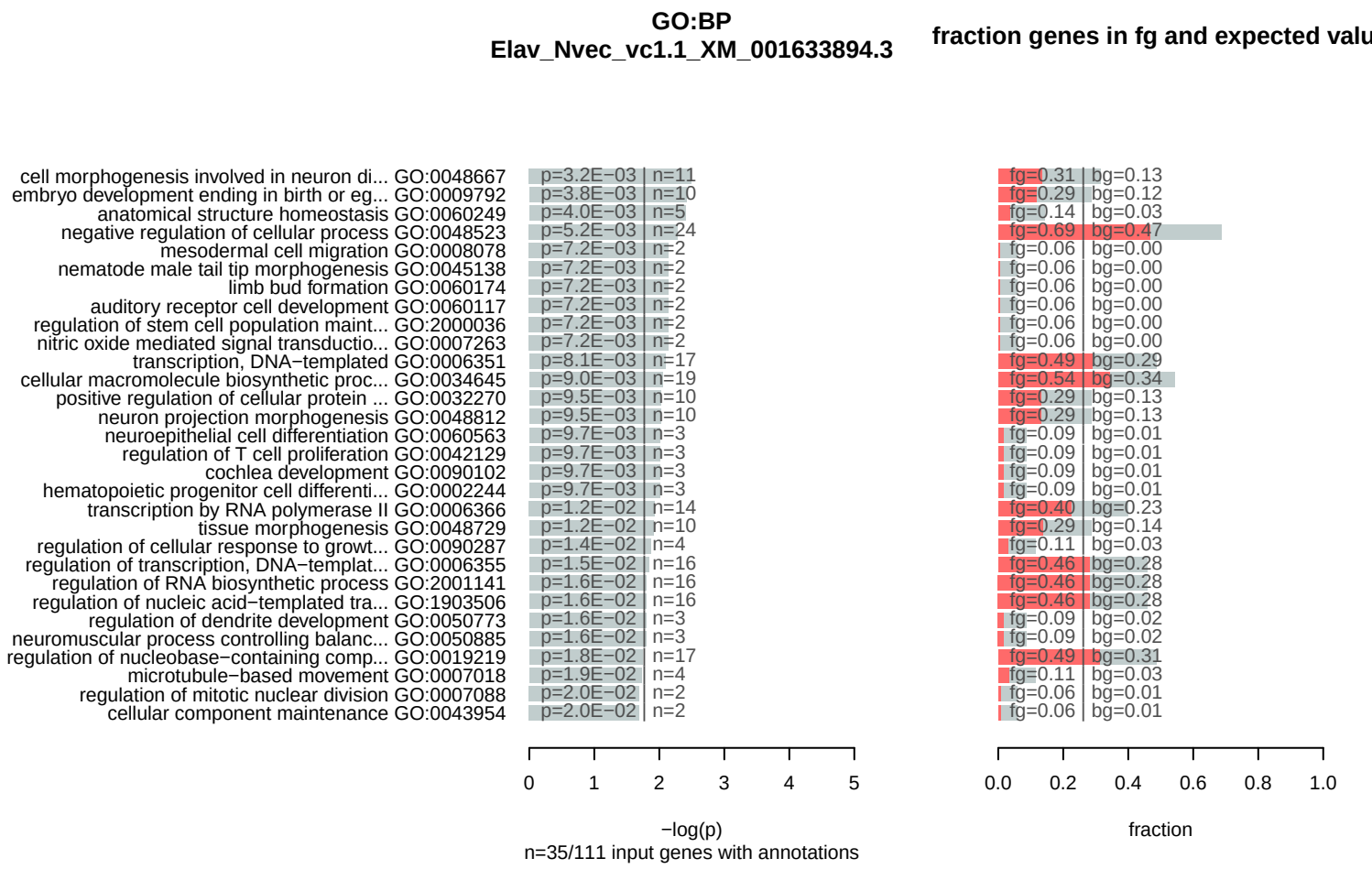
GO:BP
Elav_Nvec_vc1.1_XM_001633894.3
fraction genes in fg and expected valu
cell morphogenesis involved in neuron di... GO:0048667 p=3.2E−03 n=11 fg=0.31 bg=0.13
embryo development ending in birth or eg... GO:0009792 p=3.8E−03 n=10 fg=0.29 bg=0.12
anatomical structure homeostasis GO:0060249 p=4.0E−03 n=5 fg=0.14 bg=0.03
negative regulation of cellular process GO:0048523 p=5.2E−03 n=24 fg=0.69 bg=0.47
mesodermal cell migration GO:0008078 p=7.2E−03 n=2 fg=0.06 bg=0.00
nematode male tail tip morphogenesis GO:0045138 p=7.2E−03 n=2 fg=0.06 bg=0.00
limb bud formation GO:0060174 p=7.2E−03 n=2 fg=0.06 bg=0.00
auditory receptor cell development GO:0060117 p=7.2E−03 n=2 fg=0.06 bg=0.00
regulation of stem cell population maint... GO:2000036 p=7.2E−03 n=2 fg=0.06 bg=0.00
nitric oxide mediated signal transductio... GO:0007263 p=7.2E−03 n=2 fg=0.06 bg=0.00
transcription, DNA−templated GO:0006351 p=8.1E−03 n=17 fg=0.49 bg=0.29
cellular macromolecule biosynthetic proc... GO:0034645 p=9.0E−03 n=19 fg=0.54 bg=0.34
positive regulation of cellular protein ... GO:0032270 p=9.5E−03 n=10 fg=0.29 bg=0.13
neuron projection morphogenesis GO:0048812 p=9.5E−03 n=10 fg=0.29 bg=0.13
neuroepithelial cell differentiation GO:0060563 p=9.7E−03 n=3 fg=0.09 bg=0.01
regulation of T cell proliferation GO:0042129 p=9.7E−03 n=3 fg=0.09 bg=0.01
cochlea development GO:0090102 p=9.7E−03 n=3 fg=0.09 bg=0.01
hematopoietic progenitor cell differenti... GO:0002244 p=9.7E−03 n=3 fg=0.09 bg=0.01
transcription by RNA polymerase II GO:0006366 p=1.2E−02 n=14 fg=0.40 bg=0.23
tissue morphogenesis GO:0048729 p=1.2E−02 n=10 fg=0.29 bg=0.14
regulation of cellular response to growt... GO:0090287 p=1.4E−02 n=4 fg=0.11 bg=0.03
regulation of transcription, DNA−templat... GO:0006355 p=1.5E−02 n=16 fg=0.46 bg=0.28
regulation of RNA biosynthetic process GO:2001141 p=1.6E−02 n=16 fg=0.46 bg=0.28
regulation of nucleic acid−templated tra... GO:1903506 p=1.6E−02 n=16 fg=0.46 bg=0.28
regulation of dendrite development GO:0050773 p=1.6E−02 n=3 fg=0.09 bg=0.02
neuromuscular process controlling balanc... GO:0050885 p=1.6E−02 n=3 fg=0.09 bg=0.02
regulation of nucleobase−containing comp... GO:0019219 p=1.8E−02 n=17 fg=0.49 bg=0.31
microtubule−based movement GO:0007018 p=1.9E−02 n=4 fg=0.11 bg=0.03
regulation of mitotic nuclear division GO:0007088 p=2.0E−02 n=2 fg=0.06 bg=0.01
cellular component maintenance GO:0043954 p=2.0E−02 n=2 fg=0.06 bg=0.01
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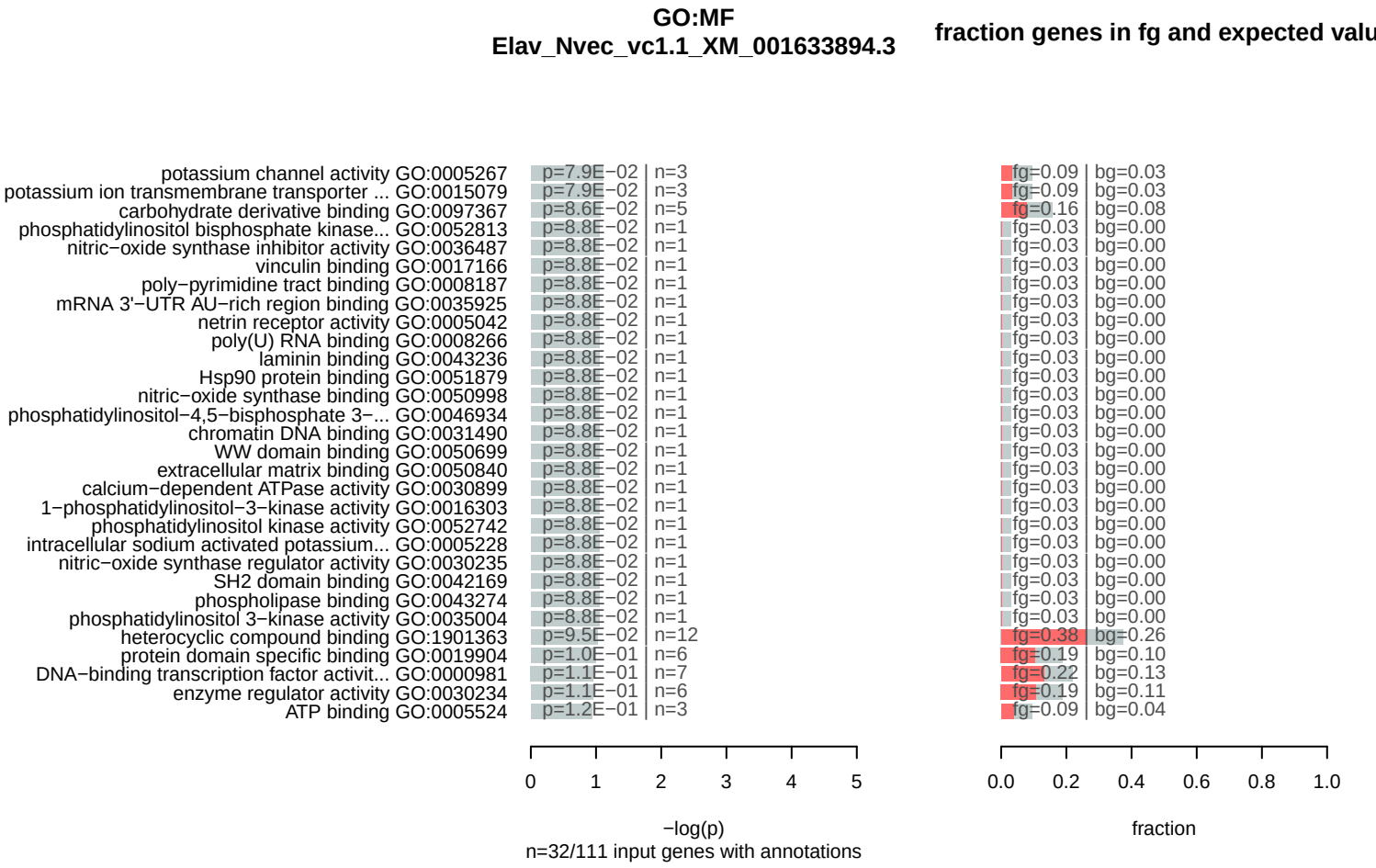
−log(p)
n=35/111 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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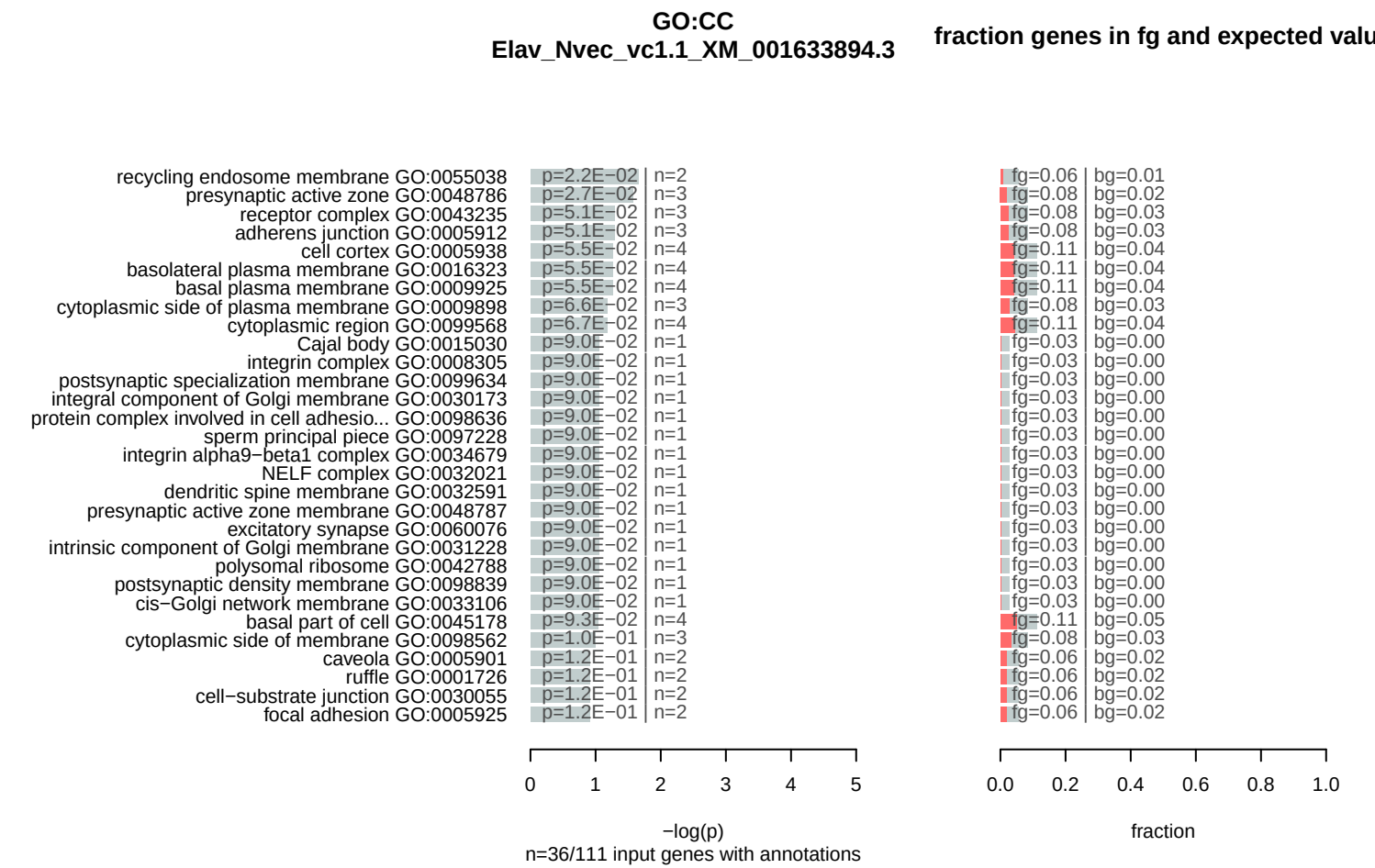
potassium ion transmembrane transporter ... GO:0015079 p=7.9E−02 n=3 fg=0.09 bg=0.03
carbohydrate derivative binding GO:0097367 p=8.6E−02 n=5 fg=0.16 bg=0.08
phosphatidylinositol bisphosphate kinase... GO:0052813 p=8.8E−02 n=1 fg=0.03 bg=0.00
nitric−oxide synthase inhibitor activity GO:0036487 p=8.8E−02 n=1 fg=0.03 bg=0.00
vinculin binding GO:0017166 p=8.8E−02 n=1 fg=0.03 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=8.8E−02 n=1 fg=0.03 bg=0.00
mRNA 3'−UTR AU−rich region binding GO:0035925 p=8.8E−02 n=1 fg=0.03 bg=0.00
netrin receptor activity GO:0005042 p=8.8E−02 n=1 fg=0.03 bg=0.00
poly(U) RNA binding GO:0008266 p=8.8E−02 n=1 fg=0.03 bg=0.00
laminin binding GO:0043236 p=8.8E−02 n=1 fg=0.03 bg=0.00
Hsp90 protein binding GO:0051879 p=8.8E−02 n=1 fg=0.03 bg=0.00
nitric−oxide synthase binding GO:0050998 p=8.8E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=8.8E−02 n=1 fg=0.03 bg=0.00
chromatin DNA binding GO:0031490 p=8.8E−02 n=1 fg=0.03 bg=0.00
WW domain binding GO:0050699 p=8.8E−02 n=1 fg=0.03 bg=0.00
extracellular matrix binding GO:0050840 p=8.8E−02 n=1 fg=0.03 bg=0.00
calcium−dependent ATPase activity GO:0030899 p=8.8E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=8.8E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol kinase activity GO:0052742 p=8.8E−02 n=1 fg=0.03 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=8.8E−02 n=1 fg=0.03 bg=0.00
nitric−oxide synthase regulator activity GO:0030235 p=8.8E−02 n=1 fg=0.03 bg=0.00
SH2 domain binding GO:0042169 p=8.8E−02 n=1 fg=0.03 bg=0.00
phospholipase binding GO:0043274 p=8.8E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol 3−kinase activity GO:0035004 p=8.8E−02 n=1 fg=0.03 bg=0.00
heterocyclic compound binding GO:1901363 p=9.5E−02 n=12 fg=0.38 bg=0.26
protein domain specific binding GO:0019904 p=1.0E−01 n=6 fg=0.19 bg=0.10
DNA−binding transcription factor activit... GO:0000981 p=1.1E−01 n=7 fg=0.22 bg=0.13
enzyme regulator activity GO:0030234 p=1.1E−01 n=6 fg=0.19 bg=0.11
ATP binding GO:0005524 p=1.2E−01 n=3 fg=0.09 bg=0.04
0 1 2 3 4 5
−log(p)
n=32/111 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Elav_Nvec_vc1.1_XM_001633894.3
fraction genes in fg and expected valu
recycling endosome membrane GO:0055038 p=2.2E−02 n=2 fg=0.06 bg=0.01
presynaptic active zone GO:0048786 p=2.7E−02 n=3 fg=0.08 bg=0.02
receptor complex GO:0043235 p=5.1E−02 n=3 fg=0.08 bg=0.03
adherens junction GO:0005912 p=5.1E−02 n=3 fg=0.08 bg=0.03
cell cortex GO:0005938 p=5.5E−02 n=4 fg=0.11 bg=0.04
basolateral plasma membrane GO:0016323 p=5.5E−02 n=4 fg=0.11 bg=0.04
basal plasma membrane GO:0009925 p=5.5E−02 n=4 fg=0.11 bg=0.04
cytoplasmic side of plasma membrane GO:0009898 p=6.6E−02 n=3 fg=0.08 bg=0.03
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Cajal body GO:0015030 p=9.0E−02 n=1 fg=0.03 bg=0.00
integrin complex GO:0008305 p=9.0E−02 n=1 fg=0.03 bg=0.00
postsynaptic specialization membrane GO:0099634 p=9.0E−02 n=1 fg=0.03 bg=0.00
integral component of Golgi membrane GO:0030173 p=9.0E−02 n=1 fg=0.03 bg=0.00
protein complex involved in cell adhesio... GO:0098636 p=9.0E−02 n=1 fg=0.03 bg=0.00
sperm principal piece GO:0097228 p=9.0E−02 n=1 fg=0.03 bg=0.00
integrin alpha9−beta1 complex GO:0034679 p=9.0E−02 n=1 fg=0.03 bg=0.00
NELF complex GO:0032021 p=9.0E−02 n=1 fg=0.03 bg=0.00
dendritic spine membrane GO:0032591 p=9.0E−02 n=1 fg=0.03 bg=0.00
presynaptic active zone membrane GO:0048787 p=9.0E−02 n=1 fg=0.03 bg=0.00
excitatory synapse GO:0060076 p=9.0E−02 n=1 fg=0.03 bg=0.00
intrinsic component of Golgi membrane GO:0031228 p=9.0E−02 n=1 fg=0.03 bg=0.00
polysomal ribosome GO:0042788 p=9.0E−02 n=1 fg=0.03 bg=0.00
postsynaptic density membrane GO:0098839 p=9.0E−02 n=1 fg=0.03 bg=0.00
cis−Golgi network membrane GO:0033106 p=9.0E−02 n=1 fg=0.03 bg=0.00
basal part of cell GO:0045178 p=9.3E−02 n=4 fg=0.11 bg=0.05
cytoplasmic side of membrane GO:0098562 p=1.0E−01 n=3 fg=0.08 bg=0.03
caveola GO:0005901 p=1.2E−01 n=2 fg=0.06 bg=0.02
ruffle GO:0001726 p=1.2E−01 n=2 fg=0.06 bg=0.02
cell−substrate junction GO:0030055 p=1.2E−01 n=2 fg=0.06 bg=0.02
focal adhesion GO:0005925 p=1.2E−01 n=2 fg=0.06 bg=0.02
0 1 2 3 4 5
−log(p)
n=36/111 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction