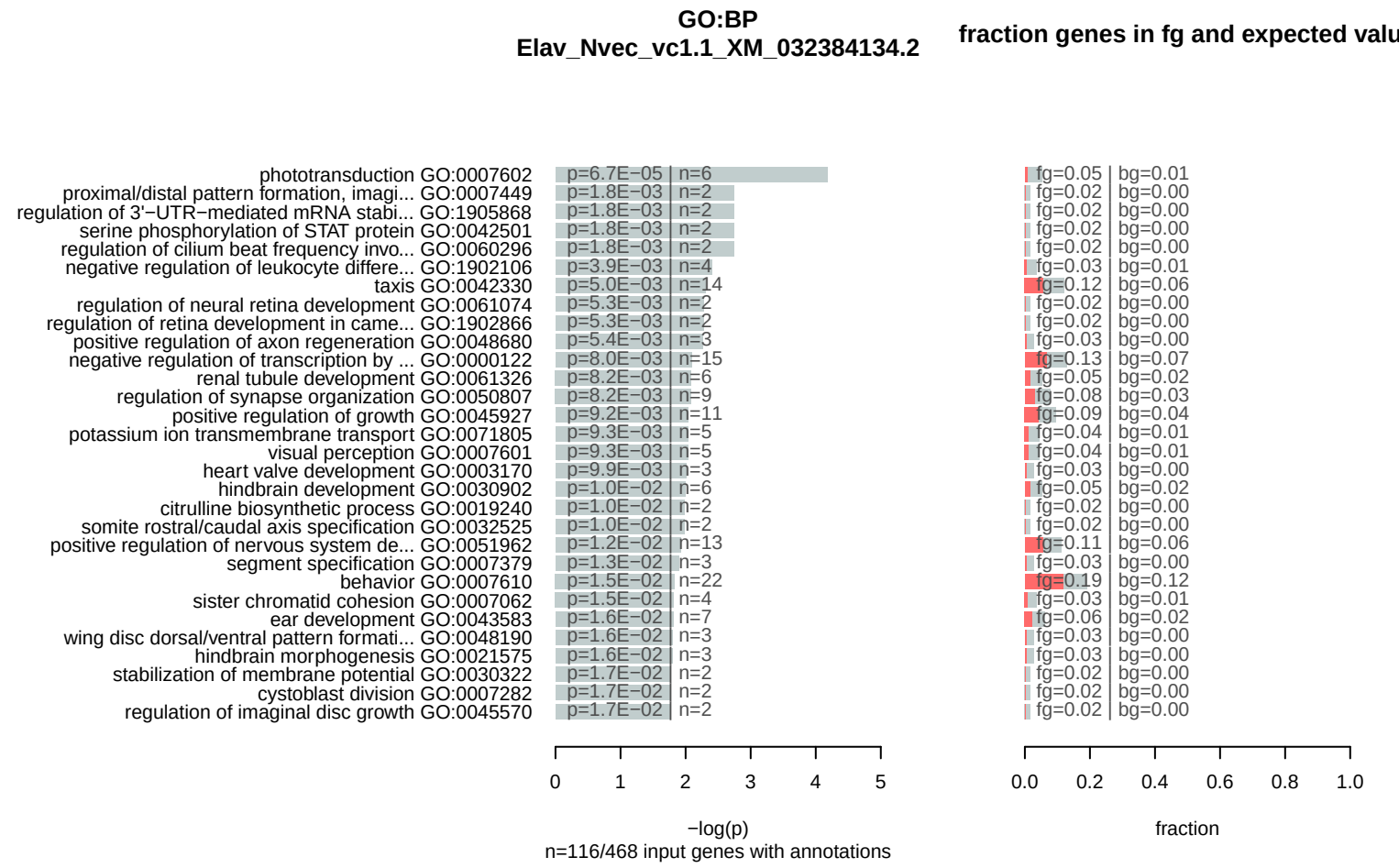
GO:BP
Elav_Nvec_vc1.1_XM_032384134.2
fraction genes in fg and expected valu
phototransduction GO:0007602 p=6.7E−05 n=6 fg=0.05 bg=0.01
proximal/distal pattern formation, imagi... GO:0007449 p=1.8E−03 n=2 fg=0.02 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=1.8E−03 n=2 fg=0.02 bg=0.00
serine phosphorylation of STAT protein GO:0042501 p=1.8E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=1.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of leukocyte differe... GO:1902106 p=3.9E−03 n=4 fg=0.03 bg=0.01
taxis GO:0042330 p=5.0E−03 n=14 fg=0.12 bg=0.06
regulation of neural retina development GO:0061074 p=5.3E−03 n=2 fg=0.02 bg=0.00
regulation of retina development in came... GO:1902866 p=5.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of axon regeneration GO:0048680 p=5.4E−03 n=3 fg=0.03 bg=0.00
negative regulation of transcription by ... GO:0000122 p=8.0E−03 n=15 fg=0.13 bg=0.07
renal tubule development GO:0061326 p=8.2E−03 n=6 fg=0.05 bg=0.02
regulation of synapse organization GO:0050807 p=8.2E−03 n=9 fg=0.08 bg=0.03
positive regulation of growth GO:0045927 p=9.2E−03 n=11 fg=0.09 bg=0.04
potassium ion transmembrane transport GO:0071805 p=9.3E−03 n=5 fg=0.04 bg=0.01
visual perception GO:0007601 p=9.3E−03 n=5 fg=0.04 bg=0.01
heart valve development GO:0003170 p=9.9E−03 n=3 fg=0.03 bg=0.00
hindbrain development GO:0030902 p=1.0E−02 n=6 fg=0.05 bg=0.02
citrulline biosynthetic process GO:0019240 p=1.0E−02 n=2 fg=0.02 bg=0.00
somite rostral/caudal axis specification GO:0032525 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of nervous system de... GO:0051962 p=1.2E−02 n=13 fg=0.11 bg=0.06
segment specification GO:0007379 p=1.3E−02 n=3 fg=0.03 bg=0.00
behavior GO:0007610 p=1.5E−02 n=22 fg=0.19 bg=0.12
sister chromatid cohesion GO:0007062 p=1.5E−02 n=4 fg=0.03 bg=0.01
ear development GO:0043583 p=1.6E−02 n=7 fg=0.06 bg=0.02
wing disc dorsal/ventral pattern formati... GO:0048190 p=1.6E−02 n=3 fg=0.03 bg=0.00
hindbrain morphogenesis GO:0021575 p=1.6E−02 n=3 fg=0.03 bg=0.00
stabilization of membrane potential GO:0030322 p=1.7E−02 n=2 fg=0.02 bg=0.00
cystoblast division GO:0007282 p=1.7E−02 n=2 fg=0.02 bg=0.00
regulation of imaginal disc growth GO:0045570 p=1.7E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=116/468 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032384134.2
fraction genes in fg and expected valu
DNA−binding transcription activator acti... GO:0001228 p=1.2E−03 n=10 fg=0.10 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.3E−03 n=10 fg=0.10 bg=0.03
potassium channel activity GO:0005267 p=6.7E−03 n=4 fg=0.04 bg=0.01
structural constituent of nuclear pore GO:0017056 p=7.9E−03 n=3 fg=0.03 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=1.1E−02 n=3 fg=0.03 bg=0.00
cAMP binding GO:0030552 p=1.1E−02 n=2 fg=0.02 bg=0.00
voltage−gated cation channel activity GO:0022843 p=1.4E−02 n=4 fg=0.04 bg=0.01
mRNA binding GO:0003729 p=1.5E−02 n=8 fg=0.08 bg=0.03
RNA methyltransferase activity GO:0008173 p=1.6E−02 n=4 fg=0.04 bg=0.01
microtubule motor activity GO:0003777 p=1.7E−02 n=3 fg=0.03 bg=0.01
acetylcholine receptor binding GO:0033130 p=1.8E−02 n=2 fg=0.02 bg=0.00
leak channel activity GO:0022840 p=1.8E−02 n=2 fg=0.02 bg=0.00
potassium ion leak channel activity GO:0022841 p=1.8E−02 n=2 fg=0.02 bg=0.00
narrow pore channel activity GO:0022842 p=1.8E−02 n=2 fg=0.02 bg=0.00
cyclic nucleotide binding GO:0030551 p=1.8E−02 n=2 fg=0.02 bg=0.00
E−box binding GO:0070888 p=2.1E−02 n=3 fg=0.03 bg=0.01
O−methyltransferase activity GO:0008171 p=2.5E−02 n=2 fg=0.02 bg=0.00
adrenergic receptor binding GO:0031690 p=3.5E−02 n=2 fg=0.02 bg=0.00
MAP kinase activity GO:0004707 p=3.5E−02 n=2 fg=0.02 bg=0.00
voltage−gated ion channel activity GO:0005244 p=3.6E−02 n=4 fg=0.04 bg=0.01
voltage−gated channel activity GO:0022832 p=3.6E−02 n=4 fg=0.04 bg=0.01
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.4E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=4.4E−02 n=1 fg=0.01 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=4.4E−02 n=1 fg=0.01 bg=0.00
taste receptor binding GO:0031883 p=4.4E−02 n=1 fg=0.01 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=4.4E−02 n=1 fg=0.01 bg=0.00
glutamate−5−semialdehyde dehydrogenase a... GO:0004350 p=4.4E−02 n=1 fg=0.01 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=4.4E−02 n=1 fg=0.01 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=4.4E−02 n=1 fg=0.01 bg=0.00
amine transmembrane transporter activity GO:0005275 p=4.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=104/468 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032384134.2
fraction genes in fg and expected valu
photoreceptor inner segment GO:0001917 p=1.8E−03 n=4 fg=0.03 bg=0.00
hippocampal mossy fiber GO:0097457 p=1.9E−03 n=2 fg=0.02 bg=0.00
photoreceptor outer segment GO:0001750 p=4.2E−03 n=4 fg=0.03 bg=0.01
synapse GO:0045202 p=6.4E−03 n=18 fg=0.15 bg=0.08
voltage−gated potassium channel complex GO:0008076 p=7.8E−03 n=3 fg=0.03 bg=0.00
exon−exon junction complex GO:0035145 p=1.1E−02 n=2 fg=0.02 bg=0.00
lipid droplet GO:0005811 p=1.9E−02 n=4 fg=0.03 bg=0.01
plasma membrane raft GO:0044853 p=4.0E−02 n=4 fg=0.03 bg=0.01
transverse filament GO:0000802 p=4.4E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=4.4E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=4.4E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber expansion GO:1990026 p=4.4E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=4.4E−02 n=1 fg=0.01 bg=0.00
pigment granule membrane GO:0090741 p=4.4E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=4.4E−02 n=1 fg=0.01 bg=0.00
chromatin GO:0000785 p=5.0E−02 n=10 fg=0.08 bg=0.05
dendrite GO:0030425 p=5.1E−02 n=12 fg=0.10 bg=0.06
dendritic tree GO:0097447 p=5.3E−02 n=12 fg=0.10 bg=0.06
cortical actin cytoskeleton GO:0030864 p=5.4E−02 n=3 fg=0.03 bg=0.01
pigment granule GO:0048770 p=6.8E−02 n=2 fg=0.02 bg=0.00
dendritic spine GO:0043197 p=7.4E−02 n=5 fg=0.04 bg=0.02
neuron spine GO:0044309 p=7.4E−02 n=5 fg=0.04 bg=0.02
caveola GO:0005901 p=7.6E−02 n=3 fg=0.03 bg=0.01
cortical cytoskeleton GO:0030863 p=7.6E−02 n=3 fg=0.03 bg=0.01
RNA polymerase III transcription regulat... GO:0090576 p=8.6E−02 n=1 fg=0.01 bg=0.00
spermatoproteasome complex GO:1990111 p=8.6E−02 n=1 fg=0.01 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=8.6E−02 n=1 fg=0.01 bg=0.00
BBSome GO:0034464 p=8.6E−02 n=1 fg=0.01 bg=0.00
tRNA−splicing ligase complex GO:0072669 p=8.6E−02 n=1 fg=0.01 bg=0.00
calcineurin complex GO:0005955 p=8.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=118/468 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction