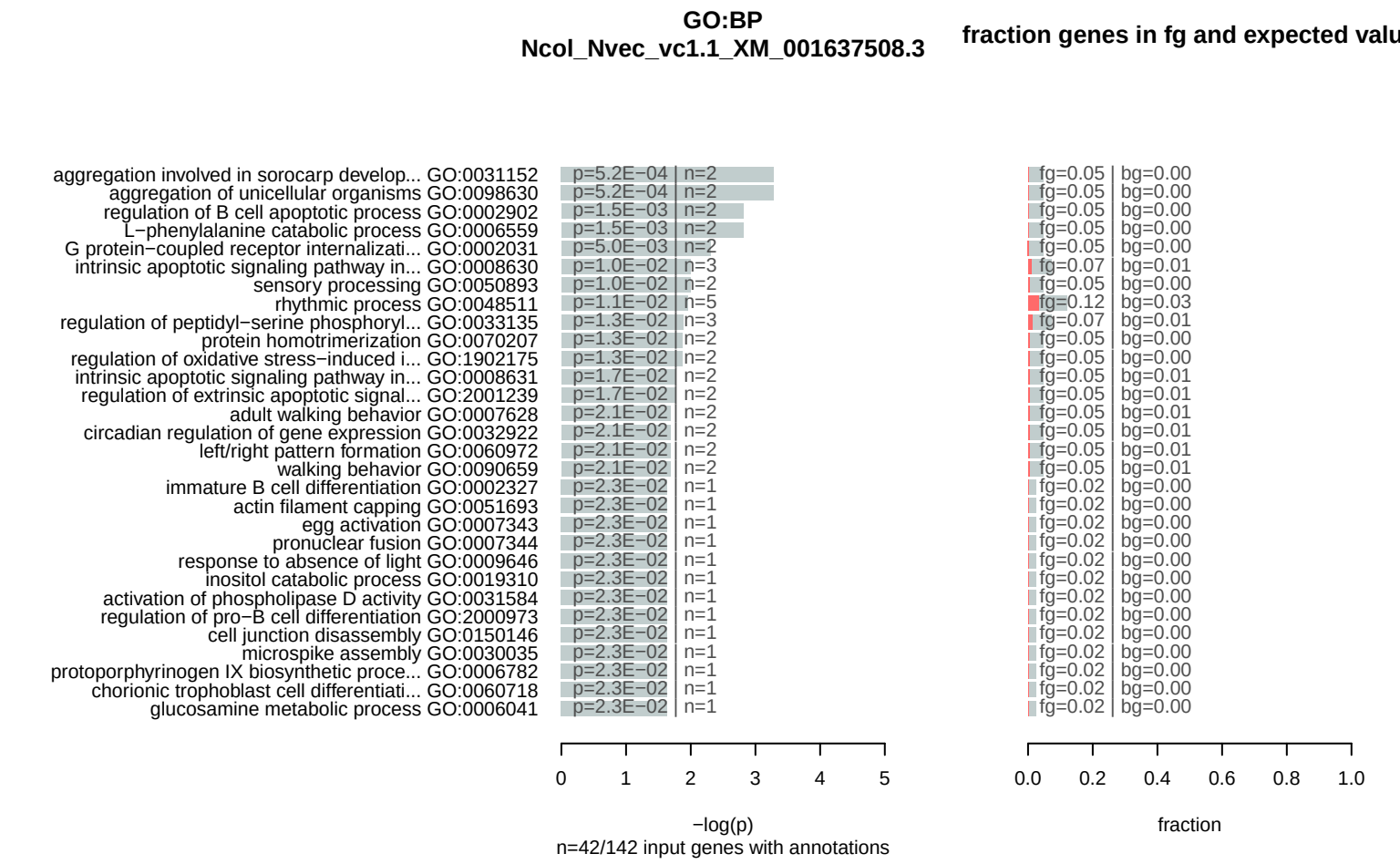
GO:BP
Ncol_Nvec_vc1.1_XM_001637508.3
fraction genes in fg and expected valu
aggregation involved in sorocarp develop... GO:0031152 p=5.2E−04 n=2 fg=0.05 bg=0.00
aggregation of unicellular organisms GO:0098630 p=5.2E−04 n=2 fg=0.05 bg=0.00
regulation of B cell apoptotic process GO:0002902 p=1.5E−03 n=2 fg=0.05 bg=0.00
L−phenylalanine catabolic process GO:0006559 p=1.5E−03 n=2 fg=0.05 bg=0.00
G protein−coupled receptor internalizati... GO:0002031 p=5.0E−03 n=2 fg=0.05 bg=0.00
intrinsic apoptotic signaling pathway in... GO:0008630 p=1.0E−02 n=3 fg=0.07 bg=0.01
sensory processing GO:0050893 p=1.0E−02 n=2 fg=0.05 bg=0.00
rhythmic process GO:0048511 p=1.1E−02 n=5 fg=0.12 bg=0.03
regulation of peptidyl−serine phosphoryl... GO:0033135 p=1.3E−02 n=3 fg=0.07 bg=0.01
protein homotrimerization GO:0070207 p=1.3E−02 n=2 fg=0.05 bg=0.00
regulation of oxidative stress−induced i... GO:1902175 p=1.3E−02 n=2 fg=0.05 bg=0.00
intrinsic apoptotic signaling pathway in... GO:0008631 p=1.7E−02 n=2 fg=0.05 bg=0.01
regulation of extrinsic apoptotic signal... GO:2001239 p=1.7E−02 n=2 fg=0.05 bg=0.01
adult walking behavior GO:0007628 p=2.1E−02 n=2 fg=0.05 bg=0.01
circadian regulation of gene expression GO:0032922 p=2.1E−02 n=2 fg=0.05 bg=0.01
left/right pattern formation GO:0060972 p=2.1E−02 n=2 fg=0.05 bg=0.01
walking behavior GO:0090659 p=2.1E−02 n=2 fg=0.05 bg=0.01
immature B cell differentiation GO:0002327 p=2.3E−02 n=1 fg=0.02 bg=0.00
actin filament capping GO:0051693 p=2.3E−02 n=1 fg=0.02 bg=0.00
egg activation GO:0007343 p=2.3E−02 n=1 fg=0.02 bg=0.00
pronuclear fusion GO:0007344 p=2.3E−02 n=1 fg=0.02 bg=0.00
response to absence of light GO:0009646 p=2.3E−02 n=1 fg=0.02 bg=0.00
inositol catabolic process GO:0019310 p=2.3E−02 n=1 fg=0.02 bg=0.00
activation of phospholipase D activity GO:0031584 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of pro−B cell differentiation GO:2000973 p=2.3E−02 n=1 fg=0.02 bg=0.00
cell junction disassembly GO:0150146 p=2.3E−02 n=1 fg=0.02 bg=0.00
microspike assembly GO:0030035 p=2.3E−02 n=1 fg=0.02 bg=0.00
protoporphyrinogen IX biosynthetic proce... GO:0006782 p=2.3E−02 n=1 fg=0.02 bg=0.00
chorionic trophoblast cell differentiati... GO:0060718 p=2.3E−02 n=1 fg=0.02 bg=0.00
glucosamine metabolic process GO:0006041 p=2.3E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=42/142 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001637508.3
fraction genes in fg and expected valu
oxidoreductase activity, acting on singl... GO:0016701 p=5.0E−04 n=2 fg=0.06 bg=0.00
actin monomer binding GO:0003785 p=2.9E−03 n=2 fg=0.06 bg=0.00
excitatory extracellular ligand−gated io... GO:0005231 p=9.7E−03 n=2 fg=0.06 bg=0.00
iron ion binding GO:0005506 p=9.7E−03 n=2 fg=0.06 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.3E−02 n=1 fg=0.03 bg=0.00
citrate (Si)−synthase activity GO:0004108 p=2.3E−02 n=1 fg=0.03 bg=0.00
L−alanine:2−oxoglutarate aminotransferas... GO:0004021 p=2.3E−02 n=1 fg=0.03 bg=0.00
iron−responsive element binding GO:0030350 p=2.3E−02 n=1 fg=0.03 bg=0.00
ferric iron binding GO:0008199 p=2.3E−02 n=1 fg=0.03 bg=0.00
inositol oxygenase activity GO:0050113 p=2.3E−02 n=1 fg=0.03 bg=0.00
3−hydroxyisobutyryl−CoA hydrolase activi... GO:0003860 p=2.3E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on singl... GO:0016702 p=2.3E−02 n=1 fg=0.03 bg=0.00
ferrochelatase activity GO:0004325 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=2.3E−02 n=1 fg=0.03 bg=0.00
acyltransferase activity, acyl groups co... GO:0046912 p=2.3E−02 n=1 fg=0.03 bg=0.00
citrate synthase activity GO:0036440 p=2.3E−02 n=1 fg=0.03 bg=0.00
homogentisate 1,2−dioxygenase activity GO:0004411 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=2.3E−02 n=1 fg=0.03 bg=0.00
alanine−oxo−acid transaminase activity GO:0047635 p=2.3E−02 n=1 fg=0.03 bg=0.00
7SK snRNA binding GO:0097322 p=2.3E−02 n=1 fg=0.03 bg=0.00
thiolester hydrolase activity GO:0016790 p=2.4E−02 n=2 fg=0.06 bg=0.01
actin filament binding GO:0051015 p=4.3E−02 n=2 fg=0.06 bg=0.01
BH3 domain binding GO:0051434 p=4.5E−02 n=1 fg=0.03 bg=0.00
omega peptidase activity GO:0008242 p=4.5E−02 n=1 fg=0.03 bg=0.00
asparaginase activity GO:0004067 p=4.5E−02 n=1 fg=0.03 bg=0.00
neurotransmitter receptor activity invol... GO:0099529 p=4.5E−02 n=1 fg=0.03 bg=0.00
threonine−type peptidase activity GO:0070003 p=4.5E−02 n=1 fg=0.03 bg=0.00
transmitter−gated ion channel activity i... GO:1904315 p=4.5E−02 n=1 fg=0.03 bg=0.00
monooxygenase activity GO:0004497 p=4.5E−02 n=1 fg=0.03 bg=0.00
fatty acid ligase activity GO:0015645 p=4.5E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=36/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001637508.3
fraction genes in fg and expected valu
serine−type peptidase complex GO:1905286 p=2.2E−02 n=1 fg=0.03 bg=0.00
nuclear RNA−directed RNA polymerase comp... GO:0031380 p=2.2E−02 n=1 fg=0.03 bg=0.00
serine−type endopeptidase complex GO:1905370 p=2.2E−02 n=1 fg=0.03 bg=0.00
RNA−directed RNA polymerase complex GO:0031379 p=2.2E−02 n=1 fg=0.03 bg=0.00
mitochondrial matrix GO:0005759 p=2.5E−02 n=5 fg=0.12 bg=0.04
intrinsic component of plasma membrane GO:0031226 p=3.7E−02 n=7 fg=0.17 bg=0.08
plasma membrane signaling receptor compl... GO:0098802 p=4.2E−02 n=2 fg=0.05 bg=0.01
protein−lipid complex GO:0032994 p=4.4E−02 n=1 fg=0.03 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=4.4E−02 n=1 fg=0.03 bg=0.00
Nebenkern GO:0016006 p=4.4E−02 n=1 fg=0.03 bg=0.00
mitochondrial derivative GO:0016007 p=4.4E−02 n=1 fg=0.03 bg=0.00
rough endoplasmic reticulum GO:0005791 p=5.3E−02 n=2 fg=0.05 bg=0.01
side of membrane GO:0098552 p=5.5E−02 n=4 fg=0.10 bg=0.04
cytoplasmic side of plasma membrane GO:0009898 p=6.3E−02 n=3 fg=0.07 bg=0.02
U2−type prespliceosome GO:0071004 p=6.5E−02 n=1 fg=0.03 bg=0.00
Bcl−2 family protein complex GO:0097136 p=6.5E−02 n=1 fg=0.03 bg=0.00
CD40 receptor complex GO:0035631 p=6.5E−02 n=1 fg=0.03 bg=0.00
CHD−type complex GO:0090545 p=6.5E−02 n=1 fg=0.03 bg=0.00
NuRD complex GO:0016581 p=6.5E−02 n=1 fg=0.03 bg=0.00
nuclear envelope GO:0005635 p=7.2E−02 n=4 fg=0.10 bg=0.04
integral component of plasma membrane GO:0005887 p=7.4E−02 n=6 fg=0.15 bg=0.08
peroxisome GO:0005777 p=7.7E−02 n=2 fg=0.05 bg=0.01
microbody GO:0042579 p=7.7E−02 n=2 fg=0.05 bg=0.01
cytoplasmic side of membrane GO:0098562 p=8.3E−02 n=3 fg=0.07 bg=0.03
integral component of peroxisomal membra... GO:0005779 p=8.6E−02 n=1 fg=0.03 bg=0.00
cortical endoplasmic reticulum GO:0032541 p=8.6E−02 n=1 fg=0.03 bg=0.00
intrinsic component of peroxisomal membr... GO:0031231 p=8.6E−02 n=1 fg=0.03 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=8.6E−02 n=1 fg=0.03 bg=0.00
prespliceosome GO:0071010 p=8.6E−02 n=1 fg=0.03 bg=0.00
rough endoplasmic reticulum membrane GO:0030867 p=8.6E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=40/142 input genes with annotations
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fraction