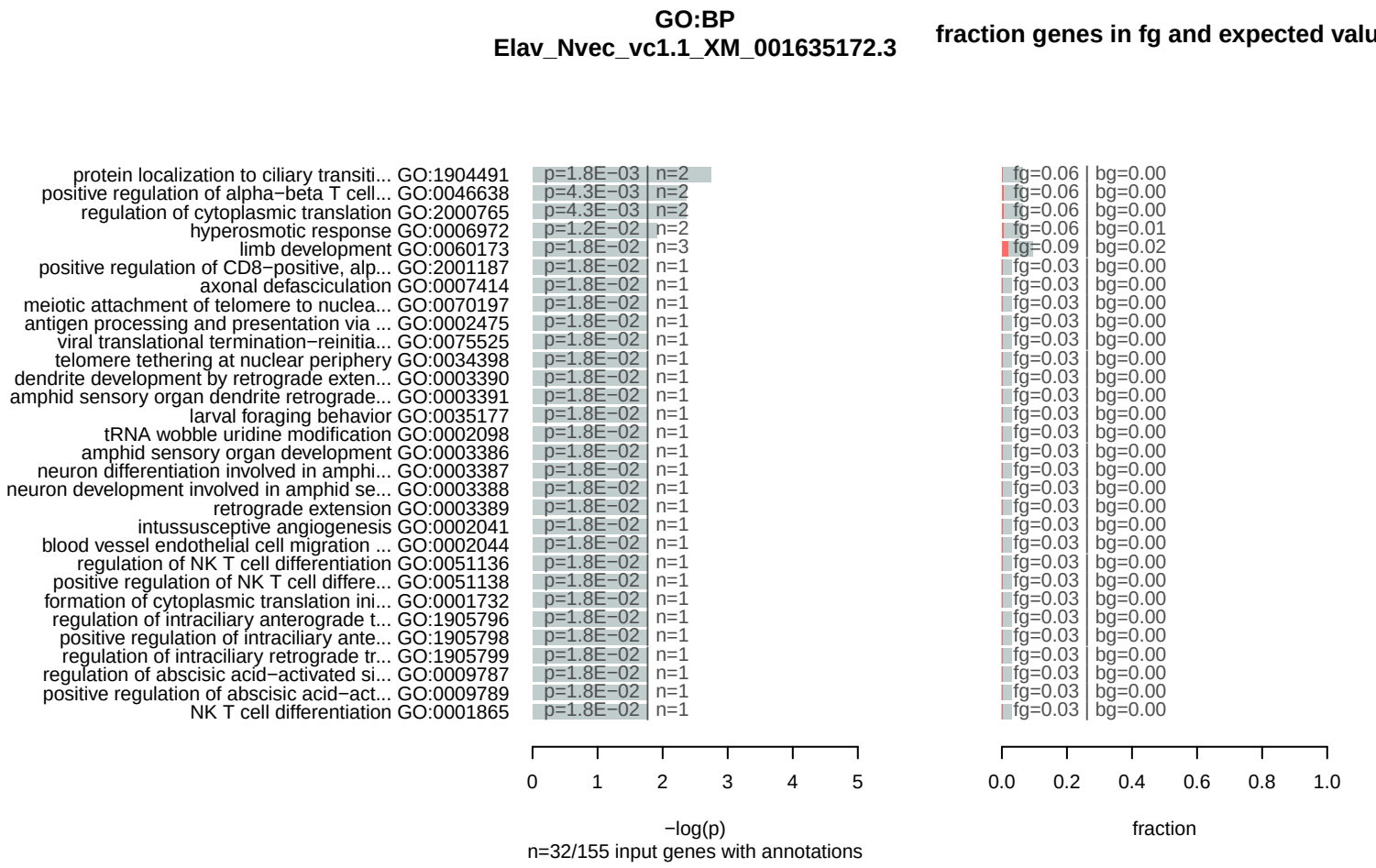
GO:BP
Elav_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
protein localization to ciliary transiti... GO:1904491 p=1.8E−03 n=2 fg=0.06 bg=0.00
positive regulation of alpha−beta T cell... GO:0046638 p=4.3E−03 n=2 fg=0.06 bg=0.00
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positive regulation of CD8−positive, alp... GO:2001187 p=1.8E−02 n=1 fg=0.03 bg=0.00
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telomere tethering at nuclear periphery GO:0034398 p=1.8E−02 n=1 fg=0.03 bg=0.00
dendrite development by retrograde exten... GO:0003390 p=1.8E−02 n=1 fg=0.03 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=1.8E−02 n=1 fg=0.03 bg=0.00
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tRNA wobble uridine modification GO:0002098 p=1.8E−02 n=1 fg=0.03 bg=0.00
amphid sensory organ development GO:0003386 p=1.8E−02 n=1 fg=0.03 bg=0.00
neuron differentiation involved in amphi... GO:0003387 p=1.8E−02 n=1 fg=0.03 bg=0.00
neuron development involved in amphid se... GO:0003388 p=1.8E−02 n=1 fg=0.03 bg=0.00
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intussusceptive angiogenesis GO:0002041 p=1.8E−02 n=1 fg=0.03 bg=0.00
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regulation of intraciliary anterograde t... GO:1905796 p=1.8E−02 n=1 fg=0.03 bg=0.00
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n=32/155 input genes with annotations
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fraction
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fraction genes in fg and expected valu
translation factor activity, RNA binding GO:0008135 p=2.6E−03 n=3 fg=0.10 bg=0.01
RNA binding GO:0003723 p=1.1E−02 n=7 fg=0.24 bg=0.09
dynein light intermediate chain binding GO:0051959 p=1.8E−02 n=1 fg=0.03 bg=0.00
poly(G) binding GO:0034046 p=1.8E−02 n=1 fg=0.03 bg=0.00
tRNA (uracil) methyltransferase activity GO:0016300 p=1.8E−02 n=1 fg=0.03 bg=0.00
hedgehog receptor activity GO:0008158 p=1.8E−02 n=1 fg=0.03 bg=0.00
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insulin−like growth factor I binding GO:0031994 p=1.8E−02 n=1 fg=0.03 bg=0.00
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phosphatidylinositol−5−phosphate binding GO:0010314 p=3.6E−02 n=1 fg=0.03 bg=0.00
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insulin−like growth factor binding GO:0005520 p=3.6E−02 n=1 fg=0.03 bg=0.00
lamin binding GO:0005521 p=3.6E−02 n=1 fg=0.03 bg=0.00
heterocyclic compound binding GO:1901363 p=5.2E−02 n=14 fg=0.48 bg=0.27
mRNA regulatory element binding translat... GO:0000900 p=5.4E−02 n=1 fg=0.03 bg=0.00
catalytic activity, acting on a glycopro... GO:0140103 p=5.4E−02 n=1 fg=0.03 bg=0.00
ribosomal small subunit binding GO:0043024 p=5.4E−02 n=1 fg=0.03 bg=0.00
rDNA binding GO:0000182 p=5.4E−02 n=1 fg=0.03 bg=0.00
glutathione binding GO:0043295 p=5.4E−02 n=1 fg=0.03 bg=0.00
pre−mRNA 3'−splice site binding GO:0030628 p=5.4E−02 n=1 fg=0.03 bg=0.00
laminin binding GO:0043236 p=5.4E−02 n=1 fg=0.03 bg=0.00
oligopeptide binding GO:1900750 p=5.4E−02 n=1 fg=0.03 bg=0.00
extracellular matrix binding GO:0050840 p=5.4E−02 n=1 fg=0.03 bg=0.00
tRNA methyltransferase activity GO:0008175 p=5.4E−02 n=1 fg=0.03 bg=0.00
mRNA binding GO:0003729 p=5.7E−02 n=3 fg=0.10 bg=0.03
0 1 2 3 4 5
−log(p)
n=29/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
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ciliary basal body GO:0036064 p=1.1E−02 n=3 fg=0.09 bg=0.01
integrin alpha3−beta1 complex GO:0034667 p=1.8E−02 n=1 fg=0.03 bg=0.00
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integrin alpha6−beta4 complex GO:0034676 p=1.8E−02 n=1 fg=0.03 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=1.8E−02 n=1 fg=0.03 bg=0.00
core−binding factor complex GO:0016513 p=1.8E−02 n=1 fg=0.03 bg=0.00
AP−3 adaptor complex GO:0030123 p=1.8E−02 n=1 fg=0.03 bg=0.00
centrosome GO:0005813 p=2.1E−02 n=5 fg=0.16 bg=0.05
NELF complex GO:0032021 p=3.5E−02 n=1 fg=0.03 bg=0.00
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intrinsic component of nuclear inner mem... GO:0031229 p=3.5E−02 n=1 fg=0.03 bg=0.00
RSF complex GO:0031213 p=3.5E−02 n=1 fg=0.03 bg=0.00
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protein complex involved in cell adhesio... GO:0098636 p=3.5E−02 n=1 fg=0.03 bg=0.00
U2AF complex GO:0089701 p=3.5E−02 n=1 fg=0.03 bg=0.00
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hemidesmosome GO:0030056 p=5.2E−02 n=1 fg=0.03 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=5.2E−02 n=1 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=5.2E−02 n=1 fg=0.03 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=5.2E−02 n=1 fg=0.03 bg=0.00
phagocytic cup GO:0001891 p=5.2E−02 n=1 fg=0.03 bg=0.00
muscle tendon junction GO:0005927 p=5.2E−02 n=1 fg=0.03 bg=0.00
intraciliary transport particle GO:0030990 p=5.2E−02 n=1 fg=0.03 bg=0.00
intraciliary transport particle A GO:0030991 p=5.2E−02 n=1 fg=0.03 bg=0.00
spot adherens junction GO:0005914 p=5.2E−02 n=1 fg=0.03 bg=0.00
ISWI−type complex GO:0031010 p=5.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction