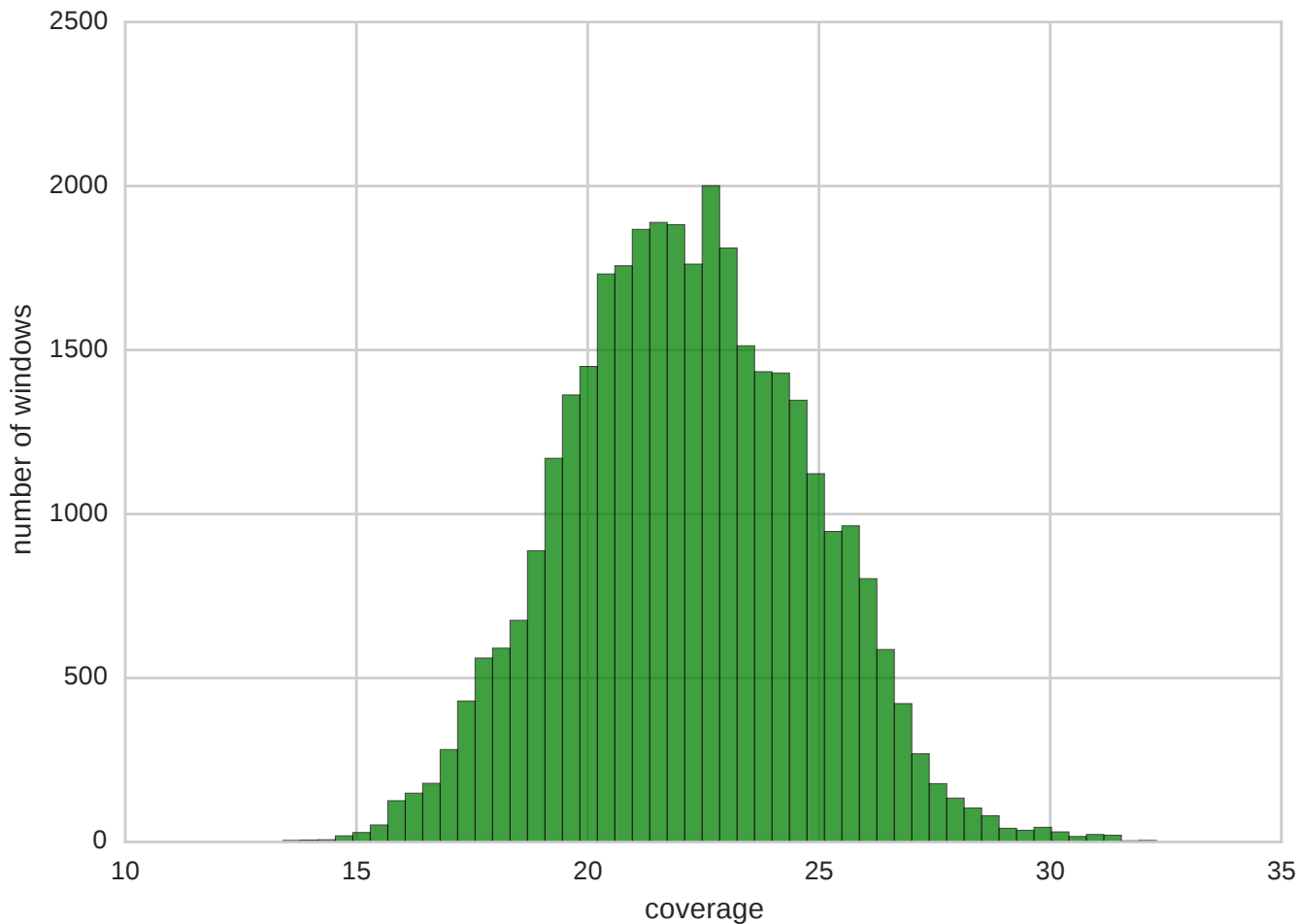
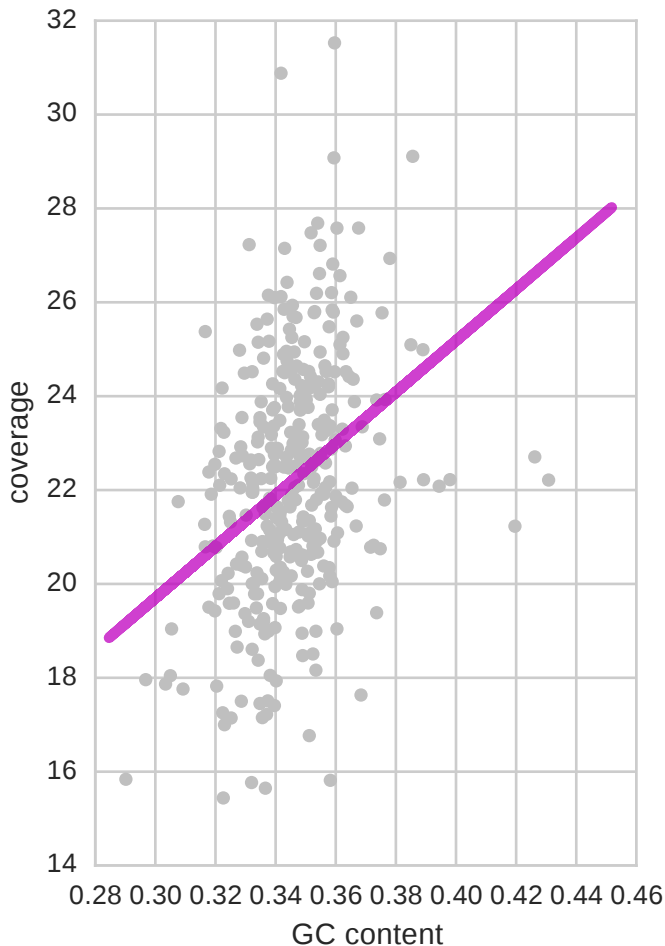


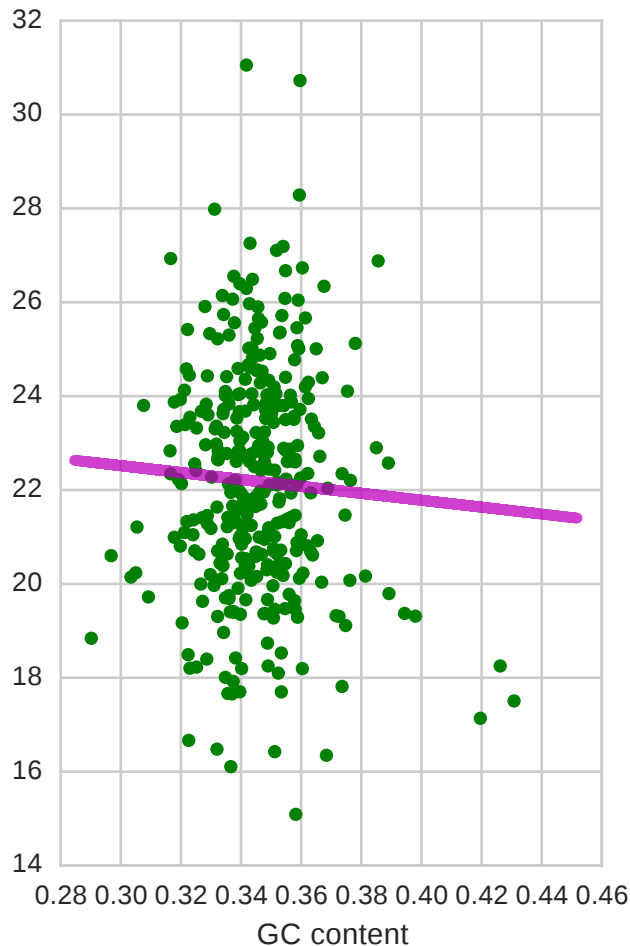
genome: ./bins/bacla_vizbin2-contigs sample: ./splitBam/bacla_vizbin2/DNA-Pieter-16
iRep: 1.41 r²: 0.99 avg. cov: 22.17 % windows: 100.00



genome: ./bins/bacla_vizbin2-contigs sample: ./splitBam/bacla_vizbin2/DNA-Pieter-16
iRep: 1.41 raw iRep: 1.44 GC r²: 0.13 GC bias: 7.33 avg. cov: 22.17 % windows: 100.00

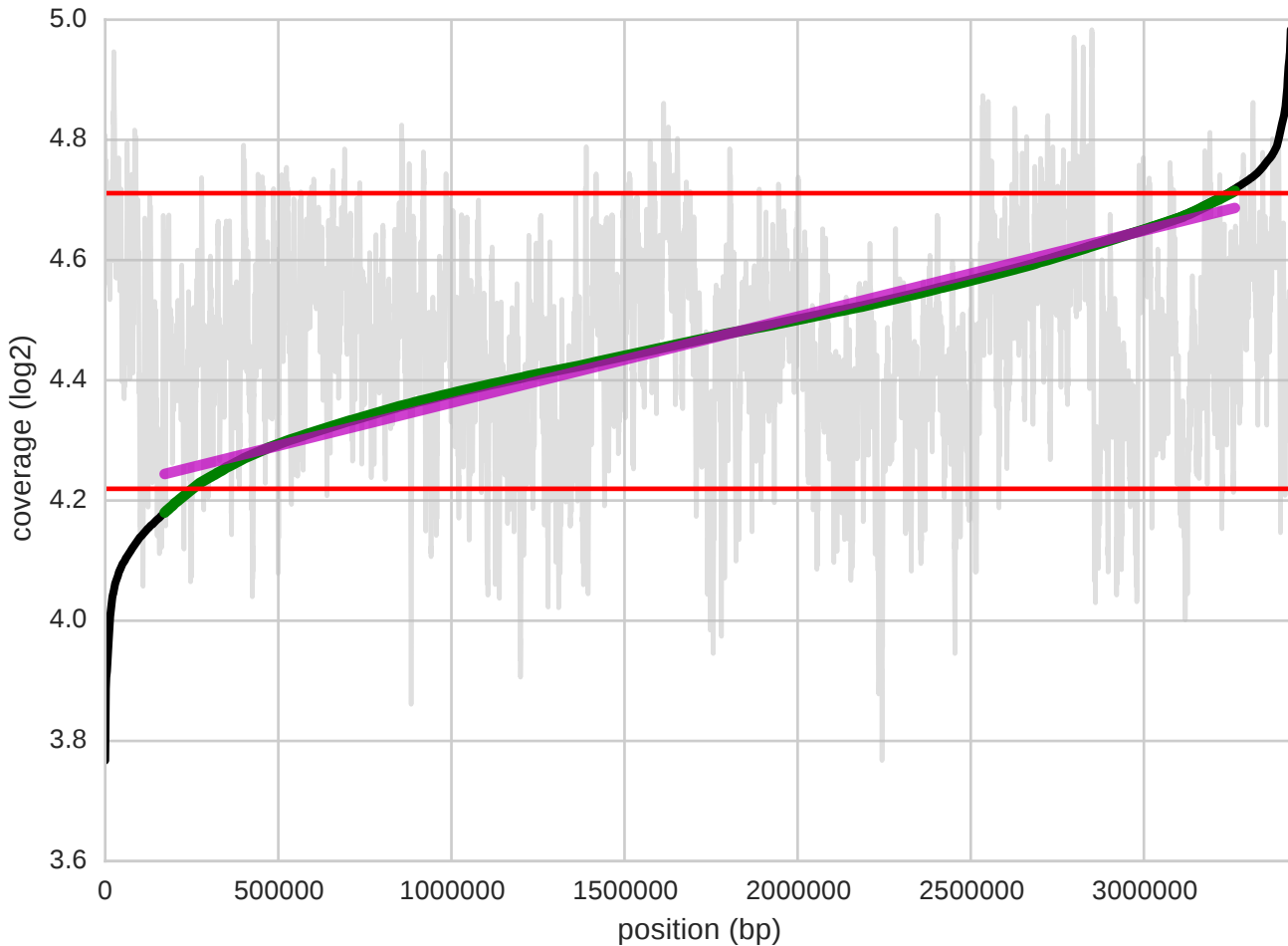


● filtered coverage
— least squares fit to GC filtered data



● corrected
— least squares fit to corrected data

genome: ./bins/bacla_vizbin2-contigs sample: ./splitBam/bacla_vizbin2/DNA-Pieter-16
iRep: 1.41 un-filtered iRep: 1.41 r^2 : 0.99 avg. cov: 22.17 % windows: 100.00



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