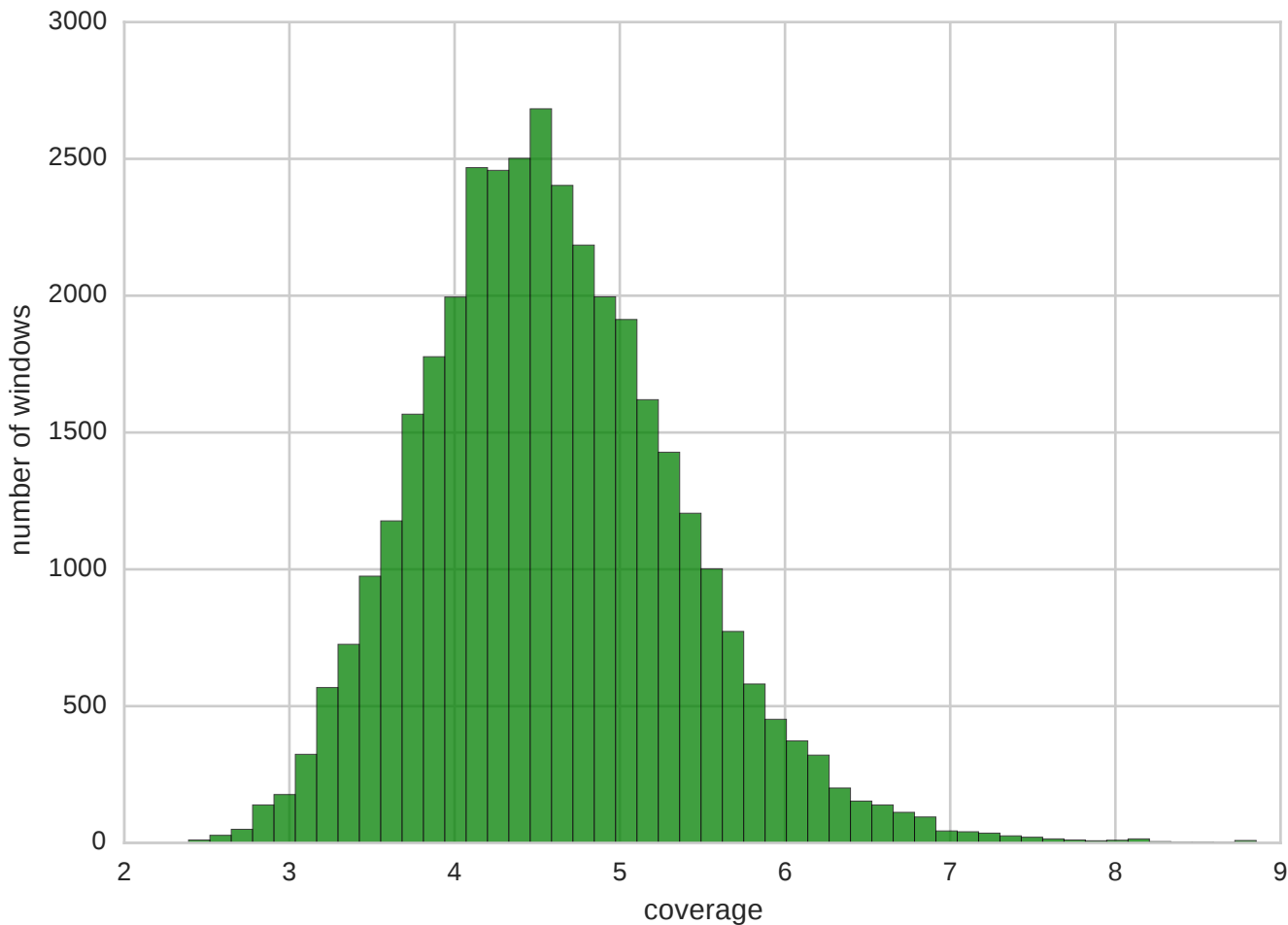
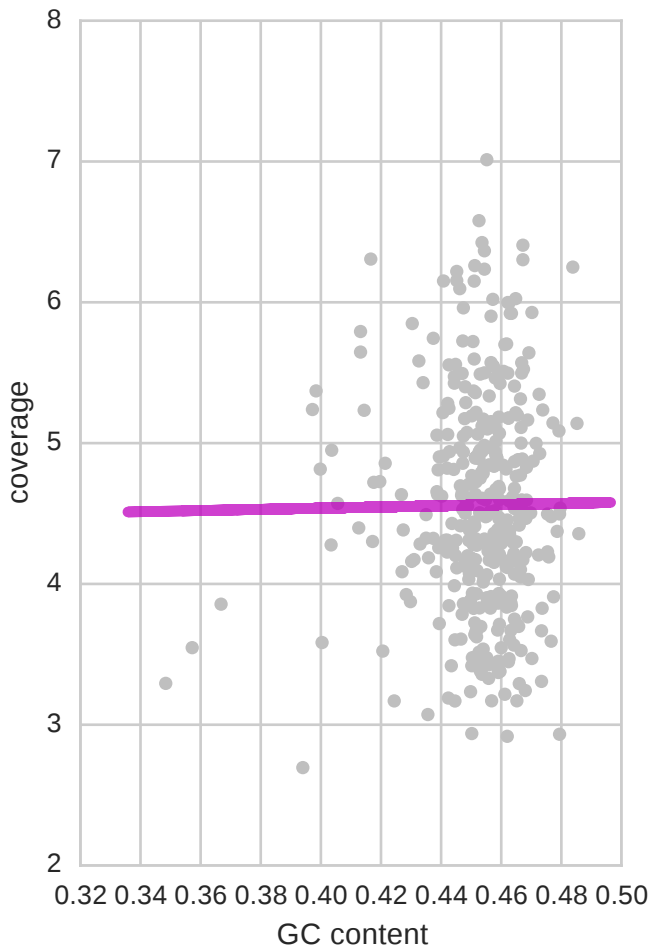


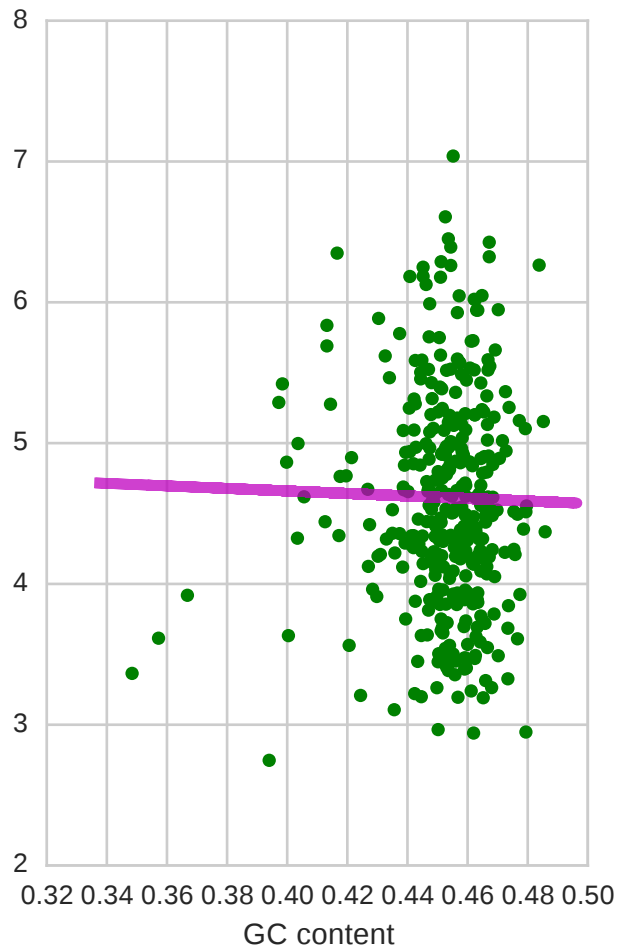
genome: ./bins/bacla\_vizbin1-contigs sample: ./splitBam/bacla\_vizbin1/DNA-Pieter-17  
iRep: n/a r<sup>2</sup>: 0.99 avg. cov: 4.59 % windows: 100.00



genome: ./bins/bacla\_vizbin1-contigs sample: ./splitBam/bacla\_vizbin1/DNA-Pieter-17  
iRep: n/a raw iRep: 1.66 GC r<sup>2</sup>: 0.00 GC bias: 0.00 avg. cov: 4.59 % windows: 100.00

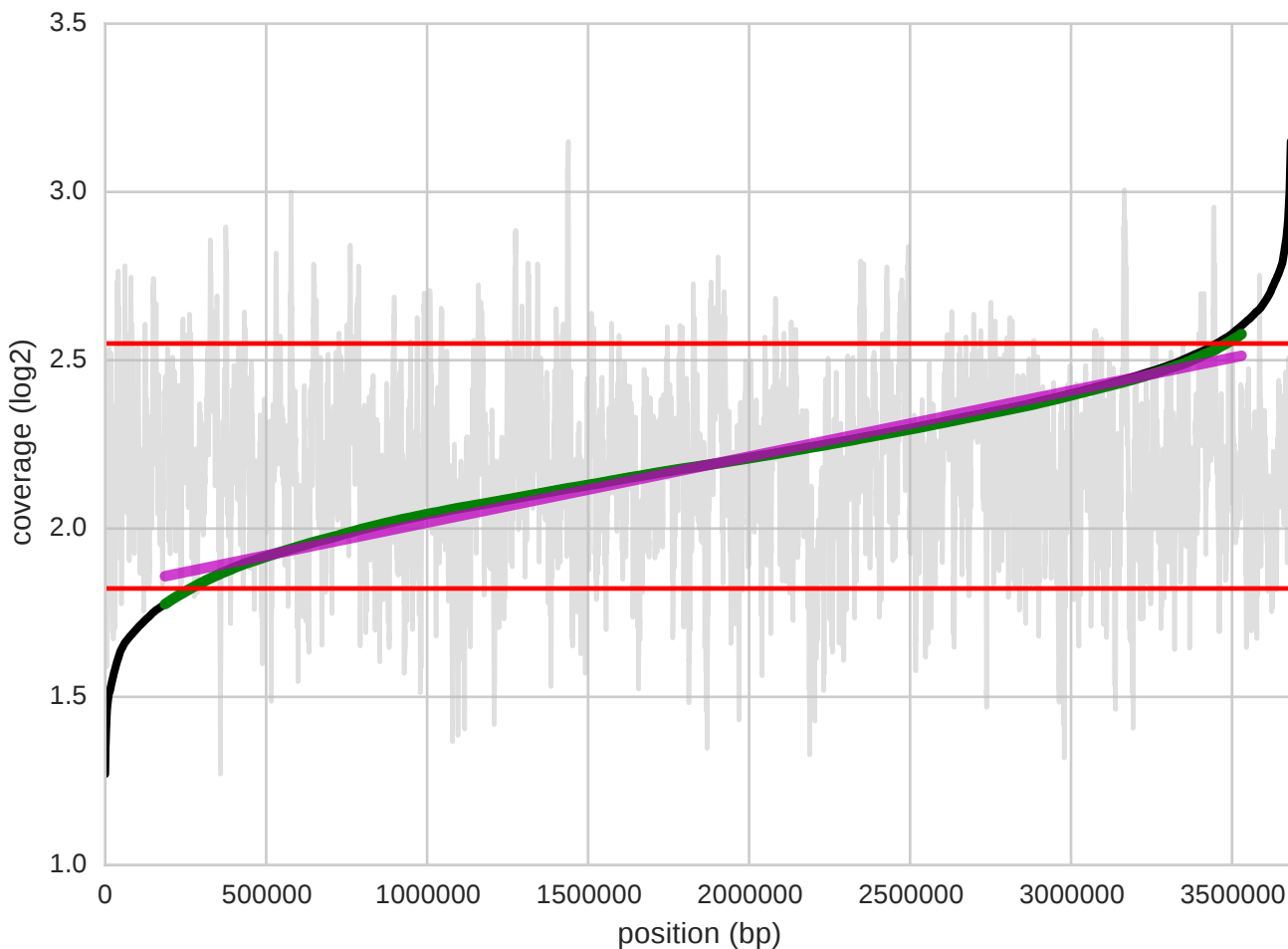


● filtered coverage  
— least squares fit to GC filtered data



● corrected  
— least squares fit to corrected data

genome: ./bins/bacla\_vizbin1-contigs sample: ./splitBam/bacla\_vizbin1/DNA-Pieter-17  
iRep: n/a un-filtered iRep: 1.66  $r^2$ : 0.99 avg. cov: 4.59 % windows: 100.00



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