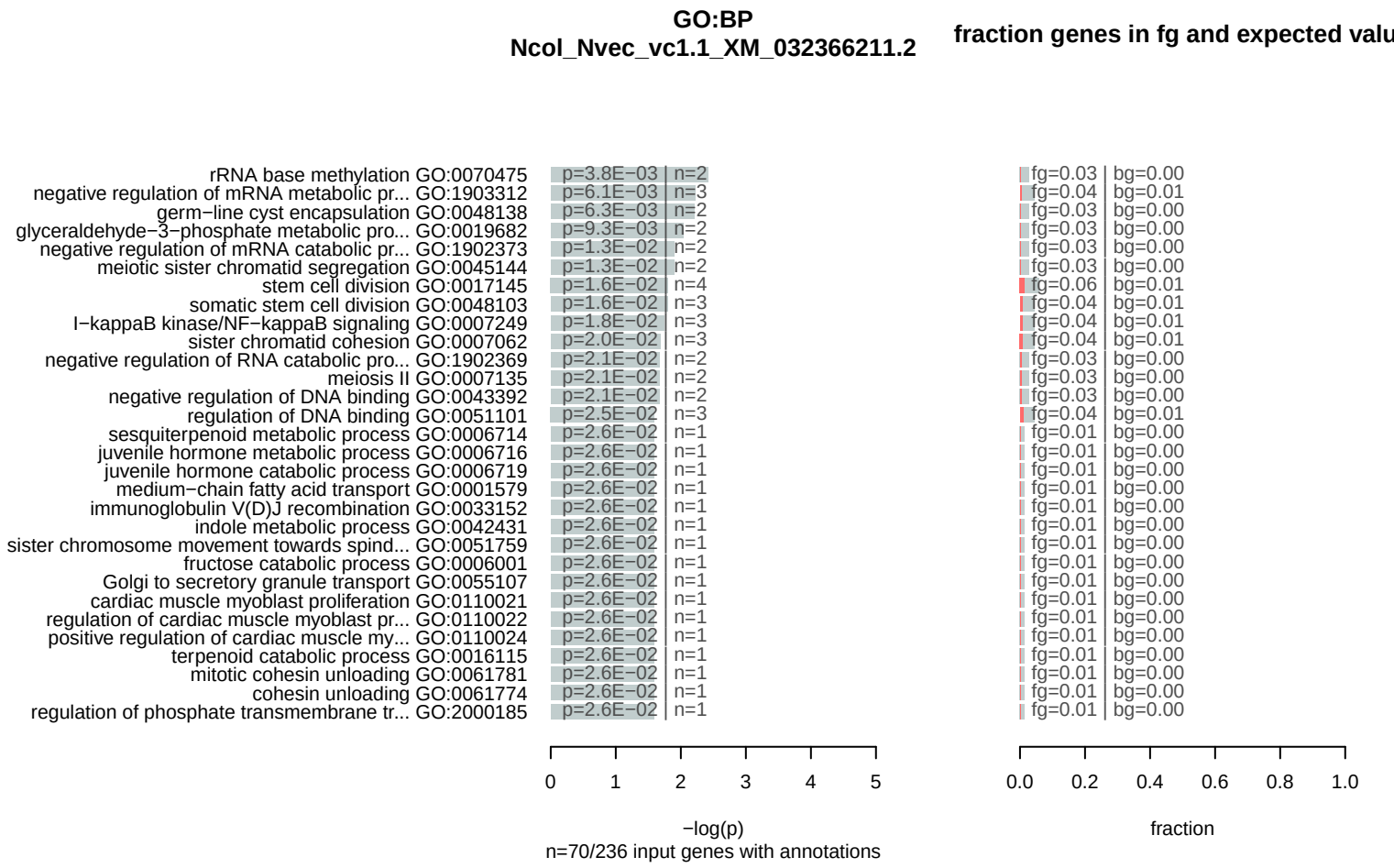
GO:BP
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
rRNA base methylation GO:0070475 p=3.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of mRNA metabolic pr... GO:1903312 p=6.1E−03 n=3 fg=0.04 bg=0.01
germ−line cyst encapsulation GO:0048138 p=6.3E−03 n=2 fg=0.03 bg=0.00
glyceraldehyde−3−phosphate metabolic pro... GO:0019682 p=9.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of mRNA catabolic pr... GO:1902373 p=1.3E−02 n=2 fg=0.03 bg=0.00
meiotic sister chromatid segregation GO:0045144 p=1.3E−02 n=2 fg=0.03 bg=0.00
stem cell division GO:0017145 p=1.6E−02 n=4 fg=0.06 bg=0.01
somatic stem cell division GO:0048103 p=1.6E−02 n=3 fg=0.04 bg=0.01
I−kappaB kinase/NF−kappaB signaling GO:0007249 p=1.8E−02 n=3 fg=0.04 bg=0.01
sister chromatid cohesion GO:0007062 p=2.0E−02 n=3 fg=0.04 bg=0.01
negative regulation of RNA catabolic pro... GO:1902369 p=2.1E−02 n=2 fg=0.03 bg=0.00
meiosis II GO:0007135 p=2.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of DNA binding GO:0043392 p=2.1E−02 n=2 fg=0.03 bg=0.00
regulation of DNA binding GO:0051101 p=2.5E−02 n=3 fg=0.04 bg=0.01
sesquiterpenoid metabolic process GO:0006714 p=2.6E−02 n=1 fg=0.01 bg=0.00
juvenile hormone metabolic process GO:0006716 p=2.6E−02 n=1 fg=0.01 bg=0.00
juvenile hormone catabolic process GO:0006719 p=2.6E−02 n=1 fg=0.01 bg=0.00
medium−chain fatty acid transport GO:0001579 p=2.6E−02 n=1 fg=0.01 bg=0.00
immunoglobulin V(D)J recombination GO:0033152 p=2.6E−02 n=1 fg=0.01 bg=0.00
indole metabolic process GO:0042431 p=2.6E−02 n=1 fg=0.01 bg=0.00
sister chromosome movement towards spind... GO:0051759 p=2.6E−02 n=1 fg=0.01 bg=0.00
fructose catabolic process GO:0006001 p=2.6E−02 n=1 fg=0.01 bg=0.00
Golgi to secretory granule transport GO:0055107 p=2.6E−02 n=1 fg=0.01 bg=0.00
cardiac muscle myoblast proliferation GO:0110021 p=2.6E−02 n=1 fg=0.01 bg=0.00
regulation of cardiac muscle myoblast pr... GO:0110022 p=2.6E−02 n=1 fg=0.01 bg=0.00
positive regulation of cardiac muscle my... GO:0110024 p=2.6E−02 n=1 fg=0.01 bg=0.00
terpenoid catabolic process GO:0016115 p=2.6E−02 n=1 fg=0.01 bg=0.00
mitotic cohesin unloading GO:0061781 p=2.6E−02 n=1 fg=0.01 bg=0.00
cohesin unloading GO:0061774 p=2.6E−02 n=1 fg=0.01 bg=0.00
regulation of phosphate transmembrane tr... GO:2000185 p=2.6E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=70/236 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
RNA methyltransferase activity GO:0008173 p=2.8E−03 n=4 fg=0.06 bg=0.01
S−adenosylmethionine−dependent methyltra... GO:0008757 p=4.1E−03 n=5 fg=0.08 bg=0.02
phosphatidylinositol−3,4−bisphosphate bi... GO:0043325 p=6.6E−03 n=2 fg=0.03 bg=0.00
rRNA methyltransferase activity GO:0008649 p=1.3E−02 n=2 fg=0.03 bg=0.00
catalytic activity, acting on a rRNA GO:0140102 p=1.3E−02 n=2 fg=0.03 bg=0.00
inositol 1,3,4,5 tetrakisphosphate bindi... GO:0043533 p=2.7E−02 n=1 fg=0.02 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=2.7E−02 n=1 fg=0.02 bg=0.00
FAD−AMP lyase (cyclizing) activity GO:0034012 p=2.7E−02 n=1 fg=0.02 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=2.7E−02 n=1 fg=0.02 bg=0.00
phosphotransferase activity, nitrogenous... GO:0016775 p=2.7E−02 n=1 fg=0.02 bg=0.00
long−chain fatty acid−CoA ligase activit... GO:0004467 p=2.7E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=2.7E−02 n=1 fg=0.02 bg=0.00
transketolase or transaldolase activity GO:0016744 p=2.7E−02 n=1 fg=0.02 bg=0.00
DNA clamp loader activity GO:0003689 p=2.7E−02 n=1 fg=0.02 bg=0.00
transketolase activity GO:0004802 p=2.7E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=2.7E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=2.7E−02 n=1 fg=0.02 bg=0.00
carbonyl reductase (NADPH) activity GO:0004090 p=2.7E−02 n=1 fg=0.02 bg=0.00
glycerone kinase activity GO:0004371 p=2.7E−02 n=1 fg=0.02 bg=0.00
very long−chain fatty acid−CoA ligase ac... GO:0031957 p=2.7E−02 n=1 fg=0.02 bg=0.00
galactosylxylosylprotein 3−beta−galactos... GO:0047220 p=2.7E−02 n=1 fg=0.02 bg=0.00
triokinase activity GO:0050354 p=2.7E−02 n=1 fg=0.02 bg=0.00
C−methyltransferase activity GO:0008169 p=2.7E−02 n=1 fg=0.02 bg=0.00
arginine kinase activity GO:0004054 p=2.7E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=2.7E−02 n=1 fg=0.02 bg=0.00
leucine zipper domain binding GO:0043522 p=2.7E−02 n=1 fg=0.02 bg=0.00
DNA polymerase activity GO:0034061 p=5.2E−02 n=2 fg=0.03 bg=0.01
ubiquitin conjugating enzyme binding GO:0031624 p=5.2E−02 n=2 fg=0.03 bg=0.01
DNA−directed DNA polymerase activity GO:0003887 p=5.2E−02 n=2 fg=0.03 bg=0.01
cAMP response element binding protein bi... GO:0008140 p=5.2E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=63/236 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
non−membrane−bounded organelle GO:0043228 p=1.8E−02 n=31 fg=0.46 bg=0.33
intracellular non−membrane−bounded organ... GO:0043232 p=1.8E−02 n=31 fg=0.46 bg=0.33
intracellular anatomical structure GO:0005622 p=1.9E−02 n=67 fg=1.00 bg=0.94
site of double−strand break GO:0035861 p=2.4E−02 n=2 fg=0.03 bg=0.00
site of DNA damage GO:0090734 p=2.4E−02 n=2 fg=0.03 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.5E−02 n=1 fg=0.01 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=2.5E−02 n=1 fg=0.01 bg=0.00
SMC loading complex GO:0032116 p=2.5E−02 n=1 fg=0.01 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=2.5E−02 n=1 fg=0.01 bg=0.00
perichromatin fibrils GO:0005726 p=2.5E−02 n=1 fg=0.01 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=2.5E−02 n=1 fg=0.01 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=2.5E−02 n=1 fg=0.01 bg=0.00
chromosome GO:0005694 p=3.3E−02 n=11 fg=0.16 bg=0.09
nucleus GO:0005634 p=3.9E−02 n=41 fg=0.61 bg=0.50
IkappaB kinase complex GO:0008385 p=4.9E−02 n=1 fg=0.01 bg=0.00
Elg1 RFC−like complex GO:0031391 p=4.9E−02 n=1 fg=0.01 bg=0.00
translation preinitiation complex GO:0070993 p=4.9E−02 n=1 fg=0.01 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=4.9E−02 n=1 fg=0.01 bg=0.00
RSF complex GO:0031213 p=4.9E−02 n=1 fg=0.01 bg=0.00
presynaptic cytoskeleton GO:0099569 p=4.9E−02 n=1 fg=0.01 bg=0.00
Lewy body GO:0097413 p=4.9E−02 n=1 fg=0.01 bg=0.00
ubiquitin ligase complex GO:0000151 p=5.3E−02 n=5 fg=0.07 bg=0.03
perinuclear region of cytoplasm GO:0048471 p=6.3E−02 n=8 fg=0.12 bg=0.06
brush border membrane GO:0031526 p=7.2E−02 n=2 fg=0.03 bg=0.01
DNA replication factor C complex GO:0005663 p=7.3E−02 n=1 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=7.3E−02 n=1 fg=0.01 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=7.3E−02 n=1 fg=0.01 bg=0.00
zymogen granule membrane GO:0042589 p=7.3E−02 n=1 fg=0.01 bg=0.00
PRC1 complex GO:0035102 p=7.3E−02 n=1 fg=0.01 bg=0.00
VCB complex GO:0030891 p=7.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=67/236 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction