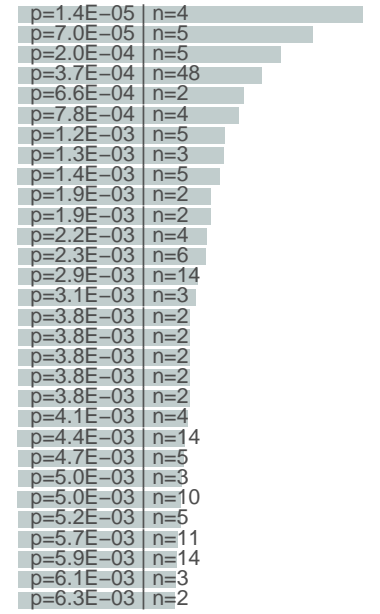


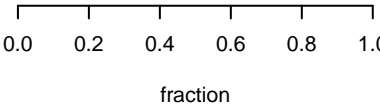
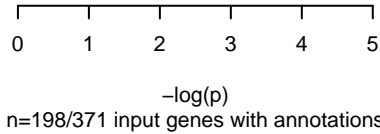
GO:BP
gc022

fraction genes in fg and expected value

positive regulation of viral entry into ...	GO:0046598
protein autoprocessing	GO:0016540
vasculogenesis	GO:0001570
proteolysis	GO:0006508
hepatic duct development	GO:0061011
positive regulation of mRNA splicing, vi...	GO:0048026
positive regulation of tumor necrosis fa...	GO:0032760
nucleosome disassembly	GO:0006337
histone deubiquitination	GO:0016578
gall bladder development	GO:0061010
hepatoblast differentiation	GO:0061017
male germ cell proliferation	GO:0002176
activation of cysteine-type endopeptidas...	GO:0006919
forebrain development	GO:0030900
melanin biosynthetic process	GO:0042438
formation of cytoplasmic translation ini...	GO:0001732
neutrophil extravasation	GO:0072672
intestinal lipid catabolic process	GO:0044258
primitive streak formation	GO:0090009
primary lung bud formation	GO:0060431
regulation of myoblast differentiation	GO:0045661
cell morphogenesis involved in neuron di...	GO:0048667
sister chromatid cohesion	GO:0007062
positive regulation of natural killer ce...	GO:0002717
homeostasis of number of cells	GO:0048872
keratinocyte differentiation	GO:0030216
response to bacterium	GO:0009617
neuron projection morphogenesis	GO:0048812
positive regulation of B cell proliferat...	GO:0030890
plasmacytoid dendritic cell activation	GO:0002270



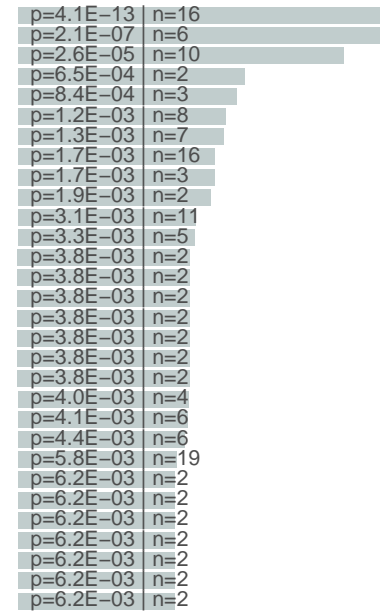
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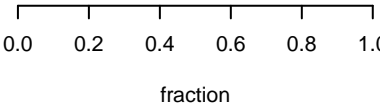
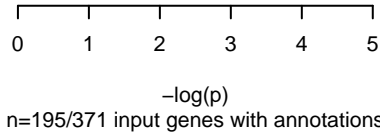
GO:MF
gc022

fraction genes in fg and expected value

serine-type endopeptidase activity	GO:0004252
scavenger receptor activity	GO:0005044
protease binding	GO:0002020
cysteine-type endopeptidase activity inv...	GO:0097200
TFIID-class transcription factor complex...	GO:0001094
exopeptidase activity	GO:0008238
hydrolase activity, hydrolyzing O-glycos...	GO:0004553
chromatin binding	GO:0003682
death domain binding	GO:0070513
HMG box domain binding	GO:0071837
protein-macromolecule adaptor activity	GO:0030674
clathrin binding	GO:0030276
proline:sodium symporter activity	GO:0005298
galactolipase activity	GO:0047714
NAD+ nucleotidase, cyclic ADP-ribose gen...	GO:0061809
1-18:1-2-16:0-monogalactosyldiacylglycer...	GO:0102549
NAD(P)+ nucleosidase activity	GO:0050135
DNA binding, bending	GO:0008301
U2 snRNA binding	GO:0030620
translation initiation factor binding	GO:0031369
translation factor activity, RNA binding	GO:0008135
ATPase binding	GO:0051117
serine-type peptidase activity	GO:0008236
spermine:oxygen oxidoreductase (spermi...	GO:0052901
spermidine:oxygen oxidoreductase (3-amin...	GO:0052902
N1-acetylspermine:oxygen oxidoreductase ...	GO:0052903
N1-acetylspermidine:oxygen oxidoreductas...	GO:0052904
MHC class II protein binding	GO:0042289
U1 snRNA binding	GO:0030619
N(1),N(12)-diacetylspermine:oxygen oxido...	GO:0052899



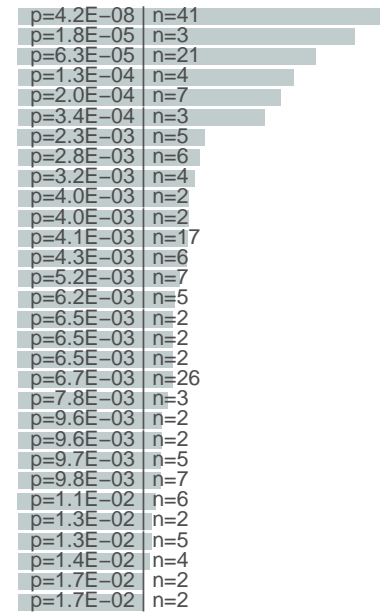
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GO:CC
gc022

fraction genes in fg and expected value

extracellular region	GO:0005576
meiotic cohesin complex	GO:0030893
extracellular space	GO:0005615
lateral element	GO:0000800
nuclear matrix	GO:0016363
box C/D RNP complex	GO:0031428
male germ cell nucleus	GO:0001673
plasma membrane raft	GO:0044853
Cajal body	GO:0015030
azurophil granule lumen	GO:0035578
dense fibrillar component	GO:0001651
cell surface	GO:0009986
vesicle coat	GO:0030120
fibrillar center	GO:0001650
basement membrane	GO:0005604
AP-2 adaptor complex	GO:0030122
nBAF complex	GO:0071565
parallel fiber to Purkinje cell synapse	GO:0098688
ribonucleoprotein complex	GO:1990904
M band	GO:0031430
GBAF complex	GO:0140288
pre-snoRNP complex	GO:0070761
acrosomal vesicle	GO:0001669
neuron projection terminus	GO:0044306
secretory granule membrane	GO:0030667
npBAF complex	GO:0071564
spliceosomal snRNP complex	GO:0097525
sex chromosome	GO:0000803
COPII vesicle coat	GO:0030127
eukaryotic translation initiation factor...	GO:0071541



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