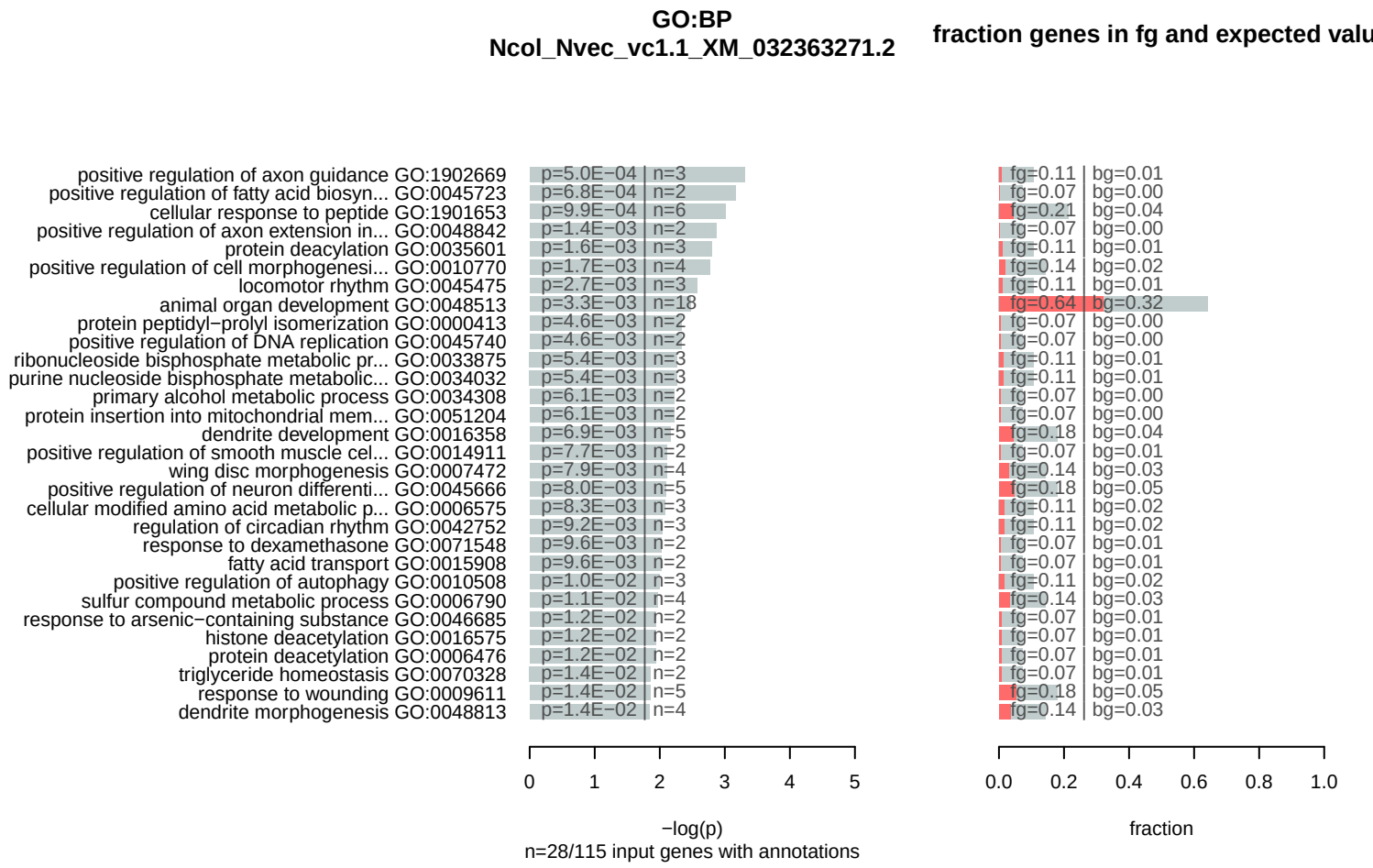
GO:BP
Ncol_Nvec_vc1.1_XM_032363271.2
fraction genes in fg and expected valu
positive regulation of axon guidance GO:1902669 p=5.0E−04 n=3 fg=0.11 bg=0.01
positive regulation of fatty acid biosyn... GO:0045723 p=6.8E−04 n=2 fg=0.07 bg=0.00
cellular response to peptide GO:1901653 p=9.9E−04 n=6 fg=0.21 bg=0.04
positive regulation of axon extension in... GO:0048842 p=1.4E−03 n=2 fg=0.07 bg=0.00
protein deacylation GO:0035601 p=1.6E−03 n=3 fg=0.11 bg=0.01
positive regulation of cell morphogenesi... GO:0010770 p=1.7E−03 n=4 fg=0.14 bg=0.02
locomotor rhythm GO:0045475 p=2.7E−03 n=3 fg=0.11 bg=0.01
animal organ development GO:0048513 p=3.3E−03 n=18 fg=0.64 bg=0.32
protein peptidyl−prolyl isomerization GO:0000413 p=4.6E−03 n=2 fg=0.07 bg=0.00
positive regulation of DNA replication GO:0045740 p=4.6E−03 n=2 fg=0.07 bg=0.00
ribonucleoside bisphosphate metabolic pr... GO:0033875 p=5.4E−03 n=3 fg=0.11 bg=0.01
purine nucleoside bisphosphate metabolic... GO:0034032 p=5.4E−03 n=3 fg=0.11 bg=0.01
primary alcohol metabolic process GO:0034308 p=6.1E−03 n=2 fg=0.07 bg=0.00
protein insertion into mitochondrial mem... GO:0051204 p=6.1E−03 n=2 fg=0.07 bg=0.00
dendrite development GO:0016358 p=6.9E−03 n=5 fg=0.18 bg=0.04
positive regulation of smooth muscle cel... GO:0014911 p=7.7E−03 n=2 fg=0.07 bg=0.01
wing disc morphogenesis GO:0007472 p=7.9E−03 n=4 fg=0.14 bg=0.03
positive regulation of neuron differenti... GO:0045666 p=8.0E−03 n=5 fg=0.18 bg=0.05
cellular modified amino acid metabolic p... GO:0006575 p=8.3E−03 n=3 fg=0.11 bg=0.02
regulation of circadian rhythm GO:0042752 p=9.2E−03 n=3 fg=0.11 bg=0.02
response to dexamethasone GO:0071548 p=9.6E−03 n=2 fg=0.07 bg=0.01
fatty acid transport GO:0015908 p=9.6E−03 n=2 fg=0.07 bg=0.01
positive regulation of autophagy GO:0010508 p=1.0E−02 n=3 fg=0.11 bg=0.02
sulfur compound metabolic process GO:0006790 p=1.1E−02 n=4 fg=0.14 bg=0.03
response to arsenic−containing substance GO:0046685 p=1.2E−02 n=2 fg=0.07 bg=0.01
histone deacetylation GO:0016575 p=1.2E−02 n=2 fg=0.07 bg=0.01
protein deacetylation GO:0006476 p=1.2E−02 n=2 fg=0.07 bg=0.01
triglyceride homeostasis GO:0070328 p=1.4E−02 n=2 fg=0.07 bg=0.01
response to wounding GO:0009611 p=1.4E−02 n=5 fg=0.18 bg=0.05
dendrite morphogenesis GO:0048813 p=1.4E−02 n=4 fg=0.14 bg=0.03
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−log(p)
n=28/115 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032363271.2
fraction genes in fg and expected valu
MAP kinase activity GO:0004707 p=3.3E−03 n=2 fg=0.07 bg=0.00
carboxylic ester hydrolase activity GO:0052689 p=3.4E−03 n=3 fg=0.10 bg=0.01
peptidyl−prolyl cis−trans isomerase acti... GO:0003755 p=6.8E−03 n=2 fg=0.07 bg=0.00
amide binding GO:0033218 p=1.1E−02 n=4 fg=0.13 bg=0.03
protein serine/threonine/tyrosine kinase... GO:0004712 p=1.1E−02 n=2 fg=0.07 bg=0.01
thiolester hydrolase activity GO:0016790 p=1.7E−02 n=2 fg=0.07 bg=0.01
vascular endothelial growth factor bindi... GO:0038085 p=1.9E−02 n=1 fg=0.03 bg=0.00
cholinesterase activity GO:0004104 p=1.9E−02 n=1 fg=0.03 bg=0.00
citrate (Si)−synthase activity GO:0004108 p=1.9E−02 n=1 fg=0.03 bg=0.00
semaphorin receptor activity GO:0017154 p=1.9E−02 n=1 fg=0.03 bg=0.00
acyltransferase activity, acyl groups co... GO:0046912 p=1.9E−02 n=1 fg=0.03 bg=0.00
pantothenate kinase activity GO:0004594 p=1.9E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acid binding GO:0036041 p=1.9E−02 n=1 fg=0.03 bg=0.00
nucleoside transmembrane transporter act... GO:0005337 p=1.9E−02 n=1 fg=0.03 bg=0.00
ribosomal protein S6 kinase activity GO:0004711 p=1.9E−02 n=1 fg=0.03 bg=0.00
citrate synthase activity GO:0036440 p=1.9E−02 n=1 fg=0.03 bg=0.00
choline binding GO:0033265 p=1.9E−02 n=1 fg=0.03 bg=0.00
glycerol−3−phosphate dehydrogenase [NAD(... GO:0047952 p=1.9E−02 n=1 fg=0.03 bg=0.00
stearic acid binding GO:0070540 p=1.9E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016901 p=1.9E−02 n=1 fg=0.03 bg=0.00
JUN kinase activity GO:0004705 p=1.9E−02 n=1 fg=0.03 bg=0.00
histone deacetylase regulator activity GO:0035033 p=1.9E−02 n=1 fg=0.03 bg=0.00
glycerol−3−phosphate dehydrogenase [NAD+... GO:0004367 p=1.9E−02 n=1 fg=0.03 bg=0.00
glycerol−3−phosphate dehydrogenase (quin... GO:0004368 p=1.9E−02 n=1 fg=0.03 bg=0.00
icosanoid binding GO:0050542 p=1.9E−02 n=1 fg=0.03 bg=0.00
icosatetraenoic acid binding GO:0050543 p=1.9E−02 n=1 fg=0.03 bg=0.00
arachidonic acid binding GO:0050544 p=1.9E−02 n=1 fg=0.03 bg=0.00
ammonium ion binding GO:0070405 p=2.0E−02 n=2 fg=0.07 bg=0.01
peptide binding GO:0042277 p=3.5E−02 n=3 fg=0.10 bg=0.02
phospholipase activity GO:0004620 p=3.5E−02 n=2 fg=0.07 bg=0.01
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−log(p)
n=30/115 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032363271.2
fraction genes in fg and expected valu
cytosol GO:0005829 p=9.1E−03 n=18 fg=0.62 bg=0.39
Sin3 complex GO:0016580 p=1.6E−02 n=1 fg=0.03 bg=0.00
semaphorin receptor complex GO:0002116 p=1.6E−02 n=1 fg=0.03 bg=0.00
glycerol−3−phosphate dehydrogenase compl... GO:0009331 p=1.6E−02 n=1 fg=0.03 bg=0.00
Dsl1/NZR complex GO:0070939 p=1.6E−02 n=1 fg=0.03 bg=0.00
mitochondrial intermembrane space GO:0005758 p=2.0E−02 n=2 fg=0.07 bg=0.01
focal adhesion GO:0005925 p=2.3E−02 n=2 fg=0.07 bg=0.01
membrane−enclosed lumen GO:0031974 p=2.5E−02 n=17 fg=0.59 bg=0.39
intracellular organelle lumen GO:0070013 p=2.5E−02 n=17 fg=0.59 bg=0.39
organelle lumen GO:0043233 p=2.5E−02 n=17 fg=0.59 bg=0.39
endoplasmic reticulum chaperone complex GO:0034663 p=3.2E−02 n=1 fg=0.03 bg=0.00
cell body fiber GO:0070852 p=3.2E−02 n=1 fg=0.03 bg=0.00
glutamate−cysteine ligase complex GO:0017109 p=3.2E−02 n=1 fg=0.03 bg=0.00
mitochondrial intermembrane space protei... GO:0042719 p=3.2E−02 n=1 fg=0.03 bg=0.00
neurofilament GO:0005883 p=3.2E−02 n=1 fg=0.03 bg=0.00
sorting endosome GO:0097443 p=3.2E−02 n=1 fg=0.03 bg=0.00
cell−substrate junction GO:0030055 p=3.2E−02 n=2 fg=0.07 bg=0.01
fibrillar center GO:0001650 p=3.6E−02 n=2 fg=0.07 bg=0.01
organelle envelope lumen GO:0031970 p=3.9E−02 n=2 fg=0.07 bg=0.01
nuclear lumen GO:0031981 p=4.3E−02 n=14 fg=0.48 bg=0.32
podosome GO:0002102 p=4.7E−02 n=1 fg=0.03 bg=0.00
TIM23 mitochondrial import inner membran... GO:0005744 p=4.7E−02 n=1 fg=0.03 bg=0.00
growth cone membrane GO:0032584 p=4.7E−02 n=1 fg=0.03 bg=0.00
intermediate filament GO:0005882 p=4.7E−02 n=1 fg=0.03 bg=0.00
Sin3−type complex GO:0070822 p=4.7E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum protein−containing... GO:0140534 p=5.9E−02 n=2 fg=0.07 bg=0.01
dendrite cytoplasm GO:0032839 p=6.3E−02 n=1 fg=0.03 bg=0.00
basal dendrite GO:0097441 p=6.3E−02 n=1 fg=0.03 bg=0.00
septin cytoskeleton GO:0032156 p=7.8E−02 n=1 fg=0.03 bg=0.00
Cul3−RING ubiquitin ligase complex GO:0031463 p=7.8E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=29/115 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction