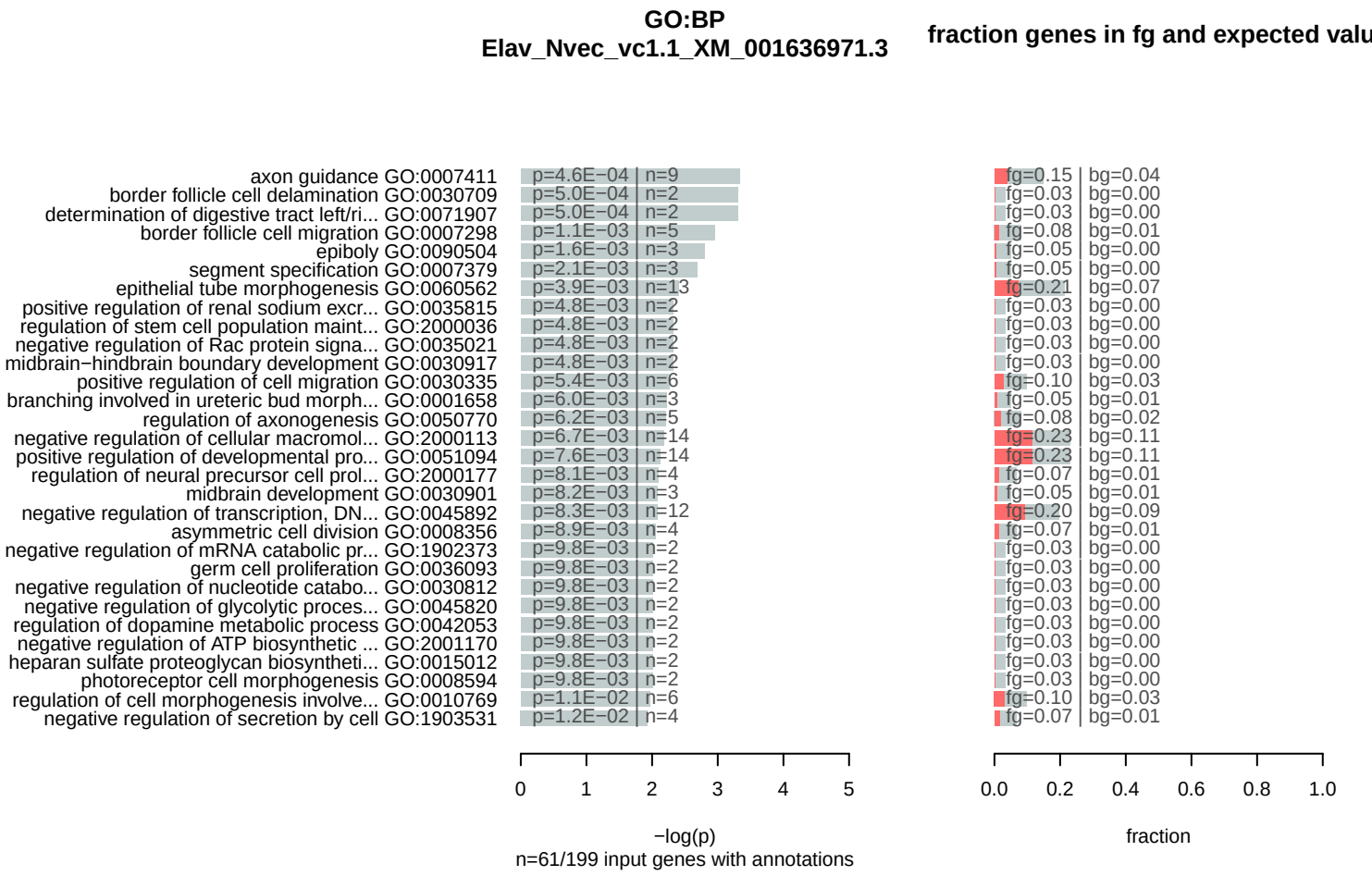
GO:BP
Elav_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
axon guidance GO:0007411 p=4.6E−04 n=9 fg=0.15 bg=0.04
border follicle cell delamination GO:0030709 p=5.0E−04 n=2 fg=0.03 bg=0.00
determination of digestive tract left/ri... GO:0071907 p=5.0E−04 n=2 fg=0.03 bg=0.00
border follicle cell migration GO:0007298 p=1.1E−03 n=5 fg=0.08 bg=0.01
epiboly GO:0090504 p=1.6E−03 n=3 fg=0.05 bg=0.00
segment specification GO:0007379 p=2.1E−03 n=3 fg=0.05 bg=0.00
epithelial tube morphogenesis GO:0060562 p=3.9E−03 n=13 fg=0.21 bg=0.07
positive regulation of renal sodium excr... GO:0035815 p=4.8E−03 n=2 fg=0.03 bg=0.00
regulation of stem cell population maint... GO:2000036 p=4.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of Rac protein signa... GO:0035021 p=4.8E−03 n=2 fg=0.03 bg=0.00
midbrain−hindbrain boundary development GO:0030917 p=4.8E−03 n=2 fg=0.03 bg=0.00
positive regulation of cell migration GO:0030335 p=5.4E−03 n=6 fg=0.10 bg=0.03
branching involved in ureteric bud morph... GO:0001658 p=6.0E−03 n=3 fg=0.05 bg=0.01
regulation of axonogenesis GO:0050770 p=6.2E−03 n=5 fg=0.08 bg=0.02
negative regulation of cellular macromol... GO:2000113 p=6.7E−03 n=14 fg=0.23 bg=0.11
positive regulation of developmental pro... GO:0051094 p=7.6E−03 n=14 fg=0.23 bg=0.11
regulation of neural precursor cell prol... GO:2000177 p=8.1E−03 n=4 fg=0.07 bg=0.01
midbrain development GO:0030901 p=8.2E−03 n=3 fg=0.05 bg=0.01
negative regulation of transcription, DN... GO:0045892 p=8.3E−03 n=12 fg=0.20 bg=0.09
asymmetric cell division GO:0008356 p=8.9E−03 n=4 fg=0.07 bg=0.01
negative regulation of mRNA catabolic pr... GO:1902373 p=9.8E−03 n=2 fg=0.03 bg=0.00
germ cell proliferation GO:0036093 p=9.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of nucleotide catabo... GO:0030812 p=9.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of glycolytic proces... GO:0045820 p=9.8E−03 n=2 fg=0.03 bg=0.00
regulation of dopamine metabolic process GO:0042053 p=9.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of ATP biosynthetic ... GO:2001170 p=9.8E−03 n=2 fg=0.03 bg=0.00
heparan sulfate proteoglycan biosyntheti... GO:0015012 p=9.8E−03 n=2 fg=0.03 bg=0.00
photoreceptor cell morphogenesis GO:0008594 p=9.8E−03 n=2 fg=0.03 bg=0.00
regulation of cell morphogenesis involve... GO:0010769 p=1.1E−02 n=6 fg=0.10 bg=0.03
negative regulation of secretion by cell GO:1903531 p=1.2E−02 n=4 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=61/199 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
MAP kinase activity GO:0004707 p=8.9E−03 n=2 fg=0.04 bg=0.00
neuropeptide receptor activity GO:0008188 p=1.2E−02 n=2 fg=0.04 bg=0.00
poly(U) RNA binding GO:0008266 p=1.5E−02 n=2 fg=0.04 bg=0.00
heterocyclic compound binding GO:1901363 p=1.6E−02 n=22 fg=0.43 bg=0.28
GTPase activating protein binding GO:0032794 p=1.8E−02 n=2 fg=0.04 bg=0.00
beta−catenin binding GO:0008013 p=1.8E−02 n=2 fg=0.04 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=1.8E−02 n=2 fg=0.04 bg=0.00
organic cyclic compound binding GO:0097159 p=1.9E−02 n=22 fg=0.43 bg=0.29
sphingolipid transfer activity GO:0120016 p=2.1E−02 n=1 fg=0.02 bg=0.00
ceramide transfer activity GO:0120017 p=2.1E−02 n=1 fg=0.02 bg=0.00
phosphopentomutase activity GO:0008973 p=2.1E−02 n=1 fg=0.02 bg=0.00
glucose−1,6−bisphosphate synthase activi... GO:0047933 p=2.1E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0046997 p=2.1E−02 n=1 fg=0.02 bg=0.00
unmethylated CpG binding GO:0045322 p=2.1E−02 n=1 fg=0.02 bg=0.00
dimethylglycine dehydrogenase activity GO:0047865 p=2.1E−02 n=1 fg=0.02 bg=0.00
heparan sulfate 2−O−sulfotransferase act... GO:0004394 p=2.1E−02 n=1 fg=0.02 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.1E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.1E−02 n=1 fg=0.02 bg=0.00
DNA end binding GO:0045027 p=2.1E−02 n=1 fg=0.02 bg=0.00
JUN kinase activity GO:0004705 p=2.1E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.1E−02 n=1 fg=0.02 bg=0.00
heparan sulfate sulfotransferase activit... GO:0034483 p=2.1E−02 n=1 fg=0.02 bg=0.00
AMP deaminase activity GO:0003876 p=2.1E−02 n=1 fg=0.02 bg=0.00
histone deacetylase regulator activity GO:0035033 p=2.1E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (NADP+) activity GO:0046554 p=2.1E−02 n=1 fg=0.02 bg=0.00
sphingolipid transporter activity GO:0046624 p=2.1E−02 n=1 fg=0.02 bg=0.00
translation regulator activity, nucleic ... GO:0090079 p=2.5E−02 n=3 fg=0.06 bg=0.01
magnesium ion binding GO:0000287 p=2.6E−02 n=4 fg=0.08 bg=0.02
G protein−coupled peptide receptor activ... GO:0008528 p=2.6E−02 n=2 fg=0.04 bg=0.01
peptide receptor activity GO:0001653 p=2.6E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=51/199 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
germinal vesicle GO:0042585 p=8.6E−03 n=2 fg=0.04 bg=0.00
cell body GO:0044297 p=1.2E−02 n=9 fg=0.16 bg=0.07
neuronal cell body GO:0043025 p=1.8E−02 n=8 fg=0.14 bg=0.06
Schmidt−Lanterman incisure GO:0043220 p=2.1E−02 n=1 fg=0.02 bg=0.00
compact myelin GO:0043218 p=2.1E−02 n=1 fg=0.02 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=2.1E−02 n=1 fg=0.02 bg=0.00
internode region of axon GO:0033269 p=2.1E−02 n=1 fg=0.02 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=2.1E−02 n=1 fg=0.02 bg=0.00
anterior cell cortex GO:0061802 p=2.1E−02 n=1 fg=0.02 bg=0.00
pinosome GO:0044352 p=2.1E−02 n=1 fg=0.02 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.1E−02 n=1 fg=0.02 bg=0.00
macropinosome GO:0044354 p=2.1E−02 n=1 fg=0.02 bg=0.00
Golgi apparatus subcompartment GO:0098791 p=3.0E−02 n=8 fg=0.14 bg=0.07
intracellular anatomical structure GO:0005622 p=3.9E−02 n=57 fg=1.00 bg=0.94
intracellular membrane−bounded organelle GO:0043231 p=4.0E−02 n=50 fg=0.88 bg=0.77
translation preinitiation complex GO:0070993 p=4.2E−02 n=1 fg=0.02 bg=0.00
lateral loop GO:0043219 p=4.2E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation elongation factor... GO:0005853 p=4.2E−02 n=1 fg=0.02 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=4.2E−02 n=1 fg=0.02 bg=0.00
growth cone filopodium GO:1990812 p=4.2E−02 n=1 fg=0.02 bg=0.00
nucleus GO:0005634 p=4.6E−02 n=36 fg=0.63 bg=0.50
somatodendritic compartment GO:0036477 p=5.0E−02 n=9 fg=0.16 bg=0.09
Golgi apparatus GO:0005794 p=5.0E−02 n=11 fg=0.19 bg=0.11
membrane−bounded organelle GO:0043227 p=5.3E−02 n=51 fg=0.89 bg=0.80
dendrite GO:0030425 p=5.4E−02 n=7 fg=0.12 bg=0.06
dendritic tree GO:0097447 p=5.6E−02 n=7 fg=0.12 bg=0.06
main axon GO:0044304 p=5.9E−02 n=2 fg=0.04 bg=0.01
organelle lumen GO:0043233 p=6.1E−02 n=30 fg=0.53 bg=0.42
intracellular organelle lumen GO:0070013 p=6.1E−02 n=30 fg=0.53 bg=0.42
membrane−enclosed lumen GO:0031974 p=6.1E−02 n=30 fg=0.53 bg=0.42
0 1 2 3 4 5
−log(p)
n=57/199 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction