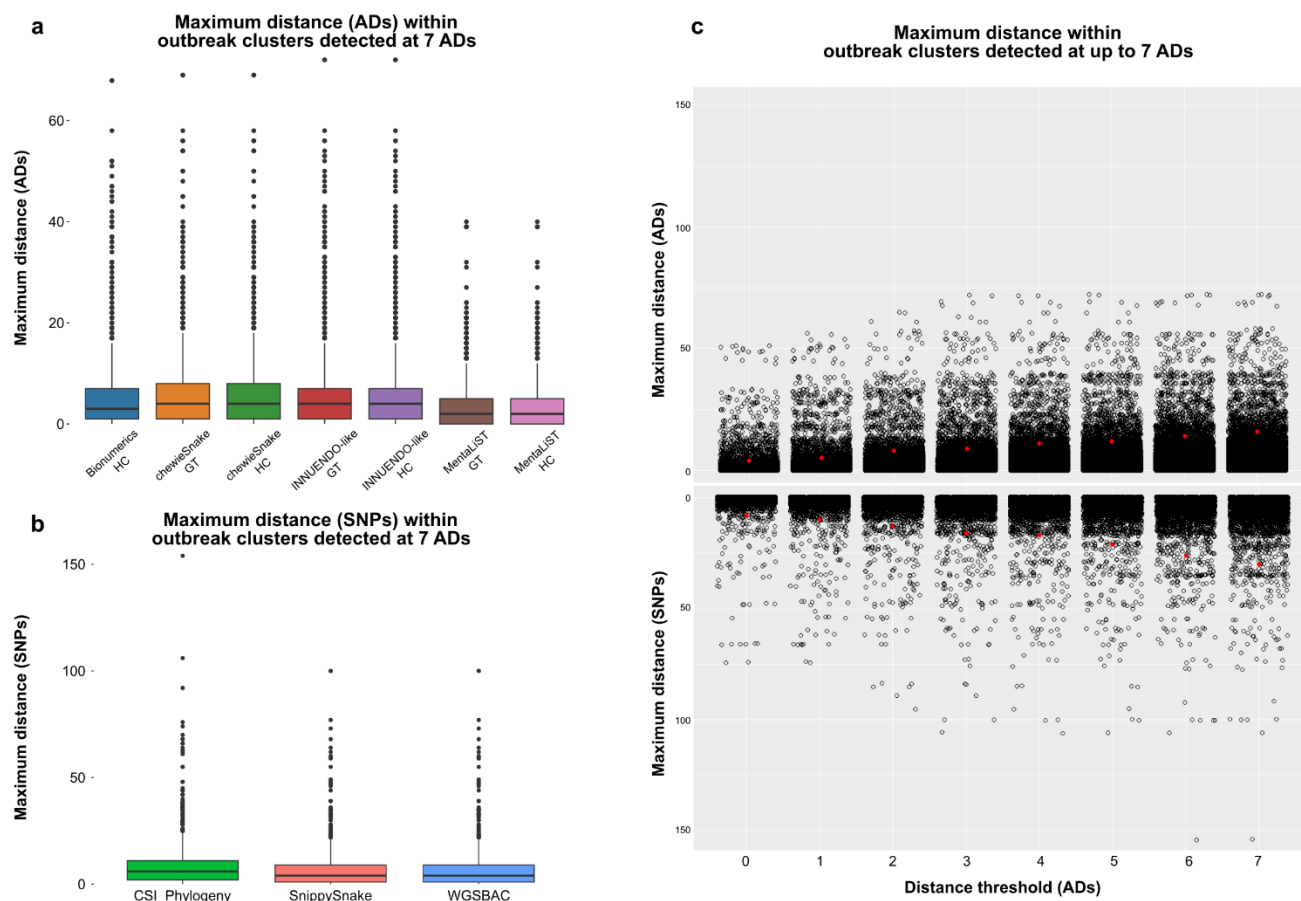
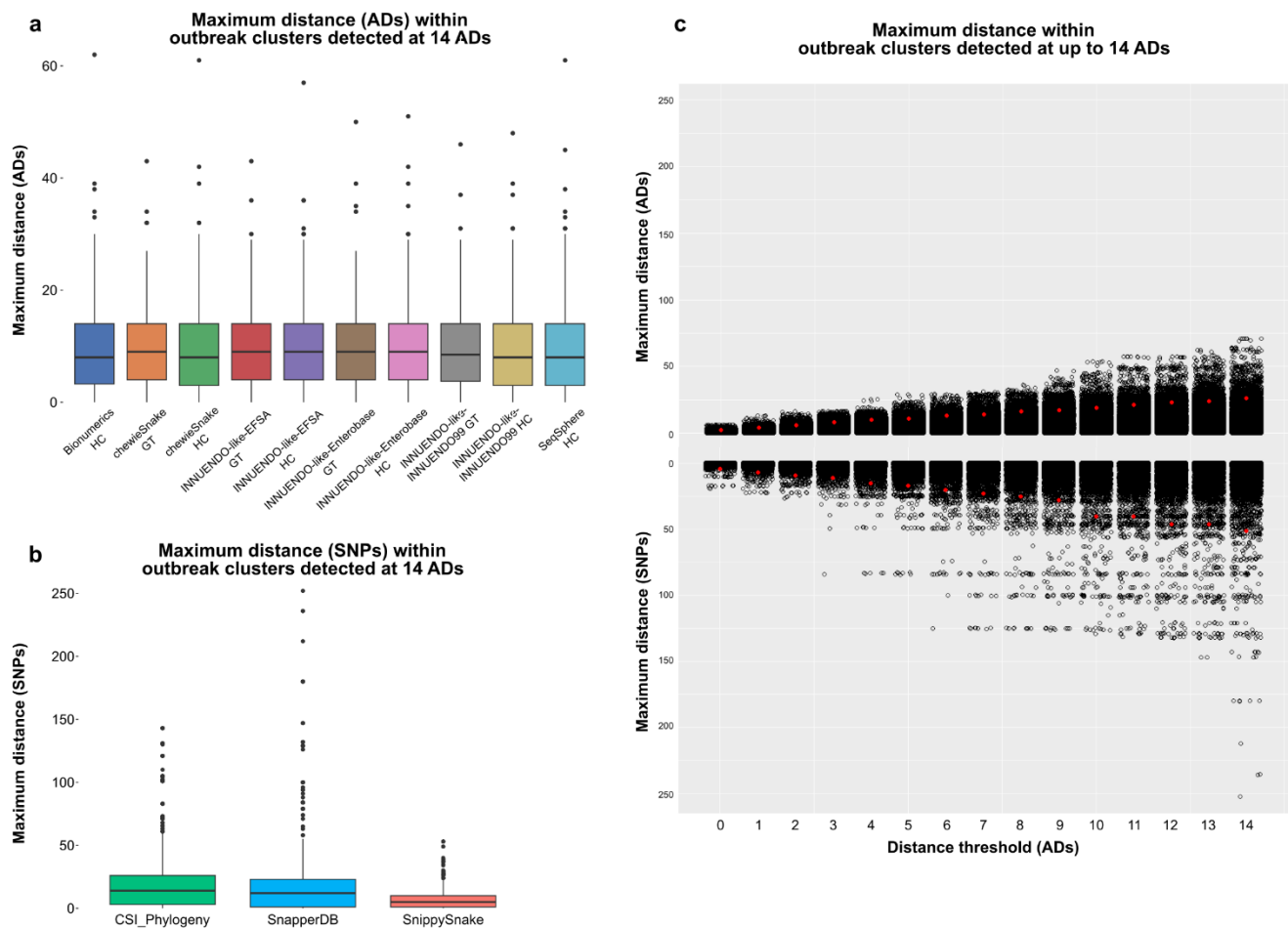


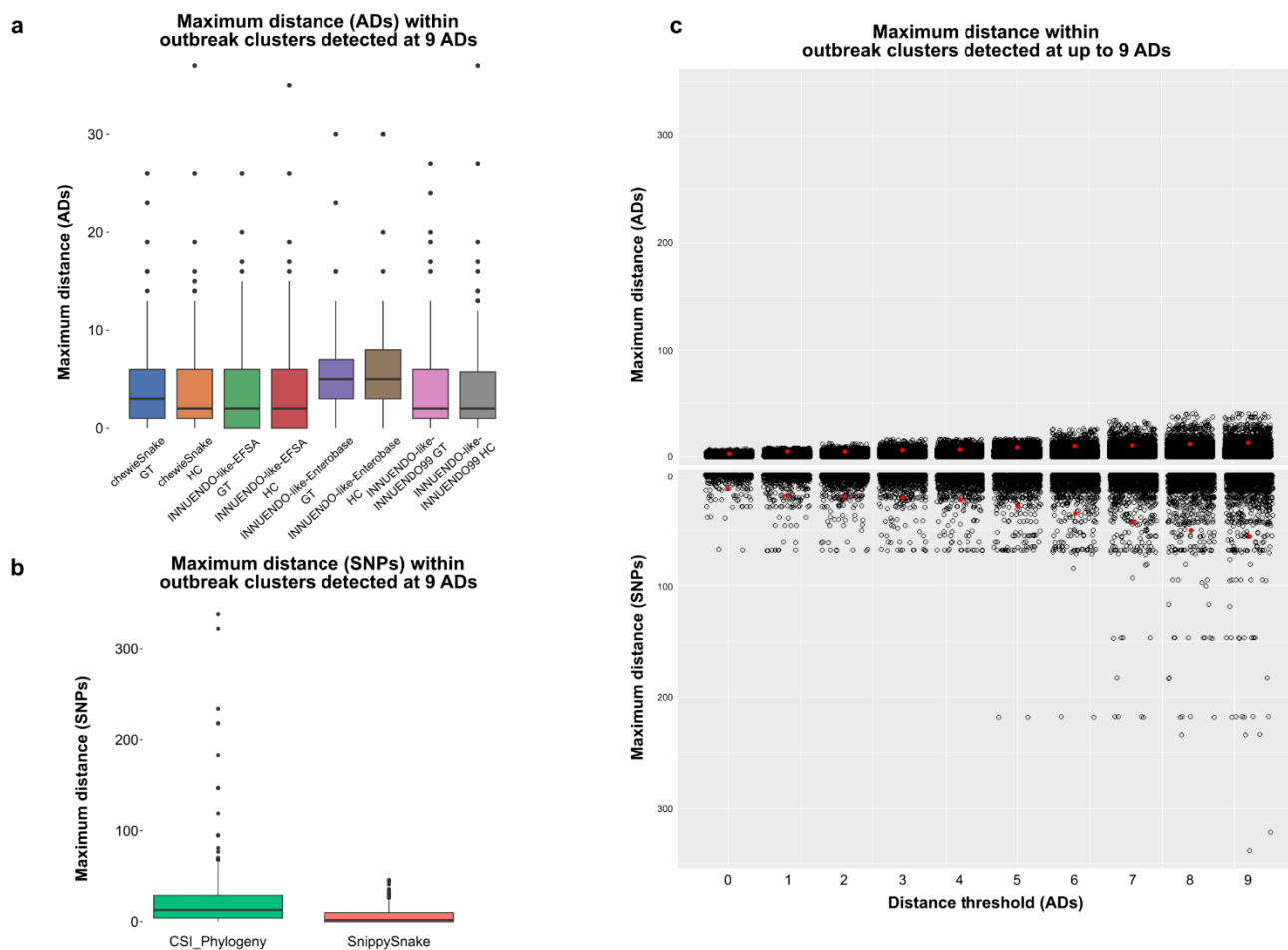
“Multi-country and intersectoral assessment of cluster congruence between pipelines for genomics surveillance of foodborne pathogens”



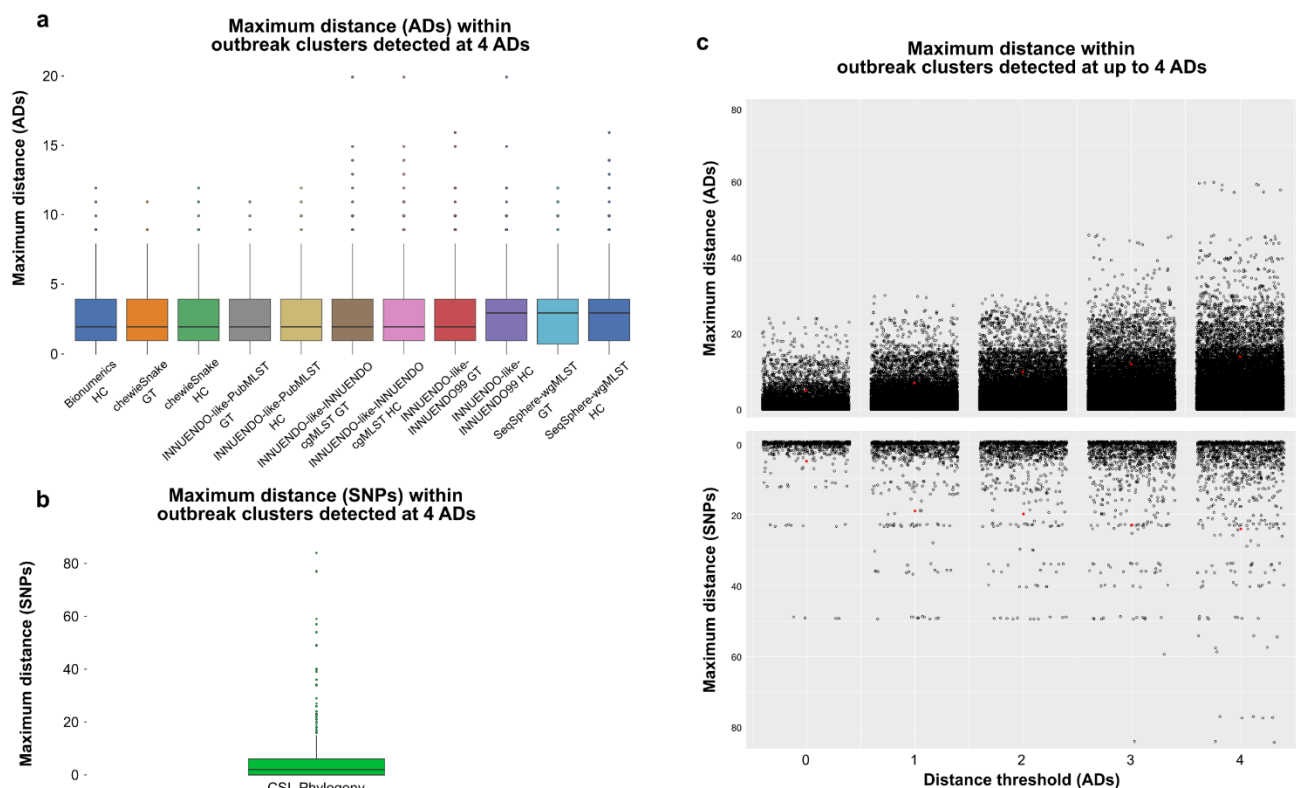
Supplementary Figure 1. Genetic diversity between potential outbreak-related isolates in the *L. monocytogenes* dataset. **a** Distribution of the maximum ADs within each “outbreak-level” cluster identified at 7 ADs by the respective pipeline. **b** Distribution of the maximum SNP distances within “outbreak-level” cgMLST clusters identified by at least an allele-based pipeline at 7 ADs. **c** Maximum allele (top) or SNP (bottom) distance threshold within each cluster determined by at least an allele-based pipeline at up to 7 ADs. The red dot indicates, for each threshold, the 95th percentile. Boxplots of panels **a** and **b** show the interquartile range (25% to 75%) and median, and whiskers extend 1.5 times the range, with outliers plotted separately. Source data are provided as a Source Data file.



Supplementary Figure 2. Genetic diversity between potential outbreak-related isolates in the *S. enterica* dataset. **a** Distribution of the maximum ADs within each cluster identified at 14 ADs by the respective pipeline. **b** Distribution of the maximum SNP distances within cgMLST clusters identified by at least an allele-based pipeline at 14 ADs. **c** Maximum allele (top) or SNP (bottom) distance threshold within each cluster determined by at least an allele-based pipeline at up to 14 ADs. The red dot indicates, for each threshold, the 95th percentile. Boxplots of panels **a** and **b** show the interquartile range (25% to 75%) and median, and whiskers extend 1.5 times the range, with outliers plotted separately. Source data are provided as a Source Data file.



Supplementary Figure 3. Genetic diversity between potential outbreak-related isolates in the *E. coli* dataset. **a** Distribution of the maximum ADs within each “outbreak-level” cluster identified at 9 ADs by the respective pipeline. **b** Distribution of the maximum SNP distances within “outbreak-level” cgMLST clusters identified by at least an allele-based pipeline at 9 ADs. **c** Maximum allele (top) or SNP (bottom) distance threshold within each cluster determined by at least an allele-based pipeline at up to 9 ADs. The red dot indicates, for each threshold, the 95th percentile. Boxplots of panels **a** and **b** show the interquartile range (25% to 75%) and median, and whiskers extend 1.5 times the range, with outliers plotted separately. Source data are provided as a Source Data file.



Supplementary Figure 4. Genetic diversity between potential outbreak-related isolates in the *C. jejuni* dataset. **a** Distribution of the maximum ADs within each “outbreak-level” cluster identified at 4 ADs by the respective pipeline. **b** Distribution of the maximum SNP distances within “outbreak-level” cgMLST clusters identified by at least an allele-based pipeline at 4 ADs. **c** Maximum allele (top) or SNP (bottom) distance threshold within each cluster determined by at least an allele-based pipeline at up to 4 ADs. The red dot indicates, for each threshold, the 95th percentile. Boxplots of panels **a** and **b** show the interquartile range (25% to 75%) and median, and whiskers extend 1.5 times the range, with outliers plotted separately. Source data are provided as a Source Data file.