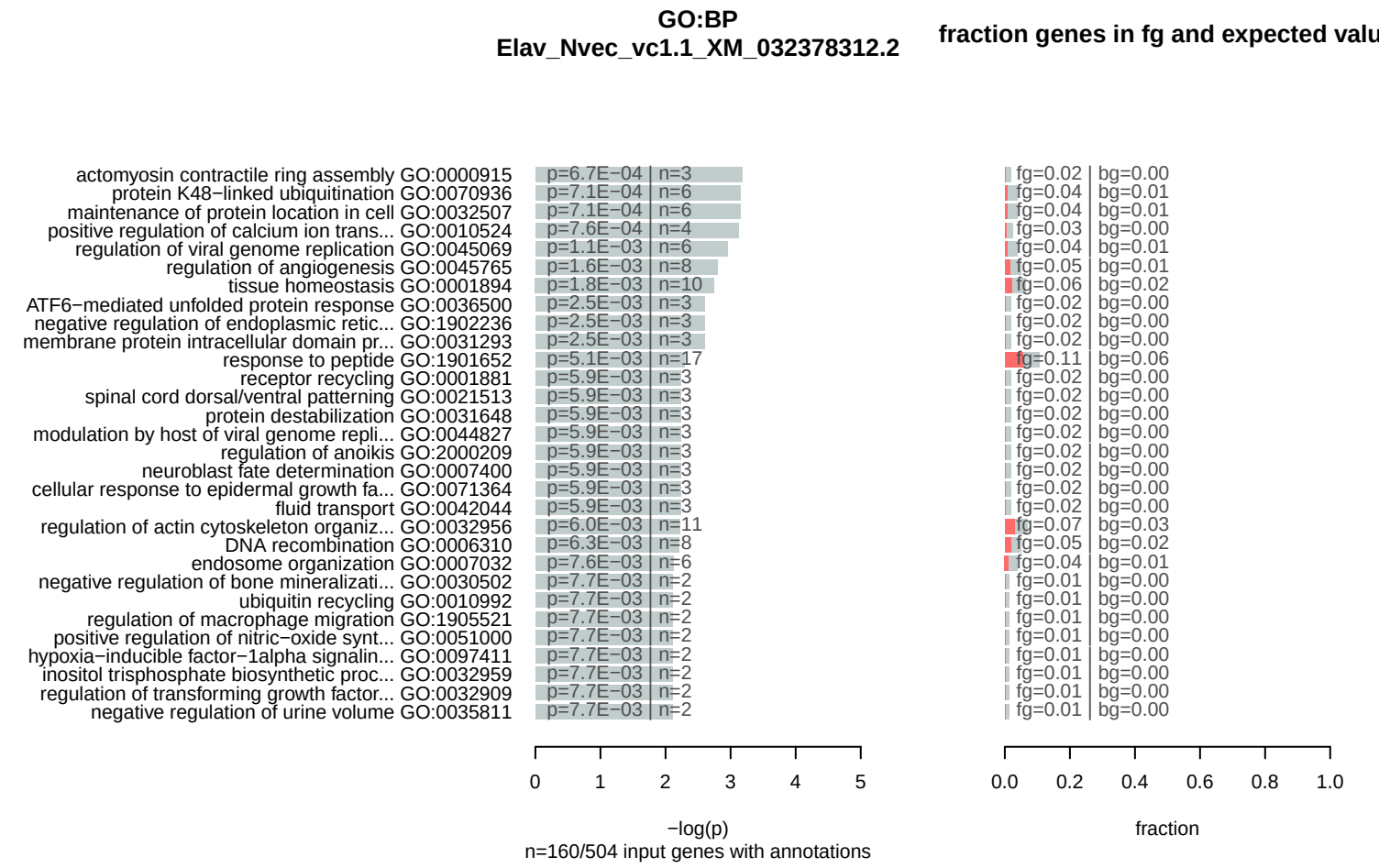
GO:BP
Elav_Nvec_vc1.1_XM_032378312.2
fraction genes in fg and expected valu
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protein K48−linked ubiquitination GO:0070936 p=7.1E−04 n=6 fg=0.04 bg=0.01
maintenance of protein location in cell GO:0032507 p=7.1E−04 n=6 fg=0.04 bg=0.01
positive regulation of calcium ion trans... GO:0010524 p=7.6E−04 n=4 fg=0.03 bg=0.00
regulation of viral genome replication GO:0045069 p=1.1E−03 n=6 fg=0.04 bg=0.01
regulation of angiogenesis GO:0045765 p=1.6E−03 n=8 fg=0.05 bg=0.01
tissue homeostasis GO:0001894 p=1.8E−03 n=10 fg=0.06 bg=0.02
ATF6−mediated unfolded protein response GO:0036500 p=2.5E−03 n=3 fg=0.02 bg=0.00
negative regulation of endoplasmic retic... GO:1902236 p=2.5E−03 n=3 fg=0.02 bg=0.00
membrane protein intracellular domain pr... GO:0031293 p=2.5E−03 n=3 fg=0.02 bg=0.00
response to peptide GO:1901652 p=5.1E−03 n=17 fg=0.11 bg=0.06
receptor recycling GO:0001881 p=5.9E−03 n=3 fg=0.02 bg=0.00
spinal cord dorsal/ventral patterning GO:0021513 p=5.9E−03 n=3 fg=0.02 bg=0.00
protein destabilization GO:0031648 p=5.9E−03 n=3 fg=0.02 bg=0.00
modulation by host of viral genome repli... GO:0044827 p=5.9E−03 n=3 fg=0.02 bg=0.00
regulation of anoikis GO:2000209 p=5.9E−03 n=3 fg=0.02 bg=0.00
neuroblast fate determination GO:0007400 p=5.9E−03 n=3 fg=0.02 bg=0.00
cellular response to epidermal growth fa... GO:0071364 p=5.9E−03 n=3 fg=0.02 bg=0.00
fluid transport GO:0042044 p=5.9E−03 n=3 fg=0.02 bg=0.00
regulation of actin cytoskeleton organiz... GO:0032956 p=6.0E−03 n=11 fg=0.07 bg=0.03
DNA recombination GO:0006310 p=6.3E−03 n=8 fg=0.05 bg=0.02
endosome organization GO:0007032 p=7.6E−03 n=6 fg=0.04 bg=0.01
negative regulation of bone mineralizati... GO:0030502 p=7.7E−03 n=2 fg=0.01 bg=0.00
ubiquitin recycling GO:0010992 p=7.7E−03 n=2 fg=0.01 bg=0.00
regulation of macrophage migration GO:1905521 p=7.7E−03 n=2 fg=0.01 bg=0.00
positive regulation of nitric−oxide synt... GO:0051000 p=7.7E−03 n=2 fg=0.01 bg=0.00
hypoxia−inducible factor−1alpha signalin... GO:0097411 p=7.7E−03 n=2 fg=0.01 bg=0.00
inositol trisphosphate biosynthetic proc... GO:0032959 p=7.7E−03 n=2 fg=0.01 bg=0.00
regulation of transforming growth factor... GO:0032909 p=7.7E−03 n=2 fg=0.01 bg=0.00
negative regulation of urine volume GO:0035811 p=7.7E−03 n=2 fg=0.01 bg=0.00
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−log(p)
n=160/504 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032378312.2
fraction genes in fg and expected valu
poly(U) RNA binding GO:0008266 p=2.8E−04 n=4 fg=0.03 bg=0.00
organic cyclic compound binding GO:0097159 p=6.6E−04 n=58 fg=0.41 bg=0.27
heterocyclic compound binding GO:1901363 p=2.9E−03 n=55 fg=0.39 bg=0.27
ATPase binding GO:0051117 p=5.9E−03 n=6 fg=0.04 bg=0.01
ubiquitin conjugating enzyme activity GO:0061631 p=1.2E−02 n=4 fg=0.03 bg=0.01
nucleic acid binding GO:0003676 p=1.6E−02 n=40 fg=0.28 bg=0.19
ubiquitin−like protein conjugating enzym... GO:0061650 p=1.7E−02 n=4 fg=0.03 bg=0.01
ubiquitin−like protein transferase activ... GO:0019787 p=1.7E−02 n=15 fg=0.11 bg=0.06
transferase activity, transferring nitro... GO:0016769 p=1.8E−02 n=3 fg=0.02 bg=0.00
GTPase binding GO:0051020 p=2.0E−02 n=16 fg=0.11 bg=0.07
cAMP response element binding GO:0035497 p=2.2E−02 n=2 fg=0.01 bg=0.00
L−histidine transmembrane transporter ac... GO:0005290 p=2.2E−02 n=2 fg=0.01 bg=0.00
basic amino acid transmembrane transport... GO:0015174 p=2.2E−02 n=2 fg=0.01 bg=0.00
peptide:proton symporter activity GO:0015333 p=2.2E−02 n=2 fg=0.01 bg=0.00
vitamin binding GO:0019842 p=2.2E−02 n=4 fg=0.03 bg=0.01
ubiquitin protein ligase binding GO:0031625 p=2.4E−02 n=11 fg=0.08 bg=0.04
metalloendopeptidase activity GO:0004222 p=2.7E−02 n=3 fg=0.02 bg=0.01
ubiquitin−protein transferase activity GO:0004842 p=2.8E−02 n=14 fg=0.10 bg=0.06
SH2 domain binding GO:0042169 p=3.8E−02 n=3 fg=0.02 bg=0.01
ubiquitin−like protein ligase binding GO:0044389 p=4.0E−02 n=11 fg=0.08 bg=0.04
azole transmembrane transporter activity GO:1901474 p=4.1E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol phosphate 5−phospha... GO:0034595 p=4.1E−02 n=2 fg=0.01 bg=0.00
aromatic amino acid transmembrane transp... GO:0015173 p=4.1E−02 n=2 fg=0.01 bg=0.00
gamma−tubulin binding GO:0043015 p=4.1E−02 n=2 fg=0.01 bg=0.00
tubulin binding GO:0015631 p=4.8E−02 n=9 fg=0.06 bg=0.03
RNA helicase activity GO:0003724 p=5.1E−02 n=3 fg=0.02 bg=0.01
p53 binding GO:0002039 p=5.6E−02 n=4 fg=0.03 bg=0.01
ubiquitin−like protein ligase activity GO:0061659 p=5.9E−02 n=9 fg=0.06 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=5.9E−02 n=9 fg=0.06 bg=0.04
phosphatidylinositol 3−kinase binding GO:0043548 p=6.5E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=141/504 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032378312.2
fraction genes in fg and expected valu
P−body GO:0000932 p=3.7E−04 n=7 fg=0.04 bg=0.01
mitochondrial large ribosomal subunit GO:0005762 p=2.6E−03 n=3 fg=0.02 bg=0.00
ribonucleoprotein complex GO:1990904 p=8.2E−03 n=22 fg=0.14 bg=0.07
nuclear membrane GO:0031965 p=1.4E−02 n=8 fg=0.05 bg=0.02
small−subunit processome GO:0032040 p=2.3E−02 n=2 fg=0.01 bg=0.00
90S preribosome GO:0030686 p=2.3E−02 n=2 fg=0.01 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=2.3E−02 n=2 fg=0.01 bg=0.00
germ plasm GO:0060293 p=2.3E−02 n=4 fg=0.02 bg=0.01
pole plasm GO:0045495 p=2.3E−02 n=4 fg=0.02 bg=0.01
neuron projection terminus GO:0044306 p=2.7E−02 n=9 fg=0.06 bg=0.03
nucleus GO:0005634 p=2.9E−02 n=89 fg=0.55 bg=0.48
membrane−bounded organelle GO:0043227 p=3.5E−02 n=140 fg=0.86 bg=0.81
cytoplasmic region GO:0099568 p=3.9E−02 n=14 fg=0.09 bg=0.05
ribonucleoprotein granule GO:0035770 p=3.9E−02 n=13 fg=0.08 bg=0.03
cytoplasmic stress granule GO:0010494 p=5.3E−02 n=3 fg=0.02 bg=0.01
ruffle membrane GO:0032587 p=5.3E−02 n=3 fg=0.02 bg=0.01
axon terminus GO:0043679 p=5.3E−02 n=8 fg=0.05 bg=0.03
heterochromatin GO:0000792 p=5.9E−02 n=4 fg=0.02 bg=0.01
clathrin−coated vesicle GO:0030136 p=6.0E−02 n=6 fg=0.04 bg=0.02
adherens junction GO:0005912 p=6.0E−02 n=7 fg=0.04 bg=0.02
cell cortex GO:0005938 p=6.1E−02 n=11 fg=0.07 bg=0.04
spliceosomal complex GO:0005681 p=6.6E−02 n=5 fg=0.03 bg=0.01
contractile ring GO:0070938 p=6.7E−02 n=2 fg=0.01 bg=0.00
terminal bouton GO:0043195 p=6.8E−02 n=6 fg=0.04 bg=0.02
presynaptic active zone GO:0048786 p=7.0E−02 n=4 fg=0.02 bg=0.01
ruffle GO:0001726 p=7.0E−02 n=4 fg=0.02 bg=0.01
cytoplasmic ribonucleoprotein granule GO:0036464 p=7.7E−02 n=12 fg=0.07 bg=0.02
synaptic vesicle membrane GO:0030672 p=8.3E−02 n=4 fg=0.02 bg=0.01
P granule GO:0043186 p=8.5E−02 n=3 fg=0.02 bg=0.01
catalytic step 2 spliceosome GO:0071013 p=8.5E−02 n=3 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
n=162/504 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction