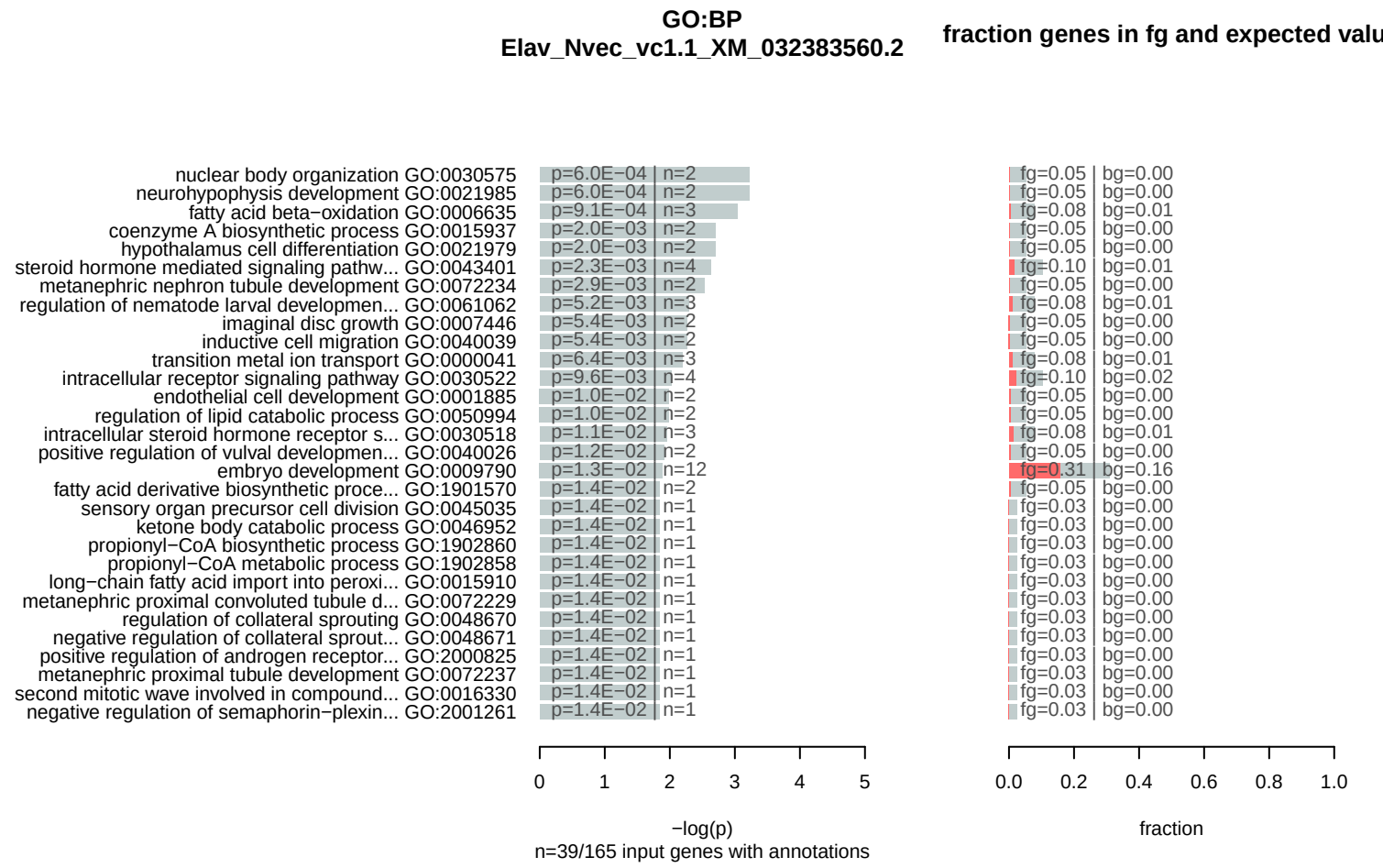
GO:BP
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fraction genes in fg and expected valu
nuclear body organization GO:0030575 p=6.0E−04 n=2 fg=0.05 bg=0.00
neurohypophysis development GO:0021985 p=6.0E−04 n=2 fg=0.05 bg=0.00
fatty acid beta−oxidation GO:0006635 p=9.1E−04 n=3 fg=0.08 bg=0.01
coenzyme A biosynthetic process GO:0015937 p=2.0E−03 n=2 fg=0.05 bg=0.00
hypothalamus cell differentiation GO:0021979 p=2.0E−03 n=2 fg=0.05 bg=0.00
steroid hormone mediated signaling pathw... GO:0043401 p=2.3E−03 n=4 fg=0.10 bg=0.01
metanephric nephron tubule development GO:0072234 p=2.9E−03 n=2 fg=0.05 bg=0.00
regulation of nematode larval developmen... GO:0061062 p=5.2E−03 n=3 fg=0.08 bg=0.01
imaginal disc growth GO:0007446 p=5.4E−03 n=2 fg=0.05 bg=0.00
inductive cell migration GO:0040039 p=5.4E−03 n=2 fg=0.05 bg=0.00
transition metal ion transport GO:0000041 p=6.4E−03 n=3 fg=0.08 bg=0.01
intracellular receptor signaling pathway GO:0030522 p=9.6E−03 n=4 fg=0.10 bg=0.02
endothelial cell development GO:0001885 p=1.0E−02 n=2 fg=0.05 bg=0.00
regulation of lipid catabolic process GO:0050994 p=1.0E−02 n=2 fg=0.05 bg=0.00
intracellular steroid hormone receptor s... GO:0030518 p=1.1E−02 n=3 fg=0.08 bg=0.01
positive regulation of vulval developmen... GO:0040026 p=1.2E−02 n=2 fg=0.05 bg=0.00
embryo development GO:0009790 p=1.3E−02 n=12 fg=0.31 bg=0.16
fatty acid derivative biosynthetic proce... GO:1901570 p=1.4E−02 n=2 fg=0.05 bg=0.00
sensory organ precursor cell division GO:0045035 p=1.4E−02 n=1 fg=0.03 bg=0.00
ketone body catabolic process GO:0046952 p=1.4E−02 n=1 fg=0.03 bg=0.00
propionyl−CoA biosynthetic process GO:1902860 p=1.4E−02 n=1 fg=0.03 bg=0.00
propionyl−CoA metabolic process GO:1902858 p=1.4E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acid import into peroxi... GO:0015910 p=1.4E−02 n=1 fg=0.03 bg=0.00
metanephric proximal convoluted tubule d... GO:0072229 p=1.4E−02 n=1 fg=0.03 bg=0.00
regulation of collateral sprouting GO:0048670 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of collateral sprout... GO:0048671 p=1.4E−02 n=1 fg=0.03 bg=0.00
positive regulation of androgen receptor... GO:2000825 p=1.4E−02 n=1 fg=0.03 bg=0.00
metanephric proximal tubule development GO:0072237 p=1.4E−02 n=1 fg=0.03 bg=0.00
second mitotic wave involved in compound... GO:0016330 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of semaphorin−plexin... GO:2001261 p=1.4E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=39/165 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032383560.2
fraction genes in fg and expected valu
light−activated ion channel activity GO:0010461 p=1.5E−02 n=1 fg=0.03 bg=0.00
C−acyltransferase activity GO:0016408 p=1.5E−02 n=1 fg=0.03 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=1.5E−02 n=1 fg=0.03 bg=0.00
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C−acetyltransferase activity GO:0016453 p=1.5E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.5E−02 n=1 fg=0.03 bg=0.00
polyamine oxidase activity GO:0046592 p=1.5E−02 n=1 fg=0.03 bg=0.00
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=1.5E−02 n=1 fg=0.03 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=1.5E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acid transporter activi... GO:0005324 p=1.5E−02 n=1 fg=0.03 bg=0.00
carbon−carbon lyase activity GO:0016830 p=2.2E−02 n=2 fg=0.06 bg=0.01
transcription coactivator activity GO:0003713 p=2.5E−02 n=4 fg=0.11 bg=0.03
primary active transmembrane transporter... GO:0015399 p=2.6E−02 n=3 fg=0.09 bg=0.02
acetyltransferase activity GO:0016407 p=2.8E−02 n=2 fg=0.06 bg=0.01
N−acetylneuraminate lyase activity GO:0008747 p=2.9E−02 n=1 fg=0.03 bg=0.00
deSUMOylase activity GO:0016929 p=2.9E−02 n=1 fg=0.03 bg=0.00
isopeptidase activity GO:0070122 p=2.9E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=2.9E−02 n=1 fg=0.03 bg=0.00
lysine−acetylated histone binding GO:0070577 p=2.9E−02 n=1 fg=0.03 bg=0.00
ligase activity, forming carbon−carbon b... GO:0016885 p=2.9E−02 n=1 fg=0.03 bg=0.00
acetylation−dependent protein binding GO:0140033 p=2.9E−02 n=1 fg=0.03 bg=0.00
dephospho−CoA kinase activity GO:0004140 p=2.9E−02 n=1 fg=0.03 bg=0.00
transferrin receptor binding GO:1990459 p=4.4E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016647 p=4.4E−02 n=1 fg=0.03 bg=0.00
LIM domain binding GO:0030274 p=4.4E−02 n=1 fg=0.03 bg=0.00
oxo−acid−lyase activity GO:0016833 p=4.4E−02 n=1 fg=0.03 bg=0.00
ubiquitin−like protein binding GO:0032182 p=4.4E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=5.1E−02 n=5 fg=0.14 bg=0.06
minor groove of adenine−thymine−rich DNA... GO:0003680 p=5.8E−02 n=1 fg=0.03 bg=0.00
SUMO binding GO:0032183 p=5.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=35/165 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032383560.2
fraction genes in fg and expected valu
peroxisome GO:0005777 p=9.8E−03 n=3 fg=0.08 bg=0.01
cyclin E1−CDK2 complex GO:0097134 p=1.3E−02 n=1 fg=0.03 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=1.3E−02 n=1 fg=0.03 bg=0.00
rhabdomere membrane GO:0033583 p=1.3E−02 n=1 fg=0.03 bg=0.00
ACF complex GO:0016590 p=1.3E−02 n=1 fg=0.03 bg=0.00
proteasome core complex, beta−subunit co... GO:0019774 p=1.3E−02 n=1 fg=0.03 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=1.3E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus GO:0035996 p=1.3E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=1.3E−02 n=1 fg=0.03 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=1.3E−02 n=1 fg=0.03 bg=0.00
Seh1−associated complex GO:0035859 p=2.6E−02 n=1 fg=0.03 bg=0.00
RSF complex GO:0031213 p=2.6E−02 n=1 fg=0.03 bg=0.00
GATOR2 complex GO:0061700 p=2.6E−02 n=1 fg=0.03 bg=0.00
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microvillus GO:0005902 p=3.1E−02 n=2 fg=0.06 bg=0.01
nuclear pore GO:0005643 p=3.4E−02 n=2 fg=0.06 bg=0.01
motile cilium GO:0031514 p=3.5E−02 n=3 fg=0.08 bg=0.02
vacuolar proton−transporting V−type ATPa... GO:0000221 p=4.0E−02 n=1 fg=0.03 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=4.0E−02 n=1 fg=0.03 bg=0.00
CHRAC GO:0008623 p=4.0E−02 n=1 fg=0.03 bg=0.00
NURF complex GO:0016589 p=4.0E−02 n=1 fg=0.03 bg=0.00
Nebenkern GO:0016006 p=4.0E−02 n=1 fg=0.03 bg=0.00
mitochondrial derivative GO:0016007 p=4.0E−02 n=1 fg=0.03 bg=0.00
mitochondrial protein−containing complex GO:0098798 p=5.0E−02 n=3 fg=0.08 bg=0.02
integral component of peroxisomal membra... GO:0005779 p=5.2E−02 n=1 fg=0.03 bg=0.00
inaD signaling complex GO:0016027 p=5.2E−02 n=1 fg=0.03 bg=0.00
Cul4A−RING E3 ubiquitin ligase complex GO:0031464 p=5.2E−02 n=1 fg=0.03 bg=0.00
proteasome core complex GO:0005839 p=5.2E−02 n=1 fg=0.03 bg=0.00
intrinsic component of peroxisomal membr... GO:0031231 p=5.2E−02 n=1 fg=0.03 bg=0.00
mitochondrial inner membrane GO:0005743 p=5.6E−02 n=4 fg=0.11 bg=0.04
0 1 2 3 4 5
−log(p)
n=36/165 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction