

Description of Additional Supplementary Files

Supplementary Data 1. Details on the study design.

Supplementary Data 2. Details on the analysis of the dataset of *Listeria monocytogenes*.

Supplementary Data 3. Minimum threshold (AD) at which each allelebased pipeline groups all samples of an *L. monocytogenes* ST into a single cluster.

Supplementary Data 4. Minimum threshold (AD) at which each allelebased pipeline groups all samples of an *L. monocytogenes* CC into a single cluster.

Supplementary Data 5. Inter-pipeline corresponding points for each pairwise comparison performed for *L. monocytogenes*.

Supplementary Data 6. Details on the r^2 and slope of the linear tendency line that fits the inter-pipeline corresponding points presented in Supplementary Data 5.

Supplementary Data 7. Number of clusters detected by each allele-based pipeline at high resolution level in *L. monocytogenes* dataset, with indication of the number of clusters detected with the exact same composition in all pipelines (exact_composition_all) or in at least another pipeline (shared_with_another), or not detected by another pipeline (exclusive).

Supplementary Data 8. Clusters detected by at least one allele-based pipeline at 7 ADs in the *L. monocytogenes* dataset, with indication of the cluster length and the minimum AD threshold at which this cluster was detected by each pipeline.

Supplementary Data 9. Percentage of *L. monocytogenes* genetic clusters that once detected by a given pipeline at a certain threshold (left) are also detected, with the exact same composition, by another pipeline (top) at another (or up to another) threshold.

Supplementary Data 10. Details on the analysis of the dataset of *Salmonella enterica*.

Supplementary Data 11. Minimum threshold (AD) at which each allelebased pipeline groups all samples of an *S. enterica* serotype into a single cluster.

Supplementary Data 12. Minimum threshold (AD) at which each allelebased pipeline groups all samples of an *S. enterica* ST into a single cluster.

Supplementary Data 13. Interpipeline corresponding points for each pairwise comparison performed for *S. enterica*.

Supplementary Data 14. Details on the r^2 and slope of the linear tendency line that fits the inter-pipeline corresponding points presented in Supplementary Data 13.

Supplementary Data 15. Number of clusters detected by each allele-based pipeline at high resolution level in *S. enterica* dataset, with indication of the number of clusters detected with the exact same

composition in all pipelines (exact_composition_all) or in at least another pipeline (shared_with_another), or not detected by another pipeline (exclusive).

Supplementary Data 16. Clusters detected by at least one allele-based pipeline at 14 ADs in the *S. enterica* dataset, with indication of the cluster length and the minimum AD threshold at which this cluster was detected by each pipeline.

Supplementary Data 17. Percentage of *S. enterica* genetic clusters that once detected by a given pipeline at a certain threshold (left) are also detected, with the exact same composition, by another pipeline (top) at another (or up to another) threshold.

Supplementary Data 18. Genetic distance within the *S. enterica* genetic clusters detected at 14 ADs by the INNUENDO-like-INNUENDO99 pipeline before and after a dynamic cluster zoom-in.

Supplementary Data 19. Details on the analysis of the dataset of *Escherichia coli*.

Supplementary Data 20. Minimum threshold (AD) at which each allelebased pipeline groups all samples of an *E. coli* serotype into a single cluster.

Supplementary Data 21. Minimum threshold (AD) at which each allelebased pipeline groups all samples of an *E. coli* ST into a single cluster.

Supplementary Data 22. Interpipeline corresponding points for each pairwise comparison performed for *E. coli*.

Supplementary Data 23. Details on the r^2 and slope of the linear tendency line that fits the inter-pipeline corresponding points presented in Supplementary Data 22.

Supplementary Data 24. Number of clusters detected by each allele-based pipeline at high resolution level in *E. coli* dataset, with indication of the number of clusters detected with the exact same composition in all pipelines (exact_composition_all) or in at least another pipeline (shared_with_another), or not detected by another pipeline (exclusive).

Supplementary Data 25. Clusters detected by at least one allele-based pipeline at 9 ADs in the *E. coli* dataset, with indication of the cluster length and the minimum AD threshold at which this cluster was detected by each pipeline.

Supplementary Data 26. Percentage of *E. coli* genetic clusters that once detected by a given pipeline at a certain threshold (left) are also detected, with the exact same composition, by another pipeline (top) at another (or up to another) threshold.

Supplementary Data 27. Genetic distance within the *E. coli* genetic clusters detected at 9 ADs by the INNUENDO-like-INNUENDO99 pipeline before and after a dynamic cluster zoom-in.

Supplementary Data 28. Details on the analysis of the dataset of *Campylobacter jejuni*.

Supplementary Data 29. Minimum threshold (AD) at which each allelebased pipeline groups all samples of a *C. jejuni* CC into a single cluster.

Supplementary Data 30. Minimum threshold (AD) at which each allelebased pipeline groups all samples of a *C. jejuni* ST into a single cluster.

Supplementary Data 31. Interpipeline corresponding points for each pairwise comparison performed for *C. jejuni*.

Supplementary Data 32. Details on the r^2 and slope of the linear tendency line that fits the inter-pipeline corresponding points presented in Supplementary Data 31.

Supplementary Data 33. Number of clusters detected by each allele-based pipeline at high resolution level in *C. jejuni* dataset, with indication of the number of clusters detected with the exact same composition in all pipelines (exact_composition_all) or in at least another pipeline (shared_with_another), or not detected by another pipeline (exclusive).

Supplementary Data 34. Clusters detected by at least one allele-based pipeline at 4 ADs in the *C. jejuni* dataset, with indication of the cluster length and the minimum AD threshold at which this cluster was detected by each pipeline.

Supplementary Data 35. Percentage of *C. jejuni* genetic clusters that once detected by a given pipeline at a certain threshold (left) are also detected, with the exact same composition, by another pipeline (top) at another (or up to another) threshold.

Supplementary Data 36. Genetic distance within the *C. jejuni* genetic clusters detected at 4 ADs by the INNUENDO-like-INNUENDO99 and the SeqSphere-wgMLST pipelines before and after a dynamic cluster zoom-in.

Supplementary Data 37. Supporting results of the assessment of the impact of applying a different assembly pipeline and updating the allele caller.

Supplementary Data 38. Details on the schemas used by each pipeline.