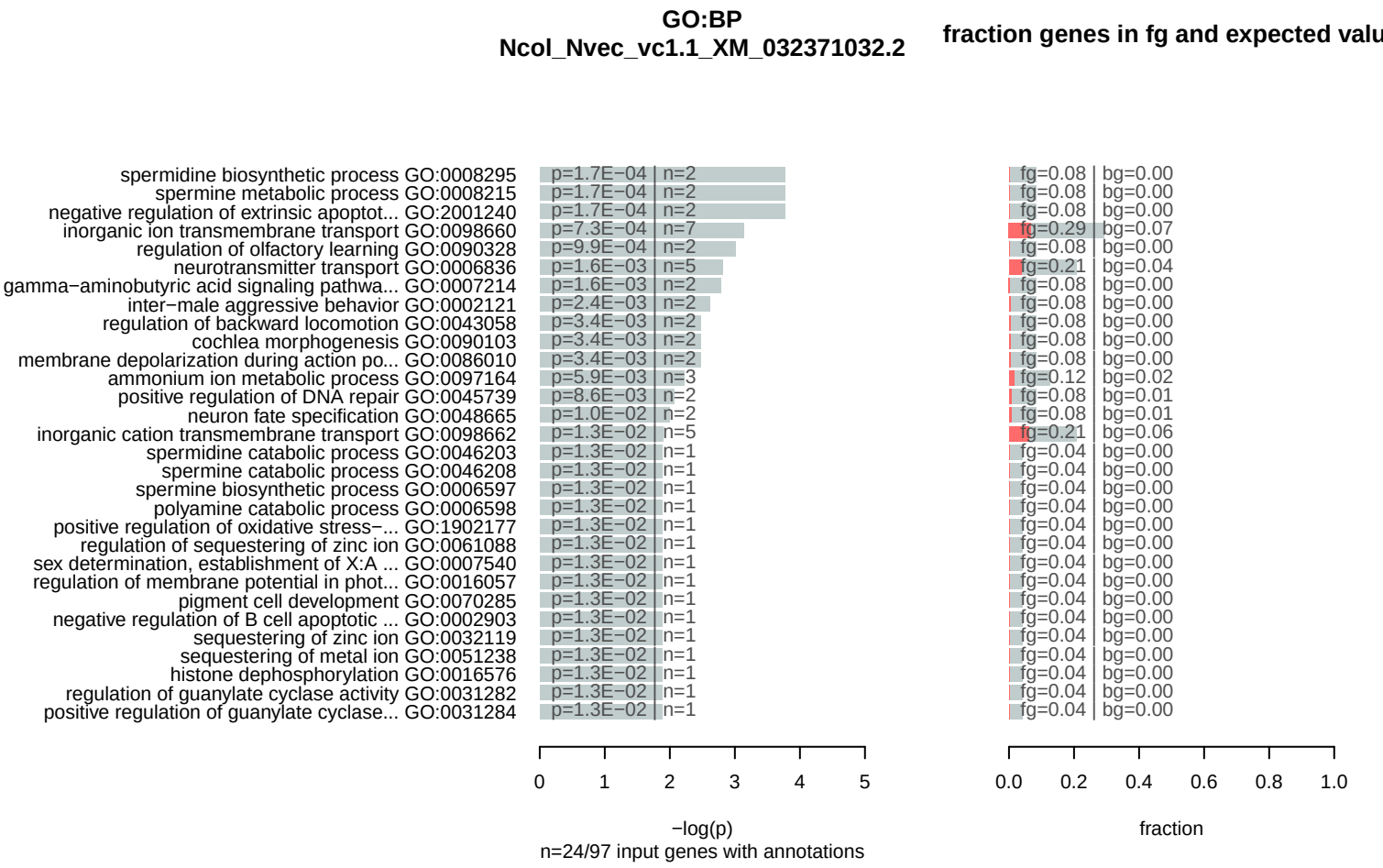
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spermine metabolic process GO:0008215 p=1.7E−04 n=2 fg=0.08 bg=0.00
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regulation of olfactory learning GO:0090328 p=9.9E−04 n=2 fg=0.08 bg=0.00
neurotransmitter transport GO:0006836 p=1.6E−03 n=5 fg=0.21 bg=0.04
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=1.6E−03 n=2 fg=0.08 bg=0.00
inter−male aggressive behavior GO:0002121 p=2.4E−03 n=2 fg=0.08 bg=0.00
regulation of backward locomotion GO:0043058 p=3.4E−03 n=2 fg=0.08 bg=0.00
cochlea morphogenesis GO:0090103 p=3.4E−03 n=2 fg=0.08 bg=0.00
membrane depolarization during action po... GO:0086010 p=3.4E−03 n=2 fg=0.08 bg=0.00
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positive regulation of DNA repair GO:0045739 p=8.6E−03 n=2 fg=0.08 bg=0.01
neuron fate specification GO:0048665 p=1.0E−02 n=2 fg=0.08 bg=0.01
inorganic cation transmembrane transport GO:0098662 p=1.3E−02 n=5 fg=0.21 bg=0.06
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spermine biosynthetic process GO:0006597 p=1.3E−02 n=1 fg=0.04 bg=0.00
polyamine catabolic process GO:0006598 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of oxidative stress−... GO:1902177 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of sequestering of zinc ion GO:0061088 p=1.3E−02 n=1 fg=0.04 bg=0.00
sex determination, establishment of X:A ... GO:0007540 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of membrane potential in phot... GO:0016057 p=1.3E−02 n=1 fg=0.04 bg=0.00
pigment cell development GO:0070285 p=1.3E−02 n=1 fg=0.04 bg=0.00
negative regulation of B cell apoptotic ... GO:0002903 p=1.3E−02 n=1 fg=0.04 bg=0.00
sequestering of zinc ion GO:0032119 p=1.3E−02 n=1 fg=0.04 bg=0.00
sequestering of metal ion GO:0051238 p=1.3E−02 n=1 fg=0.04 bg=0.00
histone dephosphorylation GO:0016576 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of guanylate cyclase activity GO:0031282 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of guanylate cyclase... GO:0031284 p=1.3E−02 n=1 fg=0.04 bg=0.00
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n=24/97 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
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GABA−gated chloride ion channel activity GO:0022851 p=4.9E−04 n=2 fg=0.10 bg=0.00
GABA−A receptor activity GO:0004890 p=4.9E−04 n=2 fg=0.10 bg=0.00
benzodiazepine receptor activity GO:0008503 p=4.9E−04 n=2 fg=0.10 bg=0.00
phospholipase A2 activity GO:0004623 p=9.8E−04 n=2 fg=0.10 bg=0.00
voltage−gated calcium channel activity GO:0005245 p=4.4E−03 n=2 fg=0.10 bg=0.01
polyamine binding GO:0019808 p=1.3E−02 n=1 fg=0.05 bg=0.00
polyamine oxidase activity GO:0046592 p=1.3E−02 n=1 fg=0.05 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=1.3E−02 n=1 fg=0.05 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=1.3E−02 n=1 fg=0.05 bg=0.00
oxidoreductase activity, acting on the C... GO:0016647 p=1.3E−02 n=1 fg=0.05 bg=0.00
adenosylmethionine decarboxylase activit... GO:0004014 p=1.3E−02 n=1 fg=0.05 bg=0.00
cyclase activator activity GO:0010853 p=1.3E−02 n=1 fg=0.05 bg=0.00
guanylate cyclase regulator activity GO:0030249 p=1.3E−02 n=1 fg=0.05 bg=0.00
phospholipase A1 activity GO:0008970 p=1.3E−02 n=1 fg=0.05 bg=0.00
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N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=1.3E−02 n=1 fg=0.05 bg=0.00
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calcium sensitive guanylate cyclase acti... GO:0008048 p=1.3E−02 n=1 fg=0.05 bg=0.00
guanylate cyclase activator activity GO:0030250 p=1.3E−02 n=1 fg=0.05 bg=0.00
sodium ion transmembrane transporter act... GO:0015081 p=1.6E−02 n=2 fg=0.10 bg=0.01
transmembrane transporter activity GO:0022857 p=1.9E−02 n=9 fg=0.43 bg=0.09
metal ion transmembrane transporter acti... GO:0046873 p=2.0E−02 n=5 fg=0.24 bg=0.04
dephospho−CoA kinase activity GO:0004140 p=2.6E−02 n=1 fg=0.05 bg=0.00
neurotransmitter:sodium symporter activi... GO:0005328 p=2.6E−02 n=1 fg=0.05 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=2.6E−02 n=1 fg=0.05 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=2.6E−02 n=1 fg=0.05 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=2.6E−02 n=1 fg=0.05 bg=0.00
calcium−dependent protein kinase regulat... GO:0010858 p=2.6E−02 n=1 fg=0.05 bg=0.00
BH3 domain binding GO:0051434 p=2.6E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=21/97 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
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neuromuscular junction GO:0031594 p=7.6E−03 n=3 fg=0.13 bg=0.02
integral component of synaptic vesicle m... GO:0030285 p=7.9E−03 n=2 fg=0.09 bg=0.01
neuronal cell body membrane GO:0032809 p=1.3E−02 n=2 fg=0.09 bg=0.01
neuron projection membrane GO:0032589 p=1.5E−02 n=2 fg=0.09 bg=0.01
cell body membrane GO:0044298 p=1.5E−02 n=2 fg=0.09 bg=0.01
Seh1−associated complex GO:0035859 p=2.5E−02 n=1 fg=0.04 bg=0.00
growth cone filopodium GO:1990812 p=2.5E−02 n=1 fg=0.04 bg=0.00
GATOR2 complex GO:0061700 p=2.5E−02 n=1 fg=0.04 bg=0.00
growth cone lamellipodium GO:1990761 p=3.8E−02 n=1 fg=0.04 bg=0.00
Bcl−2 family protein complex GO:0097136 p=3.8E−02 n=1 fg=0.04 bg=0.00
leading edge membrane GO:0031256 p=3.9E−02 n=2 fg=0.09 bg=0.01
cell leading edge GO:0031252 p=4.7E−02 n=3 fg=0.13 bg=0.04
peroxisomal matrix GO:0005782 p=5.0E−02 n=1 fg=0.04 bg=0.00
microbody lumen GO:0031907 p=5.0E−02 n=1 fg=0.04 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=6.2E−02 n=1 fg=0.04 bg=0.00
neuronal cell body GO:0043025 p=7.2E−02 n=4 fg=0.17 bg=0.07
dynactin complex GO:0005869 p=7.4E−02 n=1 fg=0.04 bg=0.00
dendritic tree GO:0097447 p=7.8E−02 n=4 fg=0.17 bg=0.07
dendrite GO:0030425 p=7.8E−02 n=4 fg=0.17 bg=0.07
presynapse GO:0098793 p=8.0E−02 n=5 fg=0.22 bg=0.05
transmembrane transporter complex GO:1902495 p=8.2E−02 n=2 fg=0.09 bg=0.02
calcium channel complex GO:0034704 p=8.6E−02 n=1 fg=0.04 bg=0.00
transporter complex GO:1990351 p=9.0E−02 n=2 fg=0.09 bg=0.02
cell body GO:0044297 p=9.0E−02 n=4 fg=0.17 bg=0.08
axon GO:0030424 p=9.8E−02 n=4 fg=0.17 bg=0.08
membrane GO:0016020 p=1.3E−01 n=15 fg=0.65 bg=0.46
respiratory chain complex I GO:0045271 p=1.4E−01 n=1 fg=0.04 bg=0.01
mitochondrial respiratory chain complex ... GO:0005747 p=1.4E−01 n=1 fg=0.04 bg=0.01
NADH dehydrogenase complex GO:0030964 p=1.4E−01 n=1 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=23/97 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction