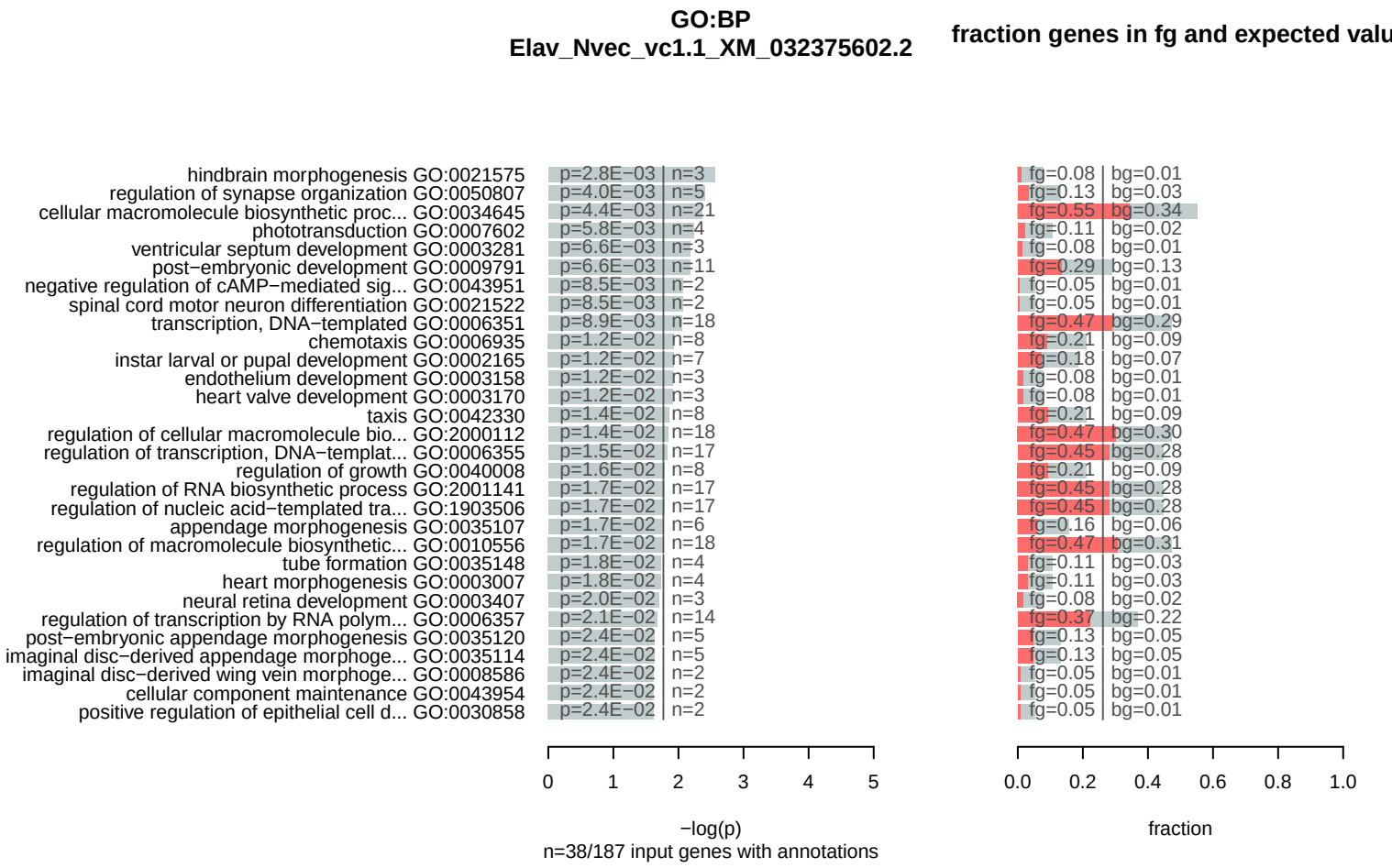
GO:BP
Elav_Nvec_vc1.1_XM_032375602.2
fraction genes in fg and expected valu
hindbrain morphogenesis GO:0021575 p=2.8E−03 n=3 fg=0.08 bg=0.01
regulation of synapse organization GO:0050807 p=4.0E−03 n=5 fg=0.13 bg=0.03
cellular macromolecule biosynthetic proc... GO:0034645 p=4.4E−03 n=21 fg=0.55 bg=0.34
phototransduction GO:0007602 p=5.8E−03 n=4 fg=0.11 bg=0.02
ventricular septum development GO:0003281 p=6.6E−03 n=3 fg=0.08 bg=0.01
post−embryonic development GO:0009791 p=6.6E−03 n=11 fg=0.29 bg=0.13
negative regulation of cAMP−mediated sig... GO:0043951 p=8.5E−03 n=2 fg=0.05 bg=0.01
spinal cord motor neuron differentiation GO:0021522 p=8.5E−03 n=2 fg=0.05 bg=0.01
transcription, DNA−templated GO:0006351 p=8.9E−03 n=18 fg=0.47 bg=0.29
chemotaxis GO:0006935 p=1.2E−02 n=8 fg=0.21 bg=0.09
instar larval or pupal development GO:0002165 p=1.2E−02 n=7 fg=0.18 bg=0.07
endothelium development GO:0003158 p=1.2E−02 n=3 fg=0.08 bg=0.01
heart valve development GO:0003170 p=1.2E−02 n=3 fg=0.08 bg=0.01
taxis GO:0042330 p=1.4E−02 n=8 fg=0.21 bg=0.09
regulation of cellular macromolecule bio... GO:2000112 p=1.4E−02 n=18 fg=0.47 bg=0.30
regulation of transcription, DNA−templat... GO:0006355 p=1.5E−02 n=17 fg=0.45 bg=0.28
regulation of growth GO:0040008 p=1.6E−02 n=8 fg=0.21 bg=0.09
regulation of RNA biosynthetic process GO:2001141 p=1.7E−02 n=17 fg=0.45 bg=0.28
regulation of nucleic acid−templated tra... GO:1903506 p=1.7E−02 n=17 fg=0.45 bg=0.28
appendage morphogenesis GO:0035107 p=1.7E−02 n=6 fg=0.16 bg=0.06
regulation of macromolecule biosynthetic... GO:0010556 p=1.7E−02 n=18 fg=0.47 bg=0.31
tube formation GO:0035148 p=1.8E−02 n=4 fg=0.11 bg=0.03
heart morphogenesis GO:0003007 p=1.8E−02 n=4 fg=0.11 bg=0.03
neural retina development GO:0003407 p=2.0E−02 n=3 fg=0.08 bg=0.02
regulation of transcription by RNA polym... GO:0006357 p=2.1E−02 n=14 fg=0.37 bg=0.22
post−embryonic appendage morphogenesis GO:0035120 p=2.4E−02 n=5 fg=0.13 bg=0.05
imaginal disc−derived appendage morphoge... GO:0035114 p=2.4E−02 n=5 fg=0.13 bg=0.05
imaginal disc−derived wing vein morphoge... GO:0008586 p=2.4E−02 n=2 fg=0.05 bg=0.01
cellular component maintenance GO:0043954 p=2.4E−02 n=2 fg=0.05 bg=0.01
positive regulation of epithelial cell d... GO:0030858 p=2.4E−02 n=2 fg=0.05 bg=0.01
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−log(p)
n=38/187 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
enzyme inhibitor activity GO:0004857 p=4.3E−03 n=4 fg=0.11 bg=0.02
acetylcholine receptor binding GO:0033130 p=9.5E−03 n=2 fg=0.06 bg=0.01
cAMP binding GO:0030552 p=2.7E−02 n=2 fg=0.06 bg=0.01
metal ion transmembrane transporter acti... GO:0046873 p=4.5E−02 n=6 fg=0.17 bg=0.08
carbohydrate derivative binding GO:0097367 p=4.5E−02 n=6 fg=0.17 bg=0.08
cyclic nucleotide binding GO:0030551 p=5.0E−02 n=2 fg=0.06 bg=0.01
phosphatidylinositol phosphate binding GO:1901981 p=6.6E−02 n=3 fg=0.08 bg=0.03
DNA−binding transcription factor activit... GO:0000981 p=8.2E−02 n=8 fg=0.22 bg=0.13
nitric−oxide synthase regulator activity GO:0030235 p=9.9E−02 n=1 fg=0.03 bg=0.00
V2 vasopressin receptor binding GO:0031896 p=9.9E−02 n=1 fg=0.03 bg=0.00
rRNA primary transcript binding GO:0042134 p=9.9E−02 n=1 fg=0.03 bg=0.00
opsin binding GO:0002046 p=9.9E−02 n=1 fg=0.03 bg=0.00
insulin−like growth factor receptor bind... GO:0005159 p=9.9E−02 n=1 fg=0.03 bg=0.00
phospholipase binding GO:0043274 p=9.9E−02 n=1 fg=0.03 bg=0.00
translation factor activity, RNA binding GO:0008135 p=9.9E−02 n=1 fg=0.03 bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762 p=9.9E−02 n=1 fg=0.03 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=9.9E−02 n=1 fg=0.03 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=9.9E−02 n=1 fg=0.03 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=9.9E−02 n=1 fg=0.03 bg=0.00
rRNA binding GO:0019843 p=9.9E−02 n=1 fg=0.03 bg=0.00
tau protein binding GO:0048156 p=9.9E−02 n=1 fg=0.03 bg=0.00
chemoattractant activity GO:0042056 p=9.9E−02 n=1 fg=0.03 bg=0.00
non−tyrosine kinase fibroblast growth fa... GO:0001571 p=9.9E−02 n=1 fg=0.03 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=9.9E−02 n=1 fg=0.03 bg=0.00
arrestin family protein binding GO:1990763 p=9.9E−02 n=1 fg=0.03 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=9.9E−02 n=1 fg=0.03 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=9.9E−02 n=1 fg=0.03 bg=0.00
triglyceride lipase activity GO:0004806 p=9.9E−02 n=1 fg=0.03 bg=0.00
TPR domain binding GO:0030911 p=9.9E−02 n=1 fg=0.03 bg=0.00
proline−rich region binding GO:0070064 p=9.9E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=36/187 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
cortical actin cytoskeleton GO:0030864 p=8.3E−03 n=2 fg=0.05 bg=0.00
plasma membrane raft GO:0044853 p=8.6E−03 n=4 fg=0.11 bg=0.02
plasma membrane protein complex GO:0098797 p=1.0E−02 n=6 fg=0.16 bg=0.05
caveola GO:0005901 p=1.9E−02 n=3 fg=0.08 bg=0.02
germ cell nucleus GO:0043073 p=2.3E−02 n=2 fg=0.05 bg=0.01
cell junction GO:0030054 p=2.6E−02 n=12 fg=0.32 bg=0.19
neuron projection GO:0043005 p=2.6E−02 n=12 fg=0.32 bg=0.19
dendritic spine GO:0043197 p=2.8E−02 n=5 fg=0.14 bg=0.05
neuron spine GO:0044309 p=2.8E−02 n=5 fg=0.14 bg=0.05
potassium channel complex GO:0034705 p=2.9E−02 n=3 fg=0.08 bg=0.02
voltage−gated potassium channel complex GO:0008076 p=2.9E−02 n=3 fg=0.08 bg=0.02
plasma membrane bounded cell projection GO:0120025 p=3.4E−02 n=14 fg=0.38 bg=0.24
cell projection GO:0042995 p=3.4E−02 n=14 fg=0.38 bg=0.24
synapse GO:0045202 p=3.7E−02 n=10 fg=0.27 bg=0.15
membrane protein complex GO:0098796 p=3.9E−02 n=6 fg=0.16 bg=0.07
cation channel complex GO:0034703 p=4.0E−02 n=4 fg=0.11 bg=0.04
somatodendritic compartment GO:0036477 p=4.1E−02 n=10 fg=0.27 bg=0.15
T−tubule GO:0030315 p=4.4E−02 n=2 fg=0.05 bg=0.01
ion channel complex GO:0034702 p=5.0E−02 n=4 fg=0.11 bg=0.04
transporter complex GO:1990351 p=5.0E−02 n=4 fg=0.11 bg=0.04
transmembrane transporter complex GO:1902495 p=5.0E−02 n=4 fg=0.11 bg=0.04
nucleus GO:0005634 p=5.7E−02 n=22 fg=0.59 bg=0.46
basolateral plasma membrane GO:0016323 p=6.0E−02 n=4 fg=0.11 bg=0.04
basal plasma membrane GO:0009925 p=6.0E−02 n=4 fg=0.11 bg=0.04
postsynapse GO:0098794 p=6.1E−02 n=6 fg=0.16 bg=0.08
dendrite GO:0030425 p=7.1E−02 n=8 fg=0.22 bg=0.12
dendritic tree GO:0097447 p=7.1E−02 n=8 fg=0.22 bg=0.12
synaptic membrane GO:0097060 p=7.3E−02 n=4 fg=0.11 bg=0.04
striated muscle thin filament GO:0005865 p=9.2E−02 n=1 fg=0.03 bg=0.00
spectrosome GO:0045170 p=9.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=37/187 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction