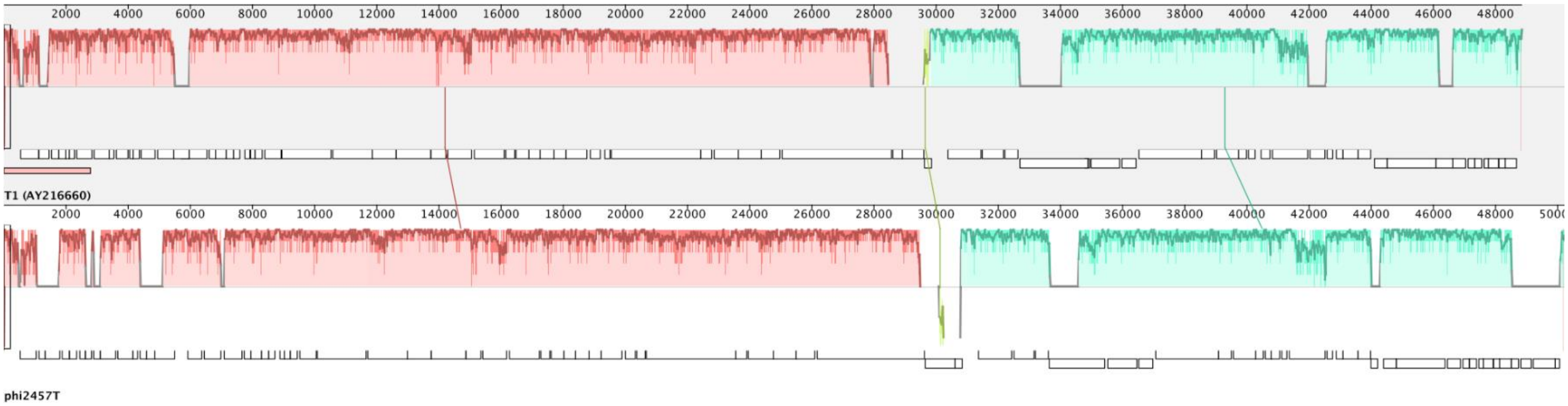
Supplementary Digital Content 1. Mauve-Sequence Alignment.



The genome of Φ2457T was aligned to the previously characterized *E. coli* phage T1 using the progressiveMauve tool (27) in Geneious R9 (Biomatters Ltd.). Colored regions indicate locally collinear blocks (LCBs) free from genomic rearrangements, with graph height indicating similarity. These alignments showed ~70% pairwise identity at the nucleotide level.