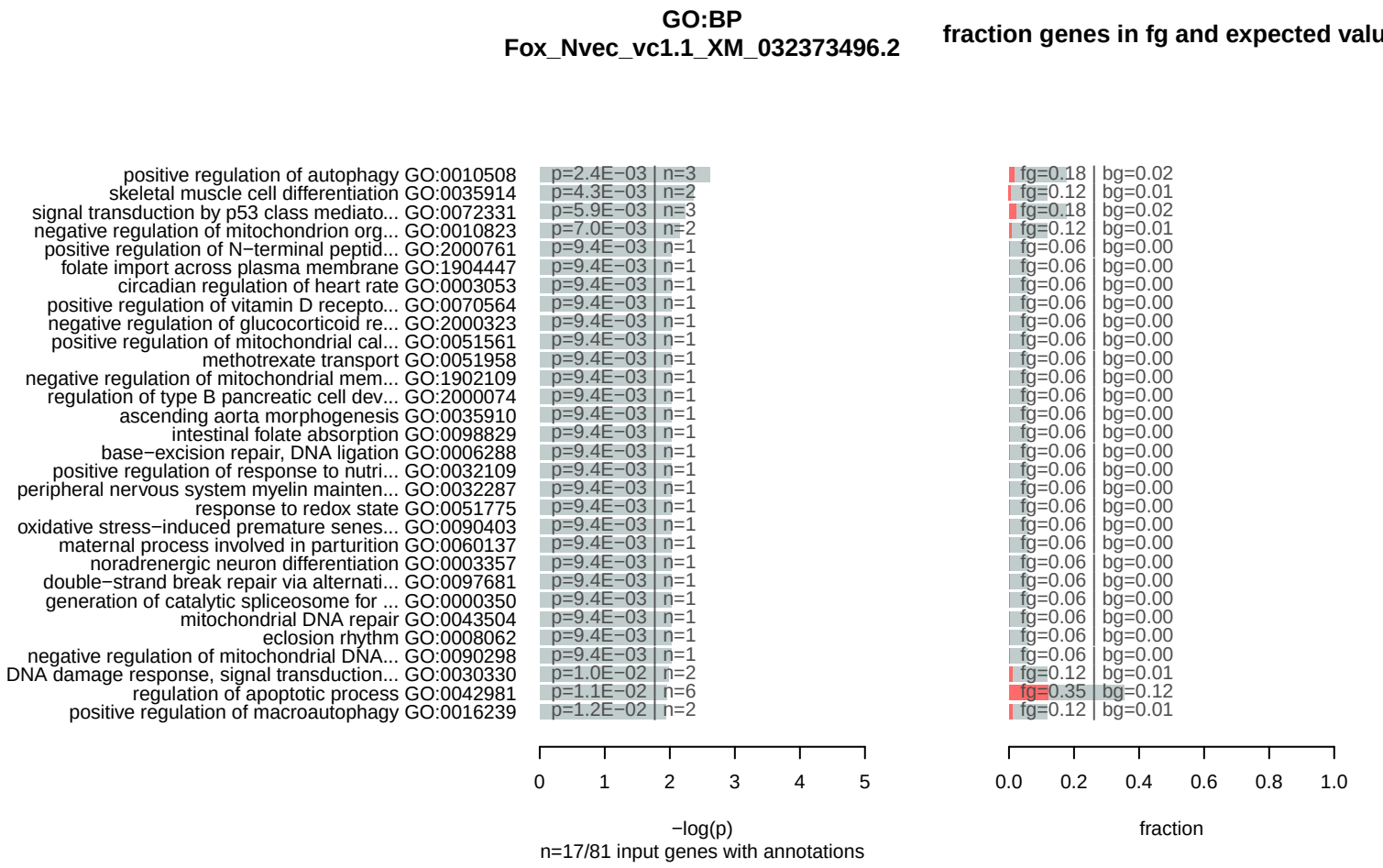
GO:BP
Fox_Nvec_vc1.1_XM_032373496.2
fraction genes in fg and expected valu
positive regulation of autophagy GO:0010508 p=2.4E−03 n=3 fg=0.18 bg=0.02
skeletal muscle cell differentiation GO:0035914 p=4.3E−03 n=2 fg=0.12 bg=0.01
signal transduction by p53 class mediato... GO:0072331 p=5.9E−03 n=3 fg=0.18 bg=0.02
negative regulation of mitochondrion org... GO:0010823 p=7.0E−03 n=2 fg=0.12 bg=0.01
positive regulation of N−terminal peptid... GO:2000761 p=9.4E−03 n=1 fg=0.06 bg=0.00
folate import across plasma membrane GO:1904447 p=9.4E−03 n=1 fg=0.06 bg=0.00
circadian regulation of heart rate GO:0003053 p=9.4E−03 n=1 fg=0.06 bg=0.00
positive regulation of vitamin D recepto... GO:0070564 p=9.4E−03 n=1 fg=0.06 bg=0.00
negative regulation of glucocorticoid re... GO:2000323 p=9.4E−03 n=1 fg=0.06 bg=0.00
positive regulation of mitochondrial cal... GO:0051561 p=9.4E−03 n=1 fg=0.06 bg=0.00
methotrexate transport GO:0051958 p=9.4E−03 n=1 fg=0.06 bg=0.00
negative regulation of mitochondrial mem... GO:1902109 p=9.4E−03 n=1 fg=0.06 bg=0.00
regulation of type B pancreatic cell dev... GO:2000074 p=9.4E−03 n=1 fg=0.06 bg=0.00
ascending aorta morphogenesis GO:0035910 p=9.4E−03 n=1 fg=0.06 bg=0.00
intestinal folate absorption GO:0098829 p=9.4E−03 n=1 fg=0.06 bg=0.00
base−excision repair, DNA ligation GO:0006288 p=9.4E−03 n=1 fg=0.06 bg=0.00
positive regulation of response to nutri... GO:0032109 p=9.4E−03 n=1 fg=0.06 bg=0.00
peripheral nervous system myelin mainten... GO:0032287 p=9.4E−03 n=1 fg=0.06 bg=0.00
response to redox state GO:0051775 p=9.4E−03 n=1 fg=0.06 bg=0.00
oxidative stress−induced premature senes... GO:0090403 p=9.4E−03 n=1 fg=0.06 bg=0.00
maternal process involved in parturition GO:0060137 p=9.4E−03 n=1 fg=0.06 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=9.4E−03 n=1 fg=0.06 bg=0.00
double−strand break repair via alternati... GO:0097681 p=9.4E−03 n=1 fg=0.06 bg=0.00
generation of catalytic spliceosome for ... GO:0000350 p=9.4E−03 n=1 fg=0.06 bg=0.00
mitochondrial DNA repair GO:0043504 p=9.4E−03 n=1 fg=0.06 bg=0.00
eclosion rhythm GO:0008062 p=9.4E−03 n=1 fg=0.06 bg=0.00
negative regulation of mitochondrial DNA... GO:0090298 p=9.4E−03 n=1 fg=0.06 bg=0.00
DNA damage response, signal transduction... GO:0030330 p=1.0E−02 n=2 fg=0.12 bg=0.01
regulation of apoptotic process GO:0042981 p=1.1E−02 n=6 fg=0.35 bg=0.12
positive regulation of macroautophagy GO:0016239 p=1.2E−02 n=2 fg=0.12 bg=0.01
0 1 2 3 4 5
−log(p)
n=17/81 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032373496.2
fraction genes in fg and expected valu
methotrexate transmembrane transporter a... GO:0015350 p=1.1E−02 n=1 fg=0.06 bg=0.00
nickel cation binding GO:0016151 p=1.1E−02 n=1 fg=0.06 bg=0.00
folic acid transmembrane transporter act... GO:0008517 p=1.1E−02 n=1 fg=0.06 bg=0.00
xenobiotic transmembrane transporter act... GO:0042910 p=1.1E−02 n=1 fg=0.06 bg=0.00
mRNA 5'−UTR binding GO:0048027 p=1.1E−02 n=1 fg=0.06 bg=0.00
protein heterodimerization activity GO:0046982 p=1.4E−02 n=4 fg=0.24 bg=0.06
DNA ligase (ATP) activity GO:0003910 p=2.1E−02 n=1 fg=0.06 bg=0.00
nuclear vitamin D receptor binding GO:0042809 p=2.1E−02 n=1 fg=0.06 bg=0.00
heme transmembrane transporter activity GO:0015232 p=2.1E−02 n=1 fg=0.06 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=2.1E−02 n=1 fg=0.06 bg=0.00
DNA ligase activity GO:0003909 p=2.1E−02 n=1 fg=0.06 bg=0.00
carbonate dehydratase activity GO:0004089 p=3.2E−02 n=1 fg=0.06 bg=0.00
RNA stem−loop binding GO:0035613 p=3.2E−02 n=1 fg=0.06 bg=0.00
sequence−specific mRNA binding GO:1990825 p=3.2E−02 n=1 fg=0.06 bg=0.00
nuclear retinoic acid receptor binding GO:0042974 p=3.2E−02 n=1 fg=0.06 bg=0.00
bHLH transcription factor binding GO:0043425 p=3.2E−02 n=1 fg=0.06 bg=0.00
phosphorylase kinase activity GO:0004689 p=3.2E−02 n=1 fg=0.06 bg=0.00
ligase activity, forming phosphoric este... GO:0016886 p=3.2E−02 n=1 fg=0.06 bg=0.00
phospholipase A2 activity GO:0004623 p=4.2E−02 n=1 fg=0.06 bg=0.00
gamma−tubulin binding GO:0043015 p=4.2E−02 n=1 fg=0.06 bg=0.00
dicarboxylic acid transmembrane transpor... GO:0005310 p=4.2E−02 n=1 fg=0.06 bg=0.00
vitamin transmembrane transporter activi... GO:0090482 p=5.2E−02 n=1 fg=0.06 bg=0.00
protein dimerization activity GO:0046983 p=5.8E−02 n=5 fg=0.29 bg=0.13
RNA polymerase II−specific DNA−binding t... GO:0061629 p=6.0E−02 n=2 fg=0.12 bg=0.02
ubiquitin−specific protease binding GO:1990381 p=6.2E−02 n=1 fg=0.06 bg=0.00
aryl hydrocarbon receptor binding GO:0017162 p=6.2E−02 n=1 fg=0.06 bg=0.00
modified amino acid transmembrane transp... GO:0072349 p=6.2E−02 n=1 fg=0.06 bg=0.00
DNA−binding transcription factor binding GO:0140297 p=6.9E−02 n=2 fg=0.12 bg=0.03
hydro−lyase activity GO:0016836 p=8.2E−02 n=1 fg=0.06 bg=0.01
Notch binding GO:0005112 p=8.2E−02 n=1 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=17/81 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
DNA ligase III−XRCC1 complex GO:0070421 p=1.1E−02 n=1 fg=0.05 bg=0.00
post−mRNA release spliceosomal complex GO:0071014 p=1.1E−02 n=1 fg=0.05 bg=0.00
SMAD protein complex GO:0071141 p=2.1E−02 n=1 fg=0.05 bg=0.00
U2−type catalytic step 2 spliceosome GO:0071007 p=2.1E−02 n=1 fg=0.05 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=3.1E−02 n=1 fg=0.05 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=3.1E−02 n=1 fg=0.05 bg=0.00
Prp19 complex GO:0000974 p=3.1E−02 n=1 fg=0.05 bg=0.00
phagophore assembly site GO:0000407 p=3.1E−02 n=1 fg=0.05 bg=0.00
Hrd1p ubiquitin ligase ERAD−L complex GO:0000839 p=3.1E−02 n=1 fg=0.05 bg=0.00
phosphorylase kinase complex GO:0005964 p=3.1E−02 n=1 fg=0.05 bg=0.00
fungal−type vacuole GO:0000324 p=4.1E−02 n=1 fg=0.05 bg=0.00
fungal−type vacuole membrane GO:0000329 p=4.1E−02 n=1 fg=0.05 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=4.1E−02 n=1 fg=0.05 bg=0.00
rough endoplasmic reticulum membrane GO:0030867 p=4.1E−02 n=1 fg=0.05 bg=0.00
chromatoid body GO:0033391 p=4.1E−02 n=1 fg=0.05 bg=0.00
ER ubiquitin ligase complex GO:0000835 p=4.1E−02 n=1 fg=0.05 bg=0.00
Hrd1p ubiquitin ligase complex GO:0000836 p=4.1E−02 n=1 fg=0.05 bg=0.00
storage vacuole GO:0000322 p=5.1E−02 n=1 fg=0.05 bg=0.00
synaptonemal complex GO:0000795 p=5.1E−02 n=1 fg=0.05 bg=0.00
synaptonemal structure GO:0099086 p=5.1E−02 n=1 fg=0.05 bg=0.00
nucleus GO:0005634 p=5.4E−02 n=13 fg=0.68 bg=0.48
Derlin−1 retrotranslocation complex GO:0036513 p=6.1E−02 n=1 fg=0.05 bg=0.00
cytoplasmic ubiquitin ligase complex GO:0000153 p=6.1E−02 n=1 fg=0.05 bg=0.00
integral component of mitochondrial memb... GO:0032592 p=8.1E−02 n=1 fg=0.05 bg=0.00
U2−type spliceosomal complex GO:0005684 p=8.1E−02 n=1 fg=0.05 bg=0.00
intrinsic component of mitochondrial mem... GO:0098573 p=8.1E−02 n=1 fg=0.05 bg=0.00
recycling endosome membrane GO:0055038 p=9.1E−02 n=1 fg=0.05 bg=0.00
condensed nuclear chromosome GO:0000794 p=1.0E−01 n=1 fg=0.05 bg=0.01
serine/threonine protein kinase complex GO:1902554 p=1.0E−01 n=1 fg=0.05 bg=0.01
nuclear lumen GO:0031981 p=1.1E−01 n=9 fg=0.47 bg=0.32
0 1 2 3 4 5
−log(p)
n=19/81 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction