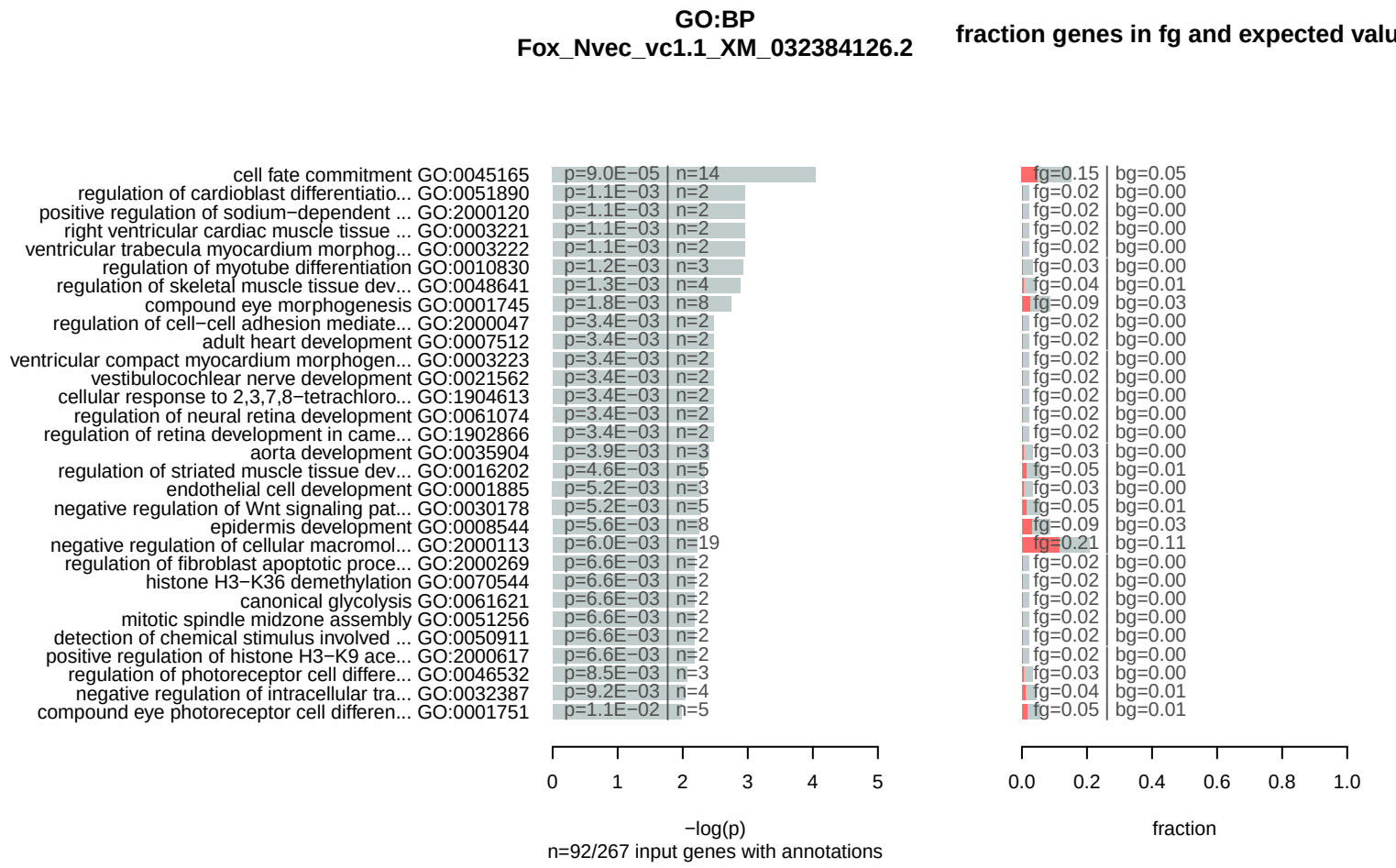
GO:BP
Fox_Nvec_vc1.1_XM_032384126.2
fraction genes in fg and expected valu
cell fate commitment GO:0045165 p=9.0E−05 n=14 fg=0.15 bg=0.05
regulation of cardioblast differentiatio... GO:0051890 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of sodium−dependent ... GO:2000120 p=1.1E−03 n=2 fg=0.02 bg=0.00
right ventricular cardiac muscle tissue ... GO:0003221 p=1.1E−03 n=2 fg=0.02 bg=0.00
ventricular trabecula myocardium morphog... GO:0003222 p=1.1E−03 n=2 fg=0.02 bg=0.00
regulation of myotube differentiation GO:0010830 p=1.2E−03 n=3 fg=0.03 bg=0.00
regulation of skeletal muscle tissue dev... GO:0048641 p=1.3E−03 n=4 fg=0.04 bg=0.01
compound eye morphogenesis GO:0001745 p=1.8E−03 n=8 fg=0.09 bg=0.03
regulation of cell−cell adhesion mediate... GO:2000047 p=3.4E−03 n=2 fg=0.02 bg=0.00
adult heart development GO:0007512 p=3.4E−03 n=2 fg=0.02 bg=0.00
ventricular compact myocardium morphogen... GO:0003223 p=3.4E−03 n=2 fg=0.02 bg=0.00
vestibulocochlear nerve development GO:0021562 p=3.4E−03 n=2 fg=0.02 bg=0.00
cellular response to 2,3,7,8−tetrachloro... GO:1904613 p=3.4E−03 n=2 fg=0.02 bg=0.00
regulation of neural retina development GO:0061074 p=3.4E−03 n=2 fg=0.02 bg=0.00
regulation of retina development in came... GO:1902866 p=3.4E−03 n=2 fg=0.02 bg=0.00
aorta development GO:0035904 p=3.9E−03 n=3 fg=0.03 bg=0.00
regulation of striated muscle tissue dev... GO:0016202 p=4.6E−03 n=5 fg=0.05 bg=0.01
endothelial cell development GO:0001885 p=5.2E−03 n=3 fg=0.03 bg=0.00
negative regulation of Wnt signaling pat... GO:0030178 p=5.2E−03 n=5 fg=0.05 bg=0.01
epidermis development GO:0008544 p=5.6E−03 n=8 fg=0.09 bg=0.03
negative regulation of cellular macromol... GO:2000113 p=6.0E−03 n=19 fg=0.21 bg=0.11
regulation of fibroblast apoptotic proce... GO:2000269 p=6.6E−03 n=2 fg=0.02 bg=0.00
histone H3−K36 demethylation GO:0070544 p=6.6E−03 n=2 fg=0.02 bg=0.00
canonical glycolysis GO:0061621 p=6.6E−03 n=2 fg=0.02 bg=0.00
mitotic spindle midzone assembly GO:0051256 p=6.6E−03 n=2 fg=0.02 bg=0.00
detection of chemical stimulus involved ... GO:0050911 p=6.6E−03 n=2 fg=0.02 bg=0.00
positive regulation of histone H3−K9 ace... GO:2000617 p=6.6E−03 n=2 fg=0.02 bg=0.00
regulation of photoreceptor cell differe... GO:0046532 p=8.5E−03 n=3 fg=0.03 bg=0.00
negative regulation of intracellular tra... GO:0032387 p=9.2E−03 n=4 fg=0.04 bg=0.01
compound eye photoreceptor cell differen... GO:0001751 p=1.1E−02 n=5 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=92/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032384126.2
fraction genes in fg and expected valu
RNA polymerase II cis−regulatory region ... GO:0000978 p=8.1E−04 n=9 fg=0.11 bg=0.03
TPR domain binding GO:0030911 p=1.2E−03 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016647 p=3.4E−03 n=2 fg=0.02 bg=0.00
promoter−specific chromatin binding GO:1990841 p=5.2E−03 n=3 fg=0.04 bg=0.00
histone H3−methyl−lysine−36 demethylase ... GO:0051864 p=6.6E−03 n=2 fg=0.02 bg=0.00
TFIID−class transcription factor complex... GO:0001094 p=1.1E−02 n=2 fg=0.02 bg=0.00
RNA polymerase II general transcription ... GO:0001091 p=1.6E−02 n=2 fg=0.02 bg=0.00
protein tyrosine/serine/threonine phosph... GO:0008138 p=2.2E−02 n=2 fg=0.02 bg=0.00
protein binding GO:0005515 p=2.6E−02 n=57 fg=0.70 bg=0.59
helicase activity GO:0004386 p=2.7E−02 n=4 fg=0.05 bg=0.01
phosphatidylinositol bisphosphate phosph... GO:0034593 p=2.8E−02 n=2 fg=0.02 bg=0.00
G−protein alpha−subunit binding GO:0001965 p=2.8E−02 n=2 fg=0.02 bg=0.00
glyceraldehyde−3−phosphate dehydrogenase... GO:0043891 p=3.4E−02 n=1 fg=0.01 bg=0.00
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=3.4E−02 n=1 fg=0.01 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=3.4E−02 n=1 fg=0.01 bg=0.00
signal recognition particle binding GO:0005047 p=3.4E−02 n=1 fg=0.01 bg=0.00
phosphatidylinositol−4,5−bisphosphate 4−... GO:0034597 p=3.4E−02 n=1 fg=0.01 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=3.4E−02 n=1 fg=0.01 bg=0.00
aminophospholipid flippase activity GO:0015247 p=3.4E−02 n=1 fg=0.01 bg=0.00
7S RNA binding GO:0008312 p=3.4E−02 n=1 fg=0.01 bg=0.00
glucose−1,6−bisphosphate synthase activi... GO:0047933 p=3.4E−02 n=1 fg=0.01 bg=0.00
histone kinase activity (H3−T3 specific) GO:0072354 p=3.4E−02 n=1 fg=0.01 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=3.4E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.4E−02 n=1 fg=0.01 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=3.4E−02 n=1 fg=0.01 bg=0.00
flippase activity GO:0140327 p=3.4E−02 n=1 fg=0.01 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=3.4E−02 n=1 fg=0.01 bg=0.00
CoA carboxylase activity GO:0016421 p=3.4E−02 n=1 fg=0.01 bg=0.00
phosphopentomutase activity GO:0008973 p=3.4E−02 n=1 fg=0.01 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=3.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=81/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032384126.2
fraction genes in fg and expected valu
mitotic spindle GO:0072686 p=1.4E−03 n=6 fg=0.07 bg=0.01
R2TP complex GO:0097255 p=3.2E−03 n=2 fg=0.02 bg=0.00
mitotic spindle midzone GO:1990023 p=1.5E−02 n=2 fg=0.02 bg=0.00
germinal vesicle GO:0042585 p=2.1E−02 n=2 fg=0.02 bg=0.00
female germ cell nucleus GO:0001674 p=2.7E−02 n=2 fg=0.02 bg=0.00
sperm connecting piece GO:0097224 p=3.3E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=3.3E−02 n=1 fg=0.01 bg=0.00
AP−4 adaptor complex GO:0030124 p=3.3E−02 n=1 fg=0.01 bg=0.00
centralspindlin complex GO:0097149 p=3.3E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=3.3E−02 n=1 fg=0.01 bg=0.00
DNA polymerase III, core complex GO:0044776 p=3.3E−02 n=1 fg=0.01 bg=0.00
translation release factor complex GO:0018444 p=3.3E−02 n=1 fg=0.01 bg=0.00
CHOP−C/EBP complex GO:0036488 p=3.3E−02 n=1 fg=0.01 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=3.3E−02 n=1 fg=0.01 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=3.3E−02 n=1 fg=0.01 bg=0.00
peroxisomal matrix GO:0005782 p=3.4E−02 n=2 fg=0.02 bg=0.00
MLL1 complex GO:0071339 p=3.4E−02 n=2 fg=0.02 bg=0.00
H4 histone acetyltransferase complex GO:1902562 p=3.4E−02 n=2 fg=0.02 bg=0.00
microbody lumen GO:0031907 p=3.4E−02 n=2 fg=0.02 bg=0.00
histone methyltransferase complex GO:0035097 p=3.5E−02 n=3 fg=0.03 bg=0.01
adherens junction GO:0005912 p=4.2E−02 n=5 fg=0.06 bg=0.02
MLL1/2 complex GO:0044665 p=5.0E−02 n=2 fg=0.02 bg=0.00
nuclear membrane GO:0031965 p=5.4E−02 n=5 fg=0.06 bg=0.02
midbody GO:0030496 p=5.7E−02 n=4 fg=0.04 bg=0.02
DNA polymerase complex GO:0042575 p=5.8E−02 n=2 fg=0.02 bg=0.00
katanin complex GO:0008352 p=6.6E−02 n=1 fg=0.01 bg=0.00
cell trailing edge GO:0031254 p=6.6E−02 n=1 fg=0.01 bg=0.00
DNA polymerase III complex GO:0009360 p=6.6E−02 n=1 fg=0.01 bg=0.00
NSL complex GO:0044545 p=6.6E−02 n=1 fg=0.01 bg=0.00
GAIT complex GO:0097452 p=6.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=90/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction