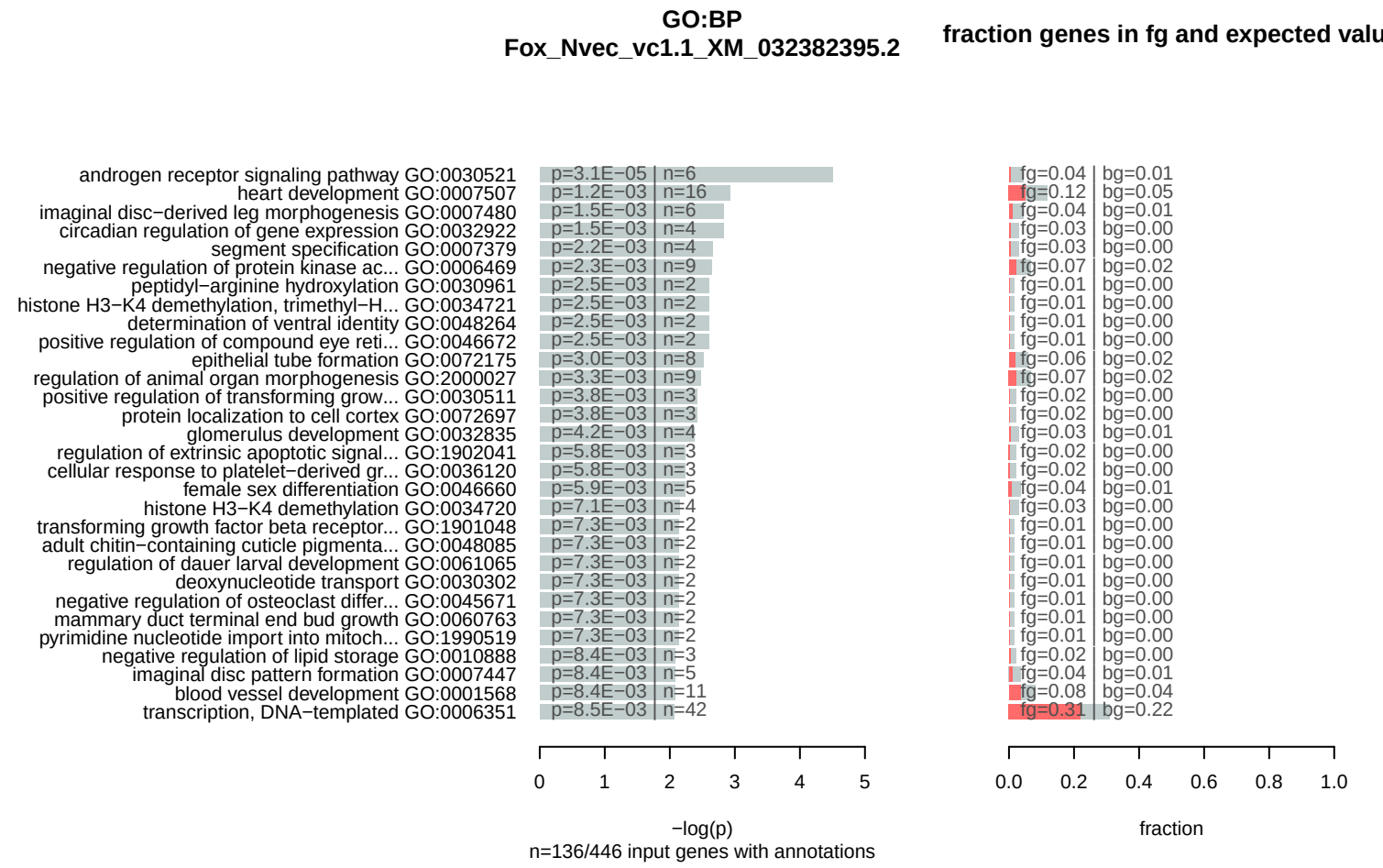
GO:BP
Fox_Nvec_vc1.1_XM_032382395.2
fraction genes in fg and expected valu
androgen receptor signaling pathway GO:0030521 p=3.1E−05 n=6 fg=0.04 bg=0.01
heart development GO:0007507 p=1.2E−03 n=16 fg=0.12 bg=0.05
imaginal disc−derived leg morphogenesis GO:0007480 p=1.5E−03 n=6 fg=0.04 bg=0.01
circadian regulation of gene expression GO:0032922 p=1.5E−03 n=4 fg=0.03 bg=0.00
segment specification GO:0007379 p=2.2E−03 n=4 fg=0.03 bg=0.00
negative regulation of protein kinase ac... GO:0006469 p=2.3E−03 n=9 fg=0.07 bg=0.02
peptidyl−arginine hydroxylation GO:0030961 p=2.5E−03 n=2 fg=0.01 bg=0.00
histone H3−K4 demethylation, trimethyl−H... GO:0034721 p=2.5E−03 n=2 fg=0.01 bg=0.00
determination of ventral identity GO:0048264 p=2.5E−03 n=2 fg=0.01 bg=0.00
positive regulation of compound eye reti... GO:0046672 p=2.5E−03 n=2 fg=0.01 bg=0.00
epithelial tube formation GO:0072175 p=3.0E−03 n=8 fg=0.06 bg=0.02
regulation of animal organ morphogenesis GO:2000027 p=3.3E−03 n=9 fg=0.07 bg=0.02
positive regulation of transforming grow... GO:0030511 p=3.8E−03 n=3 fg=0.02 bg=0.00
protein localization to cell cortex GO:0072697 p=3.8E−03 n=3 fg=0.02 bg=0.00
glomerulus development GO:0032835 p=4.2E−03 n=4 fg=0.03 bg=0.01
regulation of extrinsic apoptotic signal... GO:1902041 p=5.8E−03 n=3 fg=0.02 bg=0.00
cellular response to platelet−derived gr... GO:0036120 p=5.8E−03 n=3 fg=0.02 bg=0.00
female sex differentiation GO:0046660 p=5.9E−03 n=5 fg=0.04 bg=0.01
histone H3−K4 demethylation GO:0034720 p=7.1E−03 n=4 fg=0.03 bg=0.00
transforming growth factor beta receptor... GO:1901048 p=7.3E−03 n=2 fg=0.01 bg=0.00
adult chitin−containing cuticle pigmenta... GO:0048085 p=7.3E−03 n=2 fg=0.01 bg=0.00
regulation of dauer larval development GO:0061065 p=7.3E−03 n=2 fg=0.01 bg=0.00
deoxynucleotide transport GO:0030302 p=7.3E−03 n=2 fg=0.01 bg=0.00
negative regulation of osteoclast differ... GO:0045671 p=7.3E−03 n=2 fg=0.01 bg=0.00
mammary duct terminal end bud growth GO:0060763 p=7.3E−03 n=2 fg=0.01 bg=0.00
pyrimidine nucleotide import into mitoch... GO:1990519 p=7.3E−03 n=2 fg=0.01 bg=0.00
negative regulation of lipid storage GO:0010888 p=8.4E−03 n=3 fg=0.02 bg=0.00
imaginal disc pattern formation GO:0007447 p=8.4E−03 n=5 fg=0.04 bg=0.01
blood vessel development GO:0001568 p=8.4E−03 n=11 fg=0.08 bg=0.04
transcription, DNA−templated GO:0006351 p=8.5E−03 n=42 fg=0.31 bg=0.22
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−log(p)
n=136/446 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032382395.2
fraction genes in fg and expected valu
histone H3−tri/di/monomethyl−lysine−4 de... GO:0034647 p=2.6E−03 n=2 fg=0.02 bg=0.00
G protein−coupled serotonin receptor bin... GO:0031821 p=2.6E−03 n=2 fg=0.02 bg=0.00
ADP binding GO:0043531 p=5.9E−03 n=4 fg=0.03 bg=0.01
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=7.4E−03 n=4 fg=0.03 bg=0.00
I−SMAD binding GO:0070411 p=7.6E−03 n=2 fg=0.02 bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218 p=7.6E−03 n=2 fg=0.02 bg=0.00
DNA−binding transcription factor binding GO:0140297 p=7.7E−03 n=8 fg=0.07 bg=0.02
solute:cation symporter activity GO:0015294 p=9.4E−03 n=4 fg=0.03 bg=0.01
nuclear receptor binding GO:0016922 p=1.2E−02 n=6 fg=0.05 bg=0.02
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FAD binding GO:0071949 p=1.5E−02 n=2 fg=0.02 bg=0.00
protein kinase B binding GO:0043422 p=1.5E−02 n=2 fg=0.02 bg=0.00
transcription coactivator activity GO:0003713 p=1.6E−02 n=9 fg=0.07 bg=0.03
solute:sodium symporter activity GO:0015370 p=1.6E−02 n=3 fg=0.02 bg=0.00
RNA polymerase II−specific DNA−binding t... GO:0061629 p=1.7E−02 n=7 fg=0.06 bg=0.02
magnesium ion binding GO:0000287 p=1.7E−02 n=7 fg=0.06 bg=0.02
transcription regulator activity GO:0140110 p=1.9E−02 n=20 fg=0.16 bg=0.10
hormone receptor binding GO:0051427 p=2.1E−02 n=6 fg=0.05 bg=0.02
arrestin family protein binding GO:1990763 p=2.4E−02 n=2 fg=0.02 bg=0.00
TFIID−class transcription factor complex... GO:0001094 p=2.4E−02 n=2 fg=0.02 bg=0.00
transcription coactivator binding GO:0001223 p=2.4E−02 n=2 fg=0.02 bg=0.00
alcohol binding GO:0043178 p=2.6E−02 n=3 fg=0.02 bg=0.01
nuclear androgen receptor binding GO:0050681 p=2.6E−02 n=3 fg=0.02 bg=0.01
L−amino acid transmembrane transporter a... GO:0015179 p=3.2E−02 n=3 fg=0.02 bg=0.01
RNA polymerase II general transcription ... GO:0001091 p=3.4E−02 n=2 fg=0.02 bg=0.00
BH domain binding GO:0051400 p=3.4E−02 n=2 fg=0.02 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=3.4E−02 n=2 fg=0.02 bg=0.00
amino acid transmembrane transporter act... GO:0015171 p=3.8E−02 n=3 fg=0.02 bg=0.01
transcription coregulator activity GO:0003712 p=3.9E−02 n=11 fg=0.09 bg=0.05
DNA−binding transcription factor activit... GO:0003700 p=4.4E−02 n=14 fg=0.11 bg=0.07
0 1 2 3 4 5
−log(p)
n=122/446 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032382395.2
fraction genes in fg and expected valu
intrinsic component of the cytoplasmic s... GO:0031235 p=1.1E−03 n=3 fg=0.02 bg=0.00
brahma complex GO:0035060 p=1.4E−02 n=2 fg=0.01 bg=0.00
organelle membrane GO:0031090 p=1.8E−02 n=43 fg=0.32 bg=0.24
microtubule end GO:1990752 p=2.2E−02 n=2 fg=0.01 bg=0.00
chromatin GO:0000785 p=2.4E−02 n=12 fg=0.09 bg=0.05
histone deacetylase complex GO:0000118 p=2.4E−02 n=3 fg=0.02 bg=0.00
PcG protein complex GO:0031519 p=2.4E−02 n=3 fg=0.02 bg=0.00
cleavage furrow GO:0032154 p=3.0E−02 n=3 fg=0.02 bg=0.01
organelle inner membrane GO:0019866 p=3.1E−02 n=11 fg=0.08 bg=0.04
Golgi medial cisterna GO:0005797 p=3.6E−02 n=3 fg=0.02 bg=0.01
translation release factor complex GO:0018444 p=5.0E−02 n=1 fg=0.01 bg=0.00
septin filament array GO:0032160 p=5.0E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=5.0E−02 n=1 fg=0.01 bg=0.00
ribose phosphate diphosphokinase complex GO:0002189 p=5.0E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=5.0E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=5.0E−02 n=1 fg=0.01 bg=0.00
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lamellipodium membrane GO:0031258 p=5.0E−02 n=1 fg=0.01 bg=0.00
nuclear inner membrane GO:0005637 p=5.7E−02 n=2 fg=0.01 bg=0.00
cell division site GO:0032153 p=6.6E−02 n=3 fg=0.02 bg=0.01
cytoplasmic vesicle membrane GO:0030659 p=6.7E−02 n=14 fg=0.10 bg=0.07
membrane GO:0016020 p=7.0E−02 n=66 fg=0.49 bg=0.41
H4 histone acetyltransferase complex GO:1902562 p=7.1E−02 n=2 fg=0.01 bg=0.00
Golgi lumen GO:0005796 p=7.1E−02 n=2 fg=0.01 bg=0.00
bounding membrane of organelle GO:0098588 p=7.4E−02 n=24 fg=0.18 bg=0.13
SWI/SNF superfamily−type complex GO:0070603 p=7.5E−02 n=3 fg=0.02 bg=0.01
mitochondrial membrane GO:0031966 p=7.7E−02 n=12 fg=0.09 bg=0.06
vesicle membrane GO:0012506 p=7.7E−02 n=14 fg=0.10 bg=0.07
0 1 2 3 4 5
−log(p)
n=135/446 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction