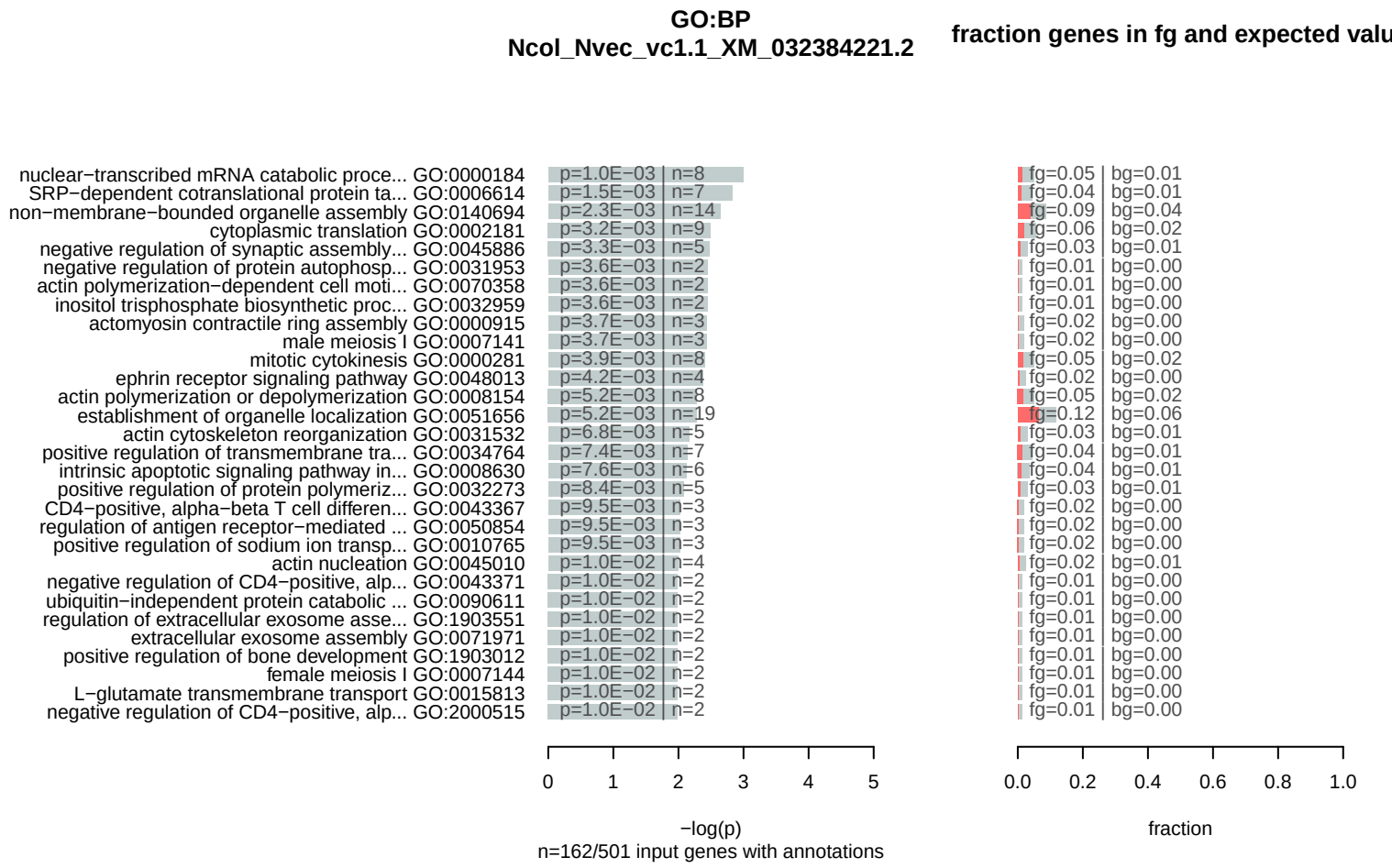
GO:BP
Ncol_Nvec_vc1.1_XM_032384221.2
fraction genes in fg and expected valu
nuclear−transcribed mRNA catabolic proce... GO:0000184 p=1.0E−03 n=8 fg=0.05 bg=0.01
SRP−dependent cotranslational protein ta... GO:0006614 p=1.5E−03 n=7 fg=0.04 bg=0.01
non−membrane−bounded organelle assembly GO:0140694 p=2.3E−03 n=14 fg=0.09 bg=0.04
cytoplasmic translation GO:0002181 p=3.2E−03 n=9 fg=0.06 bg=0.02
negative regulation of synaptic assembly... GO:0045886 p=3.3E−03 n=5 fg=0.03 bg=0.01
negative regulation of protein autophosp... GO:0031953 p=3.6E−03 n=2 fg=0.01 bg=0.00
actin polymerization−dependent cell moti... GO:0070358 p=3.6E−03 n=2 fg=0.01 bg=0.00
inositol trisphosphate biosynthetic proc... GO:0032959 p=3.6E−03 n=2 fg=0.01 bg=0.00
actomyosin contractile ring assembly GO:0000915 p=3.7E−03 n=3 fg=0.02 bg=0.00
male meiosis I GO:0007141 p=3.7E−03 n=3 fg=0.02 bg=0.00
mitotic cytokinesis GO:0000281 p=3.9E−03 n=8 fg=0.05 bg=0.02
ephrin receptor signaling pathway GO:0048013 p=4.2E−03 n=4 fg=0.02 bg=0.00
actin polymerization or depolymerization GO:0008154 p=5.2E−03 n=8 fg=0.05 bg=0.02
establishment of organelle localization GO:0051656 p=5.2E−03 n=19 fg=0.12 bg=0.06
actin cytoskeleton reorganization GO:0031532 p=6.8E−03 n=5 fg=0.03 bg=0.01
positive regulation of transmembrane tra... GO:0034764 p=7.4E−03 n=7 fg=0.04 bg=0.01
intrinsic apoptotic signaling pathway in... GO:0008630 p=7.6E−03 n=6 fg=0.04 bg=0.01
positive regulation of protein polymeriz... GO:0032273 p=8.4E−03 n=5 fg=0.03 bg=0.01
CD4−positive, alpha−beta T cell differen... GO:0043367 p=9.5E−03 n=3 fg=0.02 bg=0.00
regulation of antigen receptor−mediated ... GO:0050854 p=9.5E−03 n=3 fg=0.02 bg=0.00
positive regulation of sodium ion transp... GO:0010765 p=9.5E−03 n=3 fg=0.02 bg=0.00
actin nucleation GO:0045010 p=1.0E−02 n=4 fg=0.02 bg=0.01
negative regulation of CD4−positive, alp... GO:0043371 p=1.0E−02 n=2 fg=0.01 bg=0.00
ubiquitin−independent protein catabolic ... GO:0090611 p=1.0E−02 n=2 fg=0.01 bg=0.00
regulation of extracellular exosome asse... GO:1903551 p=1.0E−02 n=2 fg=0.01 bg=0.00
extracellular exosome assembly GO:0071971 p=1.0E−02 n=2 fg=0.01 bg=0.00
positive regulation of bone development GO:1903012 p=1.0E−02 n=2 fg=0.01 bg=0.00
female meiosis I GO:0007144 p=1.0E−02 n=2 fg=0.01 bg=0.00
L−glutamate transmembrane transport GO:0015813 p=1.0E−02 n=2 fg=0.01 bg=0.00
negative regulation of CD4−positive, alp... GO:2000515 p=1.0E−02 n=2 fg=0.01 bg=0.00
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n=162/501 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032384221.2
fraction genes in fg and expected valu
structural constituent of ribosome GO:0003735 p=1.1E−04 n=12 fg=0.08 bg=0.02
mRNA binding GO:0003729 p=4.6E−04 n=13 fg=0.09 bg=0.03
actin binding GO:0003779 p=1.1E−03 n=10 fg=0.07 bg=0.02
RNA binding GO:0003723 p=1.2E−03 n=33 fg=0.23 bg=0.10
chloride channel inhibitor activity GO:0019869 p=1.1E−02 n=2 fg=0.01 bg=0.00
mRNA 3'−UTR binding GO:0003730 p=1.4E−02 n=4 fg=0.03 bg=0.01
profilin binding GO:0005522 p=2.1E−02 n=2 fg=0.01 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=2.1E−02 n=2 fg=0.01 bg=0.00
translation factor activity, RNA binding GO:0008135 p=2.5E−02 n=5 fg=0.03 bg=0.01
ion channel inhibitor activity GO:0008200 p=3.3E−02 n=3 fg=0.02 bg=0.01
calcium−dependent phospholipid binding GO:0005544 p=3.3E−02 n=2 fg=0.01 bg=0.00
5S rRNA binding GO:0008097 p=3.3E−02 n=2 fg=0.01 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=3.3E−02 n=2 fg=0.01 bg=0.00
translation regulator activity, nucleic ... GO:0090079 p=3.3E−02 n=5 fg=0.03 bg=0.01
channel inhibitor activity GO:0016248 p=4.1E−02 n=3 fg=0.02 bg=0.01
phosphatidylinositol 3−kinase binding GO:0043548 p=4.7E−02 n=2 fg=0.01 bg=0.00
mRNA 5'−UTR binding GO:0048027 p=4.7E−02 n=2 fg=0.01 bg=0.00
structural molecule activity GO:0005198 p=5.4E−02 n=19 fg=0.13 bg=0.05
translation regulator activity GO:0045182 p=5.9E−02 n=5 fg=0.03 bg=0.01
molecular function inhibitor activity GO:0140678 p=5.9E−02 n=3 fg=0.02 bg=0.01
cadmium ion binding GO:0046870 p=6.1E−02 n=1 fg=0.01 bg=0.00
supercoiled DNA binding GO:0097100 p=6.1E−02 n=1 fg=0.01 bg=0.00
acetate−CoA ligase activity GO:0003987 p=6.1E−02 n=1 fg=0.01 bg=0.00
branched−chain amino acid transmembrane ... GO:0015658 p=6.1E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=6.1E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=6.1E−02 n=1 fg=0.01 bg=0.00
U5 snRNA binding GO:0030623 p=6.1E−02 n=1 fg=0.01 bg=0.00
aminophospholipid flippase activity GO:0015247 p=6.1E−02 n=1 fg=0.01 bg=0.00
phosphatidylglycerol binding GO:1901611 p=6.1E−02 n=1 fg=0.01 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=6.1E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=145/501 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032384221.2
fraction genes in fg and expected valu
cleavage furrow GO:0032154 p=7.7E−05 n=6 fg=0.04 bg=0.01
septin ring GO:0005940 p=2.0E−04 n=3 fg=0.02 bg=0.00
sperm annulus GO:0097227 p=2.0E−04 n=3 fg=0.02 bg=0.00
septin complex GO:0031105 p=2.0E−04 n=3 fg=0.02 bg=0.00
contractile ring GO:0070938 p=6.7E−04 n=4 fg=0.03 bg=0.00
stress fiber GO:0001725 p=1.8E−03 n=4 fg=0.03 bg=0.00
small ribosomal subunit GO:0015935 p=2.1E−03 n=6 fg=0.04 bg=0.01
eukaryotic translation elongation factor... GO:0005853 p=3.4E−03 n=2 fg=0.01 bg=0.00
cytosolic large ribosomal subunit GO:0022625 p=4.0E−03 n=6 fg=0.04 bg=0.01
non−membrane−bounded organelle GO:0043228 p=1.2E−02 n=75 fg=0.47 bg=0.33
intracellular non−membrane−bounded organ... GO:0043232 p=1.2E−02 n=75 fg=0.47 bg=0.33
transcription regulator complex GO:0005667 p=1.3E−02 n=12 fg=0.08 bg=0.04
cytosolic small ribosomal subunit GO:0022627 p=1.5E−02 n=4 fg=0.03 bg=0.01
cytoskeleton GO:0005856 p=1.6E−02 n=37 fg=0.23 bg=0.15
cytosolic ribosome GO:0022626 p=2.0E−02 n=10 fg=0.06 bg=0.02
intercellular bridge GO:0045171 p=2.7E−02 n=4 fg=0.03 bg=0.01
P−body GO:0000932 p=3.2E−02 n=4 fg=0.03 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=3.2E−02 n=4 fg=0.03 bg=0.01
multivesicular body GO:0005771 p=3.7E−02 n=3 fg=0.02 bg=0.00
spindle GO:0005819 p=4.1E−02 n=10 fg=0.06 bg=0.03
focal adhesion GO:0005925 p=4.3E−02 n=4 fg=0.03 bg=0.01
organelle membrane contact site GO:0044232 p=4.4E−02 n=2 fg=0.01 bg=0.00
nuclear protein−containing complex GO:0140513 p=4.9E−02 n=26 fg=0.16 bg=0.12
polysome GO:0005844 p=4.9E−02 n=4 fg=0.03 bg=0.01
actin cytoskeleton GO:0015629 p=4.9E−02 n=12 fg=0.08 bg=0.03
late endosome GO:0005770 p=5.1E−02 n=7 fg=0.04 bg=0.02
microtubule cytoskeleton GO:0015630 p=5.3E−02 n=23 fg=0.14 bg=0.10
neuron projection terminus GO:0044306 p=5.6E−02 n=7 fg=0.04 bg=0.02
tertiary granule GO:0070820 p=5.6E−02 n=4 fg=0.03 bg=0.01
protein farnesyltransferase complex GO:0005965 p=5.9E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=159/501 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction