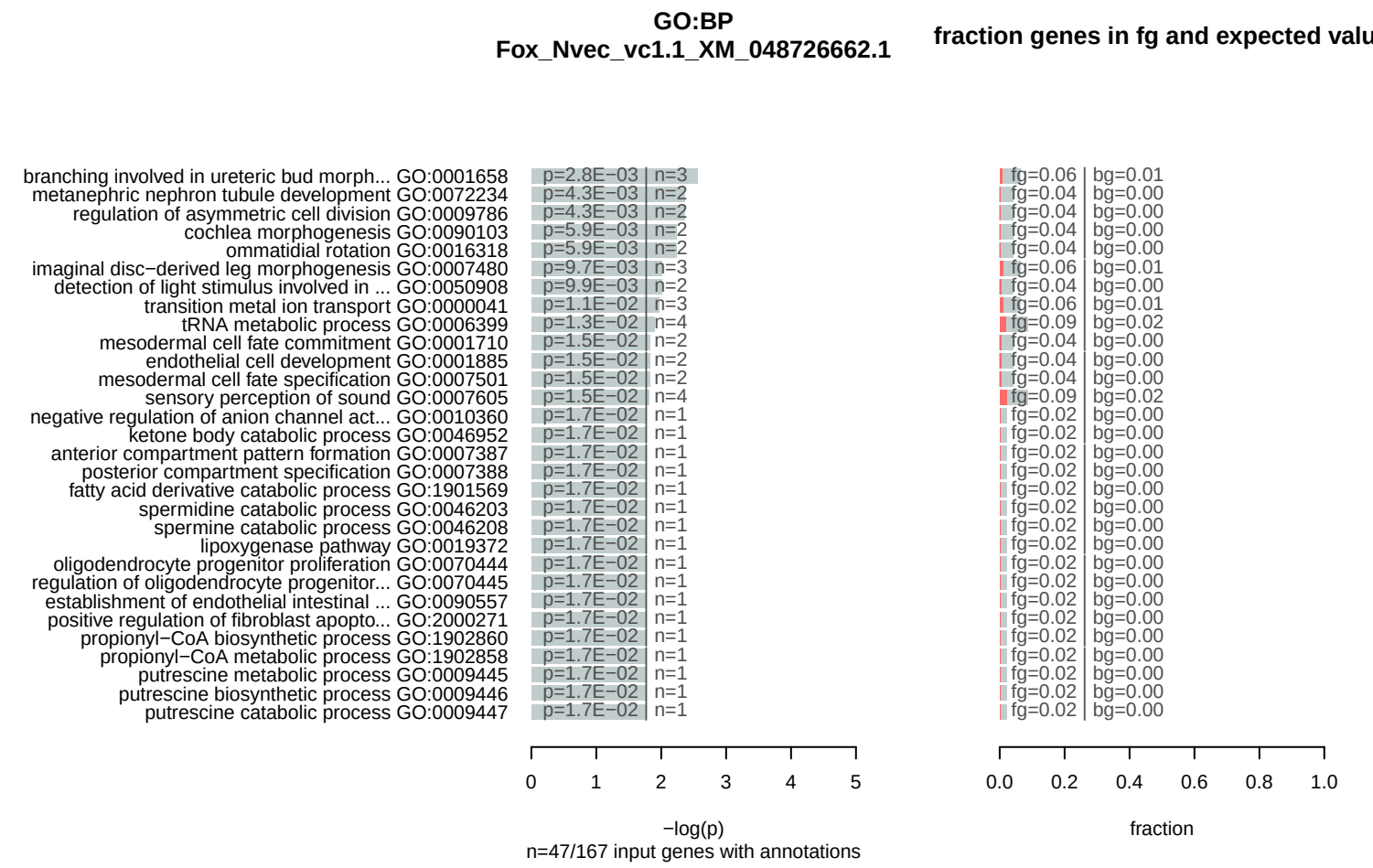
GO:BP
Fox_Nvec_vc1.1_XM_048726662.1
fraction genes in fg and expected valu
branching involved in ureteric bud morph... GO:0001658 p=2.8E−03 n=3 fg=0.06 bg=0.01
metanephric nephron tubule development GO:0072234 p=4.3E−03 n=2 fg=0.04 bg=0.00
regulation of asymmetric cell division GO:0009786 p=4.3E−03 n=2 fg=0.04 bg=0.00
cochlea morphogenesis GO:0090103 p=5.9E−03 n=2 fg=0.04 bg=0.00
ommatidial rotation GO:0016318 p=5.9E−03 n=2 fg=0.04 bg=0.00
imaginal disc−derived leg morphogenesis GO:0007480 p=9.7E−03 n=3 fg=0.06 bg=0.01
detection of light stimulus involved in ... GO:0050908 p=9.9E−03 n=2 fg=0.04 bg=0.00
transition metal ion transport GO:0000041 p=1.1E−02 n=3 fg=0.06 bg=0.01
tRNA metabolic process GO:0006399 p=1.3E−02 n=4 fg=0.09 bg=0.02
mesodermal cell fate commitment GO:0001710 p=1.5E−02 n=2 fg=0.04 bg=0.00
endothelial cell development GO:0001885 p=1.5E−02 n=2 fg=0.04 bg=0.00
mesodermal cell fate specification GO:0007501 p=1.5E−02 n=2 fg=0.04 bg=0.00
sensory perception of sound GO:0007605 p=1.5E−02 n=4 fg=0.09 bg=0.02
negative regulation of anion channel act... GO:0010360 p=1.7E−02 n=1 fg=0.02 bg=0.00
ketone body catabolic process GO:0046952 p=1.7E−02 n=1 fg=0.02 bg=0.00
anterior compartment pattern formation GO:0007387 p=1.7E−02 n=1 fg=0.02 bg=0.00
posterior compartment specification GO:0007388 p=1.7E−02 n=1 fg=0.02 bg=0.00
fatty acid derivative catabolic process GO:1901569 p=1.7E−02 n=1 fg=0.02 bg=0.00
spermidine catabolic process GO:0046203 p=1.7E−02 n=1 fg=0.02 bg=0.00
spermine catabolic process GO:0046208 p=1.7E−02 n=1 fg=0.02 bg=0.00
lipoxygenase pathway GO:0019372 p=1.7E−02 n=1 fg=0.02 bg=0.00
oligodendrocyte progenitor proliferation GO:0070444 p=1.7E−02 n=1 fg=0.02 bg=0.00
regulation of oligodendrocyte progenitor... GO:0070445 p=1.7E−02 n=1 fg=0.02 bg=0.00
establishment of endothelial intestinal ... GO:0090557 p=1.7E−02 n=1 fg=0.02 bg=0.00
positive regulation of fibroblast apopto... GO:2000271 p=1.7E−02 n=1 fg=0.02 bg=0.00
propionyl−CoA biosynthetic process GO:1902860 p=1.7E−02 n=1 fg=0.02 bg=0.00
propionyl−CoA metabolic process GO:1902858 p=1.7E−02 n=1 fg=0.02 bg=0.00
putrescine metabolic process GO:0009445 p=1.7E−02 n=1 fg=0.02 bg=0.00
putrescine biosynthetic process GO:0009446 p=1.7E−02 n=1 fg=0.02 bg=0.00
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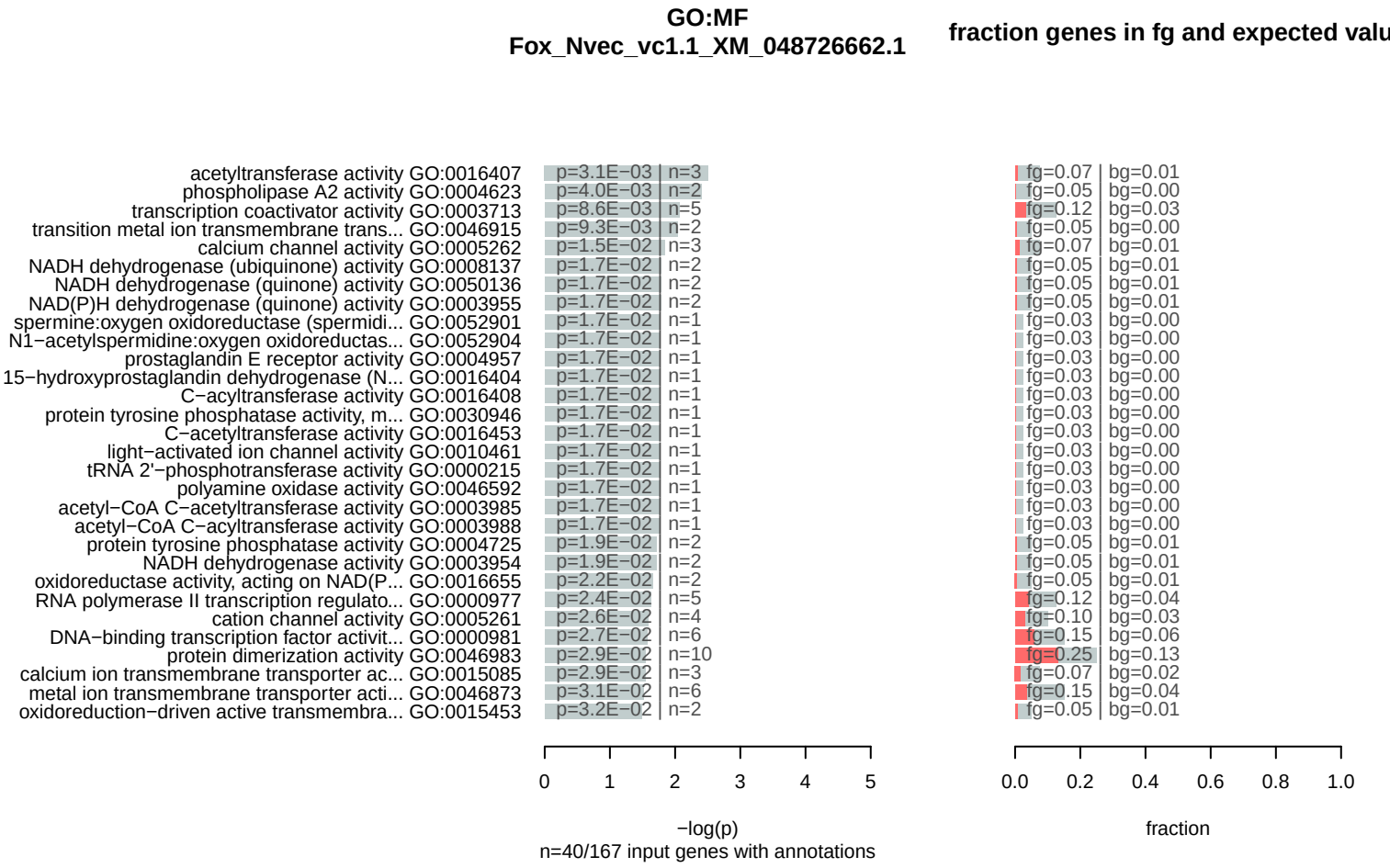
−log(p)
n=47/167 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
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fraction genes in fg and expected valu
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phospholipase A2 activity GO:0004623 p=4.0E−03 n=2 fg=0.05 bg=0.00
transcription coactivator activity GO:0003713 p=8.6E−03 n=5 fg=0.12 bg=0.03
transition metal ion transmembrane trans... GO:0046915 p=9.3E−03 n=2 fg=0.05 bg=0.00
calcium channel activity GO:0005262 p=1.5E−02 n=3 fg=0.07 bg=0.01
NADH dehydrogenase (ubiquinone) activity GO:0008137 p=1.7E−02 n=2 fg=0.05 bg=0.01
NADH dehydrogenase (quinone) activity GO:0050136 p=1.7E−02 n=2 fg=0.05 bg=0.01
NAD(P)H dehydrogenase (quinone) activity GO:0003955 p=1.7E−02 n=2 fg=0.05 bg=0.01
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=1.7E−02 n=1 fg=0.03 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=1.7E−02 n=1 fg=0.03 bg=0.00
prostaglandin E receptor activity GO:0004957 p=1.7E−02 n=1 fg=0.03 bg=0.00
15−hydroxyprostaglandin dehydrogenase (N... GO:0016404 p=1.7E−02 n=1 fg=0.03 bg=0.00
C−acyltransferase activity GO:0016408 p=1.7E−02 n=1 fg=0.03 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=1.7E−02 n=1 fg=0.03 bg=0.00
C−acetyltransferase activity GO:0016453 p=1.7E−02 n=1 fg=0.03 bg=0.00
light−activated ion channel activity GO:0010461 p=1.7E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.7E−02 n=1 fg=0.03 bg=0.00
polyamine oxidase activity GO:0046592 p=1.7E−02 n=1 fg=0.03 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=1.7E−02 n=1 fg=0.03 bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988 p=1.7E−02 n=1 fg=0.03 bg=0.00
protein tyrosine phosphatase activity GO:0004725 p=1.9E−02 n=2 fg=0.05 bg=0.01
NADH dehydrogenase activity GO:0003954 p=1.9E−02 n=2 fg=0.05 bg=0.01
oxidoreductase activity, acting on NAD(P... GO:0016655 p=2.2E−02 n=2 fg=0.05 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=2.4E−02 n=5 fg=0.12 bg=0.04
cation channel activity GO:0005261 p=2.6E−02 n=4 fg=0.10 bg=0.03
DNA−binding transcription factor activit... GO:0000981 p=2.7E−02 n=6 fg=0.15 bg=0.06
protein dimerization activity GO:0046983 p=2.9E−02 n=10 fg=0.25 bg=0.13
calcium ion transmembrane transporter ac... GO:0015085 p=2.9E−02 n=3 fg=0.07 bg=0.02
metal ion transmembrane transporter acti... GO:0046873 p=3.1E−02 n=6 fg=0.15 bg=0.04
oxidoreduction−driven active transmembra... GO:0015453 p=3.2E−02 n=2 fg=0.05 bg=0.01
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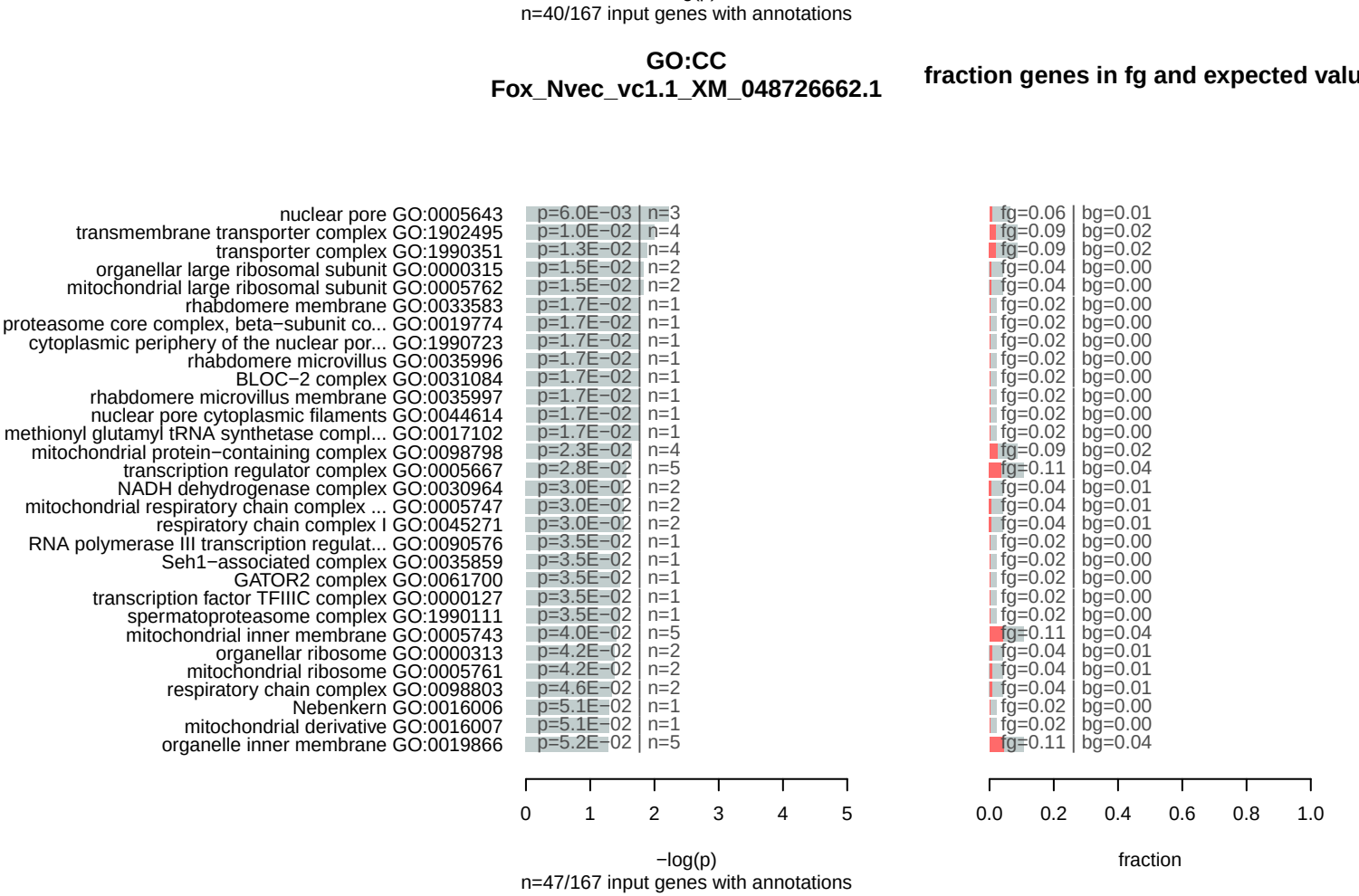
−log(p)
n=40/167 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Fox_Nvec_vc1.1_XM_048726662.1
fraction genes in fg and expected valu
nuclear pore GO:0005643 p=6.0E−03 n=3 fg=0.06 bg=0.01
transmembrane transporter complex GO:1902495 p=1.0E−02 n=4 fg=0.09 bg=0.02
transporter complex GO:1990351 p=1.3E−02 n=4 fg=0.09 bg=0.02
organellar large ribosomal subunit GO:0000315 p=1.5E−02 n=2 fg=0.04 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=1.5E−02 n=2 fg=0.04 bg=0.00
rhabdomere membrane GO:0033583 p=1.7E−02 n=1 fg=0.02 bg=0.00
proteasome core complex, beta−subunit co... GO:0019774 p=1.7E−02 n=1 fg=0.02 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=1.7E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus GO:0035996 p=1.7E−02 n=1 fg=0.02 bg=0.00
BLOC−2 complex GO:0031084 p=1.7E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=1.7E−02 n=1 fg=0.02 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=1.7E−02 n=1 fg=0.02 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=1.7E−02 n=1 fg=0.02 bg=0.00
mitochondrial protein−containing complex GO:0098798 p=2.3E−02 n=4 fg=0.09 bg=0.02
transcription regulator complex GO:0005667 p=2.8E−02 n=5 fg=0.11 bg=0.04
NADH dehydrogenase complex GO:0030964 p=3.0E−02 n=2 fg=0.04 bg=0.01
mitochondrial respiratory chain complex ... GO:0005747 p=3.0E−02 n=2 fg=0.04 bg=0.01
respiratory chain complex I GO:0045271 p=3.0E−02 n=2 fg=0.04 bg=0.01
RNA polymerase III transcription regulat... GO:0090576 p=3.5E−02 n=1 fg=0.02 bg=0.00
Seh1−associated complex GO:0035859 p=3.5E−02 n=1 fg=0.02 bg=0.00
GATOR2 complex GO:0061700 p=3.5E−02 n=1 fg=0.02 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=3.5E−02 n=1 fg=0.02 bg=0.00
spermatoproteasome complex GO:1990111 p=3.5E−02 n=1 fg=0.02 bg=0.00
mitochondrial inner membrane GO:0005743 p=4.0E−02 n=5 fg=0.11 bg=0.04
organellar ribosome GO:0000313 p=4.2E−02 n=2 fg=0.04 bg=0.01
mitochondrial ribosome GO:0005761 p=4.2E−02 n=2 fg=0.04 bg=0.01
respiratory chain complex GO:0098803 p=4.6E−02 n=2 fg=0.04 bg=0.01
Nebenkern GO:0016006 p=5.1E−02 n=1 fg=0.02 bg=0.00
mitochondrial derivative GO:0016007 p=5.1E−02 n=1 fg=0.02 bg=0.00
organelle inner membrane GO:0019866 p=5.2E−02 n=5 fg=0.11 bg=0.04
0 1 2 3 4 5
−log(p)
n=47/167 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction