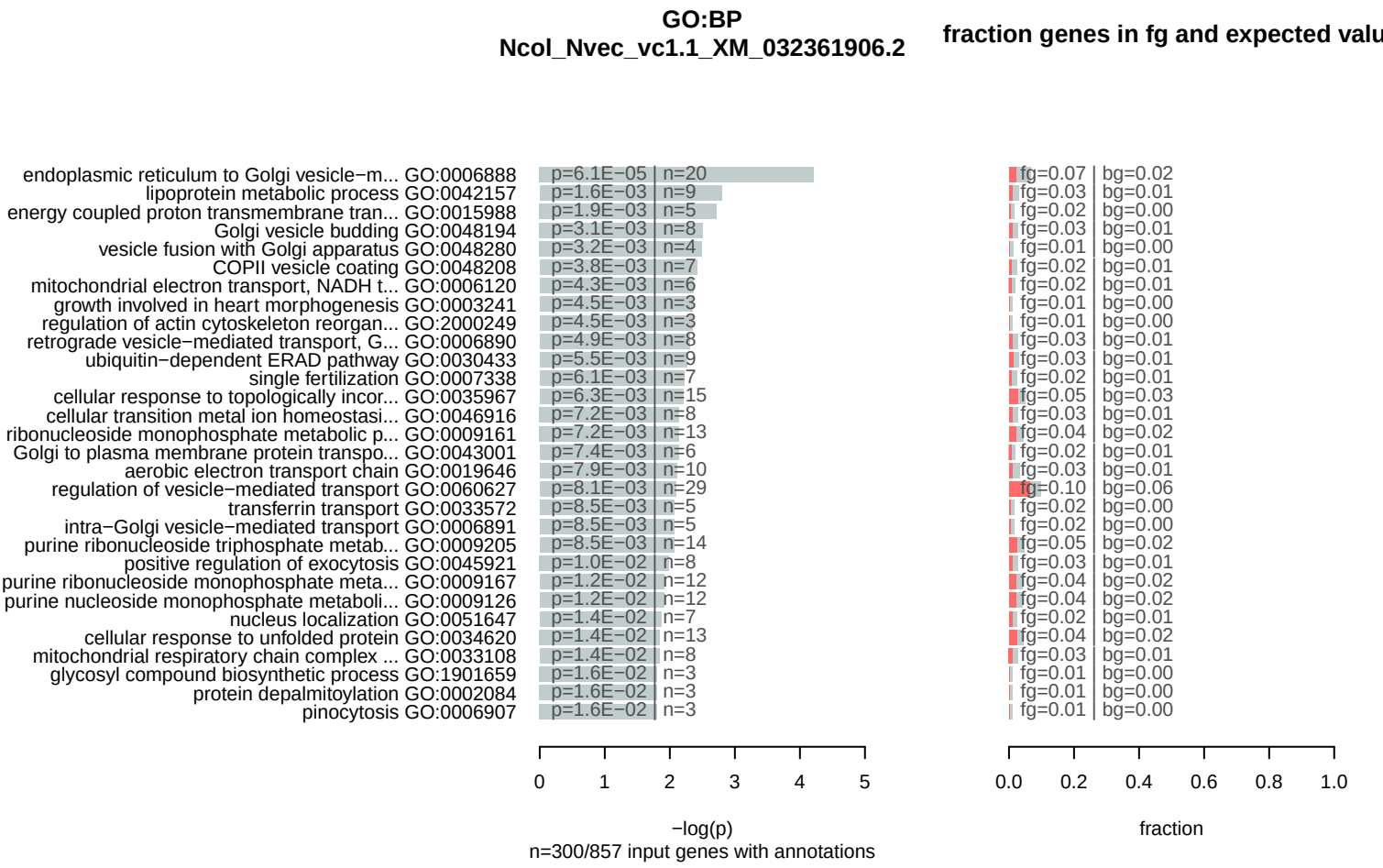
GO:BP
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fraction genes in fg and expected valu
endoplasmic reticulum to Golgi vesicle−m... GO:0006888 p=6.1E−05 n=20 fg=0.07 bg=0.02
lipoprotein metabolic process GO:0042157 p=1.6E−03 n=9 fg=0.03 bg=0.01
energy coupled proton transmembrane tran... GO:0015988 p=1.9E−03 n=5 fg=0.02 bg=0.00
Golgi vesicle budding GO:0048194 p=3.1E−03 n=8 fg=0.03 bg=0.01
vesicle fusion with Golgi apparatus GO:0048280 p=3.2E−03 n=4 fg=0.01 bg=0.00
COPII vesicle coating GO:0048208 p=3.8E−03 n=7 fg=0.02 bg=0.01
mitochondrial electron transport, NADH t... GO:0006120 p=4.3E−03 n=6 fg=0.02 bg=0.01
growth involved in heart morphogenesis GO:0003241 p=4.5E−03 n=3 fg=0.01 bg=0.00
regulation of actin cytoskeleton reorgan... GO:2000249 p=4.5E−03 n=3 fg=0.01 bg=0.00
retrograde vesicle−mediated transport, G... GO:0006890 p=4.9E−03 n=8 fg=0.03 bg=0.01
ubiquitin−dependent ERAD pathway GO:0030433 p=5.5E−03 n=9 fg=0.03 bg=0.01
single fertilization GO:0007338 p=6.1E−03 n=7 fg=0.02 bg=0.01
cellular response to topologically incor... GO:0035967 p=6.3E−03 n=15 fg=0.05 bg=0.03
cellular transition metal ion homeostasi... GO:0046916 p=7.2E−03 n=8 fg=0.03 bg=0.01
ribonucleoside monophosphate metabolic p... GO:0009161 p=7.2E−03 n=13 fg=0.04 bg=0.02
Golgi to plasma membrane protein transpo... GO:0043001 p=7.4E−03 n=6 fg=0.02 bg=0.01
aerobic electron transport chain GO:0019646 p=7.9E−03 n=10 fg=0.03 bg=0.01
regulation of vesicle−mediated transport GO:0060627 p=8.1E−03 n=29 fg=0.10 bg=0.06
transferrin transport GO:0033572 p=8.5E−03 n=5 fg=0.02 bg=0.00
intra−Golgi vesicle−mediated transport GO:0006891 p=8.5E−03 n=5 fg=0.02 bg=0.00
purine ribonucleoside triphosphate metab... GO:0009205 p=8.5E−03 n=14 fg=0.05 bg=0.02
positive regulation of exocytosis GO:0045921 p=1.0E−02 n=8 fg=0.03 bg=0.01
purine ribonucleoside monophosphate meta... GO:0009167 p=1.2E−02 n=12 fg=0.04 bg=0.02
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nucleus localization GO:0051647 p=1.4E−02 n=7 fg=0.02 bg=0.01
cellular response to unfolded protein GO:0034620 p=1.4E−02 n=13 fg=0.04 bg=0.02
mitochondrial respiratory chain complex ... GO:0033108 p=1.4E−02 n=8 fg=0.03 bg=0.01
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fraction
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fraction genes in fg and expected valu
electron transfer activity GO:0009055 p=6.4E−04 n=10 fg=0.04 bg=0.01
ubiquitin protein ligase binding GO:0031625 p=6.7E−04 n=21 fg=0.08 bg=0.04
proton transmembrane transporter activit... GO:0015078 p=2.5E−03 n=8 fg=0.03 bg=0.01
oxidoreduction−driven active transmembra... GO:0015453 p=3.1E−03 n=7 fg=0.03 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=3.6E−03 n=6 fg=0.02 bg=0.01
catalytic activity, acting on a protein GO:0140096 p=1.1E−02 n=68 fg=0.27 bg=0.20
NADH dehydrogenase activity GO:0003954 p=1.3E−02 n=5 fg=0.02 bg=0.01
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=1.4E−02 n=3 fg=0.01 bg=0.00
palmitoyl−(protein) hydrolase activity GO:0008474 p=1.4E−02 n=3 fg=0.01 bg=0.00
RNA polymerase II general transcription ... GO:0001091 p=1.4E−02 n=3 fg=0.01 bg=0.00
palmitoyl hydrolase activity GO:0098599 p=1.4E−02 n=3 fg=0.01 bg=0.00
SNAP receptor activity GO:0005484 p=2.0E−02 n=5 fg=0.02 bg=0.01
thiolester hydrolase activity GO:0016790 p=2.0E−02 n=5 fg=0.02 bg=0.01
PTB domain binding GO:0051425 p=2.6E−02 n=2 fg=0.01 bg=0.00
dipeptidase activity GO:0016805 p=2.6E−02 n=2 fg=0.01 bg=0.00
tRNA (guanine) methyltransferase activit... GO:0016423 p=2.6E−02 n=2 fg=0.01 bg=0.00
zinc ion binding GO:0008270 p=2.6E−02 n=19 fg=0.07 bg=0.05
ubiquitin−like protein ligase activity GO:0061659 p=2.9E−02 n=15 fg=0.06 bg=0.04
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oxidoreductase activity, acting on NAD(P... GO:0016651 p=3.0E−02 n=7 fg=0.03 bg=0.01
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=3.2E−02 n=3 fg=0.01 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016864 p=3.2E−02 n=3 fg=0.01 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=3.2E−02 n=3 fg=0.01 bg=0.00
flavin adenine dinucleotide binding GO:0050660 p=3.2E−02 n=3 fg=0.01 bg=0.00
ubiquitin−ubiquitin ligase activity GO:0034450 p=3.2E−02 n=3 fg=0.01 bg=0.00
proton−transporting ATPase activity, rot... GO:0046961 p=3.2E−02 n=3 fg=0.01 bg=0.00
protein disulfide isomerase activity GO:0003756 p=3.2E−02 n=3 fg=0.01 bg=0.00
NADH dehydrogenase (quinone) activity GO:0050136 p=4.2E−02 n=4 fg=0.02 bg=0.01
NAD(P)H dehydrogenase (quinone) activity GO:0003955 p=4.2E−02 n=4 fg=0.02 bg=0.01
oxidoreductase activity, acting on NAD(P... GO:0016655 p=4.2E−02 n=4 fg=0.02 bg=0.01
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032361906.2
fraction genes in fg and expected valu
plasma membrane proton−transporting V−ty... GO:0033181 p=6.0E−04 n=5 fg=0.02 bg=0.00
phagocytic vesicle membrane GO:0030670 p=1.0E−03 n=6 fg=0.02 bg=0.00
mitochondrial respiratory chain complex ... GO:0005747 p=1.1E−03 n=7 fg=0.02 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=1.4E−03 n=39 fg=0.13 bg=0.08
cytoplasm GO:0005737 p=1.7E−03 n=261 fg=0.88 bg=0.80
COPII−coated ER to Golgi transport vesic... GO:0030134 p=2.1E−03 n=7 fg=0.02 bg=0.01
oxidoreductase complex GO:1990204 p=3.9E−03 n=12 fg=0.04 bg=0.01
respiratory chain complex GO:0098803 p=4.2E−03 n=10 fg=0.03 bg=0.01
site of double−strand break GO:0035861 p=4.2E−03 n=5 fg=0.02 bg=0.00
inner mitochondrial membrane protein com... GO:0098800 p=7.6E−03 n=12 fg=0.04 bg=0.01
Derlin−1 retrotranslocation complex GO:0036513 p=8.1E−03 n=4 fg=0.01 bg=0.00
intrinsic component of endoplasmic retic... GO:0031227 p=1.1E−02 n=13 fg=0.04 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=1.1E−02 n=13 fg=0.04 bg=0.02
cytosol GO:0005829 p=1.3E−02 n=133 fg=0.45 bg=0.39
Golgi apparatus GO:0005794 p=1.4E−02 n=52 fg=0.18 bg=0.13
vacuolar proton−transporting V−type ATPa... GO:0016471 p=1.7E−02 n=4 fg=0.01 bg=0.00
ER to Golgi transport vesicle membrane GO:0012507 p=1.7E−02 n=4 fg=0.01 bg=0.00
endomembrane system GO:0012505 p=1.7E−02 n=127 fg=0.43 bg=0.34
Golgi−associated vesicle membrane GO:0030660 p=1.7E−02 n=6 fg=0.02 bg=0.01
Golgi apparatus subcompartment GO:0098791 p=1.8E−02 n=34 fg=0.11 bg=0.08
trans−Golgi network membrane GO:0032588 p=2.2E−02 n=10 fg=0.03 bg=0.02
intrinsic component of organelle membran... GO:0031300 p=2.2E−02 n=20 fg=0.07 bg=0.04
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Golgi−associated vesicle GO:0005798 p=2.5E−02 n=11 fg=0.04 bg=0.02
Golgi membrane GO:0000139 p=2.5E−02 n=26 fg=0.09 bg=0.06
proton−transporting two−sector ATPase co... GO:0033177 p=2.7E−02 n=2 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=2.7E−02 n=2 fg=0.01 bg=0.00
Golgi transport complex GO:0017119 p=2.7E−02 n=2 fg=0.01 bg=0.00
mitochondrial respiratory chain complex ... GO:0005750 p=2.7E−02 n=2 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=2.7E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=297/857 input genes with annotations
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fraction