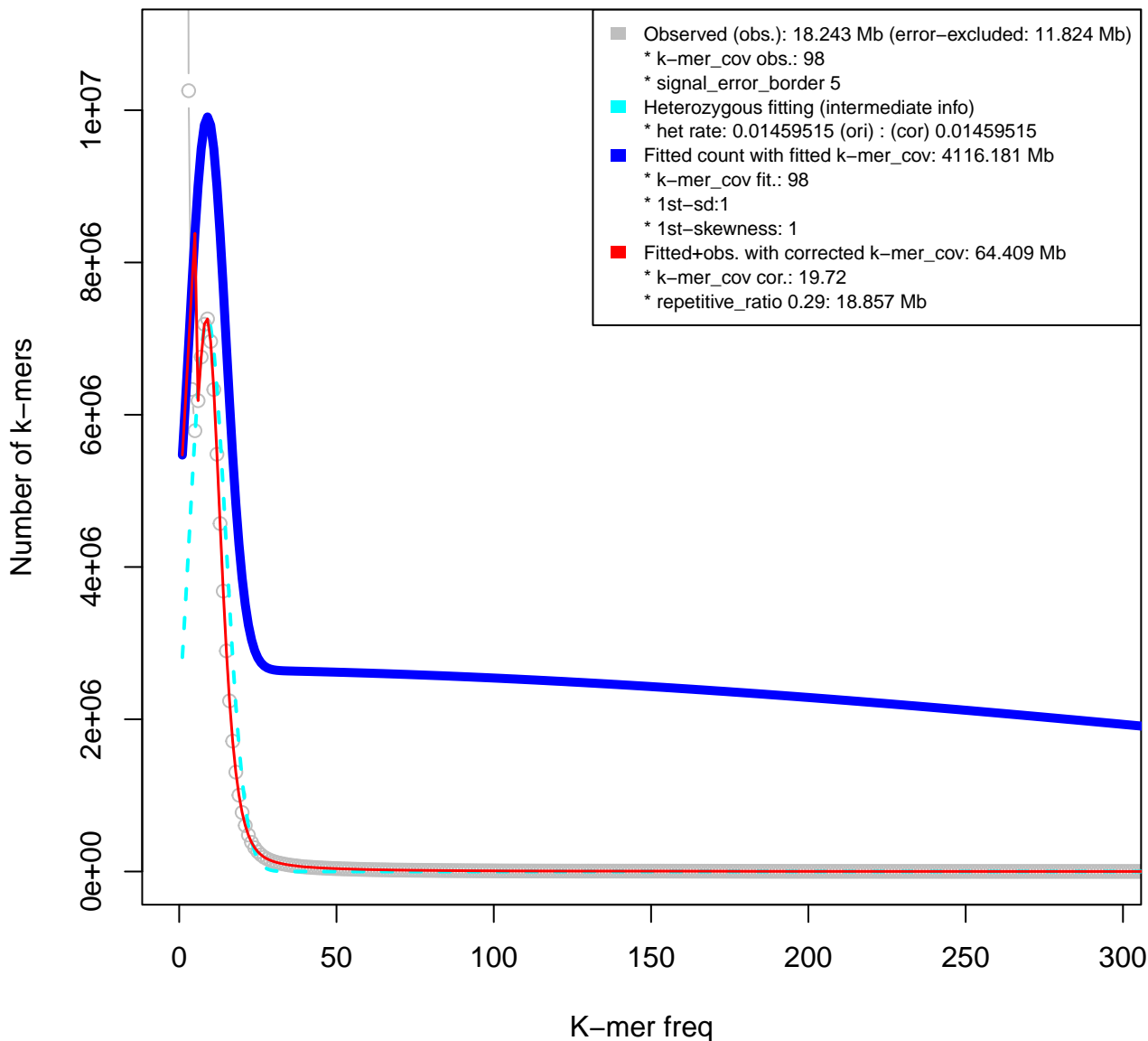


# Sample kmer\_cut\_out.histo k= 21



Genome size estimation by error–excluding, fitting, and correcting

