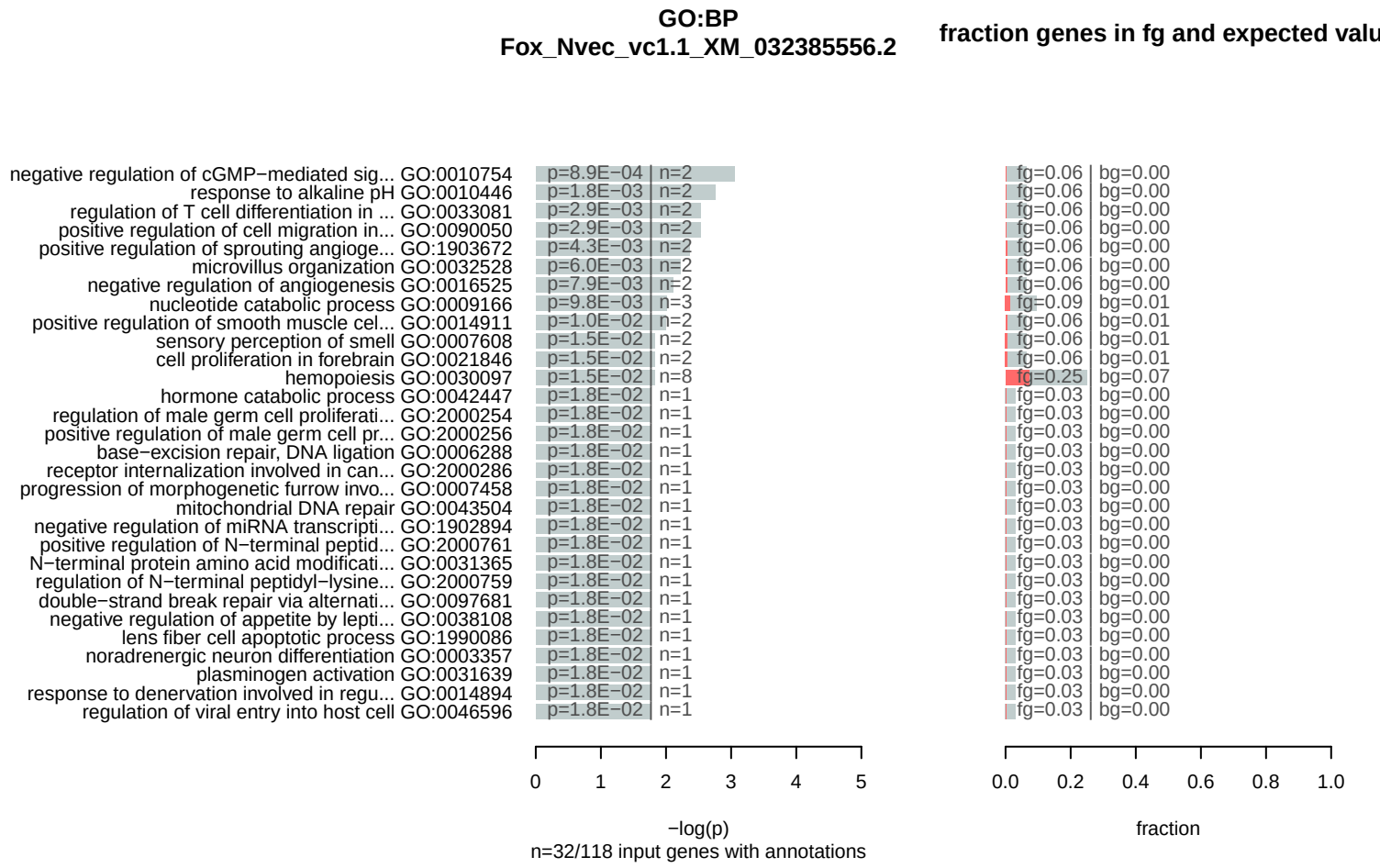
GO:BP
Fox_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
negative regulation of cGMP−mediated sig... GO:0010754 p=8.9E−04 n=2 fg=0.06 bg=0.00
response to alkaline pH GO:0010446 p=1.8E−03 n=2 fg=0.06 bg=0.00
regulation of T cell differentiation in ... GO:0033081 p=2.9E−03 n=2 fg=0.06 bg=0.00
positive regulation of cell migration in... GO:0090050 p=2.9E−03 n=2 fg=0.06 bg=0.00
positive regulation of sprouting angioge... GO:1903672 p=4.3E−03 n=2 fg=0.06 bg=0.00
microvillus organization GO:0032528 p=6.0E−03 n=2 fg=0.06 bg=0.00
negative regulation of angiogenesis GO:0016525 p=7.9E−03 n=2 fg=0.06 bg=0.00
nucleotide catabolic process GO:0009166 p=9.8E−03 n=3 fg=0.09 bg=0.01
positive regulation of smooth muscle cel... GO:0014911 p=1.0E−02 n=2 fg=0.06 bg=0.01
sensory perception of smell GO:0007608 p=1.5E−02 n=2 fg=0.06 bg=0.01
cell proliferation in forebrain GO:0021846 p=1.5E−02 n=2 fg=0.06 bg=0.01
hemopoiesis GO:0030097 p=1.5E−02 n=8 fg=0.25 bg=0.07
hormone catabolic process GO:0042447 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of male germ cell proliferati... GO:2000254 p=1.8E−02 n=1 fg=0.03 bg=0.00
positive regulation of male germ cell pr... GO:2000256 p=1.8E−02 n=1 fg=0.03 bg=0.00
base−excision repair, DNA ligation GO:0006288 p=1.8E−02 n=1 fg=0.03 bg=0.00
receptor internalization involved in can... GO:2000286 p=1.8E−02 n=1 fg=0.03 bg=0.00
progression of morphogenetic furrow invo... GO:0007458 p=1.8E−02 n=1 fg=0.03 bg=0.00
mitochondrial DNA repair GO:0043504 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of miRNA transcripti... GO:1902894 p=1.8E−02 n=1 fg=0.03 bg=0.00
positive regulation of N−terminal peptid... GO:2000761 p=1.8E−02 n=1 fg=0.03 bg=0.00
N−terminal protein amino acid modificati... GO:0031365 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of N−terminal peptidyl−lysine... GO:2000759 p=1.8E−02 n=1 fg=0.03 bg=0.00
double−strand break repair via alternati... GO:0097681 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of appetite by lepti... GO:0038108 p=1.8E−02 n=1 fg=0.03 bg=0.00
lens fiber cell apoptotic process GO:1990086 p=1.8E−02 n=1 fg=0.03 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=1.8E−02 n=1 fg=0.03 bg=0.00
plasminogen activation GO:0031639 p=1.8E−02 n=1 fg=0.03 bg=0.00
response to denervation involved in regu... GO:0014894 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of viral entry into host cell GO:0046596 p=1.8E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/118 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
transcription corepressor binding GO:0001222 p=3.0E−04 n=2 fg=0.07 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=1.9E−03 n=6 fg=0.21 bg=0.05
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555 p=4.3E−03 n=2 fg=0.07 bg=0.00
ribosome binding GO:0043022 p=1.2E−02 n=2 fg=0.07 bg=0.01
calmodulin−activated dual specificity 3'... GO:0004117 p=1.8E−02 n=1 fg=0.04 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=1.8E−02 n=1 fg=0.04 bg=0.00
beta−endorphin binding GO:0031626 p=1.8E−02 n=1 fg=0.04 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=1.8E−02 n=1 fg=0.04 bg=0.00
pantetheine hydrolase activity GO:0017159 p=1.8E−02 n=1 fg=0.04 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=1.8E−02 n=1 fg=0.04 bg=0.00
protein−membrane adaptor activity GO:0043495 p=1.8E−02 n=1 fg=0.04 bg=0.00
insulin binding GO:0043559 p=1.8E−02 n=1 fg=0.04 bg=0.00
transcription coregulator activity GO:0003712 p=2.2E−02 n=5 fg=0.18 bg=0.06
hydrolase activity, acting on carbon−nit... GO:0016811 p=3.1E−02 n=2 fg=0.07 bg=0.01
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=3.5E−02 n=1 fg=0.04 bg=0.00
DNA ligase activity GO:0003909 p=3.5E−02 n=1 fg=0.04 bg=0.00
phosphotransferase activity, carboxyl gr... GO:0016774 p=3.5E−02 n=1 fg=0.04 bg=0.00
acetyl−CoA hydrolase activity GO:0003986 p=3.5E−02 n=1 fg=0.04 bg=0.00
calcium−dependent protein kinase regulat... GO:0010858 p=3.5E−02 n=1 fg=0.04 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=3.5E−02 n=1 fg=0.04 bg=0.00
DNA ligase (ATP) activity GO:0003910 p=3.5E−02 n=1 fg=0.04 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=3.5E−02 n=1 fg=0.04 bg=0.00
calcium−dependent protein kinase inhibit... GO:0008427 p=3.5E−02 n=1 fg=0.04 bg=0.00
ubiquitination−like modification−depende... GO:0140035 p=3.5E−02 n=1 fg=0.04 bg=0.00
ubiquitin−dependent protein binding GO:0140036 p=3.5E−02 n=1 fg=0.04 bg=0.00
GPI anchor binding GO:0034235 p=3.5E−02 n=1 fg=0.04 bg=0.00
O−acetyltransferase activity GO:0016413 p=3.5E−02 n=1 fg=0.04 bg=0.00
SUMO transferase activity GO:0019789 p=3.5E−02 n=1 fg=0.04 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=3.5E−02 n=5 fg=0.18 bg=0.07
transcription regulator activity GO:0140110 p=3.7E−02 n=7 fg=0.25 bg=0.12
0 1 2 3 4 5
−log(p)
n=28/118 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
histone deacetylase complex GO:0000118 p=1.3E−02 n=2 fg=0.06 bg=0.01
RNA polymerase II transcription represso... GO:0090571 p=1.8E−02 n=1 fg=0.03 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=1.8E−02 n=1 fg=0.03 bg=0.00
A band GO:0031672 p=2.2E−02 n=2 fg=0.06 bg=0.01
extracellular region GO:0005576 p=2.4E−02 n=6 fg=0.18 bg=0.07
nuclear chromosome GO:0000228 p=3.1E−02 n=4 fg=0.12 bg=0.04
BBSome GO:0034464 p=3.6E−02 n=1 fg=0.03 bg=0.00
lipid droplet GO:0005811 p=4.5E−02 n=2 fg=0.06 bg=0.01
mitochondria−associated endoplasmic reti... GO:0044233 p=5.4E−02 n=1 fg=0.03 bg=0.00
Sin3−type complex GO:0070822 p=5.4E−02 n=1 fg=0.03 bg=0.00
peroxisomal matrix GO:0005782 p=7.1E−02 n=1 fg=0.03 bg=0.00
pericentriolar material GO:0000242 p=7.1E−02 n=1 fg=0.03 bg=0.00
microbody lumen GO:0031907 p=7.1E−02 n=1 fg=0.03 bg=0.00
Z disc GO:0030018 p=7.5E−02 n=2 fg=0.06 bg=0.01
extracellular space GO:0005615 p=7.6E−02 n=3 fg=0.09 bg=0.03
I band GO:0031674 p=8.0E−02 n=2 fg=0.06 bg=0.01
synaptonemal complex GO:0000795 p=8.8E−02 n=1 fg=0.03 bg=0.00
filopodium tip GO:0032433 p=8.8E−02 n=1 fg=0.03 bg=0.00
synaptonemal structure GO:0099086 p=8.8E−02 n=1 fg=0.03 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=8.8E−02 n=1 fg=0.03 bg=0.00
sperm fibrous sheath GO:0035686 p=8.8E−02 n=1 fg=0.03 bg=0.00
tertiary granule lumen GO:1904724 p=1.0E−01 n=1 fg=0.03 bg=0.00
centriolar satellite GO:0034451 p=1.0E−01 n=1 fg=0.03 bg=0.00
cytosolic proteasome complex GO:0031597 p=1.0E−01 n=1 fg=0.03 bg=0.00
organelle membrane contact site GO:0044232 p=1.0E−01 n=1 fg=0.03 bg=0.00
chromosome GO:0005694 p=1.1E−01 n=5 fg=0.15 bg=0.08
neuromuscular junction GO:0031594 p=1.2E−01 n=2 fg=0.06 bg=0.02
sarcomere GO:0030017 p=1.3E−01 n=2 fg=0.06 bg=0.02
azurophil granule membrane GO:0035577 p=1.4E−01 n=1 fg=0.03 bg=0.00
fusome GO:0045169 p=1.4E−01 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=33/118 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction