1_predicted	2.66±0.45
serine/arginine repetitive matrix 2 (predicted)	Srrm2_predicted	7.01±4.03
Serine/arginine-rich protein specific kinase 1	Srpk1	0.98±0.23
serine/arginine-rich protein specific kinase 2 (predicted)	Srpk2_predicted	2.39±0.22
serine/threonine kinase 11 interacting protein (predicted)	Stk11ip_predicted	0.79±0.04
serine/threonine kinase 16	Stk16	3.75±0
serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	0.42±0.17
Serine/threonine kinase 2	Slk	1.83±0.82
serine/threonine kinase 22 substrate 1 /// interferon regulatory factor 3	Irf3 /// Stk22s1	1.59±0.94
serine/threonine kinase 24 (STE20 homolog, yeast)	Stk24	2.34±0.45
serine/threonine kinase 25 (STE20 homolog, yeast)	Stk25	2.22±0.34
serine/threonine kinase 3 (STE20 homolog, yeast)	Stk3	1.81±0.12
serine/threonine kinase 38	Stk38	1.71±0.29
serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	2.39±0.33
serine/threonine kinase 4 (predicted)	Stk4_predicted	1.6±0.2
serine/threonine kinase receptor associated protein	Strap	8.51±0.14
serine/threonine/tyrosine interacting-like 1	Styxl1	0.3±0.01
serologically defined colon cancer antigen 1	Sdccag1	2.28±0.43
serologically defined colon cancer antigen 10	Sdccag10	0.32±0.03
serologically defined colon cancer antigen 3	Sdccag3	3.35±0.2
Serpine1 mRNA binding protein 1	Serbp1	14.86±1.07
SERTA domain containing 1	Sertad1	1.38±0.4
SERTA domain containing 2	Sertad2	2.08±0.45
SERTA domain containing 4	Sertad4	0.51±0.2
serum deprivation response	Sdpr	0.81±0.23
serum response factor (predicted)	Srf_predicted	1.23±0.4
serum response factor binding protein 1	Srfbp1	0.81±0.33
seryl-aminoacyl-tRNA synthetase	Sars	5.23±2.43
seryl-aminoacyl-tRNA synthetase 2	Sars2	0.36±0.09
sestrin 1 (predicted)	Sesn1_predicted	2.43±0.1
SET and MYND domain containing 1 (predicted)	Smyd1_predicted	0.29±0.16
SET and MYND domain containing 2	Smyd2	0.82±0.25
SET and MYND domain containing 3	Smyd3	0.33±0.18

SET and MYND domain containing 4 (predicted)	Smyd4_predicted	1.76±0.08
SET and MYND domain containing 5 (predicted)	Smyd5_predicted	0.64±0.11
SET binding factor 1 (predicted)	Sbf1_predicted	0.77±0.04
SET domain and mariner transposase fusion gene	Setmar	0.53±0.05
SET domain containing (lysine methyltransferase) 8 /// similar to SET domain-containing protein	LOC687538 /// LOC689	1.36±0.09
SET domain containing 2	Setd2	1.46±0.39
SET domain containing 3	Setd3	4.34±1.09
SET domain containing 4	Setd4	0.89±0.03
SET domain containing 5	Setd5	0.48±0.12
SET domain containing 6	Setd6	0.47±0.11
SET domain, bifurcated 1 (predicted)	Setdb1_predicted	1.7±0.2
SET translocation (predicted)	Set_predicted	4.75±0.71
SET translocation (predicted)	LOC502130 /// RGD15	6.29±0.92
seven in absentia 1A	Siah1a	0.53±0.03
seven in absentia 2	Siah2	0.4±0.11
sex comb on midleg homolog 1 (predicted)	Scmh1_predicted	1.43±0.14
SFT2 domain containing 1	Sft2d1	4.17±0.44
SFT2 domain containing 2	Sft2d2	9.92±1.9
SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	Sugt1	3.4±1.6
SH2 domain containing 4A	Sh2d4a	3.14±0.12
SH2 domain containing phosphatase anchor protein 1 (predicted)	Spap1_predicted	0.9±0.01
SH2-B PH domain containing signaling mediator 1	Sh2bpsm1	2.22±0.51
SH3 and PX domain containing 3 (predicted)	Sh3px3_predicted	1.16±0.13
SH3 domain and tetratricopeptide repeats 1 (predicted)	Sh3tc1_predicted	0.7±1.41
Sh3 domain YSC-like 1 (predicted)	Sh3yl1_predicted	1.83±0.69
SH3/ankyrin domain gene 2	Shank2	9.13±0.49
SH3-binding domain glutamic acid-rich protein	Sh3bgr	1.28±0.28
SH3-binding domain glutamic acid-rich protein like (predicted)	Sh3bgrl_predicted	2.26±0.81
SH3-binding kinase 1	Sbk1	0.61±0.06
SH3-domain binding protein 4	Sh3bp4	3.12±0.83
SH3-domain binding protein 5 (BTK-associated)	Sh3bp5	3.44±2.57
SH3-domain GRB2-like 1	Sh3gl1	0.99±0.04
SH3-domain GRB2-like 2	Sh3gl2	1.32±0.38
SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	1.42±0.26
SH3-domain GRB2-like endophilin B2	Sh3glb2	1.15±0.23
Sh3kbp1 binding protein 1 (predicted)	Shkbp1_predicted	0.92±0.25
SHANK-associated RH domain interacting protein	Sharpin	3.37±0.29
short coiled-coil protein	Scoc	6.94±0.72
shroom family member 2	Shroom2	1.32±0.82
Shwachman-Bodian-Diamond syndrome homolog (human)	Sbds	4.26±0.19
siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	Siahbp1	4.72±0.49
sialic acid acetylesterase (predicted)	Siae_predicted	2.57±0.06
SID1 transmembrane family, member 2 (predicted)	Sidt2_predicted	2.91±0.41
sideroflexin 3	Sfxn3	5.53±0.01
sideroflexin 4 (predicted)	Sfxn4_predicted	0.98±0.05
signal peptidase complex subunit 2 homolog (S. cerevisiae) (predicted)	Spcs2_predicted	4.04±0.5
signal peptide peptidase 3	Sppl3	4.32±0
signal peptide peptidase-like 2A	Sppl2a	1.52±0.62
signal peptide peptidase-like 2B	Sppl2b	1.49±0.51
signal recognition particle 14 (predicted)	Srp14_predicted	8.96±0.67
signal recognition particle 19 (predicted)	Srp19_predicted	2.25±0.29
signal recognition particle 54	Srp54	1.8±0.6
signal recognition particle 68 (predicted)	Srp68_predicted	3.2±0.04
signal recognition particle 72	Srp72	2.29±0.29
signal recognition particle receptor ('docking protein')	Srpr	6.68±0.62
signal recognition particle receptor, B subunit	Srprb	5.72±1.1
signal sequence receptor, alpha	Ssr1	10.11±2.31
signal sequence receptor, beta (predicted)	Ssr2_predicted	3.02±0.17
signal sequence receptor, delta	Ssr4	12.33±3.73
signal sequence receptor, gamma	Ssr3	8.22±1.05
signal transducer and activator of transcription 1	Stat1	7.38±0.61
signal transducer and activator of transcription 2	Stat2	1.56±0.14
signal transducer and activator of transcription 3	Stat3	5.47±1.57
signal transducer and activator of transcription 6 (predicted)	Stat6_predicted	0.25±0.07
signal transducing adaptor family member 2	Stap2	0.25±0.4
signal-induced proliferation-associated 1 like 1	Sipa1l1	0.81±0.05
similar to 0610007L01Rik protein	MGC94190	8.5±1.29
similar to 0610010K06Rik protein	RGD1307161	5.92±0.06
Similar to 106 kDa O-GlcNAc transferase-interacting protein (predicted)	RGD1307844_predicte	0.72±0.53
similar to 1110008L16Rik protein (predicted)	RGD1305089_predicte	2.12±0.18
similar to 1500019C06Rik protein (predicted)	RGD1560433_predicte	0.41±0.24
similar to 1700019E19Rik protein (predicted)	RGD1307392_predicte	1.04±0.9
similar to 1700113K14Rik protein (predicted)	RGD1311084_predicte	0.56±0.19
similar to 1700123O20Rik protein (predicted)	RGD1308430_predicte	2.05±0.12
similar to 2010004A03Rik protein (predicted) /// similar to 2010004A03Rik protein	LOC498951 /// RGD13	0.59±0.08
similar to 2010321M09Rik protein	RGD1359616	2.38±0.31
similar to 2210021J22Rik protein (predicted)	RGD1306001_predicte	0.41±0.07
similar to 2310044H10Rik protein	MGC93975	2.54±0.39
similar to 2310047B19Rik protein (predicted)	RGD1308026_predicte	0.82±0.12
similar to 2410001C21Rik protein	RGD1311072	3.12±0.63
similar to 2410024A21Rik protein	RGD1304878	1.02±0.23
similar to 2610027C15Rik protein (predicted)	RGD1308876_predicte	0.28±0.07
similar to 2610030H06Rik protein (predicted)	RGD1566155_predicte	0.66±0.21
similar to 2610301G19Rik protein (predicted)	RGD1309922_predicte	1.31±0.03
similar to 2610317D23Rik protein (predicted)	RGD1565411_predicte	0.92±0.27
similar to 2700029M09Rik protein (predicted)	RGD1311747_predicte	3.42±1.29
similar to 2700078E11Rik protein	RGD1308127	2.82±0.67

Similar to 2810022L02Rik protein	RGD1309930	0.33±0.34
similar to 2810422O20Rik protein	RGD1306783	0.65±0.12
similar to 2900002H16Rik protein (predicted)	RGD1307973_predicte	2.99±0.26
similar to 3000004C01Rik protein	RGD1310360	0.22±0.01
similar to 3110080A02Rik protein (predicted)	RGD1305754_predicte	0.39±0.13
similar to 3-oxoacid CoA transferase 1	LOC678860	47.52±1.66
similar to 4632419K20Rik protein	MGC94288	0.47±0.02
similar to 4921517L17Rik protein	RGD1311678	0.33±0.12
similar to 4930429A08Rik protein (predicted)	RGD1564943_predicte	2.2±0.39
similar to 4930438D12Rik protein (predicted)	RGD1563224_predicte	4.04±0.43
similar to 4930453N24Rik protein	MGC95208	1.48±0.33
Similar to 4930506M07Rik protein (predicted)	RGD1311558_predicte	1±0.47
Similar to 4930566A11Rik protein (predicted)	RGD1306674_predicte	0.45±0.04
similar to 5(3)-deoxyribonucleotidase, cytosolic type (Cytosolic 5,3-pyrimidine nucleotidase) (Deoxy-5-nucleotidase 1) (dNT-1)	LOC688261	0.73±0.21
similar to 5730403M16Rik protein	LOC308320	0.42±0.03
Similar to 5730420B22Rik protein (predicted)	RGD1306755_predicte	0.46±0.44
similar to 5930416I19Rik protein	MGC94282	0.48±0.08
similar to 5-nucleotidase, cytosolic II	LOC365090	4.39±0.53
similar to 6.8 kDa mitochondrial proteolipid	LOC691427	18.68±0.95
similar to 60S ribosomal protein L38 /// ribosomal protein L38 /// 60S ribosomal protein L38 pseudogene	LOC681221 /// LOC681	35.66±1.57
similar to 82-kD FMRP Interacting Protein	LOC687994	0.38±0.28
similar to 9130011E15Rik protein (predicted)	RGD1564887_predicte	0.91±0.19
similar to 9230105E10Rik protein	RGD1304579	1.73±0.22
similar to 9630058J23Rik protein (predicted)	RGD1564833_predicte	1.49±0
similar to 9930012K11Rik protein (predicted)	RGD1308117 predicte	0.49±0.38
Similar to a disintegrin and metalloprotease domain 4	LOC500688	1.57±0.31
Similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 10	LOC314655	0.71±0.17
similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (ACAD-8) (predicted)	RGD1564209_predicte	1.31±0.24
similar to acyl-CoA thioesterase	LOC302640	8±0.57
similar to Adaptor-related protein complex 1, mu 2 subunit (AP1M2) (predicted)	RGD1561490_predicte	4.34±0.8
similar to Adenosine deaminase CG11994-PA	LOC311352	0.4±0.2
similar to Adenylosuccinate synthetase isozyme 1 (Adenylosuccinate synthetase, muscle isozyme) (IMP--aspartate ligase 1) (AdSS 1) (A	LOC684425	0.47±0.06
similar to adipocyte-specific protein 4	RGD1308813	3.95±1.07
similar to ADP-ribosylation factor GTPase-activating protein 3 (ARF GAP 3)	LOC503165	1.48±0.15
similar to ADP-ribosylation factor-like 1	LOC688311	1.39±0.1
similar to AHA1, activator of heat shock 90kDa protein ATPase homolog 1	LOC681996	2.59±0.06
similar to AI115348 protein (predicted)	RGD1311939_predicte	1.85±0.16
Similar to AL023001 protein (predicted)	RGD1305001_predicte	1.55±0.45
similar to alcohol dehydrogenase PAN2 (predicted)	RGD1565196_predicte	2.95±2.25
similar to Alpha- and gamma-adaptin-binding protein p34	LOC498912	2.19±0.49
Similar to alternative testis transcripts open reading frame A CG4241-PA, isoform A	LOC689414	0.88±0.22
similar to AMME syndrome candidate gene 1 protein homolog (predicted)	RGD1561004_predicte	0.23±0.11
similar to AMSH-family protein	LOC687696	1.4±0.05
similar to Amyloid beta (A4) precursor-like protein 1 (predicted)	RGD1561211_predicte	0.36±0.07
similar to anaphase promoting complex subunit 13	LOC685029	5.51±1.77
similar to ankyrin repeat domain 40	LOC688144	3.25±0.28
Similar to AP2 associated kinase 1 (predicted)	RGD1563580_predicte	1.83±0.71
similar to AP-3 complex subunit sigma-2 (Adapter-related protein complex 3 sigma-2 subunit) (Sigma-adaptin 3b) (AP-3 complex sigma-3	LOC683402	2.08±0.52
Similar to APG4 autophagy 4 homolog C	LOC313391	0.78±0.11
similar to APG4-D protein	LOC686505	1.58±0.76
Similar to Apolipoprotein L3 (Apolipoprotein L-III) (ApoL-III) (TNF-inducible protein CG12-1) (CG12_1) (predicted)	RGD1309798_predicte	0.21±0
similar to apoptosis related protein APR-3; p18 protein (predicted)	RGD1311605_predicte	2.99±0.66
similar to apurinic/apyrimidinic endonuclease 2 (predicted)	RGD1565983_predicte	0.34±0.09
similar to arginyl aminopeptidase (aminopeptidase B)-like 1	LOC684035	3.33±0.13
similar to arsenate resistance protein 2	LOC686980	2.24±0.03
similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	LOC684567	46.93±7.26
similar to autophagy 5-like	LOC365601	1.85±0.03
Similar to axonemal dynein light chain 1	LOC685664	0.34±0.17
similar to B0432.8	LOC289378	1.39±0.12
similar to B0511.12	LOC690217	0.54±0.02
similar to B230212L03Rik protein	MGC95152	2.3±0.48
similar to Basic FGF-repressed Zic-binding protein (mbFZb)	LOC683512	3.03±0.81
similar to Basic helix-loop-helix transcription factor scleraxis	LOC684826	0.51±0
similar to BC003940 protein (predicted)	RGD1311925_predicte	3.59±0.71
Similar to BC021442 protein (predicted)	RGD1561413_predicte	0.38±0.46
Similar to B-cell CLL/lymphoma 7A	LOC690085	2.53±0.34
Similar to Bcl2-associated athanogene 2	LOC690038	1.52±0.21
Similar to bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (variant 1) (predicted)	RGD1306698_predicte	1.36±0.52
similar to Brain protein 44 (predicted)	RGD1563422_predicte	26.72±1.92
Similar to Breast carcinoma amplified sequence 3 homolog (K20D4) (predicted)	RGD1560788_predicte	0.75±0.17
similar to Butyrate-induced transcript 1 (predicted)	RGD1565496_predicte	2.19±0.08
similar to C11orf17 protein (predicted)	RGD1306959_predicte	0.79±0.04
similar to C184L-22 /// Sjogren's syndrome/scleroderma autoantigen 1	LOC684594 /// Sssca1	1.56±0.55
similar to C1orf25	RGD1307890	1.3±0.07
similar to C21orf70 protein	RGD1311257	0.87±0.21
similar to C530044N13Rik protein	RGD1306568	3.87±1.12
similar to capping protein (actin filament) muscle Z-line, alpha 1	LOC691149	3.26±0.27
Similar to Catechol O-methyltransferase (predicted)	RGD1561509_predicte	0.55±0.12
Similar to CCAAT displacement protein isoform b	Cutl1	3.65±0.37
similar to cDNA sequence AF155546	RGD1309387	1.01±0.19
similar to cDNA sequence AK129302 (predicted)	RGD1561708_predicte	0.76±0.04
similar to cDNA sequence BC005537	LOC498750	5.97±1
Similar to cDNA sequence BC006662	RGD1304748	29.02±17.22
similar to cDNA sequence BC013529 (predicted)	RGD1309759_predicte	4.28±0.79
similar to cDNA sequence BC017158	RGD1310127	2.29±0.2
similar to CDNA sequence BC017647 (predicted)	RGD1566149_predicte	0.87±0.31
similar to cDNA sequence BC020002 (predicted)	RGD1308432_predicte	0.59±0.15

similar to CDNA sequence BC024479	LOC500974	2.38±0.78
similar to cDNA sequence BC024814 (predicted)	RGD1311433_predicte	1±0.09
similar to cDNA sequence BC025816	LOC498957	0.56±0.06
similar to cDNA sequence BC031181 (predicted)	RGD1562987_predicte	5.49±0.36
similar to cDNA sequence BC056474 (predicted)	RGD1564058_predicte	3.5±1.33
similar to CDV-3B	LOC315970	0.72±0.1
similar to Cell division protein kinase 8 (Protein kinase K35) (predicted)	RGD1560888_predicte	1.17±0.11
similar to centrosome protein Cep63	LOC300963	0.49±0.21
similar to cervical cancer receptor (predicted)	RGD1310591_predicte	2.02±0.01
similar to CG10084-PA	RGD1308297	4.67±0.28
similar to CG11206-PA	LOC313672	0.58±0.28
similar to CG11388-PA (predicted)	RGD1308154_predicte	2.23±0.62
similar to CG12279-PA	LOC500420	1.15±0.84
similar to CG12379-PA (predicted)	RGD1308635_predicte	3.97±0.8
similar to CG12929-PA	LOC682404	1.04±0.05
similar to CG12935-PA	LOC686289 /// LOC69	3.82±0.55
similar to CG13901-PA	RGD1307648	1.75±0.01
Similar to CG13957-PA (predicted)	RGD1309995_predicte	0.56±0.64
similar to CG14286-PA	LOC686765	1.95±0.32
similar to CG14483-PA	LOC681884	2.9±0.11
similar to CG14803-PA (predicted)	RGD1304693_predicte	0.46±0.15
similar to CG14903-PA (predicted)	RGD1561792_predicte	1.74±0.05
similar to CG14967-PA	RGD1307929	6.81±0.12
similar to CG14977-PA (predicted)	RGD1309735_predicte	6.19±1.12
similar to CG14980-PB	RGD1306410	2.64±0.74
similar to CG16812-PA (predicted)	RGD1307554_predicte	0.43±0.12
similar to CG18661-PA	RGD1307155	2.86±0.77
similar to CG1998-PA	LOC691221	3.17±0.62
similar to CG31122-PA (predicted)	RGD1306941_predicte	1.9±0.71
similar to CG31613-PA	LOC684841	0.31±0.04
Similar to CG31759-PA	RGD1310975	0.33±0.04
similar to CG33331-PA	LOC362419	1.18±0.55
similar to CG33714-PB, isoform B	LOC688717	2.76±0.93
similar to CG3570-PA	LOC500034	1.42±0.28
Similar to CG3740-PA	LOC690000	3.18±0.66
similar to CG4751-PA	LOC681944	9.39±1.97
similar to CG4768-PA (predicted)	RGD1309748_predicte	2.56±0.85
similar to CG5500-PA	LOC688310	1.6±0.36
similar to CG5987-PA (predicted) /// mesenchymal stem cell protein DSC92	Ngrn /// RGD1310399_	1.89±0.16
similar to CG6105-PA	MGC72942	37.87±8.63
similar to CG6878-PA	LOC679572	8.01±2.66
similar to CG8043-PA (predicted)	RGD1306000_predicte	0.7±0.35
similar to CG8272-PA	LOC502201	0.23±0.07
similar to CG8841-PA (predicted)	RGD1311422_predicte	0.69±0.19
similar to CG9117-PA	RGD1306932	0.41±0.14
similar to CG9240-PA	LOC687395	2.64±1.02
Similar to CG9339-PA (predicted)	RGD1306143_predicte	0.32±0.06
similar to CG9346-PA (predicted)	RGD1307882_predicte	1.88±0.48
similar to CG9752-PA	RGD1311345	3.09±0.04
similar to CG9882-PA (predicted)	RGD1306157_predicte	1.2±0.17
similar to CG9886-like	LOC684314	0.21±0.01
similar to CG9967-PA, isoform A	LOC678910	1.21±0.17
Similar to CG9996-PA	LOC300173	1.47±0.46
similar to CGI-112 protein	RGD1308113	0.71±0.05
similar to CGI-35 protein (predicted)	RGD1310899_predicte	6.71±0.17
similar to Chain A, Solution Structure Of The Bola-Like Protein From Mus Musculus (predicted)	RGD1309998_predicte	5.86±0.94
similar to channel-interacting PDZ domain protein isoform 1 (predicted)	RGD1565362_predicte	2.55±0.13
similar to chr2 synaptotagmin (predicted)	RGD1565705_predicte	0.47±0.07
similar to chromosome 1 open reading frame 172	RGD1303271	0.56±0.06
similar to chromosome 1 open reading frame 2 (predicted)	RGD1306107_predicte	0.83±0.4
similar to chromosome 1 open reading frame 50 (predicted)	RGD1564804_predicte	0.58±0.24
similar to chromosome 1 open reading frame 63	RGD1359529	9.49±0.66
similar to chromosome 10 open reading frame 18 (predicted)	RGD1564456_predicte	1.44±0.24
similar to chromosome 10 open reading frame 4; similar to putative acid phosphatase F26C11.1	RGD1309482	0.87±0.12
similar to chromosome 10 open reading frame 6 (predicted)	RGD1560300_predicte	1.16±0.07
similar to chromosome 14 open reading frame 130	RGD1359144	1.57±0.14
similar to chromosome 14 open reading frame 138 (predicted)	RGD1306228_predicte	2.33±0.33
similar to chromosome 14 open reading frame 145	LOC500700	0.55±0.05
similar to chromosome 14 open reading frame 21 (predicted)	RGD1308396_predicte	0.46±0.4
similar to chromosome 14 open reading frame 35 (predicted)	RGD1559923_predicte	2.73±0.02
similar to chromosome 14 open reading frame 50	RGD1309051	4.16±0.56
similar to chromosome 14 open reading frame 94	RGD1305288	4.04±0.33
similar to chromosome 16 open reading frame 28 (predicted)	RGD1565247_predicte	0.67±0.42
similar to chromosome 16 open reading frame 33; minus -99 protein (predicted)	RGD1310922_predicte	1.63±0.28
similar to chromosome 16 open reading frame 5	RGD1310686	5.5±0.23
similar to chromosome 16 open reading frame 7 (predicted)	RGD1565149_predicte	1.73±0.21
similar to chromosome 17 open reading frame 27	LOC688296	0.2±0.18
similar to chromosome 2 open reading frame 3; transcription factor 9 (binds GC-rich sequences) (predicted)	RGD1304792_predicte	0.24±0.03
similar to chromosome 20 open reading frame 116 (predicted)	RGD1309979_predicte	3.85±0.34
similar to chromosome 20 open reading frame 30; HSPC274 protein	RGD1307399	3.5±0.27
Similar to chromosome 20 open reading frame 6	RGD1306067	2.07±0.53
similar to chromosome 3 open reading frame 10	LOC679934	2.87±0.24
similar to chromosome 6 open reading frame 106 isoform a	LOC294154	6.63±1.28
similar to chromosome 7 open reading frame 11	LOC678905	0.63±0.08
Similar to chromosome 7 open reading frame 23 (predicted)	RGD1562351_predicte	0.51±0.08
similar to chromosome 7 open reading frame 30 (predicted)	RGD1306936_predicte	3.44±0.14
Similar to chromosome 9 open reading frame 5 (predicted)	RGD1308958_predicte	0.28±0.13

similar to cleavage stimulation factor, 3 pre-RNA subunit 2	LOC683927	0.22±0.15
similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) (predicted)	RGD1566215_predicte	4.64±0.52
similar to coiled coil domain containing 28B	LOC682445	0.23±0.07
Similar to coiled-coil domain containing 6	LOC691155	0.55±1.13
similar to coiled-coil domain containing 8	MGC72567	0.52±0.16
similar to coiled-coil domain containing 9	LOC684934	0.61±0.15
similar to coiled-coil-helix-coiled-coil-helix domain containing 7	LOC684258	3.78±0.6
similar to component of oligomeric golgi complex 2	LOC678914	1.75±0.39
similar to component of oligomeric golgi complex 2 /// component of oligomeric golgi complex 2	Cog2 /// LOC678914	0.21±0.07
similar to component of oligomeric golgi complex 5 isoform 1 (predicted)	RGD1563296_predicte	0.96±0.16
similar to constitutive photomorphogenic protein 1	RGD1304773	5.76±0.3
similar to copine II	LOC498972	1.09±0.28
similar to COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase	LOC687381 /// LOC691	2.77±0.71
similar to COX11 homolog, cytochrome c oxidase assembly protein /// COX11 homolog, cytochrome c oxidase assembly protein (yeast)	Cox11 /// LOC688135	0.75±0.22
similar to CPSF4 protein	MGC108785	1.69±0.18
similar to cullin 4A (predicted)	RGD1563853_predicte	0.75±0.19
similar to cullin 7	LOC680835	1.11±0.02
similar to cyclin-dependent kinase inhibitor 2D	Cdkn2d	0.97±0.22
similar to Cysteine protease ATG4A (Autophagy-related protein 4 homolog A) (Autophagin-2) (Autophagy-related cysteine endopeptidas	LOC678769	1.72±0.01
similar to cystin 1	LOC690489	2.63±1.6
similar to cytokine receptor related protein 4	Cytor4	0.68±0.24
similar to D1Ertd622e protein (predicted)	RGD1562136_predicte	7.53±1.59
similar to D330021B20 protein	RGD1308143	1.39±0.99
similar to D3Mm3e (predicted)	RGD1561494_predicte	0.32±0.05
similar to D8Ertd354e protein (predicted)	RGD1560755_predicte	2.69±0.49
similar to dachshund b	LOC686314	0.72±0.29
similar to Dachshund homolog 1 (Dach1)	LOC306096	0.57±0.19
similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	rCG_33565	6.95±0.24
similar to death effector domain-containing DNA binding protein 2	LOC687118	0.44±0.02
similar to Dedicator of cytokinesis protein 1 (180 kDa protein downstream of CRK) (DOCK180)	LOC679295	6.21±0.72
similar to defective SPErmatogenesis family member (spe-39)	LOC681989	3.94±0.3
similar to Dehydrogenase/reductase SDR family member 7 precursor (Retinal short-chain dehydrogenase/reductase 4) (predicted)	RGD1565002_predicte	0.77±0.31
similar to Dendritic cell protein GA17 (predicted)	RGD1565840_predicte	11.37±0.56
similar to density-regulated protein	LOC689601	1.56±0.17
similar to DEP domain containing 6 (predicted)	RGD1561030_predicte	2.65±0.11
similar to Der1-like domain family, member 2	LOC687738	1.99±0.19
similar to diacylglycerol kinase epsilon	LOC497978	0.51±0.1
similar to diacylglycerol kinase, delta 130kDa isoform 1 (predicted)	RGD1563309_predicte	0.49±0.1
similar to differentially expressed in B16F10 1	LOC687029	5.35±0.71
Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle	LOC685729	11.06±4.19
similar to DIP13 alpha (predicted)	RGD1309388_predicte	1.61±0.42
similar to Disco-interacting protein 2 homolog /// DIP2 disco-interacting protein 2 homolog A (Drosophila)	Dip2a /// LOC687682	1.99±0.24
similar to divalent cation tolerant protein CUTA (predicted)	RGD1564854_predicte	1.06±0.32
similar to dJ202D23.2 (novel protein similar to C21ORF5 (KIAA0933)) (predicted)	RGD1305534_predicte	0.7±0.09
Similar to dJ55C23.6 gene product (predicted)	RGD1306962_predicte	2.76±0.7
similar to dJ842G6.1.1 (novel protein) (predicted)	RGD1309829_predicte	2.21±0.6
similar to dJ881L22.2 (novel protein) (predicted)	RGD1307696_predicte	1.04±0.06
Similar to DKFZP434B168 protein (predicted)	RGD1308014_predicte	1.02±0.54
similar to DKFZP547E1010 protein	LOC361990	4.11±1.06
similar to DKFZP547E1010 protein /// similar to Protein C1orf77 homolog	LOC361990 /// LOC50	1.05±0.18
Similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase MmuIIIA) (DNA MTase MmuIIIA) (M.MmuIIIA) (pred	RGD1305891_predicte	0.44±0.03
similar to DNA segment on chromosome X and Y (unique) 155 expressed sequence isoform 1	LOC288526	1.24±0.01
similar to DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed (predicted)	RGD1560909_predicte	0.68±0.15
Similar to DNA segment, Chr 10, University of California at Los Angeles 1 (predicted)	RGD1560401_predicte	4.04±0.1
similar to DNA segment, Chr 10, Wayne State University 102, expressed (predicted)	RGD1563365_predicte	0.45±0
similar to DNA segment, Chr 11, Wayne State University 99, expressed (predicted) /// hypothetical protein LOC619573	LOC619573 /// RGD13	1.08±0.43
similar to DNA segment, Chr 14, ERATO Doi 436, expressed (predicted)	RGD1304610_predicte	0.41±0.22
similar to DNA segment, Chr 14, ERATO Doi 449, expressed	RGD1305689	0.96±0.11
similar to DNA segment, Chr 18, Wayne State University 98, expressed (predicted)	RGD1560212_predicte	3.21±0.03
similar to DNA segment, Chr 19, ERATO Doi 386, expressed (predicted)	RGD1307934_predicte	0.24±0.02
similar to DNA segment, Chr 4, ERATO Doi 22, expressed (predicted)	RGD1560286_predicte	1.61±0.17
similar to DNA segment, Chr 5, ERATO Doi 135, expressed	LOC679383	1.18±0.03
similar to DNA segment, Chr 6, Wayne State University 163, expressed (predicted)	RGD1311164_predicte	1.15±0.31
similar to DnaJ (Hsp40) homolog, subfamily A, member 4	LOC498996	2.1±1.01
similar to DnaJ (Hsp40) homolog, subfamily B, member 10 isoform 2	LOC689593	5.74±0.6
similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (HSJ-2) (MRJ) (mDj4)	LOC690183	6.75±0.52
similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (predicted)	Dnajb6 /// LOC686213	2.13±0.12
Similar to DNA-repair protein XRCC2 (X-ray repair cross-complementing protein 2) (predicted)	RGD1564823_predicte	0.2±0.07
similar to DOC-1 related protein /// CDK2-associated protein 2	Cdk2ap2 /// LOC68378	8.72±1.54
similar to dolichyl-phosphate mannosyltransferase polypeptide 3 (Dolichol-phosphate mannose synthase subunit 3) (predicted)	rCG_63436 /// RGD156	4.85±0.04
similar to downregulated in renal cell carcinoma	RGD1306327	4.65±0.12
similar to e(y)2 protein	LOC682575	4.7±1.79
similar to early estrogen-induced gene 1 protein	LOC687750	1.37±0.12
Similar to EHM2 (predicted)	RGD1562988_predicte	1.41±0.38
similar to Elongation factor Ts, mitochondrial precursor (EF-Ts) (EF-TsMt) (2A3-2)	LOC679068	2.43±0.85
similar to Elongation of very long chain fatty acids protein 1	LOC679532	5.21±0.16
similar to elongation protein 4 homolog	LOC687694	0.75±0.38
similar to EMSY protein (predicted)	RGD1310712_predicte	0.43±0.12
similar to enoyl Coenzyme A hydratase domain containing 3	LOC684538	4.94±2.25
similar to ENSANGP00000021391 (predicted)	RGD1309779_predicte	7.54±0.87
similar to Ephrin type-B receptor 4 precursor (Tyrosine-protein kinase receptor MDK-2) (Developmental kinase 2) (Tyrosine kinase MYK-	LOC686310	1.79±0.43
similar to Erbb2 interacting protein isoform 2 (predicted)	RGD1562952_predicte	3.28±0.39
similar to erythroid differentiation-related factor 1 (predicted)	RGD1306820_predicte	0.72±0.06
similar to ES cell-expressed Ras	LOC679682	1.78±0.48
similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor-interacting protein 1) (TRIP	LOC682390	5.44±0.51
similar to Exocyst complex component Sec15B (predicted)	RGD1560638_predicte	0.91±0.01
similar to exosome component 1	LOC679140	0.83±0.11

similar to exosome component 10	LOC313707	0.49±0.13
Similar to expressed sequence AA536743 (predicted)	RGD1307468_predicte	2.76±1.64
similar to expressed sequence AA960436	RGD1305215	0.53±0.3
Similar to expressed sequence AI449175	MGC72612	0.27±0.23
similar to expressed sequence AI597479	RGD1310553	1.16±0.1
similar to expressed sequence AW209491	RGD1308147	1.76±1.14
similar to expressed sequence AW212394 (predicted)	RGD1562317_predicte	2.66±0.39
similar to expressed sequence AW413431 (predicted)	RGD1559841_predicte	0.87±0.04
similar to expressed sequence AW556797 (predicted)	RGD1305138_predicte	1.36±0.43
Similar to Ext1	LOC299907	0.35±0.02
similar to F28C1.3a	LOC308398	1.23±0.23
similar to F33H2.2	LOC689997	5.52±1.9
similar to F33H2.2	LOC684063 /// LOC689	1.33±0.18
similar to F54C1.5a	LOC499814	0.46±0.53
similar to F57G4.9	LOC690164	0.28±0.03
similar to Fam13a1 protein	RGD1309807	1.25±0.13
similar to family 53, member C protein	LOC685405	1.17±0.12
similar to family with sequence similarity 11, member A (predicted)	RGD1563037_predicte	2.78±0.52
similar to F-box only protein 27 (predicted)	RGD1563982_predicte	0.56±0.03
similar to F-box only protein 31 (predicted)	RGD1561069_predicte	0.98±0.04
similar to F-box only protein 6 (F-box/G-domain protein 2) (predicted)	RGD1305932_predicte	0.33±0.15
similar to F-box protein FBL2	RGD1308119	0.79±0.36
similar to Fbxw17 protein (predicted)	RGD1566133_predicte	0.41±0.05
similar to Fc fragment of IgG binding protein; IgG Fc binding protein	RGD1311906	0.42±0.1
similar to FKSG24 (predicted)	RGD1308064_predicte	3.41±0.8
similar to FLJ00128 protein (predicted)	RGD1308093_predicte	0.66±0.11
Similar to FLJ20298 protein isoform a (predicted)	RGD1563084_predicte	1.47±0.1
similar to Folylpolyglutamate synthase, mitochondrial precursor (Folylpoly-gamma-glutamate synthetase) (FPGS) (Tetrahydrofolate synth	LOC687266	4±0.93
similar to FUN14 domain containing 2 (predicted)	RGD1560916_predicte	2.5±0.13
Similar to G protein-coupled receptor 146 (predicted)	RGD1560731_predicte	0.74±0.03
similar to Galactosylceramide sulfotransferase (GalCer sulfotransferase) (Cerebroside sulfotransferase) (3-phosphoadenylylsulfate:galac	LOC683713	7.48±3.15
similar to gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	MGC125167	5.92±0.06
similar to GC-rich sequence DNA-binding factor homolog	LOC681004	1.16±0.41
similar to gem (nuclear organelle) associated protein 5	LOC686616	0.67±0.23
similar to gem (nuclear organelle) associated protein 7	LOC499391	1.67±0.04
similar to gene trap ROSA b-geo 22	LOC687166 /// LOC691	0.78±0.11
similar to GI:13385412-like protein splice form I	RGD735065	4.54±0.59
similar to GLI-Kruppel family member GLI4	LOC500893	0.86±0.09
similar to Glucocorticoid receptor DNA-binding factor 1	LOC686359	3.58±1.05
similar to Glucosylceramidase precursor (Beta-glucocerebrosidase) (Acid beta-glucosidase) (D-glucosyl-N-acylsphingosine glucohydrolas	LOC684536	1.22±0.25
similar to glutathione transferase GSTM7-7	MGC108896	0.35±0.05
similar to glycogen synthase 1, muscle	LOC687978 /// LOC690	3.19±0.26
similar to Golgi phosphoprotein 2 (Golgi membrane protein GP73)	LOC680692 /// LOC682	7.66±0.19
similar to GTL2, imprinted maternally expressed untranslated (predicted)	RGD1566401_predicte	0.31±0.16
similar to H43E16.1	LOC689994	0.39±0.1
similar to HCDI protein (predicted)	RGD1309307_predicte	1.16±0.3
similar to Hepatocellular carcinoma-associated antigen 58 homolog (predicted)	RGD1305020_predicte	0.41±0.16
Similar to heterogeneous nuclear ribonucleoprotein G - human	LOC302855	2.71±0.24
similar to Histidine triad nucleotide-binding protein 1 (Adenosine 5-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase	LOC690660	23.94±3.18
Similar to histocompatibility 28	LOC310968	1.6±0.93
similar to histone cell cycle regulation defective homolog A isoform 1	LOC363849	0.42±0.38
similar to Histone H1.2 (H1 VAR.1) (H1c)	LOC684681	25.18±11.6
similar to HIV-1 Rev binding protein	LOC363266	1.27±0.2
similar to HLA-B associated transcript-2 isoform a	LOC296637	4.44±1.38
similar to homeobox protein (predicted)	RGD1566402_predicte	1.63±0.55
similar to Homeobox protein Hox-D9 (Hox-4.4) (Hox-5.2)	LOC682957	3.71±0.09
similar to homeobox-containing transcription factor (predicted)	RGD1561431_predicte	2±0.52
similar to homeotic protein Hox 4.6 - mouse (predicted)	RGD1563800_predicte	1.38±0.01
similar to HSPC043 protein (predicted)	RGD1307983_predicte	1.47±0.05
similar to HSPC288 (predicted)	RGD1310769_predicte	1.16±0.05
similar to HT014 (predicted)	RGD1308048_predicte	3.4±0.5
similar to HT021 (predicted)	RGD1306063_predicte	2.96±0.27
similar to HTGN29 protein; keratinocytes associated transmembrane protein 2	RGD1310352	5.47±0.04
similar to hypothetical gene supported by AF226663 (predicted)	RGD1565146_predicte	0.72±0.14
similar to hypothetical gene supported by AK085276 (predicted)	RGD1562252_predicte	0.93±0.09
similar to hypothetical gene supported by BC025338 (predicted)	RGD1564419_predicte	1.11±0.31
similar to hypothetical MGC48595 (predicted)	RGD1566220_predicte	0.69±0.32
similar to hypothetical p38 protein (predicted)	RGD1311910_predicte	1.78±0.24
similar to hypothetical protein	RGD1306595	1.64±0.52
similar to hypothetical protein	RGD1310571	1.53±0.29
similar to hypothetical protein	RGD1307336	1.58±0.17
similar to hypothetical protein	RGD1311361	0.55±0.1
similar to hypothetical protein	RGD1310571	0.43±0.12
similar to hypothetical protein	LOC360479	0.34±0.01
similar to hypothetical protein (predicted)	RGD1305045_predicte	6.42±0.85
similar to hypothetical protein (predicted)	RGD1308489_predicte	2.03±0.22
similar to hypothetical protein (predicted)	RGD1561605_predicte	2.35±0.48
similar to hypothetical protein (predicted)	RGD1309765_predicte	1.59±0.76
similar to hypothetical protein (predicted)	RGD1565432_predicte	1.79±0.5
similar to hypothetical protein (predicted)	RGD1308489_predicte	1.97±0.11
similar to hypothetical protein (predicted)	RGD1310440_predicte	1.53±0.04
similar to hypothetical protein (predicted)	RGD1306576_predicte	1.57±0.09
similar to hypothetical protein (predicted)	RGD1560620_predicte	0.93±0.06
similar to hypothetical protein (predicted)	RGD1305269_predicte	0.43±0.16
similar to hypothetical protein (predicted)	RGD1560620_predicte	0.3±0.02
similar to hypothetical protein (predicted)	RGD1562590_predicte	0.4±0.23
similar to hypothetical protein BC011833 (predicted)	RGD1309188_predicte	5.35±1.51

similar to Hypothetical protein BC014729	MGC105560	3.66±0.49
similar to hypothetical protein BC015148 (predicted)	RGD1309095_predicte	0.26±0.14
similar to Hypothetical protein C6orf60 (predicted) /// similar to minichromosome maintenance protein 8 isoform 1 (predicted)	RGD1311294_predicte	0.38±0.01
similar to hypothetical protein CG003 (predicted)	RGD1307034_predicte	0.5±0.03
similar to Hypothetical protein CGI-99	RGD1304704	12.43±1.72
similar to hypothetical protein CL25084 (predicted)	RGD1306508_predicte	11.02±1.04
similar to hypothetical protein D030056L22	LOC499331	0.95±0.62
Similar to hypothetical protein D15Ertd785e	MGC114417	0.75±0.01
similar to hypothetical protein D2Ertd391e (predicted)	RGD1310685_predicte	3.37±0.79
similar to hypothetical protein DKFZp313N0621 (predicted)	RGD1560717_predicte	2.45±0.35
similar to hypothetical protein DKFZp434A1319 (predicted)	RGD1307357_predicte	0.24±0.27
similar to hypothetical protein DKFZp434K1815	LOC304396	0.41±0.03
similar to hypothetical protein DKFZp564D0478 (predicted)	RGD1304793_predicte	2.02±0.06
similar to hypothetical protein DKFZp761D0211 (predicted)	RGD1306151_predicte	5.2±0.45
similar to hypothetical protein ET (predicted)	RGD1307394_predicte	0.86±0.15
Similar to hypothetical protein F730001J03 (predicted)	RGD1311757_predicte	1.05±0.32
similar to hypothetical protein FLJ10154	RGD1310061	5.3±0.14
similar to hypothetical protein FLJ10342 (predicted)	RGD1307791_predicte	0.72±0.28
similar to hypothetical protein FLJ10901 (predicted)	RGD1311892_predicte	0.34±0.35
similar to hypothetical protein FLJ10925	RGD1305455	0.28±0.06
similar to hypothetical protein FLJ10986	LOC298250	2.16±0.22
similar to hypothetical protein FLJ11193 (predicted)	RGD1306502_predicte	1.36±0.45
similar to hypothetical protein FLJ11218	RGD1309804	0.43±0.53
Similar to hypothetical protein FLJ11305 (predicted)	RGD1307041_predicte	1.22±0.18
similar to hypothetical protein FLJ12118 (predicted)	RGD1311612 predicte	0.36±0.17
similar to hypothetical protein FLJ12242 (predicted)	RGD1311154_predicte	0.48±0.02
similar to hypothetical protein FLJ12661 (predicted)	RGD1309403_predicte	0.29±0.14
Similar to hypothetical protein FLJ12787	RGD1310992	0.22±0.04
similar to hypothetical protein FLJ13045 (predicted)	RGD1307615_predicte	1.17±0
similar to hypothetical protein FLJ13089	RGD1305685	0.3±0.13
similar to hypothetical protein FLJ13149 (predicted)	RGD1563839_predicte	1.72±0.41
similar to hypothetical protein FLJ13188 (predicted)	RGD1305500_predicte	0.38±0.21
similar to hypothetical protein FLJ13231 (predicted) /// hypothetical protein LOC679830	LOC679830 /// RGD13	0.3±0.07
similar to hypothetical protein FLJ14146	RGD1310587	2.17±1.35
similar to hypothetical protein FLJ14675	RGD1309592	0.73±1.15
similar to hypothetical protein FLJ20010 (predicted)	RGD1563941_predicte	3.66±0.17
similar to hypothetical protein FLJ20014	LOC497934	0.49±0.04
Similar to hypothetical protein FLJ20154	RGD1305793	3.86±1.51
similar to hypothetical protein FLJ20171 (predicted)	RGD1560481_predicte	2.07±0.14
similar to hypothetical protein FLJ20254	RGD1311324	2.32±0.73
similar to hypothetical protein FLJ20259 (predicted)	RGD1311095_predicte	0.36±0.39
similar to hypothetical protein FLJ20276 (predicted)	RGD1308101	0.2±0.02
similar to hypothetical protein FLJ20436	RGD1303127	3.57±0.52
similar to hypothetical protein FLJ20436 /// hypothetical LOC363737	LOC363737 /// RGD13	0.43±0.09
similar to hypothetical protein FLJ20487	RGD1309216	5.14±1.71
similar to hypothetical protein FLJ20507 (predicted)	RGD1309744_predicte	3.05±0.15
Similar to hypothetical protein FLJ20627 (predicted)	RGD1309546_predicte	2.33±0.41
Similar to hypothetical protein FLJ20674 (predicted)	RGD1565800_predicte	1.18±0.37
similar to hypothetical protein FLJ20729 (predicted)	RGD1308723_predicte	0.53±0.05
similar to hypothetical protein FLJ21156 (predicted)	RGD1309823 predicte	0.94±0.05
similar to hypothetical protein FLJ21820	RGD1311648	1.52±0.46
similar to hypothetical protein FLJ21827	RGD1307682	1.85±0.48
similar to hypothetical protein FLJ22175 (predicted)	RGD1306926_predicte	0.73±0.34
similar to hypothetical protein FLJ22490 (predicted)	RGD1307055_predicte	0.81±0.16
Similar to hypothetical protein FLJ22578 (predicted)	RGD1566232_predicte	0.36±0.06
similar to hypothetical protein FLJ22965 (predicted)	RGD1564541_predicte	0.95±0.36
similar to hypothetical protein FLJ23263	RGD1310414	0.31±0.12
Similar to hypothetical protein FLJ23451 (predicted)	RGD1310453_predicte	0.83±0.02
similar to hypothetical protein FLJ30596 (predicted)	RGD1306809_predicte	2.37±0.14
similar to hypothetical protein FLJ31528	RGD1307410	0.7±0.05
similar to hypothetical protein FLJ31606 (predicted)	RGD1561507_predicte	1.15±0.4
similar to hypothetical protein FLJ32796 (predicted)	RGD1311142_predicte	0.33±0.05
similar to hypothetical protein FLJ32825 (predicted)	RGD1564257_predicte	0.2±0.11
Similar to hypothetical protein FLJ32884 (predicted)	RGD1309453_predicte	1.97±0.13
similar to hypothetical protein FLJ33868 (predicted)	RGD1305797_predicte	0.94±0.06
Similar to hypothetical protein FLJ33977 (predicted)	RGD1306423_predicte	0.94±0.43
similar to hypothetical protein FLJ37953 (predicted)	RGD1311269_predicte	0.52±0.13
similar to Hypothetical protein KIAA0152	RGD1307736	0.63±0.15
similar to Hypothetical protein KIAA0373 (predicted)	RGD1311640_predicte	0.22±0.08
similar to hypothetical protein LOC284018 isoform b (predicted)	RGD1565033_predicte	1.5±0.17
similar to hypothetical protein LOC340061 (predicted)	RGD1562552_predicte	0.27±0.24
similar to Hypothetical protein MGC11690	RGD1305178	2.78±0.34
similar to hypothetical protein MGC14327 (predicted)	RGD1306304_predicte	1.92±0.1
Similar to hypothetical protein MGC17337 (predicted)	RGD1308165_predicte	0.22±0.16
Similar to hypothetical protein MGC17839 (predicted)	RGD1565079 predicte	0.85±0.04
similar to hypothetical protein MGC17943 (predicted)	RGD1563325_predicte	2.03±0.34
similar to Hypothetical protein MGC18716	RGD1307935	5.16±0.03
Similar to hypothetical protein MGC20700 (predicted)	RGD1307722_predicte	0.22±0.12
similar to hypothetical protein MGC23280 (predicted)	RGD1305508_predicte	1.84±0.06
similar to hypothetical protein MGC2494	RGD1306126	2.86±0.06
similar to hypothetical protein MGC25461 (predicted)	RGD1306717_predicte	0.24±0.01
similar to Hypothetical protein MGC25529 (predicted)	RGD1306746_predicte	1.6±0.24
Similar to hypothetical protein MGC29390 (predicted)	RGD1310490_predicte	0.45±0.15
similar to hypothetical protein MGC29875; novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7	LOC305076	0.64±0.01
similar to hypothetical protein MGC30618	RGD1305572	1.3±0.24
similar to hypothetical protein MGC3207	RGD1307789	1.59±0.68
Similar to hypothetical protein MGC36325 (predicted)	RGD1307374_predicte	0.8±0.34

similar to hypothetical protein MGC36831 (predicted)	RGD1306215_predicte	2.57±0.4
similar to hypothetical protein MGC37079 (predicted)	RGD1310484_predicte	1.8±0.24
similar to hypothetical protein MGC38960 (predicted)	RGD1310552_predicte	1.25±0.18
similar to hypothetical protein MGC40841; similar to hypothetical protein MGC4707	RGD1309540	0.97±0.26
similar to hypothetical protein MGC45873 (predicted)	RGD1310271_predicte	0.31±0.2
similar to hypothetical protein MGC52110 (predicted)	RGD1565095_predicte	26.18±0.91
similar to hypothetical protein MGC6696	RGD1309471	4.86±0.41
similar to hypothetical protein MGC7537	RGD1359380	3.48±0.16
similar to hypothetical protein MGC9912 (predicted)	RGD1309138_predicte	0.95±0.35
similar to hypothetical protein PRO0971	RGD1311435	1.7±0.04
similar to hypothetical protein supported by AL449243 (predicted) /// similar to CG17680-PA	LOC687237 /// RGD13	13.14±0.8
similar to Hypothetical UPF0184 protein C9orf16 homolog (predicted)	RGD1561113_predicte	3.31±0.37
similar to Hypothetical UPF0327 protein (predicted)	RGD1560187_predicte	25.87±4.44
similar to Interferon-alpha	LOC686326	0.39±0.36
similar to interferon-inducible GTPase	MGC108823	0.23±0.17
Similar to interleukin 17D precursor	LOC691799	0.31±0.31
similar to ionized calcium binding adapter molecule 2 (Iba2) (predicted)	RGD1305081_predicte	1.03±0.11
similar to IQ motif and Sec7 domain 1	LOC686590	5.68±0.65
similar to IQ motif and Sec7 domain 2	LOC685244	0.37±0.04
Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicte	1.59±0.04
similar to isochorismatase domain containing 2	LOC684270	3.98±0.55
similar to isopentenyl diphosphate delta-isomerase type 2 (predicted)	LOC689842 /// RGD15	0.49±0.69
similar to jumonji domain containing 1B	LOC682469	2.03±0.17
similar to jumonji domain containing 2B	LOC301128	0.63±0.16
similar to jumonji protein	LOC681740	1.84±0.24
similar to Jumonji/ARID domain-containing protein 1C (SmcX protein) (predicted)	RGD1560601_predicte	2.27±0.22
similar to K04F10.2	LOC361646	0.63±0.07
similar to K11B4.2	LOC688966	1.33±0.06
similar to K11B4.2	LOC684626 /// LOC68	0.5±0.07
similar to KB07 protein (predicted)	RGD1561940_predicte	3.78±0.4
similar to Kelch domain containing 4 (predicted)	RGD1561676_predicte	0.33±0.01
similar to Kelch-like protein 3 (predicted)	RGD1565218_predicte	0.64±0.2
similar to keratinocytes associated protein 3	LOC683980	0.89±0.16
similar to KIAA0090 protein (predicted)	RGD1310427_predicte	0.68±0.1
similar to KIAA0157 gene product is novel. (predicted)	RGD1308918_predicte	1.08±0.13
Similar to KIAA0240 (predicted)	RGD1305680_predicte	0.61±0.06
similar to KIAA0335	RGD1305314	0.76±0.31
similar to KIAA0368 (predicted)	RGD1306148_predicte	3.11±0.43
similar to KIAA0372 gene product (predicted)	RGD1306062_predicte	0.89±0.08
similar to KIAA0406-like protein (predicted)	RGD1562582_predicte	1.76±0.04
similar to KIAA0423 (predicted)	RGD1310474_predicte	1.03±0.08
similar to KIAA0467 protein (predicted)	RGD1308616_predicte	1.44±0.03
similar to KIAA0528 protein (predicted)	RGD1304592_predicte	1.38±0.77
Similar to KIAA0564 protein (predicted)	RGD1308772_predicte	0.5±0.02
Similar to KIAA0597 protein (predicted)	RGD1565757_predicte	4.05±0.47
similar to KIAA0614 protein (predicted)	RGD1309762_predicte	1.56±0.11
Similar to KIAA0672 gene product	RGD1305664	0.35±0.03
similar to KIAA0833 protein /// similar to calmodulin-binding transcription activator 1	LOC362665 /// LOC50	1.3±0.41
similar to KIAA0853 protein (predicted)	RGD1563689_predicte	1.87±1.07
Similar to KIAA0869 protein (predicted)	RGD1308329_predicte	0.42±0.01
similar to KIAA0892 protein (predicted)	RGD1308759_predicte	0.92±0.06
similar to KIAA0913 protein (predicted)	RGD1309414_predicte	1.45±0.34
similar to KIAA0947 protein (predicted)	RGD1309747_predicte	0.75±0.04
similar to KIAA0965 protein (predicted)	RGD1564793_predicte	0.78±0.06
similar to KIAA0999 protein	LOC684112	2.19±0.37
similar to KIAA1007 protein; adrenal gland protein AD-005	RGD1308009	2.88±0.16
similar to KIAA1009 protein	RGD1307365	0.31±0.03
similar to KIAA1078 protein (predicted)	RGD1310950_predicte	2.14±0.27
Similar to KIAA1183 protein (predicted)	RGD1560435_predicte	0.77±0.32
similar to KIAA1217 (predicted)	RGD1563437_predicte	2.47±0.9
similar to KIAA1267 protein (predicted)	RGD1311429_predicte	2.33±0.41
Similar to KIAA1280 protein (predicted)	RGD1560666_predicte	1.06±0.07
similar to KIAA1411 protein (predicted)	RGD1304927_predicte	0.8±0.14
similar to KIAA1582 protein (predicted)	RGD1310027_predicte	1.55±0.25
similar to KIAA1627 protein (predicted)	RGD1304822_predicte	1.91±0.16
similar to KIAA1636 protein (predicted)	RGD1309285_predicte	0.23±0.02
similar to KIAA1731 protein (predicted)	RGD1311723_predicte	0.2±0.09
similar to KIAA1841 protein (predicted)	RGD1305110_predicte	0.3±0.02
similar to KIAA2026 protein	RGD1311595	0.98±0.12
similar to kynurenine formamidase	rCG_34031	0.8±0.02
Similar to Lethal giant larvae homolog 2 (predicted)	RGD1560307_predicte	3.2±0.2
similar to leucine rich repeat and fibronectin type III domain containing 4	LOC688721	1.01±0.26
similar to LEYDIG CELL TUMOR 10 KD PROTEIN	LOC288913	3.35±0.35
similar to ligatin	LOC498225	1.78±0.22
Similar to Lmnb2 protein (predicted)	RGD1563803_predicte	0.28±0.04
similar to LOC387763 protein (predicted)	RGD1564664_predicte	0.73±0.21
similar to LOC495800 protein	LOC499770	0.25±0.29
similar to lymphocyte antigen 6 complex, locus E ligand	LOC501282	3.41±0.28
similar to lysophosphatidylglycerol acyltransferase 1	LOC679692	1.81±0.65
similar to M phase phosphoprotein 6	LOC686999	1.72±0.21
similar to Maleylacetoacetate isomerase (MAAI) (Glutathione S-transferase zeta 1) (GSTZ1-1)	LOC681913	3.41±0.84
similar to mammalian retrotransposon derived 8b	LOC678880	5.18±0.45
similar to Map4k6-pending protein /// similar to misshapen-like kinase 1 isoform 1	LOC303259 /// LOC68	6.88±0.41
similar to MASK-4E-BP3 protein	LOC682955	1.78±0.02
similar to MASK-4E-BP3 protein	LOC679725 /// LOC68	1.44±0.19
similar to MASK-4E-BP3 protein	LOC679725	0.41±0.2
similar to mbt domain containing 1	LOC688133	2.21±0.01

similar to Mediator of RNA polymerase II transcription subunit 12 (Thyroid hormone receptor-associated protein complex 230 kDa compo	LOC679693	1.28±0.09
similar to mediator of RNA polymerase II transcription, subunit 18 homolog	LOC682988	1.06±0.54
similar to melanoma inhibitory activity 3	LOC683007	3.52±0.05
similar to membrane-associated RING-CH protein IX	LOC679272	0.96±0.2
similar to Metaxin 1, isoform 2	LOC295241	2.03±0.12
similar to methionine adenosyltransferase II, beta /// methionine adenosyltransferase II, beta	Mat2b /// MGC94725	9.86±0.08
similar to Methionine-R-sulfoxide reductase (Selenoprotein X 1) (Selenoprotein R)	MGC105753	2.61±0.94
similar to microfibrillar-associated protein 1 (predicted) /// microfibrillar-associated protein 1A	Mfap1a /// RGD156414	1.78±0.14
similar to microfilament and actin filament cross-linker protein isoform b	LOC362587	3.24±0.62
similar to Microtubule-associated protein RP/EB family member 2 (APC-binding protein EB2) (End-binding protein 2) (EB2)	LOC679221	1.4±0.4
similar to Microtubule-associated serine/threonine-protein kinase 3	LOC684053	0.38±0.03
similar to mirror-image polydactyly 1	LOC687620	1.11±0.18
similar to mitochondria-associated granulocyte macrophage CSF signaling molecule (predicted)	Magmas /// RGD15644	4.83±1.42
similar to Mitochondrial 28S ribosomal protein S28 (S28mt) (MRP-S28)	LOC679330	2.62±0.8
similar to Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39)	LOC684304	2.15±0.64
similar to Mitochondrial carrier triple repeat 1 (predicted)	LOC686727 /// Mcart2_	1.85±0.64
similar to mitochondrial hepatocellular carcinoma-downregulated carrier protein	LOC684556	0.34±0.27
similar to mitochondrial ribosomal protein L10	LOC691075	2.7±0.18
similar to mKIAA0215 protein (predicted)	RGD1563945_predicte	0.24±0.3
similar to mKIAA0256 protein (predicted)	RGD1559930_predicte	0.71±0.4
similar to mKIAA0317 protein (predicted)	RGD1307597_predicte	1.35±0.05
similar to mKIAA0664 protein (predicted)	RGD1307222_predicte	10.52±1.06
similar to mKIAA0738 protein (predicted)	RGD1565474_predicte	0.4±0.15
similar to mKIAA0978 protein (predicted)	RGD1561878_predicte	1.21±0.57
similar to mKIAA0998 protein (predicted)	RGD1563583_predicte	0.63±0.33
similar to mKIAA1011 protein	LOC366669	5.85±0.38
similar to mKIAA1111 protein (predicted)	RGD1561065_predicte	1.17±0.07
Similar to mKIAA1208 protein (predicted)	RGD1564821_predicte	1.2±0.28
similar to mKIAA1402 protein (predicted)	RGD1306404_predicte	0.24±0.02
similar to mKIAA1429 protein (predicted)	RGD1559904_predicte	0.89±0.38
similar to mKIAA1450 protein (predicted)	RGD1562174_predicte	0.99±0.07
similar to mKIAA1461 protein	LOC311026	0.52±0.03
similar to mKIAA1604 protein (predicted)	RGD1565385_predicte	0.42±0.24
similar to mKIAA1737 protein (predicted)	RGD1309492_predicte	2.67±0.25
similar to mKIAA1797 protein (predicted)	RGD1311849_predicte	0.92±0.25
similar to mKIAA1924 protein (predicted)	RGD1561785_predicte	0.31±0.1
similar to mKIAA1931 protein (predicted)	RGD1562335_predicte	0.96±0.19
similar to mKIAA2005 protein (predicted)	RGD1561472_predicte	0.54±0.21
similar to mKIAA2005 protein (predicted)	LOC500013 /// RGD15	6.76±2.14
similar to Mkrn1 protein	MGC94941	1.39±0.12
similar to modulator of estrogen induced transcription	RGD1307526	2.26±0.51
similar to monogenic, audiogenic seizure susceptibility 1	LOC685383	4.11±0.22
similar to Mospd2 protein (predicted)	RGD1563952_predicte	2.39±0.9
Similar to Msx2-interacting protein (SPEN homolog) (SMART/HDAC1-associated repressor protein)	LOC690911	2.16±0.53
similar to multi sex combs CG12058-PA	LOC686883	2.93±0.24
Similar to Murine homolog of human ftp-3	LOC308650	1.4±0.3
similar to muscleblind-like 2 isoform 1	LOC680445	8.76±1.04
Similar to Myc-associated zinc finger protein (MAZI) (Purine-binding transcription factor) (Pur-1)	LOC691842	1.01±0.35
Similar to myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog	LOC301119	0.27±0.23
similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lysine N-methyltransferase, H3 lysine-4 specific MLL3	LOC502710	3.71±0.18
similar to myocyte enhancer factor 2C	LOC309957	0.95±0.41
similar to myosin XVIIIa	LOC360570	4.28±0.36
similar to MYST histone acetyltransferase monocytic leukemia 4 (predicted)	RGD1566399_predicte	1.72±0.01
similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)	LOC683547	26.09±3.03
similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) (CI-PDSW)	LOC681418 /// LOC681	19.21±3.55
similar to Naglu (predicted)	RGD1564228_predicte	4.26±1.47
similar to Negative elongation factor D (NELF-D) (TH1-like protein)	LOC679203	1.83±0.36
Similar to nemo like kinase (predicted)	RGD1561602_predicte	0.34±0.06
similar to nemo like kinase (predicted) /// nemo like kinase	Nlk /// RGD1561440_pr	1.65±0.62
similar to neurobeachin (predicted)	RGD1562629_predicte	4.07±1.3
similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27)	MGC72932	4.51±0.02
similar to NICE-3	LOC361985	7.67±1.18
similar to Nicotinamide riboside kinase 1	LOC499330	0.38±0.33
similar to NMDA receptor regulated 1-like	LOC686240	0.28±0.03
similar to NNX3 (predicted)	RGD1310358_predicte	4±1.35
similar to novel protein (HT036) (predicted)	RGD1561416_predicte	0.6±0.13
similar to novel protein (predicted)	RGD1563106_predicte	2.03±0.37
similar to novel protein (predicted)	RGD1560636_predicte	0.32±0.01
similar to novel protein (predicted)	RGD1566099_predicte	0.59±0.12
similar to novel protein of unknown function (DUF423) family member (predicted)	RGD1563438_predicte	4.62±0.65
similar to Nuclear membrane binding protein NUCLING (predicted)	RGD1560011_predicte	0.45±0.22
similar to nuclear receptor binding protein	LOC680451	5.49±0.1
similar to Nucleolar protein 11	LOC688235	1.61±0.24
similar to nucleolar protein with MIF4G domain 1	LOC682058	0.78±0.07
similar to O-acetyltransferase	LOC678772	0.77±0.31
similar to olfactory receptor 873	LOC687016	1.19±0.39
similar to Oligosaccharyl transferase 3 CG7748-PA	RGD1311563	11.21±0.96
similar to oocyte-testis gene 1 (predicted)	RGD1307158_predicte	0.57±0.17
similar to OPA3 protein (predicted)	RGD1561117_predicte	1.76±0.18
Similar to oxoglutarate dehydrogenase (lipoamide)	LOC360975	0.61±0.17
similar to p150 target of rapamycin (TOR)-scaffold protein containing WD-repeats (predicted)	RGD1311784_predicte	0.76±0.17
similar to Paired amphipathic helix protein Sin3b (Transcriptional corepressor Sin3b) (Histone deacetylase complex subunit Sin3b)	LOC683381	3.33±0.17
similar to pancreatitis-induced protein 49	RGD1308600	0.93±0.48
similar to Peptide chain release factor 1, mitochondrial precursor (MRF-1)	LOC686234	0.47±0.11
similar to peptide deformylase-like protein	LOC690214	1.04±0.35
similar to peptidyl prolyl isomerase H (predicted)	RGD1564921_predicte	1.09±0.06
similar to peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor; peptidylglycine alpha-amidating monooxygenase C	RGD1309847_predicte	0.83±0.05

similar to Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (Rotamase Pin4) (PPIase Pin4)	LOC684441	2.83±1.7
similar to peptidylprolyl isomerase D	LOC295142 /// LOC36	0.38±0.07
similar to pericentrin	LOC687681	0.85±0.09
similar to Peroxidasin CG12002-PA (predicted)	RGD1308720_predicte	0.5±0.06
similar to Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxisomal farnesylated protein)	LOC289233	1.46±0.05
similar to PES1 protein	LOC289740	0.59±0.11
Similar to PHD finger protein 14 isoform 1 (predicted)	RGD1563764_predicte	1.36±0.58
similar to PHD zinc finger containing protein JUNE1	MGC94192	1.27±0.58
similar to PHF21A protein (predicted)	RGD1560612_predicte	0.43±0.14
similar to phosphoseryl-tRNA kinase (predicted)	RGD1564300_predicte	5.28±0.56
Similar to PI-3-kinase-related kinase SMG-1	Arl6ip1	3.2±0.61
similar to Placental protein 25 homolog (PP25)	LOC685284	0.78±0.12
similar to plasma kallikrein-like protein 4 precursor /// gene trap locus 3	Gtl3 /// RGD1307877	1.55±0.65
similar to plexin 1 (predicted)	RGD1560871_predicte	1.04±0.42
similar to polyglutamine-containing protein	RGD1310994	8.39±0.84
similar to POT1-like telomere end-binding protein	LOC500054	1.41±0.03
similar to potassium channel modulatory factor 1	LOC684322	4.02±0.76
similar to praja1, RING-H2 motif containing	LOC683077	3.96±0.91
similar to predicted CDS, putative protein of bilaterial origin (4J193)	RGD1306153	0.34±0.08
similar to prefoldin 4 (predicted)	RGD1560211_predicte	2.43±0.57
similar to Prefoldin subunit 2 /// prefoldin 2	LOC678975 /// Pfdn2	0.53±0.16
similar to Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1) (VHL-binding protein 1) (VBP-1)	LOC681825	1.12±0.13
similar to PRO1853 homolog	RGD1311578	0.86±0.09
similar to Probable ATP-dependent RNA helicase DHX34 (DEAH box protein 34)	LOC684903	0.76±0.17
similar to procollagen C-endopeptidase enhancer 2	LOC684050	0.27±0.19
similar to product is unknown~seizure-related gene (predicted) /// similar to Ornithine decarboxylase antizyme 2 (ODC-Az 2) (AZ2)	LOC690789 /// RGD15	4.82±1.35
similar to Proline oxidase, mitochondrial precursor (Proline dehydrogenase)	LOC680409	1.48±0.42
similar to Protease-associated domain-containing protein of 21 kDa precursor	LOC686393	1.14±0.08
similar to Proteasome inhibitor PI31 subunit	LOC682071 /// LOC68	1.76±0.04
similar to Protein C12orf11 (Sarcoma antigen NY-SAR-95)	LOC690728	0.7±1
similar to Protein C18orf1	LOC679578	0.21±0
similar to Protein C20orf20	RGD1308612	2.51±0.26
Similar to Protein C22orf5	RGD1306591	1.9±0.81
similar to protein C33A12.3	RGD1359508	1±0.05
similar to Protein C6orf115	LOC684848 /// LOC68	0.5±0.06
similar to Protein C6orf203	LOC683897	4.68±1.69
similar to Protein C7orf26 homolog	LOC683674	2.04±0.56
similar to Protein C8orf4 (Thyroid cancer protein 1) (TC-1)	LOC684871	13.04±3.61
similar to Protein CGI-117 (Protein HSPC111) (predicted)	RGD1305727_predicte	2.36±0.24
similar to Protein disulfide-isomerase TXNDC10 precursor (Thioredoxin domain-containing protein 10)	LOC682967	3.18±0.82
similar to Protein FAM60A (Tera protein)	LOC686611	0.95±0.22
similar to Protein KIAA0280	LOC503175 /// LOC69	7.61±0.69
similar to Protein KIAA1404	LOC686701	0.8±0.17
similar to Protein KIAA1543	LOC682941 /// LOC68	1.02±0.16
similar to Protein KIAA1688	LOC500901	0.82±0.1
similar to Protein Njmu-R1 (predicted)	RGD1310429_predicte	0.47±0.02
Similar to protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	0.21±0.12
similar to Protein SYS1 homolog	LOC685079	4.34±0.4
similar to Protein transport protein SEC61 gamma subunit	LOC689134	12.54±2.81
similar to protein tyrosine phosphatase, receptor type, D (predicted)	RGD1561090_predicte	9.3±0.3
similar to Protein UNQ655/PRO1286 homolog precursor	LOC686324	2.28±0.42
Similar to putative phosphoinositide 5-phosphatase type II; C62	LOC287533	0.69±0.35
similar to Putative protein 15E1.2 (predicted)	RGD1309698_predicte	0.51±0.04
similar to putative protein, with at least 9 transmembrane domains, of eukaryotic origin (43.9 kD) (2G415)	RGD1309228	0.55±0.1
similar to putative repair and recombination helicase RAD26L (predicted)	RGD1561537_predicte	1.61±0.4
similar to putative RNA methyltransferase (predicted)	RGD1309077_predicte	0.22±0.13
similar to Putative RNA-binding protein 15 (RNA-binding motif protein 15) (One-twenty two protein)	LOC684233	2.08±0.13
similar to R31449_3 (predicted)	RGD1563634_predicte	0.67±0.17
similar to RAB11 family interacting protein 5 (class I) isoform 1	LOC312502	3.14±0.16
similar to RAB3 GTPase-activating protein (predicted)	RGD1306487_predicte	2.52±0.58
similar to ras homolog gene family, member f	LOC687609	2.42±0.95
Similar to Ras suppressor protein 1	LOC680419	0.73±0.52
similar to Ras-related protein Rab-1B /// RAB1B, member RAS oncogene family	MGC105830 /// rCG_4	4.24±0.27
similar to RCK (predicted)	RGD1564560_predicte	3.26±0.85
similar to receptor-interacting factor 1	RGD1306520	0.25±0.46
similar to Recombining binding protein suppressor of hairless (J kappa-recombination signal binding protein) (RBP-J kappa)	LOC679028	2.26±0.03
similar to reduced expression 2	LOC690559	0.22±0.29
similar to replication protein-binding trans-activator RBT1	MGC108974	0.98±0.11
similar to REST corepressor 3	LOC684192	1.65±0.24
Similar to Retinoblastoma-binding protein 2 (RBBP-2)	LOC312678	2.39±0.14
similar to Retinoic acid receptor gamma-A (RAR-gamma-A)	LOC685072	0.76±0.4
similar to Rho guanine nucleotide exchange factor (GEF) 10 (predicted)	RGD1565043_predicte	0.9±0.17
similar to ribosomal protein L22 proprotein	LOC365157	1.64±0.23
similar to ribosomal protein L27a (predicted)	RGD1560633_predicte	1.6±0.35
similar to ribosomal protein, mitochondrial, S22	LOC683519	2.11±0.14
similar to RIKEN cDNA 0610007P06	LOC293103	3.97±0.22
similar to RIKEN cDNA 0610007P22 (predicted)	RGD1565744_predicte	0.95±0.1
Similar to RIKEN cDNA 0610010D20 (predicted)	RGD1310475_predicte	3.85±0.32
similar to RIKEN cDNA 0610011L14 gene	RGD1311066	0.98±0.12
similar to RIKEN cDNA 0610037D15	LOC298442	0.34±0.05
similar to RIKEN cDNA 0610037L13	RGD1559786	2.6±0.76
similar to RIKEN cDNA 0610037P05	RGD1305823	4.13±0.62
similar to RIKEN cDNA 0610038D11 (predicted)	RGD1309710_predicte	2.79±0.05
similar to RIKEN cDNA 0610038L10 gene (predicted) /// riboflavin kinase /// similar to riboflavin kinase (predicted)	Rfk /// RGD1560961_p	6.78±1.07
similar to RIKEN cDNA 0610039J04	RGD1562218	0.86±0.37
similar to RIKEN cDNA 0610039K22 (predicted) /// similar to CG3295-PA /// similar to RIKEN cDNA 0610039K22	LOC361780 /// MGC11	0.41±0.04
similar to RIKEN cDNA 0610040J01	LOC498368	1.73±0.09

similar to RIKEN cDNA 0710008K08 (predicted)	RGD1562691_predicte	0.4±0.2
similar to RIKEN cDNA 1110001A07 gene /// hypothetical protein LOC687897 /// hypothetical protein LOC691962	LOC687897 /// LOC691	1.57±0.2
similar to RIKEN cDNA 1110001J03	MGC112899	10.49±1.22
similar to RIKEN cDNA 1110001M20 (predicted)	RGD1310313_predicte	18.7±2.12
similar to RIKEN cDNA 1110003E01	RGD1311122	3.67±0.12
similar to RIKEN cDNA 1110004E09	RGD1306954	1.89±0.27
similar to RIKEN cDNA 1110005A03	RGD1306284	2.17±0.47
similar to RIKEN cDNA 1110007C09 (predicted)	RGD1306058_predicte	3.89±0.41
similar to RIKEN cDNA 1110007L15 (predicted)	RGD1311660_predicte	2.38±0.11
similar to RIKEN cDNA 1110008F13	RGD1307752	10.36±0.12
similar to RIKEN cDNA 1110008J03 (predicted)	RGD1306772_predicte	0.41±0.3
similar to RIKEN cDNA 1110012L19 (predicted)	RGD1562747_predicte	1.38±0
similar to RIKEN cDNA 1110018J12 (predicted)	RGD1565310_predicte	1.35±0.14
Similar to RIKEN cDNA 1110020A23 (predicted)	RGD1308134_predicte	1.52±0.08
similar to RIKEN cDNA 1110031I02	RGD1305007	4±0.71
Similar to RIKEN cDNA 1110038F21 (predicted)	RGD1562059_predicte	4.5±0.19
similar to RIKEN cDNA 1110059E24	RGD1359158	1.5±0.19
similar to RIKEN cDNA 1110059G10	RGD1311745	2.67±0.35
similar to RIKEN cDNA 1190005P17 (predicted)	RGD1308261_predicte	1.23±0.62
similar to RIKEN cDNA 1200003C05 (predicted)	RGD1308917_predicte	3.92±0.02
similar to RIKEN cDNA 1200009B18; EST AA408438	RGD1310606	3.4±0.29
similar to RIKEN cDNA 1200011I18	RGD1307254	0.23±0.16
similar to RIKEN cDNA 1200011M11 (predicted)	RGD1306862_predicte	0.7±0.37
similar to RIKEN cDNA 1200013P24	RGD1308915	1.86±0.78
similar to RIKEN cDNA 1200014J11 (predicted)	RGD1308139_predicte	1.77±0.13
similar to RIKEN cDNA 1200014M14	RGD1310597	0.24±0.22
similar to RIKEN cDNA 1200016B10 (predicted)	RGD1308695_predicte	1.54±0.48
similar to RIKEN cDNA 1300018I05	RGD1307801	3.43±0.23
similar to RIKEN cDNA 1500002O20	RGD1309888	1.07±0.24
similar to RIKEN cDNA 1500003O22	RGD1308302	0.84±0.37
similar to RIKEN cDNA 1500011H22	RGD1310861	2.07±0.64
similar to RIKEN cDNA 1500031L02	RGD621352	3.17±0.22
similar to RIKEN cDNA 1600012F09 (predicted)	RGD1306613_predicte	2.69±0.69
similar to RIKEN cDNA 1600029D21	LOC363060	7.81±0.75
similar to RIKEN cDNA 1700012G19 gene (predicted)	RGD1307773_predicte	3.74±0.48
similar to RIKEN cDNA 1700023M03	RGD1305457	0.57±0.15
Similar to RIKEN cDNA 1700027M01	RGD1311815	1.93±0.15
similar to RIKEN cDNA 1700027N10 (predicted)	RGD1310693_predicte	0.69±0.27
similar to RIKEN cDNA 1700037H04	RGD1311739	1.22±0.01
similar to RIKEN cDNA 1700040L02 (predicted)	RGD1306739_predicte	2.12±0.35
similar to RIKEN cDNA 1700052N19	RGD1305235	2.62±1.35
similar to RIKEN cDNA 1700088E04	RGD1359634	0.58±0.07
similar to RIKEN cDNA 1700108L22	RGD1307509	1.53±0.55
similar to RIKEN cDNA 1810014F10 gene (predicted)	RGD1311186_predicte	5±1.28
similar to RIKEN cDNA 1810020D17 (predicted)	RGD1561459_predicte	2.55±0.27
similar to RIKEN cDNA 1810021J13	RGD1311364	2.74±0.67
similar to RIKEN cDNA 1810022C23	RGD1310224	2.23±1.37
similar to RIKEN cDNA 1810030N24 (predicted)	RGD1305158_predicte	2.54±0.8
similar to RIKEN cDNA 1810030O07 (predicted)	RGD1565685_predicte	3.38±0.97
Similar to RIKEN cDNA 1810036I24 (predicted)	RGD1306343_predicte	7.36±0.57
similar to RIKEN cDNA 1810042K04 (predicted)	RGD1305593_predicte	1.64±0.06
similar to RIKEN cDNA 1810043G02; DNA segment, Chr 10, Johns Hopkins University 13, expressed	RGD1309594	1.16±0.18
similar to RIKEN cDNA 1810046J19 (predicted)	RGD1306682_predicte	5.16±1.45
similar to RIKEN cDNA 1810063B07 gene (predicted)	RGD1310877_predicte	0.82±0.27
similar to RIKEN cDNA 1810074P20 (predicted)	RGD1309308_predicte	1.18±0.06
similar to RIKEN cDNA 2010011I20 (predicted)	RGD1311378_predicte	1.23±0.13
similar to RIKEN cDNA 2010012F05 (predicted)	RGD1309846_predicte	7.42±0.98
Similar to RIKEN cDNA 2010012O05 (predicted)	RGD1311783_predicte	3.48±0.4
similar to RIKEN cDNA 2010107G23 (predicted) /// hypothetical protein LOC679430	LOC679430 /// RGD13	6.56±0.56
similar to RIKEN cDNA 2010110K16 (predicted)	RGD1305283_predicte	1.51±0.48
similar to RIKEN cDNA 2010200O16 (predicted)	RGD1564454_predicte	2.81±0.1
similar to RIKEN cDNA 2010301N04 (predicted)	RGD1565557_predicte	0.64±0.36
similar to RIKEN cDNA 2010309E21 (predicted)	RGD1304825_predicte	1.71±0.16
similar to RIKEN cDNA 2010311D03	RGD1303272	5.65±0.69
similar to RIKEN cDNA 2010316F05 (predicted)	RGD1308179_predicte	0.4±0.17
similar to RIKEN cDNA 2210009G21 (predicted)	RGD1563120_predicte	0.32±0.06
similar to RIKEN cDNA 2210010N04 gene	RGD1306873	0.27±0.1
similar to RIKEN cDNA 2210012G02	LOC366431	0.93±0.13
similar to RIKEN cDNA 2210016L21 gene	RGD1311899	2.43±0.35
similar to RIKEN cDNA 2310001A20	RGD1308874	1.3±1.44
similar to RIKEN cDNA 2310002J15 (predicted)	RGD1560880_predicte	0.24±0.01
similar to RIKEN cDNA 2310004I24 gene	RGD1309906	0.49±0.22
Similar to RIKEN cDNA 2310005N03 gene	RGD1309105_predicte	1.36±0.45
similar to RIKEN cDNA 2310007F12 (predicted)	RGD1562416_predicte	1.03±0.27
similar to RIKEN cDNA 2310008H04 (predicted)	RGD1566036_predicte	0.57±0.33
similar to RIKEN cDNA 2310011J03	RGD1359127	3±0.61
similar to RIKEN cDNA 2310016C16 (predicted)	RGD1307506_predicte	3.6±0.56
similar to RIKEN cDNA 2310022B05 (predicted)	RGD1559896_predicte	0.34±0.26
similar to RIKEN cDNA 2310028N02	RGD1359339	0.57±0.03
similar to RIKEN cDNA 2310033P09	RGD1304587	1.45±0.34
similar to RIKEN cDNA 2310035C23 (predicted)	RGD1307235_predicte	1.66±0.25
similar to RIKEN cDNA 2310036O22 (predicted) /// similar to CG18809-PA, isoform A	LOC690331 /// RGD15	4.95±0.42
similar to RIKEN cDNA 2310042G06	MGC72955	2.81±1.07
similar to RIKEN cDNA 2310045A20 (predicted)	RGD1562860_predicte	0.21±0.1
similar to RIKEN cDNA 2310047O13 (predicted)	RGD1309605_predicte	2.57±0.17
similar to RIKEN cDNA 2310057M21	RGD1305014	0.34±0.14
similar to RIKEN cDNA 2310061F22	LOC292069	0.3±0.01

similar to RIKEN cDNA 2310079N02 (predicted)	RGD1306192_predicte	3.95±0.4
similar to RIKEN cDNA 2400003C14	RGD1307799	5.96±0.57
similar to RIKEN cDNA 2400010D15	RGD1311805	0.89±0.36
similar to RIKEN cDNA 2410002F23	RGD1309326	0.97±0.06
similar to RIKEN cDNA 2410002O22 gene	RGD1306583	3.92±0.64
similar to RIKEN cDNA 2410004B18 (predicted)	RGD1560065_predicte	1.69±0
similar to RIKEN cDNA 2410016O06 (predicted)	RGD1307704_predicte	0.4±0.03
similar to RIKEN cDNA 2410022L05 (predicted)	RGD1565675_predicte	1.79±0.34
similar to RIKEN cDNA 2410025L10 (predicted)	RGD1563342_predicte	1.78±0.13
similar to RIKEN cDNA 2510039O18 (predicted)	RGD1305350_predicte	0.77±0.31
similar to RIKEN cDNA 2600017H02 (predicted)	RGD1561781_predicte	0.52±0.53
similar to RIKEN cDNA 2610003J06	RGD1307381	1.09±0.31
similar to RIKEN cDNA 2610019F03	LOC498662	0.33±0.1
similar to RIKEN cDNA 2610029G23 (predicted)	RGD1562502_predicte	0.97±0.1
Similar to RIKEN cDNA 2610110G12	RGD1303066	0.26±0
similar to RIKEN cDNA 2610205E22	RGD1306582	2.63±0.41
similar to RIKEN cDNA 2610209A20 (predicted)	RGD1305211_predicte	0.45±0.04
similar to RIKEN cDNA 2610301B20; EST AI428449	MGC94199	0.74±0.04
similar to RIKEN cDNA 2610304G08 gene (predicted)	RGD1304782_predicte	1.18±0.47
similar to RIKEN cDNA 2610528E23	RGD1309437	0.83±0.18
similar to RIKEN cDNA 2610528J11 (predicted)	RGD1305347_predicte	6.19±0.93
similar to RIKEN cDNA 2700002I20	RGD1307279	5.94±1.5
similar to RIKEN cDNA 2700038C09	RGD1310660	2.49±0.8
similar to RIKEN cDNA 2700062C07	MGC116121	1.04±0.06
similar to RIKEN cDNA 2700081O15 (predicted)	RGD1560108 predicte	1.02±0.13
similar to RIKEN cDNA 2810002N01	RGD1304719	7.77±0.75
similar to RIKEN cDNA 2810403A07	RGD1565775	4.03±0.48
similar to RIKEN cDNA 2810428I15 (predicted)	RGD1566239_predicte	1.28±0.29
similar to RIKEN cDNA 2810432L12	RGD1307218	3.16±0.25
Similar to RIKEN cDNA 2810443J12 (predicted)	RGD1304868_predicte	0.51±0.18
similar to RIKEN cDNA 2810453I06	LOC498145	0.93±0.16
similar to RIKEN cDNA 2810485I05 (predicted)	RGD1311077_predicte	1.41±0.1
similar to RIKEN cDNA 2900010J23	LOC499779	3.86±1.5
similar to RIKEN cDNA 2900010M23 (predicted)	RGD1306917_predicte	7.68±1.38
similar to RIKEN cDNA 2900092E17	RGD1305592	0.65±0.21
similar to RIKEN cDNA 3110001D03 (predicted)	RGD1309148_predicte	2.36±0.06
similar to RIKEN cDNA 3110001I22 (predicted)	RGD1305537_predicte	0.86±0.33
similar to RIKEN cDNA 3110037I16 (predicted)	RGD1309802_predicte	0.26±0.08
similar to RIKEN cDNA 3110040N11	RGD1305713	0.74±0.01
similar to RIKEN cDNA 3110043O21	RGD1359108	0.45±0.16
Similar to RIKEN cDNA 3110050N22 (predicted)	RGD1311970_predicte	2.64±0.35
similar to RIKEN cDNA 3200002M19 (predicted)	RGD1311634_predicte	2.82±0.01
similar to RIKEN cDNA 3930401K13	RGD1309459	2.65±0.36
similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicte	3.21±0.07
similar to RIKEN cDNA 4632411B12	RGD1309220	2.03±0.13
similar to RIKEN cDNA 4732418C07 (predicted)	RGD1310351_predicte	1.73±0.42
similar to RIKEN cDNA 4833418A01 (predicted)	RGD1565551_predicte	0.35±0.03
similar to RIKEN cDNA 4921524J17 (predicted)	RGD1308706_predicte	3.05±0.49
similar to RIKEN cDNA 4930444A02	RGD1310810	1.78±0.34
similar to RIKEN cDNA 4930455F23	RGD1309708	0.7±0.16
similar to RIKEN cDNA 4930538D17	RGD1309313	0.87±0.16
similar to RIKEN cDNA 4930550C14	RGD1311251	1.04±0.47
similar to RIKEN cDNA 4930570C03	LOC300191	3.13±0.36
similar to RIKEN cDNA 4930579G22 (predicted)	RGD1560258_predicte	0.97±0.2
similar to RIKEN cDNA 4931400A14 (predicted)	RGD1307234_predicte	1.1±0.8
similar to RIKEN cDNA 4931406C07	RGD1309534	0.68±1.71
similar to RIKEN cDNA 4931406P16 (predicted)	RGD1308428_predicte	1.22±0.16
similar to RIKEN cDNA 4931414P19 (predicted)	RGD1565222_predicte	0.38±0.09
similar to RIKEN cDNA 4932432K03	RGD1308087	1.05±0.21
Similar to RIKEN cDNA 4933404M02	LOC499806	0.58±0
similar to RIKEN cDNA 4933406L09	LOC361016	0.3±0.01
similar to RIKEN cDNA 4933428G09 (predicted)	RGD1311045_predicte	0.48±0.17
similar to RIKEN cDNA 4933433P14 gene	RGD1308470	0.25±0.03
similar to RIKEN cDNA 4933435A13	RGD1306402	0.33±0.06
Similar to RIKEN cDNA 5033406L14	RGD1305755	0.79±0.5
similar to RIKEN cDNA 5033414D02 (predicted)	RGD1306839_predicte	1.4±0.47
similar to RIKEN cDNA 5133400G04	RGD1311742	0.6±0.06
similar to RIKEN cDNA 5133401N09	MGC125086	0.39±0.06
similar to RIKEN cDNA 5230400G24	RGD1310230	13.36±0.48
similar to RIKEN cDNA 5330414D10 (predicted) /// hypothetical LOC366300	LOC366300 /// RGD13(	0.33±0.09
similar to RIKEN cDNA 5330440M15 /// coiled-coil domain containing 17	Ccdc17 /// LOC313519	1.99±0.09
similar to RIKEN cDNA 5430437P03	MGC94542	5.2±0.55
similar to RIKEN cDNA 5630401D24 (predicted)	RGD1311526_predicte	0.46±0.11
similar to RIKEN cDNA 5730449L18 (predicted)	RGD1308584_predicte	2.29±0.15
similar to RIKEN cDNA 5730453I16	RGD1305441	4.61±1.3
similar to RIKEN cDNA 5730454B08 (predicted)	RGD1308290_predicte	2.14±1.42
Similar to RIKEN cDNA 5730469D23 (predicted)	RGD1308324_predicte	0.96±0.8
similar to RIKEN cDNA 5730469M10	RGD1309676	3.37±1.74
similar to RIKEN cDNA 5730509K17 gene (predicted)	RGD1561042_predicte	1.02±0.28
similar to RIKEN cDNA 5730596K20 (predicted)	RGD1309871_predicte	0.76±0.02
similar to RIKEN cDNA 5830433M19	MGC125002	1.13±0.47
Similar to RIKEN cDNA 5830446M03	RGD1307688	0.64±0.04
Similar to RIKEN cDNA 6330406I15 (predicted)	RGD1307396_predicte	9.48±0.57
similar to RIKEN cDNA 6330409N04	RGD1306437	4.46±0.4
similar to RIKEN cDNA 6330416G13 gene (predicted)	RGD1304595_predicte	0.25±0.08
similar to RIKEN cDNA 6430548M08 (predicted)	RGD1304884_predicte	0.39±0.44
similar to RIKEN cDNA 6530403A03	RGD1309020	0.45±0.04

similar to RIKEN cDNA 8430406I07	RGD1307465	1.1±0.09
Similar to RIKEN cDNA 9030221M09 gene (predicted)	RGD1305469_predicte	2.25±0.05
similar to RIKEN cDNA 9030624J02	LOC361635	1.96±0.07
similar to RIKEN cDNA 9430023L20	RGD1359310	1.5±0.2
Similar to RIKEN cDNA 9430077D24 gene	LOC290341	1.23±0.15
similar to RIKEN cDNA 9430098E02 (predicted) /// hypothetical protein LOC680815	LOC680815 /// RGD15	1.87±0.22
similar to RIKEN cDNA A030007L17; EST AA673177 (predicted) /// similar to C44B7.7	LOC685702 /// RGD13	0.22±3.73
similar to RIKEN cDNA A130042E20; open reading frame 57 (predicted)	RGD1308722_predicte	0.27±0.1
similar to RIKEN cDNA A430005L14	RGD1304567	1.76±0.2
Similar to RIKEN cDNA A430093J20 gene	LOC367113	1.99±0.35
similar to RIKEN cDNA A530088I07 gene	LOC311984	0.97±0.09
similar to RIKEN cDNA A730011L01 gene	LOC498029	0.57±0.06
similar to RIKEN cDNA A930008G19 (predicted)	RGD1310799_predicte	1.03±0.01
similar to RIKEN cDNA A930016P21 (predicted)	RGD1560629_predicte	0.98±0.4
similar to RIKEN cDNA B230118H07 (predicted)	RGD1309730_predicte	6.13±0.23
Similar to RIKEN cDNA B230312A22	RGD1311249	1.83±0.01
similar to RIKEN cDNA B230380D07 (predicted)	RGD1311456_predicte	1.96±0.14
similar to RIKEN cDNA B630019K06 (predicted)	RGD1560784_predicte	0.29±0.02
similar to RIKEN cDNA B930062P21 gene (predicted)	RGD1562562_predicte	2.18±0.03
similar to RIKEN cDNA C030006K11	MGC94207	4.56±1.34
similar to RIKEN cDNA C130022K22 gene	RGD1305225	0.63±0.02
similar to RIKEN cDNA C430004E15	LOC499749	3.29±0.29
similar to RIKEN cDNA D030070L09	RGD1310199	1.89±0.18
similar to RIKEN cDNA D130059P03 gene (predicted)	RGD1310722_predicte	2.01±0.64
similar to RIKEN cDNA D230025D16Rik	RGD621098	0.43±0.13
similar to RIKEN cDNA D530033C11 (predicted)	RGD1307179_predicte	0.97±0.21
similar to RIKEN cDNA D630029K19	RGD1307100	1.78±0.29
similar to RIKEN cDNA D930015E06	LOC679811	0.3±0.07
similar to RIKEN cDNA E130201N16 (predicted)	RGD1311589_predicte	1.79±0.18
similar to RIKEN cDNA E130308A19 (predicted)	RGD1310951_predicte	0.67±0.16
similar to RIKEN cDNA E230015L20 gene (predicted)	RGD1560873_predicte	0.86±0.02
similar to RIKEN cDNA F730014I05 (predicted)	RGD1310800_predicte	0.67±0.17
similar to ring finger protein 13	LOC681578	8.03±0.88
similar to ring finger protein 168	LOC684436	0.55±0.24
Similar to RN49018 (predicted)	RGD1305208_predicte	0.93±0.16
similar to RNA binding motif, single stranded interacting protein 3 isoform 1	LOC680726	11.14±0.58
similar to RNA binding protein gene with multiple splicing (predicted)	RGD1561067_predicte	6.93±0.45
Similar to RNA binding protein with multiple splicing 2 (predicted)	RGD1561222_predicte	4.17±0.32
similar to RNA polymerase 1-3	MGC112727	6.51±0.08
Similar to RNA-binding protein Musashi2-S (predicted)	RGD1560397_predicte	1.01±0.32
similar to RNA-binding region (RNP1, RRM) containing 3	LOC686263	1.86±0.37
similar to Rnf37-pending protein	RGD1305440	0.48±0.1
similar to scaffold attachment factor B2	LOC301126	1.7±0.01
Similar to SCO cytochrome oxidase deficient homolog 1 (yeast) (predicted)	RGD1559538_predicte	2.26±0.51
similar to Sec1 family domain containing protein 2 (Syntaxin binding protein 1-like 1) (Neuronal Sec1)	LOC498353	0.39±0.31
similar to SEC22 vesicle trafficking protein-like 3	LOC687022	1.05±0.04
similar to SEC24 related gene family, member C	LOC685144	3.08±0.8
similar to Selenoprotein H (predicted)	RGD1563348_predicte	1.07±0.98
similar to selenoprotein SelM (predicted)	RGD1565037_predicte	1.1±0.36
similar to semaF cytoplasmic domain associated protein 2	LOC365960	1.68±0.25
Similar to septin 10 isoform 1	LOC309891	2.84±0.5
similar to Ser/Thr-rich protein T10 in DGCR region (predicted)	RGD1310348_predicte	4.04±0
Similar to Serine	LOC691318	0.96±0.32
Similar to Serine/threonine protein kinase 24 (predicted)	RGD1561742_predicte	0.48±0.11
similar to serologically defined colon cancer antigen 3 isoform 1	LOC683605	0.47±0.13
similar to Serum amyloid A-3 protein precursor	LOC687992	1.57±0.44
similar to Sestrin 2 (Hi95) (predicted)	RGD1566319_predicte	3.1±0.37
similar to Sfrs4 protein (predicted)	RGD1561347_predicte	2.12±0.3
Similar to SH3-domain binding protein 3	LOC688018	6.87±0.69
similar to Shb protein (predicted)	RGD1565350_predicte	3.16±0.36
similar to sid2057p	RGD1311703	4.26±0.61
similar to signal peptidase complex subunit 3 homolog	LOC680782	5.5±1.01
similar to Signal recognition particle 9 kDa protein (SRP9) /// signal recognition particle 9	LOC682826 /// Srp9	5.53±1.28
similar to Ski protein (predicted)	RGD1565591_predicte	2.87±1.37
similar to Smad ubiquitination regulatory factor 1 isoform 2	LOC690516	0.69±0.05
similar to small nuclear ribonucleoprotein D3	LOC687711	6.49±0.32
similar to small nuclear ribonucleoprotein polypeptide G	LOC681031 /// LOC687	5.54±1.19
Similar to small nuclear RNA activating complex, polypeptide 5	LOC691501	0.97±0.32
similar to small unique nuclear receptor co-repressor (predicted) /// nuclear DNA binding protein	C1d /// RGD1560600_	1.9±0.93
similar to SMP3 mannosyltransferase /// similar to nuclear cap binding protein subunit 2	LOC684506 /// LOC68	3.44±0.68
similar to snRNP core protein SMX5	LOC684148	1.33±0.33
similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (predicted)	RGD1561141_predicte	3.17±0.6
Similar to solute carrier family 30 (zinc transporter), member 9	LOC498358	1.77±0.15
Similar to Solute carrier family 35, member E3 (predicted)	RGD1564876_predicte	2.09±0.87
similar to sorbin and SH3 domain containing 1 isoform 3	LOC678826	4.95±0.16
similar to sorting nexin 3	LOC684097	23.99±0.42
similar to Sorting nexin-9	LOC683687	2.12±0.39
similar to SPBPJ4664.02 (predicted) /// RGD1562079 (predicted)	RGD1559845_predicte	6.05±0.2
similar to specifically androgen-regulated protein	LOC498222	4.5±0.91
similar to Sperm 1 POU-domain transcription factor (SPRM-1) (predicted)	RGD1305526_predicte	2.66±0.16
similar to spindlin	LOC682571	12.05±1.15
similar to spinster-like protein	RGD1305613	2.08±0.05
similar to SPla/RYanodine receptor SPRY (1J970) (predicted)	RGD1308847_predicte	0.66±0.05
similar to Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa subunit) (U2 snRNP auxiliary factor small subunit)	LOC687575	2.52±0.59
similar to splicing factor, arginine/serine-rich 1 (ASF/SF2) /// splicing factor, arginine/serine-rich 1	LOC688114 /// Sfrs1	6.55±1.03
Similar to splicing factor, arginine/serine-rich 2, interacting protein	LOC312030	1.25±0.08
Similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Ge	LOC303057	3.25±0.32

similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Ge	LOC303057 /// Slu7	0.89±0.09
Similar to Sterile alpha motif domain containing 10 (predicted)	RGD1563203_predicte	0.59±0.09
similar to sterile alpha motif domain containing 9-like	LOC500013	1.46±0.78
similar to stromal membrane-associated protein 1	LOC684800	2.39±0.4
similar to Sulfide:quinone oxidoreductase, mitochondrial precursor	LOC691966	3.75±0.06
similar to SUMO/sentrin specific protease 2	LOC295194	1.01±0.15
similar to SUMO/sentrin specific protease 5	LOC686286	1.07±0.14
similar to suppressor of hairy wing homolog 4 isoform 1 (predicted)	RGD1560796_predicte	0.53±0.14
similar to Suppressor of S. cerevisiae gcr2 (predicted)	RGD1565023_predicte	1.07±0.04
similar to SWI	LOC684513 /// LOC68	1.36±0.35
similar to T03G11.6	LOC689540	12.21±1.99
similar to TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	RGD1562272_predicte	0.41±0.1
similar to talin 2 (predicted)	RGD1565416_predicte	0.98±0.1
similar to TBC1 domain family member 4 (Akt substrate of 160 kDa) (AS160)	LOC686547	0.61±0.1
similar to TBC1 domain family, member 8 (with GRAM domain); vascular Rab-GAP/TBC-containing (predicted)	RGD1308221_predicte	4.31±0.65
Similar to TBP-associated factor 172 (TAF-172) (TAF(II)170) (predicted)	RGD1564130_predicte	1.16±0.51
similar to TBP-associated factor 4	LOC682097	3.01±0.36
Similar to T-Brain-1	LOC311078	0.43±0.34
similar to T-cell receptor alpha chain precursor V and C regions (TRA29)	RGD1359684	3.71±0.98
similar to testhymin (predicted)	RGD1563612_predicte	0.24±0.19
similar to THO complex subunit 4 (Tho4) (RNA and export factor binding protein 1) (REF1-I) (Ally of AML-1 and LEF-1) (Aly/REF)	LOC688305	2.43±0.06
similar to thymus atrophy-related protein (predicted)	RGD1304607_predicte	1.05±0.05
Similar to TICAM-1	LOC363328	0.49±0.1
similar to topoisomerase (DNA) II beta	LOC361100	3.55±0.42
similar to TR4 orphan receptor associated protein TRA16	LOC361128	2.14±0.06
similar to transcription factor	MGC112830	3.88±1.03
similar to Transcription factor 7-like 2 (HMG box transcription factor 4) (T-cell-specific transcription factor 4) (TCF-4) (hTCF-4)	LOC683733	2.76±0.09
Similar to transcription factor 7-like 2, T-cell specific, HMG-box	LOC679869	0.21±0.06
similar to Transcription initiation factor TFIID subunit 12 (Transcription initiation factor TFIID 20 kDa subunits) (TAFII-20) (TAFII20)	LOC682902	0.46±0.24
similar to translocase of inner mitochondrial membrane 50 homolog	LOC687295	2.59±0.25
similar to translocase of the inner mitochondrial membrane 14 isoform a	LOC683663	5.49±0.94
similar to transmembrane protein 41a	LOC681708	0.68±0.17
similar to transmembrane protein 61	LOC688864	1.14±0.43
similar to Tripartite motif protein 47 /// tripartite motif-containing 47	LOC688269 /// Trim47	2.26±0.12
similar to TRS85 homolog (predicted)	RGD1309102_predicte	1.62±0.14
Similar to TSC22 domain family protein 2 (TSC22-related-inducible leucine zipper protein 4)	LOC499624	0.9±0.14
similar to TSC22 domain family protein 4 (TSC22-related-inducible leucine zipper protein 2)	LOC686226	0.77±0.67
similar to tyrosine kinase-associated leucine zipper protein LAZipII (predicted)	RGD1565584_predicte	2.17±0.25
similar to U5 snRNP-specific protein (Prp8-binding) (predicted)	RGD1309198_predicte	0.72±0.28
similar to ubiquinol-cytochrome c reductase complex 7.2kDa protein isoform b	LOC685322	47.13±0.4
similar to Ubiquitin carboxyl-terminal hydrolase 21 (Ubiquitin thiolesterase 21) (Ubiquitin-specific processing protease 21) (Deubiquitinati	LOC678925 /// LOC68	1.8±0.06
similar to ubiquitin protein ligase E3 component n-recognin 2	LOC363188	3.03±0.01
similar to ubiquitin protein ligase E3B	LOC687633	1.9±0.05
similar to ubiquitin specific protease 34	LOC360990	2.31±0.27
similar to Ubiquitin-associated protein 2-like	LOC497952	1.92±0.12
similar to ubiquitin-conjugating enzyme E2R 2	LOC689226	6.26±0.26
similar to ubiquitin-protein ligase E3-alpha (predicted)	RGD1562326_predicte	0.75±0.44
similar to uncharacterized hypothalamus protein HT013 (predicted)	RGD1307071_predicte	0.8±0.07
similar to UPF0197 protein C11orf10 homolog (predicted)	RGD1560328_predicte	6.02±0.62
similar to UPF0308 protein C9orf21	LOC498685	0.36±0.14
similar to vacuolar protein sorting 13C protein (predicted)	RGD1560364_predicte	1.51±0.05
Similar to Vacuolar protein sorting 26 homolog (VPS26 protein homolog)	LOC300472	1.69±0.07
similar to vacuolar protein sorting 37D	LOC687208	1.4±0.5
similar to Vps41 protein (predicted)	RGD1560511_predicte	5.97±0.68
similar to WAC (predicted)	RGD1562407_predicte	1.34±0.12
similar to WD repeat domain 11 protein (predicted)	RGD1564964_predicte	0.95±0.44
similar to WD repeat domain 74 /// WD repeat domain 74	LOC686449 /// Wdr74	0.89±0.1
similar to Wdr8 protein	LOC366515	0.51±0.21
Similar to XPA binding protein 1	LOC688393	0.49±0.16
similar to yippee-like 3 (predicted)	RGD1564579_predicte	5.61±1.49
similar to YY1-associated factor 2 /// YY1 associated factor 2	LOC681599 /// Yaf2	0.63±0.07
similar to Zinc finger CCCH-type domain containing protein 6	LOC678741	2.01±0.04
Similar to Zinc finger CCHC domain-containing protein 6	LOC501515	1.48±0.58
similar to zinc finger like protein 1	LOC684755	0.93±0.21
similar to Zinc finger protein 133	LOC499900	0.35±0.12
similar to zinc finger protein 146	LOC687516	1.25±0.32
similar to zinc finger protein 277 isoform 1	LOC298977	1.03±0.03
similar to Zinc finger protein 326 (Zinc finger protein-associated with nuclear matrix of 75 kDa)	LOC682914	4.42±0.12
similar to zinc finger protein 341	LOC296300	0.43±0.04
similar to zinc finger protein 385 /// zinc finger protein 385	LOC683930 /// Zfp385	1.32±0.79
similar to zinc finger protein 422, related sequence 1	LOC314600	2.17±1.28
similar to zinc finger protein 426 (predicted)	RGD1564241_predicte	0.59±0.26
similar to Zinc finger protein 551 (Zinc finger protein KOX23)	LOC691396	0.77±0.03
Similar to zinc finger protein 609 (predicted)	RGD1561651_predicte	0.81±0.16
similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3) (predicted)	RGD1560191_predicte	0.39±0.51
similar to zinc finger protein 639	LOC683504	0.59±0.11
similar to zinc finger protein 709	LOC362845	0.33±0.14
Similar to zinc finger protein 748 isoform 2	LOC680222	0.79±0.15
similar to zinc finger protein 75 (predicted)	RGD1565419_predicte	0.3±0.06
similar to zinc finger protein 84 (HPF2)	LOC691170	0.42±0.18
similar to Zinc finger protein RP-8 CG3260-PA /// programmed cell death 2-like	LOC687670 /// Pdcd2l	0.39±0.05
similar to zinc finger, matrin type 2	LOC679898	2.06±0.11
similar to zinc finger, RAN-binding domain containing 3 (predicted)	RGD1564952_predicte	0.33±0.05
similar to zinc finger, ZZ domain containing 3	LOC310958	1.6±0.56
Sin3A associated protein	Sap130	2.38±0.29
Sin3-associated polypeptide 18	Sap18	8.2±0.15
sine oculis-related homeobox 4 homolog (Drosophila) (predicted)	Six4_predicted	2.18±0.37

sine oculis-related homeobox 5 homolog (Drosophila) (predicted)	Six5_predicted	0.6±0.02
single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	Sigirr	1.21±0.3
single stranded DNA binding protein 3	Ssbp3	0.79±0.26
single stranded DNA binding protein 4	Ssbp4	0.82±0.38
single-minded homolog 1 (Drosophila)	Sim1	1.61±2.47
single-minded homolog 2 (Drosophila)	Sim2	12.25±3.07
single-stranded DNA binding protein 1	Ssbp1	2.43±0.41
single-stranded DNA binding protein 2	Ssbp2	1.23±0.03
sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	Sirt2	4.89±1
sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (predicted)	Sirt3_predicted	2.35±0.06
sirtuin 4 (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	Sirt4	0.59±0.21
sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	Sirt5	7.79±1.2
sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	Sirt6	1.37±0.06
sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae) (predicted)	Sirt7_predicted	1.35±0.18
SIVA1, apoptosis-inducing factor	Siva1	1.24±0.19
six transmembrane epithelial antigen of the prostate 2	Steap2	4.38±0.06
Sjogren syndrome antigen B	Ssb	4.92±0.57
Sjogren's syndrome nuclear autoantigen 1 (predicted)	Ssna1_predicted	1.36±0.42
skeletal muscle and kidney enriched inositol phosphatase	Skip	1.75±0.12
SLAIN motif family, member 2	Slain2	3±0.67
slingshot homolog 3 (Drosophila)	Ssh3	0.43±0.09
Smad nuclear interacting protein 1	Snip1	0.76±0.18
SMAD specific E3 ubiquitin protein ligase 2 (predicted)	Smurf2_predicted	1.54±0.43
small cell adhesion glycoprotein	Smagp	8.91±0.15
small EDRK-rich factor 2	Serf2	20.15±0.74
small G protein signaling modulator 2	Sgsm2	0.74±0.17
small G protein signaling modulator 3	Sgsm3	0.58±0.13
small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Sgta	2.72±0.01
Small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	Sgtb	0.23±0.11
small inducible cytokine subfamily E, member 1	Scye1	1.68±0.03
small muscle protein, X-linked	Smpx	15.14±0.89
small nuclear ribonucleoprotein D1 (predicted)	Snrpd1_predicted	0.71±0.07
small nuclear ribonucleoprotein D2 /// similar to small nuclear ribonucleoprotein D2	LOC686737 /// Snrpd2	11.04±1.75
small nuclear ribonucleoprotein E	Snrpe	11.9±1.96
small nuclear ribonucleoprotein N	Snrpn	2.12±0.32
small nuclear ribonucleoprotein N /// SNRPN upstream reading frame	Snrpn /// Snurf	0.97±0.32
small nuclear ribonucleoprotein polypeptide A	Snrpa	0.41±0.06
small nuclear ribonucleoprotein polypeptide F	Snrpf	3.05±0.81
small nuclear ribonucleoprotein polypeptides B and B1	Snrpb	6.5±0.71
small nuclear RNA activating complex, polypeptide 1 (predicted)	Snapc1_predicted	0.41±0.27
small nuclear RNA activating complex, polypeptide 2	Snapc2	3.64±0.15
small nuclear RNA activating complex, polypeptide 3	Snapc3	1.04±0.1
small nuclear RNA activating complex, polypeptide 4 (predicted)	Snapc4_predicted	0.24±0.1
small nuclear RNA activating complex, polypeptide 5	Snapc5	0.65±0.2
small nucleolar RNA host gene (non-protein coding) 8	Snhg8	1.47±0.4
small optic lobes homolog (Drosophila) (predicted)	Solh_predicted	0.81±0.19
SMC6 structural maintenance of chromosomes 6-like 1 (yeast) (predicted)	Smc6l1_predicted	1.38±0.27
SMEK homolog 1, suppressor of mek1 (Dictyostelium)	Smek1	3.29±0.48
SMEK homolog 2, suppressor of mek1 (Dictyostelium)	Smek2	2.87±0.61
Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	Smg5	0.25±0.01
Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) /// similar to KIAA0732 protein	RGD1309609 /// Smg6	0.61±0.02
Smith-Magenis syndrome chromosome region, candidate 7-like	Smcr7l	0.76±0.19
smoothelin	Smtn	0.34±0.15
smoothelin /// PDZ domain containing RING finger 3 (predicted)	Pdzrn3_predicted /// Sr	1.93±0.94
smoothelin-like 2	Smtnl2	5.56±0.59
smoothened homolog (Drosophila)	Smo	0.73±0.45
SMT3 suppressor of mif two 3 homolog 1 (yeast)	Sumo1	6.25±0.26
SMT3 suppressor of mif two 3 homolog 2 (yeast) /// similar to SMT3 suppressor of mif two 3 homolog 2	LOC690244 /// Sumo2	16.8±2.41
SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	Sumo3	7.6±0.05
smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	Smu1	2.36±0.29
SNAP-associated protein	Snapap	2.61±0.02
SNF1-like kinase 2 (predicted)	Snf1lk2_predicted	1.49±0.02
SNF2 histone linker PHD RING helicase (predicted)	Shprh_predicted	0.88±0.18
Snf2-related CREBBP activator protein	Srcap	0.52±0.19
SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	Snf8	4.87±0.11
sno, strawberry notch homolog 1 (Drosophila)	Sbno1	1.38±0.17
snurportin 1	Snupn	0.75±0.19
soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	0.97±0.36
sodium channel and clathrin linker 1	Sclt1	0.98±0.05
sodium channel modifier 1 (predicted)	Scnm1_predicted	0.89±0.11
sodium channel, nonvoltage-gated, type I, alpha	Scnn1a	1.91±0.35
sodium channel, voltage-gated, type I, beta	Scn1b	2.57±0.03
solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3	0.46±0.13
solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	Slc1a1	5.96±1.27
solute carrier family 1 (neutral amino acid transporter), member 5	Slc1a5	6.96±0.02
solute carrier family 10 (sodium/bile acid cotransporter family), member 3	Slc10a3	0.75±0.12
solute carrier family 10, member 2	Slc10a2	0.37±0.02
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	1.36±0.69
solute carrier family 12 (potassium/chloride transporters), member 9	Slc12a9	1.09±0.03
solute carrier family 12, member 1	Slc12a1	41.35±5.95
solute carrier family 12, member 4	Slc12a4	0.3±0
solute carrier family 12, member 6	Slc12a6	0.27±0.1
solute carrier family 12, member 7	Slc12a7	1.92±0.31
solute carrier family 15, member 4	Slc15a4	1.12±0.33
solute carrier family 16 (monocarboxylic acid transporters), member 1	Slc16a1	1.83±0.02
solute carrier family 16 (monocarboxylic acid transporters), member 7	Slc16a7	35.55±6.27
solute carrier family 17 (anion/sugar transporter), member 5	Slc17a5	1.73±0.65

solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	1.95±0.17
solute carrier family 19 (thiamine transporter), member 2	Slc19a2	5.03±1.48
solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1	6.85±1.51
solute carrier family 2 (facilitated glucose transporter), member 13	Slc2a13	1.87±0.16
solute carrier family 2 (facilitated glucose transporter), member 4	Slc2a4	5.13±0.23
solute carrier family 2, (facilitated glucose transporter) member 8	Slc2a8	0.94±0.04
solute carrier family 20 (phosphate transporter), member 1	Slc20a1	2.74±1.52
solute carrier family 20, member 2	Slc20a2	1.25±0.12
solute carrier family 22 (organic cation transporter), member 15 (predicted)	Slc22a15_predicted	0.4±0.18
solute carrier family 22 (organic cation transporter), member 17	Slc22a17	1.88±0.3
solute carrier family 22 (organic cation transporter), member 4	Slc22a4	3.19±0.18
solute carrier family 22 (organic cation transporter), member 5	Slc22a5	4.51±0.6
solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	Slc24a6	1.83±0.5
solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	3.26±0.07
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25a13	4.65±0.71
solute carrier family 25 (mitochondrial carrier, brain), member 14	Slc25a14	0.2±0.11
solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	Slc25a1	3.45±0.48
solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	0.85±0.01
solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	Slc25a29	3.58±0.19
solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 (predicted)	Slc25a17_predicted	4.46±0.19
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	Slc25a3	51.76±3.99
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	Slc25a4	23.69±2.55
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	Slc25a5	51.71±2.45
solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	Slc25a10	6.84±0.64
Solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	Slc25a15	1.02±0.03
solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	Slc25a11	7.79±0.82
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	Slc25a23	3.02±0.18
solute carrier family 25, member 28	Slc25a28	3.16±0.03
Solute carrier family 25, member 30	Slc25a30	2.93±1.8
solute carrier family 25, member 35	Slc25a35	1.78±0.7
solute carrier family 25, member 36	Slc25a36	14.5±1.23
solute carrier family 25, member 38	Slc25a38	1.69±0.33
solute carrier family 25, member 39	Slc25a39	17.1±2.38
solute carrier family 25, member 44	Slc25a44	0.88±0.28
solute carrier family 25, member 46	Slc25a46	6.84±3.23
solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	1.58±0.23
solute carrier family 27 (fatty acid transporter), member 4	Slc27a4	3.07±0.19
solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	0.23±0.06
solute carrier family 29 (nucleoside transporters), member 3	Slc29a3	0.37±0.26
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	9.91±2.14
solute carrier family 30 (zinc transporter), member 1	Slc30a1	0.31±0.35
solute carrier family 30 (zinc transporter), member 3	Slc30a3	1.07±0.05
solute carrier family 30 (zinc transporter), member 4	Slc30a4	0.81±0.09
solute carrier family 30 (zinc transporter), member 5 (predicted)	Slc30a5_predicted	2±0.24
solute carrier family 30 (zinc transporter), member 6 (predicted)	Slc30a6_predicted	1.7±0.56
solute carrier family 30 (zinc transporter), member 7	Slc30a7	0.59±0.19
solute carrier family 30 (zinc transporter), member 9	Slc30a9	0.74±0.05
solute carrier family 31 (copper transporters), member 1	Slc31a1	1.33±0.37
solute carrier family 31, member 2	Slc31a2	2.76±0.2
solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	3.78±0.4
solute carrier family 34 (sodium phosphate), member 1	Slc34a1	0.67±0.16
solute carrier family 34 (sodium phosphate), member 2	Slc34a2	0.75±0.69
solute carrier family 35 (CMP-sialic acid transporter), member 1 (predicted)	Slc35a1_predicted	5.8±0.47
Solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (predicted)	Slc35d1_predicted	0.31±0.01
solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	Slc35a3	0.42±0.18
solute carrier family 35, member A4	Slc35a4	2.16±0.27
solute carrier family 35, member A5	Slc35a5	1.9±0.25
solute carrier family 35, member B1	Slc35b1	4.12±0.55
solute carrier family 35, member B3 (predicted)	Slc35b3_predicted	2.26±1.07
solute carrier family 35, member B4 (predicted)	Slc35b4_predicted	1±0.12
solute carrier family 35, member C1 (predicted)	Slc35c1_predicted	2.06±0.12
solute carrier family 35, member C2	Slc35c2	0.61±0.07
solute carrier family 35, member E1	Slc35e1	0.76±0.08
solute carrier family 35, member E3	Slc35e3	0.72±0.01
solute carrier family 35, member E4	Slc35e4	0.55±0.05
solute carrier family 35, member F5 (predicted)	Slc35f5_predicted	2.4±0.05
solute carrier family 37 (glucose-6-phosphate transporter), member 4	Slc37a4	3.49±0.08
solute carrier family 37 (glycerol-3-phosphate transporter), member 1	Slc37a1	5.25±1
solute carrier family 38, member 1	Slc38a1	0.97±0.09
solute carrier family 38, member 10	Slc38a10	2.45±0.93
solute carrier family 38, member 2	Slc38a2	5.94±0.41
solute carrier family 38, member 4	Slc38a4	0.37±0.04
solute carrier family 38, member 6	Slc38a6	0.5±0.06
solute carrier family 39 (iron-regulated transporter), member 1	Slc40a1	2.09±0.11
solute carrier family 39 (metal ion transporter), member 13	Slc39a13	3.69±0.69
solute carrier family 39 (metal ion transporter), member 6	Slc39a6	0.37±0.13
solute carrier family 39 (zinc transporter), member 10 (predicted)	Slc39a10_predicted	1.18±0.24
solute carrier family 39 (zinc transporter), member 14 (predicted)	Slc39a14_predicted	0.79±0.15
solute carrier family 39 (zinc transporter), member 2 (predicted)	Slc39a2_predicted	0.73±0.05
solute carrier family 39 (zinc transporter), member 3	Slc39a3	0.51±0.05
solute carrier family 4 (anion exchanger), member 1, adaptor protein (predicted)	Slc4a1ap_predicted	1.07±0.32
solute carrier family 4 (anion exchanger), member 2	Slc4a2	5.2±0.85
solute carrier family 4 (anion exchanger), member 3	Slc4a3	0.4±0.1
solute carrier family 4, sodium bicarbonate cotransporter, member 7	Slc4a7	1.26±0.16
solute carrier family 41, member 1 (predicted)	Slc41a1_predicted	0.56±0.04
solute carrier family 41, member 3	Slc41a3	0.95±0.06
solute carrier family 43, member 2 (predicted)	Slc43a2_predicted	4.73±1.07

Solute carrier family 44, member 2 (predicted)	Slc44a2_predicted	2.77±1.9
solute carrier family 44, member 4	Slc44a4	1.28±0.82
solute carrier family 45, member 3 (predicted)	Slc45a3_predicted	2.42±1.27
solute carrier family 45, member 4	Slc45a4	2.25±0.22
solute carrier family 46, member 3	Slc46a3	0.58±0.19
solute carrier family 5 (inositol transporters), member 3	Slc5a3	24.15±0.41
solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Slc5a6	4.74±0.74
solute carrier family 6 (neurotransmitter transporter), member 17	Slc6a17	7.69±0.96
solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	Slc6a12	4.79±3.2
solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	13.74±1.46
solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	Slc7a5	0.39±0.17
solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (predicted)	Slc7a6_predicted	3.3±1.03
solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	0.79±1.17
solute carrier family 7, member 6 opposite strand	Slc7a6os	1.1±0.19
solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	Slc9a6	2.43±0.56
solute carrier family 9 (sodium/hydrogen exchanger), member 1	Slc9a1	0.75±0.22
solute carrier family 9 (sodium/hydrogen exchanger), member 3	Slc9a3	20.32±0.86
solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	Slc9a3r1	0.72±2.73
solute carrier organic anion transporter family, member 1a4	Slco1a4	0.21±0.42
solute carrier organic anion transporter family, member 3a1	Slco3a1	1.55±0.41
Son cell proliferation protein	Son	4.07±0.52
Son of sevenless homolog 1 (Drosophila)	Sos1	1.97±0.05
sorbin and SH3 domain containing 3	Sorbs3	1.96±0.23
sorbitol dehydrogenase	Sord	0.28±0.93
sortilin 1	Sort1	0.69±0.26
sortilin-related receptor, LDLR class A repeats-containing	Sorl1	27.54±0.81
sortilin-related VPS10 domain containing receptor 2 (predicted)	Sorcs2_predicted	0.28±0.05
sorting and assembly machinery component 50 homolog (S. cerevisiae)	Samm50	13.71±0.51
sorting nexin 1	Snx1	1.17±0.31
sorting nexin 11	Snx11	0.72±0.15
sorting nexin 12 (predicted)	Snx12_predicted	1.36±0.16
sorting nexin 13 (predicted)	Snx13_predicted	1.03±0.35
sorting nexin 14 (predicted)	Snx14_predicted	1.82±0.29
sorting nexin 15	Snx15	1.52±0.11
sorting nexin 16	Snx16	2.04±0.25
sorting nexin 17	Snx17	2.33±1.08
sorting nexin 18	Snx18	1.71±0.3
sorting nexin 19 (predicted)	Snx19_predicted	0.97±0.19
sorting nexin 2 (predicted)	Snx2_predicted	11.26±5.75
sorting nexin 25	Snx25	0.96±0.05
sorting nexin 26 (predicted)	Snx26_predicted	0.42±0.06
sorting nexin 4 (predicted)	Snx4_predicted	2.44±0.03
sorting nexin 5 (predicted)	Snx5_predicted	2.19±0.51
sorting nexin 6 (predicted)	Snx6_predicted	2.07±0.36
sorting nexin 7	Snx7	0.76±0.03
sorting nexin 8 (predicted)	Snx8_predicted	1.12±0.2
sorting nexin family member 27	Snx27	1.84±0.47
sorting nexing 24	Snx24	0.43±0.2
SP110 nuclear body protein	Sp110	0.69±0.09
SP140 nuclear body protein	Sp140	2.93±0.7
sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2 (predicted)	Spock2_predicted	2.72±0.31
spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	Spg20	0.55±0.19
spastic paraplegia 21 homolog (human)	Spg21	2.96±0.26
spastic paraplegia 7 homolog (human)	Spg7	2.25±0.27
spastin (predicted)	Spast_predicted	1.41±0.01
SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc24	0.53±0.09
SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	0.33±0.03
SPECC1-like	Specc1l	0.73±0.17
speckle-type POZ protein	Spop	2.75±0.56
spectrin beta 2	Spnb2	13.93±1.31
spectrin repeat containing, nuclear envelope 1	Syne1	0.22±0.04
speedy homolog A (Drosophila)	Spdya	0.24±0.02
sperm associated antigen 5	Spag5	0.21±0.02
sperm associated antigen 7 (predicted)	Spag7_predicted	1.67±0.24
sperm associated antigen 9 (predicted)	Spag9_predicted	4.34±0.2
sperm autoantigenic protein 17	Spa17	2.44±0.73
sperm specific antigen 2 (predicted)	Ssfa2_predicted	1.91±1.4
spermatid perinuclear RNA binding protein	Strbp	1.99±0.24
spermatogenesis associated 5 (predicted)	Spata5_predicted	0.27±0.01
spermatogenesis associated 6	Spata6	0.95±0.04
spermatogenesis associated 7	Spata7	1.38±0.31
spermatogenesis associated, serine-rich 2 (predicted)	Spats2_predicted	0.47±0.15
spermidine synthase	Srm	1.18±0.53
spermidine/spermine N1-acetyl transferase 1	Sat1	26.38±1.25
spermidine/spermine N1-acetyl transferase 2 (predicted)	Sat2 predicted	5.5±0.22
spermine oxidase (predicted)	Smox_predicted	0.34±0.09
spermine synthase	Sms	1.08±0.11
spermine synthase /// similar to spermine synthase	LOC683008 /// LOC69	0.73±0.04
S-phase kinase-associated protein 1A	Skp1a	22.84±1.86
sphingomyelin phosphodiesterase 1, acid lysosomal	Smpd1	11.04±0
sphingomyelin phosphodiesterase 2, neutral	Smpd2	0.41±0.28
sphingomyelin phosphodiesterase 4	Smpd4	0.73±0.2
sphingomyelin phosphodiesterase, acid-like 3A	Smpdl3a	9.37±0.27
sphingomyelin phosphodiesterase, acid-like 3B	Smpdl3b	1.13±0.39
sphingosine kinase 1	Sphk1	8.15±2.22
sphingosine kinase 2	Sphk2	2.95±0.17
sphingosine kinase 2 /// similar to Sphingosine kinase 2 (SK 2) (SPK 2)	LOC367812 /// Sphk2	0.21±0.06

sphingosine phosphate lyase 1	Sgpl1	0.46±0.13
sphingosine-1-phosphate phosphatase 1	Sgpp1	0.32±0.51
spindle assembly 6 homolog (C. elegans) (predicted)	Sass6_predicted	0.22±0.01
spindlin 1 /// similar to spindlin	LOC682571 /// Spin1	2.94±0.57
spindlin family, member 2	Spin2	0.71±0.05
spire homolog 1 (Drosophila) (predicted)	Spire1_predicted	1.46±0.58
splA/ryanodine receptor domain and SOCS box containing 1 (predicted)	Spsb1_predicted	0.21±0.11
splA/ryanodine receptor domain and SOCS box containing 2	Spsb2	0.39±0.23
splA/ryanodine receptor domain and SOCS box containing 3 (predicted)	Spsb3_predicted	2.59±0.58
splA/ryanodine receptor domain and SOCS box containing 4 (predicted)	Spsb4_predicted	2.61±1.32
spleen tyrosine kinase	Syk	0.71±0.39
splicing factor 1	Sf1	3.15±0.02
splicing factor 3a, subunit 1 (predicted)	Sf3a1_predicted	0.77±0.06
splicing factor 3a, subunit 2	Sf3a2	1.58±0.09
splicing factor 3a, subunit 3	Sf3a3	1.36±0.07
splicing factor 3b, subunit 1	Sf3b1	11.14±1.09
splicing factor 3b, subunit 2 (predicted)	Sf3b2_predicted	3.01±0.23
splicing factor 3b, subunit 3 (predicted)	Sf3b3_predicted	3.04±0.57
splicing factor 3b, subunit 4	Sf3b4	3.83±0.14
splicing factor 3b, subunit 5	Sf3b5	5.91±0.69
splicing factor 4	Sf4	0.61±0.06
splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	1.72±0.33
splicing factor YT521-B	Yt521	5.83±0.2
splicing factor, arginine/serine rich 9	Sfrs9	4.07±0.1
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	Sfrs10	10.47±2.56
splicing factor, arginine/serine-rich 11	Sfrs11	6.34±0.82
splicing factor, arginine/serine-rich 12	Sfrs12	0.64±0.2
splicing factor, arginine/serine-rich 14 (predicted)	Sfrs14_predicted	0.67±0.22
splicing factor, arginine/serine-rich 15	Sfrs15	1.04±0.17
Splicing factor, arginine/serine-rich 16	Sfrs16	0.54±0.05
splicing factor, arginine/serine-rich 18	Sfrs18	2.08±0.23
splicing factor, arginine/serine-rich 2 (SC-35)	Sfrs2	7.1±0.81
splicing factor, arginine/serine-rich 2, interacting protein	Sfrs2ip	0.66±0.16
splicing factor, arginine/serine-rich 3 (SRp20) (predicted)	Sfrs3_predicted	14.44±1.43
splicing factor, arginine/serine-rich 5	Sfrs5	4.69±1.15
splicing factor, arginine/serine-rich 6	Sfrs6	6.64±0.18
splicing factor, arginine/serine-rich 8	Sfrs8	0.61±0.17
split hand/foot malformation (ectrodactyly) type 1	Shfm1	10.75±0.22
spondin 1	Spon1	24.59±0.29
sprouty homolog 2 (Drosophila)	Spry2	4.3±0.92
sprouty homolog 4 (Drosophila) (predicted)	Spry4_predicted	0.2±0.37
Sprouty-related, EVH1 domain containing 2	Spred2	4.73±0.9
SPRY domain containing 3	Spryd3	1.27±0.07
SPRY domain containing 4	Spryd4	1.34±0.4
squalene epoxidase	Sqle	2.09±1.52
squamous cell carcinoma antigen recognized by T-cells 1	Sart1	2.31±0.51
squamous cell carcinoma antigen recognized by T-cells 3 (predicted)	Sart3_predicted	1.04±0.28
src family associated phosphoprotein 1	Skap1	2.28±0.33
src family associated phosphoprotein 2	Skap2	6.69±2.24
Src homology 2 domain-containing transforming protein C1	Shc1	1.75±0.11
SREBF chaperone	Scap	2.21±0.14
SRR1 domain containing	Srrd	0.58±0.01
SR-related CTD-associated factor 1	Scaf1	0.41±0.22
SRY-box containing gene 11	Sox11	0.56±0.19
SRY-box containing gene 4 (predicted)	Sox4_predicted	2.92±0.5
SRY-box containing gene 6	Sox6	0.42±0.2
Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	3.48±0.73
ST3 beta-galactoside alpha-2,3-sialyltransferase 2	St3gal2	0.75±0.23
ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	0.8±0.01
ST3 beta-galactoside alpha-2,3-sialyltransferase 4	St3gal4	0.23±0.07
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	1.34±0.36
ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	5.68±0.83
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	St6galnac2	1.57±1.77
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	St6galnac3	1.15±0.32
Stam binding protein	Stambp	1.4±0.04
stannin	Snn	5.49±1.14
staphylococcal nuclease and tudor domain containing 1	Snd1	2.88±0.22
STARD3 N-terminal like	Stard3nl	2.19±0.33
StAR-related lipid transfer (START) domain containing 5	Stard5	1.38±0.04
START domain containing 10	Stard10	6.48±0.58
START domain containing 3	Stard3	3.57±0.2
START domain containing 7 (predicted)	Stard7_predicted	8.02±0.86
START domain containing 8 (predicted)	Stard8_predicted	9.51±0.82
stathmin 1	Stmn1	8.04±0.52
staufen RNA binding protein homolog 1 (Drosophila)	Stau1	3.58±0.34
staufen, RNA binding protein, homolog 2 (Drosophila)	Stau2	1.57±0.12
STE20-like kinase (yeast)	Slk	0.42±0
STEAP family member 3	Steap3	1.23±0.7
stearoyl-Coenzyme A desaturase 2	Scd2	0.39±0.72
stem-loop binding protein	Slbp	1.31±1.18
Sterile alpha motif domain containing 4 (predicted)	Samd4_predicted	0.24±0.02
sterile alpha motif domain containing 4B	Samd4b	0.57±0.17
sterile alpha motif domain containing 8	Samd8	0.46±0.34
steroid 5 alpha-reductase 3	Srd5a3	2.95±0.23
steroid receptor RNA activator 1	Sra1	4.93±0.29
sterol carrier protein 2 /// podocan (predicted)	Podn_predicted /// Scp	30.27±1.13
Sterol O-acyltransferase 1	Soat1	1.7±0.06

sterol regulatory element binding factor 1	Srebf1	1.07±0.93
sterol regulatory element binding factor 2 (predicted)	Srebf2	3.89±0.4
sterol-C4-methyl oxidase-like	Sc4mol	6.05±4.23
sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	Sc5d	2.45±1.01
STIP1 homology and U-Box containing protein 1	Stub1	4.1±0.49
stomatin (Epb7.2)-like 2	Stoml2	3.01±0.54
stomatin-like 1	Stoml1	0.4±0.36
strawberry notch homolog 2 (Drosophila)	Sbno2	0.43±0.1
stress 70 protein chaperone, microsome-associated	Stch	1.18±0.27
stress-associated endoplasmic reticulum protein 1	Serp1	13.12±1.72
stress-induced phosphoprotein 1	Stip1	6.02±2.36
striatin, calmodulin binding protein	Strn	1.27±0.52
striatin, calmodulin binding protein 3	Strn3	4.01±0.09
striatin, calmodulin binding protein 4 (predicted)	Strn4_predicted	2.07±0.31
stromal antigen 1 (predicted)	Stag1_predicted	1.34±0.07
stromal antigen 2 (predicted)	Stag2_predicted	4.3±0.05
stromal cell derived factor 2 (predicted)	Sdf2_predicted	4.59±0.21
stromal cell derived factor 4	Sdf4	6.88±0.09
stromal cell-derived factor 2-like 1 (predicted)	Sdf2l1_predicted	0.81±0.13
stromal interaction molecule 2 (predicted)	Stim2_predicted	0.43±0.2
stromal membrane-associated GTPase-activating protein 2	Smap2	0.75±0.04
structural maintenace of chromosomes 3	Smc3	6.26±1.62
structural maintenance of chromosomes 1A	Smc1a	1.22±0.07
structural maintenance of chromosomes 2	Smc2	0.77±0.44
structural maintenance of chromosomes 4	Smc4	0.23±0.06
structural maintenance of chromosomes 5	Smc5	1.02±0.17
structure specific recognition protein 1	Ssrp1	4.19±0.17
STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	Stt3a	1.45±0.21
SUB1 homolog (S. cerevisiae)	Sub1	19.01±0.95
succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	Sdha	35.16±4.34
succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (predicted)	Sdhb_predicted	29.36±3.66
succinate dehydrogenase complex, subunit C, integral membrane protein	Sdhc	37.61±1.76
succinate dehydrogenase complex, subunit D, integral membrane protein	Sdhd	30.26±2.82
succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	19.25±0.99
succinate-Coenzyme A ligase, ADP-forming, beta subunit (predicted)	Sucla2_predicted	15.91±2.47
succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	26.28±0.69
sulfatase 2	Sulf2	5.44±0.43
sulfatase modifying factor 1 (predicted)	Sumf1_predicted	1.01±0.33
sulfatase modifying factor 2	Sumf2	0.76±0.02
sulfite oxidase	Suox	3.45±0.34
sulfotransferase family 1A, phenol-preferring, member 1	Sult1a1	2.76±4.49
sulfotransferase family, cytosolic, 2B, member 1 (predicted)	Sult2b1_predicted	1.08±0
SUMO	LOC686286 /// RGD15	0.43±0.34
SUMO/sentrin specific peptidase 2	Senp2	0.46±0.03
SUMO/sentrin specific peptidase 3	Senp3	2.1±0.05
SUMO/sentrin specific peptidase 6 (predicted)	Senp6_predicted	2.88±0.09
SUMO1 activating enzyme subunit 1	Sae1	4.05±1.04
SUMO1 activating enzyme subunit 2	Sae2	4.37±0
SUMO1/sentrin specific protease 7 (predicted)	Senp7_predicted	1.33±0.36
superkiller viralicidic activity 2-like 2 (S. cerevisiae)	Skiv2l2	2.78±0.04
superoxide dismutase 1, soluble	Sod1	17.81±1.75
superoxide dismutase 2, mitochondrial	Sod2	13.22±3.87
suppression of tumorigenicity 13	St13	5.98±0.05
suppression of tumorigenicity 14 (colon carcinoma)	St14	10.44±1.33
suppression of tumorigenicity 5 (predicted)	St5_predicted	1.79±0.07
suppression of tumorigenicity 7-like	St7l	1.01±0.35
suppressor of cytokine signaling 3	Socs3	1.53±0.34
suppressor of cytokine signaling 5	Socs5	6.94±1.46
suppressor of cytokine signaling 6 (predicted)	Socs6_predicted	2.95±0.72
suppressor of cytokine signaling 7 (predicted)	Socs7_predicted	0.58±0.14
suppressor of defective silencing 3 homolog (S. cerevisiae)	Suds3	4.38±0.13
suppressor of IKK epsilon	Sike	0.69±0.11
suppressor of Ty 16 homolog (S. cerevisiae) (predicted)	Supt16h_predicted	1.56±0.11
suppressor of Ty 3 homolog (S. cerevisiae)	Supt3h	0.65±0.08
suppressor of Ty 4 homolog 1 (S. cerevisiae)	Supt4h1	4.1±0.59
suppressor of Ty 5 homolog (S. cerevisiae)	Supt5h	4.47±1.27
suppressor of Ty 6 homolog (S. cerevisiae)	Supt6h	0.93±0.02
suppressor of Ty 7 (S. cerevisiae)-like	Supt7l	1.06±0.28
suppressor of var1, 3-like 1 (S. cerevisiae)	Supv3l1	3.56±0.92
suppressor of variegation 3-9 homolog 1 (Drosophila) (predicted)	Suv39h1_predicted	0.95±0.17
suppressor of variegation 4-20 homolog 1 (Drosophila) (predicted)	Suv420h1_predicted	1.85±0.07
suppressor of variegation 4-20 homolog 2 (Drosophila) (predicted)	Suv420h2_predicted	1.68±0.12
surfeit 1	Surf1	4.21±0.39
surfeit 4	Surf4	3.98±0.65
surfeit gene 2	Surf2	1.09±0.4
surfeit gene 6 (predicted)	Surf6_predicted	1.54±0.61
survival motor neuron 1	Smn1	0.81±0.34
survival motor neuron domain containing 1	Smndc1	3.9±0.41
survival of motor neuron protein interacting protein 1	Sip1	1.33±0.23
sushi, nidogen and EGF-like domains 1	Sned1	1.3±1.34
SWA-70 protein	Swap70	0.71±0.26
Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (predicted)	Smarcal1_predicted	0.54±0.16
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2	0.53±0.13
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Smarca4	3.56±0.27
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)	Smarca5_predicted	1.68±0.59
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	Smarcb1	2.01±0.02
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 (predicted)	Smarcc1_predicted	0.99±0.08

SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1 (predicted)	Smarcd1_predicted	0.66±0.05
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Smarcd2	1.31±0.11
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	Smarcd3	6.25±1.64
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Smarce1	8.79±0.73
SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1; (predicted)	Smarcad1_predicted	0.51±0.1
SYF2 homolog, RNA splicing factor (S. cerevisiae)	Syf2	3.94±0.05
symplekin	Sympk	0.56±0.06
synapse associated protein 1	Syap1	2.01±1.06
synapse defective 1, Rho GTPase, homolog 1 (C. elegans) (predicted)	Syde1_predicted	0.6±0.02
synaptic vesicle glycoprotein 2a	Sv2a	5.11±1.35
synaptic vesicle glycoprotein 2b	Sv2b	25.32±47.08
synaptogyrin 1	Syngr1	2.82±0.51
synaptogyrin 2	Syngr2	2.99±0.01
synaptojanin 1	Synj1	0.72±0.02
synaptojanin 2 binding protein	Synj2bp	2.51±0.06
Synaptophysin-like protein	Sypl	12.33±2.59
synaptopodin 2	Synpo2	0.5±0.19
synaptosomal-associated protein 23	Snap23	2.24±0.49
synaptosomal-associated protein 29	Snap29	1.19±0.89
Synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	1.59±0.48
Synaptotagmin III	Syt3	0.81±0.29
synaptotagmin XVII	Syt17	4.16±0.32
synaptotagmin-like 2 (predicted)	Sytl2_predicted	15.5±2.36
syndecan 1	Sdc1	0.64±0.25
syndecan 2	Sdc2	4.65±2.56
syndecan 3	Sdc3	1.19±0.3
syndecan 4	Sdc4	26.85±5.75
syndecan binding protein	Sdcbp	24.28±5.17
synovial apoptosis inhibitor 1, synoviolin	Syvn1	0.99±0.03
synovial sarcoma translocation, Chromosome 18	Ss18	2.99±0.11
synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	1.39±0.41
syntaxin 12	Stx12	1.35±0.31
syntaxin 16 (predicted)	Stx16_predicted	2.62±0.51
syntaxin 17	Stx17	0.51±0.46
syntaxin 18	Stx18	1.9±0.8
syntaxin 4A (placental)	Stx4a	3.46±0.33
syntaxin 5a	Stx5a	1.82±0.06
syntaxin 6	Stx6	1.76±0.32
syntaxin 7	Stx7	19.33±0.09
syntaxin 8	Stx8	1.46±0.1
syntaxin binding protein 1	Stxbp1	0.82±0.53
syntaxin binding protein 2	Stxbp2	1.49±0.54
syntaxin binding protein 3	Stxbp3	2.65±0.35
syntaxin binding protein 5 (tomosyn)	Stxbp5	0.28±0
syntrophin, acidic 1	Snta1	0.99±0.16
synuclein, gamma	Sncg	0.34±1.47
TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf1_predicted	0.69±0.07
TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf11	1.2±0.4
TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf13_predicted	4.04±1.39
TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	LOC364872 / LOC6880	0.22±0.74
TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf2	1.42±0.36
TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf5_predicted	0.36±0.03
TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf5l	0.6±0.32
TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf6	2.02±0
TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor (predicted)	Taf6l_predicted	0.44±0
TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factorq	Taf8	0.61±0.1
TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf9	4.45±1.18
TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor pseudogene	Taf9 /// Taf9_ps	1.08±0.43
tafazzin	Taz	1.44±0.23
talin 1	Tln1	1.75±1.36
TANK-binding kinase 1	Tbk1	1.56±0.4
tankyrase 1 binding protein 1 (predicted)	Tnks1bp1_predicted	1.03±0.06
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 (predicted)	Tnks2_predicted	3.39±0.07
TAO kinase 1	Taok1	0.97±0.02
TAP binding protein	Tapbp	0.23±0.58
TAR (HIV) RNA binding protein 2	Tarbp2	2.19±0.41
TAR DNA binding protein	Tardbp	6.78±1.07
target of EGR1, member 1 (nuclear) (predicted)	Toe1_predicted	0.34±0.15
target of myb1 homolog (chicken)	Tom1	2.8±0.59
Target of myb1-like 2 (chicken) (predicted)	Tom1l2_predicted	2.56±0.45
taspase, threonine aspartase 1 (predicted)	Tasp1_predicted	0.27±0.14
Taste receptor, type 1, member 2	Tas1r2	0.82±0.47
TATA box binding protein	Tbp	1.1±0.12
TATA box binding protein (Tbp)-associated factor, RNA polymerase I, C	Taf1c	0.24±0.26
TATA box binding protein-like 1	Tbpl1	1.8±0.98
TatD DNase domain containing 2	Tatdn2	2.96±0.13
Tax1 (human T-cell leukemia virus type I) binding protein 1	Tax1bp1	11.77±1.68
Tax1 (human T-cell leukemia virus type I) binding protein 3	Tax1bp3	5.4±0.12
TBC1 domain family, member 10a	Tbc1d10a	1.45±0.14
TBC1 domain family, member 14	Tbc1d14	8.9±1.37
TBC1 domain family, member 15	Tbc1d15	0.58±0.42
TBC1 domain family, member 17 (predicted)	Tbc1d17_predicted	0.95±0.34
TBC1 domain family, member 2 (predicted)	Tbc1d2_predicted	0.26±0.05
TBC1 domain family, member 22a (predicted)	Tbc1d22a_predicted	0.8±0.08
TBC1 domain family, member 22B	Tbc1d22b	0.97±0.02
TBC1 domain family, member 23 (predicted)	Tbc1d23_predicted	3.42±0.23
TBC1 domain family, member 2B	Tbc1d2b	0.68±0.28

TBC1 domain family, member 7 (predicted)	Tbc1d7_predicted	0.78±0.13
TBC1 domain family, member 9B	Tbc1d9b	2.97±0.22
TBCC domain containing 1	Tbccd1	0.4±0.03
T-box 19 (predicted)	Tbx19_predicted	0.42±0.15
TCDD-inducible poly(ADP-ribose) polymerase (predicted)	Tiparp_predicted	0.45±0.05
T-cell leukemia translocation altered gene	Tcta	2.88±0.02
T-cell lymphoma invasion and metastasis 1	Tiam1	0.49±0.3
T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	Tcirg1	0.76±0.25
TCF3 (E2A) fusion partner	Tfpt	0.51±0.04
t-complex 11 (mouse) like 2	Tcp11l2	0.3±0.8
t-complex protein 1	Tcp1	11.82±1.18
Tctex1 domain containing 2	Tctex1d2	0.77±0.17
TEA domain family member 3	Tead3	0.74±0.2
teashirt zinc finger family member 1	Tshz1	2.16±0.11
Tectonic 2	Tect2	0.7±0
tectonic family member 3	Tctn3	0.38±0.15
tektin 1	Tekt1	0.48±0.11
TEL2, telomere maintenance 2, homolog (S. cerevisiae)	Telo2	0.83±0.35
telomerase associated protein 1	Tep1	1.7±0
telomeric repeat binding factor 2, interacting protein	Terf2ip	2.04±0.34
tensin 1	Tns1	14.22±0.37
tensin 4	Tns4	0.2±0.02
tensin like C1 domain containing phosphatase (predicted)	Tenc1_predicted	1.05±0.41
TERF1 (TRF1)-interacting nuclear factor 2	Tinf2	0.21±0.01
terminal uridylyl transferase 1, U6 snRNA-specific	Tut1	0.55±0.25
tescalcin	Tesc	8.13±2.39
testis derived transcript	Tes	4.42±1.03
testis enhanced gene transcript	Tegt	28.31±5.03
testis expressed gene 10 (predicted)	Tex10_predicted	1.13±0.15
testis expressed gene 14 (predicted)	Tex14_predicted	4.23±0.48
testis expressed gene 15 (predicted)	Tex15_predicted	0.91±0.37
testis expressed gene 2	Tex2	2.99±0.14
testis expressed gene 261	Tex261	3.75±0.72
testis expressed gene 264	Tex264	4.15±1.18
testis specific protein kinase 1	Tesk1	0.83±0.22
testis-specific kinase 2	Tesk2	0.58±0.02
testis-specific protein, Y-encoded-like 1	Tspyl1	2.76±0.36
tetraspanin 12	Tspan12	16.11±1.8
tetraspanin 14 (predicted)	Tspan14_predicted	2.33±0.56
tetraspanin 3	Tspan3	13.12±1.51
tetraspanin 31	Tspan31	2.94±0.47
tetraspanin 33	Tspan33	4.86±0.28
tetraspanin 4	Tspan4	1.2±0.42
tetraspanin 6	Tspan6	2.79±0.92
tetraspanin 7	Tspan7	8.8±1.5
tetraspanin 8	Tspan8	23.6±3.48
tetraspanin 9 (predicted)	Tspan9_predicted	1.17±0.07
tetratricopeptide repeat domain 1	Ttc1	3.21±0.05
tetratricopeptide repeat domain 12	Ttc12	0.49±0.06
tetratricopeptide repeat domain 13	Ttc13	0.75±0.23
tetratricopeptide repeat domain 15	Ttc15	2.02±0.57
tetratricopeptide repeat domain 17	Ttc17	1.31±0.02
tetratricopeptide repeat domain 19	Ttc19	1.19±0.12
tetratricopeptide repeat domain 21B	Ttc21b	0.95±0.35
tetratricopeptide repeat domain 23	Ttc23	1.08±0.14
tetratricopeptide repeat domain 27	Ttc27	1.23±0.42
tetratricopeptide repeat domain 3 (predicted)	Ttc3_predicted	4.54±0.08
tetratricopeptide repeat domain 33	Ttc33	1.2±0.34
tetratricopeptide repeat domain 35	Ttc35	6.57±0.7
tetratricopeptide repeat domain 5	Ttc5	1.45±0.58
tetratricopeptide repeat domain 7	Ttc7	3.7±0.32
tetratricopeptide repeat domain 7B (predicted)	Ttc7b_predicted	1.28±0.18
Tetratricopeptide repeat domain 8 (predicted)	Ttc8_predicted	0.68±0.29
Tetratricopeptide repeat domain 9C	Ttc9c	2.96±0.62
TG interacting factor 1	Tgif1	1.3±1.2
THAP domain containing 11 (predicted)	Thap11_predicted	0.97±0.01
THAP domain containing 4	Thap4	25.29±6.11
THAP domain containing 7	Thap7	0.61±0.04
THAP domain containing, apoptosis associated protein 3 (predicted)	Thap3_predicted	1.76±0.35
thiamine triphosphatase	Thtpa	4.43±0.25
thioesterase superfamily member 2 (predicted)	Them2_predicted	8.63±2.07
thioesterase superfamily member 4	Them4	2.15±0.35
thioredoxin 1	Txn1	25.5±1.47
thioredoxin 2	Txn2	11.77±1.04
thioredoxin domain containing 1	Txndc1	2.51±0.21
thioredoxin domain containing 11 (predicted)	Txndc11_predicted	0.51±0.06
thioredoxin domain containing 12 (endoplasmic reticulum)	Txndc12	2.72±0.15
thioredoxin domain containing 13	Txndc13	4.03±0.38
thioredoxin domain containing 15	Txndc15	5.59±0.92
thioredoxin domain containing 17	Txndc17	5.49±0.05
thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	3.23±0.2
Thioredoxin domain containing 9	Txndc9	0.67±0.26
thioredoxin interacting protein	Txnip	45.03±7.89
thioredoxin reductase 1	Txnrd1	1.38±0.74
thioredoxin reductase 2	Txnrd2	1.51±0.3
thioredoxin-like 1	Txnl1	9.39±0.28
thioredoxin-like 4B	Txnl4b	0.74±0.05

Thioredoxin-related transmembrane protein 2	Tmx2	10.2±2.13
thiosulfate sulfurtransferase, mitochondrial	Tst	1.29±1.17
THO complex 1	Thoc1	1.54±0.64
THO complex 2 (predicted)	Thoc2_predicted	1.31±0.1
THO complex 3 (predicted)	Thoc3_predicted	0.92±0.12
THO complex 5	Thoc5	2.03±0.42
THO complex 6 homolog (Drosophila)	Thoc6	0.88±0.04
THO complex 7 homolog (Drosophila)	Thoc7	5.46±3.15
three prime histone mRNA exonuclease 1	Thex1	0.76±0.18
three prime repair exonuclease 1	Trex1	0.8±0.07
threonine synthase-like 2 (bacterial)	Thnsl2	1.76±1.59
threonyl-tRNA synthetase	Tars	1.54±0.3
threonyl-tRNA synthetase 2, mitochondrial (putative)	Tars2	1.71±0.16
THUMP domain containing 1	Thumpd1	2.17±0.1
THUMP domain containing 2	Thumpd2	0.23±0.1
THUMP domain containing 3	Thumpd3	2.26±0.18
thymidine kinase 1	Tk1	1.19±0.1
thymidine kinase 2, mitochondrial (predicted)	Tk2_predicted	0.58±0.19
thymidylate synthase	Tyms	0.31±0.03
thymine-DNA glycosylase	Tdg	1.17±0.42
thymocyte nuclear protein 1	Thyn1	1.55±0.49
Thymoma viral proto-oncogene 1	Akt1	5.37±0.05
Thymoma viral proto-oncogene 2	Akt2	1.95±0.18
thymopoietin	Tmpo	3.33±0.02
thyroid adenoma associated	Thada	0.49±0.62
thyroid hormone receptor alpha	Thra	2.13±0.46
thyroid hormone receptor associated protein 3	Thrap3	3.15±0.3
thyroid hormone receptor beta	Thrb	0.9±0.02
thyroid hormone receptor interactor 10	Trip10	1.29±0.45
thyroid hormone receptor interactor 11	Trip11	0.2±0.01
thyroid hormone receptor interactor 12	Trip12	4.88±0.69
thyroid hormone responsive protein	Thrsp	0.38±0.08
Tia1 cytotoxic granule-associated RNA binding protein-like 1	Tial1	2.13±0.14
tight junction associated protein 1 (predicted)	Tjap1_predicted	0.29±0.12
tight junction protein 1 (predicted)	Tjp1_predicted	3.72±1.27
tight junction protein 2	Tjp2	0.84±0.11
timeless homolog (Drosophila)	Timeless	0.46±0.05
TIP41, TOR signalling pathway regulator-like (S. cerevisiae) (predicted) /// similar to TIP41, TOR signalling pathway regulator-like	LOC686733 /// Tiprl_pr	1.17±0.7
tissue factor pathway inhibitor	Tfpi	1.54±0.18
Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	Timp3	2.72±10.65
tissue inhibitor of metalloproteinase 4	Timp4	0.35±0.1
tissue specific transplantation antigen P35B (predicted)	Tsta3_predicted	1.97±0.11
TLC domain containing 1	Tlcd1	3.75±0.66
TM2 domain containing 1 (predicted)	Tm2d1_predicted	4.71±0.86
TM2 domain containing 2	Tm2d2	5.48±1.51
TM2 domain containing 3 (predicted)	Tm2d3_predicted	4.25±0.75
TM2 domain containing 3 (predicted) /// threonyl-tRNA synthetase-like 2	Tarsl2 /// Tm2d3_predic	0.5±0.06
TMEM9 domain family, member B (predicted)	Tmem9b_predicted	4.18±0.42
Tnf receptor associated factor 4 (predicted)	Traf4_predicted	3.93±0.33
Tnf receptor-associated factor 2 (predicted)	Traf2_predicted	0.4±0.06
Tnf receptor-associated factor 3 (predicted)	Traf3_predicted	0.55±0.04
Tnf receptor-associated factor 6 (predicted)	Traf6_predicted	1.17±0.31
Tnf receptor-associated factor 7 (predicted)	Traf7_predicted	1.28±0.17
TNF receptor-associated protein 1	Trap1	8.9±2.17
TNFAIP3 interacting protein 1 (predicted)	Tnip1_predicted	2.19±0.01
TNFAIP3 interacting protein 2	Tnip2	0.5±0.28
TNFRSF1A-associated via death domain	Tradd	1.08±0.04
TNNI3 interacting kinase	Tnni3k	0.36±0.12
toll interacting protein (predicted)	Tollip_predicted	1.23±0.27
topoisomerase (DNA) 2 alpha	Top2a	1.25±0.53
topoisomerase (DNA) I	Top1	4.22±0.61
topoisomerase (DNA) II beta binding protein	Topbp1	0.54±0.17
topoisomerase (DNA) III beta (predicted)	Top3b_predicted	1.57±0.52
topoisomerase I binding, arginine/serine-rich (predicted)	Topors_predicted	2.83±0.63
torsin A interacting protein 1	Tor1aip1	3.15±0.58
torsin A interacting protein 2	Tor1aip2	0.23±0
torsin family 1, member B	Tor1b	0.41±0.18
torsin family 2, member A	Tor2a	1.52±0.03
torsin family 3, member A	Tor3a	0.31±0.07
tousled-like kinase 1 (predicted)	Tlk1_predicted	3.83±0.49
tousled-like kinase 2 (Arabidopsis) (predicted)	Tlk2_predicted	1.58±0.28
TOX high mobility group box family member 4	Tox4	1.69±0.11
TP53 regulated inhibitor of apoptosis 1	Triap1	3.75±0.09
TP53 regulating kinase (predicted)	Trp53rk_predicted	0.5±0.29
Tp53rk binding protein	Tprkb	1.69±0.36
TraB domain containing	Trabd	0.99±0.3
Traf and Tnf receptor associated protein	Ttrap	1.46±0.05
TRAF family member-associated Nf-kappa B activator	Tank	0.67±0.11
TRAF type zinc finger domain containing 1	Trafd1	1.08±0.33
Traf3 interacting protein 2	Traf3ip2	0.54±0
TRAF4 associated factor 1	Traf4af1	0.6±0.14
trafficking protein particle complex 1	Trappc1	4.3±0.49
trafficking protein particle complex 2	Trappc2	1.71±0.59
trafficking protein particle complex 2-like	Trappc2l	3.22±0.12
trafficking protein particle complex 3	Trappc3	4.9±0.72
trafficking protein particle complex 4	Trappc4	1.9±0.05
trafficking protein particle complex 5	Trappc5	6.98±0.09

trafficking protein particle complex 6A /// similar to trafficking protein particle complex 6A	LOC686599 /// Trappc6	3.72±0.38
trafficking protein particle complex 6B (predicted)	Trappc6b_predicted	3.34±0.56
trafficking protein, kinesin binding 2	Trak2	3.88±0.13
trans-acting transcription factor 1	Sp1	4.71±0.62
transaldolase 1	Taldo1	9.63±0.79
transcobalamin 2	Tcn2	13.48±3.51
transcription elongation factor A (SII) 1	Tcea1	7.38±0.12
transcription elongation factor A (SII)-like 1	Tceal1	0.96±0.09
transcription elongation factor A (SII)-like 8	Tceal8	2.67±0.12
transcription elongation factor B (SIII), polypeptide 1	Tceb1	8.1±0.95
transcription elongation factor B (SIII), polypeptide 2	Tceb2	16.63±3.76
transcription elongation factor B (SIII), polypeptide 3	Tceb3	1.66±0.49
transcription elongation regulator 1 (CA150) (predicted)	Tcerg1_predicted	2.17±0.36
transcription factor 19	Tcf19	3.15±0.68
transcription factor 20	Tcf20	0.33±0.11
transcription factor 25 (basic helix-loop-helix)	Tcf25	5.88±0.98
transcription factor 4	Tcf4	0.29±0.61
transcription factor A, mitochondrial	Tfam	4.64±0.52
transcription factor AP-2 beta (predicted)	Tcfap2b_predicted	5.93±1.74
transcription factor AP4 (predicted)	Tcfap4_predicted	0.43±0.27
transcription factor B1, mitochondrial	Tfb1m	0.52±0.01
transcription factor B2, mitochondrial	Tfb2m	2.37±0.01
transcription factor CP2 (predicted)	Tcfcp2_predicted	0.39±0.12
transcription factor CP2-like 1 (predicted)	Tcfcp2l1_predicted	2.98±0.55
transcription factor CP2-like 2	Tcfcp2l2	1.23±0.67
transcription factor Dp-2 (E2F dimerization partner 2)	Tfdp2	0.37±0.29
transcription factor EB	Tcfeb	1.23±0.05
transcriptional adaptor 1 (HFI1 homolog, yeast) like	Tada1l	1.24±0.35
transcriptional adaptor 3 (NGG1 homolog, yeast)-like	Tada3l	0.31±0.23
transcriptional regulator, SIN3A (yeast) (predicted)	Sin3a_predicted	1.3±0.36
transducer of ERBB2, 2	Tob2	5.69±0.54
transducer of ErbB-2.1	Tob1	17.01±7.24
transducin (beta)-like 1 X-linked (predicted)	Tbl1x_predicted	1.77±0.66
transducin (beta)-like 1X-linked receptor 1 (predicted)	Tbl1xr1_predicted	2.81±0.02
transducin (beta)-like 3	Tbl3	0.69±0.29
transducin-like enhancer of split 1, homolog of Drosophila E(spl) (predicted)	Tle1_predicted	0.46±0.22
transducin-like enhancer of split 3, homolog of Drosophila E(spl)	Tle3	0.62±0.4
transducin-like enhancer of split 4, homolog of Drosophila E(spl)	Tle4	0.4±0.08
transferrin receptor	Tfrc	20.51±6
transformation related protein 53	Trp53	1.36±0.17
transformation related protein 53 binding protein 1 (predicted)	Trp53bp1_predicted	1.41±0.11
transformation related protein 53 inducible protein 13	Trp53i13	0.58±0.11
transformation/transcription domain-associated protein (predicted)	Trrap_predicted	1.5±0.38
transformed mouse 3T3 cell double minute 1	Mdm1	0.92±0.21
transformed mouse 3T3 cell double minute 2 homolog (mouse) (predicted)	Mdm2_predicted	1.76±0.02
transformer 2 alpha homolog (Drosophila)	Tra2a	2.32±0.05
transforming growth factor beta 1 induced transcript 1	Tgfb1i1	1.07±0.48
transforming growth factor beta regulated gene 1	Tbrg1	6.36±0.39
transforming growth factor beta regulated gene 4	Tbrg4	2.25±0.47
transforming growth factor, beta receptor 1	Tgfbr1	4.71±1.37
transforming growth factor, beta receptor associated protein 1 (predicted)	Tgfbrap1_predicted	0.58±0.06
transforming, acidic coiled-coil containing protein 1	Tacc1	6.12±1.61
transglutaminase 2, C polypeptide	Tgm2	0.65±0.2
trans-golgi network protein	Tgoln1	7.2±1.46
transient receptor potential cation channel, subfamily C, member 1	Trpc1	0.65±0.19
transient receptor potential cation channel, subfamily C, member 2	Trpc2	0.38±0.02
transient receptor potential cation channel, subfamily C, member 4 associated protein	Trpc4ap	3.18±0.25
transient receptor potential cation channel, subfamily M, member 4	Trpm4	1±0.14
transient receptor potential cation channel, subfamily M, member 7	Trpm7	0.76±0.27
transient receptor potential cation channel, subfamily V, member 4	Trpv4	1.28±0.24
transient receptor potential cation channel, subfamily V, member 4	Trpv1 /// Trpv4	0.52±0.32
transient receptor potential cation channel, subfamily V, member 5	Trpv5	0.32±0.03
Transient receptor potential-related protein, ChaK	Trpm7	3.17±0.22
transketolase	Tkt	13.38±3.36
translin	Tsn	0.97±0.24
translin-associated factor X	Tsnax	3.39±0.34
translocase of inner mitochondrial membrane 10 homolog (yeast)	Timm10	6.43±0.98
translocase of inner mitochondrial membrane 13 homolog (yeast)	Timm13	15.04±1.31
translocase of inner mitochondrial membrane 17a	Timm17a	8.04±1.92
translocase of inner mitochondrial membrane 17b	Timm17b	1.65±0.21
translocase of inner mitochondrial membrane 22 homolog (yeast)	Timm22	3.45±0.81
translocase of inner mitochondrial membrane 23 homolog (yeast)	Timm23	12.63±1.22
translocase of inner mitochondrial membrane 44	Timm44	1.09±0.07
translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	Timm8a1	2.73±1.01
translocase of inner mitochondrial membrane 8 homolog b (yeast)	Timm8b	21.05±6.37
translocase of inner mitochondrial membrane 9 homolog (yeast)	Timm9	3.39±0.48
translocase of outer mitochondrial membrane 20 homolog (yeast)	Tomm20	18.05±3.33
translocase of outer mitochondrial membrane 22 homolog (yeast)	Tomm22	9.03±1.18
translocase of outer mitochondrial membrane 34 (predicted)	Tomm34_predicted	0.92±0.32
translocase of outer mitochondrial membrane 40 homolog (yeast)	Tomm40	3.74±0.27
translocase of outer mitochondrial membrane 40 homolog B (yeast)	Tomm40b	0.88±0.2
translocase of outer mitochondrial membrane 7 homolog (yeast)	Tomm7	14.91±0.37
translocase of outer mitochondrial membrane 70 homolog A (yeast)	Tomm70a	2.29±0.08
translocated promoter region	Tpr	2.11±0.57
translocating chain-associating membrane protein 1	Tram1	11.95±0.16
Translocation associated membrane protein 1	Tram1	0.3±0.17
translocation protein 1	Tloc1	17.89±1.59

translocator protein	Tspo	10.36±1.43
transmembrane 4 superfamily member 1 (predicted)	Tm4sf1_predicted	0.46±4.1
transmembrane 7 superfamily member 2	Tm7sf2	4.05±0.15
transmembrane 7 superfamily member 3	Tm7sf3	0.67±0.72
transmembrane 9 superfamily member 1	Tm9sf1	8.21±0.37
transmembrane 9 superfamily member 2	Tm9sf2	16.61±0.57
transmembrane 9 superfamily member 3	Tm9sf3	2.37±0.11
transmembrane 9 superfamily protein member 4	Tm9sf4	2.12±0.04
transmembrane and coiled coil domains 1	Tmcc1	0.46±0.2
transmembrane and coiled coil domains 3	Tmcc3	1.8±0.06
transmembrane and coiled-coil domains 1	Tmco1	5.5±0.72
transmembrane and coiled-coil domains 3 (predicted)	Tmco3_predicted	3.94±1.01
transmembrane and coiled-coil domains 4	Tmco4	1.24±0.17
transmembrane and coiled-coil domains 6	Tmco6	0.67±0.16
transmembrane and tetratricopeptide repeat containing 4	Tmtc4	4.9±0.57
transmembrane and ubiquitin-like domain containing 1	Tmub1	1±0.04
transmembrane and ubiquitin-like domain containing 2	Tmub2	3.96±0.32
transmembrane BAX inhibitor motif containing 4	Tmbim4	2.83±1.81
transmembrane channel-like gene family 4	Tmc4	13.24±1.27
transmembrane emp24 domain containing 1	Tmed1	1.29±0.24
transmembrane emp24 domain containing 3	Tmed3	2.68±0.89
transmembrane emp24 domain trafficking protein 2	Tmed2	10.78±2.35
transmembrane emp24 protein transport domain containing 4 (predicted)	Tmed4_predicted	1.55±0.35
transmembrane emp24 protein transport domain containing 5	Tmed5	0.37±0.16
transmembrane emp24 protein transport domain containing 6 (predicted)	Tmed6_predicted	5.89±1.41
transmembrane emp24 protein transport domain containing 7	Tmed7	8.53±3.12
transmembrane emp24 protein transport domain containing 9	Tmed9	5.44±0.19
transmembrane emp24-like trafficking protein 10 (yeast)	Tmed10	3.16±0.42
transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	Tpte2	0.28±0.01
transmembrane protease, serine 2	Tmprss2	9.29±0.22
transmembrane protein 1 (predicted)	Tmem1_predicted	1.69±0.09
transmembrane protein 101	Tmem101	0.98±0.08
transmembrane protein 103 (predicted)	Tmem103_predicted	0.74±0.19
transmembrane protein 106B	Tmem106b	15.4±3.82
transmembrane protein 106C	Tmem106c	1.29±0.06
transmembrane protein 109	Tmem109	2.17±0.14
transmembrane protein 11 (predicted)	Tmem11_predicted	1.97±0.12
transmembrane protein 110	Tmem110	0.41±0.02
transmembrane protein 111	Tmem111	5.31±1.05
transmembrane protein 112B	Tmem112b	1.08±0.29
transmembrane protein 115 (predicted)	Tmem115_predicted	4.79±0.3
transmembrane protein 120A	Tmem120a	0.61±0.08
transmembrane protein 123	Tmem123	21.84±0.02
transmembrane protein 126A	Tmem126a	6.09±2.29
transmembrane protein 126B	Tmem126b	4.72±0.72
transmembrane protein 128	Tmem128	1.94±0.34
transmembrane protein 129	Tmem129	1.7±0.66
transmembrane protein 131	Tmem131	1.34±0.48
transmembrane protein 132A	Tmem132a	2.33±0.19
transmembrane protein 134	Tmem134	6.31±0.78
transmembrane protein 135	Tmem135	0.33±0.07
transmembrane protein 138	Tmem138	0.62±0.13
transmembrane protein 139	Tmem139	6.65±1.35
transmembrane protein 140	Tmem140	1.36±1.83
transmembrane protein 141	Tmem141	3.54±0.82
transmembrane protein 143	Tmem143	0.71±0.03
transmembrane protein 147	Tmem147	7.81±0.74
transmembrane protein 14A (predicted)	Tmem14a_predicted	4.81±0.26
transmembrane protein 14C	Tmem14c	4.96±0.79
transmembrane protein 157	Tmem157	0.98±0.07
transmembrane protein 160	Tmem160	3.56±0.16
transmembrane protein 161A	Tmem161a	1.55±0.68
transmembrane protein 161B	Tmem161b	2.34±1.17
transmembrane protein 164	Tmem164	2.69±0.29
transmembrane protein 165	Tmem165	3.93±0.69
transmembrane protein 166	Tmem166	7.73±0.99
transmembrane protein 168	Tmem168	3.34±0.3
transmembrane protein 16F (predicted)	Tmem16f_predicted	6.52±0.27
transmembrane protein 16K	Tmem16k	1.72±0.34
transmembrane protein 17	Tmem17	0.9±0.18
transmembrane protein 171	Tmem171	1.74±1.02
transmembrane protein 177	Tmem177	1.3±0.89
transmembrane protein 179B	Tmem179b	5.67±0.68
transmembrane protein 183A	Tmem183a	3.08±0.15
transmembrane protein 185B	Tmem185b	2.46±0.46
transmembrane protein 186	Tmem186	1.06±0.32
transmembrane protein 188	Tmem188	2.18±0.14
transmembrane protein 189 /// similar to ubiquitin-conjugating enzyme E2 variant 1 (predicted)	RGD1562209_predicte	0.72±0.03
transmembrane protein 19	Tmem19	1.12±0.23
transmembrane protein 192	Tmem192	1.26±0.16
transmembrane protein 205	Tmem205	2.21±0.72
transmembrane protein 208	Tmem208	5.19±0.56
transmembrane protein 209	Tmem209	1.82±0.11
transmembrane protein 24	Tmem24	0.41±0.11
transmembrane protein 30A	Tmem30a	4.57±0.68
transmembrane protein 30B (predicted)	Tmem30b_predicted	7.42±0.1
transmembrane protein 32 (predicted)	Tmem32_predicted	6.22±0.29

transmembrane protein 33	Tmem33	1.82±0.23
transmembrane protein 34	Tmem34	3.76±0.3
transmembrane protein 37	Tmem37	15.43±6.35
transmembrane protein 38a (predicted)	Tmem38a_predicted	0.76±0.09
transmembrane protein 38B	Tmem38b	2.16±0.33
transmembrane protein 39a	Tmem39a	0.74±0.01
transmembrane protein 39b	Tmem39b	0.73±0
transmembrane protein 4	Tmem4	4.42±0.29
transmembrane protein 41B	Tmem41b	6.28±0.82
transmembrane protein 42 (predicted)	Tmem42_predicted	3.55±0.16
transmembrane protein 43	Tmem43	3.1±0.17
transmembrane protein 49	Tmem49	1.39±1.08
transmembrane protein 5	Tmem5	1.13±0.2
transmembrane protein 50A (predicted)	Tmem50a_predicted	3.82±0.38
transmembrane protein 50B	Tmem50b	14.01±0.4
transmembrane protein 51	Tmem51	0.82±0.37
transmembrane protein 53 (predicted)	Tmem53_predicted	1.37±0.24
transmembrane protein 55A	Tmem55a	4.05±1.71
transmembrane protein 55B	Tmem55b	2.12±0.12
transmembrane protein 57	Tmem57	1.48±0.17
transmembrane protein 58 (predicted)	Tmem58_predicted	0.57±0.1
transmembrane protein 60 (predicted)	Tmem60_predicted	1.91±0.3
transmembrane protein 62	Tmem62	1.31±0.03
transmembrane protein 63a (predicted)	Tmem63a_predicted	2.37±0.42
transmembrane protein 66	Tmem66	7.36±0.14
transmembrane protein 67	Tmem67	1.11±0
transmembrane protein 68 (predicted)	Tmem68_predicted	0.71±0.17
transmembrane protein 69	Tmem69	2.67±1.07
transmembrane protein 77	Tmem77	0.84±0.29
transmembrane protein 79	Tmem79	0.77±0.14
transmembrane protein 8 (five membrane-spanning domains) (predicted)	Tmem8_predicted	4.07±1.34
transmembrane protein 80	Tmem80	0.95±0.17
transmembrane protein 81	Tmem81	0.44±0.08
transmembrane protein 82	Tmem82	0.35±0.16
transmembrane protein 85	Tmem85	5.38±0.4
transmembrane protein 86A (predicted)	Tmem86a_predicted	6.84±0.3
transmembrane protein 87A (predicted)	Tmem87a_predicted	1.15±0.22
transmembrane protein 87B	Tmem87b	1±0.28
transmembrane protein 9 (predicted)	Tmem9_predicted	2.52±0.27
transmembrane protein 93 (predicted)	Tmem93_predicted	3.91±0.34
transmembrane protein 97	Tmem97	3.02±0.46
transmembrane protein 98	Tmem98	4.9±0.01
transmembrane protein with EGF-like and two follistatin-like domains 1	Tmeff1	1.34±0.22
transmembrane, prostate androgen induced RNA (predicted)	Tmepai_predicted	7.66±0.99
transporter 1, ATP-binding cassette, sub-family B (MDR	Btnl3 /// Btnl4 /// Btnl5 /	11.93±2.28
transporter 1, ATP-binding cassette, sub-family B (MDR	Btnl3 / Btnl4 / Btnl5 / Hl	3.9±2.77
transportin 1	Tnpo1	0.86±0.59
transportin 2 (importin 3, karyopherin beta 2b) (predicted)	Tnpo2_predicted	1.38±0.12
transportin 3	Tnpo3	0.9±0.28
tribbles homolog 1 (Drosophila)	Trib1	0.38±0.15
tribbles homolog 2 (Drosophila)	Trib2	3.95±1.08
trichoplein, keratin filament binding (predicted)	Tchp_predicted	0.92±0.11
trichorhinophalangeal syndrome I (human)	Trps1	0.49±0.42
trimethylguanosine synthase homolog (S. cerevisiae)	Tgs1	1.35±0.65
trimethyllysine hydroxylase, epsilon	Tmlhe	1.07±0.21
Trinucleotide repeat containing 6 (predicted)	Tnrc6_predicted	0.53±0.38
trinucleotide repeat containing 6a	Tnrc6a	1.2±0.23
trinucleotide repeat containing 6B	Tnrc6b	0.93±0.27
TRIO and F-actin binding protein	Triobp	0.89±0.15
triosephosphate isomerase 1	Tpi1	35.95±5.14
tripartite motif protein 16 (predicted)	Trim16_predicted	1.55±0.27
tripartite motif protein 2	Trim2	1.45±0.2
tripartite motif protein 32	Trim32	2.7±0.97
Tripartite motif protein 37 (predicted)	Trim37_predicted	0.79±0.11
tripartite motif protein 8 (predicted) /// tripartite motif-containing 8	Trim8 /// Trim8_predict	2.36±0.39
tripartite motif-containing 11	Trim11	0.77±0.14
tripartite motif-containing 23	Trim23	0.24±0.1
tripartite motif-containing 24	Trim24	1.7±0.84
tripartite motif-containing 25	Trim25	1.6±0.8
tripartite motif-containing 26	Trim26	0.58±0.21
tripartite motif-containing 27	Trim27	1.67±0.12
tripartite motif-containing 28	Trim28	6.77±0.1
tripartite motif-containing 3	Trim3	0.95±0.05
tripartite motif-containing 33	Trim33	1.67±0.13
tripartite motif-containing 35	Trim35	9.02±1.07
tripartite motif-containing 37	Trim37	0.56±0.13
tripartite motif-containing 39	Trim39	0.56±0.33
tripartite motif-containing 41	Trim41	1.27±0.16
tripartite motif-containing 45	Trim45	0.5±0
tripartite motif-containing 6	Trim6	1.62±0.49
tripartite motif-containing 63	Trim63	0.66±0.7
tripeptidyl peptidase I	Tpp1	3.97±0.77
tripeptidyl peptidase II	Tpp2	1.02±0.43
triple functional domain (PTPRF interacting)	Trio	2.71±0.48
Trk-fused gene	Tfg	2.58±0.14
TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	Trmt1	1.07±0
TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae) (predicted)	Trmt5_predicted	0.6±0.19

tRNA aspartic acid methyltransferase 1	Trdmt1	0.35±0.09
tRNA isopentenyltransferase 1 (predicted)	Trit1_predicted	1.05±0.52
tRNA methyltranferase 12 homolog (S. cerevisiae)	Trmt12	0.34±0.02
tRNA methyltransferase 6 homolog (S. cerevisiae)	Trmt6	0.52±0.19
tRNA nucleotidyl transferase, CCA-adding, 1	Trnt1	3.15±0.71
tRNA phosphotransferase 1 (predicted)	Trpt1_predicted	1.6±0.05
tRNA selenocysteine associated protein	Secp43	5.52±0.21
tRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	Tsen2	0.69±0.03
tRNA splicing endonuclease 34 homolog (SEN34, S. cerevisiae)	Tsen34	8.22±0.48
tRNA splicing endonuclease 54 homolog (S. cerevisiae)	Tsen54	1.37±0.17
tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	Thg1l	0.35±0.03
tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Tyw1	0.57±0.25
tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	Tyw3	1.37±0.14
tropomodulin 3	Tmod3	1.45±0.76
tropomodulin 4 (predicted)	Tmod4_predicted	3.06±0.85
tropomyosin 1, alpha	Tpm1	0.92±1.61
tropomyosin 3, gamma	Tpm3	1.79±2.33
TruB pseudouridine (psi) synthase homolog 1 (E. coli)	Trub1	0.51±0.18
TruB pseudouridine (psi) synthase homolog 2 (E. coli)	Trub2	3.25±0.24
trypsin domain containing 1 (predicted)	Tysnd1_predicted	1.11±0.32
tryptophan rich basic protein	Wrb	1.41±0.2
tryptophanyl-tRNA synthetase	Wars	1.91±0.08
TSC22 domain family 3	Tsc22d3	6.6±5.2
TSC22 domain family, member 1	Tsc22d1	6.4±7.75
TSC22 domain family, member 4	Tsc22d4	3.69±0.64
TSC22 domain family, member 4 /// similar to TSC22 domain family protein 4 (TSC22-related-inducible leucine zipper protein 2)	LOC686226 /// Tsc22d	0.66±0.3
TSPY-like 4	Tspyl4	0.93±0.13
Tu translation elongation factor, mitochondrial (predicted)	Tufm_predicted	13.83±1.89
tubby like protein 4	Tulp4	0.98±0.12
tuberous sclerosis 2	Tsc2	2.29±0.2
tubulin cofactor a	Tbca	20.2±1.47
tubulin folding cofactor B	Tbcb	2.82±0.96
Tubulin tyrosine ligase	Ttl	1.22±0.21
tubulin tyrosine ligase-like 1	Ttll1	0.26±0.06
tubulin tyrosine ligase-like family, member 12 (predicted)	Ttll12_predicted	1.33±0.37
tubulin, alpha 1A /// tubulin, alpha 1C /// tubulin, alpha 1B	Tuba1a /// Tuba1b /// T	14.73±3.05
tubulin, alpha 4A	Tuba4a	9.72±6.21
tubulin, beta 2a	Tubb2a	10.93±0.11
tubulin, beta 2c	Tubb2c	5.91±1.98
tubulin, beta 4	Tubb4	0.45±0.27
tubulin, beta 5	Tubb5	2.84±0.22
tubulin, gamma 1	Tubg1	1.97±0.73
tubulin, gamma complex associated protein 2	Tubgcp2	1.23±0.57
tubulin, gamma complex associated protein 3	Tubgcp3	0.43±0.32
tubulin, gamma complex associated protein 6 (predicted)	Tubgcp6_predicted	0.56±0.16
tubulin-specific chaperone c (predicted)	Tbcc_predicted	0.52±0.07
tubulin-specific chaperone d	Tbcd	1.39±0.28
tubulin-specific chaperone e	Tbce	1.65±0.2
tubulointerstitial nephritis antigen-like 1	Tinagl1	0.27±2.27
tudor domain containing 3	Tdrd3	1.32±0.4
tudor domain containing 7	Tdrd7	1.87±0.16
tuftelin interacting protein 11	Tfip11	0.32±0.12
tumor necrosis factor (ligand) superfamily, member 13	Tnfsf13	0.94±0.13
tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	0.3±2.86
tumor necrosis factor receptor superfamily, member 1a	Tnfrsf1a	1.6±0.71
tumor necrosis factor receptor superfamily, member 21 (predicted)	Tnfrsf21_predicted	5.28±0.7
tumor necrosis factor superfamily, member 5-induced protein 1 (predicted)	Tnfsf5ip1_predicted	2.41±0.22
tumor necrosis factor, alpha-induced protein 1 (endothelial)	Tnfaip1	4.63±0.31
tumor necrosis factor, alpha-induced protein 2	Tnfaip2	0.55±0.22
tumor necrosis factor, alpha-induced protein 8 (predicted)	Tnfaip8_predicted	0.52±0.21
tumor protein D52 (predicted)	Tpd52_predicted	2.39±0.31
tumor protein D52-like 1	Tpd52l1	1.5±0.75
tumor protein D52-like 2	Tpd52l2	0.69±0.09
tumor protein p53 inducible nuclear protein 2	Trp53inp2	12.81±0.8
tumor protein, translationally-controlled 1	Tpt1	46.79±5.04
tumor rejection antigen gp96 (predicted)	Tra1_predicted	6.5±1.47
tumor suppressing subtransferable candidate 1	Tssc1	0.25±0.15
tumor suppressor candidate 2	Tusc2	0.95±0.01
tumor suppressor candidate 3	Tusc3	5.08±0.1
tumor suppressor candidate 4	Tusc4	3.53±0.42
tumor susceptibility gene 101	Tsg101	3.37±0.37
tumor-associated calcium signal transducer 1	Tacstd1	34.14±10.17
tumor-associated calcium signal transducer 2	Tacstd2	4.5±0.85
tumor-suppressing subchromosomal transferable fragment 4	Tssc4	2.04±0.28
tweety homolog 3 (Drosophila) (predicted)	Ttyh3_predicted	1.11±0.44
twinfilin, actin-binding protein, homolog 1 (Drosophila)	Twf1	3.3±0.03
twist gene homolog 1 (Drosophila)	Twist1	0.97±0.03
TWIST neighbor (predicted)	Twistnb_predicted	1.36±0.01
twisted gastrulation homolog 1 (Drosophila) (predicted)	Twsg1_predicted	12.24±3.85
two pore channel 1	Tpcn1	4.85±1.04
two pore segment channel 2 (predicted)	Tpcn2_predicted	0.38±0.04
type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Arts1	3.21±0.83
TYRO3 protein tyrosine kinase 3	Tyro3	0.34±0.12
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Ywhab	10.39±0.65
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	15.36±3.37
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	7.43±2.6
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	5.53±0.55

tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Ywhaq	18.73±1.49
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Ywhaz	13.31±0.07
tyrosine kinase, non-receptor, 2	Tnk2	0.69±0
tyrosyl-DNA phosphodiesterase 1	Tdp1	0.93±0.23
tyrosylprotein sulfotransferase 2	Tpst2	1.6±0.3
tyrosyl-tRNA synthetase	Yars	1.75±0.19
tyrosyl-tRNA synthetase 2 (mitochondrial)	Yars2	0.95±0.55
U1 small nuclear ribonucleoprotein C /// similar to U1 small nuclear ribonucleoprotein C (U1 snRNP protein C) (U1C protein) (U1-C)	LOC685273 /// Snrpc	4.1±0.19
U1 small nuclear ribonucleoprotein polypeptide A (predicted)	Snrp70_predicted	2.72±0.74
U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 /// similar to U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b	LOC690372 /// U2af2	4.86±1.46
U2 small nuclear ribonucleoprotein B (predicted)	Snrpb2_predicted	1.39±0.83
U2 small nuclear RNA auxiliary factor 1-like 4 /// similar to Hypothetical protein MGC30332 (predicted)	RGD1563574_predicte	1.44±0.18
U2AF homology motif (UHM) kinase 1	Uhmk1	0.26±0.2
U7 snRNP-specific Sm-like protein LSM10	Lsm10	1.68±0.72
UbiA prenyltransferase domain containing 1 (predicted)	Ubiad1_predicted	0.61±0.2
ubinuclein 1 (predicted)	Ubn1_predicted	0.42±0.19
Ubiquilin 1	Ubqln1	4.54±0.16
ubiquilin 2 (predicted)	Ubqln2_predicted	2.98±0.46
ubiquilin 4 (predicted)	Ubqln4_predicted	1.5±0.13
ubiquinol cytochrome c reductase core protein 2	Uqcrc2	44.49±4.31
ubiquinol-cytochrome c reductase binding protein (predicted)	LOC687741 /// Uqcrb //	41.76±3.71
ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	35.37±4.77
ubiquinol-cytochrome c reductase hinge protein	Uqcrh	44.57±2.05
ubiquinol-cytochrome c reductase, 6.4kDa subunit	Uqcr	45.08±2.4
ubiquinol-cytochrome c reductase, complex III subunit VII	Uqcrq	39.62±6.34
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1	39.88±2.47
ubiquitin A-52 residue ribosomal protein fusion product 1	Uba52	28.89±3.47
ubiquitin associated domain containing 1	Ubac1	4.27±1.15
ubiquitin B	Ubb	49.18±5.25
ubiquitin C	Ubc	24.66±5.08
ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	LOC679036 /// RGD15	2.41±0.73
ubiquitin carboxyl-terminal esterase L5	Uchl5	3.88±0.88
ubiquitin domain containing 1	Ubtd1	0.52±0.05
ubiquitin family domain containing 1	Ubfd1	1.02±0.23
ubiquitin fusion degradation 1-like	Ufd1l	3.27±0.33
ubiquitin interaction motif containing 1	Uimc1	3.08±0.74
ubiquitin protein ligase E3A (predicted)	Ube3a_predicted	2.18±0.26
ubiquitin protein ligase E3C	Ube3c	1.54±0.21
ubiquitin related modifier 1 homolog (S. cerevisiae)	Urm1	0.63±0.31
ubiquitin specific peptdiase 1	Usp1	3.73±0.87
ubiquitin specific peptidase 10	Usp10	3.2±0.12
ubiquitin specific peptidase 11	Usp11	0.8±0.28
ubiquitin specific peptidase 12	Usp12	1.34±0.4
ubiquitin specific peptidase 14	Usp14	4.71±0.83
ubiquitin specific peptidase 15	Usp15	0.56±0.08
ubiquitin specific peptidase 18	Usp18	0.93±0.35
ubiquitin specific peptidase 19	Usp19	2.17±0.06
ubiquitin specific peptidase 2	Usp2	5.11±1.32
ubiquitin specific peptidase 20	Usp20	1.03±0.27
ubiquitin specific peptidase 25	Usp25	6.9±0.86
ubiquitin specific peptidase 28	Usp28	0.97±0.2
ubiquitin specific peptidase 3	Usp3	2.35±0.04
ubiquitin specific peptidase 33	Usp33	5.51±1.58
ubiquitin specific peptidase 35	Usp35	0.39±0.32
ubiquitin specific peptidase 36	Usp36	2.13±0.17
ubiquitin specific peptidase 38	Usp38	1.27±0.01
ubiquitin specific peptidase 39	Usp39	1.33±0.2
ubiquitin specific peptidase 4 (proto-oncogene)	Usp4	1.9±0.15
ubiquitin specific peptidase 40	Usp40	2.61±0.33
ubiquitin specific peptidase 42	Usp42	0.97±0.3
ubiquitin specific peptidase 46	Usp46	0.37±0.11
ubiquitin specific peptidase 47	Usp47	2.34±0.74
ubiquitin specific peptidase 5 (isopeptidase T)	Usp5	2.18±0.53
ubiquitin specific peptidase 52	Usp52	0.21±0.05
ubiquitin specific peptidase 54	Usp54	0.36±0.08
ubiquitin specific peptidase 7	Usp7	2.09±0.09
ubiquitin specific peptidase 8	Usp8	3.95±0.44
Ubiquitin specific peptidase 9, X chromosome (predicted)	Usp9x_predicted	3.28±0.14
ubiquitin specific peptidase like 1	Uspl1	1.42±0.15
ubiquitin specific protease 13 (isopeptidase T-3) (predicted)	Usp13_predicted	0.24±0.01
ubiquitin specific protease 24 (predicted)	Usp24_predicted	1.69±0.62
ubiquitin specific protease 32 (predicted)	Usp32_predicted	1.56±0.16
ubiquitin specific protease 43	rCG_32844	0.52±0.28
ubiquitin specific protease 48	Usp48	1.8±0.13
Ubiquitin specific protease 7 (herpes virus-associated)	Usp7	3.29±0.52
ubiquitin-activating enzyme E1C	Ube1c	4.15±1.41
ubiquitin-activating enzyme E1-domain containing 1	Ube1dc1	1.33±0.05
ubiquitin-activating enzyme E1-like 2	Ube1l2	1.45±0.49
ubiquitin-associated protein 1	Ubap1	1.49±0.33
ubiquitin-associated protein 2 (predicted)	Ubap2_predicted	2.6±0.29
ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	2.64±0.4
ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (predicted)	Ube4b_predicted	5.57±0.07
ubiquitin-conjugating enzyme E2 variant 1 (predicted)	Ube2v1_predicted	8.5±0.41
ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	0.92±0.37
Ubiquitin-conjugating enzyme E2, J1 (predicted)	Ube2j1_predicted	2.07±0.3
ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	Ube2j2	3.07±0.07
ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	Ube2a	2.84±0.43

ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	Ube2b	7.36±0.45
ubiquitin-conjugating enzyme E2C (predicted)	Ube2c_predicted	0.99±0.08
ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast) (predicted)	Ube2d1_predicted	0.96±0.1
Ubiquitin-conjugating enzyme E2D 2	Ube2d2	5.13±0.88
ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	12.18±0.15
ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	6.46±0.64
ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast) (predicted)	Ube2e3_predicted	7.3±1.55
ubiquitin-conjugating enzyme E2F (putative)	Ube2f	2.45±0.3
ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	6.77±0.01
ubiquitin-conjugating enzyme E2G 2 (predicted)	Ube2g2_predicted	0.88±0.11
ubiquitin-conjugating enzyme E2I	Ube2i	3.94±0.45
ubiquitin-conjugating enzyme E2L 3 (predicted)	Ube2l3_predicted	5.33±0.85
ubiquitin-conjugating enzyme E2L 6	Ube2l6	0.5±0.01
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (predicted)	Ube2m_predicted	5.25±0.44
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (predicted) /// chromatin modifying protein 2A	Chmp2a /// Ube2m_pre	8.74±1.87
ubiquitin-conjugating enzyme E2N	Ube2n	4.42±0.1
ubiquitin-conjugating enzyme E2O (predicted)	Ube2o_predicted	2.45±0.93
ubiquitin-conjugating enzyme E2Q (putative) 1	Ube2q1	3.43±0.18
ubiquitin-conjugating enzyme E2Q (putative) 2 (predicted)	Ube2q2_predicted	3.47±0.27
ubiquitin-conjugating enzyme E2S (predicted)	Ube2s_predicted	3.03±0.31
ubiquitin-conjugating enzyme E2T (putative) (predicted)	Ube2t_predicted	0.21±0.09
ubiquitin-conjugating enzyme E2Z (putative)	Ube2z	1.56±0.23
ubiquitin-fold modifier 1	Ufm1	4.48±0.34
ubiquitin-fold modifier conjugating enzyme 1	Ufc1	4.43±1.49
ubiquitin-like 3	Ubl3	11.92±5.34
ubiquitin-like 4	Ubl4	2.78±0.74
ubiquitin-like 5	Ubl5	15.93±0.52
ubiquitin-like 7 (bone marrow stromal cell-derived)	Ubl7	3.01±0.04
ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	5.32±0.47
ubiquitin-like modifier activating enzyme 1	Uba1	9.69±1.57
ubiquitin-like, containing PHD and RING finger domains 2 (predicted)	Uhrf2_predicted	1.84±0.21
ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	0.31±0.07
ubiquitously expressed transcript	Uxt	3.02±0.09
ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (predicted)	Utx_predicted	2.38±0.44
UBX domain containing 1	Ubxd1	2.7±0.08
UBX domain containing 2	Ubxd2	6.48±0.12
UBX domain containing 4	Ubxd4	4.54±0.03
UBX domain containing 6 (predicted)	Ubxd6_predicted	2.3±0.32
UBX domain containing 8	Ubxd8	1.26±0.42
UCHL5 interacting protein	Uchl5ip	0.95±0.04
UDP galactosyltransferase 8A	Ugt8a	1.17±0.25
UDP glycosyltransferase 1 family, polypeptide A1	Ugt1a1 /// Ugt1a2 /// Ug	14.82±0.91
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	B4galt1_predicted	3.03±0.25
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	B4galt3	2.32±0.14
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 (predicted)	B4galt5_predicted	0.26±0.02
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	B4galt6	0.97±0.47
UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1	B3galnt1	0.94±0.34
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3gnt1	2.16±1.19
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	B3gnt2	5.74±0.32
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	B3gnt7	0.64±0.24
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	B3gntl1	0.24±0.08
UDP-glucose dehydrogenase	Ugdh	6.88±1.27
UDP-glucose pyrophosphorylase 2	Ugp2	27.11±0
UDP-glucuronate decarboxylase 1	Uxs1	1.11±0.17
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	Galnt1	2.09±0.1
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	Galnt11	0.58±0.14
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13	Galnt13	0.24±0.06
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (predicted)	Galnt2_predicted	4.02±0.06
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (predicted)	Galntl4_predicted	6.4±1.24
UDP-N-acetylglucosamine pyrophosphorylase 1	Uap1	1.3±0.54
UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 (predicted)	Uap1l1_predicted	4.81±0.95
UFM1-specific peptidase 2	Ufsp2	3.86±1.41
UHRF1 (ICBP90) binding protein 1-like	Uhrf1bp1l	3.87±0.58
UNC homeobox	Uncx	0.78±0.06
UNC-119 homolog (C. elegans)	Unc119	0.73±0.08
unc-119 homolog B (C. elegans)	Unc119b	6.16±0.21
unc-13 homolog B (C. elegans)	Unc13b	0.39±0
unc-45 homolog A (C. elegans)	Unc45a	1.98±0.82
unc-5 homolog C (C. elegans)-like	Unc5cl	0.34±0.13
unc-5 homolog D (C. elegans) (predicted)	Unc5d_predicted	1.58±0.21
unc-50 homolog (C. elegans)	Unc50	4.75±0.89
Unc-51 like kinase 1 (C. elegans)	Ulk1	2.71±0.45
Unc-51 like kinase 2 (C. elegans) (predicted)	Ulk2_predicted	0.47±0.5
unc-84 homolog B (C. elegans)	Unc84b	3.52±1.38
unconventional SNARE in the ER 1 homolog (S. cerevisiae)	LOC292282 /// Use1	5.29±0.94
UPF3 regulator of nonsense transcripts homolog A (yeast)	Upf3a	1.47±0.29
UPF3 regulator of nonsense transcripts homolog B (yeast) (predicted)	Upf3b_predicted	3.07±0.23
upregulated during skeletal muscle growth 5	Usmg5	51.12±0.94
up-regulated gene 4	Urg4	0.9±0.02
up-regulator of carnitine transporter, OCTN2	LOC303140	0.61±0.1
upstream binding protein 1 (predicted)	Ubp1_predicted	2.63±0.47
upstream binding transcription factor, RNA polymerase I	Ubtf	1.47±0.11
upstream transcription factor 1	Usf1	0.61±0.03
upstream transcription factor 2	Usf2	2.2±0.15
uracil-DNA glycosylase	Ung	4.22±0.2
uridine monophosphate synthetase	Umps	3.44±1.09
uridine phosphorylase 1	Upp1	1.74±0.22

uridine-cytidine kinase 1 (predicted)	Uck1_predicted	2.96±0.34
uridine-cytidine kinase 1-like 1	Uckl1	2.12±0.19
uridine-cytidine kinase 2	Uck2	0.78±0.47
uromodulin	Umod	71.52±5.82
uroplakin 1A	Upk1a	0.64±0.6
uroporphyrinogen decarboxylase	Urod	7.62±1.07
USO1 homolog, vesicle docking protein (yeast)	Uso1	2.63±0.42
USP6 N-terminal like (predicted)	Usp6nl_predicted	0.77±0.18
UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	Utp14a	1.35±0.16
UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Utp15	0.53±0.07
UTP18, small subunit (SSU) processome component, homolog (yeast)	Utp18	0.21±0.14
UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	0.36±0.03
UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae	Utp3	2.17±0.13
UTP6, small subunit (SSU) processome component, homolog (yeast)	Utp6	0.36±0.35
Utrophin	Utrn	0.72±0.25
Vac14 homolog (S. cerevisiae)	Vac14	1.29±0.01
vaccinia related kinase 1	Vrk1	0.7±0.16
vaccinia related kinase 3	Vrk3	2.85±0.17
vacuolar protein sorting 11 (yeast) (predicted)	Vps11_predicted	1.75±0.02
vacuolar protein sorting 13D (yeast) (predicted)	Vps13d_predicted	0.7±0.1
vacuolar protein sorting 16 (yeast)	Vps16	0.61±0.25
vacuolar protein sorting 18 (yeast) (predicted)	Vps18_predicted	0.33±0.18
vacuolar protein sorting 25 homolog (S. cerevisiae)	Vps25	5.54±0.96
Vacuolar protein sorting 26 (yeast)	Vps26	2.63±0.92
vacuolar protein sorting 26 homolog A (yeast)	Vps26a	1.58±0.26
vacuolar protein sorting 28 (yeast) (predicted)	Vps28_predicted	4.26±0.06
vacuolar protein sorting 29 (S. pombe) (predicted)	Vps29_predicted	8.19±1.57
vacuolar protein sorting 33A (yeast)	Vps33a	0.76±0.15
vacuolar protein sorting 33B (yeast)	Vps33b	0.63±0.04
vacuolar protein sorting 35	Vps35	7.57±1.18
vacuolar protein sorting 36 (yeast) (predicted)	Vps36_predicted	0.99±0.14
vacuolar protein sorting 37 homolog A (S. cerevisiae)	Vps37a	0.75±0.28
vacuolar protein sorting 37B (yeast) (predicted)	Vps37b_predicted	1.22±0.24
vacuolar protein sorting 37C (yeast) (predicted)	Vps37c_predicted	1.35±0.39
vacuolar protein sorting 39 (yeast)	Vps39	0.57±0.07
vacuolar protein sorting 45 (yeast)	Vps45	0.82±0.07
vacuolar protein sorting 4a (yeast)	Vps4a	3.24±0.07
vacuolar protein sorting 4b (yeast)	Vps4b	3.58±0.37
vacuolar protein sorting 52 (yeast)	Vps52	0.58±0.3
vacuolar protein sorting 53 (yeast) (predicted)	Vps53_predicted	1.18±0.28
vacuolar protein sorting 54 (yeast)	Vps54	2.63±0.82
vacuolar protein sorting 72 (yeast) (predicted)	Vps72_predicted	1.63±0.25
vacuolar protein sorting 8 homolog (S. cerevisiae)	Vps8	1.95±0.38
valosin containing protein (p97)/p47 complex interacting protein 1	Vcpip1	0.94±0.36
valosin-containing protein	Vcp	8.45±0.96
vang-like 1 (van gogh, Drosophila)	Vangl1	0.38±0.26
vascular endothelial growth factor A	Vegfa	13.23±2.49
vascular endothelial growth factor B	Vegfb	4.51±0.22
vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	2.07±0.44
vasodilator-stimulated phosphoprotein (predicted)	Vasp_predicted	2.56±0.25
vasohibin 1	Vash1	0.54±0.08
vasorin	Vasn	0.82±0.05
VATPase, H+ transporting, lysosomal V1 subunit E1	Atp6v1e1	14.79±0.87
vav 3 oncogene	Vav3	9.51±1.75
Vav2 oncogene (predicted)	Vav2_predicted	0.85±0.06
v-crk sarcoma virus CT10 oncogene homolog (avian)	Crk	0.59±0.15
v-crk sarcoma virus CT10 oncogene homolog (avian)-like	Crkl	0.37±0.05
ventricular zone expressed PH domain homolog 1 (zebrafish) /// similar to VEPH isoform A (predicted)	RGD1565184_predicte	3.55±1.51
v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	Erbb2	1.83±0.19
versican	Vcan	1.42±0.54
very low density lipoprotein receptor	Vldlr	0.5±0.06
vesicle amine transport protein 1 homolog (T californica)	Vat1	1.1±0.32
vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	0.32±0.01
vesicle-associated membrane protein 1	Vamp1	0.45±0.05
vesicle-associated membrane protein 2	Vamp2	1.29±0.11
vesicle-associated membrane protein 3	Vamp3	3.09±0.13
vesicle-associated membrane protein 5	Vamp5	2.25±0.17
vesicle-associated membrane protein 7	Vamp7	4.31±0.52
vesicle-associated membrane protein 8	Vamp8	12.25±1
vesicle-associated membrane protein, associated protein a	Vapa	25.88±0.89
vesicle-associated membrane protein, associated protein B and C	Vapb	4.11±0.13
vestigial like 4 (Drosophila)	Vgll4	2.51±0.03
vezatin, adherens junctions transmembrane protein	Vezt	0.28±0.13
villin 2	Vil2	8.31±2.61
villin-like (predicted)	Vill_predicted	0.61±0.35
vinculin (predicted)	Vcl_predicted	1.58±0.88
virus-induced signaling adapter	Visa	5.06±0.87
vitamin D receptor	Vdr	0.25±0.01
vitamin K epoxide reductase complex, subunit 1	Vkorc1	9.13±1.19
vitamin K epoxide reductase complex, subunit 1-like 1	Vkorc1l1	0.24±0.01
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Kras	4.82±0.78
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	Mafk	0.59±0.89
voltage-dependent anion channel 1	Vdac1	20.97±1.55
voltage-dependent anion channel 2	Vdac2	33.52±0.81
voltage-dependent anion channel 3	Vdac3	34.95±8.38
von Hippel-Lindau tumor suppressor	Vhl	5.79±0.47
Vps20-associated 1 homolog (S. cerevisiae)	Vta1	2.97±0.42

v-raf murine sarcoma 3611 viral oncogene homolog	Araf	2.48±0.6
v-raf-1 murine leukemia viral oncogene homolog 1	Raf1	4.33±1.32
v-ral simian leukemia viral oncogene homolog A (ras related)	Rala	1.71±0.4
v-ral simian leukemia viral oncogene homolog B (ras related)	Ralb	2.62±0.39
v-rel reticuloendotheliosis viral oncogene homolog A (avian)	Rela	1.47±0.64
WAP four-disulfide core domain 1	Wfdc1	0.83±0.12
WAP four-disulfide core domain 10	Wfdc10	1.95±0.4
WAP four-disulfide core domain 2	Wfdc2	15.59±0.67
WAS protein homology region 2 domain containing 1	Whdc1	0.57±0.08
WAS/WASL interacting protein family, member 1	Wipf1	0.88±0.05
WAS/WASL interacting protein family, member 3	Wipf3	0.2±0.18
WD and tetratricopeptide repeats 1 (predicted)	Wdtc1_predicted	1.23±0.05
WD repeat and FYVE domain containing 1	Wdfy1	0.64±0.88
WD repeat and FYVE domain containing 2 (predicted)	Wdfy2_predicted	4.49±0.19
WD repeat and FYVE domain containing 3 (predicted)	Wdfy3_predicted	5.32±0.11
WD repeat and HMG-box DNA binding protein 1 (predicted)	Wdhd1_predicted	0.29±0.16
WD repeat and SOCS box-containing 1	Wsb1	0.25±0.07
WD repeat and SOCS box-containing 2	Wsb2	4.49±1.49
WD repeat domain 1	Wdr1	6.71±0.71
WD repeat domain 12	Wdr12	0.21±0.08
WD repeat domain 13 (predicted)	Wdr13_predicted	3.15±0.56
WD repeat domain 18	Wdr18	0.81±0.01
WD repeat domain 19 (predicted)	Wdr19_predicted	0.76±0.14
WD repeat domain 20	Wdr20	0.36±0.29
WD repeat domain 20a	Wdr20a	0.76±0.24
WD repeat domain 21 (predicted)	Wdr21_predicted	1.05±0.06
WD repeat domain 22	Wdr22	0.34±0.2
WD repeat domain 23	Wdr23	7.3±0.94
WD repeat domain 24	Wdr24	0.8±0.06
WD repeat domain 25 /// similar to pre-mRNA splicing factor-like (predicted)	RGD1562505_predicte	0.26±0.23
WD repeat domain 26	Wdr26	2.56±0.06
WD repeat domain 3 (predicted)	Wdr3_predicted	0.56±0.3
WD repeat domain 31	Wdr31	0.57±0.03
WD repeat domain 32 (predicted)	Wdr32_predicted	0.34±0.09
WD repeat domain 33 (predicted)	Wdr33_predicted	1.2±0
WD repeat domain 34	Wdr34	1.36±0.3
WD repeat domain 36 (predicted)	Wdr36_predicted	0.84±0.53
WD repeat domain 37 (predicted)	Wdr37_predicted	1.91±0.21
WD repeat domain 41 (predicted)	Wdr41_predicted	0.56±0
WD repeat domain 42A	Wdr42a	1.8±0.41
WD repeat domain 43	Wdr43	0.75±0.15
WD repeat domain 45	Wdr45	4.24±0.74
WD repeat domain 47	Wdr47	0.6±0.02
WD repeat domain 48 (predicted)	Wdr48_predicted	0.73±0.21
WD repeat domain 5	Wdr5	1.53±0.24
WD repeat domain 59	Wdr59	6.95±1.4
WD repeat domain 5B	Wdr5b	0.41±0.15
WD repeat domain 6	Wdr6	2.6±0.25
WD repeat domain 61	Wdr61	6.81±0.87
WD repeat domain 67	Wdr67	0.92±0.34
WD repeat domain 68 (predicted)	Wdr68_predicted	5.14±1.49
WD repeat domain 70	Wdr70	1.02±0.47
WD repeat domain 75	Wdr75	0.32±0.34
WD repeat domain 77	Wdr77	2.15±0.45
WD repeat domain 79	Wdr79	0.6±0.01
WD repeat domain 81	Wdr81	0.7±0.15
WD repeat domain 89	Wdr89	0.28±0.05
WD repeat domain, phosphoinositide interacting 1 (predicted)	Wipi1_predicted	0.48±0.44
WD repeat domain, phosphoinositide interacting 2	Wipi2	1.5±0.35
WD repeat, SAM and U-box domain containing 1	Wdsub1	1.83±0.03
WD repeats and SOF domain containing 1 (predicted)	Wdsof1_predicted	3±1.26
Wdr45 like (predicted)	Wdr45l_predicted	2.6±0.57
wee 1 homolog (S. pombe)	Wee1	0.25±0.06
Werner helicase interacting protein 1	Wrnip1	2.07±0.23
widely-interspaced zinc finger motifs (predicted)	Wiz_predicted	0.43±0.3
Williams Beuren syndrome chromosome region 22	LOC368084 /// Wbscr2	1.11±0.45
Williams Beuren syndrome chromosome region 27	Wbscr27	0.43±0.08
Williams-Beuren syndrome chromosome region 16 homolog (human) (predicted)	Wbscr16_predicted	0.42±0
Williams-Beuren syndrome chromosome region 18 /// similar to Williams-Beuren syndrome critical region 18	LOC680976 /// Wbscr1	2.16±0.23
Wilms' tumour 1-associating protein	Wtap	7.2±1.24
wingless related MMTV integration site 10a (predicted)	Wnt10a_predicted	1.06±0.14
Wiskott-Aldrich syndrome-like (human)	Wasl	5.68±0.77
WNK lysine deficient protein kinase 1	Wnk1	0.92±0.34
WNK lysine deficient protein kinase 4	Wnk4	3.7±0.94
Wnt inhibitory factor 1	Wif1	0.35±0.1
Wolf-Hirschhorn syndrome candidate 1 (human)	Whsc1	0.61±0.12
Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)	Whsc1l1_predicted	1.6±0.27
Wolf-Hirschhorn syndrome candidate 2 (human)	Whsc2	2.33±0.1
Wolfram syndrome 1 homolog (human)	Wfs1	0.68±0.35
WSC domain containing 1	Wscd1	2.92±0.49
WT1-interacting protein (predicted)	Wtip_predicted	0.85±0.51
WW domain binding protein 1	Wbp1	6.65±1.51
WW domain binding protein 11	Wbp11	1.41±0.52
WW domain binding protein 2	Wbp2	1.38±0.07
WW domain binding protein 4	Wbp4	0.92±0.42
WW domain binding protein 5 (predicted)	Wbp5_predicted	18.51±0.02
WW domain binding protein 7	Wbp7	1.28±0.31

WW domain containing E3 ubiquitin protein ligase 2 (predicted)	Wwp2_predicted	0.91±0.16
WW domain containing transcription regulator 1	Wwtr1	0.39±0.01
WW, C2 and coiled-coil domain containing 1	Wwc1	3.6±0.2
WW, C2 and coiled-coil domain containing 2	Wwc2	3.49±0.07
X Kell blood group precursor-related family, member 5	Xkr5	0.25±0.17
X-box binding protein 1	Xbp1	10.04±3.65
Xenotropic and polytropic retrovirus receptor 1 (predicted)	Xpr1_predicted	1.96±0.11
xeroderma pigmentosum, complementation group A (predicted)	Xpa_predicted	0.79±0.04
xeroderma pigmentosum, complementation group C (predicted)	Xpc_predicted	0.72±0.02
xin actin-binding repeat containing 1	Xirp1	0.21±0.09
X-linked myotubular myopathy gene 1	Mtm1	0.76±0.15
XPA binding protein 2	Xab2	0.98±0.17
X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Xpnpep1	3.46±1.22
X-ray repair complementing defective repair in Chinese hamster cells 1	Xrcc1	1.39±0.16
X-ray repair complementing defective repair in Chinese hamster cells 4	Xrcc4	0.48±0.01
X-ray repair complementing defective repair in Chinese hamster cells 5	Xrcc5	0.93±0.19
X-ray repair complementing defective repair in Chinese hamster cells 6	Xrcc6	0.88±0.04
XRCC6 binding protein 1	Xrcc6bp1	9.87±0.48
XTP3-transactivated protein A	Xtp3tpa	1.78±0
xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	B4galt7	0.41±0
xylosyltransferase II	Xylt2	0.99±0.38
xylulokinase homolog (H. influenzae)	Xylb	3.49±0.17
Y box protein 1	Ybx1	35.65±0.52
Y box protein 2 (predicted)	Ybx2_predicted	1.32±0.21
YEATS domain containing 2	Yeats2	0.9±0.29
YEATS domain containing 4 (predicted)	Yeats4_predicted	2.47±0.58
Yip1 domain family, member 1	Yipf1	3.86±0.15
Yip1 domain family, member 2	Yipf2	0.52±0.15
Yip1 domain family, member 3	Yipf3	0.69±0.47
Yip1 domain family, member 4	Yipf4	4.37±0.15
Yip1 domain family, member 5	Yipf5	5.56±2.07
Yip1 interacting factor homolog (S. cerevisiae)	Yif1	4.02±1.13
yippee-like 5 (Drosophila)	Ypel5	6.59±0.83
YKT6 homolog (S. Cerevisiae)	Ykt6	0.35±0.05
YLP motif containing 1	Ylpm1	1.19±0.3
YME1-like 1 (S. cerevisiae)	Yme1l1	3.65±0.42
yrdC domain containing (E.coli)	Yrdc	0.7±0.19
YTH domain family 1	Ythdf1	2.49±0.33
YTH domain family 2 (predicted)	Ythdf2_predicted	1.95±0.25
YTH domain family 3 (predicted)	Ythdf3_predicted	3.59±0.74
YY1 transcription factor	Yy1	3.83±0.49
zer-1 homolog (C. elegans)	Zer1	1.48±0.41
zinc and ring finger 1 (predicted)	Znrf1_predicted	11.62±0.68
zinc binding alcohol dehydrogenase, domain containing 1	Zadh1	10.62±1.75
zinc binding alcohol dehydrogenase, domain containing 2 (predicted)	Zadh2_predicted	1.64±0.04
zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	Zrsr2	0.27±0.26
zinc finger and BTB domain containing 1	Zbtb1	0.61±0.59
zinc finger and BTB domain containing 11 (predicted)	Zbtb11_predicted	2.78±0.99
zinc finger and BTB domain containing 17	Zbtb17	1.68±0.11
zinc finger and BTB domain containing 20 (predicted)	Zbtb20_predicted	1.92±0.76
zinc finger and BTB domain containing 24 (predicted)	Zbtb24_predicted	0.26±0.04
zinc finger and BTB domain containing 4 (predicted)	Zbtb4_predicted	3.07±0.89
zinc finger and BTB domain containing 41 homolog	Zbtb41	1.14±0.02
zinc finger and BTB domain containing 43	Zbtb43	0.93±0.15
zinc finger and BTB domain containing 44	Zbtb44	0.63±0.19
zinc finger and BTB domain containing 45	Zbtb45	1.63±0.48
zinc finger and BTB domain containing 5 (predicted)	Zbtb5_predicted	0.96±0
zinc finger and BTB domain containing 6	Zbtb6	0.33±0.02
zinc finger and BTB domain containing 7a	Zbtb7a	1.41±0.05
zinc finger and BTB domain containing 7B (predicted)	Zbtb7b_predicted	0.32±0.17
zinc finger and BTB domain containing 8 (predicted)	Zbtb8_predicted	0.69±0.03
zinc finger and BTB domain containing 8 opposite strand (predicted)	Zbtb8os_predicted	2.46±0.19
zinc finger and BTB domain containing 9	Zbtb9	0.48±0.31
zinc finger and SCAN domain containing 21	Zscan21	0.83±0.17
zinc finger and SCAN domains 20	Zscan20	0.27±0.03
zinc finger CCCH type containing 10	Zc3h10	0.52±0.19
zinc finger CCCH type containing 13	Zc3h13	0.46±0.09
zinc finger CCCH type containing 14	Zc3h14	2.73±0.07
zinc finger CCCH type containing 6 (predicted)	Zc3h6_predicted	0.59±0.06
zinc finger CCCH type containing 7 A (predicted)	Zc3h7a_predicted	1.64±0.37
zinc finger CCCH type containing 8	Zc3h8	1.09±0.17
zinc finger CCCH-type containing 15	Zc3h15	4.54±0.23
zinc finger CCCH-type containing 7B (predicted)	Zc3h7b_predicted	1.91±0.26
zinc finger CCHC-type and RNA binding motif 1	Zcrb1	1.33±0.11
zinc finger homeobox 3 (predicted)	Zfhx3_predicted	0.82±0.19
zinc finger protein 105	Zfp105	0.69±0.22
zinc finger protein 110	Zfp110	1.92±0.67
zinc finger protein 111	Zfp111	0.39±0.28
zinc finger protein 124 (HZF-16) (predicted)	Znf124_predicted	0.45±0.28
zinc finger protein 128	Zfp128	0.23±0.22
zinc finger protein 131	Zfp131	0.39±0.36
zinc finger protein 142 (clone pHZ-49) (predicted)	Znf142_predicted	0.53±0.09
zinc finger protein 143	Zfp143	0.5±0.35
zinc finger protein 148	Zfp148	3.29±0.11
zinc finger protein 157	Zfp157	0.6±0.19
zinc finger protein 161	Zfp161	0.47±0.01
zinc finger protein 180	Zfp180	2.55±0.33

zinc finger protein 189 (predicted)	Zfp189_predicted	0.74±0.18
zinc finger protein 191	Zfp191	0.72±0.38
zinc finger protein 202	Zfp202	0.37±0.1
zinc finger protein 207	Zfp207	3.05±1.1
Zinc finger protein 212	Zfp212	1.62±0.67
zinc finger protein 213 (predicted)	Znf213_predicted	1.1±0.26
zinc finger protein 213 (predicted) /// similar to Caspase-14 precursor (CASP-14)	LOC679178 /// LOC68	0.4±0.08
zinc finger protein 219	Zfp219	3.15±1.09
zinc finger protein 259	Zfp259	3.05±0.12
zinc finger protein 260	Zfp260	3.75±0.33
zinc finger protein 278	Zfp278	1.24±0.07
zinc finger protein 281	Zfp281	1.03±0.08
zinc finger protein 282 (predicted)	Zfp282_predicted	0.62±0.11
zinc finger protein 289	Zfp289	2.27±0.03
zinc finger protein 291	Znf291	1.15±0.08
zinc finger protein 292	Zfp292	0.27±0.39
zinc finger protein 294	Zfp294	2.24±0.42
zinc finger protein 297	Zfp297	0.52±0.11
zinc finger protein 313	Zfp313	1.7±0.7
zinc finger protein 316 (predicted)	Zfp316_predicted	0.33±0.03
zinc finger protein 330 (predicted)	Zfp330_predicted	4.79±1.19
zinc finger protein 335	Zfp335	0.78±0.17
zinc finger protein 346 (predicted)	Zfp346_predicted	0.42±0.01
zinc finger protein 347	Zfp347	0.56±0.13
zinc finger protein 354A	Zfp354a	0.38±0.07
zinc finger protein 358 (predicted)	Zfp358_predicted	1.29±0.38
zinc finger protein 36	Zfp36	10.71±6.43
zinc finger protein 36, C3H type-like 1	Zfp36l1	21.03±3.68
zinc finger protein 36, C3H type-like 2	Zfp36l2	5.47±0.82
zinc finger protein 362 /// zinc finger and SCAN domains 20	Zfp362 /// Zscan20	2.85±0.3
zinc finger protein 364 (predicted)	Zfp364_predicted	3.33±1.23
zinc finger protein 367	Zfp367	1.93±0.1
zinc finger protein 384	Zfp384	2.52±0.28
zinc finger protein 386 (Kruppel-like)	Zfp386	2.32±0.09
zinc finger protein 395 (predicted)	Zfp395_predicted	2.42±0.29
zinc finger protein 40	Zfp40	0.26±0.15
zinc finger protein 407	Zfp407	0.25±0.03
zinc finger protein 410 (predicted)	Zfp410_predicted	1.45±0.06
zinc finger protein 414	Zfp414	1.74±0.23
zinc finger protein 422	Zfp422	2.8±0.13
zinc finger protein 426	Zfp426	0.76±0.11
zinc finger protein 444 (predicted)	Zfp444_predicted	0.79±0.07
zinc finger protein 445	Zfp445	1.55±0.02
zinc finger protein 446 (predicted)	Zfp446_predicted	0.69±0.09
zinc finger protein 451	Zfp451	0.65±0.27
zinc finger protein 455	Zfp455	0.33±0
zinc finger protein 46 (predicted)	Zfp46_predicted	1.04±0.18
zinc finger protein 462	Zfp462	1.37±0.09
zinc finger protein 467	Zfp467	2.2±0.48
zinc finger protein 469 (predicted)	Zfp469_predicted	0.58±0.18
zinc finger protein 503 (predicted)	Zfp503_predicted	8.77±3.52
Zinc finger protein 507 (predicted)	Znf507_predicted	1.37±0.13
zinc finger protein 509 (predicted)	Zfp509_predicted	0.2±0.02
zinc finger protein 511	Zfp511	0.24±0.08
zinc finger protein 512	Zfp512	0.88±0.42
zinc finger protein 512B	Znf512b	1.12±0.04
zinc finger protein 513	Zfp513	1.55±0.15
zinc finger protein 524	Zfp524	1.38±0.26
zinc finger protein 532 (predicted)	Znf532_predicted	0.41±0.32
zinc finger protein 533 (predicted)	Zfp533_predicted	1.68±0.29
zinc finger protein 541	Zfp541	1.93±0.34
zinc finger protein 553	Zfp553	1.55±0.29
zinc finger protein 553 /// zinc finger protein 771	Zfp553 /// Zfp771	3.66±0.79
zinc finger protein 574	Zfp574	1.27±0
zinc finger protein 579	Zfp579	0.49±0.06
zinc finger protein 580 (predicted)	Zfp580_predicted	1.74±0.4
zinc finger protein 592 (predicted)	Zfp592_predicted	0.66±0.06
zinc finger protein 598 (predicted)	Zfp598_predicted	1.14±0.2
zinc finger protein 609	Zfp609	0.2±0.18
zinc finger protein 61	Zfp61	0.76±0.24
zinc finger protein 612 (predicted)	Zfp612_predicted	0.51±0.05
zinc finger protein 618 (predicted)	Znf618_predicted	3.08±0.08
zinc finger protein 622	Zfp622	1.32±0.25
zinc finger protein 629	Zfp629	1.49±0.37
Zinc finger protein 637	Zfp637	3.64±0.02
zinc finger protein 64	Zfp64	0.32±0.09
zinc finger protein 644 (predicted)	Zfp644_predicted	2.25±0.41
zinc finger protein 652	Zfp652	0.9±0.05
zinc finger protein 653 (predicted)	Zfp653_predicted	0.2±0.35
zinc finger protein 654	Zfp654	1.08±0.42
zinc finger protein 655	Zfp655	3.8±0.86
zinc finger protein 667	Zfp667	0.64±0.13
zinc finger protein 672	Zfp672	1.76±0.59
zinc finger protein 68 (predicted)	Zfp68_predicted	2.78±0.79
zinc finger protein 688 (predicted)	Zfp688_predicted	0.51±0.18
zinc finger protein 691 (predicted)	Zfp691_predicted	1.25±0.22
zinc finger protein 692 (predicted)	Zfp692_predicted	0.74±0

zinc finger protein 703	Zfp703	0.39±0.09
zinc finger protein 706	Zfp706	16.23±4.25
zinc finger protein 709	Zfp709	0.25±0.18
Zinc finger protein 710 (predicted)	Zfp710_predicted	0.26±0.16
zinc finger protein 771	Zfp771	0.98±0.07
zinc finger protein 775	Zfp775	0.51±0.12
zinc finger protein 777	Zfp777	0.83±0.08
zinc finger protein 787	Zfp787	2.46±0.3
zinc finger protein 821	Zfp821	0.97±0.11
zinc finger protein 828	Zfp828	1.71±0.37
zinc finger protein 84 (predicted)	Zfp84_predicted	0.9±0.3
zinc finger protein 91	Zfp91	2.42±0.17
zinc finger protein LOC100125361	rCG_64343	0.28±0.06
zinc finger protein X-linked (predicted)	Zfx_predicted	1.51±0.25
zinc finger protein ZFP	LOC503192	1.37±0.23
zinc finger RNA binding protein	Zfr	8.72±0.27
zinc finger with KRAB and SCAN domains 1	Zkscan1	0.29±0.22
zinc finger with KRAB and SCAN domains 17	Zkscan17	1.3±0.05
zinc finger with KRAB and SCAN domains 3	Zkscan3	3.29±1.1
zinc finger with KRAB and SCAN domains 5	Zkscan5	2.05±0.51
zinc finger with KRAB and SCAN domains 6	Zkscan6	0.75±0.13
zinc finger with UFM1-specific peptidase domain	Zufsp	0.99±0
zinc finger, AN1-type domain 1	Zfand1	0.49±0.21
zinc finger, AN1-type domain 3	Zfand3	2.28±0.11
zinc finger, AN1-type domain 5	Zfand5	5.1±1.67
zinc finger, AN1-type domain 6	Zfand6	12.47±0.01
zinc finger, BED domain containing 3	Zbed3	1.84±0.1
zinc finger, BED domain containing 4 (predicted)	Zbed4_predicted	0.65±0.21
zinc finger, C3HC-type 1 (predicted)	Zc3hc1_predicted	0.57±0.06
zinc finger, CCCH-type with G patch domain /// Lck interacting transmembrane adaptor 1	Lime1 /// Zgpat	0.58±0.11
zinc finger, CCHC domain containing 10	Zcchc10	0.87±0.01
zinc finger, CCHC domain containing 11 (predicted)	Zcchc11_predicted	0.59±0.5
zinc finger, CCHC domain containing 12	Zcchc12	0.27±0.18
zinc finger, CCHC domain containing 17	Zcchc17	1.12±0
Zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted	0.28±0.16
zinc finger, CCHC domain containing 9	Zcchc9	1.06±0.35
Zinc finger, CW-type with coiled-coil domain 1 (predicted)	Zcwcc1_predicted	0.36±0.08
zinc finger, DHHC domain containing 1	Zdhhc1	1.56±0.38
zinc finger, DHHC domain containing 13	Zdhhc13	1.8±0.19
zinc finger, DHHC domain containing 16	Zdhhc16	2.23±0.14
zinc finger, DHHC domain containing 2	Zdhhc2	0.32±0.13
zinc finger, DHHC domain containing 23	Zdhhc23	1.11±0.45
Zinc finger, DHHC domain containing 3	Zdhhc3	1.67±0.22
zinc finger, DHHC domain containing 4	Zdhhc4	1.94±0.47
zinc finger, DHHC domain containing 5	Zdhhc5	2.34±0.63
zinc finger, DHHC domain containing 6	Zdhhc6	3.87±0.23
zinc finger, DHHC domain containing 7	Zdhhc7	2.52±0.44
zinc finger, DHHC domain containing 8	Zdhhc8	0.92±0.3
zinc finger, FYVE domain containing 1 (predicted)	Zfyve1_predicted	0.58±0.25
zinc finger, FYVE domain containing 16	Zfyve16	0.59±0.31
zinc finger, FYVE domain containing 19	Zfyve19	1.04±0.14
zinc finger, FYVE domain containing 20 (predicted)	Zfyve20_predicted	0.81±0.13
zinc finger, FYVE domain containing 21 (predicted)	Zfyve21_predicted	5.03±0.09
zinc finger, FYVE domain containing 26 (predicted)	Zfyve26_predicted	1.21±0.21
zinc finger, FYVE domain containing 27	Zfyve27	0.64±0.07
zinc finger, FYVE domain containing 9 (predicted)	Zfyve9_predicted	0.61±0.14
zinc finger, HIT domain containing 1 (predicted)	Znhit1_predicted	4.78±0.71
zinc finger, HIT domain containing 2 (predicted)	Znhit2_predicted	0.62±0.21
zinc finger, HIT type 3	Znhit3	0.96±0.01
zinc finger, matrin type 2	Zmat2	0.94±0.22
zinc finger, matrin type 3	Zmat3	0.26±0.03
zinc finger, matrin type 5	Zmat5	1.31±0.02
zinc finger, matrin-like (predicted)	Zfml_predicted	1.95±1.96
zinc finger, MIZ-type containing 1	Zmiz1	7.25±0.54
zinc finger, MIZ-type containing 2	Zmiz2	4.22±0.97
zinc finger, MYM domain containing 1 (predicted)	Zmym1_predicted	0.69±0.2
zinc finger, MYM-type 2	Zmym2	3.32±0.58
zinc finger, MYM-type 4 (predicted)	Zmym4_predicted	1.19±0.08
zinc finger, MYM-type 6	Zmym6	1.61±0.39
zinc finger, MYND domain containing 11	Zmynd11	11.35±0.41
zinc finger, MYND domain containing 15 (predicted)	Zmynd15_predicted	0.21±0.24
zinc finger, MYND domain containing 19	Zmynd19	0.47±0.12
zinc finger, MYND domain-containing 10	Zmynd10	0.24±0.06
zinc finger, RAN-binding domain containing 2	Zranb2	5.25±0.73
zinc finger, SWIM domain containing 1 (predicted)	Zswim1_predicted	1.21±0.26
zinc finger, SWIM domain containing 3 (predicted)	Zswim3_predicted	0.39±0.09
zinc finger, SWIM domain containing 4 (predicted)	Zswim4_predicted	0.63±0.06
zinc finger, SWIM domain containing 5 (predicted)	Zswim5_predicted	0.58±0.06
Zinc finger, ZZ-type with EF hand domain 1 (predicted)	Zzef1_predicted	0.49±0.49
Zinc fingers and homeoboxes 2	Zhx2	0.83±0.24
zinc fingers and homeoboxes protein 1	Zhx1	1.65±0.25
Zinc metallopeptidase, STE24 homolog (S. cerevisiae) (predicted)	Zmpste24_predicted	6.76±0.4
zinc ribbon domain containing, 1	Znrd1	1.57±0.16
ZUBR1	Rbaf600	2.33±0.56
ZW10 homolog (Drosophila), centromere/kinetochore protein	Zw10	1.11±0.03
ZW10 interactor	Zwint	7.78±0.87
Zwilch, kinetochore associated, homolog (Drosophila)	Zwilch	0.39±0.13

ZXD family zinc finger C	Zxdc	0.36±0.03