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 9: Phylogenetic analysis of 115 high-confidence core profiles. Sequence data for 1013 loci that comprise the high-confidence core were collected from all members of the core-genome sequence typing database and a single randomly selected subject (red). Sequences were then aligned and concatenated. Supermatrices were analyzed with the PHYLIP “dnadist” (F84 and default settings) and “neighbor” (Neighbor-joining approach with default settings) modules. Roman numerals (I, II, and III) identify the three currently recognized evolutionary lineages.

Additional file 9