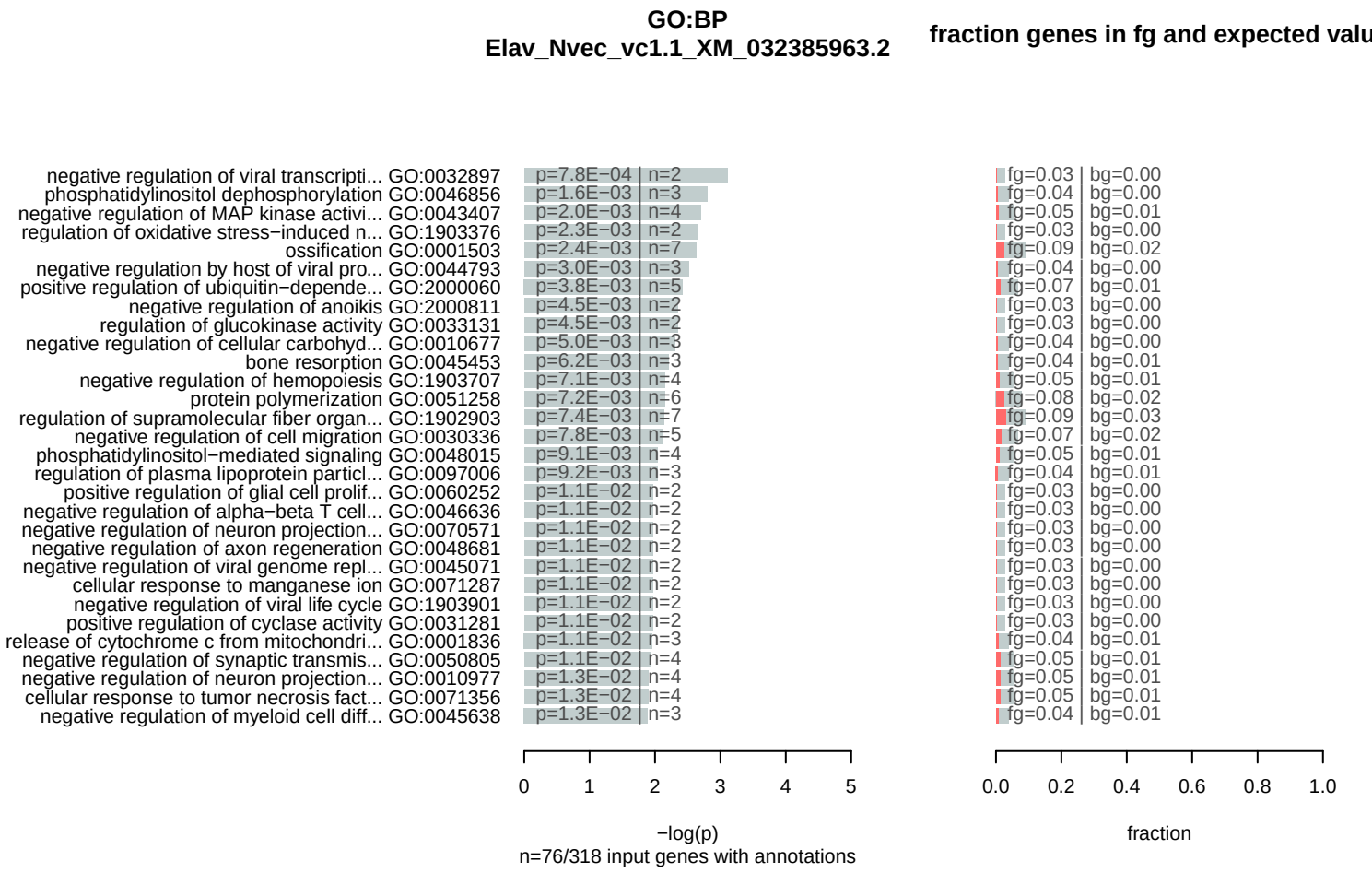
GO:BP
Elav_Nvec_vc1.1_XM_032385963.2
fraction genes in fg and expected valu
negative regulation of viral transcripti... GO:0032897 p=7.8E−04 n=2 fg=0.03 bg=0.00
phosphatidylinositol dephosphorylation GO:0046856 p=1.6E−03 n=3 fg=0.04 bg=0.00
negative regulation of MAP kinase activi... GO:0043407 p=2.0E−03 n=4 fg=0.05 bg=0.01
regulation of oxidative stress−induced n... GO:1903376 p=2.3E−03 n=2 fg=0.03 bg=0.00
ossification GO:0001503 p=2.4E−03 n=7 fg=0.09 bg=0.02
negative regulation by host of viral pro... GO:0044793 p=3.0E−03 n=3 fg=0.04 bg=0.00
positive regulation of ubiquitin−depende... GO:2000060 p=3.8E−03 n=5 fg=0.07 bg=0.01
negative regulation of anoikis GO:2000811 p=4.5E−03 n=2 fg=0.03 bg=0.00
regulation of glucokinase activity GO:0033131 p=4.5E−03 n=2 fg=0.03 bg=0.00
negative regulation of cellular carbohyd... GO:0010677 p=5.0E−03 n=3 fg=0.04 bg=0.00
bone resorption GO:0045453 p=6.2E−03 n=3 fg=0.04 bg=0.01
negative regulation of hemopoiesis GO:1903707 p=7.1E−03 n=4 fg=0.05 bg=0.01
protein polymerization GO:0051258 p=7.2E−03 n=6 fg=0.08 bg=0.02
regulation of supramolecular fiber organ... GO:1902903 p=7.4E−03 n=7 fg=0.09 bg=0.03
negative regulation of cell migration GO:0030336 p=7.8E−03 n=5 fg=0.07 bg=0.02
phosphatidylinositol−mediated signaling GO:0048015 p=9.1E−03 n=4 fg=0.05 bg=0.01
regulation of plasma lipoprotein particl... GO:0097006 p=9.2E−03 n=3 fg=0.04 bg=0.01
positive regulation of glial cell prolif... GO:0060252 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of alpha−beta T cell... GO:0046636 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of neuron projection... GO:0070571 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of axon regeneration GO:0048681 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of viral genome repl... GO:0045071 p=1.1E−02 n=2 fg=0.03 bg=0.00
cellular response to manganese ion GO:0071287 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of viral life cycle GO:1903901 p=1.1E−02 n=2 fg=0.03 bg=0.00
positive regulation of cyclase activity GO:0031281 p=1.1E−02 n=2 fg=0.03 bg=0.00
release of cytochrome c from mitochondri... GO:0001836 p=1.1E−02 n=3 fg=0.04 bg=0.01
negative regulation of synaptic transmis... GO:0050805 p=1.1E−02 n=4 fg=0.05 bg=0.01
negative regulation of neuron projection... GO:0010977 p=1.3E−02 n=4 fg=0.05 bg=0.01
cellular response to tumor necrosis fact... GO:0071356 p=1.3E−02 n=4 fg=0.05 bg=0.01
negative regulation of myeloid cell diff... GO:0045638 p=1.3E−02 n=3 fg=0.04 bg=0.01
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−log(p)
n=76/318 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032385963.2
fraction genes in fg and expected valu
phosphatidylinositol phosphate phosphata... GO:0052866 p=3.3E−03 n=3 fg=0.04 bg=0.00
actin monomer binding GO:0003785 p=7.9E−03 n=2 fg=0.03 bg=0.00
cysteine−type peptidase activity GO:0008234 p=1.1E−02 n=4 fg=0.06 bg=0.01
phosphatidylinositol phosphate 5−phospha... GO:0034595 p=1.2E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol 3−kinase binding GO:0043548 p=1.2E−02 n=2 fg=0.03 bg=0.00
inositol phosphate phosphatase activity GO:0052745 p=1.6E−02 n=2 fg=0.03 bg=0.00
phosphotyrosine residue binding GO:0001784 p=2.1E−02 n=2 fg=0.03 bg=0.00
cullin family protein binding GO:0097602 p=2.1E−02 n=2 fg=0.03 bg=0.00
protease binding GO:0002020 p=2.5E−02 n=3 fg=0.04 bg=0.01
signaling receptor complex adaptor activ... GO:0030159 p=2.6E−02 n=2 fg=0.03 bg=0.00
peptide transmembrane transporter activi... GO:1904680 p=2.6E−02 n=2 fg=0.03 bg=0.00
guanyl−nucleotide exchange factor activi... GO:0005085 p=2.7E−02 n=4 fg=0.06 bg=0.02
histone deacetylase regulator activity GO:0035033 p=2.9E−02 n=1 fg=0.01 bg=0.00
nucleoside:sodium symporter activity GO:0005415 p=2.9E−02 n=1 fg=0.01 bg=0.00
ferrochelatase activity GO:0004325 p=2.9E−02 n=1 fg=0.01 bg=0.00
pyrimidine nucleobase transmembrane tran... GO:0005350 p=2.9E−02 n=1 fg=0.01 bg=0.00
misfolded RNA binding GO:0034336 p=2.9E−02 n=1 fg=0.01 bg=0.00
MHC protein complex binding GO:0023023 p=2.9E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein complex binding GO:0023025 p=2.9E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein binding GO:0023029 p=2.9E−02 n=1 fg=0.01 bg=0.00
purine nucleoside transmembrane transpor... GO:0015211 p=2.9E−02 n=1 fg=0.01 bg=0.00
purine−nucleoside phosphorylase activity GO:0004731 p=2.9E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein binding, via antige... GO:0023030 p=2.9E−02 n=1 fg=0.01 bg=0.00
JUN kinase activity GO:0004705 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphomannomutase activity GO:0004615 p=2.9E−02 n=1 fg=0.01 bg=0.00
S−methyl−5−thioadenosine phosphorylase a... GO:0017061 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphoglycerate dehydrogenase activity GO:0004617 p=2.9E−02 n=1 fg=0.01 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=2.9E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=2.9E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=2.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=69/318 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385963.2
fraction genes in fg and expected valu
intrinsic component of the cytoplasmic s... GO:0031235 p=7.0E−03 n=2 fg=0.03 bg=0.00
axon GO:0030424 p=8.4E−03 n=11 fg=0.15 bg=0.07
cell cortex GO:0005938 p=1.3E−02 n=7 fg=0.09 bg=0.03
focal adhesion GO:0005925 p=2.4E−02 n=3 fg=0.04 bg=0.01
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=2.7E−02 n=1 fg=0.01 bg=0.00
NMDA selective glutamate receptor comple... GO:0017146 p=2.7E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=2.7E−02 n=1 fg=0.01 bg=0.00
proteasome storage granule GO:0034515 p=2.7E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber expansion GO:1990026 p=2.7E−02 n=1 fg=0.01 bg=0.00
varicosity GO:0043196 p=2.7E−02 n=1 fg=0.01 bg=0.00
cytoplasmic region GO:0099568 p=3.0E−02 n=8 fg=0.11 bg=0.05
cell−substrate junction GO:0030055 p=3.6E−02 n=3 fg=0.04 bg=0.01
proteasome accessory complex GO:0022624 p=4.1E−02 n=2 fg=0.03 bg=0.00
proteasome regulatory particle GO:0005838 p=4.1E−02 n=2 fg=0.03 bg=0.00
postsynaptic density GO:0014069 p=4.6E−02 n=4 fg=0.05 bg=0.02
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.4E−02 n=1 fg=0.01 bg=0.00
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452 p=5.4E−02 n=1 fg=0.01 bg=0.00
ionotropic glutamate receptor complex GO:0008328 p=5.4E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=5.4E−02 n=1 fg=0.01 bg=0.00
neurofilament GO:0005883 p=5.4E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=5.4E−02 n=1 fg=0.01 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=5.4E−02 n=1 fg=0.01 bg=0.00
neurotransmitter receptor complex GO:0098878 p=5.4E−02 n=1 fg=0.01 bg=0.00
extrinsic component of Golgi membrane GO:0090498 p=5.4E−02 n=1 fg=0.01 bg=0.00
Lewy body GO:0097413 p=5.4E−02 n=1 fg=0.01 bg=0.00
CA3 pyramidal cell dendrite GO:0097442 p=5.4E−02 n=1 fg=0.01 bg=0.00
mitochondrial membrane GO:0031966 p=5.5E−02 n=8 fg=0.11 bg=0.06
postsynaptic specialization GO:0099572 p=5.9E−02 n=4 fg=0.05 bg=0.02
asymmetric synapse GO:0032279 p=6.5E−02 n=4 fg=0.05 bg=0.02
neuron to neuron synapse GO:0098984 p=6.9E−02 n=4 fg=0.05 bg=0.02
0 1 2 3 4 5
−log(p)
n=74/318 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction