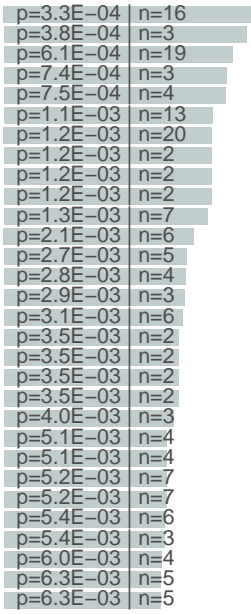


GO:BP
Fox_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

regulation of neurogenesis	GO:0050767
positive regulation of G2/M transition o...	GO:0010971
positive regulation of multicellular org...	GO:0051240
positive regulation of wound healing	GO:0090303
cell fate commitment involved in formati...	GO:0060795
regulation of neuron differentiation	GO:0045664
positive regulation of gene expression	GO:0010628
positive regulation of transcription fro...	GO:0006990
response to tunicamycin	GO:1904576
acylglycerol acyl-chain remodeling	GO:0036155
regulation of animal organ morphogenesis	GO:2000027
regulation of axonogenesis	GO:0050770
mesoderm development	GO:0007498
positive regulation of endothelial cell ...	GO:0010595
proximal/distal pattern formation	GO:0009954
cell fate specification	GO:0001708
positive regulation of peroxisome prolif...	GO:0035360
apical constriction involved in gastrula...	GO:0003384
regulation of endothelial cell different...	GO:0045601
positive regulation of cellular response...	GO:1900409
adenylate cyclase-inhibiting G protein-c...	GO:0007193
kidney morphogenesis	GO:0060993
positive regulation of chemotaxis	GO:0050921
axis specification	GO:0009798
regulation of cell morphogenesis involve...	GO:0010769
nuclear chromosome segregation	GO:0098813
positive regulation of reactive oxygen s...	GO:2000379
G protein-coupled receptor signaling pat...	GO:0007187
DNA conformation change	GO:0071103
nephron development	GO:0072006



0 1 2 3 4 5
-log(p)
n=63/199 input genes with annotations

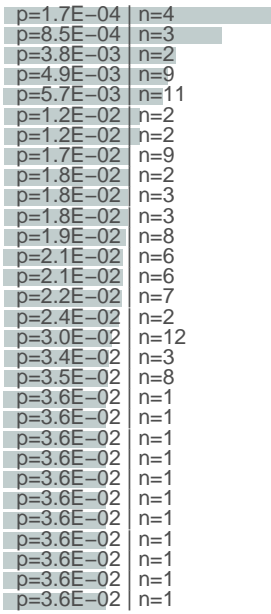
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0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
Fox_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

transcription coregulator binding	GO:0001221
ligand-gated calcium channel activity	GO:0099604
triglyceride lipase activity	GO:0004806
protein heterodimerization activity	GO:0046982
DNA-binding transcription factor activit...	GO:0003700
calcium-release channel activity	GO:0015278
transcription coactivator binding	GO:0001223
sequence-specific DNA binding	GO:0043565
peptidase activator activity	GO:0016504
single-stranded DNA binding	GO:0003697
phospholipase activity	GO:0004620
sequence-specific double-stranded DNA bi...	GO:1990837
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
RNA polymerase II transcription regulato...	GO:0000977
DNA secondary structure binding	GO:0000217
DNA binding	GO:0003677
ATPase binding	GO:0051117
double-stranded DNA binding	GO:0003690
ATP-gated ion channel activity	GO:0035381
glycogen (starch) synthase activity	GO:0004373
Rho-dependent protein serine/threonine k...	GO:0072518
heparan sulfate binding	GO:1904399
histone pre-mRNA stem-loop binding	GO:0071207
netrin receptor activity	GO:0005042
calcium- and calmodulin-responsive adeny...	GO:0008294
lysophosphatidic acid binding	GO:0035727
ATP-dependent DNA/DNA annealing activity	GO:0036310
deubiquitinase activator activity	GO:0035800
calcitonin family binding	GO:0097644



0 1 2 3 4 5
-log(p)
n=58/199 input genes with annotations

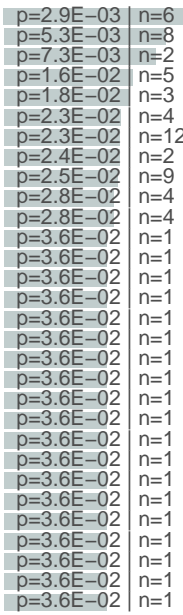
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0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
Fox_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

integral component of endoplasmic reticu...	GO:0030176
transcription regulator complex	GO:0005667
microvillus membrane	GO:0031528
extrinsic component of membrane	GO:0019898
protein-DNA complex	GO:0032993
receptor complex	GO:0043235
microtubule cytoskeleton	GO:0015630
intermediate filament cytoskeleton	GO:0045111
microtubule organizing center	GO:0005815
RNA polymerase II transcription regulato...	GO:0090575
terminal bouton	GO:0043195
histone pre-mRNA 3'end processing comple...	GO:0071204
apicomedial cortex	GO:0106037
beta-catenin-TCF7L2 complex	GO:0070369
synaptic cleft	GO:0043083
endosome to plasma membrane transport ve...	GO:0070381
amyloid-beta complex	GO:0106003
AP-3 adaptor complex	GO:0030123
single-stranded DNA-dependent ATP-depend...	GO:0017117
polytene chromosome chromocenter	GO:0005701
beta-catenin destruction complex	GO:0030877
catenin-TCF7L2 complex	GO:0071664
protein kinase CK2 complex	GO:0005956
PR-DUB complex	GO:0035517
ectoplasm	GO:0043265
apical cytoplasm	GO:0090651
intermediate-density lipoprotein particl...	GO:0034363
high-density lipoprotein particle	GO:0034364
varicosity	GO:0043196
fascia adherens	GO:0005916



0 1 2 3 4 5
-log(p)
n=65/199 input genes with annotations

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0.0 0.2 0.4 0.6 0.8 1.0
fraction