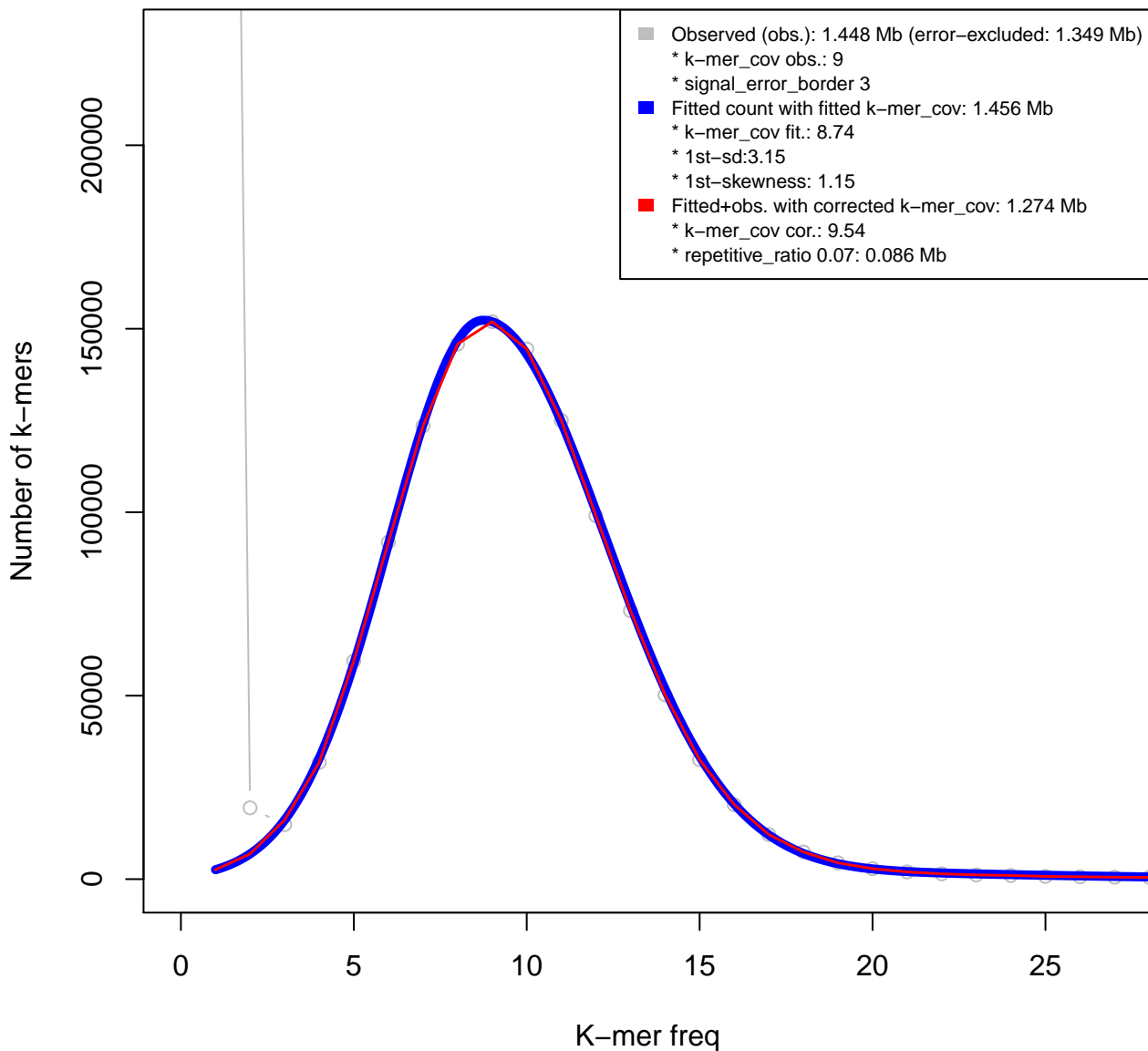


# Sample sim1.histo k= 18



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

