

Table S10. List of genes, which demonstrated decreased expression (fold change ≥ 1.5 and $p \leq 0.05$) in the differentiated cells from the late phase (day 7) when compared with the proliferating neurospheres

<u>Gene Symbol</u>	<u>Accession No.</u>	<u>Gene Definition</u>	<u>Fold Change</u>
0610007J10Rik	AK018717		0.51
0610010F05Rik	NM_027860		0.55
0610037L13Rik	NM_028754.2	RIKEN cDNA 0610037L13 gene (0610037L13Rik)	0.64
0910001A06Rik	NM_144846.4	RIKEN cDNA 0910001A06 gene (0910001A06Rik)	0.51
1100001F19Rik	XM_124187.1		0.61
1110001A07Rik	NM_025377.1	RIKEN cDNA 1110001A07 gene (1110001A07Rik)	0.65
1110001C20Rik	NM_177730		0.42
1110003F05Rik			0.35
1110007M04Rik	NM_026742.3	RIKEN cDNA 1110007M04 gene (1110007M04Rik)	0.35
1110008F13Rik	NM_026124.1	RIKEN cDNA 1110008F13 gene (1110008F13Rik)	0.45
1110012D08Rik	NM_178066.2	RIKEN cDNA 1110012D08 gene (1110012D08Rik)	0.47
1110018J23Rik	XM_140742.4		0.45
1110019N10Rik	NM_026753.1	RIKEN cDNA 1110019N10 gene (1110019N10Rik)	0.52
1110020P15Rik	NM_197979.2	RIKEN cDNA 1110020P15 gene (1110020P15Rik)	0.65
1110038B12Rik	XM_922038.2	PREDICTED: RIKEN cDNA 1110038B12 gene, transcript variant 6 (1110038B12Rik)	0.48
1110038D17Rik	NM_175133.1	RIKEN cDNA 1110038D17 gene (1110038D17Rik)	0.66
1110067D22Rik	NM_173752.3	RIKEN cDNA 1110067D22 gene (1110067D22Rik)	0.48
1110070O15Rik	AK075684		0.63
1190002F15Rik			0.53
1190009E20Rik			0.54
1200003C05Rik	NM_024205.1	RIKEN cDNA 1200003C05 gene (1200003C05Rik)	0.48
1500001M20Rik	NM_026894.1	RIKEN cDNA 1500001M20 gene (1500001M20Rik)	0.54
1500012F01Rik	NM_001081005.1	RIKEN cDNA 1500012F01 gene (1500012F01Rik)	0.48
1500032D16Rik	NM_001083891.1	RIKEN cDNA 1500032D16 gene (1500032D16Rik), transcript variant 2	0.66
1500034J01Rik	XM_912953.3	PREDICTED: RIKEN cDNA 1500034J01 gene (1500034J01Rik)	0.66
1600012H06Rik	NM_001083882.1	RIKEN cDNA 1600012H06 gene (1600012H06Rik), transcript variant 4	0.61
1700011E24Rik	XM_128789.5	PREDICTED: RIKEN cDNA 1700011E24 gene, transcript variant 2 (1700011E24Rik)	0.22
1700013A01Rik	AK005934		0.65
1700021F05Rik	NM_026411.1	RIKEN cDNA 1700021F05 gene (1700021F05Rik)	0.67
1700025G04Rik	NM_197990.2	RIKEN cDNA 1700025G04 gene (1700025G04Rik)	0.31
1700027M01Rik	NM_023544		0.66
1700029F09Rik	XM_919077.2	PREDICTED: RIKEN cDNA 1700029F09 gene, transcript variant 20 (1700029F09Rik)	0.37
1700037H04Rik	NM_026091.2	RIKEN cDNA 1700037H04 gene (1700037H04Rik)	0.66
1700041B20Rik	XM_485065		0.52
1700052N19Rik	NM_024261.2	RIKEN cDNA 1700052N19 gene (1700052N19Rik)	0.65
1700086L19Rik	XM_358420.3	PREDICTED: RIKEN cDNA 1700086L19 gene (1700086L19Rik)	0.53
1700113I22Rik	NM_026865.2	RIKEN cDNA 1700113I22 gene (1700113I22Rik)	0.48
1810006K21Rik	XM_983803.1	PREDICTED: RIKEN cDNA 1810006K21 gene (1810006K21Rik)	0.60
1810022K09Rik	XM_485210		0.60
1810055G02Rik	NM_028077.2	RIKEN cDNA 1810055G02 gene (1810055G02Rik)	0.41
1810074P20Rik	NM_026194.3	RIKEN cDNA 1810074P20 gene (1810074P20Rik)	0.66
2010003J03Rik	NM_027236.1	RIKEN cDNA 2010003J03 gene (2010003J03Rik)	0.63
2010107E04Rik	NM_027360.2	RIKEN cDNA 2010107E04 gene (2010107E04Rik)	0.60
2010309L07Rik			0.65
2010317E24Rik	XM_130053.2		0.48
2010321I05Rik			0.58
2010321M09Rik	NM_175153.3	RIKEN cDNA 2010321M09 gene (2010321M09Rik), transcript variant 1	0.59
2210412D01Rik	NM_133722.1	RIKEN cDNA 2210412D01 gene (2210412D01Rik)	0.59
2300002D11Rik	NM_001081156.1	RIKEN cDNA 2300002D11 gene (2300002D11Rik)	0.62
2310003L22Rik	NM_027093.3	RIKEN cDNA 2310003L22 gene (2310003L22Rik)	0.62
2310005E10Rik	NM_172398.3	RIKEN cDNA 2310005E10 gene (2310005E10Rik)	0.44
2310008M10Rik	NM_025509.2	RIKEN cDNA 2310008M10 gene (2310008M10Rik)	0.62
2310009B15Rik	NM_001081226.1	RIKEN cDNA 2310009B15 gene (2310009B15Rik)	0.59
2310011G17Rik			0.62
2310014H01Rik	XM_001003622.2	PREDICTED: RIKEN cDNA 2310014H01 gene, transcript variant 3 (2310014H01Rik)	0.36
2310016C08Rik	NM_023516.3	RIKEN cDNA 2310016C08 gene (2310016C08Rik)	0.41
2310036D04Rik	XM_488563		0.60
2310037I24Rik	NM_133714.2	RIKEN cDNA 2310037I24 gene (2310037I24Rik)	0.62
2310039H08Rik	NM_025966.3	RIKEN cDNA 2310039H08 gene (2310039H08Rik)	0.64
2310044H10Rik	NM_197991		0.62
2310045K21Rik	AK009823		0.53
2400010C15Rik	AK010307		0.60

2410003K15Rik	XM_132537.3		0.42
2410006H16Rik	XM_001479267.1	PREDICTED: RIKEN cDNA 2410006H16 gene (2410006H16Rik)	0.65
2410015N17Rik	NM_023203.1	RIKEN cDNA 2410015N17 gene (2410015N17Rik)	0.33
2410016O06Rik	NM_023633		0.63
2510009E07Rik	NM_001001881.1	RIKEN cDNA 2510009E07 gene (2510009E07Rik)	0.45
2600005C20Rik	NM_028244		0.44
2610002D18Rik	XM_131720.2		0.65
2610017I09Rik	XR_035175.1	PREDICTED: RIKEN cDNA 2610017I09 gene (2610017I09Rik), misc RNA.	0.46
2610019E17Rik			0.44
2610024B07Rik			0.45
2610024G14Rik	NM_019836.2	RIKEN cDNA 2610024G14 gene (2610024G14Rik)	0.52
2610024H22Rik			0.61
2610029G23Rik	NM_026312.2	RIKEN cDNA 2610029G23 gene (2610029G23Rik)	0.57
2610036L11Rik	XM_488549.3	PREDICTED: RIKEN cDNA 2610036L11 gene, transcript variant 1 (2610036L11Rik)	0.27
2610039C10Rik	NM_025642.1	RIKEN cDNA 2610039C10 gene (2610039C10Rik)	0.34
2610101N10Rik	NM_026476.1	RIKEN cDNA 2610101N10 gene (2610101N10Rik)	0.64
2610103J23Rik	NM_026002		0.62
2610207P08Rik	XM_127746.2		0.47
2610307O08Rik	XM_921606.2	PREDICTED: RIKEN cDNA 2610307O08 gene, transcript variant 12 (2610307O08Rik)	0.30
2610510J17Rik	NM_028131.1	RIKEN cDNA 2610510J17 gene (2610510J17Rik)	0.38
2700029M09Rik	XM_001474993.1	PREDICTED: RIKEN cDNA 2700029M09 gene (2700029M09Rik)	0.50
2700055A20Rik	NM_027314		0.66
2700092H06Rik	XM_132529.2		0.65
2700094K13Rik	NM_001037279.1	RIKEN cDNA 2700094K13 gene (2700094K13Rik), transcript variant 2	0.16
2810025M15Rik	XR_035184.1	PREDICTED: RIKEN cDNA 2810025M15 gene (2810025M15Rik), misc RNA.	0.37
2810026P18Rik			0.63
2810405J04Rik	NM_133747.2	RIKEN cDNA 2810405J04 gene (2810405J04Rik)	0.49
2810417H13Rik	NM_026515.2	RIKEN cDNA 2810417H13 gene (2810417H13Rik)	0.15
2810417K24Rik	AK013109		0.37
2810423A18Rik			0.62
2810452K22Rik	NM_026048.2	RIKEN cDNA 2810452K22 gene (2810452K22Rik)	0.62
2900010M23Rik	NM_026063.1	RIKEN cDNA 2900010M23 gene (2900010M23Rik)	0.65
2900056M07Rik	AK013705		0.62
2900060B14Rik			0.56
2900060P06Rik			0.39
2900072M03Rik			0.53
3000004C01Rik	NM_197959.1	RIKEN cDNA 3000004C01 gene (3000004C01Rik)	0.40
3010015K02Rik			0.67
3110009E18Rik	NM_028439.1	RIKEN cDNA 3110009E18 gene (3110009E18Rik)	0.48
3110013H01Rik	XM_203393.1		0.48
3110035E14Rik	NM_178399.4	RIKEN cDNA 3110035E14 gene (3110035E14Rik)	0.60
3110043A19Rik	XM_001476479.1	PREDICTED: RIKEN cDNA 3110043A19 gene (3110043A19Rik)	0.55
3300001G02Rik	NM_030093.1	RIKEN cDNA 3300001G02 gene (3300001G02Rik)	0.63
3632451O06Rik	NM_026142.1	RIKEN cDNA 3632451O06 gene (3632451O06Rik)	0.33
3830612M24			0.14
3930401E15Rik	AK076210		0.60
4631422C13Rik	XM_984472.1	PREDICTED: RIKEN cDNA 4631422C13 gene (4631422C13Rik)	0.64
4631427C17Rik	NM_021414.3	RIKEN cDNA 4631427C17 gene (4631427C17Rik)	0.65
4632417K18Rik	NM_026640.2	RIKEN cDNA 4632417K18 gene (4632417K18Rik)	0.27
4833424O15Rik	NM_029425.1	RIKEN cDNA 4833424O15 gene (4833424O15Rik)	0.44
4833426J09Rik			0.66
4833427B12Rik	XM_195728		0.58
4930427A07Rik	NM_134041.2	RIKEN cDNA 4930427A07 gene (4930427A07Rik)	0.64
4930430F08Rik	NM_175128		0.67
4930487N19Rik	AK015640		0.65
4930547N16Rik	NM_029249.2	RIKEN cDNA 4930547N16 gene (4930547N16Rik)	0.54
4930572J05Rik	NM_198607.1	RIKEN cDNA 4930572J05 gene (4930572J05Rik)	0.46
4932417H02Rik	NM_028898.2	RIKEN cDNA 4932417H02 gene (4932417H02Rik)	0.57
4933401P20Rik	AK016608		0.58
4933407C03Rik	XM_001004724.2	PREDICTED: RIKEN cDNA 4933407C03 gene, transcript variant 6 (4933407C03Rik)	0.49
4933407N01Rik	NM_025745.2		0.66
4933407P14Rik	NM_199019.1		0.60
4933427G23Rik	XR_005167.1	PREDICTED: RIKEN cDNA 4933427G23 gene (4933427G23Rik), misc RNA.	0.60
4933428A15Rik	NM_027756		0.60
5430417J04Rik	AK030671		0.61
5530401N12Rik			0.39
5730410I19Rik	NM_025666.1	RIKEN cDNA 5730410I19 gene (5730410I19Rik)	0.62
5730427N09Rik	NM_021552.4	RIKEN cDNA 5730427N09 gene (5730427N09Rik)	0.44

<i>5730494J16Rik</i>	AK077637		0.34
<i>5830411I20</i>			0.36
<i>5930416I19Rik</i>	NM_197981.1	RIKEN cDNA 5930416I19 gene (5930416I19Rik)	0.51
<i>6030405A18</i>	NM_177854		0.56
<i>6030405A18Rik</i>	NM_177854.2	RIKEN cDNA 6030405A18 gene (6030405A18Rik)	0.47
<i>6230416J20Rik</i>	NM_173400		0.64
<i>6330509M05Rik</i>			0.66
<i>6330549D23Rik</i>	NR_003619.1	RIKEN cDNA 6330549D23 gene (6330549D23Rik), non-coding RNA.	0.59
<i>6330569M22Rik</i>	NM_153563.1	RIKEN cDNA 6330569M22 gene (6330569M22Rik)	0.62
<i>6330578E17Rik</i>	NM_198006.3	RIKEN cDNA 6330578E17 gene (6330578E17Rik)	0.50
<i>6332401O19Rik</i>	NM_177013.3	RIKEN cDNA 6332401O19 gene (6332401O19Rik)	0.60
<i>6430402L23Rik</i>	AK078178		0.46
<i>6430527G18Rik</i>	NM_145836.1	RIKEN cDNA 6430527G18 gene (6430527G18Rik)	0.44
<i>6430537F04</i>			0.31
<i>6430706D22Rik</i>	NM_198652.1	RIKEN cDNA 6430706D22 gene (6430706D22Rik)	0.40
<i>6530401D06Rik</i>	AK018306		0.66
<i>6530418L21Rik</i>	NM_175398.3	RIKEN cDNA 6530418L21 gene (6530418L21Rik)	0.40
<i>6720458F09Rik</i>	NM_177374.2	RIKEN cDNA 6720458F09 gene (6720458F09Rik)	0.52
<i>6720460F02Rik</i>	NM_144526.2	RIKEN cDNA 6720460F02 gene (6720460F02Rik)	0.66
<i>6720463M24Rik</i>	NM_175265.4	RIKEN cDNA 6720463M24 gene (6720463M24Rik)	0.48
<i>8030402P03Rik</i>	AK078743		0.62
<i>9030024J15Rik</i>			0.48
<i>9330134C04Rik</i>	NM_001013608.1	RIKEN cDNA 9330134C04 gene (9330134C04Rik)	0.64
<i>9430008C03Rik</i>	XM_001004952.1	PREDICTED: RIKEN cDNA 9430008C03 gene (9430008C03Rik)	0.65
<i>9430065L19Rik</i>	AK034952		0.51
<i>9430080K19Rik</i>			0.46
<i>9530018I07Rik</i>			0.49
<i>9530058B02Rik</i>	NM_026633.1	RIKEN cDNA 9530058B02 gene (9530058B02Rik)	0.64
<i>9530064J02</i>	XM_489200		0.13
<i>9830001H06Rik</i>	XM_283804.7	PREDICTED: RIKEN cDNA 9830001H06 gene (9830001H06Rik)	0.66
<i>9930014A18Rik</i>	NM_177166.2		0.60
<i>A230046K03Rik</i>	NM_001033375.2	RIKEN cDNA A230046K03 gene (A230046K03Rik)	0.61
<i>A230079E18Rik</i>	AK038962		0.47
<i>A830059I20Rik</i>	NM_021427.1		0.32
<i>A930030J18Rik</i>	AK044660		0.53
<i>AA960436</i>	NM_133954.1	expressed sequence AA960436 (AA960436)	0.60
<i>Aadacl1</i>	NM_178772.2	arylacetamide deacetylase-like 1 (Aadacl1)	0.63
<i>Aard</i>	NM_175503.3	alanine and arginine rich domain containing protein (Aard)	0.32
<i>Aars</i>	NM_146217.3	alanyl-tRNA synthetase (Aars)	0.48
<i>Aatk</i>	NM_007377.3	apoptosis-associated tyrosine kinase (Aatk)	0.20
<i>Abcb7</i>	XM_907304.2	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 7, transcript variant 5 (Abcb7)	0.47
<i>Abcf1</i>	NM_013854.1	ATP-binding cassette, sub-family F (GCN20), member 1 (Abcf1)	0.66
<i>Abcf2</i>	NM_013853.1	ATP-binding cassette, sub-family F (GCN20), member 2 (Abcf2), nuclear gene encoding mitochondrial protein	0.63
<i>Abi2</i>	NM_198127.1	abl-interactor 2 (Abi2)	0.46
<i>Acadl</i>	NM_007381.3	acyl-Coenzyme A dehydrogenase, long-chain (Acadl), nuclear gene encoding mitochondrial protein	0.47
<i>Acads</i>	NM_007383.2	acyl-Coenzyme A dehydrogenase, short chain (Acads), nuclear gene encoding mitochondrial protein	0.59
<i>Acap3</i>	NM_207223.1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3 (Acap3)	0.39
<i>Acat2</i>	NM_009338.3	acetyl-Coenzyme A acetyltransferase 2 (Acat2)	0.39
<i>Acbd3</i>	NM_133225.2	acyl-Coenzyme A binding domain containing 3 (Acbd3)	0.65
<i>Acly</i>	NM_134037.2	ATP citrate lyase (Acly)	0.46
<i>Acn9</i>	XM_355744.1		0.64
<i>Aco2</i>	NM_080633.2	aconitase 2, mitochondrial (Aco2), nuclear gene encoding mitochondrial protein	0.51
<i>Acot7</i>	NM_133348.1	acyl-CoA thioesterase 7 (Acot7)	0.51
<i>Acpl2</i>	NM_153420.2	acid phosphatase-like 2 (Acpl2)	0.54
<i>Acsbg1</i>	NM_053178.2	acyl-CoA synthetase bubblegum family member 1 (Acsbg1)	0.36
<i>Acsl5</i>	NM_027976.2	acyl-CoA synthetase long-chain family member 5 (Acsl5)	0.43
<i>Acss2</i>	NM_019811.3	acyl-CoA synthetase short-chain family member 2 (Acss2)	0.51
<i>Actb</i>	NM_007393.1	actin, beta, cytoplasmic (Actb)	0.44
<i>Actl6a</i>	NM_019673.1	actin-like 6A (Actl6a)	0.53
<i>Actr3</i>	NM_023735.1	ARP3 actin-related protein 3 homolog (yeast) (Actr3)	0.56
<i>Acy1</i>	NM_025371.1	aminoacylase 1 (Acy1)	0.67
<i>Adam12</i>	NM_007400.2	a disintegrin and metallopeptidase domain 12 (meltrin alpha) (Adam12)	0.19
<i>Adam15</i>	NM_009614.2	a disintegrin and metallopeptidase domain 15 (metargidin) (Adam15), transcript variant 2	0.60
<i>Adam17</i>	NM_009615.5	a disintegrin and metallopeptidase domain 17 (Adam17)	0.53

<i>Adamts19</i>	NM_175506.3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19 (Adamts19)	0.38
<i>Adamts4</i>	NM_172845.1		0.35
<i>Adm</i>	NM_009627.1	adrenomedullin (Adm)	0.51
<i>Adnp</i>	NM_009628.2	activity-dependent neuroprotective protein (Adnp)	0.62
<i>Adpgk</i>	NM_028121.1		0.57
<i>Adrb2</i>	NM_007420.2	adrenergic receptor, beta 2 (Adrb2)	0.54
<i>Adsl</i>	NM_009634		0.62
<i>Aes</i>	NM_010347.2	amino-terminal enhancer of split (Aes)	0.41
<i>Afg31</i>	NM_054070.2	AFG3(ATPase family gene 3)-like 1 (yeast) (Afg31)	0.63
<i>Agap1</i>	NM_001037136.1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (Agap1), transcript variant 2	0.60
<i>Agfg2</i>	NM_178162.2	ArfGAP with FG repeats 2 (Agfg2), transcript variant 2	0.66
<i>Ahctf1</i>	NM_026375.1	AT hook containing transcription factor 1 (Ahctf1)	0.56
<i>Ahcy</i>	NM_016661		0.52
<i>Ahcyl1</i>	NM_145542.3	S-adenosylhomocysteine hydrolase-like 1 (Ahcyl1)	0.60
<i>AI413582</i>	NM_001002895.2	expressed sequence AI413582 (AI413582)	0.60
<i>AI448196</i>	XM_136041.3		0.48
<i>AI464131</i>	NM_001085515.1	expressed sequence AI464131 (AI464131)	0.62
<i>AI481316</i>	XM_148986.1		0.39
<i>AI593442</i>	NM_177907.2	expressed sequence AI593442 (AI593442), transcript variant 1	0.50
<i>AI851790</i>	NM_182807.2	expressed sequence AI851790 (AI851790)	0.50
<i>Ak2</i>	NM_001033966.3	adenylate kinase 2 (Ak2), transcript variant 1	0.57
<i>Akap12</i>	NM_031185.2	A kinase (PRKA) anchor protein (gravin) 12 (Akap12)	0.09
<i>Akap7</i>	NM_018747.3	A kinase (PRKA) anchor protein 7 (Akap7)	0.42
<i>Akirin1</i>	NM_023423.3	akirin 1 (Akirin1)	0.65
<i>Alad</i>	NM_008525.3	aminolevulinic acid, delta-, dehydratase (Alad)	0.58
<i>Aldh18a1</i>	NM_019698.1	aldehyde dehydrogenase 18 family, member A1 (Aldh18a1), nuclear gene encoding mitochondrial protein, transcript variant 1	0.42
<i>Aldh1a3</i>	AK043530		0.57
<i>Alg6</i>	NM_001081264.1	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase) (Alg6)	0.66
<i>Alg8</i>	NM_199035.1	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3,-glucosyltransferase) (Alg8)	0.53
<i>Alg9</i>	NM_133981.1	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase) (Alg9)	0.62
<i>Alkbh3</i>	NM_026944.1	alkB, alkylation repair homolog 3 (E. coli) (Alkbh3)	0.63
<i>Als2</i>	NM_028717.2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human) (Als2)	0.66
<i>Amot1</i>	NM_001081395.1	angiomin-like 1 (Amot1)	0.41
<i>Amph</i>	NM_175007.1	amphiphysin (Amph)	0.54
<i>Anapc5</i>	NM_021505.2	anaphase-promoting complex subunit 5 (Anapc5), transcript variant 1	0.61
<i>Angpt2</i>	NM_007426.3	angiopoietin 2 (Angpt2)	0.04
<i>Ank3</i>	NM_170687.3	ankyrin 3, epithelial (Ank3), transcript variant 6	0.22
<i>Ankrd49</i>	NM_019683.3	ankyrin repeat domain 49 (Ankrd49)	0.59
<i>Anln</i>	NM_028390.2	anillin, actin binding protein (Anln)	0.22
<i>Anp32e</i>	NM_023210.3	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E (Anp32e)	0.34
<i>Ap2b1</i>	NM_001035854.2	adaptor-related protein complex 2, beta 1 subunit (Ap2b1), transcript variant 1	0.52
<i>Apex1</i>	NM_009687.1	apurinic/apyrimidinic endonuclease 1 (Apex1)	0.65
<i>Apitd1</i>	NM_027263.1	apoptosis-inducing, TAF9-like domain 1 (Apitd1)	0.66
<i>Appbp2</i>	NM_025825		0.54
<i>Appl1</i>	NM_145221.2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1 (Appl1)	0.65
<i>Aprin</i>	NM_175310.5	androgen-induced proliferation inhibitor (Aprin)	0.46
<i>Arc</i>	NM_018790.2	activity regulated cytoskeletal-associated protein (Arc)	0.56
<i>Ard1</i>	NM_019870.1		0.59
<i>Ard1a</i>	NM_019870.2	ARD1 homolog A, N-acetyltransferase (S. cerevisiae) (Ard1a)	0.43
<i>Areg</i>	NM_009704.3	amphiregulin (Areg)	0.24
<i>Arf6</i>	NM_007481.3	ADP-ribosylation factor 6 (Arf6)	0.56
<i>Arhgap18</i>	NM_176837.2	Rho GTPase activating protein 18 (Arhgap18)	0.23
<i>Arhgap20</i>	NM_175535.3	Rho GTPase activating protein 20 (Arhgap20)	0.64
<i>Arih1</i>	NM_019927.1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) (Arih1)	0.64
<i>Arl4c</i>	NM_177305.3	ADP-ribosylation factor-like 4C (Arl4c)	0.63
<i>Armxc2</i>	NM_026139.3	armadillo repeat containing, X-linked 2 (Armxc2)	0.63
<i>Arpc1b</i>	NM_023142.1	actin related protein 2/3 complex, subunit 1B (Arpc1b)	0.33
<i>Arpc3</i>	NM_019824.3	actin related protein 2/3 complex, subunit 3 (Arpc3)	0.45
<i>Arpp21</i>	NM_028755.2	cyclic AMP-regulated phosphoprotein, 21 (Arpp21), transcript variant 1	0.46
<i>Asah1</i>	NM_019734.1	N-acylsphingosine amidohydrolase 1 (Asah1)	0.37
<i>Asb1</i>	NM_023046.4	ankyrin repeat and SOCS box-containing 1 (Asb1), transcript variant 2	0.65

<i>Ascc3</i>	XM_125617.7	PREDICTED: activating signal cointegrator 1 complex subunit 3, transcript variant 1 (<i>Ascc3</i>)	0.66
<i>Asns</i>	NM_012055.1	asparagine synthetase (<i>Asns</i>)	0.51
<i>Aspm</i>	NM_009791.4	asp (abnormal spindle)-like, microcephaly associated (<i>Drosophila</i>) (<i>Aspm</i>)	0.35
<i>Atad1</i>	NM_026487.3	ATPase family, AAA domain containing 1 (<i>Atad1</i>)	0.64
<i>Atad3a</i>	NM_179203.1	ATPase family, AAA domain containing 3A (<i>Atad3a</i>)	0.59
<i>Atf4</i>	NM_009716.2	activating transcription factor 4 (<i>Atf4</i>)	0.55
<i>Atf7ip</i>	NM_019426.2	activating transcription factor 7 interacting protein (<i>Atf7ip</i>)	0.52
<i>Atic</i>	NM_026195.1	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (<i>Atic</i>)	0.58
<i>Atp13a3</i>	XM_001480958.1	PREDICTED: ATPase type 13A3, transcript variant 1 (<i>Atp13a3</i>)	0.59
<i>Atp1b3</i>	NM_007502.3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide (<i>Atp1b3</i>)	0.57
<i>Atp5a1</i>	NM_007505.2	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 (<i>Atp5a1</i>), nuclear gene encoding mitochondrial protein	0.57
<i>Atp5c1</i>	NM_020615.3	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1 (<i>Atp5c1</i>)	0.63
<i>Atp5d</i>	NM_025313.1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (<i>Atp5d</i>)	0.57
<i>Atp5f1</i>	NM_009725.3	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 (<i>Atp5f1</i>), nuclear gene encoding mitochondrial protein	0.56
<i>Atp5g2</i>	NM_026468.1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (<i>Atp5g2</i>)	0.63
<i>Atp5g3</i>	NM_175015.2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3 (<i>Atp5g3</i>), nuclear gene encoding mitochondrial protein	0.66
<i>Atp5j</i>	NM_016755.2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F (<i>Atp5j</i>), nuclear gene encoding mitochondrial protein	0.64
<i>Atp5l</i>	NM_013795.4	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit g (<i>Atp5l</i>), nuclear gene encoding mitochondrial protein	0.57
<i>Atp5o</i>	NM_138597.2	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (<i>Atp5o</i>), nuclear gene encoding mitochondrial protein	0.61
<i>Atp6v0a1</i>	NM_016920.1		0.66
<i>AU022870</i>	NM_177682.3	expressed sequence AU022870 (AU022870)	0.63
<i>AU040320</i>	NM_133886.2	expressed sequence AU040320 (AU040320), transcript variant 3	0.50
<i>Aurka</i>	NM_011497.3	aurora kinase A (<i>Aurka</i>)	0.18
<i>Aurkaip1</i>	NM_025338.3	aurora kinase A interacting protein 1 (<i>Aurkaip1</i>)	0.63
<i>Aurkb</i>	NM_011496.1	aurora kinase B (<i>Aurkb</i>)	0.25
<i>AW120700</i>			0.38
<i>B230114H05Rik</i>	AK045406		0.53
<i>B230208H17Rik</i>	NM_001024616.1	RIKEN cDNA B230208H17 gene (B230208H17Rik)	0.62
<i>B230343A10Rik</i>			0.46
<i>B3galt6</i>	NM_080445.4	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6 (<i>B3galt6</i>)	0.49
<i>B3gnt5</i>	NM_054052.2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (<i>B3gnt5</i>)	0.58
<i>B4galt3</i>	NM_020579.1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 (<i>B4galt3</i>)	0.54
<i>Bahcc1</i>	NM_198423.2	BAH domain and coiled-coil containing 1 (<i>Bahcc1</i>)	0.42
<i>Bai2</i>	NM_173071.1	brain-specific angiogenesis inhibitor 2 (<i>Bai2</i>)	0.49
<i>Banf1</i>	NM_001038231.1	barrier to autointegration factor 1 (<i>Banf1</i>), transcript variant 2	0.28
<i>BC002199</i>	NM_145964.2	cDNA sequence BC002199 (BC002199)	0.60
<i>BC003236</i>	NM_030249		0.47
<i>BC003885</i>	NM_198609.2	cDNA sequence BC003885 (BC003885)	0.60
<i>BC003965</i>	XM_128528.2		0.55
<i>BC017647</i>	NM_145430.1	cDNA sequence BC017647 (BC017647)	0.47
<i>BC024659</i>	XM_001472442.1	PREDICTED: cDNA sequence BC024659 (BC024659)	0.58
<i>BC025076</i>	NM_175002.1		0.55
<i>BC026590</i>	NM_001081420.1	cDNA sequence BC026590 (BC026590)	0.67
<i>BC031781</i>	NM_145943.1	cDNA sequence BC031781 (BC031781)	0.66
<i>BC046331</i>	NM_177673.2	cDNA sequence BC046331 (BC046331)	0.61
<i>BC046404</i>	NM_198861.1	cDNA sequence BC046404 (BC046404)	0.57
<i>BC060632</i>	NM_198625.1	cDNA sequence BC060632 (BC060632)	0.59
<i>BC067047</i>	NM_177782.3	cDNA sequence BC067047 (BC067047)	0.42
<i>BC085271</i>	NM_001008551.1	cDNA sequence BC085271 (BC085271)	0.44
<i>Bcan</i>	NM_007529.1	brevican (<i>Bcan</i>)	0.42
<i>Bcas1</i>	NM_029815.1	breast carcinoma amplified sequence 1 (<i>Bcas1</i>)	0.32
<i>Bccip</i>	NM_025392.1	BRCA2 and CDKN1A interacting protein (<i>Bccip</i>)	0.63
<i>Bcl7c</i>	NM_009746.2	B-cell CLL/lymphoma 7C (<i>Bcl7c</i>)	0.57
<i>Bdnf</i>	NM_001048141.1	brain derived neurotrophic factor (<i>Bdnf</i>), transcript variant 3	0.55
<i>Bex2</i>	XM_977338.1	PREDICTED: brain expressed X-linked 2 (<i>Bex2</i>)	0.22
<i>Bhlhb9</i>	NM_198161.1	basic helix-loop-helix domain containing, class B9 (<i>Bhlhb9</i>)	0.61
<i>Bicd2</i>	NM_029791		0.57
<i>Bin1</i>	NM_009668.1	bridging integrator 1 (<i>Bin1</i>)	0.60
<i>Birc5</i>	NM_009689.2	baculoviral IAP repeat-containing 5 (<i>Birc5</i>), transcript variant 1	0.30

<i>Blm</i>	NM_007550.3	Bloom syndrome homolog (human) (Blm), transcript variant 1	0.39
<i>Bloc1s2</i>	XM_193940.2		0.63
<i>Bmp7</i>	NM_007557.2	bone morphogenetic protein 7 (Bmp7)	0.64
<i>Bmper</i>	NM_028472.1	BMP-binding endothelial regulator (Bmper)	0.51
<i>Bnip2</i>	NM_001008238.2	BCL2/adenovirus E1B interacting protein 2 (Bnip2), transcript variant alpha	0.47
<i>Bok</i>	NM_016778		0.35
<i>Bola2</i>	NM_175103.2	bolA-like 2 (E. coli) (Bola2)	0.59
<i>Bola3</i>	NM_175277.2	bolA-like 3 (E. coli) (Bola3)	0.65
<i>Bop1</i>	NM_013481.1	block of proliferation 1 (Bop1)	0.66
<i>Bpnt1</i>	NM_011794.3	bisphosphate 3'-nucleotidase 1 (Bpnt1)	0.56
<i>Brd2</i>	NM_001025387.2	bromodomain containing 2 (Brd2), transcript variant 2	0.61
<i>Brd3</i>	NM_023336		0.65
<i>Brip1</i>	NM_178309.1	BRCA1 interacting protein C-terminal helicase 1 (Brip1)	0.62
<i>Brp17</i>	NM_019999.1		0.53
<i>Brn1</i>	NM_144818		0.20
<i>Btaf1</i>	NM_001080706.1	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae) (Btaf1)	0.66
<i>Btbd11</i>	NM_001017525.1	BTB (POZ) domain containing 11 (Btbd11), transcript variant 2	0.38
<i>Btbd12</i>	NM_177472.4	BTB (POZ) domain containing 12 (Btbd12)	0.67
<i>Btf3</i>	NM_145455.1		0.56
<i>Btg1</i>	NM_007569.1	B-cell translocation gene 1, anti-proliferative (Btg1)	0.54
<i>Bub1b</i>	NM_009773		0.17
<i>Bves</i>	NM_024285		0.43
<i>Bxdc1</i>	NM_023323		0.56
<i>Bxdc2</i>	NM_026396.2	brix domain containing 2 (Bxdc2)	0.53
<i>Bxdc5</i>	NM_027371.2	brix domain containing 5 (Bxdc5), transcript variant 2	0.57
<i>Bzw1</i>	NM_025824		0.42
<i>Bzw2</i>	NM_025840.2	basic leucine zipper and W2 domains 2 (Bzw2)	0.38
<i>C030003D03Rik</i>	NM_029881.2	RIKEN cDNA C030003D03 gene (C030003D03Rik)	0.38
<i>C130007D14</i>	NM_177914.1		0.59
<i>C130020C13Rik</i>			0.63
<i>C130032J12Rik</i>	NM_178684.3	RIKEN cDNA C130032J12 gene (C130032J12Rik)	0.56
<i>C1galt1c1</i>	NM_021550.2	C1GALT1-specific chaperone 1 (C1galt1c1)	0.61
<i>C230043G09Rik</i>	AK048752		0.60
<i>C230053B09Rik</i>	AK048765		0.60
<i>C230071H18Rik</i>	NM_207265.2	RIKEN cDNA C230071H18 gene (C230071H18Rik)	0.60
<i>C230078M08Rik</i>	NM_176995.2	RIKEN cDNA C230078M08 gene (C230078M08Rik)	0.62
<i>C330006P03Rik</i>			0.41
<i>C330023M02Rik</i>	NM_172722		0.58
<i>C530008M17Rik</i>	XM_916109.2	PREDICTED: RIKEN cDNA C530008M17 gene, transcript variant 3 (C530008M17Rik)	0.25
<i>C730026E21Rik</i>	NM_175439		0.66
<i>C730029F17Rik</i>	AK050233		0.59
<i>C78339</i>	XM_127312		0.53
<i>C79267</i>	NM_183148		0.56
<i>C79407</i>	NM_172578.2	expressed sequence C79407 (C79407)	0.46
<i>C80913</i>	NM_011274.4	expressed sequence C80913 (C80913)	0.62
<i>C920004C08Rik</i>			0.21
<i>Cacna1h</i>	NM_021415.3	calcium channel, voltage-dependent, T type, alpha 1H subunit (Cacna1h)	0.39
<i>Cacna2d1</i>	NM_009784.1	calcium channel, voltage-dependent, alpha2/delta subunit 1 (Cacna2d1)	0.66
<i>Cacng5</i>	NM_080644.3	calcium channel, voltage-dependent, gamma subunit 5 (Cacng5)	0.57
<i>Calm2</i>	NM_007589.4	calmodulin 2 (Calm2)	0.29
<i>Calr</i>	NM_007591.3	calreticulin (Calr)	0.53
<i>Calu</i>	NM_007594.3	calumenin (Calu), transcript variant 1	0.34
<i>Camk1</i>	NM_133926.2	calcium/calmodulin-dependent protein kinase I (Camk1)	0.64
<i>Camk2b</i>	NM_007595.3	calcium/calmodulin-dependent protein kinase II, beta (Camk2b)	0.16
<i>Camk2n2</i>	XM_990809.1	PREDICTED: calcium/calmodulin-dependent protein kinase II inhibitor 2 (Camk2n2)	0.55
<i>Camkk2</i>	NM_145358.1	calcium/calmodulin-dependent protein kinase kinase 2, beta (Camkk2)	0.52
<i>Camta1</i>	NM_001081557.1	calmodulin binding transcription activator 1 (Camta1), transcript variant 1	0.61
<i>Cand1</i>	XM_125901.8	PREDICTED: cullin associated and neddylation disassociated 1, transcript variant 1 (Cand1)	0.65
<i>Caprin1</i>	NM_016739.2	cell cycle associated protein 1 (Caprin1)	0.64
<i>Car2</i>	NM_009801.3	carbonic anhydrase 2 (Car2)	0.39
<i>Cask</i>	NM_009806.2	calcium/calmodulin-dependent serine protein kinase (MAGUK family) (Cask)	0.35
<i>Cbfb</i>	NM_022309.2	core binding factor beta (Cbfb)	0.21
<i>Cbr3</i>	NM_173047.2	carbonyl reductase 3 (Cbr3)	0.61
<i>Cbx3</i>	NM_007624		0.45
<i>Cbx5</i>	NM_001076789.1	chromobox homolog 5 (Drosophila HP1a) (Cbx5), transcript variant 2	0.59
<i>Ccdc124</i>	NM_026964.3	coiled-coil domain containing 124 (Ccdc124)	0.64
<i>Ccdc28b</i>	NM_025455.2	coiled coil domain containing 28B (Ccdc28b)	0.62

<i>Ccdc41</i>	NM_029852.2	coiled-coil domain containing 41 (Ccdc41)	0.65
<i>Ccdc58</i>	NM_198645.1	coiled-coil domain containing 58 (Ccdc58)	0.64
<i>Ccdc59</i>	NM_025602.3	coiled-coil domain containing 59 (Ccdc59)	0.64
<i>Ccdc85b</i>	NM_198616.2	coiled-coil domain containing 85B (Ccdc85b)	0.59
<i>Ccdc86</i>	NM_023731.2	coiled-coil domain containing 86 (Ccdc86)	0.61
<i>Ccdc99</i>	NM_027411.1	coiled-coil domain containing 99 (Ccdc99)	0.57
<i>Ccnb1</i>	NM_172301.3	cyclin B1 (Ccnb1)	0.12
<i>Ccnd1</i>	NM_007631.1		0.04
<i>Ccnd2</i>	AK077367		0.43
<i>Ccne2</i>	NM_001037134.1	cyclin E2 (Ccne2), transcript variant 1	0.65
<i>Ccnyl1</i>	NM_001097644.1	cyclin Y-like 1 (Ccnyl1)	0.38
<i>Cct3</i>	NM_009836.1	chaperonin containing Tcp1, subunit 3 (gamma) (Cct3)	0.51
<i>Cct4</i>	NM_009837.1	chaperonin containing Tcp1, subunit 4 (delta) (Cct4)	0.56
<i>Cct6a</i>	NM_009838.1	chaperonin containing Tcp1, subunit 6a (zeta) (Cct6a)	0.48
<i>Cct8</i>	NM_009840.3	chaperonin containing Tcp1, subunit 8 (theta) (Cct8)	0.52
<i>Cd1d1</i>	NM_007639.2	CD1d1 antigen (Cd1d1)	0.49
<i>Cd276</i>	NM_133983.3	CD276 antigen (Cd276)	0.27
<i>Cdc20</i>	NM_023223.1	cell division cycle 20 homolog (S. cerevisiae) (Cdc20)	0.19
<i>Cdc25a</i>	NM_007658.3	cell division cycle 25 homolog A (S. pombe) (Cdc25a)	0.58
<i>Cdc25c</i>	NM_009860.2	cell division cycle 25 homolog C (S. pombe) (Cdc25c)	0.61
<i>Cdc2a</i>	NM_007659.3	cell division cycle 2 homolog A (S. pombe) (Cdc2a)	0.15
<i>Cdc21l</i>	NM_007661.3	cell division cycle 2-like 1 (Cdc21l)	0.65
<i>Cdc42se1</i>	NM_172395.2	CDC42 small effector 1 (Cdc42se1), transcript variant 1	0.48
<i>Cdc45l</i>	NM_009862.1	cell division cycle 45 homolog (S. cerevisiae)-like (Cdc45l)	0.47
<i>Cdc5l</i>	NM_152810.1	cell division cycle 5-like (S. pombe) (Cdc5l)	0.58
<i>Cdc6</i>	NM_011799.2	cell division cycle 6 homolog (S. cerevisiae) (Cdc6), transcript variant 1	0.55
<i>Cdc7</i>	NM_009863.2	cell division cycle 7 (S. cerevisiae) (Cdc7)	0.30
<i>Cdca2</i>	NM_175384.3	cell division cycle associated 2 (Cdca2)	0.25
<i>Cdca3</i>	NM_013538.4	cell division cycle associated 3 (Cdca3)	0.12
<i>Cdca4</i>	NM_028023.3	cell division cycle associated 4 (Cdca4)	0.44
<i>Cdca5</i>	NM_026410.1	cell division cycle associated 5 (Cdca5)	0.57
<i>Cdca7</i>	NM_025866.3	cell division cycle associated 7 (Cdca7)	0.17
<i>Cdca8</i>	NM_026560.3	cell division cycle associated 8 (Cdca8)	0.14
<i>Cdh13</i>	NM_019707.4	cadherin 13 (Cdh13)	0.20
<i>Cdh4</i>	NM_009867.1	cadherin 4 (Cdh4)	0.63
<i>Cdk2</i>	NM_183417.2	cyclin-dependent kinase 2 (Cdk2), transcript variant 1	0.31
<i>Cdk4</i>	NM_009870.2	cyclin-dependent kinase 4 (Cdk4)	0.43
<i>Cdk5r1</i>	NM_009871.2	cyclin-dependent kinase 5, regulatory subunit 1 (p35) (Cdk5r1)	0.54
<i>Cdk8</i>	NM_153599.3	cyclin-dependent kinase 8 (Cdk8)	0.59
<i>Cdkn2aipnl</i>	NM_029976.2	CDKN2A interacting protein N-terminal like (Cdkn2aipnl)	0.50
<i>Cdkn3</i>	XM_919022.2	PREDICTED: cyclin-dependent kinase inhibitor 3, transcript variant 5 (Cdkn3)	0.25
<i>Cdon</i>	AK040711		0.53
<i>Cdr2</i>	NM_007672.1	cerebellar degeneration-related 2 (Cdr2)	0.44
<i>Cdr2l</i>	NM_001080929.1	cerebellar degeneration-related protein 2-like (Cdr2l)	0.42
<i>Cdt1</i>	NM_026014.3	chromatin licensing and DNA replication factor 1 (Cdt1)	0.29
<i>Cenpa</i>	NM_007681.2	centromere protein A (Cenpa)	0.06
<i>Cenpf</i>	XM_916605.2	PREDICTED: centromere autoantigen F, transcript variant 3 (Cenpf)	0.23
<i>Cenph</i>	NM_021886.1	centromere protein H (Cenph)	0.65
<i>Cenpi</i>	NM_145924.2	centromere protein I (Cenpi)	0.57
<i>Cenpk</i>	NM_021790.1	centromere protein K (Cenpk), transcript variant 1	0.42
<i>Cenpl</i>	NM_027429.1	centromere protein L (Cenpl)	0.41
<i>Cenpm</i>	NM_025639.4	centromere protein M (Cenpm), transcript variant 1	0.63
<i>Cenpn</i>	NM_028131.3	centromere protein N (Cenpn)	0.55
<i>Cenpp</i>	NM_025495.1	centromere protein P (Cenpp)	0.59
<i>Cenpq</i>	NM_031863.3	centromere protein Q (Cenpq)	0.55
<i>Cenpt</i>	NM_177150.2	centromere protein T (Cenpt)	0.63
<i>Centd1</i>	XM_001001363.1	PREDICTED: centaurin, delta 1, transcript variant 5 (Centd1)	0.60
<i>Cep170</i>	NM_001099637.1	centrosomal protein 170 (Cep170)	0.48
<i>Cep55</i>	NM_028760.1	centrosomal protein 55 (Cep55)	0.60
<i>Cep78</i>	NM_198019.2	centrosomal protein 78 (Cep78)	0.52
<i>Cetn3</i>	NM_007684.3	centrin 3 (Cetn3)	0.62
<i>Cfl1</i>	NM_007687.2	cofilin 1, non-muscle (Cfl1)	0.41
<i>Chaf1a</i>	NM_013733.3	chromatin assembly factor 1, subunit A (p150) (Chaf1a)	0.60
<i>Chaf1b</i>	NM_028083.3	chromatin assembly factor 1, subunit B (p60) (Chaf1b)	0.31
<i>Chchd1</i>	NM_025366.2	coiled-coil-helix-coiled-coil-helix domain containing 1 (Chchd1)	0.50
<i>Chchd8</i>	NM_183270.2	coiled-coil-helix-coiled-coil-helix domain containing 8 (Chchd8)	0.64
<i>Chd1</i>	AK021188		0.58
<i>Chd4</i>	NM_145979.2	chromodomain helicase DNA binding protein 4 (Chd4)	0.63
<i>Chfr</i>	NM_172717.1	checkpoint with forkhead and ring finger domains (Chfr)	0.47
<i>Chmp4b</i>	NM_029362.3	chromatin modifying protein 4B (Chmp4b)	0.59

<i>Chn2</i>	NM_023543.1	chimerin (chimaerin) 2 (Chn2)	0.23
<i>Chrm3</i>	NM_033269.2	cholinergic receptor, muscarinic 3, cardiac (Chrm3)	0.55
<i>Chst2</i>	NM_018763.1	carbohydrate sulfotransferase 2 (Chst2)	0.35
<i>Chst7</i>	NM_021715.1	carbohydrate (N-acetylglucosamino) sulfotransferase 7 (Chst7)	0.12
<i>Chtf18</i>	NM_145409.1	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae) (Chtf18)	0.53
<i>Cirh1a</i>	NM_011574.1	cirrhosis, autosomal recessive 1A (human) (Cirh1a)	0.65
<i>Ckap2</i>	XM_134100.3		0.39
<i>Ckap2l</i>	NM_181589.2	cytoskeleton associated protein 2-like (Ckap2l)	0.56
<i>Cldnd1</i>	NM_171826.2	claudin domain containing 1 (Cldnd1)	0.52
<i>Clic4</i>	NM_013885.2	chloride intracellular channel 4 (mitochondrial) (Clic4), nuclear gene encoding mitochondrial protein	0.47
<i>Clic5</i>	NM_172621.2	chloride intracellular channel 5 (Clic5)	0.66
<i>Cln5</i>	XM_127882.3		0.56
<i>Clns1a</i>	NM_023671.1	chloride channel, nucleotide-sensitive, 1A (Clns1a)	0.55
<i>Clspn</i>	NM_175554.3	claspin homolog (Xenopus laevis) (Clspn)	0.27
<i>CltA</i>	NM_001080385.1	clathrin, light polypeptide (Lca) (CltA), transcript variant 2	0.64
<i>Cltc</i>	NM_001003908		0.58
<i>Cmas</i>	NM_009908.1	cytidine monophospho-N-acetylneuraminic acid synthetase (Cmas)	0.53
<i>Cmc1</i>	NM_026442.2	COX assembly mitochondrial protein homolog (S. cerevisiae) (Cmc1), nuclear gene encoding mitochondrial protein	0.61
<i>Cmpk</i>	NM_025647.2	cytidylate kinase (Cmpk)	0.54
<i>Cnih</i>	NM_009919.1	cornichon homolog (Drosophila) (Cnih)	0.61
<i>Cnih4</i>	NM_030131.2	cornichon homolog 4 (Drosophila) (Cnih4)	0.49
<i>Cntnap4</i>	NM_130457		0.43
<i>Col16a1</i>	NM_028266.4	collagen, type XVI, alpha 1 (Col16a1)	0.23
<i>Col18a1</i>	NM_009929.2	procollagen, type XVIII, alpha 1 (Col18a1)	0.08
<i>Col4a1</i>	NM_009931.1	procollagen, type IV, alpha 1 (Col4a1)	0.62
<i>Commd1</i>	NM_144514.2	COMM domain containing 1 (Commd1)	0.62
<i>Commd10</i>	NM_178377.4	COMM domain containing 10 (Commd10)	0.64
<i>Cops2</i>	NM_009939.2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana) (Cops2)	0.62
<i>Cops7a</i>	NM_012003.1	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (Cops7a)	0.62
<i>Coq9</i>	NM_026452.2	coenzyme Q9 homolog (yeast) (Coq9)	0.64
<i>Coro1c</i>	NM_011779.3	coronin, actin binding protein 1C (Coro1c)	0.48
<i>Cox10</i>	NM_178379.2	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (Cox10), nuclear gene encoding mitochondrial protein	0.60
<i>Cox15</i>	NM_144874.3	COX15 homolog, cytochrome c oxidase assembly protein (yeast) (Cox15), nuclear gene encoding mitochondrial protein	0.54
<i>Cox17</i>	NM_001017429.2	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast) (Cox17)	0.66
<i>Cox18</i>	NM_001033310.1	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae) (Cox18)	0.53
<i>Cox5a</i>	NM_007747.2	cytochrome c oxidase, subunit Va (Cox5a), nuclear gene encoding mitochondrial protein	0.55
<i>Cox6a1</i>	NM_007748.2		0.64
<i>Cox6c</i>	NM_053071.2	cytochrome c oxidase, subunit VIc (Cox6c)	0.65
<i>Cox7a2</i>	NM_009945.3	cytochrome c oxidase, subunit VIIa 2 (Cox7a2)	0.51
<i>Cox7a2l</i>	NM_009187.1	cytochrome c oxidase subunit VIIa polypeptide 2-like (Cox7a2l)	0.64
<i>Cpeb4</i>	NM_026252		0.60
<i>Cplx1</i>	NM_007756.2	complexin 1 (Cplx1)	0.58
<i>Cpne8</i>	NM_001033851.1	copine VIII (Cpne8), transcript variant 2	0.56
<i>Crispld2</i>	NM_030209.2	cysteine-rich secretory protein LCCL domain containing 2 (Crispld2)	0.66
<i>Crif3</i>	NM_018776.1	cytokine receptor-like factor 3 (Crif3)	0.65
<i>Crtap</i>	NM_019922.1	cartilage associated protein (Crtap)	0.53
<i>Cs</i>	NM_026444.3	citrate synthase (Cs), nuclear gene encoding mitochondrial protein	0.42
<i>Csad</i>	NM_144942.1	cysteine sulfenic acid decarboxylase (Csad)	0.57
<i>Csda</i>	NM_139117.2	cold shock domain protein A (Csda)	0.55
<i>Cse1l</i>	NM_023565.2	chromosome segregation 1-like (S. cerevisiae) (Cse1l)	0.50
<i>Csnk1d</i>	NM_027874.2	casein kinase 1, delta (Csnk1d), transcript variant 2	0.48
<i>Csnk1e</i>	NM_013767.5	casein kinase 1, epsilon (Csnk1e)	0.60
<i>Csnk1g3</i>	NM_152809.2	casein kinase 1, gamma 3 (Csnk1g3)	0.65
<i>Csnk2a1-rs3</i>	AK031617		0.59
<i>Csnk2a2</i>	NM_009974.2	casein kinase 2, alpha prime polypeptide (Csnk2a2)	0.59
<i>Cspg5</i>	NM_013884.2	chondroitin sulfate proteoglycan 5 (Cspg5)	0.36
<i>Csrp2</i>	NM_007792.3	cysteine and glycine-rich protein 2 (Csrp2)	0.47
<i>Cstf1</i>	NM_024199.2	cleavage stimulation factor, 3' pre-RNA, subunit 1 (Cstf1)	0.65
<i>Cstf2</i>	NM_133196.5	cleavage stimulation factor, 3' pre-RNA subunit 2 (Cstf2)	0.59
<i>Cstf3</i>	NM_145529.2	cleavage stimulation factor, 3' pre-RNA, subunit 3 (Cstf3), transcript variant 1	0.66

<i>Ctdspl2</i>	NM_212450.3	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2 (Ctdspl2)	0.65
<i>Ctgf</i>	NM_010217		0.63
<i>Ctps</i>	NM_016748.1	cytidine 5'-triphosphate synthase (Ctps)	0.66
<i>Ctsc</i>	NM_009982.3	cathepsin C (Ctsc)	0.34
<i>Ctnb2nl</i>	NM_030249.3	CTTNBP2 N-terminal like (Ctnb2nl)	0.40
<i>Cugbp2</i>	NM_010160.2	CUG triplet repeat, RNA binding protein 2 (Cugbp2), transcript variant 6	0.45
<i>Cul3</i>	NM_016716.4	cullin 3 (Cul3)	0.53
<i>Cx3cl1</i>	NM_009142.3	chemokine (C-X3-C motif) ligand 1 (Cx3cl1)	0.46
<i>Cxadr</i>	NM_009988		0.44
<i>Cxcl4</i>	NM_019932.2	chemokine (C-X-C motif) ligand 4 (Cxcl4)	0.46
<i>Cyb5r4</i>	NM_024195.1	cytochrome b5 reductase 4 (Cyb5r4)	0.62
<i>Cyc1</i>	NM_025567.2	cytochrome c-1 (Cyc1)	0.40
<i>Cycs</i>	NM_007808.4	cytochrome c, somatic (Cycs), nuclear gene encoding mitochondrial protein	0.37
<i>Cyp51</i>	NM_020010.2	cytochrome P450, family 51 (Cyp51)	0.30
<i>D030038A19Rik</i>	AK083512		0.55
<i>D030056L22Rik</i>	NM_177640.4	RIKEN cDNA D030056L22 gene (D030056L22Rik)	0.53
<i>D030063E12</i>			0.62
<i>D10Ert322e</i>	NM_026065.2	DNA segment, Chr 10, ERATO Doi 322, expressed (D10Ert322e)	0.57
<i>D10Wsu102e</i>	NM_026579.2	DNA segment, Chr 10, Wayne State University 102, expressed (D10Wsu102e)	0.59
<i>D10Wsu52e</i>	NM_145422.3	DNA segment, Chr 10, Wayne State University 52, expressed (D10Wsu52e)	0.61
<i>D12Ert553e</i>	NM_029758.3	DNA segment, Chr 12, ERATO Doi 553, expressed (D12Ert553e)	0.59
<i>D12Wsu95e</i>	NM_198023		0.45
<i>D130004H04Rik</i>			0.60
<i>D17H6S56E-5</i>	NM_033075.2	DNA segment, Chr 17, human D6S56E 5 (D17H6S56E-5)	0.54
<i>D17Wsu104e</i>	NM_080837.1		0.55
<i>D19Bwg1357e</i>	NM_177474.4	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed (D19Bwg1357e)	0.51
<i>D1Ert471e</i>			0.33
<i>D2Bwg1335e</i>	NM_026828.2	DNA segment, Chr 2, Brigham & Women's Genetics 1335 expressed (D2Bwg1335e)	0.51
<i>D2Ert750e</i>	NM_026412.1	DNA segment, Chr 2, ERATO Doi 750, expressed (D2Ert750e)	0.37
<i>D4Bwg0951e</i>	NM_026821.4	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed (D4Bwg0951e)	0.47
<i>D6Wsu176e</i>	NM_138587.4	DNA segment, Chr 6, Wayne State University 176, expressed (D6Wsu176e)	0.53
<i>D930028F11Rik</i>	NM_172921.2	RIKEN cDNA D930028F11 gene (D930028F11Rik)	0.56
<i>D930046M13Rik</i>			0.28
<i>D9Wsu20e</i>	NM_133718		0.43
<i>Dab2</i>	NM_023118.1		0.60
<i>Dazap1</i>	NM_133188.1	DAZ associated protein 1 (Dazap1)	0.53
<i>Dbf4</i>	NM_013726.2	DBF4 homolog (S. cerevisiae) (Dbf4)	0.25
<i>Dbt</i>	NM_010022.1	dihydrolipoamide branched chain transacylase E2 (Dbt)	0.64
<i>Dbx2</i>	XM_147966.3		0.48
<i>Dcbl1d1</i>	NM_025705.2	discoidin, CUB and LCCL domain containing 1 (Dcbl1d1)	0.60
<i>Dclk1</i>	NM_019978.2	doublecortin-like kinase 1 (Dclk1)	0.23
<i>Dclk2</i>	NM_027539.3	doublecortin-like kinase 2 (Dclk2)	0.61
<i>Dcun1d5</i>	NM_029775.2	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae) (Dcun1d5)	0.60
<i>Ddah1</i>	NM_026993		0.48
<i>Ddost</i>	NM_007838.2	dolichyl-di-phosphooligosaccharide-protein glycotransferase (Ddost)	0.58
<i>Ddx1</i>	NM_134040.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 (Ddx1)	0.63
<i>Ddx11</i>	XM_128714.3		0.36
<i>Ddx20</i>	NM_017397.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (Ddx20)	0.60
<i>Ddx21</i>	NM_019553.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 (Ddx21)	0.50
<i>Ddx25</i>	NM_013932.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (Ddx25)	0.56
<i>Ddx26</i>	NM_008715		0.56
<i>Ddx27</i>	NM_153065.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 (Ddx27)	0.67
<i>Ddx3x</i>	NM_010028.2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked (Ddx3x)	0.59
<i>Ddx54</i>	NM_028041.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54 (Ddx54)	0.54
<i>Ddx6</i>	NM_007841.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 (Ddx6)	0.51
<i>Deb1</i>	NM_026794.2	differentially expressed in B16F10 1 (Deb1)	0.53
<i>Dek</i>	NM_025900.1	DEK oncogene (DNA binding) (Dek)	0.60
<i>Dennd2a</i>	NM_172477.3	DENN/MADD domain containing 2A (Dennd2a)	0.33
<i>Dgkb</i>	NM_178681		0.55
<i>Dgkd</i>			0.52
<i>Dgkk</i>	NM_177914.2	diacylglycerol kinase kappa (Dgkk)	0.43
<i>Dgkz</i>	NM_138306.1	diacylglycerol kinase zeta (Dgkz)	0.43
<i>Dhcr24</i>	XM_131538.1		0.45
<i>Dhcr7</i>	NM_007856.2	7-dehydrocholesterol reductase (Dhcr7)	0.40
<i>Dhh</i>	NM_007857.3	desert hedgehog (Dhh)	0.41

<i>Dhrsx</i>	NM_001033326.2	dehydrogenase/reductase (SDR family) X chromosome (<i>Dhrsx</i>)	0.58
<i>Dhx15</i>	NM_007839.2	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (<i>Dhx15</i>), transcript variant 2	0.57
<i>Diras2</i>	NM_001024474.2	DIRAS family, GTP-binding RAS-like 2 (<i>Diras2</i>)	0.40
<i>Dlg5</i>	XM_981375.2	PREDICTED: discs, large homolog 5 (<i>Drosophila</i>) (<i>Dlg5</i>)	0.66
<i>Dlgap5</i>	NM_144553.1	discs, large (<i>Drosophila</i>) homolog-associated protein 5 (<i>Dlgap5</i>)	0.47
<i>Dlst</i>	NM_030225		0.53
<i>Dnahc11</i>	NM_010060.2	dynein, axonemal, heavy chain 11 (<i>Dnahc11</i>)	0.30
<i>Dnajb11</i>	XM_148071.1		0.51
<i>Dnajc2</i>	NM_009584.3	DnaJ (Hsp40) homolog, subfamily C, member 2 (<i>Dnajc2</i>)	0.48
<i>Dnclc1</i>	NM_019682		0.58
<i>Dnmt1</i>	NM_010066.3	DNA methyltransferase (cytosine-5) 1 (<i>Dnmt1</i>)	0.36
<i>Dock1</i>	NM_001033420.2	dedicator of cytokinesis 1 (<i>Dock1</i>)	0.62
<i>Dock10</i>	XM_129913.4		0.36
<i>Dos</i>	NM_015761.2	downstream of Stk11 (<i>Dos</i>)	0.60
<i>Dph2</i>	NM_026344.3	DPH2 homolog (<i>S. cerevisiae</i>) (<i>Dph2</i>)	0.63
<i>Dpp3</i>	NM_133803.1	dipeptidylpeptidase 3 (<i>Dpp3</i>)	0.66
<i>Dpy30</i>	NM_024428.3	dpy-30 homolog (<i>C. elegans</i>) (<i>Dpy30</i>)	0.61
<i>Dpysl3</i>	NM_009468.3	dihydropyrimidinase-like 3 (<i>Dpysl3</i>)	0.45
<i>Drctnb1a</i>	NM_053090		0.48
<i>Drg1</i>	NM_007879.1	developmentally regulated GTP binding protein 1 (<i>Drg1</i>)	0.65
<i>Dtymk</i>	NM_023136		0.60
<i>Dus4l</i>	NM_028002.2	dihydrouridine synthase 4-like (<i>S. cerevisiae</i>) (<i>Dus4l</i>)	0.66
<i>Dusp11</i>	NM_028099.2	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) (<i>Dusp11</i>)	0.63
<i>Dusp4</i>	NM_176933.4	dual specificity phosphatase 4 (<i>Dusp4</i>)	0.34
<i>Dusp6</i>	NM_026268.2	dual specificity phosphatase 6 (<i>Dusp6</i>)	0.10
<i>Dusp7</i>	NM_153459.2	dual specificity phosphatase 7 (<i>Dusp7</i>)	0.23
<i>Dynll1</i>	NM_019682.2	dynein light chain LC8-type 1 (<i>Dynll1</i>)	0.54
<i>E030026110Rik</i>	NM_175553		0.61
<i>E130016E03Rik</i>	NM_001039556.2	RIKEN cDNA E130016E03 gene (<i>E130016E03Rik</i>)	0.31
<i>E130306D19Rik</i>	XM_131404.3		0.47
<i>E230013M07Rik</i>	AK054036		0.25
<i>E2f1</i>	NM_007891.3	E2F transcription factor 1 (<i>E2f1</i>)	0.33
<i>E2f2</i>	NM_177733.2	E2F transcription factor 2 (<i>E2f2</i>)	0.54
<i>E330016A19Rik</i>	NM_173386.3	RIKEN cDNA E330016A19 gene (<i>E330016A19Rik</i>)	0.41
<i>E430028B21Rik</i>	NM_178668.3	RIKEN cDNA E430028B21 gene (<i>E430028B21Rik</i>)	0.60
<i>E430039I23Rik</i>	AK089103		0.58
<i>E530011J04Rik</i>	AK089133		0.55
<i>Ebna1bp2</i>	NM_026932.3	EBNA1 binding protein 2 (<i>Ebna1bp2</i>)	0.48
<i>Ece1</i>	NM_199307.1	endothelin converting enzyme 1 (<i>Ece1</i>)	0.44
<i>Ecm1</i>	NM_007899.1	extracellular matrix protein 1 (<i>Ecm1</i>)	0.58
<i>Eed</i>	NM_021876.2	embryonic ectoderm development (<i>Eed</i>)	0.65
<i>Eef1a1</i>	NM_010106.2	eukaryotic translation elongation factor 1 alpha 1 (<i>Eef1a1</i>)	0.60
<i>Eef1b2</i>	NM_018796.2	eukaryotic translation elongation factor 1 beta 2 (<i>Eef1b2</i>)	0.48
<i>Eef1d</i>	NM_023240.2	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (<i>Eef1d</i>), transcript variant 2	0.66
<i>Eef1e1</i>	NM_025380.2	eukaryotic translation elongation factor 1 epsilon 1 (<i>Eef1e1</i>)	0.34
<i>Eef1g</i>	NM_026007.4	eukaryotic translation elongation factor 1 gamma (<i>Eef1g</i>)	0.54
<i>Eef2</i>	NM_007907.1	eukaryotic translation elongation factor 2 (<i>Eef2</i>)	0.58
<i>Efnb1</i>	NM_010110.2	ephrin B1 (<i>Efnb1</i>)	0.64
<i>Efs</i>	NM_010112.3	embryonal Fyn-associated substrate (<i>Efs</i>)	0.52
<i>EG216185</i>	XM_911906.3	PREDICTED: predicted gene, EG216185 (<i>EG216185</i>)	0.58
<i>EG237361</i>	XM_905111.2	PREDICTED: predicted gene, EG237361 (<i>EG237361</i>)	0.44
<i>EG243642</i>	XM_145024.8	PREDICTED: predicted gene, EG243642 (<i>EG243642</i>)	0.41
<i>EG245297</i>	NM_001018086.2	predicted gene, EG245297 (<i>EG245297</i>)	0.65
<i>EG268795</i>	XM_921134.3	PREDICTED: predicted gene, EG268795, transcript variant 4 (<i>EG268795</i>)	0.44
<i>EG382843</i>	XM_905000.3	PREDICTED: predicted gene, EG382843 (<i>EG382843</i>)	0.66
<i>EG432681</i>	XM_484165.5	PREDICTED: predicted gene, EG432681 (<i>EG432681</i>)	0.51
<i>EG432721</i>	XM_484210.5	PREDICTED: predicted gene, EG432721 (<i>EG432721</i>)	0.44
<i>EG432879</i>	NM_001034882.2	predicted gene, EG432879 (<i>EG432879</i>)	0.55
<i>EG433144</i>	XM_484670.5	PREDICTED: predicted gene, EG433144 (<i>EG433144</i>)	0.66
<i>EG433182</i>	NM_001025388.1	predicted gene, EG433182 (<i>EG433182</i>)	0.67
<i>EG433923</i>	NM_001081233.1	predicted gene, EG433923 (<i>EG433923</i>)	0.45
<i>EG434404</i>	XM_486222.5	PREDICTED: predicted gene, EG434404 (<i>EG434404</i>)	0.58
<i>EG434858</i>	NR_002883.1	predicted gene, EG434858 (<i>EG434858</i>), non-coding RNA.	0.67
<i>EG545056</i>	NR_002889.2	predicted gene, EG545056 (<i>EG545056</i>), non-coding RNA.	0.62
<i>EG622236</i>	XM_917756.3	PREDICTED: predicted gene, EG622236, transcript variant 1 (<i>EG622236</i>)	0.50
<i>EG622339</i>	NM_001081297.1	predicted gene, EG622339 (<i>EG622339</i>)	0.64
<i>EG623818</i>	XM_888318.3	PREDICTED: predicted gene, EG623818 (<i>EG623818</i>)	0.50
<i>EG624124</i>	XM_889835.2	PREDICTED: predicted gene, EG624124, transcript variant 1 (<i>EG624124</i>)	0.55
<i>EG625917</i>	XM_917009.3	PREDICTED: predicted gene, EG625917 (<i>EG625917</i>)	0.56
<i>EG626175</i>	XM_908326.3	PREDICTED: predicted gene, EG626175 (<i>EG626175</i>)	0.41

<i>EG629595</i>	XM_894495.2	PREDICTED: predicted gene, EG629595 (EG629595)	0.51
<i>EG632248</i>	XM_001473902.1	PREDICTED: predicted gene, EG632248 (EG632248)	0.54
<i>EG633120</i>	XR_031485.1	PREDICTED: predicted gene, EG633120 (EG633120), misc RNA.	0.56
<i>EG637748</i>	XM_917238.2	PREDICTED: predicted gene, EG637748 (EG637748)	0.59
<i>EG665369</i>	XM_912043.2	PREDICTED: predicted gene, EG665369 (EG665369)	0.51
<i>EG666577</i>	XM_984280.2	PREDICTED: predicted gene, EG666577 (EG666577)	0.46
<i>EG666609</i>	XM_984926.2	PREDICTED: predicted gene, EG666609 (EG666609)	0.66
<i>EG667190</i>	XR_002058.1	PREDICTED: predicted gene, EG667190 (EG667190), misc RNA.	0.38
<i>EG667728</i>	XR_035278.1	PREDICTED: predicted gene, EG667728 (EG667728), misc RNA.	0.31
<i>EG668668</i>	NM_001081036.1	predicted gene, EG668668 (EG668668)	0.57
<i>EG668829</i>	XM_001005405.1	PREDICTED: predicted gene, EG668829 (EG668829)	0.48
<i>EG668850</i>	XR_002259.2	PREDICTED: predicted gene, EG668850 (EG668850), misc RNA.	0.60
<i>Egfr</i>	NM_007912.4	epidermal growth factor receptor (Egfr), transcript variant 2	0.64
<i>Egr3</i>	NM_018781		0.54
<i>Ehd4</i>	NM_133838.4	EH-domain containing 4 (Ehd4)	0.36
<i>Eif1a</i>	NM_010120.4	eukaryotic translation initiation factor 1A (Eif1a)	0.63
<i>Eif1ad</i>	NM_027236.2	eukaryotic translation initiation factor 1A domain containing (Eif1ad)	0.49
<i>Eif2b1</i>	NM_145371.3	eukaryotic translation initiation factor 2B, subunit 1 (alpha) (Eif2b1)	0.66
<i>Eif2b3</i>	XM_131572.4		0.62
<i>Eif2s2</i>	NM_026030.2	eukaryotic translation initiation factor 2, subunit 2 (beta) (Eif2s2)	0.46
<i>Eif2s3x</i>	NM_012010.3	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked (Eif2s3x)	0.52
<i>Eif3a</i>	NM_010123.3	eukaryotic translation initiation factor 3, subunit A (Eif3a)	0.57
<i>Eif3b</i>	NM_133916.2	eukaryotic translation initiation factor 3, subunit B (Eif3b)	0.66
<i>Eif3d</i>	NM_018749.2	eukaryotic translation initiation factor 3, subunit D (Eif3d)	0.58
<i>Eif3eip</i>	NM_145139.2	eukaryotic translation initiation factor 3, subunit E interacting protein (Eif3eip)	0.60
<i>Eif3g</i>	NM_016876.3	eukaryotic translation initiation factor 3, subunit G (Eif3g)	0.51
<i>Eif3i</i>	NM_018799.1	eukaryotic translation initiation factor 3, subunit I (Eif3i)	0.57
<i>Eif3s1</i>	NM_144545.2	eukaryotic translation initiation factor 3, subunit 1 alpha (Eif3s1)	0.66
<i>Eif3s4</i>	NM_016876.2		0.48
<i>Eif4a1</i>	NM_144958.2	eukaryotic translation initiation factor 4A1 (Eif4a1)	0.32
<i>Eif4a3</i>	NM_138669.1	eukaryotic translation initiation factor 4A, isoform 3 (Eif4a3)	0.64
<i>Eif4ebp1</i>	NM_007918.3	eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1)	0.53
<i>Eif4el3</i>	NM_023314.2		0.53
<i>Eif4g1</i>	NM_001005331.1	eukaryotic translation initiation factor 4, gamma 1 (Eif4g1), transcript variant 2	0.61
<i>Eif4g2</i>	NM_013507.2		0.66
<i>Eif4h</i>	NM_033561.1	eukaryotic translation initiation factor 4H (Eif4h)	0.62
<i>Eif5</i>	NM_173363.4	eukaryotic translation initiation factor 5 (Eif5), transcript variant 1	0.41
<i>Eif5a</i>			0.35
<i>Elavl1</i>	NM_010485.3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (Elavl1)	0.65
<i>Elk3</i>	NM_205536.1	ELK3, member of ETS oncogene family (Elk3), transcript variant 2	0.35
<i>Elmo1</i>	NM_198093.2	engulfment and cell motility 1, ced-12 homolog (C. elegans) (Elmo1), transcript variant 2	0.35
<i>Elmo2</i>	NM_080287.2	engulfment and cell motility 2, ced-12 homolog (C. elegans) (Elmo2), transcript variant 3	0.63
<i>Elov1</i>	NM_019422.2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (Elov1), transcript variant 2	0.60
<i>Elov14</i>	NM_148941.1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (Elov14)	0.51
<i>Elov15</i>	NM_134255.2	ELOVL family member 5, elongation of long chain fatty acids (yeast) (Elov15)	0.52
<i>Elov16</i>	NM_130450.2	ELOVL family member 6, elongation of long chain fatty acids (yeast) (Elov16)	0.21
<i>Emg1</i>	NM_013536.1	EMG1 nucleolar protein homolog (S. cerevisiae) (Emg1)	0.61
<i>Eno1</i>	NM_023119.1	enolase 1, alpha non-neuron (Eno1)	0.46
<i>Entpd4</i>	NM_026174.2	ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4)	0.52
<i>Epb4.111</i>	XM_487678		0.65
<i>Epn2</i>	NM_010148.2	epsin 2 (Epn2)	0.44
<i>Eprs</i>	NM_029735.1	glutamyl-prolyl-tRNA synthetase (Eprs)	0.53
<i>Ercc1</i>	NM_007948.1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (Ercc1)	0.62
<i>Ergic1</i>	NM_026170.3	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (Ergic1)	0.36
<i>Ergic2</i>	NM_026168.3	ERGIC and golgi 2 (Ergic2), transcript variant 1	0.52
<i>Erh</i>	NM_007951.1	enhancer of rudimentary homolog (Drosophila) (Erh)	0.50
<i>Erlin1</i>	NM_145502.2	ER lipid raft associated 1 (Erlin1)	0.58
<i>Ermp1</i>	NM_001081213.1	endoplasmic reticulum metalloproteinase 1 (Ermp1)	0.26
<i>Erp29</i>	NM_026129.2	endoplasmic reticulum protein 29 (Erp29)	0.64
<i>Errfi1</i>	NM_133753.1	ERBB receptor feedback inhibitor 1 (Errfi1)	0.64
<i>Esco2</i>	NM_028039.1	establishment of cohesion 1 homolog 2 (S. cerevisiae) (Esco2)	0.32
<i>Esp1</i>	NM_001014976.1	extra spindle poles-like 1 (S. cerevisiae) (Esp1)	0.64
<i>Esrra</i>	NM_007953.2	estrogen related receptor, alpha (Esrra)	0.66

<i>Esrrb</i>	NM_011934.3	estrogen related receptor, beta (<i>Esrrb</i>)	0.52
<i>Etaa1</i>	NM_026576.2	Ewing's tumor-associated antigen 1 (<i>Etaa1</i>)	0.61
<i>Etf1</i>	NM_144866.3	eukaryotic translation termination factor 1 (<i>Etf1</i>)	0.56
<i>Ets1</i>	NM_001038642.1	E26 avian leukemia oncogene 1, 5' domain (<i>Ets1</i>), transcript variant 2	0.54
<i>Ets2</i>	NM_011809.2	E26 avian leukemia oncogene 2, 3' domain (<i>Ets2</i>)	0.38
<i>Etv1</i>	NM_007960.3	ets variant gene 1 (<i>Etv1</i>)	0.29
<i>Etv4</i>	NM_008815.2	ets variant gene 4 (E1A enhancer binding protein, E1AF) (<i>Etv4</i>)	0.33
<i>Etv5</i>	NM_023794.2	ets variant gene 5 (<i>Etv5</i>)	0.20
<i>Exosc1</i>	NM_025644.3	exosome component 1 (<i>Exosc1</i>)	0.52
<i>Exosc2</i>	NM_144886.1	exosome component 2 (<i>Exosc2</i>)	0.63
<i>Exosc8</i>	NM_027148.2	exosome component 8 (<i>Exosc8</i>)	0.52
<i>Ext1</i>	NM_010162.2	exostoses (multiple) 1 (<i>Ext1</i>)	0.57
<i>Ezh2</i>	NM_007971.1	enhancer of zeste homolog 2 (<i>Drosophila</i>) (<i>Ezh2</i>)	0.27
<i>F2r</i>	NM_010169.3	coagulation factor II (thrombin) receptor (<i>F2r</i>)	0.24
<i>F630043A04Rik</i>	NM_198605.1	RIKEN cDNA F630043A04 gene (<i>F630043A04Rik</i>)	0.56
<i>Faah</i>	NM_010173.3	fatty acid amide hydrolase (<i>Faah</i>)	0.60
<i>Fabp5</i>	NM_010634.2	fatty acid binding protein 5, epidermal (<i>Fabp5</i>)	0.29
<i>Fabp7</i>	NM_021272.2		0.45
<i>Fam101a</i>	NM_028443.2	family with sequence similarity 101, member A (<i>Fam101a</i>)	0.51
<i>Fam108a</i>	NM_145421.1	family with sequence similarity 108, member A (<i>Fam108a</i>)	0.63
<i>Fam108b</i>	NM_146096.3	family with sequence similarity 108, member B (<i>Fam108b</i>)	0.66
<i>Fam120a</i>	NM_001033268.2	family with sequence similarity 120, member A (<i>Fam120a</i>)	0.48
<i>Fam131a</i>	NM_133778.2	family with sequence similarity 131, member A (<i>Fam131a</i>)	0.48
<i>Fam171a1</i>	NM_001081161.1	family with sequence similarity 171, member A1 (<i>Fam171a1</i>)	0.50
<i>Fam171b</i>	NM_175514.2	family with sequence similarity 171, member B (<i>Fam171b</i>)	0.37
<i>Fam173a</i>	NM_145410.3	family with sequence similarity 173, member A (<i>Fam173a</i>)	0.58
<i>Fam84a</i>	NM_029007.2	family with sequence similarity 84, member A (<i>Fam84a</i>)	0.33
<i>Fancd2</i>	XM_132796.4		0.66
<i>Fance</i>	XM_986338.2	PREDICTED: Fanconi anemia, complementation group E (<i>Fance</i>)	0.59
<i>Farsb</i>	NM_011811.2	phenylalanyl-tRNA synthetase, beta subunit (<i>Farsb</i>)	0.46
<i>Fblim1</i>	NM_133754.3	filamin binding LIM protein 1 (<i>Fblim1</i>)	0.54
<i>Fbln1</i>	NM_010180		0.55
<i>Fbln2</i>	NM_001081437.1	fibulin 2 (<i>Fbln2</i>), transcript variant 2	0.13
<i>Fbn1</i>	NM_007993		0.46
<i>Fbxl10</i>	NM_001005866.1	F-box and leucine-rich repeat protein 10 (<i>Fbxl10</i>), transcript variant 3	0.50
<i>Fbxl14</i>	NM_133940.1	F-box and leucine-rich repeat protein 14 (<i>Fbxl14</i>)	0.66
<i>Fchsd2</i>	NM_199012.1	FCH and double SH3 domains 2 (<i>Fchsd2</i>)	0.56
<i>Fdps</i>	NM_134469.3	farnesyl diphosphate synthetase (<i>Fdps</i>)	0.20
<i>Fen1</i>	NM_007999.3	flap structure specific endonuclease 1 (<i>Fen1</i>)	0.34
<i>Fgf1</i>	NM_010197.3	fibroblast growth factor 1 (<i>Fgf1</i>)	0.49
<i>Fgf22</i>	NM_023304.1	fibroblast growth factor 22 (<i>Fgf22</i>)	0.60
<i>Fh1</i>	NM_010209.1	fumarate hydratase 1 (<i>Fh1</i>)	0.45
<i>Fibp</i>	NM_021438.2	fibroblast growth factor (acidic) intracellular binding protein (<i>Fibp</i>)	0.54
<i>Figl1</i>	NM_021891.2	fidgetin-like 1 (<i>Figl1</i>)	0.25
<i>Fkbp11</i>	NM_024169.3	FK506 binding protein 11 (<i>Fkbp11</i>)	0.41
<i>Fkbp1a</i>	NM_008019.2	FK506 binding protein 1a (<i>Fkbp1a</i>)	0.39
<i>Fkbp4</i>	NM_010219.3	FK506 binding protein 4 (<i>Fkbp4</i>)	0.66
<i>Fkbp5</i>	NM_010220.2	FK506 binding protein 5 (<i>Fkbp5</i>)	0.61
<i>Fmn12</i>	NM_172409.2	formin-like 2 (<i>Fmn12</i>)	0.35
<i>Fnbp11</i>	NM_153118.1	formin binding protein 1-like (<i>Fnbp11</i>)	0.55
<i>Fndc3b</i>	NM_173182.1	fibronectin type III domain containing 3B (<i>Fndc3b</i>)	0.38
<i>Foxk2</i>	NM_001080932.1	forkhead box K2 (<i>Foxk2</i>)	0.62
<i>Foxm1</i>	NM_008021.4	forkhead box M1 (<i>Foxm1</i>)	0.43
<i>Foxred1</i>	NM_172291.1	FAD-dependent oxidoreductase domain containing 1 (<i>Foxred1</i>)	0.66
<i>Fpgs</i>	NM_010236.1	folylpolyglutamyl synthetase (<i>Fpgs</i>)	0.66
<i>Frm4a</i>	NM_172475		0.45
<i>Fscn1</i>	NM_007984.2	fascin homolog 1, actin bundling protein (<i>Strongylocentrotus purpuratus</i>) (<i>Fscn1</i>)	0.22
<i>Fubp3</i>	NM_001033389.2	far upstream element (FUSE) binding protein 3 (<i>Fubp3</i>)	0.61
<i>Fus</i>	NM_139149.1		0.48
<i>Fut8</i>	NM_016893.2	fucosyltransferase 8 (<i>Fut8</i>)	0.39
<i>Fxc1</i>	NM_019502.2	fractured callus expressed transcript 1 (<i>Fxc1</i>)	0.40
<i>Fxn</i>	NM_008044.1	frataxin (<i>Fxn</i>)	0.46
<i>Fxyd6</i>	NM_022004.6	FXYD domain-containing ion transport regulator 6 (<i>Fxyd6</i>)	0.48
<i>Fyn</i>	NM_008054.1	<i>Fyn</i> proto-oncogene (<i>Fyn</i>)	0.56
<i>Fzd1</i>	NM_021457.2	frizzled homolog 1 (<i>Drosophila</i>) (<i>Fzd1</i>)	0.53
<i>Fzd5</i>	NM_022721.3	frizzled homolog 5 (<i>Drosophila</i>) (<i>Fzd5</i>), transcript variant 1	0.51
<i>Fzr1</i>	NM_019757.1	fizzy/cell division cycle 20 related 1 (<i>Drosophila</i>) (<i>Fzr1</i>)	0.64
<i>G3bp1</i>	NM_013716.2	Ras-GTPase-activating protein SH3-domain binding protein 1 (<i>G3bp1</i>)	0.54
<i>G3bp2</i>	NM_001080794.1	GTPase activating protein (SH3 domain) binding protein 2 (<i>G3bp2</i>), transcript variant 2	0.62

<i>Gad1</i>	NM_008077.4	glutamic acid decarboxylase 1 (<i>Gad1</i>)	0.44
<i>Gadd45a</i>	NM_007836.1	growth arrest and DNA-damage-inducible 45 alpha (<i>Gadd45a</i>)	0.52
<i>Galnt1</i>	NM_013814.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (<i>Galnt1</i>)	0.56
<i>Galnt10</i>	NM_134189.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (<i>Galnt10</i>)	0.49
<i>Galnt2</i>	NM_139272.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (<i>Galnt2</i>)	0.60
<i>Gamt</i>	NM_010255.1	guanidinoacetate methyltransferase (<i>Gamt</i>)	0.61
<i>Ganab</i>	NM_008060.1	alpha glucosidase 2 alpha neutral subunit (<i>Ganab</i>)	0.54
<i>Gap43</i>	NM_008083.2	growth associated protein 43 (<i>Gap43</i>)	0.43
<i>Gapdh</i>	NM_008084.2	glyceraldehyde-3-phosphate dehydrogenase (<i>Gapdh</i>)	0.60
<i>Gars</i>	NM_180678.3	glycyl-tRNA synthetase (<i>Gars</i>)	0.46
<i>Gart</i>	NM_010256.2	phosphoribosylglycinamide formyltransferase (<i>Gart</i>)	0.60
<i>Gas2l3</i>	NM_001079876.1	growth arrest-specific 2 like 3 (<i>Gas2l3</i>), transcript variant 2	0.27
<i>Gas7</i>	NM_008088.1	growth arrest specific 7 (<i>Gas7</i>)	0.59
<i>Gatad1</i>	NM_026033.1	GATA zinc finger domain containing 1 (<i>Gatad1</i>)	0.59
<i>Gcap14</i>	NM_028407.3	granule cell antiserum positive 14 (<i>Gcap14</i>), transcript variant 2	0.35
<i>Gcat</i>	NM_013847		0.65
<i>Gch1</i>	NM_008102.3	GTP cyclohydrolase 1 (<i>Gch1</i>)	0.63
<i>Gcs1</i>	NM_020619.2	glucosidase 1 (<i>Gcs1</i>)	0.46
<i>Gdf15</i>	NM_011819.1	growth differentiation factor 15 (<i>Gdf15</i>)	0.30
<i>Gdpd1</i>	NM_025638.1	glycerophosphodiester phosphodiesterase domain containing 1 (<i>Gdpd1</i>)	0.56
<i>Gemin4</i>	NM_177367.2	gem (nuclear organelle) associated protein 4 (<i>Gemin4</i>)	0.53
<i>Gfm1</i>	NM_138591.1	G elongation factor, mitochondrial 1 (<i>Gfm1</i>)	0.46
<i>Gins2</i>	NM_178856.1	GINS complex subunit 2 (<i>Psf2</i> homolog) (<i>Gins2</i>)	0.53
<i>Gipc1</i>	NM_018771.3	GIPC PDZ domain containing family, member 1 (<i>Gipc1</i>)	0.54
<i>Glb1</i>	NM_009752.1	galactosidase, beta 1 (<i>Glb1</i>)	0.44
<i>Gldc</i>	NM_138595.1	glycine decarboxylase (<i>Gldc</i>)	0.46
<i>Glg1</i>	NM_009149		0.61
<i>Glrx5</i>	NM_028419.2	glutaredoxin 5 homolog (<i>S. cerevisiae</i>) (<i>Glrx5</i>)	0.58
<i>Glt25d1</i>	NM_146211.2	glycosyltransferase 25 domain containing 1 (<i>Glt25d1</i>)	0.39
<i>Glt25d2</i>	NM_177756.3	glycosyltransferase 25 domain containing 2 (<i>Glt25d2</i>)	0.59
<i>Gm444</i>	XM_144253.6	PREDICTED: gene model 444, (NCBI) (<i>Gm444</i>)	0.53
<i>Gm561</i>	NM_001033297.2	gene model 561, (NCBI) (<i>Gm561</i>)	0.45
<i>Gm949</i>	NM_001033446.2	gene model 949, (NCBI) (<i>Gm949</i>)	0.65
<i>Gmnds</i>	NM_146041.2	GDP-mannose 4, 6-dehydratase (<i>Gmnds</i>)	0.62
<i>Gna11</i>	NM_010301.3	guanine nucleotide binding protein, alpha 11 (<i>Gna11</i>)	0.66
<i>Gnai1</i>	NM_010305.1	guanine nucleotide binding protein (G protein), alpha inhibiting 1 (<i>Gnai1</i>)	0.38
<i>Gnb1</i>	NM_008142.3	guanine nucleotide binding protein (G protein), beta 1 (<i>Gnb1</i>)	0.55
<i>Gnb4</i>	NM_013531.3	guanine nucleotide binding protein (G protein), beta 4 (<i>Gnb4</i>)	0.51
<i>Gng10</i>	NM_025277.3	guanine nucleotide binding protein (G protein), gamma 10 (<i>Gng10</i>)	0.66
<i>Gng12</i>	AK005561		0.46
<i>Gng2</i>	NM_001038637.1	guanine nucleotide binding protein (G protein), gamma 2 (<i>Gng2</i>), transcript variant 2	0.60
<i>Gnl3</i>	NM_178846.1	guanine nucleotide binding protein-like 3 (nucleolar) (<i>Gnl3</i>), transcript variant 2	0.43
<i>Gnpda1</i>	NM_011937.1	glucosamine-6-phosphate deaminase 1 (<i>Gnpda1</i>)	0.51
<i>Golim4</i>	NM_175193.5	golgi integral membrane protein 4 (<i>Golim4</i>)	0.54
<i>Golm1</i>	NM_027307.4	golgi membrane protein 1 (<i>Golm1</i>), transcript variant 1	0.15
<i>Gorasp2</i>	NM_027352.3	golgi reassembly stacking protein 2 (<i>Gorasp2</i>)	0.47
<i>Got2</i>	NM_010325.2	glutamate oxaloacetate transaminase 2, mitochondrial (<i>Got2</i>), nuclear gene encoding mitochondrial protein	0.48
<i>Gpc1</i>	NM_016696.3	glypican 1 (<i>Gpc1</i>)	0.60
<i>Gpd1</i>	NM_010271.2	glycerol-3-phosphate dehydrogenase 1 (soluble) (<i>Gpd1</i>)	0.58
<i>Gpd2</i>	NM_010274.2	glycerol phosphate dehydrogenase 2, mitochondrial (<i>Gpd2</i>), nuclear gene encoding mitochondrial protein	0.58
<i>Gphn</i>	NM_172952.2	gephyrin (<i>Gphn</i>)	0.64
<i>Gpi1</i>	NM_008155.2	glucose phosphate isomerase 1 (<i>Gpi1</i>)	0.60
<i>Gpnmb</i>	NM_053110.3	glycoprotein (transmembrane) nmb (<i>Gpnmb</i>)	0.44
<i>Gpr125</i>	XM_132089.7	PREDICTED: G protein-coupled receptor 125, transcript variant 1 (<i>Gpr125</i>)	0.58
<i>Gps1</i>	NM_145370.1	G protein pathway suppressor 1 (<i>Gps1</i>)	0.61
<i>Gpsm1</i>	NM_153410.4	G-protein signalling modulator 1 (AGS3-like, <i>C. elegans</i>) (<i>Gpsm1</i>)	0.62
<i>Gpx3</i>	NM_008161.2	glutathione peroxidase 3 (<i>Gpx3</i>), transcript variant 2	0.59
<i>Grcc10</i>	NM_013535.1	gene rich cluster, C10 gene (<i>Grcc10</i>)	0.62
<i>Gria2</i>	NM_001039195.1	glutamate receptor, ionotropic, AMPA2 (alpha 2) (<i>Gria2</i>), transcript variant 1	0.55
<i>Grip1</i>	NM_028736		0.58
<i>Grm5</i>	NM_001081414.1	glutamate receptor, metabotropic 5 (<i>Grm5</i>)	0.13
<i>Grwd1</i>	NM_153419.1	glutamate-rich WD repeat containing 1 (<i>Grwd1</i>)	0.59
<i>Gsg2</i>	NM_010353.1	germ cell-specific gene 2 (<i>Gsg2</i>)	0.54
<i>Gspt1</i>	NM_146066.1	G1 to S phase transition 1 (<i>Gspt1</i>)	0.47

<i>Gstp1</i>	NM_013541.1	glutathione S-transferase, pi 1 (<i>Gstp1</i>)	0.61
<i>Gtf2e2</i>	NM_026584.2	general transcription factor II E, polypeptide 2 (beta subunit) (<i>Gtf2e2</i>)	0.54
<i>Gtf2f2</i>	NM_026816.3	general transcription factor IIF, polypeptide 2 (<i>Gtf2f2</i>)	0.56
<i>Gtf2h2</i>	NM_022011.3	general transcription factor II H, polypeptide 2 (<i>Gtf2h2</i>)	0.64
<i>Gtf3a</i>	NM_025652.1	general transcription factor III A (<i>Gtf3a</i>)	0.63
<i>Gtpbp3</i>	NM_032544.3	GTP binding protein 3 (<i>Gtpbp3</i>), nuclear gene encoding mitochondrial protein	0.42
<i>Gtpbp4</i>	NM_027000.4	GTP binding protein 4 (<i>Gtpbp4</i>)	0.50
<i>Gtse1</i>	NM_013882.1	G two S phase expressed protein 1 (<i>Gtse1</i>)	0.57
<i>Gucy1a3</i>	NM_021896.4	guanylate cyclase 1, soluble, alpha 3 (<i>Gucy1a3</i>)	0.39
<i>Gusb</i>	NM_010368.1	glucuronidase, beta (<i>Gusb</i>)	0.54
<i>H1fx</i>	NM_198622.1	H1 histone family, member X (<i>H1fx</i>)	0.53
<i>H2afx</i>	NM_010436.2	H2A histone family, member X (<i>H2afx</i>)	0.26
<i>H2afz</i>	NM_016750.1	H2A histone family, member Z (<i>H2afz</i>)	0.24
<i>Hat1</i>	NM_026115.3	histone aminotransferase 1 (<i>Hat1</i>)	0.44
<i>Hbegf</i>	NM_010415.1	heparin-binding EGF-like growth factor (<i>Hbegf</i>)	0.36
<i>Hccs</i>	NM_008222.2	holocytochrome c synthetase (<i>Hccs</i>)	0.63
<i>Hdac2</i>	NM_008229.1		0.45
<i>Heatr1</i>	NM_144835.4	HEAT repeat containing 1 (<i>Heatr1</i>)	0.53
<i>Heatr3</i>	NM_172757.3	HEAT repeat containing 3 (<i>Heatr3</i>)	0.66
<i>Hectd1</i>	XM_974905.2	PREDICTED: HECT domain containing 1 (<i>Hectd1</i>)	0.63
<i>Hectd2</i>	NM_172637.1	HECT domain containing 2 (<i>Hectd2</i>)	0.22
<i>Hes1</i>	NM_008235.2	hairy and enhancer of split 1 (<i>Drosophila</i>) (<i>Hes1</i>)	0.52
<i>Hes6</i>	NM_019479.2	hairy and enhancer of split 6 (<i>Drosophila</i>) (<i>Hes6</i>)	0.58
<i>Hip1</i>	NM_146001.1	huntingtin interacting protein 1 (<i>Hip1</i>)	0.10
<i>HIP-1</i>	AK087586		0.52
<i>Hip2</i>	NM_016786.2		0.62
<i>Hirip3</i>	NM_172746.2	HIRA interacting protein 3 (<i>Hirip3</i>)	0.51
<i>Hist1h2ad</i>	NM_178188.3	histone cluster 1, H2ad (<i>Hist1h2ad</i>)	0.18
<i>Hist1h2af</i>	NM_175661.1	histone cluster 1, H2af (<i>Hist1h2af</i>)	0.29
<i>Hist1h2ag</i>	NM_178186.2	histone cluster 1, H2ag (<i>Hist1h2ag</i>)	0.25
<i>Hist1h2ah</i>	NM_175659.1	histone cluster 1, H2ah (<i>Hist1h2ah</i>)	0.12
<i>Hist1h2ai</i>	NM_178182.1	histone cluster 1, H2ai (<i>Hist1h2ai</i>)	0.23
<i>Hist1h2ak</i>	NM_178183.1	histone cluster 1, H2ak (<i>Hist1h2ak</i>)	0.14
<i>Hist1h2an</i>	NM_178184.1	histone cluster 1, H2an (<i>Hist1h2an</i>)	0.08
<i>Hist1h2ao</i>	NM_178185.1	histone cluster 1, H2ao (<i>Hist1h2ao</i>)	0.08
<i>Hist2h2ab</i>	NM_178213.3	histone cluster 2, H2ab (<i>Hist2h2ab</i>)	0.32
<i>Hist2h2ac</i>	NM_175662.1	histone cluster 2, H2ac (<i>Hist2h2ac</i>)	0.21
<i>Hmga1</i>	NM_016660.2	high mobility group AT-hook 1 (<i>Hmga1</i>), transcript variant 1	0.36
<i>Hmgb2</i>	NM_008252.2	high mobility group box 2 (<i>Hmgb2</i>)	0.31
<i>Hmgcl</i>	NM_008254.1	3-hydroxy-3-methylglutaryl-Coenzyme A lyase (<i>Hmgcl</i>)	0.57
<i>Hmgcr</i>	NM_008255.1	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (<i>Hmgcr</i>)	0.48
<i>Hmgn2</i>	NM_016957.3	high mobility group nucleosomal binding domain 2 (<i>Hmgn2</i>)	0.56
<i>Hn1</i>	NM_008258.1	hematological and neurological expressed sequence 1 (<i>Hn1</i>)	0.29
<i>Hn1l</i>	NM_198937.2	hematological and neurological expressed 1-like (<i>Hn1l</i>)	0.54
<i>Hnrnpa2b1</i>	NM_182650.3	heterogeneous nuclear ribonucleoprotein A2/B1 (<i>Hnrnpa2b1</i>), transcript variant 2	0.37
<i>Hnrnpab</i>	NM_001048061.1	heterogeneous nuclear ribonucleoprotein A/B (<i>Hnrnpab</i>), transcript variant 1	0.38
<i>Hnrmpf</i>	NM_133834.1	heterogeneous nuclear ribonucleoprotein F (<i>Hnrmpf</i>)	0.64
<i>HnrmpH1</i>	NM_021510.2	heterogeneous nuclear ribonucleoprotein H1 (<i>HnrmpH1</i>)	0.63
<i>Hnrmpk</i>	NM_025279.2	heterogeneous nuclear ribonucleoprotein K (<i>Hnrmpk</i>)	0.56
<i>Hnrpa1</i>	NM_010447		0.34
<i>Hnrpab</i>	AK013709		0.62
<i>HnrpdI</i>	NM_016690.4	heterogeneous nuclear ribonucleoprotein D-like (<i>HnrpdI</i>)	0.65
<i>Hnrpl</i>	NM_177301.4	heterogeneous nuclear ribonucleoprotein L (<i>Hnrpl</i>)	0.44
<i>HnrplI</i>	NM_144802.3	heterogeneous nuclear ribonucleoprotein L-like (<i>HnrplI</i>)	0.50
<i>Hnrpm</i>	NM_029804.1	heterogeneous nuclear ribonucleoprotein M (<i>Hnrpm</i>)	0.60
<i>Homer1</i>	NM_152134.1	homer homolog 1 (<i>Drosophila</i>) (<i>Homer1</i>), transcript variant d	0.47
<i>Homer2</i>	XM_133550.4		0.47
<i>Hpcal1</i>	NM_016677.1	hippocalcin-like 1 (<i>Hpcal1</i>)	0.54
<i>Hprt1</i>	NM_013556.2	hypoxanthine guanine phosphoribosyl transferase 1 (<i>Hprt1</i>)	0.65
<i>Hrmt1I2</i>	NM_019830.1		0.22
<i>Hs2st1</i>	NM_011828.2	heparan sulfate 2-O-sulfotransferase 1 (<i>Hs2st1</i>)	0.65
<i>Hs6st2</i>	NM_015819.3	heparan sulfate 6-O-sulfotransferase 2 (<i>Hs6st2</i>), transcript variant 2	0.50
<i>Hsd17b12</i>	NM_019657.2	hydroxysteroid (17-beta) dehydrogenase 12 (<i>Hsd17b12</i>)	0.39
<i>Hsp90ab1</i>	NM_008302.3	heat shock protein 90kDa alpha (cytosolic), class B member 1 (<i>Hsp90ab1</i>)	0.56
<i>Hsp90b1</i>	NM_011631.1	heat shock protein 90, beta (<i>Grp94</i>), member 1 (<i>Hsp90b1</i>)	0.53
<i>Hspa8</i>	NM_031165.4	heat shock protein 8 (<i>Hspa8</i>)	0.53
<i>Hspa9</i>	NM_010481.1	heat shock protein 9 (<i>Hspa9</i>)	0.57
<i>Hspd1</i>	NM_010477.3	heat shock protein 1 (chaperonin) (<i>Hspd1</i>)	0.33
<i>Hspe1</i>	NM_008303.2	heat shock protein 1 (chaperonin 10) (<i>Hspe1</i>)	0.43

<i>Htra1</i>	NM_019564.1	HtrA serine peptidase 1 (Htra1)	0.53
<i>Htra2</i>	NM_019752.2	HtrA serine peptidase 2 (Htra2), nuclear gene encoding mitochondrial protein	0.64
<i>Hyal2</i>	NM_010489.2	hyaluronoglucosaminidase 2 (Hyal2)	0.51
<i>Iars</i>	NM_172015.1	isoleucine-tRNA synthetase (Iars)	0.49
<i>Iars2</i>	NM_198653.1	isoleucine-tRNA synthetase 2, mitochondrial (Iars2)	0.66
<i>Ibtk</i>	XM_135030.4		0.65
<i>Ick</i>	NM_019987.1	intestinal cell kinase (Ick)	0.61
<i>Ide</i>	NM_031156.2	insulin degrading enzyme (Ide)	0.42
<i>Idh1</i>	NM_010497.2	isocitrate dehydrogenase 1 (NADP+), soluble (Idh1)	0.61
<i>Idh3a</i>	NM_029573.2	isocitrate dehydrogenase 3 (NAD+) alpha (Idh3a), nuclear gene encoding mitochondrial protein	0.48
<i>Ier3</i>	NM_133662.2	immediate early response 3 (Ier3)	0.33
<i>Ier5l</i>	NM_030244.3	immediate early response 5-like (Ier5l)	0.38
<i>Igf2r</i>	NM_010515.1	insulin-like growth factor 2 receptor (Igf2r)	0.54
<i>Igfbp2</i>	NM_008342.2	insulin-like growth factor binding protein 2 (Igfbp2)	0.06
<i>Igfbp3</i>	NM_008343.2	insulin-like growth factor binding protein 3 (Igfbp3)	0.07
<i>Igfbp4</i>	NM_010517.3	insulin-like growth factor binding protein 4 (Igfbp4)	0.04
<i>Ilf2</i>	NM_026374.3	interleukin enhancer binding factor 2 (Ilf2)	0.59
<i>Immt</i>	NM_029673.2	inner membrane protein, mitochondrial (Immt), nuclear gene encoding mitochondrial protein	0.43
<i>Imp3</i>	NM_133976.1	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (Imp3)	0.46
<i>Impa2</i>	NM_053261.2	inositol (myo)-1(or 4)-monophosphatase 2 (Impa2)	0.56
<i>Impad1</i>	NM_177730.3	inositol monophosphatase domain containing 1 (Impad1)	0.42
<i>Impdh2</i>	NM_011830		0.49
<i>Incenp</i>	NM_016692.1	inner centromere protein (Incenp)	0.37
<i>Inpp5f</i>	NM_178641.3	inositol polyphosphate-5-phosphatase F (Inpp5f)	0.52
<i>Insig1</i>	NM_153526.2	insulin induced gene 1 (Insig1)	0.26
<i>Insm1</i>	NM_016889.2	insulinoma-associated 1 (Insm1)	0.66
<i>Ints7</i>	NM_178632.4	integrator complex subunit 7 (Ints7)	0.52
<i>Ipo5</i>	NM_023579.4	importin 5 (Ipo5)	0.48
<i>Ipo9</i>	NM_153774.1	importin 9 (Ipo9)	0.62
<i>Iqgap1</i>	NM_016721		0.53
<i>Iqgap3</i>	NM_001033484.1	IQ motif containing GTPase activating protein 3 (Iqgap3)	0.49
<i>Isca1</i>	NM_026921.2	iron-sulfur cluster assembly 1 homolog (S. cerevisiae) (Isca1)	0.57
<i>Isg20l2</i>	NM_177663.2	interferon stimulated exonuclease gene 20-like 2 (Isg20l2)	0.63
<i>Itgav</i>	NM_008402.1	integrin alpha V (Itgav)	0.57
<i>Itgb1</i>	NM_010578.1	integrin beta 1 (fibronectin receptor beta) (Itgb1)	0.62
<i>Itp2</i>	NM_019923.3	inositol 1,4,5-triphosphate receptor 2 (Itp2), transcript variant 1	0.33
<i>Jagn1</i>	NM_026365.2	jagunal homolog 1 (Drosophila) (Jagn1)	0.65
<i>Jam2</i>	NM_023844.2	junction adhesion molecule 2 (Jam2)	0.60
<i>Jmjd6</i>	NM_033398.2	jumonji domain containing 6 (Jmjd6)	0.52
<i>Josd2</i>	NM_025368.3	Josephin domain containing 2 (Josd2)	0.60
<i>Kars</i>	NM_053092.1	lysyl-tRNA synthetase (Kars)	0.57
<i>Kbtbd2</i>	NM_145958.1	kelch repeat and BTB (POZ) domain containing 2 (Kbtbd2)	0.63
<i>Kcnc1</i>	NM_008421.2	potassium voltage gated channel, Shaw-related subfamily, member 1 (Kcnc1)	0.37
<i>Kcnc4</i>	NM_145922.2	potassium voltage gated channel, Shaw-related subfamily, member 4 (Kcnc4)	0.35
<i>Kcnd2</i>	NM_019697.3	potassium voltage-gated channel, Shal-related family, member 2 (Kcnd2)	0.54
<i>Kcnip3</i>	NM_019789.2	Kv channel interacting protein 3, calsenilin (Kcnip3)	0.36
<i>Kcnk13</i>	NM_146037.1	potassium channel, subfamily K, member 13 (Kcnk13)	0.61
<i>Kctd12</i>	NM_177715.4	potassium channel tetramerisation domain containing 12 (Kctd12)	0.33
<i>Kdelc1</i>	NM_023645.2	KDEL (Lys-Asp-Glu-Leu) containing 1 (Kdelc1)	0.63
<i>Kdelr2</i>	NM_025841.3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (Kdelr2)	0.45
<i>Khdrbs1</i>	NM_011317.3	KH domain containing, RNA binding, signal transduction associated 1 (Khdrbs1)	0.51
<i>Kif11</i>	NM_010615.1	kinesin family member 11 (Kif11)	0.39
<i>Kif15</i>	NM_010620.1	kinesin family member 15 (Kif15)	0.36
<i>Kif18a</i>	NM_139303.1	kinesin family member 18A (Kif18a)	0.34
<i>Kif20b</i>	NM_183046.1	kinesin family member 20B (Kif20b)	0.32
<i>Kif22</i>	NM_145588.1	kinesin family member 22 (Kif22)	0.17
<i>Kif23</i>	NM_024245		0.10
<i>Kif2a</i>	NM_008442.1	kinesin family member 2A (Kif2a)	0.64
<i>Kif2c</i>	NM_134471.3	kinesin family member 2C (Kif2c)	0.26
<i>Kif3c</i>	NM_008445.2	kinesin family member 3C (Kif3c)	0.33
<i>Kif4</i>	NM_008446.1	kinesin family member 4 (Kif4)	0.32
<i>Kifc1</i>	NM_016761.1		0.51
<i>Kirrel3</i>	NM_026324.2	kin of IRRE like 3 (Drosophila) (Kirrel3)	0.42
<i>Kitl</i>	NM_013598.1	kit ligand (Kitl)	0.58
<i>Klf6</i>	NM_011803.2	Kruppel-like factor 6 (Klf6)	0.63

<i>Klf7</i>	NM_033563		0.65
<i>Klhdc2</i>	NM_027117.1	kelch domain containing 2 (<i>Klhdc2</i>)	0.60
<i>Kntc1</i>	NM_001042421.1	kinetochore associated 1 (<i>Kntc1</i>)	0.36
<i>Kpna1</i>	NM_008465.4	karyopherin (importin) alpha 1 (<i>Kpna1</i>)	0.57
<i>Kpna2</i>	NM_010655.3	karyopherin (importin) alpha 2 (<i>Kpna2</i>)	0.55
<i>Kpnb1</i>	NM_008379.3	karyopherin (importin) beta 1 (<i>Kpnb1</i>)	0.57
<i>Kras</i>	NM_021284.4	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (<i>Kras</i>)	0.60
<i>Krtcap2</i>	NM_025327.2	keratinocyte associated protein 2 (<i>Krtcap2</i>)	0.57
<i>Kti12</i>	NM_029571.2	KTI12 homolog, chromatin associated (<i>S. cerevisiae</i>) (<i>Kti12</i>)	0.61
<i>L2hgdh</i>	NM_145443.1	L-2-hydroxyglutarate dehydrogenase (<i>L2hgdh</i>), nuclear gene encoding mitochondrial protein	0.64
<i>Lama5</i>	NM_001081171.2	laminin, alpha 5 (<i>Lama5</i>)	0.49
<i>Lamc1</i>	NM_010683.1	laminin, gamma 1 (<i>Lamc1</i>)	0.48
<i>Lass2</i>	NM_029789.1	LAG1 homolog, ceramide synthase 2 (<i>Lass2</i>)	0.63
<i>Lass5</i>	NM_028015.2	LAG1 homolog, ceramide synthase 5 (<i>Lass5</i>)	0.63
<i>Lbh</i>	NM_029999.3	limb-bud and heart (<i>Lbh</i>)	0.32
<i>Lbr</i>	NM_133815		0.24
<i>Ldha</i>	NM_010699.1	lactate dehydrogenase A (<i>Ldha</i>)	0.32
<i>Leo1</i>	NM_001039522.1	Leo1, Paf1/RNA polymerase II complex component, homolog (<i>S. cerevisiae</i>) (<i>Leo1</i>)	0.64
<i>Lgals1</i>	NM_008495.1		0.16
<i>Lig1</i>	NM_010715.2	ligase I, DNA, ATP-dependent (<i>Lig1</i>), transcript variant 2	0.29
<i>Lig3</i>	NM_010716		0.64
<i>Lima1</i>	NM_023063.1	LIM domain and actin binding 1 (<i>Lima1</i>)	0.64
<i>Limd1</i>	NM_013860.1	LIM domains containing 1 (<i>Limd1</i>)	0.62
<i>Lin54</i>	NM_172714.1	lin-54 homolog (<i>C. elegans</i>) (<i>Lin54</i>)	0.49
<i>Lip1</i>	NM_021460.1		0.38
<i>Liph</i>	NM_153404.2	lipase, member H (<i>Liph</i>), transcript variant 2	0.55
<i>Litaf</i>	NM_019980.1	LPS-induced TN factor (<i>Litaf</i>)	0.42
<i>Lman1</i>	NM_027400.2	lectin, mannose-binding, 1 (<i>Lman1</i>)	0.67
<i>Lmnb1</i>	NM_010721.1	lamin B1 (<i>Lmnb1</i>)	0.13
<i>Lmo2</i>	NM_008505.3	LIM domain only 2 (<i>Lmo2</i>)	0.29
<i>LOC100039346</i>	XM_001472500.1	PREDICTED: hypothetical protein LOC100039346 (LOC100039346)	0.51
<i>LOC100039532</i>	XM_001473099.1	PREDICTED: similar to ribosomal protein L35a (LOC100039532)	0.58
<i>LOC100039571</i>	XM_001473215.1	PREDICTED: similar to ribosomal protein L23a (LOC100039571)	0.34
<i>LOC100039751</i>	XR_031048.1	PREDICTED: similar to 40S ribosomal protein S12 (LOC100039751), misc RNA.	0.61
<i>LOC100039786</i>	XM_001473500.1	PREDICTED: similar to Ywhaq protein (LOC100039786)	0.66
<i>LOC100040573</i>	XM_001475112.1	PREDICTED: similar to putative transcription factor ZNF131, transcript variant 1 (LOC100040573)	0.50
<i>LOC100040592</i>	XM_001475189.1	PREDICTED: similar to Hmgcs1 protein, transcript variant 1 (LOC100040592)	0.58
<i>LOC100040605</i>	XM_001475096.1	PREDICTED: similar to ribosomal protein L13 (LOC100040605)	0.48
<i>LOC100041500</i>	XM_001478166.1	PREDICTED: similar to LSM7 homolog, U6 small nuclear RNA associated (LOC100041500)	0.61
<i>LOC100041835</i>	XM_001478119.1	PREDICTED: similar to H+ ATP synthase (LOC100041835)	0.50
<i>LOC100042405</i>	XM_001478555.1	PREDICTED: similar to high mobility group nucleosomal binding domain 2 (LOC100042405)	0.34
<i>LOC100042427</i>	XM_001478518.1	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), transcript variant 4 (LOC100042427)	0.61
<i>LOC100042777</i>	XM_001478939.1	PREDICTED: similar to human protein homologous to DROER protein (LOC100042777)	0.62
<i>LOC100042970</i>	XM_001479207.1	PREDICTED: similar to Kifc1 protein (LOC100042970)	0.43
<i>LOC100043192</i>	XM_001479822.1	PREDICTED: similar to ribosomal protein L31 (LOC100043192)	0.60
<i>LOC100043209</i>	XM_001480293.1	PREDICTED: similar to ribosomal protein L15 (LOC100043209)	0.56
<i>LOC100043257</i>	XM_001480197.1	PREDICTED: similar to RNA binding motif protein 3 (LOC100043257)	0.44
<i>LOC100043391</i>	XM_001479903.1	PREDICTED: similar to QM protein (LOC100043391)	0.53
<i>LOC100043527</i>	XM_001480106.1	PREDICTED: similar to ribosomal protein S28 (LOC100043527)	0.58
<i>LOC100043555</i>	XM_001480194.1	PREDICTED: similar to Aak1 protein (LOC100043555)	0.52
<i>LOC100043671</i>	XM_001481024.1	PREDICTED: hypothetical protein LOC100043671 (LOC100043671)	0.53
<i>LOC100043675</i>	XM_001480621.1	PREDICTED: similar to Translocase of inner mitochondrial membrane 23 homolog (yeast) (LOC100043675)	0.61
<i>LOC100043822</i>	XM_001481025.1	PREDICTED: hypothetical protein LOC100043822 (LOC100043822)	0.59
<i>LOC100043906</i>	XM_001481214.1	PREDICTED: similar to nuclear pore-targeting complex component of 58 kDa, transcript variant 1 (LOC100043906)	0.37
<i>LOC100044322</i>	XM_001471968.1	PREDICTED: similar to UDP-glucose ceramide glucosyltransferase-like 1 (LOC100044322)	0.54
<i>LOC100044468</i>	XM_001472489.1	PREDICTED: similar to nemo-like kinase (LOC100044468)	0.54
<i>LOC100044696</i>	XM_001473268.1	PREDICTED: similar to cysteine-rich PAK1 inhibitor (LOC100044696)	0.63
<i>LOC100044756</i>	XM_001472989.1	PREDICTED: similar to PX domain-containing protein kinase-like protein (Modulator of Na,K-ATPase) (MONaKA) (LOC100044756)	0.66

LOC100044829	XM_001472872.1	PREDICTED: similar to Fibrillarin, transcript variant 1 (LOC100044829)	0.40
LOC100045040	XR_031278.1	PREDICTED: similar to ING1 protein (LOC100045040), misc RNA.	0.61
LOC100045312	XM_001473900.1	PREDICTED: similar to ribosomal protein (LOC100045312)	0.44
LOC100045343	XR_031575.1	PREDICTED: similar to CDNA sequence BC046404 (LOC100045343), misc RNA.	0.53
LOC100045542	XM_001473941.1	PREDICTED: similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1 (LOC100045542)	0.64
LOC100045668	XM_001474718.1	PREDICTED: similar to Rpl17 protein (LOC100045668)	0.64
LOC100045677	XR_031705.1	PREDICTED: similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3) (LOC100045677), misc RNA.	0.49
LOC100045737	XR_031944.1	PREDICTED: hypothetical protein LOC100045737 (LOC100045737), misc RNA.	0.64
LOC100045780	XM_001475019.1	PREDICTED: similar to metalloprotease-disintegrin meltrin beta (LOC100045780)	0.18
LOC100045887	XM_001475106.1	PREDICTED: similar to PTB-associated splicing factor (LOC100045887)	0.51
LOC100045967	XR_032154.1	PREDICTED: hypothetical protein LOC100045967 (LOC100045967), misc RNA.	0.44
LOC100045981	XM_001475298.1	PREDICTED: similar to synaptotagmin XI (LOC100045981)	0.50
LOC100045999	XM_001475422.1	PREDICTED: similar to RAN, member RAS oncogene family (LOC100045999)	0.53
LOC100046320	XR_032844.1	PREDICTED: similar to Matrin 3 (LOC100046320), misc RNA.	0.66
LOC100046343	XM_001475830.1	PREDICTED: similar to CCR4-NOT transcription complex, subunit 6 (LOC100046343)	0.50
LOC100046483	XM_001476285.1	PREDICTED: similar to casein kinase II, alpha prime subunit (LOC100046483)	0.64
LOC100046518	XM_001476353.1	PREDICTED: similar to Gprn1 protein (LOC100046518)	0.56
LOC100046650	XM_001476721.1	PREDICTED: similar to PRELI domain containing 1 (LOC100046650)	0.46
LOC100046744	XM_001475765.1	PREDICTED: similar to Serine/arginine repetitive matrix protein 2 (LOC100046744)	0.55
LOC100046853	XM_001476909.1	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein K (LOC100046853)	0.29
LOC100046855	XM_001476916.1	PREDICTED: similar to BKLf (LOC100046855)	0.38
LOC100046895	XM_001477026.1	PREDICTED: similar to Quaking protein (LOC100046895)	0.48
LOC100047155	XM_001477537.1	PREDICTED: similar to Small nuclear ribonucleoprotein polypeptide A (LOC100047155)	0.55
LOC100047167	XM_001477568.1	PREDICTED: similar to mKIAA0990 protein (LOC100047167)	0.39
LOC100047268	XM_001477774.1	PREDICTED: similar to Immediate early response 5-like (LOC100047268)	0.24
LOC100047353	XM_001477963.1	PREDICTED: similar to myocardial vascular inhibition factor (LOC100047353)	0.60
LOC100047490	XM_001478266.1	PREDICTED: similar to putative oral cancer suppressor (LOC100047490)	0.62
LOC100047606	XR_033719.1	PREDICTED: similar to neurotrophic tyrosine kinase, receptor, type 3 (LOC100047606), misc RNA.	0.67
LOC100047615	XR_033484.1	PREDICTED: similar to 40S ribosomal protein S17 (LOC100047615), misc RNA.	0.57
LOC100047619	XR_033736.1	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (LOC100047619), misc RNA.	0.19
LOC100047634	XR_032896.1	PREDICTED: similar to Eukaryotic translation initiation factor 2 alpha kinase 3 (LOC100047634), misc RNA.	0.61
LOC100047712	XM_001478724.1	PREDICTED: similar to coiled-coil domain containing 101 (LOC100047712)	0.65
LOC100047759	XM_001479214.1	PREDICTED: similar to acidic ribosomal phosphoprotein P1, transcript variant 1 (LOC100047759)	0.49
LOC100047762	XM_001478835.1	PREDICTED: similar to Aspartate aminotransferase, cytoplasmic (Transaminase A) (Glutamate oxaloacetate transaminase 1) (LOC100047762)	0.64
LOC100047827	XM_001479392.1	PREDICTED: similar to Hmgn2 protein (LOC100047827)	0.39
LOC100047888	XM_001479068.1	PREDICTED: similar to Neurocan (LOC100047888)	0.31
LOC100047915	XM_001479122.1	PREDICTED: similar to Memo1 protein (LOC100047915)	0.61
LOC100047934	XM_001478074.1	PREDICTED: hypothetical protein LOC100047934 (LOC100047934)	0.38
LOC100047935	XR_033756.1	PREDICTED: similar to ribosomal protein L5 (LOC100047935), misc RNA.	0.63
LOC100047937	XM_001479188.1	PREDICTED: similar to Aldehyde dehydrogenase 1 family, member L1 (LOC100047937)	0.64
LOC100047998	XM_001479497.1	PREDICTED: similar to ribosomal protein L37a (LOC100047998)	0.51
LOC100048413	XM_001480186.1	PREDICTED: similar to Myeloid leukemia factor 2 (LOC100048413)	0.52
LOC100048445	XM_001480467.1	PREDICTED: similar to fau (LOC100048445)	0.57
LOC100048483	XM_001480453.1	PREDICTED: similar to cytochrome c oxidase subunit VIII (LOC100048483)	0.59
LOC100048508	XM_001480806.1	PREDICTED: similar to Rpl36 protein, transcript variant 1 (LOC100048508)	0.61
LOC100048613	XM_001480380.1	PREDICTED: similar to cytochrome c oxidase, subunit VIIC, transcript variant 1 (LOC100048613)	0.56

LOC100048645	XM_001480791.1	PREDICTED: similar to cysteine and glycine-rich protein 2 binding protein (LOC100048645)	0.60
LOC209281	XR_002517.1	PREDICTED: similar to capping protein (actin filament) muscle Z-line, alpha 1 (LOC209281)	0.64
LOC212399	XM_137003.2		0.38
LOC219106	XM_139078.2		0.64
LOC219145	XM_122761.3		0.43
LOC225058	XM_140116.1		0.58
LOC225134	XR_031257.1	PREDICTED: similar to ribosomal protein S4, X-linked (LOC225134), misc RNA.	0.51
LOC226416	XM_129460.4		0.61
LOC229810	XM_124173.2		0.66
LOC230253	XM_124269.2		0.29
LOC230896	XM_124427.4		0.64
LOC231368	XR_002491.1	PREDICTED: similar to 60S acidic ribosomal protein P0 (L10E) (LOC231368)	0.41
LOC232606	XM_124826.2		0.48
LOC232887	XM_124858.2		0.66
LOC232890	XM_145374.2		0.49
LOC236831	XR_001889.1	PREDICTED: similar to 60S ribosomal protein L7a (LOC236831)	0.48
LOC237512	XM_137226.3		0.51
LOC237877	XM_111221.4		0.57
LOC238943	XM_138902.2		0.65
LOC241621	XM_917314.2	PREDICTED: similar to ribosomal protein L27a-like (LOC241621)	0.37
LOC245668	XM_142236.4		0.43
LOC245892	XM_147335.2		0.17
LOC268569	XM_195821.2		0.23
LOC268700	XM_193742.2		0.52
LOC269251	XM_193262.3		0.39
LOC269515	XM_196313.1		0.67
LOC270037	XM_193374.2		0.38
LOC271490	XM_195069.2		0.47
LOC271505	XM_195066.3		0.55
LOC272681	XM_195399.2		0.54
LOC277856	XM_204210.2		0.58
LOC329076	XM_282724.2		0.45
LOC331102	XM_284573.2		0.65
LOC331507	XM_284733.2		0.64
LOC380692	XM_354604.1		0.28
LOC380707	XM_354622.1		0.61
LOC380927	XM_354834.1		0.51
LOC380930	XM_358467.1		0.44
LOC381046	XM_354963.1		0.37
LOC381114	XM_355032.1		0.29
LOC381140	XM_355056.1		0.63
LOC381215	XM_355149.1		0.55
LOC381230	XM_355167.1		0.61
LOC381285	XM_355225.1		0.65
LOC381330	XM_355288.1		0.48
LOC381365	XM_355330.1		0.56
LOC381398	XM_355356.1		0.43
LOC381448	XM_355403.1		0.46
LOC381561	XM_355526.1		0.60
LOC381649	XM_355612.1		0.54
LOC381799	XM_355801.1		0.65
LOC381808	XM_355809.1		0.56
LOC381891	XM_355907.1		0.56
LOC381940	XM_355964.1		0.62
LOC381999	XM_356062.1		0.50
LOC382061	XM_356141.1		0.52
LOC382128	XM_356225.1		0.66
LOC382230	XM_356342.1		0.50
LOC382885	XM_356731.1		0.56
LOC383099	XM_356873.1		0.65
LOC383308	XM_356977.1		0.42
LOC383330	XM_356987.1		0.54
LOC383897	XM_357315.1		0.57
LOC383942	XM_357338.1		0.65
LOC384104	XM_357429.1		0.65
LOC384206	XM_357488.1		0.57
LOC384727	XM_357823.1		0.59

LOC385905	XR_034995.1	PREDICTED: similar to proteasome alpha7/C8 subunit (LOC385905), misc RNA.	0.65
LOC433476	XM_917865.2	PREDICTED: similar to ribosomal protein L27a (LOC433476)	0.37
LOC433745	XM_001475733.1	PREDICTED: similar to ribosomal protein L3 (LOC433745)	0.56
LOC545056	NR_002889.1	ubiquitin-conjugating enzyme E2, J2 homolog pseudogene (LOC545056) on chromosome 14.	0.57
LOC545369	XR_034542.1	PREDICTED: similar to ribosomal protein L4 (LOC545369), misc RNA.	0.59
LOC545396	XR_003545.1	PREDICTED: similar to TGF beta-inducible nuclear protein 1 (L-name-related protein 42) (LNR42) (LOC545396)	0.62
LOC545472	XM_619824.4	PREDICTED: similar to BTB (POZ) domain containing 1 (LOC545472)	0.67
LOC546015	XR_034790.1	PREDICTED: similar to ribosomal protein S9 (LOC546015), misc RNA.	0.61
LOC620678	XR_031536.1	PREDICTED: similar to 60S ribosomal protein L7 (LOC620678), misc RNA.	0.55
LOC622655	XR_032410.1	PREDICTED: similar to hCG31107 (LOC622655), misc RNA.	0.33
LOC622994	XR_031862.1	PREDICTED: hypothetical LOC622994 (LOC622994), misc RNA.	0.47
LOC623466	XR_033501.1	PREDICTED: similar to MGC27348 protein (LOC623466), misc RNA.	0.43
LOC623568	XM_001480472.1	PREDICTED: similar to ribosomal protein S20 (LOC623568)	0.41
LOC630729	XM_904332.3	PREDICTED: similar to glutathione reductase 1 (LOC630729)	0.54
LOC630936	XR_001819.2	PREDICTED: similar to nuclease sensitive element binding protein 1 (LOC630936), misc RNA.	0.27
LOC632022	XR_030945.1	PREDICTED: similar to 40S ribosomal protein S18 (LOC632022), misc RNA.	0.65
LOC632230	XR_031205.1	PREDICTED: similar to Ribosomal protein L5 (LOC632230), misc RNA.	0.56
LOC632667	XM_906862.3	PREDICTED: similar to PNG protein (LOC632667)	0.57
LOC632684	XR_031426.1	PREDICTED: hypothetical LOC632684 (LOC632684), misc RNA.	0.59
LOC633016	XM_921371.2	PREDICTED: similar to Chromobox homolog 3 (HP1 gamma homolog, Drosophila), transcript variant 2 (LOC633016)	0.46
LOC635470	XM_915945.3	PREDICTED: similar to ribosomal protein L27a-like (LOC635470)	0.43
LOC638892	XM_915073.1	PREDICTED: similar to cpn10 protein (LOC638892)	0.62
LOC640739	XM_925296.2	PREDICTED: hypothetical LOC640739 (LOC640739)	0.16
LOC640972	XM_918222.2	PREDICTED: similar to cyclin-dependent kinase 2-interacting protein (LOC640972)	0.62
LOC654426	NR_002690.1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F pseudogene (LOC654426), non-coding RNA.	0.65
LOC654467	NR_002885.1	heterogeneous nuclear ribonucleoprotein A1 pseudogene (LOC654467) on chromosome 9.	0.42
LOC654842	NM_001081681.1	hypothetical protein LOC654842 (LOC654842)	0.39
LOC665032	XM_991641.1	PREDICTED: similar to ribosomal protein (LOC665032)	0.51
LOC665235	XR_031650.1	PREDICTED: similar to hCG1642689 (LOC665235), misc RNA.	0.63
LOC665237	XR_031476.1	PREDICTED: similar to hCG31107 (LOC665237), misc RNA.	0.33
LOC665281	XR_031065.1	PREDICTED: similar to 40S ribosomal protein S12 (LOC665281), misc RNA.	0.44
LOC666559	XR_031145.1	PREDICTED: similar to farnesyl pyrophosphate synthase (LOC666559), misc RNA.	0.26
LOC666676	XR_030655.1	PREDICTED: similar to ADP-ribosylation factor (LOC666676), misc RNA.	0.49
LOC667005	XR_030797.1	PREDICTED: similar to cyclin B1 (LOC667005), misc RNA.	0.43
LOC667251	XR_032081.1	PREDICTED: similar to NADPH cytochrome B5 oxidoreductase (LOC667251), misc RNA.	0.61
LOC667609	XR_032582.1	PREDICTED: similar to mitochondrial ribosomal protein S5 (LOC667609), misc RNA.	0.66
LOC668038	XR_034201.1	PREDICTED: similar to ribosomal protein (LOC668038), misc RNA.	0.46
LOC668239	XM_001000226.2	PREDICTED: similar to Rps13 protein (LOC668239)	0.47
LOC668387	XR_031651.1	PREDICTED: similar to ribosomal protein S6 (LOC668387), misc RNA.	0.54
LOC668492	XR_034647.1	PREDICTED: similar to zinc finger CCHC-type and RNA binding motif 1 (LOC668492), misc RNA.	0.63
LOC668573	XR_035016.1	PREDICTED: similar to ribosomal protein (LOC668573), misc RNA.	0.40
LOC668706	XM_001003212.2	PREDICTED: similar to Ribosomal protein L12 (LOC668706)	0.36
LOC669658	XM_976371.1	PREDICTED: similar to melanoma antigen (LOC669658)	0.54
LOC669660	XM_976375.1	PREDICTED: similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein) (LOC669660)	0.62
LOC671641	XM_001479052.1	PREDICTED: similar to ribosomal protein S12 (LOC671641)	0.54
LOC671878	XM_001473434.1	PREDICTED: similar to spermine synthase (LOC671878)	0.37
LOC672474	XM_993721.1	PREDICTED: similar to 60S ribosomal protein L29 (LOC672474)	0.58
LOC674611	XM_980150.1	PREDICTED: similar to Su48, transcript variant 3 (LOC674611)	0.38
LOC675377	XR_005113.2	PREDICTED: similar to Ribosomal protein L8 (LOC675377), misc RNA.	0.51
LOC675440	XM_001479274.1	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae), transcript variant 1 (LOC675440)	0.62
LOC675813	XR_032773.1	PREDICTED: similar to ribosomal protein S20 (LOC675813), misc RNA.	0.58
LOC675899	XM_985882.1	PREDICTED: similar to H2A histone family, member Z (LOC675899)	0.26
LOC676420	XR_031436.1	PREDICTED: similar to ceramide kinases (LOC676420), misc RNA.	0.57
LOC676640	XM_001003712.1	PREDICTED: similar to neuron navigator 3, transcript variant 5 (LOC676640)	0.32
LOC676724	XM_992449.1	PREDICTED: hypothetical LOC676724 (LOC676724)	0.47
LOC677205	XR_034818.1	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (LOC677205), misc RNA.	0.53

<i>LOC677215</i>	XM_001001411.2	PREDICTED: similar to acidic ribosomal phosphoprotein P1, transcript variant 1 (LOC677215)	0.64
<i>LOC677317</i>	XM_001004685.1	PREDICTED: similar to Mod1 protein, transcript variant 4 (LOC677317)	0.53
<i>LOC677448</i>	XR_005062.2	PREDICTED: similar to actin (LOC677448), misc RNA.	0.57
<i>LOC677551</i>	XR_005084.2	PREDICTED: similar to Ribosomal protein L19 (LOC677551), misc RNA.	0.56
<i>Lor</i>	NM_008508.2	loricrin (Lor)	0.31
<i>Lphn3</i>	NM_198702.2	latrophilin 3 (Lphn3)	0.58
<i>Lpl</i>	NM_008509.2	lipoprotein lipase (Lpl)	0.31
<i>Lrig1</i>	NM_008377.2	leucine-rich repeats and immunoglobulin-like domains 1 (Lrig1)	0.33
<i>Lrp12</i>	NM_172814.1	low density lipoprotein-related protein 12 (Lrp12)	0.54
<i>Lrrc59</i>	NM_133807.1	leucine rich repeat containing 59 (Lrrc59)	0.44
<i>Lrrfp1</i>	NM_008515.1	leucine rich repeat (in FLII) interacting protein 1 (Lrrfp1)	0.32
<i>Lsg1</i>	NM_178069.5	large subunit GTPase 1 homolog (S. cerevisiae) (Lsg1)	0.64
<i>Lsm12</i>	NM_172947.1	LSM12 homolog (S. cerevisiae) (Lsm12)	0.62
<i>Lsm2</i>	NM_030597.2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm2)	0.44
<i>Lsm3</i>	NM_026309.1	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm3)	0.54
<i>Lsm4</i>	NM_015816.1	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm4)	0.47
<i>Lsm5</i>	NM_025520.2	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm5)	0.41
<i>Lsm6</i>	NM_030145.2	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm6)	0.48
<i>Lsm8</i>	NM_133939.1	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm8)	0.42
<i>Lss</i>	NM_146006.1	lanosterol synthase (Lss)	0.40
<i>Ltp1</i>	NM_206958.1	latent transforming growth factor beta binding protein 1 (Ltp1), transcript variant 2	0.42
<i>Ly96</i>	NM_016923.1	lymphocyte antigen 96 (Ly96)	0.58
<i>Lyar</i>	NM_025281.2	Ly1 antibody reactive clone (Lyar)	0.60
<i>Lypla2</i>	NM_011942.1	lysophospholipase 2 (Lypla2)	0.56
<i>Mad21</i>	NM_019499.2	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (Mad21)	0.27
<i>Maged1</i>	NM_019791.2	melanoma antigen, family D, 1 (Maged1)	0.36
<i>Mageh1</i>	NM_023788.3	melanoma antigen, family H, 1 (Mageh1)	0.57
<i>Magi1</i>	NM_010367.2	membrane associated guanylate kinase, WW and PDZ domain containing 1 (Magi1), transcript variant 1	0.55
<i>Mak16</i>	NM_026453.3	MAK16 homolog (S. cerevisiae) (Mak16)	0.49
<i>Mamdc2</i>	NM_174857.3	MAM domain containing 2 (Mamdc2)	0.47
<i>Man2a1</i>	NM_008549.1	mannosidase 2, alpha 1 (Man2a1)	0.48
<i>Manba</i>	NM_027288.2	mannosidase, beta A, lysosomal (Manba)	0.56
<i>Map2k2</i>	NM_023138.3	mitogen activated protein kinase kinase 2 (Map2k2)	0.65
<i>Map2k3</i>	NM_008928.3	mitogen activated protein kinase kinase 3 (Map2k3)	0.45
<i>Map2k4</i>	NM_009157.2	mitogen activated protein kinase kinase 4 (Map2k4)	0.55
<i>Map4k4</i>	NM_008696.2	mitogen-activated protein kinase kinase kinase 4 (Map4k4)	0.50
<i>Mapk1</i>	NM_011949.3	mitogen-activated protein kinase 1 (Mapk1), transcript variant 1	0.64
<i>Mapk6</i>	NM_027418.1	mitogen-activated protein kinase 6 (Mapk6), transcript variant 2	0.53
<i>Marcks</i>	NM_008538.2	myristoylated alanine rich protein kinase C substrate (Marcks)	0.60
<i>Marcks1</i>	NM_010807.3	MARCKS-like 1 (Marcks1)	0.64
<i>Mars2</i>	NM_175439.3	methionine-tRNA synthetase 2 (mitochondrial) (Mars2), nuclear gene encoding mitochondrial protein	0.62
<i>Mast2</i>	NM_008641.2	microtubule associated serine/threonine kinase 2 (Mast2), transcript variant 2	0.66
<i>Mbd3</i>	NM_013595.2	methyl-CpG binding domain protein 3 (Mbd3)	0.62
<i>Mbn1</i>	NM_020007.3	muscleblind-like 1 (Drosophila) (Mbn1)	0.54
<i>Mboat1</i>	NM_153546.3	membrane bound O-acyltransferase domain containing 1 (Mboat1)	0.63
<i>Mcat</i>	NM_001030014.2	malonyl CoA:ACP acyltransferase (mitochondrial) (Mcat), nuclear gene encoding mitochondrial protein	0.66
<i>Mcc</i>	NM_001033406.1	mutated in colorectal cancers (Mcc)	0.66
<i>Mcfd2</i>	NM_139295.2	multiple coagulation factor deficiency 2 (Mcfd2)	0.58
<i>Mcm10</i>	NM_027290.1	minichromosome maintenance deficient 10 (S. cerevisiae) (Mcm10)	0.23
<i>Mcm2</i>	NM_008564.1	minichromosome maintenance deficient 2 mitotin (S. cerevisiae) (Mcm2)	0.29
<i>Mcm3</i>	NM_008563.2	minichromosome maintenance deficient 3 (S. cerevisiae) (Mcm3)	0.53
<i>Mcm4</i>	NM_008565.2	minichromosome maintenance deficient 4 homolog (S. cerevisiae) (Mcm4)	0.28
<i>Mcm5</i>	NM_008566.2	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (Mcm5)	0.14
<i>Mcm6</i>	NM_008567.1	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (Mcm6)	0.25
<i>Mcm7</i>	NM_008568.2	minichromosome maintenance deficient 7 (S. cerevisiae) (Mcm7)	0.48
<i>Mdga2</i>	NM_207010.1	MAM domain containing glycosylphosphatidylinositol anchor 2 (Mdga2)	0.51
<i>Mdh2</i>	NM_008617.2	malate dehydrogenase 2, NAD (mitochondrial) (Mdh2), nuclear gene encoding mitochondrial protein	0.40
<i>Med10</i>	NM_138596.1	mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae) (Med10)	0.55
<i>Mef2c</i>	NM_025282.2	myocyte enhancer factor 2C (Mef2c)	0.58
<i>Mela</i>	NM_008581		0.20
<i>Melk</i>	NM_010790.2	maternal embryonic leucine zipper kinase (Melk)	0.66

<i>Mertk</i>	NM_008587.1	c-mer proto-oncogene tyrosine kinase (Mertk)	0.63
<i>Mest</i>	NM_008590.1	mesoderm specific transcript (Mest)	0.14
<i>Metap1</i>	NM_175224.4	methionyl aminopeptidase 1 (Metap1)	0.64
<i>Metap2</i>	NM_019648.3	methionine aminopeptidase 2 (Metap2)	0.66
<i>Metrn</i>	NM_133719		0.39
<i>Mex3a</i>	NM_001029890.1	mex3 homolog A (C. elegans) (Mex3a)	0.49
<i>Mfap3</i>	NM_145426.2	microfibrillar-associated protein 3 (Mfap3), transcript variant 1	0.63
<i>Mfge8</i>	NM_001045489.1	milk fat globule-EGF factor 8 protein (Mfge8), transcript variant 2	0.42
<i>Mfhas1</i>	NM_001081279.1	malignant fibrous histiocytoma amplified sequence 1 (Mfhas1)	0.42
<i>Mki67</i>	XM_001000692.2	PREDICTED: antigen identified by monoclonal antibody Ki 67 (Mki67)	0.15
<i>Mki67ip</i>	NM_026472.3	Mki67 (FHA domain) interacting nucleolar phosphoprotein (Mki67ip)	0.58
<i>mKIAA0282</i>	AK129109		0.17
<i>Mknk2</i>	NM_021462.3	MAP kinase-interacting serine/threonine kinase 2 (Mknk2)	0.62
<i>Mllt11</i>	NM_019914.3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11 (Mllt11)	0.39
<i>Mllt4</i>	NM_010806.1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (Mllt4)	0.61
<i>Mmp15</i>	NM_008609.3	matrix metallopeptidase 15 (Mmp15)	0.32
<i>Mmp17</i>	NM_011846.4	matrix metallopeptidase 17 (Mmp17)	0.55
<i>Mod1</i>	NM_008615.1	malic enzyme, supernatant (Mod1)	0.49
<i>Morc2a</i>	NM_198162.1	microorchidia 2A (Morc2a)	0.65
<i>Mphosph6</i>	NM_026758.3	M phase phosphoprotein 6 (Mphosph6)	0.53
<i>Mphosph9</i>	NM_001081323.1	M-phase phosphoprotein 9 (Mphosph9)	0.46
<i>Mpi</i>	NM_025837.2	mannose phosphate isomerase (Mpi)	0.64
<i>Mpnd</i>	NM_026530.5	MPN domain containing (Mpnd)	0.66
<i>Mre11a</i>	NM_018736.2	meiotic recombination 11 homolog A (S. cerevisiae) (Mre11a)	0.59
<i>Mrpl12</i>	NM_027204.2	mitochondrial ribosomal protein L12 (Mrpl12), nuclear gene encoding mitochondrial protein	0.46
<i>Mrpl15</i>	AK017804		0.56
<i>Mrpl17</i>	NM_025301.1		0.55
<i>Mrpl18</i>	NM_026310.3	mitochondrial ribosomal protein L18 (Mrpl18), nuclear gene encoding mitochondrial protein	0.64
<i>Mrpl20</i>	NM_025570.2	mitochondrial ribosomal protein L20 (Mrpl20), nuclear gene encoding mitochondrial protein	0.58
<i>Mrpl22</i>	NM_175001.2	mitochondrial ribosomal protein L22 (Mrpl22), nuclear gene encoding mitochondrial protein	0.61
<i>Mrpl3</i>	NM_053159.3	mitochondrial ribosomal protein L3 (Mrpl3), nuclear gene encoding mitochondrial protein	0.62
<i>Mrpl30</i>	NM_027098.2	mitochondrial ribosomal protein L30 (Mrpl30), nuclear gene encoding mitochondrial protein	0.59
<i>Mrpl34</i>	NM_053162.2	mitochondrial ribosomal protein L34 (Mrpl34), nuclear gene encoding mitochondrial protein	0.59
<i>Mrpl37</i>	NM_025500.1	mitochondrial ribosomal protein L37 (Mrpl37), nuclear gene encoding mitochondrial protein	0.63
<i>Mrpl38</i>	NM_024177.3	mitochondrial ribosomal protein L38 (Mrpl38), nuclear gene encoding mitochondrial protein	0.61
<i>Mrpl43</i>	NM_053164.3	mitochondrial ribosomal protein L43 (Mrpl43), nuclear gene encoding mitochondrial protein	0.62
<i>Mrpl52</i>	NM_026851.2	mitochondrial ribosomal protein L52 (Mrpl52), nuclear gene encoding mitochondrial protein	0.65
<i>Mrpl53</i>	NM_026744.3	mitochondrial ribosomal protein L53 (Mrpl53), nuclear gene encoding mitochondrial protein	0.46
<i>Mrpl54</i>	NM_025317.2	mitochondrial ribosomal protein L54 (Mrpl54), nuclear gene encoding mitochondrial protein	0.60
<i>Mrps10</i>	NM_183086		0.53
<i>Mrps16</i>	NM_025440.2	mitochondrial ribosomal protein S16 (Mrps16), nuclear gene encoding mitochondrial protein	0.64
<i>Mrps18b</i>	NM_025878.1	mitochondrial ribosomal protein S18B (Mrps18b), nuclear gene encoding mitochondrial protein	0.58
<i>Mrps2</i>	NM_080452.2	mitochondrial ribosomal protein S2 (Mrps2), nuclear gene encoding mitochondrial protein	0.64
<i>Mrps28</i>	NM_025434.2	mitochondrial ribosomal protein S28 (Mrps28), nuclear gene encoding mitochondrial protein	0.58
<i>Mrps30</i>	NM_021556.3	mitochondrial ribosomal protein S30 (Mrps30), nuclear gene encoding mitochondrial protein	0.63
<i>Mrps35</i>	NM_145573.2	mitochondrial ribosomal protein S35 (Mrps35), nuclear gene encoding mitochondrial protein	0.62
<i>Mrps7</i>	NM_025305.1	mitochondrial ribosomal protein S7 (Mrps7)	0.47
<i>Mrto4</i>	NM_023536.2	MRT4, mRNA turnover 4, homolog (S. cerevisiae) (Mrto4)	0.52
<i>Msl211</i>	XM_150227.8	PREDICTED: male-specific lethal 2-like 1 (Drosophila) (Msl211)	0.58

<i>Msto1</i>	NM_144898.1	misato homolog 1 (Drosophila) (Msto1)	0.64
<i>Mta2</i>	NM_011842.3	metastasis-associated gene family, member 2 (Mta2)	0.61
<i>Mtap</i>	NM_024433.1	methylthioadenosine phosphorylase (Mtap)	0.49
<i>Mtch2</i>	NM_019758.2	mitochondrial carrier homolog 2 (C. elegans) (Mtch2), nuclear gene encoding mitochondrial protein	0.66
<i>mt-Co2</i>			0.63
<i>Mtdh</i>	NM_026002.4	Metadherin (Mtdh)	0.48
<i>mtDNA_ATP8</i>			0.64
<i>Mthfd2</i>	NM_008638		0.22
<i>Mtmr11</i>	NM_181409.2	myotubularin related protein 11 (Mtmr11)	0.51
<i>Mtmr12</i>	NM_172958.3	myotubularin related protein 12 (Mtmr12)	0.56
<i>Mtmr2</i>	NM_023858.1	myotubularin related protein 2 (Mtmr2)	0.52
<i>Mvd</i>	NM_138656.1	mevalonate (diphospho) decarboxylase (Mvd)	0.56
<i>Mxra8</i>	NM_024263.3	matrix-remodelling associated 8 (Mxra8)	0.60
<i>Mybbp1a</i>	NM_016776.2	MYB binding protein (P160) 1a (Mybbp1a)	0.56
<i>Mybl2</i>	NM_008652.2	myeloblastosis oncogene-like 2 (Mybl2)	0.46
<i>Myef2</i>	NM_010852.1	myelin basic protein expression factor 2, repressor (Myef2)	0.49
<i>Myh9</i>	NM_022410.1		0.56
<i>Mylk</i>	NM_139300.3	myosin, light polypeptide kinase (Mylk)	0.22
<i>Myo1b</i>	NM_010863.2	myosin IB (Myo1b)	0.55
<i>Myo5a</i>	NM_010864.2	myosin Va (Myo5a)	0.44
<i>Myo6</i>	NM_001039546.1	myosin VI (Myo6)	0.49
<i>N4wbp5-pending</i>	AK050560		0.64
<i>N6amt1</i>	NM_026366.1	N-6 adenine-specific DNA methyltransferase 1 (putative) (N6amt1)	0.60
<i>N6amt2</i>	NM_026526.2	N-6 adenine-specific DNA methyltransferase 2 (putative) (N6amt2)	0.51
<i>Nab1</i>	NM_008667.2	Ngfi-A binding protein 1 (Nab1)	0.52
<i>Naca</i>	NM_013608.2	nascent polypeptide-associated complex alpha polypeptide (Naca)	0.50
<i>Nadk</i>	NM_138671.1	NAD kinase (Nadk)	0.66
<i>Nans</i>	NM_053179.3	N-acetylneuraminic acid synthase (sialic acid synthase) (Nans)	0.43
<i>Nap111</i>	NM_015781.3	nucleosome assembly protein 1-like 1 (Nap111)	0.35
<i>Nap114</i>	NM_008672		0.65
<i>Nap115</i>	NM_021432.2	nucleosome assembly protein 1-like 5 (Nap115)	0.59
<i>Narg1</i>	NM_053089.2	NMDA receptor-regulated gene 1 (Narg1)	0.46
<i>Nasp</i>	NM_016777.3	nuclear autoantigenic sperm protein (histone-binding) (Nasp), transcript variant 2	0.53
<i>Nat5</i>	NM_026425.1	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (Nat5)	0.56
<i>Nav1</i>	NM_173437		0.41
<i>Ncam1</i>	NM_010875.3	neural cell adhesion molecule 1 (Ncam1), transcript variant 2	0.40
<i>Ncan</i>	NM_007789.2	neurocan (Ncan)	0.13
<i>Ncapd2</i>	NM_146171.1	non-SMC condensin I complex, subunit D2 (Ncapd2)	0.24
<i>Ncapd3</i>	NM_178113.2	non-SMC condensin II complex, subunit D3 (Ncapd3)	0.45
<i>Ncapg2</i>	NM_133762.3	non-SMC condensin II complex, subunit G2 (Ncapg2)	0.62
<i>Ncaph</i>	NM_144818.1	non-SMC condensin I complex, subunit H (Ncaph)	0.16
<i>Ncdn</i>	NM_011986.2	neurochondrin (Ncdn)	0.60
<i>Ncstn</i>	NM_021607.2	nicastatin (Ncstn)	0.58
<i>Ndc80</i>	NM_023294.1	NDC80 homolog, kinetochore complex component (S. cerevisiae) (Ndc80)	0.42
<i>Ndfip1</i>	NM_022996.1	Nedd4 family interacting protein 1 (Ndfip1)	0.65
<i>Ndufa12</i>	NM_025551.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (Ndufa12)	0.64
<i>Ndufa12l</i>	XM_001476048.1	PREDICTED: Ndufa12-like (Ndufa12l)	0.66
<i>Ndufa4</i>	NM_010886.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (Ndufa4)	0.63
<i>Ndufa5</i>	NM_026614.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (Ndufa5), nuclear gene encoding mitochondrial protein	0.64
<i>Ndufb6</i>	NM_001033305.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (Ndufb6)	0.52
<i>Ndufb8</i>	NM_026061.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (Ndufb8)	0.62
<i>Ndufc1</i>	NM_025523.1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (Ndufc1)	0.56
<i>Ndufc2</i>	NM_024220.1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (Ndufc2)	0.51
<i>Ndufs2</i>	NM_153064.4	NADH dehydrogenase (ubiquinone) Fe-S protein 2 (Ndufs2)	0.58
<i>Ndufs4</i>	NM_010887.1	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Ndufs4), nuclear gene encoding mitochondrial protein	0.59
<i>Ndufv2</i>	NM_028388.1	NADH dehydrogenase (ubiquinone) flavoprotein 2 (Ndufv2)	0.59
<i>Necap1</i>	NM_026267.1	NECAP endocytosis associated 1 (Necap1)	0.62
<i>Nedd1</i>	NM_008682.1	neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1)	0.62
<i>Nek3</i>	NM_011848.2	NIMA (never in mitosis gene a)-related expressed kinase 3 (Nek3)	0.60
<i>Neo1</i>	NM_008684.1		0.53
<i>Neto2</i>	NM_001081324.1	neuropilin (NRP) and tolloid (TLL)-like 2 (Neto2)	0.40
<i>Neurl</i>	NM_021360		0.21
<i>Nfib</i>	NM_008687.2	nuclear factor I/B (Nfib)	0.56
<i>Nhs1</i>	NM_173390.3	NHS-like 1 (Nhs1)	0.63
<i>Nip7</i>	NM_025391.1	nuclear import 7 homolog (S. cerevisiae) (Nip7)	0.64
<i>Nipsnap3a</i>	NM_025623.2	nipsnap homolog 3A (C. elegans) (Nipsnap3a)	0.54

<i>Nkrf</i>	NM_029891.2	NF-kappaB repressing factor (Nkrf)	0.57
<i>Nkx2-2</i>	NM_010919.2	NK2 transcription factor related, locus 2 (Drosophila) (Nkx2-2), transcript variant 1	0.30
<i>Nme1</i>	NM_008704.2	non-metastatic cells 1, protein (NM23A) expressed in (Nme1)	0.43
<i>Nme2</i>	NM_008705.4	non-metastatic cells 2, protein (NM23B) expressed in (Nme2), transcript variant 1	0.39
<i>Nme4</i>	NM_019731.1	non-metastatic cells 4, protein expressed in (Nme4), nuclear gene encoding mitochondrial protein	0.57
<i>Nmral1</i>	NM_026393.1	NmrA-like family domain containing 1 (Nmral1)	0.58
<i>Nmt1</i>	NM_008707.3	N-myristoyltransferase 1 (Nmt1)	0.63
<i>Nob1</i>	NM_026277.1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae) (Nob1)	0.62
<i>Noc2l</i>	NM_021303.2	nucleolar complex associated 2 homolog (S. cerevisiae) (Noc2l)	0.57
<i>Noc4l</i>	NM_153570.2	nucleolar complex associated 4 homolog (S. cerevisiae) (Noc4l)	0.57
<i>Nol1</i>	NM_138747.1	nucleolar protein 1 (Nol1)	0.59
<i>Nol10</i>	NM_001008421.1	nucleolar protein 10 (Nol10)	0.63
<i>Nol5</i>	NM_018868.2	nucleolar protein 5 (Nol5)	0.24
<i>Nol5a</i>	NM_024193.2	nucleolar protein 5A (Nol5a)	0.47
<i>Nola1</i>	NM_026578.2	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) (Nola1)	0.40
<i>Nola2</i>	NM_026631.3	nucleolar protein family A, member 2 (Nola2)	0.49
<i>Nola3</i>	NM_025403.2	nucleolar protein family A, member 3 (Nola3)	0.48
<i>Nomo1</i>	NM_153057.3	nodal modulator 1 (Nomo1)	0.39
<i>Npc2</i>	NM_023409.4	Niemann Pick type C2 (Npc2)	0.66
<i>Npm1</i>	NM_008722.1	nucleophosmin 1 (Npm1)	0.41
<i>Npm3</i>	NM_008723.1	nucleoplasmin 3 (Npm3)	0.25
<i>Npm3-ps1</i>	NR_002702.1	nucleoplasmin 3, pseudogene 1 (Npm3-ps1), non-coding RNA.	0.25
<i>Nptn</i>	NM_009145.1	neuroplastin (Nptn)	0.45
<i>Nptx1</i>	NM_008730.2	neuronal pentraxin 1 (Nptx1)	0.22
<i>Nqo2</i>	NM_020282.2	NAD(P)H dehydrogenase, quinone 2 (Nqo2)	0.64
<i>Nr2c2ap</i>	NM_001025587.1	nuclear receptor 2C2-associated protein (Nr2c2ap), transcript variant 2	0.66
<i>Nrarp</i>	NM_025980.2	Notch-regulated ankyrin repeat protein (Nrarp)	0.43
<i>Nrm</i>	NM_134122.2	nurim (nuclear envelope membrane protein) (Nrm)	0.20
<i>Nrn1</i>	NM_153529.1	neuritin 1 (Nrn1)	0.42
<i>Nrp1</i>	NM_008737.1	neuropilin 1 (Nrp1)	0.35
<i>Nsbp1</i>	NM_016710.2	nucleosome binding protein 1 (Nsbp1)	0.51
<i>Nsdhl</i>	NM_010941.3	NAD(P) dependent steroid dehydrogenase-like (Nsdhl)	0.53
<i>Nsep1</i>	NM_011732		0.41
<i>Nt5dc2</i>	NM_027289.1	5'-nucleotidase domain containing 2 (Nt5dc2)	0.50
<i>Nubp1</i>	NM_011955.1	nucleotide binding protein 1 (Nubp1)	0.48
<i>Nudcd2</i>	NM_026023.4	NudC domain containing 2 (Nudcd2)	0.58
<i>Nudt21</i>	NM_026623.3	nudix (nucleoside diphosphate linked moiety X)-type motif 21 (Nudt21)	0.50
<i>Nudt5</i>	NM_016918.3	nudix (nucleoside diphosphate linked moiety X)-type motif 5 (Nudt5)	0.50
<i>Nup133</i>	NM_172288.1	nucleoporin 133 (Nup133)	0.64
<i>Nup160</i>	NM_021512.2	nucleoporin 160 (Nup160)	0.51
<i>Nup205</i>	XM_133073.7	PREDICTED: nucleoporin 205, transcript variant 1 (Nup205)	0.39
<i>Nup210</i>	NM_018815.1	nucleoporin 210 (Nup210)	0.17
<i>Nup43</i>	NM_145706.1	nucleoporin 43 (Nup43)	0.48
<i>Nup62</i>	NM_053074.1	nucleoporin 62 (Nup62)	0.36
<i>Nup85</i>	NM_001002929.3	nucleoporin 85 (Nup85)	0.54
<i>Nup88</i>	NM_172394.2	nucleoporin 88 (Nup88), transcript variant 1	0.50
<i>Nup93</i>	NM_172410		0.66
<i>Nus1</i>	NM_030250.1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae) (Nus1)	0.57
<i>Nusap1</i>	NM_001042652.1	nucleolar and spindle associated protein 1 (Nusap1), transcript variant 2	0.20
<i>Nutf2</i>	NM_026532.3	nuclear transport factor 2 (Nutf2)	0.59
<i>Nxph1</i>	NM_008751.2	neurexophilin 1 (Nxph1)	0.15
<i>Nxt1</i>	NM_019761.4	NTF2-related export protein 1 (Nxt1)	0.63
<i>Ociad2</i>	NM_026950.3	OCIA domain containing 2 (Ociad2)	0.40
<i>Ogdh</i>	NM_010956.3	oxoglutarate dehydrogenase (lipoamide) (Ogdh), nuclear gene encoding mitochondrial protein	0.59
<i>Ola1</i>	NM_025942.2	Obg-like ATPase 1 (Ola1), transcript variant 1	0.52
<i>Olfm2</i>	NM_173777.2	olfactomedin 2 (Olfm2)	0.39
<i>Olfml2b</i>	NM_177068.3	olfactomedin-like 2B (Olfml2b)	0.28
<i>Olig1</i>	NM_016968.4	oligodendrocyte transcription factor 1 (Olig1)	0.24
<i>Omg</i>	NM_019409.1	oligodendrocyte myelin glycoprotein (Omg)	0.55
<i>Opn3</i>	NM_010098.2	opsin 3 (Opn3)	0.50
<i>Oprs1</i>	NM_011014.2	opioid receptor, sigma 1 (Oprs1)	0.56
<i>Orai1</i>	NM_175423.3	ORAI calcium release-activated calcium modulator 1 (Orai1)	0.63
<i>Orc5l</i>	NM_011959.2	origin recognition complex, subunit 5-like (S. cerevisiae) (Orc5l)	0.53
<i>Orc6l</i>	NM_019716.1	origin recognition complex, subunit 6-like (S. cerevisiae) (Orc6l)	0.47
<i>Osbp16</i>	NM_145525.2	oxysterol binding protein-like 6 (Osbp16)	0.27
<i>Osbp18</i>	NM_175489.3	oxysterol binding protein-like 8 (Osbp18), transcript variant 1	0.58

<i>Ostm1</i>	NM_172416.2	osteopetrosis associated transmembrane protein 1 (Ostm1)	0.51
<i>Oxct1</i>	NM_024188.5	3-oxoacid CoA transferase 1 (Oxct1)	0.63
<i>Oxr1</i>	NM_130885.2	oxidation resistance 1 (Oxr1), transcript variant 1	0.59
<i>P2ry5</i>	NM_175116.2	purinergic receptor P2Y, G-protein coupled, 5 (P2ry5)	0.32
<i>P4hb</i>	NM_011032.2	prolyl 4-hydroxylase, beta polypeptide (P4hb)	0.54
<i>Pa2g4</i>	NM_011119.3	proliferation-associated 2G4 (Pa2g4)	0.42
<i>Pabpc1</i>	NM_008774.2	poly A binding protein, cytoplasmic 1 (Pabpc1)	0.60
<i>Pabpc4</i>	NM_130881.2	poly A binding protein, cytoplasmic 4 (Pabpc4), transcript variant 1	0.46
<i>Pabpn1</i>	NM_019402.1	poly(A) binding protein, nuclear 1 (Pabpn1)	0.52
<i>Pafah1b1</i>	NM_013625.1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit (Pafah1b1)	0.58
<i>Pafah1b3</i>	NM_008776.1	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit (Pafah1b3)	0.62
<i>Palmd</i>	NM_023245.3	palmdelphin (Palmd)	0.38
<i>Pank3</i>	NM_145962.2	pantothenate kinase 3 (Pank3)	0.54
<i>Papola</i>	NM_011112.2	poly (A) polymerase alpha (Papola)	0.61
<i>Parp1</i>	NM_007415.2	poly (ADP-ribose) polymerase family, member 1 (Parp1)	0.50
<i>Pbk</i>	NM_023209.1	PDZ binding kinase (Pbk)	0.08
<i>Pcbp1</i>	NM_011865.3	poly(rC) binding protein 1 (Pcbp1)	0.55
<i>Pcdh17</i>	NM_001013753.1	protocadherin 17 (Pcdh17)	0.33
<i>Pcdh7</i>	NM_018764.1	protocadherin 7 (Pcdh7)	0.44
<i>Pcdh9</i>	NM_001081377.1	protocadherin 9 (Pcdh9)	0.45
<i>Pcp4l1</i>	XM_484933.5	PREDICTED: Purkinje cell protein 4-like 1 (Pcp4l1)	0.64
<i>Pctk1</i>	NM_011049.4	PCTAIRE-motif protein kinase 1 (Pctk1)	0.64
<i>Pdap1</i>	NM_001033313.3	PDGFA associated protein 1 (Pdap1)	0.28
<i>Pdcd2l</i>	NM_026549.3	programmed cell death 2-like (Pdcd2l)	0.65
<i>Pde1b</i>	NM_008800		0.66
<i>Pdgfa</i>	NM_008808		0.53
<i>Pdha1</i>	NM_008810.2	pyruvate dehydrogenase E1 alpha 1 (Pdha1), nuclear gene encoding mitochondrial protein	0.65
<i>Pdhb</i>	NM_024221.3	pyruvate dehydrogenase (lipoamide) beta (Pdhb)	0.56
<i>Pdia3</i>	NM_007952.2	protein disulfide isomerase associated 3 (Pdia3)	0.57
<i>Pdia5</i>	NM_028295.1	protein disulfide isomerase associated 5 (Pdia5)	0.41
<i>Pdk3</i>	NM_145630.2	pyruvate dehydrogenase kinase, isoenzyme 3 (Pdk3)	0.64
<i>Pdlim4</i>	NM_019417.2	PDZ and LIM domain 4 (Pdlim4)	0.53
<i>Pdlim5</i>	NM_019808.1	PDZ and LIM domain 5 (Pdlim5), transcript variant 1	0.57
<i>Pdss1</i>	NM_019501.3	prenyl (solanesyl) diphosphate synthase, subunit 1 (Pdss1)	0.48
<i>Pdpx</i>	NM_020271.3	pyridoxal (pyridoxine, vitamin B6) phosphatase (Pdpx)	0.53
<i>Pdzrn4</i>	XM_001481302.1	PREDICTED: PDZ domain containing RING finger 4 (Pdzrn4)	0.33
<i>Peli1</i>	NM_023324.2	pellino 1 (Peli1)	0.49
<i>Pfdn4</i>	NM_001013369.1	prefoldin 4 (Pfdn4), transcript variant 2	0.32
<i>Pfn1</i>	NM_011072.2	profilin 1 (Pfn1)	0.52
<i>Pgam1</i>	NM_023418.2	phosphoglycerate mutase 1 (Pgam1)	0.57
<i>Pgam5</i>	NM_028273.1	phosphoglycerate mutase family member 5 (Pgam5)	0.44
<i>Pgls</i>	NM_025396.3	6-phosphogluconolactonase (Pgls)	0.57
<i>Pgp</i>	NM_025954.3	phosphoglycolate phosphatase (Pgp)	0.29
<i>Phb2</i>	NM_007531.2	prohibitin 2 (Phb2)	0.49
<i>Phc2</i>	NM_018774.3	polyhomeotic-like 2 (Drosophila) (Phc2)	0.47
<i>Phf20</i>	NM_172674.2	PHD finger protein 20 (Phf20)	0.50
<i>Phf5a</i>	NM_026737.3	PHD finger protein 5A (Phf5a)	0.60
<i>Phf6</i>	NM_027642.1	PHD finger protein 6 (Phf6)	0.54
<i>Phlda1</i>	NM_009344.1	pleckstrin homology-like domain, family A, member 1 (Phlda1)	0.34
<i>Phtf2</i>	NM_172992.2	putative homeodomain transcription factor 2 (Phtf2)	0.58
<i>Pi4ka</i>	NM_001001983.1	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (Pi4ka)	0.65
<i>Pif1</i>	NM_172453.1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae) (Pif1)	0.37
<i>Piga</i>	NM_011081.2	phosphatidylinositol glycan anchor biosynthesis, class A (Piga)	0.61
<i>Pip4k2a</i>	NM_008845.4	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha (Pip4k2a)	0.66
<i>Pip4k2b</i>	NM_054051.1	phosphatidylinositol-5-phosphate 4-kinase, type II, beta (Pip4k2b)	0.53
<i>Pitrm1</i>	NM_145131.1	pitrilysin metallopeptidase 1 (Pitrm1)	0.61
<i>Pja1</i>	NM_008853.2	praja1, RING-H2 motif containing (Pja1)	0.57
<i>Pja2</i>	NM_144859.2	praja 2, RING-H2 motif containing (Pja2), transcript variant 2	0.61
<i>Pkia</i>	NM_008862.3	protein kinase inhibitor, alpha (Pkia)	0.48
<i>Pkm2</i>	XM_131934.4		0.50
<i>Pkn2</i>	NM_178654.3	protein kinase N2 (Pkn2)	0.63
<i>Plaa</i>	NM_172695.2	phospholipase A2, activating protein (Plaa)	0.53
<i>Pld1</i>	XM_130807.1		0.51
<i>Plekha1</i>	NM_133942.2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 (Plekha1)	0.63
<i>Plekha8</i>	NM_001001335.1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8 (Plekha8)	0.63
<i>Plekhh1</i>	NM_133244.2		0.23

<i>Plk1</i>	NM_011121.3	polo-like kinase 1 (Drosophila) (Plk1)	0.11
<i>Plk2</i>	NM_152804.1	polo-like kinase 2 (Drosophila) (Plk2)	0.29
<i>Plk4</i>	NM_011495.1		0.57
<i>Plvap</i>	NM_032398.1	plasmalemma vesicle associated protein (Plvap)	0.13
<i>Plxnd1</i>	NM_026376.3	plexin D1 (Plxnd1)	0.54
<i>Pmp22</i>	NM_008885.2	peripheral myelin protein 22 (Pmp22)	0.51
<i>Pno1</i>	NM_025443.2	partner of NOB1 homolog (S. cerevisiae) (Pno1)	0.41
<i>Pola2</i>	NM_008893.2	polymerase (DNA directed), alpha 2 (Pola2)	0.64
<i>Pold1</i>	NM_011131.2	polymerase (DNA directed), delta 1, catalytic subunit (Pold1)	0.33
<i>Pold2</i>	NM_008894.1	polymerase (DNA directed), delta 2, regulatory subunit (Pold2)	0.56
<i>Pold4</i>	NM_027196		0.61
<i>Pole</i>	NM_011132.1	polymerase (DNA directed), epsilon (Pole)	0.45
<i>Pole4</i>	NM_025882.3	polymerase (DNA-directed), epsilon 4 (p12 subunit) (Pole4)	0.60
<i>Polg</i>	NM_017462.2	polymerase (DNA directed), gamma (Polg)	0.58
<i>Polr1a</i>	NM_009088.2	polymerase (RNA) I polypeptide A (Polr1a)	0.58
<i>Polr1d</i>	NM_009087.1	polymerase (RNA) I polypeptide D (Polr1d), transcript variant 1	0.64
<i>Polr1e</i>	NM_022811.2	polymerase (RNA) I polypeptide E (Polr1e)	0.60
<i>Polr2g</i>	NM_026329.2	polymerase (RNA) II (DNA directed) polypeptide G (Polr2g)	0.67
<i>Polr2h</i>	NM_145632.1	polymerase (RNA) II (DNA directed) polypeptide H (Polr2h)	0.66
<i>Polr3k</i>	NM_025901.2	polymerase (RNA) III (DNA directed) polypeptide K (Polr3k)	0.60
<i>Pop5</i>	NM_026398.2	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (Pop5)	0.60
<i>Pou3f1</i>	NM_011141.2	POU domain, class 3, transcription factor 1 (Pou3f1)	0.19
<i>Ppa1</i>	NM_026438.2	pyrophosphatase (inorganic) 1 (Ppa1)	0.48
<i>Ppa2</i>	NM_146141.1	pyrophosphatase (inorganic) 2 (Ppa2), nuclear gene encoding mitochondrial protein	0.61
<i>Ppan</i>	NM_145610		0.48
<i>Ppat</i>	XM_001002886.2	PREDICTED: phosphoribosyl pyrophosphate amidotransferase, transcript variant 8 (Ppat)	0.61
<i>Ppia</i>	NM_008907.1	peptidylprolyl isomerase A (Ppia)	0.54
<i>Ppic</i>	NM_008908.1	peptidylprolyl isomerase C (Ppic)	0.35
<i>Ppid</i>	NM_026352.2		0.61
<i>Ppif</i>	NM_134084.1	peptidylprolyl isomerase F (cyclophilin F) (Ppif), nuclear gene encoding mitochondrial protein	0.47
<i>Ppih</i>	NM_028677		0.51
<i>Ppm1b</i>	NM_011151.1	protein phosphatase 1B, magnesium dependent, beta isoform (Ppm1b)	0.64
<i>Ppm1g</i>	NM_008014.3	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (Ppm1g)	0.62
<i>Ppp1ca</i>	NM_031868.2	protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1ca)	0.65
<i>Ppp1r10</i>	NM_175934.2	protein phosphatase 1, regulatory subunit 10 (Ppp1r10)	0.62
<i>Ppp1r12a</i>	NM_027892.2	protein phosphatase 1, regulatory (inhibitor) subunit 12A (Ppp1r12a)	0.44
<i>Ppp1r14b</i>	NM_008889.1		0.54
<i>Ppp1r8</i>	NM_146154.1	protein phosphatase 1, regulatory (inhibitor) subunit 8 (Ppp1r8)	0.65
<i>Ppp1r9b</i>	NM_172261.2	protein phosphatase 1, regulatory subunit 9B (Ppp1r9b)	0.60
<i>Ppp2cb</i>	NM_017374.3	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb)	0.59
<i>Ppp2r2d</i>	NM_026391.2	protein phosphatase 2, regulatory subunit B, delta isoform (Ppp2r2d)	0.64
<i>Ppp2r5c</i>	NM_001081458.1	protein phosphatase 2, regulatory subunit B (B56), gamma isoform (Ppp2r5c), transcript variant 3	0.51
<i>Ppp3cb</i>	NM_008914		0.46
<i>Ppp3r1</i>	NM_024459.2	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I) (Ppp3r1)	0.66
<i>Ppp4r1</i>	NM_146081.1	protein phosphatase 4, regulatory subunit 1 (Ppp4r1)	0.64
<i>Ppp6c</i>	NM_024209.2	protein phosphatase 6, catalytic subunit (Ppp6c)	0.57
<i>Pprc1</i>	NM_001081214.1	peroxisome proliferative activated receptor, gamma, coactivator-related 1 (Pprc1)	0.54
<i>Prc1</i>	NM_145150.1	protein regulator of cytokinesis 1 (Prc1)	0.06
<i>Prpcp</i>	NM_028243.2	prolylcarboxypeptidase (angiotensinase C) (Prpcp)	0.36
<i>Prdx4</i>	NM_016764.3	peroxiredoxin 4 (Prdx4)	0.63
<i>Prep</i>	NM_011156.2	prolyl endopeptidase (Prep)	0.48
<i>Prkaca</i>	NM_008854.3	protein kinase, cAMP dependent, catalytic, alpha (Prkaca)	0.54
<i>Prkacb</i>	NM_011100.3	protein kinase, cAMP dependent, catalytic, beta (Prkacb)	0.46
<i>Prkar2b</i>	NM_011158.3	protein kinase, cAMP dependent regulatory, type II beta (Prkar2b)	0.40
<i>Prkcb</i>	NM_008855.1		0.15
<i>Prkcbp1</i>	NM_027230.3	protein kinase C binding protein 1 (Prkcbp1)	0.67
<i>Prkcsh</i>	NM_008925.1	protein kinase C substrate 80K-H (Prkcsh)	0.56
<i>Prkd3</i>	NM_029239.2	protein kinase D3 (Prkd3)	0.50
<i>Prkg1</i>	NM_011160		0.55
<i>Prmt3</i>	NM_133740.1	protein arginine N-methyltransferase 3 (Prmt3)	0.54

<i>Prmt5</i>	NM_013768.2	protein arginine N-methyltransferase 5 (Prmt5)	0.59
<i>Prmt7</i>	NM_145404.1	protein arginine N-methyltransferase 7 (Prmt7)	0.47
<i>Prokr1</i>	NM_021381.3	prokineticin receptor 1 (Prokr1)	0.46
<i>Prpf19</i>	NM_134129.2	PRP19/PSO4 pre-mRNA processing factor 19 homolog (<i>S. cerevisiae</i>) (Prpf19)	0.57
<i>Prpf38a</i>	NM_172697.1	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (Prpf38a)	0.60
<i>Prpf40a</i>	NM_018785.2	PRP40 pre-mRNA processing factor 40 homolog A (yeast) (Prpf40a)	0.59
<i>Prr18</i>	NM_178774.3	proline rich region 18 (Prr18)	0.33
<i>Prrc1</i>	NM_028447.2	proline-rich coiled-coil 1 (Prrc1)	0.63
<i>Prss35</i>	NM_178738.2	protease, serine, 35 (Prss35)	0.18
<i>Psip1</i>	NM_133948.4	PC4 and SFRS1 interacting protein 1 (Psip1)	0.64
<i>Psma5</i>	NM_011967.2	proteasome (prosome, macropain) subunit, alpha type 5 (Psma5)	0.59
<i>Psma7</i>	NM_011969.1	proteasome (prosome, macropain) subunit, alpha type 7 (Psma7)	0.64
<i>Psemb10</i>	NM_013640.2	proteasome (prosome, macropain) subunit, beta type 10 (Psemb10)	0.56
<i>Psemb2</i>	NM_011970.2	proteasome (prosome, macropain) subunit, beta type 2 (Psemb2)	0.62
<i>Psemb4</i>	NM_008945.2	proteasome (prosome, macropain) subunit, beta type 4 (Psemb4)	0.61
<i>Psemb7</i>	NM_011187.1	proteasome (prosome, macropain) subunit, beta type 7 (Psemb7)	0.66
<i>Psmc1</i>	NM_008947		0.60
<i>Psmc3ip</i>	NM_008949.2	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein (Psmc3ip)	0.58
<i>Psmc5</i>	NM_008950.1	protease (prosome, macropain) 26S subunit, ATPase 5 (Psmc5)	0.65
<i>Psmc1</i>	NM_027357.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (Psmc1)	0.56
<i>Psmc12</i>	NM_025894.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (Psmc12)	0.56
<i>Psmc14</i>	NM_021526.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 (Psmc14)	0.64
<i>Psmc8</i>	NM_026545.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 (Psmc8)	0.67
<i>Psmc3</i>	NM_011192.3	proteasome (prosome, macropain) 28 subunit, 3 (Psmc3)	0.59
<i>Ptcd2</i>	NM_026873.2	pentatricopeptide repeat domain 2 (Ptcd2)	0.66
<i>Pten</i>	NM_008960.2	phosphatase and tensin homolog (Pten)	0.66
<i>Ptk2</i>	NM_007982.1	PTK2 protein tyrosine kinase 2 (Ptk2)	0.36
<i>Ptn</i>	NM_008973.2	pleiotrophin (Ptn)	0.28
<i>Ptp4a2</i>	NM_008974.3	protein tyrosine phosphatase 4a2 (Ptp4a2)	0.62
<i>Ptpla</i>	NM_001012396.2	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (Ptpla), transcript variant 2	0.61
<i>Ptpn12</i>	NM_011203.2	protein tyrosine phosphatase, non-receptor type 12 (Ptpn12)	0.61
<i>Ptpre</i>	NM_011212.3	protein tyrosine phosphatase, receptor type, E (Ptpre)	0.53
<i>Ptpm</i>	NM_008984		0.65
<i>Ptpro</i>	NM_011216.2	protein tyrosine phosphatase, receptor type, O (Ptpro)	0.28
<i>Ptprz1</i>	XM_988289.1	PREDICTED: protein tyrosine phosphatase, receptor type Z, polypeptide 1, transcript variant 3 (Ptprz1)	0.19
<i>Pum2</i>	NM_030723.1	pumilio 2 (<i>Drosophila</i>) (Pum2)	0.64
<i>Purb</i>	NM_011221.2	purine rich element binding protein B (Purb)	0.64
<i>Pus7l</i>	NM_172437.2	pseudouridylate synthase 7 homolog (<i>S. cerevisiae</i>)-like (Pus7l)	0.41
<i>Pusl1</i>	XM_001476573.1	PREDICTED: pseudouridylate synthase-like 1, transcript variant 1 (Pusl1)	0.53
<i>Pvrl3</i>	NM_021495.2	poliovirus receptor-related 3 (Pvrl3), transcript variant alpha	0.55
<i>Pycr2</i>	NM_133705.1	pyrroline-5-carboxylate reductase family, member 2 (Pycr2)	0.58
<i>Qpct</i>	NM_027455.1	glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Qpct)	0.43
<i>Qrs1</i>	NM_001081054.2	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (Qrs1)	0.56
<i>R3hdm1</i>	NM_181750.2	R3H domain 1 (binds single-stranded nucleic acids) (R3hdm1)	0.67
<i>Rab26</i>	XM_283428.6	PREDICTED: RAB26, member RAS oncogene family, transcript variant 1 (Rab26)	0.06
<i>Rab31</i>	NM_133685.1	RAB31, member RAS oncogene family (Rab31)	0.64
<i>Rab34</i>	NM_033475.2	RAB34, member of RAS oncogene family (Rab34)	0.53
<i>Rab35</i>	NM_198163.1	RAB35, member RAS oncogene family (Rab35)	0.61
<i>Rab3a</i>	NM_009001.3	RAB3A, member RAS oncogene family (Rab3a)	0.50
<i>Rab3b</i>	NM_023537.4		0.36
<i>Rab3gap2</i>	XM_980542.1	PREDICTED: RAB3 GTPase activating protein subunit 2, transcript variant 4 (Rab3gap2)	0.55
<i>Rab5c</i>	NM_024456.2	RAB5C, member RAS oncogene family (Rab5c)	0.65
<i>Rab8b</i>	NM_173413.2	RAB8B, member RAS oncogene family (Rab8b)	0.43
<i>Rabggtb</i>	NM_011231.1	RAB geranylgeranyl transferase, b subunit (Rabggtb)	0.53
<i>Rabif</i>	NM_145510.1	RAB interacting factor (Rabif)	0.63
<i>Rabl3</i>	NM_026297.1		0.63
<i>Rad51</i>	NM_011234.2	RAD51 homolog (<i>S. cerevisiae</i>) (Rad51)	0.56
<i>Rad51c</i>	NM_053269.2	Rad51 homolog c (<i>S. cerevisiae</i>) (Rad51c)	0.47
<i>Rad54l</i>	NM_009015.2	RAD54 like (<i>S. cerevisiae</i>) (Rad54l)	0.49
<i>Raet1b</i>	NM_009017.1	retinoic acid early transcript beta (Raet1b)	0.34
<i>Raly</i>	NM_023130.2	hnRNP-associated with lethal yellow (Raly)	0.36
<i>Ramp2</i>	NM_019444.2	receptor (calcitonin) activity modifying protein 2 (Ramp2)	0.55
<i>Ran</i>	NM_009391.3	RAN, member RAS oncogene family (Ran)	0.59
<i>Ranbp1</i>	NM_011239.2	RAN binding protein 1 (Ranbp1)	0.39

<i>Rangap1</i>	NM_011241		0.52
<i>Rangrf</i>	NM_021329.2	RAN guanine nucleotide release factor (Rangrf)	0.54
<i>Rap1b</i>	NM_024457.2	RAS related protein 1b (Rap1b)	0.52
<i>Rap1gap</i>	NM_001081155.1	Rap1 GTPase-activating protein (Rap1gap)	0.66
<i>Rap2c</i>	NM_172413.2	RAP2C, member of RAS oncogene family (Rap2c)	0.27
<i>Rasa1</i>	NM_145452.2	RAS p21 protein activator 1 (Rasa1)	0.51
<i>Rasa3</i>	NM_009025.2	RAS p21 protein activator 3 (Rasa3)	0.29
<i>Rasal2</i>	NM_177644.4	RAS protein activator like 2 (Rasal2)	0.50
<i>Rasl11b</i>	NM_026878.1	RAS-like, family 11, member B (Rasl11b)	0.66
<i>Rassf3</i>	NM_138956.3	Ras association (RalGDS/AF-6) domain family member 3 (Rassf3)	0.20
<i>Rbbp4</i>	NM_009030.3	retinoblastoma binding protein 4 (Rbbp4)	0.60
<i>Rbbp7</i>	NM_009031.2	retinoblastoma binding protein 7 (Rbbp7)	0.58
<i>Rbl1</i>	NM_011249.1	retinoblastoma-like 1 (p107) (Rbl1)	0.41
<i>Rbm13</i>	NM_026453.1	RNA binding motif protein 13 (Rbm13)	0.41
<i>Rbms3</i>	NM_178660.2	RNA binding motif, single stranded interacting protein (Rbms3)	0.60
<i>Rbmx</i>	NM_011252.2	RNA binding motif protein, X chromosome (Rbmx)	0.32
<i>Rbx1</i>	NM_019712.3	ring-box 1 (Rbx1)	0.62
<i>Rcc1</i>	NM_133878.2	regulator of chromosome condensation 1 (Rcc1)	0.56
<i>Rcl1</i>	NM_021525.2	RNA terminal phosphate cyclase-like 1 (Rcl1)	0.62
<i>Rdh11</i>	NM_021557		0.48
<i>Reep3</i>	NM_178606.4	receptor accessory protein 3 (Reep3)	0.52
<i>Reps1</i>	NM_009048.1	RalBP1 associated Eps domain containing protein (Reps1)	0.48
<i>Rerg</i>	NM_181988.1	RAS-like, estrogen-regulated, growth-inhibitor (Rerg)	0.33
<i>Rev3l</i>	NM_011264.3	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae) (Rev3l)	0.44
<i>Rfc1</i>	NM_011258.1	replication factor C (activator 1) 1 (Rfc1)	0.64
<i>Rfc2</i>	NM_020022		0.63
<i>Rfc3</i>	XM_132528.3		0.64
<i>Rfc4</i>	NM_145480		0.36
<i>Rfc5</i>	NM_028128.1	replication factor C (activator 1) 5 (Rfc5)	0.53
<i>Rg9mtd1</i>	NM_029092.2	RNA (guanine-9-) methyltransferase domain containing 1 (Rg9mtd1)	0.66
<i>Rgs10</i>	NM_026418.2	regulator of G-protein signalling 10 (Rgs10)	0.66
<i>Rgs7</i>	NM_011880.2	regulator of G protein signaling 7 (Rgs7)	0.26
<i>Rgs7bp</i>	NM_029879.2	regulator of G-protein signalling 7 binding protein (Rgs7bp)	0.41
<i>Rhbdf1</i>	NM_010117.1	rhomboid family 1 (Drosophila) (Rhbdf1)	0.55
<i>Rhobtb1</i>	NM_001081347.1	Rho-related BTB domain containing 1 (Rhobtb1)	0.62
<i>Rhobtb2</i>	NM_153514.4	Rho-related BTB domain containing 2 (Rhobtb2)	0.66
<i>Rhoc</i>	NM_007484.1	ras homolog gene family, member C (Rhoc)	0.58
<i>Rhot1</i>	NM_021536.6	ras homolog gene family, member T1 (Rhot1)	0.65
<i>Rhot2</i>	NM_145999.2	ras homolog gene family, member T2 (Rhot2), nuclear gene encoding mitochondrial protein	0.63
<i>Riok3</i>	NM_024182.4	RIO kinase 3 (yeast) (Riok3)	0.66
<i>Rnaseh2b</i>	NM_026001.2	ribonuclease H2, subunit B (Rnaseh2b)	0.45
<i>Rnf14</i>	NM_020012.1	ring finger protein 14 (Rnf14)	0.65
<i>Rnf145</i>	NM_028862.2	ring finger protein 145 (Rnf145)	0.66
<i>Rnf26</i>	NM_153762.3	ring finger protein 26 (Rnf26)	0.46
<i>Rnf4</i>	NM_011278.1	ring finger protein 4 (Rnf4)	0.59
<i>Rnf44</i>	NM_134064.1	ring finger protein 44 (Rnf44)	0.52
<i>Rnps1</i>	NM_001080127.1	ribonucleic acid binding protein S1 (Rnps1), transcript variant 2	0.48
<i>Rnu65</i>			0.66
<i>Robo1</i>	NM_019413.2	roundabout homolog 1 (Drosophila) (Robo1)	0.44
<i>Rock2</i>	NM_009072.2	Rho-associated coiled-coil containing protein kinase 2 (Rock2)	0.62
<i>Rorb</i>	NM_001043354.1	RAR-related orphan receptor beta (Rorb), transcript variant 1	0.66
<i>Rpa3</i>	NM_026632.3	replication protein A3 (Rpa3)	0.43
<i>Rpl10a</i>	NM_011287.1	ribosomal protein L10A (Rpl10a)	0.45
<i>Rpl12</i>	NM_009076.1	ribosomal protein L12 (Rpl12)	0.37
<i>Rpl13a</i>	NM_009438.3	ribosomal protein L13a (Rpl13a)	0.27
<i>Rpl18</i>	NM_009077.2	ribosomal protein L18 (Rpl18)	0.43
<i>Rpl18a</i>	NM_029751.3	Ribosomal protein L18A (Rpl18a)	0.47
<i>Rpl19</i>	NM_009078.1	ribosomal protein L19 (Rpl19)	0.44
<i>Rpl23</i>	NM_022891.2	ribosomal protein L23 (Rpl23)	0.61
<i>Rpl24</i>	NM_024218.2	ribosomal protein L24 (Rpl24)	0.65
<i>Rpl26</i>	NM_009080.2	ribosomal protein L26 (Rpl26)	0.58
<i>Rpl27</i>	NM_011289.1	ribosomal protein L27 (Rpl27)	0.45
<i>Rpl27a</i>	NM_011975.3	ribosomal protein L27a (Rpl27a)	0.36
<i>Rpl28</i>	NM_009081		0.46
<i>Rpl29</i>	NM_009082.2	ribosomal protein L29 (Rpl29)	0.46
<i>Rpl30</i>	NM_009083.2	ribosomal protein L30 (Rpl30)	0.60
<i>Rpl31</i>	NM_053257.1	ribosomal protein L31 (Rpl31)	0.36
<i>Rpl32</i>	NM_172086		0.52
<i>Rpl34</i>	NM_026724.1	ribosomal protein L34 (Rpl34), transcript variant 1	0.54

<i>Rpl35</i>	NM_025592.3	ribosomal protein L35 (Rpl35)	0.49
<i>Rpl36a</i>	NM_019865.2	ribosomal protein L36a (Rpl36a)	0.35
<i>Rpl36al</i>	NM_025589.1	ribosomal protein L36a-like (Rpl36al)	0.45
<i>Rpl37</i>	NM_026069.2	ribosomal protein L37 (Rpl37)	0.56
<i>Rpl39</i>	NM_026055.1	ribosomal protein L39 (Rpl39)	0.56
<i>Rpl4</i>	NM_024212.2	ribosomal protein L4 (Rpl4)	0.33
<i>Rpl9</i>	NM_011292.1	ribosomal protein L9 (Rpl9)	0.58
<i>Rplp0</i>	NM_007475.4	ribosomal protein, large, P0 (Rplp0)	0.51
<i>Rplp1</i>	NM_018853.3	ribosomal protein, large, P1 (Rplp1)	0.57
<i>Rplp2</i>	NM_026020.4	ribosomal protein, large P2 (Rplp2)	0.47
<i>Rpn2</i>	NM_019642.3	ribophorin II (Rpn2)	0.54
<i>Rprm</i>	NM_023396.4	reprimo, TP53 dependent G2 arrest mediator candidate (Rprm)	0.46
<i>Rps10</i>	NM_025963.1	ribosomal protein S10 (Rps10)	0.54
<i>Rps11</i>	NM_013725.3	ribosomal protein S11 (Rps11)	0.55
<i>Rps12</i>	NM_011295.2		0.44
<i>Rps13</i>	NM_026533.1	ribosomal protein S13 (Rps13)	0.46
<i>Rps15</i>	NM_009091.1	ribosomal protein S15 (Rps15)	0.50
<i>Rps16</i>	NM_013647.1	ribosomal protein S16 (Rps16)	0.42
<i>Rps19</i>	NM_023133.1	ribosomal protein S19 (Rps19)	0.62
<i>Rps2</i>	NM_008503.4	ribosomal protein S2 (Rps2)	0.52
<i>Rps24</i>	NM_011297.2	ribosomal protein S24 (Rps24), transcript variant 1	0.61
<i>Rps25</i>	NM_024266.3	ribosomal protein S25 (Rps25)	0.50
<i>Rps26</i>	NM_013765.1	ribosomal protein S26 (Rps26)	0.38
<i>Rps27a</i>	NM_001033865.1	ribosomal protein S27a (Rps27a), transcript variant 2	0.48
<i>Rps27l</i>	NM_026467.2	ribosomal protein S27-like (Rps27l)	0.64
<i>Rps29</i>	NM_009093.1	ribosomal protein S29 (Rps29)	0.61
<i>Rps3</i>	NM_012052.1		0.51
<i>Rps3a</i>	NM_016959.2	ribosomal protein S3a (Rps3a)	0.56
<i>Rps4x</i>	NM_009094.1	ribosomal protein S4, X-linked (Rps4x)	0.45
<i>Rps5</i>	NM_009095.1	ribosomal protein S5 (Rps5)	0.43
<i>Rps6</i>	NM_009096.2	ribosomal protein S6 (Rps6)	0.53
<i>Rps6ka1</i>	NM_009097.1	ribosomal protein S6 kinase polypeptide 1 (Rps6ka1)	0.55
<i>Rps7</i>	NM_011300.2	ribosomal protein S7 (Rps7)	0.49
<i>Rps8</i>	NM_009098.2	ribosomal protein S8 (Rps8)	0.40
<i>Rps9</i>	NM_029767.2	ribosomal protein S9 (Rps9)	0.61
<i>Rrbp1</i>	NM_133626.2	ribosome binding protein 1 (Rrbp1), transcript variant 2	0.22
<i>Rrm1</i>	NM_009103.2	ribonucleotide reductase M1 (Rrm1)	0.33
<i>Rrm2</i>	NM_009104.1	ribonucleotide reductase M2 (Rrm2)	0.30
<i>Rrn3</i>	NM_001039521.1	RRN3 RNA polymerase I transcription factor homolog (yeast) (Rrn3)	0.62
<i>Rrp15</i>	NM_026041.2	ribosomal RNA processing 15 homolog (S. cerevisiae) (Rrp15)	0.55
<i>Rrp1b</i>	NM_028244.1	ribosomal RNA processing 1 homolog B (S. cerevisiae) (Rrp1b)	0.66
<i>Rsl1d1</i>	NM_025546.2	ribosomal L1 domain containing 1 (Rsl1d1)	0.52
<i>Rtkn2</i>	NM_001081346.1	rhotekin 2 (Rtkn2)	0.50
<i>Rtn3</i>	NM_001003934.1	reticulon 3 (Rtn3), transcript variant 1	0.63
<i>Rtn4ip1</i>	NM_130892.2	reticulon 4 interacting protein 1 (Rtn4ip1)	0.66
<i>Rtn4r11</i>	NM_177708.5	reticulon 4 receptor-like 1 (Rtn4r11)	0.53
<i>Ruvbl2</i>	NM_011304.3	RuvB-like protein 2 (Ruvbl2)	0.65
<i>Rwdd1</i>	NM_025614.1	RWD domain containing 1 (Rwdd1)	0.61
<i>Rybp</i>	NM_019743.3	RING1 and YY1 binding protein (Rybp)	0.63
<i>Ryk</i>	NM_001042607.1	receptor-like tyrosine kinase (Ryk), transcript variant 2	0.46
<i>Sacm1l</i>	NM_030692.1	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae) (Sacm1l)	0.55
<i>Sae1</i>	NM_019748.2	SUMO1 activating enzyme subunit 1 (Sae1)	0.55
<i>Sall3</i>	NM_178280.3	sal-like 3 (Drosophila) (Sall3)	0.54
<i>Sap30</i>	NM_021788.1	sin3 associated polypeptide (Sap30)	0.42
<i>Saps3</i>	NM_029456.1	SAPS domain family, member 3 (Saps3)	0.66
<i>Satb1</i>	NM_009122.1	special AT-rich sequence binding protein 1 (Satb1)	0.43
<i>Sav1</i>	NM_022028.2	salvador homolog 1 (Drosophila) (Sav1)	0.65
<i>Sbk</i>	NM_145587.1		0.57
<i>Sc4mol</i>	NM_025436.1	sterol-C4-methyl oxidase-like (Sc4mol)	0.58
<i>Scamp4</i>	NM_019575.4	secretory carrier membrane protein 4 (Scamp4)	0.59
<i>Scara3</i>	NM_172604.3	scavenger receptor class A, member 3 (Scara3)	0.52
<i>Scara5</i>	NM_028903.1	scavenger receptor class A, member 5 (putative) (Scara5)	0.54
<i>Scd1</i>	NM_009127.3	stearoyl-Coenzyme A desaturase 1 (Scd1)	0.57
<i>sci0001118.1_0</i>	AK002910.1		0.58
<i>sci0001849.1_2273</i>	AK031598.1		0.30
<i>sci0001978.1_6</i>	AK050665.1		0.53
<i>sci0002315.1_12</i>	XM_358429.1		0.61
<i>sci0002507.1_236</i>	AK083573.1		0.56
<i>sci0002624.1_576</i>	AK087461.1		0.55
<i>sci0002791.1_134</i>			0.63

<i>scI0004020.1_31</i>	AK081191.1		0.66
<i>Scml4</i>	NM_172938.2	sex comb on midleg-like 4 (<i>Drosophila</i>) (<i>Scml4</i>)	0.46
<i>Scoc</i>	NM_001039137.2	short coiled-coil protein (<i>Scoc</i>), transcript variant 1	0.55
<i>Scye1</i>	NM_007926.2	small inducible cytokine subfamily E, member 1 (<i>Scye1</i>)	0.67
<i>Sdc3</i>	NM_011520.3	syndecan 3 (<i>Sdc3</i>)	0.27
<i>Sdhb</i>	NM_023374.3	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (<i>Sdhb</i>), nuclear gene encoding mitochondrial protein	0.59
<i>Sdhd</i>	NM_025848.2	succinate dehydrogenase complex, subunit D, integral membrane protein (<i>Sdhd</i>), nuclear gene encoding mitochondrial protein	0.60
<i>Sdpr</i>	NM_138741.1	serum deprivation response (<i>Sdpr</i>)	0.36
<i>Sec11c</i>	NM_025468.2	SEC11 homolog C (<i>S. cerevisiae</i>) (<i>Sec11c</i>)	0.65
<i>Sec13</i>	NM_024206.4	SEC13 homolog (<i>S. cerevisiae</i>) (<i>Sec13</i>)	0.56
<i>Sec61g</i>	NM_011343.2	SEC61, gamma subunit (<i>Sec61g</i>)	0.66
<i>Sec63</i>	NM_153055		0.64
<i>Seh1l</i>	NM_001039088.1	SEH1-like (<i>S. cerevisiae</i>) (<i>Seh1l</i>), transcript variant 1	0.66
<i>Sema3a</i>	NM_009152.2	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (<i>Sema3a</i>)	0.57
<i>Sema4b</i>	NM_013659.3	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B (<i>Sema4b</i>)	0.50
<i>Sema5a</i>	NM_009154.1		0.48
<i>Septin 11</i>	NM_001009818.1	septin 11 (<i>Sept11</i>)	0.31
<i>Septin 6</i>	NM_019942.2	septin 6 (<i>Sept6</i>)	0.53
<i>Septin 9</i>	NM_017380.1	septin 9 (<i>Sept9</i>)	0.12
<i>Serbp1</i>	NM_025814.1	Serpine1 mRNA binding protein 1 (<i>Serbp1</i>)	0.47
<i>Serpine2</i>	NM_009255.2	serine (or cysteine) peptidase inhibitor, clade E, member 2 (<i>Serpine2</i>)	0.40
<i>Set</i>	AK011630		0.58
<i>Setd8</i>	NM_030241.2	SET domain containing (lysine methyltransferase) 8 (<i>Setd8</i>)	0.64
<i>Sf3b3</i>	NM_133953.2	splicing factor 3b, subunit 3 (<i>Sf3b3</i>)	0.57
<i>Sf3b4</i>	NM_153053.3	splicing factor 3b, subunit 4 (<i>Sf3b4</i>)	0.53
<i>Sfrs1</i>	NM_173374.3	splicing factor, arginine/serine-rich 1 (ASF/SF2) (<i>Sfrs1</i>), transcript variant 1	0.53
<i>Sfrs10</i>	NM_009186.4	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, <i>Drosophila</i>) (<i>Sfrs10</i>)	0.47
<i>Sfrs11</i>	NM_001093753.1	splicing factor, arginine/serine-rich 11 (<i>Sfrs11</i>), transcript variant 1	0.50
<i>Sfrs14</i>	NM_172755.2	splicing factor, arginine/serine-rich 14 (<i>Sfrs14</i>)	0.66
<i>Sfrs2</i>	NM_011358.1	splicing factor, arginine/serine-rich 2 (SC-35) (<i>Sfrs2</i>)	0.51
<i>Sfrs2ip</i>	NM_028148.2	splicing factor, arginine/serine-rich 2, interacting protein (<i>Sfrs2ip</i>)	0.67
<i>Sfrs4</i>	NM_020587.1	splicing factor, arginine/serine-rich 4 (SRp75) (<i>Sfrs4</i>)	0.63
<i>Sfrs9</i>	NM_025573.3	splicing factor, arginine/serine rich 9 (<i>Sfrs9</i>)	0.50
<i>Sfxn1</i>	NM_027324.4	sideroflexin 1 (<i>Sfxn1</i>)	0.55
<i>Sgk1</i>	NM_011361.1	serum/glucocorticoid regulated kinase 1 (<i>Sgk1</i>)	0.32
<i>Sgol1</i>	NM_028232.1	shugoshin-like 1 (<i>S. pombe</i>) (<i>Sgol1</i>)	0.49
<i>Sgol2</i>	NM_199007.1	shugoshin-like 2 (<i>S. pombe</i>) (<i>Sgol2</i>)	0.35
<i>Sgpp1</i>	NM_030750.2	sphingosine-1-phosphate phosphatase 1 (<i>Sgpp1</i>)	0.57
<i>Sh3gl2</i>	NM_019535.2	SH3-domain GRB2-like 2 (<i>Sh3gl2</i>)	0.48
<i>Sh3glb2</i>	NM_139302.1	SH3-domain GRB2-like endophilin B2 (<i>Sh3glb2</i>)	0.52
<i>Sh3kbp1</i>	NM_021389.3	SH3-domain kinase binding protein 1 (<i>Sh3kbp1</i>)	0.63
<i>Sh3pxd2b</i>	NM_177364.3	SH3 and PX domains 2B (<i>Sh3pxd2b</i>)	0.47
<i>Shcbp1</i>	NM_011369.2	Shc SH2-domain binding protein 1 (<i>Shcbp1</i>)	0.66
<i>Shmt1</i>	NM_009171		0.35
<i>Skil</i>	NM_001039090.1	SKI-like (<i>Skil</i>), transcript variant 2	0.44
<i>Skiv2l2</i>	NM_028151.2	superkiller viralicidic activity 2-like 2 (<i>S. cerevisiae</i>) (<i>Skiv2l2</i>)	0.51
<i>Skp2</i>	NM_145468.1	S-phase kinase-associated protein 2 (p45) (<i>Skp2</i>), transcript variant 2	0.31
<i>Slain2</i>	NM_153567.1	SLAIN motif family, member 2 (<i>Slain2</i>)	0.66
<i>Slc12a2</i>	NM_009194.2	solute carrier family 12, member 2 (<i>Slc12a2</i>)	0.62
<i>Slc1a4</i>	NM_018861.2	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (<i>Slc1a4</i>)	0.47
<i>Slc24a3</i>	NM_053195.2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (<i>Slc24a3</i>)	0.44
<i>Slc25a11</i>	NM_024211.2	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11 (<i>Slc25a11</i>), nuclear gene encoding mitochondrial protein	0.63
<i>Slc25a25</i>	NM_146118.2	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 (<i>Slc25a25</i>), nuclear gene encoding mitochondrial protein	0.30
<i>Slc25a3</i>	NM_133668.2	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 (<i>Slc25a3</i>)	0.59
<i>Slc25a39</i>	NM_026542.1	solute carrier family 25, member 39 (<i>Slc25a39</i>)	0.58
<i>Slc25a5</i>	NM_007451.3	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (<i>Slc25a5</i>), nuclear gene encoding mitochondrial protein	0.54
<i>Slc29a1</i>	NM_022880.1	solute carrier family 29 (nucleoside transporters), member 1 (<i>Slc29a1</i>)	0.47
<i>Slc30a5</i>	NM_022885.2	solute carrier family 30 (zinc transporter), member 5 (<i>Slc30a5</i>)	0.58

<i>Slc31a1</i>	NM_175090.3	solute carrier family 31, member 1 (Slc31a1)	0.52
<i>Slc35c2</i>	NM_144893.1	solute carrier family 35, member C2 (Slc35c2)	0.61
<i>Slc35e1</i>	NM_177766.2	solute carrier family 35, member E1 (Slc35e1)	0.57
<i>Slc35f3</i>	NM_175434.3	solute carrier family 35, member F3 (Slc35f3)	0.45
<i>Slc38a10</i>	NM_024249.4	solute carrier family 38, member 10 (Slc38a10)	0.61
<i>Slc39a6</i>	NM_139143.2	solute carrier family 39 (metal ion transporter), member 6 (Slc39a6)	0.55
<i>Slc41a2</i>	NM_177388.3	solute carrier family 41, member 2 (Slc41a2)	0.54
<i>Slc4a4</i>	NM_018760.1	solute carrier family 4 (anion exchanger), member 4 (Slc4a4)	0.50
<i>Slc4a7</i>	XM_147798.4		0.38
<i>Slc6a1</i>	NM_178703.2	solute carrier family 6 (neurotransmitter transporter, GABA), member 1 (Slc6a1)	0.64
<i>Slc6a6</i>	NM_009320.3	solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (Slc6a6)	0.36
<i>Slitrk5</i>	NM_198865.1	SLIT and NTRK-like family, member 5 (Slitrk5)	0.64
<i>Slmo2</i>	NM_025531.2	slowmo homolog 2 (Drosophila) (Slmo2)	0.47
<i>Smap2</i>	NM_133716.2	stromal membrane-associated GTPase-activating protein 2 (Smap2)	0.66
<i>Smc1a</i>	NM_019710.1	structural maintenance of chromosomes 1A (Smc1a)	0.56
<i>Smc5l1</i>	NM_153808		0.66
<i>Smn1</i>	NM_011420.2	survival motor neuron 1 (Smn1)	0.55
<i>Smtn</i>	NM_013870.2	smoothelin (Smtn)	0.29
<i>Smyd2</i>	NM_026796.1	SET and MYND domain containing 2 (Smyd2)	0.67
<i>Snopc4</i>	NM_172339.2	small nuclear RNA activating complex, polypeptide 4 (Snopc4)	0.45
<i>Snca</i>	NM_009221.2	synuclein, alpha (Snca), transcript variant 2	0.49
<i>Snd1</i>	NM_019776.2	staphylococcal nuclease and tudor domain containing 1 (Snd1)	0.65
<i>Snora65</i>	NR_002898.1	small nucleolar RNA, H/ACA box 65 (Snora65) on chromosome 2.	0.60
<i>Snrpb</i>	NM_009225.2	small nuclear ribonucleoprotein B (Snrpb)	0.53
<i>Snrpd1</i>	NM_009226.4	small nuclear ribonucleoprotein D1 (Snrpd1)	0.53
<i>Snrpd2</i>	NM_026943.1	small nuclear ribonucleoprotein D2 (Snrpd2)	0.63
<i>Snrpd3</i>	NM_026095.4	small nuclear ribonucleoprotein D3 (Snrpd3)	0.64
<i>Snrpf</i>	XM_892627.2	PREDICTED: small nuclear ribonucleoprotein polypeptide F (Snrpf)	0.41
<i>Snx9</i>	NM_025664.5	sorting nexin 9 (Snx9)	0.61
<i>Socs5</i>	NM_019654.2	suppressor of cytokine signaling 5 (Socs5)	0.38
<i>Sorcs1</i>	NM_021377.1	VPS10 domain receptor protein SORCS 1 (Sorcs1)	0.36
<i>Sorcs2</i>	NM_030889.2	sortilin-related VPS10 domain containing receptor 2 (Sorcs2)	0.54
<i>Sox11</i>	NM_009234.5	SRY-box containing gene 11 (Sox11)	0.24
<i>Sox12</i>	NM_011438.2	SRY-box containing gene 12 (Sox12)	0.57
<i>Sox5</i>	NM_011444.1	SRY-box containing gene 5 (Sox5)	0.56
<i>Sox8</i>	NM_011447.1	SRY-box containing gene 8 (Sox8)	0.43
<i>Spag5</i>	NM_017407.1	sperm associated antigen 5 (Spag5)	0.18
<i>Spag7</i>	NM_172561.1	sperm associated antigen 7 (Spag7)	0.63
<i>Spast</i>	NM_016962.1	spastin (Spast)	0.57
<i>Spata6</i>	NM_026470.3	spermatogenesis associated 6 (Spata6)	0.63
<i>Spc25</i>	NM_025565.1	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) (Spc25)	0.30
<i>Spcc3</i>	NM_029701.1	signal peptidase complex subunit 3 homolog (S. cerevisiae) (Spcc3)	0.53
<i>Specc1</i>	NM_001029936.2	sperm antigen with calponin homology and coiled-coil domains 1 (Specc1)	0.29
<i>Spg7</i>	NM_153176.4	spastic paraplegia 7 homolog (human) (Spg7), nuclear gene encoding mitochondrial protein	0.49
<i>Sphk1</i>	NM_011451.2	sphingosine kinase 1 (Sphk1), transcript variant 1	0.46
<i>Spna2</i>	XM_207079.2		0.57
<i>Spp1</i>	NM_009263.1	secreted phosphoprotein 1 (Spp1)	0.26
<i>Spred1</i>	NM_033524		0.45
<i>Spry4</i>	NM_011898.2	sprouty homolog 4 (Drosophila) (Spry4)	0.30
<i>Spsb4</i>	NM_145134.2	splA/ryanodine receptor domain and SOCS box containing 4 (Spsb4)	0.24
<i>Sqle</i>	NM_009270.3	squalene epoxidase (Sqle)	0.62
<i>Srm</i>	NM_009272.2	spermidine synthase (Srm)	0.45
<i>Srpk1</i>	NM_016795.3	serine/arginine-rich protein specific kinase 1 (Srpk1)	0.66
<i>Srprb</i>	NM_009275.4	signal recognition particle receptor, B subunit (Srprb)	0.65
<i>Srrm2</i>	NM_175229.3	serine/arginine repetitive matrix 2 (Srrm2)	0.42
<i>Ss18</i>	NM_009280.1	synovial sarcoma translocation, Chromosome 18 (Ss18)	0.60
<i>Ssbp4</i>	XM_356132.1		0.59
<i>Ssna1</i>	NM_023464.2	Sjogren's syndrome nuclear autoantigen 1 (Ssna1)	0.65
<i>Sspn</i>	NM_010656.2	sarcospan (Sspn)	0.65
<i>Ssr3</i>	NM_026155.1	signal sequence receptor, gamma (Ssr3)	0.43
<i>Sssca1</i>	NM_020491.4	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human) (Sssca1)	0.62
<i>St13</i>	NM_133726.2	suppression of tumorigenicity 13 (St13)	0.67
<i>St6gal1</i>	NM_145933.3	beta galactoside alpha 2,6 sialyltransferase 1 (St6gal1)	0.66
<i>St6galnac5</i>	NM_012028.2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1, 3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5 (St6galnac5)	0.57
<i>Stab1</i>	NM_138672.2	stabilin 1 (Stab1)	0.35
<i>Stag2</i>	NM_001077712.1	stromal antigen 2 (Stag2), transcript variant 2	0.65

<i>Stambpl1</i>	NM_029682.4	Stam binding protein like 1 (Stambpl1)	0.32
<i>Stard4</i>	NM_133774.4	StAR-related lipid transfer (START) domain containing 4 (Stard4)	0.39
<i>Stc1</i>	NM_009285.3	stanniocalcin 1 (Stc1)	0.32
<i>Stim2</i>	NM_001081103.1	stromal interaction molecule 2 (Stim2)	0.64
<i>Stip1</i>	NM_016737.1	stress-induced phosphoprotein 1 (Stip1)	0.45
<i>Stk17b</i>	NM_133810.2	serine/threonine kinase 17b (apoptosis-inducing) (Stk17b)	0.40
<i>Stk39</i>	NM_016866.2	serine/threonine kinase 39, STE20/SPS1 homolog (yeast) (Stk39)	0.64
<i>Stk4</i>	NM_021420.2	serine/threonine kinase 4 (Stk4)	0.67
<i>Strap</i>	NM_011499.2	serine/threonine kinase receptor associated protein (Strap)	0.56
<i>Stt3b</i>	NM_024222.2	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) (Stt3b)	0.59
<i>Stx4a</i>	NM_009294.3	syntaxin 4A (placental) (Stx4a)	0.60
<i>Stxbp1</i>	NM_009295.1	syntaxin binding protein 1 (Stxbp1)	0.53
<i>Styx</i>	NM_019637.3	serine/threonine/tyrosine interaction protein (Styx)	0.63
<i>Suclg2</i>	NM_011507.1	succinate-Coenzyme A ligase, GDP-forming, beta subunit (Suclg2)	0.65
<i>Sumo2</i>	NM_133354.1	SMT3 suppressor of mif two 3 homolog 2 (yeast) (Sumo2)	0.64
<i>Sumo3</i>	NM_019929.3	SMT3 suppressor of mif two 3 homolog 3 (yeast) (Sumo3)	0.66
<i>Susd4</i>	NM_144796.4	sushi domain containing 4 (Susd4)	0.64
<i>Suz12</i>	NM_199196.1	suppressor of zeste 12 homolog (Drosophila) (Suz12)	0.51
<i>Sv2a</i>	NM_022030.3	synaptic vesicle glycoprotein 2 a (Sv2a)	0.37
<i>Swap70</i>	NM_009302.2	SWA-70 protein (Swap70)	0.58
<i>Syncrip</i>	NM_019666.2	synaptotagmin binding, cytoplasmic RNA interacting protein (Syncrip), transcript variant 1	0.65
<i>Syt16</i>	NM_172804.2	synaptotagmin XVI (Syt16)	0.62
<i>Taf10</i>	NM_020024.3	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor (Taf10)	0.57
<i>Taf12</i>	BC019668		0.63
<i>Taf9</i>	NM_027139.3	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor (Taf9), transcript variant 1	0.56
<i>Tagap</i>	NM_145968.1	T-cell activation Rho GTPase-activating protein (Tagap)	0.65
<i>Tanc1</i>	NM_198294.2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 (Tanc1)	0.50
<i>Tbc1d1</i>	NM_019636.2	TBC1 domain family, member 1 (Tbc1d1)	0.40
<i>Tbc1d20</i>	NM_024196.3	TBC1 domain family, member 20 (Tbc1d20)	0.65
<i>Tbca</i>	NM_009321.2	tubulin cofactor a (Tbca)	0.59
<i>Tbrg4</i>	NM_134011.1	transforming growth factor beta regulated gene 4 (Tbrg4)	0.38
<i>Tcerg1</i>	NM_001039474.1	transcription elongation regulator 1 (CA150) (Tcerg1)	0.51
<i>Tcf12</i>	NM_011544.2	transcription factor 12 (Tcf12)	0.47
<i>Tcf19</i>	NM_025674.1	transcription factor 19 (Tcf19)	0.61
<i>Tcf4</i>	NM_013685.2	transcription factor 4 (Tcf4), transcript variant 1	0.53
<i>Tcof1</i>	NM_011552.2	Treacher Collins Franceschetti syndrome 1, homolog (Tcof1)	0.67
<i>Tcp1</i>	NM_013686.3	t-complex protein 1 (Tcp1)	0.59
<i>Tdg</i>	NM_011561.1	thymine DNA glycosylase (Tdg), transcript variant 1	0.63
<i>Tdrkh</i>	NM_028307.1	tudor and KH domain containing protein (Tdrkh)	0.66
<i>Tead2</i>	NM_011565.2	TEA domain family member 2 (Tead2)	0.32
<i>Tfdp1</i>	NM_009361.1		0.44
<i>Tfg</i>	NM_019678.2	Trk-fused gene (Tfg)	0.63
<i>Tfrc</i>	NM_011638.3	transferrin receptor (Tfrc)	0.34
<i>Tgfb1</i>	NM_009370.2	transforming growth factor, beta receptor I (Tgfb1)	0.59
<i>Thoc4</i>	NM_011568.1	THO complex 4 (Thoc4)	0.38
<i>Thoc7</i>	NM_025435.2	THO complex 7 homolog (Drosophila) (Thoc7), transcript variant 1	0.53
<i>Thumpd1</i>	NM_145585.1	THUMP domain containing 1 (Thumpd1)	0.58
<i>Thy1</i>	NM_009382.3	thymus cell antigen 1, theta (Thy1)	0.36
<i>Thyn1</i>	NM_144543.1	thymocyte nuclear protein 1 (Thyn1)	0.65
<i>Timeless</i>	NM_011589.1	timeless homolog (Drosophila) (Timeless), transcript variant 2	0.39
<i>Timm10</i>	NM_013899.1	translocase of inner mitochondrial membrane 10 homolog (yeast) (Timm10)	0.60
<i>Timm17a</i>	NM_011590.2	translocase of inner mitochondrial membrane 17a (Timm17a), nuclear gene encoding mitochondrial protein	0.47
<i>Timm8a1</i>	NM_013898.1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast) (Timm8a1)	0.60
<i>Timm8b</i>	NM_013897.1	translocase of inner mitochondrial membrane 8 homolog b (yeast) (Timm8b)	0.50
<i>Timm9</i>	NM_013896.3	translocase of inner mitochondrial membrane 9 homolog (yeast) (Timm9), nuclear gene encoding mitochondrial protein, transcript variant 1	0.56
<i>Timp1</i>	NM_011593.2	tissue inhibitor of metalloproteinase 1 (Timp1), transcript variant 2	0.35
<i>Timp4</i>	NM_080639.3	tissue inhibitor of metalloproteinase 4 (Timp4)	0.17
<i>Tipin</i>	NM_025372.1	timeless interacting protein (Tipin)	0.42
<i>Tk1</i>	NM_009387.1	thymidine kinase 1 (Tk1)	0.18
<i>Tlcd1</i>	NM_026708.1	TLC domain containing 1 (Tlcd1)	0.59
<i>Tle1</i>	NM_011599.3	transducin-like enhancer of split 1, homolog of Drosophila E(spl) (Tle1)	0.57
<i>Tle2</i>	NM_019725.1	transducin-like enhancer of split 2, homolog of Drosophila E(spl) (Tle2)	0.53

<i>Tle6</i>	NM_053254.2	transducin-like enhancer of split 6, homolog of Drosophila E(spl) (Tle6)	0.18
<i>Tmed3</i>	NM_025360.1	transmembrane emp24 domain containing 3 (Tmed3)	0.55
<i>Tmed7</i>	XM_990639.1	PREDICTED: transmembrane emp24 protein transport domain containing 7 (Tmed7)	0.59
<i>Tmed9</i>	NM_026211.1	transmembrane emp24 protein transport domain containing 9 (Tmed9)	0.55
<i>Tmem109</i>	NM_134142.1	transmembrane protein 109 (Tmem109)	0.60
<i>Tmem11</i>	NM_173453.2	transmembrane protein 11 (Tmem11)	0.55
<i>Tmem126a</i>	NM_025460.1	transmembrane protein 126A (Tmem126a)	0.61
<i>Tmem132a</i>	NM_133804.2	transmembrane protein 132A (Tmem132a)	0.46
<i>Tmem14c</i>	NM_025387.1	transmembrane protein 14C (Tmem14c)	0.54
<i>Tmem167</i>	NM_025335.2	transmembrane protein 167 (Tmem167)	0.58
<i>Tmem176a</i>	NM_025326.2	transmembrane protein 176A (Tmem176a)	0.29
<i>Tmem176b</i>	NM_023056.3	transmembrane protein 176B (Tmem176b)	0.43
<i>Tmem184b</i>	NM_172608.1	transmembrane protein 184b (Tmem184b)	0.52
<i>Tmem199</i>	NM_199199.2	transmembrane protein 199 (Tmem199)	0.58
<i>Tmem2</i>	NM_001033759.1	transmembrane protein 2 (Tmem2), transcript variant 2	0.61
<i>Tmem41a</i>	NM_025693.3	transmembrane protein 41a (Tmem41a)	0.60
<i>Tmem44</i>	NM_172614.3	transmembrane protein 44 (Tmem44)	0.36
<i>Tmem48</i>	NM_028355.3	transmembrane protein 48 (Tmem48)	0.47
<i>Tmem49</i>	NM_029478.3	transmembrane protein 49 (Tmem49)	0.48
<i>Tmem55b</i>	NM_001033271.3	transmembrane protein 55b (Tmem55b)	0.46
<i>Tmem56</i>	NM_178936.3	transmembrane protein 56 (Tmem56)	0.61
<i>Tmem63b</i>	NM_198167.2	transmembrane protein 63b (Tmem63b)	0.51
<i>Tmem68</i>	NM_028097.3	transmembrane protein 68 (Tmem68)	0.46
<i>Tmem70</i>	NM_027415.2	transmembrane protein 70 (Tmem70), transcript variant 1	0.62
<i>Tmem88</i>	NM_025915.3	transmembrane protein 88 (Tmem88)	0.64
<i>Tmem97</i>	NM_133706.2	transmembrane protein 97 (Tmem97)	0.33
<i>Tmpo</i>	NM_001080129.1	thymopoietin (Tmpo), transcript variant 3	0.61
<i>Tmsb10</i>	NM_025284.3	thymosin, beta 10 (Tmsb10)	0.53
<i>Tmsb4x</i>	NM_021278.2	thymosin, beta 4, X chromosome (Tmsb4x)	0.61
<i>Tnc</i>	NM_011607.2	tenascin C (Tnc)	0.03
<i>Tnfrsf10b</i>	NM_020275.3	tumor necrosis factor receptor superfamily, member 10b (Tnfrsf10b)	0.52
<i>Tnfrsf12a</i>	NM_013749.1	tumor necrosis factor receptor superfamily, member 12a (Tnfrsf12a)	0.38
<i>Tnfrsf21</i>	NM_178589.2	tumor necrosis factor receptor superfamily, member 21 (Tnfrsf21)	0.16
<i>Tnik</i>	XM_130797		0.61
<i>Tnpo3</i>	NM_177296.4	transportin 3 (Tnpo3)	0.62
<i>Tnrc6a</i>	NM_144925.3	trinucleotide repeat containing 6a (Tnrc6a)	0.62
<i>Tomm22</i>	NM_172609.3	translocase of outer mitochondrial membrane 22 homolog (yeast) (Tomm22), nuclear gene encoding mitochondrial protein	0.55
<i>Tomm40l</i>	NM_001037170.2	translocase of outer mitochondrial membrane 40 homolog-like (yeast) (Tomm40l), nuclear gene encoding mitochondrial protein	0.61
<i>Top1</i>	NM_009408.2	topoisomerase (DNA) I (Top1)	0.66
<i>Top2a</i>	NM_011623.1	topoisomerase (DNA) II alpha (Top2a)	0.15
<i>Tpi1</i>	NM_009415.1	triosephosphate isomerase 1 (Tpi1)	0.63
<i>Tpm3</i>	NM_022314.2	tropomyosin 3, gamma (Tpm3)	0.50
<i>Tpm4</i>	NM_001001491.1	tropomyosin 4 (Tpm4)	0.46
<i>Tpp2</i>	NM_009418.2	tripeptidyl peptidase II (Tpp2)	0.59
<i>Tpst1</i>	NM_013837.1	protein-tyrosine sulfotransferase 1 (Tpst1), transcript variant 2	0.63
<i>Tpx2</i>	NM_028109.3	TPX2, microtubule-associated protein homolog (Xenopus laevis) (Tpx2)	0.31
<i>Traf3</i>	NM_011632.2	Tnf receptor-associated factor 3 (Traf3), transcript variant 1	0.65
<i>Traf4</i>	NM_009423.3	Tnf receptor associated factor 4 (Traf4)	0.43
<i>Trak2</i>	NM_172406.2	trafficking protein, kinesin binding 2 (Trak2)	0.48
<i>Tram1</i>	NM_028173.1	translocating chain-associating membrane protein 1 (Tram1)	0.57
<i>Trappc1</i>	NM_001024206.1	trafficking protein particle complex 1 (Trappc1)	0.49
<i>Trf</i>	NM_133977.2	transferrin (Trf)	0.10
<i>Trib2</i>	NM_144551.3		0.20
<i>Trim27</i>	NM_009054.2	tripartite motif-containing 27 (Trim27)	0.64
<i>Trim28</i>	NM_011588.2	tripartite motif protein 28 (Trim28)	0.44
<i>Trim59</i>	NM_025863.2	tripartite motif-containing 59 (Trim59)	0.54
<i>Trim62</i>	NM_178110.2	tripartite motif-containing 62 (Trim62)	0.44
<i>Trim8</i>	NM_053100.1	tripartite motif protein 8 (Trim8)	0.57
<i>Trim9</i>	NM_053167.1	tripartite motif protein 9 (Trim9)	0.67
<i>Trio</i>			0.56
<i>Trip12</i>	NM_133975.4	thyroid hormone receptor interactor 12 (Trip12)	0.62
<i>Trmt1</i>	NM_027296.2	tRNA nucleotidyl transferase, CCA-adding, 1 (Trmt1)	0.65
<i>Troap</i>	XM_912265.2	PREDICTED: trophinin associated protein (Troap)	0.31
<i>Trp53</i>	NM_011640.2	transformation related protein 53 (Trp53)	0.62
<i>Trp53i11</i>	NM_001025246.1	transformation related protein 53 inducible protein 11 (Trp53i11)	0.30
<i>Trp53inp2</i>	NM_178111.3	transformation related protein 53 inducible nuclear protein 2 (Trp53inp2)	0.49
<i>Tsen15</i>	NM_025677.2	tRNA splicing endonuclease 15 homolog (S. cerevisiae) (Tsen15)	0.67

<i>Tsfm</i>	NM_025537.3	Ts translation elongation factor, mitochondrial (Tsfm), nuclear gene encoding mitochondrial protein	0.62
<i>Tspan12</i>	NM_173007.3	tetraspanin 12 (Tspan12)	0.45
<i>Tspan7</i>	NM_019634.2	tetraspanin 7 (Tspan7)	0.66
<i>Tssc4</i>	NM_138631.1	tumor-suppressing subchromosomal transferable fragment 4 (Tssc4), transcript variant 2	0.52
<i>Ttc13</i>	XM_358379.1		0.55
<i>Ttc3</i>	NM_009441.1	tetratricopeptide repeat domain 3 (Ttc3)	0.53
<i>Ttc7b</i>	XM_127105.8	PREDICTED: tetratricopeptide repeat domain 7B, transcript variant 1 (Ttc7b)	0.51
<i>Ttyh3</i>	NM_175274.3	tweety homolog 3 (Drosophila) (Ttyh3)	0.21
<i>Tuba6</i>	XM_147357.1		0.33
<i>Tubb5</i>	NM_011655.4	tubulin, beta 5 (Tubb5)	0.39
<i>Tubb6</i>	NM_026473.2	tubulin, beta 6 (Tubb6)	0.19
<i>Tubg1</i>	NM_134024.2	tubulin, gamma 1 (Tubg1)	0.45
<i>Tufm</i>	NM_172745.2	Tu translation elongation factor, mitochondrial (Tufm), nuclear gene encoding mitochondrial protein	0.62
<i>Txn1</i>	NM_011660.3	thioredoxin 1 (Txn1)	0.28
<i>Txndc12</i>	NM_025334.3	thioredoxin domain containing 12 (endoplasmic reticulum) (Txndc12)	0.61
<i>Txnl4a</i>	NM_025299.3	thioredoxin-like 4A (Txnl4a), transcript variant 1	0.65
<i>Tyms</i>	NM_021288.3	thymidylate synthase (Tyms)	0.36
<i>Tyms-ps</i>	NR_000040.1	thymidylate synthase, pseudogene (Tyms-ps), non-coding RNA.	0.39
<i>U2af1</i>	NM_024187		0.64
<i>U2af2</i>	NM_133671.1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 (U2af2)	0.64
<i>Uba1</i>	NM_009457.3	ubiquitin-like modifier activating enzyme 1 (Uba1)	0.56
<i>Uba2</i>	NM_016682.2	ubiquitin-like modifier activating enzyme 2 (Uba2)	0.49
<i>Ubap2</i>	NM_026872.1	ubiquitin-associated protein 2 (Ubap2)	0.62
<i>Ube2a</i>	NM_019668.3	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae) (Ube2a)	0.54
<i>Ube2f</i>	NM_026454.2	ubiquitin-conjugating enzyme E2F (putative) (Ube2f)	0.51
<i>Ube2g1</i>	NM_025985.4	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans) (Ube2g1)	0.54
<i>Ube2k</i>	NM_016786.3	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast) (Ube2k)	0.58
<i>Ube2m</i>	NM_145578.1	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (Ube2m)	0.64
<i>Ube2q1</i>	NM_027315.3	ubiquitin-conjugating enzyme E2Q (putative) 1 (Ube2q1)	0.65
<i>Ube2t</i>	NM_026024.2	ubiquitin-conjugating enzyme E2T (putative) (Ube2t)	0.58
<i>Ube3c</i>	NM_133907.3	ubiquitin protein ligase E3C (Ube3c)	0.58
<i>Ubr7</i>	NM_025666.2	ubiquitin protein ligase E3 component n-recogin 7 (putative) (Ubr7)	0.54
<i>Uchl3</i>	NM_016723.1	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (Uchl3)	0.56
<i>Uchl5</i>	NM_019562.1	ubiquitin carboxyl-terminal esterase L5 (Uchl5)	0.58
<i>Uck2</i>	NM_030724.3	uridine-cytidine kinase 2 (Uck2)	0.48
<i>Ugcg</i>	NM_011673		0.54
<i>Uhrf1</i>	NM_010931.2	ubiquitin-like, containing PHD and RING finger domains, 1 (Uhrf1)	0.11
<i>Uhrf2</i>	NM_144873.2	ubiquitin-like, containing PHD and RING finger domains 2 (Uhrf2)	0.59
<i>Ung</i>	NM_011677.2	uracil DNA glycosylase (Ung), transcript variant 2	0.36
<i>Upf3a</i>	NM_025924.2	UPF3 regulator of nonsense transcripts homolog A (yeast) (Upf3a)	0.59
<i>Upp1</i>	NM_009477.1	uridine phosphorylase 1 (Upp1)	0.22
<i>Uqcrc1</i>	NM_025407.2	ubiquinol-cytochrome c reductase core protein 1 (Uqcrc1)	0.57
<i>Uqcrc2</i>	NM_025899.2	ubiquinol cytochrome c reductase core protein 2 (Uqcrc2)	0.62
<i>Uqcrh</i>	NM_025641.3	ubiquinol-cytochrome c reductase hinge protein (Uqcrh)	0.54
<i>Usp1</i>	NM_146144.2	ubiquitin specific peptidase 1 (Usp1)	0.45
<i>Usp39</i>	NM_138592.3	ubiquitin specific peptidase 39 (Usp39)	0.62
<i>Usp11</i>	NM_001013378.1	ubiquitin specific peptidase like 1 (Usp11)	0.67
<i>Utp111</i>	NM_026031.3	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) (Utp111)	0.55
<i>Uxt</i>	NM_013840.2	ubiquitously expressed transcript (Uxt)	0.64
<i>Vamp3</i>	NM_009498.3	vesicle-associated membrane protein 3 (Vamp3)	0.61
<i>Vapa</i>	NM_013933.2	vesicle-associated membrane protein, associated protein A (Vapa)	0.66
<i>Vapb</i>	NM_019806.5	vesicle-associated membrane protein, associated protein B and C (Vapb)	0.63
<i>Vars</i>	NM_011690.2	valyl-tRNA synthetase (Vars), nuclear gene encoding mitochondrial protein	0.53
<i>Vav3</i>	NM_020505.2	vav 3 oncogene (Vav3), transcript variant 1	0.21
<i>Vbp1</i>	NM_011692.2	von Hippel-Lindau binding protein 1 (Vbp1)	0.54
<i>Vcp</i>	NM_009503.3	valosin containing protein (Vcp)	0.67
<i>Vdac1</i>	NM_011694.3	voltage-dependent anion channel 1 (Vdac1)	0.55
<i>Vdac2</i>	NM_011695.2	voltage-dependent anion channel 2 (Vdac2)	0.32
<i>Vdac3</i>	NM_011696.1	voltage-dependent anion channel 3 (Vdac3)	0.62
<i>Vegfa</i>	NM_009505.3	vascular endothelial growth factor A (Vegfa), transcript variant 2	0.41
<i>Vegfc</i>	NM_009506.2	vascular endothelial growth factor C (Vegfc)	0.52
<i>Vkorc111</i>	NM_027121.3	vitamin K epoxide reductase complex, subunit 1-like 1 (Vkorc111), transcript variant 1	0.49
<i>Vldlr</i>	NM_013703.1	very low density lipoprotein receptor (Vldlr)	0.47
<i>Vps29</i>	NM_019780.1	vacuolar protein sorting 29 (S. pombe) (Vps29)	0.53
<i>Vps36</i>	NM_027338.1	vacuolar protein sorting 36 (yeast) (Vps36)	0.43
<i>Vps54</i>	NM_139061.3	vacuolar protein sorting 54 (yeast) (Vps54)	0.55

<i>Vrk1</i>	NM_001029843.1	vaccinia related kinase 1 (Vrk1), transcript variant 2	0.53
<i>Wasf1</i>	NM_031877.2	WASP family 1 (Wasf1)	0.62
<i>Wasf2</i>	NM_153423		0.66
<i>Wbp11</i>	NM_021714.3	WW domain binding protein 11 (Wbp11)	0.58
<i>Wbscr17</i>	NM_145218.3	Williams-Beuren syndrome chromosome 17 homolog (human) (Wbscr17)	0.52
<i>Wdr43</i>	XM_917905.3	PREDICTED: WD repeat domain 43, transcript variant 9 (Wdr43)	0.66
<i>Wdr51b</i>	NM_027740.3	WD repeat domain 51B (Wdr51b)	0.65
<i>Wdr74</i>	NM_134139.1	WD repeat domain 74 (Wdr74)	0.65
<i>Wdr75</i>	NM_028599.1	WD repeat domain 75 (Wdr75)	0.52
<i>Wdr76</i>	NM_030234.2	WD repeat domain 76 (Wdr76)	0.56
<i>Wdr82</i>	NM_029896.1	WD repeat domain containing 82 (Wdr82)	0.64
<i>Wdr89</i>	XM_001479426.1	PREDICTED: WD repeat domain 89, transcript variant 2 (Wdr89)	0.65
<i>Whsc1</i>	XM_132006		0.43
<i>Wipf1</i>	NM_153138.3	WAS/WASL interacting protein family, member 1 (Wipf1)	0.64
<i>Wsb2</i>	NM_021539.4	WD repeat and SOCS box-containing 2 (Wsb2)	0.31
<i>Wscd1</i>	NM_177618.4	WSC domain containing 1 (Wscd1)	0.35
<i>Wwp1</i>	NM_177327.3	WW domain containing E3 ubiquitin protein ligase 1 (Wwp1)	0.62
<i>Xpnpep1</i>	NM_133216.2	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble (Xpnpep1)	0.59
<i>Xrcc6</i>	NM_010247.1	X-ray repair complementing defective repair in Chinese hamster cells 6 (Xrcc6)	0.50
<i>Yeats4</i>	NM_026570.1	YEATS domain containing 4 (Yeats4)	0.52
<i>Yrdc</i>	NM_153566.1	yrdC domain containing (E.coli) (Yrdc)	0.66
<i>Ythdf1</i>	NM_173761.3	YTH domain family 1 (Ythdf1)	0.66
<i>Ythdf2</i>	NM_145393.3	YTH domain family 2 (Ythdf2)	0.66
<i>Ywhag</i>	NM_018871.2	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (Ywhag)	0.62
<i>Ywhah</i>	NM_011738.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah)	0.31
<i>Zbed4</i>	NM_181412.3	zinc finger, BED domain containing 4 (Zbed4)	0.64
<i>Zbtb7c</i>	NM_145356.3	zinc finger and BTB domain containing 7C (Zbtb7c)	0.53
<i>Zc3h13</i>	NM_026083.2	zinc finger CCCH type containing 13 (Zc3h13)	0.61
<i>Zc3h18</i>	NM_001029993.1	zinc finger CCCH-type containing 18 (Zc3h18), transcript variant 1	0.65
<i>Zc3hc1</i>	NM_172735.1	zinc finger, C3HC type 1 (Zc3hc1)	0.66
<i>Zcchc8</i>	NM_027494.1	zinc finger, CCHC domain containing 8 (Zcchc8)	0.61
<i>Zdhhc21</i>	NM_026647.2	zinc finger, DHHC domain containing 21 (Zdhhc21)	0.49
<i>Zdhhc6</i>	NM_025883.3	zinc finger, DHHC domain containing 6 (Zdhhc6), transcript variant 2	0.59
<i>Zeb1</i>	NM_011546.2	zinc finger E-box binding homeobox 1 (Zeb1)	0.25
<i>Zfp106</i>	NM_011743.2	zinc finger protein 106 (Zfp106)	0.62
<i>Zfp131</i>	NM_028245.1	zinc finger protein 131 (Zfp131)	0.53
<i>Zfp148</i>	NM_011749.4	zinc finger protein 148 (Zfp148)	0.51
<i>Zfp207</i>	NM_011751.2	zinc finger protein 207 (Zfp207)	0.65
<i>Zfp276</i>	NM_020497		0.66
<i>Zfp326</i>	NM_018759.1	zinc finger protein 326 (Zfp326)	0.66
<i>Zfp330</i>	NM_145600.1	zinc finger protein 330 (Zfp330)	0.49
<i>Zfp365</i>	NM_178679.2	zinc finger protein 365 (Zfp365)	0.38
<i>Zfp518b</i>	NM_001081144.1	zinc finger protein 518B (Zfp518b)	0.59
<i>Zfp710</i>	NM_175433.4	zinc finger protein 710 (Zfp710)	0.53
<i>Zfp770</i>	NM_175466.2	zinc finger protein 770 (Zfp770)	0.49
<i>Zfpm2</i>	NM_011766.2	zinc finger protein, multitype 2 (Zfpm2)	0.66
<i>Zmiz1</i>	NM_183208.2	zinc finger, MIZ-type containing 1 (Zmiz1)	0.56
<i>Znrd1</i>	NM_023162.4	zinc ribbon domain containing, 1 (Znrd1)	0.67
<i>Znrf2</i>	NM_199143.1	zinc and ring finger 2 (Znrf2)	0.27
<i>Zswim6</i>	XM_358311		0.56
<i>Zwint</i>	NM_025635.1		0.59
<i>Zyx</i>	NM_011777.2	zyxin (Zyx)	0.49