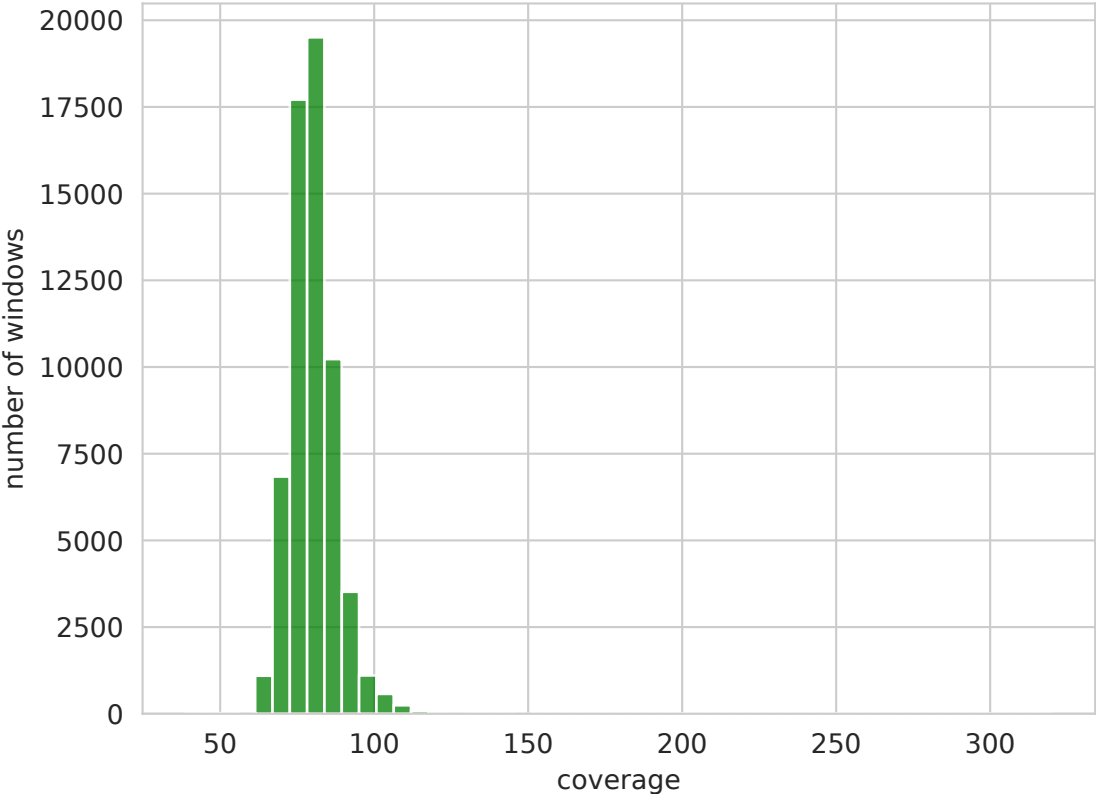
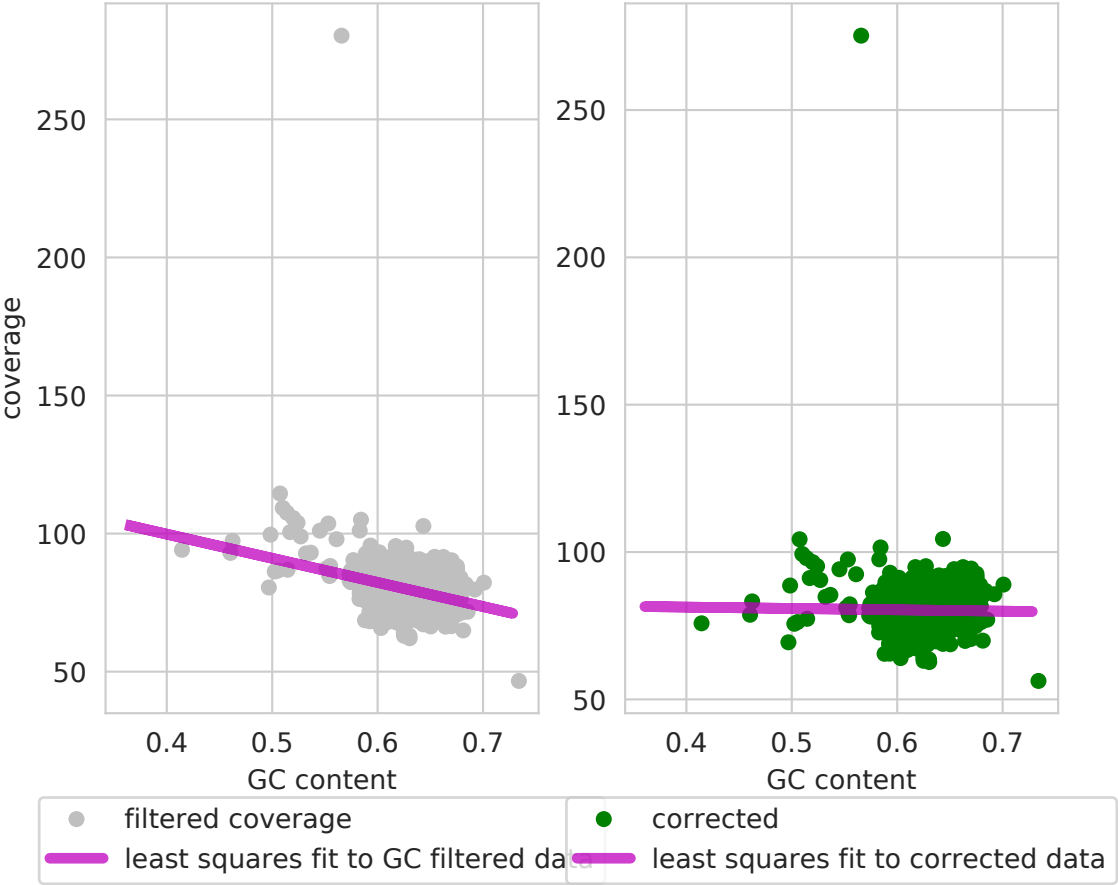


genome: /N/dc2/projects/muri2/Task2/LTDE/data/genomes\_ncbi/KBS0711/GCF\_005937955.1\_ASM593795v1\_genomic sample: /N/dc2/projects/muri2/Task2/LTDE/data/bwa\_bam/KBS0711-A  
iRep: 1.28    r<sup>2</sup>: 0.99    avg. cov: 80.32    % windows: 100.00



genome: /N/dc2/projects/muri2/Task2/LTDE/data/genomes\_ncbi/KBS0711/GCF\_005937955.1\_ASM593795v1\_genomic sample: /N/dc2/projects/muri2/Task2/LTDE/data/bwa\_bam/KBS0711-A  
iRep: 1.28 raw iRep: 1.29 GC r<sup>2</sup>: 0.17 GC bias: -14.74 avg. cov: 80.32 % windows: 100.00



genome: /N/dc2/projects/muri2/Task2/LTDE/data/genomes\_ncbi/KBS0711/GCF\_005937955.1\_ASM593795v1\_genomic sample: /N/dc2/projects/muri2/Task2/LTDE/data/bwa\_bam/KBS0711-A  
iRep: 1.28 un-filtered iRep: 1.28  $r^2$ : 0.99 avg. cov: 80.32 % windows: 100.00

