Table S3. Rat Kidney Proximal Tubule Transcriptome

Gene Title	Gene Symbol	Signal
1-acylglycerol-3-phosphate O-acyltransferase 3 (predicted)	Agpat3_predicted	2.39±0.16
1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (predicted)	Agpat5_predicted	1.03±0.1
1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Agpat6	3.13±0.26
2,3-bisphosphoglycerate mutase	Bpgm	1.65±0.09
2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	18.38±0.84
24-dehydrocholesterol reductase	Dhcr24	7.07±0.94
2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	32.98±3.02
2-4-dienoyl-Coenzyme A reductase 2, peroxisomal /// similar to mKIAA0665 protein	Decr2 /// RGD1308952	12.38±0.89
2-hydroxyacyl-CoA lyase 1	Hacl1	3.82±0.38
2-oxoglutarate and iron-dependent oxygenase domain containing 1	Ogfod1	0.42±0.09
3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	5.61±0.67
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	2.85±0.8
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	2.93±0.41
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	Hmgcs2	1.85±0.37
3-hydroxyanthranilate 3,4-dioxygenase	Haao	5.83±2.68
3-hydroxybutyrate dehydrogenase, type 2 (predicted)	Bdh2_predicted	15.79±0.81
3-hydroxyisobutyrate dehydrogenase	Hibadh	37.93±1.24
3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	4.13±0.08
3-ketodihydrosphingosine reductase	Kdsr	0.35±0.06
3-oxoacyl-ACP synthase, mitochondrial	Oxsm	1.11±0.12
3'-phosphoadenosine 5'-phosphosulfate synthase 1 (predicted)	Papss1_predicted	14.81±2.08
3'-phosphoadenosine 5'-phosphosulfate synthase 2 (predicted)	Papss2_predicted	1.2±0.1
3-phosphoglycerate dehydrogenase	Phgdh	22.31±2.41
3-phosphoinositide dependent protein kinase-1	Pdpk1	2.52±0.34
4-aminobutyrate aminotransferase	Abat	5.7±0.25
4-hydroxyphenylpyruvic acid dioxygenase	Hpd	65.65±3.62
4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	20.97±1.01
5' nucleotidase, ecto	Nt5e	9.35±0.95
5, 10-methenyltetrahydrofolate synthetase	Mthfs	5.11±0.59
5,10-methylenetetrahydrofolate reductase	Mthfr	0.46±0.11
5'-3' exoribonuclease 1 (predicted)	Xrn1_predicted	0.4±0.08
5'-3' exoribonuclease 2 (predicted)	Xrn2_predicted	6.29±0.65
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Atic	3.89±0.38
5-azacytidine induced gene 2	Azi2	1.28±0.3
5-methyltetrahydrofolate-homocysteine methyltransferase	Mtr	0.69±0.05
5-methyltetrahydrofolate-homocysteine methyltransferase reductase	Mtrr	1.85±0.2
5'-nucleotidase domain containing 1 (predicted)	Nt5dc1_predicted	2.17±0.33
5'-nucleotidase domain containing 2	Nt5dc2	0.22±0.03
5'-nucleotidase, cytosolic III (predicted)	Nt5c3_predicted	3.44±0.28
5'-nucleotidase, cytosolic III-like	Nt5c3l	1.44±0.14
5-oxoprolinase (ATP-hydrolysing)	Oplah	12.18±1.87
6-phosphogluconolactonase (predicted)	Pgls_predicted	2.44±0.64
6-pyruvoyl-tetrahydropterin synthase	Pts	1.36±0.34
7-dehydrocholesterol reductase	Dhcr7	3.35±0.39
92Aa-Protein	LOC494529	2.03±0.18
a disintegrin and metallopeptidase domain 10	Adam10	0.97±0.16
a disintegrin and metallopeptidase domain 17	Adam17	0.69±0.32
a disintegrin and metallopeptidase domain 9 (meltrin gamma)	Adam9	3.72±0.3
a disintegrin and metalloprotease domain 4	Adam4	0.23±0.07
a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	Adamts1	0.39±0.27
A kinase (PRKA) anchor protein (yotiao) 9	Akap9	2.2±0.34
A kinase (PRKA) anchor protein 1	Akap1	7.64±0.62
A kinase (PRKA) anchor protein 10 (predicted)	Akap10_predicted	1.55±0.27
A kinase (PRKA) anchor protein 11	Akap11	2.85±0.09
A kinase (PRKA) anchor protein 2	Akap2	11.01±0.57
A kinase (PRKA) anchor protein 7	Akap7	0.87±0.28
A kinase (PRKA) anchor protein 8	Akap8	1.92±0.2
A kinase (PRKA) anchor protein 8-like	Akap8l	0.68±0.1
aarF domain containing kinase 2 (predicted)	Adck2_predicted	0.59±0.05
aarF domain containing kinase 4	Adck4	0.84±0.19
aarF domain containing kinase 5	Adck5	2.08±0.16
Abelson helper integration site 1	Ahi1	0.48±0.11
abhydrolase domain containing 1	Abhd1	2.98±0.58
abhydrolase domain containing 10	Abhd10	0.4±0.06
abhydrolase domain containing 11 /// similar to abhydrolase domain containing 11	Abhd11 /// LOC686139	1.81±0.2
abhydrolase domain containing 12	Abhd12	0.31±0.23
abhydrolase domain containing 13	Abhd13	1.35±0.09
abhydrolase domain containing 14A	Abhd14a	2±0.59
abhydrolase domain containing 14b	Abhd14b	18.32±1.8
abhydrolase domain containing 3 (predicted)	Abhd3_predicted	6.9±0.03
abhydrolase domain containing 4 (predicted)	Abhd4_predicted	4.37±0.62
abhydrolase domain containing 6	Abhd6	3.68±0.75
abhydrolase domain containing 8 (predicted)	Abhd8_predicted	0.69±0.07
abl-interactor 1	Abi1	2.64±0.21
abl-interactor 2	Abi2	1.36±0.24
Ac1254	LOC362901	9.12±0.37
acetyl-coenzyme A acetyltransferase 1	Acat1	25.91±1.26
acetyl-Coenzyme A acetyltransferase 2	Acat2	3.3±0.28
acetyl-Coenzyme A acyltransferase 1 /// similar to 3-ketoacyl-CoA thiolase B, peroxisomal precursor (Beta-ketothiolase B) (predicted)	Acaa1 /// RGD1562373 predicted	21.64±1.87
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	36.61±2.72
acetyl-coenzyme A carboxylase alpha	Acaca	1.1±0.31
acetylserotonin O-methyltransferase-like (predicted)	Asmtl_predicted	1.28±0.24
achalasia, adrenocortical insufficiency, alacrimia	Aaas	0.2±0.07
acid phosphatase 1, soluble	Acp1	12.59±1.17

acid phosphatase 2, lysosomal	Acp2	7.98±1.18
acid phosphatase 5, tartrate resistant	Acp5	7.91±0.64
acid phosphatase 6, lysophosphatidic	Acp6	0.56±0.1
acid phosphatase-like 2	Acpl2	1.39±0.13
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	1.22±0.31
Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	Anp32e	3.5±0.22
acidic nuclear phosphoprotein 32 family, member B	Anp32b	2.93±0.33
acidic ribosomal phosphoprotein P0	Arbp	23±0.47
acireductone dioxygenase 1	Adi1	7.35±0.37
ACN9 homolog (S. cerevisiae)	Acn9	4.49±0.47
aconitase 1	Aco1	22.83±2.9
aconitase 2, mitochondrial	Aco2	34.62±1.16
actin binding LIM protein family, member 3	Ablim3	3.19±0.23
actin related protein 2/3 complex, subunit 1A	Arpc1a	9.78±1.08
actin related protein 2/3 complex, subunit 1B	Arpc1b	2.3±0.28
actin related protein 2/3 complex, subunit 2 (predicted)	Arpc2_predicted	16.04±1.67
actin related protein 2/3 complex, subunit 3 (predicted)	Arpc3_predicted	10.64±0.75
actin related protein 2/3 complex, subunit 4 (predicted)	Arpc4_predicted	2.45±0.72
actin related protein 2/3 complex, subunit 5	Arpc5	10.21±0.57
actin related protein 2/3 complex, subunit 5-like /// similar to actin related protein 2/3 complex, subunit 5-like (predicted)	Arpc5l /// RGD1560362_predicted	4.24±0.42
actin, beta	Actb	32.26±3.38
actin, gamma, cytoplasmic 1	Actg1 /// LOC295810 /// LOC360902 /// RGD1563410_predicted	0.44±0.21
actin, gamma, cytoplasmic 1 /// similar to Actin, cytoplasmic 2 (Gamma-actin)	Actg1 /// LOC295810	40.65±2.43
actinin alpha 4	Actn4	12.97±2.37
actinin, alpha 1	Actn1	0.24±0.33
actin-like 6A	Actl6a	3±0.09
activating signal cointegrator 1 complex subunit 1	Ascc1	1.03±0.06
activating signal cointegrator 1 complex subunit 2	Ascc2	0.37±0.06
activating signal cointegrator 1 complex subunit 3 (predicted)	Ascc3_predicted	1.15±0.15
activating signal cointegrator 1 complex subunit 3-like 1	Ascc3l1	1.79±0.14
activating transcription factor 1	Atf1	3.88±0.28
activating transcription factor 4	Atf4	7.37±0.95
Activating transcription factor 6 (predicted)	Atf6_predicted	3.54±0.72
activating transcription factor 7 interacting protein (predicted)	Atf7ip_predicted	1.32±0.16
activator of basal transcription 1	Abt1	1.22±0.17
activin receptor IIA	Acvr2a	0.95±0.12
activity-dependent neuroprotective protein	Adnp	3.76±0.07
acyl-CoA synthetase family member 2	Acsf2	8.04±1.19
acyl-CoA synthetase family member 3	Acsf3	1.83±0.41
acyl-CoA synthetase long-chain family member 1	Acsl1	13.55±0.71
acyl-CoA synthetase long-chain family member 3	Acsl3	2.26±0.26
acyl-CoA synthetase long-chain family member 4	Acsl4	9.8±1.04
acyl-CoA synthetase medium-chain family member 2A	Acsm2a	59.32±1.72
acyl-CoA synthetase medium-chain family member 3	Acsm3	18.32±3.41
acyl-CoA synthetase short-chain family member 1 (predicted)	Acss1_predicted	21.45±1.59
acyl-CoA synthetase short-chain family member 2 (predicted)	Acss2_predicted	4±2.48
acyl-CoA thioesterase 1	Acot1	24.24±1.62
acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	Acot1 /// Acot2	5.67±0.11
acyl-CoA thioesterase 2	Acot2	4.45±0.26
acyl-CoA thioesterase 3 /// acyl-CoA thioesterase 4	Acot3 /// Acot4	1.08±0.12
acyl-CoA thioesterase 4	Acot4	4.07±0.21
acyl-CoA thioesterase 7	Acot7	1.21±0.18
acyl-CoA thioesterase 8	Acot8	3.02±0.59
acyl-Coenzyme A binding domain containing 3	Acbd3	2.33±0.46
acyl-Coenzyme A binding domain containing 4	Acbd4	4.11±0.41
Acyl-Coenzyme A binding domain containing 5	Acbd5	12.06±0.15
acyl-Coenzyme A binding domain containing 6	Acbd6	1.28±0.04
acyl-Coenzyme A dehydrogenase family, member 11 (predicted)	Acad11_predicted	1.43±0.52
acyl-Coenzyme A dehydrogenase family, member 9	Acad9	3.09±0.27
acyl-Coenzyme A dehydrogenase, long-chain	Acadl	19.87±1.23
acyl-Coenzyme A dehydrogenase, medium chain	Acadm	32.48±3.65
acyl-Coenzyme A dehydrogenase, short chain	Acads	2.99±1.1
acyl-Coenzyme A dehydrogenase, short/branched chain	Acadsb	0.33±0.15
acyl-Coenzyme A dehydrogenase, very long chain	Acadvl	9.29±0.87
acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	26.97±1.91
acylglycerol kinase	Agk	0.66±0.11
acylpeptide hydrolase	Apeh	4.72±0.46
acylphosphatase 1, erythrocyte (common) type (predicted)	Acyp1_predicted	2.13±0.31
ADAMTS-like 4	Adamtsl4	0.71±0.14
adaptor protein complex AP-1, beta 1 subunit	Ap1b1	4.59±0.45
adaptor protein complex AP-1, sigma 1 (predicted)	Ap1s1_predicted	3.54±0.5
adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	8.48±0.95
adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	Appl2	2.1±0.26
adaptor-related protein complex 1, gamma 1 subunit	Ap1g1	1.91±0.14
adaptor-related protein complex 2, beta 1 subunit	Ap2b1	2.15±0.61
adaptor-related protein complex 2, mu 1 subunit	Ap2m1	19.3±0.41
adaptor-related protein complex 2, sigma 1 subunit	Ap2s1	8.57±1
adaptor-related protein complex 3, beta 1 subunit (predicted)	Ap3b1_predicted	2.72±0.24
adaptor-related protein complex 3, delta 1 subunit	Ap3d1	16.47±2.12
adaptor-related protein complex 3, mu 1 subunit	Ap3m1	4.94±0.24
adaptor-related protein complex 3, sigma 1 subunit (predicted)	Ap3s1_predicted	2.22±0.31
adaptor-related protein complex AP-1, mu subunit 1	Ap1m1	3.51±0.78
adaptor-related protein complex AP-4, beta 1 (predicted)	Ap4b1_predicted	1.31±0.14
adducin 1 (alpha)	Add1	12.13±1.42

adducin 3 (gamma)	Add3	5.41±0.66
adenine phosphoribosyl transferase (predicted)	Aprt_predicted	14.32±2.45
adenosine deaminase, RNA-specific, B1	Adarb1	0.27±0.1
adenosine kinase	Adk	22.04±1.77
adenosine monophosphate deaminase 2 (isoform L)	Ampd2	2.5±0.06
adenylate kinase 2	Ak2	33.12±1.21
adenylate kinase 3	Ak3	20.48±0.41
adenylate kinase 3-like 1	Ak3l1	22.87±3.09
adenylosuccinate lyase	Adsl	1.8±0.18
adenylosuccinate synthetase, non muscle (predicted)	Adss_predicted	11.33±0.81
adhesion molecule with Ig like domain 1	Amigo1	0.42±0.04
adhesion molecule with Ig like domain 3	Amigo3	0.39±0.18
adhesion regulating molecule 1	Adrm1	1.09±0.22
adiponectin receptor 1	Adipor1	9.56±0.79
adiponectin receptor 2	Adipor2	1.37±0.16
adipose differentiation related protein	Adfp	7.31±1.36
ADNP homeobox 2	Adnp2	0.59±0.07
ADP-dependent glucokinase	Adpgk	0.32±0.14
ADP-ribosylarginine hydrolase	Adprh	0.48±0.04
ADP-ribosylation factor 1	Arf1	29.41±0.85
ADP-ribosylation factor 2	Arf2	0.63±0.12
ADP-ribosylation factor 3	Arf3	3±0.4
ADP-ribosylation factor 4	Arf4	13.33±0.41
ADP-ribosylation factor 5	Arf5	2.85±0.62
ADP-ribosylation factor 6	Arf6	1.6±0.34
ADP-ribosylation factor GTPase activating protein 1	Arfgap1	1.04±0.06
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited) (predicted)	Arfgef1_predicted	3.9±0.62
ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	Arfgef2	1.01±0.12
ADP-ribosylation factor interacting protein 1	Arfip1	0.59±0.18
ADP-ribosylation factor interacting protein 2	Arfip2	2.46±0.5
ADP-ribosylation factor related protein 1	Arfrp1	1.87±0.14
ADP-ribosylation factor-like 1	Arl1	3.62±0.91
ADP-ribosylation factor-like 13B	Arl13b	0.87±0.11
ADP-ribosylation factor-like 2	Arl2	0.87±0.03
ADP-ribosylation factor-like 2 binding protein	Arl2bp	8.75±1.22
ADP-ribosylation factor-like 3	Arl3	5.6±0.2
ADP-ribosylation factor-like 4A	Arl4a	1.03±0.16
ADP-ribosylation factor-like 5A	Arl5a	1.77±0.15
ADP-ribosylation factor-like 6 (predicted)	Arl6_predicted	3.38±0.55
ADP-ribosylation factor-like 6 interacting protein 1	Arl6ip1	25.66±2.59
ADP-ribosylation factor-like 6 interacting protein 2	Arl6ip2	3.87±0.42
ADP-ribosylation factor-like 6 interacting protein 4	Arl6ip4	1.17±0.34
ADP-ribosylation factor-like 6 interacting protein 5	Arl6ip5	3.88±0.62
ADP-ribosylation factor-like 6 interacting protein 6	Arl6ip6	0.29±0.11
ADP-ribosylation factor-like 8A	Arl8a	1.17±0.15
ADP-ribosylation factor-like 8B	Arl8b	5.72±0.42
ADP-ribosylhydrolase like 1 /// GH regulated TBC protein 1	Adprhl1 /// Grtp1	8.35±0.58
ADP-ribosylhydrolase like 2 (predicted)	Adprhl2_predicted	0.4±0.35
adrenergic receptor kinase, beta 1	Adrbk1	0.25±0.13
adrenergic receptor, alpha 1b	Adra1b	0.6±0.04
adrenocortical dysplasia	Acd	1.7±0.23
advanced glycosylation end product-specific receptor	Ager /// Agpat1 /// Btnl7 /// Btnl8 /// C4-2 /// Crebl1 /// LOC686977 /// Notch4 /// Pbx2	2.37±0.16
Advillin	Avil	0.43±0.01
AE binding protein 1 (predicted)	Aebp1_predicted	3.04±1.07
AF4/FMR2 family, member 4 (predicted)	Aff4_predicted	2.97±0.22
afamin	Afm	0.57±0.55
AFG3(ATPase family gene 3)-like 1 (yeast) (predicted)	Afg3l1_predicted	1.14±0.13
AFG3(ATPase family gene 3)-like 2 (yeast)	Afg3l2	1.79±0.17
aftiphilin	Aftph	5±0.28
agmatine ureohydrolase (agmatinase)	Agmat	3.33±0.72
AKT1 substrate 1 (proline-rich) (predicted)	Akt1s1_predicted	1.6±0.38
alanine-glyoxylate aminotransferase 2	Agxt2	52.89±2.75
alanyl (membrane) aminopeptidase	Anpep	15.16±3.46
alanyl-tRNA synthetase	Aars	14.2±1.52
alanyl-tRNA synthetase domain containing 1	Aarsd1	1.49±0.26
alcohol dehydrogenase 1 (class I)	Adh1	34.66±3.53
alcohol dehydrogenase 4 (class II), pi polypeptide /// alcohol dehydrogenase 5	Adh4 /// Adh5	6.77±0.51
alcohol dehydrogenase, iron containing, 1	Adhfe1	19.68±1.3
aldehyde dehydrogenase 1 family, member A1	Aldh1a1	26.51±2.23
aldehyde dehydrogenase 1 family, member L1	Aldh1l1	11.43±0.25
aldehyde dehydrogenase 16 family, member A1	Aldh16a1	5.58±0.6
aldehyde dehydrogenase 2, mitochondrial	Aldh2	18.36±2.33
aldehyde dehydrogenase 9 family, member A1	Aldh9a1	17.28±1.35
aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	4.92±0.28
aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	42.12±3.45
aldehyde dehydrogenase family 7, member A1	Aldh7a1	48.44±1.78
aldo-keto reductase family 1, member A1 (aldehyde reductase)	Akr1a1	67.1±2.55
Aldo-keto reductase family 1, member B10 (aldose reductase)	Akr1b10	2.02±0.12
aldo-keto reductase family 1, member C19	Akr1c19	0.89±0.26
aldo-keto reductase family 1, member C6	Akr1c6	15.58±2.4
aldo-keto reductase family 1, member E1	Akr1e1	10.33±0.42
aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	Akr7a2	42.45±4.85
aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	Akr7a3	12.74±2.75
aldolase A	Aldoa	38.76±5.4

aldolase B	Aldob	74.15±6.16
alkaline phosphatase, liver/bone/kidney	Alpl	6.9±1.41
alkB, alkylation repair homolog (E. coli) (predicted)	Alkbh_predicted	1.51±0.16
alkB, alkylation repair homolog 2 (E. coli) (predicted)	Alkbh2_predicted	1.78±0.45
alkB, alkylation repair homolog 3 (E. coli)	Alkbh3	2.52±0.54
alkB, alkylation repair homolog 4 (E. coli) (predicted)	Alkbh4_predicted	0.26±0.07
alkB, alkylation repair homolog 5 (E. coli) (predicted)	Alkbh5_predicted	1.17±0.2
alkB, alkylation repair homolog 7 (E. coli)	Alkbh7	3.24±0.37
alpha globin regulatory element containing gene	Mare	0.77±0.16
alpha glucosidase 2 alpha neutral subunit (predicted)	Ganab_predicted	3.73±0.46
alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	2.66±0.42
alpha-2,6-sialyltransferase ST6GalNAc IV	siat7D	0.51±0.14
Alpha-kinase 3 (predicted)	Alpk3_predicted	0.32±0.08
alpha-methylacyl-CoA racemase	Amacr	13.43±1.42
alpha-spectrin 2	Spna2	17.76±2.79
amidohydrolase domain containing 2	Amdhd2	0.52±0.11
amine oxidase (flavin containing) domain 2	Aof2	0.84±0.11
amine oxidase, flavin containing 1 (predicted)	Aof1_predicted	2.3±0.4
aminoacylase 1	Acy1	42.07±3.2
aminoadipate-semialdehyde dehydrogenase	Aasdh	0.58±0.08
aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (predicted)	Aasdhppt_predicted	6.11±0.79
aminoadipate-semialdehyde synthase (predicted)	Aass_predicted	45.77±5.66
aminocarboxymuconate semialdehyde decarboxylase	Acmsd	14.46±0.35
aminolevulinate, delta-, dehydratase	Alad	9.77±1.47
aminolevulinic acid synthase 1	Alas1	2.49±0.22
aminomethyltransferase (glycine cleavage system protein T)	Amt	9.99±1.56
aminopeptidase puromycin sensitive	Npepps	1.89±0.14
aminopeptidase-like 1 (predicted)	Npepl1_predicted	2.64±0.27
amino-terminal enhancer of split	Aes	0.74±0.78
AMME chromosomal region gene 1-like	Ammecr1l	3.16±0.16
amnionless (predicted)	Amn_predicted	29.94±5.6
amplified in osteosarcoma	Os9	0.92±0.21
amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Agl	4.15±0.33
amyloid beta (A4) precursor protein	App	30.45±2.03
amyloid beta (A4) precursor protein-binding, family A, member 3	Apba3	1.22±0.15
amyloid beta (A4) precursor protein-binding, family B, member 1	Apbb1	0.27±0.05
amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	1.92±0.25
amyloid beta (A4) precursor protein-binding, family B, member 3	Apbb3	0.73±0.14
amyloid beta (A4) precursor-like protein 2	Aplp2	2.64±0.6
Amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Appbp2	2.25±0.14
amyloid beta precursor protein binding protein 1	Appbp1	2.64±0.54
amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	Als2cr2	4.46±0.14
Amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	Als2	3.04±0.23
anaphase promoting complex subunit 1 (predicted)	Anapc1_predicted	0.51±0.23
anaphase promoting complex subunit 10 (predicted)	Anapc10_predicted	0.32±0.07
anaphase promoting complex subunit 11 homolog (yeast)	Anapc11	2.16±0.35
anaphase promoting complex subunit 2	Anapc2	3.06±0.15
anaphase promoting complex subunit 4	Anapc4	2.5±0.49
anaphase promoting complex subunit 7 (predicted)	Anapc7_predicted	0.51±0.1
anaphase-promoting complex subunit 5 (predicted)	Anapc5_predicted	9.45±1.1
ancient ubiquitous protein 1	Aup1	3.02±0.29
androgen receptor	Ar	0.94±0.03
angel homolog 1 (Drosophila) (predicted)	Angel1_predicted	0.66±0.09
angel homolog 2 (Drosophila) (predicted)	Angel2_predicted	1.87±0.25
angio-associated migratory protein (predicted)	Aamp_predicted	4.43±0.32
angiogenic factor with G patch and FHA domains 1	Aggf1	0.76±0.24
angiogenin, ribonuclease A family, member 1	Ang1	1.48±0.3
angiopoietin 1	Angpt1	0.34±0.11
angiopoietin-like 2	Angptl2	0.91±0.29
angiotensin II receptor, type 1a	Agtr1a	11.58±0.78
angiotensin II, type I receptor-associated protein	Agtrap	9.84±1.19
anillin, actin binding protein (scraps homolog, Drosophila)	Anln	0.31±0.13
ankrin repeat domain 50	Ankrd50	0.33±0.08
ankyrin 2, neuronal	Ank2	0.2±0.05
ankyrin 3, epithelial	Ank3	14.46±1.14
ankyrin repeat and BTB (POZ) domain containing 1	Abtb1	0.84±0.22
ankyrin repeat and BTB (POZ) domain containing 2	Abtb2	0.87±0.24
ankyrin repeat and FYVE domain containing 1 (predicted)	Ankfy1_predicted	5.38±0.7
ankyrin repeat and IBR domain containing 1	Ankib1	3.11±0.35
ankyrin repeat and LEM domain containing 2	Ankle2	0.8±0.11
ankyrin repeat and MYND domain containing 2 (predicted)	Ankmy2_predicted	1.73±0.24
ankyrin repeat and SAM domain containing 1 (predicted)	Anks1_predicted	1.84±0.67
ankyrin repeat and SOCS box-containing protein 1 (predicted)	Asb1_predicted	0.22±0.07
ankyrin repeat and SOCS box-containing protein 13	Asb13	1.01±0.15
Ankyrin repeat and SOCS box-containing protein 3 (predicted)	Asb3_predicted	0.41±0.06
ankyrin repeat and SOCS box-containing protein 6	Asb6	0.63±0.11
ankyrin repeat and SOCS box-containing protein 8 (predicted)	Asb8_predicted	3.57±0.19
ankyrin repeat and SOCS box-containing protein 9 (predicted)	Asb9_predicted	2.57±0.44
ankyrin repeat and sterile alpha motif domain containing 3	Anks3	0.88±0.12
ankyrin repeat and zinc finger domain containing 1	Ankzf1	0.43±0.02
ankyrin repeat domain 10	Ankrd10	0.33±0.36
ankyrin repeat domain 12 (predicted)	Ankrd12_predicted	0.3±0.15
ankyrin repeat domain 13a	Ankrd13a	2.78±0.41
ankyrin repeat domain 13C	Ankrd13c	15.47±0.11
ankyrin repeat domain 15	Ankrd15	2.09±0.12
ankyrin repeat domain 17	Ankrd17	2.51±0.5
ankyrin repeat domain 24 (predicted)	Ankrd24_predicted	0.53±0.06

ankyrin repeat domain 26	Ankrd26	0.42±0.06
ankyrin repeat domain 28	Ankrd28	1.77±0.24
ankyrin repeat domain 37	Ankrd37	3.92±0.66
ankyrin repeat domain 42 (predicted)	Ankrd42_predicted	0.72±0.13
ankyrin repeat domain 46	Ankrd46	4.34±0.27
ankyrin repeat domain 49 (predicted)	Ankrd49_predicted	0.7±0.11
ankyrin repeat domain 52 (predicted)	Ankrd52_predicted	0.71±0.23
ankyrin repeat domain 54	Ankrd54	0.29±0.03
ankyrin repeat, family A (RFXANK-like), 2	Ankra2	1.06±0.12
annexin A11	Anxa11	4.07±0.68
annexin A7	Anxa7	0.29±0.35
anterior pharynx defective 1a homolog (C. elegans)	Aph1a	1.99±0.66
antigen identified by monoclonal antibody Ki-67 (predicted)	Mki67_predicted	0.87±0.29
antigenic determinant of rec-A protein	Kin	0.82±0.26
anti-Mullerian hormone type 2 receptor	Amhr2	1.14±0.24
Antisense paternally expressed gene 3	Apeg3	0.51±0.22
antizyme inhibitor 1	Azin1	2.3±0.36
AP1 gamma subunit binding protein 1	Ap1gbp1	1.84±0.28
AP2 associated kinase 1	Aak1	0.25±0.14
APAF1 interacting protein (predicted)	Apip_predicted	1.8±0.07
apelin, AGTRL1 ligand	Apln	0.73±0.34
apobec-1 complementation factor	Acf	0.36±0.06
apolipoprotein A-I binding protein (predicted)	Apoa1bp_predicted	5.81±0.76
apolipoprotein B editing complex 1	Apobec1	0.42±0.33
apolipoprotein C-II	Apoc2	1.45±0.25
apolipoprotein C-III	Apoc3	10.72±1.28
apolipoprotein E	Apoe	36.48±1.37
apolipoprotein M	Apom	33.65±3.34
apolipoprotein O-like	Apool	4.4±0.82
apoptosis antagonizing transcription factor	Aatf	0.84±0.16
Apoptosis inhibitor 5 (predicted)	Api5_predicted	6.76±0.28
apoptosis, caspase activation inhibitor (predicted)	Aven_predicted	0.79±0.18
apoptosis-inducing factor, mitochondrion-associated 1	Aifm1	14.89±1.24
apoptosis-inducing factor, mitochondrion-associated 2	Aifm2	0.55±0.13
apoptotic chromatin condensation inducer 1	Acin1	2.07±0.36
aprataxin	Aptx	0.75±0.08
apurinic/apyrimidinic endonuclease 1	Apex1	3.62±0.15
aquaporin 1	Aqp1	21.46±1.55
aquaporin 11	Aqp11	8.68±0.86
aquaporin 3	Aqp3	4.52±0.69
aquaporin 7	Aqp7	22.12±2.38
aquarius (predicted)	Aqr_predicted	1.45±0.17
archaelysin family metallopeptidase 2	Amz2	0.91±0.18
archain 1	Arcn1	4.91±0.59
arginine vasopressin-induced 1	Avpi1	1.53±0.3
arginine/serine-rich coiled-coil 1	Rsrc1	0.68±0.2
arginine-glutamic acid dipeptide (RE) repeats	Rere	1.35±0.14
arginine-rich, mutated in early stage tumors (predicted)	Armet_predicted	8.15±1.82
arginine-tRNA-protein transferase 1 (predicted)	Ate1_predicted	2.26±0.29
argininosuccinate lyase	Asl	30.77±2.63
argininosuccinate synthetase 1	Ass1	71.91±1.45
arginyl aminopeptidase (aminopeptidase B)	Rnpep	0.22±0.28
arginyl-tRNA synthetase (predicted)	Rars_predicted	2.05±0.09
arginyl-tRNA synthetase 2, mitochondrial	Rars2	1.84±0.2
ariadne homolog 2 (Drosophila) (predicted)	Arih2_predicted	0.68±0.18
Ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	Arih1	1.14±0.32
armadillo repeat containing 1 (predicted)	Armc1_predicted	6.46±0.56
armadillo repeat containing 10	Armc10	1.09±0.08
armadillo repeat containing 5	Armc5	0.37±0.07
armadillo repeat containing 8 (predicted)	Armc8_predicted	1.15±0.11
armadillo repeat containing 9 (predicted)	Armc9_predicted	0.86±0.06
armadillo repeat containing, X-linked 1	Armcx1	0.68±0.24
armadillo repeat containing, X-linked 3	Armcx3	1.29±0.16
ARP1 actin-related protein 1 homolog A (yeast) (predicted)	Actr1a_predicted	2.24±0.37
ARP1 actin-related protein 1 homolog B (yeast)	Actr1b	2.55±0.16
ARP10 actin-related protein 10 homolog (S. cerevisiae)	Actr10	4.06±0.06
ARP2 actin-related protein 2 homolog (yeast)	Actr2	13.06±2.42
ARP3 actin-related protein 3 homolog (yeast)	Actr3	6.11±0.7
ARP6 actin-related protein 6 homolog (yeast) (predicted)	Actr6_predicted	1.56±0.06
ARP8 actin-related protein 8 homolog (S. cerevisiae) (predicted)	Actr8_predicted	3.53±0.15
arrestin domain containing 1	Arrdc1	0.93±0.15
arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	Asna1	5.14±0.76
arsenic (+3 oxidation state) methyltransferase	As3mt	4.14±0.08
ARV1 homolog (yeast) (predicted)	Arv1_predicted	1±0.12
aryl hydrocarbon receptor nuclear translocator-like	Arntl	0.31±0.1
arylacetamide deacetylase (esterase)	Aadac	2.49±0.2
aryl-hydrocarbon receptor-interacting protein	Aip	1.89±0.3
arylsulfatase A	Arsa	1.29±0.34
arylsulfatase B	Arsb	7.66±0.79
arylsulfatase E (chondrodysplasia punctata 1)	Arse	0.22±0.07
arylsulfatase K	Arsk	0.8±0.11
ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (predicted)	Asf1a_predicted	1.75±0.11
ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	2.61±0.32
ash2 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash2l_predicted	1.88±0.04
asialoglycoprotein receptor 1	Asgr1	0.32±0.05
asp (abnormal spindle)-like, microcephaly associated (Drosophila) (predicted)	Aspm_predicted	0.25±0.14
asparaginase like 1	Asrgl1	4.23±1.05

asparagine synthetase domain containing 1	Asnsd1	1.84±0.14
asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase) (predicted)	Alg1_predicted	0.58±0.1
asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	Alg10b	2.11±0.23
asparagine-linked glycosylation 11 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)	Alg11	3.01±0.43
asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase) (predicted)	Alg12_predicted	1.28±0.26
asparagine-linked glycosylation 13 homolog (S. cerevisiae)	Alg13	1.26±0.29
asparagine-linked glycosylation 14 homolog (S. cerevisiae)	Alg14	1.79±0.08
asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg2	2.27±0.23
asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg3	0.8±0.09
asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	Alg5	4.21±0.83
asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	Alg8	2.06±0.27
asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase) (predicted)	Alg9_predicted	1.48±0.18
asparaginyl-tRNA synthetase	Nars	3.74±0.57
asparaginyl-tRNA synthetase 2, mitochondrial	Nars2	0.86±0.02
aspartoacylase	Aspa	12.92±1.03
aspartoacylase (aminoacylase) 3	Acy3	7.6±2.66
aspartyl aminopeptidase	Dnpep	14.05±0.45
aspartylglucosaminidase	Aga	8.82±1.1
aspartyl-tRNA synthetase	Dars	7.54±0.22
aspartyl-tRNA synthetase 2 (mitochondrial)	Dars2	1.34±0.26
AT hook containing transcription factor 1 (predicted)	Ahctf1_predicted	2.3±0.58
AT rich interactive domain 1A (Swi1 like) (predicted)	Arid1a_predicted	1.12±1.05
AT rich interactive domain 1B (Swi1 like)	Arid1b	0.31±0.02
AT rich interactive domain 2 (Arid-rfx like) (predicted)	Arid2_predicted	1.88±0.17
AT rich interactive domain 3B (Bright like) (predicted)	Arid3b_predicted	0.51±0.12
AT rich interactive domain 4A (Rbp1 like) (predicted)	Arid4a_predicted	1.19±0.12
AT rich interactive domain 4B (Rbp1 like)	Arid4b	1.16±0.06
ataxin 10	Atxn10	2.39±0.42
ataxin 2 (predicted)	Atxn2_predicted	3.19±0.51
ataxin 2-like (predicted)	Atxn2l_predicted	1.05±0.23
ATG2 autophagy related 2 homolog A (S. cerevisiae)	Atg2a	0.68±0.1
ATH1, acid trehalase-like 1 (yeast) (predicted)	Athl1_predicted	0.71±0.13
ATP binding domain 1 family, member B (predicted)	Atpbd1b_predicted	0.42±0.08
ATP binding domain 1 family, member C	Atpbd1c	0.78±0.17
ATP binding domain 4	Atpbd4	1.64±0.39
ATP citrate lyase	Acly	6.72±1.33
ATP synthase mitochondrial F1 complex assembly factor 1 (predicted)	Atpaf1_predicted	3.03±0.22
ATP synthase mitochondrial F1 complex assembly factor 2 (predicted)	Atpaf2_predicted	2.11±0.1
ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	Atp5b	57.99±0.94
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	46.99±5.34
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	Atp5g3	46.91±0.85
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Atp5g1	39.1±1.72
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	Atp5g2	23.48±4.23
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h	36.89±1.63
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	Atp5i	18.79±5.39
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Atp5j	28.83±0.6
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	Atp5s	0.79±0.08
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1	49.3±2.38
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Atp5d	21.12±3.27
ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	Atp5e	31.08±5.02
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	59.77±1.27
ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	48.4±2.88
ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted	5.25±0.58
ATP5S-like	Atp5sl	1.65±0.19
ATPase family, AAA domain containing 1	Atad1	5.29±0.67
ATPase family, AAA domain containing 2 (predicted)	Atad2_predicted	0.44±0.03
ATPase family, AAA domain containing 3A	Atad3a	1.3±0.18
ATPase inhibitory factor 1	Atpif1	8.76±2.17
ATPase type 13A1 (predicted)	Atp13a1_predicted	2.08±0.44
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	15.1±1.68
ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	4.86±0.79
ATPase, class II, type 9B	Atp9b	0.92±0.27
ATPase, class VI, type 11B	Atp11b	1.01±0.06
Atpase, class VI, type 11C (predicted)	Atp11c_predicted	2.06±0.18
ATPase, Cu++ transporting, beta polypeptide	Atp7b	0.25±0.16
ATPase, H transporting, lysosomal V0 subunit c	Atp6v0c	33.67±3.79
ATPase, H transporting, lysosomal V1 subunit B2	Atp6v1b2	23.06±2.02
ATPase, H transporting, lysosomal V1 subunit F	Atp6v1f	17.72±1.33
ATPase, H transporting, lysosomal V1 subunit G1 (predicted)	Atp6v1g1_predicted	5.79±0.38
ATPase, H+ transporting, lysosomal accessory protein 1	Atp6ap1	9.87±0.96
ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	17.77±0.53
ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	0.27±0.27
ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	0.88±0.06
ATPase, H+ transporting, lysosomal V0 subunit A4	Atp6v0a4	20.7±0.93
ATPase, H+ transporting, lysosomal V0 subunit B	Atp6v0b	10.34±0.95
ATPase, H+ transporting, lysosomal V0 subunit D1	Atp6v0d1	24.32±0.95
ATPase, H+ transporting, lysosomal V0 subunit E1	Atp6v0e	11.79±0.75
ATPase, H+ transporting, lysosomal V0 subunit E2	Atp6v0e2	10.74±1.47
ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	24.73±0.61
ATPase, H+ transporting, lysosomal V1 subunit C1	Atp6v1c1	10.11±1.23
ATPase, H+ transporting, lysosomal V1 subunit D	Atp6v1d	18.99±0.63
ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	5.67±0.3
ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	42.44±1.62
ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	51.19±1.24
ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	2.28±0.56
ATP-binding cassette, sub-family A (ABC1), member 2	Abca2	7.15±1.63
ATP-binding cassette, sub-family A (ABC1), member 3	Abca3	8.31±1.34

ATP-binding cassette, sub-family A (ABC1), member 4 (predicted)	Abca4_predicted	1.17±0.19
ATP-binding cassette, sub-family A (ABC1), member 7	Abca7	0.91±0.34
ATP-binding cassette, sub-family B (MDR/TAP), member 10	Abcb10	0.22±0.1
ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	0.65±0.15
ATP-binding cassette, sub-family B (MDR/TAP), member 1B /// ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a /// Abcb1b	0.35±0.12
ATP-binding cassette, sub-family B (MDR/TAP), member 6	Abcb6	1.66±0.29
ATP-binding cassette, sub-family B (MDR/TAP), member 8	Abcb8	1.73±0.18
ATP-binding cassette, sub-family B (MDR/TAP), member 9	Abcb9	0.3±0.03
ATP-binding cassette, sub-family C (CFTR/MRP), member 2	Abcc2	1.23±0.18
ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	6.45±0.97
ATP-binding cassette, sub-family C (CFTR/MRP), member 6	Abcc6	0.29±0.07
ATP-binding cassette, sub-family D (ALD), member 3	Abcd3	9.51±1.97
ATP-binding cassette, sub-family D (ALD), member 4	Abcd4	1.61±0.24
ATP-binding cassette, sub-family E (OABP), member 1	Abce1	3.3±0.22
ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	1.86±0.23
ATP-binding cassette, sub-family F (GCN20), member 2 (predicted)	Abcf2_predicted	1.87±0.12
ATP-binding cassette, sub-family F (GCN20), member 3	Abcf3	2.12±0.15
ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2	9.64±0.79
ATP-binding cassette, sub-family G (WHITE), member 3-like 1	Abcg3l1	2.32±0.21
atrophin 1	Atn1	1.23±0.37
attractin	Atrn	1.49±0.23
attractin like 1	Atrnl1	6.67±0.44
ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	8.48±2.05
AU RNA binding protein/enoyl-coenzyme A hydratase (predicted)	Auh_predicted	10.78±1.62
aurora kinase A interacting protein 1	Aurkaip1	5.97±0.41
aurora kinase B	Aurkb	0.22±0.06
aurora kinase C (predicted)	Aurkc_predicted	0.35±0.09
autocrine motility factor receptor (predicted)	Amfr_predicted	3.36±0.33
autophagy-related 10 (S. cerevisiae)	Atg10	0.77±0.16
autophagy-related 12 (yeast)	Atg12	2.7±0.24
autophagy-related 16-like 1 (yeast)	Atg16l1	1.17±0.33
autophagy-related 3 (yeast)	Atg3	4.02±0.63
autophagy-related 4B (yeast)	Atg4b	0.73±0.12
Autophagy-related 7 (yeast)	Atg7	1.74±0.25
autophagy-related 9A (yeast)	Atg9a	2.87±0.26
axin 1	Axin1	0.87±0.24
B9 protein domain 1	B9d1	2.49±0.18
baculoviral IAP repeat-containing 2	Birc2	1.7±0.19
BAI1-associated protein 2-like 1	Baiap2l1	0.45±0.1
Bardet-Biedl syndrome 1 homolog (human) (predicted)	Bbs1_predicted	0.86±0.23
Bardet-Biedl syndrome 2 homolog (human)	Bbs2	1.11±0.13
Bardet-Biedl syndrome 4 homolog (human) (predicted)	Bbs4_predicted	0.74±0.13
Bardet-Biedl syndrome 5	Bbs5	1.06±0.13
Bardet-Biedl syndrome 7	Bbs7	2.19±0.13
Bardet-Biedl syndrome 9	Bbs9	0.73±0.05
barrier to autointegration factor 1	Banf1	6.2±0.36
basic helix-loop-helix domain containing, class B2	Bhlhb2	1.41±0.19
basic helix-loop-helix domain containing, class B3	Bhlhb3	0.39±0.05
basic leucine zipper and W2 domains 1	Bzw1	9.16±0.61
basic leucine zipper nuclear factor 1	Blzf1	0.43±0.21
basic transcription factor 3	Btf3	23.34±1.18
basic transcription factor 3-like 4	Btf3l4	7.7±0.1
basigin	Bsg	42.9±3.01
basonuclin 2 (predicted)	Bnc2_predicted	17.7±0.57
basophilic leukemia expressed protein BLES03	Bles03	2.89±0.58
BAT2 domain containing 1	Bat2d	0.33±0.07
B-box and SPRY domain containing	Bspry	2.85±0.56
BCDIN3 domain containing	Bcdin3d	0.29±0.14
B-cell CLL/lymphoma 7B	Bcl7b	4.06±0.18
B-cell CLL/lymphoma 7C (predicted)	Bcl7c_predicted	1.05±0.35
B-cell CLL/lymphoma 9 (predicted)	Bcl9_predicted	0.51±0.16
B-cell CLL/lymphoma 9-like (predicted)	Bcl9l_predicted	0.31±0.08
B-cell leukemia/lymphoma 10	Bcl10	2.31±0.33
B-cell leukemia/lymphoma 6 (predicted)	Bcl6_predicted	1.65±1.14
B-cell receptor-associated protein 29	Bcap29	2.47±0.28
B-cell receptor-associated protein 31	Bcap31	11.81±0.55
BCL2/adenovirus E1B 19 kDa-interacting protein 3	Bnip3	19.92±0.22
BCL2/adenovirus E1B 19kDa-interacting protein 1	Bnip1	0.89±0.16
BCL2/adenovirus E1B interacting protein 3-like	Bnip3l	9.67±0.84
Bcl2-associated athanogene 1 (predicted)	Bag1_predicted	2.68±0.08
Bcl2-associated athanogene 3	Bag3	3.05±0.28
BCL2-associated athanogene 4	Bag4	0.36±0.15
BCL2-associated athanogene 5	Bag5	1.49±0.22
bcl2-associated death promoter	Bad	1.91±0.14
BCL2-associated transcription factor 1	Bclaf1	6.05±0.3
Bcl2-associated X protein	Bax	1.73±0.41
Bcl2-like 1	Bcl2l1	1.68±0.22
BCL2-like 13 (apoptosis facilitator) (predicted)	Bcl2l13_predicted	0.79±0.14
Bcl2-like 14 (apoptosis facilitator)	Bcl2l14	0.56±0.08
Bcl2-like 2	Bcl2l2	1.08±0.12
Bcl2-like 2 /// poly(A) binding protein, nuclear 1	Bcl2l2 /// Pabpn1	4.81±1.13
Bcl-2-related ovarian killer protein	Bok	0.24±0.13
BCL6 co-repressor-like 1	Bcorl1	0.26±0.16
Bcl6 interacting corepressor (predicted)	Bcor_predicted	0.5±0.14
BCS1-like (yeast)	Bcs1l	0.63±0.14
beclin 1, autophagy related	Becn1	2.79±1.15
Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	6.79±1.27

beta-2 microglobulin	B2m	52.59±3.73
betaine-homocysteine methyltransferase	Bhmt	1.33±0.24
betaine-homocysteine methyltransferase 2	Bhmt2	39.51±2.83
beta-transducin repeat containing	Btrc	0.3±0.21
BH3 interacting domain death agonist	Bid	1.63±0.13
bicaudal D homolog 2 (Drosophila)	Bicd2	0.92±0.28
bifunctional apoptosis regulator	Bfar	0.82±0.2
bile acid-Coenzyme A: amino acid N-acyltransferase	Baat	2.67±0.7
biliverdin reductase A	Blvra	1.57±0.82
biliverdin reductase B (flavin reductase (NADPH)) (predicted) /// similar to biliverdin reductase B (flavin reductase (NADPH))	Blvrb_predicted /// LOC681468	1.55±0.12
biogenesis of lysosome-related organelles complex-1, subunit 1 (predicted)	Bloc1s1_predicted	5.76±1.2
biogenesis of lysosome-related organelles complex-1, subunit 2	Bloc1s2	0.75±0.38
biotinidase	Btd	4.47±0.26
biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	20.43±3.43
bisphosphate 3'-nucleotidase 1	Bpnt1	10.13±0.24
bladder cancer associated protein homolog (human)	Blcap	2.79±0.55
bleomycin hydrolase	Blmh	2.08±0.12
block of proliferation 1	Bop1	0.65±0.1
blocked early in transport 1 homolog (S. cerevisiae)	Bet1	3.69±0.35
blocked early in transport 1 homolog (S. cerevisiae) like	Bet1l	0.91±0.17
Bloom syndrome homolog (human) (predicted)	Blm_predicted	0.37±0.09
Bm403207	LOC498525	0.79±0.1
BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	Bambi	1.33±0.49
BMS1 homolog, ribosome assembly protein (yeast)	Bms1	0.83±0.14
bobby sox homolog (Drosophila) (predicted)	Bbx_predicted	1.88±0.22
bolA homolog 3 (E. coli)	Bola3	8.57±0.78
bolA-like 1 (E. coli) (predicted)	Bola1_predicted	1.84±0.39
bone morphogenetic protein 1	Bmp1	0.5±0.1
bone morphogenetic protein 4	Bmp4	1.88±0.5
bone morphogenetic protein 7	Bmp7	8.45±0.8
bone morphogenetic protein receptor, type 1A	Bmpr1a	1.58±0.32
bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	0.35±0.1
brain abundant, membrane attached signal protein 1	Basp1	8.85±2.18
brain and reproductive organ-expressed protein	Bre	3.44±0.6
brain expressed X-linked 2 /// brain expressed gene 1	Bex1 /// Bex2	2.43±0.37
brain protein 16	Brp16	0.64±0.14
brain protein 44-like	Brp44l	38.29±0.74
brain protein I3	Bri3	12.82±2.26
brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	1.43±0.23
branched chain aminotransferase 2, mitochondrial	Bcat2	0.53±0.3
branched chain keto acid dehydrogenase E1, beta polypeptide	Bckdhb	4.36±0.65
branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	4.82±0.79
branched chain ketoacid dehydrogenase kinase	Bckdk	6.18±0.9
Brca1 associated protein 1 (predicted)	Bap1_predicted	3.06±0.36
BRCA1/BRCA2-containing complex, subunit 3	Brcc3	10.79±0.4
BRCA2 and CDKN1A interacting protein (predicted)	Bccip_predicted	2.67±0.28
breakpoint cluster region homolog (predicted)	Bcr_predicted	0.63±0.29
breast cancer anti-estrogen resistance 1	Bcar1	3.59±1.23
breast cancer anti-estrogen resistance 3 (predicted)	Bcar3_predicted	0.25±0.07
breast cancer metastasis-suppressor 1	Brms1	0.55±0.28
breast cancer metastasis-suppressor 1-like (predicted)	Brms1l_predicted	2.02±0.06
breast carcinoma amplified sequence 2 (predicted)	Bcas2_predicted	2.62±0.95
BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae) (predicted)	Brf1_predicted	0.91±0.22
BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	Brf2	0.29±0.07
Bri3 binding protein	Bri3bp	1.94±0.6
bridging integrator 1	Bin1	1.41±0.29
bridging integrator 3	Bin3	1.74±0.06
brix domain containing 1 (predicted)	Bxdc1_predicted	0.61±0.14
brix domain containing 2	Bxdc2	1.64±0.47
bromo adjacent homology domain containing 1	Bahd1	1.48±0.11
bromodomain adjacent to zinc finger domain, 1A (predicted)	Baz1a_predicted	0.62±0.09
bromodomain adjacent to zinc finger domain, 1B	Baz1b	3.26±0.45
bromodomain adjacent to zinc finger domain, 2A (predicted)	Baz2a_predicted	0.44±0.11
bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted	1.06±0.24
bromodomain and PHD finger containing, 1	Brpf1	0.21±0.07
bromodomain and WD repeat domain containing 2	Brwd2	2.74±0.04
bromodomain containing 1 (predicted)	Brd1_predicted	0.71±0.23
bromodomain containing 2	Brd2	0.37±0.22
bromodomain containing 3 (predicted)	Brd3_predicted	0.9±0.13
bromodomain containing 4	Brd4	1.4±0.36
bromodomain containing 7 (predicted)	Brd7_predicted	1.71±0.2
bromodomain containing 8	Brd8	0.25±0.15
bromodomain containing 9 (predicted)	Brd9_predicted	0.89±0.09
BSD domain containing 1	Bsdc1	1.82±0.52
BTB (POZ) domain containing 1	Btbd1	3.77±0.16
BTB (POZ) domain containing 10	Btbd10	0.89±0.11
BTB (POZ) domain containing 12	Btbd12	0.43±0.11
BTB (POZ) domain containing 14A	Btbd14a	2.05±0.32
BTB (POZ) domain containing 2	Btbd2	2.09±0.35
BTB (POZ) domain containing 3 (predicted)	Btbd3_predicted	0.52±0.05
BTB (POZ) domain containing 6	Btbd6	2±0.3
BTB (POZ) domain containing 9	Btbd9	0.51±0.14
Btg3 associated nuclear protein (predicted)	Banp_predicted	0.32±0.06
BUD13 homolog (yeast)	Bud13	0.71±0.05
budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted)	Bub1_predicted	0.29±0.09
budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	Bub3	5.04±0.13

Butyryl Coenzyme A synthetase 1 (predicted)	Bucs1_predicted	12.42±1.27
Bwk1 leukemia-related gene	Bwk1	1.29±0.21
bystin-like	Bysl	0.6±0.2
C1GALT1-specific chaperone 1	C1galt1c1	4.65±0.82
C1q and tumor necrosis factor related protein 3 (predicted)	C1qtnf3_predicted	8.1±0.25
c-abl oncogene 1, receptor tyrosine kinase	Abl1	1.08±0.13
cadherin 1	Cdh1	1.07±0.72
cadherin 16	Cdh16	20.45±1.81
cadherin 2	Cdh2	2.94±0.13
cadherin 6	Cdh6	1.07±0.19
cadherin EGF LAG seven-pass G-type receptor 2	Celsr2	3.27±0.39
calcineurin binding protein 1	Cabin1	0.76±0.17
calcitonin gene-related peptide-receptor component protein	Crcp	3.43±0.1
calcium activated nucleotidase 1	Cant1	0.64±0.1
calcium and integrin binding 1 (calmyrin)	Cib1	17.18±2.09
calcium and integrin binding family member 2	Cib2	1.88±0.42
calcium binding and coiled coil domain 1	Calcoco1	1.54±0.04
calcium binding atopy-related autoantigen 1	Cbara1	0.83±0.25
calcium binding protein 39 (predicted)	Cab39_predicted	2.94±0.21
calcium binding protein 39-like	Cab39l	2.5±0.13
calcium binding protein p22	Chp	2.69±0.28
calcium binding protein p22 /// similar to calcium binding protein P22 (predicted)	Chp /// RGD1565588_predicted	1.07±0.22
calcium homeostasis endoplasmic reticulum protein (predicted)	Cherp_predicted	1.01±0.24
calcium modulating ligand	Camlg	0.93±0.3
calcium regulated heat stable protein 1	Carhsp1	3.02±0.43
calcium/calmodulin-dependent protein kinase I	Camk1	1.76±0.25
calcium/calmodulin-dependent protein kinase II gamma	Camk2g	0.28±0.03
calcium/calmodulin-dependent protein kinase II inhibitor 1	Camk2n1	0.48±0.14
calcium/calmodulin-dependent protein kinase II, delta	Camk2d	0.35±0.14
calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Cask	0.28±0.09
calcyclin binding protein	Cacybp	7.98±0.94
calmodulin 1	Calm1	15±1.57
calmodulin 2	Calm2	6.29±2.2
calmodulin 3	Calm3	4.81±0.69
calmodulin binding transcription activator 2 (predicted)	Camta2_predicted	1.18±0.32
calmodulin regulated spectrin-associated protein 1	Camsap1	0.54±0.1
calnexin	Canx	26.56±2.64
calpain 10	Capn10	0.56±0.19
calpain 2	Capn2	1.31±0.33
calpain 7	Capn7	3.43±0.6
calpain, small subunit 1	Capns1	8.23±1.22
calpastatin	Cast	2.26±0.33
calponin 3, acidic	Cnn3	20.05±0.3
calreticulin	Calr	15.32±2
calreticulin 3	Calr3	0.58±0.13
calsequestrin 1	Casq1	1.01±0.37
calsyntenin 1	Clstn1	1.89±0.57
calsyntenin 2	Clstn2	0.31±0.08
calumenin	Calu	2.31±0.19
camello-like 1	Cml1	4.03±2.04
Camello-like 2	Cml2	0.68±0.59
camello-like 3	Cml3	9.6±3.21
camello-like 4	Cml4	6.61±5.11
camello-like 5	Cml5	2.06±1.29
cAMP responsive element binding protein 3	Creb3	1±0.12
cAMP responsive element binding protein 3-like 1	Creb3l1	0.86±0.2
cAMP responsive element binding protein-like 2	Crebl2	1.31±0.18
cAMP responsive element modulator	Crem	2.91±0.26
cAMP-regulated phosphoprotein 19	Arpp19	4.71±0.18
Cancer susceptibility candidate 3	Casc3	0.63±0.19
canopy 3 homolog (zebrafish)	Cnpy3	2.35±0.47
canopy 4 homolog (zebrafish)	Cnpy4	0.31±0.12
CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	3.37±0.67
CAP-GLY domain containing linker protein 1	Clip1	0.57±0.1
capicua homolog (Drosophila) (predicted)	Cic_predicted	1.95±0.88
capping protein (actin filament) muscle Z-line, alpha 1	Capza1	0.84±0.07
capping protein (actin filament) muscle Z-line, alpha 2	Capza2	7.43±0.88
capping protein (actin filament) muscle Z-line, beta	Capzb	9.87±0.87
cappuccino	Cno	2.3±0.24
carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Cad	0.24±0.07
carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	Chst14	0.22±0.08
carbohydrate sulfotransferase 2 (predicted)	Chst2_predicted	0.3±0.35
carbonic anhydrase 14	Car14	9.98±0.41
carbonic anhydrase 2	Ca2	30.67±1.61
carbonic anhydrase 4	Ca4	3.83±0.83
carbonic anhydrase 6	Car6	0.45±0.06
carbonic anhydrase 7 (predicted)	Car7_predicted	0.45±0.16
carbonic anhydrase VB, mitochondrial	Ca5b	10.43±0.82
carbonyl reductase 4	Cbr4	4.2±0.4
carboxylesterase 2 (intestine, liver)	Ces2	1.95±0.27
carboxylesterase 3	Ces3	7.89±1.02
carboxymethylenebutenolidase homolog (Pseudomonas)	Cmbl	44.98±3.04
carboxypeptidase D	Cpd	2.38±0.82
carboxypeptidase N, polypeptide 1	Cpn1	2.8±0.62
cardiolipin synthase 1	Crls1	7.78±0.95
cardiotrophin 1	Ctf1	0.55±0.16

carnitine acetyltransferase	Crat	6.44±1.29
carnitine O-octanoyltransferase	Crot	7.97±0.48
carnitine palmitoyltransferase 1a, liver	Cpt1a	11.01±1.49
carnitine palmitoyltransferase 2	Cpt2	1.92±0.33
cartilage associated protein	Crtap	28.51±0.42
casein kinase 1, alpha 1	Csnk1a1	5.44±0.46
casein kinase 1, delta	Csnk1d	2.56±0.36
casein kinase 1, gamma 2	Csnk1g2	1.22±0.48
casein kinase 1, gamma 3	Csnk1g3	3.8±0.21
casein kinase 2, alpha 1 polypeptide	Csnk2a1	0.92±0.14
casein kinase 2, alpha prime polypeptide	Csnk2a2	1.62±0.15
casein kinase 2, beta subunit	Csnk2b	7.58±1.01
caseinolytic peptidase X (E.coli)	Clpx	13.22±1.34
caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	Clpp	2.45±0.41
Casitas B-lineage lymphoma	Cbl	0.24±0.09
Casitas B-lineage lymphoma-like 1 (predicted)	Cbll1_predicted	0.62±0.28
cask-interacting protein 2 (predicted)	Caskin2_predicted	0.71±0.23
CASP2 and RIPK1 domain containing adaptor with death domain (predicted)	Cradd_predicted	0.6±0.04
CASP8 and FADD-like apoptosis regulator	Cflar	1.58±0.05
caspase 2	Casp2	1.32±0.24
caspase 4, apoptosis-related cysteine peptidase	Casp4	1.14±0.18
caspase 6	Casp6	2.42±0.23
caspase 7	Casp7	0.94±0.14
caspase 8	Casp8	0.25±0.06
caspase 8 associated protein 2 (predicted)	Casp8ap2_predicted	0.25±0.06
caspase 9	Casp9	0.81±0.05
catalase	Cat	41.23±1.27
catechol-O-methyltransferase	Comt	8.62±2.75
catechol-O-methyltransferase domain containing 1 (predicted)	Comtd1_predicted	5.23±0.62
catenin (cadherin associated protein), alpha 1	Ctnna1	5.16±0.55
catenin (cadherin associated protein), alpha-like 1 (predicted)	Ctnnal1_predicted	0.46±0.14
Catenin (cadherin associated protein), beta 1	Ctnnb1	26.52±2.24
catenin (cadherin associated protein), delta 1 (predicted)	Ctnnd1_predicted	1.02±0.19
catenin, beta like 1	Ctnnbl1	1.66±0.29
catenin, beta-interacting protein 1	Ctnnbip1	0.7±0.08
cathepsin B	Ctsb	58.39±2.96
cathepsin C	Ctsc	15.58±1.36
cathepsin D	Ctsd	10.96±2.93
cathepsin F	Ctsf	2.77±0.28
cathepsin H	Ctsh	67.72±2.58
cathepsin L	Ctsl	80.29±8.69
CBF1 interacting corepressor	Cir	0.88±0.15
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	5.18±0.81
CCAAT/enhancer binding protein (C/EBP), gamma	Cebpg	0.64±0.05
CCAAT/enhancer binding protein zeta (predicted)	Cebpz_predicted	2.5±0.32
CCCTC-binding factor	Ctcf	2.01±0.16
CCR4-NOT transcription complex, subunit 10	Cnot10	1.28±0.11
CCR4-NOT transcription complex, subunit 2	Cnot2	3.59±0.16
CCR4-NOT transcription complex, subunit 4	Cnot4	0.68±0.15
CCR4-NOT transcription complex, subunit 6	Cnot6	1.36±0.15
CCR4-NOT transcription complex, subunit 6-like (predicted)	Cnot6l_predicted	0.62±0.17
CCR4-NOT transcription complex, subunit 7 (predicted)	Cnot7_predicted	2.19±0.29
CCR4-NOT transcription complex, subunit 8	Cnot8	0.76±0.1
CD 81 antigen	Cd81	2.73±1.95
CD14 antigen	Cd14	0.37±0.11
CD151 antigen (Raph blood group)	Cd151	7.92±1.33
CD164 antigen	Cd164	32.83±2.33
CD1d1 antigen	Cd1d1	0.46±0.05
CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)	Cd2bp2_predicted	2.9±0.38
CD302 antigen	Cd302	2.7±0.89
CD320 antigen	Cd320	3.55±0.2
CD48 antigen	Cd48	4.65±0.76
CD59 antigen	Cd59	2.63±1.82
CD63 antigen	Cd63	58.79±3.83
CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	18.51±8.29
CD82 antigen	Cd82	4.58±0.85
CD99 antigen	Cd99	1.84±0.74
Cd99 antigen-like 2	Cd99l2	2.65±0.14
CDC like kinase 4	Clk4	3.83±0.58
CDC16 cell division cycle 16 homolog (S. cerevisiae)	Cdc16	1.62±0.11
CDC23 (cell division cycle 23, yeast, homolog)	Cdc23	0.48±0.13
CDC28 protein kinase regulatory subunit 2	Cks2	1.68±0.8
Cdc2-related kinase, arginine/serine-rich	Crkrs	0.56±0.04
Cdc42 binding protein kinase beta	Cdc42bpb	0.98±0.12
Cdc42 guanine nucleotide exchange factor (GEF) 9	Arhgef9	0.62±0.07
CDC42 small effector 1	Cdc42se1	2.02±0.21
CDC42 small effector 2	Cdc42se2	2.3±0.2
CDC91 cell division cycle 91-like 1 (S. cerevisiae)	Cdc91l1	0.77±0.1
CDC-like kinase 1	Clk1	5.01±1.75
CDC-like kinase 2	Clk2	0.29±0.06
CDC-like kinase 3	Clk3	1.53±0.13
CDGSH iron sulfur domain 1	Cisd1	40.21±2.27
CDGSH iron sulfur domain 2	Cisd2	5.21±0.44
CDK105 protein	Cdk105	5.57±1.62
CDK2 (cyclin-dependent kinase 2)-associated protein 1 (predicted) /// similar to CDK2 (cyclin-dependent kinase 2)-associated protein 1	Cdk2ap1_predicted /// LOC687549	5.97±0.48
CDK5 regulatory subunit associated protein 1-like 1 (predicted)	Cdkal1_predicted	0.61±0.09

CDK5 regulatory subunit associated protein 2	Cdk5rap2	0.53±0.11
CDKN1A interacting zinc finger protein 1 (predicted)	Ciz1_predicted	0.89±0.11
CDKN2A interacting protein	Cdkn2aip	0.64±0.14
CDKN2A interacting protein N-terminal like	Cdkn2aipnl	1.52±0.19
CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Cdipt	4.8±0.52
CDW92 antigen	Cdw92	1.14±0.26
CEA-related cell adhesion molecule 1	Ceacam1	2.07±0.1
cell adhesion molecule 1	Cadm1	0.32±0.07
cell adhesion molecule JCAM	LOC304000	2.12±0.79
cell cycle associated protein 1	Caprin1	10.09±0.35
cell cycle progression 1 (predicted)	Ccpg1_predicted	0.67±0.15
cell cycle related kinase	Ccrk	0.61±0.07
cell death-inducing DNA fragmentation factor, alpha subunit-like effector B (predicted)	Cideb_predicted	7.74±0.91
cell division cycle 123 homolog (S. cerevisiae)	Cdc123	3.37±0.32
cell division cycle 2 homolog (S.pombe)-like 1 /// similar to cell division cycle 2-like 1 (predicted)	Cdc2l1 /// RGD1566355_predicted	1.84±0.4
cell division cycle 2 homolog A (S. pombe)	Cdc2a	0.79±0.25
cell division cycle 20 homolog (S. cerevisiae)	Cdc20	0.33±0.19
cell division cycle 25 homolog A (S. pombe)	Cdc25a	0.52±0.08
cell division cycle 26	Cdc26	1.38±0.07
cell division cycle 27 homolog (S. cerevisiae)	Cdc27	0.28±0.1
cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	0.91±0.15
cell division cycle 2-like 6 (CDK8-like) (predicted)	Cdc2l6_predicted	0.54±0.2
cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted	2.2±0.16
cell division cycle 37 homolog (S. cerevisiae)	Cdc37	6.42±0.59
cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	1.74±0.35
cell division cycle 40 homolog (yeast) (predicted)	Cdc40_predicted	1.49±0.21
cell division cycle 42 homolog (S. cerevisiae)	Cdc42	21.54±2.61
cell division cycle 45 homolog (S. cerevisiae)-like	Cdc45l	0.43±0.1
cell division cycle 5-like (S. pombe)	Cdc5l	4.01±0.4
cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Cdc73	4.33±0.12
cell division cycle and apoptosis regulator 1	Ccar1	4.31±0.85
cell division cycle associated 3	Cdca3	0.94±0.28
cell division cycle associated 4	Cdca4	0.54±0.37
cell growth regulator with ring finger domain 1	Cgrrf1	3.51±0.83
cellular nucleic acid binding protein	Cnbp	9.3±2.57
cellular repressor of E1A-stimulated genes 1	Creg1	5.23±0.7
centaurin, alpha 2	Centa2	5.7±0.96
centaurin, beta 5 (predicted)	Centb5_predicted	0.36±0.18
centaurin, delta 1 (predicted)	Centd1_predicted	0.68±0.11
centaurin, delta 2	Centd2	0.3±0.22
centaurin, gamma 2 (predicted)	Centg2_predicted	1.33±0.24
centaurin, gamma 3 (predicted)	Centg3_predicted	0.69±0.09
centrin 2	Cetn2	5.41±0.59
centrin 3	Cetn3	2.95±0.29
centromere protein B	Cenpb	0.89±0.41
centromere protein J (predicted)	Cenpj_predicted	0.23±0.03
centromere protein K	Cenpk	0.32±0.12
centromere protein L	Cenpl	0.35±0.33
centromere protein N	Cenpn	0.89±0.11
centrosomal protein 152 (predicted)	Cep152_predicted	0.49±0.35
centrosomal protein 164	Cep164	0.47±0.1
centrosomal protein 250	Cep250	0.64±0.19
centrosomal protein 27 (predicted)	Cep27_predicted	0.73±0.18
centrosomal protein 27 (predicted) /// similar to Centrosomal protein of 27 kDa (Cep27 protein)	Cep27_predicted /// LOC691918	1.09±0.06
centrosomal protein 57	Cep57	1.26±0.19
centrosomal protein 68 (predicted)	Cep68_predicted	0.26±0.06
centrosomal protein 70	Cep70	0.95±0.21
centrosomal protein 78	Cep78	0.55±0.03
cerebellar degeneration-related 2	Cdr2	3.55±0.23
cereblon	Crbn	5.06±0.59
ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Cln3	0.8±0.08
ceroid-lipofuscinosis, neuronal 5 (predicted)	Cln5_predicted	0.72±0.13
ceroid-lipofuscinosis, neuronal 8	Cln8	0.74±0.48
CGG triplet repeat binding protein 1 (predicted)	Cggbp1_predicted	2.13±0.24
CGI-96 protein	Cgi-96	0.4±0.06
ChaC, cation transport regulator homolog 2 (E. coli)	Chac2	0.91±0.3
ChaC, cation transport regulator-like 1 (E. coli) (predicted)	Chac1_predicted	0.27±0.12
chaperonin containing TCP1, subunit 2 (beta)	Cct2	8.98±1.25
chaperonin subunit 3 (gamma)	Cct3	8.98±0.44
chaperonin subunit 4 (delta)	Cct4	8.1±0.25
chaperonin subunit 5 (epsilon)	Cct5	11.3±0.51
Chaperonin subunit 6a (zeta)	Cct6a	0.56±0.12
chaperonin subunit 6a (zeta) /// similar to chaperonin subunit 6a (zeta)	Cct6a /// LOC316484 /// LOC688183	11.68±1.19
chaperonin subunit 7 (eta) (predicted)	Cct7_predicted	8.1±0.32
chaperonin subunit 8 (theta) (predicted)	Cct8_predicted	7.57±1.66
Checkpoint suppressor 1 (predicted)	Ches1_predicted	0.45±0.09
checkpoint with forkhead and ring finger domains	Chfr	1.38±0.05
chemokine (C-C motif) ligand 27 (predicted)	Ccl27_predicted	0.26±0.09
chemokine (C-X3-C motif) ligand 1	Cx3cl1	1.4±0.49
chemokine (C-X-C motif) ligand 11	Cxcl11	2.66±0.22
chemokine (C-X-C motif) ligand 16	Cxcl16	15.64±0.98
chemokine-like factor	Cklf	1.05±0.16
chibby homolog 1 (Drosophila)	Cby1	1.2±0.18
chitinase domain containing 1	Chid1	0.88±0.16

chitobiase, di-N-acetyl-	Ctbs	8.09±0.74
chloride channel 2	Clcn2	0.76±0.2
chloride channel 3	Clcn3	2.63±1.37
chloride channel 4-2	Clcn4-2	7.75±0.42
Chloride channel 6 (predicted)	Clcn6_predicted	10.47±1.65
chloride channel 7	Clcn7	0.44±0.04
chloride channel calcium activated 5	Clca5	0.31±0.12
chloride channel CLIC-like 1	Clcc1	0.77±0.15
chloride channel, nucleotide-sensitive, 1A	Clns1a	2.71±0.16
chloride intracellular channel 1	Clic1	9.82±0.56
chloride intracellular channel 4 (mitochondrial)	Clic4	2.21±0.18
CHMP family, member 7 (predicted)	Chmp7_predicted	1.67±0.37
choline dehydrogenase	Chdh	5.84±1.76
choline kinase alpha	Chka	1.1±0.14
choline kinase beta	Chkb	2.86±0.29
choline phosphotransferase 1	Chpt1	40.07±2.29
choline/ethanolamine phosphotransferase 1	Cept1	7.07±0.71
chondroitin polymerizing factor	Chpf	0.57±0.12
chordin	Chrd	0.9±0.17
choroidermia	Chm	0.52±0.07
chromatin accessibility complex 1 (predicted)	Chrac1_predicted	2.89±0.3
chromatin modifying protein 1A	Chmp1a	2.36±0.16
chromatin modifying protein 1B	Chmp1b	1.88±0.23
chromatin modifying protein 2B	Chmp2b	0.98±0.84
chromatin modifying protein 4C	Chmp4c	2.05±0.13
chromatin modifying protein 5	Chmp5	12.29±1.16
chromatin modifying protein 6 (predicted)	Chmp6_predicted	2.07±0.23
chromobox homolog 1 (Drosophila HP1 beta) (predicted)	Cbx1_predicted	2.23±0.36
chromobox homolog 3 (HP1 gamma homolog, Drosophila)	Cbx3	7.08±0.46
chromobox homolog 5 (Drosophila HP1a) (predicted)	Cbx5_predicted	0.22±0.05
chromobox homolog 6	Cbx6	2.15±0.41
chromobox homolog 7	Cbx7	0.72±0.32
chromodomain helicase DNA binding protein 1 (predicted)	Chd1_predicted	1.33±0.09
chromodomain helicase DNA binding protein 1-like (predicted)	Chd1l_predicted	11.17±1.99
Chromodomain helicase DNA binding protein 2 (predicted)	Chd2_predicted	1.53±0.29
Chromodomain helicase DNA binding protein 3	Chd3	1.05±0.15
chromodomain helicase DNA binding protein 4	Chd4	5.9±0.65
chromodomain helicase DNA binding protein 7 (predicted)	Chd7_predicted	0.71±0.03
chromodomain helicase DNA binding protein 8	Chd8	1.55±0.38
chromosome segregation 1-like (S. cerevisiae) (predicted)	Cse1l_predicted	2.72±0.03
chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	Ctf8	1.95±0.04
churchill domain containing 1 (predicted)	Churc1_predicted	8.62±0.17
ciliary neurotrophic factor	Cntf	0.42±0.07
cingulin (predicted)	Cgn_predicted	0.31±0.14
cingulin-like 1	Cgnl1	27.53±4.28
cirrhosis, autosomal recessive 1A (human)	Cirh1a	9.47±0.67
cisplatin resistance-associated overexpressed protein	Crop	4.76±0.47
citrate lyase beta like	Clybl	3.83±0.31
Citrate synthase	Cs	16.71±0.72
CKLF-like MARVEL transmembrane domain containing 6	Cmtm6	7.11±0.7
clarin 3	Clrn3	10.26±0.9
clathrin, heavy polypeptide (Hc)	Cltc	32.19±0.92
clathrin, light polypeptide (Lca)	Clta	19.13±0.32
clathrin, light polypeptide (Lcb)	Cltb	1.4±0.44
claudin 1	Cldn1	0.83±0.09
claudin 10 (predicted)	Cldn10_predicted	23.24±1.35
claudin 12	Cldn12	2.91±0.52
claudin 2 (predicted)	Cldn2_predicted	23.01±3.17
claudin domain containing 1	Cldnd1	2.31±0.24
cleavage and polyadenylation factor subunit homolog (S. cerevisiae) (predicted)	Pcf11_predicted	0.82±0.11
cleavage and polyadenylation specific factor 1	Cpsf1	1.11±0.2
cleavage and polyadenylation specific factor 2 (predicted)	Cpsf2_predicted	1.49±0.32
cleavage and polyadenylation specific factor 3-like	Cpsf3l	0.91±0.09
cleavage and polyadenylation specific factor 5	Cpsf5	3.63±0.28
cleavage and polyadenylation specific factor 6	Cpsf6	1.45±0.66
cleavage and polyadenylation specificity factor 3	Cpsf3	3.91±0.51
cleavage stimulation factor, 3' pre-RNA subunit 2, tau (predicted)	Cstf2t_predicted	5.42±0.19
cleavage stimulation factor, 3' pre-RNA, subunit 1	Cstf1	0.62±0.03
cleft lip and palate associated transmembrane protein 1 (predicted)	Clptm1_predicted	7.77±0.6
CLIP associating protein 2	Clasp2	1.36±0.29
CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	Clp1	0.61±0.11
ClpB caseinolytic peptidase B homolog (E. coli)	Clpb	2.8±0.1
CLPTM1-like	Clptm1l	12.32±2.37
clusterin associated protein 1	Cluap1	3.28±0.03
c-Maf-inducing protein	Cmip	5.52±0.66
CNDP dipeptidase 2 (metallopeptidase M20 family)	Cndp2	15.94±2.09
Cnksr family member 3	Cnksr3	0.73±0.06
coactosin-like 1 (Dictyostelium) (predicted)	Cotl1_predicted	15.3±3.14
coagulation factor III	F3	11.64±1.83
coagulation factor V	F5	0.25±0.1
coatomer protein complex subunit alpha	Copa	9.67±0.65
coatomer protein complex, subunit beta 1	Copb1	6.97±0.71
coatomer protein complex, subunit beta 2 (beta prime)	Copb2	8.41±0.81
coatomer protein complex, subunit epsilon (predicted)	Cope_predicted	3.79±0.99
coatomer protein complex, subunit gamma	Copg	4.31±0.08
coatomer protein complex, subunit zeta 1 (predicted)	Copz1_predicted	5.97±1.47
Cobl-like 1 (predicted)	Cobll1_predicted	7.01±0.94

COBW domain containing 1	Cbwd1	0.43±0.14
Coenzyme A synthase	Coasy	1.42±0.05
coenzyme Q10 homolog A (yeast) (predicted)	Coq10a_predicted	1.81±0.2
coenzyme Q10 homolog B (S. cerevisiae)	Coq10b	5.7±1.41
coenzyme Q2 homolog, prenyltransferase (yeast)	Coq2	0.93±0.1
coenzyme Q3 homolog, methyltransferase (yeast)	Coq3	2.08±0.25
coenzyme Q4 homolog (yeast)	Coq4	0.62±0.09
coenzyme Q5 homolog, methyltransferase (yeast)	Coq5	0.82±0.15
Coenzyme Q6 homolog (yeast)	Coq6	12.07±1.54
cofactor of BRCA1	Cobra1	1.69±0.22
cofilin 1, non-muscle	Cfl1	18.44±2.13
cofilin 1, non-muscle	Cfl1 /// LOC502589 /// LOC688430 /// RGD1563644_predicted	1.02±0.25
cofilin 2, muscle (predicted)	Cfl2_predicted	10.83±1.2
Cohen syndrome homolog 1 (predicted)	Cohh1_predicted	2.04±0.22
coiled-coil and C2 domain containing 1A	Cc2d1a	0.53±0.4
coiled-coil and C2 domain containing 1B	Cc2d1b	1.25±0.05
coiled-coil domain containing 100	Ccdc100	0.85±0.05
coiled-coil domain containing 101	Ccdc101	0.69±0.09
coiled-coil domain containing 104	Ccdc104	1.52±0.28
coiled-coil domain containing 107	Ccdc107	1.02±0.04
coiled-coil domain containing 115	Ccdc115	0.68±0.12
coiled-coil domain containing 117	Ccdc117	0.44±0.09
coiled-coil domain containing 12 (predicted)	Ccdc12_predicted	0.96±0.11
coiled-coil domain containing 124	Ccdc124	1.36±0.41
coiled-coil domain containing 126	Ccdc126	2.43±0.21
coiled-coil domain containing 127	Ccdc127	0.53±0.12
coiled-coil domain containing 130	Ccdc130	0.51±0.13
coiled-coil domain containing 132	Ccdc132	3.39±0.18
coiled-coil domain containing 16	Ccdc16	0.62±0.2
coiled-coil domain containing 17	Ccdc17	2.01±0.33
coiled-coil domain containing 21	Ccdc21	0.8±0.24
coiled-coil domain containing 22 (predicted)	Ccdc22_predicted	1.88±0.29
coiled-coil domain containing 25 (predicted)	Ccdc25_predicted	0.68±0.07
coiled-coil domain containing 28A	Ccdc28a	0.78±0.18
coiled-coil domain containing 32	Ccdc32	0.3±0.05
coiled-coil domain containing 41	Ccdc41	0.62±0.13
coiled-coil domain containing 43	Ccdc43	1.65±0.06
coiled-coil domain containing 45	Ccdc45	0.26±0.04
coiled-coil domain containing 51	Ccdc51	0.67±0.11
coiled-coil domain containing 52	Ccdc52	0.89±0.25
coiled-coil domain containing 53 (predicted)	Ccdc53_predicted	23.85±1.94
coiled-coil domain containing 55	Ccdc55	0.23±0.07
coiled-coil domain containing 56	Ccdc56	10.85±0.35
coiled-coil domain containing 58 (predicted)	Ccdc58_predicted	2.23±0.54
coiled-coil domain containing 59 (predicted)	Ccdc59_predicted	0.56±0.16
coiled-coil domain containing 65	Ccdc65	0.34±0.03
coiled-coil domain containing 68	Ccdc68	0.65±0.12
coiled-coil domain containing 72 /// hypothetical protein LOC685117	Ccdc72 /// LOC685117	15.22±3.24
coiled-coil domain containing 84	Ccdc84	0.81±0.05
coiled-coil domain containing 86	Ccdc86	0.3±0.04
coiled-coil domain containing 90A	Ccdc90a	0.4±0.22
coiled-coil domain containing 90B	Ccdc90b	1.89±0.17
coiled-coil domain containing 91	Ccdc91	1.9±0.12
coiled-coil domain containing 92	Ccdc92	0.46±0.25
coiled-coil domain containing 93	Ccdc93	0.39±0.06
coiled-coil domain containing 95	Ccdc95	0.32±0.15
coiled-coil domain containing 96	Ccdc96	0.26±0.03
coiled-coil domain containing 97	Ccdc97	1.19±0.4
coiled-coil domain containing 98	Ccdc98	0.67±0.08
coiled-coil domain containing 99	Ccdc99	0.8±0.09
coiled-coil-helix-coiled-coil-helix domain containing 1 (predicted)	Chchd1_predicted	4.68±0.35
coiled-coil-helix-coiled-coil-helix domain containing 2	Chchd2	40.33±2.46
coiled-coil-helix-coiled-coil-helix domain containing 3 (predicted)	Chchd3_predicted	8.4±0.87
coiled-coil-helix-coiled-coil-helix domain containing 4	Chchd4	1.98±0.39
coiled-coil-helix-coiled-coil-helix domain containing 5 (predicted)	Chchd5_predicted	2.12±0.4
coiled-coil-helix-coiled-coil-helix domain containing 6 (predicted)	Chchd6_predicted	0.33±0.31
coiled-coil-helix-coiled-coil-helix domain containing 8	Chchd8	2.59±0.11
cold inducible RNA binding protein	Cirbp	0.9±0.1
cold shock domain containing E1, RNA binding	Csde1	12.66±1.37
collagen, type IV, alpha 5	Col4a5	7.15±0.24
colony stimulating factor 1 (macrophage)	Csf1	1.75±0.42
colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	Csf2rb	0.79±0.2
COMM domain containing 10	Commd10	5.06±0.19
COMM domain containing 2	Commd2	1.52±0.01
COMM domain containing 3	Commd3	16.57±2.3
COMM domain containing 4 (predicted)	Commd4_predicted	2.91±0.22
COMM domain containing 5	Commd5	1.28±0.22
COMM domain containing 6	Commd6	3.25±0.09
COMM domain containing 7	Commd7	0.62±0.07
COMM domain containing 8 (predicted)	Commd8_predicted	6.72±0.59
COMM domain containing 9	Commd9	6.09±0.91
complement component (3b/4b) receptor 1-like	Cr1l	6.15±0.52
complement component 1, q subcomponent binding protein	C1qbp	12.45±1.24

complement component 2	Bat4 /// C2 /// C4a /// Cfb /// Clic1 /// Ehmt2 /// LOC684148 /// Lsm2 /// Ly6g6c /// Ly6g6e /// Neu1 /// Ng23 /// Rdbp /// Skiv2l /// Stk19	1.94±0.16
complement component 4a	Ager /// Agpat1 /// Btnl7 /// Btnl8 /// C4-2 /// C4a /// Crebl1 /// LOC686977 /// Notch4 /// Pbx2	5.8±0.84
complement component 5	C5	10.6±0.92
complement component 8, beta polypeptide	C8b	0.51±0.14
complement component 8, gamma subunit	C8g	0.75±0.15
complement factor I	Cfi	0.36±0.06
component of oligomeric golgi complex 1 (predicted)	Cog1_predicted	1.78±0.21
component of oligomeric golgi complex 3	Cog3	0.56±0.12
component of oligomeric golgi complex 4 (predicted)	Cog4_predicted	2.07±0.43
component of oligomeric golgi complex 6	Cog6	1.28±0.26
component of oligomeric golgi complex 7	Cog7	2.61±0.12
connective tissue growth factor	Ctgf	0.3±4.81
conserved helix-loop-helix ubiquitous kinase (predicted)	Chuk_predicted	15.84±2.34
conserved nuclear protein Nhn1	Nhn1	0.57±0.27
COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	Cops2	10.24±1.08
COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	Cops3	4.38±0.58
COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	Cops4	8.26±0.09
COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	Cops5	3.96±0.73
COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) (predicted)	Cops6_predicted	8.01±0.26
COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (predicted)	Cops7a_predicted	3.85±0.28
COP9 (constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana) (predicted)	Cops7b_predicted	0.69±0.19
COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)	Cops8	5.31±0.26
Copine III (predicted)	Cpne3_predicted	2.09±0.41
copper chaperone for superoxide dismutase	Ccs	5.22±0.48
copper metabolism (Murr1) domain containing 1 (predicted)	Commd1_predicted	3.04±0.06
coproporphyrinogen oxidase	Cpox	2.05±0.31
core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	C1galt1	0.75±0.12
core binding factor beta	Cbfb	2.63±0.29
cornichon homolog (Drosophila) (predicted)	Cnih_predicted	8.21±1.1
cornichon homolog 4 (Drosophila)	Cnih4	3.19±0.27
coronin 7	Coro7	2.55±0.29
coronin, actin binding protein 1C	Coro1c	3.02±0.08
coronin, actin-binding protein, 1B	Coro1b	2.16±0.14
cortactin	Cttn	5.14±0.22
cortactin binding protein 2	Cttnbp2	1.17±0.06
cortistatin	Cort	0.39±0.17
cortistatin /// phosphogluconate dehydrogenase	Cort /// Pgd	2.35±1.02
COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	4.56±0.23
COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	Cox18	2.06±0.1
COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	Cox19	2.07±0.3
COX4 neighbor	Cox4nb	1.4±0.01
COXII /// cytochrome c oxidase subunit 3	COX2 /// COX3	68.86±6.42
CP110 protein	Cp110	0.29±0.2
craniofacial development protein 1	Cfdp1	1.65±0.11
CREB binding protein	Crebbp	1.23±0.22
CREB regulated transcription coactivator 2	Crtc2	0.6±0.1
Crn, crooked neck-like 1 (Drosophila)	Crnkl1	1.24±0.19
crumbs homolog 3 (Drosophila)	Crb3	1.89±0.64
crystallin, gamma A	Cryga	1.38±1.05
crystallin, lambda 1	Cryl1	33.61±2.65
crystallin, mu	Crym	23.55±1.8
crystallin, zeta	Cryz	17.69±0.82
crystallin, zeta (quinone reductase)-like 1	Cryzl1	1.04±0.05
c-src tyrosine kinase	Csk	0.31±0.11
CTAGE family, member 5	Ctage5	11.77±2.21
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (predicted)	Ctdp1_predicted	1.04±0.3
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	Ctdsp1	6.53±1.33
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (predicted)	Ctdspl_predicted	1.15±0.47
CTD-binding SR-like protein rA9	LOC245925	0.59±0.2
C-terminal binding protein 1	Ctbp1	4.23±0.7
C-terminal binding protein 2	Ctbp2	1.64±0.34
Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Ctr9	1.38±0.14
CTTNBP2 N-terminal like (predicted)	Cttnbp2nl_predicted	0.25±0.4
C-type lectin domain family 16, member A	Clec16a	0.72±0.1
cubilin (intrinsic factor-cobalamin receptor)	Cubn	44.41±2.61
CUE domain containing 2 (predicted)	Cuedc2_predicted	1.01±0.11
CUG triplet repeat, RNA binding protein 1	Cugbp1	1.42±0.78
CUG triplet repeat, RNA binding protein 2	Cugbp2	0.66±0.17
cullin 1 (predicted)	Cul1_predicted	8.49±0.99
cullin 2 (predicted)	Cul2_predicted	0.55±0.05
cullin 3 (predicted)	Cul3_predicted	10.59±1.01
Cullin 4B (predicted)	Cul4b_predicted	0.91±0.17
Cullin 5	Cul5	0.44±0.12
cullin associated and neddylation disassociated 1	Cand1	6.36±0.57
cutA divalent cation tolerance homolog (E. coli)	Cuta	10.65±1.09
cutC copper transporter homolog (E.coli) (predicted)	Cutc_predicted	0.87±0.04
cut-like homeobox 1	Cux1	3.15±0.12
CWC15 homolog (S. cerevisiae)	Cwc15	3.16±0.32
CXXC finger 1 (PHD domain)	Cxxc1	0.94±0.17

CXXC finger 5	Cxxc5	7.5±1.55
cyclin A2	Ccna2	0.49±0.07
cyclin B1	Ccnb1	0.74±0.18
cyclin B2	Ccnb2	0.7±0.25
cyclin C	Ccnc	3.67±0.22
cyclin D binding myb-like transcription factor 1 /// hypothetical gene supported by AF352170 (predicted)	Dmtf1 /// RGD1562889_predicted	2.1±0.23
cyclin D1	Ccnd1	9.91±2.08
cyclin D3	Ccnd3	0.22±0.26
cyclin dependent kinase 2	Cdk2	0.96±0.12
cyclin D-type binding-protein 1	Ccndbp1	2.61±0.18
cyclin E2	Ccne2	0.53±0.17
cyclin G associated kinase	Gak	2.25±0.23
cyclin G1	Ccng1	10.38±0.67
cyclin G2 (predicted)	Ccng2_predicted	1.37±0.17
cyclin H	Ccnh	4.52±0.43
cyclin I (predicted)	Ccni_predicted	9.15±2.17
cyclin J (predicted)	Ccnj_predicted	0.24±0.05
cyclin K	Ccnk	2.94±0.24
cyclin L1	Ccnl1	2.16±0.34
cyclin L2	Ccnl2	5.92±1.3
cyclin M2	Cnnm2	1.11±0.04
cyclin M3 (predicted)	Cnnm3_predicted	1.98±0.18
cyclin T2 (predicted)	Ccnt2_predicted	0.48±0.13
cyclin Y	Ccny	3.55±0.14
cyclin Y-like 1	Ccnyl1	0.88±0.19
cyclin-dependent kinase (CDC2-like) 10	Cdk10	0.74±0.26
cyclin-dependent kinase 2-interacting protein	Cinp	0.7±0.18
cyclin-dependent kinase 4	Cdk4	4.56±0.37
cyclin-dependent kinase 5	Cdk5	1.38±0.3
cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	Cdk7	2.5±0.29
cyclin-dependent kinase 9 (CDC2-related kinase)	Cdk9	3.06±0.51
cyclin-dependent kinase inhibitor 1A	Cdkn1a	0.63±0.09
cyclin-dependent kinase inhibitor 1B	Cdkn1b	3.92±0.16
cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	Cdkn2c	1.38±0.07
cyclin-dependent kinase inhibitor 3 (predicted)	Cdkn3_predicted	0.93±0.28
cylindromatosis (turban tumor syndrome)	Cyld	1.17±0.02
cystathionase (cystathionine gamma-lyase)	Cth	3.94±1.08
cystathionine beta synthase	Cbs	8.33±1.11
cystatin B	Cstb	26.16±0.57
cysteine and glycine-rich protein 2	Csrp2	7.32±0.67
cysteine and glycine-rich protein 2 binding protein (predicted)	Csrp2bp_predicted	0.76±0.36
cysteine and histidine rich 1	Cyhr1	0.89±0.24
cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 (predicted)	Chordc1_predicted	4.46±0.73
cysteine conjugate-beta lyase 1	Ccbl1	21.9±3.54
cysteine-rich hydrophobic domain 2 (predicted)	Chic2_predicted	0.25±0.04
cysteine-rich PDZ-binding protein	Cript	2.36±0.05
cysteine-rich with EGF-like domains 2	Creld2	1.5±0.8
cysteinyl-tRNA synthetase (predicted)	Cars_predicted	1.11±0.58
cytidine 5'-triphosphate synthase 2	Ctps2	2.24±0.1
cytidine and dCMP deaminase domain containing 1	Cdadc1	2.07±0.29
cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	Cmpk1	35.55±2.82
cytidine monophospho-N-acetylneuraminic acid synthetase	Cmas	6.43±0.55
Cytidine triphosphate synthase II	Ctps2	0.83±0.15
cytochrome b /// cytochrome c oxidase subunit 3	COX3 /// CYTB	66.97±4.47
cytochrome b, ascorbate dependent 3	Cybasc3	1.16±0.06
cytochrome b-245, alpha polypeptide	Cyba	25.5±0.47
cytochrome b-5	Cyb5	21.43±1.53
cytochrome b5 reductase 3	Cyb5r3	4.05±0.73
cytochrome b5 reductase 4	Cyb5r4	5.23±0.36
cytochrome b5 type B	Cyb5b	5.27±0.79
cytochrome b-561 domain containing 1 (predicted)	Cyb561d1_predicted	0.35±0.07
cytochrome b-561 domain containing 2	Cyb561d2	1.58±0.23
cytochrome c oxidase subunit IV isoform 1	Cox4i1	48.66±2.01
cytochrome c oxidase subunit Vb	Cox5b	36.16±0.92
cytochrome c oxidase subunit VIc-1	Cox6c1	0.2±0.08
cytochrome c oxidase subunit VIIa polypeptide 2 like (predicted)	Cox7a2l_predicted	8.81±0.82
cytochrome c oxidase subunit VIIb	Cox7b	41.45±4.62
cytochrome c oxidase, subunit Va	Cox5a	44.46±1.54
cytochrome c oxidase, subunit VIa, polypeptide 1	Cox6a1	45.13±3.9
cytochrome c oxidase, subunit VIb polypeptide 1	Cox6b1	42.39±1.85
cytochrome c oxidase, subunit VIc	Cox6c	48.21±3.26
cytochrome c oxidase, subunit VIIa 2	Cox7a2	58.49±2.82
cytochrome c oxidase, subunit VIIIa	Cox8a	54.73±1
cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	Cox17	4.94±0.43
cytochrome c, somatic	Cycs	54.34±1.17
cytochrome c-1 (predicted)	Cyc1_predicted	33.44±0.32
cytochrome P450 4F6	Cyp4f6	2.09±0.23
cytochrome P450 monooxygenase CYP2T1	Cyp2t1	1.33±0.14
cytochrome P450, family 2, subfamily c, polypeptide 23	Cyp2c23	63.24±2.89
cytochrome P450, family 2, subfamily d, polypeptide 2	Cyp2d2	18.89±3.78
cytochrome P450, family 2, subfamily d, polypeptide 4	Cyp2d4v1	0.67±0.2
cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	34.02±4.09
cytochrome P450, family 2, subfamily f, polypeptide 4	Cyp2f4	0.35±0.06
cytochrome P450, family 2, subfamily u, polypeptide 1	Cyp2u1	0.38±0.06
cytochrome P450, family 20, subfamily A, polypeptide 1	Cyp20a1	4.77±0.75
cytochrome P450, family 27, subfamily b, polypeptide 1	Cyp27b1	0.38±0.06

cytochrome P450, family 4, subfamily a, polypeptide 10 /// cytochrome P450, family 4, subfamily a, polypeptide 1	Cyp4a1 /// Cyp4a10	30.31±4.34
cytochrome P450, family 4, subfamily a, polypeptide 2 /// cytochrome P450, family 4, subfamily a, polypeptide 3	Cyp4a2 /// Cyp4a3	33.51±9.3
cytochrome P450, family 4, subfamily a, polypeptide 3	Cyp4a3	15.6±2.96
cytochrome P450, family 4, subfamily a, polypeptide 8	Cyp4a8	12.51±8.24
cytochrome P450, family 4, subfamily f, polypeptide 1	Cyp4f1	23.62±2.97
cytochrome P450, subfamily 51	Cyp51	5.76±0.41
cytokine induced apoptosis inhibitor 1	Ciapin1	8.14±0.84
cytokine induced protein 29 kDa	Cip29	3.85±0.68
cytokine inducible SH2-containing protein	Cish	0.9±0.74
cytoplasmic FMR1 interacting protein 1 (predicted)	Cyfip1_predicted	5.69±0.47
cytoplasmic linker associated protein 1	Clasp1	0.87±0.08
cytoplasmic polyadenylation element binding protein 2 (predicted)	Cpeb2_predicted	0.47±0.55
cytoplasmic polyadenylation element binding protein 4 (predicted)	Cpeb4_predicted	9.87±1.41
cytoskeleton associated protein 5	Ckap5	0.96±0.28
cytoskeleton-associated protein 4 (predicted)	Ckap4_predicted	1.32±0.4
cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	Ciao1	2.92±0.27
D site albumin promoter binding protein	Dbp	2.9±0.09
D-2-hydroxyglutarate dehydrogenase	D2hgdh	0.38±0.06
D4, zinc and double PHD fingers family 2 (predicted)	Dpf2_predicted	1.84±0.14
D4, zinc and double PHD fingers, family 3 (predicted)	Dpf3_predicted	1.02±0.23
damage-specific DNA binding protein 1	Ddb1	4.46±0.62
D-amino acid oxidase 1	Dao1	36.09±3.23
dapper homolog 2, antagonist of beta-catenin (xenopus) (predicted)	Dact2_predicted	1.07±0.58
DAZ associated protein 1	Dazap1	1.6±0.52
DAZ associated protein 2	Dazap2	24.62±1
DAZ interacting protein 1-like	Dzip1l	0.56±0.09
DC2 protein	Dc2	4.71±0.54
DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae) (predicted)	Dcun1d1_predicted	1.05±0.11
DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae) (predicted)	Dcun1d4_predicted	1.6±0.07
DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	Dcun1d5	2.32±0.32
DCP1 decapping enzyme homolog A (S. cerevisiae)	Dcp1a	0.29±0.04
DCP1 decapping enzyme homolog b (S. cerevisiae)	Dcp1b	0.43±0.09
DDHD domain containing 1	Ddhd1	0.25±0.06
D-dopachrome tautomerase	Ddt	19.79±2.68
DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	5.65±0.9
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	Ddx17	1.26±0.21
DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Ddx18	0.86±0.06
DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	Ddx19	35.55±1.14
DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	Ddx20	0.52±0.1
DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	Ddx21	1.08±0.32
DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 (predicted)	Ddx23_predicted	1.8±0.25
DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	3.05±0.3
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	1.07±0.3
DEAD (Asp-Glu-Ala-Asp) box polypeptide 28 (predicted)	Ddx28_predicted	0.78±0.09
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	Ddx39	1.21±0.06
DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 (predicted)	Ddx41_predicted	1.11±0.52
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (predicted)	Ddx42_predicted	1.15±0.11
DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	1.98±0.19
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	Ddx47	1.18±0.14
DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (predicted)	Ddx49_predicted	0.79±0.16
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	19.9±2.2
DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	Ddx50	1.64±0.2
DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (predicted)	Ddx51_predicted	0.99±0.24
DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	0.84±0.21
DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	0.63±0.02
DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	Ddx56	0.22±0.03
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)	Ddx58_predicted	1.58±0.19
DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	Ddx59	0.63±0.19
dead end homolog 1 (zebrafish)	Dnd1	0.79±0.29
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (predicted)	Ddx11_predicted	0.31±0.05
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	21.6±1.44
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 (predicted)	Ddx31_predicted	0.44±0.09
deafness, autosomal recessive 59	Dfnb59	1.2±0.07
DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	Dhx57	0.97±0.07
DEAH (Asp-Glu-Ala-His) box polypeptide 15 (predicted)	Dhx15_predicted	7.48±1.51
DEAH (Asp-Glu-Ala-His) box polypeptide 30	Dhx30	2.35±0.29
DEAH (Asp-Glu-Ala-His) box polypeptide 35 (predicted)	Dhx35_predicted	0.55±0.07
DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted	3.18±0.08
DEAH (Asp-Glu-Ala-His) box polypeptide 37 (predicted)	Dhx37_predicted	0.47±0.26
DEAH (Asp-Glu-Ala-His) box polypeptide 38 (predicted)	Dhx38_predicted	0.49±0.12
DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	2.55±0.24
DEAH (Asp-Glu-Ala-His) box polypeptide 8	Dhx8	0.54±0.04
DEAH (Asp-Glu-Ala-His) box polypeptide 9 (predicted)	Dhx9_predicted	5.06±0.69
death associated protein 3	Dap3	1.96±0.34
Death effector domain-containing	Dedd	3.64±0.47
death inducer-obliterator 1	Dido1	0.53±0.07
death-associated protein	Dap	9.67±0.81
death-associated protein kinase 3	Dapk3	1.48±0.25
debranching enzyme homolog 1 (S. cerevisiae)	Dbr1	0.77±0.1
decapping enzyme, scavenger	Dcps	0.8±0.31
dedicator of cytokinesis 11	Dock11	0.5±0.12
dedicator of cytokinesis 5 (predicted)	Dock5_predicted	0.33±0.08
dedicator of cytokinesis 7	Dock7	1.01±0.26
dedicator of cytokinesis 8	Dock8	1.26±0.3
dedicator of cytokinesis 9	Dock9	1.58±0.6
de-etiolated homolog 1 (Arabidopsis)	Det1	0.26±0.07
defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	Dscc1	0.28±0.16

defender against cell death 1	Dad1	8.96±0.73
deformed epidermal autoregulatory factor 1 (Drosophila)	Deaf1	0.76±0.11
degenerative spermatocyte homolog 1 (Drosophila)	Degs1	11.7±2.01
dehydrodolichyl diphosphate synthase	Dhdds	0.69±0.09
dehydrogenase E1 and transketolase domain containing 1	Dhtkd1	16.99±1.65
dehydrogenase/reductase (SDR family) member 1	Dhrs1	1.62±0.34
dehydrogenase/reductase (SDR family) member 3	Dhrs3	1.98±0.74
dehydrogenase/reductase (SDR family) member 4	Dhrs4	11.93±0.48
dehydrogenase/reductase (SDR family) member 7B	Dhrs7b	3.5±0.4
dehydrogenase/reductase (SDR family) X chromosome	Dhrsx	1.12±0.39
deiodinase, iodothyronine, type I	Dio1	2.69±0.56
DEK oncogene (DNA binding)	Dek	9.8±1.35
deltex 3 homolog (Drosophila)	Dtx3	2.72±0.24
demethyl-Q 7	Coq7	1.98±0.19
DENN/MADD domain containing 1A	Dennd1a	1.37±0.34
DENN/MADD domain containing 2D (predicted)	Dennd2d_predicted	1.59±0.09
DENN/MADD domain containing 3	Dennd3	4.47±0.72
DENN/MADD domain containing 4B	Dennd4b	0.25±0.18
deoxyguanosine kinase (predicted)	Dguok_predicted	2.33±0.43
deoxyhypusine hydroxylase/monooxygenase	Dohh	2.54±0.04
deoxyhypusine synthase	Dhps	0.97±0.14
deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	4.26±0.37
deoxynucleotidyltransferase, terminal, interacting protein 2 (predicted)	Dnttip2_predicted	3.15±0.4
deoxyribonuclease 1-like 1	Dnase1l1	0.76±0.26
deoxythymidylate kinase (predicted)	Dtymk_predicted	9.4±0.29
deoxyuridine triphosphatase	Dut	8±0.61
DEP domain containing 1a (predicted)	Depdc1a_predicted	0.23±0.04
DEP domain containing 5 (predicted)	Depdc5_predicted	0.24±0.07
DEP domain containing 7	Depdc7	6.54±0.55
dephospho-CoA kinase domain containing	Dcakd	0.68±0.22
Der1-like domain family, member 1	Derl1	6.44±0.24
desmuslin	Dmn	0.32±0.02
destrin	Dstn	11±2.21
DET1 and DDB1 associated 1	Dda1	0.98±0.29
development and differentiation enhancing (predicted)	Ddef1_predicted	0.48±0.13
development and differentiation enhancing factor 2 (predicted)	Ddef2_predicted	0.28±0.18
developmentally regulated GTP binding protein 1	Drg1	2.21±0.22
developmentally regulated GTP binding protein 2	Drg2	1.52±0.33
developmentally regulated protein TPO1	Tpo1	0.99±0.07
dexamethasone-induced transcript	Dexi	0.81±0.05
diablo homolog (Drosophila)	Diablo	3.95±0.44
diacylglycerol kinase, alpha	Dgka	1.31±0.28
diacylglycerol kinase, gamma	Dgkg	9.42±0.14
diacylglycerol lipase, beta	Daglb	0.49±0.14
diacylglycerol O-acyltransferase 1	Dgat1	3.5±0.54
diacylglycerol O-acyltransferase 2	Dgat2	1.59±0.43
Diaphanous homolog 1 (Drosophila) (predicted)	Diap1_predicted	1.95±0.58
diazepam binding inhibitor	Dbi	46.04±0.96
dicarbonyl L-xylulose reductase	Dcxr	34.88±3.61
Dicer1, Dcr-1 homolog (Drosophila)	Dicer1	0.44±0.06
differentially expressed in FDCP 8	Def8	5.47±0.59
DiGeorge syndrome critical region gene 2	Dgcr2	1.57±0.11
DiGeorge syndrome critical region gene 6 (predicted)	Dgcr6_predicted	0.99±0.29
DiGeorge syndrome critical region gene 8 (predicted)	Dgcr8_predicted	0.66±0.18
dihydrofolate reductase	Dhfr	7.64±2.51
dihydrolipoamide branched chain transacylase E2	Dbt	4.71±0.24
dihydrolipoamide dehydrogenase	Dld	15.71±2.38
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Dlat	5.67±0.43
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst	17.23±0.83
dihydroorotate dehydrogenase	Dhodh	0.93±0.11
dihydropyrimidinase	Dpys	6.54±1.09
dihydropyrimidine dehydrogenase	Dpyd	1.41±0.28
dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	Dus2l	0.95±0.05
dihydrouridine synthase 3-like (S. cerevisiae)	Dus3l	0.64±0.02
dihydroxyacetone kinase 2 homolog (yeast)	Dak	9.99±2.2
DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	Dimt1	0.55±0.06
dimethylarginine dimethylaminohydrolase 1	Ddah1	35.14±1.78
dimethylarginine dimethylaminohydrolase 2	Ddah2	0.36±0.11
dimethylglycine dehydrogenase precursor	Dmgdh	7.9±1
dipeptidase 1 (renal)	Dpep1	0.47±0.05
dipeptidyl peptidase 9	Dpp9	0.55±0.22
dipeptidylpeptidase 3	Dpp3 /// LOC678760	3.78±0.55
dipeptidylpeptidase 4	Dpp4	32.8±2.18
dipeptidylpeptidase 7	Dpp7	54.62±2.6
dipeptidylpeptidase 8 (predicted)	Dpp8_predicted	2.15±0.29
DIS3 mitotic control homolog (S. cerevisiae)-like	Dis3l	1.78±0.05
DIS3 mitotic control homolog (S. cerevisiae)-like 2	Dis3l2	0.86±0.39
disabled homolog 2 (Drosophila) interacting protein	Dab2ip	1.14±0.12
disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	Dab2	55.45±1.71
Discoidin domain receptor family, member 2	Ddr2	0.59±0.12
discs, large (Drosophila) homolog-associated protein 1	Dlgap1	0.89±0.19
Discs, large homolog 1 (Drosophila)	Dlgh1	2.2±0.13
discs, large homolog 5 (Drosophila) (predicted)	Dlg5_predicted	3.05±0.06
dishevelled associated activator of morphogenesis 1 (predicted)	Daam1_predicted	1.55±0.14
dishevelled, dsh homolog 1 (Drosophila)	Dvl1	2.26±0.47
disrupted in renal carcinoma 2	Dirc2	7.24±1.17
distrobrevin binding protein 1	Dtnbp1	7.69±1.01

DMRT-like family C1c	Dmrtc1c	0.97±1.3
Dmx-like 1 (predicted)	Dmxl1_predicted	0.41±0.11
DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae) (predicted)	Dclre1a_predicted	1±0.18
DNA fragmentation factor, alpha subunit	Dffa	1.05±0.37
DNA fragmentation factor, beta subunit	Dffb	0.21±0.04
DNA methyltransferase (cytosine-5) 1	Dnmt1	0.52±0.16
DNA methyltransferase 1-associated protein 1	Dmap1	0.69±0.05
DNA primase, p49 subunit	Prim1	1.19±0.3
DNA primase, p58 subunit	Prim2	0.34±0.22
DNA topoisomerase 1, mitochondrial	Top1mt	0.2±0.11
DNA-damage inducible transcript 3	Ddit3	0.9±0.22
DNA-damage-inducible transcript 4-like	Ddit4l	1.78±0.76
DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	19.03±3.82
DnaJ (Hsp40) homolog, subfamily A, member 2	Dnaja2	10.25±1.46
DnaJ (Hsp40) homolog, subfamily A, member 3	Dnaja3	3.46±0.58
DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	0.64±0.02
DnaJ (Hsp40) homolog, subfamily B, member 1 (predicted)	Dnajb1_predicted	3.12±0.34
DnaJ (Hsp40) homolog, subfamily B, member 11	Dnajb11	5.2±0.73
DnaJ (Hsp40) homolog, subfamily B, member 12	Dnajb12	1.32±0.17
DnaJ (Hsp40) homolog, subfamily B, member 5 (predicted)	Dnajb5_predicted	0.98±0.2
DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	0.33±0.04
DnaJ (Hsp40) homolog, subfamily B, member 9	Dnajb9	5.34±0.64
DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	2.69±0.24
DnaJ (Hsp40) homolog, subfamily C, member 11 (predicted)	Dnajc11_predicted	0.77±0.19
DnaJ (Hsp40) homolog, subfamily C, member 13 (predicted)	Dnajc13_predicted	15.97±1.43
DnaJ (Hsp40) homolog, subfamily C, member 14	Dnajc14	0.72±0.05
DnaJ (Hsp40) homolog, subfamily C, member 15 (predicted)	Dnajc15_predicted	7.59±0.63
DnaJ (Hsp40) homolog, subfamily C, member 18	Dnajc18	0.34±0.06
DnaJ (Hsp40) homolog, subfamily C, member 2	Dnajc2	1.22±0.15
DnaJ (Hsp40) homolog, subfamily C, member 21	Dnajc21	0.81±0.09
DnaJ (Hsp40) homolog, subfamily C, member 3	Dnajc3	3±0.82
DnaJ (Hsp40) homolog, subfamily C, member 4	Dnajc4	1.19±0.11
DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	0.37±0.03
DnaJ (Hsp40) homolog, subfamily C, member 6 (predicted)	Dnajc6_predicted	6.41±0.51
DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	1.5±0.75
DnaJ (Hsp40) homolog, subfamily C, member 8	Dnajc8	3.32±0.28
DnaJ (Hsp40) homolog, subfamily C, member 9 (predicted)	Dnajc9_predicted	0.76±0.21
DnaJ homolog subfamily C member 12	Dnajc12	4.51±0.16
docking protein 4 (predicted)	Dok4_predicted	0.39±0.14
dodecenoyl-coenzyme A delta isomerase	Dci	13.35±1.47
dolichol kinase	Dolk	6.18±0.81
dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	8.45±1.1
dolichol-phosphate (beta-D) mannosyltransferase 2	Dpm2	1.52±0.09
dolichyl-di-phosphooligosaccharide-protein glycotransferase (predicted)	Ddost_predicted	8.39±0.44
dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	Dpagt1	3.02±0.39
dopa decarboxylase	Ddc	33.69±0.46
DOT1-like, histone H3 methyltransferase (S. cerevisiae) (predicted)	Dot1l_predicted	0.79±0.08
doublecortin-like kinase 2	Dclk2	0.22±0.19
doublecortin-like kinase 3 (predicted)	Dclk3_predicted	0.57±0.08
Down syndrome critical region gene 3 (predicted)	Dscr3_predicted	2.39±0.09
Down syndrome critical region homolog 2 (human) (predicted)	Dscr2_predicted	2.81±0.32
down-regulator of transcription 1	Dr1	1.23±0.13
DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor in ovarian cancer 2	Dph1 /// Ovca2	2.25±0.3
DPH2 homolog (S. cerevisiae)	Dph2	0.74±0.06
DPH3, KTI11 homolog (S. cerevisiae)	Dph3	5.14±0.96
DPH4 homolog (JJJ3, S. cerevisiae)	Dph4	0.51±0.19
DPH5 homolog (S. cerevisiae)	Dph5	0.57±0.16
Dpy-19-like 1 (C. elegans) (predicted)	Dpy19l1_predicted	3.01±0.26
dpy-30 homolog (C. elegans)	Dpy30	4.5±0.49
Dr1 associated protein 1 (negative cofactor 2 alpha) (predicted)	Drap1_predicted	2.03±0.4
drebrin-like	Dbnl	3.23±0.34
D-serine modulator-1	Dsm-1	1.94±0.37
DTW domain containing 1	Dtwd1	0.42±0.07
D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	Dtd1	2.62±0.38
dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	Dusp11	1.93±0.32
dual specificity phosphatase 16 (predicted)	Dusp16_predicted	0.44±0.06
dual specificity phosphatase 19 (predicted)	Dusp19_predicted	1.4±0.17
dual specificity phosphatase 22 (predicted)	Dusp22_predicted	2.54±0.37
dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Dusp3	10.37±0.08
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	Dyrk1a	1.03±0.02
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (predicted)	Dyrk2_predicted	2.4±0.38
Dullard homolog (Xenopus laevis)	Dullard	0.66±0.03
dymeclin (predicted)	Dym_predicted	2.39±0.2
dynactin 1	Dctn1	2.65±0.64
dynactin 2	Dctn2	4.75±0.55
dynactin 3 (predicted)	Dctn3_predicted	6.18±0.27
dynactin 4	Dctn4	0.67±0.02
dynactin 4 /// similar to dynactin subunit p62	Dctn4 /// LOC498752	0.37±0.07
dynactin 5	Dctn5	4.11±0.17
dynactin 6 (predicted)	Dctn6_predicted	3.66±0.08
dynamin 1-like	Dnm1l	1.21±0.34
dynamin 3	Dnm3	0.77±0.12
dynamin binding protein	Dnmbp	0.8±0.24
dynein cytoplasmic 1 heavy chain 1	Dync1h1	8.02±0.73
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	4.86±0.59
Dynein cytoplasmic 1 light intermediate chain 1	Dync1li1	4.09±0.88
dynein cytoplasmic 2 heavy chain 1	Dync2h1	1.01±0.14

dynein cytoplasmic 2 light intermediate chain 1	Dync2li1	1.93±0.23
dynein light chain LC8-type 1	Dynll1	2.2±0.85
dynein light chain LC8-type 2	Dynll2	9.62±0.88
dynein light chain roadblock-type 1	Dynlrb1	10.52±1.63
dynein light chain Tctex-type 1	Dynlt1	3.01±0.26
dynein light chain Tctex-type 3	Dynlt3	2.21±0.46
dynein, axonemal, light chain 4	Dnalc4	2.83±0.14
dynein, cytoplasmic 1 light intermediate chain 2	Dync1li2	3.13±0.74
dyskeratosis congenita 1, dyskerin	Dkc1	1.09±0.4
dystonia 1	Dyt1	1.86±0.15
dystonin (predicted)	Dst_predicted	2.86±0.85
dystrobrevin, beta	Dtnb	0.57±0.31
dystroglycan 1	Dag1	2.91±0.4
E1A binding protein p300	Ep300	2.35±0.59
E1A binding protein p400	Ep400	1.01±0.15
E26 avian leukemia oncogene 2, 3' domain	Ets2	1.15±0.33
E2F transcription factor 5	E2f5	3.22±0.28
E2F-associated phosphoprotein	Eapp	4.38±0.41
E74-like factor 1	Elf1	0.2±0.06
E74-like factor 2	Elf2	0.41±0.1
early endosome antigen 1 (predicted)	Eea1_predicted	1.59±0.12
EBNA1 binding protein 2	Ebna1bp2	1.98±0.06
echinoderm microtubule associated protein like 4 (predicted)	Eml4_predicted	0.64±0.23
ECSIT homolog (Drosophila)	Ecsit	2.22±0.07
ect2 oncogene (predicted)	Ect2_predicted	0.73±0.23
ecto-NOX disulfide-thiol exchanger 2	Enox2	0.69±0.09
ectonucleoside triphosphate diphosphohydrolase 2	Entpd2	0.29±0.17
ectonucleoside triphosphate diphosphohydrolase 4 (predicted)	Entpd4_predicted	3.71±0.42
ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	9±2.09
ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	2.62±0.24
ectonucleotide pyrophosphatase/phosphodiesterase 2	Enpp2	3.84±0.57
ectonucleotide pyrophosphatase/phosphodiesterase 3	Enpp3	1.87±0.42
Ectonucleotide pyrophosphatase/phosphodiesterase 4 (predicted)	Enpp4_predicted	0.52±0.04
ectonucleotide pyrophosphatase/phosphodiesterase 6 (predicted)	Enpp6_predicted	9.75±1.3
EF hand domain family A1	Efha1	2.8±0.35
EF hand domain family, member A2	Efha2	4.02±0.29
EF-hand calcium binding domain 2 (predicted)	Efcab2_predicted	0.39±0.17
EF-hand calcium binding domain 4A	Efcab4a	1.15±0.51
EF-hand calcium binding domain 7	Efcab7	0.26±0.2
EF-hand domain (C-terminal) containing 2 (predicted)	Efhc2_predicted	0.82±0.03
EFR3 homolog A (S. cerevisiae)	Efr3a	3.79±0.37
EGF-containing fibulin-like extracellular matrix protein 2	Efemp2	0.5±0.06
EGL nine homolog 1 (C. elegans)	Egln1	1.26±0.23
EGL nine homolog 2 (C. elegans)	Egln2	2.4±0.51
EH domain binding protein 1 (predicted)	Ehbp1_predicted	2.38±0.45
EH-domain containing 1	Ehd1	11.94±1.63
elaC homolog 2 (E. coli)	Elac2	0.95±0.18
elastase 1, pancreatic	Ela1	3.1±0.98
ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	5.71±0.62
electron transferring flavoprotein, alpha polypeptide	Etfa	23.49±0.78
electron transferring flavoprotein, beta polypeptide	Etfb	19.11±2.95
electron-transferring-flavoprotein dehydrogenase	Etfdh	7.4±0.64
ELK4, member of ETS oncogene family (predicted)	Elk4_predicted	1.19±0.26
ELL associated factor 1 (predicted)	Eaf1_predicted	1.43±0.15
ELMO domain containing 2	Elmod2	0.98±0.15
elongation factor 1 homolog (S. cerevisiae)	Elof1	4.32±0.49
elongation factor RNA polymerase II 2	Ell2	0.98±0.08
Elongation factor RNA polymerase II-like 3	Ell3	0.74±0.14
elongation factor Tu GTP binding domain containing 1 (predicted)	Eftud1_predicted	0.58±0.07
elongation factor Tu GTP binding domain containing 2	Eftud2	2.38±0.49
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (predicted)	Elovl2_predicted	6.46±0.61
elongation protein 2 homolog (S. cerevisiae)	Elp2	2.92±0.47
ELOVL family member 5, elongation of long chain fatty acids (yeast)	Elovl5	0.67±0.18
ELOVL family member 6, elongation of long chain fatty acids (yeast)	Elovl6	0.47±0.32
embryonic ectoderm development (predicted)	Eed_predicted	1.68±0.14
EMG1 nucleolar protein homolog (S. cerevisiae) (predicted)	Emg1_predicted	0.95±0.03
emopamil binding protein-like (predicted)	Ebpl_predicted	0.3±0.12
empty spiracles homeobox 2	Emx2	1.33±0.34
empty spiracles homolog 1 (Drosophila)	Emx1	0.33±0.05
enabled homolog (Drosophila)	Enah	0.68±0.07
Ena-vasodilator stimulated phosphoprotein	Evl	4.76±0.95
endonuclease G	Endog	0.5±0.11
endonuclease/exonuclease/phosphatase family domain containing 1	Eepd1	0.86±0.39
endoplasmic reticulum (ER) to nucleus signalling 1	Ern1	1.45±0.31
endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	Sil1	0.55±0.45
endoplasmic reticulum metallopeptidase 1	Ermp1	0.26±0.25
endoplasmic reticulum protein 29	Erp29	9.34±1.64
endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	Ergic1	0.56±0.32
endosulfine alpha	Ensa	1.35±0.26
endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 4	Edg4	0.33±0.1
endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 7	Edg7	0.28±0.01
endothelial differentiation-related factor 1 (predicted)	Edf1_predicted	9.27±2.67
engulfment and cell motility 2, ced-12 homolog (C. elegans)	Elmo2	1.14±0.21
engulfment and cell motility 3, ced-12 homolog (C. elegans)	Elmo3	2.36±0.32
enhancer of polycomb homolog 1 (Drosophila) (predicted)	Epc1_predicted	1.25±0.03
enhancer of polycomb homolog 2 (Drosophila) (predicted)	Epc2_predicted	0.5±0.15
enhancer of rudimentary homolog (Drosophila)	Erh	4.57±0.38

enhancer of zeste homolog 1 (Drosophila) (predicted)	Ezh1_predicted	2.14±0.35
enhancer of zeste homolog 2 (Drosophila)	Ezh2	0.22±0.13
enolase 1, alpha non-neuron	Eno1	54.57±2.64
enolase 3, beta, muscle	Eno3	0.26±0.01
enolase-phosphatase 1	Enoph1	0.51±0.39
enoyl coenzyme A hydratase 1, peroxisomal	Ech1	10.18±1.52
enoyl Coenzyme A hydratase domain containing 1	Echdc1	6.54±0.23
enoyl Coenzyme A hydratase domain containing 2 (predicted)	Echdc2_predicted	5.88±0.27
enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Echs1	10.9±0.66
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	7.11±0.73
enthoprotin	Enth	4.12±0.15
EP300 interacting inhibitor of differentiation 1	Eid1	6.25±0.29
EP300 interacting inhibitor of differentiation 2	Eid2	1.4±0.1
Eph receptor A2 (predicted)	Epha2_predicted	0.7±0.03
Eph receptor A4	Epha4	3.34±0.56
ephrin B1	Efnb1	0.56±0.23
epidermal growth factor receptor /// peptidase D	Egfr /// Pepd	33.41±1.29
epidermal growth factor receptor pathway substrate 15	Eps15	1.61±0.21
epidermal growth factor receptor pathway substrate 15-like 1	Eps15l1	0.62±0.14
epidermal growth factor receptor pathway substrate 8 (predicted)	Eps8_predicted	6.86±0.87
EPM2A (laforin) interacting protein 1 (predicted)	Epm2aip1_predicted	5.63±0.15
epoxide hydrolase 1, microsomal	Ephx1	14.97±2.01
epoxide hydrolase 2, cytoplasmic	Ephx2	16.35±0.19
EPS8-like 2 (predicted)	Eps8l2_predicted	1.65±0.3
Epsin 1	Epn1	0.73±0.01
ER degradation enhancer, mannosidase alpha-like 1	Edem1	7.89±1.35
ER degradation enhancer, mannosidase alpha-like 2	Edem2	0.63±0.05
ER lipid raft associated 1	Erlin1	4.34±0.91
ER lipid raft associated 2	Erlin2	6.89±0.39
ERBB receptor feedback inhibitor 1	Errfi1	19.83±4.03
ERGIC and golgi 3 (predicted)	Ergic3_predicted	3.94±0.46
ERO1-like (S. cerevisiae)	Ero1l	0.44±0.13
erythrocyte membrane protein band 4.1	Epb4.1	3.49±0.53
erythrocyte protein band 4.1-like 1	Epb4.1l1	1.63±0.46
erythrocyte protein band 4.1-like 3	Epb4.1l3	29.06±1.51
erythrocyte protein band 4.1-like 4a (predicted)	Epb4.1l4a_predicted	1.9±0.26
erythrocyte protein band 4.1-like 5	Epb4.1l5	1.89±0.16
erythrocyte protein band 4.9 (predicted)	Epb4.9_predicted	5.04±0.42
ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	Esf1	1.01±0.28
espin	Espn	3.16±1.61
establishment of cohesion 1 homolog 1 (S. cerevisiae)	Esco1	2.45±0.13
esterase 22	Es22	4.3±1.11
esterase 22 /// carboxylesterase-like /// carboxylesterase ES-4	Es22 /// LOC501232 /// rCG_44273	42.98±4.4
esterase D/formylglutathione hydrolase	Esd	16.38±1.87
estrogen receptor-binding fragment-associated gene 9	Ebag9	3.76±0.28
estrogen related receptor, alpha	Esrra	2.41±0.1
Ethanolamine kinase 1 (predicted)	Etnk1_predicted	5.72±0.62
ethylmalonic encephalopathy 1 (predicted)	Ethe1_predicted	19.95±1.14
etoposide induced 2.4 mRNA	Ei24	7.15±0.3
ets variant gene 1 (predicted)	Etv1_predicted	13.21±1.79
Ets2 repressor factor (predicted)	Erf_predicted	1.18±0.21
euchromatic histone methyltransferase 1 (predicted)	Ehmt1_predicted	1.47±0.21
eukaryotic elongation factor, selenocysteine-tRNA-specific	Eefsec	4.05±0.97
eukaryotic translation elongation factor 1 alpha 1	Eef1a1	41.77±3.66
eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1 (predicted)	Eef1a1 /// RGD1566344_predicted	44.7±3.27
eukaryotic translation elongation factor 1 beta 2 (predicted)	Eef1b2_predicted	17.27±2.79
eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d	7.44±0.53
eukaryotic translation elongation factor 1 epsilon 1 (predicted)	Eef1e1_predicted	3.55±0.27
eukaryotic translation elongation factor 1 gamma	Eef1g	11.57±0.5
eukaryotic translation elongation factor 2	Eef2	16.48±1.01
eukaryotic translation initiation factor 1	Eif1	23.95±2.29
eukaryotic translation initiation factor 1A	Eif1a	0.82±0.03
eukaryotic translation initiation factor 1A domain containing	Eif1ad	1.5±0.03
eukaryotic translation initiation factor 1A, Y-linked	Eif1ay	5.37±0.46
eukaryotic translation initiation factor 1B (predicted)	Eif1b_predicted	2.87±0.12
eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	2.61±0.45
eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	1.16±0.2
eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	4.55±0.58
eukaryotic translation initiation factor 2, subunit 1 alpha /// hypothetical gene supported by NM_019356	Eif2s1 /// LOC364604 /// LOC364984	0.33±0.06
eukaryotic translation initiation factor 2, subunit 2 (beta)	Eif2s2	8.58±1.05
eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	4.74±0.73
eukaryotic translation initiation factor 2A	Eif2a	4.05±0.63
eukaryotic translation initiation factor 2-alpha kinase 2	Eif2ak2	0.71±0.18
eukaryotic translation initiation factor 2B, subunit 1 alpha	Eif2b1	2.76±0.53
eukaryotic translation initiation factor 2B, subunit 2 beta	Eif2b2	2.95±0.46
eukaryotic translation initiation factor 2B, subunit 3	Eif2b3	0.45±0.21
eukaryotic translation initiation factor 2B, subunit 4 delta	Eif2b4	1.86±0.25
eukaryotic translation initiation factor 2B, subunit 5 epsilon	Eif2b5	1.3±0.21
eukaryotic translation initiation factor 2C, 1 (predicted)	Eif2c1_predicted	1.15±0.24
eukaryotic translation initiation factor 2C, 2	Eif2c2	0.45±0.18
eukaryotic translation initiation factor 3, subunit 1 alpha (predicted)	Eif3s1_predicted	5.1±0.21
eukaryotic translation initiation factor 3, subunit 10 (theta)	Eif3s10	8.97±0.54
eukaryotic translation initiation factor 3, subunit 6 interacting protein	Eif3s6ip	10.83±0.21
eukaryotic translation initiation factor 3, subunit 9 (eta)	Eif3s9	3.8±0.7

eukaryotic translation initiation factor 3, subunit C	Eif3c	14.09±0.85
eukaryotic translation initiation factor 3, subunit D	Eif3d	4.13±0.42
eukaryotic translation initiation factor 3, subunit E	Eif3e	10.15±1.97
eukaryotic translation initiation factor 3, subunit F	Eif3f	4.07±0.23
eukaryotic translation initiation factor 3, subunit G	Eif3g	7.67±0.47
eukaryotic translation initiation factor 3, subunit H	Eif3h	11.64±0.82
eukaryotic translation initiation factor 3, subunit K	Eif3k	3.69±0.38
eukaryotic translation initiation factor 4 gamma, 1	Eif4g1	4.06±0.45
eukaryotic translation initiation factor 4 gamma, 1 /// similar to eukaryotic translation initiation factor 4, gamma 1 isoform a	Eif4g1 /// LOC683907	0.34±0.12
eukaryotic translation initiation factor 4 gamma, 3 (predicted)	Eif4g3_predicted	1.31±0.31
eukaryotic translation initiation factor 4, gamma 2 (predicted)	Eif4g2_predicted	32.66±1.48
eukaryotic translation initiation factor 4A1	Eif4a1	8.6±0.49
eukaryotic translation initiation factor 4A2	Eif4a2	17.18±0.97
eukaryotic translation initiation factor 4B	Eif4b	4.7±0.65
eukaryotic translation initiation factor 4E	Eif4e	8.19±0.58
eukaryotic translation initiation factor 4E binding protein 2	Eif4ebp2	9.67±0.32
eukaryotic translation initiation factor 4E member 2 (predicted)	Eif4e2_predicted	2.75±0.17
eukaryotic translation initiation factor 4E nuclear import factor 1	Eif4enif1	1.59±0.08
eukaryotic translation initiation factor 4H	Eif4h	9.03±0.97
eukaryotic translation initiation factor 5	Eif5	10.66±0.53
eukaryotic translation initiation factor 5A	Eif5a	18.15±1.74
eukaryotic translation initiation factor 5B	Eif5b	1.82±0.11
eukaryotic translation initiation factor 6	Eif6	8.76±0.99
Eukaryotic translation termination factor 1	Etf1	2.97±0.59
Ewing sarcoma breakpoint region 1	Ewsr1	1.96±0.19
Ewing's tumor-associated antigen 1	Etaa1	0.7±0.14
excision repair cross-complementing rodent repair deficiency, complementation group 1 (predicted)	Ercc1_predicted	0.82±0.2
excision repair cross-complementing rodent repair deficiency, complementation group 3	Ercc3	2.38±0.38
excision repair cross-complementing rodent repair deficiency, complementation group 4	Ercc4	0.7±0.18
excision repair cross-complementing rodent repair deficiency, complementation group 5	Ercc5	0.44±0.15
excision repair cross-complementing rodent repair deficiency, complementation group 6 (predicted)	Ercc6_predicted	0.26±0.06
excision repaiross-complementing rodent repair deficiency, complementation group 8	Ercc8	0.35±0.06
exocyst complex component 2	Exoc2	1.51±0.2
exocyst complex component 3	Exoc3	3.37±0.28
Exocyst complex component 4	Exoc4	1.12±0.28
exocyst complex component 5	Exoc5	2.67±0.44
exocyst complex component 6	Exoc6	4.14±0.91
exocyst complex component 7	Exoc7	0.77±0.26
exonuclease 3''-5'' domain-like 2 (predicted)	Exdl2_predicted	0.86±0.06
exosome component 3 (predicted)	Exosc3_predicted	1.39±0.19
Exosome component 4 (predicted)	Exosc4_predicted	1.49±0.02
exosome component 5 (predicted)	Exosc5_predicted	1.43±0.45
exosome component 7	Exosc7	2.21±0.11
exosome component 8 (predicted)	Exosc8_predicted	0.32±0.17
exosome component 9	Exosc9	0.71±0.09
exostoses (multiple) 1	Ext1	1.25±0.33
exostoses (multiple) 2 (predicted)	Ext2_predicted	1.74±0.23
exportin 1, CRM1 homolog (yeast)	Xpo1	3.62±0.5
exportin 4 (predicted)	Xpo4_predicted	0.91±0.1
exportin 5 (predicted)	Xpo5_predicted	0.52±0.15
exportin 6	Xpo6	3.81±0.56
exportin 7	Xpo7	2.99±0.2
Exportin, tRNA (nuclear export receptor for tRNAs) (predicted)	Xpot_predicted	8.57±1.6
expressed in non-metastatic cells 1	Nme1	2.8±0.24
expressed in non-metastatic cells 2	Nme2	35±2.2
expressed in non-metastatic cells 4	Nme4	5.81±0.79
Eyes absent 3 homolog (Drosophila) (predicted)	Eya3_predicted	1.31±0.09
F11 receptor	F11r	8.05±0.98
factor 8-associated gene A	F8a	3.36±0.49
family with sequence similarity 100, member A	Fam100a	0.48±0.17
family with sequence similarity 103, member A1	Fam103a1	4.61±0.23
family with sequence similarity 107, member B	Fam107b	13.07±0.81
family with sequence similarity 108, member A1	Fam108a1	5.35±0.93
family with sequence similarity 108, member C1	Fam108c1	34.87±0.68
family with sequence similarity 110, member C	Fam110c	0.5±0.08
family with sequence similarity 111, member A	Fam111a	0.27±0.73
family with sequence similarity 113, member A	Fam113a	0.38±0.05
family with sequence similarity 116, member A	Fam116a	0.71±0.25
family with sequence similarity 117, member A	Fam117a	0.75±0.12
family with sequence similarity 120A /// similar to Protein CXorf17 homolog /// hypothetical protein LOC683420	Fam120a /// LOC679485 /// LOC683420 /// LOC690938	15.6±0.86
family with sequence similarity 120B	Fam120b	1.23±0.1
family with sequence similarity 120C	FAM120C	0.89±0.13
family with sequence similarity 122A	Fam122a	1.32±0.46
family with sequence similarity 123A	Fam123a	1.35±0.26
family with sequence similarity 125, member A	Fam125a	2.9±0.26
family with sequence similarity 126, member B	Fam126b	5.22±0.39
family with sequence similarity 128, member B	Fam128b	1.36±0.21
family with sequence similarity 133, member B	Fam133b	2.06±0.43
family with sequence similarity 134, member A	Fam134a	3.42±0.27
family with sequence similarity 134, member B	Fam134b	28.65±0.34
family with sequence similarity 134, member C	Fam134c	0.21±0.05
family with sequence similarity 149, member B1	Fam149b1	1.04±0.08
family with sequence similarity 151, member A	Fam151a	61.73±5.12
family with sequence similarity 151, member B	Fam151b	0.94±0.15
family with sequence similarity 152, member A	Fam152a	1.96±0.53

family with sequence similarity 152, member B	Fam152b	0.57±0.16
family with sequence similarity 20, member B	Fam20b	1.12±0.45
family with sequence similarity 20, member C	Fam20c	5.59±0.89
family with sequence similarity 21, member C	Fam21c	8.72±0.68
family with sequence similarity 3, member A	Fam3a	2.92±0.44
family with sequence similarity 3, member C	Fam3c	3.49±0.77
family with sequence similarity 32, member A	Fam32a	4.28±0.81
family with sequence similarity 35, member A	Fam35a	0.96±0.23
family with sequence similarity 40, member A	Fam40a	2.9±0.36
family with sequence similarity 44, member B	Fam44b	0.91±0.13
family with sequence similarity 45, member A	Fam45a	2.17±0.28
family with sequence similarity 48, member A	Fam48a	1.62±0.29
family with sequence similarity 49, member B	Fam49b	4.58±0.74
family with sequence similarity 50, member A	FAM50A	5.71±0.74
family with sequence similarity 54, member B	Fam54b	7.33±0.23
family with sequence similarity 58, member B	Fam58b	1.02±0.17
family with sequence similarity 69, member A	Fam69a	0.39±0.1
family with sequence similarity 73, member B	Fam73b	1.53±0.27
family with sequence similarity 76, member A	Fam76a	1.4±0.17
family with sequence similarity 80, member B	Fam80b	1±0.22
family with sequence similarity 82, member A	Fam82a	2.17±0.4
family with sequence similarity 82, member C	Fam82c	3.55±0.1
family with sequence similarity 92, member A1	Fam92a1	1.27±0.17
family with sequence similarity 96, member A	Fam96a	7.45±0.91
family with sequence similarity 96, member B	Fam96b	2.14±0.06
family with sequence similarity 98, member A	Fam98a	3.1±0.33
family with sequence similarity 98, member B	Fam98b	0.67±0.04
Fanconi anemia, complementation group C	Fancc	0.76±0.08
Fanconi anemia, complementation group E	Fance	0.24±0.1
Fanconi anemia, complementation group L (predicted)	Fancl_predicted	1.01±0.04
far upstream element (FUSE) binding protein 1	Fubp1	1.4±0.39
farnesyl diphosphate farnesyl transferase 1	Fdft1	4.6±0.54
farnesyl diphosphate synthetase	Fdps	5.9±0.64
farnesyltransferase, CAAX box, alpha	Fnta	2.76±0.47
Fas (TNFRSF6) binding factor 1 (predicted)	Fbf1_predicted	0.28±0.1
Fas apoptotic inhibitory molecule	Faim	0.78±0.18
Fas death domain-associated protein	Daxx	0.5±0.23
Fas-activated serine/threonine kinase	Fastk	1.24±0.15
Fas-associated factor 1	Faf1	2.81±0.2
fasciculation and elongation protein zeta 2 (zygin II)	Fez2	1.39±0.26
FAST kinase domains 2	Fastkd2	2.2±0.23
FAST kinase domains 3	Fastkd3	1.01±0.15
FAT tumor suppressor homolog 1 (Drosophila)	Fat1	3.59±0.4
fatty acid amide hydrolase	Faah	0.7±0.06
fatty acid binding protein 3, muscle and heart	Fabp3	21.26±1.88
fatty acid desaturase 1	Fads1	16.84±0.72
fatty acid desaturase 2	Fads2	2.8±0.55
fatty acid desaturase 3	Fads3	2.99±0.32
fatty acid synthase	Fasn	2.04±0.51
F-box and leucine-rich repeat protein 10	Fbxl10	0.64±0.14
F-box and leucine-rich repeat protein 11 (predicted)	Fbxl11_predicted	1.57±0.22
F-box and leucine-rich repeat protein 12	Fbxl12	0.46±0.05
F-box and leucine-rich repeat protein 14 (predicted)	Fbxl14_predicted	0.85±0.16
F-box and leucine-rich repeat protein 3	Fbxl3	1.2±0.11
F-box and leucine-rich repeat protein 4 (predicted)	Fbxl4_predicted	2.67±0.11
F-box and leucine-rich repeat protein 5 (predicted)	Fbxl5_predicted	4.82±0.14
F-box and leucine-rich repeat protein 6	Fbxl6	0.84±0.15
F-box and WD-40 domain protein 11 (predicted)	Fbxw11_predicted	5±0.2
F-box and WD-40 domain protein 2 (predicted)	Fbxw2_predicted	1.26±0.24
F-box and WD-40 domain protein 4 (predicted)	Fbxw4_predicted	0.73±0.17
F-box and WD-40 domain protein 5	Fbxw5	6.02±0.73
F-box and WD-40 domain protein 8 (predicted)	Fbxw8_predicted	1.48±0.65
F-box and WD-40 domain protein 9	Fbxw9	1.43±0.16
F-box only protein 18 (predicted)	Fbxo18_predicted	2.46±0.06
F-box protein 11	Fbxo11	2.45±0.09
F-box protein 16	Fbxo16	0.22±0.08
F-box protein 21	Fbxo21	1.28±0.12
F-box protein 22	Fbxo22	2.58±0.23
F-box protein 25	Fbxo25	0.98±0.1
F-box protein 28 (predicted)	Fbxo28_predicted	0.55±0.04
F-box protein 3	Fbxo3	6.04±0.56
F-box protein 30	Fbxo30	1.2±0.23
F-box protein 33	Fbxo33	1.6±0.52
F-box protein 38 (predicted)	Fbxo38_predicted	1.53±0.36
F-box protein 4	Fbxo4	2.02±0.39
F-box protein 46	Fbxo46	0.24±0.09
F-box protein 6	Fbxo6	4.43±0.54
F-box protein 7	Fbxo7	2.65±0.46
F-box protein 8	Fbxo8	1.77±0.17
f-box protein 9	Fbxo9	4.51±0.1
Fc receptor, IgG, alpha chain transporter	Fcgrt	7.42±0.87
FCH and double SH3 domains 1 (predicted)	Fchsd1_predicted	2.48±0.51
FCH and double SH3 domains 2 (predicted)	Fchsd2_predicted	0.3±0.05
FCH domain only 2 (predicted)	Fcho2_predicted	11.87±0.75
feline leukemia virus subgroup C cellular receptor family, member 2	Flvcr2	0.49±0.04
fem-1 homolog c (C.elegans) (predicted)	Fem1c_predicted	1.84±0.57
feminization 1 homolog a (C. elegans)	Fem1a	2.13±0.39

fer-1-like 3, myoferlin (C. elegans)	Fer1l3	1.48±0.44
FERM domain containing 8	Frmd8	1.95±0.21
FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) (predicted)	Farp1_predicted	0.2±0.07
FERM, RhoGEF and pleckstrin domain protein 2 (predicted)	Farp2_predicted	0.57±0.06
ferredoxin 1	Fdx1	12.98±0.3
ferredoxin 1-like	Fdx1l	1.64±0.3
ferredoxin reductase	Fdxr	0.74±0.09
ferric-chelate reductase 1	Frrs1	0.72±0.07
ferritin heavy chain 1	Fth1	58.9±3.36
ferritin light chain 1	Ftl1	46.3±2.71
ferrochelatase (predicted)	Fech_predicted	2.97±0.1
fetal Alzheimer antigen (predicted)	Falz_predicted	0.47±0.21
FGF receptor activating protein 1	Frag1	0.68±0.15
FGFR1 oncogene partner 2	Fgfr1op2	0.62±0.14
fibrillarin	Fbl	3.53±0.26
fibrinogen, alpha polypeptide	Fga	0.36±0.08
fibroblast growth factor (acidic) intracellular binding protein	Fibp	2.51±0.34
fibroblast growth factor 1	Fgf1	0.38±0.16
fibroblast growth factor 13	Fgf13	2.75±0.14
fibroblast growth factor 9	Fgf9	1.78±0.3
Fibroblast growth factor receptor 1	Fgfr1	0.95±0.18
Fibroblast growth factor receptor 3	Fgfr3	1.62±0.07
fibroblast growth factor receptor 4	Fgfr4	1.58±0.38
fibroblast growth factor receptor substrate 2 (predicted)	Frs2_predicted	1.01±0.01
fibroblast growth factor receptor substrate 3	Frs3	0.26±0.15
fibronectin 1	Fn1	0.44±0.36
fibronectin type III domain containing 3a (predicted)	Fndc3a_predicted	1.98±0.17
fibronectin type III domain containing 3B (predicted)	Fndc3b_predicted	2.92±0.53
FIG4 homolog (S. cerevisiae)	Fig4	1.44±0.15
filamin, beta (predicted)	Flnb_predicted	2.51±0.02
Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) protein	Fau /// LOC687439 /// LOC687780	27.78±2.18
FIP1 like 1 (S. cerevisiae)	Fip1l1	1.46±0.39
fission 1 (mitochondrial outer membrane) homolog (yeast)	Fis1	3.58±0.97
fizzy/cell division cycle 20 related 1 (Drosophila) (predicted)	Fzr1_predicted	1.37±0.15
FK506 binding protein 11	Fkbp11	0.38±0.04
FK506 binding protein 12-rapamycin associated protein 1	Frap1	2.34±0.11
FK506 binding protein 15	Fkbp15	3.67±0.36
FK506 binding protein 1a	Fkbp1a	4.31±0.47
FK506 binding protein 2 (predicted)	Fkbp2_predicted	7.64±1.42
FK506 binding protein 3 (predicted)	Fkbp3_predicted	7.88±1.04
FK506 binding protein 4	Fkbp4	4.11±0.38
FK506 binding protein 5	Fkbp5	0.42±0.09
FK506 binding protein 8	Fkbp8	2.92±1.37
FK506 binding protein 9	Fkbp9	3.3±0.56
FK506 binding protein-like	Fkbpl	0.69±0.06
flavin adenine dinucleotide synthetase	Flad1	1.36±0.2
flavin containing monooxygenase 1	Fmo1	42.25±1.32
flavin containing monooxygenase 2	Fmo2	3.97±1.82
flavin containing monooxygenase 3	Fmo3	7.68±5.94
flavin containing monooxygenase 4	Fmo4	7.32±0.82
flavin containing monooxygenase 5	Fmo5	2.81±0.24
flightless I homolog (Drosophila)	Flii	1.86±0.19
flotillin 1	Flot1	1.82±0.26
flotillin 2	Flot2	2±0.25
FLT3-interacting zinc finger 1	Fiz1	0.53±0.22
FLYWCH-type zinc finger 1	Flywch1	1.12±0.27
folate hydrolase	Folh1	8.37±0.64
folate receptor 1 (adult)	Folr1	39.29±4.71
folliculin	Flcn	4.47±0.65
forkhead box J1	Foxj1	0.24±0.05
forkhead box J2	Foxj2	0.65±0.47
forkhead box J3 (predicted)	Foxj3_predicted	1.68±0.27
forkhead box K2 (predicted)	Foxk2_predicted	0.75±0.11
forkhead box N3	Foxn3	0.92±0.05
forkhead box O1	Foxo1	0.47±0.14
forkhead box O4	Foxo4	1.03±0.12
formin binding protein 1	Fnbp1	0.4±0.04
formin binding protein 4	Fnbp4	1.71±0.3
formin-like 1 (predicted)	Fmnl1_predicted	0.79±0.2
Forty-two-three domain containing 1	Fyttd1	2.41±0.11
four and a half LIM domains 1	Fhl1	1.5±0.25
fractured callus expressed transcript 1	Fxc1	2.02±0.14
fragile histidine triad gene	Fhit	1.12±0.11
fragile X mental retardation syndrome 1 homolog	Fmr1	2.09±0.22
fragile X mental retardation, autosomal homolog 1	Fxr1	1.68±0.39
fragile X mental retardation, autosomal homolog 2	Fxr2	0.83±0.38
frataxin (predicted)	Fxn_predicted	3.66±0.17
frizzled homolog 1 (Drosophila)	Fzd1	14.5±0.12
frizzled homolog 4 (Drosophila)	Fzd4	0.23±0.1
frizzled homolog 8 (Drosophila)	Fzd8	0.36±0.19
frizzled-related protein	Frzb	0.37±0.12
fructosamine 3 kinase	Fn3k	6.48±0.2
fructose-1,6- biphosphatase 1	Fbp1	56.11±1.12
fructose-1,6-bisphosphatase 2	Fbp2	0.37±0.1
FSHD region gene 1 (predicted)	Frg1_predicted	0.73±0.2
Ftsj homolog 1 (E. coli) (predicted)	Ftsj1_predicted	0.26±0.14

FtsJ homolog 2 (E. coli) (predicted)	Ftsj2_predicted	0.54±0.06
FtsJ homolog 3 (E. coli)	Ftsj3	0.72±0.16
fucokinase (predicted)	Fuk_predicted	0.45±0.1
fucosidase, alpha-L- 1, tissue	Fuca1	39.84±1.75
fucosidase, alpha-L- 2, plasma	Fuca2	3.87±0.54
fucosyltransferase 8	Fut8	4.69±0.45
fukutin related protein	Fkrp	0.51±0.05
Fukuyama type congenital muscular dystrophy homolog (human) (predicted)	Fcmd_predicted	2.98±0.48
fumarate hydratase 1	Fh1	24.34±2.74
fumarylacetoacetate hydrolase	Fah	23.24±2.09
fumarylacetoacetate hydrolase domain containing 1	Fahd1	14.49±1.93
fumarylacetoacetate hydrolase domain containing 2A (predicted)	Fahd2a_predicted	8.53±2.19
FUN14 domain containing 1	Fundc1	0.55±0.2
furin (paired basic amino acid cleaving enzyme)	Furin	3.67±0.29
FUS interacting protein (serine-arginine rich) 1	Fusip1	0.55±0.1
fused toes	Fts	0.94±0.51
fusion, derived from t(12;16) malignant liposarcoma (human)	Fus	3.75±0.75
FXYD domain-containing ion transport regulator 2	Fxyd2	37.39±2.74
FYVE and coiled-coil domain containing 1 (predicted)	Fyco1_predicted	4.09±0.45
G elongation factor, mitochondrial 1	Gfm1	5.86±1.92
G elongation factor, mitochondrial 2	Gfm2	0.86±0.25
G kinase anchoring protein 1	Gkap1	2.49±0.15
G patch domain and KOW motifs	Gpkow	1.12±0.08
G patch domain containing 4	Gpatch4	0.23±0.06
G protein beta subunit-like	Gbl	0.37±0.03
G protein pathway suppressor 1	Gps1	15.54±0.72
G protein pathway suppressor 2	Gps2	1.12±0.31
G protein pathway suppressor 2 (predicted)	Gps2_predicted	1.56±0.11
G protein-coupled receptor 107 (predicted)	Gpr107_predicted	0.78±0.12
G protein-coupled receptor 125 (predicted)	Gpr125_predicted	3.13±0.46
G protein-coupled receptor 137B (predicted)	Gpr137b_predicted	5.25±0.55
G protein-coupled receptor 146	Gpr146	0.39±0.09
G protein-coupled receptor 172B	Gpr172b	3.43±0.45
G protein-coupled receptor 175	Gpr175	1±0.21
G protein-coupled receptor 177	Gpr177	3.82±0.5
G protein-coupled receptor 180	Gpr180	0.51±0.11
G protein-coupled receptor 56	Gpr56	25.03±3.8
G protein-coupled receptor 89 (predicted)	Gpr89_predicted	2.16±0.1
G protein-coupled receptor associated sorting protein 1	Gprasp1	0.48±0.11
G protein-coupled receptor associated sorting protein 2	Gprasp2	0.21±0.24
G protein-coupled receptor kinase interactor 1	Git1	0.45±0.13
G protein-coupled receptor kinase-interactor 2	Git2	0.23±0.01
G protein-coupled receptor, family C, group 5, member C	Gprc5c	4.51±0.51
G0/G1 switch gene 2	G0s2	17.44±0.57
G1 to S phase transition 1	Gspt1	8.54±0.77
GA repeat binding protein, alpha (predicted)	Gabpa_predicted	2.02±0.31
GA repeat binding protein, beta 1 /// similar to GA binding protein transcription factor, beta subunit 2 (GABPB2) (predicted)	Gabpb1 /// RGD1560391_predicted	0.52±0.25
GABA(A) receptor-associated protein like 2	Gabarapl2	13.72±0.69
galactokinase 1	Galk1	1.67±0.41
galactokinase 2	Galk2	10.14±0.32
galactose mutarotase	Galm	25.84±4.74
galactose-1-phosphate uridyl transferase	Galt	1.3±0.56
galactosidase, alpha	Gla	2.04±0.22
galactosidase, beta 1 (predicted)	Glb1_predicted	37.12±3.63
galactosidase, beta 1-like 2	Glb1l2	0.69±0.18
galectin-related protein	Hspc159	1.26±0.33
gametogenetin binding protein 2	Ggnbp2	4.89±0.72
gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1 (predicted)	Gabarapl1_predicted /// MGC125167	2.73±0.42
gamma-aminobutyric acid receptor associated protein	Gabarap	31.18±2.79
gamma-glutamyl carboxylase	Ggcx	3.01±0.34
gamma-glutamyl hydrolase	Ggh	18.09±2.24
gamma-glutamyltransferase 1	Ggt1	5.4±4.87
ganglioside-induced differentiation-associated-protein 2	Gdap2	0.66±0.12
gap junction membrane channel protein beta 1	Gjb1	2.05±0.14
gap junction membrane channel protein beta 2	Gjb2	5.7±1.5
gap junction protein, alpha 1	Gja1	1.35±0.08
GATA zinc finger domain containing 1	Gatad1	2.29±0.49
GATA zinc finger domain containing 2A	Gatad2a	1.11±0.45
GATA zinc finger domain containing 2B	Gatad2b	0.25±0.22
GCD14/PCMT domain containing protein RGD1359191	RGD1359191	0.51±0.17
GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)	Gcn1l1_predicted	0.93±0.13
GC-rich promoter binding protein 1	Gpbp1	3.81±0.77
GDNF-inducible zinc finger protein 1	Gzf1	2.07±0.3
GDP dissociation inhibitor 2	Gdi2	35.55±3.25
GDP-mannose pyrophosphorylase A	Gmppa	1.72±0.33
GDP-mannose pyrophosphorylase B (predicted)	Gmppb_predicted	0.46±0.12
gem (nuclear organelle) associated protein 4	Gemin4	0.41±0.1
gem (nuclear organelle) associated protein 6	Gemin6	2.36±0.43
gem (nuclear organelle) associated protein 8	Gemin8	1.02±0.1
general transcription factor II E, polypeptide 2 (beta subunit) (predicted)	Gtf2e2_predicted	2.07±0.34
general transcription factor II H, polypeptide 1 (predicted)	Gtf2h1_predicted	1.95±0.13
general transcription factor II H, polypeptide 2 (predicted)	Gtf2h2_predicted	0.86±0.08
general transcription factor II I	Gtf2i	5.36±0.34
general transcription factor II I repeat domain-containing 1	Gtf2ird1	1.71±0.07
general transcription factor IIa 2	Gtf2a2	7.21±0.36

general transcription factor IIB	Gtf2b	2.4±0.24
general transcription factor IIF, polypeptide 1	Gtf2f1	0.93±0.1
general transcription factor IIF, polypeptide 2	Gtf2f2	0.74±0.04
general transcription factor IIH, polypeptide 3	Gtf2h3	0.67±0.17
general transcription factor IIH, polypeptide 5	Gtf2h5	5±0.44
general transcription factor III A	Gtf3a	1.03±0.22
general transcription factor IIIC, polypeptide 2, beta	Gtf3c2	1.82±0.44
general transcription factor IIIC, polypeptide 3	Gtf3c3	0.77±0.24
general transcription factor IIIC, polypeptide 4	Gtf3c4	1.12±0.2
general transcription factor IIIC, polypeptide 5 (predicted)	Gtf3c5_predicted	0.39±0.04
general transcription factor IIIC, polypeptide 6, alpha	Gtf3c6	1.13±0.16
gephyrin	Gphn	4.35±0.7
geranylgeranyl diphosphate synthase 1	Ggps1	0.58±0.16
germ cell-less homolog 1 (Drosophila)	Gmcl1	1.63±0.27
GH3 domain containing	Ghdc	0.24±0.04
GINS complex subunit 4 (Sld5 homolog)	Gins4	0.51±0.06
GIPC PDZ domain containing family, member 1	Gipc1	0.89±0.38
GIY-YIG domain containing 2	Giyd2	1±0.16
GLE1 RNA export mediator-like (yeast)	Gle1l	0.74±0.08
glia maturation factor, beta	Gmfb	0.55±0.17
glial cell line derived neurotrophic factor family receptor alpha 1	Gfra1	1.02±0.08
glial cell line derived neurotrophic factor family receptor alpha 2	Gfra2	1.17±0.11
glial cell line derived neurotrophic factor family receptor alpha 3	Gfra3	1.1±0.18
GLI-Kruppel family member HKR3	Hkr3	0.3±0.12
glioma tumor suppressor candidate region gene 2	Gltscr2	3.45±0.93
GLIS family zinc finger 1 (predicted)	Glis1_predicted	1.11±0.18
GLIS family zinc finger 2 (predicted)	Glis2_predicted	1.34±0.63
glomulin, FKBP associated protein	Glmn	0.32±0.14
glucan (1,4-alpha-), branching enzyme 1	Gbe1	6.65±0.77
glucocorticoid modulatory element binding protein 2	Gmeb2	0.51±0.11
glucosamine (N-acetyl)-6-sulfatase	Gns	29.84±2.04
glucosamine (N-acetyl)-6-sulfatase /// similar to glucosamine (N-acetyl)-6-sulfatase	Gns /// LOC688338	0.25±0.07
glucosamine-6-phosphate deaminase 2 (predicted)	Gnpda2_predicted	0.24±0.02
glucosamine-phosphate N-acetyltransferase 1	Gnpnat1	2.24±0.54
glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	Gcnt2	5.22±0.86
glucose 6 phosphatase, catalytic, 3	G6pc3	1.11±0.28
glucose phosphate isomerase	Gpi	25.61±1.35
glucose-6-phosphatase, catalytic	G6pc	44.16±3.26
glucose-6-phosphate dehydrogenase X-linked	G6pdx	2.09±0.11
glucosidase 1	Gcs1	2.77±0.47
glucosidase, alpha, acid	Gaa	7.62±0.84
glucosidase, beta, acid 3 (cytosolic) (predicted)	Gba3_predicted	31.39±0.64
glucuronidase, beta	Gusb	1.66±0.28
glucuronyl C5-epimerase	Glce	0.78±0.11
glutamate dehydrogenase 1	Glud1	34.48±0.62
glutamate oxaloacetate transaminase 1, soluble	Got1	5.23±0.89
glutamate oxaloacetate transaminase 2, mitochondrial	Got2	29.76±2.4
glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	Grina	16.49±3.18
glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Grinl1a	9.8±1.15
glutamate receptor, metabotropic 4	Grm4	0.25±0.08
glutamate-ammonia ligase (glutamine synthetase)	Glul	25.11±3.01
glutamate-rich WD repeat containing 1	Grwd1	0.53±0.17
glutamic pyruvate transaminase (alanine aminotransferase) 2 (predicted)	Gpt2_predicted	0.31±0.05
glutaminase	Gls	6.56±0.83
Glutamine and serine rich 1 (predicted)	Qser1_predicted	0.97±0.31
glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	Qrsl1	0.98±0.11
glutaminyl-tRNA synthetase /// similar to glutaminyl-tRNA synthetase (predicted)	Qars /// RGD1562301_predicted	5.92±0.96
glutamyl aminopeptidase	Enpep	14.59±0.44
glutamyl-prolyl-tRNA synthetase	Eprs	6.37±1.22
glutamyl-tRNA synthetase 2 mitochondrial (putative)	Ears2	0.29±0.13
glutaredoxin 1 (thioltransferase)	Glrx1	2.12±0.24
glutaredoxin 2 (thioltransferase)	Glrx2	6.92±0.36
glutaredoxin 3	Glrx3	8.14±2.14
glutaredoxin 5 homolog (S. cerevisiae) (predicted)	Glrx5_predicted	16.12±1.61
glutaryl-Coenzyme A dehydrogenase (predicted)	Gcdh_predicted	27.95±1.68
glutathione peroxidase 1	Gpx1	41.25±1.49
glutathione peroxidase 2	Gpx2	1.24±0.34
glutathione peroxidase 3	Gpx3	69.54±4.2
glutathione peroxidase 4	Gpx4	26.01±3.99
glutathione reductase	Gsr	2.9±0.16
glutathione S-transferase A3	Gsta2 /// Gsta3 /// LOC494499 /// Yc2	41.87±2.39
glutathione S-transferase A3 /// glutathione-S-transferase, alpha type2 /// glutathione S-transferase Yc2 subunit	Gsta2 /// Gsta3 /// Yc2	47.03±2.94
glutathione S-transferase kappa 1	Gstk1	6.89±1.02
glutathione S-transferase omega 1	Gsto1	26.99±0.63
glutathione S-transferase theta 1	Gstt1	5.03±0.99
glutathione S-transferase theta 1 /// glutathione S-transferase, theta 3	Gstt1 /// Gstt3	30.85±5.19
glutathione S-transferase, alpha 4	Gsta4	24.31±4.13
glutathione S-transferase, C-terminal domain containing	Gstcd	0.26±0.06
glutathione S-transferase, mu 1	Gstm1	4.13±0.63
glutathione S-transferase, mu type 3	Gstm3	1.9±0.16
glutathione S-transferase, theta 2	Gstt2	3.17±0.37
glutathione synthetase	Gss	2.12±1.69
glyceraldehyde-3-phosphate dehydrogenase	Gapdh	60.99±2.36
glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyde-3-phosphate dehydrogenase	Gapdh /// LOC686275 /// LOC689689	59.41±0.26

glycerol kinase	Gyk	16.71±1.19
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	14.3±1.28
glyceronephosphate O-acyltransferase	Gnpat	2.38±0.04
glycerophosphodiester phosphodiesterase 1	Gde1	21.19±2.52
glycerophosphodiester phosphodiesterase domain containing 1 (predicted)	Gdpd1_predicted	0.2±0.16
glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Gatm	67.55±5.45
glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	Gcat	6±0.74
glycine cleavage system protein H (aminomethyl carrier)	Gcsh	35.91±2.19
glycine decarboxylase (predicted)	Gldc_predicted	10.67±1.38
glycine N-methyltransferase	Gnmt	2.82±0.63
glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein	LOC246295	1.84±0.16
glycine-N-acyltransferase	Glyat	25.69±0.65
glycogen synthase kinase 3 alpha	Gsk3a	1.05±0.19
glycogen synthase kinase 3 beta	Gsk3b	0.71±0.14
glycogenin 1	Gyg1	3.28±0.15
glycolipid transfer protein domain containing 1	Gltpd1	1.17±0.06
Glycoprotein galactosyltransferase alpha 1, 3	Ggta1	0.52±0.05
glycoprotein m6a	Gpm6a	2.01±0.58
glycoprotein, synaptic 2	Gpsn2	4.53±0.41
glycosylphosphatidylinositol specific phospholipase D1	Gpld1	0.44±0.12
glycosyltransferase 25 domain containing 1 (predicted)	Glt25d1_predicted	0.78±0.12
glycosyltransferase 8 domain containing 1	Glt8d1	1.06±0.23
glycosyltransferase-like 1B	Gyltl1b	0.89±0.06
glycosyltransferase-like domain containing 1	Gtdc1	0.65±0.17
glycyl-tRNA synthetase	Gars	4.07±0.3
glyoxalase 1	Glo1	8.08±0.57
glyoxalase domain containing 4	Glod4	3.72±0.23
glyoxalase domain containing 5	Glod5	13.28±0.85
glyoxylate reductase/hydroxypyruvate reductase (predicted)	Grhpr_predicted	41.51±2.78
glypican 4	Gpc4	15.24±2.28
GM2 ganglioside activator protein	Gm2a	0.45±0.3
GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	Gnas	11.73±3.91
golgi apparatus protein 1	Glg1	1.62±0.11
golgi associated PDZ and coiled-coil motif containing (predicted)	Gopc_predicted	3.41±0.49
golgi associated, gamma adaptin ear containing, ARF binding protein 1	Gga1	0.63±0.1
golgi associated, gamma adaptin ear containing, ARF binding protein 2	Gga2	2.95±0.31
golgi autoantigen, golgin subfamily a, 2	Golga2	0.63±0.18
golgi autoantigen, golgin subfamily a, 3 (predicted)	Golga3_predicted	0.67±0.1
golgi autoantigen, golgin subfamily a, 4	Golga4	2.87±0.32
golgi autoantigen, golgin subfamily a, 5	Golga5	3.71±0.19
golgi autoantigen, golgin subfamily a, 7	Golga7	7.51±0.14
golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	1.72±0.21
golgi integral membrane protein 4	Golim4	0.31±0.07
golgi phosphoprotein 3	Golph3	1.77±0.37
golgi phosphoprotein 3-like	Golph3l	1.62±0.46
golgi reassembly stacking protein 1	Gorasp1	0.91±0.12
golgi reassembly stacking protein 2	Gorasp2	1.56±0.28
Golgi SNAP receptor complex member 1	Gosr1	1.77±0.42
golgi SNAP receptor complex member 2	Gosr2	11.2±0.71
golgi-specific brefeldin A-resistance factor 1	Gbf1	1.46±0.07
goliath	LOC652955	3.54±0.27
GPI-anchored membrane protein 1	Gpiap1	11.1±0.88
G-protein signalling modulator 2 (AGS3-like, C. elegans)	Gpsm2	0.39±0.12
GRAM domain containing 1B (predicted)	Gramd1b_predicted	1.78±0.17
GRAM domain containing 3	Gramd3	2.6±0.55
granule cell antiserum positive 14	Gcap14	3.22±0.23
granulin	Grn	14.67±1.34
Granulocyte-macrophage colony stimulating receptor alpha	Csf2ra	0.28±0.18
GRB10 interacting GYF protein 1	Gigyf1	0.47±0.22
G-rich RNA sequence binding factor 1	Grsf1	10.92±0.48
GRIP and coiled-coil domain containing 2	Gcc2	3.69±0.44
GRIP1 associated protein 1	Gripap1	0.51±0.12
growth arrest and DNA-damage-inducible 45 alpha	Gadd45a	1.45±0.69
growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	0.46±0.38
growth arrest and DNA-damage-inducible, gamma interacting protein 1	Gadd45gip1	2.5±0.53
growth arrest specific 5	Gas5	1.63±0.56
growth arrest specific 6	Gas6	0.34±0.53
growth arrest-specific 2	Gas2	11.85±0.87
growth arrest-specific 2 like 1 (predicted)	Gas2l1_predicted	0.98±0.19
growth factor receptor bound protein 10	Grb10	2.72±0.17
growth factor receptor bound protein 14	Grb14	0.27±0.05
growth factor receptor bound protein 2	Grb2	2.2±0.59
growth factor receptor bound protein 2-associated protein 1 (predicted)	Gab1_predicted	2.38±0.46
growth factor receptor bound protein 7	Grb7	0.49±0.22
growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	Gfer	1.06±0.19
growth hormone inducible transmembrane protein	Ghitm	16±1.38
growth hormone receptor	Ghr	6.06±0.31
GrpE-like 1, mitochondrial	Grpel1	10.94±0.26
GrpE-like 2, mitochondrial	Grpel2	1.08±0.23
GSG1-like /// similar to germ cell associated 1 (predicted)	Gsg1l /// LOC687697	0.52±0.17
GTP binding protein 1 (predicted)	Gtpbp1_predicted	0.74±0.18
GTP binding protein 2	Gtpbp2	0.29±0.04
GTP binding protein 3 (mitochondrial)	Gtpbp3	0.68±0.17
GTP binding protein 4	Gtpbp4 /// LOC689842 /// RGD1560805_predicted	0.3±0.19
GTP binding protein 5	Gtpbp5	1.63±0.13

GTP binding protein 6 (putative) (predicted)	Gtpbp6_predicted	0.4±0.06
GTP cyclohydrolase I feedback regulator	Gchfr	6.66±0.56
GTPase activating protein and VPS9 domains 1 (predicted)	Gapvd1_predicted	1.68±0.27
GTPase activating RANGAP domain-like 1	Garnl1	1.67±0.33
GTP-binding protein 10 (putative)	Gtpbp10	0.97±0.26
guanidinoacetate methyltransferase	Gamt	6.16±0.79
guanine deaminase	Gda	0.24±0.18
guanine monphosphate synthetase	Gmps	3.66±0.2
guanine nucleotide binding protein (G protein), beta 5	Gnb5	0.96±0.03
guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	Gnb2l1	21.3±1.35
guanine nucleotide binding protein (G protein), gamma 12	Gng12	4.1±0.5
guanine nucleotide binding protein (G protein), gamma 5	Gng5	16.36±0.95
guanine nucleotide binding protein, alpha 11	Gna11	0.3±0.07
guanine nucleotide binding protein, alpha 12	Gna12	1.07±0.15
guanine nucleotide binding protein, alpha inhibiting 1	Gnai1	3.13±0.08
guanine nucleotide binding protein, alpha inhibiting 3	Gnai3	5.41±0.52
guanine nucleotide binding protein, beta 1	Gnb1	1.9±0.3
guanine nucleotide binding protein, beta 2	Gnb2	2.57±1.03
guanine nucleotide binding protein, beta 3	Gnb3	0.57±0.06
guanine nucleotide binding protein-like 1	Gnl1	1.02±0.08
guanine nucleotide binding protein-like 2 (nucleolar)	Gnl2	1.02±0.21
guanine nucleotide binding protein-like 3 (nucleolar)	Gnl3	3.33±0.25
guanosine diphosphate dissociation inhibitor 1	Gdi1	5.5±0.29
guanosine monophosphate reductase 2	Gmpr2	1.19±0.13
guanylate cyclase activator 2b (retina)	Guca2b	0.35±0.22
guanylate kinase 1	Guk1	4.59±0.75
gypsy retrotransposon integrase 1	Gin1	0.95±0.11
H1 histone family, member 0	H1f0	1.09±0.66
H2A histone family, member J	H2afj	4.33±1.48
H2A histone family, member V (predicted)	H2afv_predicted /// LOC685909 /// RGD1560813_predicted	4.34±0.31
H2A histone family, member X	H2afx	0.64±0.2
H2A histone family, member Y	H2afy	1.45±0.85
H2A histone family, member Z	H2afz	24.61±1.64
H3 histone, family 3B	H3f3b	16.15±1.33
hairy and enhancer of split 6 (Drosophila)	Hes6	13.09±0.17
haloacid dehalogenase-like hydrolase domain containing 2	Hdhd2	1.28±0.16
haloacid dehalogenase-like hydrolase domain containing 3	Hdhd3	1.89±0.32
Harvey rat sarcoma oncogene, subgroup R (predicted)	Rras_predicted	0.56±0.26
Harvey rat sarcoma virus oncogene	Hras	4.5±0.68
Hbs1-like (S. cerevisiae)	Hbs1l	3.12±0.09
HCLS1 binding protein 3	Hs1bp3	2.05±0.75
HD domain containing 2 (predicted)	Hddc2_predicted	0.71±0.07
HD domain containing 3 (predicted)	Hddc3_predicted	4.86±0.13
headcase homolog (Drosophila) (predicted)	Heca_predicted	1.19±0.17
HEAT repeat containing 2	Heatr2	1.53±0.2
HEAT repeat containing 5A	Heatr5a	0.51±0.09
HEAT repeat containing 5B	Heatr5b	0.92±0.14
HEAT repeat containing 6	Heatr6	0.22±0.03
heat shock 10 kDa protein 1 (chaperonin 10)	Hspe1	41.5±2.92
heat shock 105kDa/110kDa protein 1	Hsph1	6.31±1.32
heat shock 70kDa protein 12A (predicted)	Hspa12a_predicted	2.32±0.28
heat shock factor 2	Hsf2	4.17±0.34
heat shock factor binding protein 1	Hsbp1	9.07±0.56
heat shock protein 1 (chaperonin)	Hspd1	41.76±1.58
heat shock protein 14	Hspa14	0.95±0.13
heat shock protein 4	Hspa4	0.27±0.46
heat shock protein 5	Hspa5	29.47±9.51
heat shock protein 8	Hspa8	44.32±1.39
heat shock protein 9	Hspa9	15.99±0.51
heat shock protein 9	Hspa9 /// LOC500372	0.26±0.08
heat shock protein 90, alpha (cytosolic), class A member 1	Hsp90aa1	30.48±2.47
heat shock protein 90kDa alpha (cytosolic), class B member 1	Hsp90ab1	15.61±0.38
heat shock transcription factor 1	Hsf1	0.3±0.08
heat-responsive protein 12	Hrsp12	53.2±6.86
hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	Herc1_predicted	1.86±0.42
hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 (predicted)	Herc2_predicted	0.85±0.17
HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (predicted)	Hace1_predicted	0.6±0.22
hect domain and RLD 3 (predicted)	Herc3_predicted	2.2±0.17
hect domain and RLD 4	Herc4	2.71±0.33
HECT domain containing 1	Hectd1	6.32±0.2
helicase with zinc finger domain (predicted)	Helz_predicted	0.5±0.23
helicase-like transcription factor	Hltf	0.2±0.13
hematological and neurological expressed 1-like	Hn1l	3.29±0.11
hematological and neurological expressed sequence 1	Hn1	1.94±0.66
heme oxygenase (decycling) 2	Hmox2	4±0.31
HemK methyltransferase family member 1 (predicted)	Hemk1_predicted	0.38±0.17
hemoglobin, theta 1 (predicted)	Hbq1_predicted	0.55±0.06
heparan sulfate 2-O-sulfotransferase 1	Hs2st1	2.71±0.1
heparan sulfate 6-O-sulfotransferase 1 (predicted)	Hs6st1_predicted	1.83±0.27
hepatic nuclear factor 4, alpha	Hnf4a	2.49±0.39
hepatitis B virus x interacting protein (predicted)	Hbxip_predicted	22.67±1.55
hepatocyte growth factor activator	Hgfac	0.69±0.1
hepatoma-derived growth factor	Hdgf	2.62±0.39
hepatoma-derived growth factor, related protein 2	Hdgfrp2	0.74±0.06
hepsin	Hpn	4.61±0.64

Hermansky-Pudlak syndrome 1 homolog (human)	Hps1	3.34±0.52
Hermansky-Pudlak syndrome 3 homolog (human) (predicted)	Hps3_predicted	0.83±0.25
Hermansky-Pudlak syndrome 4 homolog (human) (predicted)	Hps4_predicted	0.64±0.06
HERPUD family member 2	Herpud2	2.27±0.22
heterochromatin protein 1, binding protein 3	Hp1bp3	4.23±0.41
heterogeneous nuclear ribonucleoprotein A/B	Hnrpab	11.28±2.9
heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	1.73±0.51
heterogeneous nuclear ribonucleoprotein A2/B1 /// similar to heterogeneous nuclear ribonucleoprotein A2/B1 (predicted)	Hnrnpa2b1 /// RGD1562992_predicted	2±0.81
heterogeneous nuclear ribonucleoprotein A3	Hnrpa3	19.89±2.28
heterogeneous nuclear ribonucleoprotein C	Hnrnpc	4.76±0.36
heterogeneous nuclear ribonucleoprotein D	Hnrpd	1.08±0.09
heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	2.26±0.42
heterogeneous nuclear ribonucleoprotein F	Hnrpf	5.18±0.57
heterogeneous nuclear ribonucleoprotein H1	Hnrph1	7.25±1.13
heterogeneous nuclear ribonucleoprotein H3	Hnrph3	0.45±0.32
heterogeneous nuclear ribonucleoprotein K	Hnrpk	18.37±1.36
heterogeneous nuclear ribonucleoprotein L	Hnrnpl	12.54±0.46
heterogeneous nuclear ribonucleoprotein L-like (predicted)	Hnrpll_predicted	2.07±0.14
heterogeneous nuclear ribonucleoprotein M	Hnrpm	1.93±0.5
heterogeneous nuclear ribonucleoprotein R	Hnrnpr	4.04±0.22
heterogeneous nuclear ribonucleoprotein U	Hnrnpu	6.04±0.7
heterogeneous nuclear ribonucleoprotein U-like 1 (predicted)	Hnrpul1_predicted	0.72±0.2
hexamethylene bis-acetamide inducible 1	Hexim1	9.52±0.75
hexosaminidase A	Hexa	32.74±4.67
hexosaminidase B	Hexb	42.38±1.97
hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (predicted)	H6pd_predicted	1.66±0.45
HGF-regulated tyrosine kinase substrate	Hgs	2.55±0.3
HIG1 domain family, member 1A	Higd1a	8.46±0.2
HIG1 domain family, member 2A (predicted)	Higd2a_predicted	9.67±0.67
high density lipoprotein binding protein	Hdlbp	5.28±0.43
high mobility group 20 B (predicted)	Hmg20b_predicted	0.57±0.15
high mobility group 20A (predicted)	Hmg20a_predicted	0.81±0.04
high mobility group AT-hook 1	Hmga1	0.31±0.21
high mobility group box 1	Hmgb1	10.94±0.92
high mobility group box 1	Hmgb1 /// LOC678705 /// LOC679571 /// LOC680765 /// LOC681718 /// RGD1562312_predicted /// RGD1563012_predicted /// RGD1563786_predicted	16.05±0.75
high mobility group box 2	Hmgb2	1.02±0.66
high mobility group box 3	Hmgb3	1.96±0.23
high mobility group box transcription factor 1	Hbp1	2.54±0.14
high mobility group nucleosomal binding domain 1	Hmgn1	20.54±1.67
high mobility group nucleosomal binding domain 2	Hmgn2	12.5±1.71
hippocalcin-like 1	Hpcal1	3±0.87
hippocampus abundant gene transcript 1 (predicted)	Hiat1_predicted	5.29±0.14
hippocampus abundant transcript-like 1	Hiatl1	3.8±0.07
HIRA interacting protein 3	Hirip3	0.49±0.19
histidine acid phosphatase domain containing 2A	Hisppd2a	0.6±0.2
histidine triad nucleotide binding protein 2 (predicted)	Hint2_predicted	18.64±2.14
histidine triad nucleotide binding protein 3	Hint3	3.52±0.09
histidine-rich glycoprotein	Hrg	3.4±0.43
histocompatibility 13 (predicted)	H13_predicted	3.18±0.54
histone aminotransferase 1	Hat1	3.05±0.85
histone cluster 1, H2bl /// histone cluster 1, H2bh /// histone cluster 1, H2bc /// similar to Histone H2B 291B	Hist1h2bc /// Hist1h2bh /// Hist1h2bl /// LOC682558 /// LOC684797	4.71±0.05
histone cluster 1, H4b	Hist1h4b	6.69±1.32
histone cluster 2, H2aa1 /// similar to H2A histone family, member O	Hist2h2aa1 /// LOC682560 /// LOC690131	0.28±0.27
histone cluster 3, H2a	Hist3h2a	1.58±0.06
histone deacetylase 1 (predicted)	Hdac1_predicted	0.29±0.13
histone deacetylase 1 /// histone deacetylase 1 (predicted)	Hdac1 /// Hdac1_predicted	0.52±0.19
histone deacetylase 2	Hdac2	4.71±0.08
histone deacetylase 3	Hdac3	2.94±0.42
histone deacetylase 5	Hdac5	0.34±0.16
histone deacetylase 8 (predicted)	Hdac8_predicted	0.3±0.18
histone H4 variant H4-v.1 (predicted)	RGD1562378_predicted	0.23±0.12
HIV TAT specific factor 1 (predicted)	Htatsf1_predicted	1.58±0.27
HIV-1 Rev binding protein 2 (predicted)	Hrb2_predicted	1.5±0.28
HIV-1 tat interactive protein, homolog (human)	Htatip	1.06±0.18
HLA-B associated transcript 5	Bat5	4.12±0.23
HLA-B-associated transcript 1A	Bat1a	3.43±0.98
HLA-B-associated transcript 3	Bat3	0.94±0.22
HNF1 homeobox A	Hnf1a	2.81±0.24
HNF1 homeobox B	Hnf1b	2.56±0.64
hnRNP-associated with lethal yellow	Raly	0.3±0.27
holocytochrome c synthetase (predicted)	Hccs_predicted	4.82±0.6
homeo box A10	Hoxa10	1.05±0.24
homeo box A4	Hoxa4	0.42±0.18

homeo box A5	Hoxa5	1.29±0.19
homeo box A9 (predicted)	Hoxa9_predicted	1.63±0.41
homeobox A9	Hoxa9	0.51±0.12
homeodomain interacting protein kinase 1 (predicted)	Hipk1_predicted	1.3±0.09
Homeodomain interacting protein kinase 2 (predicted)	Hipk2_predicted	4.24±1.28
homer homolog 1 (Drosophila)	Homer1	4.11±0.68
homer homolog 2 (Drosophila)	Homer2	0.96±0.1
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Herpud1	7.47±1.77
homogentisate 1, 2-dioxygenase	Hgd	11.39±0.85
homolog of zebrafish ES1	RGD1303003	6.25±0.72
hook homolog 1 (Drosophila) (predicted)	Hook1_predicted	11.2±0.42
hook homolog 2 (Drosophila)	Hook2	3.25±0.08
hook homolog 3 (Drosophila)	Hook3	1.89±0.11
hormone-regulated proliferation associated protein 20	Hrpap20	3.83±0.69
host cell factor C1 (predicted)	Hcfc1_predicted	1.68±0.44
host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	3.16±0.84
host cell factor C2	Hcfc2	1.22±0.23
HpaII tiny fragments locus 9c	Htf9c	0.95±0.15
HRAS like suppressor 3	Hrasls3	4.83±0.54
HscB iron-sulfur cluster co-chaperone homolog (E. coli)	Hscb	0.95±0.13
hsp70-interacting protein	Hspbp1	1.45±0.37
Hspb associated protein 1	Hspbap1	2.96±0.9
HtrA serine peptidase 1	Htra1	5.39±0.37
HtrA serine peptidase 2	Htra2	1.49±0.16
human immunodeficiency virus type I enhancer binding protein 1	Hivep1	0.3±0.12
human immunodeficiency virus type I enhancer binding protein 2	Hivep2	0.2±0.06
huntingtin interacting protein 1 related	Hip1r	0.62±0.11
huntingtin interacting protein 2 (predicted)	Hip2_predicted	8.84±0.91
Huntingtin interacting protein K	Hypk	5.1±0.71
HUS1 checkpoint homolog (S. pombe)	Hus1	1.31±0.35
hyaluronan mediated motility receptor (RHAMM)	Hmmr	0.74±0.3
hyaluronic acid binding protein 4 (predicted)	Habp4_predicted	2.12±0.18
hyaluronoglucosaminidase 2	Hyal2	0.85±0.11
hyaluronoglucosaminidase 3	Hyal3	0.82±0.33
hydroxyacid oxidase 1, liver	Hao1	1.97±0.71
hydroxyacid oxidase 2 (long chain)	Hao2	63.55±0.41
hydroxyacyl glutathione hydrolase	Hagh	17.99±1.54
hydroxyacyl-Coenzyme A dehydrogenase	Hadh	28.06±0.9
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Hadha	10.95±1.14
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Hadhb	23.88±0.6
hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Hsd3b7	0.41±0.09
hydroxymethylbilane synthase	Hmbs	2.18±0.3
hydroxyprostaglandin dehydrogenase 15 (NAD)	Hpgd	0.81±0.63
hydroxysteroid (17-beta) dehydrogenase 1	Hsd17b1	1.36±0.11
hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	17.42±2.21
hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	11.05±0.91
hydroxysteroid (17-beta) dehydrogenase 12	Hsd17b12	5.24±0.8
hydroxysteroid (17-beta) dehydrogenase 2	Hsd17b2	2.06±0.22
hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	18.63±0.65
hydroxysteroid (17-beta) dehydrogenase 8	Hsd17b8	2.83±0.92
hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	24.97±3.07
hydroxysteroid dehydrogenase like 2	Hsdl2	14.01±2.46
hyperpolarization-activated cyclic nucleotide-gated potassium channel 1	Hcn1	0.24±0.09
hypothetical gene supported by BC088439	LOC500947	1.06±0.08
hypothetical gene supported by NM_172157	LOC497729	3.1±1.08
hypothetical LOC100125371	LOC100125371	1.55±0.22
hypothetical LOC287306 (predicted)	RGD1307036_predicted	0.73±0.08
hypothetical LOC287388 (predicted)	RGD1310324_predicted	0.46±0.03
hypothetical LOC288978	LOC288978	0.5±0.05
hypothetical LOC290577	LOC290577	3.25±0.08
hypothetical LOC291982 (predicted) /// similar to autoantigen	LOC361399 /// RGD1309136_predicted	0.48±0.14
hypothetical LOC294030	RGD1305481	3.47±0.48
hypothetical LOC294883	RGD1305844	1±0.07
hypothetical LOC298018	LOC298018	0.31±0.17
hypothetical LOC301124	LOC301124	15.88±1.52
hypothetical LOC302495	LOC302495	0.71±0.15
hypothetical LOC304650 (predicted)	RGD1310262_predicted	2.53±0.12
hypothetical LOC305452 (predicted)	RGD1309634_predicted	0.62±0.12
hypothetical LOC305552 (predicted)	RGD1309501_predicted	0.25±0.07
hypothetical LOC306766	LOC306766	29.35±4.72
hypothetical LOC308765 (predicted) /// hypothetical protein LOC685841	LOC685841 /// RGD1311021_predicted	1.17±0.18
hypothetical LOC308869	MGC72560	7.08±0.59
hypothetical LOC310540	MGC72614	3.14±0.53
hypothetical LOC311134	LOC311134	0.49±0.06
hypothetical LOC361153	LOC361153	0.82±0.25
hypothetical LOC362564	LOC362564	0.91±0.25
hypothetical LOC366300	LOC366300	5.33±0.49
hypothetical LOC500532	LOC500532	1.37±0.33
hypothetical protein Dd25	Dd25	1.54±0.16
hypothetical protein LK44	RGD735140	1.16±0.06
hypothetical protein LOC100125364	rCG_22919	1.96±0.23
hypothetical protein LOC100125365	LOC100125365	1.03±0.46
hypothetical protein LOC292764	RGD1303117	0.53±0.11

hypothetical protein LOC303332	LOC303332	2.63±0.21
hypothetical protein LOC307347	LOC307347	7.39±0.51
Hypothetical protein LOC311254	LOC311254	0.99±0.07
hypothetical protein LOC361335	LOC361335	1.71±0.21
hypothetical protein LOC498154	LOC498154	0.79±0.15
hypothetical protein LOC498606	LOC498606	1.29±0.07
hypothetical protein LOC499120	LOC499120	1.18±0.13
hypothetical protein LOC499339	LOC499339	1.05±0.17
hypothetical protein LOC499602	LOC499602	0.31±0.09
hypothetical protein LOC500251	LOC500251	0.6±0.16
hypothetical protein LOC501546	LOC501546	3.07±0.17
hypothetical protein LOC502374	LOC502374	11.79±0.44
hypothetical protein LOC595134	LOC595134	1.89±0.08
hypothetical protein LOC606294	LOC606294	4.83±0.29
Hypothetical protein LOC619558	LOC619558	0.51±0.16
hypothetical protein LOC619574	LOC619574	0.74±0.13
Hypothetical protein LOC679802	LOC679802	0.25±0.04
hypothetical protein LOC679880	LOC679880	5.66±0.6
hypothetical protein LOC680039	LOC680039	1.97±0.19
Hypothetical protein LOC680080	LOC680080	4.81±0.27
hypothetical protein LOC680262	LOC680262	0.32±0.1
Hypothetical protein LOC680422	LOC680422	0.47±0.05
Hypothetical protein LOC680817	LOC296884	1.88±0.14
hypothetical protein LOC681219	LOC681219	11.14±1.2
hypothetical protein LOC681292	LOC681292	0.27±0.08
hypothetical protein LOC681367	LOC681367	3.13±0.06
hypothetical protein LOC682679	LOC682679	2.29±0.56
hypothetical protein LOC682709	LOC682709	3.84±0.4
hypothetical protein LOC682874	LOC682874	1.51±0.18
hypothetical protein LOC682888	LOC682888	4.6±0.64
hypothetical protein LOC683034	LOC683034	1.47±0.05
Hypothetical protein LOC683140	Ak1	1.12±0.34
hypothetical protein LOC683948	LOC683948	0.41±0.09
hypothetical protein LOC684830	LOC684830	0.77±0.22
hypothetical protein LOC684993	LOC684993	1.44±0.24
hypothetical protein LOC685203	LOC685203	7.8±1.43
hypothetical protein LOC685233 /// hypothetical protein LOC688211	LOC685233 /// LOC688211	0.34±0.11
hypothetical protein LOC685545	LOC685545	12.06±1.28
hypothetical protein LOC685548	LOC685548	12.67±1.09
hypothetical protein LOC685634	LOC685634	1.04±0.24
hypothetical protein LOC685888	LOC685888	3.12±0.21
hypothetical protein LOC686032	LOC686032	6.81±0.5
hypothetical protein LOC686120	LOC686120	2.55±0.78
hypothetical protein LOC686179	MGC125239	1.91±0.23
hypothetical protein LOC686796	LOC686796	0.41±0.12
hypothetical protein LOC687090	LOC687090	6.26±0.17
hypothetical protein LOC687361	LOC687361	0.85±0.11
hypothetical protein LOC687693	LOC687693	1.88±0.15
hypothetical protein LOC688211	LOC688211	0.91±0.21
hypothetical protein LOC688300	LOC688300	2.59±0.3
Hypothetical protein LOC688495	LOC688495	5.25±0.54
hypothetical protein LOC689147	LOC689147	7.88±0.74
Hypothetical protein LOC689165	LOC689165	0.51±0.02
hypothetical protein LOC689399	LOC689399	0.31±0.05
hypothetical protein LOC689574	LOC689574	8.46±1.75
hypothetical protein LOC689959	LOC689959	0.73±0.09
hypothetical protein LOC690243	LOC690243	1.27±0.27
hypothetical protein LOC690274	LOC690274	0.6±0.1
hypothetical protein LOC690349	LOC690349	1.76±0.17
hypothetical protein LOC690422	LOC690422	0.37±0.05
hypothetical protein LOC691543	LOC691543	0.83±0.02
hypothetical protein LOC691750	LOC691750	1.85±0.22
hypothetical protein LOC691807	rCG_28701	16.08±0.7
hypothetical protein LOC691849	LOC691849	2.36±0.12
hypothetical protein LOC692032	LOC692032	0.61±0.22
hypothetical protein MGC:15854	RGD1302996	2.95±0.69
hypothetical protein MGC:72616	RGD735175	0.97±0.3
hypothetical RNA binding protein RGD1359713	RGD1359713	9.8±1.28
hypoxanthine guanine phosphoribosyl transferase 1	Hprt1	11.57±0.75
hypoxia inducible factor 1, alpha subunit	Hif1a	7.61±0.13
hypoxia up-regulated 1	Hyou1	1.18±0.24
IAP promoted placental gene (predicted)	Ipp_predicted	2.88±0.22
iduronate 2-sulfatase	Ids	5.41±0.28
IK cytokine /// WD repeat domain 55	Ik /// Wdr55	0.95±0.41
IKAROS family zinc finger 5	Ikzf5	0.33±0.05
ilvB (bacterial acetolactate synthase)-like (predicted)	Ilvbl_predicted	2±0.24
immature colon carcinoma transcript 1 (predicted)	Ict1_predicted	4.59±0.53
immediate early response 5-like	Ier5l	0.23±0.23
immunoglobulin (CD79A) binding protein 1	Igbp1	3.24±0.53
immunoglobulin superfamily, member 11	Igsf11	24.72±2.36
immunoglobulin superfamily, member 3 (predicted)	Igsf3_predicted	0.2±0.11
IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (predicted)	Imp3_predicted	1.64±0.03
IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp4	6.53±0.53
importin 11 (predicted)	Ipo11_predicted	1.62±0.25
importin 13	Ipo13	0.8±0.23
importin 4 (predicted)	Ipo4_predicted	2.52±0.22

importin 7 (predicted)	Ipo7_predicted	7.46±0.93
Importin 9 (predicted)	Ipo9_predicted	2.83±0.33
imprinted and ancient	Impact	1.12±0.11
Indian hedgehog homolog, (Drosophila)	Ihh	0.74±0.04
indolethylamine N-methyltransferase	Inmt	1.22±1.21
influenza virus NS1A binding protein (predicted)	Ivns1abp_predicted	16.44±1.4
ing finger protein 5 pseudogene	rCG_38334	4.61±0.46
inhibitor of Bruton agammaglobulinemia tyrosine kinase (predicted)	Ibtk_predicted	1.56±0.25
inhibitor of DNA binding 2	Id2	5.46±0.12
inhibitor of DNA binding 4	Id4	8.18±1.78
inhibitor of growth family, member 1	Ing1	0.63±0.19
inhibitor of growth family, member 2	Ing2	1.2±0.08
inhibitor of growth family, member 4	Ing4	1.14±0.08
inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	Ikbkap	0.98±0.08
inhibitor of kappaB kinase beta	Ikbkb	1.18±0.12
inner membrane protein, mitochondrial	Immt	23.17±1.93
INO80 complex homolog 1 (S. cerevisiae)	Inoc1	0.56±0.18
inosine 5'-phosphate dehydrogenase 2	Impdh2	1.47±0.24
inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Itpa	3.28±0.35
Inositol (myo)-1(or 4)-monophosphatase 1	Impa1	4.28±0.32
inositol (myo)-1(or 4)-monophosphatase 2	Impa2	0.76±0.15
inositol 1,4,5-triphosphate receptor 1	Itpr1	8.63±0.9
inositol hexaphosphate kinase 1	Ihpk1	4.75±0.6
inositol hexaphosphate kinase 2	Ihpk2	1.09±0.23
inositol monophosphatase domain containing 1	Impad1	1.26±0.12
inositol polyphosphate multikinase	Ipmk	4.42±0.48
inositol polyphosphate phosphatase-like 1	Inppl1	0.56±0.38
inositol polyphosphate-1-phosphatase	Inpp1	1.66±0.38
inositol polyphosphate-4-phosphatase, type 1	Inpp4a	0.83±0.14
inositol polyphosphate-5-phosphatase B	Inpp5b	6.46±0.49
insulin degrading enzyme	Ide	1.59±0.4
insulin induced gene 1	Insig1	4.39±0.61
insulin induced gene 2	Insig2	1.91±0.11
insulin receptor substrate 2	Irs2	0.55±0.05
insulin-like growth factor 1 receptor	Igf1r	2.35±0.84
insulin-like growth factor 2 receptor	Igf2r	43.42±1.73
insulin-like growth factor binding protein 2	Igfbp2	0.72±0.3
insulin-like growth factor binding protein 4	Igfbp4	1.96±0.14
insulin-like growth factor binding protein 5	Igfbp5	11.8±1.87
insulin-like growth factor binding protein 7	Igfbp7	44.87±1.7
insulin-like growth factor binding protein, acid labile subunit	Igfals	2.54±0.45
integral membrane protein 2B	Itm2b	37.61±1.47
integral membrane transport protein UST5r	Ust5r	1.29±0.53
integrator complex subunit 10	Ints10	0.65±0.2
integrator complex subunit 4	Ints4	2.31±0.08
integrator complex subunit 5 (predicted)	Ints5_predicted	0.61±0.17
integrator complex subunit 6	Ints6	1.94±0.48
integrator complex subunit 7	Ints7	0.35±0.15
integrator complex subunit 9	Ints9	1.14±0.19
integrin alpha 1	Itga1	4.97±2.21
integrin alpha 7	Itga7	0.57±0.12
integrin alpha FG-GAP repeat containing 1	Itfg1	7.85±0.49
integrin alpha FG-GAP repeat containing 2	Itfg2	0.55±0.12
integrin alpha FG-GAP repeat containing 3	Itfg3	3.08±0.49
integrin alpha V (predicted)	Itgav_predicted	0.46±0.08
integrin beta 1 (fibronectin receptor beta)	Itgb1	4.51±0.2
integrin beta 1 binding protein 1 (predicted)	Itgb1bp1_predicted	4.36±0.52
integrin beta 3 binding protein (beta3-endonexin)	Itgb3bp	0.76±0.33
integrin linked kinase	Ilk	5.84±0.5
Integrin, alpha 6	Itga6	3.06±0.25
integrin, alpha E, epithelial-associated	Itgae	0.34±0.23
integrin, beta 5	Itgb5	1.77±0.34
integrin, beta 6	Itgb6	5.53±0.63
integrin-linked kinase-associated serine/threonine phosphatase 2C	Ilkap	1.36±0.09
interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted	0.66±0.2
interferon gamma induced GTPase	Igtp	2.36±0.04
interferon gamma inducible protein 30	Ifi30	15.4±1.86
interferon gamma receptor 1	Ifngr1	0.51±0.23
interferon gamma receptor 2 (predicted)	Ifngr2_predicted	0.59±0.24
interferon induced transmembrane protein 2	Ifitm2	6.65±1.29
interferon regulatory factor 2 binding protein 1 (predicted)	Irf2bp1_predicted	0.79±0.28
interferon regulatory factor 6 (predicted)	Irf6_predicted	0.98±0.3
interferon stimulated exonuclease gene 20-like 1 (predicted)	Isg20l1_predicted	0.55±0.12
interferon-induced protein 35	Ifi35	1.1±0.58
interferon-related developmental regulator 1	Ifrd1	3.75±0.91
interferon-related developmental regulator 2 (predicted)	Ifrd2_predicted	1.54±0.27
interleukin 1 receptor accessory protein	Il1rap	0.44±0.08
interleukin 10 receptor, beta	Il10rb	3.09±0.19
interleukin 13 receptor, alpha 1	Il13ra1	1.26±0.07
interleukin 15	Il15	0.51±0.3
interleukin 17 receptor A	Il17ra	0.88±0.23
interleukin 33	Il33	4.42±0.3
interleukin 4 receptor, alpha	Il4ra	1.04±0.17
interleukin 6 signal transducer	Il6st	1.08±0.38
interleukin enhancer binding factor 2	Ilf2	3.08±0.03
interleukin enhancer binding factor 3	Ilf3	0.25±0.1
interleukin-1 receptor-associated kinase 1 (predicted)	Irak1_predicted	4.92±0.24

interleukin-1 receptor-associated kinase 1 binding protein 1 (predicted)	Irak1bp1_predicted	2.86±0.16
interleukin-1 receptor-associated kinase 2	Irak2	1.93±0.34
intersectin 1	Itsn1	0.39±0.1
intersectin 2	Itsn2	2.67±0.51
intraflagellar transport 172 homolog (Chlamydomonas)	Ift172	1.22±0.15
intraflagellar transport 20 homolog (Chlamydomonas)	Ift20	2.63±0.49
intraflagellar transport 57 homolog (Chlamydomonas) (predicted)	Ift57_predicted	0.92±0.14
intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	0.43±0.05
intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	0.74±0.11
intraflagellar transport 88 homolog (Chlamydomonas) (predicted)	Ift88_predicted	0.66±0.06
invasion inhibitory protein 45	Iip45	0.48±0.15
inversin	Invs	0.46±0.14
iodotyrosine deiodinase	Iyd	7.43±0.54
Ion transporter protein	Nritp	8.16±0.83
IQ motif and ubiquitin domain containing	Iqub	1.07±0.12
IQ motif and WD repeats 1	Iqwd1	0.59±0.1
Iron responsive element binding protein 2	Ireb2	2.41±0.09
iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	Isca1	7.19±0.84
ischemia related factor NYW-1	Nyw1	0.6±0.07
IscU iron-sulfur cluster scaffold homolog (E. coli)	Iscu	19.07±1.48
isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	Iah1	22.79±2.01
isochorismatase domain containing 1	Isoc1	7.91±0.28
isochorismatase domain containing 2b	Isoc2b	1.87±0.49
isocitrate dehydrogenase 1 (NADP+), soluble	Idh1	51.17±3.83
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	45.47±2.36
isocitrate dehydrogenase 3 (NAD), gamma	Idh3g	33.16±2.43
isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	9.01±1.1
isocitrate dehydrogenase 3 (NAD+) beta	Idh3B	20.71±1.62
isoleucine-tRNA synthetase (predicted)	Iars_predicted	1.64±0.28
isoleucine-tRNA synthetase 2, mitochondrial (predicted)	Iars2_predicted	2.23±0.14
isopentenyl-diphosphate delta isomerase	Idi1	6.29±0.57
isoprenylcysteine carboxyl methyltransferase	Icmt	0.99±0.15
isovaleryl coenzyme A dehydrogenase	Ivd	9.38±0.94
ISY1 splicing factor homolog (S. cerevisiae)	Isy1	0.84±0.18
IWS1 homolog (S. cerevisiae)	Iws1	2.17±0.18
jagunal homolog 1 (Drosophila)	Jagn1	2.76±0.56
Janus kinase 1	Jak1	3.01±0.42
Janus kinase 2	Jak2	0.9±0.15
Josephin domain containing 1	Josd1	1.01±0.37
Josephin domain containing 2 (predicted)	Josd2_predicted	0.7±0.16
Josephin domain containing 3	Josd3	0.7±0.04
JTV1 gene	Jtv1	1.47±0.05
jumonji domain containing 1A	Jmjd1a	1.31±0.11
jumonji domain containing 1C	Jmjd1c	1.47±0.48
jumonji domain containing 5	Jmjd5	0.93±0.11
jumonji domain containing 6	Jmjd6	0.9±0.13
jumonji, AT rich interactive domain 1B (Rbp2 like)	Jarid1b	1.19±0.26
jumping translocation breakpoint	Jtb	2.96±0.36
Jun D proto-oncogene	Jund	6.17±2.49
Jun oncogene	Jun	2.81±1.94
Junction adhesion molecule 2	Jam2	0.4±0.15
junction plakoglobin	Jup	1.26±0.36
junctional adhesion molecule 3	Jam3	0.38±0.17
kalirin, RhoGEF kinase	Kalrn	0.77±0.1
kaptin	Kptn	1.2±0.35
Karyopherin (importin) alpha 1	Kpna1	3.14±0.32
karyopherin (importin) alpha 2	Kpna2	4.4±0.58
Karyopherin (importin) alpha 3	Kpna3	1.79±0.08
karyopherin (importin) alpha 6	Kpna6	0.47±0.08
karyopherin (importin) beta 1	Kpnb1	0.39±0.21
katanin p60 (ATPase-containing) subunit A1	Katna1	0.61±0.23
KDEL (Lys-Asp-Glu-Leu) containing 1	Kdelc1	0.76±0.05
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	Kdelr1	8.52±0.4
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Kdelr2	5.54±0.4
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted)	Kdelr3_predicted	7.88±0.9
kelch domain containing 1 (predicted)	Klhdc1_predicted	0.39±0.1
kelch domain containing 2	Klhdc2	4.27±0.46
kelch domain containing 3	Klhdc3	1.66±0.98
kelch domain containing 5	Klhdc5	0.7±0.13
kelch repeat and BTB (POZ) domain containing 2 (predicted)	Kbtbd2_predicted	1.98±0.41
kelch repeat and BTB (POZ) domain containing 3 (predicted)	Kbtbd3_predicted	0.48±0.15
kelch repeat and BTB (POZ) domain containing 4 (predicted)	Kbtbd4_predicted	1.01±0.19
kelch-like 14 (Drosophila)	Klhl14	0.74±0.06
kelch-like 2, Mayven (Drosophila) (predicted)	Klhl2_predicted	0.52±0.09
kelch-like 22 (Drosophila) (predicted)	Klhl22_predicted	3.84±0.26
kelch-like 23 (Drosophila) (predicted)	Klhl23_predicted	1.49±0.31
kelch-like 24 (Drosophila)	Klhl24	6.72±0.51
kelch-like 25 (Drosophila)	Klhl25	3.7±0.08
kelch-like 26 (Drosophila) (predicted)	Klhl26_predicted	0.26±0.03
kelch-like 7 (Drosophila)	Klhl7	1.49±0.58
kelch-like 8 (Drosophila) (predicted)	Klhl8_predicted	0.9±0.03
kelch-like 9 (Drosophila) (predicted)	Klhl9_predicted	5.45±0.43
Kelch-like ECH-associated protein 1	Keap1	0.89±0.32
keratin 10	Krt10	0.51±0.06
keratin 7	Krt7	9.11±1.51
keratin 8	Krt8	10.06±1.69
keratinocyte associated protein 2 (predicted)	Krtcap2_predicted	5.8±0.65

ketohexokinase	Khk	18.78±2.53
KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	4.47±0.2
KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	0.29±0.04
KH-type splicing regulatory protein	Khsrp	0.49±0.95
kidney androgen regulated protein	Kap	35.17±5.66
kidney expressed gene 1	Keg1	2.09±0.42
kidney predominant protein NCU-G1	RGD1303130	30.1±1.91
kinase D-interacting substrate of 220 kDa	Kidins220	5.26±0.94
kinectin 1 (predicted)	Ktn1_predicted	2.65±0.54
kinesin family member 11	Kif11	5.97±0.44
kinesin family member 12	Kif12	7.58±0.87
kinesin family member 13A (predicted)	Kif13a_predicted	0.95±0.08
kinesin family member 16B (predicted)	Kif16b_predicted	1.84±0.15
kinesin family member 21A (predicted)	Kif21a_predicted	3.61±0.27
kinesin family member 22	Kif22	0.33±0.04
kinesin family member 2A	Kif2a	1.22±0.23
kinesin family member 3a	Kif3a	0.46±0.07
kinesin family member 3B (predicted)	Kif3b_predicted	2.09±0.08
kinesin family member 5B	Kif5b	0.57±0.2
kinesin family member C1	Kifc1	1.05±0.09
kinesin family member C2	KIFC2	4.11±0.5
kinesin family member C3	Kifc3	0.92±0.13
Kinesin heavy chain family, member 2	Kif2	0.33±0.09
kinesin light chain 1	Klc1	1.3±0.14
kinesin light chain 2 (predicted)	Klc2_predicted	1.52±0.34
kinesin light chain 4	Klc4	6.6±0.1
kinesin-associated protein 3 (predicted)	Kifap3_predicted	2.64±0.34
KiSS-1 metastasis-suppressor /// golgi transport 1 homolog A (S. cerevisiae)	Golt1a /// Kiss1	2.04±0.29
Klotho	Kl	1.46±0.27
KRAB-A domain containing 1	Krba1	0.44±0.1
KRIT1, ankyrin repeat containing (predicted)	Krit1_predicted	0.91±0.19
Kruppel-like factor 13	Klf13	0.24±0.16
Kruppel-like factor 15	Klf15	4.53±0.52
Kruppel-like factor 3 (basic)	Klf3	1.48±0.22
Kruppel-like factor 6	Klf6	0.75±0.11
Kruppel-like factor 9	Klf9	13.84±0.79
KTEL (Lys-Tyr-Glu-Leu) containing 1	Ktelc1	1.15±0.18
KTI12 homolog, chromatin associated (S. cerevisiae)	Kti12	2.07±0.19
kynureninase (L-kynurenine hydrolase)	Kynu	10.65±0.65
kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	Kmo	10.18±0.83
kynurenine aminotransferase III	Kat3	1.89±0.34
L antigen family, member 3	Lage3	8.12±0.64
l(3)mbt-like 2 (Drosophila)	L3mbtl2	0.76±0.15
l(3)mbt-like 3 (Drosophila) (predicted)	L3mbtl3_predicted	0.57±0.15
L-2-hydroxyglutarate dehydrogenase (predicted)	L2hgdh_predicted	1.28±0.13
La ribonucleoprotein domain family, member 1 (predicted)	Larp1_predicted	3.88±2.98
La ribonucleoprotein domain family, member 5 (predicted)	Larp5_predicted	4.51±1.59
lactamase, beta (predicted)	Lactb_predicted	2.51±0.16
Lactamase, beta 2	Lactb2	20.59±1.33
lactate dehydrogenase A	Ldha	5.11±1.26
lactate dehydrogenase B	Ldhb	53.64±1.76
lactate dehydrogenase D	Ldhd	5.02±0.78
lactation elevated 1	Lace1	5.74±0.51
ladinin (predicted)	Lad1_predicted	0.95±0.1
LAG1 homolog, ceramide synthase 1 /// growth differentiation factor 1 (predicted)	Gdf1_predicted /// Lass1	1.9±0.03
lamin A	Lmna	1.82±0.4
lamin B receptor	Lbr	0.83±0.13
laminin, alpha 1	Lama1	2.07±0.32
laminin, alpha 3	Lama3	0.65±0.18
laminin, alpha 5	Lama5	0.33±0.24
laminin, beta 1	Lamb1	4.49±0.43
lanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	2.44±0.53
LanC (bacterial lantibiotic synthetase component C)-like 2 (predicted)	Lancl2_predicted	1.44±0.04
Lanosterol synthase	Lss	1.07±0.26
large subunit GTPase 1 homolog (S. cerevisiae)	Lsg1	0.35±0.07
large subunit ribosomal protein L36a	LOC685642 /// LOC687717 /// LOC691991 /// RGD1566235_predicted /// Rpl36a /// Rpl36a_predicted	12.34±0.23
large subunit ribosomal protein L36a	LOC687717 /// LOC691991 /// RGD1566235_predicted /// Rpl36a /// Rpl36a_predicted	9.27±1.69
LAS1-like (S. cerevisiae) (predicted)	Las1l_predicted	0.74±0.12
latent transforming growth factor beta binding protein 4	Ltbp4	0.54±0.1
latrophilin 1	Lphn1	2.83±0.63
latrophilin 2	Lphn2	1±0.25
LEA_4 domain containing protein RGD1359600	RGD1359600	3.48±0.27
lectin, galactose binding, soluble 8	Lgals8	9.93±0.09
lectin, galactoside-binding, soluble 2	Lgals2	1.65±0.1
lectin, mannose-binding 2 (predicted)	Lman2_predicted	13.18±1.53
Lectin, mannose-binding 2-like (predicted)	Lman2l_predicted	1.98±0.33
lectin, mannose-binding, 1	Lman1	0.28±0.25
legumain	Lgmn	65.54±3.06

LEM domain containing 2	Lemd2	0.54±0.15
LEM domain containing 3	Lemd3	0.45±0.21
Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Leo1	0.48±0.12
leprecan 1	Lepre1	0.79±0.15
leptin receptor overlapping transcript	Leprot	1.57±0.3
leptin receptor overlapping transcript-like 1	Leprotl1	2.74±0.7
leucine aminopeptidase 3	Lap3	5.59±0.58
leucine carboxyl methyltransferase 1	Lcmt1	1.11±0.42
leucine rich repeat (in FLII) interacting protein 2	Lrrfip2	0.76±0.22
leucine rich repeat and sterile alpha motif containing 1	Lrsam1	0.35±0.14
leucine rich repeat containing 14	Lrrc14	0.9±0.2
leucine rich repeat containing 16	Lrrc16	2.05±0.21
leucine rich repeat containing 19	Lrrc19	32.26±0.78
leucine rich repeat containing 20	Lrrc20	0.25±0.05
leucine rich repeat containing 27	Lrrc27	0.73±0.07
leucine rich repeat containing 28 (predicted)	Lrrc28_predicted	0.68±0.11
leucine rich repeat containing 40	Lrrc40	1.4±0.35
leucine rich repeat containing 41	Lrrc41	1.46±0.16
leucine rich repeat containing 42	Lrrc42	1.12±0.18
leucine rich repeat containing 48	Lrrc48	0.36±0.03
leucine rich repeat containing 57	Lrrc57	0.74±0.01
leucine rich repeat containing 59	Lrrc59	5.94±0.51
leucine rich repeat containing 61	Lrrc61	0.44±0.09
leucine rich repeat containing 8 family, member B	Lrrc8b	5.89±0.19
leucine rich repeat containing 8 family, member E	Lrrc8e	0.28±0.07
leucine rich repeat containing 8D	Lrrc8d	11.22±1.69
leucine zipper and CTNNBIP1 domain containing	Lzic	0.4±0.07
leucine zipper protein 1	Luzp1	0.23±0.18
leucine zipper transcription factor-like 1	Lztfl1	11.51±0.83
leucine zipper-EF-hand containing transmembrane protein 1	Letm1	3.43±0.88
leucine-rich PPR-motif containing	Lrpprc	10.54±0.36
leucine-rich repeat-containing G protein-coupled receptor 4	Lgr4	1.49±0.44
leucine-rich repeats and immunoglobulin-like domains 3	Lrig3	0.62±0.17
leucine-zipper-like transcriptional regulator, 1 (predicted)	Lztr1_predicted	1.89±0.1
leucyl-tRNA synthetase	Lars	2.9±0.54
leukocyte cell-derived chemotaxin 2 (predicted)	Lect2_predicted	0.29±0.03
leukocyte receptor cluster (LRC) member 1 (predicted)	Leng1_predicted	0.2±0.05
leukocyte receptor cluster (LRC) member 4 (predicted)	Leng4_predicted	2.75±0.11
leukotriene A4 hydrolase	Lta4h	5.07±0.08
leukotriene B4 12-hydroxydehydrogenase	Ltb4dh	4.43±0.94
ligand of numb-protein X 2 (predicted)	Lnx2_predicted	1.05±0.21
ligase I, DNA, ATP-dependent	Lig1	0.4±0.11
ligase III, DNA, ATP-dependent	Lig3	0.44±0.14
LIM and cysteine-rich domains 1 (predicted)	Lmcd1_predicted	0.61±0.06
LIM and senescent cell antigen like domains 2	Lims2	7.78±0.68
LIM and SH3 protein 1	Lasp1	9.8±1.02
LIM domain binding 1 (predicted)	Ldb1_predicted	1.14±0.09
LIM domain containing preferred translocation partner in lipoma	Lpp	0.41±0.15
LIM domain only 4	Lmo4	14.63±1.86
LIM domain only 7	Lmo7	1.34±0.2
LIM domain only protein 7	LMO7	2.65±0.87
LIM domains containing 1 (predicted)	Limd1_predicted	0.81±0.21
limkain b1	Lkap	0.72±0.2
lin-37 homolog (C. elegans)	Lin37	0.6±0.37
lin-7 homolog C (C. elegans)	Lin7c	0.4±0.04
lipase maturation factor 1	Lmf1	1.07±0.07
lipin 2 (predicted)	Lpin2_predicted	1.89±0.43
lipin 3	Lpin3	0.92±0.29
lipoic acid synthetase	Lias	3.99±0.42
lipolysis stimulated lipoprotein receptor	Lsr	1.19±0.13
lipoma HMGIC fusion partner-like 2 (predicted)	Lhfpl2_predicted	3.05±0.23
liver glycogen phosphorylase	Pygl	7.18±0.42
LMBR1 domain containing 1	Lmbrd1	8.08±1.59
LOC360590 (predicted)	RGD1311564_predicted	0.23±0.09
LOC360807	LOC360807	2.84±0.41
LOC361485 /// similar to chromosome 6 open reading frame 70 (predicted)	RGD1309374 /// RGD1562376_predicted	0.85±0.21
LOC361614 (predicted)	RGD1308929_predicted	0.86±0.03
LOC361719 (predicted)	RGD1308106_predicted	0.26±0.07
LOC361774 (predicted)	RGD1306116_predicted	0.75±0.15
LOC362678 (predicted)	RGD1308923_predicted	1.31±0.09
LOC362793	RGD1307315	0.3±0.14
LOC363015 (predicted)	RGD1310444_predicted	0.61±0.24
LOC363020 (predicted)	RGD1309410_predicted	2.38±0.51
LOC500651	MGC112883	4.23±0.16
lon peptidase 1, mitochondrial	Lonp1	3.79±0.47
lon peptidase 2, peroxisomal	Lonp2	18.18±1.38
Longevity assurance homolog 2 (S. cerevisiae)	Lass2	7.28±0.53
low density lipoprotein receptor adaptor protein 1	Ldlrap1	0.24±0.05
low density lipoprotein receptor-related protein 11 (predicted)	Lrp11_predicted	6.87±0.06
low density lipoprotein receptor-related protein 2	Lrp2	51.16±1.49
low density lipoprotein receptor-related protein 3	Lrp3	1.23±0.09
low density lipoprotein receptor-related protein 4	Lrp4	1.26±0.14
low density lipoprotein receptor-related protein 6 (predicted)	Lrp6_predicted	0.48±0.12
low density lipoprotein receptor-related protein associated protein 1	Lrpap1	26.32±2.53
low density lipoprotein-related protein 12 (predicted)	Lrp12_predicted	0.46±0.06
low-density lipoprotein receptor-related protein 10	Lrp10	8.62±1.04

LPS-induced TN factor	Litaf	6.73±1.05
LPS-responsive beige-like anchor (predicted)	Lrba_predicted	1.96±0.4
LRRGT00141	LOC499235	4.45±0.31
LSM domain containing 1	Lsmd1	9.28±0.89
LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm1_predicted	1.36±0.4
LSM12 homolog (S. cerevisiae)	Lsm12	3.71±0.82
LSM14 homolog A (SCD6, S. cerevisiae) (predicted)	Lsm14a_predicted	3.89±0.37
LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm3_predicted	2.45±0.44
LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm4_predicted	1.79±0.45
LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm5_predicted	2.17±0.21
LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm6	3.19±0.86
LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm7_predicted	1.24±0.06
LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm8_predicted	1.03±0.13
LTV1 homolog (S. cerevisiae)	Ltv1	1.41±0.23
LUC7-like (S. cerevisiae)	Luc7l	1.36±0.13
LUC7-like 2 (S. cerevisiae) (predicted)	Luc7l2_predicted	3.2±0.39
lung-inducible neuralized-related C3HC4 RING domain protein	Lincr	1.06±0.23
luteinizing hormone beta	Lhb	0.64±0.06
Ly1 antibody reactive clone	Lyar	0.71±0.1
lymphocyte antigen 6 complex, locus B	Ly6b	1.53±0.76
lymphocyte antigen 96	Ly96	0.49±0.14
lymphotoxin B receptor	Ltbr	2.13±0.65
LYR motif containing 1	Lyrm1	1.29±0.24
lysine-rich coiled-coil 1	Krcc1	5.06±0.33
LysM, putative peptidoglycan-binding, domain containing 1	Lysmd1	0.46±0.06
LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	1.2±0.02
lysophospholipase 1	Lypla1	29.39±1.32
lysophospholipase 2	Lypla2	0.55±0.03
lysophospholipase 3	Lypla3	3.09±0.31
lysophospholipase-like 1 (predicted)	Lyplal1_predicted	4.95±0.36
lysosomal acid lipase A	Lipa	4.57±0.84
lysosomal membrane glycoprotein 1	Lamp1	47.74±3.45
lysosomal membrane glycoprotein 2	Lamp2	48.1±4.48
lysosomal-associated protein transmembrane 4A	Laptm4a	26.22±1.08
lysosomal-associated protein transmembrane 4B	Laptm4b	5.58±0.77
lysozyme-like 6 (predicted)	Lyzl6_predicted	0.48±0.03
lysyl-tRNA synthetase	Kars	3.71±0.36
MACRO domain containing 1	Macrod1	2.46±0.9
macrophage erythroblast attacher	Maea	5.57±0.48
macrophage migration inhibitory factor	Mif	23.63±4.83
MAD homolog 1 (Drosophila)	Smad1	0.57±0.27
MAD homolog 2 (Drosophila)	Smad2	0.71±0.19
MAD homolog 4 (Drosophila)	Smad4	2.73±0.17
MAD homolog 5 (Drosophila)	Smad5	0.45±0.13
MAD homolog 7 (Drosophila)	Smad7	0.23±0.06
MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (predicted)	Mad2l1_predicted	0.52±0.14
MAD2 mitotic arrest deficient-like 2 (yeast)	Mad2l2	0.78±0.05
MAD2L1 binding protein	Mad2l1bp	0.58±0.14
maestro	Mro	16.86±0.82
MAF1 homolog (S. cerevisiae)	Maf1	4.02±0.5
magnesium transporter 1	Magt1	2.84±0.34
magnesium-dependent phosphatase 1	Mdp1	0.97±0.11
mago-nashi homolog, proliferation-associated (Drosophila) (predicted)	Magoh_predicted	4.73±0.57
major facilitator superfamily domain containing 1 (predicted)	Mfsd1_predicted	6.2±0.56
major facilitator superfamily domain containing 3	Mfsd3	1.14±0.38
major facilitator superfamily domain containing 9	Mfsd9	0.24±0.15
major histocompatibility complex, class II, DM alpha	Hla-dma	0.75±0.38
major histocompatibility complex, class II, DM beta	Hla-dmb	3.74±1.35
major vault protein	Mvp	3.76±0.76
MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	Mak10	2.9±0.39
makorin, ring finger protein, 2	Mkrn2	0.56±0.14
malate dehydrogenase 1, NAD (soluble)	Mdh1	51.38±0.58
malate dehydrogenase 2, NAD (mitochondrial)	Mdh2	17.73±1
male-enhanced antigen 1	Mea1	6.14±1.8
male-specific lethal 2-like 1 (Drosophila) (predicted)	Msl2l1_predicted	2.15±0.23
male-specific lethal-3 homolog 1 (Drosophila)	Msl31	2.11±0.32
malic enzyme 1, NADP(+)-dependent, cytosolic	Me1	1.58±0.62
malic enzyme 3, NADP(+)-dependent, mitochondrial (predicted)	Me3_predicted	0.29±0.06
malignant T cell amplified sequence 1	Mcts1	5.6±0.52
malignant T cell amplified sequence 2	Mcts2	2.01±0.62
malonyl-CoA decarboxylase	Mlycd	1.25±0.05
mannose phosphate isomerase (mapped)	Mpi	3.36±0.16
mannose-6-phosphate protein p76	P76	5.95±1.05
mannose-6-phosphate receptor binding protein 1	M6prbp1	3.32±1.84
mannose-6-phosphate receptor, cation dependent	M6pr	16.32±2.08
mannose-P-dolichol utilization defect 1	Mpdu1	3.52±0.4
mannosidase 1, alpha (predicted)	Man1a_predicted	7.37±1.14
mannosidase 2, alpha 1	Man2a1	1.08±0.18
mannosidase 2, alpha B1	Man2b1	18±2.07
mannosidase, alpha, class 1A, member 2 (predicted)	Man1a2_predicted	0.34±0.05
mannosidase, alpha, class 1B, member 1	Man1b1	2.6±0.17
mannosidase, alpha, class 2C, member 1	Man2c1	2.65±1.13
mannosidase, beta A, lysosomal	Manba	6.75±0.72
mannosidase, beta A, lysosomal-like	Manbal	2.18±0.18
mannoside acetylglucosaminyltransferase 1	Mgat1	1.16±0.09
mannoside acetylglucosaminyltransferase 2	Mgat2	3.64±0.51
mannoside acetylglucosaminyltransferase 4, isoenzyme B	Mgat4b	2.73±0.53

MAP kinase-activated protein kinase 2	Mapkapk2	1.54±1.63
MAP kinase-activated protein kinase 5	Mapkapk5	1.4±0.04
MAP kinase-interacting serine/threonine kinase 1	Mknk1	0.48±0.1
MAP kinase-interacting serine/threonine kinase 2	Mknk2	0.93±0.12
MAP/microtubule affinity-regulating kinase 2	Mark2	1.52±0.53
MAP/microtubule affinity-regulating kinase 3	Mark3	5.58±0.15
MAP3K12 binding inhibitory protein 1 (predicted)	Mbip_predicted	0.26±0.07
MAP-kinase activating death domain	Madd	0.44±0.16
maternal G10 transcript	G10	3.73±0.23
matrin 3	Matr3	9.12±0.32
matrix metallopeptidase 11	Mmp11	1.99±0.25
matrix-remodelling associated 8	Mxra8	3.97±0.3
max binding protein (predicted)	Mnt_predicted	0.66±0.17
Max dimerization protein 4 (predicted)	Mxd4_predicted	0.77±0.27
MAX gene associated	Mga	0.84±0.06
Max interacting protein 1	Mxi1	5.3±0.95
Max protein	Max	2.79±0.37
MAX-like protein X	Mlx	4.2±0.09
MCF.2 cell line derived transforming sequence-like	Mcf2l	0.28±0.05
McKusick-Kaufman syndrome protein	Mkks	4.3±1.16
Meckel syndrome, type 1	Mks1	0.44±0.17
mediator complex subunit 1	Med1	0.9±0.08
mediator complex subunit 13	Med13	0.87±0.04
mediator complex subunit 13-like	Med13l	0.94±0.28
mediator complex subunit 14	Med14	1.87±0.33
mediator complex subunit 15	Med15	0.57±0.15
mediator complex subunit 16	Med16	2.22±0.5
mediator complex subunit 17	Med17	1.2±0.18
mediator complex subunit 20 /// similar to ubiquitin specific protease 49 (predicted)	LOC501098 /// Med20	1.64±0.25
mediator complex subunit 21	Med21	1.51±0.32
mediator complex subunit 22	Med22	0.83±0.12
mediator complex subunit 23	Med23	1.95±0.19
mediator complex subunit 24	Med24	2.16±0.59
mediator complex subunit 29	Med29	1.48±0.41
mediator complex subunit 30 (predicted)	Med30_predicted	0.78±0.2
mediator of cell motility 1	Memo1	4.23±0.13
mediator of DNA damage checkpoint 1	Mdc1	0.26±0.11
mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae)	Med10	1.5±0.26
mediator of RNA polymerase II transcription, subunit 11 homolog (S. cerevisiae)	Med11	2.03±0.14
mediator of RNA polymerase II transcription, subunit 19 homolog (yeast) (predicted)	Med19_predicted	0.52±0.07
mediator of RNA polymerase II transcription, subunit 28 homolog (yeast) (predicted)	Med28_predicted	6.86±0.34
mediator of RNA polymerase II transcription, subunit 31 homolog (yeast) (predicted)	Med31_predicted	3.5±0.5
mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	Med4	1.29±0.4
mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (predicted)	Med6_predicted	4.02±0.18
mediator of RNA polymerase II transcription, subunit 8 homolog (yeast) (predicted)	Med8_predicted	0.7±0.09
melanocyte proliferating gene 1	Myg1	1.41±0.2
melanoma antigen, family D, 1	Maged1	4.68±0.35
melanoma antigen, family H, 1	Mageh1	2.54±0.58
melanoma nuclear protein 13 /// similar to CG3420-PA	LOC688169 /// Mel13	8.85±0.93
melanophilin	Mlph	3.05±0.77
membralin	Mbrl	1.03±0.29
membrane associated guanylate kinase, WW and PDZ domain containing 1	Magi1	0.27±0.05
membrane associated guanylate kinase, WW and PDZ domain containing 3	Magi3	0.84±0.04
membrane bound O-acyltransferase domain containing 5	Mboat5	6.12±0.71
membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	6.59±0.38
membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (predicted)	Mpp6_predicted	4.06±0.62
Membrane-associated DHHC1 zinc finger protein	LOC291967	0.24±0.09
membrane-associated ring finger (C3HC4) 2	March2	10.56±0.44
membrane-associated ring finger (C3HC4) 3	March3	0.21±0.06
membrane-associated ring finger (C3HC4) 5 (predicted)	March5_predicted	8.58±1.13
Membrane-associated ring finger (C3HC4) 7	March7	5.87±0.69
membrane-associated ring finger (C3HC4) 8 (predicted)	March8_predicted	3.59±0.23
membrane-bound transcription factor peptidase, site 1	Mbtps1	2.19±0.15
menage a trois 1	Mnat1	0.59±0.22
Meningioma expressed antigen 5 (hyaluronidase)	Mgea5	3.18±0.47
meprin 1 alpha	Mep1a	22.14±3.28
mercaptopyruvate sulfurtransferase	Mpst	20.37±3.58
mesoderm development candidate 2	Mesdc2	6.5±1.3
mesoderm induction early response 1 homolog (Xenopus laevis)	Mier1	0.21±0.04
mesoderm induction early response 1, family member 3	Mier3	1.01±0.11
met proto-oncogene	Asz1 /// Cav1 /// Cav2 /// Cttnbp2 /// Met /// ST7 /// Wnt2	1.75±0.49
metadherin	Mtdh	5.25±0.78
metal response element binding transcription factor 1 (predicted)	Mtf1_predicted	1.13±0.51
metal response element binding transcription factor 2	Mtf2	1.2±0.11
metallophosphoesterase 1 (predicted)	Mppe1_predicted	1.2±0.16
metallothionein 1a	Mt1a	43.13±5.43
metallothionein 2A	Mt2A	23.85±1.01
metastasis associated 1	Mta1	0.5±0.1
metastasis suppressor 1 (predicted)	Mtss1_predicted	15.88±0.64
metastasis-associated gene family, member 2	Mta2	0.84±0.14
metaxin 2	Mtx2	5.43±0.11
meteorin, glial cell differentiation regulator	Metrn	0.32±0.46
methionine adenosyltransferase II, alpha	Mat2a	11.4±3.98
methionine aminopeptidase 2	Metap2	6.36±0.74
methionine aminopeptidase-like 1 (predicted)	Metapl1_predicted	0.56±0.07

methionine sulfoxide reductase A	Msra	9.75±1.64
methionine sulfoxide reductase B2	Msrb2	3.17±0.47
methionine-tRNA synthetase 2 (mitochondrial) (predicted)	Mars2_predicted	1.52±0.28
methionyl aminopeptidase 1 (predicted)	Metap1_predicted	2.61±0.37
methyl-CpG binding domain protein 1	Mbd1	0.74±0.21
methyl-CpG binding domain protein 2	Mbd2	9.66±1.45
methyl-CpG binding domain protein 3 (predicted)	Mbd3_predicted	3.9±0.88
methyl-CpG binding domain protein 6 (predicted)	Mbd6_predicted	0.48±0.02
methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mccc1	3.95±0.52
methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mccc2	14.38±0.93
methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	Mthfd1	18.55±0.69
methylmalonic aciduria (cobalamin deficiency) cblA type	Mmaa	0.68±0.08
methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	Mmachc	2.95±0.39
methylmalonyl CoA epimerase (predicted)	Mcee_predicted	5.83±0.34
methylmalonyl-Coenzyme A mutase	Mut	8.92±0.7
methylphosphate capping enzyme	Mepce	0.62±0.21
Methylthioadenosine phosphorylase (predicted)	Mtap_predicted	0.58±0.08
methyltransferase 10 domain containing	Mett10d	0.74±0.04
methyltransferase like 10	Mettl10	0.82±0.1
methyltransferase like 2 (predicted)	Mettl2_predicted	0.38±0.12
methyltransferase like 5	Mettl5	2.56±0.66
methyltransferase like 6	Mettl6	0.38±0.02
methyltransferase like 7B	Mettl7b	4.61±0.76
methyltransferase-like 3	Mettl3	1.4±0.12
mevalonate kinase	Mvk	0.61±0.13
microfibrillar-associated protein 3	Mfap3	0.87±0.1
microfibrillar-associated protein 3-like	Mfap3l	0.25±0.11
microrchidia 2A	Morc2a	0.24±0.23
microrchidia 3 (predicted)	Morc3_predicted	0.58±0.26
microrchidia 4	Morc4	0.86±0.07
microsomal glutathione S-transferase 1	Mgst1	34.63±2.72
microsomal glutathione S-transferase 3 (predicted)	Mgst3_predicted	60.1±1.87
microspherule protein 1	Mcrs1	2.54±0.27
microtubule associated serine/threonine kinase 2 (predicted)	Mast2_predicted	1.14±0.08
microtubule associated serine/threonine kinase family member 4	Mast4	1.07±0.13
microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	1.24±0.98
microtubule-associated protein 1 light chain 3 beta	Map1lc3b	5.49±0.22
microtubule-associated protein 7 (predicted)	Mtap7_predicted	11.38±0.66
microtubule-associated protein tau	Mapt	10.67±2.52
microtubule-associated protein, RP/EB family, member 1	Mapre1	5.16±0.45
MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	Mid1ip1	0.39±0.39
midasin homolog (yeast)	Mdn1	0.54±0.22
midasin homolog (yeast) /// LYR motif containing 2	Lyrm2 /// Mdn1	4.01±0.38
midkine	Mdk	3.32±0.58
midnolin (predicted)	Midn_predicted	0.68±0.63
MIF4G domain containing	Mif4gd	1.08±0.1
minichromosome maintenance deficient 2 mitotin (S. cerevisiae) (predicted)	Mcm2_predicted	0.82±0.06
minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (predicted)	Mcm3ap_predicted	0.73±0.04
minichromosome maintenance deficient 4 homolog (S. cerevisiae)	Mcm4	0.41±0.21
minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (predicted)	Mcm5_predicted	0.24±0.15
minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	1.09±0.36
MIS12, MIND kinetochore complex component, homolog (yeast)	Mis12	0.29±0.04
misato homolog 1 (Drosophila) (predicted)	Msto1_predicted	0.27±0.06
MIT, microtubule interacting and transport, domain containing 1	Mitd1	0.44±0.09
mitchondrial ribosomal protein S7	Mrps7	5.45±0.4
Mitochondrial acyl-CoA thioesterase 1	Mte1	2.98±0.44
mitochondrial carrier homolog 1 (C. elegans)	Mtch1	7.67±1.4
mitochondrial carrier homolog 2 (C. elegans) (predicted)	Mtch2_predicted	21.91±0.41
mitochondrial carrier triple repeat 1	Mcart1	15.68±1.21
Mitochondrial fission regulator 1 (predicted)	Mtfr1_predicted	12.94±1.61
mitochondrial intermediate peptidase	Mipep	8.55±0.13
mitochondrial methionyl-tRNA formyltransferase	Mtfmt	2.41±0.06
mitochondrial protein 18 kDa	Mtp18	2.1±0.35
mitochondrial ribosomal protein 63	Mrp63	4.11±0.29
mitochondrial ribosomal protein L1 (predicted)	Mrpl1_predicted	2.25±0.16
mitochondrial ribosomal protein L10 (predicted) /// similar to mitochondrial ribosomal protein L10	LOC688165 /// LOC691075 /// Mrpl10_predicted	1.25±0.18
mitochondrial ribosomal protein L11	mrpl11	6.71±0.42
mitochondrial ribosomal protein L12	Mrpl12	9.16±0.98
mitochondrial ribosomal protein L13	Mrpl13	3.9±0.52
mitochondrial ribosomal protein L14 (predicted)	Mrpl14_predicted	2.1±0.82
mitochondrial ribosomal protein L15 (predicted)	Mrpl15_predicted	22.5±1.12
mitochondrial ribosomal protein L16	Mrpl16	9.22±0.4
mitochondrial ribosomal protein L17	Mrpl17	15.86±1.22
mitochondrial ribosomal protein L18 (predicted)	Mrpl18_predicted	6.87±0.45
mitochondrial ribosomal protein L19	Mrpl19	2.11±0.08
mitochondrial ribosomal protein L2	Mrpl2	3.85±0.76
mitochondrial ribosomal protein L20	Mrpl20	6.64±0.69
mitochondrial ribosomal protein L21 (predicted)	Mrpl21_predicted	2.31±0.42
mitochondrial ribosomal protein L22 (predicted)	Mrpl22_predicted	5.31±0.39
mitochondrial ribosomal protein L23	Mrpl23	2.95±0.54
mitochondrial ribosomal protein L24	mrpl24	5.23±0.53
mitochondrial ribosomal protein L27 (predicted)	Mrpl27_predicted	10.06±0.87
mitochondrial ribosomal protein L28	Mrpl28	4.12±0.9
mitochondrial ribosomal protein L3 (predicted)	Mrpl3_predicted	6.03±0.94

mitochondrial ribosomal protein L30 (predicted)	Mrpl30_predicted	3.11±0.55
mitochondrial ribosomal protein L32 (predicted)	Mrpl32_predicted	5.06±0.73
mitochondrial ribosomal protein L34	Mrpl34	3.06±0.3
mitochondrial ribosomal protein L35 (predicted)	Mrpl35_predicted	4.62±0.58
mitochondrial ribosomal protein L36 (predicted)	Mrpl36_predicted	6.07±1.07
mitochondrial ribosomal protein L37	Mrpl37	4.71±0.71
mitochondrial ribosomal protein L38	Mrpl38	1.12±0.26
mitochondrial ribosomal protein L4 (predicted)	Mrpl4_predicted	4.93±1.11
mitochondrial ribosomal protein L40	Mrpl40	2.3±0.14
mitochondrial ribosomal protein L41	Mrpl41	11.23±0.36
mitochondrial ribosomal protein L42 (predicted)	Mrpl42_predicted	6.74±1.16
mitochondrial ribosomal protein L43 (predicted)	Mrpl43_predicted	4.58±0.31
mitochondrial ribosomal protein L44	Mrpl44	2.33±0.22
mitochondrial ribosomal protein L45 (predicted)	Mrpl45_predicted	2.65±0.33
mitochondrial ribosomal protein L46	Mrpl46	2.02±0.26
mitochondrial ribosomal protein L47	Mrpl47	1.87±0.75
mitochondrial ribosomal protein L48 (predicted)	Mrpl48_predicted	3.97±0.66
Mitochondrial ribosomal protein L49	Mrpl49	2.63±0.27
mitochondrial ribosomal protein L50 (predicted)	Mrpl50_predicted	6.32±0.17
mitochondrial ribosomal protein L51 (predicted)	Mrpl51_predicted	4.26±0.32
mitochondrial ribosomal protein L52 (predicted)	Mrpl52_predicted	1.37±0.08
mitochondrial ribosomal protein L53 (predicted)	Mrpl53_predicted	9.35±1.03
mitochondrial ribosomal protein L54 (predicted)	Mrpl54_predicted	7.63±1.28
mitochondrial ribosomal protein L55 (predicted)	Mrpl55_predicted	4.5±0.72
mitochondrial ribosomal protein L9	mrpl9	3.27±0.24
mitochondrial ribosomal protein S11	Mrps11	4.13±0.5
mitochondrial ribosomal protein S12 (predicted)	Mrps12_predicted	3.12±0.41
mitochondrial ribosomal protein S14 (predicted)	Mrps14_predicted	6.19±0.83
mitochondrial ribosomal protein S15	Mrps15	2.32±0.23
mitochondrial ribosomal protein S16	Mrps16	7.83±1.19
mitochondrial ribosomal protein S17 (predicted)	Mrps17_predicted	8.35±0.28
mitochondrial ribosomal protein S18A	Mrps18a	3.55±0.52
mitochondrial ribosomal protein S18C (predicted)	Mrps18c_predicted	2.55±0.31
mitochondrial ribosomal protein S2 (predicted)	Mrps2_predicted	3.4±0.3
mitochondrial ribosomal protein S21	Mrps21	5.4±0.15
mitochondrial ribosomal protein S23 (predicted)	Mrps23_predicted	6.59±0.27
mitochondrial ribosomal protein S24 (predicted)	Mrps24_predicted	3.35±0.63
mitochondrial ribosomal protein S25	Mrps25	13.57±1.89
mitochondrial ribosomal protein S26 (predicted)	Mrps26_predicted	4.87±0.19
mitochondrial ribosomal protein S27 (predicted)	Mrps27_predicted	1.09±0.02
mitochondrial ribosomal protein S30 (predicted)	Mrps30_predicted	5.56±0.56
mitochondrial ribosomal protein S31 (predicted)	Mrps31_predicted	4.85±0.69
mitochondrial ribosomal protein S33 (predicted)	Mrps33_predicted	7.27±1.24
mitochondrial ribosomal protein S34 (predicted)	Mrps34_predicted	4.04±0.2
mitochondrial ribosomal protein S35 (predicted)	Mrps35_predicted	2.63±0.59
mitochondrial ribosomal protein S36 (predicted)	Mrps36_predicted	17.47±0.97
mitochondrial ribosomal protein S5 (predicted)	Mrps5_predicted	2.02±0.56
mitochondrial ribosomal protein S9	Mrps9	3.15±0.78
mitochondrial ribosome recycling factor	Mrrf	1±0.09
mitochondrial trans-2-enoyl-CoA reductase	Mecr	1.77±0.14
mitochondrial transcription termination factor	Mterf	1.91±0.32
mitochondrial translation optimization 1 homolog (S. cerevisiae) (predicted)	Mto1_predicted	1.66±0.3
mitochondrial translational initiation factor 2	Mtif2	1.16±0.19
mitochondrial translational release factor 1-like	Mtrf1l	0.97±0.08
mitochondrial tumor suppressor 1	Mtus1	2.87±0.32
mitochondrial ubiquitin ligase activator of NFKB 1	Mul1	0.48±0.25
mitofusin 1	Mfn1	3.94±0.48
mitofusin 2	Mfn2	3.74±0.35
Mitogen activated protein kinase 1	Mapk1	3.77±1.05
mitogen activated protein kinase 14	Mapk14	4.49±0.42
mitogen activated protein kinase 3	Mapk3	0.84±0.23
mitogen activated protein kinase kinase 1	Map2k1	1.97±0.27
mitogen activated protein kinase kinase 2	Map2k2	7.43±0.77
mitogen activated protein kinase kinase 3	Map2k3	2.06±0.33
mitogen activated protein kinase kinase 4	Map2k4	0.37±0.09
mitogen activated protein kinase kinase 5	Map2k5	0.9±0.2
mitogen activated protein kinase kinase 7	Map2k7	0.51±0.09
mitogen activated protein kinase kinase kinase 12	Map3k12	1.92±0.37
mitogen activated protein kinase kinase kinase 3 (predicted)	Map3k3_predicted	0.52±0.08
mitogen activated protein kinase kinase kinase 4 (predicted)	Map3k4_predicted	3.85±0.64
Mitogen activated protein kinase kinase kinase 7 (predicted)	Map3k7_predicted	2.4±0.06
mitogen activated protein kinase kinase kinase kinase 2 (predicted)	Map4k2_predicted	0.36±0.06
mitogen-activated protein binding protein interacting protein	Mapbpip	5.75±0.94
mitogen-activated protein kinase 1 interacting protein 1	Mapk1ip1	0.63±0.18
mitogen-activated protein kinase 6	Mapk6	2.95±0.13
mitogen-activated protein kinase 8	Mapk8	0.62±0.05
mitogen-activated protein kinase 8 interacting protein 1	Mapk8ip1	6.61±1.14
mitogen-activated protein kinase 9	Mapk9	0.3±0.14
mitogen-activated protein kinase associated protein 1	Mapkap1	1.55±0.11
mitogen-activated protein kinase kinase 1 interacting protein 1	Map2k1ip1	5.58±0.09
mitogen-activated protein kinase kinase 6	Map2k6	1.16±0.09
mitogen-activated protein kinase kinase kinase 11	Map3k11	1.16±0.57
mitogen-activated protein kinase kinase kinase 7 interacting protein 1 (predicted)	Map3k7ip1_predicted	1.41±0.16
mitogen-activated protein kinase kinase kinase 7 interacting protein 2	Map3k7ip2	1.76±0.17
mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	1.86±0.34
mitogen-activated protein kinase-activated protein kinase 3	Mapkapk3	0.78±0.15
Mki67 (FHA domain) interacting nucleolar phosphoprotein	Mki67ip	3.37±0.15

MLX interacting protein-like	Mlxipl	1.09±0.32
MMR_HSR1 domain containing protein RGD1359460	RGD1359460	0.75±0.1
MOB1, Mps One Binder kinase activator-like 1A (yeast) (predicted)	Mobkl1a_predicted	0.23±0.09
MOB1, Mps One Binder kinase activator-like 1B (yeast)	Mobkl1b	2.2±0.49
MOB1, Mps One Binder kinase activator-like 3 (yeast)	Mobkl3	1.46±0.63
MOCO sulphurase C-terminal domain containing 2	Mosc2	27.85±1.59
MOCO sulphurase C-terminal domain containing-like	LOC690745	6.76±0.39
moesin	Msn	0.98±0.26
molybdenum cofactor synthesis 2	Mocs2	13.2±2.47
MON1 homolog A (yeast) (predicted)	Mon1a_predicted	0.86±0.13
MON2 homolog (yeast)	Mon2	0.29±0.06
monoamine oxidase A	Maoa	2.09±0.25
monoamine oxidase B	Maob	2.02±0.2
Monoglyceride lipase	Mgll	10.46±0.66
Morf4 family associated protein 1	Mrfap1	26.64±3.02
mortality factor 4 like 1	Morf4l1	13.27±1.48
mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b	LOC309220 /// Morf4l1	16.13±0.77
mortality factor 4 like 2	Morf4l2	12.94±0.4
motile sperm domain containing 1 /// similar to motile sperm domain containing 1	LOC686087 /// Mospd1	2.59±0.13
motile sperm domain containing 3	Mospd3	1.17±0.15
M-phase phosphoprotein 1 (predicted)	Mphosph1_predicted	0.46±0.16
M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted)	Mphosph10_predicted	0.64±0.06
M-phase phosphoprotein 8	Mphosph8	3.44±0.59
M-phase phosphoprotein 8 /// poly (ADP-ribose) polymerase family, member 4	Mphosph8 /// Parp4	1.1±0.13
Mpv17 transgene, kidney disease mutant-like (predicted)	Mpv17l_predicted	6.65±0.4
MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	Mrs2	1.16±0.18
MRT4, mRNA turnover 4, homolog (S. cerevisiae)	Mrto4	0.89±0.19
MTERF domain containing 1	Mterfd1	6.39±1.47
MTERF domain containing 2	Mterfd2	2.47±0.12
MTERF domain containing 3	Mterfd3	0.72±0.18
mucin and cadherin like	Mucdhl	13.39±2.37
mucolipin 1 (predicted)	Mcoln1_predicted	4.18±0.46
multiple coagulation factor deficiency 2	Mcfd2	4.78±0.25
multiple EGF-like-domains 8	Megf8	0.27±0.07
multiple endocrine neoplasia 1	Men1	1.52±0.19
multiple inositol polyphosphate histidine phosphatase 1	Minpp1	6.31±0.51
multiple PDZ domain protein	Mpdz	0.7±0.06
Musashi homolog 2 (Drosophila)	Msi2	8.34±1.3
muskelin 1, intracellular mediator containing kelch motifs	Mkln1	4.37±0.44
muted	Muted	1.05±0.11
mutL homolog 1 (E. coli)	Mlh1	1.59±0.14
mutL homolog 3 (E. coli) (predicted)	Mlh3_predicted	0.74±0.07
mutS homolog 2 (E. coli)	Msh2	0.79±0.2
mutS homolog 3 (E. coli)	Msh3	0.61±0.12
myb-like, SWIRM and MPN domains 1 (predicted)	Mysm1_predicted	0.45±0.11
MYC binding protein 2	Mycbp2	3.86±0.61
myc induced nuclear antigen	Mina	0.81±0.27
myelin basic protein expression factor 2, repressor	Myef2	2.27±0.44
myelin protein zero-like 2	Mpzl2	1.41±0.39
myeloid cell leukemia sequence 1	Mcl1	13.63±0.81
myeloid differentiation primary response gene 88	Myd88	2.08±0.43
myeloid leukemia factor 2 (predicted)	Mlf2_predicted	8.35±1.43
myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosophila)	Mllt10	1.72±0.21
myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog (Drosophila) (predicted)	Mllt6_predicted	1.31±0.08
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	Mllt1	0.32±0.14
myeloid/lymphoid or mixed-lineage leukemia 1	Mll1	0.65±0.23
myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	3.33±0.85
myeloma overexpressed 2	Myeov2	13.76±1.82
Myocyte enhancer factor 2D	Mef2d	0.51±0.14
myo-inositol oxygenase	Miox	52.98±2.03
myosin 5B	Myo5b	3.48±0.56
myosin binding protein C, fast-type (predicted)	Mybpc2_predicted	1.81±0.09
myosin ID	Myo1d	0.6±0.56
myosin IE	Myo1e	0.78±0.35
myosin IXb	Myo9b	0.41±0.3
myosin light chain kinase 3	Mylk3	0.34±0.13
myosin light chain, regulatory B	Mrlcb	8.54±2.53
myosin phosphatase-Rho interacting protein	M-rip	2.03±0.32
myosin Va	Myo5a	2.42±0.5
myosin VI	Myo6	10.64±0.65
myosin VIIb	Myo7b	1.8±0.16
myosin X (predicted)	Myo10_predicted	1.6±0.17
myosin, heavy polypeptide 10, non-muscle	Myh10	0.96±0.3
Myosin, heavy polypeptide 9, non-muscle	Myh9	4.25±0.3
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (predicted)	LOC684520 /// Myl6 /// Myl6b /// Myl6_predicted	27.56±1.61
myotrophin	Mtpn	14.3±0.5
Myotubularin related protein 1 (predicted)	Mtmr1_predicted	0.4±0.21
myotubularin related protein 10	Mtmr10	6.43±0.56
myotubularin related protein 14	Mtmr14	1.97±0.06
myotubularin related protein 2 (predicted)	Mtmr2_predicted	4.92±0.39
myotubularin related protein 3	Mtmr3	1.66±0.2
myotubularin related protein 4 (predicted)	Mtmr4_predicted	3.11±0.4
myotubularin related protein 6 (predicted)	Mtmr6_predicted	10.52±0.93
myotubularin related protein 9	Mtmr9	1.17±0.27
MYST histone acetyltransferase 2	Myst2	1.42±0.05
N-6 adenine-specific DNA methyltransferase 1 (putative)	N6amt1	2.34±0.34

N-6 adenine-specific DNA methyltransferase 2 (putative)	N6amt2	0.94±0.18
Na+ dependent glucose transporter 1	Naglt1	38.31±4.22
N-acetyl galactosaminidase, alpha	Naga	2.5±0.14
N-acetylglucosamine kinase	Nagk	3.78±0.45
N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (predicted)	Nagpa_predicted	0.53±0.13
N-acetylglucosamine-1-phosphotransferase, gamma subunit	Gnptg	6.95±1.1
N-acetylneuraminate pyruvate lyase	Npl	8.15±0.33
N-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	Nans_predicted	2.36±0.26
N-acetyltransferase 1 (arylamine N-acetyltransferase)	Nat1	0.77±0.05
N-acetyltransferase 11	Nat11	0.84±0.02
N-acetyltransferase 13	Nat13	1.11±0.08
N-acetyltransferase 14	Nat14	0.22±0.02
N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (predicted)	Nat5_predicted	5.56±0.91
N-acetyltransferase ARD1 homolog (S. cerevisiae) (predicted)	Ard1_predicted	0.35±0.09
N-acylsphingosine amidohydrolase 1	Asah1	4.74±0.54
NAD kinase	Nadk	4.79±0.04
NAD synthetase 1	Nadsyn1	2.63±0.21
NAD(P) dependent steroid dehydrogenase-like	Nsdhl	3.02±0.47
NAD(P) dependent steroid dehydrogenase-like	Hspc105	0.31±0.09
NAD(P)H dehydrogenase, quinone 2	Nqo2	16.08±0.49
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10-like 1 /// NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10 /// Ndufa10l1	9.23±1.63
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	Ndufa11	12.21±2.04
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	Ndufa5	4.78±0.05
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (predicted)	Ndufa1_predicted	43.76±2.79
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)	Ndufa12_predicted	23.83±2.56
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 (predicted)	Ndufa13_predicted	12.24±1.07
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (predicted)	Ndufa2_predicted	16.44±2.29
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	Ndufa4	44.95±1.05
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) (predicted)	Ndufa6_predicted	30.3±2.46
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)	Ndufa7_predicted	9.12±3.99
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	15.88±1.39
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	17.9±1.91
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (predicted)	Ndufaf1_predicted	0.68±0.15
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 (predicted)	Ndufb3_predicted	24.94±1.59
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	Ndufb4	30.72±1.19
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11 (predicted)	Ndufb11_predicted	27.56±1.2
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (predicted)	Ndufb2_predicted	25.43±2.12
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (predicted)	Ndufb5_predicted	36.39±5.06
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (predicted)	Ndufb6_predicted	22.84±1.35
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (predicted)	Ndufb7_predicted	12±2.7
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (predicted)	Ndufb9_predicted	49.68±2.66
NADH dehydrogenase (ubiquinone) 1, alpha	LOC683884 /// Ndufab1_predicted	24.96±0.92
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	Ndufc1	22.82±2.49
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	Ndufc2	24±0.29
NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	28.23±2.77
NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	22.61±0.68
NADH dehydrogenase (ubiquinone) Fe-S protein 3 (predicted)	Ndufs3_predicted	16.95±1.2
NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	2.22±0.22
NADH dehydrogenase (ubiquinone) Fe-S protein 5	Ndufs5	24.38±0.99
NADH dehydrogenase (ubiquinone) Fe-S protein 6	LOC679739 /// LOC692052 /// Ndufs6	24.91±1.41
NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	15.05±3.34
NADH dehydrogenase (ubiquinone) Fe-S protein 8 (predicted)	Ndufs8_predicted	14.95±1.67
NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	14.59±1.38
NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	23.23±1.58
NADH dehydrogenase (ubiquinone) flavoprotein 3-like	LOC682566 /// Ndufv3l	14.53±1.26
NADH dehydrogenase subunit 1	ND1	62.3±1.74
NADH dehydrogenase subunit 2	ND2	80.18±4.84
NADH dehydrogenase subunit 3	ND3	61.59±5.33
NADPH oxidase 4	Nox4	24.63±2.5
napsin A aspartic peptidase	Napsa	53.72±5.31
nardilysin, N-arginine dibasic convertase, NRD convertase 1	Nrd1	2.96±0.34
nascent-polypeptide-associated complex alpha polypeptide (predicted)	Naca_predicted	20.89±2.86
NAT9	Nat9	0.45±0.14
NCK interacting protein with SH3 domain (predicted)	Nckipsd_predicted	0.32±0.08
NCK-associated protein 1	Nckap1	28.89±1.92
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (predicted)	Ndst2_predicted	1.07±0.16
NECAP endocytosis associated 1	Necap1	2.06±0.19
NECAP endocytosis associated 2	Necap2	1.98±0.62
necdin-like 2	Ndnl2	0.69±0.12
Nedd4 binding protein 1	N4bp1	0.23±0.1
NEDD4 binding protein 2-like 2	N4bp2l2	3.49±0.74
Nedd4 family interacting protein 1	Ndfip1	20.1±1.58
Nedd4 family interacting protein 2 (predicted)	Ndfip2_predicted	15.19±1.27
NEDD8 ultimate buster-1	Nub1	1.48±0.16
NEFA-interacting nuclear protein NIP30	Nip30	3.24±0.38
nei endonuclease VIII-like 1 (E. coli)	Neil1	1.64±0.45
neighbor of Brca1 gene 1	Nbr1	9.7±0.99
neighbor of Brca1 gene 1 /// similar to neighbor of Brca1 gene 1	LOC498369 /// Nbr1	0.92±0.19
nemo like kinase	Nlk	0.26±0.09
neogenin	Neo1	1.54±0.12
nephronophthisis 1 (juvenile) homolog (human) (predicted)	Nphp1_predicted	5.08±0.32
nerve growth factor receptor (TNFRSF16) associated protein 1	Ngfrap1	8.44±0.75
N-ethylmaleimide sensitive fusion protein	Nsf	1.12±0.12
N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	9.19±0.74
N-ethylmaleimide sensitive fusion protein attachment protein gamma	Napg	2.32±0.39

neural precursor cell expressed, developmentally down-regulated gene 4	Nedd4	10.49±0.65
neural precursor cell expressed, developmentally down-regulated gene 4-like	Nedd4l	1.11±0.34
neural precursor cell expressed, developmentally down-regulated gene 8	Nedd8	19.47±0.31
neural precursor cell expressed, developmentally down-regulated gene 9	Nedd9	3.99±0.27
neural proliferation, differentiation and control, 1	Npdc1	4.34±0.32
neuralized-like 2 (Drosophila) (predicted)	Neurl2_predicted	2.47±0.36
neuraminidase 1	Neu1	4.79±0.37
neuregulin 1	Nrg1	0.84±0.19
neuroblastoma ras oncogene	Nras	0.42±0.27
neurocalcin delta	Ncald	0.92±0.08
neuroepithelial cell transforming gene 1	Net1	13.71±0.41
neurofibromatosis 2	Nf2	2.25±0.2
neuroguidin, EIF4E binding protein	Ngdn	1.03±0.14
neurolysin (metallopeptidase M3 family)	Nln	1.54±0.23
neuromedin B (predicted)	Nmb_predicted	0.83±0.04
Neuronal regeneration related protein	Nrep	28.65±3.29
Neuropilin 1	Nrp1	0.96±0.31
neuroplastin	Nptn	14.73±1.69
neurotrophin 3	Ntf3	4.94±0.72
neutral sphingomyelinase (N-SMase) activation associated factor	Nsmaf	2.27±0.22
NFKB activating protein	Nkap	0.47±0.05
NFKB inhibitor interacting Ras-like protein 1 (predicted)	Nkiras1_predicted	0.65±0.02
NFKB inhibitor interacting Ras-like protein 2 (predicted)	Nkiras2_predicted	0.79±0.12
NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	Nfu1	1.24±0.26
Ngfi-A binding protein 1	Nab1	0.57±0.2
Ngfi-A binding protein 2	Nab2	0.51±0.25
Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	0.95±0.1
N-glycanase 1	Ngly1	6.39±1.02
NHL repeat containing 2 (predicted)	Nhlrc2_predicted	0.59±0.08
NHL repeat containing 3	Nhlrc3	1.74±0.17
nibrin	Nbn	3.3±0.52
nicalin homolog (zebrafish)	Ncln	3.81±0.68
nicastrin	Ncstn	1.97±0.21
nicolin 1	Nicn1	2.61±0.29
nicotinamide nucleotide adenylyltransferase 1	Nmnat1	0.59±0.07
nicotinamide nucleotide adenylyltransferase 3	Nmnat3	2.69±0.12
nicotinamide nucleotide transhydrogenase	Nnt	27.4±1.43
nicotinate phosphoribosyltransferase domain containing 1	Naprt1	28.15±1.74
nidogen 2	Nid2	0.43±0.79
Niemann Pick type C2	Npc2	15.38±1.83
NIK and IKK{beta} binding protein	Nibp	0.69±0.18
NIMA (never in mitosis gene a)- related kinase 9 (predicted)	Nek9_predicted	4.37±0.8
NIMA (never in mitosis gene a)-related expressed kinase 3 (predicted)	Nek3_predicted	0.42±0.28
NIMA (never in mitosis gene a)-related expressed kinase 7	Nek7	4.42±0.69
NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	Nob1	2.56±0.06
ninjurin 1	Ninj1	9.37±0.73
NIPA-like domain containing 2	Npal2	0.27±0.32
Nipped-B homolog (Drosophila)	NIPBL	1.31±0.16
nischarin	Nisch	3.73±0.62
nitric oxide synthase interacting protein (predicted)	Nosip_predicted	0.92±0.34
nitric oxide synthase trafficker	Nostrin	0.89±0.22
nitrilase 1	Nit1	12.56±0.37
nitrilase family, member 2	Nit2	19.25±1.05
nitrogen fixation gene 1 (S. cerevisiae)	Nfs1	18.16±1.43
NLR family member X1	Nlrx1	1.42±0.2
NLR family, pyrin domain containing 6	Nlrp6	1.64±0.27
NMD3 homolog (S. cerevisiae) (predicted)	Nmd3_predicted	2.54±0.52
NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted	3.73±0.38
N-methylpurine-DNA glycosylase	Mpg	0.39±0.09
NmrA-like family domain containing 1	Nmral1	1.05±0.09
N-myc downstream regulated gene 1	Ndrg1	55.07±2.4
N-myc downstream regulated gene 3	Ndrg3	0.67±0.1
N-myristoyltransferase 1	Nmt1	2.49±0.23
nodal modulator 1	Nomo1	2.09±0.45
NOL1/NOP2/Sun domain family, member 2	Nsun2	2.29±0.28
NOL1/NOP2/Sun domain family, member 4 (predicted)	Nsun4_predicted	1.56±0.23
NOL1/NOP2/Sun domain family, member 5 (predicted)	Nsun5_predicted	0.4±0.13
non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) (predicted)	Nipa2_predicted	1.93±0.24
non-catalytic region of tyrosine kinase adaptor protein 1 (predicted)	Nck1_predicted	2.11±0.44
nonhomologous end-joining factor 1	Nhej1	0.58±0.09
non-metastatic cells 3, protein expressed in	Nme3	2.96±0.1
non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	Nme6	0.5±0.13
non-POU-domain-containing, octamer-binding protein	Nono	8.19±1.08
non-SMC condensin II complex, subunit D3	Ncapd3	0.43±0.14
non-SMC condensin II complex, subunit H2	Ncaph2	0.81±0.08
non-SMC element 1 homolog (S. cerevisiae)	Nsmce1	2.91±0.22
non-SMC element 2, MMS21 homolog (S. cerevisiae)	Nsmce2	1.43±0.42
non-SMC element 4 homolog A (S. cerevisiae)	Nsmce4a	5.05±0.62
notch1-induced protein	LOC493574	0.56±0.11
notchless homolog 1 (Drosophila) (predicted)	Nle1_predicted	0.46±0.15
NS5A (hepatitis C virus) transactivated protein 9	Ns5atp9	0.35±0.15
NSFL1 (p97) cofactor (p47)	Nsfl1c	2.34±0.24
N-terminal asparagine amidase	Ntan1	7.59±0.36
NTF2-related export protein 1 (predicted)	Nxt1_predicted	0.6±0.06
NUAK family, SNF1-like kinase, 2	Nuak2	3.94±0.72
nuclear autoantigenic sperm protein (histone-binding)	Nasp	0.6±0.29
nuclear cap binding protein subunit 1, 80kDa	Ncbp1	18.69±0.48

nuclear casein kinase and cyclin-dependent kinase substrate 1	Nucks1	2.59±0.19
nuclear distribution gene C homolog (Aspergillus)	Nudc	3.12±0.14
nuclear distribution gene E homolog 1 (A nidulans)	Nde1	1.05±0.07
nuclear distribution gene E-like homolog 1 (A. nidulans)	Ndel1	5.59±0.41
nuclear factor I/A	Nfia	5.39±1.9
nuclear factor I/B	Nfib	1.24±0.44
Nuclear factor I/C	Nfic	1.07±0.77
nuclear factor of activated T-cells 5 (predicted)	Nfat5_predicted	1.16±0.13
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (predicted)	Nfatc3_predicted	1.13±0.08
nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Nfkbib	1.55±0.17
nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	Nfkb1	1.55±0.44
nuclear factor related to kappa B binding protein (predicted)	Nfrkb_predicted	0.63±0.1
nuclear factor, erythroid derived 2, like 2	Nfe2l2	8.18±2.16
nuclear factor, erythroid derived 2,-like 1 (predicted)	Nfe2l1_predicted	0.69±0.2
nuclear fragile X mental retardation protein interacting protein 1	Nufip1	1.51±0.06
nuclear import 7 homolog (S. cerevisiae)	Nip7	1.91±0.08
nuclear mitotic apparatus protein 1	Numa1	0.94±0.17
nuclear pore associated protein	Npap60	0.28±0.08
nuclear pore membrane protein 121	Pom121	0.55±0.34
nuclear prelamin A recognition factor	Narf	1.9±0.46
nuclear prelamin A recognition factor-like	Narfl	1.48±0.02
nuclear protein E3-3	RGD708545	3.93±0.24
nuclear protein in the AT region (predicted)	Npat_predicted	0.46±0.17
nuclear protein localization 4 homolog (S. cerevisiae)	Nploc4	1.59±0.1
nuclear receptor binding factor 2	Nrbf2	1.39±0.19
nuclear receptor binding protein	Nrbp	0.71±0.17
Nuclear receptor binding SET domain protein 1 (predicted)	Nsd1_predicted	2.16±0.49
nuclear receptor coactivator 1 (predicted)	Ncoa1_predicted	3.26±0.81
nuclear receptor coactivator 4 (predicted)	Ncoa4_predicted	16.24±1.66
nuclear receptor coactivator 5 (predicted)	Ncoa5_predicted	0.39±0.14
nuclear receptor coactivator 6	Ncoa6	1.17±0.43
nuclear receptor coactivator 7	Ncoa7	14.07±1.46
nuclear receptor co-repressor 1	Ncor1	4.19±0.19
nuclear receptor subfamily 1, group D, member 2	Nr1d2	3.42±0.59
nuclear receptor subfamily 1, group H, member 2	Nr1h2	1.8±0.17
nuclear receptor subfamily 1, group H, member 3	Nr1h3	2.43±0.1
nuclear receptor subfamily 1, group H, member 4	Nr1h4	13.63±0.18
nuclear receptor subfamily 1, group I, member 2	Nr1i2	1.11±0.05
nuclear receptor subfamily 2, group F, member 2	Nr2f2	1±0.48
nuclear receptor subfamily 2, group F, member 6	Nr2f6	2.52±0.86
nuclear receptor subfamily 2, group F, member 6 /// similar to Orphan nuclear receptor EAR-2 (V-erbA-related protein EAR-2)	LOC688367 /// Nr2f6	0.59±0.14
nuclear receptor subfamily 3, group C, member 1	Nr3c1	4.33±0.28
nuclear RNA export factor 1	Nxf1	3.1±0.25
nuclear transcription factor, X-box binding 1	Nfx1	0.99±0.06
nuclear transcription factor-Y beta	Nfyb	0.48±0.14
nuclear transcription factor-Y gamma	Nfyc	3.53±0.49
nuclear transport factor 2	Nutf2	3.33±1.2
nuclear transport factor 2-like export factor 2 (predicted)	Nxt2_predicted	2.12±0.18
nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	Nus1	3.96±0.4
nuclear VCP-like (predicted)	Nvl_predicted	0.55±0.15
nucleobindin 1	Nucb1	8.12±1.11
nucleolar and coiled-body phosphoprotein 1	Nolc1	1±0.15
nucleolar and spindle associated protein 1 (predicted)	Nusap1_predicted	0.32±0.11
nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	0.61±0.11
nucleolar protein 1 (predicted)	Nol1_predicted	1.51±0.04
nucleolar protein 14	Nol14	0.68±0.13
nucleolar protein 5	Nol5	1.4±0.27
nucleolar protein 5A	Nol5a	3.15±0.59
nucleolar protein 7	Nol7	5.12±0.89
nucleolar protein 8 (predicted)	Nol8_predicted	0.36±0.09
nucleolar protein 9	Nol9	0.81±0.25
nucleolar protein family 6 (RNA-associated) (predicted)	Nol6_predicted	0.93±0.09
nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	Nola1	0.62±0.05
nucleolar protein family A, member 2 (predicted)	Nola2_predicted	2.44±0.11
nucleolar protein family A, member 3	Nola3	11.86±0.93
nucleolin	Ncl	7.67±0.29
nucleophosmin 1	Npm1	13.47±1.14
nucleophosmin 1 /// similar to Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)	LOC300303 /// Npm1	1.6±0.23
nucleoporin 133 (predicted)	Nup133_predicted	0.2±0.12
nucleoporin 153	Nup153	3.55±0.39
nucleoporin 155	Nup155	1.05±0.17
nucleoporin 160 (predicted)	Nup160_predicted	0.77±0.13
nucleoporin 188	Nup188	0.76±0.14
nucleoporin 205	Nup205	1.46±0.08
nucleoporin 35	Nup35	1.77±0.14
nucleoporin 37 (predicted)	Nup37_predicted	1.71±0.05
nucleoporin 54	Nup54	0.5±0.14
nucleoporin 62	Nup62	0.35±0.14
nucleoporin 85	Nup85	0.53±0.11
nucleoporin 88	Nup88	1.34±0.03
nucleoporin 93	Nup93	0.43±0.05
nucleoporin 98	Nup98	1.07±0.3
nucleoporin like 1	Nupl1	1.28±0.16
nucleoporin like 2	Nupl2	0.65±0.09
Nucleoside 2-deoxyribosyltransferase domain containing protein RGD620382	RGD620382	0.44±0.07
nucleoside phosphorylase	Np	0.54±0.91
Nucleosome assembly protein 1-like 1	Nap1l1	5.27±0.16

nucleosome assembly protein 1-like 3	Nap1l3	1.59±0.26
nucleosome assembly protein 1-like 4	Nap1l4	2.21±0.13
nucleosome binding protein 1 (predicted)	Nsbp1_predicted	0.37±0.08
nucleotide binding protein 1	Nubp1	4.59±0.39
nucleotide binding protein 2	Nubp2	6.02±0.54
nucleotide binding protein-like (predicted)	Nubpl_predicted	0.97±0.16
NudC domain containing 1 (predicted)	Nudcd1_predicted	0.43±0.06
NudC domain containing 2	Nudcd2	1.24±0.15
nudix (nucleoside diphosphate linked moiety X)-type motif 1	Nudt1	0.48±0.1
nudix (nucleoside diphosphate linked moiety X)-type motif 12 (predicted)	Nudt12_predicted	3.54±0.69
nudix (nucleoside diphosphate linked moiety X)-type motif 14 (predicted)	Nudt14_predicted	2.15±0.7
nudix (nucleoside diphosphate linked moiety X)-type motif 16 (predicted)	Nudt16_predicted	0.21±0.2
nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	Nudt16l1	7.58±0.65
nudix (nucleoside diphosphate linked moiety X)-type motif 18	Nudt18	1.17±0.18
nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	3.4±0.11
nudix (nucleoside diphosphate linked moiety X)-type motif 2	Nudt2	3.08±0.31
nudix (nucleoside diphosphate linked moiety X)-type motif 22	Nudt22	0.83±0.16
nudix (nucleoside diphosphate linked moiety X)-type motif 5	Nudt5	1.13±0.12
nudix (nucleoside diphosphate linked moiety X)-type motif 6	Nudt6	1.01±0.12
nudix (nucleoside diphosphate linked moiety X)-type motif 7 (predicted)	Nudt7_predicted	4.37±0.32
nudix (nucleoside diphosphate linked moiety X)-type motif 9	Nudt9	0.98±0.08
nudix (nucleotide diphosphate linked moiety X)-type motif 3	Nudt3	2.71±1.22
NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Nuf2	0.35±0.08
Numb gene homolog (Drosophila)	Numb	4.57±0.11
Nur77 downstream gene 2	Ndg2	49.18±3.17
O-6-methylguanine-DNA methyltransferase	Mgmt	1.28±0.03
OAF homolog (Drosophila)	Oaf	3.76±0.57
Obg-like ATPase 1	Ola1	5.43±0.57
occludin /// thiopurine methyltransferase	Ocln /// Tpmt	1.48±0.27
OCIA domain containing 1	Ociad1	10.3±1.18
oculocerebrorenal syndrome of Lowe	Ocrl	0.37±0.13
odd-skipped related 2 (Drosophila)	Osr2	0.7±0.16
olfactomedin-like 1	Olfml1	12.99±2.94
olfactomedin-like 2A (predicted)	Olfml2a_predicted	0.48±0.32
oligonucleotide/oligosaccharide-binding fold containing 1	Obfc1	0.49±0.02
oligonucleotide/oligosaccharide-binding fold containing 2A	Obfc2a	12.33±1.89
oligonucleotide/oligosaccharide-binding fold containing 2B	Obfc2b	1.58±0.19
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Ogt	4.65±0.28
OMA1 homolog, zinc metallopeptidase (S. cerevisiae) (predicted)	Oma1_predicted	3.17±0.3
open reading frame 19	ORF19	2.15±0.07
opioid growth factor receptor	Ogfr	0.98±0.4
opioid growth factor receptor-like 1	Ogfrl1	0.42±0.17
opioid receptor, sigma 1	Oprs1	1.28±0.1
opsin 3	Opn3	0.3±0.04
optic atrophy 1 homolog (human)	Opa1	1.65±0.23
optic atrophy 3	Opa3	0.93±0.14
optineurin	Optn	1.43±0.06
ORAI calcium release-activated calcium modulator 1	Orai1	0.91±0.15
ORAI calcium release-activated calcium modulator 3	Orai3	0.4±0.07
ORAI calcium release-activated calcium modulator 3 /// similar to KIAA0339 protein	Orai3 /// RGD1311624	0.73±0.06
oral cancer overexpressed 1 (predicted)	Oraov1_predicted	0.58±0.06
oral-facial-digital syndrome 1 gene homolog (human)	Ofd1	0.24±0.06
organic solute transporter alpha	Osta	4.66±0.73
origin recognition complex, subunit 2-like (S. cerevisiae)	Orc2l	0.99±0.37
origin recognition complex, subunit 3-like (S. cerevisiae)	Orc3l	0.28±0.06
origin recognition complex, subunit 4	Orc4	2.13±0.12
origin recognition complex, subunit 4-like (S. cerevisiae)	Orc4l	1.86±0.31
origin recognition complex, subunit 5-like (S. cerevisiae)	Orc5l	0.84±0.18
origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	0.39±0.15
ORM1-like 2 (S. cerevisiae) (predicted)	Ormdl2_predicted	7.82±0.59
ORM1-like 3 (S. cerevisiae)	Ormdl3	2.66±0.08
ornithine aminotransferase	Oat	7.91±1.43
ornithine decarboxylase antizyme 1	Oaz1	22.38±2.84
O-sialoglycoprotein endopeptidase	Osgep	1.02±0.09
O-sialoglycoprotein endopeptidase-like 1	Osgepl1	1.12±0.2
osteoclast stimulating factor 1	Ostf1	2.6±0.21
osteomodulin	Omd	0.32±0.06
osteopetrosis associated transmembrane protein 1	Ostm1	4.97±0.44
OTU domain containing 1	Otud1	0.65±0.47
OTU domain containing 5	Otud5	2.5±0.04
OTU domain containing 7B	Otud7b	0.43±0.05
OTU domain containing 7B /// myotubularin related protein 11	Mtmr11 /// Otud7b	1.27±0.38
OTU domain, ubiquitin aldehyde binding 1 (predicted)	Otub1_predicted	2.38±0.57
outer dense fiber of sperm tails 2-like	Odf2l	0.84±0.2
oxidase assembly 1-like	Oxa1l	8.54±0.72
oxidation resistance 1	Oxr1	1.2±0.21
oxidative stress induced growth inhibitor family member 2	Osgin2	0.25±0.14
oxidative stress responsive gene	RGD1303142	1.39±0.24
oxidative-stress responsive 1 (predicted)	Oxsr1_predicted	1.45±0.16
oxidoreductase NAD-binding domain containing 1 (predicted)	Oxnad1_predicted	2.41±0.14
oxoglutarate dehydrogenase (lipoamide)	Ogdh	29.82±2.13
oxysterol binding protein (predicted)	Osbp_predicted	1.77±0.3
oxysterol binding protein-like 11 (predicted)	Osbpl11_predicted	1.62±0.21
oxysterol binding protein-like 1A	Osbpl1a	2.46±0.25
oxysterol binding protein-like 2	Osbpl2	2.73±0.22
oxysterol binding protein-like 3	Osbpl3	0.87±0.06

oxysterol binding protein-like 7 (predicted)	Osbpl7_predicted	0.43±0.11
oxysterol binding protein-like 9 (predicted)	Osbpl9_predicted	2.89±0.53
P18SRP protein	P18srp	1.88±0.29
P21 (CDKN1A)-activated kinase 1	Pak1	1.12±0.3
P21 (CDKN1A)-activated kinase 2	Pak2	0.79±0.15
p21 (CDKN1A)-activated kinase 4 (predicted)	Pak4_predicted	0.67±0.29
p300/CBP-associated factor	Pcaf	5.11±0.24
p34 protein	P34	0.38±0.19
P450 (cytochrome) oxidoreductase	Por	7.21±1.85
p53 and DNA damage regulated 1	Pdrg1	0.7±0.21
P55	LOC362855	8.58±0.98
p55 protein	LOC652956	9.44±1.95
Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	Paf1	0.73±0.11
paired box gene 8	Pax8	4.94±1
paired-like homeodomain transcription factor 2	Pitx2	1.73±0.09
PAK1 interacting protein 1	Pak1ip1	0.43±0.16
pallidin	Pldn	1.92±0.09
palmitoyl-protein thioesterase 1	Ppt1	1.72±0.22
palmitoyl-protein thioesterase 2	Ppt2	0.83±0.15
PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	Pan3	1.34±0.07
Pannexin 1	Panx1	0.26±0.05
pantothenate kinase 1 (predicted)	Pank1_predicted	7.27±1.7
pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	0.61±0.09
pantothenate kinase 3 (predicted)	Pank3_predicted	0.37±0.05
pantothenate kinase 4	Pank4	1.06±0.15
PAP associated domain containing 1 (predicted)	Papd1_predicted	1.52±0.23
PAP associated domain containing 4	Papd4	0.8±0.09
PAP associated domain containing 5 (predicted)	Papd5_predicted	4.35±0.19
papillary renal cell carcinoma (translocation-associated) (predicted)	Prcc_predicted	0.85±0.09
par-6 (partitioning defective 6) homolog beta (C. elegans) (predicted)	Pard6b_predicted	4±0.27
par-6 (partitioning defective 6,) homolog alpha (C. elegans)	Pard6a	0.41±0.08
paralemmin	Palm	2.23±0.56
paraoxonase 2	Pon2	6.13±0.1
paraoxonase 3	Pon3	3.2±0.94
paraspeckle protein 1	Pspc1	2±0.12
parathymosin	Ptms	5.51±1.98
parathyroid hormone receptor 1	Pthr1	22.6±3.38
Parkinson disease (autosomal recessive, early onset) 7	Park7	28.39±0.68
partner of NOB1 homolog (S. cerevisiae)	Pno1	1.88±0.19
patatin-like phospholipase domain containing 2 (predicted)	Pnpla2_predicted	1.82±0.17
patatin-like phospholipase domain containing 6	Pnpla6	0.25±0.1
patatin-like phospholipase domain containing 7	Pnpla7	2±0.25
patatin-like phospholipase domain containing 8	Pnpla8	0.65±0.19
PAX interacting (with transcription-activation domain) protein 1 (predicted)	Paxip1_predicted	0.41±0.14
paxillin	Pxn	4.55±0.6
PC4 and SFRS1 interacting protein 1	Psip1	0.93±0.27
PCTAIRE-motif protein kinase 1	Pctk1	0.92±0.11
PCTAIRE-motif protein kinase 2	Pctk2	1.45±0.25
PDGFA associated protein 1	Pdap1	4.75±0.57
PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	Pds5a	2.18±0.26
PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	Pds5b	1.09±0.13
PDZ binding kinase (predicted)	Pbk_predicted	0.34±0.22
PDZ domain containing 1	Pdzk1	40.44±0.62
PDZ domain containing 11 (predicted)	Pdzd11_predicted	2.55±0.44
PDZ domain containing 3	Pdzd3	7.47±0.75
PDZ domain containing 8	Pdzd8	0.75±0.1
PDZ domain containing RING finger 3 (predicted)	Pdzrn3_predicted	1.53±0.24
PDZK1 interacting protein 1	Pdzk1ip1	28.09±2.55
pecanex homolog (Drosophila)	Pcnx	2.78±0.36
pecanex-like 3 (Drosophila)	Pcnxl3	1.6±0.17
pellino homolog 1 (Drosophila) /// similar to pellino protein (predicted)	Peli1 /// RGD1564594_predicted	1.2±0.24
pelota homolog (Drosophila)	Pelo	1.86±0.03
penta-EF hand domain containing 1	Pef1	2.27±0.09
pentatricopeptide repeat domain 1 (predicted)	Ptcd1_predicted	2.1±0.21
pentatricopeptide repeat domain 2 (predicted)	Ptcd2_predicted	0.67±0.06
Pentatricopeptide repeat domain 3	Ptcd3	18.08±3.36
peptidase (mitochondrial processing) alpha	Pmpca	3.83±0.22
peptidase (mitochondrial processing) beta	Pmpcb	6.84±0.75
peptidylglycine alpha-amidating monooxygenase	Pam	16.05±0.66
peptidylprolyl isomerase (cyclophilin)-like 1	Ppil1	0.56±0.07
peptidylprolyl isomerase (cyclophilin)-like 2	Ppil2	1.68±0.12
peptidylprolyl isomerase (cyclophilin)-like 3	Ppil3	1.48±0.5
peptidylprolyl isomerase (cyclophilin)-like 4 (predicted)	Ppil4_predicted	0.4±0.02
peptidylprolyl isomerase A	Ppia	50.27±1.08
peptidylprolyl isomerase B	Ppib	19.77±1.6
peptidylprolyl isomerase D (cyclophilin D)	Ppid	4.3±0.62
peptidylprolyl isomerase domain and WD repeat containing 1 (predicted)	Ppwd1_predicted	0.28±0.16
peptidylprolyl isomerase E (cyclophilin E)	Ppie	0.51±0.09
peptidylprolyl isomerase F (cyclophilin F)	Ppif	1.29±0.2
peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae) (predicted)	Ptrh1_predicted	0.28±0.07
Peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae) (predicted)	Tor2a	0.27±0.02
peptidyl-tRNA hydrolase 2	Ptrh2	1.17±0.09
pericentriolar material 1	Pcm1	2.11±0.29
period homolog 2 (Drosophila)	Per2	2.95±1.09
periphilin 1 (predicted)	Pphln1_predicted	1.15±0.1
peroxiredoxin 1	Prdx1	40.84±4.27

peroxiredoxin 2	Prdx2	10.76±1.61
peroxiredoxin 3	Prdx3	18.16±0.86
peroxiredoxin 4	Prdx4	1.22±0.28
peroxiredoxin 5	Prdx5	14.91±0.44
peroxiredoxin 6	Prdx6	7.05±0.35
peroxisomal biogenesis factor 11A	Pex11a	3.61±0.28
peroxisomal biogenesis factor 11b	Pex11b	1.47±0.07
peroxisomal biogenesis factor 11c (predicted)	Pex11c_predicted	0.8±0.09
peroxisomal biogenesis factor 12	Pex12	1.74±0.2
peroxisomal biogenesis factor 13 (predicted)	Pex13_predicted	8.61±1.05
peroxisomal biogenesis factor 3	Pex3	1.03±0.07
peroxisomal biogenesis factor 6	Pex6	0.66±0.28
peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	Peci	9.51±1.53
peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase /// similar to RIKEN cDNA 1810022C23	Peci /// RGD1310224	21.38±2.15
peroxisomal membrane protein 2	Pxmp2	5.79±1.03
peroxisomal membrane protein 4	Pxmp4	2.99±2.15
peroxisomal trans-2-enoyl-CoA reductase	Pecr	21.69±0.89
peroxisome biogenesis factor 1	Pex1	2.59±0.13
peroxisome biogenesis factor 10	Pex10	0.71±0.1
peroxisome biogenesis factor 16	Pex16	2.68±0.19
peroxisome biogenesis factor 19	Pex19	1.15±0.21
peroxisome biogenesis factor 19 /// similar to Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxisomal farnesylated protein)	LOC679129 /// Pex19	3.24±0.14
peroxisome biogenesis factor 2	Pex2	1.37±0.25
peroxisome biogenesis factor 26	Pex26	0.79±0.18
peroxisome biogenesis factor 5 (predicted)	Pex5_predicted	5.27±0.29
peroxisome biogenesis factor 7	Pex7	2.53±0.12
peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	0.92±0.05
peroxisome proliferative activated receptor, gamma, coactivator 1 beta	Ppargc1b	0.54±0.09
PERP, TP53 apoptosis effector (predicted)	Perp_predicted	16.99±0.79
PEST proteolytic signal containing nuclear protein	Pcnp	3.47±0.4
PET112-like (yeast) (predicted)	Pet112l_predicted	1.06±0.16
peter pan homolog (Drosophila)	Ppan	0.44±0.12
PFTAIRE protein kinase 1 (predicted)	Pftk1_predicted	1.88±0.27
PHD finger protein 12	Phf12	0.47±0.13
PHD finger protein 13 (predicted)	Phf13_predicted	0.47±0.16
PHD finger protein 14	Phf14	0.7±0.35
PHD finger protein 17 (predicted)	Phf17_predicted	6.15±0.48
PHD finger protein 2 (predicted)	Phf2_predicted	0.55±0.21
PHD finger protein 20-like 1	Phf20l1	1.56±0.19
PHD finger protein 3 (predicted)	Phf3_predicted	2.28±0.36
PHD finger protein 5A	Phf5a	2.6±0.36
phenazine biosynthesis-like protein domain containing	Pbld	19.22±1.68
phenylalanine hydroxylase	Pah	64.61±2.21
phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	1.3±0.27
Phenylalanine-tRNA synthetase-like, alpha subunit	Farsla	1.35±0.16
phenylalanyl-tRNA synthetase, beta subunit	Farsb	3.03±0.49
phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Ebp	2.11±0.09
phosducin-like	Pdcl	0.94±0.25
phosducin-like 3	Pdcl3	2.83±0.23
phosphatase and tensin homolog	Pten	1.47±0.16
phosphatase, orphan 2	Phospho2	1.81±0.05
phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	2.18±0.11
phosphate cytidylyltransferase 2, ethanolamine	Pcyt2	2.72±0.52
phosphatidic acid phosphatase type 2 domain containing 1B	Ppapdc1b	3.63±0.44
phosphatidic acid phosphatase type 2 domain containing 2	Ppapdc2	2.49±0.43
phosphatidic acid phosphatase type 2B	Ppap2b	0.81±1.11
phosphatidic acid phosphatase type 2c	Ppap2c	3.12±0.75
phosphatidylcholine transfer protein	Pctp	0.52±0.24
phosphatidylethanolamine binding protein 1	Pebp1	25.83±1.09
phosphatidylglycerophosphate synthase 1	Pgs1	0.56±0.14
phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide (predicted)	Pik3c2a_predicted	5.45±1
Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	4.91±0.21
phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	LOC685590 /// Pik3ca	0.29±0.06
phosphatidylinositol 3-kinase, catalytic, beta polypeptide	Pik3cb	0.59±0.11
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	Pik3r2	1.28±0.15
phosphatidylinositol 4-kinase type 2 alpha	Pi4k2a	0.32±0.09
phosphatidylinositol 4-kinase, catalytic, alpha	Pi4ka	2.04±0.25
phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pi4kb	3.14±0.35
Phosphatidylinositol binding clathrin assembly protein	Picalm	29.75±1.34
phosphatidylinositol glycan anchor biosynthesis, class C	Pigc	2.11±0.26
phosphatidylinositol glycan anchor biosynthesis, class L	Pigl	0.92±0.05
phosphatidylinositol glycan anchor biosynthesis, class M	Pigm	0.49±0.1
phosphatidylinositol glycan anchor biosynthesis, class O	Pigo	1.55±0.25
phosphatidylinositol glycan anchor biosynthesis, class P	Pigp	17.07±0.71
phosphatidylinositol glycan anchor biosynthesis, class Q	Pigq	2.56±0.51
phosphatidylinositol glycan anchor biosynthesis, class S	Pigs	1.5±0.07
phosphatidylinositol glycan anchor biosynthesis, class T	Pigt	4.45±0.65
phosphatidylinositol glycan anchor biosynthesis, class V	Pigv	0.64±0.16
phosphatidylinositol glycan anchor biosynthesis, class X	Pigx	4.39±0.1
phosphatidylinositol glycan anchor biosynthesis, class Y	Pigy	5.52±0.31
phosphatidylinositol glycan, class K /// ubiquitin specific peptidase 33	Pigk /// Usp33	4.81±0.44
phosphatidylinositol transfer protein, alpha	Pitpna	3.62±1.21
phosphatidylinositol transfer protein, beta	Pitpnb	4.91±0.22
phosphatidylinositol transfer protein, membrane-associated 1	Pitpnm1	0.62±0.27
phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	Pip5k3	0.39±0.07
phosphatidylinositol-4-phosphate 5-kinase, type 1, alpha (predicted)	Pip5k1a_predicted	0.29±0.08
phosphatidylinositol-4-phosphate 5-kinase, type 1, beta	Pip5k1b	0.64±0.13

phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	Pip5k1c	2.8±0.35
phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	Pip4k2a	0.59±0.21
phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	Pip4k2c	3.57±0.21
phosphatidylserine decarboxylase	Pisd	0.7±0.1
phosphatidylserine synthase 1	Ptdss1	2.7±0.66
phosphatidylserine synthase 2 (predicted)	Ptdss2_predicted	2.77±0.75
phosphodiesterase 3B, cGMP-inhibited	Pde3b	1.09±0.19
phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	1.32±0.32
phosphodiesterase 6D, cGMP-specific, rod, delta (predicted)	Pde6d_predicted	1.89±0.19
phosphodiesterase 7A	Pde7a	2.4±0.29
Phosphodiesterase 8A	Pde8a	0.87±0.27
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	57.23±2.35
phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted	1.11±0.27
phosphofructokinase, liver, B-type	Pfkl	1.18±0.35
phosphofructokinase, muscle	Pfkm	1.76±0.15
phosphoglucomutase 1	Pgm1	3.97±0.7
phosphoglucomutase 5 (predicted) /// similar to phosphoglucomutase 5	LOC687552 /// Pgm5_predicted	0.51±0.03
phosphoglycerate dehydrogenase like 1	Phgdhl1	2.47±0.33
phosphoglycerate kinase 1	Pgk1	42.88±0.53
phosphoglycerate mutase 1	Pgam1	38.59±1.6
phosphoglycerate mutase family member 5	Pgam5	2.9±0.13
phosphohistidine phosphatase 1 (predicted)	Phpt1_predicted	8.28±1.09
Phosphoinositide-3-kinase adaptor protein 1 (predicted)	Pik3ap1_predicted	1.26±0.41
phosphoinositide-3-kinase, class 3	Pik3c3	0.76±0.11
phosphoinositide-3-kinase, regulatory subunit 4, p150 (predicted)	Pik3r4_predicted	1.84±0.2
phospholipase A2, activating protein	Plaa	1.96±0.36
phospholipase A2, group VI	Pla2g6	0.69±0.5
phospholipase A2, group XIIA (predicted)	Pla2g12a_predicted	1.19±0.08
phospholipase C, beta 1	Plcb1	7.53±0.91
phospholipase C, gamma 1	Plcg1	1.06±0.42
phospholipase C-like 1	Plcl1	6.91±0.61
phospholipase D family, member 3	Pld3	1.16±0.14
phospholipid scramblase 1	Plscr1	0.8±0.16
phospholipid scramblase 2	Plscr2	15.28±0.73
phospholipid scramblase 3	Plscr3	0.43±0.26
Phospholipid transfer protein (predicted)	Pltp_predicted	4.04±0.57
phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Lhpp	4.76±0.64
phosphomannomutase 1	Pmm1	0.42±0.18
phosphomannomutase 2 (predicted)	Pmm2_predicted	2.75±0.37
phosphomevalonate kinase	Pmvk	0.46±0.31
phosphopantothenoylcysteine decarboxylase (predicted)	Ppcdc_predicted	0.29±0.1
phosphopantothenoylcysteine synthetase	Ppcs	3.42±0.53
phosphoribosyl pyrophosphate amidotransferase	Ppat	1.22±0.06
phosphoribosyl pyrophosphate synthetase 1	Prps1	1.83±0.56
phosphoribosyl pyrophosphate synthetase 2	Prps2	3.38±0.6
phosphoribosyl pyrophosphate synthetase-associated protein 1	Prpsap1	3.26±0.33
phosphoribosyl pyrophosphate synthetase-associated protein 2	Prpsap2	3.73±0.72
phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	Paics	10.54±1.22
phosphoribosylformylglycinamidine synthase (FGAR amidotransferase) (predicted)	Pfas_predicted	0.49±0.38
phosphoribosylglycinamide formyltransferase	Gart	1.01±0.11
Phosphorylase kinase alpha 1	Phka1	0.62±0.06
phosphorylase kinase, gamma 2 (testis)	Phkg2	2.02±0.25
phosphoserine aminotransferase 1	Psat1	42.59±1.08
phosphoserine phosphatase	Psph	15.52±1.32
phosphotriesterase related	Pter	16.84±2.89
phytanoyl-CoA dioxygenase domain containing 1	Phyhd1	18.9±1.63
Phytanoyl-CoA hydroxylase	Phyh	15.85±2.14
Phytn_dehydro and Pyr_redox domain containing protein RGD1303232	RGD1303232	27.3±4.46
phytoceramidase, alkaline	Phca	0.79±0.13
PIH1 domain containing 1	Pih1d1	0.99±0.1
PIN2-interacting protein 1	Pinx1	0.37±0.11
pinin	Pnn	1.93±0.61
pitrilysin metallepetidase 1 (predicted)	Pitrm1_predicted	5.06±0.56
pituitary tumor-transforming 1 interacting protein	Pttg1ip	21.27±0.97
placenta-specific 8 (predicted)	Plac8_predicted	16.76±0.71
plakophilin 2	Pkp2	1.3±0.18
plakophilin 3 (predicted)	Pkp3_predicted	0.44±0.25
plakophilin 4 (predicted)	Pkp4_predicted	5.54±1.13
plasma glutamate carboxypeptidase	Pgcp	26.16±2.57
plasma membrane proteolipid	Pllp	17.01±1.79
plasminogen activator, urokinase	Plau	28.96±2.89
plastin 1 (I isoform) (predicted)	Pls1_predicted	5±0.31
platelet derived growth factor receptor, alpha polypeptide	Pdgfra	1.3±0.35
platelet derived growth factor, alpha	Pdgfa	1.49±0.07
platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	Pafah1b3	1.05±0.14
platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	2.52±0.52
platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	Pafah1b1	3.51±0.13
platelet-activating factor receptor	Ptafr	0.32±0.27
platelet-derived growth factor, C polypeptide	Pdgfc	1.19±0.09
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	Plekha1	6.3±0.2
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	Plekha8	0.34±0.06
Pleckstrin homology domain containing, family A member 5	Plekha5	1.23±0.25
pleckstrin homology domain containing, family A member 6 (predicted)	Plekha6_predicted	1.79±0.01
pleckstrin homology domain containing, family B (evectins) member 1	Plekhb1	0.27±0.06
pleckstrin homology domain containing, family B (evectins) member 2 (predicted)	Plekhb2_predicted	24.04±3.26
pleckstrin homology domain containing, family C (with FERM domain) member 1	Plekhc1	2.33±0.49

pleckstrin homology domain containing, family F (with FYVE domain) member 1	Plekhf1	0.48±0.14
pleckstrin homology domain containing, family F (with FYVE domain) member 2 (predicted)	Plekhf2_predicted	10.31±1.16
pleckstrin homology domain containing, family G (with RhoGef domain) member 3	Plekhg3	2.85±0.1
pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)	Plekhh1_predicted	0.55±0.24
pleckstrin homology domain containing, family J member 1	Plekhj1	1.5±0.62
pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	Plekha3	2.59±0.2
pleckstrin homology, Sec7 and coiled-coil domains 2	Pscd2	2.15±0.12
pleckstrin homology-like domain, family A, member 2 (predicted)	Phlda2_predicted	0.31±0.12
pleckstrin homology-like domain, family B, member 2	Phldb2	2.54±0.2
pleiomorphic adenoma gene-like 1	Plagl1	0.51±0.53
pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	Plrg1	3.2±1.05
plexin A2 (predicted)	Plxna2_predicted	0.38±0.1
plexin B2	Plxnb2	4.73±0.54
plexin domain containing 2 (predicted)	Plxdc2_predicted	0.9±0.25
podoplanin	Pdpn	0.63±0.27
pogo transposable element with KRAB domain (predicted)	Pogk_predicted	0.22±0.06
pogo transposable element with ZNF domain (predicted)	Pogz_predicted	0.42±0.06
Poliovirus receptor-related 3 (predicted)	Pvrl3_predicted	4.2±0.22
poly (A) polymerase alpha (predicted)	Papola_predicted	2.88±0.42
poly (ADP-ribose) glycohydrolase	Parg	6.59±0.46
poly (ADP-ribose) polymerase family, member 1	Parp1	3.67±0.15
poly (ADP-ribose) polymerase family, member 12 (predicted)	Parp12_predicted	0.65±0.12
poly (ADP-ribose) polymerase family, member 16	Parp16	2.68±0.57
poly (ADP-ribose) polymerase family, member 2 (predicted)	Parp2_predicted	0.73±0.09
poly (ADP-ribose) polymerase family, member 9 (predicted)	Parp9_predicted	0.31±0.06
poly A binding protein, cytoplasmic 4	Pabpc4	5.7±0.22
poly(A) binding protein, cytoplasmic 1	Pabpc1	13.52±1.61
poly(A) polymerase gamma (predicted)	Papolg_predicted	0.36±0.21
poly(A)-specific ribonuclease (deadenylation nuclease)	Parn	0.61±0.11
poly(rC) binding protein 1	Pcbp1	14.4±0.86
poly(rC) binding protein 2	Pcbp2	10.8±2.21
poly(rC) binding protein 3	Pcbp3	0.61±0.16
poly(rC) binding protein 4 (predicted)	Pcbp4_predicted	2.3±0.64
polyadenylate binding protein-interacting protein 1 (predicted)	Paip1_predicted	4.27±0.48
polyadenylate-binding protein interacting protein 2	Paip2	9.67±0.9
polyamine modulated factor 1 binding protein 1	Pmfbp1	0.75±0.14
polyamine-modulated factor 1	Pmf1	0.23±0.18
polybromo 1	Pbrm1	3.41±0.21
polycomb group ring finger 1	Pcgf1	0.58±0.17
polycomb group ring finger 2 (predicted)	Pcgf2_predicted	0.29±0.02
polycomb group ring finger 3	Pcgf3	0.58±0.01
Polycomb group ring finger 4 (predicted)	Pcgf4_predicted	3.41±0.19
polycomb group ring finger 5 /// similar to polycomb group ring finger 5	LOC687730 /// Pcgf5	1.4±0.2
polycomb group ring finger 6	Pcgf6	1.05±0.12
polyglutamine binding protein 1	Pqbp1	1.02±0.17
polyhomeotic-like 1 (Drosophila) (predicted)	Phc1_predicted	0.52±0.18
polyhomeotic-like 2 (Drosophila)	Phc2	0.76±0.24
polymerase (DNA directed) sigma (predicted)	Pols_predicted	0.74±0.06
Polymerase (DNA directed), alpha 1	Pola1	1.4±0.02
polymerase (DNA directed), beta	Polb	1.08±0.13
polymerase (DNA directed), delta 2, regulatory subunit	Pold2	0.39±0.04
polymerase (DNA directed), epsilon 3 (p17 subunit)	Pole3	2.91±0.44
polymerase (DNA directed), gamma	Polg	1.92±0.09
polymerase (DNA directed), gamma 2, accessory subunit (predicted)	Polg2_predicted	3.71±0.23
polymerase (DNA directed), lambda	Poll	0.78±0.14
polymerase (DNA directed), mu	Polm	0.53±0.07
polymerase (DNA-directed), delta 3, accessory subunit	Pold3	0.23±0.12
polymerase (DNA-directed), delta 4	Pold4	3.03±0.61
polymerase (DNA-directed), delta interacting protein 2 (predicted)	Poldip2_predicted	3.6±0.09
polymerase (DNA-directed), delta interacting protein 3 (predicted)	Poldip3_predicted	0.82±0.18
polymerase (DNA-directed), epsilon 4 (p12 subunit) (predicted)	Pole4_predicted	4.66±1.33
polymerase (RNA) I polypeptide E	Polr1e	0.49±0.08
polymerase (RNA) II (DNA directed) polypeptide A	Polr2a	1.53±0.21
polymerase (RNA) II (DNA directed) polypeptide B (predicted)	Polr2b_predicted	3.95±0.53
polymerase (RNA) II (DNA directed) polypeptide C	Polr2c	1.78±0.52
polymerase (RNA) II (DNA directed) polypeptide C /// similar to RIKEN cDNA 2310005O14	LOC498909 /// Polr2c	15.02±1.38
polymerase (RNA) II (DNA directed) polypeptide D (predicted)	Polr2d_predicted	3.93±0.12
polymerase (RNA) II (DNA directed) polypeptide E	Polr2e	3.81±0.66
polymerase (RNA) II (DNA directed) polypeptide F	Polr2f	2.93±0.24
polymerase (RNA) II (DNA directed) polypeptide G	Polr2g	5.2±0.32
polymerase (RNA) II (DNA directed) polypeptide H (predicted)	Polr2h /// Polr2h_predicted /// RGD1565904_predicted	1.19±0.49
polymerase (RNA) II (DNA directed) polypeptide I (predicted)	Polr2i_predicted	1.51±0.05
polymerase (RNA) II (DNA directed) polypeptide J (predicted)	Polr2j_predicted	4.29±0.39
polymerase (RNA) III (DNA directed) polypeptide A	Polr3a	1.19±0.23
polymerase (RNA) III (DNA directed) polypeptide C	Polr3c	0.76±0.15
polymerase (RNA) III (DNA directed) polypeptide D	Polr3d	1.61±0.21
polymerase (RNA) III (DNA directed) polypeptide E (predicted)	Polr3e_predicted	0.47±0.08
polymerase (RNA) III (DNA directed) polypeptide F (predicted)	Polr3f_predicted	0.5±0.17
polymerase (RNA) III (DNA directed) polypeptide G	Polr3g	4.83±0.38
polymerase (RNA) III (DNA directed) polypeptide H (predicted)	Polr3h_predicted	0.66±0.17
polymerase (RNA) III (DNA directed) polypeptide K	Polr3k	1.85±0.41
polymerase (RNA) mitochondrial (DNA directed) (predicted)	Polrmt_predicted	1.65±0.21
polynucleotide kinase 3'-phosphatase	Pnkp	0.77±0.13
polypyrimidine tract binding protein 1	Ptbp1	4.98±0.3
polypyrimidine tract binding protein 2	Ptbp2	0.28±0.11

polyribonucleotide nucleotidyltransferase 1	Pnpt1	4.84±0.35
postmeiotic segregation increased 1 (S. cerevisiae)	Pms1	0.67±0.09
postmeiotic segregation increased 2 (S. cerevisiae) (predicted)	Pms2_predicted	0.32±0.08
potassium channel tetramerisation domain containing 13	Kctd13	0.34±0.09
potassium channel tetramerisation domain containing 15	Kctd15	0.6±0.12
potassium channel tetramerisation domain containing 2	Kctd2	0.9±0.26
potassium channel tetramerisation domain containing 3	Kctd3	1.55±0.17
potassium channel tetramerisation domain containing 5 (predicted)	Kctd5_predicted	5.73±0.27
potassium channel tetramerisation domain containing 6 (predicted)	Kctd6_predicted	3.09±0.29
potassium channel tetramerisation domain containing 9 (predicted)	Kctd9_predicted	2.71±0.32
potassium channel, subfamily K, member 5	Kcnk5	2.88±0.25
potassium inwardly-rectifying channel, subfamily J, member 12	Kcnj12	1.58±0.08
potassium inwardly-rectifying channel, subfamily J, member 15	Kcnj15	1.72±0.07
potassium inwardly-rectifying channel, subfamily J, member 16	Kcnj16	24.44±2.66
potassium inwardly-rectifying channel, subfamily J, member 3	Kcnj3	0.3±0.04
potassium voltage gated channel, Shab-related subfamily, member 1	Kcnb1	0.71±0.07
potassium voltage gated channel, Shaw-related subfamily, member 3	Kcnc3	0.31±0.07
potassium voltage-gated channel, shaker-related subfamily, member 2	Kcna2	0.26±0.01
POU domain, class 2, transcription factor 1	Pou2f1	0.27±0.04
PP3111 protein	Pp3111	2.75±0.33
PQ loop repeat containing 1	Pqlc1	10.07±1.17
PQ loop repeat containing 2 (predicted)	Pqlc2_predicted	0.66±0.23
PR domain containing 15 (predicted)	Prdm15_predicted	0.59±0.25
PRA1 domain family 2 (predicted)	Praf2_predicted	0.8±0.16
praja 2, RING-H2 motif containing	Pja2	3.32±0.12
pre-B-cell colony enhancing factor 1	Pbef1	2.04±0.51
pre-B-cell leukemia transcription factor 2	Pbx2	0.87±0.33
pre-B-cell leukemia transcription factor interacting protein 1	Pbxip1	0.54±0.23
prefoldin 1 (predicted)	Pfdn1_predicted	6.28±0.08
prefoldin 2	Pfdn2	5.09±0.07
prefoldin 5 (predicted)	Pfdn5_predicted	6.59±0.51
pregnancy specific beta-1-glycoprotein 4	Psg4	0.36±0.02
pregnancy-zone protein	Pzp	27.97±4.02
PRELI domain containing 1	Prelid1	15.34±1.46
pre-mRNA processing factor 8	Prpf8	4.4±0.18
prenyl (solanesyl) diphosphate synthase, subunit 2	Pdss2	0.79±0.08
Prenylated SNARE protein	Ykt6	1.07±0.49
prenylcysteine oxidase 1	Pcyox1	2.34±0.12
presenilin 1	Psen1	1.81±0.27
presenilin 2	Psen2	0.33±0.14
presenilin 2 /// chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1 /// Psen2	5.05±1.15
presenilin associated, rhomboid-like	Parl	2.85±0.2
presenilin enhancer 2 homolog (C. elegans)	Psenen	6.96±0.83
prickle homolog 4 (Drosophila)	Prickle4	9.12±0.64
prickle-like 1 (Drosophila)	Prickle1	0.54±0.03
prickle-like 2 (Drosophila) (predicted)	Prickle2_predicted	0.33±0.03
prion protein interacting protein 1	Prnpip1	1.51±0.34
PRKC, apoptosis, WT1, regulator	Pawr	1.85±0.16
Prkr interacting protein 1 (IL11 inducible)	Prkrip1	0.29±0.16
processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	Pop4	0.94±0.12
processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (predicted)	Pop5_predicted	1.14±0.17
processing of precursor 7, ribonuclease P family, (S. cerevisiae) (predicted)	Pop7_predicted	1.07±0.13
procollagen, type IV, alpha 1 /// procollagen, type IV, alpha 2 (predicted)	Col4a1 /// Col4a2_predicted	12.34±1.1
procollagen, type IV, alpha 2 (predicted)	Col4a2_predicted	2.89±1.12
procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein (predicted)	Col4a3bp_predicted	3.76±0.44
procollagen, type IV, alpha 4	Col4a4	2.08±0.08
procollagen, type IX, alpha 1	Col9a1	0.73±0.26
procollagen, type XVIII, alpha 1	Col18a1	0.74±0.29
Procollagen, type XXVII, alpha 1	Col27a1	1.02±0.69
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	Plod1	2.55±0.28
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	Plod3	1.14±0.07
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	P4ha1	4.14±1.09
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	P4ha2_predicted	0.31±0.05
profilin 1	Pfn1	9.12±1.58
progesterone receptor membrane component 1	Pgrmc1	46.48±2.88
progesterone receptor membrane component 2	Pgrmc2	3.75±0.17
progestin and adipoQ receptor family member IX (predicted)	Paqr9_predicted	3.15±0.66
progestin and adipoQ receptor family member V	Paqr5	6.22±1.12
progestin induced protein	Dd5	6.35±0.54
programmed cell death 10	Pdcd10	7.18±0.87
programmed cell death 2	Pdcd2	1.38±0.14
programmed cell death 4	Pdcd4	0.75±0.34
programmed cell death 5 (predicted)	Pdcd5_predicted	4.12±0.58
programmed cell death 6 (predicted)	Pdcd6_predicted	7.11±0.53
programmed cell death 6 interacting protein	Pdcd6ip	5.28±0.18
programmed cell death protein 11 (predicted)	Pdcd11_predicted	0.52±0.14
programmed cell death protein 7 (predicted)	Pdcd7_predicted	2.77±0.33
progressive ankylosis	Ank	0.45±0.1
Progressive ankylosis homolog (mouse)	Ank	0.34±0.16
progressive external ophthalmoplegia 1 (human)	Peo1	0.54±0.09
prohibitin	Phb	8.24±0.45
prohibitin 2	Phb2	15.15±1.08
prolactin receptor	Prlr	5.93±1.68
prolactin regulatory element binding	Preb	3.31±0.34
proliferating cell nuclear antigen	Pcna	7.94±0.6
proliferation-associated 2G4	Pa2g4	1.07±0.52

proline dehydrogenase (oxidase) 2	Prodh2	26.24±2.6
proline rich 13	Prr13	0.98±0.7
proline rich 14	Prr14	0.59±0.22
proline rich 5 (renal)	Prr5	1.95±0.64
proline synthetase co-transcribed (predicted)	Prosc_predicted	19.57±0.09
proline, glutamic acid and leucine rich protein 1	Pelp1	0.28±0.11
proline/serine-rich coiled-coil 2	Psrc2	0.71±0.18
proline-rich nuclear receptor coactivator 1	Pnrc1	2.13±1.25
proline-rich nuclear receptor coactivator 2	Pnrc2	8.19±0.55
proline-rich polypeptide 3	Prr3	0.88±0.14
proline-rich polypeptide 6	Prr6	0.83±0.19
proline-rich transmembrane protein 1 /// similar to NG5 protein	LOC683953 /// Prrt1	0.23±0.12
prolyl 4-hydroxylase, beta polypeptide	P4hb	15.88±2.8
prolyl endopeptidase-like	Prepl	0.85±0.16
promethin	LOC378467	3.56±0.36
prominin 1	Prom1	3.34±1.02
propionyl coenzyme A carboxylase, beta polypeptide	Pccb	11.99±0.23
propionyl-coenzyme A carboxylase, alpha polypeptide	Pcca	8.83±0.62
proprotein convertase subtilisin/kexin type 1 inhibitor	Pcsk1n	1.58±0.32
proprotein convertase subtilisin/kexin type 7	Pcsk7	0.78±0.15
proprotein convertase subtilisin/kexin type 9	Pcsk9	0.45±0.26
prosaposin	Psap	10.32±1.46
prostaglandin D2 synthase (brain)	Ptgds	7.13±1.67
Prostaglandin E receptor 3 (subtype EP3)	Ptger3	0.66±0.36
prostaglandin E synthase 2 (predicted)	Ptges2_predicted	4.95±0.56
prostaglandin E synthase 3 (cytosolic) (predicted)	Ptges3_predicted	15.54±0.44
prostate tumor over expressed gene 1	Ptov1	2.85±0.95
protease (prosome, macropain) 26S subunit, ATPase 1	Psmc1	3.14±0.41
protease (prosome, macropain) 26S subunit, ATPase 5	Psmc5	3.95±0.97
protease, serine, 8 (prostasin)	Prss8	11.31±0.73
proteaseome (prosome, macropain) 28 subunit, 3	Psme3	4.07±0.22
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2	12.39±2.01
proteasome (prosome, macropain) 26S subunit, ATPase 3	Psmc3	4.57±0.38
proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	Psmc3ip	0.39±0.15
proteasome (prosome, macropain) 26S subunit, ATPase, 4	Psmc4	4.89±0.3
proteasome (prosome, macropain) 26S subunit, ATPase, 6	Psmc6	4.18±0.89
proteasome (prosome, macropain) 26S subunit, ATPase, 6 /// similar to Psmc6 protein (predicted)	Psmc6 /// RGD1559647_predicted	1.01±0.16
proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	Psmd1	3.24±0.35
proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmd11_predicted	7.92±1.06
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	Psmd12	5.29±0.54
proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (predicted)	Psmd13_predicted	3.22±0.4
proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Psmd14	4.21±0.55
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Psmd2	10.39±0.78
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	Psmd3	2.6±0.3
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	Psmd4	2.72±0.15
proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (predicted)	Psmd5_predicted	3.61±0.11
proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	Psmd6	7.88±1.72
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (predicted)	Psmd7_predicted	3.27±0.44
proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	Psmd8	4.81±0.37
proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Psmd9	1.69±0.35
proteasome (prosome, macropain) 28 subunit, alpha	Psme1	2.88±0.84
proteasome (prosome, macropain) 28 subunit, beta	Psme2	2.36±0.27
proteasome (prosome, macropain) activator subunit 4	Psme4	5.78±0.89
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	6.81±1.57
proteasome (prosome, macropain) subunit, alpha type 2	Psma2	8.89±2.74
proteasome (prosome, macropain) subunit, alpha type 3 /// proteasome subunit alpha type 3-like	Psma3 /// Psma3l	11.48±1.37
proteasome (prosome, macropain) subunit, alpha type 4	Psma4	3.85±0.41
proteasome (prosome, macropain) subunit, alpha type 5	Psma5	8.36±0.29
proteasome (prosome, macropain) subunit, alpha type 6	Psma6	17.81±1.15
proteasome (prosome, macropain) subunit, alpha type 7	Psma7	9.63±0.53
proteasome (prosome, macropain) subunit, beta type 1	Psmb1	11.02±0.21
proteasome (prosome, macropain) subunit, beta type 2	Psmb2	9.21±0.52
proteasome (prosome, macropain) subunit, beta type 3	Psmb3	5.62±0.09
proteasome (prosome, macropain) subunit, beta type 4	Psmb4	19.53±0.68
proteasome (prosome, macropain) subunit, beta type 5	Psmb5	14.67±0.64
proteasome (prosome, macropain) subunit, beta type 6	Psmb6	6.71±0.69
proteasome (prosome, macropain) subunit, beta type 7	Psmb7	8.77±0.2
proteasome maturation protein	Pomp	17.88±0.37
protective protein for beta-galactosidase	Ppgb	74.29±3.56
protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (predicted)	Pin1_predicted	3.54±0.29
protein arginine N-methyltransferase 1	Prmt1	2.7±0.23
protein arginine N-methyltransferase 2	Prmt2	0.25±0.1
protein arginine N-methyltransferase 3	Prmt3	0.78±0.14
protein arginine N-methyltransferase 5 (predicted)	Prmt5_predicted	1.76±0.33
protein arginine N-methyltransferase 6 (predicted)	Prmt6_predicted	0.27±0.09
protein associated with topoisomerase II homolog 1 (yeast)	Patl1	1.01±0.07
protein C	Proc	3.43±0.42
protein disulfide isomerase associated 3	Pdia3	9.89±2.51
protein disulfide isomerase associated 4	Pdia4	2.71±0.44
protein disulfide isomerase associated 6	Pdia6	9.66±2.45
protein geranylgeranyltransferase type I, beta subunit	Pggt1b	0.41±0.04
protein inhibitor of activated STAT 1 (predicted)	Pias1_predicted	1.67±0.04
protein inhibitor of activated STAT 2	Pias2	1.71±0.28
protein inhibitor of activated STAT 3	Pias3	0.27±0.04
protein inhibitor of activated STAT, 4	Pias4	0.68±0.28
protein interacting with C kinase 1	Pick1	0.58±0.29

protein kinase C and casein kinase substrate in neurons 1	Pacsin1	0.56±0.12
protein kinase C and casein kinase substrate in neurons 2	Pacsin2	4.27±0.44
protein kinase C and casein kinase substrate in neurons 3	Pacsin3	0.28±0.04
protein kinase C binding protein 1	Prkcbp1	1.66±0.25
protein kinase C substrate 80K-H (predicted)	Prkcsh_predicted	10.5±1.8
protein kinase C, alpha	Prkca	0.48±0.07
protein kinase C, delta	Prkcd	1.83±0.18
protein kinase C, epsilon	Prkce	0.56±0.17
protein kinase C, iota	Prkci	2.4±0.75
protein kinase C, zeta	Prkcz	1.88±0.36
protein kinase D3	Prkd3	2.23±0.13
protein kinase inhibitor, gamma	Pkig	4.89±0.46
protein kinase LYK5	Lyk5	1.11±0.04
protein kinase N1	Pkn1	0.34±0.03
protein kinase N2	Pkn2	3.56±0.25
protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	9.77±0.46
protein kinase, AMP-activated, beta 1 non-catalytic subunit	Prkab1	4.51±0.46
protein kinase, AMP-activated, gamma 1 non-catalytic subunit	Prkag1	1.7±0.33
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Prkag2	0.66±0.12
Protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	3.6±0.53
protein kinase, cAMP dependent regulatory, type I, beta	Prkar1b	0.29±0.07
protein kinase, cAMP dependent, catalytic, beta	Prkacb	7.36±0.6
protein kinase, cAMP-dependent, catalytic, alpha	Prkaca	0.61±0.55
protein kinase, cAMP-dependent, catalytic, alpha /// similar to CG2662-PA (predicted)	Prkaca /// RGD1305094_predicted	0.21±0.31
protein kinase, cGMP-dependent, type II	Prkg2	0.62±0.03
protein kinase, DNA activated, catalytic polypeptide (predicted)	Prkdc_predicted	0.93±0.12
protein kinase, interferon inducible double stranded RNA dependent activator	Prkra	5.39±0.2
protein kinase, X-linked	Prkx	0.38±0.17
protein O-fucosyltransferase 2 (predicted)	Pofut2_predicted	0.65±0.19
protein phosphatase 1, catalytic subunit, alpha isoform	Ppp1ca	14.11±1.25
protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	11.79±0.96
protein phosphatase 1, catalytic subunit, gamma isoform	Ppp1cc	37.2±1.37
protein phosphatase 1, regulatory (inhibitor) subunit 11	Ppp1r11	3.31±0.56
protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	0.64±0.09
protein phosphatase 1, regulatory (inhibitor) subunit 12C	Ppp1r12c	0.9±0.28
protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	4.89±0.34
protein phosphatase 1, regulatory (inhibitor) subunit 14c	Ppp1r14c	0.2±0.05
protein phosphatase 1, regulatory (inhibitor) subunit 15b (predicted)	Ppp1r15b_predicted	2.82±0.32
protein phosphatase 1, regulatory (inhibitor) subunit 16A (predicted)	Ppp1r16a_predicted	0.25±0.05
protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	7.48±0.04
protein phosphatase 1, regulatory (inhibitor) subunit 7	Ppp1r7	2.36±0.26
protein phosphatase 1, regulatory (inhibitor) subunit 8 (predicted)	Ppp1r8_predicted	1.37±0.05
protein phosphatase 1, regulatory subunit 10	Ppp1r10	0.84±0.15
protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	1.44±0.18
protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	9.25±0.85
protein phosphatase 1D magnesium-dependent, delta isoform (predicted)	Ppm1d_predicted	0.47±0.14
protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	Ppm1g	2.11±0.34
protein phosphatase 1H (PP2C domain containing)	Ppm1h	0.9±0.08
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Ppp2ca	13.92±0.38
protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Ppp2cb	7.54±0.38
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a	4.01±0.4
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	8.48±1.08
protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Ppp2r2a	2.24±0.37
protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	Ppp2r3a	3.19±0.4
protein phosphatase 2, regulatory subunit B (B56), alpha isoform (predicted)	Ppp2r5a_predicted	9.76±1.65
protein phosphatase 2, regulatory subunit B (B56), beta isoform	Ppp2r5b	2.19±0.22
protein phosphatase 2, regulatory subunit B (B56), delta isoform	Ppp2r5d	0.5±0.18
protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (predicted)	Ppp2r5e_predicted	3.18±0.6
protein phosphatase 2, regulatory subunit B' gamma isoform	Ppp2r5c	1.32±0.2
protein phosphatase 2, regulatory subunit B, delta isoform	Ppp2r2d	3.35±0.15
protein phosphatase 2, regulatory subunit B'', gamma	Ppp2r3c	1.09±0.16
protein phosphatase 2A, regulatory subunit B (PR 53) (predicted)	Ppp2r4_predicted	3.4±0.55
protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	3.24±0.44
protein phosphatase 3, catalytic subunit, beta isoform	Ppp3cb	2.28±0.2
protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	Ppp3r1	2.43±0.59
protein phosphatase 4, catalytic subunit	Ppp4c	0.75±0.23
protein phosphatase 4, regulatory subunit 1	Ppp4r1	1.5±0.29
protein phosphatase 4, regulatory subunit 1-like	Ppp4r1l	0.49±0.05
protein phosphatase 4, regulatory subunit 2 (predicted)	Ppp4r2_predicted	4.93±0.38
protein phosphatase 5, catalytic subunit	Ppp5c	1.2±0.27
protein phosphatase 6, catalytic subunit	Ppp6c	2.77±0.37
protein phosphatase methylesterase 1	Ppme1	3.98±0.28
protein regulator of cytokinesis 1 (predicted)	Prc1_predicted	1.02±0.33
protein S (alpha)	Pros1	0.27±0.18
protein serine kinase H1 (predicted)	Pskh1_predicted	0.42±0.24
protein tyrosine phosphatase 4a1	Ptp4a1	11±1.3
protein tyrosine phosphatase 4a2	Ptp4a2	9.19±0.48
protein tyrosine phosphatase, mitochondrial 1	Ptpmt1	5.96±0.41
protein tyrosine phosphatase, non-receptor type 1	Ptpn1	0.33±0.05
Protein tyrosine phosphatase, non-receptor type 11	Ptpn11	2.14±0.46
protein tyrosine phosphatase, non-receptor type 12	Ptpn12	2.93±0.28
protein tyrosine phosphatase, non-receptor type 13	Ptpn13	4.82±0.94
Protein tyrosine phosphatase, non-receptor type 14 (predicted)	Ptpn14_predicted	0.26±0.19
protein tyrosine phosphatase, non-receptor type 2	Ptpn2	1.96±0.26
protein tyrosine phosphatase, non-receptor type 21	Ptpn21	1.72±0.12
protein tyrosine phosphatase, non-receptor type 23	Ptpn23	0.9±0.13

protein tyrosine phosphatase, non-receptor type 6	Ptpn6	0.42±0.11
protein tyrosine phosphatase, receptor type, A	Ptpra	0.41±0.19
protein tyrosine phosphatase, receptor type, F	Ptprf	2.62±0.47
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1 (predicted)	Ppfia1_predicted	0.94±0.33
Protein tyrosine phosphatase, receptor type, G	Ptprg	0.89±0.09
protein tyrosine phosphatase, receptor type, J	Ptprj	0.94±0.08
protein tyrosine phosphatase, receptor type, K, extracellular region	Ptprk	2.91±0.32
protein tyrosine phosphatase, receptor type, N	Ptprn	1.58±0.23
protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2	Ppfibp2	2.41±0.29
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	Ptpla	1.95±0.24
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b (predicted)	LOC690040 /// Ptplb_predicted	3.22±0.25
protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) (predicted)	Prkrir_predicted	1.66±0.21
protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	2.29±0.1
protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)	Pcmtd2_predicted	3.84±0.29
protein-O-mannosyltransferase 1	Pomt1	0.79±0.1
protein-O-mannosyltransferase 2	Pomt2	2.84±0.39
proteolipid protein 2	Plp2	1.15±0.08
prothymosin alpha	Ptma	13.96±0.66
Protocadherin 1 (cadherin-like 1) (predicted)	Pcdh1_predicted	0.58±0.27
protocadherin 24	Pcdh24	5.53±0.76
protocadherin alpha 4	Pcdha1 /// Pcdha10 /// Pcdha11 /// Pcdha12 /// Pcdha13 /// Pcdha2 /// Pcdha3 /// Pcdha4 /// Pcdha5 /// Pcdha6 /// Pcdha7 /// Pcdha8 /// Pcdha9 /// Pcdhac1 /// Pcdhac2	0.33±0.18
protoporphyrinogen oxidase (predicted)	Ppox_predicted	2.62±0.17
PRP18 pre-mRNA processing factor 18 homolog (yeast)	Prpf18	1.41±0.25
PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	0.74±0.16
PRP3 pre-mRNA processing factor 3 homolog (yeast) (predicted)	Prpf3_predicted	1.14±0.2
PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (predicted)	Prpf38a_predicted	2.12±0.23
PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	Prpf38b	1.25±0.2
PRP39 pre-mRNA processing factor 39 homolog (yeast) (predicted)	Prpf39_predicted	2.91±0.52
PRP4 pre-mRNA processing factor 4 homolog (yeast)	Prpf4	1.91±0.23
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	1.94±0.16
PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	Prpf40a	0.83±0.14
PRP6 pre-mRNA splicing factor 6 homolog (S. cerevisiae)	Prpf6	1.47±0.33
pseudouridine synthase 1	Pus1	1.1±0.16
pseudouridylate synthase-like 1	Pusl1	0.38±0.04
PTC7 protein phosphatase homolog (S. cerevisiae)	Pptc7	1.35±0.35
PTEN induced putative kinase 1 (predicted)	Pink1_predicted	8.18±1.35
pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	39.75±1.07
PTK2 protein tyrosine kinase 2	Ptk2	4.14±0.28
PTPRF interacting protein, binding protein 1 (liprin beta 1) (predicted)	Ppfibp1_predicted	3.68±0.53
Pumilio 1 (Drosophila) (predicted)	Pum1_predicted	3.05±0.32
pumilio 2 (Drosophila)	Pum2	7.19±0.81
purine rich element binding protein A (predicted)	Pura_predicted	5.85±0.93
purine rich element binding protein B	Purb	0.67±0.1
purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	2.88±0.71
purine-rich element binding protein G (predicted)	Purg_predicted	0.27±0.1
putative GTP-binding protein	LOC293589	2.17±0.16
putative homeodomain transcription factor 1	Phtf1	1.88±0.32
putative homeodomain transcription factor 2 (predicted)	Phtf2_predicted	1.05±0.25
putative nucleic acid binding protein RY-1	Ry1	4.87±0.67
putative scaffolding protein POSH	Sh3md2	0.68±0.14
putative UA20 protein	Ua20	7.86±1.67
PWP1 homolog (S. cerevisiae) (predicted)	Pwp1_predicted	0.67±0.02
PX domain containing serine/threonine kinase	Pxk	0.92±0.27
pyridoxal (pyridoxine, vitamin B6) kinase /// similar to pyridoxal (pyridoxine, vitamin B6) kinase (predicted)	Pdxk /// RGD1566085_predicted	1.59±0.12
pyridoxine 5'-phosphate oxidase	Pnpo	4.11±0.33
pyroglutamyl-peptidase I	Pgpep1	47.07±4.15
pyrophosphatase (inorganic) 1	Ppa1	2.95±0.43
pyrophosphatase (inorganic) 2 (predicted)	Ppa2_predicted	19.23±2.37
pyrroline-5-carboxylate reductase family, member 2	Pycr2	0.61±0.1
pyrroline-5-carboxylate reductase-like	Pycrl	1.44±0.18
pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase) (predicted)	Pycs_predicted	0.23±0.17
pyruvate carboxylase	Pcx	11.08±0.77
pyruvate dehydrogenase (lipoamide) beta	Pdhb	17.64±1.07
pyruvate dehydrogenase complex, component X	Pdhx	2.72±0.12
pyruvate dehydrogenase E1 alpha 1	Pdha1	22.71±0.59
pyruvate dehydrogenase kinase, isoenzyme 2	Pdk2	28.26±3.08
pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	1.59±0.16
pyruvate dehydrogenase phosphatase isoenzyme 2	Pdp2	9.44±0.14
pyruvate dehydrogenase phosphatase regulatory subunit	Pdpr	0.32±0.05
pyruvate kinase, liver and red blood cell	Pklr	2.08±0.41
quaking	Qk	3.95±0.59
quaking homolog, KH domain RNA binding (mouse) /// quaking	Qk /// Qki	1.32±0.46
queuine tRNA-ribosyltransferase 1	Qtrt1	0.35±0.1
quiescin Q6 sulfhydryl oxidase 2	Qsox2	0.61±0.11
quinoid dihydropteridine reductase	Qdpr	34.78±0.36
quinolinate phosphoribosyltransferase	Qprt	11.55±2.07
R3H domain 1 (binds single-stranded nucleic acids)	R3hdm1	1.6±0.18
R3H domain and coiled-coil containing 1 (predicted)	R3hcc1_predicted	1.33±0.17

R3H domain containing 2	R3hdm2	0.74±0.03
Rab acceptor 1 (prenylated)	Rabac1	6.27±0.51
Rab geranylgeranyl transferase, a subunit	Rabggta	0.81±0.16
RAB geranylgeranyl transferase, b subunit	Rabggtb	6.08±0.69
RAB GTPase activating protein 1	Rabgap1	2.58±0.1
RAB GTPase activating protein 1-like	Rabgap1l	0.3±0.04
RAB guanine nucleotide exchange factor (GEF) 1 (predicted)	Rabgef1_predicted	0.48±0
RAB interacting factor	Rabif	0.79±0.03
Rab interacting lysosomal protein-like 2	Rilpl2	5.23±0.39
RAB, member of RAS oncogene family-like 2A	Rabl2a	1.25±0.12
RAB, member of RAS oncogene family-like 3 (predicted)	Rabl3_predicted	0.63±0.02
RAB, member of RAS oncogene family-like 4 (predicted)	Rabl4_predicted	0.71±0.08
RAB, member of RAS oncogene family-like 5	Rabl5	0.33±0.01
RAB1, member RAS oncogene family	Rab1	34.03±2.4
RAB10, member RAS oncogene family	Rab10	5.26±0.49
RAB11a, member RAS oncogene family	Rab11a	15.61±0.47
RAB11B, member RAS oncogene family	Rab11b	2.94±1.2
RAB12, member RAS oncogene family	Rab12	1.04±0.55
RAB13, member RAS oncogene family	Rab13	0.66±0.21
RAB14, member RAS oncogene family	Rab14	2.81±0.53
RAB17, member RAS oncogene family	Rab17	3.85±0.18
RAB18, member RAS oncogene family	Rab18	3.44±0.44
RAB2, member RAS oncogene family	Rab2	14.6±0.25
RAB20, member RAS oncogene family	Rab20	1.34±0.23
RAB21, member RAS oncogene family	Rab21	4.33±0.46
RAB22A, member RAS oncogene family (predicted)	Rab22a_predicted	1.55±0.26
RAB23, member RAS oncogene family (predicted)	Rab23_predicted	1.28±0.11
RAB24, member RAS oncogene family	Rab24	4.21±0.34
RAB28, member RAS oncogene family	Rab28	6.68±0.61
RAB2B, member RAS oncogene family	Rab2b	5.31±0.81
RAB3 GTPase activating protein subunit 2	Rab3gap2	0.37±0.26
RAB32, member RAS oncogene family	Rab32	0.75±0.11
RAB33B, member of RAS oncogene family (predicted)	Rab33b_predicted	0.65±0.23
RAB34, member of RAS oncogene family	Rab34	7.03±0.64
RAB35, member RAS oncogene family	Rab35	1.14±0.38
RAB3A interacting protein	Rab3ip	5.12±0.41
RAB3A interacting protein (rabin3)-like 1	Rab3il1	0.55±0.12
RAB3A, member RAS oncogene family	Rab3a	1.07±0.23
Rab40b, member RAS oncogene family (predicted)	Rab40b_predicted	1.3±0.12
Rab40c, member RAS oncogene family	Rab40c	0.52±0.21
RAB4A, member RAS oncogene family	Rab4a	3.22±0.03
RAB4B, member RAS oncogene family	Rab4b	0.72±0.24
RAB5A, member RAS oncogene family	Rab5a	5.64±0.74
RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted	6.26±0.73
RAB5C, member RAS oncogene family (predicted)	Rab5c_predicted	1.7±0.8
RAB6A, member RAS oncogene family	Rab6a	9.07±0.49
RAB7, member RAS oncogene family	Rab7	18.55±0.69
RAB7, member RAS oncogene family-like 1	Rab7l1	5.54±1.8
RAB8A, member RAS oncogene family	Rab8a	2.81±0.4
Rab9 effector protein with kelch motifs	Rabepk	0.64±0.19
RAB9, member RAS oncogene family	Rab9	3.76±0.57
rabaptin, RAB GTPase binding effector protein 1	Rabep1	1.75±0.18
rabaptin, RAB GTPase binding effector protein 2	Rabep2	0.35±0.14
rad and gem related GTP binding protein 2	Rem2	0.94±0.25
RAD1 homolog (S. pombe) (predicted)	Rad1_predicted	0.58±0.11
RAD17 homolog (S. pombe)	Rad17	1.39±0.1
RAD21 homolog (S. pombe)	Rad21	11.07±0.27
RAD23a homolog (S. cerevisiae)	Rad23a	0.35±0.24
RAD23b homolog (S. cerevisiae)	Rad23b	7.95±0.41
RAD50 homolog (S. cerevisiae)	Rad50	0.38±0.07
Rad51 homolog c (S. cerevisiae)	Rad51c	0.38±0.09
RAD52 homolog (S. cerevisiae) (predicted)	Rad52_predicted	0.47±0.09
RAD52 motif 1 (predicted)	Rdm1_predicted	0.67±0.05
Rad54 like 2 (S. cerevisiae) (predicted)	Rad54l2_predicted	0.22±0.08
RAD9 homolog B (S. cerevisiae)	Rad9b	0.28±0.1
radical fringe gene homolog (Drosophila)	Rfng	1.17±0.13
radixin	Rdx	6.81±0.65
RAE1 RNA export 1 homolog (S. pombe)	Rae1	1.1±0.13
Ral guanine nucleotide dissociation stimulator,-like 1 (predicted)	Rgl1_predicted	8.72±1.29
ralA binding protein 1	Ralbp1	1.24±0.22
RalBP1 associated Eps domain containing protein (predicted)	Reps1_predicted	0.97±0.03
RAN binding protein 10 (predicted)	Ranbp10_predicted	0.71±0.31
RAN binding protein 2	Ranbp2	5.61±0.14
RAN binding protein 3	Ranbp3	1.54±0.08
RAN binding protein 5 (predicted)	Ranbp5_predicted	1.4±0.13
RAN binding protein 6 (predicted)	Ranbp6_predicted	1.01±0.46
RAN GTPase activating protein 1	Rangap1	1.76±0.4
RAN guanine nucleotide release factor	Rangrf	3.21±0.1
RAN, member RAS oncogene family	Ran	19.77±1.21
RanBP-type and C3HC4-type zinc finger containing 1	Rbck1	0.5±0.22
Rap guanine nucleotide exchange factor (GEF) 2 (predicted)	Rapgef2_predicted	1.73±0.28
Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	0.74±0.2
Rap1 interacting factor 1 homolog (yeast)	Rif1	0.44±0.08
RAP1, GTP-GDP dissociation stimulator 1 (predicted)	Rap1gds1_predicted	2.13±0.05
RAR-related orphan receptor alpha (predicted)	Rora_predicted	1.66±0.41
RAR-related orphan receptor C /// leucine rich repeat and Ig domain containing 4	Lingo4 /// Rorc	0.44±0.07
Ras and Rab interactor 2 (predicted)	Rin2_predicted	10.59±1.94

Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (predicted)	Raph1_predicted	1.06±0.19
Ras association (RalGDS/AF-6) domain family 1	Rassf1	0.98±0.21
Ras association (RalGDS/AF-6) domain family 3 (predicted)	Rassf3_predicted	0.56±0.04
Ras association (RalGDS/AF-6) domain family 7 (predicted)	Rassf7_predicted	1.4±0.12
Ras association (RalGDS/AF-6) domain family member 6	Rassf6	0.69±0.11
Ras homolog enriched in brain	Rheb	10.44±1.04
ras homolog gene family, member A	Rhoa	11.7±1.27
ras homolog gene family, member B	Rhob	7.39±2.27
ras homolog gene family, member C (predicted)	Rhoc_predicted	5.03±0.38
ras homolog gene family, member D (predicted)	Rhod_predicted	2±0.29
Ras homolog gene family, member G	Rhog	0.64±0.2
ras homolog gene family, member Q	Rhoq	2.72±0.09
ras homolog gene family, member T2	Rhot2	1.76±0.21
RAS p21 protein activator 1	Rasa1	2.4±0.11
RAS p21 protein activator 2	Rasa2	0.94±0.07
RAS p21 protein activator 3	Rasa3	0.71±0.07
RAS protein activator like 2 (predicted)	Rasal2_predicted	0.75±0.22
RAS related protein 1b	Rap1b	5.2±0.34
ras responsive element binding protein 1 (predicted)	Rreb1_predicted	3.46±0.55
Ras-GTPase-activating protein SH3-domain binding protein 1	G3bp1	3.42±0.65
RAS-like, family 10, member B (predicted)	Rasl10b_predicted	0.47±0.07
RAS-like, family 12 (predicted)	Rasl12_predicted	1.65±0.32
Ras-related C3 botulinum toxin substrate 1	Rac1	6.94±1.32
Ras-related GTP binding A	Rraga	5.91±0.11
Ras-related GTP binding B	RragB	0.37±0.07
Ras-related GTP binding C (predicted)	Rragc_predicted	6.84±0.5
Ras-related GTP binding D (predicted)	Rragd_predicted	1.27±0.4
RAS-related protein 1a	Rap1a	8.67±0.58
RB1-inducible coiled-coil 1 (predicted)	Rb1cc1_predicted	3.01±0.44
RB-associated KRAB repressor	Rbak	0.24±0.08
RBSC-skeletrophin	LOC474147	0.73±0.11
rcd1 (required for cell differentiation) homolog 1 (S. pombe)	Rqcd1	0.86±0.19
RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	Rce1	1.21±0.11
rearranged L-myc fusion sequence (predicted)	Rlf_predicted	0.37±0.11
receptor (TNFRSF)-interacting serine-threonine kinase 1 (predicted)	Ripk1_predicted	1.57±0.35
receptor accessory protein 4	Reep4	0.77±0.06
receptor interacting protein kinase 5	Ripk5	0.88±0.11
receptor-interacting serine-threonine kinase 4 (predicted)	Ripk4_predicted	2.09±0.26
receptor-like tyrosine kinase	Ryk	1.32±0.18
recombination activating gene 1 activating protein 1 (predicted)	Rag1ap1_predicted	1.97±0.15
recombining binding protein suppressor of hairless (Drosophila) (predicted)	LOC679028 /// Rbpsuh_predicted	0.54±0.02
RecQ protein-like	Recql	1.37±0.3
RecQ protein-like 5 (predicted)	Recql5_predicted	0.65±0.14
reelin	Reln	1.26±0.2
regulated endocrine-specific protein 18	Resp18	2.09±0.76
regulator of calcineurin 1	Rcan1	12.56±1.22
regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	Rcbtb1	1.18±0.17
regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	Rcbtb2	1.28±0.28
regulator of telomere elongation helicase 1	Rtel1	1.43±0.25
regulatory factor X domain containing 2 homolog (human)	Rfxdc2	1.35±0.38
regulatory factor X, 1 (influences HLA class II expression) (predicted)	Rfx1_predicted	0.64±0.14
regulatory factor X, 5 (influences HLA class II expression) (predicted)	Rfx5_predicted	1.4±0.18
regulatory factor X-associated protein	Rfxap	0.88±0.08
related RAS viral (r-ras) oncogene homolog 2	Rras2	4.83±0.36
RELT-like 2	Rell2	1.74±0.49
remodeling and spacing factor 1	Rsf1	0.95±0.19
renin binding protein	Renbp	7.21±1.03
replication factor C (activator 1) 1	Rfc1	0.48±0.09
replication factor C (activator 1) 2	Rfc2	1.34±0.38
replication factor C (activator 1) 3	Rfc3	0.24±0.12
replication factor C (activator 1) 4 (predicted)	Rfc4_predicted	1.33±0.16
replication factor C (activator 1) 5 (predicted)	Rfc5_predicted	1.07±0.04
Replication factor C 1	Recc1	0.56±0.19
Replication protein A1	Rpa1	0.64±0.01
replication protein A2	Rpa2	0.42±0.17
replication protein A3 (predicted)	Rpa3_predicted	4.02±0.16
required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Rmnd5a	3.59±0.35
RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	Rer1	8.23±1.01
resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	2.94±0.16
REST corepressor 1 (predicted)	Rcor1_predicted	0.96±0.2
reticulocalbin 2	Rcn2	3.92±0.19
reticulon 3	Rtn3	7.9±0.89
reticulon 4	Rtn4	11.02±1.67
reticulon 4 interacting protein 1	Rtn4ip1	0.88±0.14
retinitis pigmentosa 2 homolog (human) (predicted)	Rp2h_predicted	0.46±0.09
Retinitis pigmentosa 9 homolog (human) (predicted)	Rp9h_predicted	0.21±0.08
retinoblastoma 1	Rb1	1.38±0.09
retinoblastoma binding protein 4	Rbbp4	3.95±0.87
retinoblastoma binding protein 5 (predicted)	Rbbp5_predicted	0.85±0.16
retinoblastoma binding protein 6	Rbbp6	1.45±0.2
retinoblastoma binding protein 7	Rbbp7	15±0.67
retinoblastoma binding protein 9	Rbbp9	1.06±0.02
retinoblastoma-like 2	Rbl2	2.4±0.25
retinoic acid induced 1 (predicted)	Rai1_predicted	0.25±0.19
retinoic acid induced 12	Rai12	1.54±0.23
retinoic acid induced 14	Rai14	0.93±0.06

retinoic acid receptor responder (tazarotene induced) 2	Rarres2	11.7±3.49
retinoic acid receptor, alpha	Rara	0.23±0.13
retinoic acid receptor, beta	Rarb	0.87±0.22
Retinoid X receptor alpha	Rxra	6.1±0.85
retinoid X receptor beta	Rxrb	0.2±0.03
retinoid X receptor gamma	Rxrg	2.76±0.12
retinol binding protein 1, cellular	Rbp1	26.94±2.89
Retinol dehydrogenase 10 (all-trans)	Rdh10	5.14±0.28
retinol dehydrogenase 11	Rdh11	1.04±0.05
Retinol dehydrogenase 13 (all-trans and 9-cis) (predicted)	Rdh13_predicted	1.49±0.37
retinol dehydrogenase 2	Rdh2	3.52±0.45
retinol dehydrogenase 5 (predicted)	Rdh5_predicted	1.49±0.25
retinol saturase (all trans retinol 13,14 reductase)	Retsat	10.95±1.52
REV1 homolog (S. cerevisiae)	Rev1	0.81±0.24
REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	1.33±0.19
REX2, RNA exonuclease 2 homolog (S. cerevisiae)	Rexo2	4.96±0.18
REX4, RNA exonuclease 4 homolog (S. cerevisiae)	Rexo4	2.03±0.42
RFT1 homolog (S. cerevisiae) (predicted)	Rft1_predicted	0.89±0.09
RGD1559600 (predicted)	RGD1559600_predicted	0.58±0.12
RGD1559909 (predicted)	RGD1559909_predicted	1.12±0.28
RGD1560566 (predicted)	RGD1560566_predicted	2.64±0.35
RGD1561796 (predicted)	RGD1561796_predicted	0.51±0.17
RGD1561797 (predicted)	RGD1561797_predicted	0.54±0.17
RGD1562012 (predicted)	RGD1562012_predicted	0.56±0.04
RGD1562114 (predicted)	RGD1562114_predicted	3.17±0.35
RGD1562146 (predicted)	RGD1562146_predicted	1.03±0.15
RGD1563547 (predicted)	RGD1563547_predicted	6.81±0.88
RGD1564379 (predicted)	RGD1564379_predicted	2.76±0.23
RGD1564391 (predicted)	RGD1564391_predicted	11.78±0.81
RGD1564491 (predicted)	RGD1564491_predicted	0.34±0.08
RGD1564792 (predicted)	RGD1564792_predicted	0.31±0.16
RGD1564982 (predicted)	RGD1564982_predicted	0.22±0.13
RGD1565210 (predicted)	RGD1565210_predicted	1.69±0.46
RGD1565616 (predicted)	RGD1565616_predicted	6.22±0.39
RGD1565641 (predicted)	RGD1565641_predicted	4.84±0.55
RGD1565784 (predicted)	RGD1565784_predicted	2.09±0.3
RGD1566118 (predicted)	RGD1566118_predicted	0.77±0.18
RGD1566320 (predicted)	RGD1566320_predicted	2.73±0.23
Rho family GTPase 3	Rnd3	1.18±0.09
Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	3.43±1.61
Rho GTPase activating protein 10	Arhgap10	2.22±0.17
Rho GTPase activating protein 11A	Arhgap11a	0.55±0.22
Rho GTPase activating protein 12 (predicted)	Arhgap12_predicted	0.93±0.06
Rho GTPase activating protein 17	Arhgap17	10.46±0.53
Rho GTPase activating protein 18 (predicted)	Arhgap18_predicted	1.48±0.29
Rho GTPase activating protein 21 (predicted)	Arhgap21_predicted	1.78±0.36
Rho GTPase activating protein 24	Arhgap24	23.45±2.15
Rho GTPase activating protein 27	Arhgap27	1.17±0.17
Rho GTPase activating protein 5	Arhgap5	1.24±0.07
Rho GTPase activating protein 8	Arhgap8	1.32±0.19
Rho GTPase activating protein 9	Arhgap9	0.27±0.05
Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	0.74±0.12
Rho guanine nucleotide exchange factor (GEF) 15 (predicted)	Arhgef15_predicted	1.15±0.23
Rho guanine nucleotide exchange factor (GEF) 17 (predicted)	Arhgef17_predicted	0.53±0.17
Rho guanine nucleotide exchange factor (GEF) 3 (predicted)	Arhgef3_predicted	0.55±0.3
Rho guanine nucleotide exchange factor (GEF) 5	Arhgef5	0.97±0.15
Rho guanine nucleotide exchange factor 7	Arhgef7	1.09±0.14
rho/rac guanine nucleotide exchange factor (GEF) 18 (predicted)	Arhgef18_predicted	1.07±0.3
Rho-associated coiled-coil forming kinase 2	Rock2	0.44±0.12
Rho-guanine nucleotide exchange factor (predicted)	Rgnef_predicted	2.73±0.31
rhomboid domain containing 2	Rhbdd2	2.91±0.11
rhomboid family 1 (Drosophila)	Rhbdf1	1.59±0.32
rhomboid, veinlet-like 3 (Drosophila)	Rhbdl3	0.47±0.04
rhophilin, Rho GTPase binding protein 1 (predicted)	Rhpn1_predicted	2.96±0.83
Rho-related BTB domain containing 1 (predicted)	Rhobtb1_predicted	5.37±0.56
RIB43A domain with coiled-coils 1	Ribc1	0.38±0.06
riboflavin kinase /// similar to riboflavin kinase (predicted)	Rfk /// RGD1563242_predicted	13.13±1.5
ribokinase (predicted)	Rbks_predicted	2.61±0.23
ribonuclease H2, large subunit	Rnaseh2a	0.86±0.05
ribonuclease H2, subunit B	Rnaseh2b	4.37±0.06
ribonuclease III, nuclear	Rnasen	1.15±0.04
ribonuclease P 14 subunit (human)	Rpp14	1.57±0.13
ribonuclease P 21 subunit (human) /// RT1 class I, M10, gene 1	Rpp21 /// RT1-M10-1	1.08±0.2
ribonuclease P 25 subunit (human)	Rpp25	4.77±1.09
ribonuclease P 40 subunit (human)	Rpp40	0.56±0.12
ribonuclease P/MRP 30 /// similar to Ribonuclease P protein subunit p30 (RNaseP protein p30) (RNase P subunit 2)	LOC687772 /// Rpp30	0.9±0.12
ribonuclease T2 (predicted)	Rnaset2_predicted	5.81±0.94
ribonuclease, RNase A family 4	Rnase4	2.5±0.86
ribonuclease, RNase K	Rnasek	17.71±1.26
ribonuclease/angiogenin inhibitor 1	Rnh1	5.09±0.56
ribonucleic acid binding protein S1	Rnps1	1.98±0.18
ribonucleotide reductase M1	Rrm1	2.72±0.38
ribonucleotide reductase M2	Rrm2	2.48±0.62
ribophorin I	Rpn1	11.52±1.27
ribophorin II	Rpn2	17.89±2.42
ribose 5-phosphate isomerase A (predicted)	Rpia_predicted	1.99±0.34

ribose-phosphate pyrophosphokinase I -like	LOC314140	0.99±0.14
ribosomal L1 domain containing 1	Rsl1d1	1.99±0.24
ribosomal protein L10	Rpl10	24.78±0.6
ribosomal protein L10A	Rpl10a	11.02±0.54
ribosomal protein L11	Rpl11	26.17±1.53
ribosomal protein L12 (predicted) /// similar to 60S ribosomal protein L12 /// similar to similar to 60S ribosomal protein L12	LOC499782 /// LOC685320 /// LOC688511 /// Rpl12_predicted	17.43±0.4
ribosomal protein L13	Rpl13	15.58±1.7
ribosomal protein L13A	Rpl13a	15.95±2.05
ribosomal protein L14	Rpl14	12.22±0.44
ribosomal protein L15	Rpl15	17.83±0.89
ribosomal protein L17	Rpl17	20.48±2.34
ribosomal protein L18	Rpl18	27.14±3.59
ribosomal protein L18A	Rpl18a	25.9±5.29
ribosomal protein L19	Rpl19	32.27±2.18
ribosomal protein L21 /// similar to ribosomal protein L21	LOC679852 /// LOC690841 /// Rpl21	13.61±1.82
ribosomal protein L22	Rpl22	22.93±1.15
ribosomal protein L22 like 1 (predicted)	Rpl22l1_predicted	19.95±2.85
ribosomal protein L23	Rpl23	23.48±2.5
ribosomal protein L23a	Rpl23a	23.68±2.45
ribosomal protein L24	Rpl24	17.44±0.92
ribosomal protein L26	Rpl26	40.42±6.72
ribosomal protein L27	Rpl27	28.82±2.21
ribosomal protein L27a (predicted)	Rpl27a_predicted	25.48±1.03
ribosomal protein L28	Rpl28	23.63±4.01
ribosomal protein L29	Rpl29	16.61±0.59
ribosomal protein L3	Rpl3	24.11±1.46
ribosomal protein L3 /// similar to 60S ribosomal protein L3 (L4)	LOC499207 /// Rpl3	1.26±0.23
ribosomal protein L30	Rpl30	28.39±2.65
ribosomal protein L31	Rpl31	31.61±0.73
ribosomal protein L32	Rpl32	37.06±1.34
ribosomal protein L34 (predicted)	Rpl34_predicted	19.86±0.38
ribosomal protein L35	Rpl35	24.89±1.61
ribosomal protein L35a	Rpl35a	24.09±1.42
ribosomal protein L36	LOC364105 /// RGD1563135_predicted /// RGD1563687_predicted /// RGD1563867_predicted /// Rpl36	0.51±0.08
ribosomal protein L37	Rpl37	25.47±3.02
ribosomal protein L37a /// similar to 60S ribosomal protein L37a	LOC679823 /// LOC687187 /// LOC689401 /// Rpl37a	28.1±1.13
ribosomal protein L4	Rpl4	18.01±2.47
ribosomal protein L41	Rpl41	27.05±1.03
ribosomal protein L5	Rpl5	27.43±4.44
ribosomal protein L6 /// similar to 60S ribosomal protein L6 (Neoplasm-related protein C140) (predicted)	RGD1563476_predicted /// Rpl6	21.64±0.55
ribosomal protein L7	Rpl7	37.02±5.51
ribosomal protein L7a (predicted)	Rpl7a_predicted	37±1.92
ribosomal protein L7-like 1	Rpl7l1	2.94±0.22
ribosomal protein L8	Rpl8	17.39±0.93
ribosomal protein L8 /// similar to 60S ribosomal protein L8 /// similar to 60S ribosomal protein L8 (predicted)	LOC365370 /// RGD1561333_predicted /// Rpl8	2.4±0.83
ribosomal protein L9 /// EH-domain containing 2	Ehd2 /// Rpl9	38.69±0.4
ribosomal protein S10	Rps10	17±3.05
ribosomal protein S11	Rps11	18.44±1.66
ribosomal protein S12	Rps12	24.9±0.44
ribosomal protein S13 /// similar to ribosomal protein S13	LOC684988 /// Rps13	28.7±0.34
ribosomal protein S14	Rps14	30.25±3.03
ribosomal protein S15	Rps15	19.96±3.43
ribosomal protein S15a	Rps15a	15.95±0.35
ribosomal protein S16	Rps16	26.81±3.72
ribosomal protein S17	Rps17	46.45±2.28
ribosomal protein S18	Rps18	45.68±1.73
ribosomal protein S19	Rps19	22.29±1.7
ribosomal protein S2	Rps2	37.38±0.25
ribosomal protein S2 /// similar to ribosomal protein S2 (predicted) /// similar to 40S ribosomal protein S2	LOC688473 /// RGD1559516_predicted /// Rps2	37.58±3.44
ribosomal protein S20	Rps20	33.88±2.24
ribosomal protein S21	Rps21	17.95±2.55
ribosomal protein S23	Rps23	27.61±3.02
ribosomal protein S24	Rps24	26.9±0.91
ribosomal protein s25	Rps25	9.19±1.02
ribosomal protein S26	Rps26	23.21±0.41
ribosomal protein S27	Rps27	27.66±2.2
ribosomal protein S27a	Rps27a	25.91±3.76
ribosomal protein S28 /// similar to 40S ribosomal protein S28	LOC684733 /// Rps28	28.27±2.92
ribosomal protein S29	Rps29	55.08±2.78
ribosomal protein S3	Rps3	17.43±0.85

ribosomal protein S3a	Rps3a	33.17±5.43
ribosomal protein S4, X-linked	Rps4x	32.34±3.3
ribosomal protein S4, Y-linked 2	Rps4y2	0.42±0.2
ribosomal protein S5	Rps5	23.19±0.71
ribosomal protein S6	Rps6	20.14±3.48
ribosomal protein S6 kinase polypeptide 1	Rps6ka1	0.34±0.17
ribosomal protein S6 kinase polypeptide 3	Rps6ka3	1.77±0.18
ribosomal protein S6 kinase, 70kDa, polypeptide 1	Rps6kb1	0.72±0.26
ribosomal protein S6 kinase, polypeptide 4	Rps6ka4	0.68±0.14
ribosomal protein S7 /// similar to ribosomal protein S7	LOC497813 /// Rps7	17.16±1.04
ribosomal protein S8	Rps8	21.64±0.65
ribosomal protein S9	Rps9	21.83±1.61
ribosomal protein SA	Rpsa	27.91±1.59
ribosomal protein SA	LOC367035 /// LOC683125 /// LOC688911 /// RGD1563757_predicted /// Rpsa	5.3±0.53
ribosomal protein, large P2 /// hypothetical gene supported by X15098 /// similar to 60S acidic ribosomal protein P2	LOC363929 /// LOC498555 /// Rplp2	22.62±2.5
ribosomal protein, large, P1	Rplp1	43.08±3.24
ribosomal RNA processing 1 homolog (S. cerevisiae)	Rrp1	0.93±0.24
ribosomal RNA processing 1 homolog B (S. cerevisiae)	Rrp1b	0.2±0.14
ribosome binding protein 1	Rrbp1	0.78±0.03
ribulose-5-phosphate-3-epimerase	Rpe	1.66±0.22
RIM binding protein 2	Rimbp2	1.84±0.18
ring finger (C3HC4 type) and KH domain containing 1 (predicted)	Rkhd1_predicted	0.41±0.02
ring finger 111	Rnf111	1.29±0.15
ring finger and CHY zinc finger domain containing 1	Rchy1	6.04±0.74
ring finger and FYVE like domain containing protein	Rffl	0.4±0.03
ring finger and KH domain containing 2 (predicted)	Rkhd2_predicted	1.66±0.26
ring finger and WD repeat domain 3 /// similar to mixed lineage kinase domain-like	LOC690743 /// Rfwd3	0.3±0.13
ring finger protein (C3H2C3 type) 6 (predicted)	Rnf6_predicted	1.63±0.14
ring finger protein 10	Rnf10	2.55±0.78
ring finger protein 103	Rnf103	3.02±0.31
ring finger protein 11 (predicted)	Rnf11_predicted	0.79±0.11
ring finger protein 11 (predicted) /// similar to RING finger protein 11 (NEDD4 WW domain-binding protein 2) (Sid 1669)	LOC683844 /// Rnf11_predicted	5.43±0.24
ring finger protein 113A1	Rnf113a1	0.47±0.14
ring finger protein 113A2	Rnf113a2	1.32±0.31
ring finger protein 121 (predicted)	Rnf121_predicted	0.51±0.06
ring finger protein 125 (predicted)	Rnf125_predicted	0.23±0.06
ring finger protein 126	Rnf126	0.55±0.11
ring finger protein 128 /// hypothetical protein LOC680663	LOC680663 /// Rnf128	8.79±1.14
ring finger protein 135 /// ras homolog gene family, member T1 (predicted)	Rhot1_predicted /// Rnf135	4.67±0.37
ring finger protein 138	Rnf138	0.44±0.26
ring finger protein 139 (predicted)	Rnf139_predicted	3.07±0.41
ring finger protein 14	Rnf14	8.16±0.9
ring finger protein 145	Rnf145	1.01±0.21
ring finger protein 146	Rnf146	3.23±0.46
ring finger protein 149	Rnf149	9.25±1.77
ring finger protein 152 (predicted)	Rnf152_predicted	2.04±0.38
ring finger protein 166	Rnf166	0.59±0.1
ring finger protein 167	Rnf167	2.28±0.04
ring finger protein 181	Rnf181	5.93±0.48
ring finger protein 185	Rnf185	2.11±0.25
ring finger protein 187 (predicted)	Rnf187_predicted	1.97±0.44
ring finger protein 19A	Rnf19a	3.61±0.78
ring finger protein 2	Rnf2	1.1±0.05
ring finger protein 20 (predicted)	Rnf20_predicted	1.32±0.17
ring finger protein 208	Rnf208	1.32±0.55
ring finger protein 215	Rnf215	4.68±0.57
ring finger protein 216	Rnf216	1.29±0.18
ring finger protein 217	Rnf217	0.31±0.07
ring finger protein 219	Rnf219	0.22±0.05
ring finger protein 25	Rnf25	0.72±0.25
ring finger protein 26 (predicted)	Rnf26_predicted	1.15±0.22
ring finger protein 31 (predicted)	Rnf31_predicted	0.2±0.02
ring finger protein 34	Rnf34	1.3±0.06
ring finger protein 4	Rnf4	1.74±0.28
ring finger protein 41	Rnf41	1.08±0.31
Ring finger protein 44	Rnf44	1.59±0.61
ring finger protein 7 (predicted)	Rnf7_predicted	4.69±0.45
ring finger protein 8	Rnf8	0.63±0.02
RING1 and YY1 binding protein (predicted)	Rybp_predicted	1.6±0.67
ring-box 1	Rbx1	9.82±0.64
RIO kinase 1 (yeast)	Riok1	0.3±0.24
RIO kinase 2 (yeast)	Riok2	0.57±0.08
RIO kinase 3 (yeast) (predicted)	Riok3_predicted	7.38±0.59
RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	Rmi1	1.28±0.22
RNA (guanine-7-) methyltransferase	Rnmt	1.36±0.36
RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1	1.46±0.19
RNA (guanine-9-) methyltransferase domain containing 3	Rg9mtd3	0.92±0.1
RNA binding motif protein 10	Rbm10	0.76±0.01
RNA binding motif protein 12	Rbm12	0.22±0.09
RNA binding motif protein 12B	Rbm12b	1.62±0.36

RNA binding motif protein 13	Rbm13	0.38±0.06
RNA binding motif protein 15B (predicted)	Rbm15b_predicted	0.25±0.15
RNA binding motif protein 16	Rbm16	1.99±0.34
RNA binding motif protein 17	Rbm17	2.62±0.29
RNA binding motif protein 18 (predicted)	Rbm18_predicted	1.9±0.32
RNA binding motif protein 22	Rbm22	1.02±0.12
RNA binding motif protein 25 (predicted)	Rbm25_predicted	1.62±0.32
RNA binding motif protein 25 (predicted) /// similar to RNA binding motif protein 25 (predicted)	Rbm25_predicted /// RGD1565486_predicted	1.69±0.11
RNA binding motif protein 27 (predicted)	Rbm27_predicted	0.63±0.1
RNA binding motif protein 3	Rbm3	4.39±0.35
RNA binding motif protein 34	Rbm34	0.66±0.15
RNA binding motif protein 38	Rbm38	0.42±0.11
RNA binding motif protein 39	Rbm39	7.1±1.03
RNA binding motif protein 42	Rbm42	2.83±0.73
RNA binding motif protein 45	Rbm45	3.42±0.46
RNA binding motif protein 4B	Rbm4b	2.31±0.1
RNA binding motif protein 5	Rbm5	2.86±0.04
RNA binding motif protein 6	Rbm6	0.91±0.04
RNA binding motif protein 8 (predicted)	Rbm8_predicted	4.14±0.61
RNA binding motif protein, X chromosome	Rbmx	1.37±0.2
RNA binding motif protein, X chromosome retrogene (predicted)	Rbmxrt_predicted	2.07±0.24
RNA binding motif, single stranded interacting protein 2	Rbms2	0.42±0.09
RNA guanylyltransferase and 5'-phosphatase (predicted)	Rngtt_predicted	0.91±0.06
RNA polymerase 1-1	Rpo1-1	2.14±0.27
RNA polymerase 1-2	Rpo1-2	0.53±0.09
RNA polymerase II associated protein 2	Rpap2	1.01±0.12
RNA polymerase II associated protein 3	Rpap3	1.03±0.12
RNA pseudouridylate synthase domain containing 3 (predicted)	Rpusd3_predicted	0.88±0.21
RNA pseudouridylate synthase domain containing 4	Rpusd4	0.37±0.06
RNA terminal phosphate cyclase domain 1	Rtcd1	6.68±0.46
RNA terminal phosphate cyclase-like 1	Rcl1	1.02±0.14
RNA U, small nuclear RNA export adaptor	Rnuxa	2.43±0.45
rogdi homolog (Drosophila)	Rogdi	7.27±1.35
Ros1 proto-oncogene	Ros1	0.41±0.07
rosbin, round spermatid basic protein 1 (predicted)	Rsbn1_predicted	0.72±0.19
roundabout homolog 3 (Drosophila) (predicted)	Robo3_predicted	0.93±0.44
Rous sarcoma oncogene	Src	1.25±0.3
RPA interacting protein	Rpain	0.42±0.22
RRN3 RNA polymerase I transcription factor homolog (yeast)	Rrn3	1.65±0.55
rRNA promoter binding protein	LOC257642	7.53±1.05
RRP9, small subunit (SSU) processome component, homolog (yeast)	Rrp9	0.78±0.05
RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (predicted)	Rrs1_predicted	0.85±0.17
RT1 class I, CE12	RT1-CE12	0.45±0.45
RT1 class Ib gene, H2-TL-like, grc region (N3)	Dhx16 /// Ier3 /// Mrps18b /// RGD1303066 /// RT1-149 /// RT1-N2 /// RT1-N3 /// RT1-O /// RT1-S2 /// RT1-S3 /// RT1-T24-1	4.88±0.42
RT1 class Ib, locus Aw2	RT1-Aw2	6.39±2.24
RT1 class Ib, locus Aw2	Atp6v1g2 /// B3galt4 /// Cdsn /// Col11a2 /// Daxx /// Ddr1 /// Gtf2h4 /// Hcr /// Ke2 /// LOC682408 /// Lst1 /// Ltb /// Phf1 /// Pou5f1 /// Psors1c2 /// Rab2l /// RT1-A1 /// RT1-A2 /// RT1-A3 /// RT1-Aw2 /// RT1-CE1 /// RT1-CE10 /// RT1-CE11 /// RT1-CE12 /// RT1-CE13 /// RT1-CE14 /// RT1-CE15 /// RT1-CE16 /// RT1-CE2 /// RT1-CE3 /// RT1-CE4 /// RT1-CE5 /// RT1-CE7 /// RT1-Cl /// RT1-DOa /// RT1-Ha /// RT1-Ke4 /// Syngap1 /// Tapbp /// Tcf19 /// Vars2l /// Wdr46 /// Zbtb9 /// Zfp297	3.63±0.46
RT1 class II, locus Ba	RT1-Ba	5.06±2.15
Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (predicted)	Rtf1_predicted	0.45±0.02
RUN and FYVE domain containing 1	Rufy1	5.83±1.19
RUN and FYVE domain containing 3	Rufy3	1.43±0.36
RUN domain containing 1 (predicted)	Rundc1_predicted	1.27±0.03
RuvB-like protein 1	Ruvbl1	0.96±0.09
RuvB-like protein 2	Ruvbl2	0.55±0.51
RWD domain containing 2B	Rwdd2b	2.88±0.52
RWD domain containing 3	Rwdd3	0.34±0.04
RWD domain containing 4A	Rwdd4a	5.79±0.55
S1 RNA binding domain 1	Srbd1	0.53±0.08
S100 calcium binding protein A13 (predicted)	S100a13_predicted	0.2±0.21
S100 calcium binding protein A16 (predicted)	S100a16_predicted	1.69±0.36
S100 calcium binding protein G	S100g	0.44±0.12
SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	Sacm1l	6.94±1.39
saccharopine dehydrogenase (putative)	Sccpdh	12.21±0.73
S-adenosylhomocysteine hydrolase	Ahcy	6.25±0.61

S-adenosylhomocysteine hydrolase-like 1 (predicted)	Ahcyl1_predicted	12.63±0.58
S-adenosylhomocysteine hydrolase-like 2	Ahcyl2	19.33±0.68
S-adenosylmethionine decarboxylase 1	Amd1	5.89±1.05
Sal-like 1 (Drosophila) (predicted)	Sall1_predicted	2.75±0.21
salvador homolog 1 (Drosophila) (predicted)	Sav1_predicted	1.89±0.53
SAP30-like	Sap30l	1.71±0.22
SAPS domain family, member 1 (predicted)	Saps1_predicted	2.04±0.24
SAPS domain family, member 2	Saps2	0.96±0.08
SAPS domain family, member 3 (predicted)	Saps3_predicted	4.87±0.74
SAR1 gene homolog A (S. cerevisiae)	Sar1a	5.28±1.02
SAR1 gene homolog B (S. cerevisiae)	Sar1b	13.59±0.99
sarcoma antigen NY-SAR-48	Ny-sar-48	0.24±0.15
sarcosine dehydrogenase	Sardh	3.76±0.66
scaffold attachment factor B	Safb	0.41±0.12
SCAN domain-containing 1 (predicted)	Scand1_predicted	10.27±2.97
scavenger receptor class B, member 2	Scarb2	0.47±0.05
SCF apoptosis response protein 1	LOC499941	1.13±0.51
Scm-like with four mbt domains 1	Sfmbt1	0.97±0.12
scotin	MGC94600	0.57±0.17
scratch homolog 1, zinc finger protein (Drosophila) (predicted)	Scrt1_predicted	0.2±0.08
scribbled homolog (Drosophila)	Scrib	1.02±0.26
SCY1-like 1 (S. cerevisiae)	Scyl1	1.41±0.55
SCY1-like 1 binding protein 1	Scyl1bp1	0.56±0.04
SCY1-like 2 (S. cerevisiae) (predicted)	Scyl2_predicted	4.12±0.39
SCY1-like 3 (S. cerevisiae)	Scyl3	0.32±0.05
SDA1 domain containing 1	Sdad1	0.42±0.06
sec1 family domain containing 1	Scfd1	3.11±0.6
SEC11 homolog A (S. cerevisiae)	Sec11a	4.98±0.58
SEC11 homolog C (S. cerevisiae)	Sec11c	3.58±0.64
SEC13 homolog (S. cerevisiae)	Sec13	10.21±0.53
SEC14 and spectrin domains 1	Sestd1	4.07±0.13
SEC16 homolog A (S. cerevisiae)	Sec16a	1.37±0.41
SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	Sec22a	1.41±0.1
SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	Sec22b	0.92±0.18
SEC23 interacting protein	Sec23ip	0.3±0.11
SEC23A (S. cerevisiae) (predicted)	Sec23a_predicted	1.96±0.23
SEC23B (S. cerevisiae) (predicted)	Sec23b_predicted	5.39±0.51
SEC24 related gene family, member A (S. cerevisiae) (predicted)	Sec24a_predicted	2.88±0.21
SEC24 related gene family, member B (S. cerevisiae) (predicted)	Sec24b_predicted	0.74±0.16
SEC24 related gene family, member D (S. cerevisiae) (predicted)	Sec24d_predicted	4.6±0.17
SEC31 homolog A (S. cerevisiae)	Sec31a	3.03±0.15
SEC3-like 1 (S. cerevisiae)	Sec3l1	3.31±0.21
Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	3.54±0.47
Sec61 beta subunit (predicted)	Sec61b_predicted	8.21±0.77
Sec61, alpha subunit 2 (S. cerevisiae) (predicted)	Sec61a2_predicted	4.12±0.53
SEC63-like (S. cerevisiae) (predicted)	Sec63_predicted	3.28±0.17
secernin 2	Scrn2	1.66±0.28
SECIS binding protein 2	Secisbp2	0.97±0.07
secreted and transmembrane 1B	Sectm1b	0.99±0.25
secreted phosphoprotein 1	Spp1	5.1±2.76
secreted phosphoprotein 2	Spp2	63.59±6.25
secretion regulating guanine nucleotide exchange factor	Sergef	5.34±0.73
secretory carrier membrane protein 1	Scamp1	2.73±0.24
secretory carrier membrane protein 2	Scamp2	4.68±0.52
secretory carrier membrane protein 3	Scamp3	4.4±0.46
secretory carrier membrane protein 4	Scamp4	1.48±0.17
sedlin-like	LOC287274	6.88±0.21
sedoheptulokinase	Shpk	3.52±0.58
Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	Sel1h	4.78±0.58
SEL1 domain containing protein RGD735029	RGD735029	3±0.06
sel-1 suppressor of lin-12-like (C. elegans)	Sel1l	1.39±0.19
selenium binding protein 1	Selenbp1	13.71±1.84
selenocysteine lyase	Scly	22.77±0.96
selenophosphate synthetase 1	Sephs1	4.82±0.26
selenophosphate synthetase 2	Sephs2	13.32±1.59
selenoprotein	Sept15	16.1±0.48
selenoprotein K	Selk	9.71±1.28
selenoprotein P, plasma, 1	Sepp1	67.38±3.01
selenoprotein S	SELS	7.42±0.23
selenoprotein T	Selt	6.6±0.84
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B (predicted)	Sema3b_predicted	2.7±0.35
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Sema4a	3.16±0.1
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Sema4b	4.29±0.6
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted)	Sema4g_predicted	0.63±0.03
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (predicted)	Sema6d_predicted	0.22±0.41
septin 11	Sept11	2.74±0.5
septin 14	Sept14	0.23±0.03
septin 2	Sept2	4.1±0.45
septin 7	sept7	6.88±0.56
septin 8 (predicted)	Sept8_predicted	1.29±0.28
septin 9	Sept9	0.47±0.3
sequestosome 1	Sqstm1	17.26±1.53
serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	Serpinc1	26.82±2.01
serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	43.69±2.5
serine (or cysteine) peptidase inhibitor, clade F, member 2	Serpinf2	4.98±1.64
serine (or cysteine) peptidase inhibitor, clade H, member 1	Serpinh1	4.16±0.59

serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpinb1a	0.45±0.42
serine carboxypeptidase 1	Scpep1	56.6±6.14
serine hydroxymethyltransferase 1 (soluble)	Shmt1	13.06±0.46
serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	17.99±0.24
serine incorporator 1	Serinc1	27.39±1.31
serine incorporator 3	Serinc3	10.56±1.18
serine palmitoyltransferase, long chain base subunit 1 (predicted)	Sptlc1_predicted	3.31±0.26
serine peptidase inhibitor, Kazal type 3	Spink3	48.73±8.08
serine protease inhibitor, Kazal type 1	Spink1	2.86±0.19
serine protease inhibitor, Kunitz type 1	Spint1	1.18±0.17
serine protease inhibitor, Kunitz type 2	Spint2	11.19±1.12
serine racemase	Srr	2.08±0.18
serine/arginine repetitive matrix 1 (predicted)	Srrm1_predicted	1.46±0.35
serine/arginine repetitive matrix 2 (predicted)	Srrm2_predicted	6.76±2.87
Serine/arginine-rich protein specific kinase 1	Srpk1	0.5±0.15
serine/arginine-rich protein specific kinase 2 (predicted)	Srpk2_predicted	1.39±0.26
serine/threonine kinase 11 interacting protein (predicted)	Stk11ip_predicted	0.69±0.18
serine/threonine kinase 16	Stk16	3.03±0.1
serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	0.22±0.14
Serine/threonine kinase 2	Slk	0.59±0.11
serine/threonine kinase 22 substrate 1 /// interferon regulatory factor 3	Irf3 /// Stk22s1	5.68±0.52
serine/threonine kinase 24 (STE20 homolog, yeast)	Stk24	8.12±0.61
serine/threonine kinase 25 (STE20 homolog, yeast)	Stk25	1.92±0.26
serine/threonine kinase 3 (STE20 homolog, yeast)	Stk3	3.88±0.42
serine/threonine kinase 38	Stk38	0.97±0.13
serine/threonine kinase 4 (predicted)	Stk4_predicted	0.79±0.58
serine/threonine kinase 40	Stk40	0.68±0.12
serine/threonine kinase receptor associated protein	Strap	9.8±0.64
serine/threonine/tyrosine interacting-like 1	Styxl1	0.64±0.24
serologically defined colon cancer antigen 1	Sdccag1	2.89±0.4
serologically defined colon cancer antigen 10	Sdccag10	5.86±0.68
serologically defined colon cancer antigen 3	Sdccag3	2.73±0.08
Serpine1 mRNA binding protein 1	Serbp1	11.26±0.99
SERTA domain containing 1	Sertad1	1.44±0.3
SERTA domain containing 2	Sertad2	1.57±0.39
serum amyloid P-component	Apcs	47.85±6.28
serum response factor (predicted)	Srf_predicted	0.89±0.29
serum response factor binding protein 1	Srfbp1	2.04±0.06
serum/glucocorticoid regulated kinase	Sgk	27.1±4.45
seryl-aminoacyl-tRNA synthetase	Sars	3.13±0.46
seryl-aminoacyl-tRNA synthetase 2	Sars2	0.2±0.05
sestrin 1 (predicted)	Sesn1_predicted	2.75±0.34
sestrin 3 (predicted)	Sesn3_predicted	0.74±0.11
SET and MYND domain containing 2	Smyd2	2.22±0.07
SET and MYND domain containing 3	Smyd3	0.4±0.04
SET and MYND domain containing 4 (predicted)	Smyd4_predicted	0.62±0.14
SET binding factor 1 (predicted)	Sbf1_predicted	1.14±0.26
SET domain and mariner transposase fusion gene	Setmar	0.43±0.14
SET domain containing (lysine methyltransferase) 8 /// similar to SET domain-containing protein	LOC687538 /// LOC689820 /// Setd8	3.75±0.62
SET domain containing 2	Setd2	0.68±0.17
SET domain containing 3	Setd3	6.61±0.98
SET domain containing 4	Setd4	0.56±0.13
SET domain containing 5	Setd5	0.34±0.06
SET domain containing 6	Setd6	1.44±0.12
SET domain, bifurcated 1 (predicted)	Setdb1_predicted	1.11±0.19
SET translocation (predicted)	Set_predicted	4.8±0.87
SET translocation (predicted)	LOC502130 /// RGD1562760_predicted /// Set_predicted	4.39±0.08
seven in absentia 1A	Siah1a	0.39±0.02
seven in absentia 2	Siah2	0.28±0.13
sex comb on midleg homolog 1 (predicted)	Scmh1_predicted	0.31±0.23
sex hormone binding globulin	Shbg	0.33±0.06
SFT2 domain containing 1	Sft2d1	5.11±0.3
SFT2 domain containing 2	Sft2d2	3.32±0.31
SFT2 domain containing 3	Sft2d3	0.61±0.16
SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	Sugt1	3.21±0.24
SH2 domain containing phosphatase anchor protein 1 (predicted)	Spap1_predicted	1.54±0.1
SH2-B PH domain containing signaling mediator 1	Sh2bpsm1	2.21±0.28
SH3 domain and tetratricopeptide repeats 1 (predicted)	Sh3tc1_predicted	4.82±0.05
SH3 domain and tetratricopeptide repeats 2	Sh3tc2	1.75±0.33
Sh3 domain YSC-like 1 (predicted)	Sh3yl1_predicted	2.6±0.13
SH3/ankyrin domain gene 2	Shank2	0.63±0.27
SH3-binding domain glutamic acid-rich protein like (predicted)	Sh3bgrl_predicted	0.7±0.27
SH3-domain binding protein 5 (BTK-associated)	Sh3bp5	2.17±0.3
SH3-domain GRB2-like 1	Sh3gl1	0.48±0.09
SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.82±0.07
SH3-domain GRB2-like endophilin B2	Sh3glb2	0.3±0.14
Sh3kbp1 binding protein 1 (predicted)	Shkbp1_predicted	0.67±0.09
SHANK-associated RH domain interacting protein	Sharpin	2.78±0.4
short coiled-coil protein	Scoc	14.9±0.71
SHQ1 homolog (S. cerevisiae) (predicted)	Shq1_predicted	0.35±0.01
shroom family member 2	Shroom2	2.61±0.48
Shwachman-Bodian-Diamond syndrome homolog (human)	Sbds	3.42±0.4
siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	Siahbp1	1.96±0.57
sialic acid acetylesterase (predicted)	Siae_predicted	5.02±0.82

SID1 transmembrane family, member 2 (predicted)	Sidt2_predicted	4.83±0.94
sideroflexin 1	Sfxn1	19.3±0.54
sideroflexin 4 (predicted)	Sfxn4_predicted	0.48±0.12
sideroflexin 5	Sfxn5	0.57±0.06
signal peptidase complex subunit 2 homolog (S. cerevisiae) (predicted)	Spcs2_predicted	4.08±0.51
signal peptide peptidase 3	Sppl3	1.4±0.86
signal peptide peptidase-like 2A	Sppl2a	2.77±0.16
signal peptide peptidase-like 2B	Sppl2b	0.76±0.05
signal recognition particle 14 (predicted)	Srp14_predicted	10.23±0.91
signal recognition particle 19 (predicted)	Srp19_predicted	1.6±0.48
signal recognition particle 54	Srp54	4.34±0.5
signal recognition particle 68 (predicted)	Srp68_predicted	3.17±0.39
signal recognition particle 72	Srp72	3.56±0.07
signal recognition particle receptor ('docking protein')	Srpr	5.2±0.25
signal recognition particle receptor, B subunit	Srprb	4.29±0.81
signal sequence receptor, alpha	Ssr1	4.28±0.67
signal sequence receptor, beta (predicted)	Ssr2_predicted	4.93±0.32
signal sequence receptor, delta	Ssr4	8.7±1.11
signal sequence receptor, gamma	Ssr3	18.82±1.05
signal transducer and activator of transcription 1	Stat1	3.43±0.1
signal transducer and activator of transcription 2	Stat2	0.34±0.12
signal transducer and activator of transcription 3	Stat3	0.92±0.39
signal transducer and activator of transcription 5B	Stat5b	0.33±0.13
signal-induced proliferation-associated 1 like 1	Sipa1l1	0.69±0.23
signal-regulatory protein alpha	Sirpa	0.73±0.02
similar to 0610007L01Rik protein	MGC94190	6.81±0.68
similar to 0610010K06Rik protein	RGD1307161	3.27±0.24
Similar to 106 kDa O-GlcNAc transferase-interacting protein (predicted)	RGD1307844_predicted	2.16±0.17
similar to 1110008L16Rik protein (predicted)	RGD1305089_predicted	1.47±0.15
similar to 1500019C06Rik protein (predicted)	RGD1560433_predicted	0.3±0.05
similar to 1700019E19Rik protein (predicted)	RGD1307392_predicted	0.77±0.23
similar to 1700123O20Rik protein (predicted)	RGD1308430_predicted	1.26±0.03
similar to 2010004A03Rik protein (predicted) /// similar to 2010004A03Rik protein	LOC498951 /// RGD1305691_predicted	2.22±0.16
similar to 2010321M09Rik protein	RGD1359616	1.77±0.25
similar to 20-alpha-hydroxysteroid dehydrogenase (predicted)	RGD1564865_predicted	29.62±2.05
similar to 2210021J22Rik protein (predicted)	RGD1306001_predicted	0.47±0.07
similar to 2310044H10Rik protein	MGC93975	2.15±0.43
similar to 2310047B19Rik protein (predicted)	RGD1308026_predicted	1.11±0.13
similar to 2410001C21Rik protein	RGD1311072	1.99±0.11
similar to 2410024A21Rik protein	RGD1304878	1.95±0.22
similar to 2610030H06Rik protein (predicted)	RGD1566155_predicted	0.69±0.06
similar to 2610301G19Rik protein (predicted)	RGD1309922_predicted	0.94±0.28
similar to 2610317D23Rik protein (predicted)	RGD1565411_predicted	0.59±0.19
similar to 2700029M09Rik protein (predicted)	RGD1311747_predicted	2.13±0.33
similar to 2700078E11Rik protein	RGD1308127	3.08±0.02
similar to 2810422O20Rik protein	RGD1306783	0.77±0.13
similar to 2900002H16Rik protein (predicted)	RGD1307973_predicted	1.16±0.2
similar to 3000004C01Rik protein	RGD1310360	0.23±0.05
similar to 3110080A02Rik protein (predicted)	RGD1305754_predicted	0.38±0.07
similar to 3-oxoacid CoA transferase 1	LOC678860	42.23±5.28
similar to 4632419K20Rik protein	MGC94288	0.68±0.07
similar to 4921517L17Rik protein	RGD1311678	0.99±0.07
similar to 4930429A08Rik protein (predicted)	RGD1564943_predicted	1.11±0.21
similar to 4930431B09Rik protein	LOC310721	2.39±0.23
similar to 4930453N24Rik protein	MGC95208	1.1±0.09
Similar to 4930566A11Rik protein (predicted)	RGD1306674_predicted	0.24±0.04
similar to 4931417G12Rik protein (predicted)	RGD1565997_predicted	1.3±0.19
similar to 5(3)-deoxyribonucleotidase, cytosolic type (Cytosolic 5,3-pyrimidine nucleotidase) (Deoxy-5-nucleotidase 1) (dNT-1)	LOC688261	0.36±0.06
similar to 5730403M16Rik protein	LOC308320	0.3±0.06
Similar to 5730420B22Rik protein (predicted)	RGD1306755_predicted	2±0.32
similar to 5930416I19Rik protein	MGC94282	0.53±0.09
similar to 5-nucleotidase, cytosolic II	LOC365090	3.25±0.32
similar to 6.8 kDa mitochondrial proteolipid	LOC691427	26.77±1.08
similar to 60S ribosomal protein L38 /// ribosomal protein L38 /// 60S ribosomal protein L38 pseudogene	LOC681221 /// LOC681502 /// LOC682793 /// LOC685963 /// LOC688248 /// LOC689671 /// LOC690468 /// LOC690833 /// Rpl38	33.73±2.8
similar to 82-kD FMRP Interacting Protein	LOC687994	0.43±0.01
similar to 9130011E15Rik protein (predicted)	RGD1564887_predicted	0.58±0.09
similar to 9230105E10Rik protein	RGD1304579	1.19±0.19
similar to 9530008L14Rik protein	RGD1305679	5.64±0.85
similar to 9630058J23Rik protein (predicted)	RGD1564833_predicted	2.07±0.19
Similar to a disintegrin and metalloprotease domain 4	LOC500688	2.6±0.55
similar to Aa2-174	RGD1309578	1.11±0.02
similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (ACAD-8) (predicted)	RGD1564209_predicted	1.64±0.11
similar to Acylphosphatase, muscle type isozyme (Acylphosphate phosphohydrolase)	LOC682245	1.78±0.14
similar to Adenosine deaminase CG11994-PA	LOC311352	0.32±0.07
similar to adipocyte-specific protein 4	RGD1308813	5.08±0.99
similar to ADP-ribosylation factor GTPase-activating protein 3 (ARF GAP 3)	LOC503165	1.02±0.18
similar to ADP-ribosylation factor-like 1	LOC688311	0.52±0.21
similar to AHA1, activator of heat shock 90kDa protein ATPase homolog 1	LOC681996	4.22±0.4
Similar to AL023001 protein (predicted)	RGD1305001_predicted	3.05±0.58

similar to alcohol dehydrogenase PAN2 (predicted)	RGD1565196_predicted	3.27±0.71
similar to Alpha- and gamma-adaptin-binding protein p34	LOC498912	1.13±0.31
Similar to alternative testis transcripts open reading frame A CG4241-PA, isoform A	LOC689414	0.97±0.19
similar to anaphase promoting complex subunit 13	LOC685029	5.59±1.33
Similar to ankyrin repeat and SOCs box-containing protein 5	LOC361187	0.24±0.04
similar to ankyrin repeat domain 40	LOC688144	2.67±0.19
Similar to AP2 associated kinase 1 (predicted)	RGD1563580_predicted	0.6±0.25
similar to AP-3 complex subunit sigma-2 (Adapter-related protein complex 3 sigma-2 subunit) (Sigma-adaptin 3b) (AP-3 complex sigma-3B subunit) (Sigma-3B-adaptin)	LOC683402	3.88±0.39
Similar to APG4 autophagy 4 homolog C	LOC313391	2.5±0.38
similar to APG4-D protein	LOC686505	0.83±0.1
similar to apoptosis related protein APR-3; p18 protein (predicted)	RGD1311605_predicted	2.68±0.26
similar to arginyl aminopeptidase (aminopeptidase B)-like 1	LOC684035	3.21±1.22
similar to arsenate resistance protein 2	LOC686980	1.36±0.26
similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	LOC684567	42.65±1.9
similar to ATP-binding cassette, sub-family G (WHITE), member 3	LOC360997	1.43±0.08
similar to autophagy 5-like	LOC365601	2.1±0.29
similar to B0511.12	LOC690217	1.24±0.15
similar to Basic FGF-repressed Zic-binding protein (mbFZb)	LOC683512	1.82±0.24
similar to BC003940 protein (predicted)	RGD1311925_predicted	1.31±0.32
Similar to BC021442 protein (predicted)	RGD1561413_predicted	0.37±0.12
similar to BC068281 protein (predicted)	RGD1563701_predicted	0.44±0.05
Similar to B-cell CLL/lymphoma 7A	LOC690085	0.75±0.5
Similar to Bcl2-associated athanogene 2	LOC690038	0.83±0.27
Similar to bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (variant 1) (predicted)	RGD1306698_predicted	1.14±0.16
similar to BMP-2 inducible kinase	LOC289485	1.51±0.08
similar to Brain protein 44 (predicted)	RGD1563422_predicted	28.36±2.58
similar to BRCA1-associated protein (BRAP2) (Impedes mitogenic signal propagation) (IMP)	LOC687346	0.54±0.12
Similar to Breast carcinoma amplified sequence 3 homolog (K20D4) (predicted)	RGD1560788_predicted	1.1±0.26
Similar to Butyrate-induced transcript 1 (predicted)	RGD1565496_predicted	2.35±0.2
similar to C184L-22 /// Sjogren's syndrome/scleroderma autoantigen 1	LOC684594 /// Sssca1	0.95±0.18
similar to C1orf25	RGD1307890	0.86±0.12
similar to C21ORF7	LOC304131	0.2±0.09
similar to C21orf70 protein	RGD1311257	0.51±0.03
similar to C530044N13Rik protein	RGD1306568	4.77±0.43
Similar to calmodulin-like 4	LOC691455	39.03±1.65
similar to capping protein (actin filament) muscle Z-line, alpha 1	LOC691149	5.3±0.43
Similar to CCAAT displacement protein isoform b	Cutl1	4.86±0.49
similar to cDNA sequence AF155546	RGD1309387	0.67±0.11
similar to cDNA sequence AF397014	RGD1308114	4.13±0.37
similar to cDNA sequence BC005537	LOC498750	6.05±0.53
Similar to cDNA sequence BC006662	RGD1304748	4.09±0.03
similar to cDNA sequence BC013529 (predicted)	RGD1309759_predicted	7.47±0.65
similar to cDNA sequence BC017158	RGD1310127	0.43±0.09
similar to CDNA sequence BC017647 (predicted)	RGD1566149_predicted	0.72±0.12
similar to cDNA sequence BC020002 (predicted)	RGD1308432_predicted	0.41±0.13
similar to cDNA sequence BC021608	MGC95155	8.51±1.08
similar to CDNA sequence BC024479	LOC500974	0.35±0.18
similar to cDNA sequence BC024814 (predicted)	RGD1311433_predicted	0.26±0.17
similar to cDNA sequence BC031181 (predicted)	RGD1562987_predicted	8.62±0.83
similar to cDNA sequence BC056474 (predicted)	RGD1564058_predicted	6.64±0.16
similar to CDV-3B	LOC315970	0.3±0.15
similar to Cell division protein kinase 8 (Protein kinase K35) (predicted)	RGD1560888_predicted	1.47±0.11
similar to centrosome protein Cep63	LOC300963	0.43±0.08
similar to cervical cancer receptor (predicted)	RGD1310591_predicted	2.46±0.33
similar to CG10084-PA	RGD1308297	5.88±0.59
similar to CG11206-PA	LOC313672	0.21±0.03
similar to CG12279-PA	LOC500420	1.86±0.45
similar to CG12379-PA (predicted)	RGD1308635_predicted	1.27±0.21
similar to CG12929-PA	LOC682404	0.78±0.59
similar to CG12935-PA	LOC686289 /// LOC690285	5.51±0.62
similar to CG13901-PA	RGD1307648	2.05±0.2
Similar to CG13957-PA (predicted)	RGD1309995_predicted	12.02±1.22
similar to CG14286-PA	LOC686765	1.04±0.16
similar to CG14483-PA	LOC681884	2.24±0.24
similar to CG14903-PA (predicted)	RGD1561792_predicted	0.96±0.08
similar to CG14967-PA	RGD1307929	11.43±1.04
similar to CG14977-PA (predicted)	RGD1309735_predicted	7.24±1.17
similar to CG14980-PB	RGD1306410	6.01±0.64
similar to CG16812-PA (predicted)	RGD1307554_predicted	0.21±0.01
similar to CG18661-PA	RGD1307155	3.06±0.76
similar to CG31122-PA (predicted)	RGD1306941_predicted	2.24±0.07
similar to CG31613-PA	LOC684841	1.24±0.08
Similar to CG31759-PA	RGD1310975	0.73±0.03
similar to CG33331-PA	LOC362419	0.68±0.13
similar to CG33714-PB, isoform B	LOC688717	4.43±0.55
similar to CG3570-PA	LOC500034	2.7±0.12
Similar to CG3740-PA	LOC690000	4.28±0.11
similar to CG4751-PA	LOC681944	1.44±0.5
similar to CG4768-PA (predicted)	RGD1309748_predicted	2.35±0.42
similar to CG5500-PA	LOC688310	0.83±0.09
similar to CG5987-PA (predicted) /// mesenchymal stem cell protein DSC92	Ngrn /// RGD1310399_predicted	1.69±0.04
similar to CG6105-PA	MGC72942	37.23±2.22
similar to CG6878-PA	LOC679572	9.6±2.24
similar to CG8043-PA (predicted)	RGD1306000_predicted	0.59±0.14

similar to CG8272-PA	LOC502201	0.46±0.06
similar to CG9117-PA	RGD1306932	0.38±0.08
similar to CG9240-PA	LOC687395	3.12±0.11
similar to CG9346-PA (predicted)	RGD1307882_predicted	3.49±0.69
similar to CG9752-PA	RGD1311345	7.96±0.93
similar to CG9882-PA (predicted)	RGD1306157_predicted	0.47±0.1
similar to CG9886-like	LOC684314	7.72±0.56
similar to CG9967-PA, isoform A	LOC678910	0.21±0.03
Similar to CG9996-PA	LOC300173	0.64±0.28
similar to CGI-35 protein (predicted)	RGD1310899_predicted	7.03±0.9
similar to Chain A, Solution Structure Of The Bola-Like Protein From Mus Musculus (predicted)	RGD1309998_predicted /// RGD1565363_predicted	3.03±0.93
similar to channel-interacting PDZ domain protein isoform 1 (predicted)	RGD1565362_predicted	3.03±0.21
similar to chr2 synaptotagmin (predicted)	RGD1565705_predicted	0.52±0.15
similar to chromosome 1 open reading frame 172	RGD1303271	0.65±0.1
similar to chromosome 1 open reading frame 50 (predicted)	RGD1564804_predicted	0.65±0.09
similar to chromosome 1 open reading frame 63	RGD1359529	15.27±2.98
similar to chromosome 10 open reading frame 18 (predicted)	RGD1564456_predicted	1.74±0.28
similar to chromosome 10 open reading frame 4; similar to putative acid phosphatase F26C11.1	RGD1309482	0.77±0.07
similar to chromosome 10 open reading frame 6 (predicted)	RGD1560300_predicted	1.01±0.19
similar to chromosome 14 open reading frame 130	RGD1359144	2.75±0.54
similar to chromosome 14 open reading frame 138 (predicted)	RGD1306228_predicted	1.1±0.07
similar to chromosome 14 open reading frame 21 (predicted)	RGD1308396_predicted	0.33±0.07
similar to chromosome 14 open reading frame 35 (predicted)	RGD1559923_predicted	1.96±0.15
similar to chromosome 14 open reading frame 94	RGD1305288	0.66±0.3
similar to chromosome 16 open reading frame 28 (predicted)	RGD1565247_predicted	3.81±0.02
similar to chromosome 16 open reading frame 33; minus -99 protein (predicted)	RGD1310922_predicted	0.61±0.09
similar to chromosome 16 open reading frame 5	RGD1310686	1.98±0.24
similar to chromosome 16 open reading frame 7 (predicted)	RGD1565149_predicted	1.54±0.3
similar to chromosome 2 open reading frame 3; transcription factor 9 (binds GC-rich sequences) (predicted)	RGD1304792_predicted	0.31±0.1
similar to chromosome 20 open reading frame 116 (predicted)	RGD1309979_predicted	4.44±0.68
similar to chromosome 20 open reading frame 30; HSPC274 protein	RGD1307399	5.17±0.58
Similar to chromosome 20 open reading frame 6	RGD1306067	1.9±0.11
similar to chromosome 3 open reading frame 10	LOC679934	4.44±1.36
similar to chromosome 6 open reading frame 106 isoform a	LOC294154	7.41±1.65
similar to chromosome 7 open reading frame 11	LOC678905	0.94±0.14
similar to chromosome 7 open reading frame 11	LOC678905 /// LOC684996	0.53±0.26
Similar to chromosome 7 open reading frame 23 (predicted)	RGD1562351_predicted	1.07±0.26
similar to chromosome 7 open reading frame 30 (predicted)	RGD1306936_predicted	3.75±0.54
Similar to chromosome 9 open reading frame 5 (predicted)	RGD1308958_predicted	0.57±0.13
similar to cleavage stimulation factor, 3 pre-RNA subunit 2	LOC683927	0.33±0.09
similar to c-myc promoter binding protein (predicted)	RGD1562639_predicted	0.25±0.13
similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) (predicted)	RGD1566215_predicted	2.96±0.13
Similar to coiled-coil domain containing 6	LOC691155	32.21±3.02
similar to coiled-coil domain containing 9	LOC684934	0.83±0.22
similar to coiled-coil-helix-coiled-coil-helix domain containing 7	LOC684258	2.34±0.12
Similar to Complement C1q-like protein 3 precursor (Gliacolin)	LOC680404	1.62±0.32
similar to component of oligomeric golgi complex 2	LOC678914	2.48±0.26
similar to component of oligomeric golgi complex 2 /// component of oligomeric golgi complex 2	Cog2 /// LOC678914	0.39±0.06
similar to component of oligomeric golgi complex 5 isoform 1 (predicted)	RGD1563296_predicted	0.63±0.11
similar to constitutive photomorphogenic protein 1	RGD1304773	3.86±0.29
similar to COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase	LOC687381 /// LOC691853	1.79±0.11
similar to CPSF4 protein	MGC108785	2.8±0.53
similar to cullin 4A (predicted)	RGD1563853_predicted	2.02±0.19
similar to cullin 7	LOC680835	0.23±0.1
similar to Cysteine protease ATG4A (Autophagy-related protein 4 homolog A) (Autophagin-2) (Autophagy-related cysteine endopeptidase 2) (AUT-like 2 cysteine endopeptidase)	LOC678769	1.09±0.17
similar to cystin 1	LOC690489	5.17±0.31
similar to cytokine receptor related protein 4	Cytor4	0.99±0.15
similar to D1Ertd622e protein (predicted)	RGD1562136_predicted	3.25±0.17
similar to D330021B20 protein	RGD1308143	2.05±0.55
similar to D8Ertd354e protein (predicted)	RGD1560755_predicted	4.07±0.72
similar to dachshund b	LOC686314	1.21±0.18
similar to Dachshund homolog 1 (Dach1)	LOC306096	3.68±0.59
similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	rCG_33565	6.58±0.38
similar to death effector domain-containing DNA binding protein 2	LOC687118	0.27±0.05
similar to Dedicator of cytokinesis protein 1 (180 kDa protein downstream of CRK) (DOCK180)	LOC679295	2.23±0.27
similar to defective SPErmatogenesis family member (spe-39)	LOC681989	1.82±0.13
similar to Dendritic cell protein GA17 (predicted)	RGD1565840_predicted	13.47±1.97
similar to density-regulated protein	LOC689601	1.32±0.26
similar to DEP domain containing 6 (predicted)	RGD1561030_predicted	0.71±0.13
similar to Der1-like domain family, member 2	LOC687738	3.46±0.49
similar to diacylglycerol kinase, delta 130kDa isoform 1 (predicted)	RGD1563309_predicted	0.46±0.16
similar to differentially expressed in B16F10 1	LOC687029	5.72±0.4
Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle	LOC685729	8.6±2.43
similar to DIP13 alpha (predicted)	RGD1309388_predicted	1.02±0.09
similar to Disco-interacting protein 2 homolog /// DIP2 disco-interacting protein 2 homolog A (Drosophila)	Dip2a /// LOC687682	0.43±0.12
similar to divalent cation tolerant protein CUTA (predicted)	RGD1564854_predicted	0.68±0.16
similar to dJ202D23.2 (novel protein similar to C21ORF5 (KIAA0933)) (predicted)	RGD1305534_predicted	0.9±0.13
Similar to dJ55C23.6 gene product (predicted)	RGD1306962_predicted	1.9±0.51
similar to dJ842G6.1.1 (novel protein) (predicted)	RGD1309829_predicted	1.18±0.12
similar to dJ881L22.2 (novel protein) (predicted)	RGD1307696_predicted	1.92±0.27
Similar to DKFZP434B168 protein (predicted)	RGD1308014_predicted	0.56±0.24
similar to DKFZP547E1010 protein	LOC361990	2.49±0.07

similar to DKFZP547E1010 protein /// similar to Protein C1orf77 homolog	LOC361990 /// LOC500378	0.75±0.01
Similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase MmuIIIA) (DNA MTase MmuIIIA) (M.MmuIIIA) (predicted)	RGD1305891_predicted	0.62±0.23
similar to DNA segment on chromosome X and Y (unique) 155 expressed sequence isoform 1	LOC288526	0.35±0.1
similar to DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed (predicted)	RGD1560909_predicted	1.33±0.05
Similar to DNA segment, Chr 10, University of California at Los Angeles 1 (predicted)	RGD1560401_predicted	5.33±0.54
similar to DNA segment, Chr 10, Wayne State University 102, expressed (predicted)	RGD1563365_predicted	0.76±0.17
similar to DNA segment, Chr 11, Wayne State University 99, expressed (predicted) /// hypothetical protein LOC619573	LOC619573 /// RGD1309706_predicted	0.84±0.34
similar to DNA segment, Chr 14, ERATO Doi 436, expressed (predicted)	RGD1304610_predicted	0.35±0.05
similar to DNA segment, Chr 14, ERATO Doi 449, expressed	RGD1305689	0.39±0.42
similar to DNA segment, Chr 18, Wayne State University 98, expressed (predicted)	RGD1560212_predicted	4.63±0.79
similar to DNA segment, Chr 19, ERATO Doi 386, expressed (predicted)	RGD1307934_predicted	0.35±0.05
similar to DNA segment, Chr 4, Brigham & Womens Genetics 0951 expressed	RGD1308059	0.58±0.21
similar to DNA segment, Chr 4, ERATO Doi 22, expressed (predicted)	RGD1560286_predicted	1.57±0.33
similar to DNA segment, Chr 5, ERATO Doi 135, expressed	LOC679383	3.94±0.14
similar to DNA segment, Chr 6, Wayne State University 163, expressed (predicted)	RGD1311164_predicted	2.22±0.12
similar to DnaJ (Hsp40) homolog, subfamily A, member 4	LOC498996	3.85±0.88
similar to DnaJ (Hsp40) homolog, subfamily B, member 10 isoform 2	LOC689593	1.82±0.31
similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (HSJ-2) (MRJ) (mDj4)	LOC690183	5.04±0.44
similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (predicted)	Dnajb6 /// LOC686213 /// LOC690183 /// RGD1565996_predicted	1.59±0.12
similar to DOC-1 related protein /// CDK2-associated protein 2	Cdk2ap2 /// LOC683786	4.27±0.65
similar to dolichyl-phosphate mannosyltransferase polypeptide 3 (Dolichol-phosphate mannose synthase subunit 3) (predicted)	rCG_63436 /// RGD1561807_predicted	4.85±0.48
similar to downregulated in renal cell carcinoma	RGD1306327	0.68±0.19
similar to e(y)2 protein	LOC682575	11.64±1.76
similar to early estrogen-induced gene 1 protein	LOC687750	1.88±0.24
similar to ecotropic viral integration site 5-like (predicted)	RGD1561962_predicted	1.12±0.17
similar to Elongation factor Ts, mitochondrial precursor (EF-Ts) (EF-TsMt) (2A3-2)	LOC679068	3.57±0.16
similar to Elongation of very long chain fatty acids protein 1	LOC679532	10.75±1.47
similar to elongation protein 4 homolog	LOC687694	0.63±0.11
similar to enoyl Coenzyme A hydratase domain containing 3	LOC684538	1.67±0.94
similar to ENSANGP00000021391 (predicted)	RGD1309779_predicted	10.35±0.3
similar to Erbb2 interacting protein isoform 2 (predicted)	RGD1562952_predicted	6.73±0.73
similar to erythroid differentiation-related factor 1 (predicted)	RGD1306820_predicted	0.71±0.13
similar to ES cell-expressed Ras	LOC679682	3.35±0.91
similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor-interacting protein 1) (TRIP-1)	LOC682390	5.65±0.33
similar to Exocyst complex component Sec15B (predicted)	RGD1560638_predicted	0.68±0.1
similar to exosome component 1	LOC679140	0.93±0.12
similar to exosome component 10	LOC313707	0.8±0.1
similar to expressed sequence AA960436	RGD1305215	0.23±0.03
Similar to expressed sequence AI449175	MGC72612	0.22±0.09
similar to expressed sequence AI597479	RGD1310553	0.56±0.12
similar to expressed sequence AW209491	RGD1308147	2.07±0.38
similar to expressed sequence AW212394 (predicted)	RGD1562317_predicted	1.42±0.15
similar to expressed sequence AW413431 (predicted)	RGD1559841_predicted	1.72±0.27
similar to expressed sequence AW556797 (predicted)	RGD1305138_predicted	1.09±0.16
similar to F28C1.3a	LOC308398	0.43±0.29
similar to F33H2.2	LOC689997	5.23±0.76
similar to F54C1.5a	LOC499814	0.74±0.14
similar to F57G4.9	LOC690164	0.32±0.14
similar to Fam13a1 protein	RGD1309807	0.91±0.2
similar to family 53, member C protein	LOC685405	0.9±0.1
similar to family with sequence similarity 11, member A (predicted)	RGD1563037_predicted	2.98±0.32
similar to F-box only protein 31 (predicted)	RGD1561069_predicted	1.77±0.12
similar to F-box only protein 6 (F-box/G-domain protein 2) (predicted)	RGD1305932_predicted	0.33±0.18
similar to F-box protein FBL2	RGD1308119	0.43±0.19
similar to Fbxw17 protein (predicted)	RGD1566133_predicted	0.89±0.04
similar to FKSG24 (predicted)	RGD1308064_predicted	4.6±0.71
Similar to FLJ20298 protein isoform a (predicted)	RGD1563084_predicted	4.3±0.35
similar to FLJ42986 protein (predicted)	RGD1560724_predicted	0.98±0.19
similar to FUN14 domain containing 2 (predicted)	RGD1560916_predicted	4.24±0.62
Similar to G protein-coupled receptor 146 (predicted)	RGD1560731_predicted	0.58±0.12
similar to gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	MGC125167	9.36±0.81
similar to GC-rich sequence DNA-binding factor homolog	LOC681004	0.86±0.25
similar to gem (nuclear organelle) associated protein 5	LOC686616	0.66±0.08
similar to gem (nuclear organelle) associated protein 7	LOC499391	0.24±0.13
similar to gene trap ROSA b-geo 22	LOC687166 /// LOC691093	0.46±0.39
similar to germinal histone H4 gene	LOC684887	0.29±0.04
similar to GI:13385412-like protein splice form I	RGD735065	8.29±0.56
similar to GLI-Kruppel family member GLI4	LOC500893	0.55±0.17
similar to Glucocorticoid receptor DNA-binding factor 1	LOC686359	2.57±0.1
similar to Glucosylceramidase precursor (Beta-glucocerebrosidase) (Acid beta-glucosidase) (D-glucosyl-N-acylsphingosine glucohydrolase)	LOC684536	3.53±0.38
similar to glutathione transferase GSTM7-7	MGC108896	1.96±0.26
similar to glycogen synthase 1, muscle	LOC687978 /// LOC690987	0.31±0.13
similar to Golgi phosphoprotein 2 (Golgi membrane protein GP73)	LOC680692 /// LOC682869	2.21±0.3
similar to GS2 gene (predicted)	RGD1562200_predicted	0.38±0.05
similar to GTPase activating RANGAP domain-like 3 (predicted)	RGD1564019_predicted	3.16±0.64
similar to Harmonin-interacting ankyrin repeat-containing protein (Harp)	LOC687561	4.44±0.6

similar to HCDI protein (predicted)	RGD1309307_predicted	0.43±0.03
similar to Hepatocellular carcinoma-associated antigen 58 homolog (predicted)	RGD1305020_predicted	0.75±0.12
Similar to heterogeneous nuclear ribonucleoprotein G - human	LOC302855	1.36±0.35
similar to Histidine triad nucleotide-binding protein 1 (Adenosine 5-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	LOC690660	33.61±1.56
Similar to histocompatibility 28	LOC310968	0.84±0.13
similar to histone cell cycle regulation defective homolog A isoform 1	LOC363849	0.55±0.1
similar to Histone H1.2 (H1 VAR.1) (H1c)	LOC684681	3.7±1.45
similar to HIV-1 Rev binding protein	LOC363266	1.46±0.39
similar to HLA-B associated transcript-2 isoform a	LOC296637	1.09±0.45
similar to HSPC043 protein (predicted)	RGD1307983_predicted	0.56±0.04
similar to HSPC288 (predicted)	RGD1310769_predicted	1.16±0.13
similar to HT014 (predicted)	RGD1308048_predicted	2.6±0.17
similar to HT021 (predicted)	RGD1306063_predicted	1.58±0.04
similar to HTGN29 protein; keratinocytes associated transmembrane protein 2	RGD1310352	8.92±1.16
similar to hypothetical gene supported by AF226663 (predicted)	RGD1565146_predicted	0.53±0.06
similar to hypothetical gene supported by AK085276 (predicted)	RGD1562252_predicted	0.73±0.1
similar to hypothetical MGC48595 (predicted)	RGD1566220_predicted	0.47±0.13
similar to hypothetical p38 protein (predicted)	RGD1311910_predicted	1.16±0.19
similar to hypothetical protein	RGD1306595	2.01±0.37
similar to hypothetical protein	RGD1310571	1.66±0.02
similar to hypothetical protein	RGD1307336	0.91±0.08
similar to hypothetical protein	RGD1311361	0.7±0.05
similar to hypothetical protein	RGD1310571	0.28±0.19
similar to hypothetical protein	LOC360479	0.26±0.07
similar to hypothetical protein (predicted)	RGD1305045_predicted	12±1.13
similar to hypothetical protein (predicted)	RGD1308489_predicted	2.96±0.43
similar to hypothetical protein (predicted)	RGD1561605_predicted	2.46±0.13
similar to hypothetical protein (predicted)	RGD1309765_predicted	1.56±0.38
similar to hypothetical protein (predicted)	RGD1565432_predicted	1.21±0.18
similar to hypothetical protein (predicted)	RGD1308489_predicted	1.08±0.36
similar to hypothetical protein (predicted)	RGD1310440_predicted	0.93±0.2
similar to hypothetical protein (predicted)	RGD1306576_predicted	0.74±0.27
similar to hypothetical protein (predicted)	RGD1560620_predicted	0.48±0.09
similar to hypothetical protein (predicted)	RGD1305269_predicted	0.4±0.09
similar to hypothetical protein 6720484B16 (predicted)	RGD1304881_predicted	0.57±0.16
Similar to hypothetical protein A430031N04 (predicted)	RGD1559643_predicted	0.23±0.08
similar to Hypothetical protein A430033K04 (predicted)	RGD1566386_predicted	0.23±0.07
similar to hypothetical protein BC011833 (predicted)	RGD1309188_predicted	4.25±0.38
similar to Hypothetical protein BC014729	MGC105560	3.62±0.2
similar to hypothetical protein BC015148 (predicted)	RGD1309095_predicted	0.44±0.12
similar to Hypothetical protein C6orf60 (predicted) /// similar to minichromosome maintenance protein 8 isoform 1 (predicted)	RGD1311294_predicted /// RGD1560557_predicted	0.45±0.07
similar to Hypothetical protein CGI-99	RGD1304704	13.67±0.81
similar to hypothetical protein CL25084 (predicted)	RGD1306508_predicted	7.24±0.68
similar to hypothetical protein D030056L22	LOC499331	1.15±0.07
Similar to hypothetical protein D15Ertd785e	MGC114417	0.65±0.13
similar to hypothetical protein D2Ertd391e (predicted)	RGD1310685_predicted	1.57±0.23
similar to hypothetical protein DKFZp313N0621 (predicted)	RGD1560717_predicted	6.58±0.19
similar to hypothetical protein DKFZp434A1319 (predicted)	RGD1307357_predicted	0.81±0.15
similar to hypothetical protein DKFZp434K1815	LOC304396	0.33±0.07
similar to hypothetical protein DKFZp564D0478 (predicted)	RGD1304793_predicted	0.89±0.29
similar to hypothetical protein ET (predicted)	RGD1307394_predicted	1.52±0.09
Similar to hypothetical protein F730001J03 (predicted)	RGD1311757_predicted	0.83±0.02
similar to hypothetical protein FLJ10154	RGD1310061	3.71±0.96
similar to hypothetical protein FLJ10342 (predicted)	RGD1307791_predicted	0.75±0.1
similar to hypothetical protein FLJ10901 (predicted)	RGD1311892_predicted	0.54±0.05
similar to hypothetical protein FLJ10925	RGD1305455	0.71±0.21
similar to hypothetical protein FLJ10986	LOC298250	12.64±1.34
similar to hypothetical protein FLJ11193 (predicted)	RGD1306502_predicted	1.21±0.28
similar to hypothetical protein FLJ11218	RGD1309804	2.11±0.25
Similar to hypothetical protein FLJ11305 (predicted)	RGD1307041_predicted	0.94±0.07
similar to hypothetical protein FLJ12118 (predicted)	RGD1311612_predicted	0.57±0.06
similar to hypothetical protein FLJ12242 (predicted)	RGD1311154_predicted	2.59±0.54
similar to hypothetical protein FLJ12661 (predicted)	RGD1309403_predicted	0.35±0.1
Similar to hypothetical protein FLJ12787	RGD1310992	1.41±0.58
similar to hypothetical protein FLJ13045 (predicted)	RGD1307615_predicted	0.63±0.26
similar to hypothetical protein FLJ13089	RGD1305685	0.45±0.03
similar to hypothetical protein FLJ13149 (predicted)	RGD1563839_predicted	1.53±0.36
similar to hypothetical protein FLJ13188 (predicted)	RGD1305500_predicted	0.28±0.07
similar to hypothetical protein FLJ13231 (predicted) /// hypothetical protein LOC679830	LOC679830 /// RGD1310081_predicted	0.3±0.15
similar to hypothetical protein FLJ14146	RGD1310587	9.51±1.9
similar to hypothetical protein FLJ14675	RGD1309592	0.36±0.1
similar to hypothetical protein FLJ20010 (predicted)	RGD1563941_predicted	3.51±1.25
Similar to hypothetical protein FLJ20154	RGD1305793	2.68±0.44
similar to hypothetical protein FLJ20254	RGD1311324	2.15±0.31
similar to hypothetical protein FLJ20276 (predicted)	RGD1308101	0.21±0.03
similar to hypothetical protein FLJ20436	RGD1303127	1.15±0.22
similar to hypothetical protein FLJ20487	RGD1309216	5.01±0.85
similar to hypothetical protein FLJ20507 (predicted)	RGD1309744_predicted	3.89±0.23
Similar to hypothetical protein FLJ20627 (predicted)	RGD1309546_predicted	3.67±0.44
similar to hypothetical protein FLJ20729 (predicted)	RGD1308723_predicted	0.32±0.08
similar to hypothetical protein FLJ21156 (predicted)	RGD1309823_predicted	0.79±0.17
similar to hypothetical protein FLJ21820	RGD1311648	2.54±0.41
similar to hypothetical protein FLJ21827	RGD1307682	1.45±0.34

similar to hypothetical protein FLJ22490 (predicted)	RGD1307055_predicted	1.09±0.22
similar to hypothetical protein FLJ22965 (predicted)	RGD1564541_predicted	1.61±0.18
similar to hypothetical protein FLJ23263	RGD1310414	0.36±0.08
Similar to hypothetical protein FLJ23451 (predicted)	RGD1310453_predicted	0.32±0.02
similar to hypothetical protein FLJ30596 (predicted)	RGD1306809_predicted	2.09±0.28
similar to hypothetical protein FLJ31364 (predicted)	RGD1304924_predicted	0.29±0.1
similar to hypothetical protein FLJ31528	RGD1307410	0.74±0.17
similar to hypothetical protein FLJ31606 (predicted)	RGD1561507_predicted	0.22±0.11
similar to hypothetical protein FLJ32825 (predicted)	RGD1564257_predicted	5.57±0.64
Similar to hypothetical protein FLJ32884 (predicted)	RGD1309453_predicted	1.1±0.15
similar to hypothetical protein FLJ33868 (predicted)	RGD1305797_predicted	1.42±0.16
Similar to hypothetical protein FLJ33977 (predicted)	RGD1306423_predicted	0.74±0.06
similar to hypothetical protein FLJ37953 (predicted)	RGD1311269_predicted	0.72±0.27
similar to hypothetical protein FLJ38348 (predicted)	RGD1311424_predicted	0.79±0.27
similar to Hypothetical protein KIAA0152	RGD1307736	2.86±0.17
similar to Hypothetical protein KIAA0373 (predicted)	RGD1311640_predicted	0.28±0.03
similar to Hypothetical protein KIAA0539 (predicted)	RGD1304621_predicted	0.43±0.05
similar to hypothetical protein LOC168850 (predicted)	RGD1560157_predicted	0.64±0.12
similar to hypothetical protein LOC284018 isoform b (predicted)	RGD1565033_predicted	1.94±0.26
similar to Hypothetical protein MGC11690	RGD1305178	1.67±0.38
similar to hypothetical protein MGC14327 (predicted)	RGD1306304_predicted	2.6±0.16
similar to hypothetical protein MGC17943 (predicted)	RGD1563325_predicted	2.21±0.11
similar to Hypothetical protein MGC18716	RGD1307935	1.01±0.18
Similar to hypothetical protein MGC20700 (predicted)	RGD1307722_predicted	0.57±0.12
similar to hypothetical protein MGC23280 (predicted)	RGD1305508_predicted	0.58±0.16
similar to hypothetical protein MGC2494	RGD1306126	2.31±0.58
similar to hypothetical protein MGC25461 (predicted)	RGD1306717_predicted	0.26±0.06
similar to Hypothetical protein MGC25529 (predicted)	RGD1306746_predicted	1.32±0.02
Similar to hypothetical protein MGC29390 (predicted)	RGD1310490_predicted	0.79±0.02
similar to hypothetical protein MGC29875; novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7	LOC305076	0.66±0.12
similar to hypothetical protein MGC30618	RGD1305572	0.83±0.01
similar to hypothetical protein MGC3207	RGD1307789	1.49±0.06
similar to hypothetical protein MGC34760	RGD1359349	2.95±1.68
Similar to hypothetical protein MGC36325 (predicted)	RGD1307374_predicted	0.41±0.01
similar to hypothetical protein MGC36831 (predicted)	RGD1306215_predicted	1.1±0.31
similar to hypothetical protein MGC37079 (predicted)	RGD1310484_predicted	1.39±0.08
similar to Hypothetical protein MGC38513	RGD1304580	0.67±0.03
similar to hypothetical protein MGC38960 (predicted)	RGD1310552_predicted	1.56±0.15
similar to hypothetical protein MGC40841; similar to hypothetical protein MGC4707	RGD1309540	0.97±0.21
similar to hypothetical protein MGC45873 (predicted)	RGD1310271_predicted	0.24±0.12
similar to hypothetical protein MGC47256 (predicted)	RGD1308694_predicted	5.74±0.67
similar to hypothetical protein MGC52110 (predicted)	RGD1565095_predicted	18.56±0.39
similar to hypothetical protein MGC6696	RGD1309471	4.25±0.6
similar to hypothetical protein MGC7537	RGD1359380	2.45±0.53
similar to hypothetical protein MGC9912 (predicted)	RGD1309138_predicted	1.03±0.05
similar to hypothetical protein PRO0971	RGD1311435	1.63±0.19
similar to hypothetical protein supported by AL449243 (predicted) /// similar to CG17680-PA	LOC687237 /// RGD1311310_predicted	29.26±1.47
similar to Hypothetical UPF0184 protein C9orf16 homolog (predicted)	RGD1561113_predicted	1.35±0.37
similar to Hypothetical UPF0327 protein (predicted)	RGD1560187_predicted	21.98±1.24
similar to Integrin alpha-IIb precursor (Platelet membrane glycoprotein IIb) (GPalpha IIb) (GPIIb) (CD41 antigen)	LOC685269	0.54±0.11
similar to Interferon-alpha	LOC686326	0.26±0.26
similar to IQ motif and Sec7 domain 1	LOC686590	5.73±0.99
similar to IQ motif and Sec7 domain 2	LOC685244	0.58±0.06
Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	1.24±0.31
similar to isochorismatase domain containing 2	LOC684270	4.84±0.79
similar to jumonji domain containing 1B	LOC682469	1.86±0.26
similar to jumonji domain containing 2B	LOC301128	0.22±0.1
similar to jumonji protein	LOC681740	2.05±0.45
similar to Jumonji/ARID domain-containing protein 1C (SmcX protein) (predicted)	RGD1560601_predicted	1.43±0.26
similar to K11B4.2	LOC688966	2.59±0.35
similar to K11B4.2	LOC684626 /// LOC688966	0.65±0.12
similar to KB07 protein (predicted)	RGD1561940_predicted	5.3±0.4
similar to keratinocytes associated protein 3	LOC683980	0.36±0.14
similar to KIAA0090 protein (predicted)	RGD1310427_predicted	1.79±0.61
similar to KIAA0157 gene product is novel. (predicted)	RGD1308918_predicted	1.13±0.3
Similar to KIAA0240 (predicted)	RGD1305680_predicted	0.94±0.37
similar to KIAA0335	RGD1305314	0.89±0.13
similar to KIAA0368 (predicted)	RGD1306148_predicted	1.91±0.23
similar to KIAA0372 gene product (predicted)	RGD1306062_predicted	0.89±0.23
similar to KIAA0406-like protein (predicted)	RGD1562582_predicted	3.98±0.39
similar to KIAA0423 (predicted)	RGD1310474_predicted	1.8±0.18
similar to KIAA0456 protein (predicted)	RGD1566016_predicted	0.47±0.19
similar to KIAA0467 protein (predicted)	RGD1308616_predicted	0.69±0.19
similar to KIAA0528 protein (predicted)	RGD1304592_predicted	1.2±0.09
Similar to KIAA0564 protein (predicted)	RGD1308772_predicted	5.22±1.75
Similar to KIAA0597 protein (predicted)	RGD1565757_predicted	20.83±1.47
similar to KIAA0614 protein (predicted)	RGD1309762_predicted	0.2±0.02
Similar to KIAA0672 gene product	RGD1305664	0.59±0.12
similar to KIAA0833 protein /// similar to calmodulin-binding transcription activator 1	LOC362665 /// LOC500591	0.83±0.51
similar to KIAA0853 protein (predicted)	RGD1563689_predicted	2.49±0.33
Similar to KIAA0869 protein (predicted)	RGD1308329_predicted	0.29±0.12
similar to KIAA0913 protein (predicted)	RGD1309414_predicted	3.53±0.6
similar to KIAA0947 protein (predicted)	RGD1309747_predicted	0.46±0.24

similar to KIAA0965 protein (predicted)	RGD1564793_predicted	0.84±0.18
similar to KIAA0999 protein	LOC684112	3.28±0.71
similar to KIAA1007 protein; adrenal gland protein AD-005	RGD1308009	5.91±0.17
similar to KIAA1009 protein	RGD1307365	0.24±0.01
similar to KIAA1078 protein (predicted)	RGD1310950_predicted	0.59±0.14
Similar to KIAA1161 protein (predicted)	RGD1309821_predicted	0.3±0.06
similar to KIAA1267 protein (predicted)	RGD1311429_predicted	1.64±0.25
Similar to KIAA1280 protein (predicted)	RGD1560666_predicted	1.04±0.03
similar to KIAA1411 protein (predicted)	RGD1304927_predicted	2.04±0.12
similar to KIAA1582 protein (predicted)	RGD1310027_predicted	0.45±0.2
similar to KIAA1627 protein (predicted)	RGD1304822_predicted	1.86±0.15
similar to KIAA1636 protein (predicted)	RGD1309285_predicted	0.68±0.15
similar to KIAA1712 protein	RGD1308517	0.4±0.05
similar to KIAA1841 protein (predicted)	RGD1305110_predicted	0.43±0.12
similar to KIAA1919 protein (predicted)	RGD1310495_predicted	11.53±1.57
similar to KIAA2026 protein	RGD1311595	2.21±0.21
similar to kynurenine formamidase	rCG_34031	5.45±1.03
Similar to Lethal giant larvae homolog 2 (predicted)	RGD1560307_predicted	0.62±0.14
similar to LEYDIG CELL TUMOR 10 KD PROTEIN	LOC288913	2.68±0.36
similar to ligatin	LOC498225	1.98±0.15
similar to lin-9 homolog (C. elegans) /// lin-9 homolog (C. elegans)	Lin9 /// LOC360888	0.3±0.02
similar to liver-specific bHLH-Zip transcription factor	LOC686794	6.95±0.46
Similar to Lmnb2 protein (predicted)	RGD1563803_predicted	0.21±0.08
similar to LOC495800 protein	LOC499770	0.84±0.2
similar to lymphocyte antigen 6 complex, locus E ligand	LOC501282	3.32±0.27
similar to lysophosphatidylglycerol acyltransferase 1	LOC679692	6.61±0.36
similar to M phase phosphoprotein 6	LOC686999	1.24±0.22
similar to Maleylacetoacetate isomerase (MAAI) (Glutathione S-transferase zeta 1) (GSTZ1-1)	LOC681913	6.96±0.69
similar to mammalian retrotransposon derived 8b	LOC678880	8.55±1.2
similar to Map4k6-pending protein /// similar to misshapen-like kinase 1 isoform 1	LOC303259 /// LOC687705	1.7±0.18
similar to MASK-4E-BP3 protein	LOC682955	2.85±0.45
similar to MASK-4E-BP3 protein	LOC679725 /// LOC682955	2.21±0.38
similar to MASK-4E-BP3 protein	LOC679725	1.11±0.05
similar to mbt domain containing 1	LOC688133	2.09±0.3
similar to Mediator of RNA polymerase II transcription subunit 12 (Thyroid hormone receptor-associated protein complex 230 kDa component) (Trap230) (Activator-recruited cofactor 240 kDa component) (ARC240) (CAG repeat protein 45) (OPA-containing pr...	LOC679693	0.6±0.05
similar to mediator of RNA polymerase II transcription, subunit 18 homolog	LOC682988	0.44±0.46
similar to melanoma inhibitory activity 3	LOC683007	5.84±1.17
similar to membrane-associated RING-CH protein IX	LOC679272	0.97±0.32
similar to Metaxin 1, isoform 2	LOC295241	2.14±0.5
similar to methionine adenosyltransferase II, beta /// methionine adenosyltransferase II, beta	Mat2b /// MGC94725	17.22±0.5
similar to Methionine-R-sulfoxide reductase (Selenoprotein X 1) (Selenoprotein R)	MGC105753	35.33±3.33
similar to microfibrillar-associated protein 1 (predicted) /// microfibrillar-associated protein 1A	Mfap1a /// RGD1564148_predicted	1.08±0.1
similar to microfilament and actin filament cross-linker protein isoform b	LOC362587	1.5±0.23
similar to Microsomal signal peptidase 23 kDa subunit (SPase 22 kDa subunit) (SPC22/23)	MGC109340	0.81±0.07
similar to Microtubule-associated protein RP/EB family member 2 (APC-binding protein EB2) (End-binding protein 2) (EB2)	LOC679221	0.24±0.2
Similar to MIR-interacting saposin-like protein precursor (Transmembrane protein 4) (Putative secreted protein ZSIG9)	LOC685001	0.31±0.09
similar to mitochondria-associated granulocyte macrophage CSF signaling molecule (predicted)	Magmas /// RGD1564452_predicted	7.56±1.19
similar to Mitochondrial 28S ribosomal protein S28 (S28mt) (MRP-S28)	LOC679330	1.7±0.36
similar to Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39)	LOC684304	2.42±0.07
similar to Mitochondrial carrier triple repeat 1 (predicted)	LOC686727 /// Mcart2_predicted /// RGD1565119_predicted	5.55±0.64
similar to mitochondrial hepatocellular carcinoma-downregulated carrier protein	LOC684556	4.27±0.48
similar to mitochondrial ribosomal protein L10	LOC691075	2.4±0.18
similar to mKIAA0133 protein (predicted)	RGD1307980_predicted	0.33±0.05
similar to mKIAA0215 protein (predicted)	RGD1563945_predicted	0.85±0.16
similar to mKIAA0256 protein (predicted)	RGD1559930_predicted	1.55±0.52
similar to mKIAA0317 protein (predicted)	RGD1307597_predicted	1.43±0.36
similar to mKIAA0664 protein (predicted)	RGD1307222_predicted	7.81±0.69
similar to mKIAA0738 protein (predicted)	RGD1565474_predicted	0.91±0.22
similar to mKIAA0978 protein (predicted)	RGD1561878_predicted	0.42±0.12
similar to mKIAA1011 protein	LOC366669	5.97±0.8
similar to mKIAA1111 protein (predicted)	RGD1561065_predicted	0.74±0.04
Similar to mKIAA1208 protein (predicted)	RGD1564821_predicted	1.23±0.22
similar to mKIAA1402 protein (predicted)	RGD1306404_predicted	0.56±0.09
similar to mKIAA1429 protein (predicted)	RGD1559904_predicted	0.64±0.12
similar to mKIAA1450 protein (predicted)	RGD1562174_predicted	2.16±0.41
similar to mKIAA1604 protein (predicted)	RGD1565385_predicted	0.28±0.2
similar to mKIAA1737 protein (predicted)	RGD1309492_predicted	3.62±0.42
similar to mKIAA1797 protein (predicted)	RGD1311849_predicted	1.59±0.17
similar to mKIAA1931 protein (predicted)	RGD1562335_predicted	0.53±0.15
similar to Mkrn1 protein	MGC94941	1.6±0.21
similar to modulator of estrogen induced transcription	RGD1307526	2.86±0.36
similar to monogenic, audiogenic seizure susceptibility 1	LOC685383	0.95±0.17
similar to Mospd2 protein (predicted)	RGD1563952_predicted	4.05±0.26
Similar to Msx2-interacting protein (SPEN homolog) (SMART/HDAC1-associated repressor protein)	LOC690911	0.69±0.15
similar to multi sex combs CG12058-PA	LOC686883	1.79±0.57
Similar to Murine homolog of human ftp-3	LOC308650	4.74±0.21
similar to muscleblind-like 2 isoform 1	LOC680445	7.77±0.55
Similar to Myc-associated zinc finger protein (MAZI) (Purine-binding transcription factor) (Pur-1)	LOC691842	0.78±0.1

similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lysine N-methyltransferase, H3 lysine-4 specific MLL3)	LOC502710	1.58±0.23
similar to myocyte enhancer factor 2C	LOC309957	1.22±0.31
similar to myosin light chain 1 slow a	LOC684533	0.3±0.19
similar to myosin XVIIIa	LOC360570	1.95±0.24
similar to Myosin-15 (Myosin XV) (Unconventional myosin-15)	LOC688266 /// LOC690323	0.7±0.26
similar to Myosin-15 (Myosin XV) (Unconventional myosin-15)	LOC688264	0.67±0.22
similar to MYST histone acetyltransferase monocytic leukemia 4 (predicted)	RGD1566399_predicted	0.31±0.2
similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)	LOC683547	21.9±3.05
similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) (CI-PDSW)	LOC681418 /// LOC681867	11.41±1.63
similar to Naglu (predicted)	RGD1564228_predicted	2.14±0.57
similar to Negative elongation factor D (NELF-D) (TH1-like protein)	LOC679203	1.13±0.18
Similar to nemo like kinase (predicted)	RGD1561602_predicted	0.41±0.07
similar to nemo like kinase (predicted) /// nemo like kinase	Nlk /// RGD1561440_predicted	1.3±0.23
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	4.71±0.46
similar to NICE-3	LOC361985	6.61±0.25
similar to Nicotinamide riboside kinase 1	LOC499330	1.6±0.27
similar to NMDA receptor regulated 1-like	LOC686240	0.26±0.03
similar to NNX3 (predicted)	RGD1310358_predicted	1.31±0.08
similar to novel protein (HT036) (predicted)	RGD1561416_predicted	2.78±0.5
similar to novel protein (predicted)	RGD1563106_predicted	0.92±0.38
similar to novel protein (predicted)	RGD1560636_predicted	0.29±0.18
similar to novel protein of unknown function (DUF423) family member (predicted)	RGD1563438_predicted	14.74±1.6
similar to Nuclear membrane binding protein NUCLING (predicted)	RGD1560011_predicted	0.96±0.17
similar to Nucleolar protein 11	LOC688235	1.66±0.06
similar to nucleolar protein with MIF4G domain 1	LOC682058	1.94±0.39
similar to O-acetyltransferase	LOC678772	0.91±0.09
similar to olfactory receptor 873	LOC687016	0.43±0.14
similar to Oligosaccharyl transferase 3 CG7748-PA	RGD1311563	14.34±1.89
similar to oocyte-testis gene 1 (predicted)	RGD1307158_predicted	0.46±0.08
similar to OPA3 protein (predicted)	RGD1561117_predicted	2.73±0.44
similar to opposite strand transcription unit to Stag3; Gats protein	RGD1304774	3.11±0.34
similar to OTTHUMP00000040081 (predicted)	RGD1566403_predicted	0.92±0.1
similar to p150 target of rapamycin (TOR)-scaffold protein containing WD-repeats (predicted)	RGD1311784_predicted	0.54±0.12
similar to Paired amphipathic helix protein Sin3b (Transcriptional corepressor Sin3b) (Histone deacetylase complex subunit Sin3b)	LOC683381	2.63±0.46
Similar to Pellino protein homolog 2 (Pellino 2) (predicted)	RGD1565884_predicted	0.86±0.25
similar to peptide deformylase-like protein	LOC690214	1.93±0.21
similar to peptidyl prolyl isomerase H (predicted)	RGD1564921_predicted	1.18±0.16
similar to Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (Rotamase Pin4) (PPIase Pin4)	LOC684441	0.63±0.07
similar to peptidylprolyl isomerase D	LOC295142 /// LOC364127 /// LOC501602 /// Ppid /// RGD1560149_predicted	0.37±0.02
similar to pericentrin	LOC687681	0.64±0.24
similar to Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxisomal farnesylated protein)	LOC289233	0.99±0.03
similar to PES1 protein	LOC289740	1.15±0.15
Similar to PHD finger protein 14 isoform 1 (predicted)	RGD1563764_predicted	1.39±1.54
similar to PHD zinc finger containing protein JUNE1	MGC94192	1.13±0.07
similar to PHF21A protein (predicted)	RGD1560612_predicted	0.44±0.15
similar to phosphoseryl-tRNA kinase (predicted)	RGD1564300_predicted	1.76±0.42
Similar to PI-3-kinase-related kinase SMG-1	Arl6ip1	2.42±0.66
similar to Placental protein 25 homolog (PP25)	LOC685284	1.91±0.46
similar to plasma kallikrein-like protein 4 precursor /// gene trap locus 3	Gtl3 /// RGD1307877	1.66±0.05
similar to plexin 1 (predicted)	RGD1560871_predicted	0.39±0.18
similar to polyglutamine-containing protein	RGD1310994	1.25±0.58
similar to POT1-like telomere end-binding protein	LOC500054	0.62±0.02
similar to potassium channel modulatory factor 1	LOC684322	4.28±0.48
similar to praja1, RING-H2 motif containing	LOC683077	6.86±0.35
similar to prefoldin 4 (predicted)	RGD1560211_predicted	3.56±0.05
similar to Prefoldin subunit 2 /// prefoldin 2	LOC678975 /// Pfdn2	0.53±0.08
similar to Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1) (VHL-binding protein 1) (VBP-1)	LOC681825	0.36±0.08
similar to PRO1853 homolog	RGD1311578	1.35±0.27
similar to procollagen C-endopeptidase enhancer 2	LOC684050	1±0.13
similar to product is unknown~seizure-related gene (predicted) /// similar to Ornithine decarboxylase antizyme 2 (ODC-Az 2) (AZ2)	LOC690789 /// RGD1562933_predicted	3.81±0.49
similar to Proline oxidase, mitochondrial precursor (Proline dehydrogenase)	LOC680409	1.91±0.45
similar to Protease-associated domain-containing protein of 21 kDa precursor	LOC686393	1.61±0.21
similar to Proteasome inhibitor PI31 subunit	LOC682071 /// LOC689852	3.22±0.41
similar to Protein C10orf11 homolog	LOC681383	1.68±0.34
similar to Protein C12orf11 (Sarcoma antigen NY-SAR-95)	LOC690728	1.34±0.21
similar to Protein C20orf20	RGD1308612	1.11±0.27
similar to protein C33A12.3	RGD1359508	1.19±0.51
similar to Protein C6orf115	LOC684848 /// LOC685045	7.58±0.37
similar to Protein C6orf203	LOC683897	1.1±0.2
similar to Protein C7orf26 homolog	LOC683674	0.34±0.29
similar to Protein CGI-117 (Protein HSPC111) (predicted)	RGD1305727_predicted	2.56±0.13
similar to Protein disulfide-isomerase TXNDC10 precursor (Thioredoxin domain-containing protein 10)	LOC682967	1.67±0.34
similar to Protein FAM60A (Tera protein)	LOC686611	0.26±0.11
similar to Protein KIAA0280	LOC503175 /// LOC690188	6.65±0.59

similar to Protein KIAA1404	LOC686701	0.33±0.21
similar to Protein KIAA1543	LOC682941 /// LOC689074	1.49±0.41
similar to Protein KIAA1688	LOC500901	0.26±0.19
similar to Protein Njmu-R1 (predicted)	RGD1310429_predicted	0.29±0.13
similar to Protein SYS1 homolog	LOC685079	3.26±0.46
similar to Protein transport protein SEC61 gamma subunit	LOC689134	17.57±1.11
similar to protein tyrosine phosphatase, receptor type, D (predicted)	RGD1561090_predicted	13.93±1.72
similar to Protein UNQ655/PRO1286 homolog precursor	LOC686324	2.38±0.16
Similar to putative phosphoinositide 5-phosphatase type II; C62	LOC287533	0.87±0.09
similar to Putative protein 15E1.2 (predicted)	RGD1309698_predicted	0.98±0.13
similar to putative protein, with at least 9 transmembrane domains, of eukaryotic origin (43.9 kD) (2G415)	RGD1309228	0.74±0.23
similar to putative repair and recombination helicase RAD26L (predicted)	RGD1561537_predicted	1.96±0.09
similar to Putative RNA-binding protein 15 (RNA-binding motif protein 15) (One-twenty two protein)	LOC684233	1.54±0.25
similar to R31449_3 (predicted)	RGD1563634_predicted	0.91±0.34
similar to RAB11 family interacting protein 5 (class I) isoform 1	LOC312502	5.71±0.19
similar to RAB3 GTPase-activating protein (predicted)	RGD1306487_predicted	2.34±0.19
similar to Rap2-binding protein 9	MGC124740	0.49±0.04
similar to Ras GTPase-activating-like protein IQGAP2 (predicted)	RGD1561455_predicted	8.25±0.55
Similar to Ras suppressor protein 1	LOC680419	0.71±0.02
similar to Ras-related protein Rab-1B /// RAB1B, member RAS oncogene family	MGC105830 /// rCG_48149	2.74±0.64
similar to RCK (predicted)	RGD1564560_predicted	2.05±0.55
similar to receptor-interacting factor 1	RGD1306520	0.69±0.09
similar to Recombining binding protein suppressor of hairless (J kappa-recombination signal binding protein) (RBP-J kappa)	LOC679028	1.97±0.34
similar to reduced expression 2	LOC690559	0.45±0.27
similar to replication protein-binding trans-activator RBT1	MGC108974	0.48±0.14
similar to REST corepressor 3	LOC684192	0.51±0.03
Similar to Retinoblastoma-binding protein 2 (RBBP-2)	LOC312678	2.32±0.17
similar to Retinoblastoma-binding protein 8 (RBBP-8) (CtBP interacting protein) (CtIP) (Retinoblastoma-interacting protein and myosin-like) (RIM) (predicted)	RGD1308872_predicted	1.01±0.19
similar to ribosomal protein L27a (predicted)	RGD1560633_predicted	3.98±1.19
similar to ribosomal protein, mitochondrial, S22	LOC683519	2.59±0.41
similar to RIKEN cDNA 0610007P06	LOC293103	3.48±0.19
similar to RIKEN cDNA 0610007P22 (predicted)	RGD1565744_predicted	0.77±0.08
Similar to RIKEN cDNA 0610010D20 (predicted)	RGD1310475_predicted	25.19±0.91
similar to RIKEN cDNA 0610011L14 gene	RGD1311066	1.07±0.22
similar to RIKEN cDNA 0610012D14	RGD1310111	4.07±0.53
similar to RIKEN cDNA 0610037D15	LOC298442	0.25±0.09
similar to RIKEN cDNA 0610037L13	RGD1559786	1.16±0.26
similar to RIKEN cDNA 0610037P05	RGD1305823	2±0.25
similar to RIKEN cDNA 0610038D11 (predicted)	RGD1309710_predicted	2.49±0.46
similar to RIKEN cDNA 0610038L10 gene (predicted) /// riboflavin kinase /// similar to riboflavin kinase (predicted)	Rfk /// RGD1560961_predicted /// RGD1563242_predicted	7.04±0.25
similar to RIKEN cDNA 0610039J04	RGD1562218	0.88±0.11
similar to RIKEN cDNA 0610040J01	LOC498368	7.1±0.79
similar to RIKEN cDNA 1100001H23	RGD1308734	3.32±0.4
similar to RIKEN cDNA 1110001A07 gene /// hypothetical protein LOC687897 /// hypothetical protein LOC691962	LOC687897 /// LOC691962 /// RGD1307084	0.5±0.11
similar to RIKEN cDNA 1110001J03	MGC112899	5.61±0.32
similar to RIKEN cDNA 1110001M20 (predicted)	RGD1310313_predicted	23.58±1.83
similar to RIKEN cDNA 1110003E01	RGD1311122	3.85±0.06
similar to RIKEN cDNA 1110004E09	RGD1306954	2.91±0.27
similar to RIKEN cDNA 1110005A03	RGD1306284	3.4±0.74
similar to RIKEN cDNA 1110007C09 (predicted)	RGD1306058_predicted	2.62±0.32
similar to RIKEN cDNA 1110007L15 (predicted)	RGD1311660_predicted	2.22±0.4
similar to RIKEN cDNA 1110008F13	RGD1307752	15.64±1.27
similar to RIKEN cDNA 1110008J03 (predicted)	RGD1306772_predicted	0.43±0.33
similar to RIKEN cDNA 1110012L19 (predicted)	RGD1562747_predicted	0.92±0.07
similar to RIKEN cDNA 1110018J12 (predicted)	RGD1565310_predicted	1.94±0.07
Similar to RIKEN cDNA 1110020A23 (predicted)	RGD1308134_predicted	0.67±0.05
similar to RIKEN cDNA 1110031I02	RGD1305007	1.63±0.27
Similar to RIKEN cDNA 1110038F21 (predicted)	RGD1562059_predicted	0.64±0.23
similar to RIKEN cDNA 1110059E24	RGD1359158	2.3±0.13
similar to RIKEN cDNA 1110059G10	RGD1311745	2.57±0.24
similar to RIKEN cDNA 1190005P17 (predicted)	RGD1308261_predicted	1.3±0.59
similar to RIKEN cDNA 1200003C05 (predicted)	RGD1308917_predicted	6.24±1.05
similar to RIKEN cDNA 1200009B18; EST AA408438	RGD1310606	3.52±0.79
similar to RIKEN cDNA 1200011M11 (predicted)	RGD1306862_predicted	0.51±0.21
similar to RIKEN cDNA 1200014J11 (predicted)	RGD1308139_predicted	1.01±0.26
similar to RIKEN cDNA 1200014M14	RGD1310597	0.21±0.02
similar to RIKEN cDNA 1200016B10 (predicted)	RGD1308695_predicted	1.19±0.03
similar to RIKEN cDNA 1300018I05	RGD1307801	3.07±0.55
similar to RIKEN cDNA 1500002O20	RGD1309888	1.15±0.23
similar to RIKEN cDNA 1500003O22	RGD1308302	0.48±0.15
similar to RIKEN cDNA 1500011H22	RGD1310861	1.16±0.16
similar to RIKEN cDNA 1500031L02	RGD621352	2.8±0.25
similar to RIKEN cDNA 1600012F09 (predicted)	RGD1306613_predicted	1.94±0.21
similar to RIKEN cDNA 1700012G19 gene (predicted)	RGD1307773_predicted	2.2±0.43
similar to RIKEN cDNA 1700019G17 (predicted) /// similar to Camello-like 2	LOC681227 /// RGD1563507_predicted	0.56±0.36
similar to RIKEN cDNA 1700023M03	RGD1305457	0.28±0.16
Similar to RIKEN cDNA 1700027M01	RGD1311815	0.63±0.05
similar to RIKEN cDNA 1700027N10 (predicted)	RGD1310693_predicted	1.26±0.1

similar to RIKEN cDNA 1700040L02 (predicted)	RGD1306739_predicted	0.59±0.22
similar to RIKEN cDNA 1700052N19	RGD1305235	2.43±0.3
similar to RIKEN cDNA 1700088E04	RGD1359634	0.42±0.07
similar to RIKEN cDNA 1700108L22	RGD1307509	1.13±0.23
similar to RIKEN cDNA 1810007P19	RGD1306596	0.56±0.1
similar to RIKEN cDNA 1810014F10 gene (predicted)	RGD1311186_predicted	4.7±0.13
similar to RIKEN cDNA 1810020D17 (predicted)	RGD1561459_predicted	1.51±0.25
similar to RIKEN cDNA 1810021J13	RGD1311364	1.2±0.16
similar to RIKEN cDNA 1810022C23	RGD1310224	36.11±3.29
similar to RIKEN cDNA 1810029B16 (predicted)	RGD1305222_predicted	0.47±0.07
similar to RIKEN cDNA 1810030N24 (predicted)	RGD1305158_predicted	3.2±0.32
similar to RIKEN cDNA 1810030O07 (predicted)	RGD1565685_predicted	1.42±0.19
Similar to RIKEN cDNA 1810036I24 (predicted)	RGD1306343_predicted	9.29±1.24
similar to RIKEN cDNA 1810042K04 (predicted)	RGD1305593_predicted	0.9±0.15
similar to RIKEN cDNA 1810043G02; DNA segment, Chr 10, Johns Hopkins University 13, expressed	RGD1309594	0.32±0.1
similar to RIKEN cDNA 1810046J19 (predicted)	RGD1306682_predicted	6.07±0.35
similar to RIKEN cDNA 1810063B07 gene (predicted)	RGD1310877_predicted	1.45±0.05
similar to RIKEN cDNA 1810074P20 (predicted)	RGD1309308_predicted	1.34±0.26
similar to RIKEN cDNA 2010011I20 (predicted)	RGD1311378_predicted	1.45±0.23
similar to RIKEN cDNA 2010012F05 (predicted)	RGD1309846_predicted	2.72±0.26
Similar to RIKEN cDNA 2010012O05 (predicted)	RGD1311783_predicted	2.87±0.41
similar to RIKEN cDNA 2010107G23 (predicted) /// hypothetical protein LOC679430	LOC679430 /// RGD1305587 predicted	4.31±0.72
similar to RIKEN cDNA 2010110K16 (predicted)	RGD1305283_predicted	2.38±0.37
similar to RIKEN cDNA 2010200O16 (predicted)	RGD1564454_predicted	1.53±0.11
similar to RIKEN cDNA 2010301N04 (predicted)	RGD1565557_predicted	1.17±0.49
similar to RIKEN cDNA 2010305A19 (predicted)	RGD1305274_predicted	0.66±0.07
similar to RIKEN cDNA 2010309E21 (predicted)	RGD1304825_predicted	1.8±0.3
similar to RIKEN cDNA 2010311D03	RGD1303272	14.93±2.37
similar to RIKEN cDNA 2010316F05 (predicted)	RGD1308179_predicted	0.42±0.15
similar to RIKEN cDNA 2210009G21 (predicted)	RGD1563120_predicted	0.59±0.04
similar to RIKEN cDNA 2210010N04 gene	RGD1306873	0.29±0.14
similar to RIKEN cDNA 2210012G02	LOC366431	0.47±0.16
similar to RIKEN cDNA 2210016L21 gene	RGD1311899	3.1±0.15
similar to RIKEN cDNA 2310001A20	RGD1308874	38.2±0.92
similar to RIKEN cDNA 2310002J15 (predicted)	RGD1560880_predicted	0.32±0.02
similar to RIKEN cDNA 2310004I24 gene	RGD1309906	0.95±0.03
Similar to RIKEN cDNA 2310005N03 gene	RGD1309105_predicted	0.38±0.16
similar to RIKEN cDNA 2310007F12 (predicted)	RGD1562416_predicted	1.36±0.2
similar to RIKEN cDNA 2310008H04 (predicted)	RGD1566036_predicted	0.5±0.19
similar to RIKEN cDNA 2310011J03	RGD1359127	0.99±0.06
similar to RIKEN cDNA 2310022B05 (predicted)	RGD1559896_predicted	4.34±0.95
similar to RIKEN cDNA 2310028N02	RGD1359339	3.85±0.21
similar to RIKEN cDNA 2310033P09	RGD1304587	1.09±0.14
similar to RIKEN cDNA 2310035C23 (predicted)	RGD1307235_predicted	2.72±0.4
similar to RIKEN cDNA 2310036O22 (predicted) /// similar to CG18809-PA, isoform A	LOC690331 /// RGD1564093 predicted	5.9±0.94
similar to RIKEN cDNA 2310042G06	MGC72955	3.82±0.68
similar to RIKEN cDNA 2310047O13 (predicted)	RGD1309605 predicted	5.63±0.94
similar to RIKEN cDNA 2310057M21	RGD1305014	0.33±0.12
similar to RIKEN cDNA 2310061F22	LOC292069	0.21±0.07
similar to RIKEN cDNA 2310079N02 (predicted)	RGD1306192_predicted	3.65±0.1
similar to RIKEN cDNA 2400003C14	RGD1307799	4.5±0.5
similar to RIKEN cDNA 2400010D15	RGD1311805	1.13±0.1
similar to RIKEN cDNA 2410002O22 gene	RGD1306583	3.68±0.63
similar to RIKEN cDNA 2410004B18 (predicted)	RGD1560065_predicted	0.47±0.39
similar to RIKEN cDNA 2410016O06 (predicted)	RGD1307704_predicted	0.76±0.19
similar to RIKEN cDNA 2410022L05 (predicted)	RGD1565675_predicted	5.86±0.68
similar to RIKEN cDNA 2410025L10 (predicted)	RGD1563342_predicted	1.3±0.11
similar to RIKEN cDNA 2510039O18 (predicted)	RGD1305350_predicted	1.75±0.03
similar to RIKEN cDNA 2610002M06 (predicted)	RGD1566265_predicted	0.56±0.06
similar to RIKEN cDNA 2610003J06	RGD1307381	1.56±0.17
similar to RIKEN cDNA 2610029G23 (predicted)	RGD1562502_predicted	1.03±0.27
similar to RIKEN cDNA 2610205E22	RGD1306582	1.86±0.18
similar to RIKEN cDNA 2610209A20 (predicted)	RGD1305211_predicted	0.58±0.12
similar to RIKEN cDNA 2610301B20; EST AI428449	MGC94199	1.24±0.11
similar to RIKEN cDNA 2610304G08 gene (predicted)	RGD1304782_predicted	1.03±0.2
similar to RIKEN cDNA 2610528E23	RGD1309437	1.07±0.27
similar to RIKEN cDNA 2610528J11 (predicted)	RGD1305347_predicted	9.25±1.15
similar to RIKEN cDNA 2700002I20	RGD1307279	3.93±0.68
similar to RIKEN cDNA 2700038C09	RGD1310660	3.15±1.12
similar to RIKEN cDNA 2700062C07	MGC116121	0.54±0.12
similar to RIKEN cDNA 2810002N01	RGD1304719	1.48±0.19
similar to RIKEN cDNA 2810025M15 (predicted)	RGD1304982 predicted	21.87±1.04
similar to RIKEN cDNA 2810055F11 (predicted)	RGD1305721_predicted	13.23±1.07
similar to RIKEN cDNA 2810403A07	RGD1565775	2.34±0.51
similar to RIKEN cDNA 2810405K02 (predicted)	RGD1308251_predicted	14.72±1.79
similar to RIKEN cDNA 2810428I15 (predicted)	RGD1566239_predicted	0.6±0.23
Similar to RIKEN cDNA 2810443J12 (predicted)	RGD1304868_predicted	0.22±0.1
similar to RIKEN cDNA 2810451A06	RGD1311098	9.67±0.71
similar to RIKEN cDNA 2810485I05 (predicted)	RGD1311077_predicted	0.5±0.16
similar to RIKEN cDNA 2900010J23	LOC499779	0.68±1.38
similar to RIKEN cDNA 2900010M23 (predicted)	RGD1306917_predicted	1.69±0.6
similar to RIKEN cDNA 2900011O08	RGD1305733	1.03±0.08
similar to RIKEN cDNA 3010026O09 (predicted)	RGD1564036_predicted	0.33±0.04
similar to RIKEN cDNA 3110001D03 (predicted)	RGD1309148_predicted	1.87±0.16
similar to RIKEN cDNA 3110001I22 (predicted)	RGD1305537_predicted	1.09±0.09

similar to RIKEN cDNA 3110040N11	RGD1305713	1.06±0.1
similar to RIKEN cDNA 3110043O21	RGD1359108	0.23±0.04
Similar to RIKEN cDNA 3110050N22 (predicted)	RGD1311970_predicted	0.39±0.21
similar to RIKEN cDNA 3200002M19 (predicted)	RGD1311634_predicted	1.09±0.07
similar to RIKEN cDNA 3930401K13	RGD1309459	5.26±0.48
similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicted	1.32±0.37
similar to RIKEN cDNA 4632411B12	RGD1309220	1.01±0.23
similar to RIKEN cDNA 4732418C07 (predicted)	RGD1310351_predicted	1.66±0.27
similar to RIKEN cDNA 4921524J17 (predicted)	RGD1308706_predicted	2.53±0.52
similar to RIKEN cDNA 4921536K21 (predicted)	RGD1308775_predicted	0.22±0.1
similar to RIKEN cDNA 4930444A02	RGD1310810	0.48±0.08
similar to RIKEN cDNA 4930455F23	RGD1309708	0.62±0.03
similar to RIKEN cDNA 4930579G22 (predicted)	RGD1560258_predicted	0.82±0.12
similar to RIKEN cDNA 4931406C07	RGD1309534	24.34±3.81
similar to RIKEN cDNA 4931406P16 (predicted)	RGD1308428_predicted	0.23±0.03
similar to RIKEN cDNA 4931414P19 (predicted)	RGD1565222_predicted	0.28±0.06
similar to RIKEN cDNA 4932432K03	RGD1308087	1.59±0.08
similar to RIKEN cDNA 4933428G09 (predicted)	RGD1311045_predicted	0.29±0.06
similar to RIKEN cDNA 4933433P14 gene	RGD1308470	0.55±0.14
similar to RIKEN cDNA 4933435A13	RGD1306402	0.32±0.07
Similar to RIKEN cDNA 5033406L14	RGD1305755	1.29±0.11
similar to RIKEN cDNA 5033414D02 (predicted)	RGD1306839_predicted	1.6±0.28
similar to RIKEN cDNA 5133400G04	RGD1311742	0.54±0.07
similar to RIKEN cDNA 5133401N09	MGC125086	1.2±0.05
similar to RIKEN cDNA 5230400G24	RGD1310230	8.24±0.58
similar to RIKEN cDNA 5330440M15 /// coiled-coil domain containing 17	Ccdc17 /// LOC313519	1.69±0.31
similar to RIKEN cDNA 5430437P03	MGC94542	2.8±1.01
similar to RIKEN cDNA 5730449L18 (predicted)	RGD1308584_predicted	3.94±0.24
similar to RIKEN cDNA 5730453I16	RGD1305441	3.19±0.81
similar to RIKEN cDNA 5730454B08 (predicted)	RGD1308290_predicted	0.99±0.19
Similar to RIKEN cDNA 5730469D23 (predicted)	RGD1308324_predicted	0.88±0.19
similar to RIKEN cDNA 5730469M10	RGD1309676	2.27±0.35
similar to RIKEN cDNA 5730509K17 gene (predicted)	RGD1561042_predicted	1.52±0.05
similar to RIKEN cDNA 5730557B15 (predicted)	RGD1564227_predicted	0.72±0.11
similar to RIKEN cDNA 5730596K20 (predicted)	RGD1309871_predicted	0.49±0.09
similar to RIKEN cDNA 5830433M19	MGC125002	1.6±0.06
similar to RIKEN cDNA 6330409N04	RGD1306437	4.96±0.39
similar to RIKEN cDNA 6330416G13 gene (predicted)	RGD1304595_predicted	1.56±0.38
similar to RIKEN cDNA 6530403A03	RGD1309020	0.22±0.09
similar to RIKEN cDNA 8430406I07	RGD1307465	1.04±0.12
Similar to RIKEN cDNA 9030221M09 gene (predicted)	RGD1305469_predicted	1.18±0.13
similar to RIKEN cDNA 9030624J02	LOC361635	3.07±0.18
similar to RIKEN cDNA 9430023L20	RGD1359310	0.75±0.08
Similar to RIKEN cDNA 9430077D24 gene	LOC290341	1.8±0.21
similar to RIKEN cDNA 9430098E02 (predicted) /// hypothetical protein LOC680815	LOC680815 /// RGD1565407_predicted	1.87±0.34
similar to RIKEN cDNA A030007L17; EST AA673177 (predicted) /// similar to C44B7.7	LOC685702 /// RGD1304876_predicted	1.01±1.29
similar to RIKEN cDNA A430005L14	RGD1304567	2.89±0.18
Similar to RIKEN cDNA A430093J20 gene	LOC367113	2.13±0.11
similar to RIKEN cDNA A530088I07 gene	LOC311984	0.83±0.12
similar to RIKEN cDNA A930008G19 (predicted)	RGD1310799_predicted	0.57±0.05
similar to RIKEN cDNA A930016P21 (predicted)	RGD1560629_predicted	1.43±0.14
similar to RIKEN cDNA B230118H07 (predicted)	RGD1309730_predicted	1.81±0.17
Similar to RIKEN cDNA B230312A22	RGD1311249	0.45±0.05
similar to RIKEN cDNA B230380D07 (predicted)	RGD1311456_predicted	0.66±0.18
similar to RIKEN cDNA C030006K11	MGC94207	6.32±0.66
similar to RIKEN cDNA C130022K22 gene	RGD1305225	0.35±0.11
similar to RIKEN cDNA C430004E15	LOC499749	3.95±0.54
similar to RIKEN cDNA D030070L09	RGD1310199	2.15±0.33
similar to RIKEN cDNA D130059P03 gene (predicted)	RGD1310722_predicted	0.8±0.24
similar to RIKEN cDNA D230025D16Rik	RGD621098	0.64±0.02
similar to RIKEN cDNA D530033C11 (predicted)	RGD1307179_predicted	1.02±0.2
similar to RIKEN cDNA D630029K19	RGD1307100	3.01±0.5
similar to RIKEN cDNA E130201N16 (predicted)	RGD1311589_predicted	3.52±0.84
similar to RIKEN cDNA E130308A19 (predicted)	RGD1310951_predicted	0.96±0.05
similar to RIKEN cDNA E230015L20 gene (predicted)	RGD1560873_predicted	0.92±0.22
similar to RIKEN cDNA F730014I05 (predicted)	RGD1310800_predicted	0.79±0.15
similar to ring finger protein 13	LOC681578	14.14±0.57
similar to RNA binding protein gene with multiple splicing (predicted)	RGD1561067_predicted	5.46±0.9
Similar to RNA binding protein with multiple splicing 2 (predicted)	RGD1561222_predicted	3.67±0.73
similar to RNA polymerase 1-3	MGC112727	6.28±0.81
similar to RNA-binding region (RNP1, RRM) containing 3	LOC686263	1.07±0.15
similar to Rnf37-pending protein	RGD1305440	0.31±0.07
similar to scaffold attachment factor B2	LOC301126	0.78±0.25
Similar to SCO cytochrome oxidase deficient homolog 1 (yeast) (predicted)	RGD1559538_predicted	2.41±0.19
similar to Sec1 family domain containing protein 2 (Syntaxin binding protein 1-like 1) (Neuronal Sec1)	LOC498353	0.99±0.21
similar to SEC24 related gene family, member C	LOC685144	2.98±0.14
similar to Selenoprotein H (predicted)	RGD1563348_predicted	10.33±0.66
similar to semaF cytoplasmic domain associated protein 2	LOC365960	12.75±0.66
similar to Ser/Thr-rich protein T10 in DGCR region (predicted)	RGD1310348_predicted	4.55±0.27
Similar to Serine	LOC691318	0.64±0.19
similar to serologically defined colon cancer antigen 3 isoform 1	LOC683605	1.05±0.28
similar to Serum amyloid A-3 protein precursor	LOC687992	0.9±0.23
similar to Sestrin 2 (Hi95) (predicted)	RGD1566319_predicted	5.52±1.79
similar to Sfrs4 protein (predicted)	RGD1561347_predicted	0.78±0.36
Similar to SH3-domain binding protein 3	LOC688018	3.85±0.52

similar to Shb protein (predicted)	RGD1565350_predicted	1.91±0.39
similar to sid2057p	RGD1311703	3.92±0.46
similar to signal peptidase complex subunit 3 homolog	LOC680782	12.12±0.87
similar to Signal recognition particle 9 kDa protein (SRP9) /// signal recognition particle 9	LOC682826 /// Srp9	5.45±1.21
similar to Ski protein (predicted)	RGD1565591_predicted	1.61±0.51
similar to Smad ubiquitination regulatory factor 1 isoform 2	LOC690516	0.37±0.05
similar to small nuclear ribonucleoprotein D3	LOC687711	2.42±0.65
similar to small nuclear ribonucleoprotein polypeptide G	LOC681031 /// LOC687679	4.89±0.64
Similar to small nuclear RNA activating complex, polypeptide 5	LOC691501	1.78±0.3
similar to small unique nuclear receptor co-repressor (predicted)	RGD1560600_predicted	0.31±0.07
similar to small unique nuclear receptor co-repressor (predicted) /// nuclear DNA binding protein	C1d /// RGD1560600_predicted	5.71±0.4
similar to SMP3 mannosyltransferase /// similar to nuclear cap binding protein subunit 2	LOC684506 /// LOC689116	3.16±0.32
similar to snRNP core protein SMX5	LOC684148	0.86±0.4
similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (predicted)	RGD1561141_predicted	0.97±0.35
Similar to solute carrier family 30 (zinc transporter), member 9	LOC498358	2.85±0.43
Similar to Solute carrier family 35, member E3 (predicted)	RGD1564876_predicted	1.21±0.38
similar to Solute carrier family 6 (neurotransmitter transporter), member 20 (predicted)	RGD1566368_predicted	15.25±1.48
similar to sorbin and SH3 domain containing 1 isoform 3	LOC678826	4.33±0.89
similar to sorting nexin 3	LOC684097	25.33±1.52
similar to Sorting nexin-9	LOC683687	11.15±0.87
similar to SPBPJ4664.02 (predicted) /// RGD1562079 (predicted)	RGD1559845_predicted /// RGD1562079_predicted	5.39±0.31
similar to Sperm 1 POU-domain transcription factor (SPRM-1) (predicted)	RGD1305526_predicted	1±0.22
similar to spermatogenesis associated 5-like 1	LOC691729	0.33±0.14
similar to sphingomyelin phosphodiesterase 3, neutral membrane (predicted) /// similar to spermatogenesis and centriole associated 1	LOC686589 /// RGD1565316_predicted	0.39±0.04
similar to spindlin	LOC682571	4.41±0.47
similar to spinster-like protein	RGD1305613	2.64±0.39
similar to SPla/RYanodine receptor SPRY (1J970) (predicted)	RGD1308847_predicted	1.79±0.21
similar to Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa subunit) (U2 snRNP auxiliary factor small subunit)	LOC687575	1.26±0.26
similar to splicing factor, arginine/serine-rich 1 (ASF/SF2) /// splicing factor, arginine/serine-rich 1	LOC688114 /// Sfrs1	5.44±0.65
Similar to splicing factor, arginine/serine-rich 2, interacting protein	LOC312030	3.15±0.33
Similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Genetics 0878 expressed	LOC303057	2.34±0.36
similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Genetics 0878 expressed	LOC303057 /// Slu7	0.78±0.15
Similar to Sterile alpha motif domain containing 10 (predicted)	RGD1563203_predicted	0.53±0.08
similar to stromal membrane-associated protein 1	LOC684800	4.36±0.36
similar to SUMO/sentrin specific protease 2	LOC295194	1.02±0.09
similar to SUMO/sentrin specific protease 5	LOC686286	0.76±0.19
similar to SUMO/sentrin specific protease 5 (predicted) /// similar to SUMO/sentrin specific protease 5	LOC686286 /// RGD1564247_predicted	0.32±0.05
similar to suppressor of hairy wing homolog 4 isoform 1 (predicted)	RGD1560796_predicted	0.71±0.16
similar to Suppressor of S. cerevisiae gcr2 (predicted)	RGD1565023_predicted	0.86±0.08
similar to SWI	LOC684513 /// LOC685179	1.44±0.22
similar to T03G11.6	LOC689540	11.86±0.23
similar to TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	RGD1562272_predicted	0.83±0.11
similar to talin 2 (predicted)	RGD1565416_predicted	0.57±0.11
Similar to TBP-associated factor 172 (TAF-172) (TAF(II)170) (predicted)	RGD1564130_predicted	1.7±0.41
similar to TBP-associated factor 4	LOC682097	0.79±0.26
similar to testhymin (predicted)	RGD1563612_predicted	0.33±0.27
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	1.29±0.3
similar to thymus atrophy-related protein (predicted)	RGD1304607_predicted	0.76±0.12
Similar to TICAM-1	LOC363328	0.28±0.17
similar to topoisomerase (DNA) II beta	LOC361100	2.67±0.19
similar to TR4 orphan receptor associated protein TRA16	LOC361128	1.36±0.08
Similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted)	RGD1561817_predicted	0.54±0.09
similar to transcription factor	MGC112830	2.5±0.06
similar to Transcription factor 7-like 2 (HMG box transcription factor 4) (T-cell-specific transcription factor 4) (TCF-4) (hTCF-4)	LOC683733	0.7±0.28
similar to Transcription initiation factor TFIID subunit 12 (Transcription initiation factor TFIID 20 kDa subunits) (TAFII-20) (TAFII20)	LOC682902	0.41±0.17
similar to translocase of inner mitochondrial membrane 50 homolog	LOC687295	1.47±0.07
similar to translocase of the inner mitochondrial membrane 14 isoform a	LOC683663	25.52±1.53
Similar to transmembrane 6 superfamily member 2	LOC689029	1.33±0.09
similar to transmembrane protein 41a	LOC681708	5±0.39
similar to TRS85 homolog (predicted)	RGD1309102_predicted	2.15±0.29
Similar to TSC22 domain family protein 2 (TSC22-related-inducible leucine zipper protein 4)	LOC499624	0.46±0.29
similar to tyrosine kinase-associated leucine zipper protein LAZipII (predicted)	RGD1565584_predicted	0.83±0.16
similar to U5 snRNP-specific protein (Prp8-binding) (predicted)	RGD1309198_predicted	0.52±0.22
similar to ubiquinol-cytochrome c reductase complex 7.2kDa protein isoform b	LOC685322	48.89±4.43
similar to Ubiquitin carboxyl-terminal hydrolase 21 (Ubiquitin thiolesterase 21) (Ubiquitin-specific processing protease 21) (Deubiquitinating enzyme 21)	LOC678925 /// LOC688466	0.67±0.1
similar to ubiquitin protein ligase E3 component n-recognin 2	LOC363188	1.33±0.08
similar to ubiquitin protein ligase E3B	LOC687633	2.16±0.42
similar to ubiquitin specific protease 34	LOC360990	2.04±0.14
similar to Ubiquitin-associated protein 2-like	LOC497952	1.51±0.07
similar to ubiquitin-conjugating enzyme E2R 2	LOC689226	5.76±1.08
similar to ubiquitin-protein ligase E3-alpha (predicted)	RGD1562326_predicted	1.99±0.46
similar to UPF0197 protein C11orf10 homolog (predicted)	RGD1560328_predicted	7.41±0.28
similar to UPF0308 protein C9orf21	LOC498685	0.43±0.08
similar to vacuolar protein sorting 13C protein (predicted)	RGD1560364_predicted	2.74±0.07
Similar to Vacuolar protein sorting 26 homolog (VPS26 protein homolog)	LOC300472	2.94±0.71
similar to vacuolar protein sorting 37D	LOC687208	0.66±0.46

similar to vesicle transport through interaction with t-SNAREs 1B homolog (predicted)	RGD1560475_predicted	0.61±0.19
similar to Vps41 protein (predicted)	RGD1560511_predicted	8.26±0.71
similar to WAC (predicted)	RGD1562407_predicted	1.67±0.2
similar to WD repeat domain 11 protein (predicted)	RGD1564964_predicted	0.81±0.17
similar to WD repeat domain 74 /// WD repeat domain 74	LOC686449 /// Wdr74	0.86±0.3
similar to Wdr8 protein	LOC366515	0.67±0.17
Similar to XPA binding protein 1	LOC688393	0.86±0.09
similar to yippee-like 3 (predicted)	RGD1564579_predicted	0.94±0.18
similar to YY1-associated factor 2 /// YY1 associated factor 2	LOC681599 /// Yaf2	0.53±0.09
similar to Zinc finger CCCH-type domain containing protein 6	LOC678741	1.07±0.35
Similar to Zinc finger CCHC domain-containing protein 6	LOC501515	0.99±0.16
similar to zinc finger like protein 1	LOC684755	0.46±0.23
similar to Zinc finger protein 133	LOC499900	0.5±0.11
similar to zinc finger protein 146	LOC687516	0.68±0.26
similar to zinc finger protein 277 isoform 1	LOC298977	2.9±0.31
similar to zinc finger protein 322a	LOC684943	0.21±0.08
similar to Zinc finger protein 326 (Zinc finger protein-associated with nuclear matrix of 75 kDa)	LOC682914	3.44±0.37
similar to zinc finger protein 422, related sequence 1	LOC314600	1.25±0.12
similar to zinc finger protein 426 (predicted)	RGD1564241_predicted	0.36±0.05
similar to zinc finger protein 455	LOC682834	0.5±0.06
Similar to zinc finger protein 609 (predicted)	RGD1561651_predicted	0.49±0.12
similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3) (predicted)	RGD1560191_predicted	0.44±0.18
similar to zinc finger protein 639	LOC683504	0.84±0.12
similar to zinc finger protein 709	LOC362845	0.23±0.07
Similar to zinc finger protein 748 isoform 2	LOC680222	0.32±0.05
similar to zinc finger protein 75 (predicted)	RGD1565419_predicted	0.69±0.11
similar to zinc finger protein 84 (HPF2)	LOC691170	0.53±0.11
similar to Zinc finger protein RP-8 CG3260-PA /// programmed cell death 2-like	LOC687670 /// Pdcd2l	1.23±0.09
similar to zinc finger, matrin type 2	LOC679898	1.91±0.11
similar to zinc finger, RAN-binding domain containing 3 (predicted)	RGD1564952_predicted	0.3±0.07
similar to zinc finger, ZZ domain containing 3	LOC310958	1.65±0.36
Sin3A associated protein	Sap130	1.64±0.22
Sin3-associated polypeptide 18	Sap18	10.25±0.11
single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	Sigirr	3.02±0.38
single stranded DNA binding protein 3	Ssbp3	0.68±0.06
single-stranded DNA binding protein 1	Ssbp1	2.52±0.41
single-stranded DNA binding protein 2	Ssbp2	1.47±0.39
sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	Sirt2	4.37±0.47
sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (predicted)	Sirt3_predicted	2.79±0.06
sirtuin 4 (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	Sirt4	0.32±0.08
sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	Sirt5	1.61±0.22
sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	Sirt6	0.57±0.06
sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae) (predicted)	Sirt7_predicted	1.59±0.15
six transmembrane epithelial antigen of the prostate 1 (predicted)	Steap1_predicted	4.79±0.71
six transmembrane epithelial antigen of the prostate 2	Steap2	22.22±1.41
Sjogren syndrome antigen B	Ssb	4.58±0.35
Sjogren's syndrome nuclear autoantigen 1 (predicted)	Ssna1_predicted	2.78±0.38
skeletal muscle and kidney enriched inositol phosphatase	Skip	1.11±0.12
SLAIN motif family, member 2	Slain2	1.18±0.31
slingshot homolog 1 (Drosophila)	Ssh1	0.24±0.14
slingshot homolog 3 (Drosophila)	Ssh3	0.68±0.1
slit homolog 2 (Drosophila)	Slit2	1.47±0.2
Smad nuclear interacting protein 1	Snip1	1.33±0.02
SMAD specific E3 ubiquitin protein ligase 2 (predicted)	Smurf2_predicted	1.08±0.3
small cell adhesion glycoprotein	Smagp	4.9±0.37
small EDRK-rich factor 2	Serf2	20.28±3.31
small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Sgta	4.73±0.49
small inducible cytokine subfamily E, member 1	Scye1	2.11±0.29
small nuclear ribonucleoprotein D1 (predicted)	Snrpd1_predicted	0.4±0.02
small nuclear ribonucleoprotein D2 /// similar to small nuclear ribonucleoprotein D2	LOC686737 /// Snrpd2	3.06±1.05
small nuclear ribonucleoprotein E	Snrpe	10.26±0.68
small nuclear ribonucleoprotein N /// SNRPN upstream reading frame	Snrpn /// Snurf	0.44±0.19
small nuclear ribonucleoprotein polypeptide A	Snrpa	0.45±0
small nuclear ribonucleoprotein polypeptide F	Snrpf	3.05±0.24
small nuclear ribonucleoprotein polypeptides B and B1	Snrpb	8.72±0.33
small nuclear RNA activating complex, polypeptide 1 (predicted)	Snapc1_predicted	0.21±0.03
small nuclear RNA activating complex, polypeptide 2	Snapc2	0.28±0.09
small nuclear RNA activating complex, polypeptide 3	Snapc3	0.23±0.21
small nuclear RNA activating complex, polypeptide 5	Snapc5	1.28±0.39
small nucleolar RNA host gene (non-protein coding) 8	Snhg8	0.72±0.2
SMC6 structural maintenance of chromosomes 6-like 1 (yeast) (predicted)	Smc6l1_predicted	1.54±0.12
SMEK homolog 1, suppressor of mek1 (Dictyostelium)	Smek1	2.95±0.45
SMEK homolog 2, suppressor of mek1 (Dictyostelium)	Smek2	2.79±0.44
Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) /// similar to KIAA0732 protein	RGD1309609 /// Smg6	0.47±0.1
Smith-Magenis syndrome chromosome region, candidate 7-like	Smcr7l	0.54±0.12
smoothelin-like 2	Smtnl2	5.59±0.32
smoothened homolog (Drosophila)	Smo	0.3±0.03
SMT3 suppressor of mif two 3 homolog 1 (yeast)	Sumo1	6.21±0.49
SMT3 suppressor of mif two 3 homolog 2 (yeast) /// similar to SMT3 suppressor of mif two 3 homolog 2	LOC690244 /// Sumo2	7.9±0.17
SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	Sumo3	6.61±0.99
smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	Smu1	2.83±0.29
SNAP-associated protein	Snapap	3.58±0.37
SNF1-like kinase 2 (predicted)	Snf1lk2_predicted	5.67±0.65
SNF2 histone linker PHD RING helicase (predicted)	Shprh_predicted	0.86±0.06
Snf2-related CREBBP activator protein	Srcap	0.32±0.05
SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	Snf8	2.66±0.23
sno, strawberry notch homolog 1 (Drosophila)	Sbno1	3.32±0.37

snurportin 1	Snupn	0.27±0.12
soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	0.47±0.05
sodium channel and clathrin linker 1	Sclt1	0.4±0.27
sodium channel modifier 1 (predicted)	Scnm1_predicted	6.15±1.91
solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	Slc1a1	15.39±2.87
solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Slc10a1	0.28±0.09
solute carrier family 10 (sodium/bile acid cotransporter family), member 3	Slc10a3	0.3±0.09
solute carrier family 10, member 2	Slc10a2	1.69±0.01
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	8.34±1.6
solute carrier family 12 (potassium/chloride transporters), member 8	Slc12a8	7±1.52
solute carrier family 12 (potassium/chloride transporters), member 9	Slc12a9	0.57±0.06
solute carrier family 12 (sodium/potassium/chloride transporters), member 2	Slc12a2	1.95±0.11
solute carrier family 12, member 6	Slc12a6	4.07±0.85
solute carrier family 12, member 7	Slc12a7	2.94±0.29
solute carrier family 13 (sodium/sulfate symporters), member 1	Slc13a1	24.03±3.58
solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	Slc13a2	9.67±1.37
solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Slc13a3	43.6±5.03
solute carrier family 15 (oligopeptide transporter), member 1	Slc15a1	3.54±0.14
solute carrier family 15, member 4	Slc15a4	1.24±0.23
solute carrier family 16 (monocarboxylic acid transporters), member 1	Slc16a1	18.81±2.84
solute carrier family 16 (monocarboxylic acid transporters), member 10	Slc16a10	2.29±0.15
solute carrier family 16 (monocarboxylic acid transporters), member 13	Slc16a13	6.23±0.41
solute carrier family 16 (monocarboxylic acid transporters), member 6	Slc16a6	7.83±0.65
solute carrier family 17 (anion/sugar transporter), member 5	Slc17a5	8.02±1.49
solute carrier family 17 (sodium phosphate), member 1	Slc17a1	13.3±0.94
solute carrier family 17 (sodium phosphate), member 2 (predicted)	Slc17a2_predicted	3.32±0.36
solute carrier family 17 (sodium phosphate), member 3	Slc17a3	7.55±1.49
solute carrier family 17 (sodium phosphate), member 4	Slc17a4	3.02±0.26
solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	6.55±1.33
solute carrier family 19 (thiamine transporter), member 2	Slc19a2	0.63±0.38
solute carrier family 2 (facilitated glucose transporter), member 2	Slc2a2	26.18±2.14
solute carrier family 2 (facilitated glucose transporter), member 9	Slc2a9	0.5±0.06
solute carrier family 2, (facilitated glucose transporter) member 8	Slc2a8	0.66±0.08
solute carrier family 20 (phosphate transporter), member 1	Slc20a1	2.29±0.33
solute carrier family 20, member 2	Slc20a2	0.74±0.14
solute carrier family 22 (organic anion transporter), member 6	Slc22a6	33.58±3.92
solute carrier family 22 (organic anion transporter), member 8	Slc22a8	46.31±2.28
solute carrier family 22 (organic anion/cation transporter), member 12	Slc22a12	8.5±1.19
solute carrier family 22 (organic anion/cation transporter), member 9	Slc22a9	24.56±3.26
solute carrier family 22 (organic cation transporter), member 1	Slc22a1	24.22±1.7
solute carrier family 22 (organic cation transporter), member 15 (predicted)	Slc22a15_predicted	0.75±0.13
solute carrier family 22 (organic cation transporter), member 17	Slc22a17	1.23±0.19
solute carrier family 22 (organic cation transporter), member 18	Slc22a18	28.05±2.82
solute carrier family 22 (organic cation transporter), member 4	Slc22a4	2.64±0.39
solute carrier family 22 (organic cation transporter), member 5	Slc22a5	24.84±3.12
solute carrier family 22, member 23	Slc22a23	0.59±0.17
solute carrier family 23 (nucleobase transporters), member 1	Slc23a1	2.07±0.36
solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	3.41±0.37
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25a13	24.42±2.08
solute carrier family 25 (mitochondrial carrier, brain), member 14	Slc25a14	0.28±0.13
solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	Slc25a1	7.17±0.82
solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	1.3±0.18
solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	Slc25a29	1.04±0.06
solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 (predicted)	Slc25a17_predicted	4.34±0.53
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	Slc25a25	0.7±0.32
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	Slc25a3	51.28±3.76
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	Slc25a4	16.99±2.91
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	Slc25a5	57.01±2.74
solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	Slc25a10	14.41±1.94
Solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	Slc25a15	6.44±0.44
solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	Slc25a11	15.79±0.47
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	Slc25a23	6.69±1.1
solute carrier family 25, member 28	Slc25a28	1.78±0.46
Solute carrier family 25, member 30	Slc25a30	7.11±0.9
solute carrier family 25, member 36	Slc25a36	7.78±0.48
solute carrier family 25, member 37	Slc25a37	0.69±0.27
solute carrier family 25, member 38	Slc25a38	1.2±0.07
solute carrier family 25, member 39	Slc25a39	18.55±2.28
solute carrier family 25, member 44	Slc25a44	1.6±0.08
solute carrier family 25, member 46	Slc25a46	5.63±1.1
solute carrier family 26 (sulfate transporter), member 1	Slc26a1	17.3±1.24
solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	1.2±0.12
solute carrier family 27 (fatty acid transporter), member 2	Slc27a2	46.06±4.43
solute carrier family 27 (fatty acid transporter), member 4	Slc27a4	1.33±0.19
solute carrier family 27 (fatty acid transporter), member 5	Slc27a5	0.72±0.05
solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	Slc28a1	1.53±0.21
solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	0.2±0.06
solute carrier family 29 (nucleoside transporters), member 3	Slc29a3	10.79±1.49
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	37.93±1.59
solute carrier family 3, member 1	Slc3a1	47.78±4.89
solute carrier family 30 (zinc transporter), member 1	Slc30a1	0.3±0.18
solute carrier family 30 (zinc transporter), member 2	Slc30a2	4.15±0.71
solute carrier family 30 (zinc transporter), member 4	Slc30a4	4.38±0.21
solute carrier family 30 (zinc transporter), member 5 (predicted)	Slc30a5_predicted	2.3±0.46
solute carrier family 30 (zinc transporter), member 6 (predicted)	Slc30a6_predicted	1.54±0.29
solute carrier family 30 (zinc transporter), member 7	Slc30a7	0.4±0.12
solute carrier family 30 (zinc transporter), member 9	Slc30a9	0.99±0.13

solute carrier family 31 (copper transporters), member 1	Slc31a1	7.99±0.59
solute carrier family 31, member 2	Slc31a2	1.22±0.1
solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	6.84±0.53
solute carrier family 34 (sodium phosphate), member 1	Slc34a1	54.47±2.06
solute carrier family 34 (sodium phosphate), member 3	Slc34a3	31.33±2.82
solute carrier family 35 (CMP-sialic acid transporter), member 1 (predicted)	Slc35a1_predicted	12.17±0.99
Solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (predicted)	Slc35d1_predicted	2.93±0.44
solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	Slc35a3	0.73±0.12
solute carrier family 35, member A4	Slc35a4	1.32±0.3
solute carrier family 35, member A5	Slc35a5	0.64±0.04
solute carrier family 35, member B1	Slc35b1	6.71±0.88
solute carrier family 35, member B3 (predicted)	Slc35b3_predicted	2±0.81
solute carrier family 35, member B4 (predicted)	Slc35b4_predicted	2.75±0.51
solute carrier family 35, member C1 (predicted)	Slc35c1_predicted	2.13±0.16
solute carrier family 35, member C2	Slc35c2	1.98±0.04
solute carrier family 35, member E1	Slc35e1	0.5±0.06
solute carrier family 35, member E3	Slc35e3	0.47±0.03
solute carrier family 35, member F2 (predicted)	Slc35f2_predicted	1.12±0.33
solute carrier family 35, member F5 (predicted)	Slc35f5_predicted	0.63±0.13
solute carrier family 37 (glucose-6-phosphate transporter), member 4	Slc37a4	41.99±2.71
solute carrier family 38, member 10	Slc38a10	2.05±0.23
solute carrier family 38, member 2	Slc38a2	1.6±0.58
solute carrier family 38, member 6	Slc38a6	0.94±0.25
solute carrier family 38, member 7	Slc38a7	1.09±0.08
solute carrier family 39 (iron-regulated transporter), member 1	Slc40a1	4.16±0.27
solute carrier family 39 (metal ion transporter), member 13	Slc39a13	1.53±0.11
solute carrier family 39 (metal ion transporter), member 5 (predicted)	Slc39a5_predicted	0.69±0.04
solute carrier family 39 (metal ion transporter), member 8	Slc39a8	5.04±1.23
solute carrier family 39 (zinc transporter), member 10 (predicted)	Slc39a10_predicted	2.04±0.28
solute carrier family 39 (zinc transporter), member 14 (predicted)	Slc39a14_predicted	1.21±0.03
solute carrier family 39 (zinc transporter), member 3	Slc39a3	1.19±0.26
solute carrier family 4 (anion exchanger), member 1, adaptor protein (predicted)	Slc4a1ap_predicted	0.96±0.04
solute carrier family 4 (anion exchanger), member 2	Slc4a2	2.18±0.14
solute carrier family 4 (anion exchanger), member 4	Slc4a4	26.35±3.93
solute carrier family 41, member 1 (predicted)	Slc41a1_predicted	0.23±0.1
solute carrier family 43, member 2 (predicted)	Slc43a2_predicted	14.4±1.31
solute carrier family 44, member 4	Slc44a4	5.63±0.98
solute carrier family 45, member 3 (predicted)	Slc45a3_predicted	1.37±0.24
solute carrier family 45, member 4	Slc45a4	1.07±0.09
solute carrier family 46, member 1	Slc46a1	0.37±0.02
solute carrier family 47, member 1	Slc47a1	33.38±4.15
solute carrier family 5 (sodium/glucose cotransporter), member 11	Slc5a11	8.45±1.37
solute carrier family 5 (sodium/glucose cotransporter), member 12	Slc5a12	23.43±1.69
solute carrier family 5 (sodium/glucose cotransporter), member 2	Slc5a2	34.46±3.46
solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Slc5a6	1.59±0.56
solute carrier family 6 (neurotransmitter transporter), member 18	Slc6a18	1.31±1.19
solute carrier family 6 (neurotransmitter transporter), member 20	Slc6a20	1.5±0.26
solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	31.37±3.68
solute carrier family 6 (neurotransmitter transporter, GABA), member 13	Slc6a13	3.92±0.14
solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	1.05±0.14
solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	56.19±1.81
solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	Slc7a8	10.65±1.2
solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	Slc7a9	43.28±3.17
solute carrier family 7, member 6 opposite strand	Slc7a6os	0.46±0.12
solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	Slc9a6	1.95±0.38
solute carrier family 9 (sodium/hydrogen exchanger), member 1	Slc9a1	0.33±0.28
solute carrier family 9 (sodium/hydrogen exchanger), member 3	Slc9a3	10.18±0.89
solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	Slc9a3r1	19.1±2.42
Son cell proliferation protein	Son	4.69±0.86
Son of sevenless homolog 1 (Drosophila)	Sos1	1.34±0.23
sorbitol dehydrogenase	Sord	48.33±3
sortilin-related receptor, LDLR class A repeats-containing	Sorl1	1.17±1.35
sortilin-related VPS10 domain containing receptor 2 (predicted)	Sorcs2_predicted	4.77±0.59
sorting and assembly machinery component 50 homolog (S. cerevisiae)	Samm50	12.48±1.78
sorting nexin 1	Snx1	3.63±0.69
sorting nexin 11	Snx11	0.86±0.3
sorting nexin 12 (predicted)	Snx12_predicted	2.32±0.08
sorting nexin 13 (predicted)	Snx13_predicted	2.11±0.38
sorting nexin 14 (predicted)	Snx14_predicted	1.4±0.26
sorting nexin 15	Snx15	0.6±0.21
sorting nexin 16	Snx16	2.35±0.11
sorting nexin 17	Snx17	4.12±1.01
sorting nexin 18	Snx18	4.74±1.07
sorting nexin 19 (predicted)	Snx19_predicted	1.22±0.39
sorting nexin 2 (predicted)	Snx2_predicted	11.85±2.62
sorting nexin 25	Snx25	5.12±0.16
sorting nexin 4 (predicted)	Snx4_predicted	1.77±0.14
sorting nexin 5 (predicted)	Snx5_predicted	22.1±0.48
sorting nexin 6 (predicted)	Snx6_predicted	9.41±0.9
sorting nexin 7	Snx7	2.98±1.23
sorting nexin 8 (predicted)	Snx8_predicted	1.45±0.33
sorting nexin family member 27	Snx27	2.24±0.27
sorting nexing 24	Snx24	1.37±0.16
spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	Spg20	0.9±0.18
spastic paraplegia 21 homolog (human)	Spg21	6.35±0.82
spastic paraplegia 3A homolog (human)	Spg3a	0.33±0.02
spastic paraplegia 7 homolog (human)	Spg7	3.72±0.34

spastin (predicted)	Spast_predicted	1.71±0.27
SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc24	0.46±0.18
SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	0.66±0.11
SPECC1-like	Specc1l	0.94±0.15
special AT-rich sequence binding protein 1	Satb1	0.59±0.15
speckle-type POZ protein	Spop	1.04±0.04
spectrin beta 2	Spnb2	34.54±0.64
sperm associated antigen 7 (predicted)	Spag7_predicted	1.94±0.07
sperm associated antigen 9 (predicted)	Spag9_predicted	8.77±0.67
sperm autoantigenic protein 17	Spa17	3.13±0.47
sperm specific antigen 2 (predicted)	Ssfa2_predicted	6.04±0.41
spermatid perinuclear RNA binding protein	Strbp	1.32±0.2
spermatogenesis associated 5 (predicted)	Spata5_predicted	0.23±0.11
spermatogenesis associated 6	Spata6	0.71±0.21
spermatogenesis associated 7	Spata7	1.2±0.12
spermatogenesis associated, serine-rich 2 (predicted)	Spats2_predicted	2.88±0.58
spermidine synthase	Srm	0.85±0.12
spermidine/spermine N1-acetyl transferase 1	Sat1	6.28±1.86
spermidine/spermine N1-acetyl transferase 2 (predicted)	Sat2_predicted	11.23±0.43
spermine synthase	Sms	2.49±0.19
spermine synthase /// similar to spermine synthase	LOC683008 /// LOC690027 /// Sms	1.16±0.28
S-phase kinase-associated protein 1A	Skp1a	33.12±1.87
S-phase kinase-associated protein 2 (p45)	Skp2	0.25±0.12
sphingomyelin phosphodiesterase 1, acid lysosomal	Smpd1	9.03±0.42
sphingomyelin phosphodiesterase 2, neutral	Smpd2	0.78±0.12
sphingomyelin phosphodiesterase 4	Smpd4	0.87±0.01
sphingomyelin phosphodiesterase, acid-like 3A	Smpdl3a	3.46±0.09
sphingomyelin synthase 1	Sgms1	1.17±0.1
sphingosine kinase 2	Sphk2	1.3±0.52
sphingosine phosphate lyase 1	Sgpl1	0.32±0.01
sphingosine-1-phosphate phosphatase 1	Sgpp1	13.13±1.4
spindlin 1 /// similar to spindlin	LOC682571 /// Spin1	1.5±0.19
spindlin family, member 2	Spin2	0.24±0.02
spire homolog 1 (Drosophila) (predicted)	Spire1_predicted	0.27±0.13
splA/ryanodine receptor domain and SOCS box containing 2	Spsb2	0.44±0.11
splA/ryanodine receptor domain and SOCS box containing 3 (predicted)	Spsb3_predicted	2.7±0.35
splA/ryanodine receptor domain and SOCS box containing 4 (predicted)	Spsb4_predicted	0.66±0.09
splicing factor 1	Sf1	3.32±0.64
splicing factor 3a, subunit 1 (predicted)	Sf3a1_predicted	0.42±0.1
splicing factor 3a, subunit 2	Sf3a2	1.23±0.19
splicing factor 3a, subunit 3	Sf3a3	0.97±0.25
splicing factor 3b, subunit 1	Sf3b1	11.25±1.11
splicing factor 3b, subunit 2 (predicted)	Sf3b2_predicted	2.21±0.26
splicing factor 3b, subunit 3 (predicted)	Sf3b3_predicted	1.72±0.15
splicing factor 3b, subunit 4	Sf3b4	2.47±0.05
splicing factor 3b, subunit 5	Sf3b5	4.41±0.76
splicing factor 4	Sf4	0.68±0.05
splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	1.08±0.2
splicing factor YT521-B	Yt521	3.68±0.22
splicing factor, arginine/serine rich 9	Sfrs9	1.47±0.34
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	Sfrs10	11.25±1.27
splicing factor, arginine/serine-rich 11	Sfrs11	3.15±0.41
splicing factor, arginine/serine-rich 12	Sfrs12	0.93±0.15
splicing factor, arginine/serine-rich 14 (predicted)	Sfrs14_predicted	0.31±0.06
splicing factor, arginine/serine-rich 15	Sfrs15	0.69±0.17
splicing factor, arginine/serine-rich 18	Sfrs18	2.27±0.7
splicing factor, arginine/serine-rich 2 (SC-35)	Sfrs2	8.79±1.02
splicing factor, arginine/serine-rich 2, interacting protein	Sfrs2ip	2.53±0.47
splicing factor, arginine/serine-rich 3 (SRp20) (predicted)	Sfrs3_predicted	5.29±0.75
splicing factor, arginine/serine-rich 5	Sfrs5	7.6±1.7
splicing factor, arginine/serine-rich 6	Sfrs6	8.27±0.74
splicing factor, arginine/serine-rich 8	Sfrs8	0.37±0.09
split hand/foot malformation (ectrodactyly) type 1	Shfm1	12.41±0.66
sporulation protein, meiosis-specific, SPO11 homolog (S. cerevisiae) (predicted)	Spo11_predicted	0.79±0.17
sprouty homolog 4 (Drosophila) (predicted)	Spry4_predicted	0.24±0.3
Sprouty-related, EVH1 domain containing 2	Spred2	0.46±0.34
SPRY domain containing 4	Spryd4	0.89±0.07
squalene epoxidase	Sqle	1.22±0.42
squamous cell carcinoma antigen recognized by T-cells 1	Sart1	1.64±0.35
squamous cell carcinoma antigen recognized by T-cells 3 (predicted)	Sart3_predicted	0.48±0.19
src family associated phosphoprotein 2	Skap2	1.8±0.41
Src homology 2 domain containing F	Shf	0.72±0.06
Src homology 2 domain-containing transforming protein C1	Shc1	0.75±0.14
SREBF chaperone	Scap	2.87±0.54
SRR1 domain containing	Srrd	0.3±0.15
SR-related CTD-associated factor 1	Scaf1	0.44±0.15
SRY-box containing gene 13	Sox13	0.53±0.27
SRY-box containing gene 6	Sox6	0.29±0.04
Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	5.44±0.43
ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	0.66±0.07
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	3.46±0.51
ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	5.83±0.28
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	St6galnac3	7.14±0.32
Stam binding protein	Stambp	1.28±0.08
stannin	Snn	1.04±0.17
staphylococcal nuclease and tudor domain containing 1	Snd1	1.2±0.24

STARD3 N-terminal like	Stard3nl	1.46±0.32
StAR-related lipid transfer (START) domain containing 4 (predicted)	Stard4_predicted	1.68±0.07
StAR-related lipid transfer (START) domain containing 5	Stard5	0.71±0.08
START domain containing 10	Stard10	2.73±2.31
START domain containing 3	Stard3	1.74±0.55
START domain containing 7 (predicted)	Stard7_predicted	7.42±0.6
START domain containing 8 (predicted)	Stard8_predicted	1.72±0.46
stathmin 1	Stmn1	23.12±0.92
staufen RNA binding protein homolog 1 (Drosophila)	Stau1	5.25±0.2
staufen, RNA binding protein, homolog 2 (Drosophila)	Stau2	2.1±0.3
stem-loop binding protein	Slbp	1.4±0.06
Sterile alpha motif domain containing 4 (predicted)	Samd4_predicted	0.33±0.06
sterile alpha motif domain containing 4B	Samd4b	0.66±0.23
sterile alpha motif domain containing 8	Samd8	1.45±0.15
steroid receptor RNA activator 1	Sra1	5±0.99
steroid sulfatase	Sts	0.48±0.15
sterol carrier protein 2 /// podocan (predicted)	Podn_predicted /// Scp2	22.75±0.87
Sterol O-acyltransferase 1	Soat1	1.13±0.06
sterol regulatory element binding factor 1	Srebf1	1.31±0.25
sterol regulatory element binding factor 2 (predicted)	Srebf2	2.32±0.11
sterol-C4-methyl oxidase-like	Sc4mol	8.18±1.36
sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	Sc5d	5.97±1.86
stimulated by retinoic acid gene 6	Stra6	8.59±0.17
STIP1 homology and U-Box containing protein 1	Stub1	2.66±0.82
stomatin (Epb7.2)-like 2	Stoml2	3.38±0.16
strawberry notch homolog 2 (Drosophila)	Sbno2	0.6±0.07
stress 70 protein chaperone, microsome-associated	Stch	1.09±0.03
stress-associated endoplasmic reticulum protein 1	Serp1	14.44±0.26
stress-induced phosphoprotein 1	Stip1	4.8±0.45
striatin, calmodulin binding protein	Strn	0.85±0.22
striatin, calmodulin binding protein 3	Strn3	1.89±0.48
striatin, calmodulin binding protein 4 (predicted)	Strn4_predicted	0.81±0.26
stromal antigen 1 (predicted)	Stag1_predicted	1.66±0.3
stromal antigen 2 (predicted)	Stag2_predicted	4.65±0.27
stromal cell derived factor 2 (predicted)	Sdf2_predicted	4.71±1.15
stromal cell derived factor 4	Sdf4	10.62±1.51
stromal cell-derived factor 2-like 1 (predicted)	Sdf2l1_predicted	1.23±0.36
stromal interaction molecule 1 (predicted)	Stim1_predicted	0.36±0.01
stromal interaction molecule 2 (predicted)	Stim2_predicted	0.58±0.16
stromal membrane-associated GTPase-activating protein 2	Smap2	1.08±0.23
structural maintenace of chromosomes 3	Smc3	2.62±0.52
structural maintenance of chromosomes 1A	Smc1a	1.73±0.41
structural maintenance of chromosomes 2	Smc2	1.57±0.24
structural maintenance of chromosomes 4	Smc4	0.52±0.19
structural maintenance of chromosomes 5	Smc5	1.28±0.1
structure specific recognition protein 1	Ssrp1	1.55±0.18
STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	Stt3a	1.3±0.08
SUB1 homolog (S. cerevisiae)	Sub1	27.08±1.26
succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	Sdha	39.33±3.17
succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (predicted)	Sdhb_predicted	29.77±2.29
succinate dehydrogenase complex, subunit C, integral membrane protein	Sdhc	35.7±1.91
succinate dehydrogenase complex, subunit D, integral membrane protein	Sdhd	30.13±1.37
succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	28.61±1.47
succinate-Coenzyme A ligase, ADP-forming, beta subunit (predicted)	Sucla2_predicted	22.66±2.71
succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	30.37±4.67
sulfatase 2	Sulf2	0.23±0.16
sulfatase modifying factor 1 (predicted)	Sumf1_predicted	2.46±0.48
sulfatase modifying factor 2	Sumf2	1.86±0.19
sulfite oxidase	Suox	13.06±1.23
sulfotransferase family 1A, phenol-preferring, member 1	Sult1a1	0.89±0.38
sulfotransferase family 1B, member 1	Sult1b1	16.67±1.68
sulfotransferase family, cytosolic, 1C, member 2	Sult1c2	43.62±3.1
sulfotransferase family, cytosolic, 1C, member 2a	Sult1c2a	63.09±0.58
SUMO	LOC686286 /// RGD1564247_predicted /// Senp5_predicted	0.61±0.12
SUMO/sentrin specific peptidase 2	Senp2	0.61±0.07
SUMO/sentrin specific peptidase 3	Senp3	1.71±0.09
SUMO/sentrin specific peptidase 6 (predicted)	Senp6_predicted	1.91±0.14
SUMO1 activating enzyme subunit 1	Sae1	2.6±0.17
SUMO1 activating enzyme subunit 2	Sae2	2.64±0.77
SUMO1/sentrin specific protease 7 (predicted)	Senp7_predicted	0.7±0.03
superkiller viralicidic activity 2-like 2 (S. cerevisiae)	Skiv2l2	3.39±0.45
superoxide dismutase 1, soluble	Sod1	45.43±1.69
superoxide dismutase 2, mitochondrial	Sod2	13.55±0.15
superoxide dismutase 3, extracellular	Sod3	34.3±3.46
supervillin (predicted)	Svil_predicted	1.92±0.21
suppression of tumorigenicity 13	St13	19.88±1.58
suppression of tumorigenicity 7-like	St7l	0.74±0.02
suppressor of cytokine signaling 5	Socs5	1.47±0.35
suppressor of cytokine signaling 6 (predicted)	Socs6_predicted	1.47±0.04
suppressor of cytokine signaling 7 (predicted)	Socs7_predicted	0.33±0.04
suppressor of defective silencing 3 homolog (S. cerevisiae)	Suds3	2.34±0.49
suppressor of IKK epsilon	Sike	0.57±0.17
suppressor of Ty 16 homolog (S. cerevisiae) (predicted)	Supt16h_predicted	1.88±0.41
suppressor of Ty 4 homolog 1 (S. cerevisiae)	Supt4h1	2.94±0.23
suppressor of Ty 5 homolog (S. cerevisiae)	Supt5h	4.19±0.52

suppressor of Ty 6 homolog (S. cerevisiae)	Supt6h	2.35±0.49
suppressor of Ty 7 (S. cerevisiae)-like	Supt7l	0.84±0.19
suppressor of var1, 3-like 1 (S. cerevisiae)	Supv3l1	2.46±0.43
suppressor of variegation 3-9 homolog 1 (Drosophila) (predicted)	Suv39h1_predicted	0.71±0.04
suppressor of variegation 4-20 homolog 1 (Drosophila) (predicted)	Suv420h1_predicted	0.73±0.13
suppressor of variegation 4-20 homolog 2 (Drosophila) (predicted)	Suv420h2_predicted	0.36±0.06
surfeit 1	Surf1	4.87±0.62
surfeit 4	Surf4	6.78±0.67
surfeit gene 2	Surf2	4.33±0.58
surfeit gene 6 (predicted)	Surf6_predicted	0.7±0.13
survival motor neuron 1	Smn1	0.86±0.06
survival motor neuron domain containing 1	Smndc1	2.02±0.35
survival of motor neuron protein interacting protein 1	Sip1	0.61±0.11
sushi domain containing 2 (predicted)	Susd2_predicted	24.94±2.84
sushi domain containing 3 (predicted)	Susd3_predicted	3.16±0.24
sushi, nidogen and EGF-like domains 1 /// similar to CG2919-PA (predicted)	RGD1305604_predicted /// Sned1	0.28±0.18
SWA-70 protein	Swap70	3.24±0.21
Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (predicted)	Smarcal1_predicted	0.39±0.1
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Smarca4	1.05±0.09
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)	Smarca5_predicted	1.7±0.12
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	Smarcb1	2.24±0.24
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 (predicted)	Smarcc1_predicted	0.59±0.11
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1 (predicted)	Smarcd1_predicted	0.27±0.04
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Smarcd2	0.47±0.17
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Smarce1	3.24±0.38
SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1; (predicted)	Smarcad1_predicted	0.7±0.13
SYF2 homolog, RNA splicing factor (S. cerevisiae)	Syf2	2.88±0.24
symplekin	Sympk	0.31±0.14
synapse associated protein 1	Syap1	3.81±0.28
synaptic vesicle glycoprotein 2b	Sv2b	33.74±4
synaptogyrin 1	Syngr1	1±0.1
synaptogyrin 2	Syngr2	1.57±0.12
synaptojanin 1	Synj1	3.3±0.17
synaptojanin 2 binding protein	Synj2bp	18.04±2.22
synaptophysin-like 2	Sypl2	1.78±0.22
Synaptophysin-like protein	Sypl	29.81±1.53
synaptosomal-associated protein 23	Snap23	7.08±0.9
synaptosomal-associated protein 29	Snap29	2.54±0.29
Synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	2.37±0.25
Synaptotagmin III	Syt3	0.3±0.13
syndecan 1	Sdc1	2.45±0.29
syndecan 2	Sdc2	20.12±1.07
syndecan 4	Sdc4	21.21±1.7
syndecan binding protein	Sdcbp	30.97±3.88
synovial apoptosis inhibitor 1, synoviolin	Syvn1	1.55±0.36
synovial sarcoma translocation, Chromosome 18	Ss18	2.67±0.83
synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	0.56±0.18
syntaxin 12	Stx12	1.86±0.22
syntaxin 16 (predicted)	Stx16_predicted	0.98±0.27
syntaxin 18	Stx18	1.68±0.18
syntaxin 3	Stx3	0.45±0.1
syntaxin 4A (placental)	Stx4a	2.63±0.18
syntaxin 5a	Stx5a	2.05±0.26
syntaxin 6	Stx6	1.01±0.05
syntaxin 7	Stx7	9.21±0.48
syntaxin 8	Stx8	1.28±0.3
syntaxin binding protein 2	Stxbp2	2.07±0.25
syntaxin binding protein 3	Stxbp3	4.9±0.45
syntaxin binding protein 5 (tomosyn)	Stxbp5	0.89±0.2
syntrophin, acidic 1	Snta1	9.3±1.85
TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf1_predicted	0.52±0.22
TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf11	3.71±0.22
TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf13_predicted	2.69±0.36
TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf2	2.53±0.28
TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf5_predicted	0.2±0.07
TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf5l	0.59±0.07
TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf6	1.19±0.28
TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factorq	Taf8	0.49±0.02
TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf9	4.83±0.87
TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor pseudogene	Taf9 /// Taf9_ps	1.8±0.02
TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf9b	0.65±0.19
tafazzin	Taz	1.57±0.2
talin 1	Tln1	0.26±0.48
TANK-binding kinase 1	Tbk1	2.39±0.32
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 (predicted)	Tnks2_predicted	2.12±0.24
TAO kinase 1	Taok1	0.59±0.22
TAP binding protein	Tapbp	0.73±0.17
TAR (HIV) RNA binding protein 2	Tarbp2	0.72±0.14
TAR DNA binding protein	Tardbp	7±1.7
target of EGR1, member 1 (nuclear) (predicted)	Toe1_predicted	0.23±0.07
target of myb1 homolog (chicken)	Tom1	5.56±0.71
Target of myb1-like 2 (chicken) (predicted)	Tom1l2_predicted	1.67±0.3
taspase, threonine aspartase 1 (predicted)	Tasp1_predicted	0.49±0.03
TATA box binding protein	Tbp	0.79±0.03
TATA box binding protein-like 1	Tbpl1	2.33±0.22

TatD DNase domain containing 2	Tatdn2	2.58±0.2
Tax1 (human T-cell leukemia virus type I) binding protein 1	Tax1bp1	12±1.67
Tax1 (human T-cell leukemia virus type I) binding protein 3	Tax1bp3	2.17±0.52
TBC1 domain family, member 1 (predicted)	Tbc1d1_predicted	2.75±0.38
TBC1 domain family, member 10a	Tbc1d10a	3.2±1.24
TBC1 domain family, member 14	Tbc1d14	5.08±1.09
TBC1 domain family, member 15	Tbc1d15	3.59±0.13
TBC1 domain family, member 17 (predicted)	Tbc1d17_predicted	0.59±0.07
TBC1 domain family, member 19 (predicted)	Tbc1d19_predicted	1.38±0.17
TBC1 domain family, member 2 (predicted)	Tbc1d2_predicted	0.28±0.05
TBC1 domain family, member 22a (predicted)	Tbc1d22a_predicted	0.47±0.14
TBC1 domain family, member 22B	Tbc1d22b	0.82±0.31
TBC1 domain family, member 23 (predicted)	Tbc1d23_predicted	1.75±0.54
TBC1 domain family, member 7 (predicted)	Tbc1d7_predicted	0.57±0.02
TBC1 domain family, member 9B	Tbc1d9b	1.25±0.18
TBCC domain containing 1	Tbccd1	0.89±0.21
T-box 2 (predicted)	Tbx2_predicted	0.68±0.13
TCDD-inducible poly(ADP-ribose) polymerase (predicted)	Tiparp_predicted	3.03±0.17
T-cell leukemia translocation altered gene	Tcta	5.74±1.08
TCF3 (E2A) fusion partner	Tfpt	0.2±0.02
t-complex 11 (mouse) like 2	Tcp11l2	0.21±0.44
t-complex protein 1	Tcp1	11.31±1.84
Tctex1 domain containing 2	Tctex1d2	1.92±0.24
teashirt zinc finger family member 1	Tshz1	3.3±0.74
Tectonic 2	Tect2	0.28±0.05
tectonic family member 3	Tctn3	1.15±0.25
telomerase associated protein 1	Tep1	0.6±0.05
telomeric repeat binding factor 2 (predicted)	Terf2_predicted	0.41±0.11
telomeric repeat binding factor 2, interacting protein	Terf2ip	2.05±0.16
tensin 1	Tns1	15.82±1.64
TERF1 (TRF1)-interacting nuclear factor 2	Tinf2	0.75±0.09
terminal uridylyl transferase 1, U6 snRNA-specific	Tut1	0.24±0.06
testis enhanced gene transcript	Tegt	45.05±2.18
testis expressed gene 10 (predicted)	Tex10_predicted	0.2±0.13
testis expressed gene 2	Tex2	3.72±0.2
testis expressed gene 261	Tex261	3.02±0.25
testis expressed gene 264	Tex264	18.77±2.09
testis specific protein kinase 1	Tesk1	0.6±0.17
testis specific X-linked gene	Tsx	4.8±0.48
testis-specific kinase 2	Tesk2	0.43±0.08
testis-specific protein, Y-encoded-like 1	Tspyl1	5.51±0.67
tetraspanin 14 (predicted)	Tspan14_predicted	5.35±0.29
tetraspanin 18 (predicted)	Tspan18_predicted	1.44±0.19
tetraspanin 3	Tspan3	7.15±0.44
tetraspanin 31	Tspan31	4.44±0.54
tetraspanin 33	Tspan33	10.47±1.49
tetraspanin 4	Tspan4	2.17±0.36
tetraspanin 5	Tspan5	4.43±0.64
tetraspanin 6	Tspan6	2.47±0.41
tetratricopeptide repeat domain 1	Ttc1	2.14±0.61
tetratricopeptide repeat domain 12	Ttc12	0.6±0.13
tetratricopeptide repeat domain 13	Ttc13	1.42±0.18
tetratricopeptide repeat domain 15	Ttc15	2.15±0.16
tetratricopeptide repeat domain 17	Ttc17	0.85±0.04
tetratricopeptide repeat domain 19	Ttc19	0.82±0.05
tetratricopeptide repeat domain 21B	Ttc21b	0.23±0.5
tetratricopeptide repeat domain 23	Ttc23	0.69±0.07
tetratricopeptide repeat domain 27	Ttc27	0.96±0.18
tetratricopeptide repeat domain 3 (predicted)	Ttc3_predicted	4.15±0.08
tetratricopeptide repeat domain 33	Ttc33	0.71±0.1
tetratricopeptide repeat domain 35	Ttc35	9.81±1.43
tetratricopeptide repeat domain 5	Ttc5	0.63±0.13
tetratricopeptide repeat domain 7	Ttc7	0.81±0.14
tetratricopeptide repeat domain 7B (predicted)	Ttc7b_predicted	2.19±0.28
Tetratricopeptide repeat domain 8 (predicted)	Ttc8_predicted	1.14±0.18
Tetratricopeptide repeat domain 9C	Ttc9c	1.79±0.22
TG interacting factor 1	Tgif1	0.86±0.35
THAP domain containing 11 (predicted)	Thap11_predicted	0.89±0.04
THAP domain containing 4	Thap4	8.56±0.9
THAP domain containing 7	Thap7	0.8±0.19
THAP domain containing, apoptosis associated protein 3 (predicted)	Thap3_predicted	1.72±0.75
thiamine triphosphatase	Thtpa	2.47±0.43
thimet oligopeptidase 1	Thop1	0.36±0.25
thioesterase superfamily member 2 (predicted)	Them2_predicted	3.31±0.28
thioesterase superfamily member 4	Them4	0.95±0.19
thiopurine methyltransferase	Tpmt	11.47±1.43
thioredoxin 1	Txn1	46.18±2.23
thioredoxin 2	Txn2	8.71±1.09
thioredoxin domain containing 1	Txndc1	3.83±0.33
thioredoxin domain containing 11 (predicted)	Txndc11_predicted	0.77±0.06
thioredoxin domain containing 12 (endoplasmic reticulum)	Txndc12	3.57±0.13
thioredoxin domain containing 13	Txndc13	3.8±0.84
thioredoxin domain containing 15	Txndc15	5.13±1.31
thioredoxin domain containing 17	Txndc17	32.75±0.89
thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	7.95±0.76
Thioredoxin domain containing 9	Txndc9	1.04±0.1
thioredoxin reductase 1	Txnrd1	6.07±1.21

thioredoxin reductase 2	Txnrd2	2.55±0.25
thioredoxin-like 1	Txnl1	12.94±1
thioredoxin-like 4B	Txnl4b	0.58±0.13
Thioredoxin-related transmembrane protein 2	Tmx2	8.93±1.56
thiosulfate sulfurtransferase, mitochondrial	Tst	32.56±3.28
THO complex 1	Thoc1	1.88±0.41
THO complex 2 (predicted)	Thoc2_predicted	0.96±0.59
THO complex 5	Thoc5	1±0.21
THO complex 6 homolog (Drosophila)	Thoc6	0.32±0.08
THO complex 7 homolog (Drosophila)	Thoc7	7.14±1.13
three prime histone mRNA exonuclease 1	Thex1	0.48±0.1
three prime repair exonuclease 1	Trex1	0.4±0.07
threonine synthase-like 2 (bacterial)	Thnsl2	23.95±1.84
threonyl-tRNA synthetase	Tars	2.78±0.21
threonyl-tRNA synthetase 2, mitochondrial (putative)	Tars2	1.89±0.29
thrombopoietin	Thpo	0.21±0.08
THUMP domain containing 1	Thumpd1	4.38±0.42
THUMP domain containing 3	Thumpd3	1.03±0.28
thymidine kinase 1	Tk1	1.13±0.13
thymidine kinase 2, mitochondrial (predicted)	Tk2_predicted	0.47±0.25
thymidylate synthase	Tyms	0.31±0.06
thymine-DNA glycosylase	Tdg	1.52±0.21
thymocyte nuclear protein 1	Thyn1	0.97±0.05
thymocyte selection-associated high mobility group box	Tox	1.29±0.28
Thymoma viral proto-oncogene 1	Akt1	1.09±0.61
Thymoma viral proto-oncogene 2	Akt2	1.25±0.06
thymopoietin	Tmpo	2.24±0.07
thyroid adenoma associated	Thada	1.99±0.09
thyroid hormone receptor associated protein 3	Thrap3	3.03±0.47
thyroid hormone receptor beta	Thrb	0.47±0.06
thyroid hormone receptor interactor 10	Trip10	0.26±0.02
thyroid hormone receptor interactor 12	Trip12	7.04±0.81
thyrotroph embryonic factor	Tef	1.34±0.17
Tia1 cytotoxic granule-associated RNA binding protein-like 1	Tial1	2.02±0.16
Tigger transposable element derived 3 (predicted)	Tigd3_predicted	0.25±0.15
tight junction associated protein 1 (predicted)	Tjap1_predicted	0.3±0.1
tight junction protein 2	Tjp2	1.74±0.24
TIP41, TOR signalling pathway regulator-like (S. cerevisiae) (predicted) /// similar to TIP41, TOR signalling pathway regulator-like	LOC686733 /// Tiprl_predicted	1.42±0.14
tissue factor pathway inhibitor	Tfpi	4.82±0.66
tissue inhibitor of metalloproteinase 3	Timp3	34.93±1.8
Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	Timp3	34.24±3.16
tissue inhibitor of metalloproteinase 4	Timp4	0.75±0.2
tissue specific transplantation antigen P35B (predicted)	Tsta3_predicted	2.6±0.27
TLC domain containing 1	Tlcd1	1.53±0.22
TM2 domain containing 1 (predicted)	Tm2d1_predicted	6.89±0.25
TM2 domain containing 2	Tm2d2	3.74±0.25
TM2 domain containing 3 (predicted)	Tm2d3_predicted	5.99±0.65
TM2 domain containing 3 (predicted) /// threonyl-tRNA synthetase-like 2	Tarsl2 /// Tm2d3_predicted	0.4±0.06
TMEM9 domain family, member B (predicted)	Tmem9b_predicted	6.71±0.18
Tnf receptor associated factor 4 (predicted)	Traf4_predicted	3.31±0.14
Tnf receptor-associated factor 3 (predicted)	Traf3_predicted	0.67±0.13
Tnf receptor-associated factor 6 (predicted)	Traf6_predicted	1.16±0.11
Tnf receptor-associated factor 7 (predicted)	Traf7_predicted	0.75±0.11
TNF receptor-associated protein 1	Trap1	5.85±0.69
TNFAIP3 interacting protein 1 (predicted)	Tnip1_predicted	0.91±0.08
TNFRSF1A-associated via death domain	Tradd	0.28±0.21
tocopherol (alpha) transfer protein	Ttpa	0.79±0.02
toll interacting protein (predicted)	Tollip_predicted	2.23±0.41
topoisomerase (DNA) 2 alpha	Top2a	0.21±0.15
topoisomerase (DNA) I	Top1	4.56±0.48
topoisomerase (DNA) II beta binding protein	Topbp1	0.81±0.23
topoisomerase (DNA) III alpha (predicted)	Top3a_predicted	0.64±0.14
topoisomerase (DNA) III beta (predicted)	Top3b_predicted	0.9±0.07
topoisomerase I binding, arginine/serine-rich (predicted)	Topors_predicted	2.75±0.08
torsin A interacting protein 1	Tor1aip1	2.92±0.15
torsin A interacting protein 2	Tor1aip2	1.09±0.1
torsin family 1, member B	Tor1b	1.61±0.32
torsin family 2, member A	Tor2a	1.98±0.07
tousled-like kinase 1 (predicted)	Tlk1_predicted	2.49±0.03
tousled-like kinase 2 (Arabidopsis) (predicted)	Tlk2_predicted	1.13±0.17
TOX high mobility group box family member 4	Tox4	1.3±0.22
TP53 regulated inhibitor of apoptosis 1	Triap1	6.24±0.74
TP53 regulating kinase (predicted)	Trp53rk_predicted	0.79±0.02
Tp53rk binding protein	Tprkb	2.09±0.13
TraB domain containing	Trabd	2.09±0.35
Traf and Tnf receptor associated protein	Ttrap	1.23±0.11
TRAF family member-associated Nf-kappa B activator	Tank	0.32±0.04
TRAF type zinc finger domain containing 1	Trafd1	0.6±0.27
Traf3 interacting protein 2	Traf3ip2	0.6±0.13
trafficking protein particle complex 1	Trappc1	11.02±0.7
trafficking protein particle complex 2	Trappc2	1.44±0.07
trafficking protein particle complex 2-like	Trappc2l	5.39±0.28
trafficking protein particle complex 3	Trappc3	5.35±0.41
trafficking protein particle complex 4	Trappc4	1.74±0.12
trafficking protein particle complex 5	Trappc5	2.35±0.45

trafficking protein particle complex 6A /// similar to trafficking protein particle complex 6A	LOC686599 /// Trappc6a	4.62±0.61
trafficking protein particle complex 6B (predicted)	Trappc6b_predicted	1.65±0.32
trafficking protein, kinesin binding 2	Trak2	2.63±0.36
trans-acting transcription factor 1	Sp1	1.57±0.21
transaldolase 1	Taldo1	13.62±1.01
transcobalamin 2	Tcn2	43.89±3.29
transcription elongation factor A (SII) 1	Tcea1	7.8±0.28
transcription elongation factor A (SII), 3	Tcea3	2.02±1.05
transcription elongation factor A (SII)-like 1	Tceal1	1.35±0.23
transcription elongation factor A (SII)-like 8	Tceal8	2.39±0.37
transcription elongation factor B (SIII), polypeptide 1	Tceb1	11.91±1.17
transcription elongation factor B (SIII), polypeptide 2	Tceb2	14.04±1.53
transcription elongation factor B (SIII), polypeptide 3	Tceb3	1.68±0.2
transcription elongation regulator 1 (CA150) (predicted)	Tcerg1_predicted	1.85±0.1
transcription factor 19	Tcf19	0.43±0.05
transcription factor 25 (basic helix-loop-helix)	Tcf25	5.85±0.49
transcription factor A, mitochondrial	Tfam	2.91±0.44
transcription factor AP4 (predicted)	Tcfap4_predicted	0.33±0.14
transcription factor B1, mitochondrial	Tfb1m	1.44±0.19
transcription factor B2, mitochondrial	Tfb2m	3.42±0.44
transcription factor CP2 (predicted)	Tcfcp2_predicted	0.59±0.16
transcription factor CP2-like 2	Tcfcp2l2	0.41±0.16
transcription factor Dp-2 (E2F dimerization partner 2)	Tfdp2	0.64±0.27
transcription factor E3 (predicted)	Tcfe3_predicted	1.15±0.17
transcription factor EC	Tcfec	1.15±0.2
transcriptional adaptor 1 (HFI1 homolog, yeast) like	Tada1l	0.83±0.09
transcriptional adaptor 3 (NGG1 homolog, yeast)-like	Tada3l	0.63±0.17
transcriptional regulator, SIN3A (yeast) (predicted)	Sin3a_predicted	0.55±0.21
transducer of ERBB2, 2	Tob2	2.18±0.28
transducer of ErbB-2.1	Tob1	6.45±1.18
transducin (beta)-like 1 X-linked (predicted)	Tbl1x_predicted	1.03±0.33
transducin (beta)-like 1X-linked receptor 1 (predicted)	Tbl1xr1_predicted	7.15±0.52
transducin (beta)-like 3	Tbl3	0.55±0.09
transferrin receptor	Tfrc	3.11±1.44
transformation related protein 53	Trp53	1.68±0.03
transformation related protein 53 binding protein 1 (predicted)	Trp53bp1_predicted	0.36±0.07
transformation/transcription domain-associated protein (predicted)	Trrap_predicted	0.3±0.2
transformed mouse 3T3 cell double minute 1	Mdm1	0.26±0.14
transformed mouse 3T3 cell double minute 2 homolog (mouse) (predicted)	Mdm2_predicted	1.73±0.45
transformer 2 alpha homolog (Drosophila)	Tra2a	2.28±0.61
transforming growth factor beta regulated gene 1	Tbrg1	4.58±0.46
transforming growth factor beta regulated gene 4	Tbrg4	1.28±0.11
Transforming growth factor, beta 2	Tgfb2	0.27±0.07
transforming growth factor, beta receptor 1	Tgfbr1	8.52±1.18
transforming growth factor, beta receptor associated protein 1 (predicted)	Tgfbrap1_predicted	1.01±0.27
transforming, acidic coiled-coil containing protein 2	Tacc2	4.47±0.55
transgelin 2	Tagln2	6.92±1.63
transglutaminase 2, C polypeptide	Tgm2	36.44±6.29
trans-golgi network protein	Tgoln1	18.27±1.35
transient receptor potential cation channel, subfamily C, member 3	Trpc3	0.33±0.06
transient receptor potential cation channel, subfamily C, member 4 associated protein	Trpc4ap	2.17±0.37
transient receptor potential cation channel, subfamily M, member 7	Trpm7	1.37±0.15
transient receptor potential cation channel, subfamily V, member 1	Trpv1	10.38±1.03
transient receptor potential cation channel, subfamily V, member 4	Trpv4	3.94±0.29
transient receptor potential cation channel, subfamily V, member 4	Trpv1 /// Trpv4	3.17±0.31
Transient receptor potential-related protein, ChaK	Trpm7	6.06±0.45
transketolase	Tkt	22.11±0.93
translin	Tsn	0.65±0.05
translin-associated factor X	Tsnax	6.18±0.67
translocase of inner mitochondrial membrane 10 homolog (yeast)	Timm10	6.26±0.62
translocase of inner mitochondrial membrane 13 homolog (yeast)	Timm13	13.21±2.74
translocase of inner mitochondrial membrane 17a	Timm17a	8.17±0.67
translocase of inner mitochondrial membrane 17b	Timm17b	1.43±0.08
translocase of inner mitochondrial membrane 22 homolog (yeast)	Timm22	2.61±0.28
translocase of inner mitochondrial membrane 23 homolog (yeast)	Timm23	17±0.67
translocase of inner mitochondrial membrane 44	Timm44	0.89±0.04
translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	Timm8a1	2.39±0.08
translocase of inner mitochondrial membrane 8 homolog b (yeast)	Timm8b	19.36±3.04
translocase of inner mitochondrial membrane 9 homolog (yeast)	Timm9	3.82±0.68
translocase of outer mitochondrial membrane 20 homolog (yeast)	Tomm20	26.47±0.68
translocase of outer mitochondrial membrane 22 homolog (yeast)	Tomm22	6.6±0.17
translocase of outer mitochondrial membrane 34 (predicted)	Tomm34_predicted	0.57±0.14
translocase of outer mitochondrial membrane 40 homolog (yeast)	Tomm40	2.52±0.36
translocase of outer mitochondrial membrane 7 homolog (yeast)	Tomm7	15.31±2.17
translocase of outer mitochondrial membrane 70 homolog A (yeast)	Tomm70a	4.68±0.58
translocated promoter region	Tpr	1.25±0.36
translocating chain-associating membrane protein 1	Tram1	8.6±1.13
translocation protein 1	Tloc1	9.85±1.23
transmembrane 7 superfamily member 2	Tm7sf2	2.43±0.37
transmembrane 7 superfamily member 3	Tm7sf3	1.81±0.1
transmembrane 9 superfamily member 1	Tm9sf1	5.86±0.54
transmembrane 9 superfamily member 2	Tm9sf2	17.1±1.29
transmembrane 9 superfamily member 3	Tm9sf3	6.5±1.4
transmembrane 9 superfamily protein member 4	Tm9sf4	4.56±0.56
transmembrane and coiled coil domains 3	Tmcc3	1.29±0.04
transmembrane and coiled-coil domains 1	Tmco1	15.8±2.51
transmembrane and coiled-coil domains 3 (predicted)	Tmco3_predicted	1.58±0.4

transmembrane and coiled-coil domains 4	Tmco4	0.45±0.15
transmembrane and coiled-coil domains 6	Tmco6	1.27±0.37
transmembrane and tetratricopeptide repeat containing 4	Tmtc4	0.33±0.12
transmembrane and ubiquitin-like domain containing 1	Tmub1	0.54±0.02
transmembrane and ubiquitin-like domain containing 2	Tmub2	2.94±0.39
transmembrane BAX inhibitor motif containing 4	Tmbim4	6.22±0.97
transmembrane emp24 domain containing 1	Tmed1	0.87±0.34
transmembrane emp24 domain trafficking protein 2	Tmed2	9.07±1.13
transmembrane emp24 protein transport domain containing 4 (predicted)	Tmed4_predicted	4.08±0.2
transmembrane emp24 protein transport domain containing 5	Tmed5	1.07±0.14
transmembrane emp24 protein transport domain containing 7	Tmed7	6.74±0.63
transmembrane emp24 protein transport domain containing 9	Tmed9	3.28±0.37
transmembrane emp24-like trafficking protein 10 (yeast)	Tmed10	6.16±0.72
transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	Tpte2	0.98±0.23
transmembrane protease, serine 8 (intestinal)	Tmprss8	0.74±0.48
transmembrane protein 1 (predicted)	Tmem1_predicted	2.1±0.15
transmembrane protein 101	Tmem101	0.79±0.16
transmembrane protein 103 (predicted)	Tmem103_predicted	0.96±0.18
transmembrane protein 106A	Tmem106a	11.96±1.07
transmembrane protein 106B	Tmem106b	5.83±0.23
transmembrane protein 109	Tmem109	0.43±0.11
transmembrane protein 11 (predicted)	Tmem11_predicted	2.27±0.23
transmembrane protein 110	Tmem110	0.21±0.02
transmembrane protein 111	Tmem111	6.22±0.72
transmembrane protein 112B	Tmem112b	0.84±0.16
transmembrane protein 115 (predicted)	Tmem115_predicted	2.33±0.19
transmembrane protein 120A	Tmem120a	1.93±0.13
transmembrane protein 123	Tmem123	14.8±1.67
transmembrane protein 126A	Tmem126a	9.85±0.12
transmembrane protein 126B	Tmem126b	12.23±0.78
transmembrane protein 128	Tmem128	2.02±0.22
transmembrane protein 129	Tmem129	1.46±0.44
transmembrane protein 131	Tmem131	5.79±0.28
transmembrane protein 134	Tmem134	3.33±0.46
transmembrane protein 135	Tmem135	0.45±0.13
transmembrane protein 138	Tmem138	0.55±0.12
transmembrane protein 139	Tmem139	4.05±1.01
transmembrane protein 140	Tmem140	13.66±2.16
transmembrane protein 141	Tmem141	2.13±0.15
transmembrane protein 143	Tmem143	0.7±0.21
transmembrane protein 144	Tmem144	3.98±0.51
transmembrane protein 147	Tmem147	6.58±0.74
transmembrane protein 14C	Tmem14c	4.71±0.36
transmembrane protein 150	Tmem150	11.91±0.89
transmembrane protein 157	Tmem157	0.82±0.07
transmembrane protein 160	Tmem160	3.46±0.32
transmembrane protein 161B	Tmem161b	2.29±0.48
transmembrane protein 165	Tmem165	1.37±0.22
transmembrane protein 166	Tmem166	3.84±0.24
transmembrane protein 168	Tmem168	5.24±0.46
transmembrane protein 16F (predicted)	Tmem16f_predicted	4.35±0.44
transmembrane protein 16K	Tmem16k	0.85±0.26
transmembrane protein 17	Tmem17	0.51±0.11
transmembrane protein 174	Tmem174	14.91±1.76
transmembrane protein 176A	Tmem176a	0.9±1.18
transmembrane protein 176B	Tmem176b	1.99±0.56
transmembrane protein 177	Tmem177	0.67±0.07
transmembrane protein 178	Tmem178	0.43±0.35
transmembrane protein 179B	Tmem179b	4±0.21
transmembrane protein 183A	Tmem183a	8.69±0.59
transmembrane protein 185B	Tmem185b	10.39±1.88
transmembrane protein 186	Tmem186	0.8±0.24
transmembrane protein 188	Tmem188	2.66±0.28
transmembrane protein 189 /// similar to ubiquitin-conjugating enzyme E2 variant 1 (predicted)	RGD1562209_predicted /// Tmem189	0.48±0.12
transmembrane protein 19	Tmem19	0.96±0.13
transmembrane protein 192	Tmem192	2.15±0.56
transmembrane protein 205	Tmem205	8.07±1.07
transmembrane protein 208	Tmem208	4.57±0.21
transmembrane protein 209	Tmem209	2.3±0.31
transmembrane protein 24	Tmem24	8.96±0.93
transmembrane protein 27	Tmem27	67.69±6.83
transmembrane protein 30A	Tmem30a	9.51±0.55
transmembrane protein 32 (predicted)	Tmem32_predicted	6.49±1.2
transmembrane protein 33	Tmem33	4.4±0.71
transmembrane protein 34	Tmem34	3.96±0.64
transmembrane protein 37	Tmem37	13.86±0.55
transmembrane protein 38a (predicted)	Tmem38a_predicted	0.41±0.26
transmembrane protein 38B	Tmem38b	1.91±0.08
transmembrane protein 39a	Tmem39a	0.52±0.03
transmembrane protein 39b	Tmem39b	3.85±0.54
transmembrane protein 4	Tmem4	5.05±0.67
transmembrane protein 41B	Tmem41b	12.02±0.95
transmembrane protein 42 (predicted)	Tmem42_predicted	5.68±0.98
transmembrane protein 43	Tmem43	2.14±0.18
transmembrane protein 49	Tmem49	4.88±0.4
transmembrane protein 5	Tmem5	0.7±0.05

transmembrane protein 50A (predicted)	Tmem50a_predicted	6.16±0.18
transmembrane protein 50B	Tmem50b	1.6±0.21
transmembrane protein 51	Tmem51	5.12±0.28
transmembrane protein 53 (predicted)	Tmem53_predicted	0.9±0.1
transmembrane protein 55A	Tmem55a	3.23±0.66
transmembrane protein 55B	Tmem55b	2.14±0.11
transmembrane protein 57	Tmem57	1.2±0.18
transmembrane protein 60 (predicted)	Tmem60_predicted	2.23±0.21
transmembrane protein 62	Tmem62	1.18±0.25
transmembrane protein 63a (predicted)	Tmem63a_predicted	1.03±0.27
transmembrane protein 66	Tmem66	5.97±0.96
transmembrane protein 67	Tmem67	1.28±0.54
transmembrane protein 68 (predicted)	Tmem68_predicted	1.59±0.14
transmembrane protein 69	Tmem69	3.63±0.08
transmembrane protein 77	Tmem77	19.62±1.63
transmembrane protein 79	Tmem79	4.34±0.14
transmembrane protein 8 (five membrane-spanning domains) (predicted)	Tmem8_predicted	12.37±0.72
transmembrane protein 82	Tmem82	1.49±0.37
transmembrane protein 85	Tmem85	8.74±1.05
transmembrane protein 86A (predicted)	Tmem86a_predicted	11.07±1.15
transmembrane protein 87A (predicted)	Tmem87a_predicted	0.77±0.33
transmembrane protein 87B	Tmem87b	1.75±0.17
transmembrane protein 9 (predicted)	Tmem9_predicted	2.38±0.38
transmembrane protein 93 (predicted)	Tmem93_predicted	7.27±0.74
transmembrane protein 97	Tmem97	2.17±0.41
transmembrane protein 98	Tmem98	2.73±0.25
transporter 1, ATP-binding cassette, sub-family B (MDR	Btnl3 /// Btnl4 /// Btnl5 /// Hla-dma /// Hla-dmb /// Psmb9 /// RGD1562488_predicted /// RT1-Ba /// RT1-Bb /// RT1-Da /// RT1-Db1 /// RT1-DOb /// Tap1 /// Tap2 ///	7.39±3.78
transportin 1	Tnpo1	0.9±0.06
transportin 2 (importin 3, karyopherin beta 2b) (predicted)	Tnpo2_predicted	2.2±0.22
transportin 3	Tnpo3	4.49±1.32
tribbles homolog 1 (Drosophila)	Trib1	0.67±0.04
tribbles homolog 2 (Drosophila)	Trib2	0.47±0.4
trichoplein, keratin filament binding (predicted)	Tchp_predicted	0.58±0.1
trichorhinophalangeal syndrome I (human)	Trps1	2.12±0.24
trimethylguanosine synthase homolog (S. cerevisiae)	Tgs1	0.77±0.04
trimethyllysine hydroxylase, epsilon	Tmlhe	6.2±1.02
trinucleotide repeat containing 6a	Tnrc6a	0.8±0.19
trinucleotide repeat containing 6B	Tnrc6b	0.84±0.13
TRIO and F-actin binding protein	Triobp	0.59±0.12
triosephosphate isomerase 1	Tpi1	29.51±1.73
tripartite motif protein 14 (predicted)	Trim14_predicted	1.51±0.08
tripartite motif protein 32	Trim32	4±0.06
Tripartite motif protein 37 (predicted)	Trim37_predicted	0.8±0.2
tripartite motif protein 8 (predicted) /// tripartite motif-containing 8	Trim8 /// Trim8_predicted	2.25±0.44
tripartite motif-containing 11	Trim11	2±0.08
tripartite motif-containing 23	Trim23	0.41±0.08
tripartite motif-containing 24	Trim24	0.2±0.16
tripartite motif-containing 25	Trim25	1.78±0.35
tripartite motif-containing 26	Trim26	0.23±0.11
tripartite motif-containing 27	Trim27	2.04±0.31
tripartite motif-containing 28	Trim28	3.28±0.39
tripartite motif-containing 3	Trim3	1.21±0.09
tripartite motif-containing 33	Trim33	1.16±0.26
tripartite motif-containing 35	Trim35	17.36±1.41
tripartite motif-containing 37	Trim37	0.51±0.13
tripartite motif-containing 39	Trim39	0.53±0.09
tripartite motif-containing 41	Trim41	1.12±0.16
tripartite motif-containing 46	Trim46	0.38±0.16
tripartite motif-containing 59 (predicted)	Trim59_predicted	2.39±0.22
tripartite motif-containing 63	Trim63	0.36±0.05
tripeptidyl peptidase I	Tpp1	19.72±2.2
tripeptidyl peptidase II	Tpp2	3.45±0.47
triple functional domain (PTPRF interacting)	Trio	2.27±0.23
Trk-fused gene	Tfg	3.96±0.95
TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	Trmt1	1.04±0.29
TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae) (predicted)	Trmt5_predicted	0.52±0.13
tRNA isopentenyltransferase 1 (predicted)	Trit1_predicted	1.2±0.11
tRNA methyltranferase 12 homolog (S. cerevisiae)	Trmt12	0.24±0.1
tRNA methyltransferase 6 homolog (S. cerevisiae)	Trmt6	0.56±0.06
tRNA nucleotidyl transferase, CCA-adding, 1	Trnt1	3.64±0.56
tRNA selenocysteine associated protein	Secp43	4.91±0.44
tRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	Tsen2	0.34±0.03
tRNA splicing endonuclease 34 homolog (SEN34, S. cerevisiae)	Tsen34	3.9±0.7
tRNA splicing endonuclease 54 homolog (S. cerevisiae)	Tsen54	0.56±0.17
tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Tyw1	0.47±0.23
tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	Tyw3	0.77±0.18
tropomodulin 3	Tmod3	0.71±0.65
tropomyosin 3, gamma	Tpm3	12.62±0.16
TruB pseudouridine (psi) synthase homolog 1 (E. coli)	Trub1	0.54±0.02
TruB pseudouridine (psi) synthase homolog 2 (E. coli)	Trub2	2.94±0.72

trypsin domain containing 1 (predicted)	Tysnd1_predicted	2.52±0.28
tryptophan rich basic protein	Wrb	1.12±0.34
tryptophanyl-tRNA synthetase	Wars	2.9±0.22
TSC22 domain family 3	Tsc22d3	3.53±0.35
TSC22 domain family, member 1	Tsc22d1	38.58±3.38
TSPY-like 4	Tspyl4	0.95±0.23
tsukushin	Tsku	1.92±0.22
Tu translation elongation factor, mitochondrial (predicted)	Tufm_predicted	12.81±0.5
tubby like protein 4	Tulp4	0.62±0.06
tuberous sclerosis 2	Tsc2	1.28±0.25
tubulin cofactor a	Tbca	21.94±1.18
tubulin folding cofactor B	Tbcb	4.86±0.17
Tubulin tyrosine ligase	Ttl	0.49±0.07
tubulin tyrosine ligase-like family, member 7	Ttll7	0.47±0.09
tubulin, alpha 1A /// tubulin, alpha 1C /// tubulin, alpha 1B	Tuba1a /// Tuba1b /// Tuba1c	3.32±1.08
tubulin, alpha 4A	Tuba4a	9.22±0.51
tubulin, beta 2a	Tubb2a	0.21±0.43
tubulin, beta 2c	Tubb2c	14.37±1.32
tubulin, beta 4	Tubb4	0.36±0.16
tubulin, beta 5	Tubb5	0.55±0.31
tubulin, gamma 1	Tubg1	1.14±0.05
tubulin, gamma complex associated protein 2	Tubgcp2	1.24±0.15
tubulin, gamma complex associated protein 3	Tubgcp3	0.38±0.08
tubulin-specific chaperone c (predicted)	Tbcc_predicted	0.85±0.11
tubulin-specific chaperone d	Tbcd	2.04±0.15
tubulin-specific chaperone e	Tbce	2.47±0.18
tubulointerstitial nephritis antigen	Tinag	32.99±3.1
tudor domain containing 3	Tdrd3	0.37±0.37
tudor domain containing 7	Tdrd7	1.43±0.17
tumor necrosis factor (ligand) superfamily, member 13	Tnfsf13	3.94±0.21
tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	Tnfrsf14	5.22±0.56
tumor necrosis factor receptor superfamily, member 1a	Tnfrsf1a	1.16±0.41
tumor necrosis factor receptor superfamily, member 21 (predicted)	Tnfrsf21_predicted	4.83±1.11
tumor necrosis factor receptor superfamily, member 9	Tnfrsf9	0.85±0.19
tumor necrosis factor superfamily, member 5-induced protein 1 (predicted)	Tnfsf5ip1_predicted	3.02±0.31
tumor necrosis factor, alpha-induced protein 1 (endothelial)	Tnfaip1	3.57±0.3
tumor necrosis factor, alpha-induced protein 8 (predicted)	Tnfaip8_predicted	18.46±0.74
tumor protein D52 (predicted)	Tpd52_predicted	1.83±0.2
tumor protein D52-like 2	Tpd52l2	1.07±0.13
tumor protein p53 inducible nuclear protein 2	Trp53inp2	4.3±0.23
tumor protein, translationally-controlled 1	Tpt1	52.82±0.91
tumor rejection antigen gp96 (predicted)	Tra1_predicted	15.4±4.18
tumor suppressing subtransferable candidate 1	Tssc1	0.62±0.2
tumor suppressor candidate 2	Tusc2	1.11±0.07
tumor suppressor candidate 3	Tusc3	3.61±0.44
tumor suppressor candidate 4	Tusc4	1.91±0.07
tumor susceptibility gene 101	Tsg101	3.09±0.2
tumor-associated calcium signal transducer 1	Tacstd1	29.56±1.15
tumor-suppressing subchromosomal transferable fragment 4	Tssc4	1.05±0.34
tweety homolog 2 (Drosophila)	Ttyh2	1.66±0.43
tweety homolog 3 (Drosophila) (predicted)	Ttyh3_predicted	3.56±0.53
twinfilin, actin-binding protein, homolog 1 (Drosophila)	Twf1	14.58±0.81
TWIST neighbor (predicted)	Twistnb_predicted	1.74±0.21
twisted gastrulation homolog 1 (Drosophila) (predicted)	Twsg1_predicted	4.1±0.68
two pore channel 1	Tpcn1	5.98±0.34
type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Arts1	4.77±0.52
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Ywhab	8.81±0.12
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	14.95±0.7
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	1.21±0.56
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	4.18±0.35
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Ywhaq	14.89±0.42
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Ywhaz	13.99±0.32
tyrosylprotein sulfotransferase 2	Tpst2	3.03±0.34
tyrosyl-tRNA synthetase	Yars	1.84±0.54
tyrosyl-tRNA synthetase 2 (mitochondrial)	Yars2	1.69±0.23
U1 small nuclear ribonucleoprotein C /// similar to U1 small nuclear ribonucleoprotein C (U1 snRNP protein C) (U1C protein) (U1-C)	LOC685273 /// Snrpc	4.43±0.78
U1 small nuclear ribonucleoprotein polypeptide A (predicted)	Snrp70_predicted	1.7±0.43
U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 /// similar to U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b	LOC690372 /// U2af2	4.09±0.59
U2 small nuclear ribonucleoprotein B (predicted)	Snrpb2_predicted	1.23±0.22
U2 small nuclear RNA auxiliary factor 1-like 4 /// similar to Hypothetical protein MGC30332 (predicted)	RGD1563574_predicted /// U2af1l4	0.86±0.22
U7 snRNP-specific Sm-like protein LSM10	Lsm10	1.25±0.19
UbiA prenyltransferase domain containing 1 (predicted)	Ubiad1_predicted	0.44±0.2
ubinuclein 1 (predicted)	Ubn1_predicted	1.47±0.12
Ubiquilin 1	Ubqln1	6.18±0.61
ubiquilin 2 (predicted)	Ubqln2_predicted	4.03±0.67
ubiquilin 4 (predicted)	Ubqln4_predicted	0.66±0.34
ubiquinol cytochrome c reductase core protein 2	Uqcrc2	41.12±3.96
ubiquinol-cytochrome c reductase binding protein (predicted)	LOC687741 /// Uqcrb /// Uqcrb_predicted	48.31±0.5
ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	26.62±3.59
ubiquinol-cytochrome c reductase hinge protein	Uqcrh	35.91±2.04
ubiquinol-cytochrome c reductase, 6.4kDa subunit	Uqcr	28.55±3.26
ubiquinol-cytochrome c reductase, complex III subunit VII	Uqcrq	27.17±5.74
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1	40.83±3.14
ubiquitin A-52 residue ribosomal protein fusion product 1	Uba52	23.93±3.43

ubiquitin associated domain containing 1	Ubac1	2.81±0.36
ubiquitin B	Ubb	42.85±3.26
ubiquitin C	Ubc	27.37±2.15
ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	LOC679036 /// RGD1561196_predicted /// Uchl3	4.03±0.78
ubiquitin carboxyl-terminal esterase L5	Uchl5	4.67±0.58
ubiquitin family domain containing 1	Ubfd1	0.82±0.18
ubiquitin fusion degradation 1-like	Ufd1l	2.26±0.12
ubiquitin interaction motif containing 1	Uimc1	1.19±0.45
ubiquitin protein ligase E3A (predicted)	Ube3a_predicted	4.35±0.31
ubiquitin protein ligase E3C	Ube3c	1.52±0.16
ubiquitin related modifier 1 homolog (S. cerevisiae)	Urm1	0.58±0.06
ubiquitin specific peptdiase 1	Usp1	1.15±0.12
ubiquitin specific peptidase 10	Usp10	4.79±0.28
ubiquitin specific peptidase 11	Usp11	0.27±0.08
ubiquitin specific peptidase 12	Usp12	0.59±0.02
ubiquitin specific peptidase 14	Usp14	4.73±0.27
ubiquitin specific peptidase 15	Usp15	1.44±0.2
ubiquitin specific peptidase 19	Usp19	1.81±0.24
ubiquitin specific peptidase 2	Usp2	1.05±0.48
ubiquitin specific peptidase 20	Usp20	1.48±0.09
ubiquitin specific peptidase 25	Usp25	4.32±0.92
ubiquitin specific peptidase 28	Usp28	0.51±0.04
ubiquitin specific peptidase 3	Usp3	1.72±0.2
ubiquitin specific peptidase 33	Usp33	7.6±1.14
ubiquitin specific peptidase 36	Usp36	0.95±0.01
ubiquitin specific peptidase 38	Usp38	1.31±0.16
ubiquitin specific peptidase 39	Usp39	1.45±0.27
ubiquitin specific peptidase 4 (proto-oncogene)	Usp4	2.4±0.76
ubiquitin specific peptidase 40	Usp40	2.78±0.31
ubiquitin specific peptidase 42	Usp42	0.62±0.16
ubiquitin specific peptidase 46	Usp46	1.05±0.08
ubiquitin specific peptidase 47	Usp47	3.16±0.61
ubiquitin specific peptidase 5 (isopeptidase T)	Usp5	2.55±0.45
ubiquitin specific peptidase 7	Usp7	1.78±0.16
ubiquitin specific peptidase 8	Usp8	5.62±1.29
Ubiquitin specific peptidase 9, X chromosome (predicted)	Usp9x_predicted	2.9±0.23
ubiquitin specific peptidase like 1	Uspl1	0.61±0.08
ubiquitin specific protease 24 (predicted)	Usp24_predicted	1.77±0.47
ubiquitin specific protease 32 (predicted)	Usp32_predicted	1.58±0.16
ubiquitin specific protease 48	Usp48	0.9±0.26
Ubiquitin specific protease 7 (herpes virus-associated)	Usp7	2.79±0.21
ubiquitin-activating enzyme E1C	Ube1c	6.23±0.26
ubiquitin-activating enzyme E1-domain containing 1	Ube1dc1	1.79±0.48
ubiquitin-activating enzyme E1-like 2	Ube1l2	0.98±0.06
ubiquitin-associated protein 1	Ubap1	2.21±0.52
ubiquitin-associated protein 2 (predicted)	Ubap2_predicted	2.33±0.35
ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	5.43±0.9
ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (predicted)	Ube4b_predicted	1.59±0.65
ubiquitin-conjugating enzyme E2 variant 1 (predicted)	Ube2v1_predicted	5.77±1.29
ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	3.03±0.52
Ubiquitin-conjugating enzyme E2, J1 (predicted)	Ube2j1_predicted	2.44±0.42
ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	Ube2j2	1.18±0.16
ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	Ube2a	2.71±0.39
ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	Ube2b	7.93±0.5
ubiquitin-conjugating enzyme E2C (predicted)	Ube2c_predicted	0.39±0.12
ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast) (predicted)	Ube2d1_predicted	0.39±0.06
Ubiquitin-conjugating enzyme E2D 2	Ube2d2	5.92±0.42
ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	21.74±0.37
ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	5.31±0.99
ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast) (predicted)	Ube2e3_predicted	8.31±0.78
ubiquitin-conjugating enzyme E2F (putative)	Ube2f	5.42±0.56
ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	4.62±1
ubiquitin-conjugating enzyme E2G 2 (predicted)	Ube2g2_predicted	1.01±0.18
ubiquitin-conjugating enzyme E2I	Ube2i	3.7±0.25
ubiquitin-conjugating enzyme E2L 3 (predicted)	Ube2l3_predicted	7.22±0.59
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (predicted)	Ube2m_predicted	4.96±0.88
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (predicted) /// chromatin modifying protein 2A	Chmp2a /// Ube2m_predicted	7.84±0.2
ubiquitin-conjugating enzyme E2N	Ube2n	4.11±0.42
ubiquitin-conjugating enzyme E2O (predicted)	Ube2o_predicted	0.51±0.23
ubiquitin-conjugating enzyme E2Q (putative) 1	Ube2q1	4.49±0.34
ubiquitin-conjugating enzyme E2Q (putative) 2 (predicted)	Ube2q2_predicted	4.04±0.31
ubiquitin-conjugating enzyme E2S (predicted)	Ube2s_predicted	2.59±0.4
ubiquitin-conjugating enzyme E2Z (putative)	Ube2z	1.6±0.1
ubiquitin-fold modifier 1	Ufm1	6.67±0.81
ubiquitin-fold modifier conjugating enzyme 1	Ufc1	5.44±0.95
ubiquitin-like 3	Ubl3	7.84±1.57
ubiquitin-like 4	Ubl4	3.35±0.43
ubiquitin-like 5	Ubl5	12.72±1.21
ubiquitin-like 7 (bone marrow stromal cell-derived)	Ubl7	1.67±0.55
ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	3.7±0.2
ubiquitin-like modifier activating enzyme 1	Uba1	5.8±0.63
ubiquitin-like, containing PHD and RING finger domains 2 (predicted)	Uhrf2_predicted	3.49±0.61
ubiquitously expressed transcript	Uxt	3.58±0.24
ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (predicted)	Utx_predicted	2.4±0.5

UBX domain containing 1	Ubxd1	1.81±0.25
UBX domain containing 2	Ubxd2	9.56±0.26
UBX domain containing 4	Ubxd4	4.22±0.5
UBX domain containing 6 (predicted)	Ubxd6_predicted	3.31±0.49
UBX domain containing 8	Ubxd8	1.6±0.36
UCHL5 interacting protein	Uchl5ip	0.94±0.22
UDP glucuronosyltransferase 2 family, polypeptide B36	Ugt2b36	5.02±3.99
UDP glycosyltransferase 1 family, polypeptide A1	Ugt1a1 /// Ugt1a2 /// Ugt1a3 /// Ugt1a5 /// Ugt1a6 /// Ugt1a7 /// Ugt1a8 /// Ugt1a9	6.12±3.17
UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6 (predicted)	B3galt6_predicted	0.26±0.06
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	B4galt1_predicted	0.64±0.34
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	B4galt3	1.9±0.24
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 (predicted)	B4galt5_predicted	0.28±0.06
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	B4galt6	0.64±0.29
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3gnt1	3.78±0.14
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	B3gnt7	0.28±0.01
UDP-glucose dehydrogenase	Ugdh	18.04±1.73
UDP-glucose pyrophosphorylase 2	Ugp2	8.27±0.26
UDP-glucuronate decarboxylase 1	Uxs1	1.67±0.12
UDP-glucuronosyltransferase	LOC286989	1.13±0.35
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	Galnt1	4.38±0.51
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	Galnt11	19.06±4.35
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	Galnt14	3.39±0.6
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (predicted)	Galnt2_predicted	9.91±0.98
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	Galnt3	1.04±0.19
UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 (predicted)	Uap1l1_predicted	11.41±1.75
UFM1-specific peptidase 2	Ufsp2	6.71±0.76
UHRF1 (ICBP90) binding protein 1-like	Uhrf1bp1l	2.06±0.11
unc-119 homolog B (C. elegans)	Unc119b	3.92±0.19
unc-45 homolog A (C. elegans)	Unc45a	2.12±0.33
unc-5 homolog C (C. elegans)-like	Unc5cl	4.39±0.25
unc-50 homolog (C. elegans)	Unc50	5±0.76
Unc-51 like kinase 1 (C. elegans)	Ulk1	0.55±0.16
Unc-51 like kinase 2 (C. elegans) (predicted)	Ulk2_predicted	1.46±0.17
unc-84 homolog B (C. elegans)	Unc84b	1.57±0.46
unconventional SNARE in the ER 1 homolog (S. cerevisiae)	LOC292282 /// Use1	4.51±0.57
UPF3 regulator of nonsense transcripts homolog A (yeast)	Upf3a	1.4±0.15
UPF3 regulator of nonsense transcripts homolog B (yeast) (predicted)	Upf3b_predicted	2.17±0.2
upregulated during skeletal muscle growth 5	Usmg5	49.86±2.57
up-regulated gene 4	Urg4	1.36±0.13
up-regulator of carnitine transporter, OCTN2	LOC303140	0.2±0.07
upstream binding protein 1 (predicted)	Ubp1_predicted	1.61±0.3
upstream binding transcription factor, RNA polymerase I	Ubtf	0.96±0.25
upstream transcription factor 1	Usf1	0.36±0.26
upstream transcription factor 2	Usf2	1.59±0.24
uracil-DNA glycosylase	Ung	6.25±0.67
ureidopropionase, beta	Upb1	14.21±1.12
uridine monophosphate synthetase	Umps	3.96±0.27
uridine-cytidine kinase 1 (predicted)	Uck1_predicted	2.52±0.51
uridine-cytidine kinase 1-like 1	Uckl1	1.05±0.07
uroporphyrinogen decarboxylase	Urod	3.88±0.49
uroporphyrinogen III synthase	Uros	0.44±0.07
Usher syndrome 1C homolog (human)	Ush1c	7.29±1.06
USO1 homolog, vesicle docking protein (yeast)	Uso1	5.1±0.66
USP6 N-terminal like (predicted)	Usp6nl_predicted	0.45±0.19
UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	Utp14a	1.06±0.12
UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Utp15	0.5±0.14
UTP18, small subunit (SSU) processome component, homolog (yeast)	Utp18	1.55±0.1
UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	0.66±0.14
UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae	Utp3	2.46±0.3
UTP6, small subunit (SSU) processome component, homolog (yeast)	Utp6	0.35±0.09
Vac14 homolog (S. cerevisiae)	Vac14	1.42±0.23
vaccinia related kinase 1	Vrk1	0.54±0.13
vaccinia related kinase 3	Vrk3	2.95±0.12
vacuolar protein sorting 11 (yeast) (predicted)	Vps11_predicted	1.69±0.13
vacuolar protein sorting 13D (yeast) (predicted)	Vps13d_predicted	0.58±0.1
vacuolar protein sorting 16 (yeast)	Vps16	1.19±0.15
vacuolar protein sorting 18 (yeast) (predicted)	Vps18_predicted	0.34±0.05
vacuolar protein sorting 25 homolog (S. cerevisiae)	Vps25	6.78±0.62
Vacuolar protein sorting 26 (yeast)	Vps26	3.22±0.19
vacuolar protein sorting 26 homolog A (yeast)	Vps26a	2.56±0.33
vacuolar protein sorting 26 homolog B (S. pombe)	Vps26b	0.35±0.19
vacuolar protein sorting 28 (yeast) (predicted)	Vps28_predicted	6.37±0.25
vacuolar protein sorting 29 (S. pombe) (predicted)	Vps29_predicted	21.81±2.58
vacuolar protein sorting 33A (yeast)	Vps33a	0.75±0.31
vacuolar protein sorting 33B (yeast)	Vps33b	0.51±0.09
vacuolar protein sorting 35	Vps35	21.84±0.52
vacuolar protein sorting 36 (yeast) (predicted)	Vps36_predicted	0.96±0.2
vacuolar protein sorting 37 homolog A (S. cerevisiae)	Vps37a	1.86±0.08
vacuolar protein sorting 37B (yeast) (predicted)	Vps37b_predicted	0.68±0.24
vacuolar protein sorting 37C (yeast) (predicted)	Vps37c_predicted	0.45±0.07
vacuolar protein sorting 39 (yeast)	Vps39	0.43±0.1
vacuolar protein sorting 45 (yeast)	Vps45	1.25±0.1
vacuolar protein sorting 4a (yeast)	Vps4a	3.28±0.3
vacuolar protein sorting 4b (yeast)	Vps4b	4.22±0.12

vacuolar protein sorting 52 (yeast)	Vps52	0.39±0.1
vacuolar protein sorting 53 (yeast) (predicted)	Vps53_predicted	1.42±0.31
vacuolar protein sorting 54 (yeast)	Vps54	1.49±0.07
vacuolar protein sorting 72 (yeast) (predicted)	Vps72_predicted	0.22±0.26
vacuolar protein sorting 8 homolog (S. cerevisiae)	Vps8	2.06±0.26
valosin containing protein (p97)/p47 complex interacting protein 1	Vcpip1	1.13±0.03
valosin-containing protein	Vcp	14.86±0.75
valyl-tRNA synthetase 2	Vars2	0.24±0.21
vang-like 1 (van gogh, Drosophila)	Vangl1	2.48±0.37
vanin 1	Vnn1	9.86±0.13
vascular endothelial growth factor A	Vegfa	2.59±0.45
vascular endothelial growth factor B	Vegfb	3.82±0.24
vascular endothelial growth factor C	Vegfc	0.61±0.21
vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	1.52±0.17
VATPase, H+ transporting, lysosomal V1 subunit E1	Atp6v1e1	13.8±0.86
vav 3 oncogene	Vav3	0.43±0.39
Vav2 oncogene (predicted)	Vav2_predicted	0.95±0.06
ventricular zone expressed PH domain homolog 1 (zebrafish) /// similar to VEPH isoform A (predicted)	RGD1565184_predicted /// Veph1	0.58±0.03
v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	Erbb2	0.78±0.11
very low density lipoprotein receptor	Vldlr	3.92±0.09
vesicle amine transport protein 1 homolog (T californica)	Vat1	0.99±0.72
vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	0.36±0.05
vesicle-associated membrane protein 2	Vamp2	0.69±0.07
vesicle-associated membrane protein 3	Vamp3	5.86±0.33
vesicle-associated membrane protein 4 (predicted)	Vamp4_predicted	0.39±0.13
vesicle-associated membrane protein 7	Vamp7	5.3±0.63
vesicle-associated membrane protein 8	Vamp8	6.82±1.52
vesicle-associated membrane protein, associated protein a	Vapa	19.05±1.76
vesicle-associated membrane protein, associated protein B and C	Vapb	4.35±0.72
vestigial like 4 (Drosophila)	Vgll4	0.48±0.19
villin 1 (predicted)	Vil1_predicted	11.23±1.16
villin 2	Vil2	27.35±0.64
villin-like (predicted)	Vill_predicted	5.07±1.07
vinculin (predicted)	Vcl_predicted	1.5±0.52
virus-induced signaling adapter	Visa	0.62±0.05
vitamin D receptor	Vdr	0.29±0.1
vitamin K epoxide reductase complex, subunit 1	Vkorc1	11.89±1.49
vitamin K epoxide reductase complex, subunit 1-like 1	Vkorc1l1	1.2±0.21
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Kras	3.39±0.25
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	Mafg	0.33±0.1
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	Mafk	0.51±0.09
v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	Maf	5.99±1.62
voltage-dependent anion channel 1	Vdac1	26.64±2.25
voltage-dependent anion channel 2	Vdac2	26.07±1.03
voltage-dependent anion channel 3	Vdac3	22.89±3.27
von Hippel-Lindau tumor suppressor	Vhl	3.91±0.26
von Willebrand factor A domain containing 1	Vwa1	0.49±0.16
Vps20-associated 1 homolog (S. cerevisiae)	Vta1	3.57±0.13
v-raf murine sarcoma 3611 viral oncogene homolog	Araf	2.38±0.39
v-raf-1 murine leukemia viral oncogene homolog 1	Raf1	3.2±0.31
v-ral simian leukemia viral oncogene homolog A (ras related)	Rala	1.5±0.19
v-ral simian leukemia viral oncogene homolog B (ras related)	Ralb	2.91±0.41
v-rel reticuloendotheliosis viral oncogene homolog A (avian)	Rela	0.46±0.4
WAS protein homology region 2 domain containing 1	Whdc1	0.32±0.1
WAS/WASL interacting protein family, member 1	Wipf1	0.5±0.33
WASP family 1	Wasf1	0.62±0.08
WD and tetratricopeptide repeats 1 (predicted)	Wdtc1_predicted	1.62±0.33
WD repeat and FYVE domain containing 1	Wdfy1	6.24±0.84
WD repeat and FYVE domain containing 2 (predicted)	Wdfy2_predicted	1.75±0.29
WD repeat and FYVE domain containing 3 (predicted)	Wdfy3_predicted	10.84±0.39
WD repeat and SOCS box-containing 1	Wsb1	3.89±0.87
WD repeat and SOCS box-containing 2	Wsb2	5.02±0.25
WD repeat domain 1	Wdr1	7.51±0.48
WD repeat domain 12	Wdr12	0.95±0.13
WD repeat domain 13 (predicted)	Wdr13_predicted	1.58±0.24
WD repeat domain 18	Wdr18	0.86±0.13
WD repeat domain 19 (predicted)	Wdr19_predicted	0.47±0.06
WD repeat domain 20	Wdr20	0.31±0.1
WD repeat domain 20a	Wdr20a	0.43±0.05
WD repeat domain 21 (predicted)	Wdr21_predicted	0.71±0.06
WD repeat domain 23	Wdr23	7.43±1.88
WD repeat domain 24	Wdr24	0.83±0.25
WD repeat domain 25 /// similar to pre-mRNA splicing factor-like (predicted)	RGD1562505_predicted /// Wdr25	0.2±0.04
WD repeat domain 26	Wdr26	3.5±0.33
WD repeat domain 3 (predicted)	Wdr3_predicted	0.96±0.14
WD repeat domain 31	Wdr31	0.47±0.1
WD repeat domain 32 (predicted)	Wdr32_predicted	0.43±0.07
WD repeat domain 33 (predicted)	Wdr33_predicted	0.96±0.45
WD repeat domain 34	Wdr34	0.4±0.03
WD repeat domain 36 (predicted)	Wdr36_predicted	1.73±0.13
WD repeat domain 37 (predicted)	Wdr37_predicted	1.5±0.15
WD repeat domain 41 (predicted)	Wdr41_predicted	0.45±0.08
WD repeat domain 42A	Wdr42a	1.07±0.22
WD repeat domain 43	Wdr43	0.69±0.08
WD repeat domain 44	Wdr44	0.29±0.06

WD repeat domain 45	Wdr45	2.47±0.26
WD repeat domain 47	Wdr47	0.33±0.13
WD repeat domain 48 (predicted)	Wdr48_predicted	0.64±0.2
WD repeat domain 5	Wdr5	0.96±0.19
WD repeat domain 51A	Wdr51a	0.53±0.09
WD repeat domain 55	Wdr55	0.26±0.15
WD repeat domain 5B	Wdr5b	0.27±0.07
WD repeat domain 6	Wdr6	2.11±0.52
WD repeat domain 61	Wdr61	5.37±0.16
WD repeat domain 67	Wdr67	1.52±0.12
WD repeat domain 68 (predicted)	Wdr68_predicted	2.81±0.4
WD repeat domain 70	Wdr70	0.44±0.08
WD repeat domain 75	Wdr75	0.56±0.26
WD repeat domain 77	Wdr77	2.61±0.36
WD repeat domain 79	Wdr79	0.7±0.1
WD repeat domain 81	Wdr81	1.95±0.3
WD repeat domain 89	Wdr89	1.34±0.14
WD repeat domain 91	Wdr91	1.32±0.31
WD repeat domain, phosphoinositide interacting 1 (predicted)	Wipi1_predicted	3.52±0.55
WD repeat domain, phosphoinositide interacting 2	Wipi2	1.72±0.2
WD repeat, SAM and U-box domain containing 1	Wdsub1	0.96±0.13
WD repeats and SOF domain containing 1 (predicted)	Wdsof1_predicted	2.68±0.38
Wdr45 like (predicted)	Wdr45l_predicted	3.87±0.49
wee 1 homolog (S. pombe)	Wee1	0.43±0.12
Werner helicase interacting protein 1	Wrnip1	0.92±0.16
widely-interspaced zinc finger motifs (predicted)	Wiz_predicted	0.84±0.05
Williams Beuren syndrome chromosome region 22	LOC368084 /// Wbscr22	1.25±0.09
Williams-Beuren syndrome chromosome region 16 homolog (human) (predicted)	Wbscr16_predicted	0.82±0.19
Williams-Beuren syndrome chromosome region 18 /// similar to Williams-Beuren syndrome critical region 18	LOC680976 /// Wbscr18	2.7±0.06
Wilms' tumour 1-associating protein	Wtap	3.76±0.51
wingless related MMTV integration site 2b	Wnt2b	0.3±0.18
Wiskott-Aldrich syndrome-like (human)	Wasl	4.06±0.22
Wolf-Hirschhorn syndrome candidate 1 (human)	Whsc1	0.27±0.12
Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)	Whsc1l1_predicted	0.92±0.07
Wolf-Hirschhorn syndrome candidate 2 (human)	Whsc2	0.8±0.02
WW domain binding protein 1	Wbp1	2.36±0.2
WW domain binding protein 11	Wbp11	0.86±0.29
WW domain binding protein 2	Wbp2	4.65±0.28
WW domain binding protein 4	Wbp4	1.22±0.27
WW domain binding protein 5 (predicted)	Wbp5_predicted	8.18±1.83
WW domain binding protein 7	Wbp7	0.31±0.09
WW domain containing E3 ubiquitin protein ligase 1	Wwp1	1.6±0.39
WW domain containing E3 ubiquitin protein ligase 2 (predicted)	Wwp2_predicted	1.25±0.17
WW domain containing transcription regulator 1	Wwtr1	0.93±0.17
WW, C2 and coiled-coil domain containing 1	Wwc1	5.19±0.61
WW, C2 and coiled-coil domain containing 2	Wwc2	3.99±0.08
X Kell blood group precursor-related family, member 5	Xkr5	0.23±0.09
xanthine dehydrogenase	Xdh	21.99±3.2
X-box binding protein 1	Xbp1	4.99±1.19
Xenotropic and polytropic retrovirus receptor 1 (predicted)	Xpr1_predicted	5.24±0.31
xeroderma pigmentosum, complementation group A (predicted)	Xpa_predicted	0.7±0.03
xeroderma pigmentosum, complementation group C (predicted)	Xpc_predicted	1.93±0.12
X-linked myotubular myopathy gene 1	Mtm1	0.35±0.08
XPA binding protein 2	Xab2	0.77±0.34
X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Xpnpep1	13.35±2.37
X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	Xpnpep2	14.51±0.65
X-ray repair complementing defective repair in Chinese hamster cells 1	Xrcc1	0.41±0.16
X-ray repair complementing defective repair in Chinese hamster cells 4	Xrcc4	0.79±0.05
X-ray repair complementing defective repair in Chinese hamster cells 5	Xrcc5	2.86±0.49
X-ray repair complementing defective repair in Chinese hamster cells 6	Xrcc6	0.26±0.08
XRCC6 binding protein 1	Xrcc6bp1	1.46±0.29
XTP3-transactivated protein A	Xtp3tpa	0.75±0.15
xylosyltransferase II	Xylt2	0.7±0.27
xylulokinase homolog (H. influenzae)	Xylb	30.17±2.64
Y box protein 1	Ybx1	19.37±1.73
YEATS domain containing 2	Yeats2	1.91±0.23
YEATS domain containing 4 (predicted)	Yeats4_predicted	1.7±0.05
Yip1 domain family, member 1	Yipf1	4.02±0.64
Yip1 domain family, member 2	Yipf2	0.43±0.02
Yip1 domain family, member 3	Yipf3	1.04±0.35
Yip1 domain family, member 4	Yipf4	4.45±0.29
Yip1 domain family, member 5	Yipf5	10.99±1.28
Yip1 interacting factor homolog (S. cerevisiae)	Yif1	4.13±0.34
yippee-like 5 (Drosophila)	Ypel5	7.82±0.59
YKT6 homolog (S. Cerevisiae)	Ykt6	0.31±0.07
YME1-like 1 (S. cerevisiae)	Yme1l1	7.85±1.01
yrdC domain containing (E.coli)	Yrdc	0.44±0.15
YTH domain family 1	Ythdf1	1.96±0.07
YTH domain family 2 (predicted)	Ythdf2_predicted	1.85±0.13
YTH domain family 3 (predicted)	Ythdf3_predicted	4.24±0.27
YY1 transcription factor	Yy1	10.74±0.89
zer-1 homolog (C. elegans)	Zer1	0.88±0.16
zeta-chain (TCR) associated protein kinase 70	Zap70	0.2±0.03
zinc and ring finger 1 (predicted)	Znrf1_predicted	5.48±1.04
zinc binding alcohol dehydrogenase, domain containing 1	Zadh1	5.63±0.58
zinc binding alcohol dehydrogenase, domain containing 2 (predicted)	Zadh2_predicted	1.23±0.06
zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	Zrsr1	0.43±0.06

zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	Zrsr2	0.36±0.14
zinc finger and BTB domain containing 1	Zbtb1	0.4±0.2
zinc finger and BTB domain containing 11 (predicted)	Zbtb11_predicted	1.93±0.14
zinc finger and BTB domain containing 17	Zbtb17	0.6±0.26
zinc finger and BTB domain containing 2 (predicted)	Zbtb2_predicted	0.42±0.16
zinc finger and BTB domain containing 20 (predicted)	Zbtb20_predicted	4.2±1.19
zinc finger and BTB domain containing 24 (predicted)	Zbtb24_predicted	0.25±0.08
zinc finger and BTB domain containing 4 (predicted)	Zbtb4_predicted	0.86±0.22
zinc finger and BTB domain containing 41 homolog	Zbtb41	0.83±0.17
zinc finger and BTB domain containing 43	Zbtb43	0.95±0.18
zinc finger and BTB domain containing 44	Zbtb44	0.48±0.02
zinc finger and BTB domain containing 45	Zbtb45	0.39±0.13
zinc finger and BTB domain containing 5 (predicted)	Zbtb5_predicted	0.75±0.11
zinc finger and BTB domain containing 6	Zbtb6	0.23±0.07
zinc finger and BTB domain containing 7a	Zbtb7a	0.49±0.15
zinc finger and BTB domain containing 8 opposite strand (predicted)	Zbtb8os_predicted	3.36±0.37
zinc finger and SCAN domain containing 21	Zscan21	0.55±0.12
zinc finger and SCAN domains 20	Zscan20	0.61±0.1
zinc finger CCCH type containing 13	Zc3h13	0.71±0.12
zinc finger CCCH type containing 14	Zc3h14	3.65±0.41
zinc finger CCCH type containing 6 (predicted)	Zc3h6_predicted	0.24±0.07
zinc finger CCCH type containing 7 A (predicted)	Zc3h7a_predicted	1.35±0.14
zinc finger CCCH type containing 8	Zc3h8	1.07±0.21
zinc finger CCCH-type containing 15	Zc3h15	6.16±0.07
zinc finger CCCH-type containing 7B (predicted)	Zc3h7b_predicted	1.58±0.18
zinc finger CCHC-type and RNA binding motif 1	Zcrb1	1.43±0.09
zinc finger protein 105	Zfp105	0.6±0.08
zinc finger protein 110	Zfp110	2.1±0.16
zinc finger protein 124 (HZF-16) (predicted)	Znf124_predicted	0.33±0.02
zinc finger protein 131	Zfp131	0.74±0.27
zinc finger protein 143	Zfp143	0.67±0.11
zinc finger protein 148	Zfp148	2.48±0.11
zinc finger protein 157	Zfp157	0.54±0.02
zinc finger protein 161	Zfp161	0.24±0.03
zinc finger protein 180	Zfp180	2.37±0.43
zinc finger protein 189 (predicted)	Zfp189_predicted	0.32±0.18
zinc finger protein 191	Zfp191	0.61±0.08
zinc finger protein 207	Zfp207	3.04±0.31
Zinc finger protein 212	Zfp212	1±0.41
zinc finger protein 213 (predicted)	Znf213_predicted	0.38±0.02
zinc finger protein 213 (predicted) /// similar to Caspase-14 precursor (CASP-14)	LOC679178 /// LOC680728 /// Znf213_predicted	0.33±0.02
zinc finger protein 219	Zfp219	0.65±0.32
zinc finger protein 259	Zfp259	1.01±0.44
zinc finger protein 260	Zfp260	2.07±0.2
zinc finger protein 275 (predicted)	Zfp275_predicted	0.54±0.17
zinc finger protein 278	Zfp278	0.71±0.17
zinc finger protein 281	Zfp281	2.54±0.36
zinc finger protein 289	Zfp289	2.73±0.33
zinc finger protein 291	Znf291	0.43±0.11
zinc finger protein 292	Zfp292	0.88±0.14
zinc finger protein 294	Zfp294	3.02±0.55
zinc finger protein 297	Zfp297	0.46±0.07
zinc finger protein 313	Zfp313	0.73±0.12
zinc finger protein 316 (predicted)	Zfp316_predicted	0.32±0.11
zinc finger protein 329 (predicted)	Zfp329_predicted	0.4±0.05
zinc finger protein 330 (predicted)	Zfp330_predicted	4.21±0.58
zinc finger protein 335	Zfp335	0.43±0.19
zinc finger protein 346 (predicted)	Zfp346_predicted	0.77±0.14
zinc finger protein 347	Zfp347	0.71±0.13
zinc finger protein 354A	Zfp354a	15.77±2.85
zinc finger protein 358 (predicted)	Zfp358_predicted	0.87±0.16
zinc finger protein 36	Zfp36	1.57±0.91
zinc finger protein 36, C3H type-like 1	Zfp36l1	7.34±2.18
zinc finger protein 36, C3H type-like 2	Zfp36l2	0.94±0.73
zinc finger protein 362 /// zinc finger and SCAN domains 20	Zfp362 /// Zscan20	7.48±1.38
zinc finger protein 364 (predicted)	Zfp364_predicted	5.01±0.15
zinc finger protein 367	Zfp367	0.27±0.15
zinc finger protein 384	Zfp384	2.58±0.25
zinc finger protein 386 (Kruppel-like)	Zfp386	2.27±0.58
zinc finger protein 395 (predicted)	Zfp395_predicted	1.09±0.33
zinc finger protein 407	Zfp407	0.36±0.05
zinc finger protein 410 (predicted)	Zfp410_predicted	1.78±0.36
zinc finger protein 414	Zfp414	0.62±0.34
zinc finger protein 422	Zfp422	1.21±0.05
zinc finger protein 444 (predicted)	Zfp444_predicted	0.2±0.13
zinc finger protein 445	Zfp445	1.25±0.14
zinc finger protein 446 (predicted)	Zfp446_predicted	0.35±0.05
zinc finger protein 451	Zfp451	0.44±0.04
zinc finger protein 455	Zfp455	0.76±0.08
zinc finger protein 46 (predicted)	Zfp46_predicted	0.59±0.26
zinc finger protein 462	Zfp462	1.34±0.11
zinc finger protein 467	Zfp467	0.2±0.11
zinc finger protein 469 (predicted)	Zfp469_predicted	1.52±0.19
zinc finger protein 503 (predicted)	Zfp503_predicted	13.48±2.16
Zinc finger protein 507 (predicted)	Znf507_predicted	0.98±0.03

zinc finger protein 511	Zfp511	0.65±0.08
zinc finger protein 512	Zfp512	0.45±0.09
zinc finger protein 512B	Znf512b	0.7±0.17
zinc finger protein 513	Zfp513	1.42±0.17
zinc finger protein 524	Zfp524	1.08±0.1
zinc finger protein 533 (predicted)	Zfp533_predicted	0.62±0.28
zinc finger protein 541	Zfp541	0.83±0.19
zinc finger protein 553 /// zinc finger protein 771	Zfp553 /// Zfp771	2.09±0.55
zinc finger protein 574	Zfp574	0.48±0.13
zinc finger protein 580 (predicted)	Zfp580_predicted	0.28±0.18
zinc finger protein 592 (predicted)	Zfp592_predicted	0.56±0.07
zinc finger protein 598 (predicted)	Zfp598_predicted	0.96±0.25
zinc finger protein 609	Zfp609	0.52±0.15
zinc finger protein 61	Zfp61	0.46±0.14
zinc finger protein 612 (predicted)	Zfp612_predicted	0.24±0.09
zinc finger protein 618 (predicted)	Znf618_predicted	0.39±0.15
zinc finger protein 622	Zfp622	0.93±0.06
Zinc finger protein 637	Zfp637	1.28±0.14
zinc finger protein 644 (predicted)	Zfp644_predicted	1.54±0.06
zinc finger protein 653 (predicted)	Zfp653_predicted	0.59±0.05
zinc finger protein 654	Zfp654	1.03±0.09
zinc finger protein 655	Zfp655	3.65±0.38
zinc finger protein 667	Zfp667	0.34±0.07
zinc finger protein 672	Zfp672	0.89±0.11
zinc finger protein 68 (predicted)	Zfp68_predicted	1.16±0.29
zinc finger protein 688 (predicted)	Zfp688_predicted	0.58±0.07
zinc finger protein 692 (predicted)	Zfp692_predicted	0.37±0.01
zinc finger protein 706	Zfp706	9.4±0.65
zinc finger protein 709	Zfp709	0.22±0.16
zinc finger protein 771	Zfp771	0.37±0.14
zinc finger protein 777	Zfp777	0.23±0.16
zinc finger protein 787	Zfp787	1.37±0.03
zinc finger protein 821	Zfp821	0.33±0.2
zinc finger protein 828	Zfp828	0.9±0.11
zinc finger protein 84 (predicted)	Zfp84_predicted	0.43±0.12
zinc finger protein 91	Zfp91	3.86±0.17
zinc finger protein X-linked (predicted)	Zfx_predicted	0.68±0.12
zinc finger protein ZFP	LOC503192	1.05±0.13
zinc finger RNA binding protein	Zfr	5.38±0.76
zinc finger with KRAB and SCAN domains 1	Zkscan1	0.76±0.06
zinc finger with KRAB and SCAN domains 17	Zkscan17	1.66±0.21
zinc finger with KRAB and SCAN domains 3	Zkscan3	1.88±0.05
zinc finger with KRAB and SCAN domains 5	Zkscan5	0.85±0.19
zinc finger with KRAB and SCAN domains 6	Zkscan6	0.31±0.09
zinc finger with UFM1-specific peptidase domain	Zufsp	0.81±0.07
zinc finger, AN1-type domain 1	Zfand1	0.97±0.08
zinc finger, AN1-type domain 3	Zfand3	3.52±0.42
zinc finger, AN1-type domain 5	Zfand5	2.5±0.53
zinc finger, AN1-type domain 6	Zfand6	9.5±0.41
zinc finger, BED domain containing 3	Zbed3	2.1±0.49
zinc finger, BED domain containing 4 (predicted)	Zbed4_predicted	0.72±0.14
zinc finger, C3HC-type 1 (predicted)	Zc3hc1_predicted	0.36±0.18
zinc finger, CCCH-type with G patch domain	Zgpat	0.31±0.04
zinc finger, CCHC domain containing 10	Zcchc10	0.59±0.13
zinc finger, CCHC domain containing 11 (predicted)	Zcchc11_predicted	0.65±0.16
Zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted	0.85±0.09
zinc finger, CCHC domain containing 9	Zcchc9	1.83±0.12
zinc finger, DHHC domain containing 1	Zdhhc1	0.61±0.35
zinc finger, DHHC domain containing 13	Zdhhc13	0.93±0.31
zinc finger, DHHC domain containing 16	Zdhhc16	2.46±0.03
zinc finger, DHHC domain containing 2	Zdhhc2	1.06±0.22
zinc finger, DHHC domain containing 23	Zdhhc23	0.73±0.19
Zinc finger, DHHC domain containing 3	Zdhhc3	7.39±0.31
zinc finger, DHHC domain containing 4	Zdhhc4	2.06±0.11
zinc finger, DHHC domain containing 5	Zdhhc5	2.33±0.24
zinc finger, DHHC domain containing 6	Zdhhc6	2.4±0.2
zinc finger, DHHC domain containing 7	Zdhhc7	1.78±0.62
zinc finger, DHHC domain containing 9	Zdhhc9	8.15±1.18
zinc finger, DHHC-type containing 22	Zdhhc22	0.25±0.08
zinc finger, FYVE domain containing 1 (predicted)	Zfyve1_predicted	0.57±0.22
zinc finger, FYVE domain containing 16	Zfyve16	1.19±0.16
zinc finger, FYVE domain containing 20 (predicted)	Zfyve20_predicted	0.68±0.02
zinc finger, FYVE domain containing 21 (predicted)	Zfyve21_predicted	7.57±0.07
zinc finger, FYVE domain containing 26 (predicted)	Zfyve26_predicted	1.64±0.04
zinc finger, FYVE domain containing 27	Zfyve27	0.4±0.07
zinc finger, HIT domain containing 1 (predicted)	Znhit1_predicted	4.16±0.75
zinc finger, HIT domain containing 2 (predicted)	Znhit2_predicted	0.7±0.03
zinc finger, HIT type 3	Znhit3	1.21±0.14
zinc finger, matrin type 2	Zmat2	0.93±0.21
zinc finger, matrin type 3	Zmat3	0.65±0.22
zinc finger, matrin-like (predicted)	Zfml_predicted	2.2±0.36
zinc finger, MIZ-type containing 1	Zmiz1	0.75±0.77
zinc finger, MIZ-type containing 2	Zmiz2	0.43±0.34
zinc finger, MYM domain containing 1 (predicted)	Zmym1_predicted	0.71±0.12
zinc finger, MYM-type 2	Zmym2	2.59±0.09
zinc finger, MYM-type 3	Zmym3	0.23±0.1
zinc finger, MYM-type 4 (predicted)	Zmym4_predicted	0.77±0.04

zinc finger, MYM-type 6	Zmym6	1.37±0.22
zinc finger, MYND domain containing 11	Zmynd11	3.97±0.46
zinc finger, MYND domain containing 15 (predicted)	Zmynd15_predicted	0.8±0.11
zinc finger, RAN-binding domain containing 2	Zranb2	5.57±0.29
zinc finger, SWIM domain containing 1 (predicted)	Zswim1_predicted	0.81±0.17
zinc finger, SWIM domain containing 3 (predicted)	Zswim3_predicted	0.21±0.05
zinc finger, SWIM domain containing 4 (predicted)	Zswim4_predicted	0.48±0.19
zinc finger, SWIM domain containing 5 (predicted)	Zswim5_predicted	0.81±0.22
Zinc finger, ZZ-type with EF hand domain 1 (predicted)	Zzef1_predicted	0.87±0.07
Zinc fingers and homeoboxes 2	Zhx2	2.55±0.38
zinc fingers and homeoboxes protein 1	Zhx1	1.54±0.18
Zinc metallopeptidase, STE24 homolog (S. cerevisiae) (predicted)	Zmpste24_predicted	4.58±0.51
zinc ribbon domain containing, 1	Znrd1	1.64±0.16
ZUBR1	Rbaf600	1.32±0.24
ZW10 homolog (Drosophila), centromere/kinetochore protein	Zw10	1.09±0.06
ZW10 interactor	Zwint	12.09±1.06
Zwilch, kinetochore associated, homolog (Drosophila)	Zwilch	0.32±0.02
ZXD family zinc finger C	Zxdc	0.39±0.09
zyxin	Zyx	0.88±0.13