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GO term enrichment of down-regulated genes (D28 vs. D21)

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BP GO:0007067 mitotic nuclear division
Annotate: 91
Significant: 18
Expected: 3.63
topGO p-value: 0.0002
Differentially expressed genes in this GO term: Smp_004060 (cell division cycle 20); Smp_046280 (actin binding protein anillin); Smp_047620 (G2:mitotic specific cyclin B3); Smp_078920 (condensin complex subunit 3); Smp_082490 (G2:mitotic specific cyclin B2); Smp_134850 (structural maintenance of chromosomes protein 3); Smp_137780 (sister chromatid cohesion protein PDS5); Smp_137790 (sister chromatid cohesion protein PDS5); Smp_140240 (hypothetical protein); Smp_145260 (structural maintenance of chromosomes protein 3); Smp_149490 (hypothetical protein); Smp_167810 (family C50 non peptidase ue (C50 family)); Smp_169970 (kinetochore protein ndc80); Smp_171710 (structural maintenance of chromosomes protein 2); Smp_173700 (structural maintenance of chromosomes protein 4); Smp_175490 (sister chromatid cohesion protein PDS5); Smp_176010 (cytoskeleton associated protein 5); Smp_193330 (kinesin II 85 kDa subunit)

BP GO:0008285 negative regulation of cell proliferation
Annotate: 5
Significant: 3
Expected: 0.2
topGO p-value: 0.0006
Differentially expressed genes in this GO term: Smp_045470 (prospero homeobox protein 2); Smp_137780 (sister chromatid cohesion protein PDS5); Smp_175490 (sister chromatid cohesion protein PDS5)

BP GO:0030154 cell differentiation
Annotate: 79
Significant: 10
Expected: 3.15
topGO p-value: 0.0011
Differentially expressed genes in this GO term: Smp_062490 (heart and neural crest derivatives expressed); Smp_076600 (transcription factor SOX 14); Smp_132540 (protein slit); Smp_138230 (doublesex and mab-3 related transcription factor 1); Smp_142120 (achaete scute transcription factor); Smp_143190 (hypothetical protein); Smp_146790 (bone morphogenetic protein-like protein); Smp_148110 (transcription factor SOX 14); Smp_155690 (Sox family of transcription factor); Smp_167400 (transcription factor sum 1)

BP GO:0007223 Wnt signaling pathway; calcium modulating pathway
Annotate: 6
Significant: 3
Expected: 0.24
topGO p-value: 0.0011
Differentially expressed genes in this GO term: Smp_151400 (WNT); Smp_167140 (WNT); Smp_196930 (WNT)

BP GO:0030245 cellulose catabolic process

Annotate: 6

Significant: 3

Expected: 0.24

topGO p-value: 0.0011

Differentially expressed genes in this GO term: Smp_164170

(endoglycoceramidase); Smp_187070 (hypothetical protein); Smp_193630

(endoglycoceramidase)

BP GO:0006281 DNA repair

Annotate: 139

Significant: 15

Expected: 5.54

topGO p-value: 0.002

Differentially expressed genes in this GO term: Smp_042810 (chromosome transmission fidelity protein 18); Smp_055140 (crossover junction endonuclease mus81); Smp_055500 (DNA polymerase theta); Smp_083710 (Fanconi anemia); Smp_106040 (Structure specific endonuclease SLX1); Smp_124230 (dna repair protein rad51 1); Smp_128870 (nibrin); Smp_130760 (Mediator of DNA damage checkpoint protein 1); Smp_132510 (breast cancer type 1 susceptibility protein); Smp_133990 (DNA topoisomerase 2 binding protein 1); Smp_136160 (hypothetical protein); Smp_145260 (structural maintenance of chromosomes protein 3); Smp_162340 (serine:threonine protein kinase ATR); Smp_173880 (RAD9 A); Smp_181420 (Structure specific endonuclease SLX1)

BP GO:0007076 mitotic chromosome condensation

Annotate: 8

Significant: 3

Expected: 0.32

topGO p-value: 0.003

Differentially expressed genes in this GO term: Smp_145260 (structural maintenance of chromosomes protein 3); Smp_171710 (structural maintenance of chromosomes protein 2); Smp_173700 (structural maintenance of chromosomes protein 4)

BP GO:0051276 chromosome organization

Annotate: 200

Significant: 19

Expected: 7.97

topGO p-value: 0.0043

Differentially expressed genes in this GO term: Smp_002930 (histone H2A); Smp_026030 (DNA repair and recombination protein RAD54B); Smp_054840 (DNA replication licensing factor MCM2); Smp_079560 (DNA replication licensing factor MCM2); Smp_086860 (histone H2A); Smp_128870 (nibrin); Smp_134850 (structural maintenance of chromosomes protein 3); Smp_135110 (AT rich interactive domain containing protein); Smp_135650 (hypothetical protein); Smp_137110 (hypothetical protein); Smp_137780 (sister chromatid cohesion protein PDS5); Smp_137790 (sister chromatid cohesion protein PDS5); Smp_145260 (structural maintenance of chromosomes protein 3); Smp_162370 (histone H1 gamma); Smp_167810 (family C50 non peptidase ue (C50 family)); Smp_171710 (structural maintenance of chromosomes protein 2); Smp_173700 (structural maintenance of chromosomes protein 4); Smp_175490 (sister chromatid cohesion protein PDS5); Smp_194820 (dna repair and recombination protein rad54)

BP GO:0007530 sex determination
Annotate: 9
Significant: 3
Expected: 0.36
topGO p-value: 0.0046
Differentially expressed genes in this GO term: Smp_138230 (doublesex and mab-3 related transcription factor 1); Smp_143190 (hypothetical protein); Smp_148110 (transcription factor SOX 14)

BP GO:0006259 DNA metabolic process
Annotate: 319
Significant: 37
Expected: 12.72
topGO p-value: 0.0046
Differentially expressed genes in this GO term: Smp_007000 (DNA replication complex GINS protein PSF1); Smp_009030 (ribonucleoside diphosphate reductase large); Smp_032500 (DNA replication licensing factor MCM7); Smp_042810 (chromosome transmission fidelity protein 18); Smp_047610 (cell division control protein 45); Smp_052390 (origin recognition complex subunit 5); Smp_054840 (DNA replication licensing factor MCM2); Smp_055140 (crossover junction endonuclease mus81); Smp_055500 (DNA polymerase theta); Smp_067260 (dna polymerase alpha subunit b); Smp_079050 (DNA primase large subunit); Smp_079560 (DNA replication licensing factor MCM2); Smp_083710 (Fanconi anemia); Smp_094140 (DNA replication licensing factor MCM6); Smp_106040 (Structure specific endonuclease SLX1); Smp_124230 (dna repair protein rad51 1); Smp_127070 (origin recognition complex subunit); Smp_128870 (nibrin); Smp_130760 (Mediator of DNA damage checkpoint protein 1); Smp_132510 (breast cancer type 1 susceptibility protein); Smp_133990 (DNA topoisomerase 2 binding protein 1); Smp_134850 (structural maintenance of chromosomes protein 3); Smp_135650 (hypothetical protein); Smp_136160 (hypothetical protein); Smp_143490 (DNA replication licensing factor MCM5); Smp_145260 (structural maintenance of chromosomes protein 3); Smp_149120 (insect origin recognition complex subunit); Smp_151560 (dna replication licensing factor mcm9); Smp_162340 (serine:threonine protein kinase ATR); Smp_167540 (dna replication factor cdt1); Smp_171710 (structural maintenance of chromosomes protein 2); Smp_172530 (DNA replication licensing factor MCM4); Smp_173700 (structural maintenance of chromosomes protein 4); Smp_173880 (RAD9 A); Smp_178260 (DNA polymerase alpha catalytic subunit); Smp_181420 (Structure specific endonuclease SLX1); Smp_184750 (gag pol polyprotein)

BP GO:0006260 DNA replication
Annotate: 174
Significant: 21
Expected: 6.94
topGO p-value: 0.0097
Differentially expressed genes in this GO term: Smp_007000 (DNA replication complex GINS protein PSF1); Smp_009030 (ribonucleoside diphosphate reductase large); Smp_032500 (DNA replication licensing factor MCM7); Smp_042810 (chromosome transmission fidelity protein 18); Smp_047610 (cell division control protein 45); Smp_052390 (origin recognition complex subunit 5); Smp_054840 (DNA replication licensing factor MCM2); Smp_055500 (DNA polymerase theta); Smp_067260 (dna polymerase alpha subunit b); Smp_079050 (DNA primase large subunit); Smp_079560 (DNA replication licensing factor MCM2); Smp_094140 (DNA replication licensing factor MCM6); Smp_127070 (origin recognition complex subunit); Smp_135650 (hypothetical protein); Smp_143490 (DNA replication

licensing factor MCM5); Smp_149120 (insect origin recognition complex subunit); Smp_151560 (dna replication licensing factor mcm9); Smp_167540 (dna replication factor cdt1); Smp_172530 (DNA replication licensing factor MCM4); Smp_178260 (DNA polymerase alpha catalytic subunit); Smp_184750 (gag pol polyprotein)

BP GO:0007018 microtubule-based movement

Annotate: 61

Significant: 7

Expected: 2.43

topGO p-value: 0.0102

Differentially expressed genes in this GO term: Smp_027920 (Tubulin alpha 1 chain); Smp_128200 (kinesin protein kif23); Smp_149260 (kinesin family 1); Smp_169360 (kinesin protein kif26a); Smp_173450 (chromosome associated kinesin KIF4A); Smp_193330 (kinesin II 85 kDa subunit); Smp_212760 (kinesin)

BP GO:0006941 striated muscle contraction

Annotate: 160

Significant: 13

Expected: 6.38

topGO p-value: 0.0111

Differentially expressed genes in this GO term: Smp_032490 (tropomyosin); Smp_086220 (hypothetical protein); Smp_124600 (hypothetical protein); Smp_128930 (spectrin beta chain); Smp_129710 (Uveal autoantigen with coiled coil domains); Smp_134850 (structural maintenance of chromosomes protein 3); Smp_135900 (DNA double strand break repair rad50 ATPase); Smp_147890 (Rootletin); Smp_148420 (coiled coil domain containing 88A); Smp_150750 (centrosomal protein 110 kDa); Smp_150970 (RAB6 interacting protein 2 (ERC protein 1)); Smp_172210 (leucine rich repeat and coiled coil); Smp_213950 (citron Rho interacting kinase)

BP GO:0000075 cell cycle checkpoint

Annotate: 5

Significant: 2

Expected: 0.2

topGO p-value: 0.0146

Differentially expressed genes in this GO term: Smp_128870 (nibrin); Smp_167540 (dna replication factor cdt1)

BP GO:0006268 DNA unwinding involved in DNA replication

Annotate: 14

Significant: 3

Expected: 0.56

topGO p-value: 0.0164

Differentially expressed genes in this GO term: Smp_054840 (DNA replication licensing factor MCM2); Smp_079560 (DNA replication licensing factor MCM2); Smp_135650 (hypothetical protein)

BP GO:0040007 growth

Annotate: 15

Significant: 4

Expected: 0.6

topGO p-value: 0.0211

Differentially expressed genes in this GO term: Smp_128870 (nibrin); Smp_136160 (hypothetical protein); Smp_146790 (bone morphogenetic protein-like protein); Smp_194390 (suppressor of cytokine signaling 6)

BP GO:0006695 cholesterol biosynthetic process

Annotate: 6

Significant: 2

Expected: 0.24

topGO p-value: 0.0214

Differentially expressed genes in this GO term: Smp_124300 (Lamin B receptor (ERG24)); Smp_155270 (HMG-CoA synthase)

BP GO:0007126 meiotic nuclear division

Annotate: 8

Significant: 2

Expected: 0.32

topGO p-value: 0.0378

Differentially expressed genes in this GO term: Smp_055140 (crossover junction endonuclease mus81); Smp_128870 (nibrin)

BP GO:0016055 Wnt signaling pathway

Annotate: 26

Significant: 6

Expected: 1.04

topGO p-value: 0.042

Differentially expressed genes in this GO term: Smp_068680 (secreted frizzled protein); Smp_139180 (frizzled 5); Smp_151400 (WNT); Smp_167140 (WNT); Smp_168620 (ataxin 1); Smp_196930 (WNT)

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GO term enrichment of up-regulated genes (D28 vs. D21)

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BP GO:0007155 cell adhesion

Annotate: 222

Significant: 17

Expected: 8.74

topGO p-value: 0.0006

Differentially expressed genes in this GO term: Smp_078720 (hypothetical protein); Smp_123840 (neurexin 2 alpha); Smp_126540 (hypothetical protein); Smp_139380 (Spindle assembly checkpoint component MAD1); Smp_144910 (collagen type I:II:III:V:XI alpha); Smp_145900 (sphingolipid delta(4) desaturase:C4 hydroxylase); Smp_153930 (invadolysin (M08 family)); Smp_157020 (titin); Smp_157690 (von Willebrand factor type A); Smp_159920 (protocadherin 11); Smp_164590 (fibrillar collagen chain FAp1 alpha); Smp_165480 (hypothetical protein); Smp_180240 (f spondin); Smp_196840 (collagen alpha 1(II) chain); Smp_197080 (titin); Smp_197370 (hypothetical protein); Smp_213900 (type IV collagen alpha 1 chain)

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### BP      GO:0018958 phenol-containing compound metabolic process
# Annotate: 6
# Significant: 3
# Expected: 0.24
# topGO p-value: 0.0011
# Differentially expressed genes in this GO term: Smp_013540 (Tyrosinase);
Smp_050270 (Tyrosinase); Smp_135230 (Tyrosine DeCarboxylase family member (tdc
1))

### BP      GO:0006875 cellular metal ion homeostasis
# Annotate: 11
# Significant: 4
# Expected: 0.43
# topGO p-value: 0.0015
# Differentially expressed genes in this GO term: Smp_047660 (Ferritin-2 heavy
chain); Smp_063530 (apoferritin-2); Smp_151850 (inositol 1); Smp_199540 (type
inositol trisphosphate receptor; inositol trisphosphate receptor type)

### BP      GO:0008643 carbohydrate transport
# Annotate: 26
# Significant: 5
# Expected: 1.02
# topGO p-value: 0.003
# Differentially expressed genes in this GO term: Smp_012440 (glucose transport
protein); Smp_105410 (glucose transport protein); Smp_119580 (uncharacterized
MFS type transporter C19orf28); Smp_123720 (hypothetical protein); Smp_139150
(sodium dependent glucose transporter 1)

### BP      GO:1901617 organic hydroxy compound biosynthetic process
# Annotate: 24
# Significant: 4
# Expected: 0.94
# topGO p-value: 0.0078
# Differentially expressed genes in this GO term: Smp_013540 (Tyrosinase);
Smp_050270 (Tyrosinase); Smp_124750 (hypothetical protein); Smp_135230 (Tyrosine
DeCarboxylase family member (tdc 1))

### BP      GO:0019438 aromatic compound biosynthetic process
# Annotate: 1089
# Significant: 31
# Expected: 42.88
# topGO p-value: 0.0119
# Differentially expressed genes in this GO term: Smp_000660 (ornithine
aminotransferase); Smp_012560 (o methyltransferase); Smp_012810 (Four and a half
LIM domains protein 3); Smp_013540 (Tyrosinase); Smp_015020 (sodium potassium
transporting ATPase alpha subunit); Smp_025370 (lipopolysaccharide induced);
Smp_049850 (hypoxanthine guanine phosphoribosyltransferase); Smp_050270
(Tyrosinase); Smp_052470 (o methyltransferase); Smp_063520 (pre B cell leukemia
transcription factor 3); Smp_067430 (oligodendrocyte transcription factor 2);
Smp_071390 (adenylate kinase); Smp_103560 (hypoxanthine-guanine
phosphoribosyltransferase); Smp_125450 (retinal guanylyl cyclase 2); Smp_125810
(zinc finger protein 112); Smp_128460 (cation transporting atpase worm);
Smp_133490 (mitogen activated protein kinase 15); Smp_134040 (Ecdysone induced
protein 74EF B); Smp_134870 (early growth response protein); Smp_135230

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(Tyrosine DeCarboxylase family member (tdc 1)); Smp_136710 (calcium transporting atpase); Smp_142050 (Serine/Threonine Kinase); Smp_157670 (hypothetical protein); Smp_163380 (cyclin dependent kinase 2); Smp_166560 (zinc finger homeobox protein 1); Smp_179030 (hypothetical protein); Smp_196950 (one cut domain family member); Smp_212330 (DNA directed RNA polymerase III largest subunit); Smp_212430 (nuclear hormone receptor); Smp_212440 (nuclear hormone receptor); Smp_212820 (zinc finger protein)

BP GO:1901362 organic cyclic compound biosynthetic process
Annotate: 1118
Significant: 34
Expected: 44.02
topGO p-value: 0.012
Differentially expressed genes in this GO term: Smp_000660 (ornithine aminotransferase); Smp_012560 (o methyltransferase); Smp_012810 (Four and a half LIM domains protein 3); Smp_013540 (Tyrosinase); Smp_015020 (sodium potassium transporting ATPase alpha subunit); Smp_025370 (lipopolysaccharide induced); Smp_049850 (hypoxanthine guanine phosphoribosyltransferase); Smp_050270 (Tyrosinase); Smp_052470 (o methyltransferase); Smp_063520 (pre B cell leukemia transcription factor 3); Smp_067430 (oligodendrocyte transcription factor 2); Smp_071390 (adenylate kinase); Smp_103560 (hypoxanthine-guanine phosphoribosyltransferase); Smp_117920 (steroid dehydrogenase); Smp_124750 (hypothetical protein); Smp_125450 (retinal guanylyl cyclase 2); Smp_125810 (zinc finger protein 112); Smp_128460 (cation transporting atpase worm); Smp_133490 (mitogen activated protein kinase 15); Smp_134040 (Ecdysone induced protein 74EF B); Smp_134870 (early growth response protein); Smp_135230 (Tyrosine DeCarboxylase family member (tdc 1)); Smp_136710 (calcium transporting atpase); Smp_142050 (Serine/Threonine Kinase); Smp_145020 (glutamate semialdehyde dehydrogenase); Smp_157670 (hypothetical protein); Smp_163380 (cyclin dependent kinase 2); Smp_166560 (zinc finger homeobox protein 1); Smp_179030 (hypothetical protein); Smp_196950 (one cut domain family member); Smp_212330 (DNA directed RNA polymerase III largest subunit); Smp_212430 (nuclear hormone receptor); Smp_212440 (nuclear hormone receptor); Smp_212820 (zinc finger protein)

BP GO:0009058 biosynthetic process
Annotate: 1998
Significant: 60
Expected: 78.67
topGO p-value: 0.0127
Differentially expressed genes in this GO term: Smp_000660 (ornithine aminotransferase); Smp_000850 (cysteine string protein); Smp_007760 (alanine aminotransferase 2); Smp_012560 (o methyltransferase); Smp_012810 (Four and a half LIM domains protein 3); Smp_013540 (Tyrosinase); Smp_015020 (sodium potassium transporting ATPase alpha subunit); Smp_025370 (lipopolysaccharide induced); Smp_049150 (glutamine oxaloacetic transaminase; glutamic oxaloacetic transaminase); Smp_049850 (hypoxanthine guanine phosphoribosyltransferase); Smp_050270 (Tyrosinase); Smp_052470 (o methyltransferase); Smp_054300 (alpha 1); Smp_059980 (arginase); Smp_063520 (pre B cell leukemia transcription factor 3); Smp_067430 (oligodendrocyte transcription factor 2); Smp_071390 (adenylate kinase); Smp_071520 (hypothetical protein); Smp_089240 (alpha 1); Smp_099090 (hypothetical protein); Smp_103560 (hypoxanthine-guanine phosphoribosyltransferase); Smp_117920 (steroid dehydrogenase); Smp_124750 (hypothetical protein); Smp_125450 (retinal guanylyl cyclase 2); Smp_125810 (zinc finger protein 112); Smp_128370 (glutamate synthase); Smp_128460 (cation transporting atpase worm); Smp_130370 (elongation of very long chain fatty

acids); Smp_133490 (mitogen activated protein kinase 15); Smp_134040 (Ecdysone induced protein 74EF B); Smp_134870 (early growth response protein); Smp_135230 (Tyrosine DeCarboxylase family member (tdc 1)); Smp_136710 (calcium transporting atpase); Smp_137460 (cytoplasmic polyadenylation element binding); Smp_142030 (5' AMP activated protein kinase subunit gamma); Smp_142050 (Serine/Threonine Kinase); Smp_144860 (protein boule); Smp_145020 (glutamate semialdehyde dehydrogenase); Smp_149820 (glycoprotein N acetylgalactosamine); Smp_154680 (glycosyltransferase 14 family member); Smp_157670 (hypothetical protein); Smp_158510 (diacylglycerol O-acyltransferase 1); Smp_158520 (diacylglycerol O acyltransferase); Smp_161030 (hypothetical protein); Smp_163380 (cyclin dependent kinase 2); Smp_166560 (zinc finger homeobox protein 1); Smp_168550 (steroid dehydrogenase); Smp_168560 (steroid dehydrogenase); Smp_169570 (glycerol 3 phosphate dehydrogenase); Smp_179030 (hypothetical protein); Smp_195060 (hypothetical protein); Smp_196950 (one cut domain family member); Smp_209060 (alpha 1); Smp_210300 (phospholipase DDHD1); Smp_212330 (DNA directed RNA polymerase III largest subunit); Smp_212370 (SNF4:AMP activated protein kinase gamma subunit); Smp_212430 (nuclear hormone receptor); Smp_212440 (nuclear hormone receptor); Smp_212820 (zinc finger protein); Smp_214380 (alpha(13)fucosyltransferase)

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### BP      GO:0009698  phenylpropanoid metabolic process
# Annotate: 5
# Significant: 2
# Expected: 0.2
# topGO p-value: 0.0143
# Differentially expressed genes in this GO term: Smp_012560 (o
methyltransferase); Smp_052470 (o methyltransferase)
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### BP      GO:0007586  digestion
# Annotate: 5
# Significant: 2
# Expected: 0.2
# topGO p-value: 0.0143
# Differentially expressed genes in this GO term: Smp_175560 (beta site APP
cleaving enzyme 1); Smp_194090 (subfamily S1A unassigned peptidase (S01
family))
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### BP      GO:0055114  oxidation-reduction process
# Annotate: 136
# Significant: 9
# Expected: 5.35
# topGO p-value: 0.0171
# Differentially expressed genes in this GO term: Smp_010820 (peptidyl-alpha-
hydroxyglycine alpha-amidating lyase); Smp_017610 (amiloride sensitive amine
oxidase); Smp_047660 (Ferritin-2 heavy chain); Smp_050390 (aldehyde
dehydrogenase); Smp_059480 (thioredoxin peroxidase); Smp_063530 (apoferritin-2);
Smp_143840 (glycogen phosphorylase); Smp_153700 (hypothetical protein);
Smp_169570 (glycerol 3 phosphate dehydrogenase)
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### BP      GO:0006071  glycerol metabolic process
# Annotate: 6
# Significant: 2
# Expected: 0.24
# topGO p-value: 0.0209
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Differentially expressed genes in this GO term: Smp_158510 (diacylglycerol O-acyltransferase 1); Smp_158520 (diacylglycerol O acyltransferase)

BP GO:0006629 lipid metabolic process

Annotate: 270

Significant: 21

Expected: 10.63

topGO p-value: 0.021

Differentially expressed genes in this GO term: Smp_000260 (proactivator polypeptide); Smp_011000 (sterol esterase 1/lysosomal acid lipase-related/lipase 1); Smp_037780 (hypothetical protein); Smp_038970 (long chain fatty acid coenzyme A ligase); Smp_117920 (steroid dehydrogenase); Smp_121660 (IDL peptide); Smp_124750 (hypothetical protein); Smp_130370 (elongation of very long chain fatty acids); Smp_134390 (sterol O-acyltransferase 1); Smp_142030 (5' AMP activated protein kinase subunit gamma); Smp_144850 (oxysterol binding protein 1); Smp_145900 (sphingolipid delta(4) desaturase:C4 hydroxylase); Smp_149820 (glycoprotein N acetylgalactosamine); Smp_154760 (egf domain protein); Smp_158510 (diacylglycerol O-acyltransferase 1); Smp_158520 (diacylglycerol O acyltransferase); Smp_168550 (steroid dehydrogenase); Smp_168560 (steroid dehydrogenase); Smp_169570 (glycerol 3 phosphate dehydrogenase); Smp_175090 (long-chain-fatty-acid--CoA ligase); Smp_212370 (SNF4:AMP activated protein kinase gamma subunit)

BP GO:0072593 reactive oxygen species metabolic process

Annotate: 7

Significant: 2

Expected: 0.28

topGO p-value: 0.0284

Differentially expressed genes in this GO term: Smp_095980 (Extracellular superoxide dismutase (Cu Zn)); Smp_174810 (Extracellular superoxide dismutase (Cu Zn))

BP GO:0006836 neurotransmitter transport

Annotate: 31

Significant: 4

Expected: 1.22

topGO p-value: 0.032

Differentially expressed genes in this GO term: Smp_055260 (sodium dependent neurotransmitter transporter); Smp_129920 (sodium dependent neurotransmitter transporter); Smp_137990 (complexin); Smp_160360 (sodium:chloride dependent neurotransmitter)

BP GO:0015711 organic anion transport

Annotate: 60

Significant: 7

Expected: 2.36

topGO p-value: 0.0346

Differentially expressed genes in this GO term: Smp_054010 (y+1 amino acid transporter 2); Smp_123010 (high affinity cationic amino acid transporter 1); Smp_130780 (monocarboxylate transporter); Smp_134620 (monocarboxylate transporter); Smp_135020 (oxalate:formate antiporter); Smp_150090 (Monocarboxylate transporter 14); Smp_176930 (cationic amino acid transporter)

BP GO:0006879 cellular iron ion homeostasis
Annotate: 8
Significant: 2
Expected: 0.31
topGO p-value: 0.037
Differentially expressed genes in this GO term: Smp_047660 (Ferritin-2 heavy chain); Smp_063530 (apoferritin-2)

BP GO:0006166 purine ribonucleoside salvage
Annotate: 9
Significant: 2
Expected: 0.35
topGO p-value: 0.0463
Differentially expressed genes in this GO term: Smp_049850 (hypoxanthine guanine phosphoribosyltransferase); Smp_103560 (hypoxanthine-guanine phosphoribosyltransferase)