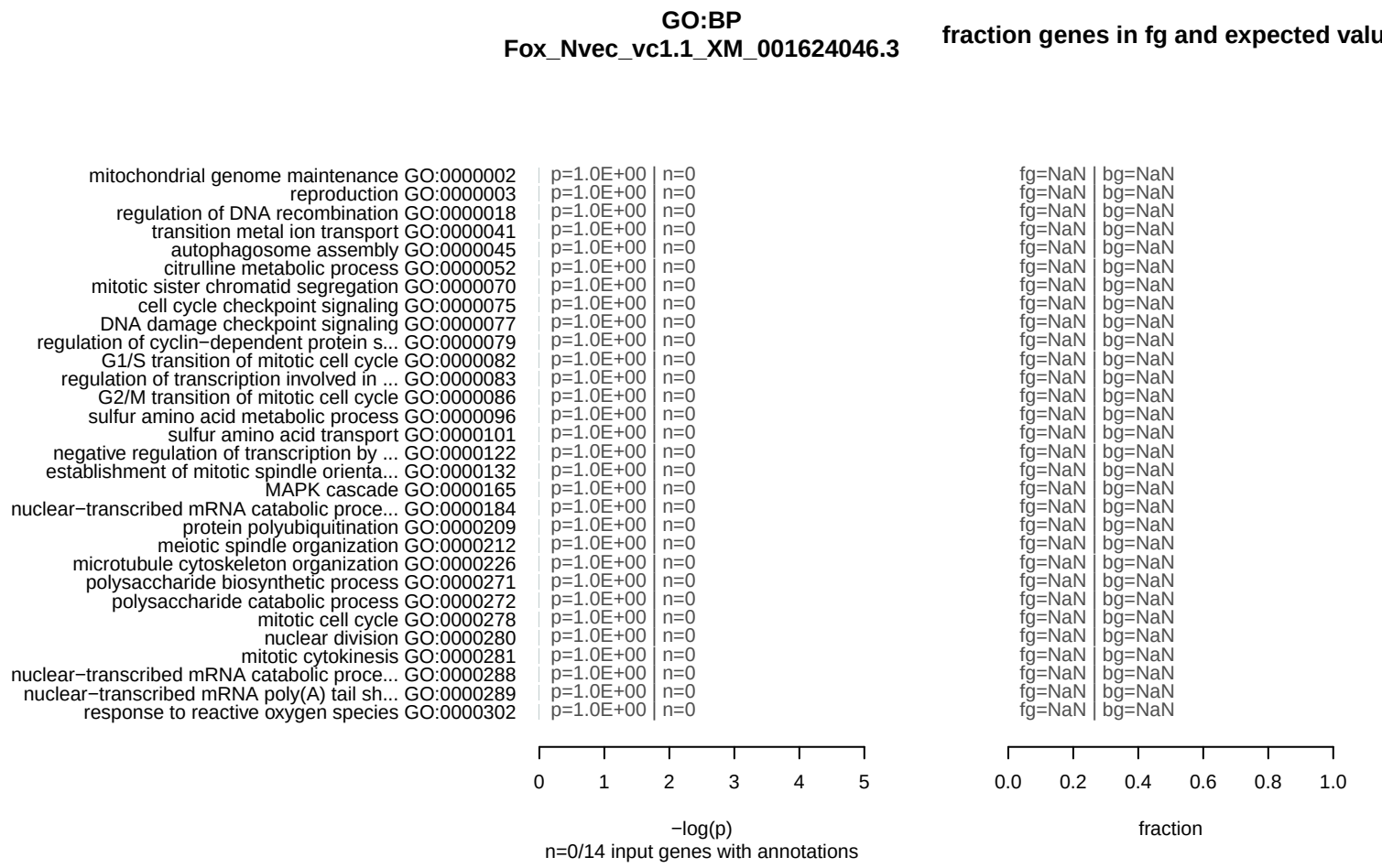
GO:BP
Fox_Nvec_vc1.1_XM_001624046.3
fraction genes in fg and expected valu
mitochondrial genome maintenance GO:0000002
reproduction GO:0000003
regulation of DNA recombination GO:0000018
transition metal ion transport GO:0000041
autophagosome assembly GO:0000045
citrulline metabolic process GO:0000052
mitotic sister chromatid segregation GO:0000070
cell cycle checkpoint signaling GO:0000075
DNA damage checkpoint signaling GO:0000077
regulation of cyclin−dependent protein s... GO:0000079
G1/S transition of mitotic cell cycle GO:0000082
regulation of transcription involved in ... GO:0000083
G2/M transition of mitotic cell cycle GO:0000086
sulfur amino acid metabolic process GO:0000096
sulfur amino acid transport GO:0000101
negative regulation of transcription by ... GO:0000122
establishment of mitotic spindle orienta... GO:0000132
MAPK cascade GO:0000165
nuclear−transcribed mRNA catabolic proce... GO:0000184
protein polyubiquitination GO:0000209
meiotic spindle organization GO:0000212
microtubule cytoskeleton organization GO:0000226
polysaccharide biosynthetic process GO:0000271
polysaccharide catabolic process GO:0000272
mitotic cell cycle GO:0000278
nuclear division GO:0000280
mitotic cytokinesis GO:0000281
nuclear−transcribed mRNA catabolic proce... GO:0000288
nuclear−transcribed mRNA poly(A) tail sh... GO:0000289
response to reactive oxygen species GO:0000302
p=1.0E+00 | n=0
fg=NaN | bg=NaN
0 1 2 3 4 5
−log(p)
n=0/14 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001624046.3
fraction genes in fg and expected valu
mannosyltransferase activity GO:0000030
sulfur amino acid transmembrane transpor... GO:0000099
microfilament motor activity GO:0000146
SNARE binding GO:0000149
nucleotide binding GO:0000166
3'−5'−exoribonuclease activity GO:0000175
DNA secondary structure binding GO:0000217
magnesium ion binding GO:0000287
adenyl−nucleotide exchange factor activi... GO:0000774
inositol hexakisphosphate binding GO:0000822
mRNA regulatory element binding translat... GO:0000900
transcription cis−regulatory region bind... GO:0000976
RNA polymerase II transcription regulato... GO:0000977
RNA polymerase II cis−regulatory region ... GO:0000978
RNA polymerase II core promoter sequence... GO:0000979
DNA−binding transcription factor activit... GO:0000981
cis−regulatory region sequence−specific ... GO:0000987
core promoter sequence−specific DNA bind... GO:0001046
transcription regulatory region nucleic ... GO:0001067
intronic transcription regulatory region... GO:0001161
RNA polymerase II intronic transcription... GO:0001162
DNA−binding transcription activator acti... GO:0001216
DNA−binding transcription repressor acti... GO:0001217
transcription coregulator binding GO:0001221
transcription corepressor binding GO:0001222
transcription coactivator binding GO:0001223
DNA−binding transcription repressor acti... GO:0001227
DNA−binding transcription activator acti... GO:0001228
amyloid−beta binding GO:0001540
non−tyrosine kinase fibroblast growth fa... GO:0001571
p=1.0E+00 | n=0
fg=NaN | bg=NaN
0 1 2 3 4 5
−log(p)
n=0/14 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001624046.3
fraction genes in fg and expected valu
histone deacetylase complex GO:0000118
histone acetyltransferase complex GO:0000123
SAGA complex GO:0000124
transcription factor TFIIIC complex GO:0000127
Golgi trans cisterna GO:0000138
Golgi membrane GO:0000139
ubiquitin ligase complex GO:0000151
nuclear ubiquitin ligase complex GO:0000152
cytoplasmic ubiquitin ligase complex GO:0000153
vacuolar proton−transporting V−type ATPa... GO:0000220
vacuolar proton−transporting V−type ATPa... GO:0000221
nuclear chromosome GO:0000228
organellar ribosome GO:0000313
organellar small ribosomal subunit GO:0000314
storage vacuole GO:0000322
lytic vacuole GO:0000323
fungal−type vacuole GO:0000324
fungal−type vacuole membrane GO:0000329
autophagosome membrane GO:0000421
DNA−directed RNA polymerase complex GO:0000428
chromosome, centromeric region GO:0000775
kinetochore GO:0000776
condensed chromosome, centromeric region GO:0000779
chromosome, telomeric region GO:0000781
chromatin GO:0000785
euchromatin GO:0000791
heterochromatin GO:0000792
condensed chromosome GO:0000793
condensed nuclear chromosome GO:0000794
synaptonemal complex GO:0000795
p=1.0E+00 | n=0
fg=NaN | bg=NaN
0 1 2 3 4 5
−log(p)
n=0/14 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction