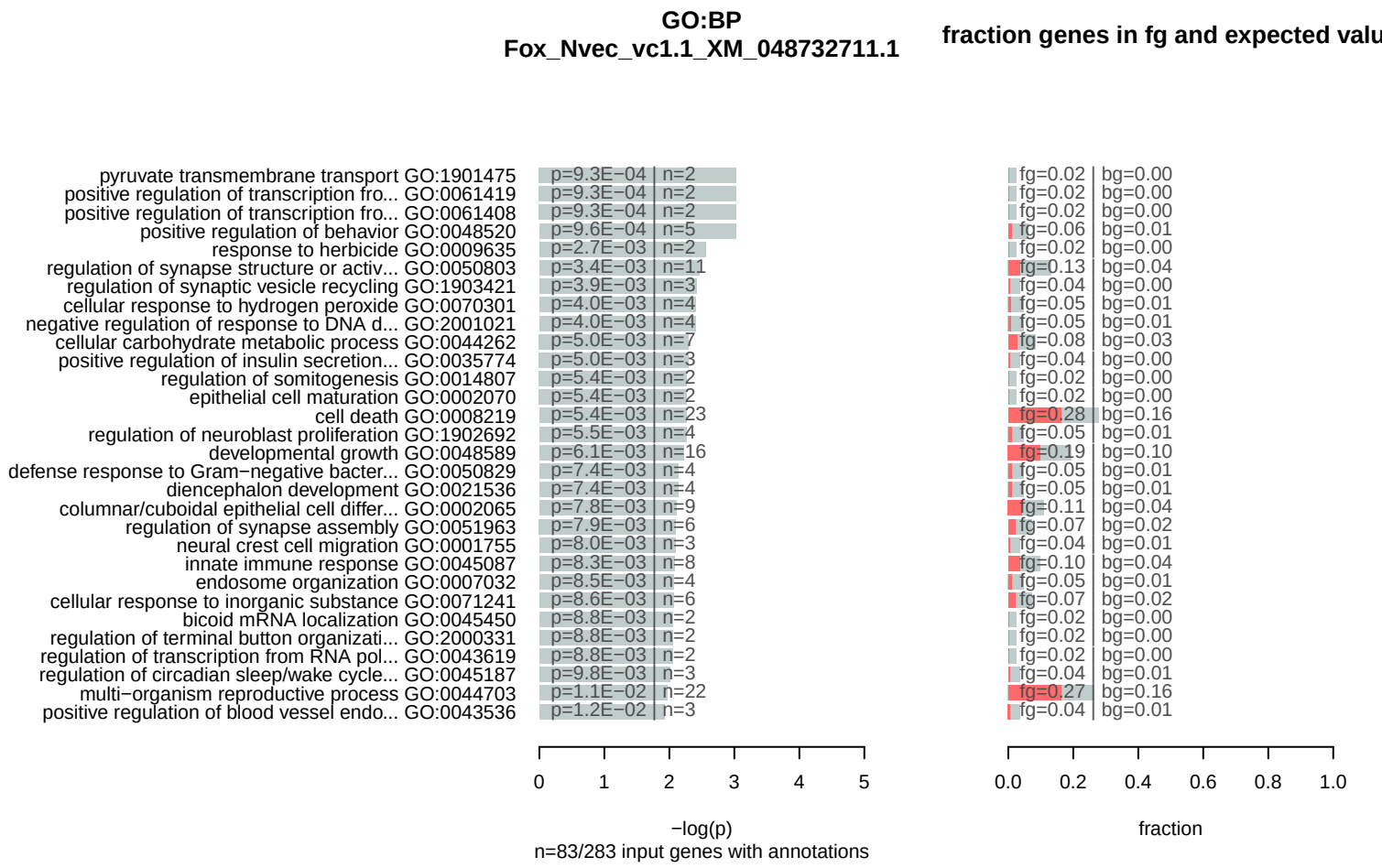
GO:BP
Fox_Nvec_vc1.1_XM_048732711.1
fraction genes in fg and expected valu
pyruvate transmembrane transport GO:1901475 p=9.3E−04 n=2 fg=0.02 bg=0.00
positive regulation of transcription fro... GO:0061419 p=9.3E−04 n=2 fg=0.02 bg=0.00
positive regulation of transcription fro... GO:0061408 p=9.3E−04 n=2 fg=0.02 bg=0.00
positive regulation of behavior GO:0048520 p=9.6E−04 n=5 fg=0.06 bg=0.01
response to herbicide GO:0009635 p=2.7E−03 n=2 fg=0.02 bg=0.00
regulation of synapse structure or activ... GO:0050803 p=3.4E−03 n=11 fg=0.13 bg=0.04
regulation of synaptic vesicle recycling GO:1903421 p=3.9E−03 n=3 fg=0.04 bg=0.00
cellular response to hydrogen peroxide GO:0070301 p=4.0E−03 n=4 fg=0.05 bg=0.01
negative regulation of response to DNA d... GO:2001021 p=4.0E−03 n=4 fg=0.05 bg=0.01
cellular carbohydrate metabolic process GO:0044262 p=5.0E−03 n=7 fg=0.08 bg=0.03
positive regulation of insulin secretion... GO:0035774 p=5.0E−03 n=3 fg=0.04 bg=0.00
regulation of somitogenesis GO:0014807 p=5.4E−03 n=2 fg=0.02 bg=0.00
epithelial cell maturation GO:0002070 p=5.4E−03 n=2 fg=0.02 bg=0.00
cell death GO:0008219 p=5.4E−03 n=23 fg=0.28 bg=0.16
regulation of neuroblast proliferation GO:1902692 p=5.5E−03 n=4 fg=0.05 bg=0.01
developmental growth GO:0048589 p=6.1E−03 n=16 fg=0.19 bg=0.10
defense response to Gram−negative bacter... GO:0050829 p=7.4E−03 n=4 fg=0.05 bg=0.01
diencephalon development GO:0021536 p=7.4E−03 n=4 fg=0.05 bg=0.01
columnar/cuboidal epithelial cell differ... GO:0002065 p=7.8E−03 n=9 fg=0.11 bg=0.04
regulation of synapse assembly GO:0051963 p=7.9E−03 n=6 fg=0.07 bg=0.02
neural crest cell migration GO:0001755 p=8.0E−03 n=3 fg=0.04 bg=0.01
innate immune response GO:0045087 p=8.3E−03 n=8 fg=0.10 bg=0.04
endosome organization GO:0007032 p=8.5E−03 n=4 fg=0.05 bg=0.01
cellular response to inorganic substance GO:0071241 p=8.6E−03 n=6 fg=0.07 bg=0.02
bicoid mRNA localization GO:0045450 p=8.8E−03 n=2 fg=0.02 bg=0.00
regulation of terminal button organizati... GO:2000331 p=8.8E−03 n=2 fg=0.02 bg=0.00
regulation of transcription from RNA pol... GO:0043619 p=8.8E−03 n=2 fg=0.02 bg=0.00
regulation of circadian sleep/wake cycle... GO:0045187 p=9.8E−03 n=3 fg=0.04 bg=0.01
multi−organism reproductive process GO:0044703 p=1.1E−02 n=22 fg=0.27 bg=0.16
positive regulation of blood vessel endo... GO:0043536 p=1.2E−02 n=3 fg=0.04 bg=0.01
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−log(p)
n=83/283 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_048732711.1
fraction genes in fg and expected valu
volume−sensitive anion channel activity GO:0005225 p=1.0E−03 n=2 fg=0.03 bg=0.00
pyruvate transmembrane transporter activ... GO:0050833 p=1.0E−03 n=2 fg=0.03 bg=0.00
cyclin−dependent protein serine/threonin... GO:0016538 p=2.3E−03 n=3 fg=0.04 bg=0.00
protein domain specific binding GO:0019904 p=3.0E−03 n=14 fg=0.18 bg=0.08
histone deacetylase binding GO:0042826 p=8.6E−03 n=4 fg=0.05 bg=0.01
mRNA binding GO:0003729 p=9.1E−03 n=7 fg=0.09 bg=0.03
RNA polymerase II transcription regulato... GO:0000977 p=1.3E−02 n=8 fg=0.11 bg=0.04
ubiquitin binding GO:0043130 p=1.8E−02 n=3 fg=0.04 bg=0.01
voltage−gated chloride channel activity GO:0005247 p=1.9E−02 n=2 fg=0.03 bg=0.00
voltage−gated anion channel activity GO:0008308 p=1.9E−02 n=2 fg=0.03 bg=0.00
Hsp90 protein binding GO:0051879 p=2.4E−02 n=3 fg=0.04 bg=0.01
transcription cis−regulatory region bind... GO:0000976 p=2.5E−02 n=8 fg=0.11 bg=0.05
metalloendopeptidase activity GO:0004222 p=3.2E−02 n=2 fg=0.03 bg=0.00
transcription coregulator binding GO:0001221 p=3.2E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol−3,5−bisphosphate 5−... GO:0043813 p=3.2E−02 n=1 fg=0.01 bg=0.00
holo−[acyl−carrier−protein] synthase act... GO:0008897 p=3.2E−02 n=1 fg=0.01 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 p=3.2E−02 n=1 fg=0.01 bg=0.00
FAD−AMP lyase (cyclizing) activity GO:0034012 p=3.2E−02 n=1 fg=0.01 bg=0.00
glycerone kinase activity GO:0004371 p=3.2E−02 n=1 fg=0.01 bg=0.00
cobalt ion binding GO:0050897 p=3.2E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase activit... GO:0046933 p=3.2E−02 n=1 fg=0.01 bg=0.00
triokinase activity GO:0050354 p=3.2E−02 n=1 fg=0.01 bg=0.00
rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039 p=3.2E−02 n=1 fg=0.01 bg=0.00
NAD+−protein ADP−ribosyltransferase acti... GO:1990404 p=3.2E−02 n=1 fg=0.01 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=3.2E−02 n=1 fg=0.01 bg=0.00
MRF binding GO:0043426 p=3.2E−02 n=1 fg=0.01 bg=0.00
gamma−catenin binding GO:0045295 p=3.2E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=3.2E−02 n=1 fg=0.01 bg=0.00
MHC class I protein binding GO:0042288 p=3.2E−02 n=1 fg=0.01 bg=0.00
telomeric repeat−containing RNA binding GO:0061752 p=3.2E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/283 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_048732711.1
fraction genes in fg and expected valu
autophagosome GO:0005776 p=1.6E−03 n=5 fg=0.06 bg=0.01
type I terminal bouton GO:0061174 p=5.0E−03 n=3 fg=0.04 bg=0.00
endocytic vesicle GO:0030139 p=6.1E−03 n=6 fg=0.07 bg=0.02
Sin3−type complex GO:0070822 p=8.8E−03 n=2 fg=0.02 bg=0.00
endosome membrane GO:0010008 p=9.7E−03 n=7 fg=0.08 bg=0.03
cell−cell contact zone GO:0044291 p=1.6E−02 n=3 fg=0.04 bg=0.01
secondary lysosome GO:0005767 p=1.8E−02 n=2 fg=0.02 bg=0.00
cell periphery GO:0071944 p=1.9E−02 n=30 fg=0.36 bg=0.25
plasma membrane GO:0005886 p=2.0E−02 n=28 fg=0.34 bg=0.23
lamellipodium GO:0030027 p=2.2E−02 n=5 fg=0.06 bg=0.02
early endosome membrane GO:0031901 p=2.5E−02 n=3 fg=0.04 bg=0.01
late endosome membrane GO:0031902 p=2.5E−02 n=3 fg=0.04 bg=0.01
cell surface GO:0009986 p=2.6E−02 n=7 fg=0.08 bg=0.04
secretory vesicle GO:0099503 p=2.7E−02 n=11 fg=0.13 bg=0.07
integral component of organelle membrane GO:0031301 p=2.9E−02 n=7 fg=0.08 bg=0.04
nuclear lamina GO:0005652 p=2.9E−02 n=2 fg=0.02 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005754 p=3.1E−02 n=1 fg=0.01 bg=0.00
dendritic growth cone GO:0044294 p=3.1E−02 n=1 fg=0.01 bg=0.00
podocyte foot GO:0098846 p=3.1E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase, cataly... GO:0045267 p=3.1E−02 n=1 fg=0.01 bg=0.00
late endosome GO:0005770 p=3.1E−02 n=5 fg=0.06 bg=0.02
intrinsic component of organelle membran... GO:0031300 p=3.5E−02 n=7 fg=0.08 bg=0.04
plasma membrane region GO:0098590 p=3.6E−02 n=12 fg=0.14 bg=0.08
intracellular membrane−bounded organelle GO:0043231 p=3.7E−02 n=73 fg=0.88 bg=0.77
exocytic vesicle GO:0070382 p=4.2E−02 n=5 fg=0.06 bg=0.02
mitotic spindle pole GO:0097431 p=4.3E−02 n=2 fg=0.02 bg=0.00
axon terminus GO:0043679 p=4.3E−02 n=7 fg=0.08 bg=0.02
phagocytic vesicle GO:0045335 p=4.4E−02 n=3 fg=0.04 bg=0.01
apical part of cell GO:0045177 p=4.4E−02 n=8 fg=0.10 bg=0.05
external side of plasma membrane GO:0009897 p=4.8E−02 n=3 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=83/283 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction