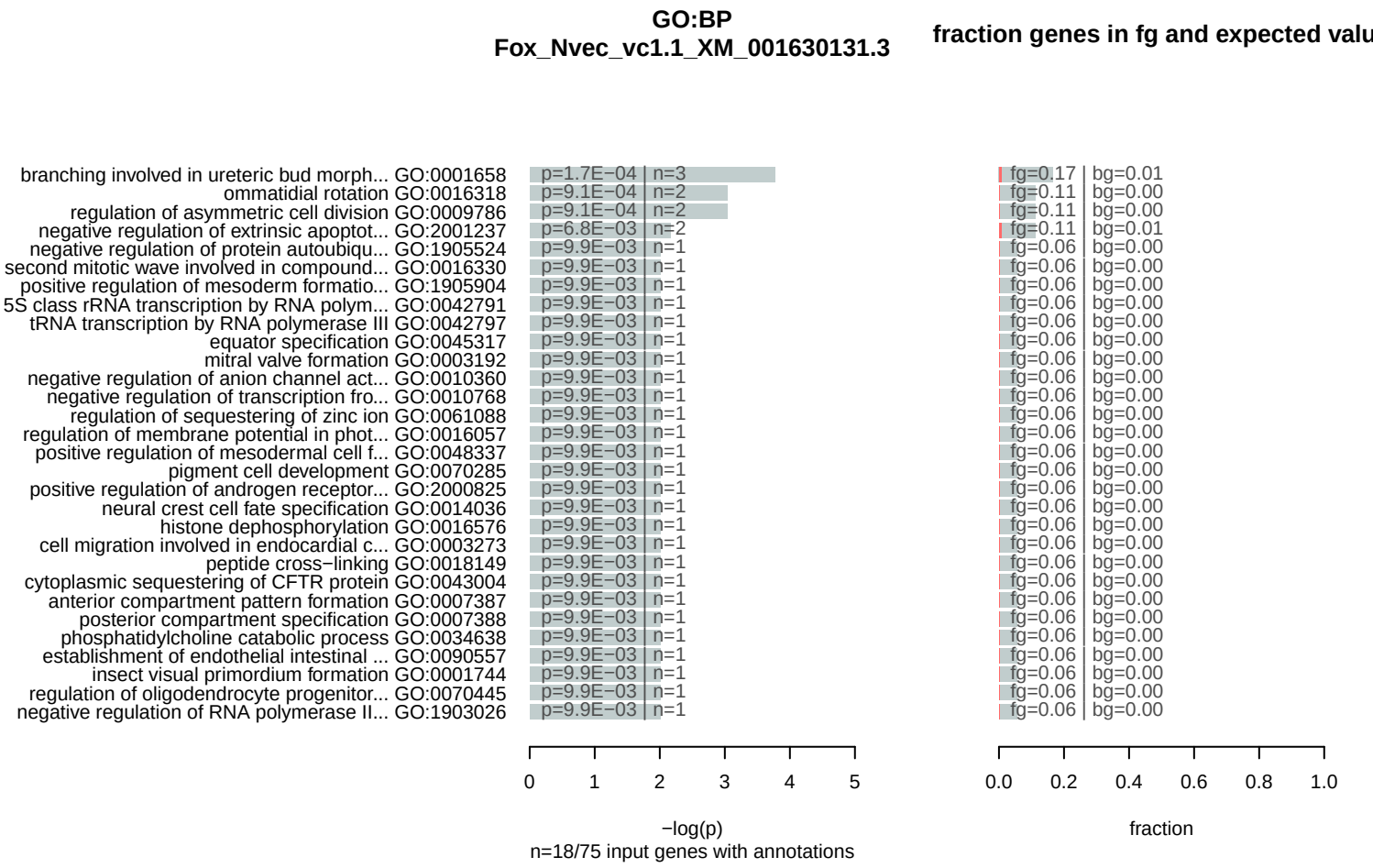
GO:BP
Fox_Nvec_vc1.1_XM_001630131.3
fraction genes in fg and expected valu
branching involved in ureteric bud morph... GO:0001658 p=1.7E−04 n=3 fg=0.17 bg=0.01
ommatidial rotation GO:0016318 p=9.1E−04 n=2 fg=0.11 bg=0.00
regulation of asymmetric cell division GO:0009786 p=9.1E−04 n=2 fg=0.11 bg=0.00
negative regulation of extrinsic apoptot... GO:2001237 p=6.8E−03 n=2 fg=0.11 bg=0.01
negative regulation of protein autoubiqu... GO:1905524 p=9.9E−03 n=1 fg=0.06 bg=0.00
second mitotic wave involved in compound... GO:0016330 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of mesoderm formatio... GO:1905904 p=9.9E−03 n=1 fg=0.06 bg=0.00
5S class rRNA transcription by RNA polym... GO:0042791 p=9.9E−03 n=1 fg=0.06 bg=0.00
tRNA transcription by RNA polymerase III GO:0042797 p=9.9E−03 n=1 fg=0.06 bg=0.00
equator specification GO:0045317 p=9.9E−03 n=1 fg=0.06 bg=0.00
mitral valve formation GO:0003192 p=9.9E−03 n=1 fg=0.06 bg=0.00
negative regulation of anion channel act... GO:0010360 p=9.9E−03 n=1 fg=0.06 bg=0.00
negative regulation of transcription fro... GO:0010768 p=9.9E−03 n=1 fg=0.06 bg=0.00
regulation of sequestering of zinc ion GO:0061088 p=9.9E−03 n=1 fg=0.06 bg=0.00
regulation of membrane potential in phot... GO:0016057 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of mesodermal cell f... GO:0048337 p=9.9E−03 n=1 fg=0.06 bg=0.00
pigment cell development GO:0070285 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of androgen receptor... GO:2000825 p=9.9E−03 n=1 fg=0.06 bg=0.00
neural crest cell fate specification GO:0014036 p=9.9E−03 n=1 fg=0.06 bg=0.00
histone dephosphorylation GO:0016576 p=9.9E−03 n=1 fg=0.06 bg=0.00
cell migration involved in endocardial c... GO:0003273 p=9.9E−03 n=1 fg=0.06 bg=0.00
peptide cross−linking GO:0018149 p=9.9E−03 n=1 fg=0.06 bg=0.00
cytoplasmic sequestering of CFTR protein GO:0043004 p=9.9E−03 n=1 fg=0.06 bg=0.00
anterior compartment pattern formation GO:0007387 p=9.9E−03 n=1 fg=0.06 bg=0.00
posterior compartment specification GO:0007388 p=9.9E−03 n=1 fg=0.06 bg=0.00
phosphatidylcholine catabolic process GO:0034638 p=9.9E−03 n=1 fg=0.06 bg=0.00
establishment of endothelial intestinal ... GO:0090557 p=9.9E−03 n=1 fg=0.06 bg=0.00
insect visual primordium formation GO:0001744 p=9.9E−03 n=1 fg=0.06 bg=0.00
regulation of oligodendrocyte progenitor... GO:0070445 p=9.9E−03 n=1 fg=0.06 bg=0.00
negative regulation of RNA polymerase II... GO:1903026 p=9.9E−03 n=1 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=18/75 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001630131.3
fraction genes in fg and expected valu
acetyltransferase activity GO:0016407 p=6.1E−03 n=2 fg=0.13 bg=0.01
protein heterodimerization activity GO:0046982 p=8.7E−03 n=4 fg=0.27 bg=0.06
protein tyrosine phosphatase activity, m... GO:0030946 p=9.4E−03 n=1 fg=0.07 bg=0.00
phospholipase A1 activity GO:0008970 p=9.4E−03 n=1 fg=0.07 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=9.4E−03 n=1 fg=0.07 bg=0.00
syntaxin binding GO:0019905 p=1.4E−02 n=2 fg=0.13 bg=0.01
metal ion transmembrane transporter acti... GO:0046873 p=1.5E−02 n=3 fg=0.20 bg=0.04
transcription coactivator activity GO:0003713 p=1.6E−02 n=3 fg=0.20 bg=0.04
calcium channel activity GO:0005262 p=1.9E−02 n=2 fg=0.13 bg=0.01
LIM domain binding GO:0030274 p=1.9E−02 n=1 fg=0.07 bg=0.00
lysine−acetylated histone binding GO:0070577 p=1.9E−02 n=1 fg=0.07 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=1.9E−02 n=1 fg=0.07 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=1.9E−02 n=1 fg=0.07 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=1.9E−02 n=1 fg=0.07 bg=0.00
acetylation−dependent protein binding GO:0140033 p=1.9E−02 n=1 fg=0.07 bg=0.00
transcription regulator activity GO:0140110 p=2.3E−02 n=5 fg=0.33 bg=0.12
calcium ion transmembrane transporter ac... GO:0015085 p=2.5E−02 n=2 fg=0.13 bg=0.02
phospholipase A2 activity GO:0004623 p=2.6E−02 n=2 fg=0.13 bg=0.00
zinc ion transmembrane transporter activ... GO:0005385 p=2.8E−02 n=1 fg=0.07 bg=0.00
histone acetyltransferase activity GO:0004402 p=2.8E−02 n=1 fg=0.07 bg=0.00
cell adhesion molecule binding GO:0050839 p=2.9E−02 n=2 fg=0.13 bg=0.02
SNARE binding GO:0000149 p=3.1E−02 n=2 fg=0.13 bg=0.02
RNA polymerase II transcription regulato... GO:0000977 p=3.5E−02 n=3 fg=0.20 bg=0.05
phosphatidic acid binding GO:0070300 p=3.7E−02 n=1 fg=0.07 bg=0.00
peptide−lysine−N−acetyltransferase activ... GO:0061733 p=3.7E−02 n=1 fg=0.07 bg=0.00
peptide N−acetyltransferase activity GO:0034212 p=3.7E−02 n=1 fg=0.07 bg=0.00
inorganic cation transmembrane transport... GO:0022890 p=4.2E−02 n=3 fg=0.20 bg=0.05
cation transmembrane transporter activit... GO:0008324 p=4.6E−02 n=3 fg=0.20 bg=0.06
transcription coactivator binding GO:0001223 p=4.6E−02 n=1 fg=0.07 bg=0.00
phosphatidylserine binding GO:0001786 p=4.6E−02 n=1 fg=0.07 bg=0.00
0 1 2 3 4 5
−log(p)
n=15/75 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001630131.3
fraction genes in fg and expected valu
RNA polymerase III transcription regulat... GO:0090576 p=1.1E−02 n=1 fg=0.05 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=1.1E−02 n=1 fg=0.05 bg=0.00
nuclear body GO:0016604 p=2.9E−02 n=4 fg=0.21 bg=0.06
trans−Golgi network membrane GO:0032588 p=4.1E−02 n=2 fg=0.11 bg=0.02
zonula adherens GO:0005915 p=4.1E−02 n=1 fg=0.05 bg=0.00
XY body GO:0001741 p=4.1E−02 n=1 fg=0.05 bg=0.00
transcription regulator complex GO:0005667 p=4.4E−02 n=3 fg=0.16 bg=0.04
RNA polymerase II transcription regulato... GO:0090575 p=4.5E−02 n=2 fg=0.11 bg=0.02
MLL1 complex GO:0071339 p=5.1E−02 n=1 fg=0.05 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=5.1E−02 n=1 fg=0.05 bg=0.00
pronucleus GO:0045120 p=6.1E−02 n=1 fg=0.05 bg=0.00
MLL1/2 complex GO:0044665 p=7.1E−02 n=1 fg=0.05 bg=0.00
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transcription factor TFIID complex GO:0005669 p=7.1E−02 n=1 fg=0.05 bg=0.00
calcium channel complex GO:0034704 p=7.1E−02 n=1 fg=0.05 bg=0.00
apical part of cell GO:0045177 p=7.8E−02 n=3 fg=0.16 bg=0.05
stereocilium GO:0032420 p=8.1E−02 n=1 fg=0.05 bg=0.00
stereocilium bundle GO:0032421 p=8.1E−02 n=1 fg=0.05 bg=0.00
trans−Golgi network transport vesicle GO:0030140 p=9.1E−02 n=1 fg=0.05 bg=0.00
sex chromosome GO:0000803 p=9.1E−02 n=1 fg=0.05 bg=0.00
Golgi−associated vesicle membrane GO:0030660 p=1.4E−01 n=1 fg=0.05 bg=0.01
trans−Golgi network GO:0005802 p=1.5E−01 n=2 fg=0.11 bg=0.04
nuclear chromosome GO:0000228 p=1.5E−01 n=2 fg=0.11 bg=0.04
histone methyltransferase complex GO:0035097 p=1.6E−01 n=1 fg=0.05 bg=0.01
protein−DNA complex GO:0032993 p=1.6E−01 n=1 fg=0.05 bg=0.01
cell−substrate junction GO:0030055 p=1.7E−01 n=1 fg=0.05 bg=0.01
presynaptic active zone GO:0048786 p=1.7E−01 n=1 fg=0.05 bg=0.01
fibrillar center GO:0001650 p=1.8E−01 n=1 fg=0.05 bg=0.01
methyltransferase complex GO:0034708 p=1.8E−01 n=1 fg=0.05 bg=0.01
chromosome GO:0005694 p=1.8E−01 n=3 fg=0.16 bg=0.08
0 1 2 3 4 5
−log(p)
n=19/75 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction