Anabolic transcriptional changes in bone of hibernating black bears (*Ursus americanus*)

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Table S1 Primer sequences used for the real-time PCR tests in this study

Gene Symbol	Forward	Reverse
B4galt6	CAT TGC AAA TGG AGG TTC TTT	CCT CGC ATT GCA CTT GAT AC
Cav1	GTC TGA CCT TGG GGA CGT TA	TGT CCA TGC CAG TGT CTG TT
Cd47	ATC TCG TGA AGG AGA AAA CCA T	ATT AAA CCA AGT CCG CAA GAA T
Cfl1	TCT TCT GGG CAC CTG AGT CT	ATC CCC GTC AGC TTT TTC TT
Dcn	CCT CCT GCT TGC ACA AGT TT	GCC TAT CCC AGA AGC CTC AT
Ect2	GGT GAT TTT AGC CAC TAG CAA AT	CAC AAT TTC CCC ATG GTC TTA C
Fn1	CTC CAC TGG CCA CTA CAA CC	CGG GAA TCT TCT CTG TCA GC
Gpc3	TCC CCA AGC TTA TCA TGA CC	AGT CCC TGG CAG TAA GAG CA
Hoxa10	AGG TCT TGC ATT GTG GGA CT	GGG AGA ATT GTG GTG TGC TT
Lnpep	CAG ATG CAC CTT TAC CAA AGA A	AGT TCG TAG CGT AGT GGC ATA A
Mapk8	CTG ATC GTT CCT GGT GTG TG	TTA CGG GAA AGT CTG CTG CT
Mef2c	CAG CCA CTT GAA CCC TCA AT	GCA GGA AAT TAA CGC CAT GT
Omg	CCA TCT GGA CTG CAA GAG AA	GGC TTT CAA GCC TGT TGT TT
Prrx1	TGC ACT TTC AGC ACA CAT TT	TTC AGA TTG GTG GCT GTT TG
Sdc2	TGG AAA CCA CGA CAC TGA AG	AGC TGG GTC CAT TTT CCT TT
Srgn	TGG ATC TGG AAG TGG TTC TG	GGA CCA AGT CCT GGT TGT CT

Timp2	GCA ATG TGT TTT TGC TGG AC	CCG AGC GAT CAC TCA AGA AT
Ube2d3	TTG GAA GTC AAA CAC CCT TTG	AGC TCC AAG CCT CCT AAC AA
Yap1	AGG AAC AAA ATG AGC ATG GA	GCC ACT CTA ACT CAC GAC CAG
Zeb1	TGA GGG AGA AGA GGC AAA AA	TTC AGA CAC CTG CTC GCT ATT
Hint1	CCC TCA AGC ACC AAC TCA TT	CCA GAT CAG CAG CAC ATT TC

Table S2 List of differentially expressed genes identified in this study. Listed genes demonstrate significant expression differences between hibernating and summer active black bears in bone tissue. Genes are ranked by log$_2$FC (Fold Change), P is a significance level. Positive significant genes are up-regulated (positive values of log$_2$FC) and negative significant genes are down-regulated (negative values of log$_2$FC) in hibernating animals. Differentially expressed genes with P<0.01 are in bold. Complete description of the black bear EST collection can be found in The Black Bear Gene Index at http://compbio.dfci.harvard.edu/tgi/cgi-bin/tgi/T_release.pl?gudb=bear

Symbol	Gene name	Array	Clone_ID	P value	Log$_2$FC
Peg3	Paternally expressed 3	BA002	007_009_B11	0.012	2.080
Ndrg2	NDRG family member 2	BA002	005-012A_B09_2006-11-15	0.049	1.973
Gpc3	Glypican 3	BA002	008_031_O10	0.012	1.922
Csrp3	Cysteine and glycine-rich protein 3 (cardiac LIM protein)	BA002	005_007_E03	0.042	1.825
Prrx1	Paired related homeobox 1	BA002	007_014_A16	0.000	1.488
Znf681	Zinc finger protein 681	BA01	5222004_000_011D_E02_10	0.005	1.441
Ahnak	AHNAK nucleoprotein	BA002	005_010_K08	0.019	1.437
Loc727893	Phosphodiesterase 4D interacting protein	BA002	005_011_B22	0.024	1.421
Nnat	Neuronatin	BA002	007_022_P12	0.043	1.384
C10orf116	Chromosome 10 open reading frame 116	BA002	005-023C_H11_2006-11-16	0.018	1.380
Fat	FAT tumor suppressor homolog 1	BA002	007_021_J10	0.035	1.356
Lmo7	LIM domain 7	BA002	005-018A_C12_2006-10-13	0.002	1.317
Ptgis	Prostaglandin I2 (prostacyclin) synthase	BA002	008_006_N12	0.020	1.261
Nfib	Nuclear factor I/B	BA002	005_010_A05	0.000	1.245
Epb41l2	Erythrocyte membrane protein band 4.1-like 2	BA01	02102004A_000_008A_B7_B07_03	0.022	1.193

Fn1	Fibronectin 1	BA002	008_005_I14	0.027	1.192
Sgcb	Sarcoglycan, beta (43kda dystrophin-associated glycoprotein)	BA002	005-023D_D06_2006-11-16	0.012	1.188
Gtdc1	Glycosyltransferase-like domain containing 1	BA002	008-001C_B03_2006-11-07	0.006	1.180
Plekha5	Pleckstrin homology domain containing, family A member 5	BA002	007_005_A10	0.015	1.177
Cabc1	Aarf domain containing kinase 3 (chaperone-ABC1-like)	BA002	005-014C_E05_2006-10-05	0.049	1.173
Map1b	Microtubule-associated protein 1B	BA002	007_010_G14	0.035	1.165
Tm4sf1	Transmembrane 4 L six family member 1	BA002	005_005_I12	0.014	1.153
Timp2	TIMP metallopeptidase inhibitor 2	BA002	005_004_P03	0.021	1.138
Hif1an	Hypoxia inducible factor 1, alpha subunit inhibitor	BA002	005-021C_D02_2006-12-05	0.003	1.136
Sumo3	SMT3 suppressor of mif two 3 homolog 3	BA002	008_006_I02	0.001	1.121
Cmya5	Cardiomyopathy associated 5	BA01	004_006A_F08	0.025	1.108
Txnip	Thioredoxin interacting protein	BA002	011-015_N19	0.011	1.108
Olfml3	Olfactomedin-like 3	BA002	008_007_M22	0.024	1.094
Znf532	Zinc finger protein 532	BA002	007_025_D18	0.002	1.084
Kiaa1217	Kiaa1217	BA002	008_023_F10	0.029	1.083
Maged1	Melanoma antigen family D, 1	BA002	005-015B_D08_2006-10-21	0.017	1.079
Ecm2	Extracellular matrix protein 2, female organ and adipocyte specific	BA002	005_010_I20	0.015	1.069
Bhlhb2	Basic helix-loop-helix family, member e40	BA002	008B-001D_G10_2006-11-08	0.000	1.067
C12orf50	Chromosome 12 open reading frame 50	BA01	04192004_000_006C_G12_14	0.006	1.057
Mef2c	Myocyte enhancer factor 2C	BA002	007_026_C14	0.013	1.055
Cav1	Caveolin 1, caveolae protein	BA002	007_011_E01	0.023	1.055
Raph1	Ras association (ralgds/AF-6) and pleckstrin homology domains 1	BA002	008_008_C09	0.004	1.043
Timp3	TIMP metallopeptidase inhibitor 3	BA01	S401692.UAF-991-M13F	0.010	1.038
Ttc3	Tetratricopeptide repeat domain 3	BA01	001_002B_F01	0.008	1.034
Pls3	Plastin 3	BA002	007_013_O03	0.005	1.033
Tead1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	BA002	008_006_C10	0.007	1.022
Rnf126	Ring finger protein 126	BA01	004_002C_H06	0.048	1.007

Caprin2	Caprin family member 2	BA01	04202004A_000_009A_D04_08	0.010	0.983
Anxa3	Annexin A3	BA002	008_002_B17	0.005	0.980
C10orf56	Zinc finger, CCHC domain containing 24	BA002	008_012_F18	0.015	0.965
Ntrk2	Neurotrophic tyrosine kinase, receptor, type 2	BA002	007_004_O21	0.020	0.961
Thbs4	Thrombospondin 4	BA002	010-003B_A08_2007-03-28	0.011	0.959
Il33	Interleukin 33	BA002	008_028_D10	0.016	0.959
Tenc1	Tensin like C1 domain containing phosphatase (tensin 2)	BA002	005-015A_E04_2006-10-25	0.005	0.957
Znf383	Zinc finger protein 383	BA002	007_002_O02	0.002	0.955
Ppp1r3b	Protein phosphatase 1, regulatory (inhibitor) subunit 3B	BA002	008_005_L18	0.040	0.952
Nuak1	NUAK family, SNF1-like kinase, 1	BA002	008_004_K18	0.026	0.952
Kif21a	Kinesin family member 21A	BA002	007_024_J07	0.000	0.949
Tceal2	Transcription elongation factor A (SII)-like 2	BA002	007-019C_B05_2006-10-17	0.010	0.938
Dcn	Decorin	BA01	004_004A_C03	0.002	0.936
Mbnl2	Muscleblind-like 2	BA002	007_010_O08	0.029	0.932
Tnni3	Troponin I type 3	BA002	005-019C_B06_2006-12-01	0.016	0.910
Thbs1	Thrombospondin 1	BA002	008_021_M01	0.028	0.905
Rbp4	Retinol binding protein 4, plasma	BA002	008_016_J20	0.022	0.898
Bhlhb9	Basic helix-loop-helix domain containing, class B, 9	BA002	005-017B_A04_2006-11-06	0.000	0.897
Akap11	A kinase (PRKA) anchor protein 11	BA002	007_006_P11	0.037	0.894
Rtn2	Reticulon 2	BA002	007_013_N22	0.017	0.893
R3hdm2	R3H domain containing 2	BA002	005-016D_H11_2006-11-10	0.002	0.892
Sdc2	Syndecan 2	BA002	007_026_A24	0.013	0.889
Kalrn	Kalirin, rhogef kinase	BA002	007_031_N14	0.023	0.884
Tmeff1	Transmembrane protein with EGF-like and two follistatin-like domains 1	BA002	007_021_F15	0.006	0.880
Cmbl	Carboxymethylenebutenolidase homolog	BA01	001_001C_G09	0.032	0.877
Zfp36l1	Zinc finger protein 36, C3H type-like 1	BA01	UAhib_3612.y1_010	0.020	0.871
C5orf13	Chromosome 5 open reading frame 13	BA002	008_024_C14	0.029	0.863
Aldh1a3	Aldehyde dehydrogenase 1 family, member A3	BA002	008_008_A10	0.005	0.861
Auts2	Autism susceptibility candidate 2	BA002	008_008_C19	0.030	0.851
Dstn	Destrin (actin depolymerizing factor)	BA002	007_022_H03	0.039	0.848
Ehbp1	EH domain binding protein 1	BA002	005_004_H20	0.036	0.847

Pfn2	Profilin 2	BA002	005_010_D03	0.000	0.841
Zeb1	Zinc finger E-box binding homeobox 1	BA002	007_008_A08	0.000	0.841
Mapk8	Mitogen-activated protein kinase 8	BA002	007_008_P23	0.006	0.837
Rbm3	RNA binding motif (RNP1, RRM) protein 3	BA01	TC146	0.021	0.833
Prosp	Protein S pseudogene (beta)	BA002	008_020_G15	0.011	0.831
Hoxa10	Homeobox A10	BA002	011-007_O17	0.008	0.831
Tef	Thyrotrophic embryonic factor	BA002	007_011_L01	0.032	0.828
Kif13a	Kinesin family member 13A	BA002	007_030_E07	0.020	0.823
Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	BA002	007-019D_F04_2006-11-01	0.010	0.820
Nudt7	Nudix (nucleoside diphosphate linked moiety X)-type motif 7	BA002	008_016_I08	0.002	0.815
Uba1	Ubiquitin-like modifier activating enzyme 1	BA01	12162003a_000_004_B6_B06_04	0.006	0.812
Kctd18	Potassium channel tetramerisation domain containing 18	BA002	008_016_M10	0.002	0.809
Arid1b	AT rich interactive domain 1B (SWI1-like)	BA002	008_023_O18	0.029	0.804
Dock9	Dedicator of cytokinesis 9	BA01	04192004_000_006C_F03_11	0.007	0.796
Bbs2	Bardet-Biedl syndrome 2	BA002	007_020_L07	0.001	0.796
Pcbp2	Poly(rc) binding protein 2	BA01	UAhib_1460.y1_058	0.003	0.796
Malat1	Metastasis associated lung adenocarcinoma transcript 1	BA002	011-011_F10	0.018	0.795
Msrb3	Methionine sulfoxide reductase B3	BA002	005_011_N19	0.016	0.785
Prepl	Prolyl endopeptidase-like	BA002	007_031_B19	0.003	0.783
Phldb2	Pleckstrin homology-like domain, family B, member 2	BA01	UAhib_1549.y1_063	0.007	0.781
Zfyve21	Zinc finger, FYVE domain containing 21	BA002	007_007_K20	0.017	0.781
Tspan7	Tetraspanin 7	BA01	TC101	0.037	0.778
Casd1	CAS1 domain containing 1	BA002	007_003_K22	0.018	0.774
Lifr	Leukemia inhibitory factor receptor alpha	BA002	005-016B_G08_2006-11-22	0.047	0.771
Schip1	Schwannomin interacting protein 1	BA01	004_004B_G05	0.025	0.769
Wwp1	WW domain containing E3 ubiquitin protein ligase 1	BA002	008_005_P09	0.008	0.769
C17orf58	Chromosome 17 open reading frame 58	BA002	007_005_F20	0.048	0.768
Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	BA002	007_020_E16	0.018	0.765

Fam13c1	Family with sequence similarity 13, member C	BA002	008_004_P15	0.034	0.765
Bhmt2	Betaine--homocysteine S-methyltransferase 2	BA002	008_014_L22	0.039	0.763
Glo1	Glyoxalase I	BA002	007_012_E21	0.005	0.760
S100a10	S100 calcium binding protein A10	BA002	005-012C_E03_2006-11-28	0.014	0.756
Ptprb	Protein tyrosine phosphatase, receptor type, B	BA002	007_009_F22	0.002	0.755
Sfpq	Splicing factor proline/glutamine-rich	BA002	008_006_F17	0.007	0.754
Fap	Fibroblast activation protein, alpha	BA002	005_008_A09	0.002	0.751
Mysm1	Myb-like, SWIRM and MPN domains 1	BA01	04122004_000-006A_E11_09	0.035	0.746
Klf10	Kruppel-like factor 10	BA002	008_023_G04	0.042	0.746
C6orf145	Chromosome 6 open reading frame 145	BA002	008_014_M09	0.001	0.743
Cald1	Caldesmon 1	BA01	UAhib_3471.y1_067	0.041	0.741
Fam54b	Family with sequence similarity 54, member B	BA002	005-023D_E10_2006-11-16	0.015	0.734
Clk1	CDC-like kinase 1	BA002	005-023B_C03_2006-11-11	0.027	0.732
Csde1	Cold shock domain containing E1, RNA-binding	BA002	008B-001C_G03_2006-11-09	0.010	0.728
Tceal4	Transcription elongation factor A (SII)-like 4	BA002	013-006_J12	0.002	0.727
Svil	Supervillin	BA002	011-005_L17	0.025	0.727
Atp2b1	Atpase, Ca++ transporting, plasma membrane 1	BA002	008_002_G24	0.027	0.724
Spink2	Serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	BA002	007_008_A16	0.047	0.718
Sptbn1	Spectrin, beta, non-erythrocytic 1	BA01	04202004A_000_009A_C06_06	0.017	0.716
Rragb	Ras-related GTP binding B	BA01	05202004A_000_011B_B01_03	0.002	0.714
Tle1	Transducin-like enhancer of split 1	BA002	005-023D_G09_2006-11-16	0.000	0.711
Jam2	Junctional adhesion molecule 2	BA002	011-013_A10	0.002	0.709
Tcea3	Transcription elongation factor A (SII), 3	BA002	011-015_D09	0.001	0.708
Ttn	Titin	BA01	004_001D_G09	0.004	0.702
Zmym5	Zinc finger, MYM-type 5	BA01	05202004_001_011A_F03_11	0.005	0.700
Fbxo25	F-box protein 25	BA002	007_029_F11	0.010	0.700
Tbc1d12	TBC1 domain family, member 12	BA002	007_003_F19	0.036	0.699
Armcx3	Armadillo repeat containing, X-linked 3	BA002	007_008_L17	0.020	0.696
Pftk1	Cyclin-dependent kinase 14	BA002	014-007_A04	0.034	0.696
Frap1	Mechanistic target of rapamycin	BA002	005-021D_B11_2006-12-05	0.000	0.695

	(serine/threonine kinase)				
Clu	Clusterin	BA01	TC231	0.014	0.693
Tacc2	Transforming, acidic coiled-coil containing protein 2	BA01	TC568	0.034	0.682
Gnai1	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	BA002	005_006_E16	0.013	0.679
Kcmf1	Potassium channel modulatory factor 1	BA01	TC322	0.012	0.677
Fhod3	Formin homology 2 domain containing 3	BA002	007_033_H06	0.014	0.675
Itm2a	Integral membrane protein 2A	BA002	007_008_B20	0.009	0.667
Anxa1	Annexin A1	BA01	TC370	0.022	0.664
Col15a1	Collagen, type XV, alpha 1	BA002	005-013A_G02_2006-10-06	0.044	0.661
Fdft1	Farnesyl-diphosphate farnesyltransferase 1	BA01	004_001C_F11	0.021	0.660
Tspan3	Tetraspanin 3	BA01	001_001D_C04	0.002	0.660
Htra1	Htra serine peptidase 1	BA002	008_032_O15	0.006	0.658
Rtn4	Reticulon 4	BA002	007_003_G04	0.030	0.657
C5orf35	Chromosome 5 open reading frame 35	BA002	005-013B_A07_2006-10-27	0.017	0.657
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	BA01	05202004A_000_011B_B05_03	0.026	0.656
Camk2d	Calcium/calmodulin-dependent protein kinase II delta	BA002	007_012_J13	0.031	0.655
Obfc1	Oligonucleotide/oligosaccharide-binding fold containing 1	BA002	007-019A_H05_2006-10-18	0.016	0.652
Ccdc76	Coiled-coil domain containing 76	BA01	UAhib_0383.y1_091	0.016	0.651
Aga	Aspartylglucosaminidase	BA002	007_011_M02	0.040	0.650
Znf510	Zinc finger protein 510	BA002	005-024A_B09_2006-11-15	0.049	0.650
Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	BA002	007_031_E24	0.018	0.647
B3galnt1	Beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	BA002	008_026_E05	0.014	0.646
Cdh5	Cadherin 5, type 2 (vascular endothelium)	BA002	008_027_D17	0.009	0.639
Myo1b	Myosin IB	BA002	006-001A_E03_2006-10-10	0.044	0.632
Lnpep	Leucyl/cystinyl aminopeptidase	BA002	007_024_F08	0.041	0.631
Flj32549	Flj32549	BA01	04122004a_000-006D_C05_05	0.040	0.628
Ndrg3	NDRG family member 3	BA01	TC424	0.027	0.626
Sphar	S-phase response (cyclin related)	BA002	007_006_O12	0.000	0.623
Tmub2	Transmembrane and ubiquitin-like domain containing 2	BA002	007_009_L03	0.004	0.622

Gtf3a	General transcription factor IIIA	BA002	008_002_F03	0.006	0.620
Dhrs3	Dehydrogenase/reductase (SDR family) member 3	BA002	008_023_I12	0.041	0.618
Ankrd13d	Ankyrin repeat domain 13 family, member D	BA002	007_030_J08	0.021	0.614
Cpsf4	Cleavage and polyadenylation specific factor 4	BA002	007_030_H22	0.025	0.611
Brd9	Bromodomain containing 9	BA002	007_001_J20	0.049	0.609
Pogk	Pogo transposable element with KRAB domain	BA002	008-001D_H06_2006-11-07	0.011	0.608
Igf1	Insulin-like growth factor 1 (somatomedin C)	BA01	TC606	0.042	0.608
Fgf13	Fibroblast growth factor 13	BA01	003_002A_G08	0.036	0.607
Mgst2	Microsomal glutathione S-transferase 2	BA002	005-015C_D03_2006-10-20	0.004	0.603
Qki	Quaking homolog, KH domain RNA binding	BA002	008_027_C15	0.048	0.603
Ggcx	Gamma-glutamyl carboxylase	BA002	008_027_K13	0.007	0.602
Gng11	Guanine nucleotide binding protein (G protein), gamma 11	BA002	005_011_P09	0.034	0.602
Echdc2	Enoyl coa hydratase domain containing 2	BA002	008B-001B_G05_2006-10-28	0.001	0.601
Blcap	Bladder cancer associated protein	BA01	003_001C_G07	0.020	0.599
Yap1	Yes-associated protein 1	BA002	005-012A_E02_2006-11-15	0.011	0.598
H3f3b	H3 histone, family 3B (H3.3B)	BA002	005-022C_A07_2006-11-22	0.018	0.598
Synpr	Synaptoporin	BA01	05202004_001_011A_D09_07	0.037	0.593
Rxra	Retinoid X receptor, alpha	BA002	008_023_N15	0.015	0.589
Flj40235	Chromosome 19 open reading frame 75	BA002	008_002_L07	0.011	0.588
Nfic	Nuclear factor I/C (CCAAT-binding transcription factor)	BA002	007_013_J18	0.030	0.588
Trim45	Tripartite motif-containing 45	BA002	010-001B_H02_2007-04-02	0.008	0.587
Bcl6	B-cell CLL/lymphoma 6	BA002	005_010_H04	0.021	0.587
Cwf19l2	CWF19-like 2, cell cycle control	BA002	007_012_P12	0.010	0.587
Vtn	Vitronectin	BA002	008-001B_G03_2006-10-27	0.006	0.586
Pdgfc	Platelet derived growth factor C	BA002	007_013_E23	0.041	0.586
Cmpk1	Cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	BA01	UAhib_1011.y1_012	0.038	0.583
Slc25a20	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	BA002	005-021B_G02_2006-12-06	0.013	0.581
Loc647307	Phosphatidylethanolamine binding protein 1	BA002	006-001A_F03_2006-10-10	0.004	0.580
Rabep1	Rabaptin, RAB gtpase binding effector protein 1	BA002	007_031_F22	0.039	0.573
Dnal1	Dynein, axonemal, light chain 1	BA002	007_009_A18	0.019	0.571

Zak	Sterile alpha motif and leucine zipper containing kinase AZK	BA002	014-001A_G02_2007-06-11	0.011	0.571
Ccnt2	Cyclin T2	BA002	005-020A_D10_2006-11-10	0.033	0.569
Sox9	SRY (sex determining region Y)-box 9	BA01	TC535	0.010	0.568
C2orf16	Chromosome 2 open reading frame 16	BA002	008_022_C22	0.001	0.565
Als2cr4	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	BA002	008_005_O12	0.047	0.565
Prpf39	PRP39 pre-mrna processing factor 39 homolog	BA002	008_025_E16	0.022	0.564
Nhp2l1	NHP2 non-histone chromosome protein 2-like 1	BA01	004_002D_F10	0.005	0.564
Socs6	Suppressor of cytokine signaling 6	BA002	008_021_N16	0.017	0.562
Homer1	Homer homolog 1	BA002	008_007_F24	0.040	0.560
C14orf143	Chromosome 14 open reading frame 143	BA002	007_010_D08	0.034	0.555
Ptprd	Protein tyrosine phosphatase, receptor type, D	BA01	12162003a_000_004_D6_D06_08	0.039	0.553
Ssfa2	Sperm specific antigen 2	BA01	05142004_000_010B_G11_13	0.035	0.552
Myst2	MYST histone acetyltransferase 2	BA01	004_005C_E02	0.018	0.549
C8orf59	Chromosome 8 open reading frame 59	BA002	008B-001B_A05_2006-10-28	0.035	0.545
Bex2	Brain expressed X-linked 2	BA002	007B-001A_H03_2006-10-18	0.011	0.543
Nfu1	NFU1 iron-sulfur cluster scaffold homolog	BA002	005-022C_G05_2006-11-22	0.011	0.541
Gltpd1	Glycolipid transfer protein domain containing 1	BA002	008_006_C09	0.015	0.539
Calcoco2	Calcium binding and coiled-coil domain 2	BA002	008_030_J20	0.036	0.536
Asphd1	Aspartate beta-hydroxylase domain containing 1	BA002	007_002_D14	0.017	0.534
Kiaa1737	Kiaa1737	BA002	007_012_A11	0.018	0.529
Prg-3	Proteoglycan 3	BA002	014-004_G07	0.022	0.529
Znf331	Zinc finger protein 331	BA002	008-001A_C08_2006-11-02	0.038	0.528
Pon1	Paraoxonase 1	BA002	006-001A_B04_2006-10-10	0.046	0.526
C14orf179	Chromosome 14 open reading frame 179	BA002	005-012C_G03_2006-11-28	0.040	0.525
Loc93622	Hypothetical LOC93622	BA002	007_028_F19	0.024	0.524
Fbxw11	F-box and WD repeat domain containing 11	BA002	007_028_J14	0.025	0.523
Chl1	Cell adhesion molecule with homology to L1CAM (close homolog of L1)	BA002	007_003_M03	0.033	0.522

Mllt11	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	BA01	12162003_000_003_D3_D03_07	0.049	0.519
Pard3	Par-3 partitioning defective 3 homolog	BA002	007_020_M15	0.020	0.519
Ctsf	Cathepsin F	BA002	007_009_A07	0.032	0.516
Igf1r	Insulin-like growth factor 1 receptor	BA01	004_003A_H12	0.005	0.515
Jmjd4	Jumonji domain containing 4	BA002	007_008_P04	0.027	0.515
Ankmy2	Ankyrin repeat and MYND domain containing 2	BA002	008-001C_B09_2006-11-08	0.025	0.515
Pnpla8	Patatin-like phospholipase domain containing 8	BA01	04022004A_000_007D_G10_14	0.014	0.512
Prox1	Prospero homeobox 1	BA002	008_027_O17	0.020	0.512
Zdhhc9	Zinc finger, DHHC-type containing 9	BA01	004_006B_C11	0.025	0.512
Prtfdc1	Phosphoribosyl transferase domain containing 1	BA01	003_003B_F06	0.012	0.506
Myo6	Myosin VI	BA002	005-018D_A01_2006-10-25	0.012	0.503
Sub1	SUB1 homolog	BA01	35_C05	0.002	-0.500
Krr1	KRR1, small subunit (SSU) processome component, homolog	BA002	007_025_F06	0.016	-0.500
Sft2d1	SFT2 domain containing 1	BA002	008_020_J12	0.037	-0.502
Ubxd2	UBX domain protein 4	BA002	005-016B_C02_2006-11-22	0.018	-0.502
Commd6	COMM domain containing 6	BA002	014-001D_E01_2007-06-15	0.030	-0.503
Chchd2	Coiled-coil-helix-coiled-coil-helix domain containing 2	BA01	TC602	0.004	-0.504
Fam108b1	Family with sequence similarity 108, member B1	BA002	007-019C_B11_2006-10-18	0.038	-0.505
Rtcd1	RNA terminal phosphate cyclase domain 1	BA01	TC337	0.017	-0.505
Rbm8a	RNA binding motif protein 8A	BA01	05222004_000_011C_A07_01	0.003	-0.507
Ccrk	Cyclin-dependent kinase 20	BA002	007_029_N06	0.035	-0.507
Aldh9a1	Aldehyde dehydrogenase 9 family, member A1	BA002	011-005_K02	0.043	-0.509
Appl2	Adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	BA002	005-017A_E12_2006-11-07	0.005	-0.509
C19orf2	Chromosome 19 open reading frame 2	BA002	008_008_G13	0.010	-0.510
Supt4h1	Suppressor of Ty 4 homolog 1	BA002	005_010_O16	0.026	-0.514
C4orf15	HAUS augmin-like complex, subunit 3	BA01	04192004_000_006C_B06_04	0.010	-0.515
Mrpl3	Mitochondrial ribosomal protein	BA002	007_029_H03	0.005	-0.515

	L3				
Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A	BA002	008_018_H05a	0.002	-0.516
Hprt1	Hypoxanthine phosphoribosyltransferase 1	BA002	005-001C_A06_2006-08-17	0.036	-0.517
Ier5	Immediate early response 5	BA002	007_025_I09	0.032	-0.517
Crym	Crystallin, mu	BA002	007_027_I23	0.013	-0.517
Tmem126b	Transmembrane protein 126B	BA002	005_006_C21	0.029	-0.518
Psma5	Proteasome (prosome, macropain) subunit, alpha type, 5	BA01	02192004_000_005A_E3_F02_12	0.049	-0.518
Nipsnap3a	Nipsnap homolog 3A	BA002	008_025_B12	0.030	-0.518
Ssbp1	Single-stranded DNA binding protein 1	BA002	005-018A_A06_2006-10-12	0.013	-0.519
Lpgat1	Lysophosphatidylglycerol acyltransferase 1	BA002	005_005_J04	0.040	-0.523
Decr1	2,4-dienoyl coa reductase 1, mitochondrial	BA01	004_003D_B10	0.014	-0.527
Elof1	Elongation factor 1 homolog	BA002	007_007_G03	0.023	-0.527
Bnip3l	BCL2/adenovirus E1B 19kda interacting protein 3-like	BA01	UAhib_1438.y1_037	0.035	-0.528
Naca	Nascent polypeptide-associated complex alpha subunit	BA01	TC645	0.034	-0.528
Rab9a	RAB9A, member RAS oncogene family	BA002	005-025B_C03_2006-10-14	0.015	-0.529
Mrpl39	Mitochondrial ribosomal protein L39	BA002	007_009_M16	0.015	-0.529
Wdr61	WD repeat domain 61	BA002	007_027_G21	0.039	-0.531
Eny2	Enhancer of yellow 2 homolog	BA002	005_010_L03	0.013	-0.531
Fbn2	Fibrillin 2	BA002	007_007_O05	0.021	-0.533
Cip29	SAP domain containing ribonucleoprotein	BA002	007_026_F11	0.016	-0.534
Rpn2	Ribophorin II	BA01	05222004_000_011C_G06_14	0.012	-0.535
Fam120a	Family with sequence similarity 120A	BA002	005_004_L02	0.022	-0.537
Ncbp2	Nuclear cap binding protein subunit 2	BA002	005-013A_C08_2006-10-06	0.031	-0.537
Itgb1bp1	Integrin beta 1 binding protein 1	BA002	007_002_H14	0.012	-0.545
Ap4m1	Adaptor-related protein complex 4, mu 1 subunit	BA002	007_003_G21	0.024	-0.546
Adam10	ADAM metallopeptidase domain 10	BA01	004_003B_B04	0.001	-0.547
Gpr22	G protein-coupled receptor 22	BA002	007_001_D22	0.031	-0.548
Mad2l1	MAD2 mitotic arrest deficient-like 1	BA01	TC470	0.002	-0.549
Ccdc72	Coiled-coil domain containing 72	BA002	005_001A_F05_F05_2006-05-12	0.018	-0.551
C21orf66	GC-rich sequence DNA-binding	BA002	007_002_A19	0.047	-0.552

	factor 1				
Amd1	Adenosylmethionine decarboxylase 1	BA002	007_020_D07	0.035	-0.552
Ints9	Integrator complex subunit 9	BA002	011-008_P12	0.015	-0.553
C1orf31	Chromosome 1 open reading frame 31	BA01	TC674	0.028	-0.554
Csnk2a1	Casein kinase 2, alpha 1 polypeptide	BA002	005-023D_F01_2006-11-16	0.023	-0.555
Arf3	ADP-ribosylation factor 3	BA002	014-004_C08	0.028	-0.555
Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	BA01	12162003_000_003_E9_E09_09	0.007	-0.556
C10orf84	Chromosome 10 open reading frame 84	BA002	005_011_F15	0.029	-0.557
Prdm2	PR domain containing 2, with ZNF domain	BA002	005_008_B15	0.022	-0.558
Vrk1	Vaccinia related kinase 1	BA01	TC500	0.017	-0.559
Ube2d3	Ubiquitin-conjugating enzyme E2D 3	BA01	UAhib_1637.y1_039	0.000	-0.559
Psenen	Presenilin enhancer 2 homolog	BA002	007_030_L01	0.006	-0.559
Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	BA002	007-019C_C03_2006-10-17	0.017	-0.561
Mtch2	Mitochondrial carrier homolog 2	BA002	007_014_C13	0.024	-0.561
Ap2b1	Adaptor-related protein complex 2, beta 1 subunit	BA002	007_031_G09	0.028	-0.563
Bcap31	B-cell receptor-associated protein 31	BA002	007_004_P19	0.039	-0.563
Pten	Phosphatase and tensin homolog	BA002	008-001B_F10_2006-10-27	0.034	-0.565
Supt16h	Suppressor of Ty 16 homolog	BA002	007_005_I19	0.045	-0.566
Loc100129513	Magnesium transporter 1	BA01	UAhib_0558.y1_062	0.006	-0.566
Prdx3	Peroxiredoxin 3	BA01	01082004_000_001_B6_B06_04	0.002	-0.566
Pold3	Polymerase (DNA-directed), delta 3, accessory subunit	BA002	007_005_I08	0.046	-0.566
Nudcd1	Nudc domain containing 1	BA002	007_007_N11	0.019	-0.566
Cct5	Chaperonin containing TCP1, subunit 5 (epsilon)	BA01	004_003B_D12	0.002	-0.569
Herc1	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	BA002	008_008_C03	0.044	-0.569
Camk2b	Calcium/calmodulin-dependent protein kinase II beta	BA002	007_031_P24	0.007	-0.569
Prickle4	Prickle homolog 4	BA002	011-003_B10	0.041	-0.570
Hnrnpa1	Heterogeneous nuclear ribonucleoprotein A1	BA002	008B-001A_E12_2006-10-31	0.040	-0.570
Myd88	Myeloid differentiation primary	BA002	008_013_L23	0.009	-0.571

	response gene (88)				
Ilf3	Interleukin enhancer binding factor 3, 90kda	BA002	008_019_L13	0.015	-0.571
Hsp90b1	Heat shock protein 90kda beta (Grp94), member 1	BA01	TC258	0.021	-0.572
Cab39	Calcium binding protein 39	BA01	04122004a_000-006D_B05_03	0.027	-0.573
Ccdc49	CWC25 spliceosome-associated protein homolog	BA002	005-016C_A01_2006-11-03	0.004	-0.576
Papola	Poly(A) polymerase alpha	BA002	008_029_K07	0.024	-0.576
Rars2	Arginyl-trna synthetase 2, mitochondrial	BA002	005_005_F11	0.039	-0.577
Dnajb4	Dnaj (Hsp40) homolog, subfamily B, member 4	BA002	007_030_K18	0.026	-0.578
Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	BA01	TC414	0.002	-0.579
Tmem183a	Transmembrane protein 183A	BA01	05152004_000_010C_E01_09	0.015	-0.581
Actr6	ARP6 actin-related protein 6 homolog	BA01	01082004A_000_002_B6_B06_04	0.004	-0.582
Mrlc2	Myosin, light chain 12B, regulatory	BA002	007B-001A_A03_2006-10-18	0.002	-0.583
Atp2c1	Atpase, Ca++ transporting, type 2C, member 1	BA002	008_012_O13	0.031	-0.583
Pip4k2c	Phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	BA002	008_032_E09	0.049	-0.584
Aig1	Androgen-induced 1	BA002	007-019C_F06_2006-10-17	0.012	-0.585
Gde1	Glycerophosphodiester phosphodiesterase 1	BA002	007_020_A08	0.043	-0.586
Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	BA002	005-015D_F07_2006-10-26	0.005	-0.586
Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3	BA002	005_005_K22	0.013	-0.587
Psmd5	Proteasome (prosome, macropain) 26S subunit, non-atpase, 5	BA002	007_024_L04	0.030	-0.587
Bckdk	Branched chain ketoacid dehydrogenase kinase	BA002	007_010_B21	0.016	-0.588
C5orf32	Chromosome 5 open reading frame 32	BA002	005-014B_E06_2006-11-03	0.031	-0.590
Lca5	Leber congenital amaurosis 5	BA002	007_023_E02	0.034	-0.591
Ppil3	Peptidylprolyl isomerase (cyclophilin)-like 3	BA002	007_006_H01	0.003	-0.592
Sfrs6	Serine/arginine-rich splicing factor 6	BA002	007_029_D22	0.018	-0.595

Ppp1cb	Protein phosphatase 1, catalytic subunit, beta isozyme	BA01	TC657	0.002	-0.597
Sugt1	SGT1, suppressor of G2 allele of SKP1	BA002	008_003_N24	0.016	-0.604
Shfm1	Split hand/foot malformation (ectrodactyly) type 1	BA002	005-017A_F03_2006-11-07	0.002	-0.606
Gpsm3	G-protein signaling modulator 3	BA002	008_010_G12	0.014	-0.606
Nolc1	Nucleolar and coiled-body phosphoprotein 1	BA002	008_014_K06	0.003	-0.607
Vps72	Vacuolar protein sorting 72 homolog	BA002	008_003_H01	0.040	-0.607
Snta1	Syntrophin, alpha 1 (dystrophin-associated protein A1, 59kda, acidic component)	BA002	011-006_G18	0.021	-0.608
Lypla2	Lysophospholipase II	BA002	007_030_J21	0.008	-0.610
Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	BA002	007_033_H08	0.013	-0.612
Ccdc56	Coiled-coil domain containing 56	BA002	008-001A_F10_2006-11-02	0.028	-0.615
Kiaa1429	Kiaa1429	BA002	007_027_M02	0.023	-0.615
Acadl	Acyl-coa dehydrogenase, long chain	BA002	008_007_C13	0.018	-0.615
C17orf37	Chromosome 17 open reading frame 37	BA002	007_001_H16	0.003	-0.615
Snrpd1	Small nuclear ribonucleoprotein D1 polypeptide	BA01	UAhib_3679.y1_068	0.002	-0.616
Hsp90aa1	Heat shock protein 90kda alpha (cytosolic), class A member 1	BA01	TC261	0.012	-0.617
Atp6v1b2	Atpase, H+ transporting, lysosomal 56/58kda, V1 subunit B2	BA01	04202004A_000_009A_B03_03	0.043	-0.618
Sult1b1	Sulfotransferase family, cytosolic, 1B, member 1	BA002	008_011_F21	0.020	-0.620
Acat1	Acetyl-coa acetyltransferase 1	BA002	007_002_I20	0.016	-0.622
Gnb1	Guanine nucleotide binding protein (G protein), beta polypeptide 1	BA002	008_031_B10	0.006	-0.623
Atp6v1d	Atpase, H+ transporting, lysosomal 34kda, V1 subunit D	BA002	007_003_H12	0.036	-0.624
Camta1	Calmodulin binding transcription activator 1	BA002	008_015_H11	0.034	-0.624
Tmem229a	Transmembrane protein 229A	BA002	007_004_M21	0.018	-0.624
Ap3b1	Adaptor-related protein complex 3, beta 1 subunit	BA01	04022004A_000_007D_H05_15	0.037	-0.624
Copz1	Coatomer protein complex, subunit zeta 1	BA002	008_013_A22	0.011	-0.631
Coro1c	Coronin, actin binding protein, 1C	BA002	007_013_B08	0.002	-0.634
Ostm1	Osteopetrosis associated	BA002	008_025_H18	0.003	-0.634

	transmembrane protein 1				
Pla2g4a	Phospholipase A2, group IVA (cytosolic, calcium-dependent)	BA002	007_027_A02	0.000	-0.635
Znf19	Zinc finger protein 19	BA002	005-013D_A08_2006-11-18	0.043	-0.636
Nola2	NHP2 ribonucleoprotein homolog	BA002	008B-001C_F04_2006-11-09	0.011	-0.637
Gbe1	Glucan (1,4-alpha-), branching enzyme 1	BA002	013-007_K20	0.014	-0.638
Nudt3	Nudix (nucleoside diphosphate linked moiety X)-type motif 3	BA01	UAhib_3067.y1_075	0.006	-0.639
Tmbim4	Transmembrane BAX inhibitor motif containing 4	BA01	004_004A_F07	0.005	-0.639
Parp6	Poly (ADP-ribose) polymerase family, member 6	BA002	005_007_E22	0.046	-0.640
Pef1	Penta-EF-hand domain containing 1	BA002	007_001_A16	0.040	-0.641
Ttll12	Tubulin tyrosine ligase-like family, member 12	BA01	003_003C_F05	0.050	-0.642
Hnrpk	Heterogeneous nuclear ribonucleoprotein K	BA002	007_031_I08	0.048	-0.643
Cnot8	CCR4-NOT transcription complex, subunit 8	BA002	007_022_L05	0.008	-0.645
Sec23b	Sec23 homolog B	BA002	008_024_E03	0.033	-0.645
Sec11a	SEC11 homolog A	BA002	007_009_F16	0.034	-0.646
Sorcs3	Sortilin-related VPS10 domain containing receptor 3	BA002	007_003_B23	0.029	-0.646
Sms	Spermine synthase	BA01	05132004A_000_010A_C04_06	0.003	-0.646
Oat	Ornithine aminotransferase	BA01	003_001C_C07	0.017	-0.648
Loc644961	Actin, cytoplasmic 2-like	BA01	05152004A_000_010D_G04_14	0.018	-0.648
Rpl15	Ribosomal protein L15	BA002	005-015A_B09_2006-10-25	0.039	-0.648
Scarna2	Small Cajal body-specific RNA 2	BA002	007_005_A19	0.015	-0.649
Ptpre	Protein tyrosine phosphatase, receptor type, E	BA002	008_016_H04	0.010	-0.650
Anxa6	Annexin A6	BA002	007_014_K12	0.047	-0.652
Tapbp	Binding protein (tapasin)	BA002	007_022_P14	0.022	-0.653
Amica1	Adhesion molecule, interacts with CXADR antigen 1	BA002	005-016D_F02_2006-11-10	0.003	-0.653
Ppp1cc	Protein phosphatase 1, catalytic subunit, gamma isozyme	BA002	008_016_H19	0.042	-0.656
Rbmx	RNA binding motif protein, X-linked	BA002	007_008_B11	0.008	-0.657
M6pr	Mannose-6-phosphate receptor (cation dependent)	BA002	005-017B_F02_2006-11-06	0.049	-0.658
Rap1b	RAP1B, member of RAS oncogene family	BA01	004_003B_A05	0.028	-0.659
Cisd2	CDGSH iron sulfur domain 2	BA002	005-024D_A12_2006-12-16	0.044	-0.660
Psma4	Proteasome (prosome,	BA002	005-016A_D09_2006-11-03	0.025	-0.661

	macropain) subunit, alpha type, 4				
Pafah1b2	Platelet-activating factor acetylhydrolase 1b, catalytic subunit 2	BA002	008_024_F22	0.000	-0.662
Pomp	Proteasome maturation protein	BA002	007_025_C17	0.005	-0.662
Mrpl34	Mitochondrial ribosomal protein L34	BA002	007_003_J03	0.014	-0.662
Slc27a5	Solute carrier family 27 (fatty acid transporter), member 5	BA002	008_011_M20	0.022	-0.665
Pafah1b1	Platelet-activating factor acetylhydrolase 1b, regulatory subunit 1	BA002	005-025C_F12_2006-12-08	0.021	-0.665
Adss	Adenylosuccinate synthase	BA002	008_003_J20	0.026	-0.667
Bcap29	B-cell receptor-associated protein 29	BA002	005_005_H15	0.033	-0.667
Mphosph6	M-phase phosphoprotein 6	BA002	008_024_E08	0.034	-0.667
Spcs3	Signal peptidase complex subunit 3 homolog	BA002	007_008_P03	0.043	-0.668
Fmnl1	Formin-like 1	BA002	007_009_P11	0.000	-0.670
C11orf73	Chromosome 11 open reading frame 73	BA002	005_007_B07	0.023	-0.671
Nup62	Nucleoporin 62kda	BA002	011-006_D19	0.003	-0.673
St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	BA002	007-019B_H10_2006-10-19a	0.003	-0.674
Ostf1	Osteoclast stimulating factor 1	BA002	007_031_J09	0.050	-0.675
Loc100131801	Hypothetical protein LOC100131801	BA01	004_005A_D10	0.035	-0.676
C10orf97	Family with sequence similarity 188, member A	BA002	001_002B_A08	0.047	-0.676
Gmfg	Glia maturation factor, gamma	BA002	008_014_A16	0.041	-0.679
Wdr12	WD repeat domain 12	BA01	05152004A_000_010D_G10_14	0.001	-0.679
Loc642384	Hypothetical LOC642384	BA01	004_005A_H10	0.043	-0.680
Cacybp	Calcyclin binding protein	BA01	TC626	0.000	-0.681
Ube2n	Ubiquitin-conjugating enzyme E2N	BA002	007_012_A17	0.001	-0.681
Gpd2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	BA002	007_012_E19	0.011	-0.682
Dap3	Death associated protein 3	BA002	007_010_D13	0.014	-0.682
Mrpl18	Mitochondrial ribosomal protein L18	BA002	008_027_G14	0.007	-0.682
Gpx4	Glutathione peroxidase 4 (phospholipid hydroperoxidase)	BA002	007_005_M04	0.038	-0.684
Mgat2	Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	BA002	008_022_E13	0.044	-0.685

Suclg2	Succinate-coa ligase, GDP-forming, beta subunit	BA002	008B-001A_C08_2006-10-30	0.015	-0.685
U2af1	U2 small nuclear RNA auxiliary factor 1	BA002	007_009_P21	0.047	-0.685
Serpinb1	Serpin peptidase inhibitor, clade B (ovalbumin), member 1	BA01	UAhib_1296.y1_082	0.001	-0.690
Chmp5	Chromatin modifying protein 5	BA01	TC168	0.002	-0.690
Pccb	Propionyl coa carboxylase, beta polypeptide	BA002	007_010_P19	0.032	-0.692
Them2	Acyl-coa thioesterase 13	BA002	005-013D_F01_2006-11-18	0.021	-0.693
Aifm1	Apoptosis-inducing factor, mitochondrion-associated, 1	BA002	005_009_F16	0.015	-0.694
Phf5a	PHD finger protein 5A	BA002	008_025_I07	0.001	-0.695
Tmem93	Transmembrane protein 93	BA002	007_011_C12	0.021	-0.695
Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B	BA01	05152004A_000_010D_B08_04	0.002	-0.697
Aarsd1	Alanyl-trna synthetase domain containing 1	BA002	005_011_O04	0.010	-0.697
Eno1	Enolase 1, (alpha)	BA002	005_009_C12	0.014	-0.698
Trappc1	Trafficking protein particle complex 1	BA002	007_031_I18	0.050	-0.699
Tfg	TRK-fused gene	BA002	008_022_L21	0.037	-0.700
Ca10	Carbonic anhydrase X	BA01	001_001B_G04	0.040	-0.700
Eif4a2	Eukaryotic translation initiation factor 4A2	BA002	007_009_K21	0.013	-0.704
Hnrnpc	Heterogeneous nuclear ribonucleoprotein C (C1/C2)	BA01	5222004_000_011D_D08_08	0.006	-0.706
Cpsf3l	Cleavage and polyadenylation specific factor 3-like	BA002	008_005_K12	0.006	-0.708
Xpo1	Exportin 1 (CRM1 homolog, yeast)	BA002	007_008_H21	0.021	-0.708
Stip1	Stress-induced-phosphoprotein 1	BA002	007_023_D23	0.003	-0.708
Alas1	Aminolevulinate, delta-, synthase 1	BA002	005_011_I10	0.008	-0.709
Rdm1	RAD52 motif 1	BA002	007_011_L23	0.042	-0.710
Mkln1	Muskelin 1, intracellular mediator containing kelch motifs	BA002	008_024_K04	0.000	-0.711
Scpep1	Serine carboxypeptidase 1	BA002	005-018B_E06_2006-10-13	0.005	-0.711
Sdf2l1	Stromal cell-derived factor 2-like 1	BA002	007-019C_E04_2006-10-17	0.011	-0.714
Dpm1	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	BA002	007_009_P02	0.015	-0.714
Rpl10a	Ribosomal protein l10a	BA002	007_009_J23	0.018	-0.714
Ormdl1	ORM1-like 1	BA002	008_012_N08	0.000	-0.715

Psma1	Proteasome (prosome, macropain) subunit, alpha type, 1	BA002	007_020_M21	0.010	-0.716
Mpp4	Membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	BA002	007_015_O17	0.002	-0.716
Polr2j	Polymerase (RNA) II (DNA directed) polypeptide J	BA002	007_007_P15	0.008	-0.719
Eif3m	Eukaryotic translation initiation factor 3, subunit M	BA002	005-020B_C06_2006-11-08	0.017	-0.720
Rap1a	RAP1A, member of RAS oncogene family	BA002	008_004_N22	0.001	-0.721
Fkbp4	FK506 binding protein 4	BA002	007-019D_D03_2006-11-01	0.018	-0.722
Tmed2	Transmembrane emp24 domain trafficking protein 2	BA002	005_009_L15	0.032	-0.724
Loc100129492	Small nuclear ribonucleoprotein Sm D1-like	BA002	012-001D_G06_2007-05-04	0.045	-0.726
Dusp11	Dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	BA002	007_027_F21	0.012	-0.729
Hipk1	Homeodomain interacting protein kinase 1	BA002	007_004_O02	0.025	-0.730
Fancl	Fanconi anemia, complementation group L	BA002	007B-001A_E11_2006-10-19	0.020	-0.733
Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	BA002	007_022_O15	0.038	-0.733
Vbp1	Von Hippel-Lindau binding protein 1	BA01	TC446	0.039	-0.735
Phyhipl	Phytanoyl-coa 2-hydroxylase interacting protein-like	BA002	007_013_J08	0.007	-0.737
Npm1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)	BA01	TC126	0.015	-0.738
Hspe1	Heat shock 10kda protein 1 (chaperonin 10)	BA01	TC556	0.026	-0.738
Sap18	Sin3A-associated protein	BA002	005-012C_D07_2006-11-28	0.001	-0.738
Wdr68	DDB1 and CUL4 associated factor 7	BA002	007_013_O13	0.029	-0.740
Atp6v1e1	Atpase, H+ transporting, lysosomal 31kda, V1 subunit E1	BA01	TC302	0.022	-0.742
Arhgap9	Rho gtpase activating protein 9	BA002	008_004_O08	0.009	-0.742
Shmt2	Serine hydroxymethyltransferase 2 (mitochondrial)	BA002	008_013_B11	0.031	-0.742
Sfrs2	Serine/arginine-rich splicing factor 2	BA002	011-008_E20	0.031	-0.742
Lsm14a	LSM14A, SCD6 homolog A	BA002	008_032_I14	0.012	-0.744
Ak2	Adenylate kinase 2	BA002	008_010_H20	0.034	-0.745

Enoph1	Enolase-phosphatase 1	BA01	004_005C_E07	0.001	-0.748
Fkbp5	FK506 binding protein 5	BA002	005-024A_F03_2006-11-14	0.038	-0.748
Pdk3	Pyruvate dehydrogenase kinase, isozyme 3	BA002	007_003_L06	0.031	-0.748
Slc2a14	Solute carrier family 2 (facilitated glucose transporter), member 14	BA01	04122004_000-006A_F02_12	0.026	-0.749
Tmsb4x	Thymosin beta 4, X-linked	BA002	011-013_C10	0.040	-0.752
Loc100133930	D-2-hydroxyglutarate dehydrogenase, mitochondrial-like	BA002	008_028_P13	0.014	-0.754
Pgk1	Phosphoglycerate kinase 1	BA002	007_001_L08	0.005	-0.754
Nop5/nop58	NOP58 ribonucleoprotein homolog	BA002	007_028_P08	0.034	-0.755
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	BA002	008_011_D18	0.001	-0.756
Ywhab	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	BA002	011-007_N12	0.010	-0.757
Rab6a	RAB6A, member RAS oncogene family	BA01	UAhib_0183.y1_091	0.011	-0.757
Ch25h	Cholesterol 25-hydroxylase	BA002	007_024_P10	0.012	-0.760
Ppp1r12a	Protein phosphatase 1, regulatory (inhibitor) subunit 12A	BA002	005-018B_F09_2006-10-13	0.003	-0.760
C2orf25	Methylmalonic aciduria (cobalamin deficiency) cbld type, with homocystinuria	BA002	008_019_E17	0.008	-0.761
Dera	Deoxyribose-phosphate aldolase (putative)	BA002	008_016_D05	0.013	-0.762
Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	BA002	008_016_D14	0.011	-0.763
Loc728851	Nonhistone chromosomal protein HMG-14	BA002	008_007_H19	0.032	-0.764
Magoh	Mago-nashi homolog, proliferation-associated	BA002	008_025_E07	0.038	-0.764
Rbx1	Ring-box 1, E3 ubiquitin protein ligase	BA002	005-023C_B01_2006-11-15	0.012	-0.765
Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1	BA002	007_030_O13	0.035	-0.765
Atp6v0b	Atpase, H+ transporting, lysosomal 21kda, V0 subunit b	BA002	008_002_K03	0.023	-0.766
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	BA002	008_018_H11	0.020	-0.769

Alg8	Asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog	BA002	007_007_P13	0.037	-0.769
Atad2	Atpase family, AAA domain containing 2	BA002	007_005_I18	0.003	-0.772
Txn	Thioredoxin	BA01	004_004D_E04	0.008	-0.773
Dync1li1	Dynein, cytoplasmic 1, light intermediate chain 1	BA002	008_004_K20	0.045	-0.775
Ap1g2	Adaptor-related protein complex 1, gamma 2 subunit	BA002	007_024_D11	0.026	-0.778
Ahsa1	AHA1, activator of heat shock 90kda protein atpase homolog 1	BA002	005-002D-Anya_B11_2006-08-25	0.007	-0.779
Cdc42se1	CDC42 small effector 1	BA002	008_009_L18	0.038	-0.780
Mrpl12	Mitochondrial ribosomal protein L12	BA002	005_010_D24	0.023	-0.781
Pcsk5	Proprotein convertase subtilisin/kexin type 5	BA002	013-003_G13	0.014	-0.783
Rrm1	Ribonucleotide reductase M1	BA01	004_004C_F01	0.005	-0.784
Hibch	3-hydroxyisobutyryl-coa hydrolase	BA002	007_009_J22	0.033	-0.784
Snrpb	Small nuclear ribonucleoprotein polypeptides B and B1	BA002	005_010_D05	0.037	-0.787
Prkacb	Protein kinase, camp-dependent, catalytic, beta	BA002	005-002D-Anya_C02_2006-08-24	0.023	-0.789
Arpc3	Actin related protein 2/3 complex, subunit 3	BA01	04022004A_000_007D_B10_04	0.009	-0.789
C9orf103	Chromosome 9 open reading frame 103	BA002	007_023_J02	0.027	-0.790
Ctss	Cathepsin S	BA002	008_004_I19	0.032	-0.792
Gla	Galactosidase, alpha	BA002	008-001A_D06_2006-11-02	0.017	-0.792
Ect2	Epithelial cell transforming sequence 2 oncogene	BA002	008_005_K10	0.047	-0.792
Psmb6	Proteasome (prosome, macropain) subunit, beta type, 6	BA002	008_008_L16a	0.037	-0.795
Doc2a	Double C2-like domains, alpha	BA002	007_006_E11	0.009	-0.797
Hnrpd	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kda)	BA002	008_014_I15	0.049	-0.799
Loc100129907	PYD and CARD domain containing	BA002	007_022_J19	0.005	-0.801
Spsb2	Spla/ryanodine receptor domain and SOCS box containing 2	BA002	008B-001C_B08_2006-11-09	0.035	-0.806
Nme1-nme2	NME1-NME2 readthrough	BA002	008_012_K14	0.030	-0.808
Napsb	Napsin B aspartic peptidase pseudogene	BA002	008_006_D06	0.030	-0.810
Cox8a	Cytochrome c oxidase subunit VIIIA (ubiquitous)	BA002	005_009_N12	0.016	-0.811

Ppih	Peptidylprolyl isomerase H (cyclophilin H)	BA002	011-013_I23	0.026	-0.811
Drp2	Dystrophin related protein 2	BA002	007_013_K24	0.003	-0.812
Map4k2	Mitogen-activated protein kinase kinase kinase kinase 2	BA002	007_030_G23	0.023	-0.814
Cct6a	Chaperonin containing TCP1, subunit 6A (zeta 1)	BA002	008_029_J13	0.004	-0.816
Rpl9	Ribosomal protein L9	BA002	007_012_C02	0.021	-0.817
Vamp8	Vesicle-associated membrane protein 8 (endobrevin)	BA002	005_011_J08	0.045	-0.818
Tmx1	Thioredoxin-related transmembrane protein 1	BA002	008_013_M10	0.030	-0.819
Stag2	Stromal antigen 2	BA002	007_011_K06	0.032	-0.820
Pmch	Pro-melanin-concentrating hormone	BA002	007_015_H04	0.002	-0.820
Abce1	ATP-binding cassette, sub-family E (OABP), member 1	BA002	007_029_A18	0.011	-0.821
Rps11	Ribosomal protein S11	BA002	011-012_N18	0.014	-0.821
Masp2	Mannan-binding lectin serine peptidase 2	BA002	008_015_G12	0.007	-0.822
Hspa5	Heat shock 70kda protein 5 (glucose-regulated protein, 78kda)	BA01	TC339	0.035	-0.822
Eif3e	Eukaryotic translation initiation factor 3, subunit E	BA002	005-002D-Anya_D08_2006-08-25	0.024	-0.823
Calm2	Calmodulin 2 (phosphorylase kinase, delta)	BA01	TC104	0.006	-0.823
Nutf2	Nuclear transport factor 2	BA002	007_023_K01	0.005	-0.824
Tmem30a	Transmembrane protein 30A	BA002	007_005_C17	0.006	-0.828
Sft2d2	SFT2 domain containing 2	BA002	008_028_M22	0.003	-0.830
Snap23	Synaptosomal-associated protein	BA002	005_005_M21	0.020	-0.831
Mrpl32	Mitochondrial ribosomal protein L32	BA002	008-001B_B06_2006-10-27	0.012	-0.832
Acly	ATP citrate lyase	BA002	008_005_B21	0.006	-0.834
Gimap5	Gtpase, IMAP family member 5	BA002	008_008_O23	0.006	-0.834
Btrc	Beta-transducin repeat containing	BA002	008_022_O06	0.035	-0.834
Exo1	Exonuclease 1	BA01	05132004A_000_010A_H04_16	0.020	-0.835
Ssu72	SSU72 RNA polymerase II CTD phosphatase homolog	BA002	008_012_I04	0.001	-0.836
Chordc1	Cysteine and histidine-rich domain (CHORD)-containing 1	BA01	12162003a_000_004_E12_E12_10	0.010	-0.840
B4galt6	UDP-Gal:betaglcnac beta 1,4-galactosyltransferase, polypeptide 6	BA002	007_009_H02	0.024	-0.843
Arf4	ADP-ribosylation factor 4	BA002	007_004_K12	0.021	-0.845

Zmat2	Zinc finger, matrin-type 2	BA002	006-001A_C10_2006-10-10	0.012	-0.847
Snrpd3	Small nuclear ribonucleoprotein D3 polypeptide 18kda	BA002	005-024C_F05_2006-11-30	0.037	-0.847
Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	BA002	007_002_M20	0.031	-0.847
Cdc42	Cell division cycle 42 (GTP binding protein, 25kda)	BA002	007_015_H02	0.000	-0.848
Derl2	Der1-like domain family, member 2	BA002	005-021B_D03_2006-12-06	0.001	-0.848
Metap2	Methionyl aminopeptidase 2	BA01	05202004A_000_011B_B11_03	0.002	-0.849
Znrf2	Zinc and ring finger 2	BA002	008_015_E19	0.000	-0.850
Prr13	Proline rich 13	BA002	005-015A_H05_2006-10-25	0.004	-0.850
Fcn1	Ficolin (collagen/fibrinogen domain containing) 1	BA002	005_007_J23	0.041	-0.852
Chfr	Checkpoint with forkhead and ring finger domains	BA002	008B-001B_F10_2006-10-28	0.009	-0.852
C6orf62	Chromosome 6 open reading frame 62	BA002	008_005_L24	0.042	-0.852
Ppa1	Pyrophosphatase (inorganic) 1	BA01	05222004_000_011C_H03_15	0.003	-0.852
Dkc1	Dyskeratosis congenita 1, dyskerin	BA002	007_026_B23	0.017	-0.854
Rnf10	Ring finger protein 10	BA01	05012004_000_009C_E11_09	0.040	-0.857
Loc440926	Histone H3.3-like	BA01	UAhib_0194.y1_086	0.035	-0.857
Ppp2r1b	Protein phosphatase 2, regulatory subunit A, beta	BA002	007_027_I05	0.009	-0.861
Ugt3a2	UDP glycosyltransferase 3 family, polypeptide A2	BA002	008_019_F10	0.007	-0.863
Mylip	Myosin regulatory light chain interacting protein	BA002	008_002_M11	0.031	-0.864
Tubb	Tubulin, beta	BA01	TC84	0.021	-0.866
Ppia	Peptidylprolyl isomerase A (cyclophilin A)	BA002	008_004_F04	0.016	-0.868
Hspa8	Heat shock 70kda protein 8	BA01	TC199	0.000	-0.868
Tmem50b	Transmembrane protein 50B	BA002	014-001A_H09_2007-06-12	0.005	-0.869
Ltb4dh	Prostaglandin reductase 1	BA002	008_004_O13	0.024	-0.870
Ilk	Integrin-linked kinase	BA002	007_012_O05	0.012	-0.871
Loc729505	Non-histone chromosomal protein HMG-17-like	BA01	004_003C_H07	0.004	-0.874
Atg3	ATG3 autophagy related 3 homolog	BA002	007B-001A_F09_2006-10-19	0.013	-0.874
Bclaf1	BCL2-associated transcription factor 1	BA002	011-007_O13	0.001	-0.878
Mrpl20	Mitochondrial ribosomal protein L20	BA002	005_010_E20	0.003	-0.880
Fcer1g	Fc fragment of ige, high affinity I,	BA002	005-012A_A11_2006-11-15	0.009	-0.884

	receptor for; gamma polypeptide				
Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	BA002	007_005_M22	0.003	-0.886
Cops2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	BA002	013-002_G01	0.002	-0.886
Tram1	Translocation associated membrane protein 1	BA002	008_031_D09	0.028	-0.887
Tmco1	Transmembrane and coiled-coil domains 1	BA01	TC341	0.002	-0.888
Fam96a	Family with sequence similarity 96, member A	BA002	005-014A_C01_2006-11-02	0.014	-0.889
Omg	Oligodendrocyte myelin glycoprotein	BA002	007-019C_H02_2006-10-17	0.006	-0.891
Clic1	Chloride intracellular channel 1	BA002	011-004_B16	0.010	-0.893
Dpyd	Dihydropyrimidine dehydrogenase	BA002	008_015_K05	0.017	-0.898
Loc642103	Similar to Maltase-glucoamylase	BA002	008_016_I03	0.047	-0.898
Calr	Calreticulin	BA002	008_032_N03	0.009	-0.901
Fbxo9	F-box protein 9	BA002	007_008_C20	0.037	-0.903
Epsti1	Epithelial stromal interaction 1	BA002	008_032_C09	0.021	-0.904
Nxt2	Nuclear transport factor 2-like export factor 2	BA01	05222004_000_011C_A03_01	0.025	-0.905
C5orf30	Chromosome 5 open reading frame 30	BA01	04122004_000-006A_G01_13	0.026	-0.905
Ckap2	Cytoskeleton associated protein 2	BA01	05222004_000_011C_D03_07	0.047	-0.907
Skiv2l	Superkiller viralicidic activity 2-like	BA002	008B-001B_A02_2006-10-28	0.029	-0.910
Hnrpm	Heterogeneous nuclear ribonucleoprotein M	BA002	011-016_O04	0.033	-0.916
Cap1	CAP, adenylate cyclase-associated protein 1	BA002	009-001D_E01_2007-02-24	0.027	-0.918
Atp6v0e1	Atpase, H+ transporting, lysosomal 9kda, V0 subunit e1	BA002	007_008_C05	0.009	-0.926
Psmd14	Proteasome (prosome, macropain) 26S subunit, non-atpase, 14	BA002	011-005_D14	0.005	-0.928
Coro1a	Coronin, actin binding protein, 1A	BA002	007_012_O16	0.015	-0.929
Cdc2l5	Cyclin-dependent kinase 13	BA002	011-013_N17	0.000	-0.934
Cyb5b	Cytochrome b5 type B (outer mitochondrial membrane)	BA002	007_025_L14	0.009	-0.935
Mtdh	Metadherin	BA002	007_022_C21	0.001	-0.935
Elovl6	ELOVL family member 6, elongation of long chain fatty	BA002	008_016_E14	0.004	-0.940

	acids				
Dhfr	Dihydrofolate reductase	BA002	008_019_P12	0.006	-0.941
Cbx3	Chromobox homolog 3	BA002	008_005_J08	0.034	-0.948
Tuba1b	Tubulin, alpha 1b	BA01	TC517	0.039	-0.949
Cep27	HAUS augmin-like complex, subunit 2	BA002	007_005_K11	0.012	-0.951
Ugp2	UDP-glucose pyrophosphorylase 2	BA002	008_008_L06	0.006	-0.951
Tkt	Transketolase	BA002	005-023C_F07_2006-11-15	0.018	-0.952
Vamp5	Vesicle-associated membrane protein 5 (myobrevin)	BA002	005-012C_E08_2006-11-28	0.002	-0.952
Hmgb1	High-mobility group box 1	BA01	01082004A_000_002_F10_F10_12	0.027	-0.954
Isy1	ISY1 splicing factor homolog	BA002	006-001A_C08_2006-10-10	0.012	-0.961
Calm3	Calmodulin 3 (phosphorylase kinase, delta)	BA002	011-011_B18	0.005	-0.963
Cdkn3	Cyclin-dependent kinase inhibitor 3	BA002	008_013_L10	0.033	-0.965
Actr3	ARP3 actin-related protein 3 homolog	BA002	007_005_O06	0.022	-0.966
Ap3s1	Adaptor-related protein complex 3, sigma 1 subunit	BA002	008_021_P12	0.029	-0.970
Ywhaz	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	BA002	013-002_H16	0.015	-0.971
Gadd45a	Growth arrest and DNA-damage-inducible, alpha	BA002	005-023A_H04_2006-11-09	0.011	-0.979
Gimap7	Gtpase, IMAP family member 7	BA002	008_015_F13	0.011	-0.985
Rad21	RAD21 homolog	BA002	008_005_A16	0.032	-0.990
Tubb2c	Tubulin, beta 2C	BA01	TC413	0.037	-0.993
Fam49b	Family with sequence similarity 49, member B	BA002	007_022_C14	0.047	-0.996
Casp7	Caspase 7, apoptosis-related cysteine peptidase	BA002	008_015_D13	0.022	-1.000
Ran	RAN, member RAS oncogene family	BA01	UAhib_0866.y1_077	0.001	-1.000
Acsl4	Acyl-coa synthetase long-chain family member 4	BA01	TC558	0.023	-1.001
Mki67ip	MKI67 (FHA domain) interacting nucleolar phosphoprotein	BA002	007-019D_G04_2006-11-01	0.038	-1.005
Fbl	Fibrillarin	BA002	008_002_F24	0.012	-1.006
Hagh	Hydroxyacylglutathione hydrolase	BA002	008_009_F11	0.000	-1.007
Cdk2ap2	Cyclin-dependent kinase 2 associated protein 2	BA002	007_004_O07	0.000	-1.010
Tmem33	Transmembrane protein 33	BA002	007_004_P15	0.001	-1.014
Nap1l1	Nucleosome assembly protein 1-	BA002	007_008_O14	0.016	-1.016

	like 1				
Gtf2a2	General transcription factor IIA, 2	BA002	008_005_E12	0.007	-1.021
Loc653566	Signal peptidase complex subunit 2-like	BA002	005-022C_D05_2006-11-22	0.019	-1.023
Rcan2	Regulator of calcineurin 2	BA002	TC6006	0.045	-1.030
Igll1	Immunoglobulin lambda-like polypeptide 1	BA002	007_009_E09	0.011	-1.031
Cp	Ceruloplasmin (ferroxidase)	BA002	008_028_J14	0.005	-1.033
Pccb	Propionyl coa carboxylase, beta polypeptide	BA002	007_004_J18	0.001	-1.033
Fos	FBJ murine osteosarcoma viral oncogene homolog	BA002	005-021A_B08_2006-11-01	0.004	-1.044
Pik3cb	Phosphoinositide-3-kinase, catalytic, beta polypeptide	BA002	007_006_G10	0.006	-1.044
B3gnt2	UDP-glcnac:betagal beta-1,3-N-acetylglucosaminyltransferase 2	BA002	008_016_O16	0.000	-1.044
Capza1	Capping protein (actin filament) muscle Z-line, alpha 1	BA002	007_010_J10	0.006	-1.045
Plp2	Proteolipid protein 2 (colonic epithelium-enriched)	BA002	007_002_G07	0.013	-1.047
Slc43a3	Solute carrier family 43, member 3	BA002	008_028_C09	0.022	-1.050
Hmgn2	High-mobility group nucleosomal binding domain 2	BA01	UAhib_1774.y1_078	0.002	-1.051
Arhgdib	Rho GDP dissociation inhibitor (GDI) beta	BA002	008_021_G21	0.017	-1.053
Mbd2	Methyl-cpg binding domain protein 2	BA002	008_004_M22	0.014	-1.054
Hspd1	Heat shock 60kda protein 1	BA01	UAhib_1847.y1_036	0.025	-1.059
Hsph1	Heat shock 105kda/110kda protein 1	BA002	007-019D_D10_2006-11-01	0.015	-1.072
Ghitm	Growth hormone inducible transmembrane protein	BA002	008_007_K05	0.001	-1.080
Actr2	ARP2 actin-related protein 2 homolog	BA002	008_031_A09	0.005	-1.081
Kiaa1949	Kiaa1949	BA002	008_013_A23	0.008	-1.085
Mtmr14	Myotubularin related protein 14	BA002	008_011_E24	0.002	-1.087
Cybb	Cytochrome b-245, beta polypeptide	BA002	008_006_E09	0.035	-1.089
Slc25a5	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	BA002	005_009_B04	0.010	-1.093
Farsb	Phenylalanyl-trna synthetase, beta subunit	BA002	007_023_O23	0.023	-1.101
Gpr177	Wntless homolog (G protein-coupled receptor 177)	BA002	007_006_H17	0.013	-1.103

C20orf3	Chromosome 20 open reading frame 3	BA002	008_016_A05	0.006	-1.103
Snx25	Sorting nexin 25	BA01	05222004_000_011C_G03_13	0.041	-1.111
Glul	Glutamate-ammonia ligase	BA002	005-013C_A07_2006-12-09	0.039	-1.111
Rexo2	REX2, RNA exonuclease 2 homolog	BA002	007_002_H10	0.043	-1.112
Pygl	Phosphorylase, glycogen	BA002	007_028_K14	0.012	-1.113
C1qa	Complement component 1, q subcomponent, A chain	BA002	007-019D_F07_2006-11-01	0.002	-1.116
Nuf2	NUF2, NDC80 kinetochore complex component, homolog	BA01	03312004_000_007A_D10_08	0.004	-1.118
Canx	Calnexin	BA002	005-012A_H03_2006-11-15	0.002	-1.123
Ube2s	Ubiquitin-conjugating enzyme E2S	BA002	005-023C_F11_2006-11-16	0.022	-1.129
Tpx2	TPX2, microtubule-associated, homolog	BA01	05202004A_000_011B_F05_11	0.035	-1.130
Fcn2	Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	BA002	008_013_G13	0.024	-1.131
Cpd	Carboxypeptidase D	BA01	05152004_000_010C_G08_14	0.025	-1.136
Stmn1	Stathmin 1	BA01	TC92	0.022	-1.145
Qpct	Glutaminyl-peptide cyclotransferase	BA002	007_023_H03	0.028	-1.146
Tmem14c	Transmembrane protein 14C	BA002	005_006_K07	0.012	-1.148
Ucp2	Uncoupling protein 2 (mitochondrial, proton carrier)	BA002	008_002_F21	0.024	-1.153
Arpc5	Actin related protein 2/3 complex, subunit 5	BA002	007_009_B20	0.006	-1.160
Loc646839	Tropomyosin 3	BA002	007_007_P08	0.001	-1.167
Spg21	Spastic paraplegia 21 (autosomal recessive, Mast syndrome)	BA002	007_021_M05	0.002	-1.173
Tegt	Transmembrane BAX inhibitor motif containing 6	BA01	TC293	0.005	-1.177
Syncrip	Synaptotagmin binding, cytoplasmic RNA interacting protein	BA002	011-008_N20	0.003	-1.178
C14orf147	Chromosome 14 open reading frame 147	BA002	005-018D_G08_2006-10-25	0.002	-1.186
Rogdi	Rogdi homolog	BA002	005-022C_C01_2006-11-22	0.009	-1.193
Atp6v1c1	Atpase, H+ transporting, lysosomal 42kda, V1 subunit C1	BA002	007_033_K08	0.011	-1.196
Atp6v1a	Atpase, H+ transporting, lysosomal 70kda, V1 subunit A	BA002	007_004_K07	0.008	-1.225
Top2a	Topoisomerase (DNA) II alpha	BA01	05142004_000_010B_D10_08	0.029	-1.225
Erp29	Endoplasmic reticulum protein 29	BA002	005_008_H24	0.001	-1.228
Mgst1	Microsomal glutathione S-	BA002	008_013_I09	0.008	-1.230

	transferase 1				
Prdx5	Peroxiredoxin 5	BA002	007-019C_C06_2006-10-17a	0.007	-1.245
Tloc1	SEC62 homolog	BA002	011-012_H12	0.031	-1.245
Mobkl1b	MOB1, Mps One Binder kinase activator-like 1B	BA002	008_005_H07	0.045	-1.248
Nek2	NIMA (never in mitosis gene a)-related kinase 2	BA01	02102004_000_005A_B9_B09_03	0.038	-1.251
Ptma	Prothymosin, alpha	BA002	007_005_G22	0.012	-1.254
Memo1	Mediator of cell motility 1	BA002	008_005_P19	0.006	-1.261
Glrx	Glutaredoxin (thioltransferase)	BA002	005-012C_A07_2006-11-28	0.002	-1.263
H2afz	H2A histone family, member Z	BA002	007_002_D06	0.008	-1.277
Cd47	CD47 molecule	BA002	008_020_E07	0.001	-1.300
Dad1	Defender against cell death 1	BA002	007_003_F16	0.002	-1.306
Hnrnpa2b1	Heterogeneous nuclear ribonucleoprotein A2/B1	BA002	011-004_D22	0.015	-1.308
Ube2t	Ubiquitin-conjugating enzyme E2T	BA002	007_022_M10	0.006	-1.311
Mboat2	Membrane bound O-acyltransferase domain containing 2	BA002	007_007_G12	0.025	-1.350
Cnih4	Cornichon homolog 4	BA002	007_029_F08	0.019	-1.377
Hmgb3	High-mobility group box 3	BA002	005-018D_F07_2006-10-25	0.018	-1.404
Kpna2	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	BA002	008_022_M22	0.008	-1.405
Hnrpf	Heterogeneous nuclear ribonucleoprotein F	BA002	008_002_J07	0.038	-1.420
Cfl1	Cofilin 1	BA002	007_005_F22	0.012	-1.429
Psmf1	Proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	BA01	004_001D_H08	0.029	-1.434
Acss1	Acyl-coa synthetase short-chain family member 1	BA002	008_021_H03	0.006	-1.436
Loc100133188	Acyl-coa desaturase (Stearoyl-coa desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)	BA01	03312004A_000_007B_H11_15	0.014	-1.483
Oxct1	3-oxoacid coa transferase 1	BA01	05152004_000_010C_A09_01	0.002	-1.488
Ccl15	Chemokine (C-C motif) ligand 15	BA002	008_028_I17	0.001	-1.538
Sri	Sorcin	BA002	007_020_E11	0.017	-1.544
Dut	Deoxyuridine triphosphatase	BA002	005-024D_A08_2006-12-15	0.031	-1.567
Dgat2	Diacylglycerol O-acyltransferase 2	BA002	007_014_K18	0.004	-1.589
Maob	Monoamine oxidase B	BA002	008_013_B02	0.006	-1.591
Hmgb2	High-mobility group box 2	BA01	12162003_000_003_A4_A04_02	0.025	-1.617
Hpcal1	Hippocalcin-like 1	BA002	007_021_K23	0.028	-1.777
Pfn1	Profilin 1	BA002	005_005_D19	0.004	-1.807

Loc100130890	Heat shock protein 67B2-like	BA002	007_007_L11	0.000	-1.860
Srgn	Serglycin	BA002	008_030_B09	0.002	-1.863
Pcm1	Pericentriolar material 1	BA01	01082004_000_001_F5_F05_11	0.024	-2.131