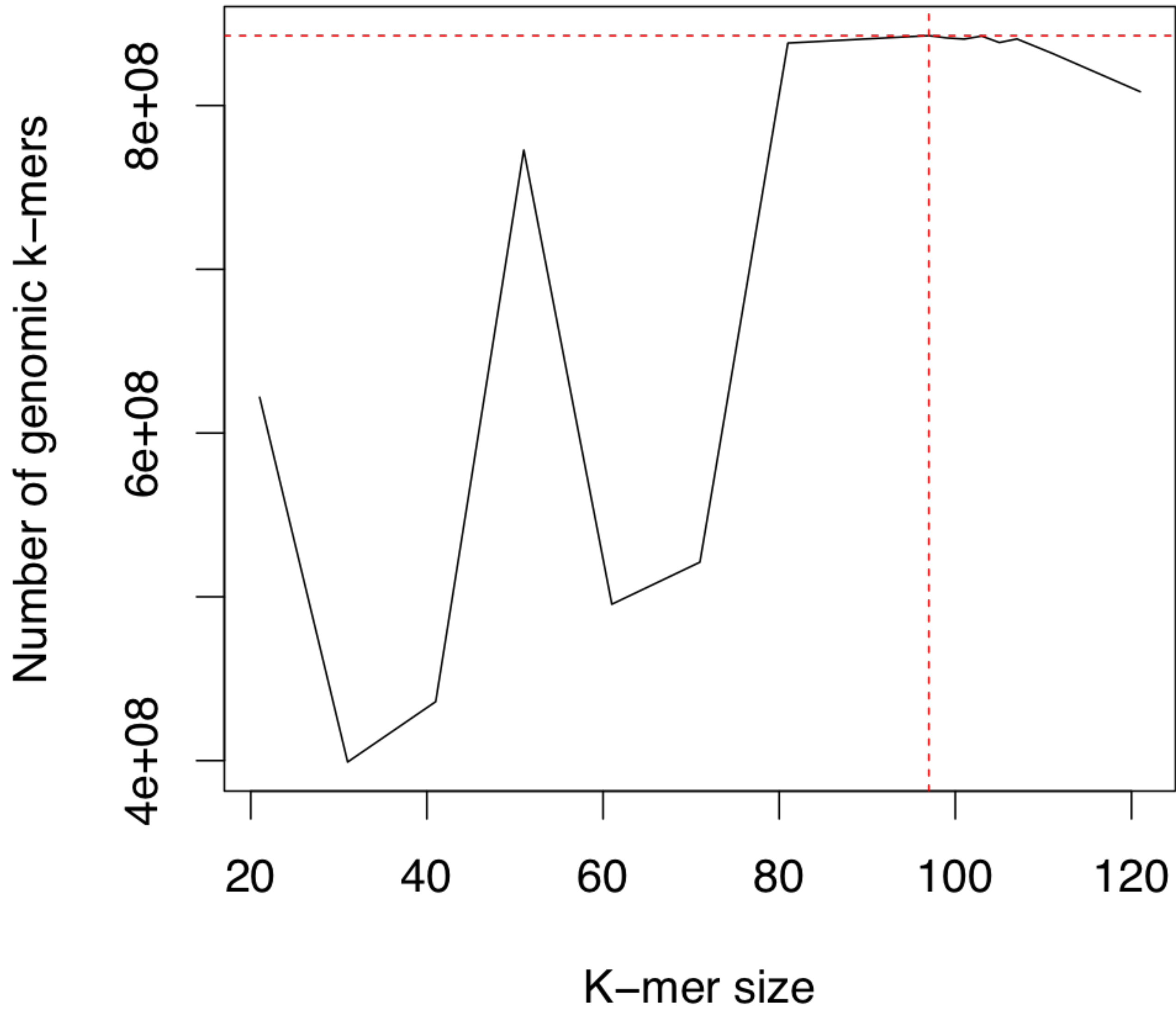


KmerGenie report

Predicted best k: 97

Predicted assembly size: 842670695 bp



The above plot should be roughly concave and have a clear global maximum. If not, the predicted best k is likely to be inaccurate.
[Click here for more details.](#)

Sampled histogram and fit for each value of k

Colors of the fits: red is the fit of the complete statistical model of the histogram (erronous k-mers + genomic k-mers). When using the diploid model, blue are only the heterozygous k-mers, green are only the homozygous k-mers.

Generated by [KmerGenie](#)