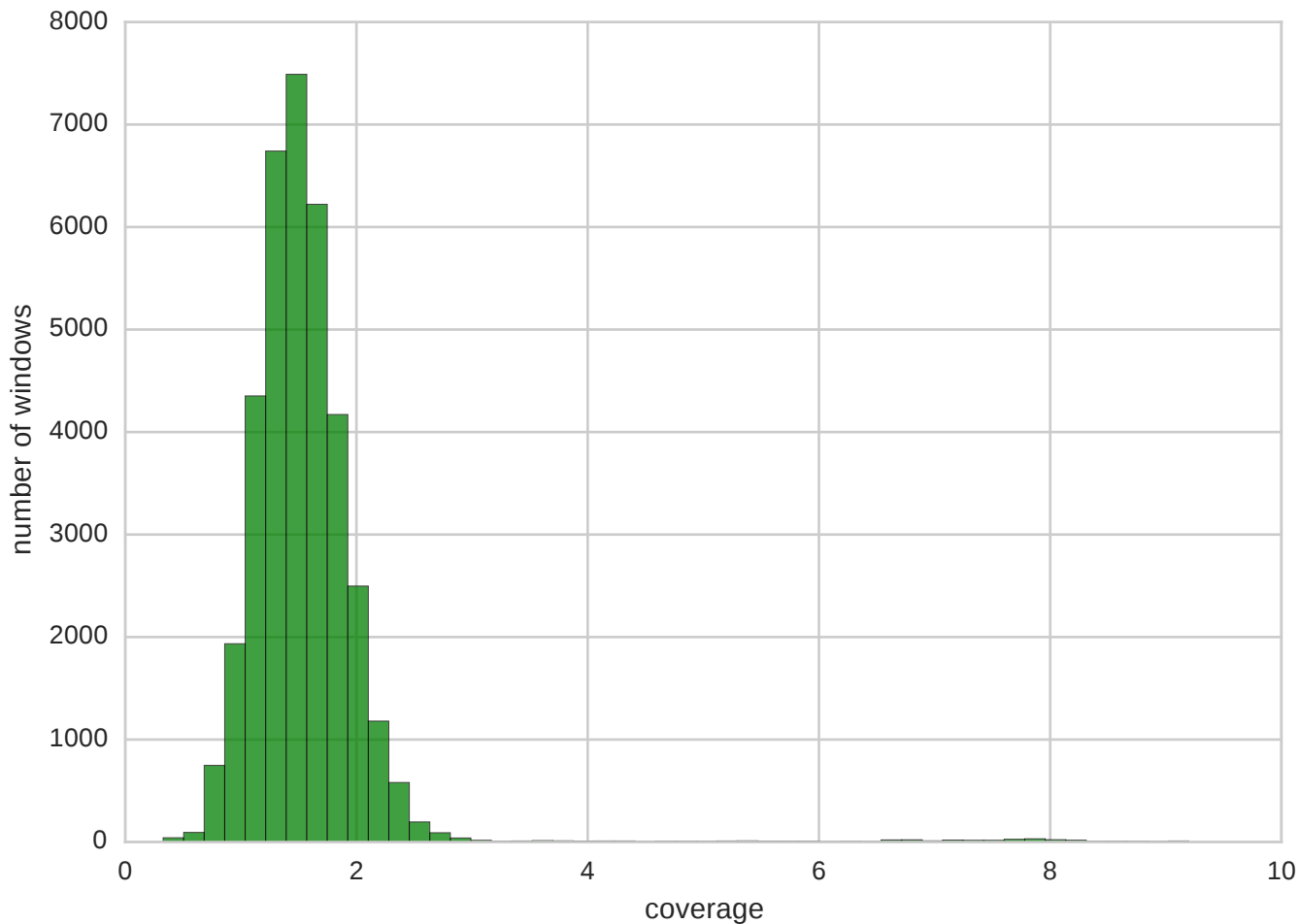
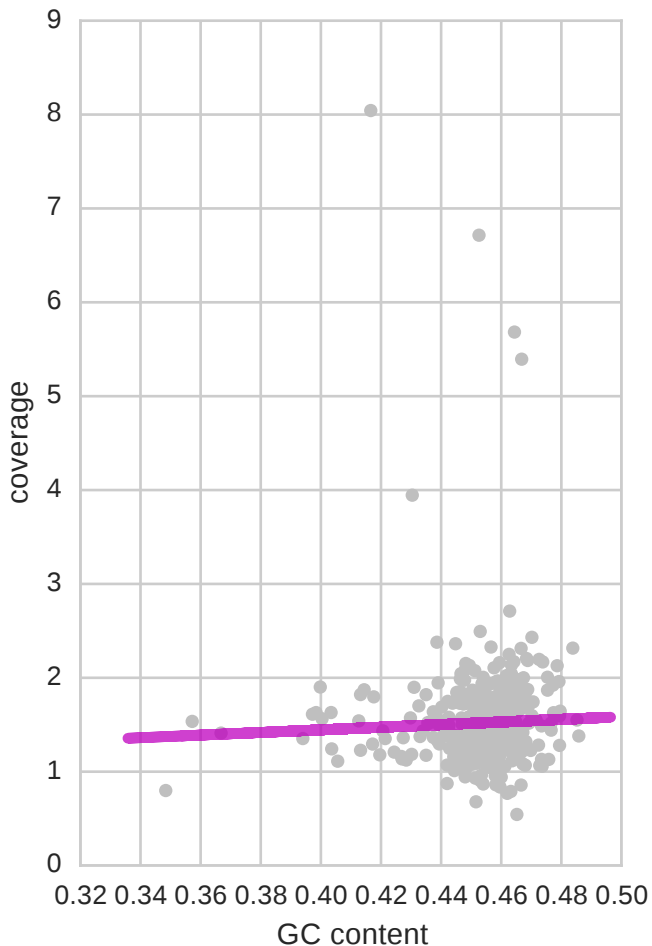


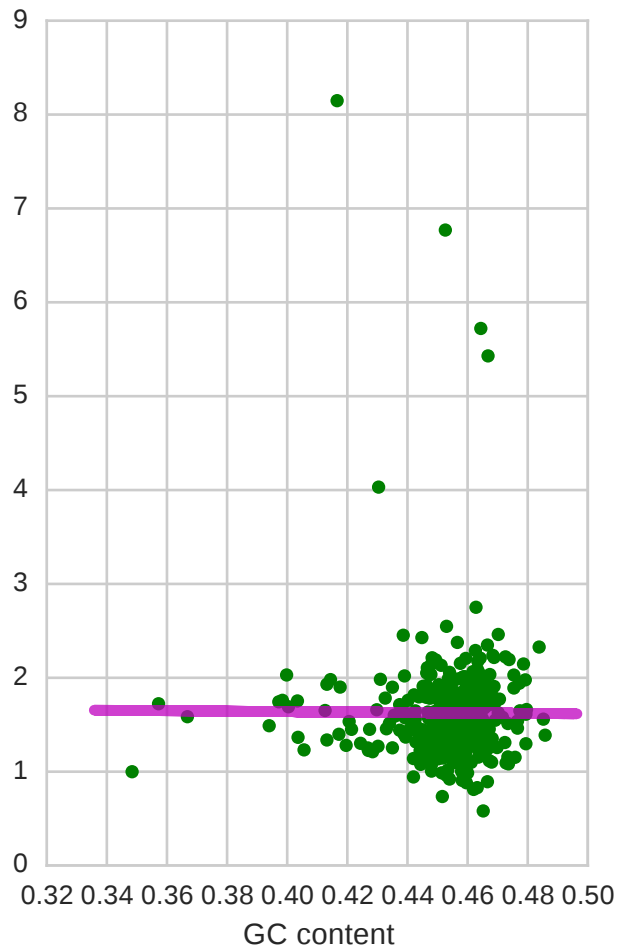
genome: ./bins/bacla\_vizbin1-contigs sample: ./splitBam/bacla\_vizbin1/DNA-Pieter-64  
iRep: n/a r<sup>2</sup>: 0.98 avg. cov: 1.57 % windows: 100.00



genome: ./bins/bacla\_vizbin1-contigs sample: ./splitBam/bacla\_vizbin1/DNA-Pieter-64  
iRep: n/a raw iRep: 2.06 GC r<sup>2</sup>: 0.00 GC bias: 0.01 avg. cov: 1.57 % windows: 100.00

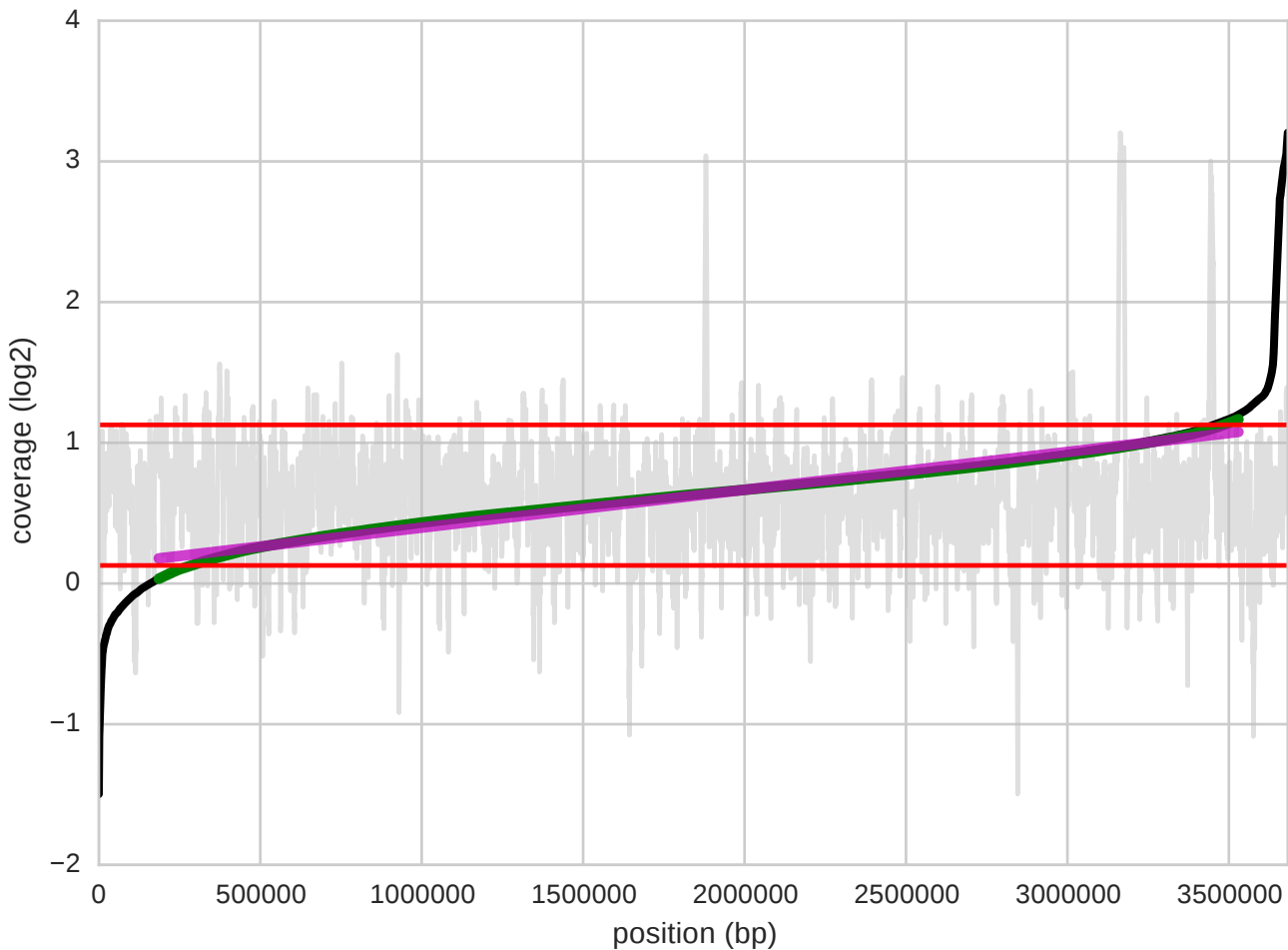


● filtered coverage  
— least squares fit to GC filtered data



● corrected  
— least squares fit to corrected data

genome: ./bins/bacla\_vizbin1-contigs sample: ./splitBam/bacla\_vizbin1/DNA-Pieter-64  
iRep: n/a un-filtered iRep: 2.00  $r^2$ : 0.98 avg. cov: 1.57 % windows: 100.00



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