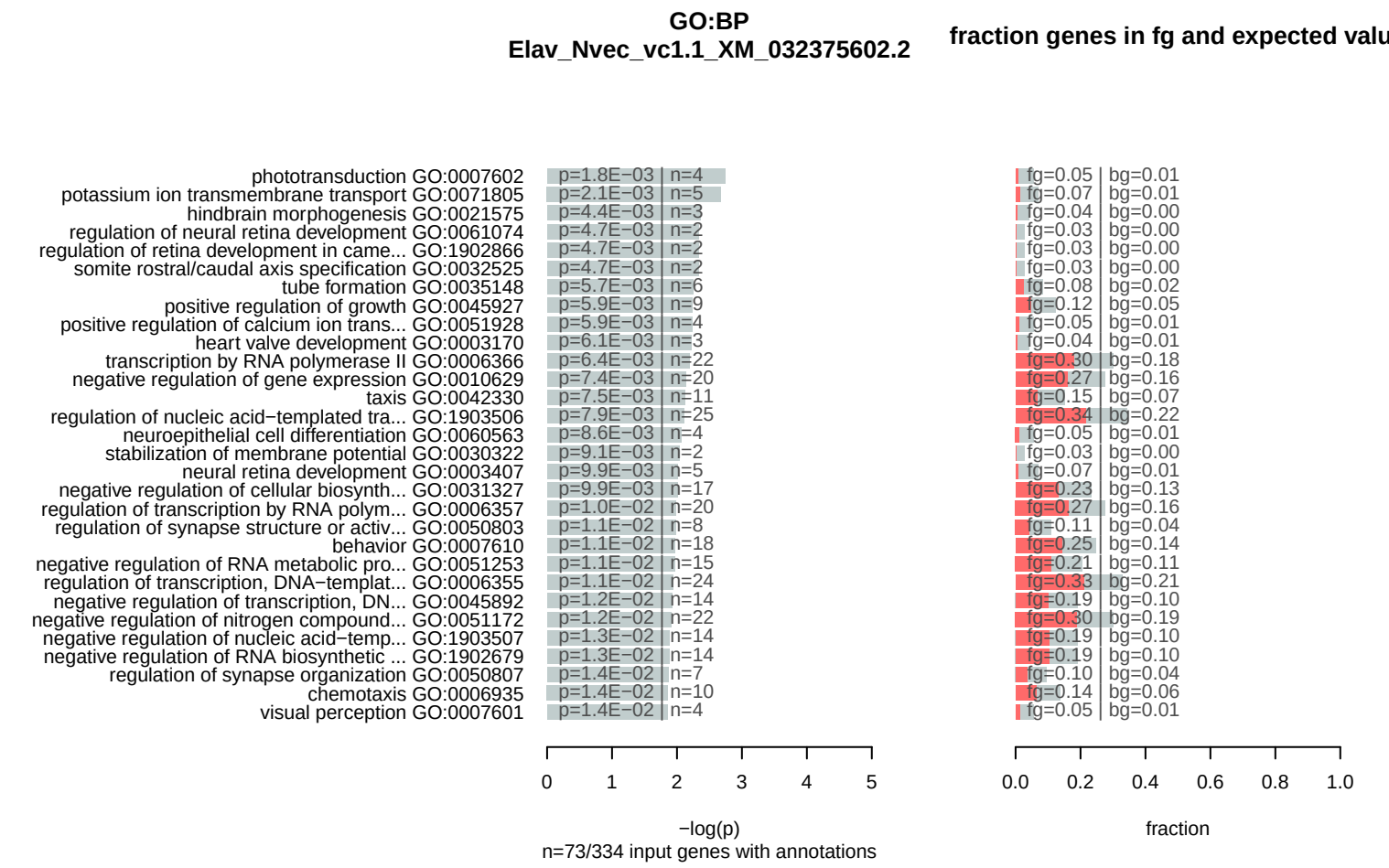
GO:BP
Elav_Nvec_vc1.1_XM_032375602.2
fraction genes in fg and expected valu
phototransduction GO:0007602 p=1.8E−03 n=4 fg=0.05 bg=0.01
potassium ion transmembrane transport GO:0071805 p=2.1E−03 n=5 fg=0.07 bg=0.01
hindbrain morphogenesis GO:0021575 p=4.4E−03 n=3 fg=0.04 bg=0.00
regulation of neural retina development GO:0061074 p=4.7E−03 n=2 fg=0.03 bg=0.00
regulation of retina development in came... GO:1902866 p=4.7E−03 n=2 fg=0.03 bg=0.00
somite rostral/caudal axis specification GO:0032525 p=4.7E−03 n=2 fg=0.03 bg=0.00
tube formation GO:0035148 p=5.7E−03 n=6 fg=0.08 bg=0.02
positive regulation of growth GO:0045927 p=5.9E−03 n=9 fg=0.12 bg=0.05
positive regulation of calcium ion trans... GO:0051928 p=5.9E−03 n=4 fg=0.05 bg=0.01
heart valve development GO:0003170 p=6.1E−03 n=3 fg=0.04 bg=0.01
transcription by RNA polymerase II GO:0006366 p=6.4E−03 n=22 fg=0.30 bg=0.18
negative regulation of gene expression GO:0010629 p=7.4E−03 n=20 fg=0.27 bg=0.16
taxis GO:0042330 p=7.5E−03 n=11 fg=0.15 bg=0.07
regulation of nucleic acid−templated tra... GO:1903506 p=7.9E−03 n=25 fg=0.34 bg=0.22
neuroepithelial cell differentiation GO:0060563 p=8.6E−03 n=4 fg=0.05 bg=0.01
stabilization of membrane potential GO:0030322 p=9.1E−03 n=2 fg=0.03 bg=0.00
neural retina development GO:0003407 p=9.9E−03 n=5 fg=0.07 bg=0.01
negative regulation of cellular biosynth... GO:0031327 p=9.9E−03 n=17 fg=0.23 bg=0.13
regulation of transcription by RNA polym... GO:0006357 p=1.0E−02 n=20 fg=0.27 bg=0.16
regulation of synapse structure or activ... GO:0050803 p=1.1E−02 n=8 fg=0.11 bg=0.04
behavior GO:0007610 p=1.1E−02 n=18 fg=0.25 bg=0.14
negative regulation of RNA metabolic pro... GO:0051253 p=1.1E−02 n=15 fg=0.21 bg=0.11
regulation of transcription, DNA−templat... GO:0006355 p=1.1E−02 n=24 fg=0.33 bg=0.21
negative regulation of transcription, DN... GO:0045892 p=1.2E−02 n=14 fg=0.19 bg=0.10
negative regulation of nitrogen compound... GO:0051172 p=1.2E−02 n=22 fg=0.30 bg=0.19
negative regulation of nucleic acid−temp... GO:1903507 p=1.3E−02 n=14 fg=0.19 bg=0.10
negative regulation of RNA biosynthetic ... GO:1902679 p=1.3E−02 n=14 fg=0.19 bg=0.10
regulation of synapse organization GO:0050807 p=1.4E−02 n=7 fg=0.10 bg=0.04
chemotaxis GO:0006935 p=1.4E−02 n=10 fg=0.14 bg=0.06
visual perception GO:0007601 p=1.4E−02 n=4 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=73/334 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032375602.2
fraction genes in fg and expected valu
voltage−gated potassium channel activity GO:0005249 p=6.9E−03 n=3 fg=0.04 bg=0.01
cAMP binding GO:0030552 p=9.9E−03 n=2 fg=0.03 bg=0.00
acetylcholine receptor binding GO:0033130 p=9.9E−03 n=2 fg=0.03 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=1.2E−02 n=10 fg=0.15 bg=0.07
leak channel activity GO:0022840 p=1.6E−02 n=2 fg=0.03 bg=0.00
potassium ion leak channel activity GO:0022841 p=1.6E−02 n=2 fg=0.03 bg=0.00
narrow pore channel activity GO:0022842 p=1.6E−02 n=2 fg=0.03 bg=0.00
structural constituent of nuclear pore GO:0017056 p=1.6E−02 n=2 fg=0.03 bg=0.00
sequence−specific DNA binding GO:0043565 p=1.6E−02 n=10 fg=0.15 bg=0.07
cis−regulatory region sequence−specific ... GO:0000987 p=3.0E−02 n=6 fg=0.09 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=3.0E−02 n=6 fg=0.09 bg=0.04
adrenergic receptor binding GO:0031690 p=3.2E−02 n=2 fg=0.03 bg=0.00
transcription corepressor activity GO:0003714 p=3.8E−02 n=4 fg=0.06 bg=0.02
phosphatidylinositol phosphate binding GO:1901981 p=3.8E−02 n=4 fg=0.06 bg=0.02
DNA−binding transcription activator acti... GO:0001228 p=4.0E−02 n=6 fg=0.09 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=4.0E−02 n=6 fg=0.09 bg=0.04
phosphatidylinositol binding GO:0035091 p=4.1E−02 n=5 fg=0.07 bg=0.03
DNA−binding transcription factor activit... GO:0003700 p=4.1E−02 n=10 fg=0.15 bg=0.08
transcription regulator activity GO:0140110 p=4.1E−02 n=13 fg=0.19 bg=0.12
opsin binding GO:0002046 p=4.2E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.2E−02 n=1 fg=0.01 bg=0.00
tRNA (uracil) methyltransferase activity GO:0016300 p=4.2E−02 n=1 fg=0.01 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=4.2E−02 n=1 fg=0.01 bg=0.00
S100 protein binding GO:0044548 p=4.2E−02 n=1 fg=0.01 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=4.2E−02 n=1 fg=0.01 bg=0.00
rRNA primary transcript binding GO:0042134 p=4.2E−02 n=1 fg=0.01 bg=0.00
purine nucleobase transmembrane transpor... GO:0005345 p=4.2E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=4.2E−02 n=1 fg=0.01 bg=0.00
nucleobase transmembrane transporter act... GO:0015205 p=4.2E−02 n=1 fg=0.01 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=4.2E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=67/334 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032375602.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=5.0E−03 n=3 fg=0.04 bg=0.01
exon−exon junction complex GO:0035145 p=5.1E−03 n=2 fg=0.03 bg=0.00
lipid droplet GO:0005811 p=6.9E−03 n=4 fg=0.05 bg=0.01
photoreceptor inner segment GO:0001917 p=9.2E−03 n=3 fg=0.04 bg=0.01
plasma membrane raft GO:0044853 p=1.0E−02 n=4 fg=0.05 bg=0.01
synapse GO:0045202 p=1.4E−02 n=14 fg=0.18 bg=0.10
dendrite GO:0030425 p=1.7E−02 n=11 fg=0.14 bg=0.07
dendritic tree GO:0097447 p=1.7E−02 n=11 fg=0.14 bg=0.07
cell junction GO:0030054 p=2.1E−02 n=17 fg=0.22 bg=0.13
photoreceptor outer segment GO:0001750 p=2.2E−02 n=3 fg=0.04 bg=0.01
neuron spine GO:0044309 p=2.4E−02 n=5 fg=0.07 bg=0.02
dendritic spine GO:0043197 p=2.4E−02 n=5 fg=0.07 bg=0.02
caveola GO:0005901 p=2.7E−02 n=3 fg=0.04 bg=0.01
neuron projection GO:0043005 p=2.8E−02 n=17 fg=0.22 bg=0.14
somatodendritic compartment GO:0036477 p=3.3E−02 n=13 fg=0.17 bg=0.10
germ cell nucleus GO:0043073 p=4.1E−02 n=2 fg=0.03 bg=0.00
transverse filament GO:0000802 p=4.2E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=4.2E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=4.2E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=4.2E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=4.2E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=4.2E−02 n=1 fg=0.01 bg=0.00
pigment granule membrane GO:0090741 p=4.2E−02 n=1 fg=0.01 bg=0.00
9+0 non−motile cilium GO:0097731 p=6.2E−02 n=3 fg=0.04 bg=0.01
photoreceptor cell cilium GO:0097733 p=6.2E−02 n=3 fg=0.04 bg=0.01
T−tubule GO:0030315 p=6.3E−02 n=2 fg=0.03 bg=0.01
pigment granule GO:0048770 p=6.3E−02 n=2 fg=0.03 bg=0.01
ciliary base GO:0097546 p=7.5E−02 n=2 fg=0.03 bg=0.01
photoreceptor connecting cilium GO:0032391 p=7.5E−02 n=2 fg=0.03 bg=0.01
lateral plasma membrane GO:0016328 p=7.5E−02 n=2 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=76/334 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction