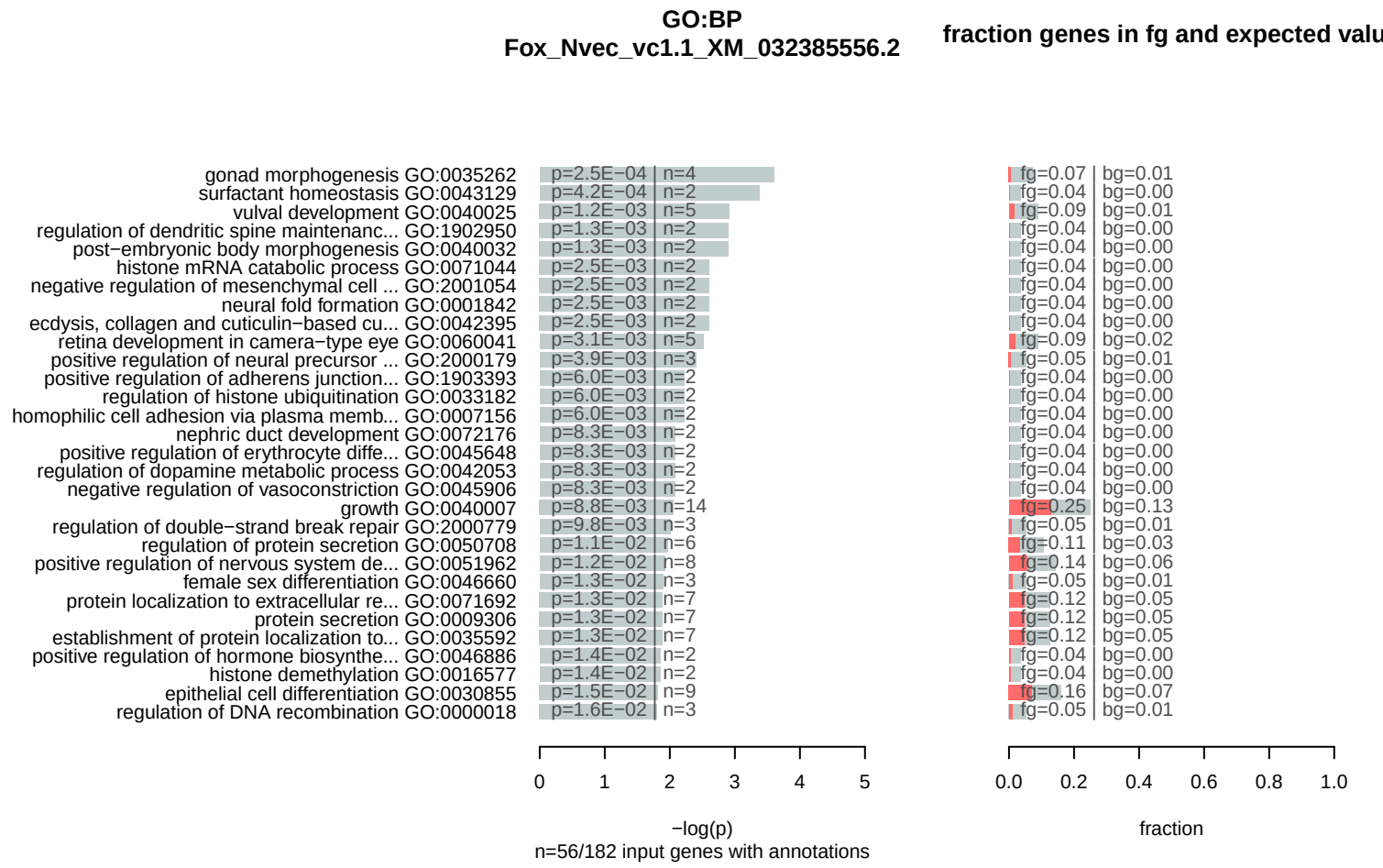
GO:BP
Fox_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
gonad morphogenesis GO:0035262 p=2.5E−04 n=4 fg=0.07 bg=0.01
surfactant homeostasis GO:0043129 p=4.2E−04 n=2 fg=0.04 bg=0.00
vulval development GO:0040025 p=1.2E−03 n=5 fg=0.09 bg=0.01
regulation of dendritic spine maintenanc... GO:1902950 p=1.3E−03 n=2 fg=0.04 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=1.3E−03 n=2 fg=0.04 bg=0.00
histone mRNA catabolic process GO:0071044 p=2.5E−03 n=2 fg=0.04 bg=0.00
negative regulation of mesenchymal cell ... GO:2001054 p=2.5E−03 n=2 fg=0.04 bg=0.00
neural fold formation GO:0001842 p=2.5E−03 n=2 fg=0.04 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=2.5E−03 n=2 fg=0.04 bg=0.00
retina development in camera−type eye GO:0060041 p=3.1E−03 n=5 fg=0.09 bg=0.02
positive regulation of neural precursor ... GO:2000179 p=3.9E−03 n=3 fg=0.05 bg=0.01
positive regulation of adherens junction... GO:1903393 p=6.0E−03 n=2 fg=0.04 bg=0.00
regulation of histone ubiquitination GO:0033182 p=6.0E−03 n=2 fg=0.04 bg=0.00
homophilic cell adhesion via plasma memb... GO:0007156 p=6.0E−03 n=2 fg=0.04 bg=0.00
nephric duct development GO:0072176 p=8.3E−03 n=2 fg=0.04 bg=0.00
positive regulation of erythrocyte diffe... GO:0045648 p=8.3E−03 n=2 fg=0.04 bg=0.00
regulation of dopamine metabolic process GO:0042053 p=8.3E−03 n=2 fg=0.04 bg=0.00
negative regulation of vasoconstriction GO:0045906 p=8.3E−03 n=2 fg=0.04 bg=0.00
growth GO:0040007 p=8.8E−03 n=14 fg=0.25 bg=0.13
regulation of double−strand break repair GO:2000779 p=9.8E−03 n=3 fg=0.05 bg=0.01
regulation of protein secretion GO:0050708 p=1.1E−02 n=6 fg=0.11 bg=0.03
positive regulation of nervous system de... GO:0051962 p=1.2E−02 n=8 fg=0.14 bg=0.06
female sex differentiation GO:0046660 p=1.3E−02 n=3 fg=0.05 bg=0.01
protein localization to extracellular re... GO:0071692 p=1.3E−02 n=7 fg=0.12 bg=0.05
protein secretion GO:0009306 p=1.3E−02 n=7 fg=0.12 bg=0.05
establishment of protein localization to... GO:0035592 p=1.3E−02 n=7 fg=0.12 bg=0.05
positive regulation of hormone biosynthe... GO:0046886 p=1.4E−02 n=2 fg=0.04 bg=0.00
histone demethylation GO:0016577 p=1.4E−02 n=2 fg=0.04 bg=0.00
epithelial cell differentiation GO:0030855 p=1.5E−02 n=9 fg=0.16 bg=0.07
regulation of DNA recombination GO:0000018 p=1.6E−02 n=3 fg=0.05 bg=0.01
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−log(p)
n=56/182 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
bHLH transcription factor binding GO:0043425 p=2.4E−03 n=2 fg=0.04 bg=0.00
3'−5' DNA helicase activity GO:0043138 p=3.9E−03 n=2 fg=0.04 bg=0.00
HMG box domain binding GO:0071837 p=7.9E−03 n=2 fg=0.04 bg=0.00
transcription coregulator activity GO:0003712 p=8.9E−03 n=7 fg=0.15 bg=0.05
protein demethylase activity GO:0140457 p=1.0E−02 n=2 fg=0.04 bg=0.00
ubiquitin−ubiquitin ligase activity GO:0034450 p=1.0E−02 n=2 fg=0.04 bg=0.00
histone demethylase activity GO:0032452 p=1.0E−02 n=2 fg=0.04 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=1.7E−02 n=5 fg=0.10 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.7E−02 n=5 fg=0.10 bg=0.03
transcription coactivator activity GO:0003713 p=1.8E−02 n=5 fg=0.10 bg=0.03
3−chloroallyl aldehyde dehydrogenase act... GO:0004028 p=2.0E−02 n=1 fg=0.02 bg=0.00
cobalt ion binding GO:0050897 p=2.0E−02 n=1 fg=0.02 bg=0.00
saccharopine dehydrogenase (NAD+, L−lysi... GO:0004754 p=2.0E−02 n=1 fg=0.02 bg=0.00
semaphorin receptor binding GO:0030215 p=2.0E−02 n=1 fg=0.02 bg=0.00
SMC family protein binding GO:0043221 p=2.0E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=2.0E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−3 demethylase... GO:0033749 p=2.0E−02 n=1 fg=0.02 bg=0.00
5'−tyrosyl−DNA phosphodiesterase activit... GO:0070260 p=2.0E−02 n=1 fg=0.02 bg=0.00
oligonucleotidase activity GO:0008946 p=2.0E−02 n=1 fg=0.02 bg=0.00
rRNA (pseudouridine) methyltransferase a... GO:0070037 p=2.0E−02 n=1 fg=0.02 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=2.0E−02 n=1 fg=0.02 bg=0.00
MRF binding GO:0043426 p=2.0E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.0E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=2.0E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=2.0E−02 n=1 fg=0.02 bg=0.00
glycogen debranching enzyme activity GO:0004133 p=2.0E−02 n=1 fg=0.02 bg=0.00
4−alpha−glucanotransferase activity GO:0004134 p=2.0E−02 n=1 fg=0.02 bg=0.00
acid−sensing ion channel activity GO:0044736 p=2.0E−02 n=1 fg=0.02 bg=0.00
amylo−alpha−1,6−glucosidase activity GO:0004135 p=2.0E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.0E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=48/182 input genes with annotations
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fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
collagen and cuticulin−based cuticle ext... GO:0060102 p=4.5E−04 n=2 fg=0.03 bg=0.00
lipid droplet GO:0005811 p=1.5E−03 n=4 fg=0.07 bg=0.01
spanning component of plasma membrane GO:0044214 p=4.3E−03 n=2 fg=0.03 bg=0.00
isoamylase complex GO:0043033 p=2.1E−02 n=1 fg=0.02 bg=0.00
plastid GO:0009536 p=2.1E−02 n=1 fg=0.02 bg=0.00
symplast GO:0055044 p=2.1E−02 n=1 fg=0.02 bg=0.00
actin cortical patch GO:0030479 p=2.1E−02 n=1 fg=0.02 bg=0.00
plasmodesma GO:0009506 p=2.1E−02 n=1 fg=0.02 bg=0.00
chloroplast GO:0009507 p=2.1E−02 n=1 fg=0.02 bg=0.00
actin rod GO:0031002 p=2.1E−02 n=1 fg=0.02 bg=0.00
catalytic step 1 spliceosome GO:0071012 p=2.1E−02 n=1 fg=0.02 bg=0.00
endocytic patch GO:0061645 p=2.1E−02 n=1 fg=0.02 bg=0.00
FANCM−MHF complex GO:0071821 p=2.1E−02 n=1 fg=0.02 bg=0.00
apoplast GO:0048046 p=2.1E−02 n=1 fg=0.02 bg=0.00
U2−type catalytic step 1 spliceosome GO:0071006 p=2.1E−02 n=1 fg=0.02 bg=0.00
cofilin−actin rod GO:0090732 p=2.1E−02 n=1 fg=0.02 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=4.3E−02 n=1 fg=0.02 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=4.3E−02 n=1 fg=0.02 bg=0.00
TRAMP complex GO:0031499 p=4.3E−02 n=1 fg=0.02 bg=0.00
Swr1 complex GO:0000812 p=4.3E−02 n=1 fg=0.02 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=4.3E−02 n=1 fg=0.02 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=6.0E−02 n=3 fg=0.05 bg=0.02
transcription regulator complex GO:0005667 p=6.1E−02 n=5 fg=0.09 bg=0.04
Fanconi anaemia nuclear complex GO:0043240 p=6.3E−02 n=1 fg=0.02 bg=0.00
R2TP complex GO:0097255 p=6.3E−02 n=1 fg=0.02 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=6.3E−02 n=1 fg=0.02 bg=0.00
proteasome core complex, alpha−subunit c... GO:0019773 p=6.3E−02 n=1 fg=0.02 bg=0.00
CIA complex GO:0097361 p=6.3E−02 n=1 fg=0.02 bg=0.00
mRNA cap binding complex GO:0005845 p=6.3E−02 n=1 fg=0.02 bg=0.00
MMXD complex GO:0071817 p=6.3E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=58/182 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction