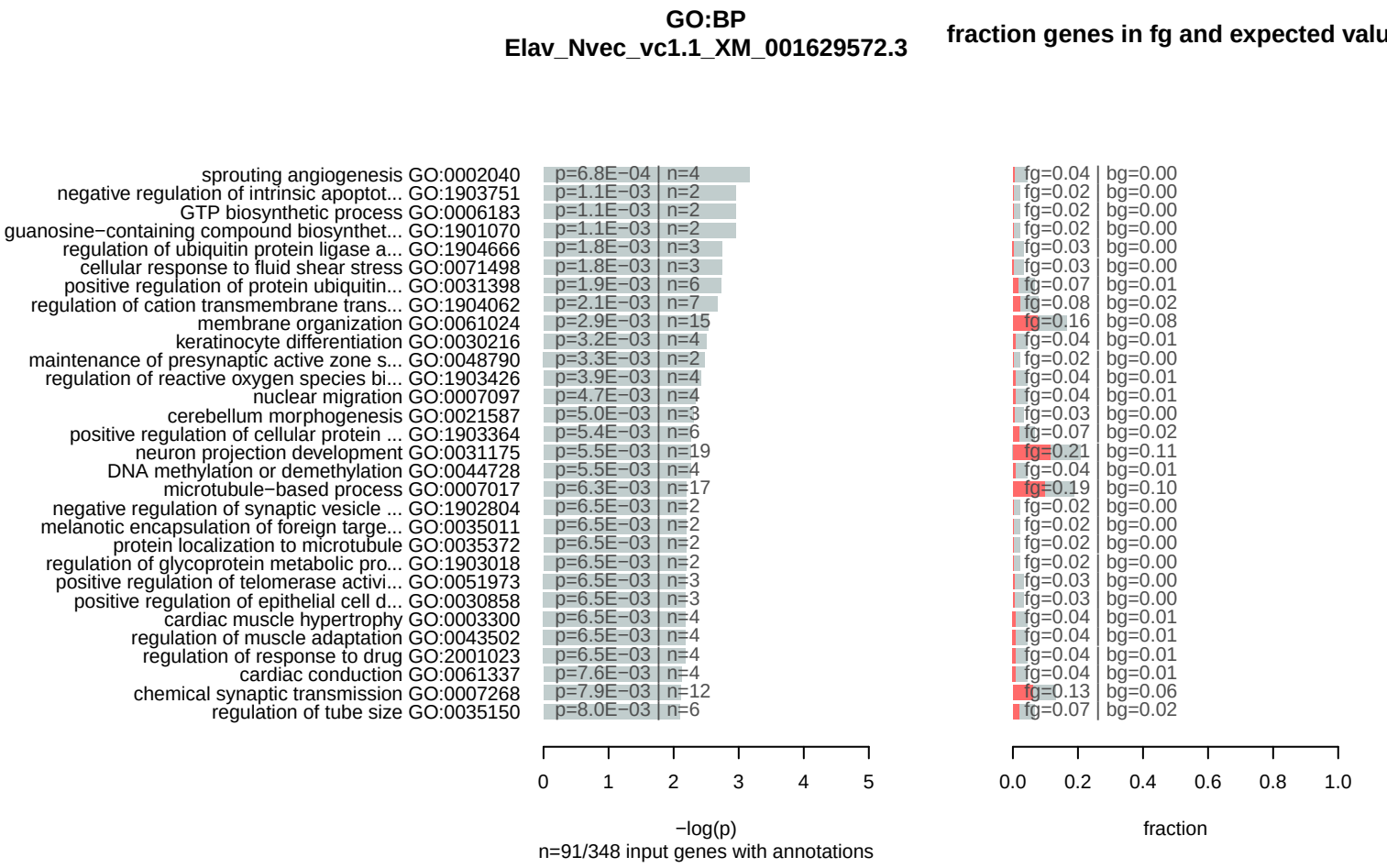
GO:BP
Elav_Nvec_vc1.1_XM_001629572.3
fraction genes in fg and expected valu
sprouting angiogenesis GO:0002040 p=6.8E−04 n=4 fg=0.04 bg=0.00
negative regulation of intrinsic apoptot... GO:1903751 p=1.1E−03 n=2 fg=0.02 bg=0.00
GTP biosynthetic process GO:0006183 p=1.1E−03 n=2 fg=0.02 bg=0.00
guanosine−containing compound biosynthet... GO:1901070 p=1.1E−03 n=2 fg=0.02 bg=0.00
regulation of ubiquitin protein ligase a... GO:1904666 p=1.8E−03 n=3 fg=0.03 bg=0.00
cellular response to fluid shear stress GO:0071498 p=1.8E−03 n=3 fg=0.03 bg=0.00
positive regulation of protein ubiquitin... GO:0031398 p=1.9E−03 n=6 fg=0.07 bg=0.01
regulation of cation transmembrane trans... GO:1904062 p=2.1E−03 n=7 fg=0.08 bg=0.02
membrane organization GO:0061024 p=2.9E−03 n=15 fg=0.16 bg=0.08
keratinocyte differentiation GO:0030216 p=3.2E−03 n=4 fg=0.04 bg=0.01
maintenance of presynaptic active zone s... GO:0048790 p=3.3E−03 n=2 fg=0.02 bg=0.00
regulation of reactive oxygen species bi... GO:1903426 p=3.9E−03 n=4 fg=0.04 bg=0.01
nuclear migration GO:0007097 p=4.7E−03 n=4 fg=0.04 bg=0.01
cerebellum morphogenesis GO:0021587 p=5.0E−03 n=3 fg=0.03 bg=0.00
positive regulation of cellular protein ... GO:1903364 p=5.4E−03 n=6 fg=0.07 bg=0.02
neuron projection development GO:0031175 p=5.5E−03 n=19 fg=0.21 bg=0.11
DNA methylation or demethylation GO:0044728 p=5.5E−03 n=4 fg=0.04 bg=0.01
microtubule−based process GO:0007017 p=6.3E−03 n=17 fg=0.19 bg=0.10
negative regulation of synaptic vesicle ... GO:1902804 p=6.5E−03 n=2 fg=0.02 bg=0.00
melanotic encapsulation of foreign targe... GO:0035011 p=6.5E−03 n=2 fg=0.02 bg=0.00
protein localization to microtubule GO:0035372 p=6.5E−03 n=2 fg=0.02 bg=0.00
regulation of glycoprotein metabolic pro... GO:1903018 p=6.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of telomerase activi... GO:0051973 p=6.5E−03 n=3 fg=0.03 bg=0.00
positive regulation of epithelial cell d... GO:0030858 p=6.5E−03 n=3 fg=0.03 bg=0.00
cardiac muscle hypertrophy GO:0003300 p=6.5E−03 n=4 fg=0.04 bg=0.01
regulation of muscle adaptation GO:0043502 p=6.5E−03 n=4 fg=0.04 bg=0.01
regulation of response to drug GO:2001023 p=6.5E−03 n=4 fg=0.04 bg=0.01
cardiac conduction GO:0061337 p=7.6E−03 n=4 fg=0.04 bg=0.01
chemical synaptic transmission GO:0007268 p=7.9E−03 n=12 fg=0.13 bg=0.06
regulation of tube size GO:0035150 p=8.0E−03 n=6 fg=0.07 bg=0.02
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−log(p)
n=91/348 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001629572.3
fraction genes in fg and expected valu
histone deacetylase activity GO:0004407 p=4.8E−03 n=3 fg=0.03 bg=0.00
transcription corepressor activity GO:0003714 p=1.0E−02 n=5 fg=0.06 bg=0.02
phosphatidylinositol 3−kinase binding GO:0043548 p=1.8E−02 n=2 fg=0.02 bg=0.00
MAP kinase activity GO:0004707 p=2.5E−02 n=2 fg=0.02 bg=0.00
scaffold protein binding GO:0097110 p=3.5E−02 n=3 fg=0.03 bg=0.01
nitrite reductase (NO−forming) activity GO:0050421 p=3.7E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.7E−02 n=1 fg=0.01 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=3.7E−02 n=1 fg=0.01 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=3.7E−02 n=1 fg=0.01 bg=0.00
amino acid:proton symporter activity GO:0005280 p=3.7E−02 n=1 fg=0.01 bg=0.00
poly(G) binding GO:0034046 p=3.7E−02 n=1 fg=0.01 bg=0.00
tricarboxylate secondary active transmem... GO:0005371 p=3.7E−02 n=1 fg=0.01 bg=0.00
RNA trimethylguanosine synthase activity GO:0071164 p=3.7E−02 n=1 fg=0.01 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=3.7E−02 n=1 fg=0.01 bg=0.00
adenylylsulfatase activity GO:0047627 p=3.7E−02 n=1 fg=0.01 bg=0.00
mitochondrion targeting sequence binding GO:0030943 p=3.7E−02 n=1 fg=0.01 bg=0.00
L−proline transmembrane transporter acti... GO:0015193 p=3.7E−02 n=1 fg=0.01 bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196 p=3.7E−02 n=1 fg=0.01 bg=0.00
polyamine oxidase activity GO:0046592 p=3.7E−02 n=1 fg=0.01 bg=0.00
adenylosuccinate synthase activity GO:0004019 p=3.7E−02 n=1 fg=0.01 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.7E−02 n=1 fg=0.01 bg=0.00
nitrite reductase activity GO:0098809 p=3.7E−02 n=1 fg=0.01 bg=0.00
m7G(5')pppN diphosphatase activity GO:0050072 p=3.7E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type I (single strand ... GO:0003917 p=3.7E−02 n=1 fg=0.01 bg=0.00
hydrolase activity, acting on acid anhyd... GO:0016819 p=3.7E−02 n=1 fg=0.01 bg=0.00
glycine transmembrane transporter activi... GO:0015187 p=3.7E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on other... GO:0016661 p=3.7E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on other... GO:0016662 p=3.7E−02 n=1 fg=0.01 bg=0.00
superoxide−generating NADPH oxidase acti... GO:0016176 p=3.7E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=3.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=87/348 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001629572.3
fraction genes in fg and expected valu
transcription repressor complex GO:0017053 p=2.8E−03 n=4 fg=0.04 bg=0.01
cytoplasmic ribonucleoprotein granule GO:0036464 p=3.6E−03 n=7 fg=0.08 bg=0.02
Golgi trans cisterna GO:0000138 p=6.9E−03 n=3 fg=0.03 bg=0.00
I band GO:0031674 p=7.9E−03 n=5 fg=0.05 bg=0.01
histone deacetylase complex GO:0000118 p=8.8E−03 n=3 fg=0.03 bg=0.00
euchromatin GO:0000791 p=1.3E−02 n=3 fg=0.03 bg=0.01
Golgi medial cisterna GO:0005797 p=1.3E−02 n=3 fg=0.03 bg=0.01
P granule GO:0043186 p=1.6E−02 n=3 fg=0.03 bg=0.01
rough endoplasmic reticulum membrane GO:0030867 p=1.6E−02 n=2 fg=0.02 bg=0.00
pole plasm GO:0045495 p=1.9E−02 n=3 fg=0.03 bg=0.01
germ plasm GO:0060293 p=1.9E−02 n=3 fg=0.03 bg=0.01
apicolateral plasma membrane GO:0016327 p=2.2E−02 n=2 fg=0.02 bg=0.00
A band GO:0031672 p=2.2E−02 n=3 fg=0.03 bg=0.01
cytosol GO:0005829 p=2.5E−02 n=47 fg=0.51 bg=0.40
Z disc GO:0030018 p=2.8E−02 n=4 fg=0.04 bg=0.01
vesicle tethering complex GO:0099023 p=2.9E−02 n=3 fg=0.03 bg=0.01
P−body GO:0000932 p=3.4E−02 n=3 fg=0.03 bg=0.01
Golgi−associated vesicle lumen GO:0070931 p=3.4E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=3.4E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=3.4E−02 n=1 fg=0.01 bg=0.00
Yb body GO:0070725 p=3.4E−02 n=1 fg=0.01 bg=0.00
PET complex GO:1990923 p=3.4E−02 n=1 fg=0.01 bg=0.00
NMDA selective glutamate receptor comple... GO:0017146 p=3.4E−02 n=1 fg=0.01 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=3.4E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=3.4E−02 n=1 fg=0.01 bg=0.00
retromer, cargo−selective complex GO:0030906 p=3.4E−02 n=1 fg=0.01 bg=0.00
endocytic vesicle lumen GO:0071682 p=3.4E−02 n=1 fg=0.01 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=3.4E−02 n=1 fg=0.01 bg=0.00
nucleotide−excision repair complex GO:0000109 p=3.4E−02 n=1 fg=0.01 bg=0.00
melanosome GO:0042470 p=3.6E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=93/348 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction