

Table S8. List of genes, which demonstrated decreased expression (fold change ≥ 1.5 and $p \leq 0.05$) in the differentiated cells from an early phase (day 2) when compared with the proliferating neurospheres

<u>Gene Symbol</u>	<u>Accession No.</u>	<u>Gene Definition</u>	<u>Fold Change</u>
0610007J10Rik	NM_017380.1		0.40
0610007P14Rik	NM_001009818.1	RIKEN cDNA 0610007P14 gene (0610007P14Rik)	0.63
0610010E21Rik	AK018717	RIKEN cDNA 0610010E21 gene (0610010E21Rik)	0.59
0610010F05Rik	NM_021446.2		0.57
0610012G03Rik	NM_001033140.3		0.56
1100001F19Rik	NM_027860		0.55
1110001A07Rik	NM_025320	RIKEN cDNA 1110001A07 gene (1110001A07Rik)	0.56
1110001C20Rik	NM_133186		0.49
1110001J03Rik	XM_124187.1	RIKEN cDNA 1110001J03 gene (1110001J03Rik)	0.50
1110001N06Rik	NM_025377.1		0.62
1110002E23Rik	NM_177730		0.57
1110003F05Rik	NM_025363.2		0.54
1110007L15Rik	AK003256	RIKEN cDNA 1110007L15 gene (1110007L15Rik)	0.55
1110007M04Rik	AK003291	RIKEN cDNA 1110007M04 gene (1110007M04Rik)	0.33
1110008B24Rik			0.62
1110008F13Rik	NM_026269.1	RIKEN cDNA 1110008F13 gene (1110008F13Rik)	0.31
1110008P14Rik	NM_026742.3	RIKEN cDNA 1110008P14 gene (1110008P14Rik)	0.38
1110012D08Rik	XM_177016.2	RIKEN cDNA 1110012D08 gene (1110012D08Rik)	0.47
1110018J23Rik	NM_026124.2		0.52
1110019N10Rik	NM_198001.1	RIKEN cDNA 1110019N10 gene (1110019N10Rik)	0.52
1110020P15Rik	NM_178066.2	RIKEN cDNA 1110020P15 gene (1110020P15Rik)	0.61
1110021J02Rik	NM_172963.3		0.57
1110021L09Rik	NM_026754.2	PREDICTED: RIKEN cDNA 1110021L09 gene (1110021L09Rik)	0.64
1110038B12Rik	XM_140742.4	PREDICTED: RIKEN cDNA 1110038B12 gene, transcript variant 6 (1110038B12Rik)	0.53
1110059E24Rik	NM_026753.1	RIKEN cDNA 1110059E24 gene (1110059E24Rik)	0.66
1110067D22Rik	NM_197979.2	RIKEN cDNA 1110067D22 gene (1110067D22Rik)	0.47
1190002F15Rik			0.53
1190009E20Rik	XM_001474669.1		0.61
1200003C05Rik		RIKEN cDNA 1200003C05 gene (1200003C05Rik)	0.50
1500001L15Rik	XM_922038.2		0.67
1500001M20Rik	NM_025423.1	RIKEN cDNA 1500001M20 gene (1500001M20Rik)	0.58
1500012F01Rik	NM_173752.3	RIKEN cDNA 1500012F01 gene (1500012F01Rik)	0.64
1500032D16Rik		RIKEN cDNA 1500032D16 gene (1500032D16Rik), transcript variant 2	0.53
1500034J01Rik	XM_147036	PREDICTED: RIKEN cDNA 1500034J01 gene (1500034J01Rik)	0.61
1600012H06Rik	NM_197988.1	RIKEN cDNA 1600012H06 gene (1600012H06Rik), transcript variant 4	0.62
1700011E24Rik	NM_001033144.1	PREDICTED: RIKEN cDNA 1700011E24 gene, transcript variant 2 (1700011E24Rik)	0.22
1700013A01Rik			0.59
1700021F05Rik	NM_024205.1	RIKEN cDNA 1700021F05 gene (1700021F05Rik)	0.62
1700025G04Rik	XM_001002205.2	RIKEN cDNA 1700025G04 gene (1700025G04Rik)	0.41
1700027M01Rik	XM_127738.3		0.64
1700029F09Rik	NM_026894.1	PREDICTED: RIKEN cDNA 1700029F09 gene, transcript variant 20 (1700029F09Rik)	0.39
1700037H04Rik	NM_001081005.1	RIKEN cDNA 1700037H04 gene (1700037H04Rik)	0.56
1700041B20Rik	NM_024283.2		0.49
1700086L19Rik	NM_025892.1	PREDICTED: RIKEN cDNA 1700086L19 gene (1700086L19Rik)	0.56
1700113I22Rik	NM_001083891.1	RIKEN cDNA 1700113I22 gene (1700113I22Rik)	0.50
1810006K21Rik	XM_912953.3	PREDICTED: RIKEN cDNA 1810006K21 gene (1810006K21Rik)	0.50
1810009A15Rik	AK028065	RIKEN cDNA 1810009A15 gene (1810009A15Rik)	0.65
1810022K09Rik	NM_001083882.1		0.52
1810027O10Rik	XM_001478332.1		0.56
1810035L17Rik	NM_027040.1	RIKEN cDNA 1810035L17 gene (1810035L17Rik)	0.59
1810055G02Rik	NM_001081275.1	RIKEN cDNA 1810055G02 gene (1810055G02Rik)	0.46
1810063B05Rik	XM_128789.5	RIKEN cDNA 1810063B05 gene (1810063B05Rik)	0.58
2010007H12Rik	AK005934	RIKEN cDNA 2010007H12 gene (2010007H12Rik)	0.67
2010107E04Rik	XM_994504.1	RIKEN cDNA 2010107E04 gene (2010107E04Rik)	0.55
2010309L07Rik	NM_029331.2		0.60
2010317E24Rik	NM_026411.1		0.51
2010321I05Rik	NM_197990.2		0.65
2010321M09Rik	NM_183254.1	RIKEN cDNA 2010321M09 gene (2010321M09Rik), transcript variant 1	0.62
2210411K11Rik	NM_023544	RIKEN cDNA 2210411K11 gene (2210411K11Rik)	0.66
2210412D01Rik	NM_029338.3	RIKEN cDNA 2210412D01 gene (2210412D01Rik)	0.64
2310003F16Rik	XM_919077.2	RIKEN cDNA 2310003F16 gene (2310003F16Rik)	0.65
2310003L22Rik	NM_001033148.2	RIKEN cDNA 2310003L22 gene (2310003L22Rik)	0.57
2310005E10Rik	NM_026091.2	RIKEN cDNA 2310005E10 gene (2310005E10Rik)	0.60
2310005N03Rik	XM_485065	RIKEN cDNA 2310005N03 gene (2310005N03Rik)	0.49

2310008M10Rik	NM_001033185.1	RIKEN cDNA 2310008M10 gene (2310008M10Rik)	0.58
2310009B15Rik	XM_358420.3	RIKEN cDNA 2310009B15 gene (2310009B15Rik)	0.57
2310014H01Rik	NM_138581.2	PREDICTED: RIKEN cDNA 2310014H01 gene, transcript variant 3 (2310014H01Rik)	0.32
2310016C08Rik	NM_026865.2	RIKEN cDNA 2310016C08 gene (2310016C08Rik)	0.41
2310016M24Rik	XM_983803.1	RIKEN cDNA 2310016M24 gene (2310016M24Rik)	0.57
2310036D04Rik	NM_172701.2		0.53
2310037I24Rik	NM_025463.2	RIKEN cDNA 2310037I24 gene (2310037I24Rik)	0.66
2310039H08Rik	NM_029631	RIKEN cDNA 2310039H08 gene (2310039H08Rik)	0.59
2310044H10Rik	XM_485210		0.52
2310045K21Rik	XM_109683.4		0.58
2310051F07Rik			0.61
2310061F22Rik	NM_026958.2	RIKEN cDNA 2310061F22 gene (2310061F22Rik)	0.66
2310079P03Rik	NM_028077.2		0.62
2400010C15Rik	NM_174987.3		0.52
2410003K15Rik	NM_027242.3		0.39
2410015M20Rik	NM_027360.2	RIKEN cDNA 2410015M20 gene (2410015M20Rik)	0.63
2410015N17Rik		RIKEN cDNA 2410015N17 gene (2410015N17Rik)	0.30
2410016F01Rik	XM_130053.2		0.67
2410016O06Rik			0.65
2410022L05Rik	NM_175153.3	RIKEN cDNA 2410022L05 gene (2410022L05Rik)	0.64
2510009E07Rik		RIKEN cDNA 2510009E07 gene (2510009E07Rik)	0.63
2600005C20Rik	NM_029384.1		0.48
2610002D18Rik	NM_133722.1		0.64
2610017I09Rik	XM_901486.2	PREDICTED: RIKEN cDNA 2610017I09 gene (2610017I09Rik), misc RNA.	0.47
2610019E17Rik	NM_026318.2		0.45
2610024B07Rik	NM_027093.3		0.50
2610024G14Rik	NM_172398.3	RIKEN cDNA 2610024G14 gene (2610024G14Rik)	0.60
2610024H22Rik	NM_025511.2		0.62
2610029G23Rik	NM_025506.2	RIKEN cDNA 2610029G23 gene (2610029G23Rik)	0.56
2610036L11Rik	NM_025857.2	PREDICTED: RIKEN cDNA 2610036L11 gene, transcript variant 1 (2610036L11Rik)	0.26
2610039C10Rik	NM_025509.2	RIKEN cDNA 2610039C10 gene (2610039C10Rik)	0.40
2610101N10Rik	NM_001081226.1	RIKEN cDNA 2610101N10 gene (2610101N10Rik)	0.65
2610103J23Rik	NM_001082975.1		0.61
2610207P08Rik	XM_001003622.2		0.59
2610307O08Rik	NM_023516.3	PREDICTED: RIKEN cDNA 2610307O08 gene, transcript variant 12 (2610307O08Rik)	0.29
2610510J17Rik	NM_183256.2	RIKEN cDNA 2610510J17 gene (2610510J17Rik)	0.39
2700029M09Rik	NM_175149.3	PREDICTED: RIKEN cDNA 2700029M09 gene (2700029M09Rik)	0.46
2700055A20Rik	XM_488563		0.62
2700092H06Rik	NM_133714.2		0.56
2700094K13Rik	NM_025966.3	RIKEN cDNA 2700094K13 gene (2700094K13Rik), transcript variant 2	0.17
2810025M15Rik	XM_912979.2	PREDICTED: RIKEN cDNA 2810025M15 gene (2810025M15Rik), misc RNA.	0.34
2810405J04Rik		RIKEN cDNA 2810405J04 gene (2810405J04Rik)	0.53
2810407C02Rik	NM_197991	RIKEN cDNA 2810407C02 gene (2810407C02Rik)	0.62
2810410M20Rik	AK009823	RIKEN cDNA 2810410M20 gene (2810410M20Rik)	0.61
2810417H13Rik		RIKEN cDNA 2810417H13 gene (2810417H13Rik)	0.16
2810417K24Rik	NM_153775.1		0.42
2810423A18Rik	AK010232		0.49
2810428I15Rik			0.65
2900010M23Rik	AK010307	RIKEN cDNA 2900010M23 gene (2900010M23Rik)	0.58
2900060B14Rik	XM_132537.3		0.61
2900060P06Rik	NM_153152.3		0.52
3000004C01Rik	NM_023203.1	RIKEN cDNA 3000004C01 gene (3000004C01Rik)	0.41
3110001D03Rik	NM_022423.1	RIKEN cDNA 3110001D03 gene (3110001D03Rik)	0.62
3110009E18Rik	NM_023633	RIKEN cDNA 3110009E18 gene (3110009E18Rik)	0.52
3110013H01Rik	NM_025556.2		0.45
3110043A19Rik	NM_028596.2	PREDICTED: RIKEN cDNA 3110043A19 gene (3110043A19Rik)	0.57
3300001G02Rik	NM_001001881.1	RIKEN cDNA 3300001G02 gene (3300001G02Rik)	0.50
3632451O06Rik	NM_028244	RIKEN cDNA 3632451O06 gene (3632451O06Rik)	0.41
3830612M24	XM_131720.2		0.18
3930401E15Rik	XR_035175.1		0.64
4631422C13Rik		PREDICTED: RIKEN cDNA 4631422C13 gene (4631422C13Rik)	0.64
4632417K18Rik		RIKEN cDNA 4632417K18 gene (4632417K18Rik)	0.30
4833424O15Rik	NM_019836.2	RIKEN cDNA 4833424O15 gene (4833424O15Rik)	0.46
4833426J09Rik			0.65
4833427B12Rik	NM_026312.2		0.58
4930427A07Rik	XM_902349.2	RIKEN cDNA 4930427A07 gene (4930427A07Rik)	0.65
4930461P20Rik	XM_488549.3	PREDICTED: RIKEN cDNA 4930461P20 gene (4930461P20Rik)	0.63
4930547N16Rik	NM_025642.1	RIKEN cDNA 4930547N16 gene (4930547N16Rik)	0.55

<i>4930572J05Rik</i>	NM_026476.1	RIKEN cDNA 4930572J05 gene (4930572J05Rik)	0.58
<i>4932417H02Rik</i>	NM_026002	RIKEN cDNA 4932417H02 gene (4932417H02Rik)	0.62
<i>4933401P20Rik</i>	NM_027426.2		0.64
<i>4933407C03Rik</i>	XM_127746.2	PREDICTED: RIKEN cDNA 4933407C03 gene, transcript variant 6 (4933407C03Rik)	0.65
<i>4933407P14Rik</i>	XM_921606.2		0.62
<i>4933427G23Rik</i>	NM_028131.1	PREDICTED: RIKEN cDNA 4933427G23 gene (4933427G23Rik), misc RNA.	0.52
<i>5430417J04Rik</i>	NM_028258.1		0.63
<i>5530401N12Rik</i>	XM_001474993.1		0.38
<i>5730410I19Rik</i>	XR_035347.1	RIKEN cDNA 5730410I19 gene (5730410I19Rik)	0.59
<i>5730427N09Rik</i>	NM_027314	RIKEN cDNA 5730427N09 gene (5730427N09Rik)	0.57
<i>5730449L18Rik</i>	NM_026528.3	RIKEN cDNA 5730449L18 gene (5730449L18Rik)	0.65
<i>5730494J16Rik</i>	XM_132529.2		0.36
<i>5730525O22Rik</i>	NM_001037279.1		0.60
<i>5730528L13Rik</i>	NM_145144.1	RIKEN cDNA 5730528L13 gene (5730528L13Rik)	0.65
<i>5830411I20</i>	XR_035184.1		0.40
<i>5930416I19Rik</i>		RIKEN cDNA 5930416I19 gene (5930416I19Rik)	0.48
<i>6030405A18</i>	NM_133747.2		0.59
<i>6230416J20Rik</i>	NM_001040396.2		0.66
<i>6330549D23Rik</i>	NM_024428.2	RIKEN cDNA 6330549D23 gene (6330549D23Rik), non-coding RNA.	0.51
<i>6330578E17Rik</i>	NM_026515.2	RIKEN cDNA 6330578E17 gene (6330578E17Rik)	0.56
<i>6332401O19Rik</i>	AK013109	RIKEN cDNA 6332401O19 gene (6332401O19Rik)	0.64
<i>6430402L23Rik</i>			0.41
<i>6430527G18Rik</i>	XM_147329.1	RIKEN cDNA 6430527G18 gene (6430527G18Rik)	0.37
<i>6430537F04</i>			0.50
<i>6430706D22Rik</i>	XM_484890	RIKEN cDNA 6430706D22 gene (6430706D22Rik)	0.48
<i>6530418L21Rik</i>	NM_026063.1	RIKEN cDNA 6530418L21 gene (6530418L21Rik)	0.44
<i>6720458F09Rik</i>	NM_144518.3	RIKEN cDNA 6720458F09 gene (6720458F09Rik)	0.48
<i>6720463M24Rik</i>	NM_172884	RIKEN cDNA 6720463M24 gene (6720463M24Rik)	0.52
<i>6720469N11Rik</i>			0.52
<i>8030402P03Rik</i>	NM_183095.1		0.62
<i>8430410K20Rik</i>		RIKEN cDNA 8430410K20 gene (8430410K20Rik)	0.65
<i>9430029K10Rik</i>	NM_197959.1		0.65
<i>9430065L19Rik</i>	AK076147		0.45
<i>9430080K19Rik</i>	XM_001002726.1		0.48
<i>9530018I07Rik</i>	NM_025849.2		0.54
<i>9530058B02Rik</i>	NM_001033167.1	RIKEN cDNA 9530058B02 gene (9530058B02Rik)	0.58
<i>9530064J02</i>	NM_028439.1		0.15
<i>9930014A18Rik</i>	XM_203393.1		0.47
<i>A230046K03Rik</i>		RIKEN cDNA A230046K03 gene (A230046K03Rik)	0.66
<i>A230079E18Rik</i>	AK014074		0.46
<i>A430005L14Rik</i>	XM_001476479.1	RIKEN cDNA A430005L14 gene (A430005L14Rik)	0.64
<i>A830059I20Rik</i>	NM_026085.2		0.33
<i>A930030J18Rik</i>	NM_030093.1		0.52
<i>AA960436</i>		expressed sequence AA960436 (AA960436)	0.60
<i>Aaas</i>	NM_026142.1	achalasia, adrenocortical insufficiency, alacrimia (Aaas)	0.63
<i>Aacs</i>	NM_178141.2	acetoacetyl-CoA synthetase (Aacs)	0.55
<i>Aadacl1</i>		arylacetamide deacetylase-like 1 (Aadacl1)	0.45
<i>Aard</i>	AK076210	alanine and arginine rich domain containing protein (Aard)	0.53
<i>Aars</i>	NM_026486.1	alanyl-tRNA synthetase (Aars)	0.46
<i>Aarsd1</i>	NM_001081295.1	alanyl-tRNA synthetase domain containing 1 (Aarsd1)	0.66
<i>Aatk</i>	XM_984472.1	apoptosis-associated tyrosine kinase (Aatk)	0.22
<i>Abcb6</i>	NM_026640.2	ATP-binding cassette, sub-family B (MDR/TAP), member 6 (Abcb6), nuclear gene encoding mitochondrial protein	0.56
<i>Abcb7</i>	AK029315	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 7, transcript variant 5 (Abcb7)	0.51
<i>Abcf1</i>		ATP-binding cassette, sub-family F (GCN20), member 1 (Abcf1)	0.63
<i>Abcf2</i>	NM_027845.1	ATP-binding cassette, sub-family F (GCN20), member 2 (Abcf2), nuclear gene encoding mitochondrial protein	0.60
<i>Abi2</i>	NM_026127.3	abl-interactor 2 (Abi2)	0.57
<i>Acap3</i>	NM_029425.1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3 (Acap3)	0.36
<i>Acat2</i>		acetyl-Coenzyme A acetyltransferase 2 (Acat2)	0.40
<i>Acbd3</i>	XM_195728	acyl-Coenzyme A binding domain containing 3 (Acbd3)	0.65
<i>Acly</i>	NM_133923.2	ATP citrate lyase (Acly)	0.43
<i>Acn9</i>	AK015050		0.65
<i>Aco2</i>	NM_134041.2	aconitase 2, mitochondrial (Aco2), nuclear gene encoding mitochondrial protein	0.56
<i>Acot7</i>	NM_027507.1	acyl-CoA thioesterase 7 (Acot7)	0.42
<i>Acpl2</i>	NM_029115.1	acid phosphatase-like 2 (Acpl2)	0.57
<i>Acsbg1</i>	XM_001473469.1	acyl-CoA synthetase bubblegum family member 1 (Acsbg1)	0.40
<i>AcsI5</i>	XM_355576.1	acyl-CoA synthetase long-chain family member 5 (AcsI5)	0.36

<i>Acss2</i>	NM_029249.2	acyl-CoA synthetase short-chain family member 2 (<i>Acss2</i>)	0.55
<i>Actb</i>	NM_026353.2	actin, beta (<i>Actb</i>)	0.52
<i>Actl6a</i>	NM_198607.1	actin-like 6A (<i>Actl6a</i>)	0.51
<i>Actr10</i>	XM_357260.1	ARP10 actin-related protein 10 homolog (<i>S. cerevisiae</i>) (<i>Actr10</i>)	0.57
<i>Actr3</i>	NM_028898.2	ARP3 actin-related protein 3 homolog (<i>yeast</i>) (<i>Actr3</i>)	0.58
<i>Adam12</i>	NM_001081025.1	a disintegrin and metallopeptidase domain 12 (meltrin alpha) (<i>Adam12</i>)	0.21
<i>Adam15</i>	XM_620624.3	a disintegrin and metallopeptidase domain 15 (metargidin) (<i>Adam15</i>), transcript variant 2	0.64
<i>Adam17</i>	AK016608	a disintegrin and metallopeptidase domain 17 (<i>Adam17</i>)	0.58
<i>Adamts19</i>	XM_001004724.2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19 (<i>Adamts19</i>)	0.43
<i>Adamts4</i>	XM_129929.1		0.36
<i>Adap1</i>	NM_199019.1	ArfGAP with dual PH domains 1 (<i>Adap1</i>)	0.55
<i>Adm</i>	NM_027707	adrenomedullin (<i>Adm</i>)	0.43
<i>Adpgk</i>	XR_005167.1		0.60
<i>Adprh</i>	NM_027728.2	ADP-ribosylarginine hydrolase (<i>Adprh</i>)	0.57
<i>Adrb2</i>	NM_001004146.1	adrenergic receptor, beta 2 (<i>Adrb2</i>)	0.53
<i>Adrbk1</i>	XM_149592.1	adrenergic receptor kinase, beta 1 (<i>Adrbk1</i>)	0.61
<i>Adrm1</i>	XM_128281	adhesion regulating molecule 1 (<i>Adrm1</i>)	0.62
<i>Adsl</i>	NM_001003948.1		0.63
<i>Aes</i>	AK030367		0.63
<i>Afg3l1</i>	NM_026606.1	AFG3(ATPase family gene 3)-like 1 (<i>yeast</i>) (<i>Afg3l1</i>)	0.64
<i>Agap1</i>	AK077378	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (<i>Agap1</i>), transcript variant 2	0.53
<i>Agfg1</i>	AK030671	ArfGAP with FG repeats 1 (<i>Agfg1</i>)	0.60
<i>Agfg2</i>		ArfGAP with FG repeats 2 (<i>Agfg2</i>), transcript variant 2	0.53
<i>Agpat6</i>	NM_145509.1	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) (<i>Agpat6</i>)	0.64
<i>Ahctf1</i>		AT hook containing transcription factor 1 (<i>Ahctf1</i>)	0.56
<i>Ahcy</i>	NM_027442		0.50
<i>Ahcyl1</i>	NM_178765.3	S-adenosylhomocysteine hydrolase-like 1 (<i>Ahcyl1</i>)	0.66
<i>AI413582</i>	NM_025666.1	expressed sequence AI413582 (AI413582)	0.56
<i>AI448196</i>	NM_021552.4		0.50
<i>AI481316</i>	NM_025677.1		0.60
<i>AI593442</i>	AK077637	expressed sequence AI593442 (AI593442), transcript variant 1	0.50
<i>AI851790</i>	AK017789	expressed sequence AI851790 (AI851790)	0.55
<i>Aip</i>	NM_028137.2	aryl-hydrocarbon receptor-interacting protein (<i>Aip</i>)	0.63
<i>Ak2</i>		adenylate kinase 2 (<i>Ak2</i>), transcript variant 2	0.55
<i>Akap12</i>	NM_197981.1	A kinase (PRKA) anchor protein (gravin) 12 (<i>Akap12</i>)	0.11
<i>Akap7</i>	NM_177854	A kinase (PRKA) anchor protein 7 (<i>Akap7</i>)	0.47
<i>Akirin1</i>	AK031346	akirin 1 (<i>Akirin1</i>)	0.65
<i>Akr1a4</i>		aldo-keto reductase family 1, member A4 (aldehyde reductase) (<i>Akr1a4</i>)	0.63
<i>AL022832</i>	NM_173400		0.63
<i>Alad</i>	NM_134022.2	aminolevulinatase, delta-, dehydratase (<i>Alad</i>)	0.58
<i>Alas1</i>	XM_358637.1	aminolevulinic acid synthase 1 (<i>Alas1</i>)	0.51
<i>Aldh18a1</i>		aldehyde dehydrogenase 18 family, member A1 (<i>Aldh18a1</i>), nuclear gene encoding mitochondrial protein, transcript variant 1	0.48
<i>Aldoa</i>	NM_001033301.2	aldolase A, fructose-bisphosphate (<i>Aldoa</i>)	0.63
<i>Alg8</i>	NR_003619.1	asparagine-linked glycosylation 8 homolog (<i>yeast</i> , alpha-1,3-glucosyltransferase) (<i>Alg8</i>)	0.56
<i>Alg9</i>	NM_198006.3	asparagine-linked glycosylation 9 homolog (<i>yeast</i> , alpha 1,2-mannosyltransferase) (<i>Alg9</i>)	0.62
<i>Amotl1</i>	NM_177013.3	angiomin-like 1 (<i>Amotl1</i>)	0.31
<i>Amph</i>	AK078178	amphiphysin (<i>Amph</i>)	0.66
<i>Anapc5</i>	NM_145836.1	anaphase-promoting complex subunit 5 (<i>Anapc5</i>), transcript variant 1	0.66
<i>Angpt2</i>		angiopoietin 2 (<i>Angpt2</i>)	0.05
<i>Ank3</i>	NM_178689.3	ankyrin 3, epithelial (<i>Ank3</i>), transcript variant 6	0.23
<i>Anln</i>	NM_172286	anillin, actin binding protein (<i>Anln</i>)	0.21
<i>Anp32e</i>	NM_172930.2	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E (<i>Anp32e</i>)	0.34
<i>Anxa3</i>	NM_198652.1	annexin A3 (<i>Anxa3</i>)	0.36
<i>Ap2b1</i>	NM_175398.3	adaptor-related protein complex 2, beta 1 subunit (<i>Ap2b1</i>), transcript variant 1	0.54
<i>Ap4s1</i>	NM_177374.2	adaptor-related protein complex AP-4, sigma 1 (<i>Ap4s1</i>)	0.67
<i>Apaf1</i>	NM_175265.4	apoptotic peptidase activating factor 1 (<i>Apaf1</i>), transcript variant 1	0.63
<i>Apex1</i>	NM_177138.2	apurinic/apyrimidinic endonuclease 1 (<i>Apex1</i>)	0.66
<i>Apitd1</i>		apoptosis-inducing, TAF9-like domain 1 (<i>Apitd1</i>)	0.66
<i>Aplp2</i>		amyloid beta (A4) precursor-like protein 2 (<i>Aplp2</i>), transcript variant 3	0.64
<i>Appbp2</i>	AK078743		0.57
<i>Aprin</i>	AK078769	androgen-induced proliferation inhibitor (<i>Aprin</i>)	0.62
<i>Aprt</i>	NM_145609.1		0.58
<i>Arc</i>	AK082376	activity regulated cytoskeletal-associated protein (<i>Arc</i>)	0.58

<i>Ard1</i>	AK020369		0.57
<i>Ard1a</i>	AK034130	ARD1 homolog A, N-acetyltransferase (<i>S. cerevisiae</i>) (<i>Ard1a</i>)	0.42
<i>Areg</i>	XM_128267	amphiregulin (<i>Areg</i>)	0.27
<i>Arf6</i>	NM_177462	ADP-ribosylation factor 6 (<i>Arf6</i>)	0.53
<i>Arhgap18</i>	XM_284281.2	Rho GTPase activating protein 18 (<i>Arhgap18</i>)	0.27
<i>Arl2bp</i>	AK034952	ADP-ribosylation factor-like 2 binding protein (<i>Arl2bp</i>), transcript variant 1	0.65
<i>Arl4c</i>		ADP-ribosylation factor-like 4C (<i>Arl4c</i>)	0.57
<i>Arl6ip1</i>		ADP-ribosylation factor-like 6 interacting protein 1 (<i>Arl6ip1</i>)	0.63
<i>Armcx2</i>	NM_026633.1	armadillo repeat containing, X-linked 2 (<i>Armcx2</i>)	0.55
<i>Arpc1b</i>	XM_489200	actin related protein 2/3 complex, subunit 1B (<i>Arpc1b</i>)	0.30
<i>Arpc2</i>	AK035833	actin related protein 2/3 complex, subunit 2 (<i>Arpc2</i>)	0.67
<i>Arpc3</i>	AK036567	actin related protein 2/3 complex, subunit 3 (<i>Arpc3</i>)	0.58
<i>Asah1</i>	AK036626	N-acylsphingosine amidohydrolase 1 (<i>Asah1</i>)	0.43
<i>Ascc2</i>	NM_172581.1	activating signal cointegrator 1 complex subunit 2 (<i>Ascc2</i>)	0.55
<i>Asns</i>	NM_177166.2	asparagine synthetase (<i>Asns</i>)	0.48
<i>Aspm</i>	NM_001033375.2	asp (abnormal spindle)-like, microcephaly associated (<i>Drosophila</i>) (<i>Aspm</i>)	0.37
<i>Atad3a</i>	XM_489103	ATPase family, AAA domain containing 3A (<i>Atad3a</i>)	0.60
<i>Atf4</i>	AK038731	activating transcription factor 4 (<i>Atf4</i>)	0.37
<i>Atf7ip</i>	AK038962	activating transcription factor 7 interacting protein (<i>Atf7ip</i>)	0.55
<i>Atg3</i>	NM_172447.2	autophagy-related 3 (yeast) (<i>Atg3</i>)	0.60
<i>Atic</i>	NM_175287.3	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (<i>Atic</i>)	0.55
<i>Atp13a3</i>	XM_989657.2	PREDICTED: ATPase type 13A3, transcript variant 1 (<i>Atp13a3</i>)	0.66
<i>Atp1b3</i>	NM_021427.1	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide (<i>Atp1b3</i>)	0.52
<i>Atp5a1</i>	NM_177118	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 (<i>Atp5a1</i>), nuclear gene encoding mitochondrial protein	0.43
<i>Atp5b</i>		ATP synthase, H ⁺ transporting mitochondrial F1 complex, beta subunit (<i>Atp5b</i>), nuclear gene encoding mitochondrial protein	0.59
<i>Atp5c1</i>	AK044025	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1 (<i>Atp5c1</i>)	0.51
<i>Atp5d</i>	NM_177225	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (<i>Atp5d</i>)	0.45
<i>Atp5f1</i>	NM_172768	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 (<i>Atp5f1</i>), nuclear gene encoding mitochondrial protein	0.52
<i>Atp5g2</i>	AK044660	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (<i>Atp5g2</i>)	0.55
<i>Atp5g3</i>	NM_133954.1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3 (<i>Atp5g3</i>), nuclear gene encoding mitochondrial protein	0.66
<i>Atp5h</i>	NM_153416.1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit d (<i>Atp5h</i>), nuclear gene encoding mitochondrial protein	0.55
<i>Atp5j</i>	NM_030210.1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F (<i>Atp5j</i>), nuclear gene encoding mitochondrial protein	0.54
<i>Atp5l</i>	NM_178772.2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit g (<i>Atp5l</i>), nuclear gene encoding mitochondrial protein	0.44
<i>Atp5o</i>	NM_175503.3	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (<i>Atp5o</i>), nuclear gene encoding mitochondrial protein	0.55
<i>Atp6v0a1</i>	NM_146217.3		0.62
<i>Atp6v1c1</i>	NM_144829.1	ATPase, H ⁺ transporting, lysosomal V1 subunit C1 (<i>Atp6v1c1</i>)	0.62
<i>Atp6v1d</i>	NM_007377.3	ATPase, H ⁺ transporting, lysosomal V1 subunit D (<i>Atp6v1d</i>)	0.63
<i>Atp6v1e1</i>	NM_172961.2	ATPase, H ⁺ transporting, lysosomal V1 subunit E1 (<i>Atp6v1e1</i>)	0.60
<i>Atp6v1h</i>	NM_023732.2	ATPase, H ⁺ transporting, lysosomal V1 subunit H (<i>Atp6v1h</i>)	0.58
<i>Atpif1</i>	XM_907304.2	ATPase inhibitory factor 1 (<i>Atpif1</i>), nuclear gene encoding mitochondrial protein	0.62
<i>Atxn10</i>	NM_172912.4	ataxin 10 (<i>Atxn10</i>)	0.49
<i>AU040320</i>	NM_001033336.2	expressed sequence AU040320 (<i>AU040320</i>), transcript variant 3	0.54
<i>Aup1</i>	NM_176839.1	ancient ubiquitous protein 1 (<i>Aup1</i>)	0.66
<i>Aurka</i>	NM_013854.1	aurora kinase A (<i>Aurka</i>)	0.19
<i>Aurkaip1</i>	NM_013853.1	aurora kinase A interacting protein 1 (<i>Aurkaip1</i>)	0.61
<i>Aurkb</i>	NR_003522.1	aurora kinase B (<i>Aurkb</i>)	0.25
<i>AV028368</i>	NM_029631.2		0.65
<i>AW120700</i>	NM_134130.1		0.55
<i>B020018G12Rik</i>	NM_198127.1	RIKEN cDNA B020018G12 gene (<i>B020018G12Rik</i>)	0.61
<i>B230114H05Rik</i>	NM_177678.6		0.58
<i>B230208H17Rik</i>	NM_177470	RIKEN cDNA B230208H17 gene (<i>B230208H17Rik</i>)	0.65
<i>B230343A10Rik</i>	NM_007382.1		0.56
<i>B2m</i>	NM_207223.1	beta-2 microglobulin (<i>B2m</i>)	0.62
<i>B3galt6</i>	NM_009338.3	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6 (<i>B3galt6</i>)	0.51
<i>B3gnt5</i>	NM_133225.2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (<i>B3gnt5</i>)	0.66
<i>B4galt3</i>	NM_134037.2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 (<i>B4galt3</i>)	0.50
<i>Bag1</i>	XM_355744.1	Bcl2-associated athanogene 1 (<i>Bag1</i>)	0.62

<i>Bahcc1</i>	NM_080633.2	BAH domain and coiled-coil containing 1 (Bahcc1)	0.42
<i>Bai2</i>	NM_012006.2	brain-specific angiogenesis inhibitor 2 (Bai2)	0.63
<i>Banf1</i>	NM_025590.3	barrier to autointegration factor 1 (Banf1), transcript variant 2	0.28
<i>Bat1a</i>	NM_133348.1	HLA-B-associated transcript 1A (Bat1a)	0.66
<i>Bax</i>	NM_153420.2	Bcl2-associated X protein (Bax)	0.64
<i>BC003236</i>	NM_053178.2		0.47
<i>BC003885</i>	NM_027976.2	cDNA sequence BC003885 (BC003885)	0.59
<i>BC003965</i>	NM_080575.1		0.52
<i>BC017647</i>	NM_019811.3	cDNA sequence BC017647 (BC017647)	0.45
<i>BC019806</i>	NM_007392.2		0.65
<i>BC024659</i>	NM_007393.3	PREDICTED: cDNA sequence BC024659 (BC024659)	0.61
<i>BC031781</i>	NM_019673.1	cDNA sequence BC031781 (BC031781)	0.66
<i>BC039210</i>	NM_134156.1	PREDICTED: cDNA sequence BC039210 (BC039210)	0.57
<i>BC046331</i>	NM_019785.1	cDNA sequence BC046331 (BC046331)	0.60
<i>BC046404</i>	NM_023735.1	cDNA sequence BC046404 (BC046404)	0.62
<i>BC051227</i>	NM_007400.2	cDNA sequence BC051227 (BC051227)	0.65
<i>BC056474</i>	NM_009614.2	cDNA sequence BC056474 (BC056474)	0.62
<i>BC060632</i>	NM_009615.5	cDNA sequence BC060632 (BC060632)	0.62
<i>BC067047</i>	NM_172053.2	cDNA sequence BC067047 (BC067047)	0.47
<i>BC085271</i>	NM_175506.3	cDNA sequence BC085271 (BC085271)	0.45
<i>Bcas1</i>	NM_172845.1	breast carcinoma amplified sequence 1 (Bcas1)	0.42
<i>Bccip</i>		BRCA2 and CDKN1A interacting protein (Bccip)	0.57
<i>Bcl7c</i>	XM_131451.2	B-cell CLL/lymphoma 7C (Bcl7c)	0.54
<i>Bcs1l</i>	NM_172723.4	BCS1-like (yeast) (Bcs1l)	0.66
<i>Bdnf</i>	NM_133770.1	brain derived neurotrophic factor (Bdnf), transcript variant 3	0.66
<i>Bex2</i>	NM_153534.2	brain expressed X-linked 2 (Bex2)	0.60
<i>Bhlhb2</i>	NM_009623.2	basic helix-loop-helix domain containing, class B2 (Bhlhb2)	0.57
<i>Bicd2</i>	NM_009627.1		0.62
<i>Bin1</i>	NM_001008533.2	bridging integrator 1 (Bin1)	0.57
<i>Birc5</i>	NM_028121.1	baculoviral IAP repeat-containing 5 (Birc5), transcript variant 1	0.30
<i>Blm</i>	NM_007414.3	Bloom syndrome homolog (human) (Blm), transcript variant 1	0.42
<i>Bloc1s2</i>	NM_007417.2		0.65
<i>Blvra</i>	NM_007420.2		0.62
<i>Bmp7</i>	NM_130863.1	bone morphogenetic protein 7 (Bmp7)	0.64
<i>Bnip2</i>	NM_019822.3	BCL2/adenovirus E1B interacting protein 2 (Bnip2), transcript variant alpha	0.55
<i>Bok</i>	NM_009634		0.31
<i>Bola2</i>	NM_010347	bolA-like 2 (E. coli) (Bola2)	0.50
<i>Bola3</i>	NM_054070.2	bolA-like 3 (E. coli) (Bola3)	0.51
<i>Bop1</i>	NM_001037136.1	block of proliferation 1 (Bop1)	0.56
<i>Bpnt1</i>	NM_010472.2	bisphosphate 3'-nucleotidase 1 (Bpnt1)	0.50
<i>Brd2</i>	NM_178162.2	bromodomain containing 2 (Brd2), transcript variant 1	0.65
<i>Brip1</i>	NM_018743.3	BRCA1 interacting protein C-terminal helicase 1 (Brip1)	0.63
<i>Brn1</i>	NM_007428.3		0.22
<i>Btaf1</i>	NM_009642.4	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, <i>S. cerevisiae</i>) (Btaf1)	0.61
<i>Btbd11</i>	NM_026375.1	BTB (POZ) domain containing 11 (Btbd11), transcript variant 2	0.40
<i>Btf3</i>	NM_016661		0.57
<i>Btg1</i>	NM_145542.3	B-cell translocation gene 1, anti-proliferative (Btg1)	0.57
<i>Bub1b</i>	NM_009643.1		0.17
<i>Bub3</i>	NM_001002895.2	budding uninhibited by benzimidazoles 3 homolog (<i>S. cerevisiae</i>) (Bub3)	0.66
<i>Bves</i>	XM_136041.3		0.59
<i>Bxdc1</i>	XM_148986.1		0.58
<i>Bxdc2</i>	NM_177907.2	brix domain containing 2 (Bxdc2)	0.56
<i>Bxdc5</i>	NM_198860.1	brix domain containing 5 (Bxdc5), transcript variant 2	0.60
<i>Bzw1</i>	NM_178926.2		0.49
<i>Bzw2</i>	NM_182807.2	basic leucine zipper and W2 domains 2 (Bzw2)	0.42
<i>C030003D03Rik</i>		RIKEN cDNA C030003D03 gene (C030003D03Rik)	0.43
<i>C030025P15Rik</i>	NM_016666.2		0.64
<i>C130007D14</i>	NM_016895.3		0.66
<i>C130032J12Rik</i>	NM_009647.4	RIKEN cDNA C130032J12 gene (C130032J12Rik)	0.55
<i>C1galt1c1</i>	NM_031185.2	C1GALT1-specific chaperone 1 (C1galt1c1)	0.60
<i>C230040D10Rik</i>	NM_001033785.1	PREDICTED: RIKEN cDNA C230040D10 gene (C230040D10Rik)	0.66
<i>C230053B09Rik</i>	NM_018747.3		0.62
<i>C230071H18Rik</i>	NM_017476.2	RIKEN cDNA C230071H18 gene (C230071H18Rik)	0.61
<i>C230078M08Rik</i>	NM_023423.3	RIKEN cDNA C230078M08 gene (C230078M08Rik)	0.64
<i>C330006P03Rik</i>	NM_021473.2		0.48
<i>C330023M02Rik</i>	NM_013916.1	RIKEN cDNA C330023M02 gene (C330023M02Rik)	0.51
<i>C530008M17Rik</i>	NM_008525.3	PREDICTED: RIKEN cDNA C530008M17 gene, transcript variant 3 (C530008M17Rik)	0.46
<i>C730029F17Rik</i>	NM_020559.1		0.58
<i>C78339</i>	NM_019698.1		0.50
<i>C79267</i>	NM_007437		0.49

<i>C79407</i>	NM_172532	expressed sequence C79407 (C79407)	0.45
<i>C920004C08Rik</i>	NM_134042.2		0.21
<i>Cacna1h</i>	NM_007438.3	calcium channel, voltage-dependent, T type, alpha 1H subunit (Cacna1h)	0.54
<i>Cad</i>	NM_009657.3	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (Cad)	0.66
<i>Calm2</i>	NM_199035.1	calmodulin 2 (Calm2)	0.22
<i>Calr</i>	NM_133981.1	calreticulin (Calr)	0.50
<i>Calu</i>	NM_001081395.1	calumenin (Calu), transcript variant 1	0.59
<i>Camk1</i>	NM_009667.2	calcium/calmodulin-dependent protein kinase I (Camk1)	0.54
<i>Camk2b</i>	NM_175007.1	calcium/calmodulin-dependent protein kinase II, beta (Camk2b)	0.32
<i>Camk2n2</i>	NM_007446.1	PREDICTED: calcium/calmodulin-dependent protein kinase II inhibitor 2 (Camk2)	0.53
<i>Camkk2</i>	NM_001042711.2	calcium/calmodulin-dependent protein kinase kinase 2, beta (Camkk2)	0.53
<i>Camta1</i>	NM_021505.2	calmodulin binding transcription activator 1 (Camta1), transcript variant 1	0.59
<i>Cand1</i>	NM_009640.3	PREDICTED: cullin associated and neddylation disassociated 1, transcript variant 1 (Cand1)	0.64
<i>Caprin1</i>	NM_007426.3	cell cycle associated protein 1 (Caprin1)	0.59
<i>Car2</i>	NM_020581.1	carbonic anhydrase 2 (Car2)	0.43
<i>Cask</i>	NM_020332.3	calcium/calmodulin-dependent serine protein kinase (MAGUK family) (Cask)	0.37
<i>Cbfb</i>	NM_170687.3	core binding factor beta (Cbfb)	0.29
<i>Cbr3</i>	NM_028390.2	carbonyl reductase 3 (Cbr3)	0.58
<i>Cbx3</i>	NM_023210.3		0.51
<i>Cbx5</i>	NM_013469.1	chromobox homolog 5 (Drosophila HP1a) (Cbx5), transcript variant 2	0.58
<i>Ccdc101</i>	NM_013470.1	coiled-coil domain containing 101 (Ccdc101)	0.65
<i>Ccdc124</i>	NM_009673.1	coiled-coil domain containing 124 (Ccdc124)	0.60
<i>Ccdc43</i>	NM_001035854.2	coiled-coil domain containing 43 (Ccdc43)	0.64
<i>Ccdc58</i>	NM_029505.1	coiled-coil domain containing 58 (Ccdc58)	0.61
<i>Ccdc86</i>	NM_021710.1	coiled-coil domain containing 86 (Ccdc86)	0.63
<i>Ccdc99</i>	NM_001042558.1	coiled-coil domain containing 99 (Ccdc99)	0.57
<i>Ccnb1</i>	NM_009687.1	cyclin B1 (Ccnb1)	0.13
<i>Ccnd1</i>	NM_027263.1		0.06
<i>Ccnd2</i>	NM_009691.2		0.23
<i>Ccne2</i>	NM_009696.2	cyclin E2 (Ccne2), transcript variant 1	0.67
<i>Ccng1</i>	NM_025825	cyclin G1 (Ccng1)	0.64
<i>Ccnh</i>	NM_175310.5	cyclin H (Ccnh)	0.61
<i>Ccny11</i>	NM_009698.1	cyclin Y-like 1 (Ccny11)	0.41
<i>Cct3</i>	NM_009700.1	chaperonin containing Tcp1, subunit 3 (gamma) (Cct3)	0.48
<i>Cct4</i>	NM_022026.2	chaperonin containing Tcp1, subunit 4 (delta) (Cct4)	0.52
<i>Cct6a</i>	NM_018790.2	chaperonin containing Tcp1, subunit 6a (zeta) (Cct6a)	0.48
<i>Cct8</i>	NM_019870.1	chaperonin containing Tcp1, subunit 8 (theta) (Cct8)	0.45
<i>Cd164</i>	NM_019870.2	CD164 antigen (Cd164)	0.62
<i>Cd276</i>	NM_009704.3	CD276 antigen (Cd276)	0.39
<i>Cd8b</i>	NM_007477.4		0.64
<i>Cdc20</i>	NM_007481.3	cell division cycle 20 homolog (S. cerevisiae) (Cdc20)	0.19
<i>Cdc25a</i>	NM_176837.2	cell division cycle 25 homolog A (S. pombe) (Cdc25a)	0.62
<i>Cdc25c</i>	NM_183019.2	cell division cycle 25 homolog C (S. pombe) (Cdc25c)	0.63
<i>Cdc2a</i>	NM_024191.1	cell division cycle 2 homolog A (S. pombe) (Cdc2a)	0.16
<i>Cdc42</i>	NM_177305.3	cell division cycle 42 homolog (S. cerevisiae) (Cdc42)	0.60
<i>Cdc42ep1</i>	NM_019419.1	CDC42 effector protein (Rho GTPase binding) 1 (Cdc42ep1)	0.65
<i>Cdc42se1</i>	NM_001081083.1	CDC42 small effector 1 (Cdc42se1), transcript variant 1	0.57
<i>Cdc45l</i>	NM_030184.2	cell division cycle 45 homolog (S. cerevisiae)-like (Cdc45l)	0.48
<i>Cdc5l</i>	NM_026139.3	cell division cycle 5-like (S. pombe) (Cdc5l)	0.60
<i>Cdc6</i>	NM_023142.1	cell division cycle 6 homolog (S. cerevisiae) (Cdc6), transcript variant 1	0.58
<i>Cdc7</i>	NM_029711.1	cell division cycle 7 (S. cerevisiae) (Cdc7)	0.31
<i>Cdca2</i>	NM_019824.3	cell division cycle associated 2 (Cdca2)	0.25
<i>Cdca3</i>	NM_178917.2	cell division cycle associated 3 (Cdca3)	0.11
<i>Cdca4</i>	NM_009712.3	cell division cycle associated 4 (Cdca4)	0.44
<i>Cdca5</i>	NM_028710.2	cell division cycle associated 5 (Cdca5)	0.58
<i>Cdca7</i>	NM_019734.1	cell division cycle associated 7 (Cdca7)	0.21
<i>Cdca8</i>	NM_029291.1	cell division cycle associated 8 (Cdca8)	0.13
<i>Cdh13</i>	NM_012055.1	cadherin 13 (Cdh13)	0.35
<i>Cdk2</i>	NM_028386.1	cyclin-dependent kinase 2 (Cdk2), transcript variant 1	0.41
<i>Cdk4</i>	NM_009791.4	cyclin-dependent kinase 4 (Cdk4)	0.47
<i>Cdk8</i>	NM_007494.3	cyclin-dependent kinase 8 (Cdk8)	0.62
<i>Cdkn1a</i>	NM_179203.1	cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a)	0.49
<i>Cdkn2aipnl</i>	NM_007498.2	CDKN2A interacting protein N-terminal like (Cdkn2aipnl)	0.55
<i>Cdkn3</i>	NM_009716.2	PREDICTED: cyclin-dependent kinase inhibitor 3, transcript variant 5 (Cdkn3)	0.24
<i>Cdon</i>	NM_019426.2		0.62
<i>Cdr2</i>	NM_026217.1	cerebellar degeneration-related 2 (Cdr2)	0.40
<i>Cdr2l</i>	NM_026402.3	cerebellar degeneration-related protein 2-like (Cdr2l)	0.44
<i>Cdt1</i>	NM_026195.1	chromatin licensing and DNA replication factor 1 (Cdt1)	0.28
<i>Cebpd</i>	XM_001480958.1	CCAAT/enhancer binding protein (C/EBP), delta (Cebpd)	0.66

<i>Cenpa</i>	NM_144900.1	centromere protein A (Cenpa)	0.06
<i>Cenpb</i>	NM_009721.4	centromere protein B (Cenpb)	0.62
<i>Cenpf</i>	NM_013415.5	PREDICTED: centromere autoantigen F, transcript variant 3 (Cenpf)	0.23
<i>Cenpi</i>	NM_007502.3	centromere protein I (Cenpi)	0.62
<i>Cenpk</i>	NM_007505.2	centromere protein K (Cenpk), transcript variant 1	0.45
<i>Cenpl</i>	NM_016774.3	centromere protein L (Cenpl)	0.41
<i>Cenpm</i>	NM_020615.3	centromere protein M (Cenpm), transcript variant 2	0.57
<i>Cenpn</i>	NM_025313.1	centromere protein N (Cenpn)	0.55
<i>Cenpp</i>	NM_009725.3	centromere protein P (Cenpp)	0.58
<i>Cenpq</i>	NM_026468.1	centromere protein Q (Cenpq)	0.57
<i>Centd1</i>	NM_175015.2	PREDICTED: centaurin, delta 1, transcript variant 5 (Centd1)	0.56
<i>Cep152</i>	NM_027862.1	centrosomal protein 152 (Cep152)	0.63
<i>Cep170</i>	NM_016755.2	centrosomal protein 170 (Cep170)	0.61
<i>Cep55</i>	NM_013795.4	centrosomal protein 55 (Cep55)	0.60
<i>Cep78</i>	NM_138597.2	centrosomal protein 78 (Cep78)	0.59
<i>Cetn3</i>	NM_016920.1	centrin 3 (Cetn3)	0.63
<i>Cfl1</i>	NM_025494.2	cofilin 1, non-muscle (Cfl1)	0.64
<i>Cggbp1</i>	NM_023721.2	CGG triplet repeat binding protein 1 (Cggbp1)	0.63
<i>Chaf1a</i>	NM_007510.2	chromatin assembly factor 1, subunit A (p150) (Chaf1a)	0.60
<i>Chaf1b</i>	NM_133826.2	chromatin assembly factor 1, subunit B (p60) (Chaf1b)	0.31
<i>Chchd1</i>	NM_009727.2	coiled-coil-helix-coiled-coil-helix domain containing 1 (Chchd1)	0.47
<i>Chchd4</i>	NM_007512.2	coiled-coil-helix-coiled-coil-helix domain containing 4 (Chchd4), nuclear gene encoding mitochondrial protein	0.61
<i>Chd1</i>	NM_009124.4		0.60
<i>Chmp4b</i>	NM_016843.3	chromatin modifying protein 4B (Chmp4b)	0.57
<i>Chmp7</i>	NM_177629.2	CHMP family, member 7 (Chmp7)	0.64
<i>Chn2</i>	NM_133886.2	chimerin (chimaerin) 2 (Chn2)	0.27
<i>Chrm3</i>	NM_007517.3	cholinergic receptor, muscarinic 3, cardiac (Chrm3)	0.56
<i>Chst11</i>	NM_011497.3	carbohydrate sulfotransferase 11 (Chst11)	0.66
<i>Chst2</i>	NM_025338.3	carbohydrate sulfotransferase 2 (Chst2)	0.49
<i>Chst7</i>	NM_011496.1	carbohydrate (N-acetylglucosamino) sulfotransferase 7 (Chst7)	0.15
<i>Chtf18</i>	NM_177672	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae) (Chtf18)	0.55
<i>Cirh1a</i>		cirrhosis, autosomal recessive 1A (human) (Cirh1a)	0.59
<i>Ckap2</i>	XM_127132.3		0.32
<i>Ckap2l</i>	NM_009465.3	cytoskeleton associated protein 2-like (Ckap2l)	0.57
<i>Cldnd1</i>	NM_001039518.1	claudin domain containing 1 (Cldnd1)	0.52
<i>Clic1</i>			0.54
<i>Clic4</i>	AK045406	chloride intracellular channel 4 (mitochondrial) (Clic4), nuclear gene encoding mitochondrial protein	0.43
<i>Cln5</i>	NM_001024616.1		0.47
<i>Clns1a</i>	XM_981366.1	chloride channel, nucleotide-sensitive, 1A (Clns1a)	0.60
<i>Clpp</i>	XM_001001884.2	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli) (Clpp)	0.61
<i>Clspn</i>	NM_133898.3	claspin homolog (Xenopus laevis) (Clspn)	0.28
<i>Clta</i>	AK046118	clathrin, light polypeptide (Lca) (Clta), transcript variant 2	0.63
<i>Cltc</i>			0.56
<i>Cmas</i>	NM_009735.2	cytidine monophospho-N-acetylneuraminic acid synthetase (Cmas)	0.61
<i>Cmc1</i>	NM_033149.2	COX assembly mitochondrial protein homolog (S. cerevisiae) (Cmc1), nuclear gene encoding mitochondrial protein	0.56
<i>Cmpk</i>	NM_080445.4	cytidylate kinase (Cmpk)	0.63
<i>Cnih</i>	NM_029792.1	cornichon homolog (Drosophila) (Cnih)	0.60
<i>Cnih4</i>	NM_054052.2	cornichon homolog 4 (Drosophila) (Cnih4)	0.43
<i>Cntnap4</i>	NM_020579.1		0.42
<i>Col16a1</i>	AK046967	collagen, type XVI, alpha 1 (Col16a1)	0.30
<i>Col18a1</i>	AK047284	procollagen, type XVIII, alpha 1 (Col18a1)	0.11
<i>Comm1d1</i>	NM_013717.2	COMM domain containing 1 (Comm1d1)	0.59
<i>Cops6</i>	NM_019517.2	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) (Cops6)	0.61
<i>Cops7a</i>	NM_009736.1	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (Cops7a)	0.61
<i>Coq7</i>	NM_198423.2	demethyl-Q 7 (Coq7)	0.64
<i>Coro1c</i>	NM_173071.1	coronin, actin binding protein 1C (Coro1c)	0.40
<i>Cox10</i>	NM_001038231.1	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (Cox10), nuclear gene encoding mitochondrial protein	0.63
<i>Cox17</i>	NM_019693.2	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast) (Cox17)	0.48
<i>Cox18</i>	NM_007527.2	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae) (Cox18)	0.60
<i>Cox5a</i>	NM_172742	cytochrome c oxidase, subunit Va (Cox5a), nuclear gene encoding mitochondrial protein	0.42

<i>Cox5b</i>	NM_133234.1		0.64
<i>Cox6a1</i>	NM_130452.1		0.57
<i>Cox6b1</i>	NM_026116.2	cytochrome c oxidase, subunit VIb polypeptide 1 (Cox6b1)	0.56
<i>Cox6c</i>	NM_175325.2	cytochrome c oxidase, subunit VIc (Cox6c)	0.62
<i>Cox7a2</i>	NM_030249	cytochrome c oxidase, subunit VIIa 2 (Cox7a2)	0.46
<i>Cox7a2l</i>	NM_198609.2	cytochrome c oxidase subunit VIIa polypeptide 2-like (Cox7a2l)	0.66
<i>Cplx1</i>	XM_128528.2	complexin 1 (Cplx1)	0.61
<i>Cpne8</i>	NM_145430.1	copine VIII (Cpne8), transcript variant 2	0.50
<i>Creld2</i>	NM_145460	cysteine-rich with EGF-like domains 2 (Creld2)	0.57
<i>Crif3</i>	NM_145450.3	cytokine receptor-like factor 3 (Crif3)	0.66
<i>Crtap</i>	NM_146237.1	cartilage associated protein (Crtap)	0.52
<i>Cs</i>	XM_001472442.1	citrate synthase (Cs), nuclear gene encoding mitochondrial protein	0.38
<i>Csad</i>	NM_173421.1		0.67
<i>Csda</i>	NM_153584.1	cold shock domain protein A (Csda)	0.52
<i>Csde1</i>	NM_145943.1	cold shock domain containing E1, RNA binding (Csde1)	0.62
<i>Cse1l</i>	XM_196478	chromosome segregation 1-like (<i>S. cerevisiae</i>) (Cse1l)	0.53
<i>Csk</i>	XM_001481316.1	c-src tyrosine kinase (Csk)	0.66
<i>Csnk1d</i>	NM_177673.2	casein kinase 1, delta (Csnk1d), transcript variant 2	0.61
<i>Csnk1e</i>	NM_198861.1	casein kinase 1, epsilon (Csnk1e)	0.64
<i>Csnk1g2</i>	NM_178418.2	casein kinase 1, gamma 2 (Csnk1g2)	0.66
<i>Csnk2a1-rs3</i>	NM_183170.2		0.56
<i>Csnk2a2</i>	NM_001001493.2	casein kinase 2, alpha prime polypeptide (Csnk2a2)	0.58
<i>Cspg5</i>	NM_198625.1	chondroitin sulfate proteoglycan 5 (Cspg5)	0.49
<i>Csrp2</i>	NM_177782.3	cysteine and glycine-rich protein 2 (Csrp2)	0.48
<i>Cstf1</i>	NM_001008551.1	cleavage stimulation factor, 3' pre-RNA, subunit 1 (Cstf1)	0.64
<i>Ctgf</i>	NM_013867.1		0.49
<i>Ctps</i>	NM_029815.1	cytidine 5'-triphosphate synthase (Ctps)	0.60
<i>Ctsc</i>	NM_138681.3	cathepsin C (Ctsc)	0.39
<i>Ctsh</i>	NM_025392.1	cathepsin H (Ctsh)	0.59
<i>Ctnbp2nl</i>	NM_207680.2	CTTNBP2 N-terminal like (Ctnbp2nl)	0.41
<i>Cugbp1</i>	NM_009746.2	CUG triplet repeat, RNA binding protein 1 (Cugbp1), transcript variant 2	0.60
<i>Cugbp2</i>	NM_025784.2	CUG triplet repeat, RNA binding protein 2 (Cugbp2), transcript variant 6	0.47
<i>Cul3</i>	NM_027208.1	cullin 3 (Cul3)	0.58
<i>Cx3cl1</i>	NM_001048141.1	chemokine (C-X3-C motif) ligand 1 (Cx3cl1)	0.42
<i>Cxadr</i>	NM_009749.1	coxsaekie virus and adenovirus receptor (Cxadr), transcript variant 1	0.33
<i>Cxcl1</i>	NM_011498.4	chemokine (C-X-C motif) ligand 1 (Cxcl1)	0.46
<i>Cxcl4</i>	NM_031397.2	chemokine (C-X-C motif) ligand 4 (Cxcl4)	0.47
<i>Cyc1</i>	NM_029791	cytochrome c-1 (Cyc1)	0.37
<i>Cycs</i>	NM_009668.1	cytochrome c, somatic (Cycs), nuclear gene encoding mitochondrial protein	0.27
<i>Cyp51</i>		cytochrome P450, family 51 (Cyp51)	0.23
<i>D030038A19Rik</i>	NM_009689.2		0.65
<i>D030056L22Rik</i>	NM_007550.3	RIKEN cDNA D030056L22 gene (D030056L22Rik)	0.58
<i>D10627</i>	XM_193940.2	cDNA sequence D10627 (D10627)	0.64
<i>D10ErtD322e</i>	NM_026678.3	DNA segment, Chr 10, ERATO Doi 322, expressed (D10ErtD322e)	0.49
<i>D10Wsu102e</i>	NM_007557.2	DNA segment, Chr 10, Wayne State University 102, expressed (D10Wsu102e)	0.60
<i>D10Wsu52e</i>	NM_007560.3	DNA segment, Chr 10, Wayne State University 52, expressed (D10Wsu52e)	0.58
<i>D12ErtD553e</i>	NM_001008238.2	DNA segment, Chr 12, ERATO Doi 553, expressed (D12ErtD553e)	0.61
<i>D12Wsu95e</i>	NM_016778		0.46
<i>D130004H04Rik</i>	NM_175103.2		0.62
<i>D15Mgi27</i>	NM_175277.2	DNA Segment, Chr 15, Mouse Genome Informatics 27 (D15Mgi27)	0.60
<i>D17H6S56E-5</i>	NM_013481.1	DNA segment, Chr 17, human D6S56E 5 (D17H6S56E-5)	0.55
<i>D17Wsu104e</i>	NM_011794.3		0.56
<i>D19Bwg1357e</i>	NM_010238.3	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed (D19Bwg1357e)	0.48
<i>D1ErtD471e</i>	NM_178309.1		0.48
<i>D2Bwg1335e</i>	NM_144818	DNA segment, Chr 2, Brigham & Women's Genetics 1335 expressed (D2Bwg1335e)	0.50
<i>D2ErtD750e</i>	NM_001080706.1	DNA segment, Chr 2, ERATO Doi 750, expressed (D2ErtD750e)	0.35
<i>D4Bwg0951e</i>	NM_001017525.1	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed (D4Bwg0951e)	0.52
<i>D6Wsu176e</i>	NM_145455.1		0.60
<i>D930046M13Rik</i>	NM_007569.1		0.41
<i>D9Wsu20e</i>	NM_009773		0.58
<i>Dad1</i>	NM_009774.3		0.63
<i>Dap3</i>	NM_024285	death associated protein 3 (Dap3), nuclear gene encoding mitochondrial protein	0.67
<i>Dazap1</i>	NM_023323		0.33
<i>Dbf4</i>	NM_026396.2	DBF4 homolog (<i>S. cerevisiae</i>) (Dbf4)	0.29
<i>Dbt</i>	NM_027371.2	dihydroipoamide branched chain transacylase E2 (Dbt)	0.61
<i>Dbx2</i>	NM_172449.1		0.56
<i>Dclk1</i>	NM_025824	doublecortin-like kinase 1 (Dclk1)	0.27
<i>Dcps</i>	NM_025840.2	decapping enzyme, scavenger (Dcps)	0.64

<i>Dcun1d5</i>	NM_029881.2	DCN1, defective in cullin neddylation 1, domain containing 5 (<i>S. cerevisiae</i>) (<i>Dcun1d5</i>)	0.62
<i>Ddost</i>		dolichyl-di-phosphooligosaccharide-protein glycotransferase (<i>Ddost</i>)	0.55
<i>Ddx1</i>	NM_177287	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 (<i>Ddx1</i>)	0.55
<i>Ddx11</i>			0.39
<i>Ddx20</i>	XM_975397.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (<i>Ddx20</i>)	0.59
<i>Ddx21</i>	NM_177914.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 (<i>Ddx21</i>)	0.53
<i>Ddx25</i>		DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (<i>Ddx25</i>)	0.61
<i>Ddx26</i>	NM_178684.3		0.64
<i>Ddx27</i>	AK081724	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 (<i>Ddx27</i>)	0.65
<i>Ddx3x</i>	NM_021550.2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked (<i>Ddx3x</i>)	0.63
<i>Ddx54</i>	NM_207233.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54 (<i>Ddx54</i>)	0.53
<i>Ddx6</i>	XM_976346.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 (<i>Ddx6</i>)	0.57
<i>Deb1</i>	AK048765	differentially expressed in B16F10 1 (<i>Deb1</i>)	0.48
<i>Dek</i>	AK082620	DEK oncogene (DNA binding) (<i>Dek</i>)	0.61
<i>Dennd2a</i>	NM_207265.2	DENN/MADD domain containing 2A (<i>Dennd2a</i>)	0.35
<i>Dgkd</i>	NM_176995.2		0.57
<i>Dgkk</i>	NM_009778.1	diacylglycerol kinase kappa (<i>Dgkk</i>)	0.49
<i>Dgkz</i>		diacylglycerol kinase zeta (<i>Dgkz</i>)	0.47
<i>Dhcr24</i>	NM_172722.3		0.37
<i>Dhcr7</i>	NM_175286.3	7-dehydrocholesterol reductase (<i>Dhcr7</i>)	0.38
<i>Dhh</i>	NM_011413.2	desert hedgehog (<i>Dhh</i>)	0.42
<i>Dhps</i>	NM_009780.1	deoxyhypusine synthase (<i>Dhps</i>)	0.66
<i>Dhrsx</i>	XM_916109.2	dehydrogenase/reductase (SDR family) X chromosome (<i>Dhrsx</i>)	0.53
<i>Dhx15</i>		DEAH (Asp-Glu-Ala-His) box polypeptide 15 (<i>Dhx15</i>), transcript variant 2	0.44
<i>Dhx30</i>	AK049826	DEAH (Asp-Glu-Ala-His) box polypeptide 30 (<i>Dhx30</i>)	0.65
<i>Diras2</i>	AK050233		0.55
<i>Dlgap5</i>	XM_127312	discs, large (<i>Drosophila</i>) homolog-associated protein 5 (<i>Dlgap5</i>)	0.46
<i>Dlst</i>	NM_183148		0.51
<i>Dnahc11</i>	NM_172578.2	dynein, axonemal, heavy chain 11 (<i>Dnahc11</i>)	0.32
<i>Dnajb11</i>			0.47
<i>Dnajc19</i>	NM_198037.1	DnaJ (Hsp40) homolog, subfamily C, member 19 (<i>Dnajc19</i>), transcript variant 2	0.65
<i>Dnajc2</i>	NM_021415.3	DnaJ (Hsp40) homolog, subfamily C, member 2 (<i>Dnajc2</i>)	0.52
<i>Dnmt1</i>	NM_009785.1	DNA methyltransferase (cytosine-5) 1 (<i>Dnmt1</i>)	0.36
<i>Dock1</i>	NM_146123.2	dedicator of cytokinesis 1 (<i>Dock1</i>)	0.65
<i>Dock10</i>	NM_023525.1		0.43
<i>Dos</i>	NM_007589.4	downstream of Stk11 (<i>Dos</i>)	0.55
<i>Dpm3</i>	NM_007591.3		0.65
<i>Dpp3</i>	NM_007594.3	dipeptidylpeptidase 3 (<i>Dpp3</i>)	0.62
<i>Dpy30</i>	NM_133926.2	dpy-30 homolog (<i>C. elegans</i>) (<i>Dpy30</i>)	0.56
<i>Dpysl3</i>	NM_007595.3	dihydropyrimidinase-like 3 (<i>Dpysl3</i>)	0.60
<i>Drg1</i>	NM_178597.4	developmentally regulated GTP binding protein 1 (<i>Drg1</i>)	0.64
<i>Dtymk</i>	XM_990809.1		0.61
<i>Dusp1</i>	NM_145358.1	dual specificity phosphatase 1 (<i>Dusp1</i>)	0.35
<i>Dusp4</i>	NM_001081557.1	dual specificity phosphatase 4 (<i>Dusp4</i>)	0.36
<i>Dusp6</i>	XM_125901.8	dual specificity phosphatase 6 (<i>Dusp6</i>)	0.10
<i>Dusp7</i>	NM_007600.2	dual specificity phosphatase 7 (<i>Dusp7</i>)	0.29
<i>Dynll1</i>	NM_007602.3	dynein light chain LC8-type 1 (<i>Dynll1</i>)	0.62
<i>E030026I10Rik</i>	NM_016739.2		0.56
<i>E130016E03Rik</i>	NM_009801.3	RIKEN cDNA E130016E03 gene (<i>E130016E03Rik</i>)	0.33
<i>E130306D19Rik</i>	NM_025821.2		0.48
<i>E230013M07Rik</i>	NM_009806.2		0.31
<i>E2f1</i>	NM_009814.1	E2F transcription factor 1 (<i>E2f1</i>)	0.32
<i>E2f2</i>	NM_009804.1	E2F transcription factor 2 (<i>E2f2</i>)	0.54
<i>E2f6</i>	NM_022309.3	E2F transcription factor 6 (<i>E2f6</i>)	0.64
<i>E330016A19Rik</i>	NM_173047.2	RIKEN cDNA E330016A19 gene (<i>E330016A19Rik</i>)	0.46
<i>E430028B21Rik</i>	NM_007624	RIKEN cDNA E430028B21 gene (<i>E430028B21Rik</i>)	0.64
<i>E430039I23Rik</i>	NM_001076789.1		0.43
<i>E530011J04Rik</i>	NM_172274.1		0.60
<i>Ebna1bp2</i>	NM_029339.2	EBNA1 binding protein 2 (<i>Ebna1bp2</i>)	0.45
<i>Ebp</i>	NM_026964.3	phenylalkylamine Ca2+ antagonist (emopamil) binding protein (<i>Ebp</i>)	0.66
<i>Ece1</i>	XM_355284.5	endothelin converting enzyme 1 (<i>Ece1</i>)	0.53
<i>Ecm1</i>	NM_026222.2	extracellular matrix protein 1 (<i>Ecm1</i>)	0.63
<i>Edf1</i>	NM_025918.3	endothelial differentiation-related factor 1 (<i>Edf1</i>)	0.56
<i>Eef1a1</i>	NM_198645.1	eukaryotic translation elongation factor 1 alpha 1 (<i>Eef1a1</i>)	0.62
<i>Eef1b2</i>	NM_023731.2	eukaryotic translation elongation factor 1 beta 2 (<i>Eef1b2</i>)	0.48
<i>Eef1e1</i>	NM_025725.2	eukaryotic translation elongation factor 1 epsilon 1 (<i>Eef1e1</i>)	0.33
<i>Eef1g</i>	NM_027411.1	eukaryotic translation elongation factor 1 gamma (<i>Eef1g</i>)	0.50
<i>Efnb1</i>	NM_172301.3	ephrin B1 (<i>Efnb1</i>)	0.66
<i>Efs</i>	NM_007631.1	embryonal Fyn-associated substrate (<i>Efs</i>)	0.42

<i>EG216185</i>	NM_009829	PREDICTED: predicted gene, EG216185 (EG216185)	0.50
<i>EG237361</i>	NM_001037134.1	PREDICTED: predicted gene, EG237361 (EG237361)	0.36
<i>EG243642</i>	NM_009831.2	PREDICTED: predicted gene, EG243642 (EG243642)	0.41
<i>EG245297</i>	NM_023243.4	predicted gene, EG245297 (EG245297)	0.64
<i>EG268795</i>	NM_001097644.1	PREDICTED: predicted gene, EG268795, transcript variant 4 (EG268795)	0.45
<i>EG269105</i>	NM_053180.2	PREDICTED: predicted gene, EG269105 (EG269105)	0.57
<i>EG382843</i>	NM_009836.1	PREDICTED: predicted gene, EG382843 (EG382843)	0.51
<i>EG432448</i>	NM_009837.1	PREDICTED: predicted gene, EG432448, transcript variant 1 (EG432448)	0.63
<i>EG432681</i>	NM_009838.1	PREDICTED: predicted gene, EG432681 (EG432681)	0.47
<i>EG432721</i>	NM_009840.3	PREDICTED: predicted gene, EG432721 (EG432721)	0.39
<i>EG432879</i>	NM_153098.2	predicted gene, EG432879 (EG432879)	0.58
<i>EG433144</i>	NM_016898.2	PREDICTED: predicted gene, EG433144 (EG433144)	0.62
<i>EG433182</i>	NM_133983.3	predicted gene, EG433182 (EG433182)	0.58
<i>EG433923</i>	NM_007652.2	predicted gene, EG433923 (EG433923)	0.53
<i>EG434404</i>	NM_007656.4	PREDICTED: predicted gene, EG434404 (EG434404)	0.57
<i>EG434858</i>	NM_009858	predicted gene, EG434858 (EG434858), non-coding RNA.	0.64
<i>EG545056</i>	NM_023223.1	predicted gene, EG545056 (EG545056), non-coding RNA.	0.65
<i>EG622236</i>	NM_007658.3	PREDICTED: predicted gene, EG622236, transcript variant 1 (EG622236)	0.49
<i>EG622339</i>	NM_009860.2	predicted gene, EG622339 (EG622339)	0.51
<i>EG623818</i>	NM_007659.3	PREDICTED: predicted gene, EG623818 (EG623818)	0.57
<i>EG624124</i>	NM_009861.1	PREDICTED: predicted gene, EG624124, transcript variant 1 (EG624124)	0.48
<i>EG625054</i>	NM_027219.3	predicted gene, EG625054 (EG625054), non-coding RNA.	0.58
<i>EG625917</i>	NM_020006.1	PREDICTED: predicted gene, EG625917 (EG625917)	0.49
<i>EG626175</i>	NM_172395.2	PREDICTED: predicted gene, EG626175 (EG626175)	0.40
<i>EG629595</i>	NM_009862.1	PREDICTED: predicted gene, EG629595 (EG629595)	0.42
<i>EG632248</i>	NM_152810.1	PREDICTED: predicted gene, EG632248 (EG632248)	0.42
<i>EG633120</i>	NM_011799.2	PREDICTED: predicted gene, EG633120 (EG633120), misc RNA.	0.53
<i>EG637748</i>	NM_009863.2	PREDICTED: predicted gene, EG637748 (EG637748)	0.49
<i>EG665369</i>	NM_175384.3	PREDICTED: predicted gene, EG665369 (EG665369)	0.52
<i>EG666577</i>	NM_013538.4	PREDICTED: predicted gene, EG666577 (EG666577)	0.45
<i>EG666609</i>	NM_028023.3	PREDICTED: predicted gene, EG666609 (EG666609)	0.61
<i>EG667190</i>	NM_026410.1	PREDICTED: predicted gene, EG667190 (EG667190), misc RNA.	0.30
<i>EG667728</i>	NM_025866.3	PREDICTED: predicted gene, EG667728 (EG667728), misc RNA.	0.22
<i>EG668668</i>	NM_026560.3	predicted gene, EG668668 (EG668668)	0.65
<i>EG668829</i>	NM_019707.4	PREDICTED: predicted gene, EG668829 (EG668829)	0.53
<i>EG668850</i>	NM_183417.2	PREDICTED: predicted gene, EG668850 (EG668850), misc RNA.	0.51
<i>Egr1</i>	NM_009870.2	early growth response 1 (Egr1)	0.60
<i>Ehd4</i>	NM_153599.3	EH-domain containing 4 (Ehd4)	0.35
<i>Eif1a</i>	NM_007669.2	eukaryotic translation initiation factor 1A (Eif1a)	0.61
<i>Eif1ad</i>	NM_029976.2	eukaryotic translation initiation factor 1A domain containing (Eif1ad)	0.46
<i>Eif2b3</i>	XM_919022.2		0.56
<i>Eif2s2</i>	NM_033037.3	eukaryotic translation initiation factor 2, subunit 2 (beta) (Eif2s2)	0.61
<i>Eif2s3x</i>	AK040711	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked (Eif2s3x)	0.56
<i>Eif3a</i>	NM_007672.1	eukaryotic translation initiation factor 3, subunit A (Eif3a)	0.50
<i>Eif3b</i>	NM_001080929.1	eukaryotic translation initiation factor 3, subunit B (Eif3b)	0.66
<i>Eif3d</i>	NM_026014.3	eukaryotic translation initiation factor 3, subunit D (Eif3d)	0.59
<i>Eif3eip</i>	NM_007679.4	eukaryotic translation initiation factor 3, subunit E interacting protein (Eif3eip)	0.65
<i>Eif3f</i>	NM_009886.2	eukaryotic translation initiation factor 3, subunit F (Eif3f)	0.66
<i>Eif3g</i>	NM_007681.2	eukaryotic translation initiation factor 3, subunit G (Eif3g)	0.49
<i>Eif3i</i>	NM_007682.2	eukaryotic translation initiation factor 3, subunit I (Eif3i)	0.58
<i>Eif3k</i>	XM_916605.2	eukaryotic translation initiation factor 3, subunit K (Eif3k)	0.62
<i>Eif3s4</i>	NM_145924.2		0.46
<i>Eif3s5</i>	NM_021790.1		0.65
<i>Eif4a1</i>	NM_027429.1	eukaryotic translation initiation factor 4A1 (Eif4a1)	0.28
<i>Eif4a3</i>	NM_178269.3	eukaryotic translation initiation factor 4A, isoform 3 (Eif4a3)	0.66
<i>Eif4ebp1</i>	NM_028131.3	eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1)	0.51
<i>Eif4el3</i>	NM_025495.1		0.55
<i>Eif4g1</i>	NM_031863.3	eukaryotic translation initiation factor 4, gamma 1 (Eif4g1), transcript variant 2	0.61
<i>Eif5</i>	XM_001001363.1	eukaryotic translation initiation factor 5 (Eif5), transcript variant 1	0.58
<i>Eif5a</i>	NM_001081091.1	eukaryotic translation initiation factor 5A (Eif5a)	0.39
<i>Eif6</i>	NM_001099637.1	eukaryotic translation initiation factor 6 (Eif6)	0.62
<i>Elavl1</i>	NM_028760.1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (Elavl1)	0.52
<i>Elk3</i>	NM_198019.2	ELK3, member of ETS oncogene family (Elk3), transcript variant 2	0.43
<i>Elmo1</i>	NM_207298.2	engulfment and cell motility 1, ced-12 homolog (C. elegans) (Elmo1), transcript variant 2	0.58
<i>Elov11</i>	NM_007684.3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (Elov11), transcript variant 2	0.51
<i>Elov14</i>	NM_145825.1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (Elov14)	0.63

<i>Elov15</i>	NM_007687.2	ELOVL family member 5, elongation of long chain fatty acids (yeast) (Elov15)	0.62
<i>Elov16</i>	NM_008823.3	ELOVL family member 6, elongation of long chain fatty acids (yeast) (Elov16)	0.21
<i>Emg1</i>	NM_178647.2	EMG1 nucleolar protein homolog (S. cerevisiae) (Emg1)	0.53
<i>Eno1</i>	NM_013733.3	enolase 1, alpha non-neuron (Eno1)	0.39
<i>Entpd4</i>	NM_028083.3	ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4)	0.52
<i>Epn2</i>	NM_025366.2		0.20
<i>Erc1</i>	NM_133928.2	excision repair cross-complementing rodent repair deficiency, complementation group 1 (Erc1)	0.64
<i>Ergic1</i>	AK021188	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (Ergic1)	0.39
<i>Ergic2</i>	NM_007695.2	ERGIC and golgi 2 (Ergic2), transcript variant 1	0.59
<i>Erh</i>	NM_001025566.1	enhancer of rudimentary homolog (Drosophila) (Erh)	0.58
<i>Erlin1</i>	NM_029362.3	ER lipid raft associated 1 (Erlin1)	0.62
<i>Ermp1</i>	NM_134078.3	endoplasmic reticulum metalloproteinase 1 (Ermp1)	0.32
<i>Erp29</i>	NM_023543.1	endoplasmic reticulum protein 29 (Erp29)	0.64
<i>Errf1</i>	NM_033269.2	ERBB receptor feedback inhibitor 1 (Errf1)	0.62
<i>Esco2</i>	NM_021439.2	establishment of cohesion 1 homolog 2 (S. cerevisiae) (Esco2)	0.31
<i>Esp1</i>	NM_018763.1	extra spindle poles-like 1 (S. cerevisiae) (Esp1)	0.65
<i>Esrra</i>	NM_021715.1	estrogen related receptor, alpha (Esrra)	0.55
<i>Esrrb</i>	NM_145409.1	estrogen related receptor, beta (Esrrb)	0.52
<i>Etf1</i>	NM_011574.1	eukaryotic translation termination factor 1 (Etf1)	0.54
<i>Ets1</i>	XM_134100.3	E26 avian leukemia oncogene 1, 5' domain (Ets1), transcript variant 2	0.66
<i>Ets2</i>	NM_181589.2	E26 avian leukemia oncogene 2, 3' domain (Ets2)	0.48
<i>Etv1</i>	NM_029437.1	ets variant gene 1 (Etv1)	0.35
<i>Etv4</i>	NM_008770.2	ets variant gene 4 (E1A enhancer binding protein, E1AF) (Etv4)	0.38
<i>Etv5</i>	NM_171826.2	ets variant gene 5 (Etv5)	0.22
<i>Exosc1</i>	NM_033444.1	exosome component 1 (Exosc1)	0.55
<i>Exosc2</i>	NM_013885.2	exosome component 2 (Exosc2)	0.66
<i>Exosc6</i>	NM_030179.2	exosome component 6 (Exosc6)	0.65
<i>Exosc7</i>	NM_001042634.1	exosome component 7 (Exosc7)	0.64
<i>Exosc8</i>	NM_007714.2	exosome component 8 (Exosc8)	0.51
<i>Ext1</i>	XM_127882.3	exostoses (multiple) 1 (Ext1)	0.61
<i>Extl3</i>	NM_023671.1	exostoses (multiple)-like 3 (Extl3)	0.58
<i>Ezh2</i>	NM_017393.1	enhancer of zeste homolog 2 (Drosophila) (Ezh2)	0.35
<i>F2r</i>	NM_175554.3	coagulation factor II (thrombin) receptor (F2r)	0.36
<i>F630043A04Rik</i>	NM_001080385.1	RIKEN cDNA F630043A04 gene (F630043A04Rik)	0.58
<i>Faah</i>	NM_001003908	fatty acid amide hydrolase (Faah)	0.66
<i>Fabp5</i>	NM_009908.1	fatty acid binding protein 5, epidermal (Fabp5)	0.30
<i>Fabp7</i>	NM_026442.2		0.58
<i>Faf1</i>	NM_023160.1	Fas-associated factor 1 (Faf1)	0.58
<i>Fahd1</i>	NM_023455.2	fumarylacetoacetate hydrolase domain containing 1 (Fahd1), nuclear gene encoding mitochondrial protein	0.62
<i>Fam101a</i>	NM_025647.2	family with sequence similarity 101, member A (Fam101a)	0.48
<i>Fam108a</i>	NM_026066.2	family with sequence similarity 108, member A (Fam108a)	0.64
<i>Fam110a</i>	NM_009919.1	family with sequence similarity 110, member A (Fam110a), transcript variant 1	0.54
<i>Fam120a</i>	NM_030131.2	family with sequence similarity 120, member A (Fam120a)	0.56
<i>Fam125a</i>	NM_009923.1	family with sequence similarity 125, member A (Fam125a)	0.65
<i>Fam131a</i>	AK039251	family with sequence similarity 131, member A (Fam131a)	0.42
<i>Fam171a1</i>	NM_130457	family with sequence similarity 171, member A1 (Fam171a1)	0.49
<i>Fam173a</i>	NM_028266.4	family with sequence similarity 173, member A (Fam173a)	0.55
<i>Fam84a</i>	NM_009929.2	family with sequence similarity 84, member A (Fam84a)	0.38
<i>Fancd2</i>	XM_907370.3	Fanconi anemia, complementation group D2 (Fancd2)	0.66
<i>Fance</i>	NM_153393.1	PREDICTED: Fanconi anemia, complementation group E (Fance)	0.56
<i>Farsb</i>	NM_199473	phenylalanyl-tRNA synthetase, beta subunit (Farsb)	0.42
<i>Fastk</i>	NM_144514.2	Fas-activated serine/threonine kinase (Fastk)	0.61
<i>Fblim1</i>	AK018238	filamin binding LIM protein 1 (Fblim1)	0.55
<i>Fbln1</i>	NM_012002.3	fibulin 1 (Fbln1)	0.37
<i>Fbln2</i>	NM_012003.1	fibulin 2 (Fbln2), transcript variant 2	0.17
<i>Fbn1</i>	NM_009940.2		0.64
<i>Fbxl10</i>	NM_011779.3	F-box and leucine-rich repeat protein 10 (Fbxl10), transcript variant 3	0.51
<i>Fbxl14</i>	NM_178379.2	F-box and leucine-rich repeat protein 14 (Fbxl14)	0.51
<i>Fbxl4</i>	NM_001017429.2	F-box and leucine-rich repeat protein 4 (Fbxl4)	0.67
<i>Fbxo9</i>	NM_001033310.1	f-box protein 9 (Fbxo9), transcript variant 1	0.62
<i>Fchsd2</i>	NM_007747.2	FCH and double SH3 domains 2 (Fchsd2)	0.63
<i>Fcmd</i>	NM_009942		0.65
<i>Fdps</i>	NM_007748.2	farnesyl diphosphate synthetase (Fdps)	0.14
<i>Fen1</i>	NM_025628.2	flap structure specific endonuclease 1 (Fen1)	0.35
<i>Fgf1</i>	NM_053071.2	fibroblast growth factor 1 (Fgf1)	0.64
<i>Fgf22</i>	NM_009945.3	fibroblast growth factor 22 (Fgf22)	0.62
<i>Fgfr1op2</i>	NM_009187.1	FGFR1 oncogene partner 2 (Fgfr1op2)	0.60
<i>Fh1</i>	NM_013494.2	fumarate hydratase 1 (Fh1)	0.37

<i>Fibp</i>	NM_007756.2	fibroblast growth factor (acidic) intracellular binding protein (Fibp)	0.51
<i>Flgn1</i>	NM_001033851.1	fidgetin-like 1 (Flgn1)	0.27
<i>Fkbp11</i>	NM_029720.1	FK506 binding protein 11 (Fkbp11)	0.39
<i>Fkbp1a</i>	NM_018776.1	FK506 binding protein 1a (Fkbp1a)	0.44
<i>Fkbp2</i>	NM_019922.1	FK506 binding protein 2 (Fkbp2)	0.60
<i>Fkbp4</i>	NM_009964.1	FK506 binding protein 4 (Fkbp4)	0.48
<i>Fkbp5</i>	NM_009967.1	FK506 binding protein 5 (Fkbp5)	0.64
<i>Fmnl2</i>	NM_026444.3	formin-like 2 (Fmnl2)	0.39
<i>Fndc3b</i>	NM_144942	fibronectin type III domain containing 3B (Fndc3b)	0.35
<i>Foxk2</i>	NM_139117.2	forkhead box K2 (Foxk2)	0.56
<i>Foxm1</i>	NM_144901.2	forkhead box M1 (Foxm1)	0.45
<i>Foxp3</i>	NM_023565.2	forkhead box P3 (Foxp3)	0.63
<i>Foxred1</i>	NM_172753.3	FAD-dependent oxidoreductase domain containing 1 (Foxred1)	0.64
<i>Fpgs</i>	NM_007783.2	folylpolyglutamyl synthetase (Fpgs)	0.62
<i>Frmd4a</i>	NM_027874.2		0.40
<i>Fscn1</i>	NM_013767.5	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus) (Fscn1)	0.32
<i>Ftl1</i>	NM_134002.1		0.63
<i>Fubp1</i>	AK031617		0.65
<i>Fus</i>	NM_009974.2		0.51
<i>Fut8</i>	NM_013884.2	fucosyltransferase 8 (Fut8)	0.35
<i>Fxc1</i>	NM_026493.3	fractured callus expressed transcript 1 (Fxc1)	0.42
<i>Fxn</i>	NM_007792.3	frataxin (Fxn)	0.51
<i>Fxr1h</i>	NM_009976.3		0.63
<i>Fxr2</i>	NM_024199.2	fragile X mental retardation, autosomal homolog 2 (Fxr2)	0.63
<i>Fyn</i>	NM_146012.1	Fyn proto-oncogene (Fyn)	0.57
<i>Fzd1</i>	NM_010217	frizzled homolog 1 (Drosophila) (Fzd1)	0.58
<i>Fzr1</i>	NM_009819.1	fizzy/cell division cycle 20 related 1 (Drosophila) (Fzr1)	0.56
<i>G3bp1</i>	NM_018761.2	Ras-GTPase-activating protein SH3-domain binding protein 1 (G3bp1)	0.44
<i>G3bp2</i>	NM_016748.1	GTPase activating protein (SH3 domain) binding protein 2 (G3bp2), transcript variant 1	0.60
<i>Gaa</i>	NM_001038492.1	glucosidase, alpha, acid (Gaa)	0.63
<i>Gad1</i>	NM_009982.3	glutamic acid decarboxylase 1 (Gad1)	0.53
<i>Gadd45a</i>	NM_007801.1	growth arrest and DNA-damage-inducible 45 alpha (Gadd45a)	0.41
<i>Galnt1</i>	NM_030249.3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (Galnt1)	0.56
<i>Galnt10</i>	NM_198683.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (Galnt10)	0.53
<i>Galnt2</i>	NM_010160.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (Galnt2)	0.59
<i>Ganab</i>	NM_016716.4	alpha glucosidase 2 alpha neutral subunit (Ganab)	0.55
<i>Gap43</i>	NM_009142.3	growth associated protein 43 (Gap43)	0.31
<i>Gapdh</i>	NM_001025192.2	glyceraldehyde-3-phosphate dehydrogenase (Gapdh)	0.44
<i>Gars</i>	NM_008176.1	glycyl-tRNA synthetase (Gars)	0.47
<i>Gart</i>	NM_019932.2	phosphoribosylglycinamide formyltransferase (Gart)	0.65
<i>Gas2l3</i>	NM_009911.2	growth arrest-specific 2 like 3 (Gas2l3), transcript variant 2	0.27
<i>Gas7</i>	NM_025567.2	growth arrest specific 7 (Gas7)	0.61
<i>Gatad1</i>	NM_007808.4	GATA zinc finger domain containing 1 (Gatad1)	0.56
<i>Gcap14</i>	NM_180962.1	granule cell antiserum positive 14 (Gcap14), transcript variant 2	0.41
<i>Gcap27</i>	NM_009994.1		0.62
<i>Gcat</i>	NM_130882.1		0.37
<i>Gcs1</i>	NM_022434.1	glucosidase 1 (Gcs1)	0.41
<i>Gdf15</i>	NM_133969.2	growth differentiation factor 15 (Gdf15)	0.27
<i>Gdpd1</i>	NM_020010.2	glycerophosphodiester phosphodiesterase domain containing 1 (Gdpd1)	0.57
<i>Gemin4</i>	NM_007825.3	gem (nuclear organelle) associated protein 4 (Gemin4)	0.56
<i>Gfm1</i>	AK050914	G elongation factor, mitochondrial 1 (Gfm1)	0.52
<i>Gga2</i>	AK083512	golgi associated, gamma adaptin ear containing, ARF binding protein 2 (Gga2)	0.65
<i>Gins2</i>	NM_177640.4	GINS complex subunit 2 (Psf2 homolog) (Gins2)	0.53
<i>Gipc1</i>	NM_053078.3	GIPC PDZ domain containing family, member 1 (Gipc1)	0.52
<i>Glb1</i>	NM_001013379.2	galactosidase, beta 1 (Glb1)	0.50
<i>Glg1</i>	NM_026065.2		0.59
<i>Glrx1</i>	NM_028027.2		0.66
<i>Glrx2</i>	NM_026579.2	glutaredoxin 2 (thioltransferase) (Glrx2), transcript variant 1	0.59
<i>Glrx3</i>	NM_145422.3	glutaredoxin 3 (Glrx3)	0.61
<i>Glrx5</i>	NM_029758.3	glutaredoxin 5 homolog (S. cerevisiae) (Glrx5)	0.53
<i>Glt25d1</i>	NM_198023	glycosyltransferase 25 domain containing 1 (Glt25d1)	0.39
<i>Gm444</i>		PREDICTED: gene model 444, (NCBI) (Gm444)	0.62
<i>Gm561</i>	NM_134100.2	gene model 561, (NCBI) (Gm561)	0.41
<i>Gmids</i>	NM_138583.1	GDP-mannose 4, 6-dehydratase (Gmids)	0.57
<i>Gmpr2</i>	NM_033075.2	guanosine monophosphate reductase 2 (Gmpr2)	0.61
<i>Gmps</i>	NM_080837.1	guanine monophosphate synthetase (Gmps)	0.61

<i>Gna11</i>	NM_177474.4		0.63
<i>Gnai1</i>		guanine nucleotide binding protein (G protein), alpha inhibiting 1 (Gnai1)	0.50
<i>Gnaq</i>	AK051822	guanine nucleotide binding protein, alpha q polypeptide (Gnaq)	0.66
<i>Gnb1</i>	NM_026828.2	guanine nucleotide binding protein (G protein), beta 1 (Gnb1)	0.49
<i>Gnb4</i>	NM_026412.1	guanine nucleotide binding protein (G protein), beta 4 (Gnb4)	0.57
<i>Gne</i>	NM_177617.2		0.66
<i>Gng12</i>	NM_001081022.1		0.39
<i>Gng2</i>	NM_026821.4	guanine nucleotide binding protein (G protein), gamma 2 (Gng2), transcript variant 2	0.64
<i>Gnl3</i>		guanine nucleotide binding protein-like 3 (nucleolar) (Gnl3), transcript variant 2	0.36
<i>Gnpda1</i>	NM_001081232.1	glucosamine-6-phosphate deaminase 1 (Gnpda1)	0.48
<i>Golga3</i>	NM_207274.1	golgi autoantigen, golgin subfamily a, 3 (Golga3)	0.66
<i>Golim4</i>	NM_138587.3	golgi integral membrane protein 4 (Golim4)	0.60
<i>Golm1</i>	NM_172681.2	golgi membrane protein 1 (Golm1), transcript variant 2	0.21
<i>Gorasp2</i>		golgi reassembly stacking protein 2 (Gorasp2)	0.49
<i>Got2</i>	NM_028181	glutamate oxaloacetate transaminase 2, mitochondrial (Got2), nuclear gene encoding mitochondrial protein	0.41
<i>Gpd1</i>	NM_133718	glycerol-3-phosphate dehydrogenase 1 (soluble) (Gpd1)	0.58
<i>Gpd2</i>	NM_010015.1	glycerol phosphate dehydrogenase 2, mitochondrial (Gpd2), nuclear gene encoding mitochondrial protein	0.57
<i>Gpi1</i>	NM_022994.2	glucose phosphate isomerase 1 (Gpi1)	0.47
<i>Gpnmb</i>	NM_134062.1	glycoprotein (transmembrane) nmb (Gpnmb)	0.40
<i>Gpr162</i>	NM_010045.2	G protein-coupled receptor 162 (Gpr162)	0.54
<i>Gpsm1</i>	AK010657	G-protein signalling modulator 1 (AGS3-like, C. elegans) (Gpsm1)	0.58
<i>Gpsn2</i>	NM_013726.2	glycoprotein, synaptic 2 (Gpsn2)	0.62
<i>Grcc10</i>	NM_010022.1	gene rich cluster, C10 gene (Grcc10)	0.54
<i>Gria3</i>	XM_147966.3	glutamate receptor, ionotropic, AMPA3 (alpha 3) (Gria3)	0.60
<i>Grip1</i>	NM_019978.2		0.56
<i>Grm5</i>	NM_027030.2	glutamate receptor, metabotropic 5 (Grm5)	0.16
<i>Grwd1</i>	NM_029775.2	glutamate-rich WD repeat containing 1 (Grwd1)	0.59
<i>Gsg2</i>	NM_028119.2	germ cell-specific gene 2 (Gsg2)	0.56
<i>Gspt1</i>	NM_027442.4	G1 to S phase transition 1 (Gspt1)	0.44
<i>Gstm5</i>	NM_007838.2	glutathione S-transferase, mu 5 (Gstm5)	0.56
<i>Gstp1</i>	NM_007584.2	glutathione S-transferase, pi 1 (Gstp1)	0.53
<i>Gstt1</i>	NM_134040.1	glutathione S-transferase, theta 1 (Gstt1)	0.52
<i>Gtf2e2</i>	XM_128714.3	general transcription factor II E, polypeptide 2 (beta subunit) (Gtf2e2)	0.58
<i>Gtf2f2</i>	NM_017397.2	general transcription factor IIF, polypeptide 2 (Gtf2f2)	0.63
<i>Gtf2h2</i>	NM_019553.2	general transcription factor II H, polypeptide 2 (Gtf2h2)	0.65
<i>Gtf3a</i>	NM_013932.3	general transcription factor III A (Gtf3a)	0.61
<i>Gtf3c1</i>	NM_008715	general transcription factor III C 1 (Gtf3c1)	0.65
<i>Gtpbp3</i>	NM_153065.3	GTP binding protein 3 (Gtpbp3), nuclear gene encoding mitochondrial protein	0.41
<i>Gtpbp4</i>	NM_010028.2	GTP binding protein 4 (Gtpbp4)	0.52
<i>Gtse1</i>	NM_012008.1	G two S phase expressed protein 1 (Gtse1)	0.47
<i>Gusb</i>	NM_028041.2	glucuronidase, beta (Gusb)	0.57
<i>H1fx</i>	NM_007841.3	H1 histone family, member X (H1fx)	0.65
<i>H2afx</i>	NM_026794.2	H2A histone family, member X (H2afx)	0.26
<i>H2afz</i>	NM_025900.1	H2A histone family, member Z (H2afz)	0.21
<i>Hat1</i>	NM_172477.3	histone aminotransferase 1 (Hat1)	0.42
<i>Hbegf</i>		heparin-binding EGF-like growth factor (Hbegf)	0.42
<i>Hccs</i>	NM_177914.2	holocytochrome c synthetase (Hccs)	0.61
<i>Hdac2</i>	NM_138306.1		0.44
<i>Hdgf</i>	XM_131538.1	hepatoma-derived growth factor (Hdgf)	0.65
<i>Heatr1</i>	NM_007856.2	HEAT repeat containing 1 (Heatr1)	0.52
<i>Hectd1</i>	NM_007857.3	PREDICTED: HECT domain containing 1 (Hectd1)	0.56
<i>Hectd2</i>	NM_001039514.1	HECT domain containing 2 (Hectd2)	0.29
<i>Herc4</i>	NM_026819.2	hect domain and RLD 4 (Herc4)	0.66
<i>Hes1</i>	NM_001033326.2	hairy and enhancer of split 1 (Drosophila) (Hes1)	0.55
<i>Hes6</i>	NM_007839.2	hairy and enhancer of split 6 (Drosophila) (Hes6)	0.66
<i>Hif1a</i>	NM_133347.1	hypoxia inducible factor 1, alpha subunit (Hif1a)	0.64
<i>Hint1</i>	NM_133941.2	histidine triad nucleotide binding protein 1 (Hint1)	0.54
<i>Hip1</i>	NM_011805.2	huntingtin interacting protein 1 (Hip1)	0.12
<i>HIP-1</i>	NM_145217.2		0.52
<i>Hip2</i>			0.53
<i>Hirip3</i>	NM_178118	HIRA interacting protein 3 (Hirip3)	0.45
<i>Hist1h2ad</i>	NM_177639.5	histone cluster 1, H2ad (Hist1h2ad)	0.09
<i>Hist1h2af</i>	NM_144553.1	histone cluster 1, H2af (Hist1h2af)	0.08
<i>Hist1h2ag</i>	NM_030225	histone cluster 1, H2ag (Hist1h2ag)	0.26
<i>Hist1h2ah</i>	NM_032418	histone cluster 1, H2ah (Hist1h2ah)	0.13
<i>Hist1h2ai</i>	NM_010060.2	histone cluster 1, H2ai (Hist1h2ai)	0.08
<i>Hist1h2ak</i>	XM_148071.1	histone cluster 1, H2ak (Hist1h2ak)	0.15

<i>Hist1h2an</i>	NM_153527.2	histone cluster 1, H2an (Hist1h2an)	0.08
<i>Hist1h2ao</i>	NM_178055.3	histone cluster 1, H2ao (Hist1h2ao)	0.09
<i>Hist2h2ab</i>	NM_013760.3	histone cluster 2, H2ab (Hist2h2ab)	0.28
<i>Hist2h2ac</i>	NM_001026211.1	histone cluster 2, H2ac (Hist2h2ac)	0.17
<i>Hmga1</i>	NM_009584.3	high mobility group AT-hook 1 (Hmga1), transcript variant 1	0.36
<i>Hmgb2</i>	NM_138664.2	high mobility group box 2 (Hmgb2)	0.31
<i>Hmgcl</i>	NM_175223.2	3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl)	0.60
<i>Hmgcr</i>	NM_152915.1	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr)	0.47
<i>Hmgn2</i>	NM_010066.3	high mobility group nucleosomal binding domain 2 (Hmgn2)	0.62
<i>Hn1</i>	NM_001033420.2	hematological and neurological expressed sequence 1 (Hn1)	0.49
<i>Hn1l</i>	XM_129913.4	hematological and neurological expressed 1-like (Hn1l)	0.52
<i>Hnrmpa2b1</i>	NM_015761.2	heterogeneous nuclear ribonucleoprotein A2/B1 (Hnrmpa2b1), transcript variant 2	0.36
<i>Hnrmpab</i>	XM_130951.1	heterogeneous nuclear ribonucleoprotein A/B (Hnrmpab), transcript variant 1	0.41
<i>Hnrmpf</i>	NM_133803.1	heterogeneous nuclear ribonucleoprotein F (Hnrmpf)	0.64
<i>HnrmpH1</i>	NM_024428.3	heterogeneous nuclear ribonucleoprotein H1 (HnrmpH1)	0.50
<i>Hnrmpk</i>	NM_009468.3	heterogeneous nuclear ribonucleoprotein K (Hnrmpk)	0.64
<i>Hnrpa1</i>	NM_011993.2		0.24
<i>Hnrpab</i>	NM_023047.2		0.64
<i>HnrpdL</i>	NM_007879.1	heterogeneous nuclear ribonucleoprotein D-like (HnrpdL)	0.63
<i>Hnrpl</i>	NM_010078.2	heterogeneous nuclear ribonucleoprotein L (Hnrpl)	0.51
<i>Hnrpll</i>	NM_019466.2	heterogeneous nuclear ribonucleoprotein L-like (Hnrpll)	0.52
<i>Hnrpm</i>	NM_172442.2	heterogeneous nuclear ribonucleoprotein M (Hnrpm)	0.60
<i>Homer1</i>	NM_023136	homer homolog 1 (Drosophila) (Homer1), transcript variant d	0.53
<i>Hpcal1</i>	NM_013642.2	hippocalcin-like 1 (Hpcal1)	0.51
<i>Hprt1</i>	NM_176933.4	hypoxanthine guanine phosphoribosyl transferase 1 (Hprt1)	0.27
<i>Hras1</i>	NM_026268.2		0.60
<i>Hrmt1l2</i>	NM_153459.2		0.23
<i>Hs2st1</i>	NM_172256.1	heparan sulfate 2-O-sulfotransferase 1 (Hs2st1)	0.62
<i>Hs3st3b1</i>	NM_019682.2	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (Hs3st3b1)	0.61
<i>Hs6st2</i>	NM_029297.1	heparan sulfate 6-O-sulfotransferase 2 (Hs6st2), transcript variant 2	0.55
<i>Hsd17b12</i>	NM_021469.2	hydroxysteroid (17-beta) dehydrogenase 12 (Hsd17b12)	0.40
<i>Hsd17b7</i>	NM_175553	hydroxysteroid (17-beta) dehydrogenase 7 (Hsd17b7)	0.60
<i>Hsp90ab1</i>	AK087162	heat shock protein 90kDa alpha (cytosolic), class B member 1 (Hsp90ab1)	0.51
<i>Hsp90b1</i>	NM_001081756.1	heat shock protein 90, beta (Grp94), member 1 (Hsp90b1)	0.40
<i>Hspa8</i>	NM_001039556.2	heat shock protein 8 (Hspa8)	0.63
<i>Hspa9</i>	NM_178791.4	heat shock protein 9 (Hspa9)	0.60
<i>Hspd1</i>	XM_131404.3	heat shock protein 1 (chaperonin) (Hspd1)	0.36
<i>Hspe1</i>	NM_001015681.1	heat shock protein 1 (chaperonin 10) (Hspe1)	0.41
<i>Hspg2</i>	AK054036		0.64
<i>Htra1</i>	NM_007891.3	HtrA serine peptidase 1 (Htra1)	0.66
<i>Htra2</i>	NM_177733.2	HtrA serine peptidase 2 (Htra2), nuclear gene encoding mitochondrial protein	0.65
<i>Hyal2</i>	NM_033270.1	hyaluronoglucosaminidase 2 (Hyal2)	0.50
<i>Iars</i>	NM_175528	isoleucine-tRNA synthetase (Iars)	0.47
<i>Iars2</i>	NM_173386.3	isoleucine-tRNA synthetase 2, mitochondrial (Iars2)	0.65
<i>Ibtk</i>	NM_173749		0.65
<i>Ick</i>	NM_178668.3	intestinal cell kinase (Ick)	0.61
<i>Ide</i>	AK089103	insulin degrading enzyme (Ide)	0.59
<i>Idh3a</i>	AK089133	isocitrate dehydrogenase 3 (NAD+) alpha (Idh3a), nuclear gene encoding mitochondrial protein	0.46
<i>Ier3</i>	NM_026932.3	immediate early response 3 (Ier3)	0.18
<i>Ier5l</i>	NM_007898.2	immediate early response 5-like (Ier5l)	0.35
<i>Igf2r</i>	NM_199307.1	insulin-like growth factor 2 receptor (Igf2r)	0.54
<i>Igfbp2</i>	NM_016772.1	insulin-like growth factor binding protein 2 (Igfbp2)	0.06
<i>Igfbp3</i>	NM_026728.1	insulin-like growth factor binding protein 3 (Igfbp3)	0.05
<i>Igfbp4</i>	NM_007899.1	insulin-like growth factor binding protein 4 (Igfbp4)	0.08
<i>Ilf2</i>	NM_021519.1	interleukin enhancer binding factor 2 (Ilf2)	0.55
<i>Ilvbl</i>	NM_010332.2	ilvB (bacterial acetolactate synthase)-like (Ilvbl)	0.63
<i>Immt</i>	NM_007904.3	inner membrane protein, mitochondrial (Immt), nuclear gene encoding mitochondrial protein	0.43
<i>Imp3</i>	NM_010106.2	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (Imp3)	0.45
<i>Impa2</i>	NM_018796.2	inositol (myo)-1(or 4)-monophosphatase 2 (Impa2)	0.59
<i>Impad1</i>	NM_025380.2	inositol monophosphatase domain containing 1 (Impad1)	0.47
<i>Impdh2</i>	NM_026007.4		0.44
<i>Incenp</i>	NM_010110.2	inner centromere protein (Incenp)	0.37
<i>Inpp5f</i>	NM_010112.3	inositol polyphosphate-5-phosphatase F (Inpp5f)	0.47
<i>Insig1</i>	XM_911906.3	insulin induced gene 1 (Insig1)	0.34
<i>Ints7</i>	NM_177689.3	integrator complex subunit 7 (Ints7)	0.64
<i>Ipo4</i>	XM_905111.2	importin 4 (Ipo4)	0.62
<i>Ipo5</i>	XM_145024.8	importin 5 (Ipo5)	0.46
<i>Ipo9</i>	NM_001018086.2	importin 9 (Ipo9)	0.53

<i>Iqgap1</i>	XM_921134.3		0.46
<i>Iqgap3</i>	XM_913807.2	IQ motif containing GTPase activating protein 3 (<i>Iqgap3</i>)	0.51
<i>Isca1</i>	XM_905000.3	iron-sulfur cluster assembly 1 homolog (<i>S. cerevisiae</i>) (<i>Isca1</i>)	0.66
<i>Isy1</i>	XM_890293.3	ISY1 splicing factor homolog (<i>S. cerevisiae</i>) (<i>Isy1</i>)	0.54
<i>Itgav</i>	XM_484165.5	integrin alpha V (<i>Itgav</i>)	0.61
<i>Itgb1</i>	XM_484210.5	integrin beta 1 (fibronectin receptor beta) (<i>Itgb1</i>)	0.60
<i>Itpr2</i>	NM_001034882.2	inositol 1,4,5-triphosphate receptor 2 (<i>Itpr2</i>), transcript variant 1	0.39
<i>Jagn1</i>	XM_484670.5	jagunal homolog 1 (<i>Drosophila</i>) (<i>Jagn1</i>)	0.62
<i>Jam2</i>	NM_001025388.1	junction adhesion molecule 2 (<i>Jam2</i>)	0.62
<i>Jmjd6</i>	NM_001081233.1	jumonji domain containing 6 (<i>Jmjd6</i>)	0.49
<i>Josd2</i>	XM_486222.5	Josephin domain containing 2 (<i>Josd2</i>)	0.56
<i>Jun</i>	NR_002883.1	Jun oncogene (<i>Jun</i>)	0.60
<i>Kars</i>	NR_002889.2	lysyl-tRNA synthetase (<i>Kars</i>)	0.54
<i>Kbtbd2</i>	XM_620762.4	kelch repeat and BTB (POZ) domain containing 2 (<i>Kbtbd2</i>)	0.64
<i>Kcnc1</i>	XM_917756.3	potassium voltage gated channel, Shaw-related subfamily, member 1 (<i>Kcnc1</i>)	0.33
<i>Kcnc4</i>	NM_001081297.1	potassium voltage gated channel, Shaw-related subfamily, member 4 (<i>Kcnc4</i>)	0.38
<i>Kcnip3</i>	XM_888318.3	Kv channel interacting protein 3, calsenilin (<i>Kcnip3</i>)	0.42
<i>Kcnk13</i>	XM_889835.2	potassium channel, subfamily K, member 13 (<i>Kcnk13</i>)	0.66
<i>Kctd12</i>	NR_003363.1	potassium channel tetramerisation domain containing 12 (<i>Kctd12</i>)	0.44
<i>Kctd20</i>	XM_917009.3	potassium channel tetramerisation domain containing 20 (<i>Kctd20</i>)	0.63
<i>Kdelc1</i>	XM_908326.3	KDEL (Lys-Asp-Glu-Leu) containing 1 (<i>Kdelc1</i>)	0.65
<i>Kdelr2</i>	XM_894495.2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (<i>Kdelr2</i>)	0.43
<i>Khdrbs1</i>	XM_001473902.1	KH domain containing, RNA binding, signal transduction associated 1 (<i>Khdrbs1</i>)	0.50
<i>Kif11</i>	XM_978542.1	kinesin family member 11 (<i>Kif11</i>)	0.40
<i>Kif15</i>	XR_031485.1	kinesin family member 15 (<i>Kif15</i>)	0.37
<i>Kif18a</i>	XM_917238.2	kinesin family member 18A (<i>Kif18a</i>)	0.37
<i>Kif20b</i>	XM_912043.2	kinesin family member 20B (<i>Kif20b</i>)	0.32
<i>Kif22</i>	NM_001081746.1	kinesin family member 22 (<i>Kif22</i>)	0.16
<i>Kif23</i>	XM_984280.2		0.11
<i>Kif2c</i>	XM_984926.2	kinesin family member 2C (<i>Kif2c</i>)	0.26
<i>Kif3c</i>	XR_002058.1	kinesin family member 3C (<i>Kif3c</i>)	0.31
<i>Kif4</i>	XR_035278.1	kinesin family member 4 (<i>Kif4</i>)	0.31
<i>Kifc1</i>	NM_001081036.1		0.50
<i>Kirrel3</i>	XM_001005405.1	kin of IRRE like 3 (<i>Drosophila</i>) (<i>Kirrel3</i>)	0.44
<i>Kitl</i>	XR_002259.2	kit ligand (<i>Kitl</i>)	0.56
<i>Klf6</i>	NM_007913.5	Kruppel-like factor 6 (<i>Klf6</i>)	0.65
<i>Klf7</i>	NM_133838.4		0.62
<i>Klhdc2</i>	NM_010120.4	kelch domain containing 2 (<i>Klhdc2</i>)	0.55
<i>Kntc1</i>	NM_027236.2	kinetochore associated 1 (<i>Kntc1</i>)	0.38
<i>Kpna1</i>	XM_131572.4	karyopherin (importin) alpha 1 (<i>Kpna1</i>)	0.64
<i>Kpna2</i>	NM_026030.2	karyopherin (importin) alpha 2 (<i>Kpna2</i>)	0.56
<i>Kpnb1</i>	NM_012010.3	karyopherin (importin) beta 1 (<i>Kpnb1</i>)	0.53
<i>Kras</i>	NM_010123.3	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (<i>Kras</i>)	0.65
<i>Krtcap2</i>	NM_133916.2	keratinocyte associated protein 2 (<i>Krtcap2</i>)	0.53
<i>Lama5</i>	NM_018749.2	laminin, alpha 5 (<i>Lama5</i>)	0.43
<i>Lamc1</i>	NM_145139.2	laminin, gamma 1 (<i>Lamc1</i>)	0.59
<i>Lass2</i>	NM_025344.1	LAG1 homolog, ceramide synthase 2 (<i>Lass2</i>)	0.54
<i>Lass5</i>	NM_016876.3	LAG1 homolog, ceramide synthase 5 (<i>Lass5</i>)	0.59
<i>Lbh</i>	NM_018799.1	limb-bud and heart (<i>Lbh</i>)	0.38
<i>Lbr</i>	NM_028659.2		0.23
<i>Ldha</i>	NM_016876.2	lactate dehydrogenase A (<i>Ldha</i>)	0.33
<i>Leo1</i>	NM_025344	Leo1, Paf1/RNA polymerase II complex component, homolog (<i>S. cerevisiae</i>) (<i>Leo1</i>)	0.58
<i>Lgals1</i>	NM_144958.2		0.17
<i>Lig1</i>	NM_138669.1	ligase I, DNA, ATP-dependent (<i>Lig1</i>), transcript variant 2	0.27
<i>Lig3</i>	NM_007918.3		0.60
<i>Limd1</i>	NM_023314.2	LIM domains containing 1 (<i>Limd1</i>)	0.61
<i>Lin54</i>	NM_001005331.1	lin-54 homolog (<i>C. elegans</i>) (<i>Lin54</i>)	0.49
<i>Lip1</i>	NM_173363.4		0.52
<i>Liph</i>	NM_181582.3	lipase, member H (<i>Liph</i>), transcript variant 2	0.58
<i>Litaf</i>	NM_010579.2	LPS-induced TN factor (<i>Litaf</i>)	0.36
<i>Lman1</i>	NM_010485.3	lectin, mannose-binding, 1 (<i>Lman1</i>)	0.59
<i>Lmnb1</i>	NM_205536.1	lamin B1 (<i>Lmnb1</i>)	0.15
<i>Lmo2</i>	NM_198093.2	LIM domain only 2 (<i>Lmo2</i>)	0.32
<i>LOC100039346</i>	NM_019422.2	PREDICTED: hypothetical protein LOC100039346 (<i>LOC100039346</i>)	0.33
<i>LOC100039532</i>	NM_148941.1	PREDICTED: similar to ribosomal protein L35a (<i>LOC100039532</i>)	0.52
<i>LOC100039571</i>	NM_134255.2	PREDICTED: similar to ribosomal protein L23a (<i>LOC100039571</i>)	0.35
<i>LOC100039751</i>	NM_130450.2	PREDICTED: similar to 40S ribosomal protein S12 (<i>LOC100039751</i>), misc RNA.	0.37
<i>LOC100039786</i>	NM_013536.1	PREDICTED: similar to Ywhaq protein (<i>LOC100039786</i>)	0.58
<i>LOC100040573</i>	NM_007929.2	PREDICTED: similar to putative transcription factor ZNF131, transcript variant 1 (<i>LOC100040573</i>)	0.59

LOC100040592	NM_028013.2	PREDICTED: similar to Hmgcs1 protein, transcript variant 1 (LOC100040592)	0.38
LOC100040605	NM_023119.1	PREDICTED: similar to ribosomal protein L13 (LOC100040605)	0.44
LOC100041500	NM_032003.1	PREDICTED: similar to LSM7 homolog, U6 small nuclear RNA associated (LOC100041500)	0.58
LOC100041835	NM_009849.1	PREDICTED: similar to H+ ATP synthase (LOC100041835)	0.41
LOC100041864	NM_026174.2	PREDICTED: similar to Rpl11 protein (LOC100041864)	0.55
LOC100042405	NM_001026214.1	PREDICTED: similar to high mobility group nucleosomal binding domain 2 (LOC100042405)	0.45
LOC100042427	NM_173447.2	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), transcript variant 4 (LOC100042427)	0.39
LOC100042777	NM_007940.3	PREDICTED: similar to human protein homologous to DROER protein (LOC100042777)	0.65
LOC100042970	NM_010148	PREDICTED: similar to Kifc1 protein (LOC100042970)	0.42
LOC100043192	NM_007948.1	PREDICTED: similar to ribosomal protein L31 (LOC100043192)	0.50
LOC100043209	NM_026170.3	PREDICTED: similar to ribosomal protein L15 (LOC100043209)	0.54
LOC100043257	NM_026168.3	PREDICTED: similar to RNA binding motif protein 3 (LOC100043257)	0.48
LOC100043391	NM_007951.1	PREDICTED: similar to QM protein (LOC100043391)	0.48
LOC100043527	NM_145502.2	PREDICTED: similar to ribosomal protein S28 (LOC100043527)	0.49
LOC100043555	NM_001081213.1	PREDICTED: similar to Aak1 protein (LOC100043555)	0.52
LOC100043671	NM_026129.2	PREDICTED: hypothetical protein LOC100043671 (LOC100043671)	0.51
LOC100043675	NM_133753.1	PREDICTED: similar to Translocase of inner mitochondrial membrane 23 homolog (yeast) (LOC100043675)	0.54
LOC100043796	NM_028039.1	PREDICTED: similar to macrophage migration inhibitory factor, transcript variant 1 (LOC100043796)	0.53
LOC100043822	NM_001014976.1	PREDICTED: hypothetical protein LOC100043822 (LOC100043822)	0.63
LOC100043906	NM_007953.2	PREDICTED: similar to nuclear pore-targeting complex component of 58 kDa, transcript variant 1 (LOC100043906)	0.36
LOC100044322	NM_011934.3	PREDICTED: similar to UDP-glucose ceramide glucosyltransferase-like 1 (LOC100044322)	0.49
LOC100044468	NM_144866.3	PREDICTED: similar to nemo-like kinase (LOC100044468)	0.58
LOC100044475	NM_001038642.1	PREDICTED: similar to SH2/SH3 adaptor protein (LOC100044475)	0.66
LOC100044696	NM_011809.2	PREDICTED: similar to cysteine-rich PAK1inhibitor (LOC100044696)	0.53
LOC100044829	NM_007960.3	PREDICTED: similar to Fibrillarin, transcript variant 1 (LOC100044829)	0.35
LOC100044948	NM_008815.2	PREDICTED: similar to macrophage migration inhibitory factor (LOC100044948)	0.45
LOC100045040	NM_023794.2	PREDICTED: similar to ING1 protein (LOC100045040), misc RNA.	0.66
LOC100045300	NM_025644.3	PREDICTED: similar to Dr1 associated protein 1 (negative cofactor 2 alpha) (LOC100045300)	0.61
LOC100045312	NM_144886.1	PREDICTED: similar to ribosomal protein (LOC100045312)	0.35
LOC100045343	NM_028274.2	PREDICTED: similar to CDNA sequence BC046404 (LOC100045343), misc RNA.	0.64
LOC100045542	NM_001081188.1	PREDICTED: similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1 (LOC100045542)	0.63
LOC100045668	NM_027148.2	PREDICTED: similar to Rpl17 protein (LOC100045668)	0.49
LOC100045677	NM_010162.2	PREDICTED: similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3) (LOC100045677), misc RNA.	0.49
LOC100045697	NM_018788.2	PREDICTED: similar to ornithine decarboxylase antizyme (LOC100045697), misc RNA.	0.65
LOC100045737	NM_007971.1	PREDICTED: hypothetical protein LOC100045737 (LOC100045737), misc RNA.	0.62
LOC100045780	NM_010169.3	PREDICTED: similar to metalloprotease-disintegrin meltrin beta (LOC100045780)	0.18
LOC100045887	NM_198605.1	PREDICTED: similar to PTB-associated splicing factor (LOC100045887)	0.51
LOC100045967	AK089303	PREDICTED: hypothetical protein LOC100045967 (LOC100045967), misc RNA.	0.34
LOC100045981	AK089567	PREDICTED: similar to synaptotagmin XI (LOC100045981)	0.65
LOC100045999	NM_010173.3	PREDICTED: similar to RAN, member RAS oncogene family (LOC100045999)	0.42
LOC100046039	NM_010634.2	PREDICTED: similar to histone deacetylase HD1 (LOC100046039)	0.64
LOC100046343	NM_021272.2	PREDICTED: similar to CCR4-NOT transcription complex, subunit 6 (LOC100046343)	0.49
LOC100046650	NM_021890.3	PREDICTED: similar to PRELI domain containing 1 (LOC100046650)	0.53
LOC100046744	NM_007983.2	PREDICTED: similar to Serine/arginine repetitive matrix protein 2 (LOC100046744)	0.59
LOC100046853	NM_010176.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein K (LOC100046853)	0.26
LOC100046855	NM_023480.2	PREDICTED: similar to BKLF (LOC100046855)	0.44
LOC100046895	NM_028443.2	PREDICTED: similar to Quaking protein (LOC100046895)	0.66
LOC100047155	NM_153560.4	PREDICTED: similar to Small nuclear ribonucleoprotein polypeptide A (LOC100047155)	0.44
LOC100047167	NM_145421.1	PREDICTED: similar to mKIAA0990 protein (LOC100047167)	0.36
LOC100047184	NM_028666.2	PREDICTED: similar to proteasome alpha7/C8 subunit (LOC100047184)	0.65

LOC100047261	NM_001033268.2	PREDICTED: similar to spermidine/spermine N1-acetyltransferase (LOC100047261), misc RNA.	0.63
LOC100047268	NM_028617.2	PREDICTED: similar to Immediate early response 5-like (LOC100047268)	0.26
LOC100047353	NM_133778.2	PREDICTED: similar to myocardial vascular inhibition factor (LOC100047353)	0.63
LOC100047579	NM_025459.2	PREDICTED: similar to transmembrane protein 20 (LOC100047579)	0.66
LOC100047615	NM_001081161.1	PREDICTED: similar to 40S ribosomal protein S17 (LOC100047615), misc RNA.	0.57
LOC100047619	NM_145410.3	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (LOC100047619), misc RNA.	0.32
LOC100047634	NM_001081428.1	PREDICTED: similar to Eukaryotic translation initiation factor 2 alpha kinase 3 (LOC100047634), misc RNA.	0.63
LOC100047651	NM_153782.1	PREDICTED: similar to FOG (LOC100047651)	0.56
LOC100047712	NM_029007.2	PREDICTED: similar to coiled-coil domain containing 101 (LOC100047712)	0.63
LOC100047759	NM_001033244.2	PREDICTED: similar to acidic ribosomal phosphoprotein P1, transcript variant 1 (LOC100047759)	0.43
LOC100047762	XM_986338.2	PREDICTED: similar to Aspartate aminotransferase, cytoplasmic (Transaminase A) (Glutamate oxaloacetate transaminase 1) (LOC100047762)	0.59
LOC100047827	NM_025850.2	PREDICTED: similar to Hmgn2 protein (LOC100047827)	0.42
LOC100047888	NM_011811.2	PREDICTED: similar to Neurocan (LOC100047888)	0.42
LOC100047934	NM_007987.1	PREDICTED: hypothetical protein LOC100047934 (LOC100047934)	0.45
LOC100047935	NM_023229.2	PREDICTED: similar to ribosomal protein L5 (LOC100047935), misc RNA.	0.52
LOC100047998	NM_133754.3	PREDICTED: similar to ribosomal protein L37a (LOC100047998)	0.43
LOC100048187	NM_010180.1	PREDICTED: similar to ribosomal protein S27 (metallopanstimulin 1) (LOC100048187)	0.59
LOC100048413	NM_001081437.1	PREDICTED: similar to Myeloid leukemia factor 2 (LOC100048413)	0.56
LOC100048445	NM_007993	PREDICTED: similar to fau (LOC100048445)	0.50
LOC100048480	NM_001005866.1	PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein (LOC100048480)	0.59
LOC100048483	NM_133940.1	PREDICTED: similar to cytochrome c oxidase subunit VIII (LOC100048483)	0.43
LOC100048508	NM_172988.1	PREDICTED: similar to Rpl36 protein, transcript variant 1 (LOC100048508)	0.43
LOC100048613	NM_176848.1	PREDICTED: similar to cytochrome c oxidase, subunit VIIc, transcript variant 1 (LOC100048613)	0.47
LOC100048645	NM_145564.3	PREDICTED: similar to cysteine and glycine-rich protein 2 binding protein (LOC100048645)	0.59
LOC100048803	NM_025785.2	PREDICTED: hypothetical protein LOC100048803 (LOC100048803)	0.54
LOC212399	NM_026346.1		0.39
LOC216443	NM_025386.2		0.59
LOC219049	NM_001001160.2		0.50
LOC219106	NM_173401.2		0.57
LOC219145	NM_023605.2		0.40
LOC225058	NM_010189.1		0.47
LOC225134	NM_199012.1	PREDICTED: similar to ribosomal protein S4, X-linked (LOC225134), misc RNA.	0.42
LOC226416	NM_139309		0.47
LOC229810	NM_134469.3		0.63
LOC230253	NM_007999.3		0.25
LOC230896	XM_001480162.1		0.55
LOC231368	NM_183171.1	PREDICTED: similar to 60S acidic ribosomal protein P0 (L10E) (LOC231368)	0.40
LOC232606	NM_199448.1		0.59
LOC232887	NM_010197.3		0.60
LOC232890	NM_023304.1		0.47
LOC236831	NM_026218.2	PREDICTED: similar to 60S ribosomal protein L7a (LOC236831)	0.43
LOC237512	NM_010209.1		0.40
LOC237877	NM_001077361.1		0.60
LOC238943	NM_021438.2		0.62
LOC241621	NM_021891.2	PREDICTED: similar to ribosomal protein L27a-like (LOC241621)	0.29
LOC245668	NM_024169.3		0.45
LOC245892	NM_008019.2		0.16
LOC268569	NM_008020.2		0.20
LOC268700	NM_010219.3		0.39
LOC269251	NM_010220.2		0.33
LOC270037	NM_201518.1		0.33
LOC271490	NM_019445.1		0.49
LOC271505	NM_172409.2		0.54
LOC272681	NM_022014.2		0.48
LOC277856	NM_173182.1		0.56
LOC280205	NM_010234.2		0.56
LOC329076	NM_008240.2		0.41
LOC329750	NM_001080932.1		0.55
LOC331102	NM_008021.4		0.51
LOC331507	NM_054039.1		0.63
LOC380692	NM_172291.1		0.26

LOC380707	NM_010236.1		0.55
LOC380927	NM_172475		0.57
LOC380930	NM_007984.2		0.48
LOC381046	NM_008047.4		0.37
LOC381114	NM_010240.1		0.27
LOC381140	NM_057172.1		0.50
LOC381215	NM_139149.1		0.49
LOC381230	NM_016893.2		0.54
LOC381330	NM_019502.2		0.42
LOC381365	NM_008044.1		0.38
LOC381398	AF124385		0.37
LOC381448	NM_011814.2		0.36
LOC381561	NM_148925.1		0.49
LOC381649	NM_008054.1		0.46
LOC381799	NM_021457.2		0.64
LOC381808	NM_008056		0.58
LOC381891	NM_019757.1		0.60
LOC381940	NM_013716.2		0.65
LOC381999	NM_011816.3		0.44
LOC382061	NM_008064.2		0.43
LOC382230	NM_021356.2		0.52
LOC382885	NM_020590.4		0.51
LOC383010	NM_008069.4		0.63
LOC383099	NM_008077.4		0.53
LOC383308	NM_007836.1		0.34
LOC383330	NM_013814.2		0.62
LOC383897	NM_134189.2		0.54
LOC383942	NM_139272.2		0.64
LOC384104	NM_001081421.1		0.52
LOC384206	NM_008060.1		0.58
LOC384727	NM_172672.2		0.55
LOC385699	NM_008083.2		0.62
LOC385905	NM_008084.2	PREDICTED: similar to proteasome alpha7/C8 subunit (LOC385905), misc RNA	0.58
LOC433476	NM_178888.4	PREDICTED: similar to ribosomal protein L27a (LOC433476)	0.28
LOC433546	NM_180678.3	PREDICTED: similar to 60S ribosomal protein L9 (LOC433546)	0.59
LOC433745	NM_010256.2	PREDICTED: similar to ribosomal protein L3 (LOC433745)	0.50
LOC433749	NM_001079876.1	PREDICTED: similar to Rho family GTPase RhoA (LOC433749)	0.66
LOC433943	NM_008088.1	PREDICTED: similar to Glutathione S-transferase Mu 1 (GST class-mu 1) (Glutathione S-transferase GT8.7) (pmGT10) (GST 1-1) (LOC433943), misc RNA.	0.66
LOC433955	NM_026033.1	PREDICTED: similar to HSPC008 (LOC433955), misc RNA.	0.64
LOC545056	XM_289726.2	ubiquitin-conjugating enzyme E2, J2 homolog pseudogene (LOC545056) on chromosome 14.	0.53
LOC545369	NM_010260.1	PREDICTED: similar to ribosomal protein L4 (LOC545369), misc RNA.	0.60
LOC545472	NM_145523.3	PREDICTED: similar to BTB (POZ) domain containing 1 (LOC545472)	0.60
LOC546015	NM_028407.3	PREDICTED: similar to ribosomal protein S9 (LOC546015), misc RNA.	0.65
LOC620678		PREDICTED: similar to 60S ribosomal protein L7 (LOC620678), misc RNA.	0.53
LOC622655	NM_013847	PREDICTED: similar to hCG31107 (LOC622655), misc RNA.	0.34
LOC622994	NM_133219.1	PREDICTED: hypothetical LOC622994 (LOC622994), misc RNA.	0.45
LOC623006	NM_020619.2	PREDICTED: similar to retinoblastoma-binding protein mRbAp46 (LOC623006), misc RNA.	0.58
LOC623466	NM_144891.1	PREDICTED: similar to MGC27348 protein (LOC623466), misc RNA.	0.42
LOC623568	NM_011819.1	PREDICTED: similar to ribosomal protein S20 (LOC623568)	0.41
LOC624662	NM_025638.1	PREDICTED: similar to MGC69457 protein (LOC624662), misc RNA.	0.65
LOC630729	NM_023608.2	PREDICTED: similar to glutathione reductase 1 (LOC630729)	0.57
LOC630936	NM_177367.2	PREDICTED: similar to nuclease sensitive element binding protein 1 (LOC630936), misc RNA.	0.31
LOC632022	NM_010277	PREDICTED: similar to 40S ribosomal protein S18 (LOC632022), misc RNA.	0.55
LOC632230	NM_138591.1	PREDICTED: similar to Ribosomal protein L5 (LOC632230), misc RNA.	0.46
LOC632667	NM_028758.2	PREDICTED: similar to PNG protein (LOC632667)	0.39
LOC632684	NM_027544.1	PREDICTED: hypothetical LOC632684 (LOC632684), misc RNA.	0.58
LOC633016	NM_178856.1	PREDICTED: similar to Chromobox homolog 3 (HP1 gamma homolog, Drosophila), transcript variant 2 (LOC633016)	0.54
LOC634015	NM_018771.3	PREDICTED: similar to Proteasome subunit beta type 3 (Proteasome theta chain) (Proteasome chain 13) (Proteasome component C10-II) (LOC634015)	0.64
LOC635470	NM_010288.2	PREDICTED: similar to ribosomal protein L27a-like (LOC635470)	0.33
LOC638892	NM_009752.1	PREDICTED: similar to cpn10 protein (LOC638892)	0.52
LOC639931		PREDICTED: similar to zinc RING finger protein SAG (LOC639931)	0.57
LOC640739	NM_009149	PREDICTED: hypothetical LOC640739 (LOC640739)	0.16

<i>LOC654426</i>	NM_027450	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F pseudogene (<i>LOC654426</i>), non-coding RNA.	0.53
<i>LOC654467</i>	NM_053108	heterogeneous nuclear ribonucleoprotein A1 pseudogene (<i>LOC654467</i>) on chromosome 9.	0.34
<i>LOC654842</i>	NM_001038592.1	hypothetical protein <i>LOC654842</i> (<i>LOC654842</i>)	0.41
<i>LOC664894</i>	NM_023140.4	PREDICTED: similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein S27a (bases 217_532) (<i>LOC664894</i>)	0.63
<i>LOC665032</i>	NM_028419.2	PREDICTED: similar to ribosomal protein (<i>LOC665032</i>)	0.50
<i>LOC665235</i>	NM_146211.2	PREDICTED: similar to hCG1642689 (<i>LOC665235</i>), misc RNA.	0.36
<i>LOC665237</i>	NM_008133.2	PREDICTED: similar to hCG31107 (<i>LOC665237</i>), misc RNA.	0.29
<i>LOC665281</i>	NM_008134.2	PREDICTED: similar to 40S ribosomal protein S12 (<i>LOC665281</i>), misc RNA.	0.36
<i>LOC666559</i>	XM_144253.6	PREDICTED: similar to farnesyl pyrophosphate synthase (<i>LOC666559</i>), misc RNA	0.20
<i>LOC666676</i>	NM_001033297.2	PREDICTED: similar to ADP-ribosylation factor (<i>LOC666676</i>), misc RNA.	0.46
<i>LOC667005</i>	NM_001013771.2	PREDICTED: similar to cyclin B1 (<i>LOC667005</i>), misc RNA.	0.43
<i>LOC667251</i>	NM_146041.2	PREDICTED: similar to NADPH cytochrome B5 oxidoreductase (<i>LOC667251</i>), misc RNA.	0.64
<i>LOC668038</i>	NM_025508.3	PREDICTED: similar to ribosomal protein (<i>LOC668038</i>), misc RNA.	0.39
<i>LOC668239</i>	NM_177992.2	PREDICTED: similar to Rps13 protein (<i>LOC668239</i>)	0.42
<i>LOC668387</i>	NM_001033300.2	PREDICTED: similar to ribosomal protein S6 (<i>LOC668387</i>), misc RNA.	0.48
<i>LOC668492</i>	NM_010301.1	PREDICTED: similar to zinc finger CCHC-type and RNA binding motif 1 (<i>LOC668492</i>), misc RNA.	0.58
<i>LOC668573</i>	NM_010305.1	PREDICTED: similar to ribosomal protein (<i>LOC668573</i>), misc RNA.	0.42
<i>LOC668706</i>	NM_010308.3	PREDICTED: similar to Ribosomal protein L12 (<i>LOC668706</i>)	0.32
<i>LOC669658</i>	NM_008139.5	PREDICTED: similar to melanoma antigen (<i>LOC669658</i>)	0.67
<i>LOC671523</i>	NM_008142.3	PREDICTED: similar to ring finger and WD repeat domain 3 (<i>LOC671523</i>)	0.66
<i>LOC671641</i>	NM_013531.3	PREDICTED: similar to ribosomal protein S12 (<i>LOC671641</i>)	0.44
<i>LOC671878</i>	NM_015828	PREDICTED: similar to spermine synthase (<i>LOC671878</i>)	0.44
<i>LOC672474</i>	AK005561	PREDICTED: similar to 60S ribosomal protein L29 (<i>LOC672474</i>)	0.55
<i>LOC674611</i>	NM_001038637.1	PREDICTED: similar to Su48, transcript variant 3 (<i>LOC674611</i>)	0.33
<i>LOC675377</i>	NM_178846.2	PREDICTED: similar to Ribosomal protein L8 (<i>LOC675377</i>), misc RNA.	0.47
<i>LOC675440</i>	NM_011937.1	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 (<i>S. cerevisiae</i>), transcript variant 1 (<i>LOC675440</i>)	0.51
<i>LOC675813</i>	NM_008146.3	PREDICTED: similar to ribosomal protein S20 (<i>LOC675813</i>), misc RNA.	0.63
<i>LOC675899</i>	NM_175193.5	PREDICTED: similar to H2A histone family, member Z (<i>LOC675899</i>)	0.22
<i>LOC676640</i>	NM_001035122.2	PREDICTED: similar to neuron navigator 3, transcript variant 5 (<i>LOC676640</i>)	0.43
<i>LOC676724</i>	NM_027352.3	PREDICTED: hypothetical <i>LOC676724</i> (<i>LOC676724</i>)	0.41
<i>LOC676974</i>	NM_029674.1	PREDICTED: similar to Glucose phosphate isomerase 1, transcript variant 2 (<i>LOC676974</i>)	0.57
<i>LOC677205</i>	NM_010325.2	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (<i>LOC677205</i>), misc RNA.	0.57
<i>LOC677213</i>	NM_008149.3	PREDICTED: similar to U2AF homology motif (UHM) kinase 1 (<i>LOC677213</i>)	0.66
<i>LOC677215</i>	NM_010271.2	PREDICTED: similar to acidic ribosomal phosphoprotein P1, transcript variant 1 (<i>LOC677215</i>)	0.58
<i>LOC677317</i>	NM_010274.2	PREDICTED: similar to Mod1 protein, transcript variant 4 (<i>LOC677317</i>)	0.50
<i>LOC677448</i>	NM_008155.2	PREDICTED: similar to actin (<i>LOC677448</i>), misc RNA.	0.55
<i>LOC677551</i>	NM_008156.2	PREDICTED: similar to Ribosomal protein L19 (<i>LOC677551</i>), misc RNA.	0.62
<i>Lor</i>	AK020224	loricrin (<i>Lor</i>)	0.33
<i>Lpl</i>	NM_053110.3	lipoprotein lipase (<i>Lpl</i>)	0.56
<i>Lrig1</i>	NM_177469.3	leucine-rich repeats and immunoglobulin-like domains 1 (<i>Lrig1</i>)	0.51
<i>Lrp12</i>	NR_003568.1	low density lipoprotein-related protein 12 (<i>Lrp12</i>)	0.62
<i>Lrrc59</i>	NM_013533.3	leucine rich repeat containing 59 (<i>Lrrc59</i>)	0.39
<i>Lrrfp1</i>	NM_001025381.1	leucine rich repeat (in FLII) interacting protein 1 (<i>Lrrfp1</i>)	0.32
<i>Lsg1</i>	NM_175271.2	large subunit GTPase 1 homolog (<i>S. cerevisiae</i>) (<i>Lsg1</i>)	0.67
<i>Lsm1</i>	NM_134438.1	LSM1 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm1</i>)	0.64
<i>Lsm12</i>	NM_022420.1	LSM12 homolog (<i>S. cerevisiae</i>) (<i>Lsm12</i>)	0.59
<i>Lsm2</i>	NM_153410.4	LSM2 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm2</i>)	0.41
<i>Lsm3</i>	NM_134118.3	LSM3 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm3</i>)	0.57
<i>Lsm4</i>	NM_008160.5	LSM4 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm4</i>)	0.42
<i>Lsm5</i>	NM_013535.1	LSM5 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm5</i>)	0.44
<i>Lsm6</i>	NM_080289.1	LSM6 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm6</i>)	0.40
<i>Lsm8</i>	NM_008165.2	LSM8 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (<i>Lsm8</i>)	0.43
<i>Lss</i>	NM_016886.2	lanosterol synthase (<i>Lss</i>)	0.37
<i>Ltbp1</i>	NM_028736	latent transforming growth factor beta binding protein 1 (<i>Ltbp1</i>), transcript variant 2	0.46
<i>Ly96</i>	NM_019497.2	lymphocyte antigen 96 (<i>Ly96</i>)	0.55
<i>Lyar</i>	NM_001081414.1	Ly1 antibody reactive clone (<i>Lyar</i>)	0.58
<i>Lypla2</i>	NM_153419.1	lysophospholipase 2 (<i>Lypla2</i>)	0.58
<i>Mad21</i>	NM_010353.1	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (<i>Mad21</i>)	0.25
<i>Mad21bp</i>	NM_146066.1	MAD2L1 binding protein (<i>Mad21bp</i>)	0.63
<i>Maged1</i>	NM_010356.3	melanoma antigen, family D, 1 (<i>Maged1</i>)	0.39

<i>Mageh1</i>	NM_010357.1	melanoma antigen, family H, 1 (Mageh1)	0.61
<i>Mak16</i>	NM_010360.2	MAK16 homolog (S. cerevisiae) (Mak16)	0.50
<i>Man2a1</i>	NM_013541.1	mannosidase 2, alpha 1 (Man2a1)	0.51
<i>Manba</i>	NM_008185.2	mannosidase, beta A, lysosomal (Manba)	0.49
<i>Map2k2</i>	NM_026584.2	mitogen activated protein kinase kinase 2 (Map2k2)	0.66
<i>Map2k3</i>	NM_026816.3	mitogen activated protein kinase kinase 3 (Map2k3)	0.48
<i>Map2k4</i>	NM_022011.3	mitogen activated protein kinase kinase 4 (Map2k4)	0.66
<i>Map3k11</i>	NM_025652.1	mitogen-activated protein kinase kinase kinase 11 (Map3k11)	0.64
<i>Map4k4</i>	NM_207239.1	mitogen-activated protein kinase kinase kinase kinase 4 (Map4k4)	0.54
<i>Mapk1ip11</i>	NM_032544.3	mitogen-activated protein kinase 1 interacting protein 1-like (Mapk1ip11)	0.64
<i>Mapk4</i>	NM_027000.4	mitogen-activated protein kinase 4 (Mapk4)	0.66
<i>Mapk6</i>	NM_013882.1	mitogen-activated protein kinase 6 (Mapk6), transcript variant 2	0.53
<i>Marcks11</i>	NM_010368.1	MARCKS-like 1 (Marcks11)	0.57
<i>Mast2</i>	NM_010376.3	microtubule associated serine/threonine kinase 2 (Mast2), transcript variant 2	0.65
<i>Mbd3</i>	NM_198622.1	methyl-CpG binding domain protein 3 (Mbd3)	0.61
<i>Mbnl1</i>	NM_010436.2	muscleblind-like 1 (Drosophila) (Mbnl1)	0.48
<i>Mboat1</i>	NM_016750.1	membrane bound O-acyltransferase domain containing 1 (Mboat1)	0.47
<i>Mcfcd2</i>	NM_010380.3	multiple coagulation factor deficiency 2 (Mcfcd2)	0.61
<i>Mcl1</i>	XM_915849.1	myeloid cell leukemia sequence 1 (Mcl1)	0.57
<i>Mcm10</i>	NM_026115.3	minichromosome maintenance deficient 10 (S. cerevisiae) (Mcm10)	0.24
<i>Mcm2</i>	NM_010415.1	minichromosome maintenance deficient 2 mitotin (S. cerevisiae) (Mcm2)	0.30
<i>Mcm3</i>	NM_153198	minichromosome maintenance deficient 3 (S. cerevisiae) (Mcm3)	0.55
<i>Mcm4</i>	NM_010406.1	minichromosome maintenance deficient 4 homolog (S. cerevisiae) (Mcm4)	0.27
<i>Mcm5</i>	NM_008222.2	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (Mcm5)	0.15
<i>Mcm6</i>	NM_008229.1	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (Mcm6)	0.26
<i>Mcm7</i>	NM_008230.4	minichromosome maintenance deficient 7 (S. cerevisiae) (Mcm7)	0.47
<i>Mdga2</i>	NM_008231.2	MAM domain containing glycosylphosphatidylinositol anchor 2 (Mdga2)	0.38
<i>Mdh1</i>	NM_144835.4	malate dehydrogenase 1, NAD (soluble) (Mdh1)	0.49
<i>Mdh2</i>	XM_974905.2	malate dehydrogenase 2, NAD (mitochondrial) (Mdh2), nuclear gene encoding mitochondrial protein	0.28
<i>Med10</i>	NM_172637.1	mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae) (Med10)	0.58
<i>Mela</i>	NM_026101.2		0.23
<i>Melk</i>	NM_008235.2	maternal embryonic leucine zipper kinase (Melk)	0.66
<i>Mest</i>	NM_019479.2	mesoderm specific transcript (Mest)	0.30
<i>Metap1</i>	NM_138753.2	methionyl aminopeptidase 1 (Metap1)	0.64
<i>Metrm</i>	NM_010423.2		0.34
<i>Mettl9</i>	NM_029095.1	methyltransferase like 9 (Mettl9)	0.65
<i>Mex3a</i>	NM_010431.1	mex3 homolog A (C. elegans) (Mex3a)	0.57
<i>Mfge8</i>	NM_008248.2		0.65
<i>Mfhas1</i>	NM_146001.1	malignant fibrous histiocytoma amplified sequence 1 (Mfhas1)	0.48
<i>Mfn1</i>	AK087586	mitofusin 1 (Mfn1)	0.58
<i>Mif</i>	NM_016786.2	macrophage migration inhibitory factor (Mif)	0.42
<i>Mki67</i>	NM_172746.2	PREDICTED: antigen identified by monoclonal antibody Ki 67 (Mki67)	0.15
<i>Mki67ip</i>	NM_178189.3	Mki67 (FHA domain) interacting nucleolar phosphoprotein (Mki67ip)	0.54
<i>mkIAA0282</i>	NM_178188.3		0.32
<i>Mkks</i>	NM_175661.1	McKusick-Kaufman syndrome protein (Mkks)	0.65
<i>Mknk2</i>	NM_178186.2	MAP kinase-interacting serine/threonine kinase 2 (Mknk2)	0.60
<i>Mllt11</i>	NM_175659.1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11 (Mllt11)	0.40
<i>Mmp14</i>	NM_178182.1	matrix metalloproteinase 14 (membrane-inserted) (Mmp14)	0.64
<i>Mmp15</i>	NM_178183.1	matrix metalloproteinase 15 (Mmp15)	0.31
<i>Mmp17</i>	NM_178184.1	matrix metalloproteinase 17 (Mmp17)	0.58
<i>Mod1</i>	NM_178185.1	malic enzyme, supernatant (Mod1)	0.51
<i>Mphosph6</i>	NM_178194.3	M phase phosphoprotein 6 (Mphosph6)	0.55
<i>Mphosph9</i>	NM_013549.1	M-phase phosphoprotein 9 (Mphosph9)	0.47
<i>Mpi</i>	NM_178212.1	mannose phosphate isomerase (Mpi)	0.58
<i>Mpnd</i>	NM_178213.3	MPN domain containing (Mpnd)	0.60
<i>Mre11a</i>	NM_175662.1	meiotic recombination 11 homolog A (S. cerevisiae) (Mre11a)	0.57
<i>Mrpl10</i>	NM_016660.2	mitochondrial ribosomal protein L10 (Mrpl10), nuclear gene encoding mitochondrial protein	0.63
<i>Mrpl12</i>	NM_008252.2	mitochondrial ribosomal protein L12 (Mrpl12), nuclear gene encoding mitochondrial protein	0.43
<i>Mrpl15</i>	NM_008254.1		0.45
<i>Mrpl17</i>	NM_008255.1		0.51
<i>Mrpl18</i>	NM_016957.3	mitochondrial ribosomal protein L18 (Mrpl18), nuclear gene encoding mitochondrial protein	0.60

<i>Mrpl2</i>	NM_008258.1	mitochondrial ribosomal protein L2 (Mrpl2), nuclear gene encoding mitochondrial protein	0.52
<i>Mrpl20</i>	NM_198937.2	mitochondrial ribosomal protein L20 (Mrpl20), nuclear gene encoding mitochondrial protein	0.49
<i>Mrpl22</i>	NM_182650.3	mitochondrial ribosomal protein L22 (Mrpl22), nuclear gene encoding mitochondrial protein	0.62
<i>Mrpl23</i>	NM_001048061.1	mitochondrial ribosomal protein L23 (Mrpl23), nuclear gene encoding mitochondrial protein	0.61
<i>Mrpl3</i>	NM_133834.1	mitochondrial ribosomal protein L3 (Mrpl3), nuclear gene encoding mitochondrial protein	0.64
<i>Mrpl30</i>	NM_021510.2	mitochondrial ribosomal protein L30 (Mrpl30), nuclear gene encoding mitochondrial protein	0.54
<i>Mrpl34</i>	NM_025279.2	mitochondrial ribosomal protein L34 (Mrpl34), nuclear gene encoding mitochondrial protein	0.51
<i>Mrpl37</i>	NM_010447	mitochondrial ribosomal protein L37 (Mrpl37), nuclear gene encoding mitochondrial protein	0.60
<i>Mrpl38</i>	AK013709	mitochondrial ribosomal protein L38 (Mrpl38), nuclear gene encoding mitochondrial protein	0.60
<i>Mrpl40</i>	NM_016690.2	mitochondrial ribosomal protein L40 (Mrpl40), nuclear gene encoding mitochondrial protein	0.61
<i>Mrpl43</i>	NM_177301.4	mitochondrial ribosomal protein L43 (Mrpl43), nuclear gene encoding mitochondrial protein	0.65
<i>Mrpl47</i>	NM_144802.3	mitochondrial ribosomal protein L47 (Mrpl47), nuclear gene encoding mitochondrial protein	0.64
<i>Mrpl50</i>	NM_029804.1	mitochondrial ribosomal protein L50 (Mrpl50), nuclear gene encoding mitochondrial protein	0.66
<i>Mrpl52</i>	NM_152134.1	mitochondrial ribosomal protein L52 (Mrpl52), nuclear gene encoding mitochondrial protein	0.54
<i>Mrpl53</i>	NM_175606.2	mitochondrial ribosomal protein L53 (Mrpl53), nuclear gene encoding mitochondrial protein	0.44
<i>Mrpl54</i>	NM_016677.1	mitochondrial ribosomal protein L54 (Mrpl54), nuclear gene encoding mitochondrial protein	0.58
<i>Mrps10</i>	NM_013556.2		0.50
<i>Mrps16</i>	NM_008284	mitochondrial ribosomal protein S16 (Mrps16), nuclear gene encoding mitochondrial protein	0.49
<i>Mrps18b</i>	NM_019830.1	mitochondrial ribosomal protein S18B (Mrps18b), nuclear gene encoding mitochondrial protein	0.50
<i>Mrps18c</i>	NM_008287.2	mitochondrial ribosomal protein S18C (Mrps18c), nuclear gene encoding mitochondrial protein	0.62
<i>Mrps2</i>	NM_011828.2	mitochondrial ribosomal protein S2 (Mrps2), nuclear gene encoding mitochondrial protein	0.64
<i>Mrps23</i>	NM_018805.2	mitochondrial ribosomal protein S23 (Mrps23), nuclear gene encoding mitochondrial protein	0.66
<i>Mrps24</i>	NM_015819.3	mitochondrial ribosomal protein S24 (Mrps24), nuclear gene encoding mitochondrial protein	0.66
<i>Mrps28</i>	NM_019657.2	mitochondrial ribosomal protein S28 (Mrps28), nuclear gene encoding mitochondrial protein	0.57
<i>Mrps30</i>	NM_010476.3	mitochondrial ribosomal protein S30 (Mrps30), nuclear gene encoding mitochondrial protein	0.61
<i>Mrps31</i>	NM_153193.2	mitochondrial ribosomal protein S31 (Mrps31), nuclear gene encoding mitochondrial protein	0.65
<i>Mrps35</i>	NM_008302.3	mitochondrial ribosomal protein S35 (Mrps35), nuclear gene encoding mitochondrial protein	0.56
<i>Mrps7</i>	NM_011631.1	mitochondrial ribosomal protein S7 (Mrps7)	0.49
<i>Mrps9</i>	NM_008301.4	mitochondrial ribosomal protein S9 (Mrps9)	0.62
<i>Mrto4</i>	NM_031165.4	MRT4, mRNA turnover 4, homolog (S. cerevisiae) (Mrto4)	0.53
<i>Msto1</i>	NM_010481.1	misato homolog 1 (Drosophila) (Msto1)	0.66
<i>Mta2</i>	NM_030704.1	metastasis-associated gene family, member 2 (Mta2)	0.66
<i>Mtap</i>	NM_010477.3	methylthioadenosine phosphorylase (Mtap)	0.56
<i>Mtap1s</i>	NM_008303.2	microtubule-associated protein 1S (Mtap1s)	0.66
<i>Mtap7d1</i>		microtubule-associated protein 7 domain containing 1 (Mtap7d1)	0.63
<i>mt-Atp6</i>	NM_016865.2		0.65
<i>Mtch2</i>	NM_019564.2	mitochondrial carrier homolog 2 (C. elegans) (Mtch2), nuclear gene encoding mitochondrial protein	0.56
<i>mt-Co2</i>	NM_019752.2		0.55
<i>Mtdh</i>	NM_010489.2	Metadherin (Mtdh)	0.49
<i>mtDNA_ATP8</i>	NM_010490.2		0.55
<i>mtDNA_ND1</i>	NM_172015.1		0.66
<i>Mthfd2</i>	NM_198653.1		0.21
<i>Mtmr11</i>	XM_135030.4	myotubularin related protein 11 (Mtmr11)	0.40

<i>Mttr12</i>	NM_019987.1	myotubularin related protein 12 (Mttr12)	0.53
<i>Mttr2</i>	NM_031166.2	myotubularin related protein 2 (Mttr2)	0.58
<i>Mtx1</i>	AK013239	metaxin 1 (Mtx1)	0.66
<i>Mvd</i>	NM_031156.2	mevalonate (diphospho) decarboxylase (Mvd)	0.56
<i>Mxra8</i>	NM_029573.2	matrix-remodelling associated 8 (Mxra8)	0.44
<i>Mybbp1a</i>	NM_133662.2	MYB binding protein (P160) 1a (Mybbp1a)	0.47
<i>Mybl2</i>	NM_030244.3	myeloblastosis oncogene-like 2 (Mybl2)	0.48
<i>Myef2</i>	NM_010501.2	myelin basic protein expression factor 2, repressor (Myef2)	0.53
<i>Myh9</i>	NM_026820.2		0.47
<i>Mylk</i>	NM_008338.2	myosin, light polypeptide kinase (Mylk)	0.27
<i>Myo1b</i>	NM_031177.2	myosin IB (Myo1b)	0.65
<i>Myo5a</i>	NM_009879.2	myosin Va (Myo5a)	0.50
<i>Myo6</i>	NM_010515.1	myosin VI (Myo6)	0.58
<i>N4wbp5-pending</i>	NM_008342.2		0.60
<i>N6amt2</i>	NM_008343.2	N-6 adenine-specific DNA methyltransferase 2 (putative) (N6amt2)	0.51
<i>Nab1</i>	NM_010517.3	Ngfi-A binding protein 1 (Nab1)	0.59
<i>Naca</i>	NM_010518.2	nascent polypeptide-associated complex alpha polypeptide (Naca)	0.43
<i>Naglu</i>	NM_008048.2	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB) (Naglu)	0.54
<i>Nans</i>	NM_018741.1	N-acetylneuraminic acid synthase (sialic acid synthase) (Nans)	0.48
<i>Nap111</i>	NM_170599.2	nucleosome assembly protein 1-like 1 (Nap111)	0.39
<i>Nap115</i>	NM_019440.2	nucleosome assembly protein 1-like 5 (Nap115)	0.60
<i>Narg1</i>	NM_010555.4	NMDA receptor-regulated gene 1 (Narg1)	0.47
<i>Nars</i>	NM_010560.2	asparaginyl-tRNA synthetase (Nars)	0.66
<i>Nasp</i>	NM_026374.3		0.45
<i>Nat5</i>	NM_173751.3	N-acetyltransferase 5 (ARD1 homolog, <i>S. cerevisiae</i>) (Nat5)	0.47
<i>Nav1</i>	NM_029673.2		0.45
<i>Ncan</i>	NM_133976.1	neurocan (Ncan)	0.31
<i>Ncapd2</i>	NM_053261.2	non-SMC condensin I complex, subunit D2 (Ncapd2)	0.22
<i>Ncapd3</i>	NM_177730.3	non-SMC condensin II complex, subunit D3 (Ncapd3)	0.58
<i>Ncaph</i>	NM_011830	non-SMC condensin I complex, subunit H (Ncaph)	0.19
<i>Ncdn</i>	NM_016692.1	neurochondrin (Ncdn)	0.56
<i>Ncl</i>	NM_133345.2	nucleolin (Ncl)	0.66
<i>Ncstn</i>	NM_178641.3	nicastrin (Ncstn)	0.57
<i>Ndc80</i>	NM_008916.2	NDC80 homolog, kinetochore complex component (<i>S. cerevisiae</i>) (Ndc80)	0.43
<i>Ndfip1</i>	NM_153526.4	Nedd4 family interacting protein 1 (Ndfip1)	0.61
<i>Ndufa12</i>	NM_013754.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (Ndufa12)	0.55
<i>Ndufa12l</i>	NM_178632.4	PREDICTED: Ndufa12-like (Ndufa12l)	0.51
<i>Ndufa3</i>	NM_024267.6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (Ndufa3)	0.67
<i>Ndufa4</i>	NM_023579.4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (Ndufa4)	0.54
<i>Ndufa5</i>	NM_153774.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (Ndufa5), nuclear gene encoding mitochondrial protein	0.54
<i>Ndufa6</i>	NM_177128.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) (Ndufa6), nuclear gene encoding mitochondrial protein	0.60
<i>Ndufa8</i>	NM_178378.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (Ndufa8), nuclear gene encoding mitochondrial protein	0.59
<i>Ndufa9</i>	NM_016721	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (Ndufa9)	0.61
<i>Ndufb10</i>	NM_001033484.1		0.62
<i>Ndufb3</i>	NM_026921.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 (Ndufb3)	0.60
<i>Ndufb5</i>	NM_133934.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (Ndufb5), nuclear gene encoding mitochondrial protein	0.58
<i>Ndufb6</i>	NM_013565.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (Ndufb6), nuclear gene encoding mitochondrial protein	0.44
<i>Ndufb8</i>	NM_008402.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (Ndufb8)	0.63
<i>Ndufc1</i>	NM_010578.1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (Ndufc1)	0.49
<i>Ndufc2</i>	NM_010580.1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (Ndufc2)	0.50
<i>Ndufs2</i>	NM_008407.1	NADH dehydrogenase (ubiquinone) Fe-S protein 2 (Ndufs2)	0.62
<i>Ndufs3</i>	NM_008410.1	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (Ndufs3)	0.63
<i>Ndufs4</i>	NM_172584.3	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Ndufs4), nuclear gene encoding mitochondrial protein	0.58
<i>Ndufs7</i>	XM_205854	NADH dehydrogenase (ubiquinone) Fe-S protein 7 (Ndufs7), nuclear gene encoding mitochondrial protein	0.62
<i>Ndufs8</i>	NM_019923.3	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (Ndufs8)	0.56
<i>Ndufv1</i>	NM_026365.2	NADH dehydrogenase (ubiquinone) flavoprotein 1 (Ndufv1), nuclear gene encoding mitochondrial protein	0.66
<i>Ndufv2</i>	NM_146145.2	NADH dehydrogenase (ubiquinone) flavoprotein 2 (Ndufv2)	0.52
<i>Necap1</i>	NM_178394.3	NECAP endocytosis associated 1 (Necap1)	0.62
<i>Nedd1</i>	NM_023844.2		0.61
<i>Nek3</i>	NM_033398.2	NIMA (never in mitosis gene a)-related expressed kinase 3 (Nek3)	0.52
<i>Nes</i>	NM_025368.3	nestin (Nes)	0.51
<i>Neto2</i>	NM_010591.1	neuroligin (NRP) and tolloid (TLL)-like 2 (Neto2)	0.56

<i>Neu1</i>	NM_172872.2	neuraminidase 1 (Neu1)	0.65
<i>Neurl</i>	NM_053092.1		0.30
<i>Nfatc3</i>	NM_145958.1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (Nfatc3)	0.61
<i>Nfib</i>	NM_013568.3	nuclear factor I/B (Nfib)	0.65
<i>Nfkbiz</i>	NM_008421.2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (Nfkbiz)	0.55
<i>Nhlrc2</i>	NM_145922.2	NHL repeat containing 2 (Nhlrc2)	0.58
<i>Nip7</i>	NM_019789.2	nuclear import 7 homolog (S. cerevisiae) (Nip7)	0.63
<i>Nipsnap3a</i>	NM_008430.1	nipsnap homolog 3A (C. elegans) (Nipsnap3a)	0.56
<i>Nkrf</i>	NM_146037.1	NF-kappaB repressing factor (Nkrf)	0.58
<i>Nkx2-2</i>	NM_010607.1	NK2 transcription factor related, locus 2 (Drosophila) (Nkx2-2), transcript variant 1	0.37
<i>Nme1</i>	NM_177715.4	non-metastatic cells 1, protein (NM23A) expressed in (Nme1)	0.37
<i>Nme2</i>	NM_025888.5	non-metastatic cells 2, protein (NM23B) expressed in (Nme2), transcript variant 1	0.35
<i>Nme4</i>	NM_027008.1	non-metastatic cells 4, protein expressed in (Nme4), nuclear gene encoding mitochondrial protein	0.58
<i>Nmral1</i>	NM_023645.2	NmrA-like family domain containing 1 (Nmral1)	0.58
<i>Nmt1</i>	NM_025841.3	N-myristoyltransferase 1 (Nmt1)	0.60
<i>Noc2l</i>	NM_011317.3	nucleolar complex associated 2 homolog (S. cerevisiae) (Noc2l)	0.52
<i>Noc4l</i>	NM_010615.1	nucleolar complex associated 4 homolog (S. cerevisiae) (Noc4l)	0.61
<i>Nol1</i>	NM_010620.1	nucleolar protein 1 (Nol1)	0.55
<i>Nol10</i>	NM_139303.1	nucleolar protein 10 (Nol10)	0.63
<i>Nol5</i>	NM_183046.1	nucleolar protein 5 (Nol5)	0.27
<i>Nol5a</i>	NM_016705.2	nucleolar protein 5A (Nol5a)	0.45
<i>Nola1</i>	NM_145588.1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) (Nola1)	0.38
<i>Nola2</i>	NM_024245	nucleolar protein family A, member 2 (Nola2)	0.47
<i>Nola3</i>	NM_134471.3	nucleolar protein family A, member 3 (Nola3)	0.40
<i>Nomo1</i>	NM_008445.2	nodal modulator 1 (Nomo1)	0.37
<i>Npc2</i>	NM_008446.1	Niemann Pick type C2 (Npc2)	0.64
<i>Npm1</i>	NM_016761.1	nucleophosmin 1 (Npm1)	0.43
<i>Npm3</i>	NM_026324.2	nucleoplasmin 3 (Npm3)	0.22
<i>Npm3-ps1</i>	NM_013598.1	nucleoplasmin 3, pseudogene 1 (Npm3-ps1), non-coding RNA.	0.20
<i>Nptn</i>	NM_011803.2	neuroplastin (Nptn)	0.54
<i>Nptx1</i>	AK086122	neuronal pentraxin 1 (Nptx1)	0.22
<i>Nqo2</i>	NM_027117.1	NAD(P)H dehydrogenase, quinone 2 (Nqo2)	0.56
<i>Nr2c2ap</i>	NM_030075.1	nuclear receptor 2C2-associated protein (Nr2c2ap), transcript variant 2	0.67
<i>Nr2f6</i>	NM_172052.1	nuclear receptor subfamily 2, group F, member 6 (Nr2f6)	0.62
<i>Nrarp</i>	NM_177261.4	Notch-regulated ankyrin repeat protein (Nrarp)	0.43
<i>Nrcam</i>	NM_001042421.1	neuron-glia-CAM-related cell adhesion molecule (Nrcam)	0.53
<i>Nrd1</i>	NM_008465.4	nardilysin, N-arginine dibasic convertase, NRD convertase 1 (Nrd1)	0.60
<i>Nrm</i>	NM_010655.3	nurim (nuclear envelope membrane protein) (Nrm)	0.24
<i>Nrn1</i>	NM_008379.3	neuritin 1 (Nrn1)	0.38
<i>Nrp1</i>	NM_021284.4	neuropilin 1 (Nrp1)	0.46
<i>Nsbp1</i>	NM_025327.2	nucleosome binding protein 1 (Nsbp1)	0.53
<i>Nsdhl</i>	NM_024291.3	NAD(P) dependent steroid dehydrogenase-like (Nsdhl)	0.44
<i>Nsep1</i>	NM_001081171.2		0.47
<i>Nsfl1c</i>	NM_008483.2	NSFL1 (p97) cofactor (p47) (Nsfl1c)	0.62
<i>Nt5c</i>	NM_010683.1	5',3'-nucleotidase, cytosolic (Nt5c)	0.65
<i>Nt5dc2</i>	NM_001017959.1	5'-nucleotidase domain containing 2 (Nt5dc2)	0.54
<i>Ntan1</i>	NM_029789.1		0.64
<i>Nubp1</i>	NM_028015.2	nucleotide binding protein 1 (Nubp1)	0.35
<i>Nucb1</i>	NM_029999.3	nucleobindin 1 (Nucb1)	0.65
<i>Nudc</i>	NM_133815	nuclear distribution gene C homolog (Aspergillus) (Nudc)	0.64
<i>Nudt19</i>	NM_010699.1	nudix (nucleoside diphosphate linked moiety X)-type motif 19 (Nudt19)	0.61
<i>Nudt21</i>	NM_001039522.1	nudix (nucleoside diphosphate linked moiety X)-type motif 21 (Nudt21)	0.44
<i>Nudt5</i>	NM_008495.1	nudix (nucleoside diphosphate linked moiety X)-type motif 5 (Nudt5)	0.44
<i>Nup133</i>	NM_010705.2	nucleoporin 133 (Nup133)	0.61
<i>Nup160</i>	NM_010706.1	nucleoporin 160 (Nup160)	0.52
<i>Nup205</i>	NM_018886.3	PREDICTED: nucleoporin 205, transcript variant 1 (Nup205)	0.36
<i>Nup210</i>	NM_145219.2	nucleoporin 210 (Nup210)	0.19
<i>Nup43</i>	NM_008133.3	nucleoporin 43 (Nup43)	0.45
<i>Nup62</i>	NM_175386.3	nucleoporin 62 (Nup62)	0.32
<i>Nup85</i>	NM_010715.2	nucleoporin 85 (Nup85)	0.51
<i>Nup88</i>	NM_010716	nucleoporin 88 (Nup88), transcript variant 1	0.48
<i>Nus1</i>	NM_013860.1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae) (Nus1)	0.57
<i>Nusap1</i>	NM_001034030.1	nucleolar and spindle associated protein 1 (Nusap1), transcript variant 2	0.21
<i>Nxph1</i>	NM_172714.1	neurexophilin 1 (Nxph1)	0.16
<i>Nxt1</i>	NM_021460.1	NTF2-related export protein 1 (Nxt1)	0.54

<i>Ociad2</i>	NM_153404.2	OCIA domain containing 2 (<i>Ociad2</i>)	0.37
<i>Ogdh</i>	NM_019980.1	oxoglutarate dehydrogenase (lipoamide) (<i>Ogdh</i>), nuclear gene encoding mitochondrial protein	0.60
<i>Ola1</i>	NM_025681.2	Obg-like ATPase 1 (<i>Ola1</i>), transcript variant 1	0.59
<i>Olfm2</i>	NM_008502.1	olfactomedin 2 (<i>Olfm2</i>)	0.43
<i>Olfml2b</i>	NM_027400.2	olfactomedin-like 2B (<i>Olfml2b</i>)	0.41
<i>Olig1</i>	NM_010721.1	oligodendrocyte transcription factor 1 (<i>Olig1</i>)	0.41
<i>Opn3</i>	NM_008505.3	opsin 3 (<i>Opn3</i>)	0.53
<i>Oprs1</i>	XM_001472500.1	opioid receptor, sigma 1 (<i>Oprs1</i>)	0.57
<i>Orai1</i>	XM_001473099.1	ORAI calcium release-activated calcium modulator 1 (<i>Orai1</i>)	0.61
<i>Orc5l</i>	XM_001473215.1	origin recognition complex, subunit 5-like (<i>S. cerevisiae</i>) (<i>Orc5l</i>)	0.62
<i>Orc6l</i>	XR_031048.1	origin recognition complex, subunit 6-like (<i>S. cerevisiae</i>) (<i>Orc6l</i>)	0.48
<i>Osbp3</i>	XM_001473500.1	oxysterol binding protein-like 3 (<i>Osbp3</i>)	0.67
<i>Osbp6</i>	XM_001475112.1	oxysterol binding protein-like 6 (<i>Osbp6</i>)	0.32
<i>Osbp8</i>	XM_001475189.1	oxysterol binding protein-like 8 (<i>Osbp8</i>), transcript variant 1	0.66
<i>Ostm1</i>	XM_001475096.1	osteopetrosis associated transmembrane protein 1 (<i>Ostm1</i>)	0.52
<i>Oxct1</i>	XM_001476627.1	3-oxoacid CoA transferase 1 (<i>Oxct1</i>)	0.65
<i>Oxr1</i>	XM_001478166.1	oxidation resistance 1 (<i>Oxr1</i>), transcript variant 1	0.59
<i>P2ry5</i>	XM_001478119.1	purinergic receptor P2Y, G-protein coupled, 5 (<i>P2ry5</i>)	0.30
<i>P4hb</i>	XM_001477137.1	prolyl 4-hydroxylase, beta polypeptide (<i>P4hb</i>)	0.54
<i>Pa2g4</i>	XM_001478555.1	proliferation-associated 2G4 (<i>Pa2g4</i>)	0.40
<i>Pabpc4</i>	XM_001478518.1	poly A binding protein, cytoplasmic 4 (<i>Pabpc4</i>), transcript variant 1	0.50
<i>Pafah1b1</i>	XM_001478939.1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit (<i>Pafah1b1</i>)	0.55
<i>Pafah1b3</i>	XM_001479207.1	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit (<i>Pafah1b3</i>)	0.66
<i>Pak4</i>	XM_001479822.1	p21 (CDKN1A)-activated kinase 4 (<i>Pak4</i>)	0.66
<i>Palmd</i>	XM_001480293.1	palmdelphin (<i>Palmd</i>)	0.41
<i>Pank1</i>	XM_001480197.1	pantothenate kinase 1 (<i>Pank1</i>), transcript variant 2	0.62
<i>Pank3</i>	XM_001479903.1	pantothenate kinase 3 (<i>Pank3</i>)	0.64
<i>Parp1</i>	XM_001480106.1	poly (ADP-ribose) polymerase family, member 1 (<i>Parp1</i>)	0.52
<i>Pbk</i>	XM_001480194.1	PDZ binding kinase (<i>Pbk</i>)	0.08
<i>Pbrm1</i>	XM_001481024.1	polybromo 1 (<i>Pbrm1</i>)	0.66
<i>Pcbp1</i>	XM_001480621.1	poly(rC) binding protein 1 (<i>Pcbp1</i>)	0.45
<i>Pcbp2</i>	XM_001481075.1	poly(rC) binding protein 2 (<i>Pcbp2</i>)	0.57
<i>Pcdh17</i>	XM_001481083.1	protocadherin 17 (<i>Pcdh17</i>)	0.46
<i>Pcdh7</i>	XM_001481017.1	protocadherin 7 (<i>Pcdh7</i>)	0.45
<i>Pcdh9</i>	XM_001481025.1	protocadherin 9 (<i>Pcdh9</i>)	0.55
<i>Pcyt2</i>	XM_001481214.1	phosphate cytidyltransferase 2, ethanolamine (<i>Pcyt2</i>)	0.64
<i>Pdap1</i>	XM_001474702.1	PDGFA associated protein 1 (<i>Pdap1</i>)	0.36
<i>Pdcd2l</i>	XM_001471637.1	programmed cell death 2-like (<i>Pdcd2l</i>)	0.62
<i>Pdgfa</i>	XM_001471968.1		0.38
<i>Pdhb</i>	XM_001472489.1	pyruvate dehydrogenase (lipoamide) beta (<i>Pdhb</i>)	0.54
<i>Pdia3</i>	XM_001472256.1	protein disulfide isomerase associated 3 (<i>Pdia3</i>)	0.49
<i>Pdia5</i>	XM_001473268.1	protein disulfide isomerase associated 5 (<i>Pdia5</i>)	0.41
<i>Pdlim4</i>	XM_001472872.1	PDZ and LIM domain 4 (<i>Pdlim4</i>)	0.63
<i>Pdlim5</i>	XM_001473652.1	PDZ and LIM domain 5 (<i>Pdlim5</i>), transcript variant 1	0.62
<i>Pdss1</i>	XR_031422.1	prenyl (solaneyl) diphosphate synthase, subunit 1 (<i>Pdss1</i>)	0.53
<i>Pdpx</i>	XR_031278.1	pyridoxal (pyridoxine, vitamin B6) phosphatase (<i>Pdpx</i>)	0.54
<i>Pdzrn4</i>	XM_001474658.1	PREDICTED: PDZ domain containing RING finger 4 (<i>Pdzrn4</i>)	0.49
<i>Peli1</i>	XM_001473900.1	pellino 1 (<i>Peli1</i>)	0.56
<i>Pfdn2</i>	XR_031575.1	prefoldin 2 (<i>Pfdn2</i>)	0.59
<i>Pfdn4</i>	XM_001474411.1	prefoldin 4 (<i>Pfdn4</i>), transcript variant 2	0.32
<i>Pfn1</i>	XM_001473941.1	profilin 1 (<i>Pfn1</i>)	0.44
<i>Pgam1</i>	XM_001474718.1	phosphoglycerate mutase 1 (<i>Pgam1</i>)	0.54
<i>Pgam5</i>	XR_031705.1	phosphoglycerate mutase family member 5 (<i>Pgam5</i>)	0.45
<i>Pgk1</i>	XM_001475152.1	phosphoglycerate kinase 1 (<i>Pgk1</i>)	0.55
<i>Pgls</i>	XR_031796.1	6-phosphogluconolactonase (<i>Pgls</i>)	0.52
<i>Pgp</i>	XR_031944.1	phosphoglycolate phosphatase (<i>Pgp</i>)	0.34
<i>Pgs1</i>	XM_001475019.1	phosphatidylglycerophosphate synthase 1 (<i>Pgs1</i>)	0.64
<i>Phb2</i>	XM_001475055.1	prohibitin 2 (<i>Phb2</i>)	0.42
<i>Phc2</i>	XM_001475106.1	polyhomeotic-like 2 (<i>Drosophila</i>) (<i>Phc2</i>)	0.41
<i>Phca</i>	XR_032154.1	phytoceramidase, alkaline (<i>Phca</i>)	0.65
<i>Phf10</i>	XM_001475298.1	PHD finger protein 10 (<i>Phf10</i>)	0.62
<i>Phf20</i>	XM_001475422.1	PHD finger protein 20 (<i>Phf20</i>)	0.46
<i>Phf5a</i>	XM_001475447.1	PHD finger protein 5A (<i>Phf5a</i>)	0.57
<i>Phf6</i>	XM_001475611.1	PHD finger protein 6 (<i>Phf6</i>)	0.61
<i>Phlda1</i>	XM_001475801.1	pleckstrin homology-like domain, family A, member 1 (<i>Phlda1</i>)	0.41
<i>Phft2</i>	XM_001475830.1	putative homeodomain transcription factor 2 (<i>Phft2</i>)	0.60
<i>Pi4ka</i>	XM_001476721.1	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (<i>Pi4ka</i>)	0.58
<i>Picalm</i>	XM_001476728.1		0.60
<i>Pif1</i>	XM_001475765.1	PIF1 5'-to-3' DNA helicase homolog (<i>S. cerevisiae</i>) (<i>Pif1</i>)	0.39
<i>Piga</i>	XM_001476780.1	phosphatidylinositol glycan anchor biosynthesis, class A (<i>Piga</i>)	0.63

<i>Pih1d1</i>	XM_001476909.1	PIH1 domain containing 1 (Pih1d1)	0.65
<i>Pip4k2b</i>	XM_001476916.1	phosphatidylinositol-5-phosphate 4-kinase, type II, beta (Pip4k2b)	0.56
<i>Pitpnb</i>	XM_001477026.1	phosphatidylinositol transfer protein, beta (Pitpnb)	0.63
<i>Pitrm1</i>	XM_001477492.1	pitrilysin metallopeptidase 1 (Pitrm1)	0.63
<i>Pja1</i>	XM_001477537.1		0.58
<i>Pja2</i>	XM_001477568.1	praja 2, RING-H2 motif containing (Pja2), transcript variant 2	0.57
<i>Pkd1</i>	XM_001477596.1	polycystic kidney disease 1 homolog (Pkd1)	0.66
<i>Pkia</i>	XR_033770.1	protein kinase inhibitor, alpha (Pkia)	0.62
<i>Pkm2</i>	XM_001477665.1		0.43
<i>Pkn2</i>	XR_033502.1	protein kinase N2 (Pkn2)	0.65
<i>Pla2g12a</i>	XR_033381.1	phospholipase A2, group X1IA (Pla2g12a), transcript variant 1	0.63
<i>Plaa</i>	XM_001477759.1	phospholipase A2, activating protein (Plaa)	0.61
<i>Pld1</i>	XM_001477774.1		0.52
<i>Plekha8</i>	XM_001477963.1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8 (Plekha8)	0.61
<i>Plekhk1</i>	XM_001478437.1		0.28
<i>Plk1</i>	XR_033484.1	polo-like kinase 1 (Drosophila) (Plk1)	0.11
<i>Plk2</i>	XR_033736.1	polo-like kinase 2 (Drosophila) (Plk2)	0.21
<i>Plk4</i>	XR_032896.1		0.57
<i>Plvap</i>	XM_001478602.1	plasmalemma vesicle associated protein (Plvap)	0.15
<i>Plxna2</i>	XM_001478657.1	plexin A2 (Plxna2)	0.59
<i>Pml</i>	XM_001478724.1	promyelocytic leukemia (Pml), transcript variant 1	0.61
<i>Pmp22</i>	XM_001478788.1	peripheral myelin protein 22 (Pmp22)	0.38
<i>Pno1</i>	XM_001479214.1	partner of NOB1 homolog (S. cerevisiae) (Pno1)	0.46
<i>Pola2</i>	XM_001478835.1	polymerase (DNA directed), alpha 2 (Pola2)	0.66
<i>Pold1</i>	XM_001479392.1	polymerase (DNA directed), delta 1, catalytic subunit (Pold1)	0.29
<i>Pold2</i>	XM_001479068.1	polymerase (DNA directed), delta 2, regulatory subunit (Pold2)	0.51
<i>Pold4</i>	XM_001478074.1		0.55
<i>Pole</i>	XR_033756.1	polymerase (DNA directed), epsilon (Pole)	0.45
<i>Pole4</i>	XR_033905.1	polymerase (DNA-directed), epsilon 4 (p12 subunit) (Pole4)	0.60
<i>Polg</i>	XM_001479497.1	polymerase (DNA directed), gamma (Polg)	0.65
<i>Polr1a</i>	XR_034387.1	polymerase (RNA) I polypeptide A (Polr1a)	0.58
<i>Polr1d</i>	XM_001480136.1	polymerase (RNA) I polypeptide D (Polr1d), transcript variant 1	0.61
<i>Polr1e</i>	XR_034509.1	polymerase (RNA) I polypeptide E (Polr1e)	0.58
<i>Polr2a</i>	XM_001480186.1		0.59
<i>Polr2g</i>	XM_001480467.1	polymerase (RNA) II (DNA directed) polypeptide G (Polr2g)	0.66
<i>Polr2h</i>	XM_001480451.1	polymerase (RNA) II (DNA directed) polypeptide H (Polr2h)	0.64
<i>Polr3k</i>	XM_001480453.1	polymerase (RNA) III (DNA directed) polypeptide K (Polr3k)	0.53
<i>Pomt2</i>	XM_001480806.1	protein-O-mannosyltransferase 2 (Pomt2)	0.63
<i>Pop5</i>	XM_001480785.1	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (Pop5)	0.57
<i>Por</i>	XM_001480380.1	P450 (cytochrome) oxidoreductase (Por)	0.60
<i>Pou3f1</i>	XM_001480791.1	POU domain, class 3, transcription factor 1 (Pou3f1)	0.20
<i>Ppa1</i>	XM_001471617.1	pyrophosphatase (inorganic) 1 (Ppa1)	0.43
<i>Ppa2</i>	XM_137003.2	pyrophosphatase (inorganic) 2 (Ppa2), nuclear gene encoding mitochondrial protein	0.56
<i>Ppan</i>	XM_125952.4		0.42
<i>Ppargc1a</i>	XM_122711.2	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha (Ppargc1a)	0.58
<i>Ppat</i>	XM_139078.2	PREDICTED: phosphoribosyl pyrophosphate amidotransferase, transcript variant 8 (Ppat)	0.59
<i>Ppia</i>	XM_122761.3	peptidylprolyl isomerase A (Ppia)	0.43
<i>Ppib</i>	XM_140116.1	peptidylprolyl isomerase B (Ppib)	0.44
<i>Ppic</i>	XR_031257.1	peptidylprolyl isomerase C (Ppic)	0.65
<i>Ppid</i>	XM_129460.4		0.58
<i>Ppif</i>	XM_124173.2	peptidylprolyl isomerase F (cyclophilin F) (Ppif), nuclear gene encoding mitochondrial protein	0.43
<i>Ppih</i>	XM_124269.2		0.56
<i>Ppm1b</i>	XM_124427.4	protein phosphatase 1B, magnesium dependent, beta isoform (Ppm1b)	0.62
<i>Ppm1g</i>	XR_002491.1	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (Ppm1g)	0.61
<i>Ppp1ca</i>	XM_124826.2	protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1ca)	0.63
<i>Ppp1r12a</i>	XM_124858.2	protein phosphatase 1, regulatory (inhibitor) subunit 12A (Ppp1r12a)	0.53
<i>Ppp1r14b</i>	XM_145374.2		0.39
<i>Ppp1r8</i>	XR_001889.1	protein phosphatase 1, regulatory (inhibitor) subunit 8 (Ppp1r8)	0.64
<i>Ppp2cb</i>	XM_137226.3	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb)	0.61
<i>Ppp2r5c</i>	XM_111221.4	protein phosphatase 2, regulatory subunit B (B56), gamma isoform (Ppp2r5c), transcript variant 3	0.41
<i>Ppp3ca</i>	XM_138902.2	protein phosphatase 3, catalytic subunit, alpha isoform (Ppp3ca)	0.66
<i>Ppp3cb</i>	XM_917314.2		0.47

<i>Ppp3r1</i>	XM_142236.4	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I) (Ppp3r1)	0.63
<i>Ppp6c</i>	XM_147335.2	protein phosphatase 6, catalytic subunit (Ppp6c)	0.60
<i>Pprc1</i>	XM_195821.2	peroxisome proliferative activated receptor, gamma, coactivator-related 1 (Pprc1)	0.54
<i>Prc1</i>	XM_193742.2	protein regulator of cytokinesis 1 (Prc1)	0.06
<i>Prpc</i>	XM_193262.3	prolylcarboxypeptidase (angiotensinase C) (Prpc)	0.33
<i>Prdx4</i>	XM_193374.2	peroxiredoxin 4 (Prdx4)	0.48
<i>Prep</i>	XM_193524.2	prolyl endopeptidase (Prep)	0.46
<i>Prkaca</i>	XM_195069.2	protein kinase, cAMP dependent, catalytic, alpha (Prkaca)	0.49
<i>Prkacb</i>	XM_195066.3	protein kinase, cAMP dependent, catalytic, beta (Prkacb)	0.63
<i>Prkar1a</i>	XM_195399.2	protein kinase, cAMP dependent regulatory, type I, alpha (Prkar1a)	0.66
<i>Prkar2b</i>	XM_204210.2	protein kinase, cAMP dependent regulatory, type II beta (Prkar2b)	0.55
<i>Prkcb</i>	XM_207178.1	protein kinase C, beta (Prkcb)	0.09
<i>Prkcbp1</i>	XM_282724.2	protein kinase C binding protein 1 (Prkcbp1)	0.61
<i>Prkcsh</i>	XM_287286.2	protein kinase C substrate 80K-H (Prkcsh)	0.60
<i>Prkd3</i>	XM_284573.2	protein kinase D3 (Prkd3)	0.61
<i>Prmt3</i>	XM_284733.2	protein arginine N-methyltransferase 3 (Prmt3)	0.58
<i>Prmt5</i>	XM_284853.2	protein arginine N-methyltransferase 5 (Prmt5)	0.60
<i>Prmt7</i>	XR_032458.1	protein arginine N-methyltransferase 7 (Prmt7)	0.47
<i>Prokr1</i>	XM_354560.1	prokineticin receptor 1 (Prokr1)	0.51
<i>Prpf19</i>	XM_354604.1	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae) (Prpf19)	0.58
<i>Prpf38a</i>	XM_354622.1	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (Prpf38a)	0.52
<i>Prr18</i>	XM_354834.1	proline rich region 18 (Prr18)	0.49
<i>Prrc1</i>	XM_358467.1	proline-rich coiled-coil 1 (Prrc1)	0.58
<i>Prss35</i>	XM_354911.1	protease, serine, 35 (Prss35)	0.27
<i>Psip1</i>	XM_354963.1	PC4 and SFRS1 interacting protein 1 (Psip1)	0.61
<i>Psm5</i>	XM_355032.1	proteasome (prosome, macropain) subunit, alpha type 5 (Psm5)	0.56
<i>Psm7</i>	XM_355049.1	proteasome (prosome, macropain) subunit, alpha type 7 (Psm7)	0.52
<i>Psm1</i>	XM_355056.1	proteasome (prosome, macropain) subunit, beta type 1 (Psm1)	0.62
<i>Psm10</i>	XM_355149.1	proteasome (prosome, macropain) subunit, beta type 10 (Psm10)	0.50
<i>Psm2</i>	XM_355167.1	proteasome (prosome, macropain) subunit, beta type 2 (Psm2)	0.65
<i>Psm3</i>	XM_355202.1	proteasome (prosome, macropain) subunit, beta type 3 (Psm3)	0.63
<i>Psm4</i>	XM_355288.1	proteasome (prosome, macropain) subunit, beta type 4 (Psm4)	0.59
<i>Psm5</i>	XM_355330.1	proteasome (prosome, macropain) subunit, beta type 5 (Psm5)	0.55
<i>Psm6</i>	XM_355356.1	proteasome (prosome, macropain) subunit, beta type 6 (Psm6)	0.66
<i>Psm7</i>	XM_355403.1	proteasome (prosome, macropain) subunit, beta type 7 (Psm7)	0.55
<i>Psm1</i>	XM_355526.1		0.53
<i>Psm2</i>	XM_355612.1	proteasome (prosome, macropain) 26S subunit, ATPase 2 (Psm2)	0.61
<i>Psm3ip</i>	XM_355721.1	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein (Psm3ip)	0.52
<i>Psm4</i>	XM_355801.1	proteasome (prosome, macropain) 26S subunit, ATPase, 4 (Psm4)	0.63
<i>Psm5</i>	XM_355809.1	protease (prosome, macropain) 26S subunit, ATPase 5 (Psm5)	0.63
<i>Psm12</i>	XM_355907.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (Psm12)	0.50
<i>Psm14</i>	XM_355964.1		0.62
<i>Psm8</i>	XM_358681.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 (Psm8)	0.57
<i>Psm3</i>	XM_356062.1	proteaseome (prosome, macropain) 28 subunit, 3 (Psm3)	0.59
<i>Ptcd2</i>	XM_356141.1	pentatricopeptide repeat domain 2 (Ptcd2)	0.64
<i>Pten</i>	XM_356263.1	phosphatase and tensin homolog (Pten)	0.65
<i>Ptk2</i>	XM_356342.1	PTK2 protein tyrosine kinase 2 (Ptk2)	0.39
<i>Ptn</i>	XM_356731.1	pleiotrophin (Ptn)	0.55
<i>Ptpn12</i>	XM_356798.1	protein tyrosine phosphatase, non-receptor type 12 (Ptpn12)	0.63
<i>Ptpro</i>	XM_356873.1	protein tyrosine phosphatase, receptor type, O (Ptpro)	0.31
<i>Ptprz1</i>	XM_356900.1	protein tyrosine phosphatase, receptor type Z, polypeptide 1 (Ptprz1)	0.46
<i>Pum2</i>	XM_356977.1	pumilio 2 (Drosophila) (Pum2)	0.64
<i>Pus7l</i>	XM_356987.1	pseudouridylate synthase 7 homolog (S. cerevisiae)-like (Pus7l)	0.48
<i>Pus1</i>	XM_357315.1	PREDICTED: pseudouridylate synthase-like 1, transcript variant 1 (Pus1)	0.58
<i>Pvrl3</i>	XM_357338.1	poliovirus receptor-related 3 (Pvrl3), transcript variant alpha	0.62
<i>Pycr2</i>	XM_357429.1	pyrroline-5-carboxylate reductase family, member 2 (Pycr2)	0.59
<i>Qpct</i>	XM_357488.1	glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Qpct)	0.55
<i>Qrs1</i>	XM_357823.1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (Qrs1)	0.55
<i>Rab26</i>	XM_358153.1	PREDICTED: RAB26, member RAS oncogene family, transcript variant 1 (Rab26)	0.06
<i>Rab34</i>	XM_358163.1	RAB34, member of RAS oncogene family (Rab34)	0.56
<i>Rab35</i>	XM_358915.1	RAB35, member RAS oncogene family (Rab35)	0.51
<i>Rab3a</i>	XM_358960.1	RAB3A, member RAS oncogene family (Rab3a)	0.47
<i>Rab3b</i>	XM_358981.1		0.37
<i>Rab3gap2</i>	XR_034995.1	PREDICTED: RAB3 GTPase activating protein subunit 2, transcript variant 4 (Rab3gap2)	0.52
<i>Rab5c</i>	XM_359014.1	RAB5C, member RAS oncogene family (Rab5c)	0.59
<i>Rab8b</i>	XM_359028.1	RAB8B, member RAS oncogene family (Rab8b)	0.38
<i>Rabggtb</i>	XM_359031.1	RAB geranylgeranyl transferase, b subunit (Rabggtb)	0.54

<i>Rabif</i>	XM_359035.1	RAB interacting factor (Rabif)	0.63
<i>Rad51</i>	XM_359058.1	RAD51 homolog (S. cerevisiae) (Rad51)	0.57
<i>Rad51c</i>	XM_359091.1	Rad51 homolog c (S. cerevisiae) (Rad51c)	0.48
<i>Rad54l</i>	XM_359123.1	RAD54 like (S. cerevisiae) (Rad54l)	0.56
<i>Raet1b</i>	XM_359142.1	retinoic acid early transcript beta (Raet1b)	0.36
<i>Rag1ap1</i>	XM_359148.1	recombination activating gene 1 activating protein 1 (Rag1ap1)	0.64
<i>Rai12</i>	XM_359163.1	retinoic acid induced 12 (Rai12)	0.65
<i>Raly</i>	XM_359184.1	hnRNP-associated with lethal yellow (Raly)	0.34
<i>Ramp2</i>	XM_917865.2	receptor (calcitonin) activity modifying protein 2 (Ramp2)	0.65
<i>Ran</i>	XM_906947.2	RAN, member RAS oncogene family (Ran)	0.57
<i>Ranbp1</i>	XM_001475733.1	RAN binding protein 1 (Ranbp1)	0.36
<i>Rangap1</i>	XM_485435.3		0.44
<i>Rangrf</i>	XR_034042.1	RAN guanine nucleotide release factor (Rangrf)	0.50
<i>Rap1b</i>	XR_033167.1	RAS related protein 1b (Rap1b)	0.50
<i>Rap2c</i>	NR_002889.1	RAP2C, member of RAS oncogene family (Rap2c)	0.29
<i>Rars</i>	XR_034542.1	arginyl-tRNA synthetase (Rars)	0.66
<i>Rasa3</i>	XM_619824.4	RAS p21 protein activator 3 (Rasa3)	0.33
<i>Rasal2</i>	XR_034790.1	RAS protein activator like 2 (Rasal2)	0.61
<i>Rassf3</i>	XR_031536.1	Ras association (RalGDS/AF-6) domain family member 3 (Rassf3)	0.18
<i>Rbbp4</i>	XR_032410.1	retinoblastoma binding protein 4 (Rbbp4)	0.64
<i>Rbbp7</i>	XR_031862.1	retinoblastoma binding protein 7 (Rbbp7)	0.57
<i>Rbl1</i>	XR_004752.1	retinoblastoma-like 1 (p107) (Rbl1)	0.39
<i>Rbm13</i>	XR_033501.1	RNA binding motif protein 13 (Rbm13)	0.37
<i>Rbm15</i>	XM_001480472.1		0.61
<i>Rbms3</i>	XR_033663.1	RNA binding motif, single stranded interacting protein (Rbms3)	0.55
<i>Rbmx</i>	XM_904332.3	RNA binding motif protein, X chromosome (Rbmx)	0.31
<i>Rbx1</i>	XR_001819.2	ring-box 1 (Rbx1)	0.60
<i>Rcc1</i>	XR_030945.1	regulator of chromosome condensation 1 (Rcc1)	0.54
<i>Rcl1</i>	XR_031205.1	RNA terminal phosphate cyclase-like 1 (Rcl1)	0.63
<i>Rdh11</i>	XM_906862.3		0.53
<i>Reps1</i>	XR_031426.1	RalBP1 associated Eps domain containing protein (Reps1)	0.52
<i>Rerg</i>	XM_921371.2	RAS-like, estrogen-regulated, growth-inhibitor (Rerg)	0.35
<i>Rev3l</i>	XM_907756.3	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae) (Rev3l)	0.59
<i>Rfc1</i>	XR_003906.1	replication factor C (activator 1) 1 (Rfc1)	0.67
<i>Rfc2</i>	XM_915945.3	replication factor C (activator 1) 2 (Rfc2)	0.60
<i>Rfc3</i>	XM_915073.1		0.65
<i>Rfc4</i>	XM_915139.3		0.33
<i>Rfc5</i>	XM_916567.2	replication factor C (activator 1) 5 (Rfc5)	0.55
<i>Rgl1</i>	XM_925296.2	ral guanine nucleotide dissociation stimulator,-like 1 (Rgl1)	0.59
<i>Rgs7</i>	NR_002690.1	regulator of G protein signaling 7 (Rgs7)	0.35
<i>Rgs7bp</i>	NR_002885.1	regulator of G-protein signalling 7 binding protein (Rgs7bp)	0.47
<i>Rhbd1</i>	NM_001081681.1	rhomboid family 1 (Drosophila) (Rhbd1)	0.59
<i>Rhobtb2</i>	XM_973311.2	Rho-related BTB domain containing 2 (Rhobtb2)	0.58
<i>Rhoc</i>	XM_991641.1	ras homolog gene family, member C (Rhoc)	0.57
<i>Rhoj</i>	XR_031650.1	ras homolog gene family, member J (Rhoj)	0.64
<i>Rhot2</i>	XR_031476.1	ras homolog gene family, member T2 (Rhot2), nuclear gene encoding mitochondrial protein	0.64
<i>Riok3</i>	XR_031065.1	RIO kinase 3 (yeast) (Riok3)	0.63
<i>Rn18s</i>	XR_031145.1	18S RNA (Rn18s), non-coding RNA.	0.28
<i>Rnaseh2b</i>	XR_030655.1	ribonuclease H2, subunit B (Rnaseh2b)	0.57
<i>Rnf14</i>	XR_030797.1	ring finger protein 14 (Rnf14)	0.62
<i>Rnf145</i>	XR_032081.1	ring finger protein 145 (Rnf145)	0.65
<i>Rnf26</i>	XM_001480084.1	ring finger protein 26 (Rnf26)	0.42
<i>Rnf4</i>	XR_034201.1	ring finger protein 4 (Rnf4)	0.63
<i>Rnf44</i>	XM_001000226.2	ring finger protein 44 (Rnf44)	0.53
<i>Rnps1</i>	XR_031651.1		0.54
<i>Robo1</i>	XR_034647.1	roundabout homolog 1 (Drosophila) (Robo1)	0.40
<i>Rpa3</i>	XR_035016.1	replication protein A3 (Rpa3)	0.46
<i>Rpl10a</i>	XM_001003212.2	ribosomal protein L10A (Rpl10a)	0.48
<i>Rpl12</i>	XM_976371.1	ribosomal protein L12 (Rpl12)	0.30
<i>Rpl13a</i>	XM_987550.1	ribosomal protein L13a (Rpl13a)	0.26
<i>Rpl18</i>	XM_001479052.1	ribosomal protein L18 (Rpl18)	0.42
<i>Rpl18a</i>	XM_001473434.1	Ribosomal protein L18A (Rpl18a)	0.42
<i>Rpl19</i>	XM_993721.1	ribosomal protein L19 (Rpl19)	0.37
<i>Rpl23</i>	XM_980150.1	ribosomal protein L23 (Rpl23)	0.58
<i>Rpl24</i>	XR_005113.2	ribosomal protein L24 (Rpl24)	0.62
<i>Rpl26</i>	XM_001479274.1	ribosomal protein L26 (Rpl26)	0.49
<i>Rpl27</i>	XM_001481199.1	ribosomal protein L27 (Rpl27)	0.45
<i>Rpl27a</i>	XR_032773.1	ribosomal protein L27a (Rpl27a)	0.30
<i>Rpl28</i>	XM_985882.1		0.43

<i>Rpl29</i>	XM_001003712.1	ribosomal protein L29 (Rpl29)	0.41
<i>Rpl3</i>	XM_992449.1	ribosomal protein L3 (Rpl3)	0.64
<i>Rpl30</i>	XM_001003154.1	ribosomal protein L30 (Rpl30)	0.54
<i>Rpl31</i>	XR_034818.1	ribosomal protein L31 (Rpl31)	0.46
<i>Rpl32</i>	XM_001001408.2		0.42
<i>Rpl34</i>	XM_001001411.2	ribosomal protein L34 (Rpl34), transcript variant 1	0.54
<i>Rpl35</i>	XM_001004685.1	ribosomal protein L35 (Rpl35)	0.40
<i>Rpl36a</i>	XR_005046.1	ribosomal protein L36a (Rpl36a)	0.37
<i>Rpl36al</i>	XM_001002943.1	ribosomal protein L36a-like (Rpl36al)	0.42
<i>Rpl37</i>	XR_005062.2	ribosomal protein L37 (Rpl37)	0.57
<i>Rpl38</i>	XR_005084.2	ribosomal protein L38 (Rpl38), transcript variant 1	0.59
<i>Rpl39</i>	NM_008508.2	ribosomal protein L39 (Rpl39)	0.46
<i>Rpl4</i>	NM_008509.2	ribosomal protein L4 (Rpl4)	0.38
<i>Rpl41</i>	NM_008377.2	ribosomal protein L41 (Rpl41)	0.63
<i>Rpl711</i>	NM_172814.1	ribosomal protein L7-like 1 (Rpl711)	0.65
<i>Rpl9</i>	NM_001081088.1	ribosomal protein L9 (Rpl9)	0.62
<i>Rplp0</i>	NM_001033371.2	ribosomal protein, large, P0 (Rplp0)	0.52
<i>Rplp1</i>	NM_029044.2	ribosomal protein, large, P1 (Rplp1)	0.51
<i>Rplp2</i>	XM_890234.2	ribosomal protein, large P2 (Rplp2)	0.43
<i>Rpn2</i>	NM_133807.1	ribophorin II (Rpn2)	0.47
<i>Rpp21</i>	NM_177725.2	ribonuclease P 21 subunit (human) (Rpp21)	0.60
<i>Rprm</i>	NM_008515.1	reprimo, TP53 dependent G2 arrest mediator candidate (Rprm)	0.40
<i>Rps10</i>	NM_008516.2	ribosomal protein S10 (Rps10)	0.50
<i>Rps11</i>	NM_178069.5	ribosomal protein S11 (Rps11)	0.52
<i>Rps12</i>	NM_026032.1		0.43
<i>Rps13</i>	NM_172947.1	ribosomal protein S13 (Rps13)	0.41
<i>Rps15</i>	NM_030597.2	ribosomal protein S15 (Rps15)	0.51
<i>Rps16</i>	NM_026309.1	ribosomal protein S16 (Rps16)	0.40
<i>Rps19</i>	NM_015816.1	ribosomal protein S19 (Rps19)	0.48
<i>Rps2</i>	NM_025520.2	ribosomal protein S2 (Rps2)	0.53
<i>Rps21</i>	NM_030145.2	ribosomal protein S21 (Rps21)	0.58
<i>Rps24</i>	NM_133939.1	ribosomal protein S24 (Rps24), transcript variant 1	0.61
<i>Rps25</i>	NM_146006.1	ribosomal protein S25 (Rps25)	0.45
<i>Rps26</i>	NM_206958.1	ribosomal protein S26 (Rps26)	0.40
<i>Rps27a</i>	NM_138680	ribosomal protein S27a (Rps27a), transcript variant 2	0.45
<i>Rps27l</i>	NM_178705.5	ribosomal protein S27-like (Rps27l)	0.55
<i>Rps29</i>	NM_016753.4	ribosomal protein S29 (Rps29)	0.53
<i>Rps3</i>	NM_016923.1		0.49
<i>Rps3a</i>	NM_025281.2	ribosomal protein S3a (Rps3a)	0.56
<i>Rps4x</i>	NM_145100.3	ribosomal protein S4, X-linked (Rps4x)	0.53
<i>Rps5</i>	NM_011942.1	ribosomal protein S5 (Rps5)	0.41
<i>Rps6</i>	NM_134147.3	ribosomal protein S6 (Rps6)	0.50
<i>Rps6ka1</i>	NM_019499.2	ribosomal protein S6 kinase polypeptide 1 (Rps6ka1)	0.61
<i>Rps7</i>	NM_025649.1	ribosomal protein S7 (Rps7)	0.48
<i>Rps8</i>	NM_019791.2	ribosomal protein S8 (Rps8)	0.49
<i>Rps9</i>	NM_023788.3	ribosomal protein S9 (Rps9)	0.62
<i>Rrbp1</i>	NM_026453.3	ribosome binding protein 1 (Rrbp1), transcript variant 2	0.23
<i>Rrm1</i>	NM_207237		0.33
<i>Rrm2</i>	NM_008549.1	ribonucleotide reductase M2 (Rrm2)	0.30
<i>Rrp12</i>	NM_027288.2	ribosomal RNA processing 12 homolog (S. cerevisiae) (Rrp12)	0.66
<i>Rrp15</i>	NM_026160.3	ribosomal RNA processing 15 homolog (S. cerevisiae) (Rrp15)	0.54
<i>Rrp1b</i>	NM_023138.3	ribosomal RNA processing 1 homolog B (S. cerevisiae) (Rrp1b)	0.63
<i>Rrp9</i>	NM_008928.3	RRP9, small subunit (SSU) processome component, homolog (yeast) (Rrp9)	0.63
<i>Rsl1d1</i>	NM_009157.2	ribosomal L1 domain containing 1 (Rsl1d1)	0.49
<i>Rtkn2</i>	NM_022012.3	rhotekin 2 (Rtkn2)	0.54
<i>Rtn3</i>	NM_138667.2		0.55
<i>Rtn4r11</i>	NM_008696.2	reticulum 4 receptor-like 1 (Rtn4r11)	0.57
<i>Ruvb1</i>	NM_178684.5	RuvB-like protein 1 (Ruvb1)	0.66
<i>Ruvb2</i>	NM_172632.2	RuvB-like protein 2 (Ruvb2)	0.53
<i>Rwdd1</i>	NM_027418.1	RWD domain containing 1 (Rwdd1)	0.58
<i>Rybp</i>	NM_011162.2	RING1 and YY1 binding protein (Rybp)	0.66
<i>Ryk</i>	NM_021921.2	receptor-like tyrosine kinase (Ryk), transcript variant 2	0.53
<i>Saal1</i>	NM_010838.2	PREDICTED: serum amyloid A-like 1, transcript variant 1 (Saal1)	0.63
<i>Sacm11</i>	NM_010807.3	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae) (Sacm11)	0.43
<i>Sae1</i>	NM_008641.2	SUMO1 activating enzyme subunit 1 (Sae1)	0.58
<i>Sall3</i>	NM_013592.2	sal-like 3 (Drosophila) (Sall3)	0.65
<i>Sap30</i>	NM_013595.2	sin3 associated polypeptide (Sap30)	0.42
<i>Sart3</i>	NM_020007.3	squamous cell carcinoma antigen recognized by T-cells 3 (Sart3)	0.62
<i>Sc4mol</i>	NM_153546.3	sterol-C4-methyl oxidase-like (Sc4mol)	0.31
<i>Scd1</i>	NM_026037.2	stearoyl-Coenzyme A desaturase 1 (Scd1)	0.52
<i>sci000118.1_0</i>	NM_139295.2		0.57

<i>scI0001284.1_18</i>	NM_008562.3		0.61
<i>scI0001849.1_2273</i>	NM_027290.1		0.33
<i>scI0001978.1_6</i>	NM_008564.1		0.59
<i>scI0002315.1_12</i>	NM_008563.2		0.63
<i>scI0002507.1_236</i>	NM_008565.2		0.60
<i>scI0002624.1_576</i>	NM_008566.2		0.56
<i>scI0002791.1_134</i>	NM_008567.1		0.65
<i>scI0004020.1_31</i>	NM_008568.2		0.65
<i>Scml4</i>	NM_207010.1	sex comb on midleg-like 4 (<i>Drosophila</i>) (<i>Scml4</i>)	0.48
<i>Scoc</i>	NM_008618.2	short coiled-coil protein (<i>Scoc</i>), transcript variant 2	0.55
<i>Scye1</i>	NM_029696.3	small inducible cytokine subfamily E, member 1 (<i>Scye1</i>)	0.65
<i>Sdc3</i>	NM_008617.2	syndecan 3 (<i>Sdc3</i>)	0.35
<i>Sdhb</i>	NM_138596.1	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (<i>Sdhb</i>), nuclear gene encoding mitochondrial protein	0.45
<i>Sdhd</i>	NM_008581	succinate dehydrogenase complex, subunit D, integral membrane protein (<i>Sdhd</i>), nuclear gene encoding mitochondrial protein	0.60
<i>Sdpr</i>	NM_010790.2	serum deprivation response (<i>Sdpr</i>)	0.51
<i>Sec11a</i>	NM_008590.1	SEC11 homolog A (<i>S. cerevisiae</i>) (<i>Sec11a</i>)	0.64
<i>Sec11c</i>	NM_175224.4	SEC11 homolog C (<i>S. cerevisiae</i>) (<i>Sec11c</i>)	0.44
<i>Sec13</i>	NM_133719	SEC13 homolog (<i>S. cerevisiae</i>) (<i>Sec13</i>)	0.54
<i>Sec61g</i>	NM_021554.2	SEC61, gamma subunit (<i>Sec61g</i>)	0.57
<i>Sec63</i>	NM_001029890.1	SEC63-like (<i>S. cerevisiae</i>) (<i>Sec63</i>)	0.53
<i>Seh1l</i>	NM_008594	SEH1-like (<i>S. cerevisiae</i>) (<i>Seh1l</i>), transcript variant 1	0.60
<i>Sema3a</i>	NM_001081279.1	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (<i>Sema3a</i>)	0.63
<i>Sema5a</i>	NM_024200.2		0.56
<i>Sept2</i>	NM_145486.4	septin 2 (<i>Sept2</i>)	0.60
<i>Sept6</i>	NM_010891.1	septin 6 (<i>Sept6</i>)	0.57
<i>Sept9</i>	NM_011889.2	septin 9 (<i>Sept9</i>)	0.13
<i>Sept11</i>	NM_019942.2	septin 11 (<i>Sept11</i>)	0.38
<i>Serbp1</i>	NM_001081259.1	Serpine1 mRNA binding protein 1 (<i>Serbp1</i>)	0.49
<i>Serf2</i>	NM_011844.3	small EDRK-rich factor 2 (<i>Serf2</i>)	0.61
<i>Serpine2</i>	NM_019946.3	serine (or cysteine) peptidase inhibitor, clade E, member 2 (<i>Serpine2</i>)	0.49
<i>Set</i>	NM_019394		0.60
<i>Setd8</i>	NM_026524.2	SET domain containing (lysine methyltransferase) 8 (<i>Setd8</i>)	0.66
<i>Sf3a1</i>	NM_010798.2	splicing factor 3a, subunit 1 (<i>Sf3a1</i>)	0.60
<i>Sf3a3</i>	XM_001000692.2	splicing factor 3a, subunit 3 (<i>Sf3a3</i>)	0.63
<i>Sf3b3</i>	NM_026472.3	splicing factor 3b, subunit 3 (<i>Sf3b3</i>)	0.51
<i>Sf3b4</i>	AK129109	splicing factor 3b, subunit 4 (<i>Sf3b4</i>)	0.51
<i>Sf3b5</i>	NM_021527.1		0.64
<i>Sfrs1</i>	NM_021462.3	splicing factor, arginine/serine-rich 1 (ASF/SF2) (<i>Sfrs1</i>), transcript variant 1	0.55
<i>Sfrs10</i>	NM_001039684.2	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, <i>Drosophila</i>) (<i>Sfrs10</i>)	0.46
<i>Sfrs11</i>	NM_133241.2	splicing factor, arginine/serine-rich 11 (<i>Sfrs11</i>), transcript variant 1	0.48
<i>Sfrs2</i>	NM_010801.1	splicing factor, arginine/serine-rich 2 (SC-35) (<i>Sfrs2</i>)	0.39
<i>Sfrs4</i>	XM_485570	splicing factor, arginine/serine-rich 4 (SRp75) (<i>Sfrs4</i>)	0.64
<i>Sfrs9</i>	NM_019914.3	splicing factor, arginine/serine rich 9 (<i>Sfrs9</i>)	0.47
<i>Sfxn1</i>	NM_026178.2	sideroflexin 1 (<i>Sfxn1</i>)	0.60
<i>Sgk1</i>	NM_175217.6	serum/glucocorticoid regulated kinase 1 (<i>Sgk1</i>)	0.45
<i>Sgk3</i>	NM_008608.2	serum/glucocorticoid regulated kinase 3 (<i>Sgk3</i>), transcript variant 1	0.64
<i>Sgol1</i>	NM_008609.3	shugoshin-like 1 (<i>S. pombe</i>) (<i>Sgol1</i>)	0.51
<i>Sgol2</i>	NM_011846.4	shugoshin-like 2 (<i>S. pombe</i>) (<i>Sgol2</i>)	0.34
<i>Sgpp1</i>	NM_008610.2	sphingosine-1-phosphate phosphatase 1 (<i>Sgpp1</i>)	0.52
<i>Sh3glb1</i>	NM_010808.3	SH3-domain GRB2-like B1 (endophilin) (<i>Sh3glb1</i>)	0.65
<i>Sh3glb2</i>	NM_008615.1	SH3-domain GRB2-like endophilin B2 (<i>Sh3glb2</i>)	0.50
<i>Sh3pxd2b</i>	NM_029309.2	SH3 and PX domains 2B (<i>Sh3pxd2b</i>)	0.39
<i>Shc1</i>	NM_010820.2	src homology 2 domain-containing transforming protein C1 (<i>Shc1</i>)	0.66
<i>Shmt1</i>	NM_026758.3		0.38
<i>Sipa1l2</i>	NM_001081323.1	signal-induced proliferation-associated 1 like 2 (<i>Sipa1l2</i>)	0.66
<i>Siva1</i>	NM_025837.2	SIVA1, apoptosis-inducing factor (<i>Siva1</i>)	0.48
<i>Skil</i>	NM_026530.5	SKI-like (<i>Skil</i>), transcript variant 2	0.52
<i>Skiv2l2</i>	NM_019939.1	superkiller viralicidic activity 2-like 2 (<i>S. cerevisiae</i>) (<i>Skiv2l2</i>)	0.50
<i>Skp2</i>	NM_033564.2	S-phase kinase-associated protein 2 (p45) (<i>Skp2</i>), transcript variant 2	0.32
<i>Slain2</i>	NM_008624.3	SLAIN motif family, member 2 (<i>Slain2</i>)	0.65
<i>Slc12a2</i>	NM_018736.2	solute carrier family 12, member 2 (<i>Slc12a2</i>)	0.62
<i>Slc19a2</i>	NM_026154.1	solute carrier family 19 (thiamine transporter), member 2 (<i>Slc19a2</i>)	0.57
<i>Slc1a4</i>	NM_027204.2	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (<i>Slc1a4</i>)	0.47
<i>Slc25a11</i>	AK003026	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11 (<i>Slc25a11</i>), nuclear gene encoding mitochondrial protein	0.57

<i>Slc25a19</i>	NM_025301.1	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 (Slc25a19), nuclear gene encoding mitochondrial protein	0.64
<i>Slc25a25</i>	NM_026310.3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 (Slc25a25), nuclear gene encoding mitochondrial protein	0.27
<i>Slc25a3</i>	NM_025302.3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 (Slc25a3)	0.53
<i>Slc25a38</i>	NM_025570.2	solute carrier family 25, member 38 (Slc25a38)	0.61
<i>Slc25a39</i>	NM_175001.2	solute carrier family 25, member 39 (Slc25a39)	0.43
<i>Slc25a5</i>	NM_011288.1	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (Slc25a5), nuclear gene encoding mitochondrial protein	0.59
<i>Slc29a1</i>	NM_053159.3	solute carrier family 29 (nucleoside transporters), member 1 (Slc29a1)	0.53
<i>Slc30a5</i>	NM_027098.2	solute carrier family 30 (zinc transporter), member 5 (Slc30a5)	0.59
<i>Slc30a7</i>	NM_053162.2	solute carrier family 30 (zinc transporter), member 7 (Slc30a7)	0.65
<i>Slc31a1</i>	NM_025500.1	solute carrier family 31, member 1 (Slc31a1)	0.56
<i>Slc35c2</i>	NM_024177.3	solute carrier family 35, member C2 (Slc35c2)	0.53
<i>Slc35e1</i>	NM_010922.1	solute carrier family 35, member E1 (Slc35e1)	0.58
<i>Slc35f3</i>	NM_053164.3	solute carrier family 35, member F3 (Slc35f3)	0.51
<i>Slc38a10</i>	NM_029017.1	solute carrier family 38, member 10 (Slc38a10)	0.57
<i>Slc39a6</i>	NM_178603.4	solute carrier family 39 (metal ion transporter), member 6 (Slc39a6)	0.56
<i>Slc39a7</i>	NM_026851.2	solute carrier family 39 (zinc transporter), member 7 (Slc39a7), transcript variant 1	0.65
<i>Slc41a2</i>	NM_026744.3	solute carrier family 41, member 2 (Slc41a2)	0.52
<i>Slc4a4</i>	NM_025317.2	solute carrier family 4 (anion exchanger), member 4 (Slc4a4)	0.61
<i>Slc4a7</i>	NM_183086		0.44
<i>Slc4a8</i>	NM_025440.2	solute carrier family 4 (anion exchanger), member 8 (Slc4a8)	0.60
<i>Slc6a1</i>	NM_025878.1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1 (Slc6a1)	0.64
<i>Slc6a6</i>	NM_026826.1	solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (Slc6a6)	0.26
<i>Slimap</i>	NM_080452.2	sarcolemma associated protein (Slimap)	0.64
<i>Slimo2</i>	NM_024174.5	slowmo homolog 2 (Drosophila) (Slimo2)	0.46
<i>Sltm</i>	NM_026080.2	SAFB-like, transcription modulator (Sltm), transcript variant 1	0.66
<i>Smad3</i>	NM_025434.2		0.63
<i>Smap2</i>	NM_021556.3	stromal membrane-associated GTPase-activating protein 2 (Smap2)	0.62
<i>Smc1a</i>	NM_020560.1	structural maintenance of chromosomes 1A (Smc1a)	0.59
<i>Smn1</i>	NM_145573.2	survival motor neuron 1 (Smn1)	0.52
<i>Smtn</i>	NM_025305.1	smoothelin (Smtn)	0.33
<i>Smyd2</i>	NM_023514.3	SET and MYND domain containing 2 (Smyd2)	0.63
<i>Snappc4</i>	NM_023536.2	small nuclear RNA activating complex, polypeptide 4 (Snappc4)	0.49
<i>Snca</i>	AK031365	synuclein, alpha (Snca), transcript variant 2	0.49
<i>Snora65</i>	NM_144898.1	small nucleolar RNA, H/ACA box 65 (Snora65) on chromosome 2.	0.65
<i>Snrpa</i>	NM_010835.2	small nuclear ribonucleoprotein polypeptide A (Snrpa), transcript variant 2	0.59
<i>Snrpb</i>	NM_008630.2	small nuclear ribonucleoprotein B (Snrpb)	0.45
<i>Snrpd1</i>	NM_013603.1	small nuclear ribonucleoprotein D1 (Snrpd1)	0.48
<i>Snrpd2</i>	NM_011842.3	small nuclear ribonucleoprotein D2 (Snrpd2)	0.58
<i>Snrpd3</i>	NM_024433.1	small nuclear ribonucleoprotein D3 (Snrpd3)	0.57
<i>Snrpf</i>	NM_173013.2	PREDICTED: small nuclear ribonucleoprotein polypeptide F (Snrpf)	0.37
<i>Snx9</i>	NM_144941.2	sorting nexin 9 (Snx9)	0.61
<i>Socs5</i>		suppressor of cytokine signaling 5 (Socs5)	0.36
<i>Sod2</i>	NM_019758.2		0.56
<i>Sorcs1</i>		VPS10 domain receptor protein SORCS 1 (Sorcs1)	0.43
<i>Sorcs2</i>	NM_026002.4	sorilin-related VPS10 domain containing receptor 2 (Sorcs2)	0.59
<i>Sox11</i>			0.42
<i>Sox5</i>		SRY-box containing gene 5 (Sox5)	0.61
<i>Spag5</i>	NM_008638	sperm associated antigen 5 (Spag5)	0.22
<i>Spag7</i>	NM_181409.2	sperm associated antigen 7 (Spag7)	0.63
<i>Spast</i>	NM_172958.3	spastin (Spast)	0.61
<i>Spata6</i>	NM_023858.1	spermatogenesis associated 6 (Spata6)	0.63
<i>Spc25</i>	NM_013604.1	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) (Spc25)	0.29
<i>Spcs3</i>	NM_138656.1	signal peptidase complex subunit 3 homolog (S. cerevisiae) (Spcs3)	0.48
<i>Specc1</i>	NM_024263.3	sperm antigen with calponin homology and coiled-coil domains 1 (Specc1)	0.45
<i>Spg7</i>	NM_016969.1	spastic paraplegia 7 homolog (human) (Spg7), nuclear gene encoding mitochondrial protein	0.64
<i>Sphk1</i>	NM_016776.2	sphingosine kinase 1 (Sphk1), transcript variant 1	0.47
<i>Spna2</i>	NM_008652.2		0.46
<i>Spp1</i>	NM_170671.1	secreted phosphoprotein 1 (Spp1)	0.26
<i>Spred1</i>	NM_010852.1		0.45
<i>Spry4</i>	NM_177369.3	sprouty homolog 4 (Drosophila) (Spry4)	0.31
<i>Spsb4</i>	NM_022410.1	sp1A/ryanodine receptor domain and SOCS box containing 4 (Spsb4)	0.23
<i>Sqle</i>	XM_977718.2	squalene epoxidase (Sqle)	0.50
<i>Srebf2</i>	NM_139300.3	sterol regulatory element binding factor 2 (Srebf2)	0.59

<i>Srgap2</i>	NM_010863.2	PREDICTED: SLIT-ROBO Rho GTPase activating protein 2, transcript variant 3 (Srgap2)	0.61
<i>Srm</i>	NM_010864.2	spermidine synthase (Srm)	0.41
<i>Srpk1</i>	NM_001039546.1	serine/arginine-rich protein specific kinase 1 (Srpk1)	0.58
<i>Srpr</i>	NM_017479.2	signal recognition particle receptor ('docking protein') (Srpr)	0.63
<i>Srprb</i>	NM_008665.3	signal recognition particle receptor, B subunit (Srprb)	0.64
<i>Srm2</i>	NM_001024917.1	serine/arginine repetitive matrix 2 (Srm2)	0.45
<i>Ssbp4</i>	AK050560		0.48
<i>Ssna1</i>	NM_026526.2	Sjogren's syndrome nuclear autoantigen 1 (Ssna1)	0.60
<i>Ssr3</i>	NM_008667.2	signal sequence receptor, gamma (Ssr3)	0.57
<i>Ssrp1</i>	NM_013608.2	structure specific recognition protein 1 (Ssrp1)	0.63
<i>Sssca1</i>	NM_001037098.1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human) (Sssca1)	0.53
<i>Ssu72</i>	NM_013792.1	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast) (Ssu72)	0.66
<i>St13</i>	NM_053179.3	suppression of tumorigenicity 13 (St13)	0.61
<i>St3gal3</i>	NM_015781.3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3 (St3gal3)	0.61
<i>St6gal1</i>	NM_021432.2	beta galactoside alpha 2,6 sialyltransferase 1 (St6gal1)	0.47
<i>St6galnac5</i>	NM_053089.2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1, 3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5 (St6galnac5)	0.62
<i>Stab1</i>	NM_027350.2	stabilin 1 (Stab1)	0.37
<i>Stag2</i>	NM_016777.2	stromal antigen 2 (Stag2), transcript variant 2	0.65
<i>Stambpl1</i>	NM_026425.1	Stam binding protein like 1 (Stambpl1)	0.35
<i>Stard4</i>	NM_173437	StAR-related lipid transfer (START) domain containing 4 (Stard4)	0.40
<i>Stau2</i>	NM_008675.1	staufen (RNA binding protein) homolog 2 (Drosophila) (Stau2), transcript variant 3	0.65
<i>Stc1</i>	NM_007789.2	stanniocalcin 1 (Stc1)	0.35
<i>Stim2</i>	NM_146171.1	stromal interaction molecule 2 (Stim2)	0.62
<i>Stip1</i>	NM_178113.2	stress-induced phosphoprotein 1 (Stip1)	0.47
<i>Stk17b</i>	NM_144818.1	serine/threonine kinase 17b (apoptosis-inducing) (Stk17b)	0.38
<i>Strap</i>	NM_011986.2	serine/threonine kinase receptor associated protein (Strap)	0.58
<i>Strn4</i>	NM_010880.3	striatin, calmodulin binding protein 4 (Strn4), transcript variant 1	0.66
<i>Stt3b</i>	NM_021607.2	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) (Stt3b)	0.66
<i>Stx4a</i>	NM_023294.1	syntaxin 4A (placental) (Stx4a)	0.53
<i>Stxbp1</i>	NM_022996.1	syntaxin binding protein 1 (Stxbp1)	0.48
<i>Suclg2</i>	NM_008681.2	succinate-Coenzyme A ligase, GDP-forming, beta subunit (Suclg2)	0.66
<i>Sulf2</i>	NM_013864	sulfatase 2 (Sulf2)	0.58
<i>Sumo2</i>	NM_008681	SMT3 suppressor of mif two 3 homolog 2 (yeast) (Sumo2)	0.53
<i>Sumo3</i>	NM_025551.3	SMT3 suppressor of mif two 3 homolog 3 (yeast) (Sumo3)	0.56
<i>Supt3h</i>	XM_001476048.1	suppressor of Ty 3 homolog (S. cerevisiae) (Supt3h)	0.64
<i>Supv311</i>	NM_025348.1	suppressor of var1, 3-like 1 (S. cerevisiae) (Supv311)	0.67
<i>Suz12</i>	NM_010886.1	suppressor of zeste 12 homolog (Drosophila) (Suz12)	0.50
<i>Sv2a</i>	NM_026614.2	synaptic vesicle glycoprotein 2 a (Sv2a)	0.39
<i>Swap70</i>	NM_025987.1	SWA-70 protein (Swap70)	0.62
<i>Syde1</i>	NM_026703.2	PREDICTED: synapse defective 1, Rho GTPase, homolog 1 (C. elegans) (Syde1)	0.63
<i>Syncrip</i>	NM_025358.2	synaptotagmin binding, cytoplasmic RNA interacting protein (Syncrip), transcript variant 2	0.59
<i>Tada1l</i>	XM_128594.4	transcriptional adaptor 1 (HFI1 homolog, yeast) like (Tada1l)	0.59
<i>Taf10</i>	NM_025597.2	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor (Taf10)	0.52
<i>Taf12</i>	NM_025316.2		0.56
<i>Taf9</i>	NM_001033305.2	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor (Taf9), transcript variant 1	0.49
<i>Tagap</i>	NM_026061.2	T-cell activation Rho GTPase-activating protein (Tagap)	0.59
<i>Tagln2</i>	NM_025523.1	transgelin 2 (Tagln2)	0.51
<i>Tanc1</i>	NM_024220.1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 (Tanc1)	0.46
<i>Tank</i>	NM_153064.4	TRAF family member-associated Nf-kappa B activator (Tank)	0.66
<i>Tbc1d1</i>	NM_026688.2	TBC1 domain family, member 1 (Tbc1d1)	0.40
<i>Tbca</i>	NM_010887.1	tubulin cofactor a (Tbca)	0.60
<i>Tbrg4</i>	NM_029272.3	transforming growth factor beta regulated gene 4 (Tbrg4)	0.39
<i>Tceal8</i>	NM_144870.4	transcription elongation factor A (SII)-like 8 (Tceal8)	0.66
<i>Tcerg1</i>	NM_133666.2	transcription elongation regulator 1 (CA150) (Tcerg1)	0.52
<i>Tcf12</i>	NM_028388.1	transcription factor 12 (Tcf12)	0.52
<i>Tcf4</i>	NM_026267.1	transcription factor 4 (Tcf4), transcript variant 1	0.60
<i>Tcn2</i>	NM_008682	transcobalamin 2 (Tcn2)	0.64
<i>Tcp1</i>	NM_031881.1	t-complex protein 1 (Tcp1)	0.37
<i>Tead2</i>	NM_017464.2	TEA domain family member 2 (Tead2)	0.45
<i>Tfdp1</i>	XM_973899.1		0.48
<i>Tfg</i>	NM_011848.2	Trk-fused gene (Tfg)	0.61
<i>Tfrc</i>	NM_177898.4	transferrin receptor (Tfrc)	0.44

<i>Thap4</i>	NM_145138.1	THAP domain containing 4 (Thap4)	0.66
<i>Them2</i>	NM_016701.3	thioesterase superfamily member 2 (Them2)	0.65
<i>Thoc4</i>	NM_001081324.1	THO complex 4 (Thoc4)	0.35
<i>Thoc7</i>	NM_010893.2	THO complex 7 homolog (Drosophila) (Thoc7), transcript variant 1	0.48
<i>Thumpd1</i>	NM_021360	THUMP domain containing 1 (Thumpd1)	0.58
<i>Thyn1</i>	NM_010901.2	thymocyte nuclear protein 1 (Thyn1)	0.54
<i>Timeless</i>	NM_177176.2	timeless homolog (Drosophila) (Timeless), transcript variant 2	0.41
<i>Timm10</i>	NM_008687.2	translocase of inner mitochondrial membrane 10 homolog (yeast) (Timm10)	0.56
<i>Timm17a</i>	NM_030612.2	translocase of inner mitochondrial membrane 17a (Timm17a), nuclear gene enc	0.44
<i>Timm50</i>	NM_019867	translocase of inner mitochondrial membrane 50 homolog (yeast) (Timm50), nuc	0.62
<i>Timm8a1</i>	NM_025811.1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast) (Timm8a1)	0.49
<i>Timm8b</i>	NM_008695.2	translocase of inner mitochondrial membrane 8 homolog b (yeast) (Timm8b)	0.50
<i>Timm9</i>	NM_025391.1	translocase of inner mitochondrial membrane 9 homolog (yeast) (Timm9), nuclear gene encoding mitochondrial protein, transcript variant 1	0.54
<i>Timp1</i>	NM_025623.2	tissue inhibitor of metalloproteinase 1 (Timp1), transcript variant 2	0.31
<i>Timp4</i>	AK036043	tissue inhibitor of metalloproteinase 4 (Timp4)	0.22
<i>Tipin</i>	NM_029891.2	timeless interacting protein (Tipin)	0.41
<i>Tk1</i>	NM_010919.2	thymidine kinase 1 (Tk1)	0.19
<i>Tlcd1</i>	NM_008704.2	TLC domain containing 1 (Tlcd1)	0.50
<i>Tle2</i>	NM_008705.4	transducin-like enhancer of split 2, homolog of Drosophila E(spl) (Tle2)	0.57
<i>Tle6</i>	NM_019731.1	transducin-like enhancer of split 6, homolog of Drosophila E(spl) (Tle6)	0.17
<i>Tlk1</i>	NM_080637.3	tousled-like kinase 1 (Tlk1)	0.61
<i>Tmed3</i>	NM_138314.2	transmembrane emp24 domain containing 3 (Tmed3)	0.54
<i>Tmed9</i>	NM_026393.1	transmembrane emp24 protein transport domain containing 9 (Tmed9)	0.59
<i>Tmem109</i>	NM_008707.3	transmembrane protein 109 (Tmem109)	0.50
<i>Tmem11</i>	NM_021303.2	transmembrane protein 11 (Tmem11)	0.49
<i>Tmem126a</i>	NM_153570.2	transmembrane protein 126A (Tmem126a)	0.49
<i>Tmem132a</i>	NM_138747.1	transmembrane protein 132A (Tmem132a)	0.39
<i>Tmem147</i>	NM_001008421.1	transmembrane protein 147 (Tmem147)	0.66
<i>Tmem14c</i>	NM_018868.2	transmembrane protein 14C (Tmem14c)	0.57
<i>Tmem176a</i>	NM_024193.2	transmembrane protein 176A (Tmem176a)	0.23
<i>Tmem176b</i>	NM_026578.2	transmembrane protein 176B (Tmem176b)	0.29
<i>Tmem184b</i>	NM_026631.3	transmembrane protein 184b (Tmem184b)	0.56
<i>Tmem185b</i>	NM_025403.2	transmembrane protein 185B (Tmem185b)	0.60
<i>Tmem199</i>	NM_153057.3	transmembrane protein 199 (Tmem199)	0.58
<i>Tmem41a</i>	NM_020043.2	transmembrane protein 41a (Tmem41a)	0.56
<i>Tmem44</i>	NM_028995.3	transmembrane protein 44 (Tmem44)	0.43
<i>Tmem48</i>	NM_023409.4	transmembrane protein 48 (Tmem48)	0.51
<i>Tmem49</i>	NM_008722.1	transmembrane protein 49 (Tmem49)	0.41
<i>Tmem55a</i>	NM_008723.1	transmembrane protein 55A (Tmem55a)	0.64
<i>Tmem55b</i>	NR_002702.1	transmembrane protein 55b (Tmem55b)	0.48
<i>Tmem56</i>	NM_009145.1	transmembrane protein 56 (Tmem56)	0.62
<i>Tmem63b</i>	NM_008730.2	transmembrane protein 63b (Tmem63b)	0.51
<i>Tmem68</i>	NM_020282.2	transmembrane protein 68 (Tmem68)	0.48
<i>Tmem70</i>	NM_001025587.1	transmembrane protein 70 (Tmem70), transcript variant 1	0.61
<i>Tmem88</i>	NM_010150.2	transmembrane protein 88 (Tmem88)	0.56
<i>Tmem97</i>	NM_025980.2	transmembrane protein 97 (Tmem97)	0.27
<i>Tmpo</i>	NM_144847.1	thymopoietin (Tmpo), transcript variant 6	0.62
<i>Tmsb10</i>	NM_176930.3	thymosin, beta 10 (Tmsb10)	0.63
<i>Tmsb4x</i>	NM_146150.2	thymosin, beta 4, X chromosome (Tmsb4x)	0.58
<i>Tnc</i>	NM_134122.2	tenascin C (Tnc)	0.04
<i>Tnfaip8</i>	NM_153529.1	tumor necrosis factor, alpha-induced protein 8 (Tnfaip8)	0.59
<i>Tnfrsf10b</i>	NM_008737.1	tumor necrosis factor receptor superfamily, member 10b (Tnfrsf10b)	0.62
<i>Tnfrsf12a</i>	NM_172544.2	tumor necrosis factor receptor superfamily, member 12a (Tnfrsf12a)	0.44
<i>Tnfrsf21</i>	NM_016710.2	tumor necrosis factor receptor superfamily, member 21 (Tnfrsf21)	0.36
<i>Tomm22</i>	NM_010941.3	translocase of outer mitochondrial membrane 22 homolog (yeast) (Tomm22), nuclear gene encoding mitochondrial protein	0.55
<i>Tomm40l</i>	NM_011732	translocase of outer mitochondrial membrane 40 homolog-like (yeast) (Tomm40l), nuclear gene encoding mitochondrial protein	0.54
<i>Tomm70a</i>	NM_198326.2	translocase of outer mitochondrial membrane 70 homolog A (yeast) (Tomm70a)	0.66
<i>Top2a</i>	NM_008741.1	topoisomerase (DNA) II alpha (Top2a)	0.16
<i>Tpi1</i>	NM_015807.1	triosephosphate isomerase 1 (Tpi1)	0.40
<i>Tpm3</i>	NM_027289.1	tropomyosin 3, gamma (Tpm3)	0.39
<i>Tpm4</i>	NM_010946.2	tropomyosin 4 (Tpm4)	0.46
<i>Tpr</i>	NM_001025074.1	translocated promoter region (Tpr)	0.64
<i>Tpst1</i>	NM_008747.2	protein-tyrosine sulfotransferase 1 (Tpst1), transcript variant 2	0.61
<i>Tpx2</i>	NM_001004363.1	TPX2, microtubule-associated protein homolog (Xenopus laevis) (Tpx2)	0.31
<i>Traf3</i>	NM_028778.3	Tnf receptor-associated factor 3 (Traf3), transcript variant 1	0.58
<i>Traf4</i>	NM_011955.1	Tnf receptor associated factor 4 (Traf4)	0.49
<i>Trak2</i>	NM_008749.1	trafficking protein, kinesin binding 2 (Trak2)	0.52
<i>Tram1</i>	NM_010948.1	translocating chain-associating membrane protein 1 (Tram1)	0.55

<i>Trap1</i>	NM_001031664.1	TNF receptor-associated protein 1 (Trap1)	0.64
<i>Trappc1</i>	NM_033080.2	trafficking protein particle complex 1 (Trappc1)	0.63
<i>Trappc4</i>	NM_026623.3	trafficking protein particle complex 4 (Trappc4)	0.58
<i>Trf</i>	NM_016918.2	transferrin (Trf)	0.13
<i>Trib2</i>	NM_172288.1		0.31
<i>Trim27</i>	NM_021512.2	tripartite motif-containing 27 (Trim27)	0.65
<i>Trim28</i>	XM_133073.7	tripartite motif protein 28 (Trim28)	0.44
<i>Trim59</i>	NM_018815.1	tripartite motif-containing 59 (Trim59)	0.49
<i>Trim62</i>	NM_145706.1	tripartite motif-containing 62 (Trim62)	0.43
<i>Trim8</i>	NM_053074.1	tripartite motif protein 8 (Trim8)	0.43
<i>Trio</i>	NM_001002929.3		0.57
<i>Trip12</i>	NM_172394.2	thyroid hormone receptor interactor 12 (Trip12)	0.58
<i>Troap</i>	NM_030250.1	PREDICTED: trophinin associated protein (Troap)	0.30
<i>Trp53</i>	NM_001042652.1	transformation related protein 53 (Trp53)	0.55
<i>Trp53i11</i>	NM_008750.4	transformation related protein 53 inducible protein 11 (Trp53i11)	0.32
<i>Trp53inp2</i>	NM_008751.2	transformation related protein 53 inducible nuclear protein 2 (Trp53inp2)	0.42
<i>Tsen15</i>	NM_019761.4	tRNA splicing endonuclease 15 homolog (S. cerevisiae) (Tsen15)	0.67
<i>Tsfm</i>	NM_016978.1	Ts translation elongation factor, mitochondrial (Tsfm), nuclear gene encoding mitochondrial protein	0.65
<i>Tsg101</i>	NM_026950.3	tumor susceptibility gene 101 (Tsg101)	0.62
<i>Tspan12</i>	NM_011858.3	tetraspanin 12 (Tspan12)	0.57
<i>Tssc4</i>	NM_010956.3	tumor-suppressing subchromosomal transferable fragment 4 (Tssc4), transcript variant 2	0.58
<i>Ttc3</i>	NM_008760.2	tetratricopeptide repeat domain 3 (Ttc3)	0.66
<i>Ttc7b</i>	NM_139144.2	PREDICTED: tetratricopeptide repeat domain 7B, transcript variant 1 (Ttc7b)	0.51
<i>Ttc9c</i>	NM_025942.2	tetratricopeptide repeat domain 9C (Ttc9c)	0.63
<i>Ttyh3</i>	NM_173777.2	tweety homolog 3 (Drosophila) (Ttyh3)	0.46
<i>Tuba6</i>	NM_172907.2		0.36
<i>Tubb5</i>	NM_177068.3	tubulin, beta 5 (Tubb5)	0.39
<i>Tubb6</i>	NM_016968.4	tubulin, beta 6 (Tubb6)	0.26
<i>Tubg1</i>	NM_153122.2	tubulin, gamma 1 (Tubg1)	0.43
<i>Tufm</i>	NM_010098.2	Tu translation elongation factor, mitochondrial (Tufm), nuclear gene encoding mitochondrial protein	0.56
<i>Txn1</i>	NM_011014.2	thioredoxin 1 (Txn1)	0.28
<i>Txndc12</i>	NM_175423.3	thioredoxin domain containing 12 (endoplasmic reticulum) (Txndc12)	0.47
<i>Txn14</i>	NM_011959.2		0.58
<i>Txn14a</i>	NM_019716.1	thioredoxin-like 4A (Txn14a), transcript variant 2	0.63
<i>Tyms</i>	NM_025661.3	thymidylate synthase (Tyms)	0.34
<i>Tyms-ps</i>	NM_027881.1	thymidylate synthase, pseudogene (Tyms-ps), non-coding RNA.	0.37
<i>U2af1</i>	NM_024289		0.63
<i>U2af2</i>	NM_145525.2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 (U2af2)	0.55
<i>Uaca</i>	NM_175489.3	uveal autoantigen with coiled-coil domains and ankyrin repeats (Uaca)	0.55
<i>Uba1</i>	NM_011019.1	ubiquitin-like modifier activating enzyme 1 (Uba1)	0.53
<i>Uba2</i>	NM_172416.2	ubiquitin-like modifier activating enzyme 2 (Uba2)	0.53
<i>Ubap2</i>	NM_024188.5	ubiquitin-associated protein 2 (Ubap2)	0.62
<i>Ube2f</i>	NM_130885.2	ubiquitin-conjugating enzyme E2F (putative) (Ube2f)	0.50
<i>Ube2g1</i>	NM_175116.2	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans) (Ube2g1)	0.63
<i>Ube2k</i>	NM_011032.2	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast) (Ube2k)	0.59
<i>Ube2m</i>	NM_011119.3	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (Ube2m)	0.60
<i>Ube2q1</i>	NM_130881.2	ubiquitin-conjugating enzyme E2Q (putative) 1 (Ube2q1)	0.63
<i>Ube2t</i>	NM_027032.2	ubiquitin-conjugating enzyme E2T (putative) (Ube2t)	0.58
<i>Ube3c</i>	NM_001081170.1	ubiquitin protein ligase E3C (Ube3c)	0.64
<i>Ubfd1</i>	NM_008812.1	ubiquitin family domain containing 1 (Ubfd1)	0.66
<i>Ubr7</i>	NM_013625.1	ubiquitin protein ligase E3 component n-recogin 7 (putative) (Ubr7)	0.58
<i>Uchl5</i>	NM_008776.1	ubiquitin carboxyl-terminal esterase L5 (Uchl5)	0.54
<i>Uck2</i>	NM_027470.3	uridine-cytidine kinase 2 (Uck2)	0.35
<i>Ugcg</i>	XM_974900.1		0.53
<i>Uhrf1</i>	NM_023245.3	ubiquitin-like, containing PHD and RING finger domains, 1 (Uhrf1)	0.12
<i>Uhrf2</i>	NM_023792.1	ubiquitin-like, containing PHD and RING finger domains 2 (Uhrf2)	0.61
<i>Ung</i>	NM_145962.2	uracil DNA glycosylase (Ung), transcript variant 2	0.37
<i>Upp1</i>	NM_027995.2	uridine phosphorylase 1 (Upp1)	0.23
<i>Uqcr</i>	NM_007415.2	ubiquinol-cytochrome c reductase (6.4kD) subunit (Uqcr)	0.66
<i>Uqcrc1</i>	NM_054056.2	ubiquinol-cytochrome c reductase core protein 1 (Uqcrc1)	0.54
<i>Uqcrc2</i>	NM_023209.1	ubiquinol cytochrome c reductase core protein 2 (Uqcrc2)	0.62
<i>Uqcrh</i>	NM_001081251.1	ubiquinol-cytochrome c reductase hinge protein (Uqcrh)	0.53
<i>Usp1</i>	NM_011865.3	ubiquitin specific peptidase 1 (Usp1)	0.47
<i>Usp39</i>	NM_011042.1	ubiquitin specific peptidase 39 (Usp39)	0.63
<i>Usp11</i>	NM_021567.2	ubiquitin specific peptidase like 1 (Usp11)	0.62
<i>Utp111</i>	NM_011043.3	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) (Utp111)	0.55
<i>Uxt</i>	NM_001013753.1	ubiquitously expressed transcript (Uxt)	0.49

<i>Vamp3</i>	NM_018764.1	vesicle-associated membrane protein 3 (Vamp3)	0.60
<i>Vapa</i>	NM_001081377.1	vesicle-associated membrane protein, associated protein A (Vapa)	0.60
<i>Vapb</i>	NM_177546.2	vesicle-associated membrane protein, associated protein B and C (Vapb)	0.58
<i>Vars</i>	NM_024229.2	valyl-tRNA synthetase (Vars), nuclear gene encoding mitochondrial protein	0.46
<i>Vav3</i>	NM_001033313.3	vav 3 oncogene (Vav3), transcript variant 1	0.28
<i>Vbp1</i>	NM_026549.3	von Hippel-Lindau binding protein 1 (Vbp1)	0.57
<i>Vdac1</i>	NM_008808	voltage-dependent anion channel 1 (Vdac1)	0.54
<i>Vdac2</i>	NM_026840.2	voltage-dependent anion channel 2 (Vdac2)	0.26
<i>Vdac3</i>	NM_024221.3	voltage-dependent anion channel 3 (Vdac3)	0.57
<i>Vegfa</i>	NM_007952.2	vascular endothelial growth factor A (Vegfa), transcript variant 2	0.40
<i>Vegfb</i>	NM_028295.1	vascular endothelial growth factor B (Vegfb)	0.54
<i>Vegfc</i>	NM_145978.1	vascular endothelial growth factor C (Vegfc)	0.56
<i>Vkorc1</i>	NM_019417.2	vitamin K epoxide reductase complex, subunit 1 (Vkorc1)	0.64
<i>Vkorc111</i>	NM_019808.1	vitamin K epoxide reductase complex, subunit 1-like 1 (Vkorc111), transcript variant 1	0.48
<i>Vldlr</i>	NM_026131	very low density lipoprotein receptor (Vldlr)	0.45
<i>Vps29</i>	NM_178939.2	vacuolar protein sorting 29 (S. pombe) (Vps29)	0.51
<i>Vps36</i>	NM_019501.3	vacuolar protein sorting 36 (yeast) (Vps36)	0.29
<i>Vps54</i>	NM_020271.3	vacuolar protein sorting 54 (yeast) (Vps54)	0.57
<i>Vrk1</i>	NM_018884.1		0.44
<i>Wasf2</i>	XM_001481302.1		0.52
<i>Wbp11</i>	NM_008556.1	WW domain binding protein 11 (Wbp11)	0.57
<i>Wbscr17</i>	NM_023324.2	Williams-Beuren syndrome chromosome region 17 homolog (human) (Wbscr17)	0.53
<i>Wdr43</i>	NM_033602	PREDICTED: WD repeat domain 43, transcript variant 9 (Wdr43)	0.65
<i>Wdr51b</i>	NM_011070.3	WD repeat domain 51B (Wdr51b)	0.61
<i>Wdr74</i>	NM_001013369.1	WD repeat domain 74 (Wdr74)	0.60
<i>Wdr75</i>	NM_008825.3	WD repeat domain 75 (Wdr75)	0.55
<i>Wdr76</i>	NM_173019.5	WD repeat domain 76 (Wdr76)	0.54
<i>Wdr82</i>	NM_011072.3	WD repeat domain containing 82 (Wdr82)	0.62
<i>Wdr89</i>	NM_023418.2	PREDICTED: WD repeat domain 89, transcript variant 2 (Wdr89)	0.56
<i>Wdsof1</i>	NM_028273.1	WD repeats and SOF domain containing 1 (Wdsof1)	0.66
<i>Whsc1</i>	NM_008828.2		0.47
<i>Wsb2</i>	NM_025396.3	WD repeat and SOCS box-containing 2 (Wsb2)	0.34
<i>Wscd1</i>	NM_025954.3	WSC domain containing 1 (Wscd1)	0.41
<i>Wwp1</i>	NM_133757.2	WW domain containing E3 ubiquitin protein ligase 1 (Wwp1)	0.65
<i>Wwtr1</i>	NM_007531.2	WW domain containing transcription regulator 1 (Wwtr1)	0.60
<i>Xbp1</i>	NM_018774.3	X-box binding protein 1 (Xbp1)	0.46
<i>Xpnpep1</i>	NM_025408.2	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble (Xpnpep1)	0.54
<i>Xpo6</i>	NM_024250.3	exportin 6 (Xpo6)	0.64
<i>Xrcc6</i>	NM_028716.1	X-ray repair complementing defective repair in Chinese hamster cells 6 (Xrcc6)	0.50
<i>Yeats4</i>	NM_172674.2	YEATS domain containing 4 (Yeats4)	0.58
<i>Ywhab</i>	NM_026737.3	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (Ywhab)	0.58
<i>Ywhag</i>	NM_027642.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (Ywhag)	0.47
<i>Ywhah</i>	NM_011079.2	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah)	0.35
<i>Ywhaq</i>	NM_009344.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (Ywhaq)	0.62
<i>Zbtb7c</i>	NM_172992.2	zinc finger and BTB domain containing 7C (Zbtb7c)	0.54
<i>Zbtb8os</i>	NM_008835.1	zinc finger and BTB domain containing 8 opposite strand (Zbtb8os)	0.63
<i>Zc3hc1</i>	NM_001001983.1	zinc finger, C3HC type 1 (Zc3hc1)	0.62
<i>Zcrb1</i>	NM_146194	zinc finger CCHC-type and RNA binding motif 1 (Zcrb1)	0.63
<i>Zdhhc21</i>	NM_172453.1	zinc finger, DHHC domain containing 21 (Zdhhc21)	0.55
<i>Zdhhc6</i>	NM_011081.2	zinc finger, DHHC domain containing 6 (Zdhhc6), transcript variant 2	0.62
<i>Zeb1</i>	NM_029406.1	zinc finger E-box binding homeobox 1 (Zeb1)	0.31
<i>Zfp106</i>	NM_178149.4	zinc finger protein 106 (Zfp106)	0.63
<i>Zfp131</i>	NM_054051.1	zinc finger protein 131 (Zfp131)	0.63
<i>Zfp148</i>	NM_019640.4	zinc finger protein 148 (Zfp148)	0.58
<i>Zfp180</i>	NM_011256.1		0.65
<i>Zfp207</i>	NM_145131.1	zinc finger protein 207 (Zfp207)	0.62
<i>Zfp330</i>	NM_008853.1	zinc finger protein 330 (Zfp330)	0.54
<i>Zfp365</i>	NM_144859.2	zinc finger protein 365 (Zfp365)	0.41
<i>Zfp518b</i>	NM_013630.2	zinc finger protein 518B (Zfp518b)	0.63
<i>Zfp710</i>	NM_008862.3	zinc finger protein 710 (Zfp710)	0.48
<i>Zfp770</i>	XM_131934.4	zinc finger protein 770 (Zfp770)	0.51
<i>Znrd1</i>	NM_023058.3	zinc ribbon domain containing, 1 (Znrd1)	0.58
<i>Znrf2</i>	NM_178654.3	zinc and ring finger 2 (Znrf2)	0.26
<i>Zswim6</i>	NM_175464.2		0.60

Zwint
Zyx

NM_023196.2
NM_013737.2

zyxin (Zyx)

0.62
0.54