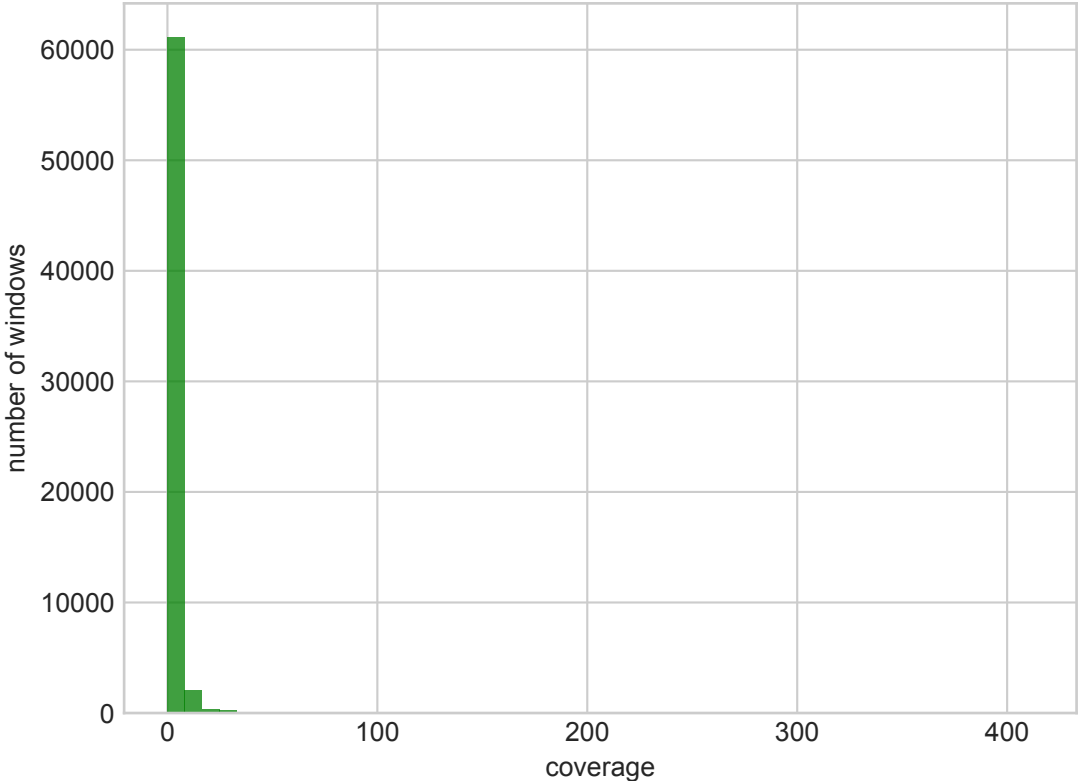
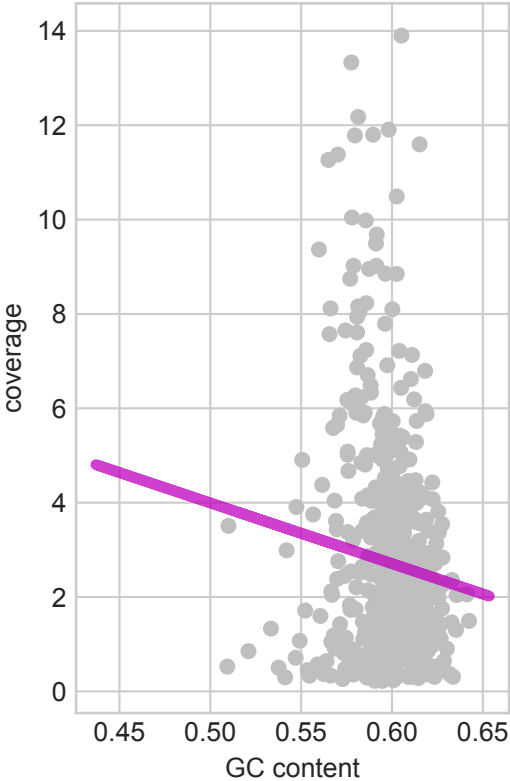


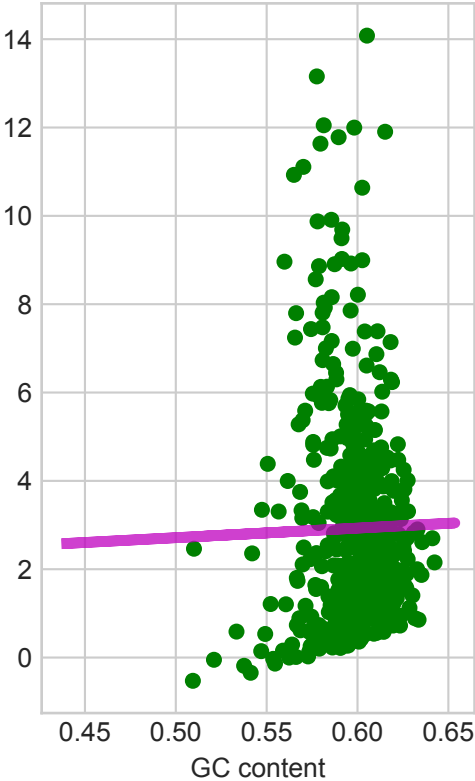
genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/ATCC43928/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/ATCC43928-A
iRep: n/a r^2: 0.97 avg. cov: 3.22 % windows: 80.07



genome: /Users/WRShoemaker/GitHub/LTDE/data/genomes/2016_KBSGenomes_Annotate/ATCC43928/G-Chr1 sample: /Users/WRShoemaker/GitHub/LTDE/data/bwa_sam/ATCC43928-A
iRep: n/a raw iRep: 13.85 GC r²: 0.01 GC bias: -0.19 avg. cov: 3.22 % windows: 80.07



● filtered coverage
— least squares fit to GC filtered data



● corrected
— least squares fit to corrected data

