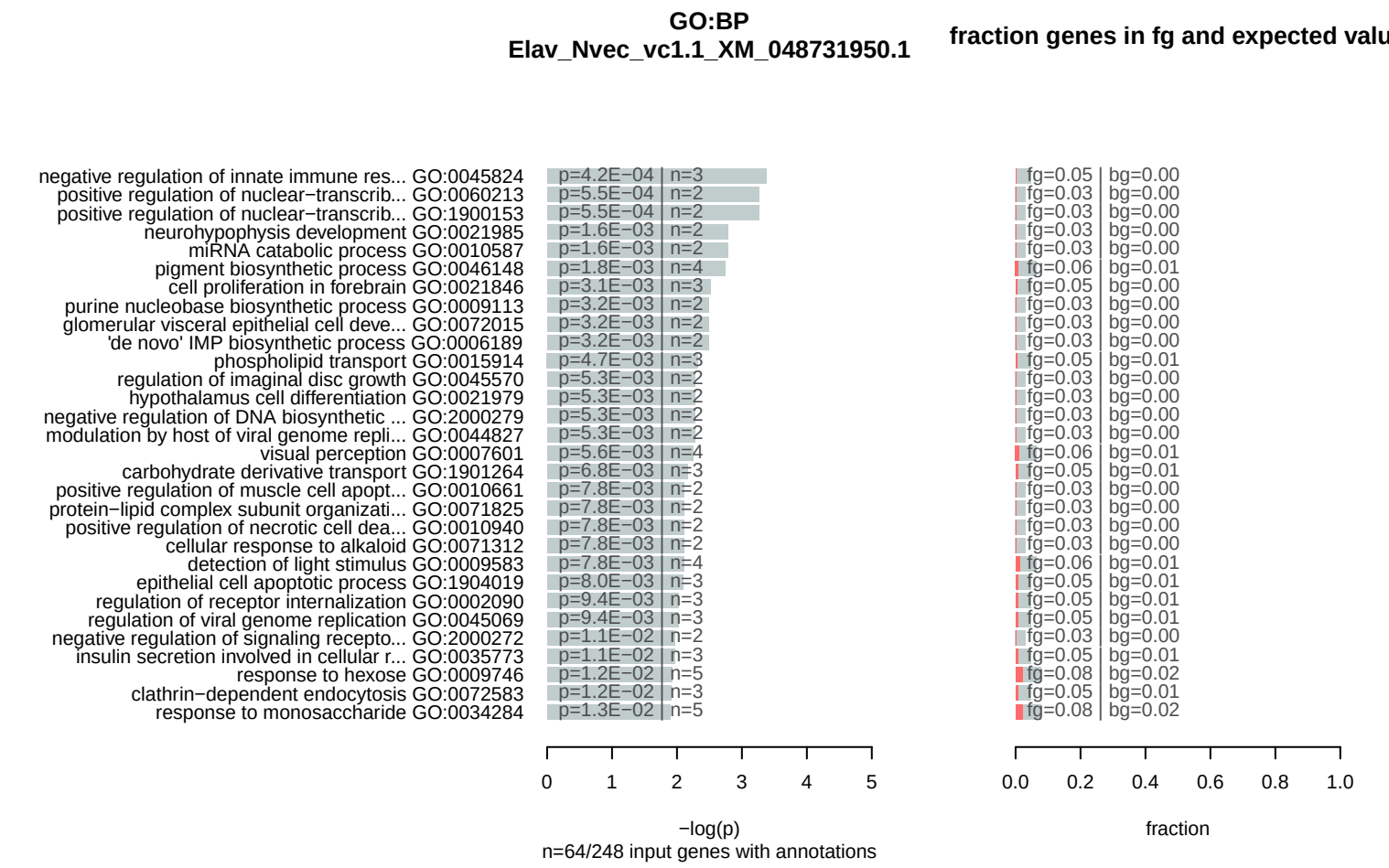
GO:BP
Elav_Nvec_vc1.1_XM_048731950.1
fraction genes in fg and expected valu
negative regulation of innate immune res... GO:0045824 p=4.2E−04 n=3 fg=0.05 bg=0.00
positive regulation of nuclear−transcrib... GO:0060213 p=5.5E−04 n=2 fg=0.03 bg=0.00
positive regulation of nuclear−transcrib... GO:1900153 p=5.5E−04 n=2 fg=0.03 bg=0.00
neurohypophysis development GO:0021985 p=1.6E−03 n=2 fg=0.03 bg=0.00
miRNA catabolic process GO:0010587 p=1.6E−03 n=2 fg=0.03 bg=0.00
pigment biosynthetic process GO:0046148 p=1.8E−03 n=4 fg=0.06 bg=0.01
cell proliferation in forebrain GO:0021846 p=3.1E−03 n=3 fg=0.05 bg=0.00
purine nucleobase biosynthetic process GO:0009113 p=3.2E−03 n=2 fg=0.03 bg=0.00
glomerular visceral epithelial cell deve... GO:0072015 p=3.2E−03 n=2 fg=0.03 bg=0.00
'de novo' IMP biosynthetic process GO:0006189 p=3.2E−03 n=2 fg=0.03 bg=0.00
phospholipid transport GO:0015914 p=4.7E−03 n=3 fg=0.05 bg=0.01
regulation of imaginal disc growth GO:0045570 p=5.3E−03 n=2 fg=0.03 bg=0.00
hypothalamus cell differentiation GO:0021979 p=5.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of DNA biosynthetic ... GO:2000279 p=5.3E−03 n=2 fg=0.03 bg=0.00
modulation by host of viral genome repli... GO:0044827 p=5.3E−03 n=2 fg=0.03 bg=0.00
visual perception GO:0007601 p=5.6E−03 n=4 fg=0.06 bg=0.01
carbohydrate derivative transport GO:1901264 p=6.8E−03 n=3 fg=0.05 bg=0.01
positive regulation of muscle cell apopt... GO:0010661 p=7.8E−03 n=2 fg=0.03 bg=0.00
protein−lipid complex subunit organizati... GO:0071825 p=7.8E−03 n=2 fg=0.03 bg=0.00
positive regulation of necrotic cell dea... GO:0010940 p=7.8E−03 n=2 fg=0.03 bg=0.00
cellular response to alkaloid GO:0071312 p=7.8E−03 n=2 fg=0.03 bg=0.00
detection of light stimulus GO:0009583 p=7.8E−03 n=4 fg=0.06 bg=0.01
epithelial cell apoptotic process GO:1904019 p=8.0E−03 n=3 fg=0.05 bg=0.01
regulation of receptor internalization GO:0002090 p=9.4E−03 n=3 fg=0.05 bg=0.01
regulation of viral genome replication GO:0045069 p=9.4E−03 n=3 fg=0.05 bg=0.01
negative regulation of signaling recepto... GO:2000272 p=1.1E−02 n=2 fg=0.03 bg=0.00
insulin secretion involved in cellular r... GO:0035773 p=1.1E−02 n=3 fg=0.05 bg=0.01
response to hexose GO:0009746 p=1.2E−02 n=5 fg=0.08 bg=0.02
clathrin−dependent endocytosis GO:0072583 p=1.2E−02 n=3 fg=0.05 bg=0.01
response to monosaccharide GO:0034284 p=1.3E−02 n=5 fg=0.08 bg=0.02
0 1 2 3 4 5
−log(p)
n=64/248 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048731950.1
fraction genes in fg and expected valu
phospholipid transporter activity GO:0005548 p=4.0E−03 n=3 fg=0.05 bg=0.01
ABC−type transporter activity GO:0140359 p=5.4E−03 n=2 fg=0.04 bg=0.00
active ion transmembrane transporter act... GO:0022853 p=6.3E−03 n=5 fg=0.09 bg=0.02
lipid transfer activity GO:0120013 p=8.0E−03 n=2 fg=0.04 bg=0.00
Wnt−protein binding GO:0017147 p=8.0E−03 n=2 fg=0.04 bg=0.00
adrenergic receptor binding GO:0031690 p=1.1E−02 n=2 fg=0.04 bg=0.00
ATPase−coupled transmembrane transporter... GO:0042626 p=1.3E−02 n=5 fg=0.09 bg=0.01
ATP hydrolysis activity GO:0016887 p=1.4E−02 n=7 fg=0.12 bg=0.05
exoribonuclease activity, producing 5'−p... GO:0016896 p=1.8E−02 n=2 fg=0.04 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=1.8E−02 n=2 fg=0.04 bg=0.00
3'−5'−exoribonuclease activity GO:0000175 p=1.8E−02 n=2 fg=0.04 bg=0.00
exoribonuclease activity GO:0004532 p=2.3E−02 n=2 fg=0.04 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016668 p=2.3E−02 n=2 fg=0.04 bg=0.00
opsin binding GO:0002046 p=2.4E−02 n=1 fg=0.02 bg=0.00
selenium binding GO:0008430 p=2.4E−02 n=1 fg=0.02 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=2.4E−02 n=1 fg=0.02 bg=0.00
histone kinase activity (H3−T11 specific... GO:0035402 p=2.4E−02 n=1 fg=0.02 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=2.4E−02 n=1 fg=0.02 bg=0.00
N6−methyladenosine−containing RNA bindin... GO:1990247 p=2.4E−02 n=1 fg=0.02 bg=0.00
very−low−density lipoprotein particle re... GO:0070326 p=2.4E−02 n=1 fg=0.02 bg=0.00
alpha−N−acetylglucosaminidase activity GO:0004561 p=2.4E−02 n=1 fg=0.02 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=2.4E−02 n=1 fg=0.02 bg=0.00
V2 vasopressin receptor binding GO:0031896 p=2.4E−02 n=1 fg=0.02 bg=0.00
amine transmembrane transporter activity GO:0005275 p=2.4E−02 n=1 fg=0.02 bg=0.00
signaling receptor inhibitor activity GO:0030547 p=2.4E−02 n=1 fg=0.02 bg=0.00
omega−amidase activity GO:0050152 p=2.4E−02 n=1 fg=0.02 bg=0.00
phosphoribosylaminoimidazole carboxylase... GO:0004638 p=2.4E−02 n=1 fg=0.02 bg=0.00
phosphoribosylaminoimidazolesuccinocarbo... GO:0004639 p=2.4E−02 n=1 fg=0.02 bg=0.00
receptor antagonist activity GO:0048019 p=2.4E−02 n=1 fg=0.02 bg=0.00
ABC−type guanine transporter activity GO:0008558 p=2.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/248 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048731950.1
fraction genes in fg and expected valu
P granule GO:0043186 p=6.5E−03 n=3 fg=0.04 bg=0.01
fibrillar center GO:0001650 p=8.2E−03 n=4 fg=0.06 bg=0.01
ribonucleoprotein complex GO:1990904 p=1.3E−02 n=12 fg=0.18 bg=0.09
P−body GO:0000932 p=1.4E−02 n=3 fg=0.04 bg=0.01
supramolecular complex GO:0099080 p=1.8E−02 n=13 fg=0.19 bg=0.08
endosome GO:0005768 p=1.9E−02 n=10 fg=0.15 bg=0.07
polysome GO:0005844 p=2.0E−02 n=3 fg=0.04 bg=0.01
ribonucleoprotein granule GO:0035770 p=2.3E−02 n=7 fg=0.10 bg=0.02
host cell nuclear part GO:0044094 p=2.5E−02 n=1 fg=0.01 bg=0.00
rough endoplasmic reticulum lumen GO:0048237 p=2.5E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=2.5E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=2.5E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=2.5E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=2.5E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=2.5E−02 n=1 fg=0.01 bg=0.00
UTP−C complex GO:0034456 p=2.5E−02 n=1 fg=0.01 bg=0.00
CURI complex GO:0032545 p=2.5E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=2.5E−02 n=1 fg=0.01 bg=0.00
pigment granule membrane GO:0090741 p=2.5E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=2.5E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=2.5E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=2.5E−02 n=1 fg=0.01 bg=0.00
other organism part GO:0044217 p=2.5E−02 n=1 fg=0.01 bg=0.00
tubulin folding cofactor complex GO:1990727 p=2.5E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber to CA3 synapse GO:0098686 p=2.5E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=2.5E−02 n=1 fg=0.01 bg=0.00
neuron projection cytoplasm GO:0120111 p=2.9E−02 n=2 fg=0.03 bg=0.00
small−subunit processome GO:0032040 p=3.4E−02 n=2 fg=0.03 bg=0.00
cytoplasmic microtubule GO:0005881 p=4.0E−02 n=2 fg=0.03 bg=0.00
smooth endoplasmic reticulum GO:0005790 p=4.0E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=67/248 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction