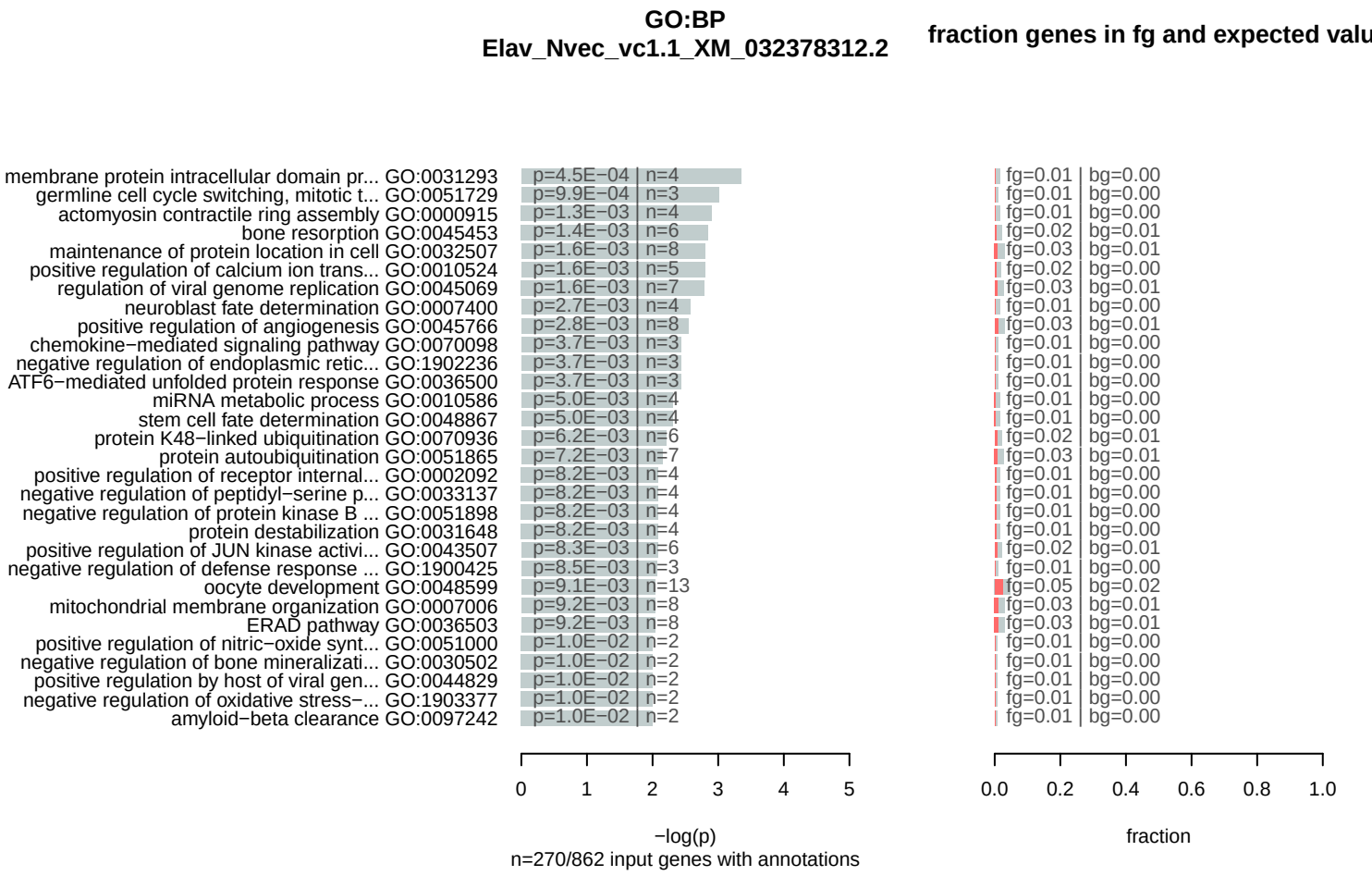
GO:BP
Elav_Nvec_vc1.1_XM_032378312.2
fraction genes in fg and expected valu
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germline cell cycle switching, mitotic t... GO:0051729 p=9.9E−04 n=3 fg=0.01 bg=0.00
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regulation of viral genome replication GO:0045069 p=1.6E−03 n=7 fg=0.03 bg=0.01
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negative regulation of endoplasmic retic... GO:1902236 p=3.7E−03 n=3 fg=0.01 bg=0.00
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miRNA metabolic process GO:0010586 p=5.0E−03 n=4 fg=0.01 bg=0.00
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positive regulation of receptor internal... GO:0002092 p=8.2E−03 n=4 fg=0.01 bg=0.00
negative regulation of peptidyl−serine p... GO:0033137 p=8.2E−03 n=4 fg=0.01 bg=0.00
negative regulation of protein kinase B ... GO:0051898 p=8.2E−03 n=4 fg=0.01 bg=0.00
protein destabilization GO:0031648 p=8.2E−03 n=4 fg=0.01 bg=0.00
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mitochondrial membrane organization GO:0007006 p=9.2E−03 n=8 fg=0.03 bg=0.01
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negative regulation of oxidative stress−... GO:1903377 p=1.0E−02 n=2 fg=0.01 bg=0.00
amyloid−beta clearance GO:0097242 p=1.0E−02 n=2 fg=0.01 bg=0.00
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fraction
GO:MF
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gamma−tubulin binding GO:0043015 p=1.2E−03 n=4 fg=0.02 bg=0.00
mRNA 3'−UTR binding GO:0003730 p=3.0E−03 n=6 fg=0.03 bg=0.01
zinc ion binding GO:0008270 p=6.8E−03 n=18 fg=0.08 bg=0.04
enzyme binding GO:0019899 p=8.8E−03 n=67 fg=0.29 bg=0.22
ubiquitin protein ligase activity GO:0061630 p=9.1E−03 n=14 fg=0.06 bg=0.03
cis−trans isomerase activity GO:0016859 p=1.2E−02 n=4 fg=0.02 bg=0.00
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GTPase binding GO:0051020 p=1.3E−02 n=21 fg=0.09 bg=0.05
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transferase activity, transferring nitro... GO:0016769 p=2.5E−02 n=3 fg=0.01 bg=0.00
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cAMP response element binding GO:0035497 p=2.7E−02 n=2 fg=0.01 bg=0.00
basic amino acid transmembrane transport... GO:0015174 p=2.7E−02 n=2 fg=0.01 bg=0.00
L−histidine transmembrane transporter ac... GO:0005290 p=2.7E−02 n=2 fg=0.01 bg=0.00
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ubiquitin−like protein ligase binding GO:0044389 p=2.8E−02 n=15 fg=0.06 bg=0.04
small GTPase binding GO:0031267 p=2.8E−02 n=17 fg=0.07 bg=0.04
amide binding GO:0033218 p=3.1E−02 n=12 fg=0.05 bg=0.03
RNA polymerase binding GO:0070063 p=3.2E−02 n=4 fg=0.02 bg=0.01
ubiquitin conjugating enzyme activity GO:0061631 p=3.2E−02 n=4 fg=0.02 bg=0.01
phosphotyrosine residue binding GO:0001784 p=3.7E−02 n=3 fg=0.01 bg=0.00
organic cyclic compound binding GO:0097159 p=3.7E−02 n=85 fg=0.36 bg=0.29
small molecule binding GO:0036094 p=4.0E−02 n=33 fg=0.14 bg=0.10
ubiquitin−like protein conjugating enzym... GO:0061650 p=4.2E−02 n=4 fg=0.02 bg=0.01
glycolipid binding GO:0051861 p=5.1E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=234/862 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032378312.2
fraction genes in fg and expected valu
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90S preribosome GO:0030686 p=1.7E−04 n=6 fg=0.02 bg=0.00
small−subunit processome GO:0032040 p=6.4E−04 n=6 fg=0.02 bg=0.00
interphase microtubule organizing center GO:0031021 p=1.1E−02 n=2 fg=0.01 bg=0.00
ribonucleoprotein complex GO:1990904 p=1.5E−02 n=41 fg=0.15 bg=0.09
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mitochondrial large ribosomal subunit GO:0005762 p=2.1E−02 n=4 fg=0.01 bg=0.00
pole plasm GO:0045495 p=2.5E−02 n=5 fg=0.02 bg=0.01
germ plasm GO:0060293 p=2.5E−02 n=5 fg=0.02 bg=0.01
apical dendrite GO:0097440 p=2.8E−02 n=3 fg=0.01 bg=0.00
Cul2−RING ubiquitin ligase complex GO:0031462 p=2.8E−02 n=3 fg=0.01 bg=0.00
centrosome GO:0005813 p=2.8E−02 n=22 fg=0.08 bg=0.05
ruffle membrane GO:0032587 p=2.9E−02 n=4 fg=0.01 bg=0.00
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membrane−bounded organelle GO:0043227 p=2.9E−02 n=236 fg=0.84 bg=0.80
endoplasmic reticulum exit site GO:0070971 p=3.0E−02 n=2 fg=0.01 bg=0.00
Cul5−RING ubiquitin ligase complex GO:0031466 p=3.0E−02 n=2 fg=0.01 bg=0.00
catalytic step 2 spliceosome GO:0071013 p=3.2E−02 n=6 fg=0.02 bg=0.01
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ribonucleoprotein granule GO:0035770 p=4.9E−02 n=17 fg=0.06 bg=0.02
microtubule organizing center GO:0005815 p=4.9E−02 n=26 fg=0.09 bg=0.07
mitochondrial intermembrane space protei... GO:0042719 p=5.6E−02 n=2 fg=0.01 bg=0.00
mitochondrial protein−containing complex GO:0098798 p=5.6E−02 n=11 fg=0.04 bg=0.02
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non−membrane−bounded organelle GO:0043228 p=7.5E−02 n=109 fg=0.39 bg=0.33
intracellular non−membrane−bounded organ... GO:0043232 p=7.5E−02 n=109 fg=0.39 bg=0.33
P granule GO:0043186 p=7.6E−02 n=4 fg=0.01 bg=0.01
SCF ubiquitin ligase complex GO:0019005 p=7.6E−02 n=4 fg=0.01 bg=0.01
0 1 2 3 4 5
−log(p)
n=280/862 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction