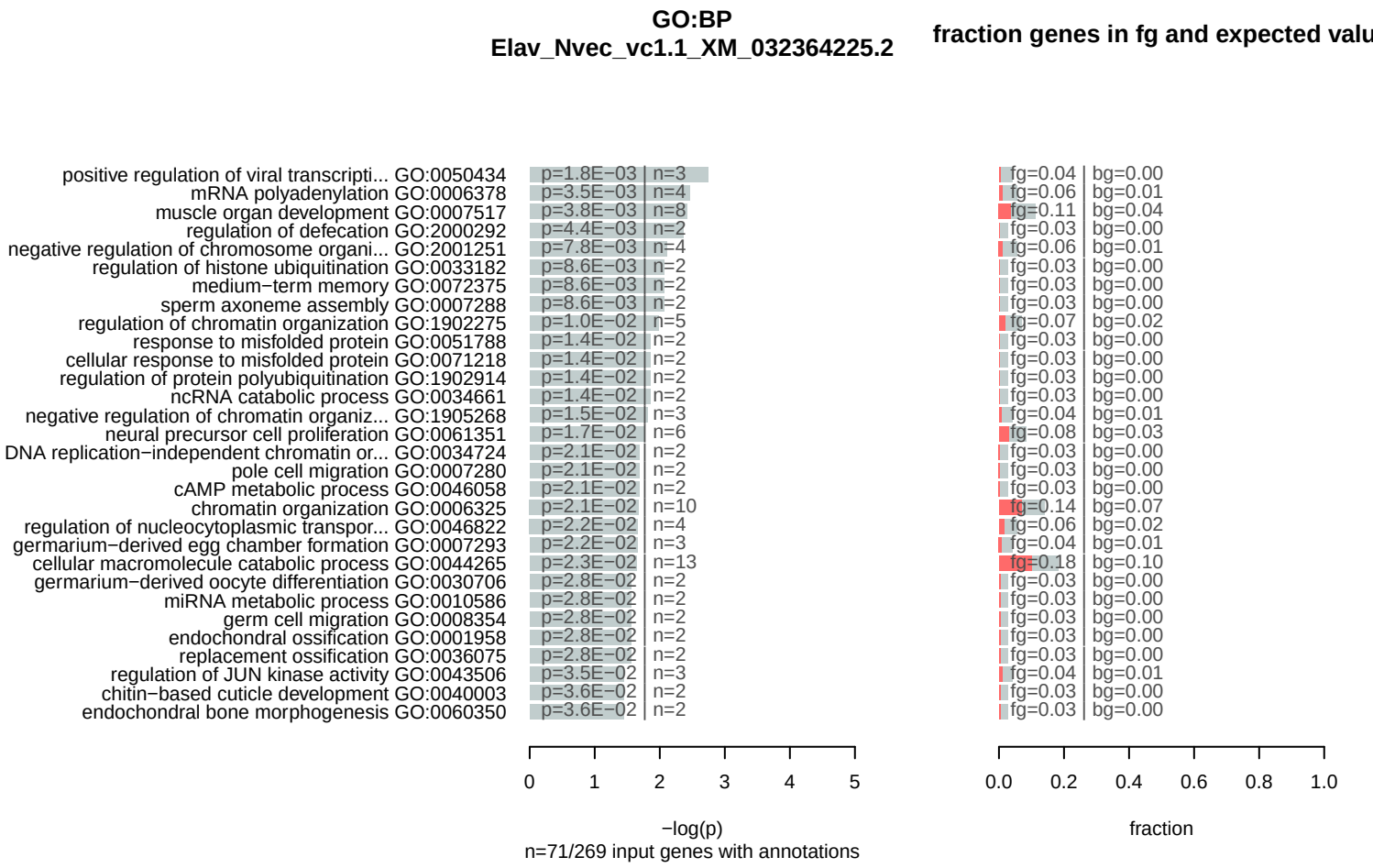
GO:BP
Elav_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
positive regulation of viral transcripti... GO:0050434 p=1.8E−03 n=3 fg=0.04 bg=0.00
mRNA polyadenylation GO:0006378 p=3.5E−03 n=4 fg=0.06 bg=0.01
muscle organ development GO:0007517 p=3.8E−03 n=8 fg=0.11 bg=0.04
regulation of defecation GO:2000292 p=4.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of chromosome organi... GO:2001251 p=7.8E−03 n=4 fg=0.06 bg=0.01
regulation of histone ubiquitination GO:0033182 p=8.6E−03 n=2 fg=0.03 bg=0.00
medium−term memory GO:0072375 p=8.6E−03 n=2 fg=0.03 bg=0.00
sperm axoneme assembly GO:0007288 p=8.6E−03 n=2 fg=0.03 bg=0.00
regulation of chromatin organization GO:1902275 p=1.0E−02 n=5 fg=0.07 bg=0.02
response to misfolded protein GO:0051788 p=1.4E−02 n=2 fg=0.03 bg=0.00
cellular response to misfolded protein GO:0071218 p=1.4E−02 n=2 fg=0.03 bg=0.00
regulation of protein polyubiquitination GO:1902914 p=1.4E−02 n=2 fg=0.03 bg=0.00
ncRNA catabolic process GO:0034661 p=1.4E−02 n=2 fg=0.03 bg=0.00
negative regulation of chromatin organiz... GO:1905268 p=1.5E−02 n=3 fg=0.04 bg=0.01
neural precursor cell proliferation GO:0061351 p=1.7E−02 n=6 fg=0.08 bg=0.03
DNA replication−independent chromatin or... GO:0034724 p=2.1E−02 n=2 fg=0.03 bg=0.00
pole cell migration GO:0007280 p=2.1E−02 n=2 fg=0.03 bg=0.00
cAMP metabolic process GO:0046058 p=2.1E−02 n=2 fg=0.03 bg=0.00
chromatin organization GO:0006325 p=2.1E−02 n=10 fg=0.14 bg=0.07
regulation of nucleocytoplasmic transpor... GO:0046822 p=2.2E−02 n=4 fg=0.06 bg=0.02
germarium−derived egg chamber formation GO:0007293 p=2.2E−02 n=3 fg=0.04 bg=0.01
cellular macromolecule catabolic process GO:0044265 p=2.3E−02 n=13 fg=0.18 bg=0.10
germarium−derived oocyte differentiation GO:0030706 p=2.8E−02 n=2 fg=0.03 bg=0.00
miRNA metabolic process GO:0010586 p=2.8E−02 n=2 fg=0.03 bg=0.00
germ cell migration GO:0008354 p=2.8E−02 n=2 fg=0.03 bg=0.00
endochondral ossification GO:0001958 p=2.8E−02 n=2 fg=0.03 bg=0.00
replacement ossification GO:0036075 p=2.8E−02 n=2 fg=0.03 bg=0.00
regulation of JUN kinase activity GO:0043506 p=3.5E−02 n=3 fg=0.04 bg=0.01
chitin−based cuticle development GO:0040003 p=3.6E−02 n=2 fg=0.03 bg=0.00
endochondral bone morphogenesis GO:0060350 p=3.6E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=71/269 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
modification−dependent protein binding GO:0140030 p=7.8E−04 n=5 fg=0.08 bg=0.01
polynucleotide adenylyltransferase activ... GO:0004652 p=2.1E−03 n=3 fg=0.05 bg=0.00
histone binding GO:0042393 p=4.2E−03 n=5 fg=0.08 bg=0.02
syntaxin−1 binding GO:0017075 p=9.6E−03 n=2 fg=0.03 bg=0.00
MAP kinase kinase kinase activity GO:0004709 p=2.3E−02 n=2 fg=0.03 bg=0.00
neurotransmitter binding GO:0042165 p=3.1E−02 n=2 fg=0.03 bg=0.00
polyubiquitin modification−dependent pro... GO:0031593 p=3.1E−02 n=2 fg=0.03 bg=0.00
hormone binding GO:0042562 p=4.0E−02 n=2 fg=0.03 bg=0.01
manganese ion transmembrane transporter ... GO:0005384 p=4.1E−02 n=1 fg=0.02 bg=0.00
nitrite reductase activity GO:0098809 p=4.1E−02 n=1 fg=0.02 bg=0.00
uridylyltransferase activity GO:0070569 p=4.1E−02 n=1 fg=0.02 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=4.1E−02 n=1 fg=0.02 bg=0.00
ribonuclease P activity GO:0004526 p=4.1E−02 n=1 fg=0.02 bg=0.00
protein kinase C inhibitor activity GO:0008426 p=4.1E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=4.1E−02 n=1 fg=0.02 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=4.1E−02 n=1 fg=0.02 bg=0.00
SMC family protein binding GO:0043221 p=4.1E−02 n=1 fg=0.02 bg=0.00
purine nucleobase transmembrane transpor... GO:0005345 p=4.1E−02 n=1 fg=0.02 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=4.1E−02 n=1 fg=0.02 bg=0.00
NAD−retinol dehydrogenase activity GO:0004745 p=4.1E−02 n=1 fg=0.02 bg=0.00
RNA uridylyltransferase activity GO:0050265 p=4.1E−02 n=1 fg=0.02 bg=0.00
U6 snRNA binding GO:0017070 p=4.1E−02 n=1 fg=0.02 bg=0.00
adipokinetic hormone receptor activity GO:0097003 p=4.1E−02 n=1 fg=0.02 bg=0.00
ABC−type guanine transporter activity GO:0008558 p=4.1E−02 n=1 fg=0.02 bg=0.00
pyrroline−5−carboxylate reductase activi... GO:0004735 p=4.1E−02 n=1 fg=0.02 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=4.1E−02 n=1 fg=0.02 bg=0.00
nucleobase transmembrane transporter act... GO:0015205 p=4.1E−02 n=1 fg=0.02 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=4.1E−02 n=1 fg=0.02 bg=0.00
phosphoserine residue binding GO:0050815 p=4.1E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=4.1E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=66/269 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
vacuolar proton−transporting V−type ATPa... GO:0016471 p=2.9E−02 n=2 fg=0.03 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=3.7E−02 n=2 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0016469 p=3.7E−02 n=2 fg=0.03 bg=0.00
kinesin complex GO:0005871 p=3.7E−02 n=2 fg=0.03 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=4.0E−02 n=1 fg=0.01 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=4.0E−02 n=1 fg=0.01 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=4.0E−02 n=1 fg=0.01 bg=0.00
nucleolar ribonuclease P complex GO:0005655 p=4.0E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=4.0E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=4.0E−02 n=1 fg=0.01 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=4.0E−02 n=1 fg=0.01 bg=0.00
CCAAT−binding factor complex GO:0016602 p=4.0E−02 n=1 fg=0.01 bg=0.00
FACT complex GO:0035101 p=4.0E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=4.0E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=4.0E−02 n=1 fg=0.01 bg=0.00
ER membrane insertion complex GO:0072379 p=4.0E−02 n=1 fg=0.01 bg=0.00
BAT3 complex GO:0071818 p=4.0E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=4.0E−02 n=1 fg=0.01 bg=0.00
pigment granule membrane GO:0090741 p=4.0E−02 n=1 fg=0.01 bg=0.00
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=4.0E−02 n=1 fg=0.01 bg=0.00
ribonuclease MRP complex GO:0000172 p=4.0E−02 n=1 fg=0.01 bg=0.00
centriole GO:0005814 p=4.8E−02 n=3 fg=0.04 bg=0.01
presynaptic membrane GO:0042734 p=7.4E−02 n=3 fg=0.04 bg=0.01
tricarboxylic acid cycle enzyme complex GO:0045239 p=7.8E−02 n=1 fg=0.01 bg=0.00
U5 snRNP GO:0005682 p=7.8E−02 n=1 fg=0.01 bg=0.00
HULC complex GO:0033503 p=7.8E−02 n=1 fg=0.01 bg=0.00
TRAMP complex GO:0031499 p=7.8E−02 n=1 fg=0.01 bg=0.00
extrinsic component of endoplasmic retic... GO:0042406 p=7.8E−02 n=1 fg=0.01 bg=0.00
muscle myosin complex GO:0005859 p=7.8E−02 n=1 fg=0.01 bg=0.00
myosin II complex GO:0016460 p=7.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=72/269 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction