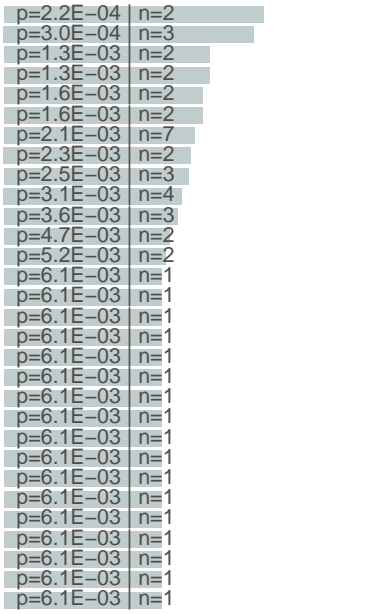


GO:BP
Placozoa_gain

negative regulation of glucokinase activ...	GO:0033132
positive regulation of peptidyl-serine p...	GO:0033138
negative regulation of CD4-positive, alp...	GO:2000515
detection of mechanical stimulus involve...	GO:0050910
auditory receptor cell stereocilium orga...	GO:0060088
cell fate determination	GO:0001709
negative regulation of transcription by ...	GO:0000122
neuron recognition	GO:0008038
positive regulation of T cell differenti...	GO:0045582
negative regulation of protein transport	GO:0051224
negative regulation of peptide hormone s...	GO:0090278
maternal behavior	GO:0042711
modification of postsynaptic structure	GO:0099010
commitment of neuronal cell to specific ...	GO:0021902
pronephric field specification	GO:0039003
positive regulation of peptidyl-serine d...	GO:1902310
positive regulation of metanephric DCT c...	GO:2000594
positive regulation of optic nerve forma...	GO:2000597
NMDA selective glutamate receptor signal...	GO:0098989
zinc ion import into synaptic vesicle	GO:0099180
cellular response to methyl methanesulfo...	GO:0072703
positive regulation of receptor binding	GO:1900122
regulation of endoplasmic reticulum stre...	GO:0060734
regulation of axon guidance	GO:1902667
ureter maturation	GO:0035799
vestibulocochlear nerve formation	GO:0021650
cell dedifferentiation	GO:0043697
plus-end specific microtubule depolymeri...	GO:0070462
optic nerve structural organization	GO:0021633
negative regulation of apoptotic process...	GO:1900215



0 1 2 3 4 5
-log(p)
n=48/96 input genes with annotations

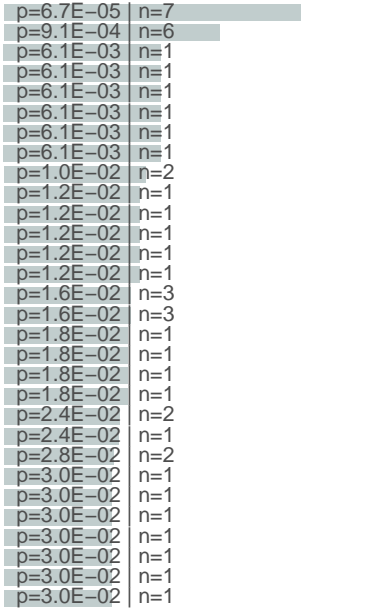
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0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
Placozoa_gain

DNA-binding transcription factor activit...	GO:0000981
RNA polymerase II cis-regulatory region ...	GO:0000978
urea channel activity	GO:0015265
water channel activity	GO:0015250
glycerol channel activity	GO:0015254
sulfonylurea receptor binding	GO:0017098
CTP binding	GO:0002135
neurexin family protein binding	GO:0042043
spectrin binding	GO:0030507
inositol 1,4,5 trisphosphate binding	GO:0070679
dATP binding	GO:0032564
adenyl deoxyribonucleotide binding	GO:0032558
nitric-oxide synthase regulator activity	GO:0030235
transmembrane monodehydroascorbate reduc...	GO:0140575
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
Rho GDP-dissociation inhibitor binding	GO:0051022
opsin binding	GO:0002046
UTP binding	GO:0002134
purine deoxyribonucleotide binding	GO:0032554
alcohol binding	GO:0043178
deoxyribonucleotide binding	GO:0032552
phosphoprotein binding	GO:0051219
GDP-dissociation inhibitor binding	GO:0051021
phospholipase C activity	GO:0004629
transforming growth factor beta binding	GO:0050431
phosphatidylinositol phospholipase C act...	GO:0004435
TPR domain binding	GO:0030911
C2H2 zinc finger domain binding	GO:0070742
tau-protein kinase activity	GO:0050321



0 1 2 3 4 5
-log(p)
n=48/96 input genes with annotations

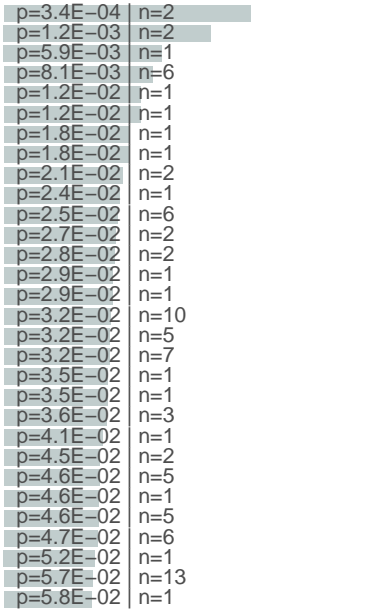
fraction genes in fg and expected value

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0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
Placozoa_gain

stereocilium tip	GO:0032426
kinocilium	GO:0060091
transcription factor AP-1 complex	GO:0035976
perinuclear region of cytoplasm	GO:0048471
core-binding factor complex	GO:0016513
dendritic growth cone	GO:0044294
chromaffin granule	GO:0042583
chromaffin granule membrane	GO:0042584
early endosome membrane	GO:0031901
sperm mitochondrial sheath	GO:0097226
cell body	GO:0044297
brush border membrane	GO:0031526
lipid droplet	GO:0005811
cytoplasmic vesicle lumen	GO:0060205
secretory granule lumen	GO:0034774
neuron projection	GO:0043005
transcription regulator complex	GO:0005667
extracellular region	GO:0005576
vesicle lumen	GO:0031983
protein phosphatase type 1 complex	GO:0000164
extrinsic component of membrane	GO:0019898
dendrite terminus	GO:0044292
extrinsic component of plasma membrane	GO:0019897
secretory vesicle	GO:0099503
BORC complex	GO:0099078
neuronal cell body	GO:0043025
somatodendritic compartment	GO:0036477
perinuclear endoplasmic reticulum	GO:0097038
plasma membrane bounded cell projection	GO:0120025
insulin-responsive compartment	GO:0032593



0 1 2 3 4 5
-log(p)
n=47/96 input genes with annotations

fraction genes in fg and expected value

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fraction