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 14: Simpson's index of diversity and 95% confidence intervals. These measurements indicate the probabilities that two strains sampled randomly from a population will be assigned to two different types.

Name	**Number of Partitions**	**Simpson's ID**	**Confidence Interval (95%)**
CGST	73	0.995	0.990-1.000
PFGE+Ribo	48	0.972	0.957-0.988
PFGE	48	0.972	0.957-0.988
ApaI	43	0.968	0.952-0.984
AscI	39	0.965	0.949-0.981
ribotype	25	0.899	0.861-0.936
MLST	25	0.889	0.844-0.934

Note: ApaI and AscI data were combined to generate the PFGE category and ApaI, AscI, and ribotype data were combined to generate the PFGE+Ribo category.