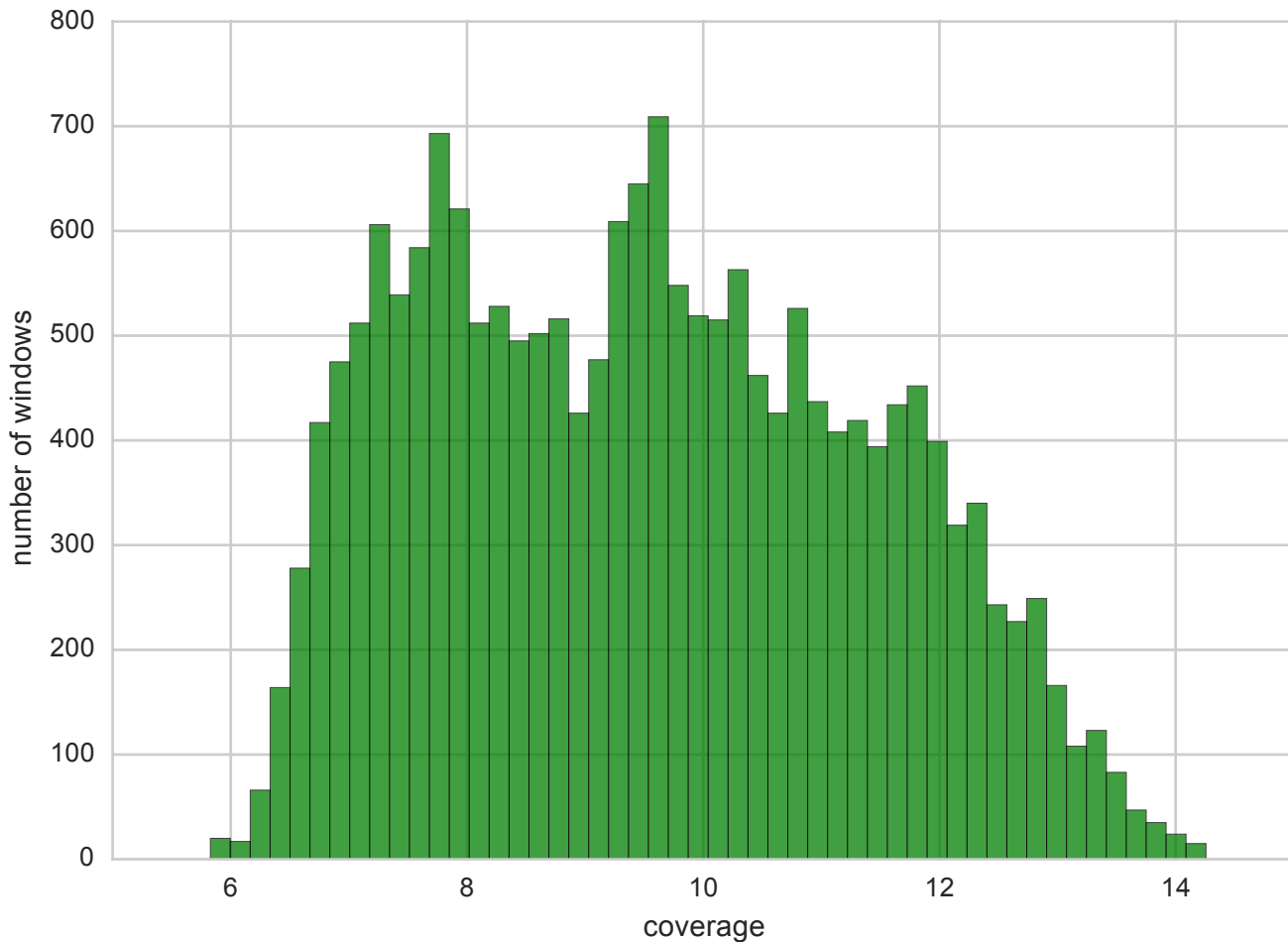
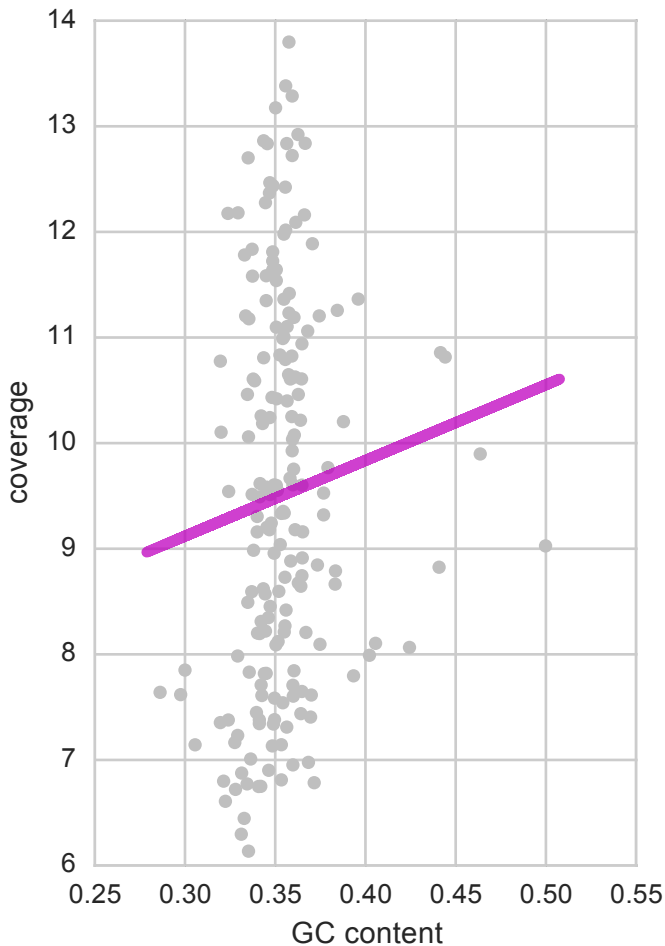


genome: l_gasseri sample: l_gasseri.fna-vs-l_gasseri_sample1-shrunk
iRep: 1.91 r^2: 1.00 avg. cov: 9.54 % windows: 100.00



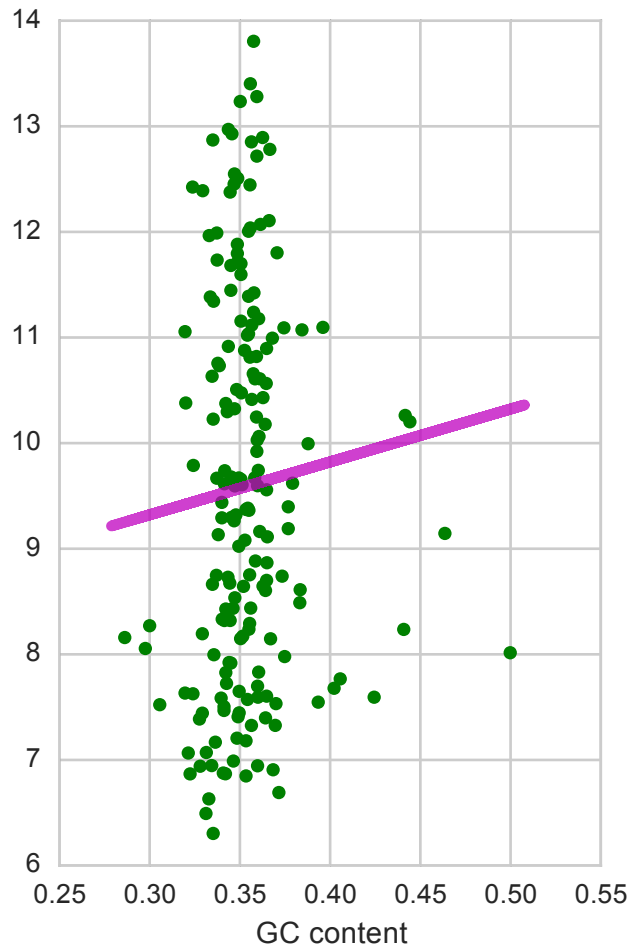
genome: l_gasseri sample: l_gasseri.fna-vs-l_gasseri_sample1-shrunk

iRep: 1.91 raw iRep: 1.92 GC r²: 0.01 GC bias: 0.08 avg. cov: 9.54 % windows: 100.00



filtered coverage

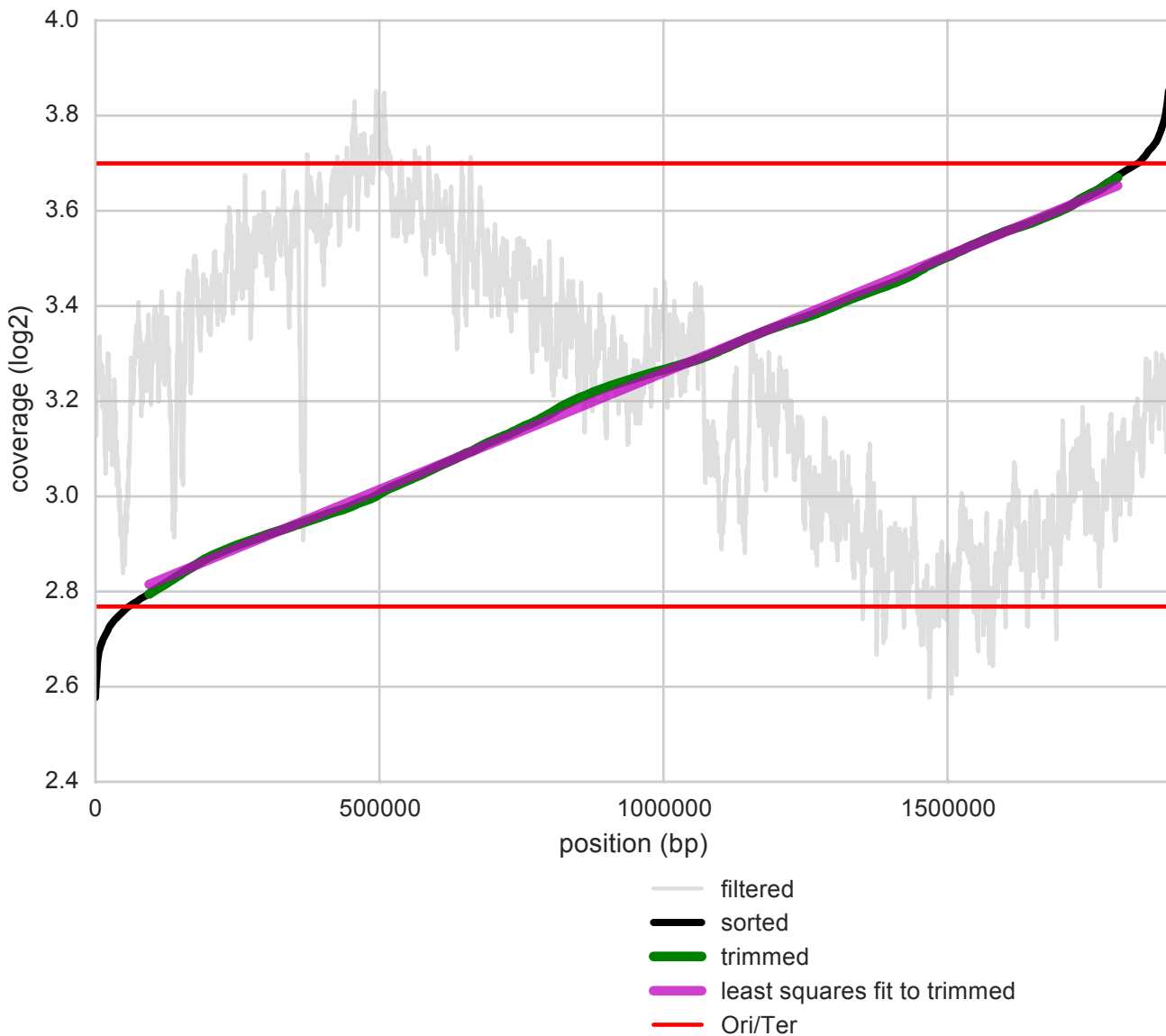
least squares fit to GC filtered data



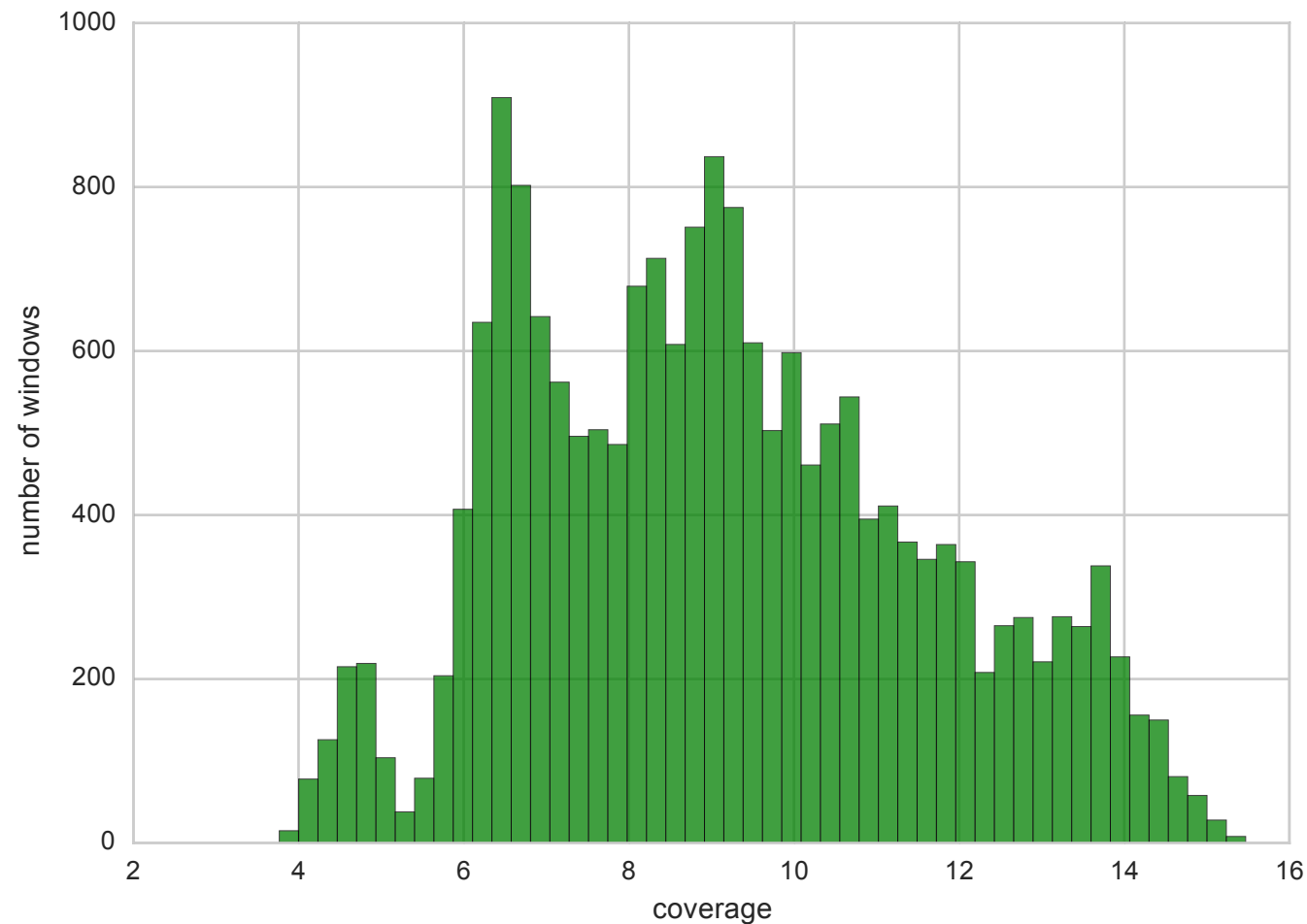
corrected

least squares fit to corrected data

genome: l_gasseri sample: l_gasseri.fna-vs-l_gasseri_sample1-shrunk
iRep: 1.91 un-filtered iRep: 1.91 r^2 : 1.00 avg. cov: 9.54 % windows: 100.00

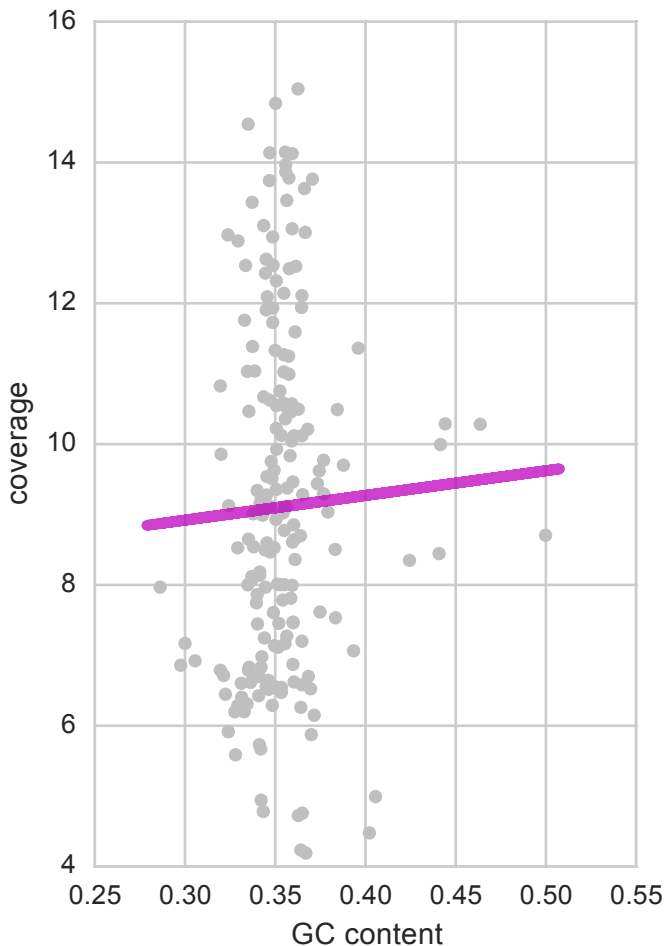


genome: l_gasseri sample: l_gasseri.fna-vs-l_gasseri_sample2-shrunk
iRep: 2.36 r^2 : 0.99 avg. cov: 9.16 % windows: 100.00



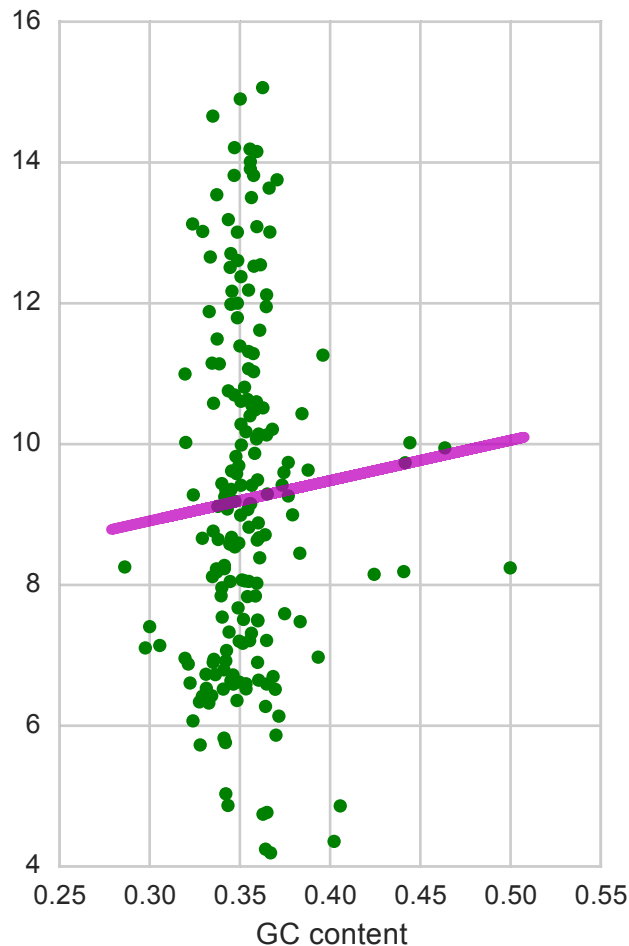
genome: l_gasseri sample: l_gasseri.fna-vs-l_gasseri_sample2-shrunk

iRep: 2.36 raw iRep: 2.38 GC r^2 : 0.00 GC bias: 0.01 avg. cov: 9.16 % windows: 100.00



filtered coverage

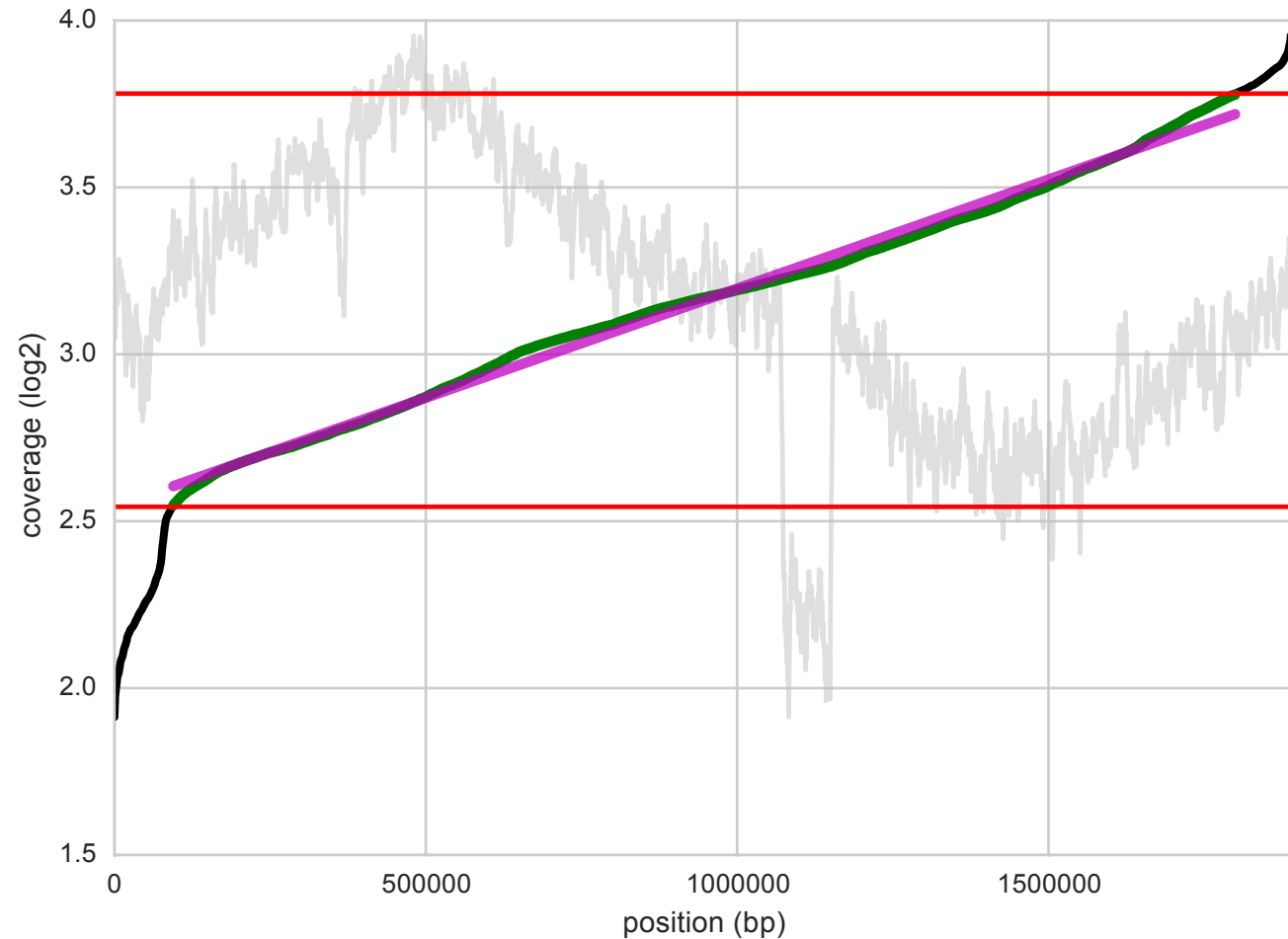
least squares fit to GC filtered data



corrected

least squares fit to corrected data

genome: l_gasseri sample: l_gasseri.fna-vs-l_gasseri_sample2-shrunk
iRep: 2.36 un-filtered iRep: 2.36 r^2 : 0.99 avg. cov: 9.16 % windows: 100.00



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