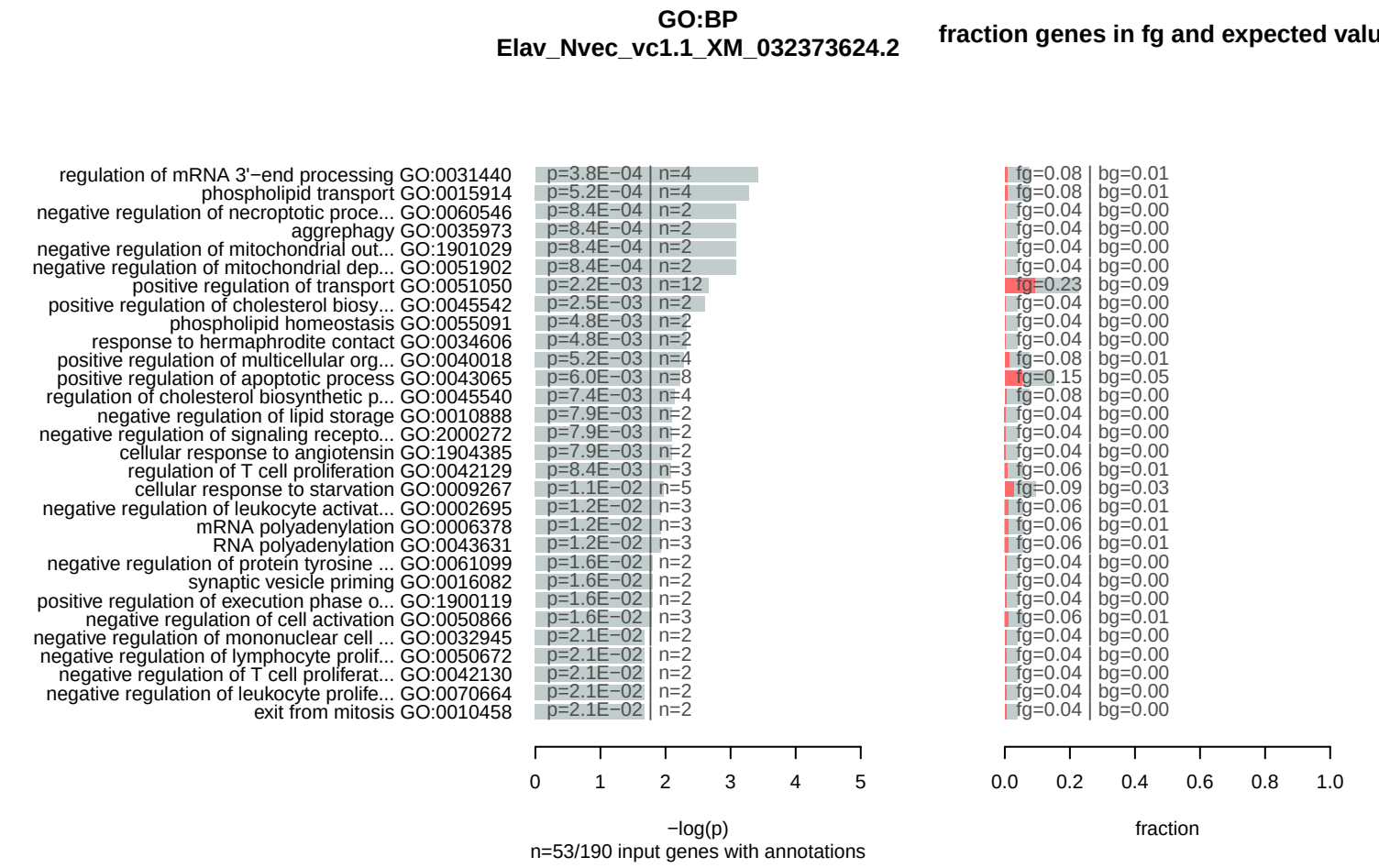
GO:BP
Elav_Nvec_vc1.1_XM_032373624.2
fraction genes in fg and expected valu
regulation of mRNA 3'−end processing GO:0031440 p=3.8E−04 n=4 fg=0.08 bg=0.01
phospholipid transport GO:0015914 p=5.2E−04 n=4 fg=0.08 bg=0.01
negative regulation of necroptotic proce... GO:0060546 p=8.4E−04 n=2 fg=0.04 bg=0.00
aggrephagy GO:0035973 p=8.4E−04 n=2 fg=0.04 bg=0.00
negative regulation of mitochondrial out... GO:1901029 p=8.4E−04 n=2 fg=0.04 bg=0.00
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positive regulation of transport GO:0051050 p=2.2E−03 n=12 fg=0.23 bg=0.09
positive regulation of cholesterol biosy... GO:0045542 p=2.5E−03 n=2 fg=0.04 bg=0.00
phospholipid homeostasis GO:0055091 p=4.8E−03 n=2 fg=0.04 bg=0.00
response to hermaphrodite contact GO:0034606 p=4.8E−03 n=2 fg=0.04 bg=0.00
positive regulation of multicellular org... GO:0040018 p=5.2E−03 n=4 fg=0.08 bg=0.01
positive regulation of apoptotic process GO:0043065 p=6.0E−03 n=8 fg=0.15 bg=0.05
regulation of cholesterol biosynthetic p... GO:0045540 p=7.4E−03 n=4 fg=0.08 bg=0.00
negative regulation of lipid storage GO:0010888 p=7.9E−03 n=2 fg=0.04 bg=0.00
negative regulation of signaling recepto... GO:2000272 p=7.9E−03 n=2 fg=0.04 bg=0.00
cellular response to angiotensin GO:1904385 p=7.9E−03 n=2 fg=0.04 bg=0.00
regulation of T cell proliferation GO:0042129 p=8.4E−03 n=3 fg=0.06 bg=0.01
cellular response to starvation GO:0009267 p=1.1E−02 n=5 fg=0.09 bg=0.03
negative regulation of leukocyte activat... GO:0002695 p=1.2E−02 n=3 fg=0.06 bg=0.01
mRNA polyadenylation GO:0006378 p=1.2E−02 n=3 fg=0.06 bg=0.01
RNA polyadenylation GO:0043631 p=1.2E−02 n=3 fg=0.06 bg=0.01
negative regulation of protein tyrosine ... GO:0061099 p=1.6E−02 n=2 fg=0.04 bg=0.00
synaptic vesicle priming GO:0016082 p=1.6E−02 n=2 fg=0.04 bg=0.00
positive regulation of execution phase o... GO:1900119 p=1.6E−02 n=2 fg=0.04 bg=0.00
negative regulation of cell activation GO:0050866 p=1.6E−02 n=3 fg=0.06 bg=0.01
negative regulation of mononuclear cell ... GO:0032945 p=2.1E−02 n=2 fg=0.04 bg=0.00
negative regulation of lymphocyte prolif... GO:0050672 p=2.1E−02 n=2 fg=0.04 bg=0.00
negative regulation of T cell proliferat... GO:0042130 p=2.1E−02 n=2 fg=0.04 bg=0.00
negative regulation of leukocyte prolife... GO:0070664 p=2.1E−02 n=2 fg=0.04 bg=0.00
exit from mitosis GO:0010458 p=2.1E−02 n=2 fg=0.04 bg=0.00
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−log(p)
n=53/190 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032373624.2
fraction genes in fg and expected valu
phospholipid transporter activity GO:0005548 p=4.3E−04 n=4 fg=0.08 bg=0.01
RNA polymerase II cis−regulatory region ... GO:0000978 p=6.2E−03 n=6 fg=0.12 bg=0.04
DNA−binding transcription activator acti... GO:0001228 p=8.6E−03 n=6 fg=0.12 bg=0.04
actin filament binding GO:0051015 p=9.1E−03 n=3 fg=0.06 bg=0.01
cholesterol binding GO:0015485 p=1.2E−02 n=2 fg=0.04 bg=0.00
sterol binding GO:0032934 p=1.7E−02 n=2 fg=0.04 bg=0.00
steroid binding GO:0005496 p=2.2E−02 n=2 fg=0.04 bg=0.01
dystroglycan binding GO:0002162 p=3.0E−02 n=1 fg=0.02 bg=0.00
steroid dehydrogenase activity GO:0016229 p=3.0E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=3.0E−02 n=1 fg=0.02 bg=0.00
glycerol−3−phosphate O−acyltransferase a... GO:0004366 p=3.0E−02 n=1 fg=0.02 bg=0.00
translation elongation factor binding GO:0061770 p=3.0E−02 n=1 fg=0.02 bg=0.00
peroxisome targeting sequence binding GO:0000268 p=3.0E−02 n=1 fg=0.02 bg=0.00
kinetochore binding GO:0043515 p=3.0E−02 n=1 fg=0.02 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=3.0E−02 n=1 fg=0.02 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=3.0E−02 n=1 fg=0.02 bg=0.00
protein serine/threonine phosphatase inh... GO:0004865 p=3.0E−02 n=1 fg=0.02 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=3.0E−02 n=1 fg=0.02 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=3.0E−02 n=1 fg=0.02 bg=0.00
alcohol binding GO:0043178 p=3.4E−02 n=2 fg=0.04 bg=0.01
protein heterodimerization activity GO:0046982 p=5.4E−02 n=6 fg=0.12 bg=0.06
soluble NSF attachment protein activity GO:0005483 p=5.9E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol 3−kinase regulator ... GO:0035014 p=5.9E−02 n=1 fg=0.02 bg=0.00
Tat protein binding GO:0030957 p=5.9E−02 n=1 fg=0.02 bg=0.00
octopamine receptor activity GO:0004989 p=5.9E−02 n=1 fg=0.02 bg=0.00
nuclear retinoid X receptor binding GO:0046965 p=5.9E−02 n=1 fg=0.02 bg=0.00
STAT family protein binding GO:0097677 p=5.9E−02 n=1 fg=0.02 bg=0.00
toxin transmembrane transporter activity GO:0019534 p=5.9E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol 3−kinase regulatory... GO:0036312 p=5.9E−02 n=1 fg=0.02 bg=0.00
sequence−specific single stranded DNA bi... GO:0098847 p=5.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=48/190 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032373624.2
fraction genes in fg and expected valu
microtubule end GO:1990752 p=8.3E−03 n=2 fg=0.04 bg=0.00
autophagosome membrane GO:0000421 p=8.3E−03 n=2 fg=0.04 bg=0.00
centrosomal corona GO:0031592 p=3.0E−02 n=1 fg=0.02 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.0E−02 n=1 fg=0.02 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=3.0E−02 n=1 fg=0.02 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=3.0E−02 n=1 fg=0.02 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=3.0E−02 n=1 fg=0.02 bg=0.00
protein kinase CK2 complex GO:0005956 p=3.0E−02 n=1 fg=0.02 bg=0.00
cortical microtubule GO:0055028 p=3.0E−02 n=1 fg=0.02 bg=0.00
CCAAT−binding factor complex GO:0016602 p=3.0E−02 n=1 fg=0.02 bg=0.00
ESCRT−0 complex GO:0033565 p=3.0E−02 n=1 fg=0.02 bg=0.00
cortical microtubule plus−end GO:1903754 p=3.0E−02 n=1 fg=0.02 bg=0.00
growth cone GO:0030426 p=3.2E−02 n=4 fg=0.07 bg=0.02
azurophil granule GO:0042582 p=3.3E−02 n=3 fg=0.06 bg=0.01
primary lysosome GO:0005766 p=3.3E−02 n=3 fg=0.06 bg=0.01
site of polarized growth GO:0030427 p=3.7E−02 n=4 fg=0.07 bg=0.02
intercellular bridge GO:0045171 p=4.8E−02 n=2 fg=0.04 bg=0.01
early endosome GO:0005769 p=5.2E−02 n=5 fg=0.09 bg=0.04
cis−Golgi network membrane GO:0033106 p=5.9E−02 n=1 fg=0.02 bg=0.00
female germline ring canal GO:0035324 p=5.9E−02 n=1 fg=0.02 bg=0.00
Seh1−associated complex GO:0035859 p=5.9E−02 n=1 fg=0.02 bg=0.00
microtubule minus−end GO:0036449 p=5.9E−02 n=1 fg=0.02 bg=0.00
growth cone filopodium GO:1990812 p=5.9E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=5.9E−02 n=1 fg=0.02 bg=0.00
GATOR2 complex GO:0061700 p=5.9E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=5.9E−02 n=1 fg=0.02 bg=0.00
Atg12−Atg5−Atg16 complex GO:0034274 p=5.9E−02 n=1 fg=0.02 bg=0.00
cytoplasmic region GO:0099568 p=6.0E−02 n=6 fg=0.11 bg=0.05
azurophil granule lumen GO:0035578 p=6.3E−02 n=2 fg=0.04 bg=0.01
focal adhesion GO:0005925 p=7.2E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=54/190 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction