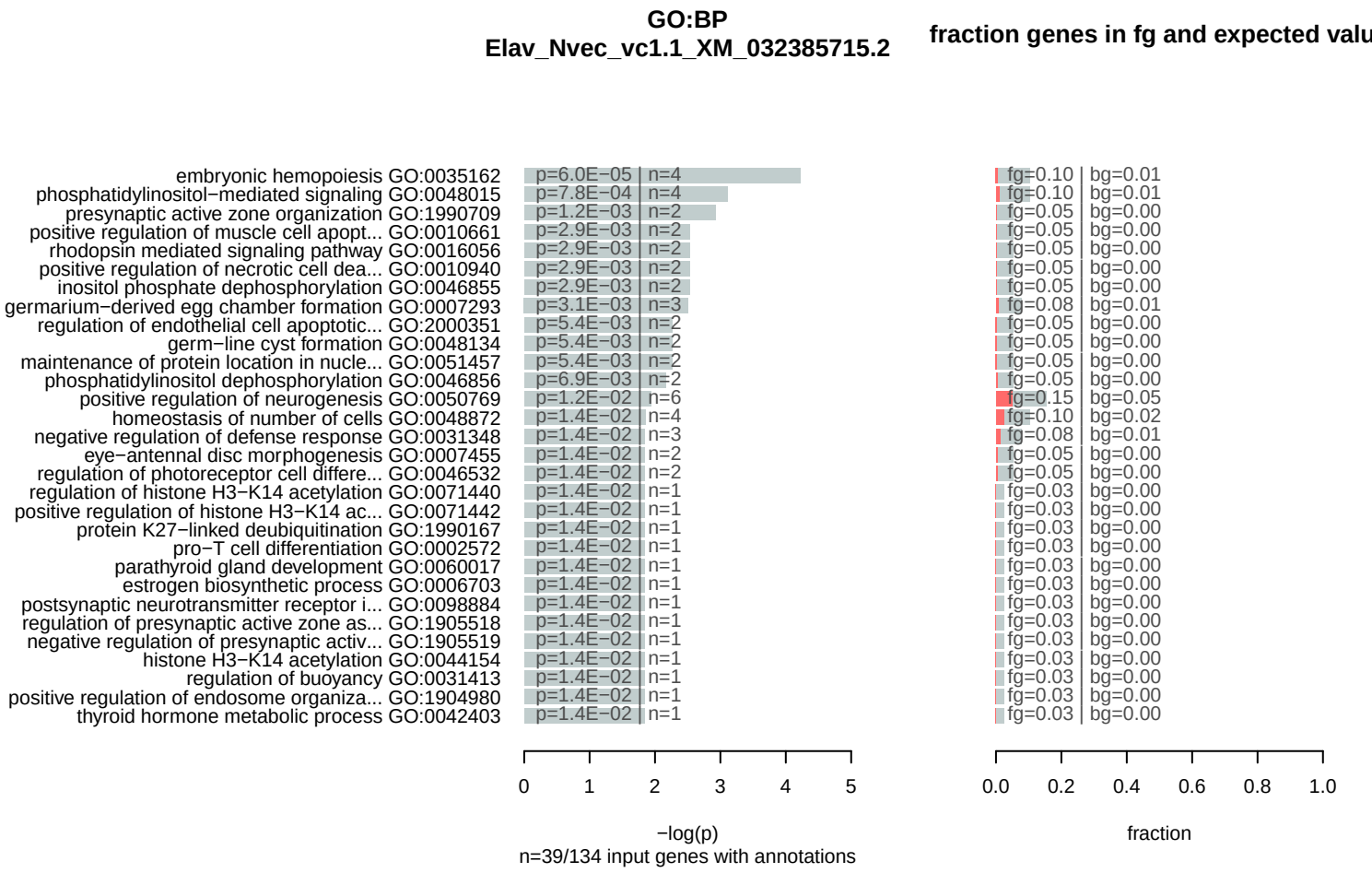
GO:BP
Elav_Nvec_vc1.1_XM_032385715.2
fraction genes in fg and expected valu
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phosphatidylinositol−mediated signaling GO:0048015 p=7.8E−04 n=4 fg=0.10 bg=0.01
presynaptic active zone organization GO:1990709 p=1.2E−03 n=2 fg=0.05 bg=0.00
positive regulation of muscle cell apopt... GO:0010661 p=2.9E−03 n=2 fg=0.05 bg=0.00
rhodopsin mediated signaling pathway GO:0016056 p=2.9E−03 n=2 fg=0.05 bg=0.00
positive regulation of necrotic cell dea... GO:0010940 p=2.9E−03 n=2 fg=0.05 bg=0.00
inositol phosphate dephosphorylation GO:0046855 p=2.9E−03 n=2 fg=0.05 bg=0.00
germarium−derived egg chamber formation GO:0007293 p=3.1E−03 n=3 fg=0.08 bg=0.01
regulation of endothelial cell apoptotic... GO:2000351 p=5.4E−03 n=2 fg=0.05 bg=0.00
germ−line cyst formation GO:0048134 p=5.4E−03 n=2 fg=0.05 bg=0.00
maintenance of protein location in nucle... GO:0051457 p=5.4E−03 n=2 fg=0.05 bg=0.00
phosphatidylinositol dephosphorylation GO:0046856 p=6.9E−03 n=2 fg=0.05 bg=0.00
positive regulation of neurogenesis GO:0050769 p=1.2E−02 n=6 fg=0.15 bg=0.05
homeostasis of number of cells GO:0048872 p=1.4E−02 n=4 fg=0.10 bg=0.02
negative regulation of defense response GO:0031348 p=1.4E−02 n=3 fg=0.08 bg=0.01
eye−antennal disc morphogenesis GO:0007455 p=1.4E−02 n=2 fg=0.05 bg=0.00
regulation of photoreceptor cell differe... GO:0046532 p=1.4E−02 n=2 fg=0.05 bg=0.00
regulation of histone H3−K14 acetylation GO:0071440 p=1.4E−02 n=1 fg=0.03 bg=0.00
positive regulation of histone H3−K14 ac... GO:0071442 p=1.4E−02 n=1 fg=0.03 bg=0.00
protein K27−linked deubiquitination GO:1990167 p=1.4E−02 n=1 fg=0.03 bg=0.00
pro−T cell differentiation GO:0002572 p=1.4E−02 n=1 fg=0.03 bg=0.00
parathyroid gland development GO:0060017 p=1.4E−02 n=1 fg=0.03 bg=0.00
estrogen biosynthetic process GO:0006703 p=1.4E−02 n=1 fg=0.03 bg=0.00
postsynaptic neurotransmitter receptor i... GO:0098884 p=1.4E−02 n=1 fg=0.03 bg=0.00
regulation of presynaptic active zone as... GO:1905518 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of presynaptic activ... GO:1905519 p=1.4E−02 n=1 fg=0.03 bg=0.00
histone H3−K14 acetylation GO:0044154 p=1.4E−02 n=1 fg=0.03 bg=0.00
regulation of buoyancy GO:0031413 p=1.4E−02 n=1 fg=0.03 bg=0.00
positive regulation of endosome organiza... GO:1904980 p=1.4E−02 n=1 fg=0.03 bg=0.00
thyroid hormone metabolic process GO:0042403 p=1.4E−02 n=1 fg=0.03 bg=0.00
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n=39/134 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032385715.2
fraction genes in fg and expected valu
phosphatidylinositol−3,5−bisphosphate 3−... GO:0052629 p=5.3E−04 n=2 fg=0.06 bg=0.00
phosphatidylinositol−3−phosphatase activ... GO:0004438 p=1.7E−03 n=2 fg=0.06 bg=0.00
inositol phosphate phosphatase activity GO:0052745 p=3.6E−03 n=2 fg=0.06 bg=0.00
metal ion transmembrane transporter acti... GO:0046873 p=4.7E−03 n=5 fg=0.16 bg=0.04
protein binding GO:0005515 p=5.6E−03 n=26 fg=0.81 bg=0.59
long−chain fatty acid transporter activi... GO:0005324 p=1.4E−02 n=1 fg=0.03 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=1.4E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−3,5−bisphosphate 5−... GO:0043813 p=1.4E−02 n=1 fg=0.03 bg=0.00
EH domain binding GO:1990175 p=1.4E−02 n=1 fg=0.03 bg=0.00
interleukin−2 receptor binding GO:0005134 p=1.4E−02 n=1 fg=0.03 bg=0.00
aminomethyltransferase activity GO:0004047 p=1.4E−02 n=1 fg=0.03 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=1.4E−02 n=1 fg=0.03 bg=0.00
light−activated ion channel activity GO:0010461 p=1.4E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.4E−02 n=1 fg=0.03 bg=0.00
semaphorin receptor binding GO:0030215 p=1.4E−02 n=1 fg=0.03 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=1.4E−02 n=1 fg=0.03 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=1.4E−02 n=1 fg=0.03 bg=0.00
enzyme binding GO:0019899 p=1.4E−02 n=13 fg=0.41 bg=0.22
E−box binding GO:0070888 p=1.5E−02 n=2 fg=0.06 bg=0.01
calcium ion transmembrane transporter ac... GO:0015085 p=1.6E−02 n=3 fg=0.09 bg=0.02
steroid dehydrogenase activity GO:0016229 p=2.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol transfer activity GO:0008526 p=2.7E−02 n=1 fg=0.03 bg=0.00
inositol−1,4,5−trisphosphate 5−phosphata... GO:0052658 p=2.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−4−phosphate phospha... GO:0043812 p=2.7E−02 n=1 fg=0.03 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=2.7E−02 n=1 fg=0.03 bg=0.00
phosphatidic acid transfer activity GO:1990050 p=2.7E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=2.7E−02 n=1 fg=0.03 bg=0.00
Hsp90 protein binding GO:0051879 p=2.9E−02 n=2 fg=0.06 bg=0.01
protein homodimerization activity GO:0042803 p=3.0E−02 n=7 fg=0.22 bg=0.10
phosphatase binding GO:0019902 p=3.5E−02 n=3 fg=0.09 bg=0.02
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−log(p)
n=32/134 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385715.2
fraction genes in fg and expected valu
nuclear pore GO:0005643 p=3.3E−03 n=3 fg=0.08 bg=0.01
motile cilium GO:0031514 p=6.8E−03 n=4 fg=0.11 bg=0.02
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=8.1E−03 n=2 fg=0.05 bg=0.00
rhabdomere GO:0016028 p=8.1E−03 n=2 fg=0.05 bg=0.00
9+2 motile cilium GO:0097729 p=1.3E−02 n=3 fg=0.08 bg=0.01
dendritic spine head GO:0044327 p=1.4E−02 n=1 fg=0.03 bg=0.00
host cell part GO:0033643 p=1.4E−02 n=1 fg=0.03 bg=0.00
host intracellular part GO:0033646 p=1.4E−02 n=1 fg=0.03 bg=0.00
host intracellular organelle GO:0033647 p=1.4E−02 n=1 fg=0.03 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=1.4E−02 n=1 fg=0.03 bg=0.00
host intracellular region GO:0043656 p=1.4E−02 n=1 fg=0.03 bg=0.00
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host cell nuclear part GO:0044094 p=1.4E−02 n=1 fg=0.03 bg=0.00
other organism part GO:0044217 p=1.4E−02 n=1 fg=0.03 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=1.4E−02 n=1 fg=0.03 bg=0.00
host cell nucleus GO:0042025 p=1.4E−02 n=1 fg=0.03 bg=0.00
host cellular component GO:0018995 p=1.4E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus GO:0035996 p=1.4E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=1.4E−02 n=1 fg=0.03 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=1.4E−02 n=1 fg=0.03 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=1.4E−02 n=1 fg=0.03 bg=0.00
host cell PML body GO:0075341 p=1.4E−02 n=1 fg=0.03 bg=0.00
rhabdomere membrane GO:0033583 p=1.4E−02 n=1 fg=0.03 bg=0.00
dendritic spine neck GO:0044326 p=2.8E−02 n=1 fg=0.03 bg=0.00
gamma−tubulin complex GO:0000930 p=2.8E−02 n=1 fg=0.03 bg=0.00
CCR4−NOT core complex GO:0030015 p=2.8E−02 n=1 fg=0.03 bg=0.00
Seh1−associated complex GO:0035859 p=2.8E−02 n=1 fg=0.03 bg=0.00
glycine cleavage complex GO:0005960 p=2.8E−02 n=1 fg=0.03 bg=0.00
GATOR2 complex GO:0061700 p=2.8E−02 n=1 fg=0.03 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=2.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=38/134 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction