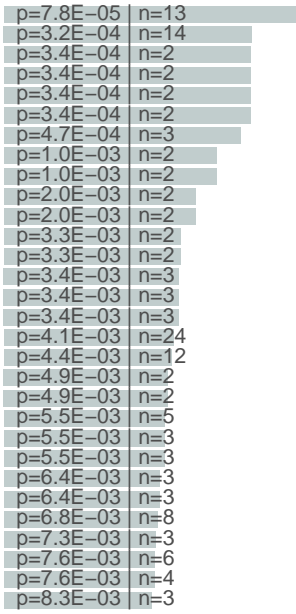


GO:BP
Fox_Nvec_vc1.1_XM_032384126.2

fraction genes in fg and expected value

negative regulation of cellular macromol...	GO:2000113
negative regulation of gene expression	GO:0010629
regulation of cardioblast differentiatio...	GO:0051890
positive regulation of sodium-dependent ...	GO:2000120
right ventricular cardiac muscle tissue ...	GO:0003221
ventricular trabecula myocardium morphog...	GO:0003222
aorta development	GO:0035904
adult heart development	GO:0007512
cellular response to 2,3,7,8-tetrachloro...	GO:1904613
regulation of brood size	GO:0060378
establishment of endothelial barrier	GO:0061028
venous blood vessel development	GO:0060841
dendrite self-avoidance	GO:0070593
female sex differentiation	GO:0046660
regulation of epithelial cell differenti...	GO:0030856
positive regulation of DNA-templated tra...	GO:2000144
positive regulation of cellular process	GO:0048522
positive regulation of gene expression	GO:0010628
regulation of myotube differentiation	GO:0010830
antennal morphogenesis	GO:0048800
post-embryonic appendage morphogenesis	GO:0035120
cardiac septum development	GO:0003279
negative regulation of intracellular tra...	GO:0032387
positive regulation of proteasomal ubiqu...	GO:0032436
response to estradiol	GO:0032355
embryonic morphogenesis	GO:0048598
negative regulation of canonical Wnt sig...	GO:0090090
embryonic organ development	GO:0048568
epidermal cell differentiation	GO:0009913
regulation of striated muscle tissue dev...	GO:0016202



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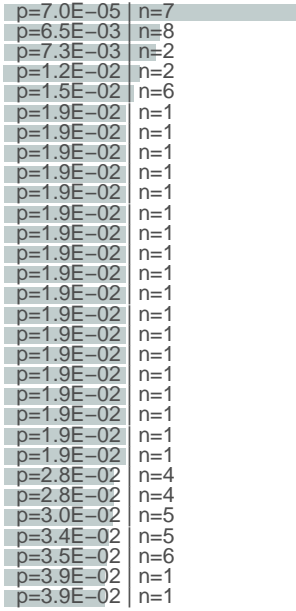
0 1 2 3 4 5
-log(p)
n=34/108 input genes with annotations

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 value

RNA polymerase II cis-regulatory region ...	GO:0000978
protein domain specific binding	GO:0019904
organophosphate ester transmembrane tran...	GO:0015605
E-box binding	GO:0070888
DNA-binding transcription factor activit...	GO:0000981
phosphatidylglycerol binding	GO:1901611
cardiolipin binding	GO:1901612
mRNA 5'-UTR binding	GO:0048027
phosphate ion binding	GO:0042301
aspartic-type endopeptidase inhibitor ac...	GO:0019828
peptidyl-cysteine S-nitrosylase activity	GO:0035605
glyceraldehyde-3-phosphate dehydrogenase...	GO:0004365
intracellular sodium activated potassium...	GO:0005228
sodium:phosphate symporter activity	GO:0005436
serum response element binding	GO:0010736
proteinase activated receptor binding	GO:0031871
ATPase-coupled intramembrane lipid trans...	GO:0140326
flippase activity	GO:0140327
cGMP-stimulated cyclic-nucleotide phosph...	GO:0004118
glyceraldehyde-3-phosphate dehydrogenase...	GO:0043891
CoA carboxylase activity	GO:0016421
propionyl-CoA carboxylase activity	GO:0004658
aminophospholipid flippase activity	GO:0015247
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
ubiquitin-protein transferase activity	GO:0004842
ubiquitin-like protein transferase activ...	GO:0019787
DNA-binding transcription factor activit...	GO:0003700
ligase activity, forming carbon-carbon b...	GO:0016885
CoA-ligase activity	GO:0016405



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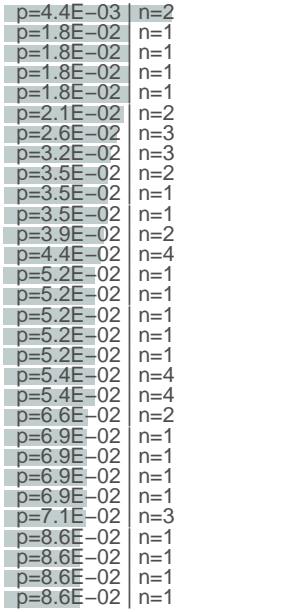
0 1 2 3 4 5
-log(p)
n=31/108 input genes with annotations

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 value

acrosomal vesicle	GO:0001669
CHOP-C/EBP complex	GO:0036488
dentate gyrus mossy fiber	GO:0044302
hippocampal mossy fiber	GO:0097457
Flemming body	GO:0090543
brush border membrane	GO:0031526
actin-based cell projection	GO:0098858
adherens junction	GO:0005912
microvillus	GO:0005902
cytosolic aryl hydrocarbon receptor comp...	GO:0034752
GAIT complex	GO:0097452
cell-substrate junction	GO:0030055
transcription regulator complex	GO:0005667
nuclear aryl hydrocarbon receptor comple...	GO:0034753
endoplasmic reticulum exit site	GO:0070971
GARP complex	GO:0000938
EARP complex	GO:1990745
muscle tendon junction	GO:0005927
cell-cell junction	GO:0005911
anchoring junction	GO:0070161
brush border	GO:0005903
aryl hydrocarbon receptor complex	GO:0034751
microvillus membrane	GO:0031528
intercellular canaliculus	GO:0046581
zonula adherens	GO:0005915
extracellular space	GO:0005615
sperm fibrous sheath	GO:0035686
sperm principal piece	GO:0097228
immunological synapse	GO:0001772
sensory dendrite	GO:0071683



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fg=0.03	bg=0.00
fg=0.03	bg=0.00
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0 1 2 3 4 5
-log(p)
n=32/108 input genes with annotations

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fraction