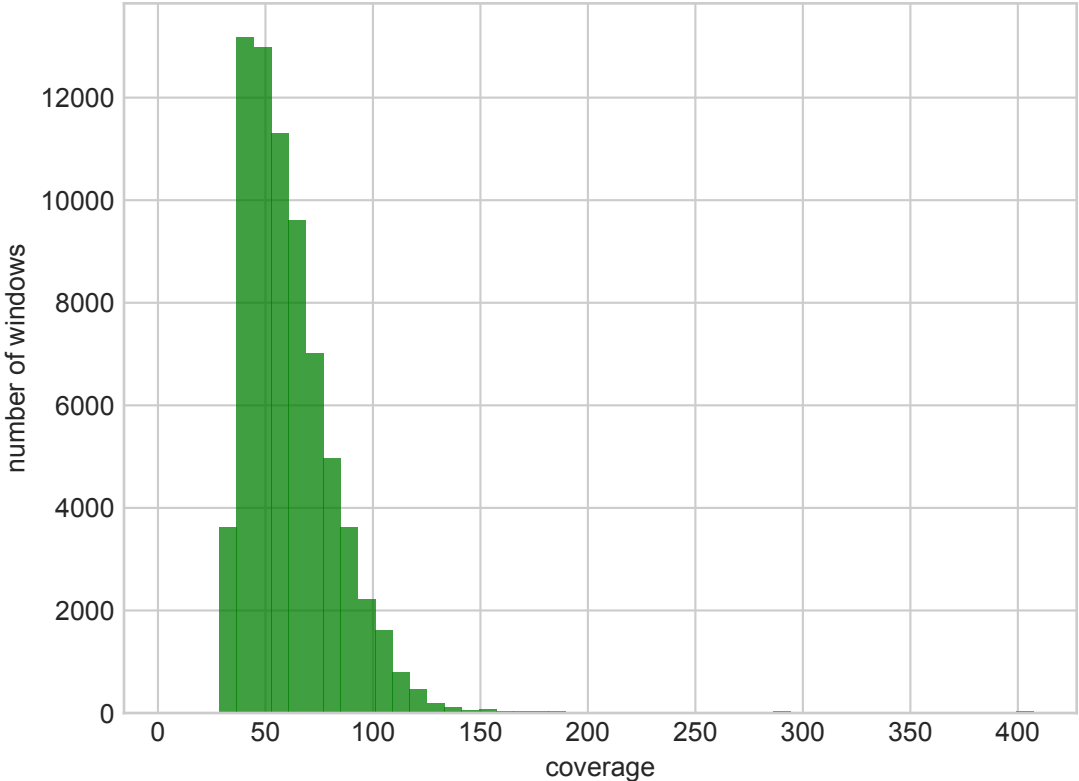
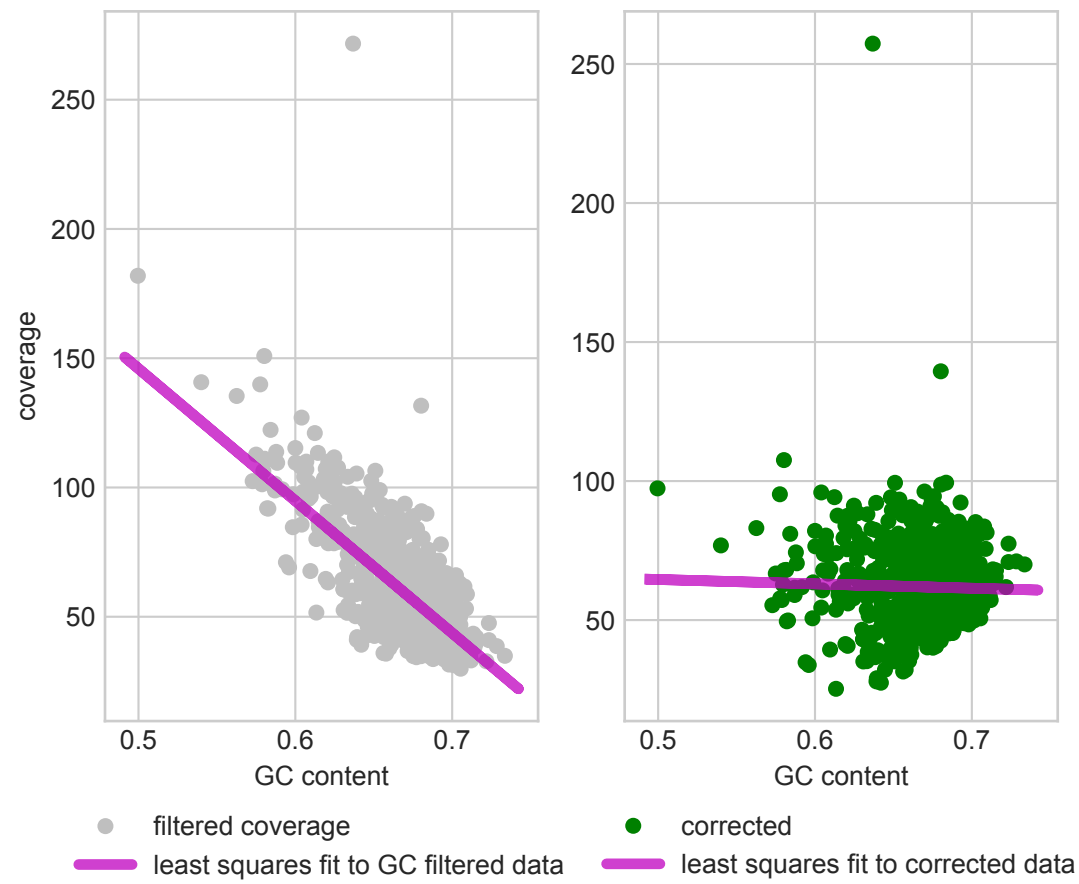


genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0801/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0801-C
iRep: 2.00 r^2: 0.99 avg. cov: 61.63 % windows: 99.99



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0801/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0801-C
iRep: 2.00 raw iRep: 2.70 GC r^2: 0.55 GC bias: -280.58 avg. cov: 61.63 % windows: 99.99



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/KBS0801/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/KBS0801-C
iRep: 2.00 un-filtered iRep: 2.00 r^2: 0.99 avg. cov: 61.63 % windows: 99.99

