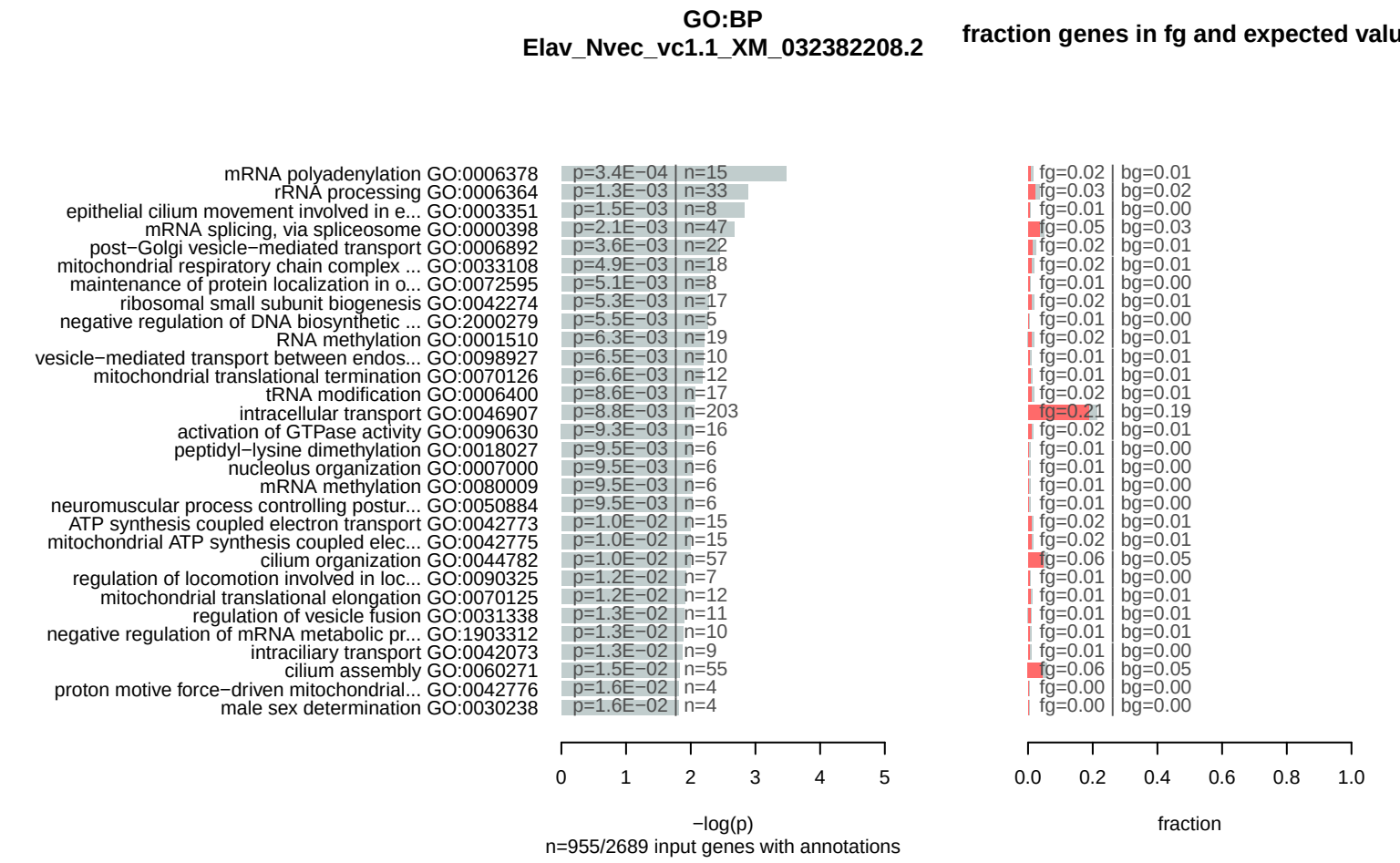
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fraction genes in fg and expected valu
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rRNA processing GO:0006364 p=1.3E−03 n=33 fg=0.03 bg=0.02
epithelial cilium movement involved in e... GO:0003351 p=1.5E−03 n=8 fg=0.01 bg=0.00
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post−Golgi vesicle−mediated transport GO:0006892 p=3.6E−03 n=22 fg=0.02 bg=0.01
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maintenance of protein localization in o... GO:0072595 p=5.1E−03 n=8 fg=0.01 bg=0.00
ribosomal small subunit biogenesis GO:0042274 p=5.3E−03 n=17 fg=0.02 bg=0.01
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RNA methylation GO:0001510 p=6.3E−03 n=19 fg=0.02 bg=0.01
vesicle−mediated transport between endos... GO:0098927 p=6.5E−03 n=10 fg=0.01 bg=0.01
mitochondrial translational termination GO:0070126 p=6.6E−03 n=12 fg=0.01 bg=0.01
tRNA modification GO:0006400 p=8.6E−03 n=17 fg=0.02 bg=0.01
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activation of GTPase activity GO:0090630 p=9.3E−03 n=16 fg=0.02 bg=0.01
peptidyl−lysine dimethylation GO:0018027 p=9.5E−03 n=6 fg=0.01 bg=0.00
nucleolus organization GO:0007000 p=9.5E−03 n=6 fg=0.01 bg=0.00
mRNA methylation GO:0080009 p=9.5E−03 n=6 fg=0.01 bg=0.00
neuromuscular process controlling postur... GO:0050884 p=9.5E−03 n=6 fg=0.01 bg=0.00
ATP synthesis coupled electron transport GO:0042773 p=1.0E−02 n=15 fg=0.02 bg=0.01
mitochondrial ATP synthesis coupled elec... GO:0042775 p=1.0E−02 n=15 fg=0.02 bg=0.01
cilium organization GO:0044782 p=1.0E−02 n=57 fg=0.06 bg=0.05
regulation of locomotion involved in loc... GO:0090325 p=1.2E−02 n=7 fg=0.01 bg=0.00
mitochondrial translational elongation GO:0070125 p=1.2E−02 n=12 fg=0.01 bg=0.01
regulation of vesicle fusion GO:0031338 p=1.3E−02 n=11 fg=0.01 bg=0.01
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proton motive force−driven mitochondrial... GO:0042776 p=1.6E−02 n=4 fg=0.00 bg=0.00
male sex determination GO:0030238 p=1.6E−02 n=4 fg=0.00 bg=0.00
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GO:MF
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alpha−tubulin binding GO:0043014 p=1.0E−03 n=8 fg=0.01 bg=0.00
O−methyltransferase activity GO:0008171 p=1.4E−03 n=6 fg=0.01 bg=0.00
small GTPase binding GO:0031267 p=2.2E−03 n=50 fg=0.06 bg=0.04
oxidoreductase activity, acting on NAD(P... GO:0016655 p=4.3E−03 n=10 fg=0.01 bg=0.01
ubiquitin protein ligase activity GO:0061630 p=5.5E−03 n=35 fg=0.04 bg=0.03
phosphatase inhibitor activity GO:0019212 p=7.2E−03 n=6 fg=0.01 bg=0.00
NADH dehydrogenase activity GO:0003954 p=9.4E−03 n=9 fg=0.01 bg=0.01
S−adenosylmethionine−dependent methyltra... GO:0008757 p=1.5E−02 n=21 fg=0.03 bg=0.02
nuclear localization sequence binding GO:0008139 p=1.9E−02 n=5 fg=0.01 bg=0.00
RNA polymerase II general transcription ... GO:0001091 p=1.9E−02 n=5 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase binding GO:0043548 p=1.9E−02 n=5 fg=0.01 bg=0.00
tRNA (guanine) methyltransferase activit... GO:0016423 p=1.9E−02 n=5 fg=0.01 bg=0.00
NAD(P)H dehydrogenase (quinone) activity GO:0003955 p=2.0E−02 n=8 fg=0.01 bg=0.01
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beta−tubulin binding GO:0048487 p=2.1E−02 n=7 fg=0.01 bg=0.00
histone binding GO:0042393 p=2.3E−02 n=20 fg=0.03 bg=0.02
catalytic activity, acting on RNA GO:0140098 p=2.9E−02 n=50 fg=0.06 bg=0.04
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deubiquitinase activity GO:0101005 p=2.9E−02 n=10 fg=0.01 bg=0.01
cysteine−type peptidase activity GO:0008234 p=2.9E−02 n=16 fg=0.02 bg=0.01
helicase activity GO:0004386 p=3.5E−02 n=17 fg=0.02 bg=0.01
RNA 7−methylguanosine cap binding GO:0000340 p=3.8E−02 n=3 fg=0.00 bg=0.00
PTB domain binding GO:0051425 p=3.8E−02 n=3 fg=0.00 bg=0.00
annealing activity GO:0140666 p=3.8E−02 n=3 fg=0.00 bg=0.00
phosphorylase kinase regulator activity GO:0008607 p=3.8E−02 n=3 fg=0.00 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=3.8E−02 n=3 fg=0.00 bg=0.00
dipeptidase activity GO:0016805 p=3.8E−02 n=3 fg=0.00 bg=0.00
pre−mRNA intronic binding GO:0097157 p=3.8E−02 n=3 fg=0.00 bg=0.00
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0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032382208.2
fraction genes in fg and expected valu
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nuclear protein−containing complex GO:0140513 p=7.6E−05 n=143 fg=0.15 bg=0.12
intracellular anatomical structure GO:0005622 p=1.1E−04 n=918 fg=0.97 bg=0.94
methyltransferase complex GO:0034708 p=1.3E−03 n=20 fg=0.02 bg=0.01
catalytic complex GO:1902494 p=2.2E−03 n=179 fg=0.19 bg=0.14
proton−transporting two−sector ATPase co... GO:0016469 p=4.8E−03 n=8 fg=0.01 bg=0.00
ribonucleoprotein complex GO:1990904 p=4.9E−03 n=106 fg=0.11 bg=0.09
Prp19 complex GO:0000974 p=5.2E−03 n=5 fg=0.01 bg=0.00
proteasome regulatory particle, lid subc... GO:0008541 p=5.2E−03 n=5 fg=0.01 bg=0.00
mitochondrial respiratory chain complex ... GO:0005747 p=6.1E−03 n=11 fg=0.01 bg=0.01
AP−type membrane coat adaptor complex GO:0030119 p=9.0E−03 n=6 fg=0.01 bg=0.00
preribosome, small subunit precursor GO:0030688 p=9.0E−03 n=6 fg=0.01 bg=0.00
RNA polymerase complex GO:0030880 p=9.6E−03 n=26 fg=0.03 bg=0.02
axoneme GO:0005930 p=9.9E−03 n=19 fg=0.02 bg=0.01
organellar ribosome GO:0000313 p=1.1E−02 n=12 fg=0.01 bg=0.01
mitochondrial ribosome GO:0005761 p=1.1E−02 n=12 fg=0.01 bg=0.01
spliceosomal complex GO:0005681 p=1.3E−02 n=23 fg=0.02 bg=0.02
non−membrane−bounded organelle GO:0043228 p=1.4E−02 n=346 fg=0.37 bg=0.33
intracellular non−membrane−bounded organ... GO:0043232 p=1.4E−02 n=346 fg=0.37 bg=0.33
RNA polymerase I complex GO:0005736 p=1.5E−02 n=4 fg=0.00 bg=0.00
small ribosomal subunit GO:0015935 p=1.6E−02 n=14 fg=0.01 bg=0.01
catalytic step 2 spliceosome GO:0071013 p=1.6E−02 n=14 fg=0.01 bg=0.01
nuclear DNA−directed RNA polymerase comp... GO:0055029 p=1.7E−02 n=24 fg=0.03 bg=0.02
trans−Golgi network GO:0005802 p=2.1E−02 n=34 fg=0.04 bg=0.03
intracellular protein−containing complex GO:0140535 p=2.2E−02 n=104 fg=0.11 bg=0.08
plasma membrane proton−transporting V−ty... GO:0033181 p=2.2E−02 n=5 fg=0.01 bg=0.00
DNA−directed RNA polymerase complex GO:0000428 p=2.2E−02 n=24 fg=0.03 bg=0.02
late endosome GO:0005770 p=2.5E−02 n=28 fg=0.03 bg=0.02
proton−transporting V−type ATPase comple... GO:0033176 p=2.5E−02 n=6 fg=0.01 bg=0.00
U12−type spliceosomal complex GO:0005689 p=2.5E−02 n=6 fg=0.01 bg=0.00
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n=946/2689 input genes with annotations
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fraction