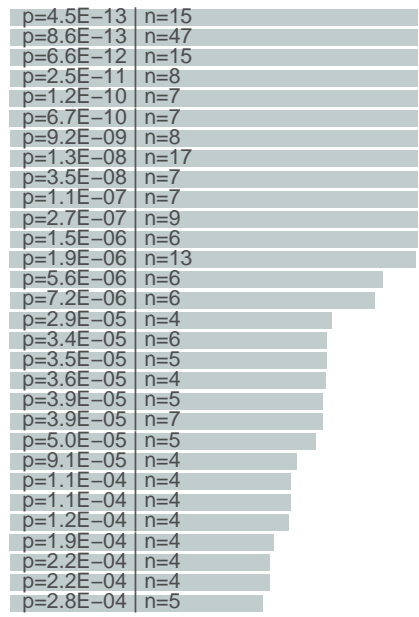


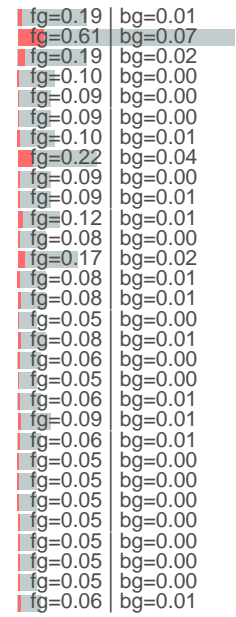
GO:BP
gc013

fraction genes in fg and expected value

phospholipase C–activating G protein–cou...	GO:0007200
G protein–coupled receptor signaling pat...	GO:0007186
adenylate cyclase–activating G protein–c...	GO:0007189
G protein–coupled receptor signaling pat...	GO:0007187
osteoblast development	GO:0002076
positive regulation of inositol phosphat...	GO:0060732
chondrocyte differentiation	GO:0002062
negative regulation of cell population p...	GO:0008285
bone resorption	GO:0045453
bone mineralization	GO:0030282
cell maturation	GO:0048469
positive regulation of mast cell degranu...	GO:0043306
positive regulation of cytosolic calcium...	GO:0007204
intestine smooth muscle contraction	GO:0014827
presynaptic modulation of chemical synap...	GO:0099171
negative regulation of epinephrine secre...	GO:0032811
adenylate cyclase–inhibiting G protein–c...	GO:0007193
operant conditioning	GO:0035106
neuron–glial cell signaling	GO:0150099
G protein–coupled adenosine receptor sig...	GO:0001973
regulation of norepinephrine secretion	GO:0014061
postsynaptic modulation of chemical syna...	GO:0099170
regulation of sensory perception of pain	GO:0051930
gamma–aminobutyric acid signaling pathwa...	GO:0007214
neuropeptide signaling pathway	GO:0007218
positive regulation of cytosolic calcium...	GO:0051482
positive regulation of acetylcholine sec...	GO:0014057
prolactin secretion	GO:0070459
negative regulation of luteinizing hormo...	GO:0033685
regulation of synaptic transmission, glu...	GO:0051966



–log(p)
n=77/261 input genes with annotations

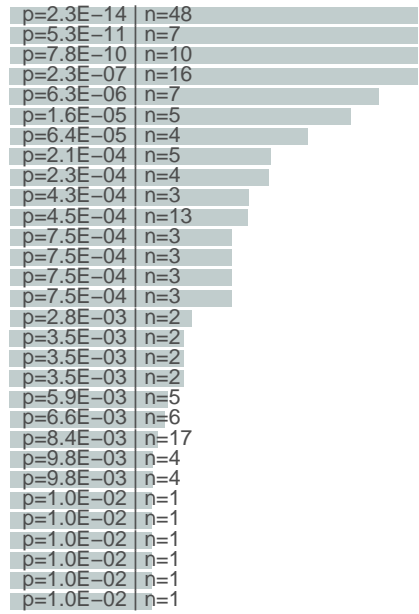


fraction

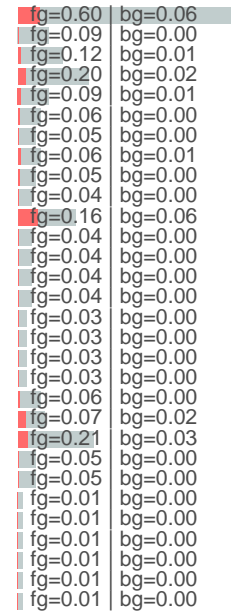
GO:MF
gc013

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
G protein–coupled peptide receptor activ...	GO:0008528
protein self–association	GO:0043621
G protein–coupled adenosine receptor act...	GO:0001609
G protein–coupled GABA receptor activity	GO:0004965
olfactory receptor activity	GO:0004984
substance K receptor activity	GO:0016497
nicotinic acid receptor activity	GO:0070553
protein homodimerization activity	GO:0042803
G protein–coupled neurotransmitter recep...	GO:0099579
purinergic nucleotide receptor activity	GO:0001614
extracellular matrix protein binding	GO:1990430
G protein–coupled neurotransmitter recep...	GO:0150047
all–trans retinal binding	GO:0005503
neuromedin U binding	GO:0042924
group II metabotropic glutamate receptor...	GO:0001641
neuromedin U receptor activity	GO:0001607
postsynaptic neurotransmitter receptor a...	GO:0098960
protein heterodimerization activity	GO:0046982
peptide binding	GO:0042277
G protein–coupled neurotransmitter recep...	GO:0099528
G protein–coupled receptor activity invo...	GO:0099530
corticotrophin–releasing factor receptor...	GO:0015056
leukotriene receptor activity	GO:0004974
corticotrophin–releasing hormone receptor...	GO:0043404
G protein–coupled neurotransmitter recep...	GO:0098872
ceramide–1–phosphate phosphatase activit...	GO:0106235
inositol 1,3,4,5 tetrakisphosphate bindi...	GO:0043533



–log(p)
n=80/261 input genes with annotations

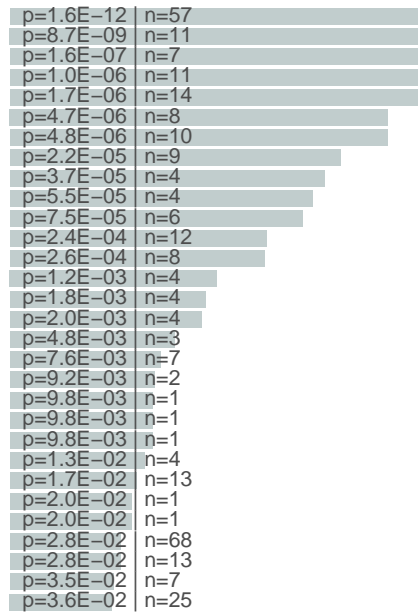


fraction

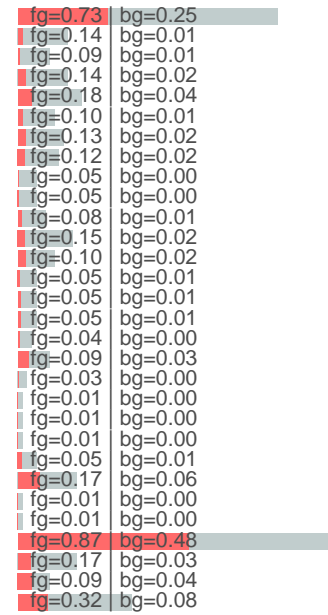
GO:CC
gc013

fraction genes in fg and expected value

plasma membrane	GO:0005886
Schaffer collateral – CA1 synapse	GO:0098685
brush border membrane	GO:0031526
presynaptic membrane	GO:0042734
glutamatergic synapse	GO:0098978
dendritic spine	GO:0043197
apical plasma membrane	GO:0016324
basolateral plasma membrane	GO:0016323
G protein–coupled GABA receptor complex	GO:1902712
G protein–coupled receptor heterodimeric...	GO:0038039
GABA–ergic synapse	GO:0098982
receptor complex	GO:0043235
postsynaptic membrane	GO:0045211
dendritic shaft	GO:0043198
sperm head	GO:0061827
sperm midpiece	GO:0097225
axolemma	GO:0030673
membrane raft	GO:0045121
astrocyte projection	GO:0097449
DNA recombinase complex	GO:0097519
nucleotide–excision repair factor 3 comp...	GO:0000112
G protein–coupled receptor homodimeric c...	GO:0038038
non–motile cilium	GO:0097730
cilium	GO:0005929
PR–DUB complex	GO:0035517
core–binding factor complex	GO:0016513
membrane	GO:0016020
synaptic membrane	GO:0097060
cell surface	GO:0009986
plasma membrane region	GO:0098590



–log(p)
n=78/261 input genes with annotations



fraction