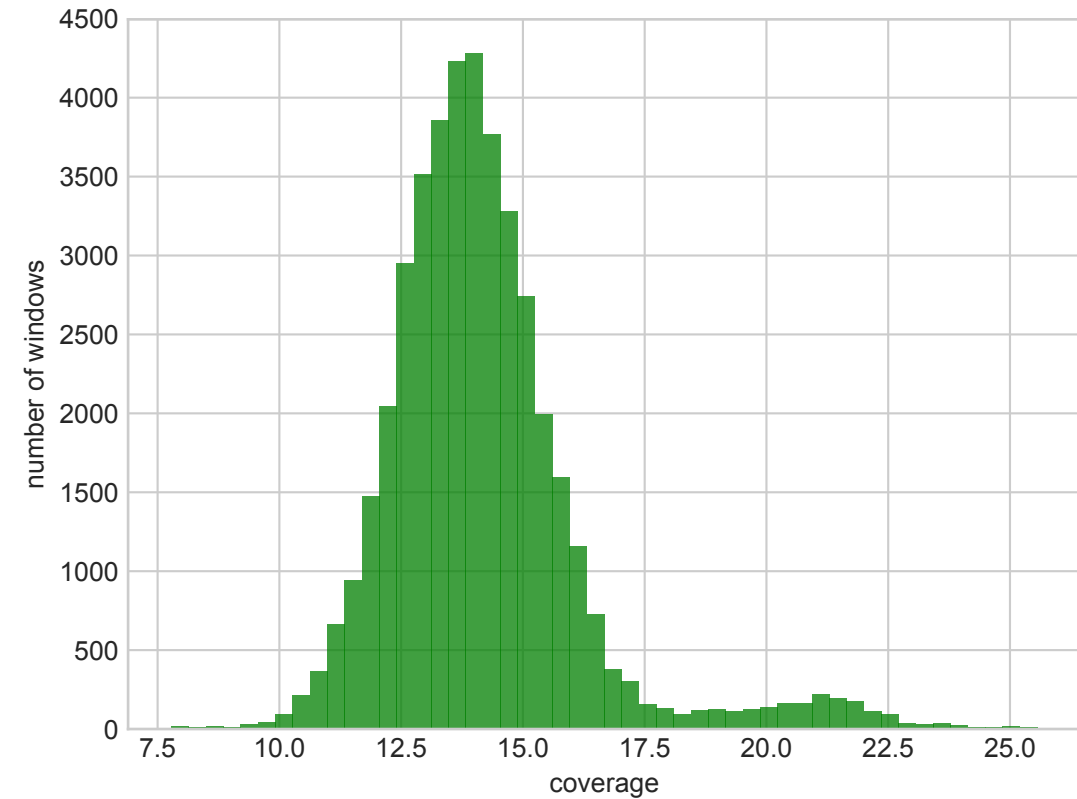
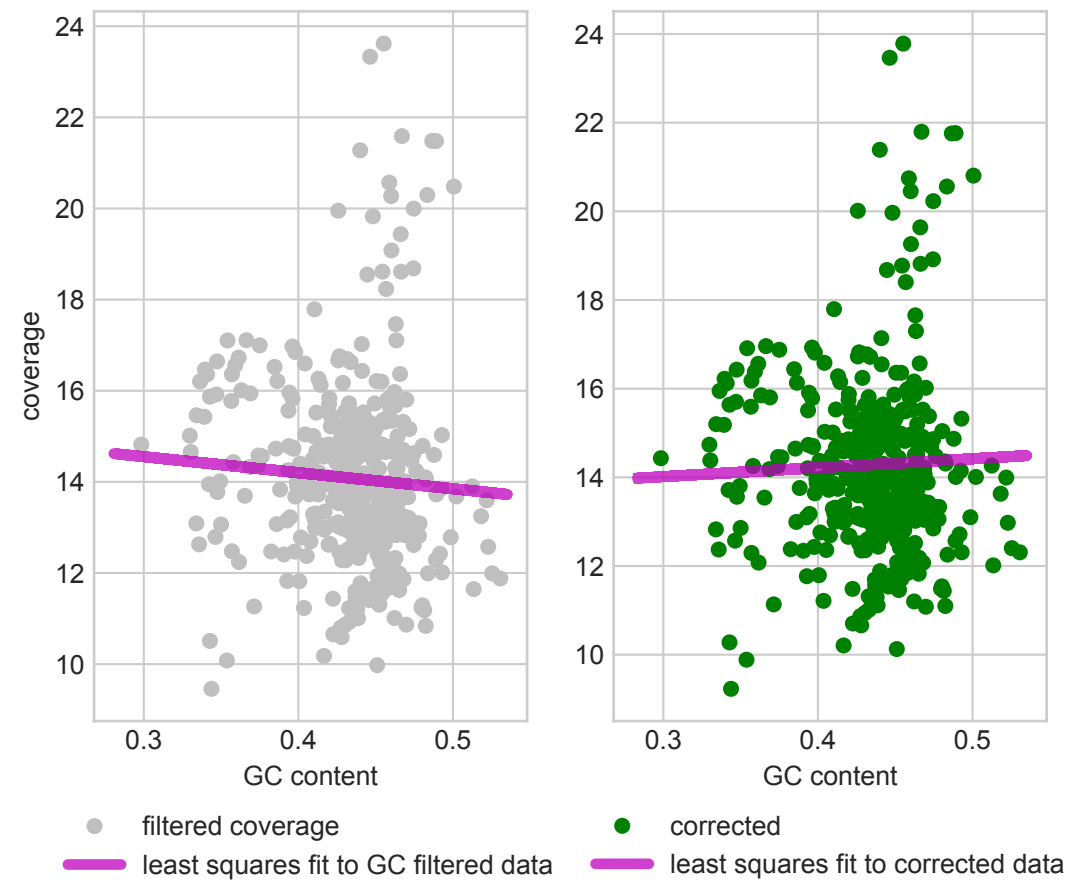


genome: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/reference\_assemblies\_task2/Bacillus\_subtilis\_NCIB\_3610/GCA\_002055965.1\_ASM205596v1\_genomic sample: /Users/WRShoemaker/GitHub/Task2/PoolPopSeq/data/bwa\_fna/D300/Sample\_L2B3-300\_mapped\_sort\_NOdup\_sort\_merged\_sort  
iRep: 1.38 r^2: 0.98 avg. cov: 14.17 % 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\_L2B3-300\_mapped\_sort\_NOdup\_sort\_merged\_sort  
iRep: 1.38 raw iRep: 1.39 GC r^2: 0.00 GC bias: -0.02 avg. cov: 14.17 % 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\_L2B3-300\_mapped\_sort\_NOdup\_sort\_merged\_sort  
iRep: 1.38 un-filtered iRep: 1.38 r^2: 0.98 avg. cov: 14.17 % windows: 100.00

