

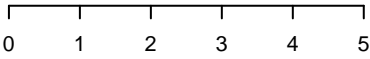
GO:BP  
gc018

fraction genes in fg and expected value

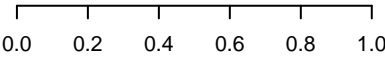
positive regulation of Notch signaling p...	GO:0035481
positive regulation of cardiac endotheli...	GO:0062000
neuroblast division in subventricular zo...	GO:0021849
regulation of postsynapse assembly	GO:0150052
endocardial cushion fusion	GO:0003274
myofibroblast contraction	GO:1990764
cardiac jelly development	GO:1905072
intestinal epithelial cell differentiati...	GO:0060575
lateral ventricle development	GO:0021670
regulation of amine transport	GO:0051952
regulation of muscle system process	GO:0090257
aortic valve morphogenesis	GO:0003180
positive regulation of multicellular org...	GO:0051240
cell motility	GO:0048870
localization of cell	GO:0051674
movement of cell or subcellular componen...	GO:0006928
negative regulation of cardiac muscle hy...	GO:0010614
negative regulation of muscle hypertroph...	GO:0014741
adherens junction organization	GO:0034332
hormone secretion	GO:0046879
hormone transport	GO:0009914
positive regulation of cell motility	GO:2000147
locomotion	GO:0040011
histamine secretion involved in inflamma...	GO:0002441
histamine secretion by mast cell	GO:0002553
histamine production involved in inflamm...	GO:0002349
positive regulation of secretion by cell	GO:1903532
positive regulation of locomotion	GO:0040017
positive regulation of cellular componen...	GO:0051272
positive regulation of secretion	GO:0051047

p=7.9E-04	n=1
p=7.9E-04	n=1
p=7.9E-04	n=1
p=1.6E-03	n=1
p=1.6E-03	n=1
p=1.6E-03	n=1
p=2.4E-03	n=1
p=3.9E-03	n=1
p=4.7E-03	n=1
p=5.2E-03	n=2
p=6.2E-03	n=2
p=7.1E-03	n=1
p=7.1E-03	n=4
p=1.0E-02	n=3
p=1.0E-02	n=3
p=1.2E-02	n=4
p=1.3E-02	n=1
p=1.3E-02	n=1
p=1.3E-02	n=1
p=1.4E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.6E-02	n=3
p=1.6E-02	n=1
p=1.6E-02	n=1
p=1.6E-02	n=1
p=1.6E-02	n=2
p=1.6E-02	n=2
p=1.6E-02	n=2
p=1.7E-02	n=2

fg=0.17	bg=0.00
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fg=0.17	bg=0.00
fg=0.33	bg=0.02
fg=0.33	bg=0.02
fg=0.17	bg=0.00
fg=0.67	bg=0.09
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fg=0.50	bg=0.09
fg=0.67	bg=0.11
fg=0.17	bg=0.00
fg=0.17	bg=0.00
fg=0.17	bg=0.00
fg=0.33	bg=0.03
fg=0.33	bg=0.03
fg=0.33	bg=0.03
fg=0.50	bg=0.10
fg=0.17	bg=0.00
fg=0.17	bg=0.00
fg=0.17	bg=0.00
fg=0.33	bg=0.03
fg=0.33	bg=0.03
fg=0.33	bg=0.03
fg=0.33	bg=0.03



-log(p)  
n=6/31 input genes with annotations



fraction

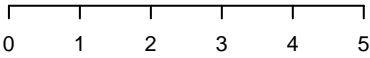
GO:MF  
gc018

fraction genes in fg and expected value

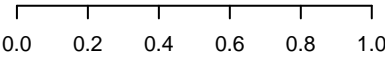
ganglioside GM1 binding	GO:1905573
substance K receptor activity	GO:0016497
G protein-coupled adenosine receptor act...	GO:0001609
tachykinin receptor activity	GO:0004995
G protein-coupled receptor activity	GO:0004930
transmembrane signaling receptor activit...	GO:0004888
neuropeptide receptor activity	GO:0008188
signaling receptor activity	GO:0038023
molecular transducer activity	GO:0060089
G protein-coupled peptide receptor activ...	GO:0008528
peptide receptor activity	GO:0001653
DNA-binding transcription factor activit...	GO:0000981
RNA polymerase II cis-regulatory region ...	GO:0000978
DNA-binding transcription factor activit...	GO:0003700
phospholipid binding	GO:0005543
cis-regulatory region sequence-specific ...	GO:0000987
GTPase activator activity	GO:0005096
GTPase regulator activity	GO:0030695
nucleoside-triphosphatase regulator acti...	GO:0060589
calcium ion binding	GO:0005509
RNA polymerase II transcription regulato...	GO:0000977
transcription cis-regulatory region bind...	GO:0000976
transcription regulatory region nucleic ...	GO:0001067
sequence-specific double-stranded DNA bi...	GO:1990837
zinc ion binding	GO:0008270
double-stranded DNA binding	GO:0003690
sequence-specific DNA binding	GO:0043565
transcription regulator activity	GO:0140110
metal ion binding	GO:0046872
transition metal ion binding	GO:0046914

p=2.6E-03	n=1
p=2.0E-02	n=1
p=2.0E-02	n=1
p=2.2E-02	n=1
p=3.4E-02	n=2
p=4.7E-02	n=2
p=4.8E-02	n=1
p=5.6E-02	n=2
p=5.6E-02	n=2
p=9.9E-02	n=1
p=1.1E-01	n=1
p=1.1E-01	n=1
p=1.2E-01	n=1
p=1.2E-01	n=1
p=1.2E-01	n=1
p=1.3E-01	n=1
p=1.3E-01	n=1
p=1.4E-01	n=1
p=1.4E-01	n=1
p=1.4E-01	n=1
p=1.4E-01	n=1
p=1.4E-01	n=1
p=1.7E-01	n=1
p=1.7E-01	n=1
p=1.7E-01	n=1
p=1.8E-01	n=1
p=1.9E-01	n=1
p=2.1E-01	n=1
p=2.1E-01	n=1
p=2.3E-01	n=1
p=2.8E-01	n=2
p=2.9E-01	n=1

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fg=0.20	bg=0.00
fg=0.20	bg=0.00
fg=0.40	bg=0.06
fg=0.40	bg=0.07
fg=0.20	bg=0.01
fg=0.40	bg=0.08
fg=0.40	bg=0.08
fg=0.20	bg=0.02
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fg=0.20	bg=0.02
fg=0.20	bg=0.03
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fg=0.20	bg=0.05
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fg=0.20	bg=0.05
fg=0.40	bg=0.21
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-log(p)  
n=5/31 input genes with annotations



fraction

GO:CC  
gc018

fraction genes in fg and expected value

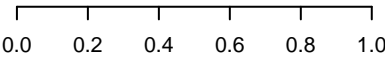
synapse	GO:0045202
synaptic membrane	GO:0097060
cell junction	GO:0030054
sperm midpiece	GO:0097225
sperm head	GO:0061827
neuromuscular junction	GO:0031594
plasma membrane region	GO:0098590
Schaffer collateral - CA1 synapse	GO:0098685
sperm flagellum	GO:0036126
9+2 motile cilium	GO:0097729
motile cilium	GO:0031514
presynaptic membrane	GO:0042734
plasma membrane	GO:0005886
cell periphery	GO:0071944
chromatin	GO:0000785
glutamatergic synapse	GO:0098978
lytic vacuole	GO:0000323
lysosome	GO:0005764
vacuole	GO:0005773
presynapse	GO:0098793
cilium	GO:0005929
extracellular region	GO:0005576
chromosome	GO:0005694
membrane	GO:0016020
plasma membrane bounded cell projection	GO:0120025
cell projection	GO:0042995
cellular anatomical entity	GO:0110165
non-membrane-bounded organelle	GO:0043228
intracellular non-membrane-bounded organ...	GO:0043232
nucleus	GO:0005634

p=1.6E-02	n=3
p=1.7E-02	n=2
p=3.1E-02	n=3
p=4.2E-02	n=1
p=4.5E-02	n=1
p=6.3E-02	n=1
p=8.0E-02	n=2
p=8.2E-02	n=1
p=8.7E-02	n=1
p=9.7E-02	n=1
p=1.3E-01	n=1
p=1.3E-01	n=1
p=1.7E-01	n=3
p=2.0E-01	n=3
p=2.0E-01	n=1
p=2.3E-01	n=1
p=2.3E-01	n=1
p=2.3E-01	n=1
p=2.6E-01	n=1
p=3.0E-01	n=1
p=3.2E-01	n=1
p=3.5E-01	n=1
p=4.0E-01	n=1
p=6.2E-01	n=3
p=6.3E-01	n=1
p=6.7E-01	n=1
p=7.8E-01	n=6
p=8.7E-01	n=1
p=8.7E-01	n=1
p=9.6E-01	n=1

fg=0.50	bg=0.10
fg=0.33	bg=0.03
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fg=0.17	bg=0.02
fg=0.17	bg=0.02
fg=0.17	bg=0.02
fg=0.50	bg=0.25
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fg=0.17	bg=0.29
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fg=0.17	bg=0.43



-log(p)  
n=6/31 input genes with annotations



fraction