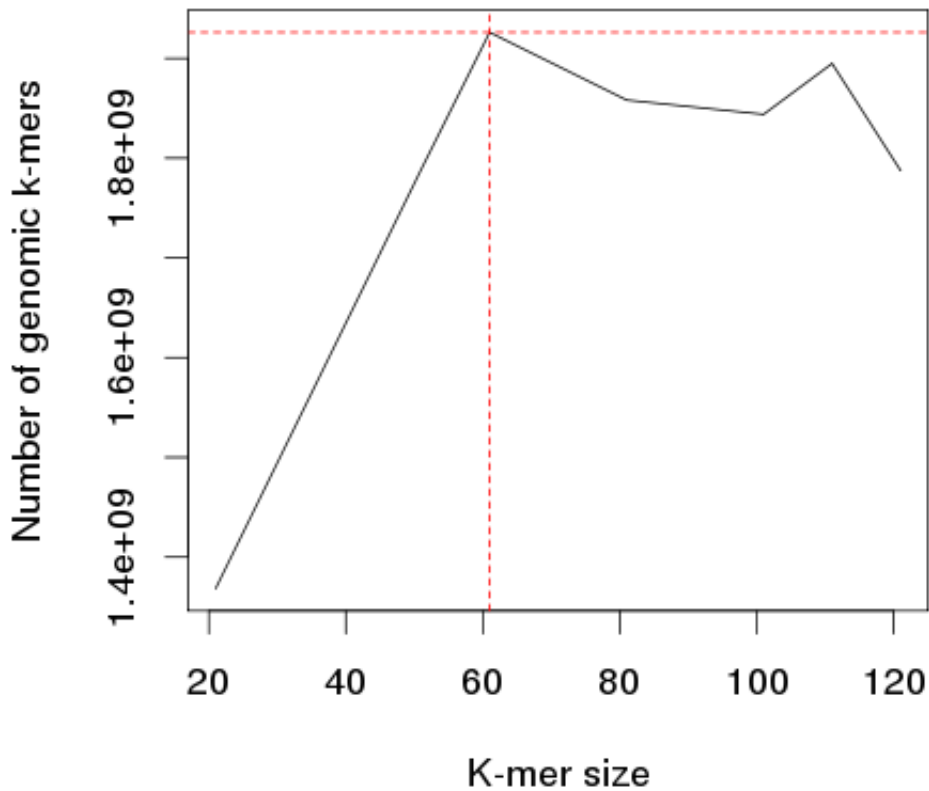


# KmerGenie report

**Predicted best k: 61**

**Predicted assembly size: 1926073727 bp**



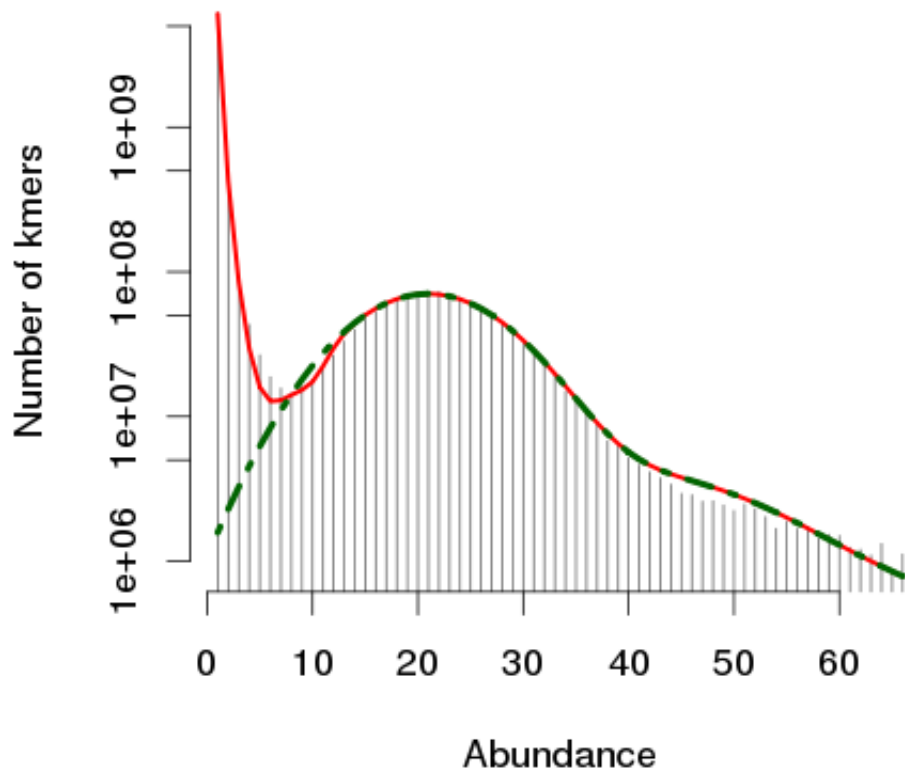
The above plot should be roughly concave and have a clear global maximum. If not, the predicted best k is likely to be inaccurate.

[Click here for more details.](#)

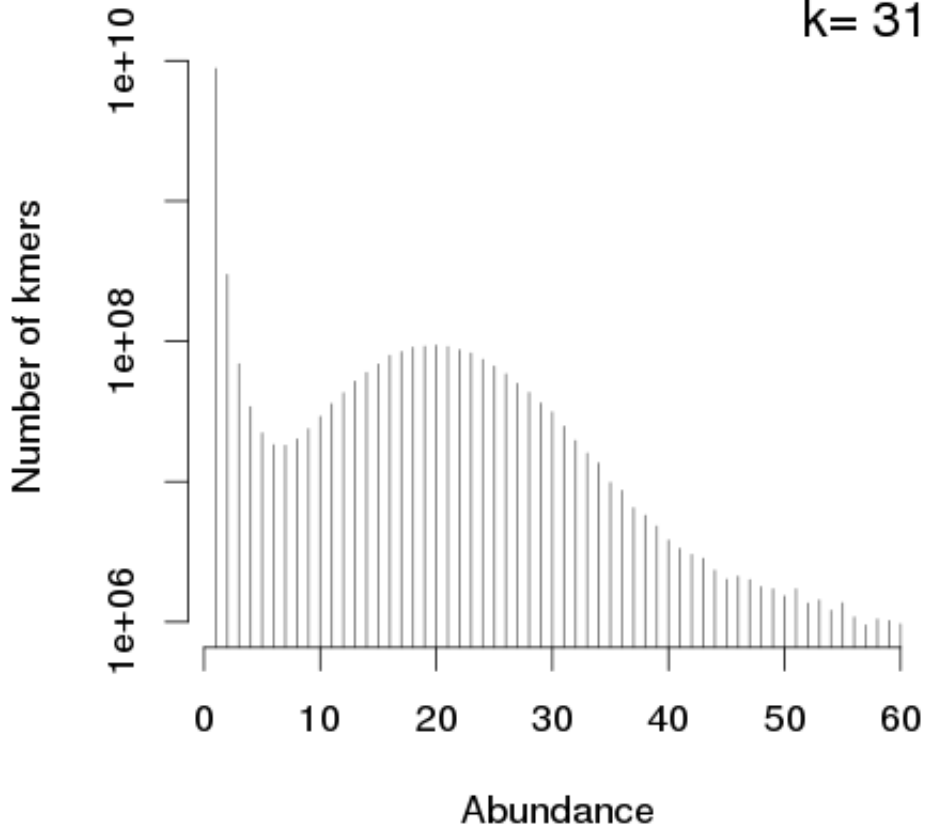
**Sampled histogram and fit for each value of k**

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.

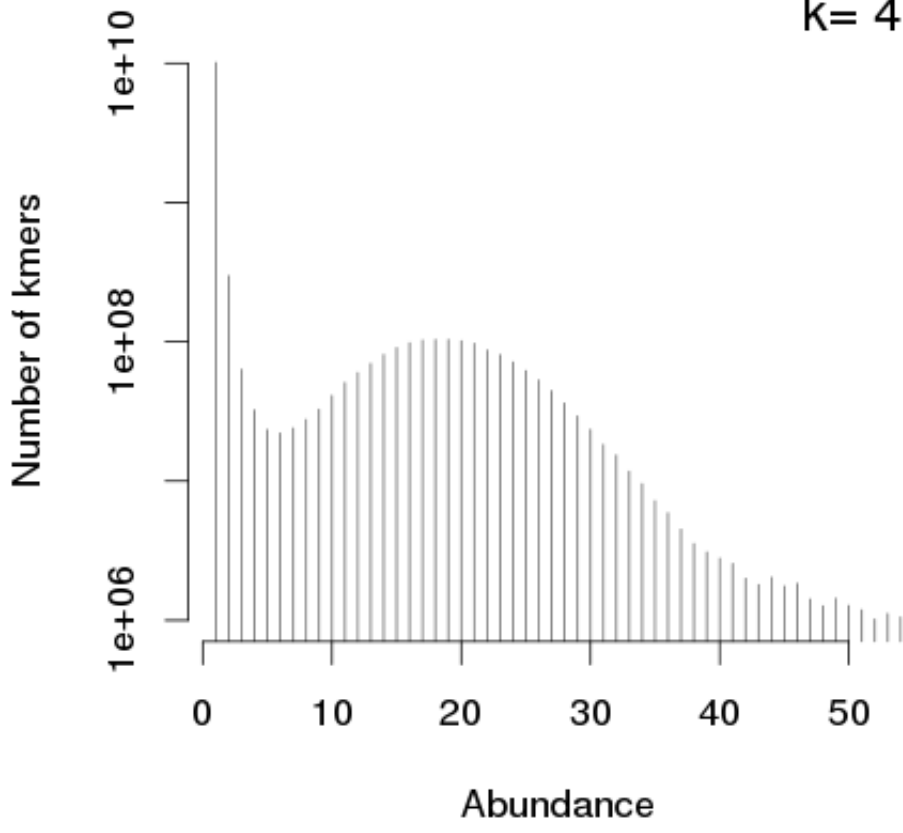
k= 21



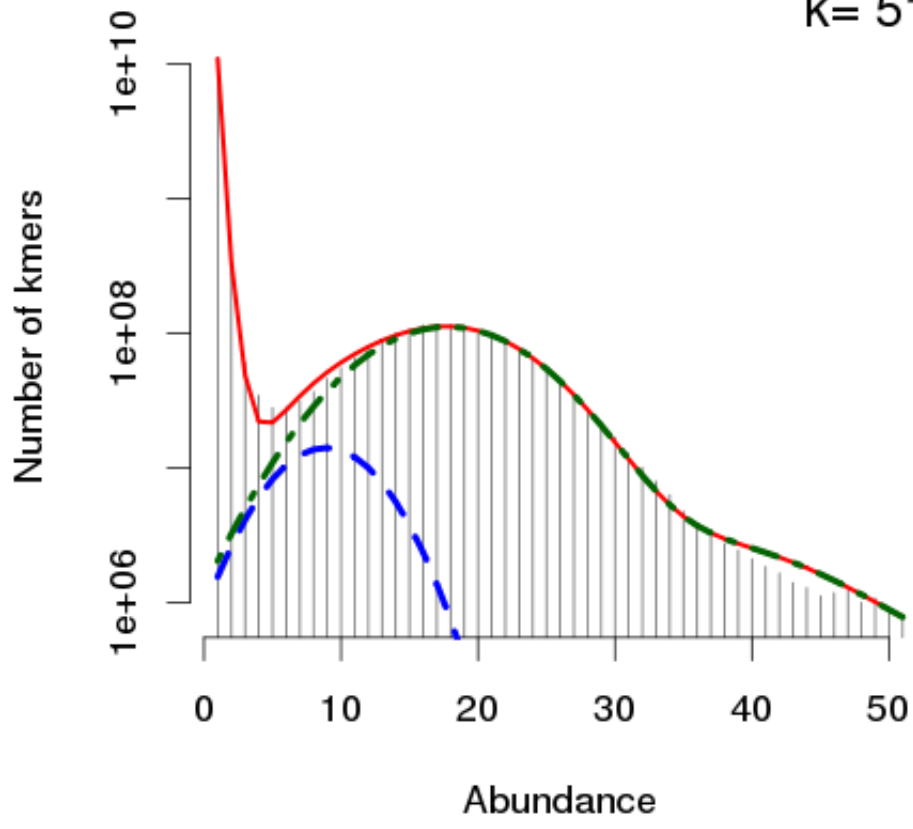
k= 31



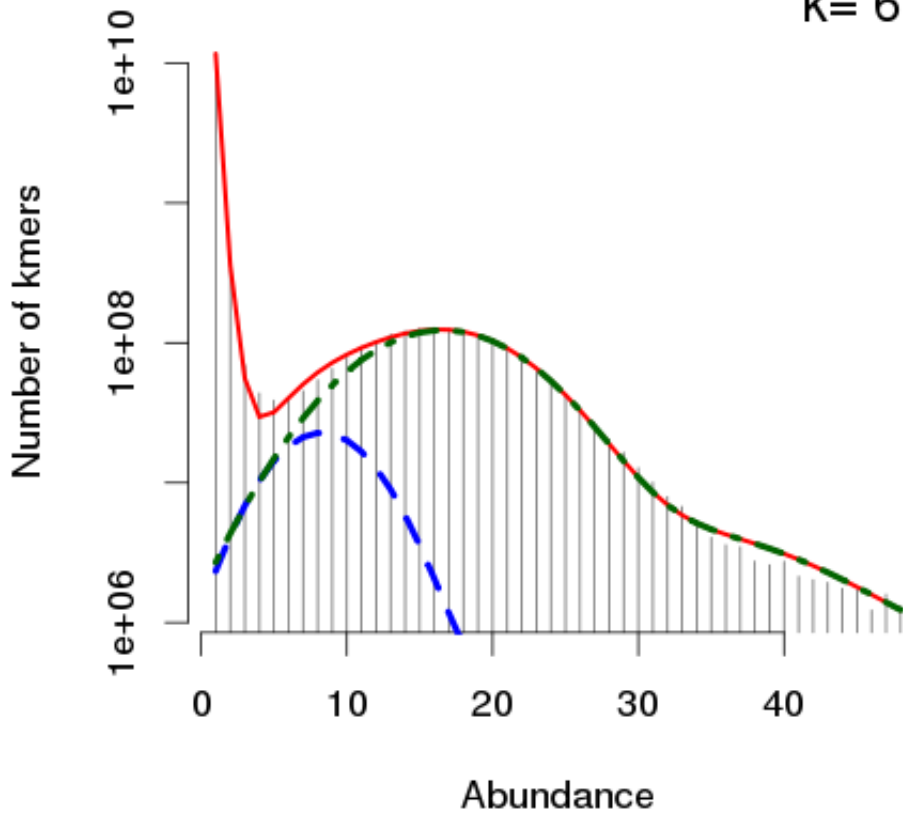
k= 41



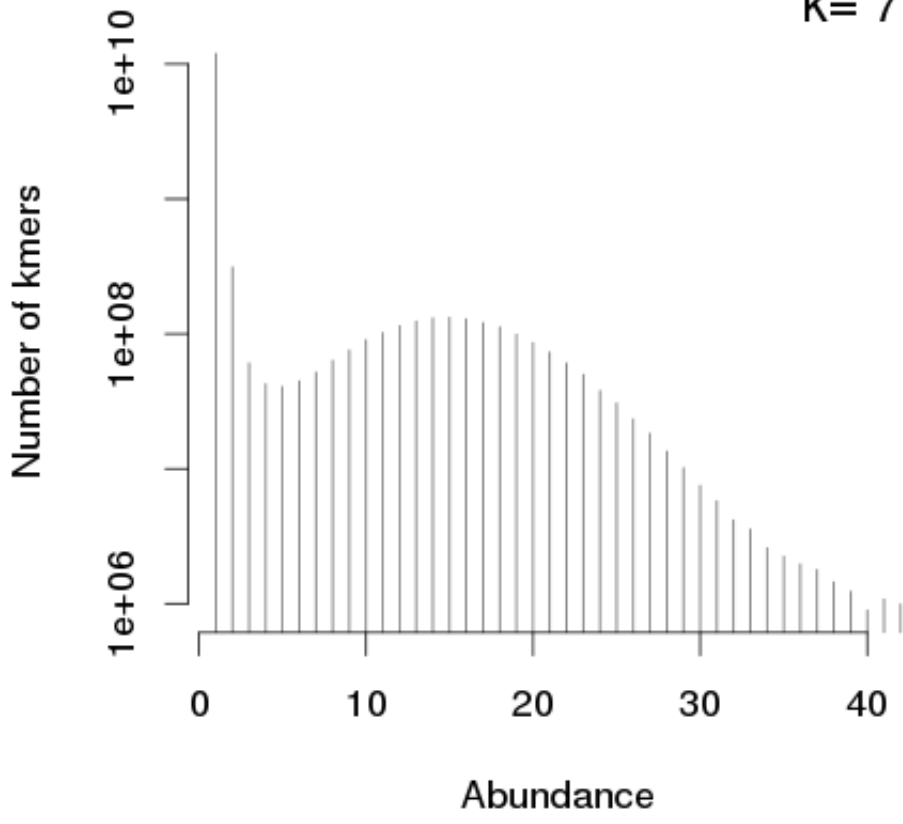
k= 51



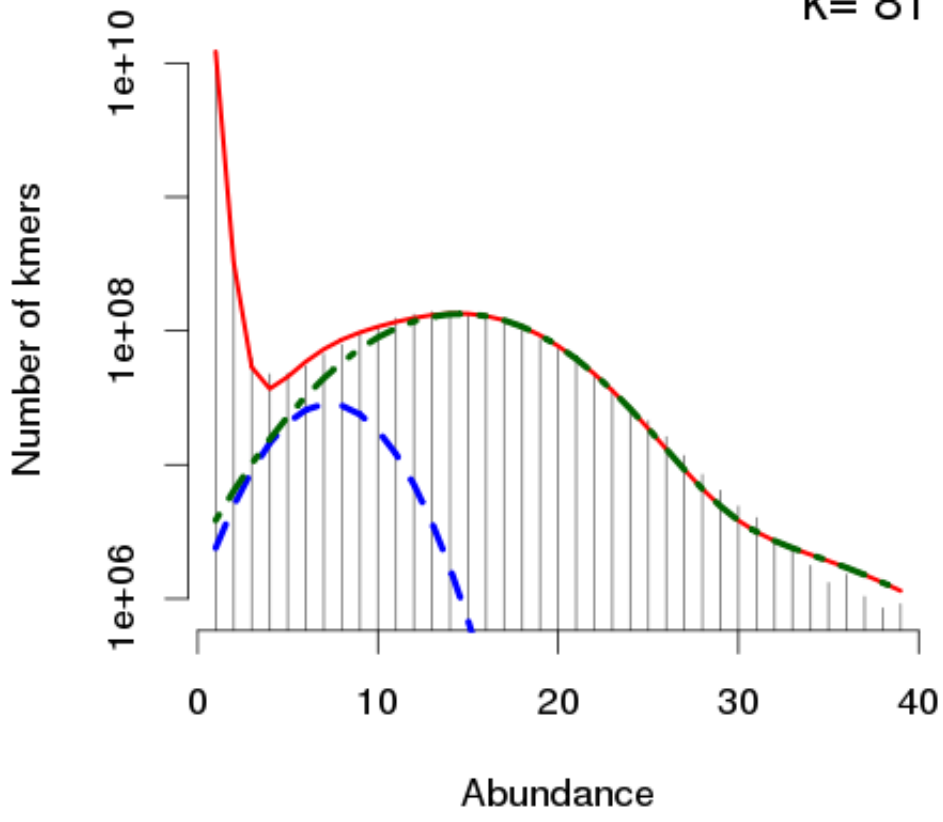
k= 61



k= 71

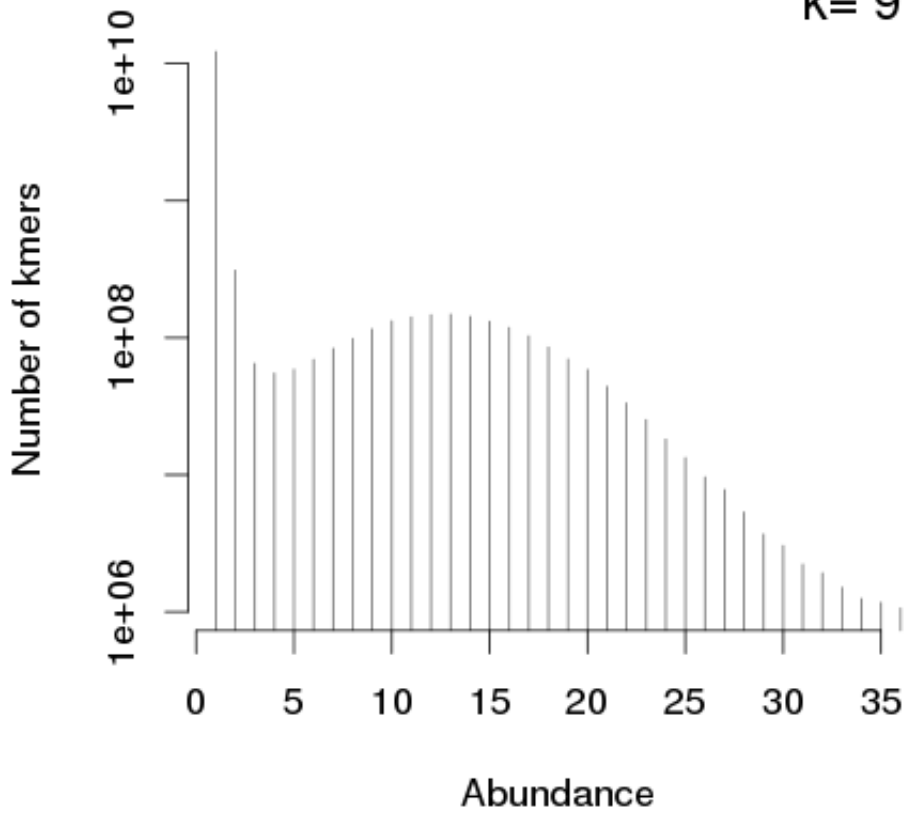


k= 81

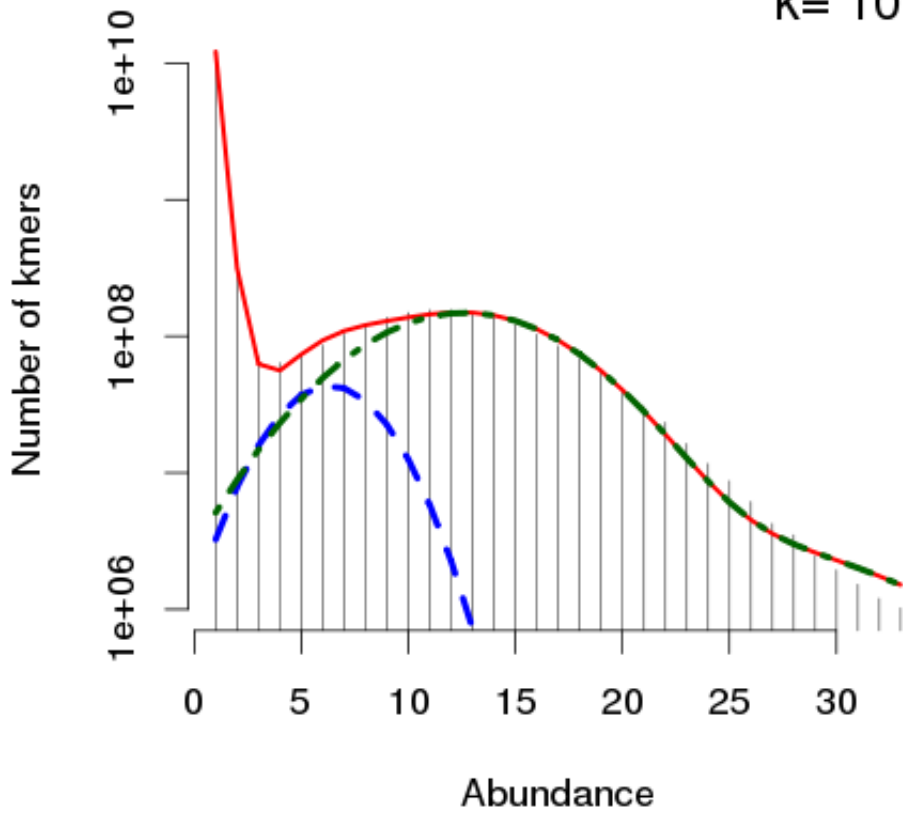




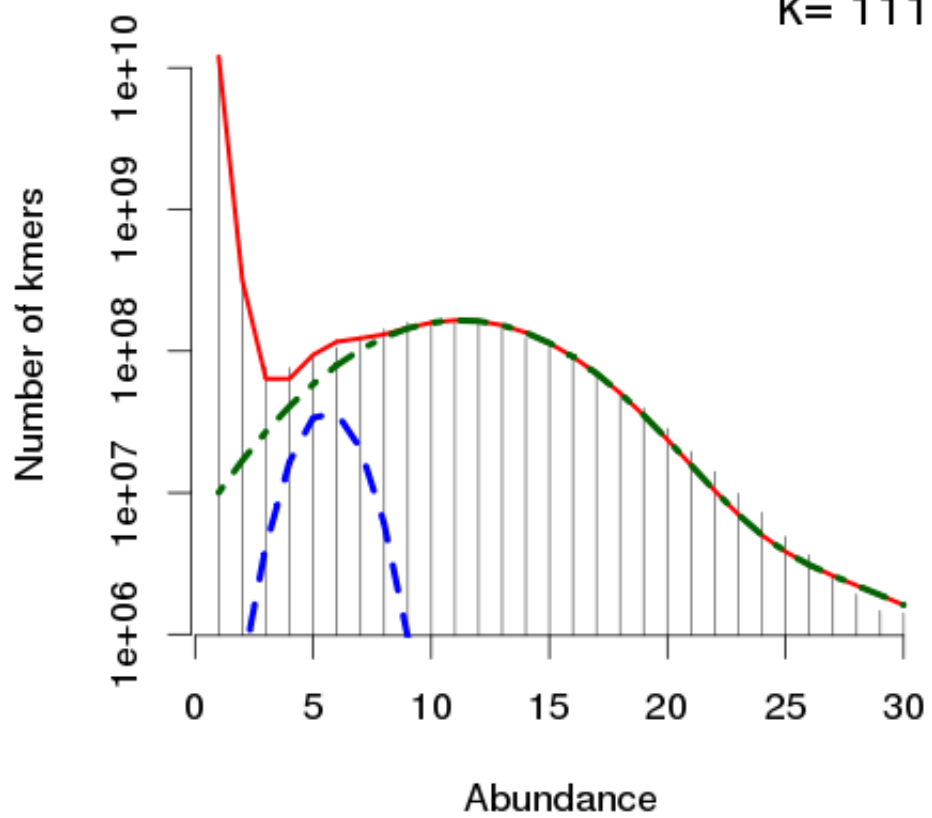
k= 91



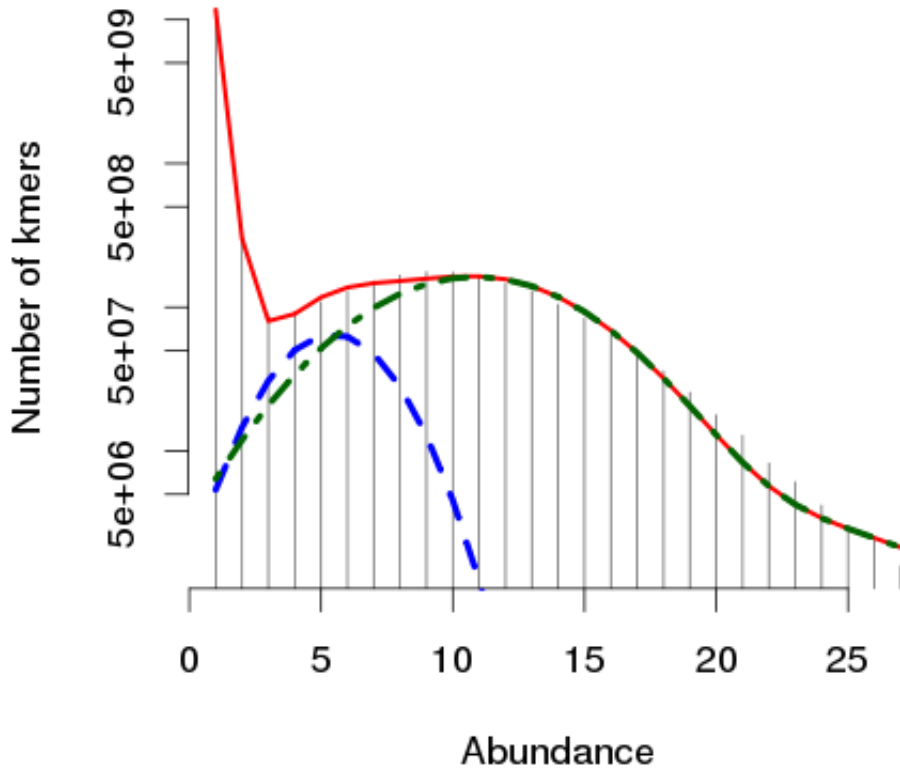
k= 101



k= 111



k= 121



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