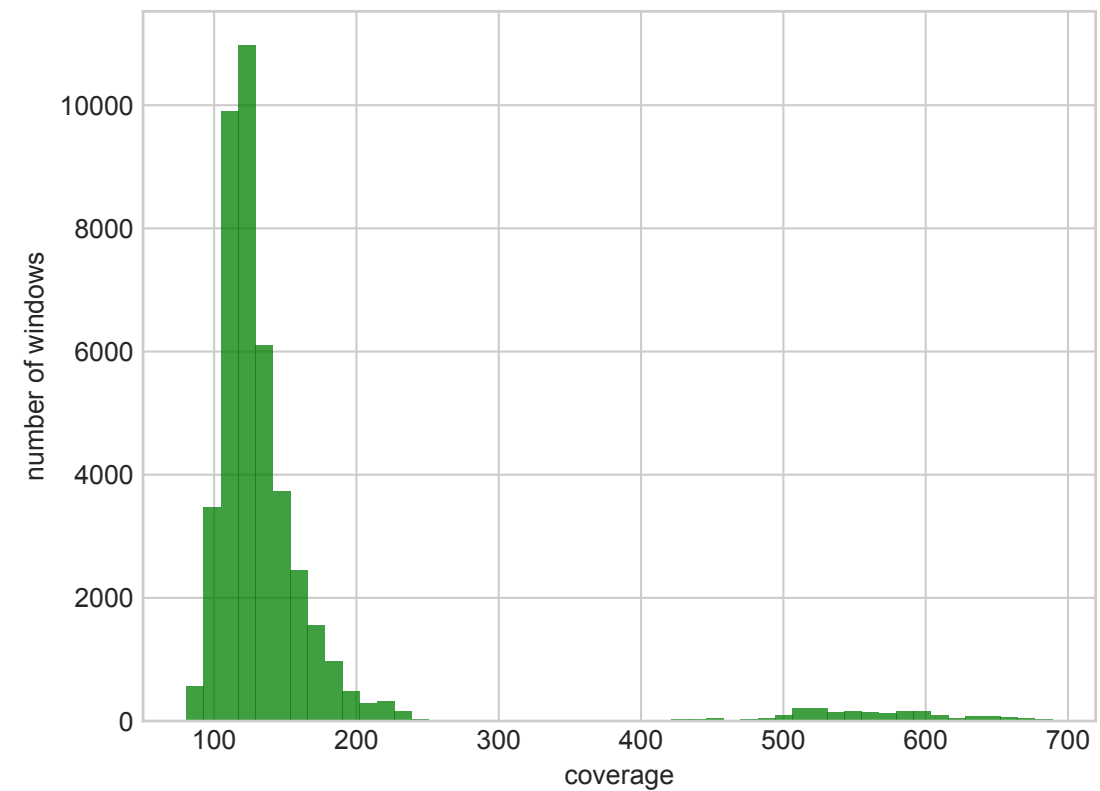
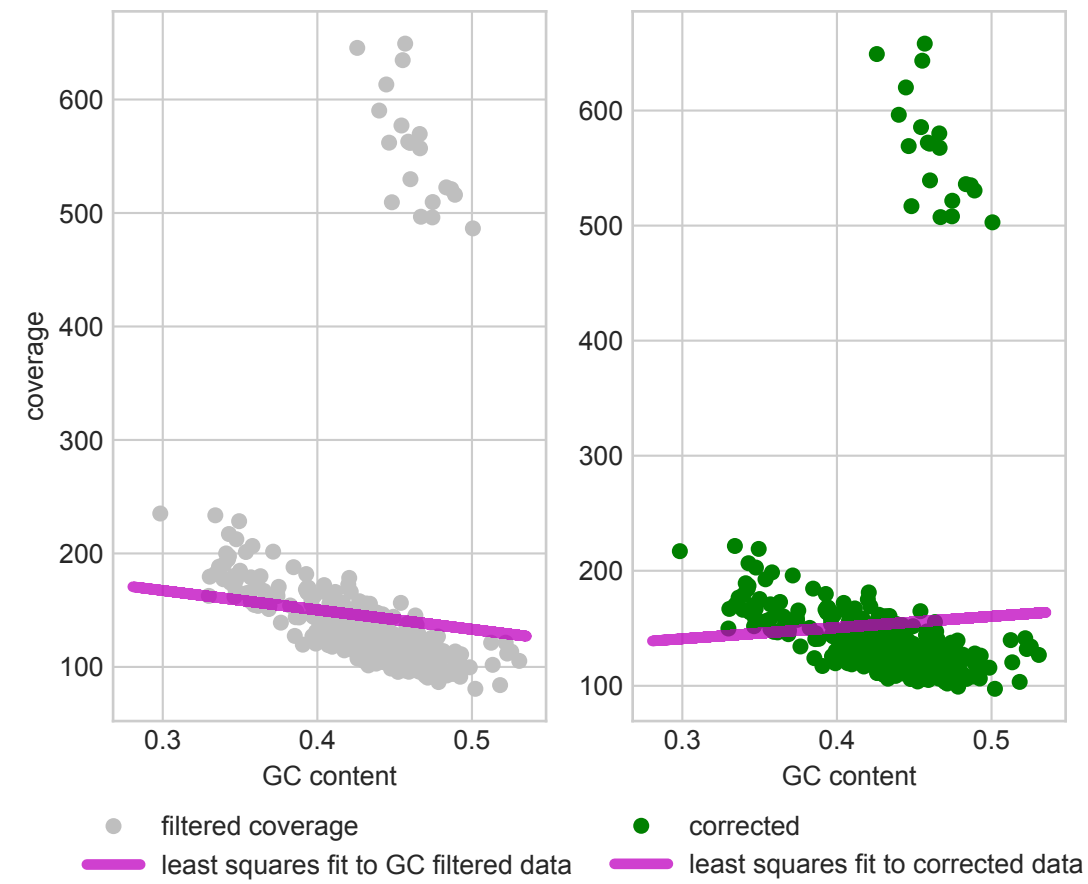


genome: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/reference_assemblies_task2/Bacillus_subtilis_NCIB_3610/GCA_002055965.1_ASM205596v1_genomic sample: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/bwa_fna/D300/Sample_L1B4-300_mapped_sort_NOdup_sort_merged_sort
iRep: 1.61 r²: 0.90 avg. cov: 149.49 % windows: 100.00



genome: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/reference_assemblies_task2/Bacillus_subtilis_NCIB_3610/GCA_002055965.1_ASM205596v1_genomic sample: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/bwa_fna/D300/Sample_L1B4-300_mapped_sort_NOdup_sort_merged_sort
iRep: 1.61 raw iRep: 1.82 GC r^2: 0.01 GC bias: -1.05 avg. cov: 149.49 % windows: 100.00



genome: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/reference_assemblies_task2/Bacillus_subtilis_NCIB_3610/GCA_002055965.1_ASM205596v1_genomic sample: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/bwa_fna/D300/Sample_L1B4-300_mapped_sort_NOdup_sort_merged_sort
iRep: 1.61 un-filtered iRep: 1.61 r^2: 0.90 avg. cov: 149.49 % windows: 100.00

