Supplemental Table 1:

Results of primary druggable genome v2 (DG2) Achilles heel siRNA screen in KMS11 multiple myeloma cells.
Results are provided per siRNA as a B-score centered on the median and normalized to the standard deviation.

All statistically validated vulnerable genes are listed in Table 1 in the paper; siRNA against other genes are unverified for sensitivity/specificity
(individual siRNA results may be inaccurate and should be examined within a robust statistical framework).

Entrez Gene	SYMBOL	Description	siRNA B_Score	Target Sequence	Vendor target annotation	Top refseq hit
1	A1BG	alpha-1-B glycoprotein	0.02	CAGAAGATGCGTATCAGTATT	NM_130786:	NM_130786:
1	A1BG	alpha-1-B glycoprotein	-1.38	CTGCGTCTACGTGGACCTGAA	NM_130786:	NM_130786:
2	A2M	alpha-2-macroglobulin	-4.22	ACGGATGAGCATGGCCTTGTA	NM_000014:	NM_000014:
2	A2M	alpha-2-macroglobulin	0.20	CACCAACTCAAAGATTCGTAA	NM_000014:	NM_000014:
53947	A4GALT	alpha 1,4-galactosyltransferase (globotriaosylceramide synthase)	0.85	AGGAGAATAATCAATAGAATA	NM_017436:	NM_017436:
53947	A4GALT	alpha 1,4-galactosyltransferase (globotriaosylceramide synthase)	1.32	CACGTGCTGGTCCTGATGAAA	NM_017436:	NM_017436:
13	AADAC	arylacetamide deacetylase (esterase)	0.67	TTGGCTGATGACAACAAATTA	NM_001086:	NM_001086:
13	AADAC	arylacetamide deacetylase (esterase)	1.06	CAGCCTCTTGATGTAGATTTA	NM_001086:	NM_001086:
22848	AAK1	AP2 associated kinase 1	-1.50	AACGTGAGTAGCGGTGATGTA	NM_014911:	NM_014911:
22848	AAK1	AP2 associated kinase 1	0.53	CCAGGTGGTAAACCTGATGAA	NM_014911:	NM_014911:
10157	AASS	aminoadipate-semialdehyde synthase	0.51	AACGATTGATCTTGTGGCTTA	NM_005763:	NM_005763:
10157	AASS	aminoadipate-semialdehyde synthase	0.50	AACGGTACATTACCTGATAAA	NM_005763:	NM_005763:
26574	AATF	apoptosis antagonizing transcription factor	0.07	TCGAGAACTCATAGAACGGAA	NM_012138:	NM_012138:
26574	AATF	apoptosis antagonizing transcription factor	-0.58	TTGGAAGGAAGGATCAAACTA	NM_012138:	NM_012138:
	AB095936		1.11	TCCGGGTGATTCACTATAGAA	AB095936	No hits found till 3 mismatches
18	ABAT	4-aminobutyrate aminotransferase	0.59	TCCCGATGATTCCATACGGAA	NM_000663:	NM_020686:NM_000663:
18	ABAT	4-aminobutyrate aminotransferase	-1.10	CACGCACTCTAAAGCCATTCA	NM_000663:	NM_020686:NM_000663:
19	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	-2.65	CCGGAACATGCTACAATACCA	NM_005502:	NM_005502:
19	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	0.29	CACCGACAATAAGCTGAATAA	NM_005502:	NM_005502:
10349	ABCA10	ATP-binding cassette, sub-family A (ABC1), member 10	0.63	AAAGAGATAAGCGTGCGTCAA	NM_080282:	NM_080282:
10349	ABCA10	ATP-binding cassette, sub-family A (ABC1), member 10	0.61	CAGCCTGTTAATCGTTAATAA	NM_080282:	NM_080282:
26154	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	-2.28	CAGGTGACTCCGATAATATAA	NM_015657:	NM_015657:
26154	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	-0.97	AAGCCTAATGATCCGACTTTA	NM_015657:	NM_015657:NM_173076:
20	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	-3.23	CTGGAAGAACGTGACGCTCAA	NM_001606:	NM_001606:
20	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	1.06	CTGGGTCAGTCCCGTATTTAT	NM_001606:	NM_001606:NM_212533:
21	ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	0.09	CCGCTTGAAGATTCAGTCGGA	NM_001089:	NM_001089:
21	ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	2.25	CCAAGTTTATCTCATCCTTTA	NM_001089:	NM_001089:
24	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	-1.42	AAGGAGCCCATTGTTGATGAA	NM_000350:	NM_000350:
24	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	-0.71	CCGTCTGAACATCACCTTCTA	NM_000350:	NM_000350:
23461	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	1.71	GTACGTAATGTTCCAATCTAA	NM_018672:	NM_018672:NM_172232:
23461	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	0.61	TGGCGAGCAATTCGAACTGCA	NM_018672:	NM_018672:NM_172232:
23460	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	1.68	ACGCGAGGCTCGCCATCGCAA	NM_080284:	NM_080284:NM_172346:
23460	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	1.80	AAGGATTACATTCTAGAGCTA	NM_080284:	NM_080284:NM_172346:
10347	ABCA7	ATP-binding cassette, sub-family A (ABC1), member 7	-0.59	CCCGGCCACGTGCGCATCAAA	NM_019112:	NM_019112:NM_033308:
10347	ABCA7	ATP-binding cassette, sub-family A (ABC1), member 7	0.80	GACGAGGATGTAGCCCGTGAA	NM_019112:	NM_019112:NM_033308:
10351	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	-0.03	TTCGTTAGCATGCAATGCCAA	NM_007168:	NM_007168:
10351	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	0.91	CTATCTGGCATTGGCGATTTA	NM_007168:	NM_007168:
10350	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	-0.06	TCGATAGTTGCTACTGATCTA	NM_080283:	NM_080283:NM_172386:
10350	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	-2.64	GAGGGCGATCATAGGGCATAA	NM_080283:	NM_080283:NM_172386:
5243	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	-0.60	ATCGAGTCACTGCCTAATAAA	NM_000927:	NM_000927:
5243	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.00	CACGGAAGGCCTAATGCCGAA	NM_000927:	NM_000927:
23456	ABCB10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	-3.24	TAGACCCTAAGAAGTAATTAA	NM_012089:	NM_012089:
23456	ABCB10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	-3.19	CTAGGTATTATTAAGAATGAA	NM_012089:	NM_012089:
8647	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	0.84	CGGGATGATAGTCAATTCCTT	NM_003742:	NM_003742:
8647	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	0.02	TCAGATCGGGATGATAGTCAA	NM_003742:	NM_003742:
5244	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	0.59	CCGACTGTCTACGGTCCGAAA	NM_000443:	NM_000443:NM_018849:NM_018850:
5244	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	-0.93	TCGGCATTTAGTGACAAAGAA	NM_000443:	NM_000443:NM_018849:NM_018850:
340273	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	1.95	TTGGAGAATATACGTACTATA	NM_178559:	NM_178559:
340273	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	-0.58	TACGTACTATAGTGTCATTAA	NM_178559:	NM_178559:
10058	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0.06	CAGGCTCTCAACTGTGGTCAA	NM_005689:	NM_005689:
10058	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	-2.04	CACCTACATTATCCAGCTGTA	NM_005689:	NM_005689:
22	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-2.24	AACCCTCATAGTATCTATTCA	NM_004299:	NM_004299:
22	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-0.48	AGCATTTATCTTGCTGGTCAA	NM_004299:	NM_004299:
11194	ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-3.83	AAGCTGGAAGCTTCCGATGAA	NM_007188:	NM_007188:
11194	ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	0.90	AGGAATTTAAGTCATCCTTCA	NM_007188:	NM_007188:
23457	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	2.53	CCCGGTCAATAAAGTGTACTA	NM_019624:	NM_019624:NM_203445:NM_203444:NM_019625:
23457	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	4.45	CTGCGTGACCACGGCCATCTA	NM_019624:	NM_019624:NM_203445:NM_203444:NM_019625:
4363	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	-1.62	CCGAGTGGAATTCCGGAACTA	NM_004996:	NM_004996:NM_019902:NM_019901:NM_019900:NM_019899:NM_019862:NM_019898:
4363	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	-0.96	TCGGATGTCATCTGAAATGGA	NM_004996:	NM_004996:NM_019902:NM_019901:NM_019900:NM_019899:NM_019862:NM_019898:
89845	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	0.01	AGCCCAGATTGTGGTAGATTA	NM_033450:	NM_033450:
89845	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	0.29	CTGCTGGTACCCGTCAACAAA	NM_033450:	NM_033450:
85320	ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	0.35	AGGCTACTTGATGGCTCTCAA	NM_032583:	NM_145186:NM_033151:NM_032583:
85320	ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	-1.84	CTCCTCCAGTTGGATCATCAA	NM_032583:	NM_145186:NM_033151:NM_032583:
94160	ABCC12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	-0.45	CGGTAGGAAATTACCCTGAAA	NM_033226:	NM_145188:NM_145190:NM_145189:NM_145187:NM_033226:
94160	ABCC12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	0.39	CCGGAAAGTCATCGTTAGGAA	NM_033226:	NM_145188:NM_145190:NM_145189:NM_145187:NM_033226:
150000	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13	1.08	CTCGCTTGAATGTATGCGATA	NM_138726:	NM_138726:
150000	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13	-0.30	TAGGGTTATCTACAATATAAA	NM_138726:	NM_138726:
1244	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	-2.38	CCGTATCAGGTTTGCCAGTTA	NM_000392:	NM_000392:
1244	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	-1.35	CTGGAGTACCTACAAGCAATA	NM_000392:	NM_000392:
8714	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	-0.43	AAGGGTGAAATCCGCATTGAT	NM_003786:	NM_020037:NM_020038:NM_003786:
8714	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.01	CCGGAATTATTCTGTGCGCTA	NM_003786:	NM_020037:NM_020038:NM_003786:
10257	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	0.07	GAGGTTAAAGACAGTCATATA	NM_005845:	NM_005845:
10257	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	-3.17	CTCCTAGTACTTAGAAATACA	NM_005845:	NM_005845:
10057	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.52	ATAGCCTATATTTACAGTGAA	NM_005688:	NM_005688:
10057	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	1.00	ATCCTTCACGATCAAACCTAA	NM_005688:	NM_005688:
368	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	-1.28	CACGTGTGCTGTGCTGAGCAA	NM_001171:	NM_001171:
368	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	-1.91	ACGGTTGACGTGGACATTCCA	NM_001171:	NM_001171:
6833	ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	0.89	CTAACTGTAAATCACTTGTAA	NM_000352:	NM_000352:
6833	ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	1.27	CAGCGGCACCATCCGATTTAA	NM_000352:	NM_000352:
10060	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	-1.01	CCCAAATTTGTTCGCCCACAA	NM_005691:	NM_005691:NM_020298:
10060	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	-1.02	CTGCATCTATAGCATCCATTA	NM_005691:	NM_005691:NM_020298:NM_020297:
215	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	0.02	CTCTTTCTACAGCCTAATTTA	NM_000033:	NM_000033:
215	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	-0.09	CCACCTCTTTCTACAGCCTAA	NM_000033:	NM_000033:
225	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	0.89	CACTCGAGAATTATAGCCAAT	NM_005164:	NM_005164:

225	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	-0.73	TCGCCTAGTAGACCACGCCTA	NM_005164:	NM_005164:
225	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	0.85	CACTCGAGAATTATAGCCAAT	NM_005164:	NM_005164:
225	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	0.08	TCGCCTAGTAGACCACGCCTA	NM_005164:	NM_005164:
5825	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	0.92	TCCATAATACATAACATTCAA	NM_002858:	NM_002858:
5825	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	-0.48	AAGGATTTAAATCATGGCAAA	NM_002858:	NM_002858:
5826	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	-0.23	CCCGTTCACCCTCGTCTACTA	NM_005050:	NM_020323:NM_020324:NM_020325:NM_020326: NM_005050:
5826	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	0.07	CCCTACCTTAACCCAAATGAA	NM_005050:	NM_020323:NM_020324:NM_020325:NM_020326: NM_005050:
6059	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	-0.20	CTGATTGACATTTGATAAATA	NM_002940:	NM_002940:
6059	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	-1.13	CCAGTTGGGTTCTAAATTGTA	NM_002940:	NM_002940:
23	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	-3.43	AAGGGAAGGCTAAGCCTCAAA	NM_001090:	NM_001090:NM_001025091:
23	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	-0.93	CAGAGTGTTAGCCAAATCGAT	NM_001090:	NM_001090:NM_001025091:
10061	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	0.07	AACTGAAGTATTATACGGGTA	NM_005692:	NM_005692:NM_007189:
10061	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	1.11	TACGGTCTCACTGGGAAACAA	NM_005692:	NM_005692:NM_007189:
55324	ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	-1.40	CGAGGCTCGACTTAAGGCAAA	NM_018358:	NM_018358:
55324	ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	-0.96	TCGGTTGGAATCATCTGGCAA	NM_018358:	NM_018358:
9619	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	-4.55	CTCGGTCGGCACCGCCATGAA	NM_004915:	NM_016818:NM_004915:
9619	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	0.52	TACGTCCTGAGTCAAGGACAA	NM_004915:	NM_016818:NM_004915:NM_207174:NM_207627: NM_207628:NM_207629:NM_207630:
9429	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	2.10	CTGGTCTAATTTATTAATCTA	NM_004827:	NM_004827:
9429	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	1.16	CTGGCGAAGAATATTTGGTAA	NM_004827:	NM_004827:
64137	ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	0.08	CTATATTTATACAGTATGCAA	NM_022169:	NM_022169:
64137	ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	0.99	AGCCATGATGGTCTCTGCTAA	NM_022169:	NM_022169:
64240	ABCG5	ATP-binding cassette, sub-family G (WHITE), member 5 (sterolin 1)	-0.92	GTGCTACTTGGTATCGTCCAA	NM_022436:	NM_022436:
64240	ABCG5	ATP-binding cassette, sub-family G (WHITE), member 5 (sterolin 1)	-1.96	ACCCTTGTCCTGAACATTCAA	NM_022436:	NM_022436:
64241	ABCG8	ATP-binding cassette, sub-family G (WHITE), member 8 (sterolin 2)	0.02	AAAGCCAACGTGAACAATTAA	NM_022437:	NM_022437:
64241	ABCG8	ATP-binding cassette, sub-family G (WHITE), member 8 (sterolin 2)	0.10	CACCATCAATACAGAAAGTGA	NM_022437:	NM_022437:
25890	ABI3BP	ABI gene family, member 3 (NESH) binding protein	-1.63	TGCGGAGGAGTTTAATAGTTA	NM_015429:	NM_015429:
25890	ABI3BP	ABI gene family, member 3 (NESH) binding protein	-1.47	TACTATGTATTTATACGTTAA	NM_015429:	NM_015429:
25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	1.48	AACACTCTAAGCATAACTAAA	NM_005157:	NM_005157:NM_007313:
25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	0.34	ACGCACGGACATCACCATGAA	NM_005157:	NM_005157:NM_007313:
27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelsc	-2.07	AACCCTGTCCTTAATAACTTA	NM_005158:	NM_005158:NM_007314:
27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelsc	2.39	ATCAAGCATCCTAATCTGGTA	NM_005158:	NM_005158:NM_007314:
31	ACACA	acetyl-Coenzyme A carboxylase alpha	0.44	CTGGATAATCTGGTCAATGTA	NM_000664:	NM_000664:NM_198838:NM_198839:NM_198837: NM_198835:NM_198836:NM_198834:
31	ACACA	acetyl-Coenzyme A carboxylase alpha	-2.15	TCGCATCACAATTGGCAATAA	NM_000664:	NM_000664:NM_198838:NM_198839:NM_198837: NM_198835:NM_198836:NM_198834:
32	ACACB	acetyl-Coenzyme A carboxylase beta	-0.54	AAGGATCGATCCAGCTTACAA	NM_001093:	NM_001093:
32	ACACB	acetyl-Coenzyme A carboxylase beta	-4.91	CCCGCTGTGCATAGAAATGTA	NM_001093:	NM_001093:
80724	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	1.14	ACAGCACAGAACAATCATTTA	NM_025247:	NM_025247:
80724	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	0.05	CTGGTGAGGTATGGCACCGAA	NM_025247:	NM_025247:
84129	ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	-1.47	CGAGATGAAGATAGCTATGTA	NM_032169:	NM_032169:
84129	ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	0.38	CAGGGAGTATATAGCAGATAT	NM_032169:	NM_032169:
33	ACADL	acyl-Coenzyme A dehydrogenase, long chain	-2.07	AAGGGACGAAAGCTACATAAA	NM_001608:	NM_001608:
33	ACADL	acyl-Coenzyme A dehydrogenase, long chain	0.19	TAGGTGTTTCATTTATCTCTA	NM_001608:	NM_001608:
34	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	1.42	CAACTTGACAGTAACTTTGTA	NM_000016:	NM_000016:
34	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	2.27	AAGGTACTTCACAAATTCAAA	NM_000016:	NM_000016:
35	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	0.32	CCAGATCAGATCACATGGGAA	NM_000017:	NM_000017:
35	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	-0.09	CACGGCCAACCTCATCTTTGA	NM_000017:	NM_000017:
37	ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	-4.41	ACGGATGGTTATGCTGCAGTA	NM_000018:	NM_000018:NM_001033859:
37	ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	-2.07	AAGCAAGCTTTGGATCAGTAA	NM_000018:	NM_000018:NM_001033859:
38	ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thio	-2.28	TAGTCTGGTTGTACTAGCAAA	NM_000019:	NM_000019:
38	ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thio	-2.28	CCAGATGTAGTGGTGAAAGAA	NM_000019:	NM_000019:
39	ACAT2 (acety	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thio	-0.03	AAACGTGGGCTTACACCTTTA	NM_005891:	NM_005891:
39	ACAT2 (acety	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thio	0.03	CGCCATGGGAGCAACATAGAA	NM_005891:	NM_005891:
64746	ACBD3	acyl-Coenzyme A binding domain containing 3	-0.57	CAGCTGTTTAGTTCAGAGTTA	NM_022735:	NM_022735:
64746	ACBD3	acyl-Coenzyme A binding domain containing 3	1.62	GAGCATTAGAGTCACAGTTTA	NM_022735:	NM_022735:
40	ACCN1	amiloride-sensitive cation channel 1, neuronal (degenerin)	-7.24	CAGCAAGACATCAGCCAAGTA	NM_001094:	NM_183377:NM_001094:
40	ACCN1	amiloride-sensitive cation channel 1, neuronal (degenerin)	-0.21	CACCCTGGAATCAGAACTGCA	NM_001094:	NM_183377:NM_001094:
41	ACCN2	amiloride-sensitive cation channel 2, neuronal	0.58	AACGAGTTCCGCTTTAGCCAA	NM_001095:	NM_020039:NM_001095:
41	ACCN2	amiloride-sensitive cation channel 2, neuronal	0.66	CCCTATCTTAATGAGAGACAA	NM_001095:	NM_020039:NM_001095:
9311	ACCN3	amiloride-sensitive cation channel 3	0.81	CCCAAATAAAGTCCTAATGCA	NM_004769:	NM_004769:NM_020321:NM_020322:
9311	ACCN3	amiloride-sensitive cation channel 3	0.02	CTGGGCAGCCATCGAACCCAA	NM_004769:	NM_004769:NM_020321:
55515	ACCN4	amiloride-sensitive cation channel 4, pituitary	0.23	CTGTACATTTGTAAATATTTA	NM_018674:	NM_018674:NM_182847:
55515	ACCN4	amiloride-sensitive cation channel 4, pituitary	-4.10	TAGGACGGTGCTGTGACTGAA	NM_018674:	NM_018674:NM_182847:
51802	ACCN5	amiloride-sensitive cation channel 5, intestinal	0.00	AGGAGTGTTAATGGTCACTTA	NM_017419:	NM_017419:
51802	ACCN5	amiloride-sensitive cation channel 5, intestinal	0.04	ATCATAGAAATTATTGAATAT	NM_017419:	NM_017419:
1636	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	-3.64	CAGCGACGAGCATGACATCAA	NM_000789:	NM_000789:NM_152830:NM_152831:
1636	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	1.31	CACCACAGAGGCTATGCTAAA	NM_000789:	NM_000789:NM_152830:NM_152831:
59272	ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	0.01	ATGCTAGATTTACACACTCAA	NM_021804:	NM_021804:
59272	ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	-1.25	ATGGAACGACAATGAAATGTA	NM_021804:	NM_021804:
43	ACHE	acetylcholinesterase (Yt blood group)	0.04	CGCCCTCTGGCTGCAAATAAA	NM_000665:	NM_015831:NM_000665:
43	ACHE	acetylcholinesterase (Yt blood group)	0.16	CCCAGGCTTCAGCAAAGACAA	NM_000665:	NM_015831:NM_000665:
47	ACLY	ATP citrate lyase	-0.06	CAGCCAGAACTTGGTAGTCAA	NM_001096:	NM_198830:NM_001096:
47	ACLY	ATP citrate lyase	0.28	CCGAGTGAAGTCGATAAACAA	NM_001096:	NM_198830:NM_001096:
48	ACO1	aconitase 1, soluble	0.35	CAGGGCAAGAACGATACACTA	NM_002197:	NM_002197:
48	ACO1	aconitase 1, soluble	-0.03	ATGGGTGTGATCCCACTTGAA	NM_002197:	NM_002197:
51	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	0.21	TAGCTATAGAGCAAATGATAA	NM_004035:	NM_004035:NM_007292:
51	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	0.27	CACAAGTAAACCAGCGTGTAA	NM_004035:	NM_004035:NM_007292:
52	ACP1	acid phosphatase 1, soluble	3.38	CCCATAGTGCACACTTGTATA	NM_004300:	NM_007099:NM_004300:NM_177554:
52	ACP1	acid phosphatase 1, soluble	-3.10	TCCGTAGGAGCTCACAGTCTA	NM_004300:	NM_007099:NM_004300:NM_177554:
53	ACP2 (acid pl	acid phosphatase 2, lysosomal	1.12	CAGCCTGAAGTCTTCGGCAAA	NM_001610:	NM_001610:
53	ACP2 (acid pl	acid phosphatase 2, lysosomal	-0.01	CTGGATGTCTACAATGGTGAA	NM_001610:	NM_001610:
54	ACP5	acid phosphatase 5, tartrate resistant	0.23	CTCGGGCAAGTCCCTCTTTAA	NM_001611:	NM_001611:
54	ACP5	acid phosphatase 5, tartrate resistant	-1.03	CTGGTACGTGCTAGCCGGAAA	NM_001611:	NM_001611:
51205	ACP6	acid phosphatase 6, lysophosphatidic	0.30	CCATGTCAGTTTATACCTTAA	NM_016361:	NM_016361:
51205	ACP6	acid phosphatase 6, lysophosphatidic	-1.20	CCCGCTGGACATGTTCTTGAA	NM_016361:	NM_016361:
55	ACPP	acid phosphatase, prostate	4.68	ACAGATGGCGCTAGATGTTTA	NM_001099:	NM_001099:
55	ACPP	acid phosphatase, prostate	2.03	CCGGACTTTGATGAGTGCTAT	NM_001099:	NM_001099:
93650	ACPT (acid pl	acid phosphatase, testicular	0.08	CCCGCCAAAGATGGAGGGAAT	NM_033068:	NM_033068:NM_080789:NM_080790:NM_080791:
93650	ACPT (acid pl	acid phosphatase, testicular	0.11	CTGGTGTTCGTGGCTCTGGTA	NM_033068:	NM_033068:NM_080791:
49	ACR (acrosin)	acrosin	-3.86	CAAGAGAGATATGTGGAGAAA	NM_001097:	NM_001097:
49	ACR (acrosin)	acrosin	0.91	TGGGAACAATAAACCAGTAAA	NM_001097:	NM_001097:
56	ACRV1	acrosomal vesicle protein 1	-1.22	CAGGCACAATATTAAATTGCT	NM_001612:	NM_001612:NM_020069:NM_020107:NM_020108: NM_020109:NM_020110:NM_020111:NM_020114:

56	ACRV1	acrosomal vesicle protein 1	0.07	ATGGAACGAGGATGCAAATTA	NM_001612:	NM_001612:NM_020069:NM_020107:NM_020108: NM_020109:NM_020110:NM_020111:NM_020113: NM_020114:NM_020115:
2182	ACSL4	acyl-CoA synthetase long-chain family member 4	-2.59	AAGGGCAGAGTTACTTGATAA	NM_004458:	NM_004458:NM_022977:
2182	ACSL4	acyl-CoA synthetase long-chain family member 4	0.18	TTGGAGCGATTTGAAATTCCA	NM_004458:	NM_004458:NM_022977:
23305	ACSL6	acyl-CoA synthetase long-chain family member 6	-0.48	TTGGAAGATATGGTGAGGTTA	NM_015256:	NM_015256:NM_001009185:
23305	ACSL6	acyl-CoA synthetase long-chain family member 6	-0.53	CCGGAGTGGAATCATCAGGAA	NM_015256:	NM_015256:NM_001009185:
6296	ACSM3	acyl-CoA synthetase medium-chain family member 3	0.44	ATGCTTGTACAGAATGATATA	NM_005622:	NM_202000:NM_005622:
6296	ACSM3	acyl-CoA synthetase medium-chain family member 3	-0.11	CAAGCTGATTGTATCAGAGAA	NM_005622:	NM_202000:NM_005622:
86	ACTL6A	actin-like 6A	0.95	AAAGCTTTAACTGGCTCTATA	NM_004301:	NM_177989:NM_178042:NM_004301:
86	ACTL6A	actin-like 6A	-0.02	CAACAGTGGAACGGAGGTTTA	NM_004301:	NM_177989:NM_178042:NM_004301:
51412	ACTL6B	actin-like 6B	0.23	CAACAGCACCATGGAGCGCAA	NM_016188:	NM_016188:
51412	ACTL6B	actin-like 6B	0.81	CTGGCATAACTACATGTGTAA	NM_016188:	NM_016188:
87	ACTN1	actinin, alpha 1	0.69	GACCATTATGATTCTCAGCAA	NM_001102:	NM_001102:
87	ACTN1	actinin, alpha 1	0.50	GCGCACCATCATGGACCATTA	NM_001102:	NM_001102:
81	ACTN4	actinin, alpha 4	-3.62	ACGCAGCATCGTGGACTACAA	NM_004924:	NM_004924:
81	ACTN4	actinin, alpha 4	1.90	CCCGCAAATCATCAACTCCAA	NM_004924:	NM_004924:
10097	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	-0.05	CAAGGTTTATTGACTGGTGTA	NM_005722:	NM_001005386:NM_005722:
10097	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	0.23	CCAGATGGACGTATCATCAAA	NM_005722:	NM_001005386:NM_005722:
10096	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	0.20	ATCGATGTTGGTTATGAGAGA	NM_005721:	NM_005721:
10096	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	0.01	CCGGCTGAAATTAAGTGAGGA	NM_005721:	NM_005721:
90	ACVR1	activin A receptor, type I	-0.33	CGGATGGTGAGCAATGGTATA	NM_001105:	NM_001105:
90	ACVR1	activin A receptor, type I	1.26	CTGGTCTGTCTTTGGATAATA	NM_001105:	NM_001105:
91	ACVR1B	activin A receptor, type IB	0.97	CCGTTCTTACGTCGCCATAAA	NM_004302:	NM_004302:
91	ACVR1B	activin A receptor, type IB	-1.50	CTGTGATTACCTCTCAATCTA	NM_004302:	NM_004302:
130399	ACVR1C	activin A receptor, type IC	0.86	TACTTTGGTAAACGAGATTTA	NM_145259:	NM_145259:
130399	ACVR1C	activin A receptor, type IC	0.30	CACAGAGTAATGAATATTTAA	NM_145259:	NM_145259:
92	ACVR2A	activin A receptor, type IIA	2.56	GAGGTATTAGAGGGTGCTATA	NM_001616:	NM_001616:
92	ACVR2A	activin A receptor, type IIA	-1.05	TCCACGGTTGCTAAATTATAA	NM_001616:	NM_001616:
93	ACVR2B	activin A receptor, type IIB	0.00	CAGCTCATGAATGACTTTGTA	NM_001106:	NM_001106:
93	ACVR2B	activin A receptor, type IIB	2.81	TACGGTCATGTGGACATCCAT	NM_001106:	NM_001106:
94	ACVRL1	activin A receptor type II-like 1	1.63	CACCGAGTTCGTCAACCACTA	NM_000020:	NM_000020:
94	ACVRL1	activin A receptor type II-like 1	1.57	CAGGAAGACGCTGGAATAAGA	NM_000020:	NM_000020:
100	ADA (adenosi	adenosine deaminase	-0.87	ATGGGCATGGTTGAATCTGAA	NM_000022:	NM_000022:
100	ADA (adenosi	adenosine deaminase	-1.17	CATGATCTCAATAGTCAGTTA	NM_000022:	NM_000022:
161823	ADAL	adenosine deaminase-like	1.93	TAGGTATTTGATAGCAGTTGA	XM_091156:	NM_001012969:
102	ADAM10	ADAM metallopeptidase domain 10	-0.81	ATGGGACACATGAGACGCTAA	NM_001110:	NM_001110:
102	ADAM10	ADAM metallopeptidase domain 10	-0.39	ACCAAACTTCACAGACTGTAA	NM_001110:	NM_001110:
4185	ADAM11	ADAM metallopeptidase domain 11	0.42	AAGTATGAGTGCTGATTCAAA	NM_002390:	NM_002390:
4185	ADAM11	ADAM metallopeptidase domain 11	-3.72	CCTGGCCGATGTGATATACAA	NM_002390:	NM_002390:
8038	ADAM12	ADAM metallopeptidase domain 12 (meltrin alpha)	-0.12	CAAGGTCTTTAAAGTGACTAA	NM_003474:	NM_003474:
8038	ADAM12	ADAM metallopeptidase domain 12 (meltrin alpha)	0.15	AAGGCGGTGCTTGATAGAAAT	NM_003474:	NM_003474:
8751	ADAM15	ADAM metallopeptidase domain 15 (metargidin)	-0.47	CTGGTGTGTATAGACCATCGA	NM_003815:	NM_207191:NM_207194:NM_207196:NM_207197: NM_207195:NM_003815:
8751	ADAM15	ADAM metallopeptidase domain 15 (metargidin)	0.59	CTGACGGACCCTGTTGTCAAA	NM_003815:	NM_207191:NM_207194:NM_207196:NM_207197: NM_207195:NM_003815:
6868	ADAM17	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, con	-3.29	AAGAAACAGAGTGCTAATTTA	NM_003183:	NM_003183:
6868	ADAM17	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, con	1.12	CAGGATGTAATTGAACGATTT	NM_003183:	NM_003183:
8749	ADAM18	ADAM metallopeptidase domain 18	0.97	AGCGATGACGTGGGACATTAA	NM_014237:	NM_014237:
8749	ADAM18	ADAM metallopeptidase domain 18	-1.94	CTGGACCATGTTGTACATCAA	NM_014237:	NM_014237:
8728	ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	1.10	TACCTCGTGGCTGATTATTTA	NM_023038:	NM_023038:NM_033274:
8728	ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	-0.04	CACCTTATTTACAGATCTGAA	NM_023038:	NM_023038:NM_033274:
2515	ADAM2	ADAM metallopeptidase domain 2 (fertilin beta)	-0.36	AACCATATACTGTGAATTTAA	NM_001464:	NM_001464:
2515	ADAM2	ADAM metallopeptidase domain 2 (fertilin beta)	1.94	TGCTATAATGGTGAAAGTTAA	NM_001464:	NM_001464:
8748	ADAM20 (AD	ADAM metallopeptidase domain 20	0.75	TTCGGTCACTGTGGTATTGTA	NM_003814:	NM_003814:
8748	ADAM20 (AD	ADAM metallopeptidase domain 20	0.65	ACGTGTAATAACCATGATATA	NM_003814:	NM_003814:
53616	ADAM22	ADAM metallopeptidase domain 22	-0.01	TCGGTCTAATTCAACTGAGTA	NM_004194:	NM_004194:NM_021721:NM_021722:
53616	ADAM22	ADAM metallopeptidase domain 22	-1.03	CCGGCCGAATGTGTCCTTGAA	NM_004194:	NM_004194:NM_021721:NM_021722:NM_021723: NM_016351:
8745	ADAM23	ADAM metallopeptidase domain 23	-0.64	GACGGATATGCATGCAATCAA	NM_003812:	NM_003812:
8745	ADAM23	ADAM metallopeptidase domain 23	-0.13	CGCGGGTGACATTTCACTATA	NM_003812:	NM_003812:
10863	ADAM28	ADAM metallopeptidase domain 28	0.13	CACACTAATCTTGGAGGAATA	NM_014265:	NM_014265:
10863	ADAM28	ADAM metallopeptidase domain 28	0.93	AAGAAATATCTCCGAAGTTAA	NM_014265:	NM_014265:
11086	ADAM29	ADAM metallopeptidase domain 29	0.13	CACAGGCACTGTGTCCATATA	NM_014269:	NM_014269:
11086	ADAM29	ADAM metallopeptidase domain 29	0.89	ACCGTAGTTGTGCAATTGTTA	NM_014269:	NM_014269:
11085	ADAM30	ADAM metallopeptidase domain 30	-0.11	TACCATGCTATTCAAGGTATA	NM_021794:	NM_021794:
11085	ADAM30	ADAM metallopeptidase domain 30	-0.27	AAGATCGGTGTTGCCAATCAA	NM_021794:	NM_021794:
80332	ADAM33	ADAM metallopeptidase domain 33	0.34	CAGAGGGAACCATTTAAGAAA	NM_025220:	NM_153202:NM_025220:
80332	ADAM33	ADAM metallopeptidase domain 33	0.04	CCGCGTCACGCAGGACGCCAA	NM_025220:	NM_153202:NM_025220:
8756	ADAM7	ADAM metallopeptidase domain 7	-12.29	TGCAACGTCTTTACAACCTTA	NM_003817:	NM_003817:
8756	ADAM7	ADAM metallopeptidase domain 7	0.59	CTGGTTATTGTCGGTATCGGA	NM_003817:	NM_003817:
101	ADAM8	ADAM metallopeptidase domain 8	0.11	CCCAGCTTTGTGTGTGTTTAA	NM_001109:	NM_001109:
101	ADAM8	ADAM metallopeptidase domain 8	-0.74	AGGCATCATCGTCTACCGCAA	NM_001109:	NM_001109:
8754	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	1.36	ACCTTAGTTATCATTAATGTA	NM_003816:	NM_003816:NM_001005845:
8754	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	-1.37	TTCTACCTTAGTTATCATTAA	NM_003816:	NM_003816:NM_001005845:
27299	ADAMDEC1	ADAM-like, decysin 1	-0.25	CGGCTAAACTATTCAGAGTTA	NM_014479:	NM_014479:
27299	ADAMDEC1	ADAM-like, decysin 1	-0.27	AGCCCTAACGTGTAAACTGAA	NM_014479:	NM_014479:
9510	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	0.58	CAGCAACGTGAAATAACGCAA	NM_006988:	NM_006988:
9510	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	-4.85	CTGAGCAGTGATATAGCATAA	NM_006988:	NM_006988:
81794	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	-0.45	CCGGAAGTTATTTATTGGGAA	NM_030957:	NM_030957:
81794	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	-0.50	ACCGATTAATGCATCTCTCAT	NM_030957:	NM_030957:
81792	ADAMTS12 (	ADAM metallopeptidase with thrombospondin type 1 motif, 12	0.01	CAGGAAAGACGGCAAACCGTA	NM_030955:	NM_030955:
81792	ADAMTS12 (	ADAM metallopeptidase with thrombospondin type 1 motif, 12	-0.68	CCGGAGAGTTCTGAAACCAAA	NM_030955:	NM_030955:
140766	ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif, 14	-5.27	CCGCTTGATCATGGTTGGCTA	NM_080722:	NM_139155:NM_080722:
140766	ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif, 14	-1.12	CAGGAGTGTGTGTACACTGGA	NM_080722:	NM_139155:NM_080722:
170689	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	0.73	CTCCAAGAAGAGATTCGACAA	NM_139055:	NM_139055:
170689	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	0.79	CGGCGCGGACCTGGAACATTA	NM_139055:	NM_139055:
170691	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17	1.15	CAGGGACTTCTATGCAAACAA	NM_139057:	NM_139057:
170691	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17	0.14	AACGACAGTGACTGCCCTCAA	NM_139057:	NM_139057:
9509	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	-5.26	CAGGCGAATGGGAGCCATGTA	NM_014244:	NM_014244:
9509	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	-1.34	CCGCCGGAGGCTGGACCACAA	NM_014244:	NM_014244:
9508	ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	-0.20	TAGGCAAATTCCAGATAGTAA	NM_014243:	NM_014243:
9508	ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	0.10	AACAATGTGATACGTAAATTA	NM_014243:	NM_014243:
9507	ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	-1.62	AAGAACTAGCATAACACTCAA	NM_005099:	NM_005099:
9507	ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	-1.81	ACAGATGTGGTTGCATCCTAA	NM_005099:	NM_005099:
11096	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5 (aggreca	-1.43	AAGCACTTGATTGTACCCGTA	NM_007038:	NM_007038:
11096	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5 (aggreca	0.07	CAGTGGTGACCTTGCAATATA	NM_007038:	NM_007038:
11173	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	-1.65	CCCGGAGAAGTACTTCCTCAA	NM_014272:	NM_014272:
11173	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	-1.66	CTGCATCAACGGCATCTGTAA	NM_014272:	NM_014272:

11095	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	-0.26	CAGCATCAAGAATTCCATCAA	NM_007037:	NM_007037:
11095	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	-1.59	CCGGGAAGGAAGTATAAATAA	NM_007037:	NM_007037:
56999	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	0.24	CACGACAAATGTGATACCTTA	NM_020249:	NM_182920:
56999	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	-0.54	AGGACGTAGAATGAAATTTAA	NM_020249:	NM_182920:
103	ADAR	adenosine deaminase, RNA-specific	-0.70	TCCCTCGATAACAGTCAGCTA	NM_001111:	NM_015840:NM_001111:NM_015841:NM_001025107:
103	ADAR	adenosine deaminase, RNA-specific	0.14	TTCCGTTACCGCAGGGATCTA	NM_001111:	NM_015840:NM_001111:NM_015841:NM_001025107:
104	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	0.38	CAGGATGGAAGTAGAATGATT	NM_001112:	NM_001033049:NM_015833:NM_001112:
104	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	1.46	CACAACTTGAGCTTTACTTAA	NM_001112:	NM_001033049:NM_015834:NM_015833:NM_001112:
113451	ADC	arginine decarboxylase	-1.63	TAGTTCAAGTATGCAACATAA	NM_052998:	NM_052998:
113451	ADC	arginine decarboxylase	0.63	CACCTCCAAGACCATCGTGTA	NM_052998:	NM_052998:
57143	ADCK1	aarF domain containing kinase 1	1.20	TAACAAGTACTTGGACCCTAA	NM_020421:	NM_020421:
57143	ADCK1	aarF domain containing kinase 1	-0.11	TACGACGGCTGTCATCAGTTA	NM_020421:	NM_020421:
90956	ADCK2	aarF domain containing kinase 2	0.94	CAGATTGACCTGCGTTACGAA	NM_052853:	NM_052853:
90956	ADCK2	aarF domain containing kinase 2	0.10	CCGGAATGTGAAAGCCGTCAA	NM_052853:	NM_052853:
79934	ADCK4	aarF domain containing kinase 4	-1.52	CAGATGCTGAGAGTTCTTGAA	NM_024876:	NM_024876:
79934	ADCK4	aarF domain containing kinase 4	-1.05	CCGGGTCCCAGCCGTGGTTAA	NM_024876:	NM_024876:
203054	ADCK5	aarF domain containing kinase 5	-1.57	AAGGCCTTTGCTGAGCAGATA	NM_174922:	NM_174922:
203054	ADCK5	aarF domain containing kinase 5	-9.11	CCGCTACTTCCTTATGGCTAA	NM_174922:	NM_174922:
107	ADCY1 (aden	adenylate cyclase 1 (brain)	0.46	CTGGAACTGCATGCCGTGAAA	NM_021116:	NM_021116:
107	ADCY1 (aden	adenylate cyclase 1 (brain)	-0.21	CAGGCACTTATTGAGAATTAA	NM_021116:	NM_021116:
108	ADCY2	adenylate cyclase 2 (brain)	0.27	CACCTGTCGAGGAATAATCAA	NM_020546:	NM_020546:
108	ADCY2	adenylate cyclase 2 (brain)	0.33	AAGGATGATTCAAGCAATTGA	NM_020546:	NM_020546:
109	ADCY3	adenylate cyclase 3	0.23	ACAGGTATTGATAAAGAACAA	NM_004036:	NM_004036:
109	ADCY3	adenylate cyclase 3	-0.21	CAGACGTATGATGAGATTGGA	NM_004036:	NM_004036:
196883	ADCY4 (aden	adenylate cyclase 4	1.45	CTCGCCTTCTAAGAACCTCAA	NM_139247:	NM_139247:
196883	ADCY4 (aden	adenylate cyclase 4	-0.26	CCCGTAGTAGCTGGAGTTATT	NM_139247:	NM_139247:
111	ADCY5 (aden	adenylate cyclase 5	-0.98	CCAGGTCACCACAGACATGTA	NM_183357:	NM_183357:
111	ADCY5 (aden	adenylate cyclase 5	-0.08	CGCCATAGACTTCTTCAACAA	NM_183357:	NM_183357:
112	ADCY6	adenylate cyclase 6	-0.90	ACCATGTATTTCAGTGAAATA	NM_015270:	NM_015270:NM_020983:
112	ADCY6	adenylate cyclase 6	-1.51	CAGCCTGAGTCTAGCATGTTT	NM_015270:	NM_015270:NM_020983:
113	ADCY7	adenylate cyclase 7	0.97	TCAGATAATAATAGTTTGTAA	NM_001114:	NM_001114:
113	ADCY7	adenylate cyclase 7	0.10	CTGGTTTCACATGAATACTAT	NM_001114:	NM_001114:
114	ADCY8	adenylate cyclase 8 (brain)	0.47	GAAGCATAATATCGAAACTTA	NM_001115:	NM_001115:
114	ADCY8	adenylate cyclase 8 (brain)	1.96	TCGGATCTACATCCATCGCTA	NM_001115:	NM_001115:
115	ADCY9 (aden	adenylate cyclase 9	0.55	ATCGGAGAGGGAAATACCAAA	NM_001116:	NM_001116:
115	ADCY9 (aden	adenylate cyclase 9	-2.53	CAGAGGGACCGTGAATGTCAA	NM_001116:	NM_001116:
117	ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	-3.51	AAGCTGGAAGGTGAACCGTTA	NM_001118:	NM_001118:
117	ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	0.34	TACGCTGAGACTCTACTTTGA	NM_001118:	NM_001118:
118	ADD1	adducin 1 (alpha)	0.58	CCTAGTTGTGATCAAAGGTAA	NM_001119:	NM_176801:NM_001119:NM_014190:NM_014189:
118	ADD1	adducin 1 (alpha)	-7.43	CAGCGATGGGTCTCCAGGCAA	NM_001119:	NM_176801:NM_001119:NM_014190:NM_014189:
123	ADFP	adipose differentiation-related protein	0.64	CTGCAGGATAGACCAGTTAAA	NM_001122:	NM_001122:
123	ADFP	adipose differentiation-related protein	0.14	TCCGTTGCAGTTGATCCACAA	NM_001122:	NM_001122:
124	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	-0.03	AGAAATGGAAATTGATGTAAA	NM_000667:	NM_000667:
124	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	-1.94	CAGGTTCACCTGCAGGAGGAA	NM_000667:	NM_000667:
125	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide	-2.67	AAGACCTTAGACATAAAGTAA	NM_000668:	NM_000668:
125	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide	1.43	AAGCCTCAATTACTAATTGTA	NM_000668:	NM_000668:
126	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	0.03	ACTGGATGCATTAATAACAAA	NM_000669:	NM_000669:
126	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	0.77	GGGAAATTATTTGTCAAGCAA	NM_000669:	NM_000669:
127	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	0.43	TCGGCCGTACTATAAATGGAA	NM_000670:	NM_000670:
127	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	0.77	AACCAGTACATTCTCTCAGTA	NM_000670:	NM_000670:
128	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	0.08	CTGCGTGTTACCTAAGACGTA	NM_000671:	NM_000671:
128	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	1.58	TACGGGAACTACCATAATTTA	NM_000671:	NM_000671:
130	ADH6	alcohol dehydrogenase 6 (class V)	0.54	AAGCTGTATACTGATAATTGA	NM_000672:	NM_000672:
130	ADH6	alcohol dehydrogenase 6 (class V)	-0.53	CAGGACGTTCTTTGAAGGGTT	NM_000672:	NM_000672:
131	ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	0.24	AACGATTAAGAATCATCATTA	NM_000673:	NM_000673:
131	ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	0.98	CAGATATAGCGTATAAAGATA	NM_000673:	NM_000673:
9370	ADIPOQ	adiponectin, C1Q and collagen domain containing	0.61	CACGCTTTCACAGTTACCCTA	NM_004797:	NM_004797:
9370	ADIPOQ	adiponectin, C1Q and collagen domain containing	-0.90	CTGGGAGCTGTTCTACTGCTA	NM_004797:	NM_004797:
51094	ADIPOR1	adiponectin receptor 1	-1.26	CAGAAGAGACTTGGCATTCAA	NM_015999:	NM_015999:
51094	ADIPOR1	adiponectin receptor 1	-0.22	AAGGACAACGACTATCTGCTA	NM_015999:	NM_015999:
79602	ADIPOR2	adiponectin receptor 2	-0.28	TCGGCTCTCCTTGAATAAGAA	NM_024551:	NM_024551:
79602	ADIPOR2	adiponectin receptor 2	1.44	TAGGGTGTCATTGTCATTTGA	NM_024551:	NM_024551:
132	ADK	adenosine kinase	0.44	AAGGGTATGGTAATGCTTGTA	NM_001123:	NM_001123:NM_006721:
132	ADK	adenosine kinase	-0.02	TAGTTTGATAGTGCCACTTAA	NM_001123:	NM_001123:NM_006721:
133	ADM	adrenomedullin	-0.02	CTGTATAATCTATTTACATAA	NM_001124:	NM_001124:
133	ADM	adrenomedullin	0.35	ACCGAGTCTCTGTATAATCTA	NM_001124:	NM_001124:
79924	ADM2	adrenomedullin 2	-1.98	TAGCGAACACTGAGCATTTAA	NM_024866:	NM_024866:
79924	ADM2	adrenomedullin 2	-0.92	CTGGTACGTCAAGGAGCCTAA	NM_024866:	NM_024866:
11318	ADMR	adrenomedullin receptor	0.76	CCCTCTCATCACAGTCTTCAA	NM_007264:	NM_007264:
11318	ADMR	adrenomedullin receptor	-0.68	CCGCTTCACTCACTACTTCTA	NM_007264:	NM_007264:
134	ADORA1	adenosine A1 receptor	1.00	CAGCATGGAGTACATGGTCTA	NM_000674:	NM_000674:
134	ADORA1	adenosine A1 receptor	-0.53	GAGGCCCATGTGACTAATAAA	NM_000674:	NM_000674:
135	ADORA2A	adenosine A2a receptor	-0.52	CAGCATGAGGCCCAGCAAGAA	NM_000675:	NM_000675:
135	ADORA2A	adenosine A2a receptor	-0.52	CAGGAGTGTCCTGATGATTCA	NM_000675:	NM_000675:
136	ADORA2B	adenosine A2b receptor	0.68	AAGGATTGACAAATATATTTA	NM_000676:	NM_000676:
136	ADORA2B	adenosine A2b receptor	0.34	ACGTATCTAGCTAATATGTAT	NM_000676:	NM_000676:
140	ADORA3	adenosine A3 receptor	1.62	AAGCGTCAACTCGTGCAAGAA	NM_000677:	NM_000677:
140	ADORA3	adenosine A3 receptor	-3.10	TCGGAACAAACTCAGTCTGAA	NM_000677:	NM_000677:
140	ADORA3	adenosine A3 receptor	-1.28	CACGGCTTCTGCCATCTGCAA	NM_020683:	NM_020683:
140	ADORA3	adenosine A3 receptor	0.56	CTCGCGTGTCCTGACTCCAAA	NM_020683:	NM_020683:
148	ADRA1A	adrenergic, alpha-1A-, receptor	1.38	AAGACGGATGGCGTTTGTGAA	NM_000680:	NM_000680:NM_033304:NM_033302:NM_033303:
148	ADRA1A	adrenergic, alpha-1A-, receptor	-1.82	CCCGTGGATCTGCCAGGATTA	NM_000680:	NM_000680:NM_033304:NM_033302:NM_033303:
147	ADRA1B	adrenergic, alpha-1B-, receptor	0.73	CCGTGTCTATATAGTGGCCAA	NM_000679:	NM_000679:
147	ADRA1B	adrenergic, alpha-1B-, receptor	0.29	GAGGGCGGACTCTAAGATGAA	NM_000679:	NM_000679:
146	ADRA1D	adrenergic, alpha-1D-, receptor	-0.80	CTACGGGAGACCGATATTTAA	NM_000678:	NM_000678:
146	ADRA1D	adrenergic, alpha-1D-, receptor	-1.14	TTGGCCGACTACAGCAACCTA	NM_000678:	NM_000678:
150	ADRA2A	adrenergic, alpha-2A-, receptor	0.05	CAAGGCTTGGTGCGAGATCTA	NM_000681:	NM_000681:
150	ADRA2A	adrenergic, alpha-2A-, receptor	-0.94	CTCCCGCCGCTTAGAAATAAA	NM_000681:	NM_000681:
151	ADRA2B	adrenergic, alpha-2B-, receptor	0.06	AAGGTCTGAGTTATTACGCTA	NM_000682:	NM_000682:
151	ADRA2B	adrenergic, alpha-2B-, receptor	0.00	CTGAGTTATTACGCTACATGA	NM_000682:	NM_000682:
152	ADRA2C	adrenergic, alpha-2C-, receptor	0.53	AAGTATTTAAATGTTTGCCAA	NM_000683:	NM_000683:
152	ADRA2C	adrenergic, alpha-2C-, receptor	0.23	CAGGAGCTTGGCAGAGAGATA	NM_000683:	NM_000683:

153	ADRB1	adrenergic, beta-1-, receptor	0.46	CCGATAGCAGGTGAACTCGAA	NM_000684:	NM_000684:
153	ADRB1	adrenergic, beta-1-, receptor	0.38	CCGCCTCTTCGTCTTCTTCAA	NM_000684:	NM_000684:
154	ADRB2	adrenergic, beta-2-, receptor, surface	0.55	CCGAGCAAAGGTCTAAAGTTT	NM_000024:	NM_000024:
154	ADRB2	adrenergic, beta-2-, receptor, surface	-0.60	GAGGGTAATAAACTTAGAATA	NM_000024:	NM_000024:
155	ADRB3	adrenergic, beta-3-, receptor	-0.11	CAGGGTTCATAAGAAGGTGAA	NM_000025:	NM_000025:
155	ADRB3	adrenergic, beta-3-, receptor	0.00	GAGGCAGTAAATTAGGCCTAA	NM_000025:	NM_000025:
156	ADRBK1	adrenergic, beta, receptor kinase 1	0.77	CCGGGAGATCTTCGACTCATA	NM_001619:	NM_001619:
156	ADRBK1	adrenergic, beta, receptor kinase 1	-0.19	CGGCTGGAGGCTCGCAAGAAA	NM_001619:	NM_001619:
157	ADRBK2	adrenergic, beta, receptor kinase 2	1.11	AAGATGTTCAGTGTTGGGTAA	NM_005160:	NM_005160:
157	ADRBK2	adrenergic, beta, receptor kinase 2	2.13	CAAGTGTATGGGATTAACTAA	NM_005160:	NM_005160:
158	ADSL (adenyl	adenylosuccinate lyase	-1.28	CTCGAGAATTGTTACCTTAAA	NM_000026:	NM_000026:
158	ADSL (adenyl	adenylosuccinate lyase	0.08	TTGGAAGAGAATTAAACGAAA	NM_000026:	NM_000026:
165	AEBP1	AE binding protein 1	-0.47	CACCCTGAGCACTACCATAGA	NM_001129:	NM_001129:
165	AEBP1	AE binding protein 1	-0.16	CCGGGAGATCATGGCCATGAA	NM_001129:	NM_001129:
166	AES	amino-terminal enhancer of split	-2.22	CAGGCCCACCTCTCCAAGGAA	NM_198970:	NM_198969:NM_198970:NM_001130:
166	AES	amino-terminal enhancer of split	-1.37	CGGCTTGAACATCGAGATGCA	NM_198970:	NM_198969:NM_198970:NM_001130:
246181	AFAR3	aflatoxin B1 aldehyde reductase 3	-0.08	CCCGCTTTGTCTAATTTAGAA	NM_201252:	NM_201252:
246181	AFAR3	aflatoxin B1 aldehyde reductase 3	0.30	CACGTTGTATGATTTCGTTTA	NM_201252:	NM_201252:
2334	AFF2	AF4/FMR2 family, member 2	-0.02	CGGCCTTATTCTCATAATTAA	NM_002025:	NM_002025:
2334	AFF2	AF4/FMR2 family, member 2	-2.07	CTGGGTAAGACTACTCAGTAA	NM_002025:	NM_002025:
10939	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	0.37	ATGATGAAGTACGAATACTTA	NM_006796:	NM_006796:
10939	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	0.02	CATGGTATTGGAGAAACCTTA	NM_006796:	NM_006796:
173	AFM	afamin	1.62	CCAGTGCATAATTAACTCAAA	NM_001133:	NM_001133:
173	AFM	afamin	2.09	GAGAACTTCAATAGTACTCAA	NM_001133:	NM_001133:
174	AFP	alpha-fetoprotein	0.32	CTGGAACGTGGTCAATGTATA	NM_001134:	NM_001134:
174	AFP	alpha-fetoprotein	-0.25	TACCAATGTACTGCAGAGATA	NM_001134:	NM_001134:
175	AGA	aspartylglucosaminidase	0.56	TACGGTGCTGCTTGCAATAAA	NM_000027:	NM_000027:
175	AGA	aspartylglucosaminidase	-1.37	CAGGATATTCCTATCCATAAA	NM_000027:	NM_000027:
79841	AGBL2	ATP/GTP binding protein-like 2	0.95	CATGTATTACCCAGAATTTAA	NM_024783:	NM_024783:
79841	AGBL2	ATP/GTP binding protein-like 2	0.99	CCAATAGATATTCTCTCTAAA	NM_024783:	NM_024783:
340351	AGBL3	ATP/GTP binding protein-like 3	0.18	CCCATCGTGCATAGCACTAAA	NM_178563:	NM_178563:
340351	AGBL3	ATP/GTP binding protein-like 3	-1.46	GACGGTGAGCCTACCCGTATA	NM_178563:	NM_178563:
84871	AGBL4	ATP/GTP binding protein-like 4	0.39	TGGGTTCTGTTTGAAATACTT	NM_032785:	NM_032785:
84871	AGBL4	ATP/GTP binding protein-like 4	0.08	CTGCCTGGAATAAGAGTTTGA	NM_032785:	NM_032785:
177	AGER	advanced glycosylation end product-specific receptor	-1.23	AAGGGAGTATCTGTGAAGGAA	NM_172197:	NM_172197:NM_001136:
177	AGER	advanced glycosylation end product-specific receptor	-0.91	CACGGCTGGTGTTCCCAATAA	NM_172197:	NM_172197:NM_001136:
178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debran	-1.33	AAGGCAGGAAACAACTATTAA	NM_000028:	NM_000028:
178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debran	0.92	ATGCAAGGTCATCATATGTAA	NM_000028:	NM_000645:NM_000642:NM_000643:NM_000028: NM_000644:NM_000646:
181	AGRP	agouti related protein homolog (mouse)	-1.43	CAAGCTGGGTACTGCCATGAA	NM_007316:	NM_007316:NM_001138:
181	AGRP	agouti related protein homolog (mouse)	-0.52	CAGCCGCACCTAGCTGGCCAA	NM_007316:	NM_007316:NM_001138:
183	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1.02	CAGAGTCTACCCAACAGCTTA	NM_000029:	NM_000029:
183	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0.93	CTGTTTGAATGCGGAACAATA	NM_000029:	NM_000029:
185	AGTR1	angiotensin II receptor, type 1	0.29	ACGCACAATGCTTGTAGCCAA	NM_000685:	NM_000685:NM_032049:NM_031850:NM_004835: NM_009585:
185	AGTR1	angiotensin II receptor, type 1	-2.92	CGCGGGTTTGATATTTGACAA	NM_000685:	NM_000685:NM_031850:
186	AGTR2	angiotensin II receptor, type 2	1.33	AGGAGTGTGTTTAGGCACTAA	NM_000686:	NM_000686:
186	AGTR2	angiotensin II receptor, type 2	0.26	CTGCATGAGTGTTGATAGGTA	NM_000686:	NM_000686:
57085	AGTRAP	angiotensin II receptor-associated protein	-2.25	CAGGGATTGCCTGAACCAAGA	NM_020350:	NM_020350:
57085	AGTRAP	angiotensin II receptor-associated protein	-6.39	CTGCTTCGTCTACCACATGTA	NM_020350:	NM_020350:
187	AGTRL1	angiotensin II receptor-like 1	-1.77	CACCACTAAGGTGCAGTGCTA	NM_005161:	NM_005161:
187	AGTRL1	angiotensin II receptor-like 1	0.04	CACTGTGGTTCATCAAATAAA	NM_005161:	NM_005161:
189	AGXT	alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycol	1.18	CTCCCGGGAATGTTTAATAAA	NM_000030:	NM_000030:
189	AGXT	alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycol	-0.36	CTGGAGAGACATCGTCAGCTA	NM_000030:	NM_000030:
64902	AGXT2	alanine-glyoxylate aminotransferase 2	0.03	CGGGATGAATTTGAAATTGTT	NM_031900:	NM_031900:
64902	AGXT2	alanine-glyoxylate aminotransferase 2	0.01	AAGGGTGAATTTGAAGAATTT	NM_031900:	NM_031900:
64850	AGXT2L1 (ala	alanine-glyoxylate aminotransferase 2-like 1	-0.80	ATGTGTCAAATTAGAGAGCAA	NM_031279:	NM_031279:
64850	AGXT2L1 (ala	alanine-glyoxylate aminotransferase 2-like 1	-0.01	CAGAATAAACCAAGTGATAAT	NM_031279:	NM_031279:
191	AHCY	S-adenosylhomocysteine hydrolase	-0.99	CACCTGGTCTGTGGACTTATA	NM_000687:	NM_000687:
191	AHCY	S-adenosylhomocysteine hydrolase	0.22	CAGCCGTCATACTGTTCCAAA	NM_000687:	NM_000687:
10768	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	0.34	CCCACTTGGATTTATAGTATA	NM_006621:	NM_006621:
10768	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-0.56	CTGATAGAACTCTATAATGCA	NM_006621:	NM_006621:
196	AHR (aryl hyd	aryl hydrocarbon receptor	0.23	TTCGTTTACCTTCAAACTTTA	NM_001621:	NM_001621:
196	AHR (aryl hyd	aryl hydrocarbon receptor	0.31	CAGGAACACCTACATCTAGAA	NM_001621:	NM_001621:
57491	AHRR	aryl-hydrocarbon receptor repressor	-1.15	TACGCAGGAGCCTATCCTGAA	NM_020731:	NM_020731:
57491	AHRR	aryl-hydrocarbon receptor repressor	0.25	CCCAACAGTTCTTAAATGAAA	NM_020731:	NM_020731:
197	AHSG	alpha-2-HS-glycoprotein	-0.24	CACATGCGATCTACATTAATA	NM_001622:	NM_001622:
197	AHSG	alpha-2-HS-glycoprotein	-0.22	CTGAAAGACCTTCCTTAATAA	NM_001622:	NM_001622:
57379	AICDA	activation-induced cytidine deaminase	0.33	CAAAGGTATATTAACTATATA	NM_020661:	NM_020661:
57379	AICDA	activation-induced cytidine deaminase	1.11	CCCAAAGGTATATTAACTATA	NM_020661:	NM_020661:
199	AIF1	allograft inflammatory factor 1	0.05	CACCTAGCAGTTGGTTGGCAA	NM_004847:	NM_004847:NM_032955:
199	AIF1	allograft inflammatory factor 1	2.83	CAGAGTCAACAAATTAAATAA	NM_004847:	NM_001623:NM_004847:NM_032955:
150209	AIFL	apoptosis-inducing factor like	-0.17	AACATGTTAGACATTACCGTA	NM_144704:	NM_144704:NM_001018060:
150209	AIFL	apoptosis-inducing factor like	1.66	CAGAAGATGCTCAACCCTCAA	NM_144704:	NM_144704:NM_001018060:
9049	AIP	aryl hydrocarbon receptor interacting protein	-2.57	CAACGTCAAGGCCTACTTCAA	NM_003977:	NM_003977:
9049	AIP	aryl hydrocarbon receptor interacting protein	-1.17	CCAGTTCCTCTGTGACATCAA	NM_003977:	NM_003977:
23746	AIPL1	aryl hydrocarbon receptor interacting protein-like 1	0.08	TACAGAAGAGCTTATGAATAA	NM_014336:	NM_001033054:NM_001033055:NM_014336:
23746	AIPL1	aryl hydrocarbon receptor interacting protein-like 1	0.01	CCCAGGCATCGTGAAGGCCTA	NM_014336:	NM_001033054:NM_001033055:NM_014336:
326	AIRE	autoimmune regulator (autoimmune polyendocrinopathy candidiasis e	0.06	CATCATGTGCCTGGAAATTAA	NM_000658:	NM_000658:NM_000659:NM_000383:
326	AIRE	autoimmune regulator (autoimmune polyendocrinopathy candidiasis e	-2.44	CCGGCCGGCTGGGATCAAGAA	NM_000658:	NM_000658:NM_000659:NM_000383:
55966	AJAP1	adherens junction associated protein 1	-1.11	ATGCTTAGTATGAGCAGAATA	NM_018836:	NM_018836:
55966	AJAP1	adherens junction associated protein 1	1.11	CTGGTTAATATACATATATAA	NM_018836:	NM_018836:
	AK001795		1.88	AACAAGTAATCCCTAGTACTA	AK001795	No hits found till 3 mismatches
203	AK1 (adenyla	adenylate kinase 1	0.96	CCGGGATGCCATGGTGGCCAA	NM_000476:	NM_000476:
203	AK1 (adenyla	adenylate kinase 1	1.61	GCGGCTGGAGACCTATTACAA	NM_000476:	NM_000476:
204	AK2	adenylate kinase 2	1.55	ATGGGTGGGAATGATAGGACA	NM_001625:	NM_001625:
204	AK2	adenylate kinase 2	-5.10	CCACATGTAAAGACTTGGTTA	NM_001625:	NM_001625:
50808	AK3	adenylate kinase 3	1.58	CCCGTGGCACTATGTAAATAA	NM_016282:	NM_016282:
50808	AK3	adenylate kinase 3	0.91	CCGTGGCACTATGTAAATAAA	NM_016282:	NM_016282:
205	AK3L1	adenylate kinase 3-like 1	1.68	CAGGAAGATGTGGTCATTCAT	NM_013410:	NM_001005353:NM_013410:NM_203464:
205	AK3L1	adenylate kinase 3-like 1	2.52	CCTGGTAACAGTGAAATTGAA	NM_013410:	NM_001005353:NM_013410:NM_203464:
26289	AK5	adenylate kinase 5	-3.29	CAGAGCTAGTCAGTACATGAA	NM_174858:	NM_012093:NM_174858:
26289	AK5	adenylate kinase 5	-1.44	CAGCATGGCAGTTGACAACAA	NM_174858:	NM_012093:NM_174858:
122481	AK7	adenylate kinase 7	0.08	CAAGATTGTCTTGACCATTTA	NM_152327:	NM_152327:
122481	AK7	adenylate kinase 7	1.28	GACGATCAATATATAATTAGA	NM_152327:	NM_152327:
8165	AKAP1	A kinase (PRKA) anchor protein 1	0.99	AGCGCTGAACTTGATTGGGAA	NM_003488:	NM_003488:NM_139275:
8165	AKAP1	A kinase (PRKA) anchor protein 1	-0.16	CACGCAGAGATGACAGTACAA	NM_003488:	NM_003488:NM_139275:
11216	AKAP10	A kinase (PRKA) anchor protein 10	-0.93	CAGATAAGCATAGAACTGATA	NM_007202:	NM_007202:
11216	AKAP10	A kinase (PRKA) anchor protein 10	0.78	TAGCAGGACAGCCACACTTAA	NM_007202:	NM_007202:

11215	AKAP11	A kinase (PRKA) anchor protein 11	0.23	ACCGGTTATCTAAATCTATTA	NM_016248:	NM_144490:NM_016248:
11215	AKAP11	A kinase (PRKA) anchor protein 11	0.00	CTGACCGGTTATCTAAATCTA	NM_016248:	NM_144490:NM_016248:
9590	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-0.08	ACGGATGTAGTGTTGAAAGTA	NM_005100:	NM_005100:NM_144497:
9590	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-0.26	CCCGAAATAATCGAACAGATT	NM_005100:	NM_005100:NM_144497:
11214	AKAP13	A kinase (PRKA) anchor protein 13	-1.19	CACGGTCATTATGAGAAACAA	NM_006738:	NM_144767:NM_006738:NM_007200:
11214	AKAP13	A kinase (PRKA) anchor protein 13	1.37	CAGGATTACACTGAAAGTAAT	NM_006738:	NM_144767:NM_006738:NM_007200:
158798	AKAP14	A kinase (PRKA) anchor protein 14	-0.75	CCCATTGTCGTTTCTTATGTA	NM_178813:	NM_001008534:NM_178813:
158798	AKAP14	A kinase (PRKA) anchor protein 14	-2.02	TACGAGGATGAATTGACTCAA	NM_178813:	NM_001008535:NM_178813:NM_001008534:
10566	AKAP3	A kinase (PRKA) anchor protein 3	0.45	AGGGATCATGACCTATGCTAA	NM_006422:	NM_006422:
10566	AKAP3	A kinase (PRKA) anchor protein 3	0.70	ATCAAGCTATCCATAATGAAA	NM_006422:	NM_006422:
8852	AKAP4	A kinase (PRKA) anchor protein 4	0.63	GTCGGTGAACACATTCTCAAA	NM_003886:	NM_139289:NM_003886:
8852	AKAP4	A kinase (PRKA) anchor protein 4	0.45	TACAGTGTCTATGCCGATCAA	NM_003886:	NM_139289:NM_003886:
9495	AKAP5	A kinase (PRKA) anchor protein 5	0.48	AGGGCTTTCATCAAGAAATTA	NM_004857:	NM_004857:
9495	AKAP5	A kinase (PRKA) anchor protein 5	1.16	ATCAGGTTGATCTTTAAATAA	NM_004857:	NM_004857:
9472	AKAP6	A kinase (PRKA) anchor protein 6	-3.02	AAGCATGTGGATGTACATCTA	NM_004274:	NM_004274:
9472	AKAP6	A kinase (PRKA) anchor protein 6	1.92	CACGTTTGTCACTGCCGTTTA	NM_004274:	NM_004274:
9465	AKAP7	A kinase (PRKA) anchor protein 7	-0.34	AACGATGGGTCTGAAGTCCAA	NM_004842:	NM_016377:NM_138633:NM_004842:
9465	AKAP7	A kinase (PRKA) anchor protein 7	-2.47	CCCGATGACGCTGAACTAGTA	NM_004842:	NM_016377:NM_138633:NM_004842:
10270	AKAP8	A kinase (PRKA) anchor protein 8	0.43	CAAGGTTAGCACGCAACAGAA	NM_005858:	NM_005858:
10270	AKAP8	A kinase (PRKA) anchor protein 8	-3.42	GAGGCCGGTAGTGATCCTCAA	NM_005858:	NM_005858:
26993	AKAP8L	A kinase (PRKA) anchor protein 8-like	-0.23	AAGGAACACTTTAAGTACGTA	NM_014371:	NM_014371:
26993	AKAP8L	A kinase (PRKA) anchor protein 8-like	-3.77	CAGGATAACACCACCAACTAT	NM_014371:	NM_014371:
10142	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	-2.40	CAGCCTATCAGTGAACATCAA	NM_005751:	NM_147171:NM_147185:NM_005751:
10142	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	-1.49	CAGCTTCAAAGGGATATACAA	NM_005751:	NM_147171:NM_147185:NM_005751:
10327	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	0.33	AAGAATGCTGATGGGACTATA	NM_006066:	NM_006066:NM_153326:
10327	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	-2.95	CAGCTGTTAAGTATGCCCTTA	NM_006066:	NM_006066:NM_153326:
231	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	-0.24	TAGCTTGATGTTGGATCTCAA	NM_001628:	NM_001628:
231	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	-0.13	CAAACCTGGCTTGAAGTATAA	NM_001628:	NM_001628:
57016	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	-0.24	GAGCAGGACGTGAGACTTCTA	NM_020299:	NM_020299:
57016	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	-0.01	GAGGATGTAAAGATCAATAAA	NM_020299:	NM_020299:
8644	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid deh	-1.48	CACCCTAATTATCCATATTCA	NM_003739:	NM_003739:
8644	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid deh	0.26	CTGGGATCTCAACGAGACAAA	NM_003739:	NM_003739:
1109	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-a	0.51	CCAGAAAGCAAACATAATAAA	NM_001818:	NM_001818:
1109	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-a	-0.24	GAGGGTGTTGCACGACATCTA	NM_001818:	NM_001818:
340811	AKR1CL1	aldo-keto reductase family 1, member C-like 1	0.21	TGGGAAAGAATTACTGCCAAA	NM_001007536:	NM_001007536:
340811	AKR1CL1	aldo-keto reductase family 1, member C-like 1	-0.06	CAAGAGAGAGGAAATATTCTA	NM_001007536:	NM_001007536:
83592	AKR1CL2	aldo-keto reductase family 1, member C-like 2	-0.89	TGGTGTCTGAATAGAACTAAA	NM_031436:	NM_031436:
83592	AKR1CL2	aldo-keto reductase family 1, member C-like 2	0.53	AGGGAAGAATATACAGATTGA	NM_031436:	NM_031436:
6718	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta	0.00	TAGTGTTACTTGGATAGCTTA	NM_005989:	NM_005989:
6718	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta	0.34	CTGGGTAGTAGCGTTGGTAAT	NM_005989:	NM_005989:
8574	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductas	0.72	TGGCCTTAAGCTGACTTAGAA	NM_003689:	NM_003689:
8574	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductas	-0.01	CCAGCTGGAGACGTCATTGAA	NM_003689:	NM_003689:
22977	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductas	-0.80	AACTGGAAGGAGCACCACTTT	NM_012067:	NM_012067:
207	AKT1	v-akt murine thymoma viral oncogene homolog 1	0.71	ACGCTACTTCCTCCTCAAGAA	NM_005163:	NM_001014432:NM_001014431:NM_005163:
207	AKT1	v-akt murine thymoma viral oncogene homolog 1	-1.26	CACGCTTGGTCCCGAGGCCAA	NM_005163:	NM_001014432:NM_001014431:NM_005163:
208	AKT2	v-akt murine thymoma viral oncogene homolog 2	-2.60	ACGGGCTAAAGTGACCATGAA	NM_001626:	NM_001626:
208	AKT2	v-akt murine thymoma viral oncogene homolog 2	0.47	CAAGCGTGGTGAATACATCAA	NM_001626:	NM_001626:
10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, ga	0.47	AACTGTTGGCTTTGGATTAAA	NM_005465:	NM_181690:
10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, ga	0.34	ACCAGAGGTGTTAGAAGATAA	NM_005465:	NM_181690:NM_005465:
210	ALAD	aminolevulinate, delta-, dehydratase	-0.52	CTCCCAATAATCAACAGCAAA	NM_000031:	NM_001003945:NM_000031:
210	ALAD	aminolevulinate, delta-, dehydratase	1.93	AAGGGTGAGCCATCAAGCTAA	NM_000031:	NM_001003945:NM_000031:
212	ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia	1.02	GACCACCTAAAGAAACTTCTA	NM_000032:	NM_001037969:NM_001037968:NM_000032:NM_001037967:
212	ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia	-0.41	CAGGGACAAGATCATGGAGAA	NM_000032:	NM_001037969:NM_001037968:NM_000032:NM_001037967:
214	ALCAM	activated leukocyte cell adhesion molecule	-2.06	CTGAAGAGAATGTTACATTAA	NM_001627:	NM_001627:
214	ALCAM	activated leukocyte cell adhesion molecule	0.09	CAAGTGTTCCCTGATAGACAA	NM_001627:	NM_001627:
126133	ALDH16A1	aldehyde dehydrogenase 16 family, member A1	1.16	CCCAATAAACTCTCTGACCAA	NM_153329:	NM_153329:
126133	ALDH16A1	aldehyde dehydrogenase 16 family, member A1	-4.69	CCGGCTGTCCTGCCTCTCCAA	NM_153329:	NM_153329:
5832	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	0.87	GAGCCAGTCATCCTTAACAAA	NM_002860:	NM_002860:NM_001017423:
5832	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	0.20	TCGCATTTAGTTGGTACTAGA	NM_002860:	NM_001017423:NM_002860:
216	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	0.45	CTGAATATAAAGCTTAATAAA	NM_000689:	NM_000689:
216	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	1.22	CCACGTGGCATCTTTAATAAA	NM_000689:	NM_000689:
8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	-0.45	TAGCCACTAACCAACTAGTTA	NM_003888:	NM_170696:NM_170697:NM_003888:
8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	0.94	GCGGGAGTACTCAGAAGTTAA	NM_003888:	NM_170696:NM_170697:NM_003888:
220	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-0.02	AACCTTGATAGTGATACGTTA	NM_000693:	NM_000693:
220	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-0.29	ACCAGTGTGTGTATAACGAAA	NM_000693:	NM_000693:
219	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	-0.88	CAGCACGTGGATGTTGACAAA	NM_000692:	NM_000692:
219	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	-0.66	TTGAACTAGGTGGATACTAAA	NM_000692:	NM_000692:
10840	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	0.91	CACTGTGTTTGTCAACACGTA	NM_012190:	NM_012190:
10840	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	-0.16	CAGGGTTCTTCTTTGAGCCAA	NM_012190:	NM_012190:
160428	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	0.70	ATGGATATAATTGATAGTCCA	XM_090294:	NM_001034173:
160428	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	0.95	ATGGTCATTTCTAAATTCCAA	XM_090294:	NM_001034173:
217	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	-1.58	CAGCCATTGATGGAAAGTTCA	NM_000690:	NM_000690:
217	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	-2.63	CACAGTCAAAGTGCCTCAGAA	NM_000690:	NM_000690:
218	ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	-0.64	CAGCAACGACAAGGTGATTAA	NM_000691:	NM_000691:
218	ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	-1.64	AGGGAACTCAGTGGTCCTCAA	NM_000691:	NM_000691:
224	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	0.32	CTCTAAGAGAGTAATCATAAA	NM_000382:	NM_001031806:NM_000382:
224	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	1.63	GAGAATGTGATTTACTTTATA	NM_000382:	NM_001031806:NM_000382:
221	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	-1.03	CAGGAGCTTGTAACTCTTTAT	NM_000694:	NM_000694:NM_001030010:
221	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	-0.08	CTGGCTGATGTCACCTGAATA	NM_000694:	NM_001030010:NM_000694:
222	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	-0.96	CCCACCCTATACCGACTGGAA	NM_000695:	NM_000695:NM_001031615:
222	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	-5.60	CACGGCCGTCTCCACCAGAAA	NM_000695:	NM_000695:NM_001031615:
8659	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	-0.52	CAGGGTAAAGTGTAACTCAGA	NM_003748:	NM_003748:
8659	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	1.61	CAACTTCTACATCAACGACAA	NM_003748:	NM_170726:NM_003748:
7915	ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehy	0.18	AAGGAGACTTATCTACATATA	NM_001080:	NM_001080:NM_170740:
7915	ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehy	0.67	TTCGGAAGTGGTACAATTTAA	NM_001080:	NM_001080:NM_170740:
4329	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	-0.59	AACCATCATCTCGAATGTCAA	NM_005589:	NM_005589:
4329	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	-0.69	CAGCTTTGTGGGATCCAACAA	NM_005589:	NM_005589:
501	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	-1.08	AAGGTCTACTTGTACTATCAA	NM_001182:	NM_001182:
501	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	0.39	TCCGATTCTCTATGTCTTTAA	NM_001182:	NM_001182:
64577	ALDH8A1	aldehyde dehydrogenase 8 family, member A1	1.10	CAAGAAGAGTACATAGTTTGA	NM_022568:	NM_022568:NM_170771:
64577	ALDH8A1	aldehyde dehydrogenase 8 family, member A1	-2.38	CTGGATAAAGCAGGTGTTCCA	NM_022568:	NM_022568:NM_170771:
223	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	0.61	TACGCAAATATTGATCACGAA	NM_000696:	NM_000696:
223	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	0.45	CCGTGTGACAATCGAATATTA	NM_000696:	NM_000696:
226	ALDOA	aldolase A, fructose-bisphosphate	0.24	GCCAAATAAACAGCTATTTAA	NM_000034:	NM_184041:NM_184043:NM_000034:
226	ALDOA	aldolase A, fructose-bisphosphate	0.47	TCCGGCACACTGCCAAATAAA	NM_000034:	NM_184041:NM_184043:NM_000034:
229	ALDOB (aldol	aldolase B, fructose-bisphosphate	-1.85	AAGGAGATAGCTGCAACCAAA	NM_000035:	NM_000035:
229	ALDOB (aldol	aldolase B, fructose-bisphosphate	0.17	CTGGAAATACAACACATGTTA	NM_000035:	NM_000035:

29929	ALG6 (aspara	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-glucosylt	0.56	CCGGTTGATCGTGGATTATTT	NM_013339:	NM_013339:
29929	ALG6 (aspara	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-glucosylt	2.02	AGGCCTTATTCTTATAGACTA	NM_013339:	NM_013339:
238	ALK	anaplastic lymphoma kinase (Ki-1)	1.21	CACCTACGTATTTAAGATGAA	NM_004304:	NM_004304:
238	ALK	anaplastic lymphoma kinase (Ki-1)	0.06	CTGGGCCTGTATACCGGATAA	NM_004304:	NM_004304:
121642	ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	-2.52	CACGGACGTGTTGCAGTGATA	NM_001001655:	NM_001001655:
121642	ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	0.04	GTGCGGTTTACCCGTGTTTAA	NM_001001655:	NM_001001655:
221120	ALKBH3	alkB, alkylation repair homolog 3 (E. coli)	0.00	ATCGCTATCATCTTTAGGCAA	NM_139178:	NM_139178:
221120	ALKBH3	alkB, alkylation repair homolog 3 (E. coli)	-1.33	CAGAGAGGATATAACTTATCA	NM_139178:	NM_139178:
91801	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	0.51	GCCGTACTCATTTGCAAGATA	NM_138775:	NM_138775:
91801	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	0.14	CTGCAAAGCTACTACGATCAA	NM_138775:	NM_138775:
239	ALOX12	arachidonate 12-lipoxygenase	-0.74	CTGGTATGCCTGGGTCCCTAA	NM_000697:	NM_000697:
239	ALOX12	arachidonate 12-lipoxygenase	0.92	CCCAAAGCTGTGCTAAACCAA	NM_000697:	NM_000697:
242	ALOX12B	arachidonate 12-lipoxygenase, 12R type	0.49	CCGATATGTCACTATAGTCAT	NM_001139:	NM_001139:
242	ALOX12B	arachidonate 12-lipoxygenase, 12R type	0.89	CTGATCCGATATGTCACTATA	NM_001139:	NM_001139:
246	ALOX15 (arac	arachidonate 15-lipoxygenase	-0.23	CCCAAATTGAGTTTAACAATA	NM_001140:	NM_001140:
246	ALOX15 (arac	arachidonate 15-lipoxygenase	-0.10	CTGGGAAATCATCTATCGGTA	NM_001140:	NM_001140:
247	ALOX15B (ara	arachidonate 15-lipoxygenase, type B	-0.62	CACCAAGAAGTGGCTGCCAAA	NM_001141:	NM_001141:
247	ALOX15B (ara	arachidonate 15-lipoxygenase, type B	-6.42	TTGGACCTTATGGTCACCCAA	NM_001141:	NM_001141:
240	ALOX5	arachidonate 5-lipoxygenase	1.46	CCCAATTCAATTACTATTGAA	NM_000698:	NM_000698:
240	ALOX5	arachidonate 5-lipoxygenase	-0.64	ACCGACGTAAAGAACTGGAAA	NM_000698:	NM_000698:
241	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	1.53	TTGGTGTTCTCATCTAATCAA	NM_001629:	NM_001629:
241	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	0.91	TGCTGGCATATTCAACTATTA	NM_001629:	NM_001629:
59344	ALOXE3	arachidonate lipoxygenase 3	-2.44	AAGCCGCTGACCAAAGTCCAA	NM_021628:	NM_021628:
59344	ALOXE3	arachidonate lipoxygenase 3	-0.26	GACGATCTCGCTGCTCTTCAA	NM_021628:	NM_021628:
248	ALPI	alkaline phosphatase, intestinal	-3.47	CACGTCCATCCTGTACGGCAA	NM_001631:	NM_001631:
248	ALPI	alkaline phosphatase, intestinal	0.00	TCCATTCTCCTAGGAGACAAA	NM_001631:	NM_001631:
80216	ALPK1	alpha-kinase 1	-3.57	CAGCCCTTGGTCCTATCTGAA	NM_025144:	NM_025144:
80216	ALPK1	alpha-kinase 1	-0.01	CAGGCCCTACATTTAAAGCTA	NM_025144:	NM_025144:
115701	ALPK2	alpha-kinase 2	-1.08	AGCGAAGACCTTGGCATTTAT	NM_052947:	NM_052947:
115701	ALPK2	alpha-kinase 2	-5.19	CGGCCTCATGCCTGTCTTCAA	NM_052947:	NM_052947:
249	ALPL	alkaline phosphatase, liver/bone/kidney	5.09	CAGGATTGGAACATCAGTTAA	NM_000478:	NM_000478:
249	ALPL	alkaline phosphatase, liver/bone/kidney	-1.33	CCGGGACTGGTACTCAGACAA	NM_000478:	NM_000478:
251	ALPPL2	alkaline phosphatase, placental-like 2	2.01	CTGGGAAACACAAAGCAATAA	X53279:	NM_031313:
251	ALPPL2	alkaline phosphatase, placental-like 2	0.55	TTGCTTTATCTTGCTCTTGAA	X53279:	NM_031313:
57679	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	-2.80	CAGAGAGTGAATACACTGGAA	NM_020919:	NM_020919:
57679	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	0.19	CGGGCCAGGATTAGGAATTTA	NM_020919:	NM_020919:
259173	ALS2CL	ALS2 C-terminal like	1.07	CAGCCTGACCCTGGCCTCAAA	NM_147129:	NM_147129:NM_182775:
259173	ALS2CL	ALS2 C-terminal like	-0.42	CCCAAGTGGCTTGTAAATCAT	NM_147129:	NM_147129:NM_182775:
55437	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candida	-8.10	CAGGAACACTGGTAACTATAA	NM_018571:	NM_018571:
55437	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candida	1.86	CCAGTGGAACTCACACAGTAA	NM_018571:	NM_018571:
65061	ALS2CR7 (an	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candida	0.31	CTGGACATAAACTAAGTCTAA	NM_139158:	NM_139158:
65061	ALS2CR7 (an	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candida	-1.99	CTGGCGTACATCCACCACCAA	NM_139158:	NM_139158:
60529	ALX4	aristaless-like homeobox 4	-4.93	CAGCCTCAGCCCAGGCCTCAA	NM_021926:	NM_021926:
60529	ALX4	aristaless-like homeobox 4	-7.34	CCGGACCACCTTCACCAGCTA	NM_021926:	NM_021926:
23600	AMACR	alpha-methylacyl-CoA racemase	0.93	GACGGGATTGTCTTTACATAA	NM_014324:	NM_203382:NM_014324:
23600	AMACR	alpha-methylacyl-CoA racemase	0.51	TTGGACTGAGTTAAGTTACAA	NM_014324:	NM_203382:NM_014324:
262	AMD1	adenosylmethionine decarboxylase 1	1.05	CTGGGCTTAATATTCTTTAAA	NM_001634:	NM_001033059:NM_001634:
265	AMELX	amelogenin (amelogenesis imperfecta 1, X-linked)	-3.10	CAGGAGTGACACAAGAACACA	NM_001142:	NM_001142:NM_182680:NM_182681:
265	AMELX	amelogenin (amelogenesis imperfecta 1, X-linked)	1.59	CAAACAGAAACTTGCACTGAA	NM_001142:	NM_001142:NM_182680:NM_182681:
267	AMFR	autocrine motility factor receptor	0.69	AAGGATCGATTTGAATATCTT	NM_138958:	NM_138958:NM_001144:
267	AMFR	autocrine motility factor receptor	1.58	CACGCTCAGTTGAAATAACAA	NM_138958:	NM_138958:NM_001144:
268	AMH	anti-Mullerian hormone	0.23	CGCGTGGCTGCTGAACTGCAA	NM_000479:	NM_000479:
268	AMH	anti-Mullerian hormone	-0.36	CCACGTGGTGCTGCTGCTGAA	NM_000479:	NM_000479:
269	AMHR2	anti-Mullerian hormone receptor, type II	0.03	CAGAATGTGCTCATTCGGGAA	NM_020547:	NM_020547:
269	AMHR2	anti-Mullerian hormone receptor, type II	0.78	ATGGCCAATATAAACCAGGTA	NM_020547:	NM_020547:
84883	AMID	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer	-1.46	CACCGACTATGTTACAGTGTA	NM_032797:	NM_032797:
84883	AMID	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer	0.83	CAGGTTTCATTTAAGAAGAAA	NM_032797:	NM_032797:
347902	AMIGO2	adhesion molecule with Ig-like domain 2	0.48	TAGCATCATCACAGACCTATA	NM_181847:	NM_181847:
347902	AMIGO2	adhesion molecule with Ig-like domain 2	2.01	TAGATGTTTCTTATAACCGAA	NM_181847:	NM_181847:
9949	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocy	-0.02	CGCCAGCATCATCATTTCCAA	NM_015365:	NM_001025580:NM_015365:
9949	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocy	-0.13	CTGACCAGGTATCGTAGTGAA	NM_015365:	NM_001025580:NM_015365:
81693	AMN	amnionless homolog (mouse)	-2.61	CAGGGTGGCCTTACTCAGTAA	NM_030943:	NM_030943:
81693	AMN	amnionless homolog (mouse)	-1.06	CAGCCACAGTTACTTCGTCAA	NM_030943:	NM_030943:
270	AMPD1	adenosine monophosphate deaminase 1 (isoform M)	0.74	TTGCTGAGGGTCTTAAATCAA	NM_000036:	NM_000036:
270	AMPD1	adenosine monophosphate deaminase 1 (isoform M)	-4.26	CGCCATGTCACCACTAAGTAA	NM_000036:	NM_000036:
271	AMPD2 (ader	adenosine monophosphate deaminase 2 (isoform L)	-4.16	CCGGACCAATGTGCCAGACAT	NM_004037:	NM_004037:NM_203404:NM_139156:
271	AMPD2 (ader	adenosine monophosphate deaminase 2 (isoform L)	0.02	CGGCTTCTCGCACAAGGTAAA	NM_004037:	NM_004037:NM_203404:NM_139156:
272	AMPD3 (ader	adenosine monophosphate deaminase (isoform E)	0.71	CCGATATGAGACCTTATGCAA	NM_000480:	NM_001025389:NM_000480:NM_001025390:
272	AMPD3 (ader	adenosine monophosphate deaminase (isoform E)	1.28	CTGCGTGACCTGTATTTGAAA	NM_000480:	NM_001025389:NM_000480:NM_001025390:
51321	AMZ2	archaemetzincins-2	-0.39	CCCGTGGAAGCCTTTAAGGAA	NM_016627:	NM_016627:NM_001033572:NM_001033574:NM_001033570:NM_001033571:NM_001033569:
51321	AMZ2	archaemetzincins-2	0.28	CAGCATTGTAGAAAGATACAA	NM_016627:	NM_016627:NM_001033572:NM_001033574:NM_001033570:NM_001033571:NM_001033569:
64682	ANAPC1	anaphase promoting complex subunit 1	0.88	AACGATTACTAATATAAGAGA	NM_022662:	NM_022662:
64682	ANAPC1	anaphase promoting complex subunit 1	-0.01	AACGTGACTTCTGCACAACAA	NM_022662:	NM_022662:
10393	ANAPC10	anaphase promoting complex subunit 10	1.10	ATCCTGTATTCAAATAATATA	NM_014885:	NM_014885:
10393	ANAPC10	anaphase promoting complex subunit 10	-0.38	CAAGGCATCCGTTATATCTAA	NM_014885:	NM_014885:
51529	ANAPC11	APC11 anaphase promoting complex subunit 11 homolog (yeast)	-3.17	CAGGCCCATTTGAGATCTTTG	NM_016476:	NM_001002246:NM_001002249:NM_016476:NM_001002248:
51529	ANAPC11	APC11 anaphase promoting complex subunit 11 homolog (yeast)	-2.57	CCGCCAGGAATGGAAGTTCAA	NM_016476:	NM_001002247:NM_001002244:NM_001002246:NM_001002249:NM_016476:NM_001002248:NM_001002245:
29882	ANAPC2	anaphase promoting complex subunit 2	-9.17	AAGGTTCTTCTACCGCATCTA	NM_013366:	NM_013366:
29882	ANAPC2	anaphase promoting complex subunit 2	-1.33	CTCACTGGATCGTATCTACAA	NM_013366:	NM_013366:
29945	ANAPC4	anaphase promoting complex subunit 4	-6.61	CAAGCTGGTGCTGCCGCTTTA	NM_013367:	NM_013367:
29945	ANAPC4	anaphase promoting complex subunit 4	-1.87	CAAGGCTAGATGAACAGTGTA	NM_013367:	NM_013367:
51433	ANAPC5	anaphase promoting complex subunit 5	-1.54	ACCCTTGATAAACCATCTCTA	NM_016237:	NM_016237:
51433	ANAPC5	anaphase promoting complex subunit 5	-0.53	CAGAATCAAACTGATGGCTGA	NM_016237:	NM_016237:
51434	ANAPC7	anaphase promoting complex subunit 7	0.78	CAGCTTCTATAGCAAACGCTA	NM_016238:	NM_016238:
51434	ANAPC7	anaphase promoting complex subunit 7	0.41	CCCAAAGGCCAGATTACATTA	NM_016238:	NM_016238:
283	ANG	angiogenin, ribonuclease, RNase A family, 5	1.10	AACGTTGTTGTTGCTTGTGAA	NM_001145:	NM_001145:
283	ANG	angiogenin, ribonuclease, RNase A family, 5	-2.21	CAGCATCAAGGCCATCTGTGA	NM_001145:	NM_001145:
284	ANGPT1	angiopoietin 1	-0.11	AACAGTTTATTAGAACATAAA	NM_001146:	NM_001146:
284	ANGPT1	angiopoietin 1	-3.16	CCGGATTTCTCTTCCCAGAAA	NM_001146:	NM_001146:
285	ANGPT2	angiopoietin 2	1.15	CAGCAACGCTATGTGCTTAAA	NM_001147:	NM_001147:
285	ANGPT2	angiopoietin 2	-0.62	TCGCAACTGACTAATCAGCAA	NM_001147:	NM_001147:
51378	ANGPT4	angiopoietin 4	0.44	CAAGACGATCTTGAGGTCGAA	NM_015985:	NM_015985:
51378	ANGPT4	angiopoietin 4	0.84	CAGGCTTTCTGTGGTCGGGTA	NM_015985:	NM_015985:
9068	ANGPTL1	angiopoietin-like 1	0.33	CGGGAGATAGATGTTCTGCAA	NM_004673:	NM_004673:

9068	ANGPTL1	angiopoietin-like 1	1.42	CTCGTGTTACTCAACTCTATA	NM_004673:	NM_004673:
23452	ANGPTL2	angiopoietin-like 2	-1.32	ACCGGCCGTATAGATAATGTA	NM_012098:	NM_012098:
23452	ANGPTL2	angiopoietin-like 2	-1.62	CCGCATCTCATCTCCAAACTA	NM_012098:	NM_012098:
27329	ANGPTL3	angiopoietin-like 3	0.59	ACCGTGGAAGACCAATATAAA	NM_014495:	NM_014495:
27329	ANGPTL3	angiopoietin-like 3	-2.54	CAGGTAGTCCATGGACATTAA	NM_014495:	NM_014495:
51129	ANGPTL4	angiopoietin-like 4	-0.27	CAGATGGAGGCTGGACAGTAA	NM_016109:	NM_139314:NM_016109:
51129	ANGPTL4	angiopoietin-like 4	0.08	CAGCCTGCAGACACAACTCAA	NM_016109:	NM_139314:NM_016109:
253935	ANGPTL5 (ar	angiopoietin-like 5	0.07	CACCGAGTGGTTTATACATAA	NM_178127:	NM_178127:
253935	ANGPTL5 (ar	angiopoietin-like 5	1.75	TACGGACTCTTCAGTAGTTAA	NM_178127:	NM_178127:
83854	ANGPTL6	angiopoietin-like 6	-2.61	CACCGTGGATAGGGACCGAGA	NM_031917:	NM_031917:
83854	ANGPTL6	angiopoietin-like 6	-0.01	GAGGCAAGATGGTTCAGTCAA	NM_031917:	NM_031917:
10218	ANGPTL7	angiopoietin-like 7	2.05	CTGAAGGTAGATGGTGTTATA	NM_021146:	NM_021146:
10218	ANGPTL7	angiopoietin-like 7	-0.05	ACCGCCTGGGTGAGCACAATA	NM_021146:	NM_021146:
287	ANK2	ankyrin 2, neuronal	0.94	ACCGTGCAAACGGGTGATATA	NM_001148:	NM_001148:
287	ANK2	ankyrin 2, neuronal	-0.22	CAGGACCCTTCTAAACATAAA	NM_001148:	NM_001148:
288	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-0.24	CTAGTCGATTATTTAAGCATA	NM_001149:	NM_001149:NM_020987:
288	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	1.17	CGCATCCTTAGCTTTACGTAA	NM_001149:	NM_001149:NM_020987:
162282	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	0.33	CAGGACAGAATAATCCTTACA	NM_153228:	NM_153228:
162282	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	0.69	CACACCAGTTCTATTACACAA	NM_153228:	NM_153228:
56172	ANKH	ankylosis, progressive homolog (mouse)	0.62	TTGAATGTAAGGCTCAGTAAA	NM_054027:	NM_054027:
56172	ANKH	ankylosis, progressive homolog (mouse)	0.30	ATCAATGAACATTGTACCTTA	NM_054027:	NM_054027:
54467	ANKIB1	ankyrin repeat and IBR domain containing 1	1.04	CCCAATATACTTCTTGCAATA	XM_377955:	XM_377955:XM_380018:
54467	ANKIB1	ankyrin repeat and IBR domain containing 1	1.08	AACGGAATGTGCACAATGAAA	XM_377955:	XM_377955:XM_380018:
255239	ANKK1	ankyrin repeat and kinase domain containing 1	-0.56	AGGAGCCGAGATGGAAATTTA	NM_178510:	NM_178510:
255239	ANKK1	ankyrin repeat and kinase domain containing 1	-2.34	GCGGACGGAGTACGCCATCAA	NM_178510:	NM_178510:
51281	ANKMY1	ankyrin repeat and MYND domain containing 1	-1.53	CAGCAAGTACTGCAAGACCAA	NM_016552:	NM_016552:NM_017844:
51281	ANKMY1	ankyrin repeat and MYND domain containing 1	0.02	CCAGAGGAACATGGACAGCAA	NM_016552:	NM_016552:NM_017844:
91074	ANKRD30A	ankyrin repeat domain 30A	2.00	AACCGTATATATCAATATGAA	NM_052997:	NM_052997:
91074	ANKRD30A	ankyrin repeat domain 30A	-0.87	CAGGAGATGCTTGTTTGCAAA	NM_052997:	NM_052997:
353322	ANKRD37	ankyrin repeat domain 37	-2.53	CCCAAATTGATTTATGTAATA	NM_181726:	NM_181726:
353322	ANKRD37	ankyrin repeat domain 37	-0.84	AAGTTTCTTACAACAATTAAA	NM_181726:	NM_181726:
54443	ANLN	anillin, actin binding protein (scraps homolog, Drosophila)	0.33	CACCGTTTCCATCGTCTCGTA	NM_018685:	NM_018685:
54443	ANLN	anillin, actin binding protein (scraps homolog, Drosophila)	0.17	CTGATGCTTGCTACAAACCTA	NM_018685:	NM_018685:
8125	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-3.14	CGGAGCTGGTTGAGCCTTCAA	NM_006305:	NM_006305:
8125	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	0.05	AACGTTGCTGTGGGAACGAGA	NM_006305:	NM_006305:
81611	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.32	CCCAGCTTAAATAAACTTCGA	NM_030920:	NM_030920:
81611	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.81	TTGGAGCTTAGTGATAATATA	NM_030920:	NM_030920:
290	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptida	-1.36	CCGAAATGCCACACTGGTCAA	NM_001150:	NM_001150:
290	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptida	-1.18	CCGGGTGAACTACGACGAAGA	NM_001150:	NM_001150:
84168	ANTXR1	anthrax toxin receptor 1	0.31	CCGAGGAACAACCTTAATGAA	NM_018153:	NM_032208:NM_018153:NM_053034:
84168	ANTXR1	anthrax toxin receptor 1	0.89	CTGACAGAAGACAGAGAACAA	NM_018153:	NM_032208:NM_018153:NM_053034:
118429	ANTXR2	anthrax toxin receptor 2	0.09	CACGTCGACGATGCCAAATTA	NM_058172:	NM_058172:
118429	ANTXR2	anthrax toxin receptor 2	0.99	CCCGAGTTCCATCTCAGTAAA	NM_058172:	NM_058172:
93550	ANUBL1	AN1, ubiquitin-like, homolog (Xenopus laevis)	0.07	CTGCCCGGGATTCGTATTATA	NM_174890:	NM_174890:
93550	ANUBL1	AN1, ubiquitin-like, homolog (Xenopus laevis)	1.41	ATGGTGTTGGAATGAATGGAA	NM_174890:	NM_174890:
301	ANXA1	annexin A1	-0.19	ATGCCTCACAGCTATCGTGAA	NM_000700:	NM_000700:
301	ANXA1	annexin A1	0.08	ATGGTTAAAGGTGTGGATGAA	NM_000700:	NM_000700:
302	ANXA2	annexin A2	0.99	TCGCTATTTAAGTTAAATTTA	NM_004039:	NM_001002857:NM_001002858:NM_004039:
302	ANXA2	annexin A2	1.21	TTAAGTTAAATTTAAATGAAA	NM_004039:	NM_001002857:NM_001002858:NM_004039:
221656	AOF1	amine oxidase (flavin containing) domain 1	-1.22	ATCGATGCGGTATGAAACCAA	XM_173173:	NM_153042:
221656	AOF1	amine oxidase (flavin containing) domain 1	-0.42	AGGGACTAAATATGACTTTAA	XM_173173:	NM_153042:
23028	AOF2	amine oxidase (flavin containing) domain 2	-0.64	CTGGAAATGACTATGATTTAA	NM_015013:	NM_015013:
23028	AOF2	amine oxidase (flavin containing) domain 2	0.79	AGGCCTAGACATTAAACTGAA	NM_015013:	NM_015013:
316	AOX1	aldehyde oxidase 1	-0.18	ACCAACAGAAATTATACCATA	NM_001159:	NM_001159:
316	AOX1	aldehyde oxidase 1	0.33	TACCCTCAACTTGCTATCAAA	NM_001159:	NM_001159:
1174	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	-0.01	CAAAGTTGTCTATAAGAGATA	NM_001283:	NM_057089:NM_001283:
1174	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	-0.23	CGAGCTGGACATCATCTTCAA	NM_001283:	NM_057089:NM_001283:
8905	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	1.19	CAGGCAGTATACATTTATTAA	NM_003916:	NM_003916:
8905	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.31	AAGGGAACTTTAGTTAATTAA	NM_003916:	NM_003916:
163	AP2B1	adaptor-related protein complex 2, beta 1 subunit	-0.68	CCGGTGCACATTAAAGATCCA	NM_001282:	NM_001282:NM_001030006:
163	AP2B1	adaptor-related protein complex 2, beta 1 subunit	2.81	TCCCATCTATGTTAAACTAGA	NM_001282:	NM_001282:NM_001030006:
1173	AP2M1	adaptor-related protein complex 2, mu 1 subunit	-1.88	TGGAGGCTTATTCATCTATAA	NM_004068:	NM_004068:NM_001025205:
1173	AP2M1	adaptor-related protein complex 2, mu 1 subunit	0.41	TGCCATCGTGTGGAAGATCAA	NM_004068:	NM_004068:NM_001025205:
8546	AP3B1	adaptor-related protein complex 3, beta 1 subunit	-0.66	TTGCCGTTACCCAGTAACATA	NM_152671:	NM_003664:
8943	AP3D1	adaptor-related protein complex 3, delta 1 subunit	1.24	CTGAGTGTTAATTTAACTCTA	NM_003938:	NM_003938:
8943	AP3D1	adaptor-related protein complex 3, delta 1 subunit	-4.10	CCGCGTGAAGGCCATCCGCAA	NM_003938:	NM_003938:
1176	AP3S1	adaptor-related protein complex 3, sigma 1 subunit	-0.49	CAAGGCGATCCTAATCTTCAA	NM_001284:	NM_001284:NM_001002924:
1176	AP3S1	adaptor-related protein complex 3, sigma 1 subunit	1.90	CAAGTATTTGTGGAAACATTA	NM_001284:	NM_001284:NM_001002924:
317	APAF1	apoptotic peptidase activating factor	-0.36	AAGGGCAATGGAGATAAATTA	NM_001160:	NM_013229:NM_181868:NM_181869:NM_181861:NM_001160:
317	APAF1	apoptotic peptidase activating factor	0.82	CAGTGAAGGTATGGAATATTA	NM_001160:	NM_013229:NM_181868:NM_181861:NM_001160:
324	APC	adenomatosis polyposis coli	-0.67	CAGACTAAGCATTGAGCATAA	NM_000038:	NM_000038:
324	APC	adenomatosis polyposis coli	0.25	CCGGTGATTGACAGTGTTTCA	NM_000038:	NM_000038:
10297	APC2	adenomatosis polyposis coli 2	0.06	CCGCGGTCTCTGGACAATCAA	NM_005883:	NM_005883:
10297	APC2	adenomatosis polyposis coli 2	1.23	CAGTGTTAAACGGACGTGTAA	NM_005883:	NM_005883:
325	APCS	amyloid P component, serum	1.04	CTGTATGTCTGCCTAATTAAA	NM_001639:	NM_001639:
325	APCS	amyloid P component, serum	2.03	AGAGGATATGTCATCATCAAA	NM_001639:	NM_001639:
10290	APEG1	aortic preferentially expressed gene 1	1.13	AACACCTATTTCTTAACTCAA	NM_005876:	NM_005876:
10290	APEG1	aortic preferentially expressed gene 1	-8.18	CAGCTGGAATAACAAGCCCAA	NM_005876:	NM_005876:
327	APEH	N-acylaminoacyl-peptide hydrolase	-3.33	CAGAGGAATGTGGGCTATGTA	NM_001640:	NM_001640:
327	APEH	N-acylaminoacyl-peptide hydrolase	-0.26	CAGGAGGAACACTTTGATGCA	NM_001640:	NM_001640:
328	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-1.82	ACCCTTAATTAAGATCCTCAA	NM_001641:	NM_001641:
328	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-0.33	CCAGATATACTGTGCCTTCAA	NM_001641:	NM_001641:NM_080648:NM_080649:
27301	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	-0.58	ACGCTGCAGCACAACAATCAA	NM_014481:	NM_014481:
27301	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	-0.11	CTGGCTATCGTTGAGGGTTAT	NM_014481:	NM_014481:
51107	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	-1.42	TTGGTGTGATAAATACCCTAA	NM_016022:	NM_016022:
51107	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	-0.08	ATGAAATTAATGGAGGCTCAA	NM_016022:	NM_016022:
8539	API5	apoptosis inhibitor 5	0.75	AAGAGTAATGGTCAATCTTAA	NM_006595:	NM_006595:
8539	API5	apoptosis inhibitor 5	1.21	CAAGTTTGCTATTCAAATCAA	NM_006595:	NM_006595:
8862	APLN	apelin, AGTRL1 ligand	0.96	CCCAAATCGGTTCTAGGTCAA	NM_017413:	NM_017413:
8862	APLN	apelin, AGTRL1 ligand	1.16	TGGGCCTGACATGGCTATATA	NM_017413:	NM_017413:
333	APLP1	amyloid beta (A4) precursor-like protein 1	-0.80	CCCTACTAACATCCCAATAAA	NM_005166:	NM_001024807:NM_005166:
333	APLP1	amyloid beta (A4) precursor-like protein 1	-0.02	CACAGACGGTGTGGATATTTA	NM_005166:	NM_001024807:NM_005166:
334	APLP2	amyloid beta (A4) precursor-like protein 2	1.02	TAGCCTGTAGCTTATATTTGA	NM_001642:	NM_001642:
334	APLP2	amyloid beta (A4) precursor-like protein 2	0.38	CAGCGTCTTCTAGAGAGCTTA	NM_001642:	NM_001642:
335	APOA1	apolipoprotein A-I	0.87	CACGCTCAGCGAGAAGGCCAA	NM_000039:	NM_000039:XM_496536:
335	APOA1	apolipoprotein A-I	1.57	CTCAGAATAAACGTTTCCAAA	NM_000039:	NM_000039:XM_496536:
336	APOA2 (apoli	apolipoprotein A-II	0.02	AGGCCAAGTCTTACTTTGAAA	NM_001643:	NM_001643:

336	APOA2 (apoli	apolipoprotein A-II	-0.30	CCCACTCTTTGCTACAATAAA	NM_001643:	NM_001643:
116519	APOA5	apolipoprotein A-V	-3.36	CTGACATAGCTCTACACCTAA	NM_052968:	NM_052968:
116519	APOA5	apolipoprotein A-V	-5.39	CTCCCGGAAGCTCACGCTCAA	NM_052968:	NM_052968:
338	APOB	apolipoprotein B (including Ag(x) antigen)	-1.00	CAGCACCTAGCTGGAAAGTTA	NM_000384:	NM_000384:
338	APOB	apolipoprotein B (including Ag(x) antigen)	-0.81	CCGGGTCAAATATACCTTGAA	NM_000384:	NM_000384:
55911	APOB48R	apolipoprotein B48 receptor	-0.66	CTGGGAATACCGTGAACTTAA	NM_018690:	NM_018690:NM_182804:
55911	APOB48R	apolipoprotein B48 receptor	-0.59	AAGGCTGGGACTCGAAAGAAA	NM_018690:	NM_018690:NM_182804:
344	APOC2	apolipoprotein C-II	-0.69	ACAATAAATAATCGTAACAAA	NM_000483:	NM_000483:
344	APOC2	apolipoprotein C-II	0.02	GTGAATAGTAACAATAAATAA	NM_000483:	NM_000483:
345	APOC3	apolipoprotein C-III	-0.15	CCCAATAAAGCTGGACAAGAA	NM_000040:	NM_000040:XM_496537:
345	APOC3	apolipoprotein C-III	1.13	CTGGAGCACCGTTAAGGACAA	NM_000040:	NM_000040:XM_496537:
348	APOE	apolipoprotein E	1.94	CCCTAGTTTAATAAAGATTCA	NM_000041:	NM_000041:
348	APOE	apolipoprotein E	-1.38	AAGGAGTTGAAGGCCTACAAA	NM_000041:	NM_000041:
319	APOF	apolipoprotein F	-0.92	ATGAGTTGCCCTGTAAATTTA	NM_001638:	NM_001638:
319	APOF	apolipoprotein F	-3.07	AAGCTATATACATGTCTTCAA	NM_001638:	NM_001638:
350	APOH	apolipoprotein H (beta-2-glycoprotein I)	0.32	CAAGTTGTAAAGCATCTTGTA	NM_000042:	NM_000042:
350	APOH	apolipoprotein H (beta-2-glycoprotein I)	-0.45	CTGGATGGCCCGGAAGAAATA	NM_000042:	NM_000042:
23780	APOL2	apolipoprotein L, 2	0.34	AAGCGGCACCAATGTAGCAAA	NM_030882:	NM_145637:NM_030882:
23780	APOL2	apolipoprotein L, 2	-0.79	CAGGTTGAGAGGGTTGTTGAA	NM_030882:	NM_145637:NM_030882:
351	APP	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer dis	0.15	AAGGATGACTACAGACATTAA	NM_000484:	NM_201414:NM_000484:NM_201413:
351	APP	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer dis	1.84	ACCCAATTAAGTCCTACTTTA	NM_000484:	NM_201414:NM_000484:NM_201413:
10513	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	0.76	AGGGATGTTTAGGATAAGTTA	NM_006380:	NM_006380:
10513	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.51	CAGCATGTACCGCATGTGTAA	NM_006380:	NM_006380:
353	APRT	adenine phosphoribosyltransferase	-3.41	CAGCCACACTGAACCCAATTA	NM_000485:	NM_000485:NM_001030018:
353	APRT	adenine phosphoribosyltransferase	0.16	CTGTGTTTCAGCCACACTGAA	NM_000485:	NM_000485:NM_001030018:
10603	APS	adaptor protein with pleckstrin homology and src homology 2 domains	0.82	CGCGGACACCTCTGCACTCAA	NM_020979:	NM_020979:
10603	APS	adaptor protein with pleckstrin homology and src homology 2 domains	0.94	CCCACTGTCAGCCATCATTGA	NM_020979:	NM_020979:
54840	APTX	aprataxin	0.00	ACAGTTGAAAGCAGAGTGTAA	NM_017692:	NM_175073:NM_175071:NM_175069:NM_017692: NM_175073:NM_175071:NM_175072:NM_175069:
54840	APTX	aprataxin	0.65	CTACTCATTTCCTAAATTAAA	NM_017692:	NM_017692:
357	APXL	apical protein-like (Xenopus laevis)	0.60	CTCAATGATGCAGGCAATAAA	NM_001649:	NM_001649:
357	APXL	apical protein-like (Xenopus laevis)	2.03	TTCACTCATTCTCAGATTAAA	NM_001649:	NM_001649:
134549	APXL2	apical protein 2	1.20	CTGGATGGACTGATTCCTTTA	NM_133456:	NM_133456:
134549	APXL2	apical protein 2	-1.07	CCGGCGCTGGCTAAGTTTGAA	NM_133456:	NM_133456:
358	AQP1	aquaporin 1 (Colton blood group)	1.17	TTGGAATTTCATTATATGTTA	NM_000385:	NM_000385:NM_198098:
358	AQP1	aquaporin 1 (Colton blood group)	-0.53	CTGAGTGACCTCCTTCTGCAA	NM_000385:	NM_000385:NM_198098:
359	AQP2	aquaporin 2 (collecting duct)	0.73	AAGCTGTGATGTTGTATATAT	NM_000486:	NM_000486:
359	AQP2	aquaporin 2 (collecting duct)	-6.63	CAGGGTAGAGAGGACAAAGAA	NM_000486:	NM_000486:
360	AQP3	aquaporin 3 (Gill blood group)	0.57	CTCCTTTAATCCTCTACTCAA	NM_004925:	NM_004925:
360	AQP3	aquaporin 3 (Gill blood group)	-0.37	CTGGATGTACATACATAAGTA	NM_004925:	NM_004925:
361	AQP4	aquaporin 4	-1.24	TACAACATGGTTGCAGAATAA	NM_001650:	NM_004028:NM_001650:
361	AQP4	aquaporin 4	0.64	GACGGATGACCTGATTCTAAA	NM_001650:	NM_004028:NM_001650:
362	AQP5 (aquap	aquaporin 5	-2.83	AACCCTCATCTTCGTCTTCTT	NM_001651:	NM_001651:
362	AQP5 (aquap	aquaporin 5	0.92	AATGAACCCAGCCCGCTCTTT	NM_001651:	NM_001651:
363	AQP6	aquaporin 6, kidney specific	-0.23	CAGGGACTGCTGTGAAATCAA	NM_001652:	NM_053286:NM_001652:
363	AQP6	aquaporin 6, kidney specific	1.59	CTAAGTTGGTTTAATAGTTAA	NM_001652:	NM_053286:NM_001652:
364	AQP7	aquaporin 7	-0.77	CCAGGAAATACTGCAGAGGAA	NM_001170:	NM_001170:
364	AQP7	aquaporin 7	0.39	GCCCATATGGTTCTAAATAAA	NM_001170:	NM_001170:
343	AQP8 (aquap	aquaporin 8	-2.96	CTGACAATTCTCACTTTGCAA	NM_001169:	NM_001169:
343	AQP8 (aquap	aquaporin 8	-0.11	GAGCGTGTTTCTTGAGAGGAA	NM_001169:	NM_001169:
366	AQP9	aquaporin 9	-0.02	ACGACTGTGCTTGTCCATTAT	NM_020980:	NM_020980:
366	AQP9	aquaporin 9	1.60	CAACCAAACCCTAAATTGAAA	NM_020980:	NM_020980:
367	AR	androgen receptor (dihydrotestosterone receptor; testicular feminizati	0.44	AAGGAACTCGATCGTATCATT	NM_000044:	NM_000044:NM_001011645:
367	AR	androgen receptor (dihydrotestosterone receptor; testicular feminizati	-2.61	CACGGGAAGTTTAGAGAGCTA	NM_000044:	NM_000044:NM_001011645:
369	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	0.05	CCCGCTGACCATGCACAATTT	NM_001654:	NM_001654:
369	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	-7.45	CCGACTCATCAAGGGACGAAA	NM_001654:	NM_001654:
8260	ARD1A	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	-0.24	CCGCCCTGCACCTCTATTCCA	NM_003491:	NM_003491:
8260	ARD1A	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	-1.98	CACAGAGAGCACAGATGTCAA	NM_003491:	NM_003491:
374	AREG	amphiregulin (schwannoma-derived growth factor)	0.38	CAGAGTTGAACAGGTAGTTAA	NM_001657:	NM_001657:
374	AREG	amphiregulin (schwannoma-derived growth factor)	-3.26	CTGCCAAGTCATAGCCATAAA	NM_001657:	NM_001657:
23647	ARFIP2	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	0.53	AAAGTTTGACATCGTCAAGAA	NM_012402:	NM_012402:
23647	ARFIP2	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	0.80	CAGGACCCAACCTCAATGAAA	NM_012402:	NM_012402:
383	ARG1 (argina	arginase, liver	-0.41	AAGCATAGAGTTATCCTTCTA	NM_000045:	NM_000045:
383	ARG1 (argina	arginase, liver	1.04	CGATATAAATCTCATAGTTAA	NM_000045:	NM_000045:
55114	ARHGAP17	Rho GTPase activating protein 17	1.31	CAGCAGACATGTACAACTTTA	NM_018054:	NM_018054:NM_001006634:
55114	ARHGAP17	Rho GTPase activating protein 17	-0.01	AAGCAGTGCGTTAACTATCTA	NM_018054:	NM_018054:NM_001006634:
23092	ARHGAP26	Rho GTPase activating protein 26	0.81	ACCGTATGGCCTATAGTTTAA	NM_015071:	NM_015071:
23092	ARHGAP26	Rho GTPase activating protein 26	-0.89	AGGGAGTATACTAGTAGGTTA	NM_015071:	NM_015071:
396	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	-0.24	ATCCAGCATACGTACAGGAAA	NM_004309:	NM_004309:
396	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	1.13	CCGCCTGGCCATCAGTATTTA	NM_004309:	NM_004309:
397	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-0.93	CACAGCTGGGTCCCTCTTCAA	NM_001175:	NM_001175:
397	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	0.00	CACTGAATAAATAGATCAGAA	NM_001175:	NM_001175:
398	ARHGDIG (R	Rho GDP dissociation inhibitor (GDI) gamma	0.40	AAGGAAGGTGTTGATTACAGA	NM_001176:	NM_001176:
398	ARHGDIG (R	Rho GDP dissociation inhibitor (GDI) gamma	-0.96	CAGAGTGAAGATCTCCTTCAA	NM_001176:	NM_001176:
9639	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	-0.78	CAGGCAGTCACCAGAAATAAA	NM_014629:	NM_014629:
9639	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	0.48	CCGAGTCTTCATGTTAAATGA	NM_014629:	NM_014629:
9826	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	0.02	CACAACGACTCTCGACCGGAA	NM_014784:	NM_014784:NM_198236:
9826	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	0.55	CTGGAGGATCAGCAAGGATAA	NM_014784:	NM_014784:NM_198236:
9828	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	1.03	CAGGAGGTTATTCAGAGCATA	NM_014786:	NM_014786:
9828	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	-0.29	CAGGCTCGAACCCGTGCCAAA	NM_014786:	NM_014786:
9181	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	-0.84	CAGCACCCTACTGCCCTTTAA	NM_004723:	NM_004723:
9181	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	0.14	CAGCGATTGGTCAATCTCTAT	NM_004723:	NM_004723:
50649	ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	0.52	CACATTTAATTTCATAAATAA	NM_015320:	NM_032995:NM_015320:
50649	ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	-4.87	CCGCGACGTGTTGTACTACAA	NM_015320:	NM_032995:NM_015320:
7984	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	1.08	TGGGAACCTTTCATCATTAAA	NM_005435:	NM_001002861:NM_005435:
7984	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	0.50	TTCAGTGATAGCCGTATGTTA	NM_005435:	NM_001002861:NM_005435:
9459	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	0.17	CTCGGTACTCTGGATAACGAA	NM_004840:	NM_004840:
9459	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-1.59	CTGTGAGAAGTTGTAATATTA	NM_004840:	NM_004840:
8289	ARID1A	AT rich interactive domain 1A (SWI- like)	1.24	AACCAAAGTTACTGTTGTTTA	NM_018450:	NM_139135:NM_006015:NM_018450:
8289	ARID1A	AT rich interactive domain 1A (SWI- like)	-7.57	CACCTTGGTTACACTCGCCAA	NM_018450:	NM_139135:NM_006015:NM_018450:
5926	ARID4A	AT rich interactive domain 4A (RBP1-like)	0.05	ACGATTGAAGTTGATAGTATT	NM_002892:	NM_002892:NM_023000:NM_023001:
5926	ARID4A	AT rich interactive domain 4A (RBP1-like)	-1.65	CTGGTTTGACATTGCTAAGTA	NM_002892:	NM_002892:NM_023000:NM_023001:
25820	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1	-1.76	CTGCGCTTTGAGCACAAACTA	NM_005744:	NM_005744:
25820	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1	-1.70	TAGAGTGCAATCGACTGTTAA	NM_005744:	NM_005744:
10425	ARIH2	ariadne homolog 2 (Drosophila)	0.14	AAAGGTTGTACAATTATACAA	NM_006321:	NM_006321:
10425	ARIH2	ariadne homolog 2 (Drosophila)	0.57	ATCGTGAACCAGAGCCAACAA	NM_006321:	NM_006321:
403	ARL3	ADP-ribosylation factor-like 3	1.24	AGGGAACAACACGGTTTAGAA	NM_004311:	NM_004311:
403	ARL3	ADP-ribosylation factor-like 3	1.14	ACCGATATTCTTATATATGTA	NM_004311:	NM_004311:

7873	ARMET	arginine-rich, mutated in early stage tumors	-2.72	CAGCCAGATATGTGAGCTTAA	NM_006010:	NM_006010:
7873	ARMET	arginine-rich, mutated in early stage tumors	0.32	CTGAAGAAGCTCCGAGTTAAA	NM_006010:	NM_006010:
405	ARNT	aryl hydrocarbon receptor nuclear translocator	0.77	CAGCCAATATACAACTGTAAA	NM_001668:	NM_001668:NM_178427:NM_178426:
405	ARNT	aryl hydrocarbon receptor nuclear translocator	-1.26	ACGGAACAAGATGACAGCCTA	NM_001668:	NM_001668:NM_178427:NM_178426:
9915	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	-0.79	GTGGACAGTTTAAGTACTTAA	NM_014862:	NM_014862:
9915	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	-0.99	CCGGAACAGCTCTAGGAATAA	NM_014862:	NM_014862:
406	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	0.06	TCGATGGTTCAGTTTCATGAA	NM_001178:	NM_001178:NM_001030272:NM_001030273:
406	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	0.92	TAGGCACATCGTGTTATGAAT	NM_001178:	NM_001178:NM_001030272:NM_001030273:
56938	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.02	CCCGGTTTGCAGTGAATGGAA	NM_020183:	NM_020183:
56938	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.05	ATGGATGCTTACCCAACTCAA	NM_020183:	NM_020183:
10776	ARPP-19	cyclic AMP phosphoprotein, 19 kD	0.29	CCCGGCCGGCTTATGATTTAA	NM_006628:	NM_006628:
10776	ARPP-19	cyclic AMP phosphoprotein, 19 kD	0.02	CGGCATGTTTGTAGCATACAA	NM_006628:	NM_006628:
407	ARR3	arrestin 3, retinal (X-arrestin)	0.98	CCACTGTAACACTCTAATAAA	NM_004312:	NM_004312:
407	ARR3	arrestin 3, retinal (X-arrestin)	-1.04	CTGGTTGTCCGGAAAGTACAA	NM_004312:	NM_004312:
408	ARRB1	arrestin, beta 1	-0.49	CTCGACGTTCTGCAAGGTCTA	NM_020251:	NM_004041:NM_020251:
408	ARRB1	arrestin, beta 1	0.55	CCAGTAGATACCAATCTCATA	NM_020251:	NM_004041:NM_020251:
409	ARRB2	arrestin, beta 2	0.25	CAAGCTGTGTTCATACCTAAA	NM_199004:	NM_004313:NM_199004:
409	ARRB2	arrestin, beta 2	-0.01	CTCGAACAAGATGACCAGGTA	NM_199004:	NM_004313:NM_199004:
410	ARSA	arylsulfatase A	0.59	TCGGCAGTCTCTCTTCTTCTA	NM_000487:	NM_000487:
410	ARSA	arylsulfatase A	0.42	CAGGGCTTCCATCGATTTCTA	NM_000487:	NM_000487:
411	ARSB	arylsulfatase B	0.28	AACCAACTTTATAGTACATAA	NM_000046:	NM_000046:
411	ARSB	arylsulfatase B	0.62	CACATTTCTTACGCAAATGAA	NM_000046:	NM_000046:
414	ARSD (arylsu	arylsulfatase D	0.62	TCGGTTGCTACGGGAACAATA	NM_001669:	NM_001669:NM_009589:
414	ARSD (arylsu	arylsulfatase D	1.11	AAGGTTCTTAATGCCATCGAA	NM_001669:	NM_001669:
415	ARSE	arylsulfatase E (chondrodysplasia punctata 1)	-0.16	AGGGAAGATGACCCACAATAA	NM_000047:	NM_000047:
415	ARSE	arylsulfatase E (chondrodysplasia punctata 1)	-0.54	CACGAGTTCCTGATGCATTAT	NM_000047:	NM_000047:
416	ARSF	arylsulfatase F	-0.17	ACGGAGGGCATTTGGAAGCTA	NM_004042:	NM_004042:
416	ARSF	arylsulfatase F	-0.60	CTGAACGAGCTGGATCCATTA	NM_004042:	NM_004042:
22901	ARSG	arylsulfatase G	-1.49	CTGGAAGACGATACCGCAGAA	NM_014960:	NM_014960:
22901	ARSG	arylsulfatase G	-6.57	AAGGACAAAGTTGACCACACA	NM_014960:	NM_014960:
347527	ARSH	arylsulfatase family, member H	-2.88	CAGCCATAAGAGAGCATCGTA	XM_293401:	NM_001011719:
347527	ARSH	arylsulfatase family, member H	-0.40	GACGTTGGAATTGCATCCTTA	XM_293401:	NM_001011719:
340075	ARSI	arylsulfatase family, member I	-0.86	CTGGCCGAATATAACCGCACA	XM_291139:	NM_001012301:
340075	ARSI	arylsulfatase family, member I	-0.54	CACGGGCAATGTGGACTATTA	XM_291139:	NM_001012301:
79642	ARSJ	arylsulfatase family, member J	-0.45	CCGATCCATTATCAACATAAA	NM_024590:	NM_024590:
79642	ARSJ	arylsulfatase family, member J	-0.15	CAGATTGATGAGGACATTCAA	NM_024590:	NM_024590:
153642	ARSK	arylsulfatase family, member K	-0.48	AAGGGTCTAGATCCAAATTAT	NM_198150:	NM_198150:
153642	ARSK	arylsulfatase family, member K	-0.57	AAGCAGTAAACTGGTTAAGAA	NM_198150:	NM_198150:
9048	ARTN	artemin	-2.09	CAGCATTTGAAGGACACATAT	NM_057090:	NM_003976:NM_057160:NM_057090:NM_057091:
9048	ARTN	artemin	-1.26	CCCGAACAGGTGAAGGGACAA	NM_057090:	NM_003976:NM_057160:NM_057090:NM_057091:
51752	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regula	0.01	TCCGAATGTATCATTGAATAA	NM_016442:	NM_016442:
51752	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regula	0.25	TCGGGCAAGTCTCATTAACAA	NM_016442:	NM_016442:
57412	AS3MT	arsenic (+3 oxidation state) methyltransferase	-0.04	CCGGCCATAAATGAATTATTT	NM_020682:	NM_020682:
57412	AS3MT	arsenic (+3 oxidation state) methyltransferase	0.15	CAGACCATAAGAAACAACAAA	NM_020682:	NM_020682:
427	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	-3.68	CACGATTAACTGTGAAATGTA	NM_004315:	NM_177924:NM_004315:
427	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	0.19	CACGTTCTGTTAATTTAGTAA	NM_004315:	NM_177924:NM_004315:
51665	ASB1	ankyrin repeat and SOCS box-containing 1	0.25	CCGCCTAAGCACTTTAGGAAA	NM_016114:	NM_016114:
51665	ASB1	ankyrin repeat and SOCS box-containing 1	-3.54	CAGGAGGGTCTTCCCAAGATA	NM_016114:	NM_016114:
51665	ASB1	ankyrin repeat and SOCS box-containing 1	-8.84	CAGGAGCTATAGTGGAGTGAA	NM_016154:	NM_016114:
136371	ASB10 (ankyr	ankyrin repeat and SOCS box-containing 10	0.20	CCGGGTGATGTCTGATGAAGA	NM_080871:	NM_080871:
136371	ASB10 (ankyr	ankyrin repeat and SOCS box-containing 10	-9.17	CAGCGCCAACACCATGGACTA	NM_080871:	NM_080871:
140456	ASB11	ankyrin repeat and SOCS box-containing 11	-1.44	CAGGCACTCTTGCTCCGTGAA	NM_080873:	NM_001012428:NM_080873:
140456	ASB11	ankyrin repeat and SOCS box-containing 11	-1.44	TAGGATAGCAGAAGAGATCTA	NM_080873:	NM_080873:
79754	ASB13	ankyrin repeat and SOCS box-containing 13	0.11	ATGGCGGGTCTTCGTCCTAAA	NM_024701:	NM_024701:
79754	ASB13	ankyrin repeat and SOCS box-containing 13	1.25	CTGGAGGACTTTGCATGATTA	NM_024701:	NM_024701:
142686	ASB14	ankyrin repeat and SOCS box-containing 14	0.34	CTCACTATATATTATAGTAAA	NM_130387:	NM_130387:
142686	ASB14	ankyrin repeat and SOCS box-containing 14	-0.04	ACGACCTTTATGGACAAGGAA	NM_130387:	NM_130387:
142685	ASB15	ankyrin repeat and SOCS box-containing 15	0.03	ATCAAACATAACACTAGCCTA	NM_080928:	NM_080928:
142685	ASB15	ankyrin repeat and SOCS box-containing 15	0.60	TAAGACACTCTGGGAATTCAA	NM_080928:	NM_080928:
127247	ASB17	ankyrin repeat and SOCS box-containing 17	-0.30	ACCATCAGGAATCAACTATTA	NM_080868:	NM_080868:
127247	ASB17	ankyrin repeat and SOCS box-containing 17	0.82	CTACTGCAATATGGAATCTTA	NM_080868:	NM_080868:
51676	ASB2	ankyrin repeat and SOCS box-containing 2	1.07	CCCAGGCAGGCTGATTAGATA	NM_016150:	NM_016150:
51676	ASB2	ankyrin repeat and SOCS box-containing 2	-0.16	CGGCGCGAACATCGACGCCTA	NM_016150:	NM_016150:
51130	ASB3	ankyrin repeat and SOCS box-containing 3	-2.73	CTGAGGATGTATGAAGTTCCA	NM_016115:	NM_145863:NM_016115:
51130	ASB3	ankyrin repeat and SOCS box-containing 3	1.56	TACGGTCTGACAGTTATATTA	NM_016115:	NM_145863:NM_016115:
51666	ASB4	ankyrin repeat and SOCS box-containing 4	1.12	CCAGAGGGAATTATTTATTAA	NM_016116:	NM_016116:
51666	ASB4	ankyrin repeat and SOCS box-containing 4	-0.98	CCCGATGATGACTTGGAGAAA	NM_016116:	NM_016116:
140459	ASB6	ankyrin repeat and SOCS box-containing 6	0.27	AAGCTTAAACTATTCATCTTA	NM_017873:	NM_177999:NM_017873:
140459	ASB6	ankyrin repeat and SOCS box-containing 6	-0.87	CAGGGCTAGACACGAAGCTTA	NM_017873:	NM_177999:NM_017873:
140460	ASB7	ankyrin repeat and SOCS box-containing 7	-0.32	CACAAGTATGTAATATAATTA	NM_024708:	NM_024708:
140460	ASB7	ankyrin repeat and SOCS box-containing 7	0.09	ACGCTTGATGTTAGAATCTGA	NM_024708:	NM_198243:NM_024708:
140461	ASB8	ankyrin repeat and SOCS box-containing 8	0.38	CCTATTGATGCTGGTGTTTAA	NM_024095:	NM_024095:
140461	ASB8	ankyrin repeat and SOCS box-containing 8	0.96	TAGGAAGATGGAAAGTACTTA	NM_024095:	NM_024095:
140462	ASB9	ankyrin repeat and SOCS box-containing 9	0.54	CTGCATACGTTTGTATTATTA	NM_024087:	NM_024087:NM_001031739:
140462	ASB9	ankyrin repeat and SOCS box-containing 9	0.49	TAGATTTGTATTTGTTATAAA	NM_024087:	NM_024087:NM_001031739:
84164	ASCC2	activating signal cointegrator 1 complex subunit 2	-1.26	CAGGAAGAAGGAAGCCAACAA	NM_032204:	NM_032204:
84164	ASCC2	activating signal cointegrator 1 complex subunit 2	-0.35	CACGCGGAGTTTGCTGAACGA	NM_032204:	NM_032204:
429	ASCL1	achaete-scute complex-like 1 (Drosophila)	0.51	ACAAACTAGTTTCGTAATAAA	NM_004316:	NM_004316:
429	ASCL1	achaete-scute complex-like 1 (Drosophila)	-0.49	CCCGCCCTTTCTTAAAGTGCA	NM_004316:	NM_004316:
430	ASCL2	achaete-scute complex-like 2 (Drosophila)	0.55	AGGGAGCGTGAACTTTATAAA	NM_005170:	NM_005170:
430	ASCL2	achaete-scute complex-like 2 (Drosophila)	0.33	GAGGGTTATCTATACATTTAA	NM_005170:	NM_005170:
432	ASGR1	asialoglycoprotein receptor 1	0.25	CAGGTTATCATTGTGAACTTT	NM_001671:	NM_001671:
432	ASGR1	asialoglycoprotein receptor 1	-2.63	TCCGAAGGTGAGGAGCTTGAA	NM_001671:	NM_001671:
433	ASGR2	asialoglycoprotein receptor 2	-5.33	CACGAGCTGGGTGGAAGTGAA	NM_080914:	NM_080914:NM_080913:NM_080912:NM_001181:
433	ASGR2	asialoglycoprotein receptor 2	0.10	GAGCAGAAATTCATTGTACAA	NM_080914:	NM_080914:NM_080913:NM_080912:NM_001181:
55870	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	-0.45	ACGGTAGTTCTTGCAATTATT	NM_018489:	NM_018489:
55870	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	1.09	TCGACTGTTATCTCACATTAA	NM_018489:	NM_018489:
9070	ASH2L	ash2 (absent, small, or homeotic)-like (Drosophila)	0.05	CCCGTTTAACAAAGATGGCTA	NM_004674:	NM_004674:
9070	ASH2L	ash2 (absent, small, or homeotic)-like (Drosophila)	1.88	CCGAGTAACTAACTTATTTAA	NM_004674:	NM_004674:
438	ASMT	acetylserotonin O-methyltransferase	0.09	CAAGACATAATAATAAAGACA	NM_004043:	NM_004043:
438	ASMT	acetylserotonin O-methyltransferase	0.93	AGCACACAAGACATAATAATA	NM_004043:	NM_004043:
440	ASNS	asparagine synthetase	0.83	ATGGTGAAATCTACAACCATA	NM_001673:	NM_133436:NM_183356:NM_001673:
440	ASNS	asparagine synthetase	0.01	TCCGTATTTGTGGCTCTGTTA	NM_001673:	NM_133436:NM_183356:NM_001673:
54529	ASNSD1	asparagine synthetase domain containing 1	-2.58	GCGGGACTAAAGGAACTACAA	NM_019048:	NM_019048:
54529	ASNSD1	asparagine synthetase domain containing 1	0.81	TCAGAATTGATCTTAAGTCTA	NM_019048:	NM_019048:

443	ASPA	aspartoacylase (Canavan disease)	0.50	TACATCTTACACGGTGTCTTA	NM_000049:	NM_000049:
443	ASPA	aspartoacylase (Canavan disease)	-3.34	CTGCGCCATTGAGGTCTATAA	NM_000049:	NM_000049:
444	ASPH	aspartate beta-hydroxylase	-0.16	ACGCAGCCTTCCAGCAATTTA	NM_004318:	NM_004318:
444	ASPH	aspartate beta-hydroxylase	-1.27	CGGGCTACACAGAGTTAGTAA	NM_004318:	NM_004318:
259266	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0.00	AAGATTGAGCATGAAGGTCAA	NM_018136:	NM_018136:
259266	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	-0.02	ACGCTATATGTCAGCGTACTA	NM_018136:	NM_018136:
445	ASS	argininosuccinate synthetase	-3.75	CCCGTGGAGCATGGATGAGAA	NM_000050:	NM_000050:NM_054012:
445	ASS	argininosuccinate synthetase	-3.17	CTGATGGAGTACGCAAAGCAA	NM_000050:	NM_000050:NM_054012:
29028	ATAD2	ATPase family, AAA domain containing 2	0.33	AAGGCATTTATAAAGATCGAA	NM_014109:	NM_014109:
29028	ATAD2	ATPase family, AAA domain containing 2	0.14	CCGGATAAAGAAGAACGGACA	NM_014109:	NM_014109:
466	ATF1	activating transcription factor 1	0.03	CTGCCAATAAATTCTAAATTA	NM_005171:	NM_005171:
466	ATF1	activating transcription factor 1	0.57	AACCTAGTACATTACTAAATA	NM_005171:	NM_005171:
1386	ATF2	activating transcription factor 2	-0.40	CGCGGGTGACCGAAAGGATCA	NM_001880:	NM_001880:
1386	ATF2	activating transcription factor 2	1.68	TCCATTTGAGAATGAATTCAA	NM_001880:	NM_001880:
9474	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	-1.60	CTAGGAGATCTCCTCAAAGAA	NM_004849:	NM_004849:
9474	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	-0.08	TCCAACTTGTTTCACGCTATA	NM_004849:	NM_004849:
472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C	1.68	AACCATGAGTCTAGTACTTAA	NM_000051:	NM_000051:
472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C	-0.05	CACCTGTTTGTTAGTTTATTA	NM_000051:	NM_000051:NM_138292:
1822	ATN1	atrophin 1	0.49	CACTAATAATTTATATATATA	NM_001940:	NM_001007026:NM_001940:
1822	ATN1	atrophin 1	-1.59	CACCCTCTGCACGAGAACGAA	NM_001940:	NM_001007026:NM_001940:
474	ATOH1	atonal homolog 1 (Drosophila)	-0.57	AACGACAAGAAGCTGTCCAAA	NM_005172:	NM_005172:
474	ATOH1	atonal homolog 1 (Drosophila)	-0.57	AAGGAGGAAAACAGCAAAACT	NM_005172:	NM_005172:
479	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	-0.36	ATGCAGCACCATCATGATCAA	NM_001676:	NM_001676:
479	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	-1.34	TTGGCGTACGAGAAAGCTGAA	NM_001676:	NM_001676:
84239	ATP13A4	ATPase type 13A4	-0.70	CCGGATAAGGACTGTAATGAT	NM_032279:	NM_032279:
476	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.13	CCCGGAAAGACTGAAAGAATA	NM_000701:	NM_001001586:NM_000701:
476	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.67	CTTGATGAACTTCATCGTAAA	NM_000701:	NM_001001586:NM_000701:
477	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	0.24	CAGATTAGACACTATGTGTTA	NM_000702:	NM_000702:
477	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	-1.40	CCGATTAATTGGAGATTACTA	NM_000702:	NM_000702:
478	ATP1A3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-0.03	CTGGACAATTATCAAATATAT	NM_152296:	NM_152296:
478	ATP1A3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	0.61	CTGGTTCTGGACAATTATCAA	NM_152296:	NM_152296:
480	ATP1A4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	-2.04	CCGGGCTGACTTTAAGGCTAA	NM_144699:	NM_144699:
480	ATP1A4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	-0.29	CTCAATGAACGATGAAATGAA	NM_144699:	NM_144699:
487	ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	0.89	TCGGAACTACCTAGAGGGATA	NM_004320:	NM_004320:
487	ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-0.61	CCCGATAGTGACACATCTTCA	NM_004320:	NM_004320:NM_173201:
488	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-0.42	AAGCAGGACATCAATGAGCAA	NM_001681:	NM_001681:NM_170665:
488	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	1.45	AAGGTGATACTTGTTCCCTTA	NM_001681:	NM_001681:NM_170665:
489	ATP2A3	ATPase, Ca++ transporting, ubiquitous	-0.09	CGCCTGTAACACGGTCATCAA	NM_174958:	NM_174958:NM_174953:NM_174954:NM_174955: NM_174956:NM_005173:NM_174957:
489	ATP2A3	ATPase, Ca++ transporting, ubiquitous	1.73	CACCAATATCACATCGGGCAA	NM_174958:	NM_174958:NM_174953:NM_174954:NM_174955: NM_174956:NM_005173:NM_174957:
490	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	0.61	TCCCATTATATAGTATGTATA	NM_001682:	NM_001001323:NM_001682:
490	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	1.75	AGGGACCGTGATGATATTGTA	NM_001682:	NM_001001323:NM_001682:
491	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	-1.92	CCGGGACGAGATGGTAAAGAA	NM_001683:	NM_001683:NM_001001331:
491	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	1.25	TGAGGTAGTGTTGAAATATTA	NM_001683:	NM_001683:NM_001001331:
492	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	0.85	CACAGATACGTAATAATTTAA	NM_021949:	NM_021949:NM_001001344:
492	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	1.05	CCGGAAGACAAGCTTTACAAA	NM_021949:	NM_021949:NM_001001344:
493	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-1.13	TTGGTCTAAGCTAGGAACCTA	NM_001684:	NM_001684:NM_001001396:
493	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	0.80	CCGGACTATCTGCATAGCTTA	NM_001684:	NM_001684:NM_001001396:
27032	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	-2.02	TACGTATTAAATGCACGTTAA	NM_014382:	NM_014382:
27032	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	-1.77	TAGGGTAACAGTGTCCATAAT	NM_014382:	NM_014382:
495	ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide	-0.31	CAGGAATAAGATCCTGGTGAT	NM_000704:	NM_000704:
495	ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide	-0.57	CAGTAAGAACTGCGTGGTCAA	NM_000704:	NM_000704:
496	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	1.23	AGGCAGCAACTCTCTAATTAA	NM_000705:	NM_000705:
496	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	0.66	TTGCAATTCCTAAGTTGTAAA	NM_000705:	NM_000705:
496	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	0.37	AGGCAGCAACTCTCTAATTAA	NM_000705:	NM_000705:
496	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	0.36	TTGCAATTCCTAAGTTGTAAA	NM_000705:	NM_000705:
498	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subu	-2.33	TTGGCTGGATTTGAAGCTTAA	NM_004046:	NM_001001935:NM_004046:NM_001001937:
498	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subu	-1.49	CCCAGTTGGTGAAGAGACTTA	NM_004046:	NM_001001935:NM_004046:NM_001001937:
506	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polype	0.87	ACCCGTGAAGGCAATGATTTA	NM_001686:	NM_001686:
506	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polype	-1.90	AAGAATTACCACTACCAAGAA	NM_001686:	NM_001686:
10159	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	-1.79	ATGGGCTAATATGGATACTAA	NM_005765:	NM_005765:
10159	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	0.06	AAGAGTGTATATGGTAGGGAA	NM_005765:	NM_005765:
523	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	0.04	ATGGAGGTTGATGGTAAGGTA	NM_001690:	NM_001690:
523	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	-3.12	ACCCAAATTGTGATAGCATAA	NM_001690:	NM_001690:
525	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 (Renal t	-0.51	CCCGGCAGTAGCTGCAACCTA	NM_001692:	NM_001692:
525	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 (Renal t	-4.71	CCGGGTCAAGTTTGCCCAGTA	NM_001692:	NM_001692:
526	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	-1.53	CTCGATTACTCAAATCCCTAT	NM_001693:	NM_001693:
526	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	-1.37	CAGGCTGGTTTGGTAAAGAAA	NM_001693:	NM_001693:
528	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	-0.26	AAGGTTTAGAATCCCAGCATA	NM_001695:	NM_001695:NM_001007254:
528	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	1.40	ATGCATTAATTCCATTTGTTA	NM_001695:	NM_001695:NM_001007254:
538	ATP7A	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	0.32	TAGCAGCTTGTAGTATTGAAA	NM_000052:	NM_000052:
538	ATP7A	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	-0.69	CAGCCAGTTATTCTTCCATTA	NM_000052:	NM_000052:
540	ATP7B	ATPase, Cu++ transporting, beta polypeptide	1.19	ACCCAGGTTGGCATCAACAAA	NM_000053:	NM_000053:NM_001005918:
540	ATP7B	ATPase, Cu++ transporting, beta polypeptide	0.86	ACCCTTGGTGAGGACAATTTA	NM_000053:	NM_000053:NM_001005918:
10079	ATP9A	ATPase, Class II, type 9A	1.17	CTCAAGTTCCATTTATATTAA	XM_030577:	NM_006045:
10079	ATP9A	ATPase, Class II, type 9A	0.96	ATGTATTGAGTGAATAGTTAA	XM_030577:	NM_006045:
545	ATR	ataxia telangiectasia and Rad3 related	-0.96	CAGGCACTAATTGTTCTTCAA	NM_001184:	NM_001184:
545	ATR	ataxia telangiectasia and Rad3 related	0.04	CCGCTAATCTTCTAACATTAA	NM_001184:	NM_001184:
8455	ATRN	attractin	0.24	GAGAGGAATATTCTAACTTAA	NM_012070:	NM_139321:NM_139322:NM_012070:
8455	ATRN	attractin	-0.36	CCAGATGTGGACCATTCTTAA	NM_012070:	NM_139321:NM_139322:NM_012070:
26033	ATRNL1	attractin-like 1	1.90	TTGGTCGTAGGTAAAGGTCAA	NM_207303:	NM_207303:
26033	ATRNL1	attractin-like 1	-2.23	CAGCTTTCCGCCTAACTAGAA	NM_207303:	NM_207303:
546	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 hom	0.77	AGGCGACGTATTAAGGTTCAA	NM_000489:	NM_000489:NM_138271:NM_138270:
546	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 hom	-1.94	CCGACAGAAACTAACCCTGTA	NM_000489:	NM_000489:NM_138271:NM_138270:
4287	ATXN3	ataxin 3	1.23	TACGATGGGATCATTATTTCA	NM_004993:	NM_030660:NM_004993:NM_001024631:
4287	ATXN3	ataxin 3	1.14	TGCGTCGGTTGTAGGACTAAA	NM_004993:	NM_030660:NM_004993:NM_001024631:
92552	ATXN3L	ataxin 3-like	1.45	AAGCTCGGCATTGATCCTATA	XM_045705:	XM_045705:
92552	ATXN3L	ataxin 3-like	-2.03	CTCGATTACAACAACAAGCAT	XM_045705:	XM_045705:
550	AUP1 (ancien	ancient ubiquitous protein 1	0.84	CCCAATGTCACATTAAATTCA	NM_012103:	NM_012103:NM_181576:NM_181575:
550	AUP1 (ancien	ancient ubiquitous protein 1	-1.64	CAGGAGCGCAAGCAAGCACTA	NM_012103:	NM_012103:NM_181576:NM_181575:
6790	AURKA	aurora kinase A	-6.85	CACCTTCGGCATCCTAATATT	NM_003600:	NM_198433:NM_003600:NM_198435:NM_198434: NM_198436:NM_198437:
6790	AURKA	aurora kinase A	0.50	CACGTGCTCTACCTCCATTTA	NM_003600:	NM_198433:NM_003600:NM_198435:NM_198434: NM_198436:NM_198437:
54998	AURKAIP1	aurora kinase A interacting protein 1	-0.13	ATCCGTAGTAATAAATTCTCA	NM_017900:	NM_017900:
54998	AURKAIP1	aurora kinase A interacting protein 1	-2.79	CTGCTGTGATCCGTAGTAATA	NM_017900:	NM_017900:
9212	AURKB	aurora kinase B	-1.96	AACGCGGCACTTCACAATTGA	NM_004217:	NM_004217:
9212	AURKB	aurora kinase B	-4.97	ACGCGGCACTTCACAATTGAT	NM_004217:	NM_004217:

6795	AURKC	aurora kinase C	1.82	AAGATGTAAGATGCTAATTAA	NM_003160:	NM_001015878:NM_001015879:NM_003160:
6795	AURKC	aurora kinase C	-0.09	CCGGGTGTACCTGATTCTGGA	NM_003160:	NM_001015878:NM_001015879:NM_003160:
551	AVP	arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes i	-0.63	CCCCTGCAGCACGGACAATAA	NM_000490:	NM_000490:
551	AVP	arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes i	0.02	CAATAAACCTCCGCCAATGCA	NM_000490:	NM_000490:
552	AVPR1A	arginine vasopressin receptor 1A	-0.01	ATGAACGGACTGGATAGTAAA	NM_000706:	NM_000706:
552	AVPR1A	arginine vasopressin receptor 1A	-2.45	TCGCAAACATAGGGTAATAAA	NM_000706:	NM_000706:
553	AVPR1B	arginine vasopressin receptor 1B	-1.53	CAGCATGTTTGCCTCCACCTA	NM_000707:	NM_000707:
553	AVPR1B	arginine vasopressin receptor 1B	-1.66	CTGGATCTACATGGGCTTCAA	NM_000707:	NM_000707:
554	AVPR2	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)	0.01	CAGCCTCAACAGCTGCACCAA	NM_000054:	NM_000054:
554	AVPR2	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)	-0.04	CCTCATTCTCTCCCTAATAAA	NM_000054:	NM_000054:
8312	AXIN1	axin 1	-5.04	CAGCTACAGATACTACTTCAA	NM_003502:	NM_003502:NM_181050:
8312	AXIN1	axin 1	0.72	CAGCATCGTTGTGGCGTACTA	NM_003502:	NM_003502:NM_181050:
8313	AXIN2	axin 2 (conductin, axil)	0.81	CAGTGAGTTGGTTGTCACTTA	NM_004655:	NM_004655:
8313	AXIN2	axin 2 (conductin, axil)	-0.23	AGCGATCCTGTTAATCCTTAT	NM_004655:	NM_004655:
558	AXL	AXL receptor tyrosine kinase	2.95	CCGGTGTTCTAAGATGTGATA	NM_001699:	NM_001699:NM_021913:
558	AXL	AXL receptor tyrosine kinase	1.81	TCCAAGATTCTAGATGATTAA	NM_001699:	NM_001699:NM_021913:
51582	AZIN1	antizyme inhibitor 1	-0.52	ATCATAGTATTTGTTGACCTA	NM_015878:	NM_015878:NM_148174:
51582	AZIN1	antizyme inhibitor 1	-2.04	CAGGTTAAGCTTGTCTGGTCA	NM_015878:	NM_015878:NM_148174:
566	AZU1	azurocidin 1 (cationic antimicrobial protein 37)	-1.75	CTGGATCGATGGTGTTCTCAA	NM_001700:	NM_001700:
566	AZU1	azurocidin 1 (cationic antimicrobial protein 37)	-0.56	CTGGCCTCCATTCAGAATCAA	NM_001700:	NM_001700:
567	B2M (beta-2-	beta-2-microglobulin	-6.79	AAGTGGGATCGAGACATGTAA	NM_004048:	NM_004048:
567	B2M (beta-2-	beta-2-microglobulin	0.80	TCCGACATTGAAGTTGACTTA	NM_004048:	NM_004048:
2583	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	1.41	CACCAAGACCTTCCTCCGTTA	NM_001478:	NM_001478:
2583	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	0.00	CAGAGGGACTCTAAGAACCTA	NM_001478:	NM_001478:
2683	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	0.63	CCCAAGAACTTCGGTCCTAAA	NM_001497:	NM_001497:
2683	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	1.61	CACAAATAGGCCTATGATTTA	NM_001497:	NM_001497:
23621	BACE1	beta-site APP-cleaving enzyme 1	-0.13	ACCAAACAACTTGGTTGTGAA	NM_012104:	NM_138973:NM_138972:NM_138971:NM_012104:
23621	BACE1	beta-site APP-cleaving enzyme 1	-1.16	CCCAAGATCATTCTACAAGTA	NM_012104:	NM_138973:NM_138972:NM_138971:NM_012104:
25825	BACE2	beta-site APP-cleaving enzyme 2	1.15	TACATGTGCCACCAACATAAA	NM_012105:	NM_138992:NM_138991:NM_012105:
25825	BACE2	beta-site APP-cleaving enzyme 2	0.43	AACCATGAACTCAGCTATTAA	NM_012105:	NM_138992:NM_138991:NM_012105:
60468	BACH2 (BTB	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-1.70	CACGAGGCATTGTGTGTTGAA	NM_021813:	NM_021813:
60468	BACH2 (BTB	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-0.20	CAGGTGATAATTATGTAGGAA	NM_021813:	NM_021813:
572	BAD	BCL2-antagonist of cell death	-0.13	ACGAGTTTGTGGACTCCTTTA	AK023420:	NM_004322:NM_032989:
573	BAG1 (BCL2-	BCL2-associated athanogene	-0.01	CCGTCTCTGGATCGGAATTTA	NM_004323:	NM_004323:
573	BAG1 (BCL2-	BCL2-associated athanogene	-0.25	CTGGATCGGAATTTACCTGAT	NM_004323:	NM_004323:
9532	BAG2	BCL2-associated athanogene 2	0.44	CAGGCGAAGATCAACGCTAAA	NM_004282:	NM_004282:
9532	BAG2	BCL2-associated athanogene 2	0.98	TCAGGCGAAGATCAACGCTAA	NM_004282:	NM_004282:
9531	BAG3	BCL2-associated athanogene 3	-0.50	CCCAATTCAAGTGATCCGCAA	NM_004281:	NM_004281:
9531	BAG3	BCL2-associated athanogene 3	0.10	CCGCAAAGAGGTGGATTCTAA	NM_004281:	NM_004281:
9530	BAG4	BCL2-associated athanogene 4	0.77	CAACATATACTTCATGTGTAA	NM_004874:	NM_004874:
9530	BAG4	BCL2-associated athanogene 4	-0.02	CTGGATATAATCTGAGACAAA	NM_004874:	NM_004874:
9529	BAG5	BCL2-associated athanogene 5	1.16	AAGGAGATATTCAGCAAGCTA	NM_004873:	NM_001015049:NM_004873:NM_001015048:
9529	BAG5	BCL2-associated athanogene 5	-0.56	CCGGATTATTCTACTCCTGCA	NM_004873:	NM_001015049:NM_004873:NM_001015048:
575	BAI1 (brain-s	brain-specific angiogenesis inhibitor 1	0.81	CCGCTGTGTTTCCATTGACTA	NM_001702:	NM_001702:
575	BAI1 (brain-s	brain-specific angiogenesis inhibitor 1	0.78	CCGGAACCGCCTCATCCGCAA	NM_001702:	NM_001702:
576	BAI2 (brain-s	brain-specific angiogenesis inhibitor 2	0.35	CCCGAACGAAAGGATACGGTA	NM_001703:	NM_001703:
576	BAI2 (brain-s	brain-specific angiogenesis inhibitor 2	0.20	CTCTCTGATTGTCACAGATAA	NM_001703:	NM_001703:
577	BAI3	brain-specific angiogenesis inhibitor 3	1.42	ATGGACTAAGGTAGAGACAAA	NM_001704:	NM_001704:
577	BAI3	brain-specific angiogenesis inhibitor 3	-0.86	TTGGATGATAATGCAGGACTA	NM_001704:	NM_001704:
10458	BAIAP2	BAI1-associated protein 2	-0.75	CTGCTTCTCCTGCCTAATAAA	NM_006340:	NM_006340:
10458	BAIAP2	BAI1-associated protein 2	-4.72	CAGCAAGAATCCTCAGAAGTA	NM_006340:	NM_017450:NM_017451:NM_006340:
55971	BAIAP2L1	BAI1-associated protein 2-like 1	0.01	CACGGAGAGCACCTACCGGAA	NM_018842:	NM_018842:
55971	BAIAP2L1	BAI1-associated protein 2-like 1	0.68	CTCAACGAGAGTCTTGATGAA	NM_018842:	NM_018842:
8938	BAIAP3	BAI1-associated protein 3	0.84	TGGGATCATGACGACGATGTA	NM_003933:	NM_003933:
8938	BAIAP3	BAI1-associated protein 3	0.64	GTCGACCTTGCTGGACATTAA	NM_003933:	NM_003933:
578	BAK1	BCL2-antagonist/killer 1	-4.14	AACCCATTCACTACAGGTGAA	NM_001188:	NM_001188:
578	BAK1	BCL2-antagonist/killer 1	-2.14	CAGGATTCAGCTATTCTGGAA	NM_001188:	NM_001188:
8314	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	0.45	CTCAATTCCTCTGTCCATCAA	NM_004656:	NM_004656:
8314	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	-0.34	CCCGCTGGTGCTGGAAGCAAA	NM_004656:	NM_004656:
580	BARD1 (BRC	BRCA1 associated RING domain 1	0.01	CTGAATATTATACCAGATGAA	NM_000465:	NM_000465:
580	BARD1 (BRC	BRCA1 associated RING domain 1	0.79	GACCATCAATACAGTCGCATA	NM_000465:	NM_000465:
7917	BAT3	HLA-B associated transcript 3	-2.25	CAGCTCCGGTCTGATATACAA	NM_004639:	NM_080703:NM_080702:NM_004639:
7917	BAT3	HLA-B associated transcript 3	0.02	CCGGTTGCTGGAGTTGTGTAA	NM_004639:	NM_080703:NM_080702:NM_004639:
581	BAX	BCL2-associated X protein	-1.35	ATCATCAGATGTGGTCTATAA	NM_004324:	NM_004324:
581	BAX	BCL2-associated X protein	-0.91	CAGCTCTGAGCAGATCATGAA	NM_004324:	NM_004324:NM_138765:NM_138763:NM_138764:NM_138761:
11177	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	-0.61	AACCCTCGTAACACAAGTGAA	NM_013448:	NM_182648:NM_013448:
11177	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	0.12	CACAAGTTAGATTGCCAGTTA	NM_013448:	NM_182648:NM_013448:
9031	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	0.41	CCGGGTCATTTCATTAGAGAA	NM_023005:	NM_023005:NM_032408:
9031	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	0.56	CAGATGCTCAGTATCCTATTA	NM_023005:	NM_023005:NM_032408:
11176	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	-1.28	CTCGGTAGCTTTGAATCTTAA	NM_013449:	NM_013449:
11176	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	1.82	CCCGCAGTGACGGCCAGTAAA	NM_013449:	NM_013449:
29994	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	0.45	AGGGCCTAAATTAAAGTATAA	NM_013450:	NM_013450:
29994	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	-0.62	CTGAAGGTAATGATAGCTATA	NM_013450:	NM_013450:
27113	BBC3	BCL2 binding component 3	-0.18	CAATCCCATTGCATAGGTTTA	AF332558:	NM_014417:
27113	BBC3	BCL2 binding component 3	0.01	CAGCCTGTAAGATACTGTATA	AF332558:	NM_014417:
583	BBS2	Bardet-Biedl syndrome 2	0.58	ATGAAGAGTCGTTATATGGAA	NM_031885:	NM_031885:
583	BBS2	Bardet-Biedl syndrome 2	2.48	CTCGGTCAGAACTTTCTGTTA	NM_031885:	NM_031885:
4059	BCAM	basal cell adhesion molecule (Lutheran blood group)	-4.95	CACGACCATTATATGCTGGAA	NM_005581:	NM_005581:NM_001013257:
4059	BCAM	basal cell adhesion molecule (Lutheran blood group)	-0.64	CAAGATCACGTGGTATCGCAA	NM_005581:	NM_005581:NM_001013257:
55973	BCAP29	B-cell receptor-associated protein 29	-0.06	ATGGCAGTGATTATAATATTA	NM_001008405:	NM_018844:NM_001008405:
55973	BCAP29	B-cell receptor-associated protein 29	-1.13	TAGGTCAGGATTACTATATAA	NM_001008405:	NM_018844:NM_001008405:
10134	BCAP31	B-cell receptor-associated protein 31	1.03	AAAGGTGAACCTCCAGAACAA	NM_005745:	NM_005745:
10134	BCAP31	B-cell receptor-associated protein 31	0.01	CAAGAAGTACATGGAGGAGAA	NM_005745:	NM_005745:
9564	BCAR1	breast cancer anti-estrogen resistance 1	-1.12	AAGCAGTTTGAACGACTGGAA	NM_014567:	NM_014567:
9564	BCAR1	breast cancer anti-estrogen resistance 1	-4.69	CTGGATGGAGGACTATGACTA	NM_014567:	NM_014567:
8412	BCAR3	breast cancer anti-estrogen resistance 3	-0.22	CAGTTATATGATATTCTTTAA	NM_003567:	NM_003567:
8412	BCAR3	breast cancer anti-estrogen resistance 3	0.24	AAGGTATCAGTTATATGATAT	NM_003567:	NM_003567:
586	BCAT1	branched chain aminotransferase 1, cytosolic	0.69	ATGGTGCACCTAATAAATTAA	NM_005504:	NM_005504:
586	BCAT1	branched chain aminotransferase 1, cytosolic	1.14	CTAGTGGTACATAGTAACTAA	NM_005504:	NM_005504:
587	BCAT2	branched chain aminotransferase 2, mitochondrial	-0.17	CTGAAGTGCAATACGAAATAA	NM_001190:	NM_001190:
587	BCAT2	branched chain aminotransferase 2, mitochondrial	1.32	CACCTGAAGTGCAATACGAAA	NM_001190:	NM_001190:
56647	BCCIP	BRCA2 and CDKN1A interacting protein	-0.06	CAGTGTGTTGAACAAATTCAA	NM_016567:	NM_078468:NM_078469:NM_016567:
56647	BCCIP	BRCA2 and CDKN1A interacting protein	-0.06	GACGAGGAAGTGAATATTGAA	NM_016567:	NM_078468:NM_078469:NM_016567:
56257	BCDIN3	bin3, bicoid-interacting 3, homolog (Drosophila)	-3.29	CAGTATGGGAATTATTGCAAA	NM_019606:	NM_019606:
56257	BCDIN3	bin3, bicoid-interacting 3, homolog (Drosophila)	-7.16	CACCAAGTGGGTGCATCTGAA	NM_019606:	NM_019606:
590	BCHE	butyrylcholinesterase	-2.45	CAGGAGTGAGTGAGTTTGGAA	NM_000055:	NM_000055:

590	BCHE	butyrylcholinesterase	1.63	CAGAACGTTGAACTTAGCTAA	NM_000055:	NM_000055:
593	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	-0.39	CTCGGCGGAGTTTATAGATAA	NM_000709:	NM_000709:
593	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	-0.36	CAAGAGCATGACACTGCTTAA	NM_000709:	NM_000709:
10295	BCKDK (bran	branched chain ketoacid dehydrogenase kinase	0.85	AACGCCCACCATGATGCTCTA	NM_005881:	NM_005881:
10295	BCKDK (bran	branched chain ketoacid dehydrogenase kinase	-0.33	CAGAACTTGGAGAGCAGGGAA	NM_005881:	NM_005881:
8915	BCL10	B-cell CLL/lymphoma 10	0.05	CACGTACTGTTTCACGACAAT	NM_003921:	NM_003921:
8915	BCL10	B-cell CLL/lymphoma 10	0.87	GTGCTGAAACTTAGAAATATA	NM_003921:	NM_003921:
64919	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-1.35	CAGAGGTGGGTTAAACTGTAA	NM_022898:	NM_022898:NM_138576:
64919	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-0.44	CAGCGGATAACAATCTTTCAA	NM_022898:	NM_022898:NM_138576:
596	BCL2	B-cell CLL/lymphoma 2	-1.37	CAGGCTTAAGATTTGGAATAA	NM_000633:	NM_000633:
596	BCL2	B-cell CLL/lymphoma 2	-3.42	CCGGGAGATAGTGATGAAGTA	NM_000633:	NM_000657:NM_000633:
597	BCL2A1	BCL2-related protein A1	0.16	AGGACACTCCATATTGTGAAA	NM_004049:	XM_375224:NM_004049:
597	BCL2A1	BCL2-related protein A1	1.24	AGGGAGGAAGGATATTATAAA	NM_004049:	NM_004049:
598	BCL2L1	BCL2-like 1	0.15	AAAGTGCAGTTCAGTAATAAA	NM_001191:	NM_138578:NM_001191:
598	BCL2L1	BCL2-like 1	0.34	AAGGCGGATTTGAATCTCTTT	NM_001191:	NM_138578:NM_001191:
10017	BCL2L10	BCL2-like 10 (apoptosis facilitator)	-2.44	ACAGATGTGTGAGAACAAGAA	NM_020396:	NM_020396:
10017	BCL2L10	BCL2-like 10 (apoptosis facilitator)	0.87	ATGACAGATGTGTGAGAACAA	NM_020396:	NM_020396:
10018	BCL2L11	BCL2-like 11 (apoptosis facilitator)	1.23	CAGCATGTTCACGTTATTTAA	NM_138627:	NM_207003:NM_138627:NM_138625:NM_138626:NM_138624:NM_138622:NM_138623:NM_006538:NM_138621:
10018	BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.67	CACCCACGAATGGTTATCTTA	NM_138627:	NM_207003:NM_138627:NM_138625:NM_138626:NM_138624:NM_138622:NM_138623:NM_006538:NM_138621:
83596	BCL2L12	BCL2-like 12 (proline rich)	0.07	CCGGGTAGCTCTCAAACTCGA	NM_052842:	NM_052842:NM_138639:
83596	BCL2L12	BCL2-like 12 (proline rich)	-0.05	CGCGGGAAAGTTGAACTAATA	NM_052842:	NM_052842:NM_138639:
23786	BCL2L13	BCL2-like 13 (apoptosis facilitator)	-0.23	CCGTGTCTTTCCAGCCCTAAA	NM_015367:	NM_015367:
23786	BCL2L13	BCL2-like 13 (apoptosis facilitator)	-0.03	TTGGGCTTATAGAGCCAGTTA	NM_015367:	NM_015367:
79370	BCL2L14	BCL2-like 14 (apoptosis facilitator)	0.03	ATGGCCTGCATTTGAGCTAAA	NM_030766:	NM_030766:
79370	BCL2L14	BCL2-like 14 (apoptosis facilitator)	1.25	TCCGTTTCTAGTACTATTTAT	NM_030766:	NM_030766:NM_138722:NM_138723:
599	BCL2L2	BCL2-like 2	-4.08	AAGGCTGAGTATGGTTCCCAA	NM_004050:	NM_004050:
599	BCL2L2	BCL2-like 2	-0.58	TCGCCAGAACGTGGGACCAAA	NM_004050:	NM_004050:
602	BCL3	B-cell CLL/lymphoma 3	-0.11	ACGGATCACGATGTAAATTAT	NM_005178:	NM_005178:
602	BCL3	B-cell CLL/lymphoma 3	-0.31	CACGATGTAAATTATTAAGCA	NM_005178:	NM_005178:
604	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)	0.01	AACCTGCATTTCCGTCACAAA	NM_001706:	NM_001706:NM_138931:
604	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)	0.31	AACCTTAGTGTGATCAATCTA	NM_001706:	NM_001706:NM_138931:
605	BCL7A	B-cell CLL/lymphoma 7A	-0.01	TGGAATGTTCATTATCGCCAA	NM_020993:	NM_020993:NM_001024808:
605	BCL7A	B-cell CLL/lymphoma 7A	-4.40	CTGCACTTCGAGAAGAATCAA	NM_020993:	NM_020993:NM_001024808:
607	BCL9	B-cell CLL/lymphoma 9	-0.17	CACAGAGTAGCCCTAAGTCAA	NM_004326:	NM_004326:
607	BCL9	B-cell CLL/lymphoma 9	0.82	CCGCATTATTCCATCTGAGAA	NM_004326:	NM_004326:
613	BCR	breakpoint cluster region	2.73	ACGGCAGTCCATGACGGTGAA	NM_004327:	NM_004327:NM_021574:
613	BCR	breakpoint cluster region	-2.39	CAGCATTCCGCTGACCATCAA	NM_004327:	NM_004327:NM_021574:
617	BCS1L	BCS1-like (yeast)	-0.06	CACGGCGGATCTTATTGTCTA	NM_004328:	NM_004328:
617	BCS1L	BCS1-like (yeast)	1.15	CCGCATTTCCACTAAGTTTGA	NM_004328:	NM_004328:
622	BDH1	3-hydroxybutyrate dehydrogenase, type 1	-6.02	CAAGCAGGTGGCAGAAGTGAA	NM_004051:	NM_004051:NM_203315:NM_203314:
622	BDH1	3-hydroxybutyrate dehydrogenase, type 1	-0.13	CAGCAGCGAAGAGGTGGAGAA	NM_004051:	NM_004051:NM_203315:NM_203314:
56898	BDH2	3-hydroxybutyrate dehydrogenase, type 2	1.03	AAGACATTAATGAGTCCAAAC	NM_020139:	NM_020139:
56898	BDH2	3-hydroxybutyrate dehydrogenase, type 2	1.24	AATCTGGCAATATTATCAACA	NM_020139:	NM_020139:
623	BDKRB1	bradykinin receptor B1	-0.50	CCGGGTCACCTGCGTGCTCAT	NM_000710:	NM_000710:
623	BDKRB1	bradykinin receptor B1	0.23	CTCCAATATCTTCATCCCATA	NM_000710:	NM_000710:
624	BDKRB2	bradykinin receptor B2	-1.46	CTGCACGGTGGCAGAGATCTA	NM_000623:	NM_000623:
624	BDKRB2	bradykinin receptor B2	-1.07	CTGGCAGGTTAGAACCTAGAA	NM_000623:	NM_000623:
627	BDNF	brain-derived neurotrophic factor	-0.33	CGGGACGGTCACAGTCCTTGA	NM_001709:	NM_170732:NM_170731:NM_170734:NM_170733:NM_170735:NM_001709:
627	BDNF	brain-derived neurotrophic factor	0.90	CTGGCGATTCATAAGGATAGA	NM_001709:	NM_170732:NM_170731:NM_170734:NM_170733:NM_170735:NM_001709:
8678	BECN1	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	0.49	ACCGACTTGTTCCTTACGGAA	NM_003766:	NM_003766:
8678	BECN1	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	0.26	AGGGTCTAAGACGTCCAACAA	NM_003766:	NM_003766:
10282	BET1	BET1 homolog (S. cerevisiae)	-0.35	CACTGATGTCGTGGCGCTTTA	NM_005868:	NM_005868:
10282	BET1	BET1 homolog (S. cerevisiae)	-0.02	CAGAATAAATTATTAGCTGAA	NM_005868:	NM_005868:
51283	BFAR	bifunctional apoptosis regulator	-0.07	CCGGGACGAGTGGAATGATTA	NM_016561:	NM_016561:
51283	BFAR	bifunctional apoptosis regulator	0.81	TCCGGTGTGCTCACAGCTTTA	NM_016561:	NM_016561:
27319	BHLHB5	basic helix-loop-helix domain containing, class B, 5	-0.59	ACGTAAGAACATGCTAAGCAA	NM_152414:	NM_152414:
27319	BHLHB5	basic helix-loop-helix domain containing, class B, 5	0.05	AGCAATAGTTGCTATACGTAA	NM_152414:	NM_152414:
637	BID	BH3 interacting domain death agonist	1.49	AAAGACAATGTTAAACTTATA	NM_001196:	NM_001196:NM_197966:NM_197967:
637	BID	BH3 interacting domain death agonist	0.00	CAGGGATGAGTGCATCACAAA	NM_001196:	NM_001196:NM_197966:NM_197967:
638	BIK	BCL2-interacting killer (apoptosis-inducing)	-1.33	CCGAGGAGCAGGAGTGCTCAA	NM_001197:	NM_001197:
638	BIK	BCL2-interacting killer (apoptosis-inducing)	2.98	TCGGCAAAGAATCTACTGGAA	NM_001197:	NM_001197:
4671	BIRC1	baculoviral IAP repeat-containing 1	-0.01	CGTGGTGAACTTTGTGAATTA	NM_004536:	NM_004536:
4671	BIRC1	baculoviral IAP repeat-containing 1	2.34	TCGAAATTCATGATACTACTA	NM_004536:	NM_004536:
329	BIRC2	baculoviral IAP repeat-containing 2	-0.16	TAGGCGTTTCTGATAACACTA	NM_001166:	NM_001166:
329	BIRC2	baculoviral IAP repeat-containing 2	0.61	TCCCAGGTCCCTCGTATCAAA	NM_001166:	NM_001166:
330	BIRC3	baculoviral IAP repeat-containing 3	-0.03	CAAGAACATGATGTTATTAAA	AF070674:	NM_182962:NM_001165:
330	BIRC3	baculoviral IAP repeat-containing 3	-4.14	CACAGACGTCTTTACAAGCAA	AF070674:	NM_182962:NM_001165:
330	BIRC3	baculoviral IAP repeat-containing 3	1.42	CAGAGTCATTTCCATGTTCTA	XR_000213:	NM_001165:
331	BIRC4	baculoviral IAP repeat-containing 4	-0.57	AGCGTATTTAATGATAGAATA	NM_001167:	NM_001167:
331	BIRC4	baculoviral IAP repeat-containing 4	-0.10	CACGTACTTGTGCGAATTATT	NM_001167:	NM_001167:
332	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	-3.63	CTCGGCTGTTCCTGAGAAATA	NM_001168:	NM_001012271:NM_001168:NM_001012270:
332	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	-0.05	CTGGCGTAAGATGATGGATTT	NM_001168:	NM_001012271:NM_001168:NM_001012270:
57448	BIRC6	baculoviral IAP repeat-containing 6 (apollon)	-0.27	ACGGATGGAACTGACAGAATA	NM_016252:	NM_016252:
57448	BIRC6	baculoviral IAP repeat-containing 6 (apollon)	1.11	CCCGATATATTGGATAATCGA	NM_016252:	NM_016252:
79444	BIRC7	baculoviral IAP repeat-containing 7 (livin)	1.54	ATGCTTCTGAATAGAAATAAA	NM_022161:	NM_139317:NM_022161:
79444	BIRC7	baculoviral IAP repeat-containing 7 (livin)	1.21	TTGGATGCTTCTGAATAGAAA	NM_022161:	NM_139317:NM_022161:
112401	BIRC8	baculoviral IAP repeat-containing 8	-0.51	CGGTTATTGATTTCAAGCAAA	NM_033341:	NM_033341:
112401	BIRC8	baculoviral IAP repeat-containing 8	0.41	AACGTTAATATTCGAGGTGAA	NM_033341:	NM_033341:
640	BLK	B lymphoid tyrosine kinase	2.84	CAGCCGTGCTGTTAAACCAAA	NM_001715:	NM_001715:
640	BLK	B lymphoid tyrosine kinase	0.14	CTGGTAAGCGACTGTCATCAA	NM_001715:	NM_001715:
641	BLM	Bloom syndrome	0.16	CCGAATCTCAATGTACATAGA	NM_000057:	NM_000057:
641	BLM	Bloom syndrome	0.01	CTGACCATCTGTGACTATAAA	NM_000057:	NM_000057:
642	BLMH	bleomycin hydrolase	0.71	CTGAAACAGAATACTGTTAAA	NM_000386:	NM_000386:
642	BLMH	bleomycin hydrolase	-2.59	AAGGATGAATGATATTCTGAA	NM_000386:	NM_000386:
29760	BLNK	B-cell linker	0.33	TGCGATTTATTGAAGCAACAA	NM_013314:	NM_013314:
29760	BLNK	B-cell linker	-0.02	CAGAGGCGAGTATATAGACAA	NM_013314:	NM_013314:
643	BLR1	Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C	0.23	CAGCCATGAACTACCCGCTAA	NM_001716:	NM_001716:
643	BLR1	Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C	-0.05	CCCGCTAACGCTGGAAATGGA	NM_001716:	NM_001716:
90427	BMF	Bcl2 modifying factor	0.13	CAGACGCTAGAAACTAAATTA	AK024472:	NM_001003942:NM_033503:NM_001003940:NM_001003943:
90427	BMF	Bcl2 modifying factor	3.02	GACGCTAGAAACTAAATTATA	AK024472:	NM_001003942:NM_033503:NM_001003940:NM_001003943:

649	BMP1	bone morphogenetic protein 1	-1.12	AAGGACTATGGCCACATTCAA	NM_001199:	NM_006131:NM_006130:NM_006132:NM_006129:NM_001199:NM_006128:
649	BMP1	bone morphogenetic protein 1	-0.33	CAGCTATATTGTGTTCACCTA	NM_001199:	NM_006131:NM_006130:NM_006132:NM_006129:NM_001199:NM_006128:
27302	BMP10	bone morphogenetic protein 10	-5.03	CCCGCTCTACATCGACTTCAA	NM_014482:	NM_014482:
27302	BMP10	bone morphogenetic protein 10	0.26	TACGATGGAGTAGACCGGAAA	NM_014482:	NM_014482:
9210	BMP15	bone morphogenetic protein 15	-0.18	TCCCGTATAAGTATGTTCCAA	NM_005448:	NM_005448:
9210	BMP15	bone morphogenetic protein 15	-0.64	ACGCCATTATTCAGAACCTTA	NM_005448:	NM_005448:
650	BMP2	bone morphogenetic protein 2	-0.95	AACGCCTTAAGTCCAGCTGTA	NM_001200:	NM_001200:
650	BMP2	bone morphogenetic protein 2	1.53	CACCGAATTAATATTTATGAA	NM_001200:	NM_001200:
55589	BMP2K	BMP2 inducible kinase	0.93	AGGCATCACCTGAATATCTTA	NM_017593:	NM_198892:NM_017593:
55589	BMP2K	BMP2 inducible kinase	-0.40	TCCGATGTGCATTGAAGCGAA	NM_017593:	NM_198892:NM_017593:
651	BMP3 (bone	bone morphogenetic protein 3 (osteogenic)	-0.59	CAGGAGATACCTCAAGGTAGA	NM_001201:	NM_001201:
651	BMP3 (bone	bone morphogenetic protein 3 (osteogenic)	-3.96	CCGCCATTTCTGAGCCAGAAA	NM_001201:	NM_001201:
652	BMP4	bone morphogenetic protein 4	-0.45	CACGAGACTGGTCCACCACAA	NM_001202:	NM_130851:NM_130850:NM_001202:
652	BMP4	bone morphogenetic protein 4	-3.38	CCCGATGGGATTCCCGTCCAA	NM_001202:	NM_001202:
653	BMP5	bone morphogenetic protein 5	1.62	AAAGATCTGTATTAAGGTTTA	NM_021073:	NM_021073:
653	BMP5	bone morphogenetic protein 5	1.27	CGGAGCAACAACCGATTTGAA	NM_021073:	NM_021073:
654	BMP6	bone morphogenetic protein 6	-0.95	ACCGTGCTGTGCGCCAACTAA	NM_001718:	NM_001718:
654	BMP6	bone morphogenetic protein 6	-1.06	CAGCATTTATCAAGTCTTACA	NM_001718:	NM_001718:
655	BMP7	bone morphogenetic protein 7 (osteogenic protein 1)	-0.08	CCCGGAAGTTCCTGTAATAAA	NM_001719:	NM_001719:
655	BMP7	bone morphogenetic protein 7 (osteogenic protein 1)	-0.04	TCCAATGAACAAGATCCTACA	NM_001719:	NM_001719:
656	BMP8B	bone morphogenetic protein 8b (osteogenic protein 2)	-0.05	ACAGATATGATGTAAAGTGAA	NM_001720:	NM_001720:
656	BMP8B	bone morphogenetic protein 8b (osteogenic protein 2)	0.13	TAGGAAAGACATGTAAGAGCA	NM_001720:	NM_001720:
657	BMPR1A	bone morphogenetic protein receptor, type IA	0.86	CAGCTACGCCGGACAATAGAA	NM_004329:	NM_004329:
657	BMPR1A	bone morphogenetic protein receptor, type IA	0.01	GCGGCAGACATTAAAGGTACA	NM_004329:	NM_004329:
657	BMPR1A	bone morphogenetic protein receptor, type IA	0.35	AAGAAATGTTATAAAGTAGAA	XM_208545:	XM_208545:NM_004329:
658	BMPR1B	bone morphogenetic protein receptor, type IB	-5.31	AACGAATGTAATAAAGACCTA	NM_001203:	NM_001203:
658	BMPR1B	bone morphogenetic protein receptor, type IB	0.54	ACGGATATTGTTTCACGATGA	NM_001203:	NM_001203:
659	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	0.57	CTCGTAAGTATGTAAAGGAAA	NM_001204:	NM_001204:
660	BMX	BMX non-receptor tyrosine kinase	2.34	AAGCTTATTCATTATCATCAA	NM_001721:	NM_203281:NM_001721:
660	BMX	BMX non-receptor tyrosine kinase	0.16	CACAGTGTCCTTATTTAGTAA	NM_001721:	NM_203281:NM_001721:
662	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	0.04	ACGAACGATCCTGGATGCAAA	NM_013979:	NM_001205:NM_013980:NM_013978:NM_013979:
662	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	-0.01	CACGTCCGGATCTGTAACCAA	NM_013979:	NM_001205:NM_013980:NM_013978:NM_013979:
664	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	0.78	ATGAATAACATTGATAATAAA	NM_004052:	NM_004052:
664	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	0.73	ATGCTAATTGTTCATAATCAA	NM_004052:	NM_004052:
665	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-0.39	AAGCTTTACACCTGTTTACAA	AL132665:	NM_004331:
665	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	0.54	GACATCGATATTGACTATTTA	AL132665:	NM_004331:
91653	BOC (Boc ho	Boc homolog (mouse)	0.09	CAGGTCCTTATATCACCTTCA	NM_033254:	NM_033254:
91653	BOC (Boc ho	Boc homolog (mouse)	-1.69	ACCCGAGATCATGGCCAGCAA	NM_033254:	NM_033254:
666	BOK	BCL2-related ovarian killer	-0.84	CAGCCTGTAAACAGAGCGTAA	NM_032515:	NM_032515:
666	BOK	BCL2-related ovarian killer	-1.62	GCCCTGCACATTCAATCTGAA	NM_032515:	NM_032515:
669	BPGM (2,3-bi	2,3-bisphosphoglycerate mutase	0.71	CAAGAATAAGCAGCAAATAAA	NM_001724:	NM_001724:NM_199186:
669	BPGM (2,3-bi	2,3-bisphosphoglycerate mutase	-0.97	CTGGAAGGTATCTCAGATGAA	NM_001724:	NM_001724:NM_199186:
670	BPHL	biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-ass	-0.16	CCAAATGAGAATAATGACATA	NM_004332:	NM_004332:
670	BPHL	biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-ass	0.81	GCAGATGAATTCAACAAGTTA	NM_004332:	NM_004332:
671	BPI (bacterici	bactericidal/permeability-increasing protein	0.80	AGGAATCGTGTTTCAATTGTA	NM_001725:	NM_001725:
671	BPI (bacterici	bactericidal/permeability-increasing protein	0.01	CAGACGTTGTCTATAAATGAA	NM_001725:	NM_001725:
80341	BPIL1	bactericidal/permeability-increasing protein-like 1	0.65	ACCATACTTAGTCATCACCAA	NM_025227:	NM_025227:
80341	BPIL1	bactericidal/permeability-increasing protein-like 1	0.01	CAGGCGAATTTCTCATTTCAA	NM_025227:	NM_025227:
254240	BPIL2 (bacter	bactericidal/permeability-increasing protein-like 2	0.21	CCCGGATTGCAGAGATCTACA	NM_174932:	NM_174932:
254240	BPIL2 (bacter	bactericidal/permeability-increasing protein-like 2	-0.17	CTCCCGGATTGCAGAGATCTA	NM_174932:	NM_174932:
128859	BPIL3	bactericidal/permeability-increasing protein-like 3	-2.86	CTGGCTGAGCTGGACATAGTA	NM_174897:	NM_174897:
128859	BPIL3	bactericidal/permeability-increasing protein-like 3	-0.87	CCTGGTCAATGTGAAGACTAA	NM_174897:	NM_174897:
673	BRAF	v-raf murine sarcoma viral oncogene homolog B1	-0.04	AAGCTAGATGCACTCCAACAA	NM_004333:	NM_004333:
673	BRAF	v-raf murine sarcoma viral oncogene homolog B1	1.20	ACACGACATGTGAATATCCTA	NM_004333:	NM_004333:
8315	BRAP	BRCA1 associated protein	2.05	CAAGATAGTTCGGATAGAGAA	NM_006768:	NM_006768:
8315	BRAP	BRCA1 associated protein	-0.72	TAGGATGTGGACGGTATGTCA	NM_006768:	NM_006768:
672	BRCA1	breast cancer 1, early onset	-0.10	ACCATACAGCTTCATAAATAA	NM_007294:	NM_007296:NM_007294:NM_007295:NM_007298:NM_007297:NM_007299:NM_007300:NM_007301:NM_007302:NM_007303:NM_007304:NM_007306:NM_007305:
672	BRCA1	breast cancer 1, early onset	0.38	ACCGTTAATAAGGCAACTTAT	NM_007294:	NM_007296:NM_007294:NM_007295:NM_007299:NM_007300:NM_007301:NM_007303:NM_007304:NM_007306:
675	BRCA2	breast cancer 2, early onset	0.07	CAGGACACAATTACAACTAAA	NM_000059:	NM_000059:
675	BRCA2	breast cancer 2, early onset	0.08	TTGGAGGAATATCGTAGGTAA	NM_000059:	NM_000059:
79184	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	0.07	ATGGACCTACATACACACAAA	NM_024332:	NM_024332:NM_001018055:
79184	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	0.81	TACGATGTTGATTATAACATT	NM_024332:	NM_024332:NM_001018055:
23774	BRD1	bromodomain containing 1	-0.13	AAGACGGGATGTAAATTTACA	NM_014577:	NM_014577:
23774	BRD1	bromodomain containing 1	0.51	ACGGTTAGAAGCTCAAGGGTA	NM_014577:	NM_014577:
10902	BRD8	bromodomain containing 8	0.01	CAGATCGTAGCTAGTTTGTAT	NM_006696:	NM_183359:NM_006696:
10902	BRD8	bromodomain containing 8	-2.52	CCGGCTGTCTCCACTACTGAA	NM_006696:	NM_139199:NM_183359:NM_006696:
26228	BRDG1	BCR downstream signaling 1	-0.01	CACCAGAATTAGAATTAAACA	NM_012108:	NM_012108:
26228	BRDG1	BCR downstream signaling 1	-0.10	AAGGAACCAACTGAAGATTAT	NM_012108:	NM_012108:
9577	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	1.15	AAGAAATAAACTCACAAATTA	NM_004899:	NM_199191:NM_199192:NM_004899:NM_199193:NM_199194:
9577	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.69	CTCGCTGTTCTTCCTCTGAAA	NM_004899:	NM_199191:NM_199192:NM_004899:NM_199193:NM_199194:
55290	BRF2	BRF2, subunit of RNA polymerase III transcription initiation factor, BR	1.35	GAGGTGGGAAATAATTCCTTA	NM_018310:	NM_018310:
55290	BRF2	BRF2, subunit of RNA polymerase III transcription initiation factor, BR	-1.03	ACCGCGGTTGCCTACTACCAA	NM_018310:	NM_018310:
83990	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.75	CCTGAACTTTACGATCCTGAA	NM_032043:	NM_032043:
83990	BRIP1	BRCA1 interacting protein C-terminal helicase 1	-0.60	AAGATAAACAGTCCACTTCAA	NM_032043:	NM_032043:
25855	BRMS1	breast cancer metastasis suppressor 1	2.92	AAGGAGAAGTTGTTCAGGGAA	NM_015399:	NM_015399:NM_001024957:NM_001024958:
25855	BRMS1	breast cancer metastasis suppressor 1	2.77	CAGGAATAAGTACGAATGTGA	NM_015399:	NM_015399:NM_001024957:NM_001024958:
84312	BRMS1L	breast cancer metastasis-suppressor 1-like	0.01	ATGCAAATTCGTACAAAGGTA	NM_032352:	NM_032352:
84312	BRMS1L	breast cancer metastasis-suppressor 1-like	-2.09	CCGCTGGCAACTTTACAGGAA	NM_032352:	NM_032352:
7862	BRPF1	bromodomain and PHD finger containing, 1	-3.56	CAGCAACTGCCTCAAGTATAA	NM_004634:	NM_001003694:NM_004634:
7862	BRPF1	bromodomain and PHD finger containing, 1	0.01	AAGGGAGACGATCAAGGTTCA	NM_004634:	NM_001003694:NM_004634:
27154	BRPF3 (brom	bromodomain and PHD finger containing, 3	-2.29	CCGGCTTGAGAAAGAGTCATA	XM_166450:	NM_015695:
27154	BRPF3 (brom	bromodomain and PHD finger containing, 3	-1.53	TACCAACTGCATGAAGTATAA	XM_166450:	NM_015695:
680	BRS3 (bomb	bombesin-like receptor 3	0.35	AGCGTGTGTATCCGACTCTAA	NM_001727:	NM_001727:
680	BRS3 (bomb	bombesin-like receptor 3	0.05	CAGCGTGTGTATCCGACTCTA	NM_001727:	NM_001727:
84446	BRSK1	BR serine/threonine kinase 1	2.52	CAACTGTGAATCTGTAAATAA	NM_032430:	NM_032430:
84446	BRSK1	BR serine/threonine kinase 1	2.15	ACAAATATTCCTCGTGCTAAA	NM_032430:	NM_032430:
9024	BRSK2	BR serine/threonine kinase 2	-2.84	CCCGACTGCCAGAGTCTGCTA	NM_003957:	NM_003957:
9024	BRSK2	BR serine/threonine kinase 2	-0.01	GCGAGCTACTGTAAACTTTAA	NM_003957:	NM_003957:

26580	BSCL2	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)	-2.81	CAGGAGGAGTCAACTCCGCAA	NM_032667:	NM_032667:
26580	BSCL2	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)	0.37	CCGCTTCTCTTTGCAGGTTAA	NM_032667:	NM_032667:
682	BSG	basigin (Ok blood group)	0.05	CCCGTAGATTCCCATCATACA	NM_001728:	NM_198591:NM_001728:NM_198590:NM_198589:
682	BSG	basigin (Ok blood group)	-2.56	CCGGTCAGAGCTACACATTGA	NM_001728:	NM_198591:NM_001728:NM_198590:NM_198589:
7809	BSND	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	0.27	TGGGATGATATGGAGGTTCAA	NM_057176:	NM_057176:
7809	BSND	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	-3.27	CTGGACATGGACTCCAGTGAA	NM_057176:	NM_057176:
54836	BSPRY	B-box and SPRY domain containing	0.05	CCAGAACAGTTGTGCCTATAA	NM_017688:	NM_017688:
54836	BSPRY	B-box and SPRY domain containing	-3.03	CTGGATGGTGAATGTCCAGAA	NM_017688:	NM_017688:
684	BST2	bone marrow stromal cell antigen 2	-3.00	AAGCGTGAGAATCGCGGACAA	NM_004335:	NM_004335:
684	BST2	bone marrow stromal cell antigen 2	-2.42	AGGGAGAGATCACTACATTAA	NM_004335:	NM_004335:
90135	BTBD6	BTB (POZ) domain containing 6	0.51	ATAGTGGACTTCTGTAATAAA	NM_033271:	NM_033271:
90135	BTBD6	BTB (POZ) domain containing 6	-0.25	TCGGGAGGCCCTCAACACCAA	NM_033271:	NM_033271:
685	BTC (betacell	betacellulin	-0.03	CAGGATTACTAGTCAAACAAA	NM_001729:	NM_001729:
685	BTC (betacell	betacellulin	0.04	CACCAGAAGTCCTGAAACTAA	NM_001729:	NM_001729:
686	BTD (biotinida	biotinidase	0.76	ATGCGATTGGTCTCAAGCTAA	NM_000060:	NM_000060:
686	BTD (biotinida	biotinidase	-0.61	CACAAATGTCGTGTTCAGCAA	NM_000060:	NM_000060:
695	BTK	Bruton agammaglobulinemia tyrosine kinase	3.22	CAGCTCGAAACTGTTTGGTAA	NM_000061:	NM_000061:
695	BTK	Bruton agammaglobulinemia tyrosine kinase	0.82	CCCTTTATGATTACATGCCAA	NM_000061:	NM_000061:
696	BTN1A1	butyrophilin, subfamily 1, member A1	-1.64	CTCATCGTCTTTACCTAATAA	NM_001732:	NM_001732:
696	BTN1A1	butyrophilin, subfamily 1, member A1	-0.55	CACCCTCAATTTGTTGATCCA	NM_001732:	NM_001732:
11120	BTN2A1	butyrophilin, subfamily 2, member A1	-0.08	AAGTATGGTATCCAAAGCAAA	NM_007049:	NM_007049:NM_078476:
11120	BTN2A1	butyrophilin, subfamily 2, member A1	2.50	TACATACATTTACAACATTTA	NM_007049:	NM_007049:NM_078476:
10385	BTN2A2	butyrophilin, subfamily 2, member A2	1.76	AACGATTAATGTTTCATTATT	NM_006995:	NM_181531:NM_006995:
10385	BTN2A2	butyrophilin, subfamily 2, member A2	-0.21	TACGTCAGCATTCAGGTTCAA	NM_006995:	NM_181531:NM_006995:
54718	BTN2A3 (buty	butyrophilin, subfamily 2, member A3	-1.06	TAGGGTCTTATGACAGCCAAA	NM_024018:	NM_024018:
54718	BTN2A3 (buty	butyrophilin, subfamily 2, member A3	-3.17	CAGGGAGAGCATTCCGGGCAA	NM_024018:	NM_024018:
11119	BTN3A1	butyrophilin, subfamily 3, member A1	1.01	AAGACTCAGTTCAGAAAGAAA	NM_194441:	NM_194441:NM_007048:
11119	BTN3A1	butyrophilin, subfamily 3, member A1	0.05	CAGATGGAGAAGTATCCAGTA	NM_194441:	NM_194441:NM_007048:
11118	BTN3A2	butyrophilin, subfamily 3, member A2	-0.56	CAGAGCGGGAAATAAGCCTAA	NM_007047:	NM_007047:
11118	BTN3A2	butyrophilin, subfamily 3, member A2	-0.05	CAGCCTGATGCTCTAATGGAA	NM_007047:	NM_007047:
10384	BTN3A3	butyrophilin, subfamily 3, member A3	0.20	CCAGCTGATATCAGAGACTTA	NM_006994:	NM_006994:NM_197974:
10384	BTN3A3	butyrophilin, subfamily 3, member A3	1.29	AAGGTGAATTAACTTTACAAA	NM_006994:	NM_006994:NM_197974:
56244	BTNL2	butyrophilin-like 2 (MHC class II associated)	0.34	GTGGGAGAAGATATACAGCTA	NM_019602:	NM_019602:
56244	BTNL2	butyrophilin-like 2 (MHC class II associated)	-1.07	ATGGAGGGACATGGAAGGAAA	NM_019602:	NM_019602:
10917	BTNL3	butyrophilin-like 3	0.29	ACCCATGGAATAGTTATTGAA	NM_006707:	NM_197975:NM_006707:
10917	BTNL3	butyrophilin-like 3	-0.31	CCCAGCATTACCTGATACCAA	NM_006707:	NM_197975:NM_006707:
79908	BTNL8	butyrophilin-like 8	-1.59	CAGGATTAGTTCCCAGTCTTA	NM_024850:	NM_024850:
79908	BTNL8	butyrophilin-like 8	-1.31	CACAGTATCAAGGCAGGACAA	NM_024850:	NM_024850:
153579	BTNL9	butyrophilin-like 9	0.49	AACATTCTTGTTCTTAGCAAA	NM_152547:	NM_152547:
153579	BTNL9	butyrophilin-like 9	-1.39	CCAGATCATCCAAGTGATTAA	NM_152547:	NM_152547:
8945	BTRC	beta-transducin repeat containing	0.01	CAGGATGAGCAACAACAGTAA	NM_003939:	NM_003939:NM_033637:
8945	BTRC	beta-transducin repeat containing	0.37	CTGGGCTAGAATAAATGTAAA	NM_003939:	NM_003939:NM_033637:
699	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	2.22	AACACTATACTAACAAGATTA	NM_004336:	NM_004336:
699	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	-1.97	CAGCTTGTGATAAAGAGTCAA	NM_004336:	NM_004336:
701	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	2.57	ACGAGAATACCTAATATGTGA	NM_001211:	NM_001211:
701	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-0.64	CAGATTTAGCACATTTACTAT	NM_001211:	NM_001211:
9184	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	0.71	CTGGTTATAGTTGCTAATTCT	NM_004725:	NM_004725:
9184	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	-0.36	TTGGACCTGTTTCTATCTCTA	NM_004725:	NM_004725:
9256	BZRAP1	benzodiazapine receptor (peripheral) associated protein 1	0.94	CACAGTGAGTATGTAACTTGA	NM_004758:	NM_004758:
9256	BZRAP1	benzodiazapine receptor (peripheral) associated protein 1	-5.18	CAGAGCTAAATGGCTCCTTAA	NM_004758:	NM_004758:
706	BZRP	benzodiazapine receptor (peripheral)	-1.17	CGGCTCCTACCTGGTCTGGAA	NM_000714:	NM_000714:NM_007311:
706	BZRP	benzodiazapine receptor (peripheral)	-0.05	CCCATCTTCTTTGGTGCCCGA	NM_000714:	NM_000714:NM_007311:
222642	BZRPL1	benzodiazapine receptor (peripheral)-like 1	0.08	CAGAGGAGTGCTGTGGAGAAA	NM_001010873:	NM_001010873:
222642	BZRPL1	benzodiazapine receptor (peripheral)-like 1	-2.76	CCCATTCTACAAAGTCTTATT	NM_001010873:	NM_001010873:
340895	C10orf112	chromosome 10 open reading frame 112	-0.60	CAGGAGTATGGGAATATTAAA	XM_295865:	XM_295865:
340895	C10orf112	chromosome 10 open reading frame 112	0.67	AAGCTGTAACTTCGTAGATAA	XM_295865:	XM_295865:
80195	C10orf57	chromosome 10 open reading frame 57	-8.21	AACCATAGAGTTAGGCATCAT	NM_025125:	NM_025125:
80195	C10orf57	chromosome 10 open reading frame 57	0.01	ACCCTGAAAGATTATGAACTA	NM_025125:	NM_025125:
118812	C10orf83	chromosome 10 open reading frame 83	0.05	AAAGGTGTTTATAAAGAATAA	NM_178832:	NM_178832:
118812	C10orf83	chromosome 10 open reading frame 83	-0.90	CAGATTGTGGTGGAAGTTATA	NM_178832:	NM_178832:
80013	C10orf97	chromosome 10 open reading frame 97	-0.44	ACGTTATTTATTATGATCCTA	NM_024948:	NM_024948:
80013	C10orf97	chromosome 10 open reading frame 97	0.66	TTGAATGATTCCGGCTTGTAA	NM_024948:	NM_024948:
747	C11orf11	chromosome 11 open reading frame 11	0.65	CCAAACTAATATTGCTGTAAA	NM_006133:	NM_006133:
747	C11orf11	chromosome 11 open reading frame 11	1.17	CTGCAGTGCTGTACATGTTTA	NM_006133:	NM_006133:
53838	C11orf24	chromosome 11 open reading frame 24	0.45	CGGAGCCTGACCTGAATTAAA	NM_022338:	NM_022338:
53838	C11orf24	chromosome 11 open reading frame 24	0.98	TCGGAGCCTGACCTGAATTAA	NM_022338:	NM_022338:
51275	C12orf47	chromosome 12 open reading frame 47	0.08	CTCCACCGATAACCTATCAAA	NM_016534:	NM_016534:
51275	C12orf47	chromosome 12 open reading frame 47	-0.77	GAGCATAAGTTAAGTAAGTAA	NM_016534:	NM_016534:
55010	C12orf48	chromosome 12 open reading frame 48	-3.67	CAGAATAGATTGTACGGCAAA	NM_017915:	NM_017915:
55010	C12orf48	chromosome 12 open reading frame 48	0.91	CCCAATTTGCTTGTACTTATA	NM_017915:	NM_017915:
57213	C13orf1	chromosome 13 open reading frame 1	1.05	GACCATGTCGAATTAAATGTA	NM_020456:	NM_020456:
57213	C13orf1	chromosome 13 open reading frame 1	0.47	TAGTGGTTGATTAGTAATGTA	NM_020456:	NM_020456:
80209	C13orf23	chromosome 13 open reading frame 23	0.38	TACAAGTAAGACTTAGGATAA	NM_025138:	NM_025138:NM_170719:
80209	C13orf23	chromosome 13 open reading frame 23	-1.00	AAGGAAGACCTAGCCGCATAA	NM_025138:	NM_025138:NM_170719:
25938	C14orf125	chromosome 14 open reading frame 125	-0.20	CTAGGCATAATATTAGCTAAA	XM_113763:	XM_113763:
25938	C14orf125	chromosome 14 open reading frame 125	-5.18	CAGCCTTACAGTGCAACATAA	XM_113763:	XM_113763:
55148	C14orf130	chromosome 14 open reading frame 130	-0.02	ATCAGTTAACTCAGCGCTGAA	NM_018108:	NM_018108:
55148	C14orf130	chromosome 14 open reading frame 130	0.17	CACAATAGTACCGATCAGTTA	NM_018108:	NM_018108:
79697	C14orf169	chromosome 14 open reading frame 169	0.80	CTGCTTGAGACAGATATTAGA	NM_024644:	NM_024644:
79697	C14orf169	chromosome 14 open reading frame 169	-0.18	ACCCAAGTGCTTGGAAATATA	NM_024644:	NM_024644:
115708	C14orf172	chromosome 14 open reading frame 172	0.05	CCAAGTGTGAGTGATGAGCAA	NM_152307:	NM_152307:
115708	C14orf172	chromosome 14 open reading frame 172	-1.62	CCGCAGCGGCACGCCCATGAA	NM_152307:	NM_152307:
64423	C14orf173	chromosome 14 open reading frame 173	-5.74	CCCGGCCTTGATGCTACAACA	NM_022489:	NM_022489:NM_001031714:
64423	C14orf173	chromosome 14 open reading frame 173	1.11	CCTGATTCTGATGATAATAAA	NM_022489:	NM_022489:
64207	C14orf4	chromosome 14 open reading frame 4	-1.26	CGGCATGGACTACGAATTGAA	NM_024496:	NM_024496:
64207	C14orf4	chromosome 14 open reading frame 4	1.09	TCGCATCGAATTCGTGATCGA	NM_024496:	NM_024496:
283600	C14orf68	chromosome 14 open reading frame 68	-0.59	CACGGTGAAGGTCAGGATCCA	NM_207117:	NM_207117:
283600	C14orf68	chromosome 14 open reading frame 68	-1.24	TTGGGAACTGTTGTCAATAAA	NM_207117:	NM_207117:
57184	C15orf17	chromosome 15 open reading frame 17	-4.65	TAGGTTCTACATGGGAAAGTA	NM_020447:	NM_020447:
57184	C15orf17	chromosome 15 open reading frame 17	0.01	CAGTCTTTGAGCTAAAGATTA	NM_020447:	NM_020447:
123591	C15orf27	chromosome 15 open reading frame 27	-1.08	CAGCAGGGCACTATATTTGTA	NM_152335:	NM_152335:
123591	C15orf27	chromosome 15 open reading frame 27	0.94	CAGCTACATCAGTCAGTATTA	NM_152335:	NM_152335:
65259	C16orf28	chromosome 16 open reading frame 28	1.06	TCCAATTAAGTGCAAATAGTA	NM_023076:	NM_023076:
65259	C16orf28	chromosome 16 open reading frame 28	1.40	ATGCGATAATATGAAGCTTTA	NM_023076:	NM_023076:
79622	C16orf33	chromosome 16 open reading frame 33	-2.45	ACGGCCTGGCCCACTGTATAA	NM_024571:	NM_024571:
79622	C16orf33	chromosome 16 open reading frame 33	1.01	CCCAGGCATGCCCAACAGTAA	NM_024571:	NM_024571:
55839	C16orf60	chromosome 16 open reading frame 60	1.04	AACACAGTACACAAAGCCAAA	NM_018455:	NM_018455:

55839	C16orf60	chromosome 16 open reading frame 60	1.34	TTGCAATTAGTGAACATGAAA	NM_018455:	NM_018455:
57674	C17orf27	chromosome 17 open reading frame 27	2.45	TCAGCGTAGCACCGAATTCAA	NM_020914:	NM_020914:
57674	C17orf27	chromosome 17 open reading frame 27	0.89	ACGAACGGTGAGATCAACCTA	NM_020914:	NM_020914:
284021	C17orf60 (chr	chromosome 17 open reading frame 60	0.78	CTGAATCGCTTTAGTAAATAA	XM_211305:	XM_211305:
284021	C17orf60 (chr	chromosome 17 open reading frame 60	1.05	CTGAACATTATGGTCATTCAA	XM_211305:	XM_211305:
64149	C17orf75	chromosome 17 open reading frame 75	-0.01	TTGAGTTACACTCCTGTTGAA	NM_022344:	NM_022344:
64149	C17orf75	chromosome 17 open reading frame 75	0.36	TTGGCAGATACTAATCTACCA	NM_022344:	NM_022344:
753	C18orf1 (chro	chromosome 18 open reading frame 1	-0.40	CGGGAGAGGGTTAGAGCTATA	NM_181483:	NM_181481:NM_181482:NM_181483:NM_004338: NM_001003674:NM_001003675:
753	C18orf1 (chro	chromosome 18 open reading frame 1	0.67	CCACGTGTTGTTTCCATCGTA	NM_181483:	NM_181481:NM_181482:NM_181483:NM_004338: NM_001003674:NM_001003675:
10438	C1D	nuclear DNA-binding protein	1.41	CACAGTAAATATGTAAAGCTA	NM_006333:	NM_006333:NM_173177:
10438	C1D	nuclear DNA-binding protein	0.64	CAGCTGTGAAATTTAAGTGAA	NM_006333:	NM_006333:NM_173177:
55732	C1orf112	chromosome 1 open reading frame 112	-0.01	CTGGGTTTGATGCTTTGTCAA	NM_018186:	NM_018186:
55732	C1orf112	chromosome 1 open reading frame 112	-1.26	CAGCCTGGCTTTCAATGGAAA	NM_018186:	NM_018186:
83932	C1orf124	chromosome 1 open reading frame 124	-0.50	CTGAACTGATGTAAATCTTCA	NM_032018:	NM_032018:NM_001010984:
83932	C1orf124	chromosome 1 open reading frame 124	-1.42	ACGACCTAGGCTAGAAGATAA	NM_032018:	NM_032018:NM_001010984:
55182	C1orf164	chromosome 1 open reading frame 164	-0.98	CTCGGTGTTCAGTGGTGTATA	NM_018150:	NM_018150:
55182	C1orf164	chromosome 1 open reading frame 164	-2.91	CCCAATCAGTATGCTGAATCA	NM_018150:	NM_018150:
79594	C1orf166	chromosome 1 open reading frame 166	-0.81	CAGGAATTAAACATGTTGCAA	NM_024544:	NM_024544:
79594	C1orf166	chromosome 1 open reading frame 166	-0.99	CAGCTTTGACATCTTGGTGTA	NM_024544:	NM_024544:
149281	C1orf184 (chr	chromosome 1 open reading frame 184	-0.03	CTGGTGAAATTGTACGCTTTA	XM_089281:	XM_089281:
149281	C1orf184 (chr	chromosome 1 open reading frame 184	-0.18	CAGTTCTATGCCAGAGCTAAA	XM_089281:	XM_089281:
51154	C1orf33	chromosome 1 open reading frame 33	-0.29	AAGGCTTGGAATTGAAACAAA	NM_016183:	NM_016183:
51154	C1orf33	chromosome 1 open reading frame 33	-0.04	TACGCCCGAGCTGGTAACAAA	NM_016183:	NM_016183:
114897	C1QTNF1	C1q and tumor necrosis factor related protein 1	2.02	TTCAGTTGAGACTCTGCTTAA	NM_030968:	NM_198594:NM_198593:NM_030968:
114897	C1QTNF1	C1q and tumor necrosis factor related protein 1	1.27	AAGGGTGACCGCGGAGATCGA	NM_030968:	NM_198594:NM_198593:NM_030968:
715	C1R (compler	complement component 1, r subcomponent	0.15	TCGGGAGAGCCCAGGATTCAA	NM_001733:	NM_001733:
715	C1R (compler	complement component 1, r subcomponent	0.22	CCCGGGAAAGAAGGAATTTAT	NM_001733:	NM_001733:
51279	C1RL	complement component 1, r subcomponent-like	0.07	CAGCTCCAAGATGCAATTATA	NM_016546:	NM_016546:
51279	C1RL	complement component 1, r subcomponent-like	1.30	CCCGGTCTGTCTGCCCGATAA	NM_016546:	NM_016546:
716	C1S (compler	complement component 1, s subcomponent	0.09	CCCGGAGTACCTATTGTAGAT	NM_001734:	NM_201442:NM_001734:
716	C1S (compler	complement component 1, s subcomponent	1.09	GAGGTAGAGTTTGATCATAGA	NM_001734:	NM_201442:NM_001734:
717	C2	complement component 2	0.63	CCCAGTTATGAAATTAATAAA	NM_000063:	NM_000063:
717	C2	complement component 2	-0.25	ACCCTGGCATGTCACTATTAA	NM_000063:	NM_000063:
92747	C20orf114	chromosome 20 open reading frame 114	0.00	ATCCCTCTCTGCAATCAATAA	NM_033197:	NM_033197:
92747	C20orf114	chromosome 20 open reading frame 114	0.05	CCGAACCAGAATGGCAAATTA	NM_033197:	NM_033197:
55184	C20orf12	chromosome 20 open reading frame 12	-0.18	TGGCTCCTAATTACTATGTAA	NM_018152:	NM_018152:
55184	C20orf12	chromosome 20 open reading frame 12	-0.58	CTGAATTATAGTCAAGTCTCA	NM_018152:	NM_018152:
81610	C20orf129	chromosome 20 open reading frame 129	-1.16	CCAGGATAGCAAGCTCTCAAA	NM_030919:	NM_030919:
81610	C20orf129	chromosome 20 open reading frame 129	-0.70	ATAGACGGATGGCAAATTAAA	NM_030919:	NM_030919:
24148	C20orf14	chromosome 20 open reading frame 14	-0.78	CACCAATTACGATGAGTTTAA	NM_012469:	NM_012469:
24148	C20orf14	chromosome 20 open reading frame 14	-0.92	TACGATGAGTTTAATGGCTAT	NM_012469:	NM_012469:
140706	C20orf160	chromosome 20 open reading frame 160	-3.28	CACCCGATAAGAGCTCAATAA	NM_080625:	NM_080625:
140706	C20orf160	chromosome 20 open reading frame 160	-1.94	CTGAGGGTTAAGACCTTAGAA	NM_080625:	NM_080625:
90203	C20orf161	chromosome 20 open reading frame 161	0.05	CTGGGCCTGGACAAACGTCAA	NM_033421:	NM_033421:
90203	C20orf161	chromosome 20 open reading frame 161	-1.25	AAGGACCTGATGAGAACAGAA	NM_033421:	NM_033421:
10616	C20orf18	chromosome 20 open reading frame 18	-2.17	CCCTGTGTGTTTCCACGTCAA	NM_006462:	NM_006462:NM_031229:NM_031228:NM_031227:
10616	C20orf18	chromosome 20 open reading frame 18	0.61	GAGGATTACCAGCGATTTCTA	NM_006462:	NM_006462:NM_031229:NM_031228:NM_031227:
359710	C20orf185	chromosome 20 open reading frame 185	0.82	CAGTGTATGCACCAAAGCTTA	NM_182658:	NM_182658:
359710	C20orf185	chromosome 20 open reading frame 185	0.65	ACGGATCGCGTTTAGAAGAAT	NM_182658:	NM_182658:
149954	C20orf186	chromosome 20 open reading frame 186	-2.12	CCCAGTATATACCAACGGCAA	NM_182519:	NM_182519:
149954	C20orf186	chromosome 20 open reading frame 186	0.79	CCCAATCTCGTGGACAATTTA	NM_182519:	NM_182519:
55614	C20orf23	chromosome 20 open reading frame 23	-0.47	AACGAACGTGTGAGAGATCTA	NM_024704:	NM_024704:
55614	C20orf23	chromosome 20 open reading frame 23	1.71	GAGGATTTATCCAAACATTTA	NM_024704:	NM_024704:
55614	C20orf23	chromosome 20 open reading frame 23	-0.77	AACGAACGTGTGAGAGATCTA	NM_024704:	NM_024704:
55614	C20orf23	chromosome 20 open reading frame 23	0.76	CACCTTTGAATTCACTGCCAA	NM_024704:	NM_024704:
79133	C20orf7	chromosome 20 open reading frame 7	-0.76	ATGGATAGCTTTAACATCTAA	NM_024120:	NM_024120:NM_199052:
79133	C20orf7	chromosome 20 open reading frame 7	0.79	AAGAGGTTACATTGCACAATA	NM_024120:	NM_024120:NM_199052:
140731	C20orf86	chromosome 20 open reading frame 86	1.45	GAGGGCGTTTGTGGCGTTGTA	NM_080674:	NM_080674:
140731	C20orf86	chromosome 20 open reading frame 86	-0.07	AACCGCAAATTCAGAACATTT	NM_080674:	NM_080674:
79019	C22orf18	chromosome 22 open reading frame 18	-3.31	CAGCAAATACAGTCTCCAGAA	NM_024053:	NM_001002876:NM_024053:
79019	C22orf18	chromosome 22 open reading frame 18	-0.40	CCTGATCGTGTTTGTGGTTAA	NM_024053:	NM_001002876:NM_024053:
51374	C2orf28	chromosome 2 open reading frame 28	-2.90	AAGCCAAGACTTCATGAACTA	NM_016085:	NM_080592:NM_016085:
51374	C2orf28	chromosome 2 open reading frame 28	0.70	CTGGAATACTATCACCTCTTA	NM_016085:	NM_080592:NM_016085:
718	C3	complement component 3	-0.59	TAGGAACACCCTCATCATCTA	NM_000064:	NM_000064:
718	C3	complement component 3	0.05	CACGGAGAAGCGAATGGACAA	NM_000064:	NM_000064:
719	C3AR1	complement component 3a receptor 1	0.49	CTGCTAGGTTAACAAGTCAAA	NM_004054:	NM_004054:
719	C3AR1	complement component 3a receptor 1	0.19	TCGCTGTCTTGTGGTATTCAA	NM_004054:	NM_004054:
64419	C3orf29	chromosome 3 open reading frame 29	-4.92	AAGGTGAAGTTTGGCATGAAT	NM_022485:	NM_022485:
64419	C3orf29	chromosome 3 open reading frame 29	-1.00	CTGCCCAGTAATCCTGTTCAA	NM_022485:	NM_022485:
285237	C3orf38	chromosome 3 open reading frame 38	-0.27	CTGGGTTTACCTGACCCTCTA	NM_173824:	NM_173824:
285237	C3orf38	chromosome 3 open reading frame 38	-0.92	ATGAAGTACGACATAATGTAA	NM_173824:	NM_173824:
93556	C3orf50 (chro	chromosome 3 open reading frame 50	1.86	CACAGCGTTTATGATACTGAA	XM_376284:	XM_376284:
93556	C3orf50 (chro	chromosome 3 open reading frame 50	0.48	TTCAATGGATTAGAAGACTAA	XM_376284:	XM_376284:
727	C5	complement component 5	-0.77	CCGCTTGAGTATGGACATCGA	NM_001735:	NM_001735:
727	C5	complement component 5	-0.02	GCCTGCGTTAATAATGATGAA	NM_001735:	NM_001735:
728	C5AR1	complement component 5a receptor 1	0.76	CCGGAACGTGTTGACTGAAGA	NM_001736:	NM_001736:
728	C5AR1	complement component 5a receptor 1	-0.81	TCGTGGGATGGTGTTACCTTA	NM_001736:	NM_001736:
79770	C5orf14	chromosome 5 open reading frame 14	-2.65	CCGGCAGAATAGTGAGTAGAA	NM_024715:	NM_024715:
79770	C5orf14	chromosome 5 open reading frame 14	-0.47	CTGCATGAACGTAATCCAGTA	NM_024715:	NM_024715:
729	C6 (complem	complement component 6	-2.87	TAGGATCCATAAAGTGATGAA	NM_000065:	NM_000065:
729	C6 (complem	complement component 6	-1.07	CATCGTGGACTTGGTAAGAAA	NM_000065:	NM_000065:
80739	C6orf25	chromosome 6 open reading frame 25	-1.40	CACGAGGACGAGAGCCGTACA	NM_025260:	NM_025260:NM_138276:NM_138277:NM_138274: NM_138275:NM_138272:NM_138273:
80739	C6orf25	chromosome 6 open reading frame 25	-2.06	CAGCCTTTCGTCGGCCGCCTA	NM_025260:	NM_025260:NM_138276:NM_138277:NM_138274: NM_138275:NM_138272:NM_138273:
222658	C6orf69	chromosome 6 open reading frame 69	-0.22	CCGGTCTGAAGTCATCTATAA	NM_173562:	NM_173562:
222658	C6orf69	chromosome 6 open reading frame 69	0.37	TAGCATCACTGTGGAAATTAA	NM_173562:	NM_173562:
80129	C6orf97	chromosome 6 open reading frame 97	-2.06	CAACCGTTCGTGAGTCATCAA	NM_025059:	NM_025059:
80129	C6orf97	chromosome 6 open reading frame 97	-0.08	AAGCTCTAGCATGAAATTAAA	NM_025059:	NM_025059:
730	C7 (complem	complement component 7	0.31	CCGAAGATTAATCGACCAGTA	NM_000587:	NM_000587:
730	C7 (complem	complement component 7	-0.72	AAGGATTAGAACACTCATTAA	NM_000587:	NM_000587:
83590	C7orf21	chromosome 7 open reading frame 21	-1.12	GCAGATTAAAGTAACTGTGAA	NM_031434:	NM_031434:
83590	C7orf21	chromosome 7 open reading frame 21	-0.57	CCCGGAACCCGTGCAGATTAA	NM_031434:	NM_031434:
64111	C7orf9	chromosome 7 open reading frame 9	0.26	AAACATTATGATGGAAATTAA	NM_022150:	NM_022150:
64111	C7orf9	chromosome 7 open reading frame 9	1.42	ATCGTGTCAAATGTTAATGAA	NM_022150:	NM_022150:

731	C8A (compler	complement component 8, alpha polypeptide	0.31	CTGGATGTTGACTGTTAACTA	NM_000562:	NM_000562:
731	C8A (compler	complement component 8, alpha polypeptide	1.67	CACTCATAGAAACATTATTAA	NM_000562:	NM_000562:
732	C8B (compler	complement component 8, beta polypeptide	-1.52	CACGAGGTTTAGGAAGCCCTA	NM_000066:	NM_000066:
732	C8B (compler	complement component 8, beta polypeptide	0.61	CTGGAGTTCATGCAAGGGCAA	NM_000066:	NM_000066:
733	C8G	complement component 8, gamma polypeptide	0.82	CCAGAGTTTCGCTGTCCTGTA	NM_000606:	NM_000606:
733	C8G	complement component 8, gamma polypeptide	0.02	GAGTGGTACCTACTTATTAAA	NM_000606:	NM_000606:
735	C9 (complem	complement component 9	1.18	GCGGAAAGGTGTTGAACTAAA	NM_001737:	NM_001737:
735	C9 (complem	complement component 9	-2.51	TAGGAGGACTCTATGAACTAA	NM_001737:	NM_001737:
51490	C9orf114	chromosome 9 open reading frame 114	0.94	CCGGCACACCTGAAAGTTCTA	NM_016390:	NM_016390:
51490	C9orf114	chromosome 9 open reading frame 114	-0.44	TCGGGTGACTGTGCGACTGAA	NM_016390:	NM_016390:
254956	C9orf18	chromosome 9 open reading frame 18	-0.03	CACGAGGGTAGTCAAGGACTA	NM_198469:	NM_198469:
254956	C9orf18	chromosome 9 open reading frame 18	0.22	TAGGAACCGCTTTCTAAGAAA	NM_198469:	NM_198469:
28989	C9orf32	chromosome 9 open reading frame 32	0.22	ACGGAGGACTTCCTGGTTCAA	NM_014064:	NM_014064:
347240	C9orf48	chromosome 9 open reading frame 48	-0.79	CCGGGTCAAAGAACTAAAGAA	NM_194313:	NM_194313:
347240	C9orf48	chromosome 9 open reading frame 48	1.21	ACCCTATTCTATCATCATATA	NM_194313:	NM_194313:
158427	C9orf97	chromosome 9 open reading frame 97	-2.34	ACCCACGTATGTGATAAATCA	NM_139246:	NM_139246:
158427	C9orf97	chromosome 9 open reading frame 97	-1.93	AAGGGTCAACTGTATAGTTTA	NM_139246:	NM_139246:
759	CA1	carbonic anhydrase I	1.77	CAGTTTATTTGAACCAATAAA	NM_001738:	NM_001738:
759	CA1	carbonic anhydrase I	0.83	CTAGCAAATAGTAATCTGTAA	NM_001738:	NM_001738:
56934	CA10	carbonic anhydrase X	0.59	AAGTTGGATCATAATGAACAA	NM_020178:	NM_020178:
56934	CA10	carbonic anhydrase X	0.62	AACCATGAGCTATATACGAAT	NM_020178:	NM_020178:
770	CA11	carbonic anhydrase XI	0.15	GACAGAATACTTCCTGTTTAA	NM_001217:	NM_001217:
770	CA11	carbonic anhydrase XI	0.04	CTCATTCACTTCAACCAGGAA	NM_001217:	NM_001217:
771	CA12	carbonic anhydrase XII	-0.68	CACACTGTAACTACAAGAAAT	NM_001218:	NM_001218:NM_206925:
771	CA12	carbonic anhydrase XII	1.63	ATCAAATATATTTCAAGCTAT	NM_001218:	NM_001218:NM_206925:
377677	CA13	carbonic anhydrase XIII	-0.04	CAGAGGGACACTAAGCATTAA	NM_198584:	NM_198584:
377677	CA13	carbonic anhydrase XIII	-0.16	CTCAGTGATGTTAGATGGAAA	NM_198584:	NM_198584:
23632	CA14 (carbon	carbonic anhydrase XIV	0.54	CGGGATCTCTCCTTAGGATAA	NM_012113:	NM_012113:
23632	CA14 (carbon	carbonic anhydrase XIV	-0.75	AAGCAGGATCCTCGTATACCA	NM_012113:	NM_012113:
760	CA2	carbonic anhydrase II	1.67	CGGGTGTTTCCCTTTAGCTAA	NM_000067:	NM_000067:
760	CA2	carbonic anhydrase II	1.08	CAGGTGTTGAAATTCCGTAAA	NM_000067:	NM_000067:
761	CA3	carbonic anhydrase III, muscle specific	0.70	GAGGTGTATGAAGATCATATA	NM_005181:	NM_005181:
761	CA3	carbonic anhydrase III, muscle specific	1.64	AAGCATAGATTTCACATTTGA	NM_005181:	NM_005181:
762	CA4	carbonic anhydrase IV	-1.35	CTGGTCCGACTTGCCATATAA	NM_000717:	NM_000717:
762	CA4	carbonic anhydrase IV	-2.49	CTGGCTACGATAAGAAGCAAA	NM_000717:	NM_000717:
763	CA5A	carbonic anhydrase VA, mitochondrial	-0.56	CACAAGGTCCTAGAGACATTA	NM_001739:	NM_001739:
763	CA5A	carbonic anhydrase VA, mitochondrial	0.85	AGCGTTGTTTCCCAAGTTTCA	NM_001739:	NM_001739:
11238	CA5B	carbonic anhydrase VB, mitochondrial	-0.01	TAGTGGTTCTATAGCACTATA	NM_007220:	NM_007220:
11238	CA5B	carbonic anhydrase VB, mitochondrial	2.18	TACAGATAAATCAGTGATCAA	NM_007220:	NM_007220:
340591	CA5BL	carbonic anhydrase VB-like	-1.10	CAGATAAATCAGGCTGTACAA	XM_291346:	XM_291346:
765	CA6	carbonic anhydrase VI	0.59	GAGGAAATTCTTGACTACTTA	NM_001215:	NM_001215:
765	CA6	carbonic anhydrase VI	-0.38	CCGAATCAGGAATACACTCTA	NM_001215:	NM_001215:
766	CA7	carbonic anhydrase VII	0.49	CTGGCTATAGCTTATACAGTA	NM_005182:	NM_005182:NM_001014435:
766	CA7	carbonic anhydrase VII	0.01	CCAGAGAGACTCAAGCAATAA	NM_005182:	NM_005182:NM_001014435:
767	CA8	carbonic anhydrase VIII	0.52	CACCTGGATATTATTCCGATA	NM_004056:	NM_004056:
767	CA8	carbonic anhydrase VIII	1.30	CACGGTTAATTTCAAAGCTTT	NM_004056:	NM_004056:
768	CA9	carbonic anhydrase IX	-2.35	CTGGCTGCTGGTGACATCCTA	NM_001216:	NM_001216:
768	CA9	carbonic anhydrase IX	-1.19	CAGCCGCTACTTCCAATATGA	NM_001216:	NM_001216:
23523	CABIN1	calcineurin binding protein 1	-1.36	CCACGATTACGTCAAATGTAA	NM_012295:	NM_012295:
23523	CABIN1	calcineurin binding protein 1	-1.38	AAGGATTGATTTGTCGGACTA	NM_012295:	NM_012295:
57685	CACHD1	cache domain containing 1	2.74	ACGACAAAGGATATACACTTA	NM_020925:	NM_020925:
57685	CACHD1	cache domain containing 1	-0.01	CCGCAGTAGATTTCTGTGTTA	NM_020925:	NM_020925:
773	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	0.42	CGGGTGCTACGACCTCTTAAA	NM_000068:	NM_000068:NM_023035:
773	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-0.01	CCGGGTGCTACGACCTCTTAA	NM_000068:	NM_000068:NM_023035:
774	CACNA1B	calcium channel, voltage-dependent, L type, alpha 1B subunit	0.40	TCGAATTGGCTCTGACCCTTA	NM_000718:	NM_000718:
774	CACNA1B	calcium channel, voltage-dependent, L type, alpha 1B subunit	-0.34	CCGGCAGTCGTTCCAGTATAA	NM_000718:	NM_000718:
775	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	0.52	CCGGAGGAGCACATTCGATAA	NM_000719:	NM_000719:
775	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	0.76	CTGGTTTGGTTCGGTTATCTA	NM_000719:	NM_000719:
776	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	0.28	CACGCGAACGAGGCAAACTAT	NM_000720:	NM_000720:
776	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	0.34	CCAGATCAATAGGAACAATAA	NM_000720:	NM_000720:
777	CACNA1E	calcium channel, voltage-dependent, alpha 1E subunit	1.12	ATGCTTTAAGGTGATTAGTAA	NM_000721:	NM_000721:
777	CACNA1E	calcium channel, voltage-dependent, alpha 1E subunit	-1.65	CCGCGTCAGGACAGAAGGCAA	NM_000721:	NM_000721:
778	CACNA1F	calcium channel, voltage-dependent, alpha 1F subunit	-0.15	CCGGACATCCCTGAAGATCAA	NM_005183:	NM_005183:
778	CACNA1F	calcium channel, voltage-dependent, alpha 1F subunit	-4.18	CTGGCCTGCACTGCTATACAA	NM_005183:	NM_005183:
8913	CACNA1G	calcium channel, voltage-dependent, alpha 1G subunit	1.07	TACGTTTGTGCAGAATCTCTA	NM_018896:	NM_198379:NM_198388:NM_198378:NM_198377:NM_018896:NM_198386:NM_198376:NM_198382:NM_198384:NM_198383:NM_198385:NM_198380:NM_198387:NM_198396:
8913	CACNA1G	calcium channel, voltage-dependent, alpha 1G subunit	-2.71	CACGGTCATCTCGCCTATCTA	NM_018896:	NM_198379:NM_198388:NM_198378:NM_198377:NM_018896:NM_198386:NM_198376:NM_198382:NM_198384:NM_198383:NM_198385:NM_198380:NM_198387:NM_198396:
8912	CACNA1H	calcium channel, voltage-dependent, alpha 1H subunit	-2.06	CACCAGGAACATCTCCACCAA	NM_021098:	NM_021098:NM_001005407:
8912	CACNA1H	calcium channel, voltage-dependent, alpha 1H subunit	0.05	CTGAAGTACGTGGGCCACATA	NM_021098:	NM_021098:NM_001005407:
8911	CACNA1I	calcium channel, voltage-dependent, alpha 1I subunit	0.99	CCGGTTAGATGTCTCTCTTTA	NM_021096:	NM_001003406:NM_021096:
8911	CACNA1I	calcium channel, voltage-dependent, alpha 1I subunit	-1.37	CAGCGTCTCTTTAATCATCAA	NM_021096:	NM_001003406:NM_021096:
779	CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	-1.75	CCGCACGGCACTCAAGATCAA	NM_000069:	NM_000069:
779	CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	-1.81	CCGGGCTGATTCCATGAGAAA	NM_000069:	NM_000069:
781	CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	0.15	CCGCCTGTTATGACCTTCTAA	NM_000722:	NM_000722:
781	CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	2.12	TTCGATAACGACAGTAAATCA	NM_000722:	NM_000722:
9254	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	-0.67	CTGGAACATTGAGGATGGAAA	NM_006030:	NM_001005505:NM_006030:
9254	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	0.38	CAACCTGATGCTGGCACTCTA	NM_006030:	NM_001005505:NM_006030:
55799	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta 3 subunit	-8.33	CAGCACTGGACCAGTCAATAA	NM_018398:	NM_018398:
55799	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta 3 subunit	2.07	AGCGATTAAGCTCTACCTAAA	NM_018398:	NM_018398:
93589	CACNA2D4 (c	calcium channel, voltage-dependent, alpha 2/delta subunit 4	0.59	TGGCATATACTAAACGCTAAA	NM_172364:	NM_172364:NM_001005737:NM_001005766:
93589	CACNA2D4 (c	calcium channel, voltage-dependent, alpha 2/delta subunit 4	-0.48	AACAGCTAAGGTTTACATGTA	NM_172364:	NM_172364:NM_001005737:NM_001005766:
782	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	-2.46	CAGCATCGTCTGGTCGGTGAA	NM_000723:	NM_000723:
782	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	-2.87	CCCGAGGAAAGTCTCAGTCCA	NM_000723:	NM_199247:NM_199248:NM_000723:
783	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	-0.89	CACCTCCTTATTATATATAAT	NM_000724:	NM_201572:NM_201593:NM_201571:NM_201596:NM_201590:NM_000724:
783	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	0.37	CTCGAGGGAAATCTCAAGCTA	NM_000724:	NM_201572:NM_201593:NM_201571:NM_201596:NM_201597:NM_201590:NM_201570:NM_000724:
784	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	-1.11	CTCACTGTCATCACTAATAAA	NM_000725:	NM_000725:
784	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	-0.68	CCGCTTGTTAGGTTAGGGTTA	NM_000725:	NM_000725:
785	CACNB4	calcium channel, voltage-dependent, beta 4 subunit	1.00	TCCAGTTGGAACCAATTTATA	NM_000726:	NM_001005747:NM_000726:NM_001005746:
785	CACNB4	calcium channel, voltage-dependent, beta 4 subunit	0.79	CTGGGTTACAGAGTCAGCGAA	NM_000726:	NM_001005747:NM_000726:NM_001005746:
786	CACNG1	calcium channel, voltage-dependent, gamma subunit 1	0.16	CACCGTCTGGATCGAGTACTA	NM_000727:	NM_000727:
786	CACNG1	calcium channel, voltage-dependent, gamma subunit 1	-0.94	CCGCGTGACCCTCTTCTGCAT	NM_000727:	NM_000727:

10369	CACNG2	calcium channel, voltage-dependent, gamma subunit 2	-0.40	TCGGTTGGGTGTTTATATAAT	NM_006078:	NM_006078:
10369	CACNG2	calcium channel, voltage-dependent, gamma subunit 2	0.28	ATCCATTATATTAGTAGTGGA	NM_006078:	NM_006078:
10368	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	-1.47	CCGAAGCAGCTAATGTAATAA	NM_006539:	NM_006539:
10368	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	-0.49	CCCGAAGCAGCTAATGTAATA	NM_006539:	NM_006539:
27092	CACNG4	calcium channel, voltage-dependent, gamma subunit 4	-0.39	CCCTGTGTGTTTCGCCAGTTA	NM_014405:	NM_014405:
27092	CACNG4	calcium channel, voltage-dependent, gamma subunit 4	0.00	CAGGAGAGCAACTTACCTTCA	NM_014405:	NM_014405:
27091	CACNG5	calcium channel, voltage-dependent, gamma subunit 5	2.39	CCAGAATGTGTCACTGTCTTA	NM_014404:	NM_014404:
27091	CACNG5	calcium channel, voltage-dependent, gamma subunit 5	0.22	AGAGACCTACTTCAACTACAA	NM_014404:	NM_014404:NM_145811:
59285	CACNG6 (cal	calcium channel, voltage-dependent, gamma subunit 6	1.09	TTGGGATTAAAGGTTTGGAAA	NM_145814:	NM_031897:NM_145815:NM_145814:
59285	CACNG6 (cal	calcium channel, voltage-dependent, gamma subunit 6	0.53	CTGGGTGGAGCTCAACACCTA	NM_145814:	NM_031897:NM_145815:NM_145814:
59284	CACNG7 (cal	calcium channel, voltage-dependent, gamma subunit 7	-2.22	CACGGCCTTCGTCATCAGCAA	NM_031896:	NM_031896:
59284	CACNG7 (cal	calcium channel, voltage-dependent, gamma subunit 7	-0.53	ACGGAGAATATTCTGAAGACA	NM_031896:	NM_031896:
59283	CACNG8 (cal	calcium channel, voltage-dependent, gamma subunit 8	-5.03	CACCAACACGCTCAACAGGAA	NM_031895:	NM_031895:
59283	CACNG8 (cal	calcium channel, voltage-dependent, gamma subunit 8	-0.62	CTGCGTGAAGATCAATCATTT	NM_031895:	NM_031895:
790	CAD (carbam	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and	0.01	GAGGAGATCCTGCTAATTAAA	NM_004341:	NM_004341:
790	CAD (carbam	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and	-4.52	CCGGGATTGATTGATGTCCAT	NM_004341:	NM_004341:
796	CALCA	calcitonin/calcitonin-related polypeptide, alpha	0.03	CTGAATGTGCTGATCATTTGA	NM_001741:	NM_001741:NM_001033952:
796	CALCA	calcitonin/calcitonin-related polypeptide, alpha	-2.58	CAGAGGATGTCTCAAACTTCA	NM_001741:	NM_001741:NM_001033952:
797	CALCB	calcitonin-related polypeptide, beta	-1.89	AACCTTGGTGATGCATTACAA	NM_000728:	NM_000728:
799	CALCR	calcitonin receptor	-0.38	AAGCCATTTCTTTACGTCGTA	NM_001742:	NM_001742:
799	CALCR	calcitonin receptor	-0.21	TTGGGATACTAAAGTAGTTTA	NM_001742:	NM_001742:
10203	CALCRL	calcitonin receptor-like	-0.01	AAGGCGTTTACTGCAACAGAA	NM_005795:	NM_005795:
10203	CALCRL	calcitonin receptor-like	0.37	CTCCTGCTTTAGGACCATCAA	NM_005795:	NM_005795:
801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	1.26	ATGCCCGTGTATGTTGGTTTA	NM_006888:	NM_006888:
801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	-0.80	CGGCAACTTACACACATTGAA	NM_006888:	NM_006888:
805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	1.53	ACAAAGGAATTGGGAACTGTA	NM_001743:	NM_001743:
805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	0.77	CAAAGGAATTGGGAACTGTAA	NM_001743:	NM_001743:
808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	0.44	CACCAATTGATTGACTGAGAA	NM_005184:	NM_005184:
808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	-0.51	CCGCAGAGCTGCGTCACGTAA	NM_005184:	NM_005184:
811	CALR	calreticulin	-0.09	CAGTATCTATGCCTATGATAA	NM_004343:	NM_004343:
811	CALR	calreticulin	-1.88	TTGGCTCACACTGAGAATGTA	NM_004343:	NM_004343:
8536	CAMK1	calcium/calmodulin-dependent protein kinase I	0.14	CAGGTGCTGGATGCTGTGAAA	NM_003656:	NM_003656:
8536	CAMK1	calcium/calmodulin-dependent protein kinase I	-1.31	CTGCATGACCTGGGCATTGTA	NM_003656:	NM_003656:
57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID	-0.90	CAGGCGCTTTCTATACTTAAT	NM_020397:	NM_020397:
57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID	0.11	CCAGGCGCTTTCTATACTTAA	NM_020397:	NM_020397:
57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG	0.82	AACAGGCCGCCTGAAACTCAA	NM_020439:	NM_020439:
57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG	-5.93	CAGGTCTTGTCGGCAGTGAAA	NM_020439:	NM_020439:
815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	2.41	CAGGAACTTCTCCGGAGGGAA	NM_015981:	NM_015981:NM_171825:
815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	2.71	CCAGGATTTCATCTCACCATA	NM_015981:	NM_015981:NM_171825:
816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	2.00	CAAGAGTTTACTCAACAAGAA	NM_001220:	NM_172080:NM_001220:NM_172082:NM_172083:NM_172079:NM_172078:NM_172081:
816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	-0.69	CCGGAAGCAGGAGATCATTAA	NM_001220:	NM_172080:NM_001220:NM_172082:NM_172083:NM_172079:NM_172084:NM_172078:NM_172081:
817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	0.47	CCGCCTGCATAGCATATATTA	NM_001221:	NM_172115:NM_172128:NM_001221:NM_172127:
817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.76	GTGCGACTTCATGATAGCATA	NM_001221:	NM_172115:NM_172128:NM_001221:NM_172127:
818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-0.14	CCGATGAGAAACCTCGTGTTA	NM_001222:	NM_172169:NM_172171:NM_172173:NM_172172:NM_172170:NM_001222:
818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	1.60	GAGGAAGAGATCTATACCCTA	NM_001222:	NM_172169:NM_172171:NM_172173:NM_172172:NM_172170:NM_001222:
55450	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.73	AGCAAGCGGGTTGTTATTGAA	NM_018584:	NM_018584:
55450	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.45	CGGGTTGTTATTGAAGATGAT	NM_018584:	NM_018584:
814	CAMK4	calcium/calmodulin-dependent protein kinase IV	0.90	CAGAAGCCTTATGCTCTCAAA	NM_001744:	NM_001744:
814	CAMK4	calcium/calmodulin-dependent protein kinase IV	1.64	TTGCAAGTTAACACAACGTAA	NM_001744:	NM_001744:
84254	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	0.49	AGCGATGAGCAAACTCTATAA	NM_032294:	NM_172206:NM_032294:
84254	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	0.77	CGGCGTTATCTGGAAAGTGGA	NM_032294:	NM_172206:NM_032294:
10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-0.60	CCGCAAGATCTTCTCTGGGAA	NM_006549:	NM_172226:NM_006549:NM_172215:NM_153500:NM_153499:NM_172216:NM_172214:
10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	0.64	CTAGCTGATTGTTGTGGTCAA	NM_006549:	NM_172226:NM_006549:NM_153500:NM_153499:NM_172216:
79012	CAMKV	CaM kinase-like vesicle-associated	-2.26	CTGCATGGCAATAACTCATAA	NM_024046:	NM_024046:
79012	CAMKV	CaM kinase-like vesicle-associated	-3.32	AAGGTAGGGCAGTATGTTTAA	NM_024046:	NM_024046:
819	CAMLG	calcium modulating ligand	-0.71	ATCGATCAATGGATACCTATA	NM_001745:	NM_001745:
819	CAMLG	calcium modulating ligand	1.19	AGGGCTGAGTTTGTATTATTA	NM_001745:	NM_001745:
821	CANX	calnexin	0.03	ACACTAGTCTGTGTAACTTTA	NM_001746:	NM_001024649:NM_001746:
821	CANX	calnexin	-0.02	CCTGCATAATGTTAAGCTTTA	NM_001746:	NM_001024649:NM_001746:
10487	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	1.27	ATGGTTCTTCTAACCAAACTA	NM_006367:	NM_006367:
10487	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	1.04	CAACACGACATTGCAAATCAA	NM_006367:	NM_006367:
823	CAPN1	calpain 1, (mu/I) large subunit	-1.53	CAGGGACTTGTGTACTGGTTA	NM_005186:	NM_005186:
823	CAPN1	calpain 1, (mu/I) large subunit	-0.05	CCGGACCATCCGCAAATGGAA	NM_005186:	NM_005186:
11132	CAPN10 (cal	calpain 10	0.96	CAGATCTTCTTTATAACTATT	NM_023083:	NM_021251:NM_023087:NM_023088:NM_023085:NM_023086:NM_023083:NM_023084:
11132	CAPN10 (cal	calpain 10	-5.71	CTCCGTCATGGCAGTGATGAA	NM_023083:	NM_021251:NM_023087:NM_023088:NM_023085:NM_023086:NM_023083:NM_023084:
11131	CAPN11	calpain 11	-2.53	ATGCGCCTGGTTATTGAGAAA	NM_007058:	NM_007058:
11131	CAPN11	calpain 11	-1.15	CACATTCTTTCTAACCATGGA	NM_007058:	NM_007058:
147968	CAPN12	calpain 12	0.14	CAGGGCAGGGTTGCTGAGCAA	NM_144691:	NM_144691:
147968	CAPN12	calpain 12	-0.35	CAAACCATCAATTAATATTAA	NM_144691:	NM_144691:
92291	CAPN13	calpain 13	-1.40	CAGTATGGTGGTTGTGATAAA	NM_144575:	NM_144575:
92291	CAPN13	calpain 13	1.09	ACGAAGGATGGTCCCAAATAA	NM_144575:	NM_144575:
824	CAPN2	calpain 2, (m/II) large subunit	0.25	CCCGAGAATACTGGAACAATA	NM_001748:	NM_001748:
824	CAPN2	calpain 2, (m/II) large subunit	0.29	AACGGATGCTATGAAGCTCTA	NM_001748:	NM_001748:
825	CAPN3	calpain 3, (p94)	0.63	ACACATGAACATCGACTTTGA	NM_000070:	NM_173090:NM_212465:NM_212464:NM_024344:NM_000070:NM_212467:NM_173088:NM_173089:NM_173087:
825	CAPN3	calpain 3, (p94)	0.00	CCGGACAATCATTCCGGTTCA	NM_000070:	NM_212465:NM_212464:NM_024344:NM_000070:NM_212467:
726	CAPN5	calpain 5	-0.51	CTGGTGTTCTCCCACCTTGAA	NM_004055:	NM_004055:
726	CAPN5	calpain 5	-4.72	CCGCGTGATCAACACATCCCA	NM_004055:	NM_004055:
827	CAPN6	calpain 6	-0.34	AAGGGTGGTCCAACTGCCAAA	NM_014289:	NM_014289:
827	CAPN6	calpain 6	0.52	CAAGGTCATTATGTCACTGCA	NM_014289:	NM_014289:
23473	CAPN7	calpain 7	-2.06	CCGGCATAATTTACCCTCAAA	NM_014296:	NM_014296:
23473	CAPN7	calpain 7	-2.26	CAGGTGTTATGAAAGAATAAA	NM_014296:	NM_014296:
10753	CAPN9	calpain 9	0.29	GAGAACTTCTATGAGATTCTA	NM_006615:	NM_016452:NM_006615:
10753	CAPN9	calpain 9	-1.92	GAGGAGTGTAGTTTCCTTGTA	NM_006615:	NM_016452:NM_006615:
826	CAPNS1	calpain, small subunit 1	0.01	CACCTGAATGAGCATCTCTAT	NM_001749:	NM_001003962:NM_001749:
826	CAPNS1	calpain, small subunit 1	-0.52	AAGGTGGCAGGCCATATACAA	NM_001749:	NM_001003962:NM_001749:

84433	CARD11	caspase recruitment domain family, member 11	0.59	CAACTCGAGATCGATCAGCTA	NM_032415:	NM_032415:
84433	CARD11	caspase recruitment domain family, member 11	2.06	CACAGTACTCGCAGTGCTTAA	NM_032415:	NM_032415:
79092	CARD14	caspase recruitment domain family, member 14	-5.92	CACCTGGATTATGAGCTCCTA	NM_024110:	NM_024110:NM_052819:
79092	CARD14	caspase recruitment domain family, member 14	-1.66	CCGCATCGTCAGTATGGACAA	NM_024110:	NM_024110:
64127	CARD15	caspase recruitment domain family, member 15	0.58	CAGTTATGGATTGAAAGTTTA	NM_022162:	NM_022162:
64127	CARD15	caspase recruitment domain family, member 15	-7.15	TAGGCCGTTCCTTCAAAGCAA	NM_022162:	NM_022162:
10392	CARD4	caspase recruitment domain family, member 4	-0.95	CAGCCTGACAAGGTCCGCAAA	NM_006092:	NM_006092:
10392	CARD4	caspase recruitment domain family, member 4	1.29	GCCCGCTCATTTGTTAATAAA	NM_006092:	NM_006092:
84674	CARD6	caspase recruitment domain family, member 6	-0.47	AACCTTCTCCATGCAAATCTA	NM_032587:	NM_032587:
84674	CARD6	caspase recruitment domain family, member 6	0.43	CCCAATTTGCTTGAATGGGAA	NM_032587:	NM_032587:
22900	CARD8	caspase recruitment domain family, member 8	0.04	CCCTGATATTCTACTTATTTA	NM_014959:	NM_014959:
22900	CARD8	caspase recruitment domain family, member 8	-0.14	CCGGATAGGTGTGTTTATGAA	NM_014959:	NM_014959:
64170	CARD9	caspase recruitment domain family, member 9	-6.76	ACGTAAGGACTCCAAGATGTA	NM_052813.1:	NM_052813:
64170	CARD9	caspase recruitment domain family, member 9	-0.27	CCGCGTCTTCTCCATGATCAT	NM_052813.1:	NM_052813:
23729	CARKL (carb	carbohydrate kinase-like	1.34	ATGAAACATATTGTCTCTTTA	NM_013276:	NM_013276:
23729	CARKL (carb	carbohydrate kinase-like	0.74	CAGGTAGTTTATTCAAAGAGA	NM_013276:	NM_013276:
10498	CARM1	coactivator-associated arginine methyltransferase 1	1.49	CACAACAACCTGATTCCTTTA	NM_199141:	NM_199141:
10498	CARM1	coactivator-associated arginine methyltransferase 1	-2.52	CAGGATAGAAATCCCATTCAA	NM_199141:	NM_199141:
833	CARS	cysteinyl-tRNA synthetase	-4.61	AAGGAAGTGTTCATACCTCAA	NM_001751:	NM_001751:NM_001014437:NM_001014438:NM_139273:
833	CARS	cysteinyl-tRNA synthetase	-3.49	CACCCTTGGGTCCTAAATTAA	NM_001751:	NM_001751:NM_001014437:NM_001014438:NM_139273:
8573	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.50	AACCAATGGGAATCACTTTAA	NM_003688:	NM_003688:
8573	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-1.29	AAGGACGACAGATCTATGTAA	NM_003688:	NM_003688:
834	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, c	-0.09	CCCAGATATACTACAACTCAA	NM_001223:	NM_001223:NM_033294:NM_033292:NM_033293:
834	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, c	-1.37	CTCATTGAACATATGCAAGAA	NM_001223:	NM_001223:NM_033294:NM_033292:NM_033295:NM_033293:
843	CASP10	caspase 10, apoptosis-related cysteine peptidase	0.95	AAGGGTTTCTCTGTTTAGAAA	NM_001230:	NM_032977:NM_032974:NM_032976:NM_001230:
843	CASP10	caspase 10, apoptosis-related cysteine peptidase	0.53	CACAGTGCATATACACAATAA	NM_001230:	NM_032977:NM_032974:NM_032976:NM_001230:
23581	CASP14	caspase 14, apoptosis-related cysteine peptidase	-7.24	CACAGATGCCTTGCACGTTTA	NM_012114:	NM_012114:
23581	CASP14	caspase 14, apoptosis-related cysteine peptidase	-4.15	GAGGAGAAATATGATATGTCA	NM_012114:	NM_012114:
835	CASP2	caspase 2, apoptosis-related cysteine peptidase (neural precursor cell	-3.23	CAGGATCATGTAAATGCTCAA	NM_001224:	NM_032983:NM_001224:NM_032982:
835	CASP2	caspase 2, apoptosis-related cysteine peptidase (neural precursor cell	1.27	CAGGATTTGGTTGTTTAAATA	NM_001224:	NM_032983:NM_001224:NM_032982:
836	CASP3	caspase 3, apoptosis-related cysteine peptidase	1.63	ACAGCATGTAATGGTATCTTA	NM_004346:	NM_004346:NM_032991:
836	CASP3	caspase 3, apoptosis-related cysteine peptidase	-0.05	CAGCATGTAATGGTATCTTAA	NM_004346:	NM_004346:NM_032991:
837	CASP4	caspase 4, apoptosis-related cysteine peptidase	1.50	AAGAAATATTACGATGCTAAA	NM_001225:	NM_033306:NM_001225:NM_033307:
837	CASP4	caspase 4, apoptosis-related cysteine peptidase	-2.49	CTGGACTATAGTGTAGATGTA	NM_001225:	NM_033306:NM_001225:NM_033307:
838	CASP5	caspase 5, apoptosis-related cysteine peptidase	-1.78	AAGAATCGCGTGGCTCATCAA	NM_004347:	NM_004347:
838	CASP5	caspase 5, apoptosis-related cysteine peptidase	1.15	TTCGTGATAAACCACATGCTA	NM_004347:	NM_004347:
839	CASP6	caspase 6, apoptosis-related cysteine peptidase	0.79	CAGGAATTAAATCATCCCTTA	NM_001226:	NM_001226:NM_032992:
839	CASP6	caspase 6, apoptosis-related cysteine peptidase	0.97	CTCAGGAAATTAGATAAATAA	NM_001226:	NM_001226:NM_032992:
840	CASP7	caspase 7, apoptosis-related cysteine peptidase	-1.97	AAGCAATGGGTCACTCATTAA	NM_001227:	NM_033338:NM_001227:NM_033339:NM_033340:
840	CASP7	caspase 7, apoptosis-related cysteine peptidase	0.60	ATGCATCATAATAAACAACAA	NM_001227:	NM_033338:NM_001227:NM_033339:NM_033340:
841	CASP8	caspase 8, apoptosis-related cysteine peptidase	0.01	AAGAGTCTGTGCCCAAATCAA	NM_001228:	NM_033357:NM_033355:NM_001228:NM_033356:NM_033358:
841	CASP8	caspase 8, apoptosis-related cysteine peptidase	0.31	AAGATAATCAACGACTATGAA	NM_001228:	NM_033357:NM_033355:NM_001228:NM_033356:NM_033358:
9994	CASP8AP2	CASP8 associated protein 2	-0.06	AACGAAGTTTCGAGATTCTTA	NM_012115:	NM_012115:
9994	CASP8AP2	CASP8 associated protein 2	-3.52	CAGTCTGATCTCAATAAGGAA	NM_012115:	NM_012115:
842	CASP9	caspase 9, apoptosis-related cysteine peptidase	-2.13	CAGCAAAGTTGTCGAAGCCAA	NM_001229:	NM_001229:NM_032996:
842	CASP9	caspase 9, apoptosis-related cysteine peptidase	-1.82	CAGGGATTAACCTCTGCACTA	NM_001229:	NM_001229:NM_032996:
845	CASQ2	calsequestrin 2 (cardiac muscle)	1.88	TAGTGTTAAGTGTGCAGTATA	NM_001232:	NM_001232:
845	CASQ2	calsequestrin 2 (cardiac muscle)	-2.41	TAGCCTAAGCTGGGATCTGAA	NM_001232:	NM_001232:
846	CASR	calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neor	-0.16	CACGCATTTACGGATATCCTA	NM_000388:	NM_000388:
846	CASR	calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neor	-1.77	CCGGCGCAATATCACGGGCAA	NM_000388:	NM_000388:
344760	CASRL1	calcium-sensing receptor like 1	0.64	TAGCGGAGATTGGCATATGTA	XM_293581:	XM_293581:
344760	CASRL1	calcium-sensing receptor like 1	0.00	AAGAGTCTCCACCACAGATAA	XM_293581:	XM_293581:
847	CAT	catalase	0.76	CTGGAGTTACATTAATGTTAA	NM_001752:	NM_001752:
847	CAT	catalase	1.52	ACCGTCATGGCTTAATGTTTA	NM_001752:	NM_001752:
117144	CATSPER1	cation channel, sperm associated 1	-0.54	CCAGTACTTCATCTTCCTCAA	NM_053054:	NM_053054:
117144	CATSPER1	cation channel, sperm associated 1	-3.24	CCGGATCCTCAAGGTCTTCAA	NM_053054:	NM_053054:
117155	CATSPER2	cation channel, sperm associated 2	1.20	TCCGTCAAATTCAAATTATTA	NM_172096:	NM_172097:NM_172095:NM_172096:NM_054020:
347732	CATSPER3	cation channel, sperm associated 3	-0.77	CCGTTTCTTTAAGATAATTAT	NM_178019:	NM_178019:
347732	CATSPER3	cation channel, sperm associated 3	0.08	GCCCAACATTCAAGAAATTTA	NM_178019:	NM_178019:
378807	CATSPER4 (	cation channel, sperm associated 4	-6.03	CCGAGATGAACTCAACATGAT	XM_371237:	NM_198137:
378807	CATSPER4 (	cation channel, sperm associated 4	0.31	AACAGCAACGAATAACCTTTA	XM_371237:	NM_198137:
857	CAV1	caveolin 1, caveolae protein, 22kDa	-0.79	CAGCCGTGTCTATTCCATCTA	NM_001753:	NM_001753:
857	CAV1	caveolin 1, caveolae protein, 22kDa	-0.29	CTGGTCAACCGCGACCCTAAA	NM_001753:	NM_001753:
858	CAV2	caveolin 2	0.02	ACGCATAATCATTACCTTAAA	NM_001233:	NM_001233:NM_198212:
858	CAV2	caveolin 2	1.49	ACGCTAATAAGTGACAAATAA	NM_001233:	NM_001233:NM_198212:
859	CAV3	caveolin 3	-0.01	TCCTTGGAAGATCATGTTTAA	NM_001234:	NM_033337:NM_001234:
859	CAV3	caveolin 3	1.11	TAGGAAGGTGGCTCCAGTAAA	NM_001234:	NM_033337:NM_001234:
865	CBFB	core-binding factor, beta subunit	0.94	TACAAAGGTAATATTGTATTA	NM_001755:	NM_001755:NM_022845:
865	CBFB	core-binding factor, beta subunit	-0.06	CAAACAATAATGCGTCATTAA	NM_001755:	NM_001755:NM_022845:
867	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	-0.26	CCCGCCGAACTCTCTCAGATA	NM_005188:	NM_005188:
867	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	0.77	CCGTACTATCTTGTCAAGATA	NM_005188:	NM_005188:
868	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	0.42	CACAGCGAGTTCAAATGTCAA	NM_170662:	NM_170662:
868	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	-0.28	TCGGTTGGCAAACGTCCGAAA	NM_170662:	NM_170662:
23624	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	-1.54	CAGCCGAAAGTGAGACTCCTA	NM_012116:	NM_012116:
23624	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	0.10	CTGGGAGGCCGTGAGTATCTA	NM_012116:	NM_012116:
79872	CBLL1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	0.06	ACCATTATAATCCTAACTCAT	NM_024814:	NM_024814:
79872	CBLL1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	-2.79	CCGCCTCAACATGGTGGTCCA	NM_024814:	NM_024814:
873	CBR1	carbonyl reductase 1	0.78	CGCACTCAGTTGACTACGTAA	NM_001757:	NM_001757:
873	CBR1	carbonyl reductase 1	0.86	CACTAATGTACTACTAATTGA	NM_001757:	NM_001757:
874	CBR3	carbonyl reductase 3	0.21	CGGAGCTTGCTGCTTAATAAA	NM_001236:	NM_001236:
874	CBR3	carbonyl reductase 3	-1.48	AAGACAGACATGGATGGGAAA	NM_001236:	NM_001236:
84869	CBR4	carbonic reductase 4	-0.61	AAGACTACGCTGCATATTCAA	NM_032783:	NM_032783:
84869	CBR4	carbonic reductase 4	0.94	CCTAGTAGAATTTGTAATTTA	NM_032783:	NM_032783:
875	CBS	cystathionine-beta-synthase	-1.48	CGCAGAGTGGATTAAAGGCAA	NM_000071:	NM_000071:
875	CBS	cystathionine-beta-synthase	0.09	TAGGATGAACACAGGCAATGA	NM_000071:	NM_000071:
11335	CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	0.01	CTGGTTACTTTGAACAAATAA	NM_007276:	NM_007276:NM_016587:
11335	CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	0.79	TCCCTTCAAGTTAAATTGAAA	NM_007276:	NM_007276:NM_016587:
8535	CBX4	chromobox homolog 4 (Pc class homolog, Drosophila)	0.18	AAGCCCTTCTTTGGGAATATA	NM_003655:	NM_003655:

8535	CBX4	chromobox homolog 4 (Pc class homolog, Drosophila)	0.99	GAGGCTGGTCGCCCAAATATA	NM_003655:	NM_003655:
1238	CCBP2	chemokine binding protein 2	-0.15	CTCAGTGACTGTGTTGCTAAA	NM_001296:	NM_001296:
1238	CCBP2	chemokine binding protein 2	0.17	CTGCATGAGCCTGGACAAGTA	NM_001296:	NM_001296:
64793	CCDC21	coiled-coil domain containing 21	-0.05	CGACGGTGAGTTACTAATTAA	NM_022778:	NM_022778:
64793	CCDC21	coiled-coil domain containing 21	-6.58	TAGCATGGAATCTACCCTCAA	NM_022778:	NM_022778:
25901	CCDC28A	coiled-coil domain containing 28A	1.33	CCGGAGTTACAGCTAAAGGAA	NM_015439:	NM_015439:
25901	CCDC28A	coiled-coil domain containing 28A	-0.02	TCGCTTGAATTTGGAGCTCTA	NM_015439:	NM_015439:
885	CCK	cholecystokinin	0.06	ACGAATGTCCATCGTTAAGAA	NM_000729:	NM_000729:
885	CCK	cholecystokinin	0.62	ACCAGAATTGTGCAAATGGAA	NM_000729:	NM_000729:
886	CCKAR	cholecystokinin A receptor	-0.11	AAGGGTGATCCGCATGCTCAT	NM_000730:	NM_000730:
886	CCKAR	cholecystokinin A receptor	-3.19	CAGAAGAAGTCTGCTAAAGAA	NM_000730:	NM_000730:
887	CCKBR	cholecystokinin B receptor	-0.51	CCCGTGTACACTGTCGTGCAA	NM_176875:	NM_176875:
887	CCKBR	cholecystokinin B receptor	0.40	CCGCCGGGTCGAGCTGAGTAA	NM_176875:	NM_176875:
6346	CCL1	chemokine (C-C motif) ligand 1	0.67	AACATTTAAATTATACAATCA	NM_002981:	NM_002981:
6346	CCL1	chemokine (C-C motif) ligand 1	0.96	AAGCTATGTTGTTGCACTTTA	NM_002981:	NM_002981:
6356	CCL11	chemokine (C-C motif) ligand 11	-0.55	AACCCAAAGTGTGACTCATTA	NM_002986:	NM_002986:
6356	CCL11	chemokine (C-C motif) ligand 11	0.98	AAGCTTTGTGCAGATTCTTTA	NM_002986:	NM_002986:
6357	CCL13	chemokine (C-C motif) ligand 13	1.19	TGGGTCCAGAATTATATGAAA	NM_005408:	NM_005408:
6357	CCL13	chemokine (C-C motif) ligand 13	1.08	ACTCTTAACCTTCAACATGAA	NM_005408:	NM_005408:
6360	CCL16	chemokine (C-C motif) ligand 16	-0.11	AGCAATCATCTTCGTCACCAA	NM_004590:	NM_004590:
6360	CCL16	chemokine (C-C motif) ligand 16	0.06	CAGGAACTTGTCCACGGTTAA	NM_004590:	NM_004590:
6361	CCL17	chemokine (C-C motif) ligand 17	0.44	AGAGTGAAGAATGCAGTTAAA	NM_002987:	NM_002987:
6361	CCL17	chemokine (C-C motif) ligand 17	-2.06	ATGCAGTTAAATACCTGCAAA	NM_002987:	NM_002987:
6362	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	-2.14	AACCAGCATTCTCACTGTGAA	NM_002988:	NM_002988:
6362	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	-0.01	TTGGCAGTACTTATTATATAA	NM_002988:	NM_002988:
6363	CCL19	chemokine (C-C motif) ligand 19	0.10	AAGAACGCATCATCCAGAGAC	NM_006274:	NM_006274:
6363	CCL19	chemokine (C-C motif) ligand 19	-0.28	AATCGTGAGGAACTTCCACTA	NM_006274:	NM_006274:
6347	CCL2	chemokine (C-C motif) ligand 2	0.20	CTGCTGTTATAACTTCACCAA	NM_002982:	NM_002982:
6347	CCL2	chemokine (C-C motif) ligand 2	-3.66	ATGGACCACCTGGACAAGCAA	NM_002982:	NM_002982:
6364	CCL20	chemokine (C-C motif) ligand 20	0.70	AAACATTAATAAGACAAATAT	NM_004591:	NM_004591:
6364	CCL20	chemokine (C-C motif) ligand 20	1.37	TTGTTGTAATTGCATTATAAA	NM_004591:	NM_004591:
6366	CCL21	chemokine (C-C motif) ligand 21	0.35	TATGATTTATACCTAACTGAA	NM_002989:	NM_002989:
6366	CCL21	chemokine (C-C motif) ligand 21	-3.49	AAGCCTGAACCCAAGATGCAA	NM_002989:	NM_002989:
6367	CCL22	chemokine (C-C motif) ligand 22	0.43	CAGGTAAAGGACATAAATGTT	NM_002990:	NM_002990:
6367	CCL22	chemokine (C-C motif) ligand 22	1.18	TAAGCTGGAGTTATATATGTA	NM_002990:	NM_002990:
6368	CCL23	chemokine (C-C motif) ligand 23	-0.53	CTCCTGGAGAGTTACTTTGAA	NM_145898:	NM_005064:NM_145898:
6368	CCL23	chemokine (C-C motif) ligand 23	-2.93	CAGGAAGAATTGAACTTGTCA	NM_145898:	NM_005064:NM_145898:
6369	CCL24	chemokine (C-C motif) ligand 24	-0.33	AGGAGTGATCTTCACCACCAA	NM_002991:	NM_002991:
6369	CCL24	chemokine (C-C motif) ligand 24	-1.85	CAGAGATATCCTGGCAACCAA	NM_002991:	NM_002991:
6370	CCL25	chemokine (C-C motif) ligand 25	-0.06	AAGAAGTTGAGTTCTGGAAAC	NM_005624:	NM_148888:NM_005624:
6370	CCL25	chemokine (C-C motif) ligand 25	0.43	AATCTGCCTGCTGCGATATTC	NM_005624:	NM_005624:
10344	CCL26	chemokine (C-C motif) ligand 26	-3.10	CAGGGCCGTCTCAGTCTCATA	NM_006072:	NM_006072:
10344	CCL26	chemokine (C-C motif) ligand 26	-0.45	AAGCTATGAATTCACCAGTAA	NM_006072:	NM_006072:
10850	CCL27	chemokine (C-C motif) ligand 27	0.55	CAGCATTGGATAATAATTTCT	NM_006664:	NM_006664:
10850	CCL27	chemokine (C-C motif) ligand 27	-1.16	TAGCCAAATAATAAAGCAGCA	NM_006664:	NM_006664:
56477	CCL28	chemokine (C-C motif) ligand 28	1.15	TAAGATGTACATAGTACTCCA	NM_019846:	NM_019846:
56477	CCL28	chemokine (C-C motif) ligand 28	1.42	TACGTATTAGGCTTTATGTAA	NM_019846:	NM_019846:
6348	CCL3	chemokine (C-C motif) ligand 3	0.28	CAGAAATATGTCAGCGACCTA	NM_002983:	NM_002983:
6351	CCL4	chemokine (C-C motif) ligand 4	-0.03	CTGTCCCTTCTCTTAATTTAA	NM_002984:	NM_002984:
6352	CCL5	chemokine (C-C motif) ligand 5	2.10	AAAGTTCTCAATGCAACCATA	NM_002985:	NM_002985:
6352	CCL5	chemokine (C-C motif) ligand 5	1.49	ACCATTAAAGTTCTCAATGCA	NM_002985:	NM_002985:
6354	CCL7	chemokine (C-C motif) ligand 7	0.21	AAGATTTGCTTTAATTGTTAA	NM_006273:	NM_006273:
6354	CCL7	chemokine (C-C motif) ligand 7	0.54	TGGAAGCATATTGTTATTATA	NM_006273:	NM_006273:
6355	CCL8	chemokine (C-C motif) ligand 8	0.11	ATCAGTGCTCCTGTAAGTCAA	NM_005623:	NM_005623:
6355	CCL8	chemokine (C-C motif) ligand 8	-0.81	CTCAACTAAGTTCACGGCAAA	NM_005623:	NM_005623:
8900	CCNA1 (cycli	cyclin A1	-0.43	CACCGATGATACATACACAAA	NM_003914:	NM_003914:
8900	CCNA1 (cycli	cyclin A1	-0.04	TTCGAAATATGAAGAGATATA	NM_003914:	NM_003914:
890	CCNA2	cyclin A2	-0.26	ACCAGAGACACTAAATCTGTA	NM_001237:	NM_001237:
890	CCNA2	cyclin A2	0.89	GCCAGCTGTCAGGATAATAAA	NM_001237:	NM_001237:
891	CCNB1	cyclin B1	0.20	AACACTTATACTAAGCACCAA	NM_031966:	NM_031966:
891	CCNB1	cyclin B1	0.01	AATGTAGTCATGGTAAATCAA	NM_031966:	NM_031966:
9133	CCNB2	cyclin B2	-0.08	ATGCTTATACCAGTTCCCAAA	NM_004701:	NM_004701:
9133	CCNB2	cyclin B2	1.06	CAAGAATGTGGTGAAAGTAAA	NM_004701:	NM_004701:
85417	CCNB3 (cycli	cyclin B3	-4.93	AAGGCTGTGTATTACAAGTAT	NM_033031:	NM_033031:NM_033670:NM_033671:
85417	CCNB3 (cycli	cyclin B3	2.43	AGGGCTAAGCATGCATGTTAA	NM_033031:	NM_033031:NM_033670:NM_033671:
892	CCNC (cyclin	cyclin C	-0.08	CAAGTACCGTATATTGATTTA	NM_005190:	NM_001013399:NM_005190:
892	CCNC (cyclin	cyclin C	1.59	TCCGAAGAATTCCATAGTGGA	NM_005190:	NM_005190:NM_001013399:
595	CCND1	cyclin D1	0.95	AAGGCCAGTATGATTTATAAA	NM_053056:	NM_053056:
595	CCND1	cyclin D1	1.96	CTCCTACGATACGCTACTATA	NM_053056:	NM_053056:
894	CCND2	cyclin D2	0.03	AAGAAATAGACTTGCACCTTA	NM_001759:	NM_001759:
894	CCND2	cyclin D2	-0.46	TCCGCAGTGCTCCTACTTCAA	NM_001759:	NM_001759:
896	CCND3 (cycli	cyclin D3	-2.33	CAGGAACCACACCACATCTAA	NM_001760:	NM_001760:
896	CCND3 (cycli	cyclin D3	0.02	GACCATCATCCTACTGTAATA	NM_001760:	NM_001760:
898	CCNE1	cyclin E1	-0.03	ACCGGGTTTACCCAAACTCAA	NM_001238:	NM_001238:NM_057182:
898	CCNE1	cyclin E1	0.03	CACCATGGAATTAATGATTAT	NM_001238:	NM_001238:NM_057182:
9134	CCNE2	cyclin E2	1.33	AAGAAGAGTATTAAATATATA	NM_004702:	NM_057749:NM_057735:
9134	CCNE2	cyclin E2	0.46	CTCCAAGTTGATGCTCTTAAA	NM_004702:	NM_057749:NM_057735:
899	CCNF	cyclin F	-2.35	CACGGACAACACTTACAAGTA	NM_001761:	NM_001761:
899	CCNF	cyclin F	-1.49	CCGGTTTATCAGTAAAGAGAT	NM_001761:	NM_001761:
900	CCNG1	cyclin G1	1.45	CACAGTATATCTTATTCTTAA	NM_004060:	NM_199246:NM_004060:
900	CCNG1	cyclin G1	1.09	CTGGATTATTACAGCACCAAA	NM_004060:	NM_199246:NM_004060:
901	CCNG2 (cycli	cyclin G2	-0.06	AAGAGTGAGTATGCTCTTAAA	NM_004354:	NM_004354:
901	CCNG2 (cycli	cyclin G2	0.17	CTGGAGAGAGTTGGTTTCTAA	NM_004354:	NM_004354:
902	CCNH	cyclin H	0.03	AGGAAGCATATCAAACGTTTA	NM_001239:	NM_001239:
902	CCNH	cyclin H	0.28	CTGAGCTTGCACTTAACGTAA	NM_001239:	NM_001239:
8812	CCNK	cyclin K	-2.60	AAGCAACTCAAAGGTGATAAA	NM_003858:	NM_003858:
8812	CCNK	cyclin K	-2.41	ATCCTGGATCTTTACTCACAA	NM_003858:	NM_003858:
57018	CCNL1	cyclin L1	1.95	CCCTAGCAGTATCTAATTAAA	NM_020307:	NM_020307:
57018	CCNL1	cyclin L1	0.51	CTCCAAGAAGACACTATAATA	NM_020307:	NM_020307:
81669	CCNL2	cyclin L2	-0.58	CGCGTATGACATGGTGAATAA	NM_030937:	NM_030937:
81669	CCNL2	cyclin L2	1.40	GAGGAGTAGTACGTTTATCTA	NM_030937:	NM_030937:
904	CCNT1	cyclin T1	0.35	AGGCTTTGAACTAACAATTGA	NM_001240:	NM_001240:
904	CCNT1	cyclin T1	-0.02	TTGGAACATGTCATCAAGGTA	NM_001240:	NM_001240:
905	CCNT2	cyclin T2	-0.51	AAGCAAGAATATACTCATAAA	NM_001241:	NM_001241:NM_058241:
905	CCNT2	cyclin T2	0.25	AAGGGCTTTCTTGGTAATTTA	NM_001241:	NM_001241:NM_058241:
1230	CCR1	chemokine (C-C motif) receptor 1	0.05	CTGGATCGACTACAAGTTGAA	NM_001295:	NM_001295:
1230	CCR1	chemokine (C-C motif) receptor 1	-0.35	GACGGAAGAGTTGAGACCTAA	NM_001295:	NM_001295:
2826	CCR10	chemokine (C-C motif) receptor 10	-0.65	CAGGCTGAGGGTCGTGGGAAA	NM_016602:	NM_016602:
2826	CCR10	chemokine (C-C motif) receptor 10	-1.16	CTGCTGGATACTGCCGATCTA	NM_016602:	NM_016602:

1231	CCR2	chemokine (C-C motif) receptor 2	0.74	CCACATCTCGTTCTCGGTTTA	NM_000647:	NM_000647:NM_000648:
1231	CCR2	chemokine (C-C motif) receptor 2	1.19	TACGGTGCTCCCTGTCATAAA	NM_000647:	NM_000647:NM_000648:
1232	CCR3	chemokine (C-C motif) receptor 3	0.43	CACCTGAATGTTAGATAGTTA	NM_001837:	NM_178329:NM_001837:
1232	CCR3	chemokine (C-C motif) receptor 3	0.10	CCGAATTATGACCAACATCTA	NM_001837:	NM_178329:NM_001837:
1233	CCR4	chemokine (C-C motif) receptor 4	-1.28	ATGGAGTAAATCGCTACCTTT	NM_005508:	NM_005508:
1233	CCR4	chemokine (C-C motif) receptor 4	-0.05	TTGAATGAAGTTGTAGGTAAT	NM_005508:	NM_005508:
1234	CCR5	chemokine (C-C motif) receptor 5	0.75	AAGATGGATTATCAAGTGTCA	NM_000579:	NM_000579:
1234	CCR5	chemokine (C-C motif) receptor 5	-0.51	TAGGTGAGGATTGATTACCTA	NM_000579:	NM_000579:
1235	CCR6	chemokine (C-C motif) receptor 6	-0.05	AGGGATCCTACGATTACTCAA	NM_031409:	NM_031409:
1235	CCR6	chemokine (C-C motif) receptor 6	-0.70	TAGCGGAGTTCCAGCAAACAA	NM_031409:	NM_031409:NM_004367:
1236	CCR7	chemokine (C-C motif) receptor 7	0.80	AAGGACGTGCGGAACTTTAAA	NM_001838:	NM_001838:
1236	CCR7	chemokine (C-C motif) receptor 7	2.04	CAAGACCATGACCGATACCTA	NM_001838:	NM_001838:
1237	CCR8	chemokine (C-C motif) receptor 8	1.41	CAGCTGTTTCACCATCAGTCA	NM_005201:	NM_005201:
1237	CCR8	chemokine (C-C motif) receptor 8	-4.78	TAGTATCAATGATTTACTCAA	NM_005201:	NM_005201:
10803	CCR9	chemokine (C-C motif) receptor 9	-0.08	AAGGGATGAATCTGAACTATA	NM_006641:	NM_006641:NM_031200:
10803	CCR9	chemokine (C-C motif) receptor 9	-0.07	CAGTCTTGTTATCCTTGTCTA	NM_006641:	NM_006641:NM_031200:
23552	CCRK	cell cycle related kinase	-3.99	AAGGAGAAGTGCAGAGAGTAA	NM_012119:	NM_178432:NM_012119:
23552	CCRK	cell cycle related kinase	-2.17	TGGCGAGATAGTTGCCCTCAA	NM_012119:	NM_178432:NM_012119:
51554	CCRL1	chemokine (C-C motif) receptor-like 1	1.57	CGCCGTGGTTGCAACTTATAA	NM_016557:	NM_178445:NM_016557:
51554	CCRL1	chemokine (C-C motif) receptor-like 1	0.98	TTCCATGGTAGTGGCAATTTA	NM_016557:	NM_178445:NM_016557:
9034	CCRL2	chemokine (C-C motif) receptor-like 2	0.84	ACGCTTGGTCCAGAACATCAA	NM_003965:	NM_003965:
9034	CCRL2	chemokine (C-C motif) receptor-like 2	-0.69	CTGGTTGTGCTTATCCTGGTA	NM_003965:	NM_003965:
9973	CCS	copper chaperone for superoxide dismutase	-6.56	CACGTTGGAGTTCGCGGTGCA	NM_005125:	NM_005125:
9973	CCS	copper chaperone for superoxide dismutase	0.23	CAGCTGTGGGAATCACTTTAA	NM_005125:	NM_005125:
10576	CCT2	chaperonin containing TCP1, subunit 2 (beta)	0.91	CAGGCAATTAATTTATAATTA	NM_006431:	NM_006431:
10576	CCT2	chaperonin containing TCP1, subunit 2 (beta)	-0.13	AAGGAGAAAGTTGAACGTATT	NM_006431:	NM_006431:
10575	CCT4	chaperonin containing TCP1, subunit 4 (delta)	-0.26	TAGAGTTGGCCCTACGATTAA	NM_006430:	NM_006430:
10575	CCT4	chaperonin containing TCP1, subunit 4 (delta)	0.34	TTGCTCATATTGACCAATTTA	NM_006430:	NM_006430:
22948	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	1.74	CACTGTAGATGCTATAATAAA	NM_012073:	NM_012073:
22948	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	-0.81	TAGCGTCCTTGTTGACATAAA	NM_012073:	NM_012073:
10694	CCT8	chaperonin containing TCP1, subunit 8 (theta)	-1.20	AAGGCTGTATTTGTAGTAGTA	NM_006585:	NM_006585:
10694	CCT8	chaperonin containing TCP1, subunit 8 (theta)	0.71	GAGGCTGTGTATAGAAACATA	NM_006585:	NM_006585:
929	CD14 (CD14	CD14 antigen	0.28	CAGCCTAGACCTGTCTGACAA	NM_000591:	NM_000591:
929	CD14 (CD14	CD14 antigen	-1.08	CTCAGAGGTTCGGAAGACTTA	NM_000591:	NM_000591:
977	CD151	CD151 antigen (Raph blood group)	0.72	CACATACAGGTGCTCAATAAA	NM_004357:	NM_139030:NM_004357:
977	CD151	CD151 antigen (Raph blood group)	-0.62	CTGCCACATACAGGTGCTCAA	NM_004357:	NM_139030:NM_004357:
11126	CD160	CD160 antigen	-0.82	AAGAGATGCTAAATATACCAA	NM_007053:	NM_007053:
11126	CD160	CD160 antigen	1.15	AAGGAACGCGACTAAACTTAA	NM_007053:	NM_007053:
9332	CD163	CD163 antigen	1.03	CGCATTATTCTTCTTGACTAA	NM_004244:	NM_004244:NM_203416:
9332	CD163	CD163 antigen	0.03	TCGCATTATTCTTCTTGACTA	NM_004244:	NM_004244:NM_203416:
283316	CD163L1	CD163 antigen-like 1	0.30	ATGGTCTAACTTGGGCCGAAA	NM_174941:	NM_174941:
283316	CD163L1	CD163 antigen-like 1	-0.14	CACAATGAGGATGTCACATTA	NM_174941:	NM_174941:
57126	CD177	CD177 antigen	-0.93	CACCATTATGACACACGGAAA	NM_020406:	NM_020406:
57126	CD177	CD177 antigen	0.57	CCCTCTGACCTCATAACCTAA	NM_020406:	NM_020406:
4064	CD180	CD180 antigen	-2.91	AAGCCTGAACTTCAATGGCAA	NM_005582:	NM_005582:
4064	CD180	CD180 antigen	-0.68	TGGGACTATCACGAAGACCAA	NM_005582:	NM_005582:
930	CD19	CD19 antigen	1.34	CCCTTTGTATTCCTTAAATAA	NM_001770:	NM_001770:
930	CD19	CD19 antigen	-1.61	CCCGGAGAGTCTGACCACCAT	NM_001770:	NM_001770:
909	CD1A	CD1a antigen	-1.04	CTCCACATGTTCACCTATTAA	NM_001763:	NM_001763:
909	CD1A	CD1a antigen	0.90	AAGCTTCTTGCAGTTAGCTTA	NM_001763:	NM_001763:
910	CD1B	CD1b antigen	-4.11	CTGAGTGTCAAGAATGCTTCA	NM_001764:	NM_001764:
910	CD1B	CD1b antigen	0.97	CTTGGTCTAAAGGTAACTTTA	NM_001764:	NM_001764:
911	CD1C	CD1c antigen	0.99	CCCGTCGACTCTCCATTTAAA	NM_001765:	NM_001765:
911	CD1C	CD1c antigen	-0.09	ACCCAGGAGCCTAGTACAATA	NM_001765:	NM_001765:
912	CD1D (CD1d	CD1d antigen	0.44	CCGGTTGTGAAACCTACTGAA	NM_001766:	NM_001766:
912	CD1D (CD1d	CD1d antigen	-0.43	TTGGGTAAACTTGGCCATTCA	NM_001766:	NM_001766:
913	CD1E	CD1e antigen	0.00	TACCTAGATATTAAGGAAATA	NM_030893:	NM_030893:
913	CD1E	CD1e antigen	0.41	CGGGCCCAGAACATCTGTAAA	NM_030893:	NM_030893:
914	CD2	CD2 antigen (p50), sheep red blood cell receptor	0.48	CCCGAATTAAACCTGTATCAA	NM_001767:	NM_001767:
914	CD2	CD2 antigen (p50), sheep red blood cell receptor	-1.81	TAAGATGAGCTTTCCATGTAA	NM_001767:	NM_001767:
131450	CD200R1	CD200 receptor 1	-0.20	ATGGTATATGTGTCAATTTAT	NM_138806:	NM_138806:NM_170780:
131450	CD200R1	CD200 receptor 1	-0.05	AACAACAAACGAGATACATTA	NM_138806:	NM_138806:NM_170780:
344807	CD200R2	CD200 cell surface glycoprotein receptor isoform 2	-2.11	AGCGTTGTCCTTACTGATCAT	NM_001008784:	NM_001008784:
344807	CD200R2	CD200 cell surface glycoprotein receptor isoform 2	-0.50	CTGATCATTCTTTATGTGAAA	NM_001008784:	NM_001008784:
50489	CD207	CD207 antigen, langerin	0.76	CAGGATGACTTTGCACGTTAA	NM_015717:	NM_015717:
50489	CD207	CD207 antigen, langerin	0.13	ACCCTGGATTCTGAAATTAAA	NM_015717:	NM_015717:
30835	CD209	CD209 antigen	0.38	CTGGTTCAACTTTGTGTAATA	NM_021155:	NM_021155:
30835	CD209	CD209 antigen	-1.38	CTGGAACGACGACAAATGTAA	NM_021155:	NM_021155:
933	CD22	CD22 antigen	-0.02	CCGGCTGTGGAGGGAAGTCAA	NM_001771:	NM_001771:
933	CD22	CD22 antigen	-0.39	CACGAATATTATGCCCAGTTT	NM_001771:	NM_001771:
10666	CD226	CD226 antigen	0.93	ACCGGTCAACCTACCAATCAA	NM_006566:	NM_006566:
10666	CD226	CD226 antigen	-0.35	TAGAATGTGTGTATCCATCAA	NM_006566:	NM_006566:
51744	CD244	CD244 natural killer cell receptor 2B4	1.46	TCCCTGCATCTCATACCTTTA	NM_016382:	NM_016382:
51744	CD244	CD244 natural killer cell receptor 2B4	1.37	CAAGTATTTGTAATCTAGAAA	NM_016382:	NM_016382:
919	CD247	CD247 antigen	-2.60	ACCCAACACATGGGACCTATA	NM_000734:	NM_000734:NM_198053:
919	CD247	CD247 antigen	-0.13	CACGCTTTCAGCGAATGACAA	NM_000734:	NM_000734:NM_198053:
57124	CD248	CD248 antigen, endosialin	-3.30	CACGCTGGCTGTCGACGGCTA	NM_020404:	NM_020404:
57124	CD248	CD248 antigen, endosialin	0.80	CCCTATGATCTCAACCAAATA	NM_020404:	NM_020404:
29126	CD274	CD274 antigen	-4.92	GCGAATTACTGTGAAAGTCAA	NM_014143:	NM_014143:
29126	CD274	CD274 antigen	-2.87	CACGGTTCCCAAGGACCTATA	NM_014143:	NM_014143:
80381	CD276	CD276 antigen	-9.28	CAGCATGACCCTGGAGCCCAA	NM_025240:	NM_001024736:NM_025240:
80381	CD276	CD276 antigen	0.22	CTGAAACACTCTGACAGCAAA	NM_025240:	NM_001024736:NM_025240:
940	CD28	CD28 antigen (Tp44)	0.68	ATGATGGTTCTTCAACTATAA	NM_006139:	NM_006139:
940	CD28	CD28 antigen (Tp44)	1.60	CAGGGATGAGGTGCTATAATA	NM_006139:	NM_006139:
23607	CD2AP	CD2-associated protein	0.71	CAGAATGAGACAATCAGTTAA	NM_012120:	NM_012120:
23607	CD2AP	CD2-associated protein	0.38	TACGATGTATAATTTACCTAA	NM_012120:	NM_012120:
10871	CD300C	CD300c antigen	-6.13	CTGGCCCAGCGTGACCAGAAA	NM_006678:	NM_006678:
10871	CD300C	CD300c antigen	-1.27	CAGTGTGAGTAACACACTGAA	NM_006678:	NM_006678:
342510	CD300E	CD300e antigen	-0.67	GAGCATGTACAAGGGATATAA	NM_181449:	NM_181449:
342510	CD300E	CD300e antigen	0.64	TCCCATCTTCCTGGTGGTGAA	NM_181449:	NM_181449:
124599	CD300LB	CD300 antigen like family member B	-0.09	AAGGATGGGAGACCTACATTA	NM_174892:	NM_174892:
124599	CD300LB	CD300 antigen like family member B	-0.29	CAGCAATATGGCAGTGTTCAT	NM_174892:	NM_174892:
146722	CD300LF	CD300 antigen like family member F	0.59	CCCAAAGATATCTGTGTCCTA	NM_139018:	NM_139018:
146722	CD300LF	CD300 antigen like family member F	-0.70	CAGAATTGCAGGAGAATAAAT	NM_139018:	NM_139018:
146894	CD300LG	CD300 antigen like family member G	1.01	CAGAGCAATTATCTTGTATAT	NM_145273:	NM_145273:
146894	CD300LG	CD300 antigen like family member G	1.05	CACGCTTGACTGCGGAGGAAA	NM_145273:	NM_145273:
9936	CD302	CD302 antigen	0.07	TAGCTAGTAATAACAATATAA	NM_014880:	NM_014880:
9936	CD302	CD302 antigen	1.20	GAGGCTATTTAAGTAAATTTA	NM_014880:	NM_014880:
945	CD33	CD33 antigen (gp67)	0.58	TAAGTGTATGATGTCACACAA	NM_001772:	NM_001772:

945	CD33	CD33 antigen (gp67)	1.18	CCCACAGGCAATGGGTTTATA	NM_001772:	NM_001772:
947	CD34 (CD34	CD34 antigen	0.34	CACGTGGTGGCTGATACCGAA	NM_001773:	NM_001025109:NM_001773:
947	CD34 (CD34	CD34 antigen	0.23	AACGGCCATTCAGCAAGACAA	NM_001773:	NM_001025109:NM_001773:
948	CD36	CD36 antigen (collagen type I receptor, thrombospondin receptor)	0.44	CAGCAGCAACATTCAAGTTAA	NM_000072:	NM_001001547:NM_001001548:NM_000072:
948	CD36	CD36 antigen (collagen type I receptor, thrombospondin receptor)	0.59	CAGGTGCTTAACACTAATTCA	NM_000072:	NM_001001547:NM_001001548:NM_000072:
952	CD38	CD38 antigen (p45)	-1.01	CTCAATGGATCCCGCAGTAAA	NM_001775:	NM_001775:
952	CD38	CD38 antigen (p45)	-1.02	CTGGAATCGATTATAAGCAAA	NM_001775:	NM_001775:
915	CD3D	CD3d antigen, delta polypeptide (TiT3 complex)	1.11	CAGGCTATATATGGTATTAAA	NM_000732:	NM_000732:
915	CD3D	CD3d antigen, delta polypeptide (TiT3 complex)	-1.90	CACGAGGAATATATAGGTGTA	NM_000732:	NM_000732:
916	CD3E	CD3e antigen, epsilon polypeptide (TiT3 complex)	-2.62	CTCCGCCATCTTAGTAAAGTA	NM_000733:	NM_000733:
916	CD3E	CD3e antigen, epsilon polypeptide (TiT3 complex)	-1.50	ATGGGTGGTATTACACAGACA	NM_000733:	NM_000733:
917	CD3G	CD3g antigen, gamma polypeptide (TiT3 complex)	-0.21	CTCGAGGGATGTATCAGTGTA	NM_000073:	NM_000073:
917	CD3G	CD3g antigen, gamma polypeptide (TiT3 complex)	0.65	CAGCCCTAAATCTAGACTCAA	NM_000073:	NM_000073:
920	CD4	CD4 antigen (p55)	-0.14	ACCGGTTTCAGAAGACATGTA	NM_000616:	NM_000616:
920	CD4	CD4 antigen (p55)	0.76	TCCAGCATAGTCTATAAGAAA	NM_000616:	NM_000616:
958	CD40	CD40 antigen (TNF receptor superfamily member 5)	-0.01	CCCAGTCGGCTTCTTCTCCAA	NM_001250:	NM_001250:NM_152854:
958	CD40	CD40 antigen (TNF receptor superfamily member 5)	2.06	TTGGTGCTGGTCTTTATCAAA	NM_001250:	NM_001250:NM_152854:
959	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	0.76	ACACAGCATGATCGAAACATA	NM_000074:	NM_000074:
959	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	1.79	TGGGAAACAGCTGACCGTTAA	NM_000074:	NM_000074:
960	CD44	CD44 antigen (Indian blood group)	1.02	ATGGCTGTATTTGTAAACTTA	NM_000610:	NM_001001390:NM_001001391:NM_001001389:NM_001001392:NM_000610:
960	CD44	CD44 antigen (Indian blood group)	0.00	CACCATTATCTTGGAAAGAAA	NM_000610:	NM_001001390:NM_001001391:NM_001001389:NM_001001392:NM_000610:
4179	CD46	CD46 antigen, complement regulatory protein	0.07	ACGAGTAGATTATAAGTGTAA	NM_172350:	NM_172356:NM_153826:NM_172358:NM_172359:NM_172350:NM_172360:NM_172351:NM_172352:NM_172361:NM_172353:NM_172355:NM_172354:NM_172357:NM_002389:
4179	CD46	CD46 antigen, complement regulatory protein	-0.01	CAGAAGCGTATATGAATTCAA	NM_172350:	NM_172356:NM_153826:NM_172358:NM_172359:NM_172350:NM_172360:NM_172351:NM_172352:NM_172361:NM_172353:NM_172355:NM_172354:NM_172357:NM_002389:
961	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transduc	-3.91	CACGATAAGTTTACTCCTCCA	NM_198793:	NM_001025080:NM_001025079:NM_001777:NM_198793:
961	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transduc	2.79	CACTACTGAAGTATACGTAAA	NM_198793:	NM_001025080:NM_001025079:NM_001777:NM_198793:
962	CD48	CD48 antigen (B-cell membrane protein)	-2.70	CAGAAGCATGCTGCTGAATTA	NM_001778:	NM_001778:
962	CD48	CD48 antigen (B-cell membrane protein)	-5.36	CTGCAAGTGCTTGACCCTGTA	NM_001778:	NM_001778:
921	CD5	CD5 antigen (p56-62)	-1.04	AAGAGTTTAGTTGAGGAGAAA	NM_014207:	NM_014207:
921	CD5	CD5 antigen (p56-62)	1.84	ATGGTCCAAGCCGCATAATAA	NM_014207:	NM_014207:
1604	CD55	CD55 antigen, decay accelerating factor for complement (Cromer bloc	-1.63	ATGAACCACATTATAAAGTAA	NM_000574:	NM_000574:
1604	CD55	CD55 antigen, decay accelerating factor for complement (Cromer bloc	-1.64	CCAGAGATACTACAATATTAA	NM_000574:	NM_000574:
965	CD58	CD58 antigen, (lymphocyte function-associated antigen 3)	1.75	AGCAATGTAAACGTAACTCAA	NM_001779:	NM_001779:
965	CD58	CD58 antigen, (lymphocyte function-associated antigen 3)	0.05	TAGCAGTAATTACAACATGTA	NM_001779:	NM_001779:
966	CD59	CD59 antigen, complement regulatory protein	0.15	CAGAATAGCTTGGTCCTTAAA	NM_000611:	NM_203329:NM_203330:NM_203331:NM_000611:
966	CD59	CD59 antigen, complement regulatory protein	1.05	CTCGGTTAAATAGAGAGTGAA	NM_000611:	NM_203329:NM_203330:NM_203331:NM_000611:
922	CD5L	CD5 antigen-like (scavenger receptor cysteine rich family)	0.11	ACGGCTACATTTACACATTTA	NM_005894:	NM_005894:
922	CD5L	CD5 antigen-like (scavenger receptor cysteine rich family)	1.03	TACGGCTACATTTACACATTT	NM_005894:	NM_005894:
923	CD6	CD6 antigen	0.72	CAGGGAGGATGCTGCCTCCAA	NM_006725:	NM_006725:
923	CD6	CD6 antigen	-0.22	CTGGCGGTTCAACAACTCCAA	NM_006725:	NM_006725:
967	CD63	CD63 antigen (melanoma 1 antigen)	0.09	CAACGAGAAGGCGATCCATAA	NM_001780:	NM_001780:
967	CD63	CD63 antigen (melanoma 1 antigen)	-0.16	CAGATGGAGAATTACCCGAAA	NM_001780:	NM_001780:
968	CD68	CD68 antigen	-3.15	CACGGTTCATCCAACAAGCAA	NM_001251:	NM_001251:
968	CD68	CD68 antigen	-3.65	CACAGTTCATCCAACAAGCAA	NM_001251:	NM_001251:
969	CD69	CD69 antigen (p60, early T-cell activation antigen)	1.52	TAGGTTTGTGACTTTCCTAAA	NM_001781:	NM_001781:
969	CD69	CD69 antigen (p60, early T-cell activation antigen)	0.60	CTAGGGAATCTTGAGAATAAA	NM_001781:	NM_001781:
924	CD7	CD7 antigen (p41)	-0.87	CCCAGCCGTACCAGAAATAAA	NM_006137:	NM_006137:
924	CD7	CD7 antigen (p41)	0.01	ACGGTGCTTCTCAGTGGACAA	NM_006137:	NM_006137:
971	CD72	CD72 antigen	0.97	CAGCTCTAACAAGGATTGGAA	NM_001782:	NM_001782:
971	CD72	CD72 antigen	-0.92	CGCACTAGGACTTATGCTCAA	NM_001782:	NM_001782:
972	CD74	CD74 antigen (invariant polypeptide of major histocompatibility compl	-0.23	CAGGGAGAAGGGATAACCCTA	NM_004355:	NM_001025158:NM_004355:NM_001025159:
972	CD74	CD74 antigen (invariant polypeptide of major histocompatibility compl	1.53	CCAAGTCGGAACAGCAGATAA	NM_004355:	NM_001025158:NM_004355:NM_001025159:
973	CD79A	CD79a antigen (immunoglobulin-associated alpha)	-0.10	CAGGGCCACTTAGTGATAATA	NM_021601:	NM_001783:NM_021601:
973	CD79A	CD79a antigen (immunoglobulin-associated alpha)	-2.29	CAGCGGGTAATGAGCCCTTAA	NM_021601:	NM_001783:NM_021601:
974	CD79B	CD79b antigen (immunoglobulin-associated beta)	-2.88	CAGCACCTTGGCACAGCTGAA	NM_021602:	NM_021602:NM_000626:
974	CD79B	CD79b antigen (immunoglobulin-associated beta)	-0.25	ACGGTGTGTCCTGAGAAACCA	NM_021602:	NM_021602:NM_000626:
941	CD80	CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)	-0.35	AAGCTATCTTCAAATGTCTAA	NM_005191:	NM_005191:
941	CD80	CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)	1.81	AAGGGATAGTCCAAAGACTTA	NM_005191:	NM_005191:
975	CD81	CD81 antigen (target of antiproliferative antibody 1)	-5.68	CACCTTCTATGTAGGCATCTA	NM_004356:	NM_004356:
975	CD81	CD81 antigen (target of antiproliferative antibody 1)	1.44	CCGCCTGTGTATATAACGTTT	NM_004356:	NM_004356:
3732	CD82	CD82 antigen	0.34	CTCAAGGGTGTGTATATTGTA	NM_002231:	NM_001024844:NM_002231:
3732	CD82	CD82 antigen	-1.36	CAGGGTTCTCTTATCAACTCA	NM_002231:	NM_001024844:NM_002231:
8832	CD84	CD84 antigen (leukocyte antigen)	-4.58	CAGAATGTGGGCTGCATATAA	NM_003874:	NM_003874:
8832	CD84	CD84 antigen (leukocyte antigen)	-1.42	CTCAGAAATCTTCACAGTGAA	NM_003874:	NM_003874:
942	CD86	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	-0.74	CAACGGAATTAGGAAGACCAA	NM_006889:	NM_175862:NM_006889:
942	CD86	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	-0.23	CCAATTTCTAATATAACAGAA	NM_006889:	NM_175862:NM_006889:
925	CD8A	CD8 antigen, alpha polypeptide (p32)	-0.11	TTGGCAGAGTTCTATAATGTA	NM_171827:	NM_001768:NM_171827:
925	CD8A	CD8 antigen, alpha polypeptide (p32)	-5.52	TAGGGTTGTACTATGCTGTTA	NM_171827:	NM_001768:NM_171827:
928	CD9	CD9 antigen (p24)	0.02	AAAGAGGTCTTCGACAATAAA	NM_001769:	NM_001769:
928	CD9	CD9 antigen (p24)	1.26	ACAAATGTCTATCAACTTTAA	NM_001769:	NM_001769:
22918	CD93	CD93 antigen	-0.13	TACGACGTTATGTTTGGGTAA	NM_012072:	NM_012072:
22918	CD93	CD93 antigen	0.07	CTGGACTGGAATCTTAGCAAA	NM_012072:	NM_012072:
10225	CD96	CD96 antigen	0.88	AACGTTATACTCAGTCCTGAA	NM_005816:	NM_198196:NM_005816:
10225	CD96	CD96 antigen	-0.03	CCCTAAGATAATTACAGGAAA	NM_005816:	NM_198196:NM_005816:
976	CD97	CD97 antigen	0.17	AAGGTTGTAGACGTTGTGTAA	NM_001784:	NM_078481:NM_001784:NM_001025160:
976	CD97	CD97 antigen	-1.07	TCGGAGCTTGGTGCTGACCTA	NM_001784:	NM_078481:NM_001784:NM_001025160:
4267	CD99	CD99 antigen	-4.59	CCGGATGGTGGTTTCGATTTA	NM_002414:	NM_002414:
4267	CD99	CD99 antigen	0.03	TGGGCGGATGATGTTTACTAA	NM_002414:	NM_002414:
8556	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.32	ACAGATATTGCTGCAAACTAA	NM_003672:	NM_033312:NM_003672:NM_033313:
8556	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.44	CAGATATTGCTGCAAACTAAA	NM_003672:	NM_033312:NM_003672:NM_033313:
8555	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	-0.79	CAAGATCAGCAAGAACCCGAA	NM_003671:	NM_033332:NM_033331:NM_003671:
8555	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	-0.29	CCGTACAGTGATGATGACGAA	NM_003671:	NM_033332:NM_033331:NM_003671:
168448	CDC14C	CDC14 cell division cycle 14 homolog C (S. cerevisiae)	-5.39	AAGCAATGAAGGGAAGCGGAA	XM_498195:	XM_499423:XM_498195:
168448	CDC14C	CDC14 cell division cycle 14 homolog C (S. cerevisiae)	-0.64	AAGAATGGTGCCAAGAATAAA	XM_498195:	XM_499423:XM_498195:
8881	CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	0.42	ATAGTGGAATAAAGAAGGTAA	NM_003903:	NM_003903:
8881	CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	-0.46	CCCATGCACTTCGGTCACGAA	NM_003903:	NM_003903:
983	CDC2	cell division cycle 2, G1 to S and G2 to M	0.14	CAGGTTATATCTCATCTTTGA	NM_001786:	NM_033379:NM_001786:
983	CDC2	cell division cycle 2, G1 to S and G2 to M	2.29	TCGGGAAATTTCTCTATTAAA	NM_001786:	NM_033379:NM_001786:

991	CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	0.36	CACCACCATGATGTTCGGGTA	NM_001255:	NM_001255:
991	CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	0.11	CTCCCTAAGCTGGAACAGCTA	NM_001255:	NM_001255:
8697	CDC23	CDC23 (cell division cycle 23, yeast, homolog)	-2.12	ACCCATCTTAATTAAGCCTTA	NM_004661:	NM_004661:
8697	CDC23	CDC23 (cell division cycle 23, yeast, homolog)	0.03	TACGAGAAACTCAATCAACTA	NM_004661:	NM_004661:
993	CDC25A	cell division cycle 25A	-5.00	AAGGCGCTATTTGGCGCTTCA	NM_001789:	NM_001789:NM_201567:
993	CDC25A	cell division cycle 25A	3.01	AAGGGTTATCTCTTTCATACA	NM_001789:	NM_001789:NM_201567:
994	CDC25B (cell	cell division cycle 25B	-0.94	CAGGAGGCTGAGGAACCTAAA	NM_004358:	NM_212530:NM_004358:NM_021874:NM_021872:NM_021873:
994	CDC25B (cell	cell division cycle 25B	-1.52	CCCAGTCTGTTGAGTTAGTTA	NM_004358:	NM_212530:NM_004358:NM_021874:NM_021872:NM_021873:
995	CDC25C	cell division cycle 25C	0.48	CAGGAAGGGCTTATGTTTAAA	NM_001790:	NM_001790:NM_022809:
995	CDC25C	cell division cycle 25C	0.07	CCAGAGCTATATATCCTTAAA	NM_001790:	NM_001790:NM_022809:
996	CDC27	cell division cycle 27	-1.17	GCGCTTGATATCAACCCTCAA	NM_001256:	NM_001256:
996	CDC27	cell division cycle 27	1.73	TACGCTTATGCCTATACTCTA	NM_001256:	NM_001256:
8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controlle	0.14	AACGACGTAGTTTCATTGGAA	NM_003718:	NM_003718:NM_031267:
8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controlle	0.64	TCAGAGTATTATCAATATGAA	NM_003718:	NM_003718:NM_031267:
23097	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	0.04	CACTGTCGTCAGGAAGATATA	NM_015076:	NM_015076:
23097	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	1.33	GAGGATTTGTTTGAGTACGAA	NM_015076:	NM_015076:
998	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	2.24	ATCAGATTTGAAATATTTAAA	NM_001791:	NM_044472:NM_001791:
998	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	-0.11	CATCAGATTTGAAATATTTAA	NM_001791:	NM_044472:NM_001791:
8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	1.51	CAGACTTTCCGTAGCAGCTTA	NM_003607:	NM_014826:NM_003607:
8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	-0.47	CAGATAATAGTCGGAAACAAA	NM_003607:	NM_014826:NM_003607:
9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	0.71	CGCCGAGATATTCCATGTATA	NM_006035:	NM_006035:
9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	0.63	TAGGACCTTAAGAGAATAGTA	NM_006035:	NM_006035:
55561	CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)	0.01	CGCCGGTGGCTTTGCACTCTA	XM_290516:	NM_017525:
55561	CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)	-1.57	CTCGCCGCCTACCAACTTCAA	XM_290516:	NM_017525:
56990	CDC42SE2	CDC42 small effector 2	-2.77	AAGGGAGGTTATGGAGGTGGA	NM_020240:	NM_020240:
56990	CDC42SE2	CDC42 small effector 2	-2.97	CAGGAGACCTGTTCAGTGGAA	NM_020240:	NM_020240:
8318	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	-0.16	TACGAGCAGTATGAATATCAT	NM_003504:	NM_003504:
8318	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	0.52	TAGGCCAGTCAATGTCGTCAA	NM_003504:	NM_003504:
8317	CDC7	CDC7 cell division cycle 7 (S. cerevisiae)	-0.61	TAGGTCAGTATATCTACCTAA	NM_003503:	NM_003503:
8317	CDC7	CDC7 cell division cycle 7 (S. cerevisiae)	-0.01	TAGAGTTATGAGCTAGGTATA	NM_003503:	NM_003503:
79577	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, ho	-1.23	AAGGATCTCGAACACCCATTA	NM_024529:	NM_024529:
79577	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, ho	-1.28	CAGCGATCTACTCAAGTCAAA	NM_024529:	NM_024529:
83540	CDCA1	cell division cycle associated 1	-15.44	AAGCATGAAGATGTTAAGCAA	NM_031423:	NM_031423:NM_145697:
83540	CDCA1	cell division cycle associated 1	0.87	GAGGATTGCAATAAAGTTCAA	NM_031423:	NM_031423:NM_145697:
113130	CDCA5	cell division cycle associated 5	0.27	CTCGGAAAGTTTCCTCGCGTA	NM_080668:	NM_080668:
113130	CDCA5	cell division cycle associated 5	0.07	GAGGAACTAAATTTAAGGAAA	NM_080668:	NM_080668:
55143	CDCA8	cell division cycle associated 8	-0.85	AAGGTAATACAGGTAGATGAA	NM_018101:	NM_018101:
55143	CDCA8	cell division cycle associated 8	0.34	CGGGAGGTTTAGGCTCAGATA	NM_018101:	NM_018101:
999	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	-1.68	CTAGGTATTGTCTACTCTGAA	NM_004360:	NM_004360:
999	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	-0.34	TCGGCCTGAAGTGACTCGTAA	NM_004360:	NM_004360:
1009	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	0.67	ACCGTCGGAATTCATTGTCAA	NM_001797:	NM_001797:
1009	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	1.48	CAGAGAGGATACATTTAATAA	NM_001797:	NM_001797:
28513	CDH19	cadherin 19, type 2	-0.53	CAAGATGTAGTCGATCCTTAT	NM_021153:	NM_021153:
28513	CDH19	cadherin 19, type 2	0.15	CTCCATCTTAATTGCCGACAA	NM_021153:	NM_021153:
1000	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	0.54	ACCAATCGACTTTGAAACAAA	NM_001792:	NM_001792:
1000	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	-1.04	CAGATCGATATATGCAGCAAA	NM_001792:	NM_001792:
28316	CDH20	cadherin 20, type 2	0.01	CAGCTTTACTTGGGTAGATTA	NM_031891:	NM_031891:
28316	CDH20	cadherin 20, type 2	-1.48	CCGCGGGTGCTTCGCGGACAA	NM_031891:	NM_031891:
1001	CDH3	cadherin 3, type 1, P-cadherin (placental)	-4.22	AAGCCTCTTACCTGCCGTAAA	NM_001793:	NM_001793:
1001	CDH3	cadherin 3, type 1, P-cadherin (placental)	0.06	CAGATGAAATCGGCAACTTTA	NM_001793:	NM_001793:
1003	CDH5	cadherin 5, type 2, VE-cadherin (vascular epithelium)	-0.15	ACCACGAAACGTGAAGTTCAA	NM_001795:	NM_001795:
1003	CDH5	cadherin 5, type 2, VE-cadherin (vascular epithelium)	0.43	ACGTATTATCACAATAACGAA	NM_001795:	NM_001795:
8558	CDK10	cyclin-dependent kinase (CDC2-like) 10	-0.40	CCGGAAGCAGCCCTACAACAA	NM_003674:	NM_052988:NM_003674:NM_052987:
8558	CDK10	cyclin-dependent kinase (CDC2-like) 10	1.23	CCGTCTGAAGTGTATTCGTAA	NM_003674:	NM_052988:NM_003674:
1017	CDK2	cyclin-dependent kinase 2	0.08	AACAATTATATTTATATTTCA	NM_001798:	NM_052827:NM_001798:
1017	CDK2	cyclin-dependent kinase 2	-0.80	CACAATGTTTATAAAGGCCAA	NM_001798:	NM_052827:NM_001798:
1018	CDK3 (cyclin-	cyclin-dependent kinase 3	-5.05	ATGGATATGTTCCAGAAGGTA	NM_001258:	NM_001258:
1018	CDK3 (cyclin-	cyclin-dependent kinase 3	0.15	CAGACTGGATTTGGAGATGGA	NM_001258:	NM_001258:
1019	CDK4	cyclin-dependent kinase 4	-0.18	AAGGTAATCCGGAGTGAGCAA	NM_000075:	NM_000075:
1019	CDK4	cyclin-dependent kinase 4	0.51	ACCCTGGTGTTTGAGCATGTA	NM_000075:	NM_000075:
1020	CDK5	cyclin-dependent kinase 5	-0.83	CACCTACGGAACTGTGTTCAA	NM_004935:	NM_004935:
1020	CDK5	cyclin-dependent kinase 5	1.32	CCCTTTGTGGACTTTATTTAA	NM_004935:	NM_004935:
1020	CDK5	cyclin-dependent kinase 5	-9.87	CCGGGAGATCTGCCTACTCAA	XM_498294:	XM_498294:NM_004935:
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	0.01	CCGGAAGGCCACGCTGTTTGA	NM_003885:	NM_003885:
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	0.03	TGAGCTGGTTTGACTCATTAA	NM_003885:	NM_003885:
8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	-5.89	CAGCAAGAAGGTGACACCCAA	NM_003936:	NM_003936:
8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	-6.62	CCGCGAGAACCTTCTCCGCAA	NM_003936:	NM_003936:
1021	CDK6	cyclin-dependent kinase 6	-3.75	AAGACTCAAGGTGGTCAGTAA	NM_001259:	NM_001259:
1021	CDK6	cyclin-dependent kinase 6	-0.32	TCCGTTGATGTGCTTAGGTTA	NM_001259:	NM_001259:
1022	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activ	-0.08	CCGGATGGCTCTGGACGTGAA	NM_001799:	NM_001799:
1022	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activ	0.71	GAGGCTTTAAGGTAGCTTTAA	NM_001799:	NM_001799:
1024	CDK8	cyclin-dependent kinase 8	1.51	CAGAAGAAATACGTATACCAA	NM_001260:	NM_001260:
1024	CDK8	cyclin-dependent kinase 8	-5.53	CCAGCTGGACAGAATATTCAA	NM_001260:	NM_001260:
1025	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	-0.02	AACCGCTGCAAGGGTAGTATA	NM_001261:	NM_001261:
1025	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	-0.04	TAGGGACATGAAGGCTGCTAA	NM_001261:	NM_001261:
8814	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-1.07	CTGGACCGAGTGACTACTATA	NM_004196:	NM_004196:
8814	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-0.15	TCGGGAAATCCGAATGCTCAA	NM_004196:	NM_004196:
8999	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	1.00	ATGATGTGTTTAGGTAATCTA	NM_003948:	NM_003948:
8999	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	1.00	TTCTACGGACTTTAAATTAAA	NM_003948:	NM_003948:
51265	CDKL3	cyclin-dependent kinase-like 3	1.46	CAACATTATTGTCATGGACTA	NM_016508:	NM_016508:
51265	CDKL3	cyclin-dependent kinase-like 3	-4.29	TGGGCAGATAGTGGCCATTAA	NM_016508:	NM_016508:
344387	CDKL4 (cyclir	cyclin-dependent kinase-like 4	0.07	CCACAAGATCGTATACCCATA	NM_001009565:	NM_001009565:
344387	CDKL4 (cyclir	cyclin-dependent kinase-like 4	-0.10	CTGAATCAAATCGTTACGCAA	NM_001009565:	NM_001009565:
6792	CDKL5	cyclin-dependent kinase-like 5	0.76	AAGATAGACGCTTCATGTTAA	NM_003159:	NM_001037343:NM_003159:
6792	CDKL5	cyclin-dependent kinase-like 5	-0.79	AAGGCAATAATGCTAATTACA	NM_003159:	NM_001037343:NM_003159:
1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	-0.48	ATGATTCTTAGTGACTTTAAA	NM_000389:	NM_078467:NM_000389:
1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	-5.36	CAGTTTGTGTGTCTTAATTAT	NM_000389:	NM_078467:NM_000389:
1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-0.43	AAAGCGTTGGATGTAGCATTA	NM_004064:	NM_004064:
1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-3.93	ACCGACGATTCTTCTACTCAA	NM_004064:	NM_004064:
1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	0.46	AAGCTTTAAGAGTCATTTATA	NM_000076:	NM_000076:
1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	-1.91	TACACTGGTCCCAAAGTGTAA	NM_000076:	NM_000076:
1029	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	-0.72	CACGCCCTAAGCGCACATTCA	NM_000077:	NM_058197:NM_058195:NM_000077:
1029	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	-5.95	CAGAACCAAAGCTCAAATAAA	NM_000077:	NM_058197:NM_058195:NM_000077:
1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0.54	CTGCTTACTTATGCCATAGAA	NM_004936:	NM_078487:NM_004936:
1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-1.56	CTGGAAAGTTAAATAAATTTA	NM_004936:	NM_078487:NM_004936:
1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0.66	CAGGCTTATGAATATATTTAA	NM_001262:	NM_001262:
1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	-1.43	TGCCTCTACTTTATCAATTAA	NM_001262:	NM_001262:NM_078626:

1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	-2.52	ACCCAAGGGCAGAGCATTTAA	NM_001800:	NM_001800:NM_079421:
1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	-5.16	ATGAGTTATGAGTTATTCATA	NM_001800:	NM_001800:NM_079421:
1033	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity	1.07	CACAATCAAGATCTGTATCAA	NM_005192:	NM_005192:
1033	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity	0.05	TCGGGACAAATTAGCTGCACA	NM_005192:	NM_005192:
1045	CDX2	caudal type homeobox transcription factor 2	-3.97	CCGGGAGGACTGGAATGGCTA	NM_001265:	NM_001265:
1045	CDX2	caudal type homeobox transcription factor 2	-2.01	TTGGGTTGTTGGTCTGTGTAA	NM_001265:	NM_001265:
1046	CDX4 (caudal	caudal type homeobox transcription factor 4	0.40	CAGGTTATAGTCTCCGAATGA	NM_005193:	NM_005193:
1046	CDX4 (caudal	caudal type homeobox transcription factor 4	0.27	CAAGGAGAGAAAGATGATCAA	NM_005193:	NM_005193:
634	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary gly	0.78	GAGGAGGAGGATTATAACTTA	NM_001712:	NM_001024912:NM_001712:
634	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary gly	-6.17	ACGGCAGTAATGCTTCTCCTA	NM_001712:	NM_001024912:NM_001712:
1050	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	-2.69	CAGCCGATATCAACACTTGTA	NM_004364:	NM_004364:
1050	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	-6.32	CTCAGCCTTGTTTGTACTGTA	NM_004364:	NM_004364:
1051	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	-0.02	CGGGCCCTGAGTAATCGCTTA	NM_005194:	NM_005194:
1051	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	0.01	ACGTCTATGTGTACAGATGAA	NM_005194:	NM_005194:
1052	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	0.07	CACCACTAAACTGCGAGAGAA	NM_005195:	NM_005195:
1052	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	-0.78	CGCCGACCTCTTCAACAGCAA	NM_005195:	NM_005195:
1053	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	-1.57	TAGACCATGGATAAATGGCAA	NM_001805:	NM_001805:
1053	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	-1.10	CTCCGATCTCTTTGCCGTGAA	NM_001805:	NM_001805:
1054	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	-0.04	CAAGGAATTAAGTGTACTCAA	NM_001806:	NM_001806:
1054	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	0.68	CAGCTTAGCGTGGAAACCATT	NM_001806:	NM_001806:
51816	CECR1	cat eye syndrome chromosome region, candidate 1	-0.13	CCAAAGCTAGTTAGTACTCAA	NM_017424:	NM_017424:NM_177405:
51816	CECR1	cat eye syndrome chromosome region, candidate 1	-0.14	CAGCTTATAATCGGATATTTA	NM_017424:	NM_017424:NM_177405:
1056	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	0.02	TCCCATGAGCCTTGGTATCAA	NM_001807:	NM_001807:
1056	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	-0.01	AGCCCTGACGCTGGCCTATAA	NM_001807:	NM_001807:
9620	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog,	1.64	CGCCAACAGTGTGATTACCTA	NM_014246:	NM_014246:
9620	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog,	0.36	CGGGATCCTGGATGTGATCAA	NM_014246:	NM_014246:
1952	CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog,	0.69	ACGACAACAATCCAACCTTTA	NM_001408:	NM_001408:
1952	CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog,	0.49	CACGTGGTGGTCTTCAACGTA	NM_001408:	NM_001408:
1951	CELSR3	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog,	-0.66	CCGGGAGGCAGTATCAGTGTA	NM_001407:	NM_001407:
1951	CELSR3	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog,	-0.90	CTGGAATTGTCCGTACAGTAA	NM_001407:	NM_001407:
1059	CENPB (cent	centromere protein B, 80kDa	-0.78	CGCCTTGAGAAGCACAGTTTA	NM_001810:	NM_001810:
1059	CENPB (cent	centromere protein B, 80kDa	0.91	TTCGAGGTCTTGGACATCAAA	NM_001810:	NM_001810:
1062	CENPE	centromere protein E, 312kDa	0.06	CACGATACTGTTAACATGAAT	NM_001813:	NM_001813:
1062	CENPE	centromere protein E, 312kDa	-5.81	CAGGTTAATCCTACCACACAA	NM_001813:	NM_001813:
1063	CENPF	centromere protein F, 350/400ka (mitosin)	-0.14	ACCGAGAGAAATTGACTTCTA	NM_016343:	NM_016343:
1063	CENPF	centromere protein F, 350/400ka (mitosin)	-0.69	CAGAATCTTAGTAGTCAAGTA	NM_016343:	NM_016343:
64946	CENPH (cent	centromere protein H	0.26	AACGTTTACAGTTGTAGTACA	NM_022909:	NM_022909:
64946	CENPH (cent	centromere protein H	0.03	ATGGATAACATGAAACACCTA	NM_022909:	NM_022909:
11033	CENTA1	centaurin, alpha 1	-1.50	GAGGCGCACTTCAAGCATAAA	NM_006869:	NM_006869:
11033	CENTA1	centaurin, alpha 1	0.11	CCGGAAGTTTGTGCTGACAGA	NM_006869:	NM_006869:
11064	CEP110	centrosomal protein 110kDa	-0.02	CAGCTATAATCTAATAGGGAA	NM_007018:	NM_007018:
11064	CEP110	centrosomal protein 110kDa	0.32	CAGGATAATTTGGCTTTGATA	NM_007018:	NM_007018:
55165	CEP55	centrosomal protein 55kDa	0.02	ATCAGCTGTTGTATTCACAAA	NM_018131:	NM_018131:
55165	CEP55	centrosomal protein 55kDa	0.00	CAGGTTATTGCTAATGGGTTA	NM_018131:	NM_018131:
64781	CERK	ceramide kinase	0.78	ATGGCATTATTTGATCTGAAA	NM_182661:	NM_182661:NM_022766:
64781	CERK	ceramide kinase	0.01	CGGCTTAAACTTTGATCTGTA	NM_182661:	NM_182661:NM_022766:
1066	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	-0.56	CTGGTTGATTCCAATGTTGAT	NM_001266:	NM_001266:
1066	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	-0.33	CCTGAAGAGCTTCAAGCTGAA	NM_001266:	NM_001266:NM_001025194:NM_001025195:
8824	CES2	carboxylesterase 2 (intestine, liver)	0.41	CTGAGAGGTCTGAAAGAATAA	NM_003869:	NM_003869:NM_198061:
8824	CES2	carboxylesterase 2 (intestine, liver)	-0.05	CACCTAAGTGTTAGAAGCCTA	NM_003869:	NM_003869:NM_198061:
51716	CES4	carboxylesterase 4-like	-2.10	ATCGATAGGAATCCAGACCTA	NM_016280:	NM_016280:
51716	CES4	carboxylesterase 4-like	1.48	ATGGAGGATTTCGGTAGATTT	NM_016280:	NM_016280:
221223	CES7	carboxylesterase 7	1.07	CAACAAGATTTCTTCAATAAA	NM_145024:	NM_145024:
221223	CES7	carboxylesterase 7	1.67	CCCGCAATCATTAGCTTCTTT	NM_145024:	NM_145024:
1068	CETN1	centrin, EF-hand protein, 1	0.32	TCGGTTCAGAAGCTAAAGTGA	NM_004066:	NM_004066:
1068	CETN1	centrin, EF-hand protein, 1	-0.08	TTCCAGCATAATGAGATGGAA	NM_004066:	NM_004066:
1069	CETN2	centrin, EF-hand protein, 2	-3.17	CAGAACGACTTTAGACAAGCA	NM_004344:	NM_004344:
1069	CETN2	centrin, EF-hand protein, 2	0.48	GCGAATTACCCTAATTCTCAA	NM_004344:	NM_004344:
1070	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	0.16	CAGTTACCATCTTATATTCTA	NM_004365:	NM_004365:
1070	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	-0.32	TCGAGCTATGATAGAAGAATT	NM_004365:	NM_004365:
1071	CETP (choles	cholesteryl ester transfer protein, plasma	0.71	CAGGCCTCCTATTCTAAGAAA	NM_000078:	NM_000078:
1071	CETP (choles	cholesteryl ester transfer protein, plasma	-2.66	CAAGGGTCATTTCATCTACAA	NM_000078:	NM_000078:
629	CFB	complement factor B	-0.13	AAGAGAAGTCGTTTCATTCAA	NM_001710:	NM_001710:
629	CFB	complement factor B	0.53	CAGCTCAATGAAATCAATTAT	NM_001710:	NM_001710:
1675	CFD	complement factor D (adipsin)	-0.35	AACCTTGTCTCTCTCTACAAA	NM_001928:	NM_001928:
1675	CFD	complement factor D (adipsin)	-0.05	CTGCATCTGGTTGGTCTTTAT	NM_001928:	NM_001928:
3075	CFH	complement factor H	0.47	CAGGTCTTCACAAGAAAGTTA	NM_000186:	NM_000186:
3075	CFH	complement factor H	0.03	ATGGTGACTACTCACCTTTAA	NM_000186:	NM_001014975:NM_000186:
3426	CFI	complement factor I	-1.06	TACGGAAATCGTTTCTATGAA	NM_000204:	NM_000204:
3426	CFI	complement factor I	-0.76	CCGACCTTAAACGTATAGTAA	NM_000204:	NM_000204:
1072	CFL1	cofilin 1 (non-muscle)	-1.48	CAAGCATGAATTGCAAGCAAA	NM_005507:	NM_005507:
1072	CFL1	cofilin 1 (non-muscle)	-3.32	CTGACAGGGATCAAGCATGAA	NM_005507:	NM_005507:
1073	CFL2 (cofilin	cofilin 2 (muscle)	0.72	AAGGAAATATCATTTATTTAA	NM_021914:	NM_021914:NM_138638:
1073	CFL2 (cofilin	cofilin 2 (muscle)	0.57	CAGAGATTAAATATTGCTTTA	NM_021914:	NM_021914:NM_138638:
8837	CFLAR	CASP8 and FADD-like apoptosis regulator	0.69	CACCGACGAGTCTCAACTAAA	NM_003879:	NM_003879:
8837	CFLAR	CASP8 and FADD-like apoptosis regulator	0.30	TCGAGGCATTACAATCGCGAA	NM_003879:	NM_003879:
1080	CFTR	cystic fibrosis transmembrane conductance regulator, ATP-binding ca	1.00	TCAGCTTATTGTCTAGTGAAA	NM_000492:	NM_000492:
1080	CFTR	cystic fibrosis transmembrane conductance regulator, ATP-binding ca	0.70	CTCGAAAGTTATGATTATTGA	NM_000492:	NM_000492:
1081	CGA	glycoprotein hormones, alpha polypeptide	0.00	CGCCATGGATTACTACAGAAA	NM_000735:	NM_000735:
1081	CGA	glycoprotein hormones, alpha polypeptide	0.16	CAAGGATATACTGCAGCTTTA	NM_000735:	NM_000735:
1081	CGA	glycoprotein hormones, alpha polypeptide	0.23	CGCCATGGATTACTACAGAAA	NM_000735:	NM_000735:
1081	CGA	glycoprotein hormones, alpha polypeptide	0.11	CAAGGATATACTGCAGCTTTA	NM_000735:	NM_000735:
10668	CGRRF1	cell growth regulator with ring finger domain 1	0.98	CCGGGAAATTTATGATATTAT	NM_006568:	NM_006568:
10668	CGRRF1	cell growth regulator with ring finger domain 1	1.42	CGGGAAATTTATGATATTATT	NM_006568:	NM_006568:
8208	CHAF1B	chromatin assembly factor 1, subunit B (p60)	-0.03	ACGGAAAGTCTGGACCCTTGA	NM_005441:	NM_005441:
8208	CHAF1B	chromatin assembly factor 1, subunit B (p60)	-3.00	CACCAATGTCAGGATCTGGAA	NM_005441:	NM_005441:
1103	CHAT	choline acetyltransferase	-0.96	CACGGAGATGTTCTGCTGCTA	NM_020549:	NM_020984:NM_020549:NM_020986:NM_020985:
1103	CHAT	choline acetyltransferase	-1.76	CCCGAGATGTTCATGGATGAA	NM_020549:	NM_020984:NM_020549:NM_020986:NM_020985:
1105	CHD1 (chrom	chromodomain helicase DNA binding protein 1	-0.04	AAGCTACTTGTTTACATTGTA	NM_001270:	NM_001270:
1105	CHD1 (chrom	chromodomain helicase DNA binding protein 1	0.46	GCGGTTTATCAAGAGCTATAA	NM_001270:	NM_001270:
1107	CHD3	chromodomain helicase DNA binding protein 3	-1.75	CCGGACCGGGTCGGAAACGAA	NM_005852:	NM_005852:NM_001005271:NM_001005273:
1107	CHD3	chromodomain helicase DNA binding protein 3	0.01	CCCATACTGCGTATAGATGAA	NM_005852:	NM_005852:NM_001005273:
1108	CHD4	chromodomain helicase DNA binding protein 4	-1.61	AAGGTTTAAGCTCTTAGAACA	NM_001273:	NM_001273:
1108	CHD4	chromodomain helicase DNA binding protein 4	-1.67	CATGAAGGTTATAAATACGAA	NM_001273:	NM_001273:
1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	0.74	AAGAAAGAGATCTGTATCAAT	NM_001274:	NM_001274:
1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	-0.60	CCACCTCATCATAACAACAAT	NM_001274:	NM_001274:
11200	CHEK2	CHK2 checkpoint homolog (S. pombe)	1.39	ACGCCGTCCTTTGAATAACAA	NM_007194:	NM_145862:NM_007194:NM_001005735:

11200	CHEK2	CHK2 checkpoint homolog (S. pombe)	1.34	AGGACTGTCTTATAAAGATTA	NM_007194:	NM_007194:NM_001005735:
1112	CHES1	checkpoint suppressor 1	-0.22	CCGGTCCTGTTTGAATAACAT	NM_005197:	NM_005197:
1112	CHES1	checkpoint suppressor 1	-0.01	TCGAAGGAGCCTTCACGTAAA	NM_005197:	NM_005197:
55743	CHFR	checkpoint with forkhead and ring finger domains	-1.55	AACCAGAGGTTTGACATGGAA	NM_018223:	NM_018223:
55743	CHFR	checkpoint with forkhead and ring finger domains	-1.00	TCCCGTGGAGCGGATCTGTAA	NM_018223:	NM_018223:
1113	CHGA	chromogranin A (parathyroid secretory protein 1)	0.99	TATGAACTTTATCTAAAGAAA	NM_001275:	NM_001275:
1113	CHGA	chromogranin A (parathyroid secretory protein 1)	-1.79	TCCAAGGATGTTATGGAGAAA	NM_001275:	NM_001275:
26511	CHIC2	cysteine-rich hydrophobic domain 2	1.43	AACGAATAACATGATGGAATA	NM_012110:	NM_012110:
26511	CHIC2	cysteine-rich hydrophobic domain 2	1.94	AAGAACCTTCCTGTTAATGTA	NM_012110:	NM_012110:
1119	CHKA	choline kinase alpha	-1.73	AGCCGGCGATTAGATACTGAA	NM_001277:	NM_001277:NM_212469:
1120	CHKB	choline kinase beta	-0.42	CTGTGTATGTAACACAATAAA	NM_005198:	NM_005198:
1121	CHM	choroideremia (Rab escort protein 1)	-0.99	CTCCAATATATTGTCATGCAT	NM_000390:	NM_000390:
1121	CHM	choroideremia (Rab escort protein 1)	1.55	CCGGAGAGTTCTGCATGTTGA	NM_000390:	NM_001037312:NM_000390:
57132	CHMP1B	chromatin modifying protein 1B	0.66	ATAACGTATATTATTAATAAA	NM_020412:	NM_020412:
57132	CHMP1B	chromatin modifying protein 1B	0.93	ATGATTGTTCTCATAACGTAT	NM_020412:	NM_020412:
79586	CHPF	chondroitin polymerizing factor	1.07	AAGCTCCCTGCCTTTAATAAA	NM_024536:	NM_024536:
79586	CHPF	chondroitin polymerizing factor	-3.49	CAGCGAGGCCTGCTTCTACAA	NM_024536:	NM_024536:
89832	CHRFAM7A	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAI	0.94	ATCGGTTAAATTTGATGCAAA	NM_139320:	NM_139320:
89832	CHRFAM7A	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAI	-2.68	CACCGCAACATTAAGATTACA	NM_139320:	NM_139320:NM_148911:
1128	CHRM1	cholinergic receptor, muscarinic 1	1.40	CCGGCTTGGCTAGTCACATAT	NM_000738:	NM_000738:
1128	CHRM1	cholinergic receptor, muscarinic 1	-1.11	TACAGTCAAGAGGCCGACTAA	NM_000738:	NM_000738:
1129	CHRM2	cholinergic receptor, muscarinic 2	0.65	CAGGTACTTCTGTGTCACAAA	NM_000739:	NM_000739:NM_001006626:NM_001006628:NM_001006627:NM_001006629:NM_001006631:NM_001006630:NM_001006632:
1129	CHRM2	cholinergic receptor, muscarinic 2	0.16	TACGGCTATTGCAGCCTTCTA	NM_000739:	NM_000739:NM_001006626:NM_001006628:NM_001006627:NM_001006629:NM_001006631:NM_001006630:NM_001006632:
1131	CHRM3	cholinergic receptor, muscarinic 3	1.06	CCGAGCCAAACGAACAACAAA	NM_000740:	NM_000740:
1131	CHRM3	cholinergic receptor, muscarinic 3	0.74	CCTGGTAATTGTGTCATTTAA	NM_000740:	NM_000740:
1132	CHRM4	cholinergic receptor, muscarinic 4	-0.07	CCCGAAGGAGAAGAAAGCCAA	NM_000741:	NM_000741:
1132	CHRM4	cholinergic receptor, muscarinic 4	-0.12	CCGCTACTTCTGCGTCACCAA	NM_000741:	NM_000741:
1133	CHRM5	cholinergic receptor, muscarinic 5	1.50	AAGAGAGTGGTCCTAGTCAAA	NM_012125:	NM_012125:
1133	CHRM5	cholinergic receptor, muscarinic 5	0.98	CGGGCCAAGCGTACTCCGAAA	NM_012125:	NM_012125:
1134	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	0.70	ACGTGTTATATTCCATACTTA	NM_000079:	NM_000079:
1134	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	-0.41	CAGGTCGACTCATTGAATTAA	NM_000079:	NM_000079:
57053	CHRNA10 (ch	cholinergic receptor, nicotinic, alpha 10	-1.51	ATCCCTGACTCAATAAAGTAA	NM_020402:	NM_020402:
57053	CHRNA10 (ch	cholinergic receptor, nicotinic, alpha 10	0.61	TGGGTTATAATGAGAAACTGA	NM_020402:	NM_020402:
1135	CHRNA2 (cho	cholinergic receptor, nicotinic, alpha 2 (neuronal)	0.48	AAGGGCTTTGAACAATGTTTA	NM_000742:	NM_000742:
1135	CHRNA2 (cho	cholinergic receptor, nicotinic, alpha 2 (neuronal)	-0.77	CACGGGCACCTACAACAGCAA	NM_000742:	NM_000742:
1136	CHRNA3	cholinergic receptor, nicotinic, alpha 3	0.17	CCCACCTTCTATCTAAGACAA	NM_000743:	NM_000743:
1136	CHRNA3	cholinergic receptor, nicotinic, alpha 3	0.21	AACTGTCTTAGTACACCATAA	NM_000743:	NM_000743:
1137	CHRNA4	cholinergic receptor, nicotinic, alpha 4	0.56	ATGAATAATTGAGGTTAGGAA	NM_000744:	NM_000744:
1137	CHRNA4	cholinergic receptor, nicotinic, alpha 4	0.77	CAGAATGAATAATTGAGGTTA	NM_000744:	NM_000744:
1138	CHRNA5 (cho	cholinergic receptor, nicotinic, alpha 5	0.64	CTGAGTAACAGCTAATCTTTA	NM_000745:	NM_000745:
1138	CHRNA5 (cho	cholinergic receptor, nicotinic, alpha 5	2.09	CTGAAGTATACATTTAGTTAA	NM_000745:	NM_000745:
8973	CHRNA6	cholinergic receptor, nicotinic, alpha 6	-0.12	CAGCATTATTTGATACACTGA	NM_004198:	NM_004198:
8973	CHRNA6	cholinergic receptor, nicotinic, alpha 6	0.12	ACAGCCTAATTATGTAATTAA	NM_004198:	NM_004198:
1139	CHRNA7	cholinergic receptor, nicotinic, alpha 7	-0.59	ACCAGACATTCTTCTCTATAA	NM_000746:	NM_000746:
1139	CHRNA7	cholinergic receptor, nicotinic, alpha 7	-1.40	CCAGATGGCCAGATTTGGAAA	NM_000746:	NM_000746:
55584	CHRNA9	cholinergic receptor, nicotinic, alpha 9	0.81	TAGCTTCAAATGAATGTCGAA	NM_017581:	NM_017581:
55584	CHRNA9	cholinergic receptor, nicotinic, alpha 9	0.22	CTGGGTAGAAATTAATACAAT	NM_017581:	NM_017581:
1140	CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	-0.02	TAGGTCGCCAGTGAAATAGAA	NM_000747:	NM_000747:
1140	CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	0.90	CCCAATAGGTTCCAGCCTGAA	NM_000747:	NM_000747:
1141	CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)	0.16	AGAGATCGACTTGGTGCTGAA	NM_000748:	NM_000748:
1141	CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)	0.56	CGCATGCAAGATTGAAGTAAA	NM_000748:	NM_000748:
1142	CHRNB3 (cho	cholinergic receptor, nicotinic, beta 3	-1.64	CAGGTAGTACAAGACTGGAAA	NM_000749:	NM_000749:
1142	CHRNB3 (cho	cholinergic receptor, nicotinic, beta 3	-0.01	CGGAGAATGGGAAATACTGAA	NM_000749:	NM_000749:
1143	CHRNB4 (cho	cholinergic receptor, nicotinic, beta 4	-0.56	CACATGAAGAATGACGATGAA	NM_000750:	NM_000750:
1143	CHRNB4 (cho	cholinergic receptor, nicotinic, beta 4	-2.95	CAGCAAGTCATGCGTGACCAA	NM_000750:	NM_000750:
1144	CHRND	cholinergic receptor, nicotinic, delta	0.25	AACAATTACAATGAGGAGAAA	NM_000751:	NM_000751:
1144	CHRND	cholinergic receptor, nicotinic, delta	-2.62	CCGCCAGGACATCACCTTCTA	NM_000751:	NM_000751:
1145	CHRNE	cholinergic receptor, nicotinic, epsilon	0.34	TACAGTACTGACAGAAAGCAA	NM_000080:	NM_000080:
1145	CHRNE	cholinergic receptor, nicotinic, epsilon	-5.41	CAGGAGGAAAGGGTTCACATA	NM_000080:	NM_000080:
1146	CHRNG	cholinergic receptor, nicotinic, gamma	0.01	CCACCAGAAGGTGGTGTTCTA	NM_005199:	NM_005199:
1146	CHRNG	cholinergic receptor, nicotinic, gamma	-1.35	CTGCTCTATCTCAGTCACCTA	NM_005199:	NM_005199:
1147	CHUK	conserved helix-loop-helix ubiquitous kinase	-2.58	CAGGAGAAGTTCGGTTTAGTA	NM_001278:	NM_001278:
1147	CHUK	conserved helix-loop-helix ubiquitous kinase	-4.43	TTCCATAAGCTTGGTGACAAA	NM_001278:	NM_001278:
114548	CIAS1	cold autoinflammatory syndrome 1	-0.11	ACAGAACTAGTTGACTATATA	NM_004895:	NM_004895:NM_183395:
114548	CIAS1	cold autoinflammatory syndrome 1	0.87	TTGATAATTTATATCTCTCAA	NM_004895:	NM_004895:NM_183395:
10518	CIB2	calcium and integrin binding family member 2	-0.75	CACCGAAGAGCAGCTAGACAA	NM_006383:	NM_006383:
10518	CIB2	calcium and integrin binding family member 2	-0.20	CTGCACCTTCTTCAATAAGAA	NM_006383:	NM_006383:
117286	CIB3	calcium and integrin binding family member 3	-5.01	CACGAGCAGCTGGAAGCGTAT	NM_054113:	NM_054113:
117286	CIB3	calcium and integrin binding family member 3	-2.11	CTGGAGCAGACGGTGACCAAA	NM_054113:	NM_054113:
1149	CIDEA	cell death-inducing DFFA-like effector a	-1.17	CGGGTGCTGGATGACAAGGAA	NM_001279:	NM_198289:NM_001279:
1149	CIDEA	cell death-inducing DFFA-like effector a	-1.65	GAGAGTCACCTTCGACTTGTA	NM_001279:	NM_198289:NM_001279:
27141	CIDEB (cell d	cell death-inducing DFFA-like effector b	-4.24	CAGGCTAGATAACCCACCCAA	NM_014430:	NM_014430:
27141	CIDEB (cell d	cell death-inducing DFFA-like effector b	-1.49	CCGATTCACCTTTGACGTGTA	NM_014430:	NM_014430:
63924	CIDEC	cell death-inducing DFFA-like effector c	-1.08	CCGTGTAACGTTTGATCTGTA	NM_022094:	NM_022094:
63924	CIDEC	cell death-inducing DFFA-like effector c	1.37	GAGGAAGGGCATCATGGCTTA	NM_022094:	NM_022094:
8483	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	1.43	AGGGTGATCATAGTTCCTCTA	NM_003613:	NM_003613:
8483	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	0.99	CTAGTGCACATTCAAAGTTAA	NM_003613:	NM_003613:
51550	CINP	cyclin-dependent kinase 2-interacting protein	-0.15	CGGCTGATTGGCACAATTTAA	NM_032630:	NM_032630:
51550	CINP	cyclin-dependent kinase 2-interacting protein	1.02	GCGGCTGATTGGCACAATTTA	NM_032630:	NM_032630:
1154	CISH	cytokine inducible SH2-containing protein	0.82	CTGATAAGACTTCATGAAATA	NM_013324:	NM_145071:
1154	CISH	cytokine inducible SH2-containing protein	0.95	ATGGACAACTACAATAGGTAA	NM_013324:	NM_145071:
11113	CIT	citron (rho-interacting, serine/threonine kinase 21)	0.43	ATGGAAGGCACTATTTCTCAA	NM_007174:	NM_007174:
11113	CIT	citron (rho-interacting, serine/threonine kinase 21)	-0.30	CAGGATATACCGTAACACGAA	NM_007174:	NM_007174:
10370	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-termina	0.37	TGGAATGTCGTCAGTGGCAAA	NM_006079:	NM_006079:
10370	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-termina	-0.02	CAGATTTACGAGTGAAAGGAA	NM_006079:	NM_006079:
26586	CKAP2	cytoskeleton associated protein 2	1.38	CACACGATTGTAGATATTCTA	NM_018204:	NM_018204:
26586	CKAP2	cytoskeleton associated protein 2	-0.14	CCGCATTTGTTACTAACTGAA	NM_018204:	NM_018204:
10970	CKAP4	cytoskeleton-associated protein 4	0.47	AGGGCGCGGATTTAAAGTCCA	NM_006825:	NM_006825:
10970	CKAP4	cytoskeleton-associated protein 4	-1.04	ACAGGTTTCGACTACCAGAAA	NM_006825:	NM_006825:
9793	CKAP5	cytoskeleton associated protein 5	-10.47	AAGGGTCGACTCAATGATTCA	NM_014756:	NM_001008938:NM_014756:
9793	CKAP5	cytoskeleton associated protein 5	-10.73	CAGGTATTATTAATGACGCAA	NM_014756:	NM_001008938:NM_014756:
1152	CKB	creatine kinase, brain	-4.57	CCAGATTGAAACTCTCTTCAA	NM_001823:	NM_001823:
1152	CKB	creatine kinase, brain	0.15	CCGGCCTCACCCAGATTGAAA	NM_001823:	NM_001823:
51192	CKLF	chemokine-like factor	-3.06	AACAACAGTATTCATGCTCAT	NM_016951:	NM_181640:NM_016951:
51192	CKLF	chemokine-like factor	-0.51	ATCGATTAATGAAGTGGTTAT	NM_016951:	NM_181641:NM_016951:

1158	CKM	creatine kinase, muscle	0.61	GACGGGCGAGTTCAAAGGGAA	NM_001824:	NM_001824:
1158	CKM	creatine kinase, muscle	-1.35	TCCACGCAAAGCGATAAATAA	NM_001824:	NM_001824:
1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	-5.74	CCTGCCTATCTTTACAATAAA	NM_001825:	NM_001825:
1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	-1.65	GAGGTTGAGCTTGTTCAGATA	NM_001825:	NM_001825:
1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	-0.11	AACATCTTTCTGATAACATTA	NM_001826:	NM_001826:
1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	-0.09	AAGAAATCTGTTCATGTTAAA	NM_001826:	NM_001826:
1164	CKS2	CDC28 protein kinase regulatory subunit 2	-0.49	AAGTTTGTATGTTGCATTTAA	NM_001827:	NM_001827:
1164	CKS2	CDC28 protein kinase regulatory subunit 2	-4.99	CTGTAAGATGTTTAAGATAAA	NM_001827:	NM_001827:
1179	CLCA1	chloride channel, calcium activated, family member 1	-2.94	AAGGTCGATCTGAAATCAGAA	NM_001285:	NM_001285:
1179	CLCA1	chloride channel, calcium activated, family member 1	0.87	ATGGAACAGCTCACAAGTATA	NM_001285:	NM_001285:
9635	CLCA2	chloride channel, calcium activated, family member 2	-1.16	ACCCATGGCCTTCGACTACAA	NM_006536:	NM_006536:
9635	CLCA2	chloride channel, calcium activated, family member 2	-0.58	CAGCAATGGGTTTGATAGGAA	NM_006536:	NM_006536:
9629	CLCA3 (chlor	chloride channel, calcium activated, family member 3	-2.21	TAGGCCCGAAATGACTAGCAA	NM_004921:	NM_004921:
9629	CLCA3 (chlor	chloride channel, calcium activated, family member 3	0.40	GAGAGCTACATTATAAGAATA	NM_004921:	NM_004921:
22802	CLCA4	chloride channel, calcium activated, family member 4	0.08	CACCATTTGAACCTTAACGAA	NM_012128:	NM_012128:
22802	CLCA4	chloride channel, calcium activated, family member 4	0.49	AAGTTCAACGTTATATCATAA	NM_012128:	NM_012128:
23529	CLCF1	cardiotrophin-like cytokine factor 1	0.01	ACAGGATTTCCTGAAAGTTTA	NM_013246:	NM_013246:
23529	CLCF1	cardiotrophin-like cytokine factor 1	0.02	TCGAATTGTCTTCCAGTATTA	NM_013246:	NM_013246:
1180	CLCN1	chloride channel 1, skeletal muscle (Thomsen disease, autosomal dor	-0.01	CAGCTGTGATTTGCTTCGAAT	NM_000083:	NM_000083:
1180	CLCN1	chloride channel 1, skeletal muscle (Thomsen disease, autosomal dor	-0.59	CAGTACTTTGTTTGACAACAA	NM_000083:	NM_000083:
1181	CLCN2	chloride channel 2	0.00	CTCATTGGAATCGTTACTCTA	NM_004366:	NM_004366:
1181	CLCN2	chloride channel 2	-4.79	CCGAATCAAGAAACTGCCCTA	NM_004366:	NM_004366:
1182	CLCN3	chloride channel 3	0.62	TTGAATTGAGCCATCTATAAA	NM_001829:	NM_173872:NM_001829:
1182	CLCN3	chloride channel 3	-1.05	CAGAAAGTCCTCGGCCATTGA	NM_001829:	NM_173872:NM_001829:
1183	CLCN4	chloride channel 4	1.00	AAGGCTGATGTTTGTAACTTA	NM_001830:	NM_001830:
1183	CLCN4	chloride channel 4	0.68	CGGCCTGTGGATGACATTCCA	NM_001830:	NM_001830:
1184	CLCN5	chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease)	0.85	ATCCTTGTTCCTGTTACAATA	NM_000084:	NM_000084:
1184	CLCN5	chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease)	-4.55	AAGGATGTGTTAAAGCATATA	NM_000084:	NM_000084:
1185	CLCN6	chloride channel 6	0.31	CCGGTGAATGTTATTGGAATT	NM_001286:	NM_021737:NM_021735:NM_021736:NM_001286:
1185	CLCN6	chloride channel 6	0.01	TCAGATTTACGTCTACCCTAA	NM_001286:	NM_021737:NM_021735:NM_021736:NM_001286:
1186	CLCN7	chloride channel 7	-0.38	CCAGCTCATCGTTCTCCTAAA	NM_001287:	NM_001287:
1186	CLCN7	chloride channel 7	0.54	CTGGCTGACCATGTTTCGAAT	NM_001287:	NM_001287:
1187	CLCNKA	chloride channel Ka	0.18	TTGGCATAACAGGCAACTCTA	NM_004070:	NM_004070:
1187	CLCNKA	chloride channel Ka	-1.89	CTGAGTGTGAGAAGATGGAAA	NM_004070:	NM_004070:
1188	CLCNKB	chloride channel Kb	-1.01	AACAATAGGTTCAGCTCCAAA	NM_000085:	NM_000085:
1188	CLCNKB	chloride channel Kb	-4.58	CCGGCTCCTGGCGGTCTTCAA	NM_000085:	NM_000085:
23562	CLDN14	claudin 14	0.98	CACGGCCGTGTCCTACCTGAA	NM_012130:	NM_012130:NM_144492:
23562	CLDN14	claudin 14	0.44	CGGGTACAGGCTGAACGACTA	NM_012130:	NM_012130:NM_144492:
10686	CLDN16	claudin 16	1.32	TAGAATTCATATTGAATTAAA	NM_006580:	NM_006580:
10686	CLDN16	claudin 16	0.63	CAGTATGGTTACATTGATAAA	NM_006580:	NM_006580:
1365	CLDN3	claudin 3	-0.62	CACGGCCACCAAGGTCGTCTA	NM_001306:	NM_001306:
1365	CLDN3	claudin 3	-1.96	CACCATTATCCGGGACTTCTA	NM_001306:	NM_001306:
1364	CLDN4	claudin 4	-3.66	CAGAGCCATATAACTGCTCAA	NM_001305:	NM_001305:
1364	CLDN4	claudin 4	-2.45	ACGGCCCACAACATCATCCAA	NM_001305:	NM_001305:
6320	CLEC11A	C-type lectin domain family 11, member A	-1.25	AAGCATCTGCAGGAAGCCCTA	NM_002975:	NM_002975:
6320	CLEC11A	C-type lectin domain family 11, member A	-1.10	CCCTGAGGACATCGTCACTTA	NM_002975:	NM_002975:
160364	CLEC12A	C-type lectin domain family 12, member A	-2.06	ACGCACCTGACTTAAATAACA	NM_138337:	NM_201623:NM_138337:NM_201625:
160364	CLEC12A	C-type lectin domain family 12, member A	0.44	TTGGTACAGTAGGTTTATAAA	NM_138337:	NM_201623:NM_138337:NM_201625:
51267	CLEC1A	C-type lectin domain family 1, member A	0.39	TGGGTTTATGCACGTATTTAA	NM_016511:	NM_016511:
51267	CLEC1A	C-type lectin domain family 1, member A	1.08	CTGAACTGTTCCATATTATAA	NM_016511:	NM_016511:
51266	CLEC1B	C-type lectin domain family 1, member B	0.16	AGGGCTTTATTGTACAATAAA	NM_016509:	NM_016509:
51266	CLEC1B	C-type lectin domain family 1, member B	-0.02	CTGACAGATACTGAAATTGTA	NM_016509:	NM_016509:
9976	CLEC2B	C-type lectin domain family 2, member B	-2.33	ACGTGTCAGGCTACACATAAA	NM_005127:	NM_005127:
9976	CLEC2B	C-type lectin domain family 2, member B	-0.16	CAGCTAGATGTTACACCGAAA	NM_005127:	NM_005127:
29121	CLEC2D	C-type lectin domain family 2, member D	0.15	CAGGAGAGTGTGCCTATTTGA	NM_001004419:	NM_013269:NM_001004420:NM_001004419:
29121	CLEC2D	C-type lectin domain family 2, member D	-1.11	TAGAAGCATATTGGAACTGAT	NM_001004419:	NM_013269:NM_001004420:NM_001004419:
50856	CLEC4A	C-type lectin domain family 4, member A	-3.79	TAGAATTTAGGTGGTCTGTCA	NM_016184:	NM_194448:NM_016184:NM_194450:NM_194447:
50856	CLEC4A	C-type lectin domain family 4, member A	-0.12	AAGGGAGGTCCATAGAATTTA	NM_016184:	NM_194448:NM_016184:NM_194450:NM_194447:
170482	CLEC4C	C-type lectin domain family 4, member C	-1.93	TTCAGTCTAGTTGCTACTTTA	NM_203503:	NM_203503:NM_130441:
170482	CLEC4C	C-type lectin domain family 4, member C	-1.45	ATGGAAGGAAAGGACATAGAA	NM_203503:	NM_203503:NM_130441:
338339	CLEC4D	C-type lectin domain family 4, member D	0.07	ATGGAAGAATAGCGTGAATAA	NM_080387:	NM_080387:
338339	CLEC4D	C-type lectin domain family 4, member D	-0.79	CAGAGTATTCTGGCATAAGAA	NM_080387:	NM_080387:
26253	CLEC4E	C-type lectin domain family 4, member E	0.05	CCGAGTCCAATAGTCAATTTA	NM_014358:	NM_014358:
26253	CLEC4E	C-type lectin domain family 4, member E	0.63	TCCCTGAATCTTACCAACAAA	NM_014358:	NM_014358:
165530	CLEC4F	C-type lectin domain family 4, member F	-1.02	CTGCCTTCATCTAACAGTATA	NM_173535:	NM_173535:
165530	CLEC4F	C-type lectin domain family 4, member F	-0.14	CACGTGCTAAGCAGAGGCTTA	NM_173535:	NM_173535:
339390	CLEC4G	C-type lectin superfamily 4, member G	-0.18	CTGAGGAAGCATCAATAAATA	NM_198492:	NM_198492:
339390	CLEC4G	C-type lectin superfamily 4, member G	0.24	CAGCCTGAGGAAGCATCAATA	NM_198492:	NM_198492:
10332	CLEC4M	C-type lectin domain family 4, member M	-2.10	CCCAACAATAGCGGGAATGAA	NM_014257:	NM_214679:NM_214677:NM_214678:NM_214676:NM_214675:NM_014257:
10332	CLEC4M	C-type lectin domain family 4, member M	0.21	TCGATGTGACGTTGACAATTA	NM_014257:	NM_214679:NM_214677:NM_214678:NM_214676:NM_214675:NM_014257:
23601	CLEC5A	C-type lectin domain family 5, member A	0.74	ACCCTTAGACTCACGAACAAA	NM_013252:	NM_013252:
23601	CLEC5A	C-type lectin domain family 5, member A	0.39	CACGGAATAAGCACATAGTAA	NM_013252:	NM_013252:
64581	CLEC7A	C-type lectin domain family 7, member A	-1.43	TAGCAGTATATCAGTTATGAA	NM_022570:	NM_197953:NM_197952:NM_197951:NM_197950:NM_197949:NM_197947:NM_022570:NM_197948:
64581	CLEC7A	C-type lectin domain family 7, member A	1.57	ATGGAATATCATCCTGATTTA	NM_022570:	NM_197953:NM_197952:NM_197954:NM_197951:NM_197950:NM_197949:NM_197947:NM_022570:NM_197948:
1192	CLIC1	chloride intracellular channel 1	1.63	AAACCCAGCACTCAATGACAA	NM_001288:	NM_001288:
1192	CLIC1	chloride intracellular channel 1	-0.23	AAGGTGTCTCTCAGAGGAAGT	NM_001288:	NM_001288:
1193	CLIC2	chloride intracellular channel 2	0.65	CCCGTGAAGAATTTACCCACA	NM_001289:	NM_001289:
1193	CLIC2	chloride intracellular channel 2	0.24	CACAATGCCTATGCCCGTGAA	NM_001289:	NM_001289:
9022	CLIC3 (chlori	chloride intracellular channel 3	0.86	AACGCTGCAGATCGAGGACTT	NM_004669:	NM_004669:
9022	CLIC3 (chlori	chloride intracellular channel 3	0.61	AACGACGTTTTCCACAAGTTC	NM_004669:	NM_004669:
25932	CLIC4	chloride intracellular channel 4	-1.96	CAGGGAAGTTAGTCAAATGAA	NM_013943:	NM_013943:
25932	CLIC4	chloride intracellular channel 4	0.18	TAGCAGTACAATGATTAGTAA	NM_013943:	NM_013943:
53405	CLIC5	chloride intracellular channel 5	0.05	AACCATGTGGTTTGAACTTGA	NM_016929:	NM_016929:
53405	CLIC5	chloride intracellular channel 5	0.11	AAGGCCTTCTCTCATGATCTA	NM_016929:	NM_016929:
54102	CLIC6	chloride intracellular channel 6	1.33	TGGTATGTGTTTGATGCTATA	NM_053277:	NM_053277:
54102	CLIC6	chloride intracellular channel 6	1.41	ACACACAATTTCATTCATATA	NM_053277:	NM_053277:
1195	CLK1	CDC-like kinase 1	-3.76	AAAGCCGGTATCAGAACCATA	NM_004071:	NM_001024646:NM_004071:
1195	CLK1	CDC-like kinase 1	-6.63	AACGTGATGAACGCACCTTAA	NM_004071:	NM_001024646:NM_004071:
1196	CLK2	CDC-like kinase 2	-0.99	CAGCTACAGACGCAACGATTA	NM_001291:	NM_003993:NM_001291:

1196	CLK2	CDC-like kinase 2	-0.26	TACAGTCTTTGTGAAATGAAA	XM_376585:	NM_001291:NM_003993:
1198	CLK3	CDC-like kinase 3	-1.69	CACGAAGATCTCGGTCCAGAA	NM_001292:	NM_003992:NM_001292:
1198	CLK3	CDC-like kinase 3	0.69	CTGCATTCTCTTTGAGTACTA	NM_001292:	NM_003992:NM_001292:
57396	CLK4	CDC-like kinase 4	0.80	AAGTCTGACTATGTAGTCAAA	NM_020666:	NM_020666:
57396	CLK4	CDC-like kinase 4	0.33	TCGAAGAATGTTAGAATATGA	NM_020666:	NM_020666:
1201	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt di	0.02	AAAGGGTCTGCTGTGGTACAT	NM_000086:	NM_000086:
1201	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt di	-0.13	AAGACGTGTGGTTCGGCTTTC	NM_000086:	NM_000086:
2055	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental re	0.94	CCCGGACAACTTGAATGAAAT	NM_018941:	NM_018941:
2055	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental re	0.26	ACCAAGGTGTATAGTAACCTA	NM_018941:	NM_018941:
9575	CLOCK	clock homolog (mouse)	-0.95	ATCCAGCAACTTGCACCTATA	NM_004898:	NM_004898:
9575	CLOCK	clock homolog (mouse)	-1.16	ATCGGCAACAAGAAGAACTAA	NM_004898:	NM_004898:
8192	CLPP (ClpP c	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homo	0.05	GCCCAGGAGTTTGGCATCTTA	NM_006012:	NM_006012:
8192	CLPP (ClpP c	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homo	-2.90	CACGATGCAGTACATCCTCAA	NM_006012:	NM_006012:
8218	CLTCL1	clathrin, heavy polypeptide-like 1	-2.73	TCGGGCAAATGTGCCAAGCAA	NM_001835:	NM_007098:NM_001835:
8218	CLTCL1	clathrin, heavy polypeptide-like 1	1.04	CCAGTTTGAAGACTACATGAA	NM_001835:	NM_007098:NM_001835:
1191	CLU	clusterin	1.71	CCGGTTTATATGATCTTCATA	NM_001831:	NM_203339:NM_001831:
1191	CLU	clusterin	0.72	GCCGGTTTATATGATCTTCAT	NM_001831:	NM_203339:NM_001831:
1215	CMA1	chymase 1, mast cell	-0.02	CAGATCCTGCAGGCAAATTAA	NM_001836:	NM_001836:
1215	CMA1	chymase 1, mast cell	-2.52	CACCACGATATCATGTTACTA	NM_001836:	NM_001836:
1240	CMKLR1	chemokine-like receptor 1	0.59	CAGCCATAGAAGCTTTACCAA	NM_004072:	NM_004072:
1240	CMKLR1	chemokine-like receptor 1	0.15	CAGCCTTGGACTAGCAATTTA	NM_004072:	NM_004072:
57007	CMKOR1	chemokine orphan receptor 1	0.45	CACTATTGGTGTACCTTATAA	NM_020311:	NM_020311:
57007	CMKOR1	chemokine orphan receptor 1	-3.18	CCGGAAGATCATCTTCTCCTA	NM_020311:	NM_020311:
51727	CMPK	cytidylate kinase	-1.13	AAGTATTGCTAAGTACTATAA	NM_016308:	NM_016308:
51727	CMPK	cytidylate kinase	-0.03	CGCGTATATATCCCTCTAGTA	NM_016308:	NM_016308:
202333	CMYA5	cardiomyopathy associated 5	0.81	TTGAGTTCTTTCCTAAATTAA	NM_153610:	NM_153610:
202333	CMYA5	cardiomyopathy associated 5	-2.60	TAGGTGCTATACATTATTCAA	NM_153610:	NM_153610:
1259	CNGA1	cyclic nucleotide gated channel alpha 1	-0.05	TCGACTCTACATAGAACCGAA	NM_000087:	NM_000087:
1259	CNGA1	cyclic nucleotide gated channel alpha 1	-0.62	TCGAAGAACGGCCAATATTAA	NM_000087:	NM_000087:
1260	CNGA2	cyclic nucleotide gated channel alpha 2	-0.61	AGCACCGACTATAGACATTTA	NM_005140:	NM_005140:
1260	CNGA2	cyclic nucleotide gated channel alpha 2	-2.52	TGGCGAGATCAGTATCCTTAA	NM_005140:	NM_005140:
1261	CNGA3	cyclic nucleotide gated channel alpha 3	0.40	TCCCTTGGAATTGCATCCCAA	NM_001298:	NM_001298:
1261	CNGA3	cyclic nucleotide gated channel alpha 3	-0.08	AAGGTTGGAATGGTGTACTAA	NM_001298:	NM_001298:
1262	CNGA4	cyclic nucleotide gated channel alpha 4	-2.26	TAGCATGAGCTCTGTCATCTA	XM_290552:	NM_001037329:
1258	CNGB1	cyclic nucleotide gated channel beta 1	-0.92	CAGAAGTTACTCCGGAAGAAA	NM_001297:	NM_001297:
1258	CNGB1	cyclic nucleotide gated channel beta 1	-3.36	CGCCATCGACGTGAACTACAA	NM_001297:	NM_001297:
54714	CNGB3	cyclic nucleotide gated channel beta 3	-0.43	TACCCTTTACTAAAGAAATAA	NM_019098:	NM_019098:
54714	CNGB3	cyclic nucleotide gated channel beta 3	0.01	TACCTAGGATTGTAACTTAAA	NM_019098:	NM_019098:
10256	CNKSR1	connector enhancer of kinase suppressor of Ras 1	-0.76	CCGCCGCTGGTTTGTGCTCAA	NM_006314:	NM_006314:
10256	CNKSR1	connector enhancer of kinase suppressor of Ras 1	0.57	CGGACTCAGCTTAGTGCTGAA	NM_006314:	NM_006314:
154043	CNKSR3	CNKSR family member 3	-1.26	CCGGAGTTGTGTTACTGCTTA	NM_173515:	NM_173515:
154043	CNKSR3	CNKSR family member 3	-4.29	CGGAGTTGTGTTACTGCTTAA	NM_173515:	NM_173515:
4850	CNOT4	CCR4-NOT transcription complex, subunit 4	0.59	ACCGAGCGGTTTATAATTCAT	NM_013316:	NM_013316:NM_001008225:
4850	CNOT4	CCR4-NOT transcription complex, subunit 4	1.27	CACCGAGCGGTTTATAATTCA	NM_013316:	NM_013316:NM_001008225:
1268	CNR1	cannabinoid receptor 1 (brain)	0.99	CACGTTAAAGTAGGACTATCA	NM_016083:	NM_016083:NM_033181:
1268	CNR1	cannabinoid receptor 1 (brain)	1.08	TTCCATAGTTTAGGTACTCAA	NM_016083:	NM_016083:NM_033181:
1269	CNR2	cannabinoid receptor 2 (macrophage)	0.15	AACCCTGTCATCTATGCTCTA	NM_001841:	NM_001841:
1269	CNR2	cannabinoid receptor 2 (macrophage)	0.07	TTCCGGAATCATCTACACCTA	NM_001841:	NM_001841:
1270	CNTF	ciliary neurotrophic factor	1.54	ACCAGTATAGACAGAAGTAAA	NM_000614:	NM_000614:
1270	CNTF	ciliary neurotrophic factor	0.61	GACCAGTATAGACAGAAGTAA	NM_000614:	NM_000614:
1271	CNTFR	ciliary neurotrophic factor receptor	0.68	CTCCTATCCCACAGTATTTAA	NM_001842:	NM_147164:NM_001842:
1271	CNTFR	ciliary neurotrophic factor receptor	-4.49	ACGCCGGGAAGGAGTACATTA	NM_001842:	NM_147164:NM_001842:
8506	CNTNAP1	contactin associated protein 1	-1.06	CCGAATCTAATTGCGGAGCTA	NM_003632:	NM_003632:
8506	CNTNAP1	contactin associated protein 1	-1.33	CCGGATCACCTTCGAGGGTAA	NM_003632:	NM_003632:
26047	CNTNAP2	contactin associated protein-like 2	0.79	CACCATCAATTAAGACATATA	NM_014141:	NM_014141:
26047	CNTNAP2	contactin associated protein-like 2	-0.01	ACCTCTTAGTTTAATCTGAAA	NM_014141:	NM_014141:
9382	COG1	component of oligomeric golgi complex 1	0.78	ACCGATTACAGACTCTGACAA	NM_018714:	NM_018714:
9382	COG1	component of oligomeric golgi complex 1	0.38	ACGCCATGTGGGAGTTACTTA	NM_018714:	NM_018714:
22796	COG2	component of oligomeric golgi complex 2	0.49	ACGTCTGACGTCGATATAATA	NM_007357:	NM_007357:
22796	COG2	component of oligomeric golgi complex 2	-0.44	CCCGATGCATTTCATGAGAAA	NM_007357:	NM_007357:
84342	COG8	component of oligomeric golgi complex 8	-0.01	AAGACCTTGTTCCGTATTTAA	NM_032382:	NM_032382:
84342	COG8	component of oligomeric golgi complex 8	-0.01	CTGGCCTTCCATCGCGCTGAA	NM_032382:	NM_032382:
1300	COL10A1 (co	collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia)	-1.03	AAGCCTGTTTCTAACTATGAA	NM_000493:	NM_000493:
1300	COL10A1 (co	collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia)	-0.10	AGCAATCTTAAGGCTCTTTAA	NM_000493:	NM_000493:
1302	COL11A2	collagen, type XI, alpha 2	1.73	CCGCAGATGGCTGGAATATTA	NM_080679:	NM_080681:NM_080680:NM_080679:
1302	COL11A2	collagen, type XI, alpha 2	-1.14	CCCGGACAGAAGGGCACCAAA	NM_080679:	NM_080681:NM_080680:NM_080679:
1277	COL1A1	collagen, type I, alpha 1	-0.60	ACCAATCACCTGCGTACAGAA	NM_000088:	NM_000088:
1277	COL1A1	collagen, type I, alpha 1	1.01	CCCAAGGGTAACAGCGGTGAA	NM_000088:	NM_000088:
1278	COL1A2	collagen, type I, alpha 2	-3.16	AACGGTGTTGTTGGTCCCACA	NM_000089:	NM_000089:
1278	COL1A2	collagen, type I, alpha 2	-0.01	CGCGGTTACCCTGGCAATATT	NM_000089:	NM_000089:
1281	COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosoma	-1.49	CTCAAGTCTGTTAATGGACAA	NM_000090:	NM_000090:
1281	COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosoma	-5.24	ACCGATGAGATTATGACTTCA	NM_000090:	NM_000090:
1285	COL4A3 (coll	collagen, type IV, alpha 3 (Goodpasture antigen)	-4.03	AGCGGATATAGAGCTAGCTAA	NM_031366:	NM_031365:NM_031364:NM_031366:NM_000091:NM_031363:NM_031362:
1285	COL4A3 (coll	collagen, type IV, alpha 3 (Goodpasture antigen)	1.30	TCCCAAGGTTACTTAATTCAA	NM_031366:	NM_031365:NM_031364:NM_031366:NM_000091:NM_031363:NM_031362:
1286	COL4A4	collagen, type IV, alpha 4	-0.03	CACGCGCTTCATACAAAGCAT	NM_000092:	NM_000092:
1286	COL4A4	collagen, type IV, alpha 4	1.42	TTGGGTTAACAGTATCTCAAA	NM_000092:	NM_000092:
1289	COL5A1 (coll	collagen, type V, alpha 1	0.28	CCGACCCATCCTGTTCGTGAA	NM_000093:	NM_000093:
1289	COL5A1 (coll	collagen, type V, alpha 1	0.03	TTCGGTGAAGCGTCACAGAAA	NM_000093:	NM_000093:
1290	COL5A2	collagen, type V, alpha 2	-0.01	CACACTAGTATATACCATTTA	NM_000393:	NM_000393:
1290	COL5A2	collagen, type V, alpha 2	0.01	TAGGTTTAAGATGACCAATGA	NM_000393:	NM_000393:
1293	COL6A3	collagen, type VI, alpha 3	-0.57	CACCACTAAGCCCATGGTTAA	NM_004369:	NM_057164:NM_057167:NM_057166:NM_004369:NM_057165:
1293	COL6A3	collagen, type VI, alpha 3	0.65	AACGACGTCTTCTTCAAATTA	NM_004369:	NM_057164:NM_057167:NM_057166:NM_004369:NM_057165:
1294	COL7A1	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominar	-2.58	AAGGGTGACAAGGGAGACTCA	NM_000094:	NM_000094:
1294	COL7A1	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominar	-1.93	CCGGGCAGCAATGGTGACCAA	NM_000094:	NM_000094:
1295	COL8A1	collagen, type VIII, alpha 1	-0.32	CAGGATATTTATTGTATCCCA	NM_001850:	NM_020351:NM_001850:
1295	COL8A1	collagen, type VIII, alpha 1	0.08	CAGTTGGAAAGTTATATGTAA	NM_001850:	NM_020351:NM_001850:
1296	COL8A2	collagen, type VIII, alpha 2	0.35	CTGACTAGCTTTGATAAACAA	NM_005202:	NM_005202:
1296	COL8A2	collagen, type VIII, alpha 2	0.79	TAACTTGGTATAGGAAGCTTA	NM_005202:	NM_005202:
1297	COL9A1	collagen, type IX, alpha 1	2.07	CACCTCCCTTGAACAAATTTA	NM_001851:	NM_001851:NM_078485:
1297	COL9A1	collagen, type IX, alpha 1	0.21	CAGCATGATTACAATGTATTA	NM_001851:	NM_001851:NM_078485:
1298	COL9A2	collagen, type IX, alpha 2	2.59	CAGGATATTGGAGTTACTCTA	NM_001852:	NM_001852:
1298	COL9A2	collagen, type IX, alpha 2	1.16	CCAGGCCTTTCTGTAAATAAA	NM_001852:	NM_001852:
8292	COLQ	collagen-like tail subunit (single strand of homotrimer) of asymmetric a	-6.54	AAGGACAAATTCCTGCTACTA	NM_005677:	NM_080540:NM_080538:NM_080541:NM_080544:NM_080539:NM_005677:NM_080543:NM_080542:

8292	COLQ	collagen-like tail subunit (single strand of homotrimer) of asymmetric a	-1.15	AAGAAGCGTGGTGGCCACAAA	NM_005677:	NM_080540:NM_080538:NM_080541:NM_080544: NM_005677:NM_080543:NM_080542:
28991	COMMD5	COMM domain containing 5	0.61	TAGGCTGAAGTCCTAACTTGA	NM_014066:	NM_014066:
28991	COMMD5	COMM domain containing 5	-1.44	CACTCATTCGATAGCAATGAA	NM_014066:	NM_014066:
1311	COMP	cartilage oligomeric matrix protein	-3.96	CACGGTCACGGATGACGACTA	NM_000095:	NM_000095:
1311	COMP	cartilage oligomeric matrix protein	-4.01	AAGGGAGATCGTGCAGACAAT	NM_000095:	NM_000095:
1312	COMT (catecl	catechol-O-methyltransferase	-1.45	CTGGCTAGCTATATTATCTTA	NM_000754:	NM_000754:NM_007310:
1312	COMT (catecl	catechol-O-methyltransferase	-1.24	CGGGCTGTGTCCTAAATGCAA	NM_000754:	NM_000754:NM_007310:
118881	COMTD1	catechol-O-methyltransferase domain containing 1	-0.38	CCGAGTGTGTGCGAAACCTAA	NM_144589:	NM_144589:
118881	COMTD1	catechol-O-methyltransferase domain containing 1	0.04	CACCTTGGCCTTCAAGATCTA	NM_144589:	NM_144589:
9276	COPB2	coatomer protein complex, subunit beta 2 (beta prime)	-4.81	ACGATTCTTCAGAGTATGCAA	NM_004766:	NM_004766:
9276	COPB2	coatomer protein complex, subunit beta 2 (beta prime)	-6.70	CAGGTTTCAAGGGTAGTGAAA	NM_004766:	NM_004766:
22820	COPG	coatomer protein complex, subunit gamma	-1.28	CCGAGCCACCTTCTACCTAAA	NM_016128:	NM_016128:
22820	COPG	coatomer protein complex, subunit gamma	-3.29	CACCGACTCCACTATGTTGAA	NM_016128:	NM_016128:
9318	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis	-0.15	AACGTACAACATCATAGTAAT	NM_004236:	NM_004236:
9318	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis	0.12	ATCCATTAATTCTATTCTTGA	NM_004236:	NM_004236:
10987	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis	-1.42	TAGGACATACCCAAAGGGCTA	NM_006837:	NM_006837:
10987	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis	0.01	CGCCTTTAGGACATACCCAAA	NM_006837:	NM_006837:
10980	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis	1.46	CCCAACCTTATAAACATGATA	NM_006833:	NM_006833:
10980	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis	0.09	CCAGTTTGTGAACAAGTTCAA	NM_006833:	NM_006833:
51805	COQ3	coenzyme Q3 homolog, methyltransferase (yeast)	-5.35	CTGGAATCAAATGGTCTGTCA	NM_017421:	NM_017421:
51805	COQ3	coenzyme Q3 homolog, methyltransferase (yeast)	0.12	AACCATATGGTTCAAATCCTA	NM_017421:	NM_017421:
84274	COQ5	coenzyme Q5 homolog, methyltransferase (yeast)	-2.79	AAGCCTGGAACTGAAGGATAA	XM_495935:	NM_032314:
84274	COQ5	coenzyme Q5 homolog, methyltransferase (yeast)	-1.22	TAGGCCCAAGTCAGAGTATTA	XM_495935:	NM_032314:
51004	COQ6	coenzyme Q6 homolog, monooxygenase (yeast)	0.71	AAGATCTTATTTAATTTAATA	NM_182476:	NM_182476:NM_182480:
51004	COQ6	coenzyme Q6 homolog, monooxygenase (yeast)	1.64	AAGAAAGATTACGTTGATGAA	NM_182476:	NM_182476:NM_182480:
57017	COQ9	coenzyme Q9 homolog (yeast)	1.22	CCGGGTTAATGATGCAATGAA	NM_020312:	NM_020312:
57017	COQ9	coenzyme Q9 homolog (yeast)	0.01	AAGGATGGCAGTGAGCTAATA	NM_020312:	NM_020312:
10699	CORIN	corin, serine peptidase	-0.19	CACGATTGTATGAAAGTTCAA	NM_006587:	NM_006587:
10699	CORIN	corin, serine peptidase	0.59	ACCACTTTACATGAACTTCTA	NM_006587:	NM_006587:
1325	CORT	cortistatin	0.08	CAGCTGGAGATTGGGCTTAAA	NM_001302:	NM_001302:
1352	COX10 (COX	COX10 homolog, cytochrome c oxidase assembly protein, heme A: fa	-0.54	TAGGTAGATAACATCCAATCA	NM_001303:	NM_001303:
1352	COX10 (COX	COX10 homolog, cytochrome c oxidase assembly protein, heme A: fa	-1.37	AAAGGGATTGTAGGTAGATAA	NM_001303:	NM_001303:
9167	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	0.16	AAGCCTGTGGTTTCCACAGAA	NM_004718:	NM_004718:
9167	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	-5.00	CCGGACTCTGGGCGTCATGTA	NM_004718:	NM_004718:
1356	CP (cerulopla	ceruloplasmin (ferroxidase)	-0.23	AAGGACCTCTACAGTGGATTA	NM_000096:	NM_000096:
1356	CP (cerulopla	ceruloplasmin (ferroxidase)	-2.07	CAGGACTCATCGGACCTTTAA	NM_000096:	NM_000096:
1357	CPA1	carboxypeptidase A1 (pancreatic)	0.98	CCCATCCAGGCAACCAAATAA	NM_001868:	NM_001868:
1357	CPA1	carboxypeptidase A1 (pancreatic)	0.15	CAGCATCATCAAGGCAATTTA	NM_001868:	NM_001868:
1358	CPA2 (carbox	carboxypeptidase A2 (pancreatic)	-5.03	CCCGGTCCAAGGTATCTGGAA	NM_001869:	NM_001869:
1358	CPA2 (carbox	carboxypeptidase A2 (pancreatic)	1.14	TACGTGTTCTCTCAAACCAAA	NM_001869:	NM_001869:
1359	CPA3 (carbox	carboxypeptidase A3 (mast cell)	1.03	AACGAAGTAGCTTTAAGTGAA	NM_001870:	NM_001870:
1359	CPA3 (carbox	carboxypeptidase A3 (mast cell)	-1.12	CAGTAGCACCATAACGAAGTA	NM_001870:	NM_001870:
51200	CPA4	carboxypeptidase A4	0.02	CGCACTGAGGCCATTGTTAAA	NM_016352:	NM_016352:
51200	CPA4	carboxypeptidase A4	0.82	CAGTGGTAGATTTCATCCAAA	NM_016352:	NM_016352:
93979	CPA5	carboxypeptidase A5	-9.13	ATCGCTGGATCCCGTTTCAAA	NM_080385:	NM_080385:
93979	CPA5	carboxypeptidase A5	-0.87	CCGCTTATGGCGGAAGAACAA	NM_080385:	NM_080385:
1360	CPB1	carboxypeptidase B1 (tissue)	1.19	CTGGGTCTATTAAACTAGGTA	NM_001871:	NM_001871:
1360	CPB1	carboxypeptidase B1 (tissue)	0.01	CCCGGGAGCTACAACAATCTA	NM_001871:	NM_001871:
1361	CPB2	carboxypeptidase B2 (plasma, carboxypeptidase U)	-1.09	CTGCCGGAGCGTTACATCAAA	NM_001872:	NM_001872:
1361	CPB2	carboxypeptidase B2 (plasma, carboxypeptidase U)	0.03	TTCCATATTCCTATACACGAA	NM_001872:	NM_001872:NM_016413:
1362	CPD (carboxy	carboxypeptidase D	0.40	CGGGTCTAATCTAATATTAGA	NM_001304:	NM_001304:
1362	CPD (carboxy	carboxypeptidase D	-1.18	CAGCCCAGTTGCCCAAATAAA	NM_001304:	NM_001304:
1363	CPE (carboxy	carboxypeptidase E	0.07	TAGTCCGTTAACACTACTTAA	NM_001873:	NM_001873:
1363	CPE (carboxy	carboxypeptidase E	-0.89	CTCGGAGTTGTGAGCACTCTA	NM_001873:	NM_001873:
10815	CPLX1	complexin 1	0.77	CACGGCCGTGTTCACTTCTAA	NM_006651:	NM_006651:
10815	CPLX1	complexin 1	-0.73	AACGTTAGACTGCAATACTAA	NM_006651:	NM_006651:
10814	CPLX2	complexin 2	-2.08	CAGATAGGTAGCAGAGACCAA	NM_001008220:	NM_006650:NM_001008220:
10814	CPLX2	complexin 2	-1.87	CAGGGTGCTTCAGATGAGCAA	NM_001008220:	NM_006650:NM_001008220:
1368	CPM (carboxy	carboxypeptidase M	-3.35	TAGGTCTTAATGCGTAGGCAA	NM_001874:	NM_001005502:NM_198320:NM_001874:
1368	CPM (carboxy	carboxypeptidase M	1.06	CAACTGGTTGTAGTTCATAAA	NM_001874:	NM_001005502:NM_198320:NM_001874:
1369	CPN1	carboxypeptidase N, polypeptide 1, 50kD	0.02	AAGACTTTAATTATCTCCATA	NM_001308:	NM_001308:
1369	CPN1	carboxypeptidase N, polypeptide 1, 50kD	-0.10	CAAGGGAATGCAAGACTTTAA	NM_001308:	NM_001308:
131034	CPNE4	copine IV	-0.10	AATGTTGATAGACGAAATATA	NM_130808:	NM_130808:
131034	CPNE4	copine IV	0.49	CACCAAGGAGGCATCGCAATA	NM_130808:	NM_130808:
130749	CPO	carboxypeptidase O	0.10	CTGGATGATGTGTATGCGAAA	NM_173077:	NM_173077:
130749	CPO	carboxypeptidase O	-2.49	CAGCAAATGCATTGAAAGCAA	NM_173077:	NM_173077:
1371	CPOX	coproporphyrinogen oxidase	0.44	ATCCCTGAATTCTGATACTTA	NM_000097:	NM_000097:
1371	CPOX	coproporphyrinogen oxidase	0.42	CCAAGTATTGAGATAAGGGAA	NM_000097:	NM_000097:
1373	CPS1 (carbar	carbamoyl-phosphate synthetase 1, mitochondrial	-2.99	CAGGCAGTACAGTGCTGGAAA	NM_001875:	NM_001875:
1373	CPS1 (carbar	carbamoyl-phosphate synthetase 1, mitochondrial	-0.36	TACGGATGTGCCACCCATCTA	NM_001875:	NM_001875:
1374	CPT1A	carnitine palmitoyltransferase 1A (liver)	0.86	CAGCAAGCACATCGTCGTGTA	NM_001876:	NM_001031847:NM_001876:
1374	CPT1A	carnitine palmitoyltransferase 1A (liver)	-0.02	CGGGAGGAAATCAAACCAATT	NM_001876:	NM_001031847:NM_001876:
126129	CPT1C	carnitine palmitoyltransferase 1C	0.11	CCGGTTCAGAGGGTCAGGGAA	NM_152359:	NM_152359:
126129	CPT1C	carnitine palmitoyltransferase 1C	-1.13	ATGGTGTTTCTTATATCTTCA	NM_152359:	NM_152359:
1376	CPT2	carnitine palmitoyltransferase II	0.21	TGGGACTAGATCACAACTGAA	NM_000098:	NM_000098:
1376	CPT2	carnitine palmitoyltransferase II	0.02	CAGCTACAGGCTTGAGCTTTA	NM_000098:	NM_000098:
54504	CPVL	carboxypeptidase, vitellogenic-like	1.01	CACCGTGAATAAGACTTACAA	NM_019029:	NM_031311:NM_019029:
54504	CPVL	carboxypeptidase, vitellogenic-like	-0.20	CGGGATTTATACAGTGCACTA	NM_019029:	NM_031311:NM_019029:
56265	CPXM	carboxypeptidase X (M14 family)	-0.11	GAGCATCGATCTTAACCATAA	NM_019609:	NM_019609:
56265	CPXM	carboxypeptidase X (M14 family)	-0.32	CAACCAGAGCATCGATCTTAA	NM_019609:	NM_019609:
119587	CPXM2	carboxypeptidase X (M14 family), member 2	0.52	CAGGTTCATCGTGGCATTAAA	NM_198148:	NM_198148:
119587	CPXM2	carboxypeptidase X (M14 family), member 2	-0.01	TCCAGATTAGGCTAAATGTAA	NM_198148:	NM_198148:
8532	CPZ	carboxypeptidase Z	0.12	TACGCCAAAGTCATCAAGAAA	NM_003652:	NM_001014447:NM_001014448:NM_003652:
8532	CPZ	carboxypeptidase Z	-5.26	CCGGATCTCAGTCAAAGGCAT	NM_003652:	NM_001014447:NM_001014448:NM_003652:
1378	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	-0.67	CTGGAGCCAATTGGATCATTA	NM_000573:	NM_000651:NM_000573:
1378	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	-1.90	CTGCATGGTGAGCATACCCTA	NM_000573:	NM_000651:NM_000573:
1379	CR1L	complement component (3b/4b) receptor 1-like	1.63	CAGTGTGTGAACGTAAATCAT	XM_114735:	XM_114735:
1379	CR1L	complement component (3b/4b) receptor 1-like	0.46	AAGGACAAGTGCAAACGTAAA	XM_114735:	XM_114735:
1380	CR2	complement component (3d/Epstein Barr virus) receptor 2	0.60	CACGCAATTATTATACAGATA	NM_001877:	NM_001877:NM_001006658:
1380	CR2	complement component (3d/Epstein Barr virus) receptor 2	0.22	TACCTTATACGTGATATCAAA	NM_001877:	NM_001877:NM_001006658:
1382	CRABP2	cellular retinoic acid binding protein 2	1.65	TAGCCTATACAGTTTAGAATA	NM_001878:	NM_001878:
1382	CRABP2	cellular retinoic acid binding protein 2	0.04	CCCTGTAGCCTATACAGTTTA	NM_001878:	NM_001878:
8738	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	-0.05	AGGCAGGTGTCTCATATGTAA	NM_003805:	NM_003805:
8738	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	-0.39	CAGGGTTTCCACTAGACATTA	NM_003805:	NM_003805:
57585	CRAMP1L	Crm, cramped-like (Drosophila)	1.04	AAGGGCCACCACTGTACGTTA	NM_020825:	NM_020825:
57585	CRAMP1L	Crm, cramped-like (Drosophila)	-5.66	CCCGACAACCTTGCCACCCAA	NM_020825:	NM_020825:
1384	CRAT	carnitine acetyltransferase	0.28	CTGTATGATATTAATGTGGAA	NM_000755:	NM_000755:NM_144782:NM_004003:
1384	CRAT	carnitine acetyltransferase	1.32	CGCCCTGCTGTATGATATTAA	NM_000755:	NM_000755:NM_144782:NM_004003:

23418	CRB1	crumbs homolog 1 (Drosophila)	-2.66	CTGCCATATGTTTACATGGAA	NM_012076:	NM_201253:NM_012076:
23418	CRB1	crumbs homolog 1 (Drosophila)	-1.94	CTCTCCCAAATTAGTAGTAAA	NM_012076:	NM_201253:NM_012076:
1385	CREB1	cAMP responsive element binding protein 1	0.53	AGGGCAGTTGTTGCTTCTTAA	NM_004379:	NM_004379:NM_134442:
1385	CREB1	cAMP responsive element binding protein 1	-2.38	CCGCATGCATAAAGTAAGTAA	NM_004379:	NM_004379:NM_134442:
1387	CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	1.05	AACGGAGGTCGCGTTTACATA	NM_004380:	NM_004380:
1387	CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	0.38	CCCGATCCTGGTGAATCCAAA	NM_004380:	NM_004380:
79174	CRELD2	cysteine-rich with EGF-like domains 2	1.15	CCGGACTTACCCTTTAAATTA	NM_024324:	NM_024324:
79174	CRELD2	cysteine-rich with EGF-like domains 2	-0.02	AAGAGCGAATATCCTGACTTA	NM_024324:	NM_024324:
1390	CREM	cAMP responsive element modulator	-0.43	TGGGATCGCATTGCATACCTT	NM_183060:	NM_182770:NM_183013:NM_182771:NM_183060:NM_182772:NM_182850:NM_182853:NM_182718:NM_182717:NM_181571:NM_182719:NM_182720:NM_182721:NM_182722:NM_182723:NM_182724:NM_182725:NM_183011:NM_182769:NM_183012:
1390	CREM	cAMP responsive element modulator	0.57	TCCCAGCATGATGGAAGTATA	NM_183060:	NM_183013:NM_183060:NM_181571:NM_001881:NM_183011:NM_183012:
1392	CRH	corticotropin releasing hormone	0.66	AAGAGAATGTTGAATACTTAT	NM_000756:	NM_000756:
1392	CRH	corticotropin releasing hormone	0.09	CAGTTTGGTTGTGTAAGAGAA	NM_000756:	NM_000756:
1394	CRHR1	corticotropin releasing hormone receptor 1	1.35	CAGGTTGGTGACAGCCGCCTA	NM_004382:	NM_004382:
1394	CRHR1	corticotropin releasing hormone receptor 1	-0.07	GCGGGTGGCTGGTATAAATAA	NM_004382:	NM_004382:
1395	CRHR2	corticotropin releasing hormone receptor 2	-0.57	ACGGATCAGCTTCCACAGCAT	NM_001883:	NM_001883:
1395	CRHR2	corticotropin releasing hormone receptor 2	-4.00	CACGGCCATTGTCATGACCTA	NM_001883:	NM_001883:
163126	CRI2	CREBBP/EP300 inhibitor 2	-0.03	TAAGATGTTAACGCTGAGTTA	NM_153232:	NM_153232:
163126	CRI2	CREBBP/EP300 inhibitor 2	-2.81	GTCGAAAGCATTATAACTGTA	NM_153232:	NM_153232:
51232	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	0.08	GACGACTAAATCTGCTCTAAA	NM_016441:	NM_016441:
51232	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.24	CAGGCAGACAATTTCTACCAA	NM_016441:	NM_016441:
1398	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	-4.69	CAGCAGCTAACTAGAGTCCTA	NM_005206:	NM_005206:NM_016823:
1398	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	0.99	CAGGATGTACCGAGCACTTTA	NM_005206:	NM_005206:NM_016823:
1399	CRKL (v-crk s	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	0.46	AAGGAAACAAATTACGTACTA	NM_005207:	NM_005207:
1399	CRKL (v-crk s	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-0.09	TAGTTTATCATTAACCACTTA	NM_005207:	NM_005207:
51755	CRKRS	Cdc2-related kinase, arginine/serine-rich	0.26	ACCGGATATCGGGAAGTTCAA	NM_016507:	NM_016507:
51755	CRKRS	Cdc2-related kinase, arginine/serine-rich	0.68	ATCGGGATATTAAGTGTTCTA	NM_016507:	NM_016507:
9244	CRLF1	cytokine receptor-like factor 1	-1.79	AACACCAACTACTCCCTCAAG	NM_004750:	NM_004750:
9244	CRLF1	cytokine receptor-like factor 1	-1.16	AACGCTGGATATCCTGGATGT	NM_004750:	NM_004750:
64109	CRLF2	cytokine receptor-like factor 2	-0.70	CAGGATCCACGTTGACATTTA	NM_022148:	NM_022148:
64109	CRLF2	cytokine receptor-like factor 2	0.30	CACATGAGTCTCTGTGTTCAA	NM_022148:	NM_022148:
51379	CRLF3	cytokine receptor-like factor 3	0.08	CTGGTTGATGTGCCTTGTTTA	NM_015986:	NM_015986:
51379	CRLF3	cytokine receptor-like factor 3	2.16	TTCGAGTAACTATAAGTTCAA	NM_015986:	NM_015986:
54677	CROT	carnitine O-octanoyltransferase	-0.41	TACCCTCTATTACACACATAA	NM_021151:	NM_021151:
54677	CROT	carnitine O-octanoyltransferase	1.66	AAGGGTATGAATTACATTATT	NM_021151:	NM_021151:
9282	CRSP2	cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa	-5.48	CACGACAAGGTGAATGCACAA	NM_004229:	NM_004229:
9282	CRSP2	cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa	-2.11	CACGTTTACCTGACATATGAA	NM_004229:	NM_004229:
9439	CRSP3	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa	0.17	AAGGGTGTTCGAGATCTCTTA	NM_015979:	NM_015979:NM_004830:
9439	CRSP3	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa	0.67	CCGCGCATTTCTCAAACGAAA	NM_015979:	NM_015979:NM_004830:
9440	CRSP6	cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa	0.24	CAGCCTACTCTAAATTATTGA	NM_004268:	NM_004268:
9440	CRSP6	cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa	-8.30	CAGGTACATGCAGTTCAGCAA	NM_004268:	NM_004268:
9441	CRSP7	cofactor required for Sp1 transcriptional activation, subunit 7, 70kDa	-0.17	ATCAACGACGTCCGCAAGAAA	NM_004831:	NM_004831:
9441	CRSP7	cofactor required for Sp1 transcriptional activation, subunit 7, 70kDa	-2.85	CAGGAGCATCCATGACCTGAA	NM_004831:	NM_004831:
9443	CRSP9	cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa	-0.66	AGGCAGTAATTTCGCTGTATA	NM_004270:	NM_004270:
9443	CRSP9	cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa	0.28	ATCAAGGAATATACGGATGAA	NM_004270:	NM_004270:
1406	CRX	cone-rod homeobox	1.79	CACAGAGTGAAACCAATTAAA	NM_000554:	NM_000554:
1406	CRX	cone-rod homeobox	-0.54	CGGGATGGCATTCCTGAGAAA	NM_000554:	NM_000554:
1407	CRY1	cryptochrome 1 (photolyase-like)	-1.88	ATCAGCAGCTTTCACGATATA	NM_004075:	NM_004075:
1407	CRY1	cryptochrome 1 (photolyase-like)	-2.57	CTGTTTGTGATTCGTGGACAA	NM_004075:	NM_004075:
1408	CRY2	cryptochrome 2 (photolyase-like)	0.74	CCGGCTTAACATTGAACGAAT	NM_021117:	NM_021117:
1408	CRY2	cryptochrome 2 (photolyase-like)	1.05	GAGGCCATAGACAGATCTAAA	NM_021117:	NM_021117:
1408	CRY2	cryptochrome 2 (photolyase-like)	1.00	CCGGCTTAACATTGAACGAAT	NM_021117:	NM_021117:
1408	CRY2	cryptochrome 2 (photolyase-like)	0.45	GAGGCCATAGACAGATCTAAA	NM_021117:	NM_021117:
1418	CRYGA	crystallin, gamma A	0.68	CCCTATCATACTAGATGCTAA	NM_014617:	NM_014617:
1418	CRYGA	crystallin, gamma A	-1.20	CCCTTTGTCCCTATCATACTA	NM_014617:	NM_014617:
1419	CRYGB	crystallin, gamma B	-0.94	AAGATCTACGACAGAGATGAA	NM_005210:	NM_005210:
1419	CRYGB	crystallin, gamma B	0.83	TAGACGAGTCATGGATTTGTA	NM_005210:	NM_005210:
1420	CRYGC	crystallin, gamma C	-0.86	CCCAACTACCAAGGTCAACAA	NM_020989:	NM_020989:
1420	CRYGC	crystallin, gamma C	0.31	GCGGAGAGTGGTGGATTTGTA	NM_020989:	NM_020989:
1421	CRYGD	crystallin, gamma D	0.22	ACCGCTTCCGCTTCAATGAAA	NM_006891:	NM_006891:
1421	CRYGD	crystallin, gamma D	1.90	TTGTTGTTTCTTAATTTGGAA	NM_006891:	NM_006891:
1429	CRYZ (crystal	crystallin, zeta (quinone reductase)	0.81	AAGCCTACTTACCTTTATAAA	NM_001889:	NM_001889:
1429	CRYZ (crystal	crystallin, zeta (quinone reductase)	0.01	CAAGCCTACTTACCTTTATAA	NM_001889:	NM_001889:
9946	CRYZL1	crystallin, zeta (quinone reductase)-like 1	-0.78	CACGTTTCTCTGCTAAGACAA	NM_005111:	NM_005111:NM_145858:
9946	CRYZL1	crystallin, zeta (quinone reductase)-like 1	0.00	TCGGATGAACATATTCCAGTA	NM_005111:	NM_005111:NM_145858:
51380	CSAD	cysteine sulfinic acid decarboxylase	-0.27	CTCCAACATGTATGCTGTAAA	NM_015989:	NM_015989:
51380	CSAD	cysteine sulfinic acid decarboxylase	-1.11	ACCAGCCAGTACACATATGAA	NM_015989:	NM_015989:
1434	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.16	CACGGTTTGGATAATCTTAAA	NM_001316:	NM_177436:NM_001316:
1434	CSE1L	CSE1 chromosome segregation 1-like (yeast)	-3.55	CAGGATAATGTTATCAAAGTA	NM_001316:	NM_177436:NM_001316:
1435	CSF1	colony stimulating factor 1 (macrophage)	-0.18	AAGAATGTCTTTAATGAAACA	NM_000757:	NM_000757:NM_172210:NM_172211:NM_172212:
1435	CSF1	colony stimulating factor 1 (macrophage)	-0.67	CACCATGCGCTTCAGAGATAA	NM_000757:	NM_000757:NM_172210:NM_172211:NM_172212:
1436	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarco	-1.93	ACCCTCAACCTCGATCAAGTA	NM_005211:	NM_005211:
1436	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarco	0.59	ATGAGCCAAGTGGCAGCTAAA	NM_005211:	NM_005211:
1437	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	0.05	ACCCAGATTATCACCTTTGAA	NM_000758:	NM_000758:
1437	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	0.42	GACAGAAATCAGTAATATTTA	NM_000758:	NM_000758:
1438	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-m	-0.06	TCGCAATTACTTTCTGGTTAA	NM_006140:	NM_172249:NM_172247:NM_172248:NM_172245:NM_172246:NM_006140:
1438	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-m	0.90	CTCGCAATTACTTTCTGGTTA	NM_006140:	NM_172249:NM_172247:NM_172248:NM_172245:NM_172246:NM_006140:
1439	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-ma	-2.46	CAGTCATTTCTGCAAAGCCAA	NM_000395:	NM_000395:
1439	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-ma	0.69	CCCGTCATTCAGCTCTTCAAA	NM_000395:	NM_000395:
1440	CSF3	colony stimulating factor 3 (granulocyte)	0.58	ACTGAACTTCAGGATAATAAA	NM_000759:	NM_000759:NM_172219:NM_172220:
1440	CSF3	colony stimulating factor 3 (granulocyte)	-1.52	CACTGTCACATTGTAACTGAA	NM_000759:	NM_000759:NM_172219:NM_172220:
1441	CSF3R	colony stimulating factor 3 receptor (granulocyte)	0.00	CAGGCGATCTGCATACTTTAA	NM_172313:	NM_000760:NM_156038:NM_156039:NM_172313:
1441	CSF3R	colony stimulating factor 3 receptor (granulocyte)	-0.01	CCAGGCGATCTGCATACTTTA	NM_172313:	NM_000760:NM_156038:NM_156039:NM_172313:
1445	CSK	c-src tyrosine kinase	-1.76	CCGGTACAGAATGTATTGCCA	NM_004383:	NM_004383:
1445	CSK	c-src tyrosine kinase	-0.18	TACGCGCCTCATTAAACCAAA	NM_004383:	NM_004383:
64478	CSMD1	CUB and Sushi multiple domains 1	-3.91	CAGGACTGATTCATAGCCATA	NM_033225:	NM_033225:
64478	CSMD1	CUB and Sushi multiple domains 1	-1.04	CAGGAAGTCGAATTCACCTAA	NM_033225:	NM_033225:
114788	CSMD3	CUB and Sushi multiple domains 3	-0.34	CACGGTTTGCACAATGGTATA	NM_052900:	NM_052900:NM_198123:NM_198124:

114788	CSMD3	CUB and Sushi multiple domains 3	-0.88	CAGGTGTATGATGGACCAAAT	NM_052900:	NM_052900:NM_198123:NM_198124:
1452	CSNK1A1	casein kinase 1, alpha 1	-2.32	AGGGCTAAAGGCTGCAACAAA	NM_001892:	NM_001892:NM_001025105:
1452	CSNK1A1	casein kinase 1, alpha 1	-0.04	CAAGAGTAACATGAAAGGTTT	NM_001892:	NM_001892:NM_001025105:
122011	CSNK1A1L	casein kinase 1, alpha 1-like	0.16	CAAGAATAATGTGAAAGATAA	NM_145203:	NM_145203:
122011	CSNK1A1L	casein kinase 1, alpha 1-like	-0.08	CAGATTATCTTTAGAATTCCA	NM_145203:	NM_145203:
1453	CSNK1D	casein kinase 1, delta	-6.00	CCGGTCTAGGATCGAAATGTT	NM_001893:	NM_139062:NM_001893:
1453	CSNK1D	casein kinase 1, delta	-1.86	CTCCCTGACGATTCCACTGTA	NM_001893:	NM_139062:NM_001893:
1454	CSNK1E	casein kinase 1, epsilon	-2.15	GAGCTTTATCGTGGTTGTTAA	NM_001894:	NM_152221:NM_001894:
1454	CSNK1E	casein kinase 1, epsilon	-3.85	GTGGTTGTTAATTTGAAGTAA	NM_001894:	NM_152221:NM_001894:
53944	CSNK1G1 (ca	casein kinase 1, gamma 1	0.15	ATGGACCATCCTAGTAGGGAA	NM_022048:	NM_022048:NM_001011664:
53944	CSNK1G1 (ca	casein kinase 1, gamma 1	-1.05	CCGGCAGACCAATACCTCATA	NM_022048:	NM_022048:
1455	CSNK1G2	casein kinase 1, gamma 2	-0.19	AAGAATCTCTATACAAATGAA	NM_001319:	NM_001319:
1455	CSNK1G2	casein kinase 1, gamma 2	0.95	TAGGAAAGAATCTCTATACAA	NM_001319:	NM_001319:
1456	CSNK1G3 (ca	casein kinase 1, gamma 3	-0.49	CAACATATCTTCGTTATGTAA	NM_004384:	NM_001031812:NM_004384:
1456	CSNK1G3 (ca	casein kinase 1, gamma 3	0.57	TACCGCAAACTTGATATGGAA	NM_004384:	NM_001031812:NM_004384:
1457	CSNK2A1	casein kinase 2, alpha 1 polypeptide	-0.43	CTGGTCGCTTACATCACTTTA	NM_001895:	NM_001895:NM_177560:NM_177559:
1459	CSNK2A2	casein kinase 2, alpha prime polypeptide	-6.29	CAGGAGTACAATGTTCGTGTA	NM_001896:	NM_001896:
1459	CSNK2A2	casein kinase 2, alpha prime polypeptide	-0.73	CTGGGACAACATTCACGGAAA	NM_001896:	NM_001896:
1460	CSNK2B	casein kinase 2, beta polypeptide	-2.31	CAGGTCCCTCACTACCGACAA	NM_001320:	NM_001320:
1460	CSNK2B	casein kinase 2, beta polypeptide	-1.59	GTGGTGGGAATATGAAATAAA	NM_001320:	NM_001320:
9126	CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	-0.13	ATGGAGGATATCGAACGCCAA	NM_005445:	NM_005445:
9126	CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	-0.83	GAGGACTAAGTTGGAGCTTAA	NM_005445:	NM_005445:
1471	CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	-0.31	AAAGGAAAGCATTCTGCTCTT	NM_000099:	NM_000099:
1471	CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	-2.99	AAAAGCCAGCAACGACATGTA	NM_000099:	NM_000099:
9150	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) ph	-4.45	CCGGCTGTACGCACACACCAT	NM_004715:	NM_004715:NM_048368:
9150	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) ph	-3.90	CTCCATGGTTTGCATTATTGA	NM_004715:	NM_004715:NM_048368:
10106	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sm	-0.52	CCCGGAAACAGCGGGAAGTAA	NM_005730:	NM_005730:
10106	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sm	0.43	TACGATCAGCGTGACAGAGTA	NM_005730:	NM_005730:
10217	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sm	0.15	CCAGTGCAACGTCAGCTTAAA	NM_005808:	NM_005808:NM_001008392:
10217	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sm	-0.96	TACGCCCAACTCTTTAGCCAA	NM_005808:	NM_001008392:NM_005808:
1490	CTGF	connective tissue growth factor	-0.24	AACACCATAGGTAGAATGTAA	NM_001901:	NM_001901:
1490	CTGF	connective tissue growth factor	0.41	CTGATCGTTCAAAGCATGAAA	NM_001901:	NM_001901:
1493	CTLA4	cytotoxic T-lymphocyte-associated protein 4	-0.84	CAGCATTATGATGTGGGTCAA	NM_005214:	NM_005214:NM_001037631:
1493	CTLA4	cytotoxic T-lymphocyte-associated protein 4	0.68	AAGCATCACTTGGGATTAATA	NM_005214:	NM_005214:NM_001037631:
1495	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	-2.23	CACCCTGATGTCGCAGCCTAT	NM_001903:	NM_001903:
1495	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	0.38	GCGAATTGTGGCAGAGTGTAA	NM_001903:	NM_001903:
1496	CTNNA2	catenin (cadherin-associated protein), alpha 2	1.90	CCCATGAATTGAACAATTTAA	NM_004389:	NM_004389:
1496	CTNNA2	catenin (cadherin-associated protein), alpha 2	0.13	TACCATTGTATTCACTAACTA	NM_004389:	NM_004389:
8727	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	0.18	AAGCTTGGGAATCCCAAATTA	NM_003798:	NM_003798:
8727	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	1.12	ACGCTTATTAATCATAAAGAT	NM_003798:	NM_003798:
1499	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	1.00	ATGGGTAGGGTAAATCAGTAA	NM_001904:	NM_001904:
1499	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	0.32	CTCGGGATGTTCACAACCGAA	NM_001904:	NM_001904:
56998	CTNNBIP1	catenin, beta interacting protein 1	0.90	CACCTGTTTGCCTGAAGTTAA	NM_020248:	NM_001012329:NM_020248:
56998	CTNNBIP1	catenin, beta interacting protein 1	-0.49	TGCGTTTATAATTGGCTTAAA	NM_020248:	NM_001012329:NM_020248:
1500	CTNND1	catenin (cadherin-associated protein), delta 1	0.01	CTGGTGTTGATCAACAAATCA	NM_001331:	NM_001331:
1500	CTNND1	catenin (cadherin-associated protein), delta 1	1.84	TGGGAGCTTATTGCTAATTTA	NM_001331:	NM_001331:
1501	CTNND2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-relat	0.44	TAACGTTAGAATAGTGGTTAA	NM_001332:	NM_001332:
1501	CTNND2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-relat	-0.05	AAGCGCGTTGTGTATATTACA	NM_001332:	NM_001332:
1497	CTNS	cystinosis, nephropathic	-5.98	CACCTACTTGAGACTCACCAA	NM_004937:	NM_004937:NM_001031681:
1497	CTNS	cystinosis, nephropathic	0.93	CGCCATTAGCATCATAAACCA	NM_004937:	NM_004937:NM_001031681:
11330	CTRC	chymotrypsin C (caldecrin)	0.14	ATCGACTGGATCAACGAGAAA	NM_007272:	NM_007272:
11330	CTRC	chymotrypsin C (caldecrin)	-2.31	CCGGGTGTCCGCCTACATCGA	NM_007272:	NM_007272:
1506	CTRL	chymotrypsin-like	-0.01	CAACCAGGTCATAGCCTACAA	NM_001907:	NM_001907:
1506	CTRL	chymotrypsin-like	0.37	CACACCCTAGCTGGAACTCTA	NM_001907:	NM_001907:
1508	CTSB	cathepsin B	1.31	CAGCATGATTCTTTAATAGAA	NM_001908:	NM_147781:NM_147782:NM_147783:NM_147780:NM_001908:
1508	CTSB	cathepsin B	0.13	CAGGATCACTGTGGAATCGAA	NM_001908:	NM_147781:NM_147782:NM_147783:NM_147780:NM_001908:
1075	CTSC	cathepsin C	0.09	ATGATCTGCATCAGTTGTAAA	NM_001814:	NM_001814:
1075	CTSC	cathepsin C	-2.24	CTGCAATGAAGCCCTGATGAA	NM_001814:	NM_001814:
1509	CTSD	cathepsin D (lysosomal aspartyl peptidase)	-1.18	CCCAGAGGACTACACGCTCAA	NM_001909:	NM_001909:
1509	CTSD	cathepsin D (lysosomal aspartyl peptidase)	0.17	TCCCGAGGTGCTCAAGAACTA	NM_001909:	NM_001909:
1510	CTSE (cathep	cathepsin E	-3.37	CTGGCAGATTGCACTGGATAA	NM_001910:	NM_001910:NM_148964:
1510	CTSE (cathep	cathepsin E	0.23	CCCAGTCACCAAGCAAGCTTA	NM_001910:	NM_001910:NM_148964:
8722	CTSF	cathepsin F	-0.86	CCCAATCTCCGTGGCCATCAA	NM_003793:	NM_003793:
8722	CTSF	cathepsin F	0.04	CACCTTTGTTGAATTGTGGTA	NM_003793:	NM_003793:
1511	CTSG	cathepsin G	0.68	CCACAGAGTATAAATAACCAA	NM_001911:	NM_001911:
1511	CTSG	cathepsin G	-1.44	CACAGTGTTGCCAGAGCCTTA	NM_001911:	NM_001911:
1512	CTSH	cathepsin H	1.01	ATGGATGTCTAAGCACCGTAA	NM_004390:	NM_004390:NM_148979:
1512	CTSH	cathepsin H	-0.51	CACCCGTGTCTATGACGCAAA	NM_004390:	NM_004390:NM_148979:
1513	CTSK	cathepsin K (pycnodysostosis)	0.01	CACGGGACTAGTTAGCTTTAA	NM_000396:	NM_000396:
1513	CTSK	cathepsin K (pycnodysostosis)	-2.30	AGGGCTGATGCTGTACAGGTA	NM_000396:	NM_000396:
1514	CTSL	cathepsin L	0.72	TAGGTTTATATTATTGATTCA	NM_001912:	NM_145918:NM_001912:
1514	CTSL	cathepsin L	-0.23	CACTGGTAAATGTTACCTCTA	NM_001912:	NM_145918:NM_001912:
1515	CTSL2	cathepsin L2	0.32	AAGACTCATTGCTTAATTCTA	NM_001333:	NM_001333:
1515	CTSL2	cathepsin L2	1.14	AACGCTTATTGTGTAAGATAA	NM_001333:	NM_001333:
1519	CTSO	cathepsin O	0.29	TCGGAAGGATTTCAAACACCA	NM_001334:	NM_001334:
1519	CTSO	cathepsin O	0.99	CACAAGAATGGCCAACCTAAA	NM_001334:	NM_001334:
1520	CTSS	cathepsin S	1.67	AGGAATCTAATTATATCGAAA	NM_004079:	NM_004079:
1520	CTSS	cathepsin S	1.56	TGGGATAATGTCATTAATATA	NM_004079:	NM_004079:
1521	CTSW	cathepsin W (lymphopain)	-1.09	CACCGTGACCATCAACATGAA	NM_001335:	NM_001335:
1521	CTSW	cathepsin W (lymphopain)	-1.57	CGCGTTCATAACTGTCCTCAA	NM_001335:	NM_001335:
1522	CTSZ	cathepsin Z	1.13	CACCATTCTTATGTCACTTTA	NM_001336:	NM_001336:
1522	CTSZ	cathepsin Z	-2.33	CAGCACCTATAAGGATGGGAA	NM_001336:	NM_001336:
2017	CTTN	cortactin	-1.04	ATGCAACTTATTGTATCTGAA	NM_005231:	NM_005231:NM_138565:
2017	CTTN	cortactin	-0.49	CACCAGGAGCATATCAACATA	NM_005231:	NM_005231:NM_138565:
8029	CUBN	cubilin (intrinsic factor-cobalamin receptor)	-1.70	CCGGTTAGAATCCATGGACAA	NM_001081:	NM_001081:
8029	CUBN	cubilin (intrinsic factor-cobalamin receptor)	0.26	CAGCTGCAATTTGAAGATCGA	NM_001081:	NM_001081:
404093	CUEDC1	CUE domain containing 1	0.33	CCGGGCGTTCCTATGGTCAAA	NM_017949:	NM_017949:
404093	CUEDC1	CUE domain containing 1	-3.76	TACGAATCCCAGAAATCTAAA	NM_017949:	NM_017949:
10658	CUGBP1	CUG triplet repeat, RNA binding protein 1	-2.97	CAGGGTCCTCACCTAGCTCTA	NM_006560:	NM_198700:NM_006560:NM_001025596:
10658	CUGBP1	CUG triplet repeat, RNA binding protein 1	1.31	CGGGAACTCTTCGAACAGTAT	NM_006560:	NM_198700:NM_006560:NM_001025596:
8454	CUL1 (cullin 1	cullin 1	0.28	AACGTAGTTATCAGCGATTCA	NM_003592:	NM_003592:
8454	CUL1 (cullin 1	cullin 1	0.25	ACCGACAGCACTCAAATTAAA	NM_003592:	NM_003592:
8453	CUL2	cullin 2	0.39	CGGCACAATGCCCTTATTCAA	NM_003591:	NM_003591:
8453	CUL2	cullin 2	-0.07	TACATCGGATGTATACAGATA	NM_003591:	NM_003591:
8452	CUL3 (cullin 3	cullin 3	-0.10	AACAACTTTCTTCAAACGCTA	NM_003590:	NM_003590:
8452	CUL3 (cullin 3	cullin 3	0.98	GACGTTAAGAATGGCAGATAA	NM_003590:	NM_003590:
8065	CUL5	cullin 5	-2.41	CAGCTGGTTATTGGAGTAAGA	NM_003478:	NM_003478:

8065	CUL5	cullin 5	-0.15	CAGGTTTGAATCAGTCACCTA	NM_003478:	NM_003478:
6376	CX3CL1	chemokine (C-X3-C motif) ligand 1	-1.85	CACCATCAAGCCACCAACATA	NM_002996:	NM_002996:
6376	CX3CL1	chemokine (C-X3-C motif) ligand 1	-0.19	CGGAGCTGTGGTAGTAATTCA	NM_002996:	NM_002996:
1524	CX3CR1	chemokine (C-X3-C motif) receptor 1	0.36	TAGAGTTGCAATCGTAATGTA	NM_001337:	NM_001337:
1524	CX3CR1	chemokine (C-X3-C motif) receptor 1	-0.61	TCAGATGTGGTAACTGTTAAA	NM_001337:	NM_001337:
1525	CXADR	coxsackie virus and adenovirus receptor	0.07	CAGGAACTGTACGGAATATAT	NM_001338:	NM_001338:
1525	CXADR	coxsackie virus and adenovirus receptor	-5.56	CAGGTAATAGGGACTTAGCAA	NM_001338:	NM_001338:
2919	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activi	1.29	TCAATCTGGATTCATATTTAA	NM_001511:	NM_001511:
2919	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activi	1.83	TCCAGTCATTATGTTAATATT	NM_001511:	NM_001511:
3627	CXCL10	chemokine (C-X-C motif) ligand 10	-0.88	CTGACTCTAAGTGGCATTCAA	NM_001565:	NM_001565:
3627	CXCL10	chemokine (C-X-C motif) ligand 10	-0.06	CAGGAAGGTAGAAATATCTGA	NM_001565:	NM_001565:
6373	CXCL11	chemokine (C-X-C motif) ligand 11	-0.62	AAGACTAGTTTAAAGAATCAA	NM_005409:	NM_005409:
6373	CXCL11	chemokine (C-X-C motif) ligand 11	0.58	CACGTTCTTACTTGTTGTATT	NM_005409:	NM_005409:
6387	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	-0.47	CTGAAGAACAACAACAGACAA	NM_000609:	NM_000609:NM_001033886:NM_199168:
6387	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	0.27	GTGCATTGACCCGAAGCTAAA	NM_000609:	NM_000609:NM_001033886:NM_199168:
10563	CXCL13	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	-0.95	ACGGAGGAGAATTAAGTCCTA	NM_006419:	NM_006419:
10563	CXCL13	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	-2.01	AAGGGTGATGTACACATGTAT	NM_006419:	NM_006419:
9547	CXCL14	chemokine (C-X-C motif) ligand 14	-0.04	CCGCATTGTACTGCTGTGTTA	NM_004887:	NM_004887:
9547	CXCL14	chemokine (C-X-C motif) ligand 14	-0.53	CCCAGTATATGCCGCATTGTA	NM_004887:	NM_004887:
58191	CXCL16	chemokine (C-X-C motif) ligand 16	1.25	CAGCCTACACGTATTTGTTAA	NM_022059:	NM_022059:
58191	CXCL16	chemokine (C-X-C motif) ligand 16	0.25	CACGTATTTGTTAATATCTAA	NM_022059:	NM_022059:
2920	CXCL2	chemokine (C-X-C motif) ligand 2	-0.02	CAGAGAGGTTTCGATATTTAT	NM_002089:	NM_002089:
2920	CXCL2	chemokine (C-X-C motif) ligand 2	0.02	TCCCATTATATTTATTGTTTA	NM_002089:	NM_002089:
2921	CXCL3	chemokine (C-X-C motif) ligand 3	0.87	AGGGCATAATGCCTTGTTTAA	NM_002090:	NM_002090:
2921	CXCL3	chemokine (C-X-C motif) ligand 3	-0.02	TACAAATGACATGATAATAAA	NM_002090:	NM_002090:
6374	CXCL5	chemokine (C-X-C motif) ligand 5	0.61	CAGAGAGAGCTTGGAATGTTA	NM_002994:	NM_002994:
6374	CXCL5	chemokine (C-X-C motif) ligand 5	0.18	CAGCATTTATGGTAGAATATA	NM_002994:	NM_002994:
6372	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	0.49	ACGCGTTACGCTGAGAGTAAA	NM_002993:	NM_002993:
6372	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	-1.00	CAAGTTTGTCTGGACCCGGAA	NM_002993:	NM_002993:
4283	CXCL9	chemokine (C-X-C motif) ligand 9	-2.54	CAGGTAGACAGTATATAACTA	NM_002416:	NM_002416:
4283	CXCL9	chemokine (C-X-C motif) ligand 9	-3.46	CCACCCGAACGTCTTATCTAA	NM_002416:	NM_002416:
2833	CXCR3	chemokine (C-X-C motif) receptor 3	-0.03	AACAAGATCGTCAGGACCAAA	NM_001504:	NM_001504:
2833	CXCR3	chemokine (C-X-C motif) receptor 3	-1.44	ACGAGAGTGACTCGTGCTGTA	NM_001504:	NM_001504:
7852	CXCR4	chemokine (C-X-C motif) receptor 4	0.00	CAGCTGTTTATGCATAGATAA	NM_003467:	NM_001008540:NM_003467:
7852	CXCR4	chemokine (C-X-C motif) receptor 4	0.56	TCCAGCTAACACAGATGTAAA	NM_003467:	NM_001008540:NM_003467:
10663	CXCR6	chemokine (C-X-C motif) receptor 6	0.01	CAGGTCATGTGCAAGAGCCTA	NM_006564:	NM_006564:
10663	CXCR6	chemokine (C-X-C motif) receptor 6	-0.66	TCGTTTCATTGTAGTGGTTAA	NM_006564:	NM_006564:
80231	CXorf21	chromosome X open reading frame 21	-1.91	CTGGAAGTCATGTGTGAATCA	NM_025159:	NM_025159:
80231	CXorf21	chromosome X open reading frame 21	-0.08	TCGCATTTACTTAAACATGAA	NM_025159:	NM_025159:
256643	CXorf23 (chrc	chromosome X open reading frame 23	0.28	CAGGCTAAGTATCAGCGTTTA	NM_198279:	NM_198279:
256643	CXorf23 (chrc	chromosome X open reading frame 23	-0.01	TAGAGAGAACTTCACCAAGTA	NM_198279:	NM_198279:
79979	CXorf34	chromosome X open reading frame 34	1.01	CTGGATTCTTGAGGTAGTTAA	NM_024917:	NM_024917:
79979	CXorf34	chromosome X open reading frame 34	-0.34	CGCGGCTGACTTAACCTTAGA	NM_024917:	NM_024917:
30827	CXXC1	CXXC finger 1 (PHD domain)	-0.25	TGGCATGAAGCTGGCAGCCAA	NM_014593:	NM_014593:
30827	CXXC1	CXXC finger 1 (PHD domain)	1.04	TCGGCAGAAGCAGAAGCACAA	NM_014593:	NM_014593:
80319	CXXC4	CXXC finger 4	-1.43	CAGCAGTTGCAGGAACCGCAA	NM_025212:	NM_025212:
80319	CXXC4	CXXC finger 4	-1.78	TTCAAGGCATTTGGAAATGAA	NM_025212:	NM_025212:
11068	CYB561D2	cytochrome b-561 domain containing 2	-1.44	CACCAGCTTGGTCATTATGAA	NM_007022:	NM_007022:
11068	CYB561D2	cytochrome b-561 domain containing 2	-2.81	CAGGTGAGCAATGCCTACCTA	NM_007022:	NM_007022:
124936	CYB5D2	cytochrome b5 domain containing 2	0.68	TGGGCAAGGCTTCAAACTTAA	NM_144611:	NM_144611:
124936	CYB5D2	cytochrome b5 domain containing 2	0.80	ACTGGTTAGCATGACATTAAA	NM_144611:	NM_144611:
51706	CYB5R1	cytochrome b5 reductase 1	1.59	AATGATTTCTTCAGATCTCAA	NM_016243:	NM_016243:
51706	CYB5R1	cytochrome b5 reductase 1	-0.68	TAGTTCCTTGATAGCATCTTA	NM_016243:	NM_016243:
51700	CYB5R2	cytochrome b5 reductase 2	0.02	CCAGGGAATCTTGGAATCAGA	NM_016229:	NM_016229:NM_001001336:
51700	CYB5R2	cytochrome b5 reductase 2	-0.01	TCAGTATTTGGAGAACATGAA	NM_016229:	NM_016229:NM_001001336:
1727	CYB5R3	cytochrome b5 reductase 3	-1.40	CAGAGTCATTTATGAGCAGAA	NM_000398:	NM_007326:NM_000398:
1727	CYB5R3	cytochrome b5 reductase 3	0.08	CTGGAGGAACTCAGGAACAAA	NM_000398:	NM_007326:NM_000398:
51167	CYB5R4	cytochrome b5 reductase 4	-0.67	TCGATCATGTTTCCATGCAAA	NM_016230:	NM_016230:
51167	CYB5R4	cytochrome b5 reductase 4	0.14	AGGCTTCACACCAATGGTTAA	NM_016230:	NM_016230:
1535	CYBA (cytoch	cytochrome b-245, alpha polypeptide	1.36	TTTACCAGGAATTACTATGTT	NM_000101:	NM_000101:
1535	CYBA (cytoch	cytochrome b-245, alpha polypeptide	-0.29	CTTTGGTGCCTACTCCATTGT	NM_000101:	NM_000101:
1536	CYBB	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	-5.65	CAGGCTAAGGATACTAACCAA	NM_000397:	NM_000397:
1536	CYBB	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	1.01	CCAGATCATTAGGACATAATA	NM_000397:	NM_000397:
1537	CYC1 (cytoch	cytochrome c-1	-0.17	CCCATCATGGGAATAAATTAA	NM_001916:	NM_001916:
1537	CYC1 (cytoch	cytochrome c-1	-1.88	TACCATGTCCCAGATAGCCAA	NM_001916:	NM_001916:
54205	CYCS	cytochrome c, somatic	-1.71	ATGATACAGGAAACATATTAA	NM_018947:	NM_018947:
54205	CYCS	cytochrome c, somatic	0.58	CTCAACTAGAATAACACTTCA	NM_018947:	NM_018947:
1540	CYLD	cylindromatosis (turban tumor syndrome)	1.74	AAGGGTAGAACCTTTGCTAAA	NM_015247:	NM_015247:
1540	CYLD	cylindromatosis (turban tumor syndrome)	0.36	AAGGTTCATCCAGTCATAATA	NM_015247:	NM_015247:
1583	CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	-1.74	CTGGAGAACTTCAGAGTTGAA	NM_000781:	NM_000781:
1583	CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	0.97	TACTGGGAATTGAGACAGAAA	NM_000781:	NM_000781:
1584	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1	-1.09	CACCTTCAGAGCCATCAACTA	NM_000497:	NM_000497:NM_001026213:
1584	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1	-2.62	CAGGTGGAGACACTAACCCAA	NM_000497:	NM_000497:NM_001026213:
1585	CYP11B2	cytochrome P450, family 11, subfamily B, polypeptide 2	-0.67	CACTAGATCATGGGATCCTAA	NM_000498:	NM_000498:
1585	CYP11B2	cytochrome P450, family 11, subfamily B, polypeptide 2	-2.95	CAGAGATGGCTTCCTTGTTTA	NM_000498:	NM_000498:
1586	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	-3.18	CAGGCTGAGGGTAGCACCTAA	NM_000102:	NM_000102:
1586	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	-3.22	CCGGAGTGACTCTATCACCAA	NM_000102:	NM_000102:
1588	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	1.95	CACCACTTTACTTGTGTTATA	NM_000103:	NM_031226:NM_000103:
1588	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	0.84	CACCTTGGAATTCGCTTTCTA	NM_000103:	NM_031226:NM_000103:
1543	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	-0.07	AACAACTACCTGAGCTAAATA	NM_000499:	NM_000499:
1543	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	0.10	AACCATTGATTTAATGTAATA	NM_000499:	NM_000499:
1544	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	0.21	CAGCCTAACTTACATTCTTAA	NM_000761:	NM_000761:
1544	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	0.17	CCAGCCTAACTTACATTCTTA	NM_000761:	NM_000761:
1545	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	-0.76	CAGTGCATAGTTGTAGACAAA	NM_000104:	NM_000104:
1545	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	-0.08	AGGGCCCAATGAATTATTATA	NM_000104:	NM_000104:
57404	CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1	-0.93	CCAGGGATTACTCCAACTGAA	NM_020674:	NM_177538:NM_020674:
57404	CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1	-4.85	CAGAGTTGAGGTTTGCATATA	NM_020674:	NM_177538:NM_020674:
1589	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-2.13	AATCCTCAAGATGCAGCCTTT	NM_000500:	NM_000500:
1589	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-2.38	AAGGCAAGAACTCCAGAGCTC	NM_000500:	NM_000500:
1591	CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	0.23	TGCAATACTTATAAGACTTAA	NM_000782:	NM_000782:
1591	CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	0.79	AAGTTAGAGATCTGTTATATA	NM_000782:	NM_000782:
1592	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	-0.29	CAGCTTATCTAACATGTCATA	NM_000783:	NM_000783:NM_057157:
1592	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	-3.17	CACCGTGTATCCTGTGGACAA	NM_000783:	NM_000783:NM_057157:
56603	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	1.34	GCCCAGATGGCTATAATATTA	NM_019885:	NM_019885:
56603	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	-0.91	AAGACTTGTCAAAGCTTGCAA	NM_019885:	NM_019885:
340665	CYP26C1	cytochrome P450, family 26, subfamily C, polypeptide 1	-0.03	CTGGAGCGTGATGTATAGCAT	NM_183374:	NM_183374:
340665	CYP26C1	cytochrome P450, family 26, subfamily C, polypeptide 1	0.71	CACCTTCGAGCTCGACGGCTA	NM_183374:	NM_183374:
1593	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	-3.25	CCGCATTGTCCTGGTTCCCAA	NM_000784:	NM_000784:
1593	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	-3.87	CACGCTGACATGGGCCCTGTA	NM_000784:	NM_000784:

1594	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	0.34	CTGGTTTACGGTTTCTTATAA	NM_000785:	NM_000785:
1594	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	-1.53	AACCACCATAGTGAAGTGTGA	NM_000785:	NM_000785:
1553	CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	0.25	CTACAAAGAGTAGTAATAATA	NM_000766:	NM_000766:
1553	CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	0.08	TACAGTATGCTACAAAGAGTA	NM_000766:	NM_000766:
1549	CYP2A7	cytochrome P450, family 2, subfamily A, polypeptide 7	-2.46	CAGCTTCTTCTCCAACCCTCA	NM_000764:	NM_030589:NM_000764:
1549	CYP2A7	cytochrome P450, family 2, subfamily A, polypeptide 7	-0.86	CCTGATGATGAGCACGTTGAA	NM_000764:	NM_030589:NM_000764:
1555	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	0.18	TCAAATCTGCTGAGAATTAAA	NM_000767:	NM_000767:
1555	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	0.72	CCCATAAACAGAATCATACAA	NM_000767:	NM_000767:
1556	CYP2B7P1	cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	-1.17	TTCGAGTTCAGTGGTCTTGAA	NR_001278:	NR_001278:
1556	CYP2B7P1	cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	0.06	CTGCCAGAGTTTCTTACTCAT	NR_001278:	NR_001278:
1562	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	-0.66	CAAGATCCAATGAACATCCAA	NM_000772:	NM_000772:
1562	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	-0.13	CCGCAGTTGTCTTACTAAGAA	NM_000772:	NM_000772:
1557	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	0.02	CAGTCTGAATTCACTATTGAA	NM_000769:	NM_000769:
1557	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	-0.01	AACCCATAACAAATTACTTAA	NM_000769:	NM_000769:
1558	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	-0.02	AAGTCAGAATTCAATATTGAA	NM_000770:	NM_000770:NM_030878:
1558	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	-0.04	ACGAAGTTACATTAGGGAGAA	NM_000770:	NM_000770:NM_030878:
1559	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	0.83	TAGAGAAATATGATTTGTGTA	NM_000771:	NM_000771:
1559	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	0.96	TAGAGTATTAATATGTTATTA	NM_000771:	NM_000771:
1571	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	0.69	CTGGCTCCAGCTTTACAATAA	NM_000773:	NM_000773:
1571	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	-0.03	AAGGCTGATGTATTTGTTTAA	NM_000773:	NM_000773:
1572	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	-0.24	TCGCGGCTTCCTGATACCCAA	NM_000774:	NM_000774:
1572	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	0.57	CACCATTATCCGCCTTATCAA	NM_000774:	NM_000774:
1573	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	0.27	TAAGTGGTTTGTAAACCATAA	NM_000775:	NM_000775:
1573	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	0.48	AAAGTTCTTGTAAGAATCAAA	NM_000775:	NM_000775:
120227	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	1.08	TGGGTTGATCACAGACGATTA	NM_024514:	NM_024514:
120227	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	0.52	TACGGAGAGATCTTCAGTTTA	NM_024514:	NM_024514:
29785	CYP2S1 (cytc	cytochrome P450, family 2, subfamily S, polypeptide 1	-0.65	CATGCTGATGACAGTCATTTA	NM_030622:	NM_030622:
29785	CYP2S1 (cytc	cytochrome P450, family 2, subfamily S, polypeptide 1	-0.13	CACAGAATTCACCAACAAGAA	NM_030622:	NM_030622:
113612	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	0.08	CGGGTGTGTATGGGAGAACAA	NM_183075:	NM_183075:
113612	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	0.05	CCGGAGGATTTCTACCCTAAT	NM_183075:	NM_183075:
54905	CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	-0.77	AAGATTCTGCAGGAGCTGAAA	NM_017781:	NM_017781:
54905	CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	-3.47	AATCGCCATCTTCCAGCTCAT	NM_017781:	NM_017781:
51302	CYP39A1 (cyt	cytochrome P450, family 39, subfamily A, polypeptide 1	0.08	CTCCTAGGCTCTATTAACATA	NM_016593:	NM_016593:
51302	CYP39A1 (cyt	cytochrome P450, family 39, subfamily A, polypeptide 1	0.39	GAGGTGATTCTCAACTAGCAA	NM_016593:	NM_016593:
1576	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	-0.03	ATGCAATGAACACTTAATAAA	NM_017460:	NM_017460:
1576	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	0.16	CTCGATGCAATGAACACTTAA	NM_017460:	NM_017460:
64816	CYP3A43 (cyt	cytochrome P450, family 3, subfamily A, polypeptide 43	-0.56	AAGGATGAATCTACAGAATTA	NM_022820:	NM_057096:NM_057095:NM_022820:
64816	CYP3A43 (cyt	cytochrome P450, family 3, subfamily A, polypeptide 43	1.14	CTCGTAGTGACATTTATATTA	NM_022820:	NM_057096:NM_057095:NM_022820:
1577	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	0.87	CAGAGATTTCAACTTAGTCAA	NM_000777:	NM_000777:
1577	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	0.03	CCCTAAGTGGAGAATGAGTTA	NM_000777:	NM_000777:
1551	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	-0.02	ATCTGTAGTATTCTATAGTAA	NM_000765:	NM_000765:
1551	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	0.40	TTCAACCACAATCATTAATAA	NM_000765:	NM_000765:
10858	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	-0.03	GCGGATGGACACATACTTTGA	NM_006668:	NM_006668:
10858	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	-0.27	AGGCTTGGTGTCCGAATGCAA	NM_006668:	NM_006668:
1579	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	1.80	CAGCTGTAAATTGTGTGCTTA	NM_000778:	NM_000778:
1579	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	1.13	ATCAATTGTATCTTGAGTTAA	NM_000778:	NM_000778:
1580	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	1.06	ACCAAATAGAAGAATGGCTTA	NM_000779:	NM_000779:
1580	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	-1.55	ATGGCTGGGTACCACCAAATA	NM_000779:	NM_000779:
57834	CYP4F11 (cyt	cytochrome P450, family 4, subfamily F, polypeptide 11	0.07	TCGGGATCCATTACAACCCAA	NM_021187:	NM_021187:
57834	CYP4F11 (cyt	cytochrome P450, family 4, subfamily F, polypeptide 11	1.11	AGGCATTGTCTGCCTTATCAA	NM_021187:	NM_021187:
66002	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	0.01	TTGCAGATTGTCATGAATAAA	NM_023944:	NM_023944:
66002	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	-8.87	CCGCAGGAAGCTGGAATTGAT	NM_023944:	NM_023944:
8529	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	0.84	CAGGTTGTTCATATAATAATA	NM_001082:	NM_001082:
8529	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	0.64	CCAGATGAAAGGATAAACAAA	NM_001082:	NM_001082:
4051	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	0.50	CTGGTGTACAATGCTAATAAA	NM_000896:	NM_000896:
4051	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	0.75	ATCATGTTATACGTACACTTA	NM_000896:	NM_000896:
11283	CYP4F8	cytochrome P450, family 4, subfamily F, polypeptide 8	0.52	CAGAGTCTAAGTAAAGACTTT	NM_007253:	NM_007253:
11283	CYP4F8	cytochrome P450, family 4, subfamily F, polypeptide 8	1.22	AGGGAATGTCTGTAACATCAA	NM_007253:	NM_007253:
285440	CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2	0.72	TGGCTGATTCATAATGGGTAA	NM_207352:	NM_207352:
285440	CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2	0.13	TAGGGTTAGATCTTTAGTTAA	NM_207352:	NM_207352:
260293	CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1	-0.08	ATAGATGTGATCATTCCTATA	NM_178033:	NM_178033:
260293	CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1	0.06	CACCAATAGACTTTCATATAT	NM_178033:	NM_178033:
199974	CYP4Z1	cytochrome P450, family 4, subfamily Z, polypeptide 1	0.18	ATGGTTGTTTGACAAATTATA	NM_178134:	NM_178134:
1595	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	-0.23	AAGGTCCTTGGGAGTAATAAA	NM_000786:	NM_000786:
1595	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	-2.25	TAGGGAATAATCGAACATCTA	NM_000786:	NM_000786:
1581	CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	-0.21	TAAGGTGACTCGAGTGTTTAA	NM_000780:	NM_000780:
1581	CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	0.27	CGGGTGTGATCATATATCATA	NM_000780:	NM_000780:
9420	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	-0.08	CAGCCGCTTGTTGTTTGGTAT	NM_004820:	NM_004820:
9420	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	0.45	TACGACTGTCCTCATATTCAA	NM_004820:	NM_004820:
1582	CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	-1.89	CAGGTTGGTTCATGAAGACTA	NM_004391:	NM_004391:
1582	CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	-0.04	TTCAACGTGATCACTATTAAA	NM_004391:	NM_004391:
3491	CYR61	cysteine-rich, angiogenic inducer, 61	0.16	AGGCAGCTATCTGCACTCTAA	NM_001554:	NM_001554:
3491	CYR61	cysteine-rich, angiogenic inducer, 61	1.98	AAGGTATTTCGAAACTGCCAA	NM_001554:	NM_001554:
10800	CYSLTR1	cysteinyl leukotriene receptor 1	0.67	AAAGCAGACATTCGTAGAGAA	NM_006639:	NM_006639:
10800	CYSLTR1	cysteinyl leukotriene receptor 1	-0.88	CTGTATATATTGGCTAGCAAA	NM_006639:	NM_006639:
57105	CYSLTR2	cysteinyl leukotriene receptor 2	-1.24	CAGGCTTTCTAAATTCTTCAA	NM_020377:	NM_020377:
57105	CYSLTR2	cysteinyl leukotriene receptor 2	-0.86	TGGGATCATATGGATCCTTAT	NM_020377:	NM_020377:
54360	CYTL1	cytokine-like 1	0.12	CTGCCAGATCGTCAGCGCTAA	NM_018659:	NM_018659:
54360	CYTL1	cytokine-like 1	-1.81	ACAGGTCTTGTGTTAGTTGTA	NM_018659:	NM_018659:
27065	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	-0.96	CCCGGATAAGGTGGTCGTGAA	NM_014392:	NM_014392:
27065	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	0.58	AGGGTTTGGATCTCAGATAAA	NM_014392:	NM_014392:
1601	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-0.77	AAGGTTGGCCTTAGTAGTCAA	NM_001343:	NM_001343:
1601	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-2.51	TAGAGCATGAACATCCAGTAA	NM_001343:	NM_001343:
1603	DAD1	defender against cell death 1	1.50	CAGATTTGACACTTACTGCTA	NM_001344:	NM_001344:
1603	DAD1	defender against cell death 1	-0.59	TTGCCTGAGAATACAGATCAA	NM_001344:	NM_001344:
1605	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	-0.19	CCGGTGGTGAATAACAGACTA	NM_004393:	NM_004393:
1605	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	-6.45	AAGGGTGTGCATTACATTTCA	NM_004393:	NM_004393:
26007	DAK	dihydroxyacetone kinase 2 homolog (yeast)	1.08	AAGAAAGTTAATAAACTATAA	NM_015533:	NM_015533:
26007	DAK	dihydroxyacetone kinase 2 homolog (yeast)	-3.20	CCGGAAGAGCCAGTTATATCA	NM_015533:	NM_015533:
1610	DAO	D-amino-acid oxidase	-0.58	CAAGTTGTACTAACATATTAA	NM_001917:	NM_001917:
1610	DAO	D-amino-acid oxidase	-0.75	ATGGAGGATAATTGAGGCTAA	NM_001917:	NM_001917:
267012	DAOA	D-amino acid oxidase activator	-0.01	AAGAGAGACGGTAACAAGGAA	NM_172370:	NM_172370:
267012	DAOA	D-amino acid oxidase activator	0.63	AGGCATTTACAGAGATCATTA	NM_172370:	NM_172370:
7818	DAP3	death associated protein 3	-1.43	TCGCTTTGTGATGCAGGTGAA	NM_033657:	NM_033657:NM_004632:
7818	DAP3	death associated protein 3	0.00	TTGGCTCTGGACCTGCATTAA	NM_033657:	NM_033657:NM_004632:
1612	DAPK1	death-associated protein kinase 1	-1.68	AAGCATGTAATGTTAATGTTA	NM_004938:	NM_004938:
1612	DAPK1	death-associated protein kinase 1	-3.34	CGGCTATTACTCTGTGGCCAA	NM_004938:	NM_004938:
23604	DAPK2	death-associated protein kinase 2	-1.55	CGGAATTTGTTGCTCCAGAAA	NM_014326:	NM_014326:
23604	DAPK2	death-associated protein kinase 2	-4.17	CTGGTTAAAGAGACCCGGAAA	NM_014326:	NM_014326:

1613	DAPK3	death-associated protein kinase 3	0.96	CCCAGAGATTGTGAACTATGA	NM_001348:	NM_001348:
1613	DAPK3	death-associated protein kinase 3	0.02	CCGGCAGAAGGGCACGGGCAA	NM_001348:	NM_001348:
27071	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	-0.57	CTGGGCCTTATTAAAGAGCAA	NM_014395:	NM_014395:
27071	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	0.00	TAGGTAGTATAATAAAGGTAA	NM_014395:	NM_014395:
2532	DARC	Duffy blood group, chemokine receptor	0.58	ACCAGTGTCCTGGGTATCCTA	NM_002036:	NM_002036:
2532	DARC	Duffy blood group, chemokine receptor	-2.46	CAGCTGGACTTCGAAGATGTA	NM_002036:	NM_002036:
1616	DAXX	death-associated protein 6	-2.17	CACCCGCTACCCAGAGGTTAA	NM_001350:	NM_001350:
1616	DAXX	death-associated protein 6	1.51	CACGGTTGAAGCGTAAGCTGA	NM_001350:	NM_001350:
10926	DBF4	DBF4 homolog (S. cerevisiae)	1.41	CAAGTTGTTGATGATATTGTA	NM_006716:	NM_006716:
10926	DBF4	DBF4 homolog (S. cerevisiae)	1.51	CAGGCTACCAAGTGGAATATA	NM_006716:	NM_006716:
1621	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	0.19	GCGGGCTAATGAGCCAATAAA	NM_000787:	NM_000787:
1621	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	-0.01	CCGGGAGTGGGAGATCGTGAA	NM_000787:	NM_000787:
1622	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme	-0.38	CAACAAAGTAGAAGAGCTAAA	NM_020548:	NM_020548:
1622	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme	0.24	CCAGTTAAACCAGCTACTCAA	NM_020548:	NM_020548:
1629	DBT	dihydrolipoamide branched chain transacylase E2	0.96	TAGCCATATACAGACAGTATA	NM_001918:	NM_001918:
1629	DBT	dihydrolipoamide branched chain transacylase E2	0.86	ACGATTTGTATCGTATGATTA	NM_001918:	NM_001918:
160365	DCAL1	dendritic cell-associated lectin-1	-1.47	TATGGTGAGATTTAACATTTA	NM_172004:	NM_172004:
160365	DCAL1	dendritic cell-associated lectin-1	0.07	AAGTTTCAACTTCATGTGTTA	NM_172004:	NM_172004:
9201	DCAMKL1	doublecortin and CaM kinase-like 1	0.03	CAGGTTTATAACTTCGACACA	NM_004734:	NM_004734:
9201	DCAMKL1	doublecortin and CaM kinase-like 1	-0.10	CCGGAAGTGATAACACGCAAA	NM_004734:	NM_004734:
166614	DCAMKL2	doublecortin and CaM kinase-like 2	-1.23	ACAGATGCTCTGAATCATCAA	NM_152619:	NM_152619:
166614	DCAMKL2	doublecortin and CaM kinase-like 2	-4.69	CTGAGCTTGACCGTTGCATAA	NM_152619:	NM_152619:
85443	DCAMKL3	doublecortin and CaM kinase-like 3	0.64	CCAGCTAATGAAGATAAACTA	XM_047355:	XM_047355:
85443	DCAMKL3	doublecortin and CaM kinase-like 3	-2.44	TCGAAGGAGCTCAGAGTTCAA	XM_047355:	XM_047355:
131566	DCBLD2	discoidin, CUB and LCCL domain containing 2	-0.77	ACGCACGGTACTGTTCTTGAA	NM_080927:	NM_080927:
131566	DCBLD2	discoidin, CUB and LCCL domain containing 2	0.11	TCGGATGTCAGTTTATTCCTA	NM_080927:	NM_080927:
1630	DCC	deleted in colorectal carcinoma	-0.54	CACCTGTGTCCAAGAACTCTA	NM_005215:	NM_005215:
1630	DCC	deleted in colorectal carcinoma	-0.84	CAGCATACCAATTACCCATAA	NM_005215:	NM_005215:
54798	DCHS2	dachsous 2 (Drosophila)	0.72	AAGCACCACTGTAATTATAAA	NM_017639:	NM_017639:
54798	DCHS2	dachsous 2 (Drosophila)	-1.56	ATGGTTGAGTTTAATAAGTAT	NM_017639:	NM_017639:
1633	DCK	deoxycytidine kinase	-2.83	AAGTTGCAAAGTGGAATTAAA	NM_000788:	NM_000788:
1633	DCK	deoxycytidine kinase	-1.74	TTGGTATAAATTAATTTGTTA	NM_000788:	NM_000788:
9937	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	0.80	CCGCATGATTCACAAGAACAA	NM_014881:	NM_014881:
9937	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	1.16	TAGCTTCATAACAATGTTACA	NM_014881:	NM_014881:
64858	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	-4.38	CACCTACAGGTATCTAAGCAA	NM_022836:	NM_022836:
64858	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	-1.41	CCAGATCTCTATAGCAAAGAA	NM_022836:	NM_022836:
64421	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	-1.98	AAGTACGGAGCCAAAGTATAA	NM_022487:	NM_001033858:NM_001033855:NM_001033857:NM_022487:
64421	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	1.13	CAGGTTCATGTGAATAAGCTA	NM_022487:	NM_001033858:NM_001033855:NM_001033857:NM_022487:
1634	DCN	decorin	-1.36	TACGTGCGCTCTGCCATTCAA	NM_133507:	NM_133504:NM_001920:NM_133503:NM_133507:NM_133506:NM_133505:
1634	DCN	decorin	-1.98	AAGCTAGATACTGGAAACCTA	NM_133507:	NM_133504:NM_001920:NM_133503:NM_133507:NM_133506:NM_133505:
149095	DCST1	DC-STAMP domain containing 1	-1.45	TACAATGACCTATTGAAGAAA	NM_152494:	NM_152494:
149095	DCST1	DC-STAMP domain containing 1	-0.52	CAGAGACAGTGATGGAATCAA	NM_152494:	NM_152494:
1639	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	-0.14	TCGGCCCAACTTATGGAGCAA	NM_004082:	NM_023019:NM_004082:
1639	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	1.23	TCGAAGATCGAGAGACAGTTA	NM_004082:	NM_023019:NM_004082:
92181	DC-UbP	dendritic cell-derived ubiquitin-like protein	0.41	AGGCAGTTAAGAAATAGATAA	NM_152277:	NM_152277:
92181	DC-UbP	dendritic cell-derived ubiquitin-like protein	1.02	AAGGCAGTTAAGAAATAGATA	NM_152277:	NM_152277:
54165	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	0.88	CAGCATTAGTGTGTTGATTAT	NM_020640:	NM_020640:
54165	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	1.64	CTGGGCCGCTCTAAACATTTA	NM_020640:	NM_020640:
1641	DCX	doublecortex; lissencephaly, X-linked (doublecortin)	-0.12	CTGAATAGACAGTCCATATAA	NM_000555:	NM_178151:NM_000555:NM_178152:NM_178153:
1641	DCX	doublecortex; lissencephaly, X-linked (doublecortin)	0.21	ACCCTGCACATTTGATTCTAA	NM_000555:	NM_178151:NM_000555:NM_178152:NM_178153:
51181	DCXR	dicarbonyl/L-xylulose reductase	0.30	AAAGGCCAAGACTATGCTGAA	NM_016286:	NM_016286:
51181	DCXR	dicarbonyl/L-xylulose reductase	0.01	AAGGAGGCCTTTGACAGATCC	NM_016286:	NM_016286:
1642	DDB1	damage-specific DNA binding protein 1, 127kDa	0.78	ATGCAGAATCGACTCAATAAA	NM_001923:	NM_001923:
1642	DDB1	damage-specific DNA binding protein 1, 127kDa	1.94	CCACTAGATCGCGATAATAAA	NM_001923:	NM_001923:
1643	DDB2 (damag	damage-specific DNA binding protein 2, 48kDa	1.38	AGGGATCAAGCAGTTATTTGA	NM_000107:	NM_000107:
1643	DDB2 (damag	damage-specific DNA binding protein 2, 48kDa	-0.24	CTGGATTCTTACCGGATATTA	NM_000107:	NM_000107:
1644	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-1.88	TCGGCTAAAGGGTTCCAACAA	NM_000790:	NM_000790:
1644	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-4.15	CAGGCTTATATCCGCAAGCAT	NM_000790:	NM_000790:
84301	DDI2	DDI1, DNA-damage inducible 1, homolog 2 (S. cerevisiae)	-0.77	CCCGAATAGATTTCAGTAGTA	XM_496347:	NM_032341:
84301	DDI2	DDI1, DNA-damage inducible 1, homolog 2 (S. cerevisiae)	1.03	CCAGTGCAGTTCCCAAACTTA	XM_496347:	NM_032341:
1649	DDIT3	DNA-damage-inducible transcript 3	-0.23	AAGGAAGTGTATCTTCATACA	NM_004083:	NM_004083:
1649	DDIT3	DNA-damage-inducible transcript 3	1.00	CAGCTTGTATATAGAGATTGT	NM_004083:	NM_004083:
780	DDR1	discoidin domain receptor family, member 1	0.49	ACGGTGTGAATCACACATCCA	NM_001954:	NM_001954:NM_013993:NM_013994:
780	DDR1	discoidin domain receptor family, member 1	0.21	CAGGAATGATTTCCTGAAAGA	NM_001954:	NM_001954:NM_013993:NM_013994:
4921	DDR2	discoidin domain receptor family, member 2	0.01	ACGCACTGTCAGTTACACCAA	NM_006182:	NM_006182:NM_001014796:
4921	DDR2	discoidin domain receptor family, member 2	-0.12	CCGGTTCATTCCAGTCACCGA	NM_006182:	NM_006182:NM_001014796:
1653	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.84	CACGGTGTTCCTTATGTTATA	NM_004939:	NM_004939:
1653	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.30	CCGGATGGTTACATTGTCAAA	NM_004939:	NM_004939:
11218	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	0.45	GGGCTCGATTTAATTGTTCAA	NM_007204:	NM_007204:
11218	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	0.42	CTGGACTATCAGTCAAATCAA	NM_007204:	NM_007204:
29118	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	1.23	AAGGGCAAGATTATTTGCTTA	NM_015191:	NM_013264:
26512	DDX26	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	-2.47	CAGACCAACTTTCATCAGACA	NM_012141:	NM_012141:
26512	DDX26	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	0.86	CACTAATGATTCGATAATACA	NM_012141:	NM_012141:
51428	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	-0.84	CCGAGCATTGATGTCAGTGAA	NM_016222:	NM_016222:
51428	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	-3.95	CCGCCTGTACTCATCTTTGCA	NM_016222:	NM_016222:
9775	DDX48	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	-14.21	AAAGAGCAGATTTACGATGTA	NM_014740:	NM_014740:
9775	DDX48	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	-11.68	CCGCATCTTGGTGAAACGTGA	NM_014740:	NM_014740:
79039	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	-4.32	CCGGCTTGACGTGGATACCAA	NM_024072:	NM_024072:
79039	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	0.39	GGCGACTATCTTTGAGATCAA	NM_024072:	NM_024072:
1666	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	0.57	CACAGCCTTCGTGACACTAGA	NM_001359:	NM_001359:
1666	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	-0.14	ATGCGATTCAATGTGATTCAA	NM_001359:	NM_001359:
26063	DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	-0.40	AAGAAAGAGGATTAAAGAGAA	NM_020664:	NM_020664:
26063	DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	-0.71	AAGATAATCTATTTACTGTAA	NM_020664:	NM_020664:
9191	DEDD	death effector domain containing	-3.49	CTGAGCCGTAAGACAAATGTA	NM_004216:	NM_032998:NM_004216:
9191	DEDD	death effector domain containing	-0.67	TGGCTTTATGAGAGCTCTTAA	NM_004216:	NM_032998:NM_004216:
162989	DEDD2	death effector domain containing 2	-0.84	ACCAATTAAACTGCCCTGGAA	NM_133328:	NM_133328:
162989	DEDD2	death effector domain containing 2	0.16	CAGGATTGATCCCACCTCCAA	NM_133328:	NM_133328:
50619	DEF6	differentially expressed in FDCP 6 homolog (mouse)	-1.75	CGGGAACAGTATGCTCTCCAA	NM_022047:	NM_022047:
50619	DEF6	differentially expressed in FDCP 6 homolog (mouse)	-0.03	CAGGCCAGCACCAACGTGAAA	NM_022047:	NM_022047:
1667	DEFA1	defensin, alpha 1	0.50	ATGGCCTGCTATTGCAGAATA	NM_004084:	NM_004084:
1668	DEFA3	defensin, alpha 3, neutrophil-specific	0.42	ATGGACTGCTATTGCAGAATA	NM_005217:	NM_005217:
1673	DEFB4	defensin, beta 4	0.18	GACGTGCGACATGTAAACCAA	NM_004942:	NM_004942:
1673	DEFB4	defensin, beta 4	0.89	GCCCTAGAAGGTATAAACAAA	NM_004942:	NM_004942:

8560	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	1.08	ACAGCCTTACTCATAAATAAA	NM_003676:	NM_144780:NM_003676:
8560	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	-0.35	CCCGAATTAGACACTGCTGAA	NM_003676:	NM_144780:NM_003676:
7913	DEK	DEK oncogene (DNA binding)	-0.82	ATCGTGGATGTCTCTGACAAA	NM_003472:	NM_003472:
7913	DEK	DEK oncogene (DNA binding)	-2.21	CAGCTTCACGATTATGACTAA	NM_003472:	NM_003472:
51071	DERA	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	0.43	ACCGAACTTAATGGAATGGAA	NM_015954:	NM_015954:
51071	DERA	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	1.39	AGAAATCGACGTGGTAATTAA	NM_015954:	NM_015954:
79139	DERL1	Der1-like domain family, member 1	0.73	TCGACTGACATCCGTTGTTAA	NM_024295:	NM_024295:
79139	DERL1	Der1-like domain family, member 1	0.48	CCATATTTAATTTATATGATA	NM_024295:	NM_024295:
1674	DES	desmin	-0.08	CAGCAGCATGAAGTGCTCTAA	NM_001927:	NM_001927:
1674	DES	desmin	0.01	CAAGAAGACGGTGATGATCAA	NM_001927:	NM_001927:
1677	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activate	-1.17	ACGGGTCAGTAGGGATAAGAA	NM_004402:	NM_004402:NM_001004286:NM_001004285:
1677	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activate	0.91	TACGATGTTTATACTCCGTAA	NM_004402:	NM_004402:NM_001004286:NM_001004285:
1687	DFNA5	deafness, autosomal dominant 5	0.45	GCGGTCCTATTTGATGATGAA	NM_004403:	NM_004403:
1687	DFNA5	deafness, autosomal dominant 5	1.08	TAGAAAGAGTCTGACCCTTTA	NM_004403:	NM_004403:
9993	DGCR2	DiGeorge syndrome critical region gene 2	2.03	GAGGTGGGATTTGATACTGTA	NM_005137:	NM_005137:
9993	DGCR2	DiGeorge syndrome critical region gene 2	-0.26	AAGCCCAGTTGTGAATATCAA	NM_005137:	NM_005137:
1606	DGKA	diacylglycerol kinase, alpha 80kDa	-1.54	ATCCATCTTCTCAACATGCAA	NM_001345:	NM_201554:NM_001345:NM_201444:NM_201445:
1606	DGKA	diacylglycerol kinase, alpha 80kDa	-1.27	CACGACCAGTGTGCCATGAAA	NM_001345:	NM_201554:NM_001345:NM_201444:NM_201445:
1607	DGKB	diacylglycerol kinase, beta 90kDa	0.00	CCCGAACTACTTCTCCTGCAA	NM_004080:	NM_004080:NM_145695:
1607	DGKB	diacylglycerol kinase, beta 90kDa	2.49	CTCATTCTAGTCCAATGGTAA	NM_004080:	NM_004080:NM_145695:
8527	DGKD	diacylglycerol kinase, delta 130kDa	-0.36	CAGCAGATTCTCTTCTATGAA	NM_003648:	NM_152879:NM_003648:
8527	DGKD	diacylglycerol kinase, delta 130kDa	-0.92	CCGCCTCGTGACCAAGTTTAA	NM_003648:	NM_152879:NM_003648:
8526	DGKE	diacylglycerol kinase, epsilon 64kDa	1.12	ATCGATGGAAAGTTCAAGTAA	NM_003647:	NM_003647:
8526	DGKE	diacylglycerol kinase, epsilon 64kDa	-2.17	CTGGAAGTCGTTGGAGTATAT	NM_003647:	NM_003647:
1608	DGKG	diacylglycerol kinase, gamma 90kDa	-0.09	ACCGCAAATGTGAATTATCAA	NM_001346:	NM_001346:
1608	DGKG	diacylglycerol kinase, gamma 90kDa	-5.34	TAGCCACTCACATAAAGTTTA	NM_001346:	NM_001346:
160851	DGKH	diacylglycerol kinase, eta	-4.28	CAGGTGGAGTATAATGACATA	NM_152910:	NM_178009:NM_152910:
160851	DGKH	diacylglycerol kinase, eta	-0.92	CCGGATCTAGATTCCGTAGAT	NM_152910:	NM_178009:NM_152910:
9162	DGKI	diacylglycerol kinase, iota	-4.02	ACGGATCGAATGGTACTTACA	NM_004717:	NM_004717:
9162	DGKI	diacylglycerol kinase, iota	-0.39	CAGAAGGATGCTTCAACTATT	NM_004717:	NM_004717:
139189	DGKK (diacyl	diacylglycerol kinase, kappa	-0.16	ATGCCGTAGATGTTACATTTA	XM_066534:	NM_001013742:
139189	DGKK (diacyl	diacylglycerol kinase, kappa	-0.69	CAGACAGACAATATCTGTTAA	XM_066534:	NM_001013742:
1609	DGKQ	diacylglycerol kinase, theta 110kDa	0.17	CAGCGACACCAGGTTTGAGAA	NM_001347:	NM_001347:
1609	DGKQ	diacylglycerol kinase, theta 110kDa	1.99	CCGGAAGGTGACGCTCACCAA	NM_001347:	NM_001347:
8525	DGKZ	diacylglycerol kinase, zeta 104kDa	0.86	CAAGAGGAACGACTTCTGTAA	NM_003646:	NM_201533:NM_201532:NM_003646:
8525	DGKZ	diacylglycerol kinase, zeta 104kDa	0.63	CTGGAGCGAGTCAGCGACATA	NM_003646:	NM_201533:NM_201532:NM_003646:
1716	DGUOK	deoxyguanosine kinase	-5.68	CACCTTTGTAAAGAATCTGTA	NM_001929:	NM_001929:NM_080918:NM_080917:NM_080916: NM_080915:
1716	DGUOK	deoxyguanosine kinase	-0.06	CAGCACGATGGTCCTACACAT	NM_001929:	NM_001929:NM_080918:NM_080917:NM_080916: NM_080915:
1718	DHCR24	24-dehydrocholesterol reductase	0.49	AACGCAAAGCTTGGTTGTTTA	NM_014762:	NM_014762:
1718	DHCR24	24-dehydrocholesterol reductase	-0.47	CCGGGTCTCTTCATTAGTTGA	NM_014762:	NM_014762:
1717	DHCR7	7-dehydrocholesterol reductase	0.40	TTGACTTCTTCTGGAACGAAA	NM_001360:	NM_001360:
1717	DHCR7	7-dehydrocholesterol reductase	-1.48	CGGGAAGTGGTTTGACTTCAA	NM_001360:	NM_001360:
1719	DHFR (dihydr	dihydrofolate reductase	-0.16	AAGGTAACTAACGGAAGGAAA	NM_000791:	NM_000791:
1719	DHFR (dihydr	dihydrofolate reductase	0.32	CAGGATAGGAAGAGCATAATA	NM_000791:	NM_000791:
200895	DHFRL1	dihydrofolate reductase-like 1	0.61	AAGACTGTAATAAGAATCATA	NM_176815:	NM_176815:
200895	DHFRL1	dihydrofolate reductase-like 1	-9.40	CAGGCAAAGAATCAAGGGTGA	NM_176815:	NM_176815:
50846	DHH	desert hedgehog homolog (Drosophila)	1.82	CCCAGGCATAGAAACCTCGAA	NM_021044:	NM_021044:
50846	DHH	desert hedgehog homolog (Drosophila)	1.35	ACCGAGTGGCCTCCACGCAAA	NM_021044:	NM_021044:
1723	DHODH	dihydroorotate dehydrogenase	-0.31	CAGGAACTTGACTGTCTTTCA	NM_001361:	NM_001361:NM_001025193:
1723	DHODH	dihydroorotate dehydrogenase	-0.54	CTCCGGGATTTATCAACTCAA	NM_001361:	NM_001361:NM_001025193:
115817	DHRS1	dehydrogenase/reductase (SDR family) member 1	-2.45	TACCCATACCCTTGATATGAA	NM_138452:	NM_138452:
115817	DHRS1	dehydrogenase/reductase (SDR family) member 1	-3.01	CAAGTGGATTATTGCCCTCTA	NM_138452:	NM_138452:
51171	DHRS10	dehydrogenase/reductase (SDR family) member 10	-1.20	CCGAGTGGTTATCTGCGACAA	NM_016246:	NM_016246:
51171	DHRS10	dehydrogenase/reductase (SDR family) member 10	-1.37	CAGCCTCTATTGAGGATTTGA	NM_016246:	NM_016246:
10202	DHRS2	dehydrogenase/reductase (SDR family) member 2	0.87	CTCTCTGTAATTTGTGCTTTA	NM_005794:	NM_182908:NM_005794:
10202	DHRS2	dehydrogenase/reductase (SDR family) member 2	0.69	TAGATTTGGCTGATCCAATTA	NM_005794:	NM_182908:NM_005794:
9249	DHRS3	dehydrogenase/reductase (SDR family) member 3	-2.43	CACCTGCATGAACACTTTCAA	NM_004753:	NM_004753:
9249	DHRS3	dehydrogenase/reductase (SDR family) member 3	0.61	ATCGACTACTGCACATCCAAA	NM_004753:	NM_004753:
10901	DHRS4	dehydrogenase/reductase (SDR family) member 4	0.28	TTGCGCGGCTTTGAATCCAAA	NM_021004:	NM_021004:
51635	DHRS7	dehydrogenase/reductase (SDR family) member 7	0.91	ACCTTTCTTGTTAGTAACATA	NM_016029:	NM_016029:
51635	DHRS7	dehydrogenase/reductase (SDR family) member 7	0.68	GCGGCTGATGTTAATCAGCAT	NM_016029:	NM_016029:
25979	DHRS7B	dehydrogenase/reductase (SDR family) member 7B	2.20	CAGATGTTATGTCACCTGAAA	NM_015510:	NM_015510:
25979	DHRS7B	dehydrogenase/reductase (SDR family) member 7B	1.28	TTGCATTTGTTGAGACTTTAA	NM_015510:	NM_015510:
201140	DHRS7C (del	dehydrogenase/reductase (SDR family) member 7C	-0.22	CCGAGCCGAAGTGGAGGAATA	XM_113912:	XM_113912:
201140	DHRS7C (del	dehydrogenase/reductase (SDR family) member 7C	0.88	TACCACGTGTATCCAGAGCAA	XM_113912:	XM_113912:
51170	DHRS8	dehydrogenase/reductase (SDR family) member 8	-1.20	CCGGCGAAATCGTGCTGATTA	NM_016245:	NM_016245:
51170	DHRS8	dehydrogenase/reductase (SDR family) member 8	0.15	AACCGTTTATTTAACATATAT	NM_016245:	NM_016245:
10170	DHRS9	dehydrogenase/reductase (SDR family) member 9	-0.45	TCGTGCTTATTTGGATTGCAA	NM_005771:	NM_005771:NM_199204:
10170	DHRS9	dehydrogenase/reductase (SDR family) member 9	-0.89	CAGCTTAAGACGGGACATGAA	NM_005771:	NM_005771:NM_199204:
207063	DHRSX	dehydrogenase/reductase (SDR family) X-linked	0.36	CCAAGTGGTCTTCAACCATAA	NM_145177:	NM_145177:
207063	DHRSX	dehydrogenase/reductase (SDR family) X-linked	-0.24	CCGCGTTAATACAACTGAGTA	NM_145177:	NM_145177:
90957	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	2.04	TAAGTTCACCTGATAACTCAA	NM_145646:	NM_145646:NM_198963:
90957	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	-0.56	ACCAAGAACGATGGATATGTA	NM_145646:	NM_145646:NM_198963:
1729	DIAPH1	diaphanous homolog 1 (Drosophila)	0.31	TAAGAGTAGCAGGAACTCTAA	NM_005219:	NM_005219:
1729	DIAPH1	diaphanous homolog 1 (Drosophila)	0.02	TTGGTTGGCCGTGCAAGCTAA	NM_005219:	NM_005219:
1730	DIAPH2	diaphanous homolog 2 (Drosophila)	0.57	CACAGATAATTCCTTTATATA	NM_006729:	NM_006729:
1730	DIAPH2	diaphanous homolog 2 (Drosophila)	-1.32	ACCGTCGAAAGCGGATTCCAA	NM_006729:	NM_006729:NM_007309:
23405	DICER1	Dicer1, Dcr-1 homolog (Drosophila)	0.04	ATCGATCCTATGTTCAATCTA	NM_030621:	NM_030621:NM_177438:
23405	DICER1	Dicer1, Dcr-1 homolog (Drosophila)	-0.28	TTGCTCCGTTAGGGTGCCTAA	NM_030621:	NM_030621:NM_177438:
11083	DIDO1	death inducer-obliterator 1	-0.14	AACGTTCACCTTAATGATTGA	NM_022105:	NM_080796:NM_022105:
11083	DIDO1	death inducer-obliterator 1	-2.49	CTGGTGAACGTTCACCTTAAT	NM_022105:	NM_080796:NM_022105:
1733	DIO1	deiodinase, iodothyronine, type I	0.02	AAGAGGAGAGTACTCACTTTA	NM_000792:	NM_000792:NM_213593:
1733	DIO1	deiodinase, iodothyronine, type I	-0.02	CCCAATCAAGACAAATTGTTA	NM_000792:	NM_000792:NM_213593:
1734	DIO2	deiodinase, iodothyronine, type II	-0.01	TCGGAAGAACATGAATCTCTA	NM_000793:	NM_001007023:NM_000793:NM_013989:
1734	DIO2	deiodinase, iodothyronine, type II	-0.61	CTGGTTAAAGGTATGATTATA	NM_000793:	NM_001007023:NM_000793:NM_013989:
1735	DIO3	deiodinase, iodothyronine, type III	-1.07	CCGGAGGGTGTAAACATCCAA	NM_001362:	NM_001362:
1735	DIO3	deiodinase, iodothyronine, type III	-0.78	CCGTGAGGTAACCACCTTAAA	NM_001362:	NM_001362:
1736	DKC1	dyskeratosis congenita 1, dyskerin	0.80	CGGCTGCACAATGCTATTGAA	NM_001363:	NM_001363:
1736	DKC1	dyskeratosis congenita 1, dyskerin	0.42	CCCAAGGTGACTGGTTGTTTA	NM_001363:	NM_001363:
222229	DKFZp434K1	hypothetical protein DKFZp434K1815	1.82	GACGGTCAATGACAACCTGAA	NM_152892:	NM_152892:
222229	DKFZp434K1	hypothetical protein DKFZp434K1815	0.81	CACAGCTAACTAACTTATTCA	NM_152892:	NM_152892:
25891	DKFZP586H2	regeneration associated muscle protease	-2.72	CCCAACTTTCAGTTATACGAA	NM_015430:	NM_001001991:NM_015430:
25891	DKFZP586H2	regeneration associated muscle protease	-2.11	CTGGATTGAAAGAAATATGAA	NM_015430:	NM_001001991:NM_015430:
157285	DKFZp761P0	hypothetical protein DKFZp761P0423	-1.62	CTGGCCCGCCTTGTAGCCAAA	XM_291277:	XM_291277:
157285	DKFZp761P0	hypothetical protein DKFZp761P0423	0.33	CAGCTGAGCGTGTCCAGTCAA	XM_291277:	XM_291277:

55355	DKFZp762E1	hypothetical protein DKFZp762E1312	-1.29	ACCGTCAGAGGGAGATTGAAA	NM_018410:	NM_018410:
55355	DKFZp762E1	hypothetical protein DKFZp762E1312	0.64	TTGCCGTAAGACAGGTTTAAA	NM_018410:	NM_018410:
22943	DKK1	dickkopf homolog 1 (Xenopus laevis)	1.32	ATGTACTATCTTAATGCTTAA	NM_012242:	NM_012242:
22943	DKK1	dickkopf homolog 1 (Xenopus laevis)	1.30	CACACTTGTCAGAGACACTAA	NM_012242:	NM_012242:
27123	DKK2	dickkopf homolog 2 (Xenopus laevis)	0.70	AAGAAACGTGATAAGAATATA	NM_014421:	NM_014421:
27123	DKK2	dickkopf homolog 2 (Xenopus laevis)	0.11	CACTAAGATGTCACATATAAA	NM_014421:	NM_014421:
27122	DKK3	dickkopf homolog 3 (Xenopus laevis)	0.91	ACCGAGAAATTCACAAGATAA	NM_013253:	NM_013253:NM_015881:NM_001018057:
27122	DKK3	dickkopf homolog 3 (Xenopus laevis)	-0.28	TAGGGCGAGGATTATAAATGA	NM_013253:	NM_013253:NM_015881:NM_001018057:
27121	DKK4	dickkopf homolog 4 (Xenopus laevis)	-0.44	CTCGATTAAGAGTATGCCAAA	NM_014420:	NM_014420:
27121	DKK4	dickkopf homolog 4 (Xenopus laevis)	0.44	AAGCCAAGTATTAAGAAATCA	NM_014420:	NM_014420:
1737	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehy	-0.07	CTCCAGCATCGTCTCATGTAA	NM_001931:	NM_001931:
1737	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehy	0.23	TTGGTTTATCATCGATGGGAA	NM_001931:	NM_001931:
1738	DLD	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydro	1.37	ACGATAGATGAAGATACAATA	NM_000108:	NM_000108:
1738	DLD	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydro	-0.01	CCCACTTATTCAAACAGAATA	NM_000108:	NM_000108:
1739	DLG1	discs, large homolog 1 (Drosophila)	0.36	AACAGTGAAATTCAATTCTAA	NM_004087:	NM_004087:
1739	DLG1	discs, large homolog 1 (Drosophila)	0.18	ACGGGTTATTAACATATTTCA	NM_004087:	NM_004087:
1740	DLG2	discs, large homolog 2, chapsyn-110 (Drosophila)	-4.22	CTCGACTAACCCACGAAGTAA	NM_001364:	NM_001364:
1740	DLG2	discs, large homolog 2, chapsyn-110 (Drosophila)	0.41	TACGCTCGATTTGAGGCCAAA	NM_001364:	NM_001364:
1742	DLG4	discs, large homolog 4 (Drosophila)	-4.49	ATCGCTCAGTATAAACCAGAA	NM_001365:	NM_001365:
1742	DLG4	discs, large homolog 4 (Drosophila)	0.01	TACGAGGAAATCACATTGGAA	NM_001365:	NM_001365:
9231	DLG5	discs, large homolog 5 (Drosophila)	-0.15	TTGCCTGTTTGTCGACTATAA	NM_004747:	NM_004747:
9231	DLG5	discs, large homolog 5 (Drosophila)	0.08	TTCGAGTAACTTGCAGTTCAA	NM_004747:	NM_004747:
9787	DLG7	discs, large homolog 7 (Drosophila)	0.68	AAGGAATACGAACGAAATAGA	NM_014750:	NM_014750:
9787	DLG7	discs, large homolog 7 (Drosophila)	0.66	TACTTTGAATTCACAAACTAA	NM_014750:	NM_014750:
8788	DLK1	delta-like 1 homolog (Drosophila)	0.60	CTCTTAATGCATGATACAGAA	NM_003836:	NM_001032997:NM_003836:
8788	DLK1	delta-like 1 homolog (Drosophila)	-0.60	CTGGACGATGGCCTCTATGAA	NM_003836:	NM_001032997:NM_003836:
10683	DLL3	delta-like 3 (Drosophila)	0.19	AAGGCTATTATTGTGATCAAA	NM_016941:	NM_016941:NM_203486:
10683	DLL3	delta-like 3 (Drosophila)	-1.11	CCTGAAGATGTAGACCCTCAA	NM_016941:	NM_016941:NM_203486:
54567	DLL4	delta-like 4 (Drosophila)	-0.72	CACGCCGGTATTGGGCACCAA	NM_019074:	NM_019074:
54567	DLL4	delta-like 4 (Drosophila)	0.12	GTCTAGTATTTCAATAATTTA	NM_019074:	NM_019074:
1747	DLX3	distal-less homeobox 3	0.07	CATCTTTATATATAATGTTAA	NM_005220:	NM_005220:
1747	DLX3	distal-less homeobox 3	1.04	TGGACTCATCTTTATATATAA	NM_005220:	NM_005220:
1755	DMBT1	deleted in malignant brain tumors 1	0.81	AGGGTTACTTACATAAAGGAA	NM_004406:	NM_017579:NM_004406:NM_007329:
1755	DMBT1	deleted in malignant brain tumors 1	0.21	CCCGGGAACTATCCAAACAAT	NM_004406:	NM_017579:NM_004406:NM_007329:
11144	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homolog	0.29	TCCCACATGTTACTAAAGAAA	NM_007068:	NM_007068:
11144	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homolog	-0.26	TCCCTGATTTATGATAACTAT	NM_007068:	NM_007068:
1760	DMPK	dystrophia myotonica-protein kinase	-0.06	AACCAGAACTTCGCCAGTCAA	NM_004409:	NM_004409:
1761	DMRT1	doublesex and mab-3 related transcription factor 1	-0.60	ATGGAGTACTTTGTTATATAA	NM_021951:	NM_021951:
1761	DMRT1	doublesex and mab-3 related transcription factor 1	0.61	TTGGTAAAGGGTGTAATTTAA	NM_021951:	NM_021951:
63946	DMRTC2 (DM	DMRT-like family C2	-0.10	CCCACAGTCTAACCTACTCTA	XM_290331:	NM_033052:
8701	DNAH11	dynein, axonemal, heavy polypeptide 11	0.06	TACGTTGTACACGCTTTGCAA	NM_003777:	NM_003777:
8701	DNAH11	dynein, axonemal, heavy polypeptide 11	0.84	GAGCTTGTTAACCATAATTAA	NM_003777:	NM_003777:
56171	DNAH7	dynein, axonemal, heavy polypeptide 7	0.24	CGGGCTAATATCATTCGATCA	NM_018897:	NM_018897:
56171	DNAH7	dynein, axonemal, heavy polypeptide 7	1.24	TCGGAAGGCAATATATTAGAA	NM_018897:	NM_018897:
1770	DNAH9	dynein, axonemal, heavy polypeptide 9	-0.20	TGGACTGACCTCAATCCCAAA	NM_001372:	NM_001372:
1770	DNAH9	dynein, axonemal, heavy polypeptide 9	0.68	AGGCATCGACATTGACTTTAA	NM_001372:	NM_001372:
27019	DNAI1	dynein, axonemal, intermediate polypeptide 1	0.26	AAGGCCCACATATTTGACTTA	NM_012144:	NM_012144:
27019	DNAI1	dynein, axonemal, intermediate polypeptide 1	-0.27	CAGCATTACCGCGATGAATTA	NM_012144:	NM_012144:
3301	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	-0.87	TCGCCTAATCATCGAATTTAA	NM_001539:	NM_001539:
3301	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	1.61	CTGGTGGACTTTGATCCAAAT	NM_001539:	NM_001539:
150353	DNAJB7	DnaJ (Hsp40) homolog, subfamily B, member 7	0.15	ACGACAGTCCGGGTAACATAA	NM_145174:	NM_145174:
150353	DNAJB7	DnaJ (Hsp40) homolog, subfamily B, member 7	-3.36	CAGGTTCAGACTACACAATTA	NM_145174:	NM_145174:
4189	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.86	CAAGTGCATGATTTCACTTTA	NM_012328:	NM_012328:
4189	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	1.45	TCGGATAGACTTATTTCTTTA	NM_012328:	NM_012328:
54431	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	0.46	CTCGACGGACTTATAATGTTT	NM_018981:	NM_018981:
54431	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	-0.07	CAGCTTAAGTTTGGTACACTA	NM_018981:	NM_018981:
23317	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	-0.92	TAGGTTGATTCTCTTCCTTAA	NM_015268:	NM_015268:
23317	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	0.14	CTGAGTTAATTTGGAATGATA	NM_015268:	NM_015268:
85406	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	-0.08	CTCCTTTATCCTGATATAATA	NM_032364:	NM_032364:
85406	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	-0.98	TTGGGTCAAGCAGAATATTAA	NM_032364:	NM_032364:
23341	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	0.13	TACGAGATTCTTTCAAATGAA	XM_497656:	NM_015291:
23341	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	0.17	CAGGAGTTTGCCGACACCTTA	XM_497656:	NM_015291:
9829	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	-3.80	AACCGTTAAGTTACTCATGAA	XM_375737:	NM_014787:
9829	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	0.05	TAGGTGTTATTTATTAACGTA	XM_375737:	NM_014787:
1773	DNASE1	deoxyribonuclease I	-0.07	ACCTGTGCTTACAGAAAGAAA	AJ298844:	NM_005223:
1773	DNASE1	deoxyribonuclease I	-2.58	TACCTGGATGTCCAAGAGAAA	AJ298844:	NM_005223:
1776	DNASE1L3	deoxyribonuclease I-like 3	-0.81	AAGGGCCTTCACCAACAGCAA	NM_004944:	NM_004944:
1776	DNASE1L3	deoxyribonuclease I-like 3	-0.36	CACGGTGAAGAAGAGCACCAA	NM_004944:	NM_004944:
1777	DNASE2	deoxyribonuclease II, lysosomal	0.21	AAGGGCCACCACGTTAGCCAA	NM_001375:	NM_001375:
1777	DNASE2	deoxyribonuclease II, lysosomal	-2.30	GACCTTGATTGTGTGCCTTAA	NM_001375:	NM_001375:
92737	DNER	delta-notch-like EGF repeat-containing transmembrane	0.63	TAGAGTATACCCGTTACTTAA	NM_139072:	NM_139072:
92737	DNER	delta-notch-like EGF repeat-containing transmembrane	-3.22	TCGGATCTGCTTGTGAAGAAA	NM_139072:	NM_139072:
1759	DNM1	dynamin 1	-1.28	CAGCTGGTCAATGCAACCACA	NM_004408:	NM_001005336:NM_004408:
1759	DNM1	dynamin 1	-2.08	CCGCATTAACCGAATCTTCCA	NM_004408:	NM_001005336:NM_004408:
1786	DNMT1	DNA (cytosine-5-)-methyltransferase 1	0.71	CCCATCGGTTTCCGCGCGAAA	NM_001379:	NM_001379:
1786	DNMT1	DNA (cytosine-5-)-methyltransferase 1	1.13	TCGCTTATCAACTAATGATTT	NM_001379:	NM_001379:
1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	-1.10	CACATTCGGTTGAGCAACATT	NM_004412:	NM_176086:NM_176084:NM_176085:NM_176081:NM_176083:NM_004412:
1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	2.22	AGCGTTATCGCCTACTTGGAA	NM_004412:	NM_176086:NM_176084:NM_176085:NM_176081:NM_176083:NM_004412:
1788	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	-1.08	AACACCGGGATCTATGTTTAA	NM_022552:	NM_022552:NM_175630:NM_175629:
1788	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	-3.85	CAGAACAAGCCCATGATTGAA	NM_022552:	NM_022552:NM_153759:NM_175629:
1789	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	-1.46	AAGGACTACTTTGCATGTGAA	NM_006892:	NM_006892:NM_175850:NM_175848:NM_175849:
1789	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	0.02	TAGAGTTTACCTTATGTTTAA	NM_006892:	NM_006892:NM_175850:NM_175848:NM_175849:
29947	DNMT3L	DNA (cytosine-5-)-methyltransferase 3-like	0.54	AAGGCTAACCAGCGAAATATA	NM_013369:	NM_175867:NM_013369:
29947	DNMT3L	DNA (cytosine-5-)-methyltransferase 3-like	-0.39	AAGCATGTGGTTGATGTCACA	NM_013369:	NM_175867:NM_013369:
23549	DNPEP	aspartyl aminopeptidase	0.05	AAGTGGATTGTCACTCAGAAA	NM_012100:	NM_012100:
23549	DNPEP	aspartyl aminopeptidase	0.33	GAGCTGAAGCTGGATTATTAA	NM_012100:	NM_012100:
30836	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	-0.38	AAGAAGAAATTTCGCAATTAA	NM_014597:	NM_014597:
30836	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	-0.77	CACGAACAGGCCAATGTTGAA	NM_014597:	NM_014597:
1793	DOCK1	dedicator of cytokinesis 1	0.07	ACGATCGTCAACGATGTGAAA	NM_001380:	NM_001380:
1793	DOCK1	dedicator of cytokinesis 1	-0.27	CACGCTGGTTTGAGACTGTTA	NM_001380:	NM_001380:
1794	DOCK2	dedicator of cytokinesis 2	0.15	AACGTAGATTCCTGAACTCAA	NM_004946:	NM_004946:
1794	DOCK2	dedicator of cytokinesis 2	-0.93	CAGGGTCTTCCTGAGAGCTAT	NM_004946:	NM_004946:
1796	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	-0.93	AGGGATCAAAGAAGATGGTTA	NM_001381:	NM_001381:
1796	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	2.18	CCGCCTGGACTGCAAAGTGAT	NM_001381:	NM_001381:
9046	DOK2	docking protein 2, 56kDa	1.38	CAGATTTCTTGGTGGCATTAA	NM_201349:	NM_201349:NM_003974:

9046	DOK2	docking protein 2, 56kDa	-0.56	CAGCAGACGTTTGGAAAGAAA	NM_201349:	NM_201349:NM_003974:
79930	DOK3	docking protein 3	1.18	TGCAGACTCACAGATAATAAA	NM_024872:	NM_024872:
79930	DOK3	docking protein 3	-1.58	CCCAGGCAATGAGCACCTCTA	NM_024872:	NM_024872:
55715	DOK4	docking protein 4	0.01	CTGGTATTTGTTGACTACCAT	NM_018110:	NM_018110:
55715	DOK4	docking protein 4	0.11	CCCTGCTGCAATGCAATTAAA	NM_018110:	NM_018110:
55816	DOK5	docking protein 5	2.00	TCAGGTGTTATCATAAGGTTA	NM_018431:	NM_177959:NM_018431:
55816	DOK5	docking protein 5	0.26	GACAGTCAGTATTGACAATAA	NM_018431:	NM_177959:NM_018431:
220164	DOK6	docking protein 6	-0.15	CTGAGCAACATGAAAGATTAA	NM_152721:	NM_152721:
220164	DOK6	docking protein 6	1.88	AACCATAATTTGGTGCATTAA	NM_152721:	NM_152721:
57171	DOLPP1	dolichyl pyrophosphate phosphatase 1	0.54	AAGAATGCACCAAACAAACAA	NM_020438:	NM_020438:
57171	DOLPP1	dolichyl pyrophosphate phosphatase 1	0.73	CAGGGTCTACCTGCTGTACCA	NM_020438:	NM_020438:
23033	DOPEY1	dopey family member 1	1.08	CCGGAGTTCTATGTACATAGA	NM_015018:	NM_015018:
23033	DOPEY1	dopey family member 1	-0.03	CCGGATTTCTGTTATGGGCAA	NM_015018:	NM_015018:
84444	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	-0.05	CCGCTGCCGGTCTACGATAAA	NM_032482:	NM_032482:
84444	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	-1.68	CCGGCCTTCGTCGAAGCAGAA	NM_032482:	NM_032482:
64174	DPEP2	dipeptidase 2	0.34	CAGGCACAAATATTTCTTGAA	NM_022355:	NM_022355:
64174	DPEP2	dipeptidase 2	0.98	CAAGGCTGTCATTGGATCCAA	NM_022355:	NM_022355:
64180	DPEP3	dipeptidase 3	1.57	ATGCTGAGAATAAACATGTTA	NM_022357:	NM_022357:
64180	DPEP3	dipeptidase 3	0.11	CAAGCATATGCTGAGAATAAA	NM_022357:	NM_022357:
8193	DPF1	D4, zinc and double PHD fingers family 1	0.21	CAGGAGGAAGAACAGGGCCAA	NM_004647:	NM_004647:
8193	DPF1	D4, zinc and double PHD fingers family 1	-1.23	CCGCATGACCTCGAGGTGGAA	NM_004647:	NM_004647:
5977	DPF2	D4, zinc and double PHD fingers family 2	-2.86	CTGGACCTGTTGAAAGAGAAA	NM_006268:	NM_006268:
5977	DPF2	D4, zinc and double PHD fingers family 2	-1.02	CTGGATGACCTCGATGATGAA	NM_006268:	NM_006268:
57628	DPP10	dipeptidyl-peptidase 10	0.17	TTGCATATAATGCACAATCTA	NM_020868:	NM_020868:NM_001004360:
57628	DPP10	dipeptidyl-peptidase 10	0.56	CAGAATGTCAAGGGCAGCTTA	NM_020868:	NM_020868:NM_001004360:
10072	DPP3	dipeptidyl-peptidase 3	-0.02	CACGTGACAGCTAGGGTTCAA	NM_005700:	NM_130443:NM_005700:
10072	DPP3	dipeptidyl-peptidase 3	0.40	CCGAGGAGAATTTGAAGGTTT	NM_005700:	NM_005700:
1803	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing prote	-2.41	ATCGGGAAGTGGCGTGTTCAA	NM_001935:	NM_001935:
1803	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing prote	0.44	CAGTAAAGAGGCGAAGTATTA	NM_001935:	NM_001935:
1804	DPP6	dipeptidyl-peptidase 6	-0.06	ACGCTAATGGTTAACCTGATA	NM_001936:	NM_001936:NM_130797:
1804	DPP6	dipeptidyl-peptidase 6	0.43	TCCCTACACGTTATTGGCTTA	NM_001936:	NM_001936:NM_130797:
54878	DPP8	dipeptidyl-peptidase 8	-1.17	ACGGTTTGTGGTAGTAATCTA	NM_017743:	NM_130434:NM_017743:NM_197961:
54878	DPP8	dipeptidyl-peptidase 8	0.53	CTGGGTGTTGAGATATTTGAA	NM_017743:	NM_130434:NM_017743:NM_197960:NM_197961:
91039	DPP9	dipeptidyl-peptidase 9	-1.87	CACCTCTACATATTATGGAAA	NM_139159:	NM_139159:
91039	DPP9	dipeptidyl-peptidase 9	-0.52	CCGAGAGAACTCCCTCCTCTA	NM_139159:	NM_139159:
1806	DPYD	dihydropyrimidine dehydrogenase	0.76	TCGAGAGTATCCTGGCTTTAA	NM_000110:	NM_000110:
1806	DPYD	dihydropyrimidine dehydrogenase	-0.82	TCGGTGAATGATGGAAAGCAA	NM_000110:	NM_000110:
1807	DPYS	dihydropyrimidinase	0.44	CGGCAGGAGATGGGAAGTTTA	NM_001385:	NM_001385:
1807	DPYS	dihydropyrimidinase	1.10	TGGGAAGTTTATTCCTCGAAA	NM_001385:	NM_001385:
1808	DPYSL2	dihydropyrimidinase-like 2	-0.19	CTCGTGTTTATTATTCCTTAA	NM_001386:	NM_001386:
1808	DPYSL2	dihydropyrimidinase-like 2	-1.85	CAGGCTTGCGTTATTGGCCTA	NM_001386:	NM_001386:
1812	DRD1	dopamine receptor D1	-0.97	ACGGTGAGTATCAATAACAAT	NM_000794:	NM_000794:
1812	DRD1	dopamine receptor D1	0.27	GACGGTGAGTATCAATAACAA	NM_000794:	NM_000794:
50632	DRD1IP	dopamine receptor D1 interacting protein	-2.02	CTGCGTGCTGATCATGTACAA	NM_015722:	NM_015722:
50632	DRD1IP	dopamine receptor D1 interacting protein	0.37	CCAGGTGGTCATCAAGACACA	NM_015722:	NM_015722:
1813	DRD2	dopamine receptor D2	-0.07	CACCGTTATCATGAAGTCTAA	NM_000795:	NM_000795:
1813	DRD2	dopamine receptor D2	-1.71	CACGGCTAAGAGGCTGCTGAA	NM_000795:	NM_016574:NM_000795:
1814	DRD3	dopamine receptor D3	0.36	ATGGCAGATTATCGACATCTT	NM_000796:	NM_033658:NM_000796:NM_033659:NM_033660:
1814	DRD3	dopamine receptor D3	2.07	CAGGTGGAGTCTGGAATTTCA	NM_000796:	NM_033663:NM_033658:NM_000796:NM_033659:NM_033660:
1815	DRD4	dopamine receptor D4	-0.37	CACCTGGCTGGGCTACGTCAA	NM_000797:	NM_000797:
1815	DRD4	dopamine receptor D4	-2.51	TTGTACGTTAATTAAACAAAT	NM_000797:	NM_000797:
1816	DRD5	dopamine receptor D5	1.22	CGGGCTGGACCTGCCAAACAA	NM_000798:	NM_000798:
1816	DRD5	dopamine receptor D5	0.85	CTGATTTATTCTGGTGTCTAA	NM_000798:	NM_000798:
57453	DSCAML1	Down syndrome cell adhesion molecule like 1	0.22	TCGATTTGTGGTGCAACCCAA	NM_020693:	NM_020693:
57453	DSCAML1	Down syndrome cell adhesion molecule like 1	-1.68	CAGGGTCATCGGCTATCCCTA	NM_020693:	NM_020693:
1828	DSG1	desmoglein 1	-1.49	CACGTTCACGATAACCGACCA	NM_001942:	NM_001942:
1828	DSG1	desmoglein 1	-3.92	CCCGTTGTTAGTGGACACCCA	NM_001942:	NM_001942:
1832	DSP	desmoplakin	0.42	AAGGGCCACGGTATTCGCTTA	NM_004415:	NM_004415:NM_001008844:
1832	DSP	desmoplakin	-3.35	CCGACATGAATCAGTAAGTAA	NM_004415:	NM_004415:NM_001008844:
1834	DSPP	dentin sialophosphoprotein	-0.43	TCGGATAGTAAAGAATATTAT	NM_014208:	NM_014208:
1834	DSPP	dentin sialophosphoprotein	-0.29	CATGATAGTAGCATAGGTCAA	NM_014208:	NM_014208:
51514	DTL	denticleless homolog (Drosophila)	-1.64	CCCAATATGGAACATGTACTA	NM_016448:	NM_016448:
51514	DTL	denticleless homolog (Drosophila)	0.24	CCGAGTCTACTGGGTATAACA	NM_016448:	NM_016448:
1837	DTNA	dystrobrevin, alpha	0.86	CCCGTTGTCATAGCTATTTCA	NM_001390:	NM_032980:NM_001390:NM_032975:
1837	DTNA	dystrobrevin, alpha	1.44	TGCGACCTATTCAATACATTA	NM_001390:	NM_032980:NM_001390:NM_032975:
84062	DTNBP1	dystrobrevin binding protein 1	-0.68	TTGGCTGTATGCGGAATTCCA	NM_032122:	NM_183041:NM_032122:
84062	DTNBP1	dystrobrevin binding protein 1	-1.65	CACCCAGCAAATGAAGCTGAA	NM_032122:	NM_183040:NM_183041:NM_032122:
1840	DTX1	deltex homolog 1 (Drosophila)	-1.42	GACCAAGAAGAAGCACCTTAA	NM_004416:	NM_004416:
1840	DTX1	deltex homolog 1 (Drosophila)	1.12	GTGGGAGTCAGCCAAGATTTA	NM_004416:	NM_004416:
113878	DTX2	deltex homolog 2 (Drosophila)	-3.84	CAAGACAGAGATGGACCGCAA	NM_020892:	NM_020892:
113878	DTX2	deltex homolog 2 (Drosophila)	2.20	CGGGACCATCCTCATAGTTTA	NM_020892:	NM_020892:
196403	DTX3	deltex 3 homolog (Drosophila)	-1.39	ACCGAATGTCATCACCTGGAA	NM_178502:	NM_178502:
196403	DTX3	deltex 3 homolog (Drosophila)	0.03	CGGCACCATTGTCATCCAGTA	NM_178502:	NM_178502:
151636	DTX3L	deltex 3-like (Drosophila)	1.18	TGGGCAAGCATTGGTAATAAA	NM_138287:	NM_138287:
151636	DTX3L	deltex 3-like (Drosophila)	1.18	TGGAATGATATTCACCACAAA	NM_138287:	NM_138287:
23220	DTX4	deltex 4 homolog (Drosophila)	-7.56	TAGCTACGTAATTGACTTCAA	XM_166213:	XM_166213:
23220	DTX4	deltex 4 homolog (Drosophila)	-5.65	CCCGGCATTCAGGGACCGGAA	XM_166213:	XM_166213:
1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	0.06	ATCAGTTGGAATTCTCCTAAA	NM_012145:	NM_012145:
1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	-0.85	TCCCGGAAAGATCAACTGAAA	NM_012145:	NM_012145:
53905	DUOX1	dual oxidase 1	0.25	CCAGTCTAACACCACAACTAA	NM_017434:	NM_017434:NM_175940:
53905	DUOX1	dual oxidase 1	-3.35	TCGGCGGAGGTTTGGCAAGAA	NM_017434:	NM_017434:NM_175940:
50506	DUOX2	dual oxidase 2	1.43	ACATCGAGGTATAATAAATAA	NM_014080:	NM_014080:
50506	DUOX2	dual oxidase 2	0.58	ATGGTATTAGAGATATCTTTA	NM_014080:	NM_014080:
1843	DUSP1	dual specificity phosphatase 1	0.24	TAGCGTCAAGACATTTGCTGA	NM_004417:	NM_004417:
1843	DUSP1	dual specificity phosphatase 1	0.36	CTGTACTATCCTGTAAATATA	NM_004417:	NM_004417:
11221	DUSP10	dual specificity phosphatase 10	0.56	ATGAGAATACAGGCTCTCTAA	NM_007207:	NM_007207:
11221	DUSP10	dual specificity phosphatase 10	-0.76	CAGGTTCATAGACCGAAGATA	NM_007207:	NM_144728:NM_007207:NM_144729:
8446	DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	0.15	CAGAAACTGTTCCTTACTTAA	NM_003584:	NM_003584:
8446	DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	-1.13	CCCTTATGTATTCAAGCTTAA	NM_003584:	NM_003584:
11266	DUSP12	dual specificity phosphatase 12	0.49	ATGCTTTACATGGCAATCAAA	NM_007240:	NM_007240:
11266	DUSP12	dual specificity phosphatase 12	0.62	TACCGTTTCACAAGGATTGAA	NM_007240:	NM_007240:
51207	DUSP13	dual specificity phosphatase 13	-2.19	ACCCTGAGATGTAAACAGCAA	NM_016364:	NM_001007271:NM_001007273:NM_001007272:NM_001007274:NM_016364:NM_001007275:
51207	DUSP13	dual specificity phosphatase 13	0.69	TCAGTCCATCTCTATAATAAA	NM_016364:	NM_001007271:NM_001007273:NM_001007272:NM_001007274:NM_016364:NM_001007275:
11072	DUSP14	dual specificity phosphatase 14	1.14	AAGGGAATGCATACATTGCTA	NM_007026:	NM_007026:

11072	DUSP14	dual specificity phosphatase 14	0.15	ACCCTTATTATTTAGCTGTTA	NM_007026:	NM_007026:
128853	DUSP15	dual specificity phosphatase 15	0.44	ACGGGCCTGGAGGGTATTAAA	NM_177991:	NM_177991:NM_001012644:NM_080611:
128853	DUSP15	dual specificity phosphatase 15	2.23	CACCACGATTGTGACAGCGTA	NM_177991:	NM_177991:NM_001012644:NM_080611:
80824	DUSP16	dual specificity phosphatase 16	0.18	AAGGTTGTAGTTTACGATCAA	NM_030640:	NM_030640:
80824	DUSP16	dual specificity phosphatase 16	0.38	CCGGCCATTTGTGGAATACAA	NM_030640:	NM_030640:
150290	DUSP18	dual specificity phosphatase 18	1.64	ACGGGTCTCTCTCCCGAAGAA	NM_152511:	NM_152511:
150290	DUSP18	dual specificity phosphatase 18	0.55	CCAGATCACCATGGTCATCAA	NM_152511:	NM_152511:
142679	DUSP19	dual specificity phosphatase 19	0.03	ATGGTCAGTATCACTGGATAA	NM_080876:	NM_080876:
142679	DUSP19	dual specificity phosphatase 19	-1.84	CAGAGTTAACCTAATGAGTCA	NM_080876:	NM_080876:
1844	DUSP2	dual specificity phosphatase 2	0.35	CAGCCTGAGAGCTCCAAGGAA	NM_004418:	NM_004418:
1844	DUSP2	dual specificity phosphatase 2	-0.05	CTGGTCCACCACCATGTTGAA	NM_004418:	NM_004418:
63904	DUSP21	dual specificity phosphatase 21	0.20	AACGTAGTAAGCCTTACCTTA	NM_022076:	NM_022076:
63904	DUSP21	dual specificity phosphatase 21	-0.22	TCGGTGGAAGTGGTCAACGTA	NM_022076:	NM_022076:
56940	DUSP22	dual specificity phosphatase 22	-5.71	CATGTTTATGTTGAGAACTAA	NM_020185:	NM_020185:
56940	DUSP22	dual specificity phosphatase 22	0.37	GGGCAACTTAGCCAAGTTTAA	NM_020185:	NM_020185:
54935	DUSP23	dual specificity phosphatase 23	-0.02	CAGTTCTACCAGCGAACGAAA	NM_017823:	NM_017823:
54935	DUSP23	dual specificity phosphatase 23	0.10	GAAGTGGACTAAAGTATTAAA	NM_017823:	NM_017823:
78986	DUSP26	dual specificity phosphatase 26 (putative)	-0.26	TCCAAGCGTCTCGAGGATAAA	NM_024025:	NM_024025:
78986	DUSP26	dual specificity phosphatase 26 (putative)	-3.88	CAGCGAAGAGATGGTGTGAAA	NM_024025:	NM_024025:
92235	DUSP27 (dua	dual specificity phosphatase 27 (putative)	-3.44	CAGAACTGGATTGCCAATGTA	XM_043739:	XM_043739:
92235	DUSP27 (dua	dual specificity phosphatase 27 (putative)	0.14	TCCGATATTCTTCCCGCAGTA	XM_043739:	XM_043739:
1845	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-relate	1.68	CCCGCGGATCTACGTGGGCAA	NM_004090:	NM_004090:
1845	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-relate	1.12	CCGTATTTACTTAACAAGATT	NM_004090:	NM_004090:
1848	DUSP6	dual specificity phosphatase 6	2.83	CTGCATTGCGAGACCAATCTA	NM_001946:	NM_001946:
1848	DUSP6	dual specificity phosphatase 6	3.19	TACGGACACTATTATCACTAA	NM_001946:	NM_001946:NM_022652:
1849	DUSP7	dual specificity phosphatase 7	3.25	CAAGGTGGTTTCAACAAGTTT	NM_001947:	NM_001947:
1849	DUSP7	dual specificity phosphatase 7	-7.81	CGGCGGCGAGTTCACCTACAA	NM_001947:	NM_001947:
1850	DUSP8	dual specificity phosphatase 8	3.59	CCGCTCCTTCGTGGAGTACAA	NM_004420:	NM_004420:
1850	DUSP8	dual specificity phosphatase 8	3.31	TCCATCGAGTTCATCGATAAA	NM_004420:	NM_004420:
1854	DUT	dUTP pyrophosphatase	-3.52	AAGCCTTGGATGACACCGAAA	NM_001948:	NM_001948:NM_001025248:NM_001025249:
1854	DUT	dUTP pyrophosphatase	-3.31	TCCCTTCTCTTCACTAGTCTA	NM_001948:	NM_001948:NM_001025248:NM_001025249:
1855	DVL1	dishevelled, dsh homolog 1 (Drosophila)	-0.26	CAGCGTTTAGATGGTTAACAT	NM_004421:	NM_181870:NM_182779:NM_004421:
1855	DVL1	dishevelled, dsh homolog 1 (Drosophila)	0.74	CTGGAGTAGGGATCTAATTTA	NM_004421:	NM_181870:NM_182779:NM_004421:
1856	DVL2 (dishev	dishevelled, dsh homolog 2 (Drosophila)	-2.57	CTGGGAGATTTGGGCCATGTA	NM_004422:	NM_004422:
1856	DVL2 (dishev	dishevelled, dsh homolog 2 (Drosophila)	-2.83	CACGCTAAACATGGAGAAGTA	NM_004422:	NM_004422:
1857	DVL3	dishevelled, dsh homolog 3 (Drosophila)	-2.14	ACCAAGTATGTTCCTCCTGAA	NM_004423:	NM_004423:
1857	DVL3	dishevelled, dsh homolog 3 (Drosophila)	0.56	CTCCTGGTTACTTCATCACAA	NM_004423:	NM_004423:
1778	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	-1.52	CAGGTGGGTGTACATTACGAA	NM_001376:	NM_001376:
1778	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	-4.52	CAGGAGGTAATTGCAGACAAA	NM_001376:	NM_001376:
1783	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	0.40	TAGAATGATAATTGTGGTATA	NM_006141:	NM_006141:
1783	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	0.29	TCGACTTGTTGTATAAGTATA	NM_006141:	NM_006141:
1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	-0.43	CAAGAATGGGTTGCCATTAAA	NM_001396:	NM_001396:NM_130437:NM_130438:NM_101395:NM_130436:
1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	-0.90	TACGGTCGCTGACTACTTGAA	NM_001396:	NM_001396:NM_130437:NM_130438:NM_101395:NM_130436:
9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	-2.90	CACGGAGATGAAGTACTATAT	NM_004714:	NM_006484:NM_004714:NM_006483:
9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	-5.52	CCGGACCTACCGCTACAGCAA	NM_004714:	NM_006484:NM_004714:NM_006483:
8445	DYRK2 (dual-	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	2.28	TAGAAGCGGTATTAAAGTAAT	NM_003583:	NM_003583:NM_006482:
8445	DYRK2 (dual-	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0.88	TGCACAGAGATTATTGTATTA	NM_003583:	NM_003583:NM_006482:
8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	3.01	AGCCAATAAGCTTAAAGCTAA	NM_003582:	NM_003582:NM_001004023:
8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	-0.75	TCGACAGTACGTGGCCCTAAA	NM_003582:	NM_003582:NM_001004023:
8798	DYRK4 (dual-	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	0.51	CTCCATATGAACAAAGTGAAA	NM_003845:	NM_003845:
8798	DYRK4 (dual-	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	-1.44	CTGCATCACGGCGGAGTTGTA	NM_003845:	NM_003845:
9666	DZIP3	zinc finger DAZ interacting protein 3	-1.30	CTGGGCTAAGTTTCATATCTA	NM_014648:	NM_014648:
9666	DZIP3	zinc finger DAZ interacting protein 3	-0.03	CTCGCTCAATTGAATAATTGA	NM_014648:	NM_014648:
1869	E2F1	E2F transcription factor 1	-0.83	ACGCTATGAGACCTCACTGAA	NM_005225:	NM_005225:
1869	E2F1	E2F transcription factor 1	-0.39	CAGATGGTTATGGTGATCAAA	NM_005225:	NM_005225:
1870	E2F2	E2F transcription factor 2	0.15	TTGAGACGAGGGATTATTTCA	NM_004091:	NM_004091:
1870	E2F2	E2F transcription factor 2	0.77	TAGGGACCAGGTAGACTTTAA	NM_004091:	NM_004091:
1871	E2F3	E2F transcription factor 3	0.30	TACAGTATTTGCGTTACTTTA	NM_001949:	NM_001949:
1871	E2F3	E2F transcription factor 3	1.00	TTGCGTTACTTTAAGTACTAA	NM_001949:	NM_001949:
1874	E2F4	E2F transcription factor 4, p107/p130-binding	-0.02	AGGTATCGGGCTAATCGAGAA	NM_001950:	NM_001950:
1874	E2F4	E2F transcription factor 4, p107/p130-binding	-1.18	AACGAATGGATTCCTATATAA	NM_001950:	NM_001950:
1875	E2F5	E2F transcription factor 5, p130-binding	0.31	AAGGACTCATTACTTGTCTTA	NM_001951:	NM_001951:
1875	E2F5	E2F transcription factor 5, p130-binding	0.97	CAACTTTAATTTAGATGATAA	NM_001951:	NM_001951:
79733	E2F8	E2F transcription factor 8	0.66	CACGTGGGAAACCAAACTTTA	NM_024680:	NM_024680:
79733	E2F8	E2F transcription factor 8	2.23	CAGAGGATGTCCATTAATCAA	NM_024680:	NM_024680:
85403	EAF1 (ELL as	ELL associated factor 1	-1.50	AACCAATAGGTTGGAAGACAA	NM_033083:	NM_033083:
85403	EAF1 (ELL as	ELL associated factor 1	-1.92	TAGCTTGAATTCAGTCCCTAA	NM_033083:	NM_033083:
9166	EBAG9	estrogen receptor binding site associated, antigen, 9	0.94	CACCCAGTTTCGGTTATTTAA	NM_198120:	NM_004215:NM_198120:
9166	EBAG9	estrogen receptor binding site associated, antigen, 9	0.11	CTCTTAGTGATTGAGACTCAA	NM_198120:	NM_004215:NM_198120:
1880	EBI2 (Epstein	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-cou	0.52	CACGAATAGCCTACTATGCAA	NM_004951:	NM_004951:
1880	EBI2 (Epstein	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-cou	-0.62	TAGAAAGGACTGAATAGATTA	NM_004951:	NM_004951:
10148	EBI3 (Epstein	Epstein-Barr virus induced gene 3	-0.46	CTGAACTGTCACTGTGAGATA	NM_005755:	NM_005755:
10148	EBI3 (Epstein	Epstein-Barr virus induced gene 3	0.00	CTGAGAAATGGAGATGTACTA	NM_005755:	NM_005755:
10682	EBP	emopamil binding protein (sterol isomerase)	-0.29	ACTGGACAACTTTGTACCTAA	NM_006579:	NM_006579:
10682	EBP	emopamil binding protein (sterol isomerase)	-0.14	CACAGTGTGCATGGAAACCAT	NM_006579:	NM_006579:
11319	ECD	ecdysoneless homolog (Drosophila)	-1.26	CAGACTACCGATAACAATTCA	NM_007265:	NM_007265:
11319	ECD	ecdysoneless homolog (Drosophila)	-0.52	CTGGTACGGGAGAATCTGTTA	NM_007265:	NM_007265:
1889	ECE1	endothelin converting enzyme 1	-4.07	CCCGCCCATGGTGAACGCCTA	NM_001397:	NM_001397:
1889	ECE1	endothelin converting enzyme 1	-2.38	CAGATGCCTGCTCAACAACTA	NM_001397:	NM_001397:
9718	ECE2	endothelin converting enzyme 2	-4.95	CACGTTTGACCGGCAAAGCAA	NM_014693:	NM_001037324:NM_014693:
9718	ECE2	endothelin converting enzyme 2	-1.46	CACGGAACCAAGCATCCTGAA	NM_014693:	NM_001037324:NM_014693:
9427	ECEL1	endothelin converting enzyme-like 1	0.70	CTGCAAAGTCTGGTCAATAAA	NM_004826:	NM_004826:
9427	ECEL1	endothelin converting enzyme-like 1	-9.04	CAGGTGCTGACTGACAAGCAT	NM_004826:	NM_004826:
1890	ECGF1	endothelial cell growth factor 1 (platelet-derived)	-0.36	CACAGCCTCCATTCTCAGTAA	NM_001953:	NM_001953:
1894	ECT2	epithelial cell transforming sequence 2 oncogene	0.22	CTCAATTTATGCAGAGATTAA	NM_018098:	NM_018098:
1894	ECT2	epithelial cell transforming sequence 2 oncogene	-0.93	TTGCCTAGAGATAGCAAGAAA	NM_018098:	NM_018098:
1896	EDA	ectodysplasin A	0.78	CTGGGATGTAAGTTTGTGTAA	NM_001399:	NM_001399:NM_001005609:
1896	EDA	ectodysplasin A	2.10	AGGCGTGTTCGCCGCAATAAA	NM_001399:	NM_001005610:NM_001005614:NM_001005612:NM_001399:NM_001005609:
60401	EDA2R	ectodysplasin A2 receptor	0.50	CCAATTGATCAGATTACTAAA	NM_021783:	NM_021783:
60401	EDA2R	ectodysplasin A2 receptor	0.15	ACCAATTGATCAGATTACTAA	NM_021783:	NM_021783:
10913	EDAR	ectodysplasin A receptor	0.04	CCAGGTATTATTTCAGGTTTA	NM_022336:	NM_022336:
10913	EDAR	ectodysplasin A receptor	1.39	CAGAACAATGAGATCATAATA	NM_022336:	NM_022336:
128178	EDARADD (E	EDAR-associated death domain	1.02	CTGAAATACGGTAAAGATTTA	NM_080738:	NM_080738:NM_145861:
128178	EDARADD (E	EDAR-associated death domain	0.65	CCCTAGCACTTTATCCTTTAA	NM_080738:	NM_080738:NM_145861:
51366	EDD1	E3 ubiquitin protein ligase, HECT domain containing, 1	-0.56	TGCGGTGAAGTCAATGTGCAA	NM_015902:	NM_015902:
51366	EDD1	E3 ubiquitin protein ligase, HECT domain containing, 1	0.42	AGGCCTGTCGACAATATCTAA	NM_015902:	NM_015902:

8721	EDF1	endothelial differentiation-related factor 1	-0.55	CACGGTGACGGTGCTGCGCAA	NM_003792:	NM_003792:NM_153200:
8721	EDF1	endothelial differentiation-related factor 1	-1.88	CAGAAGGACCTGGCCACGAAA	NM_003792:	NM_003792:NM_153200:
1901	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	1.07	ATGATCGATCATCTATAGCAA	NM_001400:	NM_001400:
1901	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	-1.53	TAGCATTGTCAAGCTCCTAAA	NM_001400:	NM_001400:
1902	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	1.68	CAAGACTTGATATATATTGAA	NM_001401:	NM_001401:NM_057159:
1902	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	0.03	CACTATAATATTGTTCCCATA	NM_001401:	NM_001401:NM_057159:
1903	EDG3	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	-2.27	CCGCAGTATCTAAGTATCTCA	NM_005226:	NM_005226:
1903	EDG3	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	-4.06	GCGGCACTTGACAATGATCAA	NM_005226:	NM_005226:
9170	EDG4	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	2.96	CCCGCGAGTCTGTCCACTATA	NM_004720:	NM_004720:
9170	EDG4	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	0.95	GACCATCGGCTTCTTCTATAA	NM_004720:	NM_004720:
9294	EDG5	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	1.18	ACCCACGTTTCTGGAGGGCAA	NM_004230:	NM_004230:
9294	EDG5	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	-0.69	CACCCTGAATTCCCTGCTCAA	NM_004230:	NM_004230:
8698	EDG6	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	3.02	CAGCCGGCTCATTGTTCTGCA	NM_003775:	NM_003775:
8698	EDG6	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	1.35	CCGGAGCTTCCACCACCGACA	NM_003775:	NM_003775:
23566	EDG7	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	0.85	ACCCAGGTGATGACTGTCTTA	NM_012152:	NM_012152:
23566	EDG7	endothelial differentiation, lysophosphatidic acid G-protein-coupled re	-0.21	ATAGAGGATAGTATTAGCCAA	NM_012152:	NM_012152:
53637	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	1.18	CACAATGTGAACAAACAGACA	NM_030760:	NM_030760:
53637	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	-0.01	CAGCCAAATCCTATCTGGTAA	NM_030760:	NM_030760:
10085	EDIL3	EGF-like repeats and discoidin I-like domains 3	-1.16	TCCGGGAGACGGGATCATGAA	NM_005711:	NM_005711:
10085	EDIL3	EGF-like repeats and discoidin I-like domains 3	-1.07	TTGGGCAATGTACAAAGTGAA	NM_005711:	NM_005711:
1906	EDN1	endothelin 1	0.12	ACCGAGCACATTGGTGACAGA	NM_001955:	NM_001955:
1906	EDN1	endothelin 1	-2.31	CAGGTCGGAGACCATGAGAAA	NM_001955:	NM_001955:
1907	EDN2	endothelin 2	1.64	CGAACTTGTGTTTATAATAAA	NM_001956:	NM_001956:
1907	EDN2	endothelin 2	2.22	GAGGGACATTTCCACAGTCAA	NM_001956:	NM_001956:
1908	EDN3	endothelin 3	0.57	TTGCAGGAAGCCGACTGTAAA	NM_000114:	NM_207034:NM_000114:NM_207032:NM_207033:
1908	EDN3	endothelin 3	-0.01	TAGACACAGATCATAGCTCTA	NM_000114:	NM_207034:NM_000114:NM_207032:NM_207033:
1909	EDNRA	endothelin receptor type A	0.47	CTGGTGAATGTTCAATGGGAA	NM_001957:	NM_001957:
1909	EDNRA	endothelin receptor type A	0.01	TAGCCTAACATGATTATTTGA	NM_001957:	NM_001957:
1910	EDNRB	endothelin receptor type B	-7.31	CAGGATATTCACACAACACTT	NM_000115:	NM_000115:
1910	EDNRB	endothelin receptor type B	-0.43	GAGCTTTAACTCGGTCTTAAA	NM_000115:	NM_000115:
8726	EED	embryonic ectoderm development	-2.29	CTGAACGCCCTGATACACCTA	NM_003797:	NM_152991:NM_003797:
8726	EED	embryonic ectoderm development	2.26	AGGCATAATTAGGATAATAAA	NM_003797:	NM_152991:NM_003797:
1917	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	-2.98	CAAGGAGAAGACCCACATCAA	NM_001958:	NM_001958:
1917	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	-0.14	CTGGAAGTTCGAGACCACCAA	NM_001958:	NM_001958:
9521	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	-0.20	CAAATCGGGCTTAATCTTAAA	NM_004280:	NM_004280:
9521	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	-1.50	CAAGAACAGACTATATACTAA	NM_004280:	NM_004280:
29904	EEF2K	eukaryotic elongation factor-2 kinase	-0.02	CAGACACTACATGAACACGAA	NM_013302:	NM_013302:
29904	EEF2K	eukaryotic elongation factor-2 kinase	-0.01	CGGGATGGCGCTCTTCTTCTA	NM_013302:	NM_013302:
30008	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	-0.03	CACGGAATGCACAGATGGCTA	NM_016938:	NM_016938:
30008	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	-0.03	CCGCTCCGCTGCCGTCATCAA	NM_016938:	NM_016938:
1942	EFNA1	ephrin-A1	0.23	CACGTGTATAGTATCTGTATA	NM_004428:	NM_004428:NM_182685:
1942	EFNA1	ephrin-A1	0.93	TACAATGTTCTTTGTCTCAAA	NM_004428:	NM_004428:NM_182685:
1943	EFNA2	ephrin-A2	-4.83	CACGGTGGAGGTGAGCATCAA	NM_001405:	NM_001405:
1943	EFNA2	ephrin-A2	-2.41	CCGCGCCAACTCGGACCGCTA	NM_001405:	NM_001405:
1944	EFNA3	ephrin-A3	1.42	CAGGCATGTACAGACTCTATA	NM_004952:	NM_004952:
1944	EFNA3	ephrin-A3	-3.31	CCGGCATGCGGTGTACTGGAA	NM_004952:	NM_004952:
1946	EFNA5	ephrin-A5	-2.89	AAGGTCCTGTCTAAAGCTCAA	NM_001962:	NM_001962:
1946	EFNA5	ephrin-A5	1.48	TTCGATGTTAACGACAAAGTA	NM_001962:	NM_001962:
1947	EFNB1	ephrin-B1	2.07	CTCACGGTAATTAATGTCTTA	NM_004429:	NM_004429:
1947	EFNB1	ephrin-B1	-4.08	ACGGACTACAGAGAACAACTA	NM_004429:	NM_004429:
1948	EFNB2	ephrin-B2	0.36	CTGGTACTATACCCACAGATA	NM_004093:	NM_004093:
1948	EFNB2	ephrin-B2	2.36	GACGTATTTATAATAGGTATA	NM_004093:	NM_004093:
1949	EFNB3	ephrin-B3	0.08	CTACTGGAACTCGGCGAATAA	NM_001406:	NM_001406:
1949	EFNB3	ephrin-B3	0.19	CACCACGATTACTACATCATT	NM_001406:	NM_001406:
1950	EGF	epidermal growth factor (beta-urogastrone)	-0.88	CTGGACTGATACAGGGATTAA	NM_001963:	NM_001963:
1950	EGF	epidermal growth factor (beta-urogastrone)	-2.29	TCGCAGGAAATGGGAATTCTA	NM_001963:	NM_001963:
346007	EGFL11	EGF-like-domain, multiple 11	-1.69	AAGCTTGGAGCAAGACATATA	NM_198283:	NM_198283:
346007	EGFL11	EGF-like-domain, multiple 11	-0.94	GAGGAATAATGCTACATGTAA	NM_198283:	NM_198283:
1954	EGFL4	EGF-like-domain, multiple 4	-1.05	TCCGATGTACCTATTTAAGAA	NM_001410:	NM_001410:
1954	EGFL4	EGF-like-domain, multiple 4	-1.61	CCCGCTGTAAGTGGTGTACCA	NM_001410:	NM_001410:
25975	EGFL6	EGF-like-domain, multiple 6	0.20	ATGCTACGTGTGTGAACTCTA	NM_015507:	NM_015507:
25975	EGFL6	EGF-like-domain, multiple 6	0.67	CTGAATGTTACTATCTTTATA	NM_015507:	NM_015507:
65989	EGFL9	EGF-like-domain, multiple 9	0.09	AAGACCTGTGAGCTTGTCTTA	NM_023932:	NM_023932:NM_206539:
65989	EGFL9	EGF-like-domain, multiple 9	0.92	AACCTGCCTTGACGGCATAAA	NM_023932:	NM_023932:NM_206539:
1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b	-1.10	CAGGAACTGGATATTCTGAAA	NM_005228:	NM_005228:NM_201284:NM_201283:NM_201282:
1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b	-6.31	CCCATCCAATTTATCAAGGAA	NM_005228:	NM_005228:
112398	EGLN2	egl nine homolog 2 (C. elegans)	0.27	CTGGCTAGGGTTACCCAGCAA	NM_017555:	NM_017555:
112398	EGLN2	egl nine homolog 2 (C. elegans)	-3.01	CAGGGAATTGTGTCTGCAGAA	NM_017555:	NM_017555:
112399	EGLN3	egl nine homolog 3 (C. elegans)	-0.59	CTGATAGATTCGGTAATACTA	NM_022073:	NM_022073:
112399	EGLN3	egl nine homolog 3 (C. elegans)	0.11	TAGGTCTACTGATATACAATA	NM_022073:	NM_022073:
1958	EGR1	early growth response 1	1.14	TTGAAATTTGCTAAAGGGAAA	NM_001964:	NM_001964:
1958	EGR1	early growth response 1	-0.70	TTGGCTTATAAACACATTGAA	NM_001964:	NM_001964:
1959	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	0.11	AAGTGTTACCTTTGTAGTCAA	NM_000399:	NM_000399:
1959	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	1.04	TCCACTCTCTACAATCCGTAA	NM_000399:	NM_000399:
10938	EHD1	EH-domain containing 1	-0.09	CTGCCCTACCCTCTCACTTAA	NM_006795:	NM_006795:
10938	EHD1	EH-domain containing 1	-0.02	ATGGAATTGTGTGCACAAGAA	NM_006795:	NM_006795:
79813	EHMT1	euchromatic histone-lysine N-methyltransferase 1	-0.10	AACGAAGAATGGGAACCTATA	NM_024757:	NM_024757:
79813	EHMT1	euchromatic histone-lysine N-methyltransferase 1	0.44	CAACGGATACATCTTAAATAA	NM_024757:	NM_024757:
10919	EHMT2	euchromatic histone-lysine N-methyltransferase 2	1.20	CCAGGAATTTAACAAGATTGA	NM_006709:	NM_025256:NM_006709:
10919	EHMT2	euchromatic histone-lysine N-methyltransferase 2	-1.59	CACCATGAACATCGATCGCAA	NM_006709:	NM_025256:NM_006709:
9538	EI24	etoposide induced 2.4 mRNA	-1.55	AACCACGTATTGTTAGTAGAA	NM_004879:	NM_001007277:NM_004879:
9538	EI24	etoposide induced 2.4 mRNA	0.86	ATCGTTGGTTCAATAAAGGAA	NM_004879:	NM_004879:
27102	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	0.01	CCCGAATATGACGAATCTGAT	NM_014413:	NM_014413:
27102	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	0.01	CTGATTAAGGGTGCAACTAAA	NM_014413:	NM_014413:
5610	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	0.22	ACGGAAAGACTTACGTTATTA	NM_002759:	NM_002759:
5610	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	-0.16	CGGAAAGACTTACGTTATTAA	NM_002759:	NM_002759:
9451	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	2.23	CACAAACTGTATAACGGTTTA	NM_004836:	NM_004836:
9451	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	0.39	CGGCAGGTCATTAGTAATTAT	NM_004836:	NM_004836:
440275	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	1.03	TCCGATAATCTTGCAGTGCAA	BX640919:	NM_001013703:
26523	EIF2C1	eukaryotic translation initiation factor 2C, 1	0.77	TAGGCTTAACATAAAGCCGAA	NM_012199:	NM_012199:
26523	EIF2C1	eukaryotic translation initiation factor 2C, 1	-2.14	CTCCAAGAATTGTGCAAGTAA	NM_012199:	NM_012199:
27161	EIF2C2	eukaryotic translation initiation factor 2C, 2	0.00	ATACGGGTCTGTGGTGATAAA	NM_012154:	NM_012154:
27161	EIF2C2	eukaryotic translation initiation factor 2C, 2	0.29	ACAGATCCATACGTCCGTGAA	NM_012154:	NM_012154:
192669	EIF2C3	eukaryotic translation initiation factor 2C, 3	0.88	CTGACTGATTCTCATCGGGTA	NM_024852:	NM_177422:NM_024852:
192669	EIF2C3	eukaryotic translation initiation factor 2C, 3	-0.68	CTCCTATAGGAAGTATCGCAA	NM_024852:	NM_177422:NM_024852:
192670	EIF2C4	eukaryotic translation initiation factor 2C, 4	1.39	TTGGACGGGATAGGGTTGATA	NM_017629:	NM_017629:

192670	EIF2C4	eukaryotic translation initiation factor 2C, 4	-0.30	AAGGCATGTATTAGCTTGGAA	NM_017629:	NM_017629:
8665	EIF3S5	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa	-0.31	TACGCGTACTACGACACTGAA	NM_003754:	NM_003754:
8663	EIF3S8	eukaryotic translation initiation factor 3, subunit 8, 110kDa	-7.80	CCGCCGACGCATGATCAGCAA	NM_003752:	NM_003752:NM_001037808:
8663	EIF3S8	eukaryotic translation initiation factor 3, subunit 8, 110kDa	-4.32	AACGAATGGATGAAGAATTTA	NM_003752:	NM_003752:NM_001037808:
1990	ELA1 (elastas	elastase 1, pancreatic	-1.84	CTGCTTACATCTCCTGGATAA	NM_001971:	NM_001971:
1990	ELA1 (elastas	elastase 1, pancreatic	-0.79	CAGGACCTTCCGGAAACCAAT	NM_001971:	NM_001971:
63036	ELA2A	elastase 2A	-0.65	CACGCGGGTCTCCAATTACAT	NM_033440:	NM_033440:
63036	ELA2A	elastase 2A	0.53	CGGCTGCAACTACTACCACAA	NM_033440:	NM_033440:
51032	ELA2B	elastase 2B	0.13	CACCGTGAAGACGAATATGAT	NM_015849:	NM_015849:
51032	ELA2B	elastase 2B	-3.99	TGGCGTGATATGCACCTGCAA	NM_015849:	NM_015849:
10136	ELA3A	elastase 3A, pancreatic	-4.47	CTGGCTTTGGCTGCAACTTCA	NM_005747:	NM_005747:
23436	ELA3B (elast	elastase 3B, pancreatic	-0.97	CTGCCGGTGGTGGACTATGAA	NM_007352:	NM_007352:
60528	ELAC2	elaC homolog 2 (E. coli)	0.84	TAGTATTTCAGCTGCAATAAA	NM_018127:	NM_018127:
60528	ELAC2	elaC homolog 2 (E. coli)	-4.70	AAAGAAGTCAGTACCCAGAAA	NM_018127:	NM_018127:
1996	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antige	1.43	CCAGTGTTGCCTAAGTATTAA	NM_021952:	NM_021952:
1996	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antige	-2.64	AAAGGTGATTCGTGACTTCAA	NM_021952:	NM_021952:
1998	ELF2	E74-like factor 2 (ets domain transcription factor)	-0.13	TACGATATCAAGTTACACTAA	NM_006874:	NM_006874:NM_201999:
1998	ELF2	E74-like factor 2 (ets domain transcription factor)	0.03	AACAACTGAACCCATCAATAA	NM_006874:	NM_006874:NM_201999:
2002	ELK1 (ELK1,	ELK1, member of ETS oncogene family	0.70	AGGGAGTCATCTCTTCCTATA	NM_005229:	NM_005229:
2002	ELK1 (ELK1,	ELK1, member of ETS oncogene family	-1.14	CCCACGTGAGCTGTAGGGAAA	NM_005229:	NM_005229:
2005	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	0.38	AAGGACAAAGTAAATAATTCA	NM_001973:	NM_001973:NM_021795:
2005	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	0.68	CTGGCTTATATTCTTCATTTA	NM_001973:	NM_001973:NM_021795:
2006	ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	-1.77	AAGCTTGTGGCCGGAAGAGAA	NM_000501:	NM_000501:
2006	ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	0.46	CAGGTGCAGATGAGGGAGTTA	NM_000501:	NM_000501:
64123	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1	0.67	ATGCCTAATCATTCTTGTTAA	BC025721.1:	XM_371262:
64123	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1	-0.45	CCCACATTATATGAACTTGAA	BC025721.1:	XM_371262:
2010	EMD	emerin (Emery-Dreifuss muscular dystrophy)	0.72	CAGGTGCATGATGACGATCTT	NM_000117:	NM_000117:
2010	EMD	emerin (Emery-Dreifuss muscular dystrophy)	-0.08	TACAATGACGACTACTATGAA	NM_000117:	NM_000117:
27436	EML4	echinoderm microtubule associated protein like 4	-2.21	TCGGATTGTAAGGACATTGAT	NM_019063:	NM_019063:
27436	EML4	echinoderm microtubule associated protein like 4	0.50	CAGGAATCGATCGGATTGTAA	NM_019063:	NM_019063:
2015	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	0.00	CACGTGGACTAAATTCACCAA	NM_001974:	NM_001974:
2015	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	-1.02	TTGCACAGTTATAGTGATCAA	NM_001974:	NM_001974:
30817	EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	0.50	AAGCATGGTGATGATATAGGA	NM_013447:	NM_152916:NM_152921:NM_013447:NM_152917: NM_152919:NM_152920:NM_152918:
30817	EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	-0.64	ACGGGTTTGATTATTTAGTCA	NM_013447:	NM_152916:NM_152921:NM_013447:NM_152917: NM_152919:NM_152920:NM_152918:
84658	EMR3 (egf-lik	egf-like module containing, mucin-like, hormone receptor-like 3	0.45	AACGATAGTGTAGCTATTGAA	NM_032571:	NM_032571:NM_152939:
84658	EMR3 (egf-lik	egf-like module containing, mucin-like, hormone receptor-like 3	0.93	GTGGTTTAGAGAGATCGTAAA	NM_032571:	NM_032571:NM_152939:
326342	EMR4	egf-like module containing, mucin-like, hormone receptor-like 4	0.84	CCGGATTGTTACGAGAACAAT	AY181245.1:	XM_377506:
326342	EMR4	egf-like module containing, mucin-like, hormone receptor-like 4	0.78	CGGATTGTTACGAGAACAATA	AY181245.1:	XM_377506:
2016	EMX1 (empty	empty spiracles homolog 1 (Drosophila)	-3.48	CCGGCCCACGGCGCTCAACTA	NM_004097:	NM_004097:
2016	EMX1 (empty	empty spiracles homolog 1 (Drosophila)	0.41	TCCAGGCACCACTGTAGTTTA	NM_004097:	NM_004097:
2018	EMX2 (empty	empty spiracles homolog 2 (Drosophila)	-0.02	CCGGTGGAGAATCGCCACCAA	NM_004098:	NM_004098:
2018	EMX2 (empty	empty spiracles homolog 2 (Drosophila)	-1.96	AAGGCTCAGATTCGCAACAAA	NM_004098:	NM_004098:
2019	EN1 (engraile	engrailed homolog 1	0.01	CCCGGATTATTTATCCGCAAA	NM_001426:	NM_001426:
2019	EN1 (engraile	engrailed homolog 1	0.70	CTGGGTGTACTGCACACGTTA	NM_001426:	NM_001426:
2020	EN2	engrailed homolog 2	0.43	CCCACGGTAAACAATATGGAA	NM_001427:	NM_001427:
2020	EN2	engrailed homolog 2	0.12	TACGTTGTACATAATAGTGTA	NM_001427:	NM_001427:
8507	ENC1	ectodermal-neural cortex (with BTB-like domain)	-0.92	ACGGCATGTATCACAGATGTA	NM_003633:	NM_003633:
8507	ENC1	ectodermal-neural cortex (with BTB-like domain)	-0.90	CAGCGGCTCCATTAACATCTA	NM_003633:	NM_003633:
23052	ENDOD1	endonuclease domain containing 1	0.97	AACGAATGGTACAATCTCAAA	XM_290546:	XM_290546:
23052	ENDOD1	endonuclease domain containing 1	0.03	CCGCCCAGGATCAATCAGAAA	XM_290546:	XM_290546:
2021	ENDOG	endonuclease G	-8.19	CCCGGGCGAGCTGGCCAAGTA	NM_004435:	NM_004435:
2021	ENDOG	endonuclease G	-4.61	CTGGAACAACCTGGAGAAATA	NM_004435:	NM_004435:
9941	ENDOGL1	endonuclease G-like 1	1.71	AACAGTGGAATCCTAAATTTA	NM_005107:	NM_005107:
9941	ENDOGL1	endonuclease G-like 1	1.60	AAGAAGCTAGAAGAACTCAAA	NM_005107:	NM_005107:
2022	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	0.50	CAGCAATGAGGCGGTGGTCAA	NM_000118:	NM_000118:
2022	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	-0.21	CGCCATGACCCTGGTACTAAA	NM_000118:	NM_000118:
2023	ENO1	enolase 1, (alpha)	0.59	CAGAGGTTTACCACAACCTGA	NM_001428:	NM_001428:
2023	ENO1	enolase 1, (alpha)	-0.75	GCGCATTGGAGCAGAGGTTTA	NM_001428:	NM_001428:
2028	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	0.75	AAGGACACGAACCTTATTAAA	NM_001977:	NM_001977:
2028	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	-1.21	CAGAGAGTAATTTCAGCTGTA	NM_001977:	NM_001977:
5167	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	-0.02	CACCGGCTCCTAATAACGGAA	NM_006208:	NM_006208:
5167	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	1.05	CAGATAAATACTATTCATTTA	NM_006208:	NM_006208:
5168	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	2.04	ATGGATCATTATGCTGCGGAA	NM_006209:	NM_006209:
5168	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	1.17	CGGACTAGATATGATATCTTA	NM_006209:	NM_006209:
5169	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	0.70	AACCTAATGTGTGATCTTCTA	NM_005021:	NM_005021:
5169	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	1.07	CTGGCTGTTAGGAGTAAATCA	NM_005021:	NM_005021:
2029	ENSA	endosulfine alpha	-0.14	TAGTTGAGAACTCAACATTAA	NM_004436:	NM_004436:NM_207042:NM_207045:NM_207046:
2029	ENSA	endosulfine alpha	1.22	TCAGTATTCGAAATAAACAAA	NM_004436:	NM_004436:NM_207042:NM_207045:NM_207046:
2033	EP300	E1A binding protein p300	-2.23	TTGGACTACCCTATCAAGTAA	NM_001429:	NM_001429:
2033	EP300	E1A binding protein p300	-4.55	CACCGATAACTCAGACTTGAA	NM_001429:	NM_001429:
2034	EPAS1	endothelial PAS domain protein 1	0.30	AACTAGGTATTTCTAACGCCA	NM_001430:	NM_001430:
2034	EPAS1	endothelial PAS domain protein 1	-1.82	CTCGGCGTCTGAACGTCTCAA	NM_001430:	NM_001430:
2035	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	0.46	TAGGATATCAGAATTGTTCAA	NM_004437:	NM_004437:NM_203343:NM_203342:
2035	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	-4.25	CACGGCCTAGTGAATGGGATA	NM_004437:	NM_004437:NM_203343:NM_203342:
2036	EPB41L1	erythrocyte membrane protein band 4.1-like 1	-0.18	CACGTTACAGTTAGCAGACGA	NM_012156:	NM_012156:NM_177996:
2036	EPB41L1	erythrocyte membrane protein band 4.1-like 1	0.56	ACGGATGTGCTTTGAAGTTAT	NM_012156:	NM_012156:NM_177996:
2038	EPB42	erythrocyte membrane protein band 4.2	-0.86	AACCCTTGTTCTACAATCTAA	NM_000119:	NM_000119:
2038	EPB42	erythrocyte membrane protein band 4.2	-0.21	CAGCTTAAACTTCCAGCTCTA	NM_000119:	NM_000119:
2041	EPHA1	EPH receptor A1	-3.19	CACCTTTAATGTGGAAGCCCA	NM_005232:	NM_005232:
2041	EPHA1	EPH receptor A1	0.06	CAGATGGGATCCCGTATCGAA	NM_005232:	NM_005232:
284656	EPHA10	EPH receptor A10	0.25	CACGGAGTACGAGATCCGATA	NM_001004338:	NM_001004338:
284656	EPHA10	EPH receptor A10	-2.15	AACATGTACGTCTTCAATAAA	NM_001004338:	NM_001004338:
1969	EPHA2	EPH receptor A2	-4.91	CAGCGCCAAGTAAACAGGGTA	NM_004431:	NM_004431:
1969	EPHA2	EPH receptor A2	-1.21	TCGGACAGACATATAGGATAT	NM_004431:	NM_004431:
2042	EPHA3	EPH receptor A3	1.81	CCGGAAAGATGTTACCTTCAA	NM_005233:	NM_182644:NM_005233:
2042	EPHA3	EPH receptor A3	-3.30	TACCTTCAACATCATATGTAA	NM_005233:	NM_182644:NM_005233:
2043	EPHA4	EPH receptor A4	-1.17	CCCGCGAATGAAGTTACCTTA	NM_004438:	NM_004438:
2043	EPHA4	EPH receptor A4	-0.01	CCGCCAGGACATTTCCTATAA	NM_004438:	NM_004438:
2044	EPHA5	EPH receptor A5	-0.05	ACCAGTTGGATCTCCAATGAA	NM_004439:	NM_004439:NM_182472:
2044	EPHA5	EPH receptor A5	-2.85	CCCGGCAGTATGTGTCTGTAA	NM_004439:	NM_004439:NM_182472:
285220	EPHA6	EPH receptor A6	-1.93	CAGGTATGTAATGTAATGGAA	XM_114973:	XM_114973:
285220	EPHA6	EPH receptor A6	0.03	AAGGGTTATTTCCGAGCTGAA	XM_114973:	XM_114973:
2045	EPHA7	EPH receptor A7	-1.47	ACCAGTCATGATAGTAATAGA	NM_004440:	NM_004440:
2045	EPHA7	EPH receptor A7	1.60	CAGGCTGCGAAGGAAGTACTA	NM_004440:	NM_004440:
2046	EPHA8	EPH receptor A8	-0.54	ACGGCCCACCAGGGTATGTAA	NM_020526:	NM_020526:

2046	EPHA8	EPH receptor A8	1.27	GAGCGTGTGCTTATCCGTTAA	NM_020526:	NM_020526:
2047	EPHB1	EPH receptor B1	-0.61	ATGGCCCTGGATTATCTACTA	NM_004441:	NM_004441:
2047	EPHB1	EPH receptor B1	-6.85	GCGGGATGATGTGACCTACAA	NM_004441:	NM_004441:
2048	EPHB2	EPH receptor B2	1.24	CACGCTTTCTAGAGGACGATA	NM_017449:	NM_017449:NM_004442:
2048	EPHB2	EPH receptor B2	-0.56	CCGAGAGGACCTCGTCTACAA	NM_017449:	NM_017449:NM_004442:
2049	EPHB3	EPH receptor B3	-1.57	CCGCAGCTGACCGCCAGATTA	NM_004443:	NM_004443:
2049	EPHB3	EPH receptor B3	-4.31	GCGGGTCTACGTGGAGCTCAA	NM_004443:	NM_004443:
2050	EPHB4	EPH receptor B4	-2.11	CCCAGCCAATAGCCACTCTAA	NM_004444:	NM_004444:
2050	EPHB4	EPH receptor B4	0.10	TCGGACAAACACGGACAGTAT	NM_004444:	NM_004444:
2051	EPHB6	EPH receptor B6	-0.37	AACCGCCAATCTCTAGATCAA	NM_004445:	NM_004445:
2051	EPHB6	EPH receptor B6	-7.08	CTGGAGCTTTGGGATACTCAT	NM_004445:	NM_004445:
2052	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	0.38	CAACATGGCTTTGATGATAAA	NM_000120:	NM_000120:
2052	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	0.80	TTCCAGGAATTCTACATTCAA	NM_000120:	NM_000120:
2054	EPIM	epimorphin	0.87	CAGCTAGTTTGTGCTAATTAA	NM_001980:	NM_001980:NM_194356:
2054	EPIM	epimorphin	1.05	TAGGGATTCATGATAATTAAA	NM_001980:	NM_001980:NM_194356:
7957	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	-1.38	AAGCTGGAGTTAATAATCTAT	NM_005670:	NM_005670:
7957	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	-0.51	CAAGGTCTCATGACCAGTCAA	NM_005670:	NM_005670:
2056	EPO	erythropoietin	-1.33	CAGCCGAGTCCTGGAGAGGTA	NM_000799:	NM_000799:
2056	EPO	erythropoietin	-0.95	CAGGATGACCTGGAGAACTTA	NM_000799:	NM_000799:
2057	EPOR	erythropoietin receptor	0.10	CCAGTGCAGACTCAAGACTTA	NM_000121:	NM_000121:
2057	EPOR	erythropoietin receptor	1.04	CAGATGATCAGGGATCCAATA	NM_000121:	NM_000121:
2058	EPRS	glutamyl-prolyl-tRNA synthetase	0.81	AAGGCGATTACTCAGTGTTAA	NM_004446:	NM_004446:
2058	EPRS	glutamyl-prolyl-tRNA synthetase	-4.15	CAGGAGGAGACTATACAACTA	NM_004446:	NM_004446:
2060	EPS15	epidermal growth factor receptor pathway substrate 15	-1.03	CAGGAAATTAGTTCAATGCAA	NM_001981:	NM_001981:
2060	EPS15	epidermal growth factor receptor pathway substrate 15	0.13	CACCTGGTATAGAATAAATAA	NM_001981:	NM_001981:
58513	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	0.69	CAGAACCTTCTAGCACACATA	NM_021235:	NM_021235:
58513	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	-0.20	AACCATCATCAAGTCCCTGAA	NM_021235:	NM_021235:
2059	EPS8 (epider	epidermal growth factor receptor pathway substrate 8	0.26	TCGGTTCTAAAGGATGATATT	NM_004447:	NM_004447:
2059	EPS8 (epider	epidermal growth factor receptor pathway substrate 8	-3.21	TTGGATATTGTGAGACCTCCA	NM_004447:	NM_004447:
54869	EPS8L1	EPS8-like 1	-2.84	CAGGGTCAAGATAGAACATGA	NM_017729:	NM_017729:
54869	EPS8L1	EPS8-like 1	-0.03	CAGCAGTGAGCTGTCGGTCAA	NM_017729:	NM_133180:NM_139204:NM_017729:
64787	EPS8L2	EPS8-like 2	0.04	CACCAGGGCTAAGCAATTAAA	NM_022772:	NM_022772:
64787	EPS8L2	EPS8-like 2	0.06	CCCACAATGCATGGAGTATTA	NM_022772:	NM_022772:
79574	EPS8L3	EPS8-like 3	-9.53	CCGGAAGGAGTACTCCCAGAA	NM_024526:	NM_133181:NM_139053:NM_024526:
79574	EPS8L3	EPS8-like 3	0.75	AGCCATTTACTTGCACCGGAA	NM_024526:	NM_133181:NM_139053:NM_024526:
8288	EPX	eosinophil peroxidase	1.36	CTCGAATTATATGTGACAATA	NM_000502:	NM_000502:
8288	EPX	eosinophil peroxidase	2.94	AAGGAAGTTCCTGAATTTGTA	NM_000502:	NM_000502:
3266	ERAS	ES cell expressed Ras	-2.03	CACATCAGGTATACTAGGGAA	NM_181532:	NM_181532:
3266	ERAS	ES cell expressed Ras	-1.29	CTGAAGGTCTTGGCCAAGAAA	NM_181532:	NM_181532:
2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glio	-1.99	AACAAAGAAATCTTAGACGAA	NM_004448:	NM_004448:NM_001005862:
2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glio	-0.42	CACGTTTGAGTCCATGCCCAA	NM_004448:	NM_004448:NM_001005862:
55914	ERBB2IP	erbb2 interacting protein	0.46	CCCGAAGAGCCAAATATAATA	NM_001006600:	NM_001006600:NM_018695:
55914	ERBB2IP	erbb2 interacting protein	1.03	CAAGATGTTATCAATTGGTTA	NM_001006600:	NM_001006600:NM_018695:
2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	1.28	ACCGGCGATGCTGAGAACCAA	NM_001982:	NM_001005915:NM_001982:
2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	-1.25	CCAGAGCTTCAAGACTGTTTA	NM_001982:	NM_001982:
2066	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	-0.06	CTACGTGTTAGTGGCTCTTAA	NM_005235:	NM_005235:
2066	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	-0.10	CTGGAGAATTTACGCATTATT	NM_005235:	NM_005235:
2067	ERCC1	excision repair cross-complementing rodent repair deficiency, comple	1.83	ACCGTGAAGTCAGTCAACAAA	NM_001983:	NM_001983:NM_202001:
2067	ERCC1	excision repair cross-complementing rodent repair deficiency, comple	-0.80	CACCGTGAAGTCAGTCAACAA	NM_001983:	NM_001983:NM_202001:
2068	ERCC2	excision repair cross-complementing rodent repair deficiency, comple	-2.09	CCCGCTCACCCTCCTTGCTAA	NM_000400:	NM_000400:
2068	ERCC2	excision repair cross-complementing rodent repair deficiency, comple	0.98	CCGATTCTATGAGGAATTTGA	NM_000400:	NM_000400:
2071	ERCC3	excision repair cross-complementing rodent repair deficiency, comple	0.97	ACCGTTCTGAATAAACAGAAT	NM_000122:	NM_000122:
2071	ERCC3	excision repair cross-complementing rodent repair deficiency, comple	-0.48	CCGGGAATATGTGGCAATCAA	NM_000122:	NM_000122:
2072	ERCC4	excision repair cross-complementing rodent repair deficiency, comple	0.01	CAGCACCTCGATGTTTATAAA	NM_005236:	NM_005236:
2072	ERCC4	excision repair cross-complementing rodent repair deficiency, comple	0.30	CTCGCCGTGTAACAAATGAAA	NM_005236:	NM_005236:
2073	ERCC5	excision repair cross-complementing rodent repair deficiency, comple	0.27	AAGAAGATGCTAAACGTATTA	NM_000123:	NM_000123:
2073	ERCC5	excision repair cross-complementing rodent repair deficiency, comple	-0.10	CCCGGACTCTTTCAGCCATTA	NM_000123:	NM_000123:
2074	ERCC6	excision repair cross-complementing rodent repair deficiency, comple	-0.01	ACGGGCATTTCTGATTATTAA	L04791:	NM_000124:
2074	ERCC6	excision repair cross-complementing rodent repair deficiency, comple	0.58	ATGGATGGTACCACTACAATA	L04791:	NM_000124:
1161	ERCC8	excision repair cross-complementing rodent repair deficiency, comple	-0.19	ATGGTCTATTCCTGACAGCTA	NM_000082:	NM_001007233:NM_000082:
1161	ERCC8	excision repair cross-complementing rodent repair deficiency, comple	0.90	CAGAGTCAACACGGAGAGTTT	NM_000082:	NM_001007233:NM_000082:NM_001007234:
2078	ERG	v-ets erythroblastosis virus E26 oncogene like (avian)	0.68	ATGCAGAATGTATGTAATAAA	NM_004449:	NM_182918:NM_004449:
2078	ERG	v-ets erythroblastosis virus E26 oncogene like (avian)	0.10	CTGGAATTGTCTGATATTTAA	NM_004449:	NM_182918:NM_004449:
114625	ERMAP	erythroblast membrane-associated protein (Scianna blood group)	0.33	TTGGAGAGTATTGATTTCAAA	NM_018538:	NM_001017922:NM_018538:
114625	ERMAP	erythroblast membrane-associated protein (Scianna blood group)	-1.69	TTGGGAAAGGCTGATGAGTAA	NM_018538:	NM_001017922:NM_018538:
2081	ERN1	endoplasmic reticulum to nucleus signalling 1	0.04	CAGCACGGACGTCAAGTTTGA	NM_001433:	NM_001433:
2081	ERN1	endoplasmic reticulum to nucleus signalling 1	0.58	CAGGACGTGAGCGACAGAATA	NM_001433:	NM_001433:
10595	ERN2	endoplasmic reticulum to nucleus signalling 2	-0.72	AAGGATGAAACTGGCTTCTAT	NM_033266:	NM_033266:
10595	ERN2	endoplasmic reticulum to nucleus signalling 2	-0.39	CACCTGCATTCTTTACACATA	NM_033266:	NM_033266:
90952	ESAM	endothelial cell adhesion molecule	0.81	ATACATAATGTTTGTATGAAA	NM_138961:	NM_138961:
90952	ESAM	endothelial cell adhesion molecule	-0.04	TCAGGTGTTGTCCTACATCAA	NM_138961:	NM_138961:
11082	ESM1	endothelial cell-specific molecule 1	-2.95	CCCGGGTTACCTGTATCTGAA	NM_007036:	NM_007036:
11082	ESM1	endothelial cell-specific molecule 1	0.38	CCCGTAATGAGGAAATGGTTA	NM_007036:	NM_007036:
9700	ESPL1	extra spindle poles like 1 (S. cerevisiae)	0.57	CAAGCTTCCCTGAATCATAAA	NM_012291:	NM_012291:
9700	ESPL1	extra spindle poles like 1 (S. cerevisiae)	-0.28	CAGCAGCTGACTGCTAAGCTA	NM_012291:	NM_012291:
2099	ESR1	estrogen receptor 1	1.56	GAGACTTGAATTAATAAGTGA	NM_000125:	NM_000125:
2099	ESR1	estrogen receptor 1	-0.39	TTCCTTTGACCTATAGGCTAA	NM_000125:	NM_000125:
2100	ESR2	estrogen receptor 2 (ER beta)	-0.13	CAGCGATTACGCATCGGGATA	NM_001437:	NM_001437:
2100	ESR2	estrogen receptor 2 (ER beta)	-3.02	CTGGTCGTGTGAAGGATGTAA	NM_001437:	NM_001437:
2101	ESRRA	estrogen-related receptor alpha	-0.01	CCGAGAGATTGTGGTCACCAT	NM_004451:	NM_004451:
2101	ESRRA	estrogen-related receptor alpha	1.10	AGAGGAGTATGTTCTACTAAA	NM_004451:	NM_004451:
2103	ESRRB	estrogen-related receptor beta	-0.13	CAGCACTTCTATAGCGTCAAA	NM_004452:	NM_004452:
2103	ESRRB	estrogen-related receptor beta	-2.17	ACGCAGGTACAAGAAGCTCAA	NM_004452:	NM_004452:
2104	ESRRG	estrogen-related receptor gamma	0.70	TGCATTATAGCCAGTAGTAAA	NM_001438:	NM_206595:NM_001438:NM_206594:
2104	ESRRG	estrogen-related receptor gamma	0.88	TTCAACTACACTATATATAAA	NM_001438:	NM_206595:NM_001438:NM_206594:
345062	ESSPL	epidermis-specific serine protease-like protein	-0.11	AAGAGAATGCATGGAGATTTA	NM_183375:	NM_183375:
345062	ESSPL	epidermis-specific serine protease-like protein	-0.01	CCAATGTAATCTACTACCAAA	NM_183375:	NM_183375:
2108	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	0.13	CAGATATTTGTGGGTATTATA	NM_000126:	NM_000126:
2108	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	0.76	CAAGACAATTGTGGCAATTAA	NM_000126:	NM_000126:
2109	ETFB	electron-transfer-flavoprotein, beta polypeptide	-0.20	GCCCAACATCATGAAAGCCAA	NM_001985:	NM_001014763:NM_001985:
2109	ETFB	electron-transfer-flavoprotein, beta polypeptide	-0.53	CACGCTGCCCAACATCATGAA	NM_001985:	NM_001014763:NM_001985:
55500	ETNK1	ethanolamine kinase 1	-0.01	CCGTATGTGGTGGATTAGAAA	NM_018638:	NM_018638:
55500	ETNK1	ethanolamine kinase 1	-0.43	TCCGTATGTGGTGGATTAGAA	NM_018638:	NM_018638:
55224	ETNK2	ethanolamine kinase 2	0.89	TCCGATTCAACCAGTACTTCA	NM_018208:	NM_018208:
55224	ETNK2	ethanolamine kinase 2	1.60	TACGTGCAAGTCAACAAGTTT	NM_018208:	NM_018208:
2113	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	-0.45	ATGCATGTCGTTCCAAACTAA	NM_005238:	NM_005238:
2113	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.16	CCGACGAGTGATGGCACTGAA	NM_005238:	NM_005238:
2114	ETS2 (v-ets e	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	1.37	AGGGATTTATGTAGCAGCTAT	NM_005239:	NM_005239:
2114	ETS2 (v-ets e	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-3.96	CTGTGATGAGTCAAGCCTTAA	NM_005239:	NM_005239:

2118	ETV4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	-2.67	CCGGAGTCATTGGGAAGGAAA	NM_001986:	NM_001986:
2118	ETV4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	-0.84	CAGCAGAGCTTTAAGCAAGAA	NM_001986:	NM_001986:
2120	ETV6	ets variant gene 6 (TEL oncogene)	-0.66	CAGGTCACCTATCACGACAAA	NM_001987:	NM_001987:
2120	ETV6	ets variant gene 6 (TEL oncogene)	1.78	GCGCCACTACTACAAACTAAA	NM_001987:	NM_001987:
51513	ETV7	ets variant gene 7 (TEL2 oncogene)	-3.67	CCCGATATGAGCCCTACATCA	NM_016135:	NM_016135:
51513	ETV7	ets variant gene 7 (TEL2 oncogene)	-3.43	GCGCCACTATTATAAGCTTAA	NM_016135:	NM_016135:
2122	EVI1	ecotropic viral integration site 1	-1.18	CAGCACTACGTCTTCCTTAAA	NM_005241:	NM_005241:
2122	EVI1	ecotropic viral integration site 1	2.38	CCAGTGCTATCCAGTCCATAA	NM_005241:	NM_005241:
2123	EVI2A	ecotropic viral integration site 2A	0.02	GAGCTAAACTGTGTAATTTAA	NM_014210:	NM_014210:NM_001003927:
2123	EVI2A	ecotropic viral integration site 2A	0.21	CATGGTAGACCTTGCAATTTA	NM_014210:	NM_014210:NM_001003927:
115704	EVI5L (ecotro	ecotropic viral integration site 5-like	-2.32	CCCGTTGTCTCTGCTGAATCA	NM_145245:	NM_145245:
115704	EVI5L (ecotro	ecotropic viral integration site 5-like	0.04	CCCGGAACACGAGTTCTTCAA	NM_145245:	NM_145245:
51466	EVL	Enah/Vasp-like	-6.34	CCGGATCAACATCTACCACAA	NM_016337:	NM_016337:
51466	EVL	Enah/Vasp-like	-0.19	CAGGTTGTGATCAATTATTCA	NM_016337:	NM_016337:
2130	EWSR1	Ewing sarcoma breakpoint region 1	-3.61	CAAGAGGGCCTCTTAACTGTA	NM_005243:	NM_005243:
2130	EWSR1	Ewing sarcoma breakpoint region 1	0.03	CTGCATTGACTACCAGATTTA	NM_005243:	NM_005243:
9156	EXO1	exonuclease 1	0.94	ATGGATGTACTTTACCTTCTA	NM_003686:	NM_003686:NM_006027:NM_130398:
9156	EXO1	exonuclease 1	0.75	CAGATGTAGCACGTAATTCAA	NM_003686:	NM_003686:NM_006027:NM_130398:
23265	EXOC7	exocyst complex component 7	0.36	AAGGCCTTTATCAGATTCATA	NM_015219:	NM_015219:NM_001013839:
23265	EXOC7	exocyst complex component 7	-0.58	CTGGTTAAAGGTGACTGATTA	NM_015219:	NM_015219:NM_001013839:
2131	EXT1	exostoses (multiple) 1	0.44	CAGATTGTGCCAACTATCCAA	NM_000127:	NM_000127:
2131	EXT1	exostoses (multiple) 1	1.83	CACGGTGCTTTCAACAACAGA	NM_000127:	NM_000127:
2132	EXT2	exostoses (multiple) 2	1.06	GAGGTTCTGGCTAACGTTAAA	NM_000401:	NM_000401:NM_207122:
2132	EXT2	exostoses (multiple) 2	-1.34	CCGGTGGTTCTGGGAAGCGTA	NM_000401:	NM_000401:NM_207122:
2138	EYA1	eyes absent homolog 1 (Drosophila)	-0.45	AACTCGGTAACTCTCATATAA	NM_000503:	NM_172059:NM_172058:NM_000503:
2138	EYA1	eyes absent homolog 1 (Drosophila)	-0.63	CAGGAAATAATTCACTCACAA	NM_000503:	NM_172059:NM_172058:NM_000503:NM_172060:
2070	EYA4	eyes absent homolog 4 (Drosophila)	-0.07	CAGTCCTATTTAGACATGTAA	NM_004100:	NM_172104:NM_172103:NM_172105:NM_004100:
2070	EYA4	eyes absent homolog 4 (Drosophila)	0.51	CAGCTTTAGCAAAGAACTCTT	NM_004100:	NM_172104:NM_172103:NM_172105:NM_004100:
2145	EZH1	enhancer of zeste homolog 1 (Drosophila)	-1.86	AAGCGCTAGCCTGTAATTGTA	NM_001991:	NM_001991:
2145	EZH1	enhancer of zeste homolog 1 (Drosophila)	-0.54	CGCGGAAAGGTCTATGACAAA	NM_001991:	NM_001991:
2146	EZH2	enhancer of zeste homolog 2 (Drosophila)	0.02	AACCATGTTTACAACTATCAA	NM_004456:	NM_152998:NM_004456:
2146	EZH2	enhancer of zeste homolog 2 (Drosophila)	-0.03	CAGGATGGTACTTTCATTGAA	NM_004456:	NM_152998:NM_004456:
2159	F10	coagulation factor X	-2.45	CCGGTTCACAAAGGAGACCTA	NM_000504:	NM_000504:
2159	F10	coagulation factor X	-1.61	AACCATTCTGAGCGAGTTCTA	NM_000504:	NM_000504:
2160	F11	coagulation factor XI (plasma thromboplastin antecedent)	-0.01	CAAGATACCCTTAGTGACCAA	NM_000128:	NM_000128:NM_019559:
2160	F11	coagulation factor XI (plasma thromboplastin antecedent)	2.84	CAGAATAACGAAGCTCGATAA	NM_000128:	NM_000128:NM_019559:
50848	F11R	F11 receptor	0.75	ACCAGTCTATTTATTAACTTA	NM_016946:	NM_016946:NM_144502:NM_144503:NM_144504:
50848	F11R	F11 receptor	-0.40	CCGAAGTGAAGGAGAATTCAA	NM_016946:	NM_016946:NM_144502:NM_144501:NM_144503:NM_144504:
2161	F12	coagulation factor XII (Hageman factor)	-0.92	CAGGATGGCGAGGAACTCAAT	NM_000505:	NM_000505:
2161	F12	coagulation factor XII (Hageman factor)	-3.64	CCCGTGGTGCTTCGTGCTGAA	NM_000505:	NM_000505:
2162	F13A1	coagulation factor XIII, A1 polypeptide	-1.43	TACAATGTAATAGAAGCTTAA	NM_000129:	NM_000129:
2162	F13A1	coagulation factor XIII, A1 polypeptide	0.09	AGCGTTGACATTCTATTGGAA	NM_000129:	NM_000129:
2165	F13B	coagulation factor XIII, B polypeptide	0.31	AGGCCTATTGTTTAGATGGAA	NM_001994:	NM_001994:
2165	F13B	coagulation factor XIII, B polypeptide	0.64	AAAGTCTTACATGGAGATTTA	NM_001994:	NM_001994:
2147	F2	coagulation factor II (thrombin)	-1.58	AAGGTACGAGCGAAACATTGA	NM_000506:	NM_000506:
2147	F2	coagulation factor II (thrombin)	0.28	CCGCACAAGGTACGAGCGAAA	NM_000506:	NM_000506:
2149	F2R	coagulation factor II (thrombin) receptor	-0.30	CAGTATAGAATAGGCACTTTA	NM_001992:	NM_001992:
2149	F2R	coagulation factor II (thrombin) receptor	-0.82	TAGAGTGTGATGTATGTGTAA	NM_001992:	NM_001992:
2150	F2RL1	coagulation factor II (thrombin) receptor-like 1	0.89	ATAGTCGTGAATCTTGTTCAA	NM_005242:	NM_005242:
2150	F2RL1	coagulation factor II (thrombin) receptor-like 1	-3.58	CCGAAGTGTCCGCACTGTAAA	NM_005242:	NM_005242:
2151	F2RL2	coagulation factor II (thrombin) receptor-like 2	-0.11	CAGGAGCCACGATTACTGTAA	NM_004101:	NM_004101:
2151	F2RL2	coagulation factor II (thrombin) receptor-like 2	0.98	CAGTTAGGATACATCACTAAA	NM_004101:	NM_004101:
9002	F2RL3	coagulation factor II (thrombin) receptor-like 3	0.26	AAGGCTGTACTGGGTCGAACA	NM_003950:	NM_003950:
9002	F2RL3	coagulation factor II (thrombin) receptor-like 3	-0.55	CACATTCACGATACTGTGCAA	NM_003950:	NM_003950:
2152	F3	coagulation factor III (thromboplastin, tissue factor)	0.50	ACTGACTTAAGTGGCATTAAA	NM_001993:	NM_001993:
2152	F3	coagulation factor III (thromboplastin, tissue factor)	-0.29	AACGAATGGTACTACAACCAA	NM_001993:	NM_001993:
2153	F5	coagulation factor V (proaccelerin, labile factor)	-0.18	CGCCATTAATGGGATGATCTA	NM_000130:	NM_000130:
2153	F5	coagulation factor V (proaccelerin, labile factor)	0.04	CCCATTCAAGACCCTGATCAA	NM_000130:	NM_000130:
2155	F7 (coagulati	coagulation factor VII (serum prothrombin conversion accelerator)	0.72	CTGGTTCTTATCCATTATCAT	NM_000131:	NM_000131:NM_019616:
2155	F7 (coagulati	coagulation factor VII (serum prothrombin conversion accelerator)	-0.08	TCGAACTGTCCTGGCACCAAA	NM_000131:	NM_000131:NM_019616:
2157	F8	coagulation factor VIII, procoagulant component (hemophilia A)	1.08	ACGAGTGTCCATAGATATAAA	NM_019863:	NM_019863:NM_000132:
2157	F8	coagulation factor VIII, procoagulant component (hemophilia A)	0.63	CAGGAGGGTGCATCCAATTTA	NM_019863:	NM_019863:NM_000132:
2158	F9	coagulation factor IX (plasma thromboplastic component, Christmas d	-0.77	CACGAAGGCAAGATTGGCATA	NM_000133:	NM_000133:
2158	F9	coagulation factor IX (plasma thromboplastic component, Christmas d	0.06	TACAAAGTTCACCATCTATAA	NM_000133:	NM_000133:
2166	FAAH	fatty acid amide hydrolase	-0.31	CAAGGCCCAACTAACAGTCAA	NM_001441:	NM_001441:
2166	FAAH	fatty acid amide hydrolase	-0.49	CCGGCGGAGTGCGACAGCGTA	NM_001441:	NM_001441:
2167	FABP4	fatty acid binding protein 4, adipocyte	1.89	CAATATGGTTACGTTGGTTAA	NM_001442:	NM_001442:
2167	FABP4	fatty acid binding protein 4, adipocyte	0.16	CCTGATTTAGCAAGCAAGTAA	NM_001442:	NM_001442:
8772	FADD	Fas (TNFRSF6)-associated via death domain	-0.68	AGCGGGATCTCGTATCTTTAA	NM_003824:	NM_003824:
8772	FADD	Fas (TNFRSF6)-associated via death domain	-1.08	CAGCGGGATCTCGTATCTTTA	NM_003824:	NM_003824:
11124	FAF1	Fas (TNFRSF6) associated factor 1	0.48	AAGGACGAGGATGAACGTGAA	NM_007051:	NM_131917:NM_007051:
11124	FAF1	Fas (TNFRSF6) associated factor 1	-0.57	CAGGCATGTACTGGCATTGAA	NM_007051:	NM_131917:NM_007051:
2184	FAH (fumaryl	fumarylacetoacetate hydrolase (fumarylacetoacetase)	0.14	CGCCATTCAGTGACAAATAAA	NM_000137:	NM_000137:
2184	FAH (fumaryl	fumarylacetoacetate hydrolase (fumarylacetoacetase)	0.52	CCGCCATTCAGTGACAAATAA	NM_000137:	NM_000137:
9214	FAIM3	Fas apoptotic inhibitory molecule 3	-0.64	CAGGGTTGGGTCTTACACAAA	NM_005449:	NM_005449:
9214	FAIM3	Fas apoptotic inhibitory molecule 3	-0.04	CCGAGTTACTCTGAAGCAATA	NM_005449:	NM_005449:
2186	FALZ	fetal Alzheimer antigen	0.17	AACGCCTTATGATGAATCTAA	NM_004459:	NM_004459:NM_182641:
2186	FALZ	fetal Alzheimer antigen	1.22	AAGCATAATGCTGTAATAGAA	NM_004459:	NM_004459:NM_182641:
54097	FAM3B	family with sequence similarity 3, member B	-0.56	CTGGGTATTTATTGCAGCAAA	NM_058186:	NM_206964:NM_058186:
54097	FAM3B	family with sequence similarity 3, member B	-1.51	CAGGTCTAGCTGGGTATTTAT	NM_058186:	NM_206964:NM_058186:
9679	FAM53B	family with sequence similarity 53, member B	1.75	TACTTGTACTGTGTAAATAAA	NM_014661:	NM_014661:
9679	FAM53B	family with sequence similarity 53, member B	-2.02	CGGGAGATGCTTCCTTCTGTA	NM_014661:	NM_014661:
79850	FAM57A	family with sequence similarity 57, member A	0.33	CCCGATCAACTAGGATGAATT	NM_024792:	NM_024792:
79850	FAM57A	family with sequence similarity 57, member A	0.78	TAGGTAGTTATTGATCGTTTA	NM_024792:	NM_024792:
57795	FAM5B	family with sequence similarity 5, member B	0.36	CCACCTGAACATCTAAGTAAA	NM_021165:	NM_021165:
57795	FAM5B	family with sequence similarity 5, member B	0.03	AAAGTGATTCTTGTCATTCAA	NM_021165:	NM_021165:
23344	FAM62A	family with sequence similarity 62 (C2 domain containing), member A	-0.47	ACGCCCGACCCTAGACATCAA	NM_015292:	NM_015292:
23344	FAM62A	family with sequence similarity 62 (C2 domain containing), member A	-0.99	GTGGGAGATAGTTCTCATAAA	NM_015292:	NM_015292:
54629	FAM63B	family with sequence similarity 63, member B	-0.78	TAGCACCATGACCAAATACAA	NM_019092:	NM_019092:
54629	FAM63B	family with sequence similarity 63, member B	-0.40	AAGCCTCTCCATCAAGTGGAA	NM_019092:	NM_019092:
54478	FAM64A	family with sequence similarity 64, member A	0.23	CCCACCCATTACGGCGATCAA	NM_019013:	NM_019013:
54478	FAM64A	family with sequence similarity 64, member A	-0.12	CCGCCAAGGCTTCATACTCAA	NM_019013:	NM_019013:
23625	FAM89B	family with sequence similarity 89, member B	-0.23	CAGGGCGCGTAGATAAATAAA	NM_152832:	NM_152832:
23625	FAM89B	family with sequence similarity 89, member B	0.20	CCCGTGCTGGATATTTAAATT	NM_152832:	NM_152832:

2175	FANCA	Fanconi anemia, complementation group A	-2.20	CAGCATATTCAGGAGGCCTTA	NM_000135:	NM_000135:
2175	FANCA	Fanconi anemia, complementation group A	-1.33	CAGCGTTGAGATATCAAAGAT	NM_000135:	NM_000135:
2176	FANCC	Fanconi anemia, complementation group C	1.27	CGCGAGGACCACCCGATTTAA	NM_000136:	NM_000136:
2176	FANCC	Fanconi anemia, complementation group C	1.74	GGCATTGTTAGTGTAACTCAA	NM_000136:	NM_000136:
2177	FANCD2	Fanconi anemia, complementation group D2	1.15	ACGGGAGAGAGTCAGAATCAA	NM_033084:	NM_001018115:NM_033084:
2177	FANCD2	Fanconi anemia, complementation group D2	-0.27	TTGGAGGAGATTGATGGTCTA	NM_033084:	NM_001018115:NM_033084:
2178	FANCE	Fanconi anemia, complementation group E	-2.91	AACGCCGAGGAGAGCTTGTAA	NM_021922:	NM_021922:
2178	FANCE	Fanconi anemia, complementation group E	-0.18	TAGCCTGAGGATAAAGGCTGA	NM_021922:	NM_021922:
2188	FANCF	Fanconi anemia, complementation group F	1.35	AACCAGCATTAGAGCTTTATA	NM_022725:	NM_022725:
2188	FANCF	Fanconi anemia, complementation group F	-0.29	ATGCCTTTGGATACTAAATTA	NM_022725:	NM_022725:
2189	FANCG	Fanconi anemia, complementation group G	0.31	CCCAGGTAATCGAGACACTTA	NM_004629:	NM_004629:
2189	FANCG	Fanconi anemia, complementation group G	-7.12	CCGCGGGAACTAACTCTTCAA	NM_004629:	NM_004629:
2191	FAP	fibroblast activation protein, alpha	0.53	CGCACTGATCAAGAAATTAAA	NM_004460:	NM_004460:
2191	FAP	fibroblast activation protein, alpha	-2.47	TCGCCTGTTGGGAGTAAATTA	NM_004460:	NM_004460:
355	FAS	Fas (TNF receptor superfamily, member 6)	-0.71	AAGGACATTACTAGTGACTCA	NM_000043:	NM_152875:NM_152876:NM_152877:NM_000043: NM_152873:NM_152871:NM_152874:NM_152872:
355	FAS	Fas (TNF receptor superfamily, member 6)	1.10	CACATTGATTAAAGATCTCAA	NM_000043:	NM_152875:NM_152876:NM_152877:NM_000043: NM_152873:NM_152871:NM_152874:NM_152872:
356	FASLG	Fas ligand (TNF superfamily, member 6)	0.25	ATCGGTGAAACTAACAGATAA	NM_000639:	NM_000639:
356	FASLG	Fas ligand (TNF superfamily, member 6)	1.69	GAGGCTTGCATAATAAGCTAA	NM_000639:	NM_000639:
2194	FASN	fatty acid synthase	-0.61	CCGCCATGCAACGGGATTGAA	NM_004104:	NM_004104:
2194	FASN	fatty acid synthase	0.53	TCCCAGGTATGCGACGGGAAA	NM_004104:	NM_004104:
10922	FASTK	Fas-activated serine/threonine kinase	-1.99	CAGCAGCAAGGTGGTACAGAA	NM_006712:	NM_006712:NM_033015:
10922	FASTK	Fas-activated serine/threonine kinase	1.26	CTGGTGGTTCAGGAAACGCAA	NM_006712:	NM_006712:NM_033015:
2195	FAT	FAT tumor suppressor homolog 1 (Drosophila)	-2.89	CAGGCTGGATTACAACTTTAA	NM_005245:	NM_005245:
2195	FAT	FAT tumor suppressor homolog 1 (Drosophila)	1.45	CCCTACTACGCCGTTGTTAAA	NM_005245:	NM_005245:
2196	FAT2	FAT tumor suppressor homolog 2 (Drosophila)	0.63	ACCAAGGTGATTGATTTGCTA	NM_001447:	NM_001447:
2196	FAT2	FAT tumor suppressor homolog 2 (Drosophila)	-0.02	CACCCACAACTTTGAATATTA	NM_001447:	NM_001447:
2197	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously ex	-0.72	AAGCCACTTAGTTCAGTCAAA	NM_001997:	NM_001997:
2197	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously ex	-4.08	CCGCCGTTCAGTCGCCAATAT	NM_001997:	NM_001997:
2200	FBN1	fibrillin 1 (Marfan syndrome)	0.87	CCGGATTTACCCAACACCATA	NM_000138:	NM_000138:
2200	FBN1	fibrillin 1 (Marfan syndrome)	0.68	CAGTGCAATGATCGTAATGAA	NM_000138:	NM_000138:
2201	FBN2	fibrillin 2 (congenital contractural arachnodactyly)	0.31	TTCATTAATACTGTAGTTATA	NM_001999:	NM_001999:
2201	FBN2	fibrillin 2 (congenital contractural arachnodactyly)	-1.14	CAGGATTGCCATATGTGCAAA	NM_001999:	NM_001999:
2203	FBP1	fructose-1,6-bisphosphatase 1	-2.87	CTCGCTCTGCACAGCAGTCAA	NM_000507:	NM_000507:
2203	FBP1	fructose-1,6-bisphosphatase 1	-0.54	TTCCTAGAGAGCAGAAATAAA	NM_000507:	NM_000507:
8789	FBP2 (fructos	fructose-1,6-bisphosphatase 2	-0.26	AGGACCCTAAATGAACGATAA	NM_003837:	NM_003837:
8789	FBP2 (fructos	fructose-1,6-bisphosphatase 2	-0.53	CAGGTTATGCGCTGTACGGTA	NM_003837:	NM_003837:
84678	FBXL10	F-box and leucine-rich repeat protein 10	1.42	AGGAGTGGACTAGAAGTTTAA	NM_032590:	NM_032590:NM_001005366:
84678	FBXL10	F-box and leucine-rich repeat protein 10	0.22	TAGGAGTGGACTAGAAGTTTA	NM_032590:	NM_032590:NM_001005366:
22992	FBXL11	F-box and leucine-rich repeat protein 11	-0.70	ACCCATTTCGTTGCTACCCAA	NM_012308:	NM_012308:
22992	FBXL11	F-box and leucine-rich repeat protein 11	-0.20	CTCACTGGAGTTCCTATAGTA	NM_012308:	NM_012308:
54850	FBXL12	F-box and leucine-rich repeat protein 12	0.37	AATGATCGATATGCTCATAAA	NM_017703:	NM_017703:
54850	FBXL12	F-box and leucine-rich repeat protein 12	2.14	TCGCGATTCAATGATCGATAT	NM_017703:	NM_017703:
144699	FBXL14	F-box and leucine-rich repeat protein 14	0.19	CAAATCATTATCATTCATTAA	NM_152441:	NM_152441:
144699	FBXL14	F-box and leucine-rich repeat protein 14	0.07	ATGTATTACTGAGAACGTAAA	NM_152441:	NM_152441:
79176	FBXL15	F-box and leucine-rich repeat protein 15	1.38	CACCCTGGAGCTTCAAATAAA	XM_370575:	NM_024326:
79176	FBXL15	F-box and leucine-rich repeat protein 15	-0.67	CTGAGCTGTAGGGAAACTGAA	XM_370575:	NM_024326:
64839	FBXL17	F-box and leucine-rich repeat protein 17	0.08	ACGAGAGGGTAGTCACATTAA	NM_022824:	NM_022824:
64839	FBXL17	F-box and leucine-rich repeat protein 17	0.11	ACGAAAGTTAATTATACATTA	NM_022824:	NM_022824:
80028	FBXL18	F-box and leucine-rich repeat protein 18	0.80	CAGCCAGTTTCTGTTGTTTGA	NM_024963:	NM_024963:
80028	FBXL18	F-box and leucine-rich repeat protein 18	-2.68	CCGCGCGGCTTTGGCAAGAAA	NM_024963:	NM_024963:
54620	FBXL19	F-box and leucine-rich repeat protein 19	1.47	TACAATACGGTTTGCTATAAA	NM_019085:	NM_019085:
54620	FBXL19	F-box and leucine-rich repeat protein 19	0.26	CCGGGTCTGTACAATACGGTT	NM_019085:	NM_019085:
25827	FBXL2	F-box and leucine-rich repeat protein 2	0.21	TAGGTTTCCATGAGACACCAA	NM_012157:	NM_012157:
25827	FBXL2	F-box and leucine-rich repeat protein 2	0.95	TACCTAGGTACGAAAGTTCTA	NM_012157:	NM_012157:
84961	FBXL20	F-box and leucine-rich repeat protein 20	-0.38	CTTGGCGAACTGAGTATTTAA	NM_032875:	NM_032875:
84961	FBXL20	F-box and leucine-rich repeat protein 20	1.50	GACCCATTTACCCAATATTAA	NM_032875:	NM_032875:
26224	FBXL3	F-box and leucine-rich repeat protein 3	0.25	AAGGCTTATCTAGATTCGAAA	NM_012158:	NM_012158:
26224	FBXL3	F-box and leucine-rich repeat protein 3	0.26	TTGGAATTACATAGTTATGTA	NM_012158:	NM_012158:
26235	FBXL4	F-box and leucine-rich repeat protein 4	0.08	AACGACTTGTTCTCTATCGAA	NM_012160:	NM_012160:
26235	FBXL4	F-box and leucine-rich repeat protein 4	0.28	TCCGAATTAGTACGCCTTGAA	NM_012160:	NM_012160:
26234	FBXL5	F-box and leucine-rich repeat protein 5	-0.01	TTGGTAATGCCATGTCATTTA	NM_012161:	NM_012161:NM_033535:
26234	FBXL5	F-box and leucine-rich repeat protein 5	1.31	ATGCCTGTTTGCACGATTTAA	NM_012161:	NM_012161:NM_033535:
23194	FBXL7	F-box and leucine-rich repeat protein 7	-2.61	AAGGTCTCACTAGGAAATTTA	NM_012304:	NM_012304:
23194	FBXL7	F-box and leucine-rich repeat protein 7	-5.30	ACCCATGGACATTCTTGTCAA	NM_012304:	NM_012304:
55336	FBXL8	F-box and leucine-rich repeat protein 8	0.00	AAGGCATGCTGCCACCTTATC	NM_018378:	NM_018378:
55336	FBXL8	F-box and leucine-rich repeat protein 8	-0.11	AATCGAGCTGCTGATGGTTCT	NM_018378:	NM_018378:
26267	FBXO10	F-box protein 10	-1.18	CCCGGGTACTTGCCAAGTGAA	XM_291314:	XM_291314:
26267	FBXO10	F-box protein 10	-0.18	CCAGGTGTGTACGAAGAGCAA	XM_291314:	XM_291314:
80204	FBXO11	F-box protein 11	0.51	CTGCTTAGAGATTACAGTAAA	NM_012167:	NM_025133:NM_018693:NM_012167:
80204	FBXO11	F-box protein 11	-3.35	CAGGTGTATGGATTACCTCAA	NM_012167:	NM_025133:NM_018693:NM_012167:
201456	FBXO15	F-box protein 15	-1.75	ATGGCATTCTTTAATTGCAAA	NM_152676:	NM_152676:
201456	FBXO15	F-box protein 15	-0.68	ATCAGTTACTGTTATATGGTA	NM_152676:	NM_152676:
157574	FBXO16	F-box protein 16	1.52	TACGGTTTAACTGGTACATCA	NM_172366:	NM_172366:
157574	FBXO16	F-box protein 16	0.03	TCCAAGGGTGTTATCTTTATA	NM_172366:	NM_172366:
115290	FBXO17	F-box protein 17	-0.05	CTGCCTGACGTTGTCAGTCAA	NM_024907:	NM_024907:NM_148169:
115290	FBXO17	F-box protein 17	1.03	CTCGGTGGACTCAGTCACAAA	NM_024907:	NM_024907:NM_148169:
84893	FBXO18	F-box protein, helicase, 18	-1.38	CACCGTCCTTACCATGAAGAA	NM_032807:	NM_032807:NM_178150:
84893	FBXO18	F-box protein, helicase, 18	-2.12	TAGGGCGGAAGTACCAGTCAA	NM_032807:	NM_032807:NM_178150:
26232	FBXO2	F-box protein 2	0.37	AACGATGAGAGCGTCAAGAAG	NM_012168:	NM_012168:
26232	FBXO2	F-box protein 2	-5.22	AAGCTCACCGTTAAGCTACTG	NM_012168:	NM_012168:
26263	FBXO22	F-box protein 22	2.28	CCAAATCTGTTTGGTCACAAA	NM_012170:	NM_012170:
26263	FBXO22	F-box protein 22	-1.02	AAGGTGGGAGCCAGTAATTAT	NM_012170:	NM_012170:NM_147188:
26261	FBXO24	F-box protein 24	-1.27	CAGGCGAGTGACTGTCAAGAA	NM_012172:	NM_033506:NM_012172:
26261	FBXO24	F-box protein 24	0.03	CCCAAGGTGTGACACAGTTTA	NM_012172:	NM_033506:NM_012172:
126433	FBXO27	F-box protein 27	0.37	CTGCCAATCATATGTAATAAA	NM_178820:	NM_178820:
126433	FBXO27	F-box protein 27	1.89	CAGCTGAAAGTCTACGTTAAA	NM_178820:	NM_178820:
23219	FBXO28	F-box protein 28	-0.01	CAAGCTTTCCTTACCCTACAA	NM_015176:	NM_015176:
23219	FBXO28	F-box protein 28	0.53	TAGGAACAAGAGACTATTAAA	NM_015176:	NM_015176:
26273	FBXO3	F-box protein 3	1.85	TCGCTAAGACCTTGACTTTAA	NM_012175:	NM_012175:
26273	FBXO3	F-box protein 3	0.98	GTCGGGTATATGAATACACAA	NM_012175:	NM_012175:NM_033406:
84085	FBXO30	F-box protein 30	0.16	CAGACCGGAAATCATATGAAA	NM_032145:	NM_032145:
84085	FBXO30	F-box protein 30	0.00	CAGAATTTACATGGTGATTCA	NM_032145:	NM_032145:
79791	FBXO31	F-box protein 31	-2.58	CAGAGTCAGAGAATTGGCAAA	NM_024735:	NM_024735:
79791	FBXO31	F-box protein 31	1.60	CCCATATGAGATGACGAGGAA	NM_024735:	NM_024735:
254170	FBXO33	F-box protein 33	-1.95	ATCCTGAGTAATAGTAGGCAA	NM_203301:	NM_203301:

254170	FBXO33	F-box protein 33	-0.92	CTGCTAGATTGTAATATTTAA	NM_203301:	NM_203301:
55030	FBXO34	F-box protein 34	-1.12	TCGGTAAAGCATCATCTCGAA	NM_017943:	NM_017943:
55030	FBXO34	F-box protein 34	-0.27	AAGAAACTCTAAATAGTTGAA	NM_017943:	NM_017943:
130888	FBXO36	F-box protein 36	1.27	AGAGGTTTCTATTGTATATAA	NM_174899:	NM_174899:
130888	FBXO36	F-box protein 36	-0.08	CACCGTCATTCTGAGGTCAAA	NM_174899:	NM_174899:
81545	FBXO38	F-box protein 38	-0.38	TTCGCTCGATACGACTTTGAA	NM_030793:	NM_030793:NM_205836:
81545	FBXO38	F-box protein 38	-0.31	CTGGATGGACACTATAGCAAA	NM_030793:	NM_030793:NM_205836:
26272	FBXO4	F-box protein 4	-2.61	CAGTGTGATTCCACAGATTCA	NM_012176:	NM_012176:NM_033484:
26272	FBXO4	F-box protein 4	-0.26	CAGATTGATGGTATTGGATCA	NM_012176:	NM_012176:NM_033484:
51725	FBXO40	F-box protein 40	0.68	CACCATATTTATGGAGAACAT	NM_016298:	NM_016298:
51725	FBXO40	F-box protein 40	0.10	GAGGAAGATACGTCTCCTAAA	NM_016298:	NM_016298:
54455	FBXO42	F-box protein 42	-0.18	CTGGGATCAAATCTCCATTAA	XM_048774:	NM_018994:
54455	FBXO42	F-box protein 42	-0.03	CTCCTGTGTGATAGATGATAA	XM_048774:	NM_018994:
93611	FBXO44	F-box protein 44	-2.35	CGGACATTGGATGAAGCCGAA	NM_033182:	NM_183412:NM_183413:NM_033182:NM_0010147 65:
93611	FBXO44	F-box protein 44	1.30	CCCGAAAGGTCTTGACCTGAA	NM_033182:	NM_183412:NM_183413:NM_033182:NM_0010147 65:
200933	FBXO45	F-box protein 45	-0.40	CAGACGTTACTATTATCCCTA	XM_117294:	XM_117294:
200933	FBXO45	F-box protein 45	-0.45	CCCATGGGACTTGAAATACAA	XM_117294:	XM_117294:
23403	FBXO46	F-box protein 46	0.47	CTAGATGGTTTGCCTATTAAA	XM_371179:	XM_371179:
23403	FBXO46	F-box protein 46	0.66	CAGCGATAGCTCCAAGGCCAA	XM_371179:	XM_371179:
26271	FBXO5	F-box protein 5	1.38	AGCGCTTGCATAACAAGGAAA	NM_012177:	NM_012177:
26271	FBXO5	F-box protein 5	-0.46	CATGTTCATTCCGGACTTAAA	NM_012177:	NM_012177:
26270	FBXO6	F-box protein 6	-0.45	AATGTTTGCATGGCAAATTGA	NM_018438:	NM_018438:
26270	FBXO6	F-box protein 6	-1.58	AATCGTGGTTAAGGACTGGTT	NM_018438:	NM_018438:
25793	FBXO7	F-box protein 7	-0.10	CACAGATTGGAAAGAACTGTA	NM_012179:	NM_012179:NM_001033024:
25793	FBXO7	F-box protein 7	0.64	GACAATACTGTCAGAGTTCAA	NM_012179:	NM_012179:NM_001033024:
26269	FBXO8	F-box protein 8	0.14	GTGCATTAGATTTGCCTGAAA	NM_012180:	NM_012180:
26269	FBXO8	F-box protein 8	0.25	ACAGCTGTTAACGAATGATAA	NM_012180:	NM_012180:
26268	FBXO9	F-box protein 9	0.71	ACACGTTATGTTAAAGGTGAA	NM_012347:	NM_012347:NM_033481:NM_033480:
26268	FBXO9	F-box protein 9	0.52	ATGATAGTACACGTTATGTTA	NM_012347:	NM_012347:NM_033481:NM_033480:
23291	FBXW11	F-box and WD-40 domain protein 11	0.16	CACTGGGATAGTCTAATTCTA	NM_012300:	NM_033644:NM_033645:NM_012300:
23291	FBXW11	F-box and WD-40 domain protein 11	0.30	CAGAAGTAAATCGACCGTCAA	NM_012300:	NM_033644:NM_033645:NM_012300:
285231	FBXW12	F-box and WD-40 domain protein 12	0.44	CACCTTTGATCTACCAACCAA	NM_207102:	NM_207102:
285231	FBXW12	F-box and WD-40 domain protein 12	0.20	CTGACTTAGCTTTGAAGCGAA	NM_207102:	NM_207102:
26190	FBXW2	F-box and WD-40 domain protein 2	0.72	CACGCAGTGCACAATCATTTA	NM_012164:	NM_012164:
26190	FBXW2	F-box and WD-40 domain protein 2	-1.38	CCAGTGGGACTTTGCCAGTTA	NM_012164:	NM_012164:
6468	FBXW4	F-box and WD-40 domain protein 4	-1.79	CAGCACCTTCACTGTCAAGTA	NM_022039:	NM_022039:
6468	FBXW4	F-box and WD-40 domain protein 4	1.07	TGGGAAGATTGGCATTCATAA	NM_022039:	NM_022039:
6468	FBXW4	F-box and WD-40 domain protein 4	-0.84	CCCAGTGAAGGTGTCTCAGAA	NM_012165:	NM_022039:
54461	FBXW5	F-box and WD-40 domain protein 5	0.12	CCCGTTCAGGGCCCTGAATAA	NM_018998:	NM_178225:NM_178226:NM_018998:
54461	FBXW5	F-box and WD-40 domain protein 5	-2.63	CACGAGGATGTGGTCAACTCA	NM_018998:	NM_178225:NM_178226:NM_018998:
55294	FBXW7	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila	1.45	CTGGTTGACTTTCTAATTAGA	NM_018315:	NM_033632:NM_018315:NM_001013415:
55294	FBXW7	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila	0.31	AAGGAACTGCAATAATATCAA	NM_018315:	NM_033632:NM_018315:NM_001013415:
26259	FBXW8	F-box and WD-40 domain protein 8	-1.36	TCCGTAGTTGTTCTAATATTA	NM_012174:	NM_153348:NM_012174:
26259	FBXW8	F-box and WD-40 domain protein 8	0.32	AACCAATAGTTAGTTAATATA	NM_012174:	NM_153348:NM_012174:
84261	FBXW9	F-box and WD-40 domain protein 9	0.15	TAGGCACTAAGCGAAATAGTA	NM_032301:	NM_032301:
84261	FBXW9	F-box and WD-40 domain protein 9	0.00	CAGGTTCTGATCAAGACCTTA	NM_032301:	NM_032301:
83953	FCAMR	Fc receptor, IgA, IgM, high affinity	1.61	CCAGGTTTAAGTACTCTTAAA	NM_032029:	NM_032029:
83953	FCAMR	Fc receptor, IgA, IgM, high affinity	-0.87	CACCAGAAGCTCGGTGACAAA	NM_032029:	NM_032029:
2219	FCN1	ficolin (collagen/fibrinogen domain containing) 1	0.98	AGGGAGAATTATGTTTCTAAA	NM_002003:	NM_002003:
2219	FCN1	ficolin (collagen/fibrinogen domain containing) 1	-3.23	CTGTCATGCTTCAAACCTCAA	NM_002003:	NM_002003:
2220	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	0.02	CTGCCATGTGTCAAACCTGAA	NM_004108:	NM_004108:NM_015837:
2220	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	-6.71	AAGGATACAATTATAGCTACA	NM_004108:	NM_004108:NM_015837:
8547	FCN3	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	-0.30	CTGCTTGCCTGTCCACATTTA	NM_003665:	NM_173452:NM_003665:
8547	FCN3	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	-0.05	ATGCATCCTGTTACCGATCAA	NM_003665:	NM_173452:NM_003665:
79368	FCRL2	Fc receptor-like 2	1.24	TCAGAAGATGGCTTACCATAA	NM_030764:	NM_030764:
79368	FCRL2	Fc receptor-like 2	-4.73	TTCAAATATAGTAAAGATAAA	NM_030764:	NM_030764:
343413	FCRL6	Fc receptor-like 6	-0.44	CAGAGAGAGGAGTGAGCCCAA	NM_001004310:	NM_001004310:
343413	FCRL6	Fc receptor-like 6	2.12	CAGACATTCACACAAACTTCA	NM_001004310:	NM_001004310:
2222	FDFT1	farnesyl-diphosphate farnesyltransferase 1	-0.39	TCCTACTACTTTAATCCCTAA	NM_004462:	NM_004462:
2222	FDFT1	farnesyl-diphosphate farnesyltransferase 1	1.75	TTGAATGTTCGTAATAGTAGA	NM_004462:	NM_004462:
2232	FDXR	ferredoxin reductase	-5.18	AAGCGTGCCCTTTGACTCCAA	NM_004110:	NM_024417:NM_004110:
2232	FDXR	ferredoxin reductase	-1.63	TGGGAACATGCTGGAAATAAA	NM_004110:	NM_024417:NM_004110:
2235	FECH	ferrochelatase (protoporphyria)	0.37	CCCAAGGGTAATAAACGTGTA	NM_000140:	NM_000140:NM_001012515:
2235	FECH	ferrochelatase (protoporphyria)	-0.31	CCGACTGGTGTGGCAATCCAA	NM_000140:	NM_000140:NM_001012515:
55527	FEM1A	fem-1 homolog a (C.elegans)	-0.77	TGCGATAAATCCACTAGCTAA	NM_018708:	NM_018708:
55527	FEM1A	fem-1 homolog a (C.elegans)	-0.39	AAGGATTGAGACCCAAGTCAT	NM_018708:	NM_018708:
10116	FEM1B	fem-1 homolog b (C. elegans)	-0.90	CAGCCCGCAATGGACACGCAA	NM_015322:	NM_015322:
10116	FEM1B	fem-1 homolog b (C. elegans)	0.47	CTGGATATGTAAAGTCGTTTA	NM_015322:	NM_015322:
2237	FEN1	flap structure-specific endonuclease 1	0.02	CAAGAGCTACTTTGGCCGTAA	NM_004111:	NM_004111:
2237	FEN1	flap structure-specific endonuclease 1	2.26	TAAGTCCATTGTTACATGAAA	NM_004111:	NM_004111:
2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	-3.57	CAGAACAACTTAGTAGGATAA	NM_005246:	NM_005246:
2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	-6.05	CAGATAGATCCTAGTACAGAA	NM_005246:	NM_005246:
2242	FES	feline sarcoma oncogene	-1.52	AAGGCCAAGTTTCTACAGGAA	NM_002005:	NM_002005:
2242	FES	feline sarcoma oncogene	-0.39	CAGCCTGAGGCTGAGTACCAA	NM_002005:	NM_002005:
54738	FEV	FEV (ETS oncogene family)	1.42	AGGCGGCAGCGCTTTAATTAA	NM_017521:	NM_017521:
54738	FEV	FEV (ETS oncogene family)	-0.07	TTCAATATCACTACTCTTTAA	NM_017521:	NM_017521:
2864	FFAR1	free fatty acid receptor 1	-0.67	TAGCCTGGTCTACGCCCTGAA	NM_005303:	NM_005303:
2864	FFAR1	free fatty acid receptor 1	1.41	TGCCTGGAGTGTGGTGCTTAA	NM_005303:	NM_005303:
2867	FFAR2	free fatty acid receptor 2	-1.56	ACCATCGTGATCATCGTTCAA	NM_005306:	NM_005306:
2867	FFAR2	free fatty acid receptor 2	-6.60	CTACGAGAACTTCACCGATAA	NM_005306:	NM_005306:
2865	FFAR3	free fatty acid receptor 3	0.74	CAGAAAGTTCCCATTGCTCAA	NM_005304:	NM_005304:
2865	FFAR3	free fatty acid receptor 3	0.05	GTGGATCATCAGAGACATTTA	NM_005304:	NM_005304:
2243	FGA	fibrinogen alpha chain	0.50	ACGCGTCGTTCATGCTCTAAA	NM_000508:	NM_021871:NM_000508:
2243	FGA	fibrinogen alpha chain	-0.37	AGGGCTTTAGCTCGTGAAGTA	NM_000508:	NM_021871:NM_000508:
2244	FGB	fibrinogen beta chain	-0.21	CAGCACGTATGACAGAGACAA	NM_005141:	NM_005141:
2244	FGB	fibrinogen beta chain	-0.58	CAGGAAATGGGATCCATATAA	NM_005141:	NM_005141:
2246	FGF1	fibroblast growth factor 1 (acidic)	-0.91	CTGATACTTATTTACCTATAA	NM_000800:	NM_033137:NM_033136:NM_000800:
2246	FGF1	fibroblast growth factor 1 (acidic)	1.35	GAGAATGATAGTAATAGGATA	NM_000800:	NM_033137:NM_033136:NM_000800:
2255	FGF10 (fibrob	fibroblast growth factor 10	-0.77	TCCAATGGTGGTACACTCATA	NM_004465:	NM_004465:
2255	FGF10 (fibrob	fibroblast growth factor 10	-2.75	CAACTATTACTTAGCCATGAA	NM_004465:	NM_004465:
9965	FGF19 (fibrob	fibroblast growth factor 19	-1.86	CCGTAAGGCGCTACTATATAA	NM_005117:	NM_005117:
9965	FGF19 (fibrob	fibroblast growth factor 19	0.06	CAACATGATATTTATGAGTAA	NM_005117:	NM_005117:
2247	FGF2	fibroblast growth factor 2 (basic)	1.15	AACAATATTAGTCGTATCCAA	NM_002006:	NM_002006:
2247	FGF2	fibroblast growth factor 2 (basic)	0.03	ATGCTAAACTTTACTGATGTA	NM_002006:	NM_002006:
8074	FGF23	fibroblast growth factor 23	0.65	TCCATTCATAAGGAGACTCAA	NM_020638:	NM_020638:
8074	FGF23	fibroblast growth factor 23	-1.92	CTCTCTTTAAATGACCACCTA	NM_020638:	NM_020638:
2248	FGF3	fibroblast growth factor 3 (murine mammary tumor virus integration sit	-1.35	TTGCTCCTGGGTGGAAATTAA	NM_005247:	NM_005247:

2248	FGF3	fibroblast growth factor 3 (murine mammary tumor virus integration sit	1.08	TTGTGTCATCACAACATTAAA	NM_005247:	NM_005247:
2249	FGF4	fibroblast growth factor 4 (heparin secretory transforming protein 1, Ka	0.89	ATGTGTATATATTGCCACCAA	NM_002007:	NM_002007:
2249	FGF4	fibroblast growth factor 4 (heparin secretory transforming protein 1, Ka	-0.66	CACCGATGAGTGCACGTTCAA	NM_002007:	NM_002007:
2250	FGF5	fibroblast growth factor 5	0.97	ACACATATATATAACAAATAA	NM_004464:	NM_033143:NM_004464:
2250	FGF5	fibroblast growth factor 5	0.99	TTGAACTAATTTATACTTTAA	NM_004464:	NM_033143:NM_004464:
2251	FGF6	fibroblast growth factor 6	0.09	AAGCATCATCTGTTCGATTGA	NM_020996:	NM_020996:
2251	FGF6	fibroblast growth factor 6	0.42	TTCGTTGCCATGAACAGTAAA	NM_020996:	NM_020996:
2252	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	-0.26	CACCCGGAGCACTACACTATA	NM_002009:	NM_002009:
2252	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	-1.63	TAGTTTGTAGCTACAGTAGAA	NM_002009:	NM_002009:
2253	FGF8	fibroblast growth factor 8 (androgen-induced)	-2.44	CTACATCTGCATGAACAAGAA	NM_006119:	NM_033164:NM_033165:NM_033163:NM_006119:
2253	FGF8	fibroblast growth factor 8 (androgen-induced)	-5.78	CAAGAGCAACGGCAAAGGCAA	NM_006119:	NM_033164:NM_033165:NM_033163:NM_006119:
2254	FGF9	fibroblast growth factor 9 (glia-activating factor)	-0.63	ATCGCAGTGAACTTAAAGCAA	NM_002010:	NM_002010:
2254	FGF9	fibroblast growth factor 9 (glia-activating factor)	0.81	GCGATACTATGTTGCATTAAA	NM_002010:	NM_002010:
2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeif	-2.88	AACAGATAACACCAAACCAAA	NM_000604:	NM_015850:NM_023111:NM_023110:NM_023109:NM_023105:NM_023108:NM_023107:NM_023106:NM_000604:
2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeif	-0.38	CAGAGATTTACCCATCGGGTA	NM_000604:	NM_015850:NM_023111:NM_023109:NM_023105:NM_023106:NM_000604:
11116	FGFR1OP	FGFR1 oncogene partner	1.30	AAGTATATTAGTATAAGTTAA	NM_007045:	NM_007045:NM_194429:
11116	FGFR1OP	FGFR1 oncogene partner	0.32	CCAGATGAAGATGATATGGAA	NM_007045:	NM_007045:NM_194429:
26127	FGFR1OP2	FGFR1 oncogene partner 2	1.19	ACGGAGGATTTGTACGCTAAA	NM_015633:	NM_015633:
26127	FGFR1OP2	FGFR1 oncogene partner 2	1.27	TAGACATATTTAGTAGGTTAA	NM_015633:	NM_015633:
2263	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratin	-2.92	CCGAATGAAGAACACGACCAA	NM_000141:	NM_023031:NM_023029:NM_023030:NM_023028:NM_022973:NM_022974:NM_000141:NM_022972:NM_022975:NM_022969:
2263	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratin	-4.15	CGGAGGAGCGTTGCCATTCAA	NM_000141:	NM_023031:NM_023029:NM_023030:NM_022976:NM_023028:NM_022973:NM_022974:NM_000141:NM_022972:NM_022975:NM_022971:NM_022969:NM_022970:
2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwa	-0.53	ACCCTACGTTACCGTGCTCAA	NM_000142:	NM_000142:NM_022965:
2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwa	0.14	CAGGAGAATTAGATTTCTATA	NM_000142:	NM_000142:NM_022965:
2264	FGFR4	fibroblast growth factor receptor 4	-1.20	CACATTGACTACTATAAGAAA	NM_002011:	NM_213647:NM_022963:NM_002011:
2264	FGFR4	fibroblast growth factor receptor 4	1.99	CAGGCTCTTCCGGCAAGTCAA	NM_002011:	NM_213647:NM_022963:NM_002011:
53834	FGFRL1	fibroblast growth factor receptor-like 1	-2.14	CACCGTGCTGCCAGACCCAAA	NM_021923:	NM_021923:NM_001004356:NM_001004358:
53834	FGFRL1	fibroblast growth factor receptor-like 1	1.15	CTTGGTATTTATATTTAAGAA	NM_021923:	NM_021923:NM_001004356:NM_001004358:
2266	FGG (fibrinog	fibrinogen gamma chain	-0.25	CCGGTGGTATTCCATGAAGAA	NM_000509:	NM_000509:NM_021870:
2266	FGG (fibrinog	fibrinogen gamma chain	-0.35	CCCGGTGGTATTCCATGAAGA	NM_000509:	NM_000509:NM_021870:
2267	FGL1	fibrinogen-like 1	0.62	TAGCCGTTATGCACAATATAA	NM_004467:	NM_201553:NM_147203:NM_004467:NM_201552:
2267	FGL1	fibrinogen-like 1	1.12	ATAGCCGTTATGCACAATATA	NM_004467:	NM_201553:NM_147203:NM_004467:NM_201552:
10875	FGL2	fibrinogen-like 2	-0.16	CCAGGTATTCGTTATCTAATA	NM_006682:	NM_006682:
10875	FGL2	fibrinogen-like 2	1.42	ATGGCAAATATTATCACCAAA	NM_006682:	NM_006682:
2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	0.25	CACGTGGAACGGCAGCACTAA	NM_005248:	NM_005248:
2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	-0.14	CAGACCTTGTCTAGTTATTTA	NM_005248:	NM_005248:
2271	FH	fumarate hydratase	0.65	TAGGATGTGCTAGGTCTAAGA	NM_000143:	NM_000143:
2271	FH	fumarate hydratase	-0.48	CAGGAATTTAGTGGTTATGTT	NM_000143:	NM_000143:
2274	FHL2	four and a half LIM domains 2	0.48	ATCGAGTAAGGCACACCCAAA	NM_001450:	NM_001450:NM_201555:NM_201556:NM_201557:
2274	FHL2	four and a half LIM domains 2	-2.62	CTCCCGTTGCGTCAAGTCTAA	NM_001450:	NM_001450:NM_201555:NM_201556:NM_201557:
9457	FHL5	four and a half LIM domains 5	-0.15	AACCAATTGAATCTGATTCTA	NM_020482:	NM_020482:
9457	FHL5	four and a half LIM domains 5	0.12	ACCAATTGAATCTGATTCTAA	NM_020482:	NM_020482:
84929	FIBCD1	fibrinogen C domain containing 1	0.39	CCCACTGAAGTTTGTGCTTAA	NM_032843:	NM_032843:
84929	FIBCD1	fibrinogen C domain containing 1	0.34	CCGGGCCATCCCTGACACGAA	NM_032843:	NM_032843:
2277	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	0.53	CAGGTGTCATATGACTGATTA	NM_004469:	NM_004469:
2277	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	-0.29	CAGGTTGTAAGTGCTTGCCAA	NM_004469:	NM_004469:
60681	FKBP10	FK506 binding protein 10, 65 kDa	0.15	GTGGGTGTTAGGGCTATGAAA	NM_021939:	NM_021939:
60681	FKBP10	FK506 binding protein 10, 65 kDa	0.12	CTGGAGAGAGAAGGAAGATTA	NM_021939:	NM_021939:
51303	FKBP11	FK506 binding protein 11, 19 kDa	0.01	TTGGGTATCACCTATACAGAA	NM_016594:	NM_016594:
51303	FKBP11	FK506 binding protein 11, 19 kDa	-0.37	CCGAGCCAACTACTGGCTAAA	NM_016594:	NM_016594:
55033	FKBP14	FK506 binding protein 14, 22 kDa	0.06	GAGGTAGAAAGTTATATTTAT	NM_017946:	NM_017946:
55033	FKBP14	FK506 binding protein 14, 22 kDa	0.01	AACACGGTTAATAACATATAA	NM_017946:	NM_017946:
2280	FKBP1A	FK506 binding protein 1A, 12kDa	-3.00	GAGGACTGAATTACTCTCCAA	NM_000801:	NM_000801:
2280	FKBP1A	FK506 binding protein 1A, 12kDa	0.83	TAGGTTAACATTAGAATAGGA	NM_000801:	NM_000801:
2281	FKBP1B	FK506 binding protein 1B, 12.6 kDa	0.92	AACAATGTCCTCTTTGAGAAA	NM_004116:	NM_004116:NM_054033:
2281	FKBP1B	FK506 binding protein 1B, 12.6 kDa	-3.62	CAGAGGGACTTGAGCCAGTTA	NM_004116:	NM_004116:NM_054033:
2286	FKBP2	FK506 binding protein 2, 13kDa	0.06	CAGGGACCAGACTGTTCCAAA	NM_004470:	NM_004470:NM_057092:
2286	FKBP2	FK506 binding protein 2, 13kDa	0.26	CGGGTTTCGCACGGTCCAATA	NM_004470:	NM_004470:
2287	FKBP3	FK506 binding protein 3, 25kDa	1.02	GTGAAGCTTAATGAAGATAAA	NM_002013:	NM_002013:
2287	FKBP3	FK506 binding protein 3, 25kDa	0.33	CACAGCCTTGACGTCACTCAA	NM_002013:	NM_002013:
2288	FKBP4	FK506 binding protein 4, 59kDa	0.75	AGCAATAAAGTGGAAACAATA	NM_002014:	NM_002014:
2288	FKBP4	FK506 binding protein 4, 59kDa	-0.26	AGGGATGAGGTCTGATAAGAA	NM_002014:	NM_002014:
2289	FKBP5	FK506 binding protein 5	-0.82	ACGGGTAAACAGATTGAGCAT	NM_004117:	NM_004117:
2289	FKBP5	FK506 binding protein 5	-1.62	TCGGCTGGCAGTCTCCCTAAA	NM_004117:	NM_004117:
51661	FKBP7	FK506 binding protein 7	-3.75	CACGATGAACTATAGCATATT	NM_016105:	NM_016105:NM_181342:
51661	FKBP7	FK506 binding protein 7	1.42	CGGAGCATTGAGACATTTAAA	NM_016105:	NM_016105:NM_181342:
23770	FKBP8	FK506 binding protein 8, 38kDa	-0.85	AATCCCATGGAAGTGGCTGTT	NM_012181:	NM_012181:
23770	FKBP8	FK506 binding protein 8, 38kDa	0.95	AAGACAACATCAAGGCTCTCT	NM_012181:	NM_012181:
11328	FKBP9	FK506 binding protein 9, 63 kDa	-0.44	CTGGTGTTTGATGTTGCATTA	NM_007270:	NM_007270:
11328	FKBP9	FK506 binding protein 9, 63 kDa	-1.91	TCGAGTCACAATCGCATGAAA	NM_007270:	NM_007270:
64105	FKSG14	leucine zipper protein FKSG14	0.01	ATGGAATCTCTTAATGTACTA	NM_022145:	NM_022145:
64105	FKSG14	leucine zipper protein FKSG14	0.35	CTCAGCTATCATTGTTAATTA	NM_022145:	NM_022145:
59347	FKSG2	apoptosis inhibitor	0.27	CACGATAATCACTAGTGTTGA	NM_021631:	NM_021631:
59347	FKSG2	apoptosis inhibitor	-1.23	TACCGTAAGGATGGTCAGTAT	NM_021631:	NM_021631:
83954	FKSG83	FKSG83	2.08	ACGTGTGTCTTTCCACTTATA	NM_032030:	NM_032030:
83954	FKSG83	FKSG83	-3.14	AAGACTGTTTATATACTACCA	NM_032030:	NM_032030:
201163	FLCN	folliculin	-0.58	CCGGGATATATCAGCCATGAT	NM_144606:	NM_144997:NM_144606:
201163	FLCN	folliculin	1.74	CAGGCCTGTTGCAGTCTCCAA	NM_144606:	NM_144997:NM_144606:
2312	FLG (filaggrin	filaggrin	-0.04	CACGTAATGAGGAACAATCAA	XM_048104:	NM_002016:
2312	FLG (filaggrin	filaggrin	-0.04	CACAGTCATCATGATAAACAT	XM_048104:	NM_002016:
55277	FLJ10986	hypothetical protein FLJ10986	-1.13	CAGCAGGGCACTCAATCAGTA	NM_018291:	NM_018291:
55277	FLJ10986	hypothetical protein FLJ10986	-0.88	CCCGGACTTCTTATCGTGGAA	NM_018291:	NM_018291:
79587	FLJ12118	hypothetical protein FLJ12118	0.16	CTCGTGGGAACGCTTATTCAA	NM_024537:	NM_024537:
79587	FLJ12118	hypothetical protein FLJ12118	0.09	CTCGCCAGTCTTTATGAGGAA	NM_024537:	NM_024537:
79807	FLJ13273	hypothetical protein FLJ13273	0.47	GAGGTTTATAGGTTTAAGTAA	NM_024751:	NM_024751:
79807	FLJ13273	hypothetical protein FLJ13273	-1.01	AAGACTCAGAATCTTAAGGAA	NM_024751:	NM_024751:

79758	FLJ13639	hypothetical protein FLJ13639	-0.16	AACAGCTGGCTCAGACATTTA	NM_024705:	NM_024705:
79758	FLJ13639	hypothetical protein FLJ13639	-1.49	CTCACAGAAGATGGACTTGAA	NM_024705:	NM_001031719:NM_024705:
79828	FLJ13984	hypothetical protein FLJ13984	-0.76	CAGGCTATTCTTAGATATACA	NM_024770:	NM_024770:
79828	FLJ13984	hypothetical protein FLJ13984	0.77	CACACCTTATTTCCAGGGAAA	NM_024770:	NM_024770:
84954	FLJ14981	hypothetical protein FLJ14981	0.14	TCAGGTAATAAAGAAACGGAA	NM_032868:	NM_032868:
84954	FLJ14981	hypothetical protein FLJ14981	-1.28	CCGGATGGGCTCAGGTAATAA	NM_032868:	NM_032868:
339761	FLJ16008	FLJ16008 protein	-0.25	CGGGAGATTGTGAAGAATTTA	NM_001001665:	NM_001001665:
339761	FLJ16008	FLJ16008 protein	0.44	AACCAAGTTATTGCTGACTTA	NM_001001665:	NM_001001665:
54962	FLJ20516	timeless-interacting protein	-3.85	AAGCTTGGCGTTACTATGTAT	NM_017858:	NM_017858:
54962	FLJ20516	timeless-interacting protein	0.52	CTGAGTTAAGTAGAAGCCTAA	NM_017858:	NM_017858:
54980	FLJ20558	hypothetical protein FLJ20558	-3.09	CTGCTCTTAGCTAAGATGCAA	NM_017880:	NM_017880:
54980	FLJ20558	hypothetical protein FLJ20558	-5.67	CACCCGTAGCTTTATCCAGAA	NM_017880:	NM_017880:
55006	FLJ20628	hypothetical protein FLJ20628	-1.86	CAGGAGCAACCGAAGACATAA	NM_017910:	NM_017910:
55006	FLJ20628	hypothetical protein FLJ20628	0.01	GGCGTGATTCATGGAAATTAA	NM_017910:	NM_017910:
55011	FLJ20643	hypothetical protein FLJ20643	-0.82	ACCGGAAGAGAAAGCAATTAA	NM_017916:	NM_017916:
55011	FLJ20643	hypothetical protein FLJ20643	-3.04	CCCGCTGCAGATCAACTCTCA	NM_017916:	NM_017916:
79984	FLJ21736	esterase 31	-1.88	CGGGCTATTGTCACAGAGAAA	NM_024922:	NM_024922:
79984	FLJ21736	esterase 31	-0.66	ACCGTCATAGATGAATACCTA	NM_024922:	NM_024922:
60526	FLJ21820	hypothetical protein FLJ21820	0.09	GAGATACTCACTGATACTAAA	NM_021925:	NM_021925:
60526	FLJ21820	hypothetical protein FLJ21820	-1.60	CTGCACTAGACAGAGAATAAA	NM_021925:	NM_021925:
79912	FLJ22028	hypothetical protein FLJ22028	0.17	AAGAATAATGATCATAGGGAA	NM_024854:	NM_024854:
79912	FLJ22028	hypothetical protein FLJ22028	1.48	TAGCAATATCTCGTTTGCTAA	NM_024854:	NM_024854:
64224	FLJ22313	hypothetical protein FLJ22313	0.51	CAGCCATAAAGCAATAAACTT	NM_022373:	NM_022373:
64224	FLJ22313	hypothetical protein FLJ22313	-0.67	AAGCACGAATGGACTACTAAA	NM_022373:	NM_022373:
79866	FLJ22624	FLJ22624 protein	-3.75	CCGGTTGATAATGGCAGTTTA	NM_024808:	NM_024808:
79866	FLJ22624	FLJ22624 protein	0.77	TACCAACTCCAGGGAAATTTA	NM_024808:	NM_024808:
84197	FLJ23356	hypothetical protein FLJ23356	1.52	AAGGTCTTGGATACACTTAGA	NM_032237:	NM_032237:
84197	FLJ23356	hypothetical protein FLJ23356	-3.35	CACGATGATCTCATGCCCTCA	NM_032237:	NM_032237:
64800	FLJ23588	CAP-binding protein complex interacting protein 1	0.05	CACCGTGTAGAGTATATTCAA	NM_022785:	NM_022785:
64800	FLJ23588	CAP-binding protein complex interacting protein 1	-4.10	CAGGGCCTGTTTCAAGGCTAA	NM_022785:	NM_022785:NM_198856:
124923	FLJ25006	hypothetical protein FLJ25006	-0.88	GAGGTTAAAGCTGATGGGATA	NM_144610:	NM_144610:
124923	FLJ25006	hypothetical protein FLJ25006	0.05	TACATGGGTGAGAGAGGTTAA	NM_144610:	NM_144610:
151516	FLJ25084	Skin ASpartic Protease	-0.49	CAAGCTGCTGTTGATGACAAA	NM_152792:	NM_152792:
151516	FLJ25084	Skin ASpartic Protease	-0.03	CAGGAGCTATCCCACTGAGAA	NM_152792:	NM_152792:
220296	FLJ25530	hepatocyte cell adhesion molecule	-6.54	ATGGATGGGCTTATTCTTATA	NM_152722:	NM_152722:
220296	FLJ25530	hepatocyte cell adhesion molecule	0.83	CACATAAACAAGGGTAACAAA	NM_152722:	NM_152722:
254048	FLJ25778	hypothetical protein FLJ25778	0.48	TAGGATCACAATCACGACATA	XM_376679:	XM_376679:XM_379933:
254048	FLJ25778	hypothetical protein FLJ25778	-0.97	CACAGAGACTTGTGACTCATA	XM_376679:	XM_376679:XM_379933:
205860	FLJ25801	hypothetical protein FLJ25801	-1.05	CGGGCAGATATCATTCTACAA	NM_173553:	NM_173553:
205860	FLJ25801	hypothetical protein FLJ25801	-2.30	CAGCATGTTCAGAGTACTCCA	NM_173553:	NM_173553:
153830	FLJ31951	hypothetical protein FLJ31951	2.00	CTGTATGATCACACTCTGCAA	NM_144726:	NM_144726:
153830	FLJ31951	hypothetical protein FLJ31951	1.26	CTGATACGTGTGAGAGAGAAA	NM_144726:	NM_144726:
147664	FLJ32214	hypothetical protein FLJ32214	-0.14	CACGACGTCCTTATGCCCAAA	NM_152473:	NM_152473:
147664	FLJ32214	hypothetical protein FLJ32214	-0.87	AACGATTATCGAGACAAGTCA	NM_152473:	NM_152473:
93233	FLJ32926	hypothetical protein FLJ32926	-0.03	TACGAGGACGCCCTGAATAAA	NM_144577:	NM_144577:
93233	FLJ32926	hypothetical protein FLJ32926	0.68	AAATGGGACTGTGGAAATAAA	NM_144577:	NM_144577:
284131	FLJ35220	hypothetical protein FLJ35220	-0.03	AAGAGAGAGATTGGTGTTAAT	NM_173627:	NM_173627:
284131	FLJ35220	hypothetical protein FLJ35220	0.26	ATGGGTGAGAGTTGAAATGAA	NM_173627:	NM_173627:
339976	FLJ36180	hypothetical protein FLJ36180	-0.46	CACAACTATTAAGACGATGAA	NM_178556:	NM_178556:
339976	FLJ36180	hypothetical protein FLJ36180	0.02	GCGGGCGATGTCTGAGACCAA	NM_178556:	NM_178556:
129804	FLJ37440	hypothetical protein FLJ37440	0.73	TAACCTGGTAATATAACTGAA	NM_153214:	NM_153214:
129804	FLJ37440	hypothetical protein FLJ37440	-1.31	CACTGTAGAGGTATCAGTGAA	NM_153214:	NM_153214:
283848	FLJ37464	hypothetical protein FLJ37464	0.03	CAGGTTGTGACATGGAGCAAA	NM_173815:	NM_173815:
283848	FLJ37464	hypothetical protein FLJ37464	1.03	AAGAGTGGGCATGAAGCTCAA	NM_173815:	NM_173815:
166979	FLJ37927	CDC20-like protein	1.21	AAGGAGATTGCAACTGGTCAA	NM_152623:	NM_152623:
166979	FLJ37927	CDC20-like protein	0.15	CAAGGACAACCTATTACCAAA	NM_152623:	NM_152623:
126410	FLJ39501	cytochrome P450, family 2, subfamily E, polypeptide 2 homolog	-0.62	CAAGAGAAGATGAGTGATTAT	NM_173483:	NM_173483:
126410	FLJ39501	cytochrome P450, family 2, subfamily E, polypeptide 2 homolog	-2.11	CTGGACAACATGCACCATGTA	NM_173483:	NM_173483:
401258	FLJ43093	FLJ43093 protein	-0.18	TTCAACAATAACAGTATTCAA	NM_207498:	NM_207498:
401258	FLJ43093	FLJ43093 protein	-3.31	CACAAATTGAATATACAACAT	NM_207498:	NM_207498:
386757	FLJ43855	similar to sodium- and chloride-dependent creatine transporter	0.01	TCACCTGAACAAAGAAGACAA	NM_198857:	NM_198857:
386757	FLJ43855	similar to sodium- and chloride-dependent creatine transporter	-1.46	CTGGACAGCATCATTTACTAT	NM_198857:	NM_198857:
346689	FLJ44186	FLJ44186 protein	0.05	CACGCAGTAGAGGAATCTAGA	NM_198508:	NM_198508:
346689	FLJ44186	FLJ44186 protein	1.07	TCGGTTATCTGTTGCTTTATA	NM_198508:	NM_198508:
400535	FLJ44674	FLJ44674 protein	0.52	CAGGTGGATGCAGACATCCAA	NM_032032:	NM_207449:XM_291770:
202018	FLJ90013	hypothetical protein FLJ90013	-0.08	TCCGCTTGAATTATTCTGTTA	NM_153365:	NM_153365:
202018	FLJ90013	hypothetical protein FLJ90013	-2.93	CAGTGTTAACTTTAAGGTATA	NM_153365:	NM_153365:
2319	FLOT2	flotillin 2	0.76	CATGCACATCATGTAGATTAA	NM_004475:	NM_004475:
2319	FLOT2	flotillin 2	0.31	CTGCCTGTCCCTTCTGGTAAA	NM_004475:	NM_004475:
23769	FLRT1	fibronectin leucine rich transmembrane protein 1	0.09	TAGAATTGTGAAAGTGTTAAA	NM_013280:	NM_013280:
23769	FLRT1	fibronectin leucine rich transmembrane protein 1	0.07	AACAATCATGTAGTCGATTAA	NM_013280:	NM_013280:
23768	FLRT2	fibronectin leucine rich transmembrane protein 2	-0.26	CCGGCCTGACAGAATCAAGAA	NM_013231:	NM_013231:
23768	FLRT2	fibronectin leucine rich transmembrane protein 2	0.41	ACGCAGATTACATTTGATAAA	NM_013231:	NM_013231:
23767	FLRT3 (fibron	fibronectin leucine rich transmembrane protein 3	0.55	CCAGTGGTATTCAATAAATCA	NM_013281:	NM_013281:NM_198391:
23767	FLRT3 (fibron	fibronectin leucine rich transmembrane protein 3	0.61	ATGCCTGAACACAATTCTATA	NM_013281:	NM_013281:NM_198391:
2321	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascu	-10.13	ACCGCATATGGTATCCCTCAA	NM_002019:	NM_002019:
2321	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascu	0.84	CACTACAGTATTAGCAAGCAA	NM_002019:	NM_002019:
2322	FLT3	fms-related tyrosine kinase 3	-0.33	CCGGCTTGAGTGAATTGTGTA	NM_004119:	NM_004119:
2322	FLT3	fms-related tyrosine kinase 3	0.39	TACGTTGATTTCAGAGAATAT	NM_004119:	NM_004119:
2323	FLT3LG (fms-	fms-related tyrosine kinase 3 ligand	-0.22	CTCCTCCGACTTCGCTGTCAA	BF688722:	NM_001459:
2323	FLT3LG (fms-	fms-related tyrosine kinase 3 ligand	-0.36	GCGCGTGAACACGGAGATACA	BF688722:	NM_001459:
2324	FLT4	fms-related tyrosine kinase 4	0.45	CACCGTGTGGGCTGAGTTTAA	NM_002020:	NM_002020:NM_182925:
2324	FLT4	fms-related tyrosine kinase 4	-2.32	CACGCTCTTGGTCAACAGGAA	NM_002020:	NM_002020:NM_182925:
28982	FLVCR	feline leukemia virus subgroup C cellular receptor	0.30	CTCAACGTTATTAAATCAAAT	NM_014053:	NM_014053:
28982	FLVCR	feline leukemia virus subgroup C cellular receptor	-1.09	AACGGTTATGTTGTCCAAGCA	NM_014053:	NM_014053:
2326	FMO1 (flavin	flavin containing monooxygenase 1	0.21	CCGAACATTCAAGGTCATCAA	NM_002021:	NM_002021:
2326	FMO1 (flavin	flavin containing monooxygenase 1	0.04	AGGCCTCACTGTACAAGTATA	NM_002021:	NM_002021:
2328	FMO3	flavin containing monooxygenase 3	1.46	AACTATGTTCTTTATATCTAA	NM_006894:	NM_001002294:NM_006894:
2328	FMO3	flavin containing monooxygenase 3	2.66	AAGAATCATGTCATGATCTTA	NM_006894:	NM_001002294:NM_006894:
2329	FMO4	flavin containing monooxygenase 4	-3.24	CACGATGGGTCACAAGAGTAT	NM_002022:	NM_002022:
2329	FMO4	flavin containing monooxygenase 4	0.40	ATCGGCCTTATCGGCCTTAAA	NM_002022:	NM_002022:
2330	FMO5 (flavin	flavin containing monooxygenase 5	-0.46	CTGGGCCACTCAGGTATTTAA	NM_001461:	NM_001461:
2330	FMO5 (flavin	flavin containing monooxygenase 5	-2.64	AACCAAAGGTTTGACCATGAA	NM_001461:	NM_001461:
2331	FMOD	fibromodulin	-3.33	CTGGATTGCTCTCCACGGCAA	NM_002023:	NM_002023:
2331	FMOD	fibromodulin	0.33	GTGGCTAACCTGACCAATAAA	NM_002023:	NM_002023:
2332	FMR1	fragile X mental retardation 1	-0.72	CAGGTTAGGCAGTATAAAGAA	NM_002024:	NM_002024:
2332	FMR1	fragile X mental retardation 1	-0.32	CTGTCAAACATTAGTACTTTA	NM_002024:	NM_002024:
2335	FN1	fibronectin 1	0.00	CCCGGTTGTTATGACAATGGA	NM_002026:	NM_002026:NM_212478:NM_212482:NM_054034: NM_212476:NM_212475:NM_212474:

2335	FN1	fibronectin 1	-1.16	CCGGTTGTTATGACAATGGAA	NM_002026:	NM_002026:NM_212478:NM_212482:NM_054034:NM_212476:NM_212475:NM_212474:
64122	FN3K (fructos	fructosamine 3 kinase	0.93	CCAGCTGTTTAACTACCTGAA	NM_022158:	NM_022158:
64122	FN3K (fructos	fructosamine 3 kinase	1.25	CCCAGTGTTCGTCAAAGTCAA	NM_022158:	NM_022158:
79672	FN3KRP	fructosamine-3-kinase-related protein	-1.00	TAGCTTAAGACCAATGCAGTA	NM_024619:	NM_024619:
79672	FN3KRP	fructosamine-3-kinase-related protein	0.21	CCGGACTAGCTTAAGACCAAT	NM_024619:	NM_024619:
64778	FNDC3B	fibronectin type III domain containing 3B	0.01	CAAGAGGTTTATTTCAATCTA	NM_022763:	NM_022763:
64778	FNDC3B	fibronectin type III domain containing 3B	-1.95	CAGAGTATTACCACACAGCAA	NM_022763:	NM_022763:
152028	FNDC6	fibronectin type III domain containing 6	0.54	CTGGAGAAACAGTGTACTATT	NM_144717:	NM_144717:
152028	FNDC6	fibronectin type III domain containing 6	0.53	CACGGACAAGGGATGAGAGAA	NM_144717:	NM_144717:
2339	FNTA	farnesyltransferase, CAAX box, alpha	0.03	CCCGTGGTCCAGATCATTTAT	NM_002027:	NM_002027:
2339	FNTA	farnesyltransferase, CAAX box, alpha	1.13	CCGGGATGCTATTGAGTTAAA	NM_002027:	NM_002027:NM_001018676:
2342	FNTB	farnesyltransferase, CAAX box, beta	1.65	CAAGGTTTATACGTTTCAATA	NM_002028:	NM_002028:
2342	FNTB	farnesyltransferase, CAAX box, beta	-3.96	CACGTCCATAGAACAGGCAAA	NM_002028:	NM_002028:
2346	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	-0.20	ACGAACTGAAGACTTCTTTAA	NM_004476:	NM_001014986:NM_004476:
2346	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	0.55	CACGAACTGAAGACTTCTTTA	NM_004476:	NM_001014986:NM_004476:
2348	FOLR1	folate receptor 1 (adult)	0.01	TAAGGATGTTTCCTACCTATA	NM_000802:	NM_016724:NM_016725:NM_016729:NM_016730:NM_016731:NM_000802:
2348	FOLR1	folate receptor 1 (adult)	-0.90	CACATGTGTCTTGAGAATTAT	NM_000802:	NM_016731:NM_000802:
2348	FOLR1	folate receptor 1 (adult)	0.81	CTCCTACACCTGCAAGAGCAA	XM_497309:	XM_497309:NM_016724:NM_016725:NM_016729:NM_016730:NM_016731:NM_000802:
2350	FOLR2	folate receptor 2 (fetal)	-1.38	ATGCTTCTATTAGTCACCTAA	NM_000803:	NM_000803:
2350	FOLR2	folate receptor 2 (fetal)	-1.69	CTGGACCTCAGGAGTTAACAA	NM_000803:	NM_000803:
2352	FOLR3	folate receptor 3 (gamma)	0.49	ACAACCTATTCTAATAGACAA	NM_000804:	NM_000804:
2352	FOLR3	folate receptor 3 (gamma)	-1.86	CTGCAGCACCTTTGAGTCCTA	NM_000804:	NM_000804:
2353	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	1.17	GACCAATATTATACTAAGAAA	NM_005252:	NM_005252:
2353	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	0.63	TGGGTTCATTATTGGAATTAA	NM_005252:	NM_005252:
2354	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	0.71	AAGGGTGCGCCGGGAACGAAA	NM_006732:	NM_006732:
2354	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	0.72	CGCCGGGAACGAAATAAACTA	NM_006732:	NM_006732:
8061	FOSL1	FOS-like antigen 1	1.67	CCCACCTAGAACACTAACTCA	NM_005438:	NM_005438:
8061	FOSL1	FOS-like antigen 1	-1.09	CCGAGTAAGGCGCGAGCGGAA	NM_005438:	NM_005438:
2355	FOSL2	FOS-like antigen 2	-0.58	GCGGATCATGTACCAGGATTA	NM_005253:	NM_005253:
2355	FOSL2	FOS-like antigen 2	-0.04	TTGGGTTTGCCAAACGCCTAA	NM_005253:	NM_005253:
2296	FOXC1	forkhead box C1	-0.16	ACGGGAATAGTAGCTGTCAAA	NM_001453:	NM_001453:
2296	FOXC1	forkhead box C1	-3.08	AACGGGAATAGTAGCTGTCAA	NM_001453:	NM_001453:
2303	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	-1.69	AAGCCCGGCAAGGGCAGTTAC	NM_005251:	NM_005251:
2303	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	0.83	AACGTGCGGGAGATGTTCAAC	NM_005251:	NM_005251:
2306	FOXD2	forkhead box D2	0.57	CCCATTGGTGTCAATTGAATA	NM_004474:	NM_004474:
2306	FOXD2	forkhead box D2	0.56	CACTGGGTGTGCATTGATTTA	NM_004474:	NM_004474:
2304	FOXE1	forkhead box E1 (thyroid transcription factor 2)	1.67	AACCTAGGCAGTAATCCTAAA	NM_004473:	NM_004473:
2304	FOXE1	forkhead box E1 (thyroid transcription factor 2)	-0.12	CTGCACTATCCTGTTCACGAA	NM_004473:	NM_004473:
2290	FOXG1B	forkhead box G1B	0.86	CCCGTGTTTGTCACTTACAAA	NM_005249:	NM_005249:
2290	FOXG1B	forkhead box G1B	0.82	CTAGGGTTGTTTATTATTCTA	NM_005249:	NM_005249:
3607	FOXK2	forkhead box K2	1.21	CCGAGCACAAACATCAAGATA	NM_004514:	NM_004514:NM_181430:NM_181431:
3607	FOXK2	forkhead box K2	-1.02	CTCGGTGACCATCGGCCGCAA	NM_004514:	NM_004514:NM_181430:NM_181431:
668	FOXL2	forkhead box L2	-0.04	AAAGATGGTTTCGTCTACCAA	NM_023067:	NM_023067:
668	FOXL2	forkhead box L2	-0.10	TAGGAGAATATATCCAATAAA	NM_023067:	NM_023067:
8456	FOXN1	forkhead box N1	0.16	CACACAAATTATTCAGATGTA	NM_003593:	NM_003593:
8456	FOXN1	forkhead box N1	-0.02	CGGGCTCACCTTAAAGGTCAA	NM_003593:	NM_003593:
2308	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	0.66	AACCAAGTAGCCTGTTATCAA	NM_002015:	NM_002015:
2308	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	-1.22	CCCGAGTTTAGTAACAGTGCA	NM_002015:	NM_002015:
2309	FOXO3A	forkhead box O3A	-0.46	CTGAATGATGGGCTGACTGAA	NM_001455:	NM_001455:NM_201559:
2309	FOXO3A	forkhead box O3A	1.90	CTGGTTAGAAACTAGAATATT	NM_001455:	NM_001455:NM_201559:
2357	FPR1	formyl peptide receptor 1	-2.21	AACCAGTGACACAGCTACCAA	NM_002029:	NM_002029:
2357	FPR1	formyl peptide receptor 1	0.53	CACCGTGAGCCTGGCCAAGAA	NM_002029:	NM_002029:
2358	FPRL1	formyl peptide receptor-like 1	-0.36	CAGGAGTTGGTTAGAATTTCT	NM_001462:	NM_001005738:NM_001462:
2359	FPRL2	formyl peptide receptor-like 2	-1.85	CCCAGTCCTAACTTCATTTAA	NM_002030:	NM_002030:
2359	FPRL2	formyl peptide receptor-like 2	0.86	TCGGCTTGCTGGTTTATTATA	NM_002030:	NM_002030:
27315	FRAG1	FGF receptor activating protein 1	0.17	TCGGGTGGAGGTGGTGTTCTA	NM_014489:	NM_014489:
27315	FRAG1	FGF receptor activating protein 1	-0.36	GAGGTGGTGTTCTATACCTAA	NM_014489:	NM_014489:
2475	FRAP1	FK506 binding protein 12-rapamycin associated protein 1	-2.85	CAGGCCTATGGTCGAGATTTA	NM_004958:	NM_004958:
2475	FRAP1	FK506 binding protein 12-rapamycin associated protein 1	-2.18	CCGGCACAATGCAGCCAACAA	NM_004958:	NM_004958:
10023	FRAT1 (frequ	frequently rearranged in advanced T-cell lymphomas	-1.71	GAGGAGAACATGAGTAGATAA	NM_005479:	NM_005479:NM_181355:
10023	FRAT1 (frequ	frequently rearranged in advanced T-cell lymphomas	1.00	GAGGTGCTGCTTAATACCAAA	NM_005479:	NM_005479:NM_181355:
23401	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	0.14	AGGAATCGCGATGGCTTTATA	NM_012083:	NM_012083:
23401	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	0.31	CCCAAACTTTAAGGTAGCTAA	NM_012083:	NM_012083:
23413	FREQ	frequenin homolog (Drosophila)	0.71	CGGAATAAACCCAATGGTTAA	NM_014286:	NM_014286:
23413	FREQ	frequenin homolog (Drosophila)	0.68	GCGGAATAAACCCAATGGTTA	NM_014286:	NM_014286:
2444	FRK	fyn-related kinase	1.01	CAGGACAGTCAAGGTGATATA	NM_002031:	NM_002031:
2444	FRK	fyn-related kinase	-0.05	CTGGGAGTACCTAGAACCCTA	NM_002031:	NM_002031:
391059	FRRS1	ferric-chelate reductase 1	-0.73	CTGAAGGTTCATGGTGCCTTA	XM_372784:	NM_001013660:
391059	FRRS1	ferric-chelate reductase 1	-0.08	CAGATTGAAGTTACTTTGTCA	XM_372784:	NM_001013660:
10818	FRS2	fibroblast growth factor receptor substrate 2	-0.14	GACGGTTAAATCAGCAAACAA	NM_006654:	NM_006654:
10818	FRS2	fibroblast growth factor receptor substrate 2	0.16	CACAGGCAGCTTAATTACATA	NM_006654:	NM_006654:
10817	FRS3	fibroblast growth factor receptor substrate 3	-0.64	CACCAAGTTCAAGGTGACAAA	NM_006653:	NM_006653:
10817	FRS3	fibroblast growth factor receptor substrate 3	0.84	CCCAAGGGTCTTCAACTTTGA	NM_006653:	NM_006653:
2487	FRZB	frizzled-related protein	0.98	CGGGCTAAAGTTAAAGAGATA	NM_001463:	NM_001463:
2487	FRZB	frizzled-related protein	0.30	ACGGGACACTGTCAACCTCTA	NM_001463:	NM_001463:
79187	FSD1	fibronectin type III and SPRY domain containing 1	0.41	AGGTCTCAAGTTTGACATGAA	NM_024333:	NM_024333:
79187	FSD1	fibronectin type III and SPRY domain containing 1	-7.53	CACGGCCAAGCACGCCAACAA	NM_024333:	NM_024333:
405752	FSD1CL	FSD1 C-terminal like	-1.61	GAGCTCTTGATTACAATTTAA	NM_207647:	NM_207647:
405752	FSD1CL	FSD1 C-terminal like	0.03	AACAGTTGCTATATTCCTTTA	NM_207647:	NM_207647:
123722	FSD2	fibronectin type III and SPRY domain containing 2	0.01	CTCAGCATCTATATACATTTA	NM_001007122:	NM_001007122:
123722	FSD2	fibronectin type III and SPRY domain containing 2	-0.05	AAGAAGATTGGCATTCTATTA	NM_001007122:	NM_001007122:
2488	FSHB (follicle	follicle stimulating hormone, beta polypeptide	-5.47	CACCAGGGATCTGGTGTATAA	NM_000510:	NM_000510:NM_001018080:
2488	FSHB (follicle	follicle stimulating hormone, beta polypeptide	-1.41	TCGTTTCTGCATAAGCATCAA	NM_000510:	NM_000510:NM_001018080:
2492	FSHR	follicle stimulating hormone receptor	0.21	CAGGTCGACTTACAACTTAAA	NM_000145:	NM_000145:
2492	FSHR	follicle stimulating hormone receptor	0.03	CCAGGTCGACTTACAACTTAA	NM_000145:	NM_000145:
10468	FST	follistatin	1.58	GCTGTTGTTGTCCGTATTTAA	NM_006350:	NM_006350:
10468	FST	follistatin	-0.10	CGCAATGAATGTGCACTCCTA	NM_006350:	NM_006350:NM_013409:
2495	FTH1	ferritin, heavy polypeptide 1	1.27	ACGAGTATTTGTATTTATTAA	NM_002032:	NM_002032:
2495	FTH1	ferritin, heavy polypeptide 1	0.57	TTGGGATGAATCAGAAATCTA	NM_002032:	NM_002032:
2512	FTL	ferritin, light polypeptide	1.11	CAGCTTTCTTAACTATCCTAA	NM_000146:	NM_000146:
2512	FTL	ferritin, light polypeptide	-4.64	TAGCTCCTTCTTGCCAACCAA	NM_000146:	NM_000146:
2517	FUCA1 (fucos	fucosidase, alpha-L- 1, tissue	-0.67	TTCGCTATGTTTACAGTGATA	NM_000147:	NM_000147:
2517	FUCA1 (fucos	fucosidase, alpha-L- 1, tissue	0.62	TACGACCTTGTTAACAGCTAT	NM_000147:	NM_000147:
2519	FUCA2	fucosidase, alpha-L- 2, plasma	1.62	AGCATGTTACTGAATACTGTA	NM_032020:	NM_032020:
2519	FUCA2	fucosidase, alpha-L- 2, plasma	0.32	CCCTGACTAATGTGATCTAAA	NM_032020:	NM_032020:
197258	FUK	fucokinase	-5.26	CCGAAGGGAGTTGATTGGACA	NM_145059:	NM_145059:

197258	FUK	fucokinase	-1.38	TGGCTTAGAGTTGTAGACTTA	NM_145059:	NM_145059:
5045	FURIN	furin (paired basic amino acid cleaving enzyme)	-0.04	GCGGCTCACCCTGTCCTATAA	NM_002569:	NM_002569:
5045	FURIN	furin (paired basic amino acid cleaving enzyme)	0.60	ACCAATGGTGTGGGCCGGAAA	NM_002569:	NM_002569:
2521	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	0.83	ACAGCCCATGATTAATTTGTA	NM_004960:	NM_001010850:NM_004960:
2521	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	0.42	CAAGCAGATTGGTATTATTAA	NM_004960:	NM_001010850:NM_004960:
2523	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H bloc	-5.05	TAGGCTTATCAGGGAGTTACA	NM_000148:	NM_000148:
2523	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H bloc	-2.21	CAGGTTGCCTCTCACAATGAA	NM_000148:	NM_000148:
2524	FUT2	fucosyltransferase 2 (secretor status included)	-0.22	CACCATCTACCTGGCCAATTA	NM_000511:	NM_000511:
2524	FUT2	fucosyltransferase 2 (secretor status included)	-1.50	CACGGGCGGAGACACCATCTA	NM_000511:	NM_000511:
2531	FVT1 (follicul	follicular lymphoma variant translocation 1	1.22	AAGAATTTACAGTTCCTTCAA	NM_002035:	NM_002035:
2531	FVT1 (follicul	follicular lymphoma variant translocation 1	0.32	TAGACTCAAATGCTTAGGGAA	NM_002035:	NM_002035:
2395	FXN	frataxin	0.64	GAGCTGAGTGATGTAGCGTAA	NM_000144:	NM_000144:NM_181425:
2395	FXN	frataxin	-0.11	CAGGCTTCTTTCAAAGTGTAA	NM_000144:	NM_000144:NM_181425:
8087	FXR1 (fragile	fragile X mental retardation, autosomal homolog 1	0.27	ACTGAAGAAGTTCCTAGTTTA	NM_005087:	NM_001013438:NM_001013439:NM_005087:
8087	FXR1 (fragile	fragile X mental retardation, autosomal homolog 1	-0.91	CAGCTAAGAATGGAACGCCTA	NM_005087:	NM_001013438:NM_001013439:NM_005087:
486	FXYD2	FXYD domain containing ion transport regulator 2	0.58	ATCAATGAAGATGAGCCGTAA	NM_001680:	NM_001680:NM_021603:
486	FXYD2	FXYD domain containing ion transport regulator 2	0.75	CCCGTTCTACTATGACTATGA	NM_001680:	NM_001680:NM_021603:
53827	FXYD5	FXYD domain containing ion transport regulator 5	-3.72	CTCAACTATCATGGACATTCA	NM_014164:	NM_144779:NM_014164:
53827	FXYD5	FXYD domain containing ion transport regulator 5	0.63	GAGGACAGACGTTGAAAGATA	NM_014164:	NM_144779:NM_014164:
2533	FYB	FYN binding protein (FYB-120/130)	-0.38	AAGGCCAGACGTCTTACTCAA	NM_199335:	NM_199335:NM_001465:
2533	FYB	FYN binding protein (FYB-120/130)	-9.00	CAGGAAGAAATGACCTGTCTA	NM_199335:	NM_199335:NM_001465:
2534	FYN	FYN oncogene related to SRC, FGR, YES	0.56	AAGAAGCAGGATGCTGATCTA	NM_002037:	NM_002037:
2534	FYN	FYN oncogene related to SRC, FGR, YES	-0.54	AAGACATGTGGTGTATATAAA	NM_002037:	NM_002037:
8321	FZD1 (frizzlec	frizzled homolog 1 (Drosophila)	-6.14	ATGCCGGTACTTAGGACCTAA	NM_003505:	NM_003505:
8321	FZD1 (frizzlec	frizzled homolog 1 (Drosophila)	0.79	CCCGCGCTTCATGAATCGCAA	NM_003505:	NM_003505:
11211	FZD10	frizzled homolog 10 (Drosophila)	0.38	CAGCCGTAGGTTAAAGAAGAA	NM_007197:	NM_007197:
11211	FZD10	frizzled homolog 10 (Drosophila)	0.52	CCCGATTATGGAGCAGTTCAA	NM_007197:	NM_007197:
2535	FZD2 (frizzlec	frizzled homolog 2 (Drosophila)	1.15	CACGGTCTACATGATCAAATA	NM_001466:	NM_001466:
2535	FZD2 (frizzlec	frizzled homolog 2 (Drosophila)	0.45	CACGTACTTGGTAGACATGCA	NM_001466:	NM_001466:
7976	FZD3	frizzled homolog 3 (Drosophila)	-0.18	ATGCTTGATGTATTATGTAAA	NM_017412:	NM_017412:
7976	FZD3	frizzled homolog 3 (Drosophila)	0.51	CAGAAGAATTTGATTAGTCTA	NM_017412:	NM_017412:
8322	FZD4	frizzled homolog 4 (Drosophila)	-1.29	CAGAATGATAGTGCCTTTAAA	NM_012193:	NM_012193:
8322	FZD4	frizzled homolog 4 (Drosophila)	1.78	TAGGTGATCGATACTTGTCAA	NM_012193:	NM_012193:
7855	FZD5	frizzled homolog 5 (Drosophila)	-2.00	CAGCATTGTGGTGGCCTGCTA	NM_003468:	NM_003468:
7855	FZD5	frizzled homolog 5 (Drosophila)	-0.12	TAAGGTTGGCGTTGTAATGAA	NM_003468:	NM_003468:
8323	FZD6	frizzled homolog 6 (Drosophila)	-4.84	AACCCACTTATTGATACCTTA	NM_003506:	NM_003506:
8323	FZD6	frizzled homolog 6 (Drosophila)	0.64	AGCGATATTAGTGCCAATCAA	NM_003506:	NM_003506:
8324	FZD7	frizzled homolog 7 (Drosophila)	-1.08	AACGGCGATGTGAATCGTCAA	NM_003507:	NM_003507:
8324	FZD7	frizzled homolog 7 (Drosophila)	0.79	CAACGGCCTGATGTACTTTAA	NM_003507:	NM_003507:
8325	FZD8	frizzled homolog 8 (Drosophila)	-7.48	CAAGTAAATATCATTGTTGAA	NM_031866:	NM_031866:
8325	FZD8	frizzled homolog 8 (Drosophila)	-0.01	CCGCTCGGTCATCAAGCAACA	NM_031866:	NM_031866:
8326	FZD9	frizzled homolog 9 (Drosophila)	-0.61	CACCTGCGTCATCGTTTGCTA	NM_003508:	NM_003508:
8326	FZD9	frizzled homolog 9 (Drosophila)	-0.47	CAGCCGGAGTTTATTTAATGA	NM_003508:	NM_003508:
51343	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	-2.55	CGGGTCGATCTTCCACATTCA	NM_016263:	NM_016263:
51343	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	0.60	TGCAGTGACGCTGTCATTAAA	NM_016263:	NM_016263:
9636	G1P2	interferon, alpha-inducible protein (clone IFI-15K)	0.08	AATGCGACGAACCTCTGAGCA	NM_005101:	NM_005101:
9636	G1P2	interferon, alpha-inducible protein (clone IFI-15K)	-1.07	AAGCACCGTGTTCATGAATCT	NM_005101:	NM_005101:
10146	G3BP	Ras-GTPase-activating protein SH3-domain-binding protein	-0.21	CAGAAAGAAATCCACAGGAAA	NM_005754:	NM_005754:NM_198395:
10146	G3BP	Ras-GTPase-activating protein SH3-domain-binding protein	-6.44	CAGGAGGAGTCTGAAGAAGAA	NM_005754:	NM_005754:NM_198395:
9908	G3BP2	Ras-GTPase activating protein SH3 domain-binding protein 2	-0.30	CCGAGTGGCTCCTGAATTTAA	NM_012297:	NM_012297:NM_203504:NM_203505:
9908	G3BP2	Ras-GTPase activating protein SH3 domain-binding protein 2	0.43	TTCAGTGAATGTCATACTAAA	NM_012297:	NM_012297:NM_203504:NM_203505:
2538	G6PC	glucose-6-phosphatase, catalytic (glycogen storage disease type I, vor	-0.91	CAGCAGGTGTATACTACGTGA	NM_000151:	NM_000151:
2538	G6PC	glucose-6-phosphatase, catalytic (glycogen storage disease type I, vor	0.13	TGGGATCCAGTCAACACATTA	NM_000151:	NM_000151:
57818	G6PC2	glucose-6-phosphatase, catalytic, 2	1.45	CAGAGTATTCATAGCAACACA	NM_021176:	NM_021176:
57818	G6PC2	glucose-6-phosphatase, catalytic, 2	0.29	CTGGTGGGTCCAAGAAACTCA	NM_021176:	NM_021176:
92579	G6PC3	glucose 6 phosphatase, catalytic, 3	1.24	CAGGTGCTGGCTGGCCTAATA	NM_138387:	NM_138387:
92579	G6PC3	glucose 6 phosphatase, catalytic, 3	-1.87	GTGGCTCAACCTCATCTTCAA	NM_138387:	NM_138387:
2539	G6PD	glucose-6-phosphate dehydrogenase	-0.35	CAGCCTCTCTGCTATAAGAAA	NM_000402:	NM_000402:
2539	G6PD	glucose-6-phosphate dehydrogenase	-3.73	CACCAAGATGATGACCAAGAA	NM_000402:	NM_000402:
2548	GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease ty	0.57	TTGGGAGATTCTAAATCTTAA	NM_000152:	NM_000152:
2548	GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease ty	1.54	CAGGAATAACACGATCGTGAA	NM_000152:	NM_000152:
2549	GAB1 (GRB2	GRB2-associated binding protein 1	-0.02	ACAGAAGACCTTGGCTCTAAA	NM_002039:	NM_207123:NM_002039:
2549	GAB1 (GRB2	GRB2-associated binding protein 1	0.02	CACGAGCATTTCCAAGTGATA	NM_002039:	NM_207123:NM_002039:
9846	GAB2	GRB2-associated binding protein 2	0.66	AACCTCAAACCTGATCGGAAA	NM_012296:	NM_012296:NM_080491:
9846	GAB2	GRB2-associated binding protein 2	-8.34	CACCAATTCTGAAGACAACTA	NM_012296:	NM_012296:NM_080491:
11337	GABARAP	GABA(A) receptor-associated protein	-0.32	AAGGTAGGAGGCACATCAATA	NM_007278:	NM_007278:
11337	GABARAP	GABA(A) receptor-associated protein	0.46	CCGGGTGCCGGTGATAGTAGA	NM_007278:	NM_007278:
2550	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	1.06	CCGAATCTGCTCCAAGTCTTA	NM_001470:	NM_001470:NM_021905:
2550	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	1.34	TGGGAAGAACATGCTATCCAA	NM_001470:	NM_021903:NM_001470:NM_021904:NM_021905:
9568	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	0.77	CACGCCTGTTCTAGCCGATAA	NM_005458:	NM_005458:
9568	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	0.19	CCCAGCAAACACGATAAAGAA	NM_005458:	NM_005458:
2554	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1	0.42	CAGCATAAATCTGTTAGCATT	NM_000806:	NM_000806:
2554	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1	1.15	CACGGTCTAAACACACTTAGA	NM_000806:	NM_000806:
2555	GABRA2 (gar	gamma-aminobutyric acid (GABA) A receptor, alpha 2	-0.15	TTCCGTTATGATACAGAACAA	NM_000807:	NM_000807:
2555	GABRA2 (gar	gamma-aminobutyric acid (GABA) A receptor, alpha 2	1.65	ATCCTTCGACTAAACAATTTA	NM_000807:	NM_000807:
2556	GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3	-0.15	CCCTCAATTCATATTTATGAA	NM_000808:	NM_000808:
2556	GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3	-5.29	CCCGACTGAGACCAAGACCTA	NM_000808:	NM_000808:
2557	GABRA4 (gar	gamma-aminobutyric acid (GABA) A receptor, alpha 4	-0.65	TTGCTATAAGATATAACCTAA	NM_000809:	NM_000809:
2557	GABRA4 (gar	gamma-aminobutyric acid (GABA) A receptor, alpha 4	0.40	CAAGTAGTAAAGGATAAATTA	NM_000809:	NM_000809:
2558	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	0.53	CCCATTGATAATTCGAGCAAA	NM_000810:	NM_000810:
2558	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	2.01	CGGCACTTTCAACTTAGTTTA	NM_000810:	NM_000810:
2559	GABRA6	gamma-aminobutyric acid (GABA) A receptor, alpha 6	1.11	TCGCAGCTGTCAACTACTTTA	NM_000811:	NM_000811:
2559	GABRA6	gamma-aminobutyric acid (GABA) A receptor, alpha 6	-0.23	CCAGGTGTCTTTCTGGATTAA	NM_000811:	NM_000811:
2560	GABRB1 (gar	gamma-aminobutyric acid (GABA) A receptor, beta 1	0.89	TCCCTGGATTTCACTGATTTA	NM_000812:	NM_000812:
2560	GABRB1 (gar	gamma-aminobutyric acid (GABA) A receptor, beta 1	-0.47	CACCCTGGAGATCGAAAGTTA	NM_000812:	NM_000812:
2561	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	-1.26	ATCCCTCAGCTTTAAGCTTAA	NM_000813:	NM_021911:NM_000813:
2561	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	1.91	TACCTATTTCCTGAACGATAA	NM_000813:	NM_021911:NM_000813:
2562	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	-1.66	TAGGCCTGATATCCAACAGAA	NM_000814:	NM_000814:NM_021912:
2562	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	0.21	CTCGTTGTAAGTACTCTAATA	NM_000814:	NM_000814:NM_021912:
2563	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta	-4.62	CACGGAGCTGATGAACTTCAA	NM_000815:	NM_000815:
2563	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta	0.70	ATCGGAGGACATCGTCTACTA	NM_000815:	NM_000815:
2564	GABRE (gam	gamma-aminobutyric acid (GABA) A receptor, epsilon	0.10	CACTCTAACCATCACAATCAA	NM_004961:	NM_021990:NM_021987:NM_021984:NM_004961:
2564	GABRE (gam	gamma-aminobutyric acid (GABA) A receptor, epsilon	-1.18	CAGGCATTACTCGCCATTGAT	NM_004961:	NM_021990:NM_021987:NM_021984:NM_004961:
2565	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1	-0.02	ACCTGGTTTGACAGTCGTTTA	NM_173536:	NM_173536:
2565	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1	0.86	AGGATTAGTTATACAATTTAA	NM_173536:	NM_173536:
2566	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	0.94	TAGATTCATAATGCAATTAGA	NM_000816:	NM_198903:NM_198904:NM_000816:

2566	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	-0.03	CACCCTAAGGTTGACAATTGA	NM_000816:	NM_198903:NM_198904:NM_000816:
2567	GABRG3 (gar	gamma-aminobutyric acid (GABA) A receptor, gamma 3	-0.09	CACCATCTTCCGCAATTCTAA	NM_033223:	NM_033223:
2567	GABRG3 (gar	gamma-aminobutyric acid (GABA) A receptor, gamma 3	0.95	ACCGACCGTAATTGACGTTGA	NM_033223:	NM_033223:
2568	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	0.44	CAGAAATAAACCAAGGCTCTA	NM_014211:	NM_014211:
2568	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	1.03	AAGTGGCTTAGCTTAAGTAAA	NM_014211:	NM_014211:
55879	GABRQ	gamma-aminobutyric acid (GABA) receptor, theta	-0.05	CTGGGTATACCATATGTATTA	NM_018558:	NM_018558:
55879	GABRQ	gamma-aminobutyric acid (GABA) receptor, theta	-0.12	TAGCAAGGAGGTGTATTTCTA	NM_018558:	NM_018558:
2569	GABRR1 (gar	gamma-aminobutyric acid (GABA) receptor, rho 1	0.46	CAGAAATAACTGTATAATGAA	NM_002042:	NM_002042:
2569	GABRR1 (gar	gamma-aminobutyric acid (GABA) receptor, rho 1	-0.19	CACCACCAAACTGGCTTTCTA	NM_002042:	NM_002042:
2570	GABRR2 (gar	gamma-aminobutyric acid (GABA) receptor, rho 2	-0.17	ATGCCATTGACAAATACTCTA	NM_002043:	NM_002043:
2570	GABRR2 (gar	gamma-aminobutyric acid (GABA) receptor, rho 2	-0.72	TACGGTCACTGCCATGTGCAA	NM_002043:	NM_002043:
200959	GABRR3	gamma-aminobutyric acid (GABA) receptor, rho 3	-3.60	CTGGATCATATTGAAACCAAA	XM_116036:	XM_116036:
200959	GABRR3	gamma-aminobutyric acid (GABA) receptor, rho 3	0.00	TACAATATTGATGCAGTTCAA	XM_116036:	XM_116036:
2571	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	0.57	CCCATTTGTAATGTATCTTAT	NM_000817:	NM_000817:
2571	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	0.48	CGCCATAAACTCAACGGCATA	NM_000817:	NM_000817:
2572	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	-0.31	CAACCTGTTCTTCCTACCAAA	NM_000818:	NM_000818:
2572	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	-0.83	CGCCTTGGACAAGATTTATAA	NM_000818:	NM_000818:
1647	GADD45A	growth arrest and DNA-damage-inducible, alpha	1.46	AAGGGTTAATCATATTTGAAA	L24498:	NM_001924:
1647	GADD45A	growth arrest and DNA-damage-inducible, alpha	1.57	ACCAAATATGTTAAAGTTTAA	L24498:	NM_001924:
4616	GADD45B	growth arrest and DNA-damage-inducible, beta	-4.30	GAGGATGACATCGCCCTGCAA	NM_015675:	NM_015675:
4616	GADD45B	growth arrest and DNA-damage-inducible, beta	0.51	TCCCAGTTTGCGAATTAATAA	NM_015675:	NM_015675:
339896	GADL1	glutamate decarboxylase-like 1	-2.11	CAGGCTGAATGTTTATCTCAA	NM_207359:	NM_207359:
339896	GADL1	glutamate decarboxylase-like 1	1.02	AAGCACAATAATTGACAGAAA	NM_207359:	NM_207359:
2580	GAK	cyclin G associated kinase	0.11	ACGCGTGTGACATTCAAGAAA	NM_005255:	NM_005255:
2580	GAK	cyclin G associated kinase	0.05	CCCGTGGTTGTCTGTACAGAA	NM_005255:	NM_005255:
2581	GALC (galact	galactosylceramidase	-0.23	TAGGAATTTATAAGAGTCTAA	NM_000153:	NM_000153:
2581	GALC (galact	galactosylceramidase	-0.88	TACACTCACGTTAACTATTAA	NM_000153:	NM_000153:
2582	GALE (UDP-g	UDP-galactose-4-epimerase	-3.10	CAGCTTTATGGCGGTCATCCA	NM_000403:	NM_000403:NM_001008216:
2582	GALE (UDP-g	UDP-galactose-4-epimerase	1.36	AGAGCTTTCCAAAGTATTTAA	NM_000403:	NM_000403:NM_001008216:
2584	GALK1	galactokinase 1	1.55	CCGCCTCATGGTGGAGAGCCA	NM_000154:	NM_000154:
2584	GALK1	galactokinase 1	0.49	GAGGTACAACTGGAAGAGCTA	NM_000154:	NM_000154:
2585	GALK2	galactokinase 2	0.33	AAAGCTCTCTATGCTTCATAA	NM_002044:	NM_001001556:NM_002044:
2585	GALK2	galactokinase 2	0.12	TGCGCGAGTGCTCCAGTTTAA	NM_002044:	NM_001001556:NM_002044:
2588	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, muc	-3.90	CAGGGCCATTGATGGCCTCAA	NM_000512:	NM_000512:
2588	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, muc	-0.08	CGGGAGATTGATGACAGCATT	NM_000512:	NM_000512:
2587	GALR1	galanin receptor 1	-3.79	CACCTGAGTGATACTAAAGAA	NM_001480:	NM_001480:
2587	GALR1	galanin receptor 1	0.55	CAGCGAGGTTGATGTAGATAA	NM_001480:	NM_001480:
8811	GALR2	galanin receptor 2	-0.10	CCCGCTCACGCGCGCCACTTA	NM_003857:	NM_003857:
8811	GALR2	galanin receptor 2	-1.26	TACCAACCTGTTCATCCTTAA	NM_003857:	NM_003857:
8484	GALR3 (galar	galanin receptor 3	1.22	CACGGACCTGTTCATCCTCAA	NM_003614:	NM_003614:
8484	GALR3 (galar	galanin receptor 3	-0.23	CTGCCCGAGGACCGGAATAAA	NM_003614:	NM_003614:
2592	GALT (galact	galactose-1-phosphate uridylyltransferase	0.25	CCGGAAATTCATGGTTGGCTA	NM_147131:	NM_147131:NM_147132:NM_000155:
2592	GALT (galact	galactose-1-phosphate uridylyltransferase	0.16	AGCAATAATCCAGTAATCTAA	NM_147131:	NM_147131:NM_147132:
2593	GAMT	guanidinoacetate N-methyltransferase	1.37	AACCCTGCCTGACGGTCACTT	NM_000156:	NM_000156:NM_138924:
2593	GAMT	guanidinoacetate N-methyltransferase	-2.04	AACACCAGTTCAACTTCATCA	NM_000156:	NM_000156:NM_138924:
8139	GAN	giant axonal neuropathy (gigaxonin)	0.31	CCGCACAGTCATGTAATTCAA	NM_022041:	NM_022041:
8139	GAN	giant axonal neuropathy (gigaxonin)	-0.35	ATCATGATGAATTGAAATGAA	NM_022041:	NM_022041:
23193	GANAB	glucosidase, alpha; neutral AB	-6.24	GAGGTGTGGTATGACATTCAA	NM_014610:	NM_014610:NM_198334:NM_198335:
23193	GANAB	glucosidase, alpha; neutral AB	-6.35	CAGCACAATGATATAATCCGA	NM_014610:	NM_014610:NM_198334:NM_198335:
2595	GANC	glucosidase, alpha; neutral C	-1.28	CTGGATGTCTATGGATACCAA	NM_198141:	NM_198141:
2595	GANC	glucosidase, alpha; neutral C	0.21	CTCAGTATATGTGAAGGCCAA	NM_198141:	NM_198141:
26330	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	-2.12	CCGAGACAAGTGAAACGGGAA	NM_014364:	NM_014364:
26330	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	-0.39	CTCCATGAACATTGTGAGCAA	NM_014364:	NM_014364:
2620	GAS2	growth arrest-specific 2	1.40	ACGTGTCTATTTGAATCGGAA	NM_005256:	NM_177553:NM_005256:
2620	GAS2	growth arrest-specific 2	1.65	TACAGAGTATTCACAATAGTA	NM_005256:	NM_177553:NM_005256:
2621	GAS6	growth arrest-specific 6	-2.99	CAGCAGCGGCCCGGTCATCAA	NM_000820:	NM_000820:
2621	GAS6	growth arrest-specific 6	0.00	TGCGACAAAGATGTCAACGAA	NM_000820:	NM_000820:
2520	GAST	gastrin	-0.14	CAGCAGCCAGATGCACCCTTA	NM_000805:	NM_000805:
2520	GAST	gastrin	-0.31	CCGCAGTGCTGAGGATGAGAA	NM_000805:	NM_000805:
2623	GATA1	GATA binding protein 1 (globin transcription factor 1)	-0.67	AAGGATGGTATTCAGACTCGA	NM_002049:	NM_002049:
2623	GATA1	GATA binding protein 1 (globin transcription factor 1)	0.68	AAGCGCCTGATTGTCAGTAAA	NM_002049:	NM_002049:
2624	GATA2	GATA binding protein 2	-0.39	AAGGCTCGTTCCTGTTCAGAA	NM_032638:	NM_032638:
2624	GATA2	GATA binding protein 2	-1.63	CTGGCGCACAACTACATGGAA	NM_032638:	NM_032638:
2628	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.41	ACCGAGCGTACAGGTCAATTA	NM_001482:	NM_001482:
2628	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.05	CAGGTCAATTATCAAAGACTA	NM_001482:	NM_001482:
2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	0.30	AAGAAGGAATCGGATATAACA	NM_000157:	NM_001005741:NM_000157:NM_001005749:NM_001005742:NM_001005750:
2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	-2.58	CCAGAACAGAAGTTCCAGAAA	NM_000157:	NM_001005741:NM_000157:NM_001005749:NM_001005742:NM_001005750:
57704	GBA2	glucosidase, beta (bile acid) 2	0.72	CCGCGTCAATGCATATTTAAT	NM_020944:	NM_020944:
57704	GBA2	glucosidase, beta (bile acid) 2	-0.17	TCCGCGTCAATGCATATTTAA	NM_020944:	NM_020944:
2632	GBE1	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme	-0.06	TCGCTACAAGTTCCTAAATAA	NM_000158:	NM_000158:
2632	GBE1	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme	0.96	ACGCTGTGTCCCGATTCTATA	NM_000158:	NM_000158:
2639	GCDH	glutaryl-Coenzyme A dehydrogenase	-1.71	CAGACTCCATTTACCCTGAAA	NM_000159:	NM_013976:NM_000159:
2639	GCDH	glutaryl-Coenzyme A dehydrogenase	-0.05	TCGTTCAGATGTGTTCCTTAA	NM_000159:	NM_013976:NM_000159:
2641	GCG	glucagon	0.35	CTGCATTATAATAATAGGAGA	NM_002054:	NM_002054:
2641	GCG	glucagon	0.46	ATGTATCAAAGATACAATTAA	NM_002054:	NM_002054:
2642	GCGR	glucagon receptor	-4.16	CAACAGAACCTTCGACAAGTA	NM_000160:	NM_000160:
2642	GCGR	glucagon receptor	-6.47	CTCCAACAATAAAGAGCTCAA	NM_000160:	NM_000160:
2643	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	-2.26	CCCGGTTTCCTTTGTGGTCTA	NM_000161:	NM_000161:NM_001024024:NM_001024071:NM_001024070:
2643	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	-2.58	CAGAATGAACTGACGGTGGAA	NM_000161:	NM_000161:NM_001024024:NM_001024071:NM_001024070:
2645	GCK	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	0.00	CAGGACTTTGATGCATTTCCA	NM_000162:	NM_033507:NM_033508:NM_000162:
2645	GCK	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	0.47	CAGCTGTATGAGAAGCTCATA	NM_000162:	NM_033507:NM_033508:NM_000162:
2729	GCLC	glutamate-cysteine ligase, catalytic subunit	0.59	TAGGATCAGTAAATCCCGATA	NM_001498:	NM_001498:
2729	GCLC	glutamate-cysteine ligase, catalytic subunit	-0.23	AAGGCTTTCTTTGGTAGGTAA	NM_001498:	NM_001498:
2730	GCLM	glutamate-cysteine ligase, modifier subunit	1.58	CTAATTGAAATTGTCTATAAA	NM_002061:	NM_002061:
2730	GCLM	glutamate-cysteine ligase, modifier subunit	0.76	TGGGATTTACTAGTAGTGTAA	NM_002061:	NM_002061:
2651	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood grc	-0.62	ATGCGGTAGAGCAACTATTAA	NM_001491:	NM_001491:
2651	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood grc	-3.11	CAGGACCTGGCTACGTAATTA	NM_001491:	NM_145655:NM_001491:NM_145649:
7841	GCS1	glucosidase I	1.08	CCCTTGGATACCAGTAATTCA	NM_006302:	NM_006302:
7841	GCS1	glucosidase I	0.97	CCGTGCCAACGTGGTAGGCAA	NM_006302:	NM_006302:
54332	GDAP1	ganglioside-induced differentiation-associated protein 1	-0.53	CGAGCGTGTCTTGAAGAGAAA	NM_018972:	NM_018972:
54332	GDAP1	ganglioside-induced differentiation-associated protein 1	-2.21	TCCCGGCTTATGCAACTACAA	NM_018972:	NM_018972:
2662	GDF10	growth differentiation factor 10	-0.66	TAGTAACGTGGGAATACTAAA	NM_004962:	NM_004962:
2662	GDF10	growth differentiation factor 10	-0.92	AACAGGATAATCGTGGTGTAA	NM_004962:	NM_004962:
10220	GDF11	growth differentiation factor 11	1.24	CTGAAATGGAGTAATAAATGA	NM_005811:	NM_005811:
10220	GDF11	growth differentiation factor 11	-1.87	CAGAGCATCGACTTCAAGCAA	NM_005811:	NM_005811:

9518	GDF15	growth differentiation factor 15	0.86	AAAGCTGTCTGAACTGTTAAA	NM_004864:	NM_004864:
9518	GDF15	growth differentiation factor 15	0.55	ATGGAACTGTGTATTTATTTA	NM_004864:	NM_004864:
2658	GDF2	growth differentiation factor 2	0.98	CACACCCATCATTGTATGTTA	NM_016204:	NM_016204:
2658	GDF2	growth differentiation factor 2	-2.17	AAGGACTGATTCAATCTGCAT	NM_016204:	NM_016204:
9573	GDF3 (growt	growth differentiation factor 3	-0.07	AAGGAGTGTTCTTAGGGTAAA	NM_020634:	NM_020634:
9573	GDF3 (growt	growth differentiation factor 3	0.96	TCCAATTATGCTTTCATGCAA	NM_020634:	NM_020634:
8200	GDF5	growth differentiation factor 5 (cartilage-derived morphogenetic protei	1.92	TAGATTTAAATGTATATTGAT	NM_000557:	NM_000557:
8200	GDF5	growth differentiation factor 5 (cartilage-derived morphogenetic protei	1.40	CTGTTAGACTGTTAGATTTAA	NM_000557:	NM_000557:
392255	GDF6 (growt	growth differentiation factor 6	0.00	ATGATATGCAATCGAATGCTA	NM_001001557:	NM_001001557:
392255	GDF6 (growt	growth differentiation factor 6	-1.65	TCAGATTGTAATTATCAGTTA	NM_001001557:	NM_001001557:
151449	GDF7 (growt	growth differentiation factor 7	0.74	AACAACGTTGTCTACAAGCAA	NM_182828:	NM_182828:
151449	GDF7 (growt	growth differentiation factor 7	-1.00	GCCGTTGCACGTGGACTTCAA	NM_182828:	NM_182828:
2660	GDF8	growth differentiation factor 8	-0.42	CTGATGCTATCTCAACAATAA	NM_005259:	NM_005259:
2660	GDF8	growth differentiation factor 8	0.82	AGGAGTATGCTTTAAAGTCTA	NM_005259:	NM_005259:
2661	GDF9 (growt	growth differentiation factor 9	-1.21	CAGCTGGTATTCCCTTCACTA	NM_005260:	NM_005260:
2661	GDF9 (growt	growth differentiation factor 9	-2.87	CAAGTCAGTCTTGCTGTACAA	NM_005260:	NM_005260:
2664	GDI1	GDP dissociation inhibitor 1	-3.38	CCGCATCAAGTTGTACAGTGA	NM_001493:	NM_001493:
2664	GDI1	GDP dissociation inhibitor 1	-0.82	ACCCTTATCTTGCAAAGTGAA	NM_001493:	NM_001493:
2668	GDNF	glial cell derived neurotrophic factor	0.00	CGCGCTGAGCAGTGACTCAAA	NM_000514:	NM_000514:
2668	GDNF	glial cell derived neurotrophic factor	-1.51	CTGGAGTTAATGTCCAACCTA	NM_000514:	NM_000514:
79153	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	-2.04	ACCCATGAGCGTAGAGATCAA	NM_024307:	NM_001031718:NM_024307:
79153	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	-2.61	CCGGACCTCCTAAGTCCAGAA	NM_024307:	NM_001031718:NM_024307:
2669	GEM	GTP binding protein overexpressed in skeletal muscle	-0.64	AACGATTATACTCCTGGATAT	NM_181702:	NM_181702:NM_005261:
2669	GEM	GTP binding protein overexpressed in skeletal muscle	1.28	CAGCTCTGCTCTATTTATTAT	NM_181702:	NM_181702:NM_005261:
50628	GEMIN4	gem (nuclear organelle) associated protein 4	-0.96	CAGCCTGGACTTTACAGTTAT	NM_015721:	NM_015721:
50628	GEMIN4	gem (nuclear organelle) associated protein 4	-0.18	CACCGCAAGTTAGAACAGCTA	NM_015721:	NM_015721:
25929	GEMIN5	gem (nuclear organelle) associated protein 5	-0.26	TCAGAAATACGGCAACACGAA	NM_015465:	NM_015465:
25929	GEMIN5	gem (nuclear organelle) associated protein 5	-0.57	CTGGTGAAGATTGTTTATCTA	NM_015465:	NM_015465:
79833	GEMIN6	gem (nuclear organelle) associated protein 6	-1.30	CAGGTGGCAATCATGAGTGAA	NM_024775:	NM_024775:
79833	GEMIN6	gem (nuclear organelle) associated protein 6	-8.03	ACCCACCATATGGTCCAGAAA	NM_024775:	NM_024775:
2672	GFI1	growth factor independent 1	-0.66	CCGCGCTCATTTCTCGTCAAA	NM_005263:	NM_005263:
2672	GFI1	growth factor independent 1	0.12	TACAAGGTGGACAAATGCTAA	NM_005263:	NM_005263:
2674	GFRA1	GDNF family receptor alpha 1	0.76	ACCGCTCTGTCCACCCTATTA	NM_005264:	NM_005264:NM_145793:
2674	GFRA1	GDNF family receptor alpha 1	0.40	ACCTCTGTATTTCCAATGGTA	NM_005264:	NM_005264:NM_145793:
2675	GFRA2	GDNF family receptor alpha 2	0.08	TGGGTTTGACATGACACCTAA	NM_001495:	NM_001495:
2675	GFRA2	GDNF family receptor alpha 2	-0.12	TAACAAGGTGATCAAACCTAA	NM_001495:	NM_001495:
2676	GFRA3 (GDN	GDNF family receptor alpha 3	0.28	ACCAGGATCACCAGAATCTAA	NM_001496:	NM_001496:
2676	GFRA3 (GDN	GDNF family receptor alpha 3	0.75	CTCCTTGGTGGCCACAATTTA	NM_001496:	NM_001496:
64096	GFRA4 (GDN	GDNF family receptor alpha 4	-2.76	CTCGGATAGCACAGCCAGCTA	NM_022139:	NM_022139:NM_145763:NM_145762:
64096	GFRA4 (GDN	GDNF family receptor alpha 4	1.11	CCAGAATTCTAGGAAATTGTA	NM_022139:	NM_022139:NM_145763:NM_145762:
26088	GGA1 (golgi	golgi associated, gamma adaptin ear containing, ARF binding protein	0.31	CCGAAGAATGTGATCTTTGAA	NM_001001560:	NM_001001560:NM_013365:
26088	GGA1 (golgi	golgi associated, gamma adaptin ear containing, ARF binding protein	-0.93	TCGGTGTGTCTCCTTCATTCA	NM_001001560:	NM_001001560:NM_013365:
23163	GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein	0.17	CAGGGTGTCTGAGAAAGTGAA	NM_014001:	NM_138619:NM_014001:
23163	GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein	0.55	CACGTTAGAGGAAGTTAACAA	NM_014001:	NM_138619:NM_014001:
2677	GGCX	gamma-glutamyl carboxylase	0.15	CAGGAAGAGGTTAGACGCAAT	NM_000821:	NM_000821:
2677	GGCX	gamma-glutamyl carboxylase	-2.77	CAGACCTTTCTTAGACGCCAA	NM_000821:	NM_000821:
8836	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydr	-0.78	CTGGCTCTGATTCTTCATTAT	NM_003878:	NM_003878:
8836	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydr	-0.39	TCAGTCCAATTTATACTGGAA	NM_003878:	NM_003878:
2688	GH1	growth hormone 1	0.88	AACAGCAAGTTCGACACAAAC	NM_000515:	NM_000515:NM_022559:NM_022560:NM_022561:NM_022562:
2689	GH2	growth hormone 2	-0.14	ACGCAGCAGAAATCTAACCTA	NM_022556:	NM_002059:NM_022558:NM_022557:NM_022556:
2689	GH2	growth hormone 2	-2.30	CACCTGAAGGACCTAGAGGAA	NM_022556:	NM_002059:NM_022558:NM_022557:NM_022556:
2690	GHR	growth hormone receptor	1.06	CAGCCTGACAACATTTCTATA	NM_000163:	NM_000163:
2690	GHR	growth hormone receptor	1.21	TAGAACCTAATTCAATTCAAA	NM_000163:	NM_000163:
2691	GHRH	growth hormone releasing hormone	-0.14	CCCATACCGGTGTGCATTTAA	NM_021081:	NM_021081:
2691	GHRH	growth hormone releasing hormone	0.94	CCCGGGCTACCTGTAGCCAAA	NM_021081:	NM_021081:
2692	GHRHR	growth hormone releasing hormone receptor	-3.14	AAGGCTCAGAGGAGCCAATAA	NM_000823:	NM_000823:
2692	GHRHR	growth hormone releasing hormone receptor	-0.79	GCCAATAAACCTGTAAATGAA	NM_000823:	NM_000823:
51738	GHRL	ghrelin, growth hormone secretagogue receptor ligand	-0.02	CGCCCGGAAGATGGAGGTCAA	NM_016362:	NM_016362:
51738	GHRL	ghrelin, growth hormone secretagogue receptor ligand	0.14	CAGGAGGCGAATAAATGTTCA	NM_016362:	NM_016362:
2693	GHSR (growt	growth hormone secretagogue receptor	-1.48	AACCACAAGCAAACCGTGAAA	NM_004122:	NM_198407:NM_004122:
2693	GHSR (growt	growth hormone secretagogue receptor	0.33	AGGGACCAGAACCACAAGCAA	NM_004122:	NM_198407:NM_004122:
2695	GIP (gastric i	gastric inhibitory polypeptide	1.50	AACCAATAAAGTTTATGCTAA	NM_004123:	NM_004123:
2695	GIP (gastric i	gastric inhibitory polypeptide	1.70	AACCCAAACCAATAAAGTTTA	NM_004123:	NM_004123:
10755	GIPC1	GIPC PDZ domain containing family, member 1	-1.99	CAGCGTGATCGACCACATCCA	NM_005716:	NM_202468:NM_202467:NM_202469:NM_202470:NM_202494:NM_005716:
10755	GIPC1	GIPC PDZ domain containing family, member 1	-0.16	AGGCCGTACCTTCACGCTGAA	NM_005716:	NM_202468:NM_202467:NM_202469:NM_202470:NM_202494:NM_005716:
2696	GIPR	gastric inhibitory polypeptide receptor	0.52	CAGGTGCATTGGAGATTCTTA	NM_000164:	NM_000164:
2696	GIPR	gastric inhibitory polypeptide receptor	0.08	CTGGGAGCGCAACGAAGTCAA	NM_000164:	NM_000164:
28964	GIT1 (G prote	G protein-coupled receptor kinase interactor 1	1.48	CAGCCTTGACTTATCCGAATT	NM_014030:	NM_014030:
28964	GIT1 (G prote	G protein-coupled receptor kinase interactor 1	0.10	GCCGCTGAGGATGTCCCGAAA	NM_014030:	NM_014030:
9815	GIT2	G protein-coupled receptor kinase interactor 2	-0.07	AAGCATCGTGCAATAAGTGAA	NM_014776:	NM_057169:NM_014776:NM_057170:
9815	GIT2	G protein-coupled receptor kinase interactor 2	0.51	CTGCCTATGGCTGAAACTATA	NM_014776:	NM_057169:NM_014776:NM_057170:
2697	GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	-2.12	ATGCTTAGAGTGGACTATTAA	NM_000165:	NM_000165:
2697	GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	0.04	CAGGGAATCAAGCCATGCTTA	NM_000165:	NM_000165:
2700	GJA3	gap junction protein, alpha 3, 46kDa (connexin 46)	-0.72	ACCGGAGGACTTGGCCATCTA	NM_021954:	NM_021954:
2700	GJA3	gap junction protein, alpha 3, 46kDa (connexin 46)	-7.02	CTGCGCGTCCCTGCTGCTCAA	NM_021954:	NM_021954:
2703	GJA8	gap junction protein, alpha 8, 50kDa (connexin 50)	-4.04	TCGGAGAAGGTGTCAAAGCAA	NM_005267:	NM_005267:
2703	GJA8	gap junction protein, alpha 8, 50kDa (connexin 50)	-0.96	CTCTGTGTCCCTATTCCTCAA	NM_005267:	NM_005267:
2705	GJB1	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Toot	0.72	GCCTGAAATGTTACACATTAA	NM_000166:	NM_000166:
2705	GJB1	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Toot	1.01	TGCCTGAAATGTTACACATTA	NM_000166:	NM_000166:
2706	GJB2	gap junction protein, beta 2, 26kDa (connexin 26)	-0.04	TGGCCTCATGTCAAATATTTA	NM_004004:	NM_004004:
2706	GJB2	gap junction protein, beta 2, 26kDa (connexin 26)	0.16	CACAAAGATTCTGACCTTAAA	NM_004004:	NM_004004:
2707	GJB3	gap junction protein, beta 3, 31kDa (connexin 31)	-0.96	CCCTGAGGACATAATGTGTAA	NM_024009:	NM_024009:NM_001005752:
2707	GJB3	gap junction protein, beta 3, 31kDa (connexin 31)	0.97	AACAAGCGAATTAACTATCTA	NM_024009:	NM_024009:NM_001005752:
10804	GJB6	gap junction protein, beta 6 (connexin 30)	-0.14	AGGGTCTATCTTGTAAATATT	NM_006783:	NM_006783:
10804	GJB6	gap junction protein, beta 6 (connexin 30)	0.04	AACAAGAGACTGCTTGACAAA	NM_006783:	NM_006783:
2710	GK	glycerol kinase	-0.30	CCACCACTTAAGTGACATAAA	NM_000167:	NM_000167:NM_203391:
2710	GK	glycerol kinase	0.04	CTGAGGGTAGCCCATTTATAA	NM_000167:	NM_000167:NM_203391:
2712	GK2	glycerol kinase 2	0.00	CTCGGGTGTGCCATAATAATA	NM_033214:	NM_033214:
2712	GK2	glycerol kinase 2	0.05	TACGTTAGAAGAGCACTGTAA	NM_033214:	NM_033214:
80318	GKAP1	G kinase anchoring protein 1	-0.43	AACGCTCAACATGATCTTCCA	NM_025211:	NM_025211:
80318	GKAP1	G kinase anchoring protein 1	0.01	CATGCTGTTTGTAACGCTCAA	NM_025211:	NM_025211:
2717	GLA	galactosidase, alpha	-0.59	CAAGGTTAAGAAGTCACATAA	NM_000169:	NM_000169:
2717	GLA	galactosidase, alpha	1.51	TTGGTGGACCTCGCTCTTATA	NM_000169:	NM_000169:
2720	GLB1 (galact	galactosidase, beta 1	0.36	CACCAAAGTTTGCATATGGAA	NM_000404:	NM_000404:

2720	GLB1 (galact	galactosidase, beta 1	-1.57	ACCACTGATGGAGCACATAAA	NM_000404:	NM_000404:
2731	GLDC	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glyci	-0.02	CTCTGTCAAGGTAAATGTAAA	NM_000170:	NM_000170:
2731	GLDC	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glyci	-2.38	AACTGCGATATTAAATGCCAA	NM_000170:	NM_000170:
2734	GLG1	golgi apparatus protein 1	-1.33	CCGCTTGGAGCCAGATCTATA	NM_012201:	NM_012201:
2734	GLG1	golgi apparatus protein 1	-2.49	CCGGATTGAGATGTGGAGTTA	NM_012201:	NM_012201:
2735	GLI1	glioma-associated oncogene homolog 1 (zinc finger protein)	-2.81	CCAGCCCAGATGAATCACCAA	NM_005269:	NM_005269:
2735	GLI1	glioma-associated oncogene homolog 1 (zinc finger protein)	-0.56	CTCGGGCACCATCCATTTCTA	NM_005269:	NM_005269:
2736	GLI2	GLI-Kruppel family member GLI2	1.80	ATGAATGAATAAAGTATGTAA	NM_005270:	NM_005270:NM_030380:NM_030381:NM_030379:
2736	GLI2	GLI-Kruppel family member GLI2	-0.08	CAAGTATATATGAATGAATAA	NM_005270:	NM_005270:NM_030380:NM_030381:NM_030379:
2737	GLI3	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndro	0.02	CACCATATAAATAACGACCAT	NM_000168:	NM_000168:
2737	GLI3	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndro	-0.10	CAGCTTGTGCACCATATAAAT	NM_000168:	NM_000168:
11146	GLMN	glomulin, FKBP associated protein	-1.26	AAGGCATATTCAATTGGATTA	NM_007070:	NM_053274:NM_007070:
11146	GLMN	glomulin, FKBP associated protein	0.84	GAGGAACTTCAGTCTATAATA	NM_007070:	NM_053274:NM_007070:
2740	GLP1R	glucagon-like peptide 1 receptor	-4.84	CAGGCTCGTTCGTGAATGTCA	NM_002062:	NM_002062:
2740	GLP1R	glucagon-like peptide 1 receptor	-0.08	CCAGACAGAGCCGCAAATCAA	NM_002062:	NM_002062:
9340	GLP2R (gluca	glucagon-like peptide 2 receptor	-0.01	ATCACTGATGATCAAGTTGAA	NM_004246:	NM_004246:
9340	GLP2R (gluca	glucagon-like peptide 2 receptor	0.06	CACAGGGTGCTGGACAACAAA	NM_004246:	NM_004246:
2741	GLRA1	glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man sync	-0.95	CCGCTTTAACTTCTCTGCCTA	NM_000171:	NM_000171:
2741	GLRA1	glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man sync	0.47	TCGGATTTCCTGGATAAGCTA	NM_000171:	NM_000171:
2742	GLRA2	glycine receptor, alpha 2	-0.16	TAGGTGTAACTACTAGTCCTA	NM_002063:	NM_002063:
2742	GLRA2	glycine receptor, alpha 2	0.94	ATAGTGTACCCTCTTAATAAA	NM_002063:	NM_002063:
8001	GLRA3 (glyci	glycine receptor, alpha 3	1.25	TCGTGTTACAGTCACAATCTA	NM_006529:	NM_006529:
8001	GLRA3 (glyci	glycine receptor, alpha 3	0.25	AATGATGACCATTGTATTAAA	NM_006529:	NM_006529:
2743	GLRB (glycin	glycine receptor, beta	0.38	TTCAGTTAGTGTAAACTGCAA	NM_000824:	NM_000824:
2743	GLRB (glycin	glycine receptor, beta	-0.08	AAGCGAATTGATCTTTATGCA	NM_000824:	NM_000824:
2745	GLRX	glutaredoxin (thioltransferase)	-1.48	CACCAAGAGTGTATCTGTGAA	NM_002064:	NM_002064:
2745	GLRX	glutaredoxin (thioltransferase)	-0.18	CTCCTTCTCCACAATGATGAA	NM_002064:	NM_002064:
29998	GLTSCR1 (gli	glioma tumor suppressor candidate region gene 1	-5.06	CCGCATCGGGCTCAAGCTCAA	NM_015711:	NM_015711:
29998	GLTSCR1 (gli	glioma tumor suppressor candidate region gene 1	-0.63	CGGGCTCAAGCTCAAGATCAA	NM_015711:	NM_015711:
29997	GLTSCR2	glioma tumor suppressor candidate region gene 2	-1.69	CCGGAGCTTCCTACAATCCAT	NM_015710:	NM_015710:
29997	GLTSCR2	glioma tumor suppressor candidate region gene 2	-0.40	CTGACAAAGAAGAGAACCAAA	NM_015710:	NM_015710:
2746	GLUD1	glutamate dehydrogenase 1	0.30	CAGAATTTGCTTACCATAATT	NM_005271:	NM_005271:
2746	GLUD1	glutamate dehydrogenase 1	0.61	CCTATAGAAATAATAAATGAA	NM_005271:	NM_005271:
2760	GM2A	GM2 ganglioside activator	0.93	CACCCTGTTACATCATAACAA	NM_000405:	NM_000405:
2760	GM2A	GM2 ganglioside activator	-0.01	AAAGATGCTATTACAATGTAA	NM_000405:	NM_000405:
2762	GMDS	GDP-mannose 4,6-dehydratase	0.69	CCGGTCAGTAGCTAAGATTTA	NM_001500:	NM_001500:
2762	GMDS	GDP-mannose 4,6-dehydratase	0.70	GAAGATCATTAATGAAGTAAA	NM_001500:	NM_001500:
10691	GMEB1	glucocorticoid modulatory element binding protein 1	-0.35	CGGCCTAACCTCGGCAATTCA	NM_006582:	NM_006582:NM_024482:
10691	GMEB1	glucocorticoid modulatory element binding protein 1	-0.45	TCGGCAATTCAGGCTGTTGAA	NM_006582:	NM_006582:NM_024482:
26205	GMEB2	glucocorticoid modulatory element binding protein 2	-0.33	CACAACCAGCTTCAGAATTAA	NM_012384:	NM_012384:
26205	GMEB2	glucocorticoid modulatory element binding protein 2	-0.11	CTAGGAAGAGTCAGATTTATA	NM_012384:	NM_012384:
51291	GMIP (GEM i	GEM interacting protein	-0.11	CAGAGGGTTCCTATAAGGAAA	NM_016573:	NM_016573:
51291	GMIP (GEM i	GEM interacting protein	-0.81	CCAGAGGGTTCCTATAAGGAA	NM_016573:	NM_016573:
2765	GML	GPI anchored molecule like protein	-2.93	AAGGGACATGTTACCCGATGA	NM_002066:	NM_002066:
2765	GML	GPI anchored molecule like protein	-1.23	CTCCTCTAGGTGGCCCATTTA	NM_002066:	NM_002066:
51053	GMNN	geminin, DNA replication inhibitor	-0.13	AAGGAACTGTATCTTCCTCTA	NM_015895:	NM_015895:
51053	GMNN	geminin, DNA replication inhibitor	0.04	ACCCTATTGCATTAAAGTACA	NM_015895:	NM_015895:
2766	GMPR (guan	guanosine monophosphate reductase	0.84	TCCGGAGCAGATATCATCAAA	NM_006877:	NM_006877:
2766	GMPR (guan	guanosine monophosphate reductase	-0.04	CTCCATGTTTACAGCAATTCA	NM_006877:	NM_006877:
51292	GMPR2	guanosine monophosphate reductase 2	-1.46	AAGATGCTGATTGGTACATAA	NM_016576:	NM_016576:NM_001002000:NM_001002002:NM_001002001:
51292	GMPR2	guanosine monophosphate reductase 2	-0.79	ATGCCTCATATTGACAACGAT	NM_016576:	NM_016576:NM_001002000:NM_001002002:NM_001002001:
2768	GNA12	guanine nucleotide binding protein (G protein) alpha 12	-2.80	CCGGATCGGCCAGCTGAATTA	NM_007353:	NM_007353:
2768	GNA12	guanine nucleotide binding protein (G protein) alpha 12	1.20	GAGGTAGTTGTGCCTCAATTA	NM_007353:	NM_007353:
10672	GNA13	guanine nucleotide binding protein (G protein), alpha 13	0.85	CACCAAATAGATATCATGTTA	NM_006572:	NM_006572:
10672	GNA13	guanine nucleotide binding protein (G protein), alpha 13	-1.46	CCCGACTGCTTACCAAATTAA	NM_006572:	NM_006572:
9630	GNA14 (guan	guanine nucleotide binding protein (G protein), alpha 14	0.37	AGGGAATTCAACCTTGTCTAA	NM_004297:	NM_004297:
9630	GNA14 (guan	guanine nucleotide binding protein (G protein), alpha 14	-0.38	ATGGTGGATGTTGGTGGCCAA	NM_004297:	NM_004297:
2769	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	0.81	TCCGTGCGGGCTGAAATTAAA	NM_002068:	NM_002068:
2769	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	-1.73	CCGGTTTGCGGACGAGAGAAA	NM_002068:	NM_002068:
2770	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity	1.15	CACGTTAGATTTGGTTTGAAA	NM_002069:	NM_002069:
2770	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity	0.74	AAGGACCTTTCTTAAATGTGA	NM_002069:	NM_002069:
2771	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity	0.43	CAGCCCAAGTCCAAATGTTTA	NM_002070:	NM_002070:
2771	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity	-3.94	CCGGGCGGTTGTCTACAGCAA	NM_002070:	NM_002070:
2773	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity	0.33	AAAGTGTGATTCGATCGTCAA	NM_006496:	NM_006496:
2773	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity	0.77	AAGCTTATGGTTGAAGGTTAA	NM_006496:	NM_006496:
2774	GNAL (guanir	guanine nucleotide binding protein (G protein), alpha activating activity	-0.45	CACCGGTGACGGCAAACATTA	NM_002071:	NM_002071:NM_182978:
2774	GNAL (guanir	guanine nucleotide binding protein (G protein), alpha activating activity	-0.30	ACGCCTGCTCTGAATCGGAAA	NM_002071:	NM_002071:
2775	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity	0.15	AACAAGAAGGACATATTTGAA	NM_138736:	NM_138736:
2775	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity	0.29	ACGGACGTCATCATCGCCAAA	NM_138736:	NM_138736:
2776	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	1.11	CAGGACACATCGTTCGATTTA	NM_002072:	NM_002072:
2776	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	0.07	CAGGAATGCTATGATAGACGA	NM_002072:	NM_002072:
2778	GNAS	GNAS complex locus	-0.15	AGGGCATGATTAACAAAGCAA	NM_000516:	NM_000516:NM_080426:NM_080425:NM_016592:
2778	GNAS	GNAS complex locus	0.18	CCAAATTTAATTAAAGCCTTA	NM_000516:	NM_000516:NM_080426:NM_080425:NM_016592:
2779	GNAT1	guanine nucleotide binding protein (G protein), alpha transducing acti	-0.61	ACGCGCCATGACCACACTCAA	NM_000172:	NM_000172:NM_144499:
2779	GNAT1	guanine nucleotide binding protein (G protein), alpha transducing acti	-1.69	CAGCATCTGTTTCCCGGACTA	NM_000172:	NM_000172:NM_144499:
2780	GNAT2	guanine nucleotide binding protein (G protein), alpha transducing acti	0.32	TGGGATAGCTATTGCAGCTTA	NM_005272:	NM_005272:
2780	GNAT2	guanine nucleotide binding protein (G protein), alpha transducing acti	-0.12	AACCAATTAGAACGAATTACA	NM_005272:	NM_005272:
2781	GNAZ (guanir	guanine nucleotide binding protein (G protein), alpha z polypeptide	0.02	CGGGACACGTGTTGTACATAA	NM_002073:	NM_002073:
2781	GNAZ (guanir	guanine nucleotide binding protein (G protein), alpha z polypeptide	1.06	AGGGCCGTGTGTAAATACGAA	NM_002073:	NM_002073:
54584	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-11.10	CAGGTGCGTGGGACTCATGAA	NM_053004:	NM_053004:
54584	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-5.43	CAGCCTTGGCCTGAAACCTCA	NM_053004:	NM_053004:
10399	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like	0.03	TTGGCACACGCTAGAAGTTTA	NM_006098:	NM_006098:
10399	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like	-0.67	CCCGCAGTTCCCGGACATGAT	NM_006098:	NM_006098:
2784	GNB3 (guanir	guanine nucleotide binding protein (G protein), beta polypeptide 3	0.74	TCCCTTAATGAGCAAGGACAA	NM_002075:	NM_002075:
2784	GNB3 (guanir	guanine nucleotide binding protein (G protein), beta polypeptide 3	-0.46	TCCGGGTGCCATTCCCACTAA	NM_002075:	NM_002075:
59345	GNB4 (guanir	guanine nucleotide binding protein (G protein), beta polypeptide 4	0.52	CTGCTCTATATATAACTTAAA	NM_021629:	NM_021629:
59345	GNB4 (guanir	guanine nucleotide binding protein (G protein), beta polypeptide 4	1.51	TACGATGACTTTAATTGTAAT	NM_021629:	NM_021629:
10681	GNB5	guanine nucleotide binding protein (G protein), beta 5	0.33	TAGAAGCAAATTCCAATTCCA	NM_006578:	NM_006578:NM_016194:
10681	GNB5	guanine nucleotide binding protein (G protein), beta 5	0.36	TTAAGGTTATTCTAAATTATA	NM_006578:	NM_006578:NM_016194:
10020	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kina	1.55	ATGGAAATACATATCGAATGA	NM_005476:	NM_005476:
10020	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kina	1.18	CCCGATCATGTTTGGCATTAA	NM_005476:	NM_005476:
2791	GNG11	guanine nucleotide binding protein (G protein), gamma 11	-0.91	CAGAGAGTATCAGATGTACAA	NM_004126:	NM_004126:
2791	GNG11	guanine nucleotide binding protein (G protein), gamma 11	-3.49	CTGGAGAGGATCCTCTAGTAA	NM_004126:	NM_004126:

55970	GNG12	guanine nucleotide binding protein (G protein), gamma 12	0.37	TCCGATATGTCAGGACCTAAA	NM_018841:	NM_018841:
55970	GNG12	guanine nucleotide binding protein (G protein), gamma 12	1.07	TAGCATGTTCACAGATTTGAA	NM_018841:	NM_018841:
51764	GNG13	guanine nucleotide binding protein (G protein), gamma 13	1.11	CACGTGATTACAGTCTGTAAA	NM_016541:	NM_016541:
51764	GNG13	guanine nucleotide binding protein (G protein), gamma 13	0.59	CCCACTCACAACATCTTGTAA	NM_016541:	NM_016541:
54331	GNG2	guanine nucleotide binding protein (G protein), gamma 2	0.11	TACAGTTAGGACGCCCATGAA	NM_053064:	NM_053064:
54331	GNG2	guanine nucleotide binding protein (G protein), gamma 2	0.22	CTCCTAGTTAATAGTGGTATA	NM_053064:	NM_053064:
2785	GNG3 (guani	guanine nucleotide binding protein (G protein), gamma 3	-0.02	CAAGATGGTGGAACAGCTTAA	NM_012202:	NM_012202:
2785	GNG3 (guani	guanine nucleotide binding protein (G protein), gamma 3	0.73	GTGGAACAGCTTAAGATTGAA	NM_012202:	NM_012202:
2786	GNG4 (guani	guanine nucleotide binding protein (G protein), gamma 4	0.93	AAGTCTGGACTTAAGAGTTTA	NM_004485:	NM_004485:
2786	GNG4 (guani	guanine nucleotide binding protein (G protein), gamma 4	1.41	CAAGTTTATATCATATTAATA	NM_004485:	NM_004485:
2788	GNG7	guanine nucleotide binding protein (G protein), gamma 7	0.62	ACGCATCCATCTCCAAGTTAA	NM_052847:	NM_052847:
2788	GNG7	guanine nucleotide binding protein (G protein), gamma 7	-0.24	ACGGCTAAACTCGGATTGTGA	NM_052847:	NM_052847:
94235	GNG8 (guani	guanine nucleotide binding protein (G protein), gamma 8	0.60	ACAGCTGAAGCTGGAGGTGAA	NM_033258:	NM_033258:
94235	GNG8 (guani	guanine nucleotide binding protein (G protein), gamma 8	-5.33	CAAGACGGTGGAACAGCTGAA	NM_033258:	NM_033258:
2792	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing ac	-3.40	AAGAGAGAGAGCTCATATGAA	NM_021955:	NM_021955:
2792	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing ac	-2.49	AGGCTGTGTGATTTCATAATA	NM_021955:	NM_021955:
2793	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing ac	0.70	AACACAAAGCATCTTGGTTAA	NM_031498:	NM_031498:
2793	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing ac	0.43	CAACAAGAGTTTGTGAAGTTA	NM_031498:	NM_031498:
27232	GNMT (glycin	glycine N-methyltransferase	0.11	GACGGAAGGGTAAACAATATA	NM_018960:	NM_018960:
27232	GNMT (glycin	glycine N-methyltransferase	-2.23	CAGACGGAAGGGTAAACAATA	NM_018960:	NM_018960:
8443	GNPAT	glyceronephosphate O-acyltransferase	1.18	CACGTAATTACTCTCATCGAA	NM_014236:	NM_014236:
8443	GNPAT	glyceronephosphate O-acyltransferase	-4.01	CTCGATCAAGGTACCTCTCAA	NM_014236:	NM_014236:
2796	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	-0.36	ACCATTACTAACATGACTTAA	NM_000825:	NM_000825:
2796	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	0.98	GACCATTACTAACATGACTTA	NM_000825:	NM_000825:
2797	GNRH2	gonadotropin-releasing hormone 2	-2.15	CCAGTGGTCCCTTCACAGGAA	NM_001501:	NM_178332:NM_001501:NM_178331:
2797	GNRH2	gonadotropin-releasing hormone 2	-3.10	CTGGAGGAAAGCGAGCCCTCA	NM_001501:	NM_178332:NM_001501:NM_178331:
2798	GNRHR	gonadotropin-releasing hormone receptor	-2.38	AAGCATGGATTGGATCAGTAA	NM_000406:	NM_001012763:NM_000406:
2798	GNRHR	gonadotropin-releasing hormone receptor	0.71	ACGGTTGCATTTGCCACTTCA	NM_000406:	NM_001012763:NM_000406:
114814	GNRHR2	gonadotropin-releasing hormone (type 2) receptor 2	-0.02	CCGCCAGGCAGCAGTACTCAA	NM_057163:	NR_002328:
114814	GNRHR2	gonadotropin-releasing hormone (type 2) receptor 2	-0.22	TCCCGTTCAGGTGTAAGGAAA	NM_057163:	NR_002328:
2799	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	0.18	ATCAGTCAACTTCCACATTAA	NM_002076:	NM_002076:
2799	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	-0.22	AAGCAAGATGCTGGTTGCCAA	NM_002076:	NM_002076:
9950	GOLGA5	golgi autoantigen, golgin subfamily a, 5	-1.90	CACGACCAACCATATGGCAAA	NM_005113:	NM_005113:
9950	GOLGA5	golgi autoantigen, golgin subfamily a, 5	0.40	AAGAAGATCTTTATCGAACAA	NM_005113:	NM_005113:
26003	GORASP2	golgi reassembly stacking protein 2, 55kDa	-0.67	CAGTATGTCACGCATCTTTAA	NM_015530:	NM_015530:
26003	GORASP2	golgi reassembly stacking protein 2, 55kDa	-0.36	ATGCCTAATACTCACACGCAA	NM_015530:	NM_015530:
9527	GOSR1	golgi SNAP receptor complex member 1	0.96	CACTGTGGTATTTATAGTATT	NM_004871:	NM_004871:NM_001007024:NM_001007025:
9527	GOSR1	golgi SNAP receptor complex member 1	0.62	CATGATAGTGTTGAAGCCTAA	NM_004871:	NM_004871:NM_001007024:NM_001007025:
9570	GOSR2	golgi SNAP receptor complex member 2	-0.19	AACGAAATCCAAGCAAGCATA	NM_004287:	NM_001012511:NM_054022:NM_004287:
9570	GOSR2	golgi SNAP receptor complex member 2	-1.83	CAGCATTCCCACAGCCTGCAA	NM_004287:	NM_004287:
2811	GP1BA	glycoprotein Ib (platelet), alpha polypeptide	-1.78	ATGCATCTATGCACAGAAGAA	NM_000173:	NM_000173:
2811	GP1BA	glycoprotein Ib (platelet), alpha polypeptide	-0.61	CTGAACTTGATCAGCCACCAA	NM_000173:	NM_000173:
2812	GP1BB	glycoprotein Ib (platelet), beta polypeptide	0.89	ACGAGTCCTGAGGAGAGAA	NM_000407:	NM_000407:
2812	GP1BB	glycoprotein Ib (platelet), beta polypeptide	-2.78	CTGGGCAACACGGGCCTGCAA	NM_000407:	NM_000407:
2813	GP2	glycoprotein 2 (zymogen granule membrane)	-2.96	CAGGACCTCAATAGTTCTGAT	NM_001502:	NM_001007240:NM_001502:NM_001007241:NM_001007242:
2813	GP2	glycoprotein 2 (zymogen granule membrane)	0.11	CCAGAACTACACGAATCCTTA	NM_001502:	NM_001007240:NM_001502:NM_001007241:NM_001007242:
2814	GP5	glycoprotein V (platelet)	-0.30	ACGGGCAAAGGTCAAGATCAT	NM_004488:	NM_004488:
2814	GP5	glycoprotein V (platelet)	1.43	ATCGTGTTTGCTATGATTAAA	NM_004488:	NM_004488:
51206	GP6	glycoprotein VI (platelet)	0.35	CCCAGGCACGGTCGTATCCAA	NM_016363:	NM_016363:
51206	GP6	glycoprotein VI (platelet)	0.90	CCCGCTTCCCTTCACATTAGA	NM_016363:	NM_016363:
2815	GP9	glycoprotein IX (platelet)	0.26	TACGGTGTCCAGAGACAGTTA	NM_000174:	NM_000174:
2815	GP9	glycoprotein IX (platelet)	0.02	CCACCAGAAGCCCAGAATAAA	NM_000174:	NM_000174:
10223	GPA33	glycoprotein A33 (transmembrane)	-0.06	CAGGGATGATTCCCACCCAAA	NM_005814:	NM_005814:
10223	GPA33	glycoprotein A33 (transmembrane)	-0.72	CCCATCCTAGTGGGCACTTAA	NM_005814:	NM_005814:
151306	GPBAR1	G protein-coupled bile acid receptor 1	-3.68	AAGCCTCATCATCACCGCGAA	NM_170699:	NM_170699:
151306	GPBAR1	G protein-coupled bile acid receptor 1	-8.49	CAGGACCAAGATGACGCCCAA	NM_170699:	NM_170699:
2817	GPC1 (glypic	glypican 1	0.04	CCGCCAGATCTACGGAGCCAA	NM_002081:	NM_002081:
2817	GPC1 (glypic	glypican 1	1.24	TACAACACAGACGATATTTAA	NM_002081:	NM_002081:
221914	GPC2	glypican 2 (cerebroglycan)	0.00	CTGCAAATAAATGGTAATGTA	NM_152742:	NM_152742:
221914	GPC2	glypican 2 (cerebroglycan)	0.62	CATGTTTATTCTGCAAATAAA	NM_152742:	NM_152742:
2719	GPC3	glypican 3	1.26	GTCAGTCAAATTATTGACAAA	NM_004484:	NM_004484:
2719	GPC3	glypican 3	1.03	CCAGTGGTCAGTCAAATTATT	NM_004484:	NM_004484:
2239	GPC4	glypican 4	-4.05	TAGGTAGAGCTGAGAATACTA	NM_001448:	NM_001448:
2239	GPC4	glypican 4	0.70	TACCAAATGATAGCTCATAAA	NM_001448:	NM_001448:
10082	GPC6	glypican 6	-1.12	CCGGCTGGTCACAGACATAAA	NM_005708:	NM_005708:
10082	GPC6	glypican 6	-0.01	CTAGAGAGAATTCTTACTCAA	NM_005708:	NM_005708:
2820	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	1.45	CAGATAGCATGTGTTATTAAA	NM_000408:	NM_000408:
2820	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.45	CAGGAAGTTTCTATATTATGA	NM_000408:	NM_000408:
122876	GPHB5	glycoprotein hormone beta 5	-1.53	TCATCGAGTCTGTACCTACAA	NM_145171:	NM_145171:
122876	GPHB5	glycoprotein hormone beta 5	-0.92	GGGAGTTTACTTTCCTGGCCA	NM_145171:	NM_145171:
10243	GPHN	gephyrin	-0.41	CCGCAGTGGGATAAATCTCAA	NM_020806:	NM_020806:NM_001024218:
10243	GPHN	gephyrin	0.56	CCCATCGGCCATGACATTAAA	NM_020806:	NM_020806:NM_001024218:
2821	GPI	glucose phosphate isomerase	-2.25	CCGCGTCTGGTATGTCTCCAA	NM_000175:	NM_000175:
2821	GPI	glucose phosphate isomerase	-0.62	GAGTTTGGAATTGACCCTCAA	NM_000175:	NM_000175:
2822	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	1.21	CGGCCGAGTATATGTATATAA	NM_001503:	NM_001503:
2822	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	0.53	TACGTACGATGACGTGTCTAA	NM_001503:	NM_001503:
10457	GPNMB	glycoprotein (transmembrane) nmb	0.52	TCCATGTAACTGTATGCATAA	NM_002510:	NM_001005340:NM_002510:
10457	GPNMB	glycoprotein (transmembrane) nmb	0.04	CTACTATTGATTAGAGCCTAA	NM_002510:	NM_001005340:NM_002510:
2825	GPR1 (G prot	G protein-coupled receptor 1	-0.35	AAGCCTTAAGTCTTAATATTA	NM_005279:	NM_005279:
2825	GPR1 (G prot	G protein-coupled receptor 1	0.26	CCGACTCCACTTTCATAGTTA	NM_005279:	NM_005279:
83550	GPR101	G protein-coupled receptor 101	-5.82	CAGCTTGGAAGTGCGAGTCAA	NM_054021:	NM_054021:
83550	GPR101	G protein-coupled receptor 101	-0.76	CCGCGGTTACCTGCTCCTCTA	NM_054021:	NM_054021:
84109	GPR103	G protein-coupled receptor 103	1.77	AGGAATTACAATGATGCGGAA	NM_198179:	NM_198179:
84109	GPR103	G protein-coupled receptor 103	0.12	ATGGAAATTCAGGAATTACAA	NM_198179:	NM_198179:
57720	GPR107	G protein-coupled receptor 107	-4.69	TAGCCTAGACCGTACAAAGAA	NM_020960:	NM_020960:
57720	GPR107	G protein-coupled receptor 107	-0.09	CAGAAGTGAGGTAAGAGTAAA	NM_020960:	NM_020960:
56927	GPR108	G protein-coupled receptor 108	-0.12	CAAGTACGTCCTGTCGGATAA	XM_290854:	XM_290854:
56927	GPR108	G protein-coupled receptor 108	-1.12	CCCGGACAAGCCCATTTGGAA	XM_290854:	XM_290854:
338442	GPR109A	G protein-coupled receptor 109A	-0.17	CTCCTTAAATAACCATGCCAA	NM_177551:	NM_177551:
338442	GPR109A	G protein-coupled receptor 109A	-1.12	TGGGCCCAACCTCTCCTTAAA	NM_177551:	NM_177551:
266977	GPR110	G protein-coupled receptor 110	-0.60	CACCTAGTGAATGAAACTCAA	NM_153840:	NM_153840:
266977	GPR110	G protein-coupled receptor 110	-1.68	CAGGTCAATGGACCTGTGATA	NM_153840:	NM_153840:
266977	GPR110	G protein-coupled receptor 110	0.13	AAAGCATATGAAAGAATTCAA	NM_025048:	NM_025048:NM_153840:
266977	GPR110	G protein-coupled receptor 110	-0.62	ATGGGCTAATTAGAATTATCA	NM_025048:	NM_025048:NM_153840:
222611	GPR111	G protein-coupled receptor 111	0.08	AAGAAGGCTATTCATAGATAA	NM_153839:	NM_153839:
222611	GPR111	G protein-coupled receptor 111	0.85	CAGCCATTTGAAGACAATATA	NM_153839:	NM_153839:
139378	GPR112	G protein-coupled receptor 112	-2.21	CACGGTAATCTCTGTCAGGAA	NM_153834:	NM_153834:

139378	GPR112	G protein-coupled receptor 112	0.77	CCGGAACTGTACCTTGGTTTA	NM_153834:	NM_153834:
165082	GPR113	G protein-coupled receptor 113	-0.76	CAGAGTGTAATGTCAACCACA	NM_153835:	NM_153835:
165082	GPR113	G protein-coupled receptor 113	0.00	TCCGTAATGGAACTGAAATAA	NM_153835:	NM_153835:
221188	GPR114	G protein-coupled receptor 114	-0.01	AGCGGCTTTGTTTCAGCCTAA	NM_153837:	NM_153837:
221188	GPR114	G protein-coupled receptor 114	0.45	AGGCATGGGTCTCGAATCTTA	NM_153837:	NM_153837:
221393	GPR115	G protein-coupled receptor 115	0.05	TAGGAGAATGTTCCCACTATA	NM_153838:	NM_153838:
221393	GPR115	G protein-coupled receptor 115	0.78	TAGGCTCTCACTTTAACATTA	NM_153838:	NM_153838:
221395	GPR116	G protein-coupled receptor 116	0.04	AAGGATCTTTCTATTAGCATA	NM_015234:	NM_015234:
221395	GPR116	G protein-coupled receptor 116	-0.38	TTGAGTCTTCATGAACATGAA	NM_015234:	NM_015234:
139760	GPR119	G protein-coupled receptor 119	-1.04	CTCCCTCATCATTGCTACTAA	NM_178471:	NM_178471:
139760	GPR119	G protein-coupled receptor 119	-1.36	CAGGAGTGTCACCTCTACCTA	NM_178471:	NM_178471:
2835	GPR12	G protein-coupled receptor 12	1.34	CGGCATTGGACTCATCACCAA	NM_005288:	NM_005288:
2835	GPR12	G protein-coupled receptor 12	0.07	CTGGATGCCTTTCACCCTCTA	NM_005288:	NM_005288:
338557	GPR120	G protein-coupled receptor 120	0.91	AAGAAATGACTTGTCGATTAT	NM_181745:	NM_181745:
338557	GPR120	G protein-coupled receptor 120	-2.76	CACAGTGAGATCACAAAGGCA	NM_181745:	NM_181745:
84435	GPR123 (G p	G protein-coupled receptor 123	-0.31	CACTGTAAAGCTCTTCACCTA	NM_032422:	NM_032422:
84435	GPR123 (G p	G protein-coupled receptor 123	-1.60	CTGCCCAAGGGTAAATTGCTA	NM_032422:	NM_032422:
25960	GPR124	G protein-coupled receptor 124	0.18	CCCACAGGAGTGGTACTTAAA	NM_032777:	NM_032777:
25960	GPR124	G protein-coupled receptor 124	-1.29	CCGACTAAACATATCTGGAAA	NM_032777:	NM_032777:
166647	GPR125	G protein-coupled receptor 125	-1.91	ATGGATTTGACGGGATCTGAA	XM_291111.1:	NM_145290:
166647	GPR125	G protein-coupled receptor 125	-3.78	CAGCTTGATAATAGTCTGACA	XM_291111.1:	NM_145290:
57211	GPR126	G protein-coupled receptor 126	1.08	ACCTAGGTAACTGCATATATA	NM_020455:	NM_001032394:NM_001032395:NM_020455:NM_198569:
57211	GPR126	G protein-coupled receptor 126	0.48	TAGAATATCCGTAGTGATTCA	NM_020455:	NM_001032394:NM_001032395:NM_020455:NM_198569:
84873	GPR128	G protein-coupled receptor 128	-1.54	ACGCGAGTGGTTGGACAGATA	NM_032787:	NM_032787:
84873	GPR128	G protein-coupled receptor 128	0.17	CACAGCTCTATTACCTTCTAA	NM_032787:	NM_032787:
29933	GPR132	G protein-coupled receptor 132	-4.99	ACGGACCATTCCCGCCAAGAA	NM_013345:	NM_013345:
29933	GPR132	G protein-coupled receptor 132	-0.15	CTGGGTCACCATCGAGATCAA	NM_013345:	NM_013345:
283383	GPR133	G protein-coupled receptor 133	0.01	CAAGCACAGATTGACACGTAA	NM_198827:	NM_198827:
283383	GPR133	G protein-coupled receptor 133	-1.73	CAGCATGCACTACTACCTGAA	NM_198827:	NM_198827:
64582	GPR135	G protein-coupled receptor 135	-0.04	ACCAAACAGCCTAAATCCGAA	NM_022571:	NM_022571:
64582	GPR135	G protein-coupled receptor 135	-2.73	CAACAGGATGTCCTCTTCCAA	NM_022571:	NM_022571:
56834	GPR137	G protein-coupled receptor 137	0.53	CCGGCTGGACACCTTCGATTA	NM_020155:	NM_020155:
56834	GPR137	G protein-coupled receptor 137	0.59	TAGCATCTACCTGGAGGCCAA	NM_020155:	NM_020155:
7107	GPR137B	G protein-coupled receptor 137B	-1.96	ACCTACCACCTTAGTCGTTTA	NM_003272:	NM_003272:
7107	GPR137B	G protein-coupled receptor 137B	-0.02	CAGGAACTTTGCAAGACTCAA	NM_003272:	NM_003272:
283554	GPR137C	G protein-coupled receptor 137C	1.01	CTGGCGGAGGTTATATGTAAA	XM_290615:	XM_290615:
283554	GPR137C	G protein-coupled receptor 137C	-3.01	TCGAAAGGAGTTGTTTATAAA	XM_290615:	XM_290615:
124274	GPR139	G protein-coupled receptor 139	0.15	ACCGTTAACCATTGACAGGTA	XM_064062.4:	NM_001002911:
353345	GPR141	G protein-coupled receptor 141	-0.72	CAAAGTGGAATTCTACAGAAA	NM_181791:	NM_181791:
353345	GPR141	G protein-coupled receptor 141	0.00	TCGCTTGACCTACCTCATCAA	NM_181791:	NM_181791:
350383	GPR142	G protein-coupled receptor 142	0.87	CCGGGTCTTCGTCATGCTCTA	NM_181790:	NM_181790:
350383	GPR142	G protein-coupled receptor 142	-6.73	AACACTGGACGAGGTCCTCAA	NM_181790:	NM_181790:
4935	GPR143	G protein-coupled receptor 143	-1.09	CAGCTAGAGCTTCTTCCCGAA	NM_000273:	NM_000273:
4935	GPR143	G protein-coupled receptor 143	0.49	TCGGATATGAACCACACGGAA	NM_000273:	NM_000273:
347088	GPR144	G protein-coupled receptor 144	-1.05	CTGGCTCAATGTGCACACAAA	NM_182611:	NM_182611:
347088	GPR144	G protein-coupled receptor 144	1.22	CCGAGTCAATGCCTTGGCCAA	NM_182611:	NM_182611:
115330	GPR146	G protein-coupled receptor 146	1.25	AGCATTCAGTTTGTCAATGAA	NM_138445:	NM_138445:
115330	GPR146	G protein-coupled receptor 146	-6.98	CAGGGTTCTGAGAACATTTCA	NM_138445:	NM_138445:
344561	GPR148	G protein-coupled receptor 148	-2.13	CAGCACAATATAATAGTGGAA	NM_207364:	NM_207364:
344561	GPR148	G protein-coupled receptor 148	0.10	CCACTTATGACTAACTTCTTA	NM_207364:	NM_207364:
344758	GPR149	G protein-coupled receptor 149	-1.30	CACCGTGAGCGTAGCGCAGAA	XM_293580.1:	XM_293580:
344758	GPR149	G protein-coupled receptor 149	0.61	CACTGTGTCAATCATTAGTAA	XM_293580.1:	XM_293580:
2838	GPR15	G protein-coupled receptor 15	-3.03	TTCAGTTTATTTGGATTATTA	NM_005290:	NM_005290:
2838	GPR15	G protein-coupled receptor 15	0.61	TTGCGGCAAGAACACTATTTA	NM_005290:	NM_005290:
285601	GPR150	G protein-coupled receptor 150	-6.21	CCTGCAGGTCTACGCGTTCTA	NM_199243:	NM_199243:
285601	GPR150	G protein-coupled receptor 150	-0.66	GCGTCGCAAGATGGACTTCCT	NM_199243:	NM_199243:
134391	GPR151	G protein-coupled receptor 151	0.09	CCGAGCTACGGCGTACTCCAA	NM_194251:	NM_194251:
134391	GPR151	G protein-coupled receptor 151	-3.03	CTCCTTCACAATGCTTGGAAA	NM_194251:	NM_194251:
390212	GPR152	G protein-coupled receptor 152	-6.14	CAGGACCATTCTGTCAGCCTA	NM_206997:	NM_206997:
390212	GPR152	G protein-coupled receptor 152	-3.31	CAAATGGACACTACCATGGAA	NM_206997:	NM_206997:
387509	GPR153	G protein-coupled receptor 153	-4.21	CAGCGTTGGCGCCAAGCAGAA	NM_207370:	NM_207370:
387509	GPR153	G protein-coupled receptor 153	-2.95	GACCACCATAGTCTTCATCTA	NM_207370:	NM_207370:
387129	GPR154	G protein-coupled receptor 154	-0.23	CACCCTGATCATATTTGGGAA	NM_207172:	NM_207172:NM_207173:
387129	GPR154	G protein-coupled receptor 154	1.60	CAGATATTAATTGGCGATTCA	NM_207172:	NM_207172:NM_207173:
151556	GPR155	G protein-coupled receptor 155	-0.04	CAGGAGATGGACCTTAAATTA	NM_152529:	NM_152529:NM_001033045:
151556	GPR155	G protein-coupled receptor 155	0.51	TACGAATATGCCAACATTATA	NM_152529:	NM_152529:NM_001033045:
165829	GPR156	G protein-coupled receptor 156	-2.28	CACGGGTTAGTTCAGTAATCA	NM_153002:	NM_153002:
165829	GPR156	G protein-coupled receptor 156	-1.65	CCCGGACAAGAGAGTGATTAT	NM_153002:	NM_153002:
57512	GPR158	G protein-coupled receptor 158	0.16	TGCGTGGCTCCTATAACTCAA	NM_020752:	NM_020752:
57512	GPR158	G protein-coupled receptor 158	-0.62	CTGCTATATTCCATACAATTA	NM_020752:	NM_020752:
26996	GPR160	G protein-coupled receptor 160	0.15	AAGGGCTATACCAGTTATTAA	NM_014373:	NM_014373:
26996	GPR160	G protein-coupled receptor 160	0.57	CAACTTTAAGATATCAACCTA	NM_014373:	NM_014373:
23432	GPR161	G protein-coupled receptor 161	0.57	AAGACAGTTCGCAAAGAACTA	NM_007369:	NM_007369:NM_153832:
23432	GPR161	G protein-coupled receptor 161	-2.11	CTGGAACAAGACAGTTCGCAA	NM_007369:	NM_007369:NM_153832:
27239	GPR162	G protein-coupled receptor 162	-0.72	ATCAATTGCAGGGATGCTTAA	NM_014449:	NM_014449:NM_019858:
27239	GPR162	G protein-coupled receptor 162	0.86	CCGACTATGACTGGAACGAGA	NM_014449:	NM_019858:
2840	GPR17	G protein-coupled receptor 17	0.65	ATCGCCTAGTCTCAACCCATA	NM_005291:	NM_005291:
2840	GPR17	G protein-coupled receptor 17	0.21	CAGCAGCTAGAGGATGTCCAA	NM_005291:	NM_005291:
29909	GPR171	G protein-coupled receptor 171	-2.22	AGGCTTGCTGCTACTCATTAA	NM_013308:	NM_013308:
29909	GPR171	G protein-coupled receptor 171	-0.39	CCCAAAGGTATTCATGAGTTA	NM_013308:	NM_013308:
79581	GPR172A	G protein-coupled receptor 172A	-2.26	CACCACTGCAAGAGCCACCAA	NM_024531:	NM_024531:
79581	GPR172A	G protein-coupled receptor 172A	0.55	TGGCGTGTTCTCCTACGTGAA	NM_024531:	NM_024531:
55065	GPR172B	G protein-coupled receptor 172B	0.50	ACCACGTGTTTCAAAGCAGAA	NM_017986:	NM_017986:
55065	GPR172B	G protein-coupled receptor 172B	0.08	TTGTGGGATTTGTGCAATAAA	NM_017986:	NM_017986:
54328	GPR173	G protein-coupled receptor 173	0.04	ACGGCTCTTCATGGACCTTCA	NM_018969:	NM_018969:
54328	GPR173	G protein-coupled receptor 173	-1.01	CACGCTGGGCTTCATGCTTAT	NM_018969:	NM_018969:
84636	GPR174	G protein-coupled receptor 174	-0.26	CAGAAGGGTGATTCTAATATT	NM_032553:	NM_032553:
84636	GPR174	G protein-coupled receptor 174	0.74	GAGCATTACGATCCACGATTA	NM_032553:	NM_032553:
131601	GPR175	G protein-coupled receptor 175	-1.34	CAAGATCCTCTTCTCCTACAA	NM_016372:	NM_016372:
131601	GPR175	G protein-coupled receptor 175	0.27	TCGGAGGAGCTTCTACGTGTA	NM_016372:	NM_016372:
11245	GPR176	G protein-coupled receptor 176	-0.04	CAGCCTCGCCATGGGACATAA	NM_007223:	NM_007223:
11245	GPR176	G protein-coupled receptor 176	0.01	CAGGTACTACTCAGTCCTCTA	NM_007223:	NM_007223:
440435	GPR179	G protein-coupled receptor 179	-0.35	CACCATCATACTCAAGCTTTA	NM_001004334:	NM_001004334:
440435	GPR179	G protein-coupled receptor 179	0.71	ACAGAAGAATTCACTACTGAA	NM_001004334:	NM_001004334:
2841	GPR18 (G prc	G protein-coupled receptor 18	-4.98	CTGGTAGTCTACGGTCACTAA	NM_005292:	NM_005292:
2841	GPR18 (G prc	G protein-coupled receptor 18	-2.47	TACGGTCACTAAGCAATATAA	NM_005292:	NM_005292:
2842	GPR19 (G prc	G protein-coupled receptor 19	-1.57	CATGTCCTCTATGAAATGTTA	NM_006143:	NM_006143:

2842	GPR19 (G pro	G protein-coupled receptor 19	-5.11	CCGGTTCTACACCATCGTCTA	NM_006143:	NM_006143:
2843	GPR20 (G pro	G protein-coupled receptor 20	-0.14	CACGCGCTTCGCTGTGTACTA	NM_005293:	NM_005293:
2843	GPR20 (G pro	G protein-coupled receptor 20	0.88	CTCAGTCATCTACACCATCAA	NM_005293:	NM_005293:
2844	GPR21 (G pro	G protein-coupled receptor 21	0.43	CACCCTGTTCATCGTGATGAT	NM_005294:	NM_005294:
2844	GPR21 (G pro	G protein-coupled receptor 21	0.96	CTGTTTCGAATCACTAGTGTA	NM_005294:	NM_005294:
2845	GPR22	G protein-coupled receptor 22	-9.42	AAGTGTCTCAACAGCAATCAA	NM_005295:	NM_005295:
2845	GPR22	G protein-coupled receptor 22	1.69	CAGGCTCTTAATATTCGAATA	NM_005295:	NM_005295:
2846	GPR23	G protein-coupled receptor 23	1.40	AGGAAGTGAGTGATCAAACAA	NM_005296:	NM_005296:
2846	GPR23	G protein-coupled receptor 23	0.59	GGGCCTATAAATATAGAACAA	NM_005296:	NM_005296:
2848	GPR25 (G pro	G protein-coupled receptor 25	0.94	CCGGAGGAACTCGCTGCGCAT	NM_005298:	NM_005298:
2848	GPR25 (G pro	G protein-coupled receptor 25	0.73	CTGCGCCAACCCGCTCATCTA	NM_005298:	NM_005298:
2849	GPR26	G protein-coupled receptor 26	-1.82	CTAGGTTTCAATTGTCTTGTA	NM_153442:	NM_153442:
2849	GPR26	G protein-coupled receptor 26	-1.07	CTGAGTTTAATGAGGATATTA	NM_153442:	NM_153442:
2850	GPR27	G protein-coupled receptor 27	-1.39	CCGCCTGCTCTTCTTCATCCA	NM_018971:	NM_018971:
2850	GPR27	G protein-coupled receptor 27	0.84	GAGGCTGTGCAAGATGTTCTA	NM_018971:	NM_018971:
2827	GPR3	G protein-coupled receptor 3	-0.28	AGCCATCACCTGAGCAACCAA	NM_005281:	NM_005281:
2827	GPR3	G protein-coupled receptor 3	-0.86	TACGTTTGAATTTCTGAGCTA	NM_005281:	NM_005281:
2852	GPR30	G protein-coupled receptor 30	0.91	CGGCCACGTCATGTCTCTAAA	NM_001505:	NM_001505:
2852	GPR30	G protein-coupled receptor 30	-0.65	CTGGATGAGCTTCGACCGCTA	NM_001505:	NM_001031682:NM_001505:
2853	GPR31 (G pro	G protein-coupled receptor 31	-2.42	CCCGGGCTTGCTCATCTCTGA	NM_005299:	NM_005299:
2853	GPR31 (G pro	G protein-coupled receptor 31	0.04	TGGCCTCATCGTGTTCTGCAA	NM_005299:	NM_005299:
2854	GPR32 (G pro	G protein-coupled receptor 32	0.56	CACCTTTGTGTTCCTCAGCTA	NM_001506:	NM_001506:
2854	GPR32 (G pro	G protein-coupled receptor 32	0.82	TTGGCAGAGATTTCCAAGAAA	NM_001506:	NM_001506:
2857	GPR34 (G pro	G protein-coupled receptor 34	-0.19	TCAGGCGAACCTGAACTTTAA	NM_005300:	NM_005300:
2857	GPR34 (G pro	G protein-coupled receptor 34	1.40	TGCGACTATTACCAAATAGAA	NM_005300:	NM_005300:
2859	GPR35 (G pro	G protein-coupled receptor 35	-0.47	CCGGCACAATTTCAACTCCAT	NM_005301:	NM_005301:
2859	GPR35 (G pro	G protein-coupled receptor 35	-0.95	CGCCCTGTACATAACCAGCAA	NM_005301:	NM_005301:
2861	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	0.07	CACCAACGTACAGATGTACTA	NM_005302:	NM_005302:
2861	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	-0.04	CGGCAGAAAGGTGCATTATTA	NM_005302:	NM_005302:
9283	GPR37L1	G protein-coupled receptor 37 like 1	1.16	GCCCTTCTTGAGAAACAATAA	NM_004767:	NM_004767:
9283	GPR37L1	G protein-coupled receptor 37 like 1	-1.03	TAGGAGGCCCTTCTTGAGAAA	NM_004767:	NM_004767:
2863	GPR39 (G pro	G protein-coupled receptor 39	-0.84	CGGCATGCCCATGGAGTTCTA	NM_001508:	NM_001508:
2863	GPR39 (G pro	G protein-coupled receptor 39	-0.53	CGGGCAGTGACTGCTCCCAAA	NM_001508:	NM_001508:
2828	GPR4 (G prot	G protein-coupled receptor 4	-0.05	CACAGGGCTCACCATACACAA	NM_005282:	NM_005282:
2828	GPR4 (G prot	G protein-coupled receptor 4	-2.07	CAGCCGATATAGAGTCATTAT	NM_005282:	NM_005282:
11251	GPR44	G protein-coupled receptor 44	0.04	CGGGCGCATTATGTGCTACTA	NM_004778:	NM_004778:
11251	GPR44	G protein-coupled receptor 44	-1.21	CTCGAGGGACTTAAGATGCTA	NM_004778:	NM_004778:
11250	GPR45	G protein-coupled receptor 45	0.74	CAGCGTGGACTTGAGCTTCAA	NM_007227:	NM_007227:
11250	GPR45	G protein-coupled receptor 45	-0.68	TGGGAACTGCAACGTCATTAA	NM_007227:	NM_007227:
9248	GPR50	G protein-coupled receptor 50	0.60	ACGGATCTTCAGTGTGCGCAA	NM_004224:	NM_004224:
9248	GPR50	G protein-coupled receptor 50	-0.61	CTGGCTTTATCTTGCAGCCTA	NM_004224:	NM_004224:
9293	GPR52	G protein-coupled receptor 52	-0.28	AACCTGGCTTGCAGTAAGTAA	NM_005684:	NM_005684:
9293	GPR52	G protein-coupled receptor 52	-0.67	CAGGTGTCCACGAGTCATTAA	NM_005684:	NM_005684:
9290	GPR55 (G pro	G protein-coupled receptor 55	1.51	CCGGTTCTTGGCCATCCGTTA	NM_005683:	NM_005683:
9290	GPR55 (G pro	G protein-coupled receptor 55	-0.10	CTGAGAGGACCTGATCATGTA	NM_005683:	NM_005683:
9289	GPR56	G protein-coupled receptor 56	1.27	GAGGGTCTGGCACATCCTTAA	NM_005682:	NM_201524:NM_201525:NM_005682:
9289	GPR56	G protein-coupled receptor 56	0.10	TCGGCCGCCCATCATGGTTAA	NM_005682:	NM_201524:NM_201525:NM_005682:
2830	GPR6 (G prot	G protein-coupled receptor 6	-0.05	ACGAATAAACCCATTACAAGA	NM_005284:	NM_005284:
2830	GPR6 (G prot	G protein-coupled receptor 6	0.66	CTGCTTAATTATAGCACTTTA	NM_005284:	NM_005284:
83873	GPR61	G protein-coupled receptor 61	1.17	CCCATTTAAGCAGCTAATAAA	NM_031936:	NM_031936:
83873	GPR61	G protein-coupled receptor 61	0.93	GTGGGATAGTCTCCCATTTAA	NM_031936:	NM_031936:
118442	GPR62	G protein-coupled receptor 62	-3.00	CCCTAAGGGCTCACAACCAAA	NM_080865:	NM_080865:
118442	GPR62	G protein-coupled receptor 62	-0.12	CTGGACCAGTTTGGTATTAGA	NM_080865:	NM_080865:
81491	GPR63	G protein-coupled receptor 63	-0.19	ACCCTTCCTGGTAATACTGTA	NM_030784:	NM_030784:
81491	GPR63	G protein-coupled receptor 63	0.02	CTCATTTATGGGCATACTCAA	NM_030784:	NM_030784:
10149	GPR64	G protein-coupled receptor 64	0.04	CCCAGTAGTCAGATTATAGAA	NM_005756:	NM_005756:
10149	GPR64	G protein-coupled receptor 64	-0.14	CCGGAGGGATTACCCTTCCAA	NM_005756:	NM_005756:
8477	GPR65	G protein-coupled receptor 65	1.98	AGCGAACTTACACAATGTATA	NM_003608:	NM_003608:
8477	GPR65	G protein-coupled receptor 65	-0.27	CGGTTGCATTAACAAGTTTAA	NM_003608:	NM_003608:
8111	GPR68	G protein-coupled receptor 68	-2.94	CAGCGTGGTCATCTGGGCCAA	NM_003485:	NM_003485:
8111	GPR68	G protein-coupled receptor 68	0.03	CCGCGTGTGCTTTGAGCACTA	NM_003485:	NM_003485:
10936	GPR75	G protein-coupled receptor 75	0.58	ATGGACTTTATTCTAACTTGA	NM_006794:	NM_006794:
10936	GPR75	G protein-coupled receptor 75	-0.02	CCAGCTCGTATCAGCCATCAA	NM_006794:	NM_006794:
27202	GPR77	G protein-coupled receptor 77	-0.48	CACGTGCTGGACAAATCTTAA	NM_018485:	NM_018485:
27202	GPR77	G protein-coupled receptor 77	-9.45	CAGCAAGAAATCCACCAGCCA	NM_018485:	NM_018485:
27201	GPR78 (G pro	G protein-coupled receptor 78	-1.15	CACGAGGAGAGAAGAAGGAAA	NM_080819:	NM_080819:
27201	GPR78 (G pro	G protein-coupled receptor 78	0.01	CAGGAAGATTGGCATTGCTAT	NM_080819:	NM_080819:
27198	GPR81	G protein-coupled receptor 81	1.93	AGGGTCATTAGTCAACTCTTA	NM_032554:	NM_032554:
27198	GPR81	G protein-coupled receptor 81	0.75	TGGGATCTATTGATCTATCAA	NM_032554:	NM_032554:
27197	GPR82 (G pro	G protein-coupled receptor 82	0.54	ATGCCTTTCATGAGTATCTAT	NM_080817:	NM_080817:
27197	GPR82 (G pro	G protein-coupled receptor 82	-0.01	CATGGCTTTACCAATCATTTA	NM_080817:	NM_080817:
10888	GPR83	G protein-coupled receptor 83	1.22	TACGCTCGTGTGGCCAAGAAA	NM_016540:	NM_016540:
10888	GPR83	G protein-coupled receptor 83	-1.17	TTCGCTGTGTTGTCTAAATAA	NM_016540:	NM_016540:
53831	GPR84	G protein-coupled receptor 84	1.30	CCCAAGGAGTATTATTAATTA	NM_020370:	NM_020370:
53831	GPR84	G protein-coupled receptor 84	0.01	TCCATTATAGAAAGAATTGAA	NM_020370:	NM_020370:
54329	GPR85	G protein-coupled receptor 85	-0.41	AAGCACAAACTAGGAAGACTA	NM_018970:	NM_018970:
54329	GPR85	G protein-coupled receptor 85	-0.05	CAAGGGAACCTTACTGTGTTA	NM_018970:	NM_018970:
53836	GPR87	G protein-coupled receptor 87	-0.38	CCGGTGCTTTATCTCATTATA	NM_023915:	NM_023915:
53836	GPR87	G protein-coupled receptor 87	-1.10	TCGGAAGTTCGCATATATTAT	NM_023915:	NM_023915:
54112	GPR88	G protein-coupled receptor 88	-3.31	ACCAGTATGAGTTGCCATTAA	NM_022049:	NM_022049:
54112	GPR88	G protein-coupled receptor 88	0.23	TACCACGACATTTAACATCAA	NM_022049:	NM_022049:
51463	GPR89A	G protein-coupled receptor 89A	-0.67	ATGGATATGATCATAAGCAAA	NM_016334:	NM_016334:
51463	GPR89A	G protein-coupled receptor 89A	-2.09	ACGGAGAACAATGTTCCAGAA	NM_016334:	NM_016334:
57121	GPR92	G protein-coupled receptor 92	0.72	ACCCGCTGGTGTACTACTTTA	NM_020400:	NM_020400:
57121	GPR92	G protein-coupled receptor 92	-9.57	CCGGAGGTGAATGCCATGCCA	NM_020400:	NM_020400:
222487	GPR97	G protein-coupled receptor 97	-0.90	AAGGTTTGACGCAGAAGGTGA	NM_170776:	NM_170776:
222487	GPR97	G protein-coupled receptor 97	-1.05	CAACATGTACGACATCTTCAA	NM_170776:	NM_170776:
9737	GPRASP1	G protein-coupled receptor associated sorting protein 1	0.22	ACGCCCTAAGAGTAAGGCCAA	NM_014710:	NM_014710:
9737	GPRASP1	G protein-coupled receptor associated sorting protein 1	-0.47	CTAGCAGTAAATCCAGACCAA	NM_014710:	NM_014710:
114928	GPRASP2	G protein-coupled receptor associated sorting protein 2	1.14	CTGGATCAGTTACTAAATCTA	NM_001004051:	NM_138437:NM_001004051:
114928	GPRASP2	G protein-coupled receptor associated sorting protein 2	0.96	ACCCTGCTATTCGTTGTTTAA	NM_001004051:	NM_138437:NM_001004051:
9052	GPRC5A	G protein-coupled receptor, family C, group 5, member A	0.16	CAACTCAAGTTTAGACCCTTA	NM_003979:	NM_003979:
9052	GPRC5A	G protein-coupled receptor, family C, group 5, member A	-0.83	CAGGATGTTATCGCTATTGAA	NM_003979:	NM_003979:
51704	GPRC5B	G protein-coupled receptor, family C, group 5, member B	0.52	CTCGCCCTGTTCCTACACTTA	NM_016235:	NM_016235:
51704	GPRC5B	G protein-coupled receptor, family C, group 5, member B	0.96	TCCGTTTAGAAGCAACGTGTA	NM_016235:	NM_016235:
55890	GPRC5C	G protein-coupled receptor, family C, group 5, member C	0.04	GAGCATGTTCGTGGAGAACAA	NM_018653:	NM_022036:NM_018653:
55890	GPRC5C	G protein-coupled receptor, family C, group 5, member C	0.00	GTGGATCGTCATGTATACTTA	NM_018653:	NM_022036:NM_018653:
55507	GPRC5D	G protein-coupled receptor, family C, group 5, member D	-0.12	CAGAGGTATGATGTTTGTGAA	NM_018654:	NM_018654:
55507	GPRC5D	G protein-coupled receptor, family C, group 5, member D	0.76	TAGCATTAACTTCATATGGTA	NM_018654:	NM_018654:

222545	GPRC6A	G protein-coupled receptor, family C, group 6, member A	-1.25	CAGAATCAATCGGACACTGAA	NM_148963:	NM_148963:
222545	GPRC6A	G protein-coupled receptor, family C, group 6, member A	0.45	CCGGGACATATCATAATTGGA	NM_148963:	NM_148963:
2873	GPS1	G protein pathway suppressor 1	-0.19	AACCTTTAACGTGGACATGTA	NM_004127:	NM_004127:NM_212492:
2873	GPS1	G protein pathway suppressor 1	-0.35	CAGCCTGGATCTGGAACAGTA	NM_004127:	NM_004127:NM_212492:
29899	GPSM2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0.68	CACCAACTCATTAATATACTA	NM_013296:	NM_013296:
29899	GPSM2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	-0.86	TAGGAAATCATGATCAAGCAA	NM_013296:	NM_013296:
2875	GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	-1.28	CCCACTGTACTTGCTCTTGAT	NM_005309:	NM_005309:
2875	GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	-0.52	CCGGGAGGACGTGGCGCGGTA	NM_005309:	NM_005309:
2876	GPX1	glutathione peroxidase 1	0.06	AACACCTTGATCTTACAGAAA	Y00433:	NM_000581:NM_201397:
2876	GPX1	glutathione peroxidase 1	-0.25	GAGGAACACCTTGATCTTACA	Y00433:	NM_000581:NM_201397:
2877	GPX2	glutathione peroxidase 2 (gastrointestinal)	-1.92	CACCATGGCTTTCATTGCCAA	NM_002083:	NM_002083:
2877	GPX2	glutathione peroxidase 2 (gastrointestinal)	-0.50	AACCCTCTGGTTGGTGATTCA	NM_002083:	NM_002083:
2878	GPX3 (glutat	glutathione peroxidase 3 (plasma)	-3.33	CTGCTCTAACTGATACCTCAA	NM_002084:	NM_002084:
2878	GPX3 (glutat	glutathione peroxidase 3 (plasma)	1.16	TTCACTTATACCTAAACCCAA	NM_002084:	NM_002084:
2879	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	-0.06	AGGGAGTAACGAAGAGATCAA	NM_002085:	NM_002085:
2879	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	0.01	GTGGATGAAGATCCAACCCAA	NM_002085:	NM_002085:
2880	GPX5 (glutat	glutathione peroxidase 5 (epididymal androgen-related protein)	-2.24	CAGCGCAATATCCTGAACTAA	NM_001509:	NM_001509:
2880	GPX5 (glutat	glutathione peroxidase 5 (epididymal androgen-related protein)	0.40	TCGCACTTAATAAGAATGAAT	NM_001509:	NM_001509:NM_003996:
257202	GPX6 (glutat	glutathione peroxidase 6 (olfactory)	1.32	CCCGAGAAGTTGTGACATCTA	NM_182701:	NM_182701:
257202	GPX6 (glutat	glutathione peroxidase 6 (olfactory)	1.02	CAGACTATCCTGTGTCCCTAA	NM_182701:	NM_182701:
2882	GPX7	glutathione peroxidase 7	2.26	CAAACAATACCTCACGATATA	NM_015696:	NM_015696:
2882	GPX7	glutathione peroxidase 7	0.86	TGGCAAATAGAAGTATATCAA	NM_015696:	NM_015696:
9402	GRAP2	GRB2-related adaptor protein 2	-0.32	AGGCATGAGGATGACGTTCAA	NM_004810:	NM_004810:
9402	GRAP2	GRB2-related adaptor protein 2	1.66	CACAGTTAATGGATCTGTAAA	NM_004810:	NM_004810:
160622	GRASP (GR	GRP1 (general receptor for phosphoinositides 1)-associated scaffold	0.24	AAACTCTATATGGGACATCAA	NM_181711:	NM_181711:
160622	GRASP (GR	GRP1 (general receptor for phosphoinositides 1)-associated scaffold	-3.30	GTGCATATTGTTGCTTCTGAA	NM_181711:	NM_181711:
2887	GRB10	growth factor receptor-bound protein 10	0.48	CTACCGTATAGTAACACTGTA	NM_005311:	NM_005311:NM_001001549:NM_001001550:NM_001001555:
2887	GRB10	growth factor receptor-bound protein 10	-0.77	CTAGATGACGGGAACACCAAA	NM_005311:	NM_005311:NM_001001549:NM_001001550:NM_001001555:
2885	GRB2	growth factor receptor-bound protein 2	1.03	AGGCTTTAAGCTCCAGCTTTA	NM_002086:	NM_002086:NM_203506:
2885	GRB2	growth factor receptor-bound protein 2	-0.49	CCCGTGAACCGGAACGTCTAA	NM_002086:	NM_002086:NM_203506:
2886	GRB7 (growt	growth factor receptor-bound protein 7	-0.93	CACACTGGTATATCCCATGAA	NM_005310:	NM_005310:NM_001030002:
2886	GRB7 (growt	growth factor receptor-bound protein 7	-0.52	CCCAACAAGCTTCGAAATGGA	NM_005310:	NM_001030002:NM_005310:
9380	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	-0.12	CACATTGGTGTTGGACACATT	NM_012203:	NM_012203:
9380	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	-0.56	AAGGTGTGATTCTCTGAGGAA	NM_012203:	NM_012203:
2890	GRIA1	glutamate receptor, ionotropic, AMPA 1	-2.62	CACCATGAAGGTGGGAGGTAA	NM_000827:	NM_000827:
2890	GRIA1	glutamate receptor, ionotropic, AMPA 1	1.95	CAGCATCCGAAAGATTGGTTA	NM_000827:	NM_000827:
2891	GRIA2	glutamate receptor, ionotropic, AMPA 2	-2.52	ACGAATGAAGGTGGCAAAGAA	NM_000826:	NM_000826:
2891	GRIA2	glutamate receptor, ionotropic, AMPA 2	1.29	TCCGTATGTTATGATGAAGAA	NM_000826:	NM_000826:
2892	GRIA3	glutamate receptor, ionotrophic, AMPA 3	0.79	CAGAATTATGCTACATACAGA	NM_000828:	NM_007325:NM_000828:
2892	GRIA3	glutamate receptor, ionotrophic, AMPA 3	1.18	ATGGACGTAGGACAAATTATA	NM_000828:	NM_007325:NM_000828:
2893	GRIA4	glutamate receptor, ionotrophic, AMPA 4	0.08	CGCCCAAGGGTTCCTCATTAA	NM_000829:	NM_000829:
2893	GRIA4	glutamate receptor, ionotrophic, AMPA 4	-0.28	CACGATGAAAGTGGGAGGAAA	NM_000829:	NM_000829:
2894	GRID1	glutamate receptor, ionotropic, delta 1	1.82	TTGGATTAAAGTTGTTTAATA	XM_043613:	NM_017551:
2894	GRID1	glutamate receptor, ionotropic, delta 1	-0.06	CTCCAAGGATTGACTCTTAAA	XM_043613:	NM_017551:
2895	GRID2	glutamate receptor, ionotropic, delta 2	1.51	CTGGCAGAAATTCATTATATT	NM_001510:	NM_001510:
2895	GRID2	glutamate receptor, ionotropic, delta 2	-0.04	CACGATTACAAATGGGATCAA	NM_001510:	NM_001510:
2897	GRIK1	glutamate receptor, ionotropic, kainate 1	1.30	ACGGATTTAGAATGTGGTAAA	NM_000830:	NM_000830:
2897	GRIK1	glutamate receptor, ionotropic, kainate 1	1.13	TGGGCATATCACCTTTAATAA	NM_000830:	NM_175611:NM_000830:
2898	GRIK2	glutamate receptor, ionotropic, kainate 2	0.42	TGCCAGGAGATGGAATATCAA	NM_021956:	NM_021956:NM_175768:
2898	GRIK2	glutamate receptor, ionotropic, kainate 2	1.58	CGCTTTATGAGTCTAATTAAA	NM_021956:	NM_021956:NM_175768:
2899	GRIK3	glutamate receptor, ionotropic, kainate 3	0.85	CCAGTGGTTCCTAATCCTCTA	NM_000831:	NM_000831:
2899	GRIK3	glutamate receptor, ionotropic, kainate 3	-4.20	CAGCGTCTTCTCCTTCCTCAA	NM_000831:	NM_000831:
2900	GRIK4	glutamate receptor, ionotropic, kainate 4	0.14	CAGGGTGTTGAATTCCAACTA	NM_014619:	NM_014619:
2900	GRIK4	glutamate receptor, ionotropic, kainate 4	0.84	CGCGTTCATATGGGACGCAAA	NM_014619:	NM_014619:
2901	GRIK5	glutamate receptor, ionotropic, kainate 5	-5.78	CCGCGAGATGCGCCTCAGCAA	NM_002088:	NM_002088:
2901	GRIK5	glutamate receptor, ionotropic, kainate 5	0.45	GAGGAGGACCATCGAGCTAAA	NM_002088:	NM_002088:
2902	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	-1.29	CACGCTGGACTCGTTCATGCA	NM_000832:	NM_007327:NM_021569:NM_000832:
2902	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	-0.40	CAAGGAGGAGTTCACAGTCAA	NM_000832:	NM_007327:NM_021569:NM_000832:
2903	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	0.04	AGGGTTGTATAGTATCTGTTA	NM_000833:	NM_000833:
2903	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	-0.16	CACAGTGGCCATTGTAGTTTA	NM_000833:	NM_000833:
2904	GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	-7.71	CGGCGGGTACATGCTCAGCAA	NM_000834:	NM_000834:
2904	GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	-0.59	CCGACGGGAGTCATCCGTCTA	NM_000834:	NM_000834:
2905	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	-1.12	CTGGACGAGATCAGCAGGGTA	NM_000835:	NM_000835:
2905	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	-0.59	CACCCACATGGTCAAGTTCAA	NM_000835:	NM_000835:
2906	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	0.26	GAGGATTTGGTCCCTCAACTA	NM_000836:	NM_000836:
2906	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	-0.68	CCGCTACTGGTCGGTCGACAA	NM_000836:	NM_000836:
116443	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	-0.25	CACCCAGGGAATAACAACTTA	NM_133445:	NM_133445:
116443	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	-0.51	ACCGACGGAAATACATCTTTA	NM_133445:	NM_133445:
116444	GRIN3B	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	-3.75	CAGCGCCGAGGCGTACATCAA	XM_290850:	NM_138690:
116444	GRIN3B	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	0.49	TACACATGTCTCGGCACTTTA	XM_290850:	NM_138690:
2907	GRINA	glutamate receptor, ionotropic, N-methyl D-asparate-associated protei	-1.62	CCGGGAGAATGTCTGGACCTA	NM_000837:	NM_000837:NM_001009184:
2907	GRINA	glutamate receptor, ionotropic, N-methyl D-asparate-associated protei	-2.27	CTGGACCTACTATGTCTCCTA	NM_000837:	NM_000837:NM_001009184:
23426	GRIP1	glutamate receptor interacting protein 1	1.93	CACGATGAGTTTGAATCATGA	XM_290559:	XM_290559:
23426	GRIP1	glutamate receptor interacting protein 1	1.42	CTGGTTATTAGTAGAAACCCA	XM_290559:	XM_290559:
80852	GRIP2 (glutar	glutamate receptor interacting protein 2	-1.62	CCCACACATGTTGGATGTTAA	XM_042936:	XM_042936:
80852	GRIP2 (glutar	glutamate receptor interacting protein 2	-0.55	TAGGGTGGTCTTCTATTCTAA	XM_042936:	XM_042936:
56850	GRIPAP1	GRIP1 associated protein 1	0.21	GAGGACCTTATGGGACAGAAA	NM_020137:	NM_207672:NM_020137:
56850	GRIPAP1	GRIP1 associated protein 1	-1.65	CCGGAAGAGCGCCATCATTGA	NM_020137:	NM_020137:
6011	GRK1	G protein-coupled receptor kinase 1	-0.06	CCAGATGAAGGCGACCGGCAA	NM_002929:	NM_002929:
6011	GRK1	G protein-coupled receptor kinase 1	-1.14	CTGGAAAGACATCGAGGACTA	NM_002929:	NM_002929:
2868	GRK4	G protein-coupled receptor kinase 4	0.24	CAGGATGTTACTCACCAAGAA	NM_182982:	NM_001004056:NM_001004057:NM_182982:
2868	GRK4	G protein-coupled receptor kinase 4	0.14	CCGGGTGTTTCAAAGACATCA	NM_182982:	NM_001004056:NM_182982:
2869	GRK5	G protein-coupled receptor kinase 5	0.49	AGCGTCATAACTAGAACTGAA	NM_005308:	NM_005308:
2869	GRK5	G protein-coupled receptor kinase 5	0.37	CAGGAACAACGCGGTAGGCAA	NM_005308:	NM_005308:
2909	GRLF1	glucocorticoid receptor DNA binding factor 1	-0.88	CAGCCTAAGGAGGAACACTAA	NM_004491:	NM_024342:NM_004491:
2909	GRLF1	glucocorticoid receptor DNA binding factor 1	-0.57	CAGGATGTTCTGGGAGAGGAA	NM_004491:	NM_024342:NM_004491:
2911	GRM1	glutamate receptor, metabotropic 1	-5.29	CCAGATTAAGGTTATACGGAA	NM_000838:	NM_000838:
2911	GRM1	glutamate receptor, metabotropic 1	0.27	CCGCCTCTCTGTGCACGTGAA	NM_000838:	NM_000838:
2912	GRM2	glutamate receptor, metabotropic 2	-6.26	CACCATCGAGCTGGCCTCCTA	NM_000839:	NM_000839:
2912	GRM2	glutamate receptor, metabotropic 2	-1.82	CTACAAGGACTTTGTGCTCAA	NM_000839:	NM_000839:
2913	GRM3	glutamate receptor, metabotropic 3	-1.39	GTCCTTGTTGTAACTAATTTA	NM_000840:	NM_000840:
2913	GRM3	glutamate receptor, metabotropic 3	1.79	TACGGTGGCAATATTATGTAA	NM_000840:	NM_000840:
2914	GRM4	glutamate receptor, metabotropic 4	-2.02	ACCAAGAACATTTCTAATAAA	NM_000841:	NM_000841:
2914	GRM4	glutamate receptor, metabotropic 4	-1.02	TAAGTACATCCGAAACGTCAA	NM_000841:	NM_000841:
2915	GRM5	glutamate receptor, metabotropic 5	-0.81	CGCCATCTATTCGATGGCCTA	NM_000842:	NM_000842:
2915	GRM5	glutamate receptor, metabotropic 5	-0.82	TACGATCCTATTCGATGAGAA	NM_000842:	NM_000842:
2916	GRM6	glutamate receptor, metabotropic 6	0.89	AGCGTGATTGACTATGAGGAA	NM_000843:	NM_000843:

2916	GRM6	glutamate receptor, metabotropic 6	0.60	TTCCATGTTTACACAATTAAA	NM_000843:	NM_000843:
2917	GRM7	glutamate receptor, metabotropic 7	-0.47	CCCAGATTAGTTATGCATCAA	NM_000844:	NM_181875:NM_181874:NM_000844:
2917	GRM7	glutamate receptor, metabotropic 7	-0.62	TCGGATTTATCGCATATTTGA	NM_000844:	NM_181875:NM_181874:NM_000844:
2918	GRM8	glutamate receptor, metabotropic 8	-0.53	CAGGAGTATGCCCATTCCATA	NM_000845:	NM_000845:
2918	GRM8	glutamate receptor, metabotropic 8	0.80	TTGGTTATATTCGGGCTGTAA	NM_000845:	NM_000845:
2896	GRN	granulin	-0.37	AAGGACACTTCTGCCATGATA	NM_002087:	NM_002087:
2896	GRN	granulin	-4.50	CCAGAGTAAGTGCCTCTCCAA	NM_002087:	NM_001012479:NM_002087:
2925	GRPR (gastri	gastrin-releasing peptide receptor	0.39	ACCATAGTTAGTATATATGTA	NM_005314:	NM_005314:
2925	GRPR (gastri	gastrin-releasing peptide receptor	0.63	CAAGATCTTCTGTACAGTCAA	NM_005314:	NM_005314:
83903	GSG2 (germ	germ cell associated 2 (haspin)	2.66	CAGTCTGTTTAAGTAAGCTAA	NM_031965:	NM_031965:
83903	GSG2 (germ	germ cell associated 2 (haspin)	-0.03	ACAGTCTGTTTAAGTAAGCTA	NM_031965:	NM_031965:
2931	GSK3A	glycogen synthase kinase 3 alpha	-0.20	CAGGGAACTAGTCGCCATCAA	NM_019884:	NM_019884:
2931	GSK3A	glycogen synthase kinase 3 alpha	0.39	CCGGGTGTAAATAGATTGTTA	NM_019884:	NM_019884:
2932	GSK3B (glyc	glycogen synthase kinase 3 beta	0.33	AACACTGGTCACGTTTGGAAA	NM_002093:	NM_002093:
2932	GSK3B (glyc	glycogen synthase kinase 3 beta	0.00	CACTCAAGAACTGTCAAGTAA	NM_002093:	NM_002093:
2934	GSN	gelsolin (amyloidosis, Finnish type)	0.83	AACGATGCCTTTGTTCTGAAA	NM_000177:	NM_198252:NM_000177:
2934	GSN	gelsolin (amyloidosis, Finnish type)	-1.29	CAGCTACATCATTCTGTACAA	NM_000177:	NM_198252:NM_000177:
2936	GSR	glutathione reductase	-1.80	ATGGTCTGTGCTAACAAGGAA	NM_000637:	NM_000637:
2936	GSR	glutathione reductase	0.68	CGGCATGATAAGGTACTTAGA	NM_000637:	NM_000637:
2937	GSS	glutathione synthetase	1.26	GAGGGTGGAGGTAACAACCTA	NM_000178:	NM_000178:
2937	GSS	glutathione synthetase	0.32	TCCGACGAACATTTGAAGATA	NM_000178:	NM_000178:
2938	GSTA1	glutathione S-transferase A1	1.07	TTGCAACAATAAAGTACTTTA	M25627:	NM_145740:
2938	GSTA1	glutathione S-transferase A1	0.64	TTGCAATACCAATGTTCTAAA	M25627:	NM_145740:
2944	GSTM1	glutathione S-transferase M1	1.26	CTGCTACAATCCAGAATTTGA	X08020:	NM_000561:NM_146421:
2944	GSTM1	glutathione S-transferase M1	0.11	TCCAGAATTTGAGAAACTGAA	X08020:	NM_000561:NM_146421:
9446	GSTO1	glutathione S-transferase omega 1	2.33	CAGCAATAAAGCTATGTCTGA	NM_004832:	NM_004832:
9446	GSTO1	glutathione S-transferase omega 1	2.25	CAGGAGTCAGCAATAAAGCTA	NM_004832:	NM_004832:
2950	GSTP1	glutathione S-transferase pi	-2.56	CCAGATCTCCTTCGCTGACTA	NM_000852:	NM_000852:
2950	GSTP1	glutathione S-transferase pi	-0.46	TCCTTTCTCCAGGACCAATAA	NM_000852:	NM_000852:
2954	GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	0.43	CGCGCTGAAATTTGGCGTGAA	NM_001513:	NM_001513:NM_145870:NM_145871:
2954	GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	-3.27	ACGGTGCCCATCAATCTCATA	NM_001513:	NM_001513:NM_145870:NM_145871:
2959	GTF2B	general transcription factor IIB	-0.84	ACGTCAAATTCTTGAATACAA	NM_001514:	NM_001514:
2959	GTF2B	general transcription factor IIB	0.00	TTGACGAATTTGGCAATTCTA	NM_001514:	NM_001514:
2962	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	-0.30	CCGGGTCGGACCAGATCGGAA	NM_002096:	NM_002096:
2962	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	0.14	CGCAAGATGATCAACGACAAA	NM_002096:	NM_002096:
2965	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	-2.16	ATGGCACAGGGTAGACCTTAA	NM_005316:	NM_005316:
2965	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	0.27	CCCAGAGCTGATGCTATTGTA	NM_005316:	NM_005316:
2966	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa	0.91	CAAGATTTAAAGCCTAATAGA	NM_001515:	NM_001515:
2966	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa	0.62	TAGACTGACGTGTACTTTAAA	NM_001515:	NM_001515:
2967	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	-0.56	TAGCAGATTCTTTGTTGGGAA	NM_001516:	NM_001516:
2967	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	0.25	TGGAGTAATGGCATTAATCAA	NM_001516:	NM_001516:
2968	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	-1.62	AGCCCACCCAGTGATGCTCAA	BC004935:	NM_001517:
2968	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	1.01	TAATAAAGTTATGATAGCTAA	BC004935:	NM_001517:
9569	GTF2IRD1	GTF2I repeat domain containing 1	-0.11	AAGGAACTCTTCAACGAGAAA	NM_005685:	NM_005685:NM_016328:
9569	GTF2IRD1	GTF2I repeat domain containing 1	0.05	CCGGAAGGAGCTACAGTCAGA	NM_005685:	NM_005685:NM_016328:
23560	GTPBP4	GTP binding protein 4	-0.05	CTGGGAAGATTTACTGGTGTA	NM_012341:	NM_012341:
23560	GTPBP4	GTP binding protein 4	0.77	AACGAAAGACTCCAACCGTTA	NM_012341:	NM_012341:
51512	GTSE1	G-2 and S-phase expressed 1	-0.44	CAAGTTCTAAGCCGAACCAAA	NM_016426:	NM_016426:
51512	GTSE1	G-2 and S-phase expressed 1	0.53	TTCGGACCCTTTGGACATAAA	NM_016426:	NM_016426:
2978	GUCA1A	guanylate cyclase activator 1A (retina)	-1.27	CACCGATACAGTGTTCTCCAA	NM_000409:	NM_000409:
2978	GUCA1A	guanylate cyclase activator 1A (retina)	-1.53	CCAGGCCATTCGCGCCATTAA	NM_000409:	NM_000409:
2979	GUCA1B	guanylate cyclase activator 1B (retina)	0.95	CAACATTGTGGAGGGAATTTA	NM_002098:	NM_002098:
2979	GUCA1B	guanylate cyclase activator 1B (retina)	-1.45	CAAGCTGAAGTGGACATTCAA	NM_002098:	NM_002098:
2981	GUCA2B	guanylate cyclase activator 2B (uroguanylin)	0.31	CCAGCTGGAATCCATGAAGAA	NM_007102:	NM_007102:
2981	GUCA2B	guanylate cyclase activator 2B (uroguanylin)	-0.90	CTGAATAAAGATTCTACAACA	NM_007102:	NM_007102:
2977	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	0.65	CCCGTTTGTGATTAGAACCAA	NM_000855:	NM_000855:
2977	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	0.62	CAGGCAATTGTAGCTGTCTTA	NM_000855:	NM_000855:
2982	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-0.78	CAGGAATAGATTAGCAACCTA	NM_000856:	NM_000856:
2982	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-0.07	TCCAGTGGAGTTATCAAAGAA	NM_000856:	NM_000856:
2974	GUCY1B2	guanylate cyclase 1, soluble, beta 2	-1.14	CCGATGTTCAGAGGCATCCAA	NM_004129:	NM_004129:
2974	GUCY1B2	guanylate cyclase 1, soluble, beta 2	-2.94	CAGTGTGCACGCAGTCTATAA	NM_004129:	NM_004129:
2983	GUCY1B3	guanylate cyclase 1, soluble, beta 3	-1.12	ACCTAACATGGTGATCTGCAA	NM_000857:	NM_000857:
2983	GUCY1B3	guanylate cyclase 1, soluble, beta 3	0.98	CAAGACTTTCTTCTAGATATA	NM_000857:	NM_000857:
2984	GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	-0.38	CTCAAGATCGATGATGACAAA	NM_004963:	NM_004963:
2984	GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	0.28	CCAGGAATCTATCACCAACAA	NM_004963:	NM_004963:
3000	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	0.33	CCGGGCCAGTTCTCTTGAGAA	NM_000180:	NM_000180:
3000	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	-0.19	CTGGACCTTATCAAGGGAATA	NM_000180:	NM_000180:
2986	GUCY2F	guanylate cyclase 2F, retinal	-2.25	AAGGCAGTTGGTGAGAAACAA	NM_001522:	NM_001522:
2986	GUCY2F	guanylate cyclase 2F, retinal	0.69	ACCGTTGTTTGGAACCATCTA	NM_001522:	NM_001522:
2987	GUK1	guanylate kinase 1	0.11	CAGGGCTGACATCCTAATAAA	NM_000858:	NM_000858:
2987	GUK1	guanylate kinase 1	0.13	CCCGGCGAGGAGAACGGCAAA	NM_000858:	NM_000858:
51454	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.59	ACCCAGTTACTGCTCAGTTTA	NM_016315:	NM_016315:
51454	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.02	CTCCAGTACCTAGTAGATCTA	NM_016315:	NM_016315:
2990	GUSB	glucuronidase, beta	-2.99	AACACTAAAGGTGGAAATAAA	NM_000181:	NM_000181:
2990	GUSB	glucuronidase, beta	-2.28	CAGAGCGAGTATGGAGCAGAA	NM_000181:	NM_000181:
2995	GYPC	glycophorin C (Gerbich blood group)	0.87	CAGCAGAAAGGAGTACTTTAT	NM_016815:	NM_016815:NM_002101:
2995	GYPC	glycophorin C (Gerbich blood group)	-0.79	CAGGAATGTGGTCGACGAGAA	NM_016815:	NM_016815:NM_002101:
3001	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine es	-0.15	ACACGCGAAGGTGACCTTAAA	NM_006144:	NM_006144:
3001	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine es	-0.15	ACCCTGTGATTGGAATGAATA	NM_006144:	NM_006144:
3002	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine es	0.37	CTGGAGCCAAGTCCAGATTTA	NM_004131:	NM_004131:
3002	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine es	0.12	TACGCCATTATTACGACAGTA	NM_004131:	NM_004131:
2999	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	-0.53	CAGGGTTGCAGGACTGTAATA	NM_033423:	NM_033423:
2999	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	0.92	CTGGATAAAGAGAACAATGAA	NM_033423:	NM_033423:
3003	GZMK	granzyme K (granzyme 3; tryptase II)	0.84	TTCACTTGTATCACTGATGTA	NM_002104:	NM_002104:
3003	GZMK	granzyme K (granzyme 3; tryptase II)	0.29	TTAGAGTTGGGTGTAAGTAAA	NM_002104:	NM_002104:
3004	GZMM	granzyme M (lymphocyte met-ase 1)	0.43	CCAATAAATCATAATGAAGAA	NM_005317:	NM_005317:
3004	GZMM	granzyme M (lymphocyte met-ase 1)	0.16	CAGGGAGGGACCAATAAATCA	NM_005317:	NM_005317:
3005	H1F0	H1 histone family, member 0	0.15	ACCAGTGAAACCCAAAGCAAA	NM_005318:	NM_005318:
3005	H1F0	H1 histone family, member 0	0.71	CAAGAAGGTAGCCACGCCAAA	NM_005318:	NM_005318:
94239	H2AFV	H2A histone family, member V	-0.79	ACCATCCTAAGTGAAGACTTA	NM_012412:	NM_138635:
94239	H2AFV	H2A histone family, member V	0.03	ACCATGGTATATTGACTCTTA	NM_012412:	NM_201436:NM_201516:NM_012412:NM_201517:
3014	H2AFX	H2A histone family, member X	-0.15	CACGACTAGAACCTTAGGCAT	NM_002105:	NM_002105:
3014	H2AFX	H2A histone family, member X	-0.11	TGCCTCCTAGGAGGACATTTA	NM_002105:	NM_002105:
3015	H2AFZ	H2A histone family, member Z	0.36	AAGGTCATATCCCAAACTAAA	NM_002106:	NM_002106:
3015	H2AFZ	H2A histone family, member Z	1.26	CTCAGGACTCTAAATACTCTA	NM_002106:	NM_002106:
113457	H2-ALPHA	alpha-tubulin isotype H2-alpha	1.42	TCCAAGTTGTTTGCAATTAAA	XM_054284:	NM_080386:
113457	H2-ALPHA	alpha-tubulin isotype H2-alpha	0.89	TTCCAAGTTGTTTGCAATTAA	XM_054284:	NM_080386:
3026	HABP2	hyaluronan binding protein 2	-0.18	CCCAATTGTACCTTCTAGAAA	NM_004132:	NM_004132:

3026	HABP2	hyaluronan binding protein 2	0.75	CCGGCATAAGCGGAGATCCAA	NM_004132:	NM_004132:
57531	HACE1 (HEC	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligas	-1.53	TACGCTATATTGTATGAATTA	NM_020771:	NM_020771:
57531	HACE1 (HEC	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligas	-0.07	AGGGCTGATGCTTCCAATTTA	NM_020771:	NM_020771:
3028	HADH2	hydroxyacyl-Coenzyme A dehydrogenase, type II	-0.90	TCGCCCTCTGTGCCTAATAAA	NM_004493:	NM_004493:NM_001037811:
3028	HADH2	hydroxyacyl-Coenzyme A dehydrogenase, type II	-2.06	CTGGGTGACCCTGCTGAGTAT	NM_004493:	NM_004493:NM_001037811:
3030	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thic	-2.46	CACGGTGTACCGGGATATTAA	NM_000182:	NM_000182:
3030	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thic	0.93	AAGGGCTTCCTAGGTCGTAAA	NM_000182:	NM_000182:
3029	HAGH	hydroxyacylglutathione hydrolase	-0.86	ACAAGTATTTATTCCCATAAA	NM_005326:	NM_005326:
3029	HAGH	hydroxyacylglutathione hydrolase	-0.98	ATCGGACATTCTAATGCATAT	NM_005326:	NM_005326:
3034	HAL	histidine ammonia-lyase	1.15	ATGCCTTAATATGCCTTCATA	NM_002108:	NM_002108:
3034	HAL	histidine ammonia-lyase	1.20	CCAGTTGACTTTCTTTGGCTA	NM_002108:	NM_002108:
9421	HAND1	heart and neural crest derivatives expressed 1	0.68	ACGCCGTCTTCTCTAATTAAA	NM_004821:	NM_004821:
9421	HAND1	heart and neural crest derivatives expressed 1	0.31	GACGCCGTCTTCTCTAATTAA	NM_004821:	NM_004821:
9464	HAND2	heart and neural crest derivatives expressed 2	-0.35	CCGGCGTGGGCGAATTCAGAA	NM_021973:	NM_021973:
9464	HAND2	heart and neural crest derivatives expressed 2	0.22	CCGGTTTATTTATGTGCAATT	NM_021973:	NM_021973:
3036	HAS1	hyaluronan synthase 1	-0.14	CTCGTTCTTATTTAATCTCCA	NM_001523:	NM_001523:
3036	HAS1	hyaluronan synthase 1	-0.02	CACGTACGTGTGGGACGGCAA	NM_001523:	NM_001523:
3037	HAS2	hyaluronan synthase 2	0.11	AACGCAATTGGTCTTGTCCAA	NM_005328:	NM_005328:
3037	HAS2	hyaluronan synthase 2	-2.26	CAGCTCGATCTAAGTGCCTTA	NM_005328:	NM_005328:
8520	HAT1 (histon	histone acetyltransferase 1	0.76	TACCGGCGTGTTATTGAACGA	NM_003642:	NM_003642:NM_001033085:
8520	HAT1 (histon	histone acetyltransferase 1	1.39	CCCTTCTTAAACAGTATAATA	NM_003642:	NM_003642:NM_001033085:
26762	HAVCR1	hepatitis A virus cellular receptor 1	-0.35	CACCATTGTACTCTTACACAA	NM_012206:	NM_012206:
26762	HAVCR1	hepatitis A virus cellular receptor 1	1.65	GGCCTTTGGAATAACAATCAA	NM_012206:	NM_012206:
84868	HAVCR2	hepatitis A virus cellular receptor 2	-1.22	TTGACAGAGAGTGGTCCCTAA	NM_032782:	NM_032782:
84868	HAVCR2	hepatitis A virus cellular receptor 2	-0.05	CTGATATAAATCTAACACAAA	NM_032782:	NM_032782:
1839	HBEGF	heparin-binding EGF-like growth factor	0.92	GCCTCTTAAATTATATATTTA	NM_001945:	NM_001945:
1839	HBEGF	heparin-binding EGF-like growth factor	-0.16	CTCCAGGATCTTTGACTGAAA	NM_001945:	NM_001945:
51773	HBXAP	hepatitis B virus x associated protein	-4.08	ACGCACAAAGATTGAGTCCAA	NM_016578:	NM_016578:
51773	HBXAP	hepatitis B virus x associated protein	-5.09	CACCGAGTCGTGTACCATGAA	NM_016578:	NM_016578:
64151	HCAP-G	chromosome condensation protein G	-0.08	ATGGTGGTCTATAAACGTGAA	NM_022346:	NM_022346:
64151	HCAP-G	chromosome condensation protein G	-0.30	TAGGTCAACAATTGATTCTAA	NM_022346:	NM_022346:
54985	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	0.31	CAAGAAGAACTGAATAAAGAT	NM_001002017:	NM_001002017:NM_017885:NM_001002018:
54985	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	-1.95	AACAGAGGACACTGAGCCCAA	NM_001002017:	NM_001002017:NM_017885:NM_001002018:
285834	HCG22	HLA complex group 22	0.11	CCCGAGCGAAGGTACGGAATA	XM_496804:	XM_496804:
285834	HCG22	HLA complex group 22	-3.84	AAGTCTGATCAAATCAATAAA	XM_496804:	XM_496804:
3055	HCK	hemopoietic cell kinase	0.40	AACGACGGGCTCTGCCAGAAA	NM_002110:	NM_002110:
3055	HCK	hemopoietic cell kinase	0.17	CGGGAGCACATCAGAGGCTTA	NM_002110:	NM_002110:
348980	HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel	-0.42	CCGACTAGATCGAATAGGAAA	NM_021072:	NM_021072:
348980	HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel	-4.18	CACGGTGTTGCTGGTGTCATT	NM_021072:	NM_021072:
610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel	-0.47	AACGACAGCATTGGCGCCAAA	NM_001194:	NM_001194:
610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel	-1.14	CGGGAAGAAGATGTACTTCAT	NM_001194:	NM_001194:
610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel	0.46	CGGCATTGTGATCGAGGACAA	XM_370845:	NM_001194:XM_370845:XM_370849:
610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel	-0.29	CCGCCAGAAGATCCACGACTA	XM_370845:	NM_001194:XM_370845:XM_370849:
57657	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel	-4.49	CCCGCCTTGGATCGTCTTCAA	NM_020897:	NM_020897:
57657	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel	-1.72	CAGCTTTCTGCCAACATGTAA	NM_020897:	NM_020897:
10021	HCN4 (hyperp	hyperpolarization activated cyclic nucleotide-gated potassium channel	0.38	TAGCAAGATCTGTATATGAAT	NM_005477:	NM_005477:
10021	HCN4 (hyperp	hyperpolarization activated cyclic nucleotide-gated potassium channel	-1.41	AACCAGGTATTCTTAGAGCTA	NM_005477:	NM_005477:
3060	HCRT	hypocretin (orexin) neuropeptide precursor	0.92	CGGCATCCTCACGCTGGGCAA	NM_001524:	NM_001524:
3060	HCRT	hypocretin (orexin) neuropeptide precursor	-0.07	CTGCCCGACTGCTGTCGTCAA	NM_001524:	NM_001524:
3061	HCRTR1	hypocretin (orexin) receptor 1	-0.62	ACGGCTCTTCTCAGTCTGTGA	NM_001525:	NM_001525:
3061	HCRTR1	hypocretin (orexin) receptor 1	0.00	TTGCTTCTTTATTGTCACCTA	NM_001525:	NM_001525:
3062	HCRTR2	hypocretin (orexin) receptor 2	-0.28	ACCGACTATGACGACGAGGAA	NM_001526:	NM_001526:
3062	HCRTR2	hypocretin (orexin) receptor 2	0.85	CCGGTGCAACATCGCCTGTAA	NM_001526:	NM_001526:
10870	HCST	hematopoietic cell signal transducer	-2.02	CCCGCCCAAGAAGATGGCAAA	NM_014266:	NM_014266:
10870	HCST	hematopoietic cell signal transducer	-0.24	CAGCAGGGTGACATCCGCTAT	NM_014266:	NM_014266:NM_001007469:
3064	HD	huntingtin (Huntington disease)	-0.56	CAGGGTAGAATTGTTTGGCAA	NM_002111:	NM_002111:
3064	HD	huntingtin (Huntington disease)	-0.15	CAGGTGTTTATTGGCTTTGTA	NM_002111:	NM_002111:
3065	HDAC1	histone deacetylase 1	-0.04	CACCCGGAGGAAAGTCTGTTA	NM_004964:	NM_004964:
3065	HDAC1	histone deacetylase 1	0.48	CCCGTTCTTAACTTTGAACCA	NM_004964:	NM_004964:
83933	HDAC10	histone deacetylase 10	0.07	CAGGTGAACAGTGGTATAGCA	NM_032019:	NM_032019:
83933	HDAC10	histone deacetylase 10	-0.86	CGCCCTTGCGCCGTTAGTAAA	NM_032019:	NM_032019:
79885	HDAC11	histone deacetylase 11	-2.03	CCCAGACAGGAGGAACCATAA	NM_024827:	NM_024827:
79885	HDAC11	histone deacetylase 11	-0.54	TAAGGTGGAGAGGAACATCAA	NM_024827:	NM_024827:
3066	HDAC2	histone deacetylase 2	-0.16	ACGGTCAATAAGACCAGATAA	NM_001527:	NM_001527:
3066	HDAC2	histone deacetylase 2	-0.59	CTGGGTTGTTTCAATCTAACA	NM_001527:	NM_001527:
8841	HDAC3	histone deacetylase 3	0.31	GACCATGACAATGACAAGGAA	NM_003883:	NM_003883:
8841	HDAC3	histone deacetylase 3	0.38	CAGGTAGTGGACTTCTACCAA	NM_003883:	NM_003883:
9759	HDAC4	histone deacetylase 4	0.52	ACGGTTTATTCTGATTGAGAA	NM_006037:	NM_006037:
9759	HDAC4	histone deacetylase 4	1.26	CCGGCATGACTTTATATTGTA	NM_006037:	NM_006037:
10014	HDAC5	histone deacetylase 5	-0.07	GCCGGGTTTGATGCTGTTGAA	NM_005474:	NM_001015053:NM_005474:
10014	HDAC5	histone deacetylase 5	0.02	CCGGCAGAAGCTAGACAGCAA	NM_005474:	NM_001015053:NM_005474:
10013	HDAC6	histone deacetylase 6	-1.12	CACCGTCAACGTGGCATGGAA	NM_006044:	NM_006044:
10013	HDAC6	histone deacetylase 6	0.68	CACTTCGAAGCGAAATATTAA	NM_006044:	NM_006044:
51564	HDAC7A	histone deacetylase 7A	-2.11	AAGGCTGGAAACAGAAACCCA	NM_015401:	NM_016596:NM_015401:
51564	HDAC7A	histone deacetylase 7A	0.92	CAGCAAGATCCTCATTGTAGA	NM_015401:	NM_016596:NM_015401:
55869	HDAC8	histone deacetylase 8	-0.52	AGGGACGGTACTACAGTGTAA	NM_018486:	NM_018486:
55869	HDAC8	histone deacetylase 8	-0.54	ACGGAATGTGCAAAGTAGCAA	NM_018486:	NM_018486:
9734	HDAC9	histone deacetylase 9	0.40	CCGAATATGAATGCTGTTATT	NM_058176:	NM_178423:NM_178425:NM_058176:
9734	HDAC9	histone deacetylase 9	0.59	CAGCAACGCATTCTAATTCAT	NM_058176:	NM_178423:NM_178425:NM_014707:NM_058176: NM_058177:
3067	HDC (histidin	histidine decarboxylase	1.04	CAGCTTGTGACATGATATATA	NM_002112:	NM_002112:
3067	HDC (histidin	histidine decarboxylase	-0.37	CCACAATAGGATACAAACGAA	NM_002112:	NM_002112:
25831	HECTD1	HECT domain containing 1	-0.78	ATGCCATACTATGAAGATCAA	NM_015382:	NM_015382:
25831	HECTD1	HECT domain containing 1	-1.35	CAGACTGGTGTGAACAATTAA	NM_015382:	NM_015382:
143279	HECTD2	HECT domain containing 2	-0.59	TTGAATCATGTACAAGACTTA	NM_182765:	NM_182765:
143279	HECTD2	HECT domain containing 2	1.06	ATGCACATTGGCAGTAAACTA	NM_182765:	NM_182765:
79654	HECTD3	HECT domain containing 3	0.33	CCCGAGGTATTTCACCTCTTA	NM_024602:	NM_024602:
79654	HECTD3	HECT domain containing 3	0.01	TCGGGACATGTATGTACCCAA	NM_024602:	NM_024602:
57520	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	-3.05	CAGGATTGGTGCGCCTTTCAA	XM_038999:	NM_020760:
57520	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	-1.33	AAGGCTCTTCTCAGAATTCTA	XM_038999:	NM_020760:
57493	HEG1	HEG homolog 1 (zebrafish)	-3.88	AACCTTCGTGACAGAGTTTAA	XM_087386:	XM_087386:
57493	HEG1	HEG homolog 1 (zebrafish)	-0.22	CAAGAGAAAGTCATTACAGAA	XM_087386:	XM_087386:
51409	HEMK1	HemK methyltransferase family member 1	0.18	ATCCACGTTCATTTAACTGAA	NM_016173:	NM_016173:
51409	HEMK1	HemK methyltransferase family member 1	-3.69	CAGGGATTGATTAGTCCTCCA	NM_016173:	NM_016173:
29104	HEMK2	HemK methyltransferase family member 2	1.50	CAAGTAAATATGTGTATTATA	NM_013240:	NM_182749:NM_013240:
29104	HEMK2	HemK methyltransferase family member 2	1.14	TTCTATTTAGTTACCATTAAA	NM_013240:	NM_182749:NM_013240:
9843	HEPH	hephaestin	0.30	AGGGAGTACCTTATTATCCTA	NM_014799:	NM_138737:NM_014799:
9843	HEPH	hephaestin	-2.93	CAGGGATGAGGGCAATCTATA	NM_014799:	NM_138737:NM_014799:
8925	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain a	-0.05	CGCAATCACAATCGACCGCAA	NM_003922:	NM_003922:

8925	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain a	1.71	TCCGAACGCTAGTTCGATTAA	NM_003922:	NM_003922:
8916	HERC3	hect domain and RLD 3	1.33	AAGATTTAAGGACGTTCTTTA	NM_014606:	NM_014606:
8916	HERC3	hect domain and RLD 3	-1.72	CCCATTGGCTCTCTACAAGAA	NM_014606:	NM_014606:
26091	HERC4	hect domain and RLD 4	0.45	GAGGGAATTATTGGATCCTAA	NM_015601:	NM_015601:NM_022079:NM_001017972:
26091	HERC4	hect domain and RLD 4	0.02	TAGAAATACTACATAGGGTAA	NM_015601:	NM_015601:NM_022079:NM_001017972:
51191	HERC5	hect domain and RLD 5	-1.28	TGGAAGTAGCATAACTGTCAA	NM_016323:	NM_016323:
51191	HERC5	hect domain and RLD 5	0.88	GAGGAGAATGGTAATGTTCAA	NM_016323:	NM_016323:
55008	HERC6	hect domain and RLD 6	0.96	TTCGTGGATGTTCAAGTCAAA	NM_017912:	NM_001013005:NM_001013002:NM_001013000:NM_017912:
55008	HERC6	hect domain and RLD 6	0.08	AAGATGCTCTGCGTCAATTAA	NM_017912:	NM_001013005:NM_001013002:NM_001013000:NM_017912:
9709	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiqu	0.98	TACACTAAGTGTACTACTTTA	NM_014685:	NM_001010990:NM_001010989:NM_014685:
9709	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiqu	-0.79	CCCAACAATAACTTACAGGAA	NM_014685:	NM_001010990:NM_001010989:NM_014685:
3280	HES1	hairy and enhancer of split 1, (Drosophila)	1.03	ACCATGCACTATATTTGTATA	NM_005524:	NM_005524:
3280	HES1	hairy and enhancer of split 1, (Drosophila)	-0.25	AAAGACGAAGAGCAAGAATAA	NM_005524:	NM_005524:
57801	HES4 (hairy a	hairy and enhancer of split 4 (Drosophila)	0.50	AAACGTATTTATTATTCCAAA	NM_021170:	NM_021170:
57801	HES4 (hairy a	hairy and enhancer of split 4 (Drosophila)	-0.23	CTCCAAGCCGGTCATGGAGAA	NM_021170:	NM_021170:
388585	HES5 (hairy a	hairy and enhancer of split 5 (Drosophila)	1.34	CACGCAGATGAAGCTGCTGTA	XM_371215:	NM_001010926:
388585	HES5 (hairy a	hairy and enhancer of split 5 (Drosophila)	-0.02	CAGCAGCATCGAGCAGCTGAA	XM_371215:	NM_001010926:
55502	HES6 (hairy a	hairy and enhancer of split 6 (Drosophila)	-1.36	TTGGAGTTAGTTACCCTTGAA	NM_018645:	NM_018645:
55502	HES6 (hairy a	hairy and enhancer of split 6 (Drosophila)	0.74	TTCCATTGACATCAAATGTGA	NM_018645:	NM_018645:
8820	HESX1	homeobox, ES cell expressed 1	-0.83	CAGGGAAAGATGGTAACTTAT	NM_003865:	NM_003865:
8820	HESX1	homeobox, ES cell expressed 1	1.58	CAGGAAGATCCCAGCCCTATA	NM_003865:	NM_003865:
3073	HEXA	hexosaminidase A (alpha polypeptide)	0.24	AAGGATTTCTACGTAGTGGAA	NM_000520:	NM_000520:
3073	HEXA	hexosaminidase A (alpha polypeptide)	0.07	GAGGTGTTTGATAATAAAGTA	NM_000520:	NM_000520:
3074	HEXB	hexosaminidase B (beta polypeptide)	-0.62	CCGGGCACAATAGTTGAAGTA	NM_000521:	NM_000521:
3074	HEXB	hexosaminidase B (beta polypeptide)	0.74	TGGATATTATTGCAACCATAA	NM_000521:	NM_000521:
23462	HEY1	hairy/enhancer-of-split related with YRPW motif 1	1.41	CAGATTAAGGTGTTGTATAAA	NM_012258:	NM_012258:
23462	HEY1	hairy/enhancer-of-split related with YRPW motif 1	0.74	TCACCTTAAAGTCGTCAGTAA	NM_012258:	NM_012258:
23493	HEY2	hairy/enhancer-of-split related with YRPW motif 2	2.86	AAGAGTCTTTACATACCACTA	NM_012259:	NM_012259:
23493	HEY2	hairy/enhancer-of-split related with YRPW motif 2	2.39	TCGATTTCGTTTAATGACAAA	NM_012259:	NM_012259:
26508	HEYL (hairy/e	hairy/enhancer-of-split related with YRPW motif-like	-0.15	ATGGGTTGTTGCGGACATCCA	NM_014571:	NM_014571:
26508	HEYL (hairy/e	hairy/enhancer-of-split related with YRPW motif-like	-1.16	CTGGGATATTGTGGAAGGAAA	NM_014571:	NM_014571:
3077	HFE	hemochromatosis	1.19	TAGTATTATTGTTGCATTAAA	NM_000410:	NM_139002:NM_000410:
3077	HFE	hemochromatosis	-0.42	ACGTGGCTAGTCATAACCTTA	NM_000410:	NM_139004:NM_000410:
3081	HGD	homogentisate 1,2-dioxygenase (homogentisate oxidase)	0.35	ACCCTACAAGTACAACCTGAA	NM_000187:	NM_000187:
3081	HGD	homogentisate 1,2-dioxygenase (homogentisate oxidase)	-0.06	CGGGAATTATACACCCTACAA	NM_000187:	NM_000187:
3082	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	-0.61	AAGGTGATACCACACCTACAA	NM_000601:	NM_001010932:NM_000601:
3082	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	0.67	TGGGAGTACTGTGCAATTAAA	NM_000601:	NM_001010931:NM_001010933:NM_001010932:NM_000601:
3083	HGFAC	HGF activator	-1.79	CACCCTGTACTCGGTGTTCAA	NM_001528:	NM_001528:
3083	HGFAC	HGF activator	-0.01	CCCTGCCTTGCTGACAATAAA	NM_001528:	NM_001528:
9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	-0.37	CCGGAACGAGCCCAAGTACAA	NM_004712:	NM_004712:
9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	0.23	GCACGTCTTTCCAGAATTCAA	NM_004712:	NM_004712:
3087	HHEX	homeobox, hematopoietically expressed	1.68	ATCTGTTTATCTCCCACTTAA	NM_002729:	NM_002729:
3087	HHEX	homeobox, hematopoietically expressed	-1.05	CCCGCGGACGGTGAACGACTA	NM_002729:	NM_002729:
10086	HHLA1	HERV-H LTR-associating 1	-0.41	CTCCAGCTAGATCATCAGTTA	NM_005712:	NM_005712:
10086	HHLA1	HERV-H LTR-associating 1	1.00	AAGCATGTTAATGTTACCATT	NM_005712:	NM_005712:
55662	HIF1AN	hypoxia-inducible factor 1, alpha subunit inhibitor	0.44	AACACATAGGCTTGCGTCTTA	NM_017902:	NM_017902:
55662	HIF1AN	hypoxia-inducible factor 1, alpha subunit inhibitor	-4.15	CAAGCTCAAGCCATACATAAA	NM_017902:	NM_017902:
64344	HIF3A	hypoxia inducible factor 3, alpha subunit	-0.26	ACCAATCTCTATACACCATAA	NM_022462:	NM_022462:
64344	HIF3A	hypoxia inducible factor 3, alpha subunit	-0.64	CGGGCGCACCCTCAACCTCAA	NM_022462:	NM_022462:NM_152796:NM_152795:NM_152794:
3092	HIP1	huntingtin interacting protein 1	-2.97	ATGGCTTAGGATCGACAAGAA	NM_005338:	NM_005338:
3092	HIP1	huntingtin interacting protein 1	-3.66	CACAACAATGGGTATCCTTAA	NM_005338:	NM_005338:
3093	HIP2	huntingtin interacting protein 2	0.73	CAGGCAGTTCTATATATAGAA	NM_005339:	NM_005339:
3093	HIP2	huntingtin interacting protein 2	1.03	CCGCACGGTATTATTGTCATT	NM_005339:	NM_005339:
204851	HIPK1	homeodomain interacting protein kinase 1	-1.50	AGGGAAGCTGTACACCACTAA	NM_152696:	NM_152696:NM_198268:NM_198269:NM_181358:
204851	HIPK1	homeodomain interacting protein kinase 1	-3.52	CTGAGCTATGTTTGTAATGCA	NM_152696:	NM_198268:NM_198269:NM_181358:
28996	HIPK2	homeodomain interacting protein kinase 2	0.61	AACCAGTACCCTTACATATAA	NM_022740:	NM_022740:
28996	HIPK2	homeodomain interacting protein kinase 2	-0.38	TCCCGAAGTCTCCATACTAAA	NM_022740:	NM_022740:
10114	HIPK3	homeodomain interacting protein kinase 3	0.91	CACGTTTGGCCAGGTAGTTAA	NM_005734:	NM_005734:
10114	HIPK3	homeodomain interacting protein kinase 3	-0.42	CTCATTCTGGTTGGAGATTAA	NM_005734:	NM_005734:
147746	HIPK4	homeodomain interacting protein kinase 4	-5.98	CAGAAAGATAGTTATCCAGAA	NM_144685:	NM_144685:
147746	HIPK4	homeodomain interacting protein kinase 4	-0.58	CACAAATTATTCTTACAGAAA	NM_144685:	NM_144685:
8348	HIST1H2BO	histone 1, H2bo	-0.21	CTCCAAGAAAGCCGTAACCAA	NM_003527:	NM_003527:
3098	HK1	hexokinase 1	0.26	CACGATGTAGTCACCTTACTA	NM_000188:	NM_033496:NM_033497:NM_033498:NM_033500:NM_000188:
3098	HK1	hexokinase 1	0.00	CCGTGTCGTATGACCTAGTAA	NM_000188:	NM_033496:NM_033497:NM_033498:NM_033500:NM_000188:
3099	HK2	hexokinase 2	0.28	CCGGCCGTGCTACAATAGGTA	NM_000189:	NM_000189:
3099	HK2	hexokinase 2	0.88	CGGCCGTGCTACAATAGGTAA	NM_000189:	NM_000189:
3101	HK3	hexokinase 3 (white cell)	0.71	CACTCAGGTTAGCAATATATA	NM_002115:	NM_002115:
3101	HK3	hexokinase 3 (white cell)	0.72	CCGGAATGCGATGTCTCCTTA	NM_002115:	NM_002115:
80201	HKDC1	hexokinase domain containing 1	0.08	AAGGATTGTTAGGTATAGGAA	NM_025130:	NM_025130:
80201	HKDC1	hexokinase domain containing 1	-3.54	CTCGATGTGATGTGACATTCA	NM_025130:	NM_025130:
284459	HKR1 (GLI-Kr	GLI-Kruppel family member HKR1	-0.98	AAGGTTTCGGCAGAAGCCTAA	NM_181786:	NM_181786:
284459	HKR1 (GLI-Kr	GLI-Kruppel family member HKR1	-1.75	AGGCTTTACTTGGAAGTCGAA	NM_181786:	NM_181786:
342945	HKR2	GLI-Kruppel family member HKR2	0.57	CAGGGTATAAGTATGCTGAGA	NM_181846:	NM_181846:
342945	HKR2	GLI-Kruppel family member HKR2	1.60	TAACCTAAAGCTTATCTGTAA	NM_181846:	NM_181846:
3104	HKR3	GLI-Kruppel family member HKR3	-3.92	CCGCCCTTTGTGGGAAACTGA	XM_290331:	NM_005341:
3110	HLXB9	homeobox HB9	-0.08	ATCGCCCACGATGGAATGTAA	NM_005515:	NM_005515:
3110	HLXB9	homeobox HB9	1.51	TGCATGCTAAATTATTATTTA	NM_005515:	NM_005515:
3145	HMBS	hydroxymethylbilane synthase	-3.57	CAGCTTAACGATGCCCATTAA	NM_000190:	NM_000190:NM_001024382:
3145	HMBS	hydroxymethylbilane synthase	-0.24	CTCTCTAAGATTGGAGAGAAA	NM_000190:	NM_000190:NM_001024382:
83872	HMCN1	hemicentin 1	-0.96	CCGAGTATATGTTCCGCCAAA	NM_031935:	NM_031935:
83872	HMCN1	hemicentin 1	1.16	TAGACTCTAAGCAATTGCCAA	NM_031935:	NM_031935:
10362	HMG20B	high-mobility group 20B	-0.28	CAGCATCCCTTTAGCTTTCAA	NM_006339:	NM_006339:
10362	HMG20B	high-mobility group 20B	-1.05	TCGGCGCTTGCGGAAGATGAA	NM_006339:	NM_006339:
3159	HMGA1	high mobility group AT-hook 1	-2.97	CACCACAACTCCAGGAAGGAA	NM_002131:	NM_002131:NM_145901:NM_145902:NM_145899:NM_145903:NM_145904:NM_145905:
3159	HMGA1	high mobility group AT-hook 1	-5.54	CTGGACAAGGCTAACATCCCA	NM_002131:	NM_002131:NM_145901:NM_145902:NM_145899:NM_145903:NM_145904:NM_145905:
8091	HMGA2	high mobility group AT-hook 2	0.41	ACCTCTGAATGTTACAACGAA	NM_003483:	NM_001015886:NM_003483:
8091	HMGA2	high mobility group AT-hook 2	-0.61	TAGGAAGAACGCGGTGTGTAA	NM_003483:	NM_001015886:NM_003483:
3146	HMGB1	high-mobility group box 1	1.29	TAAACTAATAATTGCAGTAAA	NM_002128:	NM_002128:
3146	HMGB1	high-mobility group box 1	1.42	AAGAGTAATCAATCTACTCAA	NM_002128:	NM_002128:
3148	HMGB2	high-mobility group box 2	-0.54	GAGGATTGCGTTAGAGATAAA	NM_002129:	NM_002129:

3148	HMGB2	high-mobility group box 2	0.06	TCGCTATGACAGGGAGATGAA	NM_002129:	NM_002129:
3155	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylgl	0.75	ATGGAAATGAGAATAGGTTAA	NM_000191:	NM_000191:
3155	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylgl	0.60	CATGGAAATGAGAATAGGTTA	NM_000191:	NM_000191:
3156	HMGCR (3-hy	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	-0.85	CCGAGCCTAATGAAAGGGAAA	NM_000859:	NM_000859:
3156	HMGCR (3-hy	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	1.10	GAGCTTGTTGTGAGAATGTTA	NM_000859:	NM_000859:
3157	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	0.55	CTGATGTAGATTAATAATGTA	NM_002130:	NM_002130:
3157	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	-5.04	CAGGGCATTATTAGGCTATTT	NM_002130:	NM_002130:
3158	HMGCS2 (3-h	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	1.30	CTGTCATGTGTTAGAACTTTA	NM_005518:	NM_005518:
3158	HMGCS2 (3-h	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	0.87	TAGCTGGTAAATGAATTTGAA	NM_005518:	NM_005518:
3151	HMGN2	high-mobility group nucleosomal binding domain 2	0.00	GAGCCCGAGCAGTGTGAAGAA	NM_005517:	NM_005517:
3151	HMGN2	high-mobility group nucleosomal binding domain 2	0.02	TGGATACAGTTTGGCTTGGAA	NM_005517:	XM_498948:NM_005517:
9324	HMGN3	high mobility group nucleosomal binding domain 3	-4.49	AAGCAGGAAGCTGGAAAGGAA	NM_138730:	NM_004242:NM_138730:
9324	HMGN3	high mobility group nucleosomal binding domain 3	-0.58	CTGCTGACTATTTGTGGTTTA	NM_138730:	NM_004242:NM_138730:
3161	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.76	CAGAAGAATTTGAGAATTCTA	NM_012484:	NM_012484:NM_012485:
3161	HMMR	hyaluronan-mediated motility receptor (RHAMM)	-1.32	CTGGATGAGCTTGATAAATTA	NM_012484:	NM_012484:NM_012485:
3162	HMOX1	heme oxygenase (decycling) 1	-4.28	CAGGCAATGGCCTAAACTTCA	NM_002133:	NM_002133:
3162	HMOX1	heme oxygenase (decycling) 1	-0.02	CGGGCCAGCAACAAAGTGCAA	NM_002133:	NM_002133:
51617	HMP19	HMP19 protein	1.03	CTGGGAGAATTGGTTATTTGA	NM_015980:	NM_015980:
51617	HMP19	HMP19 protein	-4.05	CCGAGTCAGGCTCATGTACAA	NM_015980:	NM_015980:
3172	HNF4A	hepatocyte nuclear factor 4, alpha	-0.99	AACCTAGAGATTGTTACAGAA	NM_000457:	NM_000457:NM_178849:
3172	HNF4A	hepatocyte nuclear factor 4, alpha	0.06	CACGTGGTCACGGCAAAGGAA	NM_000457:	NM_000457:NM_178849:
3174	HNF4G	hepatocyte nuclear factor 4, gamma	0.16	ACCCTGTAATTTATTCGTGTA	NM_004133:	NM_004133:
3174	HNF4G	hepatocyte nuclear factor 4, gamma	-4.62	CACCGGATGGATTCTGATGAA	NM_004133:	NM_004133:
3176	HNMT	histamine N-methyltransferase	1.09	CAACATAACATAAGCTAGAAA	NM_006895:	NM_006895:
3176	HNMT	histamine N-methyltransferase	1.80	TGCAGGCTCAACATAACATAA	NM_006895:	NM_006895:
3181	HNRPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	0.56	ATGGATTGGATTATTTAATAA	NM_002137:	NM_002137:NM_031243:
3181	HNRPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	2.55	TTGGATTATTTAATAACATTA	NM_002137:	NM_002137:NM_031243:
3184	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA bin	-0.44	AGCCATTAAGATTTATATGAA	NM_002138:	NM_002138:NM_031369:NM_031370:NM_001003810:
3184	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA bin	3.07	CACAATGTTGGTCTTAGTAAA	NM_002138:	NM_002138:NM_031369:NM_031370:NM_001003810:
4670	HNRPM	heterogeneous nuclear ribonucleoprotein M	-4.14	CCGGATGATGAATGGCATGAA	NM_005968:	NM_031203:NM_005968:
4670	HNRPM	heterogeneous nuclear ribonucleoprotein M	-1.15	CCCGCAGGAATGGGAATGGAA	NM_005968:	NM_031203:NM_005968:
3192	HNRPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factc	-0.25	AGGATATTATTGAATACCCAA	NM_004501:	NM_031844:NM_004501:
3192	HNRPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factc	-1.27	CTGGCCGTGGTAGTTACTCAA	NM_004501:	NM_031844:NM_004501:
11100	HNRPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	-0.53	AAGACCGAACAATAAAGCGAA	NM_007040:	NM_144732:NM_144733:NM_007040:
11100	HNRPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	0.32	CCCGCAAGAAACGCAACTATA	NM_007040:	NM_144732:NM_144733:NM_007040:
221092	HNRPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	-0.83	ACGGGCGAGATTATGAGTACA	XM_495877:	XM_495877:
221092	HNRPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	1.39	ACCCAGAATCTCCCAATGAAA	XM_495877:	XM_495877:
9456	HOMER1	homer homolog 1 (Drosophila)	-0.74	AAGCTACTAGAATGCAGCTAA	NM_004272:	NM_004272:
9456	HOMER1	homer homolog 1 (Drosophila)	0.15	ATCAATCACATCTTGATTCAA	NM_004272:	NM_004272:
9455	HOMER2	homer homolog 2 (Drosophila)	0.56	ACCGAATATGACCTTCACCAA	NM_004839:	NM_004839:NM_199330:NM_199331:NM_199332:
9455	HOMER2	homer homolog 2 (Drosophila)	-4.84	CAGAACTAGGTCTACCTTCAA	NM_004839:	NM_004839:NM_199330:NM_199331:NM_199332:
9454	HOMER3	homer homolog 3 (Drosophila)	-0.83	AGGCGCCAAGGCCATCATCAA	NM_004838:	NM_004838:
9454	HOMER3	homer homolog 3 (Drosophila)	-5.45	CAGCTGGAAGCTCTGGTGCAA	NM_004838:	NM_004838:
25900	HOM-TES-10	HOM-TES-103 tumor antigen-like	1.89	CACGGCCAAGAACGACATGAA	NM_015438:	NM_080731:NM_015438:NM_080730:
25900	HOM-TES-10	HOM-TES-103 tumor antigen-like	-3.78	CAGAATGACAGAGAAGGTGAA	NM_015438:	NM_080731:NM_015438:NM_080730:
3198	HOXA1	homeobox A1	-0.16	CAGCTCCTTTATTATAATCAA	NM_005522:	NM_005522:NM_153620:
3198	HOXA1	homeobox A1	-0.06	TAGGATGTCTGTAATAAATAA	NM_005522:	NM_005522:NM_153620:
3229	HOXC13	homeobox C13	-2.99	CGGGTGCAGAAGAGTATTTAA	NM_017410:	NM_017410:
3229	HOXC13	homeobox C13	-0.87	CCGCTTTGTACCATAACCGAA	NM_017410:	NM_017410:
3236	HOXD10	homeobox D10	-0.49	CAGGGTAACTATTATTGCGCA	NM_002148:	NM_002148:
3236	HOXD10	homeobox D10	0.66	CCCTATGAGTATATATATATA	NM_002148:	NM_002148:
3238	HOXD12	homeobox D12	-0.10	AACGCAAGGAATTGTCCAATA	NM_021193:	NM_021193:
3238	HOXD12	homeobox D12	0.17	AACGAATTCCTCGTCAACGAA	NM_021193:	NM_021193:
3239	HOXD13	homeobox D13	0.26	GCCAGTATAAAGGGACTTGAA	NM_000523:	NM_000523:
3239	HOXD13	homeobox D13	0.00	ACGAACCTATCTGAGAGACAA	NM_000523:	NM_000523:
3240	HP	haptoglobin	-2.06	CTGACCAAGACCAATGCATAA	NM_005143:	NM_005143:
3240	HP	haptoglobin	-0.23	AAGGTGTCTGTTAATGAGAGA	NM_005143:	NM_005143:
3242	HPD	4-hydroxyphenylpyruvate dioxygenase	0.71	CTGGTGGACTACGACGAGAAA	NM_002150:	NM_002150:
3242	HPD	4-hydroxyphenylpyruvate dioxygenase	0.08	CCAGGAATATGTGGACTATAA	NM_002150:	NM_002150:
3248	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-1.16	CTGGCAGTGACTAATCAGTAA	NM_000860:	NM_000860:
3248	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-0.15	CAAGAGCTTCTTAGAGTAGTA	NM_000860:	NM_000860:
3249	HPN	hepsin (transmembrane protease, serine 1)	0.93	GGGATGCTCTTTAAATAATAA	NM_002151:	NM_002151:NM_182983:
3249	HPN	hepsin (transmembrane protease, serine 1)	0.37	CAGCCAGGGAATCATTAACAA	NM_002151:	NM_002151:NM_182983:
3250	HPR	haptoglobin-related protein	0.01	AAGGTGCTTGTTAATGAGAGA	NM_020995:	NM_020995:
3250	HPR	haptoglobin-related protein	-3.77	CTGACCAATACGATTGCATAA	NM_020995:	NM_020995:
3251	HPRT1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	-0.64	ATGGGAGGCCATCACATTGTA	NM_000194:	NM_000194:
3251	HPRT1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	-0.74	CACTATTGAGTGAAACATTGA	NM_000194:	NM_000194:
55806	HR	hairless homolog (mouse)	-0.51	CTCCTTCATGATTTCCATTAA	NM_005144:	NM_018411:NM_005144:
55806	HR	hairless homolog (mouse)	-0.20	GCGGGACACATCGATAGGGAA	NM_005144:	NM_018411:NM_005144:
3265	HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	-0.01	AGGAGCGATGACGGAATATAA	NM_005343:	NM_005343:NM_176795:
3265	HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	0.21	CACAGATGGGATCACAGTAAA	NM_005343:	NM_005343:NM_176795:
57110	HRASLS	HRAS-like suppressor	0.57	CAAAGAGATATTGATATTGAA	NM_020386:	NM_020386:
57110	HRASLS	HRAS-like suppressor	1.05	CAGGAGGTGGCCTATAACTTA	NM_020386:	NM_020386:
54979	HRASLS2	HRAS-like suppressor 2	1.23	CAGCTTAGTATGAATTCTATT	NM_017878:	NM_017878:
54979	HRASLS2	HRAS-like suppressor 2	0.88	CGGGAAAGGCAATAAATCCAA	NM_017878:	NM_017878:
11145	HRASLS3	HRAS-like suppressor 3	1.67	CCCGGCGAGAAAGTTGTTAAA	NM_007069:	NM_007069:
11145	HRASLS3	HRAS-like suppressor 3	1.30	TTCCTTGTTAATGACAATAAA	NM_007069:	NM_007069:
3269	HRH1	histamine receptor H1	-2.48	CAGGACCAAAGAACACTCGAA	NM_000861:	NM_000861:
3269	HRH1	histamine receptor H1	1.06	TCCGAGTCAAGTGATTGACAA	NM_000861:	NM_000861:
3274	HRH2	histamine receptor H2	-1.47	CAGCCCAGAGTCAGTCATTGA	NM_022304:	NM_022304:
3274	HRH2	histamine receptor H2	-0.08	TAGAAGGTGTTGCTTAATTTA	NM_022304:	NM_022304:
11255	HRH3	histamine receptor H3	0.73	CAGCATCTACCTGAACATCCA	NM_007232:	NM_007232:
11255	HRH3	histamine receptor H3	-0.36	TCCCTGACTACTGGTACGAAA	NM_007232:	NM_007232:
59340	HRH4	histamine receptor H4	-0.06	AAGAACCAAGATGAATAGCAA	NM_021624:	NM_021624:
59340	HRH4	histamine receptor H4	0.53	TACACTTATGCCTTACATTAA	NM_021624:	NM_021624:
8739	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	-0.66	AGCGATCGTAGAAACACAGAA	NM_003806:	NM_003806:
8739	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	-3.01	CGAGAAGGAAGTGGAGAGTAA	NM_003806:	NM_003806:
9957	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-0.71	TGGGATCCATCTTGACCTCAA	NM_005114:	NM_005114:
9957	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0.94	ATGGTTGTTAACATTGTGTAA	NM_005114:	NM_005114:
27292	HSA9761	dimethyladenosine transferase	0.44	CTGGTCCAATCTATTCATAAT	NM_014473:	NM_014473:
27292	HSA9761	dimethyladenosine transferase	0.32	TGGGATGGTCTAGTAAGGATA	NM_014473:	NM_014473:
3290	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	0.76	CACATAAACTTTATAAATTCA	NM_005525:	NM_181755:NM_005525:
3290	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	0.35	GTGATGATTAATACAATATTA	NM_005525:	NM_181755:NM_005525:
3291	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	0.27	CTGCATGGAGGTGAATTTCTT	NM_000196:	NM_000196:
3291	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	-2.62	CCGTAGCTGCATGGAGGTGAA	NM_000196:	NM_000196:

3292	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	-0.65	CAGCTGTGGGTGGCTAATTAA	NM_000413:	NM_000413:
3292	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	-0.33	ATCCCAGAGCTTCAAAGTGTA	NM_000413:	NM_000413:
51144	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	0.44	CACCAGTAGATTTGTATTAAA	NM_016142:	NM_016142:
51144	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	-0.01	TAAGTTGATACTCTACAGGTA	NM_016142:	NM_016142:
345275	HSD17B13	hydroxysteroid (17-beta) dehydrogenase 13	0.56	CTCCCACTACATCAAGACTAA	NM_178135:	NM_178135:
345275	HSD17B13	hydroxysteroid (17-beta) dehydrogenase 13	1.74	TCCATCGATGATGGAGAGAAA	NM_178135:	NM_178135:
3294	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	0.01	TCGGAATGTCATAGTCTTGAA	NM_002153:	NM_002153:
3294	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	0.52	CTCAAAGAAGTCGGAATGTCA	NM_002153:	NM_002153:
3293	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	-0.94	AAGAGTCATTGAATTATGTCA	NM_000197:	NM_000197:
3293	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	0.61	CTGCAATGACAAAGTATCTAA	NM_000197:	NM_000197:
3295	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	-0.01	GCACACTACACTATTAATAAA	NM_000414:	NM_000414:
3295	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	-0.11	AGAGCAGTACTTAGAGTTATA	NM_000414:	NM_000414:
8630	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6	1.14	CAGAGTACTAACATGTTTATA	NM_003725:	NM_003725:
8630	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6	0.39	CAAGCATATTAAGGAGACCTA	NM_003725:	NM_003725:
51478	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	0.67	ATGGAATTCTGCCTCCGTTTA	NM_016371:	NM_016371:
7923	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	-0.41	AAACACCCATGACACAGAAAG	NM_014234:	NM_014234:
7923	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	0.10	AATCTGAAGATAGTGGATACA	NM_014234:	NM_014234:
3284	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isom	1.63	ACAGTTCAACATAAAGAGCAA	NM_000198:	NM_000198:
3284	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isom	1.92	AACAATTGTGGTCTCTCTTAA	NM_000198:	NM_000198:
83693	HSDL1	hydroxysteroid dehydrogenase like 1	0.00	AACCCTCACAATACGCGTTAA	NM_031463:	NM_031463:
83693	HSDL1	hydroxysteroid dehydrogenase like 1	0.68	TGGAATGAACTTATTCCTAGA	NM_031463:	NM_031463:
84263	HSDL2	hydroxysteroid dehydrogenase like 2	-5.39	CAGTTCATGAATCGCTAATAA	NM_032303:	NM_032303:
84263	HSDL2	hydroxysteroid dehydrogenase like 2	0.77	ACCCAGTTCATGAATCGCTAA	NM_032303:	NM_032303:
3299	HSF4	heat shock transcription factor 4	-3.59	CCGACTATCCCTGCACATAAA	NM_001538:	NM_001538:
3299	HSF4	heat shock transcription factor 4	0.05	CAGAGCCGTTTCGCCAAGGAA	NM_001538:	NM_001538:
3320	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	-9.04	CAGAATGAAGGAGAACCAGAA	NM_005348:	NM_001017963:NM_005348:
3320	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	0.39	CCGGTATGAAACTTTGACAGA	NM_005348:	NM_005348:
3326	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	0.91	CCGCATCTATCGCATGATCAA	NM_007355:	NM_007355:
3326	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	-1.60	CAAGAATGATAAGGCAGTTAA	NM_007355:	NM_007355:
7184	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	-1.01	AAGGCTAATATCACTGACTGA	NM_003299:	NM_003299:
7184	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	0.69	ATGGATTAAATGCATCACAAA	NM_003299:	NM_003299:
51182	HSPA14	heat shock 70kDa protein 14	-0.49	CTCTATTGAGATAGCATCTTA	NM_016299:	NM_016299:
51182	HSPA14	heat shock 70kDa protein 14	0.92	AATGGATTACGTGATATATTA	NM_016299:	NM_016299:
3308	HSPA4	heat shock 70kDa protein 4	0.49	CAGACTATTATAAAGCTTTAA	NM_198431:	NM_198431:NM_002154:
3308	HSPA4	heat shock 70kDa protein 4	-1.76	CAGGTATAAAGGTGACATATA	NM_198431:	NM_198431:NM_002154:
3309	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	-4.05	TAGGGTGTGTGTTCACCTTCA	NM_005347:	NM_005347:
3309	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	0.74	TGGGATAAGGAAACACTTCTA	NM_005347:	NM_005347:
26353	HSPB8	heat shock 22kDa protein 8	0.90	CCGCATGGTTTGGTTAATGAA	NM_014365:	NM_014365:
26353	HSPB8	heat shock 22kDa protein 8	1.64	CGCATGGTTTGGTTAATGAAA	NM_014365:	NM_014365:
29070	HSPC065	HSPC065 protein	0.01	TAGAGGTGTGTCACAGTTAAA	NM_014157:	NM_014157:
29070	HSPC065	HSPC065 protein	0.53	TCGCAGTTTGTCTTAACTGTA	NM_014157:	NM_014157:
51491	HSPC111	hypothetical protein HSPC111	0.09	CGGGACCTCATTGACTATGTA	NM_016391:	NM_016391:
51491	HSPC111	hypothetical protein HSPC111	0.19	TCGGAGTAAGATCAACGTCTA	NM_016391:	NM_016391:
3329	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-0.97	CACCACCAGATGAGAAGTTAA	NM_002156:	NM_199440:NM_002156:
3329	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-0.23	CAGGGTTTGGTGACAATAGAA	NM_002156:	NM_199440:NM_002156:
3336	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	-0.31	AAGGGTGGAGAGATTCAACCA	NM_002157:	NM_002157:XM_497331:XM_496430:
3336	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	-0.63	AGCGTGAAAGTTGGAGATAAA	NM_002157:	NM_002157:XM_370704:
3339	HSPG2	heparan sulfate proteoglycan 2 (perlecan)	-1.53	ACGCCTGGACGTGGAGTTCAA	NM_005529:	NM_005529:
3339	HSPG2	heparan sulfate proteoglycan 2 (perlecan)	-3.23	CACCCGAGCCATGGATTTCAA	NM_005529:	NM_005529:
10524	HTATIP	HIV-1 Tat interacting protein, 60kDa	-0.89	CTGATCGAGTTCAGCTATGAA	NM_006388:	NM_006388:NM_182709:NM_182710:
10524	HTATIP	HIV-1 Tat interacting protein, 60kDa	-5.49	CACCACATTGCCTGTCCTCTA	NM_006388:	NM_006388:NM_182709:NM_182710:
10553	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	-0.15	AACCGGCAGAGTGCTCTTAAA	NM_006410:	NM_006410:
10553	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	0.08	ATCGGTAATTTCAGGGTCTAA	NM_006410:	NM_006410:
27037	HTF9C	HpaII tiny fragments locus 9C	-0.23	CCGGGTGAACGCCCAGGACAA	NM_022727:	NM_022727:NM_182984:
27037	HTF9C	HpaII tiny fragments locus 9C	-0.55	CCAGATAACACCCTACAAGAA	NM_022727:	NM_022727:NM_182984:
3350	HTR1A	5-hydroxytryptamine (serotonin) receptor 1A	0.34	CCTGTTGGGCGCCATAATCAA	NM_000524:	NM_000524:
3350	HTR1A	5-hydroxytryptamine (serotonin) receptor 1A	1.99	CTGGTTCTCTATGGGCGCATA	NM_000524:	NM_000524:
3351	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	0.57	CACAGTGTACCGGACCCGGAA	NM_000863:	NM_000863:
3351	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	0.74	CGCCGTGGAGTACTCAGCTAA	NM_000863:	NM_000863:
3352	HTR1D	5-hydroxytryptamine (serotonin) receptor 1D	0.07	CACGAATGTCTCAAGCTTTGA	NM_000864:	NM_000864:
3352	HTR1D	5-hydroxytryptamine (serotonin) receptor 1D	0.00	CTGAGTCTTTCTTAGATTAAA	NM_000864:	NM_000864:
3354	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E	-1.04	CAGCATGGCTATAAGACCCAA	NM_000865:	NM_000865:
3354	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E	-0.75	CAGGCGAACCTTCACTCAGAA	NM_000865:	NM_000865:
3355	HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	1.29	ACCCATCAACAGACTTTGATA	NM_000866:	NM_000866:
3355	HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	0.90	CTCAATTCCCTTATAAATCCA	NM_000866:	NM_000866:
3356	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	0.00	CCGCTTCAACTCCAGAACTAA	NM_000621:	NM_000621:
3356	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	-2.42	TGGGATTGAGTTGGTTACCTA	NM_000621:	NM_000621:
3357	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	0.30	CCGGAATCCAATGGCAGAGAA	NM_000867:	NM_000867:
3357	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	0.32	TGGCATGGTTACAATGCCTTA	NM_000867:	NM_000867:
3358	HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	0.08	CCCGCGAGCATCTATAACATA	NM_000868:	NM_000868:
3358	HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	0.37	TCGGTATGTAGCAATACGTAA	NM_000868:	NM_000868:
3359	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	0.73	CAAGCTGCTATTCCACATTTA	NM_000869:	NM_000869:NM_213621:
3359	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	0.04	TACGTGTATATTCGGCATCAA	NM_000869:	NM_000869:NM_213621:
9177	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	-2.03	CCGAGCCAGGATTGTGTTCAA	NM_006028:	NM_006028:
170572	HTR3C (5-hyc	5-hydroxytryptamine (serotonin) receptor 3, family member C	-0.17	AAGGTCGAATTAAGTATGATA	NM_130770:	NM_130770:
170572	HTR3C (5-hyc	5-hydroxytryptamine (serotonin) receptor 3, family member C	0.23	CAGCAGTGAAGGTCGAATTAA	NM_130770:	NM_130770:
200909	HTR3D	5-hydroxytryptamine (serotonin) receptor 3 family member D	0.22	CCAGACCTGAATAGTCTCCTA	NM_182537:	NM_182537:
200909	HTR3D	5-hydroxytryptamine (serotonin) receptor 3 family member D	0.26	TAGTACGTCCTCATCCATCAA	NM_182537:	NM_182537:
285242	HTR3E	5-hydroxytryptamine (serotonin) receptor 3, family member E	-0.27	AAGGCCTCACAGCATATGTAA	NM_182589:	NM_182589:
285242	HTR3E	5-hydroxytryptamine (serotonin) receptor 3, family member E	2.01	ACCCATGAAGGTGGACAGTAT	NM_182589:	NM_182589:
3360	HTR4	5-hydroxytryptamine (serotonin) receptor 4	-0.04	CAGAAGTCCCGGGAAGGTAAA	NM_000870:	NM_000870:
3360	HTR4	5-hydroxytryptamine (serotonin) receptor 4	-0.65	CAGCTTTGTCCTTCAGATTAA	NM_000870:	NM_000870:
3361	HTR5A	5-hydroxytryptamine (serotonin) receptor 5A	-2.08	CCTGATCTATACGGCTTTCAA	NM_024012:	NM_024012:
3361	HTR5A	5-hydroxytryptamine (serotonin) receptor 5A	-0.01	CTCGGTCTTCGGAGTGCTTAT	NM_024012:	NM_024012:
3362	HTR6	5-hydroxytryptamine (serotonin) receptor 6	-0.36	CAGGAGGCTGCAAGTCTCCTA	NM_000871:	NM_000871:
3362	HTR6	5-hydroxytryptamine (serotonin) receptor 6	1.85	CGCCGTCAATTTCTTCAACAT	NM_000871:	NM_000871:
3363	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-couplec	-7.16	CGGCGCGATGATGGACGTTAA	NM_000872:	NM_000872:NM_019859:NM_019860:
3363	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-couplec	0.99	CTGAAGTGACCGTATATATTA	NM_000872:	NM_000872:NM_019859:NM_019860:
5654	HTRA1	HtrA serine peptidase 1	-1.36	CGACGTCATAATCAGCATCAA	NM_002775:	NM_002775:
5654	HTRA1	HtrA serine peptidase 1	0.97	AGCGTATATAATTGAAGTAAT	NM_002775:	NM_002775:
27429	HTRA2	HtrA serine peptidase 2	0.14	CCCGATGTTCAGCATGGTGTA	NM_013247:	NM_013247:
27429	HTRA2	HtrA serine peptidase 2	-1.33	CCGCGAGGTCCCTATCTCGAA	NM_013247:	NM_145074:NM_013247:
94031	HTRA3	HtrA serine peptidase 3	-3.85	CCCAGTGTTGCTTGTACTGTA	NM_053044:	NM_053044:
94031	HTRA3	HtrA serine peptidase 3	1.63	AGCAGTGGAATTTATGTGCAA	NM_053044:	NM_053044:
203100	HTRA4	HtrA serine peptidase 4	-2.04	TAGGCAGTTCTTGGCAGAATA	NM_153692:	NM_153692:
203100	HTRA4	HtrA serine peptidase 4	0.44	CCCGCTCAGGAGGAATTACAA	NM_153692:	NM_153692:
30811	HUNK (hormc	hormonally upregulated Neu-associated kinase	-4.53	CACGGGCAAAGTGCCCTGTAA	NM_014586:	NM_014586:
30811	HUNK (hormc	hormonally upregulated Neu-associated kinase	-0.52	TCGGACCAAGATCAAACCAAA	NM_014586:	NM_014586:
3364	HUS1 (HUS1	HUS1 checkpoint homolog (S. pombe)	0.35	ACCGCACATCGACACACTGTA	NM_004507:	NM_004507:

3364	HUS1 (HUS1	HUS1 checkpoint homolog (S. pombe)	1.06	AGCAATCACCTTGTTATTGAA	NM_004507:	NM_004507:
10075	HUWE1	HECT, UBA and WWE domain containing 1	1.26	CCGGCTTTCACCAGTCGCTTA	XM_497119:	NM_031407:
10075	HUWE1	HECT, UBA and WWE domain containing 1	-0.54	CAGGTTGTTGGTACAGAGGAA	XM_497119:	NM_031407:
8692	HYAL2	hyaluronoglucosaminidase 2	1.52	AAAGATGTGTATCGCCGGTTA	NM_003773:	NM_003773:NM_033158:
8692	HYAL2	hyaluronoglucosaminidase 2	-0.01	CTGCCAGTACCTCAAAGATTA	NM_003773:	NM_003773:NM_033158:
3375	IAPP	islet amyloid polypeptide	0.52	CTGGTACTAAGAGGCTATTTA	NM_000415:	NM_000415:
3375	IAPP	islet amyloid polypeptide	-0.07	TTAGAGGACAATGTAACTCTA	NM_000415:	NM_000415:
3376	IARS	isoleucine-tRNA synthetase	0.72	CACAGTAATCTTCACACTTAA	NM_002161:	NM_002161:NM_013417:
3376	IARS	isoleucine-tRNA synthetase	0.27	TCGGATAAAGTCCTTATTCAA	NM_002161:	NM_002161:NM_013417:
55699	IARS2	isoleucine-tRNA synthetase 2, mitochondrial	-2.77	AAGAGTCTTCCTATAAAGTAA	NM_018060:	NM_018060:
55699	IARS2	isoleucine-tRNA synthetase 2, mitochondrial	0.81	ACCACTGAGCATATTGTTAAA	NM_018060:	NM_018060:
127544	IBRDC3	IBR domain containing 3	0.94	CACAATTTCTTACCAGATAAA	NM_153341:	NM_153341:
127544	IBRDC3	IBR domain containing 3	-0.18	CAAGTGGACATTGAAGCCAAA	NM_153341:	NM_153341:
3381	IBSP	integrin-binding sialoprotein (bone sialoprotein, bone sialoprotein II)	-0.02	ATGGTGGGTTTGAACCTACAA	NM_004967:	NM_004967:
3381	IBSP	integrin-binding sialoprotein (bone sialoprotein, bone sialoprotein II)	0.82	AAGATGAGTACAGCTACTTTA	NM_004967:	NM_004967:
25998	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-1.35	CAGATTGAGGAGCATGCCATA	AB037838:	NM_015525:
25998	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1.11	TAGAAGAGTCATTACACCATA	AB037838:	NM_015525:
3383	ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	-0.04	CCCATGAAACCGAACACACAA	NM_000201:	NM_000201:
3383	ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	-0.70	CCAGCGGAAGATCAAGAAATA	NM_000201:	NM_000201:
59082	ICEBERG	ICEBERG caspase-1 inhibitor	1.16	AAGATATTCTCGTGAAAGAAA	NM_021571:	NM_021571:
59082	ICEBERG	ICEBERG caspase-1 inhibitor	2.28	CCAAGTCTTGCTGCAAATTTA	NM_021571:	NM_021571:
22858	ICK	intestinal cell (MAK-like) kinase	1.34	ACCTAATGACTTGGTAAATTA	NM_014920:	NM_014920:NM_016513:
22858	ICK	intestinal cell (MAK-like) kinase	1.34	CTCAGTAATCTAGCTTATATA	NM_014920:	NM_014920:NM_016513:
3397	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	1.02	AGGAAATTGCTTTGTATTGTA	NM_002165:	NM_002165:NM_181353:
3397	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-0.22	TACAATGATCACCGACTGAAA	NM_002165:	NM_002165:NM_181353:
3399	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	1.01	AAAGCAAATTCTGGAAGTTAA	NM_002167:	NM_002167:
3399	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	0.01	CAGCGCTTCCTCATTCTTTGA	NM_002167:	NM_002167:
3416	IDE	insulin-degrading enzyme	-0.15	AACACTGAGGTTGCATATTTA	NM_004969:	NM_004969:
3416	IDE	insulin-degrading enzyme	1.06	AAGCATATATGCGATCTCTTA	NM_004969:	NM_004969:
3423	IDS	iduronate 2-sulfatase (Hunter syndrome)	-0.67	TACGAAGACCATACATAATAA	NM_000202:	NM_000202:
3423	IDS	iduronate 2-sulfatase (Hunter syndrome)	0.34	CTGAGGGCTAGTTAATCCAAA	NM_000202:	NM_000202:
3425	IDUA	iduronidase, alpha-L-	-1.15	CAGGAAGCCATCGACCTTCAA	NM_000203:	NM_000203:
3425	IDUA	iduronidase, alpha-L-	-0.02	CGGGACCGTCCTGGACAGCAA	NM_000203:	NM_000203:
8870	IER3	immediate early response 3	0.61	AAGGAGAGCGTCGTTAATTTA	NM_003897:	NM_052815:NM_003897:
8870	IER3	immediate early response 3	-0.23	TTGCTCCTAATTAATATTTAT	NM_003897:	NM_052815:NM_003897:
8519	IFITM1	interferon induced transmembrane protein 1 (9-27)	1.07	ACCATATTATGTTACAGATAA	NM_003641:	NM_003641:
8519	IFITM1	interferon induced transmembrane protein 1 (9-27)	-0.59	CATAAGTAATTTGATCCTCAA	NM_003641:	NM_003641:
3439	IFNA1	interferon, alpha 1	0.67	AACTATGACCATGCTGATAAA	NM_024013:	NM_024013:
3439	IFNA1	interferon, alpha 1	0.90	AAACTGATTTATCTATTTAAA	NM_024013:	NM_024013:
3447	IFNA13 (interf	interferon, alpha 13	-0.65	CAGAAGCATCTGCAATATCTA	NM_006900:	NM_006900:
3448	IFNA14	interferon, alpha 14	0.89	CTCCTTTCATCTATTTATTTA	NM_002172:	NM_002172:
3448	IFNA14	interferon, alpha 14	-2.93	CAGGAGGACTTTGATGCTCAT	NM_002172:	NM_002172:
3449	IFNA16 (interf	interferon, alpha 16	-2.08	CAGCAACTGAATGACCTAGAA	NM_002173:	NM_002173:
3451	IFNA17	interferon, alpha 17	-4.63	CAGCAACTGAATAACCTGGAA	NM_021268:	NM_021268:
3440	IFNA2	interferon, alpha 2	1.44	CAATATTATATTCAAGATATA	NM_000605:	NM_000605:
3440	IFNA2	interferon, alpha 2	-0.11	CAGAATAACTGGTACACTTCA	NM_000605:	NM_000605:
3452	IFNA21	interferon, alpha 21	-0.17	CACCGCATGAGTTGAATCAAA	NM_002175:	NM_002175:
3452	IFNA21	interferon, alpha 21	0.03	CTGATAGATCTAATTATCTAT	NM_002175:	NM_002175:
3441	IFNA4	interferon, alpha 4	0.02	AACCTAGAGGCCGAAGTTCAA	NM_021068:	NM_021068:
3441	IFNA4	interferon, alpha 4	1.33	ACAGAGCAAAGTCTTCAGAAA	NM_021068:	NM_021068:
3442	IFNA5	interferon, alpha 5	-0.79	ATCCTTCTCTTTATCAGCAAA	NM_002169:	NM_002169:
3442	IFNA5	interferon, alpha 5	-1.43	ATGCAGGAGGTTGGAGTGGAA	NM_002169:	NM_002169:
3443	IFNA6 (interfe	interferon, alpha 6	0.76	CATCAAGAAACTTGCAAGAAA	NM_021002:	NM_021002:
3443	IFNA6 (interfe	interferon, alpha 6	-0.03	ATCCTTCTCTTCATCAAGAAA	NM_021002:	NM_021002:
3444	IFNA7	interferon, alpha 7	0.42	TAGCCTAGTGATATTTGCAAA	NM_021057:	NM_021057:
3445	IFNA8 (interfe	interferon, alpha 8	0.17	CTAATTGAACCTGACATTAAA	NM_002170:	NM_002170:
3445	IFNA8 (interfe	interferon, alpha 8	0.22	AACACGGAAATGATTCTTATA	NM_002170:	NM_002170:
3454	IFNAR1	interferon (alpha, beta and omega) receptor 1	0.43	CAGGGACCTTATTATTCATTA	NM_000629:	NM_000629:
3454	IFNAR1	interferon (alpha, beta and omega) receptor 1	0.84	CTGGAATTTGCAATCACTGAA	NM_000629:	NM_000629:
3455	IFNAR2	interferon (alpha, beta and omega) receptor 2	-1.66	AAGCACCATAGTGACACTGAA	NM_000874:	NM_207584:NM_000874:NM_207585:
3455	IFNAR2	interferon (alpha, beta and omega) receptor 2	-2.66	CACAGTGATGAGCAAGCAGTA	NM_000874:	NM_207584:NM_000874:NM_207585:
3456	IFNB1	interferon, beta 1, fibroblast	-0.94	CAGGTTACCTCCGAAACTGAA	NM_002176:	NM_002176:
3456	IFNB1	interferon, beta 1, fibroblast	-3.00	CAGAGTGGAAATCCTAAGGAA	NM_002176:	NM_002176:
338376	IFNE1	interferon epsilon 1	0.57	AGGGATAAGTAGCATATTTGA	NM_176891:	NM_176891:
338376	IFNE1	interferon epsilon 1	0.91	TCAGTGAAACTTTGTATATAA	NM_176891:	NM_176891:
3458	IFNG	interferon, gamma	1.39	TCCTGTGACTGTCTCACTTAA	NM_000619:	NM_000619:
3458	IFNG	interferon, gamma	1.20	AAGAAACGAGATGACTTCGAA	NM_000619:	NM_000619:
3459	IFNGR1	interferon gamma receptor 1	0.80	CAGCATCGCTTTAAACTCGTA	NM_000416:	NM_000416:
3459	IFNGR1	interferon gamma receptor 1	1.70	ACGGAAGTGAGATCCAGTATA	NM_000416:	NM_000416:
3460	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	1.55	AGGCTTCCCAATGGATTTCAA	NM_005534:	NM_005534:
3460	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	0.62	TCGGGCATTTAAGCAACATAT	NM_005534:	NM_005534:
56832	IFNK	interferon, kappa	0.32	CAAATTGTGGATCATGGTATA	NM_020124:	NM_020124:
56832	IFNK	interferon, kappa	0.80	CCCAAATGTTATAGCCAAAGA	NM_020124:	NM_020124:
3467	IFNW1 (interf	interferon, omega 1	1.04	AAGACTCTTATTTCGGCTTTA	NM_002177:	NM_002177:
3467	IFNW1 (interf	interferon, omega 1	2.36	AACCATGTGTTTCCTATTAAA	NM_002177:	NM_002177:
55081	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	-0.06	AAGCCTTTACACTGAATGTAA	NM_018010:	NM_018010:
55081	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	0.96	CATGGTGATTATGATGGTTAA	NM_018010:	NM_018010:
3476	IGBP1	immunoglobulin (CD79A) binding protein 1	0.30	AACACTTTATAAACTACTTAA	NM_001551:	NM_001551:
3476	IGBP1	immunoglobulin (CD79A) binding protein 1	1.83	AACGAGGGCAAAGATGCTAAA	NM_001551:	NM_001551:
3479	IGF1	insulin-like growth factor 1 (somatomedin C)	-1.42	ACGGTAATACGTGAAAGCAAA	M27544:	NM_000618:
3479	IGF1	insulin-like growth factor 1 (somatomedin C)	-0.16	ATCAATAATGTTCTATAGAAA	M27544:	NM_000618:
3480	IGF1R	insulin-like growth factor 1 receptor	0.00	AACCTTAATGACAACACTTAA	NM_000875:	NM_000875:
3480	IGF1R	insulin-like growth factor 1 receptor	-2.04	AGGATTGAGTTTCTCAACGAA	NM_000875:	NM_000875:
3481	IGF2	insulin-like growth factor 2 (somatomedin A)	-0.03	CCCGCTGTTCGGTTTGCGACA	NM_000612:	NM_000612:
3481	IGF2	insulin-like growth factor 2 (somatomedin A)	1.51	CCGAACCAAAGTGGATTAATT	NM_000612:	NM_000612:
3482	IGF2R	insulin-like growth factor 2 receptor	-2.57	ACGGAGTCTCGTACTATATAA	NM_000876:	NM_000876:
3482	IGF2R	insulin-like growth factor 2 receptor	-1.93	CAGACCAGGCTTGCTCTATAA	NM_000876:	NM_000876:
3483	IGFALS	insulin-like growth factor binding protein, acid labile subunit	0.84	CAGCTTGAGGTGCTCACGCTA	NM_004970:	NM_004970:
3483	IGFALS	insulin-like growth factor binding protein, acid labile subunit	0.47	CCGACTCTTCCTCAAGGACAA	NM_004970:	NM_004970:
3484	IGFBP1	insulin-like growth factor binding protein 1	1.75	TACACTGGATATGTTGTTAAA	NM_000596:	NM_000596:NM_001013029:
3484	IGFBP1	insulin-like growth factor binding protein 1	-3.00	AAGGAGGACGGTTAACTTGTA	NM_000596:	NM_000596:NM_001013029:
3485	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	0.06	ACAGTGCAAGATGTCTCTGAA	NM_000597:	NM_000597:
3485	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	0.66	CACACGTATTTATATTTGGAA	NM_000597:	NM_000597:
3486	IGFBP3	insulin-like growth factor binding protein 3	-0.11	CAAGGTTAATGTGGAGCTCAA	NM_000598:	NM_000598:NM_001013398:
3486	IGFBP3	insulin-like growth factor binding protein 3	1.47	CCAAATATAGTAAGATCTATA	NM_000598:	NM_000598:NM_001013398:
3488	IGFBP5	insulin-like growth factor binding protein 5	-8.49	CACCCGCATCTCCGAGCTGAA	NM_000599:	NM_000599:
3488	IGFBP5	insulin-like growth factor binding protein 5	-1.14	CTGCCCAATTGTGACCGCAAA	NM_000599:	NM_000599:
285313	IGSF10	immunoglobulin superfamily, member 10	1.35	CAGGCGTATATCACTGTATAA	NM_178822:	NM_178822:
285313	IGSF10	immunoglobulin superfamily, member 10	-1.65	ACGCATCAATTTAGGATACAA	NM_178822:	NM_178822:

84966	IGSF21	immunoglobin superfamily, member 21	0.77	CGCCGTGACTTTGAAGTGTAA	NM_032880:	NM_032880:
84966	IGSF21	immunoglobin superfamily, member 21	-0.72	CAGCGCTGAGTTCGACGGGAA	NM_032880:	NM_032880:
253559	IGSF4D	immunoglobulin superfamily, member 4D	-2.57	TAGGTATTACTTAAACCAATA	NM_153184:	NM_153184:
253559	IGSF4D	immunoglobulin superfamily, member 4D	-1.55	CACAGTTGAATAATAACCTAA	NM_153184:	NM_153184:
3549	IHH	Indian hedgehog homolog (Drosophila)	-0.20	CTGGGTGTATTACGAGTCAAA	XM_050846:	NM_002181:
3549	IHH	Indian hedgehog homolog (Drosophila)	0.60	CGGCTTTGACTGGGTGTATTA	XM_050846:	NM_002181:
9807	IHPK1	inositol hexaphosphate kinase 1	-1.35	AAGGTGGATGTCCGCATGATT	NM_153273:	NM_153273:NM_001006115:
9807	IHPK1	inositol hexaphosphate kinase 1	-0.02	CCGGCAGATGCGGAAATGCGA	NM_153273:	NM_153273:NM_001006115:
51447	IHPK2	inositol hexaphosphate kinase 2	2.42	AAGCATCGGAACCAGTACAAA	NM_016291:	NM_001005909:NM_016291:
51447	IHPK2	inositol hexaphosphate kinase 2	0.62	TCGGAACCAGTACAAATTTAT	NM_016291:	NM_001005909:NM_016291:
117283	IHPK3	inositol hexaphosphate kinase 3	-6.46	AAGACTGGTGGACAAGTGTAA	NM_054111:	NM_054111:
117283	IHPK3	inositol hexaphosphate kinase 3	-6.60	CTGAGATACGTTACCCAATTA	NM_054111:	NM_054111:
3550	IK	IK cytokine, down-regulator of HLA II	-11.06	CAGGCGCTTCAAGGAAACCAA	NM_006083:	NM_006083:
3550	IK	IK cytokine, down-regulator of HLA II	-8.59	CAGCGAGTATATGAACAACAA	NM_006083:	NM_006083:
8518	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase c	-0.78	CAGCGGTTTACTATAGACAAA	NM_003640:	NM_003640:
8518	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase c	1.14	GCGGTTTACTATAGACAAATA	NM_003640:	NM_003640:
3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase b	-0.13	CACACTGGAGGTCCTCCATTA	NM_001556:	NM_001556:
3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase b	0.22	CAGACCGACATTGTGGACTTA	NM_001556:	NM_001556:
9641	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase e	-0.51	ACGGCGGAACAAGGAGATCAT	NM_014002:	NM_014002:
9641	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase e	0.26	CCGCATCATCGAACGGCTAAA	NM_014002:	NM_014002:
8517	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase g	-1.13	CTCCTCTAGTTCAGAGACATA	NM_003639:	NM_003639:
8517	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase g	0.20	TTCGGAAATGCCTCACATATA	NM_003639:	NM_003639:
3586	IL10	interleukin 10	0.81	CCAGCTTGTTATTTATAACAA	NM_000572:	NM_000572:
3586	IL10	interleukin 10	-0.05	CCCAACCACTTCATTCTTGAA	NM_000572:	NM_000572:
3587	IL10RA	interleukin 10 receptor, alpha	-1.34	CCCGCAAATGACACATATGAA	NM_001558:	NM_001558:
3587	IL10RA	interleukin 10 receptor, alpha	-0.89	CGCAGTGACCTTGGACCTGTA	NM_001558:	NM_001558:
3588	IL10RB	interleukin 10 receptor, beta	1.55	ATGGACTTATAATGTGCAATA	NM_000628:	NM_000628:
3588	IL10RB	interleukin 10 receptor, beta	-0.57	CAGCTCAGTACCTAAGTTATA	NM_000628:	NM_000628:
3589	IL11	interleukin 11	-0.24	CAAGGTCAAGATGGTTCATTA	NM_000641:	NM_000641:
3589	IL11	interleukin 11	1.39	CCCATAGGTCTTCAATAAATA	NM_000641:	NM_000641:
3590	IL11RA	interleukin 11 receptor, alpha	0.22	CAGGTGTGAATAAAGAGAATA	NM_004512:	NM_004512:
3590	IL11RA	interleukin 11 receptor, alpha	0.32	AAGGAACGTGTGTAATGTGTA	NM_004512:	NM_004512:
3592	IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lympho	1.34	AGGGCAAATATTTATAAGCTA	NM_000882:	NM_000882:
3592	IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lympho	0.61	ACCATTGGAATTAACCAAGAA	NM_000882:	NM_000882:
3593	IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lympho	0.19	ATGGGCCTTCATGCTATTTAA	NM_002187:	NM_002187:
3593	IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lympho	-0.66	TAGATGCTAAATGCTCATTGA	NM_002187:	NM_002187:
3594	IL12RB1	interleukin 12 receptor, beta 1	0.40	TCGGATATCCAGTGATCGTTA	NM_153701:	NM_153701:NM_005535:
3594	IL12RB1	interleukin 12 receptor, beta 1	0.83	CAGCTCTACAACTCAGTTAAA	NM_153701:	NM_153701:NM_005535:
3595	IL12RB2	interleukin 12 receptor, beta 2	-0.61	CAGGCGACACGTGGAAGAATA	NM_001559:	NM_001559:
3595	IL12RB2	interleukin 12 receptor, beta 2	0.23	CCGTGGGACATTAGAATCAAA	NM_001559:	NM_001559:
3596	IL13	interleukin 13	1.29	TTCATTGACTATCAAACTGAA	NM_002188:	NM_002188:
3596	IL13	interleukin 13	1.34	AACAAGTTGTTTCATTGACTA	NM_002188:	NM_002188:
3597	IL13RA1	interleukin 13 receptor, alpha 1	-1.29	AACCATGTTTGTGGCTATTAA	NM_001560:	NM_001560:
3597	IL13RA1	interleukin 13 receptor, alpha 1	0.68	CTCAGTGATGGAGATAATTTA	NM_001560:	NM_001560:
3598	IL13RA2	interleukin 13 receptor, alpha 2	0.65	TACCATTTGGTTTCATCTTAA	NM_000640:	NM_000640:
3598	IL13RA2	interleukin 13 receptor, alpha 2	0.31	CAGGATATGGATTGCGTATAT	NM_000640:	NM_000640:
3600	IL15	interleukin 15	0.89	CCCATACAAGATCGTATTGTA	NM_000585:	NM_000585:NM_172174:
3600	IL15	interleukin 15	-0.96	CAGCTCTTCTTCAATACTTAA	NM_000585:	NM_000585:NM_172175:NM_172174:
3601	IL15RA	interleukin 15 receptor, alpha	0.20	CCCAAAGCTCTCTGTCAATTA	NM_002189:	NM_172200:NM_002189:
3601	IL15RA	interleukin 15 receptor, alpha	-3.02	CCCAGCTAAGTCCGGAGTGAA	NM_002189:	NM_172200:NM_002189:
3603	IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.63	CACAATAGTAACCTGGGTAAA	NM_004513:	NM_004513:NM_172217:
3603	IL16	interleukin 16 (lymphocyte chemoattractant factor)	-0.83	GTCGTCTTAACTCACCATAAA	NM_004513:	NM_004513:NM_172217:
3605	IL17	interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8)	0.02	ACGAACTTTAAGTATGAGAAA	NM_002190:	NM_002190:
3605	IL17	interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8)	-0.48	CAGGCTTCCTTTGGAGATTAA	NM_002190:	NM_002190:
27190	IL17B	interleukin 17B	0.03	CCAGAGAAAGTGTGAGGTCAA	NM_014443:	NM_014443:
27190	IL17B	interleukin 17B	-0.43	CTGCTGTTTCTTCTTACCATT	NM_014443:	NM_014443:
27189	IL17C	interleukin 17C	-0.09	TACGTGTATTATTAAACTGAT	NM_013278:	NM_013278:
27189	IL17C	interleukin 17C	-0.27	TAAGTGTACGTGTATTATTAA	NM_013278:	NM_013278:
53342	IL17D	interleukin 17D	0.30	TGGGTGCTTGCCAAAGAGATA	NM_138284:	NM_138284:
53342	IL17D	interleukin 17D	-0.90	TGGCTGGAAGCTGATGGGAAA	NM_138284:	NM_138284:
64806	IL17E	interleukin 17E	1.28	ATAGAGATTTATCCAAATAAA	NM_022789:	NM_172314:NM_022789:
64806	IL17E	interleukin 17E	0.60	GAAGCTGTTATTGAATGTATA	NM_022789:	NM_172314:NM_022789:
112744	IL17F	interleukin 17F	-0.09	CAGTGCTAATATAATAAAGTA	NM_052872:	NM_052872:
112744	IL17F	interleukin 17F	0.49	CACTTTATATTTGATATCTAA	NM_052872:	NM_052872:
23765	IL17R	interleukin 17 receptor	-2.42	CAGCGGTCTGGTTATCGTCTA	NM_014339:	NM_014339:
23765	IL17R	interleukin 17 receptor	0.41	CGGCACCTACGTAGTCTGCTA	NM_014339:	NM_014339:
55540	IL17RB	interleukin 17 receptor B	0.53	ACAAACAGCCTTAGTAATTAA	NM_018725:	NM_172234:NM_018725:
55540	IL17RB	interleukin 17 receptor B	-0.97	CCGCTTGTTGAAGGCCACCAA	NM_018725:	NM_172234:NM_018725:
84818	IL17RC	interleukin 17 receptor C	0.88	ACCGCAGATCATTACCTTGAA	NM_032732:	NM_032732:NM_153460:NM_153461:NM_153462:NM_153463:
84818	IL17RC	interleukin 17 receptor C	-1.15	CAGGTACGAGAAGGAACTCAA	NM_032732:	NM_032732:NM_153460:NM_153461:NM_153462:NM_153463:
54756	IL17RD	interleukin 17 receptor D	-0.10	CAGGAAGATACCTGCACTAAT	NM_017563:	NM_017563:
54756	IL17RD	interleukin 17 receptor D	-0.52	CAGCAAGTTTATCGCCGTCTA	NM_017563:	NM_017563:
132014	IL17RE	interleukin 17 receptor E	0.59	CACAAGGGACTTCGCTCTAAA	NM_144640:	NM_144640:NM_153481:NM_153482:NM_153483:NM_153480:
132014	IL17RE	interleukin 17 receptor E	0.54	CGGAAAGATGAATAAAGACAA	NM_144640:	NM_144640:NM_153481:NM_153482:NM_153483:NM_153480:
3606	IL18	interleukin 18 (interferon-gamma-inducing factor)	-1.21	ACGCTTTACTTTATAGCTGAA	NM_001562:	NM_001562:
3606	IL18	interleukin 18 (interferon-gamma-inducing factor)	1.24	CCCGGACCATATTTATTATAA	NM_001562:	NM_001562:
10068	IL18BP	interleukin 18 binding protein	0.53	ACCGATCAAGTCAACTCAGTA	NM_005699:	NM_173042:NM_173043:NM_005699:
10068	IL18BP	interleukin 18 binding protein	-1.40	CAGGATGTGGACGGACTGGTA	NM_005699:	NM_173042:NM_173043:NM_005699:
8809	IL18R1	interleukin 18 receptor 1	0.98	TTGCTATTGCATAGTCTCTAA	NM_003855:	NM_003855:
8809	IL18R1	interleukin 18 receptor 1	-0.80	AAGAGTGAGATTGTCAGTGTA	NM_003855:	NM_003855:
8807	IL18RAP	interleukin 18 receptor accessory protein	-0.92	CCCAGCCTAAGGAATGGTGAA	NM_003853:	NM_003853:
8807	IL18RAP	interleukin 18 receptor accessory protein	-1.82	CCCAGTATCTTTGAACTACAA	NM_003853:	NM_003853:
29949	IL19	interleukin 19	1.64	TCCCATCTAATTTATTGTAAA	NM_013371:	NM_153758:NM_013371:
29949	IL19	interleukin 19	-0.22	CTGCAGATCATTAAGCCCTTA	NM_013371:	NM_153758:NM_013371:
3552	IL1A	interleukin 1, alpha	-0.94	CACGCCTACTTAAGACAATTA	NM_000575:	NM_000575:
3552	IL1A	interleukin 1, alpha	-2.24	CTGAGGTGATTTATGCCTTAA	NM_000575:	NM_000575:
3553	IL1B	interleukin 1, beta	0.53	CAAGATAGAAATCAATAACAA	NM_000576:	NM_000576:
3553	IL1B	interleukin 1, beta	-0.93	CAGCCAATCTTCATTGCTCAA	NM_000576:	NM_000576:
84639	IL1F10	interleukin 1 family, member 10 (theta)	-0.57	AAGGCTCTATACACAAGAGAT	NM_032556:	NM_032556:NM_173161:
84639	IL1F10	interleukin 1 family, member 10 (theta)	0.04	GCAAGATACTACATAATTAAA	NM_032556:	NM_032556:NM_173161:
26525	IL1F5	interleukin 1 family, member 5 (delta)	-0.77	CTGGATGAAGGTAGACCTAAA	NM_012275:	NM_173170:NM_012275:
26525	IL1F5	interleukin 1 family, member 5 (delta)	-0.08	TGGCTCGAGCTCAGAAGATAA	NM_012275:	NM_173170:NM_012275:
27179	IL1F6	interleukin 1 family, member 6 (epsilon)	0.36	AAAGGATATAATGGATTTGTA	NM_014440:	NM_014440:
27179	IL1F6	interleukin 1 family, member 6 (epsilon)	0.38	CTGGGCCTGAATGGACTCAAT	NM_014440:	NM_014440:

27178	IL1F7	interleukin 1 family, member 7 (zeta)	0.23	AACACCAAACCTGCTCACTAA	NM_014439:	NM_014439:NM_173202:NM_173203:NM_173204: NM_173205:
27178	IL1F7	interleukin 1 family, member 7 (zeta)	1.52	CTAATTTGAACTAATTGTATA	NM_014439:	NM_014439:NM_173202:NM_173203:NM_173204: NM_173205:
27177	IL1F8	interleukin 1 family, member 8 (eta)	-0.29	AACGCTCTGTTTAGTATGTAT	NM_014438:	NM_014438:
27177	IL1F8	interleukin 1 family, member 8 (eta)	-0.01	TTGGAATTCACACATGCATAA	NM_014438:	NM_014438:
56300	IL1F9	interleukin 1 family, member 9	-0.17	CACGATGGCATGACTAGCACA	NM_019618:	NM_019618:
56300	IL1F9	interleukin 1 family, member 9	-0.90	CAGGAGAGCTGGGTGGTATAA	NM_019618:	NM_019618:
3554	IL1R1	interleukin 1 receptor, type I	0.21	CAGGGCCTAGCTTTCATTTGA	NM_000877:	NM_000877:
3554	IL1R1	interleukin 1 receptor, type I	1.14	ATGCAGCATATATCCAGTTAA	NM_000877:	NM_000877:
7850	IL1R2	interleukin 1 receptor, type II	-1.26	CACGCCAGGAATATTCAGAAA	NM_004633:	NM_173343:NM_004633:
7850	IL1R2	interleukin 1 receptor, type II	-0.01	AAGACTGACAATCCCGTGTAA	NM_004633:	NM_173343:NM_004633:
3556	IL1RAP	interleukin 1 receptor accessory protein	0.28	CGGGCATTAATTGATTTCCTA	NM_002182:	NM_002182:
3556	IL1RAP	interleukin 1 receptor accessory protein	1.39	CCAGTCTTCATTCGCAGTTTA	NM_002182:	NM_002182:
11141	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	-0.69	ATGCAACAAGTTGAACTCCAA	NM_014271:	NM_014271:
11141	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	-2.35	ACGCATTGTGATGACCAGCAA	NM_014271:	NM_014271:
26280	IL1RAPL2	interleukin 1 receptor accessory protein-like 2	0.51	ACCAAGCATAAAGTACACCTA	NM_017416:	NM_017416:
26280	IL1RAPL2	interleukin 1 receptor accessory protein-like 2	0.78	CAGAAGCTCTGCTGAACTCTA	NM_017416:	NM_017416:
9173	IL1RL1	interleukin 1 receptor-like 1	0.27	ACCGTAAGACTAAGTAGGAAA	NM_003856:	NM_003856:NM_016232:NM_173459:
9173	IL1RL1	interleukin 1 receptor-like 1	-1.58	CAGACTTTGGTGAACCAAGAA	NM_003856:	NM_003856:NM_016232:NM_173459:
8808	IL1RL2	interleukin 1 receptor-like 2	0.99	AAGGACTGTAACGAGATTAAA	NM_003854:	NM_003854:
8808	IL1RL2	interleukin 1 receptor-like 2	0.69	TGGGTCCAATAAAGTGGTATA	NM_003854:	NM_003854:
3557	IL1RN	interleukin 1 receptor antagonist	-0.05	CCAAATGTCAATTTAGAAGAA	NM_000577:	NM_000577:NM_173843:NM_173842:NM_173841:
3557	IL1RN	interleukin 1 receptor antagonist	-1.83	CAGCGAATGAATGCTGTATAT	NM_000577:	NM_000577:NM_173843:NM_173842:NM_173841:
3558	IL2	interleukin 2	0.62	CACCAGGATGCTCACATTTAA	NM_000586:	NM_000586:
3558	IL2	interleukin 2	-0.19	CTGGAGGAAGTGCTAAATTTA	NM_000586:	NM_000586:
50604	IL20	interleukin 20	0.19	CACGGCCAGCATGTATTTCTA	NM_018724:	NM_018724:
50604	IL20	interleukin 20	0.38	CAGATTATATTTATAACCTGA	NM_018724:	NM_018724:
53832	IL20RA	interleukin 20 receptor, alpha	-1.47	CTCAATCTTTATAGAAACGAT	NM_014432:	NM_014432:
53832	IL20RA	interleukin 20 receptor, alpha	0.14	ATGGTTTAATTTAGGGAGTAA	NM_014432:	NM_014432:
59067	IL21	interleukin 21	0.57	GAGCCCTATTAAATTATATAA	NM_021803:	NM_021803:
59067	IL21	interleukin 21	1.79	AAGGATAATCAATGTATCAAT	NM_021803:	NM_021803:
50615	IL21R	interleukin 21 receptor	-0.45	ACCTGTTGAAATGTGAATTAA	NM_021798:	NM_181078:NM_181079:NM_021798:
50615	IL21R	interleukin 21 receptor	-0.36	CCAGAGCAGACCCTCAATAAA	NM_021798:	NM_181078:NM_181079:NM_021798:
50616	IL22	interleukin 22	0.87	AACATGTTTATTTGACCTCAA	NM_020525:	NM_020525:
50616	IL22	interleukin 22	0.53	AAGGTAGACTTTCTAAGCATA	NM_020525:	NM_020525:
58985	IL22RA1	interleukin 22 receptor, alpha 1	-0.31	CGGGTACAATAACACACTGTA	NM_021258:	NM_021258:
58985	IL22RA1	interleukin 22 receptor, alpha 1	0.30	CCGGAGCAAAGCAGCATGATA	NM_021258:	NM_021258:
116379	IL22RA2	interleukin 22 receptor, alpha 2	-0.23	CTGTGTAGTGGCTGAAATATA	NM_052962:	NM_052962:NM_181309:NM_181310:
116379	IL22RA2	interleukin 22 receptor, alpha 2	-1.34	CACAGAGCGGTTGAAATTGAA	NM_052962:	NM_052962:NM_181309:NM_181310:
51561	IL23A	interleukin 23, alpha subunit p19	-1.11	CAGATTTGAGAAGAAGGCAAA	NM_016584:	NM_016584:
51561	IL23A	interleukin 23, alpha subunit p19	0.80	CCAGATTTGAGAAGAAGGCAA	NM_016584:	NM_016584:
149233	IL23R (interle	interleukin 23 receptor	0.50	ATGAGGAGTTGCCATCTATTA	NM_144701:	NM_144701:
149233	IL23R (interle	interleukin 23 receptor	0.17	TCCCATGATTACAGAGATAAA	NM_144701:	NM_144701:
11009	IL24	interleukin 24	-0.01	CAGTGGATGGGTGCTTAGTAA	NM_006850:	NM_181339:NM_006850:
11009	IL24	interleukin 24	-0.06	CTGGCTGAACTTTGTGGTCGA	NM_006850:	NM_181339:NM_006850:
55801	IL26	interleukin 26	-3.53	CAGTGTGAACTTAGTACTTAA	NM_018402:	NM_018402:
55801	IL26	interleukin 26	-0.01	CAAGTACATTGTGTCAACTTA	NM_018402:	NM_018402:
246778	IL27	interleukin 27	-0.13	CTGGACCAACATGGAGAGGAT	NM_145659:	NM_145659:
246778	IL27	interleukin 27	0.92	CAGCCTGCATCTCGCCAGGAA	NM_145659:	NM_145659:
9466	IL27RA	interleukin 27 receptor, alpha	-0.93	TTCCGCTGTAACAGAACTGAA	NM_004843:	NM_004843:
9466	IL27RA	interleukin 27 receptor, alpha	-0.64	TCCGGCTTCATCTACCAGATA	NM_004843:	NM_004843:
282616	IL28A	interleukin 28A (interferon, lambda 2)	-2.61	TAGCCACTTGTCTTAATTTAT	NM_172138:	NM_172138:
282616	IL28A	interleukin 28A (interferon, lambda 2)	0.04	CAGGAATGAAACTAGACATGA	NM_172138:	NM_172138:
163702	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	-0.50	CCCAGTTTGGATGGCACGTTA	NM_170743:	NM_170743:NM_173064:NM_173065:
163702	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	-1.41	CACTCCGTTTCTATTCTTAAA	NM_170743:	NM_170743:NM_173064:NM_173065:
282618	IL29	interleukin 29 (interferon, lambda 1)	-0.26	CGCCTTGGAAGAGTCACTCAA	NM_172140:	NM_172140:
282618	IL29	interleukin 29 (interferon, lambda 1)	-0.04	CCCTACTCCTTCCTTAATTTA	NM_172140:	NM_172140:
3559	IL2RA	interleukin 2 receptor, alpha	0.58	CCACCCTATATGTAGTATAAA	NM_000417:	NM_000417:
3559	IL2RA	interleukin 2 receptor, alpha	0.49	CTCCACCCTATATGTAGTATA	NM_000417:	NM_000417:
3560	IL2RB	interleukin 2 receptor, beta	-2.24	CCCGGATGCCTTGGAGATAGA	NM_000878:	NM_000878:
3560	IL2RB	interleukin 2 receptor, beta	-1.32	ATGGCTGAAGAAGGTCCTGAA	NM_000878:	NM_000878:
3561	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	0.05	CTAGAGGATCTTGTTACTGAA	NM_000206:	NM_000206:
3561	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	0.00	CTGAACAATCAGTGGATTATA	NM_000206:	NM_000206:
3562	IL3	interleukin 3 (colony-stimulating factor, multiple)	0.61	AGCAATTGAGAGCATTCTTAA	NM_000588:	NM_000588:
3562	IL3	interleukin 3 (colony-stimulating factor, multiple)	-0.03	CTGCTCTAACATGATCGATGA	NM_000588:	NM_000588:
133396	IL31RA	interleukin 31 receptor A	1.04	CGGGACCAGCATAAATTTCAA	NM_139017:	NM_139017:
133396	IL31RA	interleukin 31 receptor A	0.43	AAGAATAACGATCCCAGATAA	NM_139017:	NM_139017:
3565	IL4	interleukin 4	-0.59	CACCGAGTTGACCGTAACAGA	NM_000589:	NM_000589:
3565	IL4	interleukin 4	0.00	CACATTGTCACTGCAAATCGA	NM_000589:	NM_172348:NM_000589:
259307	IL4I1	interleukin 4 induced 1	0.28	ACACGAGGACCTCGCATTAAA	NM_152899:	NM_152899:NM_172374:
259307	IL4I1	interleukin 4 induced 1	0.61	CTGGGTGGAGACGGCGGTCAA	NM_152899:	NM_152899:NM_172374:
3566	IL4R	interleukin 4 receptor	0.18	CACATACATGAGGGTCTCTTA	NM_000418:	NM_000418:
3566	IL4R	interleukin 4 receptor	0.05	CCGCCTCGTGGCTATAATAAT	NM_000418:	NM_000418:
3567	IL5	interleukin 5 (colony-stimulating factor, eosinophil)	0.08	CGGAGAGTAAACCAATTCCTA	NM_000879:	NM_000879:
3567	IL5	interleukin 5 (colony-stimulating factor, eosinophil)	-0.95	AAGAAATACATTGACGGCCAA	NM_000879:	NM_000879:
3568	IL5RA	interleukin 5 receptor, alpha	-0.36	CACCAGTCTTGTATCTCTTAA	NM_000564:	NM_000564:NM_175726:
3568	IL5RA	interleukin 5 receptor, alpha	0.73	CACGCCATTGATCAAATAAAT	NM_000564:	NM_175728:NM_000564:NM_175724:NM_175725: NM_175726:NM_175727:
3569	IL6	interleukin 6 (interferon, beta 2)	1.54	TAAAGAAATATTTATATTGTA	NM_000600:	NM_000600:
3569	IL6	interleukin 6 (interferon, beta 2)	1.37	CAAATAAATGGCTAACTTATA	NM_000600:	NM_000600:
3570	IL6R	interleukin 6 receptor	1.70	ACCCAGTTAGCTCTCAAGTTA	NM_000565:	NM_181359:NM_000565:
3570	IL6R	interleukin 6 receptor	1.18	TAGTTGTAACACCATGATTAA	NM_000565:	NM_181359:NM_000565:
3572	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-0.73	CGGCCAGAAGATCTACAATTA	NM_002184:	NM_175767:NM_002184:
3572	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	1.36	CACATTGTACATGGTACGAAT	NM_002184:	NM_175767:NM_002184:
3574	IL7	interleukin 7	-1.34	TAAGAGAGTCATAAACCTTAA	NM_000880:	NM_000880:
3574	IL7	interleukin 7	1.79	CTGAATGCTCCAGTCAACAAA	NM_000880:	NM_000880:
3575	IL7R	interleukin 7 receptor	-0.91	CGGCAGCAATGTATGAGATTA	NM_002185:	NM_002185:
3575	IL7R	interleukin 7 receptor	-0.87	CTGAGTGTCGTCTATCGGGAA	NM_002185:	NM_002185:
3576	IL8	interleukin 8	-0.99	AACAATTGGGTACCCAGTTAA	NM_000584:	NM_000584:
3576	IL8	interleukin 8	-1.03	CTGCGCCAACACAGAAATTAT	NM_000584:	NM_000584:
3577	IL8RA	interleukin 8 receptor, alpha	0.43	CCCGTTGAACGTCACATCTTT	NM_000634:	NM_000634:
3577	IL8RA	interleukin 8 receptor, alpha	1.41	TCCGCCAGGCTTACCATCCAA	NM_000634:	NM_000634:
3579	IL8RB	interleukin 8 receptor, beta	0.15	AGGATTTAAGTTTACCTCAAA	NM_001557:	NM_001557:
3579	IL8RB	interleukin 8 receptor, beta	-1.96	CCCAGTCAGGATTTAAGTTTA	NM_001557:	NM_001557:
3578	IL9	interleukin 9	0.48	ATCAGTTGAAGTACTAAAGAA	NM_000590:	NM_000590:
3578	IL9	interleukin 9	0.92	TACCACCATGCAAACAAGATA	NM_000590:	NM_000590:

3581	IL9R	interleukin 9 receptor	-5.27	CAGCTATGAGCTGGCCTTCAA	NM_002186:	NM_002186:NM_176786:
3581	IL9R	interleukin 9 receptor	-0.37	AAGGACAAGGGCCAAGGTCTA	NM_002186:	NM_002186:NM_176786:
3581	IL9R	interleukin 9 receptor	-2.23	CAGGGTGAAGAGAATCTTCTA	XM_375284:	NM_002186:XM_375284:
3581	IL9R	interleukin 9 receptor	0.36	AGGCACCTTTCTAGAGATTAA	XM_375284:	NM_002186:NM_176786:XM_375284:
286676	ILDR1	immunoglobulin-like domain containing receptor 1	0.52	TGGGAATGACACAGTATATAA	NM_175924:	NM_175924:
286676	ILDR1	immunoglobulin-like domain containing receptor 1	-0.34	AAGGAAATCTATGGAGTATTA	NM_175924:	NM_175924:
3608	ILF2	interleukin enhancer binding factor 2, 45kDa	-6.85	CAGGCCCTTTGTACCACATAT	NM_004515:	NM_004515:
3608	ILF2	interleukin enhancer binding factor 2, 45kDa	-0.04	CTCCATAGAAGTGTCATTCCA	NM_004515:	NM_004515:
3609	ILF3	interleukin enhancer binding factor 3, 90kDa	-0.85	AACGATTTCACCACATCTGAA	NM_153464:	NM_004516:NM_153464:
3609	ILF3	interleukin enhancer binding factor 3, 90kDa	-0.01	CTGGTTTAGCTAGAGAGTGAA	NM_153464:	NM_004516:NM_153464:
3611	ILK	integrin-linked kinase	-0.11	AAGGAAGAGCAGGGACTTCAA	NM_004517:	NM_001014795:NM_001014794:NM_004517:
3611	ILK	integrin-linked kinase	0.48	CAGCCCGAGTCCCGAGGATAA	NM_004517:	NM_004517:
80895	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	-0.39	ATGGAGGAATTCGAGCCTCAA	NM_176799:	NM_030768:NM_176799:
80895	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	-0.89	CCCGCTAGCAGTGGCGATTCA	NM_176799:	NM_030768:NM_176799:
83943	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	1.78	CCAGTTAGGAAGAACAGTAAA	NM_032549:	NM_032549:
83943	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	1.11	CAAGAAGGAACACATATTATA	NM_032549:	NM_032549:
3612	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	1.08	ACGAAGAGTAATTGCTGCAAA	NM_005536:	NM_005536:
3612	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	-0.33	CCGGAAGAGACGAGTGCGGTA	NM_005536:	NM_005536:
3614	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	0.34	ATGGCCTGCACTCTTACGAAA	NM_183243:	NM_183243:NM_000883:
3614	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	0.13	CAGCAGCAGCCAGAAACGATA	NM_183243:	NM_183243:NM_000883:
3615	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	-0.24	CAGAACAGATATTTCAGTGAA	NM_000884:	NM_000884:
3615	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	-0.44	TGGGATCCGGCTAAAGAAATA	NM_000884:	NM_000884:
3617	IMPG1	interphotoreceptor matrix proteoglycan 1	-0.52	TCGGATCTTTCTGGATCGCAT	NM_001563:	NM_001563:
3617	IMPG1	interphotoreceptor matrix proteoglycan 1	0.11	CCGTAGAATATGAAGAATTTA	NM_001563:	NM_001563:
50939	IMPG2	interphotoreceptor matrix proteoglycan 2	-1.09	AAGGAAATTCGTGTACTTGAA	NM_016247:	NM_016247:
50939	IMPG2	interphotoreceptor matrix proteoglycan 2	0.69	TCAGGCATTCATCTAAATAAA	NM_016247:	NM_016247:
10207	INADL	InaD-like (Drosophila)	-1.44	CAGCTTCATCATACCATTCAA	NM_005799:	NM_176877:NM_176878:NM_170605:NM_005799:
10207	INADL	InaD-like (Drosophila)	-0.87	CTGCACATTATTGAACTTGAA	NM_005799:	NM_176877:NM_176878:NM_170605:NM_005799:
3619	INCENP	inner centromere protein antigens 135/155kDa	-1.19	AGCGTTTGGGAGGTAGATTAA	NM_020238:	NM_020238:
3619	INCENP	inner centromere protein antigens 135/155kDa	-3.83	CCGCATCATCTGTCACAGTTA	NM_020238:	NM_020238:
3620	INDO	indoleamine-pyrrole 2,3 dioxygenase	0.09	CCGTAAGGTCTTGCCAAGAAA	NM_002164:	NM_002164:
3620	INDO	indoleamine-pyrrole 2,3 dioxygenase	1.33	AGGAAGGTTAATGTAACCCAA	NM_002164:	NM_002164:
3621	ING1	inhibitor of growth family, member 1	0.82	CAGTTTGTTCCTCTAGTAGTA	NM_005537:	NM_198219:NM_005537:NM_198218:NM_198217:
3621	ING1	inhibitor of growth family, member 1	1.13	TAGGTTTGATTCAACACTTAA	NM_005537:	NM_198219:NM_005537:NM_198218:NM_198217:
3622	ING2	inhibitor of growth family, member 2	1.98	AACAAATATCAAGAAACGTTA	NM_001564:	NM_001564:
3622	ING2	inhibitor of growth family, member 2	0.80	AGAGCACTAATTAATAGTCAA	NM_001564:	NM_001564:
54556	ING3	inhibitor of growth family, member 3	-0.59	CTAGAGTACCTGGGTACATAA	NM_019071:	NM_198266:NM_019071:
54556	ING3	inhibitor of growth family, member 3	-0.12	AACCAAGATTGCCCTATAGAA	NM_019071:	NM_198266:NM_019071:
51147	ING4	inhibitor of growth family, member 4	0.30	TACGTACTGCTATACTATAAA	NM_016162:	NM_198287:NM_016162:
51147	ING4	inhibitor of growth family, member 4	0.17	TACATACGTACTGCTATACTA	NM_016162:	NM_198287:NM_016162:
84289	ING5	inhibitor of growth family, member 5	-0.01	ACCGTGAGGGATGTTAATTAT	NM_032329:	NM_032329:
84289	ING5	inhibitor of growth family, member 5	1.31	AACCGTGAGGGATGTTAATTA	NM_032329:	NM_032329:
3623	INHA (inhibin,	inhibin, alpha	0.06	CAGCACTGTGCTTGTATCTAA	NM_002191:	NM_002191:
3623	INHA (inhibin,	inhibin, alpha	-0.89	AAGGCAGAGTTGGGAAATAGA	NM_002191:	NM_002191:
3624	INHBA	inhibin, beta A (activin A, activin AB alpha polypeptide)	-2.86	CTGCAGTAGTGTGGACTAGAA	NM_002192:	NM_002192:
3625	INHBB (inhibi	inhibin, beta B (activin AB beta polypeptide)	0.82	CACGTGAACTATGCAATTTAA	NM_002193:	NM_002193:
3625	INHBB (inhibi	inhibin, beta B (activin AB beta polypeptide)	0.23	CCACGTGAACTATGCAATTTA	NM_002193:	NM_002193:
3626	INHBC	inhibin, beta C	-1.09	CAGCCCAAGGTTGCATGGGAA	NM_005538:	NM_005538:
3626	INHBC	inhibin, beta C	0.01	ACACCCTTAGCTCACCTTTAA	NM_005538:	NM_005538:
83729	INHBE	inhibin, beta E	-1.36	TAGGGTGATGGTCCAGAGCAA	NM_031479:	NM_031479:
83729	INHBE	inhibin, beta E	-2.63	AGGGCTGTTGAGGTACCTTAA	NM_031479:	NM_031479:
3628	INPP1	inositol polyphosphate-1-phosphatase	1.05	CCGTAATTAGTACAAGTGAAA	NM_002194:	NM_002194:
3628	INPP1	inositol polyphosphate-1-phosphatase	1.68	TAGATTCAACTTATCAGTATA	NM_002194:	NM_002194:
8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-0.68	AACGATTTGCCGCAAACTGAA	NM_003866:	NM_003866:
8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-0.16	CCCGGAAAGTGTGAGCGGAAA	NM_003866:	NM_003866:
3632	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	1.88	CGGAAGGTTATGCTCCAGTTA	NM_005539:	NM_005539:
3632	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	-1.63	TCGAGTGATGCGATGAAAGAA	NM_005539:	NM_005539:
3633	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	-0.27	TTGCGGGAACATACAATGTAA	NM_005540:	NM_005540:
3633	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	-0.89	AAGAAGAGGATTACACCTATA	NM_005540:	NM_005540:
3635	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	-2.43	CAGGTGCTATGCCACATTGAA	NM_005541:	NM_005541:NM_001017915:
3635	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	-8.37	TCCCATCAACATGGTGTCCAA	NM_005541:	NM_005541:NM_001017915:
56623	INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	-3.02	ACGCATCGTGTCTCAGATCAA	NM_019892:	NM_019892:
56623	INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	-0.50	ACGGATTTCGAAGGAGATTCA	NM_019892:	NM_019892:
22876	INPP5F	inositol polyphosphate-5-phosphatase F	-0.31	AAGACCTTTACGCATATTAAA	NM_198331:	NM_014937:NM_198331:
22876	INPP5F	inositol polyphosphate-5-phosphatase F	-0.04	CAGATCTTCCATGGTGGCTTA	NM_198331:	NM_014937:NM_198331:
3630	INS (insulin)	insulin	-1.16	AAGCGTGGCATTGTGGAACAA	NM_000207:	NM_000207:
3630	INS (insulin)	insulin	-0.01	AGGCTTCTTCTACACACCCAA	NM_000207:	NM_000207:
3638	INSIG1	insulin induced gene 1	-0.85	AAGCAGCGAGTGAATCTTTAA	NM_198337:	NM_005542:NM_198336:NM_198337:
3638	INSIG1	insulin induced gene 1	0.69	ATGGTGCTTAACAAACATGAA	NM_198337:	NM_005542:NM_198336:NM_198337:
3640	INSL3	insulin-like 3 (Leydig cell)	1.39	TTGCTGTCTCTTAGTAAATAA	NM_005543:	NM_005543:
3640	INSL3	insulin-like 3 (Leydig cell)	-0.09	CTCAGTGGCTGTACCCAACAA	NM_005543:	NM_005543:
3641	INSL4	insulin-like 4 (placenta)	-3.10	ATCCATTCTGTTGTGAAGTAA	NM_002195:	NM_002195:
3641	INSL4	insulin-like 4 (placenta)	0.02	CTGAGCCAACTCCTTAGAGAA	NM_002195:	NM_002195:
3643	INSR	insulin receptor	0.63	ACCGCTTTACGCTTCTTCAAA	NM_000208:	NM_000208:
3643	INSR	insulin receptor	-0.92	TAGGAAGACGTTTGAGGATTA	NM_000208:	NM_000208:
3645	INSRR	insulin receptor-related receptor	-3.00	CAGCTCGGATTTCGAGATCCA	NM_014215:	NM_014215:
3645	INSRR	insulin receptor-related receptor	0.67	TTGGAAGGTGACGTCCATCAA	NM_014215:	NM_014215:
79711	IPO4	importin 4	0.37	TACAGCCTATTTGCAGCCTTA	NM_024658:	NM_024658:
79711	IPO4	importin 4	-0.09	CCCAAGCATTTCGCTGTACAA	NM_024658:	NM_024658:
10527	IPO7	importin 7	-0.59	CACCTACTACTCAATACCTTA	NM_006391:	NM_006391:
10527	IPO7	importin 7	0.41	CTGACTCACGGTCTTAATGAA	NM_006391:	NM_006391:
8826	IQGAP1	IQ motif containing GTPase activating protein 1	-2.33	CAGGCGCTAGCTCATGAAGAA	NM_003870:	NM_003870:
8826	IQGAP1	IQ motif containing GTPase activating protein 1	-0.61	CTGGGAGATAATGCCCACTTA	NM_003870:	NM_003870:
10788	IQGAP2 (IQ n	IQ motif containing GTPase activating protein 2	0.21	CCGACAAAGTCCTGAATTCTA	NM_006633:	NM_006633:
10788	IQGAP2 (IQ n	IQ motif containing GTPase activating protein 2	-1.84	CGGCAGAACATTGCTTATGAA	NM_006633:	NM_006633:
128239	IQGAP3	IQ motif containing GTPase activating protein 3	-2.32	CTCCGTGGTTCCGTTGAAGAA	NM_178229:	NM_178229:
128239	IQGAP3	IQ motif containing GTPase activating protein 3	1.55	GAGCACTAAGACCACCTTCTA	NM_178229:	NM_178229:
3654	IRAK1	interleukin-1 receptor-associated kinase 1	0.61	CCGGGCAATTCAGTTTCTACA	NM_001569:	NM_001569:NM_001025242:NM_001025243:
3654	IRAK1	interleukin-1 receptor-associated kinase 1	0.42	TCCCATCGCCATGCAGATCTA	NM_001569:	NM_001569:NM_001025242:
3656	IRAK2	interleukin-1 receptor-associated kinase 2	0.26	CAGCAACGTCAAGAGCTCTAA	NM_001570:	NM_001570:
3656	IRAK2	interleukin-1 receptor-associated kinase 2	0.20	CCAGATCATCCTGAACTGGAA	NM_001570:	NM_001570:
11213	IRAK3	interleukin-1 receptor-associated kinase 3	1.01	CACATTCGAATCGGTATATTA	NM_007199:	NM_007199:
11213	IRAK3	interleukin-1 receptor-associated kinase 3	0.15	CTGGATGTTCGTCATATTGAA	NM_007199:	NM_007199:
51135	IRAK4	interleukin-1 receptor-associated kinase 4	1.99	ATCCTATTAGTCATATATTTA	NM_016123:	NM_016123:
51135	IRAK4	interleukin-1 receptor-associated kinase 4	0.26	TTGCAGGACAGTGGTTATTAA	NM_016123:	NM_016123:

3658	IREB2	iron-responsive element binding protein 2	-1.25	CAGGAAGTATCGCTAGGAATA	NM_004136:	NM_004136:
3658	IREB2	iron-responsive element binding protein 2	-2.22	CAGTGGGATGGTTACACATTA	NM_004136:	NM_004136:
3659	IRF1	interferon regulatory factor 1	-2.99	CAAGCATGGCTGGGACATCAA	NM_002198:	NM_002198:
3659	IRF1	interferon regulatory factor 1	0.08	CAGCCGAGATGCTAAGAGCAA	NM_002198:	NM_002198:
3660	IRF2	interferon regulatory factor 2	-0.03	CACCTTATCTTAAAGCACTTA	NM_002199:	NM_002199:
3660	IRF2	interferon regulatory factor 2	-1.69	ACGGTGAACATCATAGTTGTA	NM_002199:	NM_002199:
26145	IRF2BP1	interferon regulatory factor 2 binding protein 1	0.77	ACCGCTGCCGCGGATAAATTA	NM_015649:	NM_015649:
26145	IRF2BP1	interferon regulatory factor 2 binding protein 1	-0.02	TTCAAGTACCTCGAATATGAA	NM_015649:	NM_015649:
359948	IRF2BP2	interferon regulatory factor 2 binding protein 2	1.09	CTGCTTGAATTGTATATATAT	NM_182972:	NM_182972:
359948	IRF2BP2	interferon regulatory factor 2 binding protein 2	0.32	CCCAATGATTACCCTTAATTA	NM_182972:	NM_182972:
3661	IRF3 (interfer	interferon regulatory factor 3	-0.76	CAAGAGGCTCGTGATGGTCAA	NM_001571:	NM_001571:
3661	IRF3 (interfer	interferon regulatory factor 3	-4.12	CCGCTCTGCCCTCAACCGCAA	NM_001571:	NM_001571:
3662	IRF4	interferon regulatory factor 4	0.88	CAGTGATGTATACATCTTATA	NM_002460:	NM_002460:
3662	IRF4	interferon regulatory factor 4	-0.08	TAGCTAAACAGTGAAGATTTA	NM_002460:	NM_002460:
3667	IRS1	insulin receptor substrate 1	-0.05	CCGGGTGAACCTCAGTCCTAA	NM_005544:	NM_005544:
3667	IRS1	insulin receptor substrate 1	-3.13	CCGGTATCGTTTCGCATGGAA	NM_005544:	NM_005544:
8660	IRS2 (insulin	insulin receptor substrate 2	0.94	CAGTGTATTGACGCATATTTA	NM_003749:	NM_003749:
8660	IRS2 (insulin	insulin receptor substrate 2	-0.02	TCGCTATAGAATAATGCATTA	NM_003749:	NM_003749:
8471	IRS4	insulin receptor substrate 4	0.12	GAGGGTGACTACATTGAAGTA	NM_003604:	NM_003604:
8471	IRS4	insulin receptor substrate 4	1.32	GCGGCGCGTGATCACCCTATA	NM_003604:	NM_003604:
10379	ISGF3G	interferon-stimulated transcription factor 3, gamma 48kDa	-1.65	CCGGAGTGTGCTGGGATGATA	NM_006084:	NM_006084:
10379	ISGF3G	interferon-stimulated transcription factor 3, gamma 48kDa	0.04	CACGATTGACCTGTCCTCTTT	NM_006084:	NM_006084:
57611	ISLR2	immunoglobulin superfamily containing leucine-rich repeat 2	0.92	CGCGATTATCTGCGAAATCCA	NM_020851:	NM_020851:
57611	ISLR2	immunoglobulin superfamily containing leucine-rich repeat 2	0.46	CCCGGTGGCACCGTAGTCTTA	NM_020851:	NM_020851:
51477	ISYNA1	myo-inositol 1-phosphate synthase A1	-0.59	TACCCTATGTTGAACAAGAAA	NM_016368:	NM_016368:
51477	ISYNA1	myo-inositol 1-phosphate synthase A1	-6.88	CCGCTCTAAGGAGGTGTCCAA	NM_016368:	NM_016368:
51477	ISYNA1	myo-inositol 1-phosphate synthase A1	0.45	TACCCTATGTTGAACAAGAAA	NM_016368:	NM_016368:
51477	ISYNA1	myo-inositol 1-phosphate synthase A1	-5.23	CCGCTCTAAGGAGGTGTCCAA	NM_016368:	NM_016368:
83737	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	1.57	GACCGCAGACATAAATATCTA	NM_031483:	NM_031483:
83737	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	0.83	TAGAGAGTTATCTGAGTGTAA	NM_031483:	NM_031483:
55846	ITFG2	integrin alpha FG-GAP repeat containing 2	1.12	GACGTTGATAACGATACGTTA	NM_018463:	NM_018463:
55846	ITFG2	integrin alpha FG-GAP repeat containing 2	0.39	TAGGGAATATGCATTACAGAA	NM_018463:	NM_018463:
3672	ITGA1	integrin, alpha 1	-1.65	ACTGAGGACATTGGAAATGAA	NM_181501:	NM_181501:
3672	ITGA1	integrin, alpha 1	-2.35	CTGCATGTCGCCACCACTGAA	NM_181501:	NM_181501:
8515	ITGA10	integrin, alpha 10	-0.96	CTGGGTGTACCTAGGCAGTAT	NM_003637:	NM_003637:
8515	ITGA10	integrin, alpha 10	-0.89	CACAAGAGACATTCTGTACAA	NM_003637:	NM_003637:
22801	ITGA11	integrin, alpha 11	0.00	CGCCTACAGCACGGTCCTAAA	NM_012211:	NM_012211:NM_001004439:
22801	ITGA11	integrin, alpha 11	0.93	ACCTGTTTGTTTATAACGGAA	NM_012211:	NM_012211:NM_001004439:
3673	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	0.38	CCCGAGCACATCATTTATATA	NM_002203:	NM_002203:
3673	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-1.18	TCGCTAGTATTCCAACAGAAA	NM_002203:	NM_002203:
3674	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen	-4.05	CAGCCAGAATCCAAACAGCAA	NM_000419:	NM_000419:
3674	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen	0.73	CCAAACTTTACAAACCTTCAA	NM_000419:	NM_000419:
3675	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	-0.43	CACCATCAACATGGAGAACAA	NM_002204:	NM_002204:NM_005501:
3675	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	-1.61	CTGGATTGACTTTGCTGTCAA	NM_002204:	NM_002204:NM_005501:
3676	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	1.68	ACGACTCTACATGTCAAACTA	NM_000885:	NM_000885:
3676	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	0.19	CAGATTGGTAAGGCATATATA	NM_000885:	NM_000885:
3678	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	0.06	CCCATTGAATTTGACAGCAAA	NM_002205:	NM_002205:
3678	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	0.94	TGGGCCAACAAAGAACACTAA	NM_002205:	NM_002205:
3655	ITGA6	integrin, alpha 6	0.03	CAGGGTAATAAACTTAGGTAA	NM_000210:	NM_000210:
3655	ITGA6	integrin, alpha 6	-0.67	CCGGCCTGTGATTAATATTCA	NM_000210:	NM_000210:
3679	ITGA7	integrin, alpha 7	-0.21	CCCAGTGATGGTATACTTGGA	NM_002206:	NM_002206:
3679	ITGA7	integrin, alpha 7	-0.35	CACAGTGAAGTCCTCCATAAA	NM_002206:	NM_002206:
8516	ITGA8 (integri	integrin, alpha 8	0.59	CCGGATTTGGCTTTACTTTAA	NM_003638:	NM_003638:
8516	ITGA8 (integri	integrin, alpha 8	1.21	TCCGAGATAAATTATCTCCAA	NM_003638:	NM_003638:
3680	ITGA9	integrin, alpha 9	-3.28	ACCGAAGATCAGGCACCTTAA	NM_002207:	NM_002207:
3680	ITGA9	integrin, alpha 9	-0.19	CCGAAGGTACAAAGAAATTAT	NM_002207:	NM_002207:
3680	ITGA9	integrin, alpha 9	0.71	AAGAGCAATCGGCTAGGTTTA	BC028701:	NM_002207:
3681	ITGAD	integrin, alpha D	0.59	CAGCTATTTCATCATAAGAAT	XM_496142:	NM_005353:
3681	ITGAD	integrin, alpha D	-3.13	CAGGTGAGGATTCCTACGGAA	XM_496142:	NM_005353:
3682	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antiger	0.49	TTGGTATTAAATAAATTTACA	NM_002208:	NM_002208:
3682	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antiger	0.15	TAGGAAACATTTGGTATTAAA	NM_002208:	NM_002208:
3683	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associa	-9.64	CAGGGCGTGGGACATCTAGTA	NM_002209:	NM_002209:
3683	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associa	1.34	CCCTGTTTAATGATTGACGTA	NM_002209:	NM_002209:
3684	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	0.00	TCAGACATCGGTTCATATTAA	NM_000632:	NM_000632:
3684	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	-0.53	CTCGTTTGACTGGTACATCAA	NM_000632:	NM_000632:
3685	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD5	2.42	ATGTAGTAGTTTGATGAATAA	NM_002210:	NM_002210:
3685	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD5	3.03	CACATACATGATACCATCCAA	NM_002210:	NM_002210:
3687	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	-0.09	CCGGCTGCTTCTGACAGCCAA	NM_000887:	NM_000887:
3687	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	-1.45	CTCCCAGGAACACATATTTAA	NM_000887:	NM_000887:
3688	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 i	-0.22	AAGAGGGATAATACAAATGAA	NM_002211:	NM_002211:NM_033666:NM_033667:NM_033668:NM_033669:NM_133376:
3688	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 i	-0.46	ACAGATGAAGTTAACAGTGAA	NM_002211:	NM_002211:NM_033666:NM_033667:NM_033668:NM_033669:NM_133376:
3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	0.76	TGCCAATTTATTTACATTTAA	NM_000211:	NM_000211:
3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	-0.09	CAGGACATCAGTCTGATTAAA	NM_000211:	NM_000211:
3690	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.51	CACGTGTGGCCTGTTCTTCTA	NM_000212:	NM_000212:
3690	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	-4.41	CCGCTTCAATGAGGAAGTGAA	NM_000212:	NM_000212:
23421	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	1.80	TAGCATTTGTGGGTAGACTTA	NM_014288:	NM_014288:
23421	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	1.84	CAGAGAAATATTTGTAATTAA	NM_014288:	NM_014288:
3691	ITGB4	integrin, beta 4	-0.72	AACGATGACAACCGACCTATT	NM_000213:	NM_001005619:NM_001005731:NM_000213:
3691	ITGB4	integrin, beta 4	-0.69	GTGGATGAGTTCCGGAATAAA	NM_000213:	NM_001005619:NM_001005731:NM_000213:
3692	ITGB4BP	integrin beta 4 binding protein	-0.51	CTGGATCTATCATTACTGCAA	NM_002212:	NM_181466:NM_181467:NM_181468:NM_181469:NM_002212:
3692	ITGB4BP	integrin beta 4 binding protein	-3.44	AAGCTACTGTGTCTTCAGCAA	NM_002212:	NM_181466:NM_181467:NM_181468:NM_181469:NM_002212:
3693	ITGB5	integrin, beta 5	2.02	CAAGATTGTTTGGGATTGGAA	NM_002213:	NM_002213:
3693	ITGB5	integrin, beta 5	2.05	CCGCTATGAAATGGCTTCAAA	NM_002213:	NM_002213:
3694	ITGB6 (integri	integrin, beta 6	-5.94	CTGGAATTACTTGTCAGCCCA	NM_000888:	NM_000888:
3694	ITGB6 (integri	integrin, beta 6	1.25	AAGGACTCAACTTGTCATTTA	NM_000888:	NM_000888:
3695	ITGB7 (integri	integrin, beta 7	1.44	CAAGTATACAATAAAGTCTTA	NM_000889:	NM_000889:
3695	ITGB7 (integri	integrin, beta 7	-1.57	CCGGCTCTCGGTGGAAATCTA	NM_000889:	NM_000889:
3696	ITGB8 (integri	integrin, beta 8	1.26	CAGATACAACCTTAATCTTAA	NM_002214:	NM_002214:
3696	ITGB8 (integri	integrin, beta 8	0.44	ATGCAGAAACGTGACGAGCAA	NM_002214:	NM_002214:
3702	ITK	IL2-inducible T-cell kinase	0.11	CAGGACTTTAGTAGAGACTGA	NM_005546:	NM_005546:
3702	ITK	IL2-inducible T-cell kinase	-0.14	CTGGTGAGTTAAGTAAGATTA	NM_005546:	NM_005546:
55600	ITLN1	intelectin 1 (galactofuranose binding)	0.09	ACCCAGTAGCTAGAATGTTAA	NM_017625:	NM_017625:
55600	ITLN1	intelectin 1 (galactofuranose binding)	-1.28	CTGCGGGATTTGTTCAGTTCA	NM_017625:	NM_017625:
142683	ITLN2	intelectin 2	-3.24	CACCAAGAATGGTGTTGTCTA	NM_080878:	NM_080878:
142683	ITLN2	intelectin 2	1.03	TAGAAGCTGCAAAGAAATCAA	NM_080878:	NM_080878:

9445	ITM2B	integral membrane protein 2B	-3.88	TAGGTAGTAGGAAGAATTACA	NM_021999:	NM_021999:
9445	ITM2B	integral membrane protein 2B	0.69	TAGTAACTGTATGAAGTCATA	NM_021999:	NM_021999:
3704	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	-3.01	CTGGAGAAGTTAAAGCCTGAA	NM_033453:	NM_181493:NM_033453:
3704	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	-15.90	CTGGATGAGACTTGTTTCCAA	NM_033453:	NM_181493:NM_033453:
3705	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	0.45	CACGCCGTCATTGACATCAAT	NM_014216:	NM_014216:
3705	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	-0.21	CCGATTAATGTCTGTACGTCA	NM_014216:	NM_014216:
3706	ITPKA (inosit	inositol 1,4,5-trisphosphate 3-kinase A	0.17	CACCAGCGGGCTGATCCTGAA	NM_002220:	NM_002220:
3706	ITPKA (inosit	inositol 1,4,5-trisphosphate 3-kinase A	0.11	CCGGTCTAACGTCTCACACCA	NM_002220:	NM_002220:
3707	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	0.54	AAGGCCATTCGAACCACTCTA	NM_002221:	NM_002221:
3707	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	0.98	GACGTAAAGATTCTATGAATA	NM_002221:	NM_002221:
80271	ITPKC (inosit	inositol 1,4,5-trisphosphate 3-kinase C	-1.56	CCGGAAGGACATGTATGAGAA	NM_025194:	NM_025194:
80271	ITPKC (inosit	inositol 1,4,5-trisphosphate 3-kinase C	-0.15	TCGGCCGAAGCCCGAACCGAA	NM_025194:	NM_025194:
3708	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	1.05	TGGTGTGTTAATACTATGTAA	NM_002222:	NM_002222:
3708	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	-0.64	AACTACGAATTTACTATACTA	NM_002222:	NM_002222:
3709	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	0.03	CGGAATCAACATCAACGATTA	NM_002223:	NM_002223:
3709	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	0.62	CCAGTTCAACTTGACGATGAA	NM_002223:	NM_002223:
3710	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	0.53	TCAGTTTACCTTAATGCCTTA	NM_002224:	NM_002224:
3710	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	-0.45	CCGCAGCATGCCGCTGATCTA	NM_002224:	NM_002224:
160897	ITR	intimal thickness-related receptor	2.00	ATGCCTCATCTTAATAGCTAA	NM_180989:	NM_180989:
160897	ITR	intimal thickness-related receptor	-1.27	CCCAATCATAATTAAGCCGTA	NM_180989:	NM_180989:
50618	ITSN2	intersectin 2	-0.39	TTGGCGCGGCCTGATACTGAA	NM_006277:	NM_006277:NM_019595:
50618	ITSN2	intersectin 2	-3.59	CACCAGGACAGTTAATATTAA	NM_006277:	NM_147152:NM_006277:NM_019595:
3712	IVD	isovaleryl Coenzyme A dehydrogenase	-0.21	CAGCTTGTACGCAATGGGAAT	NM_002225:	NM_002225:
3712	IVD	isovaleryl Coenzyme A dehydrogenase	0.47	TCGCAGCAATGAGTTCAAGAA	NM_002225:	NM_002225:
182	JAG1	jagged 1 (Alagille syndrome)	0.34	CAGAGTAATCTTGTTGGTTCA	NM_000214:	NM_000214:
182	JAG1	jagged 1 (Alagille syndrome)	-0.57	CTGCATTTAGGGAGTATTCTA	NM_000214:	NM_000214:
3714	JAG2	jagged 2	0.62	CTGCGTCGTCACCAAATCGTA	NM_002226:	NM_002226:NM_145159:
3714	JAG2	jagged 2	0.62	CTACGTTTCTTTAACCTTGTA	NM_002226:	NM_002226:NM_145159:
3716	JAK1	Janus kinase 1 (a protein tyrosine kinase)	-16.81	ACCGGATGAGGTTCTATTTCA	NM_002227:	NM_002227:
3716	JAK1	Janus kinase 1 (a protein tyrosine kinase)	0.06	CACGGATAACATCAGCTTCAT	NM_002227:	NM_002227:
3717	JAK2 (Janus	Janus kinase 2 (a protein tyrosine kinase)	0.42	AGCCATCATACGAGATCTTAA	NM_004972:	NM_004972:
3717	JAK2 (Janus	Janus kinase 2 (a protein tyrosine kinase)	0.03	CAGAATTAGCAAACCTTATAA	NM_004972:	NM_004972:
3718	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	0.71	AGGCCTTATGAGGGTCCTCTA	NM_000215:	NM_000215:
3718	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	0.47	CGGGAGATTCAGATCCTCAAA	NM_000215:	NM_000215:
152789	JAKMIP1	janus kinase and microtubule interacting protein 1	0.75	CGCGACTGCCATCCTCCTCAA	NM_144720:	NM_144720:
152789	JAKMIP1	janus kinase and microtubule interacting protein 1	-0.56	CACGTCATTGACGACCTCTCA	NM_144720:	NM_144720:
58494	JAM2	junctional adhesion molecule 2	-0.81	CCCGCGCGGACCAGACACAAA	NM_021219:	NM_021219:
58494	JAM2	junctional adhesion molecule 2	-0.74	CTCAACATAAGTGGCATCATA	NM_021219:	NM_021219:
83700	JAM3	junctional adhesion molecule 3	0.00	TAGGGTGATCTTAAAGAGTTT	NM_032801:	NM_032801:
83700	JAM3	junctional adhesion molecule 3	1.09	ACGGAGAGACTCAGCCCTTTA	NM_032801:	NM_032801:
5927	JARID1A	Jumonji, AT rich interactive domain 1A (RBBP2-like)	0.01	AAGGAATGGTATCACAGTCTA	NM_005056:	NM_005056:
5927	JARID1A	Jumonji, AT rich interactive domain 1A (RBBP2-like)	0.26	CAGATGCTTAATTGAGCTCTA	NM_005056:	NM_005056:
10765	JARID1B	Jumonji, AT rich interactive domain 1B (RBP2-like)	0.33	GAGAACTTCGTCTGTAAGTAA	NM_005377:	NM_006618:
10765	JARID1B	Jumonji, AT rich interactive domain 1B (RBP2-like)	0.50	TCGTCCTAACATAACACTAAA	NM_006618:	NM_006618:
10765	JARID1B	Jumonji, AT rich interactive domain 1B (RBP2-like)	0.27	ACGCACCAAGCCGAAAGTAAA	NM_006618:	NM_006618:
221895	JAZF1	juxtaposed with another zinc finger gene 1	-3.73	ATGAGCCTTATTGACAATTAA	NM_175061:	NM_175061:
221895	JAZF1	juxtaposed with another zinc finger gene 1	0.89	ACGCAACTAGTTGGTGCATAA	NM_175061:	NM_175061:
221037	JMJD1C	jumonji domain containing 1C	-0.20	CTGGGATTACTTAACCTTGAA	NM_004241:	NM_004241:
221037	JMJD1C	jumonji domain containing 1C	-0.55	CACCAGTATTTCACCCACCAA	NM_004241:	NM_004241:
9682	JMJD2A	jumonji domain containing 2A	0.21	TAGGACTTAGCTTCATAACTA	NM_014663:	NM_014663:
9682	JMJD2A	jumonji domain containing 2A	1.61	ACGAGTTATCAACTCAAGATA	NM_014663:	NM_014663:
23030	JMJD2B	jumonji domain containing 2B	0.55	CACCTGACAAATCCTAGCGAA	NM_015015:	NM_015015:
23030	JMJD2B	jumonji domain containing 2B	1.50	AAGCAATGTTTATATTATAAA	NM_015015:	NM_015015:
23081	JMJD2C	jumonji domain containing 2C	0.41	AGCGGGTAGGGCGATAATTTA	NM_015061:	NM_015061:
23081	JMJD2C	jumonji domain containing 2C	0.02	CCCAGAAGTTCGATTCACTAA	NM_015061:	NM_015061:
9929	JOSD1	Josephin domain containing 1	0.78	TTTGTTTAACCAAATATTAAA	NM_014876:	NM_014876:
9929	JOSD1	Josephin domain containing 1	-0.36	CAACCTCGACTCCAAACTCAA	NM_014876:	NM_014876:
126119	JOSD2	Josephin domain containing 2	-1.37	CTGCCGCTGCTGCCTCAATAA	NM_138334:	NM_138334:
126119	JOSD2	Josephin domain containing 2	-0.03	CTGGGAAAGGCCAGCACTTCA	NM_138334:	NM_138334:
57338	JPH3	junctophilin 3	-0.07	TCGCTCCATCACCCAAACAAA	NM_020655:	NM_020655:
57338	JPH3	junctophilin 3	-0.70	CAGGACAGGAATGCGGTTCAA	NM_020655:	NM_020655:
3725	JUN	v-jun sarcoma virus 17 oncogene homolog (avian)	-1.45	AAGAAGTGTCCGAGAACTAAA	NM_002228:	NM_002228:
3725	JUN	v-jun sarcoma virus 17 oncogene homolog (avian)	-2.74	CGCGCGCGAGTCGACAAGTAA	NM_002228:	NM_002228:
3726	JUNB (jun B	jun B proto-oncogene	0.13	AAACACGCACTTAGTCTCTAA	NM_002229:	NM_002229:
3726	JUNB (jun B	jun B proto-oncogene	0.01	CTCGATTCATATTGAATATAA	NM_002229:	NM_002229:
3727	JUND (jun D	jun D proto-oncogene	0.02	GAGGATGGAAACACCCTTCTA	NM_005354:	NM_005354:
3727	JUND (jun D	jun D proto-oncogene	-0.37	GCGCCTGGAAGAGAAAGTGAA	NM_005354:	NM_005354:
3728	JUP	junction plakoglobin	0.32	ATGCGTAACTACAGTTATGAA	NM_002230:	NM_021991:NM_002230:
3728	JUP	junction plakoglobin	0.34	CCAGAGCATGATTCCCATCAA	NM_002230:	NM_021991:NM_002230:
10376	K-ALPHA-1	tubulin, alpha, ubiquitous	0.03	CCCGCCCTAGTGCGTTACTTA	NM_006082:	NM_006082:
10376	K-ALPHA-1	tubulin, alpha, ubiquitous	-1.22	AAGGAGAGGAATACTAATTAT	NM_006082:	NM_006082:
8997	KALRN	kalirin, RhoGEF kinase	0.82	TCGGCTGTGTCCAACAACAAA	NM_003947:	NM_003947:NM_001024660:
8997	KALRN	kalirin, RhoGEF kinase	-0.34	AGGACTGTCTTTGTACTTGAA	NM_003947:	NM_003947:
8997	KALRN	kalirin, RhoGEF kinase	0.40	CAGGACATCAATCAAGTCTTA	NM_007064:	NM_007064:NM_001024660:
8997	KALRN	kalirin, RhoGEF kinase	0.81	CCCATTGAGTATCAACGGAAA	NM_007064:	NM_007064:NM_001024660:
3736	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member	-0.01	AAGCTACTGACCGATGTTTAA	NM_000217:	NM_000217:
3736	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member	0.51	CCCATTATAGACAGGTCAATA	NM_000217:	NM_000217:
3744	KCNA10	potassium voltage-gated channel, shaker-related subfamily, member	-0.98	CAGCACAGACTCTCTTAATAA	NM_005549:	NM_005549:
3744	KCNA10	potassium voltage-gated channel, shaker-related subfamily, member	-0.85	CACCGGGAGACTGAGAATGAA	NM_005549:	NM_005549:
3737	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member	-3.76	CTGGTTCTGCATGGAAAGCAA	NM_004974:	NM_004974:
3737	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member	1.10	TACCATTAGTAAGTCTGATTA	NM_004974:	NM_004974:
3738	KCNA3	potassium voltage-gated channel, shaker-related subfamily, member	0.54	AACTAGAATAATGACTTGTAA	NM_002232:	NM_002232:
3738	KCNA3	potassium voltage-gated channel, shaker-related subfamily, member	1.48	AGCACATCAATTCGTAGTAAA	NM_002232:	NM_002232:
3739	KCNA4	potassium voltage-gated channel, shaker-related subfamily, member	0.59	CAGCATCTCCAAATATATTTA	NM_002233:	NM_002233:
3739	KCNA4	potassium voltage-gated channel, shaker-related subfamily, member	-3.53	CAGAGGCGGATGAACCTACTA	NM_002233:	NM_002233:
3741	KCNA5	potassium voltage-gated channel, shaker-related subfamily, member	1.55	AGGAATACTTCTGATAATTTA	NM_002234:	NM_002234:
3741	KCNA5	potassium voltage-gated channel, shaker-related subfamily, member	0.76	CAGAGGGATAACCCAAACAAA	NM_002234:	NM_002234:
3742	KCNA6	potassium voltage-gated channel, shaker-related subfamily, member	0.74	CTCGATCTTGCCATAACTTTA	NM_002235:	NM_002235:
3742	KCNA6	potassium voltage-gated channel, shaker-related subfamily, member	0.14	CTGGTGTTCGGTCTACATTTA	NM_002235:	NM_002235:
3743	KCNA7	potassium voltage-gated channel, shaker-related subfamily, member	0.61	AGGGCTTCCTTTGGTATCAAA	NM_031886:	NM_031886:
3743	KCNA7	potassium voltage-gated channel, shaker-related subfamily, member	-0.08	AGCGAGTTGAGTTGTGTTGAA	NM_031886:	NM_031886:
7881	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta mem	0.65	TAAGCTGCACTGAATACTCAA	NM_172159:	NM_172159:
7881	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta mem	0.78	GAGGTGCTGTCTAATGGGAAA	NM_172159:	NM_172159:NM_003471:NM_172160:
8514	KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta mem	-1.89	AAGAGTGTGGTTTGCATCCAA	NM_003636:	NM_003636:NM_172130:
8514	KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta mem	1.34	ATCCACGAGATTGATAGTATT	NM_003636:	NM_003636:NM_172130:
9196	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta mem	-1.59	TCGAGTAGTGATACGCATGAA	NM_004732:	NM_004732:
9196	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta mem	-1.33	CCGAGCGAGGTTTAAGCCGAA	NM_004732:	NM_004732:
3745	KCNB1	potassium voltage-gated channel, Shab-related subfamily, member 1	0.18	CACGCTTTCTTTACATCACTA	NM_004975:	NM_004975:
3745	KCNB1	potassium voltage-gated channel, Shab-related subfamily, member 1	0.73	TCGGTATTTCATAGTACCTGA	NM_004975:	NM_004975:

9312	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2	0.25	GCGGTTAATAATGCCTGTGAA	NM_004770:	NM_004770:
9312	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2	-0.07	CCCAGTTGACATAACTGTGAA	NM_004770:	NM_004770:
9312	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2	-0.25	CTGGAGCAGGCTGCCCAGGAA	XR_000198:	NM_004770:
3746	KCNC1	potassium voltage-gated channel, Shaw-related subfamily, member 1	-0.38	CAGCTGGGATCTCCCAATTAT	NM_004976:	NM_004976:
3746	KCNC1	potassium voltage-gated channel, Shaw-related subfamily, member 1	1.55	GCGCATCTTGCGCATCTTTAA	NM_004976:	NM_004976:
3747	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2	1.54	AAGCTTGTACGTGTCTTTAAA	NM_139136:	NM_139136:NM_153748:
3747	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2	1.13	GAGGCCAGATCTCTTACTTAA	NM_139136:	NM_139136:NM_153748:
3748	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	-0.05	CACACTGTTGCTGGATCTTGA	NM_004977:	NM_004977:
3748	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	-2.17	AAGCTTCTTGCCCGACCTCAA	NM_004977:	NM_004977:
3749	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	0.66	TGGGTGGAATGTCCCAAGAAA	NM_004978:	NM_004978:
3749	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	-0.13	CACATATAGTATCTATATTCA	NM_004978:	NM_004978:
3750	KCND1	potassium voltage-gated channel, Shal-related subfamily, member 1	0.05	CCGGCCTGGGATGTTTCTGAA	NM_004979:	NM_004979:
3750	KCND1	potassium voltage-gated channel, Shal-related subfamily, member 1	-0.20	CAGCATTTACATCTGCCCTAA	NM_004979:	NM_004979:
3751	KCND2	potassium voltage-gated channel, Shal-related subfamily, member 2	-2.39	AAGGTTGGTAGTGAAACACAA	NM_012281:	NM_012281:
3751	KCND2	potassium voltage-gated channel, Shal-related subfamily, member 2	1.34	ATGGAAGAGTGTGTTAAACTA	NM_012281:	NM_012281:
3752	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	1.00	CAGCCTTAATTTGAAAGCAGA	NM_172198:	NM_172198:NM_004980:
3752	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	0.02	TCGCTCCAGCCTTAATTTGAA	NM_172198:	NM_172198:NM_004980:
3753	KCNE1	potassium voltage-gated channel, Isk-related family, member 1	-2.24	AACTGGGATTCTTCGGCTTCT	NM_000219:	NM_000219:
3753	KCNE1	potassium voltage-gated channel, Isk-related family, member 1	-2.53	AAGAGAAGGACAAGGCCTATG	NM_000219:	NM_000219:
23630	KCNE1L	KCNE1-like	0.82	TAAAGGTTGTTTAAACAATAA	NM_012282:	NM_012282:
23630	KCNE1L	KCNE1-like	0.60	GTGGGATAGAATGAACTTAAT	NM_012282:	NM_012282:
9992	KCNE2	potassium voltage-gated channel, Isk-related family, member 2	1.19	TTAATCAATATCAATGATGAA	NM_172201:	NM_172201:
9992	KCNE2	potassium voltage-gated channel, Isk-related family, member 2	0.03	CCAAATTGTCTTTGCTTAGAA	NM_172201:	NM_172201:
10008	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	0.15	CGCACCTAAATTATTATTATA	NM_005472:	NM_005472:
10008	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	-0.14	TCGCACCTAAATTATTATTAT	NM_005472:	NM_005472:
23704	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	-1.46	CCAGCCCATTTGCACACTAAA	NM_080671:	NM_080671:
23704	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	-1.70	CCCAGCCCATTTGCACACTAA	NM_080671:	NM_080671:
3754	KCNF1	potassium voltage-gated channel, subfamily F, member 1	-3.77	CCGCTTCTGTATCTCCCTCAA	NM_002236:	NM_002236:
3754	KCNF1	potassium voltage-gated channel, subfamily F, member 1	0.80	CCGCATGATGGAGCTGACCAA	NM_002236:	NM_002236:
3755	KCNG1	potassium voltage-gated channel, subfamily G, member 1	0.02	CCCGGGAAGAACACTAGAACA	NM_002237:	NM_002237:
3755	KCNG1	potassium voltage-gated channel, subfamily G, member 1	-2.13	CTCGGACACCAGAGACAATAA	NM_002237:	NM_002237:
26251	KCNG2	potassium voltage-gated channel, subfamily G, member 2	-1.11	CCGCGACGAGTTCTTCTTCGA	NM_012283:	NM_012283:
26251	KCNG2	potassium voltage-gated channel, subfamily G, member 2	-1.78	CCCGGTCACCTCCATCTTCCA	NM_012283:	NM_012283:
170850	KCNG3	potassium voltage-gated channel, subfamily G, member 3	-4.07	CTGACTAATATGCCATGTTAA	NM_133329:	NM_172344:NM_133329:
170850	KCNG3	potassium voltage-gated channel, subfamily G, member 3	-3.12	TAGATTATTAGGACTAGATAA	NM_133329:	NM_172344:NM_133329:
93107	KCNG4	potassium voltage-gated channel, subfamily G, member 4	-1.64	TTGCCTATCATGCACATGTAA	NM_172347:	NM_172347:
93107	KCNG4	potassium voltage-gated channel, subfamily G, member 4	-0.08	ATGAACGATGTCAATGACCTA	NM_172347:	NM_172347:
3756	KCNH1	potassium voltage-gated channel, subfamily H (eag-related), member	1.12	TCGGCGGTCCAATGATACTAA	NM_002238:	NM_002238:NM_172362:
3756	KCNH1	potassium voltage-gated channel, subfamily H (eag-related), member	-0.96	CTGAGATACTCAGGATATTAA	NM_002238:	NM_002238:NM_172362:
3757	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member	-0.96	CTGGGCGACCAGATAGGCAAA	NM_000238:	NM_172057:NM_172056:NM_000238:
3757	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member	-0.02	CCGTGAGATCATAGCACCTAA	NM_000238:	NM_172056:NM_000238:
23416	KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member	-0.03	CAAGGACATCAGCGAAACCAA	NM_012284:	NM_012284:
23416	KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member	-1.45	CCGTACCACATTCGTGTCCAA	NM_012284:	NM_012284:
23415	KCNH4	potassium voltage-gated channel, subfamily H (eag-related), member	-1.77	CAGCCGCATGAAGGACCTCAA	NM_012285:	NM_012285:
23415	KCNH4	potassium voltage-gated channel, subfamily H (eag-related), member	0.12	CGGCACTGTACTTCACTCTAA	NM_012285:	NM_012285:
27133	KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member	0.08	CTCAACATGGTCCATGTCAAA	NM_139318:	NM_139318:NM_172375:NM_172376:
27133	KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member	-1.55	TAAGCTCATAAGGATGAACTA	NM_139318:	NM_139318:NM_172375:NM_172376:
81033	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member	-1.85	CACGCCAGCTACATTCTGGAA	NM_030779:	NM_173092:NM_030779:
81033	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member	0.01	CGCGCTAGCCGTCAAGTTCAA	NM_030779:	NM_173092:NM_030779:
90134	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member	0.34	AGCAGTTAGGATGTAAATATA	NM_033272:	NM_033272:
90134	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member	0.81	TAGAGTTGACTTTCAACCTAA	NM_033272:	NM_033272:
131096	KCNH8	potassium voltage-gated channel, subfamily H (eag-related), member	0.38	CAAGACTATCAAACAAATCTA	NM_144633:	NM_144633:
131096	KCNH8	potassium voltage-gated channel, subfamily H (eag-related), member	1.19	CAGACTTTGGTAACAATCCAA	NM_144633:	NM_144633:
30820	KCNIP1	Kv channel interacting protein 1	0.53	CTGGTAGTACAAGTCCTTTAA	NM_014592:	NM_001034837:NM_014592:NM_001034838:
30820	KCNIP1	Kv channel interacting protein 1	0.26	TCCAGAAACGAGGACCAATAA	NM_014592:	NM_001034837:NM_014592:NM_001034838:
30819	KCNIP2	Kv channel interacting protein 2	-0.02	TTCACTAGAATCTTCAATCAA	NM_014591:	NM_173342:NM_173192:NM_173194:NM_173195:NM_173191:NM_014591:NM_173193:
30819	KCNIP2	Kv channel interacting protein 2	-1.04	CAGATTATGATTGCTCAGGCA	NM_014591:	NM_173342:NM_173192:NM_173194:NM_173195:NM_173191:NM_014591:NM_173193:
30818	KCNIP3	Kv channel interacting protein 3, calsenilin	-0.36	CCCACATAATACATTCCATCA	NM_013434:	NM_013434:NM_001034914:
30818	KCNIP3	Kv channel interacting protein 3, calsenilin	-3.06	CAGGAACATTCCCACATAATA	NM_013434:	NM_013434:NM_001034914:
80333	KCNIP4	Kv channel interacting protein 4	-1.40	ACGATATGATGGGTAAATGTA	NM_025221:	NM_025221:NM_147181:NM_147182:NM_147183:NM_001035003:NM_001035004:
80333	KCNIP4	Kv channel interacting protein 4	1.64	CCCAGTGGTGTTGTTAATGAA	NM_025221:	NM_025221:NM_147181:NM_147182:NM_147183:NM_001035003:NM_001035004:
3758	KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1	1.44	TACGTTTAGACAGAGGCTAAA	NM_000220:	NM_000220:NM_153765:NM_153764:NM_153766:NM_153767:
3758	KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1	-0.05	CTCCCATAGTATCCAAGACAA	NM_000220:	NM_000220:NM_153765:NM_153764:NM_153766:NM_153767:
3766	KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	-5.13	CAGGCTTTGCTTTAAGTTGCA	NM_002241:	NM_002241:
3766	KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	0.80	TGCGTTCTCAACTTTATTCAA	NM_002241:	NM_002241:
3767	KCNJ11	potassium inwardly-rectifying channel, subfamily J, member 11	-2.04	AAGGCACTTGTCACTATGCTA	NM_000525:	NM_000525:
3767	KCNJ11	potassium inwardly-rectifying channel, subfamily J, member 11	-2.76	CAGCGCTTTGTGCCCATTGTA	NM_000525:	NM_000525:
3768	KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	0.88	TTGGGTGAGACTGTTTACAAA	NM_021012:	NM_021012:
3768	KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	-0.33	CAGCGCCAACTCCTTCTGCTA	NM_021012:	NM_021012:
3769	KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	-0.69	CACATGGATGGCAAACCTAAT	NM_002242:	NM_002242:
3769	KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	0.50	ATCGCCTTACTTGCCATACAA	NM_002242:	NM_002242:
3770	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	0.13	AAGACTGAAGTGACAGATTAA	NM_013348:	NM_170720:NM_013348:
3770	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	0.80	CTGGATTCACCTAAGATTCAA	NM_013348:	NM_170720:NM_013348:
3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	-2.53	CTGAAGGTAAGAAACTCATAA	NM_002243:	NM_002243:NM_170736:NM_170737:
3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	1.00	GACCACAGTTATCGACATGAA	NM_002243:	NM_002243:NM_170736:NM_170737:
3773	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	-0.50	AAGCTTAATATTAGAGACCCA	NM_018658:	NM_018658:NM_170741:NM_170742:
3773	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	-1.07	CCGGTAACTATTGTCCATGAA	NM_018658:	NM_018658:NM_170741:NM_170742:
3759	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	1.70	CAACTCTCTTATGGTATTATA	NM_000891:	NM_000891:
3759	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	-2.42	AGGGTCAATGAGAGCCATAAA	NM_000891:	NM_000891:
3760	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	-0.69	CTGTGTGAAGTTACACAATTA	NM_002239:	NM_002239:
3760	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	0.39	AAGGCTACTGGCATTAATTAT	NM_002239:	NM_002239:
3761	KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	0.03	CCCGCTTTATGGCATGGGCAA	NM_152868:	NM_152868:NM_004981:
3761	KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	-7.04	CTGGCGCTACATGCTCATGAT	NM_152868:	NM_152868:NM_004981:
3762	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	-0.99	CCCGGAGCTCCTACATGGATA	NM_000890:	NM_000890:
3762	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	-7.50	CTCCCATGAGATCAACCAGAA	NM_000890:	NM_000890:
3763	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6	-4.21	CCGCTGATCATTAGCCATGAA	NM_002240:	NM_002240:
3763	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6	0.15	TACCGGGTCATCACAGATAAA	NM_002240:	NM_002240:
3764	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	1.05	CCAGATCGCTGTGTTACTAAT	NM_004982:	NM_004982:
3764	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	-2.22	AAGGTGCAATTTATGACTCCA	NM_004982:	NM_004982:
3765	KCNJ9	potassium inwardly-rectifying channel, subfamily J, member 9	-2.86	CAGGCCCGACAGAGAGATGAA	NM_004983:	NM_004983:
3765	KCNJ9	potassium inwardly-rectifying channel, subfamily J, member 9	1.53	AGGGATAATTCAAACTGACAA	NM_004983:	NM_004983:
3775	KCNK1	potassium channel, subfamily K, member 1	-1.28	TAGGTAACCATTAACTATGTA	NM_002245:	NM_002245:
3775	KCNK1	potassium channel, subfamily K, member 1	0.32	TAGCTGATGGCTAAATAGCAA	NM_002245:	NM_002245:

54207	KCNK10	potassium channel, subfamily K, member 10	-0.09	CTGGAATTTGTTGGAAGCAGA	NM_021161:	NM_021161:NM_138318:NM_138317:
54207	KCNK10	potassium channel, subfamily K, member 10	1.16	CAGCGTGGAGATCCACGATAA	NM_021161:	NM_021161:NM_138318:NM_138317:
56660	KCNK12	potassium channel, subfamily K, member 12	0.67	CTGGCGCTTTCTTAATCTTTA	NM_022055:	NM_022055:
56660	KCNK12	potassium channel, subfamily K, member 12	0.06	CGCGCTGGGCATCATGAACAA	NM_022055:	NM_022055:
56659	KCNK13	potassium channel, subfamily K, member 13	0.06	TGCAAAGATGATGACTATTTA	NM_022054:	NM_022054:
56659	KCNK13	potassium channel, subfamily K, member 13	0.40	TAACTAAAGAACATAGCTTAA	NM_022054:	NM_022054:
60598	KCNK15	potassium channel, subfamily K, member 15	0.67	AACGGACTCCGGCAAGGTCTT	NM_022358:	NM_022358:
60598	KCNK15	potassium channel, subfamily K, member 15	-0.06	AACTTCGAGGGCTGGACCTTC	NM_022358:	NM_022358:
83795	KCNK16	potassium channel, subfamily K, member 16	-0.01	AATCTGGCCGCCATTGAAAGA	NM_032115:	NM_032115:
83795	KCNK16	potassium channel, subfamily K, member 16	-1.52	AAGGTCAGGTCTTCTGTGTCT	NM_032115:	NM_032115:
89822	KCNK17	potassium channel, subfamily K, member 17	0.53	CTGGGTGCAGCTATATGATTA	NM_031460:	NM_031460:
89822	KCNK17	potassium channel, subfamily K, member 17	-13.27	CAGCTCTAAGGAAGACTTCAA	NM_031460:	NM_031460:
3776	KCNK2	potassium channel, subfamily K, member 2	0.68	AGCCTAGATATGGACCATTTA	NM_014217:	NM_001017424:NM_014217:NM_001017425:
3776	KCNK2	potassium channel, subfamily K, member 2	1.65	TCGCATCATCTCAACAATCAT	NM_014217:	NM_001017424:NM_014217:NM_001017425:
3777	KCNK3	potassium channel, subfamily K, member 3	0.68	CTGATAATTACCCACTCTTAA	NM_002246:	NM_002246:
3777	KCNK3	potassium channel, subfamily K, member 3	0.11	CACCATAATTGCTGATAATTA	NM_002246:	NM_002246:
50801	KCNK4	potassium channel, subfamily K, member 4	0.42	CGAGTGGAATTTGAGTCCTAA	NM_016611:	NM_016611:
50801	KCNK4	potassium channel, subfamily K, member 4	-0.34	AAGAGGCTGTACGTGAATTAA	NM_016611:	NM_016611:
8645	KCNK5	potassium channel, subfamily K, member 5	1.58	AACGATGTCAAATGTAATTTA	NM_003740:	NM_003740:
8645	KCNK5	potassium channel, subfamily K, member 5	-0.53	TCCCAAGGATTGGGAGATCTA	NM_003740:	NM_003740:
9424	KCNK6	potassium channel, subfamily K, member 6	-1.45	ATCATCATAATACAACTTCAA	NM_004823:	NM_004823:
9424	KCNK6	potassium channel, subfamily K, member 6	-4.62	CTGGTTGAGCTCAAATCCCAA	NM_004823:	NM_004823:
10089	KCNK7	potassium channel, subfamily K, member 7	-0.10	GAGGACCAAGGTGGCATCCTA	NM_005714:	NM_005714:NM_033347:NM_033348:NM_033455:NM_033456:
10089	KCNK7	potassium channel, subfamily K, member 7	-1.52	CTGGACTAGGACTCCCATAAA	NM_005714:	NM_005714:NM_033456:
51305	KCNK9	potassium channel, subfamily K, member 9	-5.18	CCGCAACAGCATGGTCATTCA	NM_016601:	NM_016601:
51305	KCNK9	potassium channel, subfamily K, member 9	-0.31	CCTCAGGTTCTTGACCATGAA	NM_016601:	NM_016601:
3778	KCNMA1	potassium large conductance calcium-activated channel, subfamily M	1.30	TAGGCAGAGCAAGTTTATTTA	NM_002247:	NM_002247:
3778	KCNMA1	potassium large conductance calcium-activated channel, subfamily M	-0.14	ACGGGATGTTACGTCAACCAT	NM_002247:	NM_001014797:NM_002247:
3779	KCNMB1	potassium large conductance calcium-activated channel, subfamily M	-0.60	TAGGATATAAAGTGCCATATA	NM_004137:	NM_004137:
3779	KCNMB1	potassium large conductance calcium-activated channel, subfamily M	0.31	CACATTTACAGTATTACTATT	NM_004137:	NM_004137:
10242	KCNMB2	potassium large conductance calcium-activated channel, subfamily M	0.97	TTCATTTAATATCAATATCAA	NM_005832:	NM_005832:NM_181361:
10242	KCNMB2	potassium large conductance calcium-activated channel, subfamily M	0.29	AAGATGCTACTTGTTGGTAAA	NM_005832:	NM_005832:NM_181361:
27094	KCNMB3	potassium large conductance calcium-activated channel, subfamily M	-1.43	AACAAAGTTCGTAACACTTAT	NM_014407:	NM_014407:NM_171830:
27094	KCNMB3	potassium large conductance calcium-activated channel, subfamily M	-1.42	TAAGACGGTGGCCAAATTAAA	NM_014407:	NM_171828:NM_014407:NM_171829:NM_171830:
27345	KCNMB4 (pot	potassium large conductance calcium-activated channel, subfamily M	-0.97	ACCCTCAGTTTCCACTATTAA	NM_014505:	NM_014505:
27345	KCNMB4 (pot	potassium large conductance calcium-activated channel, subfamily M	-3.99	CTGGAAGACTTGGAACCTCAA	NM_014505:	NM_014505:
3780	KCNN1	potassium intermediate/small conductance calcium-activated channel	-2.45	CCGGCCTAGCCTAGAATCCTA	NM_002248:	NM_002248:
3780	KCNN1	potassium intermediate/small conductance calcium-activated channel	-2.29	ACCGTCATGTACGACCTTGTA	NM_002248:	NM_002248:
3781	KCNN2	potassium intermediate/small conductance calcium-activated channel	-0.18	TCCTGGGAACCTGAACACTAA	NM_021614:	NM_170775:NM_021614:
3781	KCNN2	potassium intermediate/small conductance calcium-activated channel	-5.44	AAGAGGATTGTTACCCTGGAA	NM_021614:	NM_170775:NM_021614:
3782	KCNN3	potassium intermediate/small conductance calcium-activated channel	1.33	CCGAGCTAATTAACTAACTCA	NM_002249:	NM_170782:NM_002249:
3782	KCNN3	potassium intermediate/small conductance calcium-activated channel	0.69	AAGAGAGACCGAGCTAATTAA	NM_002249:	NM_170782:NM_002249:
3783	KCNN4	potassium intermediate/small conductance calcium-activated channel	2.02	ATCTTTGTAATAAATGTTAAA	NM_002250:	NM_002250:
3783	KCNN4	potassium intermediate/small conductance calcium-activated channel	0.54	ATGGATATCCAGTATACCAAA	NM_002250:	NM_002250:
3784	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	-0.10	ACGGCTATGACAGTTCTGTAA	NM_000218:	NM_181798:NM_000218:NM_181797:
3784	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	0.67	CAAGAAGTCTGTGGTGGTAAA	NM_000218:	NM_181798:NM_000218:NM_181797:
3785	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	-1.54	CCCATTGACACAAACCCTCAA	NM_004518:	NM_004518:
3785	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	-2.11	AACGGTCACCGTGCCCATGTA	NM_004518:	NM_172109:NM_004518:NM_172106:NM_172108:NM_172107:
3786	KCNQ3	potassium voltage-gated channel, KQT-like subfamily, member 3	0.87	AACAGGTATTCCGATTTGAAA	NM_004519:	NM_004519:
3786	KCNQ3	potassium voltage-gated channel, KQT-like subfamily, member 3	-3.48	CTCGACATGCTTTCCAGGATA	NM_004519:	NM_004519:
9132	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	-0.10	CCGCTCCATCAGGATTCTCAA	NM_004700:	NM_172163:NM_004700:
9132	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	-0.80	CGGGCATCTCTGAGACTCAAA	NM_004700:	NM_172163:NM_004700:
56479	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	0.31	TCCAAGGTGCATCGACATTAA	NM_019842:	NM_019842:
56479	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	0.11	AAGGGCAAATCACATCAGATA	NM_019842:	NM_019842:
3787	KCNS1	potassium voltage-gated channel, delayed-rectifier, subfamily S, mem	-0.93	CACCCTTATGGTCTTGCAGAA	NM_002251:	NM_002251:
3787	KCNS1	potassium voltage-gated channel, delayed-rectifier, subfamily S, mem	-0.45	ACCCGTTGGAAGAGTCTTAAA	NM_002251:	NM_002251:
3788	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, mem	-0.03	AGGGACTATTATGCCCATAAA	NM_020697:	NM_020697:
3788	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, mem	0.49	CACCAAGTGAACTCAGTTTAA	NM_020697:	NM_020697:
3790	KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, mem	1.97	TCACATTGAGCTAACTTTAAA	NM_002252:	NM_002252:
3790	KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, mem	0.24	CCCGGTCACCTTGGCGGGAAA	NM_002252:	NM_002252:
57582	KCNT1	potassium channel, subfamily T, member 1	0.77	ACGAGGACGTAGCAAATTTAA	XM_029962:	NM_020822:
57582	KCNT1	potassium channel, subfamily T, member 1	1.43	CAGGTCATCGTGGCCATAATA	XM_029962:	NM_020822:
343450	KCNT2	potassium channel, subfamily T, member 2	0.06	CACATAGAGATTAACCAACAA	NM_198503:	NM_198503:
343450	KCNT2	potassium channel, subfamily T, member 2	0.05	CAGGGTACAAGTTGAATTCTA	NM_198503:	NM_198503:
27012	KCNV1	potassium channel, subfamily V, member 1	0.07	CTGTATCCCATTATTACTATA	NM_014379:	NM_014379:
27012	KCNV1	potassium channel, subfamily V, member 1	-2.53	CTGACACATTTGAGTGTCCAA	NM_014379:	NM_014379:
169522	KCNV2	potassium channel, subfamily V, member 2	-0.84	CTGGACAGAGGGCAACTATAA	NM_133497:	NM_133497:
169522	KCNV2	potassium channel, subfamily V, member 2	-0.33	TACGAGGAGCAGACAGACGAA	NM_133497:	NM_133497:
10945	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rece	-0.99	CACGTGTATGAAGGTGGTCTA	NM_006801:	NM_006801:
10945	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rece	0.38	CCACTGGTTGCCAAACACTAA	NM_006801:	NM_006801:
11014	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rece	0.72	AAGAAACTTAATGCTGTATTA	NM_006854:	NM_006854:
11014	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rece	1.00	CCTGATCTACCTGAAATTTAA	NM_006854:	NM_006854:
11015	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rece	0.00	TACCTTAATACCAATAACCTA	NM_006855:	NM_006855:
11015	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rece	-0.07	TCCCAACTAAAGACCAGTTAA	NM_006855:	NM_006855:
3791	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	0.34	AACGCTGACATGTACGGTCTA	NM_002253:	NM_002253:
3791	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	0.04	AAGGCTAATACAACTCTTCAA	NM_002253:	NM_002253:
3792	KEL	Kell blood group, metalloendopeptidase	-1.28	CAGCACAGAAATATCGACCAA	NM_000420:	NM_000420:
3792	KEL	Kell blood group, metalloendopeptidase	1.58	CCCGACAAGAATACAACGATA	NM_000420:	NM_000420:
3795	KHK (ketohex	ketohexokinase (fructokinase)	-0.02	TAGCCGCACCATCCTATACTA	NM_000221:	NM_000221:
3795	KHK (ketohex	ketohexokinase (fructokinase)	0.21	TAGGGTGGGTAAGGCCTTATA	NM_000221:	NM_000221:NM_006488:
8570	KHSRP	KH-type splicing regulatory protein (FUSE binding protein 2)	-0.05	CAAGAGGAGATTGAAACTGAA	NM_003685:	NM_003685:
8570	KHSRP	KH-type splicing regulatory protein (FUSE binding protein 2)	-7.25	CTGGAGTGAAGATGATCTTAA	NM_003685:	NM_003685:
9768	KIAA0101	KIAA0101	-2.10	ACCCTGGTATTCTAGAATGTA	NM_014736:	NM_014736:NM_001029989:
9768	KIAA0101	KIAA0101	-0.10	ACGGTTGATAATGCCTCTACA	NM_014736:	NM_014736:NM_001029989:
23306	KIAA0286	KIAA0286 protein	1.03	TGCCTTCATATTAATATATAA	M55632:	NM_015257:
9870	KIAA0317 (KI	KIAA0317	-0.79	TCGGCTGGCCAGTCAAGTGAA	NM_014821:	NM_014821:
9870	KIAA0317 (KI	KIAA0317	-0.17	AAGCACTATTTGATACAACCA	NM_014821:	NM_014821:
9673	KIAA0446	KIAA0446 gene product	-4.11	CCGGAAGTTTGTAGCTGACTA	NM_014655:	NM_014655:
9673	KIAA0446	KIAA0446 gene product	0.03	CACCATGGAGGACAAACGCAA	NM_014655:	NM_014655:
23277	KIAA0664	KIAA0664	-1.90	CTCGGCCAAGCACATCTTCAA	NM_015229:	NM_015229:
23277	KIAA0664	KIAA0664	-0.02	AAGGGCCATATTCAAGGTGCA	NM_015229:	NM_015229:
23307	KIAA0674 (KI	KIAA0674	-0.32	CCGGAAACAACTGGAACTCAA	XM_376903:	XM_376903:
23307	KIAA0674 (KI	KIAA0674	0.18	CCCGGCAACATAACACTGAAA	XM_376903:	XM_376903:
9914	KIAA0703	KIAA0703 gene product	-0.16	CCGAGAGTTGGCGTGAAGGAA	NM_014861:	NM_014861:
9914	KIAA0703	KIAA0703 gene product	1.70	ATGGACTTAAGTGATATTAAA	NM_014861:	NM_014861:
23255	KIAA0802 (KI	KIAA0802	0.22	ACCAAGATACTTGAGTGATTA	NM_001010844:	NM_015210:

23382	KIAA0828	KIAA0828 protein	-0.08	CAGGTTCTAAACTCTATATAT	NM_015328:	NM_015328:
23382	KIAA0828	KIAA0828 protein	0.39	AGGCAACACCAGCAAATTATA	NM_015328:	NM_015328:
51603	KIAA0859	KIAA0859	1.20	CACGTATGTCTTGTCAGATAT	NM_015935:	NM_015935:NM_001007239:NM_014955:
51603	KIAA0859	KIAA0859	0.32	CGGCCTTGCTACGATGTCATA	NM_015935:	NM_015935:NM_001007239:NM_014955:
23329	KIAA0984	KIAA0984 protein	0.07	ACGCATGACCACAGATATCAA	XM_037557:	XM_037557:
23329	KIAA0984	KIAA0984 protein	-0.14	AAGAGTTGATACCAAGTTGAA	XM_037557:	XM_037557:
23387	KIAA0999	KIAA0999 protein	-0.01	AACATTGTTCATCGTGATTTA	NM_025164:	NM_025164:
23387	KIAA0999	KIAA0999 protein	0.40	CCGGGAAGTTCAAATTATGAA	NM_025164:	NM_025164:
84162	KIAA1109	KIAA1109	-1.38	CACCTCTTAAGCGAATGGAAA	XM_371706:	XM_371706:
84162	KIAA1109	KIAA1109	0.22	CTCGAAGAGATTCACTTTCAA	XM_371706:	XM_371706:
54462	KIAA1128	KIAA1128	-2.49	CCGTATATTTATGAAGCATAA	NM_018999:	NM_018999:
54462	KIAA1128	KIAA1128	-0.73	ACCGTATATTTATGAAGCATA	NM_018999:	NM_018999:
57462	KIAA1161 (KI	KIAA1161	-4.08	CACCTCTATACCACCCATTAA	NM_020702:	NM_020702:
57462	KIAA1161 (KI	KIAA1161	-4.59	CAGGCCAGACTTCGTGCCTTA	NM_020702:	NM_020702:
57495	KIAA1239	KIAA1239 protein	-7.27	ATCCATGACATCTGTGAATTA	NM_139209:	XM_049078:
55632	KIAA1333	KIAA1333	1.42	TAGATTAATCTGTATGGTCAA	NM_017769:	NM_017769:
55632	KIAA1333	KIAA1333	-0.75	AAGGAATATTATAGCCACTTA	NM_017769:	NM_017769:
57544	KIAA1344 (KI	KIAA1344	-0.39	CGGGCAGATAACATAGATCAT	XM_051699:	NM_020784:
57544	KIAA1344 (KI	KIAA1344	1.59	AACAATGAGAGTGAACTCTAA	XM_051699:	NM_020784:
57596	KIAA1446	likely ortholog of rat brain-enriched guanylate kinase-associated prote	0.01	CGGGCGGACCATGTCACCGTA	NM_020836:	NM_020836:
57596	KIAA1446	likely ortholog of rat brain-enriched guanylate kinase-associated prote	-0.27	CTGCAGCTTCTCTGAACGCTA	NM_020836:	NM_020836:
57604	KIAA1456	KIAA1456 protein	1.16	TCCGTGCAGAATAGTGCTAAT	NM_020844:	NM_020844:
57604	KIAA1456	KIAA1456 protein	0.78	CTGGAGTAATCTGATCACTTA	NM_020844:	NM_020844:
57613	KIAA1467	KIAA1467	0.71	TTGGTTTAGTATAGAATTTGA	XM_370682:	NM_020853:
57613	KIAA1467	KIAA1467	0.44	CATGGTGTATTTGCAAACTAA	XM_370682:	NM_020853:
57650	KIAA1524	KIAA1524	-0.48	CAGAAAGAGCGCAGAGTGATA	NM_020890:	NM_020890:
57650	KIAA1524	KIAA1524	0.40	CGGCACAATCTTTCTGTTCAA	NM_020890:	NM_020890:
57661	KIAA1542	CTD-binding SR-like protein rA9	-1.24	CCGGATCAATATTCCTGGAAA	XM_290536:	NM_020901:
57661	KIAA1542	CTD-binding SR-like protein rA9	0.08	CGCGTCCTTGATAAATCTCTA	XM_290536:	NM_020901:
57687	KIAA1576	KIAA1576 protein	1.85	CAGGAGCTCATTTGATTCATA	NM_020927:	NM_020927:
57687	KIAA1576	KIAA1576 protein	0.81	TACCAATTCTGTAAATTTCAA	NM_020927:	NM_020927:
57724	KIAA1632	KIAA1632	-0.94	AAGCAGTATGTGAATCGTGAA	NM_020964:	NM_020964:
57724	KIAA1632	KIAA1632	-5.20	TAGGATCTAGGTTCTCCAGAA	NM_020964:	NM_020964:
57729	KIAA1639	KIAA1639 protein	-2.84	CCGCACGGCATGTGTCAGCAA	XM_290923:	XM_290923:
57729	KIAA1639	KIAA1639 protein	-0.53	CACAAAGACCTTCGCATTCCA	XM_290923:	XM_290923:
80789	KIAA1698	KIAA1698	0.26	CACGCGTACATTAATGGACAT	NM_030628:	NM_030628:
80789	KIAA1698	KIAA1698	-2.52	CTGGGTAATATGCATGAAGTA	NM_030628:	NM_030628:
80000	KIAA1772	KIAA1772	-0.03	CACCAATTCCCTATTCACAAA	NM_024935:	NM_024935:
80000	KIAA1772	KIAA1772	-0.49	AACGGGAAACTGTATCCATAA	NM_024935:	NM_024935:
84461	KIAA1787	KIAA1787 protein	0.36	CAGGTTCAACCTCAGAGTGAA	NM_004489:	NM_032442:NM_001005408:
84461	KIAA1787	KIAA1787 protein	-1.37	CTGCGAGAAGTTTGGGCCCAA	NM_004489:	NM_032442:NM_001005408:
84451	KIAA1804	mixed lineage kinase 4	-1.60	ACGGACCATGTCTGATGGAAA	NM_032435:	NM_032435:
84451	KIAA1804	mixed lineage kinase 4	1.27	CGGGAACTTAACATTCTGATA	NM_032435:	NM_032435:
84439	KIAA1822	KIAA1822	-0.22	GCGCATCGACGTGGACCGTAA	NM_032425:	NM_032425:
84439	KIAA1822	KIAA1822	0.21	CAGGAACACTTGATGAATAAA	NM_032425:	NM_032425:
124454	KIAA1970	KIAA1970 protein	0.27	CTGTGAGATAGTAAACGTTTA	NM_133451:	NM_133451:
124454	KIAA1970	KIAA1970 protein	1.02	AACCAGCCTCATTTAAGTTAA	NM_133451:	NM_133451:
79834	KIAA2002	KIAA2002 protein	-1.77	CAGCTTGAGAACATCATATAA	XM_370878:	XM_370878:
79834	KIAA2002	KIAA2002 protein	1.52	CCACTTAACAATAATAATGAA	XM_370878:	XM_370878:
158358	KIAA2026 (KI	KIAA2026	-6.38	TCCGGAAGCAAGCCCGATAAA	XM_088551:	NM_001017969:
158358	KIAA2026 (KI	KIAA2026	-0.41	CACGTTCTGTATCTATTTCTA	XM_088551:	NM_001017969:
57498	KIDINS220	kinase D-interacting substance of 220 kDa	1.11	CAGGCGAGACTCCTTATAATA	AB033076:	NM_020738:
57498	KIDINS220	kinase D-interacting substance of 220 kDa	1.01	TCGCAGATGCGCTATTATCTA	AB033076:	NM_020738:
3832	KIF11	kinesin family member 11	-11.07	ACGGAGGAGATAGAACGTTTA	NM_004523:	NM_004523:
3832	KIF11	kinesin family member 11	-2.50	GCCGATAAGATAGAAGATCAA	NM_004523:	NM_004523:
113220	KIF12	kinesin family member 12	-2.00	AAGAGAGGCATCAGCTCCAAA	NM_138424:	NM_138424:
113220	KIF12	kinesin family member 12	-0.35	ACAGGAGTTCATGCTAGAGAA	NM_138424:	NM_138424:
63971	KIF13A	kinesin family member 13A	-1.37	CTGGCGGGTAGCGAAAGAGTA	NM_022113:	NM_022113:
63971	KIF13A	kinesin family member 13A	0.85	CCGCAACAACTTGGTAGGAAA	NM_022113:	NM_022113:
23303	KIF13B	kinesin family member 13B	0.66	ATGTCTTAACCTAAACCATAA	NM_015254:	NM_015254:
23303	KIF13B	kinesin family member 13B	0.35	CCCACTAATGTCTTAACCTAA	NM_015254:	NM_015254:
9928	KIF14	kinesin family member 14	-1.63	ATGGTTAATCGTGCTCCAGAA	XM_375825:	NM_014875:
9928	KIF14	kinesin family member 14	0.66	CAGACATGATATATCAGATAA	XM_375825:	NM_014875:
56992	KIF15	kinesin family member 15	0.52	ACGCAATAACAAATTATCATT	NM_020242:	NM_020242:
56992	KIF15	kinesin family member 15	-0.52	TTGAGATTGACCAACTTTCAA	NM_020242:	NM_020242:
57576	KIF17	kinesin family member 17	-3.06	CAGCAACTACTTCCGATCTAA	NM_020816:	NM_020816:
57576	KIF17	kinesin family member 17	-7.12	CAGGAAGAGCCTCACACATCA	NM_020816:	NM_020816:
81930	KIF18A	kinesin family member 18A	-3.57	CAGGAGGACTTGGACTCTACA	NM_031217:	NM_031217:
81930	KIF18A	kinesin family member 18A	-3.71	CAGGTGGAACTAATCTGGTTA	NM_031217:	NM_031217:
124602	KIF19	kinesin family member 19	-5.79	CCGGGTCAAGAACATCTTGCA	NM_153209:	NM_153209:
124602	KIF19	kinesin family member 19	-6.31	CCGGGAGAAGTCCTACCTGTT	NM_153209:	NM_153209:
547	KIF1A	kinesin family member 1A	-1.19	CAACTCGGAAATTAACTATAA	NM_004321:	NM_004321:
547	KIF1A	kinesin family member 1A	-4.80	CAGCCCGATCGTTTCCAAGAA	NM_004321:	NM_004321:
23095	KIF1B	kinesin family member 1B	-5.39	CCGGTTCTATTCAAACCAGCA	NM_015074:	NM_015074:
23095	KIF1B	kinesin family member 1B	0.88	CTGGTGAATCTCCAAATTATT	NM_015074:	NM_015074:
10749	KIF1C	kinesin family member 1C	-1.33	CTGGAGAATCAGTACCGGAAA	NM_006612:	NM_006612:
10749	KIF1C	kinesin family member 1C	-0.71	CACGGTCCAGACCATTGTCAA	NM_006612:	NM_006612:
3796	KIF2	kinesin heavy chain member 2	1.54	ACCATATAACATGTGATTATA	NM_004520:	NM_004520:
3796	KIF2	kinesin heavy chain member 2	-0.88	CAGCAAGCAAATCAACCCGAA	NM_004520:	NM_004520:
10112	KIF20A	kinesin family member 20A	-1.29	AACGAACTGCTTTATGACCTA	NM_005733:	NM_005733:
10112	KIF20A	kinesin family member 20A	-0.01	CTGCTTTATGACCTATTAGAA	NM_005733:	NM_005733:
55605	KIF21A	kinesin family member 21A	-1.88	AAGGTTTCAGTCTACAGGAAA	NM_017641:	NM_017641:
55605	KIF21A	kinesin family member 21A	-1.75	AAGCTTTGTGGTGAAGTGAAA	NM_017641:	NM_017641:
23046	KIF21B	kinesin family member 21B	-0.64	CCGGGTAAAGTTGTGGAATTA	XM_371332:	NM_017596:XM_371332:
23046	KIF21B	kinesin family member 21B	-1.62	TCGCCGAGTCCTGGCCATAAA	XM_371332:	NM_017596:XM_371332:
3835	KIF22	kinesin family member 22	0.52	ATCCACATCCTGAAGAATAAA	NM_007317:	NM_007317:
3835	KIF22	kinesin family member 22	0.46	CAGGACATCTATGCAGGTTCA	NM_007317:	NM_007317:
9493	KIF23	kinesin family member 23	-1.69	AAGGCTGAAGATTATGAAGAA	NM_004856:	NM_004856:NM_138555:
9493	KIF23	kinesin family member 23	1.01	CAGAAGTTGAAGTGAAATCTA	NM_004856:	NM_004856:NM_138555:
3834	KIF25	kinesin family member 25	1.47	CCGGATTGAATGCATTAACAA	NM_005355:	NM_030615:NM_005355:
3834	KIF25	kinesin family member 25	-0.07	CACCCTCTGATTGATAAGACA	NM_005355:	NM_030615:NM_005355:
26153	KIF26A	kinesin family member 26A	0.00	GCCGTGGGAATTTGAAGACAA	XM_050278:	XM_050278:
26153	KIF26A	kinesin family member 26A	1.20	CAGCATCAATGATGAGTTTGA	XM_050278:	XM_050278:
55083	KIF26B	kinesin family member 26B	-4.06	AAGCACTTTGAGGAACCTTAA	XM_371354:	XM_371354:
55083	KIF26B	kinesin family member 26B	1.76	ATCAGTATTGCTTATGAATAA	XM_371354:	XM_371354:
55582	KIF27	kinesin family member 27	-0.70	AAGAAGGACCACAGCATGTTA	NM_017576:	NM_017576:
55582	KIF27	kinesin family member 27	0.27	TACAGGTACCACTCAAATGAA	NM_017576:	NM_017576:
84643	KIF2B (kinesi	kinesin family member 2B	-0.40	CTGGTGGAGTACACCATGATA	NM_032559:	NM_032559:
84643	KIF2B (kinesi	kinesin family member 2B	0.07	CAGAGGGATGAATTTATTAAA	NM_032559:	NM_032559:

11004	KIF2C	kinesin family member 2C	1.32	CCAGTGACGACTGCAAATAAA	NM_006845:	NM_006845:
11004	KIF2C	kinesin family member 2C	0.18	CACGCGTGCTTCCAAATTATT	NM_006845:	NM_006845:
11127	KIF3A (kinesi	kinesin family member 3A	2.05	GTGCCTTATCGTAACTCTAAA	NM_007054:	NM_007054:
11127	KIF3A (kinesi	kinesin family member 3A	-5.84	CTGGTTCAGAAAGACAGGCAA	NM_007054:	NM_007054:
9371	KIF3B	kinesin family member 3B	-1.82	AACGCTAAGGTGGGTAGCCTA	NM_004798:	NM_004798:
9371	KIF3B	kinesin family member 3B	0.43	CAGAGAATTCACCGAATCCTA	NM_004798:	NM_004798:
3797	KIF3C (kinesi	kinesin family member 3C	0.03	AAGGGCCTTGATTAGGACCAA	NM_002254:	NM_002254:
3797	KIF3C (kinesi	kinesin family member 3C	0.33	AAACGAAGATATTAACATCTA	NM_002254:	NM_002254:
24137	KIF4A	kinesin family member 4A	0.43	AAGGAACAAAGCGTTACTGAA	NM_012310:	NM_012310:
24137	KIF4A	kinesin family member 4A	0.03	CAGGTCCAGACTACTACTCTA	NM_012310:	NM_012310:
3798	KIF5A	kinesin family member 5A	0.11	CTGAGTGGTGTTAGTCACTGA	NM_004984:	NM_004984:
3798	KIF5A	kinesin family member 5A	1.04	CTGCGTTGTGAGCTTCCTAAA	NM_004984:	NM_004984:
3799	KIF5B	kinesin family member 5B	0.00	AACGTTGCAAGCAGTTAGAAA	NM_004521:	NM_004521:
3799	KIF5B	kinesin family member 5B	-0.40	CGCAATTGGAGTTATAGGAAA	NM_004521:	NM_004521:
221458	KIF6	kinesin family member 6	0.26	ACGGTCCCAACTCCTCTCTAA	NM_145027:	NM_145027:
221458	KIF6	kinesin family member 6	-3.34	AAGATTGTCAAGAACCATTAA	NM_145027:	NM_145027:
374654	KIF7	kinesin family member 7	-1.04	TTGGCCAAGAATCATCACGAA	NM_198525:	NM_198525:
374654	KIF7	kinesin family member 7	1.09	TACCCTCACTGGGATCAACAA	NM_198525:	NM_198525:
64147	KIF9	kinesin family member 9	-4.41	CAGGACTTGGTTTATGAGACA	NM_182902:	NM_182902:NM_182903:NM_022342:
64147	KIF9	kinesin family member 9	0.45	AACAGACAGACTGGTCGTTTA	NM_182902:	NM_182902:NM_182903:NM_022342:
22920	KIFAP3	kinesin-associated protein 3	-0.58	CAGCATGATGGACCAACTAAA	NM_014970:	NM_014970:
22920	KIFAP3	kinesin-associated protein 3	0.99	CACAAGAGACGTCATAATCAA	NM_014970:	NM_014970:
3833	KIFC1	kinesin family member C1	0.76	TCGGGAAACACAGGCCATTAA	XM_371813:	NM_002263:
3833	KIFC1	kinesin family member C1	0.07	TGGGACTTAAAGGGTCAGTTA	XM_371813:	NM_002263:
90990	KIFC2 (kinesi	kinesin family member C2	-5.78	CAGCATGGTGGAGATCTACAA	NM_145754:	NM_145754:
90990	KIFC2 (kinesi	kinesin family member C2	-3.15	CAGCGTCTGCATCTTCACCTA	NM_145754:	NM_145754:
3801	KIFC3	kinesin family member C3	-0.24	TCCCTCTGAAATCCTATTTAA	NM_005550:	NM_005550:
3801	KIFC3	kinesin family member C3	0.23	GACCGAGTTCACCAACCTGAA	NM_005550:	NM_005550:
3814	KISS1	KiSS-1 metastasis-suppressor	-9.69	CACCCTCTGGACATTCACCCA	NM_002256:	NM_002256:
3814	KISS1	KiSS-1 metastasis-suppressor	-0.39	CCAGGTGGTCTCGTCACCTCA	NM_002256:	NM_002256:
84634	KISS1R	KISS1 receptor	0.17	GCGGACCGTGACCAACTTCTA	NM_032551:	NM_032551:
84634	KISS1R	KISS1 receptor	-0.99	TCGGTGCAGTTTCGTTGTGAA	NM_032551:	NM_032551:
3815	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	1.03	CACGGTTGAATGTAAGGCTTA	NM_000222:	NM_000222:
3815	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	0.23	CTCGCACCTTTCCAAAGTTAA	NM_000222:	NM_000222:
4254	KITLG	KIT ligand	-1.03	CACTGAATTAATCATCTATAA	NM_000899:	NM_000899:NM_003994:
4254	KITLG	KIT ligand	1.53	CAGAAATGTCTAAATGCTGAA	NM_000899:	NM_000899:NM_003994:
64837	KLC2	kinesin light chain 2	0.49	CCCGGCCGTTGCTTCTGTATA	NM_022822:	NM_022822:
64837	KLC2	kinesin light chain 2	0.15	CAGCAGTGAGATGCTGGTAAA	NM_022822:	NM_022822:
147700	KLC3	kinesin light chain 3	-0.79	CAGACCCTCCTTAGAATCCCA	NM_145275:	NM_145275:
147700	KLC3	kinesin light chain 3	0.45	CAGACCCTCCTTAGAATGCCA	NM_145275:	NM_145275:
147700	KLC3	kinesin light chain 3	-0.94	CCGCAGCAGCTCACTCTCCAA	NM_177417:	NM_177417:
147700	KLC3	kinesin light chain 3	0.75	CGGAAGAGCTGTACAAAGAAA	NM_177417:	NM_177417:
89953	KLC4	kinesin light chain 4	-0.01	AAGGTTGCGGACGTTGCACAA	NM_201521:	NM_201521:NM_201522:NM_201523:NM_138343:
89953	KLC4	kinesin light chain 4	-8.57	CAGCGGCTACAGCGCAGTGAA	NM_201521:	NM_201521:NM_201522:NM_201523:NM_138343:
7071	KLF10	Kruppel-like factor 10	0.98	ATGGCTTATGTCATCAGTAAA	NM_005655:	NM_005655:NM_001032282:
7071	KLF10	Kruppel-like factor 10	-0.16	CCGCCTGGGTTAGGTGACTAA	NM_005655:	NM_005655:
51621	KLF13	Kruppel-like factor 13	0.68	CCCAAAGTGGTTCTCGTTTAA	NM_015995:	NM_015995:
51621	KLF13	Kruppel-like factor 13	-0.21	CACCTCAGGTGTCAAAGTAAA	NM_015995:	NM_015995:
83855	KLF16	Kruppel-like factor 16	0.41	TCCTTGTATTTAATTAATTAA	NM_031918:	NM_031918:
83855	KLF16	Kruppel-like factor 16	0.36	TGGCCTCATCCTTGTATTTAA	NM_031918:	NM_031918:
1316	KLF6	Kruppel-like factor 6	0.28	CTGCCTAGAGCTGGAACGTTA	NM_001300:	NM_001008490:NM_001300:
1316	KLF6	Kruppel-like factor 6	-0.32	TTGTATGTTGAGGATCTATTA	NM_001300:	NM_001300:
3816	KLK1	kallikrein 1, renal/pancreas/salivary	0.79	CAGAGTGCTGTCTTATGTGAA	NM_002257:	NM_002257:
3816	KLK1	kallikrein 1, renal/pancreas/salivary	0.35	CGCCGTCAGAGTGCTGTCTTA	NM_002257:	NM_002257:
5655	KLK10	kallikrein 10	-1.33	TGGGTGGTGAGTTCTGACTAA	NM_002776:	NM_145888:NM_002776:
5655	KLK10	kallikrein 10	0.46	TTCATGGTGATTGTCATGTAA	NM_002776:	NM_145888:NM_002776:
11012	KLK11	kallikrein 11	-1.67	CAGCTCCTGGCCATATATCAA	NM_006853:	NM_006853:NM_144947:
11012	KLK11	kallikrein 11	1.07	ATGCTGTCACTTAATAATCAA	NM_006853:	NM_006853:NM_144947:
43849	KLK12	kallikrein 12	0.57	TGCAATAGTCTGGAATAAATA	NM_019598:	NM_019598:NM_145895:NM_145894:
43849	KLK12	kallikrein 12	1.68	TGGGAACTTCTTGGAACTTTA	NM_019598:	NM_019598:NM_145895:NM_145894:
26085	KLK13	kallikrein 13	0.49	CTCAACAATATATGTCCTATA	NM_015596:	NM_015596:
26085	KLK13	kallikrein 13	1.33	TCAGCCCATCTCAACAATATA	NM_015596:	NM_015596:
43847	KLK14	kallikrein 14	0.45	ATGGAATCATCCTAAATTGTA	NM_022046:	NM_022046:
43847	KLK14	kallikrein 14	-0.24	CCGAATAAATAATGACAATAA	NM_022046:	NM_022046:
55554	KLK15	kallikrein 15	-3.39	CCCGCCTGACATGGAACAGAA	NM_017509:	NM_023006:NM_138564:NM_138563:NM_017509:
55554	KLK15	kallikrein 15	0.14	CCCGTGTGATCTTGAACAAGA	NM_017509:	NM_023006:NM_138564:NM_138563:NM_017509:
3817	KLK2	kallikrein 2, prostatic	-4.77	CTGAGGTTCCCTAGAGTTCAA	NM_005551:	NM_001002232:NM_001002231:NM_005551:
3817	KLK2	kallikrein 2, prostatic	0.58	TACTTGAATAATTGACCTGAA	NM_005551:	NM_001002232:NM_001002231:NM_005551:
354	KLK3	kallikrein 3, (prostate specific antigen)	1.23	CAGAAATAAAGAGCTGTTATA	NM_001648:	NM_001030049:NM_001648:NM_001030047:NM_001030048:
354	KLK3	kallikrein 3, (prostate specific antigen)	-4.76	CACAGCAAGGATGGAGCTGAA	NM_001648:	NM_001030049:NM_001648:NM_001030047:NM_001030048:
9622	KLK4	kallikrein 4 (prostase, enamel matrix, prostate)	0.21	CAGAAATAAAGTCTAAGAGAA	NM_004917:	NM_004917:
9622	KLK4	kallikrein 4 (prostase, enamel matrix, prostate)	0.77	TAGATCCAGAAATAAAGTCTA	NM_004917:	NM_004917:
25818	KLK5	kallikrein 5	0.01	AACCCTGGGAACAATTTCCAA	NM_012427:	NM_012427:
25818	KLK5	kallikrein 5	-0.67	CAGACCGGGTGTCTACACGAA	NM_012427:	NM_012427:
5653	KLK6	kallikrein 6 (neurosin, zyme)	0.15	CACCATGCACTCAATAAAGAA	NM_002774:	NM_001012964:NM_001012966:NM_002774:NM_001012965:
5653	KLK6	kallikrein 6 (neurosin, zyme)	-0.70	CTGCAGATTTCTCACCTGTAA	NM_002774:	NM_001012964:NM_001012966:NM_002774:NM_001012965:
5650	KLK7	kallikrein 7 (chymotryptic, stratum corneum)	0.32	CACAATGATATTACAAACCTA	NM_005046:	NM_005046:NM_139277:
5650	KLK7	kallikrein 7 (chymotryptic, stratum corneum)	-0.07	AACCATCAAACATGTTCCAAA	NM_005046:	NM_005046:NM_139277:
11202	KLK8	kallikrein 8 (neuropsin/ovasin)	-0.26	TAAGCACTAGATCTCCCTTAA	NM_007196:	NM_144506:NM_144507:NM_007196:NM_144505:
11202	KLK8	kallikrein 8 (neuropsin/ovasin)	-1.64	CAAGGGCTGATTCTAGGATAA	NM_007196:	NM_144506:NM_144507:NM_007196:NM_144505:
284366	KLK9	kallikrein 9	1.07	CCCAAGGAACCACTTACACAA	NM_012315:	NM_012315:
284366	KLK9	kallikrein 9	1.68	CACCTCCTTCTTGGAACAGCA	NM_012315:	NM_012315:
3818	KLKB1	kallikrein B, plasma (Fletcher factor) 1	0.24	ATGGTCTGTGCTGGCTATAAA	NM_000892:	NM_000892:
3818	KLKB1	kallikrein B, plasma (Fletcher factor) 1	-1.16	AACGTGGAATCTGGATTCTCA	NM_000892:	NM_000892:
221191	Klkbl4	plasma kallikrein-like protein 4	0.09	CAGGAAGGACATTGTCGTTAT	XM_375358:	XM_375358:
221191	Klkbl4	plasma kallikrein-like protein 4	0.31	ACCAGTTGTGGCGTCCAGAAA	XM_375358:	XM_375358:
8564	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-0.18	TGGGTACAACATCGAATAATA	NM_003679:	NM_003679:
8564	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-0.39	AAGGCTATTAATATCATACTA	NM_003679:	NM_003679:
3827	KNG1	kininogen 1	-0.98	ACCGGTGAATGTACAGATAAT	NM_000893:	NM_000893:

3827	KNG1	kininogen 1	0.30	TCCCTCTTCATGCTTAATGAA	NM_000893:	NM_000893:
3831	KNS2	kinesin 2	-3.45	CCCGATGTTGCCAAGCAGTTA	NM_182923:	NM_005552:NM_182923:
3831	KNS2	kinesin 2	1.10	TGGAGTTTATGAATCAGCTAA	NM_182923:	NM_005552:NM_182923:
3831	KNS2	kinesin 2	-2.61	CCCGATGTTGCCAAGCAGTTA	NM_182923:	NM_005552:NM_182923:
3831	KNS2	kinesin 2	1.03	TGGAGTTTATGAATCAGCTAA	NM_182923:	NM_005552:NM_182923:
9735	KNTC1	kinetochore associated 1	-1.62	TCCCGTGGATCTAGAATATCA	NM_014708:	NM_014708:
9735	KNTC1	kinetochore associated 1	0.05	TGCTCTTAATTTCGAAATTAA	NM_014708:	NM_014708:
10403	KNTC2	kinetochore associated 2	-9.59	CCGAGACCACTTAATGACAAA	NM_006101:	NM_006101:
10403	KNTC2	kinetochore associated 2	-10.26	TCCCTGGGTCGTGTCAGGAAA	NM_006101:	NM_006101:
3838	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	-4.73	ACGAATTGGCATGGTGGTGAA	NM_002266:	NM_002266:
3838	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.54	CCGGGCTGGTTTGATTCCGAA	NM_002266:	NM_002266:
23633	KPNA6	karyopherin alpha 6 (importin alpha 7)	-3.37	AACCATTCTCTTACAGTTTAA	NM_012316:	NM_012316:
23633	KPNA6	karyopherin alpha 6 (importin alpha 7)	-1.46	CTGGGTGGATTACATATGATA	NM_012316:	NM_012316:
3837	KPNB1	karyopherin (importin) beta 1	-3.14	TCGGTTATATTTGCCAAGATA	NM_002265:	NM_002265:
3837	KPNB1	karyopherin (importin) beta 1	-6.43	CAAGAACTCTTTGACATCTAA	NM_002265:	NM_002265:
3845	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.26	AAGGAGAATTTAATAAAGATA	NM_004985:	NM_004985:NM_033360:
3845	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.34	CTCCTAATTATTGTAATGTAA	NM_004985:	NM_004985:NM_033360:
83999	KREMEN1	kringle containing transmembrane protein 1	-1.22	ACCCGAGTGTTTCACAGCCAA	NM_032045:	NM_032045:
83999	KREMEN1	kringle containing transmembrane protein 1	-0.69	GACCTTAGGGATTGTCATCAA	NM_032045:	NM_153379:NM_032045:
79412	KREMEN2	kringle containing transmembrane protein 2	-0.40	CCCGGACTTCCCGGACGAGTA	NM_024507:	NM_172229:NM_024507:NM_145347:NM_145348:
79412	KREMEN2	kringle containing transmembrane protein 2	-0.24	CGCGCACAACTTCTGCCGTAA	NM_024507:	NM_172229:NM_024507:NM_145347:NM_145348:
889	KRIT1	KRIT1, ankyrin repeat containing	0.48	AACAAGGAAGATCTCCATTAA	NM_004912:	NM_194454:NM_194455:NM_001013406:NM_004912:NM_194456:
889	KRIT1	KRIT1, ankyrin repeat containing	-4.67	TAGGAGCTCCAGACTACTCAA	NM_004912:	NM_194454:NM_194455:NM_001013406:NM_004912:NM_194456:
3848	KRT1	keratin 1 (epidermolytic hyperkeratosis)	0.47	TCCACTAGAACCCATAATTTA	NM_006121:	NM_006121:
3848	KRT1	keratin 1 (epidermolytic hyperkeratosis)	-2.54	AACCCATAATTTAGAGCCCTA	NM_006121:	NM_006121:
3856	KRT8	keratin 8	-2.10	CAGGGTGACCCAGAAGTCCTA	NM_002273:	NM_002273:XM_496418:
8844	KSR1	kinase suppressor of ras 1	-0.65	AAGGGCGAAGCTGGTCCGTTA	XM_290793:	NM_014238:
283455	KSR2	kinase suppressor of ras 2	-2.80	ATCCGGTGACCTCGAATCCAA	NM_173598:	NM_173598:
283455	KSR2	kinase suppressor of ras 2	-0.41	TCCGTTGTGAGGGATGCCAAA	NM_173598:	NM_173598:
112970	KTI12	KTI12 homolog, chromatin associated (S. cerevisiae)	-0.42	CAGACTAAAGAGAATGGAGAA	NM_138417:	NM_138417:
112970	KTI12	KTI12 homolog, chromatin associated (S. cerevisiae)	0.61	AAGTAAGAAAGTTATCTACTA	NM_138417:	NM_138417:
3895	KTN1	kinectin 1 (kinesin receptor)	-0.14	AACGTGATCGTTTAACAAGTA	NM_182926:	NM_182926:
3895	KTN1	kinectin 1 (kinesin receptor)	-1.50	CACCAAGAGACTAAACAAGAA	NM_182926:	NM_182926:
3897	L1CAM	L1 cell adhesion molecule	-0.20	CCGCGGATACAATGTGACGTA	NM_000425:	NM_000425:NM_024003:
3897	L1CAM	L1 cell adhesion molecule	-4.44	CACCCTCAAGCTGTCGCCCTA	NM_000425:	NM_000425:NM_024003:
284217	LAMA1	laminin, alpha 1	1.31	CACCAGTTTGGTCTCACACAA	NM_005559:	NM_005559:
284217	LAMA1	laminin, alpha 1	1.42	CCAGACGCTATTATTATTCAA	NM_005559:	NM_005559:
3908	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	-0.84	CTGGACAGGCCTATTATGTAA	NM_000426:	NM_000426:
3908	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	0.20	CCGGCTAATAGATAAACTCAA	NM_000426:	NM_000426:
3909	LAMA3	laminin, alpha 3	-1.52	CAGGTTTAATAGCGAATCTAA	NM_000227:	NM_000227:NM_198129:
3909	LAMA3	laminin, alpha 3	-3.42	CTGGAAGATGGTTACATTGAA	NM_000227:	NM_000227:NM_198129:
3910	LAMA4	laminin, alpha 4	0.01	ACAGGTCATAGTGAAAGTCAA	NM_002290:	NM_002290:
3910	LAMA4	laminin, alpha 4	0.18	ATCAAGGTTTAATAAAGTAAA	NM_002290:	NM_002290:
3911	LAMA5	laminin, alpha 5	-0.22	CTGAAGATGGTTTAAGTTATA	NM_005560:	NM_005560:
3911	LAMA5	laminin, alpha 5	-1.52	CCGCATCAGCTTCGACAGTCA	NM_005560:	NM_005560:
3912	LAMB1	laminin, beta 1	0.51	TCCGTTCACTCCTAAAGGATA	NM_002291:	NM_002291:
3912	LAMB1	laminin, beta 1	1.06	TACCAAGATCCTGTTACTTTA	NM_002291:	NM_002291:
3913	LAMB2	laminin, beta 2 (laminin S)	-0.44	GCGAGATAGGCTTGCACTTAA	NM_002292:	NM_002292:
3913	LAMB2	laminin, beta 2 (laminin S)	-0.35	CCAGGCCACCTTTGAACGCTA	NM_002292:	NM_002292:
3914	LAMB3	laminin, beta 3	-1.01	AAGAGGGATTTGAGAGAATAA	NM_000228:	NM_000228:NM_001017402:
3914	LAMB3	laminin, beta 3	-1.31	ACCGGTTGGGTCAGAGTTCCA	NM_000228:	NM_000228:NM_001017402:
3915	LAMC1	laminin, gamma 1 (formerly LAMB2)	-2.91	TAGGGATATGATAACCACTAA	NM_002293:	NM_002293:
3915	LAMC1	laminin, gamma 1 (formerly LAMB2)	0.08	TAGGTGGCAGATGTAAATGTA	NM_002293:	NM_002293:
3918	LAMC2	laminin, gamma 2	-5.87	CAGGCATATGGATGAGTTCAA	NM_005562:	NM_018891:NM_005562:
3918	LAMC2	laminin, gamma 2	-4.84	CCGGACGGTGCTGTGGTGCAA	NM_005562:	NM_018891:NM_005562:
3920	LAMP2	lysosomal-associated membrane protein 2	1.13	TAAGGACTATAGTGATTTAAA	NM_002294:	NM_002294:
3920	LAMP2	lysosomal-associated membrane protein 2	1.05	CTGGAGCATTTCAGATAAATA	NM_002294:	NM_013995:NM_002294:
10314	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	0.98	AAGGTTGTCAAAGGTCATCAA	NM_006055:	NM_006055:
10314	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	-0.19	ACGGCTAATTCACCTAAATAA	NM_006055:	NM_006055:
55915	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	1.02	ACCCAGGTATATGTTACTAAA	NM_018697:	NM_018697:
55915	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	0.00	CTGGCAGTTCCAGAACATTTA	NM_018697:	NM_018697:
51056	LAP3	leucine aminopeptidase 3	0.91	AAGCTTAATTTGCCCATTAAT	NM_015907:	NM_015907:
51056	LAP3	leucine aminopeptidase 3	0.07	AAAGCTTAATTTGCCCATTAA	NM_015907:	NM_015907:
9215	LARGE	like-glycosyltransferase	0.17	ACCAGCGAAAGCTGCATTTAA	NM_004737:	NM_004737:NM_133642:
9215	LARGE	like-glycosyltransferase	-0.02	AAGGGTTATCATCTTACTGCA	NM_004737:	NM_004737:NM_133642:
51520	LARS	leucyl-tRNA synthetase	1.27	CACCCTGTCTGTTCTACGTAA	NM_020117:	NM_020117:
51520	LARS	leucyl-tRNA synthetase	0.03	TCGCTTGAGCTAGAACACATA	NM_020117:	NM_020117:
23395	LARS2	leucyl-tRNA synthetase 2, mitochondrial	-0.24	CTGACCTAAGCCACTGATTAA	NM_015340:	NM_015340:
23395	LARS2	leucyl-tRNA synthetase 2, mitochondrial	0.24	CCCGAGAACTGCCCTCATCAA	NM_015340:	NM_015340:
3927	LASP1	LIM and SH3 protein 1	-1.68	CTGGCCTGTTATGATTCTGAA	NM_006148:	NM_006148:
3927	LASP1	LIM and SH3 protein 1	-0.01	ACCCTACAAACCTGTATTTAA	NM_006148:	NM_006148:
253782	LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	0.23	CCGGACGAACTAGGTGTTTAA	NM_203463:	NM_203463:
253782	LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	0.51	CTGGGCTGCATCATTATATAA	NM_203463:	NM_203463:
27040	LAT	linker for activation of T cells	2.96	CCCGTAACTTATTATCACTTT	NM_014387:	NM_001014988:NM_001014989:NM_014387:NM_001014987:
27040	LAT	linker for activation of T cells	0.43	CCTCTTGTGGTTCTCAATAAA	NM_014387:	NM_001014987:NM_001014988:NM_001014989:NM_014387:
9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	1.37	CCCATGAATCCTCCTAATCAA	NM_004690:	NM_004690:
9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	0.14	CGCGATCTAGTATATGTTTAA	NM_004690:	NM_004690:
26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	-0.89	CACACTCACCTCGCCCAATAA	NM_014572:	NM_014572:
26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	1.81	CAGGACCTTCACTGCATTAAA	NM_014572:	NM_014572:
3929	LBP	lipopolysaccharide binding protein	-2.37	CACGTCTCAGAGATTCTTGAA	NM_004139:	NM_004139:
3929	LBP	lipopolysaccharide binding protein	-0.19	CAAGATCACTGGGTTCCTGAA	NM_004139:	NM_004139:
3930	LBR	lamin B receptor	1.93	TAAGGTAGCTTTAGCAATTAA	NM_002296:	NM_002296:NM_194442:
3930	LBR	lamin B receptor	0.17	TAGCAATTAAATTCTAGTGAA	NM_002296:	NM_002296:NM_194442:
3931	LCAT (lecithir	lecithin-cholesterol acyltransferase	-0.40	AACAGCATCTCAACATGGTCT	NM_000229:	NM_000229:
3931	LCAT (lecithir	lecithin-cholesterol acyltransferase	-2.55	AACCAGATGTGGTGAACTGGA	NM_000229:	NM_000229:
3932	LCK (lymphoc	lymphocyte-specific protein tyrosine kinase	0.44	AAGGGCCAGGACTTTATCTAA	NM_005356:	NM_005356:
3932	LCK (lymphoc	lymphocyte-specific protein tyrosine kinase	-0.09	AGGCATCAAGTTGACCATCAA	NM_005356:	NM_005356:
9836	LCMT2	leucine carboxyl methyltransferase 2	-0.13	CAGAGGCATTTCCTCGCGTAA	NM_014793:	NM_014793:
9836	LCMT2	leucine carboxyl methyltransferase 2	-3.86	ACCCACTAAAGTAGACAATAA	NM_014793:	NM_014793:
3938	LCT	lactase	0.32	ACGGAGGATACTGATAGGATA	NM_002299:	NM_002299:
3938	LCT	lactase	-2.32	CACGGTCAAGTTTGGACTGTA	NM_002299:	NM_002299:
3939	LDHA	lactate dehydrogenase A	-0.08	AAGTCCAATATGGCAACTCTA	NM_005566:	NM_005566:
3939	LDHA	lactate dehydrogenase A	0.01	CAGCTGATTTATAATCTTCTA	NM_005566:	NM_005566:

3945	LDHB	lactate dehydrogenase B	-2.95	CACCGCGTGATTGGAAGTGGA	NM_002300:	NM_002300:
3945	LDHB	lactate dehydrogenase B	0.92	CCAGTGGACATTCTTACGTAT	NM_002300:	NM_002300:
3949	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	-3.23	CACCGAGACCAAACTCATTCA	NM_000527:	NM_000527:
3949	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	-2.05	CACCGTGACACAATCCTCAAA	NM_000527:	NM_000527:
401944	LDLRAD2 (lo	low density lipoprotein receptor class A domain containing 2	0.01	CAGGAAGTACAGATGCCCATA	XM_377577:	NM_001013693:
401944	LDLRAD2 (lo	low density lipoprotein receptor class A domain containing 2	-0.38	CGGCTCCTACCTGCAGTTCTA	XM_377577:	NM_001013693:
143458	LDLRAD3 (lo	low density lipoprotein receptor class A domain containing 3	0.96	AACCTGTTTGACGCTAATTAA	NM_174902:	NM_174902:
143458	LDLRAD3 (lo	low density lipoprotein receptor class A domain containing 3	0.04	AAGGGACTATTTATATGTGTA	NM_174902:	NM_174902:
26119	LDLRAP1	low density lipoprotein receptor adaptor protein 1	1.60	GAGGATCGTGGCTACAGCTAA	NM_015627:	NM_015627:
26119	LDLRAP1	low density lipoprotein receptor adaptor protein 1	0.73	CTAGATTTATTTGGAAATATT	NM_015627:	NM_015627:
3950	LECT2	leukocyte cell-derived chemotaxin 2	1.80	AAGGAAATTTGAGTTTAAATA	NM_002302:	NM_002302:
3950	LECT2	leukocyte cell-derived chemotaxin 2	0.27	CAGAAAGTTTATCCTGGCATA	NM_002302:	NM_002302:
51176	LEF1	lymphoid enhancer-binding factor 1	-0.29	AAGGTGTTCAGTAGAGCTAAA	NM_016269:	NM_016269:
51176	LEF1	lymphoid enhancer-binding factor 1	-0.01	CGGGTACATAATGATGCCAAA	NM_016269:	NM_016269:
10637	LEFTY1	left-right determination factor 1	1.24	CCAGATAATAAAGACTTTGTA	NM_020997:	NM_020997:
10637	LEFTY1	left-right determination factor 1	-0.88	CTGACAAGTTACCTCACCTAA	NM_020997:	NM_020997:
7044	LEFTY2	left-right determination factor 2	1.37	AACAATAATACCCTATGATTA	NM_003240:	NM_003240:
7044	LEFTY2	left-right determination factor 2	1.03	AGCACTTACGTGAGTAAATAA	NM_003240:	NM_003240:
3952	LEP	leptin (obesity homolog, mouse)	-1.32	CCAGAGTGTGAAACTTCCTAA	NM_000230:	NM_000230:
3952	LEP	leptin (obesity homolog, mouse)	0.92	CCCAATAAACATTAAGATTGA	NM_000230:	NM_000230:
3953	LEPR	leptin receptor	1.05	ATGGAAGATGTATGAGGTTTA	NM_002303:	NM_001003680:NM_001003679:NM_002303:
3953	LEPR	leptin receptor	-0.07	TTCGCTATGGTTTAAGTGGAA	NM_002303:	NM_001003680:NM_001003679:NM_002303:
54741	LEPROT	leptin receptor overlapping transcript	-5.84	AAGCATCATCATAGAGAAGTA	NM_017526:	NM_017526:
54741	LEPROT	leptin receptor overlapping transcript	-4.93	CGGCCTTGTGTTGGCAGGCAA	NM_017526:	NM_017526:
23484	LEPROTL1	leptin receptor overlapping transcript-like 1	3.75	CAGACGGTTGGCATACGTTAT	NM_015344:	NM_015344:
23484	LEPROTL1	leptin receptor overlapping transcript-like 1	3.41	CAGAGACTTGCTGAAGGATTA	NM_015344:	NM_015344:
25875	LETMD1	LETM1 domain containing 1	1.67	CACAATATAAAGTTTCATCAA	NM_015416:	NM_015416:NM_001024668:
25875	LETMD1	LETM1 domain containing 1	1.71	CACCCAGAAATTATTAGTTAT	NM_015416:	NM_015416:NM_001024669:NM_001024668:NM_001024670:
3956	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	-2.96	CACCATCGTGTGCAACAGCAA	NM_002305:	NM_002305:
3956	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	0.86	CGCCAGCAACCTGAATCTCAA	NM_002305:	NM_002305:
3959	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.78	CAGCTTCAAGAAATTACTGGA	NM_005567:	NM_005567:
3959	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.07	CTGAGGCTCAGCTTCAAGAAA	NM_005567:	NM_005567:
9211	LGI1	leucine-rich, glioma inactivated 1	0.17	AAGATTCATTGGTGATTCCAA	NM_005097:	NM_005097:
9211	LGI1	leucine-rich, glioma inactivated 1	-0.34	AAGCAACACAATTATTCACTA	NM_005097:	NM_005097:
353174	LGICZ1	ligand-gated ion channel, zinc activated 1	0.17	CACCACGGAGACCAACTGCAA	NM_180990:	NM_180990:
353174	LGICZ1	ligand-gated ion channel, zinc activated 1	1.88	CTCGCCTGGCCTGGAACACTA	NM_180990:	NM_180990:
5641	LGMN	legumain	0.22	AAGGGTCATATTTGCTTTCTA	NM_005606:	NM_005606:NM_001008530:
5641	LGMN	legumain	-0.67	CCGTATCCACTTCACAGGATA	NM_005606:	NM_001008530:NM_005606:
55366	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	0.04	TAGGATTTCATAGTAATTCTA	NM_018490:	NM_018490:
55366	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	0.02	TAGGTGTAGTAGAGCAATATA	NM_018490:	NM_018490:
8549	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	1.20	CAGCAGTATGGACGACCTTCA	NM_003667:	NM_003667:
8549	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	0.33	CCCAAGCTTGATGTCAATTAA	NM_003667:	NM_003667:
59352	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	-0.09	CAGGAGTTTCCAGATCTCAAA	NM_021636:	NM_001017403:NM_021636:NM_001017404:
59352	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	0.42	CTGGAACTGTCTCACAATCAA	NM_021636:	NM_001017403:NM_021636:NM_001017404:
59350	LGR7	leucine-rich repeat-containing G protein-coupled receptor 7	0.40	AAAGGATGTTTAGACCTCTTA	NM_021634:	NM_021634:
59350	LGR7	leucine-rich repeat-containing G protein-coupled receptor 7	0.38	ACAGACTAGAATGGCTGATAA	NM_021634:	NM_021634:
122042	LGR8	leucine-rich repeat-containing G protein-coupled receptor 8	1.49	GCGCTTGTTTACGGGATTAAA	NM_130806:	NM_130806:
122042	LGR8	leucine-rich repeat-containing G protein-coupled receptor 8	-2.65	TCGGGTTGCACTGTCCATGAA	NM_130806:	NM_130806:
1939	LGTN	ligatin	-0.41	CCGAACGATCGTCATTAACTA	NM_006893:	NM_006893:
1939	LGTN	ligatin	-1.78	CTGGCTATTGCTTGAAGAGTA	NM_006893:	NM_006893:
3972	LHB	luteinizing hormone beta polypeptide	-0.02	CCCAGTGTGCATCACCGTCAA	NM_000894:	NM_000894:
3973	LHCGR	luteinizing hormone/choriogonadotropin receptor	-1.22	CAGTTCGAAACCCAGAATTAA	NM_000233:	NM_000233:
3973	LHCGR	luteinizing hormone/choriogonadotropin receptor	-0.67	CCCAGAATTAATGGCTACCAA	NM_000233:	NM_000233:
64077	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatas	1.54	CAGGAGGAAACTAACAGTTCA	NM_022126:	NM_022126:
64077	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatas	1.97	CCCAGTCACCTTTGCAGACAA	NM_022126:	NM_022126:
8022	LHX3	LIM homeobox 3	1.96	CTGCTATTTCTAGACATGAAA	NM_014564:	NM_178138:NM_014564:
8022	LHX3	LIM homeobox 3	-7.86	CAGCTCTTTCCAAGACTTCAA	NM_014564:	NM_178138:NM_014564:
89884	LHX4	LIM homeobox 4	-1.40	TCGAAAGTACGCCAATGTGAA	NM_033343:	NM_033343:
89884	LHX4	LIM homeobox 4	-5.53	CACCAATAGGATTTATGGCAA	NM_033343:	NM_033343:
64211	LHX5	LIM homeobox 5	0.54	AAGCAGCCTCCTGAAACCAAA	NM_022363:	NM_022363:
64211	LHX5	LIM homeobox 5	0.03	TTAGATATGCTATAAATTTAA	NM_022363:	NM_022363:
56956	LHX9 (LIM ho	LIM homeobox 9	-8.93	CCGGGCGTGTGTATATGGAAA	NM_020204:	NM_020204:
56956	LHX9 (LIM ho	LIM homeobox 9	0.08	AACCAGATAATTAATTAGTTA	NM_020204:	NM_020204:NM_001014434:
3976	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	-0.01	CTGGAAGTCGACAATGTTACA	NM_002309:	NM_002309:
3976	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	-3.22	CTGGGTAAAGGTCTGTAAGAA	NM_002309:	NM_002309:
3977	LIFR	leukemia inhibitory factor receptor	0.65	TGCAGATTCGATATTAGTAAA	NM_002310:	NM_002310:
3977	LIFR	leukemia inhibitory factor receptor	-0.39	TTGGAAGCCTTTACCCATTAA	NM_002310:	NM_002310:
3978	LIG1	ligase I, DNA, ATP-dependent	0.52	CCCGTCATTTCTTTCAATAAA	NM_000234:	NM_000234:
3978	LIG1	ligase I, DNA, ATP-dependent	0.13	CCGGACGTTTGAGAAGATCGA	NM_000234:	NM_000234:
3980	LIG3 (ligase I	ligase III, DNA, ATP-dependent	-0.31	CTGGAAGATAATGAGAAGGAA	NM_002311:	NM_002311:NM_013975:
3980	LIG3 (ligase I	ligase III, DNA, ATP-dependent	-0.30	CTGGGAAGAGCTGGAAGATAA	NM_002311:	NM_002311:NM_013975:
3981	LIG4 (ligase I	ligase IV, DNA, ATP-dependent	0.01	CAAGATGTTTACAGAAAGGAA	NM_002312:	NM_206937:NM_002312:
3981	LIG4 (ligase I	ligase IV, DNA, ATP-dependent	1.32	TTGGAATTATTGAGCACTTAA	NM_002312:	NM_206937:NM_002312:
11025	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITI	-1.20	CTGACTCAAAGATGACTAATA	NM_006864:	NM_006864:
11025	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITI	-2.28	CAGGGTGGAGCTGGACAGTCA	NM_006864:	NM_006864:
3982	LIM2	lens intrinsic membrane protein 2, 19kDa	0.47	CCCAAGCATACTGGAATGCCA	NM_030657:	NM_030657:
3982	LIM2	lens intrinsic membrane protein 2, 19kDa	1.19	ATGGACTATCCATTAGAGCAA	NM_030657:	NM_030657:
3984	LIMK1	LIM domain kinase 1	0.23	CACCATGGACTTTGGCCTCAA	NM_002314:	NM_016735:NM_002314:
3984	LIMK1	LIM domain kinase 1	0.87	CTGCCTGGTCCGCGAGAACAA	NM_002314:	NM_016735:NM_002314:
3985	LIMK2 (LIM d	LIM domain kinase 2	0.34	CAGGAGGAATCTGTTACTCGA	NM_005569:	NM_005569:NM_016733:
3985	LIMK2 (LIM d	LIM domain kinase 2	-0.14	CAGGGTGAACCTGCCTGTGAA	NM_005569:	NM_005569:NM_016733:
3987	LIMS1	LIM and senescent cell antigen-like domains 1	0.95	AAACACATGGTTAAATGTTAA	NM_004987:	NM_004987:
3987	LIMS1	LIM and senescent cell antigen-like domains 1	1.13	AACATTACTTGTCTTGATCTA	NM_004987:	NM_004987:
8825	LIN7A	lin-7 homolog A (C. elegans)	1.36	TCCGATAGTCACAAATTTGAA	NM_004664:	NM_004664:
8825	LIN7A	lin-7 homolog A (C. elegans)	1.11	CCCATTTATATCTCTCGCATA	NM_004664:	NM_004664:
64130	LIN7B	lin-7 homolog B (C. elegans)	0.73	CACGTGCACTCTCTTCCTGTA	NM_022165:	NM_022165:
64130	LIN7B	lin-7 homolog B (C. elegans)	1.06	CAGGGTAGTGGAGCTACCCAA	NM_022165:	NM_022165:
55327	LIN7C	lin-7 homolog C (C. elegans)	0.35	TGGCATATTGACCCTATATAA	NM_018362:	NM_018362:
55327	LIN7C	lin-7 homolog C (C. elegans)	1.26	TCAACCGTACATCAAATTATA	NM_018362:	NM_018362:
286826	LIN9	lin-9 homolog (C. elegans)	-0.89	CCAGTAGAATTTCTTATCCAA	NM_173083:	NM_173083:
286826	LIN9	lin-9 homolog (C. elegans)	-0.40	ACGAGTGGTTCTATTCAAATA	NM_173083:	NM_173083:
3988	LIPA	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	0.48	CCCGCTACTGTCGTTATTGAT	NM_000235:	NM_000235:
3988	LIPA	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	-0.13	CTGACTTAAGCGAGGTATAAA	NM_000235:	NM_000235:
3990	LIPC	lipase, hepatic	-6.70	CAGGAGAAACCCAGCAAAGAA	NM_000236:	NM_000236:
3990	LIPC	lipase, hepatic	-0.89	CTGAAGACGATCAGAGTCAAA	NM_000236:	NM_000236:
8513	LIPF	lipase, gastric	-1.83	CAGGCTGTTAAGTCTGGGAAA	NM_004190:	NM_004190:
8513	LIPF	lipase, gastric	0.67	CAGCAATGCCTTATTTATAAT	NM_004190:	NM_004190:
9388	LIPG	lipase, endothelial	-1.09	CAAGCCCATGGAGGAAAGTTA	NM_006033:	NM_006033:

9388	LIPG	lipase, endothelial	-2.32	CCGGGCAAGTCTTGCCAGCAA	NM_006033:	NM_006033:
200879	LIPH	lipase, member H	-0.01	TACCAATGTAATCTATGATTA	NM_139248:	NM_139248:
200879	LIPH	lipase, member H	0.86	CACACGTAGAAGGGAACGAAA	NM_139248:	NM_139248:
149998	LIPI	lipase, member I	-1.37	ACCATATAGCAGATTAGATTA	NM_198996:	NM_198996:
149998	LIPI	lipase, member I	0.08	AAGGATTCCTTCAGAGATTTA	NM_198996:	NM_198996:
142910	LIPL1	lipase-like, ab-hydrolase domain containing 1	0.83	CGCTGTGTGTTTAAAGATCTA	XM_084377:	NM_001010939:
142910	LIPL1	lipase-like, ab-hydrolase domain containing 1	-3.87	CAACTGCAATTTGGAATGGTA	XM_084377:	NM_001010939:
340654	LIPL3	lipase-like, ab-hydrolase domain containing 3	-0.09	CAGGACTAAATTGGCTGTTAA	XM_291663:	XM_291663:
340654	LIPL3	lipase-like, ab-hydrolase domain containing 3	0.21	CAGGATACTCCCTCAAATCAA	XM_291663:	XM_291663:
9516	LITAF	lipopolysaccharide-induced TNF factor	0.70	GCCAATGTAGTCTCACTTAAA	NM_004862:	NM_004862:
9516	LITAF	lipopolysaccharide-induced TNF factor	0.48	TGCCAATGTAGTCTCACTTAA	NM_004862:	NM_004862:
3996	LLGL1	lethal giant larvae homolog 1 (Drosophila)	0.04	CACGGTAGCCACCACACCTTA	NM_004140:	NM_004140:
3993	LLGL2	lethal giant larvae homolog 2 (Drosophila)	-1.39	CTCCTGCGTCTTCACCAAATA	NM_004524:	NM_001031803:NM_004524:
3993	LLGL2	lethal giant larvae homolog 2 (Drosophila)	-4.89	CTGCGCGATGAGCACACACTA	NM_004524:	NM_001031803:NM_004524:
3998	LMAN1	lectin, mannose-binding, 1	0.48	TTCGATGATCTGAGGATTTAA	NM_005570:	NM_005570:
3998	LMAN1	lectin, mannose-binding, 1	-0.16	CACGATGTAAATTCACGTCAA	NM_005570:	NM_005570:
81562	LMAN2L	lectin, mannose-binding 2-like	0.49	TCCAGGTTTGATCAAACCAAA	NM_030805:	NM_030805:
81562	LMAN2L	lectin, mannose-binding 2-like	-1.96	AACCCTTATTCCACTGCCTTA	NM_030805:	NM_030805:
55716	LMBR1L	limb region 1 homolog (mouse)-like	-5.97	CACCACAGTTTCATCCTACAA	NM_018113:	NM_018113:
55716	LMBR1L	limb region 1 homolog (mouse)-like	-0.11	TCCGCGAGTGTATTATATCAA	NM_018113:	NM_018113:
89782	LMLN	leishmanolysin-like (metallopeptidase M8 family)	-0.01	TCCGTTTGTCTAATTCAGAAA	NM_033029:	NM_033029:
89782	LMLN	leishmanolysin-like (metallopeptidase M8 family)	-1.04	ATGGGATGTTCGAGATAATAA	NM_033029:	NM_033029:
4000	LMNA	lamin A/C	-0.95	CCAGGAGCTTCTGGACATCAA	NM_005572:	NM_170707:NM_170708:NM_005572:
4000	LMNA	lamin A/C	-0.94	CCCACCAAAGTTCACCCTGAA	NM_005572:	NM_170707:NM_170708:NM_005572:
4004	LMO1	LIM domain only 1 (rhombotin 1)	0.65	CCGGACAAGCGGGTAATTAGA	NM_002315:	NM_002315:
4004	LMO1	LIM domain only 1 (rhombotin 1)	2.55	CAGGGTTATGAGCTATCAAAT	NM_002315:	NM_002315:
4005	LMO2	LIM domain only 2 (rhombotin-like 1)	0.47	CACAGATTGTTTCTATACAAA	NM_005574:	NM_005574:
4005	LMO2	LIM domain only 2 (rhombotin-like 1)	0.57	CAGATAGAGAGTTGTTGTGTA	NM_005574:	NM_005574:
55885	LMO3	LIM domain only 3 (rhombotin-like 2)	1.10	TAGTTGAATATTTATTATTAA	M86528:	NM_001001395:NM_018640:
22853	LMTK2	lemur tyrosine kinase 2	0.90	CACCTCCGACTTAAATGTGAA	NM_014916:	NM_014916:
22853	LMTK2	lemur tyrosine kinase 2	-0.18	CAGATCAGACTAAGTATAGTA	NM_014916:	NM_014916:
114783	LMTK3	lemur tyrosine kinase 3	-0.11	GCGGGAGGATGTGACAAGGAA	XM_055866:	XM_055866:
114783	LMTK3	lemur tyrosine kinase 3	-4.04	CCGGGAGACAGGACCCAGGAA	XM_055866:	XM_055866:
4012	LNPEP	leucyl/cystinyl aminopeptidase	-0.04	CACGTAAATGCCAACCATCTA	NM_005575:	NM_005575:NM_175920:
4012	LNPEP	leucyl/cystinyl aminopeptidase	-0.11	TCCAATGGAACTCAAAGCCTA	NM_005575:	NM_175920:NM_005575:
84708	LNX1	ligand of numb-protein X 1	0.36	CACAGCTAACACAGCTCTTTA	NM_032622:	NM_032622:
84708	LNX1	ligand of numb-protein X 1	1.29	CTCGCTCAGAGAATTAATTAT	NM_032622:	NM_032622:
222484	LNX2	ligand of numb-protein X 2	-2.86	CACCGTATTATAGCAGACCAA	NM_153371:	NM_153371:
222484	LNX2	ligand of numb-protein X 2	-0.48	CAGCCACTTAGTTTACCAGAA	NM_153371:	NM_153371:
112714	LOC112714	similar to alpha tubulin	1.10	TTCAAGTTGTTTGCAATTAAA	NM_207312:	NM_207312:
116143	LOC116143	monad	0.70	ACGGTGGGAGACAAACATCAA	NM_138458:	NM_138458:
116143	LOC116143	monad	-2.14	AAGGTGTGGGACCCAAGGCAA	NM_138458:	NM_138458:
124446	LOC124446	hypothetical protein BC017488	0.65	GGACAACTGGTCCTTATCACA	XM_378175:	NM_194280:XM_378175:
124446	LOC124446	hypothetical protein BC017488	0.09	TGAAGGCCTTGTGCTGACCAA	XM_378175:	NM_194280:XM_378175:
125893	LOC125893	hypothetical protein LOC125893	-1.84	CTCGAACATGTTTCAGACTAA	BC028701:	NM_001031665:
127406	LOC127406	similar to laminin receptor 1 (ribosomal protein SA)	0.16	GTGGGTTTGATAGATCCTGAA	XM_497679:	XM_497679:
127406	LOC127406	similar to laminin receptor 1 (ribosomal protein SA)	-0.78	TGGCTGGATCTTGTCCATGTA	XM_497679:	XM_497679:
130576	LOC130576	hypothetical protein LOC130576	-2.34	AACGGTGAACTTTGGAGTGAA	NM_177964:	NM_177964:
130576	LOC130576	hypothetical protein LOC130576	0.05	AAGACAAATGGTGTCCACAAA	NM_177964:	NM_177964:
133308	LOC133308	hypothetical protein BC009732	-1.48	CTGCAGAAAGTTGAACATCAA	NM_178833:	NM_178833:
133308	LOC133308	hypothetical protein BC009732	-1.10	CAACGATAATGTGCAGATCAA	NM_178833:	NM_178833:
134145	LOC134145	hypothetical protein LOC134145	-0.60	CACCTAGTCTTTGGTCCATAA	NM_199133:	NM_199133:
134145	LOC134145	hypothetical protein LOC134145	-3.87	CTGGGATAATGGTACACATAA	NM_199133:	NM_199133:
134541	LOC134541	similar to odd Oz/ten-m homolog 2	-0.65	TCAGATGAGTTTCCTAGACAA	XM_068903:	XM_068903:
134541	LOC134541	similar to odd Oz/ten-m homolog 2	0.94	GCGGACTTAGATGTCTGTTTA	XM_068903:	XM_068903:
136242	LOC136242	similar to RIKEN cDNA 1700016G05	-0.37	CACCATGAAATATGTCTTCTA	XM_379939:	NM_001008270:XM_379939:
136242	LOC136242	similar to RIKEN cDNA 1700016G05	-0.08	ACCAATGTTTACAAATATGTA	XM_379939:	NM_001008270:XM_379939:
136242	LOC136242	similar to RIKEN cDNA 1700016G05	0.12	CACCATGAAATATGTCTTCTA	XM_059830:	NM_001008270:XM_379939:
136242	LOC136242	similar to RIKEN cDNA 1700016G05	1.88	ACCAATGTTTACAAATATGTA	XM_059830:	NM_001008270:XM_379939:
145814	LOC145814	hypothetical protein LOC145814	-0.69	AACCATGGTCCTTCCAGCCAA	XM_372592:	XM_372592:
145814	LOC145814	hypothetical protein LOC145814	-0.15	CAGGAGAAAGAACACTCTGAA	XM_372592:	XM_372592:
146909	LOC146909	hypothetical protein LOC146909	1.10	CCCGACATGATCACAGAGTTT	XM_085634:	XM_085634:
146909	LOC146909	hypothetical protein LOC146909	0.57	CAAGAAGGTCTTAGTCCTGAA	XM_085634:	XM_085634:
150159	LOC150159	CG10806-like	0.15	CGCCATTATGATCCAAGCAAA	XM_375344:	XM_375344:NM_139173:
150159	LOC150159	CG10806-like	-2.89	CTCATTGATCCTAATAATACT	NM_139173:	NM_139173:
150159	LOC150159	CG10806-like	-2.86	TAAGAGGAGTATTGAATGTAA	NM_139173:	NM_139173:
158160	LOC158160	hypothetical protein LOC158160	-0.01	GAGGCACTAAATCTTGGAGAA	NM_182829:	NM_182829:
158160	LOC158160	hypothetical protein LOC158160	0.47	TCGTCTGTGTATGTCATTAAA	NM_182829:	NM_182829:
196541	LOC196541	OTTHUMP00000018663	1.01	ACGAAGTTACATGTTTAATAA	XM_116936:	NM_001010977:
196541	LOC196541	OTTHUMP00000018663	1.36	TAAGATTATCTGGTTAATCTA	XM_116936:	NM_001010977:
197350	LOC197350	hypothetical protein LOC197350	0.12	GGGGTGGCCGTGCAATAAATA	XM_113871:	XM_113871:
197350	LOC197350	hypothetical protein LOC197350	-4.17	AGCAGACATCCTGACGGTCTA	XM_113871:	XM_113871:
203427	LOC203427	similar to solute carrier family 25 , member 16	-1.22	AGCACCTATCTATGCATTTAA	NM_145305:	NM_145305:
203427	LOC203427	similar to solute carrier family 25 , member 16	-0.98	CACTTTAGAGATTCTATGTAA	NM_145305:	NM_145305:
220429	LOC220429	similar to Cutaneous T-cell lymphoma-associated antigen 5 (cTAGE-5	0.22	CCGGCTAGAGAAAGAGAAATT	XM_166966:	XM_166966:
220429	LOC220429	similar to Cutaneous T-cell lymphoma-associated antigen 5 (cTAGE-5	-0.18	AAGATTATATACCATGAGAAA	XM_166966:	XM_166966:
220594	LOC220594	TL132 protein	0.25	TAGGATTCCAAAGTTGTTAAA	NM_145809:	NM_145809:
220594	LOC220594	TL132 protein	-2.48	CTGGCTTTCTGATTAAAGATA	NM_145809:	NM_145809:
222967	LOC222967	hypothetical protein LOC222967	-3.15	CTGGATGCTGAAAGACTTTAA	NM_173565:	NM_173565:
222967	LOC222967	hypothetical protein LOC222967	-4.44	ACCGAGAACATTCGTCCAAAT	NM_173565:	NM_173565:
283116	LOC283116	similar to RING finger protein 18 (Testis-specific ring-finger protein)	-0.83	AGGCTTCATTGTATTAATCTA	XM_208043:	XM_208043:
283130	LOC283130	hypothetical protein LOC283130	-3.14	GCGCTTCTTCAGAGTCATTAA	NM_182556:	NM_182556:
283130	LOC283130	hypothetical protein LOC283130	-1.26	CCCGGCTGCCTTCACCTCTTA	NM_182556:	NM_182556:
284293	LOC284293	similar to Placental thrombin inhibitor (Cytoplasmic antiproteinase) (C	-0.58	AACAACTATGCAAACATTAAA	XM_209104:	XM_209104:
284293	LOC284293	similar to Placental thrombin inhibitor (Cytoplasmic antiproteinase) (C	-0.04	CAGCTAGACTTTGTGAATGAT	XM_209104:	XM_209104:
284672	LOC284672	similar to unactive progesterone receptor, 23 kD	-0.44	CAGCTTAGGGAAAGAGAGCTA	XM_208234:	XM_208234:
284672	LOC284672	similar to unactive progesterone receptor, 23 kD	1.55	CTGGAGAGAAGTGGACTCCAT	XM_208234:	XM_208234:
285643	LOC285643	KIF4B	0.66	GCGGTAGAAGAAGAAGCTCAA	XM_209695:	XM_209695:
285643	LOC285643	KIF4B	0.09	AAGGAAGGTATTGCAGCTCGA	XM_209695:	XM_209695:
286495	LOC286495	similar to Tetratricopeptide repeat protein 3 (TPR repeat protein 3) (TF	-0.27	CAGGAGAGTATTTACAAGTTA	XM_208438:	XM_208438:
286495	LOC286495	similar to Tetratricopeptide repeat protein 3 (TPR repeat protein 3) (TF	0.55	CAGGGTGTGCTGCATGTTCAA	XM_208438:	XM_208438:
338328	LOC338328	high density lipoprotein-binding protein	1.53	CACCAGTTCAACACTCCATTA	NM_178172:	NM_178172:
338328	LOC338328	high density lipoprotein-binding protein	1.20	AAGTACAGAGTGAGACTTAAA	NM_178172:	NM_178172:
339799	LOC339799	similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47	0.49	TACGCATACTATGACACTGAA	XM_290345:	XM_290345:
342897	LOC342897	similar to F-box only protein 2	-1.16	CCGATCCTTGATCTTCCATTA	NM_001001414:	NM_001001414:
342897	LOC342897	similar to F-box only protein 2	0.93	AACGGAGTGGGTGGCAGCAAA	NM_001001414:	NM_001001414:
342931	LOC342931	similar to ret finger protein-like 1	-3.86	AACGATCTCATCGTTTCTGAA	XM_292796:	XM_292796:
342931	LOC342931	similar to ret finger protein-like 1	-1.24	GAGGGAAATACCAGTGCTTTA	XM_292796:	XM_292796:
345051	LOC345051	similar to stromal cell derived factor receptor 2	0.11	CAGCTTCTTACCTCAGTCAAA	XM_293680:	XM_293680:

345051	LOC345051	similar to stromal cell derived factor receptor 2	1.12	CCAGCTTTGATTCACTGGAAA	XM_293680:	XM_293680:
352909	LOC352909	similar to hypothetical testis protein from macaque	-3.64	CACCCAGATGGTTCAAGTAAA	NM_178837:	NM_001031802:NM_178837:
352909	LOC352909	similar to hypothetical testis protein from macaque	0.18	TGGTCTATTCCTAGAATTCTA	NM_178837:	NM_001031802:NM_178837:
375449	LOC375449	similar to microtubule associated testis specific serine/threonine protei	0.63	ATGAATTGCCACCACATTAAA	NM_198828:	NM_198828:
375449	LOC375449	similar to microtubule associated testis specific serine/threonine protei	0.47	GAGGAGCTTGACCACATATTA	NM_198828:	NM_198828:
387870	LOC387870	similar to protein tyrosine phosphatase, receptor type, Q isoform 1 pre	1.79	TAGCAGAAAGAGGAACTTTAA	XM_291991:	XM_291991:
387870	LOC387870	similar to protein tyrosine phosphatase, receptor type, Q isoform 1 pre	-0.10	CACGATATGTTTGTCTTGGAA	XM_291991:	XM_291991:
388720	LOC388720	similar to ubiquitin and ribosomal protein S27a precursor	1.76	TCGGATACAATAGATAATGTA	XM_371330:	XM_371330:
388743	LOC388743	similar to calpain 8	-3.65	CAGGGTGGTCTAGGTGAGTAA	XM_371344:	XM_371344:
388743	LOC388743	similar to calpain 8	0.17	AAGGTCTTGGCTCCAACCAAA	XM_371344:	XM_371344:
389207	LOC389207	similar to glutaredoxin cysteine-rich 1 protein	-0.68	AACAATTTGACCAAAGTATTA	XM_371694:	XM_371694:
389207	LOC389207	similar to glutaredoxin cysteine-rich 1 protein	0.15	ATCAATAAACTTTGTTTATTA	XM_371694:	XM_371694:
389289	LOC389289	similar to annexin II receptor	0.08	TACGATTGTAGAATTCTTAGA	XM_371738:	NM_001014279:
389289	LOC389289	similar to annexin II receptor	0.92	CACGGGCTCTGCAGAGCATAA	XM_371738:	NM_001014279:
389425	LOC389425	similar to ribosomal protein S27a	-0.80	CTGATCTTTGCTGGAAAGCAA	XM_371843:	XM_371843:
390282	LOC390282	similar to eukaryotic translation initiation factor 3, subunit 5 (epsilon)	0.67	AACGTCAGAGTGAAATATGTA	XM_372447:	XM_372447:
390282	LOC390282	similar to eukaryotic translation initiation factor 3, subunit 5 (epsilon)	0.28	CGAGATCATGCTCAACGGTAA	XM_372447:	XM_372447:
390564	LOC390564	similar to Neuronal acetylcholine receptor protein, beta-4 subunit prec	-0.74	CAGGGTCAGCCGAATGCCAGA	XM_372562:	XM_372562:
390846	LOC390846	similar to 27 kDa Golgi SNARE protein (Golgi SNAP receptor complex	0.77	TTGGAGATTATTATCTGTTTA	XM_372693:	XM_372693:
390846	LOC390846	similar to 27 kDa Golgi SNARE protein (Golgi SNAP receptor complex	-0.02	TTAGTAGAAGGTGAAATCCAA	XM_372693:	XM_372693:
390874	LOC390874	similar to one cut domain, family member 3	-0.07	CACGCTGATCGCCATCTTCAA	XM_372702:	XM_372702:
390975	LOC390975	similar to SH3-binding kinase	1.86	ATGAACTAGATCCAAATCCAA	XM_372749:	XM_372749:
390975	LOC390975	similar to SH3-binding kinase	-7.98	CCCGGCAAACAGTCTGAGGAA	XM_372749:	XM_372749:
391025	LOC391025	similar to protein tyrosine phosphatase, receptor type, U isoform 2 pre	-1.08	CTCATTAATTATGATTATTGA	XM_372775:	XM_372775:
391025	LOC391025	similar to protein tyrosine phosphatase, receptor type, U isoform 2 pre	-4.07	CAAAGGATTCCGGAACAGAAA	XM_372775:	XM_372775:
391599	LOC391599	similar to Cytochrome P450 2F2 (CYPIIF2) (Naphthalene dehydrogena	0.64	TCGGACAAGGATGGAAACTTT	XM_497949:	XM_497949:
391599	LOC391599	similar to Cytochrome P450 2F2 (CYPIIF2) (Naphthalene dehydrogena	1.17	CAGGAGATATTTAGGTACCAA	XM_497949:	XM_497949:
399818	LOC399818	similar to CG9643-PA	0.01	AGGGTAGTGTAAGTTATATAA	NM_212554:	NM_212554:
399818	LOC399818	similar to CG9643-PA	-1.48	CAGCGATACATGCACAAAGAT	NM_212554:	NM_212554:
399937	LOC399937	similar to RING finger protein 18 (Testis-specific ring-finger protein)	-5.06	CAGAGTGTGAGTGATACTTTA	XM_374917:	XM_374917:
399939	LOC399939	similar to RING finger protein 18 (Testis-specific ring-finger protein)	-1.60	ACGAATCAGAATGGCAATATA	XM_208061:	XM_208061:XM_374919:
400301	LOC400301	similar to protein kinase CHK2 isoform b	-1.25	TGGGCTTAAGTACTTCTGAAA	XM_375150:	XM_375150:
400301	LOC400301	similar to protein kinase CHK2 isoform b	-1.61	CTGCTGGGATGAAGACATGAA	XM_375150:	XM_375150:
400891	LOC400891	similar to chromosome 14 open reading frame 166B	0.36	CAGACGCTGAGGATTCTTGTA	XM_497793:	NM_001013675:XM_497793:
401087	LOC401087	hypothetical LOC401087	-2.82	ACGGTCTATGGTGGCACAAGA	XM_376267:	XM_376267:
401087	LOC401087	hypothetical LOC401087	0.61	ACGAATTTGCCAAATGGACAA	XM_376267:	XM_376267:
401358	LOC401358	similar to zinc finger protein 595	0.91	AACGTGCTAAGTATCAGTAAA	XM_379495:	XM_380114:XM_379495:
401358	LOC401358	similar to zinc finger protein 595	1.49	AAGGGCATACATGGTAATTAT	XM_379495:	XM_380114:XM_379495:
401525	LOC401525	similar to CDK2-associated protein 2	-0.06	ATGGCTATTTATGAAACTGTA	XM_376869:	XM_376869:
401525	LOC401525	similar to CDK2-associated protein 2	0.15	CACTTATGTAATTATCTTATA	XM_376869:	XM_376869:
402036	LOC402036	similar to carbonic anhydrase 15	0.49	CACGGAGGTGAGAGAGAGCAA	XM_377696:	XM_377696:
402036	LOC402036	similar to carbonic anhydrase 15	-0.14	CTGGAGAATGACAGCCACACA	XM_377696:	XM_372889:XM_496497:XM_377696:
407835	LOC407835	mitogen-activated protein kinase kinase 2 pseudogene	-2.91	CTGCTGGACTATATTGTGAAA	NR_002144:	NR_002144:
440040	LOC440040	similar to Metabotropic glutamate receptor 5 precursor (mGluR5)	-1.16	CCACATGGATCATCTAACTAA	XM_495873:	XM_495873:
440059	LOC440059	similar to surface glycoprotein, Ig superfamily member	0.32	CAGCAACAATTTACATTGGAA	XM_495891:	XM_495891:
440059	LOC440059	similar to surface glycoprotein, Ig superfamily member	-0.18	CACCTCAGATGTGGCCAATAA	XM_495891:	XM_495891:
442428	LOC442428	similar to fructose-1,6-bisphosphatase 2	-0.15	CAACATTGTGACCATAGTTTA	XM_498334:	XM_498334:
442428	LOC442428	similar to fructose-1,6-bisphosphatase 2	0.75	CAAGATTAGTAAGAAAGGAAA	XM_498334:	XM_498334:
51035	LOC51035	unknown protein LOC51035	-2.10	TAGGGAGGCATGCCTAGGAAA	NM_015853:	NM_015853:
51035	LOC51035	unknown protein LOC51035	-0.41	CCAGACAAAGAGTTAGAGAAA	NM_015853:	NM_015853:
51136	LOC51136	PTD016 protein	1.53	ATGATACATTATAGTATTGTA	NM_016125:	NM_016125:
51136	LOC51136	PTD016 protein	1.11	AACAGCAATTTGAAATTAGAA	NM_016125:	NM_016125:
51255	LOC51255	hypothetical protein LOC51255	0.77	TAACCTTGAATCCTCATTAAA	NM_016494:	NM_016494:
63929	LOC63929	hypothetical protein LOC63929	-1.76	CACTAGCTACCTACCAAACAA	NM_022098:	NM_022098:
63929	LOC63929	hypothetical protein LOC63929	-0.93	TCGGTGATTGTGGGCGGCCAA	NM_022098:	NM_022098:
90826	LOC90826	hypothetical protein BC004337	1.35	CACCAAGAGGAATACAATTTA	NM_138364:	NM_138364:
90826	LOC90826	hypothetical protein BC004337	-3.33	CAGACAAGTTATGGAGCATAA	NM_138364:	NM_138364:
91461	LOC91461	hypothetical protein BC007901	1.16	CAAACGTGCAATAATGCCAAA	XM_038576:	NM_138370:
91461	LOC91461	hypothetical protein BC007901	-2.24	CAGGATGTGGGTGATTCTGTA	XM_038576:	NM_138370:
91664	LOC91664	hypothetical protein BC007307	0.01	ACCGCCGCTATTCTCCAGATA	XM_039908:	XM_039908:
91664	LOC91664	hypothetical protein BC007307	-0.15	AACCTGGTGTCAAGATACAAA	XM_039908:	XM_039908:
92312	LOC92312	hypothetical protein LOC92312	-1.09	ATCCTCGAGTACAACAATGAA	XM_044166:	XM_044166:
92312	LOC92312	hypothetical protein LOC92312	-3.21	CAGGCAAGGCTGCAAGATTAA	XM_044166:	XM_044166:
93349	LOC93349	hypothetical protein BC004921	0.03	ACACGTGAGAACCATGAACAA	NM_138402:	NM_138402:
93349	LOC93349	hypothetical protein BC004921	-1.62	CAGTTGGTAAATCAGATGCAA	NM_138402:	NM_138402:
29931	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	0.17	CCCAAGATGTTTCATGTTGTA	NM_013343:	NM_013343:
29931	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	1.33	TTGGTATAACATTGCTTGAAA	NM_013343:	NM_013343:
29931	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	0.31	CCCAAGATGTTTCATGTTGTA	NM_013343:	NM_013343:
29931	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	1.98	TTGGTATAACATTGCTTGAAA	NM_013343:	NM_013343:
83752	LONPL	peroxisomal LON protease like	0.99	CCGGTATAGACCATTACCTTA	NM_031490:	NM_031490:
83752	LONPL	peroxisomal LON protease like	0.59	CCGGATTCTTCTGGATAATGA	NM_031490:	NM_031490:
91694	LONRF1	LON peptidase N-terminal domain and ring finger 1	2.62	TACTGTGCATCTATTCATAAA	NM_152271:	NM_152271:
91694	LONRF1	LON peptidase N-terminal domain and ring finger 1	0.41	ACGCATTGAATGTGTGTCGAA	NM_152271:	NM_152271:
164832	LONRF2	LON peptidase N-terminal domain and ring finger 2	-0.20	CCGACGGATATTAGTCATCAT	NM_198461:	NM_198461:
164832	LONRF2	LON peptidase N-terminal domain and ring finger 2	0.57	CTGCATGAGATTGCTCTTTGA	NM_198461:	NM_198461:
79836	LONRF3	LON peptidase N-terminal domain and ring finger 3	0.21	CAGAGAGAAATTGAGTAGAAA	NM_024778:	NM_024778:NM_001031855:
79836	LONRF3	LON peptidase N-terminal domain and ring finger 3	-0.32	TTCGCTCAAATTATCCCTAAA	NM_024778:	NM_024778:NM_001031855:
4014	LOR	loricrin	0.32	CTCAGTCAATAAATTTGCAAA	NM_000427:	NM_000427:
4014	LOR	loricrin	0.33	CCCAGTGCCTCAGTCAATAAA	NM_000427:	NM_000427:
4015	LOX	lysyl oxidase	0.26	CTGGAACTTTAGTGAAACATA	NM_002317:	NM_002317:
4015	LOX	lysyl oxidase	0.14	CTGCACAATTTCACCGTATTA	NM_002317:	NM_002317:
4017	LOXL2	lysyl oxidase-like 2	-2.25	CCAGTCTATTATAGTCACATA	NM_002318:	NM_002318:
4017	LOXL2	lysyl oxidase-like 2	-3.16	CCGGAGTTGCCTGCTCAGAAA	NM_002318:	NM_002318:
84695	LOXL3	lysyl oxidase-like 3	-1.20	CAACAGGAGGTTTGAACGCTA	NM_032603:	NM_032603:
84695	LOXL3	lysyl oxidase-like 3	-1.94	CAACAATGCAATGAAATGTAA	NM_032603:	NM_032603:
84171	LOXL4	lysyl oxidase-like 4	-0.46	CTCATTATGGACTGCTACAAA	NM_032211:	NM_032211:
84171	LOXL4	lysyl oxidase-like 4	-2.66	CAGGATTGGTCTAAACTTCAA	NM_032211:	NM_032211:
4018	LPA	lipoprotein, Lp(a)	0.10	AACCACAGAATACTACCCAAA	NM_005577:	NM_005577:
80350	LPAL2	lipoprotein, Lp(a)-like 2	0.14	CCCAGTCAAATTCCTATTCTA	NM_024492:	NM_024492:
80350	LPAL2	lipoprotein, Lp(a)-like 2	-0.01	AACCACTCACCTTGTTCTAAA	NM_024492:	NM_024492:
22859	LPHN1	latrophilin 1	0.31	CGAGATTGAACTTCTCTATAA	NM_014921:	NM_014921:NM_001008701:
22859	LPHN1	latrophilin 1	-0.32	CTGGCTCCGAGTGGACAATTA	NM_014921:	NM_014921:NM_001008701:
23266	LPHN2	latrophilin 2	0.62	CCCTATCGTACCGATACTTTA	NM_012302:	NM_012302:
23266	LPHN2	latrophilin 2	-0.23	TACATTTATAATACCCGATTA	NM_012302:	NM_012302:
23284	LPHN3	latrophilin 3	1.07	AAGCTAAACATTGCATATCAA	NM_015236:	NM_015236:
23284	LPHN3	latrophilin 3	-1.54	CAGGAACTATAGGTGTATCAA	NM_015236:	NM_015236:
4023	LPL	lipoprotein lipase	-1.44	CCCAGGGTGCATTAACTTAAA	NM_000237:	NM_000237:
4023	LPL	lipoprotein lipase	0.86	CAGAATGCTCTTCTACGTATA	NM_000237:	NM_000237:
4025	LPO	lactoperoxidase	1.40	CTCGGAATCACTGCCAAATAA	NM_006151:	NM_006151:

4025	LPO	lactoperoxidase	-1.56	CAGCACATTAGAAGTGCTCAA	NM_006151:	NM_006151:
64748	LPPR2	lipid phosphate phosphatase-related protein type 2	0.41	CCCGTGTCTAAGCATGTGCAA	NM_022737:	NM_022737:
64748	LPPR2	lipid phosphate phosphatase-related protein type 2	-3.54	CCGGGACAACTTCAGCCCTTA	NM_022737:	NM_022737:
9404	LPXN	leupaxin	1.27	ATGACTAGGCTGATAATCTTA	NM_004811:	NM_004811:
9404	LPXN	leupaxin	1.20	CTGCTTAATAGTCTTATAGAA	NM_004811:	NM_004811:
28959	LR8	LR8 protein	-0.58	GAGGAAGTTGTTCACAGCAAT	NM_014020:	NM_014020:
28959	LR8	LR8 protein	0.08	CTGATTAAACATAATAAACAA	NM_014020:	NM_014020:
64167	LRAP	leukocyte-derived arginine aminopeptidase	0.50	AAGCGTTACCTTCTTCAGTAT	NM_022350:	NM_022350:
64167	LRAP	leukocyte-derived arginine aminopeptidase	-1.28	ATGGATGGGACCAACTCATTA	NM_022350:	NM_022350:
9227	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltran	-8.59	AAGGTTGTTTAGGAAGAGTCA	NM_004744:	NM_004744:
9227	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltran	0.82	CCAGTAGACATAATTGTATTA	NM_004744:	NM_004744:
4034	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	0.68	GCTGGTTGTGTTGACAATAAA	NM_002319:	NM_002319:
4034	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	-0.61	CAGCGTTGATAGTGGCAGCAA	NM_002319:	NM_002319:
55367	LRDD	leucine-rich repeats and death domain containing	-4.46	CCGGCTGAGCTTGGACCTGTA	NM_018494:	NM_018494:NM_145886:NM_145887:
55367	LRDD	leucine-rich repeats and death domain containing	0.53	CAGAATCTGCTTTGTCTTCTA	NM_018494:	NM_018494:NM_145886:NM_145887:
4035	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin recept	-3.40	CCGCCGGATGTATAAATGTAA	NM_002332:	NM_002332:
4035	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin recept	0.33	CCGGAGTGGTATTCTGGTATA	NM_002332:	NM_002332:
26020	LRP10	low density lipoprotein receptor-related protein 10	-0.26	CACCGGAATGCCAATTAACTA	NM_014045:	NM_014045:
26020	LRP10	low density lipoprotein receptor-related protein 10	2.43	ACCCTATGTAGCTGCTATAAA	NM_014045:	NM_014045:
29967	LRP12	low density lipoprotein-related protein 12	0.69	TAGGCAGAGTTCGATAAATTA	NM_013437:	NM_013437:
29967	LRP12	low density lipoprotein-related protein 12	-1.96	TAGGACGATCAAGTTCCCTAA	NM_013437:	NM_013437:
53353	LRP1B	low density lipoprotein-related protein 1B (deleted in tumors)	2.04	TAGATGATTCATGTAAGTTAA	NM_018557:	NM_018557:
53353	LRP1B	low density lipoprotein-related protein 1B (deleted in tumors)	-2.83	CCCTACTATACTCGTTAGCAA	NM_018557:	NM_018557:
4036	LRP2	low density lipoprotein-related protein 2	0.34	CCGAAGTGATGGCTACGTTTA	NM_004525:	NM_004525:
4036	LRP2	low density lipoprotein-related protein 2	-1.74	CTCGGTTTGATTACATTGAAA	NM_004525:	NM_004525:
4037	LRP3 (low de	low density lipoprotein receptor-related protein 3	-0.09	CCGCTTTGTAACCAGGGAATA	NM_002333:	NM_002333:
4037	LRP3 (low de	low density lipoprotein receptor-related protein 3	-0.04	CGCGCTGGGCTGCGCCTTCAA	NM_002333:	NM_002333:
4038	LRP4	low density lipoprotein receptor-related protein 4	-2.32	CAGGAAATCATTCGCAACAAA	XM_035037:	NM_002334:
4038	LRP4	low density lipoprotein receptor-related protein 4	-1.05	CCGCAAAGTACTGATCAACAA	XM_035037:	NM_002334:
4041	LRP5	low density lipoprotein receptor-related protein 5	-2.24	CAGGGCTGGGAGAACTTTGTA	NM_002335:	NM_002335:
4041	LRP5	low density lipoprotein receptor-related protein 5	0.11	CCCGTTCGGTCTGACGCAGTA	NM_002335:	NM_002335:
91355	LRP5L	low density lipoprotein receptor-related protein 5-like	-0.43	CTGGAACAAATCAGTGAACAA	NM_182492:	NM_182492:
91355	LRP5L	low density lipoprotein receptor-related protein 5-like	-0.17	CACGTGCAGCCTATATGGGAA	NM_182492:	NM_182492:
4040	LRP6	low density lipoprotein receptor-related protein 6	0.38	CTGGGCTTTATTGATACCAAA	NM_002336:	NM_002336:
4040	LRP6	low density lipoprotein receptor-related protein 6	-0.02	CGGATTGAAGTTTCTAATTTA	NM_002336:	NM_002336:
7804	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e rec	0.12	CAGTACCTTACTCATCATTTA	NM_017522:	NM_033300:NM_017522:NM_001018054:NM_004631:
7804	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e rec	-1.36	CCGGATGGTGTATGACTGGAT	NM_017522:	NM_001018054:NM_004631:NM_017522:NM_033300:
4043	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	0.66	CGGGAGTTCCTGCATCACAAA	NM_002337:	NM_002337:
4043	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	0.53	TACCATGCACAGAGTCCTTAA	NM_002337:	NM_002337:
10128	LRPPRC	leucine-rich PPR-motif containing	0.53	GTGAATATGTGAAACAGTAAA	XM_376585:	NM_133259:
10234	LRRC17	leucine rich repeat containing 17	0.23	CCCGTGTGACGTGTACACATA	NM_005824:	NM_001031692:NM_005824:
10234	LRRC17	leucine rich repeat containing 17	0.26	AAGGAACAATTGGACCCGAAA	NM_005824:	NM_001031692:NM_005824:
79442	LRRC2 (leuci	leucine rich repeat containing 2	0.64	CTGGAGCTATATATAAATCTT	NM_024512:	NM_024750:NM_024512:
79442	LRRC2 (leuci	leucine rich repeat containing 2	0.61	AAGACCAAATACTGAAGTTAA	NM_024512:	NM_024512:
127495	LRRC39	leucine rich repeat containing 39	-0.16	CTGGCTGTTAACAGAGATATA	NM_144620:	NM_144620:
127495	LRRC39	leucine rich repeat containing 39	-1.84	CTCAGCAACAATAAACTGCAA	NM_144620:	NM_144620:
64101	LRRC4	leucine rich repeat containing 4	0.33	AAGCTGTGAGATCCACAGTTA	NM_022143:	NM_022143:
64101	LRRC4	leucine rich repeat containing 4	-2.25	CAGAAGGGATTTCTGGTATAA	NM_022143:	NM_022143:
55631	LRRC40	leucine rich repeat containing 40	0.83	CTCAGTACACATTTCAACTTA	NM_017768:	NM_017768:
55631	LRRC40	leucine rich repeat containing 40	0.49	TCGGTAATTGTGTAAACTTAA	NM_017768:	NM_017768:
57470	LRRC47	leucine rich repeat containing 47	-0.01	ATGTAGATACATGGCAGGTAA	NM_020710:	NM_020710:
57470	LRRC47	leucine rich repeat containing 47	1.73	CCGCGTTTGTTTGGCCGGTTT	NM_020710:	NM_020710:
94030	LRRC4B	leucine rich repeat containing 4B	-9.35	ACGCGGTACCTGAACCTGCAA	XM_292778:	XM_292778:
94030	LRRC4B	leucine rich repeat containing 4B	-0.64	CACGCGGAGCATGAACATTGA	XM_292778:	XM_292778:
57689	LRRC4C	leucine rich repeat containing 4C	0.15	CCGAATGAACTCTAAAGACAA	NM_020929:	NM_020929:
57689	LRRC4C	leucine rich repeat containing 4C	-0.02	AAGGACTGTTGAAATTATTAA	NM_020929:	NM_020929:
255252	LRRC57	leucine rich repeat containing 57	-0.18	ACCGCCTTTGCTGATAGGAAA	NM_153260:	NM_153260:
255252	LRRC57	leucine rich repeat containing 57	-1.36	AACCAAATTACCTATCAATAA	NM_153260:	NM_153260:
116064	LRRC58 (leuc	leucine rich repeat containing 58	0.12	CACGGACCATTAAGATTCGAA	XM_057296:	XM_057296:
116064	LRRC58 (leuc	leucine rich repeat containing 58	0.35	TTGGTATTATGTGACAACAAA	XM_057296:	XM_057296:
79705	LRRK1	leucine-rich repeat kinase 1	0.02	CCCTGTTTGTTTGCACATAAT	NM_024652:	NM_024652:
79705	LRRK1	leucine-rich repeat kinase 1	-0.36	CCGAGTCATTGCCGTCTTAAA	NM_024652:	NM_024652:
120892	LRRK2	leucine-rich repeat kinase 2	0.06	ATCGAAATGCACTATCATATA	XM_058513:	XM_058513:NM_198578:
120892	LRRK2	leucine-rich repeat kinase 2	0.02	CTCGTCGACTTATACGTGTAA	XM_058513:	XM_058513:NM_198578:
57633	LRRN1	leucine rich repeat neuronal 1	1.38	AAGACTTTGCTTGAATGTTTA	NM_020873:	NM_020873:
57633	LRRN1	leucine rich repeat neuronal 1	-3.86	CTGGTTTGATTCTACACCCAA	NM_020873:	NM_020873:
10446	LRRN5	leucine rich repeat neuronal 5	-1.18	AAGGCATATTGAGGAGGGCAA	NM_006338:	NM_006338:NM_201630:
10446	LRRN5	leucine rich repeat neuronal 5	-1.08	CAAGCTGGACATCACCAATAA	NM_006338:	NM_006338:NM_201630:
84894	LRRN6A	leucine rich repeat neuronal 6A	0.20	CAAGGGCAACACAAAGCACAA	NM_032808:	NM_032808:
84894	LRRN6A	leucine rich repeat neuronal 6A	-0.93	AAGGACTTCCCTGATGTGCTA	NM_032808:	NM_032808:
158038	LRRN6C	leucine rich repeat neuronal 6C	-1.75	ACCCAGGAGGTTCAACATGAA	NM_152570:	NM_152570:
158038	LRRN6C	leucine rich repeat neuronal 6C	1.58	AAGGCGTTTCATCACCACCAA	NM_152570:	NM_152570:
339398	LRRN6D	leucine rich repeat neuronal 6D	0.13	AGCGCTAGTCAGCTAGTCTAA	NM_001004432:	NM_001004432:
339398	LRRN6D	leucine rich repeat neuronal 6D	-0.12	CACGGCTATAAGATTATTTCA	NM_001004432:	NM_001004432:
90678	LRSAM1	leucine rich repeat and sterile alpha motif containing 1	-8.96	CCGAAGCAGGAGTGTCAATAA	NM_138361:	NM_001005374:NM_138361:NM_001005373:
90678	LRSAM1	leucine rich repeat and sterile alpha motif containing 1	-0.04	CTGGAGAAACTCGAGTTTGAA	NM_138361:	NM_001005374:NM_138361:NM_001005373:
51599	LSR	lipolysis stimulated lipoprotein receptor	-0.07	CGGGACGACCTCTATGACCAA	NM_015925:	NM_205834:NM_205835:NM_015925:
51599	LSR	lipolysis stimulated lipoprotein receptor	0.15	GAGGATTACCATCACCGGAAA	NM_015925:	NM_205834:NM_205835:NM_015925:
4047	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0.61	ATGAGCATCTGCCTTAATAAA	NM_002340:	NM_002340:
4047	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0.33	CAGGTAGTGTGCATCCGTGAA	NM_002340:	NM_002340:
4049	LTA	lymphotoxin alpha (TNF superfamily, member 1)	-4.02	ACCCTCGATGAAGCCCAATAA	NM_000595:	NM_000595:
4049	LTA	lymphotoxin alpha (TNF superfamily, member 1)	0.50	CCGGAGCTTTCAAAGAAGGAA	NM_000595:	NM_000595:
4048	LTA4H (leuko	leukotriene A4 hydrolase	0.54	CGCAATTCCTTTGGCGCTAAA	NM_000895:	NM_000895:
4048	LTA4H (leuko	leukotriene A4 hydrolase	0.02	GCGGCTCTGCATTCAATCCAA	NM_000895:	NM_000895:
4050	LTB	lymphotoxin beta (TNF superfamily, member 3)	-2.51	CAGGATCAGGGAGGACTGGTA	NM_002341:	NM_002341:
4050	LTB	lymphotoxin beta (TNF superfamily, member 3)	-1.38	CCCGCAGGACGGCCTCTATTA	NM_002341:	NM_009588:NM_002341:
22949	LTB4DH	leukotriene B4 12-hydroxydehydrogenase	1.71	GGCCATTTAGATGATTAGTTA	NM_012212:	NM_012212:
22949	LTB4DH	leukotriene B4 12-hydroxydehydrogenase	0.99	CCGCATTTATGGGAATGCTGA	NM_012212:	NM_012212:
1241	LTB4R	leukotriene B4 receptor	0.56	AAGGCCCATGGTCAGATTGAA	NM_181657:	NM_181657:
1241	LTB4R	leukotriene B4 receptor	-0.76	ACACTTCCTATTAATCTTAAA	NM_181657:	NM_181657:
56413	LTB4R2	leukotriene B4 receptor 2	0.04	AAGGGACTTAACATACTCTTA	NM_019839:	NM_019839:
56413	LTB4R2	leukotriene B4 receptor 2	0.26	TAAGTACATTCTCCTAATAAA	NM_019839:	NM_019839:
4052	LTBP1 (latent	latent transforming growth factor beta binding protein 1	0.03	TACCGGGTTATAAGCGGGTTA	NM_000627:	NM_000627:NM_206943:
4052	LTBP1 (latent	latent transforming growth factor beta binding protein 1	-0.80	TTGATTAAATTTGGCATTTAA	NM_000627:	NM_000627:NM_206943:
4053	LTBP2	latent transforming growth factor beta binding protein 2	1.13	TAGGAACTTAACCTTCAGATA	NM_000428:	NM_000428:
4053	LTBP2	latent transforming growth factor beta binding protein 2	1.58	CAGGATAAATTCTTAGAACCA	NM_000428:	NM_000428:
8425	LTBP4	latent transforming growth factor beta binding protein 4	0.03	TACGAGTACGGCCCAGACTTA	NM_003573:	NM_003573:

8425	LTBP4	latent transforming growth factor beta binding protein 4	0.79	GCGGCTGGAGTGCATCGATAA	NM_003573:	NM_003573:
4055	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	-9.63	CCGCCACACGGTCACCTGCAA	NM_002342:	NM_002342:
4055	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	0.15	CCGGCGGGTCTATGACTATCA	NM_002342:	NM_002342:
4056	LTC4S	leukotriene C4 synthase	0.03	ATCCTAGTCTCTATCATTAAA	NM_000897:	NM_145867:NM_000897:
4056	LTC4S	leukotriene C4 synthase	0.61	AAAGTTCTAGTGACCGAGAAA	NM_000897:	NM_145867:NM_000897:
4057	LTF	lactotransferrin	0.32	AAGCAGTGACCCTGATCCTAA	NM_002343:	NM_002343:
4057	LTF	lactotransferrin	-1.62	CAGAGAGAGCACAGTGTTTGA	NM_002343:	NM_002343:
4058	LTK	leukocyte tyrosine kinase	1.23	ACAGATCTTTGGAGTGCCTAA	NM_002344:	NM_206961:NM_002344:
4058	LTK	leukocyte tyrosine kinase	0.41	CCTGCAGATGCTTCTAATAAA	NM_002344:	NM_206961:NM_002344:
51213	LUZP4	leucine zipper protein 4	-0.56	CTAGACGACATTATAATCTAT	NM_016383:	NM_016383:
51213	LUZP4	leucine zipper protein 4	-0.06	CTGGTAGGTAAGCTAATCTAA	NM_016383:	NM_016383:
92335	LYK5	protein kinase LYK5	0.30	CACCCAGATGCTGCTAGAGAA	NM_153335:	NM_001003786:NM_001003787:NM_153335:NM_001003788:
92335	LYK5	protein kinase LYK5	0.04	CTGGTTCTAGTTCTGGTTCTA	NM_153335:	NM_153335:
4066	LYL1 (lympho	lymphoblastic leukemia derived sequence 1	-0.12	TGGCAGAGCAGTCATAGGAAA	NM_005583:	NM_005583:
4066	LYL1 (lympho	lymphoblastic leukemia derived sequence 1	-4.51	CCGCCTAGCCATGAAGTACAT	NM_005583:	NM_005583:
4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	-0.01	CCCGGACGACTTGTCTTTCAA	NM_002350:	NM_002350:
4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0.13	CGGGAAATATGGGATGTATAA	NM_002350:	NM_002350:
66004	LYNX1	Ly6/neurotoxin 1	0.51	AAGATAATTATTTAATATGAA	NM_023946:	NM_177457:NM_023946:
66004	LYNX1	Ly6/neurotoxin 1	0.48	TTCAAAGTTATGTAAAGATAA	NM_023946:	NM_177457:NM_023946:
116372	LYPD1	LY6/PLAUR domain containing 1	0.23	CACGGTGAACGTTCAAGACAT	NM_144586:	NM_144586:
116372	LYPD1	LY6/PLAUR domain containing 1	-0.83	CACAAGCAAGAGAGAATTTAA	NM_144586:	NM_144586:
27076	LYPD3	LY6/PLAUR domain containing 3	1.90	ACCGTTGTATATATTCTGGCA	NM_014400:	NM_014400:
27076	LYPD3	LY6/PLAUR domain containing 3	-0.14	CACCAGGACCGCAGCAATTCA	NM_014400:	NM_014400:
284348	LYPD5	LY6/PLAUR domain containing 5	-1.65	CCCAATAAGCAGTATGCCCTA	NM_182573:	NM_001031749:NM_182573:
284348	LYPD5	LY6/PLAUR domain containing 5	0.20	CAGCAGTGGCCCAGTATAAAT	NM_182573:	NM_182573:
1130	LYST	lysosomal trafficking regulator	1.08	CAAGGTGTTATTAAACTATTA	NM_000081:	NM_000081:
1130	LYST	lysosomal trafficking regulator	0.79	CACGCCGACCTGATTACCTAA	NM_000081:	NM_000081:
4069	LYZ (lysozym	lysozyme (renal amyloidosis)	0.46	TACGATTATGCCCAATATTAA	NM_000239:	NM_000239:
4069	LYZ (lysozym	lysozyme (renal amyloidosis)	1.72	TAACCCAGACTTAATCTTGAA	NM_000239:	NM_000239:
11178	LZTS1	leucine zipper, putative tumor suppressor 1	-1.73	CACCGTGGCACTAGAATGCAA	NM_021020:	NM_021020:
11178	LZTS1	leucine zipper, putative tumor suppressor 1	1.68	TCGGTGACCACTCTTCTTTAA	NM_021020:	NM_021020:
84445	LZTS2	leucine zipper, putative tumor suppressor 2	-2.27	CCGGATGTGCCTGCCCACATT	NM_032429:	NM_032429:
84445	LZTS2	leucine zipper, putative tumor suppressor 2	-1.07	GAGCAAGATCAGACCGCTCAA	NM_032429:	NM_032429:
4074	M6PR	mannose-6-phosphate receptor (cation dependent)	-0.29	TTGCATCTTCTCACTAGTAAA	NM_002355:	NM_002355:
4074	M6PR	mannose-6-phosphate receptor (cation dependent)	0.44	ACAGTTGTAAGTCAGAGTTAA	NM_002355:	NM_002355:
10226	M6PRBP1	mannose-6-phosphate receptor binding protein 1	0.06	CTGGTATTCAGTATTGCCTTA	NM_005817:	NM_005817:
10226	M6PRBP1	mannose-6-phosphate receptor binding protein 1	0.31	AGGGATATAGTTCATATCCCA	NM_005817:	NM_005817:
8379	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	0.28	CAGCGATTGTGAAGAACATGA	NM_003550:	NM_001013836:NM_003550:NM_001013837:
8379	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	-5.59	CAGGCGACTGCTCATCTTCAA	NM_003550:	NM_001013836:NM_001013837:NM_003550:
4085	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	-0.13	ATGGATATTTGTACTGTTTAA	NM_002358:	NM_002358:
4085	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.11	CTGAAAGTAACTCATAATCTA	NM_002358:	NM_002358:
9587	MAD2L1BP	MAD2L1 binding protein	0.98	CCGAGCCATATTCATGGCTGA	NM_014628:	NM_014628:NM_001003690:
9587	MAD2L1BP	MAD2L1 binding protein	1.00	GAGGAGATGCTGAAGAAGAAA	NM_014628:	NM_014628:NM_001003690:
10459	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	-2.95	CCCGTGGGCATCTTCCAGAAA	NM_006341:	NM_006341:
10459	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	0.74	GTGGAAGAGCGCGCTCATAAA	NM_006341:	NM_006341:
8567	MADD	MAP-kinase activating death domain	1.30	CAGACCCACTACTATAGTAAA	NM_003682:	NM_130470:NM_003682:NM_130476:NM_130475:NM_130474:NM_130473:NM_130472:NM_130471:
8567	MADD	MAP-kinase activating death domain	-1.17	CAGGAGGGCGTTAGTGGATCA	NM_003682:	NM_130470:NM_003682:NM_130476:NM_130475:NM_130474:NM_130473:NM_130472:NM_130471:
10296	MAEA	macrophage erythroblast attacher	1.89	TAGAGTCTAATTGCTATCCAT	NM_005882:	NM_001017405:NM_005882:
10296	MAEA	macrophage erythroblast attacher	1.59	TTCCATAACTGTAGAGTCTAA	NM_005882:	NM_001017405:NM_005882:
4094	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	0.25	GAGGATCTTCCCGAGCCTGAA	NM_005360:	NM_005360:NM_001031804:
4094	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	1.10	GGCGAGAAGCATGAAGTGTTA	NM_005360:	NM_005360:NM_001031804:
389692	MAFA	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	-0.63	CACGGCCGACTTCTTCCTGTA	NM_201589:	NM_201589:
389692	MAFA	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	1.26	CCTGATGAAGTTCGAGGTGAA	NM_201589:	NM_201589:
9935	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	-0.17	ACGCCCAGTCTTGCAGGTATA	NM_005461:	NM_005461:
9935	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	-1.51	CAGCCTTGTCTTATGGTCAAA	NM_005461:	NM_005461:
23764	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0.20	AAGCCGGAGAGCAACAACAAA	NM_012323:	NM_012323:NM_152878:
23764	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0.04	CAGCAAAGCTCTAAAGATCAA	NM_012323:	NM_012323:NM_152878:
4097	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	0.04	ATGGAGGTTATTAAAGATCTA	NM_002359:	NM_002359:NM_032711:
4097	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	-1.65	CAGCGTCATCACAATAGTAAA	NM_002359:	NM_002359:NM_032711:
7975	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	0.62	CAAACCGAATAAGGCATTAAA	NM_002360:	NM_002360:
7975	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	-0.78	TGCCCGGGTTATGACGACTAA	NM_002360:	NM_002360:
4099	MAG	myelin associated glycoprotein	-0.12	ATCGCGCAATGTGACCGTGAA	NM_080600:	NM_002361:NM_080600:
4099	MAG	myelin associated glycoprotein	1.19	CCCGGTGATTGTGGAGATGAA	NM_080600:	NM_002361:NM_080600:
9500	MAGED1	melanoma antigen family D, 1	1.46	CCGCAAGATTAATAACTTGAA	NM_006986:	NM_001005333:NM_001005332:NM_006986:
9500	MAGED1	melanoma antigen family D, 1	-0.50	CTCCTTGGAGATCTAAGGAAA	NM_006986:	NM_001005333:NM_001005332:NM_006986:
9863	MAGI2	membrane associated guanylate kinase, WW and PDZ domain contai	-0.24	ACGCAGTGACTACGCAACCTA	NM_012301:	NM_012301:
9863	MAGI2	membrane associated guanylate kinase, WW and PDZ domain contai	1.07	TTGGATGTCATCCAAACTTTA	NM_012301:	NM_012301:
260425	MAGI3	membrane associated guanylate kinase, WW and PDZ domain contai	-3.21	CCCTATGATGTTGTCTTGCAA	NM_020965:	NM_020965:NM_152900:
260425	MAGI3	membrane associated guanylate kinase, WW and PDZ domain contai	-1.83	CGGGATGTCGAAGACGCTGAA	NM_020965:	NM_020965:
4117	MAK	male germ cell-associated kinase	0.35	CACAGTGTTGATATATGGGTA	NM_005906:	NM_005906:
4117	MAK	male germ cell-associated kinase	1.54	CCGGATATAATCGATCAGGTT	NM_005906:	NM_005906:
10892	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	-0.23	CACAGTTGATACATAGTTGTA	NM_006785:	NM_173844:NM_006785:
10892	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.49	CTGGTAATCCAAGTAATGTTA	NM_006785:	NM_173844:NM_006785:
161357	MAMDC1	MAM domain containing 1	1.18	ACCCTTGAGTTGACTTGTCTA	NM_182830:	NM_182830:
161357	MAMDC1	MAM domain containing 1	-4.02	CAGGGTGAAACAAAGATCTTA	NM_182830:	NM_182830:
158056	MAMDC4	MAM domain containing 4	-0.28	CTCCACCTGGCTTATTATTTA	NM_206920:	NM_206920:
158056	MAMDC4	MAM domain containing 4	0.22	CAGGCTGCAGGTCTCAGGATA	NM_206920:	NM_206920:
84441	MAML2	mastermind-like 2 (Drosophila)	0.86	CAGGATACAGTATCCAATTTA	NM_032427:	NM_032427:
84441	MAML2	mastermind-like 2 (Drosophila)	-6.39	CAGAGTTCAATTTCAGCTCAA	NM_032427:	NM_032427:
4124	MAN2A1	mannosidase, alpha, class 2A, member 1	-1.96	TACCACATACAGGGAATAGAA	NM_002372:	NM_002372:
4124	MAN2A1	mannosidase, alpha, class 2A, member 1	0.11	CGGAATGGGATTTACAGTTTA	NM_002372:	NM_002372:
4122	MAN2A2	mannosidase, alpha, class 2A, member 2	-0.10	TAAGAGTATTCTGTAAGTCAA	NM_006122:	NM_006122:
4122	MAN2A2	mannosidase, alpha, class 2A, member 2	-0.65	AAAGGTATTTCGTAAGATTTA	NM_006122:	NM_006122:
4125	MAN2B1	mannosidase, alpha, class 2B, member 1	-0.02	GCGGAGTATCGGAGCCACTAA	NM_000528:	NM_000528:
4125	MAN2B1	mannosidase, alpha, class 2B, member 1	0.01	TCGACCCACCTGGAAACTGAA	NM_000528:	NM_000528:
23324	MAN2B2	mannosidase, alpha, class 2B, member 2	0.88	CGGGCTTTCTTTGGAAGATGA	NM_015274:	NM_015274:
23324	MAN2B2	mannosidase, alpha, class 2B, member 2	0.88	CACGGGTTTCTCTATGAAACA	NM_015274:	NM_015274:
4123	MAN2C1	mannosidase, alpha, class 2C, member 1	0.41	CAGGATGCTGGCGTTATCCAA	NM_006715:	NM_006715:
4123	MAN2C1	mannosidase, alpha, class 2C, member 1	-2.59	CTCGCTCTTGCGGGCGCCTAA	NM_006715:	NM_006715:
4128	MAOA (mono	monoamine oxidase A	-0.40	CAGATGTGCCTAGACACGAAA	NM_000240:	NM_000240:
4128	MAOA (mono	monoamine oxidase A	-7.28	ACCCTGGTGTGAGGACATAAA	NM_000240:	NM_000240:
4129	MAOB	monoamine oxidase B	-1.40	AAGAGTTGCAGTAAAGTTCCA	NM_000898:	NM_000898:
4129	MAOB	monoamine oxidase B	0.30	GGGCATGAAGATTCACTTCAA	NM_000898:	NM_000898:
4130	MAP1A	microtubule-associated protein 1A	0.03	CTCGTGAGTGGTACCAACAAA	NM_002373:	NM_002373:

4130	MAP1A	microtubule-associated protein 1A	-0.01	CCGGAGGACACGGTCGCTGAA	NM_002373:	NM_002373:
254042	MAP1D	methionine aminopeptidase 1D	0.80	CGGGAAATCATCAGTCATAAT	NM_199227:	NM_199227:
254042	MAP1D	methionine aminopeptidase 1D	1.39	TCCGCAGAGGTTCTCATAGAA	NM_199227:	NM_199227:
4133	MAP2	microtubule-associated protein 2	2.49	CTCGAATATTATAACTTCTTA	NM_031845:	NM_031845:NM_002374:NM_031847:NM_031846:
4133	MAP2	microtubule-associated protein 2	-0.20	CTGGATAATTATATCAGAGTA	NM_031845:	NM_031845:NM_002374:NM_031847:NM_031846:
5604	MAP2K1	mitogen-activated protein kinase kinase 1	-0.76	CTGGAAGAATTCCTGAACAAA	NM_002755:	NM_002755:
5604	MAP2K1	mitogen-activated protein kinase kinase 1	-4.30	CTGGATCAAGTCCTGAAGAAA	NM_002755:	NM_002755:
8649	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	-2.18	ATGCCCAGGCTTGCAGAATAA	NM_021970:	NM_021970:
8649	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	0.68	TAGCATATAGATGTAATTTAT	NM_021970:	NM_021970:
5605	MAP2K2	mitogen-activated protein kinase kinase 2	0.43	CAGCATTTGCATGGAACACAT	NM_030662:	NM_030662:
5605	MAP2K2	mitogen-activated protein kinase kinase 2	-1.77	CCGGCCTGCCATGGCCATCTT	NM_030662:	NM_030662:
5606	MAP2K3	mitogen-activated protein kinase kinase 3	0.36	ACGGATATCCTGCATGTCCAA	NM_002756:	NM_145110:NM_145109:NM_002756:
5606	MAP2K3	mitogen-activated protein kinase kinase 3	-2.93	CCGGGCCACCGTGAACTCACA	NM_002756:	NM_145110:NM_145109:NM_002756:
6416	MAP2K4	mitogen-activated protein kinase kinase 4	0.20	AGGGAGAATGGTGCTGTTTAA	NM_003010:	NM_003010:
6416	MAP2K4	mitogen-activated protein kinase kinase 4	-0.65	AGGGTGTATAGTGTTCACAAA	NM_003010:	NM_003010:
5607	MAP2K5	mitogen-activated protein kinase kinase 5	-0.01	AAGACGTATGTTGGAACAAAT	NM_002757:	NM_002757:NM_145162:NM_145160:NM_145161:
5607	MAP2K5	mitogen-activated protein kinase kinase 5	-0.08	CAAGACGTATGTTGGAACAAA	NM_002757:	NM_002757:NM_145162:NM_145160:NM_145161:
5608	MAP2K6	mitogen-activated protein kinase kinase 6	0.01	AAGGCTTGCATTTCTATTGGA	NM_002758:	NM_031988:NM_002758:
5608	MAP2K6	mitogen-activated protein kinase kinase 6	-0.36	TAGACCTATGATAAATAACCA	NM_002758:	NM_031988:NM_002758:
5609	MAP2K7	mitogen-activated protein kinase kinase 7	-3.78	CCGGCGGAGGATCGACCTCAA	NM_145185:	NM_145185:
4214	MAP3K1	mitogen-activated protein kinase kinase kinase 1	-0.35	CACGCATGTCAAATTCTCATA	XM_042066:	XM_042066:
4214	MAP3K1	mitogen-activated protein kinase kinase kinase 1	-3.83	CTCCGGGTGTTTCAACTAGAA	XM_042066:	XM_042066:
4294	MAP3K10	mitogen-activated protein kinase kinase kinase 10	0.20	AAGCGGCTTGAAGTCATCGAA	NM_002446:	NM_002446:
4294	MAP3K10	mitogen-activated protein kinase kinase kinase 10	2.54	CAGGATGTTCACTCTATTTAT	NM_002446:	NM_002446:
4296	MAP3K11	mitogen-activated protein kinase kinase kinase 11	-0.16	CCCGACGTCTGGAGGACTCAA	NM_002419:	NM_002419:
4296	MAP3K11	mitogen-activated protein kinase kinase kinase 11	-5.56	CCGGAGGAGAAACGTCTTCGA	NM_002419:	NM_002419:
7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12	0.02	CAGGGAGCACTATGAAAGGAA	NM_006301:	NM_006301:
7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12	0.77	CTCGTATTCCTTGTACATAGA	NM_006301:	NM_006301:
9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13	-0.47	CAGACTCAATATGCACGGACA	NM_004721:	NM_004721:
9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13	0.09	GCGAATAATTTATACATGGAA	NM_004721:	NM_004721:
9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	-4.84	CACATGCATGTGACTCCTCAA	NM_003954:	NM_003954:
9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	-6.46	TACCTAGTGCATGCTCTGCAA	NM_003954:	NM_003954:
389840	MAP3K15	mitogen-activated protein kinase kinase kinase 15	-0.37	GCCGATCAGCATAACATTAAA	XM_372199:	NM_001001671:
389840	MAP3K15	mitogen-activated protein kinase kinase kinase 15	0.58	CTGATTGTTGCTGGACAACAA	XM_372199:	NM_001001671:
10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2	-0.16	CACAGTAATATGATTGTCCTA	NM_006609:	NM_006609:
10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2	-0.04	CAGAATGATGTCCGAGTCAAA	NM_006609:	NM_006609:
4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	-1.21	CAGGAATACTCAGATCGGGAA	NM_002401:	NM_203351:NM_002401:
4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	1.21	CCACGTGTCTGTGCACCACAA	NM_002401:	NM_203351:NM_002401:
4216	MAP3K4	mitogen-activated protein kinase kinase kinase 4	-1.36	CACCAATCCCTGAAAGATTAA	NM_005922:	NM_005922:NM_006724:
4216	MAP3K4	mitogen-activated protein kinase kinase kinase 4	0.23	CTCAAGCATCGCATAGTTTAA	NM_005922:	NM_005922:NM_006724:
4217	MAP3K5	mitogen-activated protein kinase kinase kinase 5	0.02	CAGCGAGTAGATAATATCGAA	NM_005923:	NM_005923:
4217	MAP3K5	mitogen-activated protein kinase kinase kinase 5	-3.75	CCGGGAATCTATACTCAATGA	NM_005923:	NM_005923:
9064	MAP3K6	mitogen-activated protein kinase kinase kinase 6	0.53	CACCATCCAAATGCTGTTGAA	NM_004672:	NM_004672:
9064	MAP3K6	mitogen-activated protein kinase kinase kinase 6	0.09	TCAGAGGAGCTGAGTAATGAA	NM_004672:	NM_004672:
6885	MAP3K7	mitogen-activated protein kinase kinase kinase 7	1.52	CAAGAATATATGAAAGTTCAA	NM_003188:	NM_145331:NM_003188:
6885	MAP3K7	mitogen-activated protein kinase kinase kinase 7	1.29	CCCGTGTGAACCATCCTAATA	NM_003188:	NM_145333:NM_145331:NM_145332:NM_003188:
10454	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	-1.82	CACCTTGGACAAGCCACACAA	NM_006116:	NM_006116:
10454	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	0.68	CTGCAGGTGAGAGGATTTAAA	NM_006116:	NM_006116:
23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-4.09	CAGTCAATAGCCAGACCTTAA	NM_015093:	NM_145342:NM_015093:
23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	0.92	TGGCTGGGTATCTCAGTTTAA	NM_015093:	NM_145342:NM_015093:
1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	-1.42	AAGAAAGTGATCCATCATGAT	NM_005204:	NM_005204:
1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	-1.83	AGAGATTGATTTATTAATTAA	NM_005204:	NM_005204:
4293	MAP3K9	mitogen-activated protein kinase kinase kinase 9	0.62	AGCGATGAAATTGTCGTGTAT	XM_027237:	NM_033141:
4293	MAP3K9	mitogen-activated protein kinase kinase kinase 9	2.15	CAGCGATGAAATTGTCGTGTA	XM_027237:	NM_033141:
11184	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	-0.01	CTGACTAAGAGTCCCAAGAAA	NM_007181:	NM_007181:
11184	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	-0.42	TACGTGGGTGTACTCCATCAA	NM_007181:	NM_007181:
5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	-0.37	CTGGCTCTACTGCGTGAACAA	NM_004579:	NM_004579:
5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	-1.25	TCGGTCAGCCTCAGAATTCCA	NM_004579:	NM_004579:
8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	0.10	GAGGTGGTTCTTTACAGGATA	NM_003618:	NM_003618:
8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	-3.57	TCGAGCTGTTGGATAAAGTAA	NM_003618:	NM_003618:
9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	0.94	AACCATTAATGTTTAATTTAA	NM_004834:	NM_145686:NM_004834:NM_145687:
9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	0.02	AGGCAAGATCCTACCCGGAAA	NM_004834:	NM_145686:NM_004834:NM_145687:
11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	0.34	CTTGCCTATTTGCATACTAAA	NM_006575:	NM_006575:NM_198794:
11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	-0.08	TCCGCTTATTAGGATCAGACA	NM_006575:	NM_006575:NM_198794:
9053	MAP7	microtubule-associated protein 7	0.37	CAGGCATATGGTCTTTAGTAA	NM_003980:	NM_003980:
9053	MAP7	microtubule-associated protein 7	-0.34	GTGCTCCTTCTTAGCAATCAA	NM_003980:	NM_003980:
5594	MAPK1	mitogen-activated protein kinase 1	0.40	AACACTTGTCAAGAAGCGTTA	NM_002745:	NM_002745:
5594	MAPK1	mitogen-activated protein kinase 1	0.77	ATCATGGTAGTCACTAACATA	NM_002745:	NM_002745:
5602	MAPK10	mitogen-activated protein kinase 10	0.09	CCGCATGTGTCTGTATTCATA	NM_002753:	NM_138980:NM_002753:NM_138981:NM_138982:
5602	MAPK10	mitogen-activated protein kinase 10	0.49	TCCGAGCACAATAAACTCAAA	NM_002753:	NM_138980:NM_002753:NM_138981:NM_138982:
5600	MAPK11	mitogen-activated protein kinase 11	0.08	CAGGATGGAGCTGATCCAGTA	NM_002751:	NM_002751:
5600	MAPK11	mitogen-activated protein kinase 11	-0.52	CTGAGCGACGAGCACGTTCAA	NM_002751:	NM_002751:NM_138993:
6300	MAPK12	mitogen-activated protein kinase 12	-0.22	CTGGACGTATTCACTCCTGAT	NM_002969:	NM_002969:
6300	MAPK12	mitogen-activated protein kinase 12	0.72	TGGAAGCGTGTTACTTACAAA	NM_002969:	NM_002969:
5603	MAPK13	mitogen-activated protein kinase 13	-0.01	CCGGAGTGGCATGAAGCTGTA	NM_002754:	NM_002754:
5603	MAPK13	mitogen-activated protein kinase 13	-0.94	CGGGATGAGCCTCATCCGGAA	NM_002754:	NM_002754:
1432	MAPK14	mitogen-activated protein kinase 14	-3.42	AAGGTCTCTGGAGGAATTCAA	NM_001315:	NM_001315:NM_139012:NM_139013:NM_139014:
1432	MAPK14	mitogen-activated protein kinase 14	0.45	CACACAGATGATGAAATGACA	NM_001315:	NM_001315:NM_139012:NM_139013:NM_139014:
225689	MAPK15	mitogen-activated protein kinase 15	-1.10	CCCACTGACTTCCTCCAATAA	NM_139021:	NM_139021:
225689	MAPK15	mitogen-activated protein kinase 15	-3.73	CCCAGAGAACATTCCGGGAAA	NM_139021:	NM_139021:
5595	MAPK3	mitogen-activated protein kinase 3	0.65	CCCGTCTAATATATAAATATA	NM_002746:	NM_002746:
5595	MAPK3	mitogen-activated protein kinase 3	-1.43	CTCCCTGACCCGTCTAATATA	NM_002746:	NM_002746:
5596	MAPK4	mitogen-activated protein kinase 4	0.00	AAGGATCGTTGATCAGCATTA	NM_002747:	NM_002747:
5596	MAPK4	mitogen-activated protein kinase 4	-2.21	CGCCTTAAATCTAATCAGCAA	NM_002747:	NM_002747:
5597	MAPK6	mitogen-activated protein kinase 6	0.27	CAAGTTCAATTTGAAAGGAAA	NM_002748:	NM_002748:
5597	MAPK6	mitogen-activated protein kinase 6	-0.28	CAGGCTTCCTGTTGAAATAAA	NM_002748:	NM_002748:
5598	MAPK7	mitogen-activated protein kinase 7	-0.52	CAGACCCACCTTTCAGCCTTA	NM_002749:	NM_139033:NM_139034:NM_002749:NM_139032:
5598	MAPK7	mitogen-activated protein kinase 7	-3.92	CAGGAGCGGGAGCGAAAGGAA	NM_002749:	NM_139033:NM_139034:NM_002749:NM_139032:

5599	MAPK8	mitogen-activated protein kinase 8	0.02	AAGCAGTTAGATGAAAGGGAA	NM_002750:	NM_002750:NM_139047:NM_139049:NM_139046:
5599	MAPK8	mitogen-activated protein kinase 8	-2.46	AAGCCCAGTAATATAGTAGTA	NM_002750:	NM_002750:NM_139047:NM_139049:NM_139046:
9479	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	-2.50	CTGGAGGAGTTTGAGGATGAA	NM_005456:	NM_005456:
9479	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	0.61	TGGCATCAGCTTACAGTGCAA	NM_005456:	NM_005456:
23542	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	0.01	ACAGGTAATGTCGGCTTCCAA	NM_012324:	NM_012324:NM_139124:NM_016431:
23542	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	0.66	CTGGAAGAATTTGACGACGAA	NM_012324:	NM_012324:NM_139124:
23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	-5.73	CAGCCGCAACATGGAAGTACA	NM_015133:	NM_033392:NM_015133:
23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	-0.01	GACGAGTGGTCTGATGTTCAA	NM_015133:	NM_033392:NM_015133:
5601	MAPK9	mitogen-activated protein kinase 9	-0.01	AAAGTCGATTTATGTGTATTA	NM_002752:	NM_002752:NM_139068:NM_139069:NM_139070:
5601	MAPK9	mitogen-activated protein kinase 9	0.12	ATCGTGAACTTGTCCTCTTAA	NM_002752:	NM_002752:NM_139068:NM_139069:NM_139070:
79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	-0.98	CTAGGTATCTCTGGAGACAAA	NM_024117:	NM_001006621:NM_024117:NM_001006617:NM_001006620:
79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	0.00	GACCCTGTTACGAATCAGAAA	NM_024117:	NM_001006621:NM_001006619:NM_024117:NM_001006617:NM_001006620:
9261	MAPKAPK2 (	mitogen-activated protein kinase-activated protein kinase 2	-1.75	CGCCATCATCGATGACTACAA	NM_004759:	NM_032960:NM_004759:
9261	MAPKAPK2 (	mitogen-activated protein kinase-activated protein kinase 2	1.12	CTACGAGCAGATCAAGATAAA	NM_004759:	NM_032960:NM_004759:
7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	-0.02	CAGGCTTTCACTGAGAGAGAA	NM_004635:	NM_004635:
7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	0.66	CCAGATAGTAATAAACACCAT	NM_004635:	NM_004635:
8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	0.87	ACCGACCTTTCTGATTAGTAA	NM_003668:	NM_003668:NM_139078:
8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	0.61	CCGACCTTTCTGATTAGTAAA	NM_003668:	NM_003668:NM_139078:
23005	MAPKBP1 (m	mitogen activated protein kinase binding protein 1	1.06	CAGGACCGAAATATTCGGATA	XM_031706:	NM_014994:
23005	MAPKBP1 (m	mitogen activated protein kinase binding protein 1	0.88	CCCGTTTGTACTGATGTATGA	XM_031706:	NM_014994:
22919	MAPRE1	microtubule-associated protein, RP/EB family, member 1	0.63	ACCAATTGCATCCCAGCTAAA	NM_012325:	NM_012325:
22919	MAPRE1	microtubule-associated protein, RP/EB family, member 1	-2.40	CAGAGCAACATCGGAATTCTT	NM_012325:	NM_012325:
10982	MAPRE2	microtubule-associated protein, RP/EB family, member 2	-1.18	CAGCAGGTGCAGCTAAATCAA	NM_014268:	NM_014268:
10982	MAPRE2	microtubule-associated protein, RP/EB family, member 2	-0.01	GACCTTATTAATAGGAGCATA	NM_014268:	NM_014268:
4137	MAPT	microtubule-associated protein tau	-5.94	CCGCCAGGAGTTCGAAGTGAT	NM_016835:	NM_016841:NM_016835:NM_016834:NM_005910:
4137	MAPT	microtubule-associated protein tau	-0.26	TTAGGCAACATCCATCATAAA	NM_016835:	NM_016841:NM_016835:NM_016834:NM_005910:
55016	MARCH1	membrane-associated ring finger (C3HC4) 1	1.92	TAGGCAGTAATCAAAGATTAA	NM_017923:	NM_017923:
55016	MARCH1	membrane-associated ring finger (C3HC4) 1	0.52	AAGAACTTCTCATGTAATGTA	NM_017923:	NM_017923:
51257	MARCH2	membrane-associated ring finger (C3HC4) 2	-0.32	CTCCGAGTGGAGAAAGACCAA	NM_016496:	NM_001005415:NM_001005416:NM_016496:
51257	MARCH2	membrane-associated ring finger (C3HC4) 2	-3.06	ACGGAGTTTGCAGTGGAGAAA	NM_016496:	NM_001005415:NM_001005416:NM_016496:
115123	MARCH3	membrane-associated ring finger (C3HC4) 3	1.03	CACAGTGAGCTGTTTATTTAA	NM_178450:	NM_178450:
115123	MARCH3	membrane-associated ring finger (C3HC4) 3	-2.51	CAGGTTTGCAGTCGAGCGCAA	NM_178450:	NM_178450:
220972	MARCH8	membrane-associated ring finger (C3HC4) 8	0.78	TGGATGCTAAATGGCAATTAA	NM_145021:	NM_145021:NM_001002265:NM_001002266:
220972	MARCH8	membrane-associated ring finger (C3HC4) 8	-4.51	TGGGAATTAGTGGATGCTAAA	NM_145021:	NM_145021:NM_001002265:NM_001002266:
4082	MARCKS	myristoylated alanine-rich protein kinase C substrate	-2.63	CTCCTTCAAGAAGAACAAGAA	NM_002356:	NM_002356:
4082	MARCKS	myristoylated alanine-rich protein kinase C substrate	0.41	TTGAGTTTCTTTGTTGAAGAA	NM_002356:	NM_002356:
8685	MARCO	macrophage receptor with collagenous structure	-0.93	CTGAAGTTTACTACAGTGGTA	NM_006770:	NM_006770:
8685	MARCO	macrophage receptor with collagenous structure	-1.01	CAGGATTGTCGGCAGTAGTAA	NM_006770:	NM_006770:
4139	MARK1	MAP/microtubule affinity-regulating kinase 1	-1.90	CCCGGTGTAGAAACTCCATTA	NM_018650:	NM_018650:
4139	MARK1	MAP/microtubule affinity-regulating kinase 1	-0.95	CCGGCCCAGTAGTGACTTAAA	NM_018650:	NM_018650:
2011	MARK2	MAP/microtubule affinity-regulating kinase 2	-0.40	CACCTCTAATTCTTACTCTAA	NM_004954:	NM_004954:NM_017490:
2011	MARK2	MAP/microtubule affinity-regulating kinase 2	0.29	AGCCAACGAGCTGAAGCTTTA	NM_004954:	NM_004954:NM_017490:
4140	MARK3	MAP/microtubule affinity-regulating kinase 3	-0.20	AACGGCGAACCGCAACATATA	NM_002376:	NM_002376:
4140	MARK3	MAP/microtubule affinity-regulating kinase 3	0.68	CCCGGGAACGGCGAACCGCAA	NM_002376:	NM_002376:
57787	MARK4	MAP/microtubule affinity-regulating kinase 4	-2.32	CCGCATCATGAAGGGCCTAAA	NM_031417:	NM_031417:
57787	MARK4	MAP/microtubule affinity-regulating kinase 4	-0.05	CTGCAGCCTGTTGCCCAATAA	NM_031417:	NM_031417:
4141	MARS	methionine-tRNA synthetase	0.15	CTCGACATGGCAACCAATATA	NM_004990:	NM_004990:
4141	MARS	methionine-tRNA synthetase	0.47	TAGGAGCTGAGGATAACTATA	NM_004990:	NM_004990:
92935	MARS2	methionine-tRNA synthetase 2 (mitochondrial)	0.49	CCCGAACCATTTCATCACGTA	NM_138395:	NM_138395:
92935	MARS2	methionine-tRNA synthetase 2 (mitochondrial)	2.09	CAGGATCTTTAATACAATATA	NM_138395:	NM_138395:
91862	MARVELD3	MARVEL domain containing 3	-10.63	CAGGCGCTGTACCAAAGCAAA	NM_052858:	NM_052858:
91862	MARVELD3	MARVEL domain containing 3	-4.54	CTGGGAGAGCCTGCTGCCAAA	NM_052858:	NM_052858:
4142	MAS1	MAS1 oncogene	-6.70	AAGTATCTCCTAAATGTGATA	NM_002377:	NM_002377:
4142	MAS1	MAS1 oncogene	-0.03	ACAGTTGAGACTGTCGTCTAA	NM_002377:	NM_002377:
116511	MAS1L	MAS1 oncogene-like	0.16	AGGGTCGATGTGGAAACATAA	NM_052967:	NM_052967:
116511	MAS1L	MAS1 oncogene-like	1.12	CACGAATCCCTACATGGTATA	NM_052967:	NM_052967:
5648	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating componer	0.97	CAGGCAGACGAAGCTCTCTTA	NM_001879:	NM_001879:
5648	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating componer	0.01	CCGCTACGGAGTATACTCTTA	NM_001879:	NM_001879:
10747	MASP2	mannan-binding lectin serine peptidase 2	-0.02	CTGGTGTTTCTAGATAGTGAA	NM_006610:	NM_006610:
10747	MASP2	mannan-binding lectin serine peptidase 2	0.55	TACCGATTGTTGACCATCAAA	NM_006610:	NM_006610:
84059	MASS1	monogenic, audiogenic seizure susceptibility 1 homolog (mouse)	-0.65	CACGGGAGTACTAGAATTTAA	NM_032119:	NM_032119:
84059	MASS1	monogenic, audiogenic seizure susceptibility 1 homolog (mouse)	-0.96	CAGATGGTTTATCGTGTTCAA	NM_032119:	NM_032119:
23139	MAST2	microtubule associated serine/threonine kinase 2	-2.58	CAGGAGTGTGCTGTCTGGCAA	NM_015112:	NM_015112:
23139	MAST2	microtubule associated serine/threonine kinase 2	0.31	CAGTGAAATAATAATGATGAA	NM_015112:	NM_015112:
23031	MAST3	microtubule associated serine/threonine kinase 3	0.18	CACGGAGGAAGCCATGCGAAA	XM_038150:	XM_038150:
23031	MAST3	microtubule associated serine/threonine kinase 3	0.07	TTCCTTGTGTTTACAAGACTA	XM_038150:	XM_038150:
84930	MASTL	microtubule associated serine/threonine kinase-like	0.13	ACGCCTTATTCTAGCAAATTA	NM_032844:	NM_032844:
84930	MASTL	microtubule associated serine/threonine kinase-like	0.54	CAGGACAAGTGTTATCGCTTA	NM_032844:	NM_032844:
4143	MAT1A	methionine adenosyltransferase I, alpha	0.68	TTGTATGAAACTAAAGCTTTA	NM_000429:	NM_000429:
4143	MAT1A	methionine adenosyltransferase I, alpha	-2.87	TTGGCTCACACTCGACATGAA	NM_000429:	NM_000429:
4145	MATK	megakaryocyte-associated tyrosine kinase	0.88	ACGGATTCTAAGGACTCTAAA	NM_002378:	NM_002378:NM_139354:NM_139355:
4145	MATK	megakaryocyte-associated tyrosine kinase	2.04	GACGGATTCTAAGGACTCTAA	NM_002378:	NM_002378:NM_139354:NM_139355:
4148	MATN3	matrilin 3	-0.10	TTGGTAGGAAATAGAATGAAA	NM_002381:	NM_002381:
4148	MATN3	matrilin 3	0.01	AAGGTCAGCTCGTATCTTCAA	NM_002381:	NM_002381:
4149	MAX	MYC associated factor X	0.17	CCGTGTGTATTTCTAAGAAAT	NM_002382:	NM_145113:NM_002382:NM_145112:
4149	MAX	MYC associated factor X	0.88	CCGGTTTGGAGTAATCAGAAT	NM_002382:	NM_145113:NM_002382:NM_145112:
4152	MBD1	methyl-CpG binding domain protein 1	1.62	AAGGATGATTCTGCCTCCAAA	NM_002384:	NM_002384:NM_015847:NM_015845:NM_015846:NM_015844:
4152	MBD1	methyl-CpG binding domain protein 1	-0.04	CCGGGAACAGAGAATGTTTAA	NM_002384:	NM_002384:NM_015847:NM_015845:NM_015846:NM_015844:
8932	MBD2	methyl-CpG binding domain protein 2	-2.04	AAGATGATGCCTAGTAAATTA	NM_003927:	NM_015832:NM_003927:
8932	MBD2	methyl-CpG binding domain protein 2	-1.52	TGGAAAGATGATGCCTAGTAA	NM_003927:	NM_015832:NM_003927:
53615	MBD3 (methy	methyl-CpG binding domain protein 3	0.29	CCCGGAGATGGAGCACGTCTA	NM_003926:	NM_003926:
53615	MBD3 (methy	methyl-CpG binding domain protein 3	0.70	GCCGGTGACCAAGATTACCAA	NM_003926:	NM_003926:
8930	MBD4	methyl-CpG binding domain protein 4	-0.01	AAGCTTCTCATCGCTACTATA	NM_003925:	NM_003925:
8930	MBD4	methyl-CpG binding domain protein 4	-0.87	CCGCCGAATGACCTCCGCAAA	NM_003925:	NM_003925:
4153	MBL2	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	-30.25	CACATTGAGTCTATCAATCAA	NM_000242:	NM_000242:
4153	MBL2	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	0.82	TACGATGTTTAGTAACCTCAA	NM_000242:	NM_000242:
8720	MBTPS1	membrane-bound transcription factor peptidase, site 1	-0.30	CAGGGATAATTTAAGGATGAA	NM_003791:	NM_003791:
8720	MBTPS1	membrane-bound transcription factor peptidase, site 1	1.43	CAGAACAGACTTCAACAGTAA	NM_003791:	NM_003791:
51360	MBTPS2	membrane-bound transcription factor peptidase, site 2	0.45	CAGCTATGTGGTAATATTCAT	NM_015884:	NM_015884:

51360	MBTPS2	membrane-bound transcription factor peptidase, site 2	-0.69	CTGAGTTACAGTATACAGCTA	NM_015884:	NM_015884:
4157	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone recep	0.56	CACCAGGGCTTTGGCCTTAAA	NM_002386:	NM_002386:
4157	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone recep	0.84	CACGCTCTTCATCGCCTACTA	NM_002386:	NM_002386:
4158	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	0.11	CAGCCTATATAAGATCTTGGA	NM_000529:	NM_000529:
4158	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	-0.51	CCCGCTGATGCTGGTCTTCAT	NM_000529:	NM_000529:
4159	MC3R	melanocortin 3 receptor	-0.77	CTGCTACACTGCCCACTTCAA	NM_019888:	NM_019888:
4159	MC3R	melanocortin 3 receptor	-1.85	TGGCGTGGTGTTCATCGTCTA	NM_019888:	NM_019888:
4160	MC4R	melanocortin 4 receptor	1.52	AAGCGGGTTGGGATCATCATA	NM_005912:	NM_005912:
4160	MC4R	melanocortin 4 receptor	0.37	CCATAACATTATGACAGTTAA	NM_005912:	NM_005912:
4161	MC5R (melan	melanocortin 5 receptor	-2.16	CGGCATTGTCTTCATCCTGTA	NM_005913:	NM_005913:
4161	MC5R (melan	melanocortin 5 receptor	-0.12	CTGGGAGACCATCACCATCTA	NM_005913:	NM_005913:
4162	MCAM	melanoma cell adhesion molecule	-1.14	AAGACCGAACTTGTAGTTGAA	NM_006500:	NM_006500:
4162	MCAM	melanoma cell adhesion molecule	-0.61	TACACACATTATGGCTGTAAA	NM_006500:	NM_006500:
4163	MCC	mutated in colorectal cancers	1.08	ACCAATGAAACTTCGCTTTAA	NM_002387:	NM_002387:
4163	MCC	mutated in colorectal cancers	0.27	CAGGACTGCTCCAATATCCAA	NM_002387:	NM_002387:
56922	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-0.39	ATGCATTTGGGTCACTAATTA	NM_020166:	NM_020166:
56922	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-3.28	CATGGTTATGATCGCCATGAA	NM_020166:	NM_020166:
64087	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	-0.01	CCCATAAAGCGGAGACAGTAA	NM_022132:	NM_022132:
64087	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	-0.97	ACCCTTACTATTCCAGCGCAA	NM_022132:	NM_022132:
199675	MCEMP1	mast cell-expressed membrane protein 1	0.06	CTCCCTGTTTGTGTAAACATA	NM_174918:	NM_174918:
199675	MCEMP1	mast cell-expressed membrane protein 1	0.26	CAGAAAGGTGATGAATGAATA	NM_174918:	NM_174918:
4168	MCF2	MCF.2 cell line derived transforming sequence	1.52	AGGGACTATAGCTCAAGTAAA	NM_005369:	NM_005369:
4168	MCF2	MCF.2 cell line derived transforming sequence	0.31	CACGTACTAAATGAACTGATA	NM_005369:	NM_005369:
55972	MCFP	mitochondrial carrier family protein	0.78	CAGGCCTAATTCCTCGCTTAA	NM_018843:	NM_018843:
55972	MCFP	mitochondrial carrier family protein	0.51	AACCTGGATTATAATGAAGAA	NM_018843:	NM_018843:
2847	MCHR1	melanin-concentrating hormone receptor 1	0.14	CCCAAGCTGGTGGATAATGAA	NM_005297:	NM_005297:
2847	MCHR1	melanin-concentrating hormone receptor 1	-3.11	CTAGGAGGTCTGCTTACTGAA	NM_005297:	NM_005297:
84539	MCHR2	melanin-concentrating hormone receptor 2	-2.77	CACTATAATAAGATCCAGGAA	NM_032503:	NM_032503:
84539	MCHR2	melanin-concentrating hormone receptor 2	-3.91	CTCGGATTGGATGAAGTGCAA	NM_032503:	NM_032503:
4170	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	-10.22	CCCGCCGAATTCATTAATTTA	NM_021960:	NM_182763:NM_021960:
4170	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	-2.81	CTGGTTTGGCATATCTAATAA	NM_021960:	NM_182763:NM_021960:
4171	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisia	-1.00	CTCATTGGAGATGGCATGGAA	NM_004526:	NM_004526:
4171	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisia	0.97	GAGGCCCTATGCCATCCATAA	NM_004526:	NM_004526:
4172	MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	-0.15	CACGATTTGACTTGCTCTTCA	NM_002388:	NM_002388:
4172	MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	-0.97	CGGCAGGTATGACCAGTATAA	NM_002388:	NM_002388:
57192	MCOLN1	mucolipin 1	-0.09	GTGCCTGTTCTCGCTCATCAA	NM_020533:	NM_020533:
57192	MCOLN1	mucolipin 1	0.89	CTGATCACGTTTGACAACAAA	NM_020533:	NM_020533:
255231	MCOLN2	mucolipin 2	-0.39	TACGATTATCTTTGACAATAA	NM_153259:	NM_153259:
255231	MCOLN2	mucolipin 2	0.37	CTCTATTAGTCTGTTAATTTA	NM_153259:	NM_153259:
55283	MCOLN3	mucolipin 3	0.09	CTGATACATACGAAACAATTA	NM_018298:	NM_018298:
55283	MCOLN3	mucolipin 3	0.03	ATGACTTTACTCTGACTATAA	NM_018298:	NM_018298:
28985	MCTS1	malignant T cell amplified sequence 1	1.01	CAGGTATTGAACCATGGCTTA	NM_014060:	NM_014060:
28985	MCTS1	malignant T cell amplified sequence 1	1.15	GTGGCATATGAAGACATATAA	NM_014060:	NM_014060:
266727	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	1.54	CGCGGTTGTTCTATCAATAAA	NM_153487:	NM_153487:
266727	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	2.12	CAGGTGCTGTATAGCAGCTTA	NM_153487:	NM_153487:
4190	MDH1	malate dehydrogenase 1, NAD (soluble)	-0.07	CTCCCTATTAATGATTTCTCA	NM_005917:	NM_005917:
4190	MDH1	malate dehydrogenase 1, NAD (soluble)	-3.21	AAGGAAGTTGGTGTTTATGAA	NM_005917:	NM_005917:
4191	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	0.16	CTCTGTGGGCGCATCAATAAA	NM_005918:	NM_005918:
4191	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	0.44	CACGGAGGTGGTCAAGGCTAA	NM_005918:	NM_005918:
4192	MDK	midkine (neurite growth-promoting factor 2)	-0.54	CACAATTCCATTACTAAGAAA	NM_002391:	NM_001012334:NM_002391:NM_001012333:
4192	MDK	midkine (neurite growth-promoting factor 2)	-5.08	CTGCTCGTTAGCTTTAATCAA	NM_002391:	NM_001012334:NM_002391:NM_001012333:
56890	MDM1 (Mdm4	Mdm4, transformed 3T3 cell double minute 1, p53 binding protein (mo	-0.14	TAGTAATATTATACTGTCCTA	NM_020128:	NM_020128:
56890	MDM1 (Mdm4	Mdm4, transformed 3T3 cell double minute 1, p53 binding protein (mo	-0.74	TACCATTATCTTATCTAGTAA	NM_020128:	NM_020128:
4193	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mo	-1.63	AACCTGAAATTTATTCACATA	NM_002392:	NM_006880:NM_006881:NM_002392:NM_006879:NM_006878:NM_006882:
4193	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mo	-0.27	CAGGCAAATGTGCAATACCAA	NM_002392:	NM_006880:NM_006881:NM_002392:NM_006879:NM_006878:NM_006882:
4194	MDM4	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mo	-0.63	AAAGAGGTCATGCACTATTTA	NM_002393:	NM_002393:
4194	MDM4	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mo	0.16	TCAGAGCTTCTCCGTAAAGAA	NM_002393:	NM_002393:
4204	MECP2	methyl CpG binding protein 2 (Rett syndrome)	-7.08	ACGGAGCGGATTGCAAAGCAA	NM_004992:	NM_004992:
4204	MECP2	methyl CpG binding protein 2 (Rett syndrome)	0.33	CAGAGATGTCTCTTATATCTA	NM_004992:	NM_004992:
51102	MECR	mitochondrial trans-2-enoyl-CoA reductase	-0.93	CAGCCTTAAGGTATCTAATAA	NM_016011:	NM_016011:NM_001024732:
51102	MECR	mitochondrial trans-2-enoyl-CoA reductase	0.05	CCAGCCTTAAGGTATCTAATA	NM_016011:	NM_016011:NM_001024732:
9968	MED12	mediator of RNA polymerase II transcription, subunit 12 homolog (yea	-1.59	CAGGGCTATACTCCTTATGTT	NM_005120:	NM_005120:
9968	MED12	mediator of RNA polymerase II transcription, subunit 12 homolog (yea	-2.28	CACCCAAACCCTGGTTCTATA	NM_005120:	NM_005120:
219541	MED19	mediator of RNA polymerase II transcription, subunit 19 homolog (yea	0.39	CAAGTTGGACCCAAGATTGAA	NM_153450:	NM_153450:
219541	MED19	mediator of RNA polymerase II transcription, subunit 19 homolog (yea	-0.99	TTGGAACAAGCCTATAATAAA	NM_153450:	NM_153450:
29079	MED4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeas	-0.01	CAGAGATAATATCAATTCATA	NM_014166:	NM_014166:
29079	MED4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeas	-0.24	TCGAGGGAAATTATCCATATA	NM_014166:	NM_014166:
10001	MED6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeas	-0.82	ACCCAAATTTGTGCAGCTAAA	NM_005466:	NM_005466:
10001	MED6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeas	-2.16	AAGGGTATTGGTGGCACTTCA	NM_005466:	NM_005466:
112950	MED8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeas	-2.86	CAGGGTTTAGTTGACCTCATA	NM_001001651:	NM_201542:NM_001001651:NM_052877:
112950	MED8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeas	-0.86	CAGGCTAACCTGCCTTTCTTA	NM_001001651:	NM_201542:NM_001001651:NM_052877:
4210	MEFV	Mediterranean fever	-1.69	AAGGCATATGACACCCGCGTA	NM_000243:	NM_000243:
4210	MEFV	Mediterranean fever	-0.10	CAGAGGTAAGTTAGGAACGAA	NM_000243:	NM_000243:
9833	MELK	maternal embryonic leucine zipper kinase	-0.24	CGGGTTGTCTTCCGTCAGATA	NM_014791:	NM_014791:
9833	MELK	maternal embryonic leucine zipper kinase	-1.02	CTGGATCATGCAAGATTACAA	NM_014791:	NM_014791:
4221	MEN1	multiple endocrine neoplasia I	-0.45	CCCGAGTACAGTCTGTATCAA	NM_000244:	NM_000244:NM_130800:NM_130803:NM_130802:NM_130801:NM_130799:NM_130804:
4221	MEN1	multiple endocrine neoplasia I	0.32	CCGGGAAGACGAGGAGATCTA	NM_000244:	NM_000244:NM_130800:NM_130803:NM_130802:NM_130801:NM_130799:NM_130804:
4224	MEP1A	meprin A, alpha (PABA peptide hydrolase)	0.01	GAGGCTGAACCGAATGTACAA	NM_005588:	NM_005588:
4224	MEP1A	meprin A, alpha (PABA peptide hydrolase)	-7.28	GACACCTATGATGATAGCTTA	NM_005588:	NM_005588:
4225	MEP1B (mep	meprin A, beta	0.83	TGGCCAGCTAATGAAATTAAA	NM_005925:	NM_005925:
4225	MEP1B (mep	meprin A, beta	-1.03	CGGGATGACTATGTCAGGATA	NM_005925:	NM_005925:
10461	MERTK	c-mer proto-oncogene tyrosine kinase	-0.10	CAGACGTTATTTACGTCAATA	NM_006343:	NM_006343:
10461	MERTK	c-mer proto-oncogene tyrosine kinase	0.95	CAGATGAATGTTGTTAAGGAA	NM_006343:	NM_006343:
55897	MESP1	mesoderm posterior 1 homolog (mouse)	-1.09	GTGAATTTATTTATTTGTGAA	NM_018670:	NM_018670:
55897	MESP1	mesoderm posterior 1 homolog (mouse)	1.04	CTGCCTAATGTGAATTTATTT	NM_018670:	NM_018670:
4233	MET	met proto-oncogene (hepatocyte growth factor receptor)	-0.52	ACCGAGGGAATCATCATGAAA	NM_000245:	NM_000245:
4233	MET	met proto-oncogene (hepatocyte growth factor receptor)	0.40	CCGAAAGATAAACCTCTCATA	NM_000245:	NM_000245:
23173	METAP1	methionyl aminopeptidase 1	1.15	CACTGACACATTATACTTGTA	NM_015143:	NM_015143:
23173	METAP1	methionyl aminopeptidase 1	0.72	AAAGTTTGAATGATTATCCTA	NM_015143:	NM_015143:
10988	METAP2	methionyl aminopeptidase 2	2.16	ACCGTCTAATGTAATTAACCA	NM_006838:	NM_006838:
10988	METAP2	methionyl aminopeptidase 2	1.82	AAGACTGTTCACGCAAGTTAA	NM_006838:	NM_006838:
4234	METTL1	methyltransferase like 1	0.06	CTGGTGTATACCATAACCGAT	NM_005371:	NM_023032:NM_023033:NM_005371:
4234	METTL1	methyltransferase like 1	-0.48	CAGAATATGCCTACGTGCTAA	NM_005371:	NM_023032:NM_023033:NM_005371:
339175	METTL2A	methyltransferase like 2A	-0.28	CCGCCTCGGAGCACTCCGAAA	NM_001005372:	NM_001005372:
339175	METTL2A	methyltransferase like 2A	-4.06	ACAAGTTGATTATGAGATCAA	NM_001005372:	NM_001005372:NM_181725:

29081	METTL5	methyltransferase like 5	-1.87	CACCTTATAGCTATACAAGAA	NM_014168:	NM_014168:
29081	METTL5	methyltransferase like 5	0.52	TCACACCACCTTATAGCTATA	NM_014168:	NM_014168:
131965	METTL6	methyltransferase like 6	0.93	AAACATTTACAAGGTATTAAA	NM_152396:	NM_152396:
131965	METTL6	methyltransferase like 6	0.27	GTGGATGTTGTTATGTTGATA	NM_152396:	NM_152396:
25840	METTL7A	methyltransferase like 7A	-5.54	TAGGTTGGTTAGAGGGTTTAA	NM_014033:	NM_014033:
25840	METTL7A	methyltransferase like 7A	-4.56	AAGCAATCTGTGAGTCTGTAA	NM_014033:	NM_014033:
196410	METTL7B	methyltransferase like 7B	-0.91	TTCCTTCGTTCCCATGGTAAA	NM_152637:	NM_152637:
196410	METTL7B	methyltransferase like 7B	0.44	CAGGGCAATCTCTAACTTCAA	NM_152637:	NM_152637:
4239	MFAP4 (micro	microfibrillar-associated protein 4	0.98	AACTGGCTTCATACACACAAA	NM_002404:	NM_002404:
4239	MFAP4 (micro	microfibrillar-associated protein 4	0.22	CCGCGGCTGGAATGACTACAA	NM_002404:	NM_002404:
4241	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodi	1.04	CCGCAACAAGTGTGTGGGCAA	NM_005929:	NM_005929:
4241	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodi	-4.67	CAGGCACACAACCGTCTTTGA	NM_005929:	NM_005929:
4242	MFNG (manic	manic fringe homolog (Drosophila)	-0.70	CAAGACAATCATCCACAGCTA	NM_002405:	NM_002405:
4242	MFNG (manic	manic fringe homolog (Drosophila)	0.40	CTGGCTAATGTCTCTCAGTCA	NM_002405:	NM_002405:
83552	MFRP	membrane frizzled-related protein	0.64	CTGCTCCTTCCTGTCCCTTTA	NM_031433:	NM_031433:
83552	MFRP	membrane frizzled-related protein	-2.11	CAGCATAGAACTACAGTTCCA	NM_031433:	NM_031433:
8972	MGAM	maltase-glucoamylase (alpha-glucosidase)	-16.12	TGGGAGGAATAATATACCTAA	NM_004668:	NM_004668:
8972	MGAM	maltase-glucoamylase (alpha-glucosidase)	0.81	CCCAATGGAAACGGAACTAAT	NM_004668:	NM_004668:
4245	MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltran	0.78	TTGGTAGAAGACAGAATTCGA	NM_002406:	NM_002406:
4245	MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltran	-0.17	CAGGGACAGCTTCAAGGCTTT	NM_002406:	NM_002406:
79172	MGC11266	hypothetical protein MGC11266	0.64	TTGCCACATCGTAGAAACCAA	XM_379881:	NM_024322:
84329	MGC15619	hypothetical protein MGC15619	-2.26	CAGCCCGACAAGAATAACTAT	NM_032369:	NM_032369:
84329	MGC15619	hypothetical protein MGC15619	-1.40	CAGGTTCCAGGCCATCAGTAA	NM_032369:	NM_032369:
85007	MGC15875	hypothetical protein LOC85007, isoform 2	0.00	GAGGAACATCCTGAAGTTTAA	NM_032921:	NM_032921:NM_153373:
85007	MGC15875	hypothetical protein LOC85007, isoform 2	-3.87	CAGGATCATGCCACCAGTGTA	NM_032921:	NM_032921:NM_153373:
93627	MGC16169	hypothetical protein MGC16169	0.30	GTCGATTGTGTTATTTAGAAA	NM_033115:	NM_033115:
93627	MGC16169	hypothetical protein MGC16169	0.31	CCGGAATAGTGAAGACTTTAT	NM_033115:	NM_033115:
92806	MGC16385	hypothetical protein MGC16385	-0.01	CTCGGTTGACTCGCCATCGAA	NM_145039:	NM_145039:
92806	MGC16385	hypothetical protein MGC16385	1.39	AAGGTGTAATCTCGACCTTGA	NM_145039:	NM_145039:
143630	MGC20470	hypothetical protein MGC20470	-1.55	ACCAATGTGTCTTGTACTGAA	NM_145053:	NM_145053:
143630	MGC20470	hypothetical protein MGC20470	-4.05	CAGGCACTCATTGCTACTGAA	NM_145053:	NM_145053:
147015	MGC23280	hypothetical protein MGC23280	-0.80	CCGTCTAGCTAGGTAGTTAAA	NM_144683:	NM_144683:
147015	MGC23280	hypothetical protein MGC23280	-3.87	ACCGTCTAGCTAGGTAGTTAA	NM_144683:	NM_144683:
84291	MGC2408	hypothetical protein MGC2408	-0.14	TCCGGAGTTACCGGAGCGGAA	NM_032331:	NM_032331:
84291	MGC2408	hypothetical protein MGC2408	0.02	CTGGAGGCCGGTTTATCTCAA	NM_032331:	NM_032331:
79080	MGC2574	hypothetical protein MGC2574	0.22	CCGAAAGGCCGCCGAAGACAA	NM_024098:	NM_024098:
79080	MGC2574	hypothetical protein MGC2574	-0.30	CTCGGAGTTGGCCCAGAATAA	NM_024098:	NM_024098:
284439	MGC26694	hypothetical protein MGC26694	1.91	CCCGAAGGAAATGTACAGCAA	XM_209204:	NM_178526:
284439	MGC26694	hypothetical protein MGC26694	-0.55	ATGGGTAATGGTGTGAAGGAA	XM_209204:	NM_178526:
256710	MGC26856	hypothetical protein MGC26856	-2.21	CACAACGAATGGCGTGGCAAA	NM_152779:	NM_152779:
256710	MGC26856	hypothetical protein MGC26856	0.04	TTGCCTGATACCTAAATTTAA	NM_152779:	NM_152779:
166929	MGC26963	hypothetical protein MGC26963	-2.09	AACGATTAGAAAGATGAACAA	NM_152621:	NM_152621:
166929	MGC26963	hypothetical protein MGC26963	0.40	AACGCTGTAACCAAAGGTATA	NM_152621:	NM_152621:
79089	MGC3123	hypothetical protein MGC3123	-0.09	AGGCATGGTCTTTCTCCTTTA	NM_024107:	NM_024107:NM_177441:
79089	MGC3123	hypothetical protein MGC3123	-0.63	CTGGTACTTCCGAATCAATTA	NM_024107:	NM_024107:NM_177441:
284427	MGC34725	hypothetical protein MGC34725	1.96	AATGGTGAACATGTCACACAA	NM_173637:	NM_173637:
284427	MGC34725	hypothetical protein MGC34725	0.04	ATGCATGACAACAACCTTGAA	NM_173637:	NM_173637:
219995	MGC35295	hypothetical protein MGC35295	-2.37	CGCCTTCAGCGCAGACTTCAA	NM_152717:	NM_152717:
219995	MGC35295	hypothetical protein MGC35295	0.12	AAGGACAAGGCTACCACAGAA	NM_152717:	NM_152717:
348035	MGC40069	hypothetical protein MGC40069	-0.20	CCCAGTCACCTGACAAATCTA	NM_182615:	NM_182615:
348035	MGC40069	hypothetical protein MGC40069	-0.13	AACGGGATTATTCAGTAGGAA	NM_182615:	NM_182615:
256356	MGC40579	hypothetical protein MGC40579	-1.18	CAGCCAATGGGTGTAATTTCA	NM_152776:	NM_152776:
256356	MGC40579	hypothetical protein MGC40579	-0.39	TACCATCTTGTACGAGCAATA	NM_152776:	NM_152776:
79154	MGC4172	short-chain dehydrogenase/reductase	-0.07	CCCAGTGGATTTCATGGTGAT	NM_024308:	NM_024308:
79154	MGC4172	short-chain dehydrogenase/reductase	0.20	CGCCTTCAAACTCCACGACAA	NM_024308:	NM_024308:
167359	MGC42105	hypothetical protein MGC42105	1.19	GAGCATATTCGAAATAACCAA	NM_153361:	NM_153361:
167359	MGC42105	hypothetical protein MGC42105	-1.52	CGGAATCGACTGCATCATGAA	NM_153361:	NM_153361:
254013	MGC50559	hypothetical protein MGC50559	-0.23	CTCAATGGTGGCAGCATTTAA	NM_173802:	NM_173802:
254013	MGC50559	hypothetical protein MGC50559	-0.50	ATGAATGTAATTCTTGTTAAA	NM_173802:	NM_173802:
124221	MGC52282	hypothetical protein MGC52282	-1.33	AAGGTGCTAAGCTACACAGAC	NM_178453:	NM_178453:
124221	MGC52282	hypothetical protein MGC52282	-0.14	AAGTGCTGCTGCTTGAGCTGT	NM_178453:	NM_178453:
11343	MGLL	monoglyceride lipase	2.39	TCAGAGCTTGATGCTACTGTA	NM_007283:	NM_007283:NM_001003794:
11343	MGLL	monoglyceride lipase	-0.06	CTGGACCTACCTTAATGGTTA	NM_007283:	NM_007283:NM_001003794:
4255	MGMT (O-6-n	O-6-methylguanine-DNA methyltransferase	0.36	CACCAGACAGGTGTTATGGAA	NM_002412:	NM_002412:
4255	MGMT (O-6-n	O-6-methylguanine-DNA methyltransferase	-0.98	CCGGCTCTTCACCATCCCGTT	NM_002412:	NM_002412:
4257	MGST1	microsomal glutathione S-transferase 1	-3.10	ACCCAGGTAATGGATGATGAA	NM_020300:	NM_020300:NM_145764:NM_145791:NM_145792:
4257	MGST1	microsomal glutathione S-transferase 1	0.46	AAGAAGTATCTTCGAACAGAT	NM_020300:	NM_020300:NM_145764:NM_145791:NM_145792:
4258	MGST2	microsomal glutathione S-transferase 2	0.76	TAATATGGTATCATTTGTTAA	NM_002413:	NM_002413:
4258	MGST2	microsomal glutathione S-transferase 2	-1.27	CACCATGAAGGTAATATGGTA	NM_002413:	NM_002413:
4259	MGST3	microsomal glutathione S-transferase 3	0.06	CCAGAACACGTTGGAAGTGTA	NM_004528:	NM_004528:
4259	MGST3	microsomal glutathione S-transferase 3	-3.15	CTGGTGCTGCCAGCTTTATAA	NM_004528:	NM_004528:
57534	MIB1	mindbomb homolog 1 (Drosophila)	0.16	AACGAAGAGTGCCTTTCATTA	NM_020774:	NM_020774:
57534	MIB1	mindbomb homolog 1 (Drosophila)	0.06	CTCGGAGTCCTTCTATGATTA	NM_020774:	NM_020774:
4276	MICA	MHC class I polypeptide-related sequence A	-0.06	CCGGCGTAGTCCTGAGGAGAA	NM_000247:	NM_000247:
4276	MICA	MHC class I polypeptide-related sequence A	-3.65	CTGGCTTCTATCCCTGGAATA	NM_000247:	NM_000247:
4277	MICB	MHC class I polypeptide-related sequence B	1.33	CCGTAAATGTTTACTCTTTAA	NM_005931:	NM_005931:
4277	MICB	MHC class I polypeptide-related sequence B	0.09	ATGGGTGAACTTTATGAGTGA	NM_005931:	NM_005931:
4281	MID1	midline 1 (Opitz/BBB syndrome)	-2.50	CGGGCTTTAATAATTTCTTTA	NM_033290:	NM_000381:NM_033290:NM_033291:
4281	MID1	midline 1 (Opitz/BBB syndrome)	0.85	CAGGATGTGTTTGAACCTAGT	NM_033290:	NM_000381:NM_033290:NM_033291:
11043	MID2	midline 2	-0.06	AGCGAGCGAATTGCTTGCCAA	NM_012216:	NM_052817:NM_012216:
11043	MID2	midline 2	-0.23	CACGGTTTCTACAGTCTGCAA	NM_012216:	NM_052817:NM_012216:
90007	MIDN	midnolin	0.11	ACCGTTGTTCTCGTAGGTGAA	XM_028067:	NM_177401:
90007	MIDN	midnolin	1.11	ACCGGCTTCGGCAGACAGAAA	XM_028067:	NM_177401:
4282	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	-3.59	CAGGGTCTACATCAACTATTA	NM_002415:	NM_002415:
4282	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	-0.77	CATGCCGATGTTCATCGTAAA	NM_002415:	NM_002415:
84864	MINA	MYC induced nuclear antigen	-3.26	AACCAGTATTTAAGTCTATAA	NM_032778:	NM_032778:
84864	MINA	MYC induced nuclear antigen	-1.21	TACCTGCGTATCTACTAACAA	NM_032778:	NM_032778:
50488	MINK1	misshapen-like kinase 1 (zebrafish)	-4.00	CACGTACGGGCGCATCATTAA	NM_015716:	NM_170663:NM_001024937:NM_015716:NM_153827:
50488	MINK1	misshapen-like kinase 1 (zebrafish)	0.36	CGCAGACTTTGTGTTGCTGAA	NM_015716:	NM_001024937:NM_015716:NM_153827:
9562	MINPP1	multiple inositol polyphosphate histidine phosphatase, 1	1.09	CACGGTCAAACAGATCCGCAA	NM_004897:	NM_004897:
9562	MINPP1	multiple inositol polyphosphate histidine phosphatase, 1	-1.11	CCGAGTGCAGATGTTATTAAA	NM_004897:	NM_004897:
4284	MIP	major intrinsic protein of lens fiber	1.13	CCCGATGTCTCCAATGGACAA	NM_012064:	NM_012064:
4284	MIP	major intrinsic protein of lens fiber	0.22	CCGGCTCAAGAGTATTTCTGA	NM_012064:	NM_012064:
4285	MIPEP	mitochondrial intermediate peptidase	-1.19	CTCCAAGGAACGATAGCTAAA	NM_005932:	NM_005932:
4285	MIPEP	mitochondrial intermediate peptidase	-0.71	CACATTCGTCGTAACTTTACA	NM_005932:	NM_005932:

4286	MITF	microphthalmia-associated transcription factor	-0.31	CATGATGGTATCTATAGTCAA	NM_000248:	NM_000248:NM_198159:NM_198158:NM_006722:NM_198177:NM_198178:
4286	MITF	microphthalmia-associated transcription factor	-0.15	CAGCCTACAACTGAATAGCAA	NM_000248:	NM_000248:NM_198159:NM_198158:NM_006722:NM_198177:NM_198178:
4288	MKI67	antigen identified by monoclonal antibody Ki-67	0.50	CAGGCACTCGGTAAACACGAA	NM_002417:	NM_002417:
4288	MKI67	antigen identified by monoclonal antibody Ki-67	-1.54	CGCGTTTAGGGAAACTGCAAA	NM_002417:	NM_002417:
8569	MKNK1	MAP kinase interacting serine/threonine kinase 1	-1.46	CCAGCAAAGATGATACCTTAA	NM_003684:	NM_003684:
8569	MKNK1	MAP kinase interacting serine/threonine kinase 1	-1.23	TAGATAGTGCTCTGTGCCTAA	NM_003684:	NM_003684:
2872	MKNK2	MAP kinase interacting serine/threonine kinase 2	0.34	CCGCTTCTACCTGGTGTTTGA	NM_017572:	NM_199054:NM_017572:
2872	MKNK2	MAP kinase interacting serine/threonine kinase 2	0.35	TTGGACTTTCTGCATAACAAA	NM_017572:	NM_199054:NM_017572:
23608	MKRN1	makorin, ring finger protein, 1	0.72	CTCTTGTTTAATTGCACACAA	NM_013446:	NM_013446:
23608	MKRN1	makorin, ring finger protein, 1	0.16	CACGAATTTAACTGTCAGACA	NM_013446:	NM_013446:
23609	MKRN2	makorin, ring finger protein, 2	-4.07	AGCAAACAAAGTGGAAGTATA	NM_014160:	NM_014160:
23609	MKRN2	makorin, ring finger protein, 2	-2.20	AAGGCACTGTGAGGTTCTTTA	NM_014160:	NM_014160:
7681	MKRN3	makorin, ring finger protein, 3	1.41	GAGGACTTACAAAGCACTATA	NM_005664:	NM_005664:
7681	MKRN3	makorin, ring finger protein, 3	-0.93	AAGCCAGTAATTAGCATCTAA	NM_005664:	NM_005664:
91807	MLCK	MLCK protein	-2.49	ACGGAGGACAATGACCTTGCA	NM_182493:	NM_182493:
91807	MLCK	MLCK protein	1.03	GACCATGAATTTCATTGTAAA	NM_182493:	NM_182493:
4291	MLF1 (myeloi	myeloid leukemia factor 1	-0.61	GACCAATCTCTTGCTGTTAAA	NM_022443.1:	NM_022443:
4291	MLF1 (myeloi	myeloid leukemia factor 1	1.07	CAGGAGTTCATCAATATGAAT	NM_022443.1:	NM_022443:
79682	MLF1IP	MLF1 interacting protein	0.46	AGGGCGCAAGACGTTCAAAGA	NM_024629:	NM_024629:
79682	MLF1IP	MLF1 interacting protein	0.67	ATGAGCTATAATAAACTTGTA	NM_024629:	NM_024629:
4292	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	-0.03	CCGATACAAAGTGTTGTATCA	NM_000249:	NM_000249:
4292	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	1.90	GTGGCTCATGTTACTATTACA	NM_000249:	NM_000249:
27030	MLH3	mutL homolog 3 (E. coli)	-1.72	ACGAATATAAGTTATGGGCTA	NM_014381:	NM_014381:
27030	MLH3	mutL homolog 3 (E. coli)	-1.30	CAGAAGGTTGCTATATAGTAT	NM_014381:	NM_014381:
197259	MLKL	mixed lineage kinase domain-like	1.13	CACGCTTCTCTGTTACAAATA	NM_152649:	NM_152649:
197259	MLKL	mixed lineage kinase domain-like	1.11	CAGAGTCAAATCTACAGCATA	NM_152649:	NM_152649:
4297	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	0.03	ATGGCAATAGTTCTAAGCAAA	NM_005933:	NM_005933:
4297	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	-1.74	CTCGATCAAATGCCCGCCTAA	NM_005933:	NM_005933:
8085	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	-7.73	CACCAGCATGTCTAAGGCATA	NM_003482:	NM_003482:
8085	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	1.71	CGGCCGGAGTTTGTAATCAAA	NM_003482:	NM_003482:
58508	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	-1.72	CCCAGTGAGCTTCCTCAACAA	NM_021230:	NM_170606:NM_021230:
58508	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	0.00	CTAGAACAGATTCGTAAACAA	NM_021230:	NM_170606:NM_021230:
9757	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	-0.11	CCCAGCGTTGCCAGCACTATA	NM_014727:	NM_014727:
9757	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	-0.73	TCGAATCAAAGTGCCCAACTA	NM_014727:	NM_014727:
55904	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drc	-3.18	CAGCCGAATTCCCATCAGCAA	NM_018682:	NM_018682:NM_182931:
55904	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drc	1.45	CAGCAACATACAGTCAGTTTA	NM_018682:	NM_018682:NM_182931:
4298	MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	-1.21	CTGCTTCATTTGGATATCAGA	NM_005934:	NM_005934:
4298	MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	0.82	CCGCAAAGACTCCGAGAGCAA	NM_005934:	NM_005934:
8028	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	1.12	CGACAAATACTTATTCATCAA	NM_004641:	NM_004641:NM_001009569:
8028	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	-0.10	CAGATTCGCTATGATCAACCA	NM_004641:	NM_004641:NM_001009569:
4301	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	0.26	ATGCCGGTATGTATTGTCCAA	NM_005936:	NM_005936:
4301	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	-3.76	CAGCAGTTGGGCCATATTGAA	NM_005936:	NM_005936:
4302	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	-1.42	CAGGCTGTCTCAACAGCCTTA	NM_005937:	NM_005937:
4302	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosc	0.12	CAGCCATAGCCTGAGTCATAA	NM_005937:	NM_005937:
4295	MLN	motilin	-0.54	CTCCAAGATGGTATCCCGTAA	NM_002418:	NM_002418:
4295	MLN	motilin	-8.79	AAGGAACGGAATAAAGGGCAA	NM_002418:	NM_002418:
2862	MLNR	motilin receptor	0.06	CGGGCTGCCGTTCGACCTGTA	NM_001507:	NM_001507:
2862	MLNR	motilin receptor	0.35	TGGCAGAATCATTTACATAAA	NM_001507:	NM_001507:
84458	MLR2	ligand-dependent corepressor	0.64	ACGGAGAGCGCGCTTAGTAAA	NM_032440:	NM_032440:
84458	MLR2	ligand-dependent corepressor	1.76	CTGAGAGTTGTAAATAGTGAA	NM_032440:	NM_032440:
6945	MLX	MAX-like protein X	0.08	CAGGTATAACACAGCACTACA	NM_170607:	NM_198205:NM_198204:NM_170607:
6945	MLX	MAX-like protein X	0.24	CAGATTTCTGCTCATGATCTA	NM_170607:	NM_198205:NM_198204:NM_170607:
23417	MLYCD	malonyl-CoA decarboxylase	0.08	TAGGCTTTAAATGATCAGGGA	NM_012213:	NM_012213:
23417	MLYCD	malonyl-CoA decarboxylase	-1.76	AAGTTGGATAATAGGCTTTAA	NM_012213:	NM_012213:
166785	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	0.75	CGGGATATGACATAATTCTTA	NM_172250:	NM_172250:
166785	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	-0.70	AAGGAGCGGGATATGACATAA	NM_172250:	NM_172250:
23531	MMD	monocyte to macrophage differentiation-associated	-0.40	AACCACTAATATGTATGTAAA	NM_012329:	NM_012329:
23531	MMD	monocyte to macrophage differentiation-associated	0.03	AACCATTTATGTATTTCTCTA	NM_012329:	NM_012329:
221938	MMD2	monocyte to macrophage differentiation-associated 2	0.00	AAGGTTTGTGATGCCAACATT	NM_198403:	NM_198403:
221938	MMD2	monocyte to macrophage differentiation-associated 2	-0.03	CAGTATTAAATTATCTCAACA	NM_198403:	NM_198403:
4311	MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalir	0.67	ACCGTTACAAGTATACTTATA	NM_000902:	NM_007288:NM_007289:NM_007287:NM_000902:
4311	MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalir	1.45	CACCGTTACAAGTATACTTAT	NM_000902:	NM_007288:NM_007289:NM_007287:NM_000902:
79258	MMEL1	membrane metallo-endopeptidase-like 1	-0.15	TGGCCGGAACTTCGACAAGAA	NM_033467:	NM_033467:
79258	MMEL1	membrane metallo-endopeptidase-like 1	0.20	CACGCACGGCTTTGACGACAA	NM_033467:	NM_033467:
4312	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	1.01	AAGCGTGTGACAGTAAGCTAA	NM_002421:	NM_002421:
4312	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	2.13	TGGAGGTATGATGAATATAAA	NM_002421:	NM_002421:
4319	MMP10	matrix metallopeptidase 10 (stromelysin 2)	-0.63	GACACACATATTAAAGAGTAA	NM_002425:	NM_002425:
4319	MMP10	matrix metallopeptidase 10 (stromelysin 2)	0.01	CAGGATGGTGACACACATATT	NM_002425:	NM_002425:
4320	MMP11	matrix metallopeptidase 11 (stromelysin 3)	0.64	TAAACTGAGGATTGTCATTAA	NM_005940:	NM_005940:
4320	MMP11	matrix metallopeptidase 11 (stromelysin 3)	0.43	CCGCCTCTACTGGAAGTTTGA	NM_005940:	NM_005940:
4321	MMP12	matrix metallopeptidase 12 (macrophage elastase)	-1.96	ATCCTTGGACTGAGAAATTAT	NM_002426:	NM_002426:
4321	MMP12	matrix metallopeptidase 12 (macrophage elastase)	-2.66	ACCATAGGTAATGATTATATA	NM_002426:	NM_002426:
4322	MMP13	matrix metallopeptidase 13 (collagenase 3)	-0.84	GAGGAGAAACAATGATCTTTA	NM_002427:	NM_002427:
4322	MMP13	matrix metallopeptidase 13 (collagenase 3)	-0.01	TCCGAGACTAATAGAAGAAGA	NM_002427:	NM_002427:
4323	MMP14	matrix metallopeptidase 14 (membrane-inserted)	-4.39	CACAAGGACTTTGCCTCTGAA	NM_004995:	NM_004995:
4323	MMP14	matrix metallopeptidase 14 (membrane-inserted)	-1.09	CAGCGATGAAGTCTTCACTTA	NM_004995:	NM_004995:
4324	MMP15	matrix metallopeptidase 15 (membrane-inserted)	1.01	TACATTTATTTCTGTAAATAA	NM_002428:	NM_002428:
4324	MMP15	matrix metallopeptidase 15 (membrane-inserted)	1.05	CACCAAATACTGGAAATTCGA	NM_002428:	NM_002428:
4325	MMP16	matrix metallopeptidase 16 (membrane-inserted)	0.92	CAGGAGTTTGTGGTAACTTGA	NM_005941:	NM_005941:
4325	MMP16	matrix metallopeptidase 16 (membrane-inserted)	-0.01	CCGCCACATACTGTACTGTAA	NM_005941:	NM_005941:
4326	MMP17	matrix metallopeptidase 17 (membrane-inserted)	-1.95	ATGACAGGACTTATTTCTTTA	NM_016155:	NM_016155:
4326	MMP17	matrix metallopeptidase 17 (membrane-inserted)	0.96	AAGGACAATAACGTAGAGGAA	NM_016155:	NM_016155:
4313	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa typ	-0.34	CAGGCTCTTCTCCTTTCACAA	NM_004530:	NM_004530:
4313	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa typ	-0.12	CGCGCCGTCGCCCATCATCAA	NM_004530:	NM_004530:
9313	MMP20	matrix metallopeptidase 20 (enamelysin)	-0.92	ATCGATGCTGCTGTAGAATTA	NM_004771:	NM_004771:
9313	MMP20	matrix metallopeptidase 20 (enamelysin)	0.27	CACAATGAACGTGATCAAGAA	NM_004771:	NM_004771:
118856	MMP21 (matr	matrix metallopeptidase 21	1.09	CACACTGAACATGTAATAAGA	NM_147191:	NM_147191:
118856	MMP21 (matr	matrix metallopeptidase 21	-1.77	CCGCTTATTACTCCTATGCAT	NM_147191:	NM_147191:
10893	MMP24	matrix metallopeptidase 24 (membrane-inserted)	0.17	CAGGGTCTCTTCGGAGACCCA	NM_006690:	NM_006690:
10893	MMP24	matrix metallopeptidase 24 (membrane-inserted)	0.09	TGGGAGATTTGTCTTCTTCAA	NM_006690:	NM_006690:
64386	MMP25	matrix metallopeptidase 25	1.29	ACGGCCGAATCCTCCTCTTTA	NM_022468:	NM_022718:NM_022468:
64386	MMP25	matrix metallopeptidase 25	0.48	CAGAATCACTGGGAAATTTAA	NM_022468:	NM_022718:NM_022468:
56547	MMP26	matrix metallopeptidase 26	-0.07	ACGCTACTGAGTCACAATAAA	NM_021801:	NM_021801:
56547	MMP26	matrix metallopeptidase 26	-0.68	AACGCTACTGAGTCACAATAA	NM_021801:	NM_021801:
79148	MMP28	matrix metallopeptidase 28	-1.66	CTGCCTTTGTTCCTTGAAGAA	NM_024302:	NM_024302:

79148	MMP28	matrix metallopeptidase 28	-0.90	CCCAAGGAAGGCGCCCTGAAA	NM_024302:	NM_024302:
4314	MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	0.98	CAGCCATTTCTGATAAGGAAA	NM_002422:	NM_002422:
4314	MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	-2.88	GTAGACTATTTGCTTATTTAA	NM_002422:	NM_002422:
4316	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	0.52	GTGCGCGTAGATGTCAATAAA	NM_002423:	NM_002423:
4316	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	0.80	TGGACGGATGGTAGCAGTCTA	NM_002423:	NM_002423:
4317	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	0.40	TCCCAAGGATATATCAAACTA	NM_002424:	NM_002424:
4317	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	0.58	ATGGACCAACACCTCCGCAAA	NM_002424:	NM_002424:
4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa typ	-0.50	AACCTTTGAGGGCGACCTCAA	NM_004994:	NM_004994:
4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa typ	-1.92	ACGGCTTGCCCTGGTGCAGTA	NM_004994:	NM_004994:
4328	MMPL1	matrix metallopeptidase-like 1	1.10	CAGGGATGATGGAGAGTTCAT	NM_004142:	NM_004142:
64210	MMS19L	MMS19-like (MET18 homolog, S. cerevisiae)	-0.72	ATGGCTGTACAAAGAACATAA	NM_022362:	NM_022362:
64210	MMS19L	MMS19-like (MET18 homolog, S. cerevisiae)	0.02	TTGCGTTTGAAGAAAGATCTA	NM_022362:	NM_022362:
54542	MNAB	membrane associated DNA binding protein	-0.25	CAGCAGTTGTCTGCCAATCTA	NM_018835:	NM_018835:
54542	MNAB	membrane associated DNA binding protein	-1.23	CGGGAAAGATATAACTCATTA	NM_018835:	NM_018835:
4331	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	0.02	AAGGAGGTTGAGATCAGGAAA	NM_002431:	NM_002431:
4331	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	-1.50	TCGGTGTAAGACCACCAAATA	NM_002431:	NM_002431:
84057	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	-0.14	AAGGATGTACAAGCTTGTGAA	NM_032117:	NM_032117:
84057	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	-1.77	CTCATCAAAGTAGGACAATAA	NM_032117:	NM_032117:
55233	MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	1.12	AACCTGTAGCTTATAAATTTA	NM_018221:	NM_018221:
55233	MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	1.24	CAGGGTTTATGCCCATATTTA	NM_018221:	NM_018221:
4338	MOCS2	molybdenum cofactor synthesis 2	0.08	CTGGGAGAGCATTGTTATTAA	NM_004531:	NM_176806:NM_183418:NM_004531:
4338	MOCS2	molybdenum cofactor synthesis 2	0.30	TAGGATGAAGGGTTATTTAAA	NM_004531:	NM_176806:NM_183418:NM_004531:
27304	MOCS3	molybdenum cofactor synthesis 3	0.74	ATCGTTTAAATTGCATACTAT	NM_014484:	NM_014484:
27304	MOCS3	molybdenum cofactor synthesis 3	0.83	TCCCGAGATCTTTAAAGTTTA	NM_014484:	NM_014484:
27136	MORC1	MORC family CW-type zinc finger 1	-3.63	CCGATGGAAGATGTGAATCTA	NM_014429:	NM_014429:
27136	MORC1	MORC family CW-type zinc finger 1	-0.82	CACCGGCATCAATAATAGAAA	NM_014429:	NM_014429:
79710	MORC4	MORC family CW-type zinc finger 4	-2.71	CAGAGGTAGCACAACCATAAA	NM_024657:	NM_024657:
79710	MORC4	MORC family CW-type zinc finger 4	0.65	CTGGATTGAATAACAAGACAA	NM_024657:	NM_024657:
79906	MORN1	MORN repeat containing 1	-2.70	CTCGGTGTGAATGGAAGGAAA	NM_024848:	NM_024848:
79906	MORN1	MORN repeat containing 1	0.80	CCCATTTGGGTTCGAATGCAT	NM_024848:	NM_024848:
378464	MORN2	MORN repeat containing 2	-2.20	CAGTATATGAAGGACAATTTA	NM_194270:	NM_194270:
378464	MORN2	MORN repeat containing 2	1.99	AAGGACAATTTAAGGATAATA	NM_194270:	NM_194270:
283385	MORN3	MORN repeat containing 3	0.42	CAGGCTGGTGGAAAGGTGATA	NM_173855:	NM_173855:
283385	MORN3	MORN repeat containing 3	0.60	ATGCATGAGAATAAAGAATAA	NM_173855:	NM_173855:
4342	MOS	v-mos Moloney murine sarcoma viral oncogene homolog	-0.42	CGCGAACATCTTGATCAGTGA	NM_005372:	NM_005372:
4342	MOS	v-mos Moloney murine sarcoma viral oncogene homolog	1.39	CTCGGTGTACAAGGCGACTTA	NM_005372:	NM_005372:
26002	MOXD1	monooxygenase, DBH-like 1	0.01	CAGCAAGATTACCATCTAGAA	NM_015529:	NM_001031699:NM_015529:
26002	MOXD1	monooxygenase, DBH-like 1	-0.26	CAGGAGGGTGTAAGTTCTGAA	NM_015529:	NM_015529:
4350	MPG	N-methylpurine-DNA glycosylase	-1.48	CAACCGAGGCATGTTCATGAA	NM_002434:	NM_001015054:NM_001015052:NM_002434:
4350	MPG	N-methylpurine-DNA glycosylase	-0.20	CAGGGTGTTTGTGCCTCATAA	NM_002434:	NM_002434:
9585	MPHOSPH1	M-phase phosphoprotein 1	-0.37	GAGAAAGATAGTGACCTTCAA	NM_016195:	NM_016195:
9585	MPHOSPH1	M-phase phosphoprotein 1	0.06	ATGCGTGATGAGGATAAATTA	NM_016195:	NM_016195:
4352	MPL	myeloproliferative leukemia virus oncogene	0.85	CCCGGGTACTGTTCACAGCTA	NM_005373:	NM_005373:
4352	MPL	myeloproliferative leukemia virus oncogene	-0.61	CCGCGATCTCGCTACCGTTTA	NM_005373:	NM_005373:
339501	MPN2	marapsin 2	0.00	AAGATCATTAAATATTTACAA	NM_183062:	NM_183062:
339501	MPN2	marapsin 2	-2.39	GAGATTTGATAAGATCATTAA	NM_183062:	NM_183062:
4353	MPO (myelop	myeloperoxidase	-1.73	AGGCATCACCACCGTGTCTAA	NM_000250:	NM_000250:
4353	MPO (myelop	myeloperoxidase	0.63	CTCATGTATGTGCGAAGTATA	NM_000250:	NM_000250:
4354	MPP1	membrane protein, palmitoylated 1, 55kDa	0.00	CCCGCCTTGCTTTAAGACAAA	NM_002436:	NM_002436:
4354	MPP1	membrane protein, palmitoylated 1, 55kDa	-1.46	ATGGGAAGGAGTACCACTTTA	NM_002436:	NM_002436:
4355	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2	1.02	CCAGTTCTTCCAAGTGTCTAA	NM_005374:	NM_005374:
4355	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2	0.53	AACGGCCGAGTTTGTCCCTTA	NM_005374:	NM_005374:
4356	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3	0.00	CAGAATTTAAACCCTATATTA	NM_001932:	NM_001932:
4356	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3	1.12	CCCAGGAGGAAGATCGCTTAA	NM_001932:	NM_001932:
58538	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4	0.79	TACGGTCAGAAGTTCTTTATA	NM_033066:	NM_033066:
58538	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4	1.02	TCGAGGCACAATCATGTTCAA	NM_033066:	NM_033066:
64398	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5	1.46	GAGGTCTTACCATTTAATATA	NM_022474:	NM_022474:
64398	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5	-0.61	TTGGAGCGTATTCGGCAACAA	NM_022474:	NM_022474:
51678	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6	1.96	TGGAAGGTGTACTAATATATA	NM_016447:	NM_016447:
51678	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6	0.19	CTGATGATTCAGTAAGGTTAA	NM_016447:	NM_016447:
143098	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7	-0.65	ATGATTAAATCTGCACAGATA	NM_173496:	NM_173496:
143098	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7	0.82	CTCCATCAATAGAGCGTTTGA	NM_173496:	NM_173496:
4357	MPST	mercaptopyruvate sulfurtransferase	0.04	AACCAAGTGCTAAATCTTGTA	NM_021126:	NM_001013440:NM_021126:NM_001013436:
4357	MPST	mercaptopyruvate sulfurtransferase	0.91	CAGGAATTCCGTTGACTTGTT	NM_021126:	NM_001013440:NM_021126:NM_001013436:
4359	MPZ	myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)	-6.24	CCAAATGTCCTTAAATGTTTA	NM_000530:	NM_000530:
4359	MPZ	myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)	0.85	AGGGTTTATTTAGGTTATTAT	NM_000530:	NM_000530:
9019	MPZL1	myelin protein zero-like 1	0.42	AAGGCATTACTTAGAGATTGA	NM_024569:	NM_003953:NM_024569:
9019	MPZL1	myelin protein zero-like 1	-1.71	CACCTTCTTTATAAAGCGTCA	NM_024569:	NM_003953:NM_024569:
22808	MRAS	muscle RAS oncogene homolog	-4.53	CACCTCTATAAGCCTAGTCAA	NM_012219:	NM_012219:
22808	MRAS	muscle RAS oncogene homolog	-2.01	CAGAAGGTAATGGGAACTGTA	NM_012219:	NM_012219:
9902	MRC2	mannose receptor, C type 2	0.16	CCGCACCAGCAACATATCCAA	NM_006039:	NM_006039:
9902	MRC2	mannose receptor, C type 2	-3.87	CTCCCGAAACCGGCTATTCAA	NM_006039:	NM_006039:
4361	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	0.64	AAGGGTTATTTGAGCAAGTAA	NM_005590:	NM_005590:NM_005591:
4361	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	-0.52	CACATCTTTATTGAACTTGAA	NM_005590:	NM_005590:NM_005591:
116512	MRGPRD	MAS-related GPR, member D	-0.85	CACGCCTCTCCTCGTCCGTAA	NM_198923:	NM_198923:
116512	MRGPRD	MAS-related GPR, member D	0.29	CAGCAAGTTCTTGAAATTCAA	NM_198923:	NM_198923:
116534	MRGPRE	MAS-related GPR, member E	-0.85	CAGCTCCAATGTCTACAGAAA	XM_171536:	XM_171536:
116534	MRGPRE	MAS-related GPR, member E	-2.57	CCAGGAGGATGTGGCCTTCAA	XM_171536:	XM_171536:
219928	MRGPRF	MAS-related GPR, member F	0.01	CAGGAGAAGAAAGATCTGTTT	NM_145015:	NM_145015:
219928	MRGPRF	MAS-related GPR, member F	-0.68	TAAGGCATTATCAGTGAGCAA	NM_145015:	NM_145015:
259249	MRGPRX1	MAS-related GPR, member X1	-1.15	CACGTGGACAGGGAAGTCTTA	NM_147199:	NM_147199:
259249	MRGPRX1	MAS-related GPR, member X1	-1.30	CGCCTTATATATTCCCTGTTA	NM_147199:	NM_147199:
117194	MRGPRX2	MAS-related GPR, member X2	1.30	ATCAATGTCAACACATATTTA	NM_054030:	NM_054030:
117194	MRGPRX2	MAS-related GPR, member X2	-1.60	CCGAAGAACTCGGAGCATTTA	NM_054030:	NM_054030:
117195	MRGPRX3	MAS-related GPR, member X3	1.91	AACGTCAGATTTCATTACAAT	NM_054031:	NM_054031:
117195	MRGPRX3	MAS-related GPR, member X3	-0.96	CAGGATCCACCTGGATTGGAA	NM_054031:	NM_054031:
117196	MRGPRX4	MAS-related GPR, member X4	-0.36	CACCTGAATTTGGAAGTCTTA	NM_054032:	NM_054032:
117196	MRGPRX4	MAS-related GPR, member X4	1.54	CCTGAATTTGGAAGTCTTATA	NM_054032:	NM_054032:
23164	M-RIP	myosin phosphatase-Rho interacting protein	-1.96	AAGCGGGACTTCACCAATGAA	NM_015134:	NM_201274:NM_015134:
23164	M-RIP	myosin phosphatase-Rho interacting protein	-0.02	CCGGACCAACAAGCAGAATCA	NM_015134:	NM_201274:NM_015134:
6150	MRPL23	mitochondrial ribosomal protein L23	0.92	CAGTCCCGACACCTAAATAAA	NM_021134:	NM_021134:
6150	MRPL23	mitochondrial ribosomal protein L23	0.24	CCGAACCAACTTCTTCATTCA	NM_021134:	NM_021134:
11222	MRPL3	mitochondrial ribosomal protein L3	0.34	CACATTAAATATATGAGTTAA	NM_007208:	NM_007208:
11222	MRPL3	mitochondrial ribosomal protein L3	1.64	CCGCCGAAACAGACAGTTAAA	NM_007208:	NM_007208:
51318	MRPL35 (mit	mitochondrial ribosomal protein L35	0.29	CAGAGTAAACTCTTAGATAAA	NM_016622:	NM_145644:NM_016622:
51318	MRPL35 (mit	mitochondrial ribosomal protein L35	1.34	CCAGAGTAAACTCTTAGATAA	NM_016622:	NM_145644:NM_016622:
6183	MRPS12	mitochondrial ribosomal protein S12	-1.69	CAGGACCACTATTAAGCCATA	NM_021107:	NM_033363:NM_033362:NM_021107:
6183	MRPS12	mitochondrial ribosomal protein S12	-0.32	TTCCATCAGGACCACTATTAA	NM_021107:	NM_033363:NM_033362:NM_021107:
51373	MRPS17	mitochondrial ribosomal protein S17	-8.36	CAGGCTTGTTCTGGATCCCTA	NM_015969:	NM_015969:

51373	MRPS17	mitochondrial ribosomal protein S17	0.97	TCCCTATTTATTAAAGTATTT	NM_015969:	NM_015969:
28957	MRPS28	mitochondrial ribosomal protein S28	0.29	TGCAATTAGACTAATTGTGAA	NM_014018:	NM_014018:
28957	MRPS28	mitochondrial ribosomal protein S28	0.19	TTGCGGCTATTAGATCTTGAA	NM_014018:	NM_014018:
931	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	-2.07	CACCATATATTAACATATACA	NM_021950:	NM_152866:NM_021950:
931	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	0.01	TTCAATCATGGACATACTTAA	NM_021950:	NM_152866:NM_021950:
341116	MS4A10	membrane-spanning 4-domains, subfamily A, member 10	1.23	TACATTGATGGTTTACATCAA	NM_206893:	NM_206893:
341116	MS4A10	membrane-spanning 4-domains, subfamily A, member 10	0.67	AGCGATGGTCTATACAGCAAA	NM_206893:	NM_206893:
54860	MS4A12	membrane-spanning 4-domains, subfamily A, member 12	0.47	CAACCGGGTCAAGGAAATATA	NM_017716:	NM_017716:
54860	MS4A12	membrane-spanning 4-domains, subfamily A, member 12	-0.11	ATGCAACAACTACTCAGCTAA	NM_017716:	NM_017716:
2206	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment	0.86	CAAGATTTAGGTACTTATCAA	NM_000139:	NM_000139:
2206	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment	1.86	GAGAGTATTAGTCACAATTAA	NM_000139:	NM_000139:
932	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoiet	-0.87	CACACATGCCCTGATATGTAA	NM_006138:	NM_006138:NM_001031666:NM_001031809:
932	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoiet	0.79	TAGGTGTAATAATAACAACTA	NM_006138:	NM_006138:NM_001031666:NM_001031809:
51338	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	0.82	CCGTGTATATCGGGTACACAA	NM_024021:	NM_024021:NM_148975:
51338	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	-0.62	CTGGGCATAATTATATCTTAA	NM_024021:	NM_024021:NM_148975:
64232	MS4A5	membrane-spanning 4-domains, subfamily A, member 5	0.39	GAGGATTGTGATTGTGAACAA	NM_023945:	NM_023945:
64232	MS4A5	membrane-spanning 4-domains, subfamily A, member 5	-1.56	AAGAACATGGTCTAGACTGAA	NM_023945:	NM_023945:
64231	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	-1.27	ACCGTTGATGGGACTGAGAAA	NM_022349:	NM_152851:NM_022349:NM_152852:
64231	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	1.33	TAGTTAATCATGAGAAATCAA	NM_022349:	NM_022349:
245802	MS4A6E	membrane-spanning 4-domains, subfamily A, member 6E	-0.90	ACGGAGAAATATTAATTGGAA	NM_139249:	NM_139249:
245802	MS4A6E	membrane-spanning 4-domains, subfamily A, member 6E	-0.09	AAGCATTTAAAGTAATGCATA	NM_139249:	NM_139249:
58475	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	-2.97	CACGGTCTTGGATATAAGTAA	NM_021201:	NM_206940:NM_206938:NM_206939:NM_021201:
58475	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	0.02	CACACTCATATTGCTTAAATA	NM_021201:	NM_206940:NM_206938:NM_206939:NM_021201:
83661	MS4A8B	membrane-spanning 4-domains, subfamily A, member 8B	1.02	CCCACCTAGTTTGGTGTCGAA	NM_031457:	NM_031457:
83661	MS4A8B	membrane-spanning 4-domains, subfamily A, member 8B	1.43	ACGAATGAAACTGAGCTCTAA	NM_031457:	NM_031457:
9242	MSC	musculin (activated B-cell factor-1)	1.34	ACCGCTTAAATCGGACTGGAA	NM_005098:	NM_005098:
9242	MSC	musculin (activated B-cell factor-1)	0.38	CGCGCTCTACATCCGCTTTAA	NM_005098:	NM_005098:
343930	MSGN1	mesogenin 1	-5.51	GAGGTGGACTACAATATGTTA	XM_292850:	XM_292850:
343930	MSGN1	mesogenin 1	-1.36	CACCAAGATCCAGACACTCAA	XM_292850:	XM_292850:
4436	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	2.04	CCCATGGGCTATCAACTTAAT	NM_000251:	NM_000251:
4436	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.04	TCCAGGCATGCTTGTGTTGAA	NM_000251:	NM_000251:
4437	MSH3 (mutS	mutS homolog 3 (E. coli)	1.08	CAGCAAGGAGTTATGGATTAA	NM_002439:	NM_002439:
4437	MSH3 (mutS	mutS homolog 3 (E. coli)	-2.56	CCGCTAGAATTACAATACATA	NM_002439:	NM_002439:
4438	MSH4 (mutS	mutS homolog 4 (E. coli)	0.94	ATGCAGTGAGGTCTAACATAA	NM_002440:	NM_002440:
4438	MSH4 (mutS	mutS homolog 4 (E. coli)	-1.15	TCGCTCATATTAATTGATGAA	NM_002440:	NM_002440:
4439	MSH5	mutS homolog 5 (E. coli)	-3.63	AAGAAAGATATTGTTTCTTTA	NM_002441:	NM_002441:NM_172166:NM_172165:NM_025259:
4439	MSH5	mutS homolog 5 (E. coli)	2.27	CACCTTCATGATCGACCTCAA	NM_002441:	NM_002441:NM_172166:NM_172165:NM_025259:
2956	MSH6	mutS homolog 6 (E. coli)	0.35	ATCGCCATTGTTCGAGATTTA	NM_000179:	NM_000179:
2956	MSH6	mutS homolog 6 (E. coli)	0.00	CCGAAGTTGTAGAGCTTCTAA	NM_000179:	NM_000179:
55167	MSL2L1	male-specific lethal 2-like 1 (Drosophila)	1.22	AGGGCCTTGATTGTTATGTAA	NM_018133:	NM_018133:
55167	MSL2L1	male-specific lethal 2-like 1 (Drosophila)	1.34	CAGTGTCTTATGAAACATGTA	NM_018133:	NM_018133:
10232	MSLN	mesothelin	-0.69	CTCGCGCTCAGTAAACGGGAA	NM_005823:	NM_005823:NM_013404:
10232	MSLN	mesothelin	-0.31	CGGGTCCGAATACTTCGTGAA	NM_005823:	NM_005823:NM_013404:
4478	MSN (moesin	moesin	-0.17	CAGGGATGTCAACTGACCTAA	NM_002444:	NM_002444:
4478	MSN (moesin	moesin	-9.97	GACGAATTTGAGTCTATGTAA	NM_002444:	NM_002444:
4481	MSR1	macrophage scavenger receptor 1	-0.26	ATGGGTTGTCAATAGTATTAA	NM_138715:	NM_138716:NM_138715:
4481	MSR1	macrophage scavenger receptor 1	1.21	AACTATGAAATCGCTGCTCAA	NM_138715:	NM_138716:NM_138715:
4485	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	0.10	CCGGGCAAGTTCCTCGACCAA	NM_020998:	NM_020998:
4485	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	-1.54	TCGCCATTGAATGACTTCCAA	NM_020998:	NM_020998:
4486	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	-0.02	ATGGAGCATCCTTCTCCGATA	NM_002447:	NM_002447:
4486	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	0.71	TGCCATTAAGTTTGAGTATAT	NM_002447:	NM_002447:
4487	MSX1	msh homeobox homolog 1 (Drosophila)	-1.58	CACAGATGTGTTGCAAAGGTA	NM_002448:	NM_002448:
4487	MSX1	msh homeobox homolog 1 (Drosophila)	0.01	CAGCCAGGAAGATGAATCCTA	NM_002448:	NM_002448:
4488	MSX2	msh homeobox homolog 2 (Drosophila)	1.00	CTAAATATTCTTGAACAATTA	NM_002449:	NM_002449:
4488	MSX2	msh homeobox homolog 2 (Drosophila)	0.44	AACCATTACCTATATGCTAAA	NM_002449:	NM_002449:
9112	MTA1 (metas	metastasis associated 1	-0.89	CAGGGTCGGAGACTACGTCTA	NM_004689:	NM_004689:
9112	MTA1 (metas	metastasis associated 1	-0.81	GCGCATCTTGTTGGACATATT	NM_004689:	NM_004689:
9219	MTA2	metastasis associated 1 family, member 2	-1.65	ACGCCAGTTCTCAGAAATAAA	NM_004739:	NM_004739:
9219	MTA2	metastasis associated 1 family, member 2	-1.18	CAGCCAAGCGTCAGAAACTAA	NM_004739:	NM_004739:
4507	MTAP	methylthioadenosine phosphorylase	-2.70	CACAATCTGGCTCAATGTATA	NM_002451:	NM_002451:
4507	MTAP	methylthioadenosine phosphorylase	1.45	ATGGGTTAGGAAGTCACGAAA	NM_002451:	NM_002451:
22823	MTF2	metal response element binding transcription factor 2	-1.50	TCGGGTGACACTTGATGGAAA	NM_007358:	NM_007358:
22823	MTF2	metal response element binding transcription factor 2	-1.02	CAGGAGTTACAACTCAATCAT	NM_007358:	NM_007358:
4522	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, me	1.28	ATCGTTTGGTGCCATCAGTAA	NM_005956:	NM_005956:
4522	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, me	0.29	CAGATCACCATCCATCTTCAA	NM_005956:	NM_005956:
10797	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, me	-6.65	CTCGCGGCAGTTCGAAATGAA	NM_006636:	NM_006636:
10797	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, me	-0.02	TAGGATTATTCCTTGCTATTA	NM_006636:	NM_006636:
4524	MTHFR (5,10	5,10-methylenetetrahydrofolate reductase (NADPH)	-4.67	TGCCCTGTAACTTATCTAGAA	NM_005957:	NM_005957:
4524	MTHFR (5,10	5,10-methylenetetrahydrofolate reductase (NADPH)	1.01	AACCTAGTACTCTCTGCTCTA	NM_005957:	NM_005957:
9633	MTL5	metallothionein-like 5, testis-specific (tesmin)	0.98	CCACACTGAGTTTAAATCTAA	NM_004923:	NM_004923:
9633	MTL5	metallothionein-like 5, testis-specific (tesmin)	0.52	CCCAAATTATGTGTTCTTCTA	NM_004923:	NM_004923:
4534	MTM1	myotubularin 1	1.52	CGAATAGGTCATGGTGATAAA	NM_000252:	NM_000252:
4534	MTM1	myotubularin 1	-1.10	TCGGTATGAGTGGGAAACGAA	NM_000252:	NM_000252:
8776	MTMR1 (myo	myotubularin related protein 1	-0.05	CTGGCTGACTAGGACTGTTAA	NM_003828:	NM_003828:NM_176789:
8776	MTMR1 (myo	myotubularin related protein 1	0.87	ACGCATTGGCTGGAATATATA	NM_003828:	NM_003828:NM_176789:
54545	MTMR12	myotubularin related protein 12	-2.56	CAGGGTCATGGCATACCAATA	NM_019061:	NM_019061:
54545	MTMR12	myotubularin related protein 12	0.98	TGGGATGTGGATTATGCTTAA	NM_019061:	NM_019061:
8898	MTMR2	myotubularin related protein 2	-0.39	AACGATATGAACTTTGTGATA	NM_016156:	NM_201281:NM_201278:NM_016156:
8898	MTMR2	myotubularin related protein 2	0.51	CTGAGGGAGTCTAACAAGTTA	NM_016156:	NM_201281:NM_201278:NM_016156:
8897	MTMR3	myotubularin related protein 3	0.00	GACCCTTATTACCGAACCATA	NM_021090:	NM_153050:NM_153051:NM_021090:
8897	MTMR3	myotubularin related protein 3	0.81	TTGCCTTTAGCCGAATGTAAA	NM_021090:	NM_153050:NM_153051:NM_021090:
9110	MTMR4	myotubularin related protein 4	0.14	TCGGCACTGGAGAGTACCAAA	NM_004687:	NM_004687:
9110	MTMR4	myotubularin related protein 4	0.50	TTGCCATAGATGTAACCTAAA	NM_004687:	NM_004687:
9107	MTMR6 (myo	myotubularin related protein 6	0.82	CCCGGATAGCAAGCAAACCAA	NM_004685:	NM_004685:
9107	MTMR6 (myo	myotubularin related protein 6	0.22	CCCGTAAATGATGCTCTTCGA	NM_004685:	NM_004685:
55613	MTMR8	myotubularin related protein 8	0.02	CAGCCCAAGCAGAGTATGCTA	NM_017677:	NM_017677:
55613	MTMR8	myotubularin related protein 8	0.15	CGGGAAGATCTAAGAGTCTAT	NM_017677:	NM_017677:
66036	MTMR9	myotubularin related protein 9	0.99	CAGACCTAGTATTCTAAGTTA	NM_015458:	NM_015458:
66036	MTMR9	myotubularin related protein 9	0.90	CAGGTCTAAGGATTAACTATA	NM_015458:	NM_015458:
4543	MTNR1A	melatonin receptor 1A	-7.31	CACAGTCTCAAGTACGACAAA	NM_005958:	NM_005958:
4543	MTNR1A	melatonin receptor 1A	0.47	GAGGGTGAAACCTGACCGCAA	NM_005958:	NM_005958:
4544	MTNR1B	melatonin receptor 1B	-3.99	AACCCACGGCACTGCATTCAA	NM_005959:	NM_005959:
4544	MTNR1B	melatonin receptor 1B	0.59	CACTAGCTACTTACTGGCTTA	NM_005959:	NM_005959:
25821	MTO1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	-2.75	CAATACAACAGTATAGATAAA	NM_012123:	NM_133645:NM_012123:
25821	MTO1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	-3.33	CCAAGACTGATCAATACTTAT	NM_012123:	NM_133645:NM_012123:

4548	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	0.34	TTGGGATATGATACAGACTAA	NM_000254:	NM_000254:
4548	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	-0.15	CCCAAGATATTTAACGACAAA	NM_000254:	NM_000254:
4552	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	-0.01	ATGCCCTTGTGCAAATAATAA	NM_002454:	NM_002454:NM_024010:
4552	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	0.10	TCCCATGAAGACAGCGGGAAA	NM_002454:	NM_002454:NM_024010:
9788	MTSS1	metastasis suppressor 1	-4.08	CCGACGGATGTTCCAAGCCAA	NM_014751:	NM_014751:
9788	MTSS1	metastasis suppressor 1	1.24	CCGTATGGTCATTGTTCTATA	NM_014751:	NM_014751:
4547	MTTP	microsomal triglyceride transfer protein	0.76	AACGTTCTTAGTTTACTTATA	NM_000253:	NM_000253:
4547	MTTP	microsomal triglyceride transfer protein	1.64	CCCGTTCGGCATCTACTTACA	NM_000253:	NM_000253:
57509	MTUS1	mitochondrial tumor suppressor 1	0.44	ATCGCTAGAGAAGCAAATCAA	XM_372031:	NM_020749:NM_001001924:NM_001001925:NM_001001927:NM_001001931:
57509	MTUS1	mitochondrial tumor suppressor 1	-0.12	TCCGTATTACGTGACCGGCAA	XM_372031:	NM_020749:NM_001001924:NM_001001925:NM_001001927:NM_001001931:
4582	MUC1	mucin 1, transmembrane	-2.43	ACGCAGTTCAATCAGTATAAA	NM_002456:	NM_001018016:NM_001018017:NM_001018021:NM_002456:
4582	MUC1	mucin 1, transmembrane	0.28	CAGCAGCCTCTCTTACACAAA	NM_002456:	NM_001018016:NM_002456:NM_001018017:NM_001018021:
140453	MUC17	mucin 17	-4.80	AAGGAACCACTCCGTTAGCAA	NM_001004430:	NM_001004430:
140453	MUC17	mucin 17	0.38	CTGGGAGATTCTCAAATAGAA	NM_001004430:	NM_001004430:
57876	MUC3B	mucin 3B	-2.17	CTCCATCAAGGTGAACAACAA	XM_168578:	XM_374502:XM_168578:
4585	MUC4	mucin 4, tracheobronchial	-1.80	CTCTGGTTTACTTCAAATTAA	NM_138297:	NM_138298:NM_004532:NM_138299:NM_018406:NM_138297:
4585	MUC4	mucin 4, tracheobronchial	0.19	CTCATCCTTACCGCACATTTA	NM_138297:	NM_138298:NM_004532:NM_138299:NM_018406:NM_138297:
4586	MUC5AC	mucin 5, subtypes A and C, tracheobronchial/gastric	1.99	CACCCGGAGGTGAACATTGAA	XM_495860:	XM_495860:
4586	MUC5AC	mucin 5, subtypes A and C, tracheobronchial/gastric	-4.23	ACCCTTCAAGATGTGCCTCAA	XM_495860:	XM_495860:
4588	MUC6	mucin 6, gastric	0.38	CCCGTGCATACTGGAGGGTTA	XM_290540:	XM_290540:
4588	MUC6	mucin 6, gastric	-0.14	CCCGGAAGGTACGGTCCTGAA	XM_290540:	XM_290540:
340273;402	Multiple(ABC	Annotation yielded more than one identification	0.18	TTCCAGGTTATTGATAAGAAA	XM_379995:	XM_379995:XM_377933:NM_178559:
8038;1034	Multiple(ADA	Annotation yielded more than one identification	0.19	AACCATTCTTTAACAACGTAA	NM_022122:	NM_021641:NM_080282:
117;57035	Multiple(ADC	Annotation yielded more than one identification	-1.34	AACCCGTTACTTAGCTGTGTA	NM_002596:	NM_001118:NM_207035:
1645;1646	Multiple(AKR	Annotation yielded more than one identification	-1.67	AAGGTGGAATGTCATCCTTAC	NM_001353:	NM_001353:NM_001354:NM_205845:
1645;1646	Multiple(AKR	Annotation yielded more than one identification	0.95	TGCCAGCTCATTGCTCTTATA	NM_001354:	NM_001354:NM_205845:NM_001353:
1645;1646	Multiple(AKR	Annotation yielded more than one identification	0.14	AACGGTTGAACTGGATGCAAT	NM_001354:	NM_001354:NM_205845:NM_001353:
1645;1646;	Multiple(AKR	Annotation yielded more than one identification	-0.34	AATTGTTCTGGTTGCCTATAG	NM_001353:	NM_001353:NM_001354:NM_003739:NM_205845:
22977;2461	Multiple(AKR	Annotation yielded more than one identification	-1.97	AAGCGACTGCAGAGTGAAAAT	NM_012067:	NM_012067:NM_201252:
213;51283;	Multiple(ALB;	Annotation yielded more than one identification	0.33	ACCCTAGAATTTAATCAACAA	NM_022731:	NM_000477:NM_016561:NM_016618:NM_152630:NM_173557:
262;11595	Multiple(AMD	Annotation yielded more than one identification	0.56	AAGGTGGACCTTGTTGCTAAA	NM_001634:	NM_001033059:NM_001634:NM_138783:NM_198945:
324;19992	Multiple(APC;	Annotation yielded more than one identification	1.57	GAGATTTCTTCTATAAACCAA	NM_201546:	NM_000038:NM_001004303:NM_001013357:NM_001165:NM_004728:NM_015046:NM_152701:NM_182962:XM_374115:XM_379096:
548645;552	Multiple(bA16	Annotation yielded more than one identification	-0.23	AACCGCCTACGAGACACTCAA	NM_004125:	NM_001015882:NM_004125:
85317;8531	Multiple(BAG	Annotation yielded more than one identification	-1.59	ATGGCTGGAAATGCAAATGAA	NM_181704:	NM_181704:NM_182482:
552900;595	Multiple(BOL	Annotation yielded more than one identification	0.79	AACTCGAGTCTTTAATTGTAA	NM_031211:	NM_001031833:NR_002473:NR_002453:
701;353324	Multiple(BUB	Annotation yielded more than one identification	-0.62	ATGGAAGGTAGGGATAATGTA	XM_372798:	NM_001211:NM_181727:
283651;315	Multiple(C15o	Annotation yielded more than one identification	-1.58	AAGGGTGTTTGTAGAGTTGTT	NM_003123:	NM_001005266:NM_001005267:NM_001005268:NM_001005269:NM_005517:NM_005779:NM_015221:NM_017939:NM_018098:NM_133646:NM_173609:NM_182922:NM_198718:XM_086360:XM_371754:XM_373682:
400804;597	Multiple(C1or	Annotation yielded more than one identification	0.67	TAGCGTAAACATCACGACTGA	NM_153024:	NM_001010913:NM_005612:NM_017873:NM_024989:NM_177999:
11238;3405	Multiple(CA5	Annotation yielded more than one identification	-1.84	CTCGTGGAATTTGAAGATTCT	XM_291346:	XM_291346:NM_007220:
797;796	Multiple(CAL	Annotation yielded more than one identification	0.74	CCCACCAATGTGGGTTCCAAA	NM_000728:	NM_000728:NM_001033953:
831;10484;	Multiple(CAS	Annotation yielded more than one identification	0.64	ATGAGTTTCCACCTACTTATA	NM_001001957:	NM_001750:NM_006364:NM_014323:NM_032050:NM_032052:NM_173060:NM_173062:NM_203349:
117155;440	Multiple(CAT	Annotation yielded more than one identification	-0.69	CCCGAGGTTGTGGTATTGGTA	NM_172096:	NR_002318:NM_172097:NM_172095:NM_172096:NM_054020:
10951;672	Multiple(CBX	Annotation yielded more than one identification	1.37	AAGGTGATTCTGATTCTAGAA	NM_000456:	NM_006807:NM_007294:NM_007295:NM_007296:NM_007297:NM_007299:NM_007300:NM_007301:NM_007302:NM_007306:
6358;6359	Multiple(CCL	Annotation yielded more than one identification	1.14	CTGCATGGTAACTATTATATA	NM_004166:	NM_004167:NM_004166:NM_032964:NM_032965:NM_032962:
6358;6359	Multiple(CCL	Annotation yielded more than one identification	1.19	CAGGCTTAGAGGATTAGATTA	NM_004166:	NM_004167:NM_004166:NM_032964:NM_032965:NM_032962:
414062;634	Multiple(CCL	Annotation yielded more than one identification	1.66	TGGGACTCTTCTTAACTTAAA	NM_002983:	NM_002983:NM_021006:NM_001001437:
414062;634	Multiple(CCL	Annotation yielded more than one identification	1.07	TGGGACTCTTCTTAACTTAAA	NM_021006:	NM_002983:NM_021006:NM_001001437:
414062;634	Multiple(CCL	Annotation yielded more than one identification	0.32	TGGGACTCTTCTTAACTTAAA	NM_001001437:	NM_002983:NM_021006:NM_001001437:
414062;634	Multiple(CCL	Annotation yielded more than one identification	-3.22	CAGTGTCATCTTCCTAACCAA	NM_021006:	NM_021006:NM_001001437:
414062;634	Multiple(CCL	Annotation yielded more than one identification	0.01	CAGTGTCATCTTCCTAACCAA	NM_001001437:	NM_021006:NM_001001437:
9560;6351;	Multiple(CCL	Annotation yielded more than one identification	1.44	TCCATTATTTATATTAGTTTA	NM_002984:	NM_001001435:NM_207007:NM_002984:
9560;6351;	Multiple(CCL	Annotation yielded more than one identification	0.24	TCCATTATTTATATTAGTTTA	NM_001001435:	NM_001001435:NM_207007:NM_002984:
9560;6351;	Multiple(CCL	Annotation yielded more than one identification	-0.16	TCGCAACTTTGTGGTAGATTA	NM_001001435:	NM_001001435:NM_207007:NM_002984:
9560;6351;	Multiple(CCL	Annotation yielded more than one identification	0.80	TCCATTATTTATATTAGTTTA	NM_207007:	NM_001001435:NM_207007:NM_002984:
9560;6351;	Multiple(CCL	Annotation yielded more than one identification	1.09	TCGCAACTTTGTGGTAGATTA	NM_207007:	NM_001001435:NM_207007:NM_002984:
984;985	Multiple(CDC	Annotation yielded more than one identification	-4.11	CAAGATCTACATCGTGATGAA	NM_033529:	NM_033493:NM_033488:NM_033489:NM_033486:NM_024011:NM_033492:NM_033527:NM_033528:NM_033531:NM_033532:NM_033529:NM_033536:NM_033537:NM_033490:NM_033487:NM_001787:
984;985	Multiple(CDC	Annotation yielded more than one identification	-2.42	CAGGATAAAGCTCGCCGGGAA	NM_033529:	NM_033493:NM_033488:NM_033489:NM_033486:NM_024011:NM_033492:NM_033527:NM_033528:NM_033531:NM_033532:NM_033529:NM_033534:NM_033536:NM_033537:NM_033490:NM_033487:NM_001787:
984;985	Multiple(CDC	Annotation yielded more than one identification	-1.50	CAAGATCTACATCGTGATGAA	NM_033487:	NM_033493:NM_033488:NM_033489:NM_033486:NM_024011:NM_033492:NM_033527:NM_033528:NM_033531:NM_033532:NM_033529:NM_033536:NM_033537:NM_033490:NM_033487:NM_001787:
984;985	Multiple(CDC	Annotation yielded more than one identification	-0.95	CAGGATAAAGCTCGCCGGGAA	NM_033487:	NM_033493:NM_033488:NM_033489:NM_033486:NM_024011:NM_033492:NM_033527:NM_033528:NM_033531:NM_033532:NM_033529:NM_033534:NM_033536:NM_033537:NM_033490:NM_033487:NM_001787:
1082;9365	Multiple(CGB	Annotation yielded more than one identification	0.34	CCCGAGGTATAAAGCCAGGTA	NM_000737:	NM_033142:NM_033043:NM_000737:

1082;3972;	Multiple(CGB	Annotation yielded more than one identification	-0.01	CCCACAATAAAGGCTTCTCAA	NM_000737:	NM_033142:NM_033183:NM_033043:NM_000737:NM_033377:NM_033378:NM_000894:
1082;3972;	Multiple(CGB	Annotation yielded more than one identification	0.17	CCCACAATAAAGGCTTCTCAA	NM_000894:	NM_033142:NM_033183:NM_033043:NM_000737:NM_033377:NM_033378:NM_000894:
1119;55576	Multiple(CHK	Annotation yielded more than one identification	-1.79	CCGGCCCTTACCAAACCTGAT	NM_001277:	NM_001277:NM_017564:NM_212469:
1120;1375	Multiple(CHK	Annotation yielded more than one identification	-0.93	CACGAAGATGGCGCAATTTCA	NM_005198:	NM_005198:NM_152253:NM_152247:
1143;39054	Multiple(CHR	Annotation yielded more than one identification	0.78	ATGGACGACCTTCTGAACAAA	XM_372562:	XM_372562:XM_497438:XM_372553:XM_497512:NM_000750:XM_497435:XM_497440:XM_497474:XM_497475:
548596;115	Multiple(CKM	Annotation yielded more than one identification	-2.44	ACGGATCTAGATGCCAGTAAA	NM_020990:	NM_020990:NM_001015001:
548596;115	Multiple(CKM	Annotation yielded more than one identification	-2.03	CTGGACGTTACTATAGGCTCA	NM_020990:	NM_020990:NM_001015001:
1196;1197	Multiple(CLK	Annotation yielded more than one identification	-1.76	TCGCCTGGATTGGGATGAGAA	NM_001291:	NM_003993:XR_000292:NM_001291:XR_000261:
1259;23195	Multiple(CNG	Annotation yielded more than one identification	-0.45	TAAGTCTTATGTGGTGGTTAA	NM_030757:	NM_000087:NM_014611:NM_022143:
1325;37870	Multiple(COR	Annotation yielded more than one identification	0.69	AAGCTCTGTCTTTGATTTAAA	NM_001302:	NM_198544:NM_001302:
1375;1120	Multiple(CPT1	Annotation yielded more than one identification	-1.91	CACGTGTTTGCTTGGAATAAA	NM_152246:	NM_152253:NM_152247:NM_004377:NM_152245:NM_152246:
1375;1120	Multiple(CPT1	Annotation yielded more than one identification	-2.02	CTGCCTTTACTTGGTCTCCAA	NM_152246:	NM_152253:NM_152247:NM_004377:NM_152245:NM_152246:
1457;28310	Multiple(CSN	Annotation yielded more than one identification	0.02	ACCGTTGCTTGTGGATTTATA	NM_001895:	NM_001895:NM_177560:NR_002207:NM_177559:
1485;24610	Multiple(CTA	Annotation yielded more than one identification	-4.12	CAGGGCTGAATGGATGCTGCA	NM_001327:	NM_001327:NM_139250:
1485;30848	Multiple(CTA	Annotation yielded more than one identification	1.46	TACATGTTTGTTTCTGTAGAA	NM_001327:	NM_020994:NM_001327:NM_139250:NM_172377:
56998;7567	Multiple(CTN	Annotation yielded more than one identification	-2.00	CTGGCTGTGGCACTTCACCAA	NM_012165:	NM_001012329:NM_006961:NM_020248:
440387;150	Multiple(CTR	Annotation yielded more than one identification	-1.05	CAGCATTCTGACCGTGAACAA	NM_001906:	NM_001906:NM_001025200:
440387;150	Multiple(CTR	Annotation yielded more than one identification	0.05	CAGGAGGATCACCGACGTGAT	NM_001906:	NM_001906:NM_001025200:
8065;84295	Multiple(CUL	Annotation yielded more than one identification	1.00	ATGGTCACAATTAATAAGATA	NM_152715:	NM_003478:NM_032458:NM_080745:NM_182985:
1548;1553	Multiple(CYP	Annotation yielded more than one identification	-0.68	TCGGGATTTCTTCCTCCCTAA	NM_000762:	NM_000762:NM_000766:
1548;1549	Multiple(CYP	Annotation yielded more than one identification	-6.82	CACCTTCGACTGGGTCTTCAA	NM_000762:	NM_000762:NM_000764:
1565;1564	Multiple(CYP	Annotation yielded more than one identification	0.00	GAGGCTCTAATGTACAATAAA	NM_001002910:	NR_002570:NM_000106:NM_001025161:
1565;1564	Multiple(CYP	Annotation yielded more than one identification	0.44	CAGGAGATCGACGACGTGATA	NM_001002910:	NR_002570:NM_000106:NM_001025161:
1565;1564	Multiple(CYP	Annotation yielded more than one identification	0.00	GAGGCTCTAATGTACAATAAA	NM_000106:	NR_002570:NM_000106:NM_001025161:
1565;1564	Multiple(CYP	Annotation yielded more than one identification	-0.24	CAGGAGATCGACGACGTGATA	NM_000106:	NR_002570:NM_000106:NM_001025161:
1551;38917	Multiple(CYP	Annotation yielded more than one identification	-1.45	TGGAGCCATGATTATCCACTA	NM_014627:	NM_000765:NM_001004316:NM_002093:NM_014949:NM_025080:NM_198990:XM_499124:
199974;163	Multiple(CYP	Annotation yielded more than one identification	-1.40	CTGGATGGTTCTAAATGGAAA	NM_178134:	NM_178134:XR_000161:
10521;2378	Multiple(DDX	Annotation yielded more than one identification	-0.12	CTGGGACTTTGTGATATCATA	NM_152715:	NM_006386:NM_014342:NM_020828:NM_025147:NM_030881:NM_170710:NM_173700:NM_181265:XM_374803:
1667;1668	Multiple(DEF	Annotation yielded more than one identification	-0.84	CAGGAGAACGTCGCTATGGAA	NM_005217:	NM_005217:NM_004084:
1667;1668	Multiple(DEF	Annotation yielded more than one identification	-1.10	CAGGAGAACGTCGCTATGGAA	NM_004084:	NM_005217:NM_004084:
8214;85359	Multiple(DGC	Annotation yielded more than one identification	0.61	ACCCTAGGATAGTCTCATAAA	NM_005675:	NM_005675:NM_033257:
8214;85359	Multiple(DGC	Annotation yielded more than one identification	-0.30	CTGGGCAGAGTTCATCTTCTT	NM_005675:	NM_005675:NM_033257:
10901;3177	Multiple(DHR	Annotation yielded more than one identification	-0.61	AAGGAGCAGAGTTGCAAATTA	NM_021004:	NM_198083:NM_021004:
10901;3177	Multiple(DHR	Annotation yielded more than one identification	-0.84	AAGGAGCAGAGTTGCAAATTA	NM_198083:	NM_198083:NM_021004:
10901;3177	Multiple(DHR	Annotation yielded more than one identification	-5.34	AGGAGCAGAGTTGCAAATTAA	NM_198083:	NM_198083:NM_021004:
60625;1605	Multiple(DHX	Annotation yielded more than one identification	-0.07	AAGACACAATACGGACACTAA	XM_113696:	NM_021931:NM_144973:
1740;10308	Multiple(DLG	Annotation yielded more than one identification	-1.45	CAGGACAGTTTAAATGCCAAA	XM_031744:	NM_001364:NM_003414:NM_012095:NM_199051:NM_207012:
340120;579	Multiple(DP5	Annotation yielded more than one identification	0.05	CAGAGTTGTAGTAAAGCCTAA	XM_290552:	NM_001004441:NM_002843:NM_003922:NM_030799:NM_198682:
1809;7273;	Multiple(DPY	Annotation yielded more than one identification	-0.62	AAGGAAGGAAACGAACTCCAA	NM_032032:	NM_001387:NM_003319:NM_004480:NM_005665:NM_005909:NM_006573:NM_016427:NM_022771:NM_032010:NM_052900:NM_133378:NM_133432:NM_133437:NM_152319:NM_178154:NM_178155:NM_178156:NM_198123:NM_198124:NM_206853:NM_206854:NM_206855:XM_087386:
1915;44059	Multiple(EEF1	Annotation yielded more than one identification	0.01	AAGCTGGAAGATGGCCCTAAA	NM_001402:	XM_496374:NM_001402:XM_496711:XM_496717:
1915;44103	Multiple(EEF1	Annotation yielded more than one identification	-1.60	CTGGTTAATGATAACAATGCA	NM_001402:	NM_001402:XM_496711:
8665;33979	Multiple(EIF3	Annotation yielded more than one identification	-3.21	CCGCATGAGCATCAAAGCCTA	NM_003754:	XM_290345:NM_003754:
8665;33979	Multiple(EIF3	Annotation yielded more than one identification	1.43	CCGCATGAGCATCAAAGCCTA	XM_290345:	XM_290345:NM_003754:
10136;2343	Multiple(ELA	Annotation yielded more than one identification	1.40	AAGAATAAAGATCTCTCGGAA	NM_005747:	NM_005747:NM_007352:
10136;2343	Multiple(ELA	Annotation yielded more than one identification	-0.65	CACATCCTGAATAAAGAATAA	NM_007352:	NM_005747:NM_007352:
2048;16741	Multiple(EPH	Annotation yielded more than one identification	-1.17	CACCATCAAAGCTCTATGTAA	XM_035946:	NM_004442:NM_017449:NM_153234:XM_376787:
115548;150	Multiple(FCH	Annotation yielded more than one identification	-1.54	CACAATTGATTCCAACACAAA	NM_173354:	NM_138782:NM_173354:
2224;44126	Multiple(FDP	Annotation yielded more than one identification	0.03	CAAGGAGGTCCTGGAGTACAA	NM_002004:	XM_496902:XM_499334:NM_002004:XM_497102:
2224;44126	Multiple(FDP	Annotation yielded more than one identification	-0.21	CTGGAGTACAATGCCATTGGA	NM_002004:	XM_496902:XM_499334:NM_002004:XM_497102:
2865;2866	Multiple(FFA	Annotation yielded more than one identification	-0.49	CAGCGTGGTCTACGTCATAGA	NM_005305:	NM_005304:NM_005305:
2865;2866	Multiple(FFA	Annotation yielded more than one identification	1.10	CCCGCTGATCATCACCAGCTA	NM_005305:	NM_005304:NM_005305:
388561;871	Multiple(FLJ1	Annotation yielded more than one identification	0.39	CAGGTAGTAGACAGAACAATA	NM_004522:	NM_001008401:NM_003786:NM_004490:NM_014208:NM_020037:NM_020038:
126017;802	Multiple(FLJ1	Annotation yielded more than one identification	-0.83	ATGTCTAATTGGAGATTTCAA	NM_025052:	NM_001004301:NM_001009569:NM_002489:NM_004641:NM_015349:
284071;102	Multiple(FLJ3	Annotation yielded more than one identification	2.18	AAAGATGCTAACGGTAGCATA	NM_001005241:	NM_001033659:NM_005874:
161253;576	Multiple(FLJ3	Annotation yielded more than one identification	-0.18	TAAGATAGTTCTGAAAGGTAA	XM_091156:	NM_173527:XM_371590:
400624;515	Multiple(FLJ4	Annotation yielded more than one identification	-1.27	CCGCTTGAGGCTCTCTATGAA	NM_016478:	NM_001001685:NM_016505:NM_173602:
401337;128	Multiple(FLJ4	Annotation yielded more than one identification	-1.36	TAGGGCTTCCTGAAGATTAAA	XM_085722:	NM_001001707:NM_001847:NM_002392:NM_002897:NM_016836:NM_016839:NM_018717:NM_033641:
2539;570;9	Multiple(G6P	Annotation yielded more than one identification	-3.89	CACCTGGGTGTCACACGGCAA	NM_024980:	NM_000402:NM_001701:NM_004758:NM_024630:NM_153746:XM_498553:
2548;14045	Multiple(GAA	Annotation yielded more than one identification	0.80	CACCATGTTCCTCTCCATACA	XR_000213:	NM_000152:NM_001004430:NM_001004713:NM_001037343:NM_001424:NM_003159:NM_007121:NM_018328:NM_024767:NM_182643:XM_044062:XM_498088:
2562;79365	Multiple(GAB	Annotation yielded more than one identification	0.11	TAGATTGAATTAACTCTTCTA	XM_062645:	NM_000814:NM_021912:NM_030762:NM_138347:
145781;814	Multiple(Gcon	Annotation yielded more than one identification	0.17	ATATTTGAATATTGTGTTTAA	NM_015532:	NM_001018094:NM_001018097:NM_001018092:NM_001018093:NM_001018090:NM_001018091:NM_001018098:NM_015532:NM_001018102:

145781;814	Multiple(Gcon	Annotation yielded more than one identification	-0.45	CCGGGACTTAATTAAATACAA	NM_015532:	NM_001018094:NM_001018097:NM_001018092:NM_001018093:NM_001018090:NM_001018091:NM_001018098:NM_015532:NM_001018102:
2657;10715	Multiple(GDF	Annotation yielded more than one identification	-0.50	CAAGCTCAACATTTACTTCAA	NM_001492:	NM_001492:NM_198207:NM_021267:
2657;10715	Multiple(GDF	Annotation yielded more than one identification	0.80	CTCCATCTACGCTACGCTATA	NM_001492:	NM_001492:NM_198207:NM_021267:
26088;1756	Multiple(GGA	Annotation yielded more than one identification	0.77	CAAATACAATAGAGCCACTAA	NM_172100:	NM_001001560:NM_001001561:NM_004019:NM_004578:NM_006542:NM_013365:NM_145007:NM_203349:
2688;1442;	Multiple(GH1;	Annotation yielded more than one identification	-1.01	AAAGCAGACCTACAGCAAGTT	NM_000515:	NM_000515:NM_001317:NM_001318:NM_020991:NM_022559:NM_022560:NM_022561:NM_022562:NM_022579:NM_022580:NM_022581:NM_022640:NM_022641:NM_022644:NM_022645:
2790;55289	Multiple(GNG	Annotation yielded more than one identification	1.00	CAGAACATTGTAAATGATTAA	NM_004125:	NM_001017998:NM_004125:
9950;757;5	Multiple(GOL	Annotation yielded more than one identification	0.14	CAGCATGTTAATGAATAGAAT	XM_370661:	NM_005113:NM_006134:NM_017519:NM_020732:NM_024860:NM_138959:NM_144690:NM_153681:NM_153682:NM_175863:NM_198539:XM_497010:
8843;33844	Multiple(GPR	Annotation yielded more than one identification	-0.08	CCCAGAAGGGACTGAGCTAAA	NM_006018:	NM_006018:NM_177551:
8843;33844	Multiple(GPR	Annotation yielded more than one identification	-0.01	CTGCTTTCAACCAGCGACTAA	NM_006018:	NM_006018:NM_177551:
124274;161	Multiple(GPR	Annotation yielded more than one identification	0.20	CAGTAACTTCTTCCTTAACAA	XM_059051:	NM_001002911:NM_001351:
113457;112	Multiple(H2-A	Annotation yielded more than one identification	-0.57	CAAGCTAGAGTTTGCCATTTA	NM_207312:	NM_207312:NM_080386:
392360;151	Multiple(HCT	Annotation yielded more than one identification	-3.49	CAGCTTCACAATGGCCATGAA	XM_497242:	NM_145918:NM_001023564:NM_001912:XM_497240:XM_497242:XM_497226:XM_497229:XM_497223:XM_497231:
8925;54474	Multiple(HER	Annotation yielded more than one identification	0.74	AAGGATAGCATCAACTGGCAA	NM_006028:	NM_003922:NM_019010:XM_378798:
8340;8345;	Multiple(HIST	Annotation yielded more than one identification	-0.61	CACCAAGTACACCAGCTCCAA	NM_003527:	NM_175055:NM_005692:NM_003525:NM_003527:NM_003519:NM_003524:NM_003526:NM_003528:
3292;9187;	Multiple(HSD	Annotation yielded more than one identification	-0.38	CGGCACATCCACATCCTTCTA	XM_061677:	NM_000413:NM_004727:NM_007157:NM_012306:NM_033375:NM_080625:XM_047357:XM_498958:
3446;3451	Multiple(IFNA	Annotation yielded more than one identification	0.18	CTGGTTCAACATGGCAATGAT	NM_002171:	NM_002171:NM_021268:
3446;3444;	Multiple(IFNA	Annotation yielded more than one identification	-3.88	CAGCAACTGAATGACCTGGAA	NM_002171:	NM_002171:NM_021068:NM_021057:
3447;3439	Multiple(IFNA	Annotation yielded more than one identification	0.40	ATCCCTCTCTTTATCAACAAA	NM_006900:	NM_006900:NM_024013:
3448;3449;	Multiple(IFNA	Annotation yielded more than one identification	2.24	ATCTATTTATTTAAATATTTA	NM_002173:	NM_002173:NM_021068:NM_021268:NM_002172:
3448;3449;	Multiple(IFNA	Annotation yielded more than one identification	2.24	ATCTATTTATTTAAATATTTA	NM_021268:	NM_002173:NM_021068:NM_021268:NM_002172:
3448;3444	Multiple(IFNA	Annotation yielded more than one identification	-3.38	CTGGTTCATCATGGAAATGAT	NM_021057:	NM_021057:NM_002172:
3475;9097;	Multiple(IFRD	Annotation yielded more than one identification	0.26	ATACGGGTATTCCAACAGAAA	XM_373156:	NM_001007245:NM_001037334:NM_001550:NM_005151:NM_018569:
55081;5767	Multiple(IFT5	Annotation yielded more than one identification	-3.48	AAGAATTGTCGTGCACCTCAA	XM_064062.4:	NM_018010:NM_020919:NM_024590:NM_025150:NM_153688:
282616;282	Multiple(IL28	Annotation yielded more than one identification	-0.47	CAGGCCTTTAAGAGGGCCAAA	NM_172139:	NM_172139:NM_172138:
282616;282	Multiple(IL28	Annotation yielded more than one identification	-4.18	CTGCCACATAGCCCAGTTCAA	NM_172139:	NM_172139:NM_172138:
3759;7273;	Multiple(KCN	Annotation yielded more than one identification	-0.60	CTGGAAGTCAGCTGACATTAA	XM_290793:	NM_000891:NM_003319:NM_005336:NM_006197:NM_021013:NM_133378:NM_133432:NM_133437:NM_152433:NM_198439:NM_203346:
22909;5448	Multiple(KIAA	Annotation yielded more than one identification	0.39	TAAGCTGGCTTAAGAGATCAA	NM_001005241:	NM_014967:NM_019083:NM_198990:NM_205543:XM_379030:XM_498569:XM_498572:
55605;1542	Multiple(KIF2	Annotation yielded more than one identification	-0.77	CTCAGTGATATTGGATGCAAA	NM_174980:	NM_017641:NM_152553:
3859;8702	Multiple(KRT1	Annotation yielded more than one identification	0.68	ATGGATCTCTCTCAACAACTA	NM_145185:	NM_000223:NM_003778:NM_212543:
3856;3848	Multiple(KRT	Annotation yielded more than one identification	-0.02	CAGCATCATTGCTGAGGTCAA	NM_002273:	NM_002273:NM_006121:
120824;399	Multiple(LOC	Annotation yielded more than one identification	-5.57	CCGGCCCTGTTTCTACCTCAA	XM_374920:	XM_374920:XM_062300:
123688;270	Multiple(LOC	Annotation yielded more than one identification	-0.15	TTGCATCTGATCAATGAGGAA	NM_004140:	NM_001013619:NM_002060:NM_002184:NM_004093:NM_006421:NM_015225:NM_016166:NM_016350:NM_017617:NM_017969:NM_018034:NM_020921:NM_030621:NM_152334:NM_175767:NM_177438:NM_182944:NM_182945:NM_182946:NM_199459:
158160;514	Multiple(LOC	Annotation yielded more than one identification	1.62	TTGGATAATATGCATTTGTAA	NM_016371:	NM_016371:NM_001031744:
388272;557	Multiple(LOC	Annotation yielded more than one identification	0.42	CTGTAAGTAATTTGTCTTAAA	NM_005377:	NM_001001436:NM_001008493:NM_001031804:NM_002015:NM_002544:NM_015055:NM_018212:NM_020856:NM_025106:NM_032145:NM_032730:NM_144664:XM_378751:
388524;392	Multiple(LOC	Annotation yielded more than one identification	0.21	CACGGAGGCATCTTATGTTAA	NM_001005472:	XM_498132:NM_002295:XM_370697:NM_001012321:XM_372048:XM_497061:XM_376888:NM_001005472:
388524;392	Multiple(LOC	Annotation yielded more than one identification	-0.74	CACGGAGGCATCTTATGTTAA	XM_376888:	XM_498132:NM_002295:XM_370697:NM_001012321:XM_372048:XM_497061:XM_376888:NM_001005472:
388524;392	Multiple(LOC	Annotation yielded more than one identification	-0.04	CCCGTCGTAACTTAAAGGGAA	NM_001005472:	XM_371273:NM_002295:NM_001012321:XM_372048:NM_001005472:
399937;399	Multiple(LOC	Annotation yielded more than one identification	0.57	CAGCAACTCAATGAAAGCCAA	XM_374917:	XM_374917:XM_374920:
399937;399	Multiple(LOC	Annotation yielded more than one identification	0.24	CAGCAACTCAATGAAAGCCAA	XM_374920:	XM_374917:XM_374920:
400927;717	Multiple(LOC	Annotation yielded more than one identification	0.10	ATGGATGTTCTTCTTCGAGTA	XM_376010:	NM_001034843:NM_199261:NM_130785:NM_013315:NM_199259:NM_199260:NR_001591:XM_495953:XR_000202:NM_199254:
401622;401	Multiple(LOC	Annotation yielded more than one identification	-0.49	CTGACCAGGTAAGAAACTGAA	NM_025052:	NM_001013689:NM_001018158:
402251;402	Multiple(LOC	Annotation yielded more than one identification	-1.53	CAGAAGAAGTCTTGTCATCAA	XM_379995:	XM_379995:XM_377933:
440836;189	Multiple(LOC	Annotation yielded more than one identification	-3.32	CCGCTGTGCGCGAACCCTGAA	NM_001953:	NM_001953:NM_001014440:
595101;440	Multiple(LOC	Annotation yielded more than one identification	-0.02	CTGAAGATTGGTCACTGTAAA	NM_031211:	NR_002473:NR_002453:
642859;642	Multiple(LOC	Annotation yielded more than one identification	-0.88	GAGGACACCTATTCGGAAGAA	XM_114611:	XM_378044:XM_114611:
642859;642	Multiple(LOC	Annotation yielded more than one identification	0.34	CGTGTTTCTGGTGGAGTATGT	XM_114611:	XM_378044:XM_114611:
643641;231	Multiple(LOC	Annotation yielded more than one identification	-1.41	CCCGATCTTCCTTCCACCTAA	XM_376720:	XM_376720:XM_379967:
643641;231	Multiple(LOC	Annotation yielded more than one identification	-1.02	AAGGTTATACAGGACCATTCA	XM_376720:	XM_376720:XM_379967:
4018;80350	Multiple(LPA;	Annotation yielded more than one identification	-1.04	AACAGGAAGGACATGTCAATC	NM_005577:	NM_005577:NM_024492:NM_145727:
4036;3998;	Multiple(LRP	Annotation yielded more than one identification	1.07	TCCAGGTGATCTGAACCTGAA	XM_376010:	NM_004525:NM_005570:NM_007011:NM_012098:NM_014369:NM_018995:NM_152924:NM_153045:NM_206862:
10296;5143	Multiple(MAE	Annotation yielded more than one identification	-9.99	AAGCACCGAAGCGAAACTTAA	NM_001204:	NM_001017405:NM_005882:NM_016227:
5605;40783	Multiple(MAP	Annotation yielded more than one identification	-0.60	TTCCAGGAGTTTGTCAATAAA	NR_002144:	NR_002144:NM_030662:
58508;8531	Multiple(MLL	Annotation yielded more than one identification	0.68	CTGCAGATATTTCATCAAATA	NM_181704:	XM_496404:NM_181704:NM_182481:NM_182482:NM_170606:NM_182484:NM_021230:
8028;4325;	Multiple(MLL	Annotation yielded more than one identification	-42.70	TTGGTCGTGTGAATTATTAAA	BC028192:	NM_001009569:NM_004641:NM_005941:NM_015317:NM_017672:NM_152551:
8511;8510	Multiple(MMP	Annotation yielded more than one identification	-0.56	CAGAAGATCCTCCACAAGAAA	NM_004659:	NM_006983:NM_004659:
8511;8510	Multiple(MMP	Annotation yielded more than one identification	0.06	CCGGGCGCTCATGCACCTGAA	NM_004659:	NM_006983:NM_004659:
4328;64386	Multiple(MMP	Annotation yielded more than one identification	-6.91	CTCCATTATGAGGCCCTTCTA	NM_004142:	NM_004142:NM_022718:NM_022468:

414308;436	Multiple(MRC	Annotation yielded more than one identification	-2.16	CTCCAATTATTTAGAACTTTA	NM_002438:	NM_001009567:NM_002438:
414308;436	Multiple(MRC	Annotation yielded more than one identification	2.39	ATGGAAATATGTAAACAGAAA	NM_002438:	NM_001009567:NM_002438:
503497;140	Multiple(MS4	Annotation yielded more than one identification	-0.28	TCCATCGATCTGGAATTTATA	BC028192:	NM_001012417:NM_020828:NM_205850:
2206;1282;	Multiple(MS4	Annotation yielded more than one identification	0.12	AAGATTTAGGTTAACTTCTCA	AK023420:	NM_000139:NM_001845:NM_002222:NM_032557:XM_042698:
57876;6421	Multiple(MUC	Annotation yielded more than one identification	0.68	CCCACTGATATCAGTACCTTA	XM_168578:	XM_374501:XM_168578:
9172;15731	Multiple(MYO	Annotation yielded more than one identification	-3.61	ATGCGGAATTACTCTCCTCAA	XM_062645:	NM_003970:NM_152562:
4666;34253	Multiple(NAC	Annotation yielded more than one identification	-0.52	CAGCTTGGTTTGAAATTTGTA	NM_005594:	NM_005594:XM_371715:NM_199290:
8440;1775;	Multiple(NCK	Annotation yielded more than one identification	-6.04	CAGCGCCGTGTTCGCCCTCAA	XM_059051:	NM_001004720:NM_001374:NM_003581:NM_003920:
4745;55187	Multiple(NEL	Annotation yielded more than one identification	-6.07	CTGGATAATATCACCTATAGA	NM_001462:	NM_006157:NM_015378:NM_018156:XM_496703:
654364;483	Multiple(NME	Annotation yielded more than one identification	-0.59	ATAGAGCATATTTGCCAATAA	NM_002512:	NM_001018136:NM_002512:NM_001018137:NM_001018138:NM_001018139:
654364;483	Multiple(NME	Annotation yielded more than one identification	0.74	TAGAGCATATTTGCCAATAAA	NM_002512:	NM_001018136:NM_002512:NM_001018137:NM_001018138:NM_001018139:
654364;483	Multiple(NME	Annotation yielded more than one identification	-1.59	TGGGCTGGTGAAGTACATGAA	NR_001577:	NR_001577:NM_001018136:NM_002512:NM_001018137:NM_001018138:NM_001018139:
654364;483	Multiple(NME	Annotation yielded more than one identification	0.15	CAGGTTGGCAGGAACATCATT	NR_001577:	NR_001577:NM_001018136:NM_002512:NM_001018137:NM_001018138:NM_001018139:
4893;10717	Multiple(NRA	Annotation yielded more than one identification	0.61	CCAGCTCTCATGCATAGTTTA	NM_201546:	NM_002524:NM_006594:NM_018482:
11163;4406	Multiple(NUD	Annotation yielded more than one identification	1.20	AACATTTGTTCTACAAATTAA	NM_019094:	NM_019094:NR_002212:NM_199040:
11163;4406	Multiple(NUD	Annotation yielded more than one identification	-0.41	CAGGTACTATTTGTCACATAA	NM_019094:	NM_019094:NR_002212:NM_199040:
9480;39087	Multiple(ONE	Annotation yielded more than one identification	-3.72	CGCCATCTTCAAGGAGAACAA	XM_372702:	XM_372702:NM_004852:
2652;5956	Multiple(OPN	Annotation yielded more than one identification	0.34	CAGCATCTTCACCTACACCAA	NM_020061:	NM_020061:NM_000513:
341276;144	Multiple(OR1	Annotation yielded more than one identification	-0.12	CTGGAGATTGGCTTCAACCTA	NM_001004460:	NM_001004460:NM_178168:
8385;8386	Multiple(OR1	Annotation yielded more than one identification	-5.91	AGGGTTCATGACCACATCCTA	NM_003552:	NM_003552:NM_014566:
8385;8386	Multiple(OR1	Annotation yielded more than one identification	1.13	CTCGGCCTCTAAGAAATACAA	NM_003552:	NM_003552:NM_014566:
138881;343	Multiple(OR1	Annotation yielded more than one identification	-0.67	CCCAAGATGCTTATCAACTTA	NM_001004472:	NM_001004454:NM_001004472:NM_001005479:NM_001010908:NM_012368:NM_148170:NR_001564:
401427;795	Multiple(OR2	Annotation yielded more than one identification	-2.59	AAGAGAGTGCTGGGAGTAGAA	NM_030908:	NM_001005328:NM_030908:
401427;795	Multiple(OR2	Annotation yielded more than one identification	0.27	CTGGGAGTAGAAAGGGCTTTA	NM_030908:	NM_001005328:NM_030908:
391192;262	Multiple(OR2	Annotation yielded more than one identification	-1.81	ATGGCTCTAATTGGAAACCTA	NM_001004687:	NR_002145:NM_001004687:
403239;107	Multiple(OR2	Annotation yielded more than one identification	-0.98	CTGGGCTTTCTTTGCCCTCAT	NM_175617:	NM_001001824:NM_016272:NM_021648:
219417;504	Multiple(OR8	Annotation yielded more than one identification	0.46	TAGCAGTTCCTTATAGCTATA	NM_001005204:	NM_001005204:NM_001013356:
219417;504	Multiple(OR8	Annotation yielded more than one identification	0.23	TGGGAATTTCTTGTACAAACA	NM_001005204:	NM_001005204:NM_001013356:
5004;5005	Multiple(ORM	Annotation yielded more than one identification	1.48	CACGATCTTTCTCAGAGAGTA	NM_000607:	NM_000608:NM_000607:
5004;5005	Multiple(ORM	Annotation yielded more than one identification	-4.36	CAGCACGAGAAGGAGAGGAAA	NM_000607:	NM_000608:NM_000607:
5122;8707;	Multiple(PCS	Annotation yielded more than one identification	-0.04	AACCTGGAGTATCATATTATA	NM_001010844:	NM_000439:NM_003783:NM_133646:XM_498441:XM_499121:XM_499571:
5139;23650	Multiple(PDE	Annotation yielded more than one identification	-0.41	CTGCAGGAATTTAGTAACATT	BX640919:	NM_000921:NM_012101:NM_020648:NM_032119: NM_058193:NM_152303:NM_152488:XM_208333:
5343;5342;	Multiple(PLG	Annotation yielded more than one identification	0.45	ATGAAGATACGTGAAATTCAA	XM_376111:	NM_002665:NM_001032392:XM_376111:
5343;5342;	Multiple(PLG	Annotation yielded more than one identification	-1.03	CAGAGAAGAATGTGCAGCAAA	XM_376111:	NM_002665:NM_001032392:XM_376111:
5380;5383	Multiple(PMS	Annotation yielded more than one identification	1.22	ATGGATCTCATTGAAGTTTCA	NM_174930:	NM_174930:XM_496900:XM_496904:XM_379874:XM_499331:XM_499336:NM_002679:
5380;5383;	Multiple(PMS	Annotation yielded more than one identification	0.66	CAAAGGAATATTAAGAAGAAA	NM_174930:	NM_174930:XM_496900:XM_379874:XM_499331:XM_380025:XM_377962:NM_002679:
5542;44008	Multiple(PRB	Annotation yielded more than one identification	-0.93	CAAGAAGGCAACAATCCTCAA	NM_199354:	NM_005039:NM_199353:NM_199354:NM_006248:
5542;5555	Multiple(PRB	Annotation yielded more than one identification	0.10	TAACTTCAATATACCAATAAA	NM_199354:	NM_005039:NM_199353:NM_199354:NM_005042:
5545;5554	Multiple(PRB	Annotation yielded more than one identification	0.25	CAGGAAGTGAATAAGAAGATA	NM_006250:	NM_002723:NM_006250:
5644;5645	Multiple(PRS	Annotation yielded more than one identification	-0.01	CTGGGAGAGCACAACATCGAA	NM_002770:	NM_002769:NM_002770:
5651;6847;	Multiple(PRS	Annotation yielded more than one identification	3.32	TACAGGTAATTAGATGATTTA	XM_372798:	NM_002772:NM_003176:NM_016255:NM_198520:
5757;44145	Multiple(PTM	Annotation yielded more than one identification	-1.45	TTGTCCAACAATAAACAGGAA	NM_002823:	NM_002823:XM_499153:XM_499154:
5781;8932;	Multiple(PTP	Annotation yielded more than one identification	0.26	TGGATAGTTCTATAGAATTAA	NM_032143:	NM_002834:NM_003927:NM_004438:NM_006777: NM_006901:NM_013396:NM_016649:NM_018561:
353091;803	Multiple(RAE	Annotation yielded more than one identification	-1.59	GTGGACATACTTACAGAGCAA	NM_130900:	NM_130900:NM_001001788:NM_025217:
5896;10313	Multiple(RAG	Annotation yielded more than one identification	0.62	CACTTGTACGTAAGAAGGAAA	XM_085722:	NM_000448:NM_006054:NM_018559:NM_153332: NM_201428:NM_201429:NM_201430:
5906;55720	Multiple(RAP	Annotation yielded more than one identification	-0.08	CAGAAGATCGTCAGTATTTAA	NM_002884:	NM_001010935:NM_018128:
5932;1795;	Multiple(RBB	Annotation yielded more than one identification	0.02	AAGGGCTTCTTTGATAAAGAA	NM_024980:	NM_002894:NM_004947:NM_005845:NM_007120: NM_016218:NM_016237:NM_198141:NM_203291: NM_203292:
8608;2042;	Multiple(RDH	Annotation yielded more than one identification	2.00	CAGAACTTGCGAGGTGTGCAA	XR_000198:	NM_003708:NM_005233:NM_005422:NM_014281: NM_021110:NM_025099:NM_078480:NM_182644:XM_051017:
440872;842	Multiple(RGP	Annotation yielded more than one identification	-2.71	CAGAATTATGATAATAAGCAA	NM_005054:	XM_496557:NM_001024457:XM_496581:NM_006267:NM_005054:
440872;842	Multiple(RGP	Annotation yielded more than one identification	1.57	CAGCATGGTAATAATGTTCAA	NM_005054:	XM_496557:NM_001024457:XM_496581:NM_032260:NM_005054:
139886;158	Multiple(RP11	Annotation yielded more than one identification	0.70	CTGAATGGTATCTTATATCAA	NM_006088:	NM_001012968:NM_001029857:NM_012388:NM_019006:NM_020918:NM_181723:NM_183239:
6120;10349	Multiple(RPE;	Annotation yielded more than one identification	0.87	ACCATTCTTTAACAACGTAAA	NM_022122:	NM_006916:NM_080282:NM_153207:NM_199229:
6103;94025	Multiple(RPG	Annotation yielded more than one identification	-2.94	CAGCAGTATCGGCCTTGTGTA	NM_017886:	NM_000328:NM_001023582:NM_001034853:NM_024690:
6134;28439	Multiple(RPL1	Annotation yielded more than one identification	-0.77	CCCGTTGTTACCGGTATTGTA	XM_209178:	NM_006013:XM_209178:
6134;28439	Multiple(RPL1	Annotation yielded more than one identification	1.31	CCGCACCAAGCTGCAGAACAA	XM_209178:	XM_209500:XM_496264:XM_372471:NM_006013:XM_377511:XM_371781:XM_209178:
11224;4407	Multiple(RPL	Annotation yielded more than one identification	-3.32	TGCAGCAATGGCCAAGATCAA	NM_007209:	XM_499313:NM_007209:XM_496890:XM_496446:
25873;3472	Multiple(RPL	Annotation yielded more than one identification	1.31	GCCCTCAAATTTATCAAGAAA	NM_015414:	NM_033643:NM_015414:XM_294581:
6130;38847	Multiple(RPL	Annotation yielded more than one identification	-3.53	CAGGTGAACTCGGAAGACAAA	NM_000972:	XM_371115:XM_497522:NM_000972:
6130;38847	Multiple(RPL	Annotation yielded more than one identification	-4.82	CACCACCTTGGTGGAGAACAA	NM_000972:	XM_497217:XM_371115:NM_000972:
6233;38872	Multiple(RPS	Annotation yielded more than one identification	-2.11	CTGACTTACTGTTTCAACAAA	NM_002954:	NM_002954:XM_371330:
6233;38872	Multiple(RPS	Annotation yielded more than one identification	-5.30	AAGGTGGATGAGAATGGCAAA	NM_002954:	NM_002954:XM_371330:XM_371843:
6233;38872	Multiple(RPS	Annotation yielded more than one identification	1.24	AAGGTGGATGAGAATGGCAAA	XM_371330:	NM_002954:XM_371330:XM_371843:
6233;38872	Multiple(RPS	Annotation yielded more than one identification	0.92	AAGGTGGATGAGAATGGCAAA	XM_371843:	NM_002954:XM_371330:XM_371843:
6263;23607	Multiple(RYR	Annotation yielded more than one identification	-1.90	CAGCTTATTTAAGATCCAGAA	XM_113696:	NM_001036:NM_012120:NM_145063:NM_173081:XM_039676:XM_168055:XM_371586:XM_496206:XM_498422:XM_499550:
6532;51552	Multiple(SLC	Annotation yielded more than one identification	-5.11	CTGGCAAGTGGAACAGCATAA	NM_174980:	NM_001045:NM_016322:XM_372532:

6542;23527	Multiple(SLC7	Annotation yielded more than one identification	0.97	TGGGACCTACTTTATATTAAA	XM_373038:	NM_001008539:NM_003046:NM_012287:NM_013355:NM_017964:NM_021950:NM_138995:NM_152866:NM_181806:
6606;6607	Multiple(SMN	Annotation yielded more than one identification	1.02	AAGGGTGTTGTAGTTTATAAA	NM_000344:	NM_017411:NM_022874:NM_000344:NM_022876:NM_022877:NM_022875:
6606;6607	Multiple(SMN	Annotation yielded more than one identification	0.12	TTGAATGATATTGGATAATTA	NM_000344:	NM_017411:NM_022874:NM_000344:NM_022876:NM_022877:NM_022875:
548313;675	Multiple(SSX	Annotation yielded more than one identification	-3.12	CCCGAAGATCATGCCCAAGAA	NM_003147:	NM_175698:NM_003147:NM_021014:NM_001034832:NM_174962:NM_005635:NM_173358:NM_174961:NM_005636:NM_175711:
6767;15753	Multiple(ST13	Annotation yielded more than one identification	-0.05	CACCTGCTACTCAGAAAGCTA	XM_496820:	XM_499477:XM_497315:NR_002199:XM_496820:XM_498241:NM_003932:XM_165401:
10617;5557	Multiple(STA	Annotation yielded more than one identification	1.05	AACGTTGATGAGGAATAAATT	NM_153024:	NM_006463:NM_017546:NM_017619:NM_018084:NM_020978:NM_021133:NM_025160:NM_181471:NM_201647:NM_213622:XM_378238:
7341;47433	Multiple(SUM	Annotation yielded more than one identification	-2.22	CAGGCTTGTGGTGATAAATAA	NR_002190:	NM_001005782:NM_003352:NR_002190:
7341;47433	Multiple(SUM	Annotation yielded more than one identification	-3.83	AAGGAAGGTGAATATATTAAA	NR_002190:	NM_001005781:NM_003352:NR_002190:
7027;44148	Multiple(TFD	Annotation yielded more than one identification	-4.55	CCGGATCTGGTAACATGGCAA	NM_007111:	XM_497098:NM_007111:
22797;9723	Multiple(TFE	Annotation yielded more than one identification	-2.93	AAGCAGCTGTCTTATGGCATA	XM_061677:	NM_001018058:NM_012252:NM_012431:NM_023076:NM_033516:NM_207488:
7039;8852;	Multiple(TGF	Annotation yielded more than one identification	-2.92	CACAACTGTTATTCTGCCCAA	NM_001004472:	NM_003236:NM_003886:NM_018018:NM_139289:
7048;4321;	Multiple(TGF	Annotation yielded more than one identification	0.57	CTCCAACGTGTCAGCCAACAA	AB014541:	NM_001024847:NM_002426:NM_003242:NM_014874:NM_018121:NM_024032:XM_378623:
9220;39968	Multiple(TIAF	Annotation yielded more than one identification	-1.53	TACCCGATGTATGGAAATAAA	NM_004740:	NM_203318:NM_078471:NM_004740:
7092;54801	Multiple(TLL1	Annotation yielded more than one identification	1.95	CCACTTAGAAGTATTATAGTA	NM_006088:	NM_012464:NM_017645:NM_025160:NM_080867:NM_173582:NM_199421:
7099;6658;	Multiple(TLR4	Annotation yielded more than one identification	-3.23	CAGAAGGACTGTTGCCTTGTA	XM_371709:	NM_003266:NM_005634:NM_006252:NM_014550:NM_014737:NM_014874:NM_031407:NM_138375:NM_138554:NM_138556:NM_138557:NM_170773:NM_170774:
196527;464	Multiple(TME	Annotation yielded more than one identification	0.88	ACGGCTGAATTCCAGCTGATA	NM_001001957:	NM_001025356:NM_033375:
8741;40797	Multiple(TNF	Annotation yielded more than one identification	0.35	AGCGCAGGTGTCTTCCATTTA	NM_003808:	NM_172087:NM_172088:NM_172089:NM_003808:
8741;40797	Multiple(TNF	Annotation yielded more than one identification	-0.79	CCGGGCAAGGGCGAAACTTAA	NM_003808:	NM_172087:NM_172088:NM_172089:NM_003808:
7177;6449	Multiple(TPS	Annotation yielded more than one identification	-1.06	CTGGACCTCATTAAAGTGCAT	NM_003293:	NM_003294:NM_024164:
7177;2343	Multiple(TPS	Annotation yielded more than one identification	-7.46	CAGGATCATCGTGCACCCACA	NM_003293:	NM_003294:NM_012217:NM_024164:
4591;51542	Multiple(TRIM	Annotation yielded more than one identification	-1.54	ACAGATCGTGTAGAAGAGAAA	NM_001005191:	NM_001005207:NM_001005739:NM_004734:NM_012433:NM_016516:NM_021163:NM_182631:XM_371254:
79097;3999	Multiple(TRIM	Annotation yielded more than one identification	-3.40	TTGCATTCTAATGTTATTAAA	XM_208061:	XM_208061:XM_374919:XM_495873:NM_024114:
79097;3999	Multiple(TRIM	Annotation yielded more than one identification	0.82	TTGCATTCTAATGTTATTAAA	NM_024114:	XM_208061:XM_374919:XM_495873:NM_024114:
79097;4400	Multiple(TRIM	Annotation yielded more than one identification	0.72	AAGAATCAGAATGGCAATATA	XM_495872:	XM_495872:XM_495873:NM_024114:
79097;4400	Multiple(TRIM	Annotation yielded more than one identification	-2.50	AAGAATCAGAATGGCAATATA	XM_495873:	XM_495872:XM_495873:NM_024114:
79097;4400	Multiple(TRIM	Annotation yielded more than one identification	0.49	AAGAATCAGAATGGCAATATA	NM_024114:	XM_495872:XM_495873:NM_024114:
57093;2831	Multiple(TRIM	Annotation yielded more than one identification	0.13	CAGGCCTTGTTTCTACCTCAA	XM_208043:	NM_020358:XM_208043:
57093;2831	Multiple(TRIM	Annotation yielded more than one identification	-7.51	CAGGCCTTGTTTCTACCTCAA	NM_020358:	NM_020358:XM_208043:
84767;1208	Multiple(TRIM	Annotation yielded more than one identification	-4.66	CAGCAACTCAATGAAAGCAAA	NM_032681:	NM_032681:XM_495874:XM_062300:XM_208060:
445372;538	Multiple(TRIM	Annotation yielded more than one identification	-2.80	AAGACTGTACCTAACTATTAA	NM_001003827:	NM_021616:NM_130389:NM_001003827:NM_001003819:
445372;538	Multiple(TRIM	Annotation yielded more than one identification	-0.14	CTGGGTGGATGTCACACTGAA	NM_001003827:	NM_021616:NM_130389:NM_001003827:NM_001003819:
136541;237	Multiple(TRY1	Annotation yielded more than one identification	0.30	TAGGAATTAATTATAAACTAA	XM_035946:	NM_001001317:NM_013231:NM_018284:NM_145025:NM_207645:XM_370899:XM_375029:
55720;5767	Multiple(TSR1	Annotation yielded more than one identification	0.12	GAGGCAGGGATGCTAGATTAA	NM_019841:	NM_018128:NM_020918:NM_147189:
115669;767	Multiple(TTC	Annotation yielded more than one identification	1.22	AAGGAAGATGTGGAAATCTTA	NM_002192:	NM_001007795:NM_001008727:NM_003319:NM_005231:NM_006031:NM_006356:NM_006909:NM_012091:NM_015474:NM_017815:NM_018017:NM_018224:NM_020909:NM_024960:NM_025224:NM_031439:NM_032291:NM_133378:NM_133379:NM_133432:NM_133437:NM_138565:NM_139286:NM_153637:NM_153638:NM_153639:NM_153640:NM_153641:NM_173545:NM_194319:NM_198449:NM_207358:
56604;3476	Multiple(TUB	Annotation yielded more than one identification	-1.59	CCAGCAGATGTTTGATGCTAA	XM_371207:	NM_020040:XM_371207:NM_177987:
56604;3476	Multiple(TUB	Annotation yielded more than one identification	-1.11	CCAGCAGATGTTTGATGCTAA	NM_020040:	NM_020040:XM_371207:NM_177987:
27338;4404	Multiple(UBE	Annotation yielded more than one identification	-0.03	TCCCTCCAACTCTGTCTCTAA	NM_014501:	NM_014501:XM_496186:
7360;4247	Multiple(UGP	Annotation yielded more than one identification	0.41	CCCAAAGTTAGTTACTCTTAA	NM_006759:	NM_001001521:NM_001015883:NM_002408:NM_006759:
54658;5457	Multiple(UGT	Annotation yielded more than one identification	-2.39	ATGGTTGCAATTGATCCTTAA	NM_000463:	NM_205862:NM_019077:NM_019076:NM_021027:NM_019075:NM_019078:NM_019093:NM_007120:NM_000463:NM_001072:
146862;160	Multiple(UNC	Annotation yielded more than one identification	-1.79	CTCCAGCAGCATCGACATCAA	NM_014064:	NM_001033576:NM_014203:NM_130787:NM_173167:
5976;9400;	Multiple(UPF	Annotation yielded more than one identification	-2.44	TCCGCTGAGATCAGAAGGCAA	AB014541:	NM_002911:NM_004259:NM_020383:NM_194286:XM_087089:
11274;3738	Multiple(USP	Annotation yielded more than one identification	0.10	AATCCAGTGTACCTACGGAAA	NM_017414:	NM_017414:XM_036729:
11274;3738	Multiple(USP	Annotation yielded more than one identification	-0.19	AATGCGATTCTCCATCAGGAA	NM_017414:	NM_017414:XM_036729:
9736;64062	Multiple(USP	Annotation yielded more than one identification	-0.36	ACCCAGTAACATAATATTTCA	NM_152671:	NM_014709:NM_022118:XM_047550:XM_047554:
317703;916	Multiple(VN1	Annotation yielded more than one identification	1.32	GTGCATGTTGGTAAACATCAT	NM_173857:	NM_173857:XM_039908:
6375;6846	Multiple(XCL1	Annotation yielded more than one identification	-6.23	CAGGAAATCCAACACCAGAAA	NM_003175:	NM_002995:NM_003175:
6375;6846	Multiple(XCL1	Annotation yielded more than one identification	2.01	TATGTTCTAATTAATAAATTA	NM_003175:	NM_002995:NM_003175:
7531;44091	Multiple(YWH	Annotation yielded more than one identification	0.58	AGAGAGGTTAATCACACTATA	NM_006761:	NM_006761:XM_496603:
7531;44091	Multiple(YWH	Annotation yielded more than one identification	0.59	CTGAAGCAGGTTAGCGTTGAA	NM_006761:	NM_006761:XM_496603:
9877;54852	Multiple(ZC3	Annotation yielded more than one identification	-1.55	CACGAGTAAATGAGGATGCAA	XM_031744:	NM_014827:NM_017705:NM_031423:NM_145697:NM_152701:XM_498954:
64397;2349	Multiple(ZFP1	Annotation yielded more than one identification	1.10	ACCCGGCAACATCAGTTTAAA	NM_172100:	NM_022473:NM_033044:
118813;265	Multiple(ZFY	Annotation yielded more than one identification	-0.19	CTGGGCTTCTTCACCCATTTA	NM_000456:	NM_001002261:NM_001002262:NM_001005466:NM_001115:NM_144588:NM_152701:NM_175056:NM_178844:NM_181846:NM_199044:XM_374898:
7637;83480	Multiple(ZNF	Annotation yielded more than one identification	-2.56	AAGCCTTATCCTCGGAAGTAA	NM_001004492:	NM_003428:NM_031307:
4593	MUSK	muscle, skeletal, receptor tyrosine kinase	-1.09	ACGGCCTGGAATGAACTGAAA	NM_005592:	NM_005592:
4593	MUSK	muscle, skeletal, receptor tyrosine kinase	-1.62	CCCACCAATGACGTCCTCAAA	NM_005592:	NM_005592:

4594	MUT	methylmalonyl Coenzyme A mutase	-4.23	AGGGAATACCTAAACTTCGAA	NM_000255:	NM_000255:
4594	MUT	methylmalonyl Coenzyme A mutase	1.25	CTGGGCTCACTTAATAGAGAA	NM_000255:	NM_000255:
4595	MUTYH	mutY homolog (E. coli)	-0.75	CAAGCTGACATATCAAGTATA	NM_012222:	NM_012222:
4595	MUTYH	mutY homolog (E. coli)	0.82	CAGGAGGAATTTCACACCGCA	NM_012222:	NM_012222:
4598	MVK	mevalonate kinase (mevalonic aciduria)	-7.55	CCGCTTGGCGATGCCAGCCAA	NM_000431:	NM_000431:
4598	MVK	mevalonate kinase (mevalonic aciduria)	1.30	GCGGTGGGCCTGGTTAAATAA	NM_000431:	NM_000431:
9961	MVP	major vault protein	0.09	TGGGCCTGAGATGCAGGTAAA	NM_005115:	NM_005115:NM_017458:
9961	MVP	major vault protein	0.29	GCCGAGAAAGCTCGCAAGGAA	NM_005115:	NM_005115:NM_017458:
4599	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p	-3.43	TAAGATCAAGACACTCATCAA	NM_002462:	NM_002462:
4599	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p	-0.16	TCCGTTAGCCGTGGTGATTTA	NM_002462:	NM_002462:
4600	MX2	myxovirus (influenza virus) resistance 2 (mouse)	-0.36	CAGCATTGTAACTGCTTAATA	NM_002463:	NM_002463:
4600	MX2	myxovirus (influenza virus) resistance 2 (mouse)	0.52	GAGCACGATTGAAGACATAAA	NM_002463:	NM_002463:
4084	MXD1	MAX dimerization protein 1	0.59	AGCCAAATTGCACATAAAGAA	NM_002357:	NM_002357:
4084	MXD1	MAX dimerization protein 1	0.32	TACGTTGAGTTTATTAACAAA	NM_002357:	NM_002357:
83463	MXD3	MAX dimerization protein 3	0.24	CAGCGGGCGGTCAGTGCACAA	NM_031300:	NM_031300:
83463	MXD3	MAX dimerization protein 3	1.09	CACCTGTTGGAATGGACTAAA	NM_031300:	NM_031300:
10608	MXD4	MAX dimerization protein 4	1.60	TCCTTATGTCATTGTAATATA	NM_006454:	NM_006454:
10608	MXD4	MAX dimerization protein 4	1.79	TCCAGAAGTATTAAACGTCAT	NM_006454:	NM_006454:
4601	MXI1	MAX interactor 1	0.96	TAGACACACTATCATAGTTAA	NM_005962:	NM_001008541:NM_130439:NM_005962:
4601	MXI1	MAX interactor 1	-2.72	CTCACTCTTTATAGTGCACAA	NM_005962:	NM_001008541:NM_130439:NM_005962:
25878	MXRA5	matrix-remodelling associated 5	1.04	CACGTGGGAGTTACCGGATAA	NM_015419:	NM_015419:
25878	MXRA5	matrix-remodelling associated 5	1.18	CGGTACCTTAGTGATACGGAA	NM_015419:	NM_015419:
4602	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-4.53	CTGGACGAACTGATAATGCTA	NM_005375:	NM_005375:
4602	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-0.05	TTGGGATATATCATTCCTCAA	NM_005375:	NM_005375:
4605	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0.93	CACTGGAACTCTACCATCAAA	NM_002466:	NM_002466:
4605	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	-0.13	CCAGGGCTTCTTGCAGGCCAA	NM_002466:	NM_002466:
4607	MYBPC3	myosin binding protein C, cardiac	1.14	CAGGATGTCGGCAACACGGAA	NM_000256:	NM_000256:
4607	MYBPC3	myosin binding protein C, cardiac	0.05	CCGCATAAAGGTGTCCCACAT	NM_000256:	NM_000256:
4609	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-0.11	AACGTTTATAGCAGTTACACA	NM_002467:	NM_002467:
4609	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-2.56	CCCAAGGTAGTTATCCTTAAA	NM_002467:	NM_002467:
23077	MYCBP2	MYC binding protein 2	0.24	CACGAGTTAAAGCTATTCCTA	NM_015057:	NM_015057:
23077	MYCBP2	MYC binding protein 2	-1.93	AAGGAGTAGTTTAAATAGCCA	NM_015057:	NM_015057:
4610	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma d	0.11	CTCCAGTTGGCTTTACTTTAA	NM_005376:	NM_005376:
4610	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma d	0.83	CTGTGGCTAGTGACAAATAAA	NM_005376:	NM_005376:
4613	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derive	-0.26	ATGACGCTGATACATAACTAA	BC002712:	NM_005378:
4613	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derive	-0.41	CAGCAGCAGTTGCTAAAGAAA	BC002712:	NM_005378:
4615	MYD88 (myel	myeloid differentiation primary response gene (88)	2.20	CATCCTGAGTTTATAATAATA	NM_002468:	NM_002468:
4615	MYD88 (myel	myeloid differentiation primary response gene (88)	0.71	CAGAGAGTAGCTGTGTTTGAA	NM_002468:	NM_002468:
4617	MYF5 (myoge	myogenic factor 5	0.19	CCACTTTATAAGAAAGTGTAT	NM_005593:	NM_005593:
4617	MYF5 (myoge	myogenic factor 5	1.30	TCCTGATGTATCAAATGTATA	NM_005593:	NM_005593:
4618	MYF6	myogenic factor 6 (herculin)	1.36	TCCTGGTATTGTAATATTAAA	NM_002469:	NM_002469:
4618	MYF6	myogenic factor 6 (herculin)	1.12	TGCGAGGATCCTGGTATTGTA	NM_002469:	NM_002469:
4628	MYH10	myosin, heavy polypeptide 10, non-muscle	0.52	CAGGACTAATCTATACTTATT	NM_005964:	NM_005964:
4628	MYH10	myosin, heavy polypeptide 10, non-muscle	-0.64	CCCATGTTGCTTCTTCACATA	NM_005964:	NM_005964:
57644	MYH7B	myosin, heavy polypeptide 7B, cardiac muscle, beta	-1.27	CCGGGCCAAGCTCTACGACAA	XM_371398:	NM_020884:
57644	MYH7B	myosin, heavy polypeptide 7B, cardiac muscle, beta	0.69	TCCGCGGATATTGACAGCTAT	XM_371398:	NM_020884:
4627	MYH9	myosin, heavy polypeptide 9, non-muscle	0.00	AACCGGGACGAAGCCATCAAA	NM_002473:	NM_002473:
4627	MYH9	myosin, heavy polypeptide 9, non-muscle	0.16	TCCACTGAGCATCACAATAAA	NM_002473:	NM_002473:
4634	MYL3	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow	-1.93	CACACCCAAGTGTGAGATGAA	NM_000258:	NM_000258:
4634	MYL3	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow	-0.44	CAGATTGAAGAGTTCAAGGAA	NM_000258:	NM_000258:
4637	MYL6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0.95	ACCTATGAGGATTATGTCGAA	NM_021019:	NM_021019:NM_079423:NM_079424:NM_079425:
4637	MYL6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	-4.17	TAGGCTTTCTTGTCTCAGCAA	NM_021019:	NM_021019:NM_079423:NM_079424:NM_079425:
58498	MYL7	myosin, light polypeptide 7, regulatory	-0.56	AACGTGGTTCTTCCAACGTCT	NM_021223:	NM_021223:
58498	MYL7	myosin, light polypeptide 7, regulatory	-0.10	TCGTGATGGCATCATCTGCAA	NM_021223:	NM_021223:
29116	MYLIP	myosin regulatory light chain interacting protein	-4.93	ATCGGGTGCAATACTAGCTAA	NM_013262:	NM_013262:
29116	MYLIP	myosin regulatory light chain interacting protein	1.08	AAGTAAGTGCTTAAGTATTAA	NM_013262:	NM_013262:
4638	MYLK	myosin, light polypeptide kinase	-0.94	AACCTGAAATCCGCTAGCAAA	NM_005965:	NM_005965:NM_053030:NM_053029:NM_053028:NM_053027:NM_053026:NM_053025:
4638	MYLK	myosin, light polypeptide kinase	1.07	CAGCATCCATGGCTAATGAAA	NM_005965:	NM_005965:NM_053030:NM_053029:NM_053028:NM_053027:NM_053026:NM_053025:
85366	MYLK2	myosin light chain kinase 2, skeletal muscle	-0.51	AACGCTGTAACCGACGCCTTA	NM_033118:	NM_033118:
85366	MYLK2	myosin light chain kinase 2, skeletal muscle	0.09	CGGGATCCTCTTCATGCACAA	NM_033118:	NM_033118:
53904	MYO3A	myosin IIIA	1.14	TAGGATATCAATCTATAATAA	NM_017433:	NM_017433:
53904	MYO3A	myosin IIIA	-3.40	CACGAAGAAAGGGAACTTCAA	NM_017433:	NM_017433:
140469	MYO3B (myo	myosin IIIB	0.52	AACCAGTTAAATGGAACTCTA	NM_138995:	NM_138995:
140469	MYO3B (myo	myosin IIIB	0.75	ACCCTGGTTGATAAATTTGAA	NM_138995:	NM_138995:
4653	MYOC	myocilin, trabecular meshwork inducible glucocorticoid response	-0.62	CAGCATCGAATATAAGTAAGA	NM_000261:	NM_000261:
4653	MYOC	myocilin, trabecular meshwork inducible glucocorticoid response	0.61	CAGCATTTATGGGATGTTTAA	NM_000261:	NM_000261:
4654	MYOD1	myogenic differentiation 1	0.57	TACAGGGAATTTGTACGTTTA	NM_002478:	NM_002478:
4654	MYOD1	myogenic differentiation 1	0.22	CTGCACGTCGAGCAATCCAAA	NM_002478:	NM_002478:
4656	MYOG	myogenin (myogenic factor 4)	-0.13	CTGCCCTGAATTGAGAGAGAA	NM_002479:	NM_002479:
4656	MYOG	myogenin (myogenic factor 4)	-1.28	CCAACTGAGATTGTCTTCCAA	NM_002479:	NM_002479:
11143	MYST2	MYST histone acetyltransferase 2	-2.46	ACAGCTGATCATGATGAGTCA	NM_007067:	NM_007067:
11143	MYST2	MYST histone acetyltransferase 2	0.73	CAGAAAGAGAAATATATGGAA	NM_007067:	NM_007067:
7994	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	-5.22	CAGCTGAATTTGCGACCTGTA	NM_006766:	NM_006766:
7994	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	-1.21	CTGGACTTCCGTAGTGACCAA	NM_006766:	NM_006766:
23522	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	-0.25	ACGGAACATGGCTGCATCAAA	NM_012330:	NM_012330:
23522	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	-0.70	CAGCAGTTAACTAATACACTT	NM_012330:	NM_012330:
10003	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	0.93	ACGGTGGAAACTGGTATCCGA	NM_005467:	NM_005467:
10003	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	0.67	AAGAAACATGATCAACAATTA	NM_005467:	NM_005467:
4666	NACA	nascent-polypeptide-associated complex alpha polypeptide	-8.12	CTGCTTCACAGGATCCAGAAA	NM_005594:	NM_005594:
65220	NADK	NAD kinase	-0.53	AAAGAGCGTCCTTGTCATCAA	NM_023018:	NM_023018:
65220	NADK	NAD kinase	0.55	CCAGGAGAACATGATCGTGTA	NM_023018:	NM_023018:
64753	NAG6	hypothetical protein DKFZp434G156	-0.01	CAGAGGAAATTAGATGGACTA	NM_022742:	NM_022742:
64753	NAG6	hypothetical protein DKFZp434G156	-0.35	CAGGAGCTACTCACCAAGTTA	NM_022742:	NM_022742:
4668	NAGA	N-acetylgalactosaminidase, alpha-	-2.76	ATGGTAGAGAGTGAACCTCCA	NM_000262:	NM_000262:
4668	NAGA	N-acetylgalactosaminidase, alpha-	-0.08	CAGGACATTTATTCCCTTCTA	NM_000262:	NM_000262:
55577	NAGK	N-acetylglucosamine kinase	-0.01	ACCTGAGTGAAAGCTACTTAA	NM_017567:	NM_017567:
55577	NAGK	N-acetylglucosamine kinase	-0.26	CCCGGTCTTGTTCCAGGGCAA	NM_017567:	NM_017567:
4669	NAGLU	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)	0.01	CAAGAAGATCTTCCTCAAATA	NM_000263:	NM_000263:
4669	NAGLU	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)	-0.57	CAGCCAGAACGAAGTGGTCTA	NM_000263:	NM_000263:
22861	NALP1	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1	0.02	CAGCTTCTGCTCGCCAATAAA	NM_014922:	NM_014922:NM_033004:NM_001033053:NM_033006:NM_033007:
22861	NALP1	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1	-1.45	GAGGTAAACATTCTAATTGCA	NM_014922:	NM_014922:NM_033004:NM_001033053:NM_033006:NM_033007:
204801	NALP11	NACHT, leucine rich repeat and PYD containing 11	-2.75	CAGCCATGAGAACGTCAAATA	NM_145007:	NM_145007:
204801	NALP11	NACHT, leucine rich repeat and PYD containing 11	-6.87	GCCAGGTTCAATAATACCTAA	NM_145007:	NM_145007:

9476	NAPSA	napsin A aspartic peptidase	-3.07	CCCGGGTGACGCCCAAGTGAA	NM_004851:	NM_004851:
9476	NAPSA	napsin A aspartic peptidase	-1.39	CACCACCGATTTGATCCCAAA	NM_004851:	NM_004851:
256236	NAPSB	napsin B aspartic peptidase pseudogene	-1.54	CAGGATTACGTCATCCAGTTT	XR_000169:	XR_000169:
256236	NAPSB	napsin B aspartic peptidase pseudogene	0.85	CCGGTGCTCAGAAATCCCAAA	XR_000169:	XR_000169:
80155	NARG1	NMDA receptor regulated 1	-1.13	TGGGATAAAGACAATCTTCAA	NM_057175:	NM_057175:
80155	NARG1	NMDA receptor regulated 1	-0.03	AAGAAGCTACGTAATAAACAA	NM_057175:	NM_057175:
79612	NARG1L	NMDA receptor regulated 1-like	0.19	CAGGAATCTTTGGAACATATA	NM_018527:	NM_018527:NM_024561:
79612	NARG1L	NMDA receptor regulated 1-like	2.47	CAAACGCATCTTGAAATGTTA	NM_018527:	NM_018527:NM_024561:
79664	NARG2 (NMD	NMDA receptor regulated 2	-0.12	CAGAGTAGAGATGGGATTAAA	NM_024611:	NM_001018089:NM_024611:
79664	NARG2 (NMD	NMDA receptor regulated 2	-0.32	AGGGATTTGAATCATGTGAAA	NM_024611:	NM_001018089:NM_024611:
4683	NBN	nibrin	1.66	AAGGAAGACTGCCCTACTATA	NM_002485:	NM_001024688:NM_002485:
4683	NBN	nibrin	-0.66	ATGGATATGCTCCAAAGGCAA	NM_002485:	NM_001024688:NM_002485:
4077	NBR1	neighbor of BRCA1 gene 1	0.40	CTGGTGCAGTATCATAGTAGA	NM_005899:	NM_031862:NM_005899:NM_031858:
4077	NBR1	neighbor of BRCA1 gene 1	-1.52	CAGCTTAAACTCCATAGGAAA	NM_005899:	NM_031862:NM_005899:NM_031858:
4684	NCAM1	neural cell adhesion molecule 1	-3.40	CAGCGCGGCCTCCGAGTTCAA	NM_000615:	NM_181351:NM_000615:
4684	NCAM1	neural cell adhesion molecule 1	-0.30	CCGAAACAACGTACGCCGTAA	NM_000615:	NM_181351:NM_000615:
22916	NCBP2	nuclear cap binding protein subunit 2, 20kDa	-0.93	AAGCCTCTGAAAGTTATTAAA	NM_007362:	NM_007362:
22916	NCBP2	nuclear cap binding protein subunit 2, 20kDa	-0.08	CCCGTTAAACTGAGTGTAGAA	NM_007362:	NM_007362:
4688	NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, a	-0.21	CAGTTTGGAAGTGTTAACTAT	NM_000433:	NM_000433:
4688	NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, a	-3.07	CAAGTACACGGTAGTCATGAA	NM_000433:	NM_000433:
4690	NCK1	NCK adaptor protein 1	-1.58	ACAGGCCATTGTAAATACCAA	NM_006153:	NM_006153:
4690	NCK1	NCK adaptor protein 1	-0.78	ACCGTTATGCAGAATAATCCA	NM_006153:	NM_006153:
8440	NCK2	NCK adaptor protein 2	-2.24	TCGGCTTGTTTGAATCTCACA	NM_001004720:	NM_003581:NM_001004720:NM_001004722:
8440	NCK2	NCK adaptor protein 2	0.17	TAGCCGTTTGTTGACACTAAT	NM_001004720:	NM_003581:NM_001004720:NM_001004722:
10787	NCKAP1	NCK-associated protein 1	1.17	GAGGCTATAATAAACGTATTA	NM_013436:	NM_013436:NM_205842:
10787	NCKAP1	NCK-associated protein 1	0.64	TTCACTGAGATTATTCCTATA	NM_013436:	NM_013436:NM_205842:
4691	NCL	nucleolin	-3.52	ATCCGTCTAGTTAACATTTCA	NM_005381:	NM_005381:
4691	NCL	nucleolin	0.76	TTGACTGGATATTCATATAAA	NM_005381:	NM_005381:
8648	NCOA1	nuclear receptor coactivator 1	-1.04	CTCCTAATATTTCGACATTAA	NM_003743:	NM_147223:NM_147233:NM_003743:
8648	NCOA1	nuclear receptor coactivator 1	1.80	CCCAAATTAACGAGTATTATA	NM_003743:	NM_147223:NM_147233:NM_003743:
10499	NCOA2	nuclear receptor coactivator 2	0.01	AGGGCTGTTAACATTAGCAAA	NM_006540:	NM_006540:
10499	NCOA2	nuclear receptor coactivator 2	-2.13	AAGGATTGGCATTCAGTCAAA	NM_006540:	NM_006540:
8202	NCOA3	nuclear receptor coactivator 3	-1.22	AAGGTTGTCAATATAGATACA	NM_006534:	NM_006534:NM_181659:
8202	NCOA3	nuclear receptor coactivator 3	-1.96	CAGGAGGAGATTATAATACTT	NM_006534:	NM_006534:NM_181659:
8031	NCOA4	nuclear receptor coactivator 4	-1.71	ACCGACTAAGCAAATAGGCAA	NM_005437:	NM_005437:
8031	NCOA4	nuclear receptor coactivator 4	-1.96	CTGGTCAATAGTGATTACCAA	NM_005437:	NM_005437:
57727	NCOA5	nuclear receptor coactivator 5	-0.81	CCGCGCTGGTAGCGATATTAA	NM_020967:	NM_020967:
57727	NCOA5	nuclear receptor coactivator 5	0.46	CAGAGGCATTACTGAAGCTAA	NM_020967:	NM_020967:
23054	NCOA6	nuclear receptor coactivator 6	1.12	CAGAATTTAGTCTCAAAGGAA	NM_014071:	NM_014071:
23054	NCOA6	nuclear receptor coactivator 6	2.62	CCACAGATTAATATTCCTTTA	NM_014071:	NM_014071:
96764	NCOA6IP	nuclear receptor coactivator 6 interacting protein	0.06	ATGGAAACTTACAGGACTTAA	NM_024831:	NM_024831:
96764	NCOA6IP	nuclear receptor coactivator 6 interacting protein	0.44	TCGCAATAATGCAGAAGTTTA	NM_024831:	NM_024831:
135112	NCOA7	nuclear receptor coactivator 7	0.54	CCGGAAATCGGCATCACTAGA	NM_181782:	NM_181782:
135112	NCOA7	nuclear receptor coactivator 7	0.11	AACAATTATTATACTCCTTAA	NM_181782:	NM_181782:
9611	NCOR1	nuclear receptor co-repressor 1	0.37	ACCGCAGTATTGTCCAAATTA	NM_006311:	NM_006311:
9611	NCOR1	nuclear receptor co-repressor 1	0.05	AGGCAATTCAGTGGACTATAA	NM_006311:	NM_006311:
9612	NCOR2	nuclear receptor co-repressor 2	0.78	CAGAATGAATTCGATGCGTAT	NM_006312:	NM_006312:
9612	NCOR2 (?	nuclear receptor co-repressor 2	0.69	AACGAGATTGCTGGAAACCAA	NM_006312:	NM_006312:
9437	NCR1	natural cytotoxicity triggering receptor 1	-4.96	AAGCATGTTCTTACTGCTCAA	NM_004829:	NM_004829:
9437	NCR1	natural cytotoxicity triggering receptor 1	0.46	ATGGTTGTATATTCCTAATAA	NM_004829:	NM_004829:
9436	NCR2	natural cytotoxicity triggering receptor 2	1.42	ACACACTTTGTGAATAATAAA	NM_004828:	NM_004828:
9436	NCR2	natural cytotoxicity triggering receptor 2	-0.62	CACGGGCAGTCTCTACGAGAA	NM_004828:	NM_004828:
259197	NCR3	natural cytotoxicity triggering receptor 3	0.16	AACACTGTCATTCACCCAATA	NM_147130:	NM_147130:
259197	NCR3	natural cytotoxicity triggering receptor 3	0.34	ACCGTCTATTACCAGGGCAAA	NM_147130:	NM_147130:
23385	NCSTN	nicastrin	0.13	TCAGATTGGGATTAACATAAA	NM_015331:	NM_015331:
23385	NCSTN	nicastrin	-0.11	AAGGTTTAATGTCAGGGTCAA	NM_015331:	NM_015331:
4692	NDN	necdin homolog (mouse)	1.19	CCACCGTGAGTCAACTTTAAA	NM_002487:	NM_002487:
4692	NDN	necdin homolog (mouse)	0.00	CCCACCGTGAGTCAACTTTAA	NM_002487:	NM_002487:
4693	NDP	Norrie disease (pseudoglioma)	-0.01	CACGGGCATCATTCTCTAATA	NM_000266:	NM_000266:
4693	NDP	Norrie disease (pseudoglioma)	0.76	AGCCAGCGAACTGACATTAAA	NM_000266:	NM_000266:
4724	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coe	1.72	TCCTAATAAATTGGACCTTTA	NM_002495:	NM_002495:
4724	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coe	0.70	ATCTCTTAATCTCCTAATAAA	NM_002495:	NM_002495:
4723	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	-1.41	CCGCCTCATTGAGTTCTATAA	NM_007103:	NM_007103:
4723	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	-0.14	CCGCTCGACGGACATCGTGAA	NM_007103:	NM_007103:
4729	NDUFV2 (NA	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	-31.62	CAGGCCTTTAATTTATATTGA	NM_021074:	NM_021074:
4729	NDUFV2 (NA	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	0.06	CAAGCAGGCCTTTAATTTATA	NM_021074:	NM_021074:
4703	NEB	nebulin	0.56	CCGAAGCTTACACATGATTAA	NM_004543:	NM_004543:
4703	NEB	nebulin	0.50	CCAGATGCTGTTCATATCAAA	NM_004543:	NM_004543:
4734	NEDD4	neural precursor cell expressed, developmentally down-regulated 4	-1.40	ATGGAGTTGATTAGATTACAA	NM_006154:	NM_198400:NM_006154:
4734	NEDD4	neural precursor cell expressed, developmentally down-regulated 4	0.00	CCGGAGAATTATGGGTGTCAA	NM_006154:	NM_198400:NM_006154:
23327	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-lik	0.00	CCCTTACTCCAGAGAATTTAA	NM_015277:	NM_015277:
23327	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-lik	0.73	GCGGTCAAAGACATCTTTAAA	NM_015277:	NM_015277:
4738	NEDD8	neural precursor cell expressed, developmentally down-regulated 8	1.91	CTGGAAAGAAGATGCTAATTA	NM_006156:	NM_006156:
4738	NEDD8	neural precursor cell expressed, developmentally down-regulated 8	-0.90	ATGCCCAGTAATGTATGTCTA	NM_006156:	NM_006156:
4744	NEFH	neurofilament, heavy polypeptide 200kDa	-0.56	AAGGATCAGAGTAACACAATT	NM_021076:	NM_021076:
4744	NEFH	neurofilament, heavy polypeptide 200kDa	0.32	AAGGAAGACGCTAAACCCAAA	NM_021076:	NM_021076:
4747	NEFL	neurofilament, light polypeptide 68kDa	2.20	AAAGAGTGAAATGGCACGATA	NM_006158:	NM_006158:
4747	NEFL	neurofilament, light polypeptide 68kDa	0.48	CAGGACACGATCAACAAATTA	NM_006158:	NM_006158:
79661	NEIL1	nei endonuclease VIII-like 1 (E. coli)	0.05	ATGATGTTTGTTTATGAGTTA	NM_024608:	NM_024608:
79661	NEIL1	nei endonuclease VIII-like 1 (E. coli)	0.84	CGACTGTTCGTTGGTGCTTAA	NM_024608:	NM_024608:
252969	NEIL2	nei like 2 (E. coli)	0.07	ACCCAGGTCCATGGAAAGAAA	NM_145043:	NM_145043:
252969	NEIL2	nei like 2 (E. coli)	0.42	CAGCGTTTGGGTGAACGATTT	NM_145043:	NM_145043:
55247	NEIL3	nei endonuclease VIII-like 3 (E. coli)	-0.70	ACGGATTCATTTCGGAATGAA	NM_018248:	NM_018248:
55247	NEIL3	nei endonuclease VIII-like 3 (E. coli)	-0.57	CCTGGATATTCTAACAGTGAA	NM_018248:	NM_018248:
4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1	0.27	ACCGTAGGAGATGTTCGTCAA	NM_012224:	NM_012224:
4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1	-0.01	TAGGGATAGACCATCAGTCAA	NM_012224:	NM_012224:
152110	NEK10	NIMA (never in mitosis gene a)- related kinase 10	0.25	ATGGTAGTACTTACTAGATCA	NM_152534:	NM_152534:
152110	NEK10	NIMA (never in mitosis gene a)- related kinase 10	0.34	CCGGAACACCGTCACATGTCA	NM_152534:	NM_152534:NM_001031741:
79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11	-1.94	CTGCCTATGCTTGGAGTCATA	NM_024800:	NM_024800:
79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11	1.04	TGAGATAAGCTTATAGATCAA	NM_024800:	NM_024800:
4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2	1.14	AACATGAGATGTGACATTCTA	NM_002497:	NM_002497:
4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2	2.45	CAGGCGAATTCCATACCGTTA	NM_002497:	NM_002497:
4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3	-0.73	ACGATAGAGGTGGTTCTGTAA	NM_002498:	NM_002498:NM_152720:
4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3	-0.13	CAGAGATATCAAGTCCAAGAA	NM_002498:	NM_002498:NM_152720:
6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4	-0.01	CACAATCAGTAGCGTAAATAT	NM_003157:	NM_003157:
6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4	-0.73	CAGACATATATAATGGGTGAA	NM_003157:	NM_003157:
341676	NEK5	NIMA (never in mitosis gene a)-related kinase 5	-1.20	CTCGAGACCGACCATCCATAA	XM_292160:	NM_199289:
341676	NEK5	NIMA (never in mitosis gene a)-related kinase 5	-3.39	CAGGCTGTTTATTGTAATGGA	XM_292160:	NM_199289:
10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6	-0.73	ACCACGGAAGTCGAGAATTAA	NM_014397:	NM_014397:

10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6	-0.46	ACCGGAGAGGATCCATGAGAA	NM_014397:	NM_014397:
140609	NEK7 (NIMA	NIMA (never in mitosis gene a)-related kinase 7	-4.91	ACGACCGGATATGGGCTATAA	NM_133494:	NM_133494:
140609	NEK7 (NIMA	NIMA (never in mitosis gene a)-related kinase 7	-45.65	CCGGATATGGGCTATAATACA	NM_133494:	NM_133494:
284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8	-4.94	ACGGACAGTTGGGCACCAATA	NM_178170:	NM_178170:
284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8	-3.78	CCAGAAGCTGGTGATCATCAA	NM_178170:	NM_178170:
91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9	1.35	CACGAACCAGTGAAGTCTATA	NM_033116:	NM_033116:
91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9	-6.88	TACACTTGGGTGAACATGCAA	NM_033116:	NM_033116:
26012	NELF	nasal embryonic LHRH factor	-0.55	ACCCTCATAGTGACCATTAAA	NM_015537:	NM_015537:
26012	NELF	nasal embryonic LHRH factor	0.82	ACGATGTACGATACCCTCATA	NM_015537:	NM_015537:
29937	NENF	neuron derived neurotrophic factor	0.24	ACCAAAGTGTACAAAGCCAAA	NM_013349:	NM_013349:
29937	NENF	neuron derived neurotrophic factor	0.63	CATGACCATGTTCACTTTATA	NM_013349:	NM_013349:
4756	NEO1	neogenin homolog 1 (chicken)	0.04	CAGCGCTATTACACCATTGAA	NM_002499:	NM_002499:
4756	NEO1	neogenin homolog 1 (chicken)	-1.09	CAGGATTACGTGGGCAGACAA	NM_002499:	NM_002499:
10276	NET1	neuroepithelial cell transforming gene 1	0.42	CTGGAGGATGCTATATTGATA	NM_005863:	NM_005863:
10276	NET1	neuroepithelial cell transforming gene 1	0.25	TCGGTGTGGATTGATTGGAAA	NM_005863:	NM_005863:
81832	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	1.50	CAGGCTGTCCAGACACGATAA	NM_138966:	NM_153181:NM_138966:
81832	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	-2.35	CCGGGAATGCATCTACATCAT	NM_138966:	NM_138999:NM_153181:NM_138966:
81831	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	0.30	CAGGCAGTCTATATATGTTAA	NM_018092:	NM_018092:
81831	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	0.53	AAGACCTTGATTTACCGTTAA	NM_018092:	NM_018092:
4758	NEU1	sialidase 1 (lysosomal sialidase)	-0.11	ACCACCATGACTGACTATCAA	NM_000434:	NM_000434:
4758	NEU1	sialidase 1 (lysosomal sialidase)	-1.10	CAGGTCTAGTGAGCTGTAGAA	NM_000434:	NM_000434:
9148	NEURL	neuralized-like (Drosophila)	0.50	GTCGCTGTGATTGTGAATAAA	NM_004210:	NM_004210:
9148	NEURL	neuralized-like (Drosophila)	0.03	TTGGGTCGCTGTGATTGTGAA	NM_004210:	NM_004210:
140825	NEURL2	neuralized-like 2 (Drosophila)	0.18	AACCCTCCTCGTGGAACCATA	NM_080749:	NM_080749:
140825	NEURL2	neuralized-like 2 (Drosophila)	0.28	AAGTGATACAAAGGAGCATGG	NM_080749:	NM_080749:
4760	NEUROD1	neurogenic differentiation 1	-1.87	CCCATGGTGGGTTGTCATATA	NM_002500:	NM_002500:
4760	NEUROD1	neurogenic differentiation 1	0.20	CAAGCTTGTATATACATATTA	NM_002500:	NM_002500:
4761	NEUROD2	neurogenic differentiation 2	-2.14	CAAGACAATTTGTAACTAGAA	NM_006160:	NM_006160:
4761	NEUROD2	neurogenic differentiation 2	1.01	CTCGGAGAATCTCTTGTCTTA	NM_006160:	NM_006160:
58158	NEUROD4	neurogenic differentiation 4	0.26	CACGAGGATAAATCTCCTATT	NM_021191:	NM_021191:
58158	NEUROD4	neurogenic differentiation 4	-3.40	CAGGTACTTATGGGATGCTCA	NM_021191:	NM_021191:
63974	NEUROD6	neurogenic differentiation 6	0.02	CAGGTTTGTTATCACAATGTA	NM_022728:	NM_022728:
63974	NEUROD6	neurogenic differentiation 6	-1.84	TTGGTAACTATTCCTCTTCAA	NM_022728:	NM_022728:
4762	NEUROG1	neurogenin 1	1.30	CAGACGCTTCATGTAAATAAA	NM_006161:	NM_006161:
4762	NEUROG1	neurogenin 1	-0.14	CAGGGCTGGAGAGTACTTTAA	NM_006161:	NM_006161:
91624	NEXN	nexilin (F actin binding protein)	1.86	ATGGAGAAGACTATCAATATA	NM_144573:	NM_144573:
91624	NEXN	nexilin (F actin binding protein)	0.05	CTCCATTTACTCACAAAGTGA	NM_144573:	NM_144573:
4763	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Wa	-1.69	CAGGTGGCTTGGGATCAATAA	NM_000267:	NM_000267:
4763	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Wa	-0.25	TACAGTAATAGCACTAACCAA	NM_000267:	NM_000267:
4771	NF2	neurofibromin 2 (bilateral acoustic neuroma)	-1.40	CACCGTGAGGATCGTCACCAT	NM_000268:	NM_181826:NM_000268:NM_016418:NM_181835:NM_181833:NM_181827:NM_181831:NM_181832:NM_181829:NM_181825:NM_181834:NM_181830:NM_181828:
4771	NF2	neurofibromin 2 (bilateral acoustic neuroma)	-0.68	CCGGGTCGCGCCTGCACCGAA	NM_000268:	NM_181826:NM_000268:NM_016418:NM_181835:NM_181833:NM_181827:NM_181831:NM_181832:NM_181829:NM_181825:NM_181834:NM_181830:NM_181828:
10725	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	-1.56	CAGCTGGTGCTTTGAATGTAA	NM_006599:	NM_138713:NM_138714:NM_173214:NM_173215:NM_006599:
10725	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	-0.97	CAGGAGTGCCAGAAATCTTAA	NM_006599:	NM_138713:NM_138714:NM_173214:NM_173215:NM_006599:
4772	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	0.77	CACGGAAAGAAACAACCTGAA	NM_006162:	NM_172387:NM_172389:NM_172388:NM_006162:
4772	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	0.36	AAGCATGGTTTATTCATTGAA	NM_006162:	NM_172387:NM_172389:NM_172388:NM_006162:
4773	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	0.09	CTGCCCATGGTTGAAAGACAA	NM_012340:	NM_173091:NM_012340:
4773	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	-0.86	CTGGTCTATGGCGGCCAGCAA	NM_012340:	NM_173091:NM_012340:
4775	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	0.09	TTGGATCTCAGTATCCTTTAA	NM_004555:	NM_004555:NM_173163:NM_173164:NM_173165:
4775	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	1.82	TGGGATATCATTGTTCAAATA	NM_004555:	NM_004555:NM_173163:NM_173164:NM_173165:
4776	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	1.19	AAACAGCTTATTACAATTCAA	NM_004554:	NM_004554:
4776	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	-3.89	CAGCAGCAAAGTGCCAGCCAA	NM_004554:	NM_004554:
4781	NFIB	nuclear factor I/B	0.31	ACAGAGGGCAAGTGCAATTTA	NM_005596:	NM_005596:
4781	NFIB	nuclear factor I/B	-1.65	AAGGTTAAACTGTAATGACAT	NM_005596:	NM_005596:
4790	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p	-2.79	CTGGGTATACTTCATGTGACA	NM_003998:	NM_003998:
4790	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p	1.51	GACGCCATCTATGACAGTAAA	NM_003998:	NM_003998:
4792	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhi	-2.59	AAGGGTGTACTTATATCCACA	NM_020529:	NM_020529:
4792	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhi	0.21	CTGAAAGAACATGGACTTGTA	NM_020529:	NM_020529:
4794	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhi	-0.50	CTGAGTGAGAAGAGACTGAAA	NM_004556:	NM_004556:
4794	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhi	-0.69	CTGGCTGTACATCTGGACCAA	NM_004556:	NM_004556:
64332	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhi	-0.16	TCCGACGTATCCTGAAGGGAA	NM_001005474:	NM_001005474:NM_031419:
64332	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhi	1.00	CACTAAGTCTTTGTAGATAAA	NM_001005474:	NM_001005474:NM_031419:
4799	NFX1	nuclear transcription factor, X-box binding 1	0.70	AACGGTTGTGTGGACGGCATA	NM_002504:	NM_147134:NM_147133:NM_002504:
4799	NFX1	nuclear transcription factor, X-box binding 1	-1.17	CACACAGGTTCTCTAATTGAA	NM_002504:	NM_147134:NM_147133:NM_002504:
4803	NGFB	nerve growth factor, beta polypeptide	3.04	TAAGGACTGCATGGTAATTTA	NM_002506:	NM_002506:
4803	NGFB	nerve growth factor, beta polypeptide	2.33	TGCATGGTAATTTATAGTTTA	NM_002506:	NM_002506:
4804	NGFR	nerve growth factor receptor (TNFR superfamily, member 16)	1.97	AACGTTAAGTGATGAACATTA	NM_002507:	NM_002507:
4804	NGFR	nerve growth factor receptor (TNFR superfamily, member 16)	0.99	ACGTTAAGTGATGAACATTAA	NM_002507:	NM_002507:
27018	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	-5.63	ATGGCAAATATTCACCAGGAA	NM_014380:	NM_014380:NM_206915:
27018	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	-0.77	CTGGGAAAGAATCCCGGGAAA	NM_014380:	NM_014380:
374354	NHLRC2	NHL repeat containing 2	1.17	CTGACTATCACTGTAATTTAA	NM_198514:	NM_198514:
374354	NHLRC2	NHL repeat containing 2	-0.84	AACCAACAATTTCACTACAAA	NM_198514:	NM_198514:
4811	NID1	nidogen 1	-0.30	CCCGGGCAATCTGGTCATTAA	NM_002508:	NM_002508:
4811	NID1	nidogen 1	1.49	ACGGGCGAACCTGCTATGATA	NM_002508:	NM_002508:
22795	NID2 (nidoge	nidogen 2 (osteonidogen)	0.34	CACGTATAATGCTGCCAACAA	NM_007361:	NM_007361:
22795	NID2 (nidoge	nidogen 2 (osteonidogen)	0.74	AAAGCACATGTGATCAATATA	NM_007361:	NM_007361:
10430	NIFIE14	seven transmembrane domain protein	1.30	AACAGTATTTGGAAAGTTAAA	NM_032635:	NM_032635:
10430	NIFIE14	seven transmembrane domain protein	-0.32	CCAGATGAGCATAGACTCCAA	NM_032635:	NM_032635:
123606	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	1.35	CCGATGATCTTCTCTATAATA	NM_144599:	NM_144599:
123606	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	1.04	CTCGATCATGGTGTTAGAATT	NM_144599:	NM_144599:
11188	NISCH	nischarin	-0.90	CTCGTCTTCGATGACGTGCAA	NM_007184:	NM_007184:
11188	NISCH	nischarin	0.55	CACGCTCTTCATTATCTCGGA	NM_007184:	NM_007184:
85407	NKD1 (naked	naked cuticle homolog 1 (Drosophila)	0.23	CACACACGTATTTAAGGACTA	NM_033119:	NM_033119:
85407	NKD1 (naked	naked cuticle homolog 1 (Drosophila)	2.29	CTCGAAATCTCCGAGAAGATA	NM_033119:	NM_033119:
85409	NKD2 (naked	naked cuticle homolog 2 (Drosophila)	-3.45	CACGGAGCGCAGAAACCACTA	NM_033120:	NM_033120:
85409	NKD2 (naked	naked cuticle homolog 2 (Drosophila)	-0.31	CAGCCTCATGCACACCATCTA	NM_033120:	NM_033120:
4820	NKTR	natural killer-tumor recognition sequence	0.30	CACGCTTAAACCGTAGACCAA	NM_005385:	NM_005385:NM_001012651:
4820	NKTR	natural killer-tumor recognition sequence	-0.83	CAGGATTGGCAGTAAGAGATA	NM_005385:	NM_005385:NM_001012651:

26257	NKX2-8	NK2 transcription factor related, locus 8 (Drosophila)	0.01	CTGGCGTTTCGAATACCGAAA	NM_014360:	NM_014360:
26257	NKX2-8	NK2 transcription factor related, locus 8 (Drosophila)	-0.59	TTCCTCGTAGTTCGAGAATAA	NM_014360:	NM_014360:
4824	NKX3-1	NK3 transcription factor related, locus 1 (Drosophila)	-0.54	CCGGAGTACTAGCCAGCACAA	NM_006167:	NM_006167:
4824	NKX3-1	NK3 transcription factor related, locus 1 (Drosophila)	0.03	AACTGTGTTTATTGCCTATAA	NM_006167:	NM_006167:
54475	NLE1	notchless homolog 1 (Drosophila)	0.53	CCCAGGTTCTATGACCAAATA	NM_018096:	NM_001014445:NM_018096:
54475	NLE1	notchless homolog 1 (Drosophila)	0.07	AAGGACAAATGCCTCCGGATA	NM_018096:	NM_001014445:NM_018096:
22871	NLGN1	neuroligin 1	0.03	AAGAAACATGACTGTCTCAAA	NM_014932:	NM_014932:
22871	NLGN1	neuroligin 1	0.25	GAGGAATATTATGTGAATATA	NM_014932:	NM_014932:
57555	NLGN2	neuroligin 2	0.88	AAAGATGAAGAGAATATTGTA	NM_020795:	NM_020795:
57555	NLGN2	neuroligin 2	-1.99	CCCGACAATCCCTTATCCCTA	NM_020795:	NM_020795:
54413	NLGN3	neuroligin 3	0.49	ATGGAGTTTGTCCTTTGTAAA	NM_018977:	NM_018977:
54413	NLGN3	neuroligin 3	0.12	ACGCAGATGAGTCCTCGGTAA	NM_018977:	NM_018977:
57502	NLGN4X	neuroligin 4, X-linked	0.92	ATGGCCGGACACATATGTATA	NM_020742:	NM_020742:NM_181332:
57502	NLGN4X	neuroligin 4, X-linked	0.65	ACGGTGAATATTATAGAAGAA	NM_020742:	NM_020742:NM_181332:
22829	NLGN4Y	neuroligin 4, Y-linked	0.69	AAGCAATTCTCTATATATAAA	NM_014893:	NM_014893:
22829	NLGN4Y	neuroligin 4, Y-linked	0.02	TCACCAAATAATAAATATTAA	NM_014893:	NM_014893:
51701	NLK	nemo-like kinase	-0.82	CCGGATAGACCTATTGGATAT	NM_016231:	NM_016231:
51701	NLK	nemo-like kinase	-0.36	TTGGTGTTGTCTGGTCAGTAA	NM_016231:	NM_016231:
57486	NLN	neurolysin (metallopeptidase M3 family)	0.37	ACCCACTAGAAAGTAATTGTA	NM_020726:	NM_020726:
57486	NLN	neurolysin (metallopeptidase M3 family)	0.12	TTGGGACTTTCATTTGAACAA	NM_020726:	NM_020726:
	NM_001469		-1.25	GAGGGTTAGCGTTAGCCTTAA	NM_001469	No hits found till 3 mismatches
	NM_003031:		0.69	TGGCATTGGAACTACATTCAA	NM_003031:	XM_058628:
	NM_003616		-1.79	CCGCGCCTAAGGTGTCTATTA	NM_003616	No hits found till 3 mismatches
	NM_004409		1.41	GAGCCTGAGGGCTAAATTTAA	NM_004409	No hits found till 3 mismatches
	NM_005468:		0.56	CTCCGGTGCTTTATATTTACA	NM_005468:	XM_379409:
	NM_012475		-0.05	TCGGCTTAGATCTGAATCGAT	NM_012475	No hits found till 3 mismatches
	NM_014627		0.88	ATGATTATCCACTATTCGGAA	NM_014627	No hits found till 3 mismatches
	NM_017886		0.11	TTACCTGTTACTCTACATTAA	NM_017886	No hits found till 3 mismatches
	NM_030757:		-0.40	ACCGCATGCACTAGTTCTGTA	NM_030757:	XM_295270:
	NM_030906		0.00	CAGGATGGTAATAGGTTAAGA	NM_030906	No hits found till 3 mismatches
	NM_183379:		-2.07	CAGGTGTAATTACCTGTTTGA	NM_183379:	NM_183379:
	NM_183379:		0.06	ACAGGTCACCATCTTAAACAA	NM_183379:	NM_183379:
4829	NMBR (neuro	neuromedin B receptor	-1.36	AGGGACATCGATTAAACCTAA	NM_002511:	NM_002511:
4829	NMBR (neuro	neuromedin B receptor	0.76	CCCGCGGACAGTAAACTTGCA	NM_002511:	NM_002511:
4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	-0.32	CAAGTTGGCAGGAACATTATA	NM_000269:	NM_198175:NM_000269:
4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	1.87	TAGGATTCATTGAGTTGGTTA	NM_000269:	NM_198175:NM_000269:
4832	NME3	non-metastatic cells 3, protein expressed in	-2.73	ACGCACCTTCCTGGCCGTGAA	NM_002513:	NM_002513:
4832	NME3	non-metastatic cells 3, protein expressed in	-6.69	CTGCATCGAGGTTGGCAAGAA	NM_002513:	NM_002513:
4833	NME4	non-metastatic cells 4, protein expressed in	-1.78	ACCAACTACCTCCGTCAGCAA	NM_005009:	NM_005009:
4833	NME4	non-metastatic cells 4, protein expressed in	-0.84	CAGCACATGGGTGGTACACTA	NM_005009:	NM_005009:
8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate	0.83	ATGATATTAGCTAGACATAAA	NM_003551:	NM_003551:
8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate	0.02	CATGATATTAGCTAGACATAA	NM_003551:	NM_003551:
10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate	-0.34	CAGACTTCTCCTAGACATCTA	NM_005793:	NM_005793:
10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate	0.91	CAGGATCTAGCCTTCTATCTA	NM_005793:	NM_005793:
29922	NME7 (non-m	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate	-2.93	CCCGGCATTTACGCCCTGGAA	NM_013330:	NM_013330:NM_197972:
29922	NME7 (non-m	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate	-0.03	TTCATGTAGATCACCAGTCAA	NM_013330:	NM_013330:NM_197972:
9111	NMI (N-myc (	N-myc (and STAT) interactor	0.00	ACCCGGATTACTGTAAATGTT	NM_004688:	NM_004688:
9111	NMI (N-myc (	N-myc (and STAT) interactor	0.82	TACCCTCTTTATATAAATCAA	NM_004688:	NM_004688:
4836	NMT1	N-myristoyltransferase 1	0.30	ATGGAGTTAACGGGTGAATAA	NM_021079:	NM_021079:
4836	NMT1	N-myristoyltransferase 1	-1.00	CACGTGAGAATCCCTGGCAAA	NM_021079:	NM_021079:
9397	NMT2 (N-myr	N-myristoyltransferase 2	0.12	CAGGGCATTGATAGTTTGAAT	NM_004808:	NM_004808:
9397	NMT2 (N-myr	N-myristoyltransferase 2	-0.70	TAGAAGTTACAGAGTCATGTA	NM_004808:	NM_004808:
10874	NMU (neurom	neuromedin U	-0.90	GAGCAATGCTATGGAATACAA	NM_006681:	NM_006681:
10874	NMU (neurom	neuromedin U	-1.32	CAGAGTGGACGAAGAATTCCA	NM_006681:	NM_006681:
10316	NMUR1	neuromedin U receptor 1	1.10	ACCATCAAGCATATCAGTCTA	NM_006056:	NM_006056:
10316	NMUR1	neuromedin U receptor 1	0.52	CTGCCTGGCCTCAGTGCTCAA	NM_006056:	NM_006056:
56923	NMUR2	neuromedin U receptor 2	0.54	CGCAATAAACTTGATTATTAT	NM_020167:	NM_020167:
56923	NMUR2	neuromedin U receptor 2	0.30	TCGCAATAAACTTGATTATTA	NM_020167:	NM_020167:
197358	NOD3	NOD3 protein	0.01	CAGGATGATCTCAGAGGCCAT	NM_178844:	NM_178844:
197358	NOD3	NOD3 protein	0.03	CTCCGGAGACTCAATCTTCAA	NM_178844:	NM_178844:
4838	NODAL	nodal homolog (mouse)	-0.87	AAGGATCACTGTATAGATTAA	NM_018055:	NM_018055:
4838	NODAL	nodal homolog (mouse)	1.20	AAGATTAAGGATCACTGTATA	NM_018055:	NM_018055:
9241	NOG	noggin	1.94	AAGGTCAGTATTATACGTTAA	NM_005450:	NM_005450:
9241	NOG	noggin	0.43	TTCCTGTAATGCACTGTTTAA	NM_005450:	NM_005450:
65083	NOL6	nucleolar protein family 6 (RNA-associated)	-1.98	CAGGAGATCCATCCACCTATT	NM_022917:	NM_022917:NM_139235:
65083	NOL6	nucleolar protein family 6 (RNA-associated)	-0.26	CCGGCCGCCCTTGGACATTTA	NM_022917:	NM_022917:
4841	NONO	non-POU domain containing, octamer-binding	-0.08	CCAAGTGGACCGCAACATCAA	NM_007363:	NM_007363:
4841	NONO	non-POU domain containing, octamer-binding	-3.33	CTGTGTTTGATTTGTCTCATA	NM_007363:	NM_007363:
4842	NOS1	nitric oxide synthase 1 (neuronal)	-1.83	CAGAGAATAGTTCACATCTAT	NM_000620:	NM_000620:
4842	NOS1	nitric oxide synthase 1 (neuronal)	1.62	CAGCGGCAATTTGATATCCAA	NM_000620:	NM_000620:
4843	NOS2A	nitric oxide synthase 2A (inducible, hepatocytes)	-0.54	ATCGAATTTGTCAACCAATAT	NM_000625:	NM_153292:NM_000625:
4843	NOS2A	nitric oxide synthase 2A (inducible, hepatocytes)	-2.55	CTGGGCCGTGCAAACCTTCAA	NM_000625:	NM_153292:NM_000625:
4846	NOS3	nitric oxide synthase 3 (endothelial cell)	1.03	CAGGAAGAAGACCTTTAAAGA	M95296:	NM_000603:
4846	NOS3	nitric oxide synthase 3 (endothelial cell)	0.24	CCGGGACTTCATCAACCAGTA	M95296:	NM_000603:
4851	NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	-0.05	GCGGATTAATTTGCATCTGAA	NM_017617:	NM_017617:
4851	NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	1.49	CGGCATGGTGCCGAACCAATA	NM_017617:	NM_017617:
4853	NOTCH2	Notch homolog 2 (Drosophila)	0.37	CTGACTAAACGTAGTAAGGAA	NM_024408:	NM_024408:
4853	NOTCH2	Notch homolog 2 (Drosophila)	-1.21	AAGGGAAGGTAAGATGGATAA	NM_024408:	NM_024408:
4854	NOTCH3	Notch homolog 3 (Drosophila)	0.21	AAGGAATAGTTAACACTCAAA	NM_000435:	NM_000435:
4854	NOTCH3	Notch homolog 3 (Drosophila)	-2.16	CACTCTGACATGAATGAATTA	NM_000435:	NM_000435:
4855	NOTCH4	Notch homolog 4 (Drosophila)	-0.42	TCGCTATTTAAGAACCCTAAA	NM_004557:	NM_004557:
4855	NOTCH4	Notch homolog 4 (Drosophila)	-4.21	CAGATATGTAAGGACCAGAAA	NM_004557:	NM_004557:
27035	NOX1	NADPH oxidase 1	-1.33	TCCAGTGTGAACAGCAATTTA	NM_007052:	NM_007052:NM_013954:
27035	NOX1	NADPH oxidase 1	-0.40	CAGGTTTGAGCAGTCACTTTA	NM_007052:	NM_007052:NM_013955:
50507	NOX4	NADPH oxidase 4	1.35	TCCATTTGCATCAATACTCAA	NM_016931:	NM_016931:
50507	NOX4	NADPH oxidase 4	-1.26	AACCAGGAGATTGTTGGATAA	NM_016931:	NM_016931:
4860	NP	nucleoside phosphorylase	-0.09	TAGGTTGTAGCAGAAAGGAAA	NM_000270:	NM_000270:
4860	NP	nucleoside phosphorylase	-0.95	AAGGTCATCATGGATTATGAA	NM_000270:	NM_000270:
4861	NPAS1	neuronal PAS domain protein 1	0.46	GCCCGTAGCCCTGAGAATTAA	NM_002517:	NM_002517:
4861	NPAS1	neuronal PAS domain protein 1	-7.13	CAGCGTCTTCGACTACATTCA	NM_002517:	NM_002517:
4862	NPAS2	neuronal PAS domain protein 2	0.29	TCGGGACACAATCAGCTTTAA	NM_002518:	NM_002518:
4862	NPAS2	neuronal PAS domain protein 2	-1.28	CAGGACGGGACGGCAAGTCAA	NM_002518:	NM_002518:
64067	NPAS3	neuronal PAS domain protein 3	-1.37	ACCCATCAATTTCGACAATGA	NM_022123:	NM_022123:NM_173159:
64067	NPAS3	neuronal PAS domain protein 3	0.64	CGCGTGTGACAACGACATGAA	NM_022123:	NM_022123:NM_173159:
266743	NPAS4	neuronal PAS domain protein 4	0.70	TTGAATAAGTCTGTGACTTAA	NM_178864:	NM_178864:
266743	NPAS4	neuronal PAS domain protein 4	-5.59	ACCCATTACTGCCAATAACTA	NM_178864:	NM_178864:
2831	NPBWR1	neuropeptides B/W receptor 1	-1.11	CACGCTGGTGCTGCCCATCAA	NM_005285:	NM_005285:
2831	NPBWR1	neuropeptides B/W receptor 1	-0.80	CCGCATGAAGACCGTCACCAA	NM_005285:	NM_005285:
2832	NPBWR2	neuropeptides B/W receptor 2	-0.04	GACCAACGTGTTCATCCTGAA	NM_005286:	NM_005286:

2832	NPBWR2	neuropeptides B/W receptor 2	0.49	GCCGTCATCCTTGTAATCCTA	NM_005286:	NM_005286:
4864	NPC1	Niemann-Pick disease, type C1	-0.40	CCAGTTAGATGTGGCATGAAA	NM_000271:	NM_000271:
4864	NPC1	Niemann-Pick disease, type C1	1.09	CTGGACAACTATACCCGAATA	NM_000271:	NM_000271:
29881	NPC1L1 (NP	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	-2.60	CCGAGTGATGGTGGACTCCAA	NM_013389:	NM_013389:
29881	NPC1L1 (NP	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	-6.33	AAGCCTCATGACACTCTCCAA	NM_013389:	NM_013389:
10577	NPC2	Niemann-Pick disease, type C2	0.45	CAGATCGTTTCTCATCTCTAA	NM_006432:	NM_006432:
10577	NPC2	Niemann-Pick disease, type C2	-5.28	AAGGACAGTCTTACAGCGTCA	NM_006432:	NM_006432:
79716	NPEPL1	aminopeptidase-like 1	-0.17	CAGAATTCACTTGAGGTTCAA	NM_024663:	NM_024663:
79716	NPEPL1	aminopeptidase-like 1	-0.23	CTGATTTATAGGGCAAGAGAA	NM_024663:	NM_024663:
9520	NPEPPS	aminopeptidase puromycin sensitive	-0.10	CTGGGAATGGTTAAACACAAA	NM_006310:	NM_006310:
9520	NPEPPS	aminopeptidase puromycin sensitive	0.28	GAGGGATTTGCAGTTGATAAA	NM_006310:	NM_006310:
8620	NPFF	neuropeptide FF-amide peptide precursor	-1.90	CAGGGATCCTGGAGGAATGAA	NM_003717:	NM_003717:
8620	NPFF	neuropeptide FF-amide peptide precursor	-0.56	CCCAGAGGTTTGGCAGAAATA	NM_003717:	NM_003717:
64106	NPFFR1	neuropeptide FF receptor 1	-4.82	CTGGTGGCCATTGCTGTGGAA	NM_022146:	NM_022146:
64106	NPFFR1	neuropeptide FF receptor 1	-2.06	CTGTTTCATCGTGCTCAAGAA	NM_022146:	NM_022146:
10886	NPFFR2	neuropeptide FF receptor 2	1.13	CCGGGAAGACTGGCCAAATCA	NM_004885:	NM_004885:NM_053036:
10886	NPFFR2	neuropeptide FF receptor 2	-0.63	CTGGCCATAAGTGATTTACTA	NM_004885:	NM_004885:NM_053036:
4867	NPHP1	nephronophthisis 1 (juvenile)	-0.06	CAGTAAAGATACCATGTATAA	NM_000272:	NM_000272:
4867	NPHP1	nephronophthisis 1 (juvenile)	0.04	CTCCACGATTACGTGAATAAA	NM_000272:	NM_000272:
4868	NPHS1	nephrosis 1, congenital, Finnish type (nephrin)	0.68	CTGGTTAGGTGAGCTCCATAA	NM_004646:	NM_004646:
4868	NPHS1	nephrosis 1, congenital, Finnish type (nephrin)	0.95	TCGGACCAAACCAACATTCAA	NM_004646:	NM_004646:
4869	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.42	CCGACAAAGATTATCACTTTA	NM_002520:	NM_002520:NM_001037738:NM_199185:
4869	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.42	TACGAAGGCAGTCCAATTAAA	NM_002520:	NM_002520:NM_001037738:NM_199185:
255743	NPNT	nephronectin	-1.17	CTGGCTTAGACTAGAGTATAA	NM_198278:	NM_001033047:
255743	NPNT	nephronectin	-0.77	CTCATGTATATTGGAGGCAAA	NM_198278:	NM_001033047:
4879	NPPB	natriuretic peptide precursor B	-0.49	TCCACGGTGAAATAAAGTCAA	NM_002521:	NM_002521:
4879	NPPB	natriuretic peptide precursor B	0.06	AAGATGGTTTCTTACCTTTGA	NM_002521:	NM_002521:
4881	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic pep	-3.83	AACGCATTGAGCTGACACGAA	NM_000906:	NM_000906:
4881	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic pep	-0.04	ACGCATTGAGCTGACACGAAA	NM_000906:	NM_000906:
4882	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic pep	-2.74	AAGGATGCCCTAGATGAGCTA	NM_000907:	NM_003995:NM_000907:
4882	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic pep	0.04	CAGGACAATCGCACCCGGGAA	NM_000907:	NM_003995:NM_000907:
4883	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic pep	-5.51	CCGAATTGTAGAGCATACAAA	NM_000908:	NM_000908:
4883	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic pep	0.42	GAGGATTACGTTAACATGTTT	NM_000908:	NM_000908:
27020	NPTN	neuroplastin	-0.60	CAGGTATATACAGCATATAAA	NM_012428:	NM_017455:NM_012428:
27020	NPTN	neuroplastin	-0.78	CTGGTACATAAAGATGAGTAA	NM_012428:	NM_017455:NM_012428:
23467	NPTXR	neuronal pentraxin receptor	-0.39	AAGAGAGTGTCAGAATCTTAA	NM_014293:	NM_014293:NM_058178:
23467	NPTXR	neuronal pentraxin receptor	-0.61	AACCTCATGCATGGATTGTAA	NM_014293:	NM_014293:NM_058178:
4852	NPY	neuropeptide Y	-2.88	CAGCCCATATTTCATCGTGTA	NM_000905:	NM_000905:
4852	NPY	neuropeptide Y	0.96	CTGCAATGTGGTGATGGGAAA	NM_000905:	NM_000905:
4886	NPY1R	neuropeptide Y receptor Y1	-3.14	ACGACATCAGCTGATAATCAA	NM_000909:	NM_000909:
4886	NPY1R	neuropeptide Y receptor Y1	-0.34	TCCCAACTGATTGTCACTTAA	NM_000909:	NM_000909:
4887	NPY2R (neur	neuropeptide Y receptor Y2	-8.06	CCGGGAGTATTCGCTGATTGA	NM_000910:	NM_000910:
4887	NPY2R (neur	neuropeptide Y receptor Y2	0.01	TAGAATCCAATTAATGATTCA	NM_000910:	NM_000910:
4889	NPY5R	neuropeptide Y receptor Y5	0.08	CACAGTCTTGTGGAACTTCAA	NM_006174:	NM_006174:
4889	NPY5R	neuropeptide Y receptor Y5	1.31	TTGGGCTCTATACATTTGTAA	NM_006174:	NM_006174:
1728	NQO1	NAD(P)H dehydrogenase, quinone 1	0.75	AAGATCTAATTAAATAAATAA	NM_000903:	NM_000903:NM_001025433:NM_001025434:
1728	NQO1	NAD(P)H dehydrogenase, quinone 1	0.59	TCCACTGTTGGTATTATATAA	NM_000903:	NM_000903:NM_001025433:NM_001025434:
190	NR0B1	nuclear receptor subfamily 0, group B, member 1	-1.45	ATGCTCTGTACAAAGATATAA	NM_000475:	NM_000475:
190	NR0B1	nuclear receptor subfamily 0, group B, member 1	-2.81	ATGGATGATATGATGCTGGAA	NM_000475:	NM_000475:
8431	NR0B2	nuclear receptor subfamily 0, group B, member 2	0.97	AAGGAATATGCCTGCCTGAAA	NM_021969:	NM_021969:
8431	NR0B2	nuclear receptor subfamily 0, group B, member 2	0.14	TCCTATCGACTTTATACAGAA	NM_021969:	NM_021969:
9572	NR1D1	nuclear receptor subfamily 1, group D, member 1	-3.03	CAGCGTCATAACGAGGCCCTA	NM_021724:	NM_021724:
9572	NR1D1	nuclear receptor subfamily 1, group D, member 1	-1.18	TGGCATGGTGTTACTGTGTAA	NM_021724:	NM_021724:
9975	NR1D2	nuclear receptor subfamily 1, group D, member 2	-0.48	CAGCATCTGTTTATGGTATTA	NM_005126:	NM_005126:
9975	NR1D2	nuclear receptor subfamily 1, group D, member 2	0.76	TACACACGTATTCAAAGTTTA	NM_005126:	NM_005126:
7376	NR1H2	nuclear receptor subfamily 1, group H, member 2	-3.98	CTGGGCGAGCCTGTAGACCTA	NM_007121:	NM_007121:
7376	NR1H2	nuclear receptor subfamily 1, group H, member 2	-0.35	ATCGTGGACTTCGCTAAGCAA	NM_007121:	NM_007121:
10062	NR1H3	nuclear receptor subfamily 1, group H, member 3	0.28	CATGAATGAGCTGCAACTCAA	NM_005693:	NM_005693:
10062	NR1H3	nuclear receptor subfamily 1, group H, member 3	0.77	GAGATAGTTGACTTTGCTAAA	NM_005693:	NM_005693:
9971	NR1H4	nuclear receptor subfamily 1, group H, member 4	2.41	CTCATATTAATCTGATGTATA	NM_005123:	NM_005123:
9971	NR1H4	nuclear receptor subfamily 1, group H, member 4	0.85	TCCAGATAGACAATACATAAA	NM_005123:	NM_005123:
8856	NR1I2	nuclear receptor subfamily 1, group I, member 2	0.33	CAGGAGGGCCATGAAACGCAA	NM_003889:	NM_033013:NM_003889:NM_022002:
8856	NR1I2	nuclear receptor subfamily 1, group I, member 2	-0.29	AACCTGGAGGTGAGACCCAAA	NM_003889:	NM_033013:NM_003889:NM_022002:
9970	NR1I3	nuclear receptor subfamily 1, group I, member 3	1.01	AACACTTTCATGGTACTGCAA	NM_005122:	NM_005122:
9970	NR1I3	nuclear receptor subfamily 1, group I, member 3	-1.83	CACACACTTCGCAGACATCAA	NM_005122:	NM_005122:
7181	NR2C1	nuclear receptor subfamily 2, group C, member 1	-0.14	TGGGCAGGCAGCAGAAATTAA	NM_003297:	NM_003297:
7181	NR2C1	nuclear receptor subfamily 2, group C, member 1	-1.66	CCTGCAGATTATAACTCTCAA	NM_003297:	NM_003297:
7182	NR2C2	nuclear receptor subfamily 2, group C, member 2	-0.69	TACCTTAGCTAAAGCACTTAA	NM_003298:	NM_003298:
7182	NR2C2	nuclear receptor subfamily 2, group C, member 2	0.11	TCCCAGACAATAGCAATTAAA	NM_003298:	NM_003298:
7101	NR2E1	nuclear receptor subfamily 2, group E, member 1	-2.71	CTCTATACTTATGGAAATGTA	NM_003269:	NM_003269:
7101	NR2E1	nuclear receptor subfamily 2, group E, member 1	-0.41	TCCCGTTAACATAGTGCTGAA	NM_003269:	NM_003269:
10002	NR2E3	nuclear receptor subfamily 2, group E, member 3	1.77	CACAAATGTATTCATACGTAA	NM_014249:	NM_014249:
10002	NR2E3	nuclear receptor subfamily 2, group E, member 3	-2.67	CACGGAGTTTGCCTGCATGAA	NM_014249:	NM_016346:NM_014249:
7025	NR2F1	nuclear receptor subfamily 2, group F, member 1	0.59	TCCGCAGGAACTTAACTTACA	NM_005654:	NM_005654:
7025	NR2F1	nuclear receptor subfamily 2, group F, member 1	-9.67	CCGGCGTGAATTATCCCGTAT	NM_005654:	NM_005654:
7026	NR2F2	nuclear receptor subfamily 2, group F, member 2	-0.81	CCGCTTAGTTCTTGAATTGTT	NM_021005:	NM_021005:
7026	NR2F2	nuclear receptor subfamily 2, group F, member 2	0.03	GTGGAATTTATTGGCAGCCAA	NM_021005:	NM_021005:
2063	NR2F6	nuclear receptor subfamily 2, group F, member 6	-0.37	AAGGCCAATAATAAAGACATT	NM_005234:	NM_005234:
2063	NR2F6	nuclear receptor subfamily 2, group F, member 6	-0.02	ATGACTCAAGGCCAATAATAA	NM_005234:	NM_005234:
2908	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid rece	-0.50	AAGGACGGTCTGAAGAGCCAA	NM_000176:	NM_001018076:NM_001018074:NM_001018075:NM_000176:NM_001018077:NM_001020825:NM_001024094:
2908	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid rece	0.76	GAGGATCATGACTACGCTCAA	NM_000176:	NM_001018076:NM_001018074:NM_001018075:NM_000176:NM_001018077:NM_001020825:NM_001024094:
4306	NR3C2	nuclear receptor subfamily 3, group C, member 2	-1.09	CAACATTACCTTGTCTTTCAA	NM_000901:	NM_000901:
4306	NR3C2	nuclear receptor subfamily 3, group C, member 2	0.27	CAGCAATTAATTAGATCAACA	NM_000901:	NM_000901:
3164	NR4A1	nuclear receptor subfamily 4, group A, member 1	1.13	CTGATTAATATATTTAATATA	NM_002135:	NM_002135:NM_173157:
3164	NR4A1	nuclear receptor subfamily 4, group A, member 1	-0.27	CTCCTTCCACATGTACATAAA	NM_002135:	NM_002135:NM_173157:
4929	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.73	CAGACACTATGTAGTCTGTTA	NM_006186:	NM_173172:NM_173171:NM_173173:NM_006186:
4929	NR4A2	nuclear receptor subfamily 4, group A, member 2	-2.02	CTGGATTTAGAACATGGACTA	NM_006186:	NM_173172:NM_173171:NM_173173:NM_006186:
8013	NR4A3	nuclear receptor subfamily 4, group A, member 3	1.89	AAGAGTCATTCTAATATTTGA	NM_006981:	NM_173200:NM_006981:NM_173198:
8013	NR4A3	nuclear receptor subfamily 4, group A, member 3	-0.08	ATGGCTGTTTGCTTCCATAAA	NM_006981:	NM_173200:NM_006981:NM_173198:
2516	NR5A1	nuclear receptor subfamily 5, group A, member 1	1.33	CTGGAATAAATTTCGCAATTA	NM_004959:	NM_004959:
2516	NR5A1	nuclear receptor subfamily 5, group A, member 1	0.36	AAGGATAACCGAGTTTGCTAA	NM_004959:	NM_004959:
2494	NR5A2	nuclear receptor subfamily 5, group A, member 2	-1.26	ACGACAGGAGCTGATAAGCAA	NM_003822:	NM_205860:NM_003822:
2494	NR5A2	nuclear receptor subfamily 5, group A, member 2	-0.09	ACGCATGTTAATCTATGCAAA	NM_003822:	NM_205860:NM_003822:

2649	NR6A1	nuclear receptor subfamily 6, group A, member 1	0.04	AAGCGGAGCATTTGCAACAAA	NM_001489:	NM_033334:NM_001489:NM_033335:
2649	NR6A1	nuclear receptor subfamily 6, group A, member 1	0.38	GAGGAGTATGCTTGCATGAAA	NM_001489:	NM_033334:NM_001489:NM_033335:
4893	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	-0.23	AACCGCAAACGTGAAATTCTA	NM_002524:	NM_002524:
4893	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	0.18	CTGAGATACGTCTGTGACTTA	NM_002524:	NM_002524:
29982	NRBF2	nuclear receptor binding factor 2	1.47	CAAAGGGATAGCCATATGAAA	NM_030759:	NM_030759:
29982	NRBF2	nuclear receptor binding factor 2	-0.23	CACACTTTGCACTACTCATAA	NM_030759:	NM_030759:
29959	NRBP1	nuclear receptor binding protein 1	0.39	CCGGTTGACTTCTCTGCTAGA	NM_013392:	NM_013392:
29959	NRBP1	nuclear receptor binding protein 1	-11.72	TCGGTGGAGGAGGGAGTCAAA	NM_013392:	NM_013392:
340371	NRBP2	nuclear receptor binding protein 2	1.12	ATCTTAAATATTCCAATACTA	NM_178564:	NM_178564:
340371	NRBP2	nuclear receptor binding protein 2	1.98	AACGCATATCAAATAAATTAA	NM_178564:	NM_178564:
4897	NRCAM	neuronal cell adhesion molecule	-0.48	AGGGTGGTAAATATCCAGTTA	NM_005010:	NM_005010:NM_001037132:
4897	NRCAM	neuronal cell adhesion molecule	0.35	CAGGCCTTCAGTACAAAGTTA	NM_005010:	NM_005010:NM_001037132:
4898	NRD1	nardilysin (N-arginine dibasic convertase)	-1.61	AAGGCTTTCGATTGCCCGGAA	NM_002525:	NM_002525:
4898	NRD1	nardilysin (N-arginine dibasic convertase)	-6.91	CAGGGTGAAGCCACTTCATTA	NM_002525:	NM_002525:
3084	NRG1	neuregulin 1	0.53	TCGAGATACTTGTGCAAGTAA	NM_004495:	NM_004495:
3084	NRG1	neuregulin 1	1.91	TGGGAATGAATTGAATCGAAA	NM_004495:	NM_013957:NM_013964:NM_013958:NM_004495:NM_013956:NM_013962:NM_013961:NM_013960:
9542	NRG2	neuregulin 2	0.48	ACCCGTGGTGGTGGAGGGCAA	NM_013982:	NM_013985:NM_013983:NM_013984:NM_013981:NM_004883:NM_013982:
9542	NRG2	neuregulin 2	-0.58	CCGAGACATTCGCATCAAATA	NM_013982:	NM_013985:NM_013983:NM_013984:NM_013981:NM_004883:NM_013982:
10718	NRG3	neuregulin 3	1.22	CCAACGAAATACATCAATAAA	NM_001010848:	NM_001010848:
10718	NRG3	neuregulin 3	-2.61	ACCGAGGACAGTGCAAGCGAA	NM_001010848:	NM_001010848:
4900	NRGN	neurogranin (protein kinase C substrate, RC3)	-0.53	AAGCCGGACGACGACATTCTA	NM_006176:	NM_006176:
4900	NRGN	neurogranin (protein kinase C substrate, RC3)	1.48	TGGGTTGGAATGTGAACAATA	NM_006176:	NM_006176:
8204	NRIP1	nuclear receptor interacting protein 1	0.16	AACCAACCCAATACTATATTA	NM_003489:	NM_003489:
8204	NRIP1	nuclear receptor interacting protein 1	0.57	AAGCGTGCTAACGATAAAGAA	NM_003489:	NM_003489:
83714	NRIP2	nuclear receptor interacting protein 2	-0.97	CTGCTTCTCCATTGGAATAAA	NM_031474:	NM_031474:
83714	NRIP2	nuclear receptor interacting protein 2	0.08	CAGCCAGAATTCAATACAACA	NM_031474:	NM_031474:
56675	NRIP3	nuclear receptor interacting protein 3	0.65	TACCTATGTCTTAGAATTAGA	NM_020645:	NM_020645:
56675	NRIP3	nuclear receptor interacting protein 3	-1.00	CAGGCTGCCTATATAATCTCA	NM_020645:	NM_020645:
203447	NRK	Nik related kinase	0.74	ATCGAAATGTTAGGTAATCAT	NM_198465:	NM_198465:
203447	NRK	Nik related kinase	1.45	CAGGCTAATGATGTTTGTAAA	NM_198465:	NM_198465:
4901	NRL	neural retina leucine zipper	-0.26	CTAGATAGATTAGGACCTCTA	NM_006177:	NM_006177:
4901	NRL	neural retina leucine zipper	0.82	ATCCAACAACTAGATAGATTA	NM_006177:	NM_006177:
8829	NRP1	neuropilin 1	0.83	ACGGTCATAGACAGCACCATA	NM_003873:	NM_001024628:NM_001024629:NM_003873:
8829	NRP1	neuropilin 1	-1.57	CACGCGATTCATCAGGATCTA	NM_003873:	NM_001024628:NM_001024629:NM_003873:
8828	NRP2	neuropilin 2	-4.24	CAGGCTCTGAAGATTGCTCAA	NM_003872:	NM_201264:NM_201267:NM_201279:NM_003872:NM_201266:NM_018534:
8828	NRP2	neuropilin 2	-0.14	CTCGTGATATTTGTAGGATAA	NM_003872:	NM_201264:NM_201267:NM_201279:NM_003872:NM_201266:NM_018534:
4902	NRTN	neurturin	-0.65	CGCGATAACTGTACTGAGATA	NM_004558:	NM_004558:
4902	NRTN	neurturin	-0.77	TCGGCAGGCGTTCAAAGTCAA	NM_004558:	NM_004558:
9378	NRXN1	neurexin 1	0.52	CTGGGACGACATATATCTTTA	NM_004801:	NM_138735:NM_004801:
9378	NRXN1	neurexin 1	-0.97	AGCCAGGAACTTAGACCTCAA	NM_004801:	NM_004801:
9379	NRXN2	neurexin 2	-0.72	CGCCATAGTAAGCGACGGCAA	NM_015080:	NM_015080:NM_138732:NM_138734:
9379	NRXN2	neurexin 2	-1.68	ACCCGTCAATGGCAAGTTCAA	NM_015080:	NM_015080:NM_138732:
9369	NRXN3	neurexin 3	1.45	ACCAGTGTGCGTGTAACTTTA	NM_138970:	NM_004796:NM_138970:
9369	NRXN3	neurexin 3	0.28	CAGGATTATAAAGAGATATCA	NM_138970:	NM_004796:NM_138970:
64324	NSD1	nuclear receptor binding SET domain protein 1	-0.78	AAGGCGCACTAAACCTCGTAA	NM_022455:	NM_022455:NM_172349:
64324	NSD1	nuclear receptor binding SET domain protein 1	1.23	CAGTGAGAACTCGTTAATAAA	NM_022455:	NM_022455:NM_172349:
8439	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	-0.04	CACGAGTGGATTGATCTAATA	NM_003580:	NM_003580:
8439	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	-0.21	TAGCGTGGTTACTTTCTATAA	NM_003580:	NM_003580:
197370	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	-0.93	AACCTGGTTGATCAACTTAAA	NM_145080:	NM_145080:
197370	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	0.70	CCGGCTTTGCGTCTTCCACAA	NM_145080:	NM_145080:
387338	NSUN4	NOL1/NOP2/Sun domain family, member 4	-0.70	TACGTATGTCTGGCTTGATTA	NM_199044:	NM_199044:
387338	NSUN4	NOL1/NOP2/Sun domain family, member 4	1.00	ATGAACTATAATGATACCTAA	NM_199044:	NM_199044:
221078	NSUN6	NOL1/NOP2/Sun domain family, member 6	-0.34	CAGAAGCAGTTTAATGGATTA	NM_182543:	NM_182543:
221078	NSUN6	NOL1/NOP2/Sun domain family, member 6	0.54	CTCGTCACTATTAATTCGGAA	NM_182543:	NM_182543:
4908	NTF3	neurotrophin 3	-1.70	AACGGGCAACTCTCCCGTCAA	NM_002527:	NM_002527:
4908	NTF3	neurotrophin 3	-2.47	CAAGCAGATGGTGGACGTTAA	NM_002527:	NM_002527:
4909	NTF5	neurotrophin 5 (neurotrophin 4/5)	-0.36	AATGATGATGATATAATAATA	M86528:	NM_006179:
4913	NTHL1	nth endonuclease III-like 1 (E. coli)	0.42	CACGCTGGGCAAGCTCATCTA	NM_002528:	NM_002528:
4913	NTHL1	nth endonuclease III-like 1 (E. coli)	-3.71	CTGGAGGAGCAAGGTGAAATA	NM_002528:	NM_002528:
9423	NTN1	netrin 1	-2.76	CTCGCGGGACATCGCCTGCAA	NM_004822:	NM_004822:
9423	NTN1	netrin 1	0.99	AAGCTGAAGATTAACATGAAA	NM_004822:	NM_004822:
4914	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	-1.40	CACATCATCGAGAACCCACAA	NM_002529:	NM_002529:NM_001012331:NM_001007792:
4914	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	1.32	CACGGAGGCAATCGACTGCAT	NM_002529:	NM_002529:NM_001012331:NM_001007792:
4915	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	1.46	ACCACGAACAGAAGTAATGAA	NM_006180:	NM_001007097:NM_006180:NM_001018064:NM_001018065:NM_001018066:
4915	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	-0.15	CTGACGAGTTTGTCTAGGAAA	NM_006180:	NM_001007097:NM_006180:NM_001018064:NM_001018065:NM_001018066:
4916	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.00	CACGGATAACTTTATCTTGTT	NM_002530:	NM_001012338:NM_001007156:NM_002530:
4916	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	-1.73	CTGGTTGGAGCGAATCTGCTA	NM_002530:	NM_001012338:NM_002530:
4922	NTS	neurotensin	0.18	TTGAGTTGTTTAAACAGTCAA	NM_006183:	NM_006183:
4922	NTS	neurotensin	-0.33	CAGGAAGATATTCTTGATACT	NM_006183:	NM_006183:
4923	NTSR1	neurotensin receptor 1 (high affinity)	-0.86	AAGAAGGTCGCCTAAGCCTAA	NM_002531:	NM_002531:
4923	NTSR1	neurotensin receptor 1 (high affinity)	1.34	CTGGCTTAAGAAGGTCGCCTA	NM_002531:	NM_002531:
23620	NTSR2	neurotensin receptor 2	1.50	CCGGACCTGAATGTAATGCAA	NM_012344:	NM_012344:
23620	NTSR2	neurotensin receptor 2	0.22	TCGTATGGAAGAAGACCTTTA	NM_012344:	NM_012344:
9891	NUAK1	NUAK family, SNF1-like kinase, 1	0.76	CTTGAGTTGATGATCAATTAA	NM_014840:	NM_014840:
9891	NUAK1	NUAK family, SNF1-like kinase, 1	-0.86	TAGGGATTTACTGGCATGGTA	NM_014840:	NM_014840:
81788	NUAK2	NUAK family, SNF1-like kinase, 2	0.12	CCGGTGGCTGTTGATGGTGAA	NM_030952:	NM_030952:
81788	NUAK2	NUAK family, SNF1-like kinase, 2	-0.33	CTGAACGAAGAGGATACTAAA	NM_030952:	NM_030952:
84955	NUDCD1	NudC domain containing 1	0.20	GAGCTAGTAATTGGAGATAAA	NM_032869:	NM_032869:
84955	NUDCD1	NudC domain containing 1	2.20	TCGCATGTTGACCTACGTTAA	NM_032869:	NM_032869:
53343	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2.65	CACGCTGCAGATCCCATTATA	NM_024047:	NM_198038:NM_024047:NM_198039:
53343	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	0.55	ATGGATAATCTTATGCTAGAA	NM_024047:	NM_198038:NM_024047:NM_198039:
9972	NUP153	nucleoporin 153kDa	-2.01	CGCGTTGAAATTGTAATTATA	NM_005124:	NM_005124:
9972	NUP153	nucleoporin 153kDa	0.73	ATGGAACGCGTTGAAATTGTA	NM_005124:	NM_005124:
23636	NUP62	nucleoporin 62kDa	-0.46	ACCGGCTTTGCCTTGAATTTA	NM_016553:	NM_016553:NM_153719:NM_153718:NM_012346:
23636	NUP62	nucleoporin 62kDa	0.24	CGGCTTTGCCTTGAATTTAAA	NM_016553:	NM_016553:NM_153719:NM_153718:NM_012346:
4928	NUP98	nucleoporin 98kDa	-3.01	TGGGACTACTATTAAATTTAA	NM_005387:	NM_139131:NM_016320:NM_005387:NM_139132:
4928	NUP98	nucleoporin 98kDa	-9.93	CAGTGTATTACTGCTATGAAA	NM_005387:	NM_139131:NM_016320:NM_005387:NM_139132:

11097	NUPL2	nucleoporin like 2	0.21	CAGCATCATTGCAACAGATAA	NM_007342:	NM_007342:
11097	NUPL2	nucleoporin like 2	-0.19	CAGCAATAACTTACAGAGTTA	NM_007342:	NM_007342:
64359	NXN	nucleoredoxin	1.24	AAGGTAATGGTTCATATCATA	NM_022463:	NM_022463:
64359	NXN	nucleoredoxin	-0.09	AACCGGCTGTACGGAATCCAA	NM_022463:	NM_022463:
51667	NYREN18	NEDD8 ultimate buster-1	-0.83	ATCCTCAGATGTGGTGGTTAA	NM_016118:	NM_016118:
51667	NYREN18	NEDD8 ultimate buster-1	0.36	TAGAGGCTTATGAGTATCTTA	NM_016118:	NM_016118:
4938	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	-2.03	CCCGGCGGACCCTACAGGAAA	NM_002534:	NM_001032409:NM_002534:NM_016816:
4938	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	1.11	CCCTAAGAGTAATAATAAATA	NM_002534:	NM_002534:
4939	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	-0.81	CTCGTCGTGTTCCATAACTCA	NM_002535:	NM_016817:NM_002535:
4939	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.64	ACGCTCTGAGCTTAAATGATA	NM_002535:	NM_016817:NM_002535:
8638	OASL	2'-5'-oligoadenylate synthetase-like	0.64	CAGCTGGAATTCCAAGGCCAA	NM_003733:	NM_003733:NM_198213:
8638	OASL	2'-5'-oligoadenylate synthetase-like	-0.69	CAGGTGCTCCTTAGCCAAATA	NM_003733:	NM_003733:NM_198213:
4942	OAT	ornithine aminotransferase (gyrate atrophy)	-0.35	TAACGTAACTAAATAATGTAA	NM_000274:	NM_000274:
4942	OAT	ornithine aminotransferase (gyrate atrophy)	-0.37	TTGCTTTGTAACGTAACTAAA	NM_000274:	NM_000274:
4948	OCA2	oculocutaneous albinism II (pink-eye dilution homolog, mouse)	0.25	GACCTTGACACTAACACTCTA	NM_000275:	NM_000275:
4948	OCA2	oculocutaneous albinism II (pink-eye dilution homolog, mouse)	0.21	TGGAATAGACCTTGACACTAA	NM_000275:	NM_000275:
4952	OCRL	oculocerebrorenal syndrome of Lowe	0.54	TAGGGTCATACCACAGGGAAA	NM_000276:	NM_000276:NM_001587:
4952	OCRL	oculocerebrorenal syndrome of Lowe	1.75	CTAGGTGTTGAACTTAGTTAA	NM_000276:	NM_000276:NM_001587:
4953	ODC1 (ornithi	ornithine decarboxylase 1	0.08	AAGCATTTGTAGCTTGTACAA	NM_002539:	NM_002539:
4953	ODC1 (ornithi	ornithine decarboxylase 1	-0.16	TAGCTGTTAACTGCAAGTTTA	NM_002539:	NM_002539:
10178	ODZ1	odz, odd Oz/ten-m homolog 1(Drosophila)	0.75	CTCTATGATTTCCTTACTAAA	NM_014253:	NM_014253:
10178	ODZ1	odz, odd Oz/ten-m homolog 1(Drosophila)	-3.60	AAGGCTATAATCCGGCCTTAA	NM_014253:	NM_014253:
57451	ODZ2	odz, odd Oz/ten-m homolog 2 (Drosophila)	0.50	CACCACATCCTCAATGTTAAA	XM_047995:	XM_047995:
57451	ODZ2	odz, odd Oz/ten-m homolog 2 (Drosophila)	0.98	CAGCATCTTGGAGTTACGAAA	XM_047995:	XM_047995:
55714	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	-1.58	CCGGGCTGTGTCAAAGAATAA	XM_371717:	XM_371717:
55714	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	0.01	CCCAAATTTGATTTAACAGAA	XM_371717:	XM_371717:
26011	ODZ4	odz, odd Oz/ten-m homolog 4 (Drosophila)	1.37	CCAGATCAACACAGTACTTAA	XM_166254:	XM_166254:
26011	ODZ4	odz, odd Oz/ten-m homolog 4 (Drosophila)	-0.61	CCGGCCGGCCTTTAACCTCAA	XM_166254:	XM_166254:
8481	OFD1	oral-facial-digital syndrome 1	-0.07	TACCATCGGAGAGTCATTAAA	NM_003611:	NM_003611:
8481	OFD1	oral-facial-digital syndrome 1	-0.32	CCCAGTCTTTGGCAATAACAA	NM_003611:	NM_003611:
4967	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-0.97	TTGGCTTGACCCATAAACTAA	NM_002541:	NM_002541:
4967	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	0.43	CACTCTTTCTTTCTCCTTTAA	NM_002541:	NM_002541:
11054	OGFR (opioid	opioid growth factor receptor	-7.45	CAGAATGACAGGGTCCAGAAA	NM_007346:	NM_007346:
11054	OGFR (opioid	opioid growth factor receptor	0.11	CACGCCAAACCTGAGTTTCTA	NM_007346:	NM_007346:
79627	OGFRL1	opioid growth factor receptor-like 1	0.41	TTCAAAGATATCCGATATCAA	NM_024576:	NM_024576:
79627	OGFRL1	opioid growth factor receptor-like 1	-0.60	AAGAATCACTCGTATTCTTAA	NM_024576:	NM_024576:
4968	OGG1	8-oxoguanine DNA glycosylase	0.00	CGGGACCTACACCTCAGGAAA	NM_002542:	NM_002542:NM_016819:NM_016820:NM_016821:NM_016826:NM_016828:NM_016827:NM_016829:
4968	OGG1	8-oxoguanine DNA glycosylase	-1.28	CTGGTTCTGCCTTCTGGACAA	NM_002542:	NM_002542:NM_016819:NM_016820:NM_016821:NM_016826:NM_016828:NM_016827:NM_016829:
8473	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglu	0.07	AAGATTAATGTTCTTCATAAA	NM_003605:	NM_003605:NM_181673:NM_181672:
8473	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglu	0.31	CAGGTAAGTATAAGTATTCAA	NM_003605:	NM_003605:NM_181673:NM_181672:
170392	OIT3	oncoprotein induced transcript 3	0.81	AAGCTGGGTATAATATTTCAA	NM_152635:	NM_152635:
170392	OIT3	oncoprotein induced transcript 3	0.84	ATGGTGCAATCAGACCACAAA	NM_152635:	NM_152635:
10439	OLFM1	olfactomedin 1	-1.17	CCGGGACGCGATAAATATGCA	NM_006334:	NM_006334:NM_058199:NM_014279:
10439	OLFM1	olfactomedin 1	0.81	GCAGTTTAAGGGCTAACTTAA	NM_006334:	NM_006334:
93145	OLFM2	olfactomedin 2	1.35	CAGGACCTTTGACATTTGAAA	NM_058164:	NM_058164:
93145	OLFM2	olfactomedin 2	-0.60	CACGGACGTGCCCTTCCACAA	NM_058164:	NM_058164:
10562	OLFM4	olfactomedin 4	-2.84	CAGAGTTAACCTGACCACCAA	NM_006418:	NM_006418:
10562	OLFM4	olfactomedin 4	-2.95	TAGGGATTCTTTGTACAGGAA	NM_006418:	NM_006418:
169611	OLFML2A	olfactomedin-like 2A	1.01	TCCAGTCATATTTAGAACAAA	NM_182487:	NM_182487:
169611	OLFML2A	olfactomedin-like 2A	1.32	CGGCCACATTCCAAACCTCTA	NM_182487:	NM_182487:
25903	OLFML2B	olfactomedin-like 2B	-0.01	GCGGATTTACGTAACCAACTA	NM_015441:	NM_015441:
25903	OLFML2B	olfactomedin-like 2B	-2.04	TTGTATAATATTGCAAATGTA	NM_015441:	NM_015441:
116448	OLIG1	oligodendrocyte transcription factor 1	1.32	CCGAATTTAACTGGCACTTTA	NM_138983:	NM_138983:
116448	OLIG1	oligodendrocyte transcription factor 1	1.70	TCGATTTGTTACAGACGTTAA	NM_138983:	NM_138983:
10215	OLIG2	oligodendrocyte lineage transcription factor 2	1.35	AGCGCTGATGGTCATATCCAA	NM_005806:	NM_005806:
10215	OLIG2	oligodendrocyte lineage transcription factor 2	-2.20	CTCGTTGATTTGGGAGAATAT	NM_005806:	NM_005806:
4973	OLR1	oxidised low density lipoprotein (lectin-like) receptor 1	0.95	CAGAGGCCATTCCGAAATCAA	NM_002543:	NM_002543:
4973	OLR1	oxidised low density lipoprotein (lectin-like) receptor 1	0.63	ATGCTATAATTCCGAAACATA	NM_002543:	NM_002543:
115209	OMA1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	0.11	ACCGATATTCATCAACTTTCT	NM_145243:	NM_145243:
115209	OMA1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	0.11	CAGATCAATTGGGTTATTCAT	NM_145243:	NM_145243:
4974	OMG	oligodendrocyte myelin glycoprotein	-5.41	CACCTTCTGGATTTACCTCAA	NM_002544:	NM_002544:
4974	OMG	oligodendrocyte myelin glycoprotein	1.29	CAGGTGGTCATGTGACCACAA	NM_002544:	NM_002544:
4975	OMP (olfactoı	olfactory marker protein	-2.02	CTGGAATGTCGTGCTGGACAA	NM_006189:	NM_006189:
4975	OMP (olfactoı	olfactory marker protein	0.08	CTCGGATGCCATAGATTGGAA	NM_006189:	NM_006189:
4978	OPCML	opioid binding protein/cell adhesion molecule-like	1.11	CTGGGACACTATCCTACTATA	NM_002545:	NM_001012393:NM_002545:
4978	OPCML	opioid binding protein/cell adhesion molecule-like	2.67	TAGGCCAAAGTAGCAAGCTAA	NM_002545:	NM_001012393:NM_002545:
4983	OPHN1	oligophrenin 1	0.99	TAGGGCCACAGTCCCTTTAAA	NM_002547:	NM_002547:
4983	OPHN1	oligophrenin 1	1.38	GCCCTTGGACTTAACACTGAA	NM_002547:	NM_002547:
5956	OPN1LW	opsin 1 (cone pigments), long-wave-sensitive (color blindness, protan)	-4.50	CAGCACTATCAGCATTGTGAA	NM_020061:	NM_020061:
2652	OPN1MW	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deu	1.48	CAGCATCATCGTGCTCTGCTA	NM_000513:	NM_000513:
2652	OPN1MW	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deu	1.49	CAGCGTTGTGAACCAGGTCTA	NM_000513:	NM_000513:
611	OPN1SW	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	-0.77	CAAGAGTGCTTGCATCTACAA	NM_001708:	NM_001708:
611	OPN1SW	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	0.19	CGCCATGTACATGGTCAACAA	NM_001708:	NM_001708:
23596	OPN3	opsin 3 (encephalopsin, panopsin)	2.17	ACCCGTTCTATGTAATATCAA	NM_014322:	NM_001030012:NM_014322:NM_001030011:
23596	OPN3	opsin 3 (encephalopsin, panopsin)	0.44	TACCCGTTCTATGTAATATCA	NM_014322:	NM_001030012:NM_014322:NM_001030011:
94233	OPN4	opsin 4 (melanopsin)	-1.51	ACGGTTGATGTTCCAGACCAT	NM_033282:	NM_033282:NM_001030015:
94233	OPN4	opsin 4 (melanopsin)	-1.50	TCGCGTAGTTACCTATCTGAA	NM_033282:	NM_033282:NM_001030015:
221391	OPN5	opsin 5	0.14	CAGCCTGGATCGATATTTGAA	NM_181744:	NM_181744:NM_001030051:
221391	OPN5	opsin 5	-3.10	CAGCCTTTCACCATACTGGAA	NM_181744:	NM_001030051:
221391	OPN5	opsin 5	0.82	TAGGAGTATCCAAGTATCTTA	NM_181744:	NM_181744:NM_001030051:
221391	OPN5	opsin 5	-3.14	CACCGTAACCACAGTCAGGAA	NM_181744:	NM_181744:NM_001030051:
4985	OPRD1	opioid receptor, delta 1	1.32	CAGCATCTTCACGCTCACCAT	NM_000911:	NM_000911:
4985	OPRD1	opioid receptor, delta 1	1.30	CGGCATCGTCCGGTACACTAA	NM_000911:	NM_000911:
4986	OPRK1	opioid receptor, kappa 1	0.94	CAGATGCTTTAGTTACTACAA	NM_000912:	NM_000912:
4986	OPRK1	opioid receptor, kappa 1	0.65	TAGGTTTAACTCAGATCACTA	NM_000912:	NM_000912:
4987	OPRL1	opiate receptor-like 1	-0.97	ATGGGACAGGTCAAAGCATTA	NM_000913:	NM_000913:NM_182647:
4987	OPRL1	opiate receptor-like 1	-1.21	CTGGCTGGGTATTCTTCGTAA	NM_000913:	NM_000913:NM_182647:
4988	OPRM1	opioid receptor, mu 1	-3.07	TCCAGAGTGTGAATTACCTAA	NM_000914:	NM_001008503:NM_000914:NM_001008504:NM_001008505:
4988	OPRM1	opioid receptor, mu 1	0.83	TTCACCGTAGTAACACATAAA	NM_000914:	NM_000914:
10280	OPRS1	opioid receptor, sigma 1	0.27	AGGGATATCCATGCTTATGTA	NM_005866:	NM_005866:NM_147160:NM_147157:NM_147158:NM_147159:
10280	OPRS1	opioid receptor, sigma 1	-8.56	CCGGCTTGAGCTCACCACCTA	NM_005866:	NM_005866:NM_147160:NM_147157:NM_147158:NM_147159:

10133	OPTN	optineurin	-1.25	CAGCGGAATATTCCGATTCAT	NM_021980:	NM_001008212:NM_001008213:NM_001008211:NM_021980:
10133	OPTN	optineurin	0.67	AAGCATGCTATCAGAAATCAA	NM_021980:	NM_001008212:NM_001008213:NM_001008211:NM_021980:
341276	OR10A2	olfactory receptor, family 10, subfamily A, member 2	0.95	CGGCCTAAATCAAATAATTCA	NM_001004460:	NM_001004460:
283297	OR10A4	olfactory receptor, family 10, subfamily A, member 4	0.95	ACCATTTACTTGGTTACTTTA	XM_208604.1:	NM_207186:
283297	OR10A4	olfactory receptor, family 10, subfamily A, member 4	-2.09	CTCAAGGAATAAAGAAGTGAA	XM_208604.1:	NM_207186:
144124	OR10A5	olfactory receptor, family 10, subfamily A, member 5	-0.04	CCTGACATTTCTAACTATCTA	NM_178168:	NM_178168:
144124	OR10A5	olfactory receptor, family 10, subfamily A, member 5	-0.02	GAAGTTGTTATCATTATCCTA	NM_178168:	NM_178168:
121275	OR10AD1	olfactory receptor, family 10, subfamily AD, member 1	1.06	AGCTATGTTCTCTTACATGAA	NM_001004134:	NM_001004134:
121275	OR10AD1	olfactory receptor, family 10, subfamily AD, member 1	-1.02	CTGGTTCTTTGGGCTGATCAA	NM_001004134:	NM_001004134:
26539	OR10H1 (olfa	olfactory receptor, family 10, subfamily H, member 1	2.09	AAGAAGACCTTCTTCAGTAAA	NM_013940:	NM_013940:
26539	OR10H1 (olfa	olfactory receptor, family 10, subfamily H, member 1	1.05	GACCTTCTTCAGTAAACTCTA	NM_013940:	NM_013940:
26538	OR10H2	olfactory receptor, family 10, subfamily H, member 2	1.76	CACCCTGATGGCCACCACCTA	NM_013939:	NM_013939:
26538	OR10H2	olfactory receptor, family 10, subfamily H, member 2	0.08	TTGGCCTGTGGAAATAATGTA	NM_013939:	NM_013939:
26532	OR10H3	olfactory receptor, family 10, subfamily H, member 3	0.94	CAGAACCATATCTGAATTTAT	NM_013938:	NM_013938:
26532	OR10H3	olfactory receptor, family 10, subfamily H, member 3	-0.49	CCACTGCATTACAACATGCTA	NM_013938:	NM_013938:
26476	OR10J1	olfactory receptor, family 10, subfamily J, member 1	0.00	CTGATTGTAGCAATAACGCAA	NM_012351:	NM_012351:
26476	OR10J1	olfactory receptor, family 10, subfamily J, member 1	-0.87	TGGCGTGTTCCTTGCACTATA	NM_012351:	NM_012351:
26531	OR11A1	olfactory receptor, family 11, subfamily A, member 1	0.27	AACGTTAGGCTTGGTATAGAA	NM_013937:	NM_013937:
26531	OR11A1	olfactory receptor, family 11, subfamily A, member 1	-0.52	CCAGATGTTGTATAACTATTA	NM_013937:	NM_013937:
26529	OR12D2	olfactory receptor, family 12, subfamily D, member 2	0.37	ACCTGGATATCTGTTACTCTA	NM_013936:	NM_013936:
26529	OR12D2	olfactory receptor, family 12, subfamily D, member 2	-0.74	CCGGATTGTTGCCATCATGTA	NM_013936:	NM_013936:
81797	OR12D3	olfactory receptor, family 12, subfamily D, member 3	-1.07	CACAATCAAGCTAAACCTACA	NM_030959:	NM_030959:
81797	OR12D3	olfactory receptor, family 12, subfamily D, member 3	0.83	CCCAAATAACCAAACGCGTAA	NM_030959:	NM_030959:
8383	OR1A1	olfactory receptor, family 1, subfamily A, member 1	-1.65	CACGGTTGTCTCTTTGTATTA	NM_014565:	NM_014565:
8383	OR1A1	olfactory receptor, family 1, subfamily A, member 1	0.01	CGCAGTGATCACTGTAATGTA	NM_014565:	NM_014565:
26189	OR1A2	olfactory receptor, family 1, subfamily A, member 2	0.98	AGCATTAAATCCTTTCATCTA	NM_012352:	NM_012352:
26189	OR1A2	olfactory receptor, family 1, subfamily A, member 2	-0.57	TGCAGTGATAACTGTGATGTA	NM_012352:	NM_012352:
4991	OR1D2	olfactory receptor, family 1, subfamily D, member 2	-3.90	CACTTTGTATGGTATACCTAA	NM_002548:	NM_002548:
4991	OR1D2	olfactory receptor, family 1, subfamily D, member 2	0.29	CTGGGAAGACTCCTAGATAAA	NM_002548:	NM_002548:
8387	OR1E1	olfactory receptor, family 1, subfamily E, member 1	-3.68	CAGAGTCATTCATCAGAAGAA	NM_003553:	NM_003553:
8387	OR1E1	olfactory receptor, family 1, subfamily E, member 1	0.19	TCCCAAGTTGTTACAGAACAT	NM_003553:	NM_003553:
8388	OR1E2	olfactory receptor, family 1, subfamily E, member 2	0.71	CCAAATGTACTTCTTCTTGTA	NM_003554:	NM_003554:
8388	OR1E2	olfactory receptor, family 1, subfamily E, member 2	-0.57	CTGGAAAGGGTCATTTGTAAA	NM_003554:	NM_003554:
4992	OR1F1	olfactory receptor, family 1, subfamily F, member 1	-2.76	ATGGGTGGTTGCCAACCTGAA	NM_012360:	NM_012360:
4992	OR1F1	olfactory receptor, family 1, subfamily F, member 1	0.82	CAGCACCATCATTGCTGTGTA	NM_012360:	NM_012360:
8390	OR1G1	olfactory receptor, family 1, subfamily G, member 1	-0.71	CACAGTTGCATCAGTGATGTA	NM_003555:	NM_003555:
8390	OR1G1	olfactory receptor, family 1, subfamily G, member 1	-1.52	CCTGATTATCTCTTACACGAA	NM_003555:	NM_003555:
26219	OR1J4	olfactory receptor, family 1, subfamily J, member 4	-0.09	CAGGATCAATCCATTCTTTAT	XM_294533.1:	NM_001004452:
26219	OR1J4	olfactory receptor, family 1, subfamily J, member 4	-1.34	CCCAAAGATGTTATTAAGCAT	XM_294533.1:	NM_001004452:
127623	OR2B11 (olfa	olfactory receptor, family 2, subfamily B, member 11	0.60	ACCGCTGTGAATGACACCATA	NM_001004492:	NM_001004492:
81697	OR2B2	olfactory receptor, family 2, subfamily B, member 2	0.08	CACCAGGAAAGTAATCAGTTA	NM_033057:	NM_033057:
81697	OR2B2	olfactory receptor, family 2, subfamily B, member 2	-0.68	CTGGATTAGTGGCTTTAGCAA	NM_033057:	NM_033057:
4993	OR2C1	olfactory receptor, family 2, subfamily C, member 1	-0.15	AAGCATCATCGTGATCTCCTA	NM_012368:	NM_012368:
4993	OR2C1	olfactory receptor, family 2, subfamily C, member 1	0.67	CAAGTTCATTTCCCTGTTCTA	NM_012368:	NM_012368:
81472	OR2C3	olfactory receptor, family 2, subfamily C, member 3	-0.61	CCGGCACATGGTATTAGAGAA	NM_198074:	NM_198074:
81472	OR2C3	olfactory receptor, family 2, subfamily C, member 3	0.38	TCCGTGGATAATAAACTTTGA	NM_198074:	NM_198074:
120776	OR2D2	olfactory receptor, family 2, subfamily D, member 2	1.15	CAGCTGCTATTTATCGTATTA	NM_003700:	NM_003700:
120776	OR2D2	olfactory receptor, family 2, subfamily D, member 2	0.40	CAGCAATTATCACTTACATGA	NM_003700:	NM_003700:
26211	OR2F1	olfactory receptor, family 2, subfamily F, member 1	0.54	CAGAAACAAGTTTATTGATCA	NM_012369:	NM_012369:
26211	OR2F1	olfactory receptor, family 2, subfamily F, member 1	-1.85	CTGGCAGAAACTATTATGGAA	NM_012369:	NM_012369:
26716	OR2H1	olfactory receptor, family 2, subfamily H, member 1	2.20	CCACATTAAAGTTGCAAATAA	NM_030883:	NM_030883:
26716	OR2H1	olfactory receptor, family 2, subfamily H, member 1	-0.19	TAGCTCCATAAGGCACACAAA	NM_030883:	NM_030883:
7932	OR2H2	olfactory receptor, family 2, subfamily H, member 2	-5.53	CCTCCTAACCCTAGTGGGCAA	NM_007160:	NM_007160:
7932	OR2H2	olfactory receptor, family 2, subfamily H, member 2	0.06	CTGGGTCATTGGGCTAGTGGA	NM_007160:	NM_007160:
26707	OR2J2	olfactory receptor, family 2, subfamily J, member 2	2.22	CAAGTTCGGAAGACTTCTTTA	NM_030905:	NM_030905:
26707	OR2J2	olfactory receptor, family 2, subfamily J, member 2	-0.53	CACCGAGTCTTAATCCTCTAA	NM_030905:	NM_030905:
284521	OR2L13	olfactory receptor, family 2, subfamily L, member 13	0.48	CAAGTTGATTCCAACACGCTA	NM_175911:	NM_175911:
284521	OR2L13	olfactory receptor, family 2, subfamily L, member 13	-1.40	TAGGTACATTTAAGCAGTCAA	NM_175911:	NM_175911:
391192	OR2L3 (olfact	olfactory receptor, family 2, subfamily L, member 3	-1.46	TAGGATTCTTCCCACCATCAA	NM_001004687:	NM_001004687:
26245	OR2M4	olfactory receptor, family 2, subfamily M, member 4	0.27	ACCCAAGATGATCTTCAGCTA	XM_371358:	NM_017504:
26245	OR2M4	olfactory receptor, family 2, subfamily M, member 4	-0.40	CTCCTCATCTACATAGAGAAA	XM_371358:	NM_017504:
56656	OR2S2	olfactory receptor, family 2, subfamily S, member 2	-0.35	CACCGTGGTGATCGTCTTCTA	NM_019897:	NM_019897:
56656	OR2S2	olfactory receptor, family 2, subfamily S, member 2	1.90	CGGGACCTTATTCTTCATGTA	NM_019897:	NM_019897:
343172	OR2T8	olfactory receptor, family 2, subfamily T, member 8	-0.51	GTGGCCTTAAGTCGTGAATAA	NM_001005522:	NM_001005522:
343172	OR2T8	olfactory receptor, family 2, subfamily T, member 8	-0.68	ACCTCTTATTTCATTCTCCTA	NM_001005522:	NM_001005522:
26692	OR2W1	olfactory receptor, family 2, subfamily W, member 1	1.72	CAAAGCAATTATAGTTCTTTA	NM_030903:	NM_030903:
26692	OR2W1	olfactory receptor, family 2, subfamily W, member 1	-0.51	CTGGAGTATTAGTTTGGCCAA	NM_030903:	NM_030903:
4994	OR3A1	olfactory receptor, family 3, subfamily A, member 1	-2.90	AAGCTTTCAGACAAGGATAAA	NM_002550:	NM_002550:
4994	OR3A1	olfactory receptor, family 3, subfamily A, member 1	1.28	CAAGCTTTCAGACAAGGATAA	NM_002550:	NM_002550:
4995	OR3A2	olfactory receptor, family 3, subfamily A, member 2	-1.35	AAGAGGTATCTTCAACTACAT	NM_002551:	NM_002551:
4995	OR3A2	olfactory receptor, family 3, subfamily A, member 2	1.10	CACGTGGCAGCTGCAGTTCTA	NM_002551:	NM_002551:
8392	OR3A3	olfactory receptor, family 3, subfamily A, member 3	1.19	CAGGGCGCTCTGTGTCAGCTA	NM_012373:	NM_012373:
8392	OR3A3	olfactory receptor, family 3, subfamily A, member 3	-0.87	CTGGGTTCAGTGGAATCTTCA	NM_012373:	NM_012373:
219429	OR4C11	olfactory receptor, family 4, subfamily C, member 11	0.19	TAGGGTCTTTAATACACTCTA	NM_001004700:	NM_001004700:
219429	OR4C11	olfactory receptor, family 4, subfamily C, member 11	0.09	CCCTATTTGATTGATCATTAT	NM_001004700:	NM_001004700:
256144	OR4C3	olfactory receptor, family 4, subfamily C, member 3	-0.12	CTCAGTGACCTTGGAATCTAT	NM_001004702:	NM_001004702:
256144	OR4C3	olfactory receptor, family 4, subfamily C, member 3	-1.83	CTCCTACATTGTCATCCTGTA	NM_001004702:	NM_001004702:
219432	OR4C6	olfactory receptor, family 4, subfamily C, member 6	0.04	CACGGTGGTTGTATTGTTCTT	NM_001004704:	NM_001004704:
219432	OR4C6	olfactory receptor, family 4, subfamily C, member 6	1.07	CTGAAGTCTTACAGCTCTAAA	NM_001004704:	NM_001004704:
26689	OR4D1	olfactory receptor, family 4, subfamily D, member 1	1.71	CAGACCCAAGAGCTCCAGAAA	XM_292627.2:	NM_012374:
26689	OR4D1	olfactory receptor, family 4, subfamily D, member 1	-0.63	CTCCGAAATCTAGCTCTCATA	XM_292627.2:	NM_012374:
124538	OR4D2	olfactory receptor, family 4, subfamily D, member 2	2.52	ACCAATTTGCTTAAATTAGTA	NM_001004707:	NM_001004707:
124538	OR4D2	olfactory receptor, family 4, subfamily D, member 2	-6.04	CTGGATGGCGTTATGATTTCA	NM_001004707:	NM_001004707:
79345	OR51B2	olfactory receptor, family 51, subfamily B, member 2	0.93	ATCCTCTTCTCCTATATTCTA	NM_033180:	NM_033180:
79345	OR51B2	olfactory receptor, family 51, subfamily B, member 2	0.37	CTCCTATATTCTAATTCTTAA	NM_033180:	NM_033180:
79339	OR51B4	olfactory receptor, family 51, subfamily B, member 4	-0.38	CTGTGCTGATATCACGTTTAA	NM_033179:	NM_033179:
79339	OR51B4	olfactory receptor, family 51, subfamily B, member 4	0.73	TTCTTATATACTAATCCTTAA	NM_033179:	NM_033179:
143503	OR51E1	olfactory receptor, family 51, subfamily E, member 1	0.27	CAGTTTGATGCTTGTCTGCTA	NM_152430:	NM_152430:
143503	OR51E1	olfactory receptor, family 51, subfamily E, member 1	-0.19	CTCATATCTGCTTATTCTTAA	NM_152430:	NM_152430:
81285	OR51E2	olfactory receptor, family 51, subfamily E, member 2	0.70	ACGGGTGCTGGCTATGTTCAA	NM_030774:	NM_030774:
81285	OR51E2	olfactory receptor, family 51, subfamily E, member 2	-0.04	TGGCTGGAATAGTAAACTAAA	NM_030774:	NM_030774:
23538	OR52A1	olfactory receptor, family 52, subfamily A, member 1	-0.31	CACCAGCTTGTCATTCAGATA	NM_012375:	NM_012375:
23538	OR52A1	olfactory receptor, family 52, subfamily A, member 1	-0.88	CAGAAGGAGGCTAGGTTTAAA	NM_012375:	NM_012375:
143496	OR52B4	olfactory receptor, family 52, subfamily B, member 4	1.02	ATGCATGTAATGACATTCGAA	NM_001005161:	NM_001005161:
143496	OR52B4	olfactory receptor, family 52, subfamily B, member 4	1.55	TCCCATTATTTATGGGATCAA	NM_001005161:	NM_001005161:
390067	OR52H1	olfactory receptor, family 52, subfamily H, member 1	-7.01	TACCACCATCTTGACTCCCAA	NM_001005289:	NM_001005289:
390067	OR52H1	olfactory receptor, family 52, subfamily H, member 1	0.20	CAGATCAGAGATAAGGTTATA	NM_001005289:	NM_001005289:

387748	OR56B1	olfactory receptor, family 56, subfamily B, member 1	-0.67	AAGTCTTATTATACTGTCATA	NM_001005180:	NM_001005180:
387748	OR56B1	olfactory receptor, family 56, subfamily B, member 1	-4.58	ACCCTCTTCGCTATCCATCAA	NM_001005180:	NM_001005180:
196335	OR56B4	olfactory receptor, family 56, subfamily B, member 4	-0.09	ATGGCAGTAGACAGATACATA	NM_001005181:	NM_001005181:
196335	OR56B4	olfactory receptor, family 56, subfamily B, member 4	-0.56	CTCATCATAATCACCATTCAA	NM_001005181:	NM_001005181:
10798	OR5I1	olfactory receptor, family 5, subfamily I, member 1	0.19	CTGAGAAAGTTCTAAGATCAA	NM_006637:	NM_006637:
10798	OR5I1	olfactory receptor, family 5, subfamily I, member 1	-1.67	GCGGTTGATTGTCTTGTCATA	NM_006637:	NM_006637:
26338	OR5L2	olfactory receptor, family 5, subfamily L, member 2	1.15	AACAGTGGAGATGTTGACAAA	XM_372387:	NM_001004739:
26338	OR5L2	olfactory receptor, family 5, subfamily L, member 2	0.06	CACCACTATCCTGAAGATACA	XM_372387:	NM_001004739:
120065	OR5P2	olfactory receptor, family 5, subfamily P, member 2	0.04	CCACTGCTTTATTCAACCAAA	NM_153444:	NM_153444:
120065	OR5P2	olfactory receptor, family 5, subfamily P, member 2	0.47	CCAGCTACTCTTAGTAGTTTA	NM_153444:	NM_153444:
120066	OR5P3	olfactory receptor, family 5, subfamily P, member 3	1.00	ATGGGTAATATCAGCATAATT	NM_153445:	NM_153445:
120066	OR5P3	olfactory receptor, family 5, subfamily P, member 3	0.12	CTGCATCATCTTAGTGGGCAT	NM_153445:	NM_153445:
81696	OR5V1	olfactory receptor, family 5, subfamily V, member 1	0.40	AAGGTTCTATGCAATCAATTA	NM_030876:	NM_030876:
81696	OR5V1	olfactory receptor, family 5, subfamily V, member 1	0.18	CACCATCTTCTTTCTGACTTA	NM_030876:	NM_030876:
8590	OR6A2	olfactory receptor, family 6, subfamily A, member 2	1.57	ACGTGGTATTCGACCAATATA	NM_003696:	NM_003696:
8590	OR6A2	olfactory receptor, family 6, subfamily A, member 2	-0.86	TACGTGGTATTCGACCAATAT	NM_003696:	NM_003696:
389090	OR6B2	olfactory receptor, family 6, subfamily B, member 2	-6.66	TTGGGTCAAACTTCACACTAA	NM_001005853:	NM_001005853:
389090	OR6B2	olfactory receptor, family 6, subfamily B, member 2	-0.62	CACGCCAATAATTAACCCTTT	NM_001005853:	NM_001005853:
150681	OR6B3	olfactory receptor, family 6, subfamily B, member 3	0.47	CTGGAACTTCATCTCCAAATA	NM_173351:	NM_173351:
150681	OR6B3	olfactory receptor, family 6, subfamily B, member 3	0.19	CCTGAGGAATAAGGAATTTAA	NM_173351:	NM_173351:
89883	OR6W1P	olfactory receptor, family 6, subfamily W, member 1 pseudogene	-4.44	CTCCTGGTCCCTCATCTTCAT	NM_033519:	NR_002140:
89883	OR6W1P	olfactory receptor, family 6, subfamily W, member 1 pseudogene	0.84	CTGGAGCTCCTCACTCTCTTT	NM_033519:	NR_002140:
26333	OR7A17	olfactory receptor, family 7, subfamily A, member 17	0.59	CCCTGAATTCCTTGTCACAAA	NM_030901:	NM_030901:
26333	OR7A17	olfactory receptor, family 7, subfamily A, member 17	-0.03	CGGGCCTAGGTGTGTACCTTA	NM_030901:	NM_030901:
26659	OR7A5	olfactory receptor, family 7, subfamily A, member 5	0.61	AAGCTTAGTGCCCATATATAA	NM_017506:	NM_017506:
26659	OR7A5	olfactory receptor, family 7, subfamily A, member 5	-1.24	ACAGTCAGAGATGACCTTAAA	NM_017506:	NM_017506:
26658	OR7C2	olfactory receptor, family 7, subfamily C, member 2	1.15	CTGCAGTTACACCACCTTCTA	NM_012377:	NM_012377:
26658	OR7C2	olfactory receptor, family 7, subfamily C, member 2	-1.54	CTGGTGAATATCCAAACACAA	NM_012377:	NM_012377:
162998	OR7D2	olfactory receptor, family 7, subfamily D, member 2	0.74	CAGCACGTTGATATACTTTAT	NM_175883:	NM_175883:
162998	OR7D2	olfactory receptor, family 7, subfamily D, member 2	0.24	ACCAATTACCTGAATAGTGAA	NM_175883:	NM_175883:
125958	OR7D4	olfactory receptor, family 7, subfamily D, member 4	-4.16	CTGCTCTAACACCCTCCTCAA	NM_001005191:	NM_001005191:
125958	OR7D4	olfactory receptor, family 7, subfamily D, member 4	-0.36	ACGGAGCAAAGACATCTCCTA	NM_001005191:	NM_001005191:
125958	OR7D4	olfactory receptor, family 7, subfamily D, member 4	-2.06	CTCAGATTGTCTCCTCCTTAA	NM_001005191:	NM_001005191:
79315	OR7E91P (ol	olfactory receptor, family 7, subfamily E, member 91 pseudogene	0.02	AAGAAAGGGCAAGCACATTAA	NM_145242:	NR_002185:
79315	OR7E91P (ol	olfactory receptor, family 7, subfamily E, member 91 pseudogene	1.80	TCCGCCCAGCATACAAGCTTA	NM_145242:	NR_002185:
79315	OR7E91P (ol	olfactory receptor, family 7, subfamily E, member 91 pseudogene	-0.37	AAGAAAGGGCAAGCACATTAA	NM_145242:	NR_002185:
79315	OR7E91P (ol	olfactory receptor, family 7, subfamily E, member 91 pseudogene	0.79	TCCGCCCAGCATACAAGCTTA	NM_145242:	NR_002185:
26493	OR8B8	olfactory receptor, family 8, subfamily B, member 8	0.65	CAAGGTGTCTTCCCTATTCTA	NM_012378:	NM_012378:
26493	OR8B8	olfactory receptor, family 8, subfamily B, member 8	-0.56	GAGCTTTGTCTTAAAGAAGAA	NM_012378:	NM_012378:
283159	OR8D1	olfactory receptor, family 8, subfamily D, member 1	1.68	AAAGAAGAATACAATCCTTTA	NM_001002917:	NM_001002917:
283159	OR8D1	olfactory receptor, family 8, subfamily D, member 1	0.77	CAGTTTGTCTTAGATGGTTTA	NM_001002917:	NM_001002917:
283160	OR8D2	olfactory receptor, family 8, subfamily D, member 2	0.78	CAGGGTCTGTTCCATAATGAT	NM_001002918:	NM_001002918:
283160	OR8D2	olfactory receptor, family 8, subfamily D, member 2	1.35	TGGGTCTATAACATTCATGTA	NM_001002918:	NM_001002918:
219865	OR8G5	olfactory receptor, family 8, subfamily G, member 5	-1.41	CTGTTCTAGTACTTACATTAA	NM_001005198:	NM_001005198:
219865	OR8G5	olfactory receptor, family 8, subfamily G, member 5	-2.60	CAAGGGATCACTTTCCTACAA	NM_001005198:	NM_001005198:
23594	ORC6L	origin recognition complex, subunit 6 homolog-like (yeast)	-0.17	ATGCAAGATTCTAAAGCTGAA	NM_014321:	NM_014321:
23594	ORC6L	origin recognition complex, subunit 6 homolog-like (yeast)	-0.15	CAGGATTATGAAGAATGGAAA	NM_014321:	NM_014321:
84418	ORF1-FL49	putative nuclear protein ORF1-FL49	0.76	CCGCCTGTATGTTTCAATAAA	NM_032412:	NM_032412:
84418	ORF1-FL49	putative nuclear protein ORF1-FL49	1.10	CAGGTTCAGACCCGACCGTTA	NM_032412:	NM_032412:
5007	OSBP	oxysterol binding protein	0.41	CCCGCTAATGGAAGAAGTTTA	NM_002556:	NM_002556:
5007	OSBP	oxysterol binding protein	0.28	CCGAAGGTTAGTGTTATTCCA	NM_002556:	NM_002556:
126014	OSCAR	osteoclast-associated receptor	-0.37	AAGGTAGTAGTGAGACGTGAA	NM_130771:	NM_130771:NM_133168:NM_133169:NM_206817:NM_206818:
126014	OSCAR	osteoclast-associated receptor	-0.25	CCCAGCTTCATACCACCCTAA	NM_130771:	NM_130771:NM_133168:NM_133169:NM_206817:NM_206818:
55644	OSGEP	O-sialoglycoprotein endopeptidase	0.29	CCAGGATGACTCAGCAATAAA	NM_017807:	NM_017807:
55644	OSGEP	O-sialoglycoprotein endopeptidase	-0.87	TAGCAAAGCTATAGACTCCAA	NM_017807:	NM_017807:
64172	OSGEPL1 (O	O-sialoglycoprotein endopeptidase-like 1	0.17	TAAAGGTAGTATTAAGGTTAA	NM_022353:	NM_022353:
64172	OSGEPL1 (O	O-sialoglycoprotein endopeptidase-like 1	-5.05	CAGAGAGACTTGTTACCTCAA	NM_022353:	NM_022353:
5008	OSM	oncostatin M	-0.79	TGGAGGGACATGACTAATTTA	NM_020530:	NM_020530:
5008	OSM	oncostatin M	-2.00	CTGACGTAAGGTGGATATTAA	NM_020530:	NM_020530:
9180	OSMR	oncostatin M receptor	-0.51	TAGCTCTAATCTAATATATAA	NM_003999:	NM_003999:
9180	OSMR	oncostatin M receptor	0.53	TAGACTTACCTTGAACGGATA	NM_003999:	NM_003999:
5009	OTC	ornithine carbamoyltransferase	0.53	TACGTGCTTAACTTTGCTTAA	NM_000531:	NM_000531:
5009	OTC	ornithine carbamoyltransferase	0.76	AGCATCCATCCCAATTATCAA	NM_000531:	NM_000531:
158800	OTEX	paired-like homeobox protein OTEX	-1.33	CGGGTTTGGTTTAAGAATAAA	NM_139282:	NM_139282:
158800	OTEX	paired-like homeobox protein OTEX	-5.30	TGCACTTATGTTATCAATAAA	NM_139282:	NM_139282:
9381	OTOF	otoferlin	0.69	CAGGATTGAAGCTTTAGTGAA	NM_004802:	NM_194248:NM_004802:NM_194323:NM_194322:
9381	OTOF	otoferlin	-1.66	CCGGTACAAGTGGCTCATCAT	NM_004802:	NM_194248:NM_004802:NM_194323:NM_194322:
5013	OTX1	orthodenticle homolog 1 (Drosophila)	0.77	CACCCAGGAAACAGAACTTTA	NM_014562:	NM_014562:
5013	OTX1	orthodenticle homolog 1 (Drosophila)	-0.24	TCCGTTCCAGGGACCACTTAA	NM_014562:	NM_014562:
341350	OVCH1	ovochymase 1	-0.90	TACGAGGTGCATTTGGTATAA	NM_183378:	NM_183378:
341350	OVCH1	ovochymase 1	-2.84	CAGATTCAAGTGCATGTGTTA	NM_183378:	NM_183378:
341277	OVCH2	ovochymase 2	-4.11	CCACAGTTACCTGTCAATGTA	NM_198185:	NM_198185:
341277	OVCH2	ovochymase 2	-0.12	CCACATTTCTCCACCAAGAAA	NM_198185:	NM_198185:
5017	OVOL1	ovo-like 1(Drosophila)	-0.46	AACCTTCCTCTCAACTATTAA	NM_004561:	NM_004561:
5017	OVOL1	ovo-like 1(Drosophila)	-0.40	CCCAGTGGACATCAGAGTCAA	NM_004561:	NM_004561:
165140	OXER1	oxoeicosanoid (OXE) receptor 1	1.13	CCAGCTGATAGTGCCAATCAT	NM_148962:	NM_148962:
165140	OXER1	oxoeicosanoid (OXE) receptor 1	-8.31	CCGGGTGGAGGAGACAGGCAA	NM_148962:	NM_148962:
27199	OXGR1	oxoglutarate (alpha-ketoglutarate) receptor 1	-0.64	CACCAGTTCGGATGAACTCAA	NM_080818:	NM_080818:
27199	OXGR1	oxoglutarate (alpha-ketoglutarate) receptor 1	-5.35	CCGCTACTGTGTGATCATTCA	NM_080818:	NM_080818:
92106	OXNAD1	oxidoreductase NAD-binding domain containing 1	0.42	ATGCAGTTTGCATGTTACAAA	NM_138381:	NM_138381:
92106	OXNAD1	oxidoreductase NAD-binding domain containing 1	-0.99	TACCAGCGAACTCCTGTTTAA	NM_138381:	NM_138381:
54995	OXSM	3-oxoacyl-ACP synthase, mitochondrial	0.13	CAGCATTCGATATAAACTCAA	NM_017897:	NM_017897:
54995	OXSM	3-oxoacyl-ACP synthase, mitochondrial	-0.15	CAGGTCAGCATTCGATATAAA	NM_017897:	NM_017897:
9943	OXSR1	oxidative-stress responsive 1	-0.06	CTGGAGTAGGGACTAACTATA	NM_005109:	NM_005109:
9943	OXSR1	oxidative-stress responsive 1	-0.87	TAGGGACTAACTATAGCACAA	NM_005109:	NM_005109:
5021	OXTR	oxytocin receptor	-1.88	ATGGATCACGCTAGCTGTCTA	NM_000916:	NM_000916:
5021	OXTR	oxytocin receptor	0.49	GACAATGATATGCAAGTGCAA	NM_000916:	NM_000916:
5023	P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	0.15	ACCATAGGTGACTAAATTAAA	NM_002558:	NM_002558:
5023	P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	0.57	CCGCATGGTGCTGGTGCGTAA	NM_002558:	NM_002558:
22953	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	0.08	CACAGGCGTTGTAACCTTGAA	NM_012226:	NM_016318:NM_174873:NM_174872:NM_170682:NM_170683:NM_012226:
22953	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	-2.63	CACAACATACTCAGTCCAATA	NM_012226:	NM_016318:NM_174873:NM_174872:NM_170682:NM_170683:NM_012226:
5024	P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3	0.01	ACGGGAATGCTGGCAAGTTCA	NM_002559:	NM_002559:
5024	P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3	-1.94	CTCGACAGCGTTTCTGAGAAA	NM_002559:	NM_002559:

5025	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	1.08	CGGGACGTTGAGCACAACGTA	NM_002560:	NM_175568:NM_175567:NM_002560:
5025	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	-0.54	TCGTGCATTTATGATGCTAAA	NM_002560:	NM_175568:NM_175567:NM_002560:
5026	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-0.25	CCCTGTAGAGTTCCTAGATTA	NM_002561:	NM_002561:NM_175080:
5026	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-1.47	CCGCTTTGACGTGATGGTGAA	NM_002561:	NM_002561:NM_175080:
5027	P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	1.32	CTAGGATAATGTCCAACTAAA	NM_002562:	NM_002562:NM_177427:
5027	P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	-0.02	AAAGATCTACATGAATGCAAA	NM_002562:	NM_002562:NM_177427:
9127	P2RXL1	purinergic receptor P2X-like 1, orphan receptor	0.08	CAGGGCTAAGTTGGTGATCAT	NM_005446:	NM_005446:
9127	P2RXL1	purinergic receptor P2X-like 1, orphan receptor	0.11	CTGCTGTATGTGGATAGAGAA	NM_005446:	NM_005446:
5028	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	0.01	AAGCCTGCATATATTATCGTA	NM_002563:	NM_002563:
5028	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	-0.06	ATCGATTTACCTGGTAATCAT	NM_002563:	NM_002563:
27334	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	-1.10	AAGTTGAATAGTTTACCTTAA	NM_014499:	NM_014499:NM_198333:
27334	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	1.75	CTCCCTATCATATTAACTTTA	NM_014499:	NM_014499:NM_198333:
5032	P2RY11	purinergic receptor P2Y, G-protein coupled, 11	-0.95	ACCCTAGGTGTTGCTGGAGAA	NM_002566:	NM_002566:
5032	P2RY11	purinergic receptor P2Y, G-protein coupled, 11	0.42	CCCGCTGGCCGCCTACCTCTA	NM_002566:	NM_002566:
64805	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	-2.99	CAGGGTCAGATTACAAGAGCA	NM_022788:	NM_022788:
64805	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	0.67	CCGGAGTAAATCAAACTTTAT	NM_022788:	NM_022788:NM_176876:
53829	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	0.87	AAGACTGACTGTAGACTGCAA	NM_023914:	NM_176894:NM_023914:
53829	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	0.50	CAACTGTTTATTGCTAAAGAA	NM_023914:	NM_176894:NM_023914:
9934	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	0.90	ACCCATCAGTAATTTCTCTAA	NM_014879:	NM_014879:
9934	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	-0.76	TACAAAGACTTACGTCATTTA	NM_014879:	NM_014879:
5029	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	-1.08	CAGTGTGAGGCTGTAACTTAT	NM_002564:	NM_176072:NM_176071:NM_002564:
5029	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	0.69	CTGGAATGCGTCCACCACATA	NM_002564:	NM_176072:NM_176071:NM_002564:
5030	P2RY4	pyrimidinergic receptor P2Y, G-protein coupled, 4	-6.45	CAGATAGATTGTAACACGGGA	NM_002565:	NM_002565:
5030	P2RY4	pyrimidinergic receptor P2Y, G-protein coupled, 4	-0.31	CCCAATAGTGATACCTGGTAA	NM_002565:	NM_002565:
10161	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	0.46	CCGAAATGAAACTACAACTTA	NM_005767:	NM_005767:
10161	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	-0.12	CTGCGTCCTCAAAGTCCGAAA	NM_005767:	NM_005767:
5031	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	1.42	CACGGCCGTGTACACCCTAAA	NM_176797:	NM_176797:NM_176796:NM_004154:NM_176798:
5031	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	1.56	CCACATGAGCTCCTACAGAAA	NM_176797:	NM_176797:NM_176796:NM_004154:NM_176798:
286530	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	0.18	CTGGATTATTAAGCACCCTAA	NM_178129:	NM_178129:
286530	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	-0.02	GTCGGTCATCTTCATGATCAA	NM_178129:	NM_178129:
5033	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	0.41	CAGGGTGGTAATATTGGCATT	NM_000917:	NM_000917:NM_001017962:
5033	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	0.03	CGAAATCATCATATTGCATAA	NM_000917:	NM_000917:NM_001017962:
8974	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	0.05	ATCGTGTGGCTACTTTCTTAA	NM_004199:	NM_004199:
8974	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	-0.12	GAGGATCAAGGAGATCGCAAA	NM_004199:	NM_001017974:NM_004199:NM_001017973:
283208	P4HA3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	2.10	CCCAGATGAGTGGTACATTAT	NM_182904:	NM_182904:
283208	P4HA3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	-4.81	CAGAGTAGGATGCACAGTACA	NM_182904:	NM_182904:
5034	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	-29.74	AAGATGAACTGTAATACGCAA	NM_000918:	NM_000918:
5034	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla	-1.84	CAGGACGGTCATTGATTACAA	NM_000918:	NM_000918:
63970	P53AIP1	p53-regulated apoptosis-inducing protein 1	1.62	ATGATATTTGGTAAATAACAA	NM_022112:	NM_022112:
63970	P53AIP1	p53-regulated apoptosis-inducing protein 1	1.78	CAGGTGTGTGATAATTACTTA	NM_022112:	NM_022112:
26471	P8	p8 protein (candidate of metastasis 1)	-0.01	CGAGAGGAAACTGGTGACCAA	NM_012385:	NM_012385:
26471	P8	p8 protein (candidate of metastasis 1)	0.09	CTGGATGAATCTGACCTCTAT	NM_012385:	NM_012385:
5036	PA2G4	proliferation-associated 2G4, 38kDa	2.05	ACGGAAGACTACTTTAAACGA	NM_006191:	NM_006191:
5036	PA2G4	proliferation-associated 2G4, 38kDa	0.02	CCCACTCCCTTCCAACAACAA	NM_006191:	NM_006191:
8106	PABPN1	poly(A) binding protein, nuclear 1	0.63	CTGGGTGCAGGTACACCCAAA	NM_004643:	NM_004643:
8106	PABPN1	poly(A) binding protein, nuclear 1	1.19	CCGTGAGACTGCGAATATAAA	NM_004643:	NM_004643:
135138	PACRG	PARK2 co-regulated	0.64	TTCAGTTGTATAGACAATAAA	NM_152410:	NM_152410:
135138	PACRG	PARK2 co-regulated	0.09	ACAGCTCATTATCCCGATAAA	NM_152410:	NM_152410:
29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	0.18	CAGCAGCTACATCCATGTGTA	NM_020804:	NM_020804:
29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	-1.08	CGCCATAGAGTTCCAGACATA	NM_020804:	NM_020804:
11252	PACSIN2 (prc	protein kinase C and casein kinase substrate in neurons 2	-1.78	CACCCTTAATGTCCCGAGCAA	NM_007229:	NM_007229:
11252	PACSIN2 (prc	protein kinase C and casein kinase substrate in neurons 2	0.01	GAAGCTTTACATAGAACCTTA	NM_007229:	NM_007229:
29763	PACSIN3 (prc	protein kinase C and casein kinase substrate in neurons 3	0.65	AAGGATATGCTGCTCACCTTA	NM_016223:	NM_016223:
29763	PACSIN3 (prc	protein kinase C and casein kinase substrate in neurons 3	0.00	CAGAGGACAATCAGCCGGAAA	NM_016223:	NM_016223:
5047	PAEP	progestagen-associated endometrial protein (placental protein 14, pre	-0.08	ATGGTACTTGCTGGACTTGAA	NM_002571:	NM_002571:NM_001018049:
5047	PAEP	progestagen-associated endometrial protein (placental protein 14, pre	0.68	AAAGAAGTTCAAGATCAACTA	NM_002571:	NM_002571:NM_001018049:
5050	PAFAH1B3 (p	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 2	1.03	CTGCCTTCCCACAACATTAAA	NM_002573:	NM_002573:
5050	PAFAH1B3 (p	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 2	-2.88	TCCACCTACCTCCTAAGTGAA	NM_002573:	NM_002573:
5051	PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	-0.13	GAGAAGTAGTTTGGTCAGCTA	NM_000437:	NM_000437:
5051	PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	0.25	CCCGAGGACCTGTGTTCTTTA	NM_000437:	NM_000437:
55824	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-2.96	TAGGTATGATCTCTAAAGTAA	NM_018440:	NM_018440:
55824	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-1.71	CACGACCAGTGAAACTAACAA	NM_018440:	NM_018440:
5053	PAH	phenylalanine hydroxylase	0.30	TGGGCTTAATATAAATCGTAA	NM_000277:	NM_000277:
5053	PAH	phenylalanine hydroxylase	0.94	GTCGCATTTCATCAAGATTAA	NM_000277:	NM_000277:
10606	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimic	0.87	CCCAAGGACTTCTAACAATAA	NM_006452:	NM_006452:
10606	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimic	0.00	CTCGACTAACAGGGACTATAA	NM_006452:	NM_006452:
5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	-1.10	TCCACTGATTGCTGCAGCTAA	NM_002576:	NM_002576:
5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	0.52	TTGAAGAGAACTGCAACTGAA	NM_002576:	NM_002576:
5062	PAK2	p21 (CDKN1A)-activated kinase 2	-4.50	ACGAGTAATTGTGAAGCATAA	NM_002577:	NM_002577:
5062	PAK2	p21 (CDKN1A)-activated kinase 2	0.22	CCGCGACCGGATCATACGAAA	NM_002577:	NM_002577:
5063	PAK3	p21 (CDKN1A)-activated kinase 3	0.28	CAAGAAGGAATTAATTATTAA	NM_002578:	NM_002578:
5063	PAK3	p21 (CDKN1A)-activated kinase 3	0.79	TTCCAGTACTTTGTACAGGAA	NM_002578:	NM_002578:
10298	PAK4 (p21(Cl	p21(CDKN1A)-activated kinase 4	-2.75	CGGCGCCGAGCCGATGAGTAA	NM_005884:	NM_001014831:NM_005884:NM_001014833:NM_001014835:
10298	PAK4 (p21(Cl	p21(CDKN1A)-activated kinase 4	0.73	CTGGACAACTTCATCAAGATT	NM_005884:	NM_001014831:NM_005884:NM_001014834:NM_001014833:NM_001014832:NM_001014835:
56924	PAK6	p21(CDKN1A)-activated kinase 6	-0.23	CGGAAGGACCATGTTCCGCAA	NM_020168:	NM_020168:
56924	PAK6	p21(CDKN1A)-activated kinase 6	2.03	CTGTGTTACCTTTCAAGTTTA	NM_020168:	NM_020168:
57144	PAK7	p21(CDKN1A)-activated kinase 7	-0.04	ATGATCTGGATCCGTATTATA	NM_177990:	NM_020341:NM_177990:
57144	PAK7	p21(CDKN1A)-activated kinase 7	-0.17	ATGGTGTGCACGTTTCATTAA	NM_177990:	NM_020341:NM_177990:
5066	PAM	peptidylglycine alpha-amidating monooxygenase	0.95	TTGGAACATCGATCAGTTAAA	NM_000919:	NM_138821:NM_138822:NM_138766:NM_000919:
5066	PAM	peptidylglycine alpha-amidating monooxygenase	1.08	CCAGATATGTTCAGAACCATA	NM_000919:	NM_138821:NM_138822:NM_138766:NM_000919:
255967	PAN3	PABP1-dependent poly A-specific ribonuclease subunit PAN3	1.43	TACCTATACTTTGATACTGAA	NM_175854:	NM_175854:
255967	PAN3	PABP1-dependent poly A-specific ribonuclease subunit PAN3	0.01	CCGGATACAGAAATCAAGTAA	NM_175854:	NM_175854:
53354	PANK1	pantothenate kinase 1	-1.35	AACGCTGGTTAAATTGGTGTA	NM_138316:	NM_138316:NM_148977:NM_148978:
53354	PANK1	pantothenate kinase 1	-1.20	CCGAAGGATATTACAGCCGAA	NM_138316:	NM_138316:NM_148977:NM_148978:
80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	-1.81	CAGAGCGACTTTGATCACCAT	NM_024960:	NM_153640:NM_153639:NM_153641:NM_153637:NM_153638:NM_024960:
80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	-0.95	CTGTGTGTGAACTTACTGTAA	NM_024960:	NM_153640:NM_153639:NM_153641:NM_153637:NM_153638:NM_024960:
79646	PANK3	pantothenate kinase 3	1.60	AAGCGAGAATCTGTTAGTAAA	NM_024594:	NM_024594:
79646	PANK3	pantothenate kinase 3	0.11	TCCAAAGGTGATAGCACACAA	NM_024594:	NM_024594:
55229	PANK4	pantothenate kinase 4	1.50	CTGGGAGACGTTCATATTGGA	NM_018216:	NM_018216:
55229	PANK4	pantothenate kinase 4	-0.16	TCGACATAGGCGGGTCGTTAA	NM_018216:	NM_018216:

196743	PAOX	polyamine oxidase (exo-N4-amino)	0.03	CGGAGATGCTGGACACATAAA	NM_207126:	NM_207129:NM_207127:NM_207128:NM_207125:NM_207126:NM_152911:
196743	PAOX	polyamine oxidase (exo-N4-amino)	0.21	CCGGACTTGAGTCTGAGTTCA	NM_207126:	NM_207129:NM_207127:NM_207128:NM_207125:NM_207126:NM_152911:
5069	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	-1.07	CAGGGAGTGCTTGTTTGATAT	NM_002581:	NM_002581:
5069	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	-2.42	CTGGCCAATGCTTAAATACTA	NM_002581:	NM_002581:
9061	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	-1.06	ATGGACTACTATGACTCTGAA	NM_005443:	NM_005443:
9061	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	-0.56	ATGCAGGATACCCATAAGCAA	NM_005443:	NM_005443:
9060	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	0.52	ATGGAAGGTCCTGACAGATTA	NM_004670:	NM_001015880:NM_004670:
9060	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.12	AACATTGTACCCTATACTATA	NM_004670:	NM_001015880:NM_004670:
152559	PAQR3 (prog	progestin and adipoQ receptor family member III	0.60	CTAGATTTAAATAATCACTAA	NM_177453:	NM_177453:
152559	PAQR3 (prog	progestin and adipoQ receptor family member III	-0.40	CAGTTGTTAAGCAATATATAA	NM_177453:	NM_177453:
124222	PAQR4	progestin and adipoQ receptor family member IV	0.57	ACCCTGGATGACATCAATAAA	NM_152341:	NM_152341:
124222	PAQR4	progestin and adipoQ receptor family member IV	-4.89	CAGCACTTGGACAGCCTTCAA	NM_152341:	NM_152341:
54852	PAQR5	progestin and adipoQ receptor family member V	0.30	TCGCAGTCAGTTATAGATCAA	NM_017705:	NM_017705:
54852	PAQR5	progestin and adipoQ receptor family member V	1.81	TCCATATGCATAAGAAGTTAA	NM_017705:	NM_017705:
79957	PAQR6	progestin and adipoQ receptor family member VI	0.17	CAGCAGCTATTTGCCTATAGA	NM_024897:	NM_024897:NM_198406:
79957	PAQR6	progestin and adipoQ receptor family member VI	0.26	AGGGAAGAACTAACACGACTA	NM_024897:	NM_024897:NM_198406:
164091	PAQR7	progestin and adipoQ receptor family member VII	0.22	CTGAATGGTCTTTGCTAAGAA	NM_178422:	NM_178422:
164091	PAQR7	progestin and adipoQ receptor family member VII	1.04	TCCTTGGAAGTCCAAACTCTA	NM_178422:	NM_178422:
85315	PAQR8	progestin and adipoQ receptor family member VIII	0.35	CTAGAATTGCTTATCAATCAA	NM_133367:	NM_133367:
85315	PAQR8	progestin and adipoQ receptor family member VIII	0.59	AGGAAGCTTATTCTCATATAA	NM_133367:	NM_133367:
344838	PAQR9	progestin and adipoQ receptor family member IX	0.78	CACACTCTTCGTGCACTTCTA	NM_198504:	NM_198504:
344838	PAQR9	progestin and adipoQ receptor family member IX	1.84	CAGGGCTTAACCTGCTAGAAA	NM_198504:	NM_198504:
23113	PARC	p53-associated parkin-like cytoplasmic protein	-8.58	CAGATCCTTCACCTTCCTCAA	NM_015089:	NM_015089:
23113	PARC	p53-associated parkin-like cytoplasmic protein	-9.08	CTGCTCTGCCATGGTAAGCAA	NM_015089:	NM_015089:
50855	PARD6A	par-6 partitioning defective 6 homolog alpha (C.elegans)	0.51	CCAGGTTTCCTCAGTCATAGA	NM_016948:	NM_016948:NM_001037281:
50855	PARD6A	par-6 partitioning defective 6 homolog alpha (C.elegans)	-1.90	GACGGACATGATGGTTGCCAA	NM_016948:	NM_016948:NM_001037281:
84552	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	0.51	TTCCTATTTGATACAATTAAA	NM_032510:	NM_032510:
84552	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	-0.27	AACGCCTGTAGAGACACTCTA	NM_032510:	NM_032510:
11315	PARK7	Parkinson disease (autosomal recessive, early onset) 7	0.76	CAGGCTTGTAAACATATAACA	NM_007262:	NM_007262:
11315	PARK7	Parkinson disease (autosomal recessive, early onset) 7	0.58	TGCGACGATCACTTAGAGAAA	NM_007262:	NM_007262:
142	PARP1	poly (ADP-ribose) polymerase family, member 1	-1.52	ACGGTGATCGGTAGCAACAAA	NM_001618:	NM_001618:
142	PARP1	poly (ADP-ribose) polymerase family, member 1	-0.22	CCCGGTGGCTGTGGTATGAAT	NM_001618:	NM_001618:
10038	PARP2	poly (ADP-ribose) polymerase family, member 2	-0.94	AAGTACTATCTGATTCAGCTA	NM_005484:	NM_005484:
10038	PARP2	poly (ADP-ribose) polymerase family, member 2	-0.06	CGGCAGGGCGAGAGCATTAAA	NM_005484:	NM_005484:
10039	PARP3	poly (ADP-ribose) polymerase family, member 3	-0.71	CAGCAAGGAGATGTTCAAGAA	NM_005485:	NM_001003931:NM_005485:NM_001003935:
10039	PARP3	poly (ADP-ribose) polymerase family, member 3	0.83	CACGCAGAAGCTCATCACTAA	NM_005485:	NM_001003931:NM_005485:NM_001003935:
143	PARP4	poly (ADP-ribose) polymerase family, member 4	0.05	CGGCCGTTGGTTCCTATCTTA	NM_006437:	NM_006437:
143	PARP4	poly (ADP-ribose) polymerase family, member 4	-0.56	TAAGTTGGACAGAGTCATGTA	NM_006437:	NM_006437:
23178	PASK	PAS domain containing serine/threonine kinase	-0.64	ATCCTGGTTGCTAACGACAAA	NM_015148:	NM_015148:
23178	PASK	PAS domain containing serine/threonine kinase	0.85	CGCGCTGACACTGTTTGGTTA	NM_015148:	NM_015148:
160065	PATE	expressed in prostate and testis	-0.22	AAGCCTGGAAAGAGTGATGAA	NM_138294:	NM_138294:
160065	PATE	expressed in prostate and testis	0.27	AAGGAGGAAAGGGTAGTTTAA	NM_138294:	NM_138294:
5074	PAWR	PRKC, apoptosis, WT1, regulator	-0.41	CAGAATGAAGCTGTAAACTTA	NM_002583:	NM_002583:
5074	PAWR	PRKC, apoptosis, WT1, regulator	-1.17	CGAGAAGATGCAATTACACAA	NM_002583:	NM_002583:
5076	PAX2 (paired	paired box gene 2	1.68	CCCGTAGTTGCTCTTTCGGTA	NM_000278:	NM_003988:NM_003990:NM_000278:NM_003987:NM_003989:
5076	PAX2 (paired	paired box gene 2	-0.69	CACAGCTACACGCCCATTAAA	NM_000278:	NM_003988:NM_003990:NM_000278:NM_003987:NM_003989:
5077	PAX3	paired box gene 3 (Waardenburg syndrome 1)	-2.52	TAGAGGGTACTTGAATCTTCA	NM_000438:	NM_000438:
5077	PAX3	paired box gene 3 (Waardenburg syndrome 1)	-0.03	CCGAGACAAATTACTCAAGGA	NM_000438:	NM_013942:NM_000438:NM_181460:NM_181459:NM_181461:NM_181458:NM_181457:
5080	PAX6	paired box gene 6 (aniridia, keratitis)	-0.80	CCGAGAAAGACTAGCAGCCAA	NM_000280:	NM_000280:NM_001604:
5080	PAX6	paired box gene 6 (aniridia, keratitis)	0.21	GACGGCATGTATGATAAACTA	NM_000280:	NM_000280:NM_001604:
5081	PAX7	paired box gene 7	1.75	CAGGTTTAGTGAGTTCGATTA	NM_002584:	NM_002584:
5081	PAX7	paired box gene 7	-2.02	TAGCCGCGTGCTCAGAATCAA	NM_002584:	NM_002584:NM_013945:
7849	PAX8 (paired	paired box gene 8	0.16	TCCATTATTAACACAACTCTA	NM_013992:	NM_003466:NM_013951:NM_013952:NM_013953:NM_013992:
7849	PAX8 (paired	paired box gene 8	-2.39	ATGGCTCCATTATTAACACAA	NM_013992:	NM_003466:NM_013951:NM_013952:NM_013953:NM_013992:
5083	PAX9 (paired	paired box gene 9	0.54	CGGCGTGTGCGACAAGTACAA	NM_006194:	NM_006194:
5083	PAX9 (paired	paired box gene 9	0.41	TCCGGCATCGCTGGCGTTCAA	NM_006194:	NM_006194:
55193	PB1	polybromo 1	-1.45	CAGGCTTACATCGCACATACA	NM_018165:	NM_181042:NM_181041:NM_018165:NM_018313:
55193	PB1	polybromo 1	-1.30	CCGGAGTCTTTGATCTACAAA	NM_018165:	NM_181042:NM_181041:NM_018165:NM_018313:
10135	PBEF1	pre-B-cell colony enhancing factor 1	1.13	CTGGAATGTCTAGGCACTGTA	NM_005746:	NM_005746:
10135	PBEF1	pre-B-cell colony enhancing factor 1	0.95	AGGGCCGATTATCTTTACATA	NM_005746:	NM_005746:
55872	PBK	PDZ binding kinase	0.51	AAGTGTGGCTTGCGTAAATAA	NM_018492:	NM_018492:
55872	PBK	PDZ binding kinase	0.01	CTCATTCTCCTTGGGCTGTAA	NM_018492:	NM_018492:
5087	PBX1	pre-B-cell leukemia transcription factor 1	-5.66	CAGACTGGAGGTCGAAGCAAT	NM_002585:	NM_002585:
5087	PBX1	pre-B-cell leukemia transcription factor 1	-3.08	CAGGTTGGAGCCAACGTGCAA	NM_002585:	NM_002585:
5091	PC	pyruvate carboxylase	-0.49	TGGGAAGGTGATAGACATCAA	NM_000920:	NM_000920:NM_022172:
5091	PC	pyruvate carboxylase	-5.48	CCCAGACAACGTGGTCTTCAA	NM_000920:	NM_000920:NM_022172:
8850	PCAF	p300/CBP-associated factor	-2.22	CGGAGTGTACTCCGCCTGCAA	NM_003884:	NM_003884:
8850	PCAF	p300/CBP-associated factor	1.36	CAGCAAATAATTGTCAGTCTA	NM_003884:	NM_003884:
5092	PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hep	-1.25	CTGGCCAGCTTCATCGAACAA	NM_000281:	NM_000281:
5092	PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hep	0.01	ATGGTTTAACGTGTACAACAA	NM_000281:	NM_000281:NM_001001939:
84105	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hep	0.05	CAAGCTATACTTGACCTTAAA	NM_032151:	NM_032151:
84105	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hep	0.20	CAGCAGGATGGTCGGAATTAA	NM_032151:	NM_032151:
5095	PCCA (propio	propionyl Coenzyme A carboxylase, alpha polypeptide	0.06	CTGGATAACTATGTTATTCGA	NM_000282:	NM_000282:
5095	PCCA (propio	propionyl Coenzyme A carboxylase, alpha polypeptide	-0.89	CAGGTTCTAGGTGATAAACAT	NM_000282:	NM_000282:
5096	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	-1.17	CTCAGGATGCTTGGATATTAA	NM_000532:	NM_000532:
5096	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	-0.01	CAGCACAAGCGAGGAAAGCTA	NM_000532:	NM_000532:
57575	PCDH10	protocadherin 10	0.89	CCGCCTCAAGTCTTCCTTTAA	NM_020815:	NM_020815:NM_032961:
57575	PCDH10	protocadherin 10	0.46	TAGGATATTAGCTTATGTGTA	NM_020815:	NM_020815:
65217	PCDH15	protocadherin 15	-0.01	ATGGATTTAGTAGTATGCTTA	NM_033056:	NM_033056:
65217	PCDH15	protocadherin 15	0.90	ATCGCTATGTTCAGGAACAAA	NM_033056:	NM_033056:
27253	PCDH17	protocadherin 17	0.10	CAGACTGTCCTCCGTGATTTA	NM_014459:	NM_014459:
27253	PCDH17	protocadherin 17	1.87	CCAACGTTAAACCTTATTTAA	NM_014459:	NM_014459:
54510	PCDH18	protocadherin 18	-2.65	CCGGAGAATATTTCTCTCACA	NM_019035:	NM_019035:
54510	PCDH18	protocadherin 18	-2.52	CTGCGCCATAGTAGCAGGTAA	NM_019035:	NM_019035:
64881	PCDH20	protocadherin 20	-0.27	CAACTTGTTGGTCGTACTTTA	NM_022843:	NM_022843:
64881	PCDH20	protocadherin 20	1.44	ACCCTATTTAAACATATGATA	NM_022843:	NM_022843:
92211	PCDH21	protocadherin 21	0.01	CAGGTACAACTTCTATGTGAA	NM_033100:	NM_033100:
92211	PCDH21	protocadherin 21	-0.43	CAGGTTGGTAGCAAAGATCTT	NM_033100:	NM_033100:
5099	PCDH7	BH-protocadherin (brain-heart)	0.79	CAGAAATGTGCTACTAATGGA	NM_002589:	NM_002589:
5099	PCDH7	BH-protocadherin (brain-heart)	1.37	CAGAGGTATGATAGTGTCAAT	NM_002589:	NM_032456:NM_032457:NM_002589:

5101	PCDH9 (protc	protocadherin 9	0.28	AAGGCGGTATATGACAACCAA	NM_020403:	NM_020403:NM_203487:
5101	PCDH9 (protc	protocadherin 9	-0.26	ACCGACGTGGGTTATACTTAA	NM_020403:	NM_020403:NM_203487:
9752	PCDHA9	protocadherin alpha 9	0.66	CACCTTGAATATAGTCTTATA	NM_014005:	NM_014005:
9752	PCDHA9	protocadherin alpha 9	0.15	CAGCCTTCATTTCAACTTATA	NM_014005:	NM_014005:
29930	PCDHB1	protocadherin beta 1	0.66	CTCGGCCTTGTCCATATGAAA	NM_013340:	NM_013340:
29930	PCDHB1	protocadherin beta 1	0.12	ACCAAGCATTCTAGAAAGGTA	NM_013340:	NM_013340:
57717	PCDHB16	protocadherin beta 16	0.37	AACGGGTACGGTGATAATTAA	NM_020957:	NM_020957:
57717	PCDHB16	protocadherin beta 16	-0.31	AAGCAAGAGCTGAATATAATA	NM_020957:	NM_020957:
26167	PCDHB5	protocadherin beta 5	-0.94	GACCGGCAATTTGCTTCTATA	NM_015669:	NM_015669:
26167	PCDHB5	protocadherin beta 5	0.65	TCGAGGCAACTCCATATTATA	NM_015669:	NM_015669:
648	PCGF4	polycomb group ring finger 4	-2.01	CAGAGTTCGACCTACTTGTAA	NM_005180:	NM_005180:
648	PCGF4	polycomb group ring finger 4	0.13	CTCCTATGGACGTTAATTGAA	NM_005180:	NM_005180:
5105	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	-2.10	CACAGCGGCTGCAGAACATAA	NM_002591:	NM_002591:
5105	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	0.86	TGGGACTTCAGTGAAGACCAA	NM_002591:	NM_002591:
5108	PCM1	pericentriolar material 1	0.05	CAGGCTTTAACTAATTATGGA	NM_006197:	NM_006197:
5108	PCM1	pericentriolar material 1	1.94	ACCGTGATTCACTTAGATCAA	NM_006197:	NM_006197:
5110	PCMT1 (prote	protein-L-isoaspartate (D-aspartate) O-methyltransferase	0.35	TACGTGCCTTTAACAGATAAA	NM_005389:	NM_005389:
5110	PCMT1 (prote	protein-L-isoaspartate (D-aspartate) O-methyltransferase	-0.16	CTACAAGATGGCAGCATCAAA	NM_005389:	NM_005389:
115294	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain cont	1.19	TAGACGATTACTAAACTGTTA	NM_052937:	NM_052937:
115294	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain cont	1.68	ACAATTATTCTTAGACGATTA	NM_052937:	NM_052937:
55251	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain cont	0.47	AACACAAATCATGTCAATAAA	NM_018257:	NM_018257:
55251	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain cont	1.57	CAAGTTTCAAGTTTATAGATA	NM_018257:	NM_018257:
5111	PCNA	proliferating cell nuclear antigen	-3.03	AAGGATCTTAGGCATTCTTAA	M15796:	NM_002592:NM_182649:
5111	PCNA	proliferating cell nuclear antigen	0.30	ATGGATTTAGATGTTGAACAA	M15796:	NM_002592:NM_182649:
5119	PCOLN3	procollagen (type III) N-endopeptidase	0.06	ATGCTGTTGTAAATAAACAAA	NM_002768:	NM_002768:
5119	PCOLN3	procollagen (type III) N-endopeptidase	0.50	TAGAATGCTGTTGTAAATAAA	NM_002768:	NM_002768:
51586	PCQAP	PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-asso	-2.59	CAGCATCTAATTAAATTGCAT	NM_001003891:	NM_015889:NM_001003891:
51586	PCQAP	PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-asso	-8.60	CCCGCTGACTATCCTGCCCAA	NM_001003891:	NM_015889:NM_001003891:
5122	PCSK1	proprotein convertase subtilisin/kexin type 1	-1.00	AAGGTAATTCATGGCATTGAA	NM_000439:	NM_000439:
5122	PCSK1	proprotein convertase subtilisin/kexin type 1	-0.04	TAGGCAGGATCTGTACAATAA	NM_000439:	NM_000439:
27344	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	0.14	CAGCACGTCCAGAGCAACTTA	NM_013271:	NM_013271:
27344	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	0.13	CTGCTGCGTGTGAAACGCCTA	NM_013271:	NM_013271:
5126	PCSK2	proprotein convertase subtilisin/kexin type 2	-1.11	CACAGGTGTGGTGTAATTTAT	NM_002594:	NM_002594:
5126	PCSK2	proprotein convertase subtilisin/kexin type 2	-1.10	AAGGTTATGGTCAATCCCAAA	NM_002594:	NM_002594:
54760	PCSK4	proprotein convertase subtilisin/kexin type 4	0.33	ACCTCAGAGTTTGCAAATAAA	NM_017573:	NM_017573:
54760	PCSK4	proprotein convertase subtilisin/kexin type 4	0.07	CCGCTGATCTACATCAGGGAA	NM_017573:	NM_017573:
5125	PCSK5	proprotein convertase subtilisin/kexin type 5	-1.60	CTGATGGGTCATATCAGGATA	NM_006200:	NM_006200:
5125	PCSK5	proprotein convertase subtilisin/kexin type 5	0.54	CGGAATTGCTTTCAACGCCAA	NM_006200:	NM_006200:
5046	PCSK6	proprotein convertase subtilisin/kexin type 6	-0.16	CCGGAGTATCTATTTCTACAT	NM_002570:	NM_138319:NM_002570:
5046	PCSK6	proprotein convertase subtilisin/kexin type 6	-0.33	ACGGCGCGGGTCATAAAGTTA	NM_002570:	NM_138319:NM_002570:NM_138323:NM_138320:NM_138321:NM_138324:NM_138325:
9159	PCSK7	proprotein convertase subtilisin/kexin type 7	-1.03	TCGGAGCATTGTGACCACTGA	NM_004716:	NM_004716:
9159	PCSK7	proprotein convertase subtilisin/kexin type 7	-0.64	ATGCCTTTCTATGCAGAAGAA	NM_004716:	NM_004716:
5127	PCTK1	PCTAIRE protein kinase 1	1.62	CACCATAATCGCTGTATGAAA	NM_006201:	NM_033018:NM_006201:
5127	PCTK1	PCTAIRE protein kinase 1	1.73	CACGCCAACATCGTTACGCTA	NM_006201:	NM_033018:NM_006201:
5128	PCTK2	PCTAIRE protein kinase 2	0.88	AGGCTTAATTCTTGCGTATAA	NM_002595:	NM_002595:
5128	PCTK2	PCTAIRE protein kinase 2	1.44	TAGGCTTAATTCTTGCGTATA	NM_002595:	NM_002595:
5129	PCTK3	PCTAIRE protein kinase 3	-10.06	CAGGTTGGATACGGATGGCAT	NM_002596:	NM_212503:NM_212502:NM_002596:
5132	PDC	phosducin	0.89	TCGAGTTATTAGCATTTCTTA	NM_002597:	NM_002597:NM_022576:
5132	PDC	phosducin	1.62	AACAATCGAGTTATTAGCATT	NM_002597:	NM_002597:NM_022576:
5133	PDCD1	programmed cell death 1	0.89	ATCGGAGAGCTTCGTGCTAAA	NM_005018:	NM_005018:
5133	PDCD1	programmed cell death 1	1.62	CCCATTCCTGAAATTATTTAA	NM_005018:	NM_005018:
11235	PDCD10	programmed cell death 10	-0.11	ACGCCTTAATGTGTCATTATA	NM_007217:	NM_007217:NM_145859:NM_145860:
11235	PDCD10	programmed cell death 10	1.84	TACGGATTCAGTTCCAGTTTA	NM_007217:	NM_007217:
27250	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	-0.03	CACCATGAGCTTGTATATGAA	NM_014456:	NM_145341:NM_014456:
27250	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	0.10	CTCAACGTCTGTGCTAATTTA	NM_014456:	NM_145341:NM_014456:
10016	PDCD6	programmed cell death 6	-1.47	CACGGGTGTGTGGAAGTACAT	NM_013232:	NM_013232:
10016	PDCD6	programmed cell death 6	1.70	GACGGATATATTCAGACGTTA	NM_013232:	NM_013232:
10015	PDCD6IP	programmed cell death 6 interacting protein	0.14	CCAGCTTGTTTGCAATTTATA	AB037796:	NM_013374:
10015	PDCD6IP	programmed cell death 6 interacting protein	-0.02	GAGGTACTTTATACTAACATA	AB037796:	NM_013374:
9131	PDCD8	programmed cell death 8 (apoptosis-inducing factor)	-1.54	AAGGTAGAAACTGACCACATA	NM_004208:	NM_004208:NM_145812:NM_145813:
9131	PDCD8	programmed cell death 8 (apoptosis-inducing factor)	-1.70	AGGGTACTGATTGTATCTGAA	NM_004208:	NM_004208:NM_145812:
5082	PDCL	phosducin-like	1.49	CAGGGAAGTATTGTTAGTCTA	NM_005388:	NM_005388:
5082	PDCL	phosducin-like	1.10	CAAGTAGTTTATGGATTTAAA	NM_005388:	NM_005388:
10846	PDE10A	phosphodiesterase 10A	-0.01	CAGTATTACTATACAATGTAA	NM_006661:	NM_006661:
10846	PDE10A	phosphodiesterase 10A	1.03	TAGACTCTCATTCACAATGAA	NM_006661:	NM_006661:
50940	PDE11A	phosphodiesterase 11A	-0.45	CAGGTTTACAATAGGTAAGAA	NM_016953:	NM_016953:
50940	PDE11A	phosphodiesterase 11A	1.05	ATCGTGATATATTTCGATCAA	NM_016953:	NM_016953:
5136	PDE1A	phosphodiesterase 1A, calmodulin-dependent	0.58	ACAGAGTGCTATAACTATAAA	NM_005019:	NM_005019:
5136	PDE1A	phosphodiesterase 1A, calmodulin-dependent	0.36	ACACAGAGTGCTATAACTATA	NM_005019:	NM_005019:
5153	PDE1B	phosphodiesterase 1B, calmodulin-dependent	0.38	CAGGTCTTCATTGAGTCCAAA	NM_000924:	NM_000924:
5153	PDE1B	phosphodiesterase 1B, calmodulin-dependent	0.61	ATCGTGTACAATGATCGTTCA	NM_000924:	NM_000924:
5137	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	0.38	AACAGATGATTCACAAGAGTA	NM_005020:	NM_005020:
5137	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	-1.35	AAGGATCACTCTAACATCGGA	NM_005020:	NM_005020:
5138	PDE2A	phosphodiesterase 2A, cGMP-stimulated	-0.28	ACCGCTTTGTACATGAGAATA	NM_002599:	NM_002599:
5138	PDE2A	phosphodiesterase 2A, cGMP-stimulated	-2.38	ATCGCGGAGCTGATCTACAAA	NM_002599:	NM_002599:
5139	PDE3A	phosphodiesterase 3A, cGMP-inhibited	0.15	TACAGTGAGGTACATTGTTAA	NM_000921:	NM_000921:
5139	PDE3A	phosphodiesterase 3A, cGMP-inhibited	-0.16	AACGTATAATGTGACAGATGA	NM_000921:	NM_000921:
5140	PDE3B	phosphodiesterase 3B, cGMP-inhibited	-0.11	CAGGTTATGTATACCTTATTT	NM_000922:	NM_000922:
5140	PDE3B	phosphodiesterase 3B, cGMP-inhibited	-4.45	CACAGAGTGAACAGCAAACAA	NM_000922:	NM_000922:
5141	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce	0.19	TTCGATCTTGTCTCCAATTAA	NM_006202:	NM_006202:
5141	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce	-0.01	ATGGGAAGTCGTGTCATCCTA	NM_006202:	NM_006202:
5142	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce	0.11	CAGGACATTCTCGATACCTTA	NM_002600:	NM_001037340:NM_002600:NM_001037339:NM_001037341:
5142	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce	-2.43	CACCAAGTCCTTGGAATTGTA	NM_002600:	NM_001037340:NM_002600:NM_001037339:NM_001037341:
5143	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce	1.41	TCCTTCTTTATCAAATATTTA	NM_000923:	NM_000923:
5143	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce	0.01	TAGGGAGACAATCAAGCTCTT	NM_000923:	NM_000923:
5144	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce	0.88	TACTGTAATGTTAATTGTAAA	NM_006203:	NM_006203:
5144	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce	-1.48	TACCCACTAATGGACAATCAA	NM_006203:	NM_006203:
8654	PDE5A	phosphodiesterase 5A, cGMP-specific	0.19	CAGAGATGGTGTGTTCTGCAA	NM_001083:	NM_033437:NM_001083:NM_033430:
8654	PDE5A	phosphodiesterase 5A, cGMP-specific	-1.05	TCGGATGTTTACTGACCTCAA	NM_001083:	NM_033437:NM_001083:NM_033430:
5145	PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	0.00	CGGGATCACCAACAATCGCAA	NM_000440:	NM_000440:
5145	PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	-1.35	CAGATGTATTATGAGCTCAAA	NM_000440:	NM_000440:
5158	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationar	-1.64	CCGGGAAATTGTCTTCTACAA	NM_000283:	NM_000283:
5158	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationar	-2.03	CACGCTGCTCATGACCGGCAA	NM_000283:	NM_000283:
5146	PDE6C	phosphodiesterase 6C, cGMP-specific, cone, alpha prime	-2.47	ACGGATTGATTAAATGTGGAA	NM_006204:	NM_006204:
5146	PDE6C	phosphodiesterase 6C, cGMP-specific, cone, alpha prime	-2.15	CACGGTTAGATCATATCTGAA	NM_006204:	NM_006204:
5148	PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	-6.24	CTCCGTCAGCCTCACCATGAA	NM_002602:	NM_002602:

5148	PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	-1.08	GACGACATCCCTGGAATGGAA	NM_002602:	NM_002602:
5150	PDE7A	phosphodiesterase 7A	0.02	CCGAACATACAGCAATATGAA	NM_002603:	NM_002603:
5150	PDE7A	phosphodiesterase 7A	0.35	CCCGAACATACAGCAATATGA	NM_002603:	NM_002603:
27115	PDE7B	phosphodiesterase 7B	-0.08	TTCAATGTACCCAAACTTGAA	NM_018945:	NM_018945:
27115	PDE7B	phosphodiesterase 7B	0.42	CACCTCCACAATAAAGACTTA	NM_018945:	NM_018945:
5151	PDE8A	phosphodiesterase 8A	-1.21	CCCGGATACATTCCATGACAA	NM_002605:	NM_173455:NM_002605:NM_173456:NM_173457:NM_173454:
5151	PDE8A	phosphodiesterase 8A	0.57	ACGGAGATAATATACAACAAA	NM_002605:	NM_173455:NM_002605:NM_173456:NM_173457:NM_173454:
8622	PDE8B	phosphodiesterase 8B	0.69	TTGGAAGCCATTACGCATAAA	NM_003719:	NM_001029851:NM_003719:NM_001029852:NM_001029853:NM_001029854:
8622	PDE8B	phosphodiesterase 8B	2.25	CAGGAAACGAGTATGTGTTTA	NM_003719:	NM_001029851:NM_003719:NM_001029852:NM_001029853:NM_001029854:
5152	PDE9A	phosphodiesterase 9A	0.24	AACGGATATCCTGATCCTAAT	NM_002606:	NM_001001573:NM_001001567:NM_001001568:NM_001001569:NM_001001577:NM_001001585:NM_001001579:NM_002606:NM_001001581:NM_001001578:NM_001001574:NM_001001584:NM_001001583:NM_001001571:NM_001001575:NM_001001580:NM_001001582:NM_001001576:NM_001001570:NM_001001572:
5152	PDE9A	phosphodiesterase 9A	0.14	CGCGTGGAATTGGAAGGACTA	NM_002606:	NM_001001573:NM_001001567:NM_001001568:NM_001001569:NM_001001577:NM_001001585:NM_001001579:NM_002606:NM_001001581:NM_001001578:NM_001001574:NM_001001584:NM_001001583:NM_001001571:NM_001001575:NM_001001582:NM_001001570:NM_001001572:
5154	PDGFA	platelet-derived growth factor alpha polypeptide	0.39	CAGTGTTTGGACAGAACCCAA	NM_002607:	NM_033023:NM_002607:
5154	PDGFA	platelet-derived growth factor alpha polypeptide	-0.29	AAAGAACTATGCGTCAACCAA	NM_002607:	NM_033023:NM_002607:
5155	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (	-0.08	CAGGGTTATTTAATATGGTAT	NM_002608:	NM_033016:NM_002608:
5155	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (	0.09	GCGGAAGAAGCCAATCTTTAA	NM_002608:	NM_033016:NM_002608:
56034	PDGFC	platelet derived growth factor C	-1.05	AAGGAACTATGTTGCTATGAA	NM_016205:	NM_016205:
56034	PDGFC	platelet derived growth factor C	0.86	CCCAGTGATGGAACTATATTA	NM_016205:	NM_016205:
80310	PDGFD	platelet derived growth factor D	2.38	AAGGTATATCATCAACTTCTA	NM_025208:	NM_033135:NM_025208:
80310	PDGFD	platelet derived growth factor D	-0.32	TACATCTTAGTTGATTATTAA	NM_025208:	NM_033135:NM_025208:
5156	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	-1.18	ACGCAGGAAGCCTACTATTTA	NM_006206:	NM_006206:
5156	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	0.62	CCCGAGACTCCTGTAACCTTA	NM_006206:	NM_006206:
5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	-1.73	ATCCATCAACGTCTCTGTGAA	NM_002609:	NM_002609:
5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	0.88	CCGAGCAACTTTGATCAACGA	NM_002609:	NM_002609:
5157	PDGFRL	platelet-derived growth factor receptor-like	-4.29	ACGCAGTCTATCATGATGCAA	NM_006207:	NM_006207:
5157	PDGFRL	platelet-derived growth factor receptor-like	0.21	CTGGAGGATGTTACTGGCCAA	NM_006207:	NM_006207:
5160	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	-0.48	TTGCATGCAGTTTGTACATTA	NM_000284:	NM_000284:
5160	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	0.51	AACCCAGTCAATGAAATTCAA	NM_000284:	NM_000284:
64714	PDIA2	protein disulfide isomerase family A, member 2	0.03	GAGCTGTGCATTGTGAATAAA	NM_006849:	NM_006849:
64714	PDIA2	protein disulfide isomerase family A, member 2	-1.33	CTGCGCTTGGTCAACCTTGAA	NM_006849:	NM_006849:
2923	PDIA3	protein disulfide isomerase family A, member 3	-0.63	TAGCTGCACTGTTTATGGAAA	NM_005313:	NM_005313:
2923	PDIA3	protein disulfide isomerase family A, member 3	0.61	CCCAAATATCGTCATAGCCAA	NM_005313:	NM_005313:
9601	PDIA4	protein disulfide isomerase family A, member 4	0.35	TTGAGCAAGTTTATAGAAGAA	NM_004911:	NM_004911:
9601	PDIA4	protein disulfide isomerase family A, member 4	1.02	CAAGGTGTCAAACGATGCTAA	NM_004911:	NM_004911:
10954	PDIA5	protein disulfide isomerase family A, member 5	-0.34	GAGGGAGACCATGAAAGACTA	NM_006810:	NM_006810:
10954	PDIA5	protein disulfide isomerase family A, member 5	1.24	ACCGCACAGAATTGGGATTTA	NM_006810:	NM_006810:
10130	PDIA6	protein disulfide isomerase family A, member 6	0.88	AAGATGAAATTTGCTCTGCTA	NM_005742:	NM_005742:
10130	PDIA6	protein disulfide isomerase family A, member 6	0.93	ACGGGATTAGAGGATTTCCTA	NM_005742:	NM_005742:
149420	PDIK1L	PDLIM1 interacting kinase 1 like	-3.47	AAGCTAGACTCTACCCTCTAA	NM_152835:	NM_152835:
149420	PDIK1L	PDLIM1 interacting kinase 1 like	-0.52	CAGCCAAAGTACGATCTAATA	NM_152835:	NM_152835:
204474	PDILT	protein disulfide isomerase-like protein of the testis	-0.70	CCCATCCGTCCAAATCCTAAA	NM_174924:	NM_174924:
204474	PDILT	protein disulfide isomerase-like protein of the testis	0.57	TCCGAGTCATATGGTATCATA	NM_174924:	NM_174924:
5163	PDK1 (pyruva	pyruvate dehydrogenase kinase, isozyme 1	-0.16	CCCGAACTAGAACTTGAAGAA	NM_002610:	NM_002610:
5163	PDK1 (pyruva	pyruvate dehydrogenase kinase, isozyme 1	1.29	TCGGGTTTCTATAGGAAACTA	NM_002610:	NM_002610:
5164	PDK2 (pyruva	pyruvate dehydrogenase kinase, isozyme 2	-1.15	AAGAACCTTGTTAGACCGAGA	NM_002611:	NM_002611:
5164	PDK2 (pyruva	pyruvate dehydrogenase kinase, isozyme 2	-1.15	TAGGTCTGTGATGGTCCCTAA	NM_002611:	NM_002611:
5165	PDK3 (pyruva	pyruvate dehydrogenase kinase, isozyme 3	-0.12	AACGTTGTAGGTTGAAACTGA	NM_005391:	NM_005391:
5165	PDK3 (pyruva	pyruvate dehydrogenase kinase, isozyme 3	2.75	TTCATTAGCACTAACATCCAA	NM_005391:	NM_005391:
5166	PDK4	pyruvate dehydrogenase kinase, isozyme 4	1.44	ACCCGTGTCAATTAACATTTA	NM_002612:	NM_002612:
5166	PDK4	pyruvate dehydrogenase kinase, isozyme 4	2.40	AGGCCTCTTGTTCACATCAAA	NM_002612:	NM_002612:
10611	PDLIM5	PDZ and LIM domain 5	-1.29	CAGCAGGGAAACGAACTCCGA	NM_006457:	NM_001011513:NM_006457:NM_001011514:
10611	PDLIM5	PDZ and LIM domain 5	0.55	TCCGATGTGCGCCCATTGTAA	NM_006457:	NM_001011513:NM_006457:NM_001011514:
9260	PDLIM7 (PDZ	PDZ and LIM domain 7 (enigma)	0.10	ACCCAGCGTCTCCCTCAACAA	NM_005451:	NM_213636:NM_203353:NM_005451:
9260	PDLIM7 (PDZ	PDZ and LIM domain 7 (enigma)	-0.04	CACCTCCAGTGCCACAATAAA	NM_005451:	NM_203352:NM_203353:NM_005451:
57546	PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	-0.20	CAGGACGATCATCATGGAGGA	NM_020786:	NM_020786:
57546	PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	-3.19	TAGACAGGACAGGTTAATTTA	NM_020786:	NM_020786:
5170	PDPK1	3-phosphoinositide dependent protein kinase-1	-2.52	AAGCGGTTAGGCTGTGAGGAA	NM_002613:	NM_031268:XM_496112:NM_002613:
5170	PDPK1	3-phosphoinositide dependent protein kinase-1	0.08	CACGCCTAACAGGACGTATTA	NM_002613:	NM_031268:NM_002613:
10630	PDPN	podoplanin	-0.16	ATCGAGGATCTGCCAACTTCA	NM_001006624:	NM_006474:NM_001006624:NM_198389:NM_001006625:
10630	PDPN	podoplanin	0.82	CAGGAAGTCGATAGTCTCAAA	NM_001006624:	NM_006474:NM_001006624:NM_198389:NM_001006625:
55066	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	1.23	ACCACATAGCCCAGTGATTAA	NM_017990:	NM_017990:
55066	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	0.33	ATCTCTTATCTCCTTGATATA	NM_017990:	NM_017990:
8566	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	-1.24	CCGGAGCTTCATCTAGTGATT	NM_003681:	NM_003681:
8566	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.18	TCGAGTGACTTTCTAACCCAA	NM_003681:	NM_003681:
8566	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	-0.12	CACAGGTTATACGAGGGACAA	NM_003681:	NM_003681:
8566	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.52	GAGGCTGAACAACATGAATAA	NM_003681:	NM_003681:
23037	PDZD2	PDZ domain containing 2	-3.43	TAGGTTATTGATCACCATGAA	NM_015022:	NM_178140:NM_015022:
23037	PDZD2	PDZ domain containing 2	0.44	AAGCTTGTGCTTACACATGAA	NM_015022:	NM_178140:NM_015022:
79849	PDZD3	PDZ domain containing 3	-0.03	ACCGTTGCATTTGTTATAGAA	NM_024791:	NM_024791:
79849	PDZD3	PDZ domain containing 3	0.83	TCGGGTGTTGCTGACAGTATT	NM_024791:	NM_024791:
118987	PDZD8	PDZ domain containing 8	-0.88	ACCGATCTCGTAGAACCTTCA	NM_173791:	NM_173791:
118987	PDZD8	PDZ domain containing 8	0.26	CAACATGGTGTGACTACTGTA	NM_173791:	NM_173791:
23024	PDZRN3	PDZ domain containing RING finger 3	0.30	CCCGGTGGTTAACGATTTAAT	XM_041363:	NM_015009:
23024	PDZRN3	PDZ domain containing RING finger 3	-0.21	CCCGGACGGCACTAGAGTATA	XM_041363:	NM_015009:
8682	PEA15	phosphoprotein enriched in astrocytes 15	-0.48	AAGGTGATTGATTGTATTGCA	NM_003768:	NM_003768:
8682	PEA15	phosphoprotein enriched in astrocytes 15	0.08	CTGGTTAGACAGTACTCTTAA	NM_003768:	NM_003768:
5175	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	1.11	CCCAATACACTTCACAATTGA	NM_000442:	NM_000442:
5175	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	0.00	TACGATTGTGTCACAGACTCA	NM_000442:	NM_000442:
55825	PECR	peroxisomal trans-2-enoyl-CoA reductase	0.57	ATGCCTTATGGTAATTATTGA	NM_018441:	NM_018441:
55825	PECR	peroxisomal trans-2-enoyl-CoA reductase	-0.56	AAGCTTATAGTTGGTATGGAA	NM_018441:	NM_018441:
57161	PELI2 (pellinc	pellino homolog 2 (Drosophila)	0.01	CTCGGGTACAATGGTGCTTTA	NM_021255:	NM_021255:
57161	PELI2 (pellinc	pellino homolog 2 (Drosophila)	0.57	CACGTGATATAACTGGTTATA	NM_021255:	NM_021255:

53918	PELO	pelota homolog (Drosophila)	-0.54	ACGTACTACCATCTTGATTAA	NM_015946:	NM_015946:
53918	PELO	pelota homolog (Drosophila)	0.55	CTGAAGAGGATTAATGATTGA	NM_015946:	NM_015946:
27043	PELP1	proline, glutamic acid and leucine rich protein 1	1.55	CGGGCTTGTGGTTCTCTCAAA	NM_014389:	NM_014389:
27043	PELP1	proline, glutamic acid and leucine rich protein 1	2.49	CAAGGTGTATGCGATATTAGA	NM_014389:	NM_014389:
56652	PEO1	progressive external ophthalmoplegia 1	-3.09	CTGGCAGGCTAGTGTAGATAA	NM_021830:	NM_021830:
56652	PEO1	progressive external ophthalmoplegia 1	-2.61	TAGGATAGGCTGGAGCATAAA	NM_021830:	NM_021830:
5184	PEPD	peptidase D	-1.59	CTGTCCTTTAGTAGCAAGTAA	NM_000285:	NM_000285:
5184	PEPD	peptidase D	0.18	TCGGCATTTGATCAGACCAAA	NM_000285:	NM_000285:
5187	PER1	period homolog 1 (Drosophila)	-1.10	CCAGCGCGTCATGATGACCTA	NM_002616:	NM_002616:
5187	PER1	period homolog 1 (Drosophila)	-1.00	CCCGGACTCTCCACTGTTCAA	NM_002616:	NM_002616:
8864	PER2	period homolog 2 (Drosophila)	0.49	TCGAAAGTGGACACACACAAA	NM_003894:	NM_022817:NM_003894:
8864	PER2	period homolog 2 (Drosophila)	-1.40	CAGCTGGTCCAGCTTCATCAA	NM_003894:	NM_022817:NM_003894:
8863	PER3	period homolog 3 (Drosophila)	-2.05	CAGGATCATTGCGCACTCATA	NM_016831:	NM_016831:
8863	PER3	period homolog 3 (Drosophila)	0.65	AAGGTGTATAATTGGATTCAA	NM_016831:	NM_016831:
64065	PERP	PERP, TP53 apoptosis effector	0.93	CACGTGAAACTTAACACTTTA	NM_022121:	NM_022121:
64065	PERP	PERP, TP53 apoptosis effector	-0.14	TAGAATGGACTCGGTCTGTTA	NM_022121:	NM_022121:
5189	PEX1	peroxisome biogenesis factor 1	-0.09	AAGGCAGATACCGGAGCCAAA	NM_000466:	NM_000466:
5189	PEX1	peroxisome biogenesis factor 1	-0.97	CTCATGGATACTATCCAGTTA	NM_000466:	NM_000466:
5192	PEX10	peroxisome biogenesis factor 10	0.84	ACCGTAGGCATCTTTAATAAA	NM_002617:	NM_002617:NM_153818:
5192	PEX10	peroxisome biogenesis factor 10	-0.20	AAGATTTAGTCTCAGGATTAA	NM_002617:	NM_002617:NM_153818:
5194	PEX13	peroxisome biogenesis factor 13	0.09	TTGACTTGGAATCCTTAGTAA	NM_002618:	NM_002618:
5194	PEX13	peroxisome biogenesis factor 13	-1.15	TACCAACCCAACACTAACTAA	NM_002618:	NM_002618:
5195	PEX14	peroxisomal biogenesis factor 14	0.83	TAGGACTGTATATAATTGTAA	NM_004565:	NM_004565:
5195	PEX14	peroxisomal biogenesis factor 14	0.02	CGAACTCAAGTCCGAAATTAA	NM_004565:	NM_004565:
5824	PEX19	peroxisomal biogenesis factor 19	-0.45	ATGGGTGGCTTCATGAATTAA	NM_002857:	NM_002857:
5824	PEX19	peroxisomal biogenesis factor 19	1.40	TCCCTTGAGTATTTCAATGTA	NM_002857:	NM_002857:
8504	PEX3	peroxisomal biogenesis factor 3	1.01	ATGGTGAATTCCAACAACTAT	NM_003630:	NM_003630:
8504	PEX3	peroxisomal biogenesis factor 3	1.25	TGGGTAAATCACCTATACTTA	NM_003630:	NM_003630:
5830	PEX5	peroxisomal biogenesis factor 5	-4.22	CAGCTTCCTTGGGCAGTGTAA	NM_000319:	NM_000319:
5830	PEX5	peroxisomal biogenesis factor 5	0.08	TACGTCAGCTACCTATGATAA	NM_000319:	NM_000319:
51555	PEX5L	peroxisomal biogenesis factor 5-like	-0.12	ATGGGACGATGTTAAGTTTCA	NM_016559:	NM_016559:
51555	PEX5L	peroxisomal biogenesis factor 5-like	0.64	CTCGAAATAATTGTTGATCAA	NM_016559:	NM_016559:
5190	PEX6	peroxisomal biogenesis factor 6	-1.61	CAGGATGTGTTTGTGATTGGA	NM_000287:	NM_000287:
5190	PEX6	peroxisomal biogenesis factor 6	-4.39	CCAGAGCTCATTAACATGTAT	NM_000287:	NM_000287:
5191	PEX7	peroxisomal biogenesis factor 7	1.65	TAGGTTATACGTATATAGATA	NM_000288:	NM_000288:
5191	PEX7	peroxisomal biogenesis factor 7	0.04	AAGCCTGACTCTCTTCTTGAA	NM_000288:	NM_000288:
5196	PF4	platelet factor 4 (chemokine (C-X-C motif) ligand 4)	0.32	CTGATATTTGTGTTATCCTTA	NM_002619:	NM_002619:
5196	PF4	platelet factor 4 (chemokine (C-X-C motif) ligand 4)	1.08	TACGTGTGTGCATTTGCTATA	NM_002619:	NM_002619:
5207	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	1.51	CTCCACAAAGCTCACACGATA	NM_002625:	NM_002625:
5207	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	1.46	CTGCGAGACCAAGATAAATAT	NM_002625:	NM_002625:
5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	0.08	CCAGAGCAAGATAGTCTACTA	NM_006212:	NM_001018053:NM_006212:
5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-0.37	CCGTGACAAGCCAACTAACAA	NM_006212:	NM_006212:
5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.71	CAGGGACTTGTCGCTGATCAA	NM_004566:	NM_004566:
5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	2.44	CTCCAATATCATGGAAGTTAA	NM_004566:	NM_004566:
5210	PFKFB4 (6-pł	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-0.55	ACGGAGAGCGACCATCTTTAA	NM_004567:	NM_004567:
5210	PFKFB4 (6-pł	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-1.18	CAGAAAGTGTCTGGACTTGTA	NM_004567:	NM_004567:
5211	PFKL	phosphofructokinase, liver	0.03	CACGATGGCTTCGAAGGCCTA	NM_002626:	NM_002626:NM_001002021:
5211	PFKL	phosphofructokinase, liver	0.85	CCGGACCTACTCGCACCTGAA	NM_002626:	NM_002626:NM_001002021:
5213	PFKM	phosphofructokinase, muscle	1.17	AACAGATCAGTGCCAATATAA	NM_000289:	NM_000289:
5213	PFKM	phosphofructokinase, muscle	-1.36	AAGGACTTTCGGGAACGAGAA	NM_000289:	NM_000289:
5214	PFKP	phosphofructokinase, platelet	0.22	CAGCACTTTATGCACGTATTA	NM_002627:	NM_002627:
5214	PFKP	phosphofructokinase, platelet	-0.37	CCGCCTGAAGGCTGCTTGCAA	NM_002627:	NM_002627:
5216	PFN1 (profilin	profilin 1	-2.54	CGGGTGGAACGCCTACATCGA	NM_005022:	NM_005022:
5216	PFN1 (profilin	profilin 1	-2.48	TAGCATGGATCTTCGTACCAA	NM_005022:	NM_005022:
5217	PFN2	profilin 2	0.27	CAGACAGATGAAATAAATTTA	NM_002628:	NM_002628:NM_053024:
5217	PFN2	profilin 2	0.91	CTGATTTAATATGCATTTAAA	NM_002628:	NM_002628:NM_053024:
51659	Pfs2	DNA replication complex GINS protein PSF2	-4.00	CTCCTGTTAAATCATGCTTCA	NM_016095:	NM_016095:
51659	Pfs2	DNA replication complex GINS protein PSF2	-2.17	CTGGCGATTAACCTGAAACAA	NM_016095:	NM_016095:
5218	PFTK1	PFTAIRE protein kinase 1	-2.34	AAGGGACACCTTTCACAGCTA	NM_012395:	NM_012395:
5218	PFTK1	PFTAIRE protein kinase 1	-0.03	CTGGGTCTTGTCAACATCTAA	NM_012395:	NM_012395:
5222	PGA5 (pepsin	pepsinogen 5, group I (pepsinogen A)	-0.20	GCCCACTTTAGATGTATCTAA	NM_014224:	NM_014224:
5222	PGA5 (pepsin	pepsinogen 5, group I (pepsinogen A)	-1.91	CACCATCAATGGAGTCCAGTA	NM_014224:	NM_014224:
5224	PGAM2	phosphoglycerate mutase 2 (muscle)	-2.62	CCAGGCGATCATGGAGCTGAA	NM_000290:	NM_000290:
5224	PGAM2	phosphoglycerate mutase 2 (muscle)	-0.31	CTGCTACACGTCAGTGCTGAA	NM_000290:	NM_000290:
80055	PGAP1	GPI deacylase	0.74	TCCATGCATTATGCAACTTTA	NM_024989:	NM_024989:
80055	PGAP1	GPI deacylase	0.54	TTGGGTCAGCACATTTATATA	NM_024989:	NM_024989:
84547	PGBD1	piggyBac transposable element derived 1	0.76	CCCAAGCTAAGTGAAGCTTTA	NM_032507:	NM_032507:
84547	PGBD1	piggyBac transposable element derived 1	0.25	CTGGTTTGGTTTGAACCCTAT	NM_032507:	NM_032507:
5228	PGF	placental growth factor, vascular endothelial growth factor-related prot	0.64	ACCCGGCTCGTGTATTTATTA	NM_002632:	NM_002632:
5228	PGF	placental growth factor, vascular endothelial growth factor-related prot	0.77	TGCCCTCTATTTATTAGCCAA	NM_002632:	NM_002632:
5229	PGGT1B	protein geranylgeranyltransferase type I, beta subunit	-0.47	CACTTCATATAGCATTGATAA	NM_005023:	NM_005023:
5229	PGGT1B	protein geranylgeranyltransferase type I, beta subunit	0.01	CTGGGTATTCCGTTCAATCCA	NM_005023:	NM_005023:
5230	PGK1	phosphoglycerate kinase 1	0.72	CACAATTATAGATTAGATCAA	NM_000291:	NM_000291:
5230	PGK1	phosphoglycerate kinase 1	1.20	GAGGAACGGATCAGATGTCTA	NM_000291:	NM_000291:
5232	PGK2	phosphoglycerate kinase 2	0.64	CAGCAACATGTAGTTAATATA	NM_138733:	NM_138733:
5232	PGK2	phosphoglycerate kinase 2	-1.81	CAGGCCATCAGGAACTCTTAA	NM_138733:	NM_138733:
8993	PGLYRP1	peptidoglycan recognition protein 1	-2.32	GAGGTCCAACTATGTGCTCAA	NM_005091:	NM_005091:
8993	PGLYRP1	peptidoglycan recognition protein 1	0.91	TGGCATCAGCTTCATGGGCAA	NM_005091:	NM_005091:
114770	PGLYRP2	peptidoglycan recognition protein 2	0.72	CACCTGGACAATCTCGTGCTA	NM_052890:	NM_052890:
114770	PGLYRP2	peptidoglycan recognition protein 2	0.93	CACGTCTATTCAGGAAACCTA	NM_052890:	NM_052890:
114771	PGLYRP3	peptidoglycan recognition protein 3	-0.40	CAGACTGTCGTCCGAAACATA	NM_052891:	NM_052891:
114771	PGLYRP3	peptidoglycan recognition protein 3	-0.40	CAGGATGGTGGCGTGTATGAA	NM_052891:	NM_052891:
57115	PGLYRP4	peptidoglycan recognition protein 4	1.15	TCAGCAGTGTCTGAAATTTAA	NM_020393:	NM_020393:
57115	PGLYRP4	peptidoglycan recognition protein 4	-4.82	CAGCGAAGTATGGCATCATTA	NM_020393:	NM_020393:
5239	PGM5	phosphoglucomutase 5	-1.56	CAGACTGTACGCAGAGAGCTA	NM_021965:	NM_021965:
5239	PGM5	phosphoglucomutase 5	-0.01	CTCCATTATTGCTGCCCGGAA	NM_021965:	NM_021965:
54858	PGPEP1	pyroglutamyl-peptidase I	-0.09	CTCCTTAGAGATATAACCTAT	NM_017712:	NM_017712:
54858	PGPEP1	pyroglutamyl-peptidase I	-6.88	CAGAGGTCTGGTGGAAAGCAA	NM_017712:	NM_017712:
5241	PGR	progesterone receptor	0.20	CACAGCGTTTCTATCAACTTA	NM_000926:	NM_000926:
5241	PGR	progesterone receptor	-0.34	CTGCCTCTCAATCACGCCTTA	NM_000926:	NM_000926:
10857	PGRMC1	progesterone receptor membrane component 1	0.52	ATCACTAGTGACACTAATAAA	NM_006667:	NM_006667:
10857	PGRMC1	progesterone receptor membrane component 1	0.72	CAAACTTGTAATTGTGGTTAA	NM_006667:	NM_006667:
10424	PGRMC2	progesterone receptor membrane component 2	-0.55	CAAGATAAATTAATCTCACTA	NM_006320:	NM_006320:
10424	PGRMC2	progesterone receptor membrane component 2	-0.11	CCGGCGGGTCCATATGGAATA	NM_006320:	NM_006320:
54681	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase	-1.05	CAGGGCCATGGCATTTAACTA	NM_017732:	NM_017732:
54681	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase	2.46	AACCATTGCAACTCACAGTAA	NM_017732:	NM_017732:
5245	PHB (prohibiti	prohibitin	0.34	AAGGAAACAAATGTGTATAAA	NM_002634:	NM_002634:
5245	PHB (prohibiti	prohibitin	1.82	TGGGAAGGAAACAAATGTGTA	NM_002634:	NM_002634:
5245	PHB (prohibiti	prohibitin	-1.57	AGTGAAGGAAATAAAGGTAAA	XM_496437:	XM_497140:NM_002634:XM_496437:

11331	PHB2	prohibitin 2	-2.77	AACCCAGGAATTCTCAATAAA	NM_007273:	NM_007273:
11331	PHB2	prohibitin 2	-2.25	CACAGCTGCTGTAGAAGCCAA	NM_007273:	NM_007273:
5251	PHEX	phosphate regulating endopeptidase homolog, X-linked (hypophospha	-1.59	CTGGCCCGTGCTTGAATCTAA	NM_000444:	NM_000444:
5251	PHEX	phosphate regulating endopeptidase homolog, X-linked (hypophospha	2.55	CCCGAAGATATGCCAAGCTAT	NM_000444:	NM_000444:
5252	PHF1	PHD finger protein 1	0.13	ACTCTGTATGATTGAAATAAA	NM_002636:	NM_024165:NM_002636:
5252	PHF1	PHD finger protein 1	-1.81	CCCGGACTCTGTATGATTGAA	NM_002636:	NM_024165:NM_002636:
55274	PHF10	PHD finger protein 10	-3.69	ATGGCAGTGTATGGAATGTAA	NM_018288:	NM_133325:NM_018288:
55274	PHF10	PHD finger protein 10	0.79	TCCAGGGAAGACAGAAATCAA	NM_018288:	NM_133325:NM_018288:
51131	PHF11	PHD finger protein 11	-2.22	ACAGCCCATGATAGCCTCTTA	NM_016119:	NM_016119:
51131	PHF11	PHD finger protein 11	2.26	GAGATCTTATGTCAAGTTCTA	NM_016119:	NM_016119:
57649	PHF12	PHD finger protein 12	0.67	CACAATGGTCTCGTTCCCTTA	NM_020889:	NM_020889:NM_001033561:
57649	PHF12	PHD finger protein 12	-3.73	CAGGTTCTAGCAAGAGGAGAA	NM_020889:	NM_020889:NM_001033561:
148479	PHF13	PHD finger protein 13	-0.12	ATGGCCCGTGTTCATAACTCA	NM_153812:	NM_153812:
148479	PHF13	PHD finger protein 13	-0.03	CAGCTGGTGGTTCTTAGGTTT	NM_153812:	NM_153812:
9678	PHF14 (PHD	PHD finger protein 14	-2.74	CAGAACTAGCTCGATCTACCA	XM_376578:	NM_001007157:NM_014660:
9678	PHF14 (PHD	PHD finger protein 14	-0.60	AAGAAGTACTATCATCAGAAA	XM_376578:	NM_001007157:NM_014660:
23338	PHF15	PHD finger protein 15	-0.63	AACCCTTAACGAGCAATAGAA	NM_015288:	NM_015288:
23338	PHF15	PHD finger protein 15	-0.30	ATGACAAAGGATAATGTGCAA	NM_015288:	NM_015288:
9767	PHF16	PHD finger protein 16	-0.06	ACCATGATTATCAGACACTAA	NM_014735:	NM_014735:
9767	PHF16	PHD finger protein 16	-1.46	CACCAATAGGTGGGTGAAGAA	NM_014735:	NM_014735:
79960	PHF17	PHD finger protein 17	0.16	ACCGATTAAATTCATTAGTGT	NM_024900:	NM_024900:
79960	PHF17	PHD finger protein 17	1.00	CGCCCAGAGCAAGAAATGATA	NM_024900:	NM_024900:
26147	PHF19	PHD finger protein 19	1.30	CAGCATTTCATTCATACCAGA	XM_045308:	NM_015651:
26147	PHF19	PHD finger protein 19	-0.10	CCTCGTGACTTTCGAAGATAA	XM_045308:	NM_001009936:NM_015651:
51230	PHF20	PHD finger protein 20	0.38	ATGAATTATAGGACAAGTATA	NM_016436:	NM_016436:
51230	PHF20	PHD finger protein 20	1.46	AGCGACCTTTGGAATAGTTAA	NM_016436:	NM_016436:
51105	PHF20L1	PHD finger protein 20-like 1	0.28	ACGGAAATTTAGGGTATTTAA	NM_016018:	NM_016018:
51105	PHF20L1	PHD finger protein 20-like 1	-1.30	CAGCTGAAGATTGGAATACTA	NM_016018:	NM_016018:
51317	PHF21A	PHD finger protein 21A	-0.20	ACCATGCCAAGTGAAATAATA	NM_016621:	NM_016621:
51317	PHF21A	PHD finger protein 21A	-5.22	ACCGGACAAGTTCCAAATACA	NM_016621:	NM_016621:
112885	PHF21B	PHD finger protein 21B	0.38	TCCGGGAGAAACTGTGCTGTA	NM_138415:	NM_138415:
112885	PHF21B	PHD finger protein 21B	0.18	TTGTGAGATATTTAATGTGAA	NM_138415:	NM_138415:
57117	PHF22	PHD finger protein 22	-5.99	CAGGACCTAGTGGAAGTACTA	NM_020395:	NM_020395:
57117	PHF22	PHD finger protein 22	0.15	TACGCCCACTGTACCTTTAAA	NM_020395:	NM_020395:
79142	PHF23	PHD finger protein 23	2.15	AGCCTGCGTGTTGTAAATAAA	NM_024297:	NM_024297:
79142	PHF23	PHD finger protein 23	-0.31	CAGCTCAAAGGTGGAGTACTA	NM_024297:	NM_024297:
84295	PHF6	PHD finger protein 6	-0.05	CTCTCTTTCCATGTTATACAA	NM_032458:	NM_001015877:NM_032458:
84295	PHF6	PHD finger protein 6	-2.09	TAAGATATTCACACTCCTCAA	NM_032458:	NM_032458:
51533	PHF7	PHD finger protein 7	-1.90	CCGCAAGTGCATACAGAAATA	NM_016483:	NM_173341:NM_016483:
51533	PHF7	PHD finger protein 7	-1.78	CTGTCTTATCTTATCTAGTAA	NM_016483:	NM_173341:NM_016483:
23133	PHF8	PHD finger protein 8	-3.51	GAGGATTTCTATTCACCTTTA	NM_015107:	NM_015107:
23133	PHF8	PHD finger protein 8	-2.25	TCGGCGAACCAAGATAGCAAA	NM_015107:	NM_015107:
26227	PHGDH	phosphoglycerate dehydrogenase	-0.02	CAGCAATAACCGTCTAATAAA	NM_006623:	NM_006623:
26227	PHGDH	phosphoglycerate dehydrogenase	-0.37	CACGACAGGCTTGCTGAATGA	NM_006623:	NM_006623:
337867	PHGDHL1	phosphoglycerate dehydrogenase like 1	-0.10	GAGGGTAATGTTACTTCACAA	NM_177967:	NM_177967:
337867	PHGDHL1	phosphoglycerate dehydrogenase like 1	-1.29	TGCCATTACATTAGCATGTAT	NM_177967:	NM_177967:
55023	PHIP	pleckstrin homology domain interacting protein	1.58	CAGCACGTATTTGGCAATTTA	NM_017934:	NM_017934:
55023	PHIP	pleckstrin homology domain interacting protein	0.41	CACATGAGAACTAGAAATCAA	NM_017934:	NM_017934:
5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)	-0.90	ATGGGAGTGCTTGGAACTTCA	NM_002637:	NM_002637:
5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)	0.30	CCCAATCGTCTGTACTATGAA	NM_002637:	NM_002637:
5256	PHKA2	phosphorylase kinase, alpha 2 (liver)	-3.96	CCGCCTAACAAGGTAGATGAA	NM_000292:	NM_000292:
5256	PHKA2	phosphorylase kinase, alpha 2 (liver)	-0.27	CCGGATTCTTAGTCACATATA	NM_000292:	NM_000292:
5257	PHKB	phosphorylase kinase, beta	-2.70	AGGGCTGTTCGTGGTCAGTTA	NM_000293:	NM_001031835:NM_000293:
5257	PHKB	phosphorylase kinase, beta	1.15	TCGATGGGTCTTTGAATAGAA	NM_000293:	NM_001031835:NM_000293:
5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)	-1.22	CAAGAGCCTGCAAGCACTTAA	NM_006213:	NM_006213:
5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)	-0.19	CCGGGAGATCGTCATCCGAGA	NM_006213:	NM_006213:
5261	PHKG2 (phos	phosphorylase kinase, gamma 2 (testis)	2.09	CTGCATGCACTGCATATGAAA	NM_000294:	NM_000294:
5261	PHKG2 (phos	phosphorylase kinase, gamma 2 (testis)	2.32	TACGGGCACTGGGTAAAGAAA	NM_000294:	NM_000294:
7262	PHLDA2	pleckstrin homology-like domain, family A, member 2	0.43	CGCGCTCGGCACGACATGAAA	NM_003311:	NM_003311:
7262	PHLDA2	pleckstrin homology-like domain, family A, member 2	-4.79	CTGGTTCTTTGTAGTCACATA	NM_003311:	NM_003311:
162466	PHOSPHO1 (	phosphatase, orphan 1	-2.14	CGCCAACATGTGCAAGCACAA	NM_178500:	NM_178500:
162466	PHOSPHO1 (	phosphatase, orphan 1	0.98	TCGGGTCCGGACAGCCAGTAA	NM_178500:	NM_178500:
29085	PHPT1	phosphohistidine phosphatase 1	0.36	CACGCCATTTCAACTGAGAAA	NM_014172:	NM_014172:
29085	PHPT1	phosphohistidine phosphatase 1	-1.58	TCGGGCGACATGCAGAAGCAA	NM_014172:	NM_014172:
5264	PHYH	phytanoyl-CoA 2-hydroxylase	-1.51	TAGCGTGAACTTGAAGGATAT	NM_006214:	NM_001037537:NM_006214:
5264	PHYH	phytanoyl-CoA 2-hydroxylase	0.00	TTGCCACTACATTGACGTGAA	NM_006214:	NM_001037537:NM_006214:
55300	PI4K2B	phosphatidylinositol 4-kinase type 2 beta	1.54	ATGAACTTTGTGCAAGATTTA	NM_018323:	NM_018323:
55300	PI4K2B	phosphatidylinositol 4-kinase type 2 beta	0.29	CAGAGTACTGGCCTTGTTCAA	NM_018323:	NM_018323:
55361	PI4KII	phosphatidylinositol 4-kinase type II	-0.08	ACGCAAATGTATGAATAACAA	NM_018425:	NM_018425:
55361	PI4KII	phosphatidylinositol 4-kinase type II	-1.96	CCGCATCGGGCTACCACCAAA	NM_018425:	NM_018425:
8554	PIAS1	protein inhibitor of activated STAT, 1	-1.14	CCGGATCATTCTAGAGCTTTA	NM_016166:	NM_016166:
8554	PIAS1	protein inhibitor of activated STAT, 1	-2.53	ACGAGCAAAGGGAATAAGGAA	NM_016166:	NM_016166:
27124	PIB5PA	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	0.79	CAGGTAACATTCAGTGAGGAA	NM_014422:	NM_014422:NM_001002837:
27124	PIB5PA	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	0.30	CTGGGACTGGATCGGCTTATA	NM_014422:	NM_014422:NM_001002837:
8301	PICALM	phosphatidylinositol binding clathrin assembly protein	-0.55	AAGAAGGTCTTGACATCTATA	NM_007166:	NM_001008660:NM_007166:
8301	PICALM	phosphatidylinositol binding clathrin assembly protein	0.44	CACGTTGTTTAACTTAAGCAA	NM_007166:	NM_001008660:NM_007166:
9463	PICK1	protein interacting with PRKCA 1	-0.28	CCGGTGTCAATGGCAGGTCAA	NM_012407:	NM_012407:
9463	PICK1	protein interacting with PRKCA 1	-1.62	TCGCCTCACCATCAAGAAGTA	NM_012407:	NM_012407:
10026	PIGK	phosphatidylinositol glycan, class K	0.60	GCAAACTTGGATAATAATTTA	NM_005482:	NM_005482:
10026	PIGK	phosphatidylinositol glycan, class K	0.36	ATGGCTCTAGCTAGTAGTCAA	NM_005482:	NM_005482:
5284	PIGR (polyme	polymeric immunoglobulin receptor	0.68	CAGGAAGAATACGCCTTGATA	NM_002644:	NM_002644:
5284	PIGR (polyme	polymeric immunoglobulin receptor	-0.31	TACAACCGTAAGGAAAGCAAA	NM_002644:	NM_002644:
118788	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	-0.77	ATGCTCAAGAGTCACATTAAA	NM_152309:	NM_152309:
118788	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	-1.94	CAGCAGGGTATTTAAGTGCTA	NM_152309:	NM_152309:
5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	0.68	CAAGATGGTCGAATCAAGGAA	NM_002645:	NM_002645:
5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	2.23	TACCCACTAATTGCATTGGAA	NM_002645:	NM_002645:
5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	-9.82	AAGGGTTGTCTTCCTCGCCAA	NM_002646:	NM_002646:
5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	-0.90	CAGGGTGGTCCAGTCCGTCAA	NM_002646:	NM_002646:
5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	1.20	CCAGATCAAGAAATTCGTAAA	NM_004570:	NM_004570:
5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	0.27	CCCGTAGAAATGATAACTCCA	NM_004570:	NM_004570:
5289	PIK3C3	phosphoinositide-3-kinase, class 3	0.17	AACGCGAAAGTGGAAATCGTA	NM_002647:	NM_002647:
5289	PIK3C3	phosphoinositide-3-kinase, class 3	2.20	TCGGTTGGTGCATCTAATGAA	NM_002647:	NM_002647:
5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	-2.79	CTCTGAGTCAGTATAAGTATA	NM_006218:	NM_006218:
5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	-1.53	CTGAGTCAGTATAAGTATATA	NM_006218:	NM_006218:
5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	0.03	CCCTTCGATAAGATTATTGAA	NM_006219:	NM_006219:
5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	1.14	TCGGGAAGCTACCATTTCTTA	NM_006219:	NM_006219:
5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	-5.49	CCGGTCACGCATGAAGGCAAA	NM_005026:	NM_005026:
5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	-0.27	CGCCGTGATCGAGAAAGCCAA	NM_005026:	NM_005026:
5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	-1.86	ATCGAAGTTTGCAGAGACAAA	NM_002649:	NM_002649:

5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	1.13	CACCTTTACTCTATAACTCAA	NM_002649:	NM_002649:
5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-4.50	CAGCATTAAACCAGACCTTAT	NM_181504:	NM_181523:NM_181504:NM_181524:
5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-4.09	TAGCTGGTTATGAACTAGTAA	NM_181504:	NM_181523:NM_181504:NM_181524:
5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	-0.52	CCGCGAGTATGACCAGCTTTA	NM_005027:	NM_005027:
5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	1.45	TTGGTACGTGGGCAAGATCAA	NM_005027:	NM_005027:
8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	2.00	AGGGAGGCAATAATAAGTTAA	NM_003629:	NM_003629:
8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	0.50	GAGGATATCAATCGAGTACAA	NM_003629:	NM_003629:
30849	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	0.42	AAGCAGAATTCTAGATCAGAA	NM_014602:	NM_014602:
30849	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	0.15	TAGAGGCAGAAGATTACTTAA	NM_014602:	NM_014602:
23533	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5, p101	0.63	ACCGGTGCTGCTGCAACTCTA	NM_014308:	NM_014308:
23533	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5, p101	-1.25	ATCGCAGATCAAAGTGGACAA	NM_014308:	NM_014308:
5297	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	-1.29	CATCTGGAACATGAAGACTAA	NM_002650:	NM_058004:NM_002650:
5297	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	-0.41	CCAGTTCATCTGGAACATGAA	NM_002650:	NM_058004:NM_002650:
5298	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	0.01	CCGAGAGTATTGATAATTCAT	NM_002651:	NM_002651:
5298	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	0.31	TCGGCTGATAGTGGCATGATT	NM_002651:	NM_002651:
29992	PILRA	paired immunoglobin-like type 2 receptor alpha	1.21	GACCCTGTACTCTGTCTTAAA	NM_013439:	NM_178272:NM_178273:NM_013439:
29992	PILRA	paired immunoglobin-like type 2 receptor alpha	0.21	CAGCCAGGGAACCCTTCCAAA	NM_013439:	NM_178272:NM_013439:
29990	PILRB	paired immunoglobin-like type 2 receptor beta	-0.06	TACGTTATTCTTGGGCCTCTA	NM_013440:	NM_013440:
29990	PILRB	paired immunoglobin-like type 2 receptor beta	0.33	TTGGTGTTATCTCCTGAGTTA	NM_013440:	NM_175047:NM_013440:
5292	PIM1	pim-1 oncogene	-2.02	AAACATCCTTATCGACCTCAA	NM_002648:	NM_002648:
5292	PIM1	pim-1 oncogene	1.52	AAAGATTGTAGTGGATCTAAT	NM_002648:	NM_002648:
11040	PIM2 (pim-2 c	pim-2 oncogene	0.32	CAGGTCATTACCAGTCATTAA	NM_006875:	NM_006875:
11040	PIM2 (pim-2 c	pim-2 oncogene	-0.06	CCGGGATTGTCCAATTACTAA	NM_006875:	NM_006875:
415116	PIM3	pim-3 oncogene	0.87	ATGAACATGTATAGTGGCTAA	NM_001001852:	NM_001001852:
415116	PIM3	pim-3 oncogene	-0.03	CTGTCAGAAGATGAACATGTA	NM_001001852:	NM_001001852:
5300	PIN1	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting 1	0.04	CAGTATTTATTGTTCCCACAA	NM_006221:	NM_006221:
5300	PIN1	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting 1	0.39	GACCGCCAGATTCTCCCTTAA	NM_006221:	NM_006221:
65018	PINK1	PTEN induced putative kinase 1	1.41	CCGGACGCTGTTCCTCGTTAT	NM_032409:	NM_032409:
65018	PINK1	PTEN induced putative kinase 1	0.00	GACGCTGTTCCTCGTTATGAA	NM_032409:	NM_032409:
8394	PIP5K1A (ph	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	-1.20	CAGCCTCTTGATGTCAATCCA	NM_003557:	NM_003557:
8394	PIP5K1A (ph	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	0.02	CCCTGCCTTGATAATATGTTA	NM_003557:	NM_003557:
8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	-1.15	AAGGCTCAACGTATAAGCGAA	NM_003558:	NM_003558:NM_001031687:
8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	0.54	CAGGCCTACACTCTATTCAAA	NM_003558:	NM_003558:NM_001031687:
23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	-1.08	CCGCGTCGTGGTCATGAACAA	NM_012398:	NM_012398:
23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	1.29	CGGCAAGACCTATTTATAATA	NM_012398:	NM_012398:
5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	-0.28	ATGGAATTAAGTGCCATGAAA	NM_005028:	NM_005028:
5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	-0.31	CTGCCCGATGGTCTTCCGTAA	NM_005028:	NM_005028:
8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	-1.10	CACGCCATACGATACAAAGAA	NM_003559:	NM_003559:
8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	-3.68	CCGCTTTAAGTTTAAGGAGTA	NM_003559:	NM_003559:NM_138687:
79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	-0.35	CCGGAGCAGTATGCTAAGCGA	NM_024779:	NM_024779:
79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	0.27	TTGATGTGTGATAATCTCATA	NM_024779:	NM_024779:
138429	PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase-like 1	0.16	AACGTCTCCACGAGGATGAGA	NM_173492:	NM_173492:
138429	PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase-like 1	0.13	AAGATGGAACTGGATACCACC	NM_173492:	NM_173492:
9600	PITPNM1	phosphatidylinositol transfer protein, membrane-associated 1	-0.77	CAGCGGGCAATACACACACAA	NM_004910:	NM_004910:
9600	PITPNM1	phosphatidylinositol transfer protein, membrane-associated 1	-0.31	CCAGGCGAGTACAAAGCAGAA	NM_004910:	NM_004910:
57605	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	-1.32	ACGGGAAGGCTTGGACTCCAA	NM_020845:	NM_020845:
57605	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	2.17	CTCGAGTTTCTCAACTGTTCA	NM_020845:	NM_020845:
83394	PITPNM3	PITPNM family member 3	-0.61	CCGGGAGAAGTGGCTTCGTAA	NM_031220:	NM_031220:
83394	PITPNM3	PITPNM family member 3	-4.73	CACGAAGGACATCTCTGTCTA	NM_031220:	NM_031220:
10531	PITRM1	pitrilysin metallopeptidase 1	-0.46	CCGGTGAATTACGTGGGTGAA	NM_014889:	NM_014889:
10531	PITRM1	pitrilysin metallopeptidase 1	1.56	TCCGATATTGAACCCACCATA	NM_014889:	NM_014889:
5309	PITX3	paired-like homeodomain transcription factor 3	0.77	TTCAAAGATAAATGAAATAAA	NM_005029:	NM_005029:
5309	PITX3	paired-like homeodomain transcription factor 3	-0.02	CAGCCTGCGGCTCAAAGCCAA	NM_005029:	NM_005029:
64219	PJA1	praja 1	-1.81	CCCGAGATCCTGGTCACTGAA	NM_022368:	NM_145119:NM_001032396:
64219	PJA1	praja 1	-0.04	CAGTGATGATTACTACAAATA	NM_022368:	NM_145119:NM_001032396:
9867	PJA2	praja 2, RING-H2 motif containing	0.05	CTGGCAAGTTCAGATACTAAA	NM_014819:	NM_014819:
9867	PJA2	praja 2, RING-H2 motif containing	0.10	TTGGCACATATGAGGCTTAAA	NM_014819:	NM_014819:
5310	PKD1	polycystic kidney disease 1 (autosomal dominant)	-1.05	CCCGTCCATTGTGGGTAGCAA	NM_000296:	NM_001009944:NM_000296:
5310	PKD1	polycystic kidney disease 1 (autosomal dominant)	0.02	CTGGGTCTCAGCCACGTACAA	NM_000296:	NM_001009944:NM_000296:
168507	PKD1L1	polycystic kidney disease 1 like 1	-0.48	CAGGTTGACCTCAAAGGTGTA	NM_138295:	NM_138295:
168507	PKD1L1	polycystic kidney disease 1 like 1	-0.08	AACGAGTTTCATGGAACCGAA	NM_138295:	NM_138295:
114780	PKD1L2	polycystic kidney disease 1-like 2	-1.68	CAGGGCAAGCGCATGAGTAAA	NM_052892:	NM_182740:NM_052892:
114780	PKD1L2	polycystic kidney disease 1-like 2	0.17	CCGTGTTTGCTGAATGCACAA	NM_052892:	NM_182740:NM_052892:
342372	PKD1L3 (poly	polycystic kidney disease 1-like 3	0.31	CAGCTGGATGATTTCAATTAT	NM_181536:	NM_181536:
342372	PKD1L3 (poly	polycystic kidney disease 1-like 3	0.06	ACGGAGATGCCCATTATGAAA	NM_181536:	NM_181536:
5311	PKD2	polycystic kidney disease 2 (autosomal dominant)	0.00	CTCGACAATCAAGAATGTTAT	NM_000297:	NM_000297:
5311	PKD2	polycystic kidney disease 2 (autosomal dominant)	0.49	CCCTGTGTACTGGTATTATTA	NM_000297:	NM_000297:
9033	PKD2L1	polycystic kidney disease 2-like 1	-0.25	CAGATTGATGCTGTAGGCTCA	NM_016112:	NM_016112:
9033	PKD2L1	polycystic kidney disease 2-like 1	1.08	CGCCTGGATCAAGATATTCAA	NM_016112:	NM_016112:
27039	PKD2L2 (poly	polycystic kidney disease 2-like 2	1.05	AAGTGAAAGCTGACTATTCAA	NM_014386:	NM_014386:
27039	PKD2L2 (poly	polycystic kidney disease 2-like 2	0.40	TCCCGTTGTGTTAAAGACATA	NM_014386:	NM_014386:
10343	PKDREJ (pol	polycystic kidney disease (polycystin) and REJ (sperm receptor for eg	0.92	GAGGGTTGTATCATTATGCAA	NM_006071:	NM_006071:
10343	PKDREJ (pol	polycystic kidney disease (polycystin) and REJ (sperm receptor for eg	1.75	CGGGCCAAATACAAATTCCAA	NM_006071:	NM_006071:
5314	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	-5.23	CACCGGCATATTGGAAGTGTA	NM_170724:	NM_138694:NM_170724:
5314	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	-1.92	CACGAGATAGCTGTACTTTCA	NM_170724:	NM_138694:NM_170724:
5569	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0.27	ATGATTATCATTAGAAGCTAA	NM_181839:	NM_006823:NM_181839:
5569	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	1.21	TCACTTGATCATATGACGAAA	NM_181839:	NM_006823:NM_181839:
5570	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	-0.17	CAGCATGTGTATATTAGATAA	NM_181795:	NM_181795:NM_181794:NM_032471:
5570	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	-4.90	CCGGAATGCCTTACCAGACAT	NM_181795:	NM_181795:NM_181794:NM_032471:
11142	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	0.70	CCACAAGATGTTATTTATTGA	NM_181805:	NM_181804:NM_007066:NM_181805:
11142	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	-0.17	GAGCTCCATGTCCCAGATAAA	NM_181805:	NM_181804:NM_007066:NM_181805:
5313	PKLR	pyruvate kinase, liver and RBC	-0.87	CGGGTGCAATTTGGCATTGAA	NM_000298:	NM_000298:NM_181871:
5313	PKLR	pyruvate kinase, liver and RBC	-0.96	GAGGCCTATCTGAGACTATAA	NM_000298:	NM_000298:NM_181871:
5315	PKM2	pyruvate kinase, muscle	-1.84	AACATCAAGATTATCAGCAAA	NM_182471:	NM_182470:NM_182471:NM_002654:
5315	PKM2	pyruvate kinase, muscle	-0.11	CCCGATCAGTGGAGACGTTGA	NM_182471:	NM_182470:NM_182471:NM_002654:
9088	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-3.62	CCGGCCAGAGTCCTTCTTCCA	NM_004203:	NM_182687:NM_004203:
9088	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-1.96	CTGGGAGGAACTTACCGTCTA	NM_004203:	NM_182687:NM_004203:
5585	PKN1	protein kinase N1	0.10	CAGGACAGTAAGACCAAGATT	NM_002741:	NM_213560:NM_002741:
5585	PKN1	protein kinase N1	-9.25	CCGCAAGGAGCTGAAGCTGAA	NM_002741:	NM_213560:NM_002741:
5586	PKN2	protein kinase N2	0.45	AAAGTATGATATCTACGCAAA	NM_006256:	NM_006256:
5586	PKN2	protein kinase N2	-1.19	CACGTCAAAGTATGATATCTA	NM_006256:	NM_006256:
29941	PKN3	protein kinase N3	0.53	AGGGAAATACTACGCCATCAA	NM_013355:	NM_013355:
29941	PKN3	protein kinase N3	0.92	CCCGGGAAGTTTCAAGTTTGA	NM_013355:	NM_013355:
5317	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	-0.22	CTGGTGTTAGAGAGGAATTAA	NM_000299:	NM_000299:NM_001005337:
5317	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	-1.15	TCCCGAGGGCCTTATGAGAAA	NM_000299:	NM_000299:NM_001005337:
51365	PLA1A	phospholipase A1 member A	1.27	GCAGCTTATTGTAGACCATTA	NM_015900:	NM_015900:
51365	PLA1A	phospholipase A1 member A	0.12	AAGATGGTCTGCTTACCTGAA	NM_015900:	NM_015900:
8399	PLA2G10	phospholipase A2, group X	0.22	AAGCGTCCTCTCAGTAATGAA	NM_003561:	NM_003561:
8399	PLA2G10	phospholipase A2, group X	0.58	CCCAAACTGAGTACAACTTAA	NM_003561:	NM_003561:

81579	PLA2G12A	phospholipase A2, group XIIA	-0.63	AACCTAATATATCAAGGCAAA	NM_030821:	NM_030821:
81579	PLA2G12A	phospholipase A2, group XIIA	0.09	AAAGATATTTAACCTAATATA	NM_030821:	NM_030821:
5319	PLA2G1B	phospholipase A2, group IB (pancreas)	1.09	TCCATATAACAAGGCACACAA	NM_000928:	NM_000928:
5319	PLA2G1B	phospholipase A2, group IB (pancreas)	0.29	CACACTGTACTCTCCAATAAA	NM_000928:	NM_000928:
5320	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	-0.22	CACCAAATTTCTGAGCTACAA	NM_000300:	NM_000300:
5320	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	0.05	AAACGTGGATGTGGCACCAAA	NM_000300:	NM_000300:
26279	PLA2G2D	phospholipase A2, group IID	0.92	CAGGGTAGGGAAATCTCCATA	NM_012400:	NM_012400:
26279	PLA2G2D	phospholipase A2, group IID	0.36	CAGAAAGTACTCCCTCAGTAA	NM_012400:	NM_012400:
30814	PLA2G2E (ph	phospholipase A2, group IIE	-3.35	AACCGCAAATATGCCCATTAT	NM_014589:	NM_014589:
30814	PLA2G2E (ph	phospholipase A2, group IIE	0.15	CAAGTCCGCCCTGCAGTACAA	NM_014589:	NM_014589:
64600	PLA2G2F	phospholipase A2, group IIF	-3.00	CACGCCCAACTGCAGCATCTA	NM_022819:	NM_022819:
64600	PLA2G2F	phospholipase A2, group IIF	1.39	ATCGAGAACAACACTGAGATA	NM_022819:	NM_022819:
50487	PLA2G3	phospholipase A2, group III	0.86	AGCCCTAAACCTAAATTCAAA	NM_015715:	NM_015715:
50487	PLA2G3	phospholipase A2, group III	-0.07	CCAGCCCTAAACCTAAATTCA	NM_015715:	NM_015715:
5322	PLA2G5	phospholipase A2, group V	-0.02	AAGAGCCAAATTGACTCTCTA	NM_000929:	NM_000929:
5322	PLA2G5	phospholipase A2, group V	0.32	CTGGTGTATGGGTATTAAATA	NM_000929:	NM_000929:
7941	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase	-0.43	AAGGACTCTATTGATAGGGAA	NM_005084:	NM_005084:
7941	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase	0.08	TCAGGACACTTTATTCTGCTA	NM_005084:	NM_005084:
22925	PLA2R1	phospholipase A2 receptor 1, 180kDa	-2.83	AAGGAGGTACGCTGTTAAGTA	NM_001007267:	NM_007366:NM_001007267:
22925	PLA2R1	phospholipase A2 receptor 1, 180kDa	-3.24	AAGGTTTGGCTCATAGAGAAA	NM_001007267:	NM_007366:NM_001007267:
5327	PLAT	plasminogen activator, tissue	-0.61	CAGCATATTTATAGCAATCCA	NM_000930:	NM_000930:NM_033011:NM_000931:
5327	PLAT	plasminogen activator, tissue	-4.07	CAGGAAAGACGGATTGCATTA	NM_000930:	NM_000930:NM_033011:NM_000931:
5328	PLAU	plasminogen activator, urokinase	-2.41	CCGCATGACTTTGACTGGAAT	NM_002658:	NM_002658:
5328	PLAU	plasminogen activator, urokinase	2.64	GAGCTGGTGTCTGATTGTTAA	NM_002658:	NM_002658:
5329	PLAUR	plasminogen activator, urokinase receptor	-0.29	ACCGAGGTTGTGTGTGGGTTA	NM_002659:	NM_001005376:NM_002659:NM_001005377:
5329	PLAUR	plasminogen activator, urokinase receptor	-0.39	ACCGGCACTCACGAACCGAAA	NM_002659:	NM_002659:NM_001005377:
23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	0.48	TCGAGATTACATGGATGTTAA	NM_015192:	NM_182734:NM_015192:
23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	0.02	CAGAGATGATCCGGTCATATA	NM_015192:	NM_182734:NM_015192:
5330	PLCB2	phospholipase C, beta 2	0.13	GCGGCTTGCCTGGAACAGATA	NM_004573:	NM_004573:
5330	PLCB2	phospholipase C, beta 2	-0.77	CTCCATCAATCCTGTCTGGAA	NM_004573:	NM_004573:
5331	PLCB3 (phos	phospholipase C, beta 3 (phosphatidylinositol-specific)	0.87	ACGCTTGTCAACTACATCGAA	NM_000932:	NM_000932:
5331	PLCB3 (phos	phospholipase C, beta 3 (phosphatidylinositol-specific)	-1.07	CACGCTTGTCAACTACATCGA	NM_000932:	NM_000932:
5332	PLCB4	phospholipase C, beta 4	-3.85	AACCCGGTAGTCTAGAACTAA	NM_000933:	NM_000933:NM_182797:
5332	PLCB4	phospholipase C, beta 4	0.27	CTGCAGATTCCGGATATTATA	NM_000933:	NM_000933:NM_182797:
5333	PLCD1 (phos	phospholipase C, delta 1	0.99	TCCGTTAGGAATAACAATGCA	NM_006225:	NM_006225:
5333	PLCD1 (phos	phospholipase C, delta 1	0.06	CCGCTTCTTGGTGGAAGATTA	NM_006225:	NM_006225:
113026	PLCD3 (phos	phospholipase C, delta 3	2.06	TAGGTTTGTAACTGTTTCATA	NM_133373:	NM_133373:
113026	PLCD3 (phos	phospholipase C, delta 3	0.38	AAGCAAGGGTACCGCCACATA	NM_133373:	NM_133373:
84812	PLCD4	phospholipase C, delta 4	-3.57	CTCATTCTTCCTAACAAGCAA	NM_032726:	NM_032726:
84812	PLCD4	phospholipase C, delta 4	0.97	CAGATCTTTGGCGTTCGTCTA	NM_032726:	NM_032726:
51196	PLCE1	phospholipase C, epsilon 1	-1.18	AACCCAGGTGGAGATCTTTAA	NM_016341:	NM_016341:
51196	PLCE1	phospholipase C, epsilon 1	-1.32	CCGCGGTACAATTCCCAAGAA	NM_016341:	NM_016341:
5335	PLCG1	phospholipase C, gamma 1	1.26	CACCCTTACCACCAAGATCAA	NM_002660:	NM_002660:NM_182811:
5335	PLCG1	phospholipase C, gamma 1	-0.53	CGGGACTTTGATCGCTATCAA	NM_002660:	NM_002660:NM_182811:
5336	PLCG2 (phos	phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.94	CACGTGGAAGATTGACAGCAA	NM_002661:	NM_002661:
5336	PLCG2 (phos	phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.89	GACGACGGTTGTGAATGATAA	NM_002661:	NM_002661:
5334	PLCL1	phospholipase C-like 1	1.27	CTCAGGAATATCGGTCTTAAA	NM_006226:	NM_006226:
5334	PLCL1	phospholipase C-like 1	-1.66	AAGGATGTCGGTAGATTACAA	NM_006226:	NM_006226:
23228	PLCL2	phospholipase C-like 2	-0.02	CAGGATATATTCGAGCTCTTA	NM_015184:	NM_015184:
23228	PLCL2	phospholipase C-like 2	-0.44	CAGTGTCATTGATATTATTAA	NM_015184:	NM_015184:
23007	PLCL3	phospholipase C-like 3	1.37	CACGGTCTAAATCTTACAGTA	XM_042635:	NM_014996:
23007	PLCL3	phospholipase C-like 3	-3.71	CCGAGCCAAATTCAAGGCAAA	XM_042635:	NM_014996:
9651	PLCL4	phospholipase C-like 4	0.67	ACCAATCGAAAGCGTGTAGAA	XM_371214:	NM_014638:
9651	PLCL4	phospholipase C-like 4	-5.71	CCGGCAGAAGAAGACCATGAA	XM_371214:	NM_014638:
89869	PLCZ1	phospholipase C, zeta 1	0.42	TTAGCTATGCATCGCAATAAA	NM_033123:	NM_033123:
89869	PLCZ1	phospholipase C, zeta 1	1.04	CAGCAGACTCGTGTAATTAAA	NM_033123:	NM_033123:
5338	PLD2 (phospl	phospholipase D2	0.38	CGGGACCTCCTGAGACACAAA	NM_002663:	NM_002663:
5338	PLD2 (phospl	phospholipase D2	-1.67	CAGCCTGCTGACAGACACTAA	NM_002663:	NM_002663:
5339	PLEC1	plectin 1, intermediate filament binding protein 500kDa	-0.68	CACAGTGGAGAAGATCATCAA	NM_000445:	NM_201384:NM_201382:NM_201383:NM_201380: NM_201379:NM_201381:NM_201378:NM_000445:
5339	PLEC1	plectin 1, intermediate filament binding protein 500kDa	0.82	CCAGACTAATATATTAATATA	NM_000445:	NM_201384:NM_201382:NM_201383:NM_201380: NM_201379:NM_201381:NM_201378:NM_000445:
5341	PLEK	pleckstrin	-0.25	ACCATTGACTTAGGTGCCTTA	NM_002664:	NM_002664:
5341	PLEK	pleckstrin	0.71	GAGCATTTCTCTAACGTTTAT	NM_002664:	NM_002664:
23207	PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) r	0.26	CTCGGAGTTCAGAGTAGACAA	XM_290944:	XM_290944:
23207	PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) r	0.00	CCGATTGCTGTCTGCACTGAA	XM_290944:	XM_290944:
80301	PLEKHQ1	pleckstrin homology domain containing, family Q member 1	1.38	CAAGGCTTTCGATGAGGTAAA	NM_025201:	NM_025201:
80301	PLEKHQ1	pleckstrin homology domain containing, family Q member 1	0.03	AAGCTTACTTGTAATGATCAT	NM_025201:	NM_025201:
5340	PLG	plasminogen	0.96	CAGGAAAGAAGTGTCAGTCTT	NM_000301:	NM_000301:
5340	PLG	plasminogen	-6.23	CACCACCACCACAGGAAAGAA	NM_000301:	NM_000301:
5346	PLIN	perilipin	0.89	TGGCTTGTTTATGAACATTAA	NM_002666:	NM_002666:
5346	PLIN	perilipin	1.44	GCGGGTTTCTCTAACAAATAA	NM_002666:	NM_002666:
5347	PLK1	polo-like kinase 1 (Drosophila)	-13.17	CACCATATGAATTGTACAGAA	NM_005030:	NM_005030:
5347	PLK1	polo-like kinase 1 (Drosophila)	-17.57	CCGGATCAAGAAGAATGAATA	NM_005030:	NM_005030:
10769	PLK2	polo-like kinase 2 (Drosophila)	0.16	CAGATGCTCCTGAGCAATTTA	NM_006622:	NM_006622:
10769	PLK2	polo-like kinase 2 (Drosophila)	0.04	CAGATTGTGTCTGGACTGAAA	NM_006622:	NM_006622:
1263	PLK3	polo-like kinase 3 (Drosophila)	1.06	CAGAAAGACTGTGCACTACAA	NM_004073:	NM_004073:
1263	PLK3	polo-like kinase 3 (Drosophila)	-0.03	CCCGAAATCGTAGTGCTTGTA	NM_004073:	NM_004073:
10733	PLK4	polo-like kinase 4 (Drosophila)	-1.41	CACCAAATGGTCAAACAACTA	NM_014264:	NM_014264:
10733	PLK4	polo-like kinase 4 (Drosophila)	-2.90	CTGGTAGTACTAGTTCACCTA	NM_014264:	NM_014264:
5351	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	1.96	AACTGGAGAGTTTCTATTAAA	NM_000302:	NM_000302:
5351	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	0.34	CAGAGGCGGAACACACCTTTA	NM_000302:	NM_000302:
5354	PLP1	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic parapleg	1.62	TAAGGAGATGTAAGAGCTTTA	NM_000533:	NM_199478:NM_000533:
5354	PLP1	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic parapleg	-0.19	AAGGATCTTTCACCCACAGAA	NM_000533:	NM_199478:NM_000533:
5359	PLSCR1	phospholipid scramblase 1	0.43	ACGTAAGATTCAGGAAACGAA	NM_021105:	NM_021105:
5359	PLSCR1	phospholipid scramblase 1	0.77	CACAAGATATTAAATTACCAA	NM_021105:	NM_021105:
5360	PLTP (phospl	phospholipid transfer protein	-1.49	AAGACGGGATTTGAAGCTGTA	NM_006227:	NM_006227:NM_182676:
5360	PLTP (phospl	phospholipid transfer protein	1.49	CAGGTTCCGAATCTATTCCAA	NM_006227:	NM_006227:NM_182676:
57125	PLXDC1	plexin domain containing 1	-0.04	AGGCAGGACTTGCCTGATAAA	NM_020405:	NM_020405:
57125	PLXDC1	plexin domain containing 1	0.82	CAGCTAAATTTGATAATTTAA	NM_020405:	NM_020405:
84898	PLXDC2	plexin domain containing 2	-0.08	ACAGACCACAATTACTATATA	NM_032812:	NM_032812:
84898	PLXDC2	plexin domain containing 2	0.54	CACAGTACATAGCACCTTTAA	NM_032812:	NM_032812:
5361	PLXNA1	plexin A1	0.24	AAAGACGATTTGAACAAGAAA	NM_032242:	NM_032242:
5361	PLXNA1	plexin A1	1.81	CACAGCTAGAATAGATATATT	NM_032242:	NM_032242:
5362	PLXNA2	plexin A2	-0.24	CCGGACGTCCATCAGCAGATA	NM_025179:	NM_025179:
5362	PLXNA2	plexin A2	1.59	CCGGATCAATATTTCAGAGGA	NM_025179:	NM_025179:
55558	PLXNA3	plexin A3	0.49	CTGCCTATTTATTGAATCGAA	NM_017514:	NM_017514:

55558	PLXNA3	plexin A3	-0.23	CGCGGGAGACTCAGAGTTCTA	NM_017514:	NM_017514:
91584	PLXNA4B	plexin A4, B	-7.45	CAGCCGGAAACTGACCAAGAA	NM_181775:	NM_181775:
91584	PLXNA4B	plexin A4, B	-0.34	TACCTGGGAATTCTTCCTAAA	NM_181775:	NM_181775:
5364	PLXNB1	plexin B1	-0.04	AACGCGGACAGTTCAAGTATA	NM_002673:	NM_002673:
5364	PLXNB1	plexin B1	-0.14	CCGGGTGGAATTTATCCTTGA	NM_002673:	NM_002673:
23654	PLXNB2	plexin B2	0.03	ACGAGAGTATGAGAAGATCAA	XM_371474:	XM_371474:
23654	PLXNB2	plexin B2	-0.94	CCGCAGCGAGAAAGAGCTGAA	XM_371474:	XM_371474:
5365	PLXNB3	plexin B3	0.00	CACAGGTACTATGATCAGATT	NM_005393:	NM_005393:
5365	PLXNB3	plexin B3	-0.67	CAGCGGGTCTTCTTCACCCTA	NM_005393:	NM_005393:
10154	PLXNC1	plexin C1	1.09	GACGTCGTACATATTTGGAAA	NM_005761:	NM_005761:
10154	PLXNC1	plexin C1	-0.04	TCGAGGGAAGCACAAGTTCAA	NM_005761:	NM_005761:
23129	PLXND1	plexin D1	-10.97	CACGCTCTGCAAGGTTCTCAA	NM_015103:	NM_015103:
23129	PLXND1	plexin D1	-4.70	CACGAGTACCGGGTCAAGATA	NM_015103:	NM_015103:
5366	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	-1.44	TGGGCTATATACAGTCCTCAA	NM_021127:	NM_021127:
5366	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0.47	TTCGGTCACTACACAACGTAA	NM_021127:	NM_021127:
5367	PMCH	pro-melanin-concentrating hormone	-0.28	ATCTCTCTTCCTATATATTAA	NM_002674:	NM_002674:
5367	PMCH	pro-melanin-concentrating hormone	0.22	TAGTGTTAAATGTATCAGTAA	NM_002674:	NM_002674:
5371	PML	promyelocytic leukemia	-1.60	CAGGAGCAGGATAGTGCCTTT	NM_002675:	NM_033250:NM_002675:NM_033249:NM_033244:NM_033242:NM_033238:NM_033247:NM_033239:NM_033246:NM_033240:NM_033245:
5371	PML	promyelocytic leukemia	-0.24	CAGGGTTGTCCGCTCTGATTA	NM_002675:	NM_033238:
5373	PMM2	phosphomannomutase 2	0.89	CACGTTCTTCGTGAAACTGGA	NM_000303:	NM_000303:
5373	PMM2	phosphomannomutase 2	-0.76	CGGGATGTCAGACTTCACCAA	NM_000303:	NM_000303:
23203	PMPCA	peptidase (mitochondrial processing) alpha	-0.59	TCGAGAAATGGTAGAAATCAT	NM_015160:	NM_015160:
23203	PMPCA	peptidase (mitochondrial processing) alpha	-0.81	CTCACCGAGATGATTCATGAA	NM_015160:	NM_015160:
9512	PMPCB	peptidase (mitochondrial processing) beta	0.82	TACATTTATAATAGGAGTCCA	NM_004279:	NM_004279:
9512	PMPCB	peptidase (mitochondrial processing) beta	-0.09	AAGAATGGATGCGACTCTGTA	NM_004279:	NM_004279:
5378	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	0.99	CAGCGAATGGTTTCAAGATAA	NM_000534:	NM_000534:
5378	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	0.14	TTGGAACGATACAATAGTCAA	NM_000534:	NM_000534:
5395	PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	0.06	CAGACTCGTGAATGAGGTCTA	NM_000535:	NM_000535:NM_001018040:
5395	PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	-0.06	CCGGATGTAAATTTCGAGTTT	NM_000535:	NM_000535:NM_001018040:
10654	PMVK	phosphomevalonate kinase	0.72	CCCAGTGTGGATACTAATAAA	NM_006556:	NM_006556:
10654	PMVK	phosphomevalonate kinase	-0.18	TTGGCTGTGCTTGAAGGCGAA	NM_006556:	NM_006556:
139728	PNCK	pregnancy upregulated non-ubiquitously expressed CaM kinase	-3.33	CTCGAAGATCATGGTCTCTGA	NM_198452:	NM_198452:
139728	PNCK	pregnancy upregulated non-ubiquitously expressed CaM kinase	0.18	TCCGTGTGTCACAGCCCGAAA	NM_198452:	NM_198452:
11284	PNKP	polynucleotide kinase 3'-phosphatase	-0.70	CACGTGAACAGGGACACGCTA	NM_007254:	NM_007254:
11284	PNKP	polynucleotide kinase 3'-phosphatase	1.63	CACGTGTGAGACAGCCCTGAA	NM_007254:	NM_007254:
5406	PNLIP	pancreatic lipase	0.77	AATGAATTGACTTCTAATAAA	NM_000936:	NM_000936:
5406	PNLIP	pancreatic lipase	-0.03	TAGGAGACTACTGTTATTTGA	NM_000936:	NM_000936:
5407	PNLIPRP1	pancreatic lipase-related protein 1	-5.62	CCCGATGGGTTTGCTGCATAT	NM_006229:	NM_006229:
5407	PNLIPRP1	pancreatic lipase-related protein 1	0.00	CAAGTATTACTTGGAAAGCAT	NM_006229:	NM_006229:
5408	PNLIPRP2	pancreatic lipase-related protein 2	1.18	TGCGGCTATTGCGGTAATAAA	NM_005396:	NM_005396:
5408	PNLIPRP2	pancreatic lipase-related protein 2	-0.11	CTGGAACAAACGTGGGATAAA	NM_005396:	NM_005396:
119548	PNLIPRP3 (p	pancreatic lipase-related protein 3	1.14	TAACAATATTATAATATTTAA	XM_058404:	NM_001011709:
119548	PNLIPRP3 (p	pancreatic lipase-related protein 3	1.55	AACAATATTATAATATTTAAA	XM_058404:	NM_001011709:
5409	PNMT	phenylethanolamine N-methyltransferase	-2.80	AAGCCAACATGCCTGCCTCAT	NM_002686:	NM_002686:
5409	PNMT	phenylethanolamine N-methyltransferase	0.29	AAGGACATCACCATGACAGAT	NM_002686:	NM_002686:
10957	PNRC1	proline-rich nuclear receptor coactivator 1	-0.10	CAGATTTCAGTATGTGTGTAA	NM_006813:	NM_006813:
10957	PNRC1	proline-rich nuclear receptor coactivator 1	1.25	TACACTTGTATGAGCAACCAA	NM_006813:	NM_006813:
55629	PNRC2	proline-rich nuclear receptor coactivator 2	0.25	CCCAATGGCCCTGTTTATTAA	NM_017761:	NM_017761:
55629	PNRC2	proline-rich nuclear receptor coactivator 2	0.24	ACAAGTTTATGTAGTACTTAA	NM_017761:	NM_017761:
23509	POFUT1	protein O-fucosyltransferase 1	1.20	TAGAAAGTAGAAGATGTAATA	NM_015352:	NM_015352:
23509	POFUT1	protein O-fucosyltransferase 1	-0.39	ACAAATGTGGCTGTTGATTAA	NM_015352:	NM_015352:
5422	POLA (polym	polymerase (DNA directed), alpha	0.27	CTGGAGAAACTTACTACCGAT	NM_016937:	NM_016937:
5422	POLA (polym	polymerase (DNA directed), alpha	-0.19	CTGCATGAAAGCTACACTTCA	NM_016937:	NM_016937:
5423	POLB	polymerase (DNA directed), beta	1.08	CAAGATATTGTACTAAATGAA	NM_002690:	NM_002690:
5423	POLB	polymerase (DNA directed), beta	0.67	TACGAGTTCATCCATCAATTT	NM_002690:	NM_002690:
5424	POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	-1.42	CCGAGAGAGCATGTTTGGGTA	NM_002691:	NM_002691:
5424	POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	0.27	CGGGACCAGGGAGAATTAATA	NM_002691:	NM_002691:
5426	POLE	polymerase (DNA directed), epsilon	-0.59	CCGCATCATCCTCTGTACAAA	NM_006231:	NM_006231:
5426	POLE	polymerase (DNA directed), epsilon	-0.02	CCGCCTCTCCATTGACCTGAA	NM_006231:	NM_006231:
5428	POLG	polymerase (DNA directed), gamma	0.80	CACGAGCAAATCTTCGGGCAA	NM_002693:	NM_002693:
5428	POLG	polymerase (DNA directed), gamma	0.47	CAGATGCGGGTCACACCTAAA	NM_002693:	NM_002693:
5429	POLH	polymerase (DNA directed), eta	-0.41	ATCCATTTAGGTGCTGAGTTA	NM_006502:	NM_006502:
5429	POLH	polymerase (DNA directed), eta	0.74	CTGGTTGTGAGCATTCGTGTA	NM_006502:	NM_006502:
11201	POLI	polymerase (DNA directed) iota	0.90	ACCGGGAACATCAGGCTTTAA	NM_007195:	NM_007195:
11201	POLI	polymerase (DNA directed) iota	1.40	GCGGTTTATTAAGCTCTTCTA	NM_007195:	NM_007195:
51426	POLK	polymerase (DNA directed) kappa	-1.93	CCGGGTGACGACGGGTAGAAA	NM_016218:	NM_016218:
51426	POLK	polymerase (DNA directed) kappa	-0.96	TAGGATGGGACTTAATGATAA	NM_016218:	NM_016218:
27343	POLL	polymerase (DNA directed), lambda	-1.26	CAAGAGGAGAATGGTCAGCAA	NM_013274:	NM_013274:
27343	POLL	polymerase (DNA directed), lambda	-3.38	CACCGGCTCTGCACACTTCAA	NM_013274:	NM_013274:
27434	POLM	polymerase (DNA directed), mu	-1.36	CCCAGAATGCCCAGAAGAGAA	NM_013284:	NM_013284:
27434	POLM	polymerase (DNA directed), mu	0.39	CGGGAAGGACTGCGAACCTTA	NM_013284:	NM_013284:
353497	POLN	polymerase (DNA directed) nu	-3.94	CAGGAGGCACATCAACAATTT	NM_181808:	NM_181808:
353497	POLN	polymerase (DNA directed) nu	-0.63	TTGCGCATTCTTACACATTTA	NM_181808:	NM_181808:
10721	POLQ	polymerase (DNA directed), theta	0.86	AACCAGAATGTTTATATGAAA	NM_006596:	NM_199420:
10721	POLQ	polymerase (DNA directed), theta	0.92	ACGGGCCTCTTTAGATATAAA	NM_006596:	NM_199420:
9533	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	0.15	CCCGGGTTCGAGATCATTATA	NM_004875:	NM_004875:NM_203290:
9533	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	-0.07	GTGCAGGAAGTCCAAGGTAAA	NM_004875:	NM_004875:NM_203290:
5432	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	-1.41	AAGTGGGTCATAGATAGATTA	NM_002694:	NM_032940:NM_002694:
5432	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	-3.17	CAGAGTGATGTGCTAACCATA	NM_002694:	NM_032940:NM_002694:
5443	POMC	proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-mela	0.84	TGCCTGTAGTTAGGAAATAAA	NM_000939:	NM_000939:NM_001035256:
5443	POMC	proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-mela	-1.61	CTGCCTGTAGTTAGGAAATAA	NM_000939:	NM_000939:NM_001035256:
22932	POMZP3	POM (POM121 homolog, rat) and ZP3 fusion	0.32	CCACGGGATCGTGGGACTTTA	NM_012230:	NM_012230:NM_152992:
22932	POMZP3	POM (POM121 homolog, rat) and ZP3 fusion	-0.28	CAAGTCGACAGCCAACGGAAA	NM_012230:	NM_012230:NM_152992:
5444	PON1	paraoxonase 1	0.77	CAGAATGAATCCCATAATTGA	NM_000446:	NM_000446:
5444	PON1	paraoxonase 1	0.22	ATGTCAATTGTCAGATATTAA	NM_000446:	NM_000446:
5445	PON2 (parao	paraoxonase 2	-0.74	ATGTATGGCATGTGTAGTTAA	NM_000305:	NM_000305:NM_001018161:
5445	PON2 (parao	paraoxonase 2	0.25	CATGAAAGTGCGATAACTTAA	NM_000305:	NM_000305:NM_001018161:
5447	POR	P450 (cytochrome) oxidoreductase	-2.50	CCGGCTGAAGAGCTACGAGAA	NM_000941:	NM_000941:
5447	POR	P450 (cytochrome) oxidoreductase	0.70	GAGGAACATCATCGTGTTCTA	NM_000941:	NM_000941:
10631	POSTN	periostin, osteoblast specific factor	0.72	CTGCTTATTGTTAACCCTATA	NM_006475:	NM_006475:
10631	POSTN	periostin, osteoblast specific factor	0.66	ACCAGATTCATTACAATTCAA	NM_006475:	NM_006475:
5449	POU1F1	POU domain, class 1, transcription factor 1 (Pit1, growth hormone fac	0.33	AGCCAAATATATTAACAGTAA	NM_000306:	NM_000306:
5449	POU1F1	POU domain, class 1, transcription factor 1 (Pit1, growth hormone fac	0.97	TAGGAGCTTTGTACAATGAAA	NM_000306:	NM_000306:
5451	POU2F1	POU domain, class 2, transcription factor 1	0.37	TTGGAGAACTTTCTAACCAAA	NM_002697:	NM_002697:
5451	POU2F1	POU domain, class 2, transcription factor 1	-5.38	CAGCAGAATCTCAACCTGCAA	NM_002697:	NM_002697:
5456	POU3F4	POU domain, class 3, transcription factor 4	0.53	TCTAGTATTCTTAATTATTTA	NM_000307:	NM_000307:
5456	POU3F4	POU domain, class 3, transcription factor 4	0.58	TCGCCAAACAATTCAAACAAA	NM_000307:	NM_000307:

56342	PPAN	peter pan homolog (Drosophila)	0.00	TTCCGCCACTATAGCATCAAA	NM_020230:	NM_020230:
56342	PPAN	peter pan homolog (Drosophila)	1.18	CCCTCGGTTTCCTTTCATAAA	NM_020230:	NM_020230:
8611	PPAP2A	phosphatidic acid phosphatase type 2A	0.04	AACCCTGTCTGTTTACTGTAA	NM_176895:	NM_176895:NM_003711:
8611	PPAP2A	phosphatidic acid phosphatase type 2A	0.31	CTGACATTGCCAAGTATTCAA	NM_176895:	NM_176895:NM_003711:
8613	PPAP2B	phosphatidic acid phosphatase type 2B	-0.13	AGCGATCGTCCCGGAGAGCAA	AF480883:	NM_003713:NM_177414:
8613	PPAP2B	phosphatidic acid phosphatase type 2B	0.01	CAGCACAATTTCAGAAGAAAT	AF480883:	NM_003713:NM_177414:
8612	PPAP2C	phosphatidic acid phosphatase type 2C	0.81	CCGGGTCAACTGCTCGGTCTA	NM_177543:	NM_177543:NM_177526:NM_003712:
8612	PPAP2C	phosphatidic acid phosphatase type 2C	-2.15	TCGCTCGGACTTCAACAACTA	NM_177543:	NM_177543:NM_177526:NM_003712:
5465	PPARA	peroxisome proliferative activated receptor, alpha	0.27	AGGAAGGGTTGTGGCAAATAA	NM_005036:	NM_001001930:NM_005036:NM_001001929:NM_001001928:
5465	PPARA	peroxisome proliferative activated receptor, alpha	2.39	CCGTGAGAAGTCAACAACTTA	NM_005036:	NM_001001930:NM_005036:NM_001001929:NM_001001928:
5469	PPARBP	PPAR binding protein	-3.20	AAGTTTAAGGGCAATAACCAA	NM_004774:	NM_004774:
5469	PPARBP	PPAR binding protein	-0.89	CAGTGTTTCGTTCTAAATCTA	NM_004774:	NM_004774:
5467	PPARD	peroxisome proliferative activated receptor, delta	0.80	ACTGACGAAACTTTAAATAAA	NM_006238:	NM_006238:
5467	PPARD	peroxisome proliferative activated receptor, delta	0.77	CACAGACTGACGAAACTTTAA	NM_006238:	NM_006238:
5468	PPARG	peroxisome proliferative activated receptor, gamma	-1.10	CAGCGACTTGGCAATATTTAT	NM_005037:	NM_005037:NM_015869:NM_138711:NM_138712:
5468	PPARG	peroxisome proliferative activated receptor, gamma	-0.47	CCGGAGAACAATCAGATTGAA	NM_005037:	NM_005037:NM_015869:NM_138711:NM_138712:
10891	PPARGC1A	peroxisome proliferative activated receptor, gamma, coactivator 1, alp	0.18	TAGAATAGCCATGTACTATAA	NM_013261:	NM_013261:
10891	PPARGC1A	peroxisome proliferative activated receptor, gamma, coactivator 1, alp	-0.09	CTGGAAGACATGATACACCTA	NM_013261:	NM_013261:
133522	PPARGC1B	peroxisome proliferative activated receptor, gamma, coactivator 1, bet	-1.00	TCCCTTCAAACCAGACATCAA	NM_133263:	NM_133263:
133522	PPARGC1B	peroxisome proliferative activated receptor, gamma, coactivator 1, bet	-5.63	AAGCATAGTCTAGGCAAAGAA	NM_133263:	NM_133263:
5471	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.68	AAGTCCAAGTATCATCTTATA	NM_002703:	NM_002703:
5471	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.17	TACCAAAGTGCGATAACTGAA	NM_002703:	NM_002703:
5473	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	-0.96	AACCCTCTAATTCTTGCCTAA	NM_002704:	NM_002704:
5473	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	-0.65	AAGCCTGGTTTCAACCCTCTA	NM_002704:	NM_002704:
5475	PPEF1	protein phosphatase, EF-hand calcium binding domain 1	0.13	CAGCATTAGTACCTACATATT	NM_006240:	NM_006240:NM_152224:NM_152225:NM_152226:NM_152223:
5475	PPEF1	protein phosphatase, EF-hand calcium binding domain 1	0.29	CCCAATCGGTACAATCGTTGA	NM_006240:	NM_006240:NM_152224:NM_152225:NM_152226:NM_152223:
5470	PPEF2 (prote	protein phosphatase, EF-hand calcium binding domain 2	1.31	CACATGAATATCGACATTACA	NM_006239:	NM_152933:NM_006239:NM_152934:
5470	PPEF2 (prote	protein phosphatase, EF-hand calcium binding domain 2	-0.22	CTGCAGGAGCATTGCGCTTAA	NM_006239:	NM_152933:NM_006239:NM_152934:
8500	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	-0.59	AACGGCCTATTTAATATGTTA	NM_177423:	NM_177423:
8500	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	0.68	CACGAGGTTGGTCATGAAAGA	NM_177423:	NM_003626:NM_177423:
8499	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	-0.78	AACGTTTGGGTGACTCATGAA	NM_003625:	NM_003625:
8499	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	-0.73	TACCAGCTGGATTTAGGTTAA	NM_003625:	NM_003625:
8541	PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	-0.76	ACGGCTCAACTATGACCGGAA	NM_003660:	NM_003660:
8541	PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	0.70	CACGGGTAAAGAGAACTGTTT	NM_003660:	NM_003660:
8497	PPFIA4 (prote	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	-1.54	CAGGATAGCTGGGTCCATTCA	AK126624:	NM_015053:
8497	PPFIA4 (prote	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), in	0.61	TGGGTGTGTACGTACCAATAA	AK126624:	NM_015053:
5476	PPGB	protective protein for beta-galactosidase (galactosialidosis)	-0.39	CCGGCCCTGGTTAGTGAAGTA	NM_000308:	NM_000308:
5476	PPGB	protective protein for beta-galactosidase (galactosialidosis)	1.45	ATACCAGATCCTATTATATAA	NM_000308:	NM_000308:
5479	PPIB	peptidylprolyl isomerase B (cyclophilin B)	0.77	AACAGCAAATTCCATCGTGTA	NM_000942:	NM_000942:
5479	PPIB	peptidylprolyl isomerase B (cyclophilin B)	1.41	GTGGTGTTTGGCAAAGTTCTA	NM_000942:	NM_000942:
23759	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	-0.18	CAGGGACAGCCTATTTATACA	NM_014337:	NM_014337:
23759	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	-0.61	AAGGAGGAGATCCGCATTGAT	NM_014337:	NM_148175:NM_148176:NM_014337:
122769	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	0.60	CACGAACCATATTACATAATA	NM_152329:	NM_152329:
122769	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	-0.07	ATGTGTATAGTTACTCATTTA	NM_152329:	NM_152329:NM_203466:NM_203467:
5494	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha i	0.70	AAGCGTGATTTCAAACCATAA	NM_021003:	NM_177952:NM_021003:
5494	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha i	-0.12	TTCCATGAGTATTGCAGGTAA	NM_021003:	NM_177952:NM_021003:
5495	PPM1B	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta is	0.61	CACCTAAGCATATCTACTTTA	NM_002706:	NM_001033557:NM_001033556:NM_002706:NM_177968:
5495	PPM1B	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta is	1.21	CGAGATAACATGAGTATTGTA	NM_002706:	NM_001033557:NM_177969:NM_001033556:NM_002706:NM_177968:
8493	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	-0.32	ACGGGTCTTCCTAGCACATCA	NM_003620:	NM_003620:
8493	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	0.66	CTCGGCGTCGTCGAAGATAAA	NM_003620:	NM_003620:
22843	PPM1E	protein phosphatase 1E (PP2C domain containing)	-0.06	CCCATTTAGGTCTGTACTAAA	NM_014906:	NM_014906:
22843	PPM1E	protein phosphatase 1E (PP2C domain containing)	0.92	GAGGCGGTTTATAGTCAGAAA	NM_014906:	NM_014906:
9647	PPM1F	protein phosphatase 1F (PP2C domain containing)	0.61	ATGGTTGGCCACAAACAATGA	NM_014634:	NM_014634:
9647	PPM1F	protein phosphatase 1F (PP2C domain containing)	-5.19	CACCTGGTGGTCTGATTCATA	NM_014634:	NM_014634:
5496	PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamm	-8.92	CAGGACCTGAGGACTCAACTA	NM_002707:	NM_177983:NM_002707:
5496	PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamm	-2.50	CCAGAGGATGAAGTAGAACTA	NM_002707:	NM_177983:NM_002707:
151742	PPM1L	protein phosphatase 1 (formerly 2C)-like	0.31	CAGGACTACGAGAAAGACAAA	NM_139245:	NM_139245:
151742	PPM1L	protein phosphatase 1 (formerly 2C)-like	-0.59	CTGGTGGTCTTAGGTCTATAA	NM_139245:	NM_139245:
132160	PPM1M	protein phosphatase 1M (PP2C domain containing)	-0.12	CAGAGTGACTTTACAACTTAA	NM_144641:	NM_144641:
132160	PPM1M	protein phosphatase 1M (PP2C domain containing)	0.77	CCCAGAGACTCGGATTATCAA	NM_144641:	NM_144641:
54704	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	0.25	ACCGATTAAGGCCACAGGATA	NM_018444:	NM_018444:
54704	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	0.59	CAAGATAGTAGTATTATTACA	NM_018444:	NM_018444:
51400	PPME1	protein phosphatase methylesterase 1	-1.73	AACATCGAGCTCTGTTGTAAA	NM_016147:	NM_016147:
51400	PPME1	protein phosphatase methylesterase 1	0.04	AGGCGATACATCTGAGTTCAA	NM_016147:	NM_016147:
5498	PPOX	protoporphyrinogen oxidase	-0.10	CTGCTTGGTCCATCTACACAA	NM_000309:	NM_000309:
5498	PPOX	protoporphyrinogen oxidase	-3.04	CAGGAAGCAGCTGCTACACAA	NM_000309:	NM_000309:
5499	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	-0.09	AAGAGACGCTACAACATCAAA	NM_002708:	NM_002708:NM_206873:NM_001008709:
5499	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	-5.11	CCGCAATTCCGCCAAAGCCAA	NM_002708:	NM_002708:NM_206873:NM_001008709:
5500	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	-0.69	TACGAGGATGTCGTCCAGGAA	NM_002709:	NM_002709:NM_206876:
5500	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	-1.23	TAGGAATATGGTCGGGCTGAA	NM_002709:	NM_002709:NM_206876:NM_206877:
5501	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	1.01	AACATCGACAGCATTATCCAA	NM_002710:	NM_002710:
5501	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	-0.85	CTGGTTATAACAGCAAATGAA	NM_002710:	NM_002710:
5514	PPP1R10	protein phosphatase 1, regulatory subunit 10	-1.88	CCCAGCCTGCTGAGAAAGATA	NM_002714:	NM_002714:
5514	PPP1R10	protein phosphatase 1, regulatory subunit 10	-2.92	CCGAAGGACCGTCACTACATA	NM_002714:	NM_002714:
6992	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	-2.71	AACATGAGTAGCGAACACTTA	NM_021959:	NM_021959:NM_170781:
6992	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	0.50	CGCCCTAACTTTGCTTGCTAA	NM_021959:	NM_021959:NM_170781:
4659	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1.08	ATAGTACTCAACCATAATTAA	NM_002480:	NM_002480:
4659	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	-0.29	CAGAATTAACCCGTGAGTTAA	NM_002480:	NM_002480:
4660	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-0.25	CAGGGTGTTGCCTCTAAAGAA	NM_002481:	NM_032105:NM_002481:
4660	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-3.76	CGGGAGGTAGTAATCCTACAA	NM_002481:	NM_032105:NM_002481:NM_032103:NM_032104:
54776	PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	-7.27	CAGCGGGACCTCAACCCAGAA	NM_017607:	NM_017607:
54776	PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	-2.15	CAGGAGGACCTTCGGAACCAA	NM_017607:	NM_017607:
23368	PPP1R13B	protein phosphatase 1, regulatory (inhibitor) subunit 13B	-0.40	CGCGATGATGCCGATGATATT	NM_015316:	NM_015316:
23368	PPP1R13B	protein phosphatase 1, regulatory (inhibitor) subunit 13B	0.04	CGGGCTGAGAGTCCGGTTTAA	NM_015316:	NM_015316:
94274	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	0.73	CCCGATGAGATCAACATTGAT	NM_033256:	NM_033256:
94274	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	1.59	TTGTATTTAATGGTTCTGTAA	NM_033256:	NM_033256:
81706	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	-2.26	AAGAGCTGCTTTCTCGGATAA	NM_030949:	NM_030949:
81706	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	-0.58	TAAAGTTGTATGAACCCTTAA	NM_030949:	NM_030949:
54866	PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	0.40	CAGGAGCTCTTCCAGGATCAA	NM_017726:	NM_017726:
54866	PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	-0.60	CCGCCTGACAGTGAAGTATGA	NM_017726:	NM_017726:

23645	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0.20	CCAGTTGTTGATCTTATGCAA	NM_014330:	NM_014330:
23645	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0.05	TGGGTTTATATAAGGAATAAA	NM_014330:	NM_014330:
84919	PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	1.02	AAGGTGCTAATTTGGAGCCAA	NM_032833:	NM_032833:
84919	PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	-2.13	CAGGGTTACTACCTCAGTTTA	NM_032833:	NM_032833:
26051	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	0.51	ACGGGCGAGAGTAGCAGTGAA	NM_015568:	NM_015568:
26051	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	-3.32	TCGCAGATCTTTGATATCGTA	NM_015568:	NM_015568:
5502	PPP1R1A (pr	protein phosphatase 1, regulatory (inhibitor) subunit 1A	-3.91	AAGGATCACACCCACAATGAA	NM_006741:	NM_006741:
5502	PPP1R1A (pr	protein phosphatase 1, regulatory (inhibitor) subunit 1A	-0.73	TTGCCCAGATACATACCTAAA	NM_006741:	NM_006741:
84152	PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine an	-1.70	ATAAATCTTTGTAAATAACAA	NM_181505:	NM_181505:
84152	PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine an	1.29	CAGCTTGTTTGAAGCCCTTGA	NM_181505:	NM_181505:
151242	PPP1R1C (pr	protein phosphatase 1, regulatory (inhibitor) subunit 1C	-0.01	CTCGATCTGGAATTACAGCTA	XM_087137:	XM_087137:
151242	PPP1R1C (pr	protein phosphatase 1, regulatory (inhibitor) subunit 1C	0.16	TTGGAACTGGTTAGTACCTAA	XM_087137:	XM_087137:
5504	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	0.41	CACTACACGTACTGTAATAAA	NM_006241:	NM_006241:
5504	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	-2.98	TACCACTGATTTAGAAACAAA	NM_006241:	NM_006241:
80316	PPP1R2P9	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	0.64	ACGTACAGAGATTACGATTTA	NM_025210:	NR_002191:
80316	PPP1R2P9	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	-0.78	CTGGAGGGCGGTGGACGGCTA	NM_025210:	NR_002191:
5506	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and	-0.74	CACATCAGTATAGGCCATCAA	NM_002711:	NM_002711:
5506	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and	-0.44	TCAGGTGGGATTAATTCTGAA	NM_002711:	NM_002711:
79660	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	0.91	CACCCAAGTTCTTATACGTTA	NM_024607:	NM_024607:
79660	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	0.55	CCCGCTAGATATGCCATTCAA	NM_024607:	NM_024607:
5507	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	-0.52	TACGATGAATTTCAACGACGA	NM_005398:	NM_005398:
5507	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	-0.31	TCCGGAGAATCAAGATCTTAA	NM_005398:	NM_005398:
5509	PPP1R3D	protein phosphatase 1, regulatory subunit 3D	2.41	CAGGTACCCACCAACTTTATA	NM_006242:	NM_006242:
5509	PPP1R3D	protein phosphatase 1, regulatory subunit 3D	1.03	CTGAGTTAGGCAATCACTTAA	NM_006242:	NM_006242:
89801	PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	-0.12	CGGGTTGGTACGCGTGCTGAA	NM_033215:	NM_033215:
89801	PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	1.37	AACATGGATGATAACACCTTT	NM_033215:	NM_033215:
5510	PPP1R7	protein phosphatase 1, regulatory subunit 7	0.60	CACAAACCCAATGGCAATAAA	NM_002712:	NM_002712:
5510	PPP1R7	protein phosphatase 1, regulatory subunit 7	1.33	TCAGATGCCGTTGCAATTAAA	NM_002712:	NM_002712:
5511	PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8	-2.73	CAGGCCCAGGAACTGAAGAAA	NM_002713:	NM_002713:NM_138558:
5511	PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8	0.29	TACAAATAAAGATGCCCTAAA	NM_002713:	NM_014110:NM_002713:NM_138558:
55607	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0.65	CTCCAATGTCAACAGAATTAA	XM_374491:	XM_374491:XM_371933:
55607	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	1.30	GAGGGTAATATTTATCCTCTA	XM_374491:	XM_374491:XM_371933:
84687	PPP1R9B	protein phosphatase 1, regulatory subunit 9B, spinophilin	1.26	CAACTCGAAGCTGGTCAGCAA	NM_032595:	NM_032595:
84687	PPP1R9B	protein phosphatase 1, regulatory subunit 9B, spinophilin	-0.11	CCCGGGAGGTGCGCAAGATTA	NM_032595:	NM_032595:
5515	PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.80	ATGGAACTTGACGATACTCTA	NM_002715:	NM_002715:
5515	PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	-2.62	CAAACAATCATTGGAGCTTAA	NM_002715:	NM_002715:
5516	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	0.00	CCGACAAATTACCCAAGTATA	NM_004156:	NM_004156:NM_001009552:
5516	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	1.43	TGGGATCTGTCTTGGCATTAA	NM_004156:	NM_004156:NM_001009552:
5518	PPP2R1A	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp	1.68	ACGGCTGAACATCATCTCTAA	NM_014225:	NM_014225:
5518	PPP2R1A	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp	-5.01	CTGGTGTCCGATGCCAACCAA	NM_014225:	NM_014225:
5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), bet	-0.66	CAGAAGTTAGGTCAAGATGAA	NM_002716:	NM_002716:NM_181699:
5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), bet	-4.88	CAGGAAATAACTACTAAGCAA	NM_002716:	NM_002716:NM_181699:
5520	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alp	1.47	ATGGAAGGTATAGAGATCCTA	NM_002717:	NM_002717:
5520	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alp	-0.34	CTGCAGATGATTTGCGGATTA	NM_002717:	NM_002717:
5521	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), bet	-0.16	CAGGAAATGATTGGAATAGAA	NM_004576:	NM_181678:NM_181677:NM_181674:NM_181675:NM_181676:NM_004576:
5521	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), bet	-2.66	CAGGGACTACTTGACCGTCAA	NM_004576:	NM_181678:NM_181677:NM_181674:NM_181675:NM_181676:NM_004576:
5522	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), ga	1.95	ACCGCTCATTCTTCTCGGAAA	NM_020416:	NM_181876:NM_020416:
5522	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), ga	-1.49	CCGGGACTACCTTACAGTCAA	NM_020416:	NM_181876:NM_020416:
55844	PPP2R2D	protein phosphatase 2, regulatory subunit B, delta isoform	-0.74	CAGAGACTACCTGTCGGTGAA	BC047379:	NM_018461:NM_001003656:
55844	PPP2R2D	protein phosphatase 2, regulatory subunit B, delta isoform	0.42	TAGGTGGTTACCACAACAGAA	BC047379:	NM_018461:NM_001003656:
5523	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	-0.27	ACCTGTAGTAATCATGAACAA	NM_181897:	NM_002718:NM_181897:
5523	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	-2.23	CAGGAGGATTTCATCCCTCTA	NM_181897:	NM_002718:NM_181897:
28227	PPP2R3B	protein phosphatase 2 (formerly 2A), regulatory subunit B", beta	0.04	CACGTGTCTCTGTCACGTGAA	NM_199326:	NM_199326:
28227	PPP2R3B	protein phosphatase 2 (formerly 2A), regulatory subunit B", beta	-0.04	CTGGGCCTGAGTGAGCAGTAA	NM_199326:	NM_199326:
5524	PPP2R4	protein phosphatase 2A, regulatory subunit B' (PR 53)	-0.74	CTCCGGGTGGATGACCAAATA	NM_178003:	NM_178000:NM_178001:NM_021131:NM_178003:NM_178002:
5524	PPP2R4	protein phosphatase 2A, regulatory subunit B' (PR 53)	-4.99	CTGAGGTGGCTGTTTACCTAA	NM_178003:	NM_178000:NM_178001:NM_021131:NM_178003:NM_178002:
5525	PPP2R5A	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	0.01	CAGCGTATTCTGATATAGTAA	NM_006243:	NM_006243:
5525	PPP2R5A	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	-0.78	CTGTATCATGGCCATAGTATA	NM_006243:	NM_006243:
5526	PPP2R5B	protein phosphatase 2, regulatory subunit B (B56), beta isoform	0.04	CCGCATGATCTCAGTGAATAT	NM_006244:	NM_006244:
5526	PPP2R5B	protein phosphatase 2, regulatory subunit B (B56), beta isoform	2.33	CCGGTTCATCTATGAATTCGA	NM_006244:	NM_006244:
5527	PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.13	AACGAGCTGCTTTAAGTGAAA	NM_002719:	NM_178586:NM_178587:NM_178588:NM_002719:
5527	PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	-2.92	CCCATTGGAACAAGTAAGAAA	NM_002719:	NM_178588:
5529	PPP2R5E (pr	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-0.43	CACCGGGATTGCAAATCTAAT	NM_006246:	NM_006246:
5529	PPP2R5E (pr	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	1.61	CCGGTGATATTGACAATAGGA	NM_006246:	NM_006246:
5530	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (	-0.27	TAGCGATATAGCATACCCAAA	NM_000944:	NM_000944:
5530	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (	-5.36	TCGGCCTGTATGGGACTGTAA	NM_000944:	NM_000944:
5532	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (c	0.00	AAGGGTTTGGATAGGATCAAT	NM_021132:	NM_021132:
5532	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (c	-1.70	TAGGAGATTAGATAGATTCAA	NM_021132:	NM_021132:
5533	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	0.51	CAGGCTTTCCATCACTTATTA	NM_005605:	NM_005605:
5533	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	-0.11	CCGAGGGTGCTCTTATTTCTA	NM_005605:	NM_005605:
5534	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpl	-0.37	ATCCTTTAGTACAGCGAGTAA	NM_000945:	NM_000945:
5534	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpl	-0.42	GCCCATATAATTGGTAATGGA	NM_000945:	NM_000945:
5531	PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	0.00	CGGACAATCGACCGAAAGCAA	NM_002720:	NM_002720:
5531	PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	-0.14	TCGCCAGATCACGCAGGTCTA	NM_002720:	NM_002720:
9989	PPP4R1	protein phosphatase 4, regulatory subunit 1	2.02	CAGGCGTTGTTAGATCAGTAT	NM_005134:	NM_005134:
9989	PPP4R1	protein phosphatase 4, regulatory subunit 1	2.20	TGGGAGTGCTGCAGTCTTTAA	NM_005134:	NM_005134:
5536	PPP5C	protein phosphatase 5, catalytic subunit	-2.83	CCCGTTGGCCCAGTGCATCAA	NM_006247:	NM_006247:
5536	PPP5C	protein phosphatase 5, catalytic subunit	-1.91	CTCGTGGAAACCACACTCAAA	NM_006247:	NM_006247:
5537	PPP6C (prote	protein phosphatase 6, catalytic subunit	1.89	CACAAATGAGTTTGTTCATAT	NM_002721:	NM_002721:
5537	PPP6C (prote	protein phosphatase 6, catalytic subunit	-1.80	CAGCAGCAAAGTTGTTATTCA	NM_002721:	NM_002721:
23082	PPRC1	peroxisome proliferative activated receptor, gamma, coactivator-relate	-1.15	AAGGGTGGTCTTCATTGGAAA	NM_015062:	NM_015062:
23082	PPRC1	peroxisome proliferative activated receptor, gamma, coactivator-relate	-0.41	CAGACTAATAAACATCAACTA	NM_015062:	NM_015062:
5538	PPT1	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infa	0.91	AACGTAATCTACCATTTCCTA	NM_000310:	NM_000310:
5538	PPT1	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infa	0.21	AACCCACATTAGAGTGTCTAA	NM_000310:	NM_000310:
160760	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	0.66	AAAGGGATGGTACAAGTCTAA	NM_139283:	NM_139283:
160760	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	-1.33	CACAAATTGTACGTAATGATA	NM_139283:	NM_139283:
160760	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	-3.03	TAGCGTAACATGATACATCTA	AK001795:	NM_139283:
5540	PPYR1	pancreatic polypeptide receptor 1	-1.43	CAGGCTCTTCCACTTAGCTAA	NM_005972:	NM_005972:
5540	PPYR1	pancreatic polypeptide receptor 1	0.49	CTGAGAGGCGTCATCCCTCAA	NM_005972:	NM_005972:
84106	PRAM1	PML-RARA regulated adaptor molecule 1	-2.93	CCGGAGCATCAAAGCAAAGTT	NM_032152:	NM_032152:
84106	PRAM1	PML-RARA regulated adaptor molecule 1	-0.10	CCGCAAGTTCTCACAGCCTGA	NM_032152:	NM_032152:
5544	PRB3	proline-rich protein BstNI subfamily 3	-1.46	AAGAAGGTGGTCATAGCTCTA	NM_006249:	NM_006249:
5544	PRB3	proline-rich protein BstNI subfamily 3	-1.73	CAAGAAGGTAACAAACCTCAA	NM_006249:	NM_006249:
5545	PRB4	proline-rich protein BstNI subfamily 4	-1.10	TCAGCTGAGAGTTCAAGTGAA	NM_002723:	NM_002723:

5545	PRB4	proline-rich protein BstNI subfamily 4	1.21	CAGGAAGAATCTCTCTTCCTA	NM_002723:	NM_002723:
5546	PRCC	papillary renal cell carcinoma (translocation-associated)	0.38	AGGGATGTCTGTTGAAATAAA	NM_005973:	NM_199416:NM_005973:
5546	PRCC	papillary renal cell carcinoma (translocation-associated)	-0.87	CAGGGATGTCTGTTGAAATAA	NM_005973:	NM_199416:NM_005973:
5547	PRCP	prolylcarboxypeptidase (angiotensinase C)	-0.18	ATGCCATTAATCGACTCTCAA	NM_005040:	NM_199418:NM_005040:
5547	PRCP	prolylcarboxypeptidase (angiotensinase C)	-5.56	CAGGTCCTGGGATGCCATTAA	NM_005040:	NM_199418:NM_005040:
56981	PRDM11	PR domain containing 11	-2.39	ACGCCTACAGTCAGTGTGCAA	NM_020229:	NM_020229:
56981	PRDM11	PR domain containing 11	-1.99	CAGGTTCTGGATAACCCAGAA	NM_020229:	NM_020229:
7799	PRDM2	PR domain containing 2, with ZNF domain	0.61	CAGATGTATGTCTACACGTAA	NM_015866:	NM_015866:NM_001007257:
7799	PRDM2	PR domain containing 2, with ZNF domain	0.00	CCCGGGTGATTGAGATCCAAA	NM_015866:	NM_015866:NM_001007257:
56978	PRDM8	PR domain containing 8	-1.12	CGCGCGCGCAAGCACAGTTAA	NM_020226:	NM_020226:
56978	PRDM8	PR domain containing 8	-0.08	CTCGCATAATTGACTCGGAAA	NM_020226:	NM_020226:
7001	PRDX2	peroxiredoxin 2	1.35	TGGCGCCTTCAAAGAGGTGAA	NM_005809:	NM_005809:NM_181737:NM_181738:
7001	PRDX2	peroxiredoxin 2	-0.03	TTGGTTCGGGCCGGGCATAAA	NM_005809:	NM_005809:NM_181737:NM_181738:
10549	PRDX4	peroxiredoxin 4	-0.15	AACCTGGTAGTGAAACAATAA	NM_006406:	NM_006406:
10549	PRDX4	peroxiredoxin 4	0.65	AAGCAAAGCGAAGATTTCCAA	NM_006406:	NM_006406:
25824	PRDX5	peroxiredoxin 5	-0.60	CACCTGCAGCCTGGCACCCAA	NM_012094:	NM_181652:NM_012094:NM_181651:
25824	PRDX5	peroxiredoxin 5	1.37	CTGAGTGTTAATGATGCCTTT	NM_012094:	NM_012094:
9588	PRDX6	peroxiredoxin 6	1.13	GTGGCAGAACTTGAAGTTCAA	NM_004905:	NM_004905:
9588	PRDX6	peroxiredoxin 6	2.29	TCCGATGATGTGTACATGAAA	NM_004905:	NM_004905:
5550	PREP	prolyl endopeptidase	-0.55	AAGGGCATGTTGGGATAAATA	NM_002726:	NM_002726:
5550	PREP	prolyl endopeptidase	-0.37	TCCCAAGAGGCTGACTATTAA	NM_002726:	NM_002726:
9581	PREPL	prolyl endopeptidase-like	-1.22	CAGGAGCATTGTGTAATTCTA	NM_006036:	NM_006036:
9581	PREPL	prolyl endopeptidase-like	-0.05	AAGGATCTTCAGCCTGTTAAA	NM_006036:	NM_006036:
5551	PRF1	perforin 1 (pore forming protein)	0.67	CACCGTGTGGGACAATAACAA	NM_005041:	NM_005041:
5551	PRF1	perforin 1 (pore forming protein)	-0.71	CACGGTGGAGTGCCGCTTCTA	NM_005041:	NM_005041:
5554	PRH1	proline-rich protein HaeIII subfamily 1	-0.94	TGGCATCATGCTCTAACTTCA	NM_006250:	NM_006250:
85441	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	0.50	ATGTGATTAGATATTAATTTA	NM_033405:	NM_033405:NM_001037335:
85441	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	0.38	CCCTTACTCGTCGGAAATCAA	NM_033405:	NM_033405:NM_001037335:
144165	PRICKLE1	prickle-like 1 (Drosophila)	0.05	CCCATGTAAATGAGAACTCAA	NM_153026:	NM_153026:
144165	PRICKLE1	prickle-like 1 (Drosophila)	0.34	CAGTGTCAGATTAACATTTGA	NM_153026:	NM_153026:
5557	PRIM1	primase, polypeptide 1, 49kDa	-0.37	CTGAATCTGATGTCAAACATA	NM_000946:	NM_000946:
5557	PRIM1	primase, polypeptide 1, 49kDa	0.40	CTGGGATAGTTGAGTATTTGA	NM_000946:	NM_000946:
5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	0.02	CCCACGATATTCTGTACACAA	NM_006251:	NM_006251:NM_206907:
5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	-1.42	TCGGGATCAGTTAGCAACTAT	NM_006251:	NM_006251:NM_206907:
5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	-0.11	ACGACTAAGCCCAAATCTTTA	NM_006252:	NM_006252:
5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	-0.13	CCGATTTCGGATTATCTAATA	NM_006252:	NM_006252:
5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-0.02	CACGTCTAGAAGTCACATGAA	NM_006253:	NM_006253:
5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-8.68	CTGGCTATGGAACTAAATACA	NM_006253:	NM_006253:
5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.76	ACCCAAAGTACTACTCATTTA	NM_005399:	NM_005399:
5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.66	TCCAATATTAGTTGGAGTTAA	NM_005399:	NM_005399:
5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	0.68	CAAGGACAACTCAAACTTATA	NM_002730:	NM_002730:NM_207518:
5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	-0.73	CAGAAGGTGGTGAAACTGAAA	NM_002730:	NM_002730:NM_207518:
5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	0.01	CAGCCTGTGTAGTGTGACAAA	NM_182948:	NM_182948:NM_002731:
5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	-3.70	CTGACCAATCAAGTACACTAA	NM_182948:	NM_182948:NM_002731:
5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	0.54	AACCAGCTGGATCGCCATCTA	NM_002732:	NM_002732:
5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	-4.95	CTGGATCGCCATCTATGAGAA	NM_002732:	NM_002732:
5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	-0.40	CCCTAAGATAATAGCACAACA	NM_002733:	NM_002733:NM_212461:
5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	-0.22	TTGGCCCTGATTCAACCCTAA	NM_002733:	NM_002733:NM_212461:
51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	0.03	AAGCACGAGCCTGAACGGTTA	NM_016203:	NM_016203:
51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-3.92	CCGGAAAGCATTCCTCTCGAA	NM_016203:	NM_016203:
53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	0.28	CAGATCTATGAGATTGAACAA	NM_017431:	NM_017431:
53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	-1.41	TAGCCTGTTTGAAGCTGTCTA	NM_017431:	NM_017431:
5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue spec	0.19	ATGAAATAATTTAAATTCTTA	NM_002734:	NM_002734:NM_212471:NM_212472:
5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue spec	0.47	CAAATATTGGTTAGTATTTAA	NM_002734:	NM_002734:NM_212471:NM_212472:
5575	PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	0.12	CAAGAGGAACATTCAGCGTTA	NM_002735:	NM_002735:
5575	PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	-10.67	CAGGGAGTTGAGGCCGAAGAA	NM_002735:	NM_002735:
5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	0.14	AACGGCATGTCTCTCCAACAA	NM_004157:	NM_004157:
5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	-0.03	AACTTGAAAGTCAGCACTAAA	NM_004157:	NM_004157:
5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	0.17	ACGAACATGGATATTGTTGAA	NM_002736:	NM_002736:
5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	-2.16	CACGCCATTGGGACTGTCAAA	NM_002736:	NM_002736:
5578	PRKCA	protein kinase C, alpha	0.59	CAAGACGTCTTTGGAATCCAA	NM_002737:	NM_002737:
5578	PRKCA	protein kinase C, alpha	-0.03	CAGCTGGTTATTGCTAACATA	NM_002737:	NM_002737:
5579	PRKCB1	protein kinase C, beta 1	-0.11	CAAGAGCTAAGTAGATGTGTA	NM_002738:	NM_002738:
5579	PRKCB1	protein kinase C, beta 1	0.03	CCGGATGAAACTGACCGATTT	NM_002738:	NM_212535:NM_002738:
23613	PRKCBP1	protein kinase C binding protein 1	-0.36	AGCGAACTTGTCATAGATTTA	NM_183048:	NM_183047:NM_183048:NM_012408:
23613	PRKCBP1	protein kinase C binding protein 1	-0.79	CACCATTGAACAGTTATCCTA	NM_183048:	NM_183047:NM_183048:NM_012408:
5580	PRKCD	protein kinase C, delta	-0.03	CAGCAGCAAGTGCAACATCAA	NM_006254:	NM_006254:NM_212539:
5580	PRKCD	protein kinase C, delta	-0.92	CAGGTTTATTTGTGTGTCTAA	NM_006254:	NM_006254:NM_212539:
112464	PRKCDBP	protein kinase C, delta binding protein	-0.65	AAGGAGCGAATCCTACATCCA	NM_145040:	NM_145040:
112464	PRKCDBP	protein kinase C, delta binding protein	-1.53	CACGCCCTAATAAGGAGCGAA	NM_145040:	NM_145040:
5581	PRKCE	protein kinase C, epsilon	0.03	CACGGAAACACCCGTACCTTA	NM_005400:	NM_005400:
5581	PRKCE	protein kinase C, epsilon	-2.47	CCCGACCATGGTAGTGTTCAA	NM_005400:	NM_005400:
5582	PRKCG	protein kinase C, gamma	0.55	AACGGTGAAAGCCACGCTAAA	NM_002739:	NM_002739:
5582	PRKCG	protein kinase C, gamma	0.54	GACCTTTGTGTTCAACCTGAA	NM_002739:	NM_002739:
5583	PRKCH	protein kinase C, eta	0.13	CGCCGTGTGCTCATCACTGAA	NM_006255:	NM_006255:
5583	PRKCH	protein kinase C, eta	1.21	GACCAGATTTGTGGCTTATAA	NM_006255:	NM_006255:
5584	PRKCI	protein kinase C, iota	-0.11	ACGCCGCTGGAGAAAGCTTTA	NM_002740:	NM_002740:
5584	PRKCI	protein kinase C, iota	-1.56	CACCCAATATCTTCTCTTGTA	NM_002740:	NM_002740:
5588	PRKCQ	protein kinase C, theta	0.13	CCGCAGACAAGTAATCACTAA	NM_006257:	NM_006257:
5588	PRKCQ	protein kinase C, theta	-5.80	CGGGCAGATGTATATCCAGAA	NM_006257:	NM_006257:
5589	PRKCSH	protein kinase C substrate 80K-H	0.35	ACCTGTGACCTCAATACAATA	NM_002743:	NM_001001329:NM_002743:
5589	PRKCSH	protein kinase C substrate 80K-H	-1.86	CTGCACCAACACTGGCTATAA	NM_002743:	NM_001001329:NM_002743:
5590	PRKCZ	protein kinase C, zeta	-0.10	CGGAAGCATGACAGCATTAAA	NM_002744:	NM_001033582:NM_002744:NM_001033581:
5590	PRKCZ	protein kinase C, zeta	0.79	GACCAAATTTACGCCATGAAA	NM_002744:	NM_001033582:NM_002744:NM_001033581:
5587	PRKD1	protein kinase D1	0.03	CAGGAAGGCGATCTTATTGAA	NM_002742:	NM_002742:
5587	PRKD1	protein kinase D1	0.01	CCTCAGTATATTTAAACTCAA	NM_002742:	NM_002742:
25865	PRKD2	protein kinase D2	-5.93	CACGACCAACAGATACTATAA	NM_016457:	NM_016457:
25865	PRKD2	protein kinase D2	-0.44	TTGGGTGGTTCATTACAGCAA	NM_016457:	NM_016457:
23683	PRKD3	protein kinase D3	-1.32	CACGATATGTCAGTACTGCAA	NM_005813:	NM_005813:
23683	PRKD3	protein kinase D3	-2.52	CGGGAGAGTGTTACCATTGAA	NM_005813:	NM_005813:
5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	0.42	CTCGTGTATTACAGAAGGAAA	NM_006904:	NM_006904:
5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	1.21	GACCCTGTTGACAGTACTTTA	NM_006904:	NM_006904:
5592	PRKG1	protein kinase, cGMP-dependent, type I	0.49	CCGGTGTATATACCATACAAA	NM_006258:	NM_006258:
5592	PRKG1	protein kinase, cGMP-dependent, type I	0.21	GAGGTTCGTTTGAAGATTCTA	NM_006258:	NM_006258:
5593	PRKG2	protein kinase, cGMP-dependent, type II	0.80	GACCTACAATTTGATTCTCAA	NM_006259:	NM_006259:
5593	PRKG2	protein kinase, cGMP-dependent, type II	0.94	TTGAGTACTACTAACGTTTAA	NM_006259:	NM_006259:
8575	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent a	0.89	ATGATTGATTGTTAAATTTCA	NM_003690:	NM_003690:
8575	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent a	0.69	TAAGTATGATTGATTGTTAAA	NM_003690:	NM_003690:
5612	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent i	0.23	AAGGTGTATGTAGACCACTTA	NM_004705:	NM_004705:

5612	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent i	-0.52	CTGGACAGTTACAAGAAATTA	NM_004705:	NM_004705:
5613	PRKX	protein kinase, X-linked	-0.88	CGGATGGGATTCACTTAAGAA	NM_005044:	NM_005044:
5613	PRKX	protein kinase, X-linked	0.56	TTGGAATACTCTAAGAGAATA	NM_005044:	NM_005044:
5616	PRKY (protei	protein kinase, Y-linked	0.23	CCAGAGTTCGCCTACAGATAA	NM_002760:	NM_002760:
5616	PRKY (protei	protein kinase, Y-linked	1.60	TTGGGATACAGTAAGAGAATA	NM_002760:	NM_002760:
5617	PRL (prolacti	prolactin	0.00	CCCGGAGGCTATCCTATCCAA	NM_000948:	NM_000948:
5617	PRL (prolacti	prolactin	-4.15	CAGCATATTGCGATCCTGGAA	NM_000948:	NM_000948:
2834	PRLHR	prolactin releasing hormone receptor	0.09	CACCTATCACGTGGAGCTCAA	NM_004248:	NM_004248:
2834	PRLHR	prolactin releasing hormone receptor	-0.76	CGCCATGAGTTCGGCCTGCTA	NM_004248:	NM_004248:
5618	PRLR	prolactin receptor	0.30	CCGGGACTCCTGAGAACAATA	NM_000949:	NM_000949:
5618	PRLR	prolactin receptor	0.80	CTCCTGTATGAAATTCGATTA	NM_000949:	NM_000949:
3275	PRMT2	protein arginine methyltransferase 2	0.26	ACCGTGCAAATTTCTGATCTA	NM_001535:	NM_001535:NM_206962:
3275	PRMT2	protein arginine methyltransferase 2	-0.21	AACGCGATTGAGAAATGGAAA	NM_001535:	NM_001535:
10196	PRMT3	protein arginine methyltransferase 3	0.16	CAGATTTATGTGCAAAGGTTA	NM_005788:	NM_005788:
10196	PRMT3	protein arginine methyltransferase 3	-0.35	TTGGAGTTGATCAATCTGAAA	NM_005788:	NM_005788:
55170	PRMT6	protein arginine methyltransferase 6	1.45	ATAGCCTAACATTTATTGTAA	NM_018137:	NM_018137:
55170	PRMT6	protein arginine methyltransferase 6	-0.08	CACACCTTATCTAAGTCTGAA	NM_018137:	NM_018137:
54496	PRMT7	protein arginine methyltransferase 7	0.87	ACGGCCGGAATTATTAACAAA	NM_019023:	NM_019023:
54496	PRMT7	protein arginine methyltransferase 7	0.74	AACGGCCGGAATTATTAACAA	NM_019023:	NM_019023:
56341	PRMT8	protein arginine methyltransferase 8	-0.41	CAGATGTTAAGCAGCTATGAA	NM_019854:	NM_019854:
56341	PRMT8	protein arginine methyltransferase 8	1.30	CGCGTGTGCCTAGAATATATA	NM_019854:	NM_019854:
23627	PRND	prion protein 2 (dublet)	0.92	CACAATATGAGTAATGTTTAA	NM_012409:	NM_012409:
23627	PRND	prion protein 2 (dublet)	0.34	CCCAGGAGTTGTTGAACTATA	NM_012409:	NM_012409:
5624	PROC	protein C (inactivator of coagulation factors Va and VIIIa)	0.45	TGCCTTATGAATAGAATCTTA	NM_000312:	NM_000312:
5624	PROC	protein C (inactivator of coagulation factors Va and VIIIa)	0.07	CAGCAAGAGCACCACCGACAA	NM_000312:	NM_000312:
147011	PROCA1	proline-rich cyclin A1-interacting protein	0.98	CAGGGTGGTCAGGGTGCAGAA	NM_152465:	NM_152465:
147011	PROCA1	proline-rich cyclin A1-interacting protein	0.08	CAGACGTGAGCCGATCATTAA	NM_152465:	NM_152465:
10544	PROCR	protein C receptor, endothelial (EPCR)	0.03	CAGGTGGACGGCGATGTTAAT	NM_006404:	NM_006404:
10544	PROCR	protein C receptor, endothelial (EPCR)	0.21	TTGGGATGGGACGCTGATATA	NM_006404:	NM_006404:
5625	PRODH	proline dehydrogenase (oxidase) 1	-1.47	CTGCTGTATGTTTCCAGGAAA	NM_016335:	NM_016335:
5625	PRODH	proline dehydrogenase (oxidase) 1	0.69	AGGAATATAGGCGCACACTTA	NM_016335:	NM_016335:
84432	PROK1	prokineticin 1	-3.40	CCGCTGCTCCATGGACTTGAA	NM_032414:	NM_032414:
84432	PROK1	prokineticin 1	0.01	CTCCATGGACTTGAAGAACAT	NM_032414:	NM_032414:
60675	PROK2	prokineticin 2	1.11	CGGTATTAAGTTGTAATTTAA	NM_021935:	NM_021935:
60675	PROK2	prokineticin 2	1.17	TAGCCACATCTTACCTGTAAA	NM_021935:	NM_021935:
10887	PROKR1	prokineticin receptor 1	1.10	CAGGACGTTCTTTGCTGCCAA	NM_138964:	NM_138964:
10887	PROKR1	prokineticin receptor 1	-0.88	CCGCTACAAGAAACTGCGCAA	NM_138964:	NM_138964:
128674	PROKR2	prokineticin receptor 2	-1.50	CCGGACCTTCTTCGCAGCCAA	NM_144773:	NM_144773:
128674	PROKR2	prokineticin receptor 2	-0.10	TCGGCTTACTTTGCAACAGAA	NM_144773:	NM_144773:
8842	PROM1	prominin 1	-0.17	ACCTTTGAGTTTGGTCCCTAA	NM_006017:	NM_006017:
8842	PROM1	prominin 1	0.07	CACGTTATAGTCCATGGTCCA	NM_006017:	NM_006017:
5626	PROP1 (prop	prophet of Pit1, paired-like homeodomain transcription factor	0.95	CTCACCGATTAGAAATTTAAA	NM_006261:	NM_006261:
5626	PROP1 (prop	prophet of Pit1, paired-like homeodomain transcription factor	0.92	CCGCAGAGCTAAGCAACGGAA	NM_006261:	NM_006261:
5627	PROS1	protein S (alpha)	-1.09	ATGGAGGGTCCTAATGCCTTA	NM_000313:	NM_000313:
5627	PROS1	protein S (alpha)	0.44	ATGGTGGTCTATTAAATATGA	NM_000313:	NM_000313:
8858	PROZ	protein Z, vitamin K-dependent plasma glycoprotein	1.36	CATGAGATACGTTAAATAATA	NM_003891:	NM_003891:
8858	PROZ	protein Z, vitamin K-dependent plasma glycoprotein	0.75	ACAGATCATGAACTAACTGAA	NM_003891:	NM_003891:
134285	PRP2	proline-rich protein PRP2	-1.35	CAGGACAGACACGTCAGCAAA	NM_173490:	NM_173490:
134285	PRP2	proline-rich protein PRP2	0.50	GAGACTGTGAATCTATATATA	NM_173490:	NM_173490:
27339	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae	-2.93	CACGCCAAGTTCATCGCTTCA	NM_014502:	NM_014502:
27339	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae	-5.55	CAGATCTACATCTGCAAACAA	NM_014502:	NM_014502:
26121	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	-0.31	CGGGATAAGTACTCAAAGAGA	NM_015629:	NM_015629:
26121	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	-0.79	CGAGCTGAACATCATCCATAA	NM_015629:	NM_015629:
8899	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-0.18	GAGCCGATCCTTAGAAAGAAA	NM_003913:	NM_003913:NM_176800:
8899	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.21	TCGTCTGATGATAACCTTGAA	NM_003913:	NM_003913:NM_176800:
10594	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (yeast)	-6.72	ATGGCTTGTCATCCTGAATAA	NM_006445:	NM_006445:
10594	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (yeast)	-5.90	CCGAAAGTCATATAAGATGAA	NM_006445:	NM_006445:
5631	PRPS1	phosphoribosyl pyrophosphate synthetase 1	-0.03	TTGATTAATTTAAGTATTTAA	NM_002764:	NM_002764:
5631	PRPS1	phosphoribosyl pyrophosphate synthetase 1	-1.86	AACATGCTTCCTGCTATGTAA	NM_002764:	NM_002764:
221823	PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	0.81	AACAGAATAACTTCTAGGTTA	NM_175886:	NM_175886:
221823	PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	-7.90	CCCAGCCATTTCTCGCATCAA	NM_175886:	NM_175886:
5634	PRPS2	phosphoribosyl pyrophosphate synthetase 2	-0.12	TCAGCTAAGATTAAATTTAAA	NM_002765:	NM_002765:
5634	PRPS2	phosphoribosyl pyrophosphate synthetase 2	-2.63	TAGACATATCAGAGCAGTGTA	NM_002765:	NM_002765:
5636	PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	0.95	CTGGTCTAACTCATCTTATTA	NM_002767:	NM_002767:
5636	PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	0.21	AAGAGCATCATTGGCGTGATA	NM_002767:	NM_002767:
5644	PRSS1	protease, serine, 1 (trypsin 1)	-1.56	CAGGAAGACTCTGAACAATGA	NM_002769:	NM_002769:
5644	PRSS1	protease, serine, 1 (trypsin 1)	1.12	CTGAACAATGACATCATGTTA	NM_002769:	NM_002769:
8492	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	-0.29	CTCAGTGTAGTGGAAGTGATA	NM_003619:	NM_003619:
8492	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	-0.06	AAGCGGATCATTGGTGGGAAA	NM_003619:	NM_003619:
9361	PRSS15	protease, serine, 15	0.11	TAGAAGCTATTTAATGATTAA	NM_004793:	NM_004793:
9361	PRSS15	protease, serine, 15	-1.44	CCGGGACATCATTGCCTTGAA	NM_004793:	NM_004793:
10279	PRSS16	protease, serine, 16 (thymus)	0.18	CTGTTCTTTCCTAAAGATCAA	NM_005865:	NM_005865:
10279	PRSS16	protease, serine, 16 (thymus)	-1.03	CAGAGAGTTATGGAAATATAA	NM_005865:	NM_005865:
5645	PRSS2	protease, serine, 2 (trypsin 2)	-3.32	CAGCCGGACTCTGGACAATGA	NM_002770:	NM_002770:
10942	PRSS21	protease, serine, 21 (testisin)	-2.95	CCACTTTGAGTGGATCCAGAA	NM_006799:	NM_006799:NM_144957:NM_144956:
10942	PRSS21	protease, serine, 21 (testisin)	-1.76	ACCCTTGGCCTGTAACAAGAA	NM_006799:	NM_006799:NM_144957:NM_144956:
64063	PRSS22	protease, serine, 22	1.67	CCAATTTCAATAAATTATTTA	NM_022119:	NM_022119:
64063	PRSS22	protease, serine, 22	2.11	TCCTCCAATTTCAATAAATTA	NM_022119:	NM_022119:
11098	PRSS23	protease, serine, 23	0.89	CTGCATTGTAGCAATTTGTAA	NM_007173:	NM_007173:
11098	PRSS23	protease, serine, 23	1.10	AACAGTTGTGGCCACACTAAA	NM_007173:	NM_007173:
83886	PRSS27	protease, serine 27	-2.29	AAGTGCCCTTCACCAATTACA	NM_031948:	NM_031948:
83886	PRSS27	protease, serine 27	0.14	AACCCAAAACCATCAAGAATG	NM_031948:	NM_031948:
5646	PRSS3	protease, serine, 3 (mesotrypsin)	-1.20	CAGGGACACTCTGGACAATGA	NM_002771:	NM_002771:
5646	PRSS3	protease, serine, 3 (mesotrypsin)	1.21	CTGGGAGAGCACAACATCAAA	NM_002771:	NM_002771:
260429	PRSS33	protease, serine, 33	-0.12	TACAAAGTTGTGACTTAATAA	NM_152891:	NM_152891:
260429	PRSS33	protease, serine, 33	-1.09	ACGCAGTGATGGGCAAACCAA	NM_152891:	NM_152891:
167681	PRSS35	protease, serine, 35	-3.71	CCGTAGTGAGATCACTTCATA	NM_153362:	NM_153362:
167681	PRSS35	protease, serine, 35	0.46	TACGGCTAACAGAGACCTGAA	NM_153362:	NM_153362:
146547	PRSS36	protease, serine, 36	-5.66	CCCAGCCGGCTGGAACCTCAA	NM_173502:	NM_173502:
146547	PRSS36	protease, serine, 36	-0.62	CTCGTGGGCATGGCTGTTCAA	NM_173502:	NM_173502:
5651	PRSS7	protease, serine, 7 (enterokinase)	-0.22	TAGCGCATTTCTTAAACTAAA	NM_002772:	NM_002772:
5651	PRSS7	protease, serine, 7 (enterokinase)	1.83	TACGAACTTTCCAAACAGCTA	NM_002772:	NM_002772:
5652	PRSS8	protease, serine, 8 (prostasin)	-0.15	AAGCAAGGTGACAGAACTCCA	NM_002773:	NM_002773:
5652	PRSS8	protease, serine, 8 (prostasin)	-6.30	ACCCATCACCTTCTCCCGCTA	NM_002773:	NM_002773:
56952	PRTFDC1	phosphoribosyl transferase domain containing 1	-2.13	CTCGAAACTAAGCAAGTATAA	NM_020200:	NM_020200:
56952	PRTFDC1	phosphoribosyl transferase domain containing 1	-1.37	CCGGGAATGCAGCTATTAATA	NM_020200:	NM_020200:
5657	PRTN3	proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis	2.19	TCAGGTGTTTCTGAACAACTA	NM_002777:	NM_002777:
5657	PRTN3	proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis	0.76	GAGGCGGATCTTTGGACAGAA	NM_002777:	NM_002777:
57716	PRX	periaxin	-1.28	CCCGCCGTGGAAATTGAGGAA	NM_020956:	NM_020956:NM_181882:

57716	PRX	periaxin	-1.69	AGGGATGGAATTTGGCTTCAA	NM_020956:	NM_020956:NM_181882:
5660	PSAP	prosaposin (variant Gaucher disease and variant metachromatic leukc	-4.43	CTGCCTGAATGTAACCTGCTA	NM_002778:	NM_002778:
5660	PSAP	prosaposin (variant Gaucher disease and variant metachromatic leukc	-0.05	CAAGCTGATTGACAACAACAA	NM_002778:	NM_002778:
9266	PSCD2	pleckstrin homology, Sec7 and coiled-coil domains 2 (cytohesin-2)	1.37	ACCGAACTGCTTTGAACTTTA	NM_004228:	NM_017457:NM_004228:
9266	PSCD2	pleckstrin homology, Sec7 and coiled-coil domains 2 (cytohesin-2)	-0.41	CTCACTGTTCTTTGTAATTAA	NM_004228:	NM_017457:NM_004228:
9265	PSCD3	pleckstrin homology, Sec7 and coiled-coil domains 3	0.34	AAGCCTTAAGGCAGTTCTTAT	NM_004227:	NM_004227:
9265	PSCD3	pleckstrin homology, Sec7 and coiled-coil domains 3	0.04	AAGGAGTCGCCAGATGATCAA	NM_004227:	NM_004227:
5663	PSEN1	presenilin 1 (Alzheimer disease 3)	-4.48	CAGCTCTCATTTACTCCTCAA	NM_000021:	NM_007318:NM_000021:NM_007319:
5663	PSEN1	presenilin 1 (Alzheimer disease 3)	0.05	CAGGCATATCTCATTATGATT	NM_000021:	NM_007318:NM_000021:NM_007319:
5664	PSEN2	presenilin 2 (Alzheimer disease 4)	-3.59	AAGCAAGCTATTGGAGCTGAA	NM_000447:	NM_012486:NM_000447:
5664	PSEN2	presenilin 2 (Alzheimer disease 4)	-3.98	CAGGAGAGAAATGAGCCCATA	NM_000447:	NM_012486:NM_000447:
55851	PSENEN	presenilin enhancer 2 homolog (C. elegans)	1.42	CACAGAACAGAGCCAAATCAA	NM_172341:	NM_172341:
55851	PSENEN	presenilin enhancer 2 homolog (C. elegans)	-4.74	CTCGCCCAAAGAAGACTACAA	NM_172341:	NM_172341:
5681	PSKH1 (prote	protein serine kinase H1	-5.31	CCCGATTAGGGTCGAGTGTCA	NM_006742:	NM_006742:
5681	PSKH1 (prote	protein serine kinase H1	-1.12	CCGCTCCACACGCTCCAATAA	NM_006742:	NM_006742:
85481	PSKH2 (prote	protein serine kinase H2	-0.56	AAGGACTTTATAGACAAACTA	NM_033126:	NM_033126:
85481	PSKH2 (prote	protein serine kinase H2	-0.26	GAGGATCAAGTTTACATGGTA	NM_033126:	NM_033126:
5682	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-3.38	ATGGAGTGTAATTTAAATGAA	NM_002786:	NM_148976:NM_002786:
5682	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-8.30	CACAGTTGGTCTGAAATCAAA	NM_002786:	NM_148976:NM_002786:
5683	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	2.14	GAGATACATTATGTAAATAAA	NM_002787:	NM_002787:
5683	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	-4.58	AAGGATTACTTGGCTGCCATA	NM_002787:	NM_002787:
5684	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	-10.36	CCAGTCCAATGTAACTATTTA	NM_002788:	NM_152132:NM_002788:
5684	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	-2.72	TCAGATGATGATAATATGTAA	NM_002788:	NM_152132:NM_002788:
5685	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	-6.00	AACGATGATGGTTACCCTTCA	NM_002789:	NM_002789:
5685	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	-5.51	ACAGCGCTGTGTGATATCAAA	NM_002789:	NM_002789:
5686	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	-0.81	AAGAAGTTTACCACAAGTCTA	NM_002790:	NM_002790:
5686	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	0.19	ATGCTAAGACTTTAATTGATA	NM_002790:	NM_002790:
5687	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	-1.74	CCAGGGATTGTGTTTAAAGTA	NM_002791:	NM_002791:
5687	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	-10.09	ACCGAAGTGGTTAGGACTCTA	NM_002791:	NM_002791:
5688	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	-2.45	CACACTGAGTGTCCTACAATA	NM_002792:	NM_152255:NM_002792:
5688	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	-0.54	ATGGATGAGTCTCGATGTGTA	NM_002792:	NM_152255:NM_002792:
143471	PSMA8	proteasome (prosome, macropain) subunit, alpha type, 8	0.31	ACGGAAAGGATTTAATCCAAA	NM_144662:	NM_001025096:NM_001025097:NM_144662:
143471	PSMA8	proteasome (prosome, macropain) subunit, alpha type, 8	-2.48	AGCTATCAAGTTAGCAATAAA	NM_144662:	NM_001025096:NM_001025097:NM_144662:
5699	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	-2.24	CTGCGAGAAGATCCACTTCAT	NM_002801:	NM_002801:
5699	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	-2.31	CACACGGATGGTGGCGTCCAA	NM_002801:	NM_002801:
5690	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	1.39	GTGACTATGGATATAATTGAA	NM_002794:	NM_002794:
5690	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	-0.45	CAGCAATATTGTCCAGATGAA	NM_002794:	NM_002794:
5691	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	-2.49	AACGGTTTGGCCCTTACTACA	NM_002795:	NM_002795:
5691	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	0.00	AAGGAAGGTCGGCAGATCAAA	NM_002795:	NM_002795:
5692	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	-3.42	CACATGATCAGTGGCTTTGAA	NM_002796:	NM_002796:
5692	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	0.56	ACCATTGTCTACAGAGACCAA	NM_002796:	NM_002796:
5694	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	-4.88	CTCCGGGAGCTCCTACATCTA	NM_002798:	NM_002798:
5694	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	0.05	CTGGGATTCTAGTATGCAATA	NM_002798:	NM_002798:
5695	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	-3.46	CCGCCCATACACAGTGCCCAA	NM_002799:	NM_002799:
5695	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	0.03	CTGCGTCATCAGCAAGAACAA	NM_002799:	NM_002799:
5696	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifu	1.72	CAGGGACCTAAGCCACGTTAA	NM_004159:	NM_004159:NM_148919:
5696	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifu	-1.16	CGGCCTAATCTTAGCCCTGAA	NM_004159:	NM_004159:NM_148919:
5698	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifu	1.38	CAGCACCTTTATCTATGGTTA	NM_002800:	NM_002800:NM_148954:
5698	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifu	-1.71	AAGGAGGTCAGGTATATGGAA	NM_002800:	NM_002800:NM_148954:
5702	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	-10.09	ACGGCTGAAGTGCGCAATAAA	NM_002804:	NM_002804:
5702	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	-1.57	TAAGGTAATTGCAGCCACAAA	NM_002804:	NM_002804:
29893	PSMC3IP	PSMC3 interacting protein	0.26	CAGAAAGAAATCCAGGAGTTA	NM_013290:	NM_016556:NM_013290:
29893	PSMC3IP	PSMC3 interacting protein	-0.24	CAGGATGTGTTCGGGAACCTA	NM_013290:	NM_016556:NM_013290:
5704	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	-7.11	CAGAATGTCAATGTCAAGGTA	NM_006503:	NM_006503:NM_153001:
5704	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	-6.07	CAGGATTGGTTTCTTCAATAA	NM_006503:	NM_006503:NM_153001:
5705	PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	-6.14	TTGGTCAAGGTACATCCTGAA	NM_002805:	NM_002805:
5705	PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	-7.63	AAGGTACATCCTGAAGGTAAA	NM_002805:	NM_002805:
10213	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-0.61	TTGGATACTGTCGTATTTAAA	NM_005805:	NM_005805:
10213	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-4.16	ACAGACATTATTACTCCATTA	NM_005805:	NM_005805:
5708	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	-5.10	TGGGTGTGTTCCGAAAGTTTA	NM_002808:	NM_002808:
5708	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	-0.17	CTCCGGAGGGCTGTACCTTTA	NM_002808:	NM_002808:
5713	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov3	0.95	TACCTTCAAAGATACAATTAA	NM_002811:	NM_002811:
5713	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov3	-3.28	TTCCGTATTGGTCATCATTGA	NM_002811:	NM_002811:
5723	PSPH	phosphoserine phosphatase	-1.67	CCGGCATAAGGGAGCTGGTAA	NM_004577:	NM_004577:
5723	PSPH	phosphoserine phosphatase	1.32	TGCCAATAGGCTGAAATTCTA	NM_004577:	NM_004577:
9051	PSTPIP1	proline-serine-threonine phosphatase interacting protein 1	0.09	ACCGGGCGCTCTACGATTATA	NM_003978:	NM_003978:
9051	PSTPIP1	proline-serine-threonine phosphatase interacting protein 1	0.36	CCGGCTGACCATTCTCCGCAA	NM_003978:	NM_003978:
9050	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	0.00	CCACGTTATGTCAGCAATGAA	NM_024430:	NM_024430:
9050	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	-1.56	CCGGCTAGTGCTTCTGTGATA	NM_024430:	NM_024430:
5724	PTAFR	platelet-activating factor receptor	-2.37	ACCACGGATACGGTCACTGAA	NM_000952:	NM_000952:
5724	PTAFR	platelet-activating factor receptor	0.73	CACGGTCTTGGCGGTGTTCAT	NM_000952:	NM_000952:
375743	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-2.44	CTGAATGACTCTAGCAAGCAA	XM_372117:	XM_372117:
375743	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	1.21	CACAGGTTCATTGATCAAGTA	XM_372117:	XM_372117:
5725	PTBP1	polypyrimidine tract binding protein 1	0.14	CACGCACATTCCGTTGCCTTA	NM_175847:	NM_175847:NM_031990:NM_002819:NM_031991:
5725	PTBP1	polypyrimidine tract binding protein 1	0.36	ATGGTATGAGTGTAATCTAAA	NM_175847:	NM_175847:NM_031990:NM_002819:NM_031991:
5727	PTCH	patched homolog (Drosophila)	1.33	ACAGCATACCTCCTAGGTAAA	NM_000264:	NM_000264:
5727	PTCH	patched homolog (Drosophila)	-1.48	TCGCACAGAACTCCACTCAAA	NM_000264:	NM_000264:
8643	PTCH2 (patcł	patched homolog 2 (Drosophila)	-3.41	CTGGCGATGATGACAGTGGAA	NM_003738:	NM_003738:
8643	PTCH2 (patcł	patched homolog 2 (Drosophila)	-0.62	CCGCACCTGGCTGCACTATTA	NM_003738:	NM_003738:
139411	PTCHD1	patched domain containing 1	0.85	TCCCGGTTTGAGAGCTATTTA	NM_173495:	NM_173495:
139411	PTCHD1	patched domain containing 1	-1.04	AAGGATTTCACAAGAACTAAA	NM_173495:	NM_173495:
23210	PTDSR	phosphatidylserine receptor	-1.11	AAGGAAATATCGGAACCAGAA	NM_015167:	NM_015167:
23210	PTDSR	phosphatidylserine receptor	0.00	CTGCTTCCTAAGGATAGATTA	NM_015167:	NM_015167:
5728	PTEN	phosphatase and tensin homolog (mutated in multiple advanced canc	1.20	AAGATTTATGATGCACTTATT	NM_000314:	NM_000314:
5728	PTEN	phosphatase and tensin homolog (mutated in multiple advanced canc	3.03	CAATTTGAGATTCTACAGTAA	NM_000314:	NM_000314:
5729	PTGDR	prostaglandin D2 receptor (DP)	-13.62	CCAGTATCTGAGATAATATAA	NM_000953:	NM_000953:
5729	PTGDR	prostaglandin D2 receptor (DP)	0.48	CCGGTGCAGCAATTCCACTAA	NM_000953:	NM_000953:
5731	PTGER1	prostaglandin E receptor 1 (subtype EP1), 42kDa	0.15	AACCAGAGGCCCAACGACTAA	NM_000955:	NM_000955:
5731	PTGER1	prostaglandin E receptor 1 (subtype EP1), 42kDa	1.18	CTCAGCCACTTCTAAGCACAA	NM_000955:	NM_000955:
5732	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	-2.49	TACTACCGTTATACACATATA	NM_000956:	NM_000956:
5732	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	0.52	TCGGATTTCATTAAGAACACA	NM_000956:	NM_000956:
5733	PTGER3	prostaglandin E receptor 3 (subtype EP3)	1.00	AAGCATAATTTGTTTGTACAA	NM_000957:	NM_198713:NM_198712:NM_000957:NM_198714: NM_198717:NM_198716:
5733	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-0.06	AAGGACCGATTTGAGCACTAA	NM_000957:	NM_198715:
5733	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-1.13	AAGCATAATTTGTTTGTACAA	NM_000957:	NM_198713:NM_198712:NM_000957:NM_198714: NM_198717:NM_198716:

5733	PTGER3	prostaglandin E receptor 3 (subtype EP3)	0.51	CCGCTATAGAGTATTCCATAA	NM_000957:	NM_198713:NM_198712:NM_000957:NM_198714:NM_198717:NM_198716:
5734	PTGER4	prostaglandin E receptor 4 (subtype EP4)	-0.36	ACCCATAATTGAAGTGTATAA	NM_000958:	NM_000958:
5734	PTGER4	prostaglandin E receptor 4 (subtype EP4)	0.08	AGGCTCTATTCCAATAAACTA	NM_000958:	NM_000958:
9536	PTGES	prostaglandin E synthase	1.09	TTGGGTGACCAGCCACTCAAA	NM_004878:	NM_004878:NM_198797:
9536	PTGES	prostaglandin E synthase	0.15	CGGGCTAAGAATGCAGACTTT	NM_004878:	NM_004878:NM_198797:
10728	PTGES3	prostaglandin E synthase 3 (cytosolic)	-3.08	CAGCTTAGGGAAAGAGAATAA	NM_006601:	NM_006601:
10728	PTGES3	prostaglandin E synthase 3 (cytosolic)	-0.03	CAGATATGCTGTATTTGCCTA	NM_006601:	NM_006601:
5737	PTGFR	prostaglandin F receptor (FP)	-1.37	AACCCAAGAAGTAGACATCAA	NM_000959:	NM_000959:
5737	PTGFR	prostaglandin F receptor (FP)	-0.18	ATGGGAGGTAGACACAATAAA	NM_000959:	NM_000959:
5739	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	-3.14	CCCAGGGTCCTGAATAAATAA	NM_000960:	NM_000960:
5739	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	0.06	CCCATCCATCTCATTGTCTAA	NM_000960:	NM_000960:
5740	PTGIS	prostaglandin I2 (prostacyclin) synthase	1.16	CTGTTTATTGAGACCCTTTAA	NM_000961:	NM_000961:
5740	PTGIS	prostaglandin I2 (prostacyclin) synthase	0.04	GCGGTCAACAGCATCAAACAA	NM_000961:	NM_000961:
5742	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a	0.86	AACGATGAAATAAGATATATA	M59979:	NM_080591:NM_000962:
5742	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a	-1.27	CACGCCATTGGTTGGAAGCTA	M59979:	NM_080591:NM_000962:
5743	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase a	-1.35	ACGCTTTATGCTGAAGCCCTA	NM_000963:	NM_000963:
5743	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase a	-1.77	CCCGCAGTACAGAAAGTATCA	NM_000963:	NM_000963:
5741	PTH (parathy	parathyroid hormone	1.44	ATGAAGTATTTCTCACTCAAA	NM_000315:	NM_000315:
5741	PTH (parathy	parathyroid hormone	1.28	AATGTATTAACTAAAGCTAAA	NM_000315:	NM_000315:
5744	PTHLH	parathyroid hormone-like hormone	0.52	CTCCTAGACTTTGGGATCAAA	NM_002820:	NM_002820:NM_198964:
5744	PTHLH	parathyroid hormone-like hormone	1.31	CTAGGGTAATGCCGTAGGAAA	NM_002820:	NM_002820:NM_198964:
5745	PTHR1	parathyroid hormone receptor 1	-10.36	CAGCATAATGGAATCAGACAA	NM_000316:	NM_000316:
5745	PTHR1	parathyroid hormone receptor 1	-0.67	CGCCGTGAGCATCTTCGTCAA	NM_000316:	NM_000316:
5746	PTHR2 (parat	parathyroid hormone receptor 2	0.57	AAGGTGTTACTTAATAATAGT	NM_005048:	NM_005048:
5746	PTHR2 (parat	parathyroid hormone receptor 2	1.34	TGGCATGTGGGATCAATTAAA	NM_005048:	NM_005048:
5747	PTK2	PTK2 protein tyrosine kinase 2	-0.45	AACAATTTATGTTCACATTAA	NM_005607:	NM_153831:NM_005607:
5747	PTK2	PTK2 protein tyrosine kinase 2	-0.96	CACCTGGGTACTGGTATGGAA	NM_005607:	NM_153831:NM_005607:
2185	PTK2B	PTK2B protein tyrosine kinase 2 beta	-1.66	AAGCTGATCGGCATCATTGAA	NM_173176:	NM_173174:NM_173176:NM_173175:NM_004103:
2185	PTK2B	PTK2B protein tyrosine kinase 2 beta	0.54	CAGGAGAACTTAAAGCCCAAA	NM_173176:	NM_173174:NM_173176:NM_173175:NM_004103:
5753	PTK6	PTK6 protein tyrosine kinase 6	0.28	CCGGGTCCAGGTGGCCATTAA	NM_005975:	NM_005975:
5753	PTK6	PTK6 protein tyrosine kinase 6	0.04	CGGGTTAGCCAGGCTTATCAA	NM_005975:	NM_005975:
5754	PTK7	PTK7 protein tyrosine kinase 7	-0.03	ACGGTTCGAGGTCTTCAAGAA	NM_152883:	NM_152882:NM_152883:NM_152880:NM_002821:
5754	PTK7	PTK7 protein tyrosine kinase 7	0.03	ATGGGACATGGTACCGTTGTA	NM_152883:	NM_152882:NM_152883:NM_152880:NM_002821:
5756	PTK9	PTK9 protein tyrosine kinase 9	0.03	ACCGGCATCCAAGCAAGTGAA	NM_002822:	NM_002822:
5756	PTK9	PTK9 protein tyrosine kinase 9	1.14	TCCAAGCAAGTGAAGATGTTA	NM_002822:	NM_002822:
11344	PTK9L	PTK9L protein tyrosine kinase 9-like (A6-related protein)	-1.58	AAGACAGAGATCAGTGTGGAA	NM_007284:	NM_007284:
11344	PTK9L	PTK9L protein tyrosine kinase 9-like (A6-related protein)	-1.70	TTGGGATGGTTGAATGCTGTA	NM_007284:	NM_007284:
5757	PTMA	prothymosin, alpha (gene sequence 28)	-0.43	TTGATGTATGTGTGAAACAAT	NM_002823:	NM_002823:
5764	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promotin	1.01	TACATGATAAATGATAGACAA	NM_002825:	NM_002825:
5764	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promotin	1.07	TACCGTAGGCTTTGTATTCAA	NM_002825:	NM_002825:
53635	PTOV1	prostate tumor overexpressed gene 1	-6.59	CTGGAGCAGGAGCAACAGCAA	NM_017432:	NM_017432:
53635	PTOV1	prostate tumor overexpressed gene 1	-7.57	CCGGCGTGTCATTGCCAACCA	NM_017432:	NM_017432:
7803	PTP4A1	protein tyrosine phosphatase type IVA, member 1	1.05	ACGCCTTAACACAGCTCTATA	NM_003463:	NM_003463:
7803	PTP4A1	protein tyrosine phosphatase type IVA, member 1	0.56	CCCTTTGATCACGTTAATCTA	NM_003463:	NM_003463:
8073	PTP4A2	protein tyrosine phosphatase type IVA, member 2	-0.80	AACAGCATACCTGCTAAGCTA	NM_003479:	NM_003479:
8073	PTP4A2	protein tyrosine phosphatase type IVA, member 2	-0.78	CAGAGAATGCTGGTAGCTTAA	NM_003479:	NM_003479:
11156	PTP4A3	protein tyrosine phosphatase type IVA, member 3	0.93	CACCCAAGTATTTGCACAATA	NM_007079:	NM_032611:NM_007079:
11156	PTP4A3	protein tyrosine phosphatase type IVA, member 3	0.02	CCGCGGAGCCATCAACAGCAA	NM_007079:	NM_032611:NM_007079:
138639	PTPDC1	protein tyrosine phosphatase domain containing 1	0.91	CGGAATGTTGAGTGCCTTCAA	NM_152422:	NM_152422:NM_177995:
138639	PTPDC1	protein tyrosine phosphatase domain containing 1	-0.01	TACGTAGATACCAGAGGCCAA	NM_152422:	NM_152422:NM_177995:
9200	PTPLA (prote	protein tyrosine phosphatase-like (proline instead of catalytic arginine)	1.52	ACCACTTGCCATACTTCATTA	NM_014241:	NM_014241:
9200	PTPLA (prote	protein tyrosine phosphatase-like (proline instead of catalytic arginine)	0.87	CACTGTTTAATTGGAATTGTA	NM_014241:	NM_014241:
201562	PTPLB (prote	protein tyrosine phosphatase-like (proline instead of catalytic arginine)	-1.80	CACGGCGTACCTGGTCATCTA	NM_198402:	NM_198402:
201562	PTPLB (prote	protein tyrosine phosphatase-like (proline instead of catalytic arginine)	-2.69	CAGCCAAGAAATAGTTTGGTA	NM_198402:	NM_198402:
5770	PTPN1	protein tyrosine phosphatase, non-receptor type 1	1.47	CACGTGGGTATTTAATAAGAA	NM_002827:	NM_002827:
5770	PTPN1	protein tyrosine phosphatase, non-receptor type 1	-4.51	CAGGCATGCCGCGGTAGGTAA	NM_002827:	NM_002827:
5781	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrom	-0.51	CAGAAGCACAGTACCGATTTA	NM_002834:	NM_002834:
5781	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrom	-1.45	CCGCTCATGACTATACGCTAA	NM_002834:	NM_002834:
5782	PTPN12	protein tyrosine phosphatase, non-receptor type 12	-0.07	AAGCTTAATGAGGAAATATCA	NM_002835:	NM_002835:
5782	PTPN12	protein tyrosine phosphatase, non-receptor type 12	-5.91	TTGCAGGTTATCAGAGATCAA	NM_002835:	NM_002835:
5783	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fa	0.55	CGGTCTATTCTTACTAAGAAA	NM_006264:	NM_080685:NM_080684:NM_080683:NM_006264:
5783	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fa	-0.02	TCCAGGTACATTAAAGATGAA	NM_006264:	NM_080685:NM_080684:NM_080683:NM_006264:
5784	PTPN14	protein tyrosine phosphatase, non-receptor type 14	-0.78	AAGGGCGATTACGATGTACAT	NM_005401:	NM_005401:
5784	PTPN14	protein tyrosine phosphatase, non-receptor type 14	0.18	CGGTGTGGCATTTACAATATA	NM_005401:	NM_005401:
26469	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	0.02	CAGGCAGACATCAGTCCACAT	NM_014369:	NM_014369:
26469	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	0.23	CCCAATGACTGTAGCATTCAA	NM_014369:	NM_014369:
5771	PTPN2	protein tyrosine phosphatase, non-receptor type 2	0.36	AACTGTATTCATACATGTCAA	NM_002828:	NM_002828:
5771	PTPN2	protein tyrosine phosphatase, non-receptor type 2	-0.78	CCGCTGTACTTGGAAATTCGA	NM_002828:	NM_002828:NM_080422:NM_080423:
11099	PTPN21	protein tyrosine phosphatase, non-receptor type 21	0.06	GAGGAGACCATTCAATTTCAA	NM_007039:	NM_007039:
11099	PTPN21	protein tyrosine phosphatase, non-receptor type 21	-1.14	GTGCATAGATTTCTATCTTAA	NM_007039:	NM_007039:
26191	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0.27	CCGGGTAGAACTATCCCTGAT	NM_012411:	NM_012411:NM_015967:
26191	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	-2.40	TGGGATGTACGTTGTTACCAA	NM_012411:	NM_012411:NM_015967:
25930	PTPN23	protein tyrosine phosphatase, non-receptor type 23	0.51	AACCTTGTACAGTCCATGCAA	NM_015466:	NM_015466:
25930	PTPN23	protein tyrosine phosphatase, non-receptor type 23	-0.04	CCGCCAGATCCTTACGCTCAA	NM_015466:	NM_015466:
5774	PTPN3	protein tyrosine phosphatase, non-receptor type 3	1.84	CAGGTTATTCAGCGATAGTTA	NM_002829:	NM_002829:
5774	PTPN3	protein tyrosine phosphatase, non-receptor type 3	-0.23	CCGGGTATTATTGCAGGGAAA	NM_002829:	NM_002829:
5775	PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	1.89	CTCCGAACAAATAGTAAATAA	NM_002830:	NM_002830:
5775	PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	1.99	TCCGTCATCAACACAAGCTAA	NM_002830:	NM_002830:
84867	PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	0.12	ATCGAGGAGATGAACGAGAAA	NM_032781:	NM_032781:
84867	PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	-5.84	CACCAACATCGAGGAGATGAA	NM_032781:	NM_032781:
5777	PTPN6	protein tyrosine phosphatase, non-receptor type 6	-2.36	CCGGAACAAATGCGTCCCATA	NM_002831:	NM_080549:NM_002831:NM_080548:
5777	PTPN6	protein tyrosine phosphatase, non-receptor type 6	-1.75	TAGGCCCTGATGAGAACGCTA	NM_002831:	NM_080549:NM_002831:NM_080548:
5778	PTPN7	protein tyrosine phosphatase, non-receptor type 7	-5.50	CAGGTCTACCTCAGGACTGAA	NM_002832:	NM_080588:NM_080589:NM_002832:
5778	PTPN7	protein tyrosine phosphatase, non-receptor type 7	-7.55	CTGGCATTTATGACAGACAAA	NM_002832:	NM_080588:NM_080589:NM_002832:
5780	PTPN9	protein tyrosine phosphatase, non-receptor type 9	1.74	ACCAAACTAGAGTGAAGCTAA	NM_002833:	NM_002833:
5780	PTPN9	protein tyrosine phosphatase, non-receptor type 9	-0.08	AGGAACGGAGCGAATAATATA	NM_002833:	NM_002833:
140885	PTPNS1	protein tyrosine phosphatase, non-receptor type substrate 1	-1.59	CGCCTGTAAATTACTGAGAAA	NM_080792:	NM_080792:
140885	PTPNS1	protein tyrosine phosphatase, non-receptor type substrate 1	-1.27	CTCGCTGTGGACGCCTGTAAA	NM_080792:	NM_080792:
5786	PTPRA	protein tyrosine phosphatase, receptor type, A	0.75	CAGAGTGATCATTCCAGTTAA	NM_002836:	NM_080841:NM_002836:NM_080840:
5786	PTPRA	protein tyrosine phosphatase, receptor type, A	-4.58	CCGGAGAATGGCAGACGACAA	NM_002836:	NM_080841:NM_002836:NM_080840:
5787	PTPRB	protein tyrosine phosphatase, receptor type, B	-0.48	CCCGGAGATGTGGATAACTAT	NM_002837:	NM_002837:
5787	PTPRB	protein tyrosine phosphatase, receptor type, B	-0.23	CCGGTCGACTTTATCAAGTTA	NM_002837:	NM_002837:

5788	PTPRC	protein tyrosine phosphatase, receptor type, C	0.45	AACCGTTATGTTGACATTCTT	NM_002838:	NM_002838:NM_080921:NM_080922:
5788	PTPRC	protein tyrosine phosphatase, receptor type, C	-0.31	AAGAATTGCGATTTCCGTGTA	NM_002838:	NM_002838:NM_080921:NM_080922:
5789	PTPRD	protein tyrosine phosphatase, receptor type, D	-1.91	ACGGCCAGTCCCGAACAGTAA	NM_002839:	NM_130391:NM_130392:NM_002839:NM_130393:
5789	PTPRD	protein tyrosine phosphatase, receptor type, D	-0.14	CTGGGTGTCATTGAAGCAATA	NM_002839:	NM_130391:NM_130392:NM_002839:NM_130393:
5791	PTPRE	protein tyrosine phosphatase, receptor type, E	1.31	ACCACGGGCAATTAAACTTTA	NM_006504:	NM_130435:NM_006504:
5791	PTPRE	protein tyrosine phosphatase, receptor type, E	0.72	CCGAGTGATCCTTTCCATGAA	NM_006504:	NM_130435:NM_006504:
5792	PTPRF	protein tyrosine phosphatase, receptor type, F	0.67	CAGCGCTATCTAGATAGGTAA	NM_002840:	NM_130440:NM_002840:
5792	PTPRF	protein tyrosine phosphatase, receptor type, F	-2.91	CATCGTGTTTGCAAAGGTTAA	NM_002840:	NM_130440:NM_002840:
5793	PTPRG	protein tyrosine phosphatase, receptor type, G	-1.69	AGGGTGAAGTTAAGACCTTTA	NM_002841:	NM_002841:
5793	PTPRG	protein tyrosine phosphatase, receptor type, G	0.14	TCGGTGAGCTCTATTCTAATA	NM_002841:	NM_002841:
5794	PTPRH	protein tyrosine phosphatase, receptor type, H	-2.80	CCGGGACGTTGTACAATTTCA	NM_002842:	NM_002842:
5794	PTPRH	protein tyrosine phosphatase, receptor type, H	0.30	CCGGGTCATTGTATACGTGTT	NM_002842:	NM_002842:
5795	PTPRJ	protein tyrosine phosphatase, receptor type, J	0.09	TCCGAGTATGTCTACCATTTA	NM_002843:	NM_002843:
5795	PTPRJ	protein tyrosine phosphatase, receptor type, J	-1.20	TCGGGTAGAAATAACCACCAA	NM_002843:	NM_002843:
5796	PTPRK	protein tyrosine phosphatase, receptor type, K	-0.09	CCGGGTTAAATGCTATAAATA	NM_002844:	NM_002844:
5796	PTPRK	protein tyrosine phosphatase, receptor type, K	-2.12	CTGGAGATTAGTGTATGATTA	NM_002844:	NM_002844:
5797	PTPRM	protein tyrosine phosphatase, receptor type, M	-1.07	AAGGGTCAAATGCTGCAAATA	NM_002845:	NM_002845:
5797	PTPRM	protein tyrosine phosphatase, receptor type, M	0.10	CACATCCGTAGTTATGCTAAA	NM_002845:	NM_002845:
5798	PTPRN	protein tyrosine phosphatase, receptor type, N	-0.21	CACCCTTCACTGAGTTACGAA	NM_002846:	NM_002846:
5798	PTPRN	protein tyrosine phosphatase, receptor type, N	1.11	CAGGTCTGGCTTGGCACCCAA	NM_002846:	NM_002846:
5799	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	-2.80	AAGGTGCTAAAGAGATTGATA	NM_002847:	NM_002847:NM_130843:NM_130842:
5799	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	0.76	CAGCGCAGTTTAGCAGTTAAA	NM_002847:	NM_002847:NM_130843:NM_130842:
5801	PTPRR	protein tyrosine phosphatase, receptor type, R	-2.06	CGCCACCAGATTGTCAATTCA	NM_002849:	NM_002849:
5801	PTPRR	protein tyrosine phosphatase, receptor type, R	0.37	TCGCCTCATTGGAAAGAAGAA	NM_002849:	NM_002849:
5802	PTPRS	protein tyrosine phosphatase, receptor type, S	-3.43	CACGGCATCAGGCGTGCACAA	NM_002850:	NM_130854:NM_002850:
5802	PTPRS	protein tyrosine phosphatase, receptor type, S	-1.62	CGCGTCTACTACACCATGGAA	NM_002850:	NM_130853:NM_130855:NM_130854:NM_002850:
148713	PTPRV	protein tyrosine phosphatase, receptor type, V (pseudogene)	-2.27	AACGCTGAAGCAGTATATCTA	XM_086287:	XM_086287:
148713	PTPRV	protein tyrosine phosphatase, receptor type, V (pseudogene)	-2.06	AAGGTGGGCAGTCATGTCCAA	XM_086287:	XM_086287:
5803	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	-0.91	ACGCTGGAATTTGGTAGTGAA	NM_002851:	NM_002851:
5803	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	-0.10	TAGCCATATACCAATACCTAA	NM_002851:	NM_002851:
5805	PTS	6-pyruvoyltetrahydropterin synthase	-0.24	TAGGTGAATCTTAAAGAAATA	NM_000317:	NM_000317:
5805	PTS	6-pyruvoyltetrahydropterin synthase	1.07	TTCGAGTAGGTGAATCTTAAA	NM_000317:	NM_000317:
9232	PTTG1	pituitary tumor-transforming 1	-3.35	AAGACCTGCAATAATCCAGAA	NM_004219:	NM_004219:
9232	PTTG1	pituitary tumor-transforming 1	0.21	CAGAATGGCTACTCTGATCTA	NM_004219:	NM_004219:
754	PTTG1IP	pituitary tumor-transforming 1 interacting protein	-0.04	AACCCGTATGCTAGATTTGAA	NM_004339:	NM_004339:
754	PTTG1IP	pituitary tumor-transforming 1 interacting protein	-0.59	CACAGTCTGATAAGGACTTAA	NM_004339:	NM_004339:
10744	PTTG2 (pituit	pituitary tumor-transforming 2	-0.64	AAGCTGGAGTCTAGACCTTCA	NM_006607:	NM_006607:
10744	PTTG2 (pituit	pituitary tumor-transforming 2	0.64	TACGTTGATAAGGAAATTGGA	NM_006607:	NM_006607:
5817	PVR	poliovirus receptor	-1.40	ACGGCTGACCTCATACATCAA	NM_006505:	NM_006505:
5817	PVR	poliovirus receptor	-0.24	CAACACAACTTTAATCTGCAA	NM_006505:	NM_006505:
5818	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)	0.32	ACAGATCAGTCTGTCAATAAA	NM_203286:	NM_203286:
5818	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)	-0.07	AGGGCTGTTGTCAGAATTCTA	NM_203286:	NM_203286:
5819	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	-3.18	CAGGTCATCTTTGTCCGAGAA	NM_002856:	NM_002856:
5819	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	-0.19	CTGGACGACACTGGAGTGGAA	NM_002856:	NM_002856:
25945	PVRL3	poliovirus receptor-related 3	-0.74	AAGGTGTTAATCTCAAATGTA	NM_015480:	NM_015480:
25945	PVRL3	poliovirus receptor-related 3	-0.97	CACATGTAGATGGTTCCGTAA	NM_015480:	NM_015480:
81607	PVRL4	poliovirus receptor-related 4	-3.72	CAGAGCAGTATTAATGATGCA	NM_030916:	NM_030916:
81607	PVRL4	poliovirus receptor-related 4	-0.29	CCCTGATAGTCTCAAGGACAA	NM_030916:	NM_030916:
7837	PXDN	peroxidasin homolog (Drosophila)	-0.12	CAGGAGTGGAATGTACATATT	XM_056455:	XM_056455:
7837	PXDN	peroxidasin homolog (Drosophila)	1.61	AACAACCGGATTACACATTTA	XM_056455:	XM_056455:
137902	PXDNL	peroxidasin homolog-like (Drosophila)	1.58	AAGAATATCATGGAATATTTA	NM_144651:	NM_144651:
137902	PXDNL	peroxidasin homolog-like (Drosophila)	-0.41	CAAGACTGCTGTGCAGATAAA	NM_144651:	NM_144651:
54899	PXK	PX domain containing serine/threonine kinase	-0.56	CTGGCAGATTGTTAGAAGATA	NM_017771:	NM_017771:
54899	PXK	PX domain containing serine/threonine kinase	2.28	TAAGATCCCTACAAAGTTAAA	NM_017771:	NM_017771:
5828	PXMP3	peroxisomal membrane protein 3, 35kDa (Zellweger syndrome)	0.02	ACCATTTATGTATCCTTTATA	NM_000318:	NM_000318:
5828	PXMP3	peroxisomal membrane protein 3, 35kDa (Zellweger syndrome)	0.66	CCTAATAGTGACAATACATTA	NM_000318:	NM_000318:
5829	PXN	paxillin	0.22	CCGACTGAAACTGGAACCCTT	NM_002859:	NM_002859:
5829	PXN	paxillin	0.36	TCCGACTTTGATAGATTTCTA	NM_002859:	NM_002859:
29108	PYCARD	PYD and CARD domain containing	-0.72	CAGCTTCTACCTGGAGACCTA	NM_013258:	NM_013258:NM_145182:
29108	PYCARD	PYD and CARD domain containing	1.61	CGCGAGGGTCACAAACGTTGA	NM_013258:	NM_145183:NM_013258:NM_145182:
5834	PYGB	phosphorylase, glycogen; brain	0.98	TCCTAGTTTCTTGTAAAGGAA	NM_002862:	NM_002862:
5834	PYGB	phosphorylase, glycogen; brain	-2.21	CAGGTTGAAAGTGATCTTCCT	NM_002862:	NM_002862:
5836	PYGL (phosp	phosphorylase, glycogen; liver (Hers disease, glycogen storage diseas	-0.05	AACGTGGAACCTTCAGATCTA	NM_002863:	NM_002863:
5836	PYGL (phosp	phosphorylase, glycogen; liver (Hers disease, glycogen storage diseas	-0.56	CTCCAGTGACCGAACAATTAA	NM_002863:	NM_002863:
5837	PYGM (phosp	phosphorylase, glycogen; muscle (McArdle syndrome, glycogen stora	-2.12	CAAGTTGAAGTTTGCTGCCTA	NM_005609:	NM_005609:
5837	PYGM (phosp	phosphorylase, glycogen; muscle (McArdle syndrome, glycogen stora	-0.08	TCGGGATGTGGCCAAAGTGAA	NM_005609:	NM_005609:
26108	PYGO1	pygopus homolog 1 (Drosophila)	0.18	ACGCAGAATAAGCCACGACAA	NM_015617:	NM_015617:
26108	PYGO1	pygopus homolog 1 (Drosophila)	0.31	TCGAAACAATGCAGTAAATCA	NM_015617:	NM_015617:
90780	PYGO2	pygopus homolog 2 (Drosophila)	-0.25	CAGCCCATCTGTTGCACATTA	NM_138300:	NM_138300:
90780	PYGO2	pygopus homolog 2 (Drosophila)	0.13	ACGTATCTTCTTCATACCAAA	NM_138300:	NM_138300:
5858	PZP	pregnancy-zone protein	0.05	CAGACTTGCGATGGACACAAA	NM_002864:	NM_002864:
5858	PZP	pregnancy-zone protein	0.35	TACCAGTATCTCGGTTAATAA	NM_002864:	NM_002864:
5859	QARS	glutaminyl-tRNA synthetase	-0.06	CACGTGGTGGATGCAGCATTA	NM_005051:	NM_005051:
5859	QARS	glutaminyl-tRNA synthetase	-3.74	CACCATGAATCTACTAAAGCA	NM_005051:	NM_005051:
5860	QDPR	quinoid dihydropteridine reductase	-0.37	CAGTCAGAGATGAGTATACTA	NM_000320:	NM_000320:
5860	QDPR	quinoid dihydropteridine reductase	0.15	ACCCTTAGAATTCCTAGTTGA	NM_000320:	NM_000320:
54870	QRICH1	glutamine-rich 1	0.06	CCGGAATATTAGAAGTCTTAA	NM_017730:	NM_017730:
54870	QRICH1	glutamine-rich 1	0.56	ACGGCTCAAACTGTCCATATA	NM_017730:	NM_017730:NM_198880:
5768	QSCN6	quiescin Q6	-3.00	CTGCTTGGTCTTGGCCCTCAA	NM_002826:	NM_002826:NM_001004128:
5768	QSCN6	quiescin Q6	-0.47	CAGGTCCTTCTATACCGCTTA	NM_002826:	NM_002826:NM_001004128:
10890	RAB10 (RAB	RAB10, member RAS oncogene family	0.46	CAAATTCGGTTTCATATTCTA	NM_016131:	NM_016131:
10890	RAB10 (RAB	RAB10, member RAS oncogene family	0.74	CTGATGTAACTTGCTAGGTAA	NM_016131:	NM_016131:
8766	RAB11A	RAB11A, member RAS oncogene family	-3.93	AAGAGCGATATCGAGCTATAA	NM_004663:	NM_004663:
8766	RAB11A	RAB11A, member RAS oncogene family	-2.88	TAGGCATTGTAGAGATCTGAA	NM_004663:	NM_004663:
9230	RAB11B	RAB11B, member RAS oncogene family	1.65	CCGCATCACCTCCGCGTACTA	NM_004218:	NM_004218:
9230	RAB11B	RAB11B, member RAS oncogene family	-2.25	CCGCATCGTGTCACAGAAACA	NM_004218:	NM_004218:
80223	RAB11FIP1	RAB11 family interacting protein 1 (class I)	-0.91	CACAGAGTTCGGAATTCACAA	NM_001002233:	NM_001002233:NM_001002814:
80223	RAB11FIP1	RAB11 family interacting protein 1 (class I)	0.41	CAGGTTAATGATTACAATTAA	NM_001002233:	NM_001002233:NM_025151:NM_001002814:
5872	RAB13	RAB13, member RAS oncogene family	0.89	ATGGTCTTTCTTGGTATTAAA	NM_002870:	NM_002870:
5872	RAB13	RAB13, member RAS oncogene family	0.24	CAGGGCAAACATAAATGTAAA	NM_002870:	NM_002870:
51552	RAB14	RAB14, member RAS oncogene family	1.09	CACGTTAATAGAGGTAGTACA	NM_016322:	NM_016322:
51552	RAB14	RAB14, member RAS oncogene family	0.30	TCCATTGATCCCGTATCTTAA	NM_016322:	NM_016322:
64284	RAB17	RAB17, member RAS oncogene family	0.17	CAGCCTCTGGACAGAGAGGAA	NM_022449:	NM_022449:
64284	RAB17	RAB17, member RAS oncogene family	-4.29	CAGGAAGGATTCCTTCCTCAA	NM_022449:	NM_022449:
22931	RAB18	RAB18, member RAS oncogene family	0.55	ACCAACTTGTACAGACTAATA	NM_021252:	NM_021252:
22931	RAB18	RAB18, member RAS oncogene family	-0.07	CCAGGCCAATTTATAACTAAA	NM_021252:	NM_021252:

5861	RAB1A	RAB1A, member RAS oncogene family	-0.35	AACTATAGAGTTAGACGGGAA	NM_004161:	NM_004161:
5861	RAB1A	RAB1A, member RAS oncogene family	1.00	CTGCAGGAAATAGATCGTTAT	NM_004161:	NM_004161:
389721	rab1c	small GTP-binding protein	-0.06	CCGGATATGACTGCCTGTTTA	XM_372086:	XM_497021:
389721	rab1c	small GTP-binding protein	-3.79	TGGCTTCCTCGTGGTATATGA	XM_372086:	XM_497021:
5862	RAB2	RAB2, member RAS oncogene family	0.20	ACGATATTACACGGAGAGATA	NM_002865:	NM_002865:
5862	RAB2	RAB2, member RAS oncogene family	-0.12	ATCCGTCAAATTCTTGTATAA	NM_002865:	NM_002865:
55647	RAB20	RAB20, member RAS oncogene family	-2.13	CAGCAGAATGTTGGAGTGGAA	NM_017817:	NM_017817:
55647	RAB20	RAB20, member RAS oncogene family	0.95	CGACGTGTTCATTTATACAAA	NM_017817:	NM_017817:
23011	RAB21	RAB21, member RAS oncogene family	-0.08	CAGGCCCGTAACTGTCTACTA	NM_014999:	NM_014999:
23011	RAB21	RAB21, member RAS oncogene family	0.20	CGAGAACAAGTTTAACGACAA	NM_014999:	NM_014999:
57403	RAB22A	RAB22A, member RAS oncogene family	0.81	AAGGCCTATCAGCCAATTAAA	NM_020673:	NM_020673:
57403	RAB22A	RAB22A, member RAS oncogene family	0.63	CAGGTTTAATTTGATGGTCTA	NM_020673:	NM_020673:
51715	RAB23	RAB23, member RAS oncogene family	-0.02	AAGGTTAAAGTTAAGATTCTA	NM_016277:	NM_016277:NM_183227:
51715	RAB23	RAB23, member RAS oncogene family	1.00	CAGAATTTATATTGTTTATTA	NM_016277:	NM_016277:NM_183227:
53917	RAB24 (RAB2	RAB24, member RAS oncogene family	-5.18	CCCAGCCAGAACGGAGCTTAA	NM_130781:	NM_130781:NM_001031677:
53917	RAB24 (RAB2	RAB24, member RAS oncogene family	0.84	CCGGACTGTGACATTAGGTAT	NM_130781:	NM_130781:NM_001031677:
57111	RAB25	RAB25, member RAS oncogene family	0.67	AGGGTTGAGGGCATTGAGCAA	NM_020387:	NM_020387:
57111	RAB25	RAB25, member RAS oncogene family	0.02	GAGCTCTATGACCATGCTGAA	NM_020387:	NM_020387:
25837	RAB26	RAB26, member RAS oncogene family	-0.55	CCGCAGTGTTACCCATGCCTA	NM_014353:	NM_014353:
25837	RAB26	RAB26, member RAS oncogene family	-2.10	TCCGGCTGCATGATTACGTTA	NM_014353:	NM_014353:
5873	RAB27A	RAB27A, member RAS oncogene family	0.55	AAGATAGATGTTCATATTGAA	NM_004580:	NM_183234:NM_183235:NM_183236:NM_004580:
5873	RAB27A	RAB27A, member RAS oncogene family	0.91	CACCATAATTTAAATAAAGAA	NM_004580:	NM_183234:NM_183235:NM_183236:NM_004580:
5874	RAB27B (RAB	RAB27B, member RAS oncogene family	1.37	ACCGAATGGATCTTCAGGGAA	NM_004163:	NM_004163:
5874	RAB27B (RAB	RAB27B, member RAS oncogene family	1.16	TAAGCTGTACTAGAATGAATA	NM_004163:	NM_004163:
9364	RAB28	RAB28, member RAS oncogene family	-2.36	CAGCGTATTGTCAGGGCAGAA	NM_004249:	NM_004249:
9364	RAB28	RAB28, member RAS oncogene family	-0.56	CAGGGCAGAAATAGTGAAGTA	NM_004249:	NM_004249:
84932	RAB2B	RAB2B, member RAS oncogene family	-0.98	AGGGTTCTTCTTATCCTCCTA	NM_032846:	NM_032846:
84932	RAB2B	RAB2B, member RAS oncogene family	-1.62	CAGCGGAACTCTCGTGACATA	NM_032846:	NM_032846:
27314	RAB30 (RAB3	RAB30, member RAS oncogene family	0.70	AAGAGAGATTTCGGTCCATTA	NM_014488:	NM_014488:
27314	RAB30 (RAB3	RAB30, member RAS oncogene family	0.29	TCGGTCCATTACCCAGAGTTA	NM_014488:	NM_014488:
11031	RAB31	RAB31, member RAS oncogene family	0.86	AAGGAATACGCTGAATCCATA	NM_006868:	NM_006868:
11031	RAB31	RAB31, member RAS oncogene family	0.07	CAGGATTCACATAAACATTGT	NM_006868:	NM_006868:
10981	RAB32 (RAB3	RAB32, member RAS oncogene family	0.95	CACCAAAGCTTTCCTAATGAA	NM_006834:	NM_006834:
10981	RAB32 (RAB3	RAB32, member RAS oncogene family	-2.65	CTCTGCAAAGGATAACATAAA	NM_006834:	NM_006834:
9363	RAB33A	RAB33A, member RAS oncogene family	1.06	AACGATATAAATACAAGATAA	NM_004794:	NM_004794:
9363	RAB33A	RAB33A, member RAS oncogene family	-1.07	AAGCATGGTCGAGCATTACTA	NM_004794:	NM_004794:
83452	RAB33B	RAB33B, member RAS oncogene family	0.42	AAGGTTTAGGACACACCTAAT	NM_031296:	NM_031296:
83452	RAB33B	RAB33B, member RAS oncogene family	0.95	CCGAGTTGCTTTCTTACTAAA	NM_031296:	NM_031296:
83871	RAB34	RAB34, member RAS oncogene family	-3.24	CCGCGTAATCGTAGGAACTAT	NM_031934:	NM_031934:
83871	RAB34	RAB34, member RAS oncogene family	1.12	CCGGGTTATTGTAGGAACCAT	NM_031934:	NM_031934:
11021	RAB35	RAB35, member RAS oncogene family	1.54	AGGGTGTGCTTGCAAATTCAA	NM_006861:	NM_006861:
11021	RAB35	RAB35, member RAS oncogene family	2.00	CAGTTTCGTGCCGTTATTTAA	NM_006861:	NM_006861:
9609	RAB36 (RAB3	RAB36, member RAS oncogene family	-0.99	AGGCACTGTGGTGATCCCATA	NM_004914:	NM_004914:
9609	RAB36 (RAB3	RAB36, member RAS oncogene family	-0.05	CAGCTCAGCGATTGCCAAATA	NM_004914:	NM_004914:
326624	RAB37	RAB37, member RAS oncogene family	0.74	AAGGCGGATATGAGCAGCGAA	NM_175738:	NM_175738:NM_001006637:NM_001006638:
326624	RAB37	RAB37, member RAS oncogene family	1.03	CCGAGTTAAACCAATGCAATA	NM_175738:	NM_175738:NM_001006637:
23682	RAB38	RAB38, member RAS oncogene family	0.15	ATGATTTGGACTCCAAGTTAA	NM_022337:	NM_022337:
23682	RAB38	RAB38, member RAS oncogene family	-1.45	CTCCAAGTTAAGTCTCCCTAA	NM_022337:	NM_022337:
54734	RAB39 (RAB3	RAB39, member RAS oncogene family	-0.01	CAGGAGCGGTTCAGATCAATA	NM_017516:	NM_017516:
54734	RAB39 (RAB3	RAB39, member RAS oncogene family	-0.31	TAGCTTCACAACGTCAAGTTA	NM_017516:	NM_017516:
116442	RAB39B (RAB	RAB39B, member RAS oncogene family	0.81	AAAGATTATGAGCTCTACTTA	NM_171998:	NM_171998:
116442	RAB39B (RAB	RAB39B, member RAS oncogene family	0.07	CAGGAGGCACTGTAACCCTTA	NM_171998:	NM_171998:
5864	RAB3A (RAB3	RAB3A, member RAS oncogene family	0.32	CCCGTCACCCTTATTTATTAT	NM_002866:	NM_002866:
5864	RAB3A (RAB3	RAB3A, member RAS oncogene family	-0.02	CCGGACCATCACCACCGCATA	NM_002866:	NM_002866:
5865	RAB3B (RAB3	RAB3B, member RAS oncogene family	-2.27	CCGGACCATCACAACAGCCTA	NM_002867:	NM_002867:
5865	RAB3B (RAB3	RAB3B, member RAS oncogene family	1.14	CGGGTGCAGAATCACTTTACA	NM_002867:	NM_002867:
115827	RAB3C (RAB3	RAB3C, member RAS oncogene family	-1.02	ATGCAGTACAAGATTGGTCAA	NM_138453:	NM_138453:
115827	RAB3C (RAB3	RAB3C, member RAS oncogene family	1.48	TACAAGATTGGTCAACTCAAA	NM_138453:	NM_138453:
9545	RAB3D	RAB3D, member RAS oncogene family	-0.59	CAGGCCCTGTTTAGCTGTTTA	NM_004283:	NM_004283:
9545	RAB3D	RAB3D, member RAS oncogene family	0.02	TCCGTGGTGCCTTCTAGCTTA	NM_004283:	NM_004283:
142684	RAB40A	RAB40A, member RAS oncogene family	1.76	CAGAAGAGCAAAGAATAATAA	NM_080879:	NM_080879:
142684	RAB40A	RAB40A, member RAS oncogene family	-0.17	TCGCATTGTAGATTCAAGAAA	NM_080879:	NM_080879:
10966	RAB40B	RAB40B, member RAS oncogene family	1.33	CCGTCGGACTTCGAATTTCTA	NM_006822:	NM_006822:
10966	RAB40B	RAB40B, member RAS oncogene family	0.50	TCGGCGAATGCTGCTTGCGAA	NM_006822:	NM_006822:
57799	RAB40C	RAB40C, member RAS oncogene family	-4.27	CAGTAACGGGATCGACTACAA	NM_021168:	NM_021168:
57799	RAB40C	RAB40C, member RAS oncogene family	1.18	TCCGGGAATCTTGGTCGGAAA	NM_021168:	NM_021168:
347517	RAB41 (RAB4	RAB41, member RAS homolog family	-3.83	AAGATTGATTTGGATAACAAA	XM_293398:	NM_001032726:
347517	RAB41 (RAB4	RAB41, member RAS homolog family	0.70	GTGGTTGTCTATGACATTACA	XM_293398:	NM_001032726:
339122	RAB43	RAB43, member RAS oncogene family	-1.54	CCGGCCCTTCGGCTTCTTCTA	XM_290714:	NM_198490:
339122	RAB43	RAB43, member RAS oncogene family	0.19	GCAGTACGATTTCCTGTTCAA	XM_290714:	NM_198490:
5867	RAB4A	RAB4A, member RAS oncogene family	-0.35	AACCTACAATGCGCTTACTAA	NM_004578:	NM_004578:
5867	RAB4A	RAB4A, member RAS oncogene family	0.47	CACCGTTAGATGTGTATGTAA	NM_004578:	NM_004578:
53916	RAB4B	RAB4B, member RAS oncogene family	-2.64	CCGCACTATCCTCAACAAGAT	NM_016154:	NM_016154:
5868	RAB5A	RAB5A, member RAS oncogene family	0.68	ATCAGTGTTGTAGTAACTAAA	NM_004162:	NM_004162:
5868	RAB5A	RAB5A, member RAS oncogene family	-2.06	CAAGGCCGACCTAGCAAATAA	NM_004162:	NM_004162:
5869	RAB5B (RAB5	RAB5B, member RAS oncogene family	0.23	CAGAATGCGACTGCTGATTTA	NM_002868:	NM_002868:
5869	RAB5B (RAB5	RAB5B, member RAS oncogene family	0.32	TAGGTACAAGACAGCGACTTA	NM_002868:	NM_002868:
5878	RAB5C	RAB5C, member RAS oncogene family	0.18	CACCATGATTTCTCCATATAA	NM_004583:	NM_201434:NM_004583:
5878	RAB5C	RAB5C, member RAS oncogene family	0.12	CCCGACTGGAATCCACTCTAA	NM_004583:	NM_201434:NM_004583:
5870	RAB6A	RAB6A, member RAS oncogene family	-2.30	CCCACTTATTGTCACCTTGTA	NM_002869:	NM_002869:NM_198896:
5870	RAB6A	RAB6A, member RAS oncogene family	0.01	TACGGTCTTCTTTGAGGTCAA	NM_002869:	NM_002869:NM_198896:
51560	RAB6B (RAB6	RAB6B, member RAS oncogene family	-0.33	CAGGGATCACATCACTCTTAA	NM_016577:	NM_016577:
51560	RAB6B (RAB6	RAB6B, member RAS oncogene family	-2.12	CGGCTGTTACTTAAACAACTA	NM_016577:	NM_016577:
84084	RAB6C	RAB6C, member RAS oncogene family	1.18	AGCAGAAATAACGATATCTAA	NM_032144:	NM_032144:
84084	RAB6C	RAB6C, member RAS oncogene family	0.92	CAGGTAAGCATACATAGTAGA	NM_032144:	NM_032144:
23085	RAB6IP2	RAB6 interacting protein 2	0.68	CAGGAACTTAACCCAAATCTA	NM_015064:	NM_178037:NM_178038:NM_178039:NM_178040:NM_015064:
23085	RAB6IP2	RAB6 interacting protein 2	-0.02	TAGAAGTAAATTAAAGTTGTA	NM_015064:	NM_178037:NM_178038:NM_178039:NM_178040:NM_015064:
7879	RAB7	RAB7, member RAS oncogene family	-0.03	CACGTAGGCCTTCAACACAAT	NM_004637:	NM_004637:
7879	RAB7	RAB7, member RAS oncogene family	-1.49	TAGATCAGCATTCTACTACAA	NM_004637:	NM_004637:
338382	RAB7B	RAB7B, member RAS oncogene family	-1.30	CAGCATCCTCTCCAAGATTAT	NM_177403:	NM_177403:
338382	RAB7B	RAB7B, member RAS oncogene family	-0.47	TCGAGGTACCAGAGCATCTTA	NM_177403:	NM_177403:
8934	RAB7L1	RAB7, member RAS oncogene family-like 1	0.16	AACTTCTAACGTCATAATTAA	NM_003929:	NM_003929:
8934	RAB7L1	RAB7, member RAS oncogene family-like 1	-1.02	TAGGCACTTAGTCATAGGAAA	NM_003929:	NM_003929:
4218	RAB8A	RAB8A, member RAS oncogene family	2.06	ATGCTCTGTTTACATCGATAA	NM_005370:	NM_005370:
4218	RAB8A	RAB8A, member RAS oncogene family	0.50	TCGCCAGAGATATCAAAGCAA	NM_005370:	NM_005370:

51762	RAB8B	RAB8B, member RAS oncogene family	0.57	CAGCACAATCTTAGACTCATA	NM_016530:	NM_016530:
51762	RAB8B	RAB8B, member RAS oncogene family	0.35	CAGCAGAGGTTAATATACTAA	NM_016530:	NM_016530:
9367	RAB9A	RAB9A, member RAS oncogene family	0.75	CAGCAGTGTATCATCTACTAA	NM_004251:	NM_004251:
9367	RAB9A	RAB9A, member RAS oncogene family	1.84	GACCAAGACTTTAATTATAAA	NM_004251:	NM_004251:
51209	RAB9B	RAB9B, member RAS oncogene family	0.60	CAGGGTCTTCGTGCTGTTAAA	NM_016370:	NM_016370:
51209	RAB9B	RAB9B, member RAS oncogene family	1.89	CTGGCAGAAAGAATTTATTTA	NM_016370:	NM_016370:
10244	RABEPK	Rab9 effector protein with kelch motifs	-0.80	AAGCAACATGGTACACCTTGA	NM_005833:	NM_005833:
10244	RABEPK	Rab9 effector protein with kelch motifs	1.14	ATTGATATAAGTGACATGAAA	NM_005833:	NM_005833:
5875	RABGGTA (R	Rab geranylgeranyltransferase, alpha subunit	-1.57	CAGGCCAGTGATAATGCCATA	NM_004581:	NM_182836:NM_004581:
5875	RABGGTA (R	Rab geranylgeranyltransferase, alpha subunit	-2.10	CAGGCGATGTCCAGAAAGAAT	NM_004581:	NM_182836:NM_004581:
5876	RABGGTB	Rab geranylgeranyltransferase, beta subunit	-2.72	CCGGAGAAGTTACCAGATGTA	NM_004582:	NM_004582:
5876	RABGGTB	Rab geranylgeranyltransferase, beta subunit	0.59	ACGCTGTATGACAGTATTAAT	NM_004582:	NM_004582:
11158	RABL2B (RA	RAB, member of RAS oncogene family-like 2B	0.08	AAGGACCATCCTTGTGGACTT	NM_007081:	NM_007081:NM_001003789:
11158	RABL2B (RA	RAB, member of RAS oncogene family-like 2B	-0.98	CACGGTAGATGGAAGGACCAT	NM_007081:	NM_007081:NM_001003789:
285282	RABL3	RAB, member of RAS oncogene family-like 3	-1.06	CGGACTAATAGCCAGAGTTAA	NM_173825:	NM_173825:
285282	RABL3	RAB, member of RAS oncogene family-like 3	-1.65	TCCCTTAGCTATAATCAGAAA	NM_173825:	NM_173825:
11020	RABL4	RAB, member of RAS oncogene family-like 4	-4.60	AGGAATGGATTTGGTGGTGAA	NM_006860:	NM_006860:
11020	RABL4	RAB, member of RAS oncogene family-like 4	1.44	TGGGAGAGTCCCAATGTCTTA	NM_006860:	NM_006860:
64792	RABL5	RAB, member RAS oncogene family-like 5	-0.40	CAGCCCAATGATACAACAGTA	NM_022777:	NM_022777:
64792	RABL5	RAB, member RAS oncogene family-like 5	-0.75	CCGGATGGAATTCATAAAGTA	NM_022777:	NM_022777:
5879	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP bind	-0.79	AAGGTTGGTATTATCAGGAAA	NM_006908:	NM_018890:NM_198829:NM_006908:
5879	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP bind	-0.33	ACGATGTTCTGTACAACTTAA	NM_006908:	NM_018890:NM_198829:NM_006908:
5880	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP bind	1.30	CTCAACCTGCTTAAGCAGAAA	NM_002872:	NM_002872:
5880	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP bind	-0.62	AAGGAGATTGACTCGGTGAAA	NM_002872:	NM_002872:
5881	RAC3 (ras-rel	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP bind	-0.64	CCGGGAGATTGGCTCTGTGAA	NM_005052:	NM_005052:
5881	RAC3 (ras-rel	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP bind	0.19	CGCGCCCATGCAGGCCATCAA	NM_005052:	NM_005052:
29127	RACGAP1	Rac GTPase activating protein 1	-9.84	CTGAATGTATCTCCTAGCTAT	NM_013277:	NM_013277:
29127	RACGAP1	Rac GTPase activating protein 1	0.02	CTGGTAGATAGAAGAGCTAAA	NM_013277:	NM_013277:
5810	RAD1	RAD1 homolog (S. pombe)	-0.54	CAGCACCAATGTTATTAATAA	NM_002853:	NM_001033673:NM_133377:NM_002853:
5810	RAD1	RAD1 homolog (S. pombe)	-2.31	CAGTATATGATTAGAAATGAA	NM_002853:	NM_001033673:NM_133377:NM_002853:
5884	RAD17	RAD17 homolog (S. pombe)	2.18	CAGTGGTTTCTAATAAATAAA	NM_002873:	NM_133340:NM_133344:NM_133343:NM_002873: NM_133341:NM_133338:NM_133339:NM_133342:
5884	RAD17	RAD17 homolog (S. pombe)	1.77	CTCAGTGGAGATAATAATCAA	NM_002873:	NM_133340:NM_133344:NM_133343:NM_002873: NM_133341:NM_133338:NM_133339:NM_133342:
56852	RAD18	RAD18 homolog (S. cerevisiae)	0.28	ATGGTTGTTGCCCGAGGTTAA	NM_020165:	NM_020165:
56852	RAD18	RAD18 homolog (S. cerevisiae)	-1.29	CCCGAGGTTAATGTAGTTGTT	NM_020165:	NM_020165:
5885	RAD21	RAD21 homolog (S. pombe)	-1.38	ATCGATGAGCCCATTATTGAA	NM_006265:	NM_006265:
5885	RAD21	RAD21 homolog (S. pombe)	-2.08	CTGGGAGTAGTTCGAATCTAT	NM_006265:	NM_006265:
5886	RAD23A	RAD23 homolog A (S. cerevisiae)	0.76	AAGGTGCTAAAGGAGAAGATA	NM_005053:	NM_005053:
5886	RAD23A	RAD23 homolog A (S. cerevisiae)	-2.67	CAGGCCTATTTCGCGTGTGAA	NM_005053:	NM_005053:
5887	RAD23B	RAD23 homolog B (S. cerevisiae)	0.78	CTGGGATGACTTGGGCTCATA	NM_002874:	NM_002874:XM_496632:
5887	RAD23B	RAD23 homolog B (S. cerevisiae)	1.20	TAGGTGTCTAATTACTGTTTA	NM_002874:	NM_002874:
10111	RAD50	RAD50 homolog (S. cerevisiae)	0.59	CAGAAAGTGTATAATAAGAAA	NM_005732:	NM_005732:NM_133482:
10111	RAD50	RAD50 homolog (S. cerevisiae)	-1.06	CAGGAACAGATTCAACATCTA	NM_005732:	NM_005732:NM_133482:
5888	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	-2.80	AAGGGAATTAGTGAAGCCAAA	NM_002875:	NM_002875:NM_133487:
5888	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	-0.12	CACTTCTAAATTAATGGTAAA	NM_002875:	NM_002875:NM_133487:
10635	RAD51AP1	RAD51 associated protein 1	-1.47	AAGGATGGCTTTAGATGACAA	NM_006479:	NM_006479:
10635	RAD51AP1	RAD51 associated protein 1	-0.17	CACCTTAACTTTAACTGTTCA	NM_006479:	NM_006479:
5889	RAD51C	RAD51 homolog C (S. cerevisiae)	0.80	AAGAGAATGTCTCACAAATAA	NM_002876:	NM_002876:NM_058216:NM_058217:
5889	RAD51C	RAD51 homolog C (S. cerevisiae)	1.28	CTGCAAATTATCAGAAGAGAA	NM_002876:	NM_002876:NM_058216:NM_058217:
5890	RAD51L1	RAD51-like 1 (S. cerevisiae)	1.11	CAGAGAGAAGACAGATTCTTA	NM_002877:	NM_002877:NM_133510:NM_133509:
5890	RAD51L1	RAD51-like 1 (S. cerevisiae)	0.63	CCCGGCATGGGTAGCAAGAAA	NM_002877:	NM_002877:NM_133510:NM_133509:
5892	RAD51L3	RAD51-like 3 (S. cerevisiae)	-1.58	CTGGAAGAGGTAGCTCAGAAA	NM_002878:	NM_002878:NM_133627:NM_133628:NM_133629: NM_133630:
5892	RAD51L3	RAD51-like 3 (S. cerevisiae)	1.84	CTGGGTGGAAATAAGCTTATA	NM_002878:	NM_002878:NM_133627:NM_133628:NM_133629: NM_133630:
5893	RAD52 (RAD	RAD52 homolog (S. cerevisiae)	0.64	AAGGAAGGAAATAATCATCTA	NM_002879:	NM_002879:NM_134423:NM_134422:NM_134424:
5893	RAD52 (RAD	RAD52 homolog (S. cerevisiae)	0.50	CAGGAGTGACTCAAGAATTAA	NM_002879:	NM_002879:NM_134423:NM_134422:NM_134424:
25788	RAD54B	RAD54 homolog B (S. cerevisiae)	0.83	ACCCAAGAAATTATAAATAAA	NM_012415:	NM_134434:NM_012415:
25788	RAD54B	RAD54 homolog B (S. cerevisiae)	1.15	CTGGATCAAATTAAGAATATA	NM_012415:	NM_134434:NM_012415:
8438	RAD54L	RAD54-like (S. cerevisiae)	-0.77	AAGCATTTATTCGAAGCATTT	NM_003579:	NM_003579:
8438	RAD54L	RAD54-like (S. cerevisiae)	0.71	ATGGAGGATCTAAGGATGAAA	NM_003579:	NM_003579:
5883	RAD9A	RAD9 homolog A (S. pombe)	-1.90	CAGGCTCACCTTCCTAAGGAA	NM_004584:	NM_004584:
5883	RAD9A	RAD9 homolog A (S. pombe)	-0.16	TGGCGCTGACTTGGAATTCTA	NM_004584:	NM_004584:
135250	RAET1E	retinoic acid early transcript 1E	0.89	ATGCTCCTTTGTGACATCAAA	NM_139165:	NM_139165:
135250	RAET1E	retinoic acid early transcript 1E	0.42	AGCGCAGGTCTTCTTGAATAA	NM_139165:	NM_139165:
353091	RAET1G (reti	retinoic acid early transcript 1G	0.06	TCGCGTGACTTTACCTATCAT	NM_001001788:	NM_001001788:
353091	RAET1G (reti	retinoic acid early transcript 1G	-0.82	TGCCTTGTATACAATAAATAA	NM_001001788:	NM_001001788:
154064	RAET1L (reti	retinoic acid early transcript 1L	1.07	AAGGATGTCTTGTGAGCAGAA	NM_130900:	NM_130900:
5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	-0.04	CAGATCTTAGTAAGCTATATA	NM_002880:	NM_002880:
5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	1.11	CTCAGGTTTAAGAATTGTTTA	NM_002880:	NM_002880:
5896	RAG1	recombination activating gene 1	1.10	TGGGTCTTGCATTACATCAAA	NM_000448:	NM_000448:
5896	RAG1	recombination activating gene 1	2.41	CAGCTAAATTCACATAATCAT	NM_000448:	NM_000448:
5897	RAG2 (recom	recombination activating gene 2	1.53	TCCAATGAAATCCCTCCGTAA	NM_000536:	NM_000536:
5897	RAG2 (recom	recombination activating gene 2	-0.43	CAACACTTGGGTACCATTCTA	NM_000536:	NM_000536:
5891	RAGE	renal tumor antigen	-0.30	AAAGAATAAGCTGTCGTTAAA	NM_014226:	NM_014226:
5891	RAGE	renal tumor antigen	-0.25	CCGGCTGTGTGTTCTACGAGA	NM_014226:	NM_014226:
10743	RAI1	retinoic acid induced 1	-3.73	CAGGGTCAACAGCAACTCGAA	NM_030665:	NM_030665:
10743	RAI1	retinoic acid induced 1	-0.77	TTGCATATTCATCGAAGAGAA	NM_030665:	NM_030665:
5898	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	-0.43	CCCATGTGTCCTGGTGAGAAA	NM_005402:	NM_005402:
5898	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	1.91	CGCGGTGCAGATTCTTCTTAA	NM_005402:	NM_005402:
5899	RALB (v-ral si	v-ral simian leukemia viral oncogene homolog B (ras related; GTP bin	0.43	AAGAATTGTCATAGCATCTTA	NM_002881:	NM_002881:
5899	RALB (v-ral si	v-ral simian leukemia viral oncogene homolog B (ras related; GTP bin	-0.24	CACAGAGATGGTAGAAATTAT	NM_002881:	NM_002881:
10267	RAMP1 (rece	receptor (calcitonin) activity modifying protein 1	-0.40	CAGGGACGTGACCTTGACTTA	NM_005855:	NM_005855:
10267	RAMP1 (rece	receptor (calcitonin) activity modifying protein 1	-2.93	CAGGTTCTTCCTGGCAGTGCA	NM_005855:	NM_005855:
10266	RAMP2 (rece	receptor (calcitonin) activity modifying protein 2	0.10	TGGAATCATTATAAGGATCAA	NM_005854:	NM_005854:
10266	RAMP2 (rece	receptor (calcitonin) activity modifying protein 2	-0.42	CACAAGTTCTGTAATCTTCAA	NM_005854:	NM_005854:
10268	RAMP3 (rece	receptor (calcitonin) activity modifying protein 3	-0.40	ATGCTGTTTCTTAGCACAGAA	NM_005856:	NM_005856:
10268	RAMP3 (rece	receptor (calcitonin) activity modifying protein 3	-0.47	CTGCACCGAGATGGAGGCCAA	NM_005856:	NM_005856:
5901	RAN	RAN, member RAS oncogene family	1.35	ATGTGGTTTGTACATATCAAA	NM_006325:	NM_006325:
5901	RAN	RAN, member RAS oncogene family	1.77	TTGGGAATTCTTGCTGTTAAA	NM_006325:	NM_006325:
57610	RANBP10	RAN binding protein 10	0.49	CAAGTTGGTGATAGCTTATTA	NM_020850:	NM_020850:
57610	RANBP10	RAN binding protein 10	-0.47	GAGGATGGAGAGAGAACTCTA	NM_020850:	NM_020850:
5903	RANBP2	RAN binding protein 2	-2.60	CCGCGCGAAATTGTTTCGTTT	NM_006267:	NM_006267:
5903	RANBP2	RAN binding protein 2	-0.29	CAGGTGGGAACAGGATTTAAA	NM_006267:	NM_006267:

3843	RANBP5	RAN binding protein 5	-0.38	CACGAGGCAATTAAACATGAA	NM_002271:	NM_002271:
3843	RANBP5	RAN binding protein 5	-0.01	CAGGATACTTGCGGCACTCAA	NM_002271:	NM_002271:
10048	RANBP9	RAN binding protein 9	0.48	AAGCAATGAGTGAACAGCTAA	NM_005493:	NM_005493:
10048	RANBP9	RAN binding protein 9	-1.91	CAGGTTGGGATAAGCATTCAT	NM_005493:	NM_005493:
5906	RAP1A	RAP1A, member of RAS oncogene family	-3.48	CAGGGCCAGAATTTAGCAAGA	NM_002884:	NM_001010935:NM_002884:
5908	RAP1B	RAP1B, member of RAS oncogene family	1.17	CAGTATAATGTCTTAGATTAA	NM_015646:	NM_001010942:NM_015646:
5908	RAP1B	RAP1B, member of RAS oncogene family	-0.07	GACGAGTACTGTGGATGTGAA	NM_015646:	NM_001010942:NM_015646:
5911	RAP2A	RAP2A, member of RAS oncogene family	-1.38	CAGAGATAATTGCCTATACTA	NM_021033:	NM_021033:
5911	RAP2A	RAP2A, member of RAS oncogene family	0.77	CCAGTGTATTCCGTCAAGTAA	NM_021033:	NM_021033:
5912	RAP2B	RAP2B, member of RAS oncogene family	0.13	CTCACTTAAGTTTGATATCAA	NM_002886:	NM_002886:
5912	RAP2B	RAP2B, member of RAS oncogene family	1.39	TACGGTTCTTTCGTAGAACAA	NM_002886:	NM_002886:
57826	RAP2C (RAP:	RAP2C, member of RAS oncogene family	-0.14	AAGAAGCATGTTCGTATTAGA	NM_021183:	NM_021183:
57826	RAP2C (RAP:	RAP2C, member of RAS oncogene family	-2.96	ATGGGTCAGCATGACCATTAA	NM_021183:	NM_021183:
51720	RAP80	receptor associated protein 80	-1.35	CAGTATTGACTCGGAGACAAA	NM_016290:	NM_016290:
51720	RAP80	receptor associated protein 80	-0.35	CACGTCGTGACTTAAATGAAT	NM_016290:	NM_016290:
2889	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	-1.29	CAGGAAAGATTTGGTGTTGTA	NM_005312:	NM_005312:NM_198679:
2889	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	-1.68	CAGGGTTACATTGTAATATAT	NM_005312:	NM_005312:NM_198679:
51195	RAPGEFL1	Rap guanine nucleotide exchange factor (GEF)-like 1	-1.48	ACCCAAAGCTCTGGAATTGTA	NM_016339:	NM_016339:
51195	RAPGEFL1	Rap guanine nucleotide exchange factor (GEF)-like 1	-2.18	ACGGTGGAACTAAAGATTCCA	NM_016339:	NM_016339:
5913	RAPSN	receptor-associated protein of the synapse, 43kD	-1.75	CAGGTCAAGGACTACGAGAAA	NM_005055:	NM_032645:NM_005055:
5913	RAPSN	receptor-associated protein of the synapse, 43kD	-7.21	CAGCTTCTATGCCCAGGTCAA	NM_005055:	NM_032645:NM_005055:
5914	RARA	retinoic acid receptor, alpha	1.00	TGGATAAAGAATAAAGTTCTA	NM_000964:	NM_001033603:NM_001024809:NM_000964:
5914	RARA	retinoic acid receptor, alpha	-1.46	CCACATCTTCATCACCAGCAA	NM_000964:	NM_001033603:NM_001024809:NM_000964:
5915	RARB	retinoic acid receptor, beta	1.01	CTGCCAGTTCAGTTAATCAAA	NM_000965:	NM_016152:NM_000965:
5915	RARB	retinoic acid receptor, beta	-0.06	ATGGAATAGTCAAGACATCAA	NM_000965:	NM_016152:NM_000965:
5916	RARG	retinoic acid receptor, gamma	-0.33	CAGTTTGTATTTAGCTGCCAA	NM_000966:	NM_000966:
5916	RARG	retinoic acid receptor, gamma	-1.88	ATGCTTCGTGTGCAATGACAA	NM_000966:	NM_000966:
5918	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	1.71	CCGCGCGTGGATTAATCCAAA	NM_002888:	NM_002888:NM_206963:
5918	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	0.66	CCAGACCAACCATCAATGTAA	NM_002888:	NM_002888:NM_206963:
5919	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	-2.47	CTGGAAGAAACCCGAGTGCAA	NM_002889:	NM_002889:
5919	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	0.24	CAGGGAGAGGAACCCGTTCTA	NM_002889:	NM_002889:
5920	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	0.96	TTGCGATTAGGAGATACCAAA	NM_004585:	NM_004585:
5920	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	0.58	CCCGCTGTAAACAGGTGGAAA	NM_004585:	NM_004585:
5917	RARS	arginyl-tRNA synthetase	1.31	TCCCGCCAAGAGTTAAATAAA	NM_002887:	NM_002887:
5917	RARS	arginyl-tRNA synthetase	1.35	CTGCATATCCAGATTTGGAAA	NM_002887:	NM_002887:
57038	RARSL	arginyl-tRNA synthetase-like	2.45	TAAGACAACTAAAGAACTCAA	NM_020320:	NM_020320:
57038	RARSL	arginyl-tRNA synthetase-like	0.11	TAGATCGAATGGACAAGTATA	NM_020320:	NM_020320:
5921	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1.50	ACGGACCTGTCCCGTGATTTA	NM_002890:	NM_022650:NM_002890:
5921	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.00	CAGCTCCCATATACCATTAAA	NM_002890:	NM_022650:NM_002890:
10156	RASA4	RAS p21 protein activator 4	0.70	ACGGGAGACCTCGATCGTGAA	NM_006989:	NM_006989:
10156	RASA4	RAS p21 protein activator 4	0.90	CCAGAACTTTATAATAAGAGA	NM_006989:	NM_006989:
51655	RASD1	RAS, dexamethasone-induced 1	1.02	CGCGCTGGCGACACAACCTAA	NM_016084:	NM_016084:
51655	RASD1	RAS, dexamethasone-induced 1	0.53	AGGGTGGATTTATCTTCTCAA	NM_016084:	NM_016084:
23551	RASD2	RASD family, member 2	0.31	ATGGATCTCCGTGTACACTAT	NM_014310:	NM_014310:
23551	RASD2	RASD family, member 2	0.75	TCCGTGTACACTATCAATAAA	NM_014310:	NM_014310:
158158	RASEF	RAS and EF-hand domain containing	0.01	CAGCCATATGAACATGTTATA	NM_152573:	NM_152573:
158158	RASEF	RAS and EF-hand domain containing	-0.22	CCGGAAGCTACATGACAGTAA	NM_152573:	NM_152573:
5923	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	0.33	CACCAACTAAATCTCCAACAA	NM_002891:	NM_153815:NM_002891:
5923	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	-1.57	CCGGCGGAAGCTCTCCCTGAA	NM_002891:	NM_153815:NM_002891:
115727	RASGRP4 (R	RAS guanyl releasing protein 4	-0.13	CCAGGTGAAGGTAGAATGTAA	NM_052949:	NM_052949:NM_170602:NM_170603:NM_170604:
115727	RASGRP4 (R	RAS guanyl releasing protein 4	-1.02	CGCGGGAAGCATGAACAGAAA	NM_052949:	NM_052949:NM_170602:NM_170603:NM_170604:
11186	RASSF1	Ras association (RalGDS/AF-6) domain family 1	0.45	CTGGCCCAGGTTCATACCTTA	NM_007182:	NM_170716:NM_007182:NM_170712:NM_170713:NM_170714:NM_170715:NM_170717:
11186	RASSF1	Ras association (RalGDS/AF-6) domain family 1	0.71	TTGGCTCAATAAAGATTTCAA	NM_007182:	NM_170716:NM_007182:NM_170712:NM_170713:NM_170714:NM_170715:NM_170717:
283349	RASSF3	Ras association (RalGDS/AF-6) domain family 3	-1.20	CAAGTTGAAGATGACCTTGAA	NM_178169:	NM_178169:
283349	RASSF3	Ras association (RalGDS/AF-6) domain family 3	0.12	CTGCCAAGTTTGCACTTTATA	NM_178169:	NM_178169:
83937	RASSF4	Ras association (RalGDS/AF-6) domain family 4	-0.08	ATGGAGAATTTCAGGAATGAA	NM_032023:	NM_178145:NM_032023:
83937	RASSF4	Ras association (RalGDS/AF-6) domain family 4	0.87	TCCGTGGATGGCAGATTTAAA	NM_032023:	NM_178145:NM_032023:
83593	RASSF5	Ras association (RalGDS/AF-6) domain family 5	-0.58	AAGCAGGGTAATGCTCATAAA	NM_031437:	NM_182664:NM_182663:NM_182665:NM_031437:
83593	RASSF5	Ras association (RalGDS/AF-6) domain family 5	0.83	CAGATTTATTTGTATTATTAA	NM_031437:	NM_182664:NM_182663:NM_182665:NM_031437:
30062	RAX	retina and anterior neural fold homeobox	0.68	CCAGATAACCATAACAGGGAA	NM_013435:	NM_013435:
30062	RAX	retina and anterior neural fold homeobox	0.03	CAGGCTGAAGCTCCTAAACTT	NM_013435:	NM_013435:
5925	RB1	retinoblastoma 1 (including osteosarcoma)	-1.30	AAGGTTCAACTACGCGTGTAA	NM_000321:	NM_000321:
5925	RB1	retinoblastoma 1 (including osteosarcoma)	-0.79	CAGGGTTGTGTCGAAATTGGA	NM_000321:	NM_000321:
9821	RB1CC1	RB1-inducible coiled-coil 1	-0.67	ACGCAAATCAGTTGATGATTA	NM_014781:	NM_014781:
9821	RB1CC1	RB1-inducible coiled-coil 1	1.24	CTGGGACGGATACAAATCCAA	NM_014781:	NM_014781:
57786	RBAK	RB-associated KRAB repressor	-0.01	CAGAACATTCTTGTGGTACAA	NM_021163:	NM_021163:
57786	RBAK	RB-associated KRAB repressor	-0.03	CTGAGAGTTCGTGTTCCTGAA	NM_021163:	NM_021163:
5928	RBBP4	retinoblastoma binding protein 4	-1.08	ACCGATAATGCTATTAGCCCA	NM_005610:	NM_005610:
5928	RBBP4	retinoblastoma binding protein 4	0.97	CAGCTATCCCTCTATATAATA	NM_005610:	NM_005610:
5929	RBBP5	retinoblastoma binding protein 5	0.97	ACGGCAGATCGAATAATCAGA	NM_005057:	NM_005057:
5929	RBBP5	retinoblastoma binding protein 5	0.94	TCCATTTAAACCGAAACTCTA	NM_005057:	NM_005057:
5930	RBBP6	retinoblastoma binding protein 6	-0.01	CCCAGTTAAGTCATTCCTCTA	NM_006910:	NM_006910:NM_018703:
5930	RBBP6	retinoblastoma binding protein 6	0.61	ATAGTGGTTCTTCGTATTCAA	NM_006910:	NM_006910:NM_018703:
5931	RBBP7	retinoblastoma binding protein 7	-1.93	CCGACGCAAGATGGCGAGTAA	NM_002893:	NM_002893:
5931	RBBP7	retinoblastoma binding protein 7	1.34	GCGGATAAGACCGTAGCTTTA	NM_002893:	NM_002893:
64080	RBKS	ribokinase	0.30	AACACAGTCATCTTACCCTTA	NM_022128:	NM_022128:
64080	RBKS	ribokinase	1.53	CAGGTGGTAATCATTACCTTA	NM_022128:	NM_022128:
5933	RBL1	retinoblastoma-like 1 (p107)	-0.16	ACAGGCTAATGTGGAGTATAA	NM_002895:	NM_002895:NM_183404:
5933	RBL1	retinoblastoma-like 1 (p107)	-0.04	CACCAAGTGACCAACTTATAA	NM_002895:	NM_002895:NM_183404:
5934	RBL2	retinoblastoma-like 2 (p130)	0.02	ACCCTATATTAGGAAACTTTA	NM_005611:	NM_005611:
5934	RBL2	retinoblastoma-like 2 (p130)	0.50	CAGTGTTCTAATCGTAAAGAA	NM_005611:	NM_005611:
8241	RBM10	RNA binding motif protein 10	-1.27	ACCACTCACTATCGACGGCAA	NM_005676:	NM_005676:NM_152856:
8241	RBM10	RNA binding motif protein 10	0.11	CTCCAACGTGCGCGTCATAAA	NM_005676:	NM_005676:NM_152856:
10432	RBM14	RNA binding motif protein 14	-1.19	CACGCTATTCGGGCTCCTATA	NM_006328:	NM_006328:
10432	RBM14	RNA binding motif protein 14	-1.55	CGGCAAAGAAGTGAAGGGCAA	NM_006328:	NM_006328:
221662	RBM24	RNA binding motif protein 24	-3.95	AACGATATATTGCTAGTTTCA	NM_153020:	NM_153020:
221662	RBM24	RNA binding motif protein 24	0.19	AAGGTTAATGATAATGTGGTT	NM_153020:	NM_153020:
5936	RBM4	RNA binding motif protein 4	0.04	ACCGAGCAATATAATGAGCAA	NM_002896:	NM_002896:
5936	RBM4	RNA binding motif protein 4	-1.59	CTCAGGAACCGTGGACCTTAA	NM_002896:	NM_002896:
10181	RBM5	RNA binding motif protein 5	0.62	CCAACTCGCAATACTACTATA	NM_005778:	NM_005778:
10181	RBM5	RNA binding motif protein 5	-0.74	CAGGATATTACTATGATCCGA	NM_005778:	NM_005778:
9939	RBM8A	RNA binding motif protein 8A	-1.51	ACACGACAAATTCGCAGAATA	NM_005105:	NM_005105:
9939	RBM8A	RNA binding motif protein 8A	-0.08	CAGGTCTAGGGTTAAGGATTA	NM_005105:	NM_005105:

23543	RBM9	RNA binding motif protein 9	-6.37	AACGGTATAAAGAGAGATCAA	NM_014309:	NM_014309:NM_001031695:
23543	RBM9	RNA binding motif protein 9	-3.83	ACGGCTGCTTTGAAAGGTTTA	NM_014309:	NM_014309:NM_001031695:
5950	RBP4 (retinol	retinol binding protein 4, plasma	-0.34	CTGGATCGTCGACACAGACTA	NM_006744:	NM_006744:
5950	RBP4 (retinol	retinol binding protein 4, plasma	-0.21	CCCTGCCAAGTTCAAGATGAA	NM_006744:	NM_006744:
11317	RBPSUHL	recombining binding protein suppressor of hairless (Drosophila)-like	-0.43	CAGGTCCTTCCTGGAATATTA	NM_014276:	NM_014276:
11317	RBPSUHL	recombining binding protein suppressor of hairless (Drosophila)-like	-0.09	CCCATGATCATCCGTAAAGTA	NM_014276:	NM_014276:
9978	RBX1	ring-box 1	-1.12	AAGAAGCGCTTTGAAGTGAAA	NM_014248:	NM_014248:
9978	RBX1	ring-box 1	0.07	CTGCTGTTACCTAATTACAAA	NM_014248:	NM_014248:
149041	RC3H1	ring finger and CCCH-type zinc finger domains 1	1.55	CAGCAAACTTGAACCGACTAA	XM_086409:	NM_172071:
149041	RC3H1	ring finger and CCCH-type zinc finger domains 1	-0.09	CTGCAAGCAATTCAGATTAAA	XM_086409:	NM_172071:
25898	RCHY1	ring finger and CHY zinc finger domain containing 1	3.18	TTCAAGGAAGACACAAGTGTA	NM_015436:	NM_015436:NM_001008925:NM_001009922:
25898	RCHY1	ring finger and CHY zinc finger domain containing 1	1.75	TTGGAGAATATTATTGCGATA	NM_015436:	NM_015436:NM_001008925:NM_001009922:
27297	RCP9	calcitonin gene-related peptide-receptor component protein	0.37	CAGAGAGTTACTCTAAGTTAA	NM_014478:	NM_014478:
27297	RCP9	calcitonin gene-related peptide-receptor component protein	-0.69	CCGGCGTTTCATGAAGTCAGA	NM_014478:	NM_014478:
157506	RDH10 (retin	retinol dehydrogenase 10 (all-trans)	1.03	TGGAGACCTAATTATCCTAAA	NM_172037:	NM_172037:
157506	RDH10 (retin	retinol dehydrogenase 10 (all-trans)	-0.03	CCGAATCAGGAAAGAAATTGA	NM_172037:	NM_172037:
51109	RDH11	retinol dehydrogenase 11 (all-trans and 9-cis)	0.71	GACCATTAAGCTATATGTTTA	NM_016026:	NM_016026:
51109	RDH11	retinol dehydrogenase 11 (all-trans and 9-cis)	-1.43	TAGCCCTTTAAGGATTAACTA	NM_016026:	NM_016026:
145226	RDH12	retinol dehydrogenase 12 (all-trans and 9-cis)	0.49	CACCATCACTGCCTATTTCTA	NM_152443:	NM_152443:
145226	RDH12	retinol dehydrogenase 12 (all-trans and 9-cis)	0.11	AAGGAGAAGGCCAACCCTAAA	NM_152443:	NM_152443:
112724	RDH13 (retin	retinol dehydrogenase 13 (all-trans and 9-cis)	-1.04	AAGTACTTCGATGGACTCAAA	NM_138412:	NM_138412:
112724	RDH13 (retin	retinol dehydrogenase 13 (all-trans and 9-cis)	0.04	ACGAGGAAGTATAACACCAAA	NM_138412:	NM_138412:
57665	RDH14	retinol dehydrogenase 14 (all-trans and 9-cis)	-0.61	CAAGCATGGATGACATATTAA	NM_020905:	NM_020905:
57665	RDH14	retinol dehydrogenase 14 (all-trans and 9-cis)	-0.30	CTGCCTGGTGTGTGCACACAA	NM_020905:	NM_020905:
5959	RDH5	retinol dehydrogenase 5 (11-cis and 9-cis)	0.33	GTGGGTGGAGATGCACGTTAA	NM_002905:	NM_002905:
5959	RDH5	retinol dehydrogenase 5 (11-cis and 9-cis)	-1.48	CAGCAATGCCTTTGTCTTCAT	NM_002905:	NM_002905:
50700	RDH8	retinol dehydrogenase 8 (all-trans)	0.29	CACACCAGCAATGTATGTATA	NM_015725:	NM_015725:
50700	RDH8	retinol dehydrogenase 8 (all-trans)	-6.60	CAGCTGTCTCTGGGAAAGCAA	NM_015725:	NM_015725:
195814	RDHE2	retinal short chain dehydrogenase reductase isoform 1	1.69	TAGGCAGTGATCCTAGACCAA	NM_138969:	NM_138969:
195814	RDHE2	retinal short chain dehydrogenase reductase isoform 1	-0.52	TCGGCGATGTTTCCATCCTAA	NM_138969:	NM_138969:
5961	RDS	retinal degeneration, slow	-0.57	CACGGATTTAGTCCCACCCTA	NM_000322:	NM_000322:
5961	RDS	retinal degeneration, slow	0.03	GAGGAGCGATGTGATGAATAA	NM_000322:	NM_000322:
5962	RDX (radixin)	radixin	-0.02	GAGGAAGAACGTGTAACCGAA	NM_002906:	NM_002906:
5962	RDX (radixin)	radixin	0.21	TCGCGAGCACATGTTCATATA	NM_002906:	NM_002906:
9401	RECQL4	RecQ protein-like 4	-5.07	CCGGGAGTACCGCACTCTGAA	NM_004260:	NM_004260:
9401	RECQL4	RecQ protein-like 4	0.45	CCTCGATTCCATTATCATTTA	NM_004260:	NM_004260:
65055	REEP1	receptor accessory protein 1	-1.90	CCCAGAATTATCAGAAACGAA	NM_022912:	NM_022912:
65055	REEP1	receptor accessory protein 1	-4.84	AAGCCTGTAAGTGTACATGTA	NM_022912:	NM_022912:
51308	REEP2	receptor accessory protein 2	-0.11	AACGCTGTCCAACAAGGAGAA	NM_016606:	NM_016606:
51308	REEP2	receptor accessory protein 2	-2.97	CACGTGAAGGAGAAAGAGAAA	NM_016606:	NM_016606:
221035	REEP3	receptor accessory protein 3	-0.37	CAAGGACATAATGTAAGATAA	NM_001001330:	NM_001001330:
221035	REEP3	receptor accessory protein 3	-1.68	TTCCAAATATTGACTACTAAA	NM_001001330:	NM_001001330:
80346	REEP4	receptor accessory protein 4	0.28	CAGGGATGCACCCACAATGTA	NM_025232:	NM_025232:
80346	REEP4	receptor accessory protein 4	-0.11	CCCTTTCTACTATGAGATCAA	NM_025232:	NM_025232:
7905	REEP5	receptor accessory protein 5	0.83	CCAAATCGTTATAGAGAGCAA	NM_005669:	NM_005669:
7905	REEP5	receptor accessory protein 5	-0.75	CTGCACATGACTACATAGTAA	NM_005669:	NM_005669:
92840	REEP6	receptor accessory protein 6	0.30	CGGAATAACCAGGAACGTCAA	NM_138393:	NM_138393:
92840	REEP6	receptor accessory protein 6	0.84	CTGCTAGGAGGCTCCAATAAA	NM_138393:	NM_138393:
5068	REG3A	regenerating islet-derived 3 alpha	0.28	AAGGCTTTAAAGAGCAATAAA	NM_002580:	NM_002580:NM_138937:NM_138938:
5068	REG3A	regenerating islet-derived 3 alpha	1.90	CTGGAAGAGAATATTCGCTTA	NM_002580:	NM_002580:NM_138937:NM_138938:
5966	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	0.31	CCCGTATATAGAGATAATTGA	NM_002908:	NM_002908:
5966	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	0.21	CCGGTGCGTATAACCCGTATA	NM_002908:	NM_002908:
5970	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of	-0.04	ATGGAGTACCCTGAGGCTATA	NM_021975:	NM_021975:
5970	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of	1.19	CCGGATTGAGGAGAAACGTAA	NM_021975:	NM_021975:
5971	RELB	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of	0.26	CCAGATTGCCATTGTGTTCAA	NM_006509:	NM_006509:
5971	RELB	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of	0.89	GCGGATTTGCCGAATTAACAA	NM_006509:	NM_006509:
5649	RELN	reelin	0.02	TAGGGTGAACCAAGCTATAAA	NM_005045:	NM_005045:NM_173054:
5649	RELN	reelin	-2.73	AAGGAACGCTTTGACAGTGAA	NM_005045:	NM_005045:NM_173054:
28954	REM1	RAS (RAD and GEM)-like GTP-binding 1	1.77	CAGTGCCTATGTCATCGTATA	NM_014012:	NM_014012:
28954	REM1	RAS (RAD and GEM)-like GTP-binding 1	-1.48	CGCTGTGGTGTTCGACTGTAA	NM_014012:	NM_014012:
5972	REN	renin	0.32	CAGGAATCCTACAGTAGTAAA	NM_000537:	NM_000537:
5972	REN	renin	-1.86	CAGCGCGGACTATGTATTTCA	NM_000537:	NM_000537:
85004	RERG	RAS-like, estrogen-regulated, growth inhibitor	-0.20	CTAGTAGAAGATGTAGAATTA	NM_032918:	NM_032918:
85004	RERG	RAS-like, estrogen-regulated, growth inhibitor	1.02	CTGGTTTATGTTAAGCTATTT	NM_032918:	NM_032918:
5979	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyro	1.12	CAGGGTCGGATTCCAGTTAAA	NM_20975:	NM_020630:NM_020975:
5979	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyro	0.90	CCCACATGTCATCAAATTGTA	NM_20975:	NM_020630:NM_020975:
56729	RETN	resistin	-1.58	CCCTAATATTTAGGGCAATAA	NM_020415:	NM_020415:
56729	RETN	resistin	-2.01	CTCCATGGAAGAAGCCATCAA	NM_020415:	NM_020415:
51455	REV1L	REV1-like (yeast)	0.15	AGGAGATATGTCAGTATTGAA	NM_016316:	NM_001037872:NM_016316:
51455	REV1L	REV1-like (yeast)	-4.03	CAGCGCATCTGTGCCAAAGAA	NM_016316:	NM_001037872:NM_016316:
5980	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	0.14	ATGAGTATGGATCATATACAA	NM_002912:	NM_002912:
5980	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	0.19	CGGGATGTAGTCAAACTGCAA	NM_002912:	NM_002912:
5982	RFC2	replication factor C (activator 1) 2, 40kDa	-1.98	AACCATGGAAATCTACTCTAA	NM_002914:	NM_002914:NM_181471:
5982	RFC2	replication factor C (activator 1) 2, 40kDa	0.26	GAGGAGAACCATGGAAATCTA	NM_002914:	NM_002914:NM_181471:
5984	RFC4	replication factor C (activator 1) 4, 37kDa	0.25	CAGAAGTCTATTATCACAGAA	NM_002916:	NM_002916:NM_181573:
5984	RFC4	replication factor C (activator 1) 4, 37kDa	0.57	CCGATTCTGTCTTATCTGTAA	NM_002916:	NM_002916:NM_181573:
117584	RFFL	ring finger and FYVE-like domain containing 1	-0.77	TTGGTGAGAAATGAAATACAA	NM_057178:	NM_001017368:NM_057178:
117584	RFFL	ring finger and FYVE-like domain containing 1	0.13	ATCGGTTTCTTCAGTGCCTTA	NM_057178:	NM_001017368:NM_057178:
55312	RFK	riboflavin kinase	0.72	ACGATGTAATTTAATGCTAAA	NM_018339:	NM_018339:
55312	RFK	riboflavin kinase	-0.07	CACGATGTAATTTAATGCTAA	NM_018339:	NM_018339:
5987	RFP	ret finger protein	0.08	CATGCAGATTGTGAAATGTAA	NM_030950:	NM_030950:NM_006510:
5987	RFP	ret finger protein	-1.39	TTGGATCATGAGACACTCGAA	NM_030950:	NM_030950:NM_006510:
5988	RFPL1	ret finger protein-like 1	-0.02	TAGTTTATAAATTGAGTCCTA	NM_021026:	NM_021026:
5988	RFPL1	ret finger protein-like 1	0.88	ACAATTCATGATTATACTTAA	NM_021026:	NM_021026:
10739	RFPL2	ret finger protein-like 2	1.05	CAAGTTCAAATTAATGTATTA	NM_006605:	NM_006605:
10739	RFPL2	ret finger protein-like 2	1.64	CTGCAAGTTCAAATTAATGTA	NM_006605:	NM_006605:
10738	RFPL3 (ret fir	ret finger protein-like 3	-0.03	ATGGGACATTTCTATAATCTA	NM_006604:	NM_006604:
10738	RFPL3 (ret fir	ret finger protein-like 3	0.93	TAAGTTCAAATCAATGTTTAA	NM_006604:	NM_006604:
55159	RFWD3	ring finger and WD repeat domain 3	0.89	AGGGACGTTATGTGAATCTTA	NM_018124:	NM_018124:
55159	RFWD3	ring finger and WD repeat domain 3	0.22	CTGAGTTGTCCTGTCACTTAA	NM_018124:	NM_018124:
5989	RFX1	regulatory factor X, 1 (influences HLA class II expression)	0.53	CCGTGCGAAACTGTTAACTTA	NM_002918:	NM_002918:
5989	RFX1	regulatory factor X, 1 (influences HLA class II expression)	-2.77	CACCGTTGGCATGGCAACACA	NM_002918:	NM_002918:
5990	RFX2	regulatory factor X, 2 (influences HLA class II expression)	1.18	CGCGATTTCTAACGAAATGCA	NM_000635:	NM_000635:NM_134433:
5990	RFX2	regulatory factor X, 2 (influences HLA class II expression)	0.52	CTCACAGTTAACGGATTGTAA	NM_000635:	NM_000635:NM_134433:
8625	RFXANK	regulatory factor X-associated ankyrin-containing protein	0.72	AACAGGCGGCTACACAGACAT	NM_003721:	NM_003721:NM_134440:
8625	RFXANK	regulatory factor X-associated ankyrin-containing protein	0.17	AACTGTGGTCCTCAGTCTCTT	NM_003721:	NM_003721:NM_134440:
57529	RGAG1	retrotransposon gag domain containing 1	-7.33	AAGGCCCATACCAACAAGTAA	NM_020769:	NM_020769:
57529	RGAG1	retrotransposon gag domain containing 1	-4.79	CAGGGCATATATGACTCCCTA	NM_020769:	NM_020769:
5863	RGL2	ral guanine nucleotide dissociation stimulator-like 2	0.50	ATCCTGAATGGTGGCAATTAT	NM_004761:	NM_004761:

5863	RGL2	ral guanine nucleotide dissociation stimulator-like 2	1.05	CCGAAACTTCTCTTCAGTTTA	NM_004761:	NM_004761:
5995	RGR (retinal (	retinal G protein coupled receptor	-5.10	AACCATCACCCTAATAATATA	NM_002921:	NM_002921:NM_001012722:NM_001012720:
5995	RGR (retinal (	retinal G protein coupled receptor	0.50	CACGATCAATGCCATCAACTA	NM_002921:	NM_002921:NM_001012722:NM_001012720:
8786	RGS11	regulator of G-protein signalling 11	1.18	AGCGTCCAGCACACAAATAAA	NM_003834:	NM_183337:NM_003834:
8786	RGS11	regulator of G-protein signalling 11	0.34	CCCAAGGTTCCTGAAGTCTGA	NM_003834:	NM_183337:NM_003834:
6002	RGS12	regulator of G-protein signalling 12	0.28	TAGGCAAGTCTAATTCTATTA	NM_198430:	NM_198227:NM_198230:NM_002926:NM_198229:NM_198430:
6002	RGS12	regulator of G-protein signalling 12	-6.33	CAGGACTTTGGCACCCGAGAA	NM_198430:	NM_198587:NM_198227:NM_198230:NM_002926:NM_198229:NM_198430:
6003	RGS13	regulator of G-protein signalling 13	-0.69	CCAGAGTGCCATCGAAGGTAA	NM_144766:	NM_144766:NM_002927:
6003	RGS13	regulator of G-protein signalling 13	-0.22	CACAGTGACGAGAATATTCAA	NM_144766:	NM_144766:NM_002927:
10636	RGS14 (regul	regulator of G-protein signalling 14	0.57	ACCCACATAGACTATACTGTA	NM_006480:	NM_006480:
10636	RGS14 (regul	regulator of G-protein signalling 14	-1.31	CCCAGTGAACATCGACCGTCA	NM_006480:	NM_006480:
6004	RGS16	regulator of G-protein signalling 16	0.81	CAGCATGTTATATTCTTATAA	NM_002928:	NM_002928:
6004	RGS16	regulator of G-protein signalling 16	-0.65	TGCGAGATATTTATACCTCAA	NM_002928:	NM_002928:
26575	RGS17	regulator of G-protein signalling 17	-0.48	AGGGCTGAGATGGGAAATAAA	NM_012419:	NM_012419:
26575	RGS17	regulator of G-protein signalling 17	0.11	TAGGATGATATATGAAGATTA	NM_012419:	NM_012419:
10287	RGS19	regulator of G-protein signalling 19	1.50	TTATATGTTCATGAACTTTAA	NM_005873:	NM_005873:
10287	RGS19	regulator of G-protein signalling 19	0.00	GCGGGAGGGCATCAACAAGAA	NM_005873:	NM_005873:
5997	RGS2	regulator of G-protein signalling 2, 24kDa	0.76	CTCATGCTACATGAAATGTAA	NM_002923:	NM_002923:
5997	RGS2	regulator of G-protein signalling 2, 24kDa	-0.41	CTCACTGTGTACAGAACGCAA	NM_002923:	NM_002923:
8601	RGS20	regulator of G-protein signalling 20	-1.22	CTGCTATATATTCACCATGTA	NM_003702:	NM_170587:NM_003702:
8601	RGS20	regulator of G-protein signalling 20	0.79	CACATATTCGATGATGCTCAA	NM_003702:	NM_170587:NM_003702:
5998	RGS3	regulator of G-protein signalling 3	0.71	CGCGTTGACCAAGTTCCTTAA	NM_130795:	NM_144488:NM_021106:NM_130795:NM_144489:NM_134427:
5998	RGS3	regulator of G-protein signalling 3	0.22	CAGACGGATAGACATACGGAA	NM_130795:	NM_144488:NM_021106:NM_130795:NM_144489:NM_134427:
5999	RGS4	regulator of G-protein signalling 4	-0.29	CTGAGACTAAATGAGAGGAAA	NM_005613:	NM_005613:
5999	RGS4	regulator of G-protein signalling 4	0.31	GTACGTGTTATTATTATTATA	NM_005613:	NM_005613:
8490	RGS5	regulator of G-protein signalling 5	-0.19	ACAGGCTAAGGCATAGACAAA	NM_003617:	NM_003617:
8490	RGS5	regulator of G-protein signalling 5	0.52	AACGAGAGCAATGACTATTTA	NM_003617:	NM_003617:
9628	RGS6	regulator of G-protein signalling 6	0.53	ATCGACAGACATTGTTTGAAA	NM_004296:	NM_004296:
9628	RGS6	regulator of G-protein signalling 6	-0.51	CACGACTATCACTTGAGATTA	NM_004296:	NM_004296:
6000	RGS7 (regula	regulator of G-protein signalling 7	-4.09	ACGGATCATCTTGTAGCATGA	NM_002924:	NM_002924:
6000	RGS7 (regula	regulator of G-protein signalling 7	0.33	AAGTATATATCAATAAGTATA	NM_002924:	NM_002924:
85397	RGS8	regulator of G-protein signalling 8	-0.09	AAGATCATATTCTAATGTGAA	NM_033345:	NM_033345:
85397	RGS8	regulator of G-protein signalling 8	-1.20	ACAGCTATTCTTCCAGACAAA	NM_033345:	NM_033345:
8787	RGS9	regulator of G-protein signalling 9	1.04	CTGACACCAGTTTCAAATTTA	NM_003835:	NM_003835:
8787	RGS9	regulator of G-protein signalling 9	1.73	CAAATAGGTGTTTGAACTGTA	NM_003835:	NM_003835:
6005	RHAG	Rh-associated glycoprotein	0.11	TTGCAACGAGCTCAAATGCTA	NM_000324:	NM_000324:
6005	RHAG	Rh-associated glycoprotein	-1.66	CAGTGAGTAAATACAGAGTAA	NM_000324:	NM_000324:
25807	RHBDD3	rhomboid domain containing 3	0.11	CTAGTACGTGTTTAGAATAAA	NM_012265:	NM_012265:
25807	RHBDD3	rhomboid domain containing 3	-1.37	CCCGAGCTCCTACTCTGTCTA	NM_012265:	NM_012265:
64285	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	-0.02	CCACCTCATGTGGCCAATAAA	NM_022450:	NM_022450:
64285	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	0.10	CGGGCATTTATTATACTACTT	NM_022450:	NM_022450:
6010	RHO	rhodopsin (opsin 2, rod pigment) (retinitis pigmentosa 4, autosomal dc	-2.24	CACGCTCAAGCCGGAGGTCAA	NM_000539:	NM_000539:
6010	RHO	rhodopsin (opsin 2, rod pigment) (retinitis pigmentosa 4, autosomal dc	0.01	CTCGTGTGGAATCGACTACTA	NM_000539:	NM_000539:
387	RHOA	ras homolog gene family, member A	-1.01	TAGGCTGTAACTACTTTATAA	NM_001664:	NM_001664:
387	RHOA	ras homolog gene family, member A	-2.14	TACCTTATAGTTACTGTGTAA	NM_001664:	NM_001664:
388	RHOB	ras homolog gene family, member B	0.74	CACAATTGTTTCATTGTTTGA	NM_004040:	NM_004040:
388	RHOB	ras homolog gene family, member B	0.29	CCCAGTGGTACTTCTACTAAA	NM_004040:	NM_004040:
389	RHOC	ras homolog gene family, member C	1.11	CACCATGGCTGCAATCCGAAA	NM_175744:	NM_175744:
389	RHOC	ras homolog gene family, member C	-1.42	CCCTACTGTCTTTGAGAACTA	NM_175744:	NM_175744:
57381	RHOJ	ras homolog gene family, member J	0.04	CCCGATTATAAGAAGACATGA	NM_020663:	NM_020663:
57381	RHOJ	ras homolog gene family, member J	0.05	ACCAAATTAGCCTAAAGACAA	NM_020663:	NM_020663:
58480	RHOU	ras homolog gene family, member U	-0.25	ACCCAGTTACTTATGATTTAA	NM_021205:	NM_021205:
58480	RHOU	ras homolog gene family, member U	-1.55	CCCAGGTATTACACAAGCCAA	NM_021205:	NM_021205:
9743	RICS	Rho GTPase-activating protein	0.11	ACCGCTGTAACTCCTATGATA	NM_014715:	NM_014715:
9743	RICS	Rho GTPase-activating protein	-0.05	CCCGCTCAGATTATCATGTCA	NM_014715:	NM_014715:
6015	RING1	ring finger protein 1	-1.20	CAGCCAATAAGAGGACACAAA	NM_002931:	NM_002931:
6015	RING1	ring finger protein 1	-3.61	CTGGAGCTGGTGAATGAGAAA	NM_002931:	NM_002931:
83732	RIOK1	RIO kinase 1 (yeast)	1.65	GCCCAACAAGATAATATTCTA	NM_031480:	NM_031480:NM_153005:
83732	RIOK1	RIO kinase 1 (yeast)	-0.73	TACCATGTCCAGAACCAATAA	NM_031480:	NM_031480:NM_153005:
55781	RIOK2	RIO kinase 2 (yeast)	0.97	AACGCGATTATCATAAACATA	NM_018343:	NM_018343:
55781	RIOK2	RIO kinase 2 (yeast)	-0.24	CGCGGTTGAAATGGGCATGAA	NM_018343:	NM_018343:
8780	RIOK3	RIO kinase 3 (yeast)	-0.14	ATGCGGCAGTTATATCATGAA	NM_003831:	NM_003831:NM_145906:
8780	RIOK3	RIO kinase 3 (yeast)	-2.62	CTGGCTGTATTAGTACAGGAA	NM_003831:	NM_003831:NM_145906:
8737	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	-0.56	CCGACATTTCCTGGCATTGAA	NM_003804:	NM_003804:
8737	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	-0.07	TACCACTAGTCTGACGGATAA	NM_003804:	NM_003804:
8767	RIPK2	receptor-interacting serine-threonine kinase 2	1.58	ACGTATGATCTCTCTAATAGA	NM_003821:	NM_003821:
8767	RIPK2	receptor-interacting serine-threonine kinase 2	0.03	CACAAGGACATCGACCTGTTA	NM_003821:	NM_003821:
11035	RIPK3	receptor-interacting serine-threonine kinase 3	0.48	ACCGCTCGTTAACATATACAA	NM_006871:	NM_006871:
11035	RIPK3	receptor-interacting serine-threonine kinase 3	-0.03	CAGCCTGATGTCGTGCGTCAA	NM_006871:	NM_006871:
54101	RIPK4	receptor-interacting serine-threonine kinase 4	-0.66	AAGCCTGATGACGAAGTGAAA	NM_020639:	NM_020639:
54101	RIPK4	receptor-interacting serine-threonine kinase 4	-0.22	CACACGCAGTATGAAGATAAA	NM_020639:	NM_020639:
25778	RIPK5	receptor interacting protein kinase 5	1.44	TAGAGCTTGTTTGATGTTAAA	NM_015375:	NM_199462:NM_015375:
25778	RIPK5	receptor interacting protein kinase 5	0.71	TTGCTTCATCGTAAACCTAAA	NM_015375:	NM_199462:NM_015375:
25907	RIS1	Ras-induced senescence 1	-2.33	GCCGGTGTGCTTCGTGCTGTA	NM_015444:	NM_015444:
25907	RIS1	Ras-induced senescence 1	-2.42	CCGCTGCATTTCTGCTGCCTA	NM_015444:	NM_015444:
51320	RKHD2	ring finger and KH domain containing 2	0.20	TAGGCTAAAGTTGTTAGTAAA	NM_016626:	NM_016626:
51320	RKHD2	ring finger and KH domain containing 2	1.45	CCGCGCAAGAATGATATCCAA	NM_016626:	NM_016626:
84206	RKHD3	ring finger and KH domain containing 3	0.93	CCACTTGTTTATGTATATGTA	NM_032246:	NM_032246:
84206	RKHD3	ring finger and KH domain containing 3	0.81	CACAACGGAAACAATAACAAT	NM_032246:	NM_032246:
6017	RLBP1	retinaldehyde binding protein 1	-0.41	TACGACTTAGAGTCTGTGAAA	NM_000326:	NM_000326:
6017	RLBP1	retinaldehyde binding protein 1	-0.03	TTGTGTAAGGTTGTATTTCAA	NM_000326:	NM_000326:
117579	RLN3	relaxin 3	-1.63	CCGGATGCAGATGCTGATGAA	NM_080864:	NM_080864:
117579	RLN3	relaxin 3	-1.92	CCCGGTGGAGACGATCAGACA	NM_080864:	NM_080864:
51289	RLN3R1	relaxin 3 receptor 1	-0.09	CACGATAGCCACCATGAATAA	NM_016568:	NM_016568:
51289	RLN3R1	relaxin 3 receptor 1	-1.76	CTGGCGCAAGTCCTCTATCAA	NM_016568:	NM_016568:
339403	RLN3R2	relaxin 3 receptor 2	-0.31	CCGATGCCTGTCAAATTCCTA	NM_181885:	NM_181885:
339403	RLN3R2	relaxin 3 receptor 2	1.37	CAGGCGGTGGGTCGCAAGCAA	NM_181885:	NM_181885:
6041	RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	0.13	CACCTGGACATGTCAATTAAA	NM_021133:	NM_021133:
6041	RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	0.02	CCAGACTACACTAGTCCATAA	NM_021133:	NM_021133:
9921	RNF10	ring finger protein 10	-1.99	CAGGATTGAGATAGAGGAGAA	NM_014868:	NM_014868:
9921	RNF10	ring finger protein 10	-0.01	TTCGATGAAGAAACCACGGAA	NM_014868:	NM_014868:
7844	RNF103	ring finger protein 103	1.66	CTAGCAAGACTTTACAAGATA	NM_005667:	NM_005667:
7844	RNF103	ring finger protein 103	0.48	AAGCGATTTGTGGTTCTCATA	NM_005667:	NM_005667:
26994	RNF11	ring finger protein 11	1.39	TAGATTATCAGGTTCTGTTAA	NM_014372:	NM_014372:
26994	RNF11	ring finger protein 11	1.50	ATGGAAAGACTTAAAGATGAA	NM_014372:	NM_014372:

54778	RNF111	ring finger protein 111	-0.46	AAGAGCATACCTTATGATTAA	NM_017610:	NM_017610:
54778	RNF111	ring finger protein 111	-0.04	CCAAGCCTTGATAATTATGAA	NM_017610:	NM_017610:
7737	RNF113A	ring finger protein 113A	-3.76	TAGGTTTCCCATAATTCTTAA	NM_006978:	NM_006978:
7737	RNF113A	ring finger protein 113A	2.59	AGCGAAAGAATTGATTGCTAA	NM_006978:	NM_006978:
140432	RNF113B	ring finger protein 113B	-4.74	AAGGATCACATGCTACAACTA	NM_178861:	NM_178861:
140432	RNF113B	ring finger protein 113B	0.01	AACGGGAAGGAAATCCTCTTA	NM_178861:	NM_178861:
51132	RNF12	ring finger protein 12	0.04	TAGCACAAGTTAAATTTACAA	NM_016120:	NM_183353:NM_016120:
51132	RNF12	ring finger protein 12	1.36	CAGACACAAACTGGTTTCATA	NM_016120:	NM_183353:NM_016120:
55298	RNF121	ring finger protein 121	1.35	TAACTTATTATTCAAGATCAA	NM_018320:	NM_018320:NM_194453:
55298	RNF121	ring finger protein 121	1.79	TGGTCTTAACTTATTATTCAA	NM_018320:	NM_018320:NM_194453:
79845	RNF122	ring finger protein 122	0.51	CTAGTTCTATACTTAAATTGA	NM_024787:	NM_024787:
79845	RNF122	ring finger protein 122	0.37	AGGGCTAGTTCTATACTTAAA	NM_024787:	NM_024787:
63891	RNF123	ring finger protein 123	0.00	CAGGGCCACAGTGAGCATTAA	NM_022064:	NM_022064:
63891	RNF123	ring finger protein 123	-0.67	CTGCGCTACTATTGGGATGAA	NM_022064:	NM_022064:
54941	RNF125	ring finger protein 125	-1.45	ATGGTTAGGCACGATAACTAA	NM_017831:	NM_017831:
54941	RNF125	ring finger protein 125	0.56	CTCGGTTTGCAAATTAGATAA	NM_017831:	NM_017831:
55658	RNF126	ring finger protein 126	-0.58	TACACTACTTACAAAGAGAAA	NM_017876:	NM_194460:NM_017876:
55658	RNF126	ring finger protein 126	-0.01	CCGGATTATATCTGTCCAAGA	NM_017876:	NM_194460:NM_017876:
11342	RNF13	ring finger protein 13	0.28	CAGAACTAATGATGTATTGAA	NM_007282:	NM_183382:NM_183383:NM_183384:NM_183381:NM_007282:
11342	RNF13	ring finger protein 13	0.36	TTGGAATGAAAGTATAGCCAA	NM_007282:	NM_183382:NM_183383:NM_183384:NM_183381:NM_007282:
55819	RNF130	ring finger protein 130	1.49	TCCGAGAACAGGAGAAATCAA	NM_018434:	NM_018434:
55819	RNF130	ring finger protein 130	0.06	CAAGCTGTTAACCGAAGATCA	NM_018434:	NM_018434:
168433	RNF133	ring finger protein 133	0.10	AACGCTATAAGCCTAATGACA	NM_139175:	NM_139175:
168433	RNF133	ring finger protein 133	-4.34	ACCGGAGATGGCAGCGATTAA	NM_139175:	NM_139175:
84282	RNF135	ring finger protein 135	-2.14	CTCCTGGGAGATAACCTCTAA	NM_032322:	NM_032322:NM_197939:
84282	RNF135	ring finger protein 135	0.00	CAAGCTGAGGAGACTAAGTTA	NM_032322:	NM_032322:NM_197939:
379013	RNF138P1 (ri	ring finger protein 138 pseudogene 1	0.43	AAGGTGTACCACGGTTGTAAA	NM_022731:	NR_001575:
11236	RNF139	ring finger protein 139	1.00	TCCGTTTACTGTGATGTGCTA	NM_007218:	NM_007218:
11236	RNF139	ring finger protein 139	1.38	AAGGGAGCCGCTTACAAGAAA	NM_007218:	NM_007218:
9604	RNF14	ring finger protein 14	-0.35	CGGGATATTTAGGGTACTATT	NM_004290:	NM_004290:NM_183398:NM_183399:NM_183400:NM_183401:
9604	RNF14	ring finger protein 14	0.53	AGCAGAGTTATTTGCCCGTTA	NM_004290:	NM_004290:NM_183398:NM_183399:NM_183400:NM_183401:
50862	RNF141	ring finger protein 141	0.63	CTCGATTTCCTTATATCTAAT	NM_016422:	NM_016422:
50862	RNF141	ring finger protein 141	-1.14	CACTGATAAATTGTGCAATAA	NM_016422:	NM_016422:
9781	RNF144	ring finger protein 144	1.13	CAGGAATAACTGTCCAAATTA	NM_014746:	NM_014746:
9781	RNF144	ring finger protein 144	2.91	GTGGAGAAAGTGTATTCTTTA	NM_014746:	NM_014746:
81847	RNF146	ring finger protein 146	0.63	TGGCATAAGACCATTACTAAA	NM_030963:	NM_030963:
81847	RNF146	ring finger protein 146	1.33	CTGATGGACAGTGCACAGTAA	NM_030963:	NM_030963:
284996	RNF149	ring finger protein 149	0.74	TAGAGTTTAAGCAGATTTAAT	NM_173647:	NM_173647:
284996	RNF149	ring finger protein 149	-0.57	CCCATCTGTAGTGTATGTGAA	NM_173647:	NM_173647:
57484	RNF150	ring finger protein 150	-1.28	CCGGAACGCGTTCCTGCAGAA	XM_371709:	NM_020724:
146310	RNF151	ring finger protein 151	-5.43	TCCGGTGGCTAGCCAGACAAA	XM_370927:	XM_370927:
146310	RNF151	ring finger protein 151	0.45	AAGGTTGTCCACATGAATAAA	XM_370927:	XM_370927:
114804	RNF157 (ring	ring finger protein 157	0.58	TCGGGTAGCCATCACCATCTA	XM_290732:	NM_052916:
114804	RNF157 (ring	ring finger protein 157	-0.71	AAGCGTGAAAGCACTGGACAA	XM_290732:	NM_052916:
115992	RNF166	ring finger protein 166	-1.48	CAGTTACTCTTCATATTGCAA	NM_178841:	NM_178841:
115992	RNF166	ring finger protein 166	-0.15	CTGGTGAAGCACTGTGTGGAA	NM_178841:	NM_178841:
26001	RNF167	ring finger protein 167	0.10	CTGGATCCCGTCTGTATTTAT	NM_015528:	NM_015528:
26001	RNF167	ring finger protein 167	-1.89	ATGGTGTGGAATAGTGAGGAA	NM_015528:	NM_015528:
81790	RNF170	ring finger protein 170	1.33	ATACTTCGATATCATATTCTA	NM_030954:	NM_030954:
81790	RNF170	ring finger protein 170	1.44	CAGCAGGTACCTATATGATAA	NM_030954:	NM_030954:
221687	RNF182	ring finger protein 182	-0.21	AAACCCATTACTAATGATTAA	NM_152737:	NM_152737:
221687	RNF182	ring finger protein 182	0.99	AAGACTTTGTGTTGTAGTCTA	NM_152737:	NM_152737:
138065	RNF183	ring finger protein 183	1.63	AAGTGTTCTGTATTCATTAAA	NM_145051:	NM_145051:
138065	RNF183	ring finger protein 183	-0.17	GAGCTTCAATTCTGTGGGTAA	NM_145051:	NM_145051:
91445	RNF185	ring finger protein 185	-1.54	CTGAATCTTATTGAGGGACTA	NM_152267:	NM_152267:
91445	RNF185	ring finger protein 185	0.09	ACCACCATCCTCAGAAGCCAA	NM_152267:	NM_152267:
54546	RNF186	ring finger protein 186	1.20	TAGAATAGAACTGGAATTCCA	NM_019062:	NM_019062:
54546	RNF186	ring finger protein 186	1.68	TGCAGTATTGATGCCATTGTA	NM_019062:	NM_019062:
25897	RNF19	ring finger protein 19	1.94	AACCTCAATGATAGCAGTTAA	NM_015435:	NM_015435:NM_183419:
25897	RNF19	ring finger protein 19	3.17	CAGGCTTTAGTGAATAACTTT	NM_015435:	NM_015435:NM_183419:
6045	RNF2	ring finger protein 2	-0.11	GAGAGTTATTTGTGACTATAA	NM_007212:	NM_007212:
6045	RNF2	ring finger protein 2	0.69	TTGGGTTGCCACATCAGTTTA	NM_007212:	NM_007212:
56254	RNF20	ring finger protein 20	1.12	CAGGAACTTATTCATTAACCA	NM_019592:	NM_019592:
56254	RNF20	ring finger protein 20	0.84	ACGGGTGAATTCCAAAGGTTA	NM_019592:	NM_019592:
11237	RNF24	ring finger protein 24	-0.09	ACCTGCTATCAAATCATCTAA	NM_007219:	NM_007219:
11237	RNF24	ring finger protein 24	-0.90	CTGCGGGTTTGCCTCAAGAAA	NM_007219:	NM_007219:
64320	RNF25	ring finger protein 25	0.19	CAAGGAGCCCATGGACCTAAA	NM_022453:	NM_022453:
64320	RNF25	ring finger protein 25	1.51	TGGGCGAAACCCAGAAAGCTA	NM_022453:	NM_022453:
79102	RNF26	ring finger protein 26	-0.38	CACTAGGGTCCAAATACAGAA	NM_032015:	NM_032015:
79102	RNF26	ring finger protein 26	1.61	TCGGATGATCTTAAACCTTTG	NM_032015:	NM_032015:
55072	RNF31	ring finger protein 31	1.17	CAGGACAATAACGTCATGTTT	NM_017999:	NM_017999:
55072	RNF31	ring finger protein 31	-1.34	ACGCATGAACGACCCAGAATA	NM_017999:	NM_017999:
140545	RNF32	ring finger protein 32	-0.05	TTCAGTGGTATTCAACATCAA	NM_030936:	NM_030936:
140545	RNF32	ring finger protein 32	-0.04	CCGCTAATAGTCTGTCCTAAA	NM_030936:	NM_030936:
80196	RNF34	ring finger protein 34	0.49	CACTTTATTAGTCATGTATAT	NM_025126:	NM_025126:NM_194271:
80196	RNF34	ring finger protein 34	0.51	CGGCACAGGTACAAAGTGAAA	NM_025126:	NM_025126:NM_194271:
140691	RNF36	ring finger protein 36	0.22	ATGAGTCATAATATTATACAA	NM_080745:	NM_080745:NM_182985:
140691	RNF36	ring finger protein 36	0.12	AAGGAACCAAACTGATCTAAA	NM_080745:	NM_080745:NM_182985:
152006	RNF38	ring finger protein 38	-3.85	GAGAGGGTTGTTGGTAATAAA	NM_022781:	NM_194331:NM_194332:NM_194329:NM_194330:NM_022781:NM_194328:
152006	RNF38	ring finger protein 38	0.50	ACGTGTGTATGAGATCCTATA	NM_022781:	NM_194331:NM_194332:NM_194329:NM_194330:NM_022781:NM_194328:
80352	RNF39	ring finger protein 39	0.65	TTGCAGGAGTATTAATAGCAA	NM_025236:	NM_025236:NM_170769:NM_170770:
80352	RNF39	ring finger protein 39	0.09	CCCAACATCCAAGTCATCTAA	NM_025236:	NM_025236:NM_170769:
9810	RNF40	ring finger protein 40	-3.45	AAGCGGAAGCTTCGAGAAGTA	NM_014771:	NM_014771:NM_194352:
9810	RNF40	ring finger protein 40	-0.56	GCGCATCGAGTTTGAGCAGAA	NM_014771:	NM_014771:NM_194352:
54894	RNF43	ring finger protein 43	-0.65	CAGGCACTATGTTAAGAAATA	NM_017763:	NM_017763:
54894	RNF43	ring finger protein 43	1.23	CAGGCATTATCCCATTTGGAA	NM_017763:	NM_017763:
6049	RNF6	ring finger protein (C3H2C3 type) 6	-1.77	AGGGTCTAACATAGCAAACAA	NM_005977:	NM_183043:NM_005977:NM_183044:
6049	RNF6	ring finger protein (C3H2C3 type) 6	1.05	CGGGATAGTATTGCAAATAGA	NM_005977:	NM_183043:NM_005977:NM_183044:
9616	RNF7	ring finger protein 7	0.58	CCAGTGAACAGGGTAAATAAA	NM_014245:	NM_014245:NM_183063:NM_183237:
9616	RNF7	ring finger protein 7	1.35	GGCCCAGATGATATAATTTAA	NM_014245:	NM_014245:NM_183063:NM_183237:
8732	RNGTT	RNA guanylyltransferase and 5'-phosphatase	-0.04	CAGGGTTGTTAAGTTGTACTA	NM_003800:	NM_003800:
8732	RNGTT	RNA guanylyltransferase and 5'-phosphatase	-0.69	CGGGATTTCTATATGGACATA	NM_003800:	NM_003800:
6051	RNPEP	arginyl aminopeptidase (aminopeptidase B)	-1.50	CACCAGGAAGATTTCTGGAAA	NM_020216:	NM_020216:

6051	RNPEP	arginyl aminopeptidase (aminopeptidase B)	-2.98	CTGGACATGAAGGCCATTGAA	NM_020216:	NM_020216:
57140	RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	0.36	CCGGGCAGGGCTGGAATTCGA	NM_018226:	NM_018226:
57140	RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	-4.67	CCGAGCCTATGTGGAGAAGTA	NM_018226:	NM_018226:
10073	RNUT1	RNA, U transporter 1	1.26	CAGATCCACAATGTAAATATA	NM_005701:	NM_005701:
10073	RNUT1	RNA, U transporter 1	0.01	CAGGCGAAACTCAACAGCAAA	NM_005701:	NM_005701:
6091	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	-2.93	CTGGCTTTATCGACACCGCAA	NM_002941:	NM_133631:NM_002941:
6091	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	-0.04	ATGACACATGACGCCAGATAA	NM_002941:	NM_133631:NM_002941:
6092	ROBO2	roundabout, axon guidance receptor, homolog 2 (Drosophila)	1.46	CACATTCAAAGCAATAATCAA	XM_031246:	NM_002942:
6092	ROBO2	roundabout, axon guidance receptor, homolog 2 (Drosophila)	0.06	CACGAGCTTGCCAGTAAATAA	XM_031246:	NM_002942:
64221	ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)	-0.64	CCCGGACGACAGATATTACAA	NM_022370:	NM_022370:
64221	ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)	-0.10	CCACCTGAGACTTGTTTATAA	NM_022370:	NM_022370:
54538	ROBO4	roundabout homolog 4, magic roundabout (Drosophila)	-3.53	CTCCTGTAGATTACTCCTGAA	NM_019055:	NM_019055:
54538	ROBO4	roundabout homolog 4, magic roundabout (Drosophila)	-1.20	CACCTCAGGAAGTGACTCTAA	NM_019055:	NM_019055:
6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	0.63	AACGGTTAGAACAAGAGGTAA	NM_005406:	NM_005406:
6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	0.06	CAAGCTCGAATTACATCTTTA	NM_005406:	NM_005406:
9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	-0.08	AAGCTACATATGGAGCTTAAA	NM_004850:	NM_004850:
9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	-12.17	ATGCACTTGTATAAAGCCATA	NM_004850:	NM_004850:
9991	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	-0.43	AAGTCTGACCCTTGTAGGAAA	NM_005156:	NM_005156:
9991	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	-0.50	CAGCCTTAATGTGAAATATAA	NM_005156:	NM_005156:
6094	ROM1	retinal outer segment membrane protein 1	-1.28	CAGAGCAATGTAGAAGGCCTA	NM_000327:	NM_000327:
6094	ROM1	retinal outer segment membrane protein 1	0.14	CTGGAGGCTGATTCTGATATA	NM_000327:	NM_000327:
54763	ROPN1	ropporin, rhophilin associated protein 1	0.55	TACACACTAATAAACAATTAA	NM_017578:	NM_017578:
54763	ROPN1	ropporin, rhophilin associated protein 1	0.16	AGGATAGCAATTTATCTCAAA	NM_017578:	NM_017578:
4919	ROR1	receptor tyrosine kinase-like orphan receptor 1	-0.37	CCCAGTGAGTAATCTCAGTAA	NM_005012:	NM_005012:
4919	ROR1	receptor tyrosine kinase-like orphan receptor 1	-2.61	CCGTACTGCGATGAAACTTCA	NM_005012:	NM_005012:
4920	ROR2	receptor tyrosine kinase-like orphan receptor 2	-6.00	CCGGTTTGGGAAAGTCTACAA	NM_004560:	NM_004560:
4920	ROR2	receptor tyrosine kinase-like orphan receptor 2	0.15	CTGGTGCTTTACGCAGAATAA	NM_004560:	NM_004560:
6095	RORA	RAR-related orphan receptor A	-2.27	CACCGAGAAGATGGAATACTA	NM_002943:	NM_002943:NM_134262:NM_134261:NM_134260:
6095	RORA	RAR-related orphan receptor A	-0.36	CCCGACGTCTTCAAATCCTTA	NM_002943:	NM_002943:NM_134262:NM_134261:NM_134260:
6096	RORB	RAR-related orphan receptor B	0.26	CAGGCTCTCTTCTATGATTTA	NM_006914:	NM_006914:
6096	RORB	RAR-related orphan receptor B	-0.16	CCTGTTGATTGTTCAAATATA	NM_006914:	NM_006914:
6097	RORC	RAR-related orphan receptor C	-0.03	CGGGTTCATCTGAGTAAACAT	NM_005060:	NM_001001523:NM_005060:
6097	RORC	RAR-related orphan receptor C	-0.19	AAGGAGCTCTTCAGCACTGAA	NM_005060:	NM_001001523:NM_005060:
6098	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	0.06	AAGGTAATTGCTCTAACTTTA	NM_002944:	NM_002944:
6098	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	1.20	ACCGAGAAGGGTTAAACTATA	NM_002944:	NM_002944:
6101	RP1	retinitis pigmentosa 1 (autosomal dominant)	0.03	ATGGTGTGGATCAGACTTCTA	NM_006269:	NM_006269:
6101	RP1	retinitis pigmentosa 1 (autosomal dominant)	0.44	AGGCTATTGCTCATCATTCAA	NM_006269:	NM_006269:
26095	RP11-142I17.	protein tyrosine phosphatase, non-receptor type 20B	-0.02	CCCACCCTAACACTTAACATA	NM_015605:	NM_015605:
26095	RP11-142I17.	protein tyrosine phosphatase, non-receptor type 20B	1.09	CTGGTGACAAGCTATACCTAA	NM_015605:	NM_015605:
340156	RP11-145H9.	hypothetical protein LOC340156	0.46	TTGGTGTTGATAAGAAATTAA	XM_373109:	NM_001012418:
340156	RP11-145H9.	hypothetical protein LOC340156	1.53	AAGAATAAACATGGACCTTAT	XM_373109:	NM_001012418:
84061	RP11-217H1.	implantation-associated protein	-4.25	CAGTGTGTCGTTTGCAAGCAA	NM_032121:	NM_032121:
84061	RP11-217H1.	implantation-associated protein	1.17	ACCGAGAAATTACTCCGTTAT	NM_032121:	NM_032121:
139596	RP11-311P8.	hypothetical protein MGC23937 similar to CG4798	-0.36	CCCATTAATGTCCTCATTCAA	NM_145052:	NM_145052:
139596	RP11-311P8.	hypothetical protein MGC23937 similar to CG4798	0.46	ACCGAATTCAACAATGAAGTA	NM_145052:	NM_145052:
8227	RP13-297E1	DNA segment on chromosome X and Y (unique) 155 expressed seque	0.22	CGGGATGAAACTCATGTACAA	NM_005088:	NM_005088:
8227	RP13-297E1	DNA segment on chromosome X and Y (unique) 155 expressed seque	1.10	TACAAGTCCTTTAAGATCAAA	NM_005088:	NM_005088:
6102	RP2	retinitis pigmentosa 2 (X-linked recessive)	0.06	CATCCTGTTATGATTATATTA	NM_006915:	NM_006915:
6102	RP2	retinitis pigmentosa 2 (X-linked recessive)	-0.01	TCCCTTAGTTAAGCTAAATTA	NM_006915:	NM_006915:
391013	RP3-340N1.3	similar to Group IIC secretory phospholipase A2 precursor (Phosphati	0.60	CCAGCCTGTGTTGAACAGCTA	XM_372769:	XM_372769:
391013	RP3-340N1.3	similar to Group IIC secretory phospholipase A2 precursor (Phosphati	-0.20	AAGTGCCTTCTTCTCATATTA	XM_372769:	XM_372769:
80020	RP5-1119A7.	hypothetical protein FLJ23322	-3.21	CAGTCCGTCGATAGCAACAAA	NM_024955:	NM_024955:
80020	RP5-1119A7.	hypothetical protein FLJ23322	-4.88	TCGAGCTAGCTACGAATCCAA	NM_024955:	NM_024955:
51765	RP6-213H19.	Mst3 and SOK1-related kinase	1.24	CAGCAAGTCGTTGCTATTAAA	NM_016542:	NM_016542:
51765	RP6-213H19.	Mst3 and SOK1-related kinase	0.24	CCAAACCTACGTCAAGATTAA	NM_016542:	NM_016542:
6117	RPA1	replication protein A1, 70kDa	-0.74	CAGGAATTATGTCGTAAGTCA	NM_002945:	NM_002945:
6117	RPA1	replication protein A1, 70kDa	0.62	CCGTGTGACGATCCCATGTTA	NM_002945:	NM_002945:
6118	RPA2	replication protein A2, 32kDa	2.43	AACAGTGGATTCGAAAGCTAT	NM_002946:	NM_002946:
6118	RPA2	replication protein A2, 32kDa	0.12	TACCAGGAGAGTACTTACATA	NM_002946:	NM_002946:
6119	RPA3	replication protein A3, 14kDa	-1.90	AAGGGAGTAAATCGACCCTCA	NM_002947:	NM_002947:
6119	RPA3	replication protein A3, 14kDa	-2.29	TCGCTGATTGGTGCCGAGAAA	NM_002947:	NM_002947:
29935	RPA4	replication protein A4, 34kDa	-4.96	AACGGTCAATGCACACATGAT	NM_013347:	NM_013347:
29935	RPA4	replication protein A4, 34kDa	-1.29	ACGGTGATGGATAAATTGACA	NM_013347:	NM_013347:
6121	RPE65	retinal pigment epithelium-specific protein 65kDa	0.89	TACGTAACTGCTCAAAGATTA	NM_000329:	NM_000329:
6121	RPE65	retinal pigment epithelium-specific protein 65kDa	0.68	AGGGACTATCATCTAAGATTA	NM_000329:	NM_000329:
6103	RPGR	retinitis pigmentosa GTPase regulator	0.64	ATGAGCCTGAATTCCAATGAA	NM_000328:	NM_001034853:NM_001023582:NM_000328:
6103	RPGR	retinitis pigmentosa GTPase regulator	0.75	CACAGCTTTGATAACAGATAT	NM_000328:	NM_001034853:NM_001023582:NM_000328:
57096	RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	-0.36	CACTTTCACTTTAGCAAGGTA	NM_020366:	NM_020366:
57096	RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	0.13	TTCATAGGTGATGGCTTTAAA	NM_020366:	NM_020366:
6134	RPL10	ribosomal protein L10	-0.91	CAGAAACAGGTTGACAACTCA	NM_006013:	NM_006013:
6134	RPL10	ribosomal protein L10	0.54	TGGCCTTATGTCAGTTGTCTA	NM_006013:	NM_006013:
6137	RPL13	ribosomal protein L13	0.81	CAAGCCCTGGATAATGCTTTA	NM_000977:	NM_033251:NM_000977:
6137	RPL13	ribosomal protein L13	1.91	TTGGTTAGTGACTGATGTAAA	NM_000977:	NM_033251:NM_000977:
6155	RPL27 (ribos	ribosomal protein L27	-2.44	ATCGCCAAGAGATCAAAGATA	NM_000988:	NM_000988:
6155	RPL27 (ribos	ribosomal protein L27	-2.53	CACAAGGTACTCTGTGGATAT	NM_000988:	XM_499470:NM_000988:XM_498236:
11224	RPL35 (ribos	ribosomal protein L35	-4.90	CCGTGTTCTCACAGTTATTAA	NM_007209:	NM_007209:
25873	RPL36	ribosomal protein L36	0.28	CTGCCCTCTCCCTGAAATAAA	NM_015414:	NM_033643:NM_015414:
6169	RPL38 (ribos	ribosomal protein L38	-3.14	AACGTGAAGTTTAAAGTTCGA	NM_000999:	NM_000999:NM_001035258:
6169	RPL38 (ribos	ribosomal protein L38	-2.89	TAAGGACAACGTGAAGTTTAA	NM_000999:	NM_000999:NM_001035258:
6124	RPL4	ribosomal protein L4	2.16	CAGGCAGTGAGAAACATGAAA	NM_000968:	NM_000968:
6124	RPL4	ribosomal protein L4	-0.68	ACAGGCAGTGAGAAACATGAA	NM_000968:	NM_000968:
6181	RPLP2	ribosomal protein, large, P2	-1.99	CAAGGTTATCAGTGAGCTGAA	NM_001004:	NM_001004:XM_498057:
6181	RPLP2	ribosomal protein, large, P2	-5.46	AAGGAGGAGTCTGAAGAGTCA	NM_001004:	NM_001004:
10557	RPP38	ribonuclease P/MRP 38kDa subunit	-2.11	CTCCAAAGTAATCTTGCATAA	NM_006414:	NM_183005:NM_006414:
10557	RPP38	ribonuclease P/MRP 38kDa subunit	0.32	ACGCTTGAGGACAGGCTTAAA	NM_006414:	NM_183005:NM_006414:
6223	RPS19	ribosomal protein S19	-1.06	AACAAGAAGCATTAGAACAAA	NM_001022:	NM_001022:
6223	RPS19	ribosomal protein S19	-4.45	CTGGGTTAATAAATTGCCTCA	NM_001022:	NM_001022:
6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	0.39	CCCAACATCATCACTCTGAAA	NM_002953:	NM_001006665:NM_002953:
6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	-0.06	TGCCACGTACTCCGCACTCAA	NM_002953:	NM_001006665:NM_002953:
6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	0.04	CCGAGTGAGATCGAAGATGGA	NM_021135:	NM_021135:NM_001006932:
6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	-0.45	CCGGAGGTCCTGAAGCGTCAA	NM_021135:	NM_021135:NM_001006932:
6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	0.31	AGCGCTGAGAATGGACAGCAA	NM_004586:	NM_004586:
6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	0.57	TCCAAACATTATCACTCTAAA	NM_004586:	NM_004586:
8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	-0.36	CAGGCTGTGCCTTTGACTTTA	NM_003942:	NM_003942:NM_001006944:
8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	-0.72	CGCCACCTTCATGGCATTCAA	NM_003942:	NM_003942:NM_001006944:
9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.19	AAGCCAGTCATTCGAGATGAA	NM_004755:	NM_004755:NM_182398:
9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.17	CTGGATCTCTTACGTAATTCA	NM_004755:	NM_182398:

27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	-0.25	CAGCGGTATACTGCTGAACAA	NM_014496:	NM_014496:
27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	0.35	GGCGAGGTAAATGGTCTTAAA	NM_014496:	NM_014496:
6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	0.44	AAGAAGGGTATCCTTTCATTA	NM_003161:	NM_003161:
6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-0.48	CAGAGAGTCAATGTCATTACA	NM_003161:	NM_003161:
6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-0.40	ACCGCAGAGAACCGGAAGAAA	NM_003952:	NM_001007071:NM_003952:
6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-3.16	CGGGCTGAGCGGAACATTCTA	NM_003952:	NM_001007071:NM_003952:
26750	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	0.18	CAGGATTGGTTTATATGATTA	NM_012424:	NM_012424:
26750	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	-0.01	CCGGGTTGTTTCACGAAGAAA	NM_012424:	NM_012424:
83694	RPS6KL1	ribosomal protein S6 kinase-like 1	-0.98	CGCGATGTTAGTGAGGACTAT	NM_031464:	NM_031464:
83694	RPS6KL1	ribosomal protein S6 kinase-like 1	0.03	CTGAATTTGATTGGAAAGGAA	NM_031464:	NM_031464:
3921	RPSA	ribosomal protein SA	1.24	TCGACATGAGTTGTACTTCTA	NM_002295:	NM_002295:NM_001012321:
3921	RPSA	ribosomal protein SA	0.66	TACCTGGGATTGCATATCAAA	NM_002295:	NM_002295:NM_001012321:
6237	RRAS (relate	related RAS viral (r-ras) oncogene homolog	-0.31	CCGGGTCACTGCTGTATATAA	NM_006270:	NM_006270:
6237	RRAS (relate	related RAS viral (r-ras) oncogene homolog	-1.77	CTCGGCCAAACTGCGTCTCAA	NM_006270:	NM_006270:
22800	RRAS2	related RAS viral (r-ras) oncogene homolog 2	0.45	AACAGTTAGCACGGCAGCTTA	NM_012250:	NM_012250:
22800	RRAS2	related RAS viral (r-ras) oncogene homolog 2	0.13	CTGAAGCTACAGGTTGTGAAA	NM_012250:	NM_012250:
6238	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	1.01	AAGAGATTGTAGAGAAGCTAA	NM_004587:	NM_004587:
6238	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	1.25	ATGGATATTTACGACACTCAA	NM_004587:	NM_004587:
10692	RRH (retinal	retinal pigment epithelium-derived rhodopsin homolog	0.75	CACAAATGCAATTATTATTAA	NM_006583:	NM_006583:
10692	RRH (retinal	retinal pigment epithelium-derived rhodopsin homolog	-1.31	CAGACATGGATCATTGTCCTA	NM_006583:	NM_006583:
6240	RRM1	ribonucleotide reductase M1 polypeptide	-8.92	CTGGTGGGTCTCTAGAAGCAA	NM_001033:	NM_001033:
6240	RRM1	ribonucleotide reductase M1 polypeptide	-4.24	AACGGATATATTGAGAATCAA	NM_001033:	NM_001033:
6241	RRM2	ribonucleotide reductase M2 polypeptide	0.61	CGGCGATAATAGCTTGATTTA	NM_001034:	NM_001034:
6241	RRM2	ribonucleotide reductase M2 polypeptide	0.58	GCGGGATTAAACAGTCCTTTA	NM_001034:	NM_001034:
50484	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	-1.24	AACCAGGAGGTTATCATGGTA	NM_015713:	NM_015713:
50484	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	-0.04	GAGCAGTTCAGTGGTACATAA	NM_015713:	NM_015713:
6248	RSC1A1	regulatory solute carrier protein, family 1, member 1	0.08	ATCCAATTTCATATTGGTTAA	NM_006511:	NM_006511:
6248	RSC1A1	regulatory solute carrier protein, family 1, member 1	-0.32	CTCAATCAGACTTCTGAGCAA	NM_006511:	NM_006511:
84870	RSPO3	R-spondin 3 homolog (Xenopus laevis)	1.32	CTCGATATCCAGATATAAATA	NM_032784:	NM_032784:
84870	RSPO3	R-spondin 3 homolog (Xenopus laevis)	0.66	AAGGGAAGCATTACTGGGTTA	NM_032784:	NM_032784:
89970	RSPRY1	ring finger and SPRY domain containing 1	0.04	CCTGATTATCTGAAACGTCAA	NM_133368:	NM_133368:
89970	RSPRY1	ring finger and SPRY domain containing 1	0.74	GCCCATTGTGTCGTAAAGAAA	NM_133368:	NM_133368:
6251	RSU1	Ras suppressor protein 1	-1.68	CACCGAGATATGCTAATTTAA	NM_012425:	NM_152724:NM_012425:
6251	RSU1	Ras suppressor protein 1	1.46	CAGCAAGAAAGCATTAGTAAA	NM_012425:	NM_152724:NM_012425:
83546	RTBDN	retbindin	-1.06	AACCTCGGGAATGATGGATTA	NM_031429:	NM_031429:
83546	RTBDN	retbindin	-0.27	CACCTTGGAGCTCTTATCTCA	NM_031429:	NM_031429:
27156	RTDR1	rhabdoid tumor deletion region gene 1	-1.14	CAACAGTATGGTGCGCATAAA	NM_014433:	NM_014433:
27156	RTDR1	rhabdoid tumor deletion region gene 1	0.18	CACAGTGATCACTGAAGGGAA	NM_014433:	NM_014433:
51750	RTEL1	regulator of telomere elongation helicase 1	-0.21	AAGCAGCAAGCCGACATCATA	NM_016434:	NM_016434:NM_032957:
51750	RTEL1	regulator of telomere elongation helicase 1	-0.73	CCAGATCACGTTTCAGACCAA	NM_016434:	NM_016434:NM_032957:
84816	RTN4IP1	reticulon 4 interacting protein 1	2.02	ACGAGGAAAGACTGTAATTAA	NM_032730:	NM_032730:
84816	RTN4IP1	reticulon 4 interacting protein 1	0.56	CACGAGGAAAGACTGTAATTA	NM_032730:	NM_032730:
65078	RTN4R	reticulon 4 receptor	-1.25	CGCGGTATATAGAGATATGCA	NM_023004:	NM_023004:
65078	RTN4R	reticulon 4 receptor	0.31	CAGCTGGACCTCAGCGATAAT	NM_023004:	NM_023004:
146760	RTN4RL1	reticulon 4 receptor-like 1	0.48	CAGAAACGCTGAATCCAATTA	NM_178568:	NM_178568:
146760	RTN4RL1	reticulon 4 receptor-like 1	1.02	ACCCTGCCATGTGGATTATAA	NM_178568:	NM_178568:
349667	RTN4RL2	reticulon 4 receptor-like 2	0.54	CACCCTGTGGCTCTTCTCCAA	NM_178570:	NM_178570:
349667	RTN4RL2	reticulon 4 receptor-like 2	0.00	CACCATCCTCTACCTGTTCAA	NM_178570:	NM_178570:
132112	RTP1	receptor transporter protein 1	-0.67	AAGACAGGATATCTTCCATAA	NM_153708:	NM_153708:
132112	RTP1	receptor transporter protein 1	0.81	TTGGGCAAGATCATTGGTTTA	NM_153708:	NM_153708:
344892	RTP2	receptor transporter protein 2	-1.32	TAGGGTGTCGTACTTACCATA	NM_001004312:	NM_001004312:
344892	RTP2	receptor transporter protein 2	-0.92	CGGAATGAGAGGATTGCATTA	NM_001004312:	NM_001004312:
83597	RTP3	receptor transporter protein 3	0.03	AAGCAAATGTTTCAGGAGTTA	NM_031440:	NM_031440:
83597	RTP3	receptor transporter protein 3	0.49	CAAGGTGGAGGAGGTAGTTAA	NM_031440:	NM_031440:
64108	RTP4	receptor transporter protein 4	1.30	CATAATGGATTTAGTAATAAA	NM_022147:	NM_022147:
64108	RTP4	receptor transporter protein 4	1.38	AACGAGCAAACCTGAAAGCTA	NM_022147:	NM_022147:
25914	RTTN	rotatin	-0.99	GTGGAAGTTTACTGACAGGAA	M55632:	NM_173630:
861	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 onc	0.91	CAGGAAAGTTAAGGTATCAAT	NM_001754:	NM_001001890:NM_001754:
861	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 onc	0.58	CTCCCTTTCATGTTAATCAAA	NM_001754:	NM_001001890:NM_001754:
860	RUNX2	runt-related transcription factor 2	-0.07	CAGCACGCTATTAAATCCAAA	NM_004348:	NM_001015051:NM_001024630:NM_004348:
860	RUNX2	runt-related transcription factor 2	-2.35	CAGCAGCACTCCATATCTCTA	NM_004348:	NM_001015051:NM_001024630:NM_004348:
6256	RXRA	retinoid X receptor, alpha	-0.67	TCCGTACGATTGTCTCTGAAA	NM_002957:	NM_002957:
6256	RXRA	retinoid X receptor, alpha	0.86	TTCGTGTAAGCAAGTACATAA	NM_002957:	NM_002957:
6257	RXRB	retinoid X receptor, beta	0.14	AGGGATCTGCTTGATATCCCA	NM_021976:	NM_021976:
6257	RXRB	retinoid X receptor, beta	0.07	GAGGGCAATCATTCTGTTTAA	NM_021976:	NM_021976:
6258	RXRG	retinoid X receptor, gamma	-0.63	CAGGGTGGAATGAATTGCTGA	NM_006917:	NM_006917:
6258	RXRG	retinoid X receptor, gamma	-1.67	CCGGATCTCTGGTTAAACACA	NM_006917:	NM_006917:
23429	RYBP	RING1 and YY1 binding protein	0.58	TAGCTTGAGTAAACTGTTCTA	NM_012234:	NM_012234:
23429	RYBP	RING1 and YY1 binding protein	0.66	TAGCCTGCATTTGCAATGGAA	NM_012234:	NM_012234:
6259	RYK	RYK receptor-like tyrosine kinase	0.02	CGGTCTTGATGCAGAACTTTA	NM_002958:	NM_001005861:NM_002958:
6259	RYK	RYK receptor-like tyrosine kinase	-1.39	CTGATCGGTCTTGATGCAGAA	NM_002958:	NM_001005861:NM_002958:
6261	RYR1	ryanodine receptor 1 (skeletal)	0.81	CCGAAGCGGATGAGAACGAAA	NM_000540:	NM_000540:
6261	RYR1	ryanodine receptor 1 (skeletal)	0.18	CTGGGAATGGACGATAGAGAA	NM_000540:	NM_000540:
6262	RYR2	ryanodine receptor 2 (cardiac)	-1.82	AAGAGTTGTCATGATGAGGAA	NM_001035:	NM_001035:
6262	RYR2	ryanodine receptor 2 (cardiac)	0.94	GAGGATGAAGTACGAGATATA	NM_001035:	NM_001035:
6263	RYR3 (ryano	ryanodine receptor 3	-0.29	ACGAGAAGATATGGAGACTAA	NM_001036:	NM_001036:
6263	RYR3 (ryano	ryanodine receptor 3	1.05	CACGACTGATTAACGATGTAA	NM_001036:	NM_001036:
6284	S100A13 (S1	S100 calcium binding protein A13	2.04	AACCGCACTCTTCCCAAATAA	XM_371380:	NM_001024211:NM_005979:NM_001024210:NM_001024213:NM_001024212:
6284	S100A13 (S1	S100 calcium binding protein A13	0.43	CAGGAAGAAGAAAGACCTGAA	XM_371380:	NM_001024211:NM_005979:NM_001024210:NM_001024213:NM_001024212:
6289	SAA2 (serum	serum amyloid A2	-4.43	AAGCTGAGATATGGCATATAA	NM_030754:	NM_030754:
6289	SAA2 (serum	serum amyloid A2	-0.01	ATGGCATATAATAGGCATCTA	NM_030754:	NM_030754:
55811	SAC	testicular soluble adenylyl cyclase	1.74	ACCGTGGACAATCATTTCTAA	NM_018417:	NM_018417:
55811	SAC	testicular soluble adenylyl cyclase	-2.40	CTGGCACAACTTTACCGGCAA	NM_018417:	NM_018417:
22908	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	0.69	AACGGTATGTAAGGTAGTATA	NM_014016:	NM_014016:
22908	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	0.76	AAGGACCAACTTAAACGTTAA	NM_014016:	NM_014016:
26278	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	-0.47	CCGGACAGACTTACTCTCAAA	NM_014363:	NM_014363:
26278	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	1.35	CCGCAAAGACTTGTTTATGAA	NM_014363:	NM_014363:
6294	SAFB	scaffold attachment factor B	-4.29	ACGGACTGTAGTAATGGATAA	NM_002967:	NM_002967:
6294	SAFB	scaffold attachment factor B	-0.09	CTGCCATATTGTAGCTCAATA	NM_002967:	NM_002967:
6295	SAG	S-antigen; retina and pineal gland (arrestin)	0.20	CGCCATAATCTGAAAGATGCA	NM_000541:	NM_000541:
6295	SAG	S-antigen; retina and pineal gland (arrestin)	0.09	CTCGAGTGATTATTACGTCAA	NM_000541:	NM_000541:
6299	SALL1	sal-like 1 (Drosophila)	-0.62	AAGGAGATCGTCACGAGTTAA	NM_002968:	NM_002968:
6299	SALL1	sal-like 1 (Drosophila)	-2.03	CACGACTAAAGGCAATCTTAA	NM_002968:	NM_002968:
6297	SALL2	sal-like 2 (Drosophila)	-2.39	AAGCTGGGCACTGCTTACCAA	NM_005407:	NM_005407:
6297	SALL2	sal-like 2 (Drosophila)	-0.61	CCCGGGAATGTCTCGGCGAAA	NM_005407:	NM_005407:
10284	SAP18	Sin3A-associated protein, 18kDa	0.49	AGCCACGGGATTGTATGAAAT	NM_005870:	NM_005870:
10284	SAP18	Sin3A-associated protein, 18kDa	0.02	AACGGCCTATAGGATTGTTAA	NM_005870:	NM_005870:

8819	SAP30 (Sin3	Sin3A-associated protein, 30kDa	-1.09	CCAGAGGTTGATTTATACCAA	NM_003864:	NM_003864:
8819	SAP30 (Sin3	Sin3A-associated protein, 30kDa	0.36	GACGTGGAATTGAGACTAATA	NM_003864:	NM_003864:
23098	SARM1	sterile alpha and TIR motif containing 1	-1.03	AGCGGTGTTGGCGACTAACAA	NM_015077:	NM_015077:
23098	SARM1	sterile alpha and TIR motif containing 1	-0.43	CTGCTATTAAATCCACATTAA	NM_015077:	NM_015077:
6303	SAT	spermidine/spermine N1-acetyltransferase	1.48	CAAGGTGGTGTGATCTTAATA	NM_002970:	NM_002970:
6303	SAT	spermidine/spermine N1-acetyltransferase	1.52	CTCCTTGAATATCTTTCGATA	NM_002970:	NM_002970:
6304	SATB1 (speci	special AT-rich sequence binding protein 1 (binds to nuclear matrix/sc	-0.03	TCCAAGCAATTCATACTATAA	NM_002971:	NM_002971:
6304	SATB1 (speci	special AT-rich sequence binding protein 1 (binds to nuclear matrix/sc	1.46	ACCGAATATACCAGGACGAAA	NM_002971:	NM_002971:
6305	SBF1	SET binding factor 1	0.36	CAGCGCCGAGCTCTTCCGTAA	NM_002972:	NM_002972:
6305	SBF1	SET binding factor 1	0.11	CCGCGTGGTGTGGCCCTGTTA	NM_002972:	NM_002972:
388228	SBK1	SH3-binding domain kinase 1	-3.13	ACGGGAGGTGAGCATCACCAA	XM_370948:	NM_001024401:
388228	SBK1	SH3-binding domain kinase 1	-2.99	CAGCGACGTCACCAAGCACTA	XM_370948:	NM_001024401:
6309	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	1.17	ATCGATATCACCATGATTTAA	NM_006918:	NM_006918:NM_001024956:
6309	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	0.98	AACGTTGGTATGATAATGATA	NM_006918:	NM_006918:NM_001024956:
22937	SCAP	SREBP cleavage-activating protein	-1.36	CTGGCCGACGCTCTTCAGCTA	NM_012235:	NM_012235:
22937	SCAP	SREBP cleavage-activating protein	1.47	CCTGACTGTAATAATATTAAA	NM_012235:	NM_012235:
51435	SCARA3	scavenger receptor class A, member 3	-0.84	CACCATCTTCACCAACATCAA	NM_016240:	NM_182826:NM_016240:
51435	SCARA3	scavenger receptor class A, member 3	-0.55	CCAGAGGAAGAGACCATGAAA	NM_016240:	NM_182826:NM_016240:
286133	SCARA5	scavenger receptor class A, member 5 (putative)	-0.07	AAGGTTTGCATTTAAGTTAAA	NM_173833:	NM_173833:
286133	SCARA5	scavenger receptor class A, member 5 (putative)	-2.04	CTGGGCCATACACGTGTTCAA	NM_173833:	NM_173833:
949	SCARB1	scavenger receptor class B, member 1	-1.04	CCGATCCATGAAGCTAATGTA	NM_005505:	NM_005505:
949	SCARB1	scavenger receptor class B, member 1	-1.54	TAGGGAGAGGCTCGTCAACAA	NM_005505:	NM_005505:
950	SCARB2	scavenger receptor class B, member 2	0.24	AAGACAGTTACCTTAACTTTA	NM_005506:	NM_005506:
950	SCARB2	scavenger receptor class B, member 2	-0.35	CTGGTCTAACTTCATTCAGTA	NM_005506:	NM_005506:
8578	SCARF1	scavenger receptor class F, member 1	0.21	AACCTACATGTTTGCTGATAA	NM_003693:	NM_145350:NM_145349:NM_145352:NM_003693: NM_145351:
8578	SCARF1	scavenger receptor class F, member 1	0.95	TAGATTGAATTTGATAAAGTA	NM_003693:	NM_145350:NM_145349:NM_145352:NM_003693: NM_145351:
91179	SCARF2	scavenger receptor class F, member 2	-2.11	CCGCTTAAAGACCGCCTCTTA	NM_153334:	NM_153334:NM_182895:
91179	SCARF2	scavenger receptor class F, member 2	0.74	CCGGAGGCAGAAACTACCCAA	NM_153334:	NM_153334:NM_182895:
374875	SCDR10	short-chain dehydrogenase/reductase 10	1.24	TCGCTGGCTCATGCAGGTAAA	NM_198705:	NM_198533:NM_198704:NM_198705:NM_198706: NM_198707:NM_198708:
374875	SCDR10	short-chain dehydrogenase/reductase 10	-3.90	CGCCTATTATTGGGATGACAA	NM_198705:	NM_198533:NM_198705:NM_198706:NM_198708:
29106	SCG3	secretogranin III	-1.22	AAGAGTGGATTGGATCATAAA	NM_013243:	NM_013243:
29106	SCG3	secretogranin III	2.38	ATGGTGAAATATGGAACAATA	NM_013243:	NM_013243:
7356	SCGB1A1	secretoglobin, family 1A, member 1 (uteroglobin)	-3.14	AAAGCCCAGAGAAAGCATCAT	NM_003357:	NM_003357:
7356	SCGB1A1	secretoglobin, family 1A, member 1 (uteroglobin)	-1.83	AATGAGGCTGCCATGGAACTT	NM_003357:	NM_003357:
6336	SCN10A	sodium channel, voltage-gated, type X, alpha	-0.02	CCGCTCCATGGCACTCTCTAA	NM_006514:	NM_006514:
6336	SCN10A	sodium channel, voltage-gated, type X, alpha	-3.94	CACAGGCGAATGTGTCATGAA	NM_006514:	NM_006514:
11280	SCN11A	sodium channel, voltage-gated, type XI, alpha	-2.25	CACGCCTACCTCATAGCTTCA	NM_014139:	NM_014139:
11280	SCN11A	sodium channel, voltage-gated, type XI, alpha	-1.43	CAGGAGGAGCTTGGTATACTA	NM_014139:	NM_014139:
6323	SCN1A	sodium channel, voltage-gated, type I, alpha	0.81	AAGCTTCCTTTACGTACAATA	NM_006920:	NM_006920:
6323	SCN1A	sodium channel, voltage-gated, type I, alpha	0.32	ACGCATCAATCTGGTGTTCAT	NM_006920:	NM_006920:
6324	SCN1B	sodium channel, voltage-gated, type I, beta	-1.09	ACCGCCATGCATGATGGGTAA	NM_001037:	NM_001037:
6324	SCN1B	sodium channel, voltage-gated, type I, beta	-1.10	CAGAGATGATTTACTGCTACA	NM_001037:	NM_001037:
6326	SCN2A2	sodium channel, voltage-gated, type II, alpha 2	-0.20	CTCGTATGATAGTGTGACCAA	NM_021007:	NM_021007:
6326	SCN2A2	sodium channel, voltage-gated, type II, alpha 2	-0.28	CACTGGTTAGCTTAACTGCAA	NM_021007:	NM_021007:
6327	SCN2B (sodiu	sodium channel, voltage-gated, type II, beta	0.60	CTCCATCTGTTTAGTAGAAAT	NM_004588:	NM_004588:
6327	SCN2B (sodiu	sodium channel, voltage-gated, type II, beta	-0.20	CCGCGTGGAGTTCTCAGGGAA	NM_004588:	NM_004588:
6328	SCN3A	sodium channel, voltage-gated, type III, alpha	0.18	CTCCCATAATAAATTATATAA	NM_006922:	NM_006922:
6328	SCN3A	sodium channel, voltage-gated, type III, alpha	0.93	TTGGATTTATGTGAGGTCAAA	NM_006922:	NM_006922:
55800	SCN3B	sodium channel, voltage-gated, type III, beta	-0.86	CCCAATAGCTCGTGTATCTAA	NM_018400:	NM_018400:
55800	SCN3B	sodium channel, voltage-gated, type III, beta	-1.24	CCAGACCGTTAACACATTAAA	NM_018400:	NM_018400:
6329	SCN4A	sodium channel, voltage-gated, type IV, alpha	-1.31	CTGGCTCAATGTCAAGGTCAA	NM_000334:	NM_000334:
6329	SCN4A	sodium channel, voltage-gated, type IV, alpha	0.49	CAAGATTGCCTTGGACTGCAA	NM_000334:	NM_000334:
6331	SCN5A	sodium channel, voltage-gated, type V, alpha (long QT syndrome 3)	0.04	TCCTGTAAGAGTATTAACAAA	NM_000335:	NM_198056:NM_000335:
6331	SCN5A	sodium channel, voltage-gated, type V, alpha (long QT syndrome 3)	-0.52	CTGGACCAAGGTGAAAGTCAA	NM_000335:	NM_198056:NM_000335:
6332	SCN7A	sodium channel, voltage-gated, type VII, alpha	-0.12	CCGATGGTAATTAAGCTTGTA	NM_002976:	NM_002976:
6332	SCN7A	sodium channel, voltage-gated, type VII, alpha	1.72	AGAGATGTTCATGCTACTAAA	NM_002976:	NM_002976:
6334	SCN8A	sodium channel, voltage gated, type VIII, alpha	0.02	AACAACCAACTAATTGACTAA	NM_014191:	NM_014191:
6334	SCN8A	sodium channel, voltage gated, type VIII, alpha	1.68	TCGCAAGTGAAAGATTGTTTA	NM_014191:	NM_014191:
6335	SCN9A	sodium channel, voltage-gated, type IX, alpha	1.59	ATGATTCTTTAAGAATCGTAA	NM_002977:	NM_002977:
6335	SCN9A	sodium channel, voltage-gated, type IX, alpha	1.50	TCGGATAGTGAATACAGCAAA	NM_002977:	NM_002977:
6337	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	-0.52	CCCGATGTATGGAAACTGCTA	NM_001038:	NM_001038:
6337	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	1.50	TACAGGTACCCGGAAATTAAA	NM_001038:	NM_001038:
6338	SCNN1B	sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)	0.19	CTGCAATGACACCCAGTACAA	NM_000336:	NM_000336:
6338	SCNN1B	sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)	-0.52	TCGGCCAACCCTGGAACTGAA	NM_000336:	NM_000336:
6339	SCNN1D	sodium channel, nonvoltage-gated 1, delta	-1.30	CACACTTGGGCTGCTCTGAAA	NM_002978:	NM_002978:
6339	SCNN1D	sodium channel, nonvoltage-gated 1, delta	-2.03	CTGCAGGGAGGCAGAAGGCAA	NM_002978:	NM_002978:
6340	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	-1.23	ATCCCGGGACCTGAACTATTA	NM_001039:	NM_001039:
6340	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	-0.46	CAAGGCCGGCAAGTAAACAAA	NM_001039:	NM_001039:
9997	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	-0.28	CGGCCTCTTCACGGATTACTA	NM_005138:	NM_005138:
9997	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	0.98	CCCGAGCGGGACGACGTTGAA	NM_005138:	NM_005138:
59342	SCPEP1	serine carboxypeptidase 1	-0.02	CTGGGAAATACAGGTACCCAA	NM_021626:	NM_021626:
59342	SCPEP1	serine carboxypeptidase 1	1.20	AAGCAAATGATGTGATTTATA	NM_021626:	NM_021626:
6343	SCT (secretin	secretin	0.84	GTGGTACTTGGCACCAATAAA	NM_021920:	NM_021920:
6343	SCT (secretin	secretin	0.47	ACCAATAAAGGAGGAATCAGA	NM_021920:	NM_021920:
6344	SCTR	secretin receptor	-4.44	CCGGATGCTCACCAGCAGAAA	NM_002980:	NM_002980:
6344	SCTR	secretin receptor	0.56	CTCCTTCTTCTCTGAAAGAAA	NM_002980:	NM_002980:
80274	SCUBE1 (sig	signal peptide, CUB domain, EGF-like 1	-1.55	CCCGGCTTTGACCTTGCCCAA	NM_173050:	NM_173050:
80274	SCUBE1 (sig	signal peptide, CUB domain, EGF-like 1	-4.81	CACGTGTGGTTGCCACCAGAA	NM_173050:	NM_173050:
222663	SCUBE3	signal peptide, CUB domain, EGF-like 3	0.35	CACCCTGTCCACACCTAATAA	NM_152753:	NM_152753:
222663	SCUBE3	signal peptide, CUB domain, EGF-like 3	0.94	CCCGTGAGATGTAAAGAAACA	NM_152753:	NM_152753:
9255	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyt	-0.50	ACTGGTCATATTATAATAATA	NM_004757:	NM_004757:
9255	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyt	0.50	CACATAGATAACTAACTAGAT	NM_004757:	NM_004757:
57410	SCYL1	SCY1-like 1 (S. cerevisiae)	-0.01	ACAGATGTATTTATTGTACAA	NM_020680:	NM_020680:
57410	SCYL1	SCY1-like 1 (S. cerevisiae)	-0.58	CTCACTGTAGATCCTGAGAAA	NM_020680:	NM_020680:
55681	SCYL2	SCY1-like 2 (S. cerevisiae)	1.48	ATGCGTTATTAACCATCTTAA	NM_017988:	NM_017988:
55681	SCYL2	SCY1-like 2 (S. cerevisiae)	0.48	ACGGGTTACAGAATAAACATA	NM_017988:	NM_017988:
57147	SCYL3	SCY1-like 3 (S. cerevisiae)	-1.94	AAGCTCTATTATGAAATACAA	NM_020423:	NM_181093:NM_020423:
57147	SCYL3	SCY1-like 3 (S. cerevisiae)	-1.18	CAGGACAATTCCGGAAGTAAA	NM_020423:	NM_020423:
6382	SDC1	syndecan 1	0.00	CAGGAGGAATTCTATGCCTGA	NM_002997:	NM_002997:NM_001006946:
6382	SDC1	syndecan 1	-3.26	CAGGGCCTCCTGGACAGGAAA	NM_002997:	NM_002997:NM_001006946:
6383	SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated,	0.30	AAGGTACGAGTAGAGGTTTAA	NM_002998:	NM_002998:
6383	SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated,	1.59	ATGAATAGACATAAATTGTAA	NM_002998:	NM_002998:
6385	SDC4	syndecan 4 (amphiglycan, ryudocan)	1.48	CAGAAGAGACATTGTCTTCTA	NM_002999:	NM_002999:
6385	SDC4	syndecan 4 (amphiglycan, ryudocan)	0.71	CCAGCTCTGATTACCTTTGAA	NM_002999:	NM_002999:

6386	SDCBP	syndecan binding protein (syntenin)	1.81	TGGGATGGTCTTAGAATATTT	NM_005625:	NM_005625:NM_001007068:NM_001007067:NM_001007069:NM_001007070:
6386	SDCBP	syndecan binding protein (syntenin)	1.28	TTGACTCTTAAGATTATGTAA	NM_005625:	NM_005625:NM_001007068:NM_001007067:NM_001007069:NM_001007070:
6389	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-2.02	AAGAGGGCATCTGCTAAAGTT	NM_004168:	NM_004168:
6389	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-1.07	AACCAGCTATTTTGTGGAGTA	NM_004168:	NM_004168:
6390	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-4.55	CAGCTCAGAGCTGAACATAAT	NM_003000:	NM_003000:
6390	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-0.01	CATGCTAAACATGATTTATAA	NM_003000:	NM_003000:
6391	SDHC	succinate dehydrogenase complex, subunit C, integral membrane prot	0.53	CACAGTGTTATTGAAAGAAGA	NM_003001:	NM_003001:NM_001035511:NM_001035512:NM_001035513:
6391	SDHC	succinate dehydrogenase complex, subunit C, integral membrane prot	-0.02	CTGGTAGACCATAATAGTGGA	NM_003001:	NM_003001:NM_001035511:NM_001035512:NM_001035513:
121214	SDR-O	orphan short-chain dehydrogenase / reductase	-0.91	CAGAGTCAGAGATGTCATCAA	NM_148897:	NM_148897:
121214	SDR-O	orphan short-chain dehydrogenase / reductase	0.85	GAGGATTATTTCCGCATCTAT	NM_148897:	NM_148897:
23478	SEC11L1	SEC11-like 1 (S. cerevisiae)	-3.04	CCGTCATACCTCCTTCTATTA	NM_014300:	NM_014300:
23478	SEC11L1	SEC11-like 1 (S. cerevisiae)	-1.61	CACGAGTTTGAAACCGTCATA	NM_014300:	NM_014300:
157708	SEC11L2	SEC11-like 2 (S. cerevisiae)	-0.13	CAGCTTCCTCATCATCTTAAA	XM_088367:	XM_088367:
157708	SEC11L2	SEC11-like 2 (S. cerevisiae)	0.31	CTGCATTGCCTTGGAAGGGAA	XM_088367:	XM_088367:
6400	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	-2.22	ACGGCACAAGGAAGCATTGAA	NM_005065:	NM_005065:
6400	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	-0.05	CAGGATATTCACCTTGCGAAA	NM_005065:	NM_005065:
6401	SELE	selectin E (endothelial adhesion molecule 1)	-1.80	CAGGTTGAATGCACCACTCAA	NM_000450:	NM_000450:
6401	SELE	selectin E (endothelial adhesion molecule 1)	0.69	CGGAAAGTATTTCAAGCCTAA	NM_000450:	NM_000450:
6402	SELL	selectin L (lymphocyte adhesion molecule 1)	-0.35	CACGATATTATTAGTAAGAAA	NM_000655:	NM_000655:
6402	SELL	selectin L (lymphocyte adhesion molecule 1)	-0.03	CTGGAATCTGGTCAAATCCTA	NM_000655:	NM_000655:
6403	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	0.13	CCGATATAGTTCGGTGTGATA	NM_003005:	NM_003005:
6403	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	0.35	CTGGGCTGATAATGAACCTAA	NM_003005:	NM_003005:
6404	SELPLG	selectin P ligand	-1.11	ACGGAGGCACAGACCACTCAA	NM_003006:	NM_003006:
6404	SELPLG	selectin P ligand	-0.76	ATGGAGATACAGACCACTCAA	NM_003006:	NM_003006:
55829	SELS	selenoprotein S	0.20	AGGCCTCTAGATGATTAGCAA	NM_018445:	NM_018445:
55829	SELS	selenoprotein S	-1.75	AACCCTTAACCCTCGATTCAA	NM_018445:	NM_018445:
56920	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secre	-0.29	CCCTGCCCTATTGAAACTCAA	NM_020163:	NM_020163:
56920	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secre	-0.02	CAGGCTTCACTTTGTAAACCA	NM_020163:	NM_020163:
10507	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (	-0.64	ACGGATAGCAAGAGTGTGCAA	NM_006378:	NM_006378:
10507	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (	-0.57	CCGGCACATCCTGCGAACCAA	NM_006378:	NM_006378:
80031	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain	0.48	CAGGTTGAGTACCTTAGAATA	NM_020858:	NM_153616:NM_024966:NM_153617:NM_153618:NM_153619:NM_020858:
80031	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain	0.06	TACAGACATAATACAAATCAA	NM_020858:	NM_153616:NM_024966:NM_153617:NM_153618:NM_153619:NM_020858:
29843	SENP1	SUMO1/sentrin specific peptidase 1	0.25	TCGATTTGGACTATGAATCAA	NM_014554:	NM_014554:
29843	SENP1	SUMO1/sentrin specific peptidase 1	0.30	TCGCCTGACCATTACACGCAA	NM_014554:	NM_014554:
59343	SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	-0.09	AAGAACAAACGCTAACTAATA	NM_021627:	NM_021627:
59343	SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	0.61	CCACACAAGAACAAACGCTAA	NM_021627:	NM_021627:
26168	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	-1.56	CAGGCAGAGGCGGTAAAGAAA	NM_015670:	NM_015670:
26168	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	1.21	GACGAATTCCTTCAAACGTAT	NM_015670:	NM_015670:
205564	SENP5	SUMO1/sentrin specific peptidase 5	0.38	CAGAACATCGTTCTAATACCA	NM_152699:	NM_152699:
205564	SENP5	SUMO1/sentrin specific peptidase 5	0.30	GTGCCTGATTGCCACACTAAA	NM_152699:	NM_152699:
26054	SENP6	SUMO1/sentrin specific peptidase 6	-1.04	AAGGCGTATGTATTAAGTAAA	NM_015571:	NM_015571:
26054	SENP6	SUMO1/sentrin specific peptidase 6	-1.30	CAGAACAATGTGTCAATAGTA	NM_015571:	NM_015571:
57337	SENP7	SUMO1/sentrin specific peptidase 7	0.24	GTGGCATTATATATGATTAAA	NM_020654:	NM_020654:
57337	SENP7	SUMO1/sentrin specific peptidase 7	0.51	ACCGTGAGACAACTAATGAAA	NM_020654:	NM_020654:
123228	SENP8	SUMO/sentrin specific peptidase family member 8	-1.37	CCAGCTATCTATATAATGTTT	NM_145204:	NM_145204:
123228	SENP8	SUMO/sentrin specific peptidase family member 8	0.53	TCCCTTATCCACATTGGCTTA	NM_145204:	NM_145204:
57190	SEPN1	selenoprotein N, 1	0.19	CCCAACATGCCCTGTAATAAA	NM_020451:	NM_206926:NM_020451:
57190	SEPN1	selenoprotein N, 1	-0.01	TACACGCACCTTCTCACTTAA	NM_020451:	NM_206926:NM_020451:
10801	SEPT9	septin 9	-2.92	ACGCACGATATTGAGGAGAAA	NM_006640:	NM_006640:
10801	SEPT9	septin 9	-1.20	CACGCACGATATTGAGGAGAA	NM_006640:	NM_006640:
5265	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.88	CCCGAGGTCAAGTTCAACAAA	NM_000295:	NM_001002236:NM_001002235:NM_000295:
5265	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-3.31	CACCCACGATATCATCACCAA	NM_000295:	NM_001002236:NM_001002235:NM_000295:
51156	SERPINA10	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-0.30	ACCATGGTTGACCATGGTTAA	NM_016186:	NM_016186:
51156	SERPINA10	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.73	TAGGGTGTTCTCAAATAAATA	NM_016186:	NM_016186:
256394	SERPINA11 (	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.77	CAGAATTGACCTGACAAATAT	XM_170754:	XM_170754:
256394	SERPINA11 (	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-0.74	CACCAACATACTCAACTTAGA	XM_170754:	XM_170754:
145264	SERPINA12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-0.05	CTCGTCGTCAAGATAGACAAA	NM_173850:	NM_173850:
145264	SERPINA12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-2.98	ATCAATGACTTTATCAGTCAA	NM_173850:	NM_173850:
388007	SERPINA13	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-5.69	AAGGATAGTAATGGTGATCAA	NM_207378:	NM_207378:
388007	SERPINA13	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	1.00	TCCGTGCATGATTGCTTTGAA	NM_207378:	NM_207378:
390502	SERPINA2	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.24	CACGGCAAGTGGAAAGATAAA	XM_372532:	XM_372532:
390502	SERPINA2	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-1.78	CGGCAGTAGCCTGTTTGTTAA	XM_372532:	XM_372532:
12	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-1.08	AAGGACCATTGTGCGTTTCAA	NM_001085:	NM_001085:
12	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-0.33	AAGGCTGTGCTTGATGTATTT	NM_001085:	NM_001085:
5267	SERPINA4	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-4.25	CAGGCTGGTTGTACCGAGTAA	NM_006215:	NM_006215:
5267	SERPINA4	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.10	AAGGATGACACCGAAGGTCCA	NM_006215:	NM_006215:
5104	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-0.50	AAGGTGGAAATGGCCCATTTA	NM_000624:	NM_000624:
5104	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-2.85	CACCAGCATGGTAGTGGCAAA	NM_000624:	NM_000624:
866	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	-3.32	CACCCTAAACCTGACGTCCAA	NM_001756:	NM_001756:
866	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.46	CAACAGCTATGTCAAGAATAA	NM_001756:	NM_001756:
6906	SERPINA7	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	1.37	TAGGGAAAGTTGTGAACCCAA	NM_000354:	NM_000354:
6906	SERPINA7	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	1.53	ACCCTATTATCCAAATTGATA	NM_000354:	NM_000354:
327657	SERPINA9	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.35	CCCTGAATATACAAGAAAGAA	NM_175739:	NM_175739:
327657	SERPINA9	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin)	0.17	AAGGTTGTAGACATAATCCAA	NM_175739:	NM_175739:
1992	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	1.58	TTCGGCATAATTCCTCAGGTA	NM_030666:	NM_030666:
1992	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	1.55	CTCGATTTCATTGAAGTTAAT	NM_030666:	NM_030666:
5273	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	-2.88	CAGGAATGTCTTCAGCAAGAA	NM_005024:	NM_005024:
5273	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	1.56	AACGATGACTACTTACTTAAA	NM_005024:	NM_005024:
89778	SERPINB11	serpin peptidase inhibitor, clade B (ovalbumin), member 11	-1.71	CACGATCCTATTCTGTGGCAA	NM_080475:	NM_080475:
89778	SERPINB11	serpin peptidase inhibitor, clade B (ovalbumin), member 11	0.21	CAGATTCAAACTTGAAATTAA	NM_080475:	NM_080475:
89777	SERPINB12	serpin peptidase inhibitor, clade B (ovalbumin), member 12	-1.39	TTGGGTGGAGTTTAATGCCAA	NM_080474:	NM_080474:
89777	SERPINB12	serpin peptidase inhibitor, clade B (ovalbumin), member 12	-1.37	ACGATCTTGGGTGGAGTTTAA	NM_080474:	NM_080474:
5275	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	0.24	TTGGAAAGCTCTGAATCTATA	NM_012397:	NM_012397:
5275	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	1.01	ACCAGTGTTACTCATATGATT	NM_012397:	NM_012397:
5055	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	-0.17	AACCTATGACAAACTCAACAA	NM_002575:	NM_002575:
5055	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	-2.35	CAGAAGGGTAGTTATCCTGAT	NM_002575:	NM_002575:
6317	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	-1.11	TCGGATCATCACCTACTTCAA	NM_006919:	NM_006919:
6317	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	-0.52	TAGGATTCGGATCATCACCTA	NM_006919:	NM_006919:
6318	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	-0.18	TCGAATTATCATCTCCTTCAA	NM_002974:	NM_002974:
6318	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	0.27	ACCGCTGTAGTAGTAGTCGAA	NM_002974:	NM_002974:
5268	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	-0.02	GCCGTTGATCTGTTCAAACAA	NM_002639:	NM_002639:
5268	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	0.61	TTCCTTGACATGCATTGTAAA	NM_002639:	NM_002639:
5269	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	0.02	CCGCGGTTTAAACTAGAGGAA	NM_004568:	NM_004568:

5269	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	-1.78	CACCGAGGAGAGACTGTTTAA	NM_004568:	NM_004568:
8710	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	-1.18	ATCGCAGATATTCTAGCTTCA	NM_003784:	NM_003784:
8710	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	-0.96	CACGCTCATTTCTATCATTCT	NM_003784:	NM_003784:
5271	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	0.14	TTAGACAGTTTGAGTAATTAA	NM_002640:	NM_002640:NM_198833:
5271	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	-0.08	ACCACTGAGTCCTCTAACTAA	NM_002640:	NM_002640:NM_198833:
5272	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.67	TCCTATGTAATGAGCTAGAAA	NM_004155:	NM_004155:
5272	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	-1.04	CACTGCGAATACATTCCTTAA	NM_004155:	NM_004155:
462	SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	0.80	CCAACCCTTGTGTTAAGTAAA	NM_000488:	NM_000488:
462	SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	-0.01	ACCGATGTCATTCCCTCGGAA	NM_000488:	NM_000488:
3053	SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	1.49	TGGGCTAATGTTAGGGCTTAA	NM_000185:	NM_000185:
3053	SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	-1.91	CCCAAGGAGGGTACACAACTA	NM_000185:	NM_000185:
5054	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibi	-0.09	TTGATGGAAATTGACCATACA	NM_000602:	NM_000602:
5054	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibi	0.55	TTGGAGGACCTTTAGGTCAAA	NM_000602:	NM_000602:
5270	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibi	-1.35	CAGGATGGCTGGAACACTGTA	NM_006216:	NM_006216:
5270	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibi	0.18	CTGGGAGGTATTGGAGGGAAA	NM_006216:	NM_006216:
5176	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epith	-0.06	CTGCTGGACGCTGGATTAGAA	NM_002615:	NM_002615:
5176	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epith	-0.02	TCCGAGTTCATTCATGACATA	NM_002615:	NM_002615:
5345	SERPINF2	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epith	1.83	AAGCTGTATCTGAAACACCAA	NM_000934:	NM_000934:
5345	SERPINF2	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epith	1.51	ACCCACCCACTTTGAATGGAA	NM_000934:	NM_000934:
710	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioede	0.69	TCACCAGACTCTATAAATAAA	NM_000062:	NM_000062:NM_001032295:
710	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioede	-0.12	AACCTGAAACATCGTCTTGAA	NM_000062:	NM_000062:NM_001032295:
871	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1,	0.07	CAAGAACTTATTTGTACATTT	NM_001235:	NM_001235:
871	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1,	-8.80	CCCAACCTCTCCCAACTATAA	NM_001235:	NM_001235:
5274	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	0.68	AACAATATATGTAAATTATAA	NM_005025:	NM_005025:
5274	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	0.08	CAAGTTATTGTCGACCATCCA	NM_005025:	NM_005025:
5276	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	0.51	CTGGCTCAAAGCCAATTTATA	NM_006217:	NM_006217:
5276	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	-0.69	CTCCCTAGATTTAAAGTAGAA	NM_006217:	NM_006217:
91404	SESTD1	SEC14 and spectrin domains 1	-0.36	ATCCCGCATGTTGTCAACATA	NM_178123:	NM_178123:
91404	SESTD1	SEC14 and spectrin domains 1	0.08	CAGCGTCGATTTAATGGCTCA	NM_178123:	NM_178123:
6418	SET	SET translocation (myeloid leukemia-associated)	-0.42	CAGGAATCTTGCTCCAATAAA	NM_003011:	NM_003011:
6418	SET	SET translocation (myeloid leukemia-associated)	-2.31	CAGCATAGGTATGCTTACTAT	NM_003011:	NM_003011:
9739	SETD1A	SET domain containing 1A	-2.47	CAGCGTATTATGAAAGCTGGA	XM_049380:	NM_014712:
9739	SETD1A	SET domain containing 1A	-2.48	CACGCCTAACTGCTACGCCAA	XM_049380:	NM_014712:
23067	SETD1B	SET domain containing 1B	0.08	CTGAATGATAACATCCGTGAA	XM_037523:	XM_037523:
23067	SETD1B	SET domain containing 1B	-0.35	CAGGATTTCTGTTTAACTCCA	XM_037523:	XM_037523:
29072	SETD2	SET domain containing 2	-0.10	CCCAAGTCTGATAAATTTAAA	NM_012271:	NM_012271:NM_014159:
29072	SETD2	SET domain containing 2	-2.50	CGGCTAATGGTTAGAATTGAA	NM_012271:	NM_012271:NM_014159:
55209	SETD5	SET domain containing 5	0.40	AACGCGCTTGAACAACACCTA	XM_371614:	XM_371614:
55209	SETD5	SET domain containing 5	0.17	CACCTACATTCTAGCAAGGAA	XM_371614:	XM_371614:
80854	SETD7	SET domain containing (lysine methyltransferase) 7	-1.34	CACCTGGACGATGACGGATTA	NM_030648:	NM_030648:
80854	SETD7	SET domain containing (lysine methyltransferase) 7	0.34	CAGGGAGTTTACACTTACGAA	NM_030648:	NM_030648:
387893	SETD8	SET domain containing (lysine methyltransferase) 8	-2.21	AAGAATAGATGAATTGATTGA	NM_020382:	NM_020382:
387893	SETD8	SET domain containing (lysine methyltransferase) 8	-2.72	CTGCAGTCTGAAGAAAGGAAA	NM_020382:	NM_020382:
9869	SETDB1	SET domain, bifurcated 1	0.02	ACCCATGGGATTGCAATTAAA	NM_012432:	NM_012432:
9869	SETDB1	SET domain, bifurcated 1	0.13	ACCCGAGGCTTTGCTCTTAAA	NM_012432:	NM_012432:
83852	SETDB2	SET domain, bifurcated 2	1.13	CCGAGAGCATCTGAACTCTAA	NM_031915:	NM_031915:
83852	SETDB2	SET domain, bifurcated 2	-3.88	ACGGGAGAGATGAGAATACTA	NM_031915:	NM_031915:
6419	SETMAR (SE	SET domain and mariner transposase fusion gene	0.04	TTGACCCTACTTATATAGGAA	NM_006515:	NM_006515:
6419	SETMAR (SE	SET domain and mariner transposase fusion gene	-0.04	ATGTTTATAATGGGCAGGTAA	NM_006515:	NM_006515:
124925	SEZ6 (seizure	seizure related 6 homolog (mouse)	-0.20	TGGCGTGGAAATCAAGGTCAA	NM_178860:	NM_178860:
124925	SEZ6 (seizure	seizure related 6 homolog (mouse)	-2.42	TAGCTGGAGCACAAGCATCAA	NM_178860:	NM_178860:
23544	SEZ6L (seizu	seizure related 6 homolog (mouse)-like	-0.25	CCCGTGTGTAAAGTTAATCAA	NM_021115:	NM_021115:
23544	SEZ6L (seizu	seizure related 6 homolog (mouse)-like	-0.58	ACGGATCTTCTTAGATATCCA	NM_021115:	NM_021115:
26470	SEZ6L2	seizure related 6 homolog (mouse)-like 2	0.72	CCCAGTTCTGTGTAATAACAA	NM_012410:	NM_201575:NM_012410:
26470	SEZ6L2	seizure related 6 homolog (mouse)-like 2	-0.09	GGGCTTCGTATTGCACTTCAA	NM_012410:	NM_201575:NM_012410:
10291	SF3A1	splicing factor 3a, subunit 1, 120kDa	-1.26	CAGCATGTAGGTAGCGTCCTA	NM_005877:	NM_001005409:NM_005877:
10291	SF3A1	splicing factor 3a, subunit 1, 120kDa	-10.28	CAGGATAAGACGGAATGGAAA	NM_005877:	NM_001005409:NM_005877:
2810	SFN (stratifin)	stratifin	0.16	ACCATGTTTCCTCTCAATAAA	NM_006142:	NM_006142:
2810	SFN (stratifin)	stratifin	-3.79	CCGGGAGAAGGTGGAGACTGA	NM_006142:	NM_006142:
6422	SFRP1	secreted frizzled-related protein 1	-0.04	AAGGGCCATTTAGATTAGGAA	NM_003012:	NM_003012:
6422	SFRP1	secreted frizzled-related protein 1	0.32	CAGCCTGCAGGGAATAACATA	NM_003012:	NM_003012:
6424	SFRP4	secreted frizzled-related protein 4	0.57	CACCCTGAGAATAATTTGACA	NM_003014:	NM_003014:
6424	SFRP4	secreted frizzled-related protein 4	0.55	CCCGATCGGTGCAAGTGTAAA	NM_003014:	NM_003014:
6425	SFRP5	secreted frizzled-related protein 5	-2.73	CCGCTGGGACAAGAAGAATAA	NM_003015:	NM_003015:
6425	SFRP5	secreted frizzled-related protein 5	-3.06	CTGCGAGGAGTACGACTACTA	NM_003015:	NM_003015:
6434	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosop	-1.26	CCCGATCTGAATCTAGGTCTA	NM_004593:	NM_004593:
6434	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosop	0.04	CGGGACTACTATAGCAGATCA	NM_004593:	NM_004593:
9169	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	-0.16	AAGGAGGTGATCCATTGGAAA	NM_004719:	NM_004719:
9169	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	-3.14	CTGGACAGGATTCTAGCCTAA	NM_004719:	NM_004719:
8683	SFRS9	splicing factor, arginine/serine-rich 9	-2.47	CAGGGCCATATTAGCAGTGAA	NM_003769:	NM_003769:
8683	SFRS9	splicing factor, arginine/serine-rich 9	-1.25	TTGCTCTACTATGGAGATCAA	NM_003769:	NM_003769:
6441	SFTPD	surfactant, pulmonary-associated protein D	0.63	AGGAGTTTGGCCAGAAGTCAA	NM_003019:	NM_003019:
6441	SFTPD	surfactant, pulmonary-associated protein D	-3.45	CTACCTGGAAGCAGAAATGAA	NM_003019:	NM_003019:
94097	SFXN5	sideroflexin 5	0.23	CAGGCTGGTAAATTTAGGATA	NM_144579:	NM_144579:
94097	SFXN5	sideroflexin 5	-6.87	CAGCCGGACAGTGGTGTACAA	NM_144579:	NM_144579:
6442	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	-0.02	AAGGACATTCAGAATAAATAT	NM_000023:	NM_000023:
6442	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	-4.94	CAGGCTCTAAACAAGCAGGGA	NM_000023:	NM_000023:
6443	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	0.02	CACTTTGAATTGTGCACATAA	NM_000232:	NM_000232:
6443	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	-0.92	ATGCAGATTTCTAGTGCATTA	NM_000232:	NM_000232:
6445	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	1.03	CAAGATGTAGTTAAAGGAATA	NM_000231:	NM_000231:
6445	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	-0.26	CCGTGTGGAGTTAATGTATGA	NM_000231:	NM_000231:
6446	SGK	serum/glucocorticoid regulated kinase	-0.02	CACAGCTGAAATGTACGACAA	NM_005627:	NM_005627:
6446	SGK	serum/glucocorticoid regulated kinase	-0.71	CTGGGCTGTGATGACGAATAT	NM_005627:	NM_005627:
10110	SGK2	serum/glucocorticoid regulated kinase 2	-2.91	CAGGGCCAATGGGAACATCAA	NM_016276:	NM_016276:NM_170693:
10110	SGK2	serum/glucocorticoid regulated kinase 2	0.03	TGGGTACGTGACTATCCCTAA	NM_016276:	NM_016276:NM_170693:
23678	SGK3	serum/glucocorticoid regulated kinase family, member 3	0.94	ACCAACTAACTTACATGCTTA	NM_013257:	NM_170709:NM_001033578:NM_013257:
23678	SGK3	serum/glucocorticoid regulated kinase family, member 3	0.51	CCACAGCGAGACCCTAGTTAA	NM_013257:	NM_170709:NM_001033578:NM_013257:
8879	SGPL1	sphingosine-1-phosphate lyase 1	0.23	TGGGTGTGAGGTATACTCTAA	NM_003901:	NM_003901:
8879	SGPL1	sphingosine-1-phosphate lyase 1	0.65	CAGGCAGGAGGCGTTTACATA	NM_003901:	NM_003901:
81537	SGPP1	sphingosine-1-phosphate phosphatase 1	2.17	AGAGATTAACTTTCCATATAA	NM_030791:	NM_030791:
81537	SGPP1	sphingosine-1-phosphate phosphatase 1	0.72	ATCGGTATATTACCTATGGAA	NM_030791:	NM_030791:
6448	SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase)	-5.44	CCGCCTCGTGCACAACCTCAA	NM_000199:	NM_000199:
6448	SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase)	0.75	CCGGGCACTGCTGAACCCTTA	NM_000199:	NM_000199:
6449	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	-1.88	AACGAGCAGATGAAAGTGGAA	NM_003021:	NM_003021:
6449	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	0.93	CAGACCCTTCTTGAAACGAGA	NM_003021:	NM_003021:
4068	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndro	0.96	CTGGGAATTCTGGATTGTGTA	NM_002351:	NM_002351:
4068	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndro	0.24	CACTGTCTTGTTGGACGAGAA	NM_002351:	NM_002351:
10045	SH2D3A	SH2 domain containing 3A	-1.23	CACCTCTGTGTCGGCCTTTAA	NM_005490:	NM_005490:
10045	SH2D3A	SH2 domain containing 3A	-2.01	AAGGAAGTGGAGCAACAGTCA	NM_005490:	NM_005490:

10044	SH2D3C	SH2 domain containing 3C	0.33	CCACACCAATGCTGAAGTCAA	NM_005489:	NM_170600:NM_005489:
10044	SH2D3C	SH2 domain containing 3C	-3.51	CAGGCGAGAGCTACACACACA	NM_005489:	NM_170600:NM_005489:
6452	SH3BP2	SH3-domain binding protein 2	0.26	TAGGAAGTAAACGATCTGCAA	NM_003023:	NM_003023:
6452	SH3BP2	SH3-domain binding protein 2	0.99	TAGCACCTTATGTCAGGGAAA	NM_003023:	NM_003023:
23677	SH3BP4	SH3-domain binding protein 4	0.00	CAGCTCGTTGCCAATCACATA	NM_014521:	NM_014521:
23677	SH3BP4	SH3-domain binding protein 4	-1.35	CAGGCAGAATGTACAGTAATA	NM_014521:	NM_014521:
6455	SH3GL1	SH3-domain GRB2-like 1	-2.80	ACGCCCTAAGCGGGAGTATAA	NM_003025:	NM_003025:
6455	SH3GL1	SH3-domain GRB2-like 1	-0.32	ACGGTCCAGGGCAAACTGAAA	NM_003025:	NM_003025:
30011	SH3KBP1	SH3-domain kinase binding protein 1	1.40	CTCTGAGATCTCAATGCGAAA	NM_031892:	NM_031892:NM_001024666:
30011	SH3KBP1	SH3-domain kinase binding protein 1	0.72	TAGCTTATATATGACGGTATA	NM_031892:	NM_031892:NM_001024666:
81858	SHARPIN	SHANK-associated RH domain interactor	-0.17	AGGCTGCAGGTCACACTTGAA	NM_030974:	NM_030974:
81858	SHARPIN	SHANK-associated RH domain interactor	-4.29	CAGGCTGCAGGTCACACTTGA	NM_030974:	NM_030974:
6462	SHBG	sex hormone-binding globulin	-2.37	CAGGCAGAATTCAATCTCCGA	NM_001040:	NM_001040:
6462	SHBG	sex hormone-binding globulin	0.11	AAGCTGTGATGTAGAATCAAA	NM_001040:	NM_001040:
6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	0.68	AAAGTTGGAGCGGTAACCTAA	NM_003029:	NM_003029:
6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	-1.10	AGCGAACTGTGTCTACAGCAA	NM_003029:	NM_183001:NM_003029:
6469	SHH	sonic hedgehog homolog (Drosophila)	0.60	CCCGCTGGGCATGGCGGTCAA	NM_000193:	NM_000193:
6469	SHH	sonic hedgehog homolog (Drosophila)	1.04	CCAGGGCACCATTCTCATCAA	NM_000193:	NM_000193:
8036	SHOC2	soc-2 suppressor of clear homolog (C. elegans)	0.05	CCCATGGTCTTGGAAACCTTA	NM_007373:	NM_007373:
8036	SHOC2	soc-2 suppressor of clear homolog (C. elegans)	0.99	TACCTTCGCTTTAATCGTATA	NM_007373:	NM_007373:
257218	SHPRH	SNF2 histone linker PHD RING helicase	0.43	AAGAGCTTTCATGTACATTTA	NM_173082:	NM_173082:
257218	SHPRH	SNF2 histone linker PHD RING helicase	1.14	TCGGGAGGTGTTAATCCAGAA	NM_173082:	NM_173082:
6476	SI (sucrase-is	sucrase-isomaltase (alpha-glucosidase)	1.56	CTAACGTATAACGGAAATAAA	NM_001041:	NM_001041:
6476	SI (sucrase-is	sucrase-isomaltase (alpha-glucosidase)	-0.45	ATGCTTCTTATGACACAATAA	NM_001041:	NM_001041:
6477	SIAH1	seven in absentia homolog 1 (Drosophila)	1.20	CCCATTAATCAGTTCATTAGA	NM_003031:	NM_001006610:NM_003031:
6478	SIAH2	seven in absentia homolog 2 (Drosophila)	0.03	TTGGGTGGATTGCCTAGGAAA	NM_005067:	NM_005067:
6478	SIAH2	seven in absentia homolog 2 (Drosophila)	0.66	ACCCGGAGTGCTTATCTTAAA	NM_005067:	NM_005067:
89790	SIGLEC10	sialic acid binding Ig-like lectin 10	1.25	GGCGGATTATGCAGAAGTCAA	NM_033130:	NM_033130:
89790	SIGLEC10	sialic acid binding Ig-like lectin 10	-0.03	CCCAGCTGTCAGACATTTAAA	NM_033130:	NM_033130:
114132	SIGLEC11 (si	sialic acid binding Ig-like lectin 11	0.23	CCCGTTGATGACCATGCTCTT	NM_052884:	NM_052884:
114132	SIGLEC11 (si	sialic acid binding Ig-like lectin 11	0.03	CCCATTCAAATGGAGCACGAA	NM_052884:	NM_052884:
89858	SIGLEC12	sialic acid binding Ig-like lectin 12	-0.17	ATGGAACTACATATATGACAA	NM_033329:	NM_053003:NM_033329:
89858	SIGLEC12	sialic acid binding Ig-like lectin 12	0.86	CCGAGACTGATTCCTTTAGAA	NM_033329:	NM_053003:NM_033329:
8778	SIGLEC5	sialic acid binding Ig-like lectin 5	-1.84	CAGGAACGGCATAGCCCTAGA	NM_003830:	NM_003830:
8778	SIGLEC5	sialic acid binding Ig-like lectin 5	0.77	AAAGGTTGTTGTGAACATTAA	NM_003830:	NM_003830:
946	SIGLEC6	sialic acid binding Ig-like lectin 6	0.49	CCAGAAACTATAATAACATAA	NM_198846:	NM_198845:NM_198846:NM_001245:
946	SIGLEC6	sialic acid binding Ig-like lectin 6	-1.15	ACCGAGTGACATAAACACAGA	NM_198846:	NM_198845:NM_198846:NM_001245:
27036	SIGLEC7	sialic acid binding Ig-like lectin 7	-1.91	CTGGAGGAGTCTGACCCTGTA	NM_014385:	NM_016543:NM_014385:
27036	SIGLEC7	sialic acid binding Ig-like lectin 7	0.91	TAGTGAGATTGTAACGTGAAA	NM_014385:	NM_016543:NM_014385:
27181	SIGLEC8	sialic acid binding Ig-like lectin 8	0.83	TGCCCGTTGTATCATAATTTA	NM_014442:	NM_014442:
27181	SIGLEC8	sialic acid binding Ig-like lectin 8	0.11	CCGCACCCAGCTTGCATTGAA	NM_014442:	NM_014442:
27180	SIGLEC9	sialic acid binding Ig-like lectin 9	-1.75	CACACAGGCTTTAGAGTCAAA	NM_014441:	NM_014441:
27180	SIGLEC9	sialic acid binding Ig-like lectin 9	0.18	TCAAAGTATCTCAAACCTGAA	NM_014441:	NM_014441:
6492	SIM1 (single-	single-minded homolog 1 (Drosophila)	0.37	TCACCTGGTATCCATTATAAA	NM_005068:	NM_005068:
6492	SIM1 (single-	single-minded homolog 1 (Drosophila)	0.93	CACACTAAACTTCTTAACGAA	NM_005068:	NM_005068:
6493	SIM2	single-minded homolog 2 (Drosophila)	-1.22	CCGTGATTCTTGAAAGGTGTA	NM_005069:	NM_005069:
6493	SIM2	single-minded homolog 2 (Drosophila)	0.03	CCGGCAAATGCGCACGACCTA	NM_005069:	NM_005069:
25942	SIN3A	SIN3 homolog A, transcription regulator (yeast)	-4.29	CTGGTCACTCGAGCACATCTA	NM_015477:	NM_015477:
25942	SIN3A	SIN3 homolog A, transcription regulator (yeast)	-1.24	GAGCGTGTAAGCAAGCGTCTA	NM_015477:	NM_015477:
8487	SIP1	survival of motor neuron protein interacting protein 1	-0.20	CCAGATGTTGTGGTAGCTCAA	NM_003616:	NM_003616:NM_001009183:NM_001009182:
6494	SIPA1	signal-induced proliferation-associated gene 1	-3.26	CAGGCGGAGTCTGAGAGTGCA	NM_006747:	NM_153253:NM_006747:
6494	SIPA1	signal-induced proliferation-associated gene 1	-0.20	CCGGAAGCGCCACATTGGCAA	NM_006747:	NM_153253:NM_006747:
10326	SIRPB1	signal-regulatory protein beta 1	-1.53	CTGCTCAATGTCACTTCATTA	NM_006065:	NM_006065:
10326	SIRPB1	signal-regulatory protein beta 1	0.04	AACCTCAGAGTTAAATCCCTA	NM_006065:	NM_006065:
128646	SIRPD	signal-regulatory protein delta	1.02	CAGGGCCAAACCGGAAATTAA	NM_178460:	NM_178460:
128646	SIRPD	signal-regulatory protein delta	-2.65	CCGGAAATTAATCTACAATTT	NM_178460:	NM_178460:
55423	SIRPG	signal-regulatory protein gamma	0.63	CGCCTTGAGACTGACCGTAAA	NM_018556:	NM_080816:NM_018556:
55423	SIRPG	signal-regulatory protein gamma	-0.32	CTGGTGAACATATCTGACCAA	NM_018556:	NM_018556:
23411	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cere	0.01	ATAGCTGTTCTTTATGCATAA	NM_012238:	NM_012238:
23411	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cere	0.52	CAGGATTATTGTATTTACGTT	NM_012238:	NM_012238:
22933	SIRT2	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cere	0.84	AGGCATGGACTTTGACTCCAA	NM_012237:	NM_030593:NM_012237:
22933	SIRT2	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cere	-2.31	CAGCGCGTTTCTTCTCCTGTA	NM_012237:	NM_030593:NM_012237:
23410	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cere	0.98	TTCCAGCATGAAATACATTTA	NM_012239:	NM_001017524:NM_012239:
23410	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cere	0.15	CTGTGCCTAGTTGAACGGCAA	NM_012239:	NM_001017524:NM_012239:
23409	SIRT4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cere	-0.01	CACCTGGGAGAAACTCGGAAA	NM_012240:	NM_012240:
23409	SIRT4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cere	0.56	CCAGCGGTACTGGGCGAGAAA	NM_012240:	NM_012240:
23408	SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cere	-0.19	CTGGAAAGTTAATTCATATTA	NM_012241:	NM_012241:
23408	SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cere	-0.10	CTGGAGATCCATGGTAGCTTA	NM_012241:	NM_012241:NM_031244:
51548	SIRT6	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cere	0.14	CTCCCTGGTCTCCAGCTTAAA	NM_016539:	NM_016539:
51548	SIRT6	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cere	-0.75	CCGGCTCTGCACCGTGGCTAA	NM_016539:	NM_016539:
51547	SIRT7	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cere	-0.86	CTCACCGTATTTCTACTACTA	NM_016538:	NM_016538:
51547	SIRT7	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cere	0.69	CACCTTTCTGTGAGAACGGAA	NM_016538:	NM_016538:
10572	SIVA	CD27-binding (Siva) protein	0.16	TCCTAATGACAGAATGAATAA	NM_006427:	NM_021709:NM_006427:
10572	SIVA	CD27-binding (Siva) protein	0.53	CAGAATGAATAAACCTCTTTA	NM_006427:	NM_021709:NM_006427:
6496	SIX3	sine oculis homeobox homolog 3 (Drosophila)	1.61	CTGCATGACGATTTATTTGTA	NM_005413:	NM_005413:
6496	SIX3	sine oculis homeobox homolog 3 (Drosophila)	0.65	CCCAACCATACACACATACAA	NM_005413:	NM_005413:
6497	SKI	v-ski sarcoma viral oncogene homolog (avian)	-0.32	CCGACTTTATAGAGCAGTCAA	NM_003036:	NM_003036:
6497	SKI	v-ski sarcoma viral oncogene homolog (avian)	0.76	GCGAGTGTTTGTAACCATGTA	NM_003036:	NM_003036:
6498	SKIL	SKI-like	0.64	AGGCAAGTAAGTCCATATCAA	NM_005414:	NM_005414:
6498	SKIL	SKI-like	-0.03	CGGCGGGCACAGATTAATTAA	NM_005414:	NM_005414:
51763	SKIP	skeletal muscle and kidney enriched inositol phosphatase	-1.19	CAGCCAAGTGTCGTCCACATA	NM_016532:	NM_130766:NM_016532:
51763	SKIP	skeletal muscle and kidney enriched inositol phosphatase	-1.91	CTGGAATTAGCCGCTTAAATA	NM_016532:	NM_130766:NM_016532:
80309	SKIP	SPHK1 (sphingosine kinase type 1) interacting protein	-2.55	CTGAAATTCTGGACACCTTAA	XM_051221:	NM_030623:
80309	SKIP	SPHK1 (sphingosine kinase type 1) interacting protein	1.25	GGCAAGTATGCTACAAATTTA	XM_051221:	NM_030623:
6500	SKP1A	S-phase kinase-associated protein 1A (p19A)	0.49	AAAGTTGGCATTGTAAATAAA	NM_006930:	NM_170679:NM_006930:
6500	SKP1A	S-phase kinase-associated protein 1A (p19A)	1.10	AGGGTACTTTAGAGCAACTTA	NM_006930:	NM_006930:
6502	SKP2	S-phase kinase-associated protein 2 (p45)	0.19	AAGTGATAGTGTCATGCTAAA	NM_005983:	NM_032637:NM_005983:
6502	SKP2	S-phase kinase-associated protein 2 (p45)	-0.41	ACCCTTCAACTGTTAAAGGAA	NM_005983:	NM_005983:
6503	SLA	Src-like-adaptor	0.56	CCCGGTACTTTATTCTAAGAA	NM_006748:	NM_006748:
6503	SLA	Src-like-adaptor	-3.22	CTGGATCGGGTAGGTAAGAAT	NM_006748:	NM_006748:
84174	SLA2	Src-like-adaptor 2	-0.01	CAGGTTCTCAATTAAAGATTT	NM_032214:	NM_175077:NM_032214:
84174	SLA2	Src-like-adaptor 2	0.95	CATCAACAGGTTCTCAATTAA	NM_032214:	NM_175077:NM_032214:
6504	SLAMF1	signaling lymphocytic activation molecule family member 1	0.81	AACAAATTCCATCACAGTCTA	NM_003037:	NM_003037:
6504	SLAMF1	signaling lymphocytic activation molecule family member 1	-1.44	CAGAGTCTGTCCAGGAAACAA	NM_003037:	NM_003037:
114836	SLAMF6	SLAM family member 6	0.48	CACAATTTACTCCACAATTAA	NM_052931:	NM_052931:
114836	SLAMF6	SLAM family member 6	0.21	CAGGGAATGTAGTTTCACAAA	NM_052931:	NM_052931:
57823	SLAMF7	SLAM family member 7	0.46	CACTAATAGAACAATCCTAAA	NM_021181:	NM_021181:
57823	SLAMF7	SLAM family member 7	0.46	AACAGATATTGTGAGATTCAA	NM_021181:	NM_021181:
56833	SLAMF8	SLAM family member 8	-1.39	ACCATGGACTTTGGTATGGAA	NM_020125:	NM_020125:

56833	SLAMF8	SLAM family member 8	-0.22	CACTTGGGAATCAGTAGTCAA	NM_020125:	NM_020125:
89886	SLAMF9	SLAM family member 9	-2.47	CTGGCTGGCAATAAAGTCAAA	NM_033438:	NM_033438:
89886	SLAMF9	SLAM family member 9	-2.50	TCAGGGCTTTACCAAGCTCAA	NM_033438:	NM_033438:
6554	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-0.62	CACAAGTGCTGTAGAATTAAA	NM_003049:	NM_003049:
6554	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), membe	1.73	AGGGATCGTCCTCAAATCCAA	NM_003049:	NM_003049:
6555	SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family), membe	1.37	GCCTCTGAGTATCATATTAAA	NM_000452:	NM_000452:
6555	SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-0.15	CTCCTACACATTTCCCATCAA	NM_000452:	NM_000452:
8273	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-0.19	CATGGTGTTAATGCAGGACAA	NM_019848:	NM_019848:
8273	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-0.32	GCGGAGAGACTTCTGCATCAA	NM_019848:	NM_019848:
201780	SLC10A4	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-6.72	ACCAAACGTTGTCACAAATTA	NM_152679:	NM_152679:
201780	SLC10A4	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-0.80	ACCGCTCAGACTTCTCTCTAA	NM_152679:	NM_152679:
347051	SLC10A5	solute carrier family 10 (sodium/bile acid cotransporter family), membe	0.09	ATCAATTGGAATAGTCATCAA	XM_376781:	NM_001010893:
347051	SLC10A5	solute carrier family 10 (sodium/bile acid cotransporter family), membe	0.02	ATGCCTGTCAATTCTTATATA	XM_376781:	NM_001010893:
345274	SLC10A6	solute carrier family 10 (sodium/bile acid cotransporter family), membe	-0.96	TTGCAGCATATCAGACGTACA	NM_197965:	NM_197965:
345274	SLC10A6	solute carrier family 10 (sodium/bile acid cotransporter family), membe	0.83	CAGCTGATAGATGGATTTCTT	NM_197965:	NM_197965:
6557	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), men	-0.14	CTGGTGATTGGATATAAGAAA	NM_000338:	NM_000338:
6557	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), men	0.15	ACCAATGACATCCGGATTATA	NM_000338:	NM_000338:
6558	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), men	-1.20	CAGAGTATTCATTGGTGGAAA	NM_001046:	NM_001046:
6558	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), men	-0.16	CAGGATTTACACCACTAATTT	NM_001046:	NM_001046:
6559	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	-3.97	CAGGATGGACCAGGAGAGAAA	NM_000339:	NM_000339:
6559	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	-0.18	CAAGAAGACCATAGACATCTA	NM_000339:	NM_000339:
84561	SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	-0.17	CAAGCATAAAGTGTATCTCTA	NM_024628:	NM_024628:
84561	SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	-0.42	CTCGCAGGTGTCAAATGGATA	NM_024628:	NM_024628:
56996	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	-0.25	CTGGTGTTGATCGGAATCTAT	NM_020246:	NM_020246:
56996	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.57	CCCACTGGTGTTGATCGGAAT	NM_020246:	NM_020246:
64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter),	0.49	CAGATGAATCATGATTTCTAA	NM_022829:	NM_022829:NM_001011554:
64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter),	0.75	CCCAGTGATTACTTTCGATTA	NM_022829:	NM_022829:NM_001011554:
6572	SLC18A3	solute carrier family 18 (vesicular acetylcholine), member 3	0.22	TACGGAGAGCGAAGACGTGAA	NM_003055:	NM_003055:
6572	SLC18A3	solute carrier family 18 (vesicular acetylcholine), member 3	-2.62	CTGCTTGATGAGCCACCGCAA	NM_003055:	NM_003055:
10560	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-0.16	CTGCCTTTGTTTCTAAAGGTA	NM_006996:	NM_006996:
10560	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	0.31	AAGGTGTACGTATCATTTCTA	NM_006996:	NM_006996:
6505	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate trans	-0.08	ACGACCTACATCTGAAATCTA	NM_004170:	NM_004170:
6505	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate trans	-1.15	GAGGACTGTTCTAACTAGTAA	NM_004170:	NM_004170:
6509	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), men	0.28	CAGCCTTAGGTAAACAACTTA	NM_003038:	NM_003038:
6509	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), men	0.97	CCGCACATTGTCAAGTTAGAA	NM_003038:	NM_003038:
6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	-0.99	CACGCTGCCGCTGATGATGAA	NM_005628:	NM_005628:
6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	1.87	CAGCCTTTCGCTCATACTCTA	NM_005628:	NM_005628:
6574	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	0.00	CAAGCCGTCAGCAACCAAATA	NM_005415:	NM_005415:
6574	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	-1.50	CAGCTCGGTTTCTGTGCCGTA	NM_005415:	NM_005415:
6575	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	0.84	TGCCTAGAAGTCAATATTCAA	NM_006749:	NM_006749:
6575	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	0.39	TGCAGTTACTTATATATTAAA	NM_006749:	NM_006749:
51310	SLC22A17	solute carrier family 22 (organic cation transporter), member 17	0.52	AACATCCTCCTTTTCCTTTGC	NM_020372:	NM_016609:NM_020372:
51310	SLC22A17	solute carrier family 22 (organic cation transporter), member 17	0.73	AAGGCTGCCATCACCACTTTC	NM_020372:	NM_016609:NM_020372:
5002	SLC22A18	solute carrier family 22 (organic cation transporter), member 18	0.10	CAGACACAGACTGGCAATAAA	NM_002555:	NM_183233:NM_002555:
5002	SLC22A18	solute carrier family 22 (organic cation transporter), member 18	1.42	CACGTGCAGGTTGCTATCAAT	NM_002555:	NM_183233:NM_002555:
10864	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	0.47	CAGAGGCTGAAATTCAATAAA	NM_006672:	NM_006672:NM_153320:
10864	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	-0.08	CTCAAATGAGTTACTGAATAA	NM_006672:	NM_006672:NM_153320:
9187	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	0.82	ACTGCAGATTATGATGGTAAA	NM_004727:	NM_004727:
9187	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	0.02	CACAATGGGCATGGATCAGAA	NM_004727:	NM_004727:
25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	0.01	AAGGCGAGTCTGAGAATAGTA	NM_020344:	NM_020344:
25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	-0.19	AAGATTCTGGATTATACTCCA	NM_020344:	NM_020344:
57419	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	2.06	CAGAGCTAAGACACACTTATT	NM_020689:	NM_020689:
57419	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	-0.48	CACCATGCTTGTTCACTTGTA	NM_020689:	NM_020689:
123041	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	0.27	TCCGATTTGATGCACTTTGAA	NM_153646:	NM_153647:NM_153646:NM_153648:
123041	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	-0.18	TCCAGTTATTTATATGCCCAA	NM_153646:	NM_153647:NM_153646:NM_153648:
283652	SLC24A5	solute carrier family 24, member 5	-5.10	CTGCCTGTGGTTTGCTATCTA	NM_205850:	NM_205850:
283652	SLC24A5	solute carrier family 24, member 5	-3.26	ATGGATATCCGCATTTACATA	NM_205850:	NM_205850:
80024	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	0.92	CCGCCTTATGTTGCCGAAATA	NM_024959:	NM_024959:
80024	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), memb	1.22	CCGGGTATCTTCTAATACCAA	NM_024959:	NM_024959:
6576	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), men	-0.07	AAACACTCCTCTGGATGTGAT	NM_005984:	NM_005984:
6576	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), men	-1.07	AAAGCCCATGAACCCTCTGAT	NM_005984:	NM_005984:
8402	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), me	-0.77	TTGGATTGATGACACCAGCAA	NM_003562:	NM_003562:
8402	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), me	-0.81	CGGGCTGGACGTGCTGTTCAA	NM_003562:	NM_003562:
8604	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	-0.75	TCCCGAAATTTAAGTCTCCTA	NM_003705:	NM_003705:
8604	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	-0.62	CCGAGTCTGCTTACAGATTCA	NM_003705:	NM_003705:
10165	SLC25A13	solute carrier family 25, member 13 (citrin)	-1.23	CAGTATCTACCTCAAAGGCTA	NM_014251:	NM_014251:
10165	SLC25A13	solute carrier family 25, member 13 (citrin)	0.28	TAGCAGATTTATATGAGCCAA	NM_014251:	NM_014251:
9016	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	-0.58	ACCAGTCTATGATATTACTAA	NM_003951:	NM_022810:NM_003951:
9016	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	1.29	ACCGATGTTCTAAAGATTCGA	NM_003951:	NM_022810:NM_003951:
10166	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) m	0.56	AGGCCGTCCATTAGAGATTTA	NM_014252:	NM_014252:
10166	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) m	-0.06	ATAGGCCTGGATCGAAGTAAA	NM_014252:	NM_014252:
8034	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoant	-0.61	CAGGTCATGTGCACAGATTAA	NM_152707:	NM_152707:
8034	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoant	0.79	AGGGTTGGTTATATTGCAATA	NM_152707:	NM_152707:
10478	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane	1.35	ACCCAAATGATTCTCTTATAA	NM_006358:	NM_006358:
10478	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane	-3.21	CTGGACCTGTTGTCACCTTAA	NM_006358:	NM_006358:
60386	SLC25A19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), memb	1.77	ACCTATTTAATAGACATTAAA	NM_021734:	NM_021734:
60386	SLC25A19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), memb	0.29	AACCTATTTAATAGACATTAA	NM_021734:	NM_021734:
83884	SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) m	0.24	CCCTATGTACCTAATCTGAAA	NM_031947:	NM_031947:
83884	SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) m	1.00	TACCCTAAATCTTAACTTTAT	NM_031947:	NM_031947:
788	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 2	-1.73	AAGGAGTAGTAAGCAGAACTA	NM_000387:	NM_000387:
788	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 2	-1.92	CAGCTAGTGGAATGTATTTCA	NM_000387:	NM_000387:
79085	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), men	-8.66	CCGGCTTCTCATGACATGAAA	NM_024103:	NM_024103:
79085	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), men	-6.86	CCGGACGAGTTCTCAAAGCAA	NM_024103:	NM_024103:
29957	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), men	0.55	CCGAGAGTTGAAGATAGTATA	NM_013386:	NM_013386:NM_213651:
29957	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), men	-0.74	CTGACTATTTCTGAACAACAA	NM_013386:	NM_013386:NM_213651:
114789	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), men	0.74	GACGTTAGAAGTTGTCATTTA	NM_052901:	NM_052901:NM_001006641:NM_001006643:NM_001006642:
114789	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), men	0.85	CAGAGTTATGTCCTAACTATT	NM_052901:	NM_052901:NM_001006641:NM_001006643:NM_001006642:
9481	SLC25A27	solute carrier family 25, member 27	1.41	ATGAATCAACCACGAGATAAA	NM_004277:	NM_004277:
9481	SLC25A27	solute carrier family 25, member 27	0.88	CTCACGGTTTATCAAGTTTAT	NM_004277:	NM_004277:
123096	SLC25A29	solute carrier family 25, member 29	0.04	CTCAGGCTGCCTGTCCATAAA	NM_152333:	NM_152333:
123096	SLC25A29	solute carrier family 25, member 29	-0.78	CACCGTTATCCTGGAAACTGA	NM_152333:	NM_152333:
83447	SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	0.68	ATGGTATGACATATTTCTTAA	NM_031291:	NM_031291:
83447	SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	1.07	TCGGGAGAGTAAATTAAGAAA	NM_031291:	NM_031291:
81034	SLC25A32	solute carrier family 25, member 32	-4.05	ATGAGTCATTGTAGACATCTA	NM_030780:	NM_030780:
81034	SLC25A32	solute carrier family 25, member 32	2.39	TGGATCTAGATCCCAAATAAA	NM_030780:	NM_030780:
55186	SLC25A36	solute carrier family 25, member 36	0.42	AACCAATGAAATAGCGTCTAA	NM_018155:	NM_018155:
55186	SLC25A36	solute carrier family 25, member 36	-0.28	TGGCCTTTCGGTAATGTGAAA	NM_018155:	NM_018155:

291	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	0.18	CTGAATGTGAAACATCAATAA	NM_001151:	NM_001151:
291	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	-0.78	CAGATCCATTGTGTGGTTTAA	NM_001151:	NM_001151:
292	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	0.94	ATGTTGTATTCTATAACACAA	NM_001152:	NM_001152:
292	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	-1.57	CGGAAGATTGCTCGTGATGAA	NM_001152:	NM_001152:
293	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	0.76	AACCAAGAGAACCACGTAGAA	NM_001636:	NM_001636:
293	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran	0.89	AACAGAGGACGCAGAGGTCAA	NM_001636:	NM_001636:
1836	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	0.43	ACCAATCTATGTAATAGGCTA	NM_000112:	NM_000112:
1836	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	-0.58	CTGGTTAGCCTCTACACAATA	NM_000112:	NM_000112:
1811	SLC26A3	solute carrier family 26, member 3	-0.11	ATGCATAGGTTTAGCAGTATA	NM_000111:	NM_000111:
1811	SLC26A3	solute carrier family 26, member 3	0.21	TTGGCTTTAGTCCACTTCGAA	NM_000111:	NM_000111:
5172	SLC26A4	solute carrier family 26, member 4	1.25	AAGAGTGAATGTAATAGTCTT	NM_000441:	NM_000441:
5172	SLC26A4	solute carrier family 26, member 4	0.35	TCACGAATGATTAATCATAAA	NM_000441:	NM_000441:
6513	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	0.19	CAGGCTTGAAATCGCATTATT	NM_006516:	NM_006516:
6513	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	0.21	CAGACACTAAGTTATAGTATA	NM_006516:	NM_006516:
6514	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	0.30	CAGGGTGCTAACGTATCTCTA	NM_000340:	NM_000340:
6514	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	1.27	CAGACTTTAGCTTACAGTCAA	NM_000340:	NM_000340:
6517	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	-3.81	CACCTTGGACTCCTCCCACAA	NM_001042:	NM_001042:
6517	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	-0.21	ACGCTGCTGCCTCCTATGAAA	NM_001042:	NM_001042:
347734	SLC35B2	solute carrier family 35, member B2	-0.06	CAGCTTTATGGTACCTGGCTA	NM_178148:	NM_178148:
347734	SLC35B2	solute carrier family 35, member B2	1.30	CCCGATGTGGCAGGCCCTGAA	NM_178148:	NM_178148:
51006	SLC35C2	solute carrier family 35, member C2	0.17	CTCGCTGTACACAATGACCAA	NM_015945:	NM_173073:NM_015945:NM_173179:
51006	SLC35C2	solute carrier family 35, member C2	-0.39	CAGGAAATAAATGAATGTTTA	NM_015945:	NM_173073:NM_015945:NM_173179:
54407	SLC38A2	solute carrier family 38, member 2	-0.99	CTCATCAGGCATAATGTCTAA	NM_018976:	NM_018976:
54407	SLC38A2	solute carrier family 38, member 2	-0.12	TACGAACATGTTGAGTCAGAA	NM_018976:	NM_018976:
25800	SLC39A6	solute carrier family 39 (zinc transporter), member 6	-0.23	CTGGTTGATATGGTACCTGAA	NM_012319:	NM_012319:
25800	SLC39A6	solute carrier family 39 (zinc transporter), member 6	0.16	AAGGCTTATCAAGTGGTTTAA	NM_012319:	NM_012319:
6519	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transpo	0.52	CCGGCAGACCATGGACCAATA	NM_000341:	NM_000341:
6519	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transpo	-1.17	CCCGGACACGGTCACACAATA	NM_000341:	NM_000341:
30061	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	-1.01	AACCGTTTATATGCACTTTCA	NM_014585:	NM_014585:
30061	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	1.55	CAGATTCTTATCTGTACTAGA	NM_014585:	NM_014585:
51151	SLC45A2	solute carrier family 45, member 2	-0.62	ATGGACGGCCTTCCTGTCCAA	NM_016180:	NM_001012509:NM_016180:
51151	SLC45A2	solute carrier family 45, member 2	0.53	TCGCAGGGCAATGACATTAAA	NM_016180:	NM_001012509:NM_016180:
6521	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte memb	-1.64	CCGCATCTTGCTTCTGTTCAA	NM_000342:	NM_000342:
6521	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte memb	-5.54	CAGGATACCTACACCCAGAAA	NM_000342:	NM_000342:
57282	SLC4A10 (sol	solute carrier family 4, sodium bicarbonate transporter-like, member 1	-0.20	TAGCTTAGCATTAGTGACTTA	NM_022058:	NM_022058:
57282	SLC4A10 (sol	solute carrier family 4, sodium bicarbonate transporter-like, member 1	0.44	CACAGGCATCGTGGTCATAAA	NM_022058:	NM_022058:
8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	1.51	CTGTGATATATCCTAACTATA	NM_003759:	NM_003759:
8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	0.41	TAACGTGGTATTTAAAGGTAA	NM_003759:	NM_003759:
9497	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.86	ATAGAGTAAATTGTTAATGTA	NM_003615:	NM_003615:
9497	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-0.74	CCGTGGAGACTATGTATTTAA	NM_003615:	NM_003615:
9498	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	1.93	GACGGCTATCTTAAAGTTTAT	NM_004858:	NM_004858:
9498	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	-1.53	AGCCGTCATTATTAACAGGAA	NM_004858:	NM_004858:
83697	SLC4A9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	-1.80	TAGGGTGAAGCTGTTGTTGAT	NM_031467:	NM_031467:
83697	SLC4A9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	-0.19	CAGCAGCATTCAGTTCACTAA	NM_031467:	NM_031467:
6523	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	-0.55	GAGGACAGTGTTGAACGTCAA	NM_000343:	NM_000343:
6523	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	0.03	AAGGAGACCATTGAAATAGAA	NM_000343:	NM_000343:
6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	0.03	CTGGATTGCCTTGTATGCAAA	NM_000453:	NM_000453:
6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	-3.79	CAGCTTCTATGCCATCTCCTA	NM_000453:	NM_000453:
6529	SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member	1.91	CGGGCGTTATGTAAGTTTCTA	NM_003042:	NM_003042:
6529	SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member	0.70	CACGTAAGGTCTCATTTGATA	NM_003042:	NM_003042:
6538	SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member	-0.02	CCCACGGATGGTGACAGTTAA	NM_014229:	NM_014229:
6538	SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member	-0.71	CCGGCCACCGTCGCTCATTAA	NM_014229:	NM_014229:
6539	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), m	-3.72	CAGGCCAGTGTCTTCCCATTA	NM_003044:	NM_003044:
6539	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), m	0.92	AAGGCCGATATTGCTAACTGA	NM_003044:	NM_003044:
6540	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member	0.26	CTCATCCTTCATTCCATTAAA	NM_016615:	NM_016615:
6540	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member	-0.39	TCCGCTGACCTACAACAAGAA	NM_016615:	NM_016615:
11254	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	-0.27	CAGGTGATAACTTGCATACTA	NM_007231:	NM_007231:
11254	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	0.32	CCGGAATGAGATCTCATTGAA	NM_007231:	NM_007231:
55117	SLC6A15	solute carrier family 6, member 15	-1.45	CCCAATGGACGGTATGGAATA	NM_182767:	NM_182767:
55117	SLC6A15	solute carrier family 6, member 15	0.92	CCAGCAGATATTACTACTATA	NM_182767:	NM_182767:
28968	SLC6A16	solute carrier family 6, member 16	0.35	CACCAGCTAACACCCAGTAAA	NM_014037:	NM_014037:
28968	SLC6A16	solute carrier family 6, member 16	0.76	ATCGTCGTTGTCGTATTTGAA	NM_014037:	NM_014037:
388662	SLC6A17	solute carrier family 6, member 17	0.89	CTGGATTTATGGAACCAAGAA	XM_371280:	NM_001010898:
388662	SLC6A17	solute carrier family 6, member 17	-0.96	GTGGTCGAGAATGCTGAGAAA	XM_371280:	NM_001010898:
348932	SLC6A18	solute carrier family 6, member 18	-4.66	GTGGGTGTCGTTTATGTTTAT	NM_182632:	NM_182632:
348932	SLC6A18	solute carrier family 6, member 18	1.48	CAGCCTCATCAACGACTTTGA	NM_182632:	NM_182632:
340024	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	0.35	CAGGTTCAATAAGGACATCGA	NM_001003841:	NM_001003841:
340024	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	-1.74	CTCGGTGATTGTGTCCATCAT	NM_001003841:	NM_001003841:
6530	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), me	-0.23	GCCCATCTACGTCATCTATAA	NM_001043:	NM_001043:
6530	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), me	-0.03	CGCCCTGTTCTGCATAACCAA	NM_001043:	NM_001043:
54716	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	0.38	TCCAATTATATGGAAGAGTTA	NM_020208:	NM_020208:NM_022405:
54716	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	-1.09	CCCGTGGATTCAATCTTCTTA	NM_020208:	NM_020208:NM_022405:
6531	SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine), memb	-4.08	CAGCATCGTGTGGGTCCCTAA	NM_001044:	NM_001044:
6531	SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine), memb	-2.78	TAGTTTGAATTCATGCCTCAA	NM_001044:	NM_001044:
6532	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), memb	1.81	TCACTGTTCATGAATACGTAA	NM_001045:	NM_001045:
6532	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), memb	-1.73	CCGCTTGAATGCTGTGTAACA	NM_001045:	NM_001045:
6533	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member	-0.60	TCAGACCAAATTCTAGACCAA	NM_003043:	NM_003043:
6533	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member	-1.00	CACCCATCTTAAGGTGGTATA	NM_003043:	NM_003043:
6534	SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), membe	-1.16	CACGTTTCACCAGAACATCTA	NM_014228:	NM_014228:
6534	SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), membe	-0.44	CCTGGTGTATAGCATCGTCAA	NM_014228:	NM_014228:
6535	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), membe	-0.21	AAGGTGAATGCCAGATGTAAA	NM_005629:	NM_005629:
6535	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), membe	0.69	GAGAGTATATATAGATCTCTA	NM_005629:	NM_005629:
6536	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member	-1.07	CACCATGGCTTCCTACAACAA	NM_006934:	NM_006934:NM_001024845:NM_201649:
6536	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member	-0.97	ACGGCATCATGTACTACCTAA	NM_006934:	NM_006934:NM_001024845:NM_201649:
6541	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.80	GAGGGTTGGTTTATTATCAAA	NM_003045:	NM_003045:
6541	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.01	ACGCTTATGACTCCTAATGTA	NM_003045:	NM_003045:
56301	SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) me	-0.85	CAGCTTCATCTCAGAGCCTAT	NM_019849:	NM_019849:
56301	SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) me	-0.03	CACGTTCACCAACATTGCCTA	NM_019849:	NM_019849:
23657	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) me	-0.71	CACACCTTAATTATCATTCAA	NM_014331:	NM_014331:
23657	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) me	0.27	AACCACCTGTTTCACTAATAA	NM_014331:	NM_014331:
157724	SLC7A13	solute carrier family 7, (cationic amino acid transporter, y+ system) me	-4.92	AAGGTTAAACATATGATAGAA	NM_138817:	NM_138817:
157724	SLC7A13	solute carrier family 7, (cationic amino acid transporter, y+ system) me	0.20	CGGGTTCATTATGGTCTATAT	NM_138817:	NM_138817:
6542	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-0.23	CAGCATCTTGGTGAACATTTA	NM_003046:	NM_003046:NM_001008539:
6542	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-1.86	CAGGGTAACCTCGAAGAGTGA	NM_003046:	NM_003046:NM_001008539:
84889	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-0.01	TCGGCATATCTCTACAGCTAT	NM_032803:	NM_032803:
84889	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), me	1.10	TAGCTGCTTACCAACTTTAAA	NM_032803:	NM_032803:
6545	SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.02	CAGAGCCTTCTTGTTTATGAT	NM_004173:	NM_004173:
6545	SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-0.74	AGGGCTGAACTCCACACACTA	NM_004173:	NM_004173:
8140	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-1.23	ACGCACGACGTCAGCCTCTTA	NM_003486:	NM_003486:

8140	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.40	AAGGGTGTTGTGTCCAATCTA	NM_003486:	NM_003486:
9057	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-1.09	CAATAGGCTGATTGTATTTAA	NM_003983:	NM_003983:
9057	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-5.65	CAGGATCTGGGCCAACCTCAA	NM_003983:	NM_003983:
9056	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-0.54	CAGGTGCTGGATGACAATAAA	NM_003982:	NM_003982:
9056	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-2.45	TAGAGAGACATGAAACTATCA	NM_003982:	NM_003982:
23428	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.97	CCCGAATTCTGTCTGCTTAAA	NM_012244:	NM_012244:NM_182728:
23428	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), me	-0.17	CAGGCGGTTGAGGAACATATT	NM_012244:	NM_012244:NM_182728:
11136	SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.80	TGACATAAACTCGTTAGTCAA	NM_014270:	NM_014270:
11136	SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), me	0.36	TGGTATCATAGCAACGATTTA	NM_014270:	NM_014270:
6548	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antip	0.06	CAGACCAATCTTAGTTTCTAA	NM_003047:	NM_003047:
6548	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antip	1.00	CCGGTTTAATAAGAAATATGT	NM_003047:	NM_003047:
6549	SLC9A2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	-0.43	CAGGTGATCTATGCTGATCTA	NM_003048:	NM_003048:
6549	SLC9A2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	1.42	ATGGGTAGCAATCGTATTATT	NM_003048:	NM_003048:
6550	SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	-1.25	CACCACCATCATCGTAGTGTT	NM_004174:	NM_004174:
6550	SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	1.02	TGCGCAGAATTTCACCATCAA	NM_004174:	NM_004174:
9368	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regula	-1.54	AGCGAGGAGCTGAATTCCCAA	NM_004252:	NM_004252:
9368	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regula	-0.44	CACCAGAAACGCAGCAGCAAA	NM_004252:	NM_004252:
9351	SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regula	0.15	CCGAGACAGATGAACACTTCA	NM_004785:	NM_004785:
9351	SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regula	1.01	CGCGCTCTAAATAATTGCAAT	NM_004785:	NM_004785:
389015	SLC9A4	solute carrier family 9 (sodium/hydrogen exchanger), member 4	-2.97	TACGGTCTATTTCATAATTGA	AL833048:	NM_001011552:
389015	SLC9A4	solute carrier family 9 (sodium/hydrogen exchanger), member 4	-8.03	ACAAGCGTGATTAATCAGTAA	AL833048:	NM_001011552:
6553	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	0.39	CTGGGTCTAAGTCTAAACCTT	NM_004594:	NM_004594:
6553	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	-1.41	AAGCAAGAGCATCATTCCTAT	NM_004594:	NM_004594:
10479	SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0.39	AAGCTTACTAATACTCACTTA	NM_006359:	NM_006359:
10479	SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0.12	CCGCTAAATTTGTTAGATAAT	NM_006359:	NM_006359:
84679	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), member 7	0.76	TCCGAAGAGGACCAGAATGAA	NM_032591:	NM_032591:
84679	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), member 7	0.23	CAACGTGACTAAGTTTACCAA	NM_032591:	NM_032591:
23315	SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0.38	TTGGCTCACCTTGGTAACAAA	NM_015266:	NM_015266:
23315	SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	-0.69	CAGAGTCGCCTTAGTCCAGAA	NM_015266:	NM_015266:
285195	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0.43	CCACTGTTTGTTAGGCCTTAA	NM_173653:	NM_173653:
285195	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0.11	AAGGGAATGCCCAGCTATTTA	NM_173653:	NM_173653:
10599	SLCO1B1	solute carrier organic anion transporter family, member 1B1	-1.04	TAGCTACATATTTGTGGTTAA	NM_006446:	NM_006446:
10599	SLCO1B1	solute carrier organic anion transporter family, member 1B1	2.35	TGGGCTTGTCTTCAATGTTAA	NM_006446:	NM_006446:
28234	SLCO1B3	solute carrier organic anion transporter family, member 1B3	0.79	TTCATCTATGTTGCAATTCAA	NM_019844:	NM_019844:
28234	SLCO1B3	solute carrier organic anion transporter family, member 1B3	-2.23	TAGCTATGCCTTTATGGTTAA	NM_019844:	NM_019844:
6585	SLIT1	slit homolog 1 (Drosophila)	-0.67	CCGGATCTGAACCCATGTCAA	NM_003061:	NM_003061:
6585	SLIT1	slit homolog 1 (Drosophila)	-5.20	CACGGCAGAACTGCGATTGAA	NM_003061:	NM_003061:
9353	SLIT2	slit homolog 2 (Drosophila)	0.09	ACGAATTGACCTGAGCAATAA	NM_004787:	NM_004787:
9353	SLIT2	slit homolog 2 (Drosophila)	0.38	CACCGAGAGACTGGATTTAAA	NM_004787:	NM_004787:
6586	SLIT3	slit homolog 3 (Drosophila)	-1.60	CACCCAGTACAAGAAACTGAA	NM_003062:	NM_003062:
6586	SLIT3	slit homolog 3 (Drosophila)	0.33	CCAGACTAGATTTGAGTGAAA	NM_003062:	NM_003062:
84189	SLITRK6	SLIT and NTRK-like family, member 6	0.21	CTGGAACTTGACAATTATAAA	NM_032229:	NM_032229:
84189	SLITRK6	SLIT and NTRK-like family, member 6	-0.03	AGGGTCAAATATGAAATACAA	NM_032229:	NM_032229:
9748	SLK	STE20-like kinase (yeast)	-0.41	CCAGATCAGGACCGTGATAAA	NM_014720:	NM_014720:
9748	SLK	STE20-like kinase (yeast)	-6.42	TAGCATCTTGTGATCACCCAA	NM_014720:	NM_014720:
57152	SLURP1	secreted LY6/PLAUR domain containing 1	-1.03	CAGGACCATTACCCGCTGCAA	NM_020427:	NM_020427:
57152	SLURP1	secreted LY6/PLAUR domain containing 1	-7.20	CAGGGCGGAAGGTGCTCCTCA	NM_020427:	NM_020427:
4086	SMAD1	SMAD, mothers against DPP homolog 1 (Drosophila)	-0.02	CAGGACTTTGTGTACAGTTAA	NM_005900:	NM_001003688:NM_005900:
4086	SMAD1	SMAD, mothers against DPP homolog 1 (Drosophila)	0.19	CACACACACCTTGGTAACATA	NM_005900:	NM_001003688:NM_005900:
4087	SMAD2	SMAD, mothers against DPP homolog 2 (Drosophila)	-0.20	CAGGTAATGTATCATGATCCA	NM_005901:	NM_001003652:NM_005901:
4087	SMAD2	SMAD, mothers against DPP homolog 2 (Drosophila)	-1.95	CTAGAAATACTCTCCCATTAA	NM_005901:	NM_001003652:NM_005901:
4088	SMAD3	SMAD, mothers against DPP homolog 3 (Drosophila)	0.58	AAGGAGCACCTTGACAGACTT	NM_005902:	NM_005902:
4088	SMAD3	SMAD, mothers against DPP homolog 3 (Drosophila)	-1.20	ATCAAGGGATTTCCTATGGAA	NM_005902:	NM_005902:
4089	SMAD4	SMAD, mothers against DPP homolog 4 (Drosophila)	-0.79	AAGCAGCGTCACTCTACCTAA	NM_005359:	NM_005359:
4089	SMAD4	SMAD, mothers against DPP homolog 4 (Drosophila)	-0.77	CCCTGTTAAACAGTAGTTGTA	NM_005359:	NM_005359:
4090	SMAD5	SMAD, mothers against DPP homolog 5 (Drosophila)	0.02	AACATCTGATGTACCAATTTA	NM_005903:	NM_005903:NM_001001419:NM_001001420:
4090	SMAD5	SMAD, mothers against DPP homolog 5 (Drosophila)	0.40	CTGAGGTGAAATCCAGAGTAA	NM_005903:	NM_005903:NM_001001419:NM_001001420:
4091	SMAD6	SMAD, mothers against DPP homolog 6 (Drosophila)	0.23	TACCAGTCACTCGATAATAAA	NM_005585:	NM_005585:
4091	SMAD6	SMAD, mothers against DPP homolog 6 (Drosophila)	-0.24	AAGACGCACTTTGGCTTATAA	NM_005585:	NM_005585:
4092	SMAD7	SMAD, mothers against DPP homolog 7 (Drosophila)	-2.45	AAGGAGTTTATGTTCCATTAA	NM_005904:	NM_005904:
4092	SMAD7	SMAD, mothers against DPP homolog 7 (Drosophila)	0.21	CAGGCATTCCTCGGAAGTCAA	NM_005904:	NM_005904:
6595	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chro	0.50	AGGCGTCTACATAAGGTGTTA	NM_003070:	NM_139045:NM_003070:
6595	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chro	0.01	GCCCGCATAGCTCATAGGATA	NM_003070:	NM_139045:NM_003070:
6596	SMARCA3	SWI/SNF related, matrix associated, actin dependent regulator of chro	0.82	AACAATGTGAATGGAAATCAA	NM_003071:	NM_003071:NM_139048:
6596	SMARCA3	SWI/SNF related, matrix associated, actin dependent regulator of chro	0.96	ACGGGAGTAGTTAATAATAAT	NM_003071:	NM_003071:NM_139048:
6597	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chro	-0.11	CCCGTGGACTTCAAGAAGATA	NM_003072:	NM_003072:
6597	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chro	0.62	CCGCGCTACAACCAGATGAAA	NM_003072:	NM_003072:
56916	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chro	0.48	CAGCATAGGTACCTCAGATTA	NM_020159:	NM_020159:
56916	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chro	0.78	AAGGGTGATAGAGTTGTGTTA	NM_020159:	NM_020159:
50485	SMARCAL1	SWI/SNF related, matrix associated, actin dependent regulator of chro	-0.62	CAGCTTTGACCTTCTTAGCAA	NM_014140:	NM_014140:
50485	SMARCAL1	SWI/SNF related, matrix associated, actin dependent regulator of chro	0.86	TTGAGTTATGAGTTAGGTCAA	NM_014140:	NM_014140:
6604	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chro	-3.53	CAGTCGCTACTTCTACTGCAA	NM_003078:	NM_003078:NM_001003801:NM_001003802:
6604	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chro	-0.98	CTCAAGGTGATGACAGATGTA	NM_003078:	NM_003078:NM_001003801:NM_001003802:
8243	SMC1L1	SMC1 structural maintenance of chromosomes 1-like 1 (yeast)	1.10	CACCATCACACTTTAATTCCA	NM_006306:	NM_006306:
8243	SMC1L1	SMC1 structural maintenance of chromosomes 1-like 1 (yeast)	0.60	CGGCGTATTGATGAAATCAAT	NM_006306:	NM_006306:
10592	SMC2L1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	-0.06	CAGGTGGTTATTGGTGGTAGA	NM_006444:	NM_006444:
10592	SMC2L1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	-0.19	CTGAAACGTCGATACACTATA	NM_006444:	NM_006444:
23347	SMCHD1	structural maintenance of chromosomes flexible hinge domain contain	0.18	CCCGTTCGTCTCAATGTTAAA	XM_113962:	XM_113962:
23347	SMCHD1	structural maintenance of chromosomes flexible hinge domain contain	-0.01	AGGACCAATTATCTCAGTCTA	XM_113962:	XM_113962:
8242	SMCX	Smcy homolog, X-linked (mouse)	-0.32	CCGAGAGGAGCTAGAGCCAAA	NM_004187:	NM_004187:
8242	SMCX	Smcy homolog, X-linked (mouse)	-0.11	CCCAGAGAAGCTAGACCTGAA	NM_004187:	NM_004187:
8284	SMCY	Smcy homolog, Y-linked (mouse)	0.31	CAGGGTAGAAACGTTGAGAAT	NM_004653:	NM_004653:
8284	SMCY	Smcy homolog, Y-linked (mouse)	1.00	CCCAGAGACGTTGGATCTCAA	NM_004653:	NM_004653:
23049	SMG1	PI-3-kinase-related kinase SMG-1	-2.40	ATCGATGTTGCCAGACTACTA	NM_014006:	NM_015092:
23049	SMG1	PI-3-kinase-related kinase SMG-1	0.40	CACCATGGTATTACAGGTTCA	NM_014006:	NM_015092:
6608	SMO	smoothened homolog (Drosophila)	-2.91	CCGGGACTATGTGCTATGTCA	NM_005631:	NM_005631:
6608	SMO	smoothened homolog (Drosophila)	1.17	CTGGCGGAACTCGAATCGCTA	NM_005631:	NM_005631:
54498	SMOX	spermine oxidase	-0.74	CCGGCACGATAAACCAGTCAA	NM_019025:	NM_175842:NM_175840:NM_175839:NM_019025:
54498	SMOX	spermine oxidase	-1.06	ACCGACAAGATCTTTCTGGAA	NM_019025:	NM_175842:NM_175840:NM_175839:NM_019025:
6609	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomye	0.47	CTGGTTTAGCTGGATATGGGA	NM_000543:	NM_001007593:NM_000543:
6609	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomye	1.15	TGGAATTATTACCGAATTGTA	NM_000543:	NM_001007593:NM_000543:
23583	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	-2.44	AAGCATGGGACATGAAATTAA	NM_014311:	NM_014311:
23583	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	-1.52	CTCGAAGTCATTCTTGGCCAA	NM_014311:	NM_014311:
57154	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	0.36	AACCTCGATGATGTAAATCCA	NM_020429:	NM_181349:NM_020429:
57154	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	-0.14	AAGGATAACCTCGATGATGTA	NM_020429:	NM_181349:NM_020429:
64750	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	-1.29	CACCCTATGAAAGCTATGAAA	NM_022739:	NM_022739:
64750	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	1.46	CCGGATCTTCACAACAGTTTA	NM_022739:	NM_022739:

150572	SMYD1	SET and MYND domain containing 1	-1.34	CAACTGTACTGTCATATTTAA	NM_198274:	NM_198274:
150572	SMYD1	SET and MYND domain containing 1	-3.16	CGGGATGATCTGCAAAGCCTA	NM_198274:	NM_198274:
56950	SMYD2	SET and MYND domain containing 2	-0.02	GAGGTTAGTCTGAATCTTGAA	NM_020197:	NM_020197:
56950	SMYD2	SET and MYND domain containing 2	-2.46	CCGGAGGGCCAAGCACTATAA	NM_020197:	NM_020197:
10322	SMYD5	SMYD family member 5	0.54	AACATTGAAGTCTTCCAGAAA	NM_006062:	NM_006062:
10322	SMYD5	SMYD family member 5	-2.16	CTGGCCTTATGGAGTATGGAA	NM_006062:	NM_006062:
6615	SNAI1	snail homolog 1 (Drosophila)	0.44	AAGCAGTTAATTTATATATTA	NM_005985:	NM_005985:
6615	SNAI1	snail homolog 1 (Drosophila)	0.48	CCGAATGTCCCTGCTCCACAA	NM_005985:	NM_005985:
6591	SNAI2	snail homolog 2 (Drosophila)	-2.39	CACACTGAGTGACGCAATCAA	NM_003068:	NM_003068:
6591	SNAI2	snail homolog 2 (Drosophila)	0.28	CCGAAGCCAAATGACAAATAA	NM_003068:	NM_003068:
8773	SNAP23	synaptosomal-associated protein, 23kDa	0.51	CTGGCAAGGCTTATAAGACAA	NM_003825:	NM_003825:
8773	SNAP23	synaptosomal-associated protein, 23kDa	-1.49	CAGGCCTATTAACATCATACA	NM_003825:	NM_130798:NM_003825:
6616	SNAP25	synaptosomal-associated protein, 25kDa	-0.34	AAGGTTGTACATAGTGGTCAT	NM_003081:	NM_130811:NM_003081:
6616	SNAP25	synaptosomal-associated protein, 25kDa	-1.54	AAGATTAAGTTATACCAGCAA	NM_003081:	NM_130811:NM_003081:
9342	SNAP29	synaptosomal-associated protein, 29kDa	-0.38	CAGAAGATCGACAGCAACCTA	NM_004782:	NM_004782:
9342	SNAP29	synaptosomal-associated protein, 29kDa	1.90	CAGACCTAAGCTAATTATTTA	NM_004782:	NM_004782:
6622	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	0.57	CATGCTTATAAGCAACATGAA	NM_000345:	NM_007308:NM_000345:
6622	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	1.33	CCCAGTCATGACATTTCTCAA	NM_000345:	NM_007308:NM_000345:
27044	SND1	staphylococcal nuclease domain containing 1	-0.01	ATCCACCGTGTTGCAGATATA	NM_014390:	NM_014390:
27044	SND1	staphylococcal nuclease domain containing 1	0.03	CAGGCTGAACCTGTGGCGCTA	NM_014390:	NM_014390:
25992	SNED1	sushi, nidogen and EGF-like domains 1	1.17	CACCTAGGCTTCAGCCTTAAA	XM_059482:	XM_059482:
25992	SNED1	sushi, nidogen and EGF-like domains 1	0.64	CAGGTAGTAAACACGATCTTA	XM_059482:	XM_059482:
150094	SNF1LK	SNF1-like kinase	0.50	AGCGAAATAAGCAATACGTTA	NM_173354:	NM_173354:
23235	SNF1LK2	SNF1-like kinase 2	0.13	CCGAAGGATGTTGGTCCTAGA	NM_015191:	NM_015191:
54861	SNRK	SNF related kinase	0.26	ACCACTGAATTGGAACGGATA	NM_017719:	NM_017719:
54861	SNRK	SNF related kinase	0.63	CACCACTGAATTGGAACGGAT	NM_017719:	NM_017719:
6625	SNRP70	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	-0.80	AAGATTGAGCGGCGACAGCAA	NM_003089:	NM_003089:NM_001009820:
6625	SNRP70	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	-3.36	CCGGAGAGAGTTTGAGGTGTA	NM_003089:	NM_003089:NM_001009820:
6627	SNRPA1 (sma	small nuclear ribonucleoprotein polypeptide A'	-9.61	AGCCTTGTTTGTGTTAGCAAA	NM_003090:	NM_003090:
6627	SNRPA1 (sma	small nuclear ribonucleoprotein polypeptide A'	-6.89	CAGCATTGTTGAAATGCTTAA	NM_003090:	NM_003090:
6632	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	1.15	CAGAGCTGTCTATTTAGTATA	NM_006938:	NM_006938:
6632	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	1.35	TAGGCTAAACTTAACAATATA	NM_006938:	NM_006938:
6634	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	0.77	AAGGACTTTGTGTTCATTTGA	NM_004175:	NM_004175:
6634	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	-8.49	ACCCATGTTAAAGAGCATGAA	NM_004175:	NM_004175:
6637	SNRPG	small nuclear ribonucleoprotein polypeptide G	1.03	AAGAATCTTATTAAATGCGAA	NM_003096:	NM_003096:
6637	SNRPG	small nuclear ribonucleoprotein polypeptide G	1.06	CTGGTTGACATTGATTTCAAA	NM_003096:	NM_003096:
22938	SNW1	SNW domain containing 1	-5.91	CCCGATGAAGAAGCTATTAAA	NM_012245:	NM_012245:
22938	SNW1	SNW domain containing 1	-5.80	CTGGATATGGGACGAAAGAAA	NM_012245:	NM_012245:
6642	SNX1	sorting nexin 1	1.89	CTCGGGTGACTCAATATGAAA	NM_003099:	NM_003099:NM_148955:NM_152826:
6642	SNX1	sorting nexin 1	-0.36	CGCGGTGGTCAGTAAACATCA	NM_003099:	NM_003099:NM_148955:NM_152826:
23161	SNX13	sorting nexin 13	0.62	ACGGGTGCCAATATAATTGAT	NM_015132:	NM_015132:
23161	SNX13	sorting nexin 13	0.50	GAGCTTATTAGTCATAGTAAA	NM_015132:	NM_015132:
9784	SNX17	sorting nexin 17	-0.12	CTGGCCCTCGATGCCAAATTA	NM_014748:	NM_014748:
9784	SNX17	sorting nexin 17	0.75	CAGCGAGACTTTCAACAGTTT	NM_014748:	NM_014748:
8723	SNX4 (sorting	sorting nexin 4	1.92	CTCGTTATTTCTAATGATGTA	NM_003794:	NM_003794:
8723	SNX4 (sorting	sorting nexin 4	-0.86	CCCATCCTTTGTAGAGACAAA	NM_003794:	NM_003794:
58533	SNX6	sorting nexin 6	0.50	CCGCGGACTTAAAGCAATAAA	NM_021249:	NM_152233:NM_021249:
58533	SNX6	sorting nexin 6	-0.02	TCGCCAGTAGTTATATTACAA	NM_021249:	NM_152233:NM_021249:
51429	SNX9	sorting nexin 9	-0.15	TACCCAGTGTCAGATAATTAA	NM_016224:	NM_016224:
51429	SNX9	sorting nexin 9	-0.02	CCCATCATTGTTGGAGATTAT	NM_016224:	NM_016224:
8651	SOCS1	suppressor of cytokine signaling 1	-1.49	CTGGTTGTTGTAGCAGCTTAA	NM_003745:	NM_003745:
8651	SOCS1	suppressor of cytokine signaling 1	-0.48	CCCGCCGTGCACGCAGCATTA	NM_003745:	NM_003745:
8835	SOCS2	suppressor of cytokine signaling 2	1.22	TAGGCATTCTACCCTTTGAAA	NM_003877:	NM_003877:
8835	SOCS2	suppressor of cytokine signaling 2	-0.06	AAGAGGTAGCTAGGTGTTTAA	NM_003877:	NM_003877:
9021	SOCS3	suppressor of cytokine signaling 3	0.25	AAACATTTCAGTAATTTATAA	NM_003955:	NM_003955:
9021	SOCS3	suppressor of cytokine signaling 3	0.62	TTGCACATATTTATATTTATA	NM_003955:	NM_003955:
122809	SOCS4	suppressor of cytokine signaling 4	-0.04	TAGGTGATACTTGTAACTCGA	NM_080867:	NM_199421:NM_080867:
122809	SOCS4	suppressor of cytokine signaling 4	-0.62	CAGTAAGATATTGGACACAAA	NM_080867:	NM_199421:NM_080867:
9655	SOCS5	suppressor of cytokine signaling 5	0.26	TCCAATGACATATTATAGTAA	NM_014011:	NM_014011:NM_144949:
9655	SOCS5	suppressor of cytokine signaling 5	-1.34	CAGAGTTAATGAACAGTCTAA	NM_014011:	NM_014011:NM_144949:
9306	SOCS6	suppressor of cytokine signaling 6	-0.61	CGGGTACAAATTGGCATAACA	NM_004232:	NM_004232:
9306	SOCS6	suppressor of cytokine signaling 6	0.93	TTGATCTAATTGAGCATTCAA	NM_004232:	NM_004232:
30837	SOCS7	suppressor of cytokine signaling 7	-0.58	ACCAAATTAAGCTACCATGAA	NM_014598:	NM_014598:
30837	SOCS7	suppressor of cytokine signaling 7	-0.10	CCGAAAGTTCTACTACTATGA	NM_014598:	NM_014598:
6647	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult	-0.95	ATGGCACTTATTATGAGGCTA	NM_000454:	NM_000454:
6647	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult	0.50	CCAGTGCAGGTCCTCACTTTA	NM_000454:	NM_000454:
6648	SOD2	superoxide dismutase 2, mitochondrial	1.02	ATCGTTATGCTGAGTATGTTA	NM_000636:	NM_000636:
6648	SOD2	superoxide dismutase 2, mitochondrial	0.88	CTAAATTACAATTGTCATTTA	NM_000636:	NM_000636:
6649	SOD3	superoxide dismutase 3, extracellular	0.10	AACCTTTGTGTTACAGATTAA	NM_003102:	NM_003102:
6649	SOD3	superoxide dismutase 3, extracellular	1.29	CTCCTTCATCTCTTTAATAAT	NM_003102:	NM_003102:
6650	SOLH	small optic lobes homolog (Drosophila)	-2.01	CAGGCAGGTCCTGGTGATCTT	NM_005632:	NM_005632:
6650	SOLH	small optic lobes homolog (Drosophila)	-2.01	ACGGGTGTCCTCGGCCCAGAA	NM_005632:	NM_005632:
10580	SORBS1	sorbin and SH3 domain containing 1	-1.66	ACCCGGCAACACGAAAGCAAA	NM_006434:	NM_006434:NM_015385:NM_001034954:NM_001034955:NM_001034956:NM_024991:NM_001034957:
10580	SORBS1	sorbin and SH3 domain containing 1	1.17	CAGGATTCCAGTCCTCTACTA	NM_006434:	NM_006434:NM_024991:NM_001034957:
114815	SORCS1	sortilin-related VPS10 domain containing receptor 1	-0.72	CCGGCTGAACTTCTACATTCA	NM_052918:	NM_001013031:NM_052918:
114815	SORCS1	sortilin-related VPS10 domain containing receptor 1	-0.12	CAGGAAGGTGGTTTCCAATAA	NM_052918:	NM_001013031:NM_052918:
57537	SORCS2 (sor	sortilin-related VPS10 domain containing receptor 2	-2.61	CACCCGCTCCTTGTTGAGTAA	NM_020777:	NM_020777:
57537	SORCS2 (sor	sortilin-related VPS10 domain containing receptor 2	1.91	CACCGTCATCGACAATTTCTA	NM_020777:	NM_020777:
22986	SORCS3	sortilin-related VPS10 domain containing receptor 3	0.56	CACAACTTCCTTAAAGTCAAA	NM_014978:	NM_014978:
22986	SORCS3	sortilin-related VPS10 domain containing receptor 3	-3.77	AAGGCAGTCAGTGGATCTTAA	NM_014978:	NM_014978:
6652	SORD	sorbitol dehydrogenase	-0.10	CTGGTAAGATTTAGACCTAAA	NM_003104:	NM_003104:
6652	SORD	sorbitol dehydrogenase	-1.19	CACTTCCAGTTTAGAACGCAA	NM_003104:	NM_003104:
6653	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-0.86	TACGGACAGGTTAGTCTGAAT	NM_003105:	NM_003105:
6653	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	0.94	CTGGGATTTATCGGAGCAATA	NM_003105:	NM_003105:
6272	SORT1	sortilin 1	1.46	CAGCAGAGAATTGACTAGATA	NM_002959:	NM_002959:
6272	SORT1	sortilin 1	-0.74	CCCACGTCAGTTACACATTAA	NM_002959:	NM_002959:
6654	SOS1	son of sevenless homolog 1 (Drosophila)	0.49	ACGAGTAGAATCAGATATCAA	NM_005633:	NM_005633:
6654	SOS1	son of sevenless homolog 1 (Drosophila)	1.13	TGGGTTGAATCCATCACTAAA	NM_005633:	NM_005633:
50964	SOST	sclerosteosis	-1.63	ATGAATCATGACCGAAAGAAA	NM_025237:	NM_025237:
50964	SOST	sclerosteosis	-0.04	GACAATGTTAATATTGCTTTA	NM_025237:	NM_025237:
6659	SOX4	SRY (sex determining region Y)-box 4	-4.27	AAGGACAGACGAAGAGTTTAA	NM_003107:	NM_003107:
6659	SOX4	SRY (sex determining region Y)-box 4	-0.51	CACGGTCAAACTGAAATGGAT	NM_003107:	NM_003107:
6662	SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosor	-5.47	CAGCCCACTGACAGACCTTAA	NM_000346:	NM_000346:
6662	SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosor	0.24	ATGGGAGTAAACAATAGTCTA	NM_000346:	NM_000346:
6667	SP1 (Sp1 trar	Sp1 transcription factor	-1.72	CAGCAAGTTCTGACAGGACTA	NM_138473:	NM_138473:
6667	SP1 (Sp1 trar	Sp1 transcription factor	-0.11	CTAGGACGCAATAAATTTATA	NM_138473:	NM_138473:
3431	SP110	SP110 nuclear body protein	-0.02	CCCAGACACTTCATAGGATTA	NM_004509:	NM_080424:NM_004509:

3431	SP110	SP110 nuclear body protein	0.02	AAGGAAAGGCTGATTACGGAA	NM_004509:	NM_080424:NM_004509:
11262	SP140	SP140 nuclear body protein	1.03	CAGTGTCTAGTGAACTAGAAA	NM_007237:	NM_007237:
11262	SP140	SP140 nuclear body protein	-3.37	AACAGCAATGCCTGTCATGAA	NM_007237:	NM_007237:
6670	SP3	Sp3 transcription factor	0.47	CGGGTTTCTCCTGATATTAAT	NM_003111:	NM_001017371:NM_003111:
6670	SP3	Sp3 transcription factor	-2.23	CTGCGCGAGATGATACTTTGA	NM_003111:	NM_001017371:NM_003111:
10615	SPAG5	sperm associated antigen 5	-0.27	CCAAATTAGCTCTACTCCTAA	NM_006461:	NM_006461:
10615	SPAG5	sperm associated antigen 5	-0.11	TCCCGACAACTCACAGAGAAA	NM_006461:	NM_006461:
6677	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida bin	-1.36	CTGGGTGCTTCTGGAATTGTA	NM_003117:	NM_003117:NM_153189:
6677	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida bin	0.39	ACCGGGCAAGGTGTTACAATA	NM_003117:	NM_003117:NM_153189:
6678	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	0.07	ACCCAAGACATGACATTCTTA	NM_003118:	NM_003118:
6678	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	1.30	CAAGGTGCTAACATAGATTTA	NM_003118:	NM_003118:
8404	SPARCL1	SPARC-like 1 (mast9, hevin)	-0.51	ACCCTAATAAAGAGTCCATAA	NM_004684:	NM_004684:
8404	SPARCL1	SPARC-like 1 (mast9, hevin)	-0.90	CTGCATTGACTTATGAGATAA	NM_004684:	NM_004684:
6683	SPAST	spastin	0.81	TCAGGTTAATACTATCTTAAA	NM_014946:	NM_014946:NM_199436:
6683	SPAST	spastin	0.22	AACGTTATTGATACTTGGATA	NM_014946:	NM_014946:NM_199436:
64847	SPATA20	spermatogenesis associated 20	-0.56	CTCACCCTAGAATAAACTTAA	NM_022827:	NM_022827:
64847	SPATA20	spermatogenesis associated 20	-5.89	CCGCCTGATGCGGACCTGCTA	NM_022827:	NM_022827:
147841	SPBC24	spindle pole body component 24 homolog (S. cerevisiae)	0.36	CCCAGCTGCCCTTATAGTTAA	NM_182513:	NM_182513:
147841	SPBC24	spindle pole body component 24 homolog (S. cerevisiae)	0.07	CTCAACTTTACCACCAAGTTA	NM_182513:	NM_182513:
57405	SPBC25	spindle pole body component 25 homolog (S. cerevisiae)	0.01	CCACGGTTTATAATTAACATA	NM_020675:	NM_020675:
57405	SPBC25	spindle pole body component 25 homolog (S. cerevisiae)	0.68	CTCGTCATTTCATTAGGTATA	NM_020675:	NM_020675:
23013	SPEN	spen homolog, transcriptional regulator (Drosophila)	-0.35	TACGATCAGGATTACTATAGA	NM_015001:	NM_015001:
23013	SPEN	spen homolog, transcriptional regulator (Drosophila)	-4.29	CCCGTGGATATGGTTCAACTT	NM_015001:	NM_015001:
51062	SPG3A	spastic paraplegia 3A (autosomal dominant)	1.22	ACAGCAGAAGCTAACAATTTA	NM_015915:	NM_015915:NM_181598:
51062	SPG3A	spastic paraplegia 3A (autosomal dominant)	0.89	CCCGAGAGCCTAGATATTAAA	NM_015915:	NM_015915:NM_181598:
8877	SPHK1	sphingosine kinase 1	2.02	CACGAACCAAATCCAAATAAA	NM_021972:	NM_021972:NM_182965:
8877	SPHK1	sphingosine kinase 1	-3.69	CCGGCTGCTGTCACCCATGAA	NM_021972:	NM_021972:NM_182965:
56848	SPHK2 (sphir	sphingosine kinase 2	-2.52	CAGGATTGCGCTCGCTTTCAT	NM_020126:	NM_020126:
56848	SPHK2 (sphir	sphingosine kinase 2	-0.25	CCGAGGGTAGTGCCTGATCAA	NM_020126:	NM_020126:
6690	SPINK1	serine peptidase inhibitor, Kazal type 1	0.03	CTGGCCTTATTGTTGAATAAA	NM_003122:	NM_003122:
6690	SPINK1	serine peptidase inhibitor, Kazal type 1	-0.80	CTGGGCCTTGCTGAGAACCAA	NM_003122:	NM_003122:
6692	SPINT1	serine peptidase inhibitor, Kunitz type 1	-1.77	CTGGGCAGGCATAGACTTGAA	NM_003710:	NM_181642:NM_001032367:NM_003710:
6692	SPINT1	serine peptidase inhibitor, Kunitz type 1	-1.83	CGGGAAGAAGAGTGCATTCTA	NM_003710:	NM_181642:NM_001032367:NM_003710:
23626	SPO11	SPO11 meiotic protein covalently bound to DSB-like (S. cerevisiae)	0.02	CAGAGTGTACTTACCTAACAA	NM_012444:	NM_198265:NM_012444:
23626	SPO11	SPO11 meiotic protein covalently bound to DSB-like (S. cerevisiae)	0.16	TACATATATTATCTACATCAA	NM_012444:	NM_198265:NM_012444:
6696	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-ly	1.71	ACGGTTGTCCAGCAATTAATA	NM_000582:	NM_000582:
6696	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-ly	-0.11	CAGGCTGATTCTGGAAGTTCT	NM_000582:	NM_000582:
6697	SPR (sepiapt	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	1.11	AAGGAAAGGCTGCTCGTGATA	NM_003124:	NM_003124:
6697	SPR (sepiapt	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	-0.14	AACTGCTGAGCTTACTGGAAA	NM_003124:	NM_003124:
10252	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	1.18	ACGAAGAAAGTACATATGTTA	NM_005841:	NM_005841:NM_199327:
10252	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	-0.07	TAGATTCGCCTTACAATGTAA	NM_005841:	NM_005841:NM_199327:
10253	SPRY2	sprouty homolog 2 (Drosophila)	0.20	CCCATGTATTGCATAAGCTAA	NM_005842:	NM_005842:
10253	SPRY2	sprouty homolog 2 (Drosophila)	-0.88	CAGAGCCATCCGAAACACCAA	NM_005842:	NM_005842:
84926	SPRYD3	SPRY domain containing 3	1.19	CCGGTTTGTTCTCATGAACAA	NM_032840:	NM_032840:
84926	SPRYD3	SPRY domain containing 3	-0.02	CCAGTTTGGGTCAAAGTGCAA	NM_032840:	NM_032840:
283377	SPRYD4 (SPI	SPRY domain containing 4	0.29	TACCAGATGGCTGAAGAGTAA	NM_207344:	NM_207344:
283377	SPRYD4 (SPI	SPRY domain containing 4	0.10	AAAGCTAGGCATACAGCCAAA	NM_207344:	NM_207344:
80176	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	-0.53	ATGGTTGATAATAGTCAGTAA	NM_025106:	NM_025106:
80176	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	0.45	CAGGTACAATAGATGACTTTA	NM_025106:	NM_025106:
84727	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	3.09	ATAGTAAGAGATGTTGTTATA	NM_032641:	NM_032641:
84727	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	0.73	CAAGGCTATGACAGTCTGCTA	NM_032641:	NM_032641:
90864	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	0.25	AAATGTAGAGTTGATGTCTAA	NM_080861:	NM_080861:
90864	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	-0.62	CAAGATGACCTCTCCCGTCTA	NM_080861:	NM_080861:
92369	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	-0.01	ATGAAGAGCGTTTCTAATAAA	NM_080862:	NM_080862:
92369	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	-1.12	AAGCTTTATTTGAGCAAATTA	NM_080862:	NM_080862:
6709	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	0.04	CACGGTGGATCCGAACAGAGA	NM_003127:	NM_003127:
6709	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	-1.48	CCGGCTGCGTACGTGAAGAAA	NM_003127:	NM_003127:
6710	SPTB	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)	-1.26	CAGGATGTCTCCTATGATGAA	NM_000347:	NM_001024858:NM_000347:
6710	SPTB	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)	1.94	CACTCTCTGGATCAACGACAA	NM_000347:	NM_001024858:NM_000347:
10558	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	1.16	TCCTAAGTGAGCAATAATTTA	NM_006415:	NM_006415:
10558	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	-1.15	CGGCGTTTCATTGTAGTAGAA	NM_006415:	NM_006415:
6713	SQLE (squale	squalene epoxidase	2.41	ATGCTTTAATTTGCAATTTAA	NM_003129:	NM_003129:
6713	SQLE (squale	squalene epoxidase	2.38	TAGTACCATACCACTTATAAA	NM_003129:	NM_003129:
58472	SQRDL	sulfide quinone reductase-like (yeast)	-0.10	AAAGAGTTCCTTGATGGGTAA	NM_021199:	NM_021199:
58472	SQRDL	sulfide quinone reductase-like (yeast)	-0.10	CACGAAGGACTTGGAACCTAT	NM_021199:	NM_021199:
8878	SQSTM1	sequestosome 1	-0.23	AACAATCTAATTAAATGGCAT	NM_003900:	NM_003900:
8878	SQSTM1	sequestosome 1	-2.14	TAGGGTGCAAGAAGCCATTTA	NM_003900:	NM_003900:
6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	0.23	AAGCAGTGCCTGCCTATGAAA	NM_005417:	NM_005417:NM_198291:
6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	0.30	CGGCTTGTGGGTGATGTTTGA	NM_005417:	NM_005417:NM_198291:
136853	SRCRB4D	scavenger receptor cysteine rich domain containing, group B (4 doma	-1.26	CAAGGAAGATGTTAACCAGTA	NM_080744:	NM_080744:
136853	SRCRB4D	scavenger receptor cysteine rich domain containing, group B (4 doma	0.04	AAGATCCTTCCTCCTCCTAAA	NM_080744:	NM_080744:
6715	SRD5A1 (ster	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid	0.03	GAGGCTTATTTGAATACGTAA	NM_001047:	NM_001047:
6715	SRD5A1 (ster	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid	-4.76	CTCCGGAAATTTGAAGAGTAT	NM_001047:	NM_001047:
6715	SRD5A1 (ster	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid	1.59	GAGGCTTATTTGAATACGTAA	NM_001047:	NM_001047:
6715	SRD5A1 (ster	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid	-3.32	CTCCGGAAATTTGAAGAGTAT	NM_001047:	NM_001047:
6716	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid	0.00	CACCAGATGTCCACAACAATA	NM_000348:	NM_000348:
6716	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid	-0.03	ATCCAAATAATGAGTAGTGTA	NM_000348:	NM_000348:
6716	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid	0.09	CACCAGATGTCCACAACAATA	NM_000348:	NM_000348:
6716	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid	0.49	ATCCAAATAATGAGTAGTGTA	NM_000348:	NM_000348:
6720	SREBF1	sterol regulatory element binding transcription factor 1	-1.62	ACCCACTCCATTGAAGATGTA	NM_004176:	NM_001005291:NM_004176:
6720	SREBF1	sterol regulatory element binding transcription factor 1	-1.04	TGCGGAGAAGCTGCCTATCAA	NM_004176:	NM_001005291:NM_004176:
6721	SREBF2	sterol regulatory element binding transcription factor 2	-0.32	CCGCAGTGTCCTGTCATTCGA	NM_004599:	NM_004599:
6721	SREBF2	sterol regulatory element binding transcription factor 2	0.73	CTGCAATTTGTCAGTAATCAA	NM_004599:	NM_004599:
6722	SRF (serum r	serum response factor (c-fos serum response element-binding transcr	-2.15	CAAGATGGAGTTCATCGACAA	NM_003131:	NM_003131:
6722	SRF (serum r	serum response factor (c-fos serum response element-binding transcr	-3.55	CTGGATTGTTTCCAGGAGAAA	NM_003131:	NM_003131:
6717	SRI	sorcin	0.98	AGGATTCACCTTAGAAGTTTA	NM_003130:	NM_198901:NM_003130:
6717	SRI	sorcin	-3.98	CAGGCTGTGAATTCAATTGCA	NM_003130:	NM_198901:NM_003130:
6725	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-termin	0.30	CAGACCAACCCTGGTACTTTA	NM_080823:	NM_080823:
6725	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-termin	-0.78	CCGGGTCTCCATGGCAGCTGA	NM_080823:	NM_080823:
6726	SRP9	signal recognition particle 9kDa	0.21	CACGTGTGGTTCTCAAATATA	NM_003133:	NM_003133:
6726	SRP9	signal recognition particle 9kDa	0.51	TAGAAGCACGATATTTGATAA	NM_003133:	NM_003133:
6732	SRPK1	SFRS protein kinase 1	0.06	CAGACTCTTGTACACCTATAA	NM_003137:	NM_003137:
6732	SRPK1	SFRS protein kinase 1	0.60	TACCATGTGATCCGAAAGTTA	NM_003137:	NM_003137:
6733	SRPK2	SFRS protein kinase 2	0.16	AACGGTGACTCTCATTCTTTA	NM_182692:	NM_182691:NM_182692:
6733	SRPK2	SFRS protein kinase 2	0.51	CCGGTATCATGTTATTAGAAA	NM_182692:	NM_182691:NM_182692:
6734	SRPR	signal recognition particle receptor ('docking protein')	0.88	CACGGTGACTTCCACAGTAAA	NM_003139:	NM_003139:
6734	SRPR	signal recognition particle receptor ('docking protein')	1.26	CAGAGAAATAAGTAATTTATA	NM_003139:	NM_003139:
58477	SRPRB	signal recognition particle receptor, B subunit	-1.00	CCCAGATAATAGAACTGGAAA	NM_021203:	NM_021203:
58477	SRPRB	signal recognition particle receptor, B subunit	-0.87	CAAGATGTGGTTAGAAACATT	NM_021203:	NM_021203:

27286	SRPX2	sushi-repeat-containing protein, X-linked 2	-0.12	GAAGATTAACGTCAACGTCAA	NM_014467:	NM_014467:
27286	SRPX2	sushi-repeat-containing protein, X-linked 2	-1.68	CCCGATGGTGTTATACATTAA	NM_014467:	NM_014467:
6760	SS18	synovial sarcoma translocation, chromosome 18	0.93	CCGAGGTTGCATTCTAGATAA	NM_005637:	NM_005637:NM_001007559:
6760	SS18	synovial sarcoma translocation, chromosome 18	-2.48	ATCAGGGAACTTAGTAAGTAA	NM_005637:	NM_005637:NM_001007559:
6742	SSBP1	single-stranded DNA binding protein 1	0.52	AGCCTAAAGATTAGACTGTAA	NM_003143:	NM_003143:
6742	SSBP1	single-stranded DNA binding protein 1	0.23	TCGGGTTAGATCGTCAGGAAA	NM_003143:	NM_003143:
54434	SSH1	slingshot homolog 1 (Drosophila)	0.44	CTCGGAGAACCTAAACAACAA	NM_018984:	NM_018984:
54434	SSH1	slingshot homolog 1 (Drosophila)	0.67	AAAGAGATTCGTAATGAATTA	NM_018984:	NM_018984:
85464	SSH2	slingshot homolog 2 (Drosophila)	0.06	CAGATTTAGTCTAGCATGAAA	NM_033389:	NM_033389:
85464	SSH2	slingshot homolog 2 (Drosophila)	1.32	TTGAGGATGAATTAAACTTAA	NM_033389:	NM_033389:
54961	SSH3	slingshot homolog 3 (Drosophila)	-2.40	CAGGCCAGAGATAGTCTTCTT	NM_017857:	NM_018276:NM_017857:
54961	SSH3	slingshot homolog 3 (Drosophila)	-2.47	TCCCACGAGTCTTCACATGAA	NM_017857:	NM_018276:NM_017857:
8082	SSPN	sarcospan (Kras oncogene-associated gene)	-1.19	AAGCGTTAAGTCGGTAAGCTA	NM_005086:	NM_005086:
8082	SSPN	sarcospan (Kras oncogene-associated gene)	0.18	ATACACTTTACTAATCATGAA	NM_005086:	NM_005086:
6745	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	-9.79	AAAGATTTGAACGGCAATGTA	NM_003144:	NM_003144:
6745	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	0.23	CAGATAGAAGTTATTGTATAA	NM_003144:	NM_003144:
6746	SSR2	signal sequence receptor, beta (translocon-associated protein beta)	-0.45	CAAAGGGTATCTTAAATGCAA	NM_003145:	NM_003145:
6746	SSR2	signal sequence receptor, beta (translocon-associated protein beta)	1.76	CACCTCGGCAACAATTACTTA	NM_003145:	NM_003145:
6747	SSR3	signal sequence receptor, gamma (translocon-associated protein gam	0.52	TACAGTTAGGGTAACACTTTA	NM_007107:	NM_007107:
6747	SSR3	signal sequence receptor, gamma (translocon-associated protein gam	1.09	CCGAGCTGTTATTATTTATTA	NM_007107:	NM_007107:
6748	SSR4	signal sequence receptor, delta (translocon-associated protein delta)	-0.61	CAGGAAGGCTCAGAGGAATAA	NM_006280:	NM_006280:
6748	SSR4	signal sequence receptor, delta (translocon-associated protein delta)	-2.13	ATGCAAGAACAGGGTCCAGAA	NM_006280:	NM_006280:
6750	SST	somatostatin	-3.38	ACGGAGAATGATGCCCTGGAA	NM_001048:	NM_001048:
6750	SST	somatostatin	-0.23	CCCTTGCATTAGAAACTGAAA	NM_001048:	NM_001048:
6751	SSTR1	somatostatin receptor 1	0.32	CACGAACTCATTAACAACTCA	NM_001049:	NM_001049:
6751	SSTR1	somatostatin receptor 1	0.84	CGCGCTGGTGGTGCCTATTAA	NM_001049:	NM_001049:
6752	SSTR2 (soma	somatostatin receptor 2	-14.48	AGGGTTCATCATCTACACTTT	NM_001050:	NM_001050:
6752	SSTR2 (soma	somatostatin receptor 2	0.57	CTACCTGTTCATTATCATCAA	NM_001050:	NM_001050:
6753	SSTR3 (soma	somatostatin receptor 3	-0.82	CACCAACGTCTACATCCTCAA	NM_001051:	NM_001051:
6753	SSTR3 (soma	somatostatin receptor 3	0.28	CAGCACGATGCGCATCAGCTA	NM_001051:	NM_001051:
6754	SSTR4 (soma	somatostatin receptor 4	0.38	CAGCCTTGATGCCACCGTCAA	NM_001052:	NM_001052:
6754	SSTR4 (soma	somatostatin receptor 4	0.39	CAGCGTGGCCAAGCTCATCAA	NM_001052:	NM_001052:
6755	SSTR5 (soma	somatostatin receptor 5	-0.59	CGGGAACACGCTGGTCATCTA	NM_001053:	NM_001053:
6755	SSTR5 (soma	somatostatin receptor 5	0.62	CGGGCTTATGCAGACCAGCAA	NM_001053:	NM_001053:
29101	SSU72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	-2.04	ACGCCAGATGAAAGCAATCAA	NM_014188:	NM_014188:
29101	SSU72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	1.37	ACGGTAGCATTACCCAAATAA	NM_014188:	NM_014188:
6757	SSX2	synovial sarcoma, X breakpoint 2	-0.19	TTGGTCGATTCAGTTTGTCAA	NM_003147:	NM_003147:
6767	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting	0.63	TACCACATTTCTGAAATCATA	NM_003932:	NM_003932:
6767	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting	1.19	TAACCTAATTATATTCTAATA	NM_003932:	NM_003932:
6768	ST14	suppression of tumorigenicity 14 (colon carcinoma)	-0.10	AACGTCGTCACTTGTACCAAA	NM_021978:	NM_021978:
6768	ST14	suppression of tumorigenicity 14 (colon carcinoma)	-2.71	CCAGTTCGTCGTCACCAGCAA	NM_021978:	NM_021978:
23166	STAB1	stabilin 1	0.40	TAGGAACAATGGTCACTTGTA	NM_015136:	NM_015136:
23166	STAB1	stabilin 1	-0.33	CACGCCAACTGTAGCCAGGTA	NM_015136:	NM_015136:
55576	STAB2	stabilin 2	-0.14	TACGACTTTGGCAACAAACAA	NM_017564:	NM_017564:
55576	STAB2	stabilin 2	0.96	TAGGAACGTAAAGTCCTTTAA	NM_017564:	NM_017564:
10274	STAG1	stromal antigen 1	0.60	CACGTAGAATCAGATGTTCTA	NM_005862:	NM_005862:
10274	STAG1	stromal antigen 1	-1.91	CAGGATGTCGAGGTACTGTGA	NM_005862:	NM_005862:
10617	STAMBP	STAM binding protein	-0.61	CAGAAATTTGGAAGCCATTTA	NM_006463:	NM_201647:NM_006463:NM_213622:
10617	STAMBP	STAM binding protein	-0.79	CAACTGTAACTCAGAAATTAA	NM_006463:	NM_201647:NM_006463:NM_213622:
57559	STAMBPL1	STAM binding protein-like 1	-0.02	CCCAAATACTATGGCCAGATA	NM_020799:	NM_020799:
57559	STAMBPL1	STAM binding protein-like 1	-2.04	ACCGTCAACATCAGACACCTA	NM_020799:	NM_020799:
6770	STAR	steroidogenic acute regulator	1.34	CAGTCAGAATAAAGAATCATA	NM_000349:	NM_001007243:NM_000349:
6770	STAR	steroidogenic acute regulator	0.00	CTGGCAGTACATGTGCACAAA	NM_000349:	NM_001007243:NM_000349:
6772	STAT1	signal transducer and activator of transcription 1, 91kDa	0.36	CAGAAAGAGCTTGACAGTAAA	NM_007315:	NM_139266:NM_007315:
6772	STAT1	signal transducer and activator of transcription 1, 91kDa	0.00	CCAGATGTCTATGATCATTTA	NM_007315:	NM_139266:NM_007315:
6773	STAT2	signal transducer and activator of transcription 2, 113kDa	-0.15	AACGTTCAGGTGGTTCAGGAA	NM_005419:	NM_005419:
6773	STAT2	signal transducer and activator of transcription 2, 113kDa	0.30	TAGGCCGATTAACTACCCTAA	NM_005419:	NM_005419:
6774	STAT3	signal transducer and activator of transcription 3 (acute-phase respons	-0.82	CAGCCTCTCTGCAGAATTCAA	NM_003150:	NM_139276:NM_003150:NM_213662:
6774	STAT3	signal transducer and activator of transcription 3 (acute-phase respons	-0.26	CAGGCTGGTAATTTATATAAT	NM_003150:	NM_139276:NM_003150:NM_213662:
6775	STAT4 (signa	signal transducer and activator of transcription 4	-3.62	CAGCCTCGATTTCAAGAGAAA	NM_003151:	NM_003151:
6775	STAT4 (signa	signal transducer and activator of transcription 4	-1.26	TTGGTACAACGTGTCAACCAA	NM_003151:	NM_003151:
6776	STAT5A	signal transducer and activator of transcription 5A	0.27	AACCTTGTCGACAAAGAGGTA	NM_003152:	NM_003152:
6776	STAT5A	signal transducer and activator of transcription 5A	-0.47	CGGCACATTCTGTACAATGAA	NM_003152:	NM_003152:
6777	STAT5B	signal transducer and activator of transcription 5B	0.04	GCCACCCTAATTTGACATCAA	NM_012448:	NM_012448:
6777	STAT5B	signal transducer and activator of transcription 5B	-0.86	CCGCTTGGGAGACTTGAATTA	NM_012448:	NM_012448:
6778	STAT6	signal transducer and activator of transcription 6, interleukin-4 inducec	-0.04	ACGGATAGGCAGGAACATACA	NM_003153:	NM_003153:
6778	STAT6	signal transducer and activator of transcription 6, interleukin-4 inducec	-1.64	CAGGATGGCTCTCCACAGATA	NM_003153:	NM_003153:
6781	STC1	stanniocalcin 1	-0.10	AACGACTAACCTATCTATGAA	NM_003155:	NM_003155:
6781	STC1	stanniocalcin 1	1.51	CTGCTTAAACAAAGCAGTATA	NM_003155:	NM_003155:
8614	STC2	stanniocalcin 2	-2.78	CCGACGGGAGGTTAATACCAA	NM_003714:	NM_003714:
8614	STC2	stanniocalcin 2	-1.67	CTGGTGAATTCTGCACTTACA	NM_003714:	NM_003714:
79689	STEAP4	STEAP family member 4	-0.05	ACCATGATGAATTCTAGTGAA	NM_024636:	NM_024636:
79689	STEAP4	STEAP family member 4	-1.10	CACAATGGTGACCACTGATAA	NM_024636:	NM_024636:
6793	STK10	serine/threonine kinase 10	-3.24	CACGGAATTAGAGAACCTGGA	NM_005990:	NM_005990:
6793	STK10	serine/threonine kinase 10	-1.41	CAGCTCAAACTGATGAAGAAA	NM_005990:	NM_005990:
6794	STK11	serine/threonine kinase 11	0.82	CAGGAGTGTGCGGTCAATATT	NM_000455:	NM_000455:
6794	STK11	serine/threonine kinase 11	-0.16	GAGGGCCGTCAAGATCCTCAA	NM_000455:	NM_000455:
114790	STK11IP	serine/threonine kinase 11 interacting protein	-2.84	AAAGTTGTTTCCAACTCATAA	NM_052902:	NM_052902:
114790	STK11IP	serine/threonine kinase 11 interacting protein	-1.27	CTCTGCGTTTCTTGAACCTAA	NM_052902:	NM_052902:
8576	STK16	serine/threonine kinase 16	0.39	CACATAGTGTTCTGACTCCAA	NM_003691:	NM_001008910:NM_003691:
8576	STK16	serine/threonine kinase 16	-2.83	CAGGAGAATGTGTAACAAGAA	NM_003691:	NM_001008910:NM_003691:
9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)	-0.06	AACCAGGATATTTAACAGGTA	NM_004760:	NM_004760:
9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)	1.49	TCCATTGTAACCGAAGAGTTA	NM_004760:	NM_004760:
9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	2.22	AGCATATATGTTGTTAACTCA	NM_004226:	NM_004226:
9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	1.34	CATGTTAATGAAATAATTCAA	NM_004226:	NM_004226:
8859	STK19	serine/threonine kinase 19	-0.29	CCCGGAGACCTTTGGAGTTAA	NM_004197:	NM_032454:NM_004197:
8859	STK19	serine/threonine kinase 19	0.00	CTGTTATTACTCTGTCTTGAA	NM_004197:	NM_032454:NM_004197:
26576	STK23	serine/threonine kinase 23	0.37	AAGATGAGGCGCAAACGGAAA	NM_014370:	NM_014370:
26576	STK23	serine/threonine kinase 23	-2.42	AAGCGCTTTGTGGCCCTCAAA	NM_014370:	NM_014370:
8428	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	0.34	CCCACCGACGTTGGAAGGAAA	NM_003576:	NM_001032296:NM_003576:
8428	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	-0.02	CTGGAGGGAGCACGAACCTAA	NM_003576:	NM_003576:
10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	-4.53	AAGGGCATCGATAACCACACA	NM_006374:	NM_006374:
10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	-2.24	CACCAAGCTATGGATCATCAT	NM_006374:	NM_006374:
6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	0.14	CCGGCGCCTAAGAGTAAACTA	NM_006281:	NM_006281:
6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	0.11	CGGCGCCTAAGAGTAAACTAA	NM_006281:	NM_006281:
56164	STK31	serine/threonine kinase 31	0.61	CACAGTACAAGCTAAGTACAA	NM_031414:	NM_031414:NM_032944:
56164	STK31	serine/threonine kinase 31	-2.76	CCCAGTGTGGATCACTTGCTA	NM_031414:	NM_031414:NM_032944:
202374	STK32A	serine/threonine kinase 32A	1.16	CCGGATAGTATAAATCGAGGA	NM_145001:	NM_145001:
202374	STK32A	serine/threonine kinase 32A	-0.78	ATGGGTGTTTCTGCCCGGATA	NM_145001:	NM_145001:

55351	STK32B	serine/threonine kinase 32B	-1.92	CTGGGACGCGGTGTTCAAGAA	NM_018401:	NM_018401:
55351	STK32B	serine/threonine kinase 32B	-0.51	TTGGGCTGAGTTCACGAATTA	NM_018401:	NM_018401:
282974	STK32C	serine/threonine kinase 32C	0.81	CCGGGCTTCGTGCCCAACAAA	NM_173575:	NM_173575:
282974	STK32C	serine/threonine kinase 32C	0.29	TCCGAGAATGACTATCTTCAA	NM_173575:	NM_173575:
65975	STK33 (serine	serine/threonine kinase 33	-2.67	ATGTGTCTAGTGCATCCTTAA	NM_030906:	NM_030906:
140901	STK35	serine/threonine kinase 35	-6.39	CTCGGCTGTTAGGGATCTGAA	NM_080836:	NM_080836:
140901	STK35	serine/threonine kinase 35	0.00	TTGGGTTGGTATGATACATTA	NM_080836:	NM_080836:
27148	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	0.97	ATGGATGCTGACCTCCTTATA	NM_015690:	NM_015690:
27148	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	-2.77	CCAGTTGGTGTCAGCCCTGTA	NM_015690:	NM_015690:
11329	STK38	serine/threonine kinase 38	0.37	AACCTTATCGCTCAACATGAA	NM_007271:	NM_007271:
11329	STK38	serine/threonine kinase 38	-0.19	TACGTCGGCCATAAACAGCTA	NM_007271:	NM_007271:
23012	STK38L	serine/threonine kinase 38 like	1.13	AGGGAGATGTACTGTATTATA	NM_015000:	NM_015000:
23012	STK38L	serine/threonine kinase 38 like	0.10	CAGCAGCAATCCCTATAGAAA	NM_015000:	NM_015000:
27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	1.48	TGGAATAGTCTCAGATCTAAA	NM_013233:	NM_013233:
27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	1.27	TTGGAGTATTTGTAACTTCTA	NM_013233:	NM_013233:
6789	STK4	serine/threonine kinase 4	0.57	AGGATTCATAGCATCACTATA	NM_006282:	NM_006282:
6789	STK4	serine/threonine kinase 4	0.63	CACCATTTGCTGTGCGAATTA	NM_006282:	NM_006282:
83931	STK40	serine/threonine kinase 40	-2.63	CAGCGCTACCTGCGGAAATAA	NM_032017:	NM_032017:
83931	STK40	serine/threonine kinase 40	-0.27	CCGGATGGTTAAGAAGATGAA	NM_032017:	NM_032017:
30968	STOML2	stomatin (EPB72)-like 2	-0.98	CTCGACAATGTAACTCTGCAA	NM_013442:	NM_013442:
30968	STOML2	stomatin (EPB72)-like 2	1.07	TTGAACTTTAGTCGTGTAATA	NM_013442:	NM_013442:
11171	STRAP	serine/threonine kinase receptor associated protein	0.98	AAACTTTATAAGTATGATTAT	NM_007178:	NM_007178:
11171	STRAP	serine/threonine kinase receptor associated protein	1.47	AACTTTATAAGTATGATTATA	NM_007178:	NM_007178:
412	STS	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	0.44	TAGATTAATGACGTATACATA	NM_000351:	NM_000351:
412	STS	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	-0.20	AAGCCTCCTATGGAATGTAAA	NM_000351:	NM_000351:
84959	STS-1	Cbl-interacting protein Sts-1	1.72	CCGCTTAAGGATGCTAACATT	NM_032873:	NM_032873:
84959	STS-1	Cbl-interacting protein Sts-1	-1.21	CCGGCTTATTTGAGTGGACAA	NM_032873:	NM_032873:
10273	STUB1	STIP1 homology and U-box containing protein 1	-1.18	CCAGCTGGAGATGGAGAGCTA	NM_005861:	NM_005861:
10273	STUB1	STIP1 homology and U-box containing protein 1	-0.91	CCGGGCCTTGTGCTACCTGAA	NM_005861:	NM_005861:
8677	STX10	syntaxin 10	0.50	CTGGAAGAGACCATCGGTATA	NM_003765:	NM_003765:
8677	STX10	syntaxin 10	-6.32	CAGAGAGATACTCGCAGGCAA	NM_003765:	NM_003765:
8676	STX11 (synta	syntaxin 11	-1.36	CGCCAGGTTCAAGAATTGCAA	NM_003764:	NM_003764:
8676	STX11 (synta	syntaxin 11	0.09	AGCACTCAAATTGAAGTATCA	NM_003764:	NM_003764:
23673	STX12	syntaxin 12	0.41	CTGGGTTTAAAGTTTACTTCA	NM_177424:	NM_177424:
23673	STX12	syntaxin 12	1.05	TCCTTCTGTTATTATACTTAA	NM_177424:	NM_177424:
8675	STX16	syntaxin 16	-1.08	CCGGATTAAGCAGAAGATGAA	NM_001001433:	NM_003763:NM_001001433:NM_001001434:
8675	STX16	syntaxin 16	0.95	ACCATCATTGATGTTAATTAA	NM_001001433:	NM_003763:NM_001001433:NM_001001434:
55014	STX17	syntaxin 17	-4.11	ACCCTGAATTGGAGACCTTAA	NM_017919:	NM_017919:
55014	STX17	syntaxin 17	-0.23	CTCCTATAACCTCTAGGTAAA	NM_017919:	NM_017919:
415117	STX19	syntaxin 19	-0.77	CAGGCAGAATACATCAACAGA	NM_001001850:	NM_001001850:
415117	STX19	syntaxin 19	-0.04	TACAGAAATCAATATCACTAA	NM_001001850:	NM_001001850:
6804	STX1A	syntaxin 1A (brain)	0.67	CGACATAAAGAAGACAGCAAA	NM_004603:	NM_004603:
6804	STX1A	syntaxin 1A (brain)	-0.46	AGAACTCATGTCCGACATAAA	NM_004603:	NM_004603:
112755	STX1B2 (synt	syntaxin 1B2	0.05	AAGGTTCGGTCCAAATTGAAA	NM_052874:	NM_052874:
112755	STX1B2 (synt	syntaxin 1B2	0.64	ACCTAATGCAACAGCAACAAA	NM_052874:	NM_052874:
6809	STX3A (synta	syntaxin 3A	0.15	CAGCCTTAAATTAAGCTCTTA	NM_004177:	NM_004177:
6809	STX3A (synta	syntaxin 3A	0.10	CCCGGAAGAAATTGATAATTA	NM_004177:	NM_004177:
6810	STX4A	syntaxin 4A (placental)	-5.92	AAGCGAGGTGTTTGTGTCCAA	NM_004604:	NM_004604:
6810	STX4A	syntaxin 4A (placental)	-0.02	TCCGGACAATTCGGCAGACTA	NM_004604:	NM_004604:
6811	STX5A	syntaxin 5A	0.47	ATCAATAGCCTCAACAAACAA	NM_003164:	NM_003164:
6811	STX5A	syntaxin 5A	0.08	AAGTCCCTCTTTGATGATAAA	NM_003164:	NM_003164:
10228	STX6 (syntaxi	syntaxin 6	-1.83	AACCTAGTCATTAATGAGTAA	NM_005819:	NM_005819:
10228	STX6 (syntaxi	syntaxin 6	0.81	CTGAAGCTAAATAGAGAACAA	NM_005819:	NM_005819:
8417	STX7 (syntaxi	syntaxin 7	0.77	TCTGATGAAATTAGCGAATAA	NM_003569:	NM_003569:
8417	STX7 (syntaxi	syntaxin 7	-4.11	CAGCAGTATACTAACCAGCTT	NM_003569:	NM_003569:
9482	STX8	syntaxin 8	-0.75	AACCTCTTGGATGATCTTGTA	NM_004853:	NM_004853:
9482	STX8	syntaxin 8	0.96	AACGAAATCAATATGAACGAA	NM_004853:	NM_004853:
55359	STYK1	serine/threonine/tyrosine kinase 1	-0.62	CTGGGCTGCAAGATATCAATA	NM_018423:	NM_018423:
55359	STYK1	serine/threonine/tyrosine kinase 1	-0.82	TTCACCTTAGGTATAGATAAA	NM_018423:	NM_018423:
6815	STYX (serine/	serine/threonine/tyrosine interacting protein	-1.03	AAGAGGTACTATGCAAAGTAA	NM_145251:	NM_145251:
6815	STYX (serine/	serine/threonine/tyrosine interacting protein	2.05	ATGATTCTAAATAGAATCTAA	NM_145251:	NM_145251:
51657	STYXL1	serine/threonine/tyrosine interacting-like 1	-0.04	AAGCTTCTGCACATCCGGATA	NM_016086:	NM_016086:
51657	STYXL1	serine/threonine/tyrosine interacting-like 1	0.64	CAAGATTCAGAAGGACTTGAA	NM_016086:	NM_016086:
56670	SUCNR1	succinate receptor 1	-0.47	AACCTTAGAGTTACTACCCAT	NM_033050:	NM_033050:
56670	SUCNR1	succinate receptor 1	-1.53	TACCATTGTTGTTTACGGCTA	NM_033050:	NM_033050:
51684	SUFU	suppressor of fused homolog (Drosophila)	-0.50	CCAGGTTACCGCTATCGTCAA	NM_016169:	NM_016169:
51684	SUFU	suppressor of fused homolog (Drosophila)	-1.12	GAGCGTACATCTGAAATTCAA	NM_016169:	NM_016169:
129025	SUHW1	suppressor of hairy wing homolog 1 (Drosophila)	-6.74	CCCGGAGGTGGAGACAAGGAA	NM_080740:	NM_080740:
129025	SUHW1	suppressor of hairy wing homolog 1 (Drosophila)	1.27	CTGGATGCACTCGCAACTTTA	NM_080740:	NM_080740:
140883	SUHW2	suppressor of hairy wing homolog 2 (Drosophila)	1.32	CCCAACTTGAATCGAGATCAA	NM_080764:	NM_080764:
140883	SUHW2	suppressor of hairy wing homolog 2 (Drosophila)	0.52	TAGCCGTTAGTGGAGAATGAA	NM_080764:	NM_080764:
23213	SULF1	sulfatase 1	0.48	CTGGTGTTTGCGTACAGTTAA	NM_015170:	NM_015170:
23213	SULF1	sulfatase 1	0.26	TCCGTCGAATTTGAAGGTGAA	NM_015170:	NM_015170:
55959	SULF2	sulfatase 2	0.08	ATGACAGATTCTGGAGGATAA	NM_018837:	NM_198596:NM_018837:
55959	SULF2	sulfatase 2	-6.33	TCGAAAGTGGCCAGAAATGAA	NM_018837:	NM_018837:
7341	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	1.46	CAGTTACCTAATCATGTTGAA	NM_003352:	NM_001005782:NM_001005781:NM_003352:
7341	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	0.70	CTGAATCAAGGATTTAATTAA	NM_003352:	NM_001005782:NM_001005781:NM_003352:
6613	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (yeast)	0.53	GCGTCTTGTTGTTTAAATAAA	NM_006937:	NM_001005849:NM_006937:
6613	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (yeast)	0.49	GTCAAGCGTCTTGTTGTTTAA	NM_006937:	NM_001005849:NM_006937:
6612	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	0.11	TTGGGATCTATACCAATTAAA	NM_006936:	NM_006936:
6612	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	-2.47	CAGTTATGTTGTCGTGTATAA	NM_006936:	NM_006936:
11198	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.22	ACCGGAGTAATCCGAAACTGA	NM_007192:	NM_007192:
11198	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	-5.69	ACCGCATATTCGGGAAATGAA	NM_007192:	NM_007192:
6834	SURF1 (surfe	surfeit 1	-2.33	CTGGATCATGTGCTACTGGTA	NM_003172:	NM_003172:
6834	SURF1 (surfe	surfeit 1	0.94	CTGGATAATGCAGTATTTCAA	NM_003172:	NM_003172:
6839	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0.55	CAGGTGTACAACGTCTTCATA	NM_003173:	NM_003173:
6839	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0.31	GCGGGTCCGTATTGAATGCAA	NM_003173:	NM_003173:
79723	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0.30	AAGCGTTAAGCTGATAATGTA	NM_024670:	NM_024670:
79723	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	1.48	CGCGGAGGATATGGAATATTA	NM_024670:	NM_024670:
51111	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.65	CAAGAGTTAGTCAATCATTAA	NM_016028:	NM_016028:
51111	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-0.87	CTGGTGGGTTGTATTGCCGAA	NM_016028:	NM_017635:NM_016028:
84787	SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	-0.49	AATGACTTCAGCATCATGTAC	NM_032701:	NM_032701:
84787	SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	-1.32	AAGAAGAATGAGCACTGTGAA	NM_032701:	NM_032701:
6840	SVIL	supervillin	2.74	CCGAGTATTTATCCCGCTATA	NM_003174:	NM_003174:NM_021738:
6840	SVIL	supervillin	-5.50	CAGGACTGATGTCAAGGCATA	NM_003174:	NM_003174:NM_021738:
6850	SYK (spleen t	spleen tyrosine kinase	-0.03	CAGCGGGTGGAATAATCTCAA	NM_003177:	NM_003177:
6850	SYK (spleen t	spleen tyrosine kinase	0.38	CCCGCTCTTAAAGATGAGTTA	NM_003177:	NM_003177:
23345	SYNE1	spectrin repeat containing, nuclear envelope 1	-0.66	CAGGAGCTTCAGAGAGACATA	NM_015293:	NM_015293:NM_033071:NM_133650:NM_182961:

23345	SYNE1	spectrin repeat containing, nuclear envelope 1	-0.73	CTCGGAAGAAATACAGAGAAA	NM_015293:	NM_015293:NM_033071:NM_133650:NM_182961:
23224	SYNE2	spectrin repeat containing, nuclear envelope 2	-1.33	CAGAACTAGTTGATTAGTTTA	NM_015180:	NM_015180:NM_182910:NM_182912:NM_182913:NM_182914:
23224	SYNE2	spectrin repeat containing, nuclear envelope 2	-3.15	CTGGTAGAACGTCAACCTCAA	NM_015180:	NM_015180:NM_182910:NM_182912:NM_182913:NM_182914:
8831	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	0.33	ACGCTTGCCACTAAAGCCATA	NM_006772:	NM_006772:
8831	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	-0.03	CCCGGCTGATGCAAAGCTTTA	NM_006772:	NM_006772:
8867	SYNJ1	synaptojanin 1	-2.61	CAGAAAGATAACGCCATGCAA	NM_003895:	NM_203446:NM_003895:
8867	SYNJ1	synaptojanin 1	-2.24	AAGGCTCAGCTATCTGTTCAA	NM_003895:	NM_203446:NM_003895:
8871	SYNJ2	synaptojanin 2	0.52	TTCGTTCCAGATACCAAATAA	NM_003898:	NM_003898:
8871	SYNJ2	synaptojanin 2	0.71	CACCATCTAGTCCTTATTAAA	NM_003898:	NM_003898:
84447	SYVN1	synovial apoptosis inhibitor 1, synoviolin	-0.66	CTGGTCTTTCCAGTTTAGAAA	NM_032431:	NM_032431:NM_172230:
84447	SYVN1	synovial apoptosis inhibitor 1, synoviolin	0.89	TGGCAGAACTTCTGAAGTTTA	NM_032431:	NM_032431:NM_172230:
134864	TAAR1	trace amine associated receptor 1	-0.73	AGGCGCTGAAGAGATATATTA	NM_138327:	NM_138327:
134864	TAAR1	trace amine associated receptor 1	1.15	CAGAATATATCTTATCGCTAA	NM_138327:	NM_138327:
9287	TAAR2	trace amine associated receptor 2	0.15	CACATGTAATCCGTTAATATA	NM_014626:	NM_014626:NM_001033080:
9287	TAAR2	trace amine associated receptor 2	-0.10	CAGGATCCATATTCATCACAA	NM_014626:	NM_014626:NM_001033080:
9038	TAAR5	trace amine associated receptor 5	1.28	CACCATAGACACGATGGTCGA	NM_003967:	NM_003967:
9038	TAAR5	trace amine associated receptor 5	-0.62	CTGCCTCATTATGATCAGCTT	NM_003967:	NM_003967:
319100	TAAR6	trace amine associated receptor 6	-1.78	ACCCATGGTTTAGGAAAGCAA	NM_175067:	NM_175067:
319100	TAAR6	trace amine associated receptor 6	0.12	CCGGGTGATTCTGTACATAGT	NM_175067:	NM_175067:
83551	TAAR8	trace amine associated receptor 8	-0.08	ATGGGCTGGAGGAATTAGTAA	NM_053278:	NM_053278:
83551	TAAR8	trace amine associated receptor 8	0.65	GTGAATGGATCTTGTATTGAA	NM_053278:	NM_053278:
134860	TAAR9	trace amine associated receptor 9	2.20	CATGGTGTTTATATACAGTAA	NM_175057:	NM_175057:
134860	TAAR9	trace amine associated receptor 9	-0.30	TAAGGACTGATTCGTCAACAA	NM_175057:	NM_175057:
257397	TAB3	TAK1-binding protein 3	0.88	CTCGGTATAGTACAAATCCAA	NM_152787:	NM_198312:NM_152787:
257397	TAB3	TAK1-binding protein 3	0.26	GCGGTTGAAGTCTGAAGTTAA	NM_152787:	NM_198312:NM_152787:
6863	TAC1	tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neur	0.03	ATGCACTATGAGGAATAATTA	NM_003182:	NM_013997:NM_003182:NM_013996:NM_013998:
6863	TAC1	tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neur	-0.03	CACTGTATTTGTATCTCTGAA	NM_003182:	NM_013997:NM_003182:NM_013996:NM_013998:
6866	TAC3	tachykinin 3 (neuromedin K, neurokinin beta)	-3.03	CCCGAGAAACGTGACATGCAT	NM_001006667:	NM_001006667:NM_013251:
6866	TAC3	tachykinin 3 (neuromedin K, neurokinin beta)	0.14	TCCTGTAGTGTCCTACATTAA	NM_001006667:	NM_001006667:NM_013251:
6869	TACR1	tachykinin receptor 1	-2.31	CACTAACACCTCGGAACCCAA	NM_001058:	NM_015727:NM_001058:
6869	TACR1	tachykinin receptor 1	0.60	TACGCCTAGCTTCGAAATGGA	NM_001058:	NM_001058:
6865	TACR2	tachykinin receptor 2	-7.66	CGCGGTGATGTTTGTAGCCTA	NM_001057:	NM_001057:
6865	TACR2	tachykinin receptor 2	1.76	CTCCCTCTCCACGAGAGTCAA	NM_001057:	NM_001057:
6870	TACR3	tachykinin receptor 3	-0.63	CGCCTTCAACACGTTGGTCAA	NM_001059:	NM_001059:
6870	TACR3	tachykinin receptor 3	1.24	TACCATATTATCGTCATTATA	NM_001059:	NM_001059:
4070	TACSTD2	tumor-associated calcium signal transducer 2	0.12	CTCGAAATAAGTGGTACTATT	NM_002353:	NM_002353:
4070	TACSTD2	tumor-associated calcium signal transducer 2	-0.40	TTGCGACATTGTGAAGGCTTA	NM_002353:	NM_002353:
6881	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associate	-0.70	AAGGACCGCAAGTACACTCTA	NM_006284:	NM_006284:
6881	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associate	-0.17	CACCTGAGCCACCCAACCTAA	NM_006284:	NM_006284:
8148	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associate	0.64	TCAGGCTATGATCAACATCAA	NM_003487:	NM_003487:NM_139215:
8148	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associate	2.02	CTCCAGTTATGGACAAAGTTA	NM_003487:	NM_003487:
83860	TAF3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated	-5.01	CCGGAGTGTACTACTCCCAAA	XM_291729:	XM_291729:
83860	TAF3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated	1.98	CTGCATCATGCCACCAAATAA	XM_291729:	XM_291729:
389932	tAKR	aldo-keto reductase, truncated	0.63	AAGGTTGCTATGAGTAATGTA	XM_372302:	XM_372302:
389932	tAKR	aldo-keto reductase, truncated	0.49	AAGATATATTCTATACCACAA	XM_372302:	XM_372302:
6886	TAL1	T-cell acute lymphocytic leukemia 1	0.85	TCGGGAAGATTTCTAAATAAA	NM_003189:	NM_003189:
6886	TAL1	T-cell acute lymphocytic leukemia 1	-1.22	TCCGTCAACGTTGTACTGTAT	NM_003189:	NM_003189:
6887	TAL2 (T-cell	T-cell acute lymphocytic leukemia 2	0.61	AAACGCTTCGCCTGGCAATGA	NM_005421:	NM_005421:
6887	TAL2 (T-cell	T-cell acute lymphocytic leukemia 2	-1.37	CCCACTCACCCTCCAGACAAA	NM_005421:	NM_005421:
6888	TALDO1	transaldolase 1	-2.20	CCGCAACACGGGCGAGATCAA	NM_006755:	NM_006755:
6888	TALDO1	transaldolase 1	0.51	TACAAGAAGTTTAGCTACAAA	NM_006755:	NM_006755:
10010	TANK	TRAF family member-associated NFKB activator	-0.26	ATCCTTTATAGTGATGCTACA	NM_004180:	NM_004180:NM_133484:
10010	TANK	TRAF family member-associated NFKB activator	0.26	CAGACTATTATTGACAAGCTA	NM_004180:	NM_004180:NM_133484:
57551	TAOK1	TAO kinase 1	0.04	AAGGATCGGGATAGCAGTATA	NM_020791:	NM_020791:
57551	TAOK1	TAO kinase 1	1.89	CAGCTGGAATATAATAAGCGA	NM_020791:	NM_020791:
9344	TAOK2	TAO kinase 2	0.08	AACGGAAACCACCGCTCTTTA	NM_004783:	NM_004783:NM_016151:
9344	TAOK2	TAO kinase 2	0.06	ATCGAGCTGGCTGAACGGAAA	NM_004783:	NM_004783:NM_016151:
9344	TAOK2	TAO kinase 2	0.18	AACGGAAACCACCGCTCTTTA	NM_016151:	NM_004783:NM_016151:
9344	TAOK2	TAO kinase 2	-0.02	ATCGAGCTGGCTGAACGGAAA	NM_016151:	NM_004783:NM_016151:
51347	TAOK3	TAO kinase 3	0.39	CAAACAGTATAAAGCACTCAA	NM_016281:	NM_016281:
51347	TAOK3	TAO kinase 3	-6.18	CAGCTCCTCCGTCGTGCATAA	NM_016281:	NM_016281:
6890	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.04	AGGGCGAAGCCCAGAAGTTTA	NM_000593:	NM_000593:
6890	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.29	CGGGATCTATAACAACACCAT	NM_000593:	NM_000593:
6891	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	1.13	CCCTATGAGGTTGGTTATTAT	NM_000544:	NM_000544:
6891	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	-0.19	TAGCGACATTGGTAACAGCTA	NM_000544:	NM_000544:
6892	TAPBP	TAP binding protein (tapasin)	-0.68	TCGTGTAGGAATAAAGCTGTA	NM_003190:	NM_003190:
6892	TAPBP	TAP binding protein (tapasin)	0.28	TAGCTGCTGGATGTTGACGAA	NM_003190:	NM_003190:
55080	TAPBPL	TAP binding protein-like	-3.46	TAGCATCTCCTTGGTGATGAA	NM_018009:	NM_018009:
55080	TAPBPL	TAP binding protein-like	0.06	AAGGGCCTCCCTTGTGCTGAA	NM_018009:	NM_018009:
6897	TARS	threonyl-tRNA synthetase	0.43	CACCGTTATTGCTAAAGTAAA	NM_152295:	NM_152295:
6897	TARS	threonyl-tRNA synthetase	0.37	GAGGAACAGCGTTTCCGTAAA	NM_152295:	NM_152295:
80835	TAS1R1	taste receptor, type 1, member 1	0.24	CAAGGACACTGTGGCGTTTAA	NM_138697:	NM_138697:NM_177541:NM_177540:
80835	TAS1R1	taste receptor, type 1, member 1	-2.16	CTCCATGAGTTCTGCCTACAA	NM_138697:	NM_138697:NM_177539:
80834	TAS1R2	taste receptor, type 1, member 2	-0.01	CACACTGAAGATGAATATGAA	NM_152232:	NM_152232:
80834	TAS1R2	taste receptor, type 1, member 2	0.19	CAGCGTGTACTCTGCGGTCTA	NM_152232:	NM_152232:
50834	TAS2R1	taste receptor, type 2, member 1	-1.48	CTGGACACTCTCTCATCTTAA	NM_019599:	NM_019599:
50834	TAS2R1	taste receptor, type 2, member 1	1.00	TGCAATTCTCTTATTTATAAA	NM_019599:	NM_019599:
50833	TAS2R16	taste receptor, type 2, member 16	0.97	ATCACCATTATAGGTACTCTA	NM_016945:	NM_016945:
50833	TAS2R16	taste receptor, type 2, member 16	-4.22	TACCGTGTTCTACTGCATCAA	NM_016945:	NM_016945:
50831	TAS2R3	taste receptor, type 2, member 3	1.05	AGGGATAATAATGCAAATTAT	NM_016943:	NM_016943:
50831	TAS2R3	taste receptor, type 2, member 3	0.12	CAGGGATAATAATGCAAATTA	NM_016943:	NM_016943:
5726	TAS2R38	taste receptor, type 2, member 38	-1.95	AAGGCACATGAGGACAATGAA	NM_176817:	NM_176817:
5726	TAS2R38	taste receptor, type 2, member 38	-0.38	AAGGCTCAACTGGCAGAATAA	NM_176817:	NM_176817:
50832	TAS2R4	taste receptor, type 2, member 4	-0.04	CAGGACATTCTGTTCTCATTA	NM_016944:	NM_016944:
50832	TAS2R4	taste receptor, type 2, member 4	-3.08	CTGGTTTGTGACCTTGCTCAA	NM_016944:	NM_016944:
54429	TAS2R5	taste receptor, type 2, member 5	0.63	GCCGTTGGCTTCGCTATCTTA	NM_018980:	NM_018980:
54429	TAS2R5	taste receptor, type 2, member 5	-0.10	TCGGTTTAATTGGAAATGGAA	NM_018980:	NM_018980:
338398	TAS2R60	taste receptor, type 2, member 60	-2.07	CAGGCTGAGAGCTGTGCTGAA	NM_177437:	NM_177437:
338398	TAS2R60	taste receptor, type 2, member 60	-0.80	TCCGATGGCCTTCCCATACAA	NM_177437:	NM_177437:
50835	TAS2R9	taste receptor, type 2, member 9	-0.58	CTGGCTGAAGCTAAAGATCAA	NM_023917:	NM_023917:
50835	TAS2R9	taste receptor, type 2, member 9	0.88	TGGATTCATTGTACTAGTTAA	NM_023917:	NM_023917:
6898	TAT (tyrosine	tyrosine aminotransferase	0.51	CAAGCTATTGACCTTTGTTTA	NM_000353:	NM_000353:
6898	TAT (tyrosine	tyrosine aminotransferase	-3.64	TCGGGCAAATATAATGGCTAT	NM_000353:	NM_000353:
8887	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	1.14	CAGATCAATCAGCTAATAATA	NM_006024:	NM_006024:

8887	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	-0.08	CAGTCTTTGGCTTATCAATAA	NM_006024:	NM_006024:
23216	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	0.80	TTCCGCTAGATGTAACTTATA	NM_015173:	NM_015173:
23216	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	-0.56	AAGGATGTGCCATACAAAGAA	NM_015173:	NM_015173:
25771	TBC1D22A	TBC1 domain family, member 22A	-0.23	TGGGATTCAAATGAAAGTGAA	NM_014346:	NM_014346:
25771	TBC1D22A	TBC1 domain family, member 22A	-1.19	TACGTTCAGGGTATAAATGAT	NM_014346:	NM_014346:
55773	TBC1D23	TBC1 domain family, member 23	1.36	AGCGCTGAATTCTGTAGTTAA	NM_018309:	NM_018309:
55773	TBC1D23	TBC1 domain family, member 23	0.70	AGGGAGATTGTTTCACGGAAA	NM_018309:	NM_018309:
6905	TBCE	tubulin-specific chaperone e	-0.78	CCGGGCTCCATGACAATTCAA	NM_003193:	NM_003193:
6905	TBCE	tubulin-specific chaperone e	0.33	CTGAAATATGGTGCACCTGAA	NM_003193:	NM_003193:
29110	TBK1	TANK-binding kinase 1	0.28	CAGAACGTAGATTAGCTTATA	NM_013254:	NM_013254:
29110	TBK1	TANK-binding kinase 1	0.68	CTGACTTGACACGTTTGTAAA	NM_013254:	NM_013254:
79718	TBL1XR1	transducin (beta)-like 1X-linked receptor 1	-1.99	AAGCAAGATAACGGCATATAA	NM_024665:	NM_024665:
79718	TBL1XR1	transducin (beta)-like 1X-linked receptor 1	1.67	ATCACAAATGATCATACTTAA	NM_024665:	NM_024665:
10607	TBL3	transducin (beta)-like 3	-1.69	CCGGCCGTGACAAGATATGTA	NM_006453:	NM_006453:
10607	TBL3	transducin (beta)-like 3	-1.37	CCGTATCTGGAGAATGAACAA	NM_006453:	NM_006453:
6908	TBP	TATA box binding protein	0.63	TGCCCGAAACGCCGAATATAA	NM_003194:	NM_003194:
6908	TBP	TATA box binding protein	-0.35	CACCAACAATTTAGTAGTTAT	NM_003194:	NM_003194:
10716	TBR1	T-box, brain, 1	-1.09	AAGTCTCGGCCTCCACATTAA	NM_006593:	NM_006593:
10716	TBR1	T-box, brain, 1	0.56	ATGGCCGTCTGCAGCGAATAA	NM_006593:	NM_006593:
30009	TBX21	T-box 21	0.48	AACAAATACACGTATGTTATA	NM_013351:	NM_013351:
30009	TBX21	T-box 21	-5.50	CCGCCTGGACCCAACTGTCAA	NM_013351:	NM_013351:
6926	TBX3	T-box 3 (ulnar mammary syndrome)	-1.67	CTGCCTATAGAGATATATTCA	NM_005996:	NM_005996:NM_016569:
6926	TBX3	T-box 3 (ulnar mammary syndrome)	0.67	TCGGGACAAGTGAACACATTA	NM_005996:	NM_005996:NM_016569:
6910	TBX5	T-box 5	-1.68	TACCATTGTACCAAGAGGAAA	NM_000192:	NM_080717:NM_000192:NM_181486:NM_080718:
6910	TBX5	T-box 5	1.36	CCACAAGATCACGCAATTAAA	NM_000192:	NM_080717:NM_000192:NM_181486:NM_080718:
6915	TBXA2R	thromboxane A2 receptor	0.09	CCCGCAGATGAGGTCTCTGAA	NM_001060:	NM_001060:NM_201636:
6915	TBXA2R	thromboxane A2 receptor	0.02	CGGGCTGTCCTTCCTGCTGAA	NM_001060:	NM_001060:NM_201636:
6916	TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfa	-0.37	CCGCTGCAGCTAGAATCCAAA	NM_001061:	NM_030984:NM_001061:
6916	TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfa	-2.74	ACCGCTGCAGCTAGAATCCAA	NM_001061:	NM_030984:NM_001061:
6921	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin (	1.07	TGCGAACTTCTTAGATTGTTA	NM_005648:	NM_005648:
6921	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin (	0.03	TACCTGTAGTTCAGTTAGTAA	NM_005648:	NM_005648:
6923	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin E	0.75	ACACCTTTAATAAACAGTCTA	NM_007108:	NM_007108:NM_207013:
6923	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin E	-0.16	CTGGTTTGACAGCATGTTCAA	NM_007108:	NM_007108:NM_207013:
6927	TCF1	transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), a	2.12	GCGAGTGGCACGTTTATTTAA	NM_000545:	NM_000545:
6927	TCF1	transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), a	-9.57	CAGGACAAGCATGGTCCCACA	NM_000545:	NM_000545:
6938	TCF12	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	-0.03	CACCCGTATTTCCTTATCCTA	NM_003205:	NM_207036:NM_207037:NM_207038:NM_207040: NM_003205:
6938	TCF12	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	-0.51	CAGATTATCTGAAGACACAAA	NM_003205:	NM_207036:NM_207037:NM_207038:NM_207040: NM_003205:
6939	TCF15	transcription factor 15 (basic helix-loop-helix)	0.88	TGGTTGGTAAAGAAATCTTAA	NM_004609:	NM_004609:
6939	TCF15	transcription factor 15 (basic helix-loop-helix)	0.58	ATGGTTGGTAAAGAAATCTTA	NM_004609:	NM_004609:
6941	TCF19	transcription factor 19 (SC1)	-5.71	CAGCCTAAGGTCCACCGCCAA	NM_007109:	NM_007109:
6941	TCF19	transcription factor 19 (SC1)	0.11	CCGGGCTGGCATTCAGCCTAA	NM_007109:	NM_007109:
6928	TCF2	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor	1.28	TAAGGTTATAACTGTGGCTAA	NM_006481:	NM_006481:
6928	TCF2	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor	1.62	GCGGTGTAATAAGATCCTATA	NM_006481:	NM_006481:
6942	TCF20	transcription factor 20 (AR1)	0.99	TCCGATGACAAGTGAAATTTA	NM_005650:	NM_181492:NM_005650:
6942	TCF20	transcription factor 20 (AR1)	-3.37	CAGGAGTTGCACGTAGAGAAA	NM_005650:	NM_181492:NM_005650:
6943	TCF21	transcription factor 21	0.70	ATCTTTCTTTATATTGCTAAA	NM_003206:	NM_003206:
6943	TCF21	transcription factor 21	0.99	CAAGTGCAATATGTAATTATA	NM_003206:	NM_003206:
6929	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E	-0.52	CCCGGATCACTCAAGCAATAA	NM_003200:	NM_003200:
6929	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E	-1.46	CCGGGCACATGTGAAAGGTAT	NM_003200:	NM_003200:
6925	TCF4	transcription factor 4	-1.61	ACGACTTTCTTTAACATATCA	NM_003199:	NM_003199:
6925	TCF4	transcription factor 4	-0.03	CACGAAATCTTCGGAGGACAA	NM_003199:	NM_003199:
6932	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-1.92	CTGGGCAGCTTGAGAGGGCAA	NM_003202:	NM_201634:NM_213648:NM_003202:NM_201632:
6932	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-0.86	AACAGAAATAATCTGACACTA	NM_003202:	NM_201634:NM_213648:NM_003202:NM_201632:
83439	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	0.21	CCAGCACACTTGTCTAATAAA	NM_031283:	NM_031283:
83439	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	-2.75	TAGCGTGCTATTCGTCCTGTA	NM_031283:	NM_031283:
6934	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	-0.94	TCGGCTCACTCCATAGTTCAA	NM_030756:	NM_030756:
6934	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	-4.48	CAGCCGGGAGAGACCAATGAA	NM_030756:	NM_030756:
10732	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	1.77	TGGAACAAGTTAAATTGTTAA	NM_006602:	NM_006602:
10732	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	0.79	CTCGGCTAGTCTGACTCGAAA	NM_006602:	NM_006602:
8115	TCL1A	T-cell leukemia/lymphoma 1A	0.31	GCCCTTAACCATCGAGATAAA	NM_021966:	NM_021966:
8115	TCL1A	T-cell leukemia/lymphoma 1A	-2.19	GCGCTTAGTGTACCACATCAA	NM_021966:	NM_021966:
6948	TCN2	transcobalamin II; macrocytic anemia	-0.36	CTGGGAAGTCTTTCTGGCCAA	NM_000355:	NM_000355:
6948	TCN2	transcobalamin II; macrocytic anemia	1.09	TAGGAGGATTCACATATGAAA	NM_000355:	NM_000355:
6949	TCOF1	Treacher Collins-Franceschetti syndrome 1	-0.04	ACGGTTGAAGGTGGAGATCAA	NM_000356:	NM_000356:NM_001008656:
6949	TCOF1	Treacher Collins-Franceschetti syndrome 1	1.92	CAAGCAGTGAGGAATCAGATA	NM_000356:	NM_001008657:NM_000356:NM_001008656:
255394	TCP11L2	t-complex 11 (mouse) like 2	-0.15	ATGGGTAATATTAGCATTACA	NM_152772:	NM_152772:
255394	TCP11L2	t-complex 11 (mouse) like 2	-1.20	CAAGCTAATCTTATAGGTCAA	NM_152772:	NM_152772:
6996	TDG (thymine	thymine-DNA glycosylase	1.14	AGGACGTATTCTAGTACAGAA	NM_003211:	NM_003211:NM_001008411:
6996	TDG (thymine	thymine-DNA glycosylase	2.04	TAGGTATTGCTTTGGTATATA	NM_003211:	NM_003211:NM_001008411:
6997	TDGF1	teratocarcinoma-derived growth factor 1	1.87	TTGAATTATATGTTCAGATTA	NM_003212:	NM_003212:
6997	TDGF1	teratocarcinoma-derived growth factor 1	1.40	CTGCCTTTCTATACAAAGCTA	NM_003212:	NM_003212:
55775	TDP1	tyrosyl-DNA phosphodiesterase 1	1.36	CCAGAACTGTATGGAAGTAAA	NM_018319:	NM_018319:NM_001008744:
55775	TDP1	tyrosyl-DNA phosphodiesterase 1	1.58	CTGGAGTTAAGCCAAAGTATA	NM_018319:	NM_018319:NM_001008744:
81550	TDRD3	tudor domain containing 3	-1.03	AAGACGAATAGGACCTATTAA	NM_030794:	NM_030794:
81550	TDRD3	tudor domain containing 3	0.03	CAGGGACAATACAGATCATCA	NM_030794:	NM_030794:
7006	TEC	tec protein tyrosine kinase	0.80	CAGTACAAAGTCGCAATCAAA	NM_003215:	NM_003215:
7006	TEC	tec protein tyrosine kinase	-0.63	CCGCAGCTAATCAGAATCAGA	NM_003215:	NM_003215:
7009	TEGT	testis enhanced gene transcript (BAX inhibitor 1)	-1.73	AAGGCCGAACATGGAGATCAA	NM_003217:	NM_003217:
7009	TEGT	testis enhanced gene transcript (BAX inhibitor 1)	1.69	CTGATTATGTGTATCAAGGTA	NM_003217:	NM_003217:
7010	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cuta	-0.14	ACGGGCCAGATTGTAAGCTTA	NM_000459:	NM_000459:
7010	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cuta	0.36	TCGGTGCTACTTAACAACTTA	NM_000459:	NM_000459:
23371	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	0.06	ACAGCACGTGGTCGTACTATA	NM_198316:	NM_015319:NM_198316:NM_170754:
23371	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	-1.82	CAAGGTGGCGACGCACAGAAA	NM_198316:	NM_015319:NM_198316:NM_170754:
132612	Tenr	testis nuclear RNA-binding protein	0.93	CTGCAATGTTAAGTCGGTTTA	NM_139243:	NM_139243:
132612	Tenr	testis nuclear RNA-binding protein	0.85	AACAGACCTCATATTAGTTTA	NM_139243:	NM_139243:
7015	TERT	telomerase reverse transcriptase	-0.36	CTGGGAATTTGGAGTGACCAA	NM_003219:	NM_198254:NM_198255:NM_198253:NM_003219:
7015	TERT	telomerase reverse transcriptase	0.03	CCAGAACGTTCCGCAGAGAAA	NM_003219:	NM_198254:NM_198255:NM_198253:NM_003219:
7016	TESK1 (testis	testis-specific kinase 1	-1.89	CAGGACCGCCCTGACACACAA	NM_006285:	NM_006285:
7016	TESK1 (testis	testis-specific kinase 1	0.03	CTGCGGTACCTGCACTCCAAA	NM_006285:	NM_006285:
10420	TESK2 (testis	testis-specific kinase 2	0.61	CCGGGAAGAATCGCTATCTGA	NM_007170:	NM_007170:
10420	TESK2 (testis	testis-specific kinase 2	1.18	CGAGATGAGCCCTATAATGAA	NM_007170:	NM_007170:

56157	TEX13A	testis expressed sequence 13A	-0.61	CCACATCTTATTTCTCTGGAA	NM_031274:	NM_031274:
56157	TEX13A	testis expressed sequence 13A	-0.23	CTCCATGGAGACCACAGAGAA	NM_031274:	NM_031274:
7018	TF	transferrin	-0.22	TGCACTTTCCGTAGACCTTAA	NM_001063:	NM_001063:
7018	TF	transferrin	-2.79	CACCGAAGACTGCATCGCCAA	NM_001063:	NM_001063:
7019	TFAM	transcription factor A, mitochondrial	-2.17	AAGATTGAGATGTGTTCACAA	NM_003201:	NM_003201:
7019	TFAM	transcription factor A, mitochondrial	1.16	CACAATAAAGAAACAACGAAA	NM_003201:	NM_003201:
7020	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2	0.37	CACACGGACAACAACGCCAAA	NM_003220:	NM_003220:NM_001032280:
7020	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2	-0.44	GAGGAAGATCTTTAAGAGAAA	NM_003220:	NM_003220:NM_001032280:
7021	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 b	0.57	TCGGAGAAACGTTGGTGTCAA	NM_003221:	NM_003221:
7021	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 b	1.50	TTCGAGTTTAGTAATACTGAT	NM_003221:	NM_003221:
7022	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein	-0.36	TAGGAAACTTGTAGAAACGAA	NM_003222:	NM_003222:
7022	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein	0.37	AGCCCTGATTGTCATAGACAA	NM_003222:	NM_003222:
7023	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)	0.70	CAAGGAGAAGCTATTATATTT	NM_003223:	NM_003223:
7023	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)	-3.06	CCTGGGATTGTCAGCCTTCAA	NM_003223:	NM_003223:
7027	TFDP1	transcription factor Dp-1	0.43	CGGCGCGTCTACGATGCCTTA	NM_007111:	NM_007111:
7029	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	0.96	AAGGCAGAAATGAACATGAAA	NM_006286:	NM_006286:
7029	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	-0.95	CGCTACTTCTTAAGTACTTAA	NM_006286:	NM_006286:
7030	TFE3	transcription factor binding to IGHM enhancer 3	-3.34	CAGCTCCGAATTCAGGAACTA	NM_006521:	NM_006521:
7030	TFE3	transcription factor binding to IGHM enhancer 3	0.69	TCGCAGGCGATTCAACATTAA	NM_006521:	NM_006521:
7942	TFEB	transcription factor EB	-0.22	AAGCAGGAGCTGCCTAGCGAA	NM_007162:	NM_007162:
7942	TFEB	transcription factor EB	-10.78	CCGCCTGGAGATGACCAACAA	NM_007162:	NM_007162:
22797	TFEC	transcription factor EC	0.35	CGGAGTCCAAATCCACTTAAA	NM_012252:	NM_012252:NM_001018058:
22797	TFEC	transcription factor EC	-1.79	ACGGTTGATTTAGGTGCTCAT	NM_012252:	NM_012252:NM_001018058:
7031	TFF1	trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed	0.09	TCGGCTCACAACACAGATTGA	NM_003225:	NM_003225:
7031	TFF1	trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed	-5.40	CAGCTGTGCCTCGGCTCACAA	NM_003225:	NM_003225:
7032	TFF2	trefoil factor 2 (spasmolytic protein 1)	-0.09	CACCGGGTGTTCCGAAACCAA	NM_005423:	NM_005423:
7032	TFF2	trefoil factor 2 (spasmolytic protein 1)	-0.26	AACATATAATTTCTTTAAATA	NM_005423:	NM_005423:
7036	TFR2	transferrin receptor 2	1.38	TGGAGTTTCAATATCAATAAA	NM_003227:	NM_003227:
7036	TFR2	transferrin receptor 2	1.48	GACGGTCATACTGTCGGTTAA	NM_003227:	NM_003227:
7037	TFRC	transferrin receptor (p90, CD71)	-0.17	CCCATTCGTGGTGATCAATTA	NM_003234:	NM_003234:
7037	TFRC	transferrin receptor (p90, CD71)	-1.23	TCCGTGCTACTTCCAGACTAA	NM_003234:	NM_003234:
7038	TG	thyroglobulin	-0.29	CCGAGGAAACGTCTTCATGTA	NM_003235:	NM_003235:
7038	TG	thyroglobulin	0.89	AGCGTTTAGGAGTGAATGTTA	NM_003235:	NM_003235:
7039	TGFA	transforming growth factor, alpha	0.48	CTAGCTTATTACATCGTGAAA	NM_003236:	NM_003236:
7039	TGFA	transforming growth factor, alpha	0.63	CTCGGTAAGTATGTTTAGAAA	NM_003236:	NM_003236:
7040	TGFB1	transforming growth factor, beta 1 (Camurati-Engelmann disease)	-5.29	CACGTGGAGCTGTACCAGAAA	NM_000660:	NM_000660:
7040	TGFB1	transforming growth factor, beta 1 (Camurati-Engelmann disease)	0.45	CAGCATATATATGTTCTTCAA	NM_000660:	NM_000660:
7041	TGFB1I1	transforming growth factor beta 1 induced transcript 1	-0.52	TCGGTTGCTTCAGGAACTTAA	NM_015927:	NM_015927:
7041	TGFB1I1	transforming growth factor beta 1 induced transcript 1	-0.65	ACCGGTGGTGAGCTCCACAAA	NM_015927:	NM_015927:
7042	TGFB2	transforming growth factor, beta 2	-3.44	AAGGCCTTATTCTACATTTCA	NM_003238:	NM_003238:
7042	TGFB2	transforming growth factor, beta 2	0.58	TCCCAAGATTTAGAACCTCTA	NM_003238:	NM_003238:
7043	TGFB3	transforming growth factor, beta 3	0.31	AAGTATGAATATTACTCTCAA	NM_003239:	NM_003239:
7043	TGFB3	transforming growth factor, beta 3	0.31	ACGCATAGACTGAGGTATAAA	NM_003239:	NM_003239:
7045	TGFBI	transforming growth factor, beta-induced, 68kDa	1.46	TGGAGAAATGGCATCATTATA	NM_000358:	NM_000358:
7045	TGFBI	transforming growth factor, beta-induced, 68kDa	0.33	CCGCACCATAATGAGATGTGA	NM_000358:	NM_000358:
7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-li	0.62	CTGCCTTATTATGATCTTGTA	NM_004612:	NM_004612:
7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-li	-0.03	TCCATTGGTGGAATTCATGAA	NM_004612:	NM_004612:
7048	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	0.46	CTCCAATATCCTCGTGAAGAA	NM_003242:	NM_003242:NM_001024847:
7048	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-0.57	TCGCTTTGCTGAGGTCTATAA	NM_003242:	NM_003242:NM_001024847:
7049	TGFBR3 (tra	transforming growth factor, beta receptor III (betaglycan, 300kDa)	0.00	ACCTGAAATCGTGGTGTTTAA	NM_003243:	NM_003243:
7049	TGFBR3 (tra	transforming growth factor, beta receptor III (betaglycan, 300kDa)	-5.57	CCCGCAAGCTGACATGGATAA	NM_003243:	NM_003243:
9392	TGFBRAP1	transforming growth factor, beta receptor associated protein 1	-0.68	CACAGAGGTAGCAAATGGCTA	NM_004257:	NM_004257:
9392	TGFBRAP1	transforming growth factor, beta receptor associated protein 1	-2.65	CACCCACTTAGCTGTGCTGTA	NM_004257:	NM_004257:
7050	TGIF	TGFB-induced factor (TALE family homeobox)	0.70	CACATACTGTCTAATTAATAA	NM_003244:	NM_173208:NM_173209:NM_173210:NM_173211: NM_003244:NM_173207:NM_170695:NM_174886:
7050	TGIF	TGFB-induced factor (TALE family homeobox)	0.92	TCCAAGAACTATAAACTTAAA	NM_003244:	NM_173208:NM_173209:NM_173210:NM_173211: NM_003244:NM_173207:NM_170695:NM_174886:
7051	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine	-0.46	CCGCCGCACAGTGAAACTGCA	NM_000359:	NM_000359:
7051	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine	1.50	TGGCAGCTTCAAGATTGTTTA	NM_000359:	NM_000359:
7052	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamy	-5.08	CCGCGTCGTGACCAACTACAA	NM_004613:	NM_198951:NM_004613:
7052	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamy	-0.27	CCGCAAGGAGCAAACACTGAA	NM_004613:	NM_004613:
7053	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamy	-0.84	AACGGCACGCTTGTACATGAA	NM_003245:	NM_003245:
7053	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamy	0.42	TCGCATGGACGTCACGGACAA	NM_003245:	NM_003245:
7047	TGM4	transglutaminase 4 (prostate)	0.00	CAGGGCCACCATTGTCTCAAT	NM_003241:	NM_003241:
7047	TGM4	transglutaminase 4 (prostate)	0.00	ACCCAAGAAATTTATCGTCAA	NM_003241:	NM_003241:
9333	TGM5	transglutaminase 5	0.74	CAGATCCAAGCTAATATGAGA	NM_004245:	NM_004245:NM_201631:
9333	TGM5	transglutaminase 5	-2.46	CTCCCAGTTCAAGGACCTCAA	NM_004245:	NM_004245:NM_201631:
343641	TGM6	transglutaminase 6	0.35	GCCGGGAGCGTGTATACTCAA	NM_198994:	NM_198994:
343641	TGM6	transglutaminase 6	-0.05	ACGGGTCGTGTCCAACTTCAA	NM_198994:	NM_198994:
116179	TGM7	transglutaminase 7	-1.43	CGCGCACAACGTGGATAGGAA	NM_052955:	NM_052955:
116179	TGM7	transglutaminase 7	0.69	CAAGAGCCTGTATCACTTAAA	NM_052955:	NM_052955:
7054	TH	tyrosine hydroxylase	0.52	CCCAATCACCGTCACAATAAA	NM_000360:	NM_000360:NM_199293:NM_199292:
7054	TH	tyrosine hydroxylase	-1.22	CTCCGTGAAGTTCGACCCGTA	NM_000360:	NM_000360:NM_199293:NM_199292:
7056	THBD	thrombomodulin	0.70	ATGATTCATGCCAATTAGCAA	NM_000361:	NM_000361:
7056	THBD	thrombomodulin	-0.17	CTGCATGATTCATGCCAATTA	NM_000361:	NM_000361:
7057	THBS1	thrombospondin 1	-0.33	TACGAATGTAGAGATCCCTAA	NM_003246:	NM_003246:
7057	THBS1	thrombospondin 1	0.37	TAGCTGATTAACCCATGTAAA	NM_003246:	NM_003246:
7058	THBS2	thrombospondin 2	-0.08	AGCGTTGGGATACTTCATTAA	NM_003247:	NM_003247:
7058	THBS2	thrombospondin 2	0.02	CAAGAGAGTGTCGAATGATAA	NM_003247:	NM_003247:
7059	THBS3	thrombospondin 3	-0.47	ATCGATGGCTACCCAGACCAA	NM_007112:	NM_007112:
7059	THBS3	thrombospondin 3	0.11	CTGCATGGAAGTGTACGAGTA	NM_007112:	NM_007112:
7060	THBS4	thrombospondin 4	1.11	CTGACATTGATGAGTGTCGAA	NM_003248:	NM_003248:
7060	THBS4	thrombospondin 4	2.15	TTCGACCGCTTCGATAATTAA	NM_003248:	NM_003248:
117145	THEM4	thioesterase superfamily member 4	2.02	AGCCAACTTGATAAAGTTGAA	NM_053055:	NM_053055:NM_176853:
117145	THEM4	thioesterase superfamily member 4	1.50	CAGAGGCGACAAGCTTATTTA	NM_053055:	NM_053055:NM_176853:
7064	THOP1	thimet oligopeptidase 1	-0.75	CAGCAAGGTTGGCATGGATTA	NM_003249:	NM_003249:
7064	THOP1	thimet oligopeptidase 1	-2.45	CAAGTTCTACCTGGACCTGTA	NM_003249:	NM_003249:
7066	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, m	-0.12	CAGATCTTTACTCTTGAGAAA	NM_000460:	NM_199356:NM_199228:NM_000460:
7066	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, m	-1.52	CCCGGATACCTGAACAGGATA	NM_000460:	NM_199356:NM_199228:NM_000460:
7067	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a	-2.66	CCCGATGACATTGGCCAGTCA	NM_003250:	NM_199334:NM_003250:
7067	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a	-1.37	CTGGATGGAATTGAAGTGAAT	NM_003250:	NM_199334:NM_003250:
9969	THRAP1	thyroid hormone receptor associated protein 1	-2.95	ACGGTGTTTAATGAACAGGAA	NM_005121:	NM_005121:
9969	THRAP1	thyroid hormone receptor associated protein 1	0.31	CCCAGTCATGTTAAATGAATA	NM_005121:	NM_005121:
23389	THRAP2	thyroid hormone receptor associated protein 2	0.71	ATGGCTTAAATGGGACGCTAA	NM_015335:	NM_015335:
23389	THRAP2	thyroid hormone receptor associated protein 2	-1.09	CAGCCTATTGATACCACCTAA	NM_015335:	NM_015335:
9967	THRAP3	thyroid hormone receptor associated protein 3	-1.05	CGCAAGCTTTGCCGAGATCTA	NM_005119:	NM_005119:
9967	THRAP3	thyroid hormone receptor associated protein 3	-0.21	AACGCTTTACTAAATACCTAA	NM_005119:	NM_005119:

9862	THRAP4	thyroid hormone receptor associated protein 4	-0.02	ATCGAGCATTCTCTCTTGAAA	NM_014815:	NM_014815:
9862	THRAP4	thyroid hormone receptor associated protein 4	-1.15	CGGCGTCTACTGGTTCTGCAA	NM_014815:	NM_014815:
10025	THRAP5	thyroid hormone receptor associated protein 5	-0.18	CACGTGCAGCCCAGTATGGTA	NM_005481:	NM_005481:
10025	THRAP5	thyroid hormone receptor associated protein 5	1.15	TGGGAAGGACAGGTCCAATAA	NM_005481:	NM_005481:
90390	THRAP6	thyroid hormone receptor associated protein 6	-1.80	CAGGAAGCTGAGATTGGTATA	NM_080651:	NM_080651:
90390	THRAP6	thyroid hormone receptor associated protein 6	-1.92	CTGAGATTGGTATATGACAAA	NM_080651:	NM_080651:
7068	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a)	0.12	AAGTGAGACTTTAACCTTGAA	NM_000461:	NM_000461:
7068	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a)	1.95	TCCAGAATGATTACTAACCTA	NM_000461:	NM_000461:
7068	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a)	0.19	ACGAAATTCATTGGCAGATTA	XM_379184:	NM_000461:
7068	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a)	-2.77	TAGATATTTATTATCCAGGTA	XM_379184:	NM_000461:
80745	THUMPD2	THUMP domain containing 2	0.46	TGCGTTCATATGTAAATATAA	NM_025264:	NM_025264:
80745	THUMPD2	THUMP domain containing 2	-0.03	CAGGCGCCTTACAGATTGTAA	NM_025264:	NM_025264:
7072	TIA1 (TIA1 cy	TIA1 cytotoxic granule-associated RNA binding protein	-0.14	AACGATTTGGGAGGTAGTGAA	NM_022173:	NM_022173:NM_022037:
7072	TIA1 (TIA1 cy	TIA1 cytotoxic granule-associated RNA binding protein	-1.19	CTGGGCTAACAGAACAACTAA	NM_022173:	NM_022173:NM_022037:
9220	TIAF1	TGFB1-induced anti-apoptotic factor 1	0.15	AGGAGTGTCATTTGTCCCTAA	NM_004740:	NM_004740:
9220	TIAF1	TGFB1-induced anti-apoptotic factor 1	0.70	TCCCTTTACTCCGGTGCTTTA	NM_005468:	NM_004740:
7073	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	0.41	ATCGGATGCCCGGGTAGTTAA	NM_022333:	NM_003252:NM_001033925:
7073	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	0.60	TCCTAGGTTGACTATAGTCAA	NM_022333:	NM_001033925:NM_003252:
7074	TIAM1 (T-cell	T-cell lymphoma invasion and metastasis 1	-0.28	ACGGCGAGCTTTAAGAAGAAA	NM_003253:	NM_003253:
7074	TIAM1 (T-cell	T-cell lymphoma invasion and metastasis 1	-3.02	CTGGTTCTGTCTGCCCAATAA	NM_003253:	NM_003253:
148022	TICAM1	toll-like receptor adaptor molecule 1	-1.41	ATCATCGGAACAGAAATTCTA	NM_014261:	NM_014261:NM_182919:
148022	TICAM1	toll-like receptor adaptor molecule 1	0.68	CTCCCAGATCTTCGCCAGGAA	NM_014261:	NM_014261:NM_182919:
353376	TICAM2	toll-like receptor adaptor molecule 2	-0.77	TTGCCTGAGATGAAACATATA	NM_021649:	NM_021649:
353376	TICAM2	toll-like receptor adaptor molecule 2	0.75	TCGGGTACTATCACCCAGAAA	NM_021649:	NM_021649:
7075	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	2.13	CCCAGTGAGAACGTGACGTTA	NM_005424:	NM_005424:
7075	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	1.55	GCGCTTCAAGGTCAATGTGAA	NM_005424:	NM_005424:
91937	TIMD4	T-cell immunoglobulin and mucin domain containing 4	-0.19	AGGGAAACTCATGGAAACCTA	NM_138379:	NM_138379:
91937	TIMD4	T-cell immunoglobulin and mucin domain containing 4	-0.14	ATGGAATGAGGGTGACCTCAA	NM_138379:	NM_138379:
1678	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	-2.22	CAGGTAGAGGTGCATGCCTAA	NM_004085:	NM_004085:
1678	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	-0.01	CTAGAGGCCTTTAGTTATAAA	NM_004085:	NM_004085:
7076	TIMP1	TIMP metallopeptidase inhibitor 1	0.77	AAGATGTATAAAGGGTTCCAA	NM_003254:	NM_003254:
7076	TIMP1	TIMP metallopeptidase inhibitor 1	-0.82	TCCCATCTTTCTTCCGGACAA	NM_003254:	NM_003254:
7077	TIMP2	TIMP metallopeptidase inhibitor 2	-2.39	CTCGACATCGAGGACCCATAA	NM_003255:	NM_003255:
7077	TIMP2	TIMP metallopeptidase inhibitor 2	-2.38	CTCGCTGGACGTTGGAGGAAA	NM_003255:	NM_003255:
7078	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoin	-0.03	CACGCTGGTCTACACCATCAA	NM_000362:	NM_000362:
7078	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoin	0.22	CGGCGGCATTATTCCCTATAA	NM_000362:	NM_000362:
7079	TIMP4 (TIMP	TIMP metallopeptidase inhibitor 4	0.97	AGGATGTTCAGTATATCTATA	NM_003256:	NM_003256:
7079	TIMP4 (TIMP	TIMP metallopeptidase inhibitor 4	0.03	CGGTATGAAATCAAACAGATA	NM_003256:	NM_003256:
27283	TINAG	tubulointerstitial nephritis antigen	0.27	TAAGGTCATGCCTTTAAGTAA	NM_014464:	NM_014464:
27283	TINAG	tubulointerstitial nephritis antigen	0.35	ATGAACCATAACATATCATTA	NM_014464:	NM_014464:
64129	TINAGL1	tubulointerstitial nephritis antigen-like 1	0.49	CAGCCCTGTATTCTTATTCTT	NM_022164:	NM_022164:
64129	TINAGL1	tubulointerstitial nephritis antigen-like 1	-7.98	CCGGCCTGGGATCCAGGCTAA	NM_022164:	NM_022164:
114609	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	1.05	TACACTGGTATCCCTCCTAAA	NM_052887:	NM_052887:
114609	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	0.42	CCGGAAATTGGAGTGAAGCTA	NM_052887:	NM_052887:
7080	TITF1	thyroid transcription factor 1	-2.89	CTCCGTTACGTGTACATCCAA	NM_003317:	NM_003317:
7080	TITF1	thyroid transcription factor 1	-3.67	TACCTTGTCATCAGCATGTAA	NM_003317:	NM_003317:
7082	TJP1	tight junction protein 1 (zona occludens 1)	0.08	AAGGTCTAAAGGCAAATTAAA	NM_003257:	NM_003257:NM_175610:
7082	TJP1	tight junction protein 1 (zona occludens 1)	1.09	CTGGATTAAACTTAATCTAAA	NM_003257:	NM_003257:NM_175610:
7083	TK1	thymidine kinase 1, soluble	-0.76	CCGGGAAGCCGCCTATACCAA	NM_003258:	NM_003258:
7083	TK1	thymidine kinase 1, soluble	-0.30	CGGGCCGATGTTCTCAGGAAA	NM_003258:	NM_003258:
7084	TK2 (thymidin	thymidine kinase 2, mitochondrial	-4.29	ATGCCAGAAGTGGACTATGTA	NM_004614:	NM_004614:
7084	TK2 (thymidin	thymidine kinase 2, mitochondrial	-0.36	CGGGATCGAATATTAACTCCA	NM_004614:	NM_004614:
7086	TKT	transketolase (Wernicke-Korsakoff syndrome)	0.34	ACCGTGGAGGACCATTATTAT	NM_001064:	NM_001064:
7086	TKT	transketolase (Wernicke-Korsakoff syndrome)	-0.11	CAAGGTGGTCCTGAAGAGCAA	NM_001064:	NM_001064:
8277	TKTL1	transketolase-like 1	-0.26	AAGTGTTTCCTTCGTGAATAA	NM_012253:	NM_012253:
8277	TKTL1	transketolase-like 1	1.91	CCGGATCATTACAGTGGAGGA	NM_012253:	NM_012253:
9874	TLK1	tousled-like kinase 1	-1.23	CAGAGAGTATAGAATACACAA	NM_012290:	NM_012290:
9874	TLK1	tousled-like kinase 1	-0.38	CCGGAGAAGAAACAATCGGAA	NM_012290:	NM_012290:
11011	TLK2	tousled-like kinase 2	-3.92	AAGGTTCATCTGTCCATGCAA	NM_006852:	NM_006852:
11011	TLK2	tousled-like kinase 2	1.01	CAAGAGAATACGATTCTTAAA	NM_006852:	NM_006852:
7092	TLL1	tolloid-like 1	1.42	CAGCATTACAAGGATATTTGA	NM_012464:	NM_012464:
7092	TLL1	tolloid-like 1	-1.75	TAGAATCAATCTCGACCTATA	NM_012464:	NM_012464:
7093	TLL2	tolloid-like 2	-0.34	CAGAGAATTGTCTTAGGACAA	NM_012465:	NM_012465:
7093	TLL2	tolloid-like 2	0.11	CACCTCAAGGTATAATTTAAA	NM_012465:	NM_012465:
7094	TLN1	talin 1	-1.35	CAGCTCGAGATGGCAAGCTTA	NM_006289:	NM_006289:
7094	TLN1	talin 1	1.04	CCGCATTGGCATCACCAATCA	NM_006289:	NM_006289:
83660	TLN2	talin 2	-1.34	CTGCATGATCGTGATGTCACA	NM_015059:	NM_015059:
83660	TLN2	talin 2	0.05	CAGATGTTGTATGCAGCCAAA	NM_015059:	NM_015059:
7095	TLOC1	translocation protein 1	0.44	TGGAGTTATACTAACTAATAA	NM_003262:	NM_003262:
7095	TLOC1	translocation protein 1	0.42	CAGTTTCTTTAAGATGTGTAA	NM_003262:	NM_003262:
7096	TLR1	toll-like receptor 1	-0.52	CAGGGTCTTCATGAACACTAA	NM_003263:	NM_003263:
7096	TLR1	toll-like receptor 1	-0.42	CCGCAAAGTTATATCTATGAA	NM_003263:	NM_003263:
81793	TLR10	toll-like receptor 10	1.19	TCGGTTCTATTGCTTAATAAA	NM_030956:	NM_030956:NM_001017388:
81793	TLR10	toll-like receptor 10	-0.39	CCGGTGTACCTGTGAATTAAA	NM_030956:	NM_030956:NM_001017388:
7097	TLR2	toll-like receptor 2	-0.46	CCGCAACTCAAAGAACTTTAT	NM_003264:	NM_003264:
7097	TLR2	toll-like receptor 2	-0.33	CAGGTAAAGTGGAAACGTTAA	NM_003264:	NM_003264:
7098	TLR3	toll-like receptor 3	-2.46	CTGGATATCTTTGCCAATTCA	NM_003265:	NM_003265:
7098	TLR3	toll-like receptor 3	-0.19	CAGCACAATGAGCTATCTCAA	NM_003265:	NM_003265:
7099	TLR4	toll-like receptor 4	1.40	CTCGATGATATTATTGACTTA	NM_003266:	NM_138557:NM_138554:NM_138556:NM_003266:
7099	TLR4	toll-like receptor 4	0.44	CTCGATGTCATTCCAAAGTTA	NM_003266:	NM_138554:NM_138556:NM_003266:
7100	TLR5	toll-like receptor 5	-4.38	CAGGTGCTTATCTGACCTTAA	NM_003268:	NM_003268:
7100	TLR5	toll-like receptor 5	-1.69	GAGGGACTTTCTCATCTTCAA	NM_003268:	NM_003268:
10333	TLR6 (toll-like	toll-like receptor 6	0.74	CCAAGTGAACATATCAGTTAA	NM_006068:	NM_006068:
10333	TLR6 (toll-like	toll-like receptor 6	0.06	CAGAGGTTCAACCTTACTGAA	NM_006068:	NM_006068:
51284	TLR7 (toll-like	toll-like receptor 7	0.88	CAGCATGTTTAAACAATTTAA	NM_016562:	NM_016562:
51284	TLR7 (toll-like	toll-like receptor 7	0.07	CAGACCTTGGATCTAAGTAAA	NM_016562:	NM_016562:
51311	TLR8	toll-like receptor 8	-2.88	TCGCGCCATAATAAAGATGCA	NM_016610:	NM_138636:NM_016610:
51311	TLR8	toll-like receptor 8	0.03	CCCAAATGAAGCATTCCTTAA	NM_016610:	NM_138636:NM_016610:
54106	TLR9	toll-like receptor 9	1.06	CACTCAATAAATGCTACCGAA	NM_017442:	NM_017442:NM_138688:
54106	TLR9	toll-like receptor 9	-0.39	CGGCAACTGTTATTACAAGAA	NM_017442:	NM_017442:NM_138688:
83941	TM2D1	TM2 domain containing 1	2.47	ACGCAATTATATCCATAAATA	NM_032027:	NM_032027:
83941	TM2D1	TM2 domain containing 1	1.96	AAGTAGTTACATTATAGATTA	NM_032027:	NM_032027:
83877	TM2D2	TM2 domain containing 2	-0.08	TGGATTGTAATACACACTGAA	NM_031940:	NM_078473:NM_031940:NM_001024380:NM_001024381:
83877	TM2D2	TM2 domain containing 2	-0.23	CACTACTTCATAACCACTTTA	NM_031940:	NM_078473:NM_031940:NM_001024380:NM_001024381:
80213	TM2D3	TM2 domain containing 3	0.68	CAGAATGTTTATGTCTAGTTA	NM_025141:	NM_025141:NM_078474:
80213	TM2D3	TM2 domain containing 3	-1.62	CTGAACTATGCTAATCTGGAA	NM_025141:	NM_025141:NM_078474:

51768	TM7SF3 (tran	transmembrane 7 superfamily member 3	1.66	CAGTATGATGTCTATCAGTAT	NM_016551:	NM_016551:
51768	TM7SF3 (tran	transmembrane 7 superfamily member 3	0.94	TCGGAGGGAGTTTATTATTGA	NM_016551:	NM_016551:
81501	TM7SF4	transmembrane 7 superfamily member 4	1.58	TCAGCATAGAATAATGTTCAA	NM_030788:	NM_030788:
81501	TM7SF4	transmembrane 7 superfamily member 4	-0.33	ATGCCGGATAATAGAGAACTA	NM_030788:	NM_030788:
79838	TMC5	transmembrane channel-like 5	0.68	CGCGATTATTGCTAATTGGAA	NM_024780:	NM_024780:
79838	TMC5	transmembrane channel-like 5	-0.11	CAGGAATGATTGGTTCTTAGA	NM_024780:	NM_024780:
55002	TMCO3	transmembrane and coiled-coil domains 3	0.51	TAGTCAAATATTTGTTATTAA	NM_017905:	NM_017905:
55002	TMCO3	transmembrane and coiled-coil domains 3	-1.95	GAGGAGCAGCCAGTACATCAA	NM_017905:	NM_017905:
11018	TMED1	transmembrane emp24 protein transport domain containing 1	-0.17	CTGGGCATTGGAGTCAATAAA	NM_006858:	NM_006858:
11018	TMED1	transmembrane emp24 protein transport domain containing 1	-3.97	CCGGCCAAAGTCTAGGCAGAA	NM_006858:	NM_006858:
7109	TMEM1	transmembrane protein 1	1.62	ACCATTGTATTAAGACTTTAA	NM_003274:	NM_003274:
7109	TMEM1	transmembrane protein 1	-0.03	AGCCGTATACTTATGAATTTA	NM_003274:	NM_003274:
66000	TMEM108	transmembrane protein 108	-0.29	CCCTCTATTGCCAACTGTTAA	NM_023943:	NM_023943:
66000	TMEM108	transmembrane protein 108	-1.09	CACTGGGATGGTCCTTGTTAA	NM_023943:	NM_023943:
8834	TMEM11	transmembrane protein 11	-0.46	CCCGGTGGTGCTGGTCCGGAA	NM_003876:	NM_003876:
8834	TMEM11	transmembrane protein 11	-1.36	CCGTATGATTTCAGTAGAACA	NM_003876:	NM_003876:
89894	TMEM116	transmembrane protein 116	0.01	CACCGTCAATTACATCTGGTA	NM_138341:	NM_138341:
89894	TMEM116	transmembrane protein 116	-0.04	ATGGCTACTCTGAGTGTTATA	NM_138341:	NM_138341:
338440	TMEM16J	transmembrane protein 16J	-0.45	CGGGAGCAGCCAGTTGATGAA	XM_374860:	NM_001012302:
338440	TMEM16J	transmembrane protein 16J	-0.16	GACCATCATCATCATGACCAA	XM_374860:	NM_001012302:
27112	TMEM28	transmembrane protein 28	-1.73	CTCGTGCTGCATAAATACTTA	NM_015686:	NM_015686:
27112	TMEM28	transmembrane protein 28	-0.63	TCCAGACATGCTTATGTATAA	NM_015686:	NM_015686:
55754	TMEM30A	transmembrane protein 30A	0.74	AACGATTTAAAGGTACAACAA	NM_018247:	NM_018247:
55754	TMEM30A	transmembrane protein 30A	0.81	CTCGAGATGATAGTCAACTAA	NM_018247:	NM_018247:
757	TMEM50B	transmembrane protein 50B	-2.22	ATGGAGTAGATTGTACATTAA	NM_006134:	NM_006134:
757	TMEM50B	transmembrane protein 50B	0.59	AAGCTGGGATACAGCATTTAA	NM_006134:	NM_006134:
255043	TMEM86B	transmembrane protein 86B	-0.66	CGCGGTTAATGACAGCAGAAA	NM_173804:	NM_173804:
255043	TMEM86B	transmembrane protein 86B	-0.58	TCGCGGTTAATGACAGCAGAA	NM_173804:	NM_173804:
25963	TMEM87A	transmembrane protein 87A	1.24	CTGGCTTAATTTAAACAGTTA	NM_015497:	NM_015497:
25963	TMEM87A	transmembrane protein 87A	-0.60	AGCGCTGATTGTTACAATGAA	NM_015497:	NM_015497:
84910	TMEM87B	transmembrane protein 87B	0.01	CCGTATAAGAAATGTAGTTAA	NM_032824:	NM_032824:
84910	TMEM87B	transmembrane protein 87B	0.17	AAGATGGGTTTCATATCTTTA	NM_032824:	NM_032824:
56937	TMEPAI	transmembrane, prostate androgen induced RNA	0.30	CACGGATCAATTCTCACTTAA	NM_020182:	NM_199169:NM_020182:NM_199170:NM_199171:
56937	TMEPAI	transmembrane, prostate androgen induced RNA	0.33	CGCACTTGTAAAGATGATTAA	NM_020182:	NM_199169:NM_020182:NM_199170:NM_199171:
339967	TMPRSS11A	transmembrane protease, serine 11A	-0.04	TAGAGTGATTAGTTAATCAAA	NM_182606:	NM_182606:
339967	TMPRSS11A	transmembrane protease, serine 11A	-1.48	CACAACGTAAGTTATTTAGAA	NM_182606:	NM_182606:
132724	TMPRSS11B	transmembrane protease, serine 11B	0.80	TACACTGAGTCTTTCAATTTA	NM_182502:	NM_182502:
132724	TMPRSS11B	transmembrane protease, serine 11B	-0.07	CACTATGGACTACGATCTTTA	NM_182502:	NM_182502:
9407	TMPRSS11D	transmembrane protease, serine 11D	-1.10	TACCTTGACTGGATTAGGCAA	NM_004262:	NM_004262:
9407	TMPRSS11D	transmembrane protease, serine 11D	-0.70	CAGGAGTGTATACTCGAGTGA	NM_004262:	NM_004262:
28983	TMPRSS11E	transmembrane protease, serine 11E	0.24	CAAGCTTACAATGACGCCATA	NM_014058:	NM_014058:
28983	TMPRSS11E	transmembrane protease, serine 11E	-0.12	ACCCATCACATGACTATGATA	NM_014058:	NM_014058:
389208	TMPRSS11F	transmembrane protease, serine 11F	-1.01	CACGAGCTGAATATCAAAGAA	NM_207407:	NM_207407:
389208	TMPRSS11F	transmembrane protease, serine 11F	-4.25	CTGGGCTTATATCTAATAATA	NM_207407:	NM_207407:
283471	TMPRSS12	transmembrane protease, serine 12	0.03	GTGATTGGAACTAATAATATA	NM_182559:	NM_182559:
283471	TMPRSS12	transmembrane protease, serine 12	-1.49	CCAAATAATAGTTTATAATTA	NM_182559:	NM_182559:
84000	TMPRSS13	transmembrane protease, serine 13	-2.20	ACGGGAATGCATCTCCAGCAA	NM_032046:	NM_032046:
84000	TMPRSS13	transmembrane protease, serine 13	-0.01	CTGGAAATTACCTGGAGACAA	NM_032046:	NM_032046:
7113	TMPRSS2	transmembrane protease, serine 2	-0.19	ACGGACTGGATTTATCGACAA	NM_005656:	NM_005656:
7113	TMPRSS2	transmembrane protease, serine 2	-0.46	CAGGAGTGTACGGGAATGTGA	NM_005656:	NM_005656:
64699	TMPRSS3	transmembrane protease, serine 3	0.23	AAGCTATGTGAGTTCAGATAA	NM_024022:	NM_032401:NM_024022:NM_032405:NM_032404:
64699	TMPRSS3	transmembrane protease, serine 3	-0.49	CTGGAAGGGTCACTACGCAAA	NM_024022:	NM_032401:NM_024022:NM_032405:NM_032404:
56649	TMPRSS4	transmembrane protease, serine 4	0.15	CTGGATGTTGTTGAAATCACA	NM_019894:	NM_183247:NM_019894:
56649	TMPRSS4	transmembrane protease, serine 4	0.68	CAGGATCTGGATGTTGTTGAA	NM_019894:	NM_183247:NM_019894:
80975	TMPRSS5	transmembrane protease, serine 5 (spinesin)	-0.04	AAAGTGATATATGGTCTTGAA	NM_030770:	NM_030770:
80975	TMPRSS5	transmembrane protease, serine 5 (spinesin)	0.75	AACAGTATCTTTCAGAATAAA	NM_030770:	NM_030770:
164656	TMPRSS6 (tr	transmembrane protease, serine 6	-0.12	CACGGCCGGGATCACCATCAA	NM_153609:	NM_153609:
164656	TMPRSS6 (tr	transmembrane protease, serine 6	-3.42	CACGCTGGGTTGTTACCGCTA	NM_153609:	NM_153609:
344805	TMPRSS7 (tr	transmembrane protease, serine 7	0.23	TCGGATTACTCGTCAACCATA	XM_293599:	XM_293599:
344805	TMPRSS7 (tr	transmembrane protease, serine 7	1.47	CCCGAGCTACTATCCTCCAAA	XM_293599:	XM_293599:
360200	TMPRSS9	transmembrane protease, serine 9	0.24	CGGGCCAACCTGCCAACTCAA	NM_182973:	NM_182973:
360200	TMPRSS9	transmembrane protease, serine 9	0.89	CACGCGCATCACCAGGCTAAA	NM_182973:	NM_182973:
3371	TNC	tenascin C (hexabrachion)	-0.19	CCGGGCATCAGTCACCGGTTA	NM_002160:	NM_002160:
3371	TNC	tenascin C (hexabrachion)	-0.37	CTGGGATGCCCTCAAACTCAA	NM_002160:	NM_002160:
7124	TNF	tumor necrosis factor (TNF superfamily, member 2)	-0.05	CCGACTCAGCGCTGAGATCAA	NM_000594:	NM_000594:
7124	TNF	tumor necrosis factor (TNF superfamily, member 2)	0.69	TAGGGTCGGAACCCAAGCTTA	NM_000594:	NM_000594:
7126	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	0.05	ACCCATGTCTTTCTACCCTAA	NM_021137:	NM_021137:
7126	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-0.73	CAGGAGGTGAGTTCCTCTTTA	NM_021137:	NM_021137:
7127	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	-2.79	CAGGGTGATGCTGAAGATGAT	NM_006291:	NM_006291:
7127	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	-2.44	CCGGATGTCCATGGAGCAGAA	NM_006291:	NM_006291:
7128	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	-2.02	CAGCCTTTACTCATACTATTA	NM_006290:	NM_006290:
7128	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	0.30	CCGAGCTGTTCCACTTGTTAA	NM_006290:	NM_006290:
7130	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	-0.69	AAGGCGGTGTGTGAATTTGAA	NM_007115:	NM_007115:
7130	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	1.46	TGGCGTCTTTACAGATCCAAA	NM_007115:	NM_007115:
25816	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	0.33	CCGAGTACATGTGAGCGGTAA	NM_014350:	NM_014350:
25816	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	-0.12	TAGCATTGATGGAGAAATTTA	NM_014350:	NM_014350:
8797	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	1.48	ATCAAACTTCATGATCAATCA	NM_003844:	NM_003844:
8797	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	0.56	CCGGGTCCACAAGACCTTCAA	NM_003844:	NM_003844:
8795	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	1.13	CCGACTTCACTTGATACTATA	AF016266:	NM_003842:NM_147187:
8795	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	0.32	CTGGACAACCTTACAAGTATA	AF016266:	NM_003842:NM_147187:
8794	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy withou	0.37	ACCAACGCTTCCAACAATGAA	NM_003841:	NM_003841:
8794	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy withou	0.59	ATCGTAGGGATCATAGTTCTA	NM_003841:	NM_003841:
8793	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with t	-2.17	CCGGAGTGACATCAAGTGCAA	NM_003840:	NM_003840:
8793	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with t	0.48	TAGAACGGGATTATCTTGTTA	NM_003840:	NM_003840:
8792	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activa	1.13	ACCCGCTAGGTGGTTAATTTA	NM_003839:	NM_003839:
8792	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activa	-2.01	CCCGCTAGGTGGTTAATTTAT	NM_003839:	NM_003839:
4982	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotege	0.02	CACAATGTACAAATTGTATCA	NM_002546:	NM_002546:
4982	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotege	1.43	TACCTTCATTATGACGAAGAA	NM_002546:	NM_002546:
51330	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	1.22	GAGGGAGAATTTATTAATAAA	NM_016639:	NM_016639:
51330	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	-6.39	CAGCTGACACTGACTAAGGAA	NM_016639:	NM_016639:
23495	TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	-0.39	AACCCTAAGCAATGTGCATAC	NM_012452:	NM_012452:
23495	TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	0.24	AAAGGAGCAAGGCAAGTTCTA	NM_012452:	NM_012452:
115650	TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C	-0.93	CCGGGAATCTCTGATGCCACA	NM_052945:	NM_052945:
115650	TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C	-4.24	CTCCTGTTCCTGTGCCTTCAA	NM_052945:	NM_052945:
8764	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus e	-14.86	CACCTACATTGCCCACCTCAA	NM_003820:	NM_003820:

8764	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus e	-0.76	CTGCTGGAGTTCATCCTGCTA	NM_003820:	NM_003820:
608	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	0.10	AACCATTAAAGGACGAGTTTA	NM_001192:	NM_001192:
608	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	1.79	CTCGAGCAGTGCCACTTTAAA	NM_001192:	NM_001192:
8784	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	-2.24	CAGGAGGGAGAGAGAGACACA	NM_004195:	NM_004195:NM_148901:NM_148902:
8784	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	-1.74	TCGGGATTCTCAGGTCATGAA	NM_004195:	NM_004195:NM_148901:NM_148902:
55504	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	0.62	CAGCAGCTACTGATTTATCTA	NM_018647:	NM_018647:NM_148957:
55504	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	-0.40	TTGGATTCAAATAGCAGTCAA	NM_018647:	NM_018647:NM_148957:
84957	TNFRSF19L	tumor necrosis factor receptor superfamily, member 19-like	0.51	CACATCTTGATTGGAACTCAA	NM_032871:	NM_032871:NM_152222:
84957	TNFRSF19L	tumor necrosis factor receptor superfamily, member 19-like	-0.05	CCCGGGAAACTTGGACCGAGA	NM_032871:	NM_032871:
7132	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	-0.15	ACCGGCATTATTGGAGTGAAA	NM_001065:	NM_001065:
7132	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	0.32	CCCGGTGACTGTCCCAACTTT	NM_001065:	NM_001065:
7133	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	1.77	AGGGTGATAAATTGTTGATAA	NM_001066:	NM_001066:
7133	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	-1.65	CAGCCTTGGGTCTACTAATAA	NM_001066:	NM_001066:
27242	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0.02	ACCGTGTAGAATGCTTGATTA	NM_014452:	NM_014452:
27242	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0.21	TCAAGTGTACTAATTTATTAA	NM_014452:	NM_014452:
8718	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-0.45	CGCGGTATTAAATCTGTGAAA	NM_003790:	NM_148973:NM_148974:NM_148965:NM_148966:NM_148967:NM_148968:NM_148969:NM_148970:NM_003790:NM_148971:NM_148972:
8718	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-1.18	CACCGTCCAGTTGGTGGGTAA	NM_003790:	NM_148973:NM_148974:NM_148965:NM_148966:NM_148967:NM_148968:NM_148969:NM_148970:NM_003790:NM_148971:NM_148972:
939	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	-2.70	AAGGTTGGCTTGCCACCTGAA	NM_001242:	NM_001242:
939	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	-4.27	ACCGAGTGTGATCCTCTTCCA	NM_001242:	NM_001242:
943	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	2.07	CACGGAGCACACCAATAACAA	NM_001243:	NM_152942:NM_001243:
943	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	-1.51	TCCGGCAGGGATGATTGTCAA	NM_001243:	NM_001243:
3604	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	-0.35	ATCCGCTATCACAGCTTTCAA	NM_001561:	NM_001561:
3604	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	0.02	TCCGTGGGTTCTGTCATGTAA	NM_001561:	NM_001561:
8743	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1.18	AACACAAAGAACGACAAACAA	NM_003810:	NM_003810:
8743	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1.02	ATGGTCCAATATATTTACAAA	NM_003810:	NM_003810:
8600	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	-1.06	ACGGGTTGACCTTATGAGAAA	NM_003701:	NM_033012:NM_003701:
8600	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	2.04	CAGATGGATCCTAATAGAATA	NM_003701:	NM_033012:NM_003701:
8742	TNFSF12	tumor necrosis factor (ligand) superfamily, member 12	0.26	CAGGGCATTGTGTTCACTGTA	NM_003809:	NM_003809:NM_153012:
8742	TNFSF12	tumor necrosis factor (ligand) superfamily, member 12	-0.16	TTAAATAGAATAAGTCATAAA	NM_003809:	NM_003809:NM_153012:
10673	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	-0.60	CACGCCTTACTTCTTGCCTTA	NM_006573:	NM_006573:
10673	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	0.02	CGGAGGGTAAATGCCAGCAAA	NM_006573:	NM_006573:
8740	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	-2.50	AAGCTGGCTACTACTACATCT	NM_003807:	NM_003807:NM_172014:
8740	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	0.30	AAGCTGATACAAGAGCGAAGG	NM_003807:	NM_003807:NM_172014:
9966	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	0.01	AACGGTTTAGCTATGAAATTT	NM_005118:	NM_005118:
9966	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	0.28	ACCGAATGAACTATACCAACA	NM_005118:	NM_005118:
8995	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	-0.51	ATGGCTAAGTTTGGACCATTA	NM_005092:	NM_005092:
8995	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	0.47	CACCATAGACTTGATATTCAA	NM_005092:	NM_005092:
7292	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptior	0.99	AACGTTTATGACTATAGGTAA	NM_003326:	NM_003326:
7292	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptior	-1.57	CAGGCCAAGATTCGAGAGGAA	NM_003326:	NM_003326:
944	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	-2.67	AAGGACTCTCTCACACAGGAA	NM_001244:	NM_001244:
944	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	-0.44	ACCCATATCAAGGGTGACTAA	NM_001244:	NM_001244:
8744	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	0.17	CAAGTTGGACCTTGATATTTA	NM_003811:	NM_003811:
8744	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	-0.12	CTGAGTTATGGTAATACGTGA	NM_003811:	NM_003811:
23043	TNIK	TRAF2 and NCK interacting kinase	0.72	AAGGACCATATTGATAGAACA	XM_039796:	NM_015028:
23043	TNIK	TRAF2 and NCK interacting kinase	-3.09	CTGGAATATAAGCGCAAACAA	XM_039796:	NM_015028:
8711	TNK1	tyrosine kinase, non-receptor, 1	-6.26	AAGGATCTAGTCTGCCCACTA	NM_003985:	NM_003985:
8711	TNK1	tyrosine kinase, non-receptor, 1	1.34	ATCGGTCATGATGAACTTGGA	NM_003985:	NM_003985:
10188	TNK2	tyrosine kinase, non-receptor, 2	-2.71	ACGCAAGTCGTGGATGAGTAA	NM_005781:	NM_005781:NM_001010938:
10188	TNK2	tyrosine kinase, non-receptor, 2	-5.80	CGGCAGTCAGATCCTGCATAA	NM_005781:	NM_005781:NM_001010938:
63923	TNN	tenascin N	-0.35	CTGCGTAACGTCAAGAATGAA	XM_040527:	NM_022093:
63923	TNN	tenascin N	0.19	CTGGTGTTATGAGGAAGAATA	XM_040527:	NM_022093:
7137	TNNI3	troponin I type 3 (cardiac)	-0.05	ACGGAGCCGCACGCCAAGAAA	NM_000363:	NM_000363:
7137	TNNI3	troponin I type 3 (cardiac)	0.11	TAAGATCTCCGCCTCGAGAAA	NM_000363:	NM_000363:
51086	TNNI3K	TNNI3 interacting kinase	-0.01	CAGCATTCGGCGTATACCTAA	NM_015978:	NM_015978:
51086	TNNI3K	TNNI3 interacting kinase	0.95	GGAGCTAATGTCAATATTCAA	NM_015978:	NM_015978:
7138	TNNT1	troponin T type 1 (skeletal, slow)	1.18	CCATCGGTAGCTTGAAATAAA	NM_003283:	NM_003283:
7138	TNNT1	troponin T type 1 (skeletal, slow)	0.20	AAGGCTCAGCCTCAAGATTCA	NM_003283:	NM_003283:
7139	TNNT2	troponin T type 2 (cardiac)	-8.88	CAGGATCAACGATAACCAGAA	NM_000364:	NM_001001430:NM_001001432:NM_001001431:NM_000364:
7139	TNNT2	troponin T type 2 (cardiac)	1.48	CCGAAACAGGATCAACGATAA	NM_000364:	NM_001001430:NM_001001432:NM_001001431:NM_000364:
3842	TNPO1	transportin 1	-0.67	CTGGAACAACTTAATCAGTAT	NM_002270:	NM_002270:NM_153188:
3842	TNPO1	transportin 1	1.38	CAGCATGTTAAGCCTTGTATA	NM_002270:	NM_002270:NM_153188:
23534	TNPO3	transportin 3	-13.53	ACCGAATGTCTTAGTGAACTA	NM_012470:	NM_012470:
23534	TNPO3	transportin 3	-9.69	CTGGAGATCCTTACAGTGTTA	NM_012470:	NM_012470:
7143	TNR (tenascir	tenascin R (restrictin, janusin)	-2.07	TCGCAGGAATCCGCTGGCTAA	NM_003285:	NM_003285:
7143	TNR (tenascir	tenascin R (restrictin, janusin)	0.56	ACCCAGCTACCGAATACGAAA	NM_003285:	NM_003285:
57690	TNRC6C	trinucleotide repeat containing 6C	-3.43	CCGGTACGATTTAATCCAGAA	NM_018996:	NM_018996:
57690	TNRC6C	trinucleotide repeat containing 6C	0.22	CAGCTGGCATACCAACGTTTA	NM_018996:	NM_018996:
7145	TNS1	tensin 1	0.93	CCACAGATGAATCGAAAGATA	NM_022648:	NM_022648:
7145	TNS1	tensin 1	-4.32	CTGGGTAGATGGAAACTGCAA	NM_022648:	NM_022648:
64759	TNS3	tensin 3	1.77	CAGGACCTCGATATTATCGAT	NM_022748:	NM_022748:
64759	TNS3	tensin 3	-0.06	CGGTGTGATTGTGGACTACAA	NM_022748:	NM_022748:
7148	TNXB	tenascin XB	0.10	CTCCTTCGTGGTCCAGTACAA	NM_019105:	NM_019105:
7148	TNXB	tenascin XB	1.05	CCCGTGTCTGCTGTTGGTTTA	NM_019105:	NM_019105:
10140	TOB1	transducer of ERBB2, 1	0.02	CAGATATGGCCTCTTACAGTA	NM_005749:	NM_005749:
10140	TOB1	transducer of ERBB2, 1	-1.30	CCAGCCTGTTATGGCTAACTA	NM_005749:	NM_005749:
54472	TOLLIP	toll interacting protein	0.07	CACGCTTGCCGCCATCTCTTA	NM_019009:	NM_019009:
54472	TOLLIP	toll interacting protein	0.49	CCCACTGATAACGGACAGAAA	NM_019009:	NM_019009:
10043	TOM1 (target	target of myb1 (chicken)	0.76	AACGGTTTGAACGGTTCCGAA	NM_005488:	NM_005488:
10043	TOM1 (target	target of myb1 (chicken)	0.10	CACCAGCGAAGAATTTGACAA	NM_005488:	NM_005488:
9804	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-0.81	AACGATGAGAGTAAGTTGCAA	NM_014765:	NM_014765:
9804	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.21	CACAGTTTCAGAACTGAGTAA	NM_014765:	NM_014765:
56993	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	1.12	TTGGGTCTATGTACTTCTTTA	NM_020243:	NM_020243:
56993	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	1.28	ATGACACTGTGTAATTATAAA	NM_020243:	NM_020243:
10953	TOMM34	translocase of outer mitochondrial membrane 34	0.19	CACCTGGAACTCTGTAGTAAT	NM_006809:	NM_006809:
10953	TOMM34	translocase of outer mitochondrial membrane 34	0.16	ACCGAGCAGCATGTCACTTGA	NM_006809:	NM_006809:
10452	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0.02	CTCGGTATAAATCATGTTTAT	NM_006114:	NM_006114:
10452	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0.86	TCGGTATAAATCATGTTTATA	NM_006114:	NM_006114:
84134	TOMM40L	translocase of outer mitochondrial membrane 40 homolog-like (yeast)	0.01	CTGCAGTAGACTATTCAATTA	NM_032174:	NM_032174:
84134	TOMM40L	translocase of outer mitochondrial membrane 40 homolog-like (yeast)	0.79	TAGAGGCTTGGTGGATAGTAA	NM_032174:	NM_032174:
7150	TOP1	topoisomerase (DNA) I	0.73	CGGGAAGGACTCCATCAGATA	NM_003286:	NM_003286:
7150	TOP1	topoisomerase (DNA) I	-0.01	GCCCGAGGATATAATCATCAA	NM_003286:	NM_003286:
116447	TOP1MT	topoisomerase (DNA) I, mitochondrial	1.71	GTGGAGAAGATCTACAGCAAA	NM_052963:	NM_052963:
116447	TOP1MT	topoisomerase (DNA) I, mitochondrial	-4.38	CCAGACGAAGATCCAGGCAAA	NM_052963:	NM_052963:

7153	TOP2A	topoisomerase (DNA) II alpha 170kDa	-1.63	ACGAATAACCATAGAAATGAA	NM_001067:	NM_001067:
7153	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.60	CACGTAGGCTGTTTAAAGAAA	NM_001067:	NM_001067:
7155	TOP2B	topoisomerase (DNA) II beta 180kDa	0.31	TCGGGCTAGGAAAGAAGTAAA	NM_001068:	NM_001068:
7155	TOP2B	topoisomerase (DNA) II beta 180kDa	-2.73	CAGCCGAAAGACCTAAATACA	NM_001068:	NM_001068:
7156	TOP3A	topoisomerase (DNA) III alpha	0.53	CTGTGTACAGGTTAAAGTTAA	NM_004618:	NM_004618:
7156	TOP3A	topoisomerase (DNA) III alpha	0.01	TTCTCGAAAGTTGAGAATAAA	NM_004618:	NM_004618:
10210	TOPORS	topoisomerase I binding, arginine/serine-rich	1.98	CTGGAAATGTGTTATAAGCTA	NM_005802:	NM_005802:
10210	TOPORS	topoisomerase I binding, arginine/serine-rich	0.89	CAAGAGCTGGATATTAATGTA	NM_005802:	NM_005802:
1861	TOR1A	torsin family 1, member A (torsin A)	0.45	CCAGTGAATGTTCCTGTTTGA	NM_000113:	NM_000113:
1861	TOR1A	torsin family 1, member A (torsin A)	-0.38	CACCAAGTTAGATTATTACTA	NM_000113:	NM_000113:
9760	TOX	thymus high mobility group box protein TOX	0.09	TACAGTAGCTTTCACATTAAA	NM_004522:	NM_014729:
7157	TP53	tumor protein p53 (Li-Fraumeni syndrome)	-2.06	CAGCATCTTATCCGAGTGGAA	NM_000546:	NM_000546:
7157	TP53	tumor protein p53 (Li-Fraumeni syndrome)	0.66	TTGCAGTTAAGGGTTAGTTTA	NM_000546:	NM_000546:
7158	TP53BP1	tumor protein p53 binding protein, 1	0.38	CAGGACAGTCTTTCCACGAAT	NM_005657:	NM_005657:
7158	TP53BP1	tumor protein p53 binding protein, 1	1.04	TTGTTTGACCAGAGCAATAAA	NM_005657:	NM_005657:
7159	TP53BP2	tumor protein p53 binding protein, 2	0.41	ACCGTGTATCTCAGTAACAAT	NM_005426:	NM_005426:NM_001031685:
7159	TP53BP2	tumor protein p53 binding protein, 2	-2.10	CACGAGCGTCGAAGAGACAAA	NM_005426:	NM_005426:NM_001031685:
9537	TP53I11	tumor protein p53 inducible protein 11	-2.06	CCCGTTAGTCCCTGATCCCAA	AK054815:	NM_006034:
9537	TP53I11	tumor protein p53 inducible protein 11	0.85	TAGGCAATGAAATCAAGTTTA	AK054815:	NM_006034:
9540	TP53I3	tumor protein p53 inducible protein 3	0.04	AAGCTGATATGAGGAAATAAA	NM_004881:	NM_147184:NM_004881:
9540	TP53I3	tumor protein p53 inducible protein 3	1.02	CAGAGCCGTTTAAAGCTGATA	NM_004881:	NM_147184:NM_004881:
94241	TP53INP1	tumor protein p53 inducible nuclear protein 1	-0.01	CCGCGTCAGTACAATTACTAA	NM_033285:	NM_033285:
94241	TP53INP1	tumor protein p53 inducible nuclear protein 1	-0.62	CTGGGAGACACTAGTAGTATA	NM_033285:	NM_033285:
112858	TP53RK	TP53 regulating kinase	1.65	AAGTATTGGCGTATAACATTA	NM_033550:	NM_033550:
112858	TP53RK	TP53 regulating kinase	-0.04	TAAGTTTATACCGCTAAACAA	NM_033550:	NM_033550:
112858	TP53RK	TP53 regulating kinase	0.41	CACAATGATGATATAGGGATA	NM_032279:	NM_033550:
7161	TP73	tumor protein p73	-0.01	ATCGAGTATTTCACCTCCCAA	NM_005427:	NM_005427:
7161	TP73	tumor protein p73	0.33	CCCGGGATGCTCAACAACCAT	NM_005427:	NM_005427:
8626	TP73L	tumor protein p73-like	0.46	AAGGGCCAGCGTGGCTCTAAA	NM_003722:	NM_003722:
8626	TP73L	tumor protein p73-like	0.71	CACCCTTATAGTCTAAGACTA	NM_003722:	NM_003722:
53373	TPCN1	two pore segment channel 1	-0.71	CGAGCTGTATTTCATCATGAA	NM_017901:	NM_017901:
53373	TPCN1	two pore segment channel 1	1.28	TAACACAATAGTATTACTCTA	NM_017901:	NM_017901:
219931	TPCN2	two pore segment channel 2	-0.90	CAGGTGTTTCTGGATGCATAT	NM_139075:	NM_139075:
219931	TPCN2	two pore segment channel 2	0.35	CTGGTGGTGGTCTACTACGTA	NM_139075:	NM_139075:
89882	TPD52L3	tumor protein D52-like 3	-3.98	ATGGACCTAACTATACATCTT	NM_033516:	NM_033516:
89882	TPD52L3	tumor protein D52-like 3	1.08	TAGACGAAATGTGCCATTATA	NM_033516:	NM_033516:
89882	TPD52L3	tumor protein D52-like 3	1.12	ATCATATACTTCAGACATCAA	BC033792:	NM_001001874:
89882	TPD52L3	tumor protein D52-like 3	-3.74	ATGGACCTAACTATACATCTT	BC033792:	NM_033516:
7166	TPH1	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	-0.19	CGGAGTATTCAGATCCTGAAA	NM_004179:	NM_004179:
7166	TPH1	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	1.04	TCCATTTGGAGTGAAGTATAA	NM_004179:	NM_004179:
121278	TPH2	tryptophan hydroxylase 2	0.56	CTGAAATAACGTATTATGTTT	NM_173353:	NM_173353:
121278	TPH2	tryptophan hydroxylase 2	-0.22	CTCAGTATACTTCAATCCCTA	NM_173353:	NM_173353:
27010	TPK1	thiamin pyrophosphokinase 1	-5.61	AACCTGGTGCATCGAAATGTA	NM_022445:	NM_022445:
27010	TPK1	thiamin pyrophosphokinase 1	-1.37	CAGGTTGTCTGTAGAGAATGA	NM_022445:	NM_022445:
7168	TPM1	tropomyosin 1 (alpha)	0.23	AACGATATGACTTCCATGTAA	NM_000366:	NM_000366:
7168	TPM1	tropomyosin 1 (alpha)	0.60	TGCGGAGAGGTCAGTAACTAA	NM_000366:	NM_001018020:NM_001018006:NM_001018008:NM_001018005:NM_001018007:NM_000366:NM_001018004:
7172	TPMT (thiopu	thiopurine S-methyltransferase	-1.66	ACCGGTTGAATGGACAACTAA	NM_000367:	NM_000367:
7172	TPMT (thiopu	thiopurine S-methyltransferase	-9.64	CACCGGTTGAATGGACAACTA	NM_000367:	NM_000367:
7173	TPO	thyroid peroxidase	0.29	TGCGAGGTGCAGAAACACCAA	NM_000547:	NM_175722:NM_175720:NM_175719:NM_000547:
7173	TPO	thyroid peroxidase	-6.78	AAGGCTCTTTGTGCTGTCCAA	NM_000547:	NM_175722:NM_175721:NM_175720:NM_000547:
7174	TPP2 (tripepti	tripeptidyl peptidase II	0.32	CCCGATTATTGCGTATTCTAA	NM_003291:	NM_003291:
7174	TPP2 (tripepti	tripeptidyl peptidase II	0.75	ATGGAAGCATAATATAATTTA	NM_003291:	NM_003291:
23430	TPSD1	tryptase delta 1	0.21	AACCACCTTTGCAACGCGGAA	NM_012217:	NM_012217:
23430	TPSD1	tryptase delta 1	-0.03	AATGGAACCGGACATCAAGGA	NM_012217:	NM_012217:
25823	TPSG1	tryptase gamma 1	1.71	CCAAGTGCATTTCTTAAATAA	NM_012467:	NM_012467:
25823	TPSG1	tryptase gamma 1	1.57	CCCGGCCTCTTCCTTCTGCTA	NM_012467:	NM_012467:
7179	TPTE	transmembrane phosphatase with tensin homology	-0.68	CAGATTGGCAACCAAGACTAA	NM_013315:	NM_199261:NM_013315:NM_199259:NM_199260:
7179	TPTE	transmembrane phosphatase with tensin homology	0.34	CTGAAATATGTTCAACTGCAA	NM_013315:	NM_199261:NM_013315:NM_199259:NM_199260:
93492	TPTE2	transmembrane phosphoinositide 3-phosphatase and tensin homolog	1.33	ACCTGGAGAACTGATAATAAA	NM_130785:	NM_130785:NM_199254:NM_199255:
93492	TPTE2	transmembrane phosphoinositide 3-phosphatase and tensin homolog	-4.94	CTGATAATAAATTGTGGTTTA	NM_130785:	NM_130785:NM_199254:NM_199255:
22974	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	-9.65	AAGGATGATATTAACCTGTTA	NM_012112:	NM_012112:
22974	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	0.70	AAGGCTAATAATGAGATGTAA	NM_012112:	NM_012112:
126382	TRA16	TR4 orphan receptor associated protein TRA16	-2.47	CAGGGTGAGTTCAGTGCTGAA	NM_176880:	NM_176880:
126382	TRA16	TR4 orphan receptor associated protein TRA16	-0.99	CAAGAGCTATTCGCAGAGAAA	NM_176880:	NM_176880:
8717	TRADD	TNFRSF1A-associated via death domain	1.45	AGCAATGATAATAAAGTATAA	NM_003789:	NM_153425:NM_003789:
8717	TRADD	TNFRSF1A-associated via death domain	0.97	CCCGAATGTTAAGCAATGATA	NM_003789:	NM_153425:NM_003789:
7185	TRAF1	TNF receptor-associated factor 1	-1.52	AGGGCTCCACTAGGACTTCAA	NM_005658:	NM_005658:
7185	TRAF1	TNF receptor-associated factor 1	-2.61	CAGACTGATCAGGACCTCCAA	NM_005658:	NM_005658:
7186	TRAF2	TNF receptor-associated factor 2	-0.12	CACGAGGGCATATATGAAGAA	NM_021138:	NM_021138:
7186	TRAF2	TNF receptor-associated factor 2	-0.41	CTGGACCAAGACAAGATTGAA	NM_021138:	NM_021138:
7187	TRAF3	TNF receptor-associated factor 3	0.87	AGAGAGCATCGTTAAAGATAA	NM_003300:	NM_145725:NM_145726:NM_003300:
7187	TRAF3	TNF receptor-associated factor 3	-0.11	TCCGATGATCGCGCTGCAGAA	NM_003300:	NM_145725:NM_145726:NM_003300:
26146	TRAF3IP1	TNF receptor-associated factor 3 interacting protein 1	0.50	CAACTAGTATTTCGGATGATA	NM_015650:	NM_015650:
26146	TRAF3IP1	TNF receptor-associated factor 3 interacting protein 1	0.01	AAGAAGCTAATATTAACTCAA	NM_015650:	NM_015650:
80342	TRAF3IP3	TRAF3 interacting protein 3	0.52	CAGACTTGGCACCAACATTAA	NM_025228:	NM_025228:
80342	TRAF3IP3	TRAF3 interacting protein 3	-0.66	TAGCAGGGACTTACAGATGAA	NM_025228:	NM_025228:
9618	TRAF4	TNF receptor-associated factor 4	-0.76	CACCAGGACATTCGAAAGCGA	NM_004295:	NM_004295:NM_145751:
9618	TRAF4	TNF receptor-associated factor 4	-3.66	CCGGAGCTGGAAGTACAAGTA	NM_004295:	NM_004295:NM_145751:
7188	TRAF5	TNF receptor-associated factor 5	0.19	AGGGTACTTGCTATAATGGAA	NM_004619:	NM_004619:NM_145759:NM_001033910:
7188	TRAF5	TNF receptor-associated factor 5	-0.22	CTGGAGGGTACTTGCTATAAT	NM_004619:	NM_004619:NM_145759:NM_001033910:
7189	TRAF6	TNF receptor-associated factor 6	0.60	AGGGATGAGTTTAAACCCTAA	NM_004620:	NM_004620:NM_145803:
7189	TRAF6	TNF receptor-associated factor 6	-0.04	CAGGGATGAGTTTAAACCCTA	NM_004620:	NM_004620:NM_145803:
84231	TRAF7	TNF receptor-associated factor 7	-1.60	CACGCTGGTCTCCTCACACAA	NM_032271:	NM_206835:NM_032271:
84231	TRAF7	TNF receptor-associated factor 7	0.87	GCGGGACGCATCCATGTTAAA	NM_032271:	NM_206835:NM_032271:
10293	TRAIP	TRAF interacting protein	0.59	CCGTGATGATATTGATCTCAA	NM_005879:	NM_005879:
10293	TRAIP	TRAF interacting protein	-0.35	CGGGACCAGCCTGAGGTGTAA	NM_005879:	NM_005879:
66008	TRAK2	trafficking protein, kinesin binding 2	-2.10	CACGACCAGGTGTCATTACTA	NM_015049:	NM_015049:
66008	TRAK2	trafficking protein, kinesin binding 2	0.14	CAGGCACATTAAATTATTGTA	NM_015049:	NM_015049:
23471	TRAM1	translocation associated membrane protein 1	-3.84	CAGGGTAACATGGAAATACTA	NM_014294:	NM_014294:
23471	TRAM1	translocation associated membrane protein 1	-1.20	ATGGTGTGAATGGAACATTAA	NM_014294:	NM_014294:
10131	TRAP1	TNF receptor-associated protein 1	0.30	CGCGCTCATCAAGAAGCTGAA	NM_016292:	NM_016292:
10131	TRAP1	TNF receptor-associated protein 1	-2.18	CCGCTACACCCTGCACTATAA	NM_016292:	NM_016292:
6399	TRAPPC2	trafficking protein particle complex 2	1.22	AGGAATAGTGATCCTGCTATA	NM_014563:	NM_014563:NM_001011658:

6399	TRAPPC2	trafficking protein particle complex 2	-0.15	TAGGTTGATCTTAATGTAACA	NM_014563:	NM_014563:NM_001011658:
51399	TRAPPC4	trafficking protein particle complex 4	0.13	CCGAAAGATTTATGAGATTTA	NM_016146:	NM_016146:
51399	TRAPPC4	trafficking protein particle complex 4	2.04	ATGGAGGAGCTAGGTCCATAA	NM_016146:	NM_016146:
50852	TRAT1	T cell receptor associated transmembrane adaptor 1	-4.91	AAGGATGGAGATGAGCAACTA	NM_016388:	NM_016388:
50852	TRAT1	T cell receptor associated transmembrane adaptor 1	-1.15	AAGCATGAATGCGTTCTGGAA	NM_016388:	NM_016388:
54210	TREM1	triggering receptor expressed on myeloid cells 1	1.35	TCCGAGCTGCAACTAAATTAA	NM_018643:	NM_018643:
54210	TREM1	triggering receptor expressed on myeloid cells 1	0.63	GAGGATCATACTAGAAGACTA	NM_018643:	NM_018643:
54209	TREM2	triggering receptor expressed on myeloid cells 2	0.10	ATCCAAGACTGTCATATTTAA	NM_018965:	NM_018965:
54209	TREM2	triggering receptor expressed on myeloid cells 2	-1.84	AAGGAAGATGATGGGAGGAAA	NM_018965:	NM_018965:
340205	TREML1	triggering receptor expressed on myeloid cells-like 1	-0.13	CACCACCTTCATTTGACAATA	NM_178174:	NM_178174:
340205	TREML1	triggering receptor expressed on myeloid cells-like 1	1.45	CAGGCGTACGTTTCTCACAGA	NM_178174:	NM_178174:
79865	TREML2	triggering receptor expressed on myeloid cells-like 2	-1.31	CCGATACTGGTGCATGCGCAA	NM_024807:	NM_024807:
79865	TREML2	triggering receptor expressed on myeloid cells-like 2	-1.22	CTGCTGACAGTGTATACACAA	NM_024807:	NM_024807:
285852	TREML4	triggering receptor expressed on myeloid cells-like 4	1.87	TCAAGTTGAACTAACAATAAA	NM_198153:	NM_198153:
285852	TREML4	triggering receptor expressed on myeloid cells-like 4	-0.97	GCCCAAATTCTGTTTACTTAA	NM_198153:	NM_198153:
55809	TRERF1	transcriptional regulating factor 1	-2.30	ACCCAGGTGTTTGCCAACCAA	NM_018415:	NM_033501:NM_033502:NM_018415:
55809	TRERF1	transcriptional regulating factor 1	-1.52	AAGCCGAAATGCACACATGAA	NM_018415:	NM_033501:NM_033502:NM_018415:
11277	TREX1	three prime repair exonuclease 1	-5.42	CAGCAGGAACTGCCCAGAGAA	NM_016381:	NM_033629:NM_032166:NM_016381:NM_033628: NM_130384:NM_033627:
11277	TREX1	three prime repair exonuclease 1	-0.97	CTCCTTTCCTTACCACATCAA	NM_016381:	NM_033629:NM_032166:NM_016381:NM_033628: NM_130384:NM_033627:
11219	TREX2 (three	three prime repair exonuclease 2	-0.35	CACAATGGCTTTGATTATGAT	NM_007205:	NM_080701:
11219	TREX2 (three	three prime repair exonuclease 2	-0.36	CACGACGAGTCTGGTGCCCTA	NM_007205:	NM_080701:
7200	TRH	thyrotropin-releasing hormone	1.29	ATGACAGTCATCCTAATGATA	NM_007117:	NM_007117:
7200	TRH	thyrotropin-releasing hormone	0.70	TGGTTTGTATATAACCCTCTA	NM_007117:	NM_007117:
29953	TRHDE	thyrotropin-releasing hormone degrading enzyme	-0.24	CACCACTGAATTCATGTAATA	NM_013381:	NM_013381:
29953	TRHDE	thyrotropin-releasing hormone degrading enzyme	0.01	CCGAATCTATAGAATAAAGTA	NM_013381:	NM_013381:
7201	TRHR (thyrotr	thyrotropin-releasing hormone receptor	-0.29	CAGGACTCTAGTGGTTGTCAA	NM_003301:	NM_003301:
7201	TRHR (thyrotr	thyrotropin-releasing hormone receptor	0.32	CTCAATATTAGCACCTACAAA	NM_003301:	NM_003301:
10221	TRIB1	tribbles homolog 1 (Drosophila)	0.48	TCAGACTAACTTCCAGAATTA	NM_025195:	NM_025195:
10221	TRIB1	tribbles homolog 1 (Drosophila)	0.05	CCAGCCGAACGTGGAACAGTA	NM_025195:	NM_025195:
28951	TRIB2	tribbles homolog 2 (Drosophila)	-0.07	CACGTGGACTCTAGTATGTAA	NM_021643:	NM_021643:
28951	TRIB2	tribbles homolog 2 (Drosophila)	-1.92	CAGGTTGTCCCACATGTATAA	NM_021643:	NM_021643:
57761	TRIB3	tribbles homolog 3 (Drosophila)	1.38	TACCATGAGTATGTATGTTTA	NM_021158:	NM_021158:
57761	TRIB3	tribbles homolog 3 (Drosophila)	0.35	ATGAGGCTAGTTCTTGTCTAA	NM_021158:	NM_021158:
10107	TRIM10	tripartite motif-containing 10	0.71	CAGTTGTATGACTTTAAACAA	NM_006778:	NM_006778:NM_052828:
10107	TRIM10	tripartite motif-containing 10	0.07	TCCAATAATGTTAGAGTTCAT	NM_006778:	NM_006778:NM_052828:
81559	TRIM11	tripartite motif-containing 11	0.70	AGAGTAGATGTCCTATAATAA	NM_145214:	NM_145214:
81559	TRIM11	tripartite motif-containing 11	0.33	CAGAGAGTAGATGTCCTATAA	NM_145214:	NM_145214:
9830	TRIM14	tripartite motif-containing 14	1.43	AAGCAGAGCTGCGTAAAGTTA	NM_014788:	NM_014788:NM_033221:
9830	TRIM14	tripartite motif-containing 14	-4.21	CAGGTGCCTATCACTGAGTAA	NM_014788:	NM_014788:NM_033221:
89870	TRIM15	tripartite motif-containing 15	-0.59	ATCCGTGATTTCCACAGGAAA	NM_033229:	NM_033229:
89870	TRIM15	tripartite motif-containing 15	-6.71	CCGGCTTGGAGCCCAGGTCAA	NM_033229:	NM_033229:
10626	TRIM16	tripartite motif-containing 16	-1.56	AGGCAGTGAAGTCCTGTCTAA	NM_006470:	NM_006470:
10626	TRIM16	tripartite motif-containing 16	-0.06	GCCGCATCAGGTGAACATCAA	NM_006470:	NM_006470:
51127	TRIM17	tripartite motif-containing 17	-0.04	CCCGGACAGATTGAAGTGCTA	NM_016102:	NM_016102:NM_001024940:NM_001024941:
51127	TRIM17	tripartite motif-containing 17	-0.22	CAGGGACAACGTGAGCCGGAA	NM_016102:	NM_016102:NM_001024940:NM_001024941:
6737	TRIM21	tripartite motif-containing 21	-6.99	CAGAGCATACCTGGAAATGAA	NM_003141:	NM_003141:
6737	TRIM21	tripartite motif-containing 21	-5.89	CCGGCAGCGCTTTCTGCTCAA	NM_003141:	NM_003141:
10346	TRIM22	tripartite motif-containing 22	0.64	CAAGAAGTCCATAGTAATTTA	NM_006074:	NM_006074:
10346	TRIM22	tripartite motif-containing 22	-0.18	AAGCTCTATGATCTTAAATAA	NM_006074:	NM_006074:
373	TRIM23	tripartite motif-containing 23	0.26	CAAGTGTATAGCCGTAGTCTA	NM_001656:	NM_033228:NM_001656:NM_033227:
373	TRIM23	tripartite motif-containing 23	0.09	TAGGATGAAGTTAAATCTTAA	NM_001656:	NM_001656:
8805	TRIM24	tripartite motif-containing 24	-4.14	TAGGTGTACTGTACTGAAGAA	NM_003852:	NM_015905:NM_003852:
8805	TRIM24	tripartite motif-containing 24	0.88	ACGCCAGTTGCTTAAATAATA	NM_003852:	NM_015905:NM_003852:
7706	TRIM25	tripartite motif-containing 25	0.91	CAAGGTCCACCTGATGTATAA	NM_005082:	NM_005082:
7706	TRIM25	tripartite motif-containing 25	1.07	CAGCAAGTTTGACACCATTTA	NM_005082:	NM_005082:
7726	TRIM26	tripartite motif-containing 26	-1.33	ACCCATTGCTCGAGTGGTTAA	NM_003449:	NM_003449:
7726	TRIM26	tripartite motif-containing 26	2.04	ACCGGAGAATTCTCAGATAAA	NM_003449:	NM_003449:
51592	TRIM33	tripartite motif-containing 33	-0.49	TCCCGTAGTATCGGTACACAA	NM_015906:	NM_033020:NM_015906:
51592	TRIM33	tripartite motif-containing 33	-0.53	CTGGGCAAAGAATGTAGTCAA	NM_015906:	NM_033020:NM_015906:
23087	TRIM35	tripartite motif-containing 35	-0.22	CCGGATTAGTTGGTTTCCATA	NM_015066:	NM_171982:NM_015066:
23087	TRIM35	tripartite motif-containing 35	-0.69	CAGGGTTCCAGAGTACTTAAA	NM_015066:	NM_171982:NM_015066:
55521	TRIM36	tripartite motif-containing 36	0.43	AGCGTTAACCTTCGTAACTAA	NM_018700:	NM_018700:
55521	TRIM36	tripartite motif-containing 36	0.78	CCGTGTGGAACCATATTCATA	NM_018700:	NM_018700:
4591	TRIM37	tripartite motif-containing 37	-0.87	CTGTAGATTAGTGAACAGAAA	NM_015294:	NM_015294:
4591	TRIM37	tripartite motif-containing 37	-1.24	CTAGAGCTTAGTTGTGTTTAA	NM_015294:	NM_015294:
10475	TRIM38	tripartite motif-containing 38	-0.11	CCGGCCCTATTTCCAGGTTTA	NM_006355:	NM_006355:
10475	TRIM38	tripartite motif-containing 38	0.35	AACCACTGACATGTTGTTTAA	NM_006355:	NM_006355:
56658	TRIM39	tripartite motif-containing 39	-0.99	AGGGCAGAGATTGGACATCAA	NM_021253:	NM_021253:NM_172016:
56658	TRIM39	tripartite motif-containing 39	0.49	TCGGGTAATCTTCACAGAAAT	NM_021253:	NM_021253:NM_172016:
89122	TRIM4	tripartite motif-containing 4	0.21	CCGCAGTATAGGCTTAAGTCA	NM_033017:	NM_033017:NM_033091:
89122	TRIM4	tripartite motif-containing 4	0.88	CGCCCTTATTGTATAAGACAA	NM_033017:	NM_033017:NM_033091:
90933	TRIM41	tripartite motif-containing 41	-4.38	AAGGCGTGCTGTGGAAATAAA	NM_033549:	NM_201627:NM_033549:
90933	TRIM41	tripartite motif-containing 41	0.48	AGGGTAGAGCTGGGTAATAAA	NM_033549:	NM_033549:
129868	TRIM43 (tripa	tripartite motif-containing 43	-0.86	CCGGTTCTCCATAAGGAAGAA	NM_138800:	NM_138800:
129868	TRIM43 (tripa	tripartite motif-containing 43	-1.12	CGGGAGAAACTCTTAAAGCAA	NM_138800:	NM_138800:
80128	TRIM46	tripartite motif-containing 46	0.91	GTCATGGTTTATAAACAATAA	NM_025058:	NM_025058:
80128	TRIM46	tripartite motif-containing 46	-0.68	CACCACCTGCCTGGCACTATA	NM_025058:	NM_025058:
91107	TRIM47	tripartite motif-containing 47	2.34	CTGCAGCTGTTTGGAACCAAA	NM_033452:	NM_033452:
91107	TRIM47	tripartite motif-containing 47	-0.08	CAGGGACTATTTCCTCAAGTT	NM_033452:	NM_033452:
57093	TRIM49	tripartite motif-containing 49	0.28	ATGATATCTTTCTGTATGAAA	NM_020358:	NM_020358:
85363	TRIM5	tripartite motif-containing 5	-0.97	CAGGGTGTGGATGGCGTCATA	NM_033034:	NM_033092:NM_033093:NM_033034:
85363	TRIM5	tripartite motif-containing 5	1.80	TCGGTTATTACGCAATGTATA	NM_033034:	NM_033093:NM_033034:
135892	TRIM50A	tripartite motif-containing 50A	-0.63	CAGCCAAGGGTGTATTTGTAA	NM_178125:	NM_178125:
135892	TRIM50A	tripartite motif-containing 50A	1.14	TCCCTGGAACATGTAATGATA	NM_178125:	NM_178125:
84767	TRIM51	tripartite motif-containing 51	1.42	CAGAGTGTGAATGATACTTTA	NM_032681:	NM_032681:XM_208060:
25893	TRIM58	tripartite motif-containing 58	-2.82	CCGGTGAAATTTCATTCTACA	NM_015431:	NM_015431:
25893	TRIM58	tripartite motif-containing 58	-0.68	ATGGAGCAATCTCAACCTCTA	NM_015431:	NM_015431:
286827	TRIM59	tripartite motif-containing 59	-0.29	AACATTACAGGCAACCATTAA	NM_173084:	NM_173084:
286827	TRIM59	tripartite motif-containing 59	0.34	CCCGTTGAAATTTATCCTCGA	NM_173084:	NM_173084:
117854	TRIM6	tripartite motif-containing 6	-1.75	TAGGAAGTTCTGATCTGTTAA	NM_001003818:	NM_001003818:NM_058166:
117854	TRIM6	tripartite motif-containing 6	1.57	CTACACTTTCTCTAAATATTA	NM_001003818:	NM_001003818:NM_058166:
166655	TRIM60	tripartite motif-containing 60	1.14	CAGATTATGTTTCCACATTAA	NM_152620:	NM_152620:
166655	TRIM60	tripartite motif-containing 60	-0.07	CCGTTTGGCCTTATTTCTATA	NM_152620:	NM_152620:
55223	TRIM62	tripartite motif-containing 62	0.06	CACTCAGTTCCCAAATCTAAA	NM_018207:	NM_018207:
55223	TRIM62	tripartite motif-containing 62	-1.33	CCGCGAGAAGTTCCCTGGCAA	NM_018207:	NM_018207:
120146	TRIM64	tripartite motif-containing 64	1.17	ATGGATGATTGTGGCAAGTTA	XM_061890:	XM_061890:
120146	TRIM64	tripartite motif-containing 64	0.89	TACTTTCTTGTAGTTTATCAA	XM_061890:	XM_061890:

201292	TRIM65	tripartite motif-containing 65	0.57	ATCAAGTTTATTTATCCATTA	NM_173547:	NM_173547:
201292	TRIM65	tripartite motif-containing 65	0.00	ATGGATAAATATTTCACAATA	NM_173547:	NM_173547:
440730	TRIM67	tripartite motif-containing 67	0.32	CACAACTATCTCAGGCCTTAA	NM_001004342:	NM_001004342:
440730	TRIM67	tripartite motif-containing 67	0.05	CCGGGAAGTGTACGTCGGTAA	NM_001004342:	NM_001004342:
55128	TRIM68	tripartite motif-containing 68	-3.55	AAGAGAGATCCTGAAGACTTA	NM_018073:	NM_018073:
55128	TRIM68	tripartite motif-containing 68	-2.36	TAGGCCAAACTGGAGAAATAA	NM_018073:	NM_018073:
81786	TRIM7	tripartite motif-containing 7	0.64	TGGGAATATTAATACAATAAA	NM_033342:	NM_033342:
81786	TRIM7	tripartite motif-containing 7	-0.24	CGGAAGCATCTTGTAATGGAA	NM_033342:	NM_033342:
114088	TRIM9	tripartite motif-containing 9	-0.01	CAGGGCAACACTAGTTTGATA	NM_015163:	NM_015163:
114088	TRIM9	tripartite motif-containing 9	-0.53	CAGCAGAGCATCAATAGCCTA	NM_015163:	NM_015163:
7204	TRIO	triple functional domain (PTPRF interacting)	0.41	ACCGTTGTTCTTAGATGTCGA	NM_007118:	NM_007118:
7204	TRIO	triple functional domain (PTPRF interacting)	0.27	CCGGGAATGTATGGATACGTA	NM_007118:	NM_007118:
9322	TRIP10	thyroid hormone receptor interactor 10	-0.30	ACGGCTAGACCAGGATATCAA	NM_004240:	NM_004240:
9322	TRIP10	thyroid hormone receptor interactor 10	-5.03	ACGGCTGAAATTGGAAGTGCA	NM_004240:	NM_004240:
9321	TRIP11	thyroid hormone receptor interactor 11	0.95	ACCCAGCTTTGTGTTATCGTA	NM_004239:	NM_004239:
9321	TRIP11	thyroid hormone receptor interactor 11	0.55	CAGAATGAGGTTCAACGTTTA	NM_004239:	NM_004239:
9320	TRIP12	thyroid hormone receptor interactor 12	-0.17	CACAATTTAGAGGAGTATCTA	XM_376178:	NM_004238:
9320	TRIP12	thyroid hormone receptor interactor 12	0.94	CAGATGTTTCATCATTTGAAA	XM_376178:	NM_004238:
9319	TRIP13	thyroid hormone receptor interactor 13	0.89	GAGGATTCACATTAATATAAT	NM_004237:	NM_004237:
9319	TRIP13	thyroid hormone receptor interactor 13	0.87	TTGACACAGAATTAAAGGTTA	NM_004237:	NM_004237:
9325	TRIP4	thyroid hormone receptor interactor 4	0.74	AGGATTTGGACTAGAGTTCAA	NM_016213:	NM_016213:
9325	TRIP4	thyroid hormone receptor interactor 4	-0.02	CAGAAATCAGGCGACCATCTA	NM_016213:	NM_016213:
7205	TRIP6	thyroid hormone receptor interactor 6	0.08	CACGGGCTCCCTGAAGCCAAA	NM_003302:	NM_003302:
7205	TRIP6	thyroid hormone receptor interactor 6	-0.06	CTGTATGACTTTGTCACCAAA	NM_003302:	NM_003302:
55621	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	-0.26	CAGCATCAGCGCTGACTTCTA	NM_017722:	NM_017722:
55621	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	-3.42	ACGCCGGAATGTCCAGCTCAA	NM_017722:	NM_017722:
8989	TRPA1	transient receptor potential cation channel, subfamily A, member 1	0.28	CTGGTTCTAACTTTCAATTTA	NM_007332:	NM_007332:
8989	TRPA1	transient receptor potential cation channel, subfamily A, member 1	0.23	CACGAATTCATATCTAATAAA	NM_007332:	NM_007332:
7220	TRPC1	transient receptor potential cation channel, subfamily C, member 1	0.87	TTCGGACTTCTAAATATGCTA	NM_003304:	NM_003304:
7220	TRPC1	transient receptor potential cation channel, subfamily C, member 1	-0.02	TGGGTCCATTACAGATTTCAA	NM_003304:	NM_003304:
7222	TRPC3	transient receptor potential cation channel, subfamily C, member 3	0.13	TTGGCTTTGACTATAGCACAA	NM_003305:	NM_003305:
7222	TRPC3	transient receptor potential cation channel, subfamily C, member 3	1.08	CACGTTATCAGCAGATAATGA	NM_003305:	NM_003305:
7223	TRPC4	transient receptor potential cation channel, subfamily C, member 4	-6.62	AACGAAAGGGTTAACCTGCAA	NM_016179:	NM_016179:
7223	TRPC4	transient receptor potential cation channel, subfamily C, member 4	-1.45	CGAGATGACAATAGTCTCATA	NM_016179:	NM_016179:
26133	TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 as	-0.47	CTGCTTGAGTATCCTGTATAA	NM_015638:	NM_015638:NM_199368:
26133	TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 as	0.82	AACCACTTATCCAAATACTTA	NM_015638:	NM_015638:NM_199368:
7224	TRPC5	transient receptor potential cation channel, subfamily C, member 5	-3.68	ACCAGCTATCAGATAAGGCAA	NM_012471:	NM_012471:
7224	TRPC5	transient receptor potential cation channel, subfamily C, member 5	0.65	CACACTAAGTCCATCTTACAA	NM_012471:	NM_012471:
7225	TRPC6	transient receptor potential cation channel, subfamily C, member 6	-1.19	CACTTAGCCATTGAATGTAAA	NM_004621:	NM_004621:
7225	TRPC6	transient receptor potential cation channel, subfamily C, member 6	0.27	CCCTATTTAGTTTGTGGCTAA	NM_004621:	NM_004621:
57113	TRPC7	transient receptor potential cation channel, subfamily C, member 7	-0.15	CAGGCTTACGTCAACAGTCTA	NM_020389:	NM_020389:
57113	TRPC7	transient receptor potential cation channel, subfamily C, member 7	0.35	CGGATCAAACTCGCCATTAAA	NM_020389:	NM_020389:
4308	TRPM1	transient receptor potential cation channel, subfamily M, member 1	0.76	CACCATTAGGTCACTTAAGAA	NM_002420:	NM_002420:
4308	TRPM1	transient receptor potential cation channel, subfamily M, member 1	-0.62	CAAGATTATACAATCTCTTTA	NM_002420:	NM_002420:
7226	TRPM2	transient receptor potential cation channel, subfamily M, member 2	-0.71	CAGGCCTATGTCTGTGAGGAA	NM_003307:	NM_001001188:NM_003307:
7226	TRPM2	transient receptor potential cation channel, subfamily M, member 2	-0.02	CTGCAGGAAGAGCATAAAGAA	NM_003307:	NM_001001188:NM_003307:
80036	TRPM3	transient receptor potential cation channel, subfamily M, member 3	0.64	CAAGGTAACAGTCATAGTTCA	NM_020952:	NM_024971:NM_206946:NM_206947:NM_206945: NM_206944:NM_001007471:NM_020952:
80036	TRPM3	transient receptor potential cation channel, subfamily M, member 3	-0.11	ATCATCGTGTATAGACATCTA	NM_020952:	NM_024971:NM_206946:NM_206947:NM_206945: NM_206944:NM_001007471:NM_020952:
54795	TRPM4	transient receptor potential cation channel, subfamily M, member 4	-5.21	AACGTGGGAATCGGTGCATAA	NM_017636:	NM_017636:
54795	TRPM4	transient receptor potential cation channel, subfamily M, member 4	-1.51	CGGGTTTACCTTTCTAAGGAA	NM_017636:	NM_017636:
29850	TRPM5	transient receptor potential cation channel, subfamily M, member 5	-1.58	CTGACTTGTGTTGCCTGACAA	NM_014555:	NM_014555:
29850	TRPM5	transient receptor potential cation channel, subfamily M, member 5	-0.96	CAGAGTGGACTTCATTGCCAA	NM_014555:	NM_014555:
140803	TRPM6	transient receptor potential cation channel, subfamily M, member 6	-4.69	TTGCCCAATTGCCAAACTAAA	NM_017662:	NM_017662:
140803	TRPM6	transient receptor potential cation channel, subfamily M, member 6	-2.05	GAGCAGAATCCTGCACATTAA	NM_017662:	NM_017662:
54822	TRPM7	transient receptor potential cation channel, subfamily M, member 7	-1.45	CGGGAGGAAATTGTTTGGTAA	NM_017672:	NM_017672:
54822	TRPM7	transient receptor potential cation channel, subfamily M, member 7	-2.14	CTGGTTTAACACGTTGGCATA	NM_017672:	NM_017672:
79054	TRPM8	transient receptor potential cation channel, subfamily M, member 8	0.96	AAGGTTAGATTCCAATAAATA	NM_024080:	NM_024080:
79054	TRPM8	transient receptor potential cation channel, subfamily M, member 8	-2.76	CAGAATGTTATCATACTACAT	NM_024080:	NM_024080:
7227	TRPS1	trichorhinophalangeal syndrome I	0.81	CACGATAGATCTTATTCCATA	NM_014112:	NM_014112:
7227	TRPS1	trichorhinophalangeal syndrome I	0.49	GAGGGTGTTCTTGACGATTAA	NM_014112:	NM_014112:
7227	TRPS1	trichorhinophalangeal syndrome I	0.24	AGGGTACCACTTATTCTTCAA	NM_152700:	NM_014112:
7442	TRPV1	transient receptor potential cation channel, subfamily V, member 1	-0.21	CCCGAGGAAGTTTATCTGCGA	NM_018727:	NM_080705:NM_080704:NM_018727:NM_080706:
7442	TRPV1	transient receptor potential cation channel, subfamily V, member 1	0.51	CTCAATTGCTGTGCAGGTTAA	NM_018727:	NM_080705:NM_080704:NM_018727:NM_080706:
51393	TRPV2	transient receptor potential cation channel, subfamily V, member 2	-0.08	CCAGTGAATTCTGGTGGCAAA	NM_016113:	NM_016113:
51393	TRPV2	transient receptor potential cation channel, subfamily V, member 2	-0.29	CAGAGGATCTTTCCAACCACA	NM_016113:	NM_016113:
162514	TRPV3	transient receptor potential cation channel, subfamily V, member 3	0.43	CCCGGAAACCTCGGTGTAGAA	NM_145068:	NM_145068:
162514	TRPV3	transient receptor potential cation channel, subfamily V, member 3	-1.21	CACGTCTCCTTCCTTAACGAA	NM_145068:	NM_145068:
59341	TRPV4	transient receptor potential cation channel, subfamily V, member 4	-1.50	CTGGGATTTGCCGGTGCTCAA	NM_147204:	NM_021625:NM_147204:
59341	TRPV4	transient receptor potential cation channel, subfamily V, member 4	-2.31	CTGGAGTGAATTCTCTCTTCA	NM_147204:	NM_021625:NM_147204:
56302	TRPV5	transient receptor potential cation channel, subfamily V, member 5	-3.35	CAGGAGCATCCATCTGAGAAA	NM_019841:	NM_019841:
55503	TRPV6	transient receptor potential cation channel, subfamily V, member 6	-0.68	CTGCATGTCAGAGCACTTTAA	NM_018646:	NM_018646:
55503	TRPV6	transient receptor potential cation channel, subfamily V, member 6	-0.37	GAGGAGTAGCATGAACGCCAA	NM_018646:	NM_018646:
8295	TRRAP	transformation/transcription domain-associated protein	-1.64	CAGACCTTTGTAACAAGTGTA	NM_003496:	NM_003496:
8295	TRRAP	transformation/transcription domain-associated protein	0.51	ATCGAGGAAATACTTAGCCAA	NM_003496:	NM_003496:
136541	TRY1	trypsin X3	-1.79	TAGAGATATCATGAACTTCAA	NM_001001317:	NM_001001317:
136541	TRY1	trypsin X3	-1.56	CAGGAGGCGTCTGTAGAGATA	NM_001001317:	NM_001001317:
7249	TSC2	tuberous sclerosis 2	-0.37	TGGCACGATGACATCATGCAA	NM_000548:	NM_021056:NM_000548:NM_021055:
7249	TSC2	tuberous sclerosis 2	0.44	AGCATTAATCTCTTACCATAA	NM_000548:	NM_021056:NM_000548:NM_021055:
7251	TSG101	tumor susceptibility gene 101	-2.85	ACCCGTTTAGATCAAGAAGTA	NM_006292:	NM_006292:
7251	TSG101	tumor susceptibility gene 101	-4.29	CAGCTGAGGGCACTAATGCAA	NM_006292:	NM_006292:
95681	TSGA14	testis specific, 14	1.17	TCAGACAACTTTGGAGTATTA	NM_018718:	NM_018718:
95681	TSGA14	testis specific, 14	0.05	CAGTATTAGTCTAATTGAGTA	NM_018718:	NM_018718:
7252	TSHB	thyroid stimulating hormone, beta	0.75	AAGACAAACTACTGTACCAAA	NM_000549:	NM_000549:
7252	TSHB	thyroid stimulating hormone, beta	-0.66	CTGCATACATGAAGCCATCAA	NM_000549:	NM_000549:
7253	TSHR	thyroid stimulating hormone receptor	-1.43	AGCACTGATATTCAGGTTCAA	NM_000369:	NM_000369:
7253	TSHR	thyroid stimulating hormone receptor	-0.15	TACGCAGACTCTGAAGCTTAT	NM_000369:	NM_000369:NM_001018036:
60385	TSKS	testis-specific kinase substrate	-0.97	AACCAACGTCTTGAAGCAGAA	NM_021733:	NM_021733:
60385	TSKS	testis-specific kinase substrate	-3.95	CACCAACGTGTCACTGCTCAA	NM_021733:	NM_021733:
85480	TSLP	thymic stromal lymphopoietin	-0.06	CTGGAACAAGTGTCACAATTA	NM_033035:	NM_138551:NM_033035:
85480	TSLP	thymic stromal lymphopoietin	2.81	AGCACCTAAACTTACATTTAA	NM_033035:	NM_138551:NM_033035:
203062	TSNARE1	t-SNARE domain containing 1	0.68	CCGCGACGTTGTGGACCTGAA	NM_145003:	NM_145003:
203062	TSNARE1	t-SNARE domain containing 1	-0.24	CCAGCTGAGCACCCGAATAAA	NM_145003:	NM_145003:
29122	TSP50	testes-specific protease 50	1.57	GAGGTGCTCAATTAAACATTA	NM_013270:	NM_013270:
29122	TSP50	testes-specific protease 50	-0.27	CAGGGAGAAGTTCTGCTATGA	NM_013270:	NM_013270:
27075	TSPAN13	tetraspanin 13	1.34	CTCCCATAATTTGAAATTGAA	NM_014399:	NM_014399:

27075	TSPAN13	tetraspanin 13	1.70	CAGGAAGTATATCTATATGAT	NM_014399:	NM_014399:
6302	TSPAN31	tetraspanin 31	-0.31	CTGGCTATTAACCGAAGCAAA	NM_005981:	NM_005981:
6302	TSPAN31	tetraspanin 31	-1.15	CTGGTGTGGCTCTAAGGGTAA	NM_005981:	NM_005981:
7102	TSPAN7	tetraspanin 7	-1.98	CAGGCTGCCTAAGACATGTAA	NM_004615:	NM_004615:
7102	TSPAN7	tetraspanin 7	0.39	CCGGTTCATCACGGCCAATCA	NM_004615:	NM_004615:
64061	TSPYL2	TSPY-like 2	1.12	CACAAACATGGTGATTGTCAA	NM_022117:	NM_022117:
64061	TSPYL2	TSPY-like 2	-0.46	CCAGAGGTTAGTTGACCCGAA	NM_022117:	NM_022117:
7260	TSSC1 (tumo	tumor suppressing subtransferable candidate 1	1.12	CGCAGTCTCTTAAATATGATA	NM_003310:	NM_003310:
7260	TSSC1 (tumo	tumor suppressing subtransferable candidate 1	0.15	CGGGTGAAATCTGGCATATTA	NM_003310:	NM_003310:
10078	TSSC4 (tumo	tumor suppressing subtransferable candidate 4	-1.23	CCCGGTGGTGCTGAAGTGGAA	NM_005706:	NM_005706:
10078	TSSC4 (tumo	tumor suppressing subtransferable candidate 4	1.04	CCGCTTGGCTGTCCAATCACA	NM_005706:	NM_005706:
83942	TSSK1	testis-specific serine kinase 1	-0.03	CCAGCTTTCCTTGGCCATCAA	NM_032028:	NM_032028:
83942	TSSK1	testis-specific serine kinase 1	0.87	TAGAAGCTGATTTAACACCAA	NM_032028:	NM_032028:
23617	TSSK2	testis-specific serine kinase 2	-0.25	CAAGTTCAATGTGGCTGTCAA	NM_053006:	NM_053006:
23617	TSSK2	testis-specific serine kinase 2	0.98	GTCGGCCTTCACGTAAACTAA	NM_053006:	NM_053006:
23617	TSSK2	testis-specific serine kinase 2	0.07	CGACAAGGACTTCAACATCAA	XM_497791:	NM_053006:XM_497791:
81629	TSSK3	testis-specific serine kinase 3	1.49	ATGGCAAGTGCTCTCCAATAA	NM_052841:	NM_052841:
81629	TSSK3	testis-specific serine kinase 3	0.90	TGGCAAGTGCTCTCCAATAAA	NM_052841:	NM_052841:
283629	TSSK4	testis-specific serine kinase 4	-2.48	CAGGGTGGTGATGTCCTTGAA	NM_174944:	NM_174944:
283629	TSSK4	testis-specific serine kinase 4	-1.85	CCGTGAAATACAGGTAATGAA	NM_174944:	NM_174944:
83983	TSSK6	testis-specific serine kinase 6	1.30	ATCGAGGTGTGCAACGGGAAA	NM_032037:	NM_032037:
83983	TSSK6	testis-specific serine kinase 6	-0.30	CCGGTTGGAACCTGCAATAAA	NM_032037:	NM_032037:
7263	TST	thiosulfate sulfurtransferase (rhodanese)	-1.27	CTGGTGGATTCAAGGTCTCAA	NM_003312:	NM_003312:
7263	TST	thiosulfate sulfurtransferase (rhodanese)	-2.36	CCGCACCGTATCAGTGCTCAA	NM_003312:	NM_003312:
7264	TSTA3	tissue specific transplantation antigen P35B	-0.50	CAAGTCGGATGGGCAGTTTAA	NM_003313:	NM_003313:
7264	TSTA3	tissue specific transplantation antigen P35B	0.08	TCCGCGGAGGCAGTTCATATA	NM_003313:	NM_003313:
84630	TTBK1	tau tubulin kinase 1	0.12	CAGGAACGAGAAGTTTAACTA	XM_166453:	NM_032538:
84630	TTBK1	tau tubulin kinase 1	0.02	TGGCAGGAACGAGAAGTTTAA	XM_166453:	NM_032538:
146057	TTBK2	tau tubulin kinase 2	-4.13	ACGGCCCAGGTTAAATGGAAA	NM_173500:	NM_173500:
146057	TTBK2	tau tubulin kinase 2	0.46	CACATTGGTCATGACATGTTA	NM_173500:	NM_173500:
7267	TTC3	tetratricopeptide repeat domain 3	-2.00	ATCCATAAGAATTGAGCGCTA	NM_003316:	NM_003316:NM_001001894:
7267	TTC3	tetratricopeptide repeat domain 3	-0.52	CACGCCTTAGTTTGAAACAGA	NM_003316:	NM_003316:NM_001001894:
7272	TTK	TTK protein kinase	-1.12	CAGCAATACCTTGGATGATTA	NM_003318:	NM_003318:
7272	TTK	TTK protein kinase	-0.28	TCCGACTTTATGATTATGAAA	NM_003318:	NM_003318:
150465	TTL	tubulin tyrosine ligase	0.62	CGCGACTGCTTCAGAACTATA	XM_379881:	NM_153712:
7273	TTN	titin	0.06	ATCGACTATTACATCGTAGAA	NM_003319:	NM_133437:NM_133378:NM_003319:NM_133432:
7273	TTN	titin	0.26	CGCATTCTAGCTCGAGTCAAA	NM_003319:	NM_133437:NM_133378:NM_003319:NM_133432:
7274	TTPA	tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamir	0.20	ACGGATTCACATGCATGGGAA	NM_000370:	NM_000370:
7274	TTPA	tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamir	0.36	ACGGATTCATTTCCATTGAAA	NM_000370:	NM_000370:
51567	TTRAP	TRAF and TNF receptor associated protein	1.10	ACCGAAATAGTTAATATTTGA	NM_016614:	NM_016614:
51567	TTRAP	TRAF and TNF receptor associated protein	0.58	CGGAACGAATGAATCAGTTAA	NM_016614:	NM_016614:
7277	TUBA1	tubulin, alpha 1 (testis specific)	0.27	AACAGTTTCCTTGCACGGTTA	NM_006000:	NM_006000:
7277	TUBA1	tubulin, alpha 1 (testis specific)	-0.08	GAGGATGAGGGAGAAGAATAA	NM_006000:	NM_006000:
7278	TUBA2	tubulin, alpha 2	-5.53	CCCGGTCATCTCAGCCGAGAA	NM_006001:	NM_006001:NM_079836:
7278	TUBA2	tubulin, alpha 2	1.62	TTCAAGTTCTTTGCAATTAAA	NM_006001:	NM_006001:NM_079836:
7846	TUBA3	tubulin, alpha 3	-0.72	CCGCCTAAGAGTCGCGCTGTA	NM_006009:	NM_006009:
7846	TUBA3	tubulin, alpha 3	0.96	CTGAATAGGTTAATAGGTCAA	NM_006009:	NM_006009:
80086	TUBA4	tubulin, alpha 4	-2.41	CTGTGTGTCTGTCCTACATAA	NM_025019:	NM_025019:
80086	TUBA4	tubulin, alpha 4	1.15	AGGCTTTAAGGTTGATATCAA	NM_025019:	NM_025019:
51807	TUBA8	tubulin, alpha 8	0.40	TCCGGGCATCATCTAGACTTA	NM_018943:	NM_018943:
51807	TUBA8	tubulin, alpha 8	1.67	GAGCAGCTTTGTGTCACTAAA	NM_018943:	NM_018943:
79861	TUBAL3	tubulin, alpha-like 3	0.39	ACAGCACATGTTGATTACGAA	NM_024803:	NM_024803:
79861	TUBAL3	tubulin, alpha-like 3	-2.67	CTGCCGTGGTAGAGCCTTATA	NM_024803:	NM_024803:
203068	TUBB	tubulin, beta	-4.38	CAGCAAGATCCGAGAAGAATA	XM_047083:	NM_178014:XM_047083:
203068	TUBB	tubulin, beta	0.08	CAGTTAATACTTCCTCTTAAA	NM_178014:	NM_178014:
203068	TUBB	tubulin, beta	-0.37	CTCCAGAAACGTCTTCTTAAT	NM_178014:	NM_178014:
81027	TUBB1	tubulin, beta 1	0.39	TCCGAGTACCAACAATTTCAA	NM_030773:	NM_030773:
81027	TUBB1	tubulin, beta 1	-3.51	CAGCGAAGGGATGGACATAAA	NM_030773:	NM_030773:
7280	TUBB2A	tubulin, beta 2A	0.38	GAAGGTATCTATACTAATAAA	NM_001069:	NM_001069:
7280	TUBB2A	tubulin, beta 2A	-3.28	CTGTGAAGGTATCTATACTAA	NM_001069:	NM_001069:
347733	TUBB2B	tubulin, beta 2B	0.00	ACAGTTAAGATGAGAGATCAA	NM_178012:	NM_178012:
347733	TUBB2B	tubulin, beta 2B	1.22	CAGGCACGATGGATTCGGTTA	NM_178012:	NM_178012:
10381	TUBB3	tubulin, beta 3	0.36	TTGCTGTCAGATACCCTTAAA	NM_006086:	NM_006086:
10381	TUBB3	tubulin, beta 3	-1.19	GCGGATCAGCGTCTACTACAA	NM_006086:	NM_006086:
10382	TUBB4	tubulin, beta 4	-0.28	CTGACCTTGCCTCACCTTTAA	NM_006087:	NM_006087:
10382	TUBB4	tubulin, beta 4	-0.04	CTGCCTCACCCTCAATAAATA	NM_006087:	NM_006087:
56604	TUBB4Q (tub	tubulin, beta polypeptide 4, member Q	-2.48	CACAGCCGTCCAGGAACTCAA	NM_020040:	NM_020040:
84617	TUBB6	tubulin, beta 6	-2.14	CAGTATGGGACTTTGAAATAA	NM_032525:	NM_032525:
84617	TUBB6	tubulin, beta 6	1.72	CCGTGTTGCCTTATATGAATA	NM_032525:	NM_032525:
347688	TUBB8	tubulin, beta 8	0.44	CTGGTGTCTGAATATCAGCAA	XM_371207:	XM_371684:XM_371207:NM_177987:
51174	TUBD1	tubulin, delta 1	0.34	CAACAGCCAGTTCTTAGTAAA	NM_016261:	NM_016261:
51174	TUBD1	tubulin, delta 1	-0.15	TTGGTCATTCTTCGTGGGAAA	NM_016261:	NM_016261:
51175	TUBE1	tubulin, epsilon 1	0.06	TAGTGAAATCTTAGTACCTTA	NM_016262:	NM_016262:
51175	TUBE1	tubulin, epsilon 1	0.64	CAAGATTTGAAGGGTCCCTTA	NM_016262:	NM_016262:
7283	TUBG1	tubulin, gamma 1	-0.47	CCGAGGGAAATCATCACCCTA	NM_001070:	NM_001070:
7283	TUBG1	tubulin, gamma 1	-0.13	CTCCTCTTATGAGACTATTTA	NM_001070:	NM_001070:
27175	TUBG2	tubulin, gamma 2	0.68	AAGCTTGGTTGTCAGTATAAA	NM_016437:	NM_016437:
27175	TUBG2	tubulin, gamma 2	-2.48	CCGGGAGATCATCACCCTGCA	NM_016437:	NM_016437:
10844	TUBGCP2	tubulin, gamma complex associated protein 2	-4.91	CAGCGTCTGGATCAGCAACAA	NM_006659:	NM_006659:
10844	TUBGCP2	tubulin, gamma complex associated protein 2	1.20	CCAGGAGGATTACAACGACAA	NM_006659:	NM_006659:
10426	TUBGCP3	tubulin, gamma complex associated protein 3	-0.25	TACCGCGAATGCATCAGCTAA	NM_006322:	NM_006322:
10426	TUBGCP3	tubulin, gamma complex associated protein 3	-1.55	TACGACTTTGTATCAGCATAA	NM_006322:	NM_006322:
85378	TUBGCP6	tubulin, gamma complex associated protein 6	-5.67	GCGCATCAACTTCAACAACTA	NM_020461:	NM_020461:NM_001008658:
85378	TUBGCP6	tubulin, gamma complex associated protein 6	-4.50	CCACATCTCCTTGGTGAACAA	NM_020461:	NM_020461:NM_001008658:
7287	TULP1	tubby like protein 1	-2.13	CCGGCGCATGACCGTCATCAT	NM_003322:	NM_003322:
7287	TULP1	tubby like protein 1	1.11	CCGCTTCACGGTCTTTGACAA	NM_003322:	NM_003322:
7289	TULP3	tubby like protein 3	0.88	AGGACTGACAGTAATGTGATA	NM_003324:	NM_003324:
7289	TULP3	tubby like protein 3	0.95	ATGGGTGAGAGATGATTTAAA	NM_003324:	NM_003324:
56995	TULP4	tubby like protein 4	-0.17	ATGCATTACTGTAAACATGAT	NM_020245:	NM_020245:NM_001007466:
56995	TULP4	tubby like protein 4	-0.38	CACACTGTGTTGGACCAACAA	NM_020245:	NM_020245:NM_001007466:
11334	TUSC2	tumor suppressor candidate 2	-4.85	CAAGCTGAGGCGAGTGCATAA	NM_007275:	NM_007275:
11334	TUSC2	tumor suppressor candidate 2	-0.52	CCGCGGCTCTATGTTCTATGA	NM_007275:	NM_007275:
7991	TUSC3	tumor suppressor candidate 3	0.19	ATGGTAGCATTTAGTAATCTA	NM_006765:	NM_178234:NM_006765:
7991	TUSC3	tumor suppressor candidate 3	0.36	CAGGATTGAAATAAATGACAA	NM_006765:	NM_178234:NM_006765:
10641	TUSC4	tumor suppressor candidate 4	0.09	CCGGGATGTGTTCCAGCTATA	NM_006545:	NM_006545:
10641	TUSC4	tumor suppressor candidate 4	1.13	CGCCCTCGAGCCCATTGTTAA	NM_006545:	NM_006545:
7291	TWIST1	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome	-2.08	TGGGATCAAACTGGCCTGCAA	NM_000474:	NM_000474:

7291	TWIST1	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome	1.51	AAGAACACCTTTAGAAATAAA	NM_000474:	NM_000474:
117581	TWIST2	twist homolog 2 (Drosophila)	0.95	CTGCATGATTGTTTCAAGTCA	NM_057179:	NM_057179:
117581	TWIST2	twist homolog 2 (Drosophila)	-0.04	CAGAAATGCATTCTTGTACAA	NM_057179:	NM_057179:
7294	TXK	TXK tyrosine kinase	0.24	CAGCTGGGTTTAGCTACGAAA	NM_003328:	NM_003328:
7294	TXK	TXK tyrosine kinase	-1.12	CCCGGTGACATTCTATTTCCA	NM_003328:	NM_003328:
200081	TXLNA	taxilin alpha	0.17	CCGGACCTATGTGGCAAGGAA	NM_175852:	NM_175852:
200081	TXLNA	taxilin alpha	-0.05	CTGGTGTATCCTTCACATCTA	NM_175852:	NM_175852:
7295	TXN	thioredoxin	0.76	CACCATTAATGAATTAGTCTA	NM_003329:	NM_003329:
7295	TXN	thioredoxin	0.54	AACCAGCCATTGGCTATTTAA	NM_003329:	NM_003329:
25828	TXN2	thioredoxin 2	-0.21	CCCAAACTAGTGAGAGTAATA	NM_012473:	NM_012473:
25828	TXN2	thioredoxin 2	0.03	CGGGAAGGTGGTGATGGCCAA	NM_012473:	NM_012473:
81542	TXNDC	thioredoxin domain containing	0.77	TAGATTTACAGTATCGTAATA	NM_030755:	NM_030755:
81542	TXNDC	thioredoxin domain containing	1.06	ATGGTAATACAGGATATGCTA	NM_030755:	NM_030755:
54495	TXNDC10	thioredoxin domain containing 10	1.16	TAGGATATTAAGACTATCAAT	NM_019022:	NM_019022:
54495	TXNDC10	thioredoxin domain containing 10	-0.07	ATGCTGTTAATTTAACAAGTA	NM_019022:	NM_019022:
51061	TXNDC11	thioredoxin domain containing 11	-1.07	GCGGCAATTGTTGACGTGAAA	NM_015914:	NM_015914:
51061	TXNDC11	thioredoxin domain containing 11	-0.54	TGCGGCAATTGTTGACGTGAA	NM_015914:	NM_015914:
51060	TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)	1.50	AAGTGTAAATCAGTTATTCTA	NM_015913:	NM_015913:
51060	TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)	-0.86	AACAATTAAGCCGACCAGGAA	NM_015913:	NM_015913:
56255	TXNDC13	thioredoxin domain containing 13	-0.09	CTCCAGTACCTGAAAGTGAAA	NM_021156:	NM_021156:
56255	TXNDC13	thioredoxin domain containing 13	1.44	CTGGGTCTTGAACTACTTTAA	NM_021156:	NM_021156:
51075	TXNDC14	thioredoxin domain containing 14	-0.01	TTCGTTTATGGTCTTCATTAA	NM_015959:	NM_015959:
51075	TXNDC14	thioredoxin domain containing 14	0.52	CTAGATTTAACCCTAAGGTAA	NM_015959:	NM_015959:
84203	TXNDC2	thioredoxin domain containing 2 (spermatozoa)	0.61	CAGAATTAAAGTAAACATGTA	NM_032243:	NM_032243:
84203	TXNDC2	thioredoxin domain containing 2 (spermatozoa)	0.37	AGCAGTCATTGCAGAATTAAA	NM_032243:	NM_032243:
51314	TXNDC3	thioredoxin domain containing 3 (spermatozoa)	-1.21	CACGTCAATATACAACCATTT	NM_016616:	NM_016616:
51314	TXNDC3	thioredoxin domain containing 3 (spermatozoa)	0.61	CAGCTAATGTTGCTAAGTTCA	NM_016616:	NM_016616:
23071	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	0.99	CACCATCAGGCGTTTATTTAA	NM_015051:	NM_015051:
23071	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	1.55	TTGAGAGTAGTTATTATGAAA	NM_015051:	NM_015051:
81567	TXNDC5	thioredoxin domain containing 5	0.67	ATCGAGCTACTTCCCATAATA	NM_022085:	NM_030810:NM_022085:
81567	TXNDC5	thioredoxin domain containing 5	-0.15	CACATACAGGCTTAAGCTCTA	NM_022085:	NM_030810:NM_022085:
347736	TXNDC6	thioredoxin domain containing 6	-0.33	CTCCATCTCTTATATATAACA	NM_178130:	NM_178130:
347736	TXNDC6	thioredoxin domain containing 6	1.85	TACTTCTGATTGCCTAATAAA	NM_178130:	NM_178130:
255220	TXNDC8	thioredoxin domain containing 8	0.80	AACCCTATTCTCAAGAATCAA	NM_001003936:	NM_001003936:
255220	TXNDC8	thioredoxin domain containing 8	1.12	TCGCAGCACTTGAATCAATAA	NM_001003936:	NM_001003936:
10190	TXNDC9	thioredoxin domain containing 9	0.17	TACAGTTGTATCACATCGAAA	NM_005783:	NM_005783:
10190	TXNDC9	thioredoxin domain containing 9	0.38	AGCCACCATTTCAGAACCAAA	NM_005783:	NM_005783:
10628	TXNIP	thioredoxin interacting protein	0.16	AAGAGCCAATTTAACAAACTA	NM_006472:	NM_006472:
10628	TXNIP	thioredoxin interacting protein	-0.81	AAGAATACCTTAATTCCTTAA	NM_006472:	NM_006472:
9352	TXNL1	thioredoxin-like 1	1.03	ACAGAGGATGATATTAAAGAA	NM_004786:	NM_004786:
9352	TXNL1	thioredoxin-like 1	1.16	CTGACAGAGGATGATATTAAA	NM_004786:	NM_004786:
10539	TXNL2	thioredoxin-like 2	0.05	TACCCTCAGCTGTATGTGAAA	NM_006541:	NM_006541:
10539	TXNL2	thioredoxin-like 2	0.90	TTCGATATATTGGAGGATGAA	NM_006541:	NM_006541:
10907	TXNL4A	thioredoxin-like 4A	-0.19	AAGGTTTACTCTGGTTATAAA	NM_006701:	XM_499552:NM_006701:
10907	TXNL4A	thioredoxin-like 4A	0.16	TGGCCTAATCTTAACTAATTA	NM_006701:	XM_499552:NM_006701:
54957	TXNL4B	thioredoxin-like 4B	0.19	TCGATATGCTAAGAAGAACAA	NM_017853:	NM_017853:
54957	TXNL4B	thioredoxin-like 4B	-1.02	CTCGTGGTGGTTATTGAAACA	NM_017853:	NM_017853:
84817	TXNL5	thioredoxin-like 5	1.66	AAACAATAGAGTGCTATTAAA	NM_032731:	NM_032731:
84817	TXNL5	thioredoxin-like 5	0.48	CTGGCATGTGTCTAAACAATA	NM_032731:	NM_032731:
115861	TXNL6	thioredoxin-like 6	0.15	CTCAAGGACATGCCAAAGAAA	NM_138454:	NM_138454:
115861	TXNL6	thioredoxin-like 6	-0.70	AGCCCAGAGGTTCGAGATCAA	NM_138454:	NM_138454:
7296	TXNRD1	thioredoxin reductase 1	1.41	TGCCTGGCATTTGGTAGTATA	NM_003330:	NM_003330:NM_182743:NM_182742:NM_182729:
7296	TXNRD1	thioredoxin reductase 1	-1.75	CCGACTCAGAGTAGTAGCTCA	NM_003330:	NM_003330:NM_182743:NM_182742:NM_182729:
10587	TXNRD2	thioredoxin reductase 2	0.24	AACGCAGGCGAAGTTACTCAA	NM_006440:	NM_145747:NM_006440:NM_145748:
10587	TXNRD2	thioredoxin reductase 2	-1.83	CAGGAGCATGTTGAGGTCTAT	NM_006440:	NM_145747:NM_006440:NM_145748:
7297	TYK2	tyrosine kinase 2	0.08	CACCATCTGGTAATAAACTCA	NM_003331:	NM_003331:
7297	TYK2	tyrosine kinase 2	-0.33	CGGGTCTGTGCTGAATGTGTA	NM_003331:	NM_003331:
7298	TYMS	thymidylate synthetase	-0.88	AAGGATGTTGCCACTGGCAAA	NM_001071:	NM_001071:
7298	TYMS	thymidylate synthetase	-1.59	CCGTGACCTATCAGTTATTAA	NM_001071:	NM_001071:
7301	TYRO3	TYRO3 protein tyrosine kinase	0.48	AACGGTGACCTTTAGTGCCAA	NM_006293:	NM_006293:
7301	TYRO3	TYRO3 protein tyrosine kinase	-3.22	CGGACTGACCAAATCACCCAA	NM_006293:	NM_006293:
7305	TYROBP	TYRO protein tyrosine kinase binding protein	-0.38	CCGAATCATGACAGTCAGCAA	NM_003332:	NM_003332:NM_198125:
7305	TYROBP	TYRO protein tyrosine kinase binding protein	-1.34	CTGGATCCAGCCATTCCTGAA	NM_003332:	NM_003332:NM_198125:
7306	TYRP1	tyrosinase-related protein 1	1.01	TAGATTGAGTTATTAACTGTA	NM_000550:	NM_000550:
7306	TYRP1	tyrosinase-related protein 1	-0.18	CCTATTGGACATAATAGACAA	NM_000550:	NM_000550:
219743	TYSND1	trypsin domain containing 1	0.54	CAGCAGAAACCTTGCTCTGAA	NM_173555:	NM_173555:
219743	TYSND1	trypsin domain containing 1	-5.75	CAGCAGTACAGCCAGACCCAA	NM_173555:	NM_173555:
7311	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	0.01	AATACAACTGCGACAAGATGA	NM_003333:	NM_001033930:NM_003333:
7311	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	0.27	AAACTGCCGCAAGAAGAAGTG	NM_003333:	NM_001033930:NM_003333:
10422	UBADC1	ubiquitin associated domain containing 1	0.96	AATGTCAAGCATGCTAATTTA	NM_016172:	NM_016172:
10422	UBADC1	ubiquitin associated domain containing 1	0.03	CCCAGAGTTAATGTCAAGCAT	NM_016172:	NM_016172:
9898	UBAP2L	ubiquitin associated protein 2-like	0.19	CCCAATTCAGTCGACAACCTA	NM_014847:	NM_014847:
9898	UBAP2L	ubiquitin associated protein 2-like	-4.50	CAGCAGATATCTCAGGGCTAA	NM_014847:	NM_014847:
53347	UBASH3A	ubiquitin associated and SH3 domain containing, A	-4.00	AACAGGTGTAATAGTCAATAA	NM_001001895:	NM_018961:NM_001001895:
53347	UBASH3A	ubiquitin associated and SH3 domain containing, A	-6.90	ACGGCCAAACTCATCCTGGAA	NM_001001895:	NM_018961:NM_001001895:
	UBB	ubiquitin B	-13.12	UBB		
	UBB	ubiquitin B	-11.94	UBB		
7316	UBC	ubiquitin C	-0.59	GAGGTTGATCTTTGCCGGAAA	NM_021009:	NM_021009:
7316	UBC	ubiquitin C	-2.74	GAGGTTGATCTTTGCTGGGAA	NM_021009:	NM_021009:
10537	UBD	ubiquitin D	0.04	AACCCATATGACAGCGTGAAA	NM_006398:	NM_006398:
10537	UBD	ubiquitin D	0.87	ATGGGATTTAATGACCTTTGA	NM_006398:	NM_006398:
7318	UBE1L	ubiquitin-activating enzyme E1-like	-0.31	ATGCTTGTTAAAGGAAGGCAA	NM_003335:	NM_003335:
7318	UBE1L	ubiquitin-activating enzyme E1-like	-0.04	CAGCAGAAGGAACTGAACAAA	NM_003335:	NM_003335:
7319	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	1.77	AACACCCTCTATGAAATCAAA	NM_003336:	NM_181777:NM_181762:NM_003336:
7319	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	0.01	AAGCGTGTTTCTGCAATAGTA	NM_003336:	NM_181777:NM_181762:NM_003336:
7320	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	-0.83	ACCTCTCATTAGAAAGGCTAA	NM_003337:	NM_003337:
7320	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.05	CCCAGTATTAGCAATGAATTA	NM_003337:	NM_003337:
11065	UBE2C	ubiquitin-conjugating enzyme E2C	1.06	AGCCCTTGTATATTAAATAAA	NM_007019:	NM_181803:NM_181799:NM_181802:NM_007019:NM_181800:NM_181801:
11065	UBE2C	ubiquitin-conjugating enzyme E2C	0.21	GAGCCCTTGTATATTAAATAA	NM_007019:	NM_181803:NM_181799:NM_181802:NM_007019:NM_181800:NM_181801:
7327	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	1.43	AAGATTTACGTTTGTATATTA	NM_003343:	NM_182688:NM_003343:
7327	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	0.53	AAGGGACTCTACCATATCTTA	NM_003343:	NM_182688:NM_003343:
7334	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	1.36	CAGATTTGTGTTAAGATAGTA	NM_003348:	NM_003348:
7334	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	-1.93	TAGCCAGTCATAAATACATAA	NM_003348:	NM_003348:
27338	UBE2S	ubiquitin-conjugating enzyme E2S	-0.14	CCCGATGGCATCAAGGTCTTT	NM_014501:	NM_014501:
29089	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-2.18	TCGGCTGACATAATCCTCGAA	NM_139209:	NM_014176:

29089	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-8.19	ATCCTCAGAATTTAAATATAA	NM_014176:	NM_014176:
29089	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-3.65	TCGCAACTGTGTTGACCTCTA	NM_014176:	NM_014176:
7335	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	-3.60	AAGGAAGACTTGAACCTAGAA	NM_021988:	NM_199144:NM_022442:NM_021988:
7335	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	-0.38	CACGGGAATTATTATTGTCAA	NM_021988:	NM_199144:NM_022442:NM_021988:
7336	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	0.94	CAAGGAGTCCTAGGTATTATA	NM_003350:	NM_003350:
7336	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	-3.38	CAGAAGCTCCTCCGTCAGTTA	NM_003350:	NM_003350:
7337	UBE3A	ubiquitin protein ligase E3A (human papilloma virus E6-associated prc	-0.30	CAGACTGTGGTCTAAATACAA	NM_000462:	NM_130839:NM_130838:NM_000462:
7337	UBE3A	ubiquitin protein ligase E3A (human papilloma virus E6-associated prc	0.51	CCAGATTGCTCTCTAATGAAA	NM_000462:	NM_130839:NM_130838:NM_000462:
89910	UBE3B	ubiquitin protein ligase E3B	0.10	AAGGTTGATGCCGGATTCGAA	NM_130466:	NM_183414:NM_130466:NM_183415:
89910	UBE3B	ubiquitin protein ligase E3B	-9.14	CAGCATGGGTTGAGTGTACAA	NM_130466:	NM_183414:NM_130466:NM_183415:
9690	UBE3C	ubiquitin protein ligase E3C	-0.72	TAGGTCAAAGACAATCATCAA	XM_376730:	NM_014671:
9690	UBE3C	ubiquitin protein ligase E3C	0.87	CCCATAGAAGTTGTAGGTCAA	XM_376730:	NM_014671:
9354	UBE4A	ubiquitination factor E4A (UFD2 homolog, yeast)	0.07	TACCAAGAGGCTAATACTAAA	NM_004788:	NM_004788:
9354	UBE4A	ubiquitination factor E4A (UFD2 homolog, yeast)	0.70	CTCAGTGTGTGAGATATATAA	NM_004788:	NM_004788:
5412	UBL3	ubiquitin-like 3	1.33	CGCGTAGTATATAGAACAATA	NM_007106:	NM_007106:
5412	UBL3	ubiquitin-like 3	-1.13	AAGGACGATTTCTACATGGAA	NM_007106:	NM_007106:
8266	UBL4A	ubiquitin-like 4A	1.42	TAGGCTGTTTCTGATATCCAA	NM_014235:	NM_014235:
8266	UBL4A	ubiquitin-like 4A	-0.92	CAGGGACACACTCGTGAGCAT	NM_014235:	NM_014235:
164153	UBL4B	ubiquitin-like 4B	-3.47	CTGCTTGTGCTTCCAGCTTAA	NM_203412:	NM_203412:
164153	UBL4B	ubiquitin-like 4B	-4.75	GAGGCAGCAGCTGATCAGTAA	NM_203412:	NM_203412:
84993	UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)	-0.26	TACCTGATGGTCAACTCTCAA	NM_032907:	NM_201265:NM_032907:
84993	UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)	1.54	CCCAATATACCTGATGGTCAA	NM_032907:	NM_201265:NM_032907:
134510	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	0.75	CAGCTGTGTCTTAGTATGAGA	NM_145049:	NM_145049:
134510	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	0.04	GCGCACCTAAATCGTGATAAA	NM_145049:	NM_145049:
29855	UBN1	ubinuclein 1	0.45	CTCCAGGCTTTCTGCCCTAAA	NM_175617:	NM_016936:
22888	UBOX5	U-box domain containing 5	0.26	TCCGGTGTGCTTGTGTTCTTA	NM_014948:	NM_014948:NM_199415:
22888	UBOX5	U-box domain containing 5	-0.02	CCGGCACATTCCTTTCCTTTA	NM_014948:	NM_014948:NM_199415:
56061	UBPH	ubiquitin-binding protein homolog	-1.87	CCGAACATGTTGTGTGGAATA	NM_019116:	NM_019116:
56061	UBPH	ubiquitin-binding protein homolog	-0.17	CTGTCCGGCATGTACAATAAA	NM_019116:	NM_019116:
29979	UBQLN1	ubiquilin 1	0.22	TGGGATAGTGTCATAACTAAT	NM_013438:	NM_013438:
29979	UBQLN1	ubiquilin 1	0.06	GTGGGATAGTGTCATAACTAA	NM_013438:	NM_013438:
29978	UBQLN2	ubiquilin 2	0.40	TCCCATAAAGAGACCCTAATA	NM_013444:	NM_013444:
29978	UBQLN2	ubiquilin 2	0.73	CTGAAGGATCAGTGTAGTAAT	NM_013444:	NM_013444:
50613	UBQLN3	ubiquilin 3	-3.42	TTGAGATGCAATTACACCCAA	NM_017481:	NM_017481:
50613	UBQLN3	ubiquilin 3	1.14	CAAGATTTAGTTAGTACAAAT	NM_017481:	NM_017481:
56893	UBQLN4	ubiquilin 4	-0.09	CCAGAGGAAATTCGTGTGAAA	NM_020131:	NM_020131:
56893	UBQLN4	ubiquilin 4	0.37	CACACTGGCCTTTGTAAATAA	NM_020131:	XM_209569:NM_020131:
197131	UBR1	ubiquitin protein ligase E3 component n-recognin 1	-0.28	CAGGAATATTGGGATACTGTA	NM_174916:	NM_174916:
197131	UBR1	ubiquitin protein ligase E3 component n-recognin 1	-1.92	AACCCACAATATGGACAGAAA	NM_174916:	NM_174916:
23304	UBR2	ubiquitin protein ligase E3 component n-recognin 2	-4.13	CAGGTAAATGCTACAGATGAA	NM_015255:	NM_015255:
23304	UBR2	ubiquitin protein ligase E3 component n-recognin 2	-4.74	CAGAACAATACTCTAATAGAA	NM_015255:	NM_015255:
80019	UBTD1	ubiquitin domain containing 1	0.25	ATCTGCATATTTATCAATAAA	NM_024954:	NM_024954:
80019	UBTD1	ubiquitin domain containing 1	-0.13	TATCTGCATATTTATCAATAA	NM_024954:	NM_024954:
7345	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	-0.37	CAGCCACACCCAGGCACTTAA	NM_004181:	NM_004181:
7345	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	0.03	GTGGCCAATAATCAAGACAAA	NM_004181:	NM_004181:
7347	UCHL3 (ubiqu	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	1.22	AACTGTATTATTTGCAACTAA	NM_006002:	NM_006002:
7347	UCHL3 (ubiqu	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	1.17	TAGAAGTTTGCAAGAAGTTTA	NM_006002:	NM_006002:
51377	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	-6.89	AACGATATTCCTTATCTGTAA	NM_015984:	NM_015984:
51377	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	-1.70	TCGATTTAATTTAATGGCCAT	NM_015984:	NM_015984:
83549	UCK1	uridine-cytidine kinase 1	-2.00	AACGGTGGAGGTGCCGACCTA	NM_031432:	NM_031432:
83549	UCK1	uridine-cytidine kinase 1	0.28	TGCGGTTTAAAGATCCCTCTA	NM_031432:	NM_031432:
7371	UCK2	uridine-cytidine kinase 2	-1.19	CCGGATGCCTTTGACAATGAA	NM_012474:	NM_012474:
7371	UCK2	uridine-cytidine kinase 2	1.28	TCAGTACATTACGTTCGTCAA	NM_012474:	NM_012474:
54963	UCKL1	uridine-cytidine kinase 1-like 1	-2.34	ACCCAGGACTGTTGAATACAA	NM_017859:	NM_017859:
54963	UCKL1	uridine-cytidine kinase 1-like 1	0.14	TACAATGAACACGGCACGCAA	NM_017859:	NM_017859:
7349	UCN	urocortin	2.42	GCAGAACCGCATCATATTCGA	NM_003353:	NM_003353:
7349	UCN	urocortin	0.30	CCGCATCATATTCGACTCGGT	NM_003353:	NM_003353:
90226	UCN2	urocortin 2	-0.47	CTGGACATTGGACATTGCTAA	NM_033199:	NM_033199:
90226	UCN2	urocortin 2	-3.12	CAGCTTGGATGCTGCCACGTA	NM_033199:	NM_033199:
7350	UCP1	uncoupling protein 1 (mitochondrial, proton carrier)	-0.02	AACGAGAACTGTCAAAGTCAA	NM_021833:	NM_021833:
7350	UCP1	uncoupling protein 1 (mitochondrial, proton carrier)	0.16	TGCAATGAAAGTGTTCACTAA	NM_021833:	NM_021833:
7351	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	0.02	AGCCCACTTGTCATCCATAAA	NM_003355:	NM_003355:
7351	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	-0.91	TAGCCCACTTGTCATCCATAA	NM_003355:	NM_003355:
7352	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	0.38	CGGGAAATTATTATGACTCAA	NM_003356:	NM_003356:
7352	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	-0.11	TCGGGAAATTATTATGACTCA	NM_003356:	NM_003356:
56886	UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	-2.58	CCGGGCGAAAGTATCATATCA	NM_020120:	NM_020120:NM_001025777:
56886	UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	-1.66	TGGCGTGGAATTGGCCATTAA	NM_020120:	NM_020120:NM_001025777:
7360	UGP2	UDP-glucose pyrophosphorylase 2	1.41	CGAGTTCAAGTCTGTATCAAA	NM_006759:	NM_006759:NM_001001521:
54658	UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1	0.87	TTCCCACTTACTGCACAACAA	NM_000463:	NM_000463:
54600	UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A9	0.68	AGGAGTTTGTTTAAAGACAAA	NM_021027:	NM_021027:
54600	UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A9	0.62	TACGAAGTATATATTCTCTAT	NM_021027:	NM_021027:
7363	UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	1.64	AGGAAGCTAATAAATAATTAA	NM_021139:	NM_021139:
7363	UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	-0.61	ATGAGGTTATATTGAAATGTA	NM_021139:	NM_021139:
127933	UHMK1	U2AF homology motif (UHM) kinase 1	0.70	AAGCAGTACTGTAGTACTGAA	NM_144624:	NM_175866:
127933	UHMK1	U2AF homology motif (UHM) kinase 1	-1.32	CCACATATGAATGCAGGACTA	NM_144624:	NM_175866:
29128	UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	1.34	CACCTCCTTATTCTTAGATTA	NM_013282:	NM_013282:
29128	UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	1.72	ACCAAGAAAGATATAACGTTA	NM_013282:	NM_013282:
115426	UHRF2	ubiquitin-like, containing PHD and RING finger domains, 2	1.94	CACTATATTCCCTAAAGTATA	NM_152306:	NM_152306:NM_152896:
115426	UHRF2	ubiquitin-like, containing PHD and RING finger domains, 2	-0.04	CAGATATGATGGCATTTATAA	NM_152306:	NM_152306:NM_152896:
80329	ULBP1	UL16 binding protein 1	1.10	TCGGGATATACCCACAGGAAA	NM_025218:	NM_025218:
80329	ULBP1	UL16 binding protein 1	0.06	TATGATGATAATTGTATAATA	NM_025218:	NM_025218:
80328	ULBP2	UL16 binding protein 2	-0.07	CAGCAGTTATACCTAACATAT	NM_025217:	NM_025217:
80328	ULBP2	UL16 binding protein 2	0.04	TTGTTCTGTACTGATATTTAA	NM_025217:	NM_025217:
79465	ULBP3	UL16 binding protein 3	0.05	CCAGGCTTAGCTCAACCCAAA	NM_024518:	NM_024518:
79465	ULBP3	UL16 binding protein 3	-0.41	CTGGTATAACTTCACCATCAT	NM_024518:	NM_024518:
8408	ULK1	unc-51-like kinase 1 (C. elegans)	1.53	CGCGCGGTACCTCCAGAGCAA	NM_003565:	NM_003565:
8408	ULK1	unc-51-like kinase 1 (C. elegans)	1.37	TGCCCTTTGCGTTATATTGTA	NM_003565:	NM_003565:
9706	ULK2	unc-51-like kinase 2 (C. elegans)	-0.37	ACCGGGAAGTTATCAGATCAA	NM_014683:	NM_014683:
9706	ULK2	unc-51-like kinase 2 (C. elegans)	1.08	ATCGGTACAGTTATTCTTAAA	NM_014683:	NM_014683:
25989	ULK3	unc-51-like kinase 3 (C. elegans)	-25.02	CACGTACGCCACGGTGTACAA	NM_015518:	NM_015518:
25989	ULK3	unc-51-like kinase 3 (C. elegans)	-3.83	AAGGACACTCGTGAAGTGGTA	NM_015518:	NM_015518:
7372	UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferas	1.66	CACCGCATTGATACTATAATA	NM_000373:	NM_000373:
7372	UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferas	-1.52	AAGCTTCTCAGGCTTATGCAA	NM_000373:	NM_000373:
9094	UNC119	unc-119 homolog (C. elegans)	-1.28	CCGGCTGGTGATGCACAATAA	NM_005148:	NM_005148:NM_054035:
9094	UNC119	unc-119 homolog (C. elegans)	0.59	CAGGCCATTTAGAGTTGTAAA	NM_005148:	NM_005148:NM_054035:
23025	UNC13A	unc-13 homolog A (C. elegans)	-0.72	CCGCCCTATTATACTACGTCA	XM_038604:	XM_038604:
23025	UNC13A	unc-13 homolog A (C. elegans)	1.26	TGCGACCAAATCCAAGAACAA	XM_038604:	XM_038604:
10497	UNC13B	unc-13 homolog B (C. elegans)	1.33	CTGCTCTGCGTGCGCGTTAAA	NM_006377:	NM_006377:
10497	UNC13B	unc-13 homolog B (C. elegans)	1.23	ACCAGATAAATTTAACACATA	NM_006377:	NM_006377:

440279	UNC13C	unc-13 homolog C (C. elegans)	-0.92	CAAGCTGATCTAATACGTTAA	XM_496070:	XM_496070:
440279	UNC13C	unc-13 homolog C (C. elegans)	0.36	ATGGGAATGTTTAGTTCACTA	XM_496070:	XM_496070:
90249	UNC5A	unc-5 homolog A (C. elegans)	-3.29	CACCATGGAGGTCCGCATTAA	NM_133369:	NM_133369:
90249	UNC5A	unc-5 homolog A (C. elegans)	0.28	CCGCATTAATGTCTCAAGGCA	NM_133369:	NM_133369:
219699	UNC5B	unc-5 homolog B (C. elegans)	1.14	CAGCCTTAAGGTCAAGGTCTA	NM_170744:	NM_170744:
219699	UNC5B	unc-5 homolog B (C. elegans)	0.96	CACCGTCATCGTCTACGTGAA	NM_170744:	NM_170744:
8633	UNC5C	unc-5 homolog C (C. elegans)	0.03	CGGCCTCGTCTTGCAATCCAA	NM_003728:	NM_003728:
8633	UNC5C	unc-5 homolog C (C. elegans)	2.40	CTATTTCAGATTAGTAATTTA	NM_003728:	NM_003728:
137970	UNC5D	unc-5 homolog D (C. elegans)	-0.05	TACATAGGATTTCTATAGAAA	NM_080872:	NM_080872:
137970	UNC5D	unc-5 homolog D (C. elegans)	-0.04	CAAGATGTCCTGGTAGACTAA	NM_080872:	NM_080872:
7374	UNG	uracil-DNA glycosylase	0.02	ATGGGATTTGTTGCAGAAGAA	NM_003362:	NM_080911:NM_003362:
7374	UNG	uracil-DNA glycosylase	0.71	TACGCGAGGTTTGTTAATAAA	NM_003362:	NM_080911:NM_003362:
389400	UNQ9356	IVFI9356	0.68	GAGGAATTCATCATACTGTAA	NM_207410:	NM_207410:
389400	UNQ9356	IVFI9356	-2.74	CACAGTTGGCCTCTTACCTTA	NM_207410:	NM_207410:
203074	UNQ9391	tryptophan/serine protease	-0.41	AGGGAAGAACTCGGTATTCCA	NM_198464:	NM_198464:
203074	UNQ9391	tryptophan/serine protease	0.41	CACCTCGTTGGTGAACTACAA	NM_198464:	NM_198464:
387990	UNQ9438	TIMM9	-1.33	TGGGAGAACTTTGGTTATCTA	NM_207377:	NM_207377:
387990	UNQ9438	TIMM9	0.83	TCCAGTGAGAATACTATGGTA	NM_207377:	NM_207377:
5976	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	-0.62	ACGGAGCGCTGCACACCGAAA	NM_002911:	NM_002911:
5976	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	-0.49	CATCTTATTCTGGGTAATAAA	NM_002911:	NM_002911:
7384	UQCRC1	ubiquinol-cytochrome c reductase core protein I	0.80	CCACAGGTGACCACCAATAAA	NM_003365:	NM_003365:
7384	UQCRC1	ubiquinol-cytochrome c reductase core protein I	-6.99	CCGGACAATGTGGCCTTGCAA	NM_003365:	NM_003365:
7385	UQCRC2 (ubi	ubiquinol-cytochrome c reductase core protein II	-0.77	AAGGCTGCCTATAATCAAGTA	NM_003366:	NM_003366:
7385	UQCRC2 (ubi	ubiquinol-cytochrome c reductase core protein II	0.70	ATCAAGGCTGCCTATAATCAA	NM_003366:	NM_003366:
7388	UQCRH	ubiquinol-cytochrome c reductase hinge protein	1.32	CGTGTTGAATCTAGAACCGTA	NM_006004:	NM_006004:
7388	UQCRH	ubiquinol-cytochrome c reductase hinge protein	0.71	TTCTATGTAATTCGCAATGAT	NM_006004:	NM_006004:
7389	UROD	uroporphyrinogen decarboxylase	0.22	ACCGTATACCTTTACCCTCAA	NM_000374:	NM_000374:
7389	UROD	uroporphyrinogen decarboxylase	-0.67	CTGGATGACTTTGGACCACAT	NM_000374:	NM_000374:
7390	UROS (uropo	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	-1.08	CAGCAGGAAGGAAGTCAAATA	NM_000375:	NM_000375:
7390	UROS (uropo	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	0.40	ATCGATCAAATTAAGTTTGCA	NM_000375:	NM_000375:
7391	USF1	upstream transcription factor 1	-1.23	CGGATTAGAGGTCGTCATCAA	NM_007122:	NM_207005:NM_007122:
7391	USF1	upstream transcription factor 1	-2.70	CAGAGTAAAGGTGGGATTCTA	NM_007122:	NM_207005:NM_007122:
7392	USF2	upstream transcription factor 2, c-fos interacting	-0.10	AAGAGCCCAGCACAACGAAGT	NM_003367:	NM_207291:NM_003367:
7392	USF2	upstream transcription factor 2, c-fos interacting	-0.68	AAGACTGTAACGCAGACAACA	NM_003367:	NM_003367:NM_207291:
9100	USP10	ubiquitin specific peptidase 10	0.00	CAGCTTTGTTCGGCTAATGAA	NM_005153:	NM_005153:
9100	USP10	ubiquitin specific peptidase 10	-0.93	AAGGGAACTGGTGCTACATTA	NM_005153:	NM_005153:
8237	USP11	ubiquitin specific peptidase 11	-4.64	CTGCGTCGGGTACGTGATGAA	NM_004651:	NM_004651:
8237	USP11	ubiquitin specific peptidase 11	-0.97	ACCGATTCTATTGGCCTAGTA	NM_004651:	NM_004651:
219333	USP12	ubiquitin specific peptidase 12	0.19	CCGATCATGGTAGTTGATTTA	NM_182488:	NM_182488:
219333	USP12	ubiquitin specific peptidase 12	0.76	ATGGATCAACTTCATCGATAT	NM_182488:	NM_182488:
8975	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	-0.08	TCGCTTATGAACTAACGAGAA	NM_003940:	NM_003940:
8975	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	0.48	TCCGGTGAAATCTGAACTCAT	NM_003940:	NM_003940:
9097	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	1.20	CCCATCCTTTGCCTTATCTAA	NM_005151:	NM_005151:NM_001037334:
9097	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	-0.32	CAGAGTTGAAATGCCTTTCAA	NM_005151:	NM_005151:NM_001037334:
9958	USP15	ubiquitin specific peptidase 15	0.34	TATGTCGGAATTCTTAATTAA	NM_006313:	NM_006313:
9958	USP15	ubiquitin specific peptidase 15	-1.53	AAGATGATACCAGGCATATAA	NM_006313:	NM_006313:
10869	USP19	ubiquitin specific peptidase 19	-1.09	CCGGGCTGTGGAGAAGGATAA	XM_496642:	NM_006677:
10868	USP20	ubiquitin specific peptidase 20	0.43	CCGGATGATGAAACAGGGATA	NM_006676:	NM_001008563:NM_006676:
10868	USP20	ubiquitin specific peptidase 20	-3.49	CAGGCTTGTTGAAACGACCAA	NM_006676:	NM_001008563:NM_006676:
27005	USP21	ubiquitin specific peptidase 21	1.53	CAACCTAATGTGGAAACGTTA	NM_012475:	NM_012475:NM_001014443:
23358	USP24	ubiquitin specific peptidase 24	0.30	CACAATACTGTGACCGTATAA	XM_371254:	XM_371254:
23358	USP24	ubiquitin specific peptidase 24	-0.48	CCGAGTCTGATGAGAATTGTA	XM_371254:	XM_371254:
9960	USP3	ubiquitin specific peptidase 3	-0.09	CTCCAAATCATCATTCACCAA	NM_006537:	NM_006537:
9960	USP3	ubiquitin specific peptidase 3	1.66	CTGGATCGGATAAACTTTAAT	NM_006537:	NM_006537:
57478	USP31	ubiquitin specific peptidase 31	0.50	CCCGAAATATTTAGGCCTGAA	NM_020718:	NM_020718:
57478	USP31	ubiquitin specific peptidase 31	-1.62	CCGAGTTCATGAAGACCTCAA	NM_020718:	NM_020718:
84669	USP32	ubiquitin specific peptidase 32	1.60	CACTAGAAGGAGGACGATTAA	NM_032582:	NM_032582:
84669	USP32	ubiquitin specific peptidase 32	0.65	CGCACTGATGATATTCCTGAA	NM_032582:	NM_032582:
23032	USP33	ubiquitin specific peptidase 33	-0.08	CCGGTTGTTCATGTTGATCCA	NM_015017:	NM_201624:NM_015017:
23032	USP33	ubiquitin specific peptidase 33	-0.70	CTGCAAGTAGTGGACACTATA	NM_015017:	NM_201624:NM_015017:NM_201626:
9736	USP34	ubiquitin specific peptidase 34	1.06	TCAGCCTGTGTCGATACAATA	NM_014709:	NM_014709:
9736	USP34	ubiquitin specific peptidase 34	0.84	CTGGATTGAGTCAGATAACAA	NM_014709:	NM_014709:
57558	USP35 (ubiqu	ubiquitin specific peptidase 35	1.23	ACCCATGTTCATAAATAAATA	XM_290527:	XM_290527:
57558	USP35 (ubiqu	ubiquitin specific peptidase 35	1.86	CCCTTCTAACTTCTAACCGAA	XM_290527:	XM_290527:
57602	USP36	ubiquitin specific peptidase 36	-5.74	CCGCATCGAGATGCCATGCAT	NM_025090:	NM_025090:
57602	USP36	ubiquitin specific peptidase 36	-1.74	CCCGAGTGTGATTCCAGATCA	NM_025090:	NM_025090:
84640	USP38	ubiquitin specific peptidase 38	1.56	CAGCATAGTACTAATGGTTTA	NM_032557:	NM_032557:
84640	USP38	ubiquitin specific peptidase 38	-2.81	CAGGAAGTAGCTAGTAAAGCA	NM_032557:	NM_032557:
7375	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	1.15	AAGAACAAACTGAATGGTAAA	NM_003363:	NM_003363:NM_199443:
7375	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	-0.75	CAGGCAGACCTTGCAGTCAAA	NM_003363:	NM_003363:NM_199443:
84132	USP42	ubiquitin specific peptidase 42	-4.03	CACGACAGAACTGCACTTGTA	XM_374396:	NM_032172:
84132	USP42	ubiquitin specific peptidase 42	0.00	TTGGAGGATACCTAAGATCTA	XM_374396:	NM_032172:
124739	USP43	ubiquitin specific peptidase 43	1.38	CAAGAACTGATATTTACTAAA	XM_371015:	XM_371015:
124739	USP43	ubiquitin specific peptidase 43	-0.61	CACCTTTCAGAGAGTCAAATA	XM_371015:	XM_371015:
84101	USP44	ubiquitin specific peptidase 44	0.04	TTGCATGTGACAACAAATCAA	NM_032147:	NM_032147:
84101	USP44	ubiquitin specific peptidase 44	0.33	CAGATACAGTAGTATATCAAA	NM_032147:	NM_032147:
85015	USP45	ubiquitin specific peptidase 45	-1.06	CAGGAAATTATCGGAACATAA	XM_371838:	XM_371838:
85015	USP45	ubiquitin specific peptidase 45	1.27	CGGGTGAAAGATCCAACTAAA	XM_371838:	XM_371838:
64854	USP46	ubiquitin specific peptidase 46	0.15	CAGTTATTTAATCGAAGTAAT	NM_022832:	NM_022832:
64854	USP46	ubiquitin specific peptidase 46	-0.47	TAGGGAAATGTTTGTACTATA	NM_022832:	NM_022832:
84196	USP48	ubiquitin specific peptidase 48	-0.32	ACCAGATGCGTTGGTCCATAA	NM_032236:	NM_032236:
84196	USP48	ubiquitin specific peptidase 48	0.01	CCGAAGTATGCGACATAGAAA	NM_032236:	NM_032236:
8078	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	-0.05	TACGTCTGCCACATCAAGAAA	NM_003481:	NM_003481:
8078	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	-0.25	CCAGAACAGAAGGAAGTTCAA	NM_003481:	NM_003481:
373509	USP50 (ubiqu	ubiquitin specific peptidase 50	0.41	CAGCTCAATTATAGCATCGTA	NM_203494:	NM_203494:
373509	USP50 (ubiqu	ubiquitin specific peptidase 50	-3.91	CCCGGAGAAGATCATATGAGA	NM_203494:	NM_203494:
158880	USP51 (ubiqu	ubiquitin specific peptidase 51	0.60	CCCAGAGACTAGGAAACGTAA	NM_201286:	NM_201286:
158880	USP51 (ubiqu	ubiquitin specific peptidase 51	0.75	GAGGACTTACTCTACAGTGAA	NM_201286:	NM_201286:
9098	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	0.02	GCGGAAGGACATACTTATGAA	NM_004505:	NM_004505:
9098	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	0.46	TGCGGAGAGGTTCACAACAAA	NM_004505:	NM_004505:
9712	USP6NL	USP6 N-terminal like	-0.46	CCCGGAAACATCGCAATAGCA	XM_374768:	XM_374768:
9712	USP6NL	USP6 N-terminal like	0.69	AGGGACCTGTATAGTAAATTA	XM_374768:	XM_374768:
7874	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	1.09	CGAGTATGAAGTAAATTTGAA	NM_003470:	NM_003470:
7874	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	-0.84	CGGGCCGACACCAGTACATAA	NM_003470:	NM_003470:
9101	USP8	ubiquitin specific peptidase 8	-2.86	CAGGGTCAATTCAAATCTACA	NM_005154:	NM_005154:
9101	USP8	ubiquitin specific peptidase 8	-1.86	CAGGTTCAGGCAAGCCATTTA	NM_005154:	NM_005154:
8239	USP9X	ubiquitin specific peptidase 9, X-linked	-2.58	CCGCCTGCAGTGGAAAGTGTA	NM_004652:	NM_004652:NM_021906:
8239	USP9X	ubiquitin specific peptidase 9, X-linked	-2.03	CAGCTAGTATTTAGCCCAAAT	NM_004652:	NM_004652:NM_021906:
8287	USP9Y	ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	-1.68	ATGACTGGTCCTAATCTGTAA	NM_004654:	NM_004654:

8287	USP9Y	ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	-2.41	CACTAAGGTCTTATAGTCCAA	NM_004654:	NM_004654:
8287	USP9Y	ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	-1.99	CTGCGGTTCCATATTCATATA	AB095936:	NM_004654:
7402	UTRN	utrophin (homologous to dystrophin)	-0.69	CAGAGTCTGAAGATTGGATTA	NM_007124:	NM_007124:
7402	UTRN	utrophin (homologous to dystrophin)	-1.72	CTGGCTGGTATTAATCGACCA	NM_007124:	NM_007124:
257313	UTS2D	urotensin 2 domain containing	-0.13	CTGCTGATTAATATCTTGCTA	NM_198152:	NM_198152:
257313	UTS2D	urotensin 2 domain containing	-0.55	ATGGATAAGATAGGGTTGTAA	NM_198152:	NM_198152:
2837	UTS2R	urotensin 2 receptor	0.80	CACCTGCCTCACCTACGGCAA	NM_018949:	NM_018949:
2837	UTS2R	urotensin 2 receptor	-0.10	CACGCTGCTCACCAGGAACTA	NM_018949:	NM_018949:
8409	UXT	ubiquitously-expressed transcript	1.73	CAAGGACTCCATGAATATCAA	NM_004182:	NM_004182:NM_153477:
8409	UXT	ubiquitously-expressed transcript	0.66	CAGCTGGCCAAATACCTTCAA	NM_004182:	NM_004182:NM_153477:
6844	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	1.13	CCCATTAGTTCTTGTATCACA	NM_014232:	NM_014232:
6844	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	-0.11	TCCCTTCATTTGCATCTGCTA	NM_014232:	NM_014232:
7407	VARS	valyl-tRNA synthetase	-2.04	CCGGTTTGGATTATGTGCCTA	NM_006295:	NM_006295:
7407	VARS	valyl-tRNA synthetase	-0.21	CACGAGGAAGGCATCATCTAT	NM_006295:	NM_006295:
57176	VARSL	valyl-tRNA synthetase like	0.34	CGCTTTATCCTCAATGCTTTA	XM_373419:	NM_020442:
57176	VARSL	valyl-tRNA synthetase like	-0.94	CATGCAGGAATTGCTACACAA	XM_373419:	NM_020442:
7408	VASP (vasodi	vasodilator-stimulated phosphoprotein	-0.02	CCGGGCCACTGTGATGCTTTA	NM_003370:	NM_001008736:NM_003370:
7408	VASP (vasodi	vasodilator-stimulated phosphoprotein	1.46	TAGATTCACTTTAACGCTTAA	NM_003370:	NM_001008736:NM_003370:
10493	VAT1	vesicle amine transport protein 1 homolog (T californica)	-1.20	CTGGGCTTGACCAGTTCCCAA	NM_006373:	NM_006373:
10493	VAT1	vesicle amine transport protein 1 homolog (T californica)	-0.70	AAGGGAGAAGTTGGGAAGCTA	NM_006373:	NM_006373:
7409	VAV1	vav 1 oncogene	0.49	CAGCATTAAATATAACGTCGA	NM_005428:	NM_005428:
7409	VAV1	vav 1 oncogene	-1.66	CAGGTGGAGTCAGCCAGCAAA	NM_005428:	NM_005428:
7410	VAV2 (vav 2	vav 2 oncogene	0.76	CTGAAAGTCTGCCACGATAAA	NM_003371:	NM_003371:
7410	VAV2 (vav 2	vav 2 oncogene	1.18	TTGGCGATGTACATCAATGAA	NM_003371:	NM_003371:
10451	VAV3 (vav 3	vav 3 oncogene	0.16	ACCGAACTTATTAATAGGGTA	NM_006113:	NM_006113:
10451	VAV3 (vav 3	vav 3 oncogene	0.12	CACGACTTTCTCGAACACCTA	NM_006113:	NM_006113:
7411	VBP1	von Hippel-Lindau binding protein 1	0.09	AGGGTTTATAATTGGGATGTA	NM_003372:	NM_003372:
7411	VBP1	von Hippel-Lindau binding protein 1	-1.64	CTTGACTTTCTTCGAGATCAA	NM_003372:	NM_003372:
7412	VCAM1	vascular cell adhesion molecule 1	0.01	CAGGAAGTCCCTGGAAACCAA	NM_001078:	NM_080682:NM_001078:
7412	VCAM1	vascular cell adhesion molecule 1	0.21	CTGGAGTAAGAAATTAGATAA	NM_001078:	NM_080682:NM_001078:
7414	VCL (vinculin)	vinculin	-0.75	CTGATATAAATGCAATATTAA	NM_003373:	NM_003373:NM_014000:
7414	VCL (vinculin)	vinculin	-0.78	TAGGTGTTTGTTCATCTGTAA	NM_003373:	NM_003373:NM_014000:
7417	VDAC2	voltage-dependent anion channel 2	0.12	TGGTTTCTAGTTGGTTATCTA	NM_003375:	NM_003375:
7417	VDAC2	voltage-dependent anion channel 2	0.26	ACCATTGAATGAGATGGATCA	NM_003375:	NM_003375:
7417	VDAC2	voltage-dependent anion channel 2	-0.02	CAGATTTGTCAAGGTTTGAAA	XM_496551:	XM_496551:NM_003375:
7417	VDAC2	voltage-dependent anion channel 2	-6.08	CCGGTTCATCTAATACAGACA	XM_496551:	XM_496551:NM_003375:
7419	VDAC3	voltage-dependent anion channel 3	1.60	CAGTTCTGAAGTGTTATTAAA	NM_005662:	NM_005662:
7419	VDAC3	voltage-dependent anion channel 3	0.18	CAGGAGTCAAATTGACTTTAT	NM_005662:	NM_005662:
7421	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	-0.39	TACCACTGATTTGGAGATATT	NM_000376:	NM_000376:NM_001017535:
7421	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	0.70	TCAGACTCCATTTGTATTATA	NM_000376:	NM_000376:NM_001017535:
7422	VEGF	vascular endothelial growth factor	0.36	AAGAAAGATAGAGCAAGACAA	AF022375:	NM_001033756:NM_001025368:NM_001025366:NM_003376:NM_001025367:NM_001025369:NM_001025370:
7422	VEGF	vascular endothelial growth factor	-0.41	ATAGAGAATTCTACATACTAA	AF022375:	NM_001033756:NM_001025368:NM_001025366:NM_003376:NM_001025367:NM_001025369:NM_001025370:
7423	VEGFB	vascular endothelial growth factor B	-3.17	AAGACCCAAACCTCTGCATAA	NM_003377:	NM_003377:
7423	VEGFB	vascular endothelial growth factor B	-0.65	CAGTGTGAATGCAGACCTAAA	NM_003377:	NM_003377:
7424	VEGFC	vascular endothelial growth factor C	0.28	ACCCTTGTGGGTCCATGCTAA	NM_005429:	NM_005429:
7424	VEGFC	vascular endothelial growth factor C	1.32	TTGCTGCAGCACATTATAATA	NM_005429:	NM_005429:
259232	VGCNL1	voltage gated channel like 1	0.16	CAGTGTGTCAAAGAACTTAAA	NM_052867:	NM_052867:
259232	VGCNL1	voltage gated channel like 1	-1.51	CCAGATCTTTATCATTCACAA	NM_052867:	NM_052867:
7428	VHL	von Hippel-Lindau tumor suppressor	0.34	AAGGAGGTTTGTATAAGTAAT	NM_000551:	NM_000551:NM_198156:
7428	VHL	von Hippel-Lindau tumor suppressor	-5.68	CAGGAGCGCATTGCACATCAA	NM_000551:	NM_000551:NM_198156:
7430	VIL2	villin 2 (ezrin)	0.59	CACGTGTAAACAGGATTATTA	NM_003379:	NM_003379:
7430	VIL2	villin 2 (ezrin)	0.40	CAGGACTGATTGAATTACGGA	NM_003379:	NM_003379:
7432	VIP	vasoactive intestinal peptide	0.82	ATGGAATGCTGTGTTAAATAA	NM_003381:	NM_194435:NM_003381:
7432	VIP	vasoactive intestinal peptide	-0.74	CCCGACTTTCCAGAAGAGTTA	NM_003381:	NM_194435:NM_003381:
7433	VIPR1	vasoactive intestinal peptide receptor 1	-2.72	AAGCACGGACTCTTACTGCTA	NM_004624:	NM_004624:
7433	VIPR1	vasoactive intestinal peptide receptor 1	1.04	CCGGTGGATCCTCAAACAACA	NM_004624:	NM_004624:
7434	VIPR2	vasoactive intestinal peptide receptor 2	-3.63	AACGGAGACCTCGGTCATCTA	NM_003382:	NM_003382:
7434	VIPR2	vasoactive intestinal peptide receptor 2	0.66	CCCGCTGTTCGGCGTCCACTA	NM_003382:	NM_003382:
7436	VLDLR	very low density lipoprotein receptor	-0.08	CAAGATCGTAGGATAGTACTA	NM_003383:	NM_001018056:NM_003383:
7436	VLDLR	very low density lipoprotein receptor	1.18	CAAGGTTGGTAGACATGTTAA	NM_003383:	NM_001018056:NM_003383:
7439	VMD2	vitelliform macular dystrophy 2 (Best disease, bestrophin)	-3.25	CACCTTAGTATACTGCCCAAA	NM_004183:	NM_004183:
7439	VMD2	vitelliform macular dystrophy 2 (Best disease, bestrophin)	0.38	ATGGTTAGCTTAATAGATAAA	NM_004183:	NM_004183:
57191	VN1R1	vomeronasal 1 receptor 1	-0.41	ACGGACTTGATTCTCAGCCAA	NM_020633:	NM_020633:
57191	VN1R1	vomeronasal 1 receptor 1	-0.17	ATGGATACTGTTACACAAAGA	NM_020633:	NM_020633:
317701	VN1R2	vomeronasal 1 receptor 2	-0.13	CACGGAGAGAAACCCACCAAA	NM_173856:	NM_173856:
317701	VN1R2	vomeronasal 1 receptor 2	-0.66	CGCCCTTTCCTTCATCACCTA	NM_173856:	NM_173856:
317703	VN1R4	vomeronasal 1 receptor 4	0.87	TTGGATAATCCCAATAGTTTA	NM_173857:	NM_173857:
317705	VN1R5	vomeronasal 1 receptor 5	0.34	CACAGATATCCTTTGCTTTAA	NM_173858:	NM_173858:
317705	VN1R5	vomeronasal 1 receptor 5	1.63	TAGTCCTTTGATGCTAATTTA	NM_173858:	NM_173858:
8875	VNN2	vanin 2	-0.51	CAGCAATAACTTACCTGCTAA	NM_004665:	NM_004665:NM_078488:
8875	VNN2	vanin 2	0.75	AGGAGCTTTGCTGTCATTTAA	NM_004665:	NM_004665:NM_078488:
7441	VPREB1	pre-B lymphocyte gene 1	-0.11	AGACTGCATTAGGGAATTAAA	NM_007128:	NM_007128:
7441	VPREB1	pre-B lymphocyte gene 1	0.02	TCCCAGGTTCCTGCTGAGATA	NM_007128:	NM_007128:
29802	VPREB3	pre-B lymphocyte gene 3	0.75	AAATGGGTTAATAATATTCAA	NM_013378:	NM_013378:
29802	VPREB3	pre-B lymphocyte gene 3	1.42	TGGGTTAATAATATTCAACAT	NM_013378:	NM_013378:
55823	VPS11	vacuolar protein sorting 11 (yeast)	0.59	AAGGGACTTTGTACTGATTAT	NM_021729:	NM_021729:
55823	VPS11	vacuolar protein sorting 11 (yeast)	0.65	CAGCAATATATCCGAACCATT	NM_021729:	NM_021729:
64601	VPS16	vacuolar protein sorting 16 (yeast)	0.45	GAGGCCAGTGCTCGATATATA	NM_022575:	NM_080413:NM_022575:
64601	VPS16	vacuolar protein sorting 16 (yeast)	-1.78	CAGCATGGACTGGGACCTGAA	NM_022575:	NM_080413:NM_022575:
23339	VPS39	vacuolar protein sorting 39 (yeast)	-0.38	CAGGATGATCTCACCGTGGTA	NM_015289:	NM_015289:
23339	VPS39	vacuolar protein sorting 39 (yeast)	-0.27	ACGGTTCAATCAAGTGCTCAA	NM_015289:	NM_015289:
27072	VPS41	vacuolar protein sorting 41 (yeast)	-0.73	CACCATTATGTTTACTAATCA	NM_014396:	NM_014396:NM_080631:
27072	VPS41	vacuolar protein sorting 41 (yeast)	1.60	TGGCTCATTCTTTATATAGTA	NM_014396:	NM_014396:NM_080631:
7443	VRK1	vaccinia related kinase 1	0.94	CAGGTTATACTCCTTAAGTTA	NM_003384:	NM_003384:
7443	VRK1	vaccinia related kinase 1	0.91	CCAGGTGTACTTGGTAGATTA	NM_003384:	NM_003384:
7444	VRK2 (vaccin	vaccinia related kinase 2	-0.64	CACACAATAGGTTAATCGAAA	NM_006296:	NM_006296:
7444	VRK2 (vaccin	vaccinia related kinase 2	-2.11	CTGGAGGATTTGGATTGATAT	NM_006296:	NM_006296:
51231	VRK3 (vaccin	vaccinia related kinase 3	0.01	AACCAGGGCATTCTCTATGAA	NM_016440:	NM_001025778:NM_016440:
51231	VRK3 (vaccin	vaccinia related kinase 3	-3.12	CTCACTCAAACTGGATGCCAA	NM_016440:	NM_001025778:NM_016440:
23584	VSIG2	V-set and immunoglobulin domain containing 2	0.01	ATCCAACTGGTTCTAAGTCAA	NM_014312:	NM_014312:
23584	VSIG2	V-set and immunoglobulin domain containing 2	0.36	CCCACCAGATTTCTACACCAA	NM_014312:	NM_014312:
7447	VSNL1	visinin-like 1	0.72	AGCGTTTACCCGAATTAAATA	NM_003385:	NM_003385:
7447	VSNL1	visinin-like 1	0.16	CAGAGACGGCTTAAGCGTTTA	NM_003385:	NM_003385:
10490	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeas	-0.61	CAGTATGATATACCAAGGTAA	NM_006370:	NM_006370:
10490	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeas	1.03	AAGGTAATAAATGCTGTTTAT	NM_006370:	NM_006370:

10490	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeas	-2.63	AAGCAACAGGAAGCAAATGAA	XM_371718:	NM_006370:XM_371718:
7448	VTN	vitronectin	-1.18	CAGCCCAATAAAGGTCCCTTA	NM_000638:	NM_000638:
7448	VTN	vitronectin	-4.30	CCAGTTCATGTAATCTCCCAA	NM_000638:	NM_000638:
7450	VWF	von Willebrand factor	-2.71	AAGGGACGAGATCGTTAGCTA	NM_000542:	NM_000552:
7450	VWF	von Willebrand factor	-3.15	ACGGCTTGCACCATTCAGCTA	NM_000542:	NM_000552:
7450	VWF	von Willebrand factor	-1.85	ACGGCTTGCACCATTCAGCTA	NM_000552:	NM_000552:
7450	VWF	von Willebrand factor	-5.60	CCCACCATCTCTGGTCTACAA	NM_000552:	NM_000552:
7453	WARS	tryptophanyl-tRNA synthetase	0.73	AGGGTTCCAAGTATACTCTTA	NM_004184:	NM_213646:NM_213645:NM_173701:NM_004184:
7453	WARS	tryptophanyl-tRNA synthetase	-4.54	CAGGTTCTTGATGCCTATGAA	NM_004184:	NM_213646:NM_213645:NM_173701:NM_004184:
10352	WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	-1.67	AAGGTAGATCTATCAAGCCAA	NM_015836:	NM_201263:NM_015836:
10352	WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	0.62	GCCAATGGATGCGAACTTAAA	NM_015836:	NM_201263:NM_015836:
7454	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	0.68	ACGCCGAGACCTCTAAACTTA	NM_000377:	NM_000377:
7454	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	-3.11	CCGGCAGGGAATTCAGCTGAA	NM_000377:	NM_000377:
8936	WASF1	WAS protein family, member 1	0.34	CAAGAACGTGTGGACCGTTTA	NM_003931:	NM_003931:NM_001024934:NM_001024935:NM_001024936:
8936	WASF1	WAS protein family, member 1	1.22	GCCCTATAACCGATTAATTAA	NM_003931:	NM_003931:NM_001024934:
10163	WASF2	WAS protein family, member 2	-1.19	TAGGATTAGATCATTAGCTCA	NM_006990:	NM_006990:
10163	WASF2	WAS protein family, member 2	0.18	TGGTTTGGTAATGATCTGCAA	NM_006990:	NM_006990:
10810	WASF3	WAS protein family, member 3	0.11	CACCACTAGGCTGTCACTATA	NM_006646:	NM_006646:
10810	WASF3	WAS protein family, member 3	-0.06	TCGAATGGGAATTCAACTGAA	NM_006646:	NM_006646:
8976	WASL	Wiskott-Aldrich syndrome-like	0.45	AACCTTAATGTAATTTACTTA	NM_003941:	NM_003941:
8976	WASL	Wiskott-Aldrich syndrome-like	1.13	CAGATACGACAGGGTATCCAA	NM_003941:	NM_003941:
114049	WBSCR22	Williams Beuren syndrome chromosome region 22	-3.51	CAGGGAGTCTGTGTTCACCAA	NM_017528:	NM_017528:
114049	WBSCR22	Williams Beuren syndrome chromosome region 22	-5.30	CCCTAACAGTGCCAAAGCAAA	NM_017528:	NM_017528:
11169	WDHD1	WD repeat and HMG-box DNA binding protein 1	-1.18	CAGGTAGTATTAATGGTCTAA	NM_007086:	NM_007086:NM_001008396:
11169	WDHD1	WD repeat and HMG-box DNA binding protein 1	-2.91	CTGCACTTAGTCGAACTACAA	NM_007086:	NM_007086:NM_001008396:
84219	WDR24	WD repeat domain 24	1.15	TCCGTGGAAGTCAGACATGAA	NM_032259:	NM_032259:
84219	WDR24	WD repeat domain 24	-0.01	CCGTAGCATCTTCAAGATCTA	NM_032259:	NM_032259:
10885	WDR3	WD repeat domain 3	-3.03	CCGGGATGTTATCGGCTTCAA	NM_006784:	NM_006784:
10885	WDR3	WD repeat domain 3	-1.38	TCCGCTGATAGGAATGTGAAA	NM_006784:	NM_006784:
9277	WDR46	WD repeat domain 46	-1.89	TGCCCTTGATTGGGTAACAAA	NM_005452:	NM_005452:
9277	WDR46	WD repeat domain 46	-1.42	CCGAAAGCTACCACATTCTAA	NM_005452:	NM_005452:
11091	WDR5	WD repeat domain 5	-1.43	CCCGCAAGAGACTGTCGGGAA	NM_017588:	NM_017588:NM_052821:
11091	WDR5	WD repeat domain 5	0.48	GACCACCAGAAAGTTCTTAAA	NM_017588:	NM_017588:NM_052821:
25886	WDR51A	WD repeat domain 51A	-0.28	CCGGGAATGTGTCCACTCGTA	NM_015426:	NM_015426:
25886	WDR51A	WD repeat domain 51A	-1.88	CTCCAGTGACTCAACCCTGAA	NM_015426:	NM_015426:
54554	WDR5B	WD repeat domain 5B	0.77	ATCAGAGTTACTAGTAGGGTA	NM_019069:	NM_019069:
54554	WDR5B	WD repeat domain 5B	0.39	TAGCACAATAATTTAACTGAA	NM_019069:	NM_019069:
151525	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	-4.06	TCGCATCAGATGGCTATTCAT	NM_152528:	NM_152528:
151525	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	0.56	AACATCAGCTGAAGCAATTTA	NM_152528:	NM_152528:
7465	WEE1	WEE1 homolog (S. pombe)	-12.45	CAGGGTAGATTACCTCGGATA	NM_003390:	NM_003390:
7465	WEE1	WEE1 homolog (S. pombe)	-1.18	TACCTGTGTGTCCATCTTATA	NM_003390:	NM_003390:
7466	WFS1	Wolfram syndrome 1 (wolframin)	0.04	TCGCCTTAAGCTGCTGGCCAA	NM_006005:	NM_006005:
7466	WFS1	Wolfram syndrome 1 (wolframin)	0.02	CCGCGTGACTGACATCGACAA	NM_006005:	NM_006005:
7468	WHSC1	Wolf-Hirschhorn syndrome candidate 1	-6.72	CTGGATGGAATTTAGCATCAA	NM_007331:	NM_133331:NM_133332:NM_014919:NM_133333:NM_133334:NM_133330:NM_133335:NM_007331:
7468	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.10	CAGAGTGTTCTAAGAACGGAA	NM_007331:	NM_133331:NM_133332:NM_014919:NM_133333:NM_133330:NM_007331:
54904	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	0.01	CACGAGAACAGTGTAACTAAT	NM_023034:	NM_023034:
54904	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	-2.53	CCGGAATGCCTAAGCATAGAA	NM_023034:	NM_023034:
11197	WIF1	WNT inhibitory factor 1	0.26	AAGCAATATAATATATTGTAA	NM_007191:	NM_007191:
11197	WIF1	WNT inhibitory factor 1	0.14	TTGCATTGGCTTGAAGCAATA	NM_007191:	NM_007191:
147179	WIRE	WIRE protein	0.81	CCCGCCTACAACAGAGAGAAA	NM_133264:	NM_133264:
147179	WIRE	WIRE protein	0.88	CAGGTATATTATATTTCATCA	NM_133264:	NM_133264:
8840	WISP1	WNT1 inducible signaling pathway protein 1	-0.74	CCGGTTGTTTAGAAACAGAAA	NM_003882:	NM_003882:
8840	WISP1	WNT1 inducible signaling pathway protein 1	0.90	TAGATGGAATTTGGAACAATA	NM_003882:	NM_003882:
8839	WISP2	WNT1 inducible signaling pathway protein 2	0.63	ATGGGACAAGCAGTCCCTTAA	NM_003881:	NM_003881:
8839	WISP2	WNT1 inducible signaling pathway protein 2	-0.04	CATGCAGAACACCAATATTAA	NM_003881:	NM_003881:
8838	WISP3	WNT1 inducible signaling pathway protein 3	-0.76	CAGCAATATATTAAAGACAAT	NM_003880:	NM_003880:NM_198239:NM_130396:
8838	WISP3	WNT1 inducible signaling pathway protein 3	0.60	CAGCCTTGCGACAGCAATATA	NM_003880:	NM_003880:NM_198239:NM_130396:
51352	WIT1	Wilms tumor upstream neighbor 1	0.77	CAGTCTGAGGTTACAATTAGA	NM_015855:	NM_015855:
51352	WIT1	Wilms tumor upstream neighbor 1	-1.06	TAGGCCCATGAAATTGATGAA	NM_015855:	NM_015855:
65125	WNK1	WNK lysine deficient protein kinase 1	-0.01	CTAGAGGATCTTGATGCTCAA	NM_018979:	NM_018979:
65125	WNK1	WNK lysine deficient protein kinase 1	-1.14	CTGCGACGACTACGAGATAAA	NM_018979:	NM_018979:
65268	WNK2	WNK lysine deficient protein kinase 2	1.09	AACGTTCATCGAGCAGATGAA	NM_006648:	NM_006648:
65268	WNK2	WNK lysine deficient protein kinase 2	0.36	ACCTATAAGTCTAGTAGCAAA	NM_006648:	NM_006648:
65267	WNK3	WNK lysine deficient protein kinase 3	-0.26	AAGATTGGTGATCTAGGATTA	NM_020922:	NM_001002838:NM_020922:
65267	WNK3	WNK lysine deficient protein kinase 3	-0.28	CCGGGTGACGCCAATAAAGAA	NM_020922:	NM_001002838:NM_020922:
65266	WNK4	WNK lysine deficient protein kinase 4	-4.90	CAGCTTGTTGGGCGTTTCCAA	NM_032387:	NM_032387:
65266	WNK4	WNK lysine deficient protein kinase 4	-0.81	CAGGAGGAGCCAGCACCATTA	NM_032387:	NM_032387:
7471	WNT1	wingless-type MMTV integration site family, member 1	0.67	AACGGCGTTTATCTTCGCTAT	NM_005430:	NM_005430:
7471	WNT1	wingless-type MMTV integration site family, member 1	0.17	CAGCGGCGTCTGATACGCCAA	NM_005430:	NM_005430:
7480	WNT10B	wingless-type MMTV integration site family, member 10B	1.48	ACGAATGCGAATCCACAACAA	NM_003394:	NM_003394:
7480	WNT10B	wingless-type MMTV integration site family, member 10B	-0.96	CAGGATCGGCTGAGGGCCAAA	NM_003394:	NM_003394:
7473	WNT3	wingless-type MMTV integration site family, member 3	-1.61	CCGCAATTACATCGAGATCAT	NM_030753:	NM_030753:
7473	WNT3	wingless-type MMTV integration site family, member 3	-1.63	CGGCTGTGACTCGCATCATAA	NM_030753:	NM_030753:
89780	WNT3A	wingless-type MMTV integration site family, member 3A	-0.79	ACCGCCATCCTCTGCCTCAAA	NM_033131:	NM_033131:
89780	WNT3A	wingless-type MMTV integration site family, member 3A	-1.73	CCCGACTGTGCTGCTCGCGAA	NM_033131:	NM_033131:
54361	WNT4	wingless-type MMTV integration site family, member 4	-1.34	CAGACCTAAGGTGGAGTAACA	NM_030761:	NM_030761:
54361	WNT4	wingless-type MMTV integration site family, member 4	0.31	CTCATGTTATTTATTGCCGAA	NM_030761:	NM_030761:
7474	WNT5A	wingless-type MMTV integration site family, member 5A	-0.04	CACACAAACTTTACACTTTAA	NM_003392:	NM_003392:
7474	WNT5A	wingless-type MMTV integration site family, member 5A	0.49	CCGGGTCTGCAGAGAATGAAA	NM_003392:	NM_003392:
7476	WNT7A (wing	wingless-type MMTV integration site family, member 7A	0.31	CAGCAATATTTAACAATTTAT	NM_004625:	NM_004625:
7476	WNT7A (wing	wingless-type MMTV integration site family, member 7A	-1.44	CCGAAAGATCCTGGAGGAGAA	NM_004625:	NM_004625:
7486	WRN	Werner syndrome	0.29	ATGGAGATGCTTAAGCATTTA	NM_000553:	NM_000553:
7486	WRN	Werner syndrome	0.81	CGGATTGTATACGTAACTCCA	NM_000553:	NM_000553:
26118	WSB1	WD repeat and SOCS box-containing 1	-0.14	CTAGTTTACCCTTGTGGTATA	NM_015626:	NM_134264:NM_134265:NM_015626:
26118	WSB1	WD repeat and SOCS box-containing 1	0.01	ACCGGTGGGTACGATCTGTAT	NM_015626:	NM_134264:NM_134265:NM_015626:
55884	WSB2	WD repeat and SOCS box-containing 2	0.38	AAAGATGTCTTAATTGTGTAA	NM_018639:	NM_018639:
55884	WSB2	WD repeat and SOCS box-containing 2	-3.27	CACGGCTTCTTACGATACCAA	NM_018639:	NM_018639:
7490	WT1	Wilms tumor 1	0.60	AAGAAATAAATCAGAGAGCAA	NM_000378:	NM_024425:NM_024426:NM_000378:NM_024424:
7490	WT1	Wilms tumor 1	0.73	AGGGAGGGAATTTATTATTTA	NM_000378:	NM_024425:NM_024426:NM_000378:NM_024424:
9589	WTAP	Wilms tumor 1 associated protein	-0.47	ATGCAAGAGTGTACTACTCAA	NM_004906:	NM_152858:NM_152857:NM_004906:
9589	WTAP	Wilms tumor 1 associated protein	-0.15	CAGACTAAAGACAAACTGGAA	NM_004906:	NM_152858:NM_152857:NM_004906:

51741	WWOX	WW domain containing oxidoreductase	0.32	TTGGGCGATGCTGGCTTATAA	NM_016373:	NM_016373:NM_018560:
51741	WWOX	WW domain containing oxidoreductase	0.10	CCCATCGATTTACAGATATTA	NM_016373:	NM_016373:NM_018560:
11060	WWP2	WW domain containing E3 ubiquitin protein ligase 2	0.75	CAGCCAATGAAGGTTTGTCTA	NM_007014:	NM_199424:NM_007014:
11060	WWP2	WW domain containing E3 ubiquitin protein ligase 2	0.57	CTCACCTACTTTCGCTTTATA	NM_007014:	NM_199424:NM_007014:
25937	WWTR1	WW domain containing transcription regulator 1	2.97	ACAGTAGTACCAAATGCTTTA	NM_015472:	NM_015472:
25937	WWTR1	WW domain containing transcription regulator 1	3.01	CTGCGTTCTTGTGACAGATTA	NM_015472:	NM_015472:
56949	XAB2	XPA binding protein 2	-0.66	CACGTACAACACGCAGGTCAA	NM_020196:	NM_020196:
56949	XAB2	XPA binding protein 2	-6.32	CCGCGTGTACAAGTCACTGAA	NM_020196:	NM_020196:
6375	XCL1	chemokine (C motif) ligand 1	0.99	AAGAAACTTTATTCAAGTAAA	NM_002995:	NM_002995:
6375	XCL1	chemokine (C motif) ligand 1	-2.52	ACCCTTTGAATTGGACAATAA	NM_002995:	NM_002995:
2829	XCR1	chemokine (C motif) receptor 1	0.86	CTGGGAGACTTCCTCTGCAAA	NM_005283:	NM_001024644:NM_005283:
2829	XCR1	chemokine (C motif) receptor 1	0.53	TCGGGCTGTGATTATTCCGAA	NM_005283:	NM_001024644:NM_005283:
7498	XDH	xanthine dehydrogenase	-0.06	ACAGGTAATAACGTGAAGGAA	NM_000379:	NM_000379:
7498	XDH	xanthine dehydrogenase	-0.30	CCGGATTGTGGTTCGAGTGAA	NM_000379:	NM_000379:
10894	XLKD1	extracellular link domain containing 1	-1.36	AACACTCAAACTGCAACACAA	NM_006691:	NM_006691:
10894	XLKD1	extracellular link domain containing 1	1.02	ATGGAGATTCTCATAACTTGA	NM_006691:	NM_006691:
	XM_018432:		-1.19	CTGCAGTCGTTCCGACACAAA	XM_018432:	XM_018432:
	XM_018432:		-6.87	CAGTATGAACCTACTGTCAAA	XM_018432:	XM_018432:
	XM_039393:		-1.28	CAGGTTTGCCTCGGAGATGAA	XM_039393:	XM_039393:XM_379927:
	XM_039393:		-0.70	CAGCCCTTTAGTGGATGGTTA	XM_039393:	XM_039393:XM_379927:
	XM_047083:		-3.67	CAGCATCTAGGGCATATTCCA	XM_047083:	XM_047083:
	XM_051264:		-7.32	CCGGGTGGTGATCTTCAGCAA	XM_051264:	XM_051264:
	XM_051264:		0.17	CACGACTTTGGAAATCACAAA	XM_051264:	XM_051264:
	XM_059923:		0.66	AAAGGATTTATGAATAATTAA	XM_059923:	XM_059923:
	XM_059923:		-0.59	CTGGAAGAAGTTTGCAGCAAA	XM_059923:	XM_059923:
	XM_061864:		0.60	CCGATAGATGTGGAATACAAA	XM_061864:	XM_061864:
	XM_061864:		-0.77	TACGATGTGAGCATAAGTGAA	XM_061864:	XM_061864:
	XM_070277:		-1.50	CCCGGAGGAATTTGAGTCTTA	XM_070277:	XM_070277:
	XM_070277:		-0.61	CAGCAAGAAGATCATATGTGA	XM_070277:	XM_070277:
	XM_086725:		0.32	TTCGTCTAATATATTCTAAGA	XM_086725:	XM_086725:
	XM_086725:		0.19	CTCGCTGTGATTGTCAGTGAT	XM_086725:	XM_086725:
	XM_208545:		-5.17	TTGGAACGGATGAAGCATTTA	XM_208545:	XM_208545:
	XM_209616:		0.11	GACATTCTTAATTACAGGTAA	XM_209616:	XM_209616:
	XM_209616:		-0.43	TGGCAGCTACTGCAAGGTTAA	XM_209616:	XM_209616:
	XM_211557:		0.70	AACCCTCAGGTTATTACAGTA	XM_211557:	XM_211557:
	XM_211557:		-0.08	CAGTATTCAGACAAACTGAAA	XM_211557:	XM_211557:
	XM_290780:		3.65	CAGAAGGAGATCAACGACCAA	XM_290780:	XM_290780:
	XM_290780:		-5.12	CACAGCAAGTTGGCATCTAAA	XM_290780:	XM_290780:
	XM_290822:		1.79	TACCTCGAGTATGGCTGGAAA	XM_290822:	XM_290822:
	XM_290822:		-1.83	ACGGCACAGGGAAATCAGGAA	XM_290822:	XM_290822:
	XM_290866:		0.89	AGCCTGTGTGATGATGCTCTA	XM_290866:	XM_290866:
	XM_290866:		0.28	TCCAGGAAATTGGATGATAAT	XM_290866:	XM_290866:
	XM_291105:		0.10	AACCCATTGTACAAAGTTCAA	XM_291105:	XM_291105:
	XM_291105:		-3.09	CCGGCGAAACGGGATCACCAA	XM_291105:	XM_291105:
	XM_291141:		-2.06	ACGATACTTCCTTGAATTACA	XM_291141:	XM_291141:
	XM_291141:		0.46	ACCTATTAATTTAGAAGAGAA	XM_291141:	XM_291141:
	XM_292027:		-0.20	ATGATGCATATTCTTAGTCAA	XM_292027:	XM_292027:
	XM_292027:		-3.05	TGGCATGAGCATAAATACAAA	XM_292027:	XM_292027:
	XM_293360:		0.01	TCGCTTCATGTTAGTCTTGCA	XM_293360:	XM_293360:
	XM_293360:		0.89	TAGAGACTGCTTAATCTTTGA	XM_293360:	XM_293360:
	XM_370621:		0.19	AAGAATACGAATGACAATATA	XM_370621:	XM_370621:
	XM_370621:		0.70	CACGATGAGCCAACAGTCATA	XM_370621:	XM_370621:
	XM_370639:		-0.01	CCCAACAATTAGAGAATTGTA	XM_370639:	XM_370639:
	XM_370639:		-3.79	CAGAAACATAGTTAAACTTTA	XM_370639:	XM_370639:
	XM_370660:		0.02	CCCGGGATAGGACATATATGA	XM_370660:	XM_370660:
	XM_370660:		1.62	GAGGACTACTTCCGCCATTTA	XM_370660:	XM_370660:
	XM_370661		-1.54	TCCATCGAACTTATATTCCAA	XM_370661	No hits found till 3 mismatches
	XM_370716:		-1.79	CGCGATTTGCTTCCTCATATA	XM_370716:	XM_370716:
	XM_370716:		0.84	AACCAGGCAGTCGGAATGAAA	XM_370716:	XM_370716:
	XM_371145:		-0.28	CGCCTTCAGTACTTTCCACAA	XM_371145:	XM_371145:
	XM_371145:		0.48	CGGGACCCAGTTTATGGGAAA	XM_371145:	XM_371145:
	XM_371249:		-1.00	AAGAATGGAAGGATAAATATA	XM_371249:	XM_371249:
	XM_371249:		0.74	CAGTTATCTTTCCCACAATAA	XM_371249:	XM_371249:
	XM_371663:		0.50	AAGGAACAACTGTATCTTATA	XM_371663:	XM_371663:
	XM_371663:		0.72	CACACAGTATTTGTTTCTTCA	XM_371663:	XM_371663:
	XM_371718:		0.02	CACCAAGAGTAGACTGATAAA	XM_371718:	XM_371718:
	XM_371837:		-0.63	CAGGGTTCCATGATGGGTCAA	XM_371837:	XM_371837:
	XM_371837:		-0.92	CAGCACGTACCTGATGATCAA	XM_371837:	XM_371837:
	XM_372092:		0.75	CACGTACACACGGGAGCGCAA	XM_372092:	XM_372092:
	XM_372092:		-0.57	CCACGCAGAGATGACAGCCAA	XM_372092:	XM_372092:
	XM_372121:		0.85	TAGCATCATCAGAGTATCATA	XM_372121:	XM_372121:
	XM_372121:		-0.28	ATGGAACAAGACTTCTCTGAA	XM_372121:	XM_372121:
	XM_372128:		-1.01	TACATTCTAGTAAGCATCTTA	XM_372128:	XM_372128:
	XM_372128:		0.32	TAGTTTAAATATATACAATAA	XM_372128:	XM_372128:
	XM_372254:		0.98	AGGCCCAAATTTAGAAAGTTA	XM_372254:	XM_372254:
	XM_372254:		-0.24	TAGAAAGTTATGACTGTGATA	XM_372254:	XM_372254:
	XM_372323:		-0.80	AAGGTTGTTATCTTTATTGAT	XM_372323:	XM_372323:
	XM_372323:		0.00	CAGCCAGAGACAAGAAGAGTA	XM_372323:	XM_372323:
	XM_372329:		-0.69	AGCGAAGAGGACGAATCTCTA	XM_372329:	XM_372329:
	XM_372329:		0.48	CACCAGACACATTACTCACAA	XM_372329:	XM_372329:
	XM_372424:		-0.78	CACTCTGATTACTCAATCTTA	XM_372424:	XM_372424:
	XM_372424:		-0.32	ACCCAGACTATGTGTCATTAA	XM_372424:	XM_372424:
	XM_372639:		0.66	TCGGATTTAACAGGAAGGAAT	XM_372639:	XM_372639:
	XM_372639:		-1.07	AAGACGTTCCCTGAAGCAGAA	XM_372639:	XM_372639:
	XM_372663:		-1.27	TTGGAGTTCTTTGTTGGAGAA	XM_372663:	XM_372663:
	XM_372663:		-5.57	CACGTGTTGAGACTGAACTAA	XM_372663:	XM_372663:
	XM_373038		2.05	ACAGCACATCGTAAACTTATA	XM_373038	No hits found till 3 mismatches
	XM_373097:		0.47	CTCGACAGGGATTAAATGGAA	XM_373097:	XM_373097:
	XM_373097:		-1.15	ACCCTAATTTGAACAGCTTTA	XM_373097:	XM_373097:
	XM_373156		0.03	AAGAATGATACGGGTATTCCA	XM_373156	No hits found till 3 mismatches
	XM_373786:		-2.08	TAGCGTGTTCACCGAGTGGAA	XM_373786:	XM_373786:
	XM_373786:		0.02	CAGGCTGTGCAGGTCCTGGAA	XM_373786:	XM_373786:
	XM_374002:		-1.49	CACGTCGGTGGAACTCCTAAA	XM_374002:	XM_374002:
	XM_374002:		0.57	CACGACGGTACGGTTATGCTA	XM_374002:	XM_374002:
	XM_374879:		-0.36	CAGCTGCGGCTCAGCACAGTA	XM_374879:	XM_374879:
	XM_374879:		-0.76	CACCTTGGACAACCTCCAGAA	XM_374879:	XM_374879:
	XM_375344:		-1.58	CCAGCATTAGAACATCATTAA	XM_375344:	XM_375344:
	XM_375619:		0.81	TCCCTTGTGCTTGTAACCTAA	XM_375619:	XM_375619:
	XM_375619:		0.99	CAGAGAAGGTATCTGATCAAA	XM_375619:	XM_375619:

	XM_375714:		-0.01	CGAGCACGAGACAATGATGCA	XM_375714:	XM_375714:
	XM_375714:		-1.99	TGGGAGGAACGTGCTCTGTGA	XM_375714:	XM_375714:
	XM_375914:		0.19	CTGGGATTATTGATTACAACA	XM_375914:	XM_375914:
	XM_375914:		0.00	TTCATACAGAATGGCACTAAA	XM_375914:	XM_375914:
	XM_376001:		-2.99	GCCCTCTACTCAGCATGGATA	XM_376001:	XM_376001:
	XM_376001:		-0.06	CTGACACTAAGCTCGGCTTCA	XM_376001:	XM_376001:
	XM_376684:		0.36	ACCGACAGTCTTTCCCGATTA	XM_376684:	XM_379940:XM_376684:
	XM_376684:		1.49	TACGTGGAGGTTACTGATAAA	XM_376684:	XM_379940:XM_376684:
	XM_376888:		-0.73	CAGACTGGTTTGAAGGAAGAA	XM_376888:	XM_376888:
	XM_377824:		0.20	TCGGACGGAGATGACAATGAA	XM_377824:	XM_377824:
	XM_377824:		0.88	AAGAAACAAGGCTGCAGCTAA	XM_377824:	XM_377824:
	XM_377925:		-0.01	CCAGATCTGAACGGCATGGAA	XM_377925:	XM_379986:XM_377925:
	XM_377925:		0.43	CACCCGCTCAATGACGCAGAA	XM_377925:	XM_379986:XM_377925:
	XM_379264:		0.06	CGGCAGGGAAATCTCATCCAA	XM_379264:	XM_379264:
	XM_379264:		-0.28	CAGGCTGAAGTGACCCTCCAA	XM_379264:	XM_379264:
	XM_380143:		0.06	TTCCAAGTATTTAATACACAA	XM_380143:	XM_380143:XM_379518:
	XM_380143:		-0.30	CTGCTGGGAGAAAGAATGGAA	XM_380143:	XM_380143:XM_379518:
	XM_495806:		0.67	TAGGTATTCAATAGCATTAGA	XM_495806:	XM_495806:
	XM_495806:		0.16	AAGATGCAGGATCATGGCCAA	XM_495806:	XM_495806:
	XM_495815:		1.02	TCGGATGTGCTTCATCACCTA	XM_495815:	XM_495815:
	XM_495815:		-1.37	CTGGGTGTGGCTGATTATAAT	XM_495815:	XM_495815:
	XM_495872:		-0.05	TTGCCTCCTAATGTTATTAAA	XM_495872:	XM_495872:XM_370621:
	XM_495967:		0.32	CAGGCCTCAGATAGACGCCAA	XM_495967:	XM_378064:XM_495971:XM_497993:
	XM_495967:		0.35	CAGCAACTTCACAACCCAGTA	XM_495967:	XM_496597:
	XM_496123:		0.03	CTGGCTGTGAAGGACCCTTTA	XM_496123:	XM_496123:
	XM_496123:		-4.01	CAAAGAAATGTAGTTTATTTA	XM_496123:	XM_496123:
	XM_496151:		-0.07	AAGGCCTGGAACGGTCCGAAA	XM_496151:	XM_496151:
	XM_496151:		0.38	CTGGTTCTCAATAGCCGGGAA	XM_496151:	XM_496151:
	XM_496161:		-0.03	CGCGGGCGTCTAGGCAAGAAA	XM_496161:	XM_496161:
	XM_496161:		-1.93	ATGGACAAGAAGAAAGAGTAA	XM_496161:	XM_496151:XM_496161:
	XM_496165:		0.69	CTCCTACTTGTCAACCGGAAA	XM_496165:	XM_496165:
	XM_496165:		-0.94	CTGGGACTCACTGTCGACCAA	XM_496165:	XM_496165:
	XM_496291:		0.60	CTGAAGAACGGTGATCCTAAA	XM_496291:	XM_496291:
	XM_496291:		-0.26	AAAGAAGTTGTCAGATGAGAA	XM_496291:	XM_496291:
	XM_496404:		0.86	GTGCAATTCGTCAGAACTTAA	XM_496404:	XM_496404:
	XM_496404:		0.25	AGGAATGAACATAAGTTTCTA	XM_496404:	XM_496404:
	XM_496405:		0.07	TAGCATTAAGTTGCTTGACTA	XM_496405:	XM_496405:
	XM_496405:		-1.70	CTGCAACTTAGCCTAGCATTA	XM_496405:	XM_496405:
	XM_496434:		0.26	AACAGGAAATAGTGTAATCTA	XM_496434:	XM_496434:
	XM_496434:		0.90	GCGGACAGAAATCATACAATA	XM_496434:	XM_496434:
	XM_496437:		-0.23	AAATTTCATGATTGACTTAAA	XM_496437:	XM_496437:
	XM_496642		1.10	ACCCGCATTATAAACATTATA	XM_496642	No hits found till 3 mismatches
	XM_496820:		0.31	TTGGAAGAGATTCTTATTAAA	XM_496820:	XM_496820:
	XM_497211:		-0.25	ATGCGGCGTTCTTCTACCAAA	XM_497211:	XM_497211:
	XM_497211:		-0.04	TTGCCAAGAAATACAATAGAA	XM_497211:	XM_497211:
	XM_497242:		1.11	CAGGAATACAGCCAAGGGAAA	XM_497242:	XM_497240:XM_497242:XM_497226:XM_497229:XM_497223:XM_497231:
	XM_497249:		0.27	CAGCATGAGATACACCAACAA	XM_497249:	XM_497249:
	XM_497249:		-0.40	CTCAATGACGTGTACAGTTTA	XM_497249:	XM_497249:
	XM_497309:		0.96	CTGCCTGCAAACGGCACTTTA	XM_497309:	XM_497309:
	XM_497353:		-0.05	CACATCTATACATTCACGAAA	XM_497353:	XM_497353:
	XM_497353:		0.20	CAGAGAATCTGCCAACCGCAA	XM_497353:	XM_497353:
	XM_497509:		0.10	CCCTCGAGAGTTGGAAGTCAA	XM_497509:	XM_497509:
	XM_497509:		-0.16	CCAGGCCGCTTTGGAAGCGAA	XM_497509:	XM_497509:
	XM_497611:		-2.97	AAGCCGGAGGTCATAATGTAT	XM_497611:	XM_497611:
	XM_497611:		0.12	CTCAGCCACCATTGCACCAAA	XM_497611:	XM_497611:
	XM_497684:		-5.49	ATGTATAACGATGACCTAGAA	XM_497684:	XM_497684:
	XM_497684:		1.28	TGCCACATTGGTGATCCTCTA	XM_497684:	XM_497684:
	XM_497715:		0.22	CTGGATTTAACGGAAGTAATT	XM_497715:	XM_497715:
	XM_497715:		0.72	CAGTTTCATTTGACTCCTCAA	XM_497715:	XM_497715:
	XM_497791:		-0.19	ACAGTGGCCAACAGAGATTAA	XM_497791:	XM_497791:
	XM_497793:		0.16	CCCGAAAGATGTGGGCATTAA	XM_497793:	XM_497793:
	XM_497912:		-1.58	CCGGAGTCCGCGGTTACTCAA	XM_497912:	XM_497912:
	XM_497912:		-2.18	CCCATCAGAGGCAGCACTCAA	XM_497912:	XM_497912:
	XM_497921:		-1.26	CTCCAAGTTTCAGGAAGATAA	XM_497921:	XM_497921:
	XM_497921:		-2.87	AACAGTGGGCACATCAGCAAA	XM_497921:	XM_497921:
	XM_498271:		-0.22	CTCGTCATGGTTACCATTTCA	XM_498271:	XM_498271:
	XM_498271:		-4.06	AAGAGCCCTGCTCAAAGTTTA	XM_498271:	XM_498271:
	XM_498294:		0.47	TGGGACAGTGTTCAAGGCCAA	XM_498294:	XM_498294:
	XM_498308:		-1.22	AGCCCTCAATTTCGCCTTCAA	XM_498308:	XM_498308:
	XM_498308:		-7.80	CTGCCTAGTGAAGATCAGCAA	XM_498308:	XM_498308:
7507	XPA	xeroderma pigmentosum, complementation group A	-2.54	AAGAATTGCGGCGAGCAGTAA	NM_000380:	NM_000380:
7507	XPA	xeroderma pigmentosum, complementation group A	0.96	CTGATGATAAACACAAGCTTA	NM_000380:	NM_000380:
7508	XPC	xeroderma pigmentosum, complementation group C	-0.61	CCGGCTGGTATTGTCTCTACA	NM_004628:	NM_004628:
7508	XPC	xeroderma pigmentosum, complementation group C	0.44	TAGCAAATGGCTTCTATCGAA	NM_004628:	NM_004628:
7511	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-1.23	CCCGACTTCTTTGGCCAGTGA	NM_020383:	NM_020383:
7511	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-2.70	CCCGACTGGAACCAAAGGTCA	NM_020383:	NM_020383:
7512	XPNPEP2 (X-	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	0.69	CACAGCTACAATGCTGTTAAA	NM_003399:	NM_003399:
7512	XPNPEP2 (X-	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	0.89	ATGGAACCCATGATTCCTAAA	NM_003399:	NM_003399:
7514	XPO1	exportin 1 (CRM1 homolog, yeast)	-3.67	CAGCAAAGAATGGCTCAAGAA	NM_003400:	NM_003400:
7514	XPO1	exportin 1 (CRM1 homolog, yeast)	-3.45	CCCATTGTAAAGCGACTTCAA	NM_003400:	NM_003400:
57510	XPO5	exportin 5	-0.99	CTGTCTCGAATTGTAGTGGAA	NM_020750:	NM_020750:
57510	XPO5	exportin 5	0.54	CCAGATGTTTCGAACACTAAA	NM_020750:	NM_020750:
23039	XPO7	exportin 7	0.38	CAAGCTTGTATCACGCACAAA	NM_015024:	NM_015024:
23039	XPO7	exportin 7	-0.07	AAGGCTGACATGGCTGGTTTA	NM_015024:	NM_015024:
11260	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	0.55	AAGAGTTATCCTAGAACCTTA	NM_007235:	NM_007235:
11260	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	-1.25	CACGCCTATTACAACCAGAAA	NM_007235:	NM_007235:
9213	XPR1	xenotropic and polytropic retrovirus receptor	0.83	AAGGCTCGTGACACTAAGGTA	NM_004736:	NM_004736:
9213	XPR1	xenotropic and polytropic retrovirus receptor	-0.10	TCGGATCCTATGGACTCCAAA	NM_004736:	NM_004736:
	XR_000088:		-1.25	ACCACCCAGCATCTAATACAA	XR_000088:	XR_000088:
	XR_000088:		0.98	TAAGATTGGCTCGTATAACAA	XR_000088:	XR_000088:
	XR_000278:		0.86	CAGCCTGATGGAGGACTCTTA	XR_000278:	XR_000278:
	XR_000278:		0.09	CAGAGTAGTCTTGTCTCCGAA	XR_000278:	XR_000278:
	XR_000282:		-0.47	TCCGGGTTCCCAAGAACTAAA	XR_000282:	XR_000282:
	XR_000282:		-3.44	CAGGTGTAGATCACCTATTAT	XR_000282:	XR_000282:
7515	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells	-2.38	CCGATACGTCACAGCCTTCAA	NM_006297:	NM_006297:
7515	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells	-1.40	CCGATGGATCTACAGTTGCAA	NM_006297:	NM_006297:
7516	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells	-4.99	CAGGGTACTACGCAAGCCTTA	NM_005431:	NM_005431:
7516	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells	-0.43	TTGCAACGACACAAACTATAA	NM_005431:	NM_005431:

7517	XRCC3 (X-ray	X-ray repair complementing defective repair in Chinese hamster cells	0.47	CAGAATTATTGCTGCAATTAA	NM_005432:	NM_005432:
7517	XRCC3 (X-ray	X-ray repair complementing defective repair in Chinese hamster cells	0.13	GAGACACTTAAGGGAAATTAA	NM_005432:	NM_005432:
7518	XRCC4 (X-ray	X-ray repair complementing defective repair in Chinese hamster cells	-0.50	CACATTTATCATATTCATTCA	NM_003401:	NM_022550:NM_022406:NM_003401:
7518	XRCC4 (X-ray	X-ray repair complementing defective repair in Chinese hamster cells	1.52	CAGCTGATGTATACACGTTTA	NM_003401:	NM_022550:NM_022406:NM_003401:
7520	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells	0.95	AAGCATAACTATGAGTGTTTA	NM_021141:	NM_021141:
7520	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells	-5.61	AAGCGAGTAACCAGCTCATAA	NM_021141:	NM_021141:
2547	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells	-0.16	CGCCTAGTGAGCAGTAGCCAA	NM_001469:	NM_001469:
9942	XYLB	xylulokinase homolog (H. influenzae)	1.41	CTGAAATTATTGGACGTCATA	NM_005108:	NM_005108:
9942	XYLB	xylulokinase homolog (H. influenzae)	1.19	TCAGGACTCCAGCTAAATCAA	NM_005108:	NM_005108:
10138	YAF2	YY1 associated factor 2	0.22	ACCAAACATTTCCAGACTTAA	NM_005748:	NM_001012424:NM_005748:
10138	YAF2	YY1 associated factor 2	-0.28	GACAGATACATTCATGCACAA	NM_005748:	NM_001012424:NM_005748:
10413	YAP1	Yes-associated protein 1, 65kDa	-0.71	CAGGTGATACTATCAACCAAA	NM_006106:	NM_006106:
10413	YAP1	Yes-associated protein 1, 65kDa	0.80	TAGAGTAGTAATGAAATTCTA	NM_006106:	NM_006106:
8565	YARS	tyrosyl-tRNA synthetase	-0.68	CTGAAGGAGCGGGAACTTAAA	NM_003680:	NM_003680:
8565	YARS	tyrosyl-tRNA synthetase	0.01	AACAGAGAACCTAGTGGTCTA	NM_003680:	NM_003680:
51067	YARS2	tyrosyl-tRNA synthetase 2 (mitochondrial)	0.01	CCCGAGGGTATCGAATGATAA	NM_015936:	NM_015936:
51067	YARS2	tyrosyl-tRNA synthetase 2 (mitochondrial)	-0.61	AAGCTTGTTCATGGACGAGAA	NM_015936:	NM_015936:
8089	YEATS4	YEATS domain containing 4	-0.27	TTGGTAGTAAGCTAAACTGAA	NM_006530:	NM_006530:
8089	YEATS4	YEATS domain containing 4	0.11	CTCCATATGAAATTACTGAAA	NM_006530:	NM_006530:
7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	0.36	AACAGTCAGTATGCAATCTTA	NM_005433:	NM_005433:
7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	0.84	AAGTATAATGCAGTACATTAA	NM_005433:	NM_005433:
10730	YME1L1	YME1-like 1 (S. cerevisiae)	1.03	TCCGTTGATCCAGAAATTATA	NM_014263:	NM_139312:NM_139313:NM_014263:
10730	YME1L1	YME1-like 1 (S. cerevisiae)	1.43	TCGGCATTTATGGACTTCTAA	NM_014263:	NM_139312:NM_139313:NM_014263:
51646	YPEL5	yippee-like 5 (Drosophila)	2.07	TAAAGGTTTCTTTACCCTAAA	NM_016494:	NM_016061:
7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	-2.03	CAGCAATATGTTCACTATGTT	NM_003404:	NM_003404:NM_139323:
7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	-0.01	CTGGATAATACCTTTAAGAAT	NM_003404:	NM_003404:NM_139323:
7532	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	1.71	ACCAGTGTTAGCTTAATCTTA	NM_012479:	NM_012479:
7532	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	-1.47	CCGATTAGGCCTGGCTCTTAA	NM_012479:	NM_012479:
7533	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	0.23	CAGGCTACAGTTGATATTTAA	NM_003405:	NM_003405:
7533	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	0.81	TTCCATCAGCTTTATAATAAA	NM_003405:	NM_003405:
10971	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	-0.22	CAAACGATAGATAATTCCCAA	NM_006826:	NM_006826:
10971	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	-0.60	CTGGAATTGTTGGATAAATAT	NM_006826:	NM_006826:
7528	YY1	YY1 transcription factor	0.58	AACCTGAAATCTCACATCTTA	NM_003403:	NM_003403:
7528	YY1	YY1 transcription factor	0.26	ATGCCTCTCCTTTGTATATTA	NM_003403:	NM_003403:
145482	ZADH1	zinc binding alcohol dehydrogenase, domain containing 1	-0.05	ACAAATGTTTGTAAACATGAA	NM_152444:	NM_152444:
145482	ZADH1	zinc binding alcohol dehydrogenase, domain containing 1	0.69	TACATGATTCTTAAACTGAAA	NM_152444:	NM_152444:
284273	ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	0.00	TACGATGGTCTCAACACCTTT	NM_175907:	NM_175907:
284273	ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	-0.47	ACGCTTACATTCAATTCTTTA	NM_175907:	NM_175907:
51776	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	-0.53	ACGTGGTAGTATATCACTCAA	NM_016653:	NM_016653:
51776	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	0.41	TCGGGTAGCAACAAACTTATT	NM_016653:	NM_016653:
7455	ZAN (zonadhe	zonadhesin	-2.04	CAGCTTAAGAATGGCCAGTAT	NM_173059:	NM_173055:NM_173056:NM_003386:NM_173059:NM_173057:NM_173058:
7455	ZAN (zonadhe	zonadhesin	-1.65	CCCGGCTATGTGCTGAGTGAA	NM_173059:	NM_173055:NM_173056:NM_003386:NM_173059:NM_173057:NM_173058:
7535	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	0.30	CCGCAACGTCCTGCTGGTTAA	NM_001079:	NM_207519:NM_001079:
7535	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	1.32	GGCGTAGATCACCAGAATAAA	NM_001079:	NM_207519:NM_001079:
9189	ZBED1	zinc finger, BED-type containing 1	0.64	ATGCTTTGCTGTAAATACTTA	NM_004729:	NM_004729:
9189	ZBED1	zinc finger, BED-type containing 1	0.91	CGAGATCGACATGTTTCTCAA	NM_004729:	NM_004729:
27107	ZBTB11	zinc finger and BTB domain containing 11	0.10	ACGGACCCATATACTTTATAA	NM_152700:	NM_014415:
7704	ZBTB16	zinc finger and BTB domain containing 16	1.71	AGGAAGGACTATGACAAATAA	NM_006006:	NM_006006:NM_001018011:
7704	ZBTB16	zinc finger and BTB domain containing 16	0.23	CCGGGATGAGAGCACACTCAA	NM_006006:	NM_006006:NM_001018011:
51530	ZC3HC1	zinc finger, C3HC-type containing 1	-0.37	AGGGAGAATGGTGGAACTGAA	NM_016478:	NM_016478:
23390	ZDHHC17	zinc finger, DHHC-type containing 17	0.28	CAGTACCTGTTTGATACGAAA	NM_015336:	NM_015336:
23390	ZDHHC17	zinc finger, DHHC-type containing 17	0.39	CCGGATGAGTACGATACCGAA	NM_015336:	NM_015336:
51304	ZDHHC3	zinc finger, DHHC-type containing 3	-0.01	CTCACCGAAGATGGATGCTTA	NM_016598:	NM_016598:
51304	ZDHHC3	zinc finger, DHHC-type containing 3	0.59	TCCGTTCTCATGAATGTTTAA	NM_016598:	NM_016598:
9839	ZFHX1B	zinc finger homeobox 1b	0.06	CACGATCCAGACCGCAATTAA	NM_014795:	NM_014795:
9839	ZFHX1B	zinc finger homeobox 1b	0.64	CCACCATGAATAGTAATTTAA	NM_014795:	NM_014795:
7545	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)	-0.01	CCCAGGAAGATAAACCGCAAA	NM_003412:	NM_003412:
7545	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)	0.63	GTGAATTACTTTGTACGATTA	NM_003412:	NM_003412:
7546	ZIC2	Zic family member 2 (odd-paired homolog, Drosophila)	-0.35	CAGAGGAAACAATATTTATAA	NM_007129:	NM_007129:
7546	ZIC2	Zic family member 2 (odd-paired homolog, Drosophila)	-2.31	CAACCTGATTGTAAACTTCAT	NM_007129:	NM_007129:
7547	ZIC3	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	0.37	TAGGCTTAAGTACCTCCTTTA	NM_003413:	NM_003413:
7547	ZIC3	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	-2.17	AAGGCTGATTTGTTTGCTGTA	NM_003413:	NM_003413:
10269	ZMPSTE24	zinc metallopeptidase (STE24 homolog, yeast)	-0.71	CAGAACAGGAAAGACGAATTA	NM_005857:	NM_005857:
10269	ZMPSTE24	zinc metallopeptidase (STE24 homolog, yeast)	-0.09	ACGAAGGTGTATGTTGTGGAA	NM_005857:	NM_005857:
10771	ZMYND11	zinc finger, MYND domain containing 11	0.18	TAGGAATGGATCGATAGTTGA	NM_006624:	NM_006624:
10771	ZMYND11	zinc finger, MYND domain containing 11	-0.04	CACCTCATGTATCGTAAGTTA	NM_006624:	NM_006624:
116225	ZMYND19	zinc finger, MYND-type containing 19	0.58	CAGGACGGTTCTCATTATTTA	NM_138462:	NM_138462:
116225	ZMYND19	zinc finger, MYND-type containing 19	-0.55	CACGGGAGTTGTGTCCACAAA	NM_138462:	NM_138462:
94039	ZNF101	zinc finger protein 101	0.98	CACAGTAACACCAACTCGAAA	NM_033204:	NM_033204:
94039	ZNF101	zinc finger protein 101	-1.99	CACGGCGCACAGTAACACCAA	NM_033204:	NM_033204:
10168	ZNF197	zinc finger protein 197	-0.01	CACCTACACTTTAGACAATTA	NM_006991:	NM_006991:NM_001024855:
10168	ZNF197	zinc finger protein 197	-1.45	TCCCAACTTTCAAGTCTACAA	NM_006991:	NM_006991:
7750	ZNF198	zinc finger protein 198	-2.56	ACGCTGGGTATTACCATGTAA	NM_003453:	NM_003453:NM_197968:
7750	ZNF198	zinc finger protein 198	-1.98	CACGCTGGGTATTACCATGTA	NM_003453:	NM_003453:NM_197968:
9406	ZNF265	zinc finger protein 265	0.57	AAGGAAGTTGAAGATAAAGAA	NM_005455:	NM_005455:NM_203350:
9406	ZNF265	zinc finger protein 265	0.32	GTGGTGTTTGTTAGAAATAAA	NM_005455:	NM_005455:NM_203350:
23528	ZNF281	zinc finger protein 281	-2.13	CCCAATGGCCTTTATCATCTA	NM_003123:	NM_012482:
63925	ZNF335	zinc finger protein 335	-0.60	TGGCCTGTCAGTCTCAATAAA	NM_022095:	NM_022095:
63925	ZNF335	zinc finger protein 335	-8.93	CAGGCGCTTCCTAGGCAAGAA	NM_022095:	NM_022095:
23567	ZNF346	zinc finger protein 346	1.30	ACGCAAAGAACTTAAAGCTGA	NM_012279:	NM_012279:
23567	ZNF346	zinc finger protein 346	0.37	CGCAAAGAACTTAAAGCTGAA	NM_012279:	NM_012279:
27246	ZNF364	zinc finger protein 364	0.16	CTGAATAGAATTAATTCCTTA	NM_014455:	NM_014455:
27246	ZNF364	zinc finger protein 364	0.25	AGGGCTGTGGTAATCATCTTA	NM_014455:	NM_014455:
57541	ZNF398	zinc finger protein 398	0.00	CAGCAGGTTGATAGTAGATTA	NM_020781:	NM_170686:NM_020781:
57541	ZNF398	zinc finger protein 398	-0.29	CTGGACCTATACCATGGGAAA	NM_020781:	NM_170686:NM_020781:
10224	ZNF443	zinc finger protein 443	0.70	TCGGTCATTATGATAACTTAA	NM_005815:	NM_005815:
10224	ZNF443	zinc finger protein 443	1.47	TTCGGTCATTATGATAACTTA	NM_005815:	NM_005815:
55311	ZNF444	zinc finger protein 444	0.91	CAGCATCCATAGAGTAATAAA	NM_018337:	NM_018337:
55311	ZNF444	zinc finger protein 444	-1.21	CTGGGTCTTGTCCCTAGGAAT	NM_018337:	NM_018337:
168544	ZNF467	zinc finger protein 467	-1.70	CAGGAAAGAGTGGTTATTTAT	NM_207336:	NM_207336:
168544	ZNF467	zinc finger protein 467	-0.16	CCCGCTCTTCTTCTGAGCCTA	NM_207336:	NM_207336:
169270	ZNF596	zinc finger protein 596	1.32	CAGCACTTCTATAATAGATCA	NM_173539:	NM_173539:
169270	ZNF596	zinc finger protein 596	0.35	TACCACTTTGCTCAACCTAAA	NM_173539:	NM_173539:
90850	ZNF598	zinc finger protein 598	-1.67	CCGCCCTGTTGGCACACTCAA	NM_178167:	NM_178167:
90850	ZNF598	zinc finger protein 598	-1.79	AAGCACTTTCTGTGTGAGGAA	NM_178167:	NM_178167:
80095	ZNF606	zinc finger protein 606	1.17	TCCCACATTATTTACTAGAAA	NM_025027:	NM_025027:
80095	ZNF606	zinc finger protein 606	1.92	AGAGTTTAGCCAGAACTTAAA	NM_025027:	NM_025027:

58491	ZNF71	zinc finger protein 71 (Cos26)	-0.10	CAGCAGCAGGTTTGATATTCA	NM_021216:	NM_021216:
58491	ZNF71	zinc finger protein 71 (Cos26)	0.00	CCGAAGCTCGTCCCTGATAAA	NM_021216:	NM_021216:
7639	ZNF85	zinc finger protein 85 (HPF4, HTF1)	0.90	CAGCATCAGAAAGTACTTAAT	NM_003429:	NM_003429:
7639	ZNF85	zinc finger protein 85 (HPF4, HTF1)	1.97	AAAGCTTTAATCAATTTACAA	NM_003429:	NM_003429:
7555	ZNF9	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	-1.42	CACATAGATGGTGATGGCAAA	NM_003418:	NM_003418:
7555	ZNF9	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	0.09	CTGACCTCAGTAGCTATTAAA	NM_003418:	NM_003418:
10320	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	-0.49	CACCGCTTCCACATGAGCTAA	NM_006060:	NM_006060:
10320	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	1.65	AAGTAACGTCGCCAAACGTAA	NM_006060:	NM_006060:
9326	ZNHIT3	zinc finger, HIT type 3	0.62	ACAGTTGATAGACATCATAAA	NM_004773:	NM_004773:
9326	ZNHIT3	zinc finger, HIT type 3	-3.38	CTCATGAGAGCTTACATGCAA	NM_004773:	NM_004773:
84937	ZNRF1	zinc and ring finger 1	-0.11	CAGCGGAGAAACACTAAAGAA	NM_032268:	NM_032268:
84937	ZNRF1	zinc and ring finger 1	0.51	AAGTGTTATACAATCAAGAAA	NM_032268:	NM_032268:
223082	ZNRF2	zinc and ring finger 2	0.68	CGCCAAAGTTAACTGATTTAA	NM_147128:	NM_147128:
223082	ZNRF2	zinc and ring finger 2	0.52	ACGCCAAAGTTAACTGATTTA	NM_147128:	NM_147128:
84133	ZNRF3	zinc and ring finger 3	-3.80	CTGCTGCTTCTATGAAGAGAA	XM_290972:	XM_290972:
84133	ZNRF3	zinc and ring finger 3	-0.54	CCCGGTTCCCGCCGAACTCTA	XM_290972:	XM_290972:
148066	ZNRF4	zinc and ring finger 4	-0.58	AAGAATAAAGTGGGTTTGAAA	NM_181710:	NM_181710:
148066	ZNRF4	zinc and ring finger 4	-2.56	CAGCTTTGACTCCACCACCTA	NM_181710:	NM_181710:
54764	ZRANB1	zinc finger, RAN-binding domain containing 1	-0.40	CAGATCTGTAATGACCCTAAA	NM_017580:	NM_017580:
54764	ZRANB1	zinc finger, RAN-binding domain containing 1	0.38	CAAGGGTGAAATCTTCGTATA	NM_017580:	NM_017580:
84083	ZRANB3	zinc finger, RAN-binding domain containing 3	-1.95	CCGGATTCACATCTATACTAA	NM_032143:	NM_032143:
9183	ZW10	ZW10, kinetochore associated, homolog (Drosophila)	-0.49	ACCGGTGAATTTACAGACTTA	NM_004724:	NM_004724:
9183	ZW10	ZW10, kinetochore associated, homolog (Drosophila)	0.04	TACCACGAAGTGATGAATTTA	NM_004724:	NM_004724:
11130	ZWINT	ZW10 interactor	1.58	CAAATAAATATTTAAGGTTAA	NM_007057:	NM_001005413:NM_001005414:NM_007057:NM_032997:
11130	ZWINT	ZW10 interactor	2.49	CTGGTTTCAGATGTTCATTTA	NM_007057:	NM_032997:NM_007057:NM_001005413:NM_001005414: