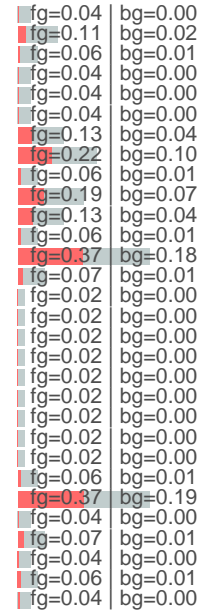
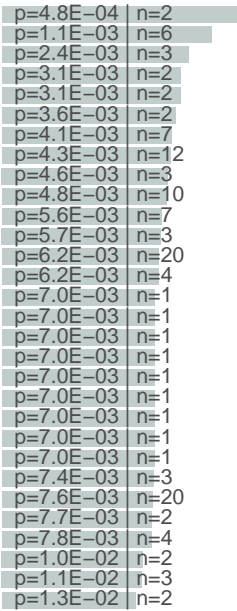


GO:BP  
gc023

fraction genes in fg and expected value

lateral ventricle development	GO:0021670
axonogenesis	GO:0007409
vasodilation	GO:0042311
negative regulation of blood pressure	GO:0045776
negative regulation of telomere maintena...	GO:0032211
protein O-linked mannosylation	GO:0035269
cell junction organization	GO:0034330
cell-cell signaling	GO:0007267
negative regulation of neurogenesis	GO:0050768
G protein-coupled receptor signaling pat...	GO:0007186
negative regulation of cell population p...	GO:0008285
positive regulation of endothelial cell ...	GO:0001938
regulation of cell communication	GO:0010646
catecholamine transport	GO:0051937
neuroblast division in subventricular zo...	GO:0021849
protein stearoylation	GO:0140438
cellular ammonium homeostasis	GO:0097275
cellular creatinine homeostasis	GO:0097276
cellular urea homeostasis	GO:0097277
negative regulation of protein kinase C ...	GO:0090038
plus-end specific microtubule depolymeri...	GO:0070462
rRNA acetylation involved in maturation ...	GO:1904812
axonemal microtubule depolymerization	GO:0060404
cyclic-nucleotide-mediated signaling	GO:0019935
regulation of signaling	GO:0023051
positive regulation of smoothened signal...	GO:0045880
smooth muscle contraction	GO:0006939
gamma-aminobutyric acid signaling pathwa...	GO:0007214
cell-cell junction organization	GO:0045216
astrocyte differentiation	GO:0048708



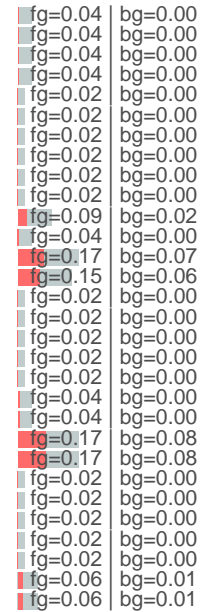
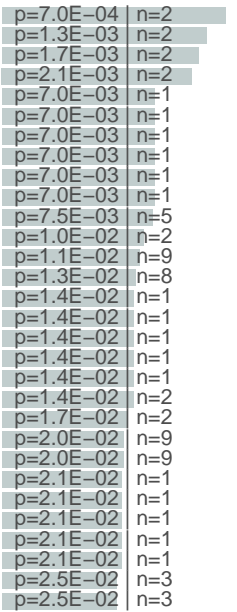
0 1 2 3 4 5  
-log(p)  
n=54/98 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0  
fraction

GO:MF  
gc023

fraction genes in fg and expected value

dolichyl-phosphate-mannose-protein manno...	GO:0004169
cadherin binding	GO:0045296
angiotensin receptor binding	GO:0031701
3',5'-cyclic-nucleotide phosphodiesteras...	GO:0004114
5'-3' DNA/RNA helicase activity	GO:0033678
rRNA cytidine N-acetyltransferase activi...	GO:1990883
beta-maltose 4-alpha-glucanotransferase ...	GO:0102500
4-alpha-glucanotransferase activity	GO:0004134
amylo-alpha-1,6-glucosidase activity	GO:0004135
mRNA N-acetyltransferase activity	GO:0106162
DNA-binding transcription factor activit...	GO:0000981
alpha-tubulin binding	GO:0043014
transmembrane signaling receptor activit...	GO:0004888
G protein-coupled receptor activity	GO:0004930
beta-2 adrenergic receptor binding	GO:0031698
bradykinin receptor activity	GO:0004947
C-rich single-stranded DNA binding	GO:1990829
polypeptide N-acetylgalactosaminyltransf...	GO:0004653
semaphorin receptor activity	GO:0017154
postsynaptic neurotransmitter receptor a...	GO:0098960
neurotransmitter receptor activity	GO:0030594
molecular transducer activity	GO:0060089
signaling receptor activity	GO:0038023
inositol-1,4,5-trisphosphate 5-phosphata...	GO:0052658
inositol-1,3,4,5-tetrakisphosphate 5-pho...	GO:0052659
Rho GDP-dissociation inhibitor binding	GO:0051022
type 1 angiotensin receptor binding	GO:0031702
polysaccharide binding	GO:0030247
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216



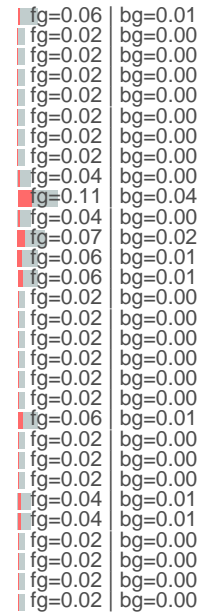
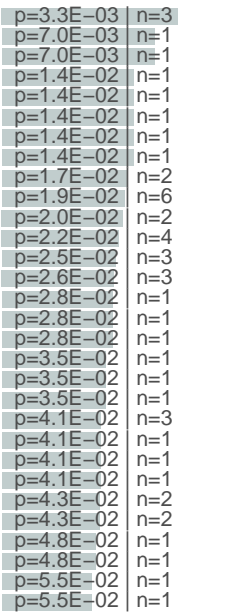
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-log(p)  
n=53/98 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0  
fraction

GO:CC  
gc023

fraction genes in fg and expected value

caveola	GO:0005901
epididymosome	GO:0098875
zonula adherens	GO:0005915
nuclear membrane microtubule tethering c...	GO:0106094
semaphorin receptor complex	GO:0002116
microtubule organizing center attachment...	GO:0034992
meiotic nuclear membrane microtubule tet...	GO:0034993
nuclear membrane protein complex	GO:0106083
ciliary membrane	GO:0060170
glutamatergic synapse	GO:0098978
kinesin complex	GO:0005871
cell leading edge	GO:0031252
dendritic spine	GO:0043197
neuron spine	GO:0044309
photoreceptor outer segment membrane	GO:0042622
presynaptic active zone cytoplasmic comp...	GO:0098831
guanylate cyclase complex, soluble	GO:0008074
cornified envelope	GO:0001533
Golgi lumen	GO:0005796
desmosome	GO:0030057
Schaffer collateral - CA1 synapse	GO:0098685
catenin complex	GO:0016342
cytosolic proteasome complex	GO:0031597
messenger ribonucleoprotein complex	GO:1990124
acrosomal vesicle	GO:0001669
dendritic shaft	GO:0043198
NSL complex	GO:0044545
dendritic spine neck	GO:0044326
nuclear outer membrane	GO:0005640
dendritic spine head	GO:0044327



0 1 2 3 4 5  
-log(p)  
n=54/98 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0  
fraction