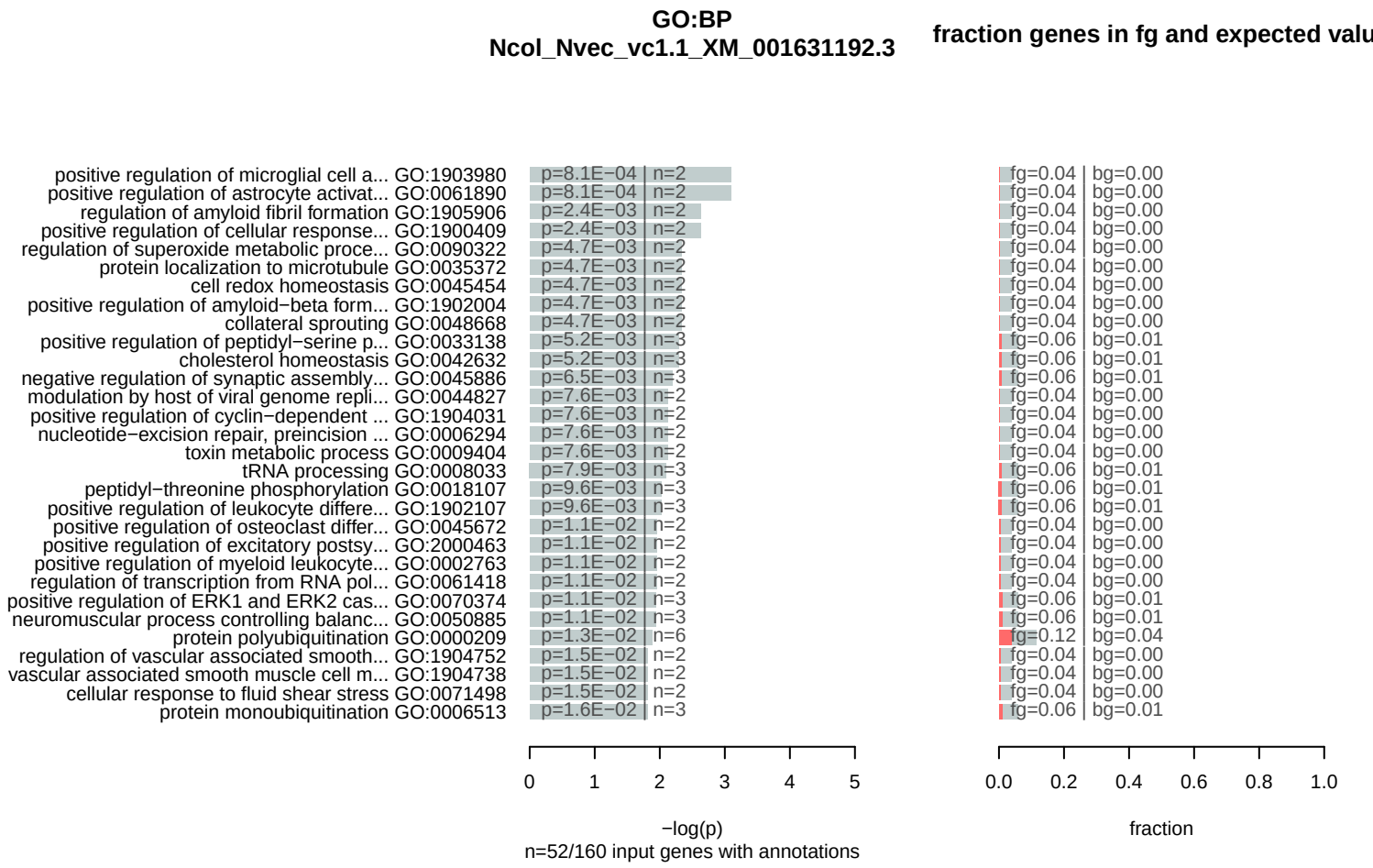
GO:BP
Ncol_Nvec_vc1.1_XM_001631192.3
fraction genes in fg and expected valu
positive regulation of microglial cell a... GO:1903980 p=8.1E−04 n=2 fg=0.04 bg=0.00
positive regulation of astrocyte activat... GO:0061890 p=8.1E−04 n=2 fg=0.04 bg=0.00
regulation of amyloid fibril formation GO:1905906 p=2.4E−03 n=2 fg=0.04 bg=0.00
positive regulation of cellular response... GO:1900409 p=2.4E−03 n=2 fg=0.04 bg=0.00
regulation of superoxide metabolic proce... GO:0090322 p=4.7E−03 n=2 fg=0.04 bg=0.00
protein localization to microtubule GO:0035372 p=4.7E−03 n=2 fg=0.04 bg=0.00
cell redox homeostasis GO:0045454 p=4.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of amyloid−beta form... GO:1902004 p=4.7E−03 n=2 fg=0.04 bg=0.00
collateral sprouting GO:0048668 p=4.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of peptidyl−serine p... GO:0033138 p=5.2E−03 n=3 fg=0.06 bg=0.01
cholesterol homeostasis GO:0042632 p=5.2E−03 n=3 fg=0.06 bg=0.01
negative regulation of synaptic assembly... GO:0045886 p=6.5E−03 n=3 fg=0.06 bg=0.01
modulation by host of viral genome repli... GO:0044827 p=7.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of cyclin−dependent ... GO:1904031 p=7.6E−03 n=2 fg=0.04 bg=0.00
nucleotide−excision repair, preincision ... GO:0006294 p=7.6E−03 n=2 fg=0.04 bg=0.00
toxin metabolic process GO:0009404 p=7.6E−03 n=2 fg=0.04 bg=0.00
tRNA processing GO:0008033 p=7.9E−03 n=3 fg=0.06 bg=0.01
peptidyl−threonine phosphorylation GO:0018107 p=9.6E−03 n=3 fg=0.06 bg=0.01
positive regulation of leukocyte differe... GO:1902107 p=9.6E−03 n=3 fg=0.06 bg=0.01
positive regulation of osteoclast differ... GO:0045672 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of excitatory postsy... GO:2000463 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of myeloid leukocyte... GO:0002763 p=1.1E−02 n=2 fg=0.04 bg=0.00
regulation of transcription from RNA pol... GO:0061418 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of ERK1 and ERK2 cas... GO:0070374 p=1.1E−02 n=3 fg=0.06 bg=0.01
neuromuscular process controlling balanc... GO:0050885 p=1.1E−02 n=3 fg=0.06 bg=0.01
protein polyubiquitination GO:0000209 p=1.3E−02 n=6 fg=0.12 bg=0.04
regulation of vascular associated smooth... GO:1904752 p=1.5E−02 n=2 fg=0.04 bg=0.00
vascular associated smooth muscle cell m... GO:1904738 p=1.5E−02 n=2 fg=0.04 bg=0.00
cellular response to fluid shear stress GO:0071498 p=1.5E−02 n=2 fg=0.04 bg=0.00
protein monoubiquitination GO:0006513 p=1.6E−02 n=3 fg=0.06 bg=0.01
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−log(p)
n=52/160 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001631192.3
fraction genes in fg and expected valu
PTB domain binding GO:0051425 p=7.5E−04 n=2 fg=0.05 bg=0.00
peptide binding GO:0042277 p=3.7E−03 n=5 fg=0.11 bg=0.02
protein−containing complex binding GO:0044877 p=4.9E−03 n=11 fg=0.25 bg=0.11
peptidase activator activity GO:0016504 p=1.0E−02 n=2 fg=0.05 bg=0.00
hormone binding GO:0042562 p=1.9E−02 n=2 fg=0.05 bg=0.01
ion gated channel activity GO:0022839 p=2.6E−02 n=4 fg=0.09 bg=0.03
translation release factor activity GO:0003747 p=2.8E−02 n=1 fg=0.02 bg=0.00
neurotransmitter receptor regulator acti... GO:0099602 p=2.8E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=2.8E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=2.8E−02 n=1 fg=0.02 bg=0.00
alanine−tRNA ligase activity GO:0004813 p=2.8E−02 n=1 fg=0.02 bg=0.00
selenium binding GO:0008430 p=2.8E−02 n=1 fg=0.02 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.8E−02 n=1 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016812 p=2.8E−02 n=1 fg=0.02 bg=0.00
DNA topoisomerase binding GO:0044547 p=2.8E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=2.8E−02 n=1 fg=0.02 bg=0.00
translation termination factor activity GO:0008079 p=2.8E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=2.8E−02 n=1 fg=0.02 bg=0.00
heparan sulfate binding GO:1904399 p=2.8E−02 n=1 fg=0.02 bg=0.00
interferon binding GO:0019961 p=2.8E−02 n=1 fg=0.02 bg=0.00
acid sphingomyelin phosphodiesterase act... GO:0061750 p=2.8E−02 n=1 fg=0.02 bg=0.00
interferon−gamma binding GO:0019964 p=2.8E−02 n=1 fg=0.02 bg=0.00
5−oxoprolinase (ATP−hydrolyzing) activit... GO:0017168 p=2.8E−02 n=1 fg=0.02 bg=0.00
AMP deaminase activity GO:0003876 p=2.8E−02 n=1 fg=0.02 bg=0.00
thioredoxin−disulfide reductase activity GO:0004791 p=2.8E−02 n=1 fg=0.02 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.8E−02 n=1 fg=0.02 bg=0.00
2 iron, 2 sulfur cluster binding GO:0051537 p=2.8E−02 n=1 fg=0.02 bg=0.00
endonuclease activity, active with eithe... GO:0016894 p=2.8E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.8E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor regulator activit... GO:0030548 p=2.8E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=44/160 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001631192.3
fraction genes in fg and expected valu
growth cone filopodium GO:1990812 p=8.1E−04 n=2 fg=0.04 bg=0.00
growth cone lamellipodium GO:1990761 p=2.4E−03 n=2 fg=0.04 bg=0.00
ciliary transition zone GO:0035869 p=3.6E−03 n=4 fg=0.08 bg=0.01
transporter complex GO:1990351 p=5.0E−03 n=5 fg=0.10 bg=0.02
Cul3−RING ubiquitin ligase complex GO:0031463 p=7.7E−03 n=2 fg=0.04 bg=0.00
main axon GO:0044304 p=9.6E−03 n=3 fg=0.06 bg=0.01
dendritic shaft GO:0043198 p=1.3E−02 n=3 fg=0.06 bg=0.01
MKS complex GO:0036038 p=2.0E−02 n=2 fg=0.04 bg=0.00
inner mitochondrial membrane protein com... GO:0098800 p=2.1E−02 n=3 fg=0.06 bg=0.01
transmembrane transporter complex GO:1902495 p=2.2E−02 n=4 fg=0.08 bg=0.02
clathrin−coated pit GO:0005905 p=2.6E−02 n=2 fg=0.04 bg=0.01
neuron spine GO:0044309 p=2.6E−02 n=4 fg=0.08 bg=0.02
dendritic spine GO:0043197 p=2.6E−02 n=4 fg=0.08 bg=0.02
nuclear SCF ubiquitin ligase complex GO:0043224 p=2.9E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=2.9E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=2.9E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.9E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.9E−02 n=1 fg=0.02 bg=0.00
lipoprotein particle GO:1990777 p=2.9E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=2.9E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=2.9E−02 n=1 fg=0.02 bg=0.00
apoptosome GO:0043293 p=2.9E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.9E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=2.9E−02 n=1 fg=0.02 bg=0.00
Cul5−RING ubiquitin ligase complex GO:0031466 p=2.9E−02 n=1 fg=0.02 bg=0.00
Cul7−RING ubiquitin ligase complex GO:0031467 p=2.9E−02 n=1 fg=0.02 bg=0.00
SCF ubiquitin ligase complex GO:0019005 p=3.8E−02 n=2 fg=0.04 bg=0.01
NADH dehydrogenase complex GO:0030964 p=4.4E−02 n=2 fg=0.04 bg=0.01
mitochondrial respiratory chain complex ... GO:0005747 p=4.4E−02 n=2 fg=0.04 bg=0.01
respiratory chain complex I GO:0045271 p=4.4E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=52/160 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction