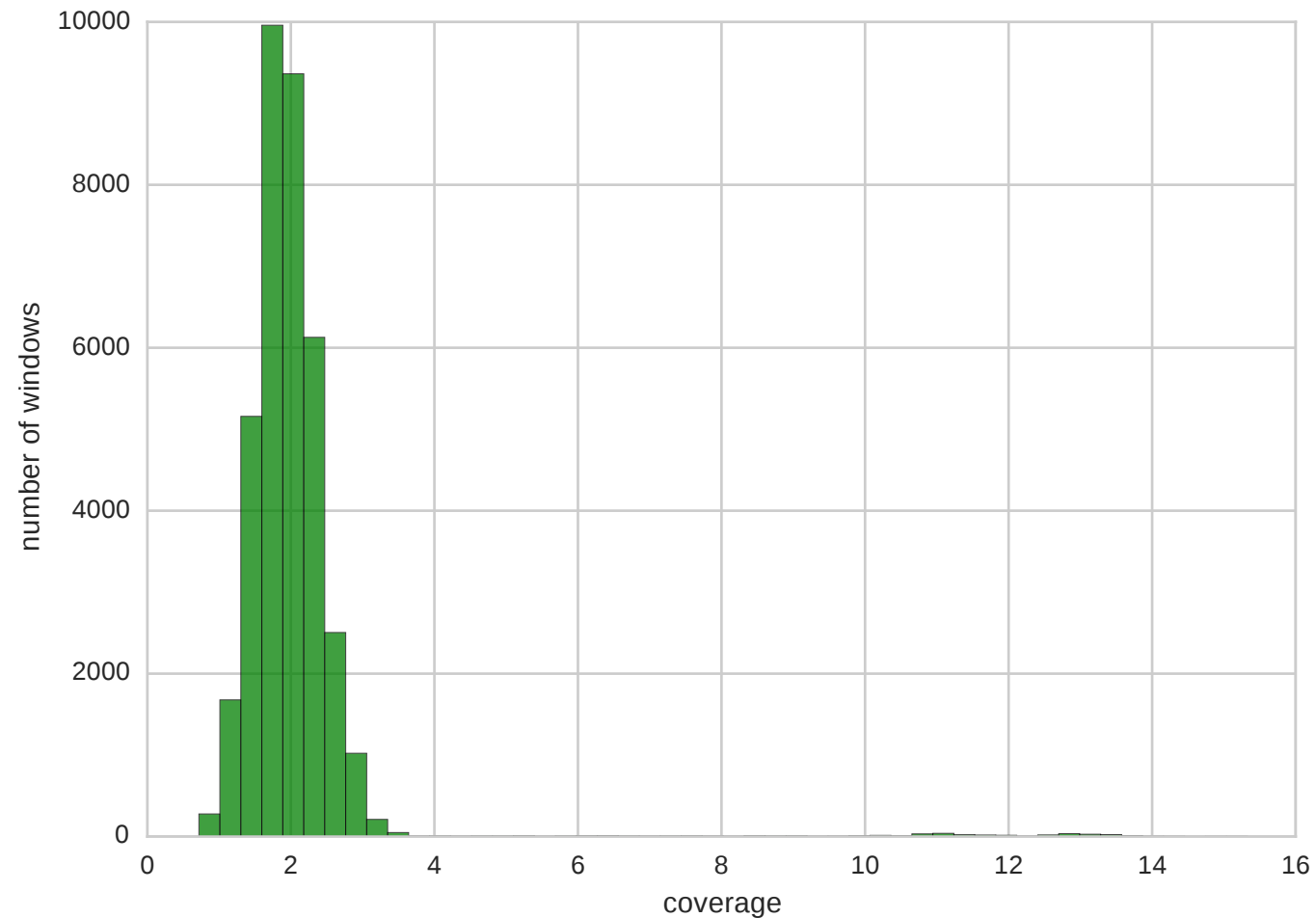
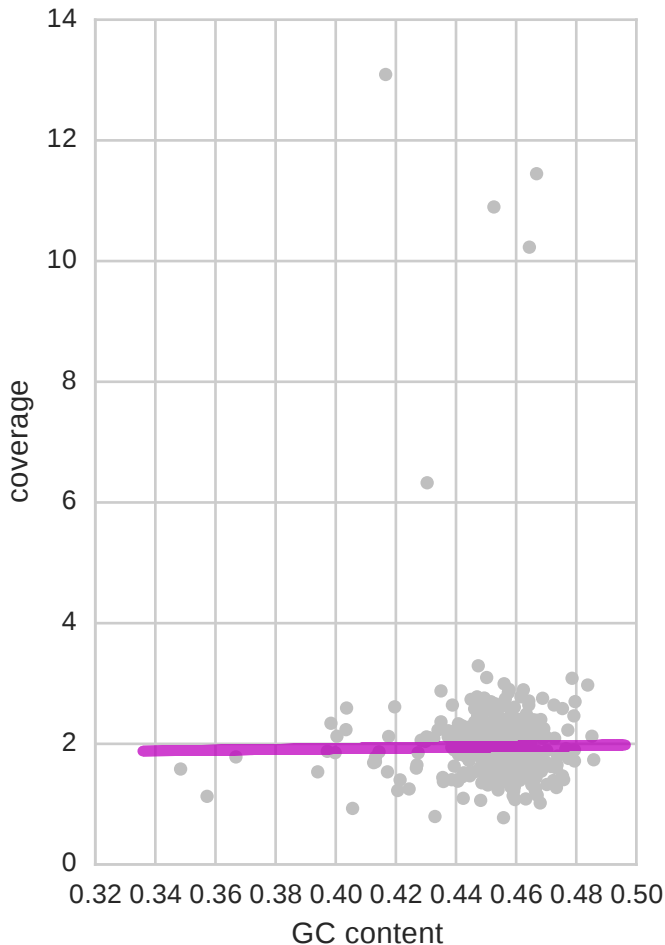


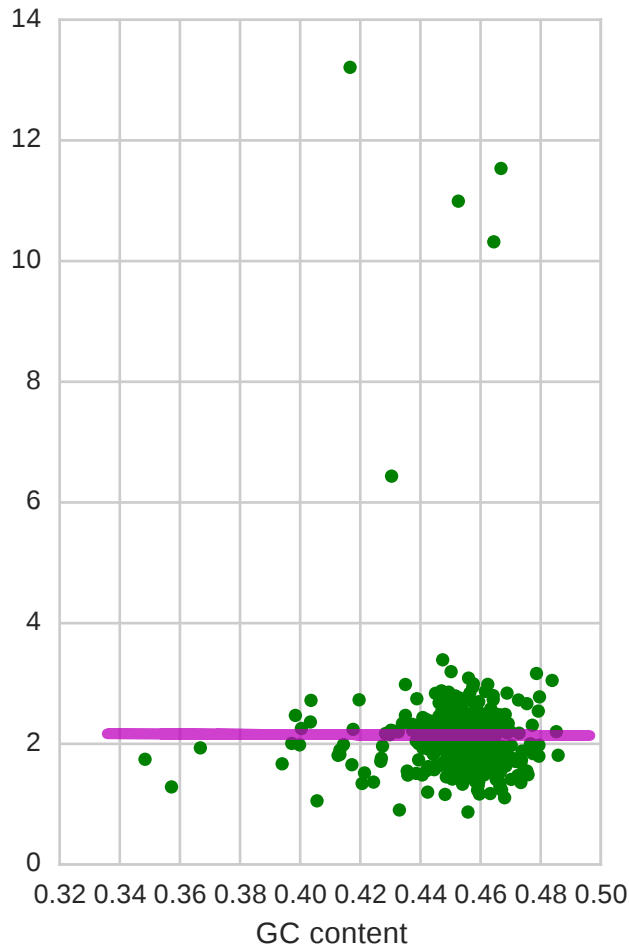
genome: ./bins/bacla_vizbin1-contigs sample: ./splitBam/bacla_vizbin1/DNA-Pieter-65
iRep: n/a r²: 0.98 avg. cov: 2.05 % windows: 100.00



genome: ./bins/bacla_vizbin1-contigs sample: ./splitBam/bacla_vizbin1/DNA-Pieter-65
iRep: n/a raw iRep: 1.94 GC r²: 0.00 GC bias: 0.00 avg. cov: 2.05 % windows: 100.00

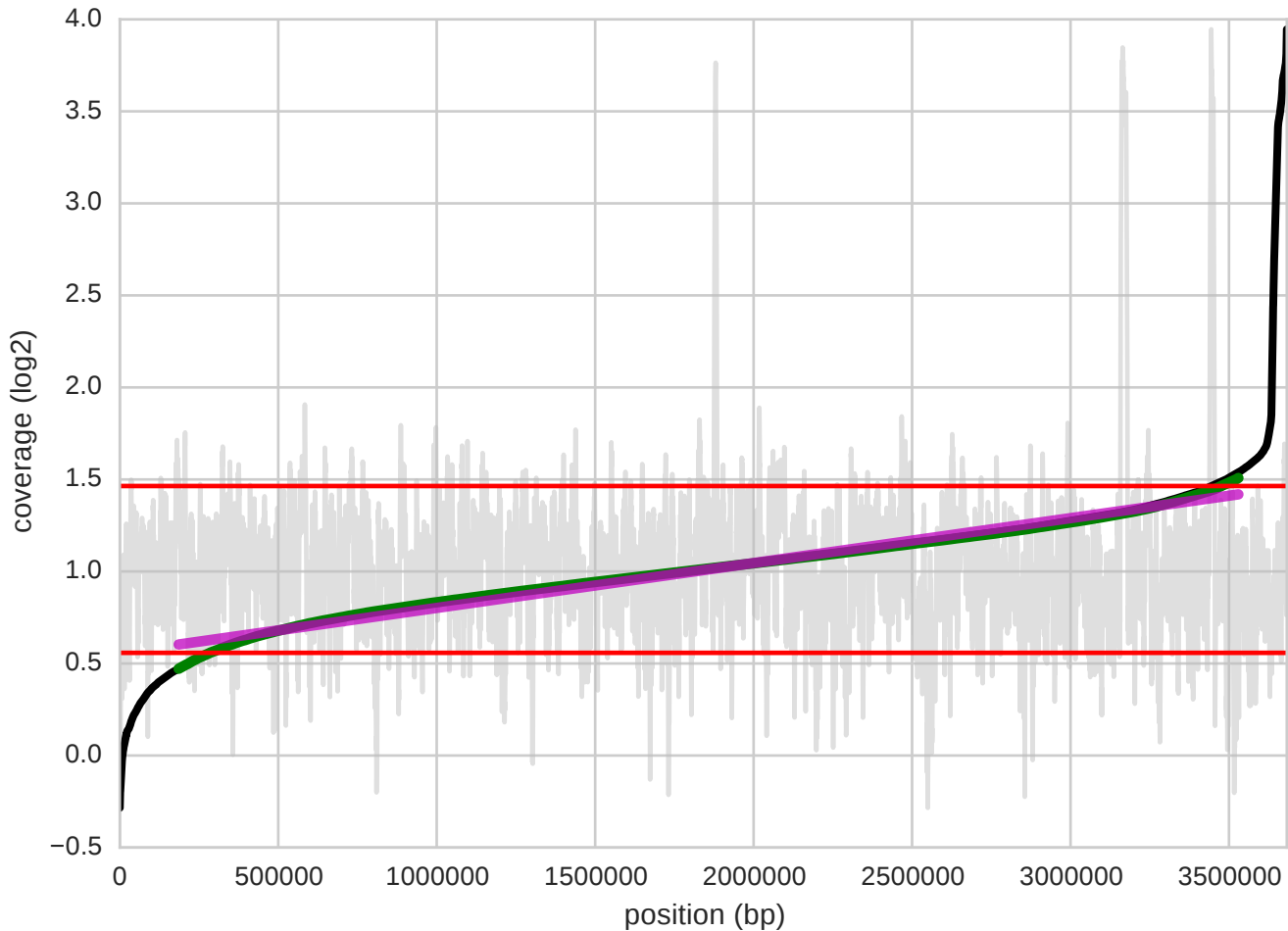


● filtered coverage
— least squares fit to GC filtered data



● corrected
— least squares fit to corrected data

genome: ./bins/bacla_vizbin1-contigs sample: ./splitBam/bacla_vizbin1/DNA-Pieter-65
iRep: n/a un-filtered iRep: 1.87 r^2 : 0.98 avg. cov: 2.05 % windows: 100.00



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