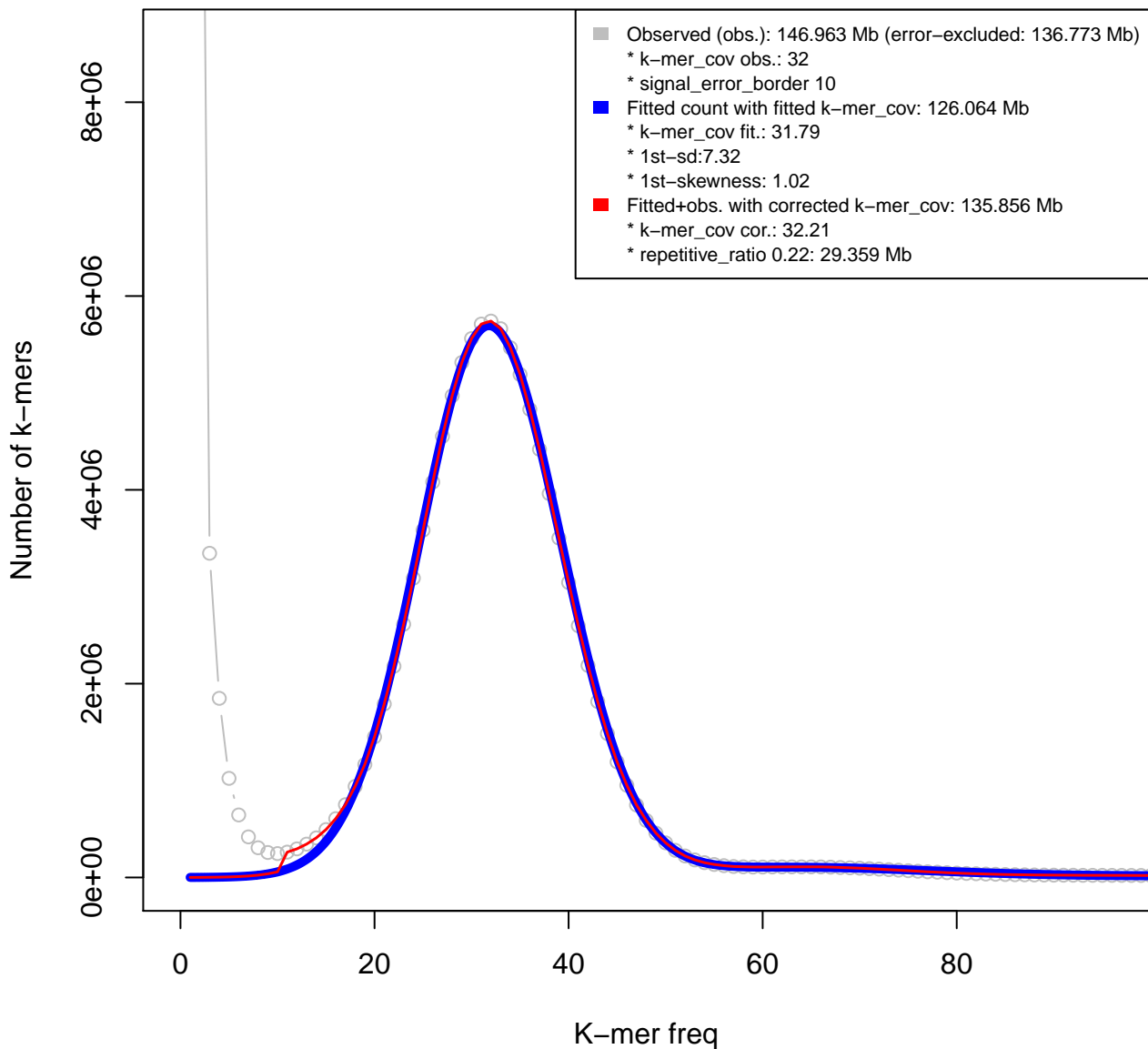


# Sample 10002.21mer.histo k= 21



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

