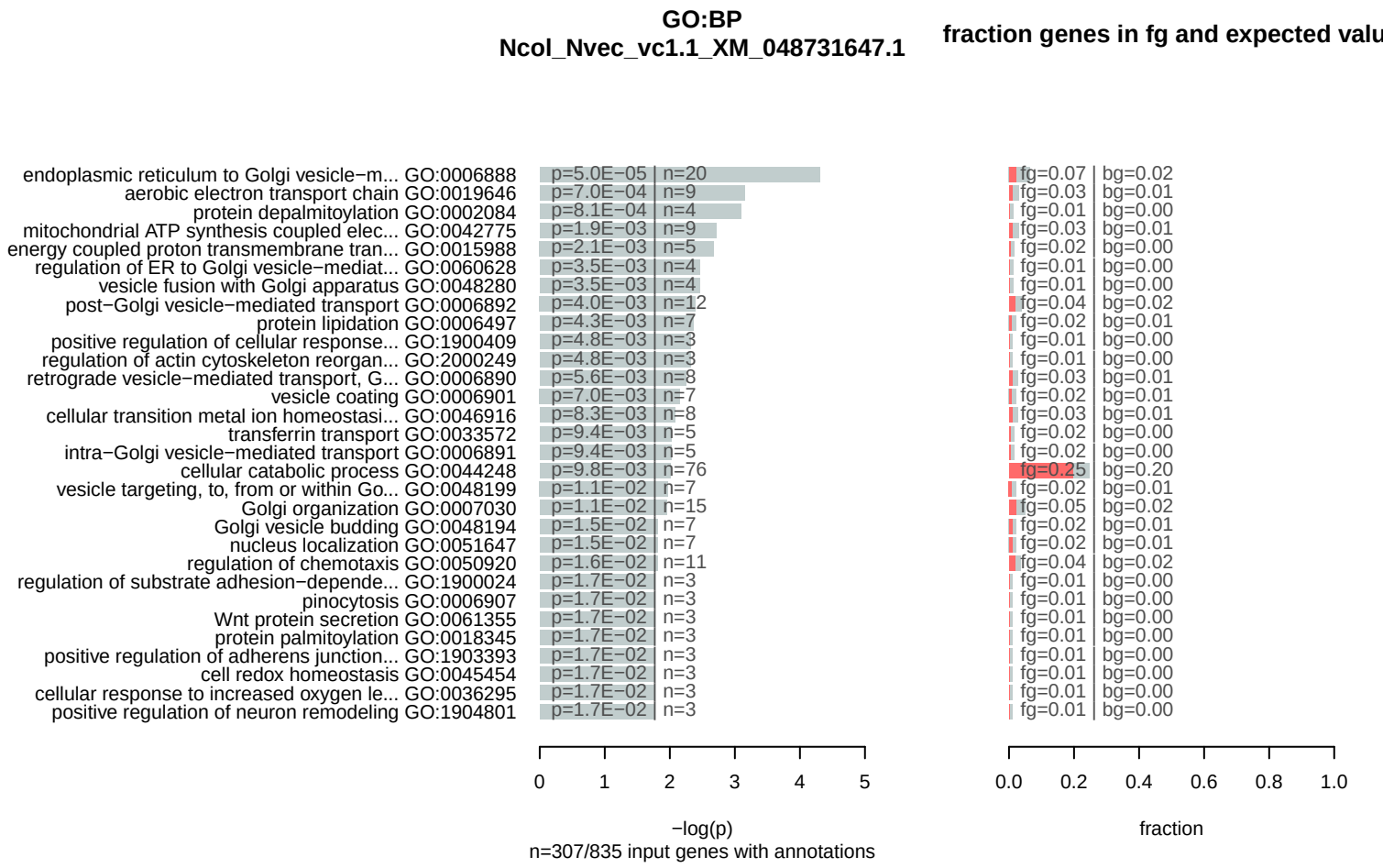
GO:BP
Ncol_Nvec_vc1.1_XM_048731647.1
fraction genes in fg and expected valu
endoplasmic reticulum to Golgi vesicle−m... GO:0006888 p=5.0E−05 n=20 fg=0.07 bg=0.02
aerobic electron transport chain GO:0019646 p=7.0E−04 n=9 fg=0.03 bg=0.01
protein depalmitoylation GO:0002084 p=8.1E−04 n=4 fg=0.01 bg=0.00
mitochondrial ATP synthesis coupled elec... GO:0042775 p=1.9E−03 n=9 fg=0.03 bg=0.01
energy coupled proton transmembrane tran... GO:0015988 p=2.1E−03 n=5 fg=0.02 bg=0.00
regulation of ER to Golgi vesicle−mediat... GO:0060628 p=3.5E−03 n=4 fg=0.01 bg=0.00
vesicle fusion with Golgi apparatus GO:0048280 p=3.5E−03 n=4 fg=0.01 bg=0.00
post−Golgi vesicle−mediated transport GO:0006892 p=4.0E−03 n=12 fg=0.04 bg=0.02
protein lipidation GO:0006497 p=4.3E−03 n=7 fg=0.02 bg=0.01
positive regulation of cellular response... GO:1900409 p=4.8E−03 n=3 fg=0.01 bg=0.00
regulation of actin cytoskeleton reorgan... GO:2000249 p=4.8E−03 n=3 fg=0.01 bg=0.00
retrograde vesicle−mediated transport, G... GO:0006890 p=5.6E−03 n=8 fg=0.03 bg=0.01
vesicle coating GO:0006901 p=7.0E−03 n=7 fg=0.02 bg=0.01
cellular transition metal ion homeostasi... GO:0046916 p=8.3E−03 n=8 fg=0.03 bg=0.01
transferrin transport GO:0033572 p=9.4E−03 n=5 fg=0.02 bg=0.00
intra−Golgi vesicle−mediated transport GO:0006891 p=9.4E−03 n=5 fg=0.02 bg=0.00
cellular catabolic process GO:0044248 p=9.8E−03 n=76 fg=0.25 bg=0.20
vesicle targeting, to, from or within Go... GO:0048199 p=1.1E−02 n=7 fg=0.02 bg=0.01
Golgi organization GO:0007030 p=1.1E−02 n=15 fg=0.05 bg=0.02
Golgi vesicle budding GO:0048194 p=1.5E−02 n=7 fg=0.02 bg=0.01
nucleus localization GO:0051647 p=1.5E−02 n=7 fg=0.02 bg=0.01
regulation of chemotaxis GO:0050920 p=1.6E−02 n=11 fg=0.04 bg=0.02
regulation of substrate adhesion−depende... GO:1900024 p=1.7E−02 n=3 fg=0.01 bg=0.00
pinocytosis GO:0006907 p=1.7E−02 n=3 fg=0.01 bg=0.00
Wnt protein secretion GO:0061355 p=1.7E−02 n=3 fg=0.01 bg=0.00
protein palmitoylation GO:0018345 p=1.7E−02 n=3 fg=0.01 bg=0.00
positive regulation of adherens junction... GO:1903393 p=1.7E−02 n=3 fg=0.01 bg=0.00
cell redox homeostasis GO:0045454 p=1.7E−02 n=3 fg=0.01 bg=0.00
cellular response to increased oxygen le... GO:0036295 p=1.7E−02 n=3 fg=0.01 bg=0.00
positive regulation of neuron remodeling GO:1904801 p=1.7E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=307/835 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048731647.1
fraction genes in fg and expected valu
palmitoyl−(protein) hydrolase activity GO:0008474 p=7.9E−04 n=4 fg=0.01 bg=0.00
ubiquitin protein ligase binding GO:0031625 p=3.4E−03 n=20 fg=0.07 bg=0.04
protein disulfide isomerase activity GO:0003756 p=3.4E−03 n=4 fg=0.01 bg=0.00
proton transmembrane transporter activit... GO:0015078 p=3.5E−03 n=8 fg=0.03 bg=0.01
electron transfer activity GO:0009055 p=4.3E−03 n=9 fg=0.03 bg=0.01
SNAP receptor activity GO:0005484 p=4.7E−03 n=6 fg=0.02 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=4.7E−03 n=6 fg=0.02 bg=0.01
primary active transmembrane transporter... GO:0015399 p=1.1E−02 n=12 fg=0.04 bg=0.02
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=1.7E−02 n=3 fg=0.01 bg=0.00
oxidoreduction−driven active transmembra... GO:0015453 p=1.9E−02 n=6 fg=0.02 bg=0.01
PTB domain binding GO:0051425 p=2.8E−02 n=2 fg=0.01 bg=0.00
dipeptidase activity GO:0016805 p=2.8E−02 n=2 fg=0.01 bg=0.00
caspase binding GO:0089720 p=2.8E−02 n=2 fg=0.01 bg=0.00
tRNA (guanine) methyltransferase activit... GO:0016423 p=2.8E−02 n=2 fg=0.01 bg=0.00
catalytic activity, acting on a protein GO:0140096 p=3.3E−02 n=73 fg=0.27 bg=0.20
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=3.6E−02 n=3 fg=0.01 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=3.6E−02 n=3 fg=0.01 bg=0.00
flavin adenine dinucleotide binding GO:0050660 p=3.6E−02 n=3 fg=0.01 bg=0.00
ubiquitin−ubiquitin ligase activity GO:0034450 p=3.6E−02 n=3 fg=0.01 bg=0.00
proton−transporting ATPase activity, rot... GO:0046961 p=3.6E−02 n=3 fg=0.01 bg=0.00
ubiquitin−like protein ligase activity GO:0061659 p=4.4E−02 n=15 fg=0.06 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=4.4E−02 n=15 fg=0.06 bg=0.04
SNARE binding GO:0000149 p=5.2E−02 n=9 fg=0.03 bg=0.02
demethylase activity GO:0032451 p=6.4E−02 n=3 fg=0.01 bg=0.00
phosphatidylinositol phosphate phosphata... GO:0052866 p=6.4E−02 n=3 fg=0.01 bg=0.00
signaling receptor activator activity GO:0030546 p=6.4E−02 n=3 fg=0.01 bg=0.00
receptor ligand activity GO:0048018 p=6.4E−02 n=3 fg=0.01 bg=0.00
NADH dehydrogenase activity GO:0003954 p=7.1E−02 n=4 fg=0.01 bg=0.01
calmodulin−dependent protein kinase acti... GO:0004683 p=7.1E−02 n=4 fg=0.01 bg=0.01
small GTPase binding GO:0031267 p=7.2E−02 n=20 fg=0.07 bg=0.05
0 1 2 3 4 5
−log(p)
n=268/835 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048731647.1
fraction genes in fg and expected valu
inner mitochondrial membrane protein com... GO:0098800 p=8.6E−05 n=13 fg=0.04 bg=0.01
cytoplasm GO:0005737 p=4.2E−04 n=271 fg=0.89 bg=0.80
plasma membrane proton−transporting V−ty... GO:0033181 p=6.7E−04 n=5 fg=0.02 bg=0.00
phagocytic vesicle membrane GO:0030670 p=1.1E−03 n=6 fg=0.02 bg=0.00
endoplasmic reticulum protein−containing... GO:0140534 p=1.2E−03 n=11 fg=0.04 bg=0.01
trans−Golgi network membrane GO:0032588 p=2.8E−03 n=12 fg=0.04 bg=0.02
endoplasmic reticulum membrane GO:0005789 p=3.1E−03 n=36 fg=0.12 bg=0.08
respiratory chain complex GO:0098803 p=4.5E−03 n=9 fg=0.03 bg=0.01
endosome membrane GO:0010008 p=5.4E−03 n=19 fg=0.06 bg=0.03
mitochondrial respiratory chain complex ... GO:0005747 p=8.0E−03 n=6 fg=0.02 bg=0.01
Golgi membrane GO:0000139 p=1.0E−02 n=28 fg=0.09 bg=0.06
COPII−coated ER to Golgi transport vesic... GO:0030134 p=1.3E−02 n=6 fg=0.02 bg=0.01
intrinsic component of organelle membran... GO:0031300 p=1.4E−02 n=21 fg=0.07 bg=0.04
intrinsic component of mitochondrial inn... GO:0031304 p=1.6E−02 n=3 fg=0.01 bg=0.00
integral component of mitochondrial inne... GO:0031305 p=1.6E−02 n=3 fg=0.01 bg=0.00
membrane protein complex GO:0098796 p=1.7E−02 n=48 fg=0.16 bg=0.09
vacuolar proton−transporting V−type ATPa... GO:0016471 p=1.8E−02 n=4 fg=0.01 bg=0.00
SNARE complex GO:0031201 p=1.9E−02 n=6 fg=0.02 bg=0.01
integral component of organelle membrane GO:0031301 p=2.2E−02 n=20 fg=0.07 bg=0.04
cytosol GO:0005829 p=2.4E−02 n=134 fg=0.44 bg=0.39
proton−transporting two−sector ATPase co... GO:0033177 p=2.8E−02 n=2 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=2.8E−02 n=2 fg=0.01 bg=0.00
endoplasmic reticulum chaperone complex GO:0034663 p=2.8E−02 n=2 fg=0.01 bg=0.00
Golgi transport complex GO:0017119 p=2.8E−02 n=2 fg=0.01 bg=0.00
mitochondrial respiratory chain complex ... GO:0005750 p=2.8E−02 n=2 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=2.8E−02 n=2 fg=0.01 bg=0.00
nuclear stress granule GO:0097165 p=2.8E−02 n=2 fg=0.01 bg=0.00
m−AAA complex GO:0005745 p=2.8E−02 n=2 fg=0.01 bg=0.00
ionotropic glutamate receptor complex GO:0008328 p=2.8E−02 n=2 fg=0.01 bg=0.00
platelet alpha granule membrane GO:0031092 p=2.8E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=304/835 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction