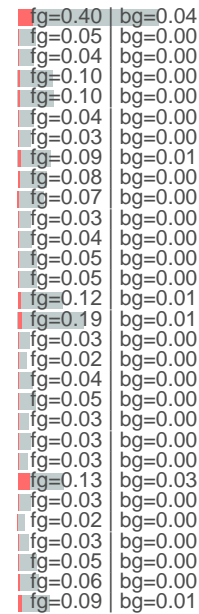
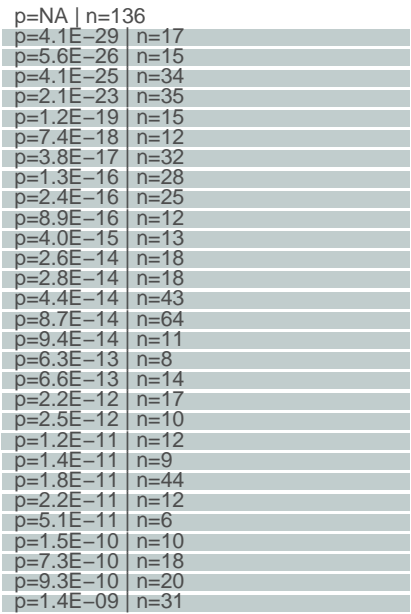


GO:BP
gc021

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
meiotic chromosome condensation	GO:0010032
mitotic cytokinesis	GO:0000281
positive regulation of chromosome segreg...	GO:0051984
positive regulation of cytokinesis	GO:0032467
positive regulation of ubiquitin protein...	GO:1904668
actomyosin contractile ring assembly	GO:0000915
anaphase-promoting complex-dependent cat...	GO:0031145
positive regulation of mitotic sister ch...	GO:1901970
mitotic spindle assembly	GO:0090307
mitotic spindle organization	GO:0007052
positive regulation of mitotic cell cycl...	GO:0090267
spindle assembly involved in female meio...	GO:0007057
protein K11-linked ubiquitination	GO:0070979
kinetochore organization	GO:0051383
positive regulation of mitotic cytokines...	GO:1903490
protein localization to kinetochore	GO:0034501
kinetochore assembly	GO:0051382
cilium assembly	GO:0060271
establishment of mitotic spindle orienta...	GO:0000132
septin ring organization	GO:0031106
positive regulation of mitotic metaphase...	GO:0045842
regulation of attachment of spindle micr...	GO:0051988
regulation of mitotic spindle organizati...	GO:0060236
G2/M transition of mitotic cell cycle	GO:0000086



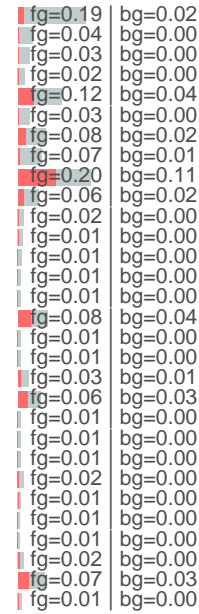
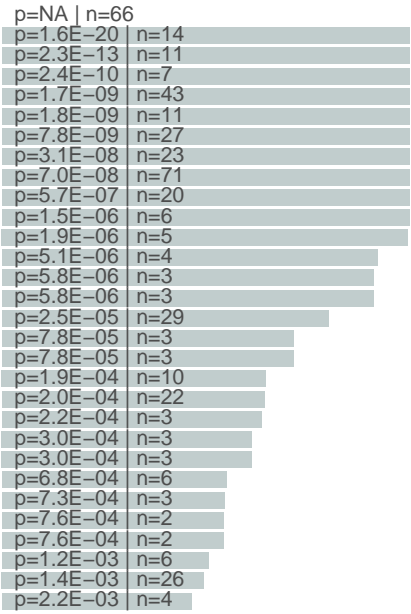
0 1 2 3 4 5
-log(p)
n=344/495 input genes with annotations

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
plus-end-directed microtubule motor acti...	GO:0008574
kinetochore binding	GO:0043515
protein kinase binding	GO:0019901
cyclin-dependent protein serine/threonin...	GO:0016538
ATP hydrolysis activity	GO:0016887
microtubule motor activity	GO:0003777
ATP binding	GO:0005524
protein C-terminus binding	GO:0008022
microtubule plus-end binding	GO:0051010
ubiquitin ligase activator activity	GO:1990757
histone methyltransferase activity (H4-K...	GO:0042799
microtubule plus end polymerase	GO:0061863
LEM domain binding	GO:0097726
chromatin binding	GO:0003682
histone kinase activity (H3-S28 specific...	GO:0044022
DNA topoisomerase type II (double strand...	GO:0003918
histone deacetylase binding	GO:0042826
GTPase activator activity	GO:0005096
centromeric DNA binding	GO:0019237
leukotriene-C4 synthase activity	GO:0004464
GTPase inhibitor activity	GO:0005095
ubiquitin conjugating enzyme activity	GO:0061631
hyaluronic acid binding	GO:0005540
kinetochore adaptor activity	GO:0140483
thromboxane A2 receptor binding	GO:0031870
kinesin binding	GO:0019894
protein serine/threonine kinase activity	GO:0004674
structural constituent of chromatin	GO:0030527



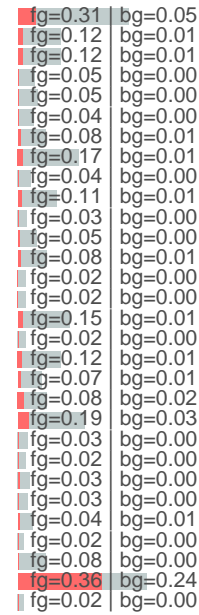
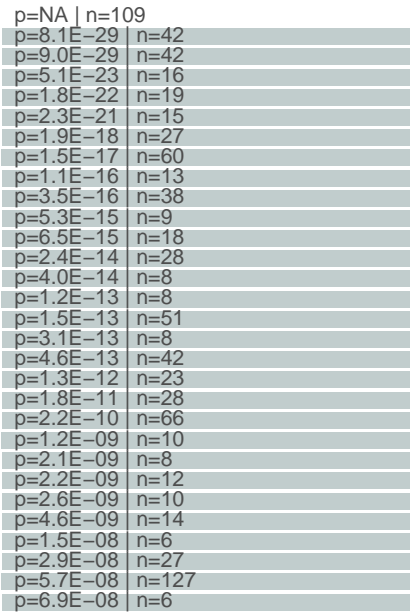
0 1 2 3 4 5
-log(p)
n=348/495 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
gc021

fraction genes in fg and expected value

centrosome	GO:0005813
midbody	GO:0030496
centriole	GO:0005814
mitotic spindle midzone	GO:1990023
anaphase-promoting complex	GO:0005680
condensin complex	GO:0000796
centriolar satellite	GO:0034451
mitotic spindle	GO:0072686
outer kinetochore	GO:0000940
spindle pole	GO:0000922
centralspindlin complex	GO:0097149
kinesin complex	GO:0005871
spindle microtubule	GO:0005876
chromosome passenger complex	GO:0032133
Ndc80 complex	GO:0031262
condensed chromosome, centromeric region	GO:0000779
mitotic spindle astral microtubule	GO:0061673
kinetochore	GO:0000776
condensed nuclear chromosome	GO:0000794
ciliary basal body	GO:0036064
microtubule	GO:0005874
cleavage furrow	GO:0032154
spindle pole centrosome	GO:0031616
mitotic spindle pole	GO:0097431
microtubule plus-end	GO:0035371
intercellular bridge	GO:0045171
actomyosin contractile ring	GO:0005826
spindle midzone	GO:0051233
nucleoplasm	GO:0005654
chromocenter	GO:0010369



0 1 2 3 4 5
-log(p)
n=351/495 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction