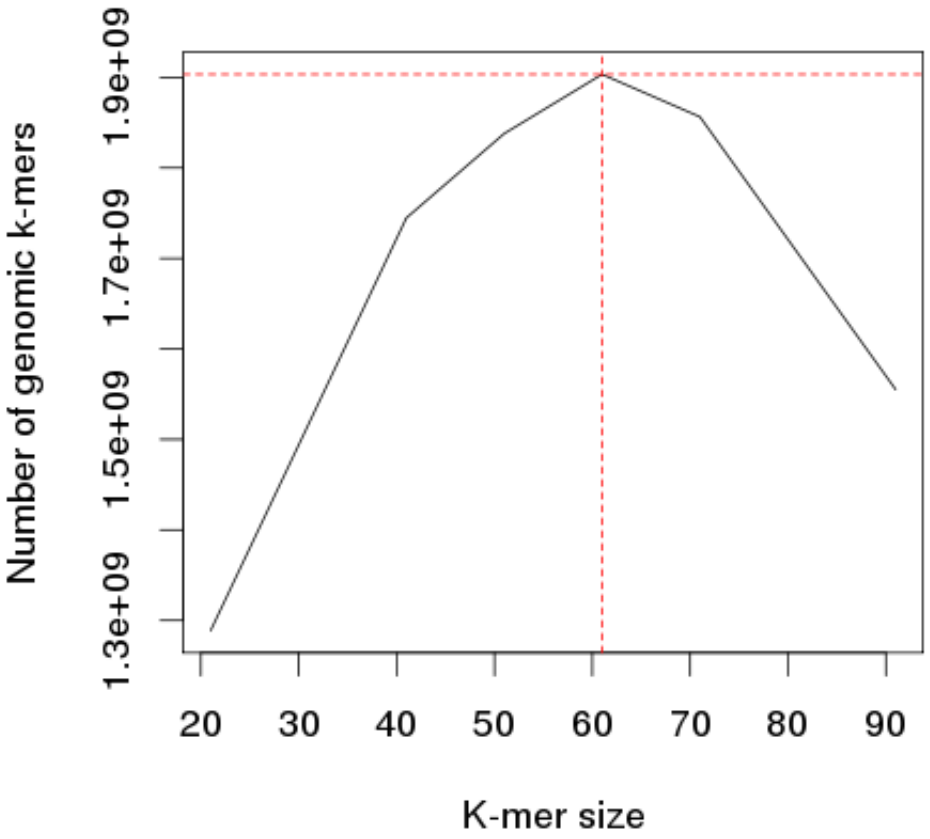
KmerGenie report

Predicted best k: 61

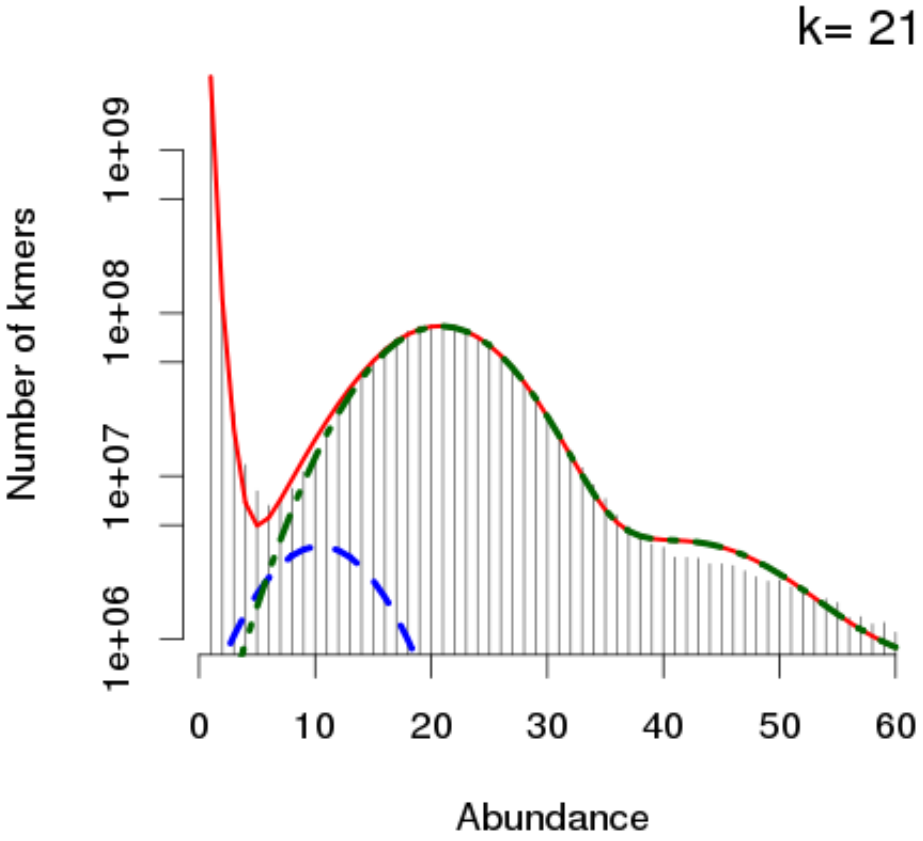
Predicted assembly size: 1903304894 bp

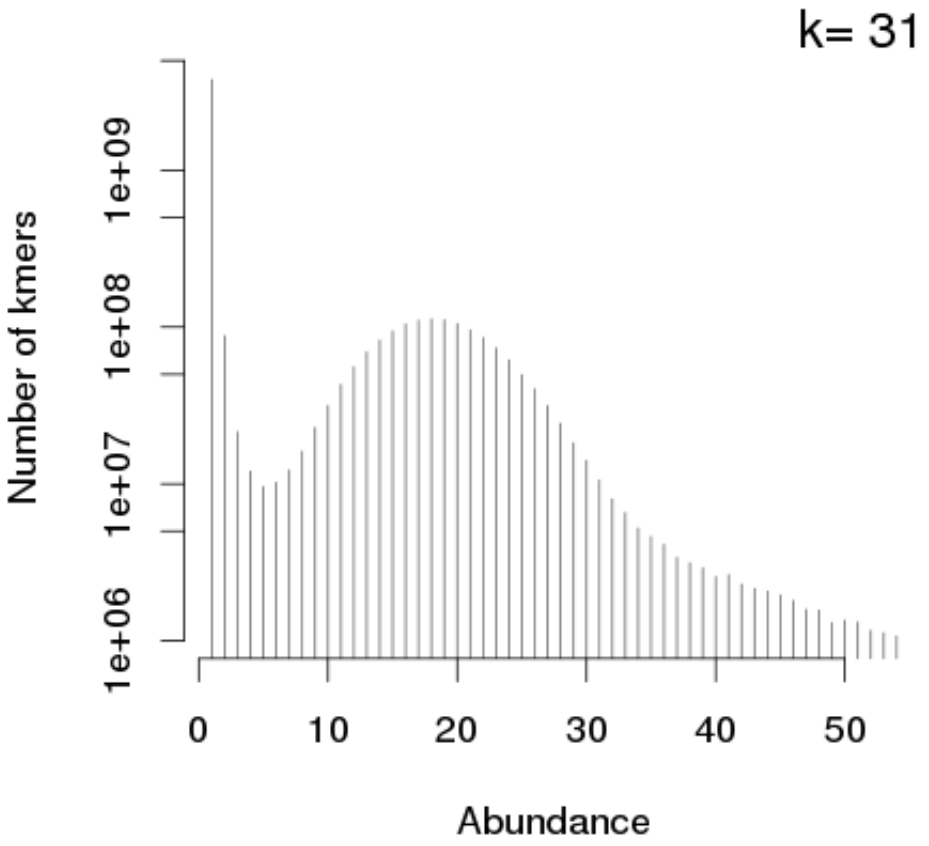


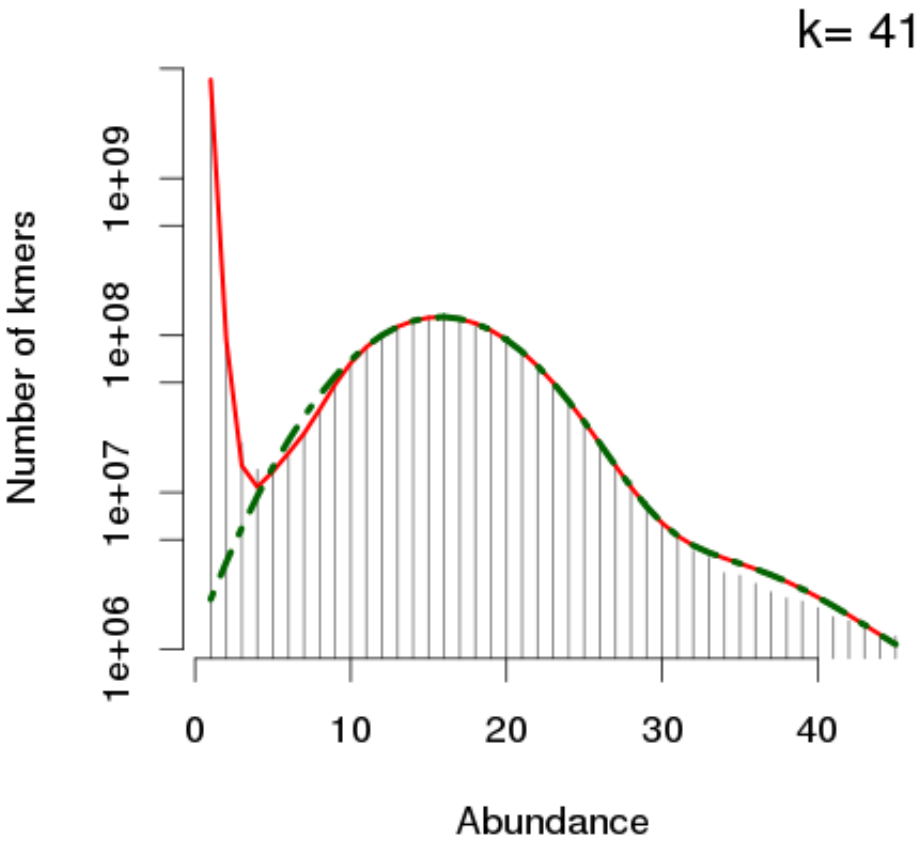
The above plot should be roughly concave and have a clear global maximum. If not, the predicted best k is likely to be inaccurate.
Click here for more details.

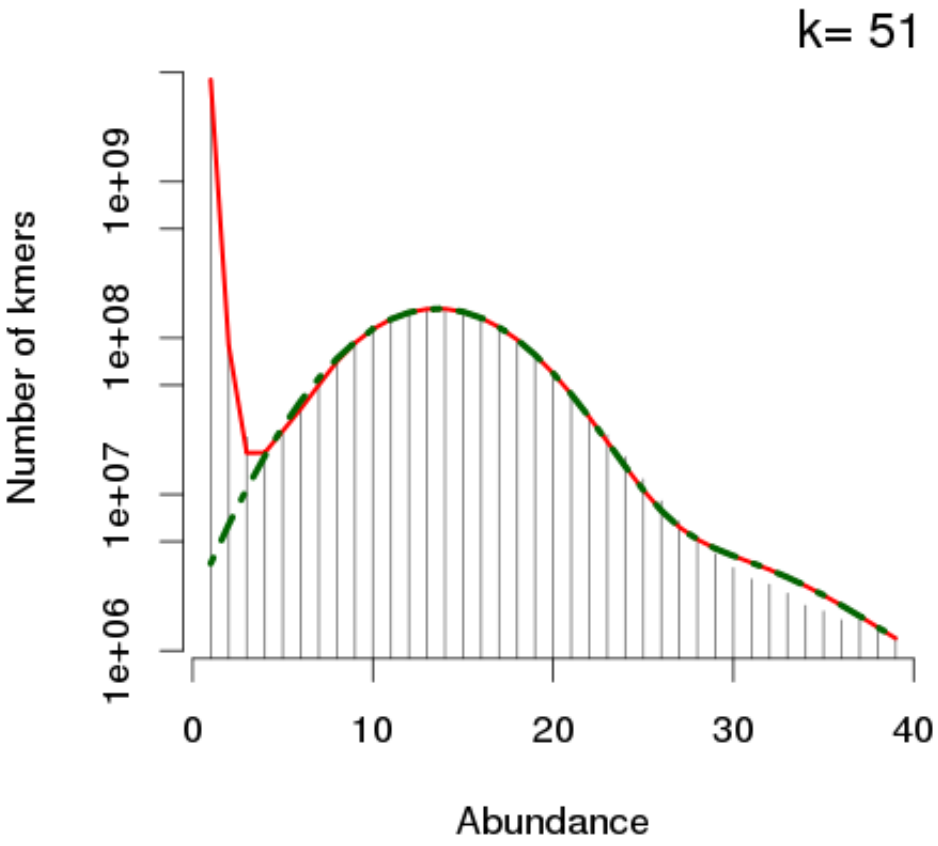
Sampled histogram and fit for each value of k

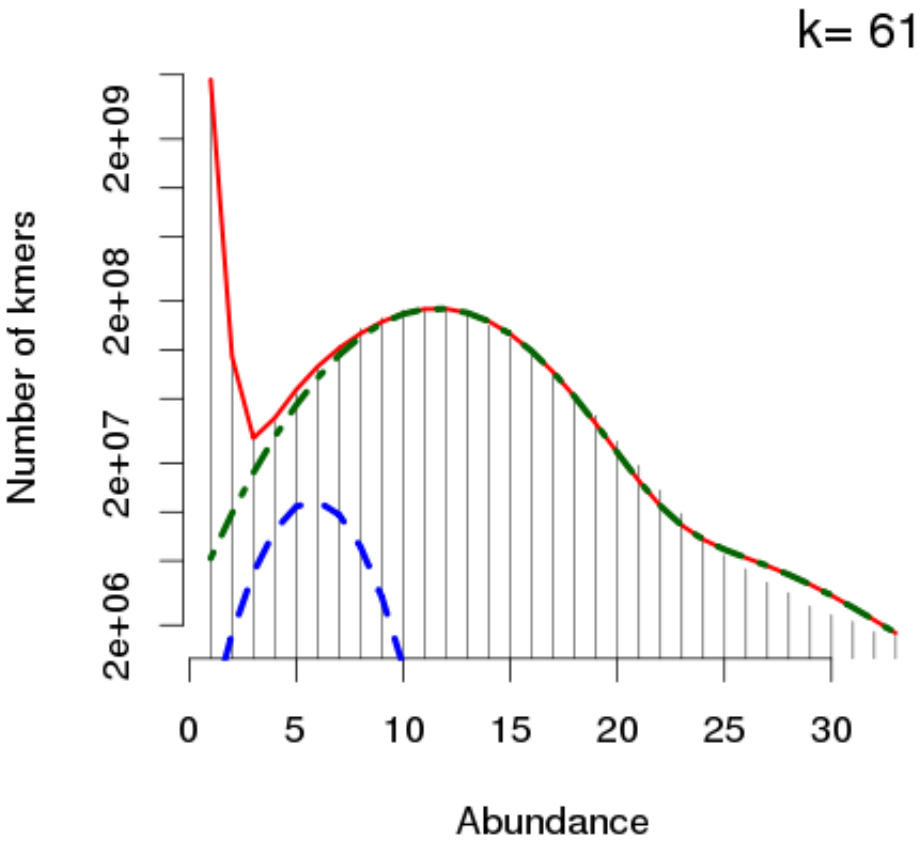
Colors of the fits: red is the fit of the complete statistical model of the histogram (erronous k-mers + genomic k-mers). When using the diploid model, green are only the heterozygous k-mers, green are only the homozygous k-mers.

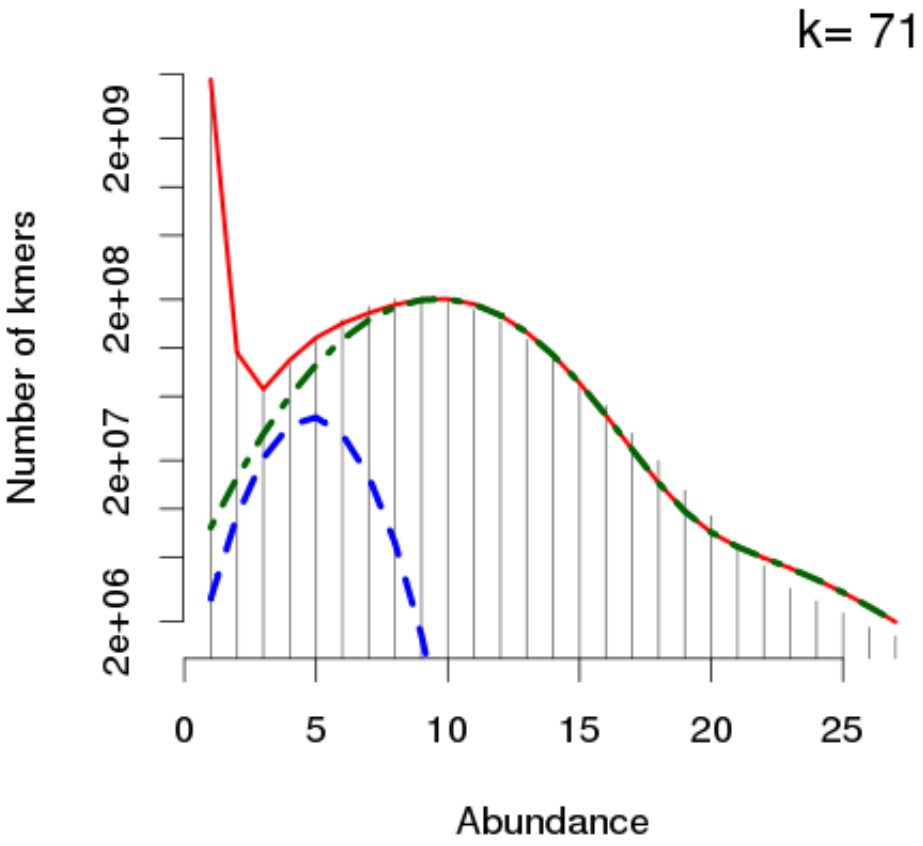


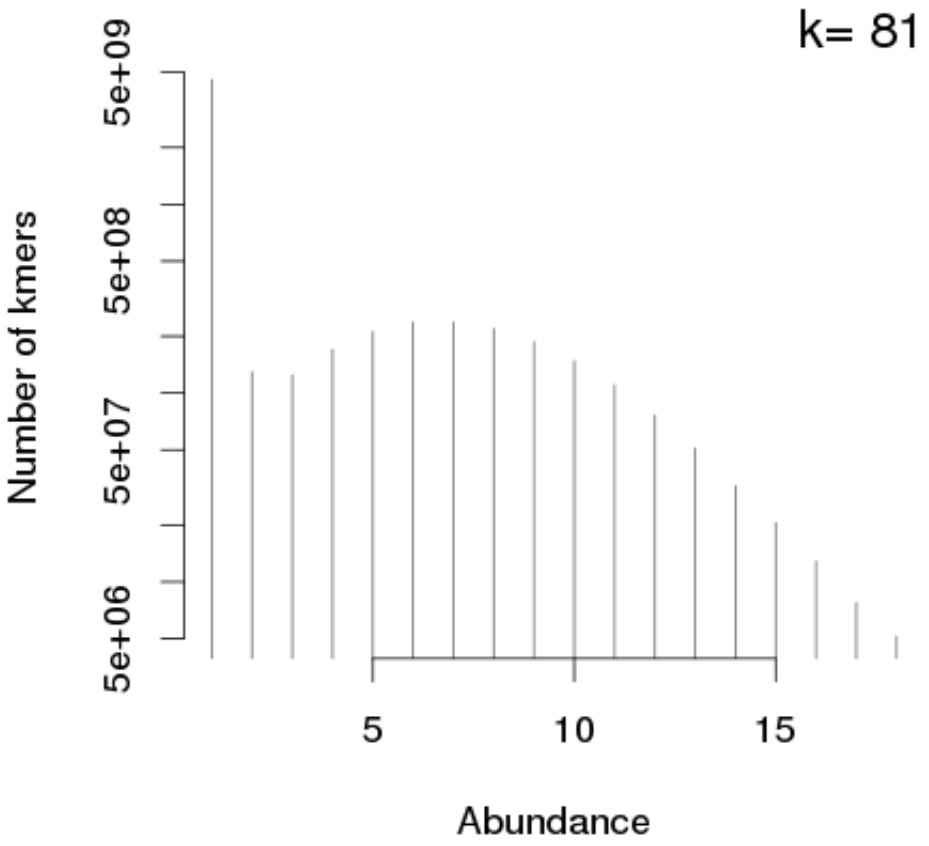

k= 31
Number of kmers
1e+06
1e+07
1e+08
1e+09
0
10
20
30
40
50
Abundance

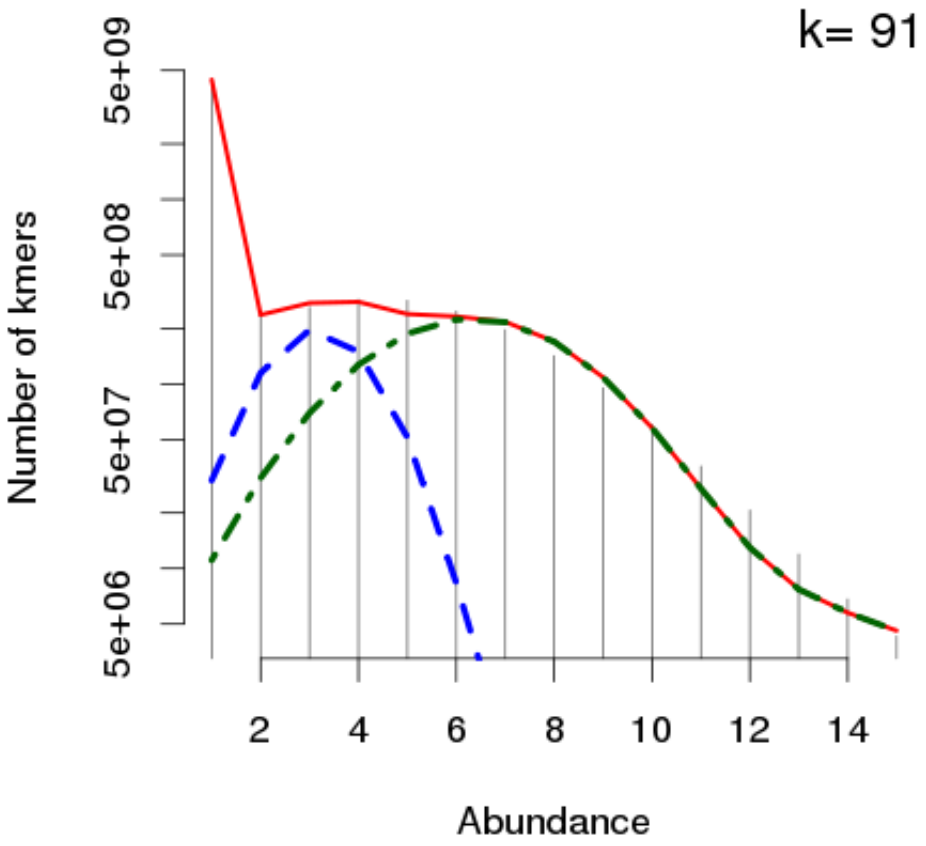

k= 41
Number of kmers
1e+06
1e+07
1e+08
1e+09
0
10
20
30
40
Abundance

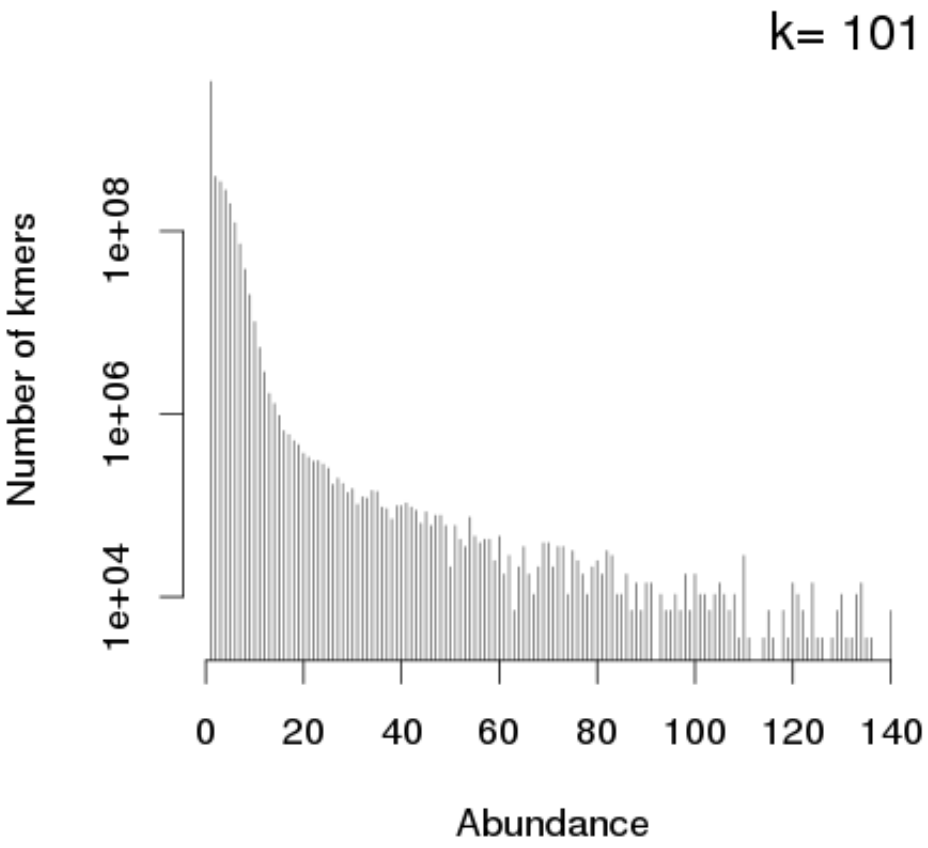

k= 51
Number of kmers
1e+06
1e+07
1e+08
1e+09
0
10
20
30
40
Abundance

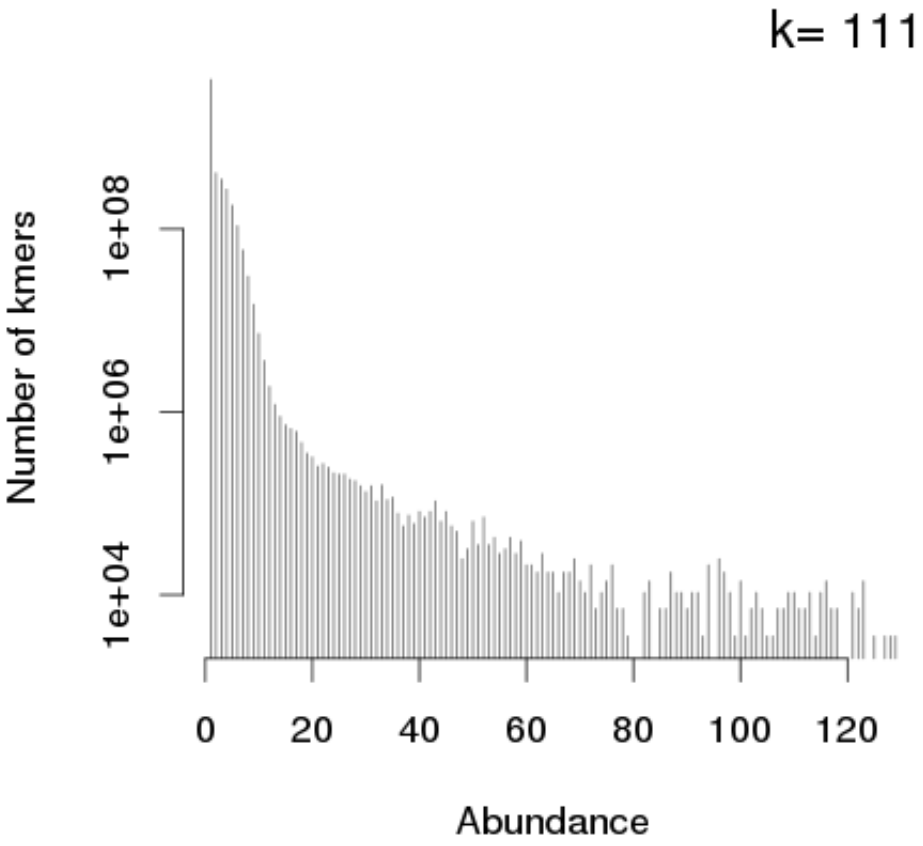

k= 61
Number of kmers
2e+06
2e+07
2e+08
2e+09
0
5
10
15
20
25
30
Abundance

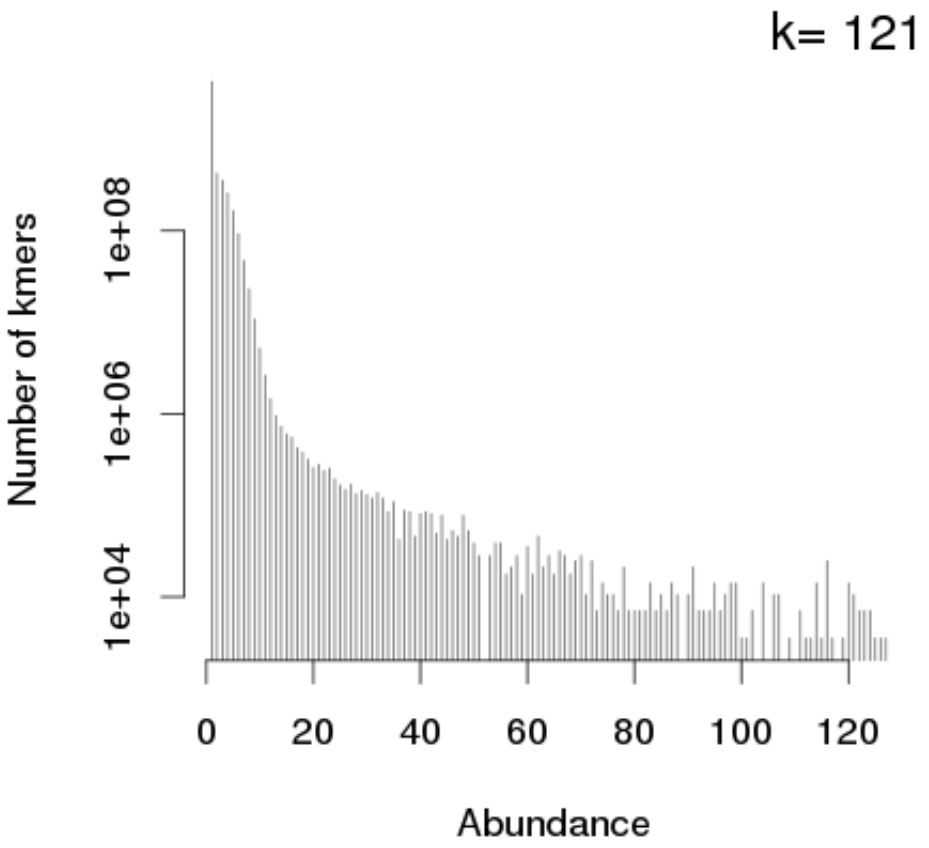

k= 71
Number of kmers
2e+06
2e+07
2e+08
2e+09
0
5
10
15
20
25
Abundance


k= 81
Number of kmers
5e+06
5e+07
5e+08
5e+09
5
10
15
Abundance


k= 91
Number of kmers
5e+06
5e+07
5e+08
5e+09
2
4
6
8
10
12
14
Abundance


k= 101
Number of kmers
1e+04
1e+06
1e+08
0
20
40
60
80
100
120
140
Abundance


k= 111
Number of kmers
1e+04
1e+06
1e+08
0
20
40
60
80
100
120
Abundance



Generated by KmerGenie