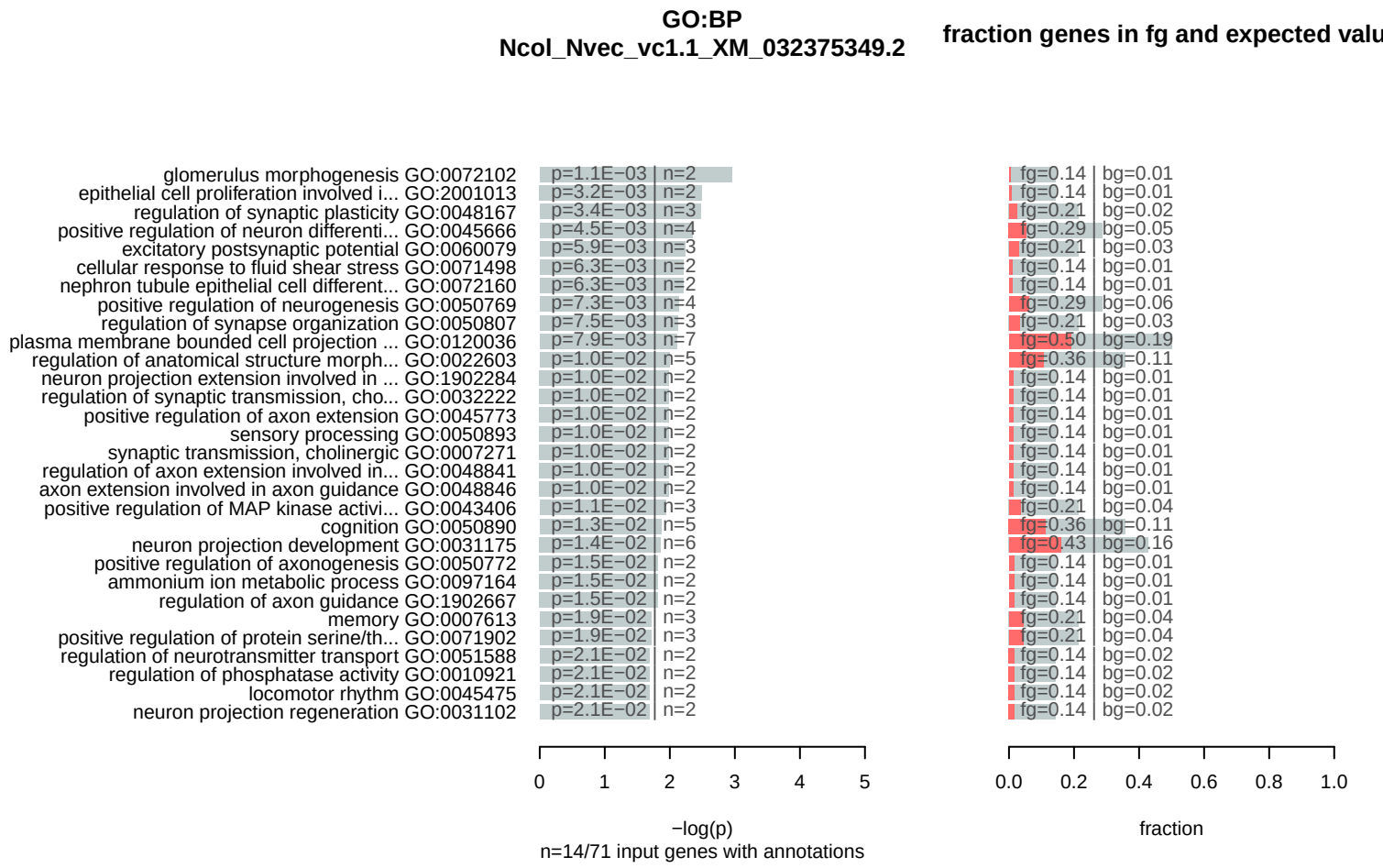
GO:BP
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fraction genes in fg and expected valu
glomerulus morphogenesis GO:0072102 p=1.1E−03 n=2 fg=0.14 bg=0.01
epithelial cell proliferation involved i... GO:2001013 p=3.2E−03 n=2 fg=0.14 bg=0.01
regulation of synaptic plasticity GO:0048167 p=3.4E−03 n=3 fg=0.21 bg=0.02
positive regulation of neuron differenti... GO:0045666 p=4.5E−03 n=4 fg=0.29 bg=0.05
excitatory postsynaptic potential GO:0060079 p=5.9E−03 n=3 fg=0.21 bg=0.03
cellular response to fluid shear stress GO:0071498 p=6.3E−03 n=2 fg=0.14 bg=0.01
nephron tubule epithelial cell different... GO:0072160 p=6.3E−03 n=2 fg=0.14 bg=0.01
positive regulation of neurogenesis GO:0050769 p=7.3E−03 n=4 fg=0.29 bg=0.06
regulation of synapse organization GO:0050807 p=7.5E−03 n=3 fg=0.21 bg=0.03
plasma membrane bounded cell projection ... GO:0120036 p=7.9E−03 n=7 fg=0.50 bg=0.19
regulation of anatomical structure morph... GO:0022603 p=1.0E−02 n=5 fg=0.36 bg=0.11
neuron projection extension involved in ... GO:1902284 p=1.0E−02 n=2 fg=0.14 bg=0.01
regulation of synaptic transmission, cho... GO:0032222 p=1.0E−02 n=2 fg=0.14 bg=0.01
positive regulation of axon extension GO:0045773 p=1.0E−02 n=2 fg=0.14 bg=0.01
sensory processing GO:0050893 p=1.0E−02 n=2 fg=0.14 bg=0.01
synaptic transmission, cholinergic GO:0007271 p=1.0E−02 n=2 fg=0.14 bg=0.01
regulation of axon extension involved in... GO:0048841 p=1.0E−02 n=2 fg=0.14 bg=0.01
axon extension involved in axon guidance GO:0048846 p=1.0E−02 n=2 fg=0.14 bg=0.01
positive regulation of MAP kinase activi... GO:0043406 p=1.1E−02 n=3 fg=0.21 bg=0.04
cognition GO:0050890 p=1.3E−02 n=5 fg=0.36 bg=0.11
neuron projection development GO:0031175 p=1.4E−02 n=6 fg=0.43 bg=0.16
positive regulation of axonogenesis GO:0050772 p=1.5E−02 n=2 fg=0.14 bg=0.01
ammonium ion metabolic process GO:0097164 p=1.5E−02 n=2 fg=0.14 bg=0.01
regulation of axon guidance GO:1902667 p=1.5E−02 n=2 fg=0.14 bg=0.01
memory GO:0007613 p=1.9E−02 n=3 fg=0.21 bg=0.04
positive regulation of protein serine/th... GO:0071902 p=1.9E−02 n=3 fg=0.21 bg=0.04
regulation of neurotransmitter transport GO:0051588 p=2.1E−02 n=2 fg=0.14 bg=0.02
regulation of phosphatase activity GO:0010921 p=2.1E−02 n=2 fg=0.14 bg=0.02
locomotor rhythm GO:0045475 p=2.1E−02 n=2 fg=0.14 bg=0.02
neuron projection regeneration GO:0031102 p=2.1E−02 n=2 fg=0.14 bg=0.02
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−log(p)
n=14/71 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032375349.2
fraction genes in fg and expected valu
excitatory extracellular ligand−gated io... GO:0005231 p=9.4E−03 n=2 fg=0.17 bg=0.01
identical protein binding GO:0042802 p=1.3E−02 n=6 fg=0.50 bg=0.19
transmitter−gated ion channel activity i... GO:1904315 p=3.3E−02 n=1 fg=0.08 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=3.3E−02 n=1 fg=0.08 bg=0.00
O−acyltransferase activity GO:0008374 p=3.3E−02 n=1 fg=0.08 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.3E−02 n=1 fg=0.08 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=3.3E−02 n=1 fg=0.08 bg=0.00
acetylcholine binding GO:0042166 p=3.3E−02 n=1 fg=0.08 bg=0.00
neurotransmitter receptor activity invol... GO:0099529 p=3.3E−02 n=1 fg=0.08 bg=0.00
toxic substance binding GO:0015643 p=3.3E−02 n=1 fg=0.08 bg=0.00
chloride channel regulator activity GO:0017081 p=3.3E−02 n=1 fg=0.08 bg=0.00
postsynaptic neurotransmitter receptor a... GO:0098960 p=3.3E−02 n=1 fg=0.08 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=3.3E−02 n=1 fg=0.08 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=3.3E−02 n=1 fg=0.08 bg=0.00
nuclear steroid receptor activity GO:0003707 p=3.3E−02 n=1 fg=0.08 bg=0.00
acetylcholine−gated cation−selective cha... GO:0022848 p=3.3E−02 n=1 fg=0.08 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=3.3E−02 n=1 fg=0.08 bg=0.00
acetylcholine receptor activity GO:0015464 p=3.3E−02 n=1 fg=0.08 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=3.3E−02 n=1 fg=0.08 bg=0.00
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protein dimerization activity GO:0046983 p=4.2E−02 n=5 fg=0.42 bg=0.18
protein homodimerization activity GO:0042803 p=4.5E−02 n=4 fg=0.33 bg=0.12
minor groove of adenine−thymine−rich DNA... GO:0003680 p=6.5E−02 n=1 fg=0.08 bg=0.01
neurotransmitter binding GO:0042165 p=6.5E−02 n=1 fg=0.08 bg=0.01
DNA secondary structure binding GO:0000217 p=6.5E−02 n=1 fg=0.08 bg=0.01
actin monomer binding GO:0003785 p=6.5E−02 n=1 fg=0.08 bg=0.01
ribonucleoside binding GO:0032549 p=9.6E−02 n=1 fg=0.08 bg=0.01
lysophospholipid acyltransferase activit... GO:0071617 p=9.6E−02 n=1 fg=0.08 bg=0.01
MAP kinase kinase kinase activity GO:0004709 p=9.6E−02 n=1 fg=0.08 bg=0.01
purine ribonucleoside binding GO:0032550 p=9.6E−02 n=1 fg=0.08 bg=0.01
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−log(p)
n=12/71 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375349.2
fraction genes in fg and expected valu
actin−based cell projection GO:0098858 p=3.2E−02 n=2 fg=0.13 bg=0.02
9+2 non−motile cilium GO:0097732 p=3.7E−02 n=1 fg=0.07 bg=0.00
anchored component of plasma membrane GO:0046658 p=3.7E−02 n=1 fg=0.07 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=3.7E−02 n=1 fg=0.07 bg=0.00
septin collar GO:0032173 p=3.7E−02 n=1 fg=0.07 bg=0.00
kinocilium GO:0060091 p=3.7E−02 n=1 fg=0.07 bg=0.00
distal axon GO:0150034 p=6.5E−02 n=3 fg=0.20 bg=0.06
stress fiber GO:0001725 p=7.3E−02 n=1 fg=0.07 bg=0.00
septin cytoskeleton GO:0032156 p=7.3E−02 n=1 fg=0.07 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=7.3E−02 n=1 fg=0.07 bg=0.00
azurophil granule membrane GO:0035577 p=7.3E−02 n=1 fg=0.07 bg=0.00
contractile actin filament bundle GO:0097517 p=7.3E−02 n=1 fg=0.07 bg=0.00
septin ring GO:0005940 p=7.3E−02 n=1 fg=0.07 bg=0.00
stereocilium GO:0032420 p=7.3E−02 n=1 fg=0.07 bg=0.00
stereocilium bundle GO:0032421 p=7.3E−02 n=1 fg=0.07 bg=0.00
septin complex GO:0031105 p=7.3E−02 n=1 fg=0.07 bg=0.00
sperm annulus GO:0097227 p=7.3E−02 n=1 fg=0.07 bg=0.00
anchored component of membrane GO:0031225 p=7.3E−02 n=1 fg=0.07 bg=0.00
actin filament bundle GO:0032432 p=7.3E−02 n=1 fg=0.07 bg=0.00
axon GO:0030424 p=8.0E−02 n=4 fg=0.27 bg=0.11
growth cone GO:0030426 p=8.0E−02 n=2 fg=0.13 bg=0.03
actin cytoskeleton GO:0015629 p=9.1E−02 n=2 fg=0.13 bg=0.03
site of polarized growth GO:0030427 p=9.1E−02 n=2 fg=0.13 bg=0.03
synaptic vesicle GO:0008021 p=1.0E−01 n=2 fg=0.13 bg=0.04
cleavage furrow GO:0032154 p=1.1E−01 n=1 fg=0.07 bg=0.01
filopodium GO:0030175 p=1.1E−01 n=1 fg=0.07 bg=0.01
actomyosin GO:0042641 p=1.1E−01 n=1 fg=0.07 bg=0.01
plasma membrane signaling receptor compl... GO:0098802 p=1.1E−01 n=1 fg=0.07 bg=0.01
exocytic vesicle GO:0070382 p=1.2E−01 n=2 fg=0.13 bg=0.04
plasma membrane bounded cell projection GO:0120025 p=1.2E−01 n=6 fg=0.40 bg=0.24
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−log(p)
n=15/71 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction