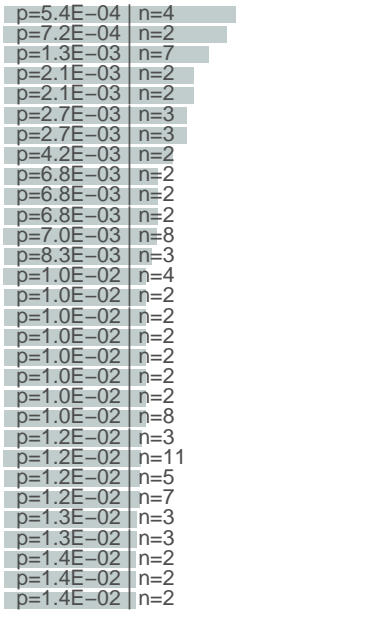


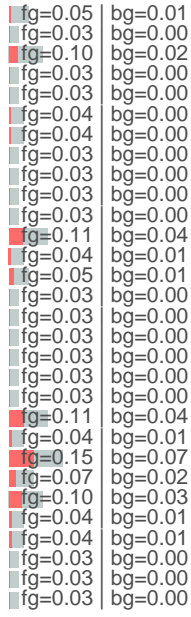
GO:BP
Fox_Nvec_vc1.1_XM_001622708.3

fraction genes in fg and expected value

establishment of ommatidial planar polar... GO:0042067
negative regulation of myofibroblast dif... GO:1904761
heart morphogenesis GO:0003007
collagen catabolic process GO:0030574
renal sodium ion absorption GO:0070294
coronary vasculature development GO:0060976
extracellular matrix disassembly GO:0022617
negative regulation of gastrulation GO:2000542
signal peptide processing GO:0006465
positive regulation of tyrosine phosphor... GO:0042531
cardioblast differentiation GO:0010002
positive regulation of neuron differenti... GO:0045666
negative regulation of peptidyl-tyrosine... GO:0050732
muscle cell proliferation GO:0033002
dendrite self-avoidance GO:0070593
negative regulation of cardiocyte differ... GO:1905208
regulation of extracellular matrix disas... GO:0010715
membranous septum morphogenesis GO:0003149
negative regulation of cardiac muscle ti... GO:0055026
homophilic cell adhesion via plasma memb... GO:0007156
negative regulation of organelle organiz... GO:0010639
negative regulation of chromatin organiz... GO:1905268
negative regulation of cellular componen... GO:0051129
positive regulation of cell growth GO:0030307
developmental growth involved in morphog... GO:0060560
regulation of cardiac muscle tissue deve... GO:0055024
midbrain development GO:0030901
negative regulation of cell fate specifi... GO:0009996
negative regulation of striated muscle t... GO:0045843
regulation of smooth muscle cell differe... GO:0051150



-log(p)
n=73/214 input genes with annotations

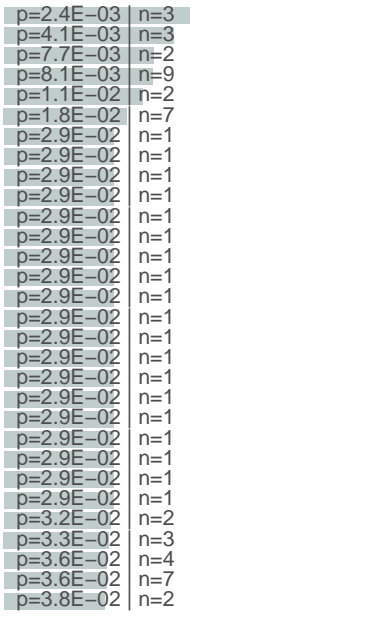


fraction

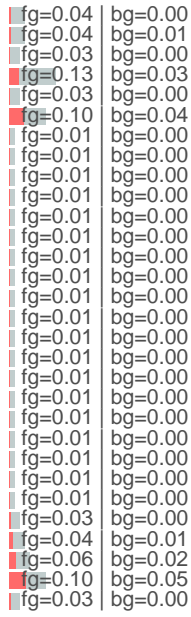
GO:MF
Fox_Nvec_vc1.1_XM_001622708.3

fraction genes in fg and expected value

phosphatidylinositol-3-phosphate binding GO:0032266
phosphatidylinositol-4-phosphate binding GO:0070273
phosphatidylinositol-5-phosphate binding GO:0010314
phosphatidylinositol binding GO:0035091
Wnt-protein binding GO:0017147
GTPase regulator activity GO:0030695
glycine N-choloyltransferase activity GO:0047963
medium-chain acyl-CoA hydrolase activity GO:0052815
long-chain acyl-CoA hydrolase activity GO:0052816
sphingolipid transfer activity GO:0120016
very long chain acyl-CoA hydrolase activ... GO:0052817
ceramide transfer activity GO:0120017
neurotrophin binding GO:0043121
G-protein beta-subunit binding GO:0031681
superoxide-generating NADPH oxidase acti... GO:0016176
non-sequence-specific DNA binding, bendi... GO:0044378
guanine/thymine mispair binding GO:0032137
inositol oxygenase activity GO:0050113
oxidative DNA demethylase activity GO:0035516
nerve growth factor binding GO:0048406
unmethylated CpG binding GO:0045322
delta-catenin binding GO:0070097
SMC family protein binding GO:0043221
interleukin-4 receptor binding GO:0005136
sphingolipid transporter activity GO:0046624
heparin binding GO:0008201
SH3 domain binding GO:0017124
cell adhesion molecule binding GO:0050839
nucleoside-triphosphatase regulator acti... GO:0060589
serine-type endopeptidase activity GO:0004252



-log(p)
n=68/214 input genes with annotations

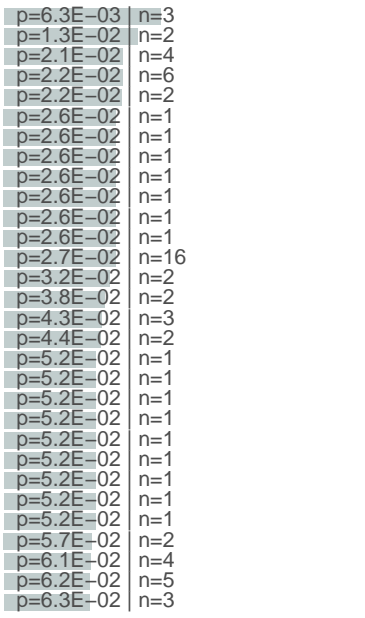


fraction

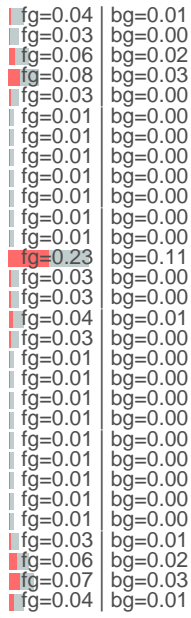
GO:CC
Fox_Nvec_vc1.1_XM_001622708.3

fraction genes in fg and expected value

Golgi medial cisterna GO:0005797
apicolateral plasma membrane GO:0016327
Golgi-associated vesicle GO:0005798
early endosome GO:0005769
chromocenter GO:0010369
dosage compensation complex GO:0046536
neuronal ribonucleoprotein granule GO:0071598
MSL complex GO:0072487
X chromosome located dosage compensation... GO:0016456
chiasma GO:0005712
recombination nodule GO:0005713
late recombination nodule GO:0005715
Golgi apparatus GO:0005794
neuron projection cytoplasm GO:0120111
Golgi trans cisterna GO:0000138
coated vesicle membrane GO:0030662
PcG protein complex GO:0031519
MutLalpha complex GO:0032389
U2AF complex GO:0089701
THO complex part of transcription export... GO:0000445
THO complex GO:0000347
TRAMP complex GO:0031499
signal peptidase complex GO:0005787
trans-Golgi network transport vesicle me... GO:0012510
Wnt signalosome GO:1990909
beta-catenin destruction complex GO:0030877
euchromatin GO:0000791
coated vesicle GO:0030135
extracellular space GO:0005615
clathrin-coated vesicle GO:0030136



-log(p)
n=71/214 input genes with annotations



fraction