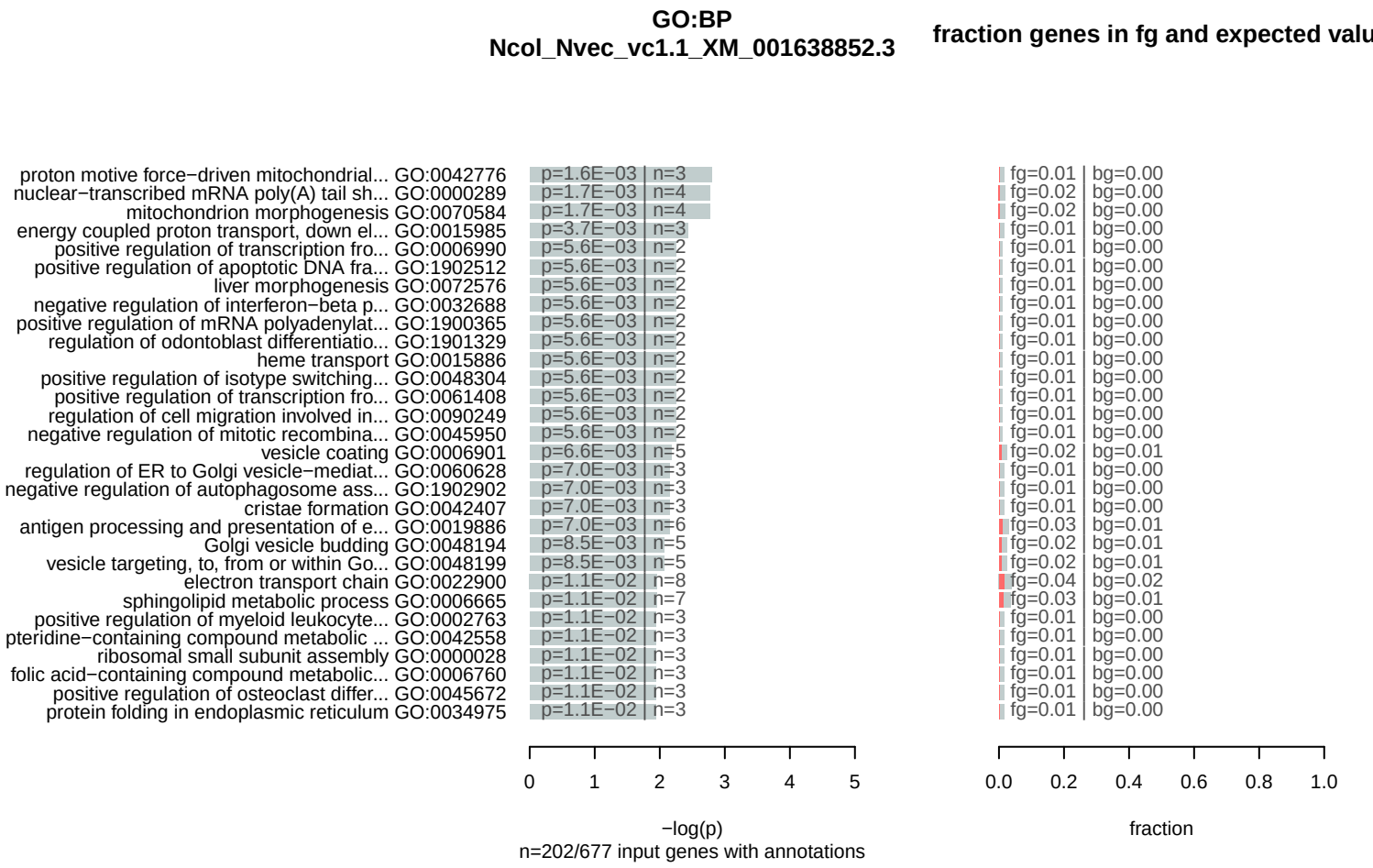
GO:BP
Ncol_Nvec_vc1.1_XM_001638852.3
fraction genes in fg and expected valu
proton motive force−driven mitochondrial... GO:0042776 p=1.6E−03 n=3 fg=0.01 bg=0.00
nuclear−transcribed mRNA poly(A) tail sh... GO:0000289 p=1.7E−03 n=4 fg=0.02 bg=0.00
mitochondrion morphogenesis GO:0070584 p=1.7E−03 n=4 fg=0.02 bg=0.00
energy coupled proton transport, down el... GO:0015985 p=3.7E−03 n=3 fg=0.01 bg=0.00
positive regulation of transcription fro... GO:0006990 p=5.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of apoptotic DNA fra... GO:1902512 p=5.6E−03 n=2 fg=0.01 bg=0.00
liver morphogenesis GO:0072576 p=5.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of interferon−beta p... GO:0032688 p=5.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of mRNA polyadenylat... GO:1900365 p=5.6E−03 n=2 fg=0.01 bg=0.00
regulation of odontoblast differentiatio... GO:1901329 p=5.6E−03 n=2 fg=0.01 bg=0.00
heme transport GO:0015886 p=5.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of isotype switching... GO:0048304 p=5.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of transcription fro... GO:0061408 p=5.6E−03 n=2 fg=0.01 bg=0.00
regulation of cell migration involved in... GO:0090249 p=5.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of mitotic recombina... GO:0045950 p=5.6E−03 n=2 fg=0.01 bg=0.00
vesicle coating GO:0006901 p=6.6E−03 n=5 fg=0.02 bg=0.01
regulation of ER to Golgi vesicle−mediat... GO:0060628 p=7.0E−03 n=3 fg=0.01 bg=0.00
negative regulation of autophagosome ass... GO:1902902 p=7.0E−03 n=3 fg=0.01 bg=0.00
cristae formation GO:0042407 p=7.0E−03 n=3 fg=0.01 bg=0.00
antigen processing and presentation of e... GO:0019886 p=7.0E−03 n=6 fg=0.03 bg=0.01
Golgi vesicle budding GO:0048194 p=8.5E−03 n=5 fg=0.02 bg=0.01
vesicle targeting, to, from or within Go... GO:0048199 p=8.5E−03 n=5 fg=0.02 bg=0.01
electron transport chain GO:0022900 p=1.1E−02 n=8 fg=0.04 bg=0.02
sphingolipid metabolic process GO:0006665 p=1.1E−02 n=7 fg=0.03 bg=0.01
positive regulation of myeloid leukocyte... GO:0002763 p=1.1E−02 n=3 fg=0.01 bg=0.00
pteridine−containing compound metabolic ... GO:0042558 p=1.1E−02 n=3 fg=0.01 bg=0.00
ribosomal small subunit assembly GO:0000028 p=1.1E−02 n=3 fg=0.01 bg=0.00
folic acid−containing compound metabolic... GO:0006760 p=1.1E−02 n=3 fg=0.01 bg=0.00
positive regulation of osteoclast differ... GO:0045672 p=1.1E−02 n=3 fg=0.01 bg=0.00
protein folding in endoplasmic reticulum GO:0034975 p=1.1E−02 n=3 fg=0.01 bg=0.00
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001638852.3
fraction genes in fg and expected valu
cAMP response element binding protein bi... GO:0008140 p=5.9E−03 n=2 fg=0.01 bg=0.00
acyl−CoA dehydrogenase activity GO:0003995 p=5.9E−03 n=2 fg=0.01 bg=0.00
heme transmembrane transporter activity GO:0015232 p=5.9E−03 n=2 fg=0.01 bg=0.00
pre−mRNA intronic binding GO:0097157 p=1.7E−02 n=2 fg=0.01 bg=0.00
phenylalanine−tRNA ligase activity GO:0004826 p=1.7E−02 n=2 fg=0.01 bg=0.00
cAMP response element binding GO:0035497 p=1.7E−02 n=2 fg=0.01 bg=0.00
magnesium ion transmembrane transporter ... GO:0015095 p=1.7E−02 n=2 fg=0.01 bg=0.00
ATP hydrolysis activity GO:0016887 p=1.7E−02 n=15 fg=0.08 bg=0.05
ATP−dependent activity GO:0140657 p=2.0E−02 n=16 fg=0.09 bg=0.05
vitamin transmembrane transporter activi... GO:0090482 p=2.6E−02 n=3 fg=0.02 bg=0.00
acetylgalactosaminyltransferase activity GO:0008376 p=3.2E−02 n=2 fg=0.01 bg=0.00
transcription regulatory region nucleic ... GO:0001067 p=3.7E−02 n=16 fg=0.09 bg=0.05
core promoter sequence−specific DNA bind... GO:0001046 p=4.4E−02 n=4 fg=0.02 bg=0.01
nucleoside−triphosphatase activity GO:0017111 p=4.7E−02 n=19 fg=0.10 bg=0.07
azole transmembrane transporter activity GO:1901474 p=5.0E−02 n=2 fg=0.01 bg=0.00
intronic transcription regulatory region... GO:0001161 p=5.0E−02 n=2 fg=0.01 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=5.0E−02 n=2 fg=0.01 bg=0.00
poly(A) binding GO:0008143 p=5.0E−02 n=2 fg=0.01 bg=0.00
misfolded protein binding GO:0051787 p=5.0E−02 n=2 fg=0.01 bg=0.00
single−stranded RNA binding GO:0003727 p=5.1E−02 n=5 fg=0.03 bg=0.01
chromatin DNA binding GO:0031490 p=5.2E−02 n=4 fg=0.02 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=5.8E−02 n=10 fg=0.05 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=5.8E−02 n=10 fg=0.05 bg=0.03
flavin adenine dinucleotide binding GO:0050660 p=5.9E−02 n=3 fg=0.02 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=6.2E−02 n=16 fg=0.09 bg=0.06
heat shock protein binding GO:0031072 p=6.4E−02 n=7 fg=0.04 bg=0.02
hydrolase activity, acting on acid anhyd... GO:0016817 p=6.6E−02 n=19 fg=0.10 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016818 p=6.6E−02 n=19 fg=0.10 bg=0.07
pyrophosphatase activity GO:0016462 p=6.6E−02 n=19 fg=0.10 bg=0.07
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=7.2E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=182/677 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001638852.3
fraction genes in fg and expected valu
Golgi−associated vesicle GO:0005798 p=8.0E−04 n=10 fg=0.05 bg=0.02
protein phosphatase type 2A complex GO:0000159 p=4.0E−03 n=3 fg=0.01 bg=0.00
Prp19 complex GO:0000974 p=4.0E−03 n=3 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000275 p=5.9E−03 n=2 fg=0.01 bg=0.00
COPII vesicle coat GO:0030127 p=5.9E−03 n=2 fg=0.01 bg=0.00
phenylalanine−tRNA ligase complex GO:0009328 p=5.9E−03 n=2 fg=0.01 bg=0.00
intracellular organelle GO:0043229 p=1.4E−02 n=186 fg=0.89 bg=0.83
proton−transporting two−sector ATPase co... GO:0033177 p=1.7E−02 n=2 fg=0.01 bg=0.00
Bcl−2 family protein complex GO:0097136 p=1.7E−02 n=2 fg=0.01 bg=0.00
CCR4−NOT complex GO:0030014 p=1.7E−02 n=2 fg=0.01 bg=0.00
organelle GO:0043226 p=2.0E−02 n=188 fg=0.90 bg=0.85
euchromatin GO:0000791 p=2.4E−02 n=4 fg=0.02 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=2.6E−02 n=23 fg=0.11 bg=0.07
trans−Golgi network transport vesicle GO:0030140 p=2.7E−02 n=3 fg=0.01 bg=0.00
nuclear outer membrane−endoplasmic retic... GO:0042175 p=3.2E−02 n=23 fg=0.11 bg=0.07
organelle subcompartment GO:0031984 p=3.2E−02 n=35 fg=0.17 bg=0.12
small ribosomal subunit GO:0015935 p=3.3E−02 n=5 fg=0.02 bg=0.01
endoplasmic reticulum subcompartment GO:0098827 p=3.3E−02 n=23 fg=0.11 bg=0.07
membrane−bounded organelle GO:0043227 p=3.6E−02 n=178 fg=0.86 bg=0.80
ficolin−1−rich granule GO:0101002 p=4.3E−02 n=7 fg=0.03 bg=0.02
tertiary granule lumen GO:1904724 p=4.7E−02 n=3 fg=0.01 bg=0.00
ficolin−1−rich granule lumen GO:1904813 p=4.8E−02 n=6 fg=0.03 bg=0.01
clathrin−coated vesicle GO:0030136 p=4.8E−02 n=6 fg=0.03 bg=0.01
condensed chromosome GO:0000793 p=4.9E−02 n=9 fg=0.04 bg=0.02
sperm fibrous sheath GO:0035686 p=5.1E−02 n=2 fg=0.01 bg=0.00
nucleoplasm GO:0005654 p=5.3E−02 n=71 fg=0.34 bg=0.29
Golgi−associated vesicle membrane GO:0030660 p=5.3E−02 n=4 fg=0.02 bg=0.01
endomembrane system GO:0012505 p=5.3E−02 n=76 fg=0.37 bg=0.31
M band GO:0031430 p=5.9E−02 n=3 fg=0.01 bg=0.00
mitochondrial outer membrane GO:0005741 p=6.7E−02 n=6 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=208/677 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction