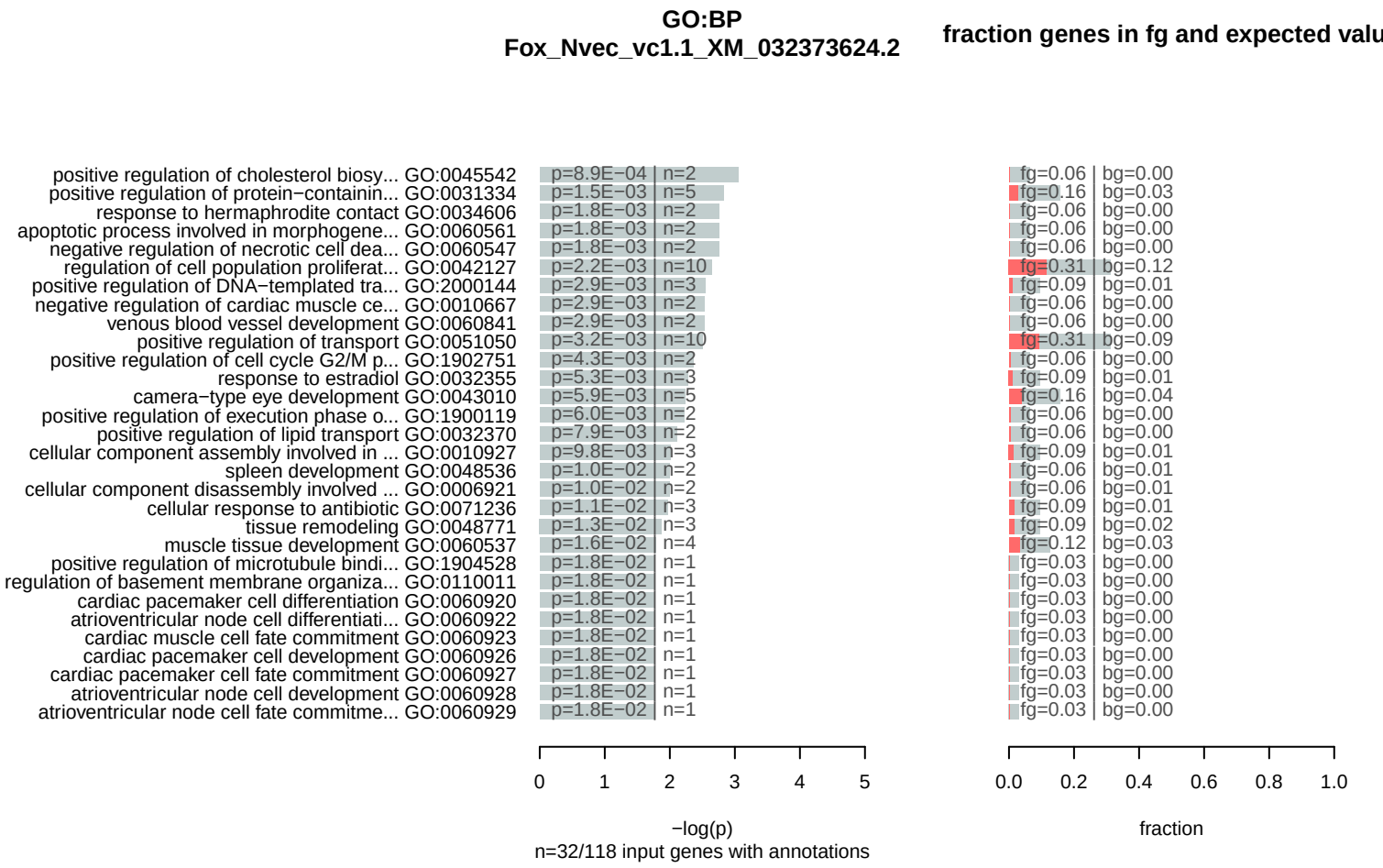
GO:BP
Fox_Nvec_vc1.1_XM_032373624.2
fraction genes in fg and expected valu
positive regulation of cholesterol biosy... GO:0045542 p=8.9E−04 n=2 fg=0.06 bg=0.00
positive regulation of protein−containin... GO:0031334 p=1.5E−03 n=5 fg=0.16 bg=0.03
response to hermaphrodite contact GO:0034606 p=1.8E−03 n=2 fg=0.06 bg=0.00
apoptotic process involved in morphogene... GO:0060561 p=1.8E−03 n=2 fg=0.06 bg=0.00
negative regulation of necrotic cell dea... GO:0060547 p=1.8E−03 n=2 fg=0.06 bg=0.00
regulation of cell population proliferat... GO:0042127 p=2.2E−03 n=10 fg=0.31 bg=0.12
positive regulation of DNA−templated tra... GO:2000144 p=2.9E−03 n=3 fg=0.09 bg=0.01
negative regulation of cardiac muscle ce... GO:0010667 p=2.9E−03 n=2 fg=0.06 bg=0.00
venous blood vessel development GO:0060841 p=2.9E−03 n=2 fg=0.06 bg=0.00
positive regulation of transport GO:0051050 p=3.2E−03 n=10 fg=0.31 bg=0.09
positive regulation of cell cycle G2/M p... GO:1902751 p=4.3E−03 n=2 fg=0.06 bg=0.00
response to estradiol GO:0032355 p=5.3E−03 n=3 fg=0.09 bg=0.01
camera−type eye development GO:0043010 p=5.9E−03 n=5 fg=0.16 bg=0.04
positive regulation of execution phase o... GO:1900119 p=6.0E−03 n=2 fg=0.06 bg=0.00
positive regulation of lipid transport GO:0032370 p=7.9E−03 n=2 fg=0.06 bg=0.00
cellular component assembly involved in ... GO:0010927 p=9.8E−03 n=3 fg=0.09 bg=0.01
spleen development GO:0048536 p=1.0E−02 n=2 fg=0.06 bg=0.01
cellular component disassembly involved ... GO:0006921 p=1.0E−02 n=2 fg=0.06 bg=0.01
cellular response to antibiotic GO:0071236 p=1.1E−02 n=3 fg=0.09 bg=0.01
tissue remodeling GO:0048771 p=1.3E−02 n=3 fg=0.09 bg=0.02
muscle tissue development GO:0060537 p=1.6E−02 n=4 fg=0.12 bg=0.03
positive regulation of microtubule bindi... GO:1904528 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of basement membrane organiza... GO:0110011 p=1.8E−02 n=1 fg=0.03 bg=0.00
cardiac pacemaker cell differentiation GO:0060920 p=1.8E−02 n=1 fg=0.03 bg=0.00
atrioventricular node cell differentiati... GO:0060922 p=1.8E−02 n=1 fg=0.03 bg=0.00
cardiac muscle cell fate commitment GO:0060923 p=1.8E−02 n=1 fg=0.03 bg=0.00
cardiac pacemaker cell development GO:0060926 p=1.8E−02 n=1 fg=0.03 bg=0.00
cardiac pacemaker cell fate commitment GO:0060927 p=1.8E−02 n=1 fg=0.03 bg=0.00
atrioventricular node cell development GO:0060928 p=1.8E−02 n=1 fg=0.03 bg=0.00
atrioventricular node cell fate commitme... GO:0060929 p=1.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=32/118 input genes with annotations
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fraction
GO:MF
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protein heterodimerization activity GO:0046982 p=1.4E−03 n=7 fg=0.23 bg=0.06
actin filament binding GO:0051015 p=2.6E−03 n=3 fg=0.10 bg=0.01
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.1E−03 n=5 fg=0.16 bg=0.04
DNA−binding transcription factor activit... GO:0003700 p=1.0E−02 n=7 fg=0.23 bg=0.08
E−box binding GO:0070888 p=1.2E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=1.5E−02 n=6 fg=0.19 bg=0.07
dystroglycan binding GO:0002162 p=1.9E−02 n=1 fg=0.03 bg=0.00
amine N−methyltransferase activity GO:0030748 p=1.9E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=1.9E−02 n=1 fg=0.03 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=1.9E−02 n=1 fg=0.03 bg=0.00
thioether S−methyltransferase activity GO:0004790 p=1.9E−02 n=1 fg=0.03 bg=0.00
serum response element binding GO:0010736 p=1.9E−02 n=1 fg=0.03 bg=0.00
kinetochore binding GO:0043515 p=1.9E−02 n=1 fg=0.03 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=1.9E−02 n=1 fg=0.03 bg=0.00
pyridine N−methyltransferase activity GO:0030760 p=1.9E−02 n=1 fg=0.03 bg=0.00
phosphatidyl−N−methylethanolamine N−meth... GO:0000773 p=1.9E−02 n=1 fg=0.03 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=1.9E−02 n=1 fg=0.03 bg=0.00
dimethyl selenide methyltransferase acti... GO:0098615 p=1.9E−02 n=1 fg=0.03 bg=0.00
DNA/DNA annealing activity GO:1990814 p=1.9E−02 n=1 fg=0.03 bg=0.00
S−methyltransferase activity GO:0008172 p=1.9E−02 n=1 fg=0.03 bg=0.00
phosphatidyl−N−dimethylethanolamine N−me... GO:0080101 p=1.9E−02 n=1 fg=0.03 bg=0.00
nicotinamide N−methyltransferase activit... GO:0008112 p=1.9E−02 n=1 fg=0.03 bg=0.00
N−methyltransferase activity GO:0008170 p=2.1E−02 n=2 fg=0.06 bg=0.01
transcription regulator activity GO:0140110 p=2.2E−02 n=8 fg=0.26 bg=0.12
phospholipid transporter activity GO:0005548 p=2.5E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=2.8E−02 n=4 fg=0.13 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=2.8E−02 n=4 fg=0.13 bg=0.04
protein tyrosine kinase binding GO:1990782 p=2.9E−02 n=2 fg=0.06 bg=0.01
RNA polymerase II−specific DNA−binding t... GO:0061629 p=3.6E−02 n=3 fg=0.10 bg=0.02
Hsp90 protein binding GO:0051879 p=3.7E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=31/118 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032373624.2
fraction genes in fg and expected valu
microtubule end GO:1990752 p=2.9E−03 n=2 fg=0.06 bg=0.00
transcription regulator complex GO:0005667 p=1.0E−02 n=5 fg=0.16 bg=0.04
centrosomal corona GO:0031592 p=1.8E−02 n=1 fg=0.03 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.8E−02 n=1 fg=0.03 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=1.8E−02 n=1 fg=0.03 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=1.8E−02 n=1 fg=0.03 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=1.8E−02 n=1 fg=0.03 bg=0.00
protein kinase CK2 complex GO:0005956 p=1.8E−02 n=1 fg=0.03 bg=0.00
cortical microtubule GO:0055028 p=1.8E−02 n=1 fg=0.03 bg=0.00
ESCRT−0 complex GO:0033565 p=1.8E−02 n=1 fg=0.03 bg=0.00
cortical microtubule plus−end GO:1903754 p=1.8E−02 n=1 fg=0.03 bg=0.00
focal adhesion GO:0005925 p=2.8E−02 n=2 fg=0.06 bg=0.01
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cis−Golgi network membrane GO:0033106 p=3.5E−02 n=1 fg=0.03 bg=0.00
myosin V complex GO:0031475 p=3.5E−02 n=1 fg=0.03 bg=0.00
muscle myosin complex GO:0005859 p=3.5E−02 n=1 fg=0.03 bg=0.00
inner dynein arm GO:0036156 p=3.5E−02 n=1 fg=0.03 bg=0.00
myosin II complex GO:0016460 p=3.5E−02 n=1 fg=0.03 bg=0.00
microtubule minus−end GO:0036449 p=3.5E−02 n=1 fg=0.03 bg=0.00
nuclear stress granule GO:0097165 p=3.5E−02 n=1 fg=0.03 bg=0.00
U2AF complex GO:0089701 p=3.5E−02 n=1 fg=0.03 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=3.5E−02 n=1 fg=0.03 bg=0.00
cell−substrate junction GO:0030055 p=3.9E−02 n=2 fg=0.06 bg=0.01
condensed chromosome, centromeric region GO:0000779 p=5.2E−02 n=2 fg=0.06 bg=0.01
myosin VI complex GO:0031476 p=5.2E−02 n=1 fg=0.03 bg=0.00
myosin VII complex GO:0031477 p=5.2E−02 n=1 fg=0.03 bg=0.00
microtubule plus−end GO:0035371 p=5.2E−02 n=1 fg=0.03 bg=0.00
axonemal dynein complex GO:0005858 p=5.2E−02 n=1 fg=0.03 bg=0.00
kinetochore microtubule GO:0005828 p=5.2E−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