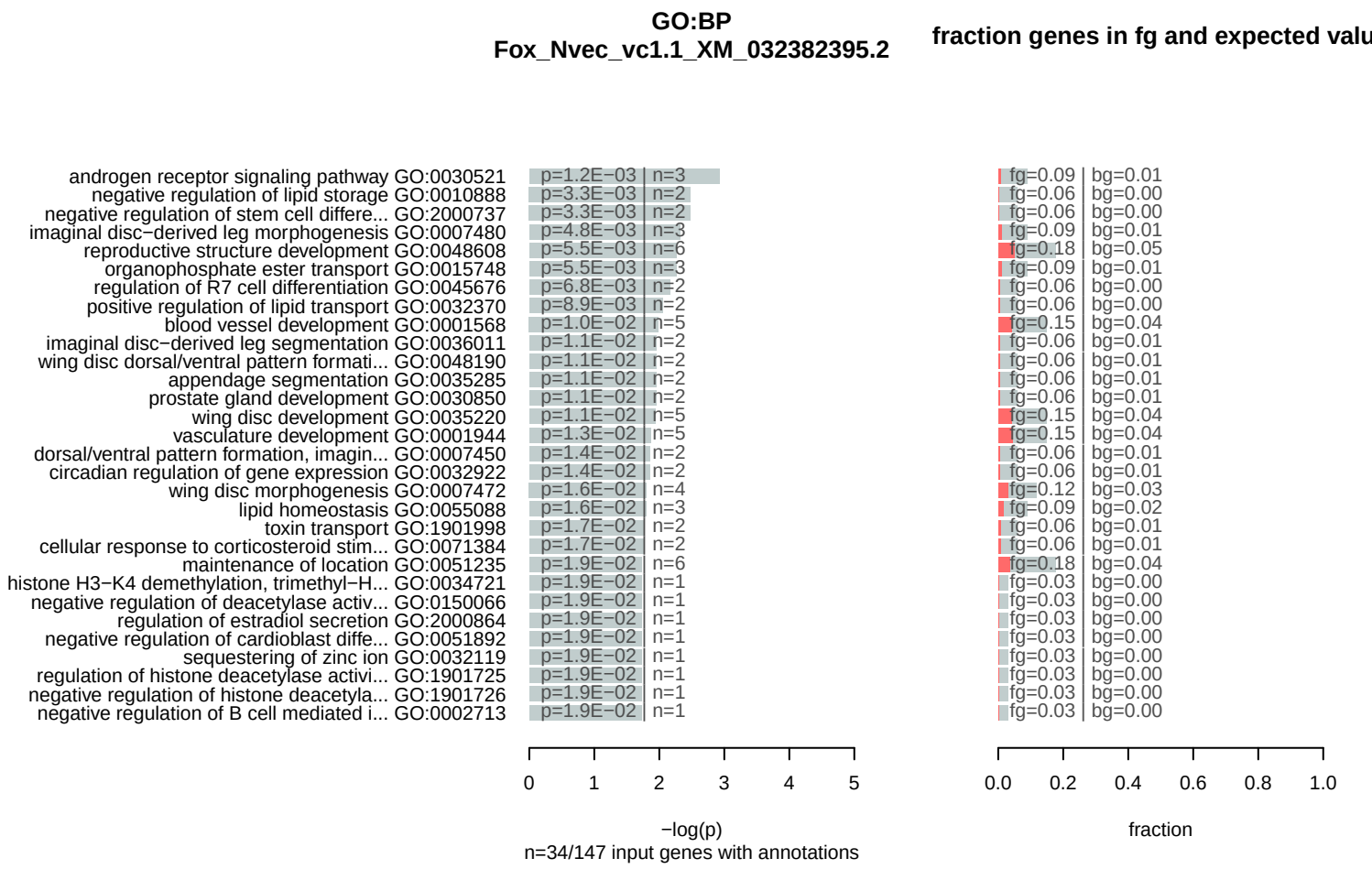
GO:BP
Fox_Nvec_vc1.1_XM_032382395.2
fraction genes in fg and expected valu
androgen receptor signaling pathway GO:0030521 p=1.2E−03 n=3 fg=0.09 bg=0.01
negative regulation of lipid storage GO:0010888 p=3.3E−03 n=2 fg=0.06 bg=0.00
negative regulation of stem cell differe... GO:2000737 p=3.3E−03 n=2 fg=0.06 bg=0.00
imaginal disc−derived leg morphogenesis GO:0007480 p=4.8E−03 n=3 fg=0.09 bg=0.01
reproductive structure development GO:0048608 p=5.5E−03 n=6 fg=0.18 bg=0.05
organophosphate ester transport GO:0015748 p=5.5E−03 n=3 fg=0.09 bg=0.01
regulation of R7 cell differentiation GO:0045676 p=6.8E−03 n=2 fg=0.06 bg=0.00
positive regulation of lipid transport GO:0032370 p=8.9E−03 n=2 fg=0.06 bg=0.00
blood vessel development GO:0001568 p=1.0E−02 n=5 fg=0.15 bg=0.04
imaginal disc−derived leg segmentation GO:0036011 p=1.1E−02 n=2 fg=0.06 bg=0.01
wing disc dorsal/ventral pattern formati... GO:0048190 p=1.1E−02 n=2 fg=0.06 bg=0.01
appendage segmentation GO:0035285 p=1.1E−02 n=2 fg=0.06 bg=0.01
prostate gland development GO:0030850 p=1.1E−02 n=2 fg=0.06 bg=0.01
wing disc development GO:0035220 p=1.1E−02 n=5 fg=0.15 bg=0.04
vasculature development GO:0001944 p=1.3E−02 n=5 fg=0.15 bg=0.04
dorsal/ventral pattern formation, imagin... GO:0007450 p=1.4E−02 n=2 fg=0.06 bg=0.01
circadian regulation of gene expression GO:0032922 p=1.4E−02 n=2 fg=0.06 bg=0.01
wing disc morphogenesis GO:0007472 p=1.6E−02 n=4 fg=0.12 bg=0.03
lipid homeostasis GO:0055088 p=1.6E−02 n=3 fg=0.09 bg=0.02
toxin transport GO:1901998 p=1.7E−02 n=2 fg=0.06 bg=0.01
cellular response to corticosteroid stim... GO:0071384 p=1.7E−02 n=2 fg=0.06 bg=0.01
maintenance of location GO:0051235 p=1.9E−02 n=6 fg=0.18 bg=0.04
histone H3−K4 demethylation, trimethyl−H... GO:0034721 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of deacetylase activ... GO:0150066 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of estradiol secretion GO:2000864 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of cardioblast diffe... GO:0051892 p=1.9E−02 n=1 fg=0.03 bg=0.00
sequestering of zinc ion GO:0032119 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of histone deacetylase activi... GO:1901725 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of histone deacetyla... GO:1901726 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of B cell mediated i... GO:0002713 p=1.9E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=34/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032382395.2
fraction genes in fg and expected valu
RNA polymerase II−specific DNA−binding t... GO:0061629 p=7.7E−03 n=4 fg=0.12 bg=0.02
nuclear receptor binding GO:0016922 p=1.5E−02 n=3 fg=0.09 bg=0.02
aspartate−tRNA ligase activity GO:0004815 p=2.1E−02 n=1 fg=0.03 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=2.1E−02 n=1 fg=0.03 bg=0.00
myosin VI binding GO:0070853 p=2.1E−02 n=1 fg=0.03 bg=0.00
myosin VI heavy chain binding GO:0070854 p=2.1E−02 n=1 fg=0.03 bg=0.00
N−acetylneuraminate lyase activity GO:0008747 p=2.1E−02 n=1 fg=0.03 bg=0.00
lipoprotein lipase activity GO:0004465 p=2.1E−02 n=1 fg=0.03 bg=0.00
histone H3−tri/di/monomethyl−lysine−4 de... GO:0034647 p=2.1E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016649 p=2.1E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=2.1E−02 n=1 fg=0.03 bg=0.00
aminoacylase activity GO:0004046 p=2.1E−02 n=1 fg=0.03 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.1E−02 n=1 fg=0.03 bg=0.00
lysophosphatidic acid binding GO:0035727 p=2.1E−02 n=1 fg=0.03 bg=0.00
electron−transferring−flavoprotein dehyd... GO:0004174 p=2.1E−02 n=1 fg=0.03 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=2.1E−02 n=1 fg=0.03 bg=0.00
AMP deaminase activity GO:0003876 p=2.1E−02 n=1 fg=0.03 bg=0.00
mono−olein transacylation activity GO:0051264 p=2.1E−02 n=1 fg=0.03 bg=0.00
diolein transacylation activity GO:0051265 p=2.1E−02 n=1 fg=0.03 bg=0.00
NAD(P)H oxidase H2O2−forming activity GO:0016174 p=2.1E−02 n=1 fg=0.03 bg=0.00
platelet−derived growth factor receptor ... GO:0005161 p=2.1E−02 n=1 fg=0.03 bg=0.00
hormone receptor binding GO:0051427 p=2.2E−02 n=3 fg=0.09 bg=0.02
actin binding GO:0003779 p=3.1E−02 n=3 fg=0.09 bg=0.02
transcription coactivator activity GO:0003713 p=3.4E−02 n=4 fg=0.12 bg=0.04
transcription regulator activity GO:0140110 p=3.7E−02 n=8 fg=0.24 bg=0.12
actin filament binding GO:0051015 p=3.9E−02 n=2 fg=0.06 bg=0.01
death receptor binding GO:0005123 p=4.2E−02 n=1 fg=0.03 bg=0.00
oxo−acid−lyase activity GO:0016833 p=4.2E−02 n=1 fg=0.03 bg=0.00
toxin transmembrane transporter activity GO:0019534 p=4.2E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acyl−CoA binding GO:0036042 p=4.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=34/147 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=2.4E−03 n=2 fg=0.05 bg=0.00
microtubule end GO:1990752 p=3.9E−03 n=2 fg=0.05 bg=0.00
dendritic microtubule GO:1901588 p=2.1E−02 n=1 fg=0.03 bg=0.00
brahma complex GO:0035060 p=4.1E−02 n=1 fg=0.03 bg=0.00
npBAF complex GO:0071564 p=4.1E−02 n=1 fg=0.03 bg=0.00
nBAF complex GO:0071565 p=4.1E−02 n=1 fg=0.03 bg=0.00
aminoacyl−tRNA synthetase multienzyme co... GO:0017101 p=4.1E−02 n=1 fg=0.03 bg=0.00
SWI/SNF complex GO:0016514 p=4.1E−02 n=1 fg=0.03 bg=0.00
microtubule minus−end GO:0036449 p=4.1E−02 n=1 fg=0.03 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=4.1E−02 n=1 fg=0.03 bg=0.00
lipid droplet GO:0005811 p=5.6E−02 n=2 fg=0.05 bg=0.01
microtubule plus−end GO:0035371 p=6.0E−02 n=1 fg=0.03 bg=0.00
respiratory chain complex IV GO:0045277 p=6.0E−02 n=1 fg=0.03 bg=0.00
nuclear aryl hydrocarbon receptor comple... GO:0034753 p=6.0E−02 n=1 fg=0.03 bg=0.00
spindle pole centrosome GO:0031616 p=6.0E−02 n=1 fg=0.03 bg=0.00
Sin3−type complex GO:0070822 p=6.0E−02 n=1 fg=0.03 bg=0.00
lamellar body GO:0042599 p=6.0E−02 n=1 fg=0.03 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=6.0E−02 n=1 fg=0.03 bg=0.00
costamere GO:0043034 p=7.9E−02 n=1 fg=0.03 bg=0.00
aryl hydrocarbon receptor complex GO:0034751 p=7.9E−02 n=1 fg=0.03 bg=0.00
cytochrome complex GO:0070069 p=9.8E−02 n=1 fg=0.03 bg=0.00
microtubule associated complex GO:0005875 p=1.2E−01 n=2 fg=0.05 bg=0.02
apicolateral plasma membrane GO:0016327 p=1.3E−01 n=1 fg=0.03 bg=0.00
axonal growth cone GO:0044295 p=1.5E−01 n=1 fg=0.03 bg=0.00
cytoplasmic microtubule GO:0005881 p=1.5E−01 n=1 fg=0.03 bg=0.00
fusome GO:0045169 p=1.5E−01 n=1 fg=0.03 bg=0.00
mitochondrial inner membrane GO:0005743 p=1.5E−01 n=3 fg=0.08 bg=0.04
mediator complex GO:0016592 p=1.7E−01 n=1 fg=0.03 bg=0.00
nuclear membrane GO:0031965 p=1.7E−01 n=2 fg=0.05 bg=0.02
cleavage furrow GO:0032154 p=1.9E−01 n=1 fg=0.03 bg=0.01
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−log(p)
n=37/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction