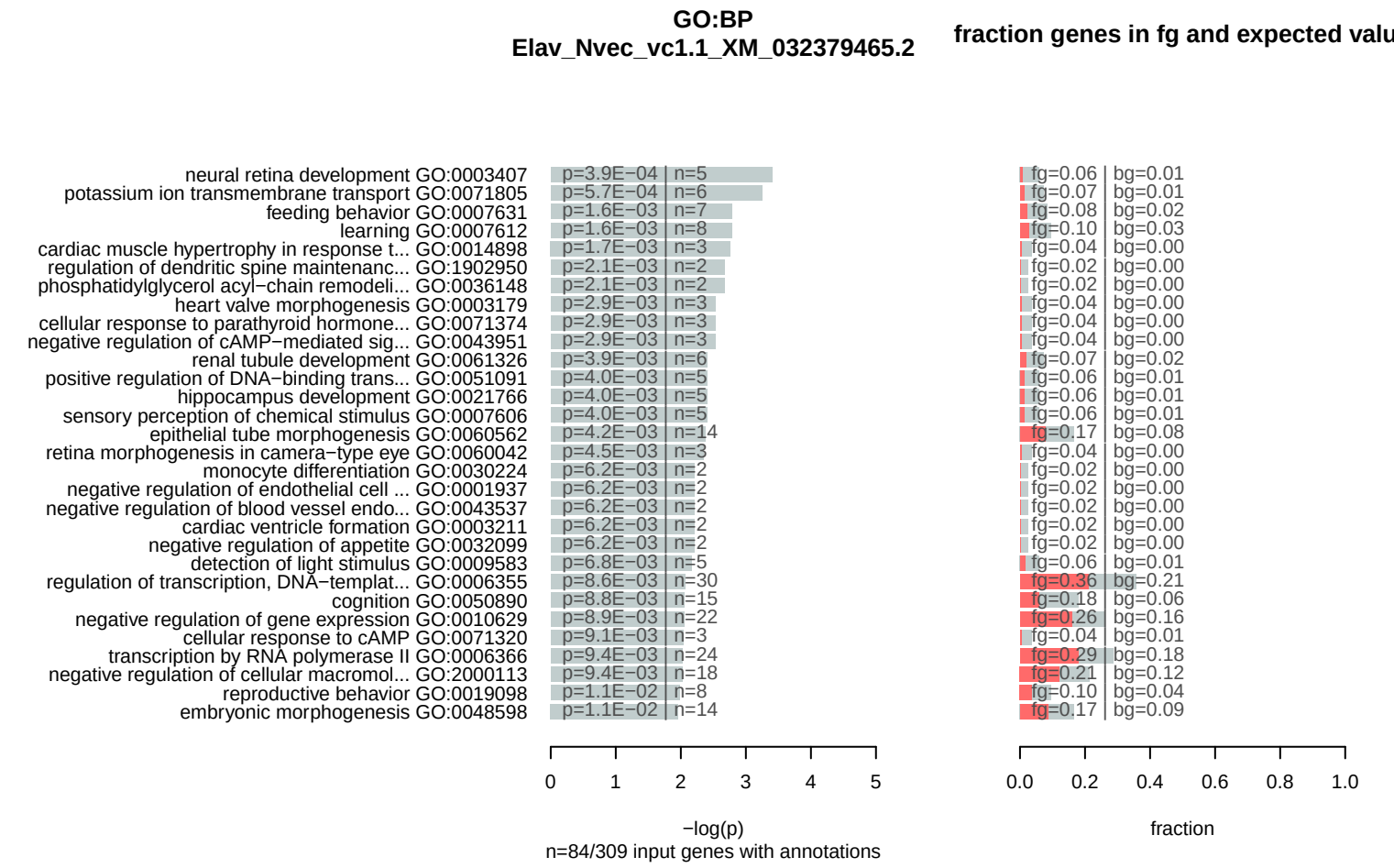
GO:BP
Elav_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
neural retina development GO:0003407 p=3.9E−04 n=5 fg=0.06 bg=0.01
potassium ion transmembrane transport GO:0071805 p=5.7E−04 n=6 fg=0.07 bg=0.01
feeding behavior GO:0007631 p=1.6E−03 n=7 fg=0.08 bg=0.02
learning GO:0007612 p=1.6E−03 n=8 fg=0.10 bg=0.03
cardiac muscle hypertrophy in response t... GO:0014898 p=1.7E−03 n=3 fg=0.04 bg=0.00
regulation of dendritic spine maintenanc... GO:1902950 p=2.1E−03 n=2 fg=0.02 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=2.1E−03 n=2 fg=0.02 bg=0.00
heart valve morphogenesis GO:0003179 p=2.9E−03 n=3 fg=0.04 bg=0.00
cellular response to parathyroid hormone... GO:0071374 p=2.9E−03 n=3 fg=0.04 bg=0.00
negative regulation of cAMP−mediated sig... GO:0043951 p=2.9E−03 n=3 fg=0.04 bg=0.00
renal tubule development GO:0061326 p=3.9E−03 n=6 fg=0.07 bg=0.02
positive regulation of DNA−binding trans... GO:0051091 p=4.0E−03 n=5 fg=0.06 bg=0.01
hippocampus development GO:0021766 p=4.0E−03 n=5 fg=0.06 bg=0.01
sensory perception of chemical stimulus GO:0007606 p=4.0E−03 n=5 fg=0.06 bg=0.01
epithelial tube morphogenesis GO:0060562 p=4.2E−03 n=14 fg=0.17 bg=0.08
retina morphogenesis in camera−type eye GO:0060042 p=4.5E−03 n=3 fg=0.04 bg=0.00
monocyte differentiation GO:0030224 p=6.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of endothelial cell ... GO:0001937 p=6.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=6.2E−03 n=2 fg=0.02 bg=0.00
cardiac ventricle formation GO:0003211 p=6.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of appetite GO:0032099 p=6.2E−03 n=2 fg=0.02 bg=0.00
detection of light stimulus GO:0009583 p=6.8E−03 n=5 fg=0.06 bg=0.01
regulation of transcription, DNA−templat... GO:0006355 p=8.6E−03 n=30 fg=0.36 bg=0.21
cognition GO:0050890 p=8.8E−03 n=15 fg=0.18 bg=0.06
negative regulation of gene expression GO:0010629 p=8.9E−03 n=22 fg=0.26 bg=0.16
cellular response to cAMP GO:0071320 p=9.1E−03 n=3 fg=0.04 bg=0.01
transcription by RNA polymerase II GO:0006366 p=9.4E−03 n=24 fg=0.29 bg=0.18
negative regulation of cellular macromol... GO:2000113 p=9.4E−03 n=18 fg=0.21 bg=0.12
reproductive behavior GO:0019098 p=1.1E−02 n=8 fg=0.10 bg=0.04
embryonic morphogenesis GO:0048598 p=1.1E−02 n=14 fg=0.17 bg=0.09
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−log(p)
n=84/309 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
voltage−gated potassium channel activity GO:0005249 p=7.3E−04 n=4 fg=0.05 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.2E−03 n=4 fg=0.05 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=2.9E−03 n=12 fg=0.16 bg=0.07
P−type calcium transporter activity GO:0005388 p=6.2E−03 n=2 fg=0.03 bg=0.00
tumor necrosis factor receptor binding GO:0005164 p=6.2E−03 n=2 fg=0.03 bg=0.00
bHLH transcription factor binding GO:0043425 p=6.2E−03 n=2 fg=0.03 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=6.2E−03 n=2 fg=0.03 bg=0.00
acetylcholine receptor binding GO:0033130 p=1.2E−02 n=2 fg=0.03 bg=0.00
cAMP binding GO:0030552 p=1.2E−02 n=2 fg=0.03 bg=0.00
chemoattractant activity GO:0042056 p=1.2E−02 n=2 fg=0.03 bg=0.00
poly(U) RNA binding GO:0008266 p=1.9E−02 n=2 fg=0.03 bg=0.00
ephrin receptor binding GO:0046875 p=1.9E−02 n=2 fg=0.03 bg=0.00
leak channel activity GO:0022840 p=1.9E−02 n=2 fg=0.03 bg=0.00
potassium ion leak channel activity GO:0022841 p=1.9E−02 n=2 fg=0.03 bg=0.00
narrow pore channel activity GO:0022842 p=1.9E−02 n=2 fg=0.03 bg=0.00
cyclic nucleotide binding GO:0030551 p=1.9E−02 n=2 fg=0.03 bg=0.00
phospholipid transporter activity GO:0005548 p=2.0E−02 n=3 fg=0.04 bg=0.01
protein kinase binding GO:0019901 p=2.0E−02 n=11 fg=0.15 bg=0.08
mRNA binding GO:0003729 p=2.3E−02 n=6 fg=0.08 bg=0.03
SMAD binding GO:0046332 p=2.4E−02 n=3 fg=0.04 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=2.7E−02 n=8 fg=0.11 bg=0.05
kinase binding GO:0019900 p=2.8E−02 n=11 fg=0.15 bg=0.08
receptor ligand activity GO:0048018 p=2.8E−02 n=2 fg=0.03 bg=0.00
G−protein alpha−subunit binding GO:0001965 p=2.8E−02 n=2 fg=0.03 bg=0.00
HMG box domain binding GO:0071837 p=2.8E−02 n=2 fg=0.03 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=2.8E−02 n=2 fg=0.03 bg=0.00
signaling receptor activator activity GO:0030546 p=2.8E−02 n=2 fg=0.03 bg=0.00
sequence−specific DNA binding GO:0043565 p=3.1E−02 n=10 fg=0.14 bg=0.07
calcium ion binding GO:0005509 p=3.2E−02 n=5 fg=0.07 bg=0.02
histone deacetylase activity GO:0004407 p=3.8E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=74/309 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=4.4E−04 n=4 fg=0.05 bg=0.00
growth cone filopodium GO:1990812 p=2.1E−03 n=2 fg=0.02 bg=0.00
plasma membrane GO:0005886 p=4.8E−03 n=36 fg=0.43 bg=0.27
growth cone lamellipodium GO:1990761 p=6.1E−03 n=2 fg=0.02 bg=0.00
stress fiber GO:0001725 p=6.4E−03 n=3 fg=0.04 bg=0.00
dendritic spine GO:0043197 p=8.5E−03 n=6 fg=0.07 bg=0.02
transcription repressor complex GO:0017053 p=1.9E−02 n=3 fg=0.04 bg=0.01
sarcomere GO:0030017 p=2.0E−02 n=5 fg=0.06 bg=0.02
contractile fiber GO:0043292 p=2.2E−02 n=6 fg=0.07 bg=0.03
main axon GO:0044304 p=3.4E−02 n=3 fg=0.04 bg=0.01
myofibril GO:0030016 p=3.7E−02 n=5 fg=0.06 bg=0.02
cell body GO:0044297 p=4.4E−02 n=11 fg=0.13 bg=0.08
endoplasmic reticulum lumen GO:0005788 p=4.5E−02 n=4 fg=0.05 bg=0.02
RNA polymerase II transcription represso... GO:0090571 p=4.6E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=4.6E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=4.6E−02 n=1 fg=0.01 bg=0.00
nucleolar ribonuclease P complex GO:0005655 p=4.6E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=4.6E−02 n=1 fg=0.01 bg=0.00
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=4.6E−02 n=1 fg=0.01 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=4.6E−02 n=1 fg=0.01 bg=0.00
ribonuclease MRP complex GO:0000172 p=4.6E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=4.6E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=4.6E−02 n=1 fg=0.01 bg=0.00
nuclear outer membrane GO:0005640 p=4.6E−02 n=1 fg=0.01 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=4.6E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=4.6E−02 n=1 fg=0.01 bg=0.00
interphase microtubule organizing center GO:0031021 p=4.6E−02 n=1 fg=0.01 bg=0.00
plasma lipoprotein particle GO:0034358 p=4.6E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=4.6E−02 n=1 fg=0.01 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=4.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=83/309 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction