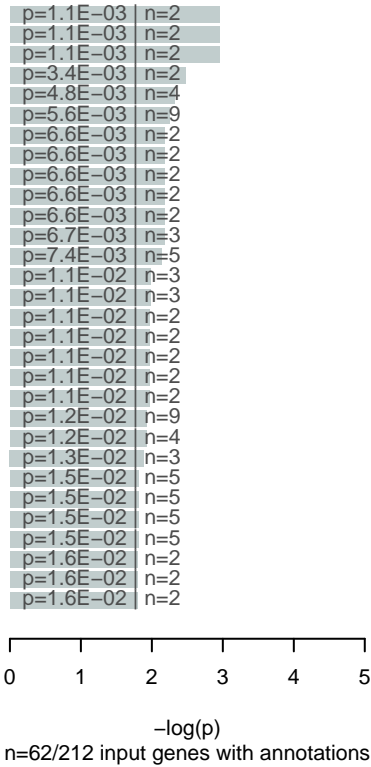
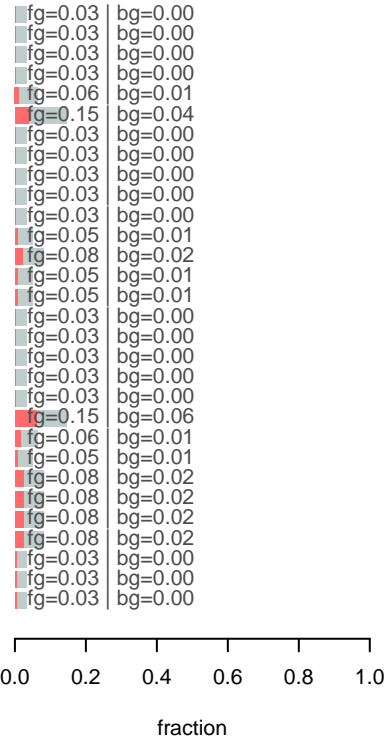


GO:BP
Fox_Nvec_vc1.1_XM_048726885.1

cellular response to copper ion	GO:0071280
regulation of iron ion transmembrane tra...	GO:0034759
protein maturation by copper ion transfe...	GO:0015680
cellular metabolic compound salvage	GO:0043094
peripheral nervous system development	GO:0007422
renal system development	GO:0072001
glomerulus morphogenesis	GO:0072102
glycerophospholipid catabolic process	GO:0046475
intraciliary retrograde transport	GO:0035721
regulation of apoptotic DNA fragmentatio...	GO:1902510
adherens junction maintenance	GO:0034334
defense response to fungus	GO:0050832
purine ribonucleoside monophosphate meta...	GO:0009167
ribonucleoside monophosphate biosyntheti...	GO:0009156
response to cadmium ion	GO:0046686
copper ion transport	GO:0006825
positive regulation of oxidoreductase ac...	GO:0051353
intraciliary transport involved in ciliu...	GO:0035735
cellular response to estradiol stimulus	GO:0071392
receptor recycling	GO:0001881
spermatogenesis	GO:0007283
cellular response to antibiotic	GO:0071236
nucleoside monophosphate biosynthetic pr...	GO:0009124
ribonucleoside triphosphate metabolic pr...	GO:0009199
nucleoside triphosphate metabolic proces...	GO:0009141
purine nucleoside triphosphate metabolic...	GO:0009144
purine ribonucleoside triphosphate metab...	GO:0009205
peripheral nervous system axon ensheathm...	GO:0032292
myelination in peripheral nervous system	GO:0022011
response to ischemia	GO:0002931

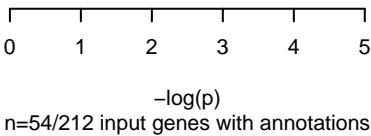


fraction genes in fg and expected value

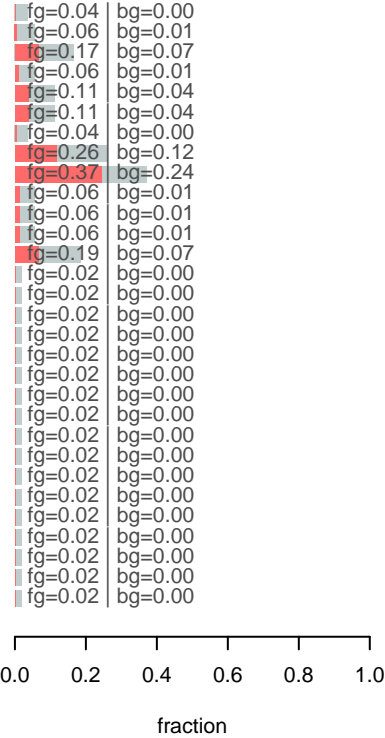


GO:MF
Fox_Nvec_vc1.1_XM_048726885.1

superoxide dismutase copper chaperone ac...	GO:0016532
E-box binding	GO:0070888
DNA-binding transcription factor activit...	GO:0000981
single-stranded DNA binding	GO:0003697
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
HMG box domain binding	GO:0071837
DNA binding	GO:0003677
enzyme binding	GO:0019899
DNA-binding transcription repressor acti...	GO:0001227
DNA-binding transcription repressor acti...	GO:0001217
electron transfer activity	GO:0009055
double-stranded DNA binding	GO:0003690
RNA polymerase I core binding	GO:0001042
oxidoreductase activity, acting on NAD(P...	GO:0050664
protein-membrane adaptor activity	GO:0043495
stearoyl-CoA 9-desaturase activity	GO:0004768
sphingomyelin phosphodiesterase D activi...	GO:0050290
oxidoreductase activity, acting on the C...	GO:0016649
UDP-N-acetylglucosamine-dolichyl-phospha...	GO:0003975
adenosine-phosphate deaminase activity	GO:0047623
electron-transferring-flavoprotein dehyd...	GO:0004174
aspartic-type endopeptidase inhibitor ac...	GO:0019828
oxidoreductase activity, acting on paire...	GO:0016717
glyceraldehyde-3-phosphate dehydrogenase...	GO:0004365
NAD(P)H oxidase H2O2-forming activity	GO:0016174
acyl-CoA desaturase activity	GO:0016215
glyceraldehyde-3-phosphate dehydrogenase...	GO:0043891
cuprous ion binding	GO:1903136
P-type divalent copper transporter activ...	GO:0043682

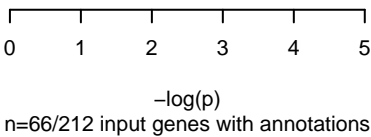


fraction genes in fg and expected value



GO:CC
Fox_Nvec_vc1.1_XM_048726885.1

intraciliary transport particle A	GO:0030991
sperm fibrous sheath	GO:0035686
ciliary tip	GO:0097542
sperm flagellum	GO:0036126
outer dense fiber	GO:0001520
protein kinase CK2 complex	GO:0005956
polytene chromosome chromocenter	GO:0005701
intraciliary transport particle B	GO:0030992
9+2 motile cilium	GO:0097729
apical junction complex	GO:0043296
motile cilium	GO:0031514
phagocytic vesicle membrane	GO:0030670
adherens junction	GO:0005912
transcription regulator complex	GO:0005667
photoreceptor connecting cilium	GO:0032391
intrinsic component of endoplasmic retic...	GO:0031227
integral component of endoplasmic reticu...	GO:0030176
histone locus body	GO:0035363
NSL complex	GO:0044545
GAIT complex	GO:0097452
nuclear stress granule	GO:0097165
cytosolic aryl hydrocarbon receptor comp...	GO:0034752
anchoring junction	GO:0070161
cell-cell junction	GO:0005911
mitochondrial outer membrane	GO:0005741
organelle outer membrane	GO:0031968
outer membrane	GO:0019867
endocytic vesicle	GO:0030139
mitochondrial intermembrane space	GO:0005758
nucleus	GO:0005634



fraction genes in fg and expected value

