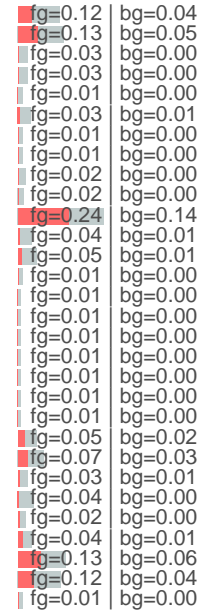
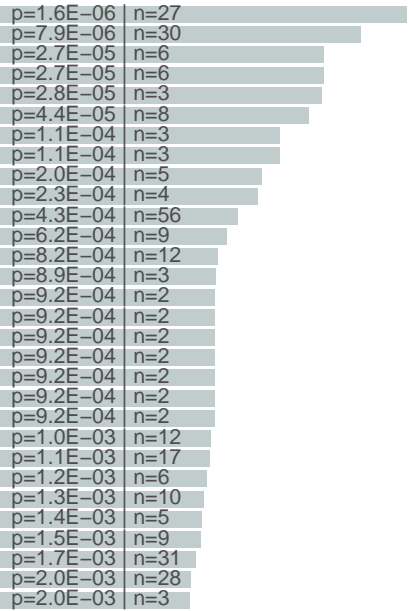


GO:BP
gc004

fraction genes in fg and expected value

negative regulation of transcription by ...	GO:0000122
positive regulation of transcription by ...	GO:0045944
calcium-dependent activation of synaptic...	GO:0099502
calcium ion-regulated exocytosis of neur...	GO:0048791
maintenance of presynaptic active zone s...	GO:0048790
regulation of G protein-coupled receptor...	GO:0008277
spontaneous neurotransmitter secretion	GO:0061669
regulation of calcium-dependent activati...	GO:0150037
negative regulation of cellular carbohyd...	GO:0010677
positive regulation of calcium ion-depen...	GO:0045956
intracellular signal transduction	GO:0035556
organelle localization by membrane tethe...	GO:0140056
regulation of synaptic plasticity	GO:0048167
cell fate determination	GO:0001709
cGMP catabolic process	GO:0046069
cranial nerve structural organization	GO:0021604
negative regulation of transcription fro...	GO:1990441
ionotropic glutamate receptor signaling ...	GO:0035235
mesenchymal to epithelial transition	GO:0060231
lens induction in camera-type eye	GO:0060235
negative regulation of isotype switching...	GO:0048294
rhythmic process	GO:0048511
negative regulation of cell differentiat...	GO:0045596
regulation of osteoblast differentiation	GO:0045667
synaptic vesicle fusion to presynaptic a...	GO:0031629
long-term synaptic potentiation	GO:0060291
positive regulation of autophagy	GO:0010508
regulation of protein localization	GO:0032880
enzyme linked receptor protein signaling...	GO:0007167
negative regulation of peptidyl-threonin...	GO:0010801



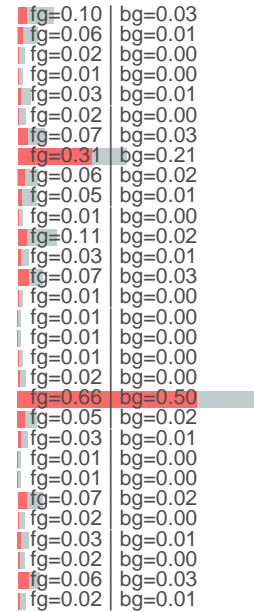
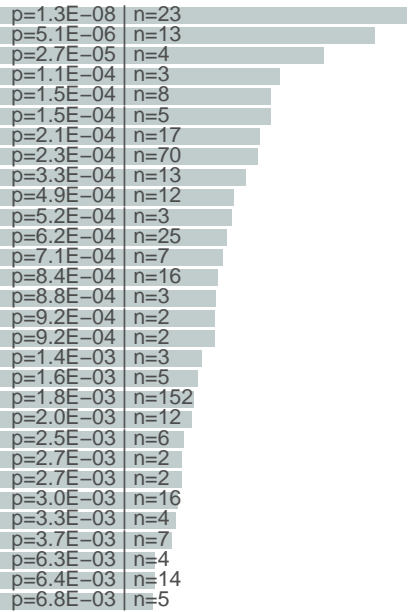
0 1 2 3 4 5
-log(p)
n=231/361 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
gc004

fraction genes in fg and expected value

RNA polymerase II cis-regulatory region ...	GO:0000978
DNA-binding transcription activator acti...	GO:0001228
3',5'-cyclic-GMP phosphodiesterase activ...	GO:0047555
high voltage-gated calcium channel activ...	GO:0008331
DNA-binding transcription repressor acti...	GO:0001227
calcium-dependent phospholipid binding	GO:0005544
GTP binding	GO:0005525
metal ion binding	GO:0046872
GTPase activity	GO:0003924
SNARE binding	GO:0000149
cAMP response element binding protein bi...	GO:0008140
DNA-binding transcription factor activit...	GO:0000981
histone deacetylase binding	GO:0042826
protein serine/threonine kinase activity	GO:0004674
SUMO transferase activity	GO:0019789
structural constituent of presynaptic ac...	GO:0098882
syntaxin-3 binding	GO:0030348
peroxisome proliferator activated recept...	GO:0042975
syntaxin-1 binding	GO:0017075
protein binding	GO:0005515
ubiquitin protein ligase binding	GO:0031625
chromatin DNA binding	GO:0031490
voltage-gated calcium channel activity i...	GO:0099626
water transmembrane transporter activity	GO:0005372
DNA-binding transcription factor binding	GO:0140297
anion:cation symporter activity	GO:0015296
transcription corepressor activity	GO:0003714
myosin binding	GO:0017022
GTPase regulator activity	GO:0030695
potassium ion transmembrane transporter ...	GO:0015079



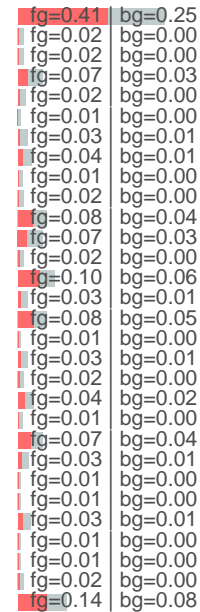
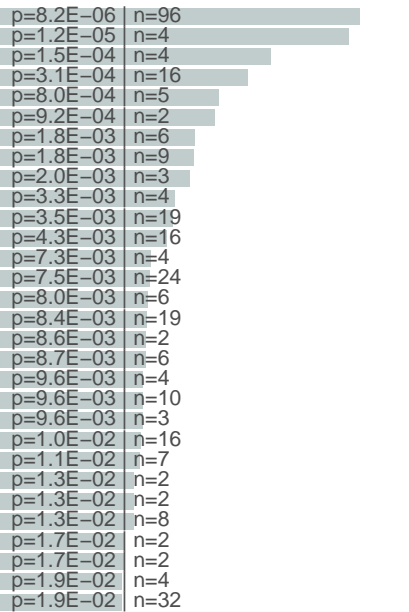
0 1 2 3 4 5
-log(p)
n=229/361 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
gc004

fraction genes in fg and expected value

plasma membrane	GO:0005886
voltage-gated calcium channel complex	GO:0005891
dense core granule	GO:0031045
synaptic vesicle	GO:0008021
presynaptic active zone membrane	GO:0048787
cytoskeleton of presynaptic active zone	GO:0048788
phagocytic vesicle	GO:0045335
neuron projection terminus	GO:0044306
heterotrimeric G-protein complex	GO:0005834
hippocampal mossy fiber to CA3 synapse	GO:0098686
glutamatergic synapse	GO:0098978
transcription regulator complex	GO:0005667
presynaptic cytosol	GO:0099523
endosome	GO:0005768
perikaryon	GO:0043204
cytoplasmic vesicle membrane	GO:0030659
Lewy body	GO:0097413
sarcolemma	GO:0042383
transcription repressor complex	GO:0017053
distal axon	GO:0150034
zymogen granule	GO:0042588
perinuclear region of cytoplasm	GO:0048471
axon terminus	GO:0043679
neuronal dense core vesicle	GO:0098992
protein phosphatase type 1 complex	GO:0000164
RNA polymerase II transcription regulato...	GO:0090575
voltage-gated potassium channel complex	GO:0008076
NSL complex	GO:0044545
SNARE complex	GO:0031201
plasma membrane region	GO:0098590



0 1 2 3 4 5
-log(p)
n=232/361 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction