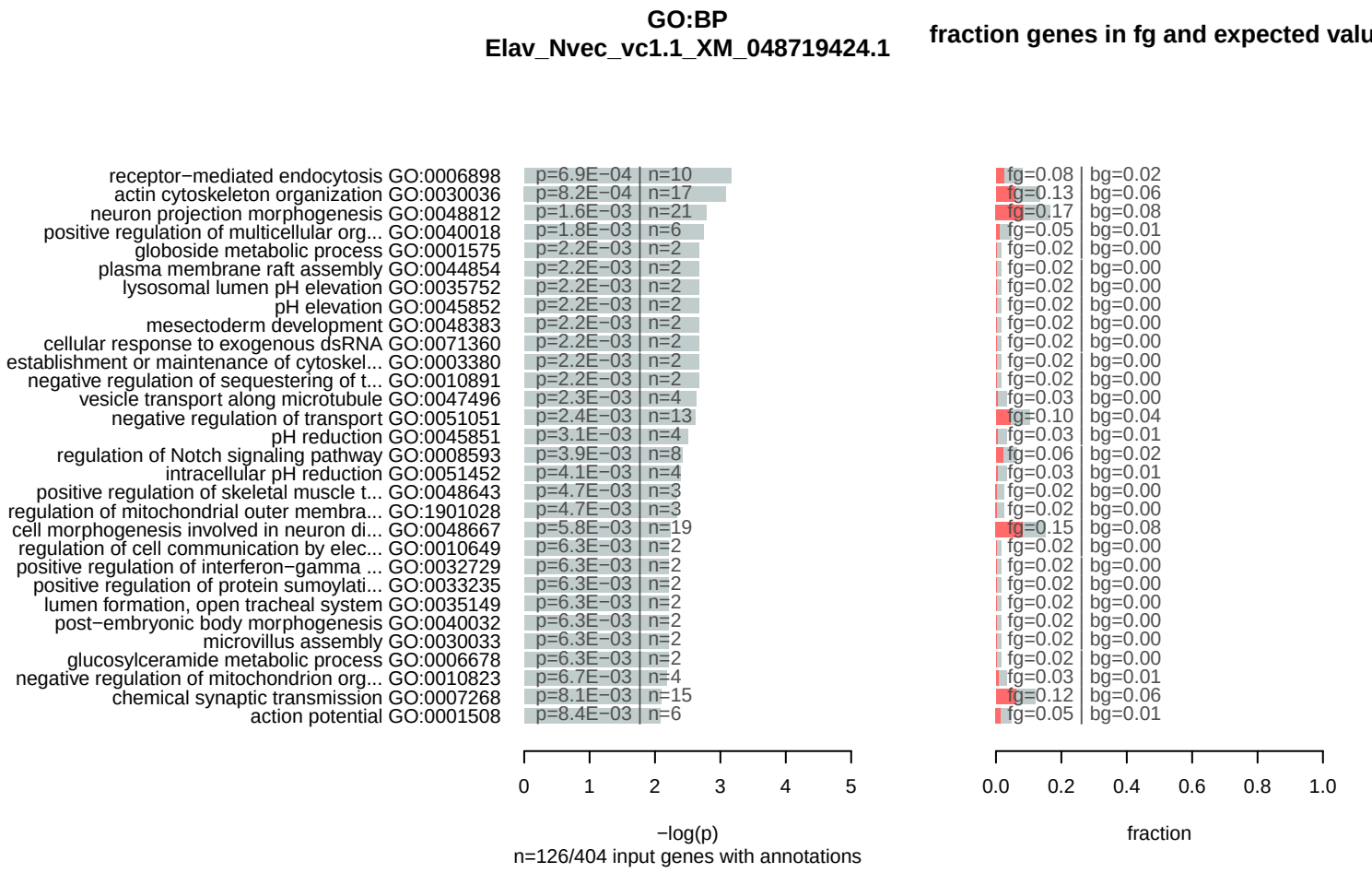
GO:BP
Elav_Nvec_vc1.1_XM_048719424.1
fraction genes in fg and expected valu
receptor−mediated endocytosis GO:0006898 p=6.9E−04 n=10 fg=0.08 bg=0.02
actin cytoskeleton organization GO:0030036 p=8.2E−04 n=17 fg=0.13 bg=0.06
neuron projection morphogenesis GO:0048812 p=1.6E−03 n=21 fg=0.17 bg=0.08
positive regulation of multicellular org... GO:0040018 p=1.8E−03 n=6 fg=0.05 bg=0.01
globoside metabolic process GO:0001575 p=2.2E−03 n=2 fg=0.02 bg=0.00
plasma membrane raft assembly GO:0044854 p=2.2E−03 n=2 fg=0.02 bg=0.00
lysosomal lumen pH elevation GO:0035752 p=2.2E−03 n=2 fg=0.02 bg=0.00
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mesectoderm development GO:0048383 p=2.2E−03 n=2 fg=0.02 bg=0.00
cellular response to exogenous dsRNA GO:0071360 p=2.2E−03 n=2 fg=0.02 bg=0.00
establishment or maintenance of cytoskel... GO:0003380 p=2.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of sequestering of t... GO:0010891 p=2.2E−03 n=2 fg=0.02 bg=0.00
vesicle transport along microtubule GO:0047496 p=2.3E−03 n=4 fg=0.03 bg=0.00
negative regulation of transport GO:0051051 p=2.4E−03 n=13 fg=0.10 bg=0.04
pH reduction GO:0045851 p=3.1E−03 n=4 fg=0.03 bg=0.01
regulation of Notch signaling pathway GO:0008593 p=3.9E−03 n=8 fg=0.06 bg=0.02
intracellular pH reduction GO:0051452 p=4.1E−03 n=4 fg=0.03 bg=0.01
positive regulation of skeletal muscle t... GO:0048643 p=4.7E−03 n=3 fg=0.02 bg=0.00
regulation of mitochondrial outer membra... GO:1901028 p=4.7E−03 n=3 fg=0.02 bg=0.00
cell morphogenesis involved in neuron di... GO:0048667 p=5.8E−03 n=19 fg=0.15 bg=0.08
regulation of cell communication by elec... GO:0010649 p=6.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of interferon−gamma ... GO:0032729 p=6.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of protein sumoylati... GO:0033235 p=6.3E−03 n=2 fg=0.02 bg=0.00
lumen formation, open tracheal system GO:0035149 p=6.3E−03 n=2 fg=0.02 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=6.3E−03 n=2 fg=0.02 bg=0.00
microvillus assembly GO:0030033 p=6.3E−03 n=2 fg=0.02 bg=0.00
glucosylceramide metabolic process GO:0006678 p=6.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of mitochondrion org... GO:0010823 p=6.7E−03 n=4 fg=0.03 bg=0.01
chemical synaptic transmission GO:0007268 p=8.1E−03 n=15 fg=0.12 bg=0.06
action potential GO:0001508 p=8.4E−03 n=6 fg=0.05 bg=0.01
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n=126/404 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048719424.1
fraction genes in fg and expected valu
structural constituent of cytoskeleton GO:0005200 p=2.0E−03 n=4 fg=0.03 bg=0.01
phosphatidylcholine binding GO:0031210 p=3.5E−03 n=3 fg=0.03 bg=0.00
spectrin binding GO:0030507 p=3.5E−03 n=3 fg=0.03 bg=0.00
amino acid binding GO:0016597 p=6.3E−03 n=4 fg=0.03 bg=0.01
phosphatidylethanolamine binding GO:0008429 p=1.3E−02 n=2 fg=0.02 bg=0.00
disordered domain specific binding GO:0097718 p=1.8E−02 n=3 fg=0.03 bg=0.01
5S rRNA binding GO:0008097 p=2.2E−02 n=2 fg=0.02 bg=0.00
G−protein beta/gamma−subunit complex bin... GO:0031683 p=2.2E−02 n=2 fg=0.02 bg=0.00
calcium−dependent protein binding GO:0048306 p=2.3E−02 n=3 fg=0.03 bg=0.01
potassium channel regulator activity GO:0015459 p=2.3E−02 n=3 fg=0.03 bg=0.01
ammonium ion binding GO:0070405 p=2.3E−02 n=3 fg=0.03 bg=0.01
ion channel regulator activity GO:0099106 p=2.3E−02 n=5 fg=0.04 bg=0.01
phospholipid transporter activity GO:0005548 p=2.8E−02 n=3 fg=0.03 bg=0.01
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channel regulator activity GO:0016247 p=2.9E−02 n=5 fg=0.04 bg=0.02
BH domain binding GO:0051400 p=3.1E−02 n=2 fg=0.02 bg=0.00
proteoglycan binding GO:0043394 p=3.1E−02 n=2 fg=0.02 bg=0.00
histone deacetylase binding GO:0042826 p=3.5E−02 n=4 fg=0.03 bg=0.01
phospholipid binding GO:0005543 p=3.7E−02 n=11 fg=0.09 bg=0.04
ATPase−coupled ion transmembrane transpo... GO:0042625 p=4.0E−02 n=3 fg=0.03 bg=0.01
GTPase activator activity GO:0005096 p=4.2E−02 n=6 fg=0.05 bg=0.02
3R−hydroxyacyl−CoA dehydratase activity GO:0080023 p=4.9E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=4.9E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=4.9E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=4.9E−02 n=1 fg=0.01 bg=0.00
misfolded RNA binding GO:0034336 p=4.9E−02 n=1 fg=0.01 bg=0.00
beta−1,4−N−acetylgalactosaminyltransfera... GO:0033207 p=4.9E−02 n=1 fg=0.01 bg=0.00
pyrimidine nucleobase transmembrane tran... GO:0005350 p=4.9E−02 n=1 fg=0.01 bg=0.00
mono−olein transacylation activity GO:0051264 p=4.9E−02 n=1 fg=0.01 bg=0.00
diolein transacylation activity GO:0051265 p=4.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=116/404 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048719424.1
fraction genes in fg and expected valu
heterotrimeric G−protein complex GO:0005834 p=1.7E−03 n=3 fg=0.02 bg=0.00
uropod GO:0001931 p=2.1E−03 n=2 fg=0.02 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=2.1E−03 n=2 fg=0.02 bg=0.00
microvillus membrane GO:0031528 p=2.9E−03 n=3 fg=0.02 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=6.1E−03 n=2 fg=0.02 bg=0.00
FAR/SIN/STRIPAK complex GO:0090443 p=6.1E−03 n=2 fg=0.02 bg=0.00
clathrin−coated pit GO:0005905 p=6.5E−03 n=3 fg=0.02 bg=0.00
cytosolic large ribosomal subunit GO:0022625 p=6.7E−03 n=5 fg=0.04 bg=0.01
plasma membrane raft GO:0044853 p=1.1E−02 n=5 fg=0.04 bg=0.01
cytoplasmic side of membrane GO:0098562 p=1.1E−02 n=10 fg=0.08 bg=0.02
eukaryotic translation initiation factor... GO:0071541 p=1.2E−02 n=2 fg=0.02 bg=0.00
recycling endosome membrane GO:0055038 p=1.2E−02 n=3 fg=0.02 bg=0.00
plasma membrane protein complex GO:0098797 p=1.3E−02 n=11 fg=0.09 bg=0.03
endosome GO:0005768 p=1.4E−02 n=16 fg=0.13 bg=0.07
membrane microdomain GO:0098857 p=1.7E−02 n=8 fg=0.06 bg=0.03
membrane raft GO:0045121 p=1.7E−02 n=8 fg=0.06 bg=0.03
caveola GO:0005901 p=1.9E−02 n=4 fg=0.03 bg=0.01
pericentriolar material GO:0000242 p=1.9E−02 n=2 fg=0.02 bg=0.00
sperm fibrous sheath GO:0035686 p=1.9E−02 n=2 fg=0.02 bg=0.00
sensory dendrite GO:0071683 p=1.9E−02 n=2 fg=0.02 bg=0.00
sarcomere GO:0030017 p=2.3E−02 n=6 fg=0.05 bg=0.02
supramolecular polymer GO:0099081 p=2.4E−02 n=12 fg=0.10 bg=0.05
supramolecular fiber GO:0099512 p=2.4E−02 n=12 fg=0.10 bg=0.05
exocytic vesicle GO:0070382 p=2.4E−02 n=7 fg=0.06 bg=0.02
I band GO:0031674 p=2.5E−02 n=5 fg=0.04 bg=0.01
axon cytoplasm GO:1904115 p=2.8E−02 n=2 fg=0.02 bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181 p=2.8E−02 n=2 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0005852 p=2.8E−02 n=2 fg=0.02 bg=0.00
spindle midzone GO:0051233 p=2.9E−02 n=3 fg=0.02 bg=0.01
cell leading edge GO:0031252 p=3.0E−02 n=9 fg=0.07 bg=0.04
0 1 2 3 4 5
−log(p)
n=124/404 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction