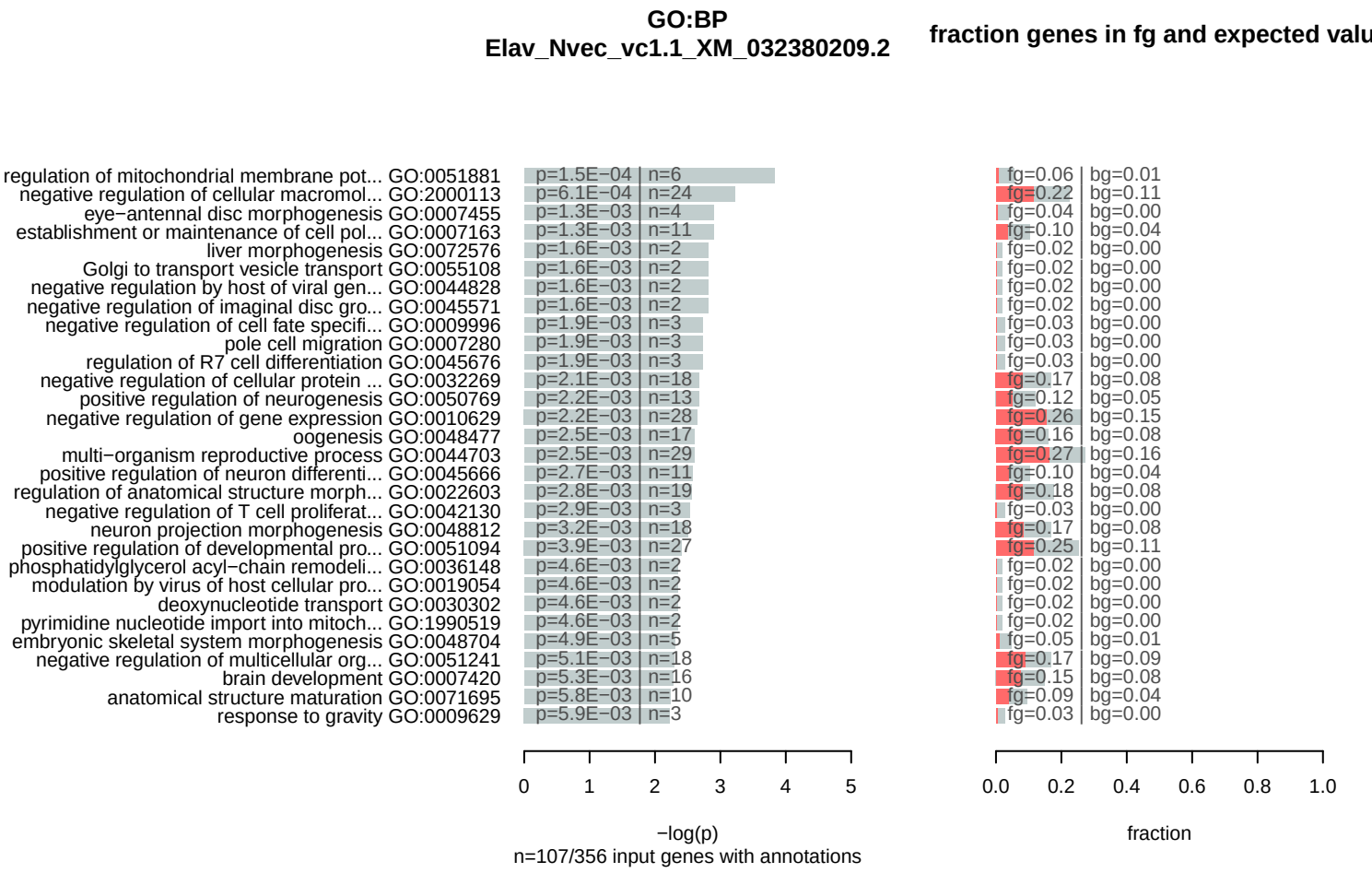
GO:BP
Elav_Nvec_vc1.1_XM_032380209.2
fraction genes in fg and expected valu
regulation of mitochondrial membrane pot... GO:0051881 p=1.5E−04 n=6 fg=0.06 bg=0.01
negative regulation of cellular macromol... GO:2000113 p=6.1E−04 n=24 fg=0.22 bg=0.11
eye−antennal disc morphogenesis GO:0007455 p=1.3E−03 n=4 fg=0.04 bg=0.00
establishment or maintenance of cell pol... GO:0007163 p=1.3E−03 n=11 fg=0.10 bg=0.04
liver morphogenesis GO:0072576 p=1.6E−03 n=2 fg=0.02 bg=0.00
Golgi to transport vesicle transport GO:0055108 p=1.6E−03 n=2 fg=0.02 bg=0.00
negative regulation by host of viral gen... GO:0044828 p=1.6E−03 n=2 fg=0.02 bg=0.00
negative regulation of imaginal disc gro... GO:0045571 p=1.6E−03 n=2 fg=0.02 bg=0.00
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positive regulation of neurogenesis GO:0050769 p=2.2E−03 n=13 fg=0.12 bg=0.05
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multi−organism reproductive process GO:0044703 p=2.5E−03 n=29 fg=0.27 bg=0.16
positive regulation of neuron differenti... GO:0045666 p=2.7E−03 n=11 fg=0.10 bg=0.04
regulation of anatomical structure morph... GO:0022603 p=2.8E−03 n=19 fg=0.18 bg=0.08
negative regulation of T cell proliferat... GO:0042130 p=2.9E−03 n=3 fg=0.03 bg=0.00
neuron projection morphogenesis GO:0048812 p=3.2E−03 n=18 fg=0.17 bg=0.08
positive regulation of developmental pro... GO:0051094 p=3.9E−03 n=27 fg=0.25 bg=0.11
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=4.6E−03 n=2 fg=0.02 bg=0.00
modulation by virus of host cellular pro... GO:0019054 p=4.6E−03 n=2 fg=0.02 bg=0.00
deoxynucleotide transport GO:0030302 p=4.6E−03 n=2 fg=0.02 bg=0.00
pyrimidine nucleotide import into mitoch... GO:1990519 p=4.6E−03 n=2 fg=0.02 bg=0.00
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anatomical structure maturation GO:0071695 p=5.8E−03 n=10 fg=0.09 bg=0.04
response to gravity GO:0009629 p=5.9E−03 n=3 fg=0.03 bg=0.00
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n=107/356 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032380209.2
fraction genes in fg and expected valu
DNA replication origin binding GO:0003688 p=1.7E−03 n=2 fg=0.02 bg=0.00
phosphotyrosine residue binding GO:0001784 p=3.4E−03 n=3 fg=0.03 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=4.5E−03 n=5 fg=0.05 bg=0.01
pyrimidine nucleotide transmembrane tran... GO:0015218 p=5.0E−03 n=2 fg=0.02 bg=0.00
mRNA 3'−UTR AU−rich region binding GO:0035925 p=5.0E−03 n=2 fg=0.02 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=5.0E−03 n=2 fg=0.02 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=1.2E−02 n=8 fg=0.08 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.2E−02 n=8 fg=0.08 bg=0.03
channel regulator activity GO:0016247 p=1.5E−02 n=5 fg=0.05 bg=0.02
nucleoside monophosphate kinase activity GO:0050145 p=1.6E−02 n=2 fg=0.02 bg=0.00
transcription regulator activity GO:0140110 p=2.1E−02 n=20 fg=0.20 bg=0.10
myosin binding GO:0017022 p=2.1E−02 n=4 fg=0.04 bg=0.01
RNA polymerase II−specific DNA−binding t... GO:0061629 p=2.1E−02 n=6 fg=0.06 bg=0.02
DNA−binding transcription factor activit... GO:0003700 p=2.2E−02 n=16 fg=0.16 bg=0.07
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1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=2.3E−02 n=2 fg=0.02 bg=0.00
aryl hydrocarbon receptor binding GO:0017162 p=2.3E−02 n=2 fg=0.02 bg=0.00
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single−stranded DNA binding GO:0003697 p=3.0E−02 n=4 fg=0.04 bg=0.01
acylglycerol O−acyltransferase activity GO:0016411 p=3.2E−02 n=2 fg=0.02 bg=0.00
nuclear receptor activity GO:0004879 p=3.2E−02 n=2 fg=0.02 bg=0.00
adenylate cyclase binding GO:0008179 p=3.2E−02 n=2 fg=0.02 bg=0.00
ubiquitin−specific protease binding GO:1990381 p=3.2E−02 n=2 fg=0.02 bg=0.00
ligand−activated transcription factor ac... GO:0098531 p=3.2E−02 n=2 fg=0.02 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=3.3E−02 n=7 fg=0.07 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=3.3E−02 n=7 fg=0.07 bg=0.03
lysophosphatidic acid acyltransferase ac... GO:0042171 p=4.1E−02 n=2 fg=0.02 bg=0.00
lysophospholipid acyltransferase activit... GO:0071617 p=4.1E−02 n=2 fg=0.02 bg=0.00
transcription cis−regulatory region bind... GO:0000976 p=4.1E−02 n=9 fg=0.09 bg=0.05
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−log(p)
n=99/356 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032380209.2
fraction genes in fg and expected valu
Lewy body GO:0097413 p=1.6E−03 n=2 fg=0.02 bg=0.00
lysosomal membrane GO:0005765 p=2.4E−03 n=7 fg=0.07 bg=0.02
postsynaptic density GO:0014069 p=3.1E−03 n=7 fg=0.07 bg=0.02
supramolecular complex GO:0099080 p=4.1E−03 n=17 fg=0.16 bg=0.08
dendrite GO:0030425 p=4.5E−03 n=14 fg=0.13 bg=0.06
myelin sheath abaxonal region GO:0035748 p=4.5E−03 n=2 fg=0.02 bg=0.00
intracellular organelle GO:0043229 p=6.9E−03 n=99 fg=0.93 bg=0.83
microvillus GO:0005902 p=8.3E−03 n=4 fg=0.04 bg=0.01
cytoplasmic stress granule GO:0010494 p=1.0E−02 n=3 fg=0.03 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=1.4E−02 n=2 fg=0.02 bg=0.00
contractile fiber GO:0043292 p=1.8E−02 n=7 fg=0.07 bg=0.03
cytoplasmic side of plasma membrane GO:0009898 p=1.8E−02 n=6 fg=0.06 bg=0.02
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primary lysosome GO:0005766 p=2.9E−02 n=4 fg=0.04 bg=0.01
ribonucleoprotein granule GO:0035770 p=3.4E−02 n=6 fg=0.06 bg=0.02
cytoplasmic side of membrane GO:0098562 p=3.4E−02 n=6 fg=0.06 bg=0.02
membrane−bounded organelle GO:0043227 p=3.4E−02 n=94 fg=0.88 bg=0.80
nucleus GO:0005634 p=3.5E−02 n=63 fg=0.59 bg=0.50
chromosome, centromeric region GO:0000775 p=3.6E−02 n=5 fg=0.05 bg=0.02
immunological synapse GO:0001772 p=3.7E−02 n=2 fg=0.02 bg=0.00
microvesicle GO:1990742 p=4.0E−02 n=1 fg=0.01 bg=0.00
sperm connecting piece GO:0097224 p=4.0E−02 n=1 fg=0.01 bg=0.00
sperm mitochondrial sheath GO:0097226 p=4.0E−02 n=1 fg=0.01 bg=0.00
Ndc80 complex GO:0031262 p=4.0E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=4.0E−02 n=1 fg=0.01 bg=0.00
apicomedial cortex GO:0106037 p=4.0E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=4.0E−02 n=1 fg=0.01 bg=0.00
alpha−heterochromatin GO:0005723 p=4.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=107/356 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction