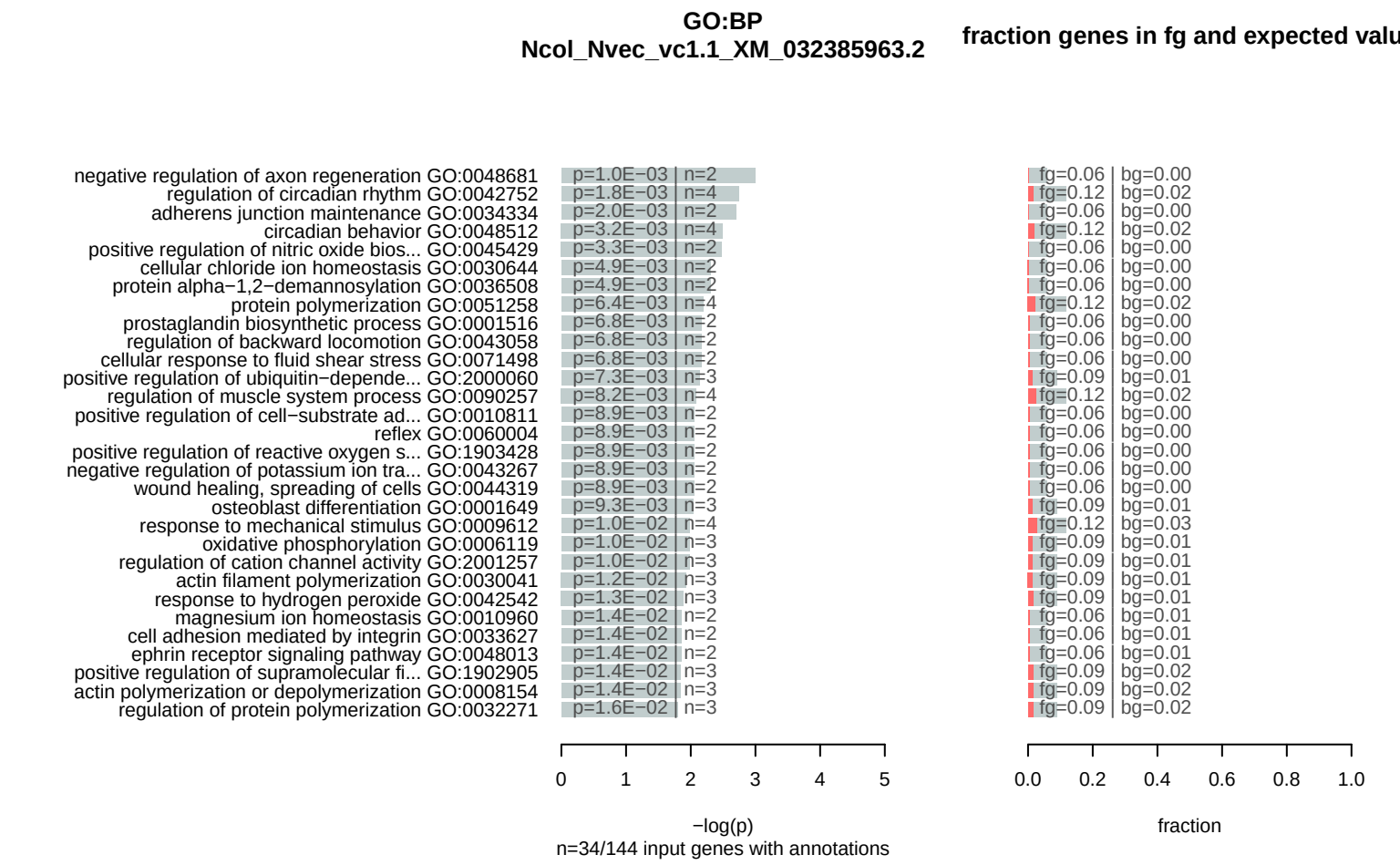
GO:BP
Ncol_Nvec_vc1.1_XM_032385963.2
fraction genes in fg and expected valu
negative regulation of axon regeneration GO:0048681 p=1.0E−03 n=2 fg=0.06 bg=0.00
regulation of circadian rhythm GO:0042752 p=1.8E−03 n=4 fg=0.12 bg=0.02
adherens junction maintenance GO:0034334 p=2.0E−03 n=2 fg=0.06 bg=0.00
circadian behavior GO:0048512 p=3.2E−03 n=4 fg=0.12 bg=0.02
positive regulation of nitric oxide bios... GO:0045429 p=3.3E−03 n=2 fg=0.06 bg=0.00
cellular chloride ion homeostasis GO:0030644 p=4.9E−03 n=2 fg=0.06 bg=0.00
protein alpha−1,2−demannosylation GO:0036508 p=4.9E−03 n=2 fg=0.06 bg=0.00
protein polymerization GO:0051258 p=6.4E−03 n=4 fg=0.12 bg=0.02
prostaglandin biosynthetic process GO:0001516 p=6.8E−03 n=2 fg=0.06 bg=0.00
regulation of backward locomotion GO:0043058 p=6.8E−03 n=2 fg=0.06 bg=0.00
cellular response to fluid shear stress GO:0071498 p=6.8E−03 n=2 fg=0.06 bg=0.00
positive regulation of ubiquitin−depende... GO:2000060 p=7.3E−03 n=3 fg=0.09 bg=0.01
regulation of muscle system process GO:0090257 p=8.2E−03 n=4 fg=0.12 bg=0.02
positive regulation of cell−substrate ad... GO:0010811 p=8.9E−03 n=2 fg=0.06 bg=0.00
reflex GO:0060004 p=8.9E−03 n=2 fg=0.06 bg=0.00
positive regulation of reactive oxygen s... GO:1903428 p=8.9E−03 n=2 fg=0.06 bg=0.00
negative regulation of potassium ion tra... GO:0043267 p=8.9E−03 n=2 fg=0.06 bg=0.00
wound healing, spreading of cells GO:0044319 p=8.9E−03 n=2 fg=0.06 bg=0.00
osteoblast differentiation GO:0001649 p=9.3E−03 n=3 fg=0.09 bg=0.01
response to mechanical stimulus GO:0009612 p=1.0E−02 n=4 fg=0.12 bg=0.03
oxidative phosphorylation GO:0006119 p=1.0E−02 n=3 fg=0.09 bg=0.01
regulation of cation channel activity GO:2001257 p=1.0E−02 n=3 fg=0.09 bg=0.01
actin filament polymerization GO:0030041 p=1.2E−02 n=3 fg=0.09 bg=0.01
response to hydrogen peroxide GO:0042542 p=1.3E−02 n=3 fg=0.09 bg=0.01
magnesium ion homeostasis GO:0010960 p=1.4E−02 n=2 fg=0.06 bg=0.01
cell adhesion mediated by integrin GO:0033627 p=1.4E−02 n=2 fg=0.06 bg=0.01
ephrin receptor signaling pathway GO:0048013 p=1.4E−02 n=2 fg=0.06 bg=0.01
positive regulation of supramolecular fi... GO:1902905 p=1.4E−02 n=3 fg=0.09 bg=0.02
actin polymerization or depolymerization GO:0008154 p=1.4E−02 n=3 fg=0.09 bg=0.02
regulation of protein polymerization GO:0032271 p=1.6E−02 n=3 fg=0.09 bg=0.02
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−log(p)
n=34/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032385963.2
fraction genes in fg and expected valu
actin monomer binding GO:0003785 p=2.4E−03 n=2 fg=0.06 bg=0.00
cysteine−type peptidase activity GO:0008234 p=9.6E−03 n=3 fg=0.09 bg=0.01
heme binding GO:0020037 p=1.4E−02 n=2 fg=0.06 bg=0.01
tetrapyrrole binding GO:0046906 p=1.7E−02 n=2 fg=0.06 bg=0.01
voltage−gated potassium channel activity GO:0005249 p=1.7E−02 n=2 fg=0.06 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=2.0E−02 n=2 fg=0.06 bg=0.01
protein methyltransferase activity GO:0008276 p=2.0E−02 n=2 fg=0.06 bg=0.01
open rectifier potassium channel activit... GO:0005252 p=2.1E−02 n=1 fg=0.03 bg=0.00
phorbol ester receptor activity GO:0001565 p=2.1E−02 n=1 fg=0.03 bg=0.00
histone deacetylase regulator activity GO:0035033 p=2.1E−02 n=1 fg=0.03 bg=0.00
JUN kinase activity GO:0004705 p=2.1E−02 n=1 fg=0.03 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=2.1E−02 n=1 fg=0.03 bg=0.00
iron−responsive element binding GO:0030350 p=2.1E−02 n=1 fg=0.03 bg=0.00
ferrochelatase activity GO:0004325 p=2.1E−02 n=1 fg=0.03 bg=0.00
S100 protein binding GO:0044548 p=2.1E−02 n=1 fg=0.03 bg=0.00
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=2.1E−02 n=1 fg=0.03 bg=0.00
3−phosphoinositide−dependent protein kin... GO:0043423 p=2.1E−02 n=1 fg=0.03 bg=0.00
integrin binding GO:0005178 p=2.4E−02 n=2 fg=0.06 bg=0.01
potassium channel activity GO:0005267 p=3.3E−02 n=2 fg=0.06 bg=0.01
oxidoreduction−driven active transmembra... GO:0015453 p=3.3E−02 n=2 fg=0.06 bg=0.01
kinesin binding GO:0019894 p=3.3E−02 n=2 fg=0.06 bg=0.01
actin filament binding GO:0051015 p=3.7E−02 n=2 fg=0.06 bg=0.01
calcium−dependent cysteine−type endopept... GO:0004198 p=4.1E−02 n=1 fg=0.03 bg=0.00
inositol monophosphate 4−phosphatase act... GO:0052833 p=4.1E−02 n=1 fg=0.03 bg=0.00
inositol monophosphate phosphatase activ... GO:0052834 p=4.1E−02 n=1 fg=0.03 bg=0.00
calcium−dependent protein serine/threoni... GO:0004723 p=4.1E−02 n=1 fg=0.03 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=4.7E−02 n=2 fg=0.06 bg=0.01
voltage−gated cation channel activity GO:0022843 p=5.2E−02 n=2 fg=0.06 bg=0.01
ion gated channel activity GO:0022839 p=5.4E−02 n=3 fg=0.09 bg=0.03
gated channel activity GO:0022836 p=6.0E−02 n=3 fg=0.09 bg=0.03
0 1 2 3 4 5
−log(p)
n=33/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032385963.2
fraction genes in fg and expected valu
core−binding factor complex GO:0016513 p=2.0E−02 n=1 fg=0.03 bg=0.00
NMDA selective glutamate receptor comple... GO:0017146 p=2.0E−02 n=1 fg=0.03 bg=0.00
smooth muscle contractile fiber GO:0030485 p=2.0E−02 n=1 fg=0.03 bg=0.00
intercalated disc GO:0014704 p=2.6E−02 n=2 fg=0.06 bg=0.01
neuronal cell body membrane GO:0032809 p=3.0E−02 n=2 fg=0.06 bg=0.01
cell body membrane GO:0044298 p=3.4E−02 n=2 fg=0.06 bg=0.01
respiratory chain complex GO:0098803 p=3.4E−02 n=2 fg=0.06 bg=0.01
neuronal cell body GO:0043025 p=3.6E−02 n=6 fg=0.17 bg=0.07
cell leading edge GO:0031252 p=3.8E−02 n=4 fg=0.11 bg=0.04
transmembrane transporter complex GO:1902495 p=3.8E−02 n=3 fg=0.08 bg=0.02
cell−cell contact zone GO:0044291 p=3.9E−02 n=2 fg=0.06 bg=0.01
neurotransmitter receptor complex GO:0098878 p=3.9E−02 n=1 fg=0.03 bg=0.00
ionotropic glutamate receptor complex GO:0008328 p=3.9E−02 n=1 fg=0.03 bg=0.00
type Ib terminal bouton GO:0061176 p=3.9E−02 n=1 fg=0.03 bg=0.00
type Is terminal bouton GO:0061177 p=3.9E−02 n=1 fg=0.03 bg=0.00
dendrite GO:0030425 p=4.0E−02 n=6 fg=0.17 bg=0.07
dendritic tree GO:0097447 p=4.0E−02 n=6 fg=0.17 bg=0.07
transporter complex GO:1990351 p=4.3E−02 n=3 fg=0.08 bg=0.02
presynapse GO:0098793 p=4.3E−02 n=5 fg=0.14 bg=0.05
mitochondrial respirasome GO:0005746 p=4.8E−02 n=2 fg=0.06 bg=0.01
respirasome GO:0070469 p=4.8E−02 n=2 fg=0.06 bg=0.01
cell body GO:0044297 p=5.0E−02 n=6 fg=0.17 bg=0.08
asymmetric synapse GO:0032279 p=5.2E−02 n=3 fg=0.08 bg=0.02
synaptic vesicle membrane GO:0030672 p=5.3E−02 n=2 fg=0.06 bg=0.01
neuron to neuron synapse GO:0098984 p=5.5E−02 n=3 fg=0.08 bg=0.02
synapse GO:0045202 p=5.8E−02 n=7 fg=0.19 bg=0.10
exocytic vesicle membrane GO:0099501 p=5.8E−02 n=2 fg=0.06 bg=0.01
respiratory chain complex IV GO:0045277 p=5.9E−02 n=1 fg=0.03 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=5.9E−02 n=1 fg=0.03 bg=0.00
muscle cell projection GO:0036194 p=5.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction