Supporting Information for:

The *Listeria monocytogenes* Core-Genome Sequence Typer (LmCGST): a bioinformatic

pipeline for molecular characterization with next-generation sequence data

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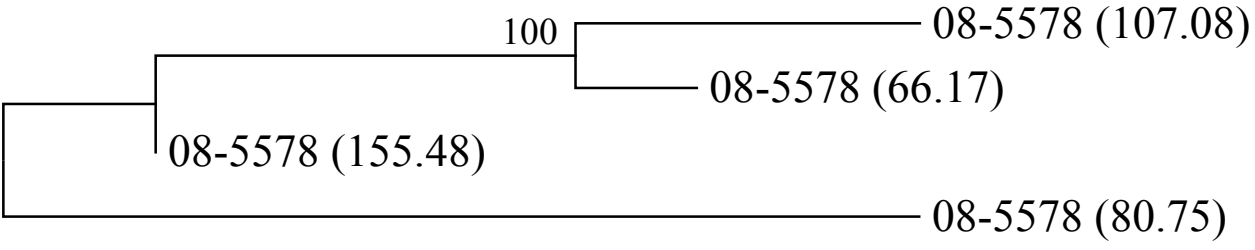
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Additional file 16: Phylogenetic analysis of *de-novo* assemblies calculated from short-read sequence data obtained from four sequencing runs of a single *Listeria monocytogenes* strain 08-5578 DNA extraction. DNA was isolated and divided into four subsamples. The subsamples were analyzed on an Illumina MiSeq benchtop sequencer. Reads were assembled *de-novo* with SPAdes v3.0.0, aligned with Mauve v2.3.1, and 3,138,152 nucleotide positions were phylogenetically analyzed with RAxML v8.1.1 (GTRCATI+25γ). The best of 100 bootstrap replicates is shown. The estimated sequence coverage for each assembly are indicated in parenthesis.

Additional file 16

100 ── 08-5578 (107.08)

── 08-5578 (66.17)

08-5578 (155.48)

── 08-5578 (80.75)

├───────┤
0.1 substitutions/site