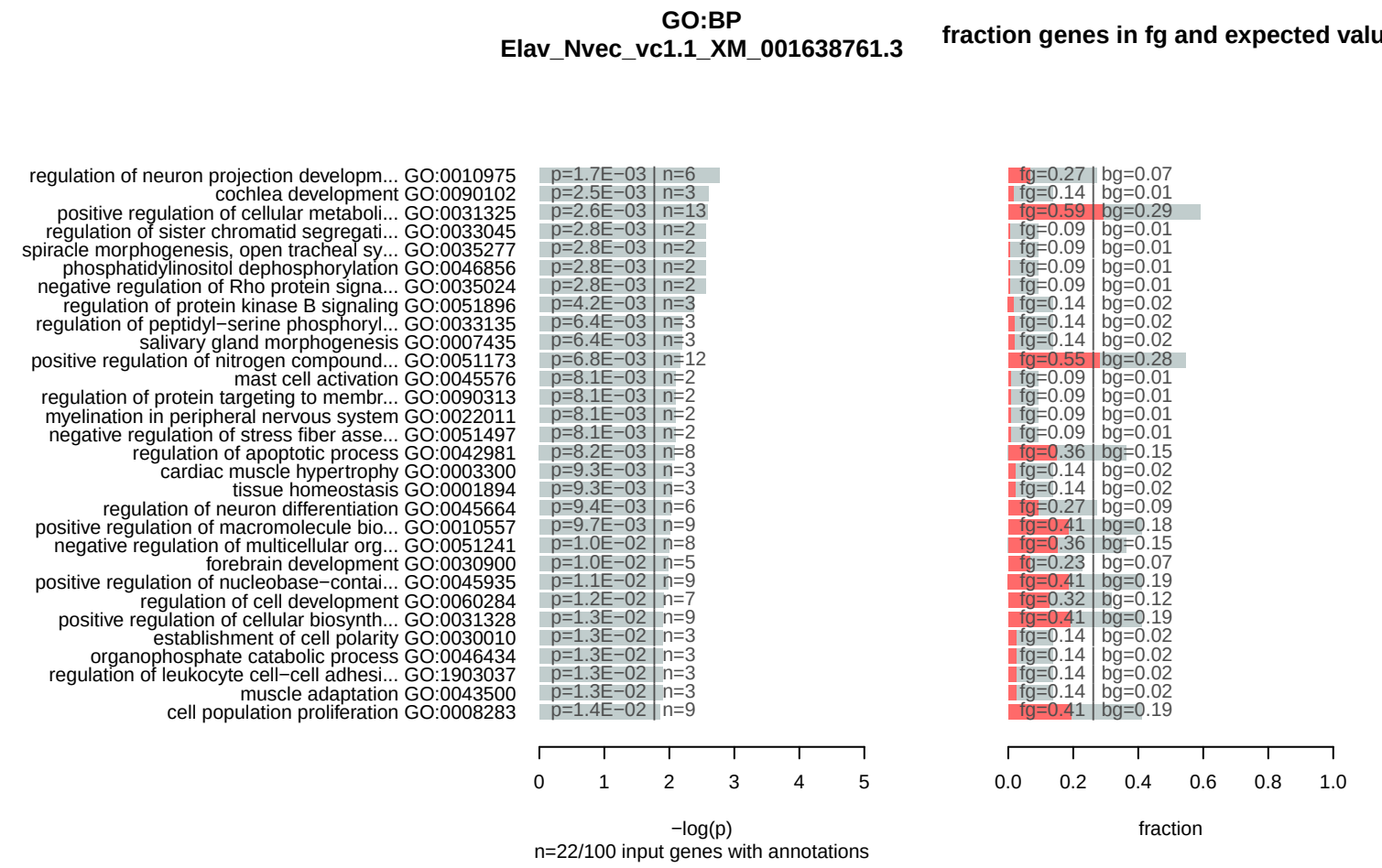
GO:BP
Elav_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
regulation of neuron projection developm... GO:0010975 p=1.7E−03 n=6 fg=0.27 bg=0.07
cochlea development GO:0090102 p=2.5E−03 n=3 fg=0.14 bg=0.01
positive regulation of cellular metaboli... GO:0031325 p=2.6E−03 n=13 fg=0.59 bg=0.29
regulation of sister chromatid segregati... GO:0033045 p=2.8E−03 n=2 fg=0.09 bg=0.01
spiracle morphogenesis, open tracheal sy... GO:0035277 p=2.8E−03 n=2 fg=0.09 bg=0.01
phosphatidylinositol dephosphorylation GO:0046856 p=2.8E−03 n=2 fg=0.09 bg=0.01
negative regulation of Rho protein signa... GO:0035024 p=2.8E−03 n=2 fg=0.09 bg=0.01
regulation of protein kinase B signaling GO:0051896 p=4.2E−03 n=3 fg=0.14 bg=0.02
regulation of peptidyl−serine phosphoryl... GO:0033135 p=6.4E−03 n=3 fg=0.14 bg=0.02
salivary gland morphogenesis GO:0007435 p=6.4E−03 n=3 fg=0.14 bg=0.02
positive regulation of nitrogen compound... GO:0051173 p=6.8E−03 n=12 fg=0.55 bg=0.28
mast cell activation GO:0045576 p=8.1E−03 n=2 fg=0.09 bg=0.01
regulation of protein targeting to membr... GO:0090313 p=8.1E−03 n=2 fg=0.09 bg=0.01
myelination in peripheral nervous system GO:0022011 p=8.1E−03 n=2 fg=0.09 bg=0.01
negative regulation of stress fiber asse... GO:0051497 p=8.1E−03 n=2 fg=0.09 bg=0.01
regulation of apoptotic process GO:0042981 p=8.2E−03 n=8 fg=0.36 bg=0.15
cardiac muscle hypertrophy GO:0003300 p=9.3E−03 n=3 fg=0.14 bg=0.02
tissue homeostasis GO:0001894 p=9.3E−03 n=3 fg=0.14 bg=0.02
regulation of neuron differentiation GO:0045664 p=9.4E−03 n=6 fg=0.27 bg=0.09
positive regulation of macromolecule bio... GO:0010557 p=9.7E−03 n=9 fg=0.41 bg=0.18
negative regulation of multicellular org... GO:0051241 p=1.0E−02 n=8 fg=0.36 bg=0.15
forebrain development GO:0030900 p=1.0E−02 n=5 fg=0.23 bg=0.07
positive regulation of nucleobase−contai... GO:0045935 p=1.1E−02 n=9 fg=0.41 bg=0.19
regulation of cell development GO:0060284 p=1.2E−02 n=7 fg=0.32 bg=0.12
positive regulation of cellular biosynth... GO:0031328 p=1.3E−02 n=9 fg=0.41 bg=0.19
establishment of cell polarity GO:0030010 p=1.3E−02 n=3 fg=0.14 bg=0.02
organophosphate catabolic process GO:0046434 p=1.3E−02 n=3 fg=0.14 bg=0.02
regulation of leukocyte cell−cell adhesi... GO:1903037 p=1.3E−02 n=3 fg=0.14 bg=0.02
muscle adaptation GO:0043500 p=1.3E−02 n=3 fg=0.14 bg=0.02
cell population proliferation GO:0008283 p=1.4E−02 n=9 fg=0.41 bg=0.19
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−log(p)
n=22/100 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
phosphatidylinositol phosphate 5−phospha... GO:0034595 p=2.9E−03 n=2 fg=0.10 bg=0.01
inositol phosphate phosphatase activity GO:0052745 p=2.9E−03 n=2 fg=0.10 bg=0.01
sequence−specific double−stranded DNA bi... GO:1990837 p=5.4E−03 n=6 fg=0.30 bg=0.09
DNA−binding transcription activator acti... GO:0001228 p=1.1E−02 n=5 fg=0.25 bg=0.07
DNA−binding transcription activator acti... GO:0001216 p=1.1E−02 n=5 fg=0.25 bg=0.07
HMG box domain binding GO:0071837 p=1.6E−02 n=2 fg=0.10 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=1.7E−02 n=5 fg=0.25 bg=0.08
cis−regulatory region sequence−specific ... GO:0000987 p=1.8E−02 n=4 fg=0.20 bg=0.06
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.8E−02 n=4 fg=0.20 bg=0.06
transcription cis−regulatory region bind... GO:0000976 p=2.3E−02 n=5 fg=0.25 bg=0.09
histone acetyltransferase binding GO:0035035 p=2.6E−02 n=2 fg=0.10 bg=0.01
transcription regulatory region nucleic ... GO:0001067 p=2.9E−02 n=5 fg=0.25 bg=0.09
DNA−binding transcription factor activit... GO:0000981 p=3.5E−02 n=6 fg=0.30 bg=0.13
guanyl ribonucleotide binding GO:0032561 p=3.8E−02 n=2 fg=0.10 bg=0.02
guanyl nucleotide binding GO:0019001 p=3.8E−02 n=2 fg=0.10 bg=0.02
chromatin binding GO:0003682 p=4.5E−02 n=4 fg=0.20 bg=0.07
SH2 domain binding GO:0042169 p=5.5E+02 n=1 fg=0.05 bg=0.00
kinase activator activity GO:0019209 p=5.5E+02 n=1 fg=0.05 bg=0.00
triplex DNA binding GO:0045142 p=5.5E+02 n=1 fg=0.05 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485 p=5.5E+02 n=1 fg=0.05 bg=0.00
inositol trisphosphate phosphatase activ... GO:0046030 p=5.5E+02 n=1 fg=0.05 bg=0.00
G−quadruplex DNA binding GO:0051880 p=5.5E+02 n=1 fg=0.05 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=5.5E+02 n=1 fg=0.05 bg=0.00
phosphatidylinositol bisphosphate phosph... GO:0034593 p=5.5E+02 n=1 fg=0.05 bg=0.00
phosphatidylinositol trisphosphate phosp... GO:0034594 p=5.5E+02 n=1 fg=0.05 bg=0.00
C2H2 zinc finger domain binding GO:0070742 p=5.5E+02 n=1 fg=0.05 bg=0.00
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=5.5E+02 n=1 fg=0.05 bg=0.00
inositol monophosphate 4−phosphatase act... GO:0052833 p=5.5E+02 n=1 fg=0.05 bg=0.00
inositol monophosphate phosphatase activ... GO:0052834 p=5.5E+02 n=1 fg=0.05 bg=0.00
lipid phosphatase activity GO:0042577 p=5.5E+02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=20/100 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
ruffle GO:0001726 p=3.8E−03 n=3 fg=0.14 bg=0.02
adherens junction GO:0005912 p=1.2E−02 n=3 fg=0.14 bg=0.02
ruffle membrane GO:0032587 p=1.5E−02 n=2 fg=0.10 bg=0.01
spindle pole GO:0000922 p=1.5E−02 n=2 fg=0.10 bg=0.01
centrosome GO:0005813 p=2.5E−02 n=3 fg=0.14 bg=0.03
focal adhesion GO:0005925 p=4.7E−02 n=2 fg=0.10 bg=0.02
cell−substrate junction GO:0030055 p=4.7E−02 n=2 fg=0.10 bg=0.02
spindle GO:0005819 p=4.7E−02 n=2 fg=0.10 bg=0.02
mitotic spindle pole GO:0097431 p=5.2E+02 n=1 fg=0.05 bg=0.00
extracellular exosome GO:0070062 p=5.2E+02 n=1 fg=0.05 bg=0.00
extracellular vesicle GO:1903561 p=5.2E+02 n=1 fg=0.05 bg=0.00
interphase microtubule organizing center GO:0031021 p=5.2E+02 n=1 fg=0.05 bg=0.00
postsynapse of neuromuscular junction GO:0098975 p=5.2E+02 n=1 fg=0.05 bg=0.00
extracellular membrane−bounded organelle GO:0065010 p=5.2E+02 n=1 fg=0.05 bg=0.00
muscle cell postsynaptic specialization GO:0097482 p=5.2E+02 n=1 fg=0.05 bg=0.00
hemidesmosome GO:0030056 p=5.2E+02 n=1 fg=0.05 bg=0.00
U5 snRNP GO:0005682 p=5.2E+02 n=1 fg=0.05 bg=0.00
extracellular organelle GO:0043230 p=5.2E+02 n=1 fg=0.05 bg=0.00
presynaptic active zone membrane GO:0048787 p=5.2E+02 n=1 fg=0.05 bg=0.00
microtubule organizing center GO:0005815 p=6.0E+02 n=3 fg=0.14 bg=0.04
recycling endosome GO:0055037 p=7.5E−02 n=2 fg=0.10 bg=0.02
perinuclear region of cytoplasm GO:0048471 p=7.5E−02 n=4 fg=0.19 bg=0.08
cell−cell junction GO:0005911 p=8.9E−02 n=3 fg=0.14 bg=0.05
anchoring junction GO:0070161 p=8.9E−02 n=3 fg=0.14 bg=0.05
cytoskeleton GO:0005856 p=9.1E−02 n=5 fg=0.24 bg=0.12
transcription regulator complex GO:0005667 p=9.9E−02 n=3 fg=0.14 bg=0.05
MLL1/2 complex GO:0044665 p=1.0E−01 n=1 fg=0.05 bg=0.00
small nuclear ribonucleoprotein complex GO:0030532 p=1.0E−01 n=1 fg=0.05 bg=0.00
NSL complex GO:0044545 p=1.0E−01 n=1 fg=0.05 bg=0.00
clathrin−coated endocytic vesicle GO:0045334 p=1.0E−01 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=21/100 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction