

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 8: *Listeria monocytogenes* high-confidence core profiles grouped by nucleotide distances. A cladogram was calculated by aligning and concatenating 1,013 loci that comprise the *L. monocytogenes* high-confidence core (HCC) genomes of 114 taxa and analyzing the resulting alignment of 1,067,173 nucleotide positions with the Randomized Accelerated Maximum Likelihood tool (GTRCATI+25 γ). The best of 100 bootstrap replicates is shown. Nucleotide distances were measured with PHYLIP. Taxa were grouped by evolutionary lineage (I, II, or III) and those that have 100 and 10 or fewer nucleotide differences, while unique HCC profiles that differ by no more than 10 nucleotides were numbered in the order that they were processed.

Additional file 8

