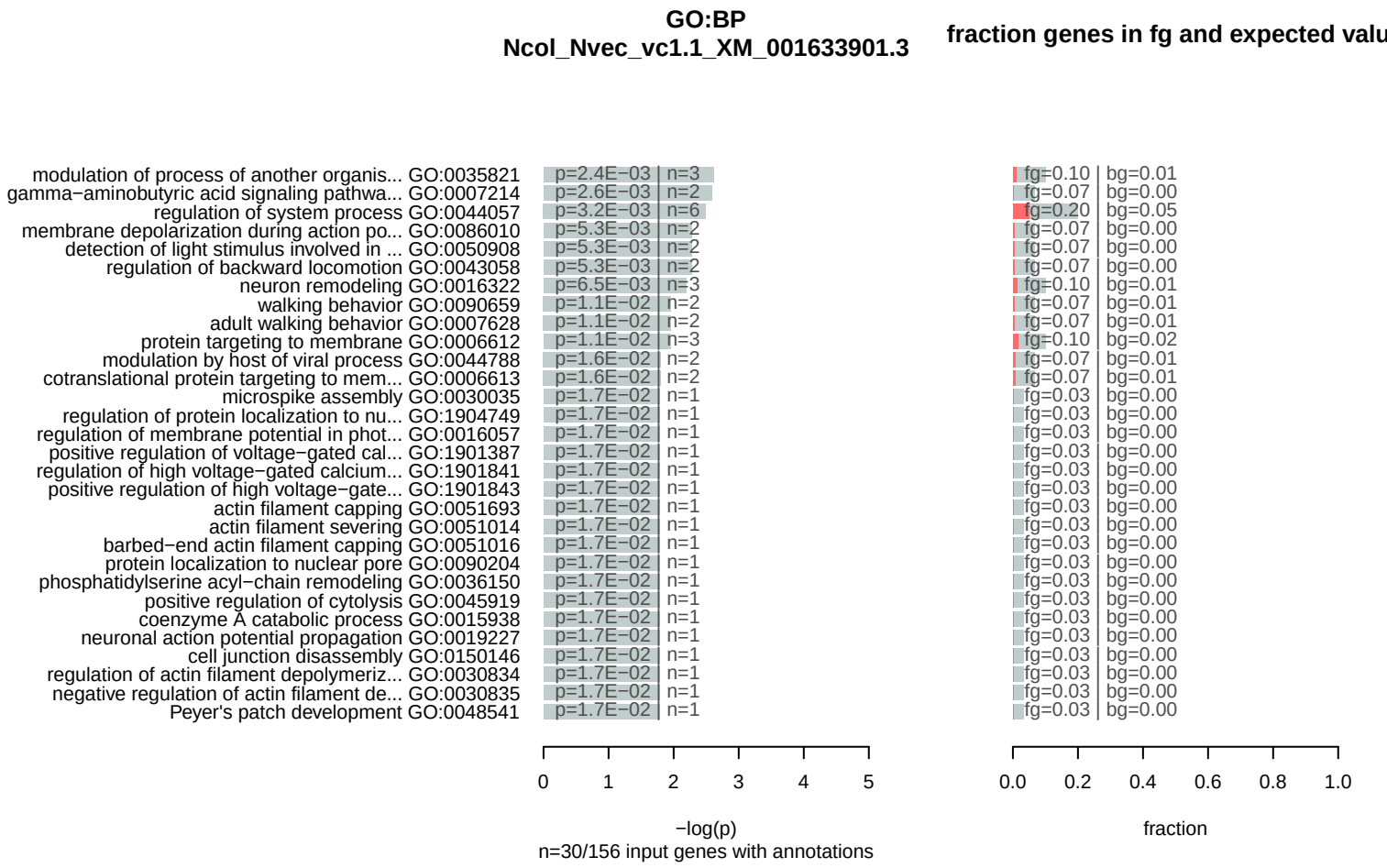
GO:BP
Ncol_Nvec_vc1.1_XM_001633901.3
fraction genes in fg and expected valu
modulation of process of another organis... GO:0035821 p=2.4E−03 n=3 fg=0.10 bg=0.01
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=2.6E−03 n=2 fg=0.07 bg=0.00
regulation of system process GO:0044057 p=3.2E−03 n=6 fg=0.20 bg=0.05
membrane depolarization during action po... GO:0086010 p=5.3E−03 n=2 fg=0.07 bg=0.00
detection of light stimulus involved in ... GO:0050908 p=5.3E−03 n=2 fg=0.07 bg=0.00
regulation of backward locomotion GO:0043058 p=5.3E−03 n=2 fg=0.07 bg=0.00
neuron remodeling GO:0016322 p=6.5E−03 n=3 fg=0.10 bg=0.01
walking behavior GO:0090659 p=1.1E−02 n=2 fg=0.07 bg=0.01
adult walking behavior GO:0007628 p=1.1E−02 n=2 fg=0.07 bg=0.01
protein targeting to membrane GO:0006612 p=1.1E−02 n=3 fg=0.10 bg=0.02
modulation by host of viral process GO:0044788 p=1.6E−02 n=2 fg=0.07 bg=0.01
cotranslational protein targeting to mem... GO:0006613 p=1.6E−02 n=2 fg=0.07 bg=0.01
microspike assembly GO:0030035 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of protein localization to nu... GO:1904749 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of membrane potential in phot... GO:0016057 p=1.7E−02 n=1 fg=0.03 bg=0.00
positive regulation of voltage−gated cal... GO:1901387 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of high voltage−gated calcium... GO:1901841 p=1.7E−02 n=1 fg=0.03 bg=0.00
positive regulation of high voltage−gate... GO:1901843 p=1.7E−02 n=1 fg=0.03 bg=0.00
actin filament capping GO:0051693 p=1.7E−02 n=1 fg=0.03 bg=0.00
actin filament severing GO:0051014 p=1.7E−02 n=1 fg=0.03 bg=0.00
barbed−end actin filament capping GO:0051016 p=1.7E−02 n=1 fg=0.03 bg=0.00
protein localization to nuclear pore GO:0090204 p=1.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylserine acyl−chain remodeling GO:0036150 p=1.7E−02 n=1 fg=0.03 bg=0.00
positive regulation of cytolysis GO:0045919 p=1.7E−02 n=1 fg=0.03 bg=0.00
coenzyme A catabolic process GO:0015938 p=1.7E−02 n=1 fg=0.03 bg=0.00
neuronal action potential propagation GO:0019227 p=1.7E−02 n=1 fg=0.03 bg=0.00
cell junction disassembly GO:0150146 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of actin filament depolymeriz... GO:0030834 p=1.7E−02 n=1 fg=0.03 bg=0.00
negative regulation of actin filament de... GO:0030835 p=1.7E−02 n=1 fg=0.03 bg=0.00
Peyer's patch development GO:0048541 p=1.7E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=30/156 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001633901.3
fraction genes in fg and expected valu
high voltage−gated calcium channel activ... GO:0008331 p=2.8E−04 n=2 fg=0.07 bg=0.00
actin monomer binding GO:0003785 p=1.6E−03 n=2 fg=0.07 bg=0.00
actin filament binding GO:0051015 p=1.7E−03 n=3 fg=0.11 bg=0.01
ion gated channel activity GO:0022839 p=4.7E−03 n=4 fg=0.15 bg=0.03
protein methyltransferase activity GO:0008276 p=1.4E−02 n=2 fg=0.07 bg=0.01
thiolester hydrolase activity GO:0016790 p=1.4E−02 n=2 fg=0.07 bg=0.01
hydroxymethylglutaryl−CoA hydrolase acti... GO:0047994 p=1.7E−02 n=1 fg=0.04 bg=0.00
succinyl−CoA hydrolase activity GO:0004778 p=1.7E−02 n=1 fg=0.04 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=1.7E−02 n=1 fg=0.04 bg=0.00
S100 protein binding GO:0044548 p=1.7E−02 n=1 fg=0.04 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=1.7E−02 n=1 fg=0.04 bg=0.00
acetyl−CoA hydrolase activity GO:0003986 p=3.4E−02 n=1 fg=0.04 bg=0.00
Tat protein binding GO:0030957 p=3.4E−02 n=1 fg=0.04 bg=0.00
oxysterol binding GO:0008142 p=3.4E−02 n=1 fg=0.04 bg=0.00
snoRNA binding GO:0030515 p=3.4E−02 n=1 fg=0.04 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=3.4E−02 n=1 fg=0.04 bg=0.00
RNA polymerase II CTD heptapeptide repea... GO:0008420 p=3.4E−02 n=1 fg=0.04 bg=0.00
phosphoprotein binding GO:0051219 p=4.0E−02 n=2 fg=0.07 bg=0.01
phosphatidylinositol binding GO:0035091 p=4.1E−02 n=3 fg=0.11 bg=0.03
GABA−gated chloride ion channel activity GO:0022851 p=5.0E−02 n=1 fg=0.04 bg=0.00
GABA receptor activity GO:0016917 p=5.0E−02 n=1 fg=0.04 bg=0.00
cyclosporin A binding GO:0016018 p=5.0E−02 n=1 fg=0.04 bg=0.00
G protein−coupled photoreceptor activity GO:0008020 p=5.0E−02 n=1 fg=0.04 bg=0.00
photoreceptor activity GO:0009881 p=5.0E−02 n=1 fg=0.04 bg=0.00
GABA−A receptor activity GO:0004890 p=5.0E−02 n=1 fg=0.04 bg=0.00
benzodiazepine receptor activity GO:0008503 p=5.0E−02 n=1 fg=0.04 bg=0.00
methyltransferase activity GO:0008168 p=5.2E−02 n=2 fg=0.07 bg=0.01
isomerase activity GO:0016853 p=5.6E−02 n=2 fg=0.07 bg=0.01
transferase activity, transferring one−c... GO:0016741 p=5.6E−02 n=2 fg=0.07 bg=0.01
protein heterodimerization activity GO:0046982 p=6.6E−02 n=4 fg=0.15 bg=0.06
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−log(p)
n=27/156 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001633901.3
fraction genes in fg and expected valu
endoplasmic reticulum chaperone complex GO:0034663 p=2.7E−04 n=2 fg=0.07 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=2.6E−03 n=2 fg=0.07 bg=0.00
smooth endoplasmic reticulum GO:0005790 p=1.6E−02 n=2 fg=0.07 bg=0.01
L−type voltage−gated calcium channel com... GO:1990454 p=1.7E−02 n=1 fg=0.03 bg=0.00
smooth muscle contractile fiber GO:0030485 p=1.7E−02 n=1 fg=0.03 bg=0.00
presynapse GO:0098793 p=2.1E−02 n=5 fg=0.17 bg=0.05
cytoplasmic side of plasma membrane GO:0009898 p=3.1E−02 n=3 fg=0.10 bg=0.02
Gtr1−Gtr2 GTPase complex GO:1990131 p=3.3E−02 n=1 fg=0.03 bg=0.00
presynaptic active zone GO:0048786 p=3.5E−02 n=2 fg=0.07 bg=0.01
cytoplasmic side of membrane GO:0098562 p=4.1E−02 n=3 fg=0.10 bg=0.03
transport vesicle GO:0030133 p=4.2E−02 n=4 fg=0.13 bg=0.04
synaptic vesicle GO:0008021 p=4.3E−02 n=3 fg=0.10 bg=0.03
muscle cell projection GO:0036194 p=4.9E−02 n=1 fg=0.03 bg=0.00
muscle cell projection membrane GO:0036195 p=4.9E−02 n=1 fg=0.03 bg=0.00
exocytic vesicle GO:0070382 p=6.0E−02 n=3 fg=0.10 bg=0.03
extracellular space GO:0005615 p=6.0E−02 n=3 fg=0.10 bg=0.03
pericentriolar material GO:0000242 p=6.5E−02 n=1 fg=0.03 bg=0.00
dendrite cytoplasm GO:0032839 p=6.5E−02 n=1 fg=0.03 bg=0.00
spindle midzone GO:0051233 p=6.5E−02 n=1 fg=0.03 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=6.5E−02 n=1 fg=0.03 bg=0.00
cortical endoplasmic reticulum GO:0032541 p=6.5E−02 n=1 fg=0.03 bg=0.00
septin cytoskeleton GO:0032156 p=8.0E−02 n=1 fg=0.03 bg=0.00
basement membrane GO:0005604 p=8.0E−02 n=1 fg=0.03 bg=0.00
EMC complex GO:0072546 p=8.0E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum subcompartment GO:0098827 p=8.4E−02 n=5 fg=0.17 bg=0.08
endoplasmic reticulum lumen GO:0005788 p=8.7E−02 n=2 fg=0.07 bg=0.02
intrinsic component of plasma membrane GO:0031226 p=8.8E−02 n=5 fg=0.17 bg=0.08
side of membrane GO:0098552 p=9.3E−02 n=3 fg=0.10 bg=0.04
sarcoplasm GO:0016528 p=9.6E−02 n=1 fg=0.03 bg=0.00
sarcoplasmic reticulum GO:0016529 p=9.6E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=30/156 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction