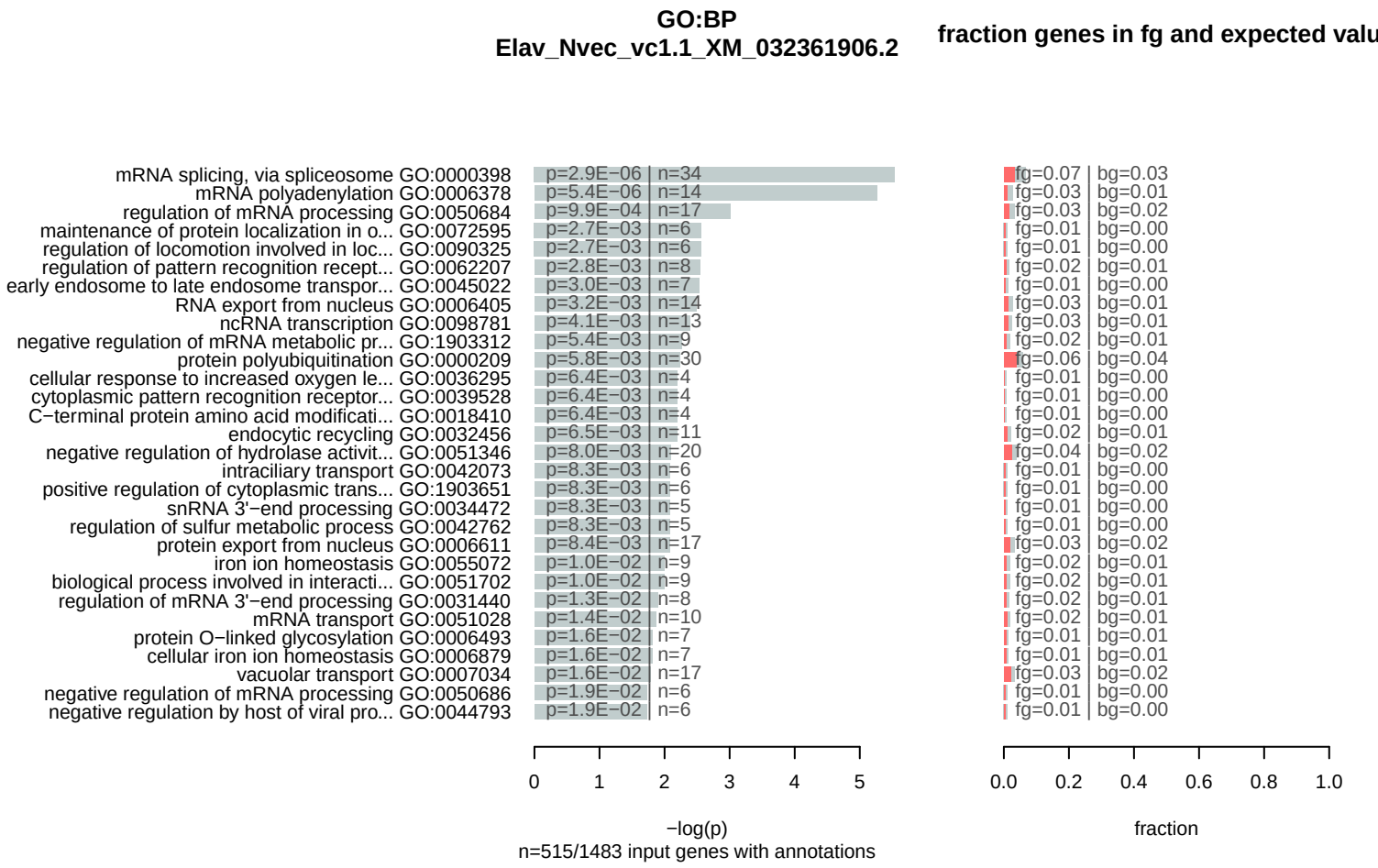
GO:BP
Elav_Nvec_vc1.1_XM_032361906.2
fraction genes in fg and expected valu
mRNA splicing, via spliceosome GO:0000398 p=2.9E−06 n=34 fg=0.07 bg=0.03
mRNA polyadenylation GO:0006378 p=5.4E−06 n=14 fg=0.03 bg=0.01
regulation of mRNA processing GO:0050684 p=9.9E−04 n=17 fg=0.03 bg=0.02
maintenance of protein localization in o... GO:0072595 p=2.7E−03 n=6 fg=0.01 bg=0.00
regulation of locomotion involved in loc... GO:0090325 p=2.7E−03 n=6 fg=0.01 bg=0.00
regulation of pattern recognition recept... GO:0062207 p=2.8E−03 n=8 fg=0.02 bg=0.01
early endosome to late endosome transpor... GO:0045022 p=3.0E−03 n=7 fg=0.01 bg=0.00
RNA export from nucleus GO:0006405 p=3.2E−03 n=14 fg=0.03 bg=0.01
ncRNA transcription GO:0098781 p=4.1E−03 n=13 fg=0.03 bg=0.01
negative regulation of mRNA metabolic pr... GO:1903312 p=5.4E−03 n=9 fg=0.02 bg=0.01
protein polyubiquitination GO:0000209 p=5.8E−03 n=30 fg=0.06 bg=0.04
cellular response to increased oxygen le... GO:0036295 p=6.4E−03 n=4 fg=0.01 bg=0.00
cytoplasmic pattern recognition receptor... GO:0039528 p=6.4E−03 n=4 fg=0.01 bg=0.00
C−terminal protein amino acid modificati... GO:0018410 p=6.4E−03 n=4 fg=0.01 bg=0.00
endocytic recycling GO:0032456 p=6.5E−03 n=11 fg=0.02 bg=0.01
negative regulation of hydrolase activit... GO:0051346 p=8.0E−03 n=20 fg=0.04 bg=0.02
intraciliary transport GO:0042073 p=8.3E−03 n=6 fg=0.01 bg=0.00
positive regulation of cytoplasmic trans... GO:1903651 p=8.3E−03 n=6 fg=0.01 bg=0.00
snRNA 3'−end processing GO:0034472 p=8.3E−03 n=5 fg=0.01 bg=0.00
regulation of sulfur metabolic process GO:0042762 p=8.3E−03 n=5 fg=0.01 bg=0.00
protein export from nucleus GO:0006611 p=8.4E−03 n=17 fg=0.03 bg=0.02
iron ion homeostasis GO:0055072 p=1.0E−02 n=9 fg=0.02 bg=0.01
biological process involved in interacti... GO:0051702 p=1.0E−02 n=9 fg=0.02 bg=0.01
regulation of mRNA 3'−end processing GO:0031440 p=1.3E−02 n=8 fg=0.02 bg=0.01
mRNA transport GO:0051028 p=1.4E−02 n=10 fg=0.02 bg=0.01
protein O−linked glycosylation GO:0006493 p=1.6E−02 n=7 fg=0.01 bg=0.01
cellular iron ion homeostasis GO:0006879 p=1.6E−02 n=7 fg=0.01 bg=0.01
vacuolar transport GO:0007034 p=1.6E−02 n=17 fg=0.03 bg=0.02
negative regulation of mRNA processing GO:0050686 p=1.9E−02 n=6 fg=0.01 bg=0.00
negative regulation by host of viral pro... GO:0044793 p=1.9E−02 n=6 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=515/1483 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032361906.2
fraction genes in fg and expected valu
RNA binding GO:0003723 p=1.1E−03 n=54 fg=0.13 bg=0.09
ubiquitin protein ligase activity GO:0061630 p=1.4E−03 n=26 fg=0.06 bg=0.04
protein phosphatase inhibitor activity GO:0004864 p=5.1E−03 n=4 fg=0.01 bg=0.00
small GTPase binding GO:0031267 p=5.4E−03 n=34 fg=0.08 bg=0.05
ATP−dependent activity GO:0140657 p=1.1E−02 n=32 fg=0.08 bg=0.05
polynucleotide adenylyltransferase activ... GO:0004652 p=1.7E−02 n=5 fg=0.01 bg=0.00
pre−mRNA intronic binding GO:0097157 p=1.9E−02 n=3 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase binding GO:0043548 p=2.0E−02 n=4 fg=0.01 bg=0.00
nuclear localization sequence binding GO:0008139 p=2.0E−02 n=4 fg=0.01 bg=0.00
helicase activity GO:0004386 p=2.2E−02 n=10 fg=0.02 bg=0.01
ATP hydrolysis activity GO:0016887 p=2.6E−02 n=28 fg=0.07 bg=0.05
catalytic activity, acting on a nucleic ... GO:0140640 p=3.4E−02 n=30 fg=0.07 bg=0.05
nucleoside−triphosphatase activity GO:0017111 p=3.5E−02 n=40 fg=0.09 bg=0.07
signal sequence binding GO:0005048 p=3.6E−02 n=5 fg=0.01 bg=0.01
single−stranded RNA binding GO:0003727 p=4.3E−02 n=9 fg=0.02 bg=0.01
pyrophosphatase activity GO:0016462 p=5.2E−02 n=40 fg=0.09 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016817 p=5.2E−02 n=40 fg=0.09 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016818 p=5.2E−02 n=40 fg=0.09 bg=0.07
proton transmembrane transporter activit... GO:0015078 p=5.7E−02 n=8 fg=0.02 bg=0.01
ligand−activated transcription factor ac... GO:0098531 p=6.1E−02 n=3 fg=0.01 bg=0.00
endonuclease activity, active with eithe... GO:0016893 p=6.1E−02 n=3 fg=0.01 bg=0.00
RNA polymerase II general transcription ... GO:0001091 p=6.1E−02 n=3 fg=0.01 bg=0.00
nuclear receptor activity GO:0004879 p=6.1E−02 n=3 fg=0.01 bg=0.00
adenylyltransferase activity GO:0070566 p=6.3E−02 n=5 fg=0.01 bg=0.01
ubiquitination−like modification−depende... GO:0140035 p=7.1E−02 n=2 fg=0.00 bg=0.00
ubiquitin−dependent protein binding GO:0140036 p=7.1E−02 n=2 fg=0.00 bg=0.00
PTB domain binding GO:0051425 p=7.1E−02 n=2 fg=0.00 bg=0.00
telomerase RNA binding GO:0070034 p=7.1E−02 n=2 fg=0.00 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=7.1E−02 n=2 fg=0.00 bg=0.00
eukaryotic translation initiation factor... GO:0004694 p=7.1E−02 n=2 fg=0.00 bg=0.00
0 1 2 3 4 5
−log(p)
n=426/1483 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032361906.2
fraction genes in fg and expected valu
nucleoplasm GO:0005654 p=1.0E−04 n=170 fg=0.34 bg=0.27
intracellular anatomical structure GO:0005622 p=4.0E−04 n=492 fg=0.97 bg=0.94
nuclear protein−containing complex GO:0140513 p=1.4E−03 n=77 fg=0.15 bg=0.11
intracellular protein−containing complex GO:0140535 p=2.2E−03 n=59 fg=0.12 bg=0.09
methyltransferase complex GO:0034708 p=5.6E−03 n=11 fg=0.02 bg=0.01
catalytic step 2 spliceosome GO:0071013 p=5.7E−03 n=8 fg=0.02 bg=0.01
plasma membrane proton−transporting V−ty... GO:0033181 p=7.7E−03 n=5 fg=0.01 bg=0.00
nuclear envelope lumen GO:0005641 p=7.7E−03 n=5 fg=0.01 bg=0.00
RNA polymerase complex GO:0030880 p=1.5E−02 n=14 fg=0.03 bg=0.02
microtubule organizing center GO:0005815 p=1.9E−02 n=44 fg=0.09 bg=0.07
centrosome GO:0005813 p=2.0E−02 n=35 fg=0.07 bg=0.05
MLL1/2 complex GO:0044665 p=2.1E−02 n=5 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0016471 p=2.1E−02 n=5 fg=0.01 bg=0.00
GARP complex GO:0000938 p=2.2E−02 n=3 fg=0.01 bg=0.00
mRNA editing complex GO:0045293 p=2.2E−02 n=3 fg=0.01 bg=0.00
EARP complex GO:1990745 p=2.2E−02 n=3 fg=0.01 bg=0.00
RNA N6−methyladenosine methyltransferase... GO:0036396 p=2.2E−02 n=3 fg=0.01 bg=0.00
exon−exon junction complex GO:0035145 p=2.2E−02 n=3 fg=0.01 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=2.2E−02 n=3 fg=0.01 bg=0.00
Prp19 complex GO:0000974 p=2.2E−02 n=3 fg=0.01 bg=0.00
catalytic complex GO:1902494 p=2.5E−02 n=91 fg=0.18 bg=0.14
endosome membrane GO:0010008 p=2.7E−02 n=25 fg=0.05 bg=0.03
ribonucleoprotein complex GO:1990904 p=2.8E−02 n=49 fg=0.10 bg=0.07
polytene chromosome GO:0005700 p=2.9E−02 n=14 fg=0.03 bg=0.02
nuclear DNA−directed RNA polymerase comp... GO:0055029 p=3.5E−02 n=12 fg=0.02 bg=0.01
RNA polymerase II, holoenzyme GO:0016591 p=3.5E−02 n=12 fg=0.02 bg=0.01
intracellular organelle GO:0043229 p=3.6E−02 n=443 fg=0.88 bg=0.84
nuclear body GO:0016604 p=3.8E−02 n=41 fg=0.08 bg=0.06
vacuolar membrane GO:0005774 p=4.0E−02 n=24 fg=0.05 bg=0.03
cytosol GO:0005829 p=4.1E−02 n=213 fg=0.42 bg=0.39
0 1 2 3 4 5
−log(p)
n=505/1483 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction