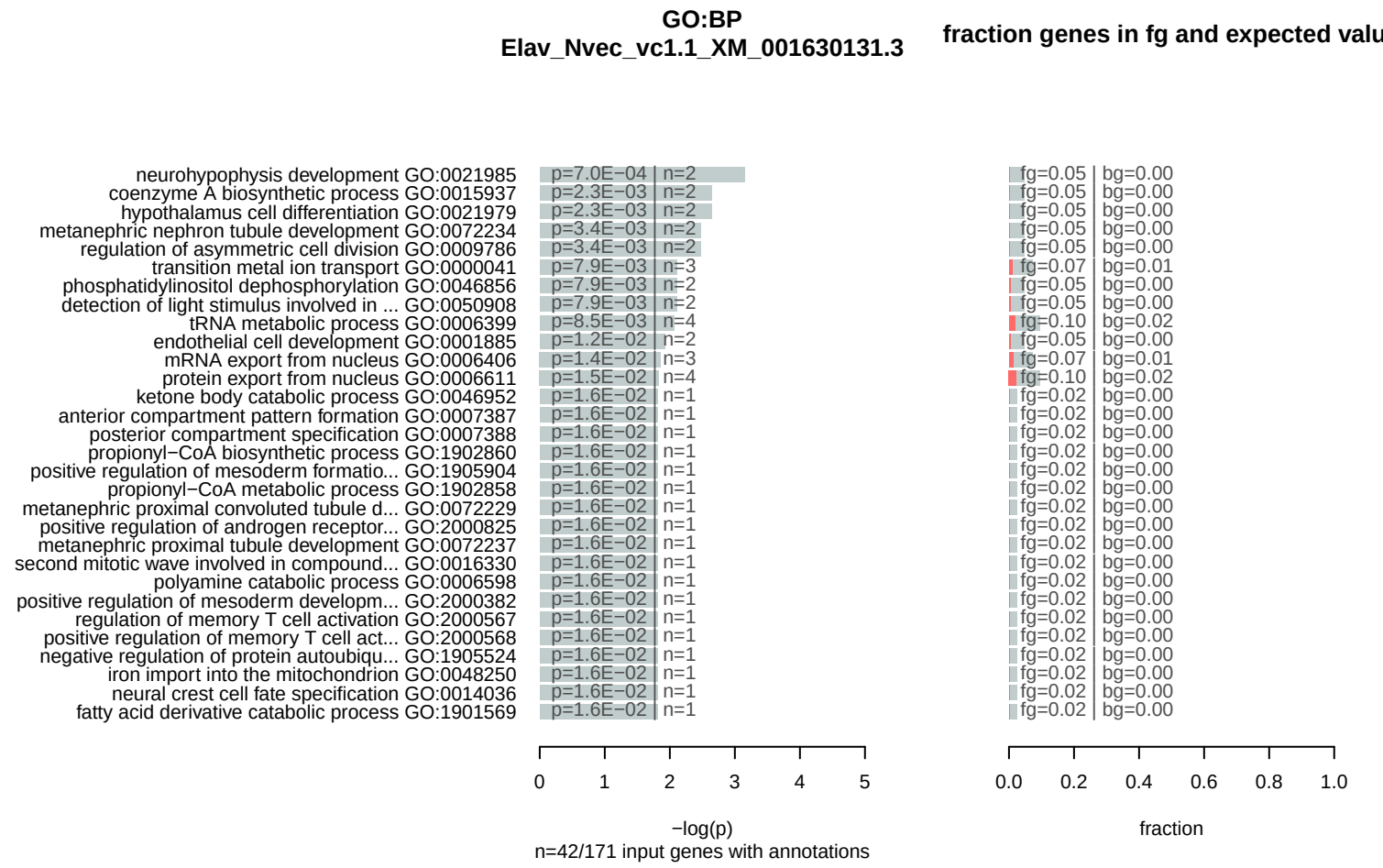
GO:BP
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fraction genes in fg and expected valu
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coenzyme A biosynthetic process GO:0015937 p=2.3E−03 n=2 fg=0.05 bg=0.00
hypothalamus cell differentiation GO:0021979 p=2.3E−03 n=2 fg=0.05 bg=0.00
metanephric nephron tubule development GO:0072234 p=3.4E−03 n=2 fg=0.05 bg=0.00
regulation of asymmetric cell division GO:0009786 p=3.4E−03 n=2 fg=0.05 bg=0.00
transition metal ion transport GO:0000041 p=7.9E−03 n=3 fg=0.07 bg=0.01
phosphatidylinositol dephosphorylation GO:0046856 p=7.9E−03 n=2 fg=0.05 bg=0.00
detection of light stimulus involved in ... GO:0050908 p=7.9E−03 n=2 fg=0.05 bg=0.00
tRNA metabolic process GO:0006399 p=8.5E−03 n=4 fg=0.10 bg=0.02
endothelial cell development GO:0001885 p=1.2E−02 n=2 fg=0.05 bg=0.00
mRNA export from nucleus GO:0006406 p=1.4E−02 n=3 fg=0.07 bg=0.01
protein export from nucleus GO:0006611 p=1.5E−02 n=4 fg=0.10 bg=0.02
ketone body catabolic process GO:0046952 p=1.6E−02 n=1 fg=0.02 bg=0.00
anterior compartment pattern formation GO:0007387 p=1.6E−02 n=1 fg=0.02 bg=0.00
posterior compartment specification GO:0007388 p=1.6E−02 n=1 fg=0.02 bg=0.00
propionyl−CoA biosynthetic process GO:1902860 p=1.6E−02 n=1 fg=0.02 bg=0.00
positive regulation of mesoderm formatio... GO:1905904 p=1.6E−02 n=1 fg=0.02 bg=0.00
propionyl−CoA metabolic process GO:1902858 p=1.6E−02 n=1 fg=0.02 bg=0.00
metanephric proximal convoluted tubule d... GO:0072229 p=1.6E−02 n=1 fg=0.02 bg=0.00
positive regulation of androgen receptor... GO:2000825 p=1.6E−02 n=1 fg=0.02 bg=0.00
metanephric proximal tubule development GO:0072237 p=1.6E−02 n=1 fg=0.02 bg=0.00
second mitotic wave involved in compound... GO:0016330 p=1.6E−02 n=1 fg=0.02 bg=0.00
polyamine catabolic process GO:0006598 p=1.6E−02 n=1 fg=0.02 bg=0.00
positive regulation of mesoderm developm... GO:2000382 p=1.6E−02 n=1 fg=0.02 bg=0.00
regulation of memory T cell activation GO:2000567 p=1.6E−02 n=1 fg=0.02 bg=0.00
positive regulation of memory T cell act... GO:2000568 p=1.6E−02 n=1 fg=0.02 bg=0.00
negative regulation of protein autoubiqu... GO:1905524 p=1.6E−02 n=1 fg=0.02 bg=0.00
iron import into the mitochondrion GO:0048250 p=1.6E−02 n=1 fg=0.02 bg=0.00
neural crest cell fate specification GO:0014036 p=1.6E−02 n=1 fg=0.02 bg=0.00
fatty acid derivative catabolic process GO:1901569 p=1.6E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=42/171 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001630131.3
fraction genes in fg and expected valu
phosphatidylinositol−3−phosphatase activ... GO:0004438 p=2.3E−03 n=2 fg=0.05 bg=0.00
transition metal ion transmembrane trans... GO:0046915 p=8.0E−03 n=2 fg=0.05 bg=0.00
calcium channel activity GO:0005262 p=1.2E−02 n=3 fg=0.08 bg=0.01
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=1.6E−02 n=1 fg=0.03 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=1.6E−02 n=1 fg=0.03 bg=0.00
MHC class Ib protein binding, via antige... GO:0023030 p=1.6E−02 n=1 fg=0.03 bg=0.00
C−acyltransferase activity GO:0016408 p=1.6E−02 n=1 fg=0.03 bg=0.00
C−acetyltransferase activity GO:0016453 p=1.6E−02 n=1 fg=0.03 bg=0.00
light−activated ion channel activity GO:0010461 p=1.6E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.6E−02 n=1 fg=0.03 bg=0.00
polyamine oxidase activity GO:0046592 p=1.6E−02 n=1 fg=0.03 bg=0.00
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MHC class Ib protein complex binding GO:0023025 p=1.6E−02 n=1 fg=0.03 bg=0.00
MHC class Ib protein binding GO:0023029 p=1.6E−02 n=1 fg=0.03 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=1.6E−02 n=1 fg=0.03 bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988 p=1.6E−02 n=1 fg=0.03 bg=0.00
cation channel activity GO:0005261 p=2.0E−02 n=4 fg=0.11 bg=0.03
calcium ion transmembrane transporter ac... GO:0015085 p=2.3E−02 n=3 fg=0.08 bg=0.02
metal ion transmembrane transporter acti... GO:0046873 p=2.3E−02 n=6 fg=0.16 bg=0.04
transcription coactivator activity GO:0003713 p=3.0E−02 n=4 fg=0.11 bg=0.03
ligase activity, forming carbon−carbon b... GO:0016885 p=3.1E−02 n=1 fg=0.03 bg=0.00
isopeptidase activity GO:0070122 p=3.1E−02 n=1 fg=0.03 bg=0.00
lysine−acetylated histone binding GO:0070577 p=3.1E−02 n=1 fg=0.03 bg=0.00
phospholipase A1 activity GO:0008970 p=3.1E−02 n=1 fg=0.03 bg=0.00
deSUMOylase activity GO:0016929 p=3.1E−02 n=1 fg=0.03 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=3.1E−02 n=1 fg=0.03 bg=0.00
acetylation−dependent protein binding GO:0140033 p=3.1E−02 n=1 fg=0.03 bg=0.00
dephospho−CoA kinase activity GO:0004140 p=3.1E−02 n=1 fg=0.03 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=3.1E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=3.1E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=37/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001630131.3
fraction genes in fg and expected valu
nuclear pore GO:0005643 p=3.8E−03 n=3 fg=0.07 bg=0.01
motile cilium GO:0031514 p=8.2E−03 n=4 fg=0.10 bg=0.02
organellar large ribosomal subunit GO:0000315 p=1.1E−02 n=2 fg=0.05 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=1.1E−02 n=2 fg=0.05 bg=0.00
sperm flagellum GO:0036126 p=1.3E−02 n=3 fg=0.07 bg=0.01
transcription regulator complex GO:0005667 p=1.5E−02 n=5 fg=0.12 bg=0.04
rhabdomere membrane GO:0033583 p=1.5E−02 n=1 fg=0.03 bg=0.00
proteasome core complex, beta−subunit co... GO:0019774 p=1.5E−02 n=1 fg=0.03 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=1.5E−02 n=1 fg=0.03 bg=0.00
sperm cytoplasmic droplet GO:0097598 p=1.5E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus GO:0035996 p=1.5E−02 n=1 fg=0.03 bg=0.00
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nuclear pore cytoplasmic filaments GO:0044614 p=1.5E−02 n=1 fg=0.03 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=1.5E−02 n=1 fg=0.03 bg=0.00
9+2 motile cilium GO:0097729 p=1.5E−02 n=3 fg=0.07 bg=0.01
RNA polymerase III transcription regulat... GO:0090576 p=2.9E−02 n=1 fg=0.03 bg=0.00
Seh1−associated complex GO:0035859 p=2.9E−02 n=1 fg=0.03 bg=0.00
growth cone filopodium GO:1990812 p=2.9E−02 n=1 fg=0.03 bg=0.00
GATOR2 complex GO:0061700 p=2.9E−02 n=1 fg=0.03 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=2.9E−02 n=1 fg=0.03 bg=0.00
spermatoproteasome complex GO:1990111 p=2.9E−02 n=1 fg=0.03 bg=0.00
organellar ribosome GO:0000313 p=3.1E−02 n=2 fg=0.05 bg=0.01
mitochondrial ribosome GO:0005761 p=3.1E−02 n=2 fg=0.05 bg=0.01
transmembrane transporter complex GO:1902495 p=3.6E−02 n=3 fg=0.07 bg=0.02
actin−based cell projection GO:0098858 p=3.8E−02 n=3 fg=0.07 bg=0.02
outer dynein arm GO:0036157 p=4.4E−02 n=1 fg=0.03 bg=0.00
Nebenkern GO:0016006 p=4.4E−02 n=1 fg=0.03 bg=0.00
mitochondrial derivative GO:0016007 p=4.4E−02 n=1 fg=0.03 bg=0.00
transporter complex GO:1990351 p=4.4E−02 n=3 fg=0.07 bg=0.02
cation channel complex GO:0034703 p=5.6E−02 n=2 fg=0.05 bg=0.01
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−log(p)
n=40/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction