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 3: Pan- and core-genome sizes of 29 closed *Listeria monocytogenes* chromosome sequences. The numbers of translated open reading frames (ORFs) in the pan- and core-genomes were calculated by identifying homologs with a 60% sequence identity and 80% coverage. Chromosomes were added 1000 times with replacement in a randomized order. The total numbers of ORFs (pan-genome; open circles) and the numbers of mutually conserved ORFs (core-genome; closed circles) was noted. Grey circles indicate mean numbers of ORFs. Each diamond indicates the numbers of ORFs calculated by Kuenne *et al*. [24].

Additional file 3