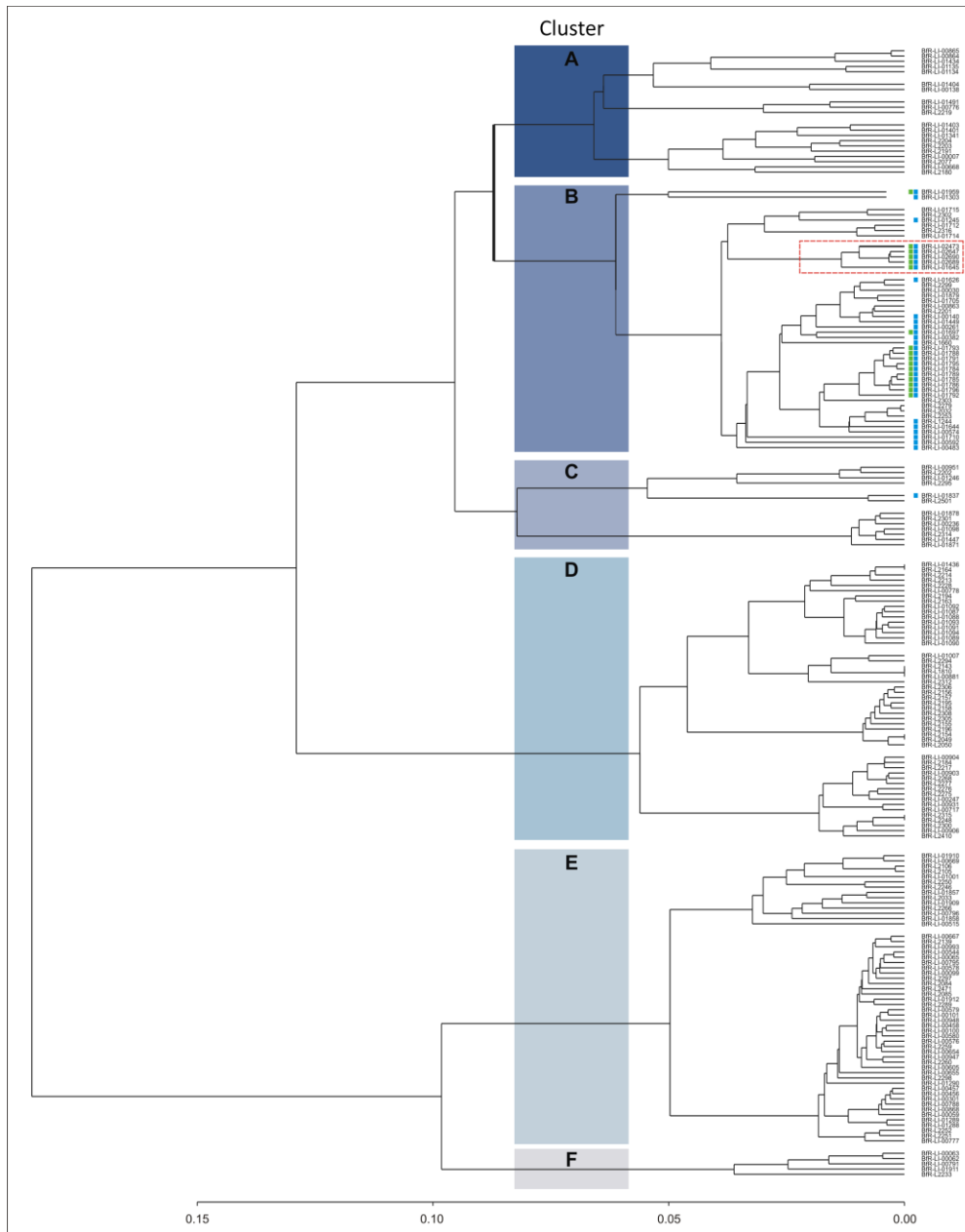


# Molecular Tracing to Find Source of Protracted Invasive Listeriosis Outbreak, Southern Germany, 2012–2016

## Technical Appendix



**Technical Appendix Figure.** Maximum parsimony tree of 174 *Listeria monocytogenes* isolates from food samples collected in Bavaria, Baden-Württemberg, and Hesse, Germany, 2012–2016. For mapping and single nucleotide polymorphism calling, we used an in-house pipeline of Eurofins Medigenomix (Ebersberg, Germany). The red box displays the outbreak cluster including a human isolate (BfR-LI-01645, PFGE 13a/54, core-genome MLST cluster type 1248) and isolates from smoked pork bellies that were distributed by the meat manufacturing plant suspected of being the outbreak source. Another 14 *L. monocytogenes* isolates from food that were not related to the outbreak but displayed the PFGE pattern 13a/54 (green squares) or PFGE pattern similar to ( $\geq 90\%$ ) *Apal* 54 (blue squares) were included in sequence analysis. Scale bar indicates mean number of nucleotide substitutions per site. MLST, multilocus sequence typing; PFGE, pulsed-field gel electrophoresis.