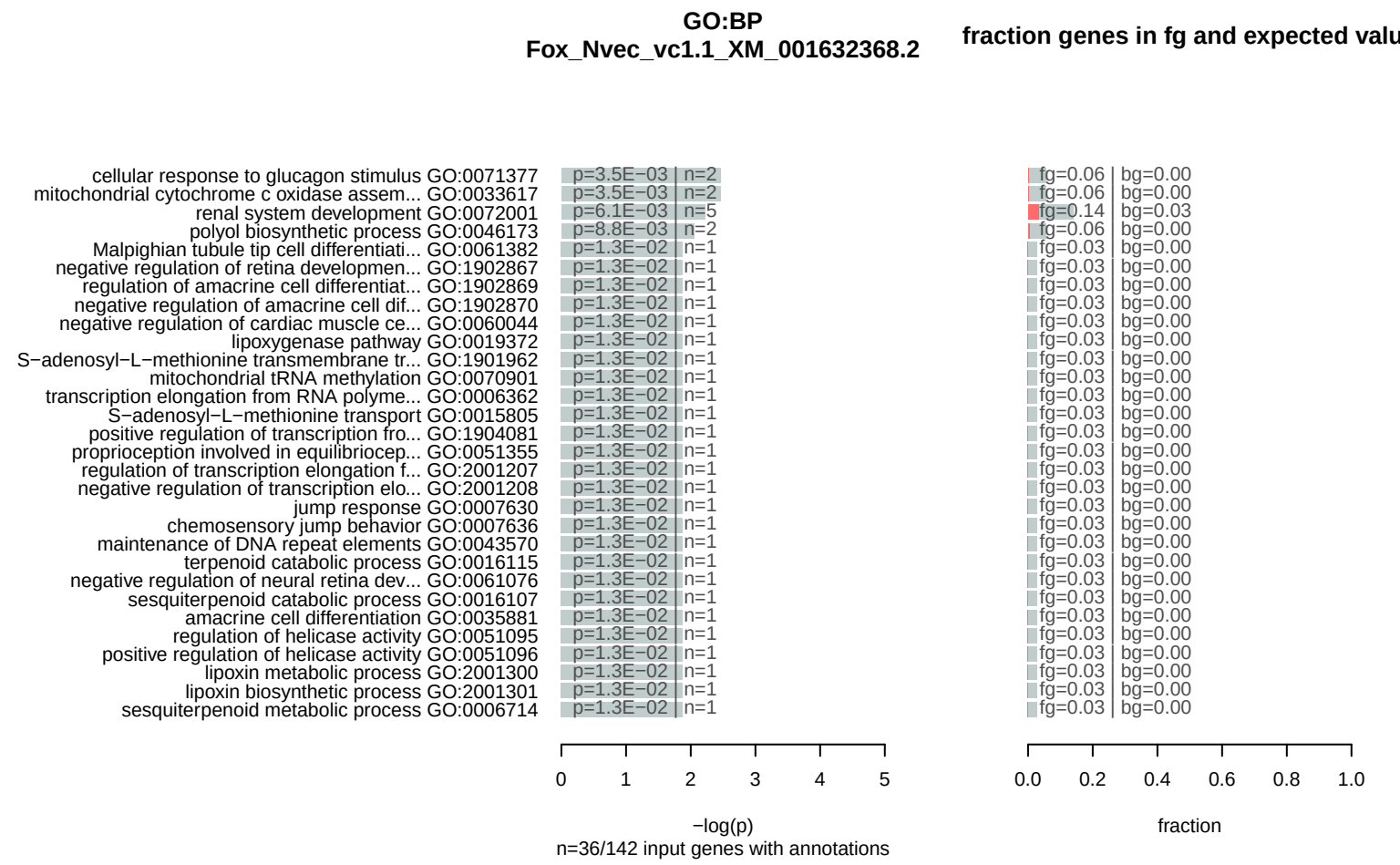
GO:BP
Fox_Nvec_vc1.1_XM_001632368.2
fraction genes in fg and expected valu
cellular response to glucagon stimulus GO:0071377 p=3.5E−03 n=2 fg=0.06 bg=0.00
mitochondrial cytochrome c oxidase assem... GO:0033617 p=3.5E−03 n=2 fg=0.06 bg=0.00
renal system development GO:0072001 p=6.1E−03 n=5 fg=0.14 bg=0.03
polyol biosynthetic process GO:0046173 p=8.8E−03 n=2 fg=0.06 bg=0.00
Malpighian tubule tip cell differentiati... GO:0061382 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of retina developmen... GO:1902867 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of amacrine cell differentiat... GO:1902869 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of amacrine cell dif... GO:1902870 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of cardiac muscle ce... GO:0060044 p=1.3E−02 n=1 fg=0.03 bg=0.00
lipoxygenase pathway GO:0019372 p=1.3E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:1901962 p=1.3E−02 n=1 fg=0.03 bg=0.00
mitochondrial tRNA methylation GO:0070901 p=1.3E−02 n=1 fg=0.03 bg=0.00
transcription elongation from RNA polyme... GO:0006362 p=1.3E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transport GO:0015805 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of transcription fro... GO:1904081 p=1.3E−02 n=1 fg=0.03 bg=0.00
proprioception involved in equilibriocep... GO:0051355 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of transcription elongation f... GO:2001207 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of transcription elo... GO:2001208 p=1.3E−02 n=1 fg=0.03 bg=0.00
jump response GO:0007630 p=1.3E−02 n=1 fg=0.03 bg=0.00
chemosensory jump behavior GO:0007636 p=1.3E−02 n=1 fg=0.03 bg=0.00
maintenance of DNA repeat elements GO:0043570 p=1.3E−02 n=1 fg=0.03 bg=0.00
terpenoid catabolic process GO:0016115 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of neural retina dev... GO:0061076 p=1.3E−02 n=1 fg=0.03 bg=0.00
sesquiterpenoid catabolic process GO:0016107 p=1.3E−02 n=1 fg=0.03 bg=0.00
amacrine cell differentiation GO:0035881 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of helicase activity GO:0051095 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of helicase activity GO:0051096 p=1.3E−02 n=1 fg=0.03 bg=0.00
lipoxin metabolic process GO:2001300 p=1.3E−02 n=1 fg=0.03 bg=0.00
lipoxin biosynthetic process GO:2001301 p=1.3E−02 n=1 fg=0.03 bg=0.00
sesquiterpenoid metabolic process GO:0006714 p=1.3E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=36/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001632368.2
fraction genes in fg and expected valu
15−hydroxyprostaglandin dehydrogenase (N... GO:0016404 p=1.3E−02 n=1 fg=0.03 bg=0.00
DNA insertion or deletion binding GO:0032135 p=1.3E−02 n=1 fg=0.03 bg=0.00
heteroduplex DNA loop binding GO:0000404 p=1.3E−02 n=1 fg=0.03 bg=0.00
double−strand/single−strand DNA junction... GO:0000406 p=1.3E−02 n=1 fg=0.03 bg=0.00
poly(ADP−ribose) glycohydrolase activity GO:0004649 p=1.3E−02 n=1 fg=0.03 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=1.3E−02 n=1 fg=0.03 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=1.3E−02 n=1 fg=0.03 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=1.3E−02 n=1 fg=0.03 bg=0.00
centromeric DNA binding GO:0019237 p=1.3E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate 4−... GO:0034597 p=1.3E−02 n=1 fg=0.03 bg=0.00
beta−1,3−galactosyl−O−glycosyl−glycoprot... GO:0047223 p=1.3E−02 n=1 fg=0.03 bg=0.00
prostaglandin E receptor activity GO:0004957 p=1.3E−02 n=1 fg=0.03 bg=0.00
non−tyrosine kinase fibroblast growth fa... GO:0001571 p=1.3E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=1.3E−02 n=1 fg=0.03 bg=0.00
protein kinase inhibitor activity GO:0004860 p=2.1E−02 n=2 fg=0.07 bg=0.01
kinase inhibitor activity GO:0019210 p=2.1E−02 n=2 fg=0.07 bg=0.01
beta−2 adrenergic receptor binding GO:0031698 p=2.5E−02 n=1 fg=0.03 bg=0.00
Y−form DNA binding GO:0000403 p=2.5E−02 n=1 fg=0.03 bg=0.00
NAD+ binding GO:0070403 p=2.5E−02 n=1 fg=0.03 bg=0.00
mismatched DNA binding GO:0030983 p=2.5E−02 n=1 fg=0.03 bg=0.00
protein tag GO:0031386 p=2.5E−02 n=1 fg=0.03 bg=0.00
gamma−butyrobetaine dioxygenase activity GO:0008336 p=2.5E−02 n=1 fg=0.03 bg=0.00
manganese ion binding GO:0030145 p=2.8E−02 n=2 fg=0.07 bg=0.01
double−stranded DNA binding GO:0003690 p=2.8E−02 n=5 fg=0.17 bg=0.06
structural constituent of ribosome GO:0003735 p=3.4E−02 n=3 fg=0.10 bg=0.02
oxidoreductase activity, acting on CH−OH... GO:0016614 p=3.6E−02 n=2 fg=0.07 bg=0.01
inosine kinase activity GO:0008906 p=3.8E−02 n=1 fg=0.03 bg=0.00
cAMP response element binding GO:0035497 p=3.8E−02 n=1 fg=0.03 bg=0.00
phosphoenolpyruvate carboxykinase activi... GO:0004611 p=3.8E−02 n=1 fg=0.03 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=3.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=30/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001632368.2
fraction genes in fg and expected valu
MutSbeta complex GO:0032302 p=1.3E−02 n=1 fg=0.03 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000276 p=1.3E−02 n=1 fg=0.03 bg=0.00
proton−transporting ATP synthase complex... GO:0045263 p=1.3E−02 n=1 fg=0.03 bg=0.00
proton−transporting ATP synthase, centra... GO:0045269 p=1.3E−02 n=1 fg=0.03 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005756 p=1.3E−02 n=1 fg=0.03 bg=0.00
mitochondrion GO:0005739 p=1.8E−02 n=10 fg=0.29 bg=0.14
cytosolic ribosome GO:0022626 p=2.1E−02 n=3 fg=0.09 bg=0.02
mitochondrial proton−transporting ATP sy... GO:0000275 p=2.6E−02 n=1 fg=0.03 bg=0.00
proton−transporting ATP synthase complex... GO:0045261 p=2.6E−02 n=1 fg=0.03 bg=0.00
proton−transporting ATP synthase complex GO:0045259 p=2.6E−02 n=1 fg=0.03 bg=0.00
cytosolic region GO:0099522 p=2.6E−02 n=1 fg=0.03 bg=0.00
postsynaptic cytosol GO:0099524 p=2.6E−02 n=1 fg=0.03 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005753 p=2.6E−02 n=1 fg=0.03 bg=0.00
mismatch repair complex GO:0032300 p=3.8E−02 n=1 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=3.8E−02 n=1 fg=0.03 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=3.8E−02 n=1 fg=0.03 bg=0.00
phagophore assembly site membrane GO:0034045 p=3.8E−02 n=1 fg=0.03 bg=0.00
ESC/E(Z) complex GO:0035098 p=3.8E−02 n=1 fg=0.03 bg=0.00
ribosomal subunit GO:0044391 p=4.3E−02 n=3 fg=0.09 bg=0.02
cytosolic large ribosomal subunit GO:0022625 p=4.7E−02 n=2 fg=0.06 bg=0.01
sperm head GO:0061827 p=5.1E−02 n=1 fg=0.03 bg=0.00
chromatoid body GO:0033391 p=5.1E−02 n=1 fg=0.03 bg=0.00
pi−body GO:0071546 p=5.1E−02 n=1 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=5.1E−02 n=1 fg=0.03 bg=0.00
ribosome GO:0005840 p=6.0E−02 n=3 fg=0.09 bg=0.03
proton−transporting two−sector ATPase co... GO:0033178 p=6.3E−02 n=1 fg=0.03 bg=0.00
phagophore assembly site GO:0000407 p=6.3E−02 n=1 fg=0.03 bg=0.00
spindle pole centrosome GO:0031616 p=7.5E−02 n=1 fg=0.03 bg=0.00
large ribosomal subunit GO:0015934 p=8.6E−02 n=2 fg=0.06 bg=0.01
preribosome, small subunit precursor GO:0030688 p=8.7E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction