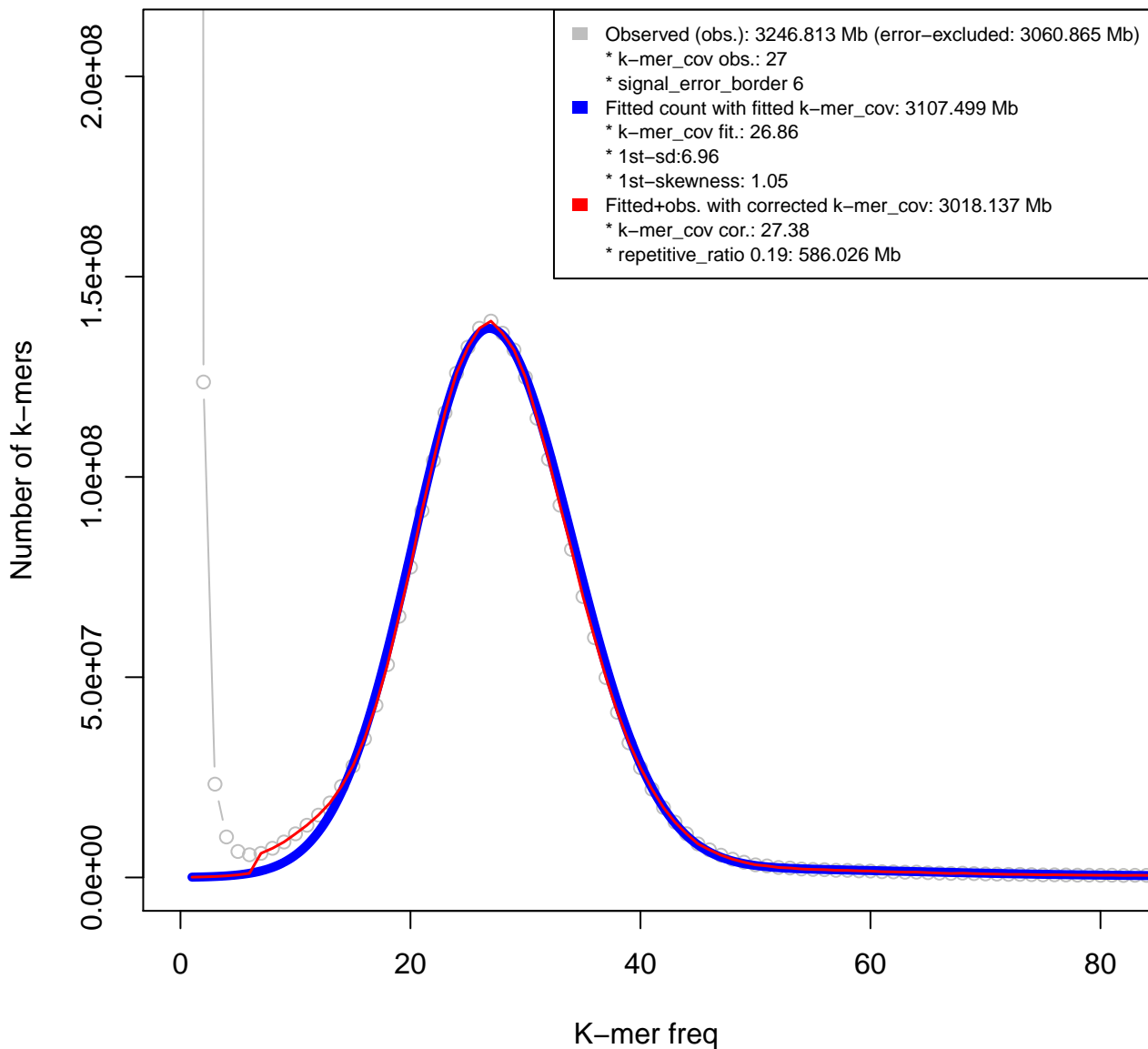


# Sample output.histo k= 27



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

