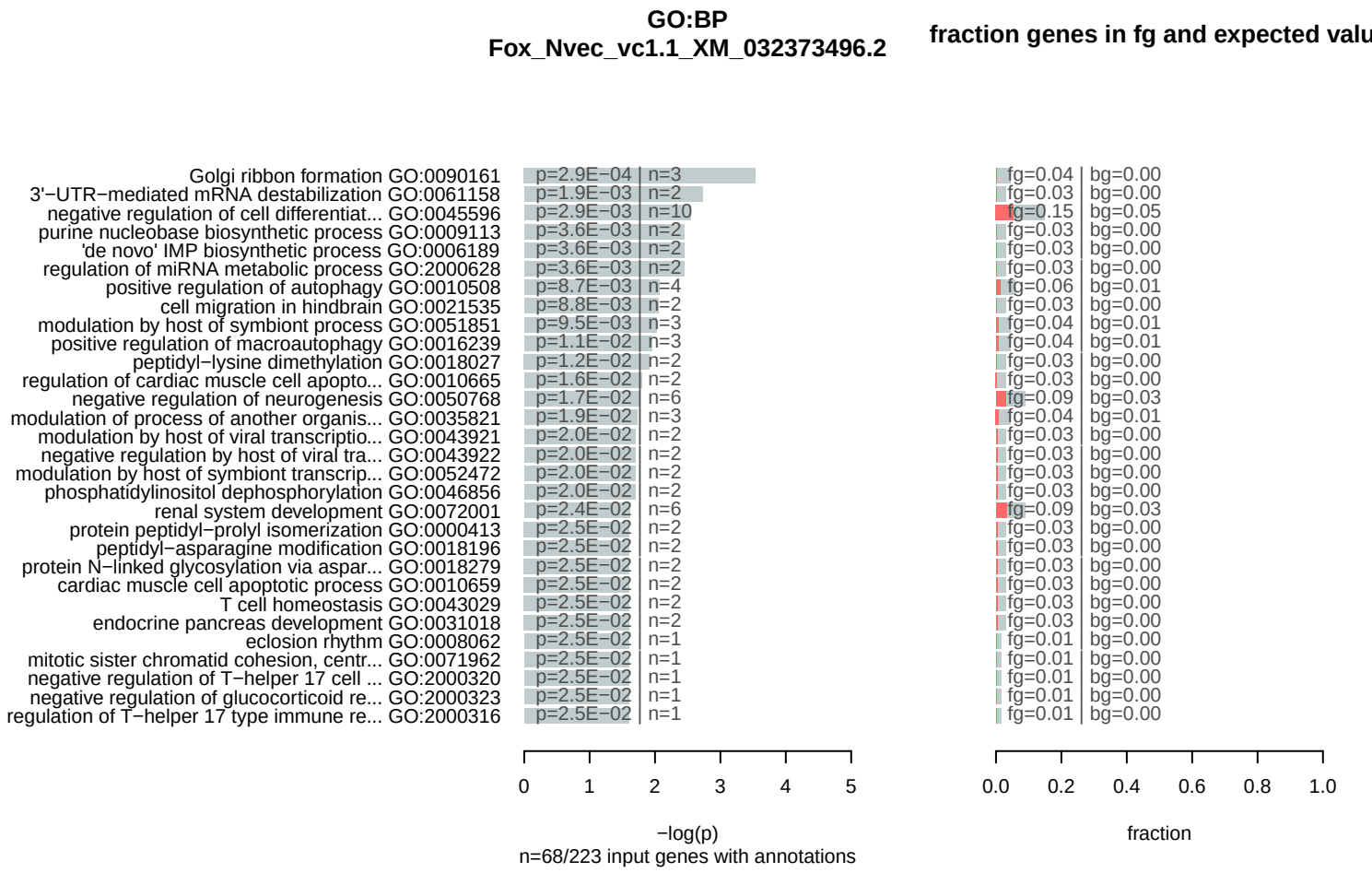
GO:BP
Fox_Nvec_vc1.1_XM_032373496.2
fraction genes in fg and expected valu
Golgi ribbon formation GO:0090161 p=2.9E−04 n=3 fg=0.04 bg=0.00
3'−UTR−mediated mRNA destabilization GO:0061158 p=1.9E−03 n=2 fg=0.03 bg=0.00
negative regulation of cell differentiat... GO:0045596 p=2.9E−03 n=10 fg=0.15 bg=0.05
purine nucleobase biosynthetic process GO:0009113 p=3.6E−03 n=2 fg=0.03 bg=0.00
'de novo' IMP biosynthetic process GO:0006189 p=3.6E−03 n=2 fg=0.03 bg=0.00
regulation of miRNA metabolic process GO:2000628 p=3.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of autophagy GO:0010508 p=8.7E−03 n=4 fg=0.06 bg=0.01
cell migration in hindbrain GO:0021535 p=8.8E−03 n=2 fg=0.03 bg=0.00
modulation by host of symbiont process GO:0051851 p=9.5E−03 n=3 fg=0.04 bg=0.01
positive regulation of macroautophagy GO:0016239 p=1.1E−02 n=3 fg=0.04 bg=0.01
peptidyl−lysine dimethylation GO:0018027 p=1.2E−02 n=2 fg=0.03 bg=0.00
regulation of cardiac muscle cell apopto... GO:0010665 p=1.6E−02 n=2 fg=0.03 bg=0.00
negative regulation of neurogenesis GO:0050768 p=1.7E−02 n=6 fg=0.09 bg=0.03
modulation of process of another organis... GO:0035821 p=1.9E−02 n=3 fg=0.04 bg=0.01
modulation by host of viral transcriptio... GO:0043921 p=2.0E−02 n=2 fg=0.03 bg=0.00
negative regulation by host of viral tra... GO:0043922 p=2.0E−02 n=2 fg=0.03 bg=0.00
modulation by host of symbiont transcrip... GO:0052472 p=2.0E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol dephosphorylation GO:0046856 p=2.0E−02 n=2 fg=0.03 bg=0.00
renal system development GO:0072001 p=2.4E−02 n=6 fg=0.09 bg=0.03
protein peptidyl−prolyl isomerization GO:0000413 p=2.5E−02 n=2 fg=0.03 bg=0.00
peptidyl−asparagine modification GO:0018196 p=2.5E−02 n=2 fg=0.03 bg=0.00
protein N−linked glycosylation via aspar... GO:0018279 p=2.5E−02 n=2 fg=0.03 bg=0.00
cardiac muscle cell apoptotic process GO:0010659 p=2.5E−02 n=2 fg=0.03 bg=0.00
T cell homeostasis GO:0043029 p=2.5E−02 n=2 fg=0.03 bg=0.00
endocrine pancreas development GO:0031018 p=2.5E−02 n=2 fg=0.03 bg=0.00
eclosion rhythm GO:0008062 p=2.5E−02 n=1 fg=0.01 bg=0.00
mitotic sister chromatid cohesion, centr... GO:0071962 p=2.5E−02 n=1 fg=0.01 bg=0.00
negative regulation of T−helper 17 cell ... GO:2000320 p=2.5E−02 n=1 fg=0.01 bg=0.00
negative regulation of glucocorticoid re... GO:2000323 p=2.5E−02 n=1 fg=0.01 bg=0.00
regulation of T−helper 17 type immune re... GO:2000316 p=2.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=68/223 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
RNA stem−loop binding GO:0035613 p=3.7E−03 n=2 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate ph... GO:0106019 p=6.0E−03 n=2 fg=0.03 bg=0.00
cyclosporin A binding GO:0016018 p=8.9E−03 n=2 fg=0.03 bg=0.00
symporter activity GO:0015293 p=9.6E−03 n=3 fg=0.05 bg=0.01
mRNA binding GO:0003729 p=1.1E−02 n=6 fg=0.10 bg=0.03
cis−trans isomerase activity GO:0016859 p=2.5E−02 n=2 fg=0.03 bg=0.00
peptidyl−prolyl cis−trans isomerase acti... GO:0003755 p=2.5E−02 n=2 fg=0.03 bg=0.00
amidophosphoribosyltransferase activity GO:0004044 p=2.5E−02 n=1 fg=0.02 bg=0.00
phosphoribosylaminoimidazole carboxylase... GO:0004638 p=2.5E−02 n=1 fg=0.02 bg=0.00
phosphoribosylaminoimidazolesuccinocarbo... GO:0004639 p=2.5E−02 n=1 fg=0.02 bg=0.00
semaphorin receptor binding GO:0030215 p=2.5E−02 n=1 fg=0.02 bg=0.00
methotrexate transmembrane transporter a... GO:0015350 p=2.5E−02 n=1 fg=0.02 bg=0.00
MAP kinase kinase kinase kinase activity GO:0008349 p=2.5E−02 n=1 fg=0.02 bg=0.00
protein−L−isoaspartate (D−aspartate) O−m... GO:0004719 p=2.5E−02 n=1 fg=0.02 bg=0.00
nickel cation binding GO:0016151 p=2.5E−02 n=1 fg=0.02 bg=0.00
carboxyl−O−methyltransferase activity GO:0010340 p=2.5E−02 n=1 fg=0.02 bg=0.00
beta−1,3−galactosyl−O−glycosyl−glycoprot... GO:0047223 p=2.5E−02 n=1 fg=0.02 bg=0.00
hedgehog receptor activity GO:0008158 p=2.5E−02 n=1 fg=0.02 bg=0.00
protein carboxyl O−methyltransferase act... GO:0051998 p=2.5E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol−4,5−bisphosphate 4−... GO:0034597 p=2.5E−02 n=1 fg=0.02 bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581 p=2.5E−02 n=1 fg=0.02 bg=0.00
calmodulin binding GO:0005516 p=2.6E−02 n=3 fg=0.05 bg=0.01
ubiquitin−like protein ligase activity GO:0061659 p=3.4E−02 n=5 fg=0.08 bg=0.03
ubiquitin protein ligase activity GO:0061630 p=3.4E−02 n=5 fg=0.08 bg=0.03
amide transmembrane transporter activity GO:0042887 p=3.5E−02 n=2 fg=0.03 bg=0.01
organic acid transmembrane transporter a... GO:0005342 p=3.9E−02 n=3 fg=0.05 bg=0.01
carboxylic acid transmembrane transporte... GO:0046943 p=3.9E−02 n=3 fg=0.05 bg=0.01
SNAP receptor activity GO:0005484 p=4.1E−02 n=2 fg=0.03 bg=0.01
xenobiotic transmembrane transporter act... GO:0042910 p=5.0E−02 n=1 fg=0.02 bg=0.00
heme transmembrane transporter activity GO:0015232 p=5.0E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=60/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032373496.2
fraction genes in fg and expected valu
Prp19 complex GO:0000974 p=6.0E−03 n=2 fg=0.03 bg=0.00
trans−Golgi network GO:0005802 p=8.6E−03 n=6 fg=0.09 bg=0.03
cytoplasmic ubiquitin ligase complex GO:0000153 p=1.2E−02 n=2 fg=0.03 bg=0.00
U2−type catalytic step 2 spliceosome GO:0071007 p=1.6E−02 n=2 fg=0.03 bg=0.00
catalytic step 2 spliceosome GO:0071013 p=2.1E−02 n=3 fg=0.04 bg=0.01
polytene chromosome band GO:0005704 p=2.5E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=2.5E−02 n=1 fg=0.01 bg=0.00
sarcoplasmic reticulum lumen GO:0033018 p=2.5E−02 n=1 fg=0.01 bg=0.00
phagocytic vesicle GO:0045335 p=2.6E−02 n=3 fg=0.04 bg=0.01
microtubule GO:0005874 p=3.3E−02 n=4 fg=0.06 bg=0.02
cytoplasmic stress granule GO:0010494 p=3.5E−02 n=2 fg=0.03 bg=0.00
Golgi trans cisterna GO:0000138 p=3.5E−02 n=2 fg=0.03 bg=0.00
mediator complex GO:0016592 p=3.5E−02 n=2 fg=0.03 bg=0.00
integral component of Golgi membrane GO:0030173 p=4.1E−02 n=2 fg=0.03 bg=0.00
supramolecular complex GO:0099080 p=4.1E−02 n=10 fg=0.15 bg=0.08
trans−Golgi network membrane GO:0032588 p=4.5E−02 n=3 fg=0.04 bg=0.01
fibrillar center GO:0001650 p=4.9E−02 n=3 fg=0.04 bg=0.01
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.0E−02 n=1 fg=0.01 bg=0.00
SMAD protein complex GO:0071141 p=5.0E−02 n=1 fg=0.01 bg=0.00
axonemal central apparatus GO:1990716 p=5.0E−02 n=1 fg=0.01 bg=0.00
nuclear SCF ubiquitin ligase complex GO:0043224 p=5.0E−02 n=1 fg=0.01 bg=0.00
Cul7−RING ubiquitin ligase complex GO:0031467 p=5.0E−02 n=1 fg=0.01 bg=0.00
post−mRNA release spliceosomal complex GO:0071014 p=5.0E−02 n=1 fg=0.01 bg=0.00
t−UTP complex GO:0034455 p=5.0E−02 n=1 fg=0.01 bg=0.00
COPII−coated ER to Golgi transport vesic... GO:0030134 p=5.3E−02 n=2 fg=0.03 bg=0.01
intrinsic component of Golgi membrane GO:0031228 p=5.3E−02 n=2 fg=0.03 bg=0.01
coated vesicle GO:0030135 p=5.3E−02 n=4 fg=0.06 bg=0.02
brush border GO:0005903 p=5.6E−02 n=3 fg=0.04 bg=0.01
late endosome GO:0005770 p=5.6E−02 n=4 fg=0.06 bg=0.02
cytoplasmic ribonucleoprotein granule GO:0036464 p=5.9E−02 n=4 fg=0.06 bg=0.02
0 1 2 3 4 5
−log(p)
n=68/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction