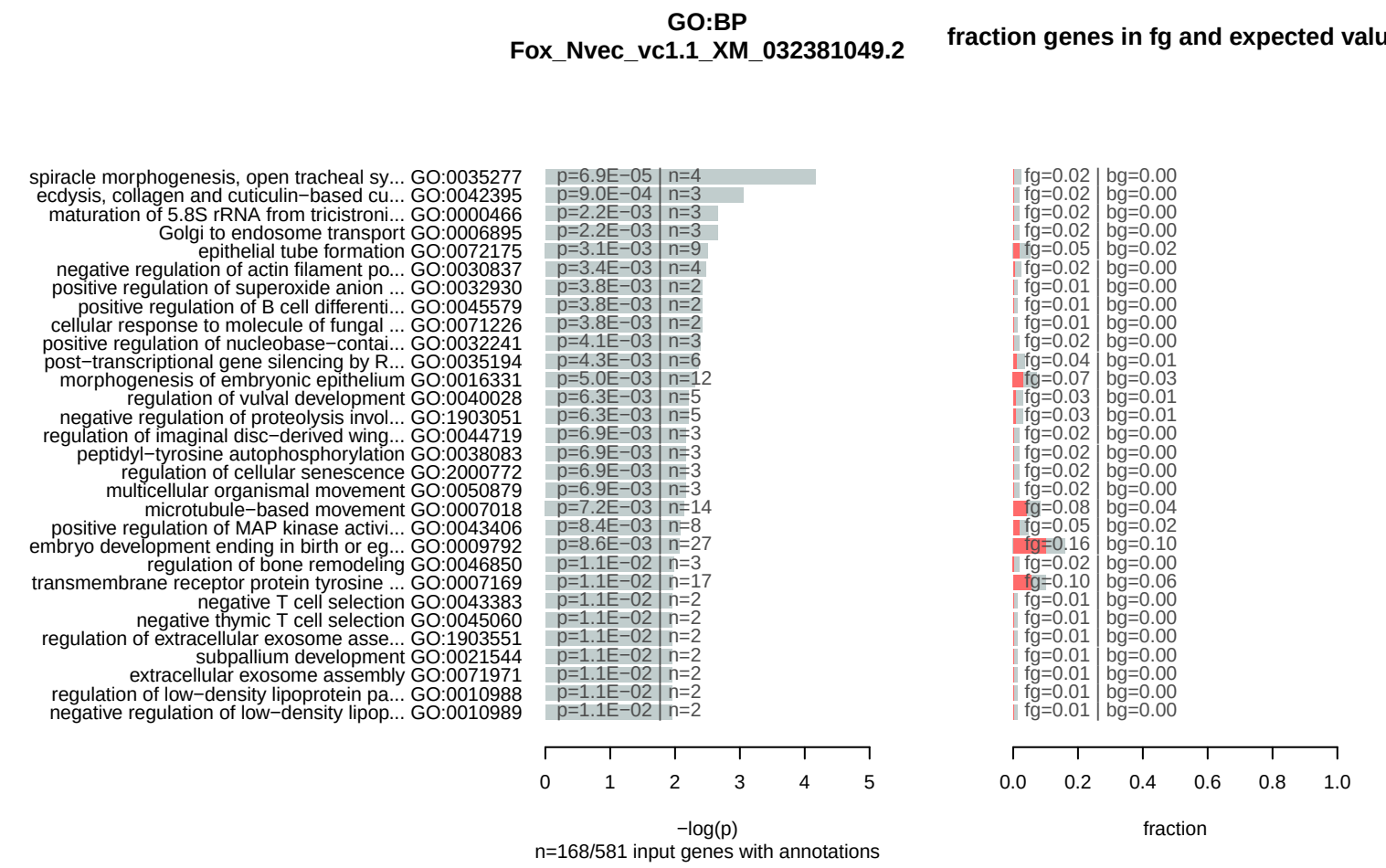
GO:BP
Fox_Nvec_vc1.1_XM_032381049.2
fraction genes in fg and expected valu
spiracle morphogenesis, open tracheal sy... GO:0035277 p=6.9E−05 n=4 fg=0.02 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=9.0E−04 n=3 fg=0.02 bg=0.00
maturation of 5.8S rRNA from tricistroni... GO:0000466 p=2.2E−03 n=3 fg=0.02 bg=0.00
Golgi to endosome transport GO:0006895 p=2.2E−03 n=3 fg=0.02 bg=0.00
epithelial tube formation GO:0072175 p=3.1E−03 n=9 fg=0.05 bg=0.02
negative regulation of actin filament po... GO:0030837 p=3.4E−03 n=4 fg=0.02 bg=0.00
positive regulation of superoxide anion ... GO:0032930 p=3.8E−03 n=2 fg=0.01 bg=0.00
positive regulation of B cell differenti... GO:0045579 p=3.8E−03 n=2 fg=0.01 bg=0.00
cellular response to molecule of fungal ... GO:0071226 p=3.8E−03 n=2 fg=0.01 bg=0.00
positive regulation of nucleobase−contai... GO:0032241 p=4.1E−03 n=3 fg=0.02 bg=0.00
post−transcriptional gene silencing by R... GO:0035194 p=4.3E−03 n=6 fg=0.04 bg=0.01
morphogenesis of embryonic epithelium GO:0016331 p=5.0E−03 n=12 fg=0.07 bg=0.03
regulation of vulval development GO:0040028 p=6.3E−03 n=5 fg=0.03 bg=0.01
negative regulation of proteolysis invol... GO:1903051 p=6.3E−03 n=5 fg=0.03 bg=0.01
regulation of imaginal disc−derived wing... GO:0044719 p=6.9E−03 n=3 fg=0.02 bg=0.00
peptidyl−tyrosine autophosphorylation GO:0038083 p=6.9E−03 n=3 fg=0.02 bg=0.00
regulation of cellular senescence GO:2000772 p=6.9E−03 n=3 fg=0.02 bg=0.00
multicellular organismal movement GO:0050879 p=6.9E−03 n=3 fg=0.02 bg=0.00
microtubule−based movement GO:0007018 p=7.2E−03 n=14 fg=0.08 bg=0.04
positive regulation of MAP kinase activi... GO:0043406 p=8.4E−03 n=8 fg=0.05 bg=0.02
embryo development ending in birth or eg... GO:0009792 p=8.6E−03 n=27 fg=0.16 bg=0.10
regulation of bone remodeling GO:0046850 p=1.1E−02 n=3 fg=0.02 bg=0.00
transmembrane receptor protein tyrosine ... GO:0007169 p=1.1E−02 n=17 fg=0.10 bg=0.06
negative T cell selection GO:0043383 p=1.1E−02 n=2 fg=0.01 bg=0.00
negative thymic T cell selection GO:0045060 p=1.1E−02 n=2 fg=0.01 bg=0.00
regulation of extracellular exosome asse... GO:1903551 p=1.1E−02 n=2 fg=0.01 bg=0.00
subpallium development GO:0021544 p=1.1E−02 n=2 fg=0.01 bg=0.00
extracellular exosome assembly GO:0071971 p=1.1E−02 n=2 fg=0.01 bg=0.00
regulation of low−density lipoprotein pa... GO:0010988 p=1.1E−02 n=2 fg=0.01 bg=0.00
negative regulation of low−density lipop... GO:0010989 p=1.1E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=168/581 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
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fraction genes in fg and expected valu
apolipoprotein binding GO:0034185 p=4.0E−03 n=2 fg=0.01 bg=0.00
ubiquitin ligase inhibitor activity GO:1990948 p=4.0E−03 n=2 fg=0.01 bg=0.00
proteoglycan binding GO:0043394 p=4.3E−03 n=3 fg=0.02 bg=0.00
non−membrane spanning protein tyrosine k... GO:0004715 p=7.2E−03 n=3 fg=0.02 bg=0.00
tRNA (cytosine) methyltransferase activi... GO:0016427 p=1.1E−02 n=2 fg=0.01 bg=0.00
heparan sulfate proteoglycan binding GO:0043395 p=1.1E−02 n=2 fg=0.01 bg=0.00
sulfur compound binding GO:1901681 p=1.3E−02 n=6 fg=0.04 bg=0.01
poly(U) RNA binding GO:0008266 p=1.6E−02 n=3 fg=0.02 bg=0.00
frizzled binding GO:0005109 p=2.1E−02 n=3 fg=0.02 bg=0.00
GTPase activating protein binding GO:0032794 p=2.1E−02 n=3 fg=0.02 bg=0.00
receptor ligand activity GO:0048018 p=2.1E−02 n=3 fg=0.02 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=2.1E−02 n=3 fg=0.02 bg=0.00
catalytic activity, acting on RNA GO:0140098 p=2.2E−02 n=12 fg=0.08 bg=0.04
cytokine activity GO:0005125 p=2.2E−02 n=2 fg=0.01 bg=0.00
glycosaminoglycan binding GO:0005539 p=2.8E−02 n=3 fg=0.02 bg=0.00
signaling receptor activator activity GO:0030546 p=2.8E−02 n=3 fg=0.02 bg=0.00
growth factor binding GO:0019838 p=2.8E−02 n=4 fg=0.03 bg=0.01
ephrin receptor binding GO:0046875 p=3.5E−02 n=2 fg=0.01 bg=0.00
G−protein beta/gamma−subunit complex bin... GO:0031683 p=3.5E−02 n=2 fg=0.01 bg=0.00
N−acetyltransferase activity GO:0008080 p=3.6E−02 n=3 fg=0.02 bg=0.01
SH2 domain binding GO:0042169 p=3.6E−02 n=3 fg=0.02 bg=0.01
signaling receptor regulator activity GO:0030545 p=3.6E−02 n=3 fg=0.02 bg=0.01
G protein−coupled receptor binding GO:0001664 p=4.2E−02 n=6 fg=0.04 bg=0.02
GDP binding GO:0019003 p=4.4E−02 n=3 fg=0.02 bg=0.01
poly−purine tract binding GO:0070717 p=5.1E−02 n=2 fg=0.01 bg=0.00
catalytic activity, acting on a glycopro... GO:0140103 p=5.1E−02 n=2 fg=0.01 bg=0.00
mRNA 5'−UTR binding GO:0048027 p=5.1E−02 n=2 fg=0.01 bg=0.00
O−methyltransferase activity GO:0008171 p=5.1E−02 n=2 fg=0.01 bg=0.00
protein tyrosine kinase activity GO:0004713 p=5.2E−02 n=6 fg=0.04 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=5.4E−02 n=3 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
n=150/581 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032381049.2
fraction genes in fg and expected valu
extrinsic component of cytoplasmic side ... GO:0031234 p=1.2E−03 n=6 fg=0.04 bg=0.01
endosome lumen GO:0031904 p=3.7E−03 n=2 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.7E−03 n=2 fg=0.01 bg=0.00
cilium GO:0005929 p=5.6E−03 n=19 fg=0.12 bg=0.06
intracellular non−membrane−bounded organ... GO:0043232 p=7.4E−03 n=70 fg=0.42 bg=0.33
ciliary tip GO:0097542 p=2.6E−02 n=3 fg=0.02 bg=0.00
extracellular space GO:0005615 p=2.6E−02 n=10 fg=0.06 bg=0.03
RNA polymerase II, core complex GO:0005665 p=3.3E−02 n=2 fg=0.01 bg=0.00
intraciliary transport particle GO:0030990 p=3.3E−02 n=2 fg=0.01 bg=0.00
cell cortex region GO:0099738 p=3.6E−02 n=4 fg=0.02 bg=0.01
ciliary basal body GO:0036064 p=4.0E−02 n=6 fg=0.04 bg=0.02
extracellular region GO:0005576 p=4.5E−02 n=18 fg=0.11 bg=0.07
organelle membrane contact site GO:0044232 p=4.7E−02 n=2 fg=0.01 bg=0.00
dendrite terminus GO:0044292 p=4.7E−02 n=2 fg=0.01 bg=0.00
ciliary base GO:0097546 p=5.0E−02 n=3 fg=0.02 bg=0.01
cytosolic ribosome GO:0022626 p=5.8E−02 n=6 fg=0.04 bg=0.02
ribosome GO:0005840 p=6.1E−02 n=8 fg=0.05 bg=0.03
intermediate−density lipoprotein particl... GO:0034363 p=6.1E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=6.1E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=6.1E−02 n=1 fg=0.01 bg=0.00
plasma lipoprotein particle GO:0034358 p=6.1E−02 n=1 fg=0.01 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=6.1E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=6.1E−02 n=1 fg=0.01 bg=0.00
DNA recombinase mediator complex GO:0033061 p=6.1E−02 n=1 fg=0.01 bg=0.00
CatSper complex GO:0036128 p=6.1E−02 n=1 fg=0.01 bg=0.00
pinosome GO:0044352 p=6.1E−02 n=1 fg=0.01 bg=0.00
macropinosome GO:0044354 p=6.1E−02 n=1 fg=0.01 bg=0.00
interleukin−5 receptor complex GO:0005895 p=6.1E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=6.1E−02 n=1 fg=0.01 bg=0.00
Swi5−Swi2 complex GO:0034974 p=6.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=165/581 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction