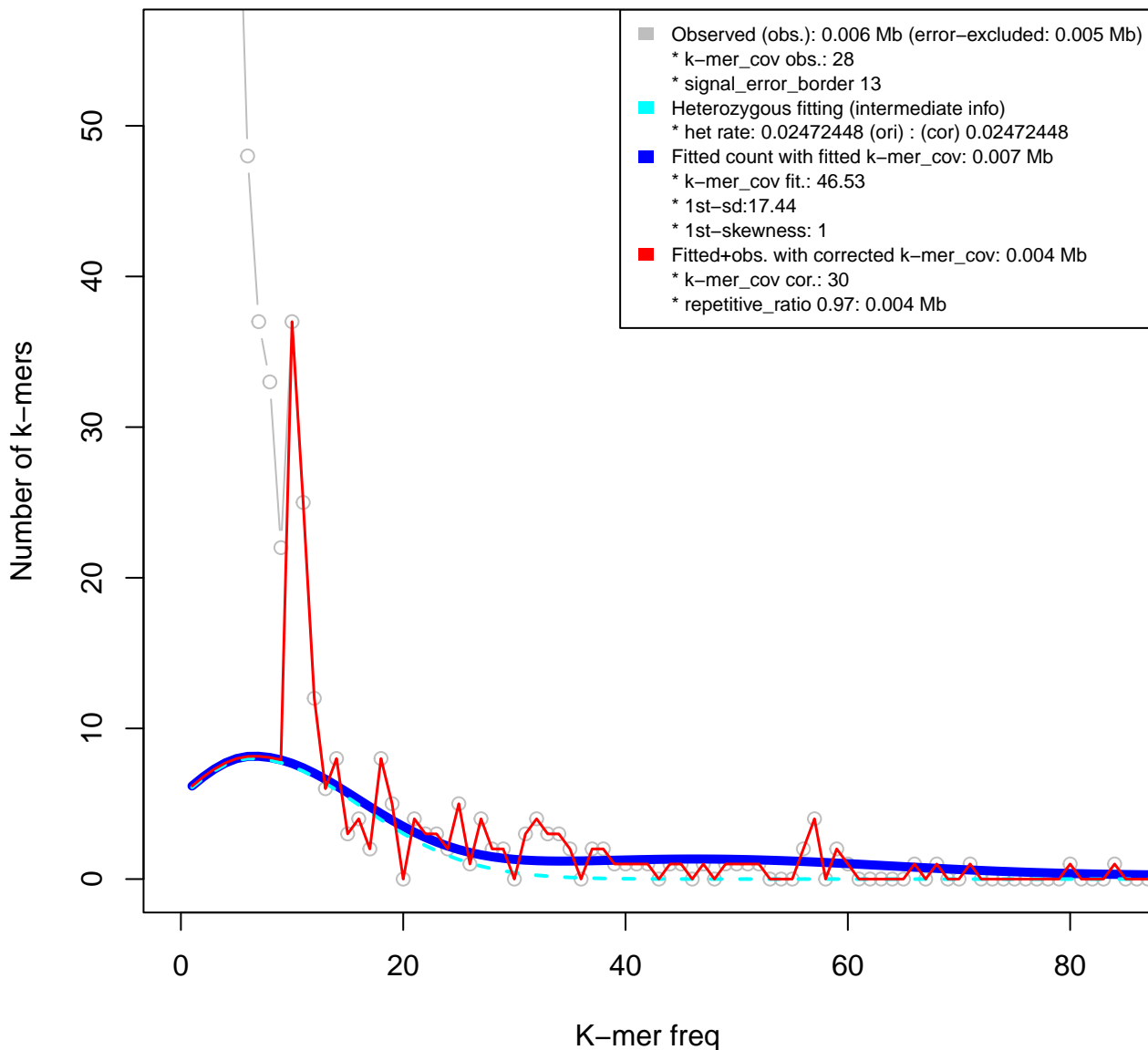


Sample kmer_Teleaulax.histo k= 19



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

