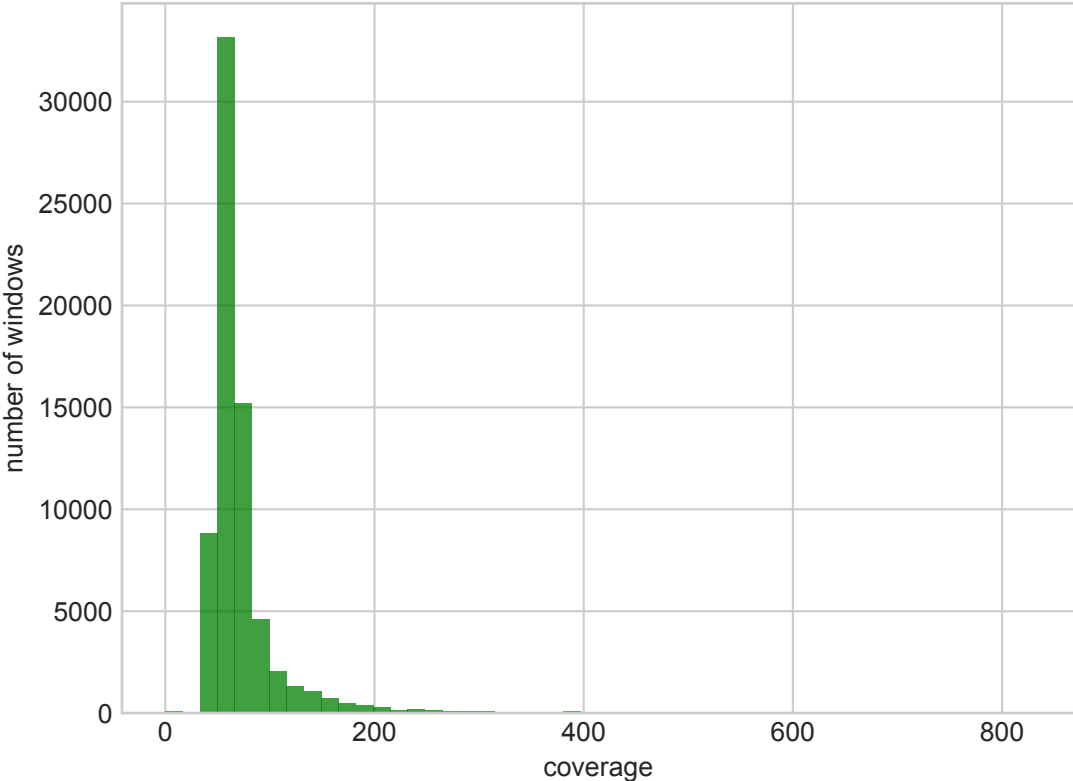
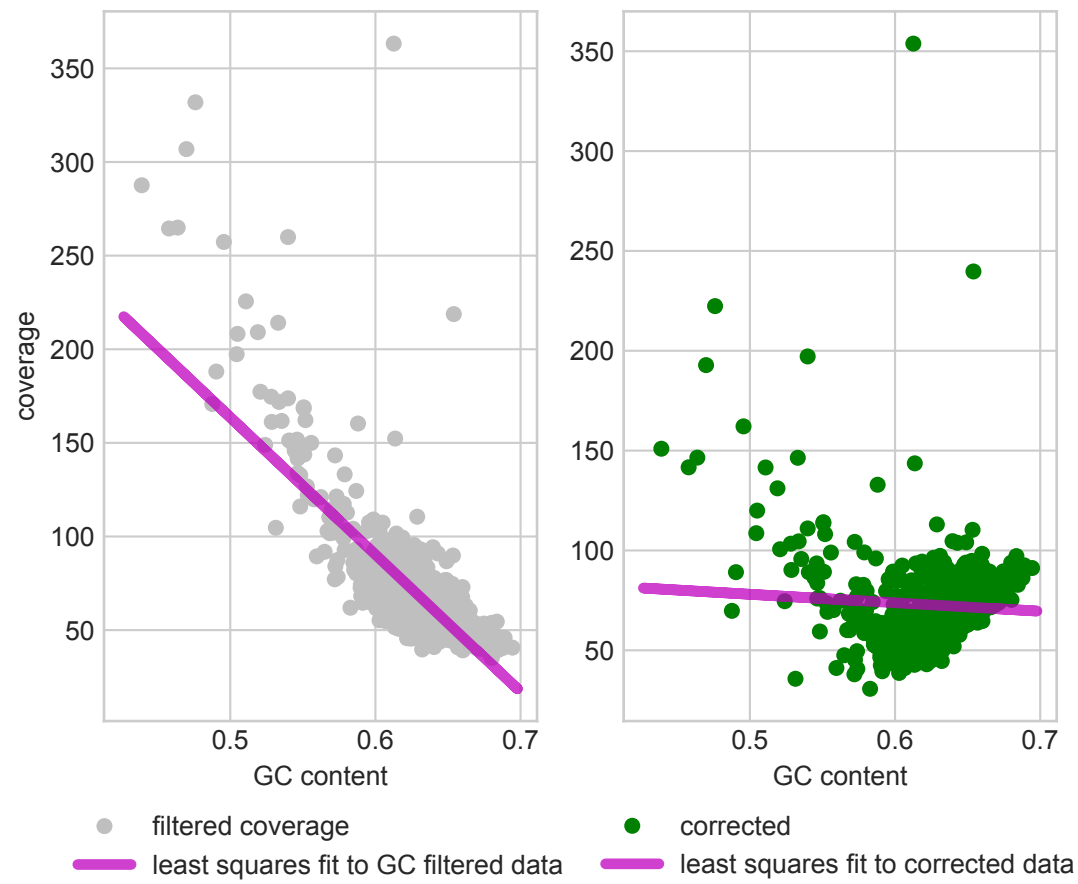


genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016\_KBSGenomes\_Annotate/ATCC13985/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa\_sam/ATCC13985-C  
iRep: 1.76 r^2: 0.98 avg. cov: 72.05 % windows: 99.85



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016\_KBSGenomes\_Annotate/ATCC13985/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa\_sam/ATCC13985-C  
iRep: 1.76 raw iRep: 2.27 GC r^2: 0.73 GC bias: -535.17 avg. cov: 72.05 % windows: 99.85



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016\_KBSGenomes\_Annotate/ATCC13985/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa\_sam/ATCC13985-C  
iRep: 1.76 un-filtered iRep: 1.76 r^2: 0.98 avg. cov: 72.05 % windows: 99.85

