

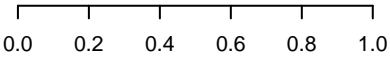
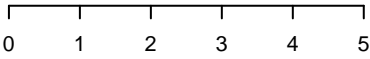
GO:BP
gc003a

fraction genes in fg and expected value

positive regulation of macrophage migrat...	GO:2000448
positive regulation of DNA helicase acti...	GO:1905776
hematopoietic stem cell migration	GO:0035701
positive regulation of mesenchymal stem ...	GO:1905322
response to tacrolimus	GO:1901327
CXCL12-activated CXCR4 signaling pathway	GO:0038160
germ cell migration	GO:0008354
positive regulation of mitochondrial DNA...	GO:0090297
positive regulation of vascular wound he...	GO:0035470
regulation of systemic arterial blood pr...	GO:0003050
negative regulation of filopodium assemb...	GO:0051490
G protein-coupled receptor signaling pat...	GO:0007186
detection of temperature stimulus involv...	GO:0050965
endothelial tube morphogenesis	GO:0061154
myelin maintenance	GO:0043217
regulation of presynaptic cytosolic calc...	GO:0099509
regulation of peptide hormone secretion	GO:0090276
detection of mechanical stimulus involve...	GO:0050966
regulation of peptide secretion	GO:0002791
regulation of peptide transport	GO:0090087
positive regulation of oligodendrocyte d...	GO:0048714
positive regulation of developmental gro...	GO:0048639
motor neuron axon guidance	GO:0008045
muscle contraction	GO:0006936
positive regulation of dendrite extensio...	GO:1903861
regulation of cytosolic calcium ion conc...	GO:0051480
branching involved in blood vessel morph...	GO:0001569
regulation of dendrite extension	GO:1903859
positive regulation of response to exter...	GO:0032103
regulation of small intestine smooth mus...	GO:1904347

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p=1.6E-02	n=2
p=1.8E-02	n=1
p=1.9E-02	n=2
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-log(p)
n=10/22 input genes with annotations

fraction

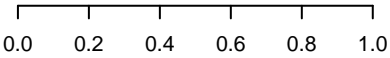
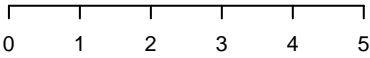
GO:MF
gc003a

fraction genes in fg and expected value

C-X-C motif chemokine 12 receptor activi...	GO:0038147
peptide binding	GO:0042277
C-C chemokine receptor activity	GO:0016493
myosin light chain binding	GO:0032027
C-C chemokine binding	GO:0019957
guanyl-nucleotide exchange factor activi...	GO:0005085
glutathione binding	GO:0043295
G protein-coupled receptor activity	GO:0004930
low-density lipoprotein particle recepto...	GO:0050750
lipoprotein particle receptor binding	GO:0070325
growth hormone-releasing hormone recepto...	GO:0016520
growth hormone secretagogue receptor act...	GO:0001616
transmembrane signaling receptor activit...	GO:0004888
G protein activity	GO:0003925
molecular transducer activity	GO:0060089
signaling receptor activity	GO:0038023
glutathione transferase activity	GO:0004364
PDZ domain binding	GO:0030165
protein domain specific binding	GO:0019904
ubiquitin binding	GO:0043130
SH3 domain binding	GO:0017124
ubiquitin-like protein binding	GO:0032182
peptide hormone binding	GO:0017046
transferase activity, transferring alkyl...	GO:0016765
hormone binding	GO:0042562
single-stranded DNA binding	GO:0003697
GTPase activity	GO:0003924
identical protein binding	GO:0042802
actin binding	GO:0003779
ubiquitin protein ligase binding	GO:0031625

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p=5.2E-03	n=2
p=8.9E-03	n=1
p=1.4E-02	n=4
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p=1.9E-02	n=1
p=2.1E-02	n=1
p=2.1E-02	n=1
p=2.3E-02	n=4
p=2.4E-02	n=1
p=3.0E-02	n=4
p=3.0E-02	n=4
p=4.8E-02	n=1
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p=5.9E-02	n=2
p=6.4E-02	n=1
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fraction

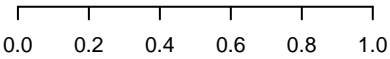
GO:CC
gc003a

fraction genes in fg and expected value

Golgi to plasma membrane transport vesic...	GO:0070319
plasma membrane	GO:0005886
proximal dendrite	GO:1990635
plasma membrane bounded cell projection	GO:0120025
distal axon	GO:0150034
neuron projection	GO:0043005
terminal bouton	GO:0043195
nucleoid	GO:0009295
mitochondrial nucleoid	GO:0042645
cell surface	GO:0009986
axon	GO:0030424
cell projection	GO:0042995
axon terminus	GO:0043679
neuron projection terminus	GO:0044306
external side of plasma membrane	GO:0009897
growth cone	GO:0030426
cilium	GO:0005929
site of polarized growth	GO:0030427
cell junction	GO:0030054
Schaffer collateral - CA1 synapse	GO:0098685
external encapsulating structure	GO:0030312
extracellular matrix	GO:0031012
late endosome	GO:0005770
cell-cell junction	GO:0005911
early endosome	GO:0005769
cell leading edge	GO:0031252
side of membrane	GO:0098552
anchoring junction	GO:0070161
membrane raft	GO:0045121
membrane microdomain	GO:0098857

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p=6.4E-02	n=2
p=7.1E-02	n=7
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p=1.2E-01	n=2
p=1.2E-01	n=1
p=1.2E-01	n=3
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