

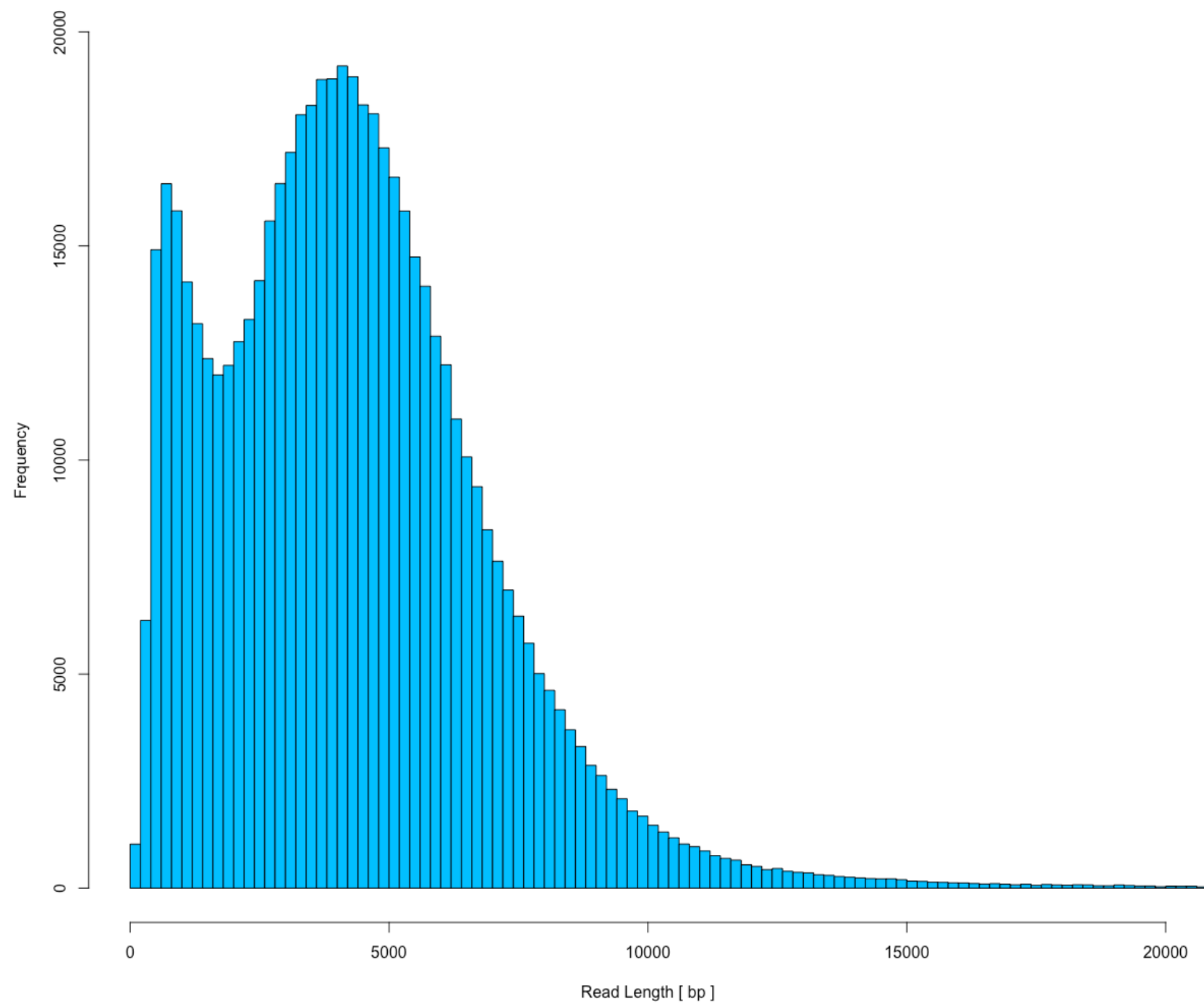


Figure S1. Histogram of the length of raw reads derived from MinION. Much short reads under 500 bp were removed by means of purification using 0.4x magnetic beads before library preparation.

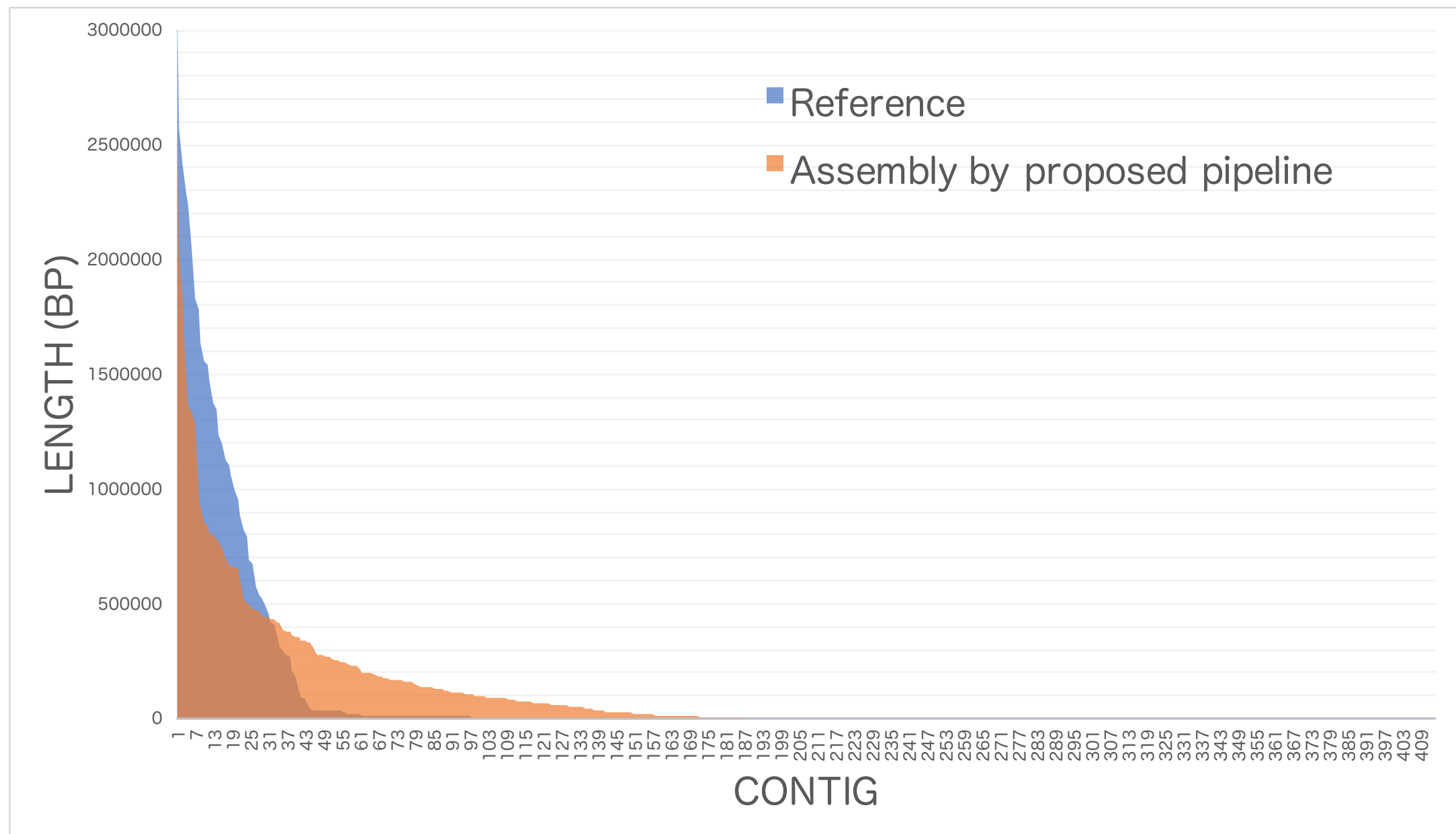


Figure S2. The contigs of assembled genomes of *C. variabilis* sorted in descending order of the length. Reference were previously assembled genome, assembly were assembled genome using the pipeline constructed in this study.