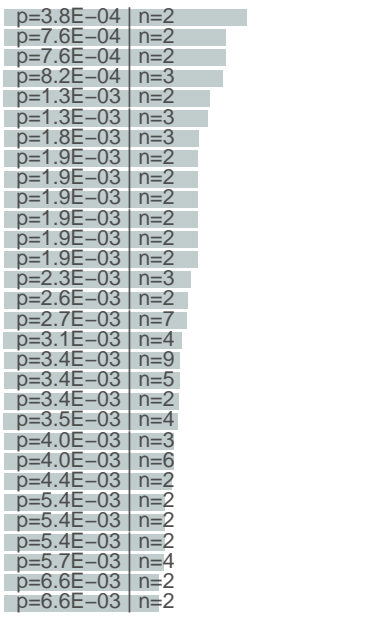


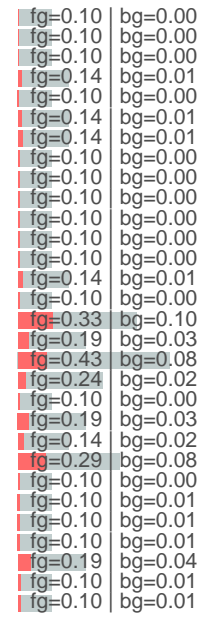
GO:BP
Fox_Nvec_vc1.1_XM_048732711.1

fraction genes in fg and expected value

olfactory nerve development GO:0021553
endodermal cell fate specification GO:0001714
olfactory bulb development GO:0021772
somatic stem cell population maintenance GO:0035019
lens morphogenesis in camera-type eye GO:0002089
osteoclast differentiation GO:0030316
bone mineralization GO:0030282
ventricular cardiac muscle tissue morpho... GO:0055010
trabecula morphogenesis GO:0061383
regulation of mesoderm formation GO:1905902
innervation GO:0060384
regulation of mesoderm development GO:2000380
regulation of mesodermal cell fate speci... GO:0042661
embryonic limb morphogenesis GO:0030326
lens fiber cell differentiation GO:0070306
positive regulation of transcription by ... GO:0045944
dorsal/ventral pattern formation GO:0009953
immune system development GO:0002520
stem cell differentiation GO:0048863
developmental induction GO:0031128
blood vessel morphogenesis GO:0048514
tissue remodeling GO:0048771
epithelial tube morphogenesis GO:0060562
proximal/distal pattern formation GO:0009954
embryonic digestive tract development GO:0048566
histone exchange GO:0043486
positive regulation of organ growth GO:0046622
embryonic organ morphogenesis GO:0048562
regulation of hematopoietic stem cell di... GO:1902036
cell proliferation in forebrain GO:0021846



0 1 2 3 4 5
-log(p)
n=21/89 input genes with annotations

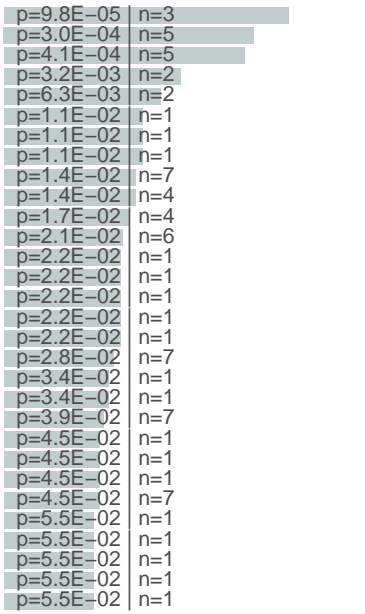


0.0 0.2 0.4 0.6 0.8 1.0
fraction

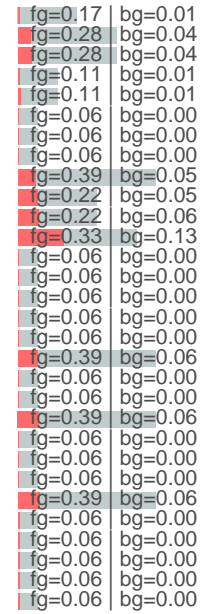
GO:MF
Fox_Nvec_vc1.1_XM_048732711.1

fraction genes in fg and expected value

transcription coregulator binding GO:0001221
RNA polymerase II cis-regulatory region ... GO:0000978
DNA-binding transcription activator acti... GO:0001228
methylated histone binding GO:0035064
DNA helicase activity GO:0003678
phosphatidyl-N-dimethylethanolamine N-me... GO:0080101
phosphatidyl-N-methylethanolamine N-meth... GO:0000773
saccharopine dehydrogenase (NAD+, L-lysi... GO:0004754
RNA polymerase II transcription regulato... GO:0000977
chromatin binding GO:0003682
protein heterodimerization activity GO:0046982
protein dimerization activity GO:0046983
transcription corepressor binding GO:0001222
gamma-butyrobetaine dioxygenase activity GO:0008336
1-phosphatidylinositol binding GO:0005545
armadillo repeat domain binding GO:0070016
saccharopine dehydrogenase activity GO:0004753
transcription cis-regulatory region bind... GO:0000976
fibroblast growth factor-activated recep... GO:0005007
receptor-receptor interaction GO:0090722
sequence-specific double-stranded DNA bi... GO:1990837
actin monomer binding GO:0003785
oxidoreductase activity, acting on the C... GO:0016646
tachykinin receptor activity GO:0004995
transcription regulatory region nucleic ... GO:0001067
phosphatidylinositol 3-kinase activity GO:0035004
phosphatidylinositol bisphosphate kinase... GO:0052813
phosphatidylinositol-4,5-bisphosphate 3-... GO:0046934
transcription coactivator binding GO:0001223
leak channel activity GO:0022840



0 1 2 3 4 5
-log(p)
n=18/89 input genes with annotations

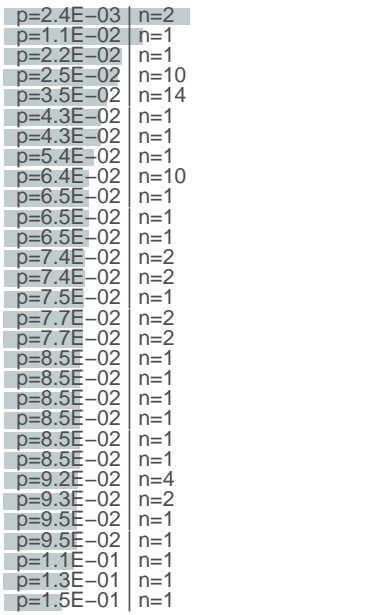


0.0 0.2 0.4 0.6 0.8 1.0
fraction

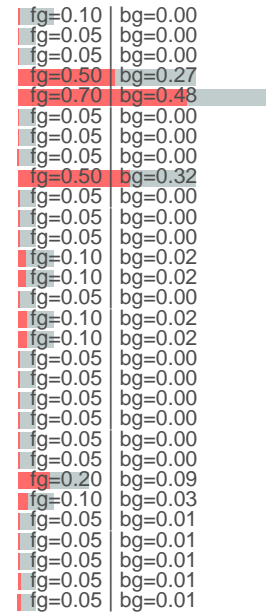
GO:CC
Fox_Nvec_vc1.1_XM_048732711.1

fraction genes in fg and expected value

polytene chromosome puff GO:0005703
apical cytoplasm GO:0090651
preribosome, small subunit precursor GO:0030688
nucleoplasm GO:0005654
nucleus GO:0005634
XY body GO:0001741
extrinsic component of endosome membrane GO:0031313
MLL1 complex GO:0071339
nuclear lumen GO:0031981
heterotrimeric G-protein complex GO:0005834
excitatory synapse GO:0060076
GTPase complex GO:1905360
integral component of endoplasmic reticu... GO:0030176
intrinsic component of endoplasmic retic... GO:0031227
MLL1/2 complex GO:0044665
cytoplasmic side of plasma membrane GO:0009898
extrinsic component of membrane GO:0019898
site of DNA damage GO:0090734
site of double-strand break GO:0035861
polytene chromosome interband GO:0005705
preribosome GO:0030684
chromosome, telomeric region GO:0000781
rhabdomere GO:0016028
endosome GO:0005768
cytoplasmic side of membrane GO:0098562
sex chromosome GO:0000803
extrinsic component of organelle membran... GO:0031312
nuclear pore GO:0005643
intercellular bridge GO:0045171
extrinsic component of cytoplasmic side ... GO:0031234



0 1 2 3 4 5
-log(p)
n=20/89 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0
fraction