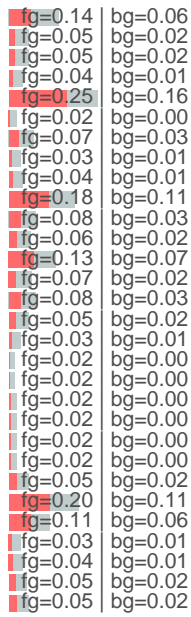
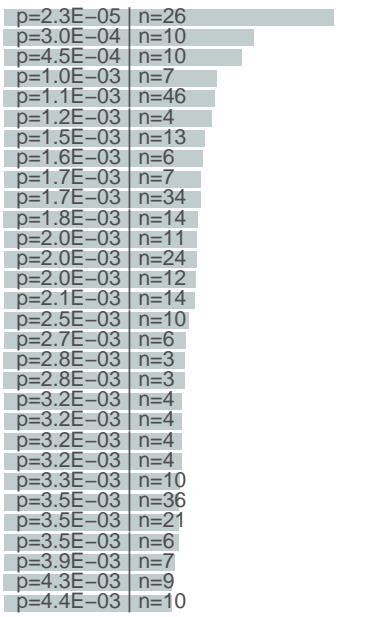


GO:BP
Fox_Nvec_vc1.1_XM_001629694.3

fraction genes in fg and expected value

aging GO:0007568
insulin receptor signaling pathway GO:0008286
open tracheal system development GO:0007424
positive regulation of chemotaxis GO:0050921
multi-organism reproductive process GO:0044703
unidimensional cell growth GO:0009826
synapse assembly GO:0007416
positive regulation of ion transmembrane... GO:0032414
response to anesthetic GO:0072347
negative regulation of signal transducti... GO:0009968
Ras protein signal transduction GO:0007265
cell fate specification GO:0001708
epithelial cell differentiation GO:0030855
response to nutrient GO:0007584
response to acid chemical GO:0001101
calcium-mediated signaling GO:0019722
response to activity GO:0014823
response to immobilization stress GO:0035902
R7 cell fate commitment GO:0007465
morphogenesis of an epithelial fold GO:0060571
cellular response to epidermal growth fa... GO:0071364
response to morphine GO:0043278
gastrulation with mouth forming second GO:0001702
regulation of small GTPase mediated sign... GO:0051056
positive regulation of developmental pro... GO:0051094
metal ion transport GO:0030001
negative regulation of synapse organizat... GO:1905809
actin-mediated cell contraction GO:0070252
response to ammonium ion GO:0060359
maintenance of location in cell GO:0051651



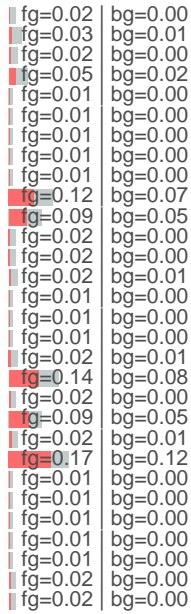
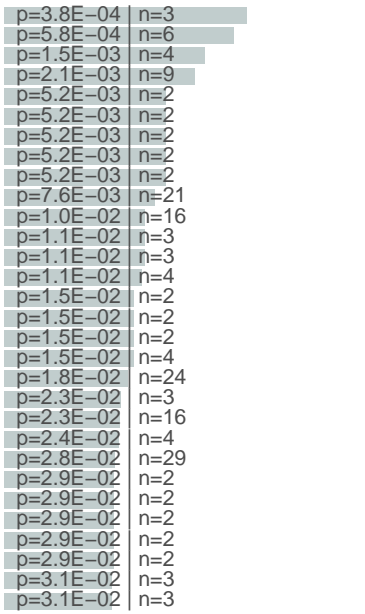
-log(p)
n=184/685 input genes with annotations

fraction

GO:MF
Fox_Nvec_vc1.1_XM_001629694.3

fraction genes in fg and expected value

mRNA regulatory element binding translat... GO:0000900
mRNA 3'-UTR binding GO:0003730
phosphotyrosine residue binding GO:0001784
G protein-coupled receptor binding GO:0001664
adenylate cyclase activity GO:0004016
sodium:bicarbonate symporter activity GO:0008510
acid-ammonia (or amide) ligase activity GO:0016880
sodium:phosphate symporter activity GO:0005436
BH3 domain binding GO:0051434
DNA-binding transcription factor activit... GO:0003700
lipid binding GO:0008289
dopamine receptor binding GO:0050780
cyclin binding GO:0030332
glutamate receptor binding GO:0035254
miRNA binding GO:0035198
phosphate ion transmembrane transporter ... GO:0015114
mRNA 3'-UTR AU-rich region binding GO:0035925
ribosome binding GO:0043022
protein domain specific binding GO:0019904
protein-disulfide reductase (NAD(P)) act... GO:0047134
transcription regulatory region nucleic ... GO:0001067
ATPase-coupled ion transmembrane transpo... GO:0042625
DNA binding GO:0003677
glycolipid binding GO:0051861
regulatory RNA binding GO:0061980
guanylate cyclase activity GO:0004383
bHLH transcription factor binding GO:0043425
Lys63-specific deubiquitinase activity GO:0061578
P-type transmembrane transporter activit... GO:0140358
receptor ligand activity GO:0048018



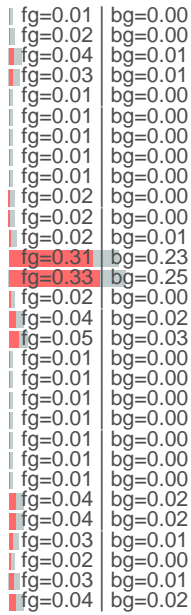
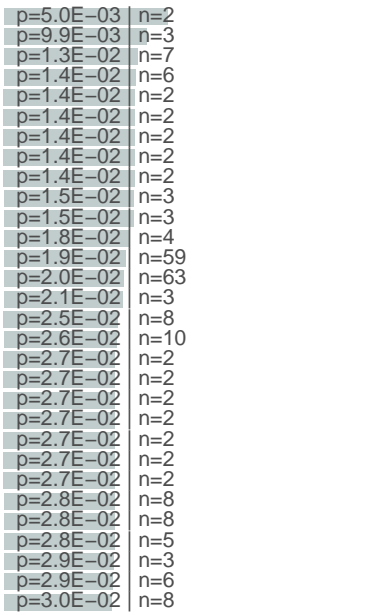
-log(p)
n=172/685 input genes with annotations

fraction

GO:CC
Fox_Nvec_vc1.1_XM_001629694.3

fraction genes in fg and expected value

mitochondrial permeability transition po... GO:0005757
microvillus membrane GO:0031528
I band GO:0031674
preribosome GO:0030684
catenin complex GO:0016342
TORC1 complex GO:0031931
TOR complex GO:0008201
Bcl-2 family protein complex GO:0097136
oligosaccharyltransferase complex GO:0008250
proton-transporting V-type ATPase comple... GO:0033176
DNA repair complex GO:1990391
intercalated disc GO:0014704
plasma membrane GO:0005886
cell periphery GO:0071944
Golgi lumen GO:0005796
growth cone GO:0030426
basal part of cell GO:0045178
growth cone lamellipodium GO:1990761
subapical complex GO:0035003
guanylate cyclase complex, soluble GO:0008074
myofilament GO:0036379
flotillin complex GO:0016600
dendritic spine membrane GO:0032591
striated muscle thin filament GO:0005865
neuron spine GO:0044309
dendritic spine GO:0043197
condensed nuclear chromosome GO:0000794
proton-transporting two-sector ATPase co... GO:0016469
Z disc GO:0030018
lamellipodium GO:0030027



-log(p)
n=191/685 input genes with annotations

fraction