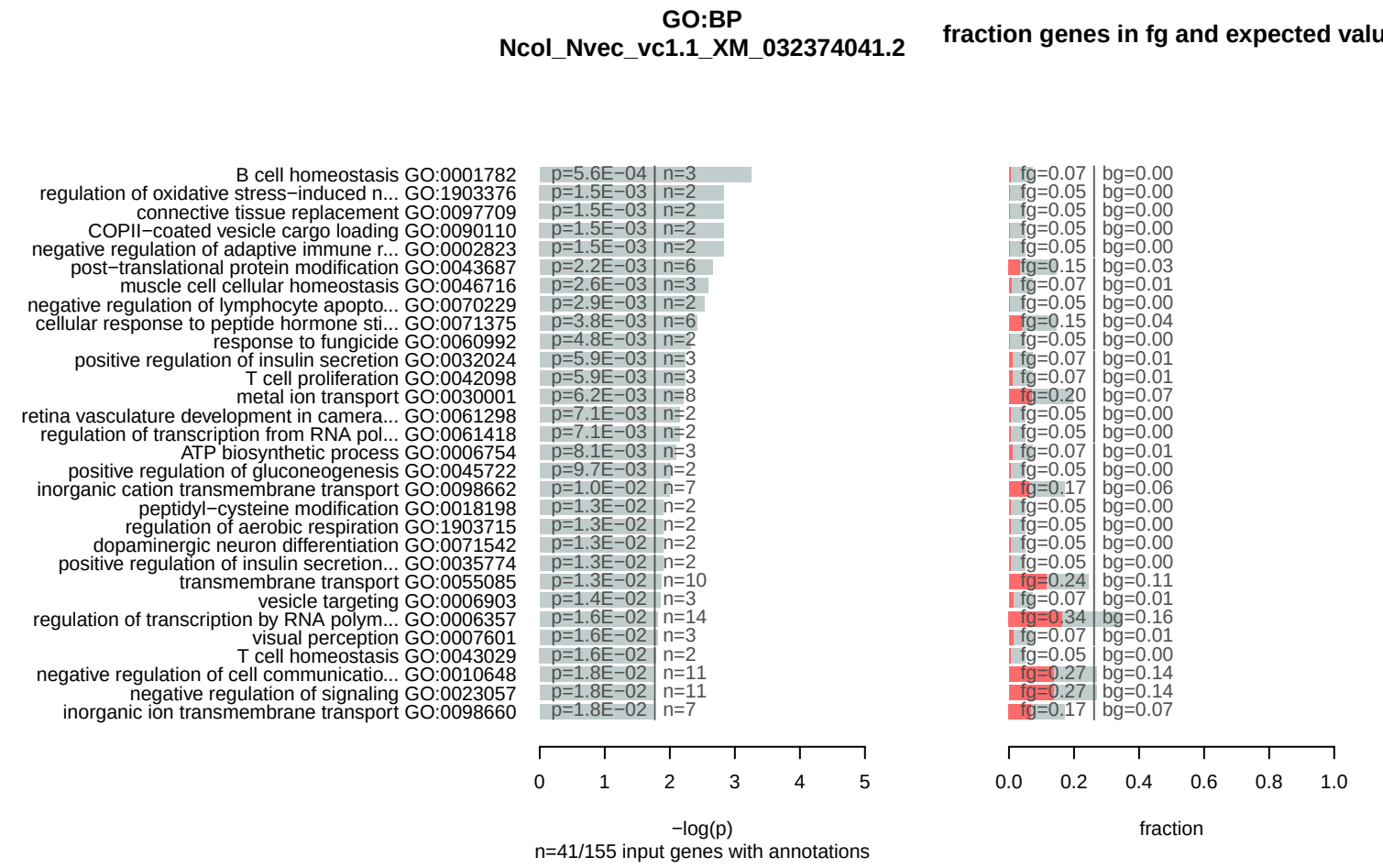
GO:BP
Ncol_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
B cell homeostasis GO:0001782 p=5.6E−04 n=3 fg=0.07 bg=0.00
regulation of oxidative stress−induced n... GO:1903376 p=1.5E−03 n=2 fg=0.05 bg=0.00
connective tissue replacement GO:0097709 p=1.5E−03 n=2 fg=0.05 bg=0.00
COPII−coated vesicle cargo loading GO:0090110 p=1.5E−03 n=2 fg=0.05 bg=0.00
negative regulation of adaptive immune r... GO:0002823 p=1.5E−03 n=2 fg=0.05 bg=0.00
post−translational protein modification GO:0043687 p=2.2E−03 n=6 fg=0.15 bg=0.03
muscle cell cellular homeostasis GO:0046716 p=2.6E−03 n=3 fg=0.07 bg=0.01
negative regulation of lymphocyte apopto... GO:0070229 p=2.9E−03 n=2 fg=0.05 bg=0.00
cellular response to peptide hormone sti... GO:0071375 p=3.8E−03 n=6 fg=0.15 bg=0.04
response to fungicide GO:0060992 p=4.8E−03 n=2 fg=0.05 bg=0.00
positive regulation of insulin secretion GO:0032024 p=5.9E−03 n=3 fg=0.07 bg=0.01
T cell proliferation GO:0042098 p=5.9E−03 n=3 fg=0.07 bg=0.01
metal ion transport GO:0030001 p=6.2E−03 n=8 fg=0.20 bg=0.07
retina vasculature development in camera... GO:0061298 p=7.1E−03 n=2 fg=0.05 bg=0.00
regulation of transcription from RNA pol... GO:0061418 p=7.1E−03 n=2 fg=0.05 bg=0.00
ATP biosynthetic process GO:0006754 p=8.1E−03 n=3 fg=0.07 bg=0.01
positive regulation of gluconeogenesis GO:0045722 p=9.7E−03 n=2 fg=0.05 bg=0.00
inorganic cation transmembrane transport GO:0098662 p=1.0E−02 n=7 fg=0.17 bg=0.06
peptidyl−cysteine modification GO:0018198 p=1.3E−02 n=2 fg=0.05 bg=0.00
regulation of aerobic respiration GO:1903715 p=1.3E−02 n=2 fg=0.05 bg=0.00
dopaminergic neuron differentiation GO:0071542 p=1.3E−02 n=2 fg=0.05 bg=0.00
positive regulation of insulin secretion... GO:0035774 p=1.3E−02 n=2 fg=0.05 bg=0.00
transmembrane transport GO:0055085 p=1.3E−02 n=10 fg=0.24 bg=0.11
vesicle targeting GO:0006903 p=1.4E−02 n=3 fg=0.07 bg=0.01
regulation of transcription by RNA polym... GO:0006357 p=1.6E−02 n=14 fg=0.34 bg=0.16
visual perception GO:0007601 p=1.6E−02 n=3 fg=0.07 bg=0.01
T cell homeostasis GO:0043029 p=1.6E−02 n=2 fg=0.05 bg=0.00
negative regulation of cell communicatio... GO:0010648 p=1.8E−02 n=11 fg=0.27 bg=0.14
negative regulation of signaling GO:0023057 p=1.8E−02 n=11 fg=0.27 bg=0.14
inorganic ion transmembrane transport GO:0098660 p=1.8E−02 n=7 fg=0.17 bg=0.07
0 1 2 3 4 5
−log(p)
n=41/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
protein−cysteine S−palmitoyltransferase ... GO:0019706 p=6.2E−04 n=2 fg=0.05 bg=0.00
channel activity GO:0015267 p=3.7E−03 n=6 fg=0.15 bg=0.04
inorganic molecular entity transmembrane... GO:0015318 p=5.4E−03 n=8 fg=0.20 bg=0.07
ion transmembrane transporter activity GO:0015075 p=6.6E−03 n=8 fg=0.20 bg=0.07
neurotransmitter transmembrane transport... GO:0005326 p=8.7E−03 n=2 fg=0.05 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=1.3E−02 n=8 fg=0.20 bg=0.08
DNA−binding transcription factor activit... GO:0000981 p=1.5E−02 n=7 fg=0.17 bg=0.07
ion channel activity GO:0005216 p=1.5E−02 n=5 fg=0.12 bg=0.04
inorganic cation transmembrane transport... GO:0022890 p=1.7E−02 n=6 fg=0.15 bg=0.05
metal ion binding GO:0046872 p=1.9E−02 n=9 fg=0.23 bg=0.11
ion gated channel activity GO:0022839 p=1.9E−02 n=4 fg=0.10 bg=0.03
calcium channel regulator activity GO:0005246 p=2.0E−02 n=2 fg=0.05 bg=0.01
cation transmembrane transporter activit... GO:0008324 p=2.0E−02 n=6 fg=0.15 bg=0.06
voltage−gated channel activity GO:0022832 p=2.1E−02 n=3 fg=0.07 bg=0.01
voltage−gated ion channel activity GO:0005244 p=2.1E−02 n=3 fg=0.07 bg=0.01
gated channel activity GO:0022836 p=2.2E−02 n=4 fg=0.10 bg=0.03
ion binding GO:0043167 p=2.4E−02 n=14 fg=0.35 bg=0.21
cobalt ion binding GO:0050897 p=2.5E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acid binding GO:0036041 p=2.5E−02 n=1 fg=0.03 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.5E−02 n=1 fg=0.03 bg=0.00
stearic acid binding GO:0070540 p=2.5E−02 n=1 fg=0.03 bg=0.00
DNA topoisomerase binding GO:0044547 p=2.5E−02 n=1 fg=0.03 bg=0.00
icosanoid binding GO:0050542 p=2.5E−02 n=1 fg=0.03 bg=0.00
icosatetraenoic acid binding GO:0050543 p=2.5E−02 n=1 fg=0.03 bg=0.00
arachidonic acid binding GO:0050544 p=2.5E−02 n=1 fg=0.03 bg=0.00
CoA carboxylase activity GO:0016421 p=2.5E−02 n=1 fg=0.03 bg=0.00
acetylcholine transmembrane transporter ... GO:0005277 p=2.5E−02 n=1 fg=0.03 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=2.5E−02 n=1 fg=0.03 bg=0.00
acetate ester transmembrane transporter ... GO:1901375 p=2.5E−02 n=1 fg=0.03 bg=0.00
calmodulin−dependent protein phosphatase... GO:0033192 p=2.5E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=40/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
ficolin−1−rich granule GO:0101002 p=2.7E−03 n=4 fg=0.10 bg=0.01
cytoplasmic ubiquitin ligase complex GO:0000153 p=7.1E−03 n=2 fg=0.05 bg=0.00
ficolin−1−rich granule lumen GO:1904813 p=1.1E−02 n=3 fg=0.07 bg=0.01
sarcolemma GO:0042383 p=1.1E−02 n=3 fg=0.07 bg=0.01
proteasome accessory complex GO:0022624 p=1.3E−02 n=2 fg=0.05 bg=0.00
proteasome regulatory particle GO:0005838 p=1.3E−02 n=2 fg=0.05 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=1.4E−02 n=8 fg=0.20 bg=0.08
brush border GO:0005903 p=1.6E−02 n=3 fg=0.07 bg=0.01
melanosome GO:0042470 p=1.6E−02 n=2 fg=0.05 bg=0.00
endoplasmic reticulum−Golgi intermediate... GO:0033116 p=1.6E−02 n=2 fg=0.05 bg=0.00
pigment granule GO:0048770 p=2.0E−02 n=2 fg=0.05 bg=0.01
T−tubule GO:0030315 p=2.0E−02 n=2 fg=0.05 bg=0.01
syntrophin complex GO:0016013 p=2.3E−02 n=1 fg=0.02 bg=0.00
calcineurin complex GO:0005955 p=2.3E−02 n=1 fg=0.02 bg=0.00
cluster of actin−based cell projections GO:0098862 p=2.4E−02 n=3 fg=0.07 bg=0.02
proteasome complex GO:0000502 p=2.4E−02 n=2 fg=0.05 bg=0.01
postsynapse GO:0098794 p=2.8E−02 n=5 fg=0.12 bg=0.04
integral component of plasma membrane GO:0005887 p=3.0E−02 n=7 fg=0.17 bg=0.08
transport vesicle membrane GO:0030658 p=3.1E−02 n=3 fg=0.07 bg=0.02
plasma membrane GO:0005886 p=3.2E−02 n=17 fg=0.41 bg=0.27
brush border membrane GO:0031526 p=3.3E−02 n=2 fg=0.05 bg=0.01
endopeptidase complex GO:1905369 p=3.8E−02 n=2 fg=0.05 bg=0.01
cell junction GO:0030054 p=4.1E−02 n=10 fg=0.24 bg=0.13
synapse GO:0045202 p=4.3E−02 n=8 fg=0.20 bg=0.10
protein serine/threonine phosphatase com... GO:0008287 p=4.4E−02 n=2 fg=0.05 bg=0.01
endoplasmic reticulum chaperone complex GO:0034663 p=4.5E−02 n=1 fg=0.02 bg=0.00
proteasome regulatory particle, lid subc... GO:0008541 p=4.5E−02 n=1 fg=0.02 bg=0.00
VCB complex GO:0030891 p=4.5E−02 n=1 fg=0.02 bg=0.00
phagophore assembly site membrane GO:0034045 p=4.5E−02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=4.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=41/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction