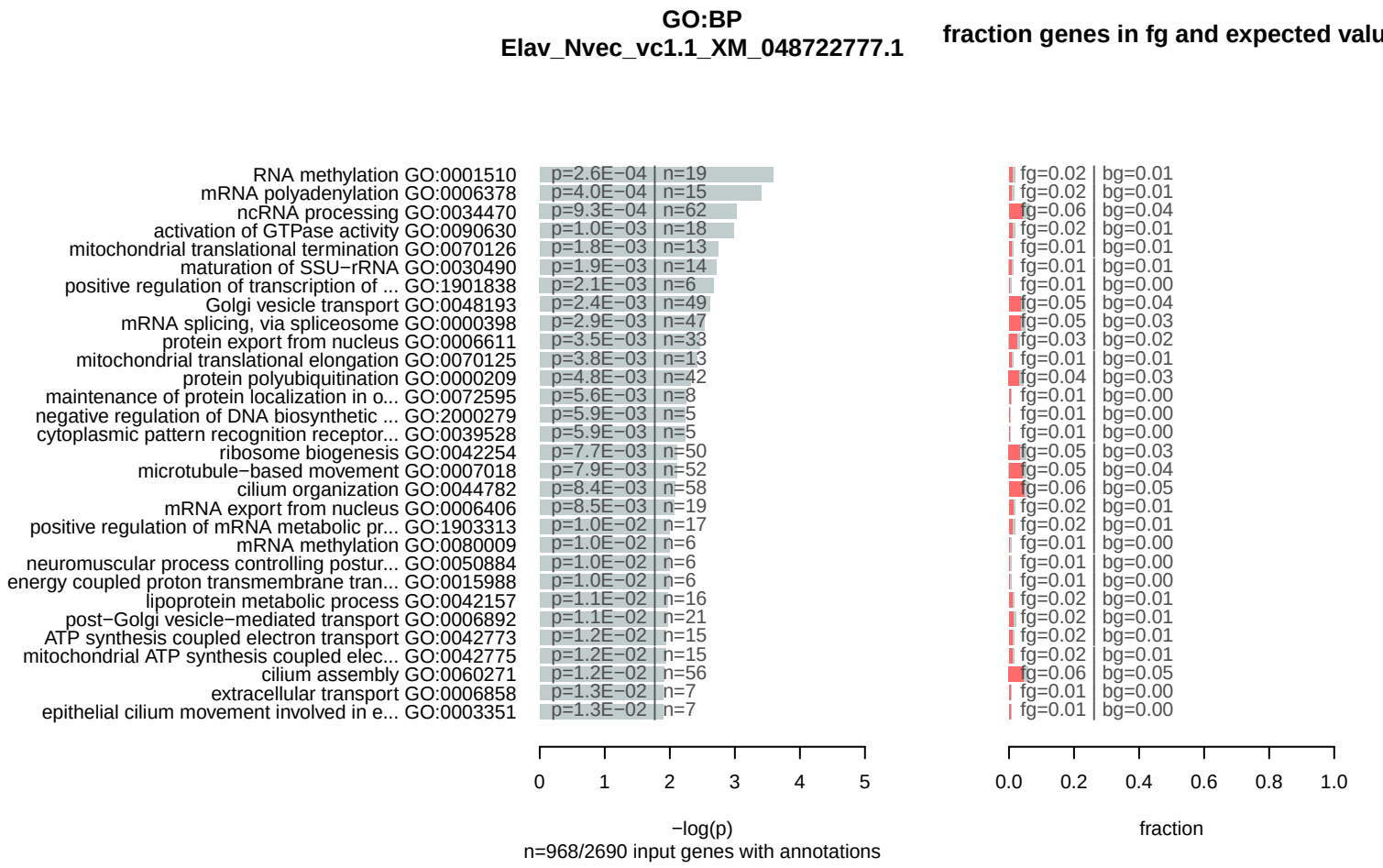
GO:BP
Elav_Nvec_vc1.1_XM_048722777.1
fraction genes in fg and expected valu
RNA methylation GO:0001510 p=2.6E−04 n=19 fg=0.02 bg=0.01
mRNA polyadenylation GO:0006378 p=4.0E−04 n=15 fg=0.02 bg=0.01
ncRNA processing GO:0034470 p=9.3E−04 n=62 fg=0.06 bg=0.04
activation of GTPase activity GO:0090630 p=1.0E−03 n=18 fg=0.02 bg=0.01
mitochondrial translational termination GO:0070126 p=1.8E−03 n=13 fg=0.01 bg=0.01
maturation of SSU−rRNA GO:0030490 p=1.9E−03 n=14 fg=0.01 bg=0.01
positive regulation of transcription of ... GO:1901838 p=2.1E−03 n=6 fg=0.01 bg=0.00
Golgi vesicle transport GO:0048193 p=2.4E−03 n=49 fg=0.05 bg=0.04
mRNA splicing, via spliceosome GO:0000398 p=2.9E−03 n=47 fg=0.05 bg=0.03
protein export from nucleus GO:0006611 p=3.5E−03 n=33 fg=0.03 bg=0.02
mitochondrial translational elongation GO:0070125 p=3.8E−03 n=13 fg=0.01 bg=0.01
protein polyubiquitination GO:0000209 p=4.8E−03 n=42 fg=0.04 bg=0.03
maintenance of protein localization in o... GO:0072595 p=5.6E−03 n=8 fg=0.01 bg=0.00
negative regulation of DNA biosynthetic ... GO:2000279 p=5.9E−03 n=5 fg=0.01 bg=0.00
cytoplasmic pattern recognition receptor... GO:0039528 p=5.9E−03 n=5 fg=0.01 bg=0.00
ribosome biogenesis GO:0042254 p=7.7E−03 n=50 fg=0.05 bg=0.03
microtubule−based movement GO:0007018 p=7.9E−03 n=52 fg=0.05 bg=0.04
cilium organization GO:0044782 p=8.4E−03 n=58 fg=0.06 bg=0.05
mRNA export from nucleus GO:0006406 p=8.5E−03 n=19 fg=0.02 bg=0.01
positive regulation of mRNA metabolic pr... GO:1903313 p=1.0E−02 n=17 fg=0.02 bg=0.01
mRNA methylation GO:0080009 p=1.0E−02 n=6 fg=0.01 bg=0.00
neuromuscular process controlling postur... GO:0050884 p=1.0E−02 n=6 fg=0.01 bg=0.00
energy coupled proton transmembrane tran... GO:0015988 p=1.0E−02 n=6 fg=0.01 bg=0.00
lipoprotein metabolic process GO:0042157 p=1.1E−02 n=16 fg=0.02 bg=0.01
post−Golgi vesicle−mediated transport GO:0006892 p=1.1E−02 n=21 fg=0.02 bg=0.01
ATP synthesis coupled electron transport GO:0042773 p=1.2E−02 n=15 fg=0.02 bg=0.01
mitochondrial ATP synthesis coupled elec... GO:0042775 p=1.2E−02 n=15 fg=0.02 bg=0.01
cilium assembly GO:0060271 p=1.2E−02 n=56 fg=0.06 bg=0.05
extracellular transport GO:0006858 p=1.3E−02 n=7 fg=0.01 bg=0.00
epithelial cilium movement involved in e... GO:0003351 p=1.3E−02 n=7 fg=0.01 bg=0.00
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n=968/2690 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048722777.1
fraction genes in fg and expected valu
RNA methyltransferase activity GO:0008173 p=5.7E−04 n=16 fg=0.02 bg=0.01
ubiquitin protein ligase activity GO:0061630 p=8.3E−04 n=38 fg=0.05 bg=0.03
alpha−tubulin binding GO:0043014 p=1.2E−03 n=8 fg=0.01 bg=0.00
small GTPase binding GO:0031267 p=1.9E−03 n=51 fg=0.06 bg=0.04
oxidoreductase activity, acting on NAD(P... GO:0016655 p=5.0E−03 n=10 fg=0.01 bg=0.01
cysteine−type peptidase activity GO:0008234 p=5.5E−03 n=18 fg=0.02 bg=0.01
deubiquitinase activity GO:0101005 p=1.0E−02 n=11 fg=0.01 bg=0.01
NADH dehydrogenase activity GO:0003954 p=1.1E−02 n=9 fg=0.01 bg=0.01
catalytic activity, acting on RNA GO:0140098 p=1.2E−02 n=52 fg=0.06 bg=0.04
palmitoyl hydrolase activity GO:0098599 p=1.4E−02 n=4 fg=0.00 bg=0.00
palmitoyl−(protein) hydrolase activity GO:0008474 p=1.4E−02 n=4 fg=0.00 bg=0.00
ATP−dependent activity GO:0140657 p=1.7E−02 n=53 fg=0.07 bg=0.05
RNA binding GO:0003723 p=1.9E−02 n=99 fg=0.12 bg=0.10
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=2.0E−02 n=5 fg=0.01 bg=0.00
O−methyltransferase activity GO:0008171 p=2.0E−02 n=5 fg=0.01 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=2.0E−02 n=5 fg=0.01 bg=0.00
proton−transporting ATPase activity, rot... GO:0046961 p=2.0E−02 n=5 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase binding GO:0043548 p=2.0E−02 n=5 fg=0.01 bg=0.00
oxidoreductase activity, acting on the a... GO:0016903 p=2.0E−02 n=5 fg=0.01 bg=0.00
tRNA (guanine) methyltransferase activit... GO:0016423 p=2.0E−02 n=5 fg=0.01 bg=0.00
nucleotidyltransferase activity GO:0016779 p=2.1E−02 n=20 fg=0.02 bg=0.02
SNARE binding GO:0000149 p=2.1E−02 n=17 fg=0.02 bg=0.01
NAD(P)H dehydrogenase (quinone) activity GO:0003955 p=2.2E−02 n=8 fg=0.01 bg=0.01
NADH dehydrogenase (ubiquinone) activity GO:0008137 p=2.2E−02 n=8 fg=0.01 bg=0.01
NADH dehydrogenase (quinone) activity GO:0050136 p=2.2E−02 n=8 fg=0.01 bg=0.01
beta−tubulin binding GO:0048487 p=2.3E−02 n=7 fg=0.01 bg=0.00
histone binding GO:0042393 p=2.8E−02 n=20 fg=0.02 bg=0.02
ATP hydrolysis activity GO:0016887 p=3.2E−02 n=47 fg=0.06 bg=0.05
oxidoreduction−driven active transmembra... GO:0015453 p=3.3E−02 n=10 fg=0.01 bg=0.01
RNA 7−methylguanosine cap binding GO:0000340 p=4.0E−02 n=3 fg=0.00 bg=0.00
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−log(p)
n=813/2690 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048722777.1
fraction genes in fg and expected valu
nucleoplasm GO:0005654 p=4.4E−07 n=335 fg=0.35 bg=0.29
intracellular anatomical structure GO:0005622 p=7.6E−05 n=937 fg=0.97 bg=0.94
nuclear protein−containing complex GO:0140513 p=1.7E−04 n=147 fg=0.15 bg=0.12
ribonucleoprotein complex GO:1990904 p=1.0E−03 n=111 fg=0.12 bg=0.09
methyltransferase complex GO:0034708 p=1.7E−03 n=20 fg=0.02 bg=0.01
plasma membrane proton−transporting V−ty... GO:0033181 p=2.0E−03 n=6 fg=0.01 bg=0.00
intracellular protein−containing complex GO:0140535 p=2.8E−03 n=108 fg=0.11 bg=0.08
intracellular non−membrane−bounded organ... GO:0043232 p=3.3E−03 n=362 fg=0.38 bg=0.33
endopeptidase complex GO:1905369 p=3.5E−03 n=16 fg=0.02 bg=0.01
mitochondrial ribosome GO:0005761 p=3.6E−03 n=13 fg=0.01 bg=0.01
trans−Golgi network GO:0005802 p=4.0E−03 n=37 fg=0.04 bg=0.03
catalytic complex GO:1902494 p=4.3E−03 n=183 fg=0.19 bg=0.14
axoneme GO:0005930 p=4.6E−03 n=20 fg=0.02 bg=0.01
RNA polymerase complex GO:0030880 p=5.6E−03 n=27 fg=0.03 bg=0.02
proton−transporting two−sector ATPase co... GO:0033178 p=5.7E−03 n=5 fg=0.01 bg=0.00
Prp19 complex GO:0000974 p=5.7E−03 n=5 fg=0.01 bg=0.00
mediator complex GO:0016592 p=6.3E−03 n=9 fg=0.01 bg=0.00
mitochondrial respiratory chain complex ... GO:0005747 p=7.1E−03 n=11 fg=0.01 bg=0.01
mitochondrial protein−containing complex GO:0098798 p=9.0E−03 n=36 fg=0.04 bg=0.02
AP−type membrane coat adaptor complex GO:0030119 p=9.9E−03 n=6 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0016471 p=9.9E−03 n=6 fg=0.01 bg=0.00
preribosome, small subunit precursor GO:0030688 p=9.9E−03 n=6 fg=0.01 bg=0.00
proteasome complex GO:0000502 p=1.2E−02 n=13 fg=0.01 bg=0.01
trans−Golgi network membrane GO:0032588 p=1.3E−02 n=18 fg=0.02 bg=0.01
DNA−directed RNA polymerase complex GO:0000428 p=1.4E−02 n=25 fg=0.03 bg=0.02
RNA polymerase I complex GO:0005736 p=1.6E−02 n=4 fg=0.00 bg=0.00
spliceosomal complex GO:0005681 p=1.7E−02 n=23 fg=0.02 bg=0.02
centrosome GO:0005813 p=1.9E−02 n=62 fg=0.06 bg=0.05
small ribosomal subunit GO:0015935 p=1.9E−02 n=14 fg=0.01 bg=0.01
catalytic step 2 spliceosome GO:0071013 p=1.9E−02 n=14 fg=0.01 bg=0.01
0 1 2 3 4 5
−log(p)
n=962/2690 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction