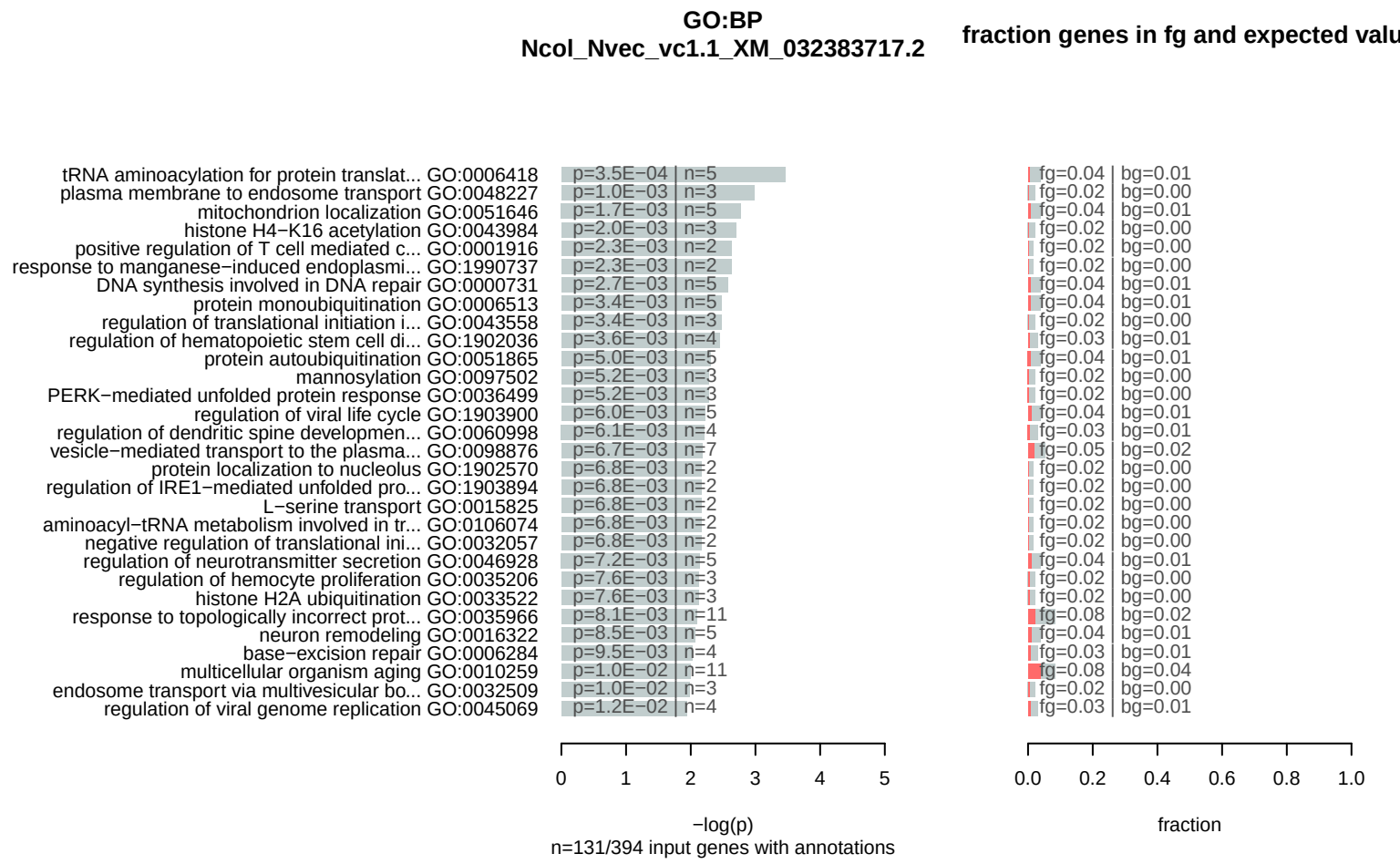
GO:BP
Ncol_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
tRNA aminoacylation for protein translat... GO:0006418 p=3.5E−04 n=5 fg=0.04 bg=0.01
plasma membrane to endosome transport GO:0048227 p=1.0E−03 n=3 fg=0.02 bg=0.00
mitochondrion localization GO:0051646 p=1.7E−03 n=5 fg=0.04 bg=0.01
histone H4−K16 acetylation GO:0043984 p=2.0E−03 n=3 fg=0.02 bg=0.00
positive regulation of T cell mediated c... GO:0001916 p=2.3E−03 n=2 fg=0.02 bg=0.00
response to manganese−induced endoplasmi... GO:1990737 p=2.3E−03 n=2 fg=0.02 bg=0.00
DNA synthesis involved in DNA repair GO:0000731 p=2.7E−03 n=5 fg=0.04 bg=0.01
protein monoubiquitination GO:0006513 p=3.4E−03 n=5 fg=0.04 bg=0.01
regulation of translational initiation i... GO:0043558 p=3.4E−03 n=3 fg=0.02 bg=0.00
regulation of hematopoietic stem cell di... GO:1902036 p=3.6E−03 n=4 fg=0.03 bg=0.01
protein autoubiquitination GO:0051865 p=5.0E−03 n=5 fg=0.04 bg=0.01
mannosylation GO:0097502 p=5.2E−03 n=3 fg=0.02 bg=0.00
PERK−mediated unfolded protein response GO:0036499 p=5.2E−03 n=3 fg=0.02 bg=0.00
regulation of viral life cycle GO:1903900 p=6.0E−03 n=5 fg=0.04 bg=0.01
regulation of dendritic spine developmen... GO:0060998 p=6.1E−03 n=4 fg=0.03 bg=0.01
vesicle−mediated transport to the plasma... GO:0098876 p=6.7E−03 n=7 fg=0.05 bg=0.02
protein localization to nucleolus GO:1902570 p=6.8E−03 n=2 fg=0.02 bg=0.00
regulation of IRE1−mediated unfolded pro... GO:1903894 p=6.8E−03 n=2 fg=0.02 bg=0.00
L−serine transport GO:0015825 p=6.8E−03 n=2 fg=0.02 bg=0.00
aminoacyl−tRNA metabolism involved in tr... GO:0106074 p=6.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of translational ini... GO:0032057 p=6.8E−03 n=2 fg=0.02 bg=0.00
regulation of neurotransmitter secretion GO:0046928 p=7.2E−03 n=5 fg=0.04 bg=0.01
regulation of hemocyte proliferation GO:0035206 p=7.6E−03 n=3 fg=0.02 bg=0.00
histone H2A ubiquitination GO:0033522 p=7.6E−03 n=3 fg=0.02 bg=0.00
response to topologically incorrect prot... GO:0035966 p=8.1E−03 n=11 fg=0.08 bg=0.02
neuron remodeling GO:0016322 p=8.5E−03 n=5 fg=0.04 bg=0.01
base−excision repair GO:0006284 p=9.5E−03 n=4 fg=0.03 bg=0.01
multicellular organism aging GO:0010259 p=1.0E−02 n=11 fg=0.08 bg=0.04
endosome transport via multivesicular bo... GO:0032509 p=1.0E−02 n=3 fg=0.02 bg=0.00
regulation of viral genome replication GO:0045069 p=1.2E−02 n=4 fg=0.03 bg=0.01
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n=131/394 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
aminoacyl−tRNA ligase activity GO:0004812 p=2.0E−03 n=4 fg=0.03 bg=0.01
translation release factor activity GO:0003747 p=2.4E−03 n=2 fg=0.02 bg=0.00
glycolipid mannosyltransferase activity GO:0004376 p=2.4E−03 n=2 fg=0.02 bg=0.00
four−way junction DNA binding GO:0000400 p=2.4E−03 n=2 fg=0.02 bg=0.00
translation initiation factor activity GO:0003743 p=6.3E−03 n=4 fg=0.03 bg=0.01
cAMP response element binding GO:0035497 p=6.9E−03 n=2 fg=0.02 bg=0.00
L−serine transmembrane transporter activ... GO:0015194 p=6.9E−03 n=2 fg=0.02 bg=0.00
aminoacyl−tRNA editing activity GO:0002161 p=6.9E−03 n=2 fg=0.02 bg=0.00
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ubiquitin binding GO:0043130 p=9.8E−03 n=4 fg=0.03 bg=0.01
acetyltransferase activity GO:0016407 p=9.8E−03 n=4 fg=0.03 bg=0.01
purine ribonucleoside triphosphate bindi... GO:0035639 p=1.7E−02 n=13 fg=0.11 bg=0.06
GDP binding GO:0019003 p=2.3E−02 n=3 fg=0.03 bg=0.01
ribonucleotide binding GO:0032553 p=4.0E−02 n=13 fg=0.11 bg=0.07
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UDP−glycosyltransferase activity GO:0008194 p=4.0E−02 n=4 fg=0.03 bg=0.01
translation regulator activity GO:0045182 p=4.2E−02 n=9 fg=0.08 bg=0.01
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damaged DNA binding GO:0003684 p=4.7E−02 n=3 fg=0.03 bg=0.01
3'−flap−structured DNA binding GO:0070337 p=4.9E−02 n=1 fg=0.01 bg=0.00
macrophage migration inhibitory factor b... GO:0035718 p=4.9E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=4.9E−02 n=1 fg=0.01 bg=0.00
branched−chain amino acid transmembrane ... GO:0015658 p=4.9E−02 n=1 fg=0.01 bg=0.00
importin−alpha family protein binding GO:0061676 p=4.9E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=4.9E−02 n=1 fg=0.01 bg=0.00
ubiquitin−like protein−specific endopept... GO:0070137 p=4.9E−02 n=1 fg=0.01 bg=0.00
SUMO−specific endopeptidase activity GO:0070139 p=4.9E−02 n=1 fg=0.01 bg=0.00
MHC protein complex binding GO:0023023 p=4.9E−02 n=1 fg=0.01 bg=0.00
glutamate−5−semialdehyde dehydrogenase a... GO:0004350 p=4.9E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein complex binding GO:0023025 p=4.9E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=116/394 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
multi−eIF complex GO:0043614 p=1.2E−04 n=3 fg=0.02 bg=0.00
translation preinitiation complex GO:0070993 p=2.5E−03 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=7.2E−03 n=2 fg=0.01 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=7.9E−03 n=18 fg=0.13 bg=0.07
mitochondrial nucleoid GO:0042645 p=8.2E−03 n=3 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0005852 p=3.3E−02 n=2 fg=0.01 bg=0.00
male germ cell nucleus GO:0001673 p=4.4E−02 n=2 fg=0.01 bg=0.00
aminoacyl−tRNA synthetase multienzyme co... GO:0017101 p=4.4E−02 n=2 fg=0.01 bg=0.00
translation release factor complex GO:0018444 p=5.0E−02 n=1 fg=0.01 bg=0.00
anchored component of synaptic vesicle m... GO:0098993 p=5.0E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=5.0E−02 n=1 fg=0.01 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=5.0E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0009330 p=5.0E−02 n=1 fg=0.01 bg=0.00
endocytic vesicle lumen GO:0071682 p=5.0E−02 n=1 fg=0.01 bg=0.00
RNA nuclear export complex GO:0042565 p=5.0E−02 n=1 fg=0.01 bg=0.00
Holliday junction resolvase complex GO:0048476 p=5.0E−02 n=1 fg=0.01 bg=0.00
eukaryotic 48S preinitiation complex GO:0033290 p=5.0E−02 n=1 fg=0.01 bg=0.00
astrocyte end−foot GO:0097450 p=5.0E−02 n=1 fg=0.01 bg=0.00
glial limiting end−foot GO:0097451 p=5.0E−02 n=1 fg=0.01 bg=0.00
gamma DNA polymerase complex GO:0005760 p=5.0E−02 n=1 fg=0.01 bg=0.00
longitudinal sarcoplasmic reticulum GO:0014801 p=5.0E−02 n=1 fg=0.01 bg=0.00
ribbon synapse GO:0097470 p=5.0E−02 n=1 fg=0.01 bg=0.00
nuclear RNA export factor complex GO:0042272 p=5.0E−02 n=1 fg=0.01 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=5.0E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network GO:0031094 p=5.0E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network membrane GO:0031095 p=5.0E−02 n=1 fg=0.01 bg=0.00
cation−transporting ATPase complex GO:0090533 p=5.0E−02 n=1 fg=0.01 bg=0.00
calcium ion−transporting ATPase complex GO:0090534 p=5.0E−02 n=1 fg=0.01 bg=0.00
synaptic cleft GO:0043083 p=5.0E−02 n=1 fg=0.01 bg=0.00
endodeoxyribonuclease complex GO:1905347 p=5.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=135/394 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction