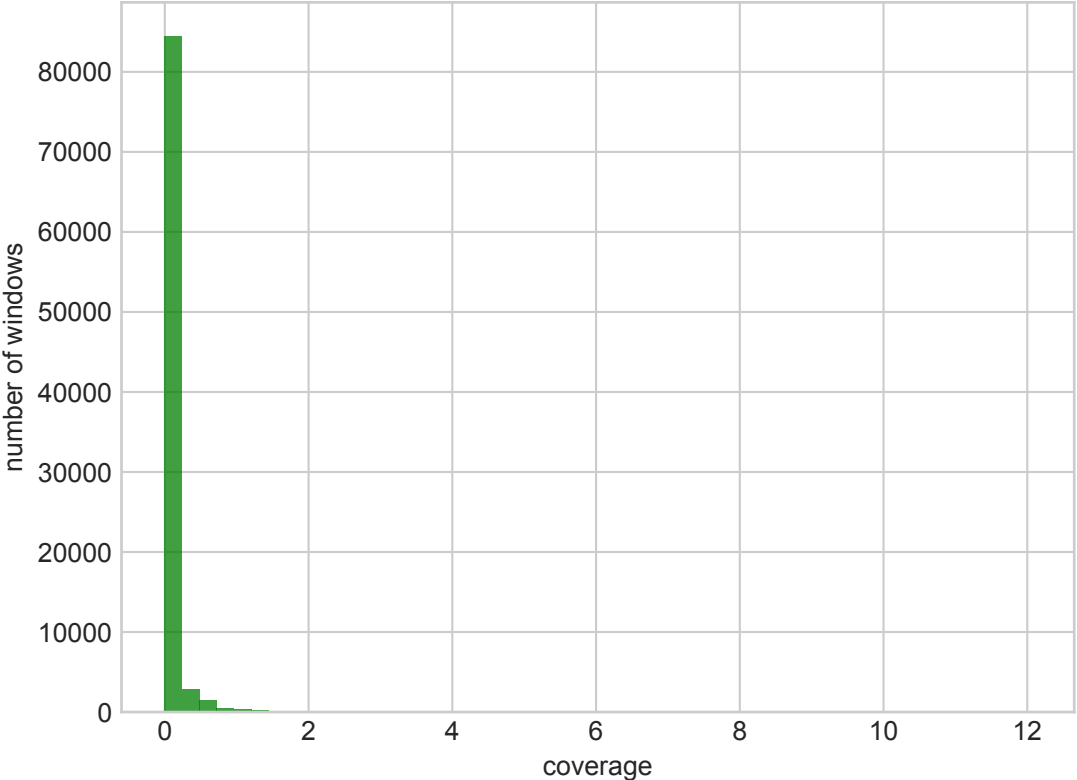
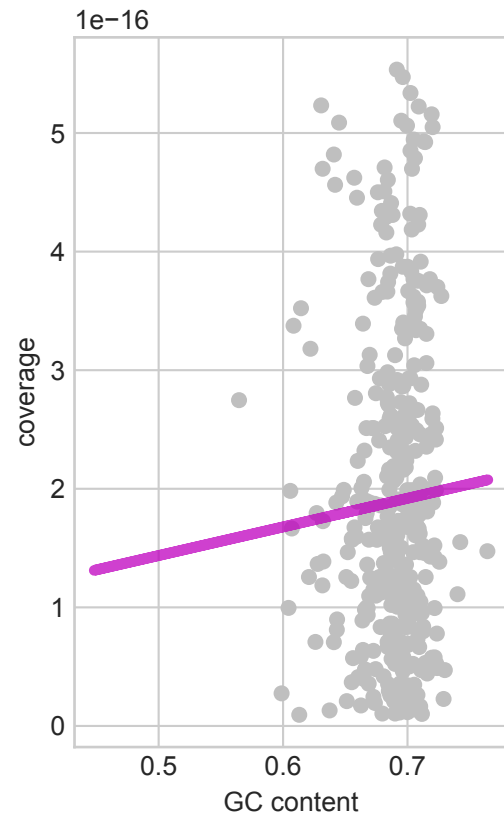


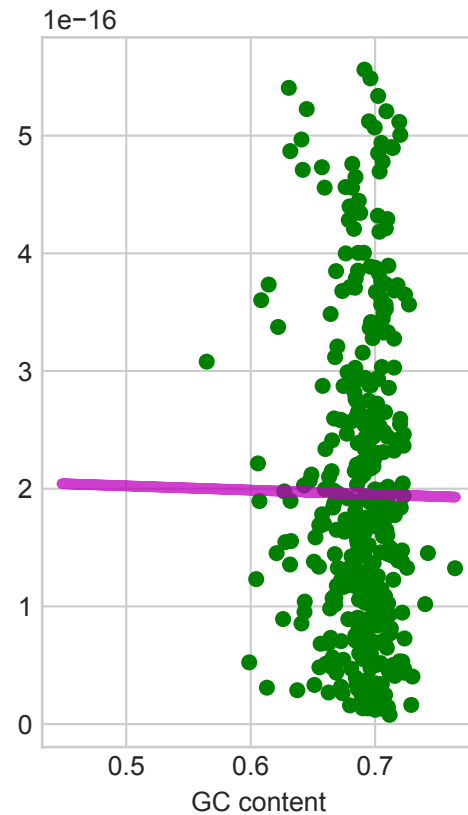
genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2015\_SoilGenomes\_Annotate/KBS0706/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa\_sam/KBS0706-C  
iRep: n/a r^2: 0.97 avg. cov: 0.05 % windows: 40.66



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2015\_SoilGenomes\_Annotate/KBS0706/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa\_sam/KBS0706-C  
iRep: n/a raw iRep: 16.04 GC r<sup>2</sup>: 0.00 GC bias: 0.00 avg. cov: 0.05 % windows: 40.66



● filtered coverage  
— least squares fit to GC filtered data



● corrected  
— least squares fit to corrected data

genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2015\_SoilGenomes\_Annotate/KBS0706/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa\_sam/KBS0706-C  
iRep: n/a un-filtered iRep: 14.62 r^2: 0.97 avg. cov: 0.05 % windows: 40.66

