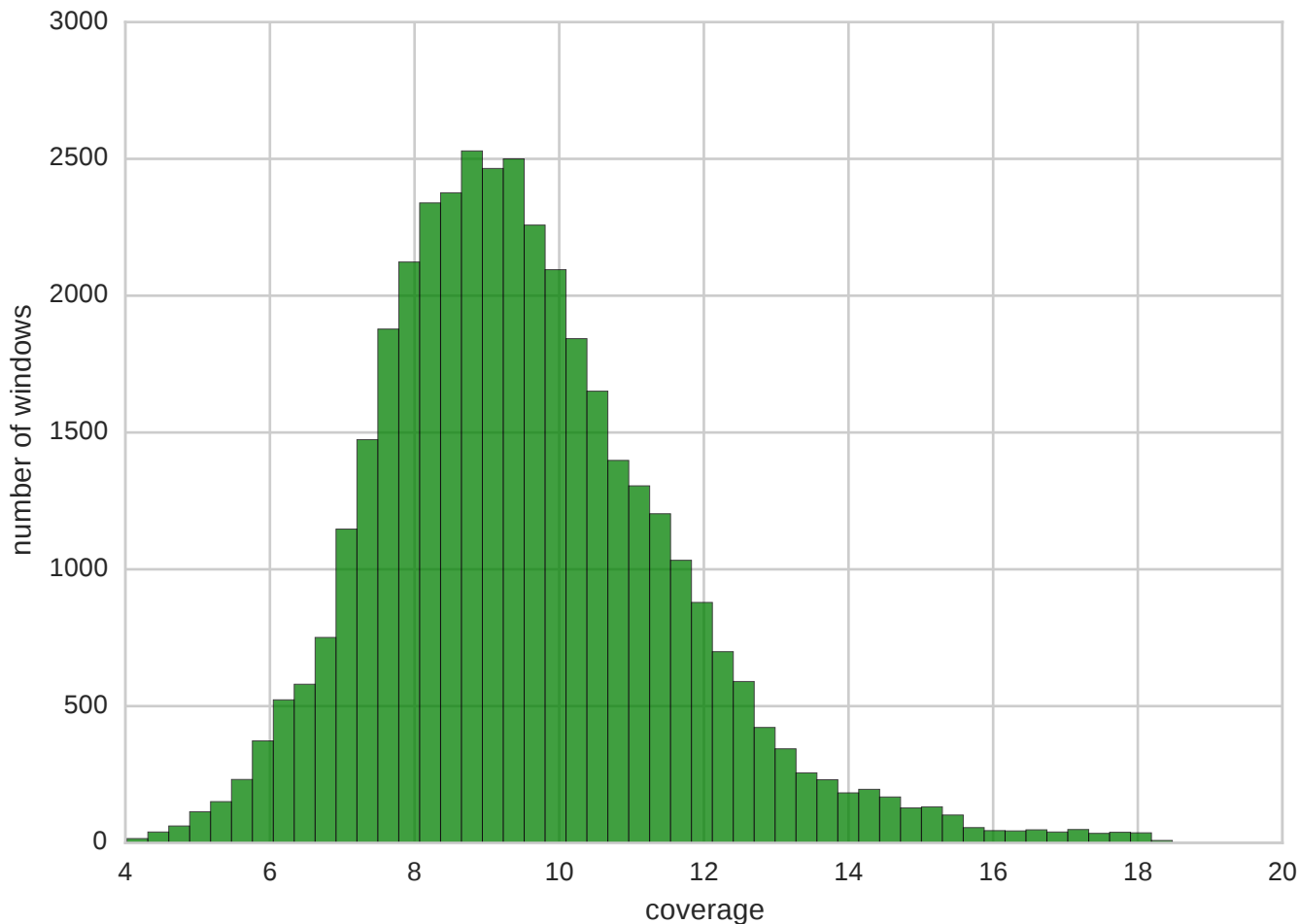
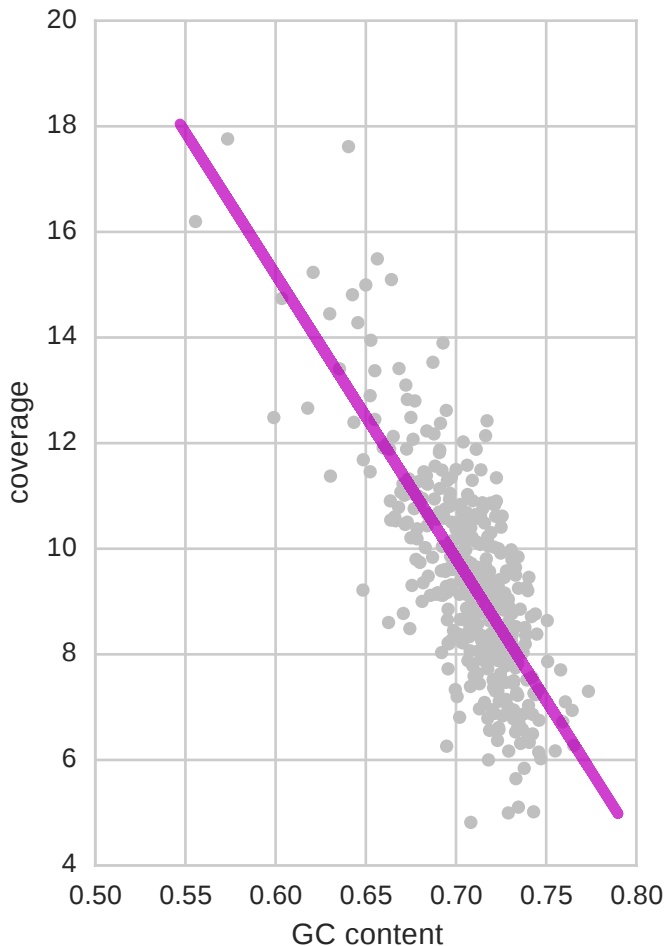


genome: ./bins/Betla\_bin-contigs sample: ./splitBam/Betla\_bin/DNA-Pieter-17  
iRep: 1.54  $r^2$ : 0.99 avg. cov: 9.50 % windows: 100.00



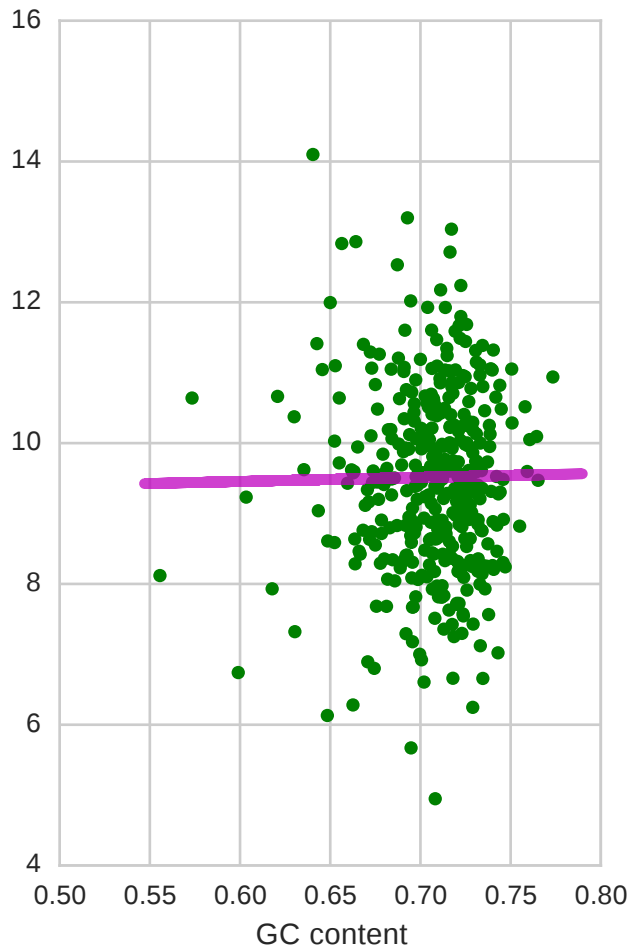
genome: ./bins/Betla\_bin-contigs sample: ./splitBam/Betla\_bin/DNA-Pieter-17

iRep: 1.54 raw iRep: 1.85 GC  $r^2$ : 0.56 GC bias: -30.21 avg. cov: 9.50 % windows: 100.00



filtered coverage

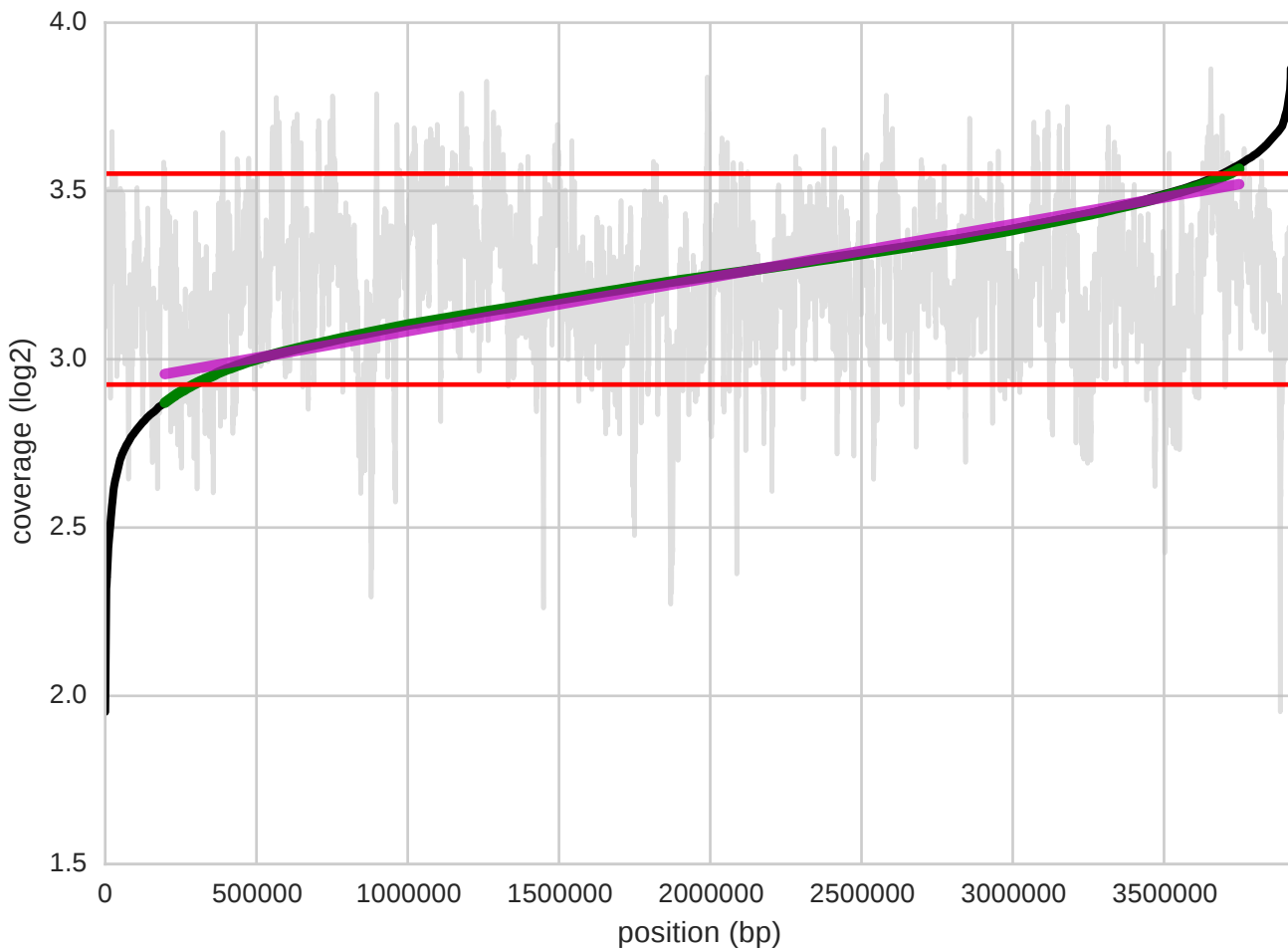
least squares fit to GC filtered data



corrected

least squares fit to corrected data

genome: ./bins/Betla\_bin-contigs sample: ./splitBam/Betla\_bin/DNA-Pieter-17  
iRep: 1.54 un-filtered iRep: 1.54  $r^2$ : 0.99 avg. cov: 9.50 % windows: 100.00



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