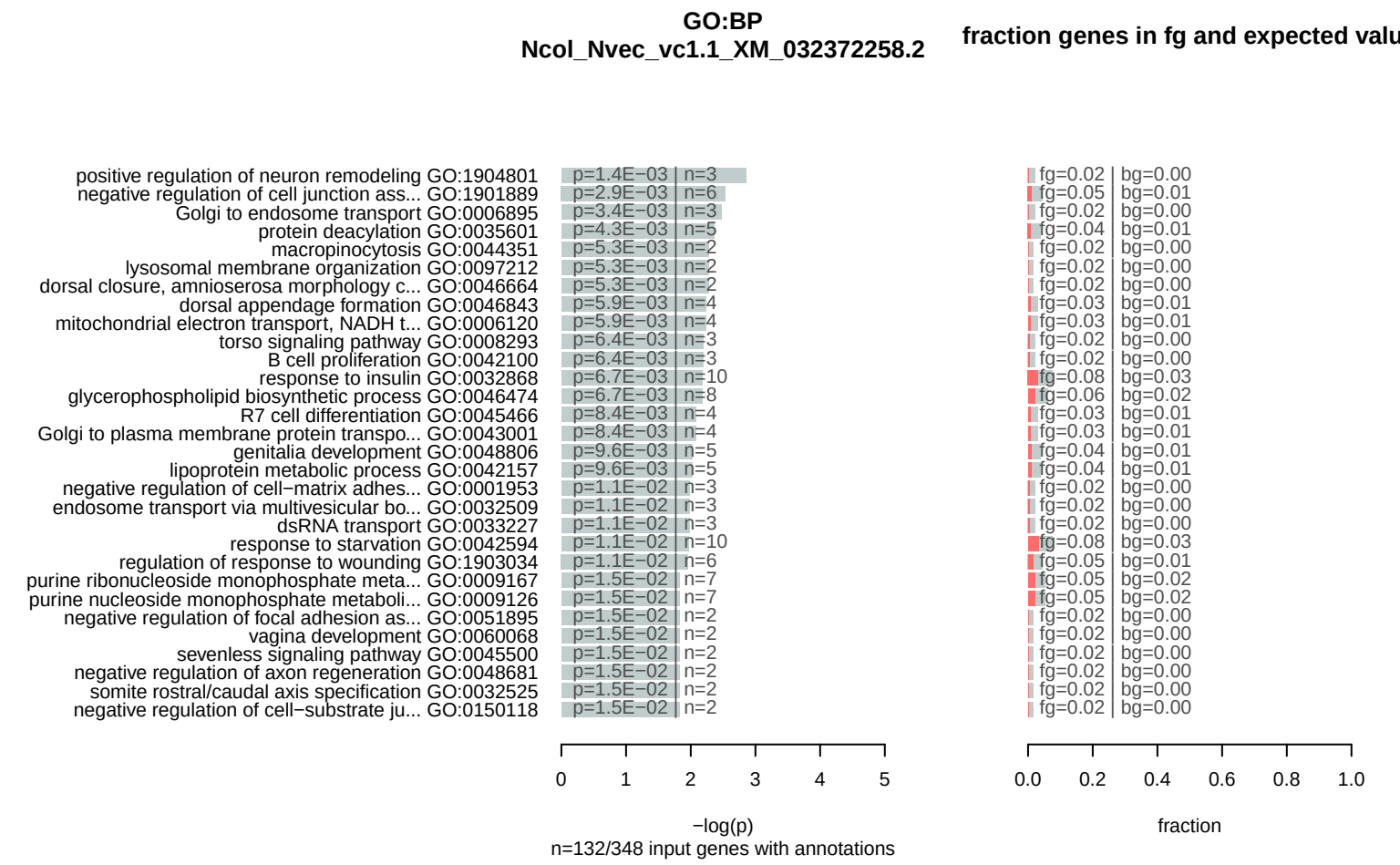
GO:BP
Ncol_Nvec_vc1.1_XM_032372258.2
fraction genes in fg and expected valu
positive regulation of neuron remodeling GO:1904801 p=1.4E−03 n=3 fg=0.02 bg=0.00
negative regulation of cell junction ass... GO:1901889 p=2.9E−03 n=6 fg=0.05 bg=0.01
Golgi to endosome transport GO:0006895 p=3.4E−03 n=3 fg=0.02 bg=0.00
protein deacylation GO:0035601 p=4.3E−03 n=5 fg=0.04 bg=0.01
macropinocytosis GO:0044351 p=5.3E−03 n=2 fg=0.02 bg=0.00
lysosomal membrane organization GO:0097212 p=5.3E−03 n=2 fg=0.02 bg=0.00
dorsal closure, amnioserosa morphology c... GO:0046664 p=5.3E−03 n=2 fg=0.02 bg=0.00
dorsal appendage formation GO:0046843 p=5.9E−03 n=4 fg=0.03 bg=0.01
mitochondrial electron transport, NADH t... GO:0006120 p=5.9E−03 n=4 fg=0.03 bg=0.01
torso signaling pathway GO:0008293 p=6.4E−03 n=3 fg=0.02 bg=0.00
B cell proliferation GO:0042100 p=6.4E−03 n=3 fg=0.02 bg=0.00
response to insulin GO:0032868 p=6.7E−03 n=10 fg=0.08 bg=0.03
glycerophospholipid biosynthetic process GO:0046474 p=6.7E−03 n=8 fg=0.06 bg=0.02
R7 cell differentiation GO:0045466 p=8.4E−03 n=4 fg=0.03 bg=0.01
Golgi to plasma membrane protein transpo... GO:0043001 p=8.4E−03 n=4 fg=0.03 bg=0.01
genitalia development GO:0048806 p=9.6E−03 n=5 fg=0.04 bg=0.01
lipoprotein metabolic process GO:0042157 p=9.6E−03 n=5 fg=0.04 bg=0.01
negative regulation of cell−matrix adhes... GO:0001953 p=1.1E−02 n=3 fg=0.02 bg=0.00
endosome transport via multivesicular bo... GO:0032509 p=1.1E−02 n=3 fg=0.02 bg=0.00
dsRNA transport GO:0033227 p=1.1E−02 n=3 fg=0.02 bg=0.00
response to starvation GO:0042594 p=1.1E−02 n=10 fg=0.08 bg=0.03
regulation of response to wounding GO:1903034 p=1.1E−02 n=6 fg=0.05 bg=0.01
purine ribonucleoside monophosphate meta... GO:0009167 p=1.5E−02 n=7 fg=0.05 bg=0.02
purine nucleoside monophosphate metaboli... GO:0009126 p=1.5E−02 n=7 fg=0.05 bg=0.02
negative regulation of focal adhesion as... GO:0051895 p=1.5E−02 n=2 fg=0.02 bg=0.00
vagina development GO:0060068 p=1.5E−02 n=2 fg=0.02 bg=0.00
sevenless signaling pathway GO:0045500 p=1.5E−02 n=2 fg=0.02 bg=0.00
negative regulation of axon regeneration GO:0048681 p=1.5E−02 n=2 fg=0.02 bg=0.00
somite rostral/caudal axis specification GO:0032525 p=1.5E−02 n=2 fg=0.02 bg=0.00
negative regulation of cell−substrate ju... GO:0150118 p=1.5E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=132/348 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032372258.2
fraction genes in fg and expected valu
electron transfer activity GO:0009055 p=1.2E−02 n=5 fg=0.05 bg=0.01
nucleobase−containing compound transmemb... GO:0015932 p=1.9E−02 n=3 fg=0.03 bg=0.01
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=2.5E−02 n=2 fg=0.02 bg=0.00
palmitoyl hydrolase activity GO:0098599 p=2.5E−02 n=2 fg=0.02 bg=0.00
palmitoyl−(protein) hydrolase activity GO:0008474 p=2.5E−02 n=2 fg=0.02 bg=0.00
NADH dehydrogenase activity GO:0003954 p=2.6E−02 n=3 fg=0.03 bg=0.01
transmembrane transporter activity GO:0022857 p=3.5E−02 n=16 fg=0.15 bg=0.09
MAP kinase activity GO:0004707 p=4.1E−02 n=2 fg=0.02 bg=0.00
MAP kinase kinase activity GO:0004708 p=4.1E−02 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016651 p=4.3E−02 n=4 fg=0.04 bg=0.01
phosphatidylinositol phosphate phosphata... GO:0052866 p=5.8E−02 n=2 fg=0.02 bg=0.00
carbohydrate derivative transmembrane tr... GO:1901505 p=5.8E−02 n=2 fg=0.02 bg=0.00
protein tyrosine kinase binding GO:1990782 p=6.5E−02 n=3 fg=0.03 bg=0.01
ribosomal large subunit binding GO:0043023 p=6.8E−02 n=1 fg=0.01 bg=0.00
5S rDNA binding GO:0080084 p=6.8E−02 n=1 fg=0.01 bg=0.00
tropomyosin binding GO:0005523 p=6.8E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=6.8E−02 n=1 fg=0.01 bg=0.00
protein phosphatase 5 binding GO:1990634 p=6.8E−02 n=1 fg=0.01 bg=0.00
acetylcholine transmembrane transporter ... GO:0005277 p=6.8E−02 n=1 fg=0.01 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=6.8E−02 n=1 fg=0.01 bg=0.00
carbohydrate:cation symporter activity GO:0005402 p=6.8E−02 n=1 fg=0.01 bg=0.00
RNA polymerase III core binding GO:0000994 p=6.8E−02 n=1 fg=0.01 bg=0.00
carbohydrate:proton symporter activity GO:0005351 p=6.8E−02 n=1 fg=0.01 bg=0.00
glucose transmembrane transporter activi... GO:0005355 p=6.8E−02 n=1 fg=0.01 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=6.8E−02 n=1 fg=0.01 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=6.8E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=6.8E−02 n=1 fg=0.01 bg=0.00
butyryl−CoA dehydrogenase activity GO:0004085 p=6.8E−02 n=1 fg=0.01 bg=0.00
7S RNA binding GO:0008312 p=6.8E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0052890 p=6.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=109/348 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032372258.2
fraction genes in fg and expected valu
Golgi transport complex GO:0017119 p=5.0E−03 n=2 fg=0.02 bg=0.00
Golgi stack GO:0005795 p=6.6E−03 n=8 fg=0.06 bg=0.02
mitochondrial respiratory chain complex ... GO:0005747 p=7.6E−03 n=4 fg=0.03 bg=0.01
oxidoreductase complex GO:1990204 p=1.4E−02 n=7 fg=0.05 bg=0.01
microtubule plus−end GO:0035371 p=1.4E−02 n=2 fg=0.02 bg=0.00
cytoplasmic microtubule GO:0005881 p=1.5E−02 n=3 fg=0.02 bg=0.00
Golgi membrane GO:0000139 p=1.8E−02 n=14 fg=0.11 bg=0.06
trans−Golgi network membrane GO:0032588 p=1.9E−02 n=6 fg=0.05 bg=0.02
bounding membrane of organelle GO:0098588 p=1.9E−02 n=29 fg=0.23 bg=0.16
mitochondrial protein−containing complex GO:0098798 p=2.5E−02 n=9 fg=0.07 bg=0.02
intrinsic component of the cytoplasmic s... GO:0031235 p=2.7E−02 n=2 fg=0.02 bg=0.00
organelle membrane GO:0031090 p=3.1E−02 n=45 fg=0.35 bg=0.26
membrane protein complex GO:0098796 p=3.4E−02 n=20 fg=0.16 bg=0.09
intracellular membrane−bounded organelle GO:0043231 p=3.5E−02 n=110 fg=0.86 bg=0.78
trans−Golgi network GO:0005802 p=4.3E−02 n=9 fg=0.07 bg=0.04
microtubule end GO:1990752 p=4.3E−02 n=2 fg=0.02 bg=0.00
intrinsic component of Golgi membrane GO:0031228 p=4.8E−02 n=3 fg=0.02 bg=0.01
membrane−bounded organelle GO:0043227 p=5.4E−02 n=112 fg=0.88 bg=0.81
sarcoplasm GO:0016528 p=6.2E−02 n=2 fg=0.02 bg=0.00
sarcoplasmic reticulum GO:0016529 p=6.2E−02 n=2 fg=0.02 bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181 p=6.2E−02 n=2 fg=0.02 bg=0.00
polymeric cytoskeletal fiber GO:0099513 p=6.5E−02 n=6 fg=0.05 bg=0.02
microtubule GO:0005874 p=7.0E−02 n=5 fg=0.04 bg=0.02
Sin3 complex GO:0016580 p=7.1E−02 n=1 fg=0.01 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=7.1E−02 n=1 fg=0.01 bg=0.00
cortical microtubule plus−end GO:1903754 p=7.1E−02 n=1 fg=0.01 bg=0.00
sarcoplasmic reticulum lumen GO:0033018 p=7.1E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=7.1E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=7.1E−02 n=1 fg=0.01 bg=0.00
BAX complex GO:0097144 p=7.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=128/348 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction