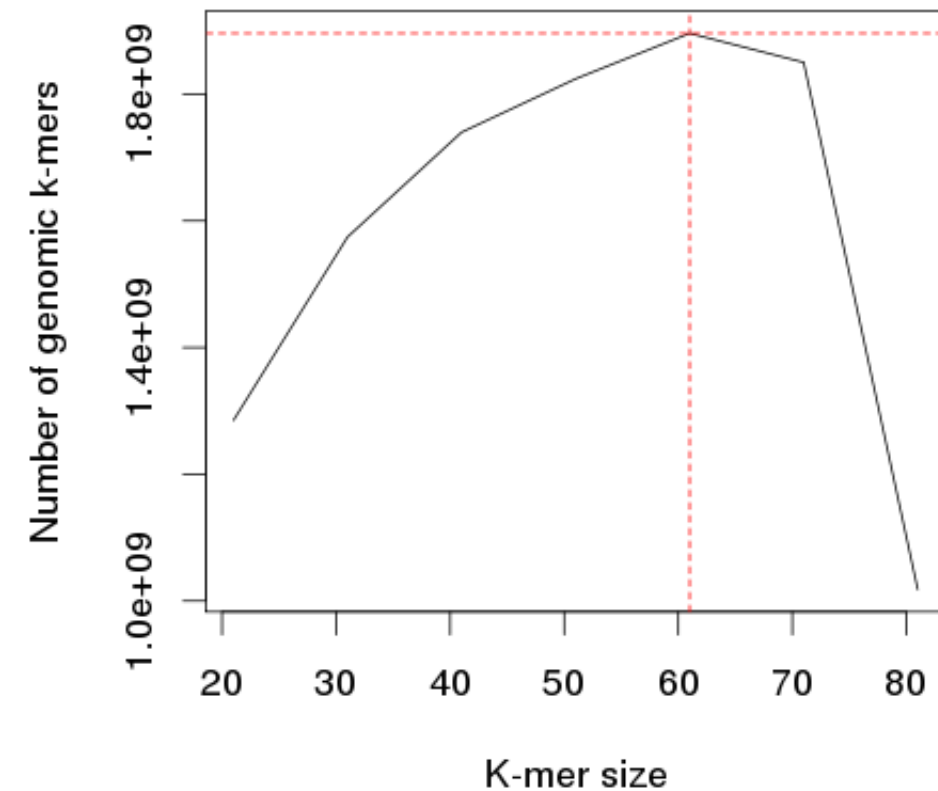


KmerGenie report

Predicted best k: 61

Predicted assembly size: 1895923629 bp



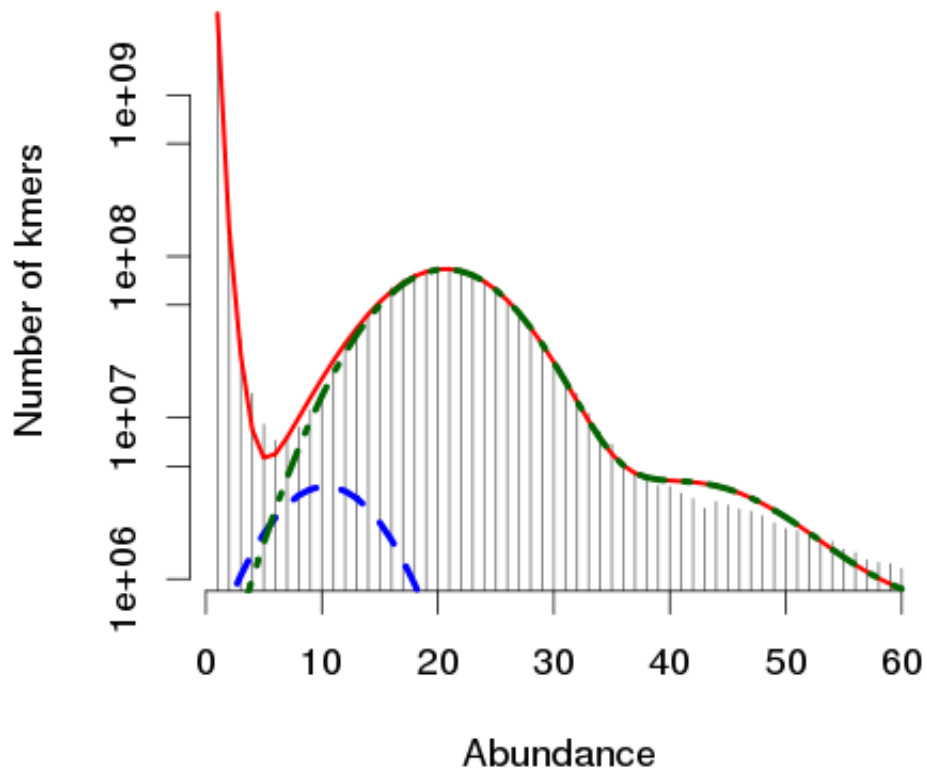
The above plot should be roughly concave and have a clear global maximum. If not, the predicted best k is likely to be inaccurate.

[Click here for more details.](#)

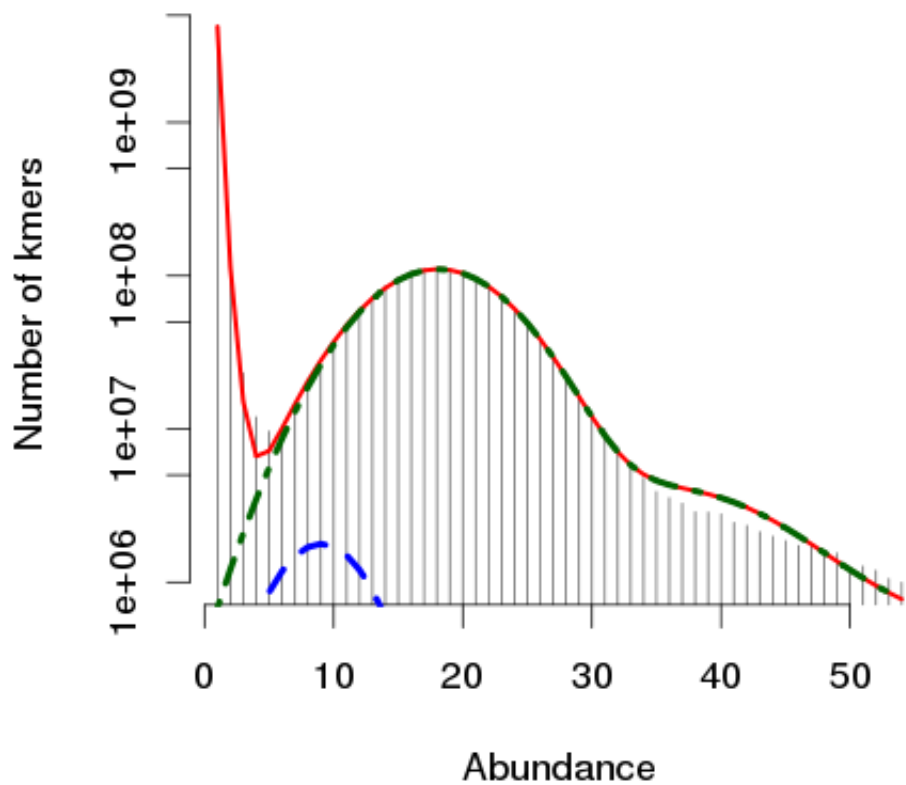
Sampled histogram and fit for each value of k

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

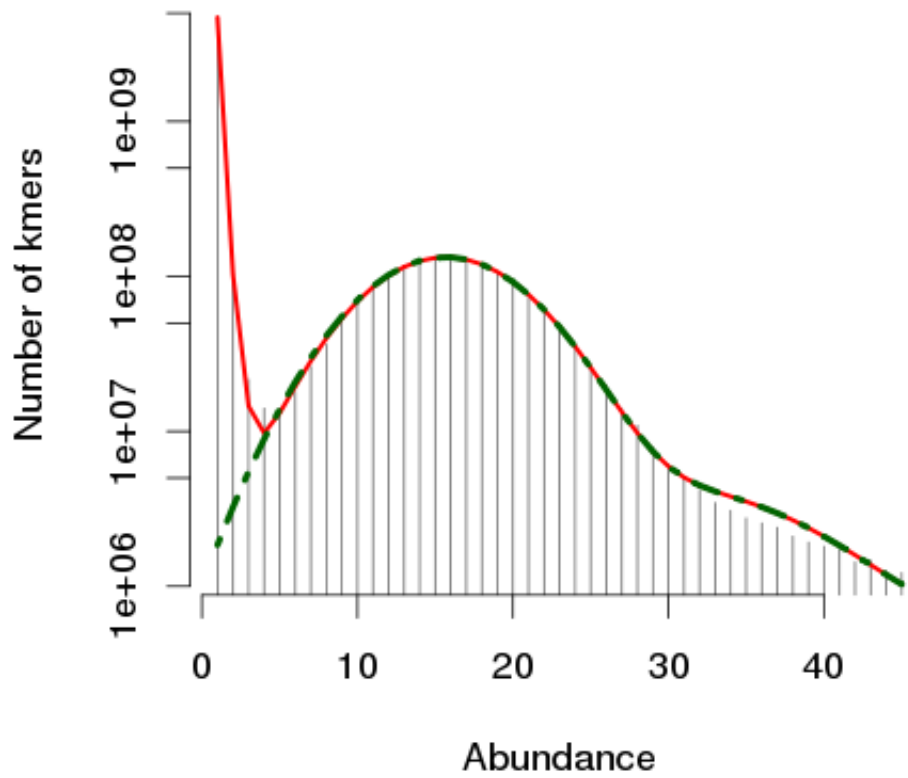
k= 21



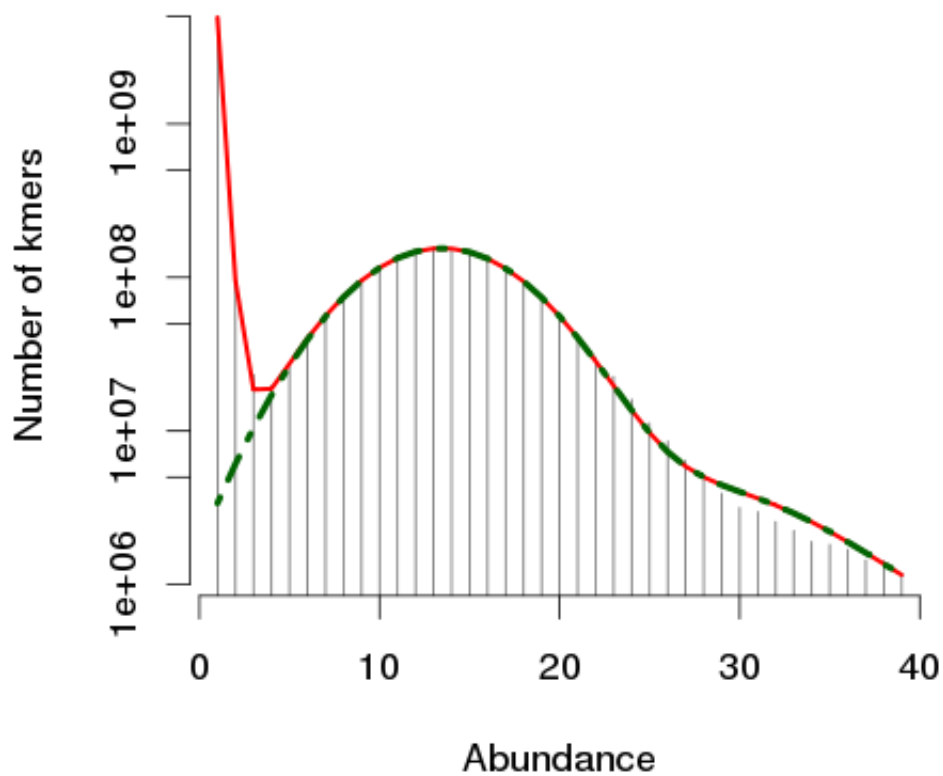
k= 31



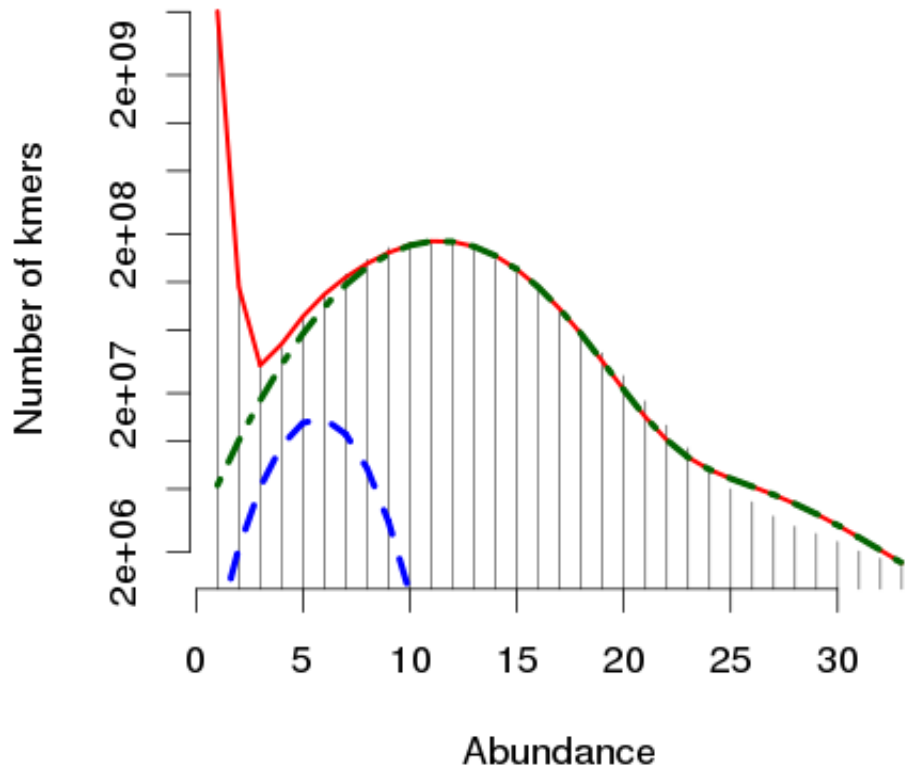
k= 41



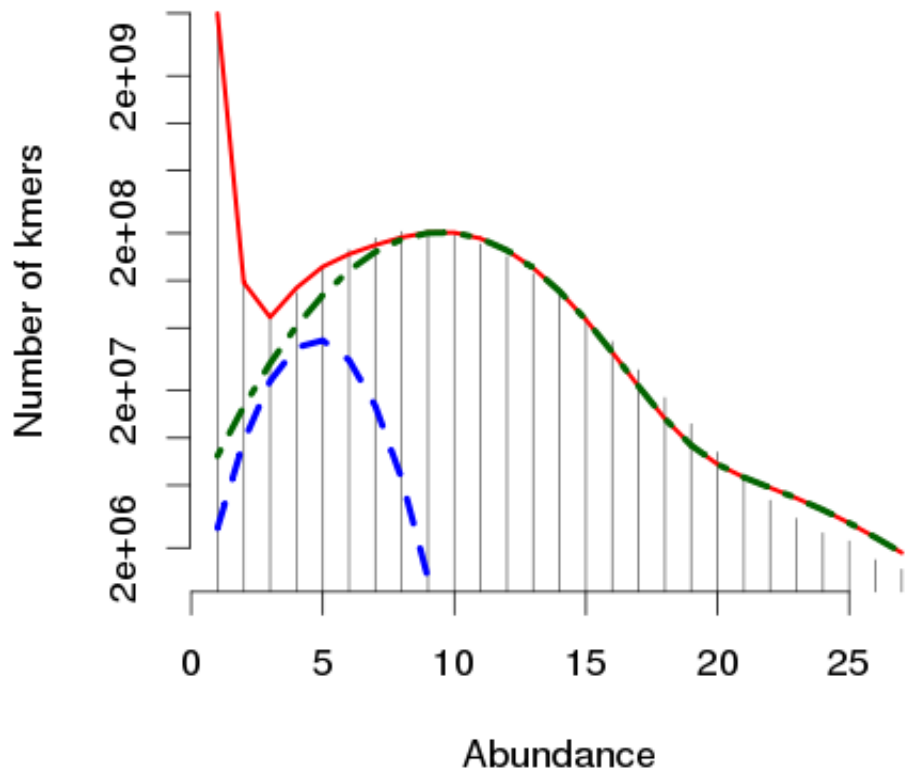
k= 51



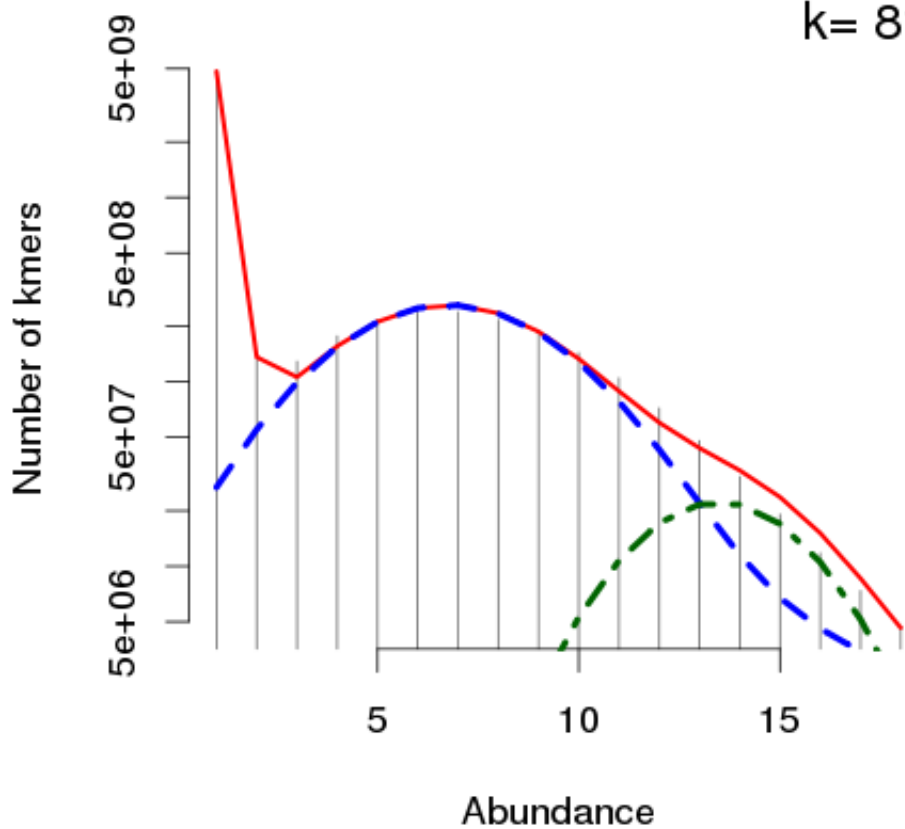
k= 61



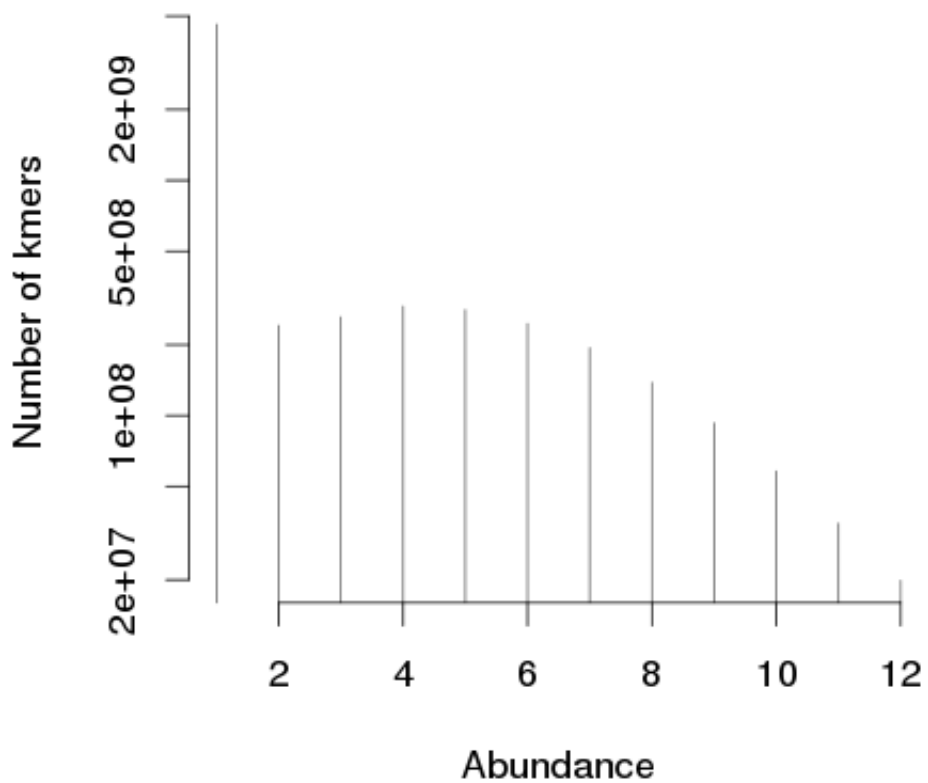
k= 71



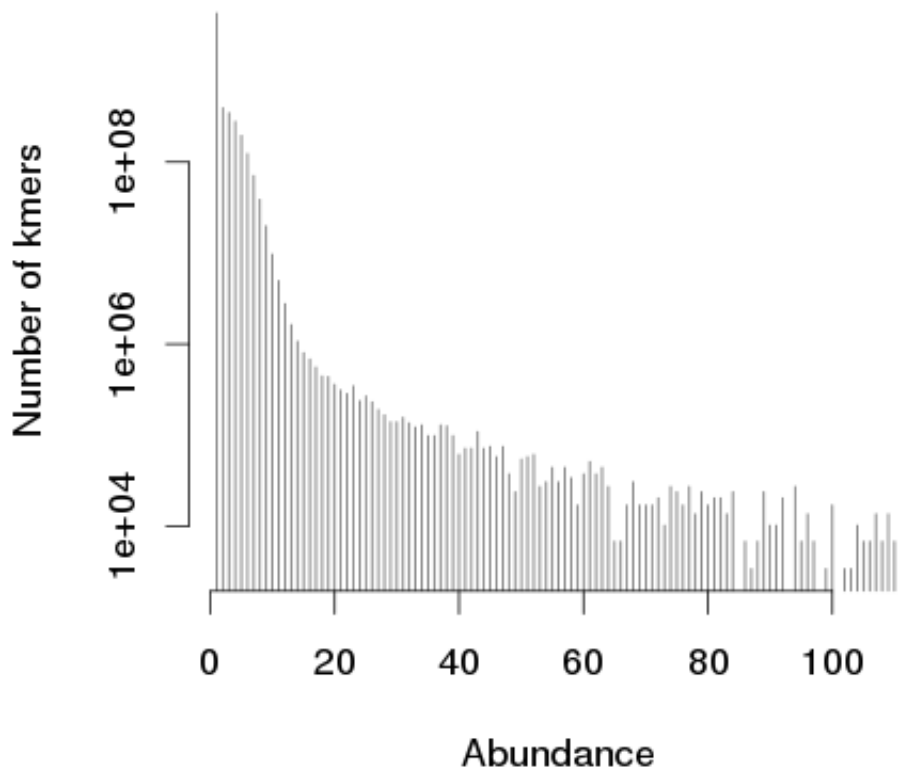
k= 81



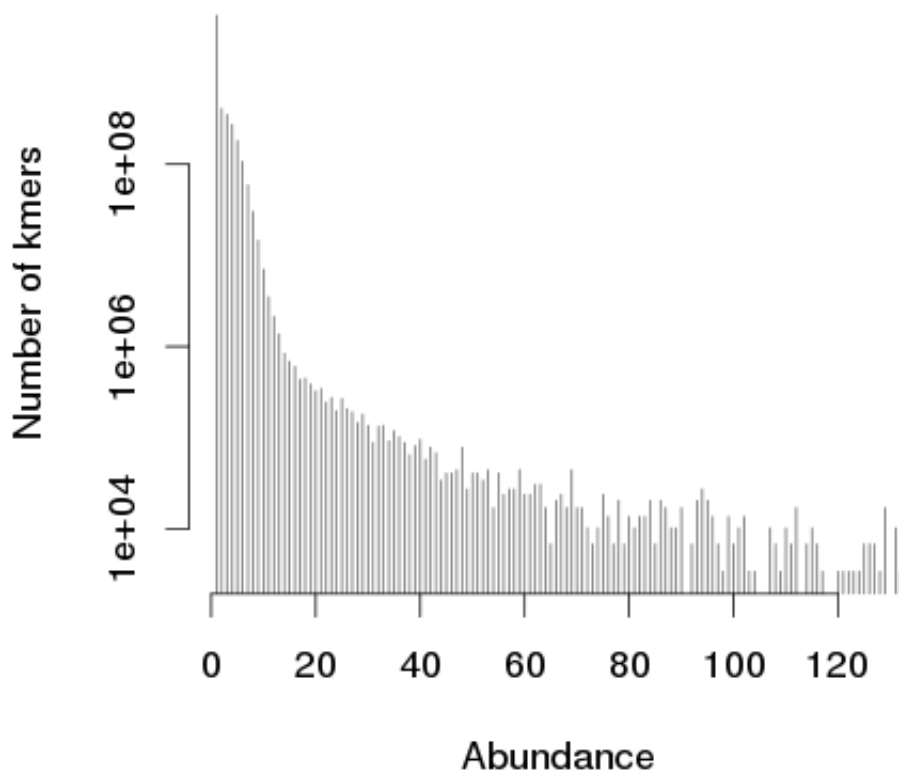
k= 91



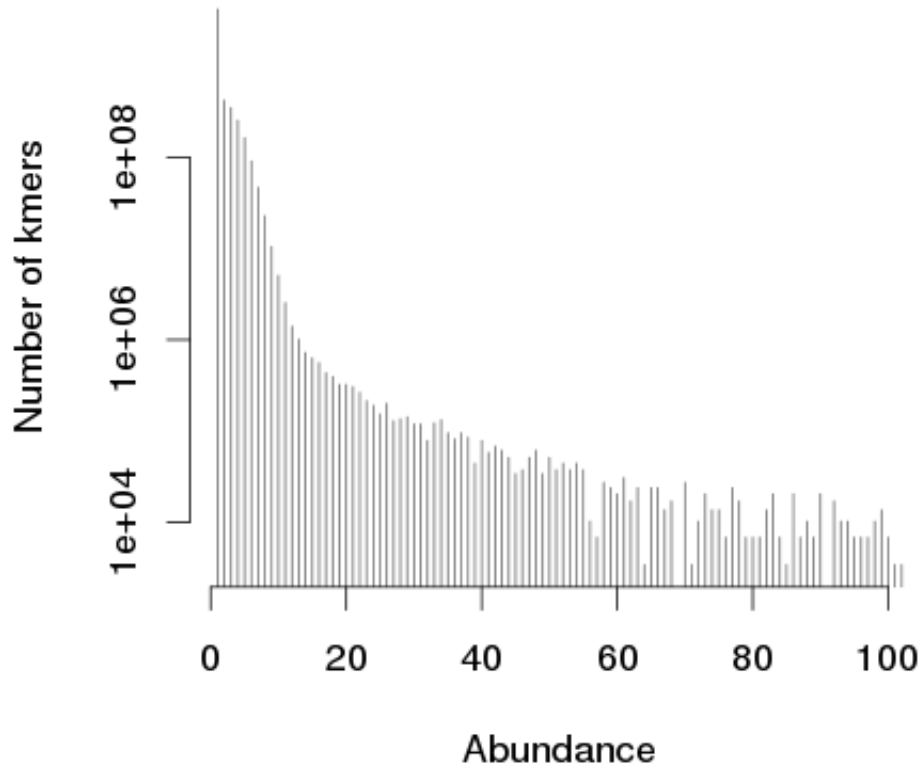
k= 101



k= 111



k= 121



Generated by [KmerGenie](#)