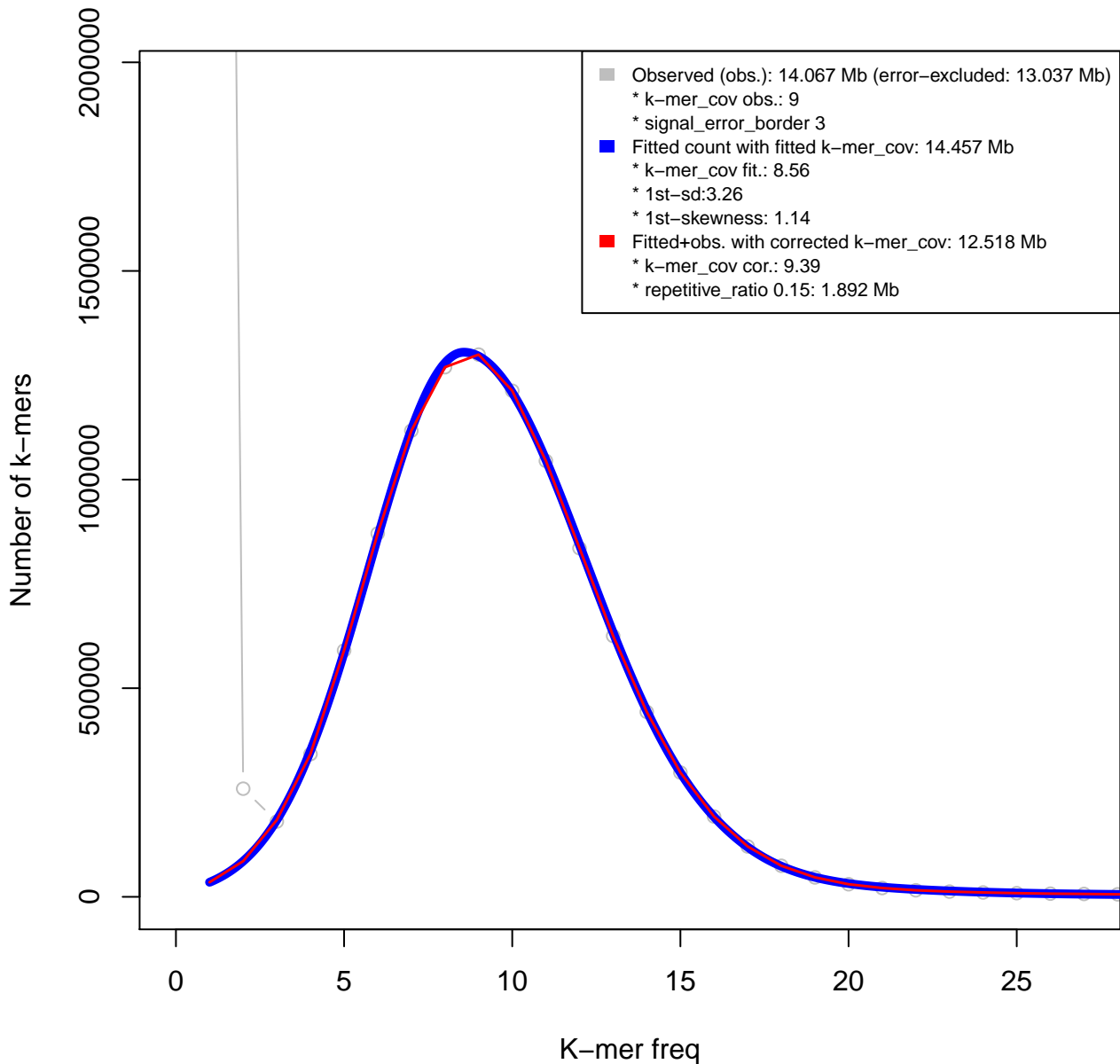


# Sample sim\_m21\_2.histo k= 21



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

