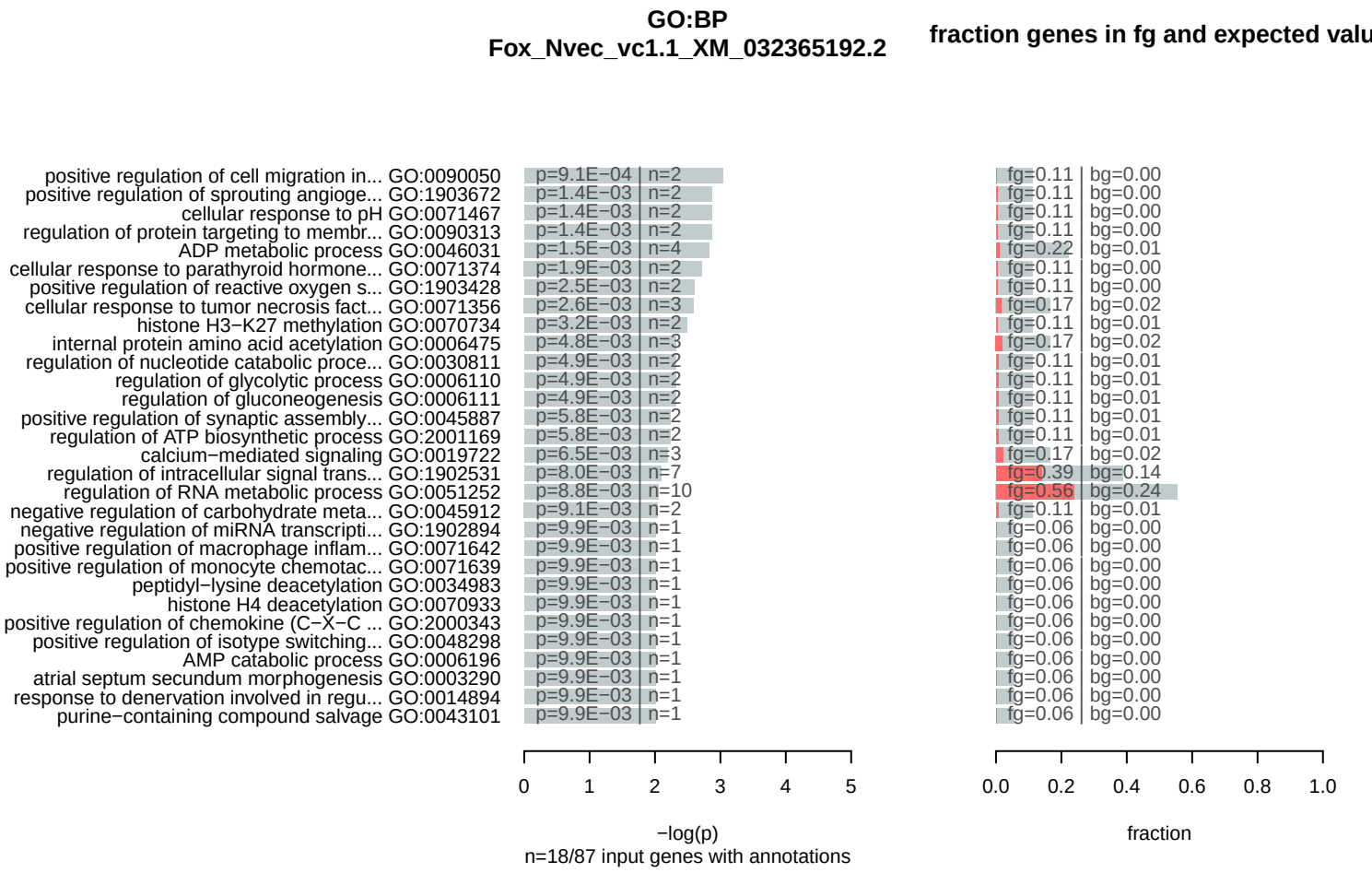
GO:BP
Fox_Nvec_vc1.1_XM_032365192.2
fraction genes in fg and expected valu
positive regulation of cell migration in... GO:0090050 p=9.1E−04 n=2 fg=0.11 bg=0.00
positive regulation of sprouting angioge... GO:1903672 p=1.4E−03 n=2 fg=0.11 bg=0.00
cellular response to pH GO:0071467 p=1.4E−03 n=2 fg=0.11 bg=0.00
regulation of protein targeting to membr... GO:0090313 p=1.4E−03 n=2 fg=0.11 bg=0.00
ADP metabolic process GO:0046031 p=1.5E−03 n=4 fg=0.22 bg=0.01
cellular response to parathyroid hormone... GO:0071374 p=1.9E−03 n=2 fg=0.11 bg=0.00
positive regulation of reactive oxygen s... GO:1903428 p=2.5E−03 n=2 fg=0.11 bg=0.00
cellular response to tumor necrosis fact... GO:0071356 p=2.6E−03 n=3 fg=0.17 bg=0.02
histone H3−K27 methylation GO:0070734 p=3.2E−03 n=2 fg=0.11 bg=0.01
internal protein amino acid acetylation GO:0006475 p=4.8E−03 n=3 fg=0.17 bg=0.02
regulation of nucleotide catabolic proce... GO:0030811 p=4.9E−03 n=2 fg=0.11 bg=0.01
regulation of glycolytic process GO:0006110 p=4.9E−03 n=2 fg=0.11 bg=0.01
regulation of gluconeogenesis GO:0006111 p=4.9E−03 n=2 fg=0.11 bg=0.01
positive regulation of synaptic assembly... GO:0045887 p=5.8E−03 n=2 fg=0.11 bg=0.01
regulation of ATP biosynthetic process GO:2001169 p=5.8E−03 n=2 fg=0.11 bg=0.01
calcium−mediated signaling GO:0019722 p=6.5E−03 n=3 fg=0.17 bg=0.02
regulation of intracellular signal trans... GO:1902531 p=8.0E−03 n=7 fg=0.39 bg=0.14
regulation of RNA metabolic process GO:0051252 p=8.8E−03 n=10 fg=0.56 bg=0.24
negative regulation of carbohydrate meta... GO:0045912 p=9.1E−03 n=2 fg=0.11 bg=0.01
negative regulation of miRNA transcripti... GO:1902894 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of macrophage inflam... GO:0071642 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of monocyte chemotac... GO:0071639 p=9.9E−03 n=1 fg=0.06 bg=0.00
peptidyl−lysine deacetylation GO:0034983 p=9.9E−03 n=1 fg=0.06 bg=0.00
histone H4 deacetylation GO:0070933 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of chemokine (C−X−C ... GO:2000343 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of isotype switching... GO:0048298 p=9.9E−03 n=1 fg=0.06 bg=0.00
AMP catabolic process GO:0006196 p=9.9E−03 n=1 fg=0.06 bg=0.00
atrial septum secundum morphogenesis GO:0003290 p=9.9E−03 n=1 fg=0.06 bg=0.00
response to denervation involved in regu... GO:0014894 p=9.9E−03 n=1 fg=0.06 bg=0.00
purine−containing compound salvage GO:0043101 p=9.9E−03 n=1 fg=0.06 bg=0.00
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−log(p)
n=18/87 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032365192.2
fraction genes in fg and expected valu
histone methyltransferase activity (H3−K... GO:0046976 p=1.1E−02 n=1 fg=0.06 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=1.1E−02 n=1 fg=0.06 bg=0.00
intracellular phosphatidylinositol−3,5−b... GO:0097682 p=1.1E−02 n=1 fg=0.06 bg=0.00
rRNA (adenine) methyltransferase activit... GO:0016433 p=1.1E−02 n=1 fg=0.06 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=1.1E−02 n=1 fg=0.06 bg=0.00
AMP deaminase activity GO:0003876 p=1.1E−02 n=1 fg=0.06 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=1.1E−02 n=1 fg=0.06 bg=0.00
protein−membrane adaptor activity GO:0043495 p=1.1E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol binding GO:0035091 p=1.2E−02 n=3 fg=0.18 bg=0.03
ion binding GO:0043167 p=1.3E−02 n=8 fg=0.47 bg=0.21
mRNA binding GO:0003729 p=1.4E−02 n=3 fg=0.18 bg=0.03
S−adenosylmethionine−dependent methyltra... GO:0008757 p=1.7E−02 n=2 fg=0.12 bg=0.01
hydrolase activity, acting on carbon−nit... GO:0016810 p=2.0E−02 n=2 fg=0.12 bg=0.01
calcium−dependent protein kinase inhibit... GO:0008427 p=2.1E−02 n=1 fg=0.06 bg=0.00
S−adenosyl−L−methionine binding GO:1904047 p=2.1E−02 n=1 fg=0.06 bg=0.00
histone methyltransferase activity (H3−K... GO:0046975 p=2.1E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol−3,5−bisphosphate bi... GO:0080025 p=2.1E−02 n=1 fg=0.06 bg=0.00
transcription corepressor binding GO:0001222 p=2.1E−02 n=1 fg=0.06 bg=0.00
histone methyltransferase activity (H4−K... GO:0042799 p=2.1E−02 n=1 fg=0.06 bg=0.00
calcium−dependent protein kinase regulat... GO:0010858 p=2.1E−02 n=1 fg=0.06 bg=0.00
NAADP−sensitive calcium−release channel ... GO:0072345 p=2.1E−02 n=1 fg=0.06 bg=0.00
catalytic activity, acting on a rRNA GO:0140102 p=2.1E−02 n=1 fg=0.06 bg=0.00
SUMO transferase activity GO:0019789 p=2.1E−02 n=1 fg=0.06 bg=0.00
histone methyltransferase activity (H3−K... GO:0042800 p=2.1E−02 n=1 fg=0.06 bg=0.00
nuclear retinoid X receptor binding GO:0046965 p=2.1E−02 n=1 fg=0.06 bg=0.00
rRNA methyltransferase activity GO:0008649 p=2.1E−02 n=1 fg=0.06 bg=0.00
methyltransferase activity GO:0008168 p=2.2E−02 n=2 fg=0.12 bg=0.01
transferase activity, transferring one−c... GO:0016741 p=2.4E−02 n=2 fg=0.12 bg=0.01
sequence−specific DNA binding GO:0043565 p=2.7E−02 n=4 fg=0.24 bg=0.07
nucleic acid binding GO:0003676 p=2.9E−02 n=7 fg=0.41 bg=0.19
0 1 2 3 4 5
−log(p)
n=17/87 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032365192.2
fraction genes in fg and expected valu
integral component of lysosomal membrane GO:1905103 p=1.1E−02 n=1 fg=0.05 bg=0.00
autosome GO:0030849 p=1.1E−02 n=1 fg=0.05 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=1.1E−02 n=1 fg=0.05 bg=0.00
plus−end kinesin complex GO:0005873 p=1.1E−02 n=1 fg=0.05 bg=0.00
histone methyltransferase complex GO:0035097 p=1.1E−02 n=2 fg=0.11 bg=0.01
methyltransferase complex GO:0034708 p=1.6E−02 n=2 fg=0.11 bg=0.01
intrinsic component of vacuolar membrane GO:0031310 p=2.1E−02 n=1 fg=0.05 bg=0.00
integral component of vacuolar membrane GO:0031166 p=2.1E−02 n=1 fg=0.05 bg=0.00
endolysosome membrane GO:0036020 p=3.1E−02 n=1 fg=0.05 bg=0.00
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extrinsic component of endosome membrane GO:0031313 p=4.1E−02 n=1 fg=0.05 bg=0.00
X chromosome GO:0000805 p=4.1E−02 n=1 fg=0.05 bg=0.00
neuromuscular junction GO:0031594 p=4.5E−02 n=2 fg=0.11 bg=0.02
chromatin GO:0000785 p=4.8E−02 n=3 fg=0.16 bg=0.04
zymogen granule GO:0042588 p=5.1E−02 n=1 fg=0.05 bg=0.00
pericentric heterochromatin GO:0005721 p=5.1E−02 n=1 fg=0.05 bg=0.00
filopodium tip GO:0032433 p=5.1E−02 n=1 fg=0.05 bg=0.00
late endosome GO:0005770 p=7.9E−02 n=2 fg=0.11 bg=0.02
euchromatin GO:0000791 p=8.1E−02 n=1 fg=0.05 bg=0.00
kinesin complex GO:0005871 p=8.1E−02 n=1 fg=0.05 bg=0.00
multivesicular body GO:0005771 p=9.1E−02 n=1 fg=0.05 bg=0.00
extrinsic component of organelle membran... GO:0031312 p=9.1E−02 n=1 fg=0.05 bg=0.00
sex chromosome GO:0000803 p=9.1E−02 n=1 fg=0.05 bg=0.00
ruffle membrane GO:0032587 p=1.0E−01 n=1 fg=0.05 bg=0.01
histone deacetylase complex GO:0000118 p=1.0E−01 n=1 fg=0.05 bg=0.01
lateral plasma membrane GO:0016328 p=1.1E−01 n=1 fg=0.05 bg=0.01
A band GO:0031672 p=1.3E−01 n=1 fg=0.05 bg=0.01
actomyosin GO:0042641 p=1.3E−01 n=1 fg=0.05 bg=0.01
transcription repressor complex GO:0017053 p=1.3E−01 n=1 fg=0.05 bg=0.01
endosome membrane GO:0010008 p=1.4E−01 n=2 fg=0.11 bg=0.03
0 1 2 3 4 5
−log(p)
n=19/87 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction