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GO term enrichment of up-regulated genes

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BP GO:0006879 cellular iron ion homeostasis
Annotate: 8
Significant: 2
Expected: 0.04
topGO p-value: 0.0006
Differentially expressed genes in this GO term: Smp_047660 (Ferritin-2 heavy chain); Smp_047680 (Ferritin-2 heavy chain)

BP GO:0006166 purine ribonucleoside salvage
Annotate: 9
Significant: 2
Expected: 0.04
topGO p-value: 0.0007
Differentially expressed genes in this GO term: Smp_049850 (hypoxanthine guanine phosphoribosyltransferase); Smp_148820 (hypoxanthine guanine phosphoribosyltransferase)

BP GO:0006826 iron ion transport
Annotate: 12
Significant: 2
Expected: 0.06
topGO p-value: 0.0013
Differentially expressed genes in this GO term: Smp_047660 (Ferritin-2 heavy chain); Smp_047680 (Ferritin-2 heavy chain)

BP GO:0007186 G-protein coupled receptor signaling pathway
Annotate: 163
Significant: 5
Expected: 0.75
topGO p-value: 0.0049
Differentially expressed genes in this GO term: Smp_012920 (class A rhodopsin G protein coupled); Smp_041700 (G protein coupled receptor fragment); Smp_157100 (sphingoid long chain base kinase); Smp_170610 (rhodopsin orphan GPCR); Smp_186780 (hypothetical protein)

BP GO:0007205 protein kinase C-activating G-protein coupled receptor signaling pathway
Annotate: 5
Significant: 1
Expected: 0.02
topGO p-value: 0.0229
Differentially expressed genes in this GO term: Smp_157100 (sphingoid long chain base kinase)

BP GO:0055114 oxidation-reduction process
Annotate: 136
Significant: 3

Expected: 0.63
topGO p-value: 0.0239
Differentially expressed genes in this GO term: Smp_047660 (Ferritin-2 heavy chain); Smp_047680 (Ferritin-2 heavy chain); Smp_062900 (tryparedoxin peroxidase)

BP GO:0042439 ethanolamine-containing compound metabolic process
Annotate: 6
Significant: 1
Expected: 0.03
topGO p-value: 0.0274
Differentially expressed genes in this GO term: Smp_212180 (glucose dehydrogenase (acceptor))

BP GO:0030245 cellulose catabolic process
Annotate: 6
Significant: 1
Expected: 0.03
topGO p-value: 0.0274
Differentially expressed genes in this GO term: Smp_164170 (endoglycoceramidase)

BP GO:0072593 reactive oxygen species metabolic process
Annotate: 7
Significant: 1
Expected: 0.03
topGO p-value: 0.0319
Differentially expressed genes in this GO term: Smp_193400 (hypothetical protein)

BP GO:0097164 ammonium ion metabolic process
Annotate: 9
Significant: 1
Expected: 0.04
topGO p-value: 0.0408
Differentially expressed genes in this GO term: Smp_212180 (glucose dehydrogenase (acceptor))

BP GO:0009116 nucleoside metabolic process
Annotate: 150
Significant: 3
Expected: 0.69
topGO p-value: 0.043
Differentially expressed genes in this GO term: Smp_049850 (hypoxanthine guanine phosphoribosyltransferase); Smp_148820 (hypoxanthine guanine phosphoribosyltransferase); Smp_179110 (purine nucleoside phosphorylase)

BP GO:0016126 sterol biosynthetic process
Annotate: 10
Significant: 1
Expected: 0.05
topGO p-value: 0.0452

Differentially expressed genes in this GO term: Smp_124750 (hypothetical protein)

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GO term enrichment of down-regulated genes

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BP GO:0009968 negative regulation of signal transduction
Annotate: 16
Significant: 2
Expected: 0.09
topGO p-value: 0.0039
Differentially expressed genes in this GO term: Smp_099440 (bone morphogenetic protein antagonist noggin); Smp_194390 (suppressor of cytokine signaling 6)

BP GO:0006865 amino acid transport
Annotate: 23
Significant: 2
Expected: 0.14
topGO p-value: 0.008
Differentially expressed genes in this GO term: Smp_127000 (Large neutral amino acids transporter small); Smp_147070 (sodium coupled neutral amino acid)

BP GO:0006813 potassium ion transport
Annotate: 78
Significant: 3
Expected: 0.46
topGO p-value: 0.0107
Differentially expressed genes in this GO term: Smp_046640 (twik family of potassium channels); Smp_046650 (TWiK family of potassium channels protein 7); Smp_147190 (hypothetical protein)

BP GO:0030154 cell differentiation
Annotate: 79
Significant: 3
Expected: 0.47
topGO p-value: 0.0111
Differentially expressed genes in this GO term: Smp_022870 (protein lin 54); Smp_099440 (bone morphogenetic protein antagonist noggin); Smp_142120 (achaete scute transcription factor)

BP GO:0019370 leukotriene biosynthetic process
Annotate: 5
Significant: 1
Expected: 0.03
topGO p-value: 0.0293
Differentially expressed genes in this GO term: Smp_007550 (leukotriene A 4 hydrolase)

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### BP      GO:0009103 lipopolysaccharide biosynthetic process
# Annotate: 5
# Significant: 1
# Expected: 0.03
# topGO p-value: 0.0293
# Differentially expressed genes in this GO term: Smp_058670 (procollagen
galactosyltransferase 1)

### BP      GO:0051216 cartilage development
# Annotate: 5
# Significant: 1
# Expected: 0.03
# topGO p-value: 0.0293
# Differentially expressed genes in this GO term: Smp_099440 (bone morphogenetic
protein antagonist noggin)

### BP      GO:0030509 BMP signaling pathway
# Annotate: 5
# Significant: 1
# Expected: 0.03
# topGO p-value: 0.0293
# Differentially expressed genes in this GO term: Smp_099440 (bone morphogenetic
protein antagonist noggin)

### BP      GO:0006633 fatty acid biosynthetic process
# Annotate: 55
# Significant: 3
# Expected: 0.33
# topGO p-value: 0.0321
# Differentially expressed genes in this GO term: Smp_007550 (leukotriene A 4
hydrolase); Smp_010770 (elongation of very long chain fatty acids); Smp_102190
(steroid dehydrogenase)

### BP      GO:0006071 glycerol metabolic process
# Annotate: 6
# Significant: 1
# Expected: 0.04
# topGO p-value: 0.0351
# Differentially expressed genes in this GO term: Smp_158510 (diacylglycerol O-
acyltransferase 1)

### BP      GO:0009082 branched-chain amino acid biosynthetic process
# Annotate: 7
# Significant: 1
# Expected: 0.04
# topGO p-value: 0.0408
# Differentially expressed genes in this GO term: Smp_075380 (hypothetical
protein)

### BP      GO:0007160 cell-matrix adhesion
# Annotate: 8

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# Significant: 1
# Expected: 0.05
# topGO p-value: 0.0465
# Differentially expressed genes in this GO term: Smp_170280 (integrin alpha ps)
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