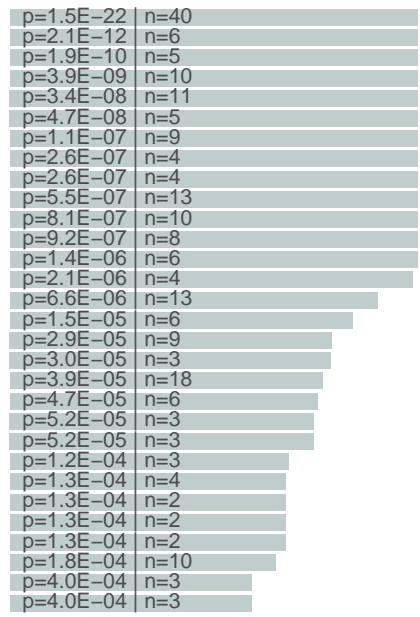


GO:BP
gc021

fraction genes in fg and expected value

cell division	GO:0051301
mitotic spindle midzone assembly	GO:0051256
positive regulation of chromosome conden...	GO:1905821
mitotic spindle assembly checkpoint sign...	GO:0007094
positive regulation of chromosome separa...	GO:1905820
mitotic chromosome condensation	GO:0007076
positive regulation of chromosome segreg...	GO:0051984
meiotic chromosome condensation	GO:0010032
actomyosin contractile ring assembly	GO:0000915
mitotic spindle assembly	GO:0090307
mitotic cytokinesis	GO:0000281
positive regulation of cytokinesis	GO:0032467
positive regulation of mitotic sister ch...	GO:1901970
positive regulation of ubiquitin protein...	GO:1904668
cilium assembly	GO:0060271
anaphase-promoting complex-dependent cat...	GO:0031145
mitotic metaphase plate congression	GO:0007080
positive regulation of mitotic cytokines...	GO:1903490
mitotic spindle organization	GO:0007052
regulation of attachment of spindle micr...	GO:0051988
kinetochore assembly	GO:0051382
positive regulation of attachment of mit...	GO:1902425
positive regulation of mitotic cell cycl...	GO:0090267
protein K11-linked ubiquitination	GO:0070979
lateral attachment of mitotic spindle mi...	GO:0099607
septin ring organization	GO:0031106
positive regulation of anaphase-promotin...	GO:1905786
G2/M transition of mitotic cell cycle	GO:0000086
positive regulation of mitotic metaphase...	GO:0045842
protein localization to kinetochore	GO:0034501



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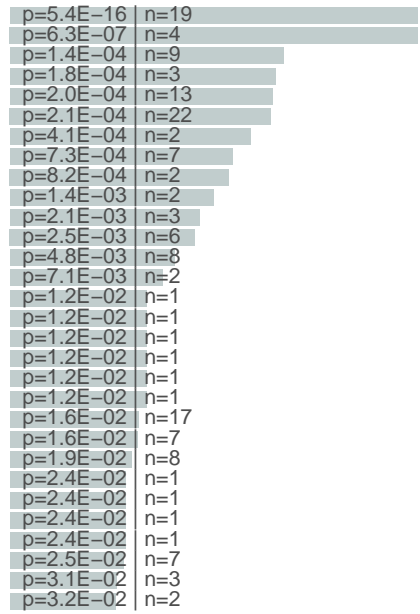
0 1 2 3 4 5
-log(p)
n=92/134 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
gc021

fraction genes in fg and expected value

microtubule binding	GO:0008017
anaphase-promoting complex binding	GO:0010997
ATP hydrolysis activity	GO:0016887
plus-end-directed microtubule motor acti...	GO:0008574
protein kinase binding	GO:0019901
ATP binding	GO:0005524
histone methyltransferase activity (H4-K...	GO:0042799
microtubule motor activity	GO:0003777
kinetochore binding	GO:0043515
ubiquitin ligase activator activity	GO:1990757
cyclin-dependent protein serine/threonin...	GO:0016538
protein C-terminus binding	GO:0008022
protein serine/threonine kinase activity	GO:0004674
histone kinase activity	GO:0035173
LEM domain binding	GO:0097726
microtubule plus end polymerase	GO:0061863
thromboxane A2 receptor binding	GO:0031870
calcium-dependent ATPase activity	GO:0030899
UMP kinase activity	GO:0033862
CMP kinase activity	GO:0036430
enzyme regulator activity	GO:0030234
protein kinase regulator activity	GO:0019887
chromatin binding	GO:0003682
uridylate kinase activity	GO:0009041
DNA topoisomerase type II (double strand...	GO:0003918
prostanoid receptor binding	GO:0031862
histone kinase activity (H3-S28 specific...	GO:0044022
kinase regulator activity	GO:0019207
histone deacetylase binding	GO:0042826
ubiquitin conjugating enzyme activity	GO:0061631



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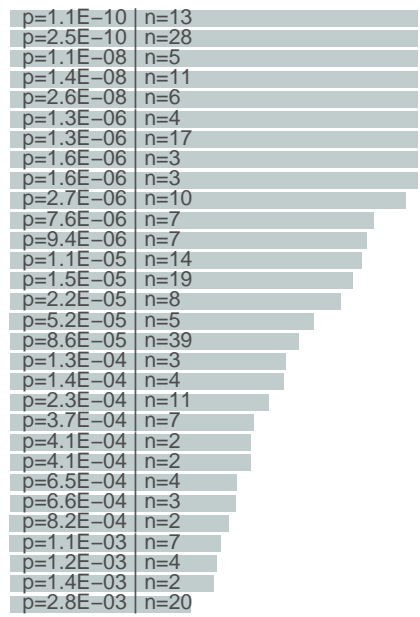
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n=93/134 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
gc021

fraction genes in fg and expected value

midbody	GO:0030496
centrosome	GO:0005813
condensin complex	GO:0000796
centriole	GO:0005814
anaphase-promoting complex	GO:0005680
mitotic spindle midzone	GO:1990023
mitotic spindle	GO:0072686
chromosome passenger complex	GO:0032133
centralspindlin complex	GO:0097149
spindle pole	GO:0000922
condensed nuclear chromosome	GO:0000794
centriolar satellite	GO:0034451
condensed chromosome, centromeric region	GO:0000779
microtubule	GO:0005874
spindle microtubule	GO:0005876
kinesin complex	GO:0005871
nucleoplasm	GO:0005654
outer kinetochore	GO:0000940
pericentric heterochromatin	GO:0005721
kinetochore	GO:0000776
spindle midzone	GO:0051233
mitotic spindle astral microtubule	GO:0061673
Ndc80 complex	GO:0031262
cyclin-dependent protein kinase holoenzy...	GO:0000307
cleavage furrow	GO:0032154
actomyosin contractile ring	GO:0005826
ciliary basal body	GO:0036064
intercellular bridge	GO:0045171
chromocenter	GO:0010369
condensed chromosome	GO:0000793



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0 1 2 3 4 5
-log(p)
n=94/134 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction