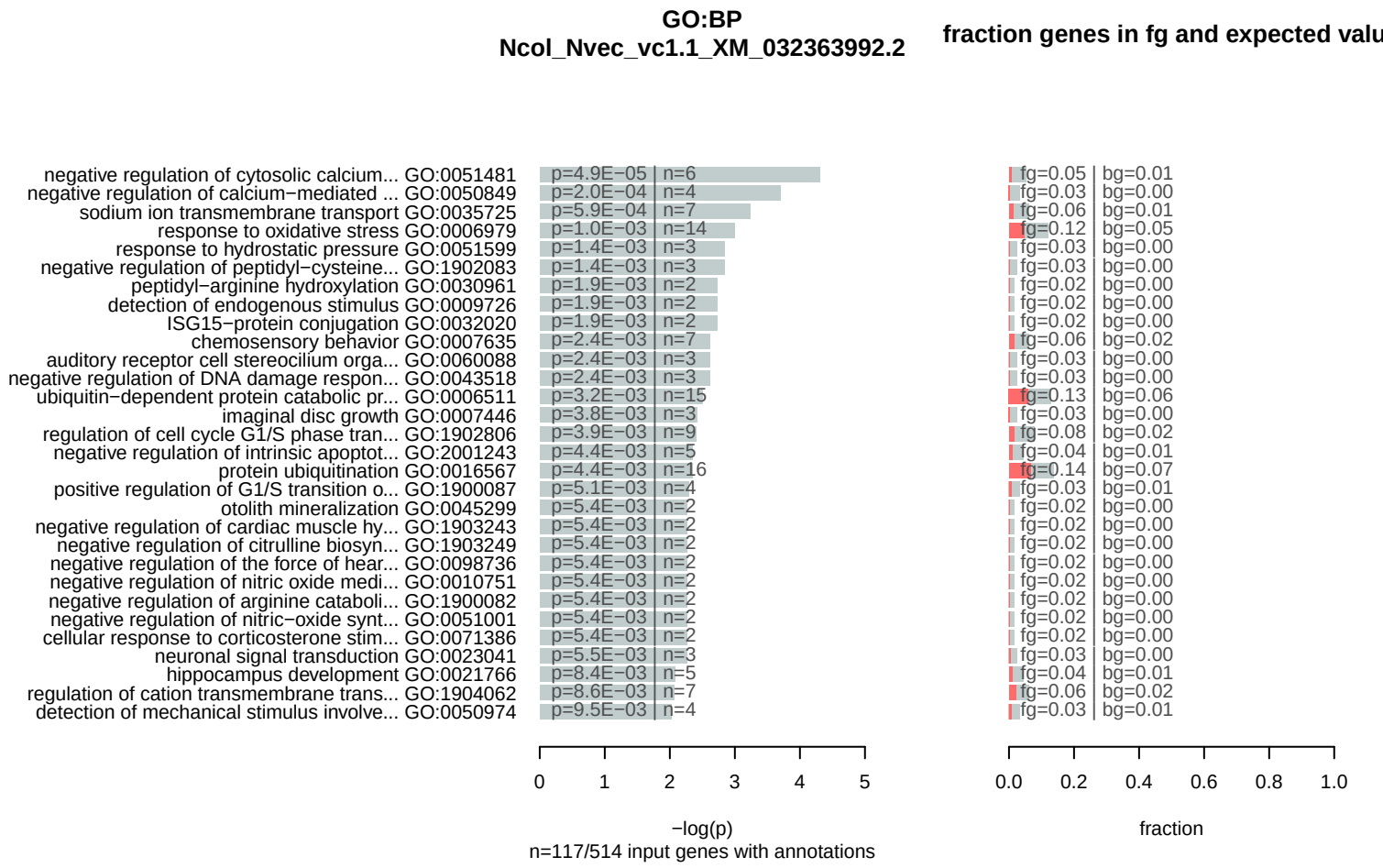
GO:BP
Ncol_Nvec_vc1.1_XM_032363992.2
fraction genes in fg and expected valu
negative regulation of cytosolic calcium... GO:0051481 p=4.9E−05 n=6 fg=0.05 bg=0.01
negative regulation of calcium−mediated ... GO:0050849 p=2.0E−04 n=4 fg=0.03 bg=0.00
sodium ion transmembrane transport GO:0035725 p=5.9E−04 n=7 fg=0.06 bg=0.01
response to oxidative stress GO:0006979 p=1.0E−03 n=14 fg=0.12 bg=0.05
response to hydrostatic pressure GO:0051599 p=1.4E−03 n=3 fg=0.03 bg=0.00
negative regulation of peptidyl−cysteine... GO:1902083 p=1.4E−03 n=3 fg=0.03 bg=0.00
peptidyl−arginine hydroxylation GO:0030961 p=1.9E−03 n=2 fg=0.02 bg=0.00
detection of endogenous stimulus GO:0009726 p=1.9E−03 n=2 fg=0.02 bg=0.00
ISG15−protein conjugation GO:0032020 p=1.9E−03 n=2 fg=0.02 bg=0.00
chemosensory behavior GO:0007635 p=2.4E−03 n=7 fg=0.06 bg=0.02
auditory receptor cell stereocilium orga... GO:0060088 p=2.4E−03 n=3 fg=0.03 bg=0.00
negative regulation of DNA damage respon... GO:0043518 p=2.4E−03 n=3 fg=0.03 bg=0.00
ubiquitin−dependent protein catabolic pr... GO:0006511 p=3.2E−03 n=15 fg=0.13 bg=0.06
imaginal disc growth GO:0007446 p=3.8E−03 n=3 fg=0.03 bg=0.00
regulation of cell cycle G1/S phase tran... GO:1902806 p=3.9E−03 n=9 fg=0.08 bg=0.02
negative regulation of intrinsic apoptot... GO:2001243 p=4.4E−03 n=5 fg=0.04 bg=0.01
protein ubiquitination GO:0016567 p=4.4E−03 n=16 fg=0.14 bg=0.07
positive regulation of G1/S transition o... GO:1900087 p=5.1E−03 n=4 fg=0.03 bg=0.01
otolith mineralization GO:0045299 p=5.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of cardiac muscle hy... GO:1903243 p=5.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of citrulline biosyn... GO:1903249 p=5.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of the force of hear... GO:0098736 p=5.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of nitric oxide medi... GO:0010751 p=5.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of arginine cataboli... GO:1900082 p=5.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of nitric−oxide synt... GO:0051001 p=5.4E−03 n=2 fg=0.02 bg=0.00
cellular response to corticosterone stim... GO:0071386 p=5.4E−03 n=2 fg=0.02 bg=0.00
neuronal signal transduction GO:0023041 p=5.5E−03 n=3 fg=0.03 bg=0.00
hippocampus development GO:0021766 p=8.4E−03 n=5 fg=0.04 bg=0.01
regulation of cation transmembrane trans... GO:1904062 p=8.6E−03 n=7 fg=0.06 bg=0.02
detection of mechanical stimulus involve... GO:0050974 p=9.5E−03 n=4 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=117/514 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032363992.2
fraction genes in fg and expected valu
calcium ion binding GO:0005509 p=3.1E−05 n=11 fg=0.10 bg=0.02
ion gated channel activity GO:0022839 p=9.3E−04 n=9 fg=0.08 bg=0.02
ISG15 transferase activity GO:0042296 p=2.2E−03 n=2 fg=0.02 bg=0.00
mitogen−activated protein kinase p38 bin... GO:0048273 p=2.2E−03 n=2 fg=0.02 bg=0.00
sodium ion transmembrane transporter act... GO:0015081 p=3.5E−03 n=5 fg=0.05 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=4.7E−03 n=3 fg=0.03 bg=0.00
D2 dopamine receptor binding GO:0031749 p=6.3E−03 n=2 fg=0.02 bg=0.00
nitric−oxide synthase inhibitor activity GO:0036487 p=6.3E−03 n=2 fg=0.02 bg=0.00
calcium−dependent ATPase activity GO:0030899 p=6.3E−03 n=2 fg=0.02 bg=0.00
alpha−actinin binding GO:0051393 p=6.8E−03 n=3 fg=0.03 bg=0.00
signaling adaptor activity GO:0035591 p=8.4E−03 n=4 fg=0.04 bg=0.01
transcription coactivator activity GO:0003713 p=8.7E−03 n=9 fg=0.08 bg=0.03
voltage−gated calcium channel activity GO:0005245 p=9.4E−03 n=3 fg=0.03 bg=0.00
active transmembrane transporter activit... GO:0022804 p=1.1E−02 n=9 fg=0.08 bg=0.03
NEDD8 transferase activity GO:0019788 p=1.2E−02 n=2 fg=0.02 bg=0.00
MAP−kinase scaffold activity GO:0005078 p=1.2E−02 n=2 fg=0.02 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=1.2E−02 n=2 fg=0.02 bg=0.00
voltage−gated sodium channel activity GO:0005248 p=1.2E−02 n=2 fg=0.02 bg=0.00
scaffold protein binding GO:0097110 p=1.2E−02 n=4 fg=0.04 bg=0.01
solute:sodium symporter activity GO:0015370 p=1.3E−02 n=3 fg=0.03 bg=0.00
disordered domain specific binding GO:0097718 p=1.6E−02 n=3 fg=0.03 bg=0.01
calcium−dependent phospholipid binding GO:0005544 p=2.0E−02 n=2 fg=0.02 bg=0.00
transaminase activity GO:0008483 p=2.0E−02 n=2 fg=0.02 bg=0.00
nitric−oxide synthase binding GO:0050998 p=2.0E−02 n=2 fg=0.02 bg=0.00
P−type calcium transporter activity GO:0005388 p=2.0E−02 n=2 fg=0.02 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=2.0E−02 n=2 fg=0.02 bg=0.00
acetylcholine receptor binding GO:0033130 p=2.0E−02 n=2 fg=0.02 bg=0.00
nuclear androgen receptor binding GO:0050681 p=2.0E−02 n=3 fg=0.03 bg=0.01
intracellular ligand−gated ion channel a... GO:0005217 p=2.0E−02 n=3 fg=0.03 bg=0.01
potassium channel regulator activity GO:0015459 p=2.0E−02 n=3 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=111/514 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032363992.2
fraction genes in fg and expected valu
dendritic spine membrane GO:0032591 p=3.2E−04 n=3 fg=0.03 bg=0.00
cytoplasmic side of plasma membrane GO:0009898 p=4.3E−04 n=9 fg=0.08 bg=0.02
neuronal cell body membrane GO:0032809 p=5.9E−04 n=5 fg=0.04 bg=0.01
postsynaptic membrane GO:0045211 p=1.2E−03 n=7 fg=0.06 bg=0.01
contractile fiber GO:0043292 p=2.7E−03 n=9 fg=0.08 bg=0.03
ubiquitin ligase complex GO:0000151 p=2.8E−03 n=10 fg=0.08 bg=0.03
presynapse GO:0098793 p=6.0E−03 n=12 fg=0.10 bg=0.05
voltage−gated potassium channel complex GO:0008076 p=7.8E−03 n=3 fg=0.03 bg=0.00
main axon GO:0044304 p=8.1E−03 n=4 fg=0.03 bg=0.01
growth cone lamellipodium GO:1990761 p=1.1E−02 n=2 fg=0.02 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234 p=1.2E−02 n=4 fg=0.03 bg=0.01
presynaptic membrane GO:0042734 p=1.3E−02 n=5 fg=0.04 bg=0.01
Z disc GO:0030018 p=1.5E−02 n=5 fg=0.04 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=1.6E−02 n=17 fg=0.14 bg=0.07
methylosome GO:0034709 p=1.7E−02 n=2 fg=0.02 bg=0.00
postsynaptic specialization membrane GO:0099634 p=1.7E−02 n=2 fg=0.02 bg=0.00
myosin II complex GO:0016460 p=1.7E−02 n=2 fg=0.02 bg=0.00
platelet alpha granule lumen GO:0031093 p=1.7E−02 n=2 fg=0.02 bg=0.00
presynaptic periactive zone GO:0036062 p=1.7E−02 n=2 fg=0.02 bg=0.00
postsynaptic density membrane GO:0098839 p=1.7E−02 n=2 fg=0.02 bg=0.00
myosin V complex GO:0031475 p=1.7E−02 n=2 fg=0.02 bg=0.00
anchored component of plasma membrane GO:0046658 p=1.7E−02 n=2 fg=0.02 bg=0.00
muscle myosin complex GO:0005859 p=1.7E−02 n=2 fg=0.02 bg=0.00
sarcomere GO:0030017 p=1.8E−02 n=6 fg=0.05 bg=0.02
I band GO:0031674 p=2.1E−02 n=5 fg=0.04 bg=0.01
intracellular canaliculus GO:0046691 p=2.5E−02 n=2 fg=0.02 bg=0.00
myosin VI complex GO:0031476 p=2.5E−02 n=2 fg=0.02 bg=0.00
myosin VII complex GO:0031477 p=2.5E−02 n=2 fg=0.02 bg=0.00
juxtaparanode region of axon GO:0044224 p=2.5E−02 n=2 fg=0.02 bg=0.00
organelle membrane contact site GO:0044232 p=2.5E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=118/514 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction