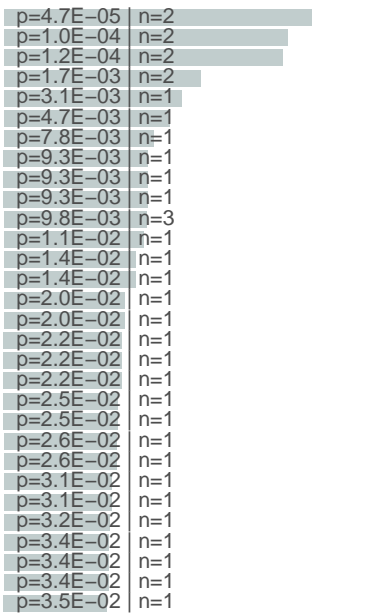


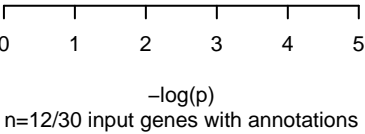
GO:BP
gc003a

fraction genes in fg and expected value

regulation of neutrophil mediated cytoto...	GO:0070948
regulation of acute inflammatory respons...	GO:0002673
neutrophil activation involved in immune...	GO:0002283
DNA catabolic process, endonucleolytic	GO:0000737
negative regulation of filopodium assemb...	GO:0051490
pancreatic A cell differentiation	GO:0003310
intestinal epithelial cell differentiati...	GO:0060575
phenotypic switching	GO:0036166
DNA methylation on cytosine within a CG ...	GO:0010424
cellular response to cocaine	GO:0071314
negative regulation of transcription by ...	GO:0000122
positive regulation of oligodendrocyte d...	GO:0048714
type B pancreatic cell differentiation	GO:0003309
negative regulation of oligodendrocyte d...	GO:0048715
type B pancreatic cell proliferation	GO:0044342
negative regulation of glial cell differ...	GO:0045686
regulation of histone H3–K9 methylation	GO:0051570
synaptonemal complex assembly	GO:0007130
peptidyl–lysine dimethylation	GO:0018027
histone H3–K9 methylation	GO:0051567
neuron fate specification	GO:0048665
positive regulation of glial cell differ...	GO:0045687
synaptonemal complex organization	GO:0070193
long–term memory	GO:0007616
regulation of DNA methylation	GO:0044030
positive regulation of neuron differenti...	GO:0045666
histone H3–K9 modification	GO:0061647
behavioral response to cocaine	GO:0048148
negative regulation of gliogenesis	GO:0014014
neuropeptide signaling pathway	GO:0007218



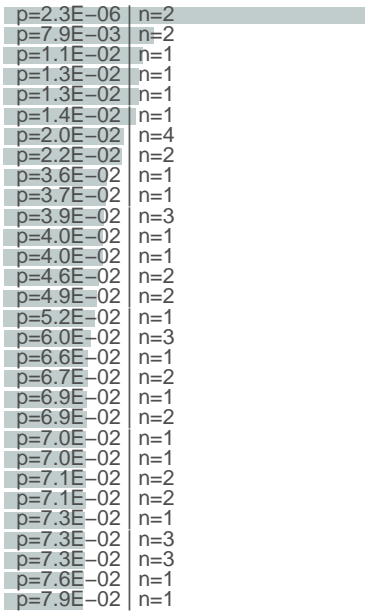
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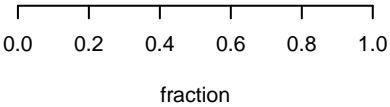
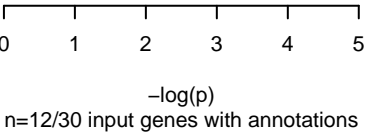
GO:MF
gc003a

fraction genes in fg and expected value

deoxyribonuclease I activity	GO:0004530
guanyl–nucleotide exchange factor activi...	GO:0005085
histone methyltransferase activity (H3–K...	GO:0046974
neuropeptide Y receptor activity	GO:0004983
histone methyltransferase activity (H3–K...	GO:0046976
C2H2 zinc finger domain binding	GO:0070742
DNA binding	GO:0003677
actin binding	GO:0003779
histone–lysine N–methyltransferase activ...	GO:0018024
transcription corepressor binding	GO:0001222
G protein–coupled receptor activity	GO:0004930
lysine N–methyltransferase activity	GO:0016278
protein–lysine N–methyltransferase activ...	GO:0016279
peptide binding	GO:0042277
RNA polymerase II transcription regulato...	GO:0000977
histone methyltransferase activity	GO:0042054
transmembrane signaling receptor activit...	GO:0004888
transcription coregulator binding	GO:0001221
chromatin binding	GO:0003682
promoter–specific chromatin binding	GO:1990841
amide binding	GO:0033218
PDZ domain binding	GO:0030165
p53 binding	GO:0002039
transcription cis–regulatory region bind...	GO:0000976
transcription regulatory region nucleic ...	GO:0001067
protein methyltransferase activity	GO:0008276
molecular transducer activity	GO:0060089
signaling receptor activity	GO:0038023
N–methyltransferase activity	GO:0008170
DNA–binding transcription repressor acti...	GO:0001227



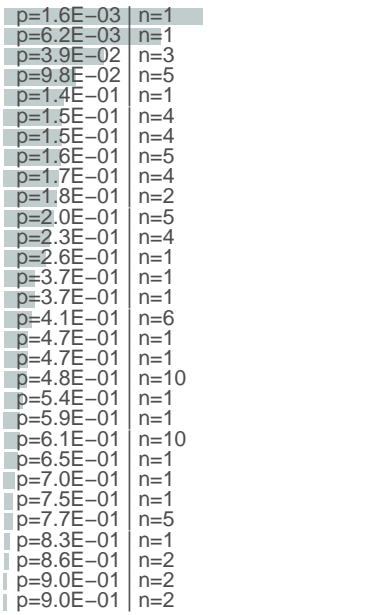
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GO:CC
gc003a

fraction genes in fg and expected value

Golgi to plasma membrane transport vesic...	GO:0070319
proximal dendrite	GO:1990635
cilium	GO:0005929
cell projection	GO:0042995
non–motile cilium	GO:0097730
cytoplasmic vesicle	GO:0031410
intracellular vesicle	GO:0097708
plasma membrane	GO:0005886
vesicle	GO:0031982
extracellular region	GO:0005576
cell periphery	GO:0071944
plasma membrane bounded cell projection	GO:0120025
nuclear speck	GO:0016607
perinuclear region of cytoplasm	GO:0048471
chromatin	GO:0000785
nucleus	GO:0005634
centrosome	GO:0005813
nuclear body	GO:0016604
membrane–bounded organelle	GO:0043227
microtubule organizing center	GO:0005815
nucleolus	GO:0005730
organelle	GO:0043226
chromosome	GO:0005694
microtubule cytoskeleton	GO:0015630
Golgi apparatus	GO:0005794
membrane	GO:0016020
cytoskeleton	GO:0005856
cytosol	GO:0005829
non–membrane–bounded organelle	GO:0043228
intracellular non–membrane–bounded organ...	GO:0043232



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