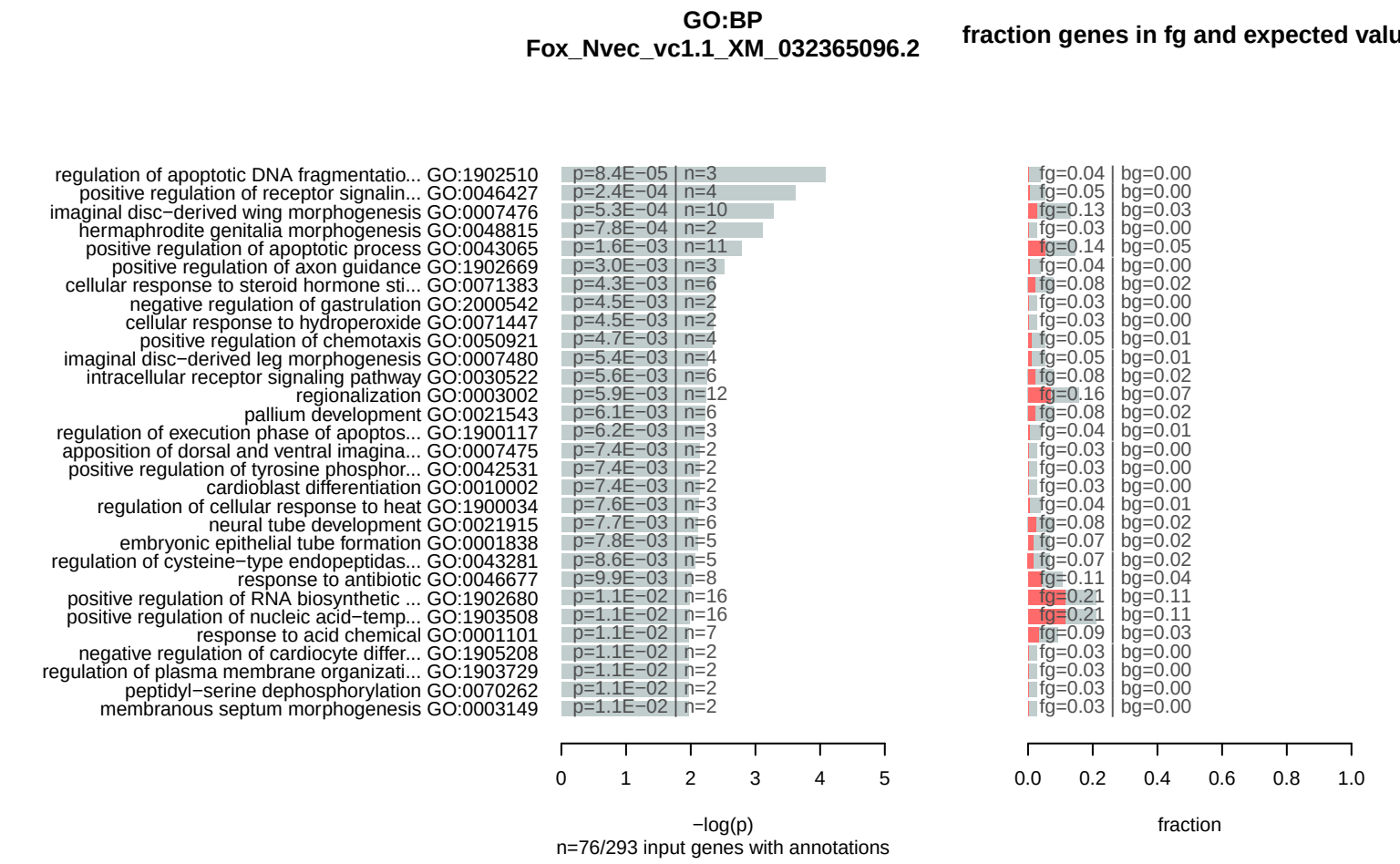
GO:BP
Fox_Nvec_vc1.1_XM_032365096.2
fraction genes in fg and expected valu
regulation of apoptotic DNA fragmentatio... GO:1902510 p=8.4E−05 n=3 fg=0.04 bg=0.00
positive regulation of receptor signalin... GO:0046427 p=2.4E−04 n=4 fg=0.05 bg=0.00
imaginal disc−derived wing morphogenesis GO:0007476 p=5.3E−04 n=10 fg=0.13 bg=0.03
hermaphrodite genitalia morphogenesis GO:0048815 p=7.8E−04 n=2 fg=0.03 bg=0.00
positive regulation of apoptotic process GO:0043065 p=1.6E−03 n=11 fg=0.14 bg=0.05
positive regulation of axon guidance GO:1902669 p=3.0E−03 n=3 fg=0.04 bg=0.00
cellular response to steroid hormone sti... GO:0071383 p=4.3E−03 n=6 fg=0.08 bg=0.02
negative regulation of gastrulation GO:2000542 p=4.5E−03 n=2 fg=0.03 bg=0.00
cellular response to hydroperoxide GO:0071447 p=4.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of chemotaxis GO:0050921 p=4.7E−03 n=4 fg=0.05 bg=0.01
imaginal disc−derived leg morphogenesis GO:0007480 p=5.4E−03 n=4 fg=0.05 bg=0.01
intracellular receptor signaling pathway GO:0030522 p=5.6E−03 n=6 fg=0.08 bg=0.02
regionalization GO:0003002 p=5.9E−03 n=12 fg=0.16 bg=0.07
pallium development GO:0021543 p=6.1E−03 n=6 fg=0.08 bg=0.02
regulation of execution phase of apoptos... GO:1900117 p=6.2E−03 n=3 fg=0.04 bg=0.01
apposition of dorsal and ventral imagina... GO:0007475 p=7.4E−03 n=2 fg=0.03 bg=0.00
positive regulation of tyrosine phosphor... GO:0042531 p=7.4E−03 n=2 fg=0.03 bg=0.00
cardioblast differentiation GO:0010002 p=7.4E−03 n=2 fg=0.03 bg=0.00
regulation of cellular response to heat GO:1900034 p=7.6E−03 n=3 fg=0.04 bg=0.01
neural tube development GO:0021915 p=7.7E−03 n=6 fg=0.08 bg=0.02
embryonic epithelial tube formation GO:0001838 p=7.8E−03 n=5 fg=0.07 bg=0.02
regulation of cysteine−type endopeptidas... GO:0043281 p=8.6E−03 n=5 fg=0.07 bg=0.02
response to antibiotic GO:0046677 p=9.9E−03 n=8 fg=0.11 bg=0.04
positive regulation of RNA biosynthetic ... GO:1902680 p=1.1E−02 n=16 fg=0.21 bg=0.11
positive regulation of nucleic acid−temp... GO:1903508 p=1.1E−02 n=16 fg=0.21 bg=0.11
response to acid chemical GO:0001101 p=1.1E−02 n=7 fg=0.09 bg=0.03
negative regulation of cardiocyte differ... GO:1905208 p=1.1E−02 n=2 fg=0.03 bg=0.00
regulation of plasma membrane organizati... GO:1903729 p=1.1E−02 n=2 fg=0.03 bg=0.00
peptidyl−serine dephosphorylation GO:0070262 p=1.1E−02 n=2 fg=0.03 bg=0.00
membranous septum morphogenesis GO:0003149 p=1.1E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/293 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032365096.2
fraction genes in fg and expected valu
frizzled binding GO:0005109 p=2.4E−03 n=3 fg=0.04 bg=0.00
nuclear receptor coactivator activity GO:0030374 p=4.1E−03 n=3 fg=0.04 bg=0.01
hormone receptor binding GO:0051427 p=6.9E−03 n=5 fg=0.07 bg=0.02
JUN kinase binding GO:0008432 p=7.7E−03 n=2 fg=0.03 bg=0.00
protein self−association GO:0043621 p=8.0E−03 n=3 fg=0.04 bg=0.01
DEAD/H−box RNA helicase binding GO:0017151 p=1.5E−02 n=2 fg=0.03 bg=0.00
Hsp90 protein binding GO:0051879 p=1.8E−02 n=3 fg=0.04 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=2.0E−02 n=2 fg=0.03 bg=0.00
cyclin−dependent protein serine/threonin... GO:0004693 p=2.6E−02 n=2 fg=0.03 bg=0.00
cyclin−dependent protein kinase activity GO:0097472 p=2.6E−02 n=2 fg=0.03 bg=0.00
malate dehydrogenase (NADP+) activity GO:0046554 p=2.9E−02 n=1 fg=0.01 bg=0.00
CCR5 chemokine receptor binding GO:0031730 p=2.9E−02 n=1 fg=0.01 bg=0.00
D−lactate dehydrogenase activity GO:0008720 p=2.9E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=2.9E−02 n=1 fg=0.01 bg=0.00
betaine−aldehyde dehydrogenase activity GO:0008802 p=2.9E−02 n=1 fg=0.01 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=2.9E−02 n=1 fg=0.01 bg=0.00
NAD(P)H oxidase H2O2−forming activity GO:0016174 p=2.9E−02 n=1 fg=0.01 bg=0.00
MRF binding GO:0043426 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphoribosylaminoimidazolecarboxamide ... GO:0004643 p=2.9E−02 n=1 fg=0.01 bg=0.00
CCR chemokine receptor binding GO:0048020 p=2.9E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=2.9E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=2.9E−02 n=1 fg=0.01 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=2.9E−02 n=1 fg=0.01 bg=0.00
cysteine desulfurase activity GO:0031071 p=2.9E−02 n=1 fg=0.01 bg=0.00
mRNA (guanine−N7−)−methyltransferase act... GO:0004482 p=2.9E−02 n=1 fg=0.01 bg=0.00
IMP cyclohydrolase activity GO:0003937 p=2.9E−02 n=1 fg=0.01 bg=0.00
telomeric repeat−containing RNA binding GO:0061752 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphatidyl−N−dimethylethanolamine N−me... GO:0080101 p=2.9E−02 n=1 fg=0.01 bg=0.00
translation elongation factor binding GO:0061770 p=2.9E−02 n=1 fg=0.01 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=68/293 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032365096.2
fraction genes in fg and expected valu
centrosome GO:0005813 p=3.6E−03 n=12 fg=0.16 bg=0.05
pericentriolar material GO:0000242 p=7.6E−03 n=2 fg=0.03 bg=0.00
P granule GO:0043186 p=9.6E−03 n=3 fg=0.04 bg=0.01
mitotic spindle GO:0072686 p=2.2E−02 n=4 fg=0.05 bg=0.01
fusome GO:0045169 p=2.5E−02 n=2 fg=0.03 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=2.9E−02 n=1 fg=0.01 bg=0.00
piP−body GO:0071547 p=2.9E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=2.9E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=2.9E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=2.9E−02 n=1 fg=0.01 bg=0.00
desmosome GO:0030057 p=2.9E−02 n=1 fg=0.01 bg=0.00
apoptosome GO:0043293 p=2.9E−02 n=1 fg=0.01 bg=0.00
mRNA cap methyltransferase complex GO:0031533 p=2.9E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=2.9E−02 n=1 fg=0.01 bg=0.00
endocytic vesicle membrane GO:0030666 p=2.9E−02 n=3 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=3.1E−02 n=2 fg=0.03 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=3.1E−02 n=2 fg=0.03 bg=0.00
pronucleus GO:0045120 p=3.7E−02 n=2 fg=0.03 bg=0.00
lateral plasma membrane GO:0016328 p=4.4E−02 n=2 fg=0.03 bg=0.00
kinesin complex GO:0005871 p=4.4E−02 n=2 fg=0.03 bg=0.00
spindle GO:0005819 p=4.5E−02 n=6 fg=0.08 bg=0.03
autophagosome GO:0005776 p=4.8E−02 n=3 fg=0.04 bg=0.01
PML body GO:0016605 p=5.1E−02 n=2 fg=0.03 bg=0.00
eukaryotic translation initiation factor... GO:0016281 p=5.6E−02 n=1 fg=0.01 bg=0.00
nuclear stress granule GO:0097165 p=5.6E−02 n=1 fg=0.01 bg=0.00
L−cysteine desulfurase complex GO:1990221 p=5.6E−02 n=1 fg=0.01 bg=0.00
core mediator complex GO:0070847 p=5.6E−02 n=1 fg=0.01 bg=0.00
elongin complex GO:0070449 p=5.6E−02 n=1 fg=0.01 bg=0.00
post−mRNA release spliceosomal complex GO:0071014 p=5.6E−02 n=1 fg=0.01 bg=0.00
U4 snRNP GO:0005687 p=5.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=77/293 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction