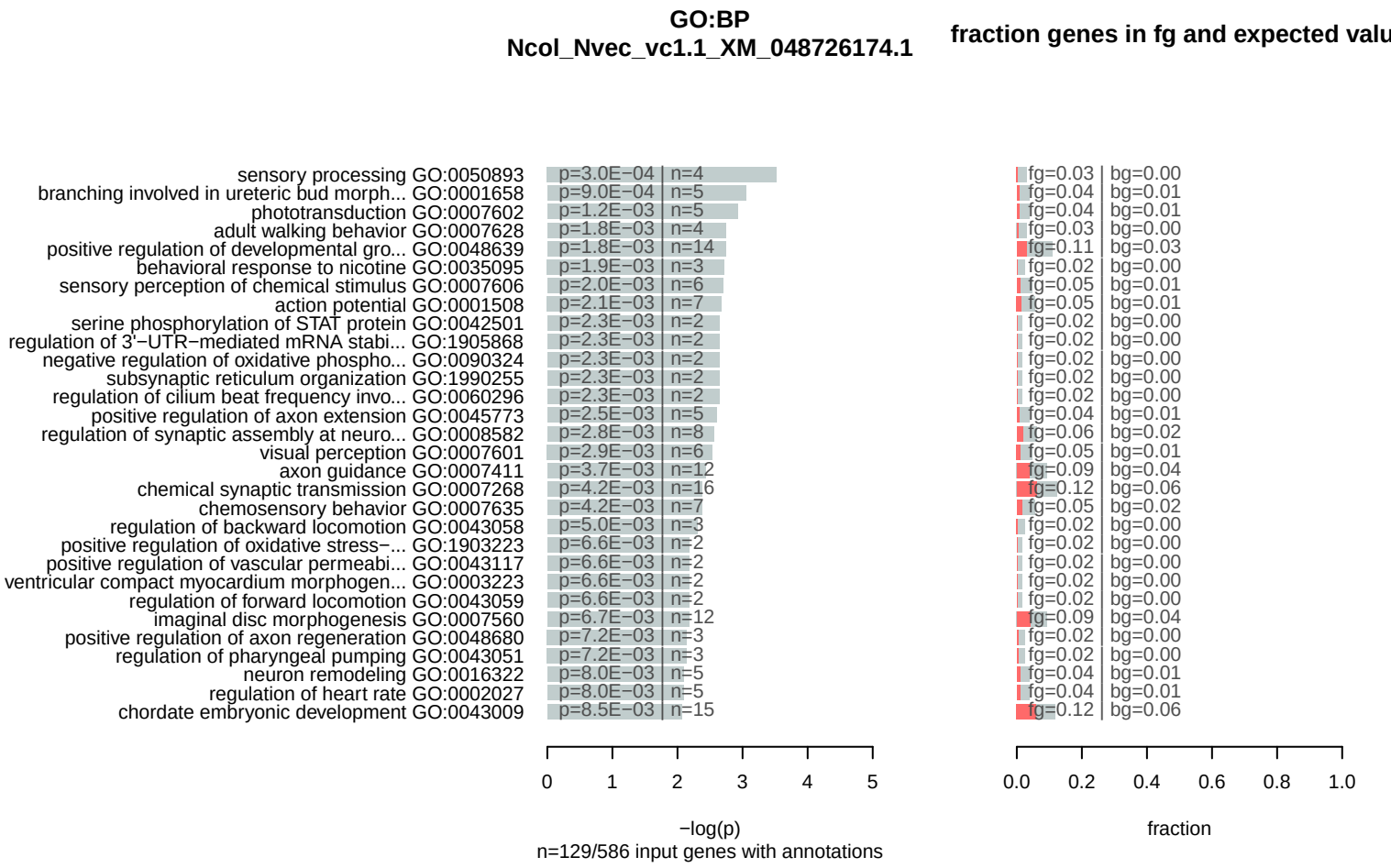
GO:BP
Ncol_Nvec_vc1.1_XM_048726174.1
fraction genes in fg and expected valu
sensory processing GO:0050893 p=3.0E−04 n=4 fg=0.03 bg=0.00
branching involved in ureteric bud morph... GO:0001658 p=9.0E−04 n=5 fg=0.04 bg=0.01
phototransduction GO:0007602 p=1.2E−03 n=5 fg=0.04 bg=0.01
adult walking behavior GO:0007628 p=1.8E−03 n=4 fg=0.03 bg=0.00
positive regulation of developmental gro... GO:0048639 p=1.8E−03 n=14 fg=0.11 bg=0.03
behavioral response to nicotine GO:0035095 p=1.9E−03 n=3 fg=0.02 bg=0.00
sensory perception of chemical stimulus GO:0007606 p=2.0E−03 n=6 fg=0.05 bg=0.01
action potential GO:0001508 p=2.1E−03 n=7 fg=0.05 bg=0.01
serine phosphorylation of STAT protein GO:0042501 p=2.3E−03 n=2 fg=0.02 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=2.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of oxidative phospho... GO:0090324 p=2.3E−03 n=2 fg=0.02 bg=0.00
subsynaptic reticulum organization GO:1990255 p=2.3E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=2.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of axon extension GO:0045773 p=2.5E−03 n=5 fg=0.04 bg=0.01
regulation of synaptic assembly at neuro... GO:0008582 p=2.8E−03 n=8 fg=0.06 bg=0.02
visual perception GO:0007601 p=2.9E−03 n=6 fg=0.05 bg=0.01
axon guidance GO:0007411 p=3.7E−03 n=12 fg=0.09 bg=0.04
chemical synaptic transmission GO:0007268 p=4.2E−03 n=16 fg=0.12 bg=0.06
chemosensory behavior GO:0007635 p=4.2E−03 n=7 fg=0.05 bg=0.02
regulation of backward locomotion GO:0043058 p=5.0E−03 n=3 fg=0.02 bg=0.00
positive regulation of oxidative stress−... GO:1903223 p=6.6E−03 n=2 fg=0.02 bg=0.00
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ventricular compact myocardium morphogen... GO:0003223 p=6.6E−03 n=2 fg=0.02 bg=0.00
regulation of forward locomotion GO:0043059 p=6.6E−03 n=2 fg=0.02 bg=0.00
imaginal disc morphogenesis GO:0007560 p=6.7E−03 n=12 fg=0.09 bg=0.04
positive regulation of axon regeneration GO:0048680 p=7.2E−03 n=3 fg=0.02 bg=0.00
regulation of pharyngeal pumping GO:0043051 p=7.2E−03 n=3 fg=0.02 bg=0.00
neuron remodeling GO:0016322 p=8.0E−03 n=5 fg=0.04 bg=0.01
regulation of heart rate GO:0002027 p=8.0E−03 n=5 fg=0.04 bg=0.01
chordate embryonic development GO:0043009 p=8.5E−03 n=15 fg=0.12 bg=0.06
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−log(p)
n=129/586 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048726174.1
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=3.0E−04 n=10 fg=0.09 bg=0.02
high voltage−gated calcium channel activ... GO:0008331 p=2.4E−03 n=2 fg=0.02 bg=0.00
ligand−gated anion channel activity GO:0099095 p=5.5E−03 n=3 fg=0.03 bg=0.00
excitatory extracellular ligand−gated io... GO:0005231 p=7.9E−03 n=3 fg=0.03 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=9.4E−03 n=9 fg=0.08 bg=0.03
structural constituent of nuclear pore GO:0017056 p=1.1E−02 n=3 fg=0.03 bg=0.00
extracellularly glutamate−gated chloride... GO:0008068 p=1.4E−02 n=2 fg=0.02 bg=0.00
cAMP binding GO:0030552 p=1.4E−02 n=2 fg=0.02 bg=0.00
extracellularly glutamate−gated ion chan... GO:0005234 p=1.4E−02 n=2 fg=0.02 bg=0.00
bHLH transcription factor binding GO:0043425 p=1.4E−02 n=2 fg=0.02 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=1.5E−02 n=3 fg=0.03 bg=0.00
promoter−specific chromatin binding GO:1990841 p=1.5E−02 n=3 fg=0.03 bg=0.00
sequence−specific DNA binding GO:0043565 p=1.6E−02 n=14 fg=0.12 bg=0.06
methylated histone binding GO:0035064 p=1.9E−02 n=3 fg=0.03 bg=0.01
methylation−dependent protein binding GO:0140034 p=1.9E−02 n=3 fg=0.03 bg=0.01
14−3−3 protein binding GO:0071889 p=2.2E−02 n=2 fg=0.02 bg=0.00
cyclic nucleotide binding GO:0030551 p=2.2E−02 n=2 fg=0.02 bg=0.00
microtubule motor activity GO:0003777 p=2.3E−02 n=3 fg=0.03 bg=0.01
DNA−binding transcription factor activit... GO:0003700 p=2.8E−02 n=18 fg=0.15 bg=0.07
cis−regulatory region sequence−specific ... GO:0000987 p=2.9E−02 n=8 fg=0.07 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.9E−02 n=8 fg=0.07 bg=0.03
glutamate binding GO:0016595 p=3.2E−02 n=2 fg=0.02 bg=0.00
mitogen−activated protein kinase kinase ... GO:0031434 p=3.2E−02 n=2 fg=0.02 bg=0.00
2−oxoglutarate−dependent dioxygenase act... GO:0016706 p=3.5E−02 n=3 fg=0.03 bg=0.01
identical protein binding GO:0042802 p=3.7E−02 n=28 fg=0.24 bg=0.17
cation channel activity GO:0005261 p=3.8E−02 n=9 fg=0.08 bg=0.03
SMAD binding GO:0046332 p=4.1E−02 n=3 fg=0.03 bg=0.01
transmitter−gated channel activity GO:0022835 p=4.3E−02 n=2 fg=0.02 bg=0.00
MAP kinase activity GO:0004707 p=4.3E−02 n=2 fg=0.02 bg=0.00
adrenergic receptor binding GO:0031690 p=4.3E−02 n=2 fg=0.02 bg=0.00
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−log(p)
n=117/586 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048726174.1
fraction genes in fg and expected valu
synapse GO:0045202 p=2.3E−03 n=21 fg=0.16 bg=0.08
hippocampal mossy fiber GO:0097457 p=2.4E−03 n=2 fg=0.01 bg=0.00
cation channel complex GO:0034703 p=7.9E−03 n=5 fg=0.04 bg=0.01
neuron projection GO:0043005 p=9.5E−03 n=27 fg=0.20 bg=0.12
potassium channel complex GO:0034705 p=1.1E−02 n=3 fg=0.02 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=1.1E−02 n=3 fg=0.02 bg=0.00
plasma membrane protein complex GO:0098797 p=1.3E−02 n=9 fg=0.07 bg=0.03
exon−exon junction complex GO:0035145 p=1.4E−02 n=2 fg=0.01 bg=0.00
dendrite GO:0030425 p=1.4E−02 n=15 fg=0.11 bg=0.06
dendritic tree GO:0097447 p=1.5E−02 n=15 fg=0.11 bg=0.06
somatodendritic compartment GO:0036477 p=1.8E−02 n=19 fg=0.14 bg=0.09
neuromuscular junction GO:0031594 p=1.8E−02 n=6 fg=0.04 bg=0.02
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presynapse GO:0098793 p=3.7E−02 n=11 fg=0.08 bg=0.05
photoreceptor outer segment GO:0001750 p=4.2E−02 n=3 fg=0.02 bg=0.01
procollagen−proline 4−dioxygenase comple... GO:0016222 p=5.0E−02 n=1 fg=0.01 bg=0.00
kinocilium GO:0060091 p=5.0E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=5.0E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=5.0E−02 n=1 fg=0.01 bg=0.00
smooth muscle contractile fiber GO:0030485 p=5.0E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=5.0E−02 n=1 fg=0.01 bg=0.00
syntrophin complex GO:0016013 p=5.0E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber expansion GO:1990026 p=5.0E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=5.0E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=5.0E−02 n=1 fg=0.01 bg=0.00
chromatin GO:0000785 p=5.0E−02 n=11 fg=0.08 bg=0.05
tertiary granule membrane GO:0070821 p=5.6E−02 n=2 fg=0.01 bg=0.00
postsynapse GO:0098794 p=5.7E−02 n=9 fg=0.07 bg=0.04
calcium channel complex GO:0034704 p=7.0E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=134/586 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction