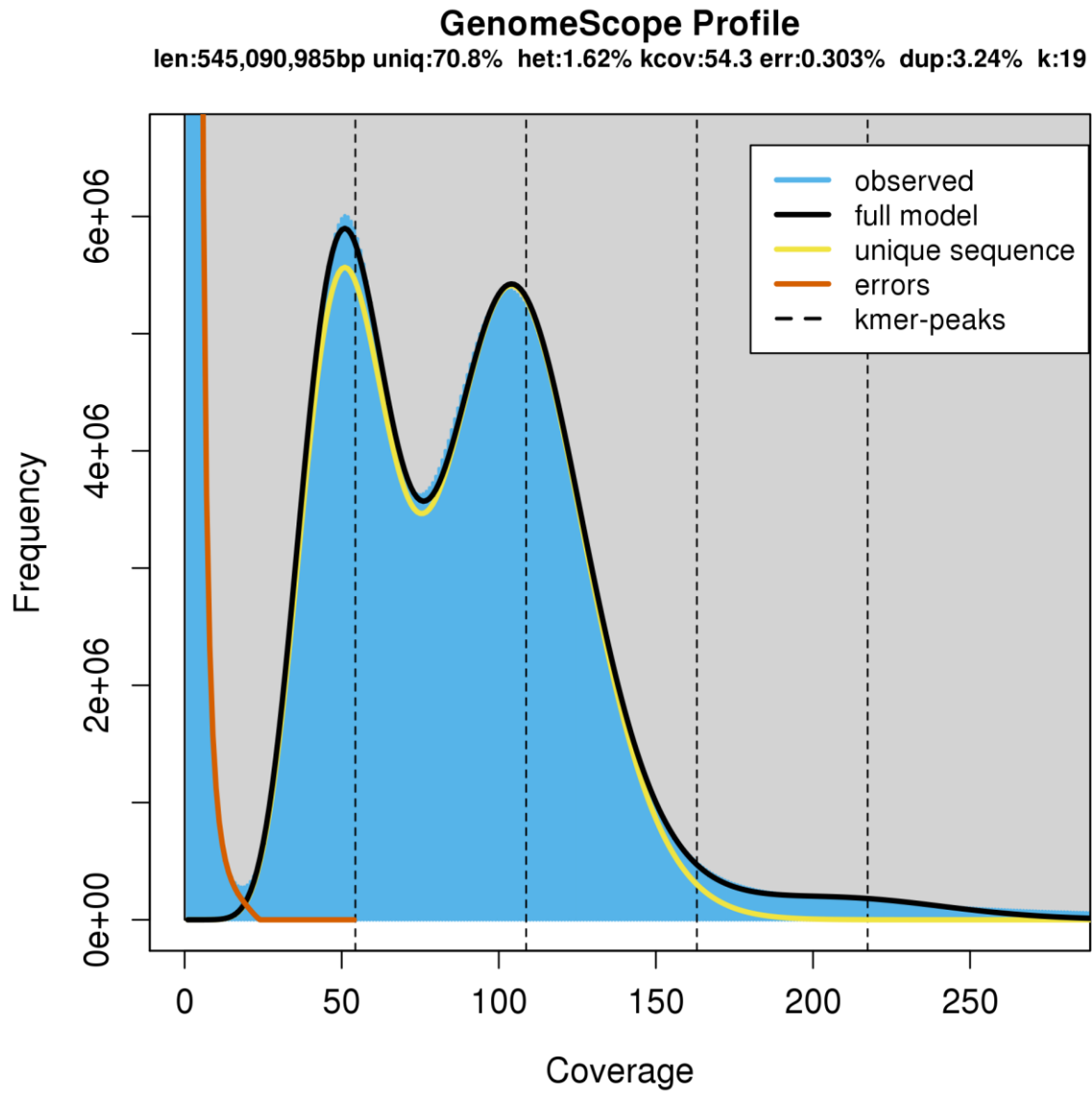


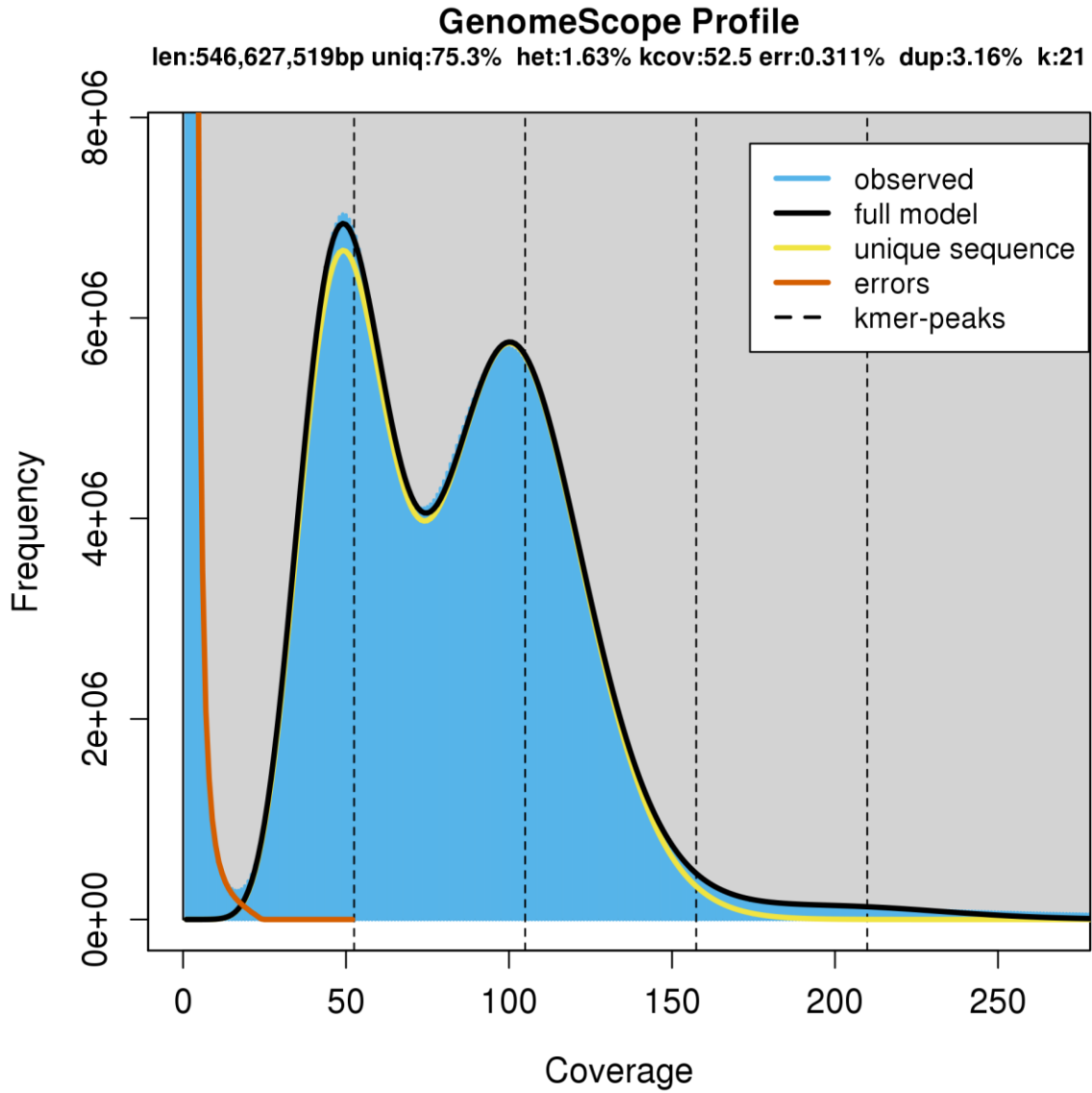
**Supplementary.** Estimation of genome size, repeat content and heterozygosity by GenomeScope, based on 19-, 21- and 25-mers in Illumina NovaSeq sequence reads (*max kmer coverage* disabled).

**19-mer**



**Supplementary.** Estimation of genome size, repeat content and heterozygosity by GenomeScope, based on 19-, 21- and 25-mers in Illumina NovaSeq sequence reads (*max kmer coverage disabled*).

**21-mer**



**Supplementary.** Estimation of genome size, repeat content and heterozygosity by GenomeScope, based on 19-, 21- and 25-mers in Illumina NovaSeq sequence reads (*max kmer coverage* disabled).

**25-mer**

