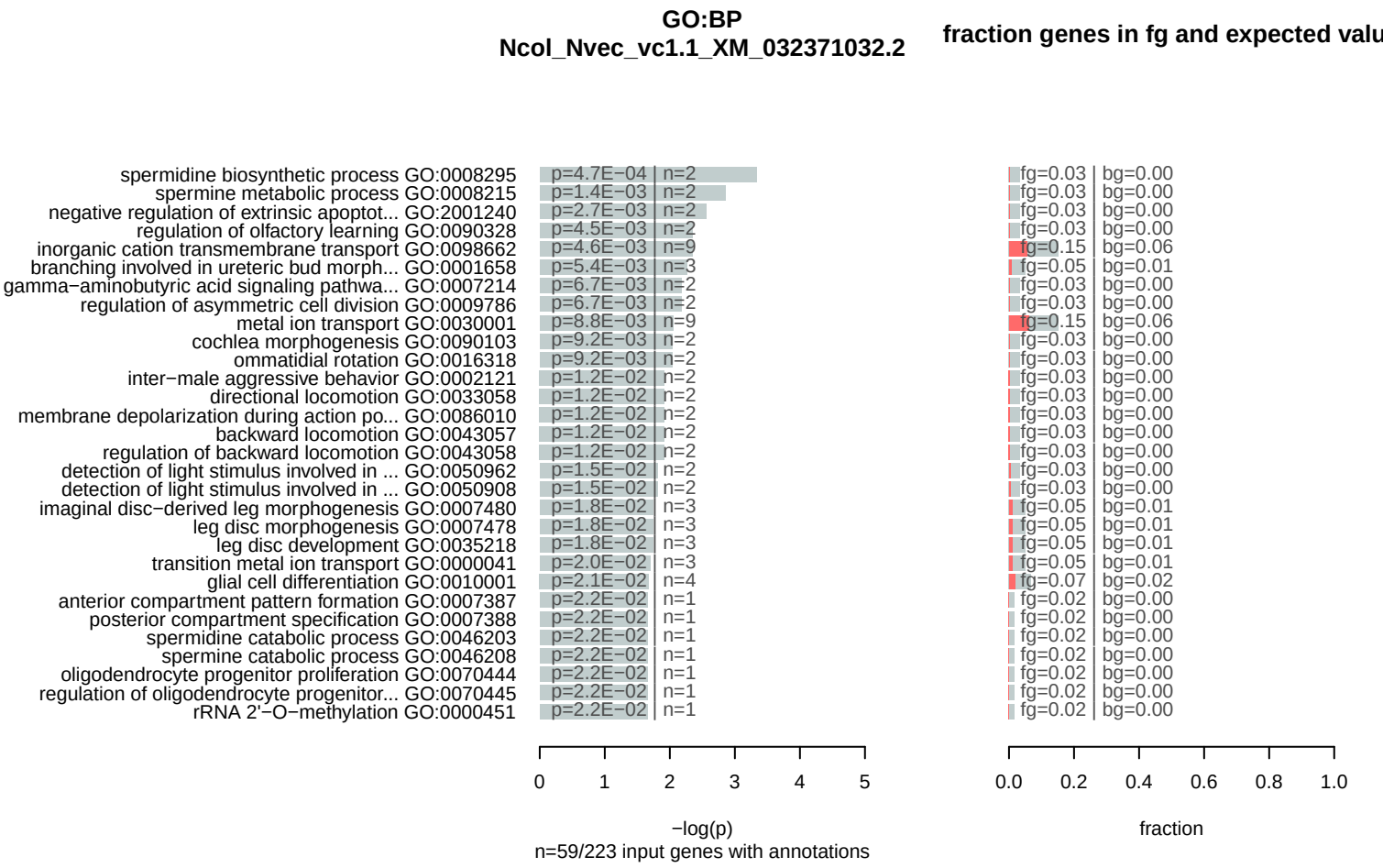
GO:BP
Ncol_Nvec_vc1.1_XM_032371032.2
fraction genes in fg and expected valu
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spermine metabolic process GO:0008215 p=1.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of extrinsic apoptot... GO:2001240 p=2.7E−03 n=2 fg=0.03 bg=0.00
regulation of olfactory learning GO:0090328 p=4.5E−03 n=2 fg=0.03 bg=0.00
inorganic cation transmembrane transport GO:0098662 p=4.6E−03 n=9 fg=0.15 bg=0.06
branching involved in ureteric bud morph... GO:0001658 p=5.4E−03 n=3 fg=0.05 bg=0.01
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=6.7E−03 n=2 fg=0.03 bg=0.00
regulation of asymmetric cell division GO:0009786 p=6.7E−03 n=2 fg=0.03 bg=0.00
metal ion transport GO:0030001 p=8.8E−03 n=9 fg=0.15 bg=0.06
cochlea morphogenesis GO:0090103 p=9.2E−03 n=2 fg=0.03 bg=0.00
ommatidial rotation GO:0016318 p=9.2E−03 n=2 fg=0.03 bg=0.00
inter−male aggressive behavior GO:0002121 p=1.2E−02 n=2 fg=0.03 bg=0.00
directional locomotion GO:0033058 p=1.2E−02 n=2 fg=0.03 bg=0.00
membrane depolarization during action po... GO:0086010 p=1.2E−02 n=2 fg=0.03 bg=0.00
backward locomotion GO:0043057 p=1.2E−02 n=2 fg=0.03 bg=0.00
regulation of backward locomotion GO:0043058 p=1.2E−02 n=2 fg=0.03 bg=0.00
detection of light stimulus involved in ... GO:0050962 p=1.5E−02 n=2 fg=0.03 bg=0.00
detection of light stimulus involved in ... GO:0050908 p=1.5E−02 n=2 fg=0.03 bg=0.00
imaginal disc−derived leg morphogenesis GO:0007480 p=1.8E−02 n=3 fg=0.05 bg=0.01
leg disc morphogenesis GO:0007478 p=1.8E−02 n=3 fg=0.05 bg=0.01
leg disc development GO:0035218 p=1.8E−02 n=3 fg=0.05 bg=0.01
transition metal ion transport GO:0000041 p=2.0E−02 n=3 fg=0.05 bg=0.01
glial cell differentiation GO:0010001 p=2.1E−02 n=4 fg=0.07 bg=0.02
anterior compartment pattern formation GO:0007387 p=2.2E−02 n=1 fg=0.02 bg=0.00
posterior compartment specification GO:0007388 p=2.2E−02 n=1 fg=0.02 bg=0.00
spermidine catabolic process GO:0046203 p=2.2E−02 n=1 fg=0.02 bg=0.00
spermine catabolic process GO:0046208 p=2.2E−02 n=1 fg=0.02 bg=0.00
oligodendrocyte progenitor proliferation GO:0070444 p=2.2E−02 n=1 fg=0.02 bg=0.00
regulation of oligodendrocyte progenitor... GO:0070445 p=2.2E−02 n=1 fg=0.02 bg=0.00
rRNA 2'−O−methylation GO:0000451 p=2.2E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=59/223 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032371032.2
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=1.4E−03 n=6 fg=0.11 bg=0.02
GABA−gated chloride ion channel activity GO:0022851 p=3.0E−03 n=2 fg=0.04 bg=0.00
GABA−A receptor activity GO:0004890 p=3.0E−03 n=2 fg=0.04 bg=0.00
benzodiazepine receptor activity GO:0008503 p=3.0E−03 n=2 fg=0.04 bg=0.00
calcium channel activity GO:0005262 p=4.8E−03 n=4 fg=0.07 bg=0.01
metal ion transmembrane transporter acti... GO:0046873 p=4.8E−03 n=9 fg=0.17 bg=0.04
phospholipase A2 activity GO:0004623 p=7.2E−03 n=2 fg=0.04 bg=0.00
voltage−gated cation channel activity GO:0022843 p=1.3E−02 n=3 fg=0.06 bg=0.01
transition metal ion transmembrane trans... GO:0046915 p=1.7E−02 n=2 fg=0.04 bg=0.00
transcription regulator activity GO:0140110 p=1.7E−02 n=11 fg=0.20 bg=0.10
voltage−gated calcium channel activity GO:0005245 p=2.0E−02 n=2 fg=0.04 bg=0.00
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=2.3E−02 n=1 fg=0.02 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=2.3E−02 n=1 fg=0.02 bg=0.00
adenosylmethionine decarboxylase activit... GO:0004014 p=2.3E−02 n=1 fg=0.02 bg=0.00
MHC class Ib protein binding, via antige... GO:0023030 p=2.3E−02 n=1 fg=0.02 bg=0.00
light−activated ion channel activity GO:0010461 p=2.3E−02 n=1 fg=0.02 bg=0.00
guanylate cyclase regulator activity GO:0030249 p=2.3E−02 n=1 fg=0.02 bg=0.00
rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039 p=2.3E−02 n=1 fg=0.02 bg=0.00
putrescine binding GO:0019810 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=2.3E−02 n=1 fg=0.02 bg=0.00
calcium sensitive guanylate cyclase acti... GO:0008048 p=2.3E−02 n=1 fg=0.02 bg=0.00
polyamine oxidase activity GO:0046592 p=2.3E−02 n=1 fg=0.02 bg=0.00
beta−1,3−galactosyl−O−glycosyl−glycoprot... GO:0047223 p=2.3E−02 n=1 fg=0.02 bg=0.00
polyamine binding GO:0019808 p=2.3E−02 n=1 fg=0.02 bg=0.00
cyclase activator activity GO:0010853 p=2.3E−02 n=1 fg=0.02 bg=0.00
MHC protein complex binding GO:0023023 p=2.3E−02 n=1 fg=0.02 bg=0.00
MHC class Ib protein complex binding GO:0023025 p=2.3E−02 n=1 fg=0.02 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=2.3E−02 n=1 fg=0.02 bg=0.00
MHC class Ib protein binding GO:0023029 p=2.3E−02 n=1 fg=0.02 bg=0.00
guanylate cyclase activator activity GO:0030250 p=2.3E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=54/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032371032.2
fraction genes in fg and expected valu
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=2.2E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus GO:0035996 p=2.2E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=2.2E−02 n=1 fg=0.02 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=2.2E−02 n=1 fg=0.02 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=2.2E−02 n=1 fg=0.02 bg=0.00
rhabdomere membrane GO:0033583 p=2.2E−02 n=1 fg=0.02 bg=0.00
proteasome core complex, beta−subunit co... GO:0019774 p=2.2E−02 n=1 fg=0.02 bg=0.00
transmembrane transporter complex GO:1902495 p=2.2E−02 n=4 fg=0.07 bg=0.02
mitochondrial large ribosomal subunit GO:0005762 p=2.3E−02 n=2 fg=0.03 bg=0.00
organellar large ribosomal subunit GO:0000315 p=2.3E−02 n=2 fg=0.03 bg=0.00
transporter complex GO:1990351 p=2.9E−02 n=4 fg=0.07 bg=0.02
integral component of synaptic vesicle m... GO:0030285 p=3.1E−02 n=2 fg=0.03 bg=0.00
intrinsic component of synaptic vesicle ... GO:0098563 p=3.6E−02 n=2 fg=0.03 bg=0.01
organelle envelope GO:0031967 p=4.1E−02 n=11 fg=0.19 bg=0.11
envelope GO:0031975 p=4.1E−02 n=11 fg=0.19 bg=0.11
core mediator complex GO:0070847 p=4.3E−02 n=1 fg=0.02 bg=0.00
Seh1−associated complex GO:0035859 p=4.3E−02 n=1 fg=0.02 bg=0.00
spermatoproteasome complex GO:1990111 p=4.3E−02 n=1 fg=0.02 bg=0.00
growth cone filopodium GO:1990812 p=4.3E−02 n=1 fg=0.02 bg=0.00
GATOR2 complex GO:0061700 p=4.3E−02 n=1 fg=0.02 bg=0.00
NADH dehydrogenase complex GO:0030964 p=4.6E−02 n=2 fg=0.03 bg=0.01
mitochondrial respiratory chain complex ... GO:0005747 p=4.6E−02 n=2 fg=0.03 bg=0.01
respiratory chain complex I GO:0045271 p=4.6E−02 n=2 fg=0.03 bg=0.01
mitochondrial protein−containing complex GO:0098798 p=4.7E−02 n=4 fg=0.07 bg=0.02
large ribosomal subunit GO:0015934 p=4.9E−02 n=3 fg=0.05 bg=0.01
membrane GO:0016020 p=5.1E−02 n=31 fg=0.53 bg=0.41
neuronal cell body membrane GO:0032809 p=5.2E−02 n=2 fg=0.03 bg=0.01
postsynaptic membrane GO:0045211 p=5.2E−02 n=3 fg=0.05 bg=0.01
cell body membrane GO:0044298 p=5.7E−02 n=2 fg=0.03 bg=0.01
RNA polymerase II transcription regulato... GO:0090575 p=6.2E−02 n=3 fg=0.05 bg=0.02
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−log(p)
n=59/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction