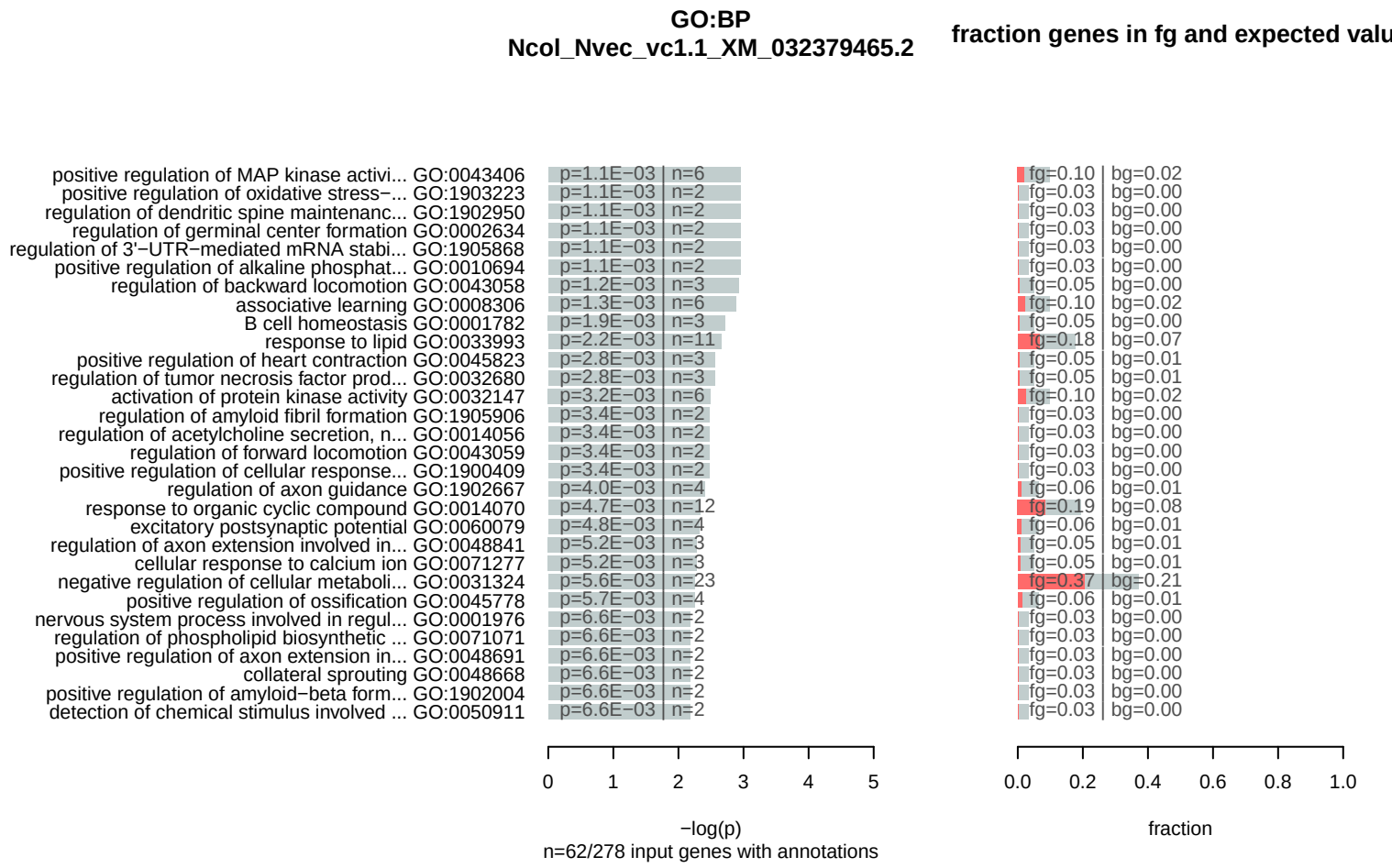
GO:BP
Ncol_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
positive regulation of MAP kinase activi... GO:0043406 p=1.1E−03 n=6 fg=0.10 bg=0.02
positive regulation of oxidative stress−... GO:1903223 p=1.1E−03 n=2 fg=0.03 bg=0.00
regulation of dendritic spine maintenanc... GO:1902950 p=1.1E−03 n=2 fg=0.03 bg=0.00
regulation of germinal center formation GO:0002634 p=1.1E−03 n=2 fg=0.03 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=1.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of alkaline phosphat... GO:0010694 p=1.1E−03 n=2 fg=0.03 bg=0.00
regulation of backward locomotion GO:0043058 p=1.2E−03 n=3 fg=0.05 bg=0.00
associative learning GO:0008306 p=1.3E−03 n=6 fg=0.10 bg=0.02
B cell homeostasis GO:0001782 p=1.9E−03 n=3 fg=0.05 bg=0.00
response to lipid GO:0033993 p=2.2E−03 n=11 fg=0.18 bg=0.07
positive regulation of heart contraction GO:0045823 p=2.8E−03 n=3 fg=0.05 bg=0.01
regulation of tumor necrosis factor prod... GO:0032680 p=2.8E−03 n=3 fg=0.05 bg=0.01
activation of protein kinase activity GO:0032147 p=3.2E−03 n=6 fg=0.10 bg=0.02
regulation of amyloid fibril formation GO:1905906 p=3.4E−03 n=2 fg=0.03 bg=0.00
regulation of acetylcholine secretion, n... GO:0014056 p=3.4E−03 n=2 fg=0.03 bg=0.00
regulation of forward locomotion GO:0043059 p=3.4E−03 n=2 fg=0.03 bg=0.00
positive regulation of cellular response... GO:1900409 p=3.4E−03 n=2 fg=0.03 bg=0.00
regulation of axon guidance GO:1902667 p=4.0E−03 n=4 fg=0.06 bg=0.01
response to organic cyclic compound GO:0014070 p=4.7E−03 n=12 fg=0.19 bg=0.08
excitatory postsynaptic potential GO:0060079 p=4.8E−03 n=4 fg=0.06 bg=0.01
regulation of axon extension involved in... GO:0048841 p=5.2E−03 n=3 fg=0.05 bg=0.01
cellular response to calcium ion GO:0071277 p=5.2E−03 n=3 fg=0.05 bg=0.01
negative regulation of cellular metaboli... GO:0031324 p=5.6E−03 n=23 fg=0.37 bg=0.21
positive regulation of ossification GO:0045778 p=5.7E−03 n=4 fg=0.06 bg=0.01
nervous system process involved in regul... GO:0001976 p=6.6E−03 n=2 fg=0.03 bg=0.00
regulation of phospholipid biosynthetic ... GO:0071071 p=6.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of axon extension in... GO:0048691 p=6.6E−03 n=2 fg=0.03 bg=0.00
collateral sprouting GO:0048668 p=6.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of amyloid−beta form... GO:1902004 p=6.6E−03 n=2 fg=0.03 bg=0.00
detection of chemical stimulus involved ... GO:0050911 p=6.6E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=62/278 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=2.6E−03 n=6 fg=0.11 bg=0.03
voltage−gated potassium channel activity GO:0005249 p=3.9E−03 n=3 fg=0.05 bg=0.01
extracellular ligand−gated ion channel a... GO:0005230 p=3.9E−03 n=3 fg=0.05 bg=0.01
DNA−binding transcription repressor acti... GO:0001227 p=4.9E−03 n=4 fg=0.07 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=5.3E−03 n=12 fg=0.22 bg=0.07
integrin binding GO:0005178 p=6.9E−03 n=3 fg=0.05 bg=0.01
transmitter−gated ion channel activity GO:0022824 p=1.1E−02 n=2 fg=0.04 bg=0.00
transmitter−gated channel activity GO:0022835 p=1.1E−02 n=2 fg=0.04 bg=0.00
BH domain binding GO:0051400 p=1.1E−02 n=2 fg=0.04 bg=0.00
ephrin receptor binding GO:0046875 p=1.1E−02 n=2 fg=0.04 bg=0.00
ligand−gated anion channel activity GO:0099095 p=2.2E−02 n=2 fg=0.04 bg=0.00
excitatory extracellular ligand−gated io... GO:0005231 p=2.2E−02 n=2 fg=0.04 bg=0.00
hormone binding GO:0042562 p=2.9E−02 n=2 fg=0.04 bg=0.01
heparan sulfate binding GO:1904399 p=3.5E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.5E−02 n=1 fg=0.02 bg=0.00
Roundabout binding GO:0048495 p=3.5E−02 n=1 fg=0.02 bg=0.00
glycogen binding GO:2001069 p=3.5E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=3.5E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=3.5E−02 n=1 fg=0.02 bg=0.00
BH4 domain binding GO:0051435 p=3.5E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=3.5E−02 n=1 fg=0.02 bg=0.00
neuropilin binding GO:0038191 p=3.5E−02 n=1 fg=0.02 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=3.5E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.5E−02 n=1 fg=0.02 bg=0.00
acetate ester transmembrane transporter ... GO:1901375 p=3.5E−02 n=1 fg=0.02 bg=0.00
C−acetyltransferase activity GO:0016453 p=3.5E−02 n=1 fg=0.02 bg=0.00
acetylcholine transmembrane transporter ... GO:0005277 p=3.5E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor regulator activit... GO:0030548 p=3.5E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor activator activit... GO:0030549 p=3.5E−02 n=1 fg=0.02 bg=0.00
phorbol ester receptor activity GO:0001565 p=3.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/278 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=3.0E−03 n=3 fg=0.05 bg=0.01
neuron projection membrane GO:0032589 p=1.4E−02 n=3 fg=0.05 bg=0.01
postsynapse GO:0098794 p=1.7E−02 n=7 fg=0.11 bg=0.04
synapse GO:0045202 p=2.0E−02 n=12 fg=0.19 bg=0.10
dendritic shaft GO:0043198 p=2.4E−02 n=3 fg=0.05 bg=0.01
striated muscle dense body GO:0055120 p=3.0E−02 n=2 fg=0.03 bg=0.00
lipoprotein particle GO:1990777 p=3.5E−02 n=1 fg=0.02 bg=0.00
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=3.5E−02 n=1 fg=0.02 bg=0.00
syntrophin complex GO:0016013 p=3.5E−02 n=1 fg=0.02 bg=0.00
smooth muscle contractile fiber GO:0030485 p=3.5E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=3.5E−02 n=1 fg=0.02 bg=0.00
9+2 non−motile cilium GO:0097732 p=3.5E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=3.5E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=3.5E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=3.5E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=3.5E−02 n=1 fg=0.02 bg=0.00
kinocilium GO:0060091 p=3.5E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=3.5E−02 n=1 fg=0.02 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=3.5E−02 n=1 fg=0.02 bg=0.00
septin collar GO:0032173 p=3.5E−02 n=1 fg=0.02 bg=0.00
dendrite GO:0030425 p=3.6E−02 n=9 fg=0.14 bg=0.07
dendritic tree GO:0097447 p=3.6E−02 n=9 fg=0.14 bg=0.07
stress fiber GO:0001725 p=3.8E−02 n=2 fg=0.03 bg=0.01
contractile actin filament bundle GO:0097517 p=3.8E−02 n=2 fg=0.03 bg=0.01
actin filament bundle GO:0032432 p=3.8E−02 n=2 fg=0.03 bg=0.01
cell junction GO:0030054 p=4.1E−02 n=14 fg=0.22 bg=0.13
exocytic vesicle GO:0070382 p=4.2E−02 n=5 fg=0.08 bg=0.03
cell periphery GO:0071944 p=4.4E−02 n=27 fg=0.42 bg=0.29
somatodendritic compartment GO:0036477 p=4.7E−02 n=11 fg=0.17 bg=0.10
neuron spine GO:0044309 p=5.0E−02 n=4 fg=0.06 bg=0.02
0 1 2 3 4 5
−log(p)
n=64/278 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction