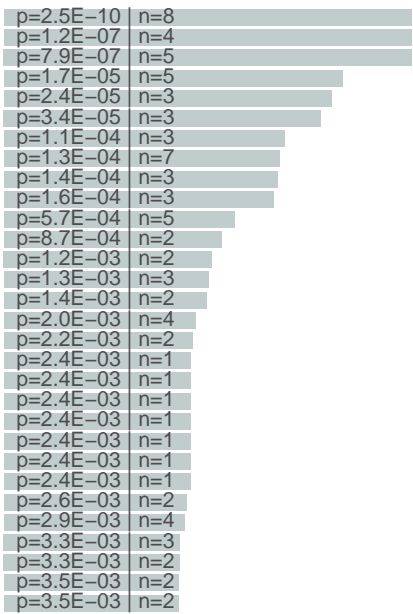


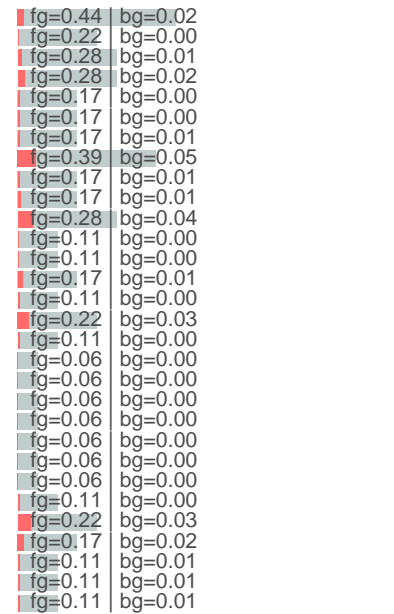
GO:BP
gc019

fraction genes in fg and expected value

adenylate cyclase-activating G protein-c...	GO:0007189
osteoblast development	GO:0002076
phospholipase C-activating G protein-cou...	GO:0007200
positive regulation of cytosolic calcium...	GO:0007204
positive regulation of inositol phosphat...	GO:0060732
G protein-coupled receptor signaling pat...	GO:0007187
bone resorption	GO:0045453
positive regulation of cell population p...	GO:0008284
bone mineralization	GO:0030282
chondrocyte differentiation	GO:0002062
negative regulation of cell population p...	GO:0008285
neutrophil activation	GO:0042119
positive regulation of chemokine product...	GO:0032722
cell maturation	GO:0048469
positive regulation of leukocyte chemota...	GO:0002690
endocytosis	GO:0006897
positive regulation of interleukin-6 pro...	GO:0032755
B cell adhesion	GO:0097323
cell-cell signaling involved in mammary ...	GO:0060764
negative regulation of neutrophil apopto...	GO:0033030
interleukin-8-mediated signaling pathway	GO:0038112
positive regulation of skeletal muscle a...	GO:1904395
Norrin signaling pathway	GO:0110135
mesodermal cell migration	GO:0008078
regulation of cyclase activity	GO:0031279
in utero embryonic development	GO:0001701
regulation of peptide hormone secretion	GO:0090276
regulation of lyase activity	GO:0051339
epidermal growth factor receptor signali...	GO:0007173
vasodilation	GO:0042311



0 1 2 3 4 5
-log(p)
n=18/56 input genes with annotations

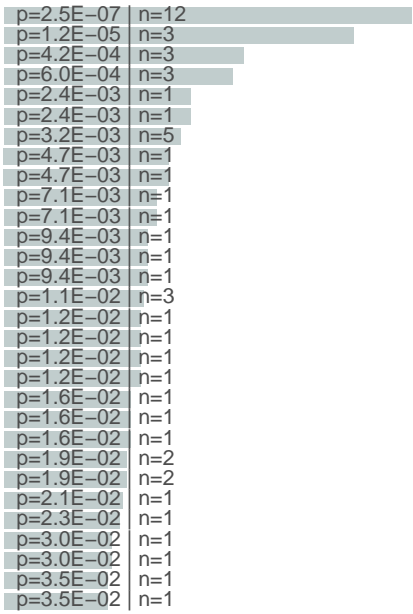


0.0 0.2 0.4 0.6 0.8 1.0
fraction

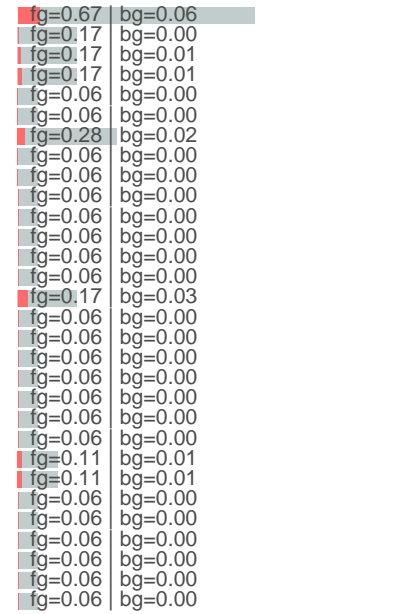
GO:MF
gc019

fraction genes in fg and expected value

G protein-coupled receptor activity	GO:0004930
parathyroid hormone receptor activity	GO:0004991
peptide hormone binding	GO:0017046
protein self-association	GO:0043621
interleukin-8 binding	GO:0019959
interleukin-8 receptor activity	GO:0004918
G protein-coupled peptide receptor activ...	GO:0008528
Wnt-activated receptor activity	GO:0042813
coreceptor activity involved in Wnt sign...	GO:0071936
C-C chemokine binding	GO:0019957
C-C chemokine receptor activity	GO:0016493
proteinase activated receptor activity	GO:0001648
potassium channel activator activity inv...	GO:0099108
thrombin-activated receptor activity	GO:0015057
calcium ion binding	GO:0005509
cyclase inhibitor activity	GO:0010852
adenylate cyclase regulator activity	GO:0010854
adenylate cyclase inhibitor activity	GO:0010855
heterotrimeric G-protein binding	GO:0032795
Wnt-protein binding	GO:0017147
cyclase regulator activity	GO:0010851
G-protein beta-subunit binding	GO:0031681
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
calcium channel inhibitor activity	GO:0019855
mannose binding	GO:0005537
exogenous protein binding	GO:0140272
virus receptor activity	GO:0001618
channel inhibitor activity	GO:0016248
ion channel inhibitor activity	GO:0008200



0 1 2 3 4 5
-log(p)
n=18/56 input genes with annotations

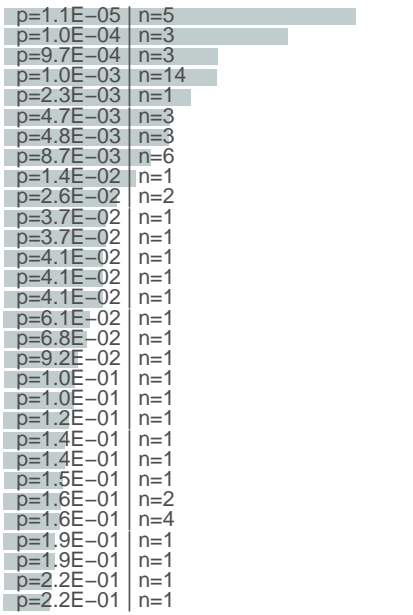


0.0 0.2 0.4 0.6 0.8 1.0
fraction

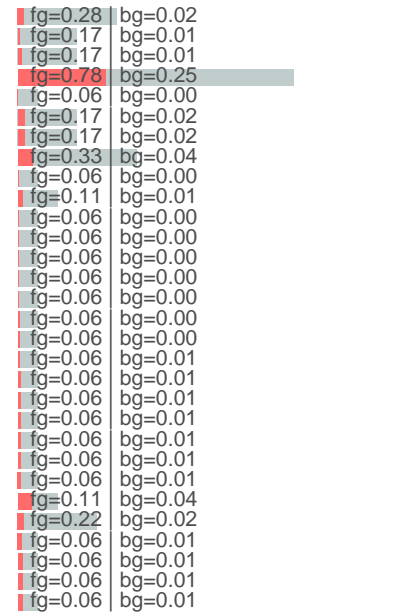
GO:CC
gc019

fraction genes in fg and expected value

receptor complex	GO:0043235
brush border membrane	GO:0031526
external side of plasma membrane	GO:0009897
plasma membrane	GO:0005886
mast cell granule	GO:0042629
apical plasma membrane	GO:0016324
basolateral plasma membrane	GO:0016323
cell surface	GO:0009986
pseudopodium	GO:0031143
Schaffer collateral - CA1 synapse	GO:0098685
GABA receptor complex	GO:1902710
G protein-coupled GABA receptor complex	GO:1902712
G protein-coupled receptor complex	GO:0097648
G protein-coupled receptor dimeric compl...	GO:0038037
G protein-coupled receptor heterodimeric...	GO:0038039
axolemma	GO:0030673
neuron projection membrane	GO:0032589
main axon	GO:0044304
plasma membrane signaling receptor compl...	GO:0098802
dendritic shaft	GO:0043198
leading edge membrane	GO:0031256
intrinsic component of plasma membrane	GO:0031226
integral component of plasma membrane	GO:0005887
GABA-ergic synapse	GO:0098982
glutamatergic synapse	GO:0098978
cell projection membrane	GO:0031253
dendritic spine	GO:0043197
neuron spine	GO:0044309
RNA polymerase II transcription regulato...	GO:0090575
mitotic spindle	GO:0072686



0 1 2 3 4 5
-log(p)
n=18/56 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0
fraction