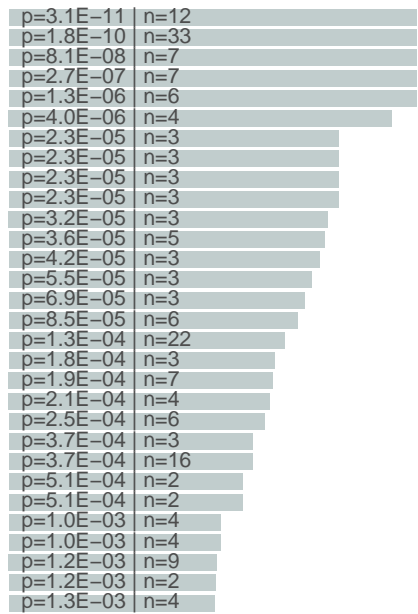


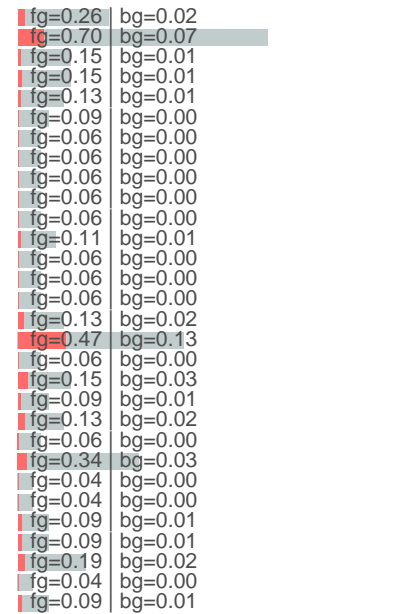
GO:BP
gc020

fraction genes in fg and expected value

adenylate cyclase-activating G protein-c...	GO:0007189
G protein-coupled receptor signaling pat...	GO:0007186
hair follicle development	GO:0001942
phospholipase C-activating G protein-cou...	GO:0007200
activation of adenylate cyclase activity	GO:0007190
epithelial cell proliferation involved i...	GO:2001013
lateral sprouting involved in lung morph...	GO:0060490
orthogonal dichotomous subdivision of te...	GO:0060488
planar dichotomous subdivision of termin...	GO:0060489
establishment of body hair planar orient...	GO:0048105
protein localization involved in establi...	GO:0090251
adenylate cyclase-inhibiting G protein-c...	GO:0007193
motor neuron migration	GO:0097475
apical protein localization	GO:0045176
planar cell polarity pathway involved in...	GO:0090179
hormone-mediated signaling pathway	GO:0009755
cell surface receptor signaling pathway	GO:0007166
activation of phospholipase C activity	GO:0007202
locomotory behavior	GO:0007626
oocyte differentiation	GO:0009994
positive regulation of cytosolic calcium...	GO:0007204
homophilic cell adhesion via plasma memb...	GO:0007156
adenylate cyclase-modulating G protein-c...	GO:0007188
cellular response to 1-oleoyl-sn-glycero...	GO:1904566
positive regulation of smooth muscle cel...	GO:0071673
positive regulation of canonical Wnt sig...	GO:0090263
anterior/posterior pattern specification	GO:0009952
inner ear development	GO:0048839
regulation of synaptic vesicle cycle	GO:0098693
positive regulation of multicellular org...	GO:0040018



-log(p)
n=47/130 input genes with annotations

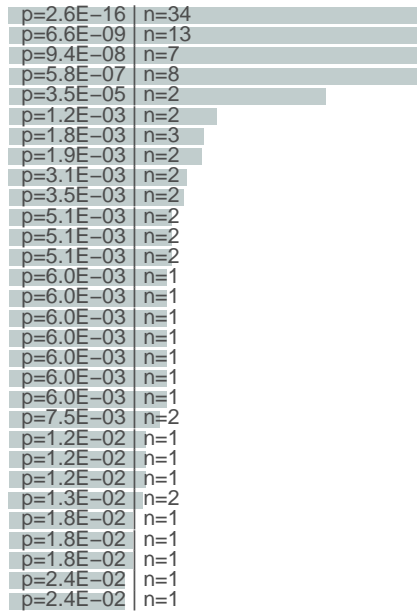


fraction

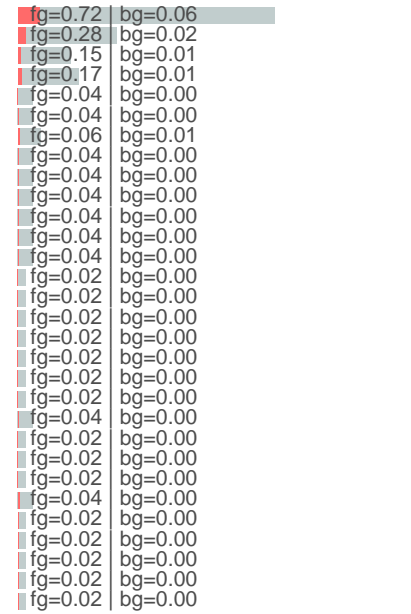
GO:MF
gc020

fraction genes in fg and expected value

G protein-coupled receptor activity	GO:0004930
G protein-coupled peptide receptor activ...	GO:0008528
peptide hormone binding	GO:0017046
protein-hormone receptor activity	GO:0016500
vasoactive intestinal polypeptide recept...	GO:0004999
lysophosphatidic acid receptor activity	GO:0070915
thyroid-stimulating hormone receptor act...	GO:0004996
lysophosphatidic acid binding	GO:0035727
bombesin receptor activity	GO:0004946
parathyroid hormone receptor activity	GO:0004991
extracellular matrix protein binding	GO:1990430
G protein-coupled neurotransmitter recep...	GO:0099579
G protein-coupled neurotransmitter recep...	GO:0150047
UDP-galactose:beta-N-acetylglucosamine b...	GO:0008499
all-trans retinoic acid 18-hydroxylase a...	GO:0062183
complement component C5a binding	GO:0001856
complement component C5a receptor activi...	GO:0004878
cannabinoid receptor activity	GO:0004949
glucosaminylgalactosylglucosylceramide b...	GO:0047275
glucagon receptor activity	GO:0004967
G protein-coupled GABA receptor activity	GO:0004965
coenzyme A transmembrane transporter act...	GO:0015228
FMN transmembrane transporter activity	GO:0044610
AMP transmembrane transporter activity	GO:0080122
G-protein alpha-subunit binding	GO:0001965
ADP transmembrane transporter activity	GO:0015217
Roundabout binding	GO:0048495
NAD transmembrane transporter activity	GO:0051724
ATP transmembrane transporter activity	GO:0005347
FAD transmembrane transporter activity	GO:0015230



-log(p)
n=47/130 input genes with annotations

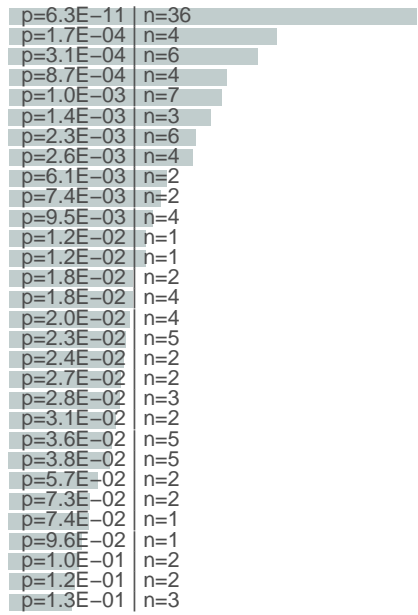


fraction

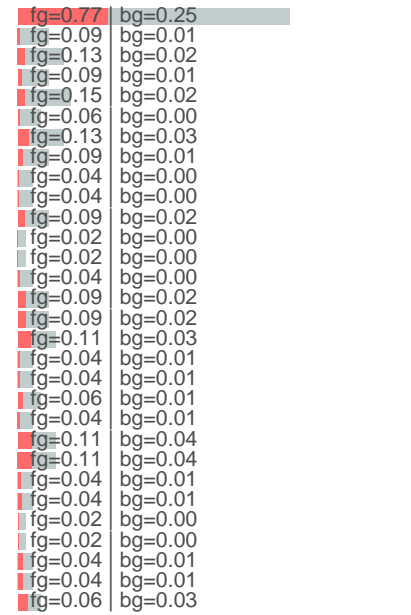
GO:CC
gc020

fraction genes in fg and expected value

plasma membrane	GO:0005886
dendritic shaft	GO:0043198
basolateral plasma membrane	GO:0016323
GABA-ergic synapse	GO:0098982
receptor complex	GO:0043235
trans-Golgi network membrane	GO:0032588
membrane raft	GO:0045121
dendritic spine	GO:0043197
G protein-coupled GABA receptor complex	GO:1902712
G protein-coupled receptor heterodimeric...	GO:0038039
cell projection membrane	GO:0031253
NLRP3 inflammasome complex	GO:0072559
inflammasome complex	GO:0061702
axolemma	GO:0030673
postsynaptic membrane	GO:0045211
presynaptic membrane	GO:0042734
synaptic membrane	GO:0097060
neuron projection membrane	GO:0032589
brush border membrane	GO:0031526
Schaffer collateral - CA1 synapse	GO:0098685
main axon	GO:0044304
glutamatergic synapse	GO:0098978
cell surface	GO:0009986
leading edge membrane	GO:0031256
brush border	GO:0005903
transcription factor TFIIIC complex	GO:0033276
exon-exon junction complex	GO:0035145
endocytic vesicle	GO:0030139
cluster of actin-based cell projections	GO:0098862
apical part of cell	GO:0045177



-log(p)
n=47/130 input genes with annotations



fraction