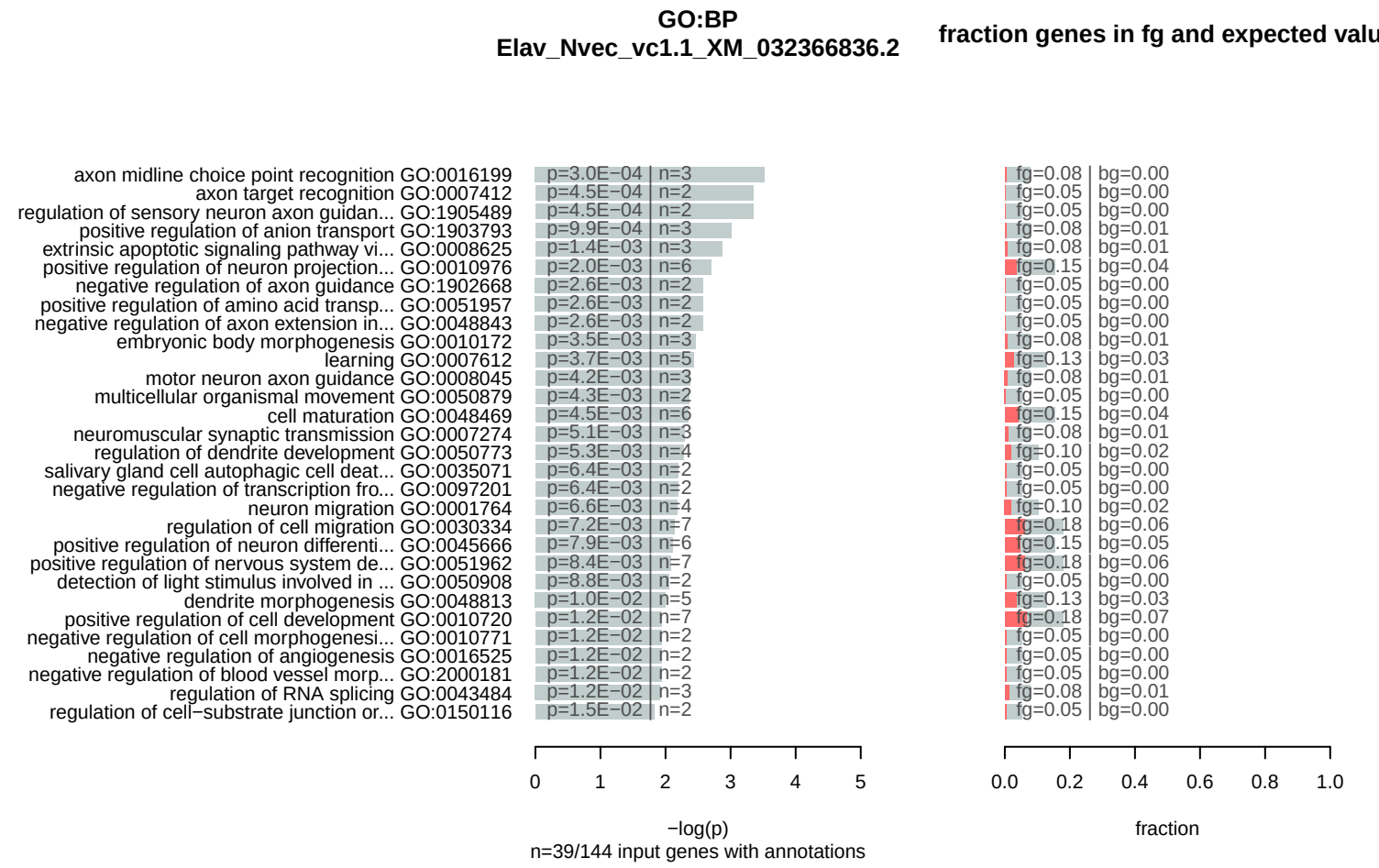
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fraction genes in fg and expected valu
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axon target recognition GO:0007412 p=4.5E−04 n=2 fg=0.05 bg=0.00
regulation of sensory neuron axon guidan... GO:1905489 p=4.5E−04 n=2 fg=0.05 bg=0.00
positive regulation of anion transport GO:1903793 p=9.9E−04 n=3 fg=0.08 bg=0.01
extrinsic apoptotic signaling pathway vi... GO:0008625 p=1.4E−03 n=3 fg=0.08 bg=0.01
positive regulation of neuron projection... GO:0010976 p=2.0E−03 n=6 fg=0.15 bg=0.04
negative regulation of axon guidance GO:1902668 p=2.6E−03 n=2 fg=0.05 bg=0.00
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learning GO:0007612 p=3.7E−03 n=5 fg=0.13 bg=0.03
motor neuron axon guidance GO:0008045 p=4.2E−03 n=3 fg=0.08 bg=0.01
multicellular organismal movement GO:0050879 p=4.3E−03 n=2 fg=0.05 bg=0.00
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neuromuscular synaptic transmission GO:0007274 p=5.1E−03 n=3 fg=0.08 bg=0.01
regulation of dendrite development GO:0050773 p=5.3E−03 n=4 fg=0.10 bg=0.02
salivary gland cell autophagic cell deat... GO:0035071 p=6.4E−03 n=2 fg=0.05 bg=0.00
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neuron migration GO:0001764 p=6.6E−03 n=4 fg=0.10 bg=0.02
regulation of cell migration GO:0030334 p=7.2E−03 n=7 fg=0.18 bg=0.06
positive regulation of neuron differenti... GO:0045666 p=7.9E−03 n=6 fg=0.15 bg=0.05
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detection of light stimulus involved in ... GO:0050908 p=8.8E−03 n=2 fg=0.05 bg=0.00
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positive regulation of cell development GO:0010720 p=1.2E−02 n=7 fg=0.18 bg=0.07
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negative regulation of angiogenesis GO:0016525 p=1.2E−02 n=2 fg=0.05 bg=0.00
negative regulation of blood vessel morp... GO:2000181 p=1.2E−02 n=2 fg=0.05 bg=0.00
regulation of RNA splicing GO:0043484 p=1.2E−02 n=3 fg=0.08 bg=0.01
regulation of cell−substrate junction or... GO:0150116 p=1.5E−02 n=2 fg=0.05 bg=0.00
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−log(p)
n=39/144 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032366836.2
fraction genes in fg and expected valu
phospholipase binding GO:0043274 p=4.0E−03 n=2 fg=0.06 bg=0.00
histone acetyltransferase binding GO:0035035 p=1.7E−02 n=2 fg=0.06 bg=0.01
enzyme binding GO:0019899 p=2.0E−02 n=15 fg=0.45 bg=0.24
double−stranded RNA binding GO:0003725 p=2.0E−02 n=2 fg=0.06 bg=0.01
nuclease inhibitor activity GO:0140721 p=2.1E−02 n=1 fg=0.03 bg=0.00
amino acid:proton symporter activity GO:0005280 p=2.1E−02 n=1 fg=0.03 bg=0.00
cyclohydrolase activity GO:0019238 p=2.1E−02 n=1 fg=0.03 bg=0.00
Rho−dependent protein serine/threonine k... GO:0072518 p=2.1E−02 n=1 fg=0.03 bg=0.00
L−proline transmembrane transporter acti... GO:0015193 p=2.1E−02 n=1 fg=0.03 bg=0.00
amino acid:cation symporter activity GO:0005416 p=2.1E−02 n=1 fg=0.03 bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196 p=2.1E−02 n=1 fg=0.03 bg=0.00
lipoprotein lipase activity GO:0004465 p=2.1E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=2.1E−02 n=1 fg=0.03 bg=0.00
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formate−tetrahydrofolate ligase activity GO:0004329 p=2.1E−02 n=1 fg=0.03 bg=0.00
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mono−olein transacylation activity GO:0051264 p=2.1E−02 n=1 fg=0.03 bg=0.00
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nickel cation binding GO:0016151 p=2.1E−02 n=1 fg=0.03 bg=0.00
ribonuclease inhibitor activity GO:0008428 p=2.1E−02 n=1 fg=0.03 bg=0.00
netrin receptor activity GO:0005042 p=2.1E−02 n=1 fg=0.03 bg=0.00
mRNA 3'−UTR AU−rich region binding GO:0035925 p=4.1E−02 n=1 fg=0.03 bg=0.00
alanine transmembrane transporter activi... GO:0022858 p=4.1E−02 n=1 fg=0.03 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=4.1E−02 n=1 fg=0.03 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=4.1E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=33/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032366836.2
fraction genes in fg and expected valu
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Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=8.9E−03 n=2 fg=0.05 bg=0.00
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plasma membrane GO:0005886 p=1.9E−02 n=17 fg=0.44 bg=0.27
cell cortex GO:0005938 p=1.9E−02 n=5 fg=0.13 bg=0.04
contractile fiber GO:0043292 p=1.9E−02 n=4 fg=0.10 bg=0.03
spectrosome GO:0045170 p=2.2E−02 n=1 fg=0.03 bg=0.00
apicomedial cortex GO:0106037 p=2.2E−02 n=1 fg=0.03 bg=0.00
spectrin GO:0008091 p=2.2E−02 n=1 fg=0.03 bg=0.00
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cortical actin cytoskeleton GO:0030864 p=3.0E−02 n=2 fg=0.05 bg=0.01
supramolecular fiber GO:0099512 p=4.0E−02 n=5 fg=0.13 bg=0.05
supramolecular polymer GO:0099081 p=4.0E−02 n=5 fg=0.13 bg=0.05
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cortical cytoskeleton GO:0030863 p=4.0E−02 n=2 fg=0.05 bg=0.01
mitochondrial pyruvate dehydrogenase (li... GO:0019910 p=4.3E−02 n=1 fg=0.03 bg=0.00
pyruvate dehydrogenase (lipoamide) phosp... GO:0045253 p=4.3E−02 n=1 fg=0.03 bg=0.00
NSL complex GO:0044545 p=4.3E−02 n=1 fg=0.03 bg=0.00
growth cone filopodium GO:1990812 p=4.3E−02 n=1 fg=0.03 bg=0.00
PTW/PP1 phosphatase complex GO:0072357 p=4.3E−02 n=1 fg=0.03 bg=0.00
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histone methyltransferase complex GO:0035097 p=4.5E−02 n=2 fg=0.05 bg=0.01
cytoplasmic region GO:0099568 p=5.0E−02 n=5 fg=0.13 bg=0.05
phosphatase complex GO:1903293 p=5.0E−02 n=2 fg=0.05 bg=0.01
mitochondrial membrane GO:0031966 p=5.4E−02 n=5 fg=0.13 bg=0.05
0 1 2 3 4 5
−log(p)
n=39/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction