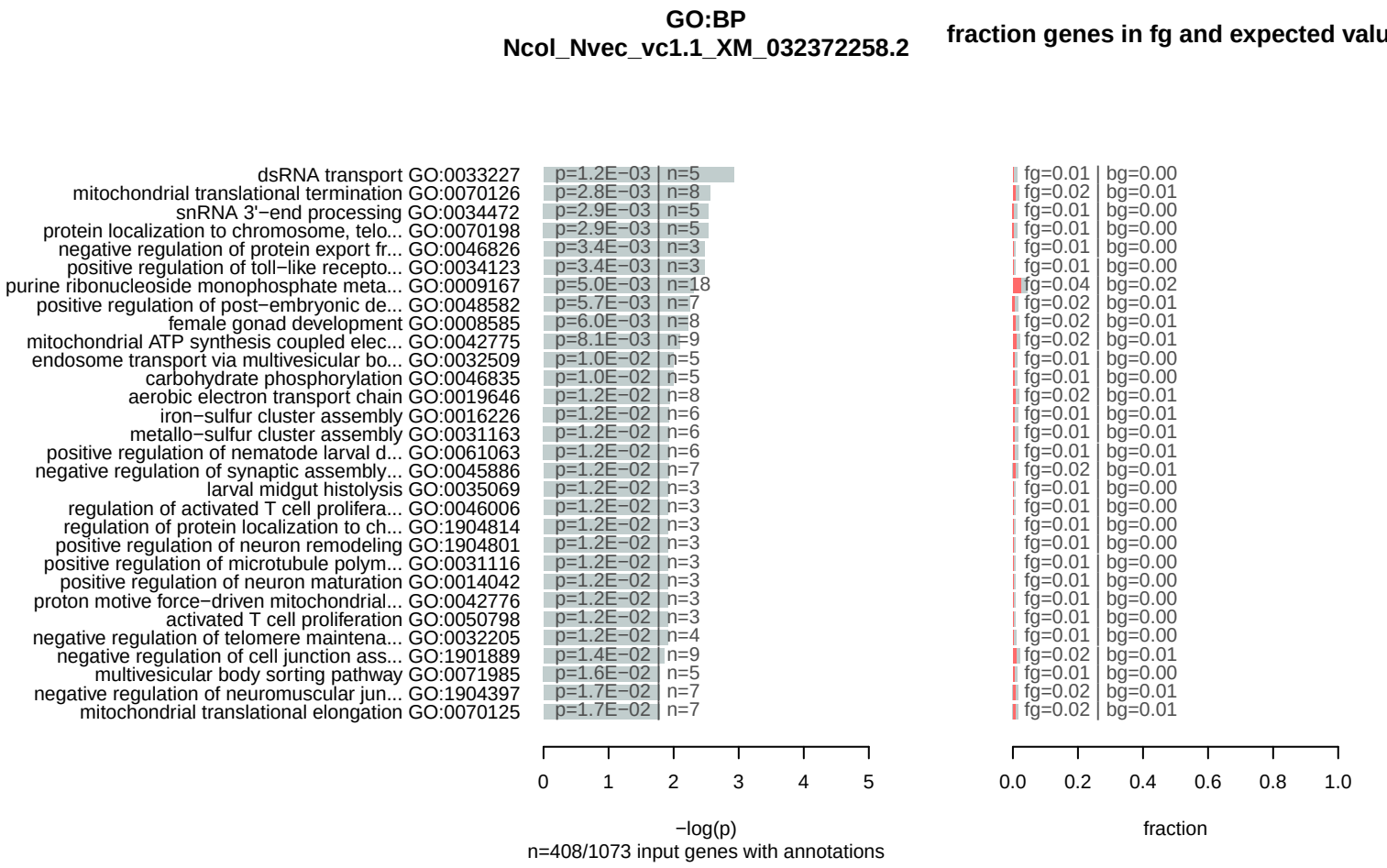
GO:BP
Ncol_Nvec_vc1.1_XM_032372258.2
fraction genes in fg and expected valu
dsRNA transport GO:0033227 p=1.2E−03 n=5 fg=0.01 bg=0.00
mitochondrial translational termination GO:0070126 p=2.8E−03 n=8 fg=0.02 bg=0.01
snRNA 3'−end processing GO:0034472 p=2.9E−03 n=5 fg=0.01 bg=0.00
protein localization to chromosome, telo... GO:0070198 p=2.9E−03 n=5 fg=0.01 bg=0.00
negative regulation of protein export fr... GO:0046826 p=3.4E−03 n=3 fg=0.01 bg=0.00
positive regulation of toll−like recepto... GO:0034123 p=3.4E−03 n=3 fg=0.01 bg=0.00
purine ribonucleoside monophosphate meta... GO:0009167 p=5.0E−03 n=18 fg=0.04 bg=0.02
positive regulation of post−embryonic de... GO:0048582 p=5.7E−03 n=7 fg=0.02 bg=0.01
female gonad development GO:0008585 p=6.0E−03 n=8 fg=0.02 bg=0.01
mitochondrial ATP synthesis coupled elec... GO:0042775 p=8.1E−03 n=9 fg=0.02 bg=0.01
endosome transport via multivesicular bo... GO:0032509 p=1.0E−02 n=5 fg=0.01 bg=0.00
carbohydrate phosphorylation GO:0046835 p=1.0E−02 n=5 fg=0.01 bg=0.00
aerobic electron transport chain GO:0019646 p=1.2E−02 n=8 fg=0.02 bg=0.01
iron−sulfur cluster assembly GO:0016226 p=1.2E−02 n=6 fg=0.01 bg=0.01
metallo−sulfur cluster assembly GO:0031163 p=1.2E−02 n=6 fg=0.01 bg=0.01
positive regulation of nematode larval d... GO:0061063 p=1.2E−02 n=6 fg=0.01 bg=0.01
negative regulation of synaptic assembly... GO:0045886 p=1.2E−02 n=7 fg=0.02 bg=0.01
larval midgut histolysis GO:0035069 p=1.2E−02 n=3 fg=0.01 bg=0.00
regulation of activated T cell prolifera... GO:0046006 p=1.2E−02 n=3 fg=0.01 bg=0.00
regulation of protein localization to ch... GO:1904814 p=1.2E−02 n=3 fg=0.01 bg=0.00
positive regulation of neuron remodeling GO:1904801 p=1.2E−02 n=3 fg=0.01 bg=0.00
positive regulation of microtubule polym... GO:0031116 p=1.2E−02 n=3 fg=0.01 bg=0.00
positive regulation of neuron maturation GO:0014042 p=1.2E−02 n=3 fg=0.01 bg=0.00
proton motive force−driven mitochondrial... GO:0042776 p=1.2E−02 n=3 fg=0.01 bg=0.00
activated T cell proliferation GO:0050798 p=1.2E−02 n=3 fg=0.01 bg=0.00
negative regulation of telomere maintena... GO:0032205 p=1.2E−02 n=4 fg=0.01 bg=0.00
negative regulation of cell junction ass... GO:1901889 p=1.4E−02 n=9 fg=0.02 bg=0.01
multivesicular body sorting pathway GO:0071985 p=1.6E−02 n=5 fg=0.01 bg=0.00
negative regulation of neuromuscular jun... GO:1904397 p=1.7E−02 n=7 fg=0.02 bg=0.01
mitochondrial translational elongation GO:0070125 p=1.7E−02 n=7 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
n=408/1073 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
telomeric DNA binding GO:0042162 p=1.9E−02 n=5 fg=0.01 bg=0.01
electron transfer activity GO:0009055 p=1.9E−02 n=9 fg=0.03 bg=0.01
U1 snRNA binding GO:0030619 p=2.0E−02 n=2 fg=0.01 bg=0.00
inositol monophosphate 4−phosphatase act... GO:0052833 p=2.0E−02 n=2 fg=0.01 bg=0.00
inositol monophosphate phosphatase activ... GO:0052834 p=2.0E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0004694 p=2.0E−02 n=2 fg=0.01 bg=0.00
polysaccharide binding GO:0030247 p=2.0E−02 n=2 fg=0.01 bg=0.00
structural constituent of ribosome GO:0003735 p=2.4E−02 n=14 fg=0.04 bg=0.02
NADH dehydrogenase activity GO:0003954 p=2.7E−02 n=5 fg=0.01 bg=0.01
cyclin−dependent protein kinase activity GO:0097472 p=2.8E−02 n=4 fg=0.01 bg=0.00
cyclin−dependent protein serine/threonin... GO:0004693 p=2.8E−02 n=4 fg=0.01 bg=0.00
phosphotransferase activity, alcohol gro... GO:0016773 p=3.8E−02 n=29 fg=0.09 bg=0.06
rDNA binding GO:0000182 p=4.1E−02 n=3 fg=0.01 bg=0.00
GTPase activating protein binding GO:0032794 p=4.1E−02 n=4 fg=0.01 bg=0.00
protein phosphatase regulator activity GO:0019888 p=5.0E−02 n=5 fg=0.01 bg=0.01
protein serine/threonine kinase activato... GO:0043539 p=5.5E−02 n=2 fg=0.01 bg=0.00
mRNA binding GO:0003729 p=5.6E−02 n=16 fg=0.05 bg=0.03
adenylyltransferase activity GO:0070566 p=5.8E−02 n=4 fg=0.01 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016651 p=6.2E−02 n=8 fg=0.02 bg=0.01
polynucleotide adenylyltransferase activ... GO:0004652 p=6.4E−02 n=3 fg=0.01 bg=0.00
carbohydrate kinase activity GO:0019200 p=6.4E−02 n=3 fg=0.01 bg=0.00
metal cluster binding GO:0051540 p=6.4E−02 n=3 fg=0.01 bg=0.00
iron−sulfur cluster binding GO:0051536 p=6.4E−02 n=3 fg=0.01 bg=0.00
proton transmembrane transporter activit... GO:0015078 p=6.5E−02 n=6 fg=0.02 bg=0.01
RNA binding GO:0003723 p=6.6E−02 n=43 fg=0.13 bg=0.10
NADH dehydrogenase (quinone) activity GO:0050136 p=7.7E−02 n=4 fg=0.01 bg=0.01
NAD(P)H dehydrogenase (quinone) activity GO:0003955 p=7.7E−02 n=4 fg=0.01 bg=0.01
NADH dehydrogenase (ubiquinone) activity GO:0008137 p=7.7E−02 n=4 fg=0.01 bg=0.01
oxidoreduction−driven active transmembra... GO:0015453 p=8.1E−02 n=5 fg=0.01 bg=0.01
primary active transmembrane transporter... GO:0015399 p=8.3E−02 n=10 fg=0.03 bg=0.02
0 1 2 3 4 5
−log(p)
n=336/1073 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
catalytic complex GO:1902494 p=2.7E−04 n=80 fg=0.20 bg=0.14
mitochondrial protein−containing complex GO:0098798 p=4.3E−04 n=20 fg=0.05 bg=0.02
mitochondrial ribosome GO:0005761 p=3.5E−03 n=8 fg=0.02 bg=0.01
integrator complex GO:0032039 p=9.0E−03 n=5 fg=0.01 bg=0.00
NuRD complex GO:0016581 p=1.1E−02 n=3 fg=0.01 bg=0.00
CHD−type complex GO:0090545 p=1.1E−02 n=3 fg=0.01 bg=0.00
mitochondrial membrane GO:0031966 p=1.2E−02 n=33 fg=0.08 bg=0.06
inner mitochondrial membrane protein com... GO:0098800 p=1.3E−02 n=10 fg=0.03 bg=0.01
organellar large ribosomal subunit GO:0000315 p=1.5E−02 n=5 fg=0.01 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=1.5E−02 n=5 fg=0.01 bg=0.00
organelle envelope GO:0031967 p=1.6E−02 n=55 fg=0.14 bg=0.11
envelope GO:0031975 p=1.6E−02 n=55 fg=0.14 bg=0.11
protein−containing complex GO:0032991 p=1.7E−02 n=206 fg=0.52 bg=0.42
respirasome GO:0070469 p=1.8E−02 n=8 fg=0.02 bg=0.01
mitochondrial respirasome GO:0005746 p=1.8E−02 n=8 fg=0.02 bg=0.01
organelle inner membrane GO:0019866 p=1.9E−02 n=26 fg=0.07 bg=0.04
nuclear protein−containing complex GO:0140513 p=1.9E−02 n=63 fg=0.16 bg=0.12
SWI/SNF superfamily−type complex GO:0070603 p=2.0E−02 n=7 fg=0.02 bg=0.01
respiratory chain complex GO:0098803 p=2.0E−02 n=7 fg=0.02 bg=0.01
U12−type spliceosomal complex GO:0005689 p=2.0E−02 n=4 fg=0.01 bg=0.00
intracellular anatomical structure GO:0005622 p=2.0E−02 n=385 fg=0.97 bg=0.94
NADH dehydrogenase complex GO:0030964 p=2.1E−02 n=6 fg=0.02 bg=0.01
mitochondrial respiratory chain complex ... GO:0005747 p=2.1E−02 n=6 fg=0.02 bg=0.01
respiratory chain complex I GO:0045271 p=2.1E−02 n=6 fg=0.02 bg=0.01
protein serine/threonine phosphatase com... GO:0008287 p=2.1E−02 n=6 fg=0.02 bg=0.01
Atg12−Atg5−Atg16 complex GO:0034274 p=2.2E−02 n=2 fg=0.01 bg=0.00
ESCRT II complex GO:0000814 p=2.2E−02 n=2 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000275 p=2.2E−02 n=2 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005753 p=2.2E−02 n=2 fg=0.01 bg=0.00
proton−transporting ATP synthase complex... GO:0045261 p=2.2E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=398/1073 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction