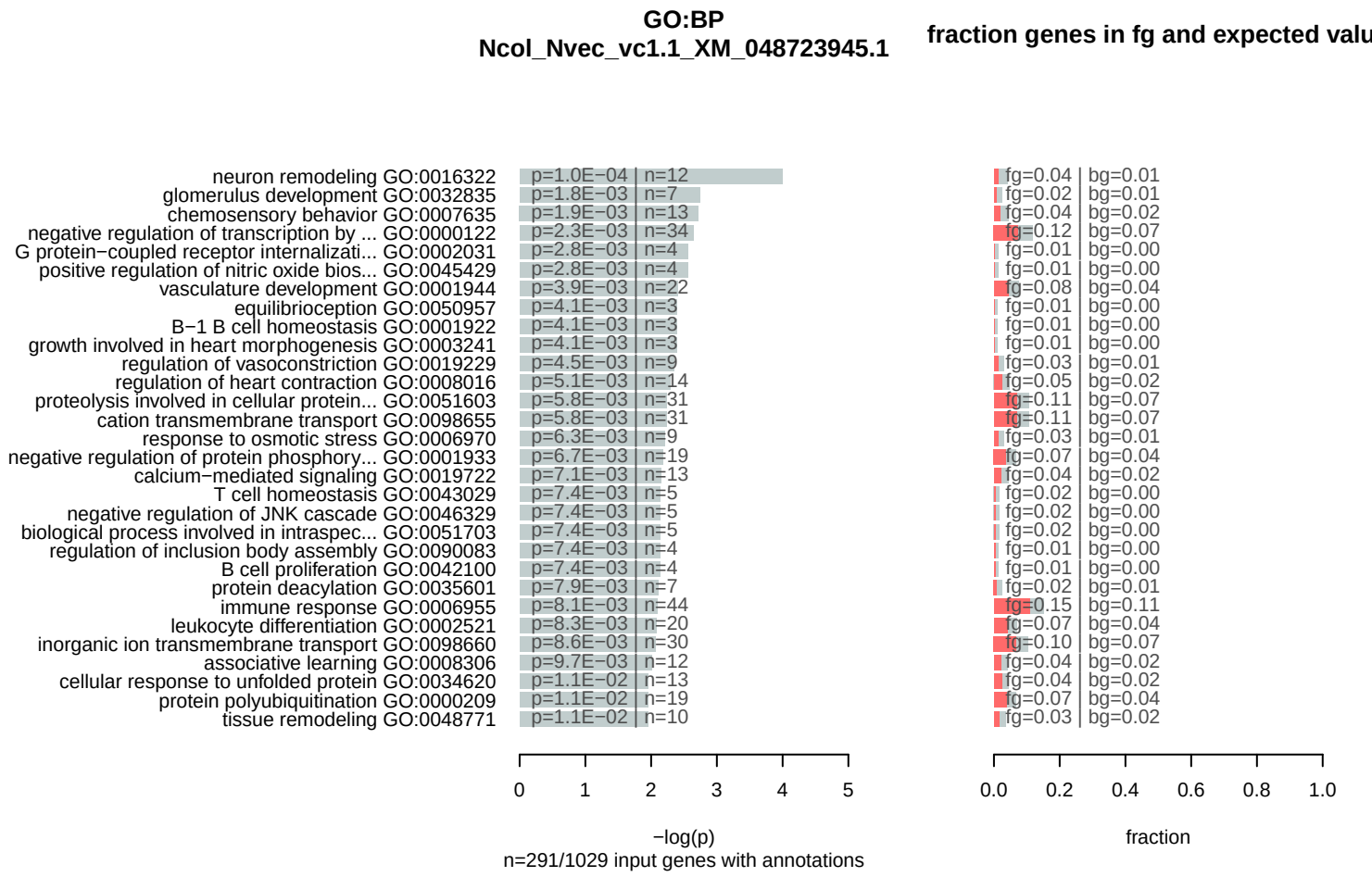
GO:BP
Ncol_Nvec_vc1.1_XM_048723945.1
fraction genes in fg and expected valu
neuron remodeling GO:0016322 p=1.0E−04 n=12 fg=0.04 bg=0.01
glomerulus development GO:0032835 p=1.8E−03 n=7 fg=0.02 bg=0.01
chemosensory behavior GO:0007635 p=1.9E−03 n=13 fg=0.04 bg=0.02
negative regulation of transcription by ... GO:0000122 p=2.3E−03 n=34 fg=0.12 bg=0.07
G protein−coupled receptor internalizati... GO:0002031 p=2.8E−03 n=4 fg=0.01 bg=0.00
positive regulation of nitric oxide bios... GO:0045429 p=2.8E−03 n=4 fg=0.01 bg=0.00
vasculature development GO:0001944 p=3.9E−03 n=22 fg=0.08 bg=0.04
equilibrioception GO:0050957 p=4.1E−03 n=3 fg=0.01 bg=0.00
B−1 B cell homeostasis GO:0001922 p=4.1E−03 n=3 fg=0.01 bg=0.00
growth involved in heart morphogenesis GO:0003241 p=4.1E−03 n=3 fg=0.01 bg=0.00
regulation of vasoconstriction GO:0019229 p=4.5E−03 n=9 fg=0.03 bg=0.01
regulation of heart contraction GO:0008016 p=5.1E−03 n=14 fg=0.05 bg=0.02
proteolysis involved in cellular protein... GO:0051603 p=5.8E−03 n=31 fg=0.11 bg=0.07
cation transmembrane transport GO:0098655 p=5.8E−03 n=31 fg=0.11 bg=0.07
response to osmotic stress GO:0006970 p=6.3E−03 n=9 fg=0.03 bg=0.01
negative regulation of protein phosphory... GO:0001933 p=6.7E−03 n=19 fg=0.07 bg=0.04
calcium−mediated signaling GO:0019722 p=7.1E−03 n=13 fg=0.04 bg=0.02
T cell homeostasis GO:0043029 p=7.4E−03 n=5 fg=0.02 bg=0.00
negative regulation of JNK cascade GO:0046329 p=7.4E−03 n=5 fg=0.02 bg=0.00
biological process involved in intraspec... GO:0051703 p=7.4E−03 n=5 fg=0.02 bg=0.00
regulation of inclusion body assembly GO:0090083 p=7.4E−03 n=4 fg=0.01 bg=0.00
B cell proliferation GO:0042100 p=7.4E−03 n=4 fg=0.01 bg=0.00
protein deacylation GO:0035601 p=7.9E−03 n=7 fg=0.02 bg=0.01
immune response GO:0006955 p=8.1E−03 n=44 fg=0.15 bg=0.11
leukocyte differentiation GO:0002521 p=8.3E−03 n=20 fg=0.07 bg=0.04
inorganic ion transmembrane transport GO:0098660 p=8.6E−03 n=30 fg=0.10 bg=0.07
associative learning GO:0008306 p=9.7E−03 n=12 fg=0.04 bg=0.02
cellular response to unfolded protein GO:0034620 p=1.1E−02 n=13 fg=0.04 bg=0.02
protein polyubiquitination GO:0000209 p=1.1E−02 n=19 fg=0.07 bg=0.04
tissue remodeling GO:0048771 p=1.1E−02 n=10 fg=0.03 bg=0.02
0 1 2 3 4 5
−log(p)
n=291/1029 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048723945.1
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=1.3E−03 n=15 fg=0.06 bg=0.03
voltage−gated potassium channel activity GO:0005249 p=1.9E−03 n=6 fg=0.02 bg=0.01
enzyme binding GO:0019899 p=5.5E−03 n=79 fg=0.31 bg=0.24
ubiquitin−like protein ligase binding GO:0044389 p=1.1E−02 n=19 fg=0.07 bg=0.04
palmitoyl−(protein) hydrolase activity GO:0008474 p=1.5E−02 n=3 fg=0.01 bg=0.00
palmitoyl hydrolase activity GO:0098599 p=1.5E−02 n=3 fg=0.01 bg=0.00
phospholipase A2 activity GO:0004623 p=1.5E−02 n=3 fg=0.01 bg=0.00
cis−trans isomerase activity GO:0016859 p=1.5E−02 n=4 fg=0.02 bg=0.00
signaling receptor regulator activity GO:0030545 p=1.5E−02 n=4 fg=0.02 bg=0.00
peptidyl−prolyl cis−trans isomerase acti... GO:0003755 p=1.5E−02 n=4 fg=0.02 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=1.5E−02 n=4 fg=0.02 bg=0.00
transcription corepressor activity GO:0003714 p=1.9E−02 n=10 fg=0.04 bg=0.02
histone binding GO:0042393 p=2.0E−02 n=9 fg=0.04 bg=0.02
cysteine−type endopeptidase activity GO:0004197 p=2.1E−02 n=5 fg=0.02 bg=0.01
voltage−gated cation channel activity GO:0022843 p=2.5E−02 n=10 fg=0.04 bg=0.01
PTB domain binding GO:0051425 p=2.6E−02 n=2 fg=0.01 bg=0.00
BH3 domain binding GO:0051434 p=2.6E−02 n=2 fg=0.01 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=2.6E−02 n=2 fg=0.01 bg=0.00
calcium−dependent protein kinase regulat... GO:0010858 p=2.6E−02 n=2 fg=0.01 bg=0.00
protein−cysteine S−palmitoyltransferase ... GO:0019706 p=2.6E−02 n=2 fg=0.01 bg=0.00
protein−cysteine S−acyltransferase activ... GO:0019707 p=2.6E−02 n=2 fg=0.01 bg=0.00
STAT family protein binding GO:0097677 p=2.6E−02 n=2 fg=0.01 bg=0.00
chemokine receptor binding GO:0042379 p=2.6E−02 n=2 fg=0.01 bg=0.00
calcium−dependent protein kinase inhibit... GO:0008427 p=2.6E−02 n=2 fg=0.01 bg=0.00
neurotransmitter:sodium symporter activi... GO:0005328 p=2.6E−02 n=2 fg=0.01 bg=0.00
S−acyltransferase activity GO:0016417 p=2.6E−02 n=2 fg=0.01 bg=0.00
methylation−dependent protein binding GO:0140034 p=2.7E−02 n=4 fg=0.02 bg=0.01
methylated histone binding GO:0035064 p=2.7E−02 n=4 fg=0.02 bg=0.01
voltage−gated calcium channel activity GO:0005245 p=2.7E−02 n=4 fg=0.02 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=2.7E−02 n=25 fg=0.10 bg=0.07
0 1 2 3 4 5
−log(p)
n=256/1029 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048723945.1
fraction genes in fg and expected valu
sensory dendrite GO:0071683 p=3.1E−03 n=4 fg=0.01 bg=0.00
cation channel complex GO:0034703 p=6.6E−03 n=11 fg=0.04 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=8.1E−03 n=5 fg=0.02 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=1.5E−02 n=3 fg=0.01 bg=0.00
calcium channel complex GO:0034704 p=1.6E−02 n=4 fg=0.01 bg=0.00
plasma membrane GO:0005886 p=2.0E−02 n=98 fg=0.33 bg=0.27
SCF ubiquitin ligase complex GO:0019005 p=2.2E−02 n=5 fg=0.02 bg=0.01
actomyosin contractile ring GO:0005826 p=2.7E−02 n=2 fg=0.01 bg=0.00
mitochondrial permeability transition po... GO:0005757 p=2.7E−02 n=2 fg=0.01 bg=0.00
growth cone filopodium GO:1990812 p=2.7E−02 n=2 fg=0.01 bg=0.00
ionotropic glutamate receptor complex GO:0008328 p=2.7E−02 n=2 fg=0.01 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=2.7E−02 n=2 fg=0.01 bg=0.00
pore complex GO:0046930 p=2.7E−02 n=2 fg=0.01 bg=0.00
neurotransmitter receptor complex GO:0098878 p=2.7E−02 n=2 fg=0.01 bg=0.00
Cul3−RING ubiquitin ligase complex GO:0031463 p=3.4E−02 n=3 fg=0.01 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=3.4E−02 n=3 fg=0.01 bg=0.00
apical part of cell GO:0045177 p=3.5E−02 n=23 fg=0.08 bg=0.05
apical plasma membrane GO:0016324 p=3.6E−02 n=18 fg=0.06 bg=0.04
dendrite GO:0030425 p=3.7E−02 n=32 fg=0.11 bg=0.07
dendritic tree GO:0097447 p=3.7E−02 n=32 fg=0.11 bg=0.07
sarcolemma GO:0042383 p=4.3E−02 n=7 fg=0.02 bg=0.01
cell periphery GO:0071944 p=4.5E−02 n=101 fg=0.34 bg=0.29
stress fiber GO:0001725 p=4.5E−02 n=4 fg=0.01 bg=0.00
contractile actin filament bundle GO:0097517 p=4.5E−02 n=4 fg=0.01 bg=0.00
actin filament bundle GO:0032432 p=4.5E−02 n=4 fg=0.01 bg=0.00
lamellipodium GO:0030027 p=4.8E−02 n=10 fg=0.03 bg=0.02
extracellular space GO:0005615 p=5.3E−02 n=14 fg=0.05 bg=0.03
cell leading edge GO:0031252 p=5.3E−02 n=16 fg=0.05 bg=0.04
transport vesicle GO:0030133 p=5.8E−02 n=19 fg=0.06 bg=0.04
Derlin−1 retrotranslocation complex GO:0036513 p=5.9E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=296/1029 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction