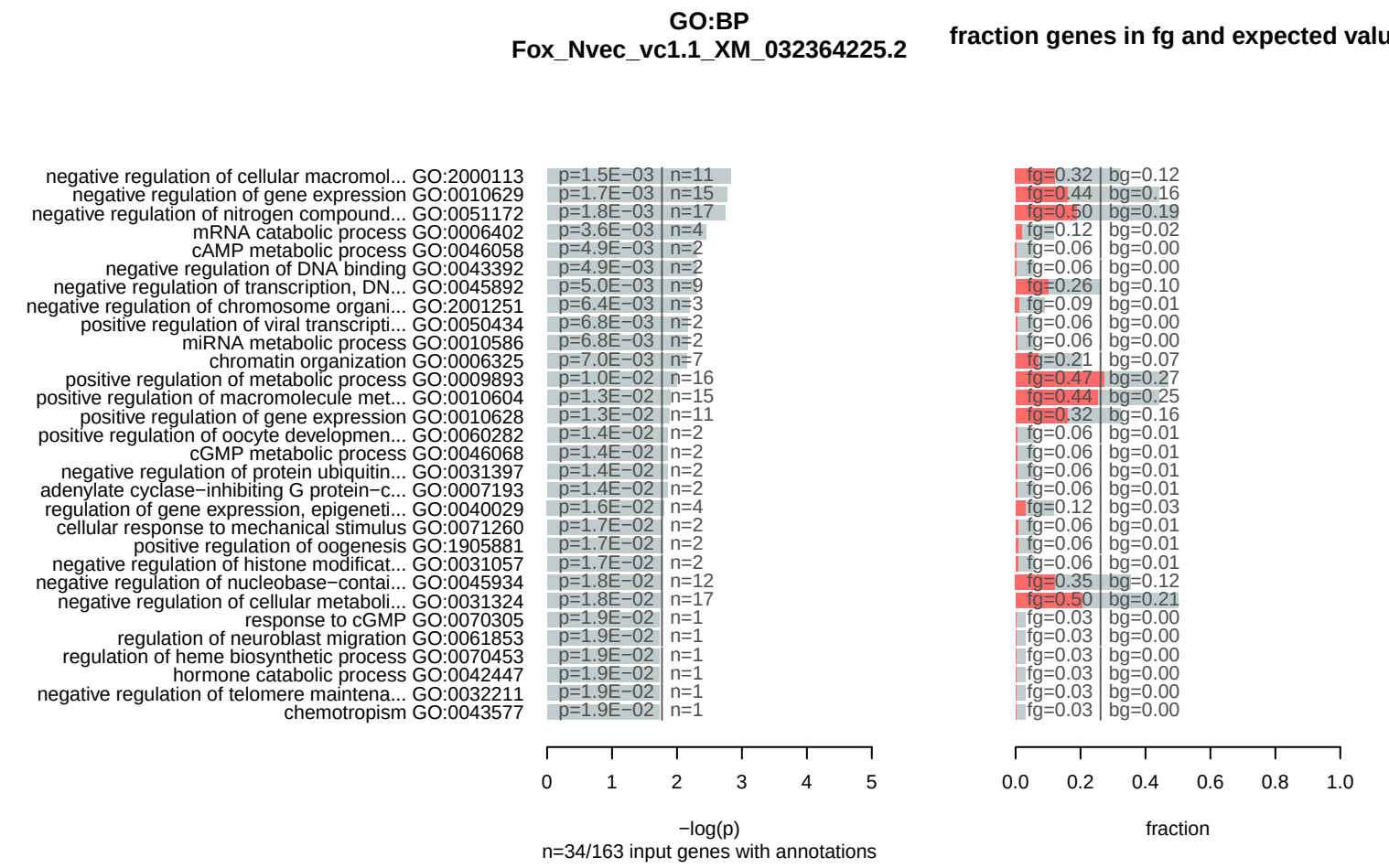
GO:BP
Fox_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
negative regulation of cellular macromol... GO:2000113 p=1.5E−03 n=11 fg=0.32 bg=0.12
negative regulation of gene expression GO:0010629 p=1.7E−03 n=15 fg=0.44 bg=0.16
negative regulation of nitrogen compound... GO:0051172 p=1.8E−03 n=17 fg=0.50 bg=0.19
mRNA catabolic process GO:0006402 p=3.6E−03 n=4 fg=0.12 bg=0.02
cAMP metabolic process GO:0046058 p=4.9E−03 n=2 fg=0.06 bg=0.00
negative regulation of DNA binding GO:0043392 p=4.9E−03 n=2 fg=0.06 bg=0.00
negative regulation of transcription, DN... GO:0045892 p=5.0E−03 n=9 fg=0.26 bg=0.10
negative regulation of chromosome organi... GO:2001251 p=6.4E−03 n=3 fg=0.09 bg=0.01
positive regulation of viral transcripti... GO:0050434 p=6.8E−03 n=2 fg=0.06 bg=0.00
miRNA metabolic process GO:0010586 p=6.8E−03 n=2 fg=0.06 bg=0.00
chromatin organization GO:0006325 p=7.0E−03 n=7 fg=0.21 bg=0.07
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positive regulation of gene expression GO:0010628 p=1.3E−02 n=11 fg=0.32 bg=0.16
positive regulation of oocyte developmen... GO:0060282 p=1.4E−02 n=2 fg=0.06 bg=0.01
cGMP metabolic process GO:0046068 p=1.4E−02 n=2 fg=0.06 bg=0.01
negative regulation of protein ubiquitin... GO:0031397 p=1.4E−02 n=2 fg=0.06 bg=0.01
adenylate cyclase−inhibiting G protein−c... GO:0007193 p=1.4E−02 n=2 fg=0.06 bg=0.01
regulation of gene expression, epigeneti... GO:0040029 p=1.6E−02 n=4 fg=0.12 bg=0.03
cellular response to mechanical stimulus GO:0071260 p=1.7E−02 n=2 fg=0.06 bg=0.01
positive regulation of oogenesis GO:1905881 p=1.7E−02 n=2 fg=0.06 bg=0.01
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response to cGMP GO:0070305 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of neuroblast migration GO:0061853 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of heme biosynthetic process GO:0070453 p=1.9E−02 n=1 fg=0.03 bg=0.00
hormone catabolic process GO:0042447 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of telomere maintena... GO:0032211 p=1.9E−02 n=1 fg=0.03 bg=0.00
chemotropism GO:0043577 p=1.9E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=34/163 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
ubiquitin−protein transferase regulator ... GO:0055106 p=1.2E−03 n=2 fg=0.06 bg=0.00
JUN kinase binding GO:0008432 p=3.8E−03 n=2 fg=0.06 bg=0.00
MAP kinase kinase kinase activity GO:0004709 p=5.6E−03 n=2 fg=0.06 bg=0.00
hormone binding GO:0042562 p=1.0E−02 n=2 fg=0.06 bg=0.01
mitogen−activated protein kinase binding GO:0051019 p=1.6E−02 n=2 fg=0.06 bg=0.01
calcium− and calmodulin−responsive adeny... GO:0008294 p=2.0E−02 n=1 fg=0.03 bg=0.00
adipokinetic hormone receptor activity GO:0097003 p=2.0E−02 n=1 fg=0.03 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=2.0E−02 n=1 fg=0.03 bg=0.00
NAD−retinol dehydrogenase activity GO:0004745 p=2.0E−02 n=1 fg=0.03 bg=0.00
ubiquitin ligase inhibitor activity GO:1990948 p=2.0E−02 n=1 fg=0.03 bg=0.00
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ubiquitin−protein transferase inhibitor ... GO:0055105 p=2.0E−02 n=1 fg=0.03 bg=0.00
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beta−endorphin binding GO:0031626 p=2.0E−02 n=1 fg=0.03 bg=0.00
JUN kinase kinase kinase activity GO:0004706 p=2.0E−02 n=1 fg=0.03 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=2.0E−02 n=1 fg=0.03 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=2.0E−02 n=1 fg=0.03 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=2.0E−02 n=1 fg=0.03 bg=0.00
SMC family protein binding GO:0043221 p=2.0E−02 n=1 fg=0.03 bg=0.00
co−SMAD binding GO:0070410 p=4.0E−02 n=1 fg=0.03 bg=0.00
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dipeptidase activity GO:0016805 p=4.0E−02 n=1 fg=0.03 bg=0.00
sphingolipid binding GO:0046625 p=4.0E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=4.0E−02 n=1 fg=0.03 bg=0.00
magnesium ion transmembrane transporter ... GO:0015095 p=4.0E−02 n=1 fg=0.03 bg=0.00
adenylate cyclase activity GO:0004016 p=4.0E−02 n=1 fg=0.03 bg=0.00
5S rRNA binding GO:0008097 p=4.0E−02 n=1 fg=0.03 bg=0.00
peroxisome proliferator activated recept... GO:0042975 p=4.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032364225.2
fraction genes in fg and expected valu
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=1.9E−02 n=1 fg=0.03 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=1.9E−02 n=1 fg=0.03 bg=0.00
endocytic vesicle lumen GO:0071682 p=1.9E−02 n=1 fg=0.03 bg=0.00
hippocampal mossy fiber GO:0097457 p=1.9E−02 n=1 fg=0.03 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=1.9E−02 n=1 fg=0.03 bg=0.00
polysome GO:0005844 p=2.1E−02 n=2 fg=0.06 bg=0.01
oligosaccharyltransferase complex GO:0008250 p=3.8E−02 n=1 fg=0.03 bg=0.00
TRAMP complex GO:0031499 p=3.8E−02 n=1 fg=0.03 bg=0.00
cytoplasmic side of rough endoplasmic re... GO:0098556 p=3.8E−02 n=1 fg=0.03 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=3.8E−02 n=1 fg=0.03 bg=0.00
RSF complex GO:0031213 p=3.8E−02 n=1 fg=0.03 bg=0.00
filamentous actin GO:0031941 p=3.8E−02 n=1 fg=0.03 bg=0.00
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rough endoplasmic reticulum GO:0005791 p=4.1E−02 n=2 fg=0.06 bg=0.01
lipid droplet GO:0005811 p=5.1E−02 n=2 fg=0.06 bg=0.01
intercalary heterochromatin GO:0005725 p=5.7E−02 n=1 fg=0.03 bg=0.00
PRC1 complex GO:0035102 p=5.7E−02 n=1 fg=0.03 bg=0.00
manchette GO:0002177 p=5.7E−02 n=1 fg=0.03 bg=0.00
polysomal ribosome GO:0042788 p=5.7E−02 n=1 fg=0.03 bg=0.00
beta−catenin−TCF complex GO:1990907 p=5.7E−02 n=1 fg=0.03 bg=0.00
muscle tendon junction GO:0005927 p=5.7E−02 n=1 fg=0.03 bg=0.00
ISWI−type complex GO:0031010 p=5.7E−02 n=1 fg=0.03 bg=0.00
microbody lumen GO:0031907 p=7.5E−02 n=1 fg=0.03 bg=0.00
microvillus membrane GO:0031528 p=7.5E−02 n=1 fg=0.03 bg=0.00
guanylate cyclase complex, soluble GO:0008074 p=7.5E−02 n=1 fg=0.03 bg=0.00
rough endoplasmic reticulum membrane GO:0030867 p=7.5E−02 n=1 fg=0.03 bg=0.00
cytosolic large ribosomal subunit GO:0022625 p=7.5E−02 n=1 fg=0.03 bg=0.00
peroxisomal matrix GO:0005782 p=7.5E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum protein−containing... GO:0140534 p=8.3E−02 n=2 fg=0.06 bg=0.01
EMC complex GO:0072546 p=9.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction