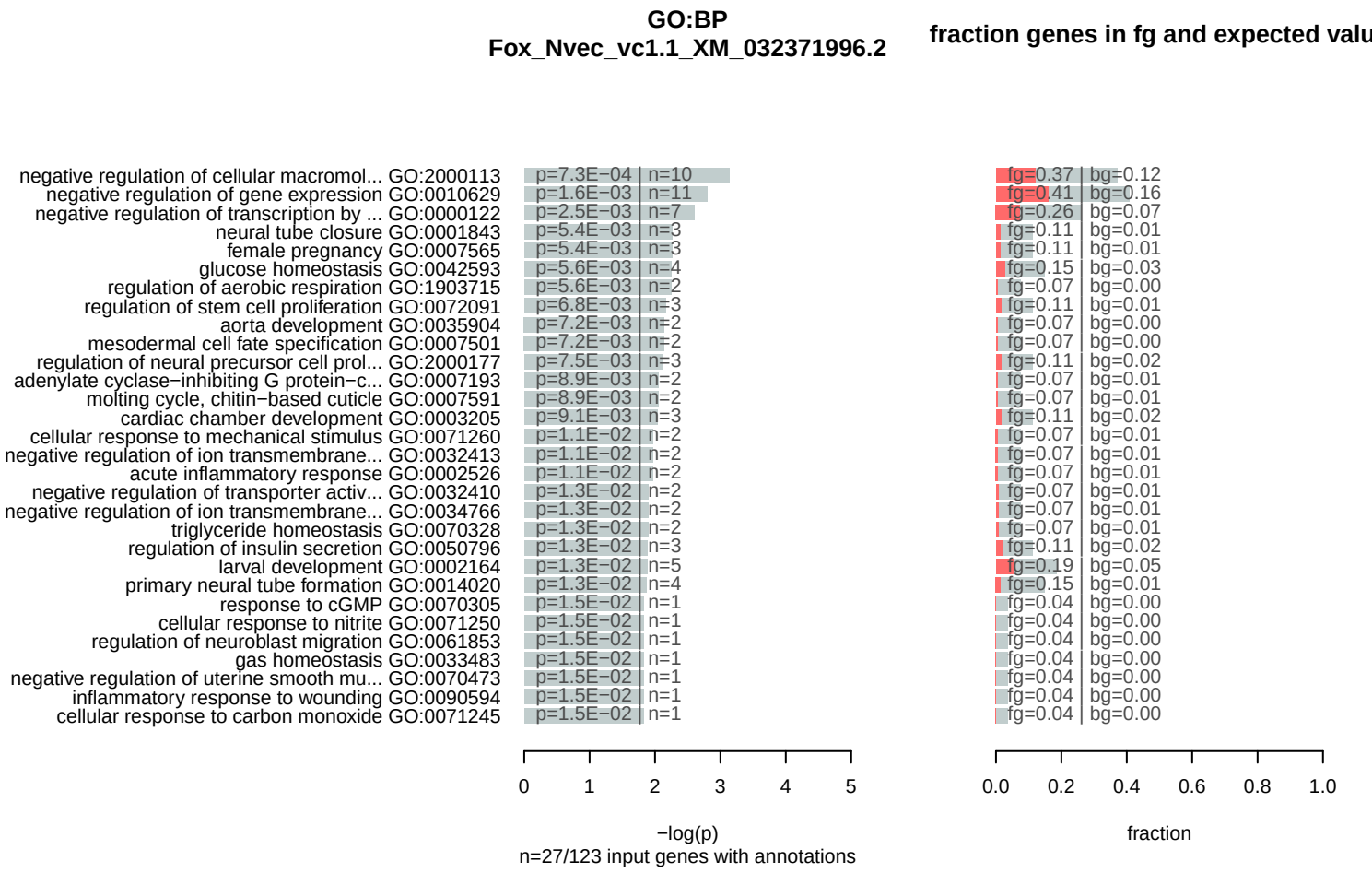
GO:BP
Fox_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
negative regulation of cellular macromol... GO:2000113 p=7.3E−04 n=10 fg=0.37 bg=0.12
negative regulation of gene expression GO:0010629 p=1.6E−03 n=11 fg=0.41 bg=0.16
negative regulation of transcription by ... GO:0000122 p=2.5E−03 n=7 fg=0.26 bg=0.07
neural tube closure GO:0001843 p=5.4E−03 n=3 fg=0.11 bg=0.01
female pregnancy GO:0007565 p=5.4E−03 n=3 fg=0.11 bg=0.01
glucose homeostasis GO:0042593 p=5.6E−03 n=4 fg=0.15 bg=0.03
regulation of aerobic respiration GO:1903715 p=5.6E−03 n=2 fg=0.07 bg=0.00
regulation of stem cell proliferation GO:0072091 p=6.8E−03 n=3 fg=0.11 bg=0.01
aorta development GO:0035904 p=7.2E−03 n=2 fg=0.07 bg=0.00
mesodermal cell fate specification GO:0007501 p=7.2E−03 n=2 fg=0.07 bg=0.00
regulation of neural precursor cell prol... GO:2000177 p=7.5E−03 n=3 fg=0.11 bg=0.02
adenylate cyclase−inhibiting G protein−c... GO:0007193 p=8.9E−03 n=2 fg=0.07 bg=0.01
molting cycle, chitin−based cuticle GO:0007591 p=8.9E−03 n=2 fg=0.07 bg=0.01
cardiac chamber development GO:0003205 p=9.1E−03 n=3 fg=0.11 bg=0.02
cellular response to mechanical stimulus GO:0071260 p=1.1E−02 n=2 fg=0.07 bg=0.01
negative regulation of ion transmembrane... GO:0032413 p=1.1E−02 n=2 fg=0.07 bg=0.01
acute inflammatory response GO:0002526 p=1.1E−02 n=2 fg=0.07 bg=0.01
negative regulation of transporter activ... GO:0032410 p=1.3E−02 n=2 fg=0.07 bg=0.01
negative regulation of ion transmembrane... GO:0034766 p=1.3E−02 n=2 fg=0.07 bg=0.01
triglyceride homeostasis GO:0070328 p=1.3E−02 n=2 fg=0.07 bg=0.01
regulation of insulin secretion GO:0050796 p=1.3E−02 n=3 fg=0.11 bg=0.02
larval development GO:0002164 p=1.3E−02 n=5 fg=0.19 bg=0.05
primary neural tube formation GO:0014020 p=1.3E−02 n=4 fg=0.15 bg=0.01
response to cGMP GO:0070305 p=1.5E−02 n=1 fg=0.04 bg=0.00
cellular response to nitrite GO:0071250 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of neuroblast migration GO:0061853 p=1.5E−02 n=1 fg=0.04 bg=0.00
gas homeostasis GO:0033483 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of uterine smooth mu... GO:0070473 p=1.5E−02 n=1 fg=0.04 bg=0.00
inflammatory response to wounding GO:0090594 p=1.5E−02 n=1 fg=0.04 bg=0.00
cellular response to carbon monoxide GO:0071245 p=1.5E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=27/123 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
protein heterodimerization activity GO:0046982 p=1.4E−03 n=6 fg=0.26 bg=0.06
transcription factor binding GO:0008134 p=5.4E−03 n=6 fg=0.26 bg=0.07
DNA−binding transcription factor activit... GO:0003700 p=8.4E−03 n=6 fg=0.26 bg=0.08
histone acetyltransferase binding GO:0035035 p=8.4E−03 n=2 fg=0.09 bg=0.01
ubiquitin ligase inhibitor activity GO:1990948 p=1.4E−02 n=1 fg=0.04 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=1.4E−02 n=1 fg=0.04 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=1.4E−02 n=1 fg=0.04 bg=0.00
NAD−retinol dehydrogenase activity GO:0004745 p=1.4E−02 n=1 fg=0.04 bg=0.00
adipokinetic hormone receptor activity GO:0097003 p=1.4E−02 n=1 fg=0.04 bg=0.00
alpha−adrenergic receptor activity GO:0004936 p=1.4E−02 n=1 fg=0.04 bg=0.00
cobalt ion binding GO:0050897 p=1.4E−02 n=1 fg=0.04 bg=0.00
alpha2−adrenergic receptor activity GO:0004938 p=1.4E−02 n=1 fg=0.04 bg=0.00
adiponectin binding GO:0055100 p=1.4E−02 n=1 fg=0.04 bg=0.00
ubiquitin−protein transferase inhibitor ... GO:0055105 p=1.4E−02 n=1 fg=0.04 bg=0.00
alpha−2C adrenergic receptor binding GO:0031696 p=1.4E−02 n=1 fg=0.04 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=1.6E−02 n=5 fg=0.22 bg=0.07
protein kinase binding GO:0019901 p=2.5E−02 n=5 fg=0.22 bg=0.08
histone deacetylase binding GO:0042826 p=2.7E−02 n=2 fg=0.09 bg=0.01
protein−hormone receptor activity GO:0016500 p=2.9E−02 n=1 fg=0.04 bg=0.00
TPR domain binding GO:0030911 p=2.9E−02 n=1 fg=0.04 bg=0.00
octopamine receptor activity GO:0004989 p=2.9E−02 n=1 fg=0.04 bg=0.00
UDP−galactose transmembrane transporter ... GO:0005459 p=2.9E−02 n=1 fg=0.04 bg=0.00
dipeptidase activity GO:0016805 p=2.9E−02 n=1 fg=0.04 bg=0.00
adrenergic receptor activity GO:0004935 p=2.9E−02 n=1 fg=0.04 bg=0.00
norepinephrine binding GO:0051380 p=2.9E−02 n=1 fg=0.04 bg=0.00
thioesterase binding GO:0031996 p=2.9E−02 n=1 fg=0.04 bg=0.00
peroxisome proliferator activated recept... GO:0042975 p=2.9E−02 n=1 fg=0.04 bg=0.00
co−SMAD binding GO:0070410 p=2.9E−02 n=1 fg=0.04 bg=0.00
GAF domain binding GO:0036004 p=2.9E−02 n=1 fg=0.04 bg=0.00
5S rRNA binding GO:0008097 p=2.9E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/123 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
actin cortical patch GO:0030479 p=1.5E−02 n=1 fg=0.04 bg=0.00
endocytic patch GO:0061645 p=1.5E−02 n=1 fg=0.04 bg=0.00
hippocampal mossy fiber GO:0097457 p=1.5E−02 n=1 fg=0.04 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=1.5E−02 n=1 fg=0.04 bg=0.00
transcription regulator complex GO:0005667 p=2.9E−02 n=4 fg=0.14 bg=0.04
SWI/SNF complex GO:0016514 p=3.1E−02 n=1 fg=0.04 bg=0.00
Lewy body GO:0097413 p=3.1E−02 n=1 fg=0.04 bg=0.00
brahma complex GO:0035060 p=3.1E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of rough endoplasmic re... GO:0098556 p=3.1E−02 n=1 fg=0.04 bg=0.00
npBAF complex GO:0071564 p=3.1E−02 n=1 fg=0.04 bg=0.00
nBAF complex GO:0071565 p=3.1E−02 n=1 fg=0.04 bg=0.00
muscle tendon junction GO:0005927 p=4.6E−02 n=1 fg=0.04 bg=0.00
beta−catenin−TCF complex GO:1990907 p=4.6E−02 n=1 fg=0.04 bg=0.00
polysomal ribosome GO:0042788 p=4.6E−02 n=1 fg=0.04 bg=0.00
cytosolic large ribosomal subunit GO:0022625 p=6.1E−02 n=1 fg=0.04 bg=0.00
rough endoplasmic reticulum membrane GO:0030867 p=6.1E−02 n=1 fg=0.04 bg=0.00
pi−body GO:0071546 p=6.1E−02 n=1 fg=0.04 bg=0.00
chromatoid body GO:0033391 p=6.1E−02 n=1 fg=0.04 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=7.5E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of endoplasmic reticulu... GO:0098554 p=7.5E−02 n=1 fg=0.04 bg=0.00
mitochondrial inner membrane GO:0005743 p=8.2E−02 n=3 fg=0.11 bg=0.04
GTPase complex GO:1905360 p=8.9E−02 n=1 fg=0.04 bg=0.00
heterotrimeric G−protein complex GO:0005834 p=8.9E−02 n=1 fg=0.04 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=9.1E−02 n=2 fg=0.07 bg=0.02
precatalytic spliceosome GO:0071011 p=1.0E−01 n=1 fg=0.04 bg=0.00
organelle inner membrane GO:0019866 p=1.0E−01 n=3 fg=0.11 bg=0.04
motile cilium GO:0031514 p=1.0E−01 n=2 fg=0.07 bg=0.02
large ribosomal subunit GO:0015934 p=1.2E−01 n=1 fg=0.04 bg=0.00
rhabdomere GO:0016028 p=1.2E−01 n=1 fg=0.04 bg=0.00
ribonucleoprotein complex GO:1990904 p=1.3E−01 n=4 fg=0.14 bg=0.07
0 1 2 3 4 5
−log(p)
n=28/123 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction