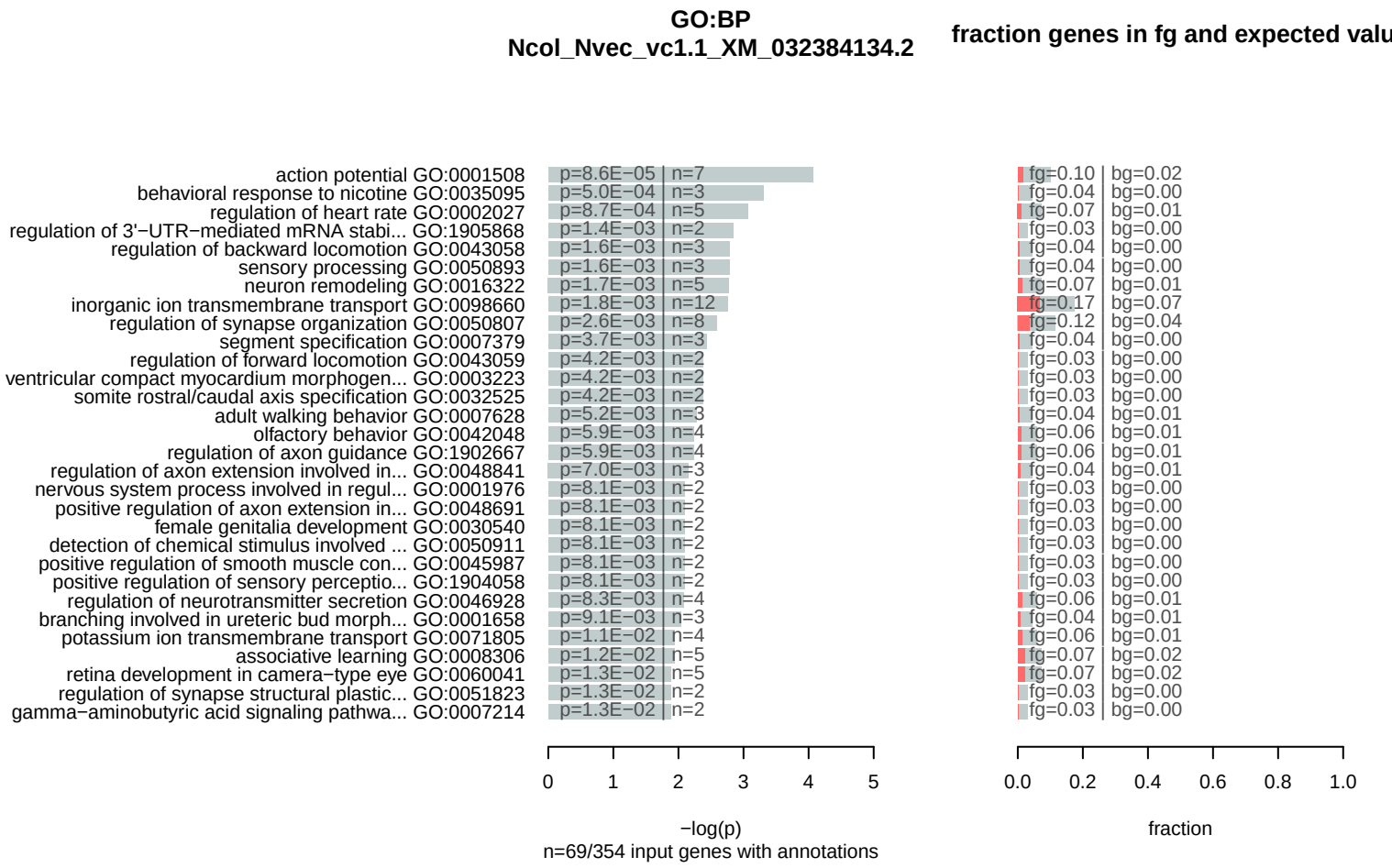
GO:BP
Ncol_Nvec_vc1.1_XM_032384134.2
fraction genes in fg and expected valu
action potential GO:0001508 p=8.6E−05 n=7 fg=0.10 bg=0.02
behavioral response to nicotine GO:0035095 p=5.0E−04 n=3 fg=0.04 bg=0.00
regulation of heart rate GO:0002027 p=8.7E−04 n=5 fg=0.07 bg=0.01
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=1.4E−03 n=2 fg=0.03 bg=0.00
regulation of backward locomotion GO:0043058 p=1.6E−03 n=3 fg=0.04 bg=0.00
sensory processing GO:0050893 p=1.6E−03 n=3 fg=0.04 bg=0.00
neuron remodeling GO:0016322 p=1.7E−03 n=5 fg=0.07 bg=0.01
inorganic ion transmembrane transport GO:0098660 p=1.8E−03 n=12 fg=0.17 bg=0.07
regulation of synapse organization GO:0050807 p=2.6E−03 n=8 fg=0.12 bg=0.04
segment specification GO:0007379 p=3.7E−03 n=3 fg=0.04 bg=0.00
regulation of forward locomotion GO:0043059 p=4.2E−03 n=2 fg=0.03 bg=0.00
ventricular compact myocardium morphogen... GO:0003223 p=4.2E−03 n=2 fg=0.03 bg=0.00
somite rostral/caudal axis specification GO:0032525 p=4.2E−03 n=2 fg=0.03 bg=0.00
adult walking behavior GO:0007628 p=5.2E−03 n=3 fg=0.04 bg=0.01
olfactory behavior GO:0042048 p=5.9E−03 n=4 fg=0.06 bg=0.01
regulation of axon guidance GO:1902667 p=5.9E−03 n=4 fg=0.06 bg=0.01
regulation of axon extension involved in... GO:0048841 p=7.0E−03 n=3 fg=0.04 bg=0.01
nervous system process involved in regul... GO:0001976 p=8.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of axon extension in... GO:0048691 p=8.1E−03 n=2 fg=0.03 bg=0.00
female genitalia development GO:0030540 p=8.1E−03 n=2 fg=0.03 bg=0.00
detection of chemical stimulus involved ... GO:0050911 p=8.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of smooth muscle con... GO:0045987 p=8.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of sensory perceptio... GO:1904058 p=8.1E−03 n=2 fg=0.03 bg=0.00
regulation of neurotransmitter secretion GO:0046928 p=8.3E−03 n=4 fg=0.06 bg=0.01
branching involved in ureteric bud morph... GO:0001658 p=9.1E−03 n=3 fg=0.04 bg=0.01
potassium ion transmembrane transport GO:0071805 p=1.1E−02 n=4 fg=0.06 bg=0.01
associative learning GO:0008306 p=1.2E−02 n=5 fg=0.07 bg=0.02
retina development in camera−type eye GO:0060041 p=1.3E−02 n=5 fg=0.07 bg=0.02
regulation of synapse structural plastic... GO:0051823 p=1.3E−02 n=2 fg=0.03 bg=0.00
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=1.3E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=69/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032384134.2
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=1.9E−05 n=9 fg=0.15 bg=0.03
high voltage−gated calcium channel activ... GO:0008331 p=1.5E−03 n=2 fg=0.03 bg=0.00
methylated histone binding GO:0035064 p=2.7E−03 n=3 fg=0.05 bg=0.01
promoter−specific chromatin binding GO:1990841 p=4.0E−03 n=3 fg=0.05 bg=0.01
voltage−gated potassium channel activity GO:0005249 p=5.6E−03 n=3 fg=0.05 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=6.8E−03 n=10 fg=0.16 bg=0.07
extracellularly glutamate−gated chloride... GO:0008068 p=8.5E−03 n=2 fg=0.03 bg=0.00
ion channel regulator activity GO:0099106 p=1.2E−02 n=4 fg=0.06 bg=0.02
glutamate binding GO:0016595 p=1.4E−02 n=2 fg=0.03 bg=0.00
transmitter−gated ion channel activity GO:0022824 p=1.4E−02 n=2 fg=0.03 bg=0.00
transmitter−gated channel activity GO:0022835 p=1.4E−02 n=2 fg=0.03 bg=0.00
channel regulator activity GO:0016247 p=1.6E−02 n=4 fg=0.06 bg=0.02
extracellular ligand−gated ion channel a... GO:0005230 p=1.9E−02 n=4 fg=0.06 bg=0.01
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.9E−02 n=1 fg=0.02 bg=0.00
glucuronosyl−N−acetylgalactosaminyl−prot... GO:0047238 p=3.9E−02 n=1 fg=0.02 bg=0.00
glycogen binding GO:2001069 p=3.9E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=3.9E−02 n=1 fg=0.02 bg=0.00
glutamate 5−kinase activity GO:0004349 p=3.9E−02 n=1 fg=0.02 bg=0.00
rRNA primary transcript binding GO:0042134 p=3.9E−02 n=1 fg=0.02 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=3.9E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.9E−02 n=1 fg=0.02 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=3.9E−02 n=1 fg=0.02 bg=0.00
acetate ester transmembrane transporter ... GO:1901375 p=3.9E−02 n=1 fg=0.02 bg=0.00
C−acetyltransferase activity GO:0016453 p=3.9E−02 n=1 fg=0.02 bg=0.00
acetylcholine transmembrane transporter ... GO:0005277 p=3.9E−02 n=1 fg=0.02 bg=0.00
amino acid kinase activity GO:0019202 p=3.9E−02 n=1 fg=0.02 bg=0.00
delta1−pyrroline−5−carboxylate synthetas... GO:0017084 p=3.9E−02 n=1 fg=0.02 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=3.9E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.9E−02 n=1 fg=0.02 bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988 p=3.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=62/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032384134.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=4.1E−03 n=3 fg=0.04 bg=0.00
ion channel complex GO:0034702 p=1.4E−02 n=6 fg=0.08 bg=0.01
voltage−gated calcium channel complex GO:0005891 p=1.4E−02 n=2 fg=0.03 bg=0.00
neuron projection membrane GO:0032589 p=1.9E−02 n=3 fg=0.04 bg=0.01
calcium channel complex GO:0034704 p=2.8E−02 n=2 fg=0.03 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.9E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=3.9E−02 n=1 fg=0.01 bg=0.00
smooth muscle contractile fiber GO:0030485 p=3.9E−02 n=1 fg=0.01 bg=0.00
syntrophin complex GO:0016013 p=3.9E−02 n=1 fg=0.01 bg=0.00
kinocilium GO:0060091 p=3.9E−02 n=1 fg=0.01 bg=0.00
synapse GO:0045202 p=4.2E−02 n=12 fg=0.17 bg=0.10
plasma membrane protein complex GO:0098797 p=4.7E−02 n=8 fg=0.11 bg=0.03
integral component of membrane GO:0016021 p=6.6E−02 n=19 fg=0.27 bg=0.16
PcG protein complex GO:0031519 p=6.6E−02 n=2 fg=0.03 bg=0.01
leading edge membrane GO:0031256 p=7.2E−02 n=3 fg=0.04 bg=0.01
cation channel complex GO:0034703 p=7.3E−02 n=5 fg=0.07 bg=0.01
mitochondrial crista GO:0030061 p=7.7E−02 n=1 fg=0.01 bg=0.00
pleated septate junction GO:0005919 p=7.7E−02 n=1 fg=0.01 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=7.7E−02 n=1 fg=0.01 bg=0.00
cell junction GO:0030054 p=8.7E−02 n=14 fg=0.20 bg=0.13
presynapse GO:0098793 p=8.9E−02 n=7 fg=0.10 bg=0.05
transmembrane transporter complex GO:1902495 p=9.4E−02 n=6 fg=0.08 bg=0.02
intrinsic component of membrane GO:0031224 p=9.4E−02 n=19 fg=0.27 bg=0.17
integral component of plasma membrane GO:0005887 p=1.0E−01 n=11 fg=0.15 bg=0.08
neuronal cell body membrane GO:0032809 p=1.0E−01 n=2 fg=0.03 bg=0.01
transporter complex GO:1990351 p=1.1E−01 n=6 fg=0.08 bg=0.02
postsynaptic membrane GO:0045211 p=1.1E−01 n=3 fg=0.04 bg=0.02
glycogen granule GO:0042587 p=1.1E−01 n=1 fg=0.01 bg=0.00
muscle cell projection GO:0036194 p=1.1E−01 n=1 fg=0.01 bg=0.00
muscle cell projection membrane GO:0036195 p=1.1E−01 n=1 fg=0.01 bg=0.00
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−log(p)
n=71/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction