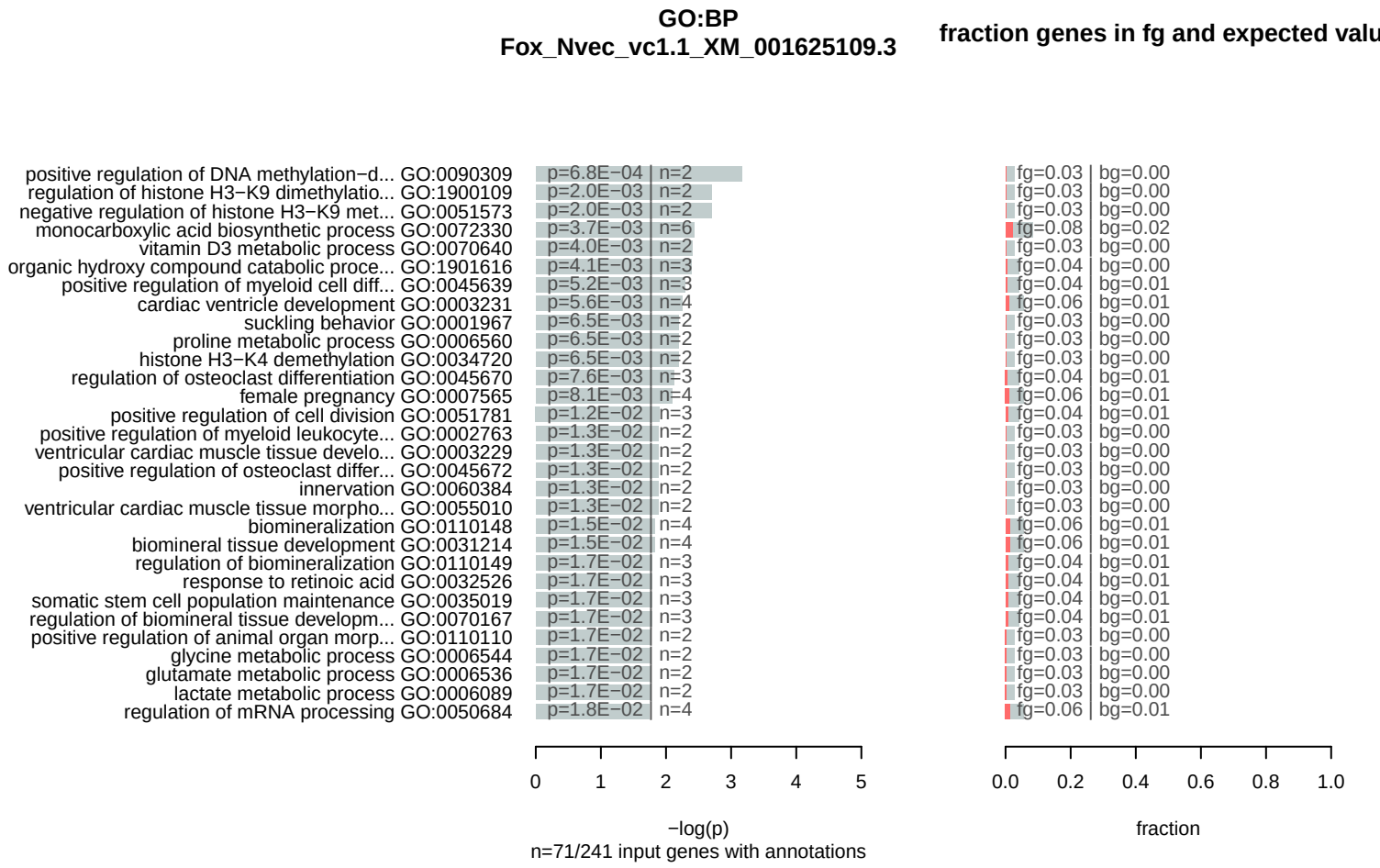
GO:BP
Fox_Nvec_vc1.1_XM_001625109.3
fraction genes in fg and expected valu
positive regulation of DNA methylation−d... GO:0090309 p=6.8E−04 n=2 fg=0.03 bg=0.00
regulation of histone H3−K9 dimethylatio... GO:1900109 p=2.0E−03 n=2 fg=0.03 bg=0.00
negative regulation of histone H3−K9 met... GO:0051573 p=2.0E−03 n=2 fg=0.03 bg=0.00
monocarboxylic acid biosynthetic process GO:0072330 p=3.7E−03 n=6 fg=0.08 bg=0.02
vitamin D3 metabolic process GO:0070640 p=4.0E−03 n=2 fg=0.03 bg=0.00
organic hydroxy compound catabolic proce... GO:1901616 p=4.1E−03 n=3 fg=0.04 bg=0.00
positive regulation of myeloid cell diff... GO:0045639 p=5.2E−03 n=3 fg=0.04 bg=0.01
cardiac ventricle development GO:0003231 p=5.6E−03 n=4 fg=0.06 bg=0.01
suckling behavior GO:0001967 p=6.5E−03 n=2 fg=0.03 bg=0.00
proline metabolic process GO:0006560 p=6.5E−03 n=2 fg=0.03 bg=0.00
histone H3−K4 demethylation GO:0034720 p=6.5E−03 n=2 fg=0.03 bg=0.00
regulation of osteoclast differentiation GO:0045670 p=7.6E−03 n=3 fg=0.04 bg=0.01
female pregnancy GO:0007565 p=8.1E−03 n=4 fg=0.06 bg=0.01
positive regulation of cell division GO:0051781 p=1.2E−02 n=3 fg=0.04 bg=0.01
positive regulation of myeloid leukocyte... GO:0002763 p=1.3E−02 n=2 fg=0.03 bg=0.00
ventricular cardiac muscle tissue develo... GO:0003229 p=1.3E−02 n=2 fg=0.03 bg=0.00
positive regulation of osteoclast differ... GO:0045672 p=1.3E−02 n=2 fg=0.03 bg=0.00
innervation GO:0060384 p=1.3E−02 n=2 fg=0.03 bg=0.00
ventricular cardiac muscle tissue morpho... GO:0055010 p=1.3E−02 n=2 fg=0.03 bg=0.00
biomineralization GO:0110148 p=1.5E−02 n=4 fg=0.06 bg=0.01
biomineral tissue development GO:0031214 p=1.5E−02 n=4 fg=0.06 bg=0.01
regulation of biomineralization GO:0110149 p=1.7E−02 n=3 fg=0.04 bg=0.01
response to retinoic acid GO:0032526 p=1.7E−02 n=3 fg=0.04 bg=0.01
somatic stem cell population maintenance GO:0035019 p=1.7E−02 n=3 fg=0.04 bg=0.01
regulation of biomineral tissue developm... GO:0070167 p=1.7E−02 n=3 fg=0.04 bg=0.01
positive regulation of animal organ morp... GO:0110110 p=1.7E−02 n=2 fg=0.03 bg=0.00
glycine metabolic process GO:0006544 p=1.7E−02 n=2 fg=0.03 bg=0.00
glutamate metabolic process GO:0006536 p=1.7E−02 n=2 fg=0.03 bg=0.00
lactate metabolic process GO:0006089 p=1.7E−02 n=2 fg=0.03 bg=0.00
regulation of mRNA processing GO:0050684 p=1.8E−02 n=4 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=71/241 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001625109.3
fraction genes in fg and expected valu
manganese ion binding GO:0030145 p=2.1E−03 n=4 fg=0.06 bg=0.01
fibroblast growth factor−activated recep... GO:0005007 p=4.2E−03 n=2 fg=0.03 bg=0.00
bHLH transcription factor binding GO:0043425 p=4.2E−03 n=2 fg=0.03 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=6.8E−03 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on paire... GO:0016705 p=1.3E−02 n=3 fg=0.05 bg=0.01
polynucleotide adenylyltransferase activ... GO:0004652 p=1.4E−02 n=2 fg=0.03 bg=0.00
fibroblast growth factor binding GO:0017134 p=1.8E−02 n=2 fg=0.03 bg=0.00
poly(U) RNA binding GO:0008266 p=2.3E−02 n=2 fg=0.03 bg=0.00
all−trans retinal binding GO:0005503 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−3 demethylase... GO:0033749 p=2.7E−02 n=1 fg=0.02 bg=0.00
U12 snRNA binding GO:0030626 p=2.7E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=2.7E−02 n=1 fg=0.02 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=2.7E−02 n=1 fg=0.02 bg=0.00
glutamate 5−kinase activity GO:0004349 p=2.7E−02 n=1 fg=0.02 bg=0.00
all−trans−retinol binding GO:1904768 p=2.7E−02 n=1 fg=0.02 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=2.7E−02 n=1 fg=0.02 bg=0.00
single−stranded DNA 3'−5' exodeoxyribonu... GO:0008310 p=2.7E−02 n=1 fg=0.02 bg=0.00
all−trans retinol 3,4−desaturase activit... GO:0061896 p=2.7E−02 n=1 fg=0.02 bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897 p=2.7E−02 n=1 fg=0.02 bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898 p=2.7E−02 n=1 fg=0.02 bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899 p=2.7E−02 n=1 fg=0.02 bg=0.00
MRF binding GO:0043426 p=2.7E−02 n=1 fg=0.02 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=2.7E−02 n=1 fg=0.02 bg=0.00
poly(ADP−ribose) glycohydrolase activity GO:0004649 p=2.7E−02 n=1 fg=0.02 bg=0.00
prostaglandin E receptor activity GO:0004957 p=2.7E−02 n=1 fg=0.02 bg=0.00
amidinotransferase activity GO:0015067 p=2.7E−02 n=1 fg=0.02 bg=0.00
glycine amidinotransferase activity GO:0015068 p=2.7E−02 n=1 fg=0.02 bg=0.00
delta1−pyrroline−5−carboxylate synthetas... GO:0017084 p=2.7E−02 n=1 fg=0.02 bg=0.00
calcidiol 1−monooxygenase activity GO:0004498 p=2.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=64/241 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001625109.3
fraction genes in fg and expected valu
polytene chromosome band GO:0005704 p=2.8E−02 n=1 fg=0.01 bg=0.00
Grb2−Sos complex GO:0070618 p=2.8E−02 n=1 fg=0.01 bg=0.00
nascent polypeptide−associated complex GO:0005854 p=2.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005756 p=2.8E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase complex... GO:0045263 p=2.8E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase, centra... GO:0045269 p=2.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000276 p=2.8E−02 n=1 fg=0.01 bg=0.00
nuclear body GO:0016604 p=3.8E−02 n=9 fg=0.12 bg=0.06
integral component of Golgi membrane GO:0030173 p=5.0E−02 n=2 fg=0.03 bg=0.00
nucleoplasm GO:0005654 p=5.1E−02 n=29 fg=0.38 bg=0.29
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.6E−02 n=1 fg=0.01 bg=0.00
BLOC−1 complex GO:0031083 p=5.6E−02 n=1 fg=0.01 bg=0.00
COPII vesicle coat GO:0030127 p=5.6E−02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=5.6E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005753 p=5.6E−02 n=1 fg=0.01 bg=0.00
microtubule minus−end GO:0036449 p=5.6E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase complex... GO:0045261 p=5.6E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000275 p=5.6E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase complex GO:0045259 p=5.6E−02 n=1 fg=0.01 bg=0.00
glycine cleavage complex GO:0005960 p=5.6E−02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=5.6E−02 n=1 fg=0.01 bg=0.00
cleavage furrow GO:0032154 p=5.7E−02 n=2 fg=0.03 bg=0.01
nuclear lumen GO:0031981 p=5.7E−02 n=33 fg=0.43 bg=0.34
intrinsic component of Golgi membrane GO:0031228 p=6.5E−02 n=2 fg=0.03 bg=0.01
chromosome, telomeric region GO:0000781 p=6.5E−02 n=2 fg=0.03 bg=0.01
R2TP complex GO:0097255 p=8.2E−02 n=1 fg=0.01 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=8.2E−02 n=1 fg=0.01 bg=0.00
phagophore assembly site membrane GO:0034045 p=8.2E−02 n=1 fg=0.01 bg=0.00
zymogen granule membrane GO:0042589 p=8.2E−02 n=1 fg=0.01 bg=0.00
Smc5−Smc6 complex GO:0030915 p=8.2E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/241 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction