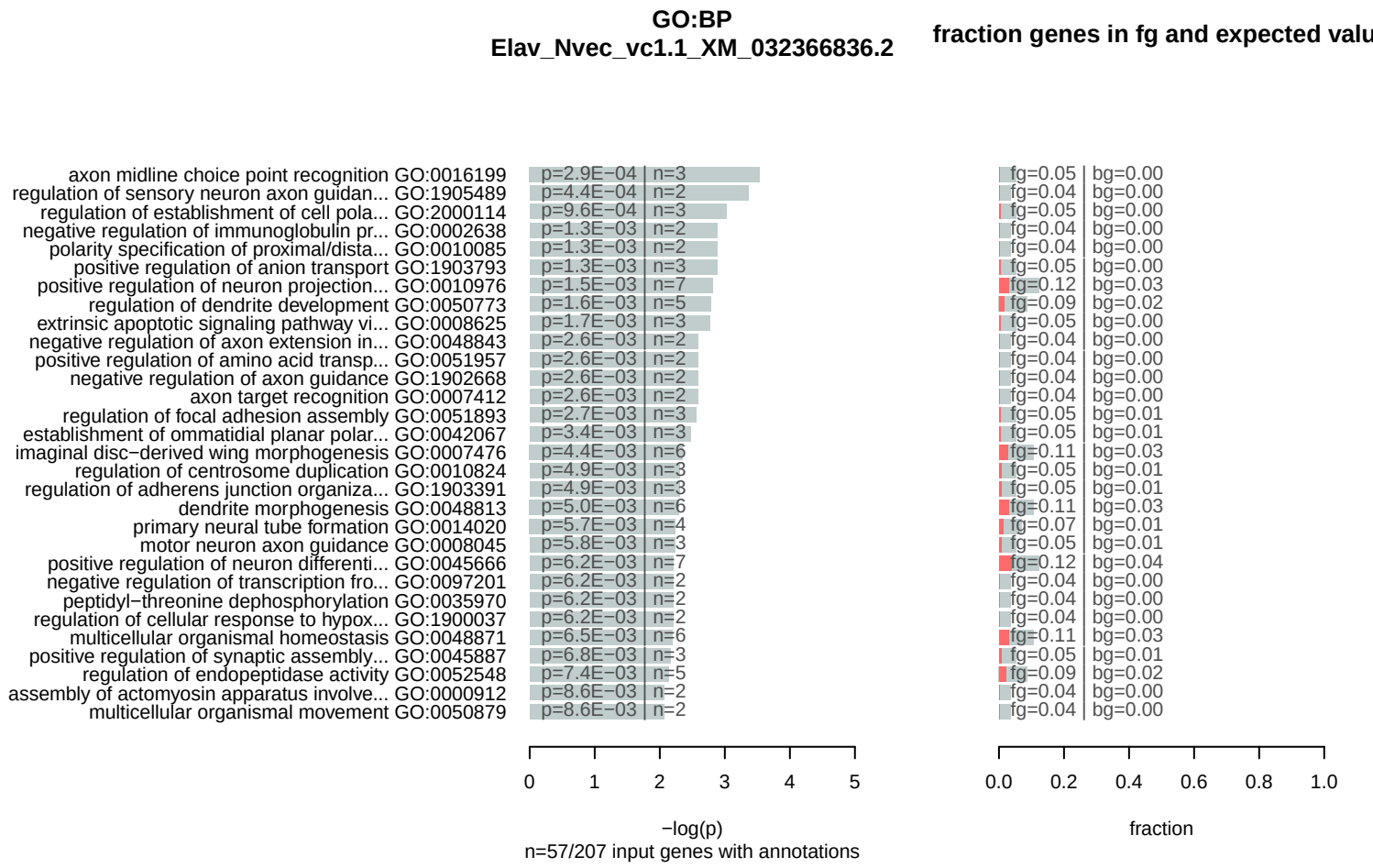
GO:BP
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fraction genes in fg and expected valu
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regulation of sensory neuron axon guidan... GO:1905489 p=4.4E−04 n=2 fg=0.04 bg=0.00
regulation of establishment of cell pola... GO:2000114 p=9.6E−04 n=3 fg=0.05 bg=0.00
negative regulation of immunoglobulin pr... GO:0002638 p=1.3E−03 n=2 fg=0.04 bg=0.00
polarity specification of proximal/dista... GO:0010085 p=1.3E−03 n=2 fg=0.04 bg=0.00
positive regulation of anion transport GO:1903793 p=1.3E−03 n=3 fg=0.05 bg=0.00
positive regulation of neuron projection... GO:0010976 p=1.5E−03 n=7 fg=0.12 bg=0.03
regulation of dendrite development GO:0050773 p=1.6E−03 n=5 fg=0.09 bg=0.02
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negative regulation of axon extension in... GO:0048843 p=2.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of amino acid transp... GO:0051957 p=2.6E−03 n=2 fg=0.04 bg=0.00
negative regulation of axon guidance GO:1902668 p=2.6E−03 n=2 fg=0.04 bg=0.00
axon target recognition GO:0007412 p=2.6E−03 n=2 fg=0.04 bg=0.00
regulation of focal adhesion assembly GO:0051893 p=2.7E−03 n=3 fg=0.05 bg=0.01
establishment of ommatidial planar polar... GO:0042067 p=3.4E−03 n=3 fg=0.05 bg=0.01
imaginal disc−derived wing morphogenesis GO:0007476 p=4.4E−03 n=6 fg=0.11 bg=0.03
regulation of centrosome duplication GO:0010824 p=4.9E−03 n=3 fg=0.05 bg=0.01
regulation of adherens junction organiza... GO:1903391 p=4.9E−03 n=3 fg=0.05 bg=0.01
dendrite morphogenesis GO:0048813 p=5.0E−03 n=6 fg=0.11 bg=0.03
primary neural tube formation GO:0014020 p=5.7E−03 n=4 fg=0.07 bg=0.01
motor neuron axon guidance GO:0008045 p=5.8E−03 n=3 fg=0.05 bg=0.01
positive regulation of neuron differenti... GO:0045666 p=6.2E−03 n=7 fg=0.12 bg=0.04
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peptidyl−threonine dephosphorylation GO:0035970 p=6.2E−03 n=2 fg=0.04 bg=0.00
regulation of cellular response to hypox... GO:1900037 p=6.2E−03 n=2 fg=0.04 bg=0.00
multicellular organismal homeostasis GO:0048871 p=6.5E−03 n=6 fg=0.11 bg=0.03
positive regulation of synaptic assembly... GO:0045887 p=6.8E−03 n=3 fg=0.05 bg=0.01
regulation of endopeptidase activity GO:0052548 p=7.4E−03 n=5 fg=0.09 bg=0.02
assembly of actomyosin apparatus involve... GO:0000912 p=8.6E−03 n=2 fg=0.04 bg=0.00
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−log(p)
n=57/207 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032366836.2
fraction genes in fg and expected valu
phospholipase binding GO:0043274 p=8.2E−03 n=2 fg=0.04 bg=0.00
endopeptidase regulator activity GO:0061135 p=1.7E−02 n=2 fg=0.04 bg=0.00
Rho−dependent protein serine/threonine k... GO:0072518 p=2.1E−02 n=1 fg=0.02 bg=0.00
peroxynitrite reductase activity GO:0072541 p=2.1E−02 n=1 fg=0.02 bg=0.00
glycine transmembrane transporter activi... GO:0015187 p=2.1E−02 n=1 fg=0.02 bg=0.00
thioredoxin peroxidase activity GO:0008379 p=2.1E−02 n=1 fg=0.02 bg=0.00
peroxiredoxin activity GO:0051920 p=2.1E−02 n=1 fg=0.02 bg=0.00
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nickel cation binding GO:0016151 p=2.1E−02 n=1 fg=0.02 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=2.1E−02 n=1 fg=0.02 bg=0.00
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methylenetetrahydrofolate dehydrogenase ... GO:0004488 p=2.1E−02 n=1 fg=0.02 bg=0.00
netrin receptor activity GO:0005042 p=2.1E−02 n=1 fg=0.02 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=2.1E−02 n=1 fg=0.02 bg=0.00
amino acid:proton symporter activity GO:0005280 p=2.1E−02 n=1 fg=0.02 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=2.1E−02 n=1 fg=0.02 bg=0.00
dolichyl pyrophosphate Man9GlcNAc2 alpha... GO:0042281 p=2.1E−02 n=1 fg=0.02 bg=0.00
mono−olein transacylation activity GO:0051264 p=2.1E−02 n=1 fg=0.02 bg=0.00
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L−proline transmembrane transporter acti... GO:0015193 p=2.1E−02 n=1 fg=0.02 bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196 p=2.1E−02 n=1 fg=0.02 bg=0.00
lysophosphatidic acid binding GO:0035727 p=2.1E−02 n=1 fg=0.02 bg=0.00
dolichyl−phosphate−glucose−glycolipid al... GO:0004583 p=2.1E−02 n=1 fg=0.02 bg=0.00
SH2 domain binding GO:0042169 p=2.4E−02 n=2 fg=0.04 bg=0.01
histone acetyltransferase binding GO:0035035 p=2.8E−02 n=2 fg=0.04 bg=0.01
double−stranded RNA binding GO:0003725 p=2.8E−02 n=2 fg=0.04 bg=0.01
peptidase regulator activity GO:0061134 p=3.3E−02 n=2 fg=0.04 bg=0.01
phospholipid binding GO:0005543 p=3.3E−02 n=5 fg=0.10 bg=0.04
adenyl nucleotide binding GO:0030554 p=3.5E−02 n=6 fg=0.12 bg=0.05
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−log(p)
n=49/207 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032366836.2
fraction genes in fg and expected valu
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cortical actin cytoskeleton GO:0030864 p=7.9E−03 n=3 fg=0.05 bg=0.01
mitochondrial membrane GO:0031966 p=1.4E−02 n=8 fg=0.14 bg=0.06
contractile fiber GO:0043292 p=1.4E−02 n=5 fg=0.09 bg=0.03
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=1.8E−02 n=2 fg=0.04 bg=0.00
mitochondrial envelope GO:0005740 p=2.1E−02 n=8 fg=0.14 bg=0.06
spectrosome GO:0045170 p=2.1E−02 n=1 fg=0.02 bg=0.00
spectrin GO:0008091 p=2.1E−02 n=1 fg=0.02 bg=0.00
apicomedial cortex GO:0106037 p=2.1E−02 n=1 fg=0.02 bg=0.00
plastid GO:0009536 p=2.1E−02 n=1 fg=0.02 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=2.1E−02 n=1 fg=0.02 bg=0.00
symplast GO:0055044 p=2.1E−02 n=1 fg=0.02 bg=0.00
plasmodesma GO:0009506 p=2.1E−02 n=1 fg=0.02 bg=0.00
chloroplast GO:0009507 p=2.1E−02 n=1 fg=0.02 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=2.1E−02 n=1 fg=0.02 bg=0.00
actin rod GO:0031002 p=2.1E−02 n=1 fg=0.02 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=2.1E−02 n=1 fg=0.02 bg=0.00
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cofilin−actin rod GO:0090732 p=2.1E−02 n=1 fg=0.02 bg=0.00
Cajal body GO:0015030 p=2.1E−02 n=2 fg=0.04 bg=0.00
growth cone GO:0030426 p=2.1E−02 n=4 fg=0.07 bg=0.02
cytoplasmic region GO:0099568 p=2.3E−02 n=7 fg=0.12 bg=0.05
cell junction GO:0030054 p=2.4E−02 n=12 fg=0.21 bg=0.11
cytoplasmic stress granule GO:0010494 p=2.5E−02 n=2 fg=0.04 bg=0.00
site of polarized growth GO:0030427 p=2.6E−02 n=4 fg=0.07 bg=0.02
membrane GO:0016020 p=3.0E−02 n=31 fg=0.54 bg=0.41
cell periphery GO:0071944 p=3.1E−02 n=23 fg=0.40 bg=0.25
supramolecular complex GO:0099080 p=3.5E−02 n=9 fg=0.16 bg=0.08
organelle membrane GO:0031090 p=3.5E−02 n=20 fg=0.35 bg=0.24
extrinsic component of membrane GO:0019898 p=4.0E−02 n=4 fg=0.07 bg=0.02
0 1 2 3 4 5
−log(p)
n=57/207 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction