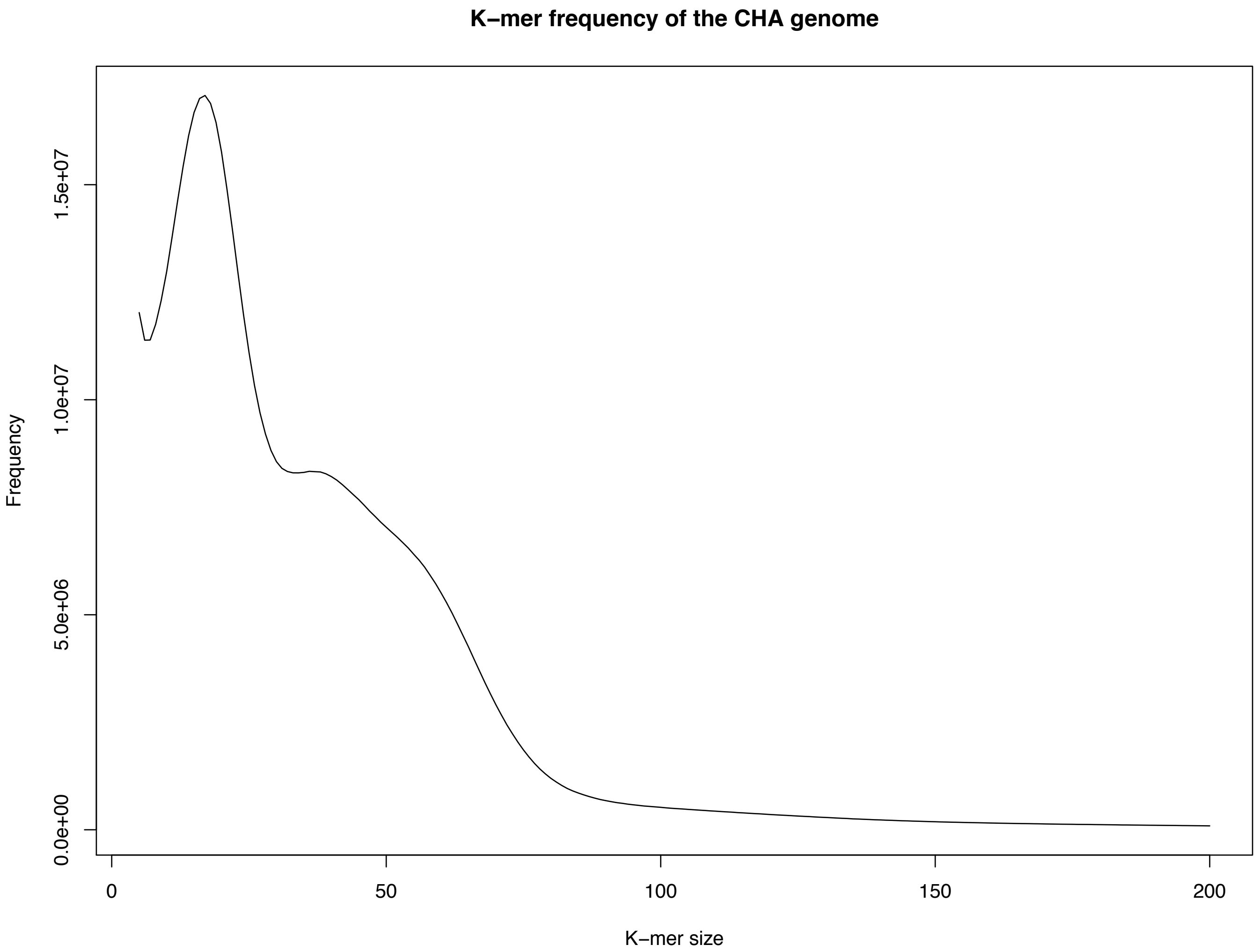
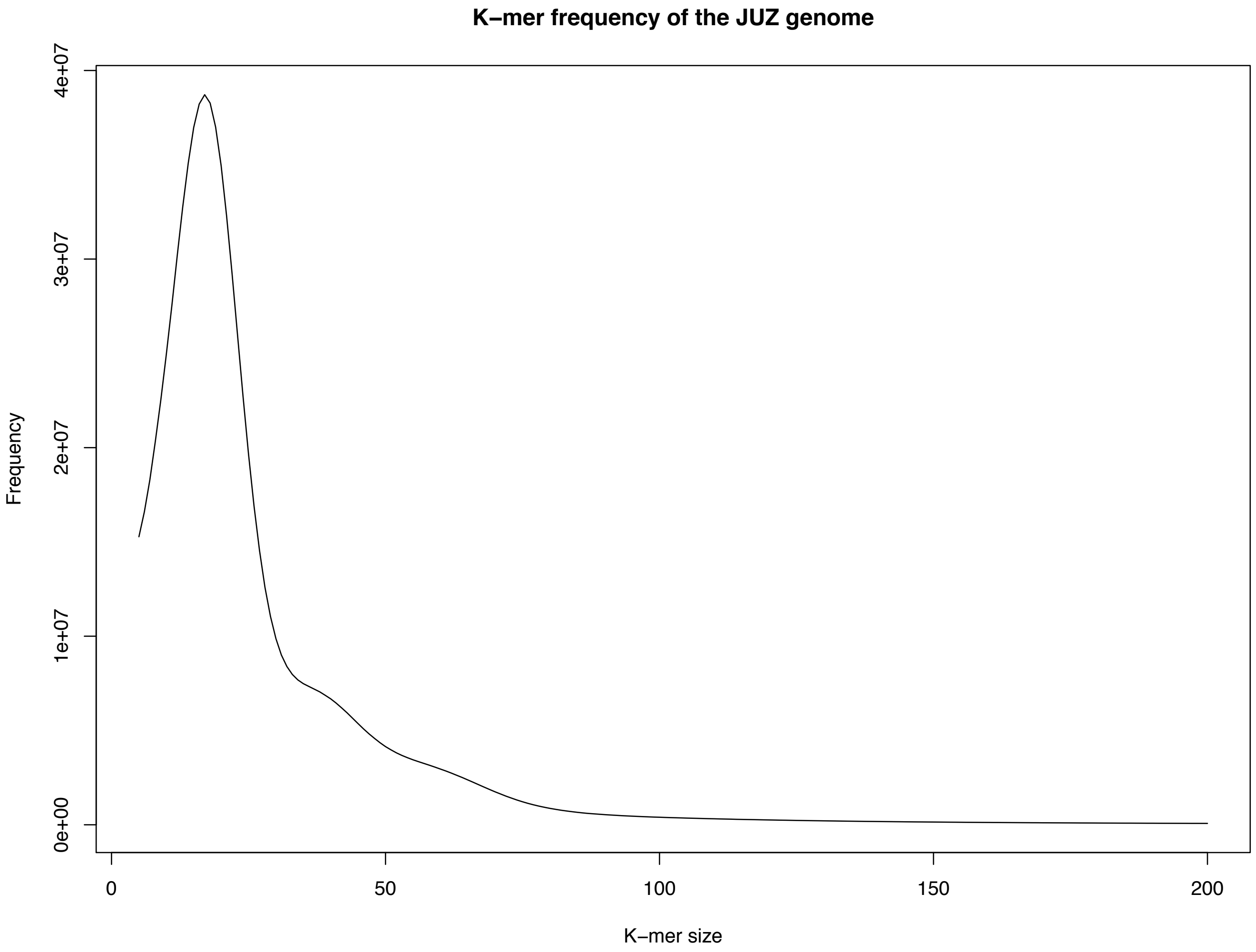
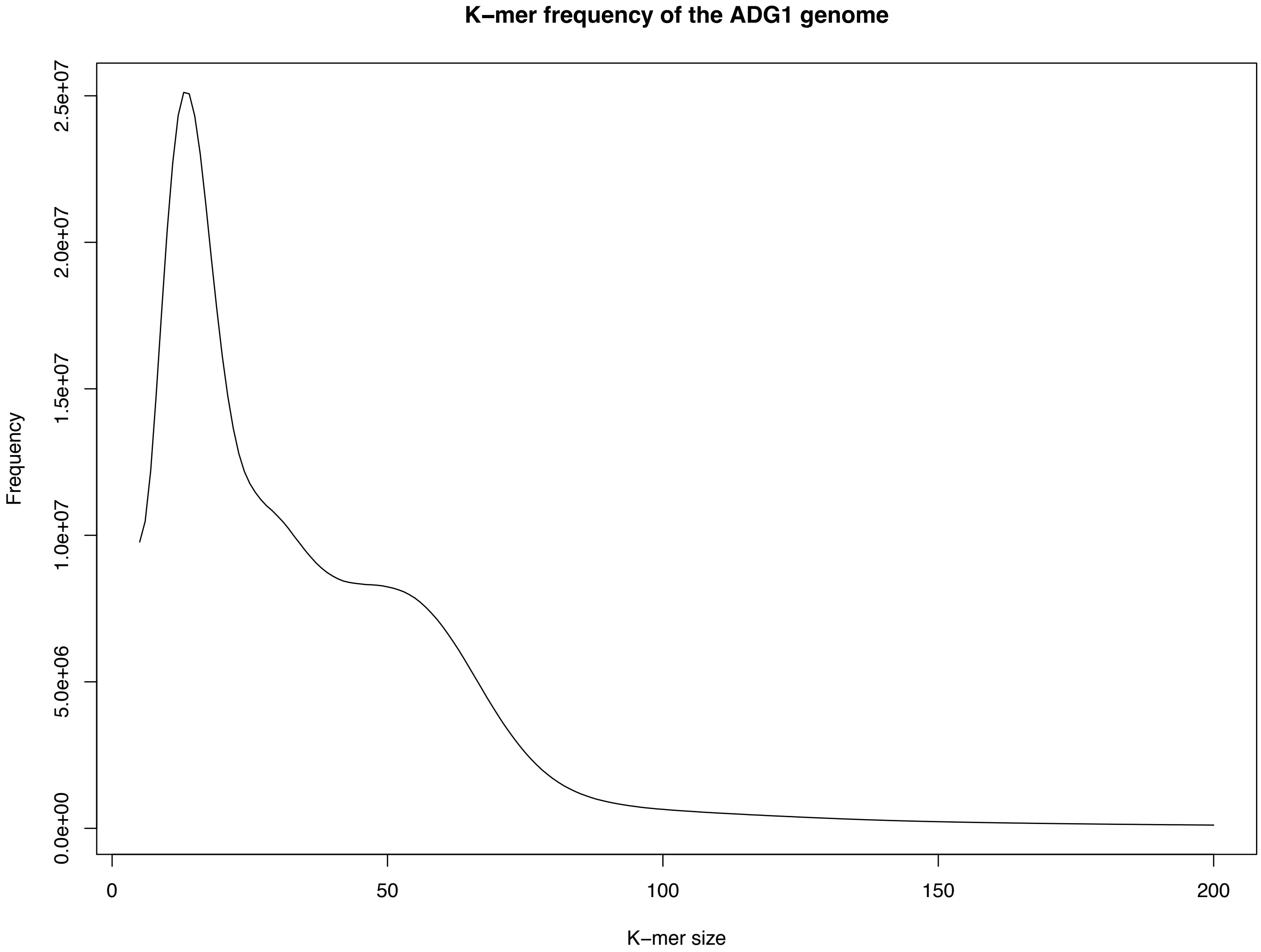


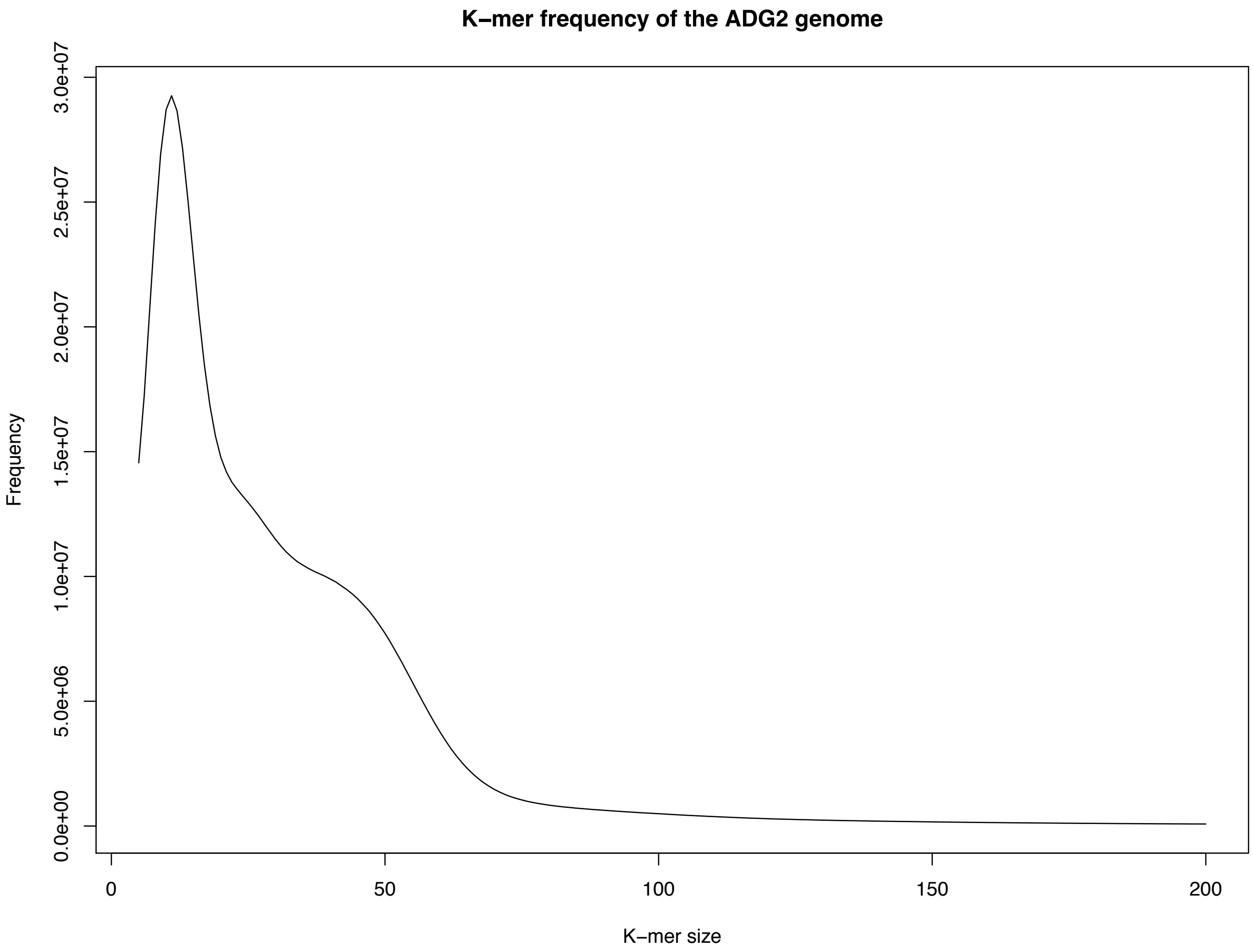
Supplementary Figure 1: The k-mer frequency of the CHA genome. The increased heterozygosity of the genome is validated by the tendency towards bimodal distribution of the k-mer frequency.



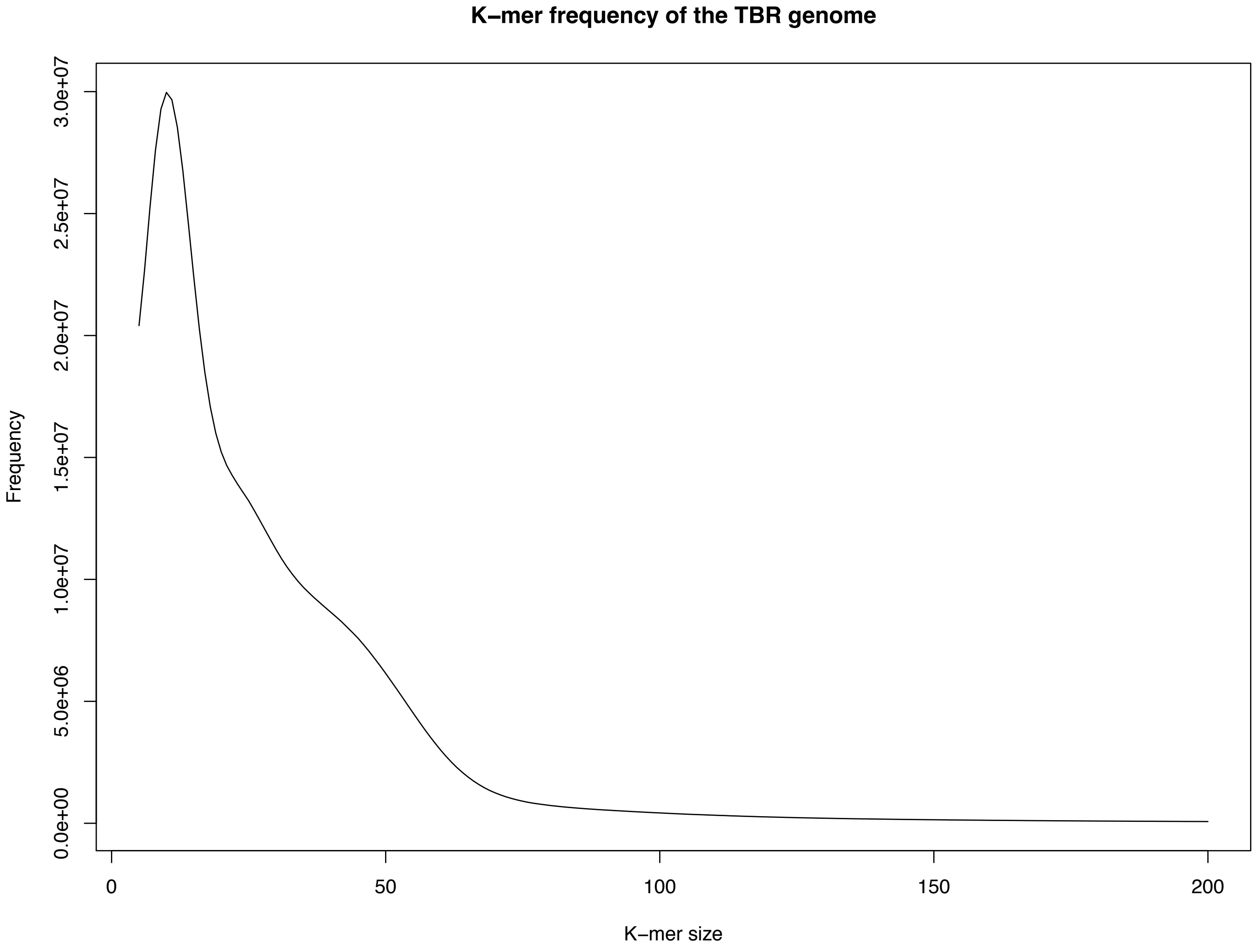
Supplementary Figure 2: The k-mer frequency of the JUZ genome. The increased heterozygosity of the genome is validated by the tendency towards bimodal distribution of the k-mer frequency.



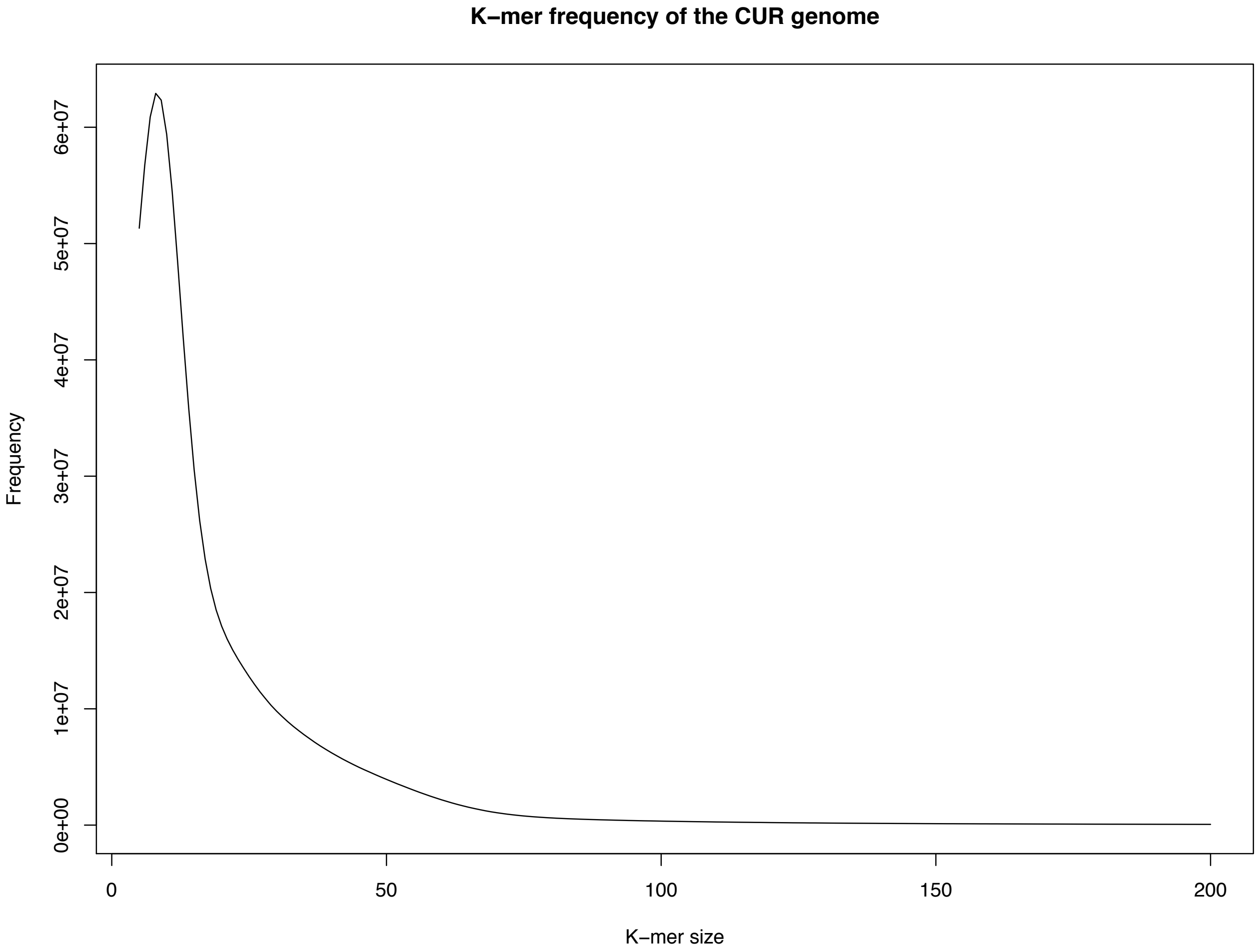
Supplementary Figure 3: The k-mer frequency of the ADG1 genome. The increased heterozygosity of the genome is validated by the tendency towards bimodal distribution of the k-mer frequency.



Supplementary Figure 4: The k-mer frequency of the ADG2 genome. The increased heterozygosity of the genome is validated by the tendency towards bimodal distribution of the k-mer frequency.



Supplementary Figure 5: The k-mer frequency of the TBR genome. The increased heterozygosity of the genome is validated by the tendency towards bimodal distribution of the k-mer frequency.



Supplementary Figure 6: The k-mer frequency of the CUR genome. The increased heterozygosity of the genome is validated by the tendency towards bimodal distribution of the k-mer frequency.