

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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Additional file 1: Phylogenetic analysis of 68 aligned *Listeria monocytogenes* genomes. Trees were calculated from 2,963,005 aligned nucleotides with the Randomized Axelerated Maximum Likelihood tool (GTRCATI+25 γ). The best of 100 bootstrap replicates is shown. Red labels indicate closed high-quality genome sequences used for calculation of the *L. monocytogenes* core-genome.

Additional file 1

