

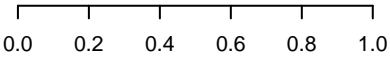
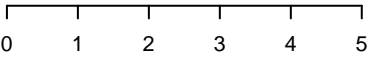
GO:BP
gc017

fraction genes in fg and expected value

positive regulation of respiratory gaseo...	GO:1903942
bombesin receptor signaling pathway	GO:0031989
positive regulation of osteoclast prolif...	GO:0090290
positive regulation of Rho protein signa...	GO:0035025
antiviral innate immune response	GO:0140374
positive regulation of interferon- α ...	GO:0032727
positive regulation of cytosolic calcium...	GO:0051482
blastocyst hatching	GO:0001835
response to symbiotic bacterium	GO:0009609
stabilization of membrane potential	GO:0030322
positive regulation of male germ cell pr...	GO:2000256
thrombopoietin-mediated signaling pathwa...	GO:0038163
G protein-coupled receptor signaling pat...	GO:0007186
inorganic cation import across plasma me...	GO:0098659
endomitotic cell cycle	GO:0007113
negative regulation of megakaryocyte dif...	GO:0045653
positive regulation of cell migration in...	GO:0090050
negative regulation of interleukin-6 pro...	GO:0032715
protein kinase B signaling	GO:0043491
negative regulation of inflammatory resp...	GO:0002862
positive regulation of cytochrome-c oxid...	GO:1904960
positive regulation of calcineurin-NFAT ...	GO:0070886
positive regulation of calcineurin-media...	GO:0106058
positive regulation of translational ini...	GO:0045948
platelet formation	GO:0030220
receptor guanylyl cyclase signaling path...	GO:0007168
positive regulation of protein targeting...	GO:0090314
regulation of transmembrane receptor pro...	GO:0090092
potassium ion import across plasma membr...	GO:1990573
positive regulation of pathway-restrict...	GO:0010862

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p=2.5E-03	n=9
p=4.7E-03	n=2
p=4.8E-03	n=1
p=4.8E-03	n=1
p=7.2E-03	n=1
p=7.3E-03	n=2
p=7.8E-03	n=2
p=9.6E-03	n=1
p=9.6E-03	n=1
p=1.2E-02	n=1
p=1.2E-02	n=1
p=1.9E-02	n=1
p=1.9E-02	n=1
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-log(p)
n=19/60 input genes with annotations

fraction

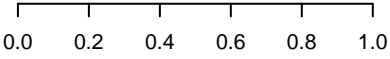
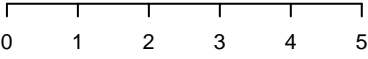
GO:MF
gc017

fraction genes in fg and expected value

lysophosphatidic acid receptor activity	GO:0070915
bombesin receptor activity	GO:0004946
pyroglutamyl-peptidase activity	GO:0016920
outward rectifier potassium channel acti...	GO:0015271
potassium ion leak channel activity	GO:0022841
calcium-dependent protein kinase inhibit...	GO:0008427
G protein-coupled receptor activity	GO:0004930
ribosomal protein S6 kinase activity	GO:0004711
neuropeptide receptor activity	GO:0008188
natriuretic peptide receptor activity	GO:0016941
glutathione peroxidase activity	GO:0004602
protein-membrane adaptor activity	GO:0043495
poly(A) binding	GO:0008143
guanylate cyclase activity	GO:0004383
group III metabotropic glutamate recepto...	GO:0001642
poly-purine tract binding	GO:0070717
cyclase activity	GO:0009975
toxic substance binding	GO:0015643
peroxidase activity	GO:0004601
oxidoreductase activity, acting on perox...	GO:0016684
phosphorus-oxygen lyase activity	GO:0016849
G protein-coupled glutamate receptor act...	GO:0098988
adenylate cyclase inhibiting G protein-c...	GO:0001640
protein serine/threonine kinase inhibito...	GO:0030291
glutamate receptor activity	GO:0008066
substance K receptor activity	GO:0016497
SMAD binding	GO:0046332
tachykinin receptor activity	GO:0004995
antioxidant activity	GO:0016209
single-stranded RNA binding	GO:0003727

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p=8.2E-03	n=4
p=1.5E-02	n=1
p=2.3E-02	n=1
p=3.0E-02	n=1
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p=4.5E-02	n=1
p=4.7E-02	n=1
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-log(p)
n=20/60 input genes with annotations

fraction

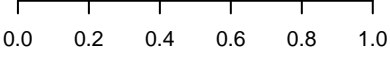
GO:CC
gc017

fraction genes in fg and expected value

plasma membrane	GO:0005886
filopodium tip	GO:0032433
mitochondrial respiratory chain complex ...	GO:0005751
respiratory chain complex IV	GO:0045277
site of polarized growth	GO:0030427
new growing cell tip	GO:0035841
growing cell tip	GO:0035838
cell tip	GO:0051286
cell pole	GO:0060187
cytochrome complex	GO:0070069
mitochondrial respiratory chain complex ...	GO:0005747
NADH dehydrogenase complex	GO:0030964
respiratory chain complex I	GO:0045271
filopodium	GO:0030175
cytoplasmic stress granule	GO:0010494
mitochondrial respirasome	GO:0005746
respiratory chain complex	GO:0098803
respirasome	GO:0070469
sperm head	GO:0061827
sperm midpiece	GO:0097225
sarcolemma	GO:0042383
lamellipodium	GO:0030027
oxidoreductase complex	GO:1990204
inner mitochondrial membrane protein com...	GO:0098800
actin-based cell projection	GO:0098858
growth cone	GO:0030426
dendrite	GO:0030425
dendritic tree	GO:0097447
neuronal cell body	GO:0043025
non-motile cilium	GO:0097730

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-log(p)
n=20/60 input genes with annotations

fraction