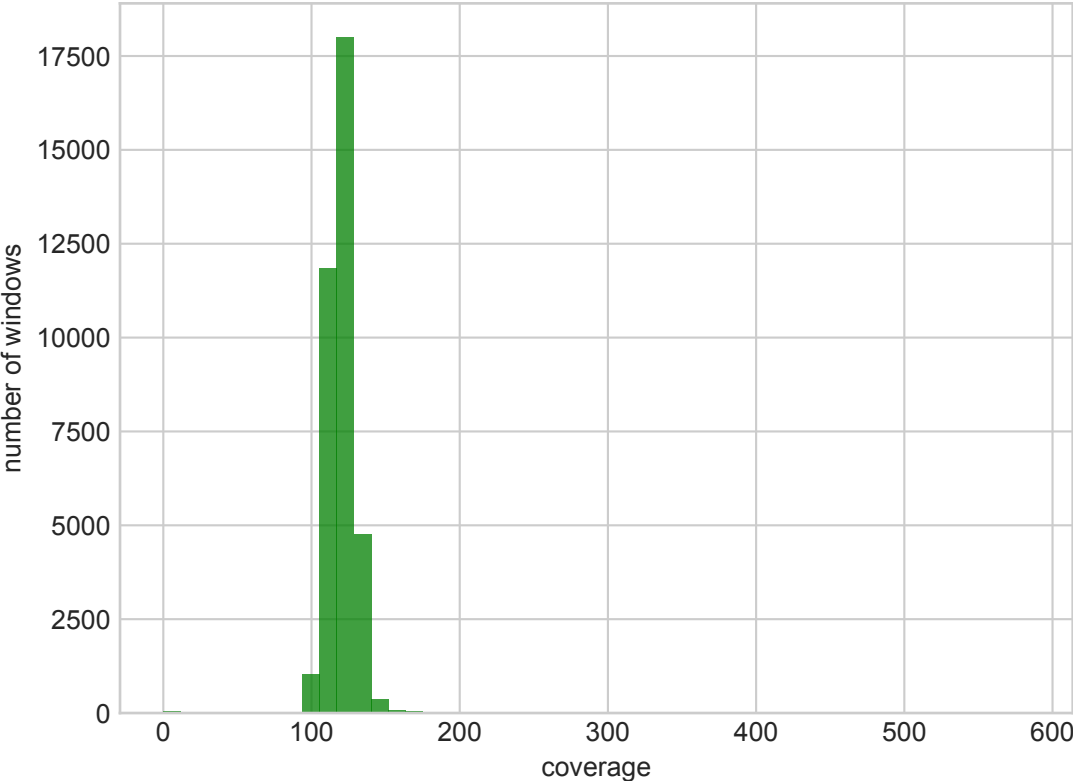
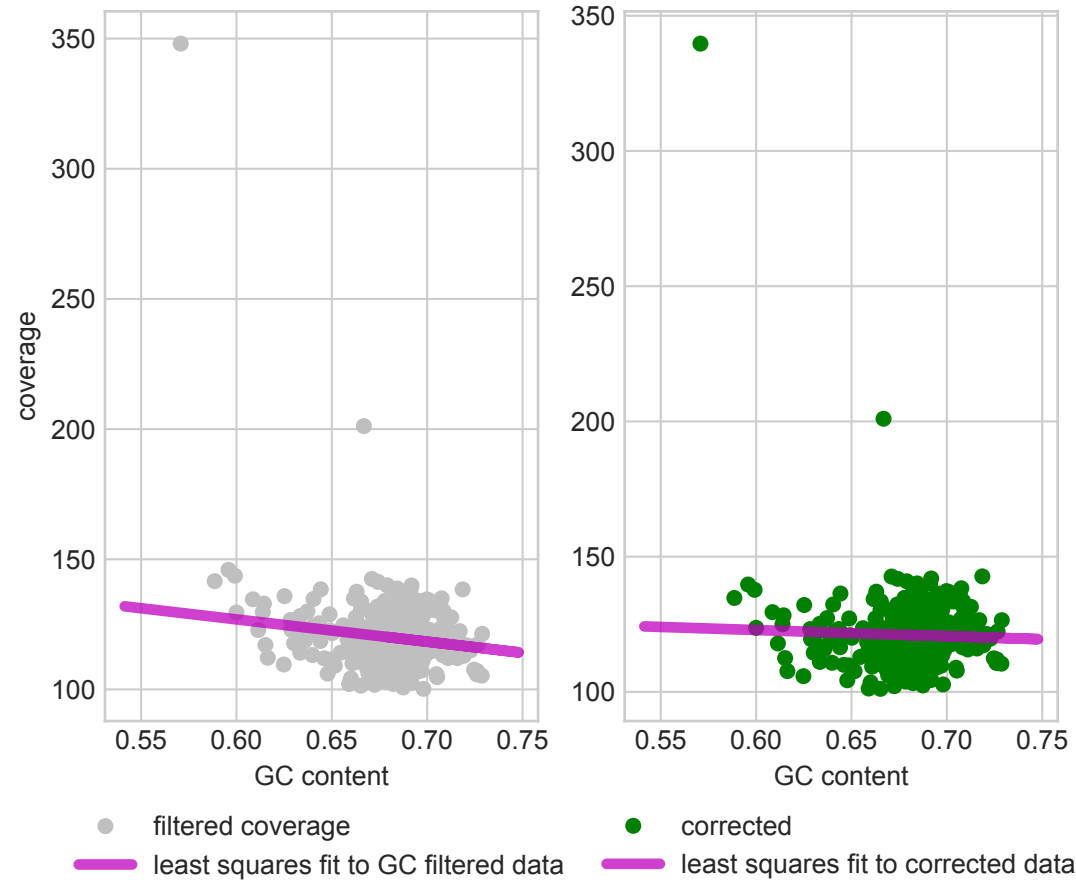


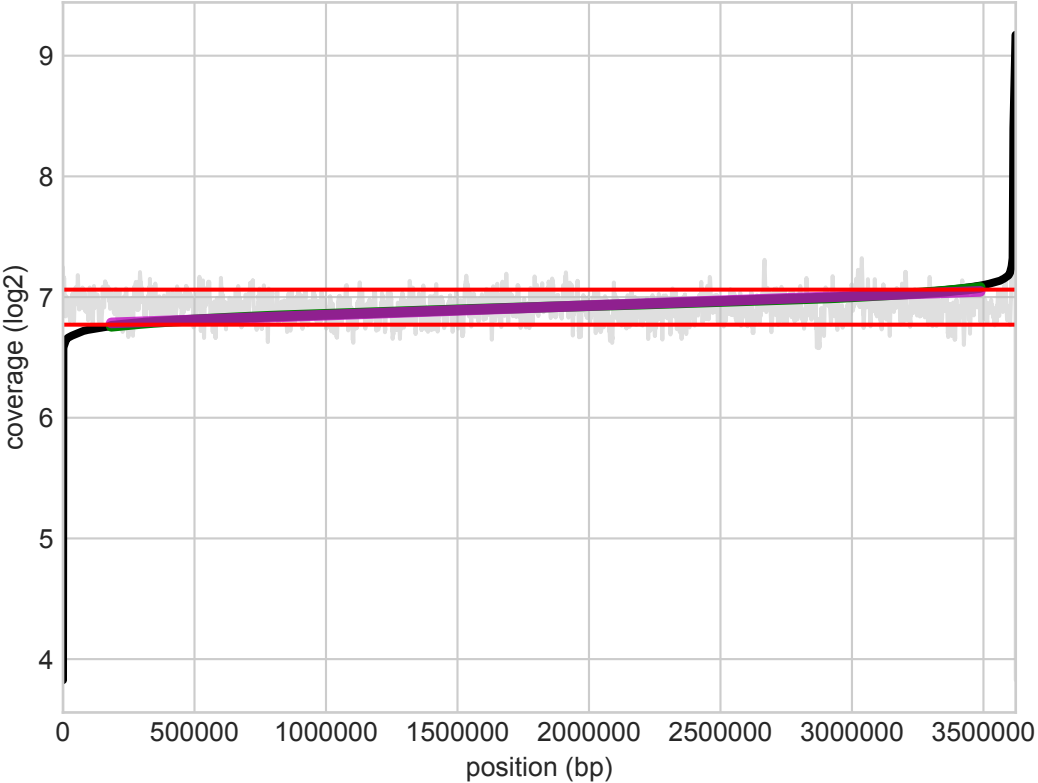
genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0702/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0702-C
iRep: 1.22 r^2: 0.99 avg. cov: 120.85 % windows: 99.90



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0702/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0702-C
iRep: 1.22 raw iRep: 1.23 GC r^2: 0.06 GC bias: -5.20 avg. cov: 120.85 % 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-C
iRep: 1.22 un-filtered iRep: 1.22 r^2 : 0.99 avg. cov: 120.85 % windows: 99.90



- filtered
- sorted
- trimmed
- least squares fit to trimmed
- Ori/Ter