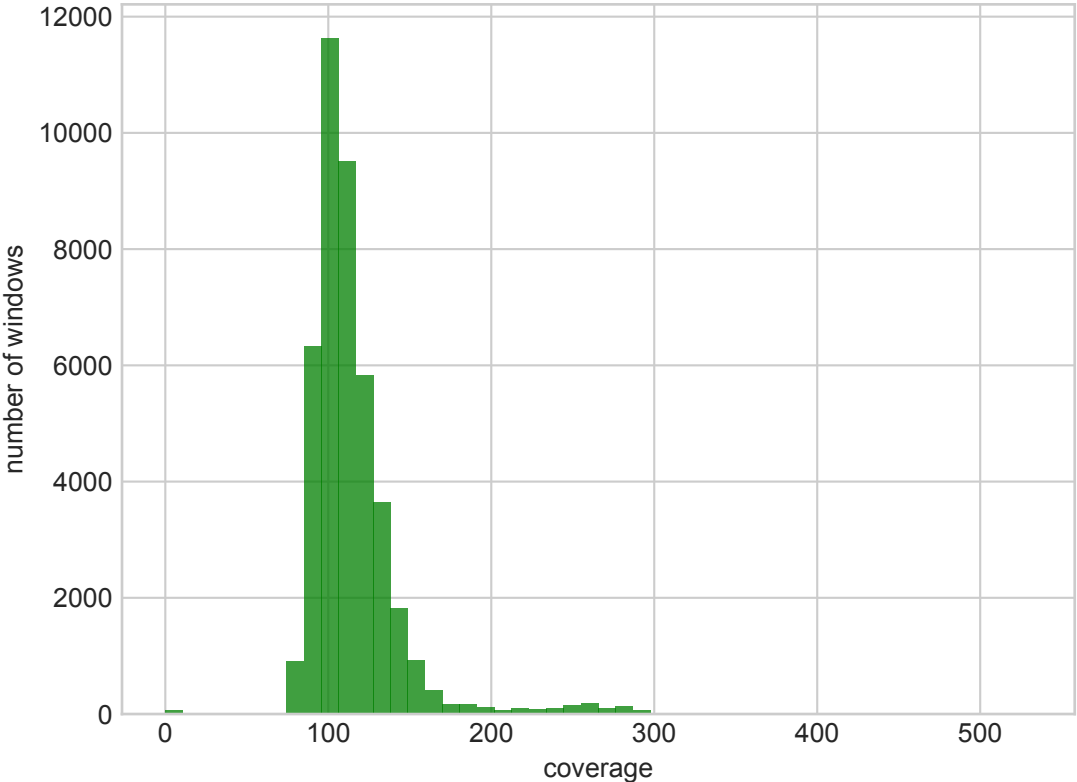
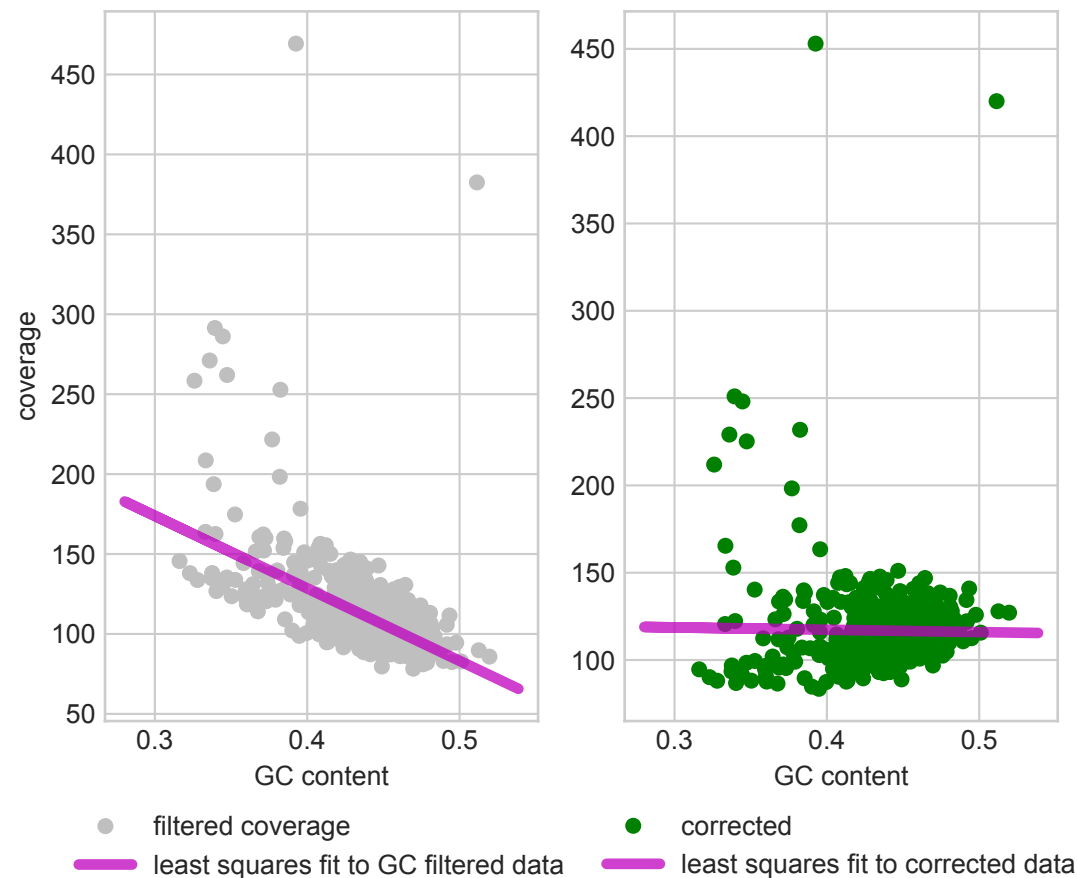
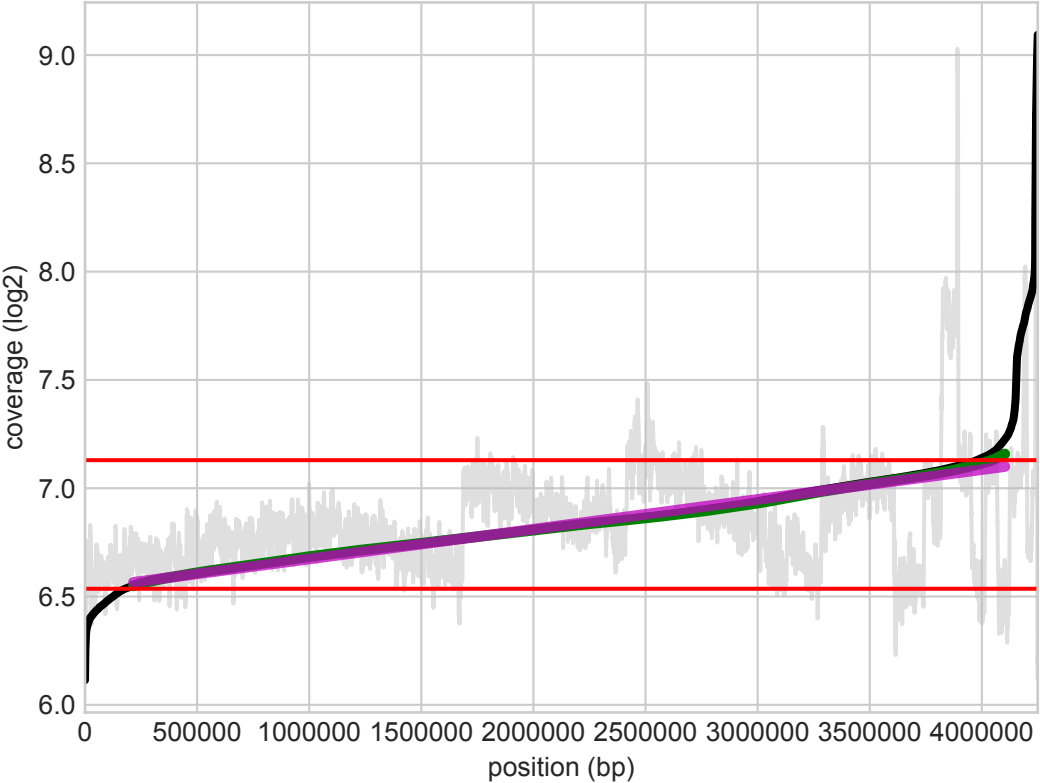


genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0812/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0812-D
iRep: 1.51 r^2: 0.99 avg. cov: 115.35 % windows: 99.85



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0812/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0812-D
iRep: 1.51 raw iRep: 1.63 GC r^2: 0.43 GC bias: -195.52 avg. cov: 115.35 % windows: 99.85





filtered
sorted
trimmed
least squares fit to trimmed
Ori/Ter