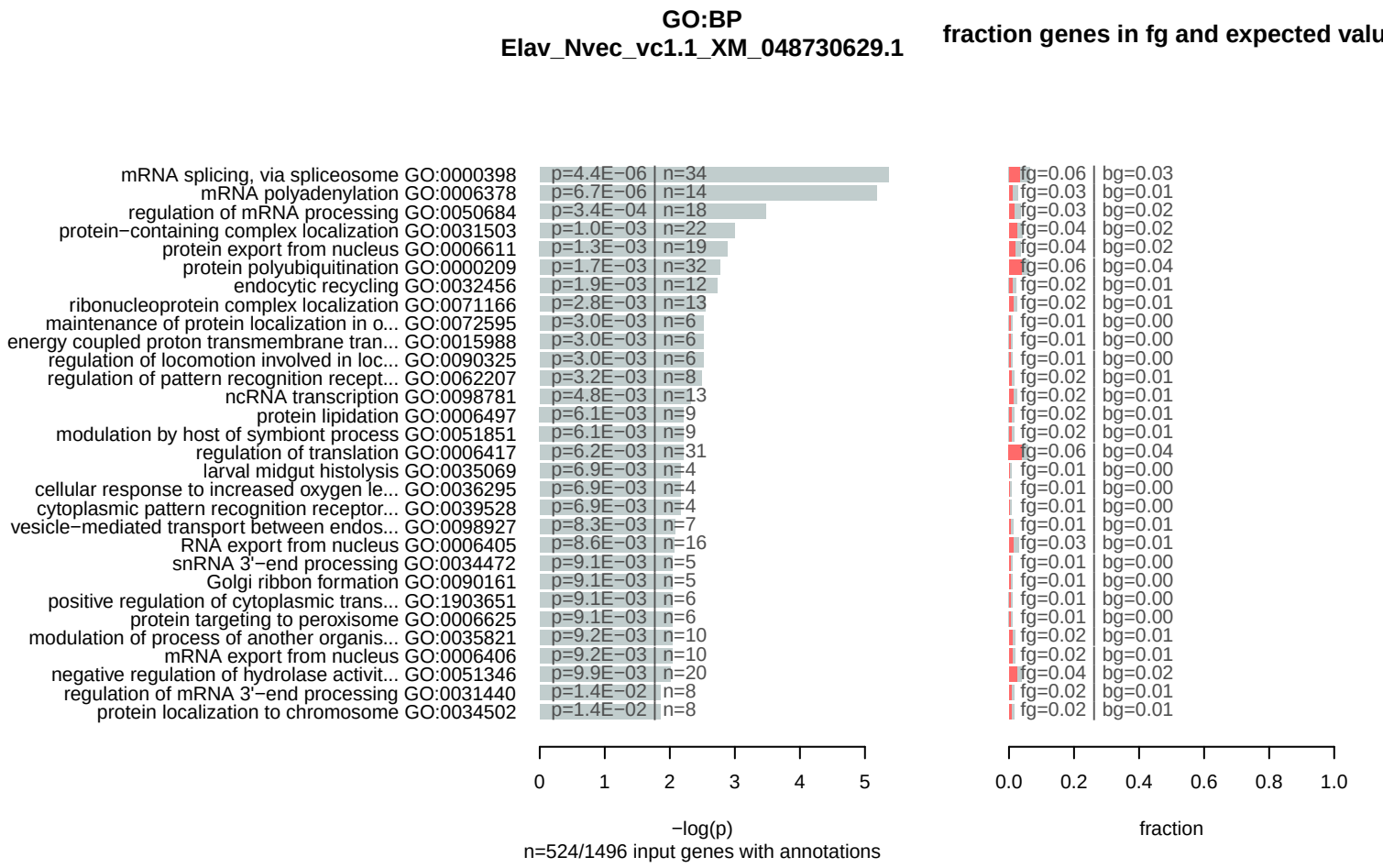
GO:BP
Elav_Nvec_vc1.1_XM_048730629.1
fraction genes in fg and expected valu
mRNA splicing, via spliceosome GO:0000398 p=4.4E−06 n=34 fg=0.06 bg=0.03
mRNA polyadenylation GO:0006378 p=6.7E−06 n=14 fg=0.03 bg=0.01
regulation of mRNA processing GO:0050684 p=3.4E−04 n=18 fg=0.03 bg=0.02
protein−containing complex localization GO:0031503 p=1.0E−03 n=22 fg=0.04 bg=0.02
protein export from nucleus GO:0006611 p=1.3E−03 n=19 fg=0.04 bg=0.02
protein polyubiquitination GO:0000209 p=1.7E−03 n=32 fg=0.06 bg=0.04
endocytic recycling GO:0032456 p=1.9E−03 n=12 fg=0.02 bg=0.01
ribonucleoprotein complex localization GO:0071166 p=2.8E−03 n=13 fg=0.02 bg=0.01
maintenance of protein localization in o... GO:0072595 p=3.0E−03 n=6 fg=0.01 bg=0.00
energy coupled proton transmembrane tran... GO:0015988 p=3.0E−03 n=6 fg=0.01 bg=0.00
regulation of locomotion involved in loc... GO:0090325 p=3.0E−03 n=6 fg=0.01 bg=0.00
regulation of pattern recognition recept... GO:0062207 p=3.2E−03 n=8 fg=0.02 bg=0.01
ncRNA transcription GO:0098781 p=4.8E−03 n=13 fg=0.02 bg=0.01
protein lipidation GO:0006497 p=6.1E−03 n=9 fg=0.02 bg=0.01
modulation by host of symbiont process GO:0051851 p=6.1E−03 n=9 fg=0.02 bg=0.01
regulation of translation GO:0006417 p=6.2E−03 n=31 fg=0.06 bg=0.04
larval midgut histolysis GO:0035069 p=6.9E−03 n=4 fg=0.01 bg=0.00
cellular response to increased oxygen le... GO:0036295 p=6.9E−03 n=4 fg=0.01 bg=0.00
cytoplasmic pattern recognition receptor... GO:0039528 p=6.9E−03 n=4 fg=0.01 bg=0.00
vesicle−mediated transport between endos... GO:0098927 p=8.3E−03 n=7 fg=0.01 bg=0.01
RNA export from nucleus GO:0006405 p=8.6E−03 n=16 fg=0.03 bg=0.01
snRNA 3'−end processing GO:0034472 p=9.1E−03 n=5 fg=0.01 bg=0.00
Golgi ribbon formation GO:0090161 p=9.1E−03 n=5 fg=0.01 bg=0.00
positive regulation of cytoplasmic trans... GO:1903651 p=9.1E−03 n=6 fg=0.01 bg=0.00
protein targeting to peroxisome GO:0006625 p=9.1E−03 n=6 fg=0.01 bg=0.00
modulation of process of another organis... GO:0035821 p=9.2E−03 n=10 fg=0.02 bg=0.01
mRNA export from nucleus GO:0006406 p=9.2E−03 n=10 fg=0.02 bg=0.01
negative regulation of hydrolase activit... GO:0051346 p=9.9E−03 n=20 fg=0.04 bg=0.02
regulation of mRNA 3'−end processing GO:0031440 p=1.4E−02 n=8 fg=0.02 bg=0.01
protein localization to chromosome GO:0034502 p=1.4E−02 n=8 fg=0.02 bg=0.01
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n=524/1496 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048730629.1
fraction genes in fg and expected valu
ubiquitin protein ligase activity GO:0061630 p=2.9E−04 n=28 fg=0.06 bg=0.04
ATP hydrolysis activity GO:0016887 p=2.4E−03 n=32 fg=0.07 bg=0.05
RNA binding GO:0003723 p=2.6E−03 n=59 fg=0.14 bg=0.09
mRNA binding GO:0003729 p=5.5E−03 n=22 fg=0.05 bg=0.03
single−stranded RNA binding GO:0003727 p=1.6E−02 n=10 fg=0.02 bg=0.01
polynucleotide adenylyltransferase activ... GO:0004652 p=1.9E−02 n=5 fg=0.01 bg=0.00
pre−mRNA intronic binding GO:0097157 p=2.0E−02 n=3 fg=0.01 bg=0.00
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=2.2E−02 n=4 fg=0.01 bg=0.00
proton−transporting ATPase activity, rot... GO:0046961 p=2.2E−02 n=4 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase binding GO:0043548 p=2.2E−02 n=4 fg=0.01 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=2.2E−02 n=4 fg=0.01 bg=0.00
phosphatase inhibitor activity GO:0019212 p=2.2E−02 n=4 fg=0.01 bg=0.00
proton transmembrane transporter activit... GO:0015078 p=2.2E−02 n=9 fg=0.02 bg=0.01
helicase activity GO:0004386 p=2.5E−02 n=10 fg=0.02 bg=0.01
small GTPase binding GO:0031267 p=2.6E−02 n=32 fg=0.07 bg=0.05
catalytic activity, acting on a nucleic ... GO:0140640 p=2.6E−02 n=31 fg=0.07 bg=0.05
GTPase binding GO:0051020 p=2.9E−02 n=38 fg=0.09 bg=0.07
ATPase−coupled ion transmembrane transpo... GO:0042625 p=3.8E−02 n=7 fg=0.02 bg=0.01
Notch binding GO:0005112 p=3.9E−02 n=5 fg=0.01 bg=0.01
microtubule motor activity GO:0003777 p=3.9E−02 n=5 fg=0.01 bg=0.01
SNARE binding GO:0000149 p=4.2E−02 n=13 fg=0.03 bg=0.02
nucleotidyltransferase activity GO:0016779 p=4.8E−02 n=9 fg=0.02 bg=0.01
catalytic activity, acting on RNA GO:0140098 p=5.0E−02 n=20 fg=0.05 bg=0.03
ATP−dependent activity, acting on RNA GO:0008186 p=5.1E−02 n=6 fg=0.01 bg=0.01
oxidoreductase activity, acting on the a... GO:0016903 p=6.5E−02 n=3 fg=0.01 bg=0.00
5'−3' RNA polymerase activity GO:0034062 p=6.5E−02 n=3 fg=0.01 bg=0.00
RNA polymerase activity GO:0097747 p=6.5E−02 n=3 fg=0.01 bg=0.00
protein phosphatase inhibitor activity GO:0004864 p=6.5E−02 n=3 fg=0.01 bg=0.00
adenylyltransferase activity GO:0070566 p=6.9E−02 n=5 fg=0.01 bg=0.01
ubiquitination−like modification−depende... GO:0140035 p=7.5E−02 n=2 fg=0.00 bg=0.00
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−log(p)
n=435/1496 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_048730629.1
fraction genes in fg and expected valu
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intracellular anatomical structure GO:0005622 p=1.2E−04 n=503 fg=0.98 bg=0.94
plasma membrane proton−transporting V−ty... GO:0033181 p=5.2E−04 n=6 fg=0.01 bg=0.00
nuclear protein−containing complex GO:0140513 p=8.0E−04 n=79 fg=0.15 bg=0.11
ribonucleoprotein complex GO:1990904 p=2.5E−03 n=54 fg=0.11 bg=0.07
vacuolar proton−transporting V−type ATPa... GO:0016471 p=2.7E−03 n=6 fg=0.01 bg=0.00
centrosome GO:0005813 p=4.4E−03 n=38 fg=0.07 bg=0.05
recycling endosome GO:0055037 p=5.3E−03 n=19 fg=0.04 bg=0.02
intracellular protein−containing complex GO:0140535 p=6.0E−03 n=63 fg=0.12 bg=0.09
RNA polymerase complex GO:0030880 p=6.4E−03 n=15 fg=0.03 bg=0.02
catalytic step 2 spliceosome GO:0071013 p=6.5E−03 n=8 fg=0.02 bg=0.01
peroxisomal matrix GO:0005782 p=6.5E−03 n=4 fg=0.01 bg=0.00
methyltransferase complex GO:0034708 p=6.5E−03 n=11 fg=0.02 bg=0.01
cytosol GO:0005829 p=1.8E−02 n=220 fg=0.43 bg=0.39
trans−Golgi network GO:0005802 p=2.2E−02 n=27 fg=0.05 bg=0.04
DNA−directed RNA polymerase complex GO:0000428 p=2.2E−02 n=13 fg=0.03 bg=0.01
MLL1/2 complex GO:0044665 p=2.2E−02 n=5 fg=0.01 bg=0.00
GARP complex GO:0000938 p=2.3E−02 n=3 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=2.3E−02 n=3 fg=0.01 bg=0.00
proton−transporting two−sector ATPase co... GO:0033178 p=2.3E−02 n=3 fg=0.01 bg=0.00
mRNA editing complex GO:0045293 p=2.3E−02 n=3 fg=0.01 bg=0.00
EARP complex GO:1990745 p=2.3E−02 n=3 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=2.3E−02 n=3 fg=0.01 bg=0.00
RNA N6−methyladenosine methyltransferase... GO:0036396 p=2.3E−02 n=3 fg=0.01 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=2.3E−02 n=3 fg=0.01 bg=0.00
Prp19 complex GO:0000974 p=2.3E−02 n=3 fg=0.01 bg=0.00
intracellular organelle GO:0043229 p=2.4E−02 n=456 fg=0.89 bg=0.84
organelle GO:0043226 p=2.9E−02 n=462 fg=0.90 bg=0.85
nucleus GO:0005634 p=3.0E−02 n=285 fg=0.55 bg=0.48
membrane−bounded organelle GO:0043227 p=3.1E−02 n=441 fg=0.86 bg=0.81
0 1 2 3 4 5
−log(p)
n=514/1496 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction