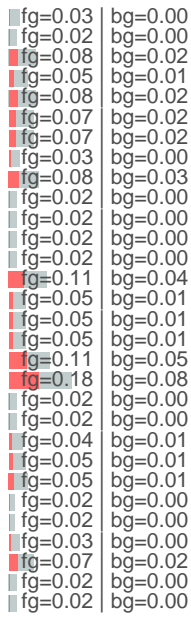
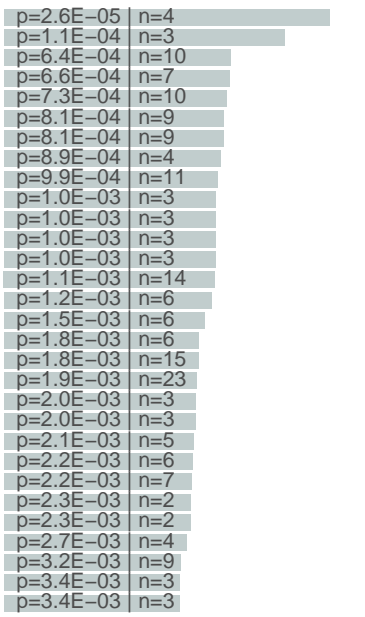


GO:BP
Fox_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

negative regulation of endothelial cell ... GO:2000352
acylglycerol acyl-chain remodeling GO:0036155
regulation of animal organ morphogenesis GO:2000027
Rho protein signal transduction GO:0007266
activation of protein kinase activity GO:0032147
regulation of axonogenesis GO:0050770
protein localization to plasma membrane GO:0072659
regulation of establishment of cell pola... GO:2000114
regulation of metal ion transport GO:0010959
cleavage furrow ingression GO:0036090
neuroblast migration GO:0097402
positive regulation of transcription reg... GO:2000679
suckling behavior GO:0001967
positive regulation of growth GO:0045927
positive regulation of angiogenesis GO:0045766
neuroepithelial cell differentiation GO:0060563
positive regulation of chromatin organiz... GO:1905269
positive regulation of neurogenesis GO:0050769
positive regulation of transcription by ... GO:0045944
positive regulation of membrane protein ... GO:0051044
sympathetic nervous system development GO:0048485
smooth muscle contraction GO:0006939
kidney morphogenesis GO:0060993
positive regulation of cellular amide me... GO:0034250
positive regulation of transcription fro... GO:0006990
response to tunicamycin GO:1904576
establishment or maintenance of cytoskel... GO:0030952
oocyte development GO:0048599
positive regulation of G2/M transition o... GO:0010971
acylglycerol catabolic process GO:0046464



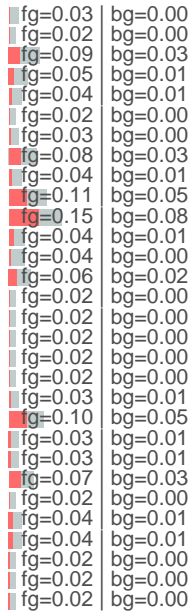
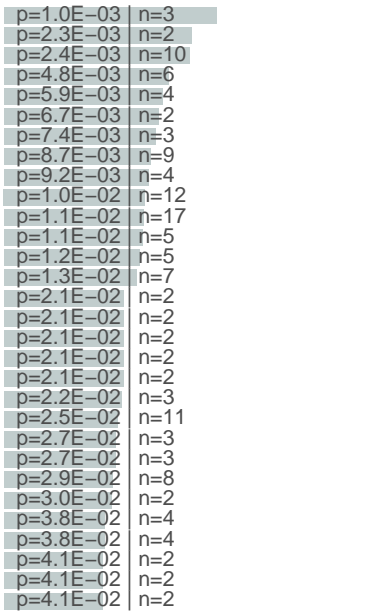
-log(p)
n=131/464 input genes with annotations

fraction

GO:MF
Fox_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

transcription coactivator binding GO:0001223
alpha-1B adrenergic receptor binding GO:0031692
DNA-binding transcription activator acti... GO:0001228
ion channel regulator activity GO:0099106
mRNA 3'-UTR binding GO:0003730
triglyceride lipase activity GO:0004806
ligand-gated calcium channel activity GO:0099604
RNA polymerase II cis-regulatory region ... GO:0000978
transmembrane transporter binding GO:0044325
transcription coregulator activity GO:0003712
protein domain specific binding GO:0019904
single-stranded DNA binding GO:0003697
transcription coregulator binding GO:0001221
enzyme inhibitor activity GO:0004857
ephrin receptor binding GO:0046875
14-3-3 protein binding GO:0071889
ionotropic glutamate receptor binding GO:0035255
arrestin family protein binding GO:1990763
acetylcholine receptor binding GO:0033130
potassium channel regulator activity GO:0015459
lipid binding GO:0008289
calcium channel regulator activity GO:0005246
peptidase regulator activity GO:0061134
transcription coactivator activity GO:0003713
mitogen-activated protein kinase kinase ... GO:0031434
DNA-binding transcription repressor acti... GO:0001227
DNA-binding transcription repressor acti... GO:0001217
calcium-release channel activity GO:0015278
peptidase activator activity GO:0016504
HMG box domain binding GO:0071837



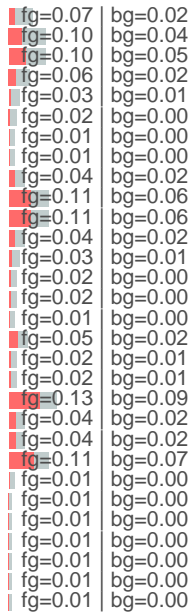
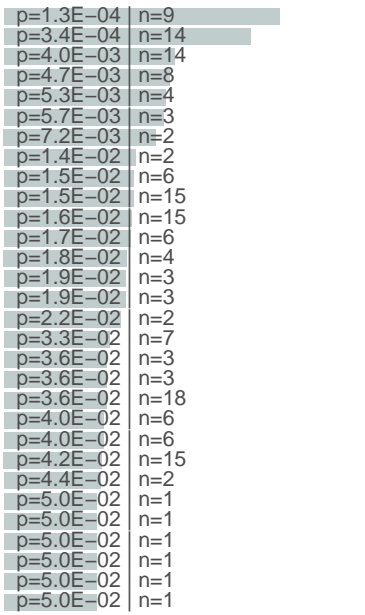
-log(p)
n=114/464 input genes with annotations

fraction

GO:CC
Fox_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

terminal bouton GO:0043195
transcription regulator complex GO:0005667
chromatin GO:0000785
integral component of endoplasmic reticu... GO:0030176
COPII-coated ER to Golgi transport vesic... GO:0030134
immunological synapse GO:0001772
skeletal muscle myofibril GO:0098723
subsynaptic reticulum GO:0071212
Golgi-associated vesicle GO:0005798
dendrite GO:0030425
dendritic tree GO:0097447
RNA polymerase II transcription regulato... GO:0090575
microvillus GO:0005902
lateral plasma membrane GO:0016328
type I terminal bouton GO:0061174
protein phosphatase type 1 complex GO:0000164
extrinsic component of membrane GO:0019898
inclusion body GO:0016234
euchromatin GO:0000791
somatodendritic compartment GO:0036477
actin-based cell projection GO:0098858
growth cone GO:0030426
vesicle membrane GO:0012506
microvillus membrane GO:0031528
mannosyltransferase complex GO:0031501
endosome to plasma membrane transport ve... GO:0070381
apicomedial cortex GO:0106037
lipoprotein particle GO:1990777
amyloid-beta complex GO:0106003
dolichol-phosphate-mannose synthase comp... GO:0033185



-log(p)
n=135/464 input genes with annotations

fraction