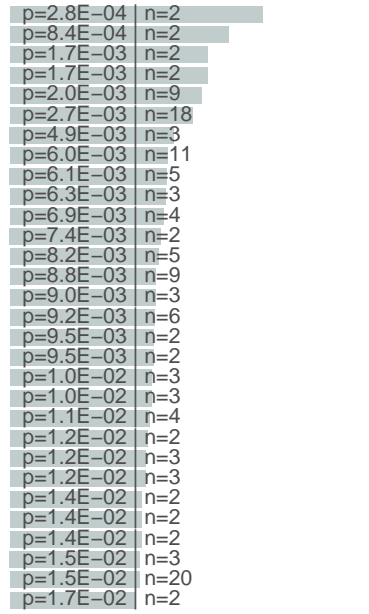


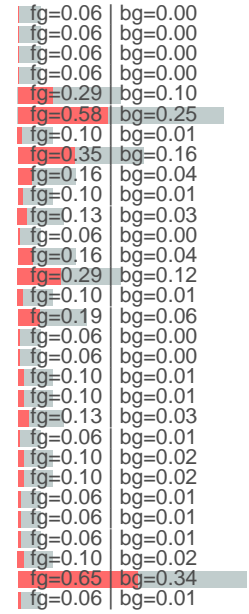
GO:BP
Fox_Nvec_vc1.1_XM_032374843.2

fraction genes in fg and expected value

regulation of cardioblast differentiatio... GO:0051890
cardiac ventricle formation GO:0003211
cardiac right ventricle morphogenesis GO:0003215
atrial septum morphogenesis GO:0060413
positive regulation of transcription by ... GO:0045944
regulation of cellular macromolecule bio... GO:2000112
neuroepithelial cell differentiation GO:0060563
positive regulation of gene expression GO:0010628
renal system development GO:0072001
adenylate cyclase–modulating G protein–c... GO:0007188
neural tube development GO:0021915
convergent extension involved in gastrul... GO:0060027
Wnt signaling pathway GO:0016055
negative regulation of cellular macromol... GO:2000113
regulation of cell cycle G1/S phase tran... GO:1902806
muscle structure development GO:0061061
regulation of cardiac conduction GO:1903779
aorta development GO:0035904
cellular response to antibiotic GO:0071236
cAMP–mediated signaling GO:0019933
canonical Wnt signaling pathway GO:0060070
cellular response to glucocorticoid stim... GO:0071385
neural tube formation GO:0001841
sodium ion transport GO:0006814
adenylate cyclase–activating G protein–c... GO:0007189
cellular response to corticosteroid stim... GO:0071384
ventricular septum morphogenesis GO:0060412
cyclic–nucleotide–mediated signaling GO:0019935
cellular nitrogen compound biosynthetic ... GO:0044271
establishment or maintenance of cytoskel... GO:0030952



–log(p)
n=31/167 input genes with annotations

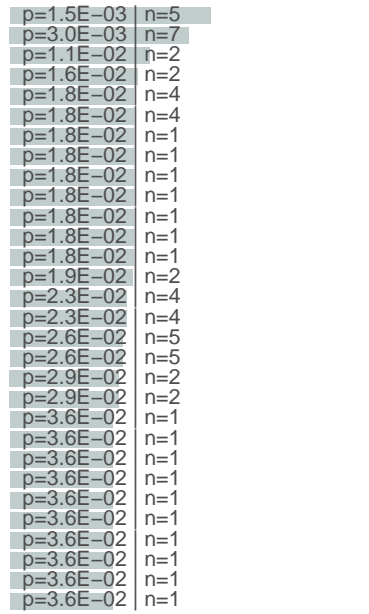


fraction

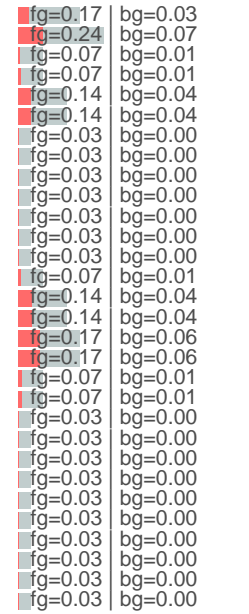
GO:MF
Fox_Nvec_vc1.1_XM_032374843.2

fraction genes in fg and expected value

mRNA binding GO:0003729
sequence–specific DNA binding GO:0043565
E–box binding GO:0070888
ubiquitin conjugating enzyme activity GO:0061631
cis–regulatory region sequence–specific ... GO:0000987
RNA polymerase II cis–regulatory region ... GO:0000978
mevalonate kinase activity GO:0004496
D5 dopamine receptor binding GO:0031752
serum response element binding GO:0010736
malate dehydrogenase (decarboxylating) (... GO:0004471
malate dehydrogenase (decarboxylating) (... GO:0004473
sphingomyelin phosphodiesterase D activi... GO:0050290
siRNA binding GO:0035197
ubiquitin–like protein conjugating enzym... GO:0061650
DNA–binding transcription activator acti... GO:0001228
DNA–binding transcription activator acti... GO:0001216
transcription coregulator activity GO:0003712
sequence–specific double–stranded DNA bi... GO:1990837
oxidoreductase activity, acting on CH–OH... GO:0016614
manganese ion binding GO:0030145
nitric–oxide synthase regulator activity GO:0030235
sodium:bicarbonate symporter activity GO:0008510
malate dehydrogenase activity GO:0016615
nitric–oxide synthase inhibitor activity GO:0036487
ISG15 transferase activity GO:0042296
calcium–dependent ATPase activity GO:0030899
malic enzyme activity GO:0004470
sphingomyelin phosphodiesterase activity GO:0004767
ATPase inhibitor activity GO:0042030
methyl–CpG binding GO:0008327



–log(p)
n=29/167 input genes with annotations

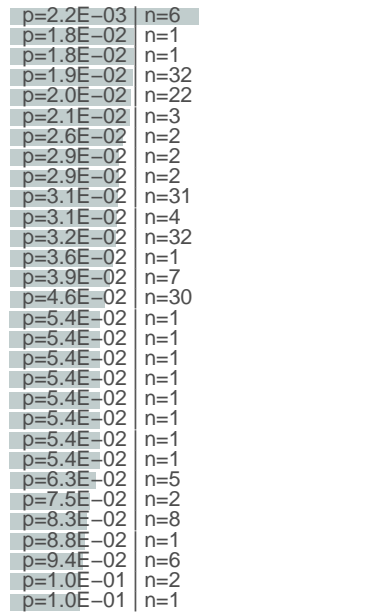


fraction

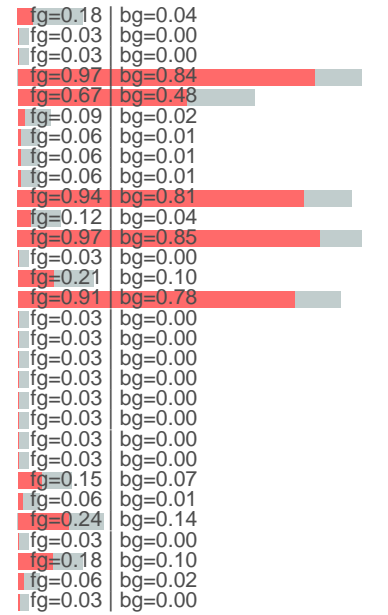
GO:CC
Fox_Nvec_vc1.1_XM_032374843.2

fraction genes in fg and expected value

transcription regulator complex GO:0005667
synaptic cleft GO:0043083
TSC1–TSC2 complex GO:0033596
intracellular organelle GO:0043229
nucleus GO:0005634
RNA polymerase II transcription regulato... GO:0090575
neuronal cell body membrane GO:0032809
cell body membrane GO:0044298
neuron projection membrane GO:0032589
membrane–bounded organelle GO:0043227
cell projection membrane GO:0031253
organelle GO:0043226
inner dynein arm GO:0036156
microtubule cytoskeleton GO:0015630
intracellular membrane–bounded organelle GO:0043231
exon–exon junction complex GO:0035145
axonemal dynein complex GO:0005858
postsynaptic specialization membrane GO:0099634
dendritic spine membrane GO:0032591
CHD–type complex GO:0090545
postsynaptic density membrane GO:0098839
NuRD complex GO:0016581
chaperone complex GO:0101031
microtubule organizing center GO:0005815
leading edge membrane GO:0031256
cytoskeleton GO:0005856
sperm principal piece GO:0097228
plasma membrane region GO:0098590
postsynaptic membrane GO:0045211
GTPase complex GO:1905360



–log(p)
n=33/167 input genes with annotations



fraction