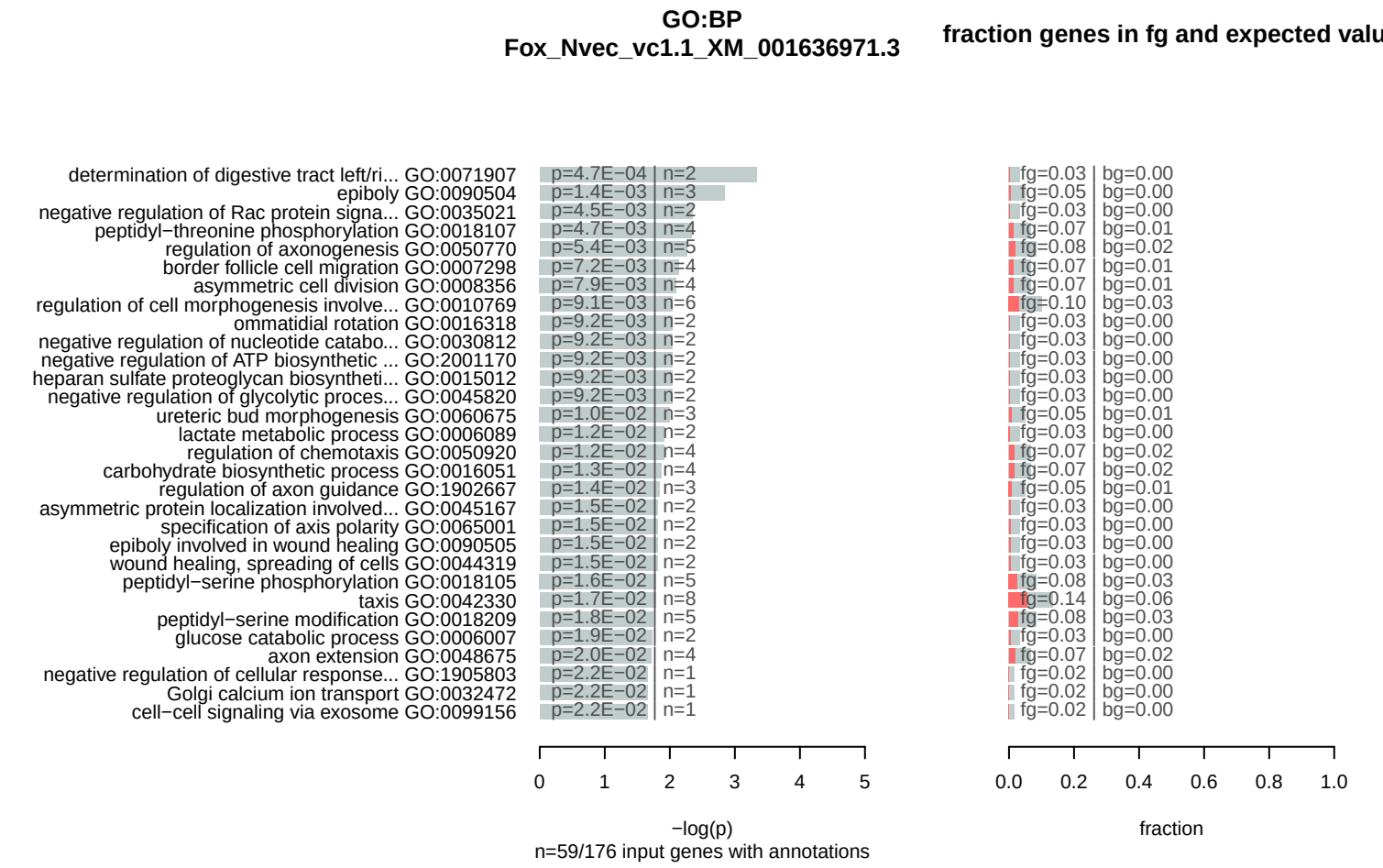
GO:BP
Fox_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
determination of digestive tract left/ri... GO:0071907 p=4.7E−04 n=2 fg=0.03 bg=0.00
epiboly GO:0090504 p=1.4E−03 n=3 fg=0.05 bg=0.00
negative regulation of Rac protein signa... GO:0035021 p=4.5E−03 n=2 fg=0.03 bg=0.00
peptidyl−threonine phosphorylation GO:0018107 p=4.7E−03 n=4 fg=0.07 bg=0.01
regulation of axonogenesis GO:0050770 p=5.4E−03 n=5 fg=0.08 bg=0.02
border follicle cell migration GO:0007298 p=7.2E−03 n=4 fg=0.07 bg=0.01
asymmetric cell division GO:0008356 p=7.9E−03 n=4 fg=0.07 bg=0.01
regulation of cell morphogenesis involve... GO:0010769 p=9.1E−03 n=6 fg=0.10 bg=0.03
ommatidial rotation GO:0016318 p=9.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of nucleotide catabo... GO:0030812 p=9.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of ATP biosynthetic ... GO:2001170 p=9.2E−03 n=2 fg=0.03 bg=0.00
heparan sulfate proteoglycan biosyntheti... GO:0015012 p=9.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of glycolytic proces... GO:0045820 p=9.2E−03 n=2 fg=0.03 bg=0.00
ureteric bud morphogenesis GO:0060675 p=1.0E−02 n=3 fg=0.05 bg=0.01
lactate metabolic process GO:0006089 p=1.2E−02 n=2 fg=0.03 bg=0.00
regulation of chemotaxis GO:0050920 p=1.2E−02 n=4 fg=0.07 bg=0.02
carbohydrate biosynthetic process GO:0016051 p=1.3E−02 n=4 fg=0.07 bg=0.02
regulation of axon guidance GO:1902667 p=1.4E−02 n=3 fg=0.05 bg=0.01
asymmetric protein localization involved... GO:0045167 p=1.5E−02 n=2 fg=0.03 bg=0.00
specification of axis polarity GO:0065001 p=1.5E−02 n=2 fg=0.03 bg=0.00
epiboly involved in wound healing GO:0090505 p=1.5E−02 n=2 fg=0.03 bg=0.00
wound healing, spreading of cells GO:0044319 p=1.5E−02 n=2 fg=0.03 bg=0.00
peptidyl−serine phosphorylation GO:0018105 p=1.6E−02 n=5 fg=0.08 bg=0.03
taxis GO:0042330 p=1.7E−02 n=8 fg=0.14 bg=0.06
peptidyl−serine modification GO:0018209 p=1.8E−02 n=5 fg=0.08 bg=0.03
glucose catabolic process GO:0006007 p=1.9E−02 n=2 fg=0.03 bg=0.00
axon extension GO:0048675 p=2.0E−02 n=4 fg=0.07 bg=0.02
negative regulation of cellular response... GO:1905803 p=2.2E−02 n=1 fg=0.02 bg=0.00
Golgi calcium ion transport GO:0032472 p=2.2E−02 n=1 fg=0.02 bg=0.00
cell−cell signaling via exosome GO:0099156 p=2.2E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=59/176 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
MAP kinase activity GO:0004707 p=8.9E−03 n=2 fg=0.04 bg=0.00
phosphatidylinositol phosphate binding GO:1901981 p=1.6E−02 n=4 fg=0.08 bg=0.02
histone deacetylase binding GO:0042826 p=1.7E−02 n=3 fg=0.06 bg=0.01
phosphatidylinositol−3−phosphate binding GO:0032266 p=1.8E−02 n=2 fg=0.04 bg=0.00
beta−catenin binding GO:0008013 p=1.8E−02 n=2 fg=0.04 bg=0.00
transcription regulatory region nucleic ... GO:0001067 p=1.9E−02 n=7 fg=0.14 bg=0.05
ATP binding GO:0005524 p=2.1E−02 n=6 fg=0.12 bg=0.04
glucose−1,6−bisphosphate synthase activi... GO:0047933 p=2.1E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.1E−02 n=1 fg=0.02 bg=0.00
heparan sulfate 2−O−sulfotransferase act... GO:0004394 p=2.1E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (NADP+) activity GO:0046554 p=2.1E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0046997 p=2.1E−02 n=1 fg=0.02 bg=0.00
dimethylglycine dehydrogenase activity GO:0047865 p=2.1E−02 n=1 fg=0.02 bg=0.00
histone deacetylase regulator activity GO:0035033 p=2.1E−02 n=1 fg=0.02 bg=0.00
JUN kinase activity GO:0004705 p=2.1E−02 n=1 fg=0.02 bg=0.00
N−acylneuraminate−9−phosphatase activity GO:0050124 p=2.1E−02 n=1 fg=0.02 bg=0.00
sphingolipid transporter activity GO:0046624 p=2.1E−02 n=1 fg=0.02 bg=0.00
phosphopentomutase activity GO:0008973 p=2.1E−02 n=1 fg=0.02 bg=0.00
DNA end binding GO:0045027 p=2.1E−02 n=1 fg=0.02 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.1E−02 n=1 fg=0.02 bg=0.00
deUFMylase activity GO:0071567 p=2.1E−02 n=1 fg=0.02 bg=0.00
AMP deaminase activity GO:0003876 p=2.1E−02 n=1 fg=0.02 bg=0.00
heparan sulfate sulfotransferase activit... GO:0034483 p=2.1E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.1E−02 n=1 fg=0.02 bg=0.00
sphingolipid transfer activity GO:0120016 p=2.1E−02 n=1 fg=0.02 bg=0.00
ceramide transfer activity GO:0120017 p=2.1E−02 n=1 fg=0.02 bg=0.00
magnesium ion binding GO:0000287 p=2.6E−02 n=4 fg=0.08 bg=0.02
phosphatidylinositol−4−phosphate binding GO:0070273 p=2.6E−02 n=2 fg=0.04 bg=0.01
double−stranded DNA binding GO:0003690 p=2.7E−02 n=7 fg=0.14 bg=0.06
transcription cis−regulatory region bind... GO:0000976 p=3.1E−02 n=6 fg=0.12 bg=0.05
0 1 2 3 4 5
−log(p)
n=51/176 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
compact myelin GO:0043218 p=2.1E−02 n=1 fg=0.02 bg=0.00
anterior cell cortex GO:0061802 p=2.1E−02 n=1 fg=0.02 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=2.1E−02 n=1 fg=0.02 bg=0.00
internode region of axon GO:0033269 p=2.1E−02 n=1 fg=0.02 bg=0.00
pinosome GO:0044352 p=2.1E−02 n=1 fg=0.02 bg=0.00
macropinosome GO:0044354 p=2.1E−02 n=1 fg=0.02 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.1E−02 n=1 fg=0.02 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=2.1E−02 n=1 fg=0.02 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=2.1E−02 n=1 fg=0.02 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=4.1E−02 n=1 fg=0.02 bg=0.00
lateral loop GO:0043219 p=4.1E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation elongation factor... GO:0005853 p=4.1E−02 n=1 fg=0.02 bg=0.00
translation preinitiation complex GO:0070993 p=4.1E−02 n=1 fg=0.02 bg=0.00
trans−Golgi network GO:0005802 p=6.0E−02 n=4 fg=0.07 bg=0.03
eukaryotic translation initiation factor... GO:0005850 p=6.1E−02 n=1 fg=0.02 bg=0.00
multi−eIF complex GO:0043614 p=6.1E−02 n=1 fg=0.02 bg=0.00
Pwp2p−containing subcomplex of 90S preri... GO:0034388 p=6.1E−02 n=1 fg=0.02 bg=0.00
Golgi apparatus subcompartment GO:0098791 p=7.0E−02 n=7 fg=0.12 bg=0.07
inner dynein arm GO:0036156 p=8.0E−02 n=1 fg=0.02 bg=0.00
filamentous actin GO:0031941 p=8.0E−02 n=1 fg=0.02 bg=0.00
basal dendrite GO:0097441 p=8.0E−02 n=1 fg=0.02 bg=0.00
spot adherens junction GO:0005914 p=8.0E−02 n=1 fg=0.02 bg=0.00
subapical complex GO:0035003 p=8.0E−02 n=1 fg=0.02 bg=0.00
Golgi apparatus GO:0005794 p=9.3E−02 n=10 fg=0.18 bg=0.11
membrane−bounded organelle GO:0043227 p=9.8E−02 n=49 fg=0.88 bg=0.80
cytoplasmic side of apical plasma membra... GO:0098592 p=1.0E−01 n=1 fg=0.02 bg=0.00
guanyl−nucleotide exchange factor comple... GO:0032045 p=1.0E−01 n=1 fg=0.02 bg=0.00
zonula adherens GO:0005915 p=1.0E−01 n=1 fg=0.02 bg=0.00
podosome GO:0002102 p=1.0E−01 n=1 fg=0.02 bg=0.00
dendrite cytoplasm GO:0032839 p=1.0E−01 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=56/176 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction