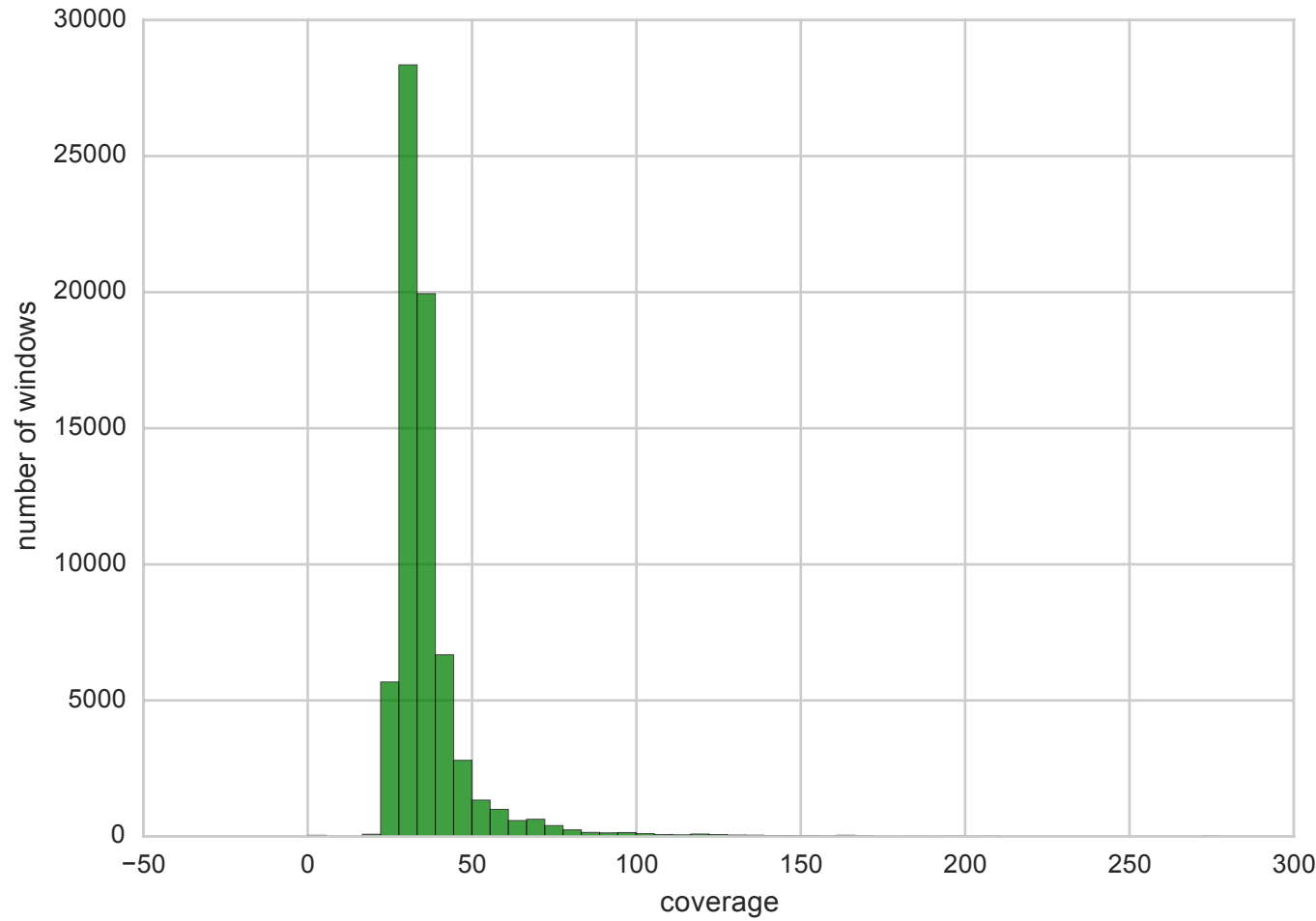
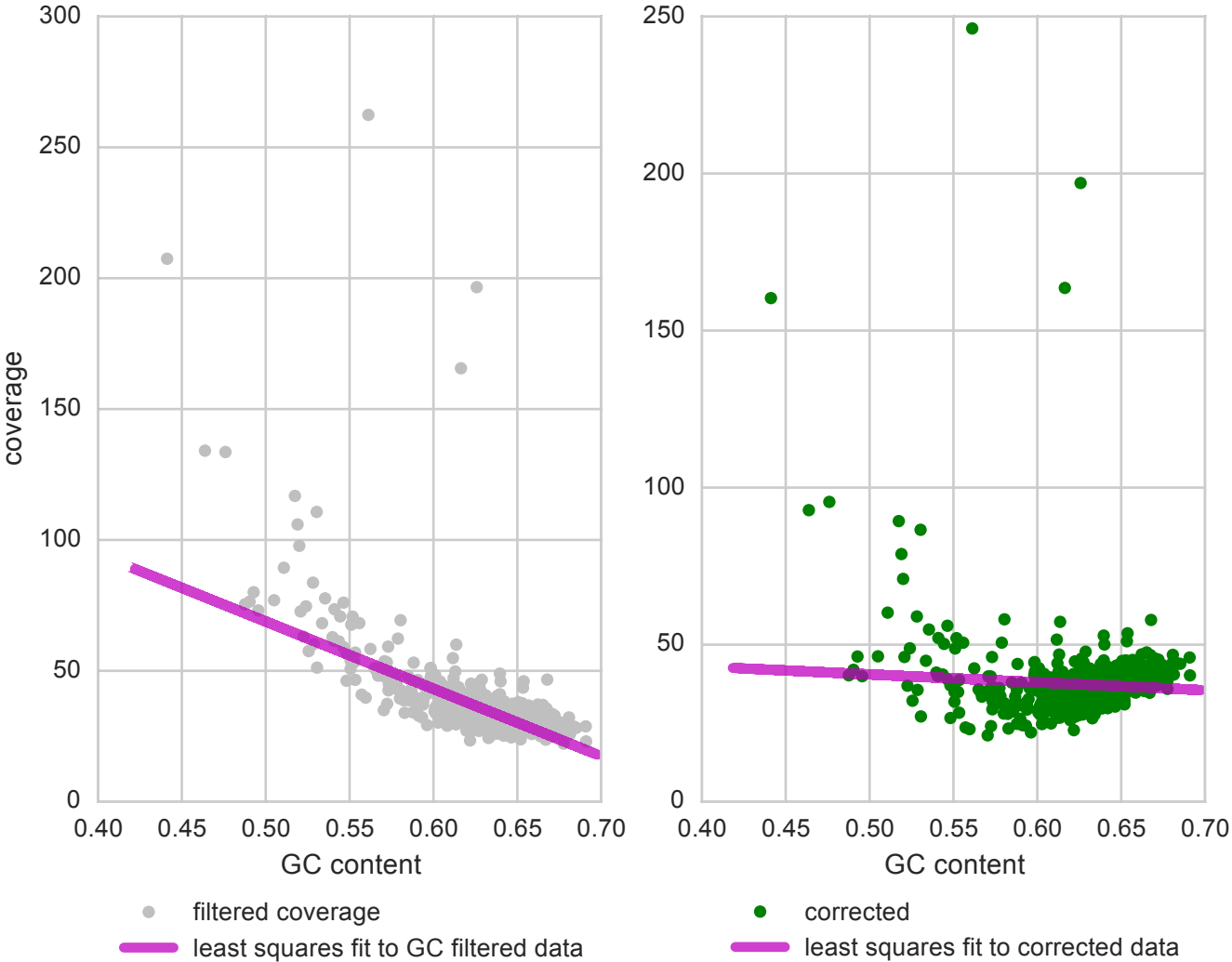
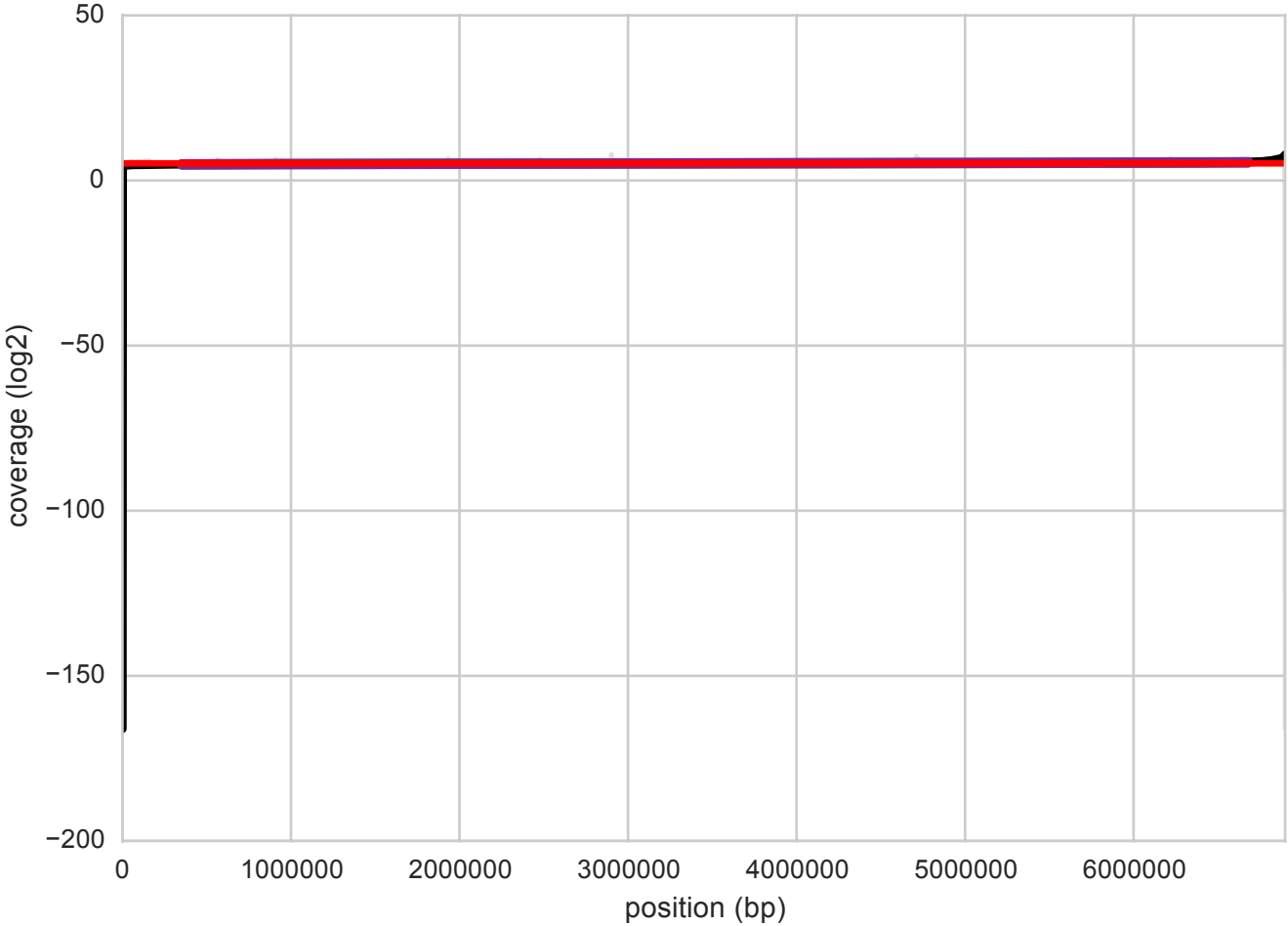


genome: /Users/WRShoemaker/github/Task2/LTDE/data/2016\_KBSGenomes\_Annotate/ATCC13985/G-Chr1 sample: /Users/WRShoemaker/github/Task2/LTDE/data/iRep/ATCC13985/GSF1046-ATCC13985-A\_S1\_mapped\_sort\_NOdup\_  
iRep: 1.51 r^2: 0.98 avg. cov: 36.91 % windows: 99.91



genome: /Users/WRShoemaker/github/Task2/LTDE/data/2016\_KBSGenomes\_Annotate/ATCC13985/G-Chr1 sample: /Users/WRShoemaker/github/Task2/LTDE/data/iRep/ATCC13985/GSF1046-ATCC13985-A\_S1\_mapped\_sort\_NOdup\_  
iRep: 1.51 raw iRep: 1.77 GC r^2: 0.67 GC bias: -172.06 avg. cov: 36.91 % windows: 99.91





— filtered  
— sorted  
— trimmed  
— least squares fit to trimmed  
— Ori/Ter