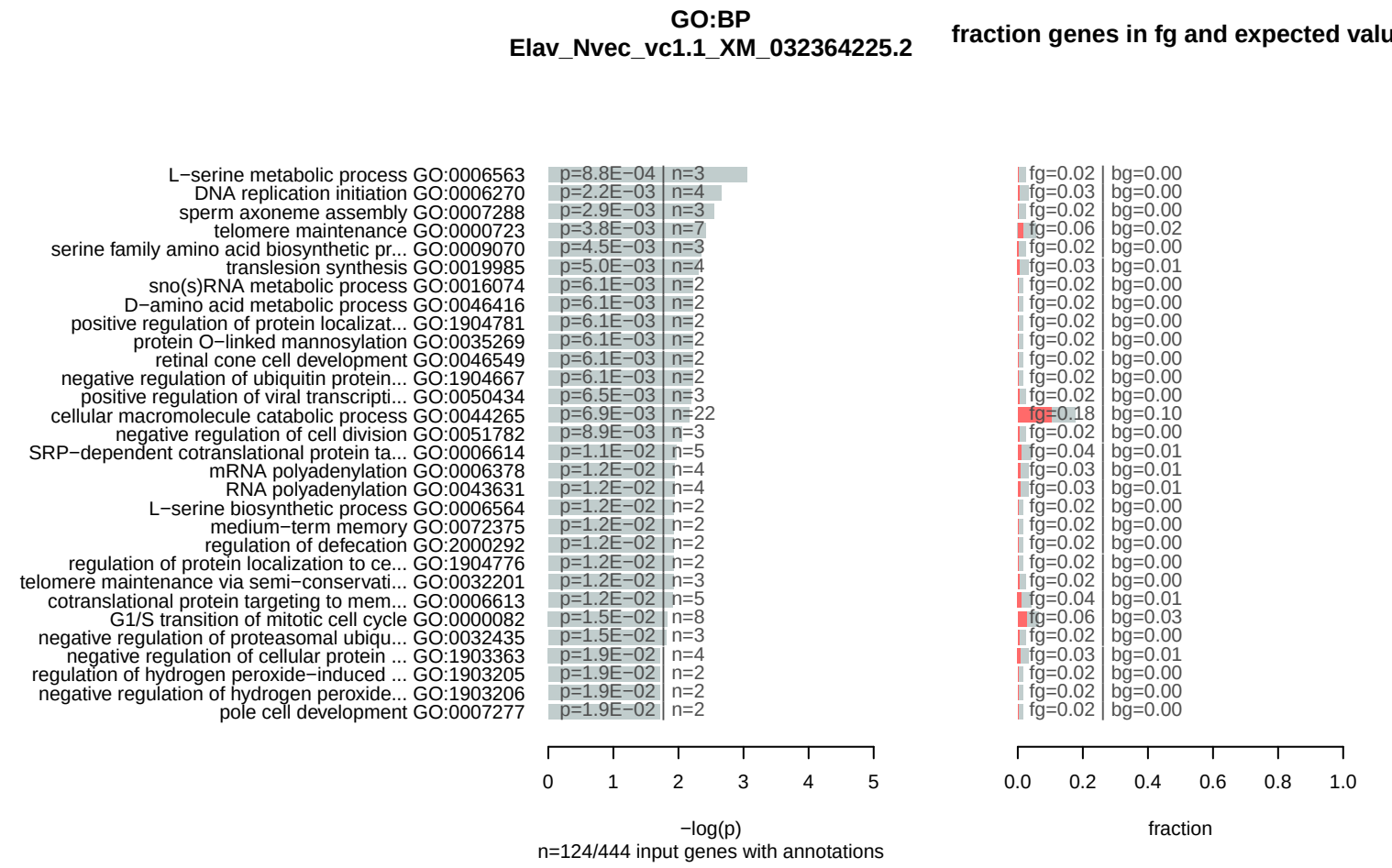
GO:BP
Elav_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
L−serine metabolic process GO:0006563 p=8.8E−04 n=3 fg=0.02 bg=0.00
DNA replication initiation GO:0006270 p=2.2E−03 n=4 fg=0.03 bg=0.00
sperm axoneme assembly GO:0007288 p=2.9E−03 n=3 fg=0.02 bg=0.00
telomere maintenance GO:0000723 p=3.8E−03 n=7 fg=0.06 bg=0.02
serine family amino acid biosynthetic pr... GO:0009070 p=4.5E−03 n=3 fg=0.02 bg=0.00
translesion synthesis GO:0019985 p=5.0E−03 n=4 fg=0.03 bg=0.01
sno(s)RNA metabolic process GO:0016074 p=6.1E−03 n=2 fg=0.02 bg=0.00
D−amino acid metabolic process GO:0046416 p=6.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of protein localizat... GO:1904781 p=6.1E−03 n=2 fg=0.02 bg=0.00
protein O−linked mannosylation GO:0035269 p=6.1E−03 n=2 fg=0.02 bg=0.00
retinal cone cell development GO:0046549 p=6.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of ubiquitin protein... GO:1904667 p=6.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of viral transcripti... GO:0050434 p=6.5E−03 n=3 fg=0.02 bg=0.00
cellular macromolecule catabolic process GO:0044265 p=6.9E−03 n=22 fg=0.18 bg=0.10
negative regulation of cell division GO:0051782 p=8.9E−03 n=3 fg=0.02 bg=0.00
SRP−dependent cotranslational protein ta... GO:0006614 p=1.1E−02 n=5 fg=0.04 bg=0.01
mRNA polyadenylation GO:0006378 p=1.2E−02 n=4 fg=0.03 bg=0.01
RNA polyadenylation GO:0043631 p=1.2E−02 n=4 fg=0.03 bg=0.01
L−serine biosynthetic process GO:0006564 p=1.2E−02 n=2 fg=0.02 bg=0.00
medium−term memory GO:0072375 p=1.2E−02 n=2 fg=0.02 bg=0.00
regulation of defecation GO:2000292 p=1.2E−02 n=2 fg=0.02 bg=0.00
regulation of protein localization to ce... GO:1904776 p=1.2E−02 n=2 fg=0.02 bg=0.00
telomere maintenance via semi−conservati... GO:0032201 p=1.2E−02 n=3 fg=0.02 bg=0.00
cotranslational protein targeting to mem... GO:0006613 p=1.2E−02 n=5 fg=0.04 bg=0.01
G1/S transition of mitotic cell cycle GO:0000082 p=1.5E−02 n=8 fg=0.06 bg=0.03
negative regulation of proteasomal ubiqu... GO:0032435 p=1.5E−02 n=3 fg=0.02 bg=0.00
negative regulation of cellular protein ... GO:1903363 p=1.9E−02 n=4 fg=0.03 bg=0.01
regulation of hydrogen peroxide−induced ... GO:1903205 p=1.9E−02 n=2 fg=0.02 bg=0.00
negative regulation of hydrogen peroxide... GO:1903206 p=1.9E−02 n=2 fg=0.02 bg=0.00
pole cell development GO:0007277 p=1.9E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=124/444 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
NAD(P)+ transhydrogenase activity GO:0008746 p=2.3E−03 n=2 fg=0.02 bg=0.00
polynucleotide adenylyltransferase activ... GO:0004652 p=3.4E−03 n=3 fg=0.03 bg=0.00
racemase and epimerase activity GO:0016854 p=6.8E−03 n=2 fg=0.02 bg=0.00
neurotransmitter binding GO:0042165 p=7.6E−03 n=3 fg=0.03 bg=0.00
modification−dependent protein binding GO:0140030 p=1.1E−02 n=5 fg=0.04 bg=0.01
ubiquitin−protein transferase regulator ... GO:0055106 p=1.3E−02 n=2 fg=0.02 bg=0.00
syntaxin−1 binding GO:0017075 p=1.3E−02 n=2 fg=0.02 bg=0.00
xylosyltransferase activity GO:0042285 p=1.3E−02 n=2 fg=0.02 bg=0.00
UDP−xylosyltransferase activity GO:0035252 p=1.3E−02 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016616 p=1.4E−02 n=4 fg=0.03 bg=0.01
JUN kinase binding GO:0008432 p=2.1E−02 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on CH−OH... GO:0016614 p=2.6E−02 n=4 fg=0.03 bg=0.01
DNA−directed DNA polymerase activity GO:0003887 p=2.7E−02 n=3 fg=0.03 bg=0.01
DNA polymerase activity GO:0034061 p=2.7E−02 n=3 fg=0.03 bg=0.01
histone binding GO:0042393 p=4.2E−02 n=5 fg=0.04 bg=0.02
telomerase RNA binding GO:0070034 p=4.2E−02 n=2 fg=0.02 bg=0.00
MAP kinase kinase kinase activity GO:0004709 p=4.2E−02 n=2 fg=0.02 bg=0.00
adiponectin binding GO:0055100 p=4.9E−02 n=1 fg=0.01 bg=0.00
nitrite reductase (NO−forming) activity GO:0050421 p=4.9E−02 n=1 fg=0.01 bg=0.00
amino−acid racemase activity GO:0047661 p=4.9E−02 n=1 fg=0.01 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=4.9E−02 n=1 fg=0.01 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=4.9E−02 n=1 fg=0.01 bg=0.00
RNA uridylyltransferase activity GO:0050265 p=4.9E−02 n=1 fg=0.01 bg=0.00
amine transmembrane transporter activity GO:0005275 p=4.9E−02 n=1 fg=0.01 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=4.9E−02 n=1 fg=0.01 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=4.9E−02 n=1 fg=0.01 bg=0.00
3−hydroxyacyl−CoA dehydrogenase activity GO:0003857 p=4.9E−02 n=1 fg=0.01 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=4.9E−02 n=1 fg=0.01 bg=0.00
histone serine kinase activity GO:0035174 p=4.9E−02 n=1 fg=0.01 bg=0.00
histone kinase activity (H3−S10 specific... GO:0035175 p=4.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=115/444 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
nuclear replisome GO:0043601 p=4.7E−04 n=4 fg=0.03 bg=0.00
alpha DNA polymerase:primase complex GO:0005658 p=1.2E−02 n=2 fg=0.02 bg=0.00
centriole GO:0005814 p=1.3E−02 n=5 fg=0.04 bg=0.01
DNA polymerase complex GO:0042575 p=1.6E−02 n=3 fg=0.02 bg=0.00
nucleoplasm GO:0005654 p=2.4E−02 n=47 fg=0.37 bg=0.29
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=2.9E−02 n=2 fg=0.02 bg=0.00
chaperone complex GO:0101031 p=3.9E−02 n=2 fg=0.02 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0016471 p=3.9E−02 n=2 fg=0.02 bg=0.00
axon hillock GO:0043203 p=4.7E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=4.7E−02 n=1 fg=0.01 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=4.7E−02 n=1 fg=0.01 bg=0.00
BAT3 complex GO:0071818 p=4.7E−02 n=1 fg=0.01 bg=0.00
CCAAT−binding factor complex GO:0016602 p=4.7E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=4.7E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=4.7E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=4.7E−02 n=1 fg=0.01 bg=0.00
ER membrane insertion complex GO:0072379 p=4.7E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=4.7E−02 n=1 fg=0.01 bg=0.00
chromosome passenger complex GO:0032133 p=4.7E−02 n=1 fg=0.01 bg=0.00
endocytic vesicle lumen GO:0071682 p=4.7E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=4.7E−02 n=1 fg=0.01 bg=0.00
pigment granule membrane GO:0090741 p=4.7E−02 n=1 fg=0.01 bg=0.00
meiotic spindle midzone GO:1990385 p=4.7E−02 n=1 fg=0.01 bg=0.00
FACT complex GO:0035101 p=4.7E−02 n=1 fg=0.01 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=5.0E−02 n=2 fg=0.02 bg=0.00
intracellular protein−containing complex GO:0140535 p=6.3E−02 n=16 fg=0.13 bg=0.08
proton−transporting two−sector ATPase co... GO:0016469 p=7.6E−02 n=2 fg=0.02 bg=0.00
ubiquitin ligase complex GO:0000151 p=9.0E−02 n=7 fg=0.06 bg=0.03
pronucleus GO:0045120 p=9.0E−02 n=2 fg=0.02 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=9.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=126/444 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction