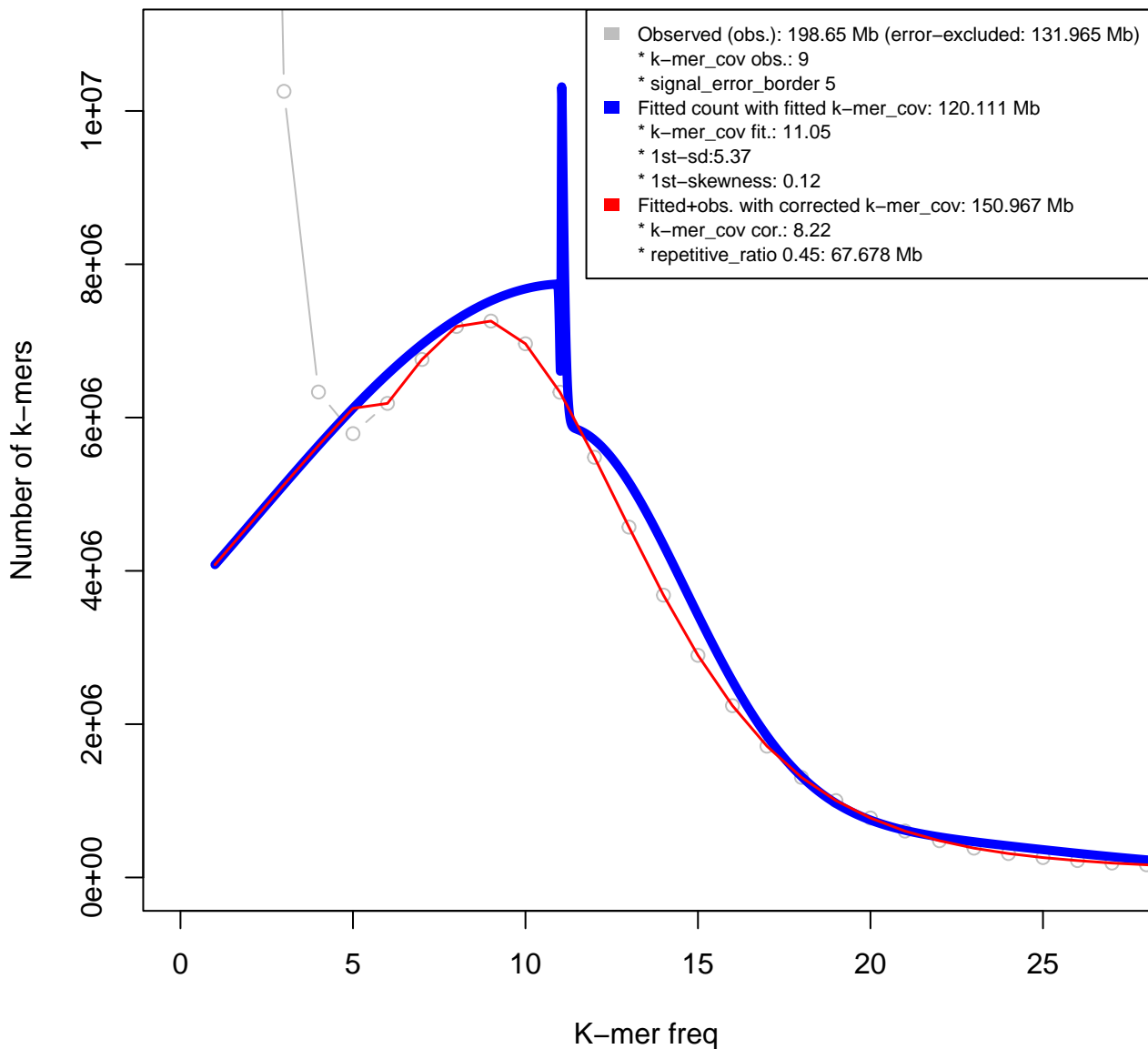


# Sample 21mer\_cut.histo k= 21



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

