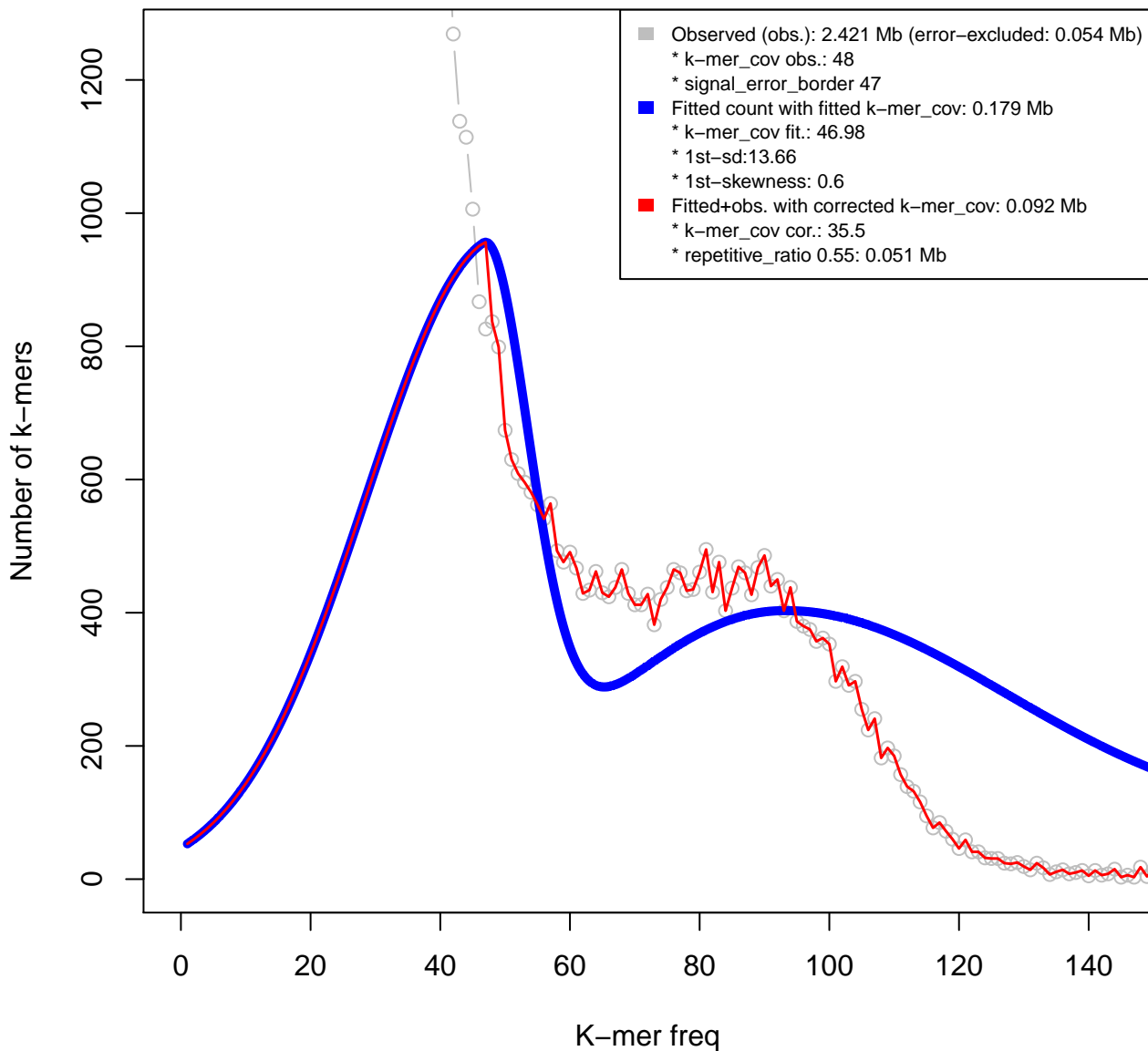


# Sample sim\_k25\_2.histo k= 25



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

