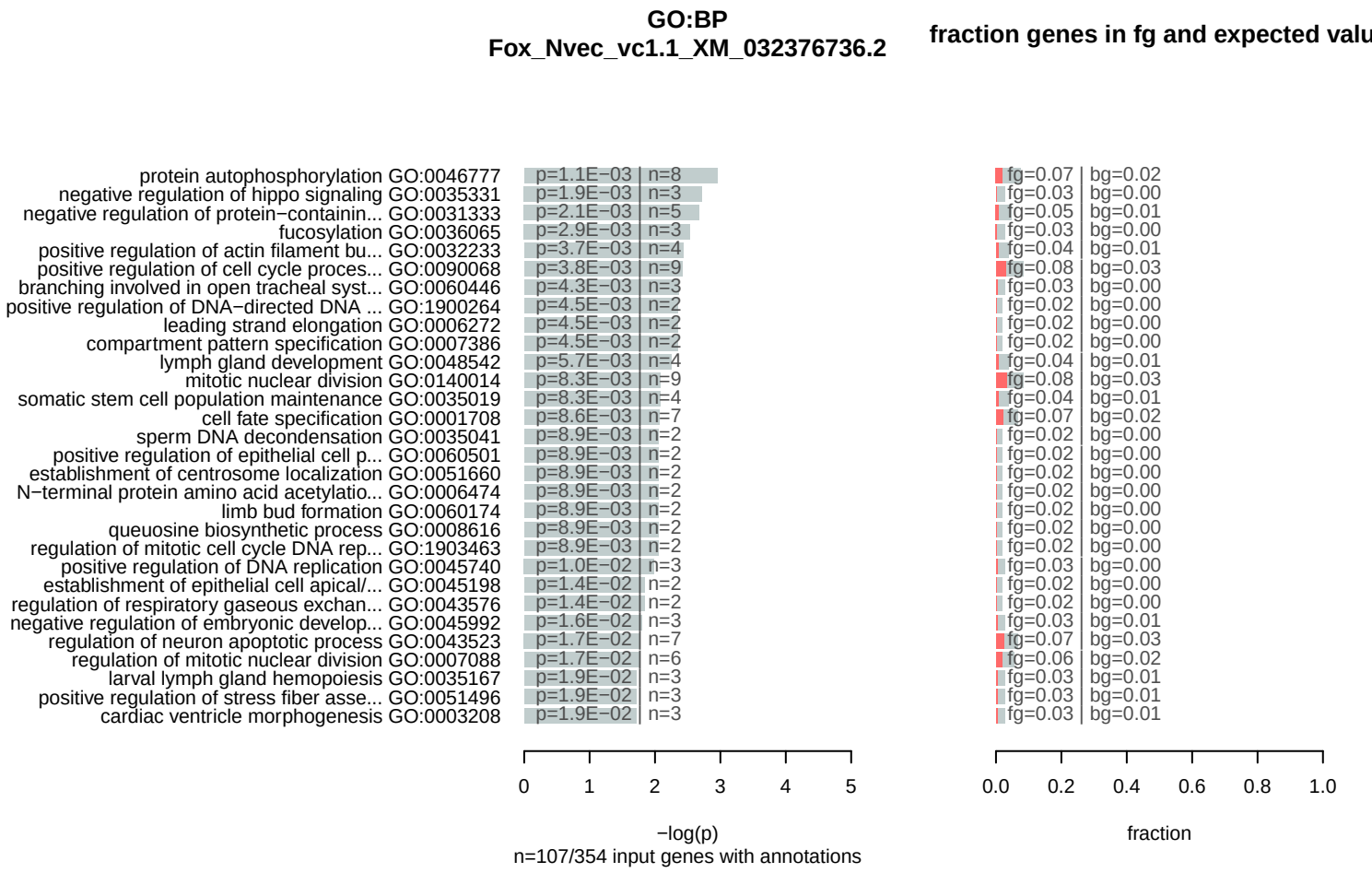
GO:BP
Fox_Nvec_vc1.1_XM_032376736.2
fraction genes in fg and expected valu
protein autophosphorylation GO:0046777 p=1.1E−03 n=8 fg=0.07 bg=0.02
negative regulation of hippo signaling GO:0035331 p=1.9E−03 n=3 fg=0.03 bg=0.00
negative regulation of protein−containin... GO:0031333 p=2.1E−03 n=5 fg=0.05 bg=0.01
fucosylation GO:0036065 p=2.9E−03 n=3 fg=0.03 bg=0.00
positive regulation of actin filament bu... GO:0032233 p=3.7E−03 n=4 fg=0.04 bg=0.01
positive regulation of cell cycle proces... GO:0090068 p=3.8E−03 n=9 fg=0.08 bg=0.03
branching involved in open tracheal syst... GO:0060446 p=4.3E−03 n=3 fg=0.03 bg=0.00
positive regulation of DNA−directed DNA ... GO:1900264 p=4.5E−03 n=2 fg=0.02 bg=0.00
leading strand elongation GO:0006272 p=4.5E−03 n=2 fg=0.02 bg=0.00
compartment pattern specification GO:0007386 p=4.5E−03 n=2 fg=0.02 bg=0.00
lymph gland development GO:0048542 p=5.7E−03 n=4 fg=0.04 bg=0.01
mitotic nuclear division GO:0140014 p=8.3E−03 n=9 fg=0.08 bg=0.03
somatic stem cell population maintenance GO:0035019 p=8.3E−03 n=4 fg=0.04 bg=0.01
cell fate specification GO:0001708 p=8.6E−03 n=7 fg=0.07 bg=0.02
sperm DNA decondensation GO:0035041 p=8.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of epithelial cell p... GO:0060501 p=8.9E−03 n=2 fg=0.02 bg=0.00
establishment of centrosome localization GO:0051660 p=8.9E−03 n=2 fg=0.02 bg=0.00
N−terminal protein amino acid acetylatio... GO:0006474 p=8.9E−03 n=2 fg=0.02 bg=0.00
limb bud formation GO:0060174 p=8.9E−03 n=2 fg=0.02 bg=0.00
queuosine biosynthetic process GO:0008616 p=8.9E−03 n=2 fg=0.02 bg=0.00
regulation of mitotic cell cycle DNA rep... GO:1903463 p=8.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of DNA replication GO:0045740 p=1.0E−02 n=3 fg=0.03 bg=0.00
establishment of epithelial cell apical/... GO:0045198 p=1.4E−02 n=2 fg=0.02 bg=0.00
regulation of respiratory gaseous exchan... GO:0043576 p=1.4E−02 n=2 fg=0.02 bg=0.00
negative regulation of embryonic develop... GO:0045992 p=1.6E−02 n=3 fg=0.03 bg=0.01
regulation of neuron apoptotic process GO:0043523 p=1.7E−02 n=7 fg=0.07 bg=0.03
regulation of mitotic nuclear division GO:0007088 p=1.7E−02 n=6 fg=0.06 bg=0.02
larval lymph gland hemopoiesis GO:0035167 p=1.9E−02 n=3 fg=0.03 bg=0.01
positive regulation of stress fiber asse... GO:0051496 p=1.9E−02 n=3 fg=0.03 bg=0.01
cardiac ventricle morphogenesis GO:0003208 p=1.9E−02 n=3 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=107/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032376736.2
fraction genes in fg and expected valu
caspase binding GO:0089720 p=4.7E−03 n=2 fg=0.02 bg=0.00
protein serine/threonine kinase activity GO:0004674 p=5.0E−03 n=10 fg=0.11 bg=0.04
alpha−(1−>3)−fucosyltransferase activity GO:0046920 p=1.5E−02 n=2 fg=0.02 bg=0.00
fucosyltransferase activity GO:0008417 p=1.5E−02 n=2 fg=0.02 bg=0.00
polynucleotide adenylyltransferase activ... GO:0004652 p=2.9E−02 n=2 fg=0.02 bg=0.00
NAD(P)+ transhydrogenase (AB−specific) a... GO:0008750 p=4.0E−02 n=1 fg=0.01 bg=0.00
Rho GDP−dissociation inhibitor binding GO:0051022 p=4.0E−02 n=1 fg=0.01 bg=0.00
apolipoprotein receptor binding GO:0034190 p=4.0E−02 n=1 fg=0.01 bg=0.00
apolipoprotein A−I receptor binding GO:0034191 p=4.0E−02 n=1 fg=0.01 bg=0.00
G−protein beta−subunit binding GO:0031681 p=4.0E−02 n=1 fg=0.01 bg=0.00
ribokinase activity GO:0004747 p=4.0E−02 n=1 fg=0.01 bg=0.00
RNA uridylyltransferase activity GO:0050265 p=4.0E−02 n=1 fg=0.01 bg=0.00
adenylate cyclase activator activity GO:0010856 p=4.0E−02 n=1 fg=0.01 bg=0.00
5−phosphoribosyl 1−pyrophosphate pyropho... GO:0043135 p=4.0E−02 n=1 fg=0.01 bg=0.00
DNA clamp loader activity GO:0003689 p=4.0E−02 n=1 fg=0.01 bg=0.00
inorganic phosphate transmembrane transp... GO:0005315 p=4.0E−02 n=1 fg=0.01 bg=0.00
high−affinity inorganic phosphate:sodium... GO:0005316 p=4.0E−02 n=1 fg=0.01 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=4.0E−02 n=1 fg=0.01 bg=0.00
NAD(P)+ transhydrogenase (B−specific) ac... GO:0003957 p=4.0E−02 n=1 fg=0.01 bg=0.00
short−branched−chain−acyl−CoA dehydrogen... GO:0016937 p=4.0E−02 n=1 fg=0.01 bg=0.00
ribonuclease P RNA binding GO:0033204 p=4.0E−02 n=1 fg=0.01 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=4.0E−02 n=1 fg=0.01 bg=0.00
3−hydroxyacyl−CoA dehydrogenase activity GO:0003857 p=4.0E−02 n=1 fg=0.01 bg=0.00
acid−sensing ion channel activity GO:0044736 p=4.0E−02 n=1 fg=0.01 bg=0.00
O−fucosylpeptide 3−beta−N−acetylglucosam... GO:0033829 p=4.0E−02 n=1 fg=0.01 bg=0.00
GBD domain binding GO:0032427 p=4.0E−02 n=1 fg=0.01 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=4.0E−02 n=1 fg=0.01 bg=0.00
SMC family protein binding GO:0043221 p=4.0E−02 n=1 fg=0.01 bg=0.00
sodium:inorganic phosphate symporter act... GO:0015319 p=4.0E−02 n=1 fg=0.01 bg=0.00
kinase binding GO:0019900 p=4.5E−02 n=12 fg=0.13 bg=0.07
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−log(p)
n=95/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032376736.2
fraction genes in fg and expected valu
Elg1 RFC−like complex GO:0031391 p=1.5E−03 n=2 fg=0.02 bg=0.00
DNA replication factor C complex GO:0005663 p=4.4E−03 n=2 fg=0.02 bg=0.00
FAR/SIN/STRIPAK complex GO:0090443 p=4.4E−03 n=2 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=4.4E−03 n=2 fg=0.02 bg=0.00
endocytic vesicle GO:0030139 p=4.8E−03 n=7 fg=0.07 bg=0.02
pseudopodium GO:0031143 p=8.5E−03 n=2 fg=0.02 bg=0.00
spindle midzone GO:0051233 p=1.8E−02 n=3 fg=0.03 bg=0.01
ATPase complex GO:1904949 p=1.9E−02 n=4 fg=0.04 bg=0.01
mitotic spindle midzone GO:1990023 p=2.0E−02 n=2 fg=0.02 bg=0.00
Golgi apparatus GO:0005794 p=2.3E−02 n=19 fg=0.18 bg=0.11
preribosome GO:0030684 p=2.4E−02 n=4 fg=0.04 bg=0.01
preribosome, small subunit precursor GO:0030688 p=2.8E−02 n=2 fg=0.02 bg=0.00
vesicle coat GO:0030120 p=3.6E−02 n=2 fg=0.02 bg=0.00
bleb GO:0032059 p=3.9E−02 n=1 fg=0.01 bg=0.00
sperm individualization complex GO:0070864 p=3.9E−02 n=1 fg=0.01 bg=0.00
investment cone GO:0070865 p=3.9E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=3.9E−02 n=1 fg=0.01 bg=0.00
microspike GO:0044393 p=3.9E−02 n=1 fg=0.01 bg=0.00
Schwann cell microvillus GO:0097454 p=3.9E−02 n=1 fg=0.01 bg=0.00
nucleotide−excision repair complex GO:0000109 p=3.9E−02 n=1 fg=0.01 bg=0.00
NatB complex GO:0031416 p=3.9E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=3.9E−02 n=1 fg=0.01 bg=0.00
ACF complex GO:0016590 p=3.9E−02 n=1 fg=0.01 bg=0.00
translocon complex GO:0071256 p=3.9E−02 n=1 fg=0.01 bg=0.00
nuclear speck GO:0016607 p=4.3E−02 n=7 fg=0.07 bg=0.03
Golgi cisterna membrane GO:0032580 p=4.5E−02 n=2 fg=0.02 bg=0.00
nuclear body GO:0016604 p=5.1E−02 n=11 fg=0.10 bg=0.06
filopodium GO:0030175 p=5.1E−02 n=3 fg=0.03 bg=0.01
intracellular membrane−bounded organelle GO:0043231 p=5.2E−02 n=89 fg=0.85 bg=0.77
mitotic spindle GO:0072686 p=5.8E−02 n=4 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=105/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction