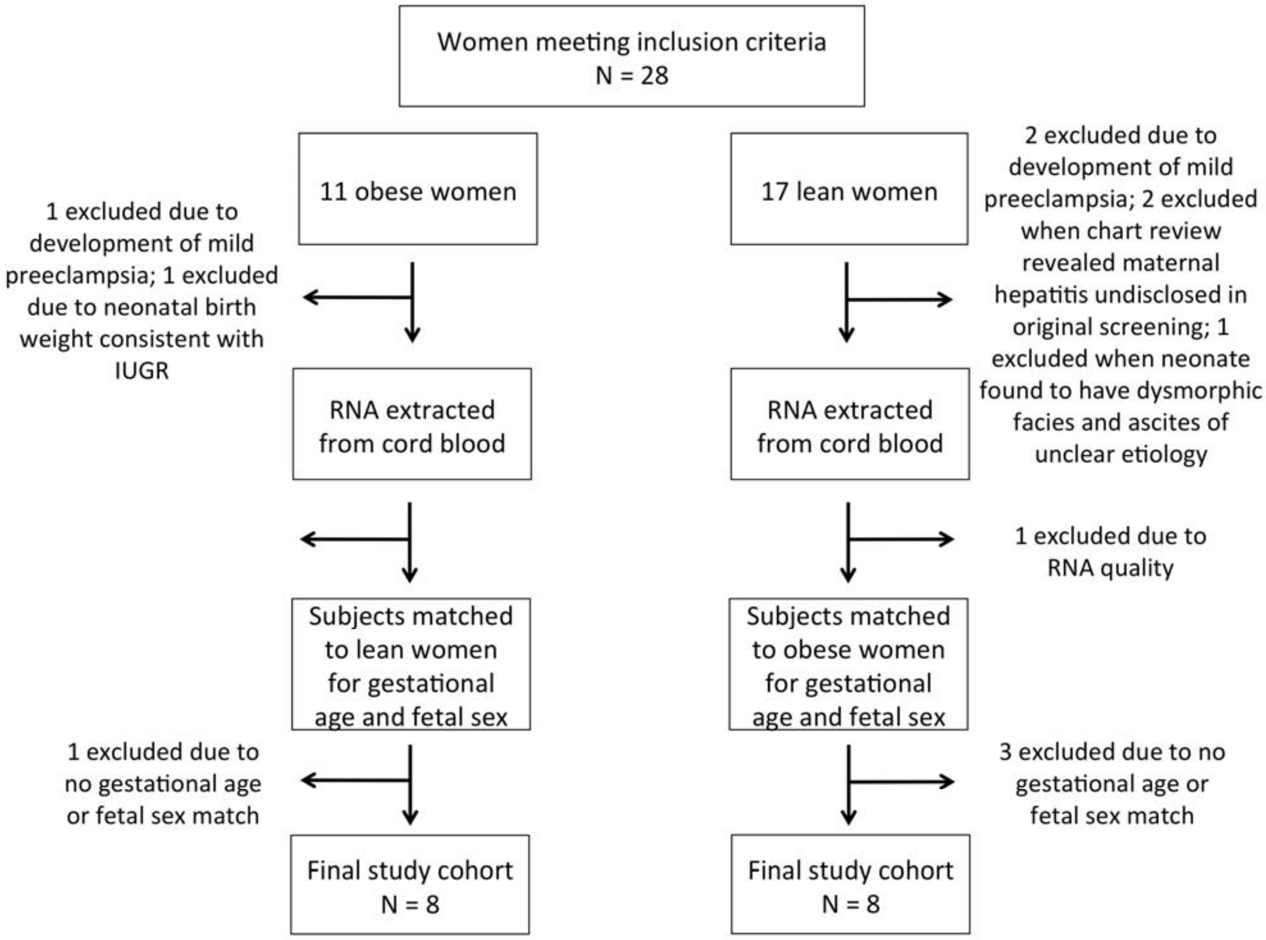
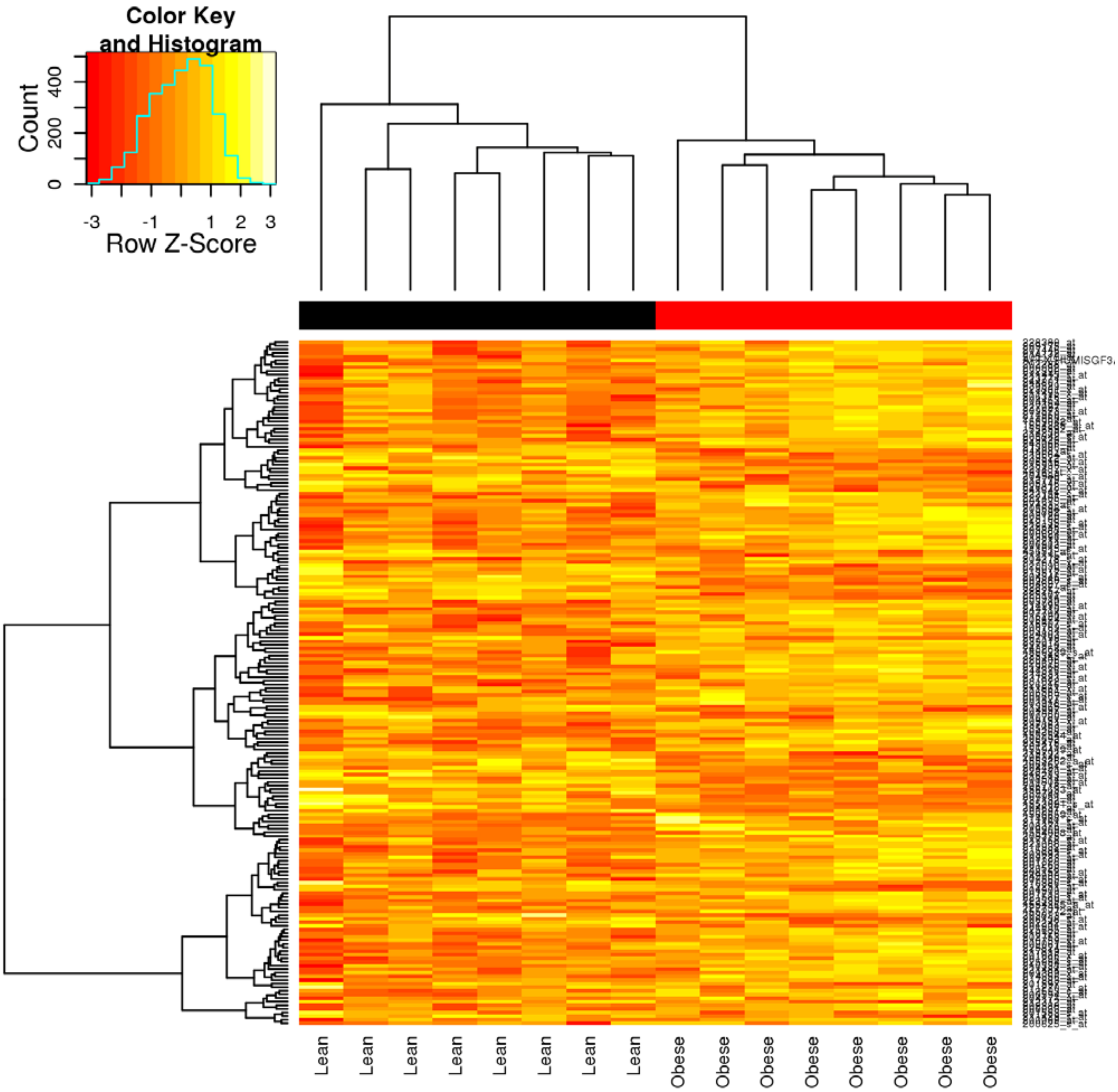


Figure S1. Flow of Subjects Through the Study



This heatmap representation of expression of the 190 genes downstream from significantly activated or inhibited upstream regulators confirms that expression clusters by maternal body mass index (BMI).

Figure S2. Heatmap of Genes Affected by Significant Upstream Regulators

Table S1. Glucose tolerance test results by subject*

Obese Subject	BMI (kg/m^2)	1-hour GLT (mg/dL)	3-hour GTT (mg/dL)	Lean Subject	BMI (kg/m^2)	1-hour GLT (mg/dL)	3-hour GTT (mg/dL)
1	36.4	124	N/A	1	20.2	144	68-125-123-110
2	35.5	156	89-129-133-85	2	19.8	173	76-158-132-118
3	53.4	71	N/A	3	23.08	65	
4	38.0	124	N/A	4	17.75	133	
5	39.9	111, 99	N/A	5	21.2	94	
6	57.8	87 (early) 100 (3rd trimester)	N/A	6	24.4	84	
7	32.6	107	N/A	7	17.6	134	
8	34.1	117 (early), 124 (3rd trimester)	N/A	8	18.6	102	

BMI: body mass index
GLT: glucose loading test
GTT: glucose tolerance test
N/A: not applicable

*Per standard obstetrical care in the United States, all patients underwent glucose tolerance testing with a 50-gram glucose drink and measurement of serum glucose one hour later (glucose loading test or GLT). If serum glucose level was ≥140 mg/dL on this screening test, patients then completed a fasting 3-hour oral glucose tolerance test with a 100-gram glucose challenge (GTT, Carpenter/Coustan diagnostic criteria used). The screening GLT was performed at 26-28 weeks, as per usual obstetrical care. Some obese subjects have two GLT values listed, because these individuals underwent an early glucose tolerance testing in addition to the 26-28 week test. This reflects some practitioners' preference for early glucose testing in the obese patient population to identify pre-pregnancy glucose intolerance or diabetes.

Table S2. Significantly differentially regulated genes in fetuses of obese women at term

Gene Name	Symbol	Affymetrix Probe ID	Fold Change	BH- p value
aminoadipate-semialdehyde synthase	*AASS*	210852_s_at	-1.76	0.00
ATP-binding cassette, sub-family A (ABC1), member 5	*ABCA5*	241705_at	1.85	0.02
ABRA C-terminal like	*ABRACL*	223361_at	1.43	0.01
ankyrin repeat and BTB (POZ) domain containing 1	*ABTB1*	242567_at	2.81	0.00
acetyl-CoA acetyltransferase 1	*ACAT1*	1559239_s_at	2.49	0.03
acyl-CoA binding domain containing 3	*ACBD3*	202323_s_at	-1.92	0.02
adenosine A1 receptor	*ADORA1*	216220_s_at	1.63	0.04
androgen-dependent TFPI-regulating protein	*ADTRP*	229070_at	1.47	0.03
ArfGAP with GTPase domain, ankyrin repeat and PH domain 6	*AGAP6 (includes others)*	221850_x_at	1.45	0.00
ArfGAP with FG repeats 1	*AGFG1*	226561_at	2.00	0.04
agmatine ureohydrolase (agmatinase)	*AGMAT*	219792_at	-2.07	0.00
1-acylglycerol-3-phosphate O-acyltransferase 1	*AGPAT1*	32836_at	-1.40	0.04
1-acylglycerol-3-phosphate O-acyltransferase 2	*AGPAT2*	32837_at	-1.37	0.00
A kinase (PRKA) anchor protein 1	*AKAP1*	201675_at	1.52	0.01
A kinase (PRKA) anchor protein 17A	*AKAP17A*	203624_at	1.38	0.04
A kinase (PRKA) anchor protein 9	*AKAP9*	210962_s_at	1.36	0.01
aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	*AKR7A2*	214259_s_at	-1.40	0.04
AKT interacting protein	*AKTIP*	223894_s_at	1.80	0.04
aldolase B, fructose-bisphosphate	*ALDOB*	243901_at	-2.14	0.00
arachidonate 5-lipoxygenase-activating protein	*ALOX5AP*	204174_at	1.54	0.05
alpha-kinase 3	*ALPK3*	228342_s_at	1.94	0.00
amyotrophic lateral sclerosis 2 (juvenile)	*ALS2*	1555284_at	-2.18	0.00
adenosine monophosphate deaminase 2	*AMPD2*	212360_at	-1.60	0.00
amylase, alpha 2A (pancreatic)	*AMY2A*	208498_s_at	1.94	0.00
anaphase promoting complex subunit 4	*ANAPC4*	232524_x_at	1.77	0.00
angel homolog 2 (Drosophila)	*ANGEL2*	217630_at	2.36	0.00
angel homolog 2 (Drosophila)	*ANGEL2*	221825_at	1.54	0.00
ankyrin repeat and FYVE domain containing 1	*ANKFY1*	219868_s_at	3.12	0.00
ankyrin repeat domain 13 family, member D	*ANKRD13D*	238642_at	-2.03	0.00
ankyrin repeat domain 40	*ANKRD40*	241032_at	-4.06	0.00
ankyrin repeat domain 52	*ANKRD52*	228257_at	-1.43	0.01
ankyrin repeat domain 65	*ANKRD65*	1556181_at	-1.98	0.02
adaptor-related protein complex 1 associated regulatory protein	*AP1AR*	242753_x_at	2.41	0.00
adaptor-related protein complex 1,	*AP1G1*	203350_at	1.28	0.04

gamma 1 subunit				
adaptor-related protein complex 2, alpha 1 subunit	*AP2A1*	223237_x_at	-1.56	0.00
adaptor-related protein complex 4, epsilon 1 subunit	*AP4E1*	228164_at	1.58	0.04
adaptor-related protein complex 5, mu 1 subunit	*AP5M1*	1555448_at	-1.28	0.03
adaptor-related protein complex 5, zeta 1 subunit	*AP5Z1*	209912_s_at	-1.24	0.04
amyloid beta (A4) precursor protein-binding, family A, member 3	*APBA3*	205146_x_at	-1.68	0.01
apoptosis inhibitor 5	*API5*	214960_at	2.32	0.00
adipocyte plasma membrane associated protein	*APMAP*	227857_at	1.41	0.00
ADP-ribosylation factor GTPase activating protein 3	*ARFGAP3*	202211_at	1.64	0.00
Rho GTPase activating protein 18	*ARHGAP18*	225173_at	-1.54	0.02
Rho GTPase activating protein 21	*ARHGAP21*	241701_at	-1.84	0.01
Rho GTPase activating protein 28	*ARHGAP28*	220381_at	-2.62	0.00
artemin	*ARTN*	210237_at	-2.64	0.01
ankyrin repeat and SOCS box containing 14	*ASB14*	237785_at	-2.59	0.00
ASMTL antisense RNA 1	*ASMTL-AS1*	244875_at	-1.57	0.00
ATPase, Na+/K+ transporting, beta 3 polypeptide	*ATP1B3*	226570_at	1.58	0.03
ATPase, Ca++ transporting, plasma membrane 4	*ATP2B4*	212135_s_at	1.57	0.01
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	*ATP5C1*	214132_at	2.13	0.01
ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (factor B)	*ATP5S*	238799_at	1.43	0.01
ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	*ATP6V1B1*	1554847_at	2.83	0.02
ATPase inhibitory factor 1	*ATPIF1*	223339_at	1.37	0.00
axin 2	*AXIN2*	224176_s_at	-1.36	0.02
beta-1,4-N-acetyl-galactosaminyl transferase 4	*B4GALNT4*	238060_s_at	-1.46	0.01
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	*B4GALT5*	221484_at	1.83	0.05
Bardet-Biedl syndrome 1	*BBS1*	218471_s_at	1.54	0.04
BCL2-like 1	*BCL2L1*	212312_at	-1.37	0.02
BEN domain containing 3	*BEND3*	227920_at	1.79	0.00
betaine--homocysteine S-methyltransferase 2	*BHMT2*	219902_at	-2.12	0.04
bicaudal D homolog 2 (Drosophila)	*BICD2*	1553021_s_at	-1.22	0.04
bromodomain and WD repeat domain containing 1	*BRWD1*	219280_at	1.52	0.00
BTB (POZ) domain containing 1	*BTBD1*	217945_at	1.49	0.01
BTB (POZ) domain containing 11	*BTBD11*	238692_at	4.68	0.00

BTG family, member 2	*BTG2*	201236_s_at	1.26	0.02
butyrophilin, subfamily 2, member A1	*BTN2A1*	215493_x_at	1.95	0.03
chromosome 11 open reading frame 95	*C11orf95*	218641_at	1.12	0.03
chromosome 12 open reading frame 60	*C12orf60*	229888_at	3.54	0.00
chromosome 12 open reading frame 73	*C12orf73*	226943_at	1.32	0.00
chromosome 14 open reading frame 119	*C14orf119*	223060_at	1.34	0.03
chromosome 14 open reading frame 2	*C14orf2*	210532_s_at	1.20	0.00
chromosome 15 open reading frame 39	*C15orf39*	215087_at	-1.85	0.00
chromosome 1 open reading frame 111	*C1orf111*	231163_at	-3.25	0.01
chromosome 2 open reading frame 40	*C2orf40*	223623_at	-2.08	0.00
chromosome 2 open reading frame 68	*C2orf68*	221878_at	1.62	0.01
chromosome 2 open reading frame 68	*C2orf68*	65472_at	1.40	0.00
chromosome 5 open reading frame 24	*C5orf24*	229098_s_at	-2.30	0.01
chromosome 6 open reading frame 141	*C6orf141*	1552575_a_at	-1.95	0.02
chromosome 6 open reading frame 165	*C6orf165*	230273_at	-1.69	0.00
calcium channel flower domain containing 1	*CACFD1*	61874_at	-1.43	0.01
calcium channel, voltage-dependent, beta 2 subunit	*CACNB2*	1559419_at	2.95	0.04
calcium/calmodulin-dependent protein kinase II gamma	*CAMK2G*	212757_s_at	1.41	0.05
CAP, adenylate cyclase-associated protein 1 (yeast)	*CAP1*	200625_s_at	1.08	0.02
calpain 6	*CAPN6*	202965_s_at	-2.91	0.01
caspase 4, apoptosis-related cysteine peptidase	*CASP4*	213596_at	1.60	0.00
caspase 4, apoptosis-related cysteine peptidase	*CASP4*	209310_s_at	1.14	0.04
chromobox homolog 6	*CBX6*	202047_s_at	-1.37	0.02
coiled-coil domain containing 157	*CCDC157*	232920_at	1.42	0.04
coiled-coil domain containing 18	*CCDC18*	228022_at	1.31	0.00
coiled-coil domain containing 186	*CCDC186*	229399_at	1.57	0.04
cyclin J	*CCNJ*	1557830_at	2.00	0.02
cyclin K	*CCNK*	225824_at	1.43	0.00
chemokine (C-C motif) receptor 2	*CCR2*	207794_at	2.48	0.01
chemokine (C-C motif) receptor 4	*CCR4*	208376_at	3.37	0.00
chemokine (C-C motif) receptor 6	*CCR6*	206983_at	1.31	0.04
chaperonin containing TCP1, subunit 8 (theta)	*CCT8*	200873_s_at	1.27	0.00
CD28 molecule	*CD28*	211861_x_at	3.32	0.04
CD59 molecule, complement regulatory protein	*CD59*	228748_at	3.05	0.03
cytidine and dCMP deaminase domain containing 1	*CDADC1*	223527_s_at	2.10	0.00
cell division cycle 42	*CDC42*	214230_at	1.79	0.02
CDC42 effector protein (Rho GTPase binding) 2	*CDC42EP2*	209850_s_at	-1.47	0.01
CDC42 effector protein (Rho GTPase binding) 3	*CDC42EP3*	225685_at	1.44	0.00
cell division cycle associated 7-like	*CDCA7L*	225081_s_at	1.27	0.04

cyclin-dependent kinase 17	*CDK17*	206474_at	1.35	0.04
cyclin-dependent kinase 2	*CDK2*	211804_s_at	-2.36	0.00
cyclin-dependent kinase 3	*CDK3*	207188_at	3.42	0.00
cyclin-dependent kinase inhibitor 1C (p57, Kip2)	*CDKN1C*	219533_at	-1.18	0.04
CCAAT/enhancer binding protein (C/EBP), delta	*CEBPD*	213006_at	3.28	0.04
centrosomal protein 128kDa	*CEP128*	233859_at	3.47	0.04
centrosomal protein 63kDa	*CEP63*	222151_s_at	1.35	0.00
ceramide synthase 5	*CERS5*	224951_at	1.36	0.00
carboxylesterase 1 pseudogene 1	*CES1P1*	206824_at	-1.27	0.05
cilia and flagella associated protein 36	*CFAP36*	224968_at	1.73	0.05
cilia and flagella associated protein 70	*CFAP70*	215849_x_at	-3.58	0.00
cilia and flagella associated protein 99	*CFAP99*	1569172_a_at	-2.15	0.00
cripto, FRL-1, cryptic family 1	*CFC1/CFC1B*	223753_s_at	3.37	0.00
complement factor H-related 1	*CFHR1*	215388_s_at	2.43	0.00
glycoprotein hormones, alpha polypeptide	*CGA*	204637_at	-2.03	0.00
chromodomain helicase DNA binding protein 5	*CHD5*	213965_s_at	-1.75	0.03
choline dehydrogenase	*CHDH*	230484_at	-4.48	0.00
checkpoint kinase 1	*CHEK1*	229423_at	1.67	0.02
charged multivesicular body protein 2B	*CHMP2B*	202537_s_at	1.26	0.00
carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	*CHST2*	1556592_at	1.70	0.01
carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	*CHST2*	1556593_s_at	1.63	0.00
CTF8, chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	*CHTF8*	228178_s_at	-1.46	0.01
churchill domain containing 1	*CHURC1*	226736_at	3.59	0.00
chloride channel, voltage-sensitive Ka	*CLCNKA*	207047_s_at	1.55	0.01
C-type lectin domain family 4, member D	*CLEC4D*	1552772_at	2.59	0.00
C-type lectin domain family 4, member D	*CLEC4D*	1552773_at	2.40	0.01
CKLF-like MARVEL transmembrane domain containing 5	*CMTM5*	230942_at	-2.05	0.01
CKLF-like MARVEL transmembrane domain containing 7	*CMTM7*	226017_at	-1.20	0.02
CCHC-type zinc finger, nucleic acid binding protein	*CNBP*	206158_s_at	1.32	0.04
CCHC-type zinc finger, nucleic acid binding protein	*CNBP*	227731_at	1.34	0.00
ciliary neurotrophic factor	*CNTF*	226812_at	-1.59	0.04
cytochrome c oxidase assembly factor 1 homolog (S. cerevisiae)	*COA1*	209446_s_at	-1.52	0.02
collagen, type III, alpha 1	*COL3A1*	211161_s_at	3.77	0.04
collagen, type IV, alpha 5	*COL4A5*	234387_at	-2.79	0.00
coronin 6	*CORO6*	1552301_a_at	-1.79	0.04
cytochrome c oxidase assembly homolog 15 (yeast)	*COX15*	221550_at	1.41	0.00
cytochrome c oxidase subunit VIIa	*COX7A2*	201597_at	-1.21	0.02

polypeptide 2 (liver)				
carboxypeptidase A3 (mast cell)	*CPA3*	205624_at	-1.77	0.05
casein beta	*CSN2*	207951_at	-1.91	0.03
cysteine-serine-rich nuclear protein 3	*CSRNP3*	220462_at	-1.73	0.04
CTD nuclear envelope phosphatase 1	*CTDNEP1*	200035_at	-1.37	0.03
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	*CTDSPL2*	223271_s_at	1.77	0.02
CWC27 spliceosome-associated protein homolog (S. cerevisiae)	*CWC27*	1555495_a_at	1.76	0.02
cytochrome P450, family 4, subfamily V, polypeptide 2	*CYP4V2*	229959_at	1.94	0.01
death associated protein 3	*DAP3*	232516_x_at	-1.60	0.01
diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	*DBI*	209389_x_at	1.38	0.03
dephospho-CoA kinase domain containing	*DCAKD*	224522_s_at	-1.98	0.02
decapping enzyme, scavenger	*DCPS*	218774_at	1.25	0.02
DEAD (Asp-Glu-Ala-Asp) box helicase 21	*DDX21*	208152_s_at	1.30	0.00
DEAD (Asp-Glu-Ala-Asp) box helicase 21	*DDX21*	224654_at	1.21	0.04
DEAD (Asp-Glu-Ala-Asp) box helicase 5	*DDX5*	200033_at	1.62	0.02
DEAD (Asp-Glu-Ala-Asp) box helicase 5	*DDX5*	225886_at	1.56	0.04
DEAD (Asp-Glu-Ala-Asp) box helicase 6	*DDX6*	204909_at	-1.65	0.04
2,4-dienoyl CoA reductase 2, peroxisomal	*DECR2*	219664_s_at	-1.54	0.00
defensin, alpha 6, Paneth cell-specific	*DEFA6*	207814_at	-1.67	0.03
defensin, beta 124	*DEFB124*	1568375_at	-2.85	0.03
defensin, beta 124	*DEFB124*	1568377_x_at	-2.03	0.04
DENN/MADD domain containing 6B	*DENND6B*	220713_at	-2.85	0.04
density-regulated protein	*DENR*	231896_s_at	1.60	0.02
deiodinase, iodothyronine, type III	*DIO3*	207154_at	-2.92	0.02
disrupted in schizophrenia 1	*DISC1*	217330_at	-2.22	0.02
distal-less homeobox 2	*DLX2*	207147_at	4.67	0.02
dystrophin	*DMD*	207660_at	-1.95	0.00
aspartyl aminopeptidase	*DNPEP*	215135_at	-2.15	0.00
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	*DYRK1B*	204954_s_at	-2.29	0.05
E2F transcription factor 3	*E2F3*	203693_s_at	1.80	0.04
estrogen receptor binding site associated, antigen, 9	*EBAG9*	204278_s_at	1.30	0.00
endogenous Bornavirus-like nucleoprotein 3	*EBLN3*	225640_at	-1.27	0.03
EH domain binding protein 1-like 1	*EHBP1L1*	1557228_at	-1.60	0.04
ELK4, ETS-domain protein (SRF accessory protein 1)	*ELK4*	205994_at	1.41	0.05
ELK4, ETS-domain protein (SRF accessory protein 1)	*ELK4*	214831_at	3.35	0.02
engulfment and cell motility 2	*ELMO2*	221528_s_at	1.42	0.00
engulfment and cell motility 2	*ELMO2*	55692_at	1.24	0.01
ER membrane protein complex subunit 4	*EMC4*	223043_at	1.22	0.04
EMI domain containing 1	*EMID1*	213779_at	-2.14	0.01

echinoderm microtubule associated protein like 4	*EML4*	223068_at	1.59	0.00
energy homeostasis associated	*ENHO*	228403_at	-2.43	0.03
ectonucleotide pyrophosphatase/phosphodiesterase 2	*ENPP2*	209392_at	1.92	0.02
epsin 3	*EPN3*	223895_s_at	-2.33	0.02
ERC2 intronic transcript 1 (non-protein coding)	*ERC2-IT1*	208247_at	-3.24	0.04
ERO1-like (S. cerevisiae)	*ERO1L*	222646_s_at	2.16	0.03
estrogen receptor 2 (ER beta)	*ESR2*	210780_at	-1.67	0.01
v-ets avian erythroblastosis virus E26 oncogene homolog 2	*ETS2*	201328_at	1.73	0.02
exocyst complex component 5	*EXOC5*	222726_s_at	1.74	0.04
exosome component 9	*EXOSC9*	205061_s_at	1.38	0.02
coagulation factor X	*F10*	205620_at	3.30	0.02
FAM170B antisense RNA 1	*FAM170B-AS1*	1557660_s_at	-2.03	0.00
family with sequence similarity 178, member A	*FAM178A*	203481_at	1.82	0.00
family with sequence similarity 198, member B	*FAM198B*	219872_at	3.43	0.00
family with sequence similarity 49, member B	*FAM49B*	228987_at	1.23	0.02
Fanconi anemia, complementation group F	*FANCF*	222713_s_at	1.52	0.02
F-box and leucine-rich repeat protein 8	*FBXL8*	220080_at	-3.20	0.00
F-box protein 27	*FBXO27*	235169_at	-2.84	0.01
F-box protein 32	*FBXO32*	225345_s_at	2.41	0.00
fer (fps/fes related) tyrosine kinase	*FER*	206412_at	2.21	0.00
fermitin family member 3	*FERMT3*	223303_at	-1.20	0.02
fibroblast growth factor 2 (basic)	*FGF2*	204421_s_at	-2.01	0.02
fumarate hydratase	*FH*	203032_s_at	1.99	0.03
farnesyltransferase, CAAX box, alpha	*FNTA*	209471_s_at	1.44	0.02
farnesyltransferase, CAAX box, beta	*FNTB*	204764_at	2.10	0.02
formyl peptide receptor 1	*FPR1*	205118_at	2.25	0.03
ferritin, heavy polypeptide-like 17	*FTHL17*	224379_at	-1.94	0.01
GTPase activating protein (SH3 domain) binding protein 1	*G3BP1*	244396_at	2.26	0.00
growth arrest and DNA-damage-inducible, gamma interacting protein 1	*GADD45GIP1*	225495_x_at	-1.54	0.03
galanin/GMAP prepropeptide	*GAL*	214240_at	-2.88	0.04
galactokinase 1	*GALK1*	229458_s_at	-1.64	0.04
growth arrest-specific 2 like 1	*GAS2L1*	209729_at	-1.81	0.03
GATA zinc finger domain containing 2A	*GATAD2A*	218131_s_at	1.31	0.02
glutamyl-tRNA(Gln) amidotransferase, subunit B	*GATB*	233593_at	2.69	0.00
GRIP and coiled-coil domain containing 1	*GCC1*	243306_s_at	-2.08	0.03
ganglioside induced differentiation associated protein 2	*GDAP2*	219473_at	2.36	0.01
GDP dissociation inhibitor 2	*GDI2*	200009_at	1.10	0.00

G elongation factor, mitochondrial 2	*GFM2*	231917_at	2.70	0.02
G elongation factor, mitochondrial 2	*GFM2*	231918_s_at	2.81	0.00
glutamine--fructose-6-phosphate transaminase 1	*GFPT1*	227027_at	2.20	0.05
golgi-associated, gamma adaptin ear containing, ARF binding protein 2	*GGA2*	210658_s_at	1.49	0.03
gamma-glutamyltransferase 1	*GGT1*	233837_at	-2.07	0.01
GINS complex subunit 4 (Sld5 homolog)	*GINS4*	240778_at	-2.97	0.02
glucagon-like peptide 1 receptor	*GLP1R*	208400_at	-2.05	0.01
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	*GNAI2*	215996_at	-1.59	0.03
guanine nucleotide binding protein (G protein), beta polypeptide 4	*GNB4*	223487_x_at	-1.73	0.02
glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	*GNE*	205042_at	1.85	0.00
golgin A7	*GOLGA7*	217819_at	1.41	0.00
golgi transport 1B	*GOLT1B*	222552_at	2.27	0.03
golgi-associated PDZ and coiled-coil motif containing	*GOPC*	227214_at	1.70	0.02
glycoprotein Ib (platelet), beta polypeptide	*GP1BB*	206655_s_at	-1.75	0.00
glycosylphosphatidylinositol anchor attachment 1	*GPAA1*	215690_x_at	-1.39	0.01
glycosylphosphatidylinositol anchor attachment 1	*GPAA1*	201618_x_at	-1.47	0.02
G patch domain containing 4	*GPATCH4*	220596_at	-1.64	0.03
glycerol-3-phosphate dehydrogenase 1 (soluble)	*GPD1*	204997_at	-2.64	0.00
glycerol-3-phosphate dehydrogenase 1 (soluble)	*GPD1*	1563035_x_at	-2.62	0.05
G protein-coupled receptor 39	*GPR39*	229105_at	-3.02	0.02
growth factor receptor-bound protein 2	*GRB2*	215075_s_at	-1.54	0.00
glutamate receptor, ionotropic, kainate 5	*GRIK5*	217509_x_at	-2.53	0.00
G-rich RNA sequence binding factor 1	*GRSF1*	221917_s_at	1.67	0.01
3-hydroxyacyl-CoA dehydratase 3	*HACD3*	222405_at	1.33	0.00
HMG-box transcription factor 1	*HBP1*	209102_s_at	1.44	0.03
HLA complex group 11 (non-protein coding)	*HCG11*	1557169_x_at	4.15	0.00
headcase homolog (Drosophila)	*HECA*	230582_at	-1.61	0.02
HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	*HERC6*	1563659_at	1.98	0.00
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	*HERPUD1*	217168_s_at	1.34	0.02
human immunodeficiency virus type I enhancer binding protein 2	*HIVEP2*	243254_at	2.10	0.00
high mobility group AT-hook 2	*HMGA2*	1561633_at	-1.63	0.02
hepatocyte nuclear factor 4, alpha	*HNF4A*	230914_at	-3.27	0.00
hepatocyte nuclear factor 4, alpha	*HNF4A*	230772_at	-2.21	0.01
heterogeneous nuclear ribonucleoprotein	*HNRNPA3*	206809_s_at	1.38	0.01

A3				
heterogeneous nuclear ribonucleoprotein A3	*HNRNPA3*	211932_at	1.26	0.03
heterogeneous nuclear ribonucleoprotein D-like	*HNRNPDL*	1554678_s_at	1.49	0.04
heterogeneous nuclear ribonucleoprotein D-like	*HNRNPDL*	201993_x_at	1.40	0.02
heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	*HNRNPU*	200594_x_at	1.37	0.04
HOXB cluster antisense RNA 3	*HOXB-AS3*	230743_at	1.72	0.01
heat shock factor binding protein 1	*HSBP1*	200942_s_at	1.36	0.04
heat shock 70kDa protein 4	*HSPA4*	211015_s_at	1.27	0.04
heat shock 70kDa protein 8	*HSPA8*	208687_x_at	1.30	0.00
heat shock 70kDa protein 8	*HSPA8*	210338_s_at	1.52	0.04
heat shock 70kDa protein 8	*HSPA8*	224187_x_at	1.22	0.00
HUS1 checkpoint homolog (S. pombe)	*HUS1*	217618_x_at	1.36	0.04
isoleucyl-tRNA synthetase 2, mitochondrial	*IARS2*	217900_at	1.74	0.04
interferon, alpha 1	*IFNA1/IFNA13*	208375_at	2.09	0.01
interferon gamma receptor 1	*IFNGR1*	242903_at	1.30	0.02
intraflagellar transport 74	*IFT74*	61732_r_at	1.57	0.01
immunoglobulin lambda constant 1 (Mcg marker)	*IGLC1*	1565495_at	-2.88	0.04
IKAROS family zinc finger 1 (Ikaros)	*IKZF1*	227346_at	1.17	0.00
interleukin 12 receptor, beta 1	*IL12RB1*	239522_at	-1.29	0.04
interleukin 7	*IL7*	206693_at	2.33	0.04
interleukin enhancer binding factor 3, 90kDa	*ILF3*	217805_at	1.51	0.00
inverted formin, FH2 and WH2 domain containing	*INF2*	222534_s_at	-2.38	0.00
insulin receptor	*INSR*	226216_at	2.14	0.04
integrator complex subunit 5	*INTS5*	53968_at	-1.49	0.00
integrator complex subunit 7	*INTS7*	218783_at	1.59	0.04
inversin	*INVS*	210114_at	-1.56	0.01
ISY1 splicing factor homolog (S. cerevisiae)	*ISY1*	223831_x_at	1.43	0.02
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	*ITGB3*	204627_s_at	-2.23	0.00
inter-alpha-trypsin inhibitor heavy chain family, member 6	*ITIH6*	234894_at	-1.99	0.01
integral membrane protein 2C	*ITM2C*	221004_s_at	-1.44	0.00
intersectin 2	*ITSN2*	209907_s_at	1.57	0.00
influenza virus NS1A binding protein	*IVNS1ABP*	206245_s_at	1.37	0.03
Janus kinase 2	*JAK2*	205842_s_at	1.78	0.00
jumonji domain containing 4	*JMJD4*	230810_at	2.53	0.00
katanin p80 (WD repeat containing) subunit B 1	*KATNB1*	203162_s_at	-1.37	0.00
potassium channel, voltage gated subfamily A regulatory beta subunit 1	*KCNAB1*	210078_s_at	-1.58	0.04

potassium channel, voltage gated subfamily E regulatory beta subunit 1	*KCNE1*	208514_at	-1.99	0.02
potassium channel tetramerization domain containing 13	*KCTD13*	45653_at	-1.18	0.01
KH domain containing, RNA binding, signal transduction associated 1	*KHDRBS1*	214185_at	1.45	0.00
KH domain containing, RNA binding, signal transduction associated 1	*KHDRBS1*	200040_at	1.39	0.04
KIAA0368	*KIAA0368*	214356_s_at	1.43	0.01
KIAA0753	*KIAA0753*	204711_at	1.47	0.02
KIAA1211	*KIAA1211*	227231_at	3.95	0.01
KIAA1468	*KIAA1468*	225506_at	2.07	0.04
KIAA1614 antisense RNA 1	*KIAA1614-AS1*	232320_at	-1.44	0.01
kinesin family member 14	*KIF14*	236641_at	4.91	0.02
kinesin family member 3B	*KIF3B*	225205_at	1.22	0.00
kinesin family member 5A	*KIF5A*	229921_at	-1.83	0.01
Kruppel-like factor 14	*KLF14*	1552814_a_at	-1.75	0.03
kelch-like family member 17	*KLHL17*	1555650_at	-2.03	0.02
kelch-like family member 35	*KLHL35*	215748_at	3.15	0.03
lysine (K)-specific methyltransferase 2A	*KMT2A*	244110_at	2.01	0.00
kinetochore associated 1	*KNTC1*	206316_s_at	1.88	0.01
karyopherin alpha 4 (importin alpha 3)	*KPNA4*	213567_at	-1.50	0.02
keratin 8 pseudogene 12	*KRT8P12*	222060_at	-1.59	0.03
laminin, alpha 2	*LAMA2*	213519_s_at	-1.68	0.03
lysosomal-associated membrane protein 1	*LAMP1*	201553_s_at	-1.07	0.00
leucine aminopeptidase 3	*LAP3*	217933_s_at	1.32	0.00
La ribonucleoprotein domain family, member 7	*LARP7*	215246_at	2.38	0.03
LIM domain binding 1	*LDB1*	35160_at	-1.66	0.00
LIM domain binding 1	*LDB1*	203451_at	-1.55	0.01
low density lipoprotein receptor class A domain containing 4	*LDLRAD4*	209573_s_at	1.91	0.00
leucine zipper-EF-hand containing transmembrane protein 1	*LETM1*	218939_at	-1.59	0.02
lectin, galactoside-binding-like	*LGALSL*	219998_at	-1.73	0.03
lipoma HMGIC fusion partner	*LHFP*	231411_at	3.13	0.05
lin-52 DREAM MuvB core complex component	*LIN52*	228583_at	1.58	0.04
long intergenic non-protein coding RNA 173	*LINC00173*	1563369_at	-1.57	0.01
long intergenic non-protein coding RNA 556	*LINC00556*	1560988_a_at	-2.26	0.00
long intergenic non-protein coding RNA 883	*LINC00883*	235606_at	6.23	0.01
long intergenic non-protein coding RNA 1204	*LINC01204*	1561352_at	-2.41	0.04
long intergenic non-protein coding RNA 1314	*LINC01314*	215126_at	1.80	0.01
long intergenic non-protein coding RNA	*LINC01526*	1562157_at	1.55	0.03

1526				
long intergenic non-protein coding RNA 1532	*LINC01532*	1559303_at	-1.75	0.02
LIM domain only 1 (rhombotin 1)	*LMO1*	206718_at	-1.78	0.02
uncharacterized LOC100271832	*LOC100271832*	1556999_at	11.54	0.00
uncharacterized LOC100288123	*LOC100288123*	230940_at	-2.48	0.04
uncharacterized LOC100506083	*LOC100506083*	1568787_at	2.73	0.00
uncharacterized LOC100506122	*LOC100506122*	1561228_at	-1.68	0.01
uncharacterized LOC100506142	*LOC100506142*	1556662_at	1.76	0.00
uncharacterized LOC100506403	*LOC100506403*	209359_x_at	-2.12	0.02
uncharacterized LOC100507388	*LOC100507388*	221183_at	-2.80	0.01
uncharacterized LOC101593348	*LOC101593348*	243272_at	4.42	0.01
uncharacterized LOC101927151	*LOC101927151*	240121_x_at	-1.20	0.01
uncharacterized LOC101927539	*LOC101927539*	1570182_at	-1.53	0.02
uncharacterized LOC101927723	*LOC101927723*	1562902_at	-3.01	0.01
uncharacterized LOC101928417	*LOC101928417*	1562857_at	-2.43	0.03
uncharacterized LOC101928921	*LOC101928921*	1554957_at	-2.30	0.04
uncharacterized LOC101929172	*LOC101929172*	1562078_at	-3.14	0.01
uncharacterized LOC103611081	*LOC103611081*	235660_at	-1.81	0.01
uncharacterized LOC283214	*LOC283214*	1561491_at	2.22	0.02
uncharacterized LOC286272	*LOC286272*	232182_at	2.18	0.02
uncharacterized LOC339988	*LOC339988*	1562698_x_at	-1.39	0.00
uncharacterized LOC339988	*LOC339988*	1562697_at	-1.30	0.02
uncharacterized LOC400692	*LOC400692*	1555798_at	2.26	0.02
uncharacterized LOC440173	*LOC440173*	229761_at	-3.43	0.00
putative POM121-like protein 1-like	*LOC728093*	213605_s_at	1.36	0.00
lipid phosphate phosphatase-related protein type 1	*LPPR1*	1570250_at	-2.26	0.01
leucine-rich repeats and calponin homology (CH) domain containing 2	*LRCH2*	227688_at	-2.12	0.05
leucine rich repeat and fibronectin type III domain containing 1	*LRFN1*	232486_at	-1.36	0.04
leucine rich repeat and fibronectin type III domain containing 5	*LRFN5*	230644_at	2.52	0.02
leucine rich repeat containing 14	*LRRC14*	203495_at	-1.62	0.04
leucine rich repeat containing 27	*LRRC27*	228884_at	-1.59	0.01

leucine-rich repeats and death domain containing 1	*LRRD1*	1569783_at	-2.55	0.00
LSM14B, SCD6 homolog B (S. cerevisiae)	*LSM14B*	224171_at	1.40	0.05
LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	*LSM8*	219119_at	1.40	0.03
LURAP1L antisense RNA 1	*LURAP1L-AS1*	242893_at	-2.02	0.00
Ly1 antibody reactive	*LYAR*	223414_s_at	1.30	0.04
melanoma antigen family H1	*MAGEH1*	218573_at	1.18	0.03
metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	*MALAT1*	224558_s_at	2.18	0.03
mitogen-activated protein kinase kinase 5	*MAP2K5*	216765_at	2.41	0.02
mitogen-activated protein kinase kinase 6	*MAP2K6*	205698_s_at	1.47	0.01
membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase	*MARCH1*	219574_at	2.21	0.03
methionine adenosyltransferase II, alpha	*MAT2A*	200769_s_at	1.61	0.02
matrin 3	*MATR3*	200624_s_at	1.63	0.00
methyl-CpG binding domain protein 2	*MBD2*	202485_s_at	-2.53	0.00
multiple coagulation factor deficiency 2	*MCFD2*	212245_at	1.47	0.05
malic enzyme 2, NAD(+)-dependent, mitochondrial	*ME2*	210154_at	1.91	0.01
MYST/Esa1-associated factor 6	*MEAF6*	228517_at	1.64	0.00
mediator complex subunit 23	*MED23*	242706_s_at	2.92	0.02
mediator complex subunit 6	*MED6*	207079_s_at	1.59	0.01
mesenteric estrogen-dependent adipogenesis	*MEDAG*	1565763_at	-2.13	0.03
maternally expressed 3 (non-protein coding)	*MEG3*	212732_at	-2.59	0.00
meteorin, glial cell differentiation regulator	*METRN*	219051_x_at	-1.82	0.03
methyltransferase like 10	*METTL10*	226634_at	1.41	0.05
methyltransferase like 12	*METTL12*	238680_at	2.74	0.01
methyltransferase like 15	*METTL15*	242247_at	2.14	0.00
methyltransferase like 7A	*METTL7A*	244376_at	1.81	0.03
methyltransferase like 7B	*METTL7B*	227055_at	4.86	0.00
major facilitator superfamily domain containing 10	*MFSD10*	209215_at	-1.45	0.00
maltase-glucoamylase (alpha-glucosidase)	*MGAM*	206522_at	1.57	0.00
monoglyceride lipase	*MGLL*	225102_at	-1.86	0.00
midnolin	*MIDN*	225954_s_at	1.47	0.03
MYC induced nuclear antigen	*MINA*	229675_at	3.11	0.02
myeloid leukemia factor 2	*MLF2*	200948_at	-1.41	0.05
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	*MLLT10*	205408_at	-1.58	0.00
matrix metallopeptidase 28	*MMP28*	219909_at	2.88	0.02
M-phase phosphoprotein 9	*MPHOSPH9*	221965_at	1.41	0.03

membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	*MPP5*	226092_at	1.57	0.01
myelin protein zero-like 2	*MPZL2*	203780_at	1.82	0.04
myelin protein zero-like 3	*MPZL3*	227747_at	1.39	0.05
mitochondrial ribosomal protein L20	*MRPL20*	224803_s_at	2.38	0.02
membrane-spanning 4-domains, subfamily A, member 6A	*MS4A6A*	219666_at	1.49	0.00
metadherin	*MTDH*	212251_at	-1.38	0.00
myotubularin related protein 1	*MTMR1*	216095_x_at	1.25	0.02
myotubularin related protein 4	*MTMR4*	214268_s_at	1.24	0.01
myotubularin related protein 9	*MTMR9*	233101_at	1.46	0.04
mitochondrial tRNA translation optimization 1	*MTO1*	224430_s_at	1.42	0.01
mechanistic target of rapamycin (serine/threonine kinase)	*MTOR*	202288_at	1.46	0.01
metastasis suppressor 1-like	*MTSS1L*	213978_at	-2.39	0.01
metaxin 1	*MTX1*	210386_s_at	-1.68	0.00
myeloma overexpressed 2	*MYEOV2*	226845_s_at	-1.46	0.01
myosin IG	*MYO1G*	244654_at	-1.30	0.00
mitotic spindle organizing protein 1	*MZT1*	228530_at	1.71	0.03
NAALADL2 antisense RNA 3	*NAALADL2-AS3*	241587_at	-2.64	0.01
nuclear apoptosis inducing factor 1	*NAIF1*	1554664_at	3.68	0.02
N-acetyltransferase 6 (GCN5-related)	*NAT6*	210874_s_at	-1.59	0.04
nicalin	*NCLN*	222206_s_at	-1.78	0.00
nuclear receptor coactivator 3	*NCOA3*	209061_at	1.33	0.02
NADH dehydrogenase (ubiquinone) complex I, assembly factor 5	*NDUFAF5*	222894_x_at	1.50	0.00
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	*NDUFB5*	203621_at	1.51	0.01
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	*NDUFB6*	1559042_at	3.27	0.00
N-terminal EF-hand calcium binding protein 2	*NECAB2*	215005_at	-1.60	0.00
NME/NM23 family member 8	*NME8*	220384_at	1.88	0.02
neuronal PAS domain protein 2	*NPAS2*	205460_at	-1.32	0.01
neuronal PAS domain protein 3	*NPAS3*	233865_at	-3.83	0.03
nephronophthisis 3 (adolescent)	*NPHP3*	1553389_at	1.85	0.03
N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	*NPL*	243066_at	1.77	0.00
nuclear receptor subfamily 2, group E, member 1	*NR2E1*	207443_at	7.04	0.04
neurogranin (protein kinase C substrate, RC3)	*NRGN*	204081_at	-2.30	0.02
neurotrophic tyrosine kinase, receptor, type 3	*NTRK3*	206462_s_at	-2.24	0.00
neurotensin	*NTS*	206291_at	-1.67	0.01
nucleotide binding protein 2	*NUBP2*	218227_at	-1.69	0.01
nuclear mitotic apparatus protein 1	*NUMA1*	1554663_a_at	-6.01	0.03
nucleoporin 107kDa	*NUP107*	218768_at	1.74	0.01

nucleoporin 160kDa	*NUP160*	214962_s_at	1.75	0.01
occludin	*OCLN*	231022_at	7.26	0.01
O-linked N-acetylglucosamine (GlcNAc) transferase	*OGT*	207563_s_at	1.56	0.03
oncoprotein induced transcript 3	*OIT3*	230478_at	3.05	0.00
olfactory receptor, family 4, subfamily D, member 1	*OR4D1*	1567069_at	-2.15	0.01
olfactory receptor, family 51, subfamily B, member 2 (gene/pseudogene)	*OR51B2*	234486_at	-2.07	0.02
oxysterol binding protein	*OSBP*	1563051_at	1.52	0.02
oxysterol binding protein-like 9	*OSBPL9*	218047_at	1.54	0.03
OSER1 antisense RNA 1 (head to head)	*OSER1-AS1*	1569745_at	1.47	0.04
oncostatin M receptor	*OSMR*	1554008_at	1.64	0.01
oligosaccharyltransferase complex subunit (non-catalytic)	*OSTC*	223001_at	1.45	0.02
peptidyl arginine deiminase, type II	*PADI2*	1554385_a_at	2.19	0.00
peptidyl arginine deiminase, type II	*PADI2*	209791_at	1.71	0.03
peptidyl arginine deiminase, type IV	*PADI4*	211413_s_at	2.80	0.04
pregnancy-associated plasma protein A, pappalysin 1	*PAPPA*	232748_at	-1.35	0.01
par-3 family cell polarity regulator	*PARD3*	210094_s_at	-1.58	0.00
paired box 3	*PAX3*	231666_at	-2.68	0.01
PCBP1 antisense RNA 1	*PCBP1-AS1*	235909_at	3.00	0.04
poly(rC) binding protein 2	*PCBP2*	213517_at	-1.80	0.02
protocadherin 1	*PCDH1*	203918_at	3.49	0.01
protocadherin 10	*PCDH10*	1556329_a_at	-2.55	0.02
protocadherin gamma subfamily C, 3	*PCDHGC3*	215836_s_at	-2.40	0.01
pericentriolar material 1	*PCM1*	202174_s_at	1.30	0.00
pecanex-like 4 (Drosophila)	*PCNXL4*	219972_s_at	2.30	0.05
programmed cell death 4 (neoplastic transformation inhibitor)	*PDCD4*	212593_s_at	1.29	0.03
phosphodiesterase 11A	*PDE11A*	237248_at	-2.29	0.02
peroxisomal biogenesis factor 5-like	*PEX5L*	241833_at	-1.91	0.02
phosphoglycerate kinase 1	*PGK1*	217383_at	1.78	0.04
putative homeodomain transcription factor 1	*PHTF1*	210191_s_at	3.52	0.01
peptidase inhibitor 15	*PI15*	207938_at	-3.01	0.01
phosphatidylinositol 4-kinase, catalytic, beta	*PI4KB*	206138_s_at	-1.21	0.01
protein inhibitor of activated STAT, 2	*PIAS2*	37433_at	1.40	0.04
phosphatidylinositol binding clathrin assembly protein	*PICALM*	203134_at	2.20	0.00
phospholipase B domain containing 1	*PLBD1*	222639_s_at	2.34	0.00
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	*PLEKHA2*	217677_at	1.65	0.03
plastin 3	*PLS3*	201215_at	5.03	0.04
polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	*POLR2J4*	222208_s_at	1.52	0.04
pyrophosphatase (inorganic) 2	*PPA2*	1554499_s_at	2.83	0.04

pyrophosphatase (inorganic) 2	*PPA2*	1556285_s_at	1.63	0.00
phosphopantothenoylcysteine synthetase	*PPCS*	218341_at	1.83	0.00
peptidylprolyl isomerase G (cyclophilin G)	*PPIG*	208993_s_at	1.47	0.00
protein phosphatase 1, regulatory subunit 12A	*PPP1R12A*	201602_s_at	1.28	0.02
protein phosphatase 2, regulatory subunit B', gamma	*PPP2R5C*	1554365_a_at	1.69	0.00
PR domain containing 6	*PRDM6*	230311_s_at	-1.68	0.03
prolactin receptor	*PRLR*	206346_at	-2.14	0.03
pre-mRNA processing factor 18	*PRPF18*	221547_at	1.55	0.02
pre-mRNA processing factor 38A	*PRPF38A*	223230_at	1.30	0.00
proline rich 7 (synaptic)	*PRR7*	219742_at	-2.90	0.00
proteasome (prosome, macropain) subunit, alpha type, 1	*PSMA1*	211746_x_at	1.34	0.02
proteasome (prosome, macropain) subunit, alpha type, 1	*PSMA1*	210759_s_at	1.49	0.00
proteasome (prosome, macropain) subunit, beta type, 7	*PSMB7*	244801_at	1.38	0.03
proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	*PSMD6*	202753_at	1.21	0.01
polypyrimidine tract binding protein 1	*PTBP1*	211270_x_at	-1.30	0.04
pre T-cell antigen receptor alpha	*PTCRA*	211252_x_at	-1.63	0.04
protein tyrosine phosphatase, receptor type, S	*PTPRS*	210823_s_at	-2.05	0.03
poliovirus receptor	*PVR*	216283_s_at	-2.24	0.03
peptide YY	*PYY*	211253_x_at	3.00	0.02
quiescin Q6 sulfhydryl oxidase 2	*QSOX2*	235239_at	-1.57	0.00
queuine tRNA-ribosyltransferase domain containing 1	*QTRTD1*	219178_at	1.25	0.01
RAB21, member RAS oncogene family	*RAB21*	239329_at	1.48	0.01
RAB3 GTPase activating protein subunit 2 (non-catalytic)	*RAB3GAP2*	202373_s_at	1.57	0.00
RAB9B, member RAS oncogene family pseudogene 1	*RAB9BP1*	208245_at	-1.46	0.01
RAB, member RAS oncogene family-like 6	*RABL6*	223166_x_at	-1.30	0.03
RAD23 homolog B (S. cerevisiae)	*RAD23B*	223598_at	1.39	0.00
Ral GTPase activating protein, alpha subunit 1 (catalytic)	*RALGAPA1*	214855_s_at	2.24	0.00
RAN binding protein 2	*RANBP2*	201713_s_at	1.37	0.00
RAP1, GTP-GDP dissociation stimulator 1	*RAP1GDS1*	237856_at	4.29	0.00
RAP2A, member of RAS oncogene family	*RAP2A*	1556808_at	4.29	0.00
arginyl-tRNA synthetase 2, mitochondrial	*RARS2*	232901_at	2.45	0.02
Ras protein-specific guanine nucleotide-releasing factor 1	*RASGRF1*	214905_at	1.89	0.02
Ras association (RalGDS/AF-6) domain family member 1	*RASSF1*	204346_s_at	-1.41	0.02
RanBP-type and C3HC4-type zinc finger containing 1	*RBCK1*	207713_s_at	-1.56	0.02
RNA binding protein, fox-1 homolog (C. elegans) 3	*RBFOX3*	229406_at	-2.59	0.00
RNA binding motif protein 17	*RBM17*	224780_at	1.56	0.02

RNA binding motif protein 25	*RBM25*	1557081_at	1.56	0.00
RNA binding motif, single stranded interacting protein 2	*RBMS2*	235439_at	-3.03	0.01
RNA binding motif protein, Y-linked, family 2, member F pseudogene	*RBMY2FP*	216544_at	-1.18	0.05
RNA binding motif protein, Y-linked, family 3, member A pseudogene	*RBMY3AP*	1565320_at	-2.17	0.04
retinol dehydrogenase 13 (all-trans/9-cis)	*RDH13*	227360_at	-1.83	0.00
ring finger and FYVE-like domain containing E3 ubiquitin protein ligase	*RFFL*	1552651_a_at	-1.39	0.04
regulatory factor X, 1 (influences HLA class II expression)	*RFX1*	226786_at	-1.41	0.01
regulatory factor X, 1 (influences HLA class II expression)	*RFX1*	206321_at	1.72	0.04
regulatory factor X, 3 (influences HLA class II expression)	*RFX3*	238810_at	2.92	0.05
regulator of G-protein signaling 2	*RGS2*	202388_at	1.49	0.01
regulator of G-protein signaling 3	*RGS3*	203823_at	-1.36	0.01
ras homolog family member H	*RHOH*	236293_at	1.64	0.04
RIC8 guanine nucleotide exchange factor B	*RIC8B*	229637_at	1.84	0.00
Rab interacting lysosomal protein	*RILP*	227366_at	-1.41	0.04
ring finger protein 144B	*RNF144B*	239012_at	3.16	0.03
ring finger protein 145	*RNF145*	238949_at	-3.46	0.00
ring finger protein 187	*RNF187*	228470_at	-2.92	0.03
rhophilin associated tail protein 1	*ROPN1*	224191_x_at	1.64	0.01
RPA interacting protein	*RPAIN*	228288_at	2.00	0.00
ribosomal protein L26-like 1	*RPL26L1*	218830_at	1.39	0.00
ribosomal protein L7-like 1	*RPL7L1*	224738_x_at	1.38	0.01
ribosomal protein L9	*RPL9*	200032_s_at	1.23	0.00
regulation of nuclear pre-mRNA domain containing 1A	*RPRD1A*	222558_at	1.94	0.04
ribosome binding protein 1	*RRBP1*	213495_s_at	-1.30	0.04
RNA 3'-terminal phosphate cyclase	*RTCA*	215351_at	1.74	0.03
reticulon 2	*RTN2*	34408_at	-1.60	0.00
RUN and FYVE domain containing 3	*RUFY3*	213430_at	1.57	0.00
RWD domain containing 1	*RWDD1*	240214_at	2.75	0.03
S100 calcium binding protein A2	*S100A2*	204268_at	2.88	0.02
sterile alpha motif domain containing 14	*SAMD14*	213866_at	-1.84	0.01
secretory carrier membrane protein 1	*SCAMP1*	212417_at	-1.83	0.01
secretory carrier membrane protein 1	*SCAMP1*	206667_s_at	2.61	0.02
scavenger receptor class B, member 2	*SCARB2*	215754_at	-1.46	0.04
sec1 family domain containing 1	*SCFD1*	215548_s_at	1.31	0.04
sodium channel and clathrin linker 1	*SCLT1*	1569495_at	-2.40	0.01
SEC16 homolog B (S. cerevisiae)	*SEC16B*	239618_at	1.67	0.02
SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	*SEC22C*	235120_at	-1.67	0.00
SEC23 interacting protein	*SEC23IP*	209175_at	1.64	0.02
selenoprotein O	*SELO*	233168_s_at	-1.46	0.04
SUMO1/sentrin/SMT3 specific peptidase	*SENP2*	228380_at	1.47	0.00

2				
selenoprotein P, plasma, 1	*SEPP1*	201427_s_at	4.24	0.04
stress-associated endoplasmic reticulum protein 1	*SERP1*	235475_at	3.05	0.00
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	*SERPINA1*	211429_s_at	-1.14	0.03
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	*SERPINA12*	1552544_at	3.52	0.03
serpin peptidase inhibitor, clade B (ovalbumin), member 9	*SERPINB9*	209723_at	1.22	0.03
splicing factor 3b, subunit 4, 49kDa	*SF3B4*	209044_x_at	-1.28	0.04
SH3-domain GRB2-like endophilin B2	*SH3GLB2*	224432_at	-1.80	0.02
SH3 and PX domains 2B	*SH3PXD2B*	231823_s_at	1.52	0.02
SHC (Src homology 2 domain containing) transforming protein 1 pseudogene 1	*SHC1P1*	217048_at	-2.38	0.04
sialic acid binding Ig-like lectin 17, pseudogene	*SIGLEC17P*	232686_at	1.63	0.04
SKI-like proto-oncogene	*SKIL*	232379_at	2.74	0.04
solute carrier family 12 (potassium/chloride transporter), member 6	*SLC12A6*	223596_at	-1.29	0.00
solute carrier family 22 (organic anion transporter), member 7	*SLC22A7*	221661_at	2.37	0.00
solute carrier family 25 (mitochondrial carnitine/acylcarnitine carrier), member 29	*SLC25A29*	225306_s_at	-1.73	0.01
solute carrier family 25, member 51	*SLC25A51*	232092_at	-1.52	0.00
solute carrier family 2 (facilitated glucose transporter), member 8	*SLC2A8*	218985_at	-1.30	0.02
solute carrier family 2 (facilitated glucose transporter), member 8	*SLC2A8*	239426_at	-1.84	0.01
solute carrier family 39 (zinc transporter), member 2	*SLC39A2*	220413_at	2.11	0.01
solute carrier family 43 (amino acid system L transporter), member 2	*SLC43A2*	228918_at	-1.47	0.00
solute carrier family 44, member 5	*SLC44A5*	1569112_at	1.66	0.05
solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	*SLC7A1*	206566_at	2.12	0.04
solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9	*SLC9A9*	242587_at	3.25	0.03
small leucine-rich protein 1	*SMLR1*	230716_at	-1.88	0.05
small nucleolar RNA host gene 12 (non-protein coding)	*SNHG12*	223774_at	1.52	0.03
small nucleolar RNA, H/ACA box 65	*SNORA65*	1558081_at	2.92	0.00
sorting nexin 1	*SNX1*	213364_s_at	1.82	0.03
sorting nexin 13	*SNX13*	215820_x_at	2.38	0.02
SON DNA binding protein	*SON*	201086_x_at	1.47	0.00
son of sevenless homolog 1 (Drosophila)	*SOS1*	212777_at	1.49	0.02
SRY (sex determining region Y)-box 30	*SOX30*	207678_s_at	3.60	0.00
spastic paraplegia 21 (autosomal recessive, Mast syndrome)	*SPG21*	215383_x_at	-2.13	0.00

small proline-rich protein 1A	*SPRR1A*	214549_x_at	-1.32	0.01
splicing regulatory glutamine/lysine-rich protein 1	*SREK1*	1568783_at	2.75	0.04
serine/arginine-rich splicing factor 11	*SRSF11*	236948_x_at	3.42	0.03
serine/arginine-rich splicing factor 3	*SRSF3*	232392_at	2.29	0.01
single-stranded DNA binding protein 1, mitochondrial	*SSBP1*	214060_at	2.15	0.00
StAR-related lipid transfer (START) domain containing 5	*STARD5*	213820_s_at	1.26	0.04
signal transducer and activator of transcription 1, 91kDa	*STAT1*	AFFX-HUMISGF3A/M97935_MB_at	1.48	0.03
stromal interaction molecule 1	*STIM1*	1557477_at	-1.50	0.00
striatin, calmodulin binding protein	*STRN*	236388_at	1.75	0.00
SUCLA2 antisense RNA 1	*SUCLA2-AS1*	1569859_at	-1.55	0.04
sulfatase modifying factor 1	*SUMF1*	226850_at	1.29	0.00
SV2 related protein homolog (rat)	*SVOP*	1568625_at	-2.57	0.01
synaptojanin 2 binding protein	*SYNJ2BP*	227274_at	1.61	0.02
TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	*TAF1D*	221580_s_at	1.25	0.02
TAO kinase 2	*TAOK2*	204986_s_at	-1.84	0.00
TAR DNA binding protein	*TARDBP*	200020_at	1.11	0.02
threonyl-tRNA synthetase	*TARS*	201263_at	1.41	0.00
taste receptor, type 2, member 9	*TAS2R9*	221461_at	-2.13	0.01
tyrosine aminotransferase	*TAT*	206916_x_at	-1.67	0.00
TBC1 domain family, member 20	*TBC1D20*	226409_at	1.54	0.04
TBC1 domain family, member 25	*TBC1D25*	227820_at	-1.45	0.00
T-box 2	*TBX2*	40560_at	-1.63	0.02
TRPM8 channel-associated factor 1	*TCAF1*	212981_s_at	2.21	0.03
transcription factor 3	*TCF3*	209151_x_at	3.01	0.02
telomerase reverse transcriptase	*TERT*	207199_at	-1.64	0.00
transforming growth factor, beta 2	*TGFB2*	220406_at	3.31	0.03
thrombomodulin	*THBD*	203888_at	2.19	0.02
thioesterase superfamily member 5	*THEM5*	1562490_at	-2.66	0.01
thyroid hormone receptor, alpha	*THRA*	1316_at	-1.52	0.02
thrombospondin, type I, domain containing 7A	*THSD7A*	230008_at	-2.33	0.00
translocase of inner mitochondrial membrane 21 homolog (yeast)	*TIMM21*	223181_at	1.86	0.00
TOR signaling pathway regulator	*TIPRL*	214773_x_at	-1.88	0.04
tight junction protein 2	*TJP2*	237132_at	-2.26	0.02
tousled-like kinase 1	*TLK1*	241642_x_at	-1.91	0.04
toll-like receptor 1	*TLR1*	210176_at	1.42	0.00
toll-like receptor 6	*TLR6*	207446_at	1.99	0.03
transmembrane 6 superfamily member 1	*TM6SF1*	219892_at	2.10	0.03
transmembrane and coiled-coil domain family 1	*TMCC1*	213351_s_at	-1.59	0.00
transmembrane emp24 protein transport	*TMED4*	1558053_s_at	-2.05	0.00

domain containing 4				
transmembrane protein 105	*TMEM105*	1561243_at	-2.88	0.00
transmembrane protein 131	*TMEM131*	235972_at	-1.88	0.00
transmembrane protein 218	*TMEM218*	235654_at	2.52	0.00
transmembrane protein 259	*TMEM259*	213985_s_at	4.19	0.02
transmembrane protein 88	*TMEM88*	229452_at	-1.24	0.03
transmembrane protein 95	*TMEM95*	1560281_a_at	-1.67	0.02
thymopoietin	*TMPO*	237863_at	2.09	0.03
thioredoxin-related transmembrane protein 4	*TMX4*	201581_at	1.54	0.01
tumor necrosis factor (ligand) superfamily, member 13	*TNFSF13*	209499_x_at	1.42	0.00
tumor necrosis factor (ligand) superfamily, member 13	*TNFSF13*	211495_x_at	1.61	0.00
translocase of outer mitochondrial membrane 20 homolog (yeast)	*TOMM20*	200662_s_at	1.45	0.02
torsin A interacting protein 2	*TOR1AIP2*	1569676_at	1.96	0.02
torsin A interacting protein 2	*TOR1AIP2*	235453_at	3.40	0.00
tumor protein p53 binding protein 2	*TP53BP2*	203120_at	1.55	0.04
tubulin polyglutamylase complex subunit 2	*TPGS2*	244233_at	1.53	0.01
taperin	*TPRN*	225891_at	-1.65	0.01
transformer 2 beta homolog (Drosophila)	*TRA2B*	200893_at	1.34	0.00
TraB domain containing 2B	*TRABD2B*	244472_at	-2.13	0.03
trafficking protein particle complex 2-like	*TRAPPC2L*	238628_s_at	-1.75	0.01
trafficking protein particle complex 6B	*TRAPPC6B*	225537_at	1.83	0.02
tripartite motif containing 38	*TRIM38*	235084_x_at	-1.53	0.01
tripartite motif containing 4	*TRIM4*	224159_x_at	-1.39	0.00
transformation/transcription domain-associated protein	*TRRAP*	214908_s_at	2.68	0.01
tetraspanin 7	*TSPAN7*	202242_at	-1.25	0.04
TSPY-like 1	*TSPYL1*	1560647_at	1.87	0.03
tubulin, gamma complex associated protein 5	*TUBGCP5*	227967_at	1.60	0.02
taurine up-regulated 1 (non-protein coding)	*TUG1*	228397_at	2.25	0.04
tumor suppressor candidate 7 (non-protein coding)	*TUSC7*	1558602_a_at	-3.52	0.00
taxilin gamma	*TXLNG*	1557954_at	1.99	0.00
UBA-like domain containing 2	*UBALD2*	224785_at	-1.60	0.00
ubiquitin-like domain containing CTD phosphatase 1	*UBLCP1*	227413_at	1.66	0.00
ubinuclein 2	*UBN2*	238349_at	-1.73	0.00
ubinuclein 2	*UBN2*	238350_at	-1.56	0.00
ubiquilin 2	*UBQLN2*	215884_s_at	1.55	0.00
ubiquitin carboxyl-terminal hydrolase L5	*UCHL5*	219960_s_at	1.87	0.00
UPF3 regulator of nonsense transcripts homolog A (yeast)	*UPF3A*	206959_s_at	1.32	0.00
uroplakin 1B	*UPK1B*	210064_s_at	2.00	0.00
ubiquinol-cytochrome c reductase	*UQCC1*	229672_at	1.99	0.01

complex assembly factor 1				
ubiquitin specific peptidase 12	*USP12*	215886_x_at	-2.02	0.00
ubiquitin specific peptidase 16	*USP16*	228822_s_at	1.35	0.02
ubiquitin specific peptidase 27, X-linked	*USP27X*	217605_at	-1.62	0.02
ubiquitin specific peptidase 34	*USP34*	242647_at	1.62	0.01
ubiquitin specific peptidase 8	*USP8*	229501_s_at	1.21	0.02
urotensin 2 receptor	*UTS2R*	1553262_a_at	-1.94	0.01
vesicle-associated membrane protein 5	*VAMP5*	214115_at	-1.40	0.00
VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	*VAPA*	225198_at	1.79	0.01
valyl-tRNA synthetase 2, mitochondrial	*VARS2*	226200_at	-2.24	0.00
voltage-dependent anion channel 3	*VDAC3*	208846_s_at	1.37	0.04
vezatin, adherens junctions transmembrane protein	*VEZT*	223090_x_at	1.65	0.01
vanin 3	*VNN3*	220528_at	1.60	0.02
WDFY family member 4	*WDFY4*	229597_s_at	-1.32	0.00
WAS protein homolog associated with actin, golgi membranes and microtubules	*WHAMM*	228953_at	1.37	0.03
WAS/WASL interacting protein family, member 3	*WIPF3*	232389_at	-1.44	0.00
widely interspaced zinc finger motifs	*WIZ*	221785_at	3.63	0.00
WW and C2 domain containing 1	*WWC1*	236725_at	-3.07	0.04
WW domain containing E3 ubiquitin protein ligase 2	*WWP2*	1552737_s_at	1.69	0.00
X antigen family, member 1E	*XAGE1B/XAGE1E*	220057_at	-1.90	0.03
X-prolyl aminopeptidase 3, mitochondrial	*XPNPEP3*	227910_at	2.66	0.00
X-ray repair complementing defective repair in Chinese hamster cells 4	*XRCC4*	205071_x_at	2.54	0.00
X-ray repair complementing defective repair in Chinese hamster cells 4	*XRCC4*	210813_s_at	1.76	0.00
5'-3' exoribonuclease 2	*XRN2*	233878_s_at	1.93	0.00
Yae1 domain containing 1	*YAE1D1*	223433_at	1.83	0.00
Yes-associated protein 1	*YAP1*	224894_at	2.20	0.00
YTH domain containing 2	*YTHDC2*	205835_s_at	2.25	0.00
YY1 transcription factor	*YY1*	201901_s_at	-1.44	0.00
YY1 transcription factor	*YY1*	213494_s_at	-1.38	0.00
zinc finger and BTB domain containing 6	*ZBTB6*	206098_at	2.74	0.03
zinc finger and BTB domain containing 8 opposite strand	*ZBTB8OS*	228970_at	1.32	0.01
zinc finger CCCH-type containing 14	*ZC3H14*	213064_at	1.64	0.03
zinc finger, CCHC domain containing 11	*ZCCHC11*	217594_at	3.61	0.00
zinc finger, CCHC domain containing 5	*ZCCHC5*	1552935_at	2.14	0.00
zinc finger, DHHC-type containing 22	*ZDHHC22*	229805_at	-1.31	0.01
zinc finger, FYVE domain containing 16	*ZFYVE16*	1555011_at	-2.00	0.02
zinc finger, GRF-type containing 1	*ZGRF1*	231204_at	1.85	0.02
zinc fingers and homeoboxes 1	*ZHX1*	223213_s_at	1.39	0.00
zinc finger, MYM-type 4	*ZMYM4*	202051_s_at	1.56	0.01
zinc finger protein 17	*ZNF17*	1558183_at	2.70	0.04
zinc finger protein 182	*ZNF182*	244024_at	1.31	0.00

zinc finger protein 221	*ZNF221*	233848_x_at	2.28	0.01
zinc finger protein 280D	*ZNF280D*	239107_at	-1.91	0.02
zinc finger protein 304	*ZNF304*	207753_at	1.87	0.03
zinc finger protein 33A	*ZNF33A*	224276_at	1.55	0.04
zinc finger protein 41	*ZNF41*	1553216_at	6.41	0.00
zinc finger protein 45	*ZNF45*	207304_at	3.24	0.03
zinc finger protein 506	*ZNF506*	221625_at	1.64	0.05
zinc finger protein 671	*ZNF671*	219849_at	1.49	0.02
zinc finger protein 697	*ZNF697*	1553702_at	-2.17	0.03
zinc finger protein 75a	*ZNF75A*	239204_at	2.29	0.00
zinc finger protein 777	*ZNF777*	228687_at	-1.64	0.04
ZNF790 antisense RNA 1	*ZNF790-AS1*	1558809_s_at	4.70	0.04
zinc finger protein 804A	*ZNF804A*	215767_at	3.81	0.03
zinc finger protein 84	*ZNF84*	204453_at	1.97	0.01
zinc finger and SCAN domain containing 12	*ZSCAN12*	240181_at	-4.25	0.03
zinc finger and SCAN domain containing 30	*ZSCAN30*	228125_at	1.46	0.02

Table S3. Significantly dysregulated biofunctions in fetuses of obese women identified by IPA

Category	Disease or Functional Annotation	P-Value[a]	False Discovery Rate[b]	Activation Z-score	Number of Genes
Cancer, Cellular Development, Cellular Growth and Proliferation	tumorigenesis of melanoma cell lines	0.00	0.26	-2	4
Cell Death and Survival, Nervous System Development and Function	survival of sensory neurons	0.00	0.26	-2.219	5
Infectious Disease	infection of cells	0.01	0.26	2.959	51
Cellular Development, Embryonic Development	differentiation of embryonic cells	0.01	0.26	-2.296	14
Neurological Disease	Neurodegeneration	0.02	0.26	2.201	13
Infectious Disease, Organismal Injury and Abnormalities	infection of embryonic cell lines	0.03	0.26	2.923	18
Dermatological Diseases and Conditions, Infectious Disease	tuberculoid leprosy	0.00	0.13		7
Infectious Disease	Viral Infection	0.00	0.26	1.598	101
Cell Cycle	arrest in cell cycle progression	0.00	0.26		26
Tissue Morphology	abnormality of trophoblast giant cells	0.00	0.26		6
Cancer, Endocrine System Disorders, Reproductive System Disease	clear-cell ovarian carcinoma	0.00	0.26		6
Embryonic Development, Tissue Development	proliferation of embryonic tissue	0.00	0.26		9
Endocrine System Development and Function, Molecular Transport, Protein Synthesis, Small Molecule Biochemistry	quantity of IGF1 in blood	0.00	0.26	0.728	7
Behavior	parental behavior	0.00	0.26		6
Dermatological Diseases and Conditions, Infectious Disease	leprosy	0.00	0.26		10
Tissue Morphology	abnormal morphology of trophoblast	0.00	0.26		8
RNA Post-Transcriptional Modification	processing of RNA	0.00	0.26	1.633	22

Cellular Assembly and Organization, Cellular Function and Maintenance	hyperpolarization of mitochondria	0.00	0.26		3
Hematological Disease, Immunological Disease, Infectious Disease	infection of myeloid cells	0.00	0.26	-0.447	5
Cell Cycle	interphase of T lymphocytes	0.00	0.26	1	5
Hereditary Disorder, Neurological Disease	hereditary spastic paraplegia	0.00	0.26		6
Hematological Disease, Immunological Disease, Infectious Disease	infection of phagocytes	0.00	0.26	-0.555	6
Hereditary Disorder, Infectious Disease	familial atypical mycobacteriosis	0.00	0.26		3
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	infiltration by monocyte-derived macrophages	0.00	0.26		3
Molecular Transport, RNA Trafficking	transport of mRNA	0.00	0.26		7
Behavior, Reproductive System Development and Function	maternal behavior	0.00	0.26		5
Cell Death and Survival	apoptosis of muscle cells	0.00	0.26	0.169	20
Endocrine System Development and Function, Organ Development	activation of thyroid gland	0.00	0.26		3
Cell Cycle	cell cycle progression of eye cells	0.00	0.26		3
Cancer, Neurological Disease	hyperplasia of brain cells	0.00	0.26		3
Hematological Disease, Immunological Disease, Infectious Disease	infection of leukocytes	0.00	0.26	0.092	7
Infectious Disease	infection by mycobacteria	0.00	0.26		4
Cell Cycle	arrest in interphase of bone cancer cell lines	0.00	0.26		6
Endocrine System Development and Function, Organ Morphology	abnormal morphology of thyroid follicle	0.00	0.26		3
Cell Signaling	Ras protein signal transduction	0.00	0.26		7

Cell Signaling	small GTPase mediated signal transduction	0.00	0.26		14
Neurological Disease, Organismal Injury and Abnormalities	gliosis of brain	0.00	0.26	0.555	5
Cell Death and Survival	cell death of muscle cells	0.00	0.26	0.998	23
Cell Cycle	cycling of centrosome	0.00	0.26		7
Cardiovascular System Development and Function, Cellular Movement	chemotaxis of vascular endothelial cells	0.00	0.26	0	4
Hereditary Disorder, Neurological Disease	hereditary motor and sensory neuropathy	0.00	0.26		8
Molecular Transport, RNA Trafficking	export of mRNA	0.00	0.26		6
Cell Death and Survival	apoptosis of T lymphocytes	0.00	0.26	0.184	20
Cancer	development of breast carcinoma	0.00	0.26		3
Cancer, Cellular Development	immortalization of leukocytes	0.00	0.26		3
Cellular Development, Cellular Growth and Proliferation	proliferation of biliary epithelial cells	0.00	0.26		3
Cellular Development	immortalization	0.00	0.26	-0.425	7
Cell Cycle	arrest in cell cycle progression of blood cells	0.00	0.26		4
Cell Cycle	interphase of leukemia cell lines	0.00	0.26		5
Endocrine System Development and Function, Organ Morphology	morphology of thyroid gland	0.00	0.26		5
Infectious Disease	replication of RNA virus	0.00	0.26	-0.774	33
Molecular Transport, Protein Trafficking	transport of protein	0.01	0.26		20
Cellular Development, Cellular Growth and Proliferation, Connective Tissue Development and Function	arrest in growth of fibroblasts	0.01	0.26		4
Cancer, Endocrine System Disorders	hyperplasia of neuroendocrine cells	0.01	0.26	-0.205	4
Cancer	cell transformation	0.01	0.26	0.599	31

Cell Cycle	G1 phase of T lymphocytes	0.01	0.26		3
Cell Cycle	arrest in G2/M phase of breast cancer cell lines	0.01	0.26		3
Cell-mediated Immune Response, Cellular Development, Cellular Function and Maintenance, Hematological System Development and Function, Hematopoiesis, Lymphoid Tissue Structure and Development	development of TREG cells	0.01	0.26		3
Cardiovascular System Development and Function, Embryonic Development, Tissue Development	septation of outflow tract	0.01	0.26		3
Cellular Compromise, Organismal Injury and Abnormalities	atrophy of cells	0.01	0.26	0	6
Cell Death and Survival	necrosis	0.01	0.26	0.54	126
Cellular Function and Maintenance	maintenance of cells	0.01	0.26	1.461	9
Cell Death and Survival	apoptosis of lymphocytes	0.01	0.26	0.574	23
Cellular Assembly and Organization	transport of endosomes	0.01	0.26		5
Cancer	hyperplasia of cells	0.01	0.26	-1.103	18
Cell Morphology, Skeletal and Muscular System Development and Function	size of muscle cells	0.01	0.26	1.177	10
Embryonic Development, Organismal Development, Tissue Development	formation of anlage	0.01	0.26		4
DNA Replication, Recombination, and Repair	DNA replication	0.01	0.26	-0.286	18
Cellular Growth and Proliferation, Nervous System Development and Function, Tissue Development	generation of neurons	0.01	0.26	-0.665	6
Cell Cycle	cell cycle progression of T lymphocytes	0.01	0.26		5
Cancer, Immunological Disease	development of lymphoma	0.01	0.26		5
Cell Cycle	arrest in interphase	0.01	0.26		26
Cell Cycle	S phase of T	0.01	0.26		3

	lymphocytes				
Embryonic Development, Organismal Development, Tissue Development	development of allantois	0.01	0.26		3
Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Cellular Function and Maintenance, Tissue Development	formation of focal complexes	0.01	0.26		3
Endocrine System Development and Function, Molecular Transport, Protein Synthesis, Small Molecule Biochemistry	quantity of TSH in blood	0.01	0.26		3
Cell Death and Survival, Hematological System Development and Function	survival of pro-B lymphocytes	0.01	0.26		3
Cell Cycle	G0 phase	0.01	0.26		8
Cell Cycle	G1 phase of tumor cell lines	0.01	0.26	-1.109	15
Cellular Function and Maintenance	maintenance of T lymphocytes	0.01	0.26	1.177	4
Cell Cycle	G1 phase	0.01	0.26	-0.156	25
Embryonic Development, Tissue Development	proliferation of embryoblast	0.01	0.26		6
Cardiovascular System Development and Function, Cell Morphology, Skeletal and Muscular System Development and Function	size of cardiomyocytes	0.01	0.26	0.391	6
Cell-To-Cell Signaling and Interaction	activation of tumor cell lines	0.01	0.26	1.069	8
Gene Expression	transactivation	0.01	0.26	1.391	37
Cell Cycle	cell cycle progression	0.01	0.26	0.777	60
Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function	proliferation of B-lymphocyte derived cell lines	0.01	0.26	-0.114	10
Cell Signaling, Post-Translational Modification	activation of MAP kinase kinase	0.01	0.26		5
Cell-To-Cell Signaling and Interaction	activation of leukemia cell lines	0.01	0.26	1.264	5
Cancer, Endocrine System Disorders	hyperplasia of endocrine cells	0.01	0.26	0.138	5

Cell-To-Cell Signaling and Interaction	sensitization of cells	0.01	0.26	1.109	5
Gene Expression	transactivation of RNA	0.01	0.26	1.065	36
Cell Cycle, Connective Tissue Development and Function	G1/S phase transition of fibroblast cell lines	0.01	0.26		4
Cancer, Endocrine System Disorders, Reproductive System Disease	mucinous ovarian cancer	0.01	0.26		4
Cellular Development, Cellular Growth and Proliferation, Nervous System Development and Function	proliferation of neuroglia	0.01	0.26	-0.277	10
Cell Cycle	arrest in cell cycle progression of T lymphocytes	0.01	0.26		3
Cell Death and Survival, Nervous System Development and Function	cell viability of striatal neurons	0.01	0.26		3
Hereditary Disorder, Neurological Disease	familial amyotrophic lateral sclerosis	0.01	0.26		3
Metabolic Disease	impaired glucose tolerance	0.01	0.26		3
Cancer	onset of tumorigenesis	0.01	0.26		3
Cell Cycle	delay in initiation of interphase	0.01	0.26	-1.706	6

IPA, Ingenuity Pathways Analysis
[a]Right-tailed Fisher's exact p-value
[b]Benjamini-Hochberg p-value

Table S4. Significantly activated and inhibited upstream regulators in fetuses of obese women

Symbol	Upstream Regulator Name	Molecule Function[a]	Predicted Activation State	Activation Z-score	Number of downstream target genes
CREM	cAMP responsive element modulator	cAMP-mediated signaling, cell differentiation. Implicated in neurodegeneration, circadian regulation of gene expression, fatty acid metabolism, glucose metabolism, regulation of apoptosis, diabetes mellitus/insulin resistance	Activated	2.00	7
N/A	salmonella minnesota R595 lipopolysaccharides	Cytokine-mediated and toll-like receptor inflammatory signaling	Activated	2.00	4
KAT5	K(lysine) acetyltransferase 5	Androgen-receptor signaling, cellular response to estradiol, DNA damage response, negative regulation of transcription from RNA polymerase II promoter	Activated	2.00	4
OSM	oncostatin M	Cytokine-mediated and acute phase response signaling, recognition of bacteria and viruses, immune response, positive regulation of acute inflammatory response, positive regulation of apoptotic signaling, peripheral nervous system development, behavioral response to pain	Activated	2.08	25
TNF	Tumor necrosis factor	Pro-inflammatory cytokine secreted by macrophages. Implicated in inflammatory response, cell proliferation, apoptosis induction, lipid metabolism, coagulation	Activated	2.15	55
etoposide	etoposide	Topoisomerase inhibitor. Used to treat a wide range of cancers including leukemias, lymphomas and solid cancers	Activated	2.16	8

FIGF, PDGFC, PGF, PROK1, VEGFA, VEGFB, VEGFC	Vascular endothelial growth factor group	Vegf signaling, angiogenesis, axonal guidance signaling, mTOR signaling, cytokine-mediated signaling	Activated	2.16	11
MYD88	Myeloid differentiation primary response 88	Adapter protein central to innate and adaptive immune response, essential signal transducer in IL-1 and toll-like receptor signaling pathways, activates numerous proinflammatory genes. Implicated in acute phase response, cytokine-mediated signaling, recognition of bacteria and viruses, response to LPS	Activated	2.17	5
TP53	Tumor protein p53	Tumor suppressor protein, responds to cellular stress to induce cell cycle arrest, apoptosis, senescence, or DNA repair. Mutations associated with human cancers	Activated	2.17	45
H89	H89	Protein kinase A inhibitor; also inhibits several other kinases, and regulates *CREB, Erk1/2, TNF, NOS3, FOS, MAPK.* Used to treat dopaminergic, GABAnergic, and excitotoxic disorders	Activated	2.18	5
N/A	streptozocin	Aminoglycoside antibiotic used as an anticancer agent. Regulates glucose, insulin, inflammatory regulators. Implicated in apoptosis, necrosis, cell proliferation, cell destruction	Activated	2.19	8
N/A	metribolone: methyltrienolone	Synthetic non-aromatizable androgen and anabolic steroid. Binds strongly to antrogen receptor	Activated	2.19	6

N/A	resveratrol: 3,4',5-trihydroxystilbene	Antioxidant phenol derivative found in plants. Anti-inflammatory, anticoagulant, anti-atherogenic properties. Investigated for treatment of obesity, metabolic syndrome, disorders of lipid metabolism, insulin resistance, Alzheimer's disease, Friedreich ataxia, cancers	Activated	2.19	6
N/A	6-hydroxydopamine: oxidopamine	Neurotransmitter analogue that depletes noradrenergic stores in nerve endings, reduces brain dopamine levels. Produces cytolytic free radicals. Implicated in cell death, apoptosis, neurodegeneration, Parkinson's disease	Activated	2.22	5
IFNG	interferon gamma	Member of type II interferon family. Cytokine with antiviral, immunoregulatory and anti-tumor properties, potent macrophage activator. Implicated in adaptive immune response, antigen processing, apoptosis, T cell differentiation and proliferation	Activated	2.29	37
N/A	bucladesine: dibutyryl cAMP	Cyclic nucleotide derivative that mimics endogeous cAMP. Vasodilatory properties, used as a cardiac stimulant in treatment of heart failure. Investigated as a treatment for metabolic disorders	Activated	2.38	9
TICAM1	toll-like receptor adaptor molecule 1	Toll-like receptor signaling, response to bacteria and viruses, apoptotic signaling pathway, Innate immune response; lipopolysaccharide-mediated signaling pathway; positive regulation of B cell	Activated	2.43	6

		proliferation and differentiation			
MYC	v-myc avian myelocytomatosis viral oncogene homolog	Cell cycle regulation, DNA damage response, apoptosis regulation, canonical Wnt receptor signaling pathway, Notch signaling pathway, cellular response to carbohydrate and estradiol stimulus, cellular response to growth hormone	Activated	2.45	33
IFNA1/IFNA13, IFNA21, IFNA5, IFNB1	Interferon alpha/beta group	Cytokine-mediated signaling, communication between innate and adaptive immune cells, recognition of bacteria and viruses, B cell proliferation and differentiation, T-cell activation	Activated	2.45	6
N/A	calcitriol (1,25-dihydroxyvitamin D3)	1,25-dihydroxyvitamin D3 biosynthesis; IL-12 signaling	Activated	2.48	14
LPS	lipopolysaccharide	Cytokine-mediated signaling, toll-like receptor signaling, crosstalk between innate and adaptive immune cells, recognition of bacteria and viruses, reactive oxygen production in macrophages	Activated	3.09	56
miR-16-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	Cell cycle progression, apoptotic signaling	Inhibited	-2.64	11
miR-155-5p	miR-155-5p (miRNAs w/seed UAAUGCU)	Cytokine-mediated signaling. Regulated by LPS, enterotoxin, Vegf	Inhibited	-2.61	7
Ins1	Insulin 1	Insulin-receptor signaling, glucose homeostasis, adipogenesis, fatty acid metabolism, negative regulation of acute phase response	Inhibited	-2.60	12

STAT5A	signal transducer and activator of transcription 5A	Cytokine-mediated signaling, growth hormone and JAK/STAT signaling, glucocorticoid receptor signaling, negative regulation of apoptosis, positive regulation of B and T cell proliferation and differentiation	Inhibited	-2.37	6
HRAS, KRAS, MRAS, NRAS, RRAS, RRAS2	Rat sarcoma viral oncogene homolog family	Cell cycle progression, growth and differentiation; cytokine and acute phase response signaling; apoptosis	Inhibited	-2.22	5
EPAS1	Endothelial PAS domain protein 1	Induction of genes regulated by low oxygen levels, angiogenesis, cellular response to hypoxia and oxidative stress, iron homeostasis	Inhibited	-2.20	7
STAT5B	Signal transducer and activator of transcription 5B	Acute phase response, cellular response to growth factor stimulus, cytokine-mediated signaling, positive regulation of inflammatory response, positive regulation of T and B- cell proliferation and differentiation, fatty acid metabolism, lipid storage	Inhibited	-2.18	8
miR -1-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	Axonal guidance/BDNF-signaling, estrogen signaling, cardiac morphogenesis, limb and branchial arch development, growth hormone signaling	Inhibited	-2.08	16
N/A	Sirolimus	mTOR inhibitor/immunosuppressant, inhibits IL-2 and other cytokine receptor-dependent signal transduction, ultimately inhibits activation of T and B lymphocytes	Inhibited	-2.06	22
INSIG1	Insulin induced gene 1	Insulin-induced gene involved in regulation of cholesterol homeostasis, lipid metabolism	Inhibited	-2.00	4

ADRB1, ADRB2, ADRB3	Beta Adrenergic Receptor Family	Adrenergic/epinephrine and norepinephrine-mediated signaling; fear response; regulation of cardiomyocyte development; positive regulation of heart rate and contractility; lipid homeostasis; brown fat cell differentiation;thermogenesis	Inhibited	-2.00	4

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[a] Gene/molecule functions obtained from the following databases: UniProt, EntrezGene, PubChem, Ingenuity Knowledge Base. Descriptions modified due to space constraints.

Table S5. Significantly dysregulated gene sets in fetuses of obese women identified by GSEA/DFLAT

Gene Set	Number of Genes in Gene Set	Normalized Enrichment Score	P-value[a]	FDR q-value[b]
JAK-STAT CASCADE	45	2.03	0.00	0.02
JAK-STAT CASCADE INVOLVED IN GROWTH HORMONE SIGNALING PATHWAY	24	1.97	0.00	0.04
GROWTH HORMONE RECEPTOR SIGNALING PATHWAY	27	1.91	0.00	0.09
RESPONSE TO GROWTH HORMONE STIMULUS	27	1.91	0.00	0.07
REGULATION OF RESPONSE TO INTERFERON-GAMMA	20	1.90	0.00	0.07
CELLULAR RESPONSE TO GROWTH HORMONE STIMULUS	27	1.89	0.00	0.06
NEGATIVE REGULATION OF AXON EXTENSION	16	1.85	0.00	0.11
REGULATION OF CHROMOSOME SEGREGATION	23	1.85	0.00	0.10
REGULATION OF INTERFERON-GAMMA-MEDIATED SIGNALING PATHWAY	19	1.84	0.00	0.10
TELENCEPHALON CELL MIGRATION	38	1.83	0.00	0.11
REGULATION OF MRNA PROCESSING	28	1.82	0.00	0.12
FOREBRAIN CELL MIGRATION	41	1.82	0.00	0.13
REGULATION OF EPIDERMIS DEVELOPMENT	15	1.81	0.00	0.13
M PHASE OF MITOTIC CELL CYCLE	143	1.81	0.00	0.13
NEGATIVE REGULATION OF DEVELOPMENTAL GROWTH	24	1.81	0.00	0.12
NUCLEAR DIVISION	135	1.80	0.00	0.13
MITOSIS	135	1.79	0.00	0.13
REGULATION OF ANDROGEN RECEPTOR SIGNALING PATHWAY	20	1.78	0.00	0.15
ORGANELLE FISSION	149	1.78	0.00	0.15
REGULATION OF INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY	35	1.77	0.00	0.17
NUCLEAR-TRANSCRIBED MRNA POLY(A) TAIL SHORTENING	20	1.76	0.00	0.18
PEPTIDYL-SERINE MODIFICATION	57	1.75	0.00	0.19
MICROTUBULE CYTOSKELETON ORGANIZATION	132	1.75	0.00	0.18

NATURAL KILLER CELL DIFFERENTIATION	13	1.75	0.00	0.18
NEGATIVE REGULATION OF AXONOGENESIS	39	1.75	0.00	0.18
NUCLEAR PORE ORGANIZATION	10	1.75	0.00	0.18
NCRNA CATABOLIC PROCESS	9	1.75	0.00	0.17
CELLULAR RESPONSE TO IONIZING RADIATION	22	1.74	0.00	0.17
REGULATION OF TRANSLATION	106	1.74	0.00	0.17
REGULATION OF KERATINOCYTE DIFFERENTIATION	11	1.74	0.00	0.18
'DE NOVO' POSTTRANSLATIONAL PROTEIN FOLDING	29	1.73	0.00	0.19
PROTEIN HOMOTETRAMERIZATION	26	1.73	0.00	0.18
GENE SILENCING	44	1.73	0.00	0.19
'DE NOVO' PROTEIN FOLDING	33	1.73	0.00	0.18
SPINDLE ASSEMBLY	22	1.73	0.00	0.18
REGULATION OF EPIDERMAL CELL DIFFERENTIATION	12	1.73	0.01	0.17
REGULATION OF HELICASE ACTIVITY	8	1.73	0.00	0.17
POST-GOLGI VESICLE-MEDIATED TRANSPORT	62	1.72	0.00	0.18
RESPONSE TO IONIZING RADIATION	47	1.72	0.00	0.18
RNA 3'-END PROCESSING	62	1.72	0.00	0.18
NUCLEAR IMPORT	50	1.71	0.00	0.18
POSITIVE REGULATION OF NEURON DEATH	13	1.71	0.00	0.18
ORGANELLE LOCALIZATION	107	1.71	0.00	0.18
REGULATION OF MICROTUBULE-BASED PROCESS	59	1.71	0.00	0.18
CENTRAL NERVOUS SYSTEM NEURON AXONOGENESIS	23	1.71	0.01	0.18
G2/M TRANSITION OF MITOTIC CELL CYCLE	97	1.70	0.00	0.18
EMBRYONIC CRANIAL SKELETON MORPHOGENESIS	36	1.70	0.00	0.18
PORE COMPLEX ASSEMBLY	9	1.70	0.00	0.18
CYTOKINESIS	67	1.70	0.00	0.18
MITOCHONDRIAL FISSION	8	1.70	0.00	0.19
REGULATION OF RNA SPLICING	32	1.70	0.00	0.18
NEGATIVE REGULATION OF EPITHELIAL CELL PROLIFERATION	47	1.70	0.00	0.18
REGULATION OF NUCLEAR-TRANSCRIBED MRNA CATABOLIC PROCESS, DEADENYLATION-DEPENDENT DECAY	9	1.70	0.00	0.18

MITOTIC PROMETAPHASE	71	1.69	0.00	0.18
RNA STABILIZATION	20	1.69	0.01	0.18
REGULATION OF ALTERNATIVE MRNA SPLICING, VIA SPLICEOSOME	8	1.69	0.01	0.18
POSITIVE REGULATION OF EPIDERMIS DEVELOPMENT	8	1.69	0.01	0.19
MRNA 3'-END PROCESSING	55	1.68	0.00	0.18
PROTEIN TARGETING TO NUCLEUS	49	1.68	0.00	0.18
REGULATION OF NUCLEAR-TRANSCRIBED MRNA POLY(A) TAIL SHORTENING	9	1.68	0.00	0.18
REGULATION OF MICROTUBULE CYTOSKELETON ORGANIZATION	49	1.68	0.00	0.18
NEGATIVE REGULATION OF CYTOSKELETON ORGANIZATION	33	1.68	0.01	0.19
MRNA STABILIZATION	20	1.68	0.00	0.18
PEPTIDYL-SERINE PHOSPHORYLATION	54	1.68	0.00	0.18
NEGATIVE REGULATION OF MAP KINASE ACTIVITY	39	1.68	0.00	0.18
REGULATION OF CELL CYCLE PHASE TRANSITION	123	1.68	0.00	0.18
NEGATIVE REGULATION OF AXON EXTENSION INVOLVED IN AXON GUIDANCE	7	1.67	0.01	0.19
PROTEIN IMPORT INTO NUCLEUS	49	1.67	0.00	0.19
REGULATION OF MITOTIC CELL CYCLE PHASE TRANSITION	123	1.67	0.00	0.19
VIRAL ENTRY INTO HOST CELL	10	1.67	0.01	0.19
REGULATION OF B CELL PROLIFERATION	27	1.67	0.01	0.19
CELL DIVISION	102	1.67	0.00	0.19
NUCLEOCYTOPLASMIC TRANSPORT	121	1.66	0.00	0.19
DENTATE GYRUS DEVELOPMENT	14	1.66	0.01	0.20
T CELL DIFFERENTIATION	105	1.66	0.00	0.20
REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	55	1.66	0.00	0.20
NEGATIVE REGULATION OF G1/S TRANSITION OF MITOTIC CELL CYCLE	74	1.65	0.00	0.20
POSITIVE REGULATION OF NUCLEAR-TRANSCRIBED MRNA POLY(A) TAIL SHORTENING	8	1.65	0.02	0.20
KERATINOCYTE DIFFERENTIATION	50	1.65	0.00	0.21
NEGATIVE REGULATION OF MITOTIC CELL CYCLE PHASE TRANSITION	102	1.65	0.00	0.21

CEREBRAL CORTEX NEURON DIFFERENTIATION	16	1.65	0.01	0.21
PROTEIN TETRAMERIZATION	47	1.65	0.00	0.20
ESTABLISHMENT OF ORGANELLE LOCALIZATION	75	1.65	0.00	0.20
SPINDLE ORGANIZATION	37	1.65	0.01	0.21
GOLGI VESICLE TRANSPORT	116	1.64	0.00	0.21
POSITIVE REGULATION OF MRNA PROCESSING	15	1.64	0.01	0.21
REGULATION OF MRNA CATABOLIC PROCESS	12	1.64	0.01	0.21
REGULATION OF ANION TRANSPORT	23	1.64	0.01	0.20
PEPTIDYL-THREONINE MODIFICATION	27	1.64	0.00	0.21
NEGATIVE REGULATION OF CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY	48	1.64	0.00	0.21
BRAIN MORPHOGENESIS	27	1.64	0.01	0.21
TOLL-LIKE RECEPTOR 2 SIGNALING PATHWAY	63	1.64	0.00	0.21
CHAPERONE-MEDIATED PROTEIN FOLDING	12	1.63	0.00	0.21
REGULATION OF G1/S TRANSITION OF MITOTIC CELL CYCLE	86	1.63	0.00	0.21
NEGATIVE REGULATION OF CELL CYCLE PHASE TRANSITION	102	1.63	0.00	0.21
REGULATION OF MITOTIC METAPHASE/ANAPHASE TRANSITION	34	1.63	0.01	0.21
REGULATION OF DENDRITIC SPINE MORPHOGENESIS	14	1.63	0.01	0.21
NEGATIVE REGULATION OF CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY INVOLVED IN APOPTOTIC PROCESS	45	1.63	0.00	0.21
RESPONSE TO ANTIBIOTIC	16	1.63	0.01	0.22
RESPONSE TO INTERLEUKIN-6	13	1.63	0.01	0.22
POSITIVE REGULATION OF NEURON APOPTOTIC PROCESS	12	1.62	0.01	0.22
MICROTUBULE-BASED MOVEMENT	68	1.62	0.00	0.22
AEROBIC RESPIRATION	31	1.62	0.01	0.22
REGULATION OF FILOPODIUM ASSEMBLY	18	1.62	0.01	0.22
VISUAL LEARNING	10	1.62	0.01	0.22
REGULATION OF MRNA SPLICING, VIA SPLICEOSOME	14	1.62	0.01	0.22

POSITIVE REGULATION OF CELL CYCLE	74	1.62	0.00	0.23
REGULATION OF EPITHELIAL CELL DIFFERENTIATION	31	1.62	0.00	0.23
OLFACTORY LOBE DEVELOPMENT	24	1.62	0.01	0.22
SIGNAL TRANSDUCTION IN RESPONSE TO DNA DAMAGE	88	1.62	0.00	0.23
FAT CELL DIFFERENTIATION	74	1.61	0.00	0.23
CEREBRAL CORTEX CELL MIGRATION	29	1.61	0.01	0.23
GOLGI ORGANIZATION	29	1.61	0.01	0.23
TYPE B PANCREATIC CELL DEVELOPMENT	11	1.61	0.01	0.23
PROTEIN POLYUBIQUITINATION	144	1.61	0.00	0.23
REGULATION OF LYMPHOCYTE CHEMOTAXIS	12	1.61	0.01	0.23
ACTIVATION OF SIGNALING PROTEIN ACTIVITY INVOLVED IN UNFOLDED PROTEIN RESPONSE	63	1.61	0.00	0.23
NEGATIVE REGULATION OF ORGANELLE ORGANIZATION	111	1.61	0.00	0.23
PANTOTHENATE METABOLIC PROCESS	11	1.61	0.01	0.23
NUCLEAR TRANSPORT	124	1.61	0.00	0.23
OLFACTORY BULB DEVELOPMENT	24	1.61	0.01	0.23
REGULATION OF RELEASE OF SEQUESTERED CALCIUM ION INTO CYTOSOL BY SARCOPLASMIC RETICULUM	15	1.61	0.02	0.23
GTP METABOLIC PROCESS	89	1.61	0.00	0.23
PROTEIN MODIFICATION BY SMALL PROTEIN REMOVAL	70	1.60	0.00	0.23
GTP CATABOLIC PROCESS	88	1.60	0.00	0.23
NEGATIVE REGULATION OF TRANSLATION	45	1.60	0.00	0.22
SIGNAL TRANSDUCTION BY PHOSPHORYLATION	29	1.60	0.01	0.23
NEGATIVE REGULATION OF PROTEIN DEPOLYMERIZATION	19	1.60	0.01	0.23
MICROTUBULE ORGANIZING CENTER ORGANIZATION	39	1.60	0.01	0.23
CILIUM MORPHOGENESIS	83	1.60	0.00	0.24
T CELL DIFFERENTIATION IN THYMUS	49	1.60	0.01	0.24
GENE SILENCING BY RNA	31	1.60	0.01	0.24
CEREBRAL CORTEX RADIAL GLIA GUIDED MIGRATION	11	1.60	0.01	0.23
NEGATIVE REGULATION OF CELL CYCLE PROCESS	137	1.59	0.00	0.24

ER TO GOLGI VESICLE-MEDIATED TRANSPORT	26	1.59	0.01	0.24
RENAL TUBULE MORPHOGENESIS	18	1.59	0.02	0.24
REGULATION OF PHOSPHATIDYLINOSITOL 3-KINASE CASCADE	44	1.59	0.01	0.24
PROTEIN COMPLEX LOCALIZATION	17	1.59	0.01	0.24
TOLL-LIKE RECEPTOR 1 SIGNALING PATHWAY	61	1.59	0.00	0.24
REGULATION OF NUCLEASE ACTIVITY	71	1.59	0.00	0.24
MYD88-DEPENDENT TOLL-LIKE RECEPTOR SIGNALING PATHWAY	66	1.59	0.00	0.24
N-ACETYLGLUCOSAMINE METABOLIC PROCESS	8	1.59	0.02	0.25
GENE SILENCING BY MIRNA	23	1.59	0.01	0.24
EPIDERMAL CELL DIFFERENTIATION	61	1.58	0.00	0.24
GUANOSINE-CONTAINING COMPOUND CATABOLIC PROCESS	90	1.58	0.00	0.24
CELLULAR RESPONSE TO INTERLEUKIN-6	10	1.58	0.01	0.24
REGULATION OF ATTACHMENT OF SPINDLE MICROTUBULES TO KINETOCHORE	7	1.58	0.01	0.24
TRICARBOXYLIC ACID CYCLE	20	1.58	0.01	0.24
ENTRY INTO HOST CELL	13	1.58	0.02	0.24
LAYER FORMATION IN CEREBRAL CORTEX	7	1.58	0.02	0.24
LEARNING	23	1.58	0.02	0.24
REGULATION OF MRNA 3'-END PROCESSING	13	1.58	0.02	0.24
PROTEIN AUTOPHOSPHORYLATION	119	1.58	0.00	0.24
GUANOSINE-CONTAINING COMPOUND METABOLIC PROCESS	95	1.58	0.00	0.24
PROTEIN DEUBIQUITINATION	57	1.58	0.00	0.24
POSITIVE REGULATION OF MRNA CATABOLIC PROCESS	11	1.58	0.02	0.24
PROTEIN FOLDING	89	1.58	0.00	0.24
REGULATION OF COFACTOR METABOLIC PROCESS	11	1.58	0.02	0.24
REGULATION OF ACYL-COA BIOSYNTHETIC PROCESS	11	1.58	0.02	0.24
NUCLEUS ORGANIZATION	34	1.58	0.01	0.24
CELLULAR RESPONSE TO CALCIUM ION	19	1.58	0.02	0.24
MOVEMENT IN HOST ENVIRONMENT	13	1.58	0.02	0.24

REGULATION OF COENZYME METABOLIC PROCESS	11	1.58	0.01	0.24
RENAL TUBULE DEVELOPMENT	23	1.57	0.02	0.24
ASSOCIATIVE LEARNING	12	1.57	0.02	0.25
ENTRY INTO CELL OF OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	13	1.57	0.03	0.24
NEGATIVE REGULATION OF MAPK CASCADE	64	1.57	0.00	0.25
POSITIVE REGULATION OF NUCLEAR-TRANSCRIBED MRNA CATABOLIC PROCESS, DEADENYLATION-DEPENDENT DECAY	7	1.57	0.02	0.24
REGULATION OF ACETYL-COA BIOSYNTHETIC PROCESS FROM PYRUVATE	11	1.57	0.01	0.24
INTEGRIN-MEDIATED SIGNALING PATHWAY	22	1.57	0.01	0.24
POSTTRANSCRIPTIONAL GENE SILENCING	24	1.57	0.02	0.24
B CELL ACTIVATION	82	1.57	0.00	0.24
REGULATION OF MUSCLE CELL DIFFERENTIATION	70	1.57	0.00	0.24
CEREBRAL CORTEX DEVELOPMENT	64	1.57	0.01	0.24
POSITIVE REGULATION OF EPITHELIAL CELL DIFFERENTIATION	12	1.57	0.03	0.24
CAMERA-TYPE EYE PHOTORECEPTOR CELL DIFFERENTIATION	14	1.57	0.02	0.24
NEGATIVE REGULATION OF TRANSLATION, NCRNA-MEDIATED	8	1.57	0.02	0.24
POSITIVE REGULATION OF NUCLEASE ACTIVITY	65	1.57	0.00	0.24
REGULATION OF MUSCLE ADAPTATION	18	1.57	0.02	0.24
POSTTRANSCRIPTIONAL GENE SILENCING BY RNA	24	1.57	0.01	0.24
POSITIVE REGULATION OF PHOSPHATIDYLINOSITOL 3-KINASE ACTIVITY	18	1.56	0.02	0.24
MOVEMENT IN ENVIRONMENT OF OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	13	1.56	0.02	0.24
ENTRY INTO OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	13	1.56	0.02	0.24

NUCLEAR PORE COMPLEX ASSEMBLY	7	1.56	0.02	0.24
ESTABLISHMENT OF SPINDLE LOCALIZATION	12	1.56	0.02	0.24
SOMATIC CELL DNA RECOMBINATION	31	1.56	0.01	0.24
PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE	32	1.56	0.02	0.24
CELLULAR RESPONSE TO ABIOTIC STIMULUS	103	1.56	0.00	0.24
REGULATION OF RESPONSE TO CYTOKINE STIMULUS	69	1.56	0.00	0.23
TYPE B PANCREATIC CELL DIFFERENTIATION	12	1.56	0.02	0.24
REGULATION OF TRANSLATION, NCRNA-MEDIATED	8	1.56	0.02	0.24
NEGATIVE REGULATION OF MITOTIC METAPHASE/ANAPHASE TRANSITION	28	1.56	0.01	0.24
ENTRY INTO HOST	13	1.56	0.02	0.24
SIGNAL TRANSDUCTION INVOLVED IN CELL CYCLE CHECKPOINT	65	1.56	0.01	0.24
SPINDLE LOCALIZATION	12	1.56	0.01	0.24
SPINDLE CHECKPOINT	31	1.56	0.01	0.24
PROTEIN IMPORT	70	1.56	0.01	0.23
NEGATIVE REGULATION OF ENDOTHELIAL CELL PROLIFERATION	19	1.56	0.02	0.23
PROTEIN LOCALIZATION TO NUCLEUS	69	1.56	0.00	0.23
REGULATION OF INTERPHASE OF MITOTIC CELL CYCLE	98	1.56	0.00	0.23
DNA DAMAGE CHECKPOINT	106	1.56	0.00	0.24
MITOCHONDRION ORGANIZATION	117	1.56	0.00	0.24
REGULATION OF BINDING	104	1.55	0.00	0.24
ORGANELLE ASSEMBLY	52	1.55	0.00	0.24
SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS VIA GERMLINE RECOMBINATION WITHIN A SINGLE LOCUS	31	1.55	0.02	0.23
PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN-DEPENDENT PROTEIN CATABOLIC PROCESS	21	1.55	0.02	0.23
NEGATIVE REGULATION OF NEUROGENESIS	79	1.55	0.01	0.24
SPINDLE ASSEMBLY CHECKPOINT	27	1.55	0.01	0.24

NEGATIVE REGULATION OF INTRACELLULAR PROTEIN KINASE CASCADE	96	1.55	0.00	0.24
VESICLE LOCALIZATION	56	1.55	0.01	0.24
PROTEIN SUMOYLATION	17	1.55	0.01	0.24
SIGNAL TRANSDUCTION INVOLVED IN DNA INTEGRITY CHECKPOINT	64	1.55	0.01	0.24
REGULATION OF INTRACELLULAR ESTROGEN RECEPTOR SIGNALING PATHWAY	15	1.55	0.02	0.24
SIGNAL TRANSDUCTION INVOLVED IN MITOTIC CELL CYCLE CHECKPOINT	63	1.55	0.01	0.24
DNA INTEGRITY CHECKPOINT	108	1.55	0.00	0.24
NEGATIVE REGULATION OF TRANSLATION INVOLVED IN GENE SILENCING BY MIRNA	8	1.55	0.03	0.24
CHROMOSOME SEGREGATION	72	1.55	0.01	0.24
SIGNAL TRANSDUCTION INVOLVED IN DNA DAMAGE CHECKPOINT	64	1.55	0.01	0.24
HEMATOPOIETIC PROGENITOR CELL DIFFERENTIATION	29	1.55	0.01	0.24
SMOOTH MUSCLE CONTRACTION	24	1.55	0.01	0.24
PLATELET-DERIVED GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	12	1.55	0.02	0.24
TRANSEPITHELIAL TRANSPORT	9	1.54	0.02	0.24
CEREBRAL CORTEX GABAERGIC INTERNEURON DIFFERENTIATION	9	1.54	0.02	0.24
CENTRAL NERVOUS SYSTEM PROJECTION NEURON AXONOGENESIS	18	1.54	0.03	0.24
REGULATION OF AXON EXTENSION INVOLVED IN AXON GUIDANCE	8	1.54	0.02	0.24
NEGATIVE REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	15	1.54	0.02	0.24
REGULATION OF NITRIC-OXIDE SYNTHASE BIOSYNTHETIC PROCESS	9	1.54	0.02	0.24
DEVELOPMENT OF SECONDARY SEXUAL CHARACTERISTICS	10	1.54	0.01	0.24
PROTEIN ACETYLATION	66	1.54	0.01	0.24
POSITIVE REGULATION OF B CELL PROLIFERATION	19	1.54	0.02	0.24
CILIUM ORGANIZATION	64	1.54	0.00	0.24

B CELL RECEPTOR SIGNALING PATHWAY	19	1.54	0.03	0.24
VISUAL BEHAVIOR	12	1.54	0.02	0.24
VESICLE TARGETING	30	1.54	0.02	0.24
CELLULAR RESPONSE TO FLUID SHEAR STRESS	8	1.54	0.02	0.24
REGULATION OF PROTEASOMAL UBIQUITIN-DEPENDENT PROTEIN CATABOLIC PROCESS	47	1.54	0.01	0.24
SIGNAL TRANSDUCTION INVOLVED IN MITOTIC G1 DNA DAMAGE CHECKPOINT	63	1.54	0.01	0.24
POSITIVE REGULATION OF TUMOR NECROSIS FACTOR BIOSYNTHETIC PROCESS	8	1.54	0.02	0.24
CENTROSOME ORGANIZATION	35	1.54	0.01	0.24
NEGATIVE REGULATION OF VIRAL TRANSCRIPTION	13	1.54	0.03	0.24
REGULATION OF TUMOR NECROSIS FACTOR BIOSYNTHETIC PROCESS	11	1.53	0.02	0.25
CYTOSKELETON-DEPENDENT INTRACELLULAR TRANSPORT	45	1.53	0.01	0.24
PROSTATE GLAND DEVELOPMENT	39	1.53	0.01	0.25
MITOTIC DNA DAMAGE CHECKPOINT	71	1.53	0.01	0.24
SPLICEOSOMAL COMPLEX ASSEMBLY	15	1.53	0.02	0.25
DNA DAMAGE RESPONSE, SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR RESULTING IN CELL CYCLE ARREST	63	1.53	0.01	0.25
CELLULAR RESPONSE TO RADIATION	48	1.53	0.01	0.25
MITOTIC CELL CYCLE CHECKPOINT	116	1.53	0.00	0.24
CILIUM ASSEMBLY	64	1.53	0.01	0.24
PROTEIN EXPORT FROM NUCLEUS	15	1.53	0.03	0.24
HIPPOCAMPUS DEVELOPMENT	44	1.53	0.01	0.24
VIRAL GENOME REPLICATION	9	1.53	0.02	0.24
MITOTIC SPINDLE ASSEMBLY CHECKPOINT	26	1.53	0.02	0.24
DENDRITE DEVELOPMENT	67	1.53	0.01	0.24
REGULATION OF DENDRITIC SPINE DEVELOPMENT	18	1.53	0.02	0.24
SPHINGOLIPID METABOLIC PROCESS	74	1.53	0.01	0.24
MITOTIC SPINDLE CHECKPOINT	29	1.53	0.01	0.24

SOMATIC RECOMBINATION OF IMMUNOGLOBULIN GENE SEGMENTS	23	1.53	0.03	0.25
REGULATION OF FATTY ACID OXIDATION	29	1.53	0.02	0.24
INOSITOL LIPID-MEDIATED SIGNALING	52	1.53	0.01	0.24
MICROTUBULE-BASED TRANSPORT	43	1.53	0.02	0.24
NEGATIVE REGULATION OF GENE EXPRESSION, EPIGENETIC	16	1.53	0.02	0.24
NOTCH SIGNALING PATHWAY	77	1.53	0.00	0.25
EMBRYONIC HEMOPOIESIS	23	1.52	0.02	0.25
SUBSTRATE ADHESION-DEPENDENT CELL SPREADING	22	1.52	0.03	0.25
REGULATION OF T CELL CHEMOTAXIS	8	1.52	0.02	0.25
REGULATION OF TRANSLATIONAL INITIATION	32	1.52	0.02	0.25
POSITIVE REGULATION OF MRNA 3'-END PROCESSING	12	1.52	0.02	0.25
REGULATION OF GLUCOSE TRANSPORT	57	1.52	0.01	0.25
DOUBLE-STRAND BREAK REPAIR VIA NONHOMOLOGOUS END JOINING	11	1.52	0.01	0.25
PEPTIDYL-THREONINE PHOSPHORYLATION	24	1.52	0.02	0.25
PHOSPHATIDYLINOSITOL-MEDIATED SIGNALING	52	1.52	0.01	0.25
PROTEIN K63-LINKED DEUBIQUITINATION	15	1.52	0.02	0.25
PROTEIN K48-LINKED UBIQUITINATION	34	1.52	0.01	0.25
SOMATIC HYPERMUTATION OF IMMUNOGLOBULIN GENES	7	1.52	0.03	0.25
REGULATION OF MESENCHYMAL CELL PROLIFERATION	15	1.52	0.04	0.25
POSITIVE REGULATION OF WNT RECEPTOR SIGNALING PATHWAY	44	1.52	0.01	0.25
NEGATIVE REGULATION OF MITOSIS	32	1.52	0.02	0.25
REGULATION OF FOCAL ADHESION ASSEMBLY	20	1.52	0.03	0.25
NCRNA PROCESSING	71	1.52	0.01	0.25
RESPONSE TO X-RAY	7	1.52	0.02	0.25
NEGATIVE REGULATION OF DNA METABOLIC PROCESS	46	1.52	0.01	0.25

SOMATIC RECOMBINATION OF IMMUNOGLOBULIN GENES INVOLVED IN IMMUNE RESPONSE	18	1.52	0.02	0.25
POSITIVE REGULATION OF T CELL CHEMOTAXIS	8	1.51	0.02	0.25
PHOSPHOLIPID TRANSPORT	24	1.51	0.03	0.25
NEGATIVE REGULATION OF TRANSCRIPTION BY COMPETITIVE PROMOTER BINDING	9	1.51	0.01	0.25
SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS	33	1.51	0.02	0.25
REGULATION OF DENDRITE MORPHOGENESIS	31	1.51	0.02	0.25
CELLULAR RESPONSE TO BMP STIMULUS	9	1.51	0.04	0.25
SUPEROXIDE METABOLIC PROCESS	18	1.51	0.03	0.25
FOREBRAIN MORPHOGENESIS	14	1.51	0.03	0.25
REGULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR PRODUCTION	18	1.51	0.02	0.25
NEGATIVE REGULATION OF MUSCLE TISSUE DEVELOPMENT	8	-2.06	0.01	0.19
NEGATIVE REGULATION OF MUSCLE ORGAN DEVELOPMENT	8	-2.03	0.01	0.18
GLUCOCORTICOID METABOLIC PROCESS	10	-2.02	0.01	0.17

GSEA/DFLAT, Gene Set Enrichment Analysis with Developmental FunctionaL Annotation at Tufts

[a] Nominal or raw p-value

[b] False discovery rate q –value