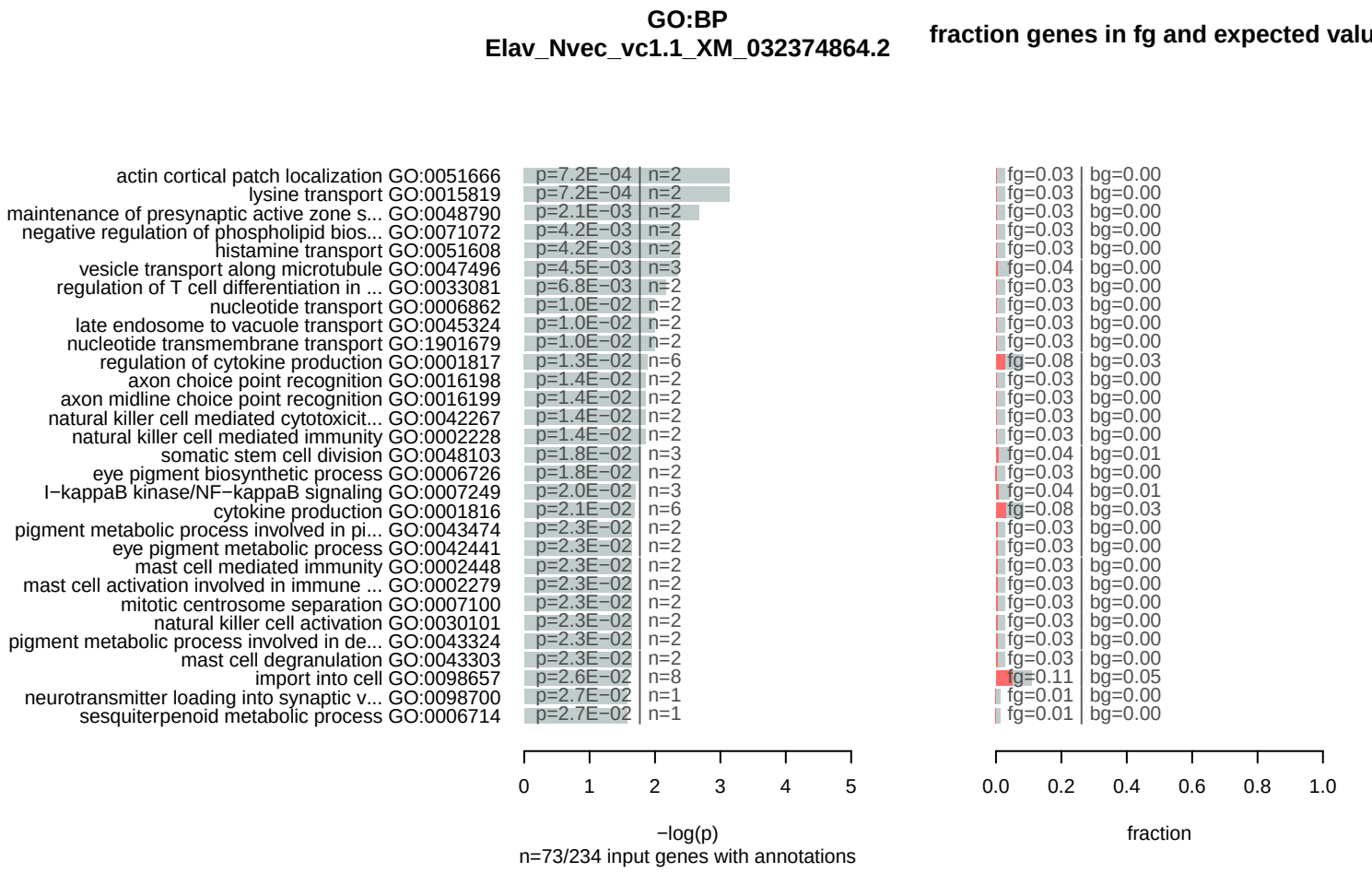
GO:BP
Elav_Nvec_vc1.1_XM_032374864.2
fraction genes in fg and expected valu
actin cortical patch localization GO:0051666 p=7.2E−04 n=2 fg=0.03 bg=0.00
lysine transport GO:0015819 p=7.2E−04 n=2 fg=0.03 bg=0.00
maintenance of presynaptic active zone s... GO:0048790 p=2.1E−03 n=2 fg=0.03 bg=0.00
negative regulation of phospholipid bios... GO:0071072 p=4.2E−03 n=2 fg=0.03 bg=0.00
histamine transport GO:0051608 p=4.2E−03 n=2 fg=0.03 bg=0.00
vesicle transport along microtubule GO:0047496 p=4.5E−03 n=3 fg=0.04 bg=0.00
regulation of T cell differentiation in ... GO:0033081 p=6.8E−03 n=2 fg=0.03 bg=0.00
nucleotide transport GO:0006862 p=1.0E−02 n=2 fg=0.03 bg=0.00
late endosome to vacuole transport GO:0045324 p=1.0E−02 n=2 fg=0.03 bg=0.00
nucleotide transmembrane transport GO:1901679 p=1.0E−02 n=2 fg=0.03 bg=0.00
regulation of cytokine production GO:0001817 p=1.3E−02 n=6 fg=0.08 bg=0.03
axon choice point recognition GO:0016198 p=1.4E−02 n=2 fg=0.03 bg=0.00
axon midline choice point recognition GO:0016199 p=1.4E−02 n=2 fg=0.03 bg=0.00
natural killer cell mediated cytotoxicit... GO:0042267 p=1.4E−02 n=2 fg=0.03 bg=0.00
natural killer cell mediated immunity GO:0002228 p=1.4E−02 n=2 fg=0.03 bg=0.00
somatic stem cell division GO:0048103 p=1.8E−02 n=3 fg=0.04 bg=0.01
eye pigment biosynthetic process GO:0006726 p=1.8E−02 n=2 fg=0.03 bg=0.00
I−kappaB kinase/NF−kappaB signaling GO:0007249 p=2.0E−02 n=3 fg=0.04 bg=0.01
cytokine production GO:0001816 p=2.1E−02 n=6 fg=0.08 bg=0.03
pigment metabolic process involved in pi... GO:0043474 p=2.3E−02 n=2 fg=0.03 bg=0.00
eye pigment metabolic process GO:0042441 p=2.3E−02 n=2 fg=0.03 bg=0.00
mast cell mediated immunity GO:0002448 p=2.3E−02 n=2 fg=0.03 bg=0.00
mast cell activation involved in immune ... GO:0002279 p=2.3E−02 n=2 fg=0.03 bg=0.00
mitotic centrosome separation GO:0007100 p=2.3E−02 n=2 fg=0.03 bg=0.00
natural killer cell activation GO:0030101 p=2.3E−02 n=2 fg=0.03 bg=0.00
pigment metabolic process involved in de... GO:0043324 p=2.3E−02 n=2 fg=0.03 bg=0.00
mast cell degranulation GO:0043303 p=2.3E−02 n=2 fg=0.03 bg=0.00
import into cell GO:0098657 p=2.6E−02 n=8 fg=0.11 bg=0.05
neurotransmitter loading into synaptic v... GO:0098700 p=2.7E−02 n=1 fg=0.01 bg=0.00
sesquiterpenoid metabolic process GO:0006714 p=2.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=73/234 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032374864.2
fraction genes in fg and expected valu
phosphatidylinositol bisphosphate bindin... GO:1902936 p=6.2E−03 n=4 fg=0.06 bg=0.01
phosphatidylinositol−3,4−bisphosphate bi... GO:0043325 p=6.4E−03 n=2 fg=0.03 bg=0.00
nucleotide transmembrane transporter act... GO:0015215 p=9.4E−03 n=2 fg=0.03 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0005547 p=1.1E−02 n=3 fg=0.05 bg=0.01
phosphatidylinositol−4,5−bisphosphate bi... GO:0005546 p=1.8E−02 n=3 fg=0.05 bg=0.01
inositol 1,3,4,5 tetrakisphosphate bindi... GO:0043533 p=2.6E−02 n=1 fg=0.02 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=2.6E−02 n=1 fg=0.02 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=2.6E−02 n=1 fg=0.02 bg=0.00
FAD−AMP lyase (cyclizing) activity GO:0034012 p=2.6E−02 n=1 fg=0.02 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=2.6E−02 n=1 fg=0.02 bg=0.00
phosphotransferase activity, nitrogenous... GO:0016775 p=2.6E−02 n=1 fg=0.02 bg=0.00
long−chain fatty acid−CoA ligase activit... GO:0004467 p=2.6E−02 n=1 fg=0.02 bg=0.00
ABC−type guanine transporter activity GO:0008558 p=2.6E−02 n=1 fg=0.02 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=2.6E−02 n=1 fg=0.02 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=2.6E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=2.6E−02 n=1 fg=0.02 bg=0.00
DNA clamp loader activity GO:0003689 p=2.6E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=2.6E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=2.6E−02 n=1 fg=0.02 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=2.6E−02 n=1 fg=0.02 bg=0.00
glycerone kinase activity GO:0004371 p=2.6E−02 n=1 fg=0.02 bg=0.00
very long−chain fatty acid−CoA ligase ac... GO:0031957 p=2.6E−02 n=1 fg=0.02 bg=0.00
galactosylxylosylprotein 3−beta−galactos... GO:0047220 p=2.6E−02 n=1 fg=0.02 bg=0.00
amine transmembrane transporter activity GO:0005275 p=2.6E−02 n=1 fg=0.02 bg=0.00
triokinase activity GO:0050354 p=2.6E−02 n=1 fg=0.02 bg=0.00
C−methyltransferase activity GO:0008169 p=2.6E−02 n=1 fg=0.02 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=2.6E−02 n=1 fg=0.02 bg=0.00
arginine kinase activity GO:0004054 p=2.6E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=2.6E−02 n=1 fg=0.02 bg=0.00
leucine zipper domain binding GO:0043522 p=2.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=62/234 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032374864.2
fraction genes in fg and expected valu
fungal−type vacuole membrane GO:0000329 p=6.7E−03 n=2 fg=0.03 bg=0.00
cell tip GO:0051286 p=9.8E−03 n=2 fg=0.03 bg=0.00
spindle microtubule GO:0005876 p=1.5E−02 n=3 fg=0.04 bg=0.01
intracellular anatomical structure GO:0005622 p=1.6E−02 n=72 fg=1.00 bg=0.94
cortical cytoskeleton GO:0030863 p=2.2E−02 n=3 fg=0.04 bg=0.01
eukaryotic 43S preinitiation complex GO:0016282 p=2.7E−02 n=1 fg=0.01 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.7E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=2.7E−02 n=1 fg=0.01 bg=0.00
perichromatin fibrils GO:0005726 p=2.7E−02 n=1 fg=0.01 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=2.7E−02 n=1 fg=0.01 bg=0.00
SMC loading complex GO:0032116 p=2.7E−02 n=1 fg=0.01 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=2.7E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=2.7E−02 n=1 fg=0.01 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=2.7E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=2.7E−02 n=1 fg=0.01 bg=0.00
pigment granule membrane GO:0090741 p=2.7E−02 n=1 fg=0.01 bg=0.00
site of double−strand break GO:0035861 p=2.8E−02 n=2 fg=0.03 bg=0.00
site of DNA damage GO:0090734 p=2.8E−02 n=2 fg=0.03 bg=0.00
striated muscle dense body GO:0055120 p=2.8E−02 n=2 fg=0.03 bg=0.00
recycling endosome membrane GO:0055038 p=3.3E−02 n=2 fg=0.03 bg=0.00
intracellular organelle GO:0043229 p=3.8E−02 n=66 fg=0.92 bg=0.83
M band GO:0031430 p=3.9E−02 n=2 fg=0.03 bg=0.00
integral component of organelle membrane GO:0031301 p=4.4E−02 n=6 fg=0.08 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=5.2E−02 n=6 fg=0.08 bg=0.04
IkappaB kinase complex GO:0008385 p=5.3E−02 n=1 fg=0.01 bg=0.00
presynaptic cytoskeleton GO:0099569 p=5.3E−02 n=1 fg=0.01 bg=0.00
RSF complex GO:0031213 p=5.3E−02 n=1 fg=0.01 bg=0.00
translation preinitiation complex GO:0070993 p=5.3E−02 n=1 fg=0.01 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=5.3E−02 n=1 fg=0.01 bg=0.00
Lewy body GO:0097413 p=5.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=72/234 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction