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GO term enrichment of down-regulated genes (D35 vs. D28)

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### BP GO:0006355 regulation of transcription; DNA-templated  
# Annotate: 856  
# Significant: 18  
# Expected: 9.87  
# topGO p-value: 0.007  
# Differentially expressed genes in this GO term: Smp\_009020 (zinc finger protein); Smp\_009040 (POU domain); Smp\_009630 (homeobox protein SIX6); Smp\_051130 (ergs ets transcription factor; erg1 ets transcription factor); Smp\_124600 (hypothetical protein); Smp\_130870 (ETS domain containing protein Elk 4); Smp\_142120 (achaete scute transcription factor); Smp\_142580 (hypothetical protein); Smp\_142940 (paired box protein pax); Smp\_143550 (hypothetical protein); Smp\_145200 (homeobox protein engrailed-like SMOX-2); Smp\_148110 (transcription factor SOX 14); Smp\_162760 (homeobox protein prospero:prox 1:ceh 26); Smp\_168620 (ataxin 1); Smp\_174150 (myeloid ecotropic viral integration site 1); Smp\_194660 (transcription factor collier); Smp\_214390 (Labial-like protein); Smp\_241480 (hypothetical protein)

### BP GO:0007186 G-protein coupled receptor signaling pathway  
# Annotate: 163  
# Significant: 6  
# Expected: 1.88  
# topGO p-value: 0.011  
# Differentially expressed genes in this GO term: Smp\_008850 (fmrfamide receptor); Smp\_052660 (metabotropic glutamate receptor 3); Smp\_123350 (galanin receptor type 2); Smp\_140250 (G protein coupled receptor fragment); Smp\_150180 (octopamine receptor oamb); Smp\_173010 (neuropeptide receptor a)

### BP GO:0046797 viral procapsid maturation  
# Annotate: 23  
# Significant: 2  
# Expected: 0.27  
# topGO p-value: 0.028  
# Differentially expressed genes in this GO term: Smp\_028150 (hypothetical protein); Smp\_123370 (serine rich repeat protein 2)

### BP GO:0015074 DNA integration  
# Annotate: 29  
# Significant: 2  
# Expected: 0.33  
# topGO p-value: 0.044  
# Differentially expressed genes in this GO term: Smp\_028150 (hypothetical protein); Smp\_123370 (serine rich repeat protein 2)

### BP GO:0007275 multicellular organism development  
# Annotate: 283  
# Significant: 8  
# Expected: 3.26  
# topGO p-value: 0.047

# Differentially expressed genes in this GO term: Smp\_142120 (achaete scute transcription factor); Smp\_142580 (hypothetical protein); Smp\_142940 (paired box protein pax); Smp\_145200 (homeobox protein engrailed-like SMOX-2); Smp\_148110 (transcription factor SOX 14); Smp\_162760 (homeobox protein prospero:prox 1:ceh 26); Smp\_174430 (hypothetical protein); Smp\_194660 (transcription factor collier)

### BP GO:0032196 transposition

# Annotate: 31

# Significant: 2

# Expected: 0.36

# topGO p-value: 0.049

# Differentially expressed genes in this GO term: Smp\_028150 (hypothetical protein); Smp\_123370 (serine rich repeat protein 2)

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GO term enrichment of up-regulated genes (D35 vs. D28)

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### BP GO:0018958 phenol-containing compound metabolic process

# Annotate: 6

# Significant: 2

# Expected: 0.04

# topGO p-value: 0.0005

# Differentially expressed genes in this GO term: Smp\_013540 (Tyrosinase); Smp\_050270 (Tyrosinase)

### BP GO:1901362 organic cyclic compound biosynthetic process

# Annotate: 1118

# Significant: 5

# Expected: 6.81

# topGO p-value: 0.0019

# Differentially expressed genes in this GO term: Smp\_000340 (ecdysone-induced protein E78); Smp\_013540 (Tyrosinase); Smp\_050270 (Tyrosinase); Smp\_145020 (glutamate semialdehyde dehydrogenase); Smp\_198020 (o methyltransferase)

### BP GO:0009072 aromatic amino acid family metabolic process

# Annotate: 11

# Significant: 2

# Expected: 0.07

# topGO p-value: 0.0019

# Differentially expressed genes in this GO term: Smp\_013540 (Tyrosinase); Smp\_050270 (Tyrosinase)

### BP GO:0046148 pigment biosynthetic process

# Annotate: 11

# Significant: 2

# Expected: 0.07

# topGO p-value: 0.0019

# Differentially expressed genes in this GO term: Smp\_013540 (Tyrosinase);  
Smp\_050270 (Tyrosinase)

### BP GO:0019438 aromatic compound biosynthetic process  
# Annotate: 1089  
# Significant: 4  
# Expected: 6.64  
# topGO p-value: 0.0042  
# Differentially expressed genes in this GO term: Smp\_000340 (ecdysone-induced protein E78); Smp\_013540 (Tyrosinase); Smp\_050270 (Tyrosinase); Smp\_198020 (o methyltransferase)

### BP GO:1901617 organic hydroxy compound biosynthetic process  
# Annotate: 24  
# Significant: 2  
# Expected: 0.15  
# topGO p-value: 0.0092  
# Differentially expressed genes in this GO term: Smp\_013540 (Tyrosinase);  
Smp\_050270 (Tyrosinase)

### BP GO:0050790 regulation of catalytic activity  
# Annotate: 24  
# Significant: 2  
# Expected: 0.15  
# topGO p-value: 0.0092  
# Differentially expressed genes in this GO term: Smp\_103610 (cathepsin B-like cysteine proteinase); Smp\_179950 (cathepsin B peptidase (C01 family))

### BP GO:1901605 alpha-amino acid metabolic process  
# Annotate: 78  
# Significant: 3  
# Expected: 0.48  
# topGO p-value: 0.0136  
# Differentially expressed genes in this GO term: Smp\_013540 (Tyrosinase);  
Smp\_050270 (Tyrosinase); Smp\_145020 (glutamate semialdehyde dehydrogenase)

### BP GO:0046942 carboxylic acid transport  
# Annotate: 28  
# Significant: 2  
# Expected: 0.17  
# topGO p-value: 0.0294  
# Differentially expressed genes in this GO term: Smp\_054010 (y+l amino acid transporter 2); Smp\_160160 (solute carrier family 17)

### BP GO:0033578 protein glycosylation in Golgi  
# Annotate: 5  
# Significant: 1  
# Expected: 0.03  
# topGO p-value: 0.0301  
# Differentially expressed genes in this GO term: Smp\_138730 (alpha fucosyltransferase m; alpha fucosyltransferase k; alpha fucosyltransferase j; alpha fucosyltransferase i)

### BP GO:0009698 phenylpropanoid metabolic process  
# Annotate: 5  
# Significant: 1  
# Expected: 0.03  
# topGO p-value: 0.0301  
# Differentially expressed genes in this GO term: Smp\_198020 (o  
methyltransferase)

### BP GO:0006071 glycerol metabolic process  
# Annotate: 6  
# Significant: 1  
# Expected: 0.04  
# topGO p-value: 0.036  
# Differentially expressed genes in this GO term: Smp\_158520 (diacylglycerol O  
acyltransferase)