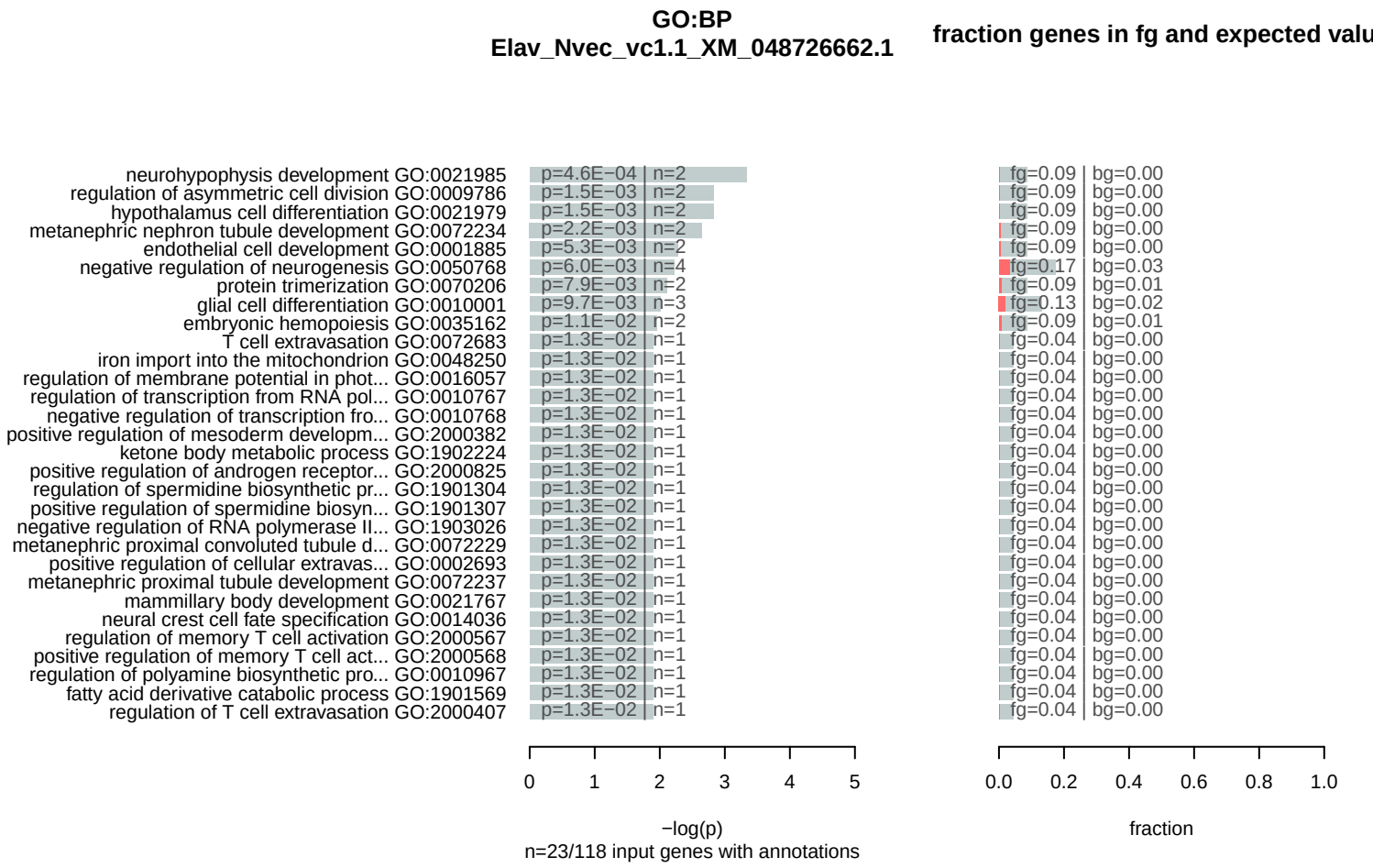
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fraction genes in fg and expected valu
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regulation of asymmetric cell division GO:0009786 p=1.5E−03 n=2 fg=0.09 bg=0.00
hypothalamus cell differentiation GO:0021979 p=1.5E−03 n=2 fg=0.09 bg=0.00
metanephric nephron tubule development GO:0072234 p=2.2E−03 n=2 fg=0.09 bg=0.00
endothelial cell development GO:0001885 p=5.3E−03 n=2 fg=0.09 bg=0.00
negative regulation of neurogenesis GO:0050768 p=6.0E−03 n=4 fg=0.17 bg=0.03
protein trimerization GO:0070206 p=7.9E−03 n=2 fg=0.09 bg=0.01
glial cell differentiation GO:0010001 p=9.7E−03 n=3 fg=0.13 bg=0.02
embryonic hemopoiesis GO:0035162 p=1.1E−02 n=2 fg=0.09 bg=0.01
T cell extravasation GO:0072683 p=1.3E−02 n=1 fg=0.04 bg=0.00
iron import into the mitochondrion GO:0048250 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of membrane potential in phot... GO:0016057 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of transcription from RNA pol... GO:0010767 p=1.3E−02 n=1 fg=0.04 bg=0.00
negative regulation of transcription fro... GO:0010768 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of mesoderm developm... GO:2000382 p=1.3E−02 n=1 fg=0.04 bg=0.00
ketone body metabolic process GO:1902224 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of androgen receptor... GO:2000825 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of spermidine biosynthetic pr... GO:1901304 p=1.3E−02 n=1 fg=0.04 bg=0.00
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negative regulation of RNA polymerase II... GO:1903026 p=1.3E−02 n=1 fg=0.04 bg=0.00
metanephric proximal convoluted tubule d... GO:0072229 p=1.3E−02 n=1 fg=0.04 bg=0.00
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neural crest cell fate specification GO:0014036 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of memory T cell activation GO:2000567 p=1.3E−02 n=1 fg=0.04 bg=0.00
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regulation of polyamine biosynthetic pro... GO:0010967 p=1.3E−02 n=1 fg=0.04 bg=0.00
fatty acid derivative catabolic process GO:1901569 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of T cell extravasation GO:2000407 p=1.3E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=23/118 input genes with annotations
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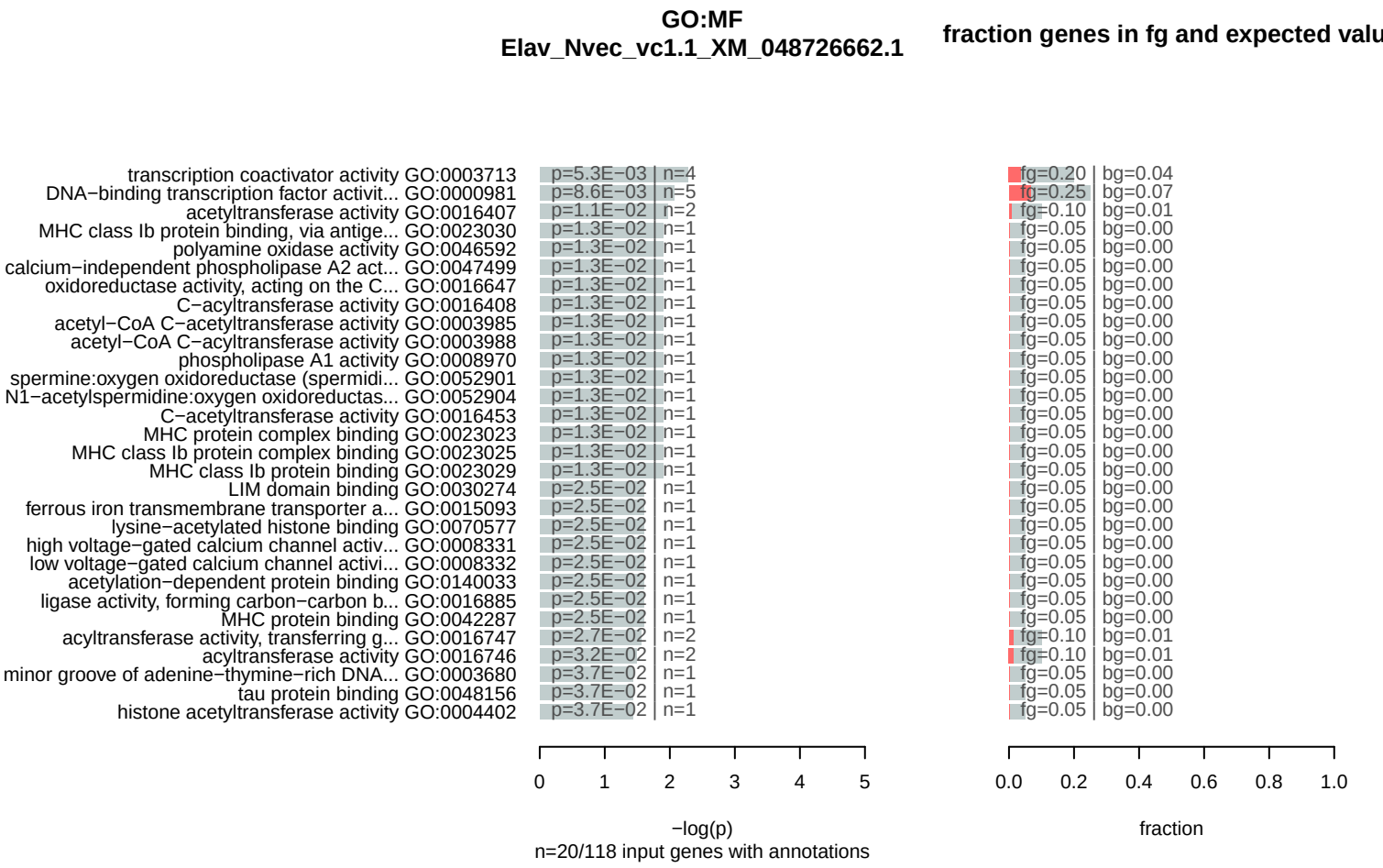
fraction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DNA−binding transcription factor activit... GO:0000981 p=8.6E−03 n=5 fg=0.25 bg=0.07
acetyltransferase activity GO:0016407 p=1.1E−02 n=2 fg=0.10 bg=0.01
MHC class Ib protein binding, via antige... GO:0023030 p=1.3E−02 n=1 fg=0.05 bg=0.00
polyamine oxidase activity GO:0046592 p=1.3E−02 n=1 fg=0.05 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=1.3E−02 n=1 fg=0.05 bg=0.00
oxidoreductase activity, acting on the C... GO:0016647 p=1.3E−02 n=1 fg=0.05 bg=0.00
C−acyltransferase activity GO:0016408 p=1.3E−02 n=1 fg=0.05 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=1.3E−02 n=1 fg=0.05 bg=0.00
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phospholipase A1 activity GO:0008970 p=1.3E−02 n=1 fg=0.05 bg=0.00
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=1.3E−02 n=1 fg=0.05 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=1.3E−02 n=1 fg=0.05 bg=0.00
C−acetyltransferase activity GO:0016453 p=1.3E−02 n=1 fg=0.05 bg=0.00
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LIM domain binding GO:0030274 p=2.5E−02 n=1 fg=0.05 bg=0.00
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lysine−acetylated histone binding GO:0070577 p=2.5E−02 n=1 fg=0.05 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=2.5E−02 n=1 fg=0.05 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=2.5E−02 n=1 fg=0.05 bg=0.00
acetylation−dependent protein binding GO:0140033 p=2.5E−02 n=1 fg=0.05 bg=0.00
ligase activity, forming carbon−carbon b... GO:0016885 p=2.5E−02 n=1 fg=0.05 bg=0.00
MHC protein binding GO:0042287 p=2.5E−02 n=1 fg=0.05 bg=0.00
acyltransferase activity, transferring g... GO:0016747 p=2.7E−02 n=2 fg=0.10 bg=0.01
acyltransferase activity GO:0016746 p=3.2E−02 n=2 fg=0.10 bg=0.01
minor groove of adenine−thymine−rich DNA... GO:0003680 p=3.7E−02 n=1 fg=0.05 bg=0.00
tau protein binding GO:0048156 p=3.7E−02 n=1 fg=0.05 bg=0.00
histone acetyltransferase activity GO:0004402 p=3.7E−02 n=1 fg=0.05 bg=0.00
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−log(p)
n=20/118 input genes with annotations
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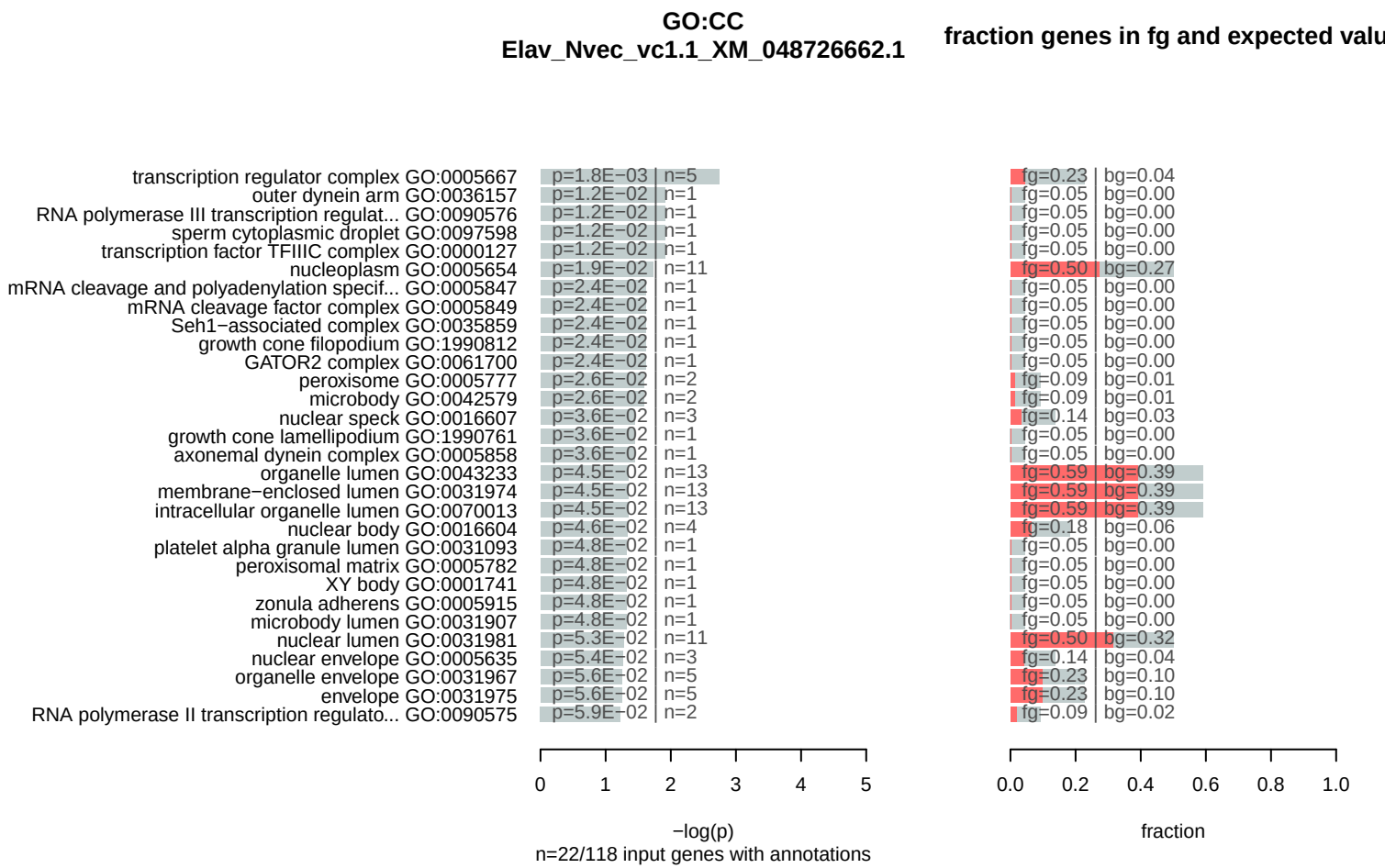
fraction


GO:CC
Elav_Nvec_vc1.1_XM_048726662.1
fraction genes in fg and expected valu
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outer dynein arm GO:0036157 p=1.2E−02 n=1 fg=0.05 bg=0.00
RNA polymerase III transcription regulat... GO:0090576 p=1.2E−02 n=1 fg=0.05 bg=0.00
sperm cytoplasmic droplet GO:0097598 p=1.2E−02 n=1 fg=0.05 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=1.2E−02 n=1 fg=0.05 bg=0.00
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Seh1−associated complex GO:0035859 p=2.4E−02 n=1 fg=0.05 bg=0.00
growth cone filopodium GO:1990812 p=2.4E−02 n=1 fg=0.05 bg=0.00
GATOR2 complex GO:0061700 p=2.4E−02 n=1 fg=0.05 bg=0.00
peroxisome GO:0005777 p=2.6E−02 n=2 fg=0.09 bg=0.01
microbody GO:0042579 p=2.6E−02 n=2 fg=0.09 bg=0.01
nuclear speck GO:0016607 p=3.6E−02 n=3 fg=0.14 bg=0.03
growth cone lamellipodium GO:1990761 p=3.6E−02 n=1 fg=0.05 bg=0.00
axonemal dynein complex GO:0005858 p=3.6E−02 n=1 fg=0.05 bg=0.00
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membrane−enclosed lumen GO:0031974 p=4.5E−02 n=13 fg=0.59 bg=0.39
intracellular organelle lumen GO:0070013 p=4.5E−02 n=13 fg=0.59 bg=0.39
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platelet alpha granule lumen GO:0031093 p=4.8E−02 n=1 fg=0.05 bg=0.00
peroxisomal matrix GO:0005782 p=4.8E−02 n=1 fg=0.05 bg=0.00
XY body GO:0001741 p=4.8E−02 n=1 fg=0.05 bg=0.00
zonula adherens GO:0005915 p=4.8E−02 n=1 fg=0.05 bg=0.00
microbody lumen GO:0031907 p=4.8E−02 n=1 fg=0.05 bg=0.00
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nuclear envelope GO:0005635 p=5.4E−02 n=3 fg=0.14 bg=0.04
organelle envelope GO:0031967 p=5.6E−02 n=5 fg=0.23 bg=0.10
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RNA polymerase II transcription regulato... GO:0090575 p=5.9E−02 n=2 fg=0.09 bg=0.02
0 1 2 3 4 5
−log(p)
n=22/118 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction