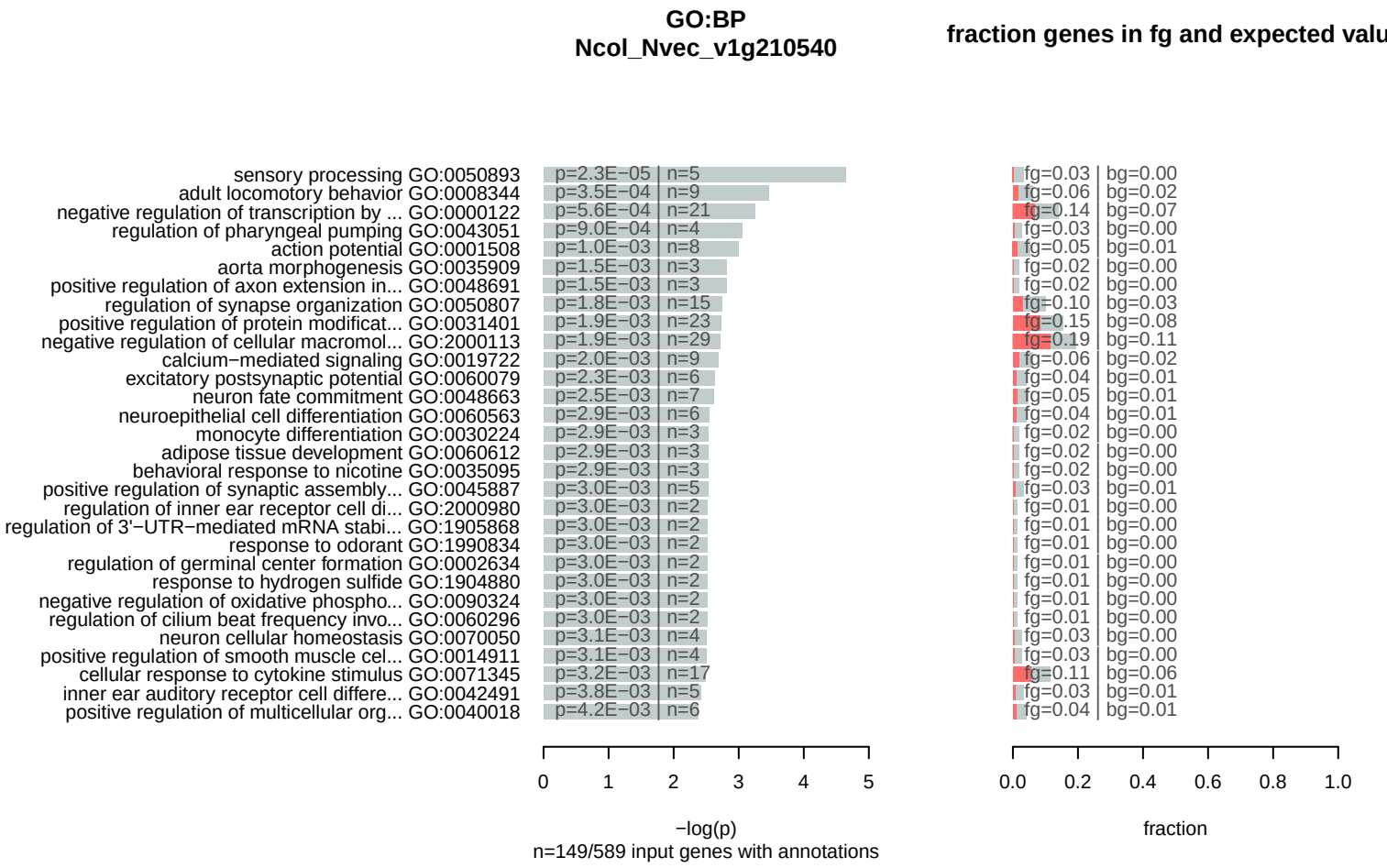
GO:BP
Ncol_Nvec_v1g210540
fraction genes in fg and expected valu
sensory processing GO:0050893 p=2.3E−05 n=5 fg=0.03 bg=0.00
adult locomotory behavior GO:0008344 p=3.5E−04 n=9 fg=0.06 bg=0.02
negative regulation of transcription by ... GO:0000122 p=5.6E−04 n=21 fg=0.14 bg=0.07
regulation of pharyngeal pumping GO:0043051 p=9.0E−04 n=4 fg=0.03 bg=0.00
action potential GO:0001508 p=1.0E−03 n=8 fg=0.05 bg=0.01
aorta morphogenesis GO:0035909 p=1.5E−03 n=3 fg=0.02 bg=0.00
positive regulation of axon extension in... GO:0048691 p=1.5E−03 n=3 fg=0.02 bg=0.00
regulation of synapse organization GO:0050807 p=1.8E−03 n=15 fg=0.10 bg=0.03
positive regulation of protein modificat... GO:0031401 p=1.9E−03 n=23 fg=0.15 bg=0.08
negative regulation of cellular macromol... GO:2000113 p=1.9E−03 n=29 fg=0.19 bg=0.11
calcium−mediated signaling GO:0019722 p=2.0E−03 n=9 fg=0.06 bg=0.02
excitatory postsynaptic potential GO:0060079 p=2.3E−03 n=6 fg=0.04 bg=0.01
neuron fate commitment GO:0048663 p=2.5E−03 n=7 fg=0.05 bg=0.01
neuroepithelial cell differentiation GO:0060563 p=2.9E−03 n=6 fg=0.04 bg=0.01
monocyte differentiation GO:0030224 p=2.9E−03 n=3 fg=0.02 bg=0.00
adipose tissue development GO:0060612 p=2.9E−03 n=3 fg=0.02 bg=0.00
behavioral response to nicotine GO:0035095 p=2.9E−03 n=3 fg=0.02 bg=0.00
positive regulation of synaptic assembly... GO:0045887 p=3.0E−03 n=5 fg=0.03 bg=0.01
regulation of inner ear receptor cell di... GO:2000980 p=3.0E−03 n=2 fg=0.01 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=3.0E−03 n=2 fg=0.01 bg=0.00
response to odorant GO:1990834 p=3.0E−03 n=2 fg=0.01 bg=0.00
regulation of germinal center formation GO:0002634 p=3.0E−03 n=2 fg=0.01 bg=0.00
response to hydrogen sulfide GO:1904880 p=3.0E−03 n=2 fg=0.01 bg=0.00
negative regulation of oxidative phospho... GO:0090324 p=3.0E−03 n=2 fg=0.01 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=3.0E−03 n=2 fg=0.01 bg=0.00
neuron cellular homeostasis GO:0070050 p=3.1E−03 n=4 fg=0.03 bg=0.00
positive regulation of smooth muscle cel... GO:0014911 p=3.1E−03 n=4 fg=0.03 bg=0.00
cellular response to cytokine stimulus GO:0071345 p=3.2E−03 n=17 fg=0.11 bg=0.06
inner ear auditory receptor cell differe... GO:0042491 p=3.8E−03 n=5 fg=0.03 bg=0.01
positive regulation of multicellular org... GO:0040018 p=4.2E−03 n=6 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=149/589 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_v1g210540
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=7.9E−06 n=13 fg=0.10 bg=0.02
DNA−binding transcription activator acti... GO:0001228 p=1.8E−04 n=13 fg=0.10 bg=0.03
extracellularly glutamate−gated chloride... GO:0008068 p=6.8E−04 n=3 fg=0.02 bg=0.00
beta−catenin binding GO:0008013 p=1.6E−03 n=4 fg=0.03 bg=0.00
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.7E−03 n=13 fg=0.10 bg=0.03
promoter−specific chromatin binding GO:1990841 p=2.4E−03 n=4 fg=0.03 bg=0.00
glutamate binding GO:0016595 p=3.1E−03 n=3 fg=0.02 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=3.2E−03 n=2 fg=0.01 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=8.4E−03 n=24 fg=0.18 bg=0.07
ion channel activity GO:0005216 p=8.7E−03 n=15 fg=0.11 bg=0.04
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=9.2E−03 n=2 fg=0.01 bg=0.00
cAMP response element binding GO:0035497 p=9.2E−03 n=2 fg=0.01 bg=0.00
SMAD binding GO:0046332 p=1.0E−02 n=4 fg=0.03 bg=0.01
structural constituent of nuclear pore GO:0017056 p=1.6E−02 n=3 fg=0.02 bg=0.00
cAMP binding GO:0030552 p=1.8E−02 n=2 fg=0.01 bg=0.00
bHLH transcription factor binding GO:0043425 p=1.8E−02 n=2 fg=0.01 bg=0.00
kinase binding GO:0019900 p=1.8E−02 n=17 fg=0.13 bg=0.07
protein kinase binding GO:0019901 p=2.0E−02 n=16 fg=0.12 bg=0.07
voltage−gated potassium channel activity GO:0005249 p=2.1E−02 n=3 fg=0.02 bg=0.00
methylated histone binding GO:0035064 p=2.7E−02 n=3 fg=0.02 bg=0.01
methylation−dependent protein binding GO:0140034 p=2.7E−02 n=3 fg=0.02 bg=0.01
cation channel activity GO:0005261 p=2.8E−02 n=10 fg=0.07 bg=0.03
14−3−3 protein binding GO:0071889 p=2.8E−02 n=2 fg=0.01 bg=0.00
cyclic nucleotide binding GO:0030551 p=2.8E−02 n=2 fg=0.01 bg=0.00
nitric−oxide synthase binding GO:0050998 p=2.8E−02 n=2 fg=0.01 bg=0.00
transcription factor binding GO:0008134 p=3.0E−02 n=15 fg=0.11 bg=0.07
cytoskeletal motor activity GO:0003774 p=3.2E−02 n=4 fg=0.03 bg=0.01
microtubule motor activity GO:0003777 p=3.3E−02 n=3 fg=0.02 bg=0.01
glutamate receptor binding GO:0035254 p=3.3E−02 n=3 fg=0.02 bg=0.01
E−box binding GO:0070888 p=4.1E−02 n=3 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
n=134/589 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_v1g210540
fraction genes in fg and expected valu
cation channel complex GO:0034703 p=2.6E−03 n=6 fg=0.04 bg=0.01
presynapse GO:0098793 p=7.5E−03 n=14 fg=0.09 bg=0.05
exocytic vesicle GO:0070382 p=7.7E−03 n=9 fg=0.06 bg=0.02
neuron projection GO:0043005 p=9.8E−03 n=28 fg=0.18 bg=0.12
synaptic vesicle GO:0008021 p=1.2E−02 n=8 fg=0.05 bg=0.02
synapse GO:0045202 p=1.5E−02 n=25 fg=0.16 bg=0.08
voltage−gated potassium channel complex GO:0008076 p=1.6E−02 n=3 fg=0.02 bg=0.00
potassium channel complex GO:0034705 p=1.6E−02 n=3 fg=0.02 bg=0.00
exon−exon junction complex GO:0035145 p=1.8E−02 n=2 fg=0.01 bg=0.00
cell periphery GO:0071944 p=2.1E−02 n=50 fg=0.33 bg=0.25
plasma membrane protein complex GO:0098797 p=2.7E−02 n=9 fg=0.06 bg=0.03
plasma membrane GO:0005886 p=2.8E−02 n=46 fg=0.30 bg=0.23
intrinsic component of plasma membrane GO:0031226 p=2.9E−02 n=17 fg=0.11 bg=0.07
integral component of plasma membrane GO:0005887 p=3.1E−02 n=16 fg=0.11 bg=0.06
T−tubule GO:0030315 p=3.3E−02 n=3 fg=0.02 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=4.1E−02 n=2 fg=0.01 bg=0.00
synaptic membrane GO:0097060 p=4.2E−02 n=7 fg=0.05 bg=0.02
postsynapse GO:0098794 p=5.2E−02 n=10 fg=0.07 bg=0.04
kinocilium GO:0060091 p=5.6E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=5.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=5.6E−02 n=1 fg=0.01 bg=0.00
procollagen−proline 4−dioxygenase comple... GO:0016222 p=5.6E−02 n=1 fg=0.01 bg=0.00
nuclear pore inner ring GO:0044611 p=5.6E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=5.6E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=5.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=5.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=5.6E−02 n=1 fg=0.01 bg=0.00
insulin−responsive compartment GO:0032593 p=5.6E−02 n=1 fg=0.01 bg=0.00
smooth muscle contractile fiber GO:0030485 p=5.6E−02 n=1 fg=0.01 bg=0.00
syntrophin complex GO:0016013 p=5.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=152/589 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction