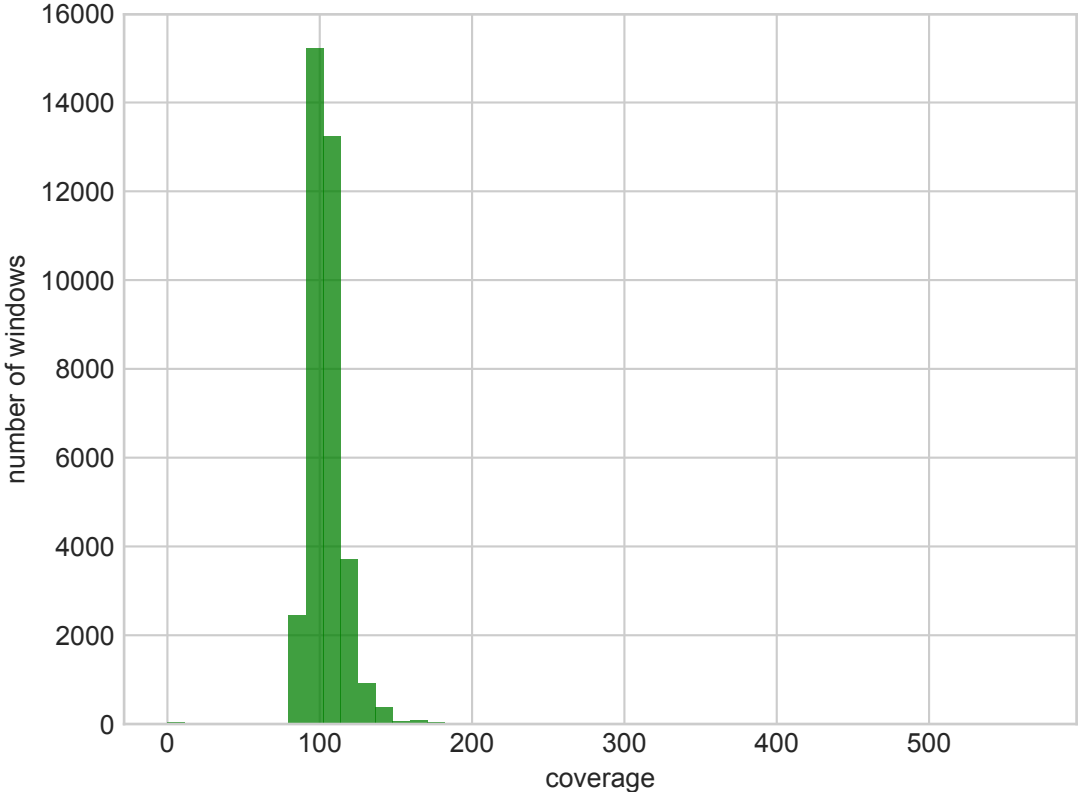
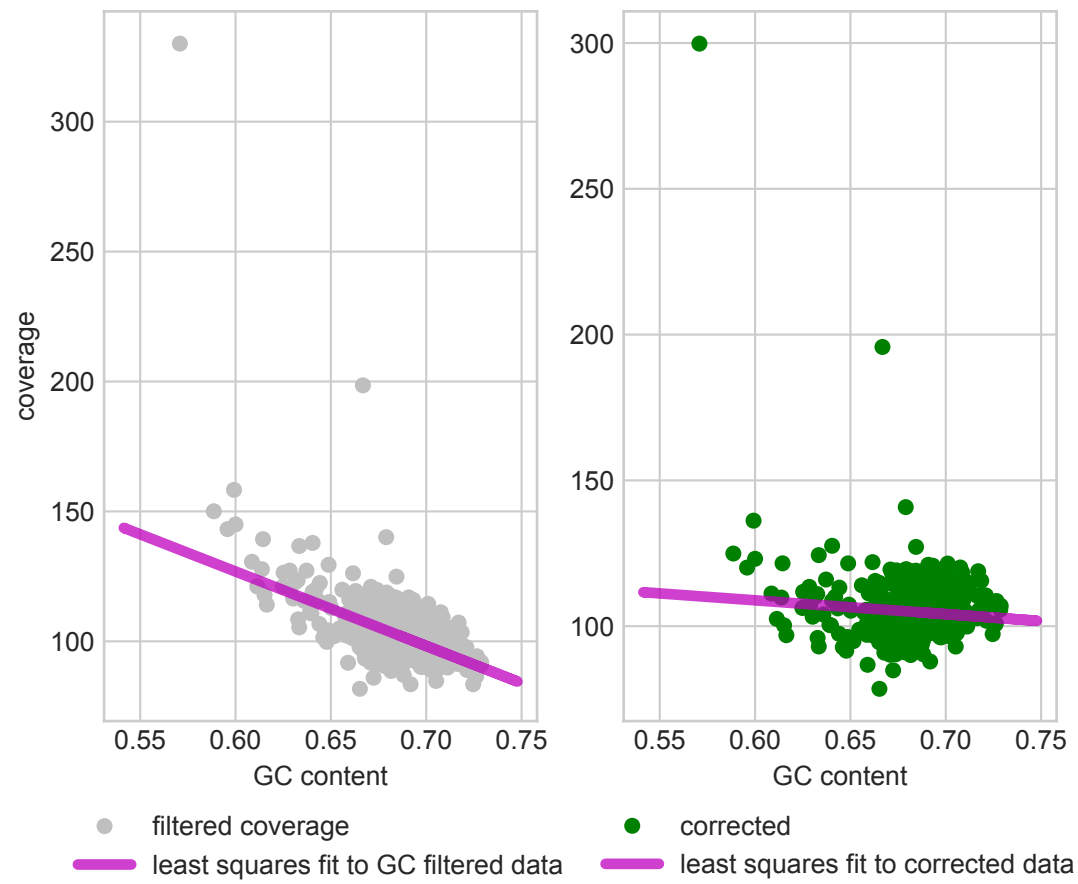


genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0702/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0702-B
iRep: 1.26 r^2: 0.99 avg. cov: 104.86 % windows: 99.90



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0702/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0702-B
iRep: 1.26 raw iRep: 1.31 GC r^2: 0.42 GC bias: -119.23 avg. cov: 104.86 % windows: 99.90



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0702/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0702-B
iRep: 1.26 un-filtered iRep: 1.26 r^2: 0.99 avg. cov: 104.86 % windows: 99.90

