

Supplementary Data 10

Details on the analysis of the dataset of *Salmonella enterica*

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Section 1 – Supporting data

Table S1.1. Characterization of allele-based pipelines clustering results, with indication of the number of samples passing the quality control (QC) tests of each pipeline, the size of the schema utilized, the maximum number of partitions obtained, and the threshold ranges with highest congruence with ST and serotype. CS – Congruence Score.

Pipeline	N	QC PASS	QC PASS (%)	Schema size	N partitions	Highest congruence point with ST (ADs)	CS with ST	Highest congruence point with serotype (ADs)	CS with serotype
chewieSnake_HC	2974	2959	99.50	3000	2615	207	2,65	1304	2.31
chewieSnake_GT	2974	2959	99.50	3000	2801	256	2,66	1663	2.31
INNUENDO-like_HC (INNUENDO wgMLST schema)	2974	2962	99.60	3088/8558	2881	217	2,64	1384	2.31
INNUENDO-like_GT (INNUENDO wgMLST schema)	2974	2962	99.60	3088/8558	2998	282	2,66	1514	2.31
INNUENDO-like_HC (Enterobase schema)	2974	2956	99.39	3000	2800	208	2.65	1371	2.31
INNUENDO-like_GT (Enterobase schema)	2974	2956	99.39	3000	2895	276	2.66	1423	2.31
INNUENDO-like_HC (EFSA schema)	2974	2947	99.09	3255	2948	220	2.64	1451	2.31
INNUENDO-like_GT (EFSA schema)	2974	2947	99.09	3255	2998	310	2.66	1580	2.31
Ridom SeqSphere_HC	2974	2960	99.53	3000	2602	205	2,65	1261	2.31
Bionumerics_HC	2974	2954	99.33	3000	2844	213	2,68	1379	2.31
Mentalist_HC	2974	2928	98.45	1461/8558	1323	-	-	-	-
Mentalist_GT	2974	2928	98.45	1461/8558	1423	-	-	-	-

NOTE: EFSA schema corresponds to the INNUENDO cgMLST schema (hosted in Chewie-NS).

Supplementary Data 10. Details on the analysis of the dataset of *Salmonella enterica*.
Section 1 – Supporting data

Table S1.2. Characterization of SNP-based pipelines clustering results, with indication of the samples passing the quality control (QC) tests of each pipeline and the maximum number of partitions obtained.

Serotype	Pipeline	N	QC PASS	QC PASS (%)	N partitions
Enteritidis	snippySnake_HC	725	725	100.00	1289
	CSI Phylogeny_HC	725	725	100.00	1833
Typhimurium	snippySnake_HC	880	880	100.00	4369
	CSI Phylogeny_HC	880	880	100.00	7642
	SnapperDB_HC	880	853	96.93	1045
Infantis	snippySnake_HC	120	120	100.00	9409
	CSI Phylogeny_HC	120	120	100.00	15512
	SnapperDB_HC	120	116	96.67	553

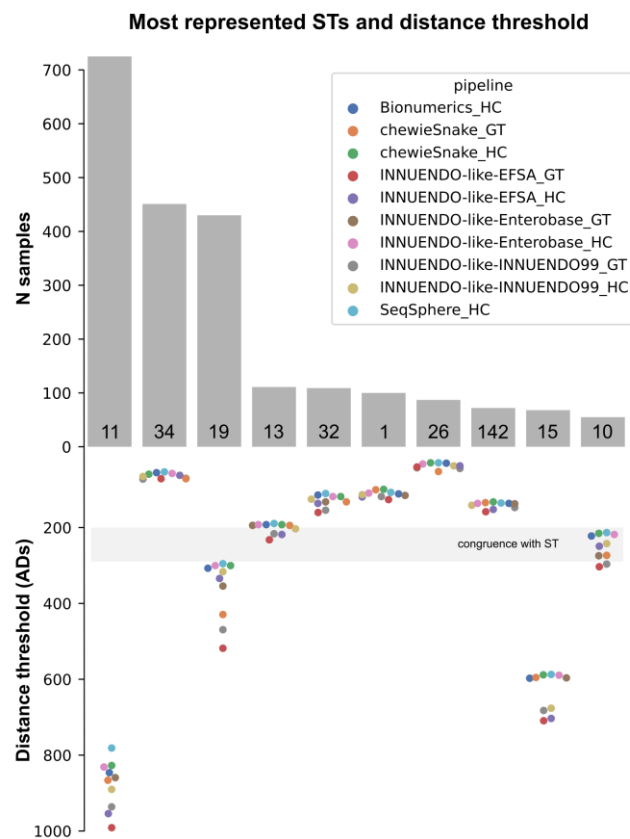


Figure S1. Allele-based clustering congruence with ST. Barplot (top) with the number of samples of the top represented STs (≥ 50 samples) present in the *S. enterica* dataset, with a swarmplot (bottom) indicating the ADs at which each pipeline clusters together all samples of each of these STs.

Section 2 – Comparison of allele-based pipelines

1. Bionumerics single-linkage vs. chewieSnake single-linkage

Table S2.1. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	Bionumerics single-linkage	chewieSnake single-linkage
Pipeline version	v8.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2844	2615

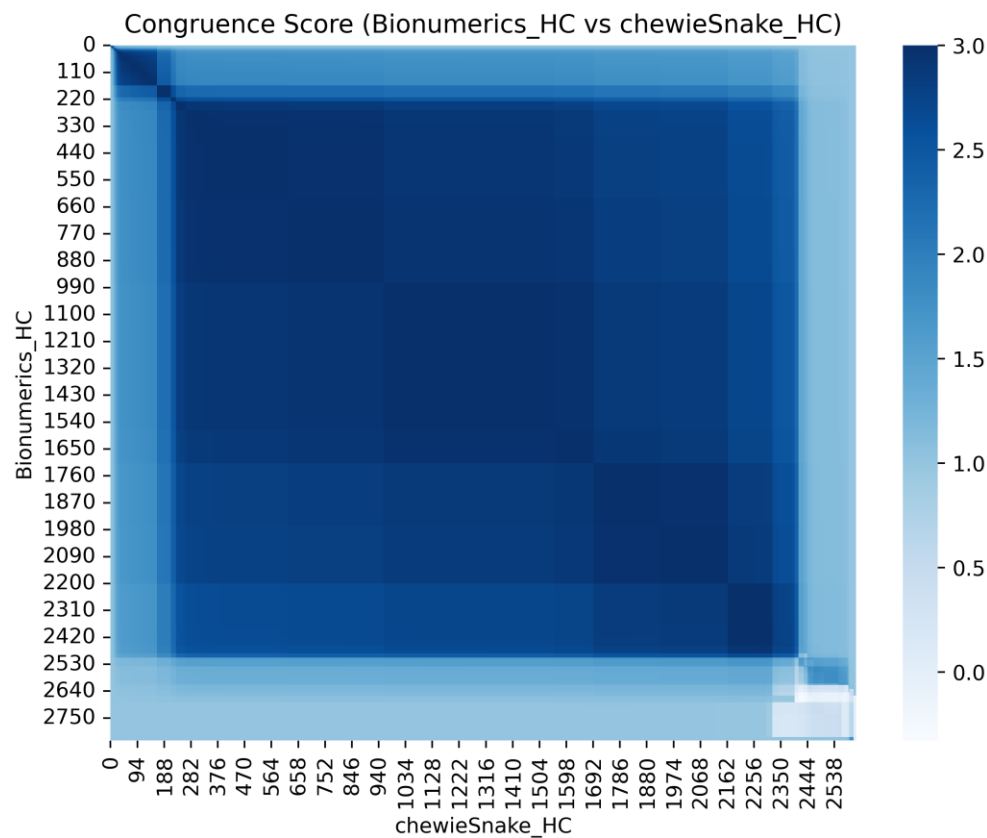


Figure S2.1.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

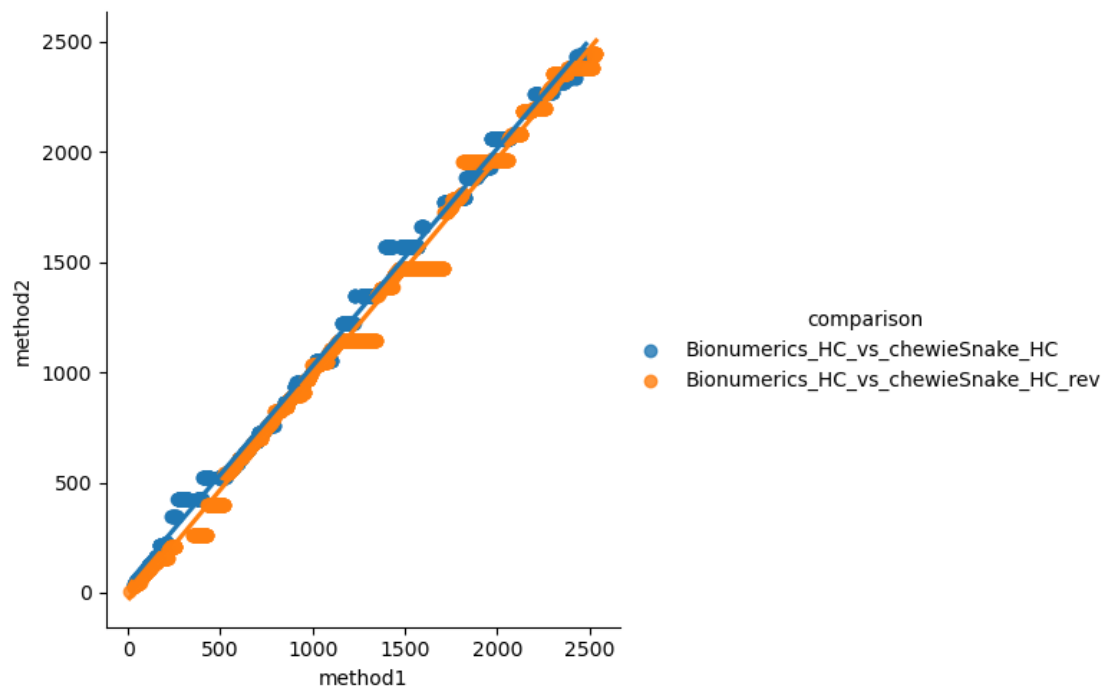


Figure S2.1.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1561 (blue) and 2418 (orange) points is presented.

2. Bionumerics single-linkage vs. INNUENDO-like-EFSA GrapeTree

Table S2.2. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	Bionumerics single-linkage	INNUENDO-like-EFSA GrapeTree
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2844	2998

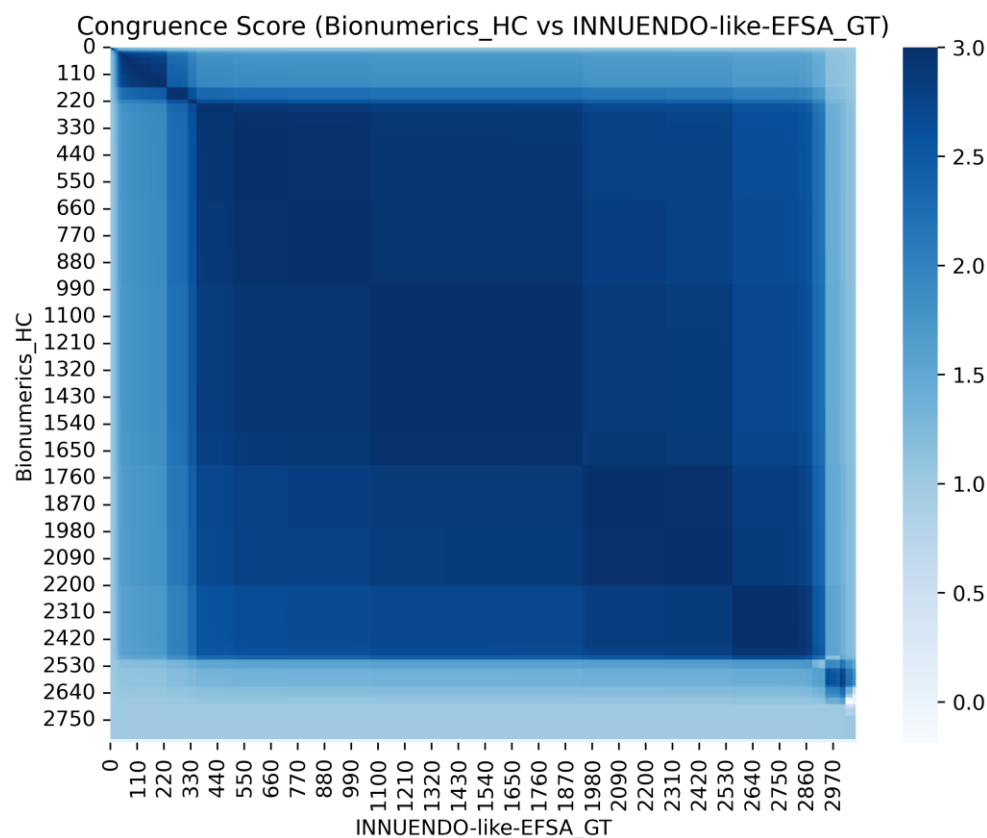


Figure S2.2.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

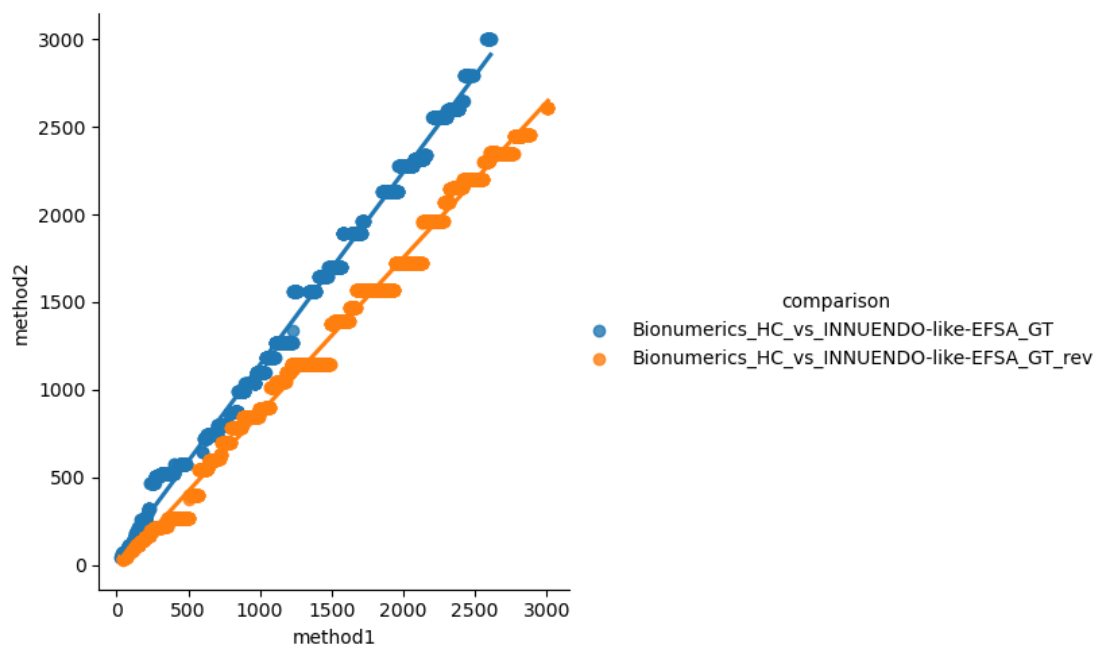


Figure S2.2.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1595 (blue) and 2309 (orange) points is presented.

3. Bionumerics single-linkage vs. INNUENDO-like-EFSA single-linkage

Table S2.3. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	Bionumerics single-linkage	INNUENDO-like-EFSA single-linkage
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2844	2948

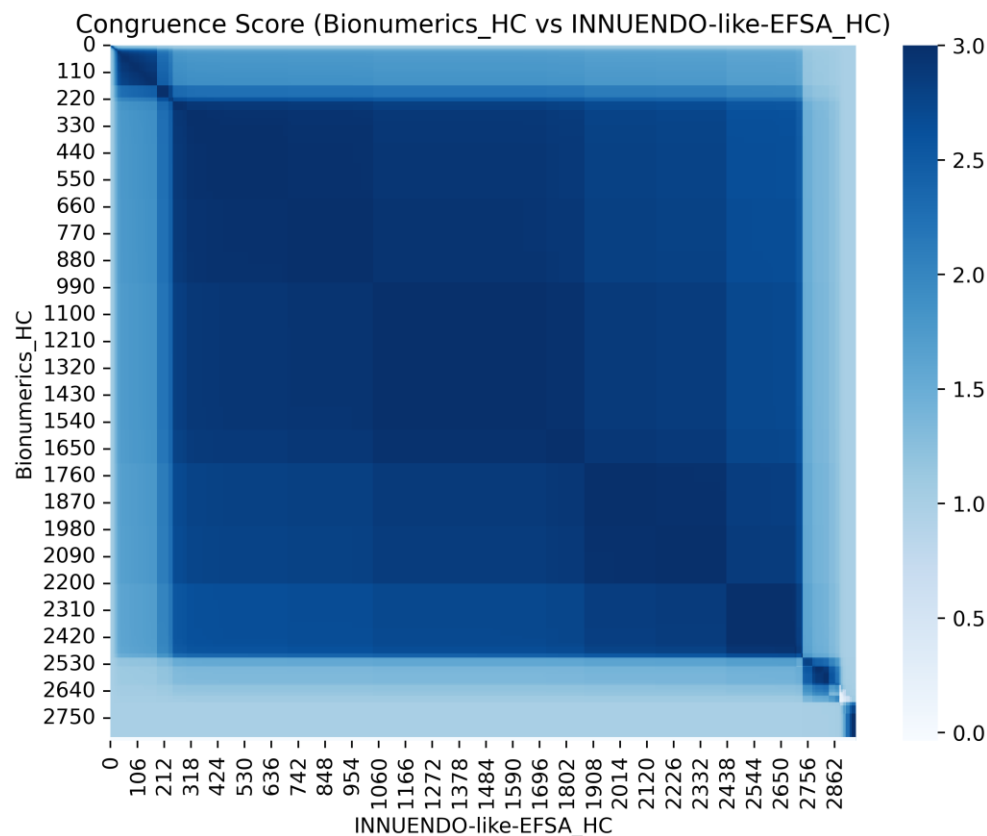


Figure S2.3.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

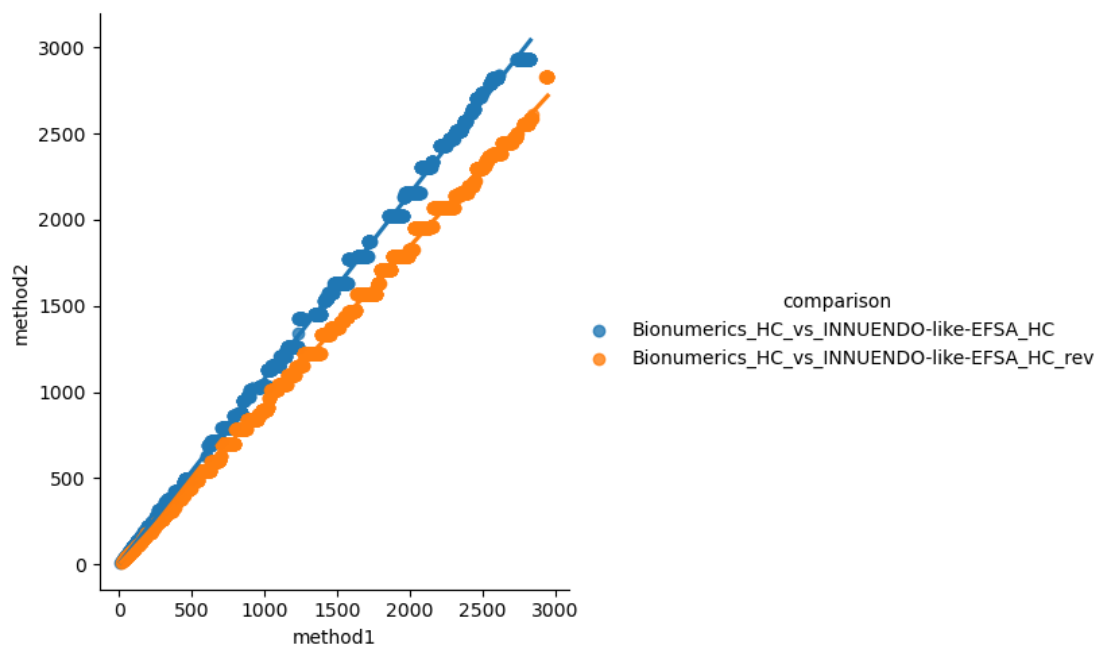


Figure S2.3.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1737 (blue) and 2841 (orange) points is presented.

4. **Bionumerics single-linkage vs. INNUENDO-like-Enterobase GrapeTree**

Table S2.4. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	Bionumerics single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2844	2895

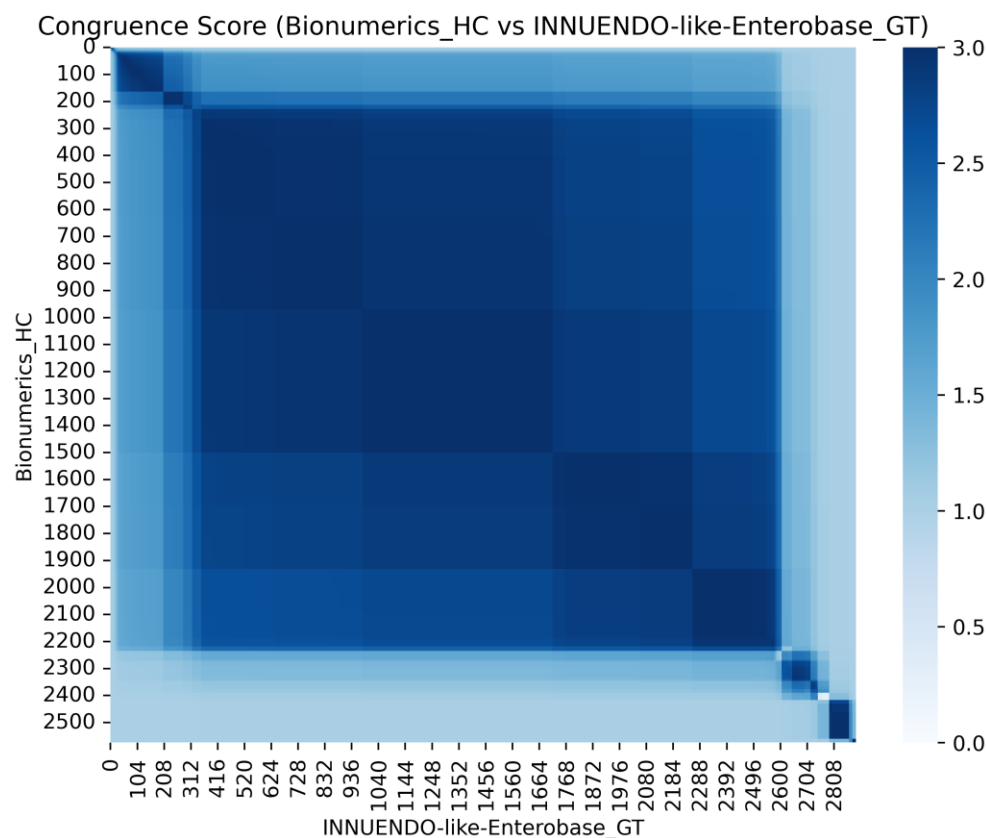


Figure S2.4.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

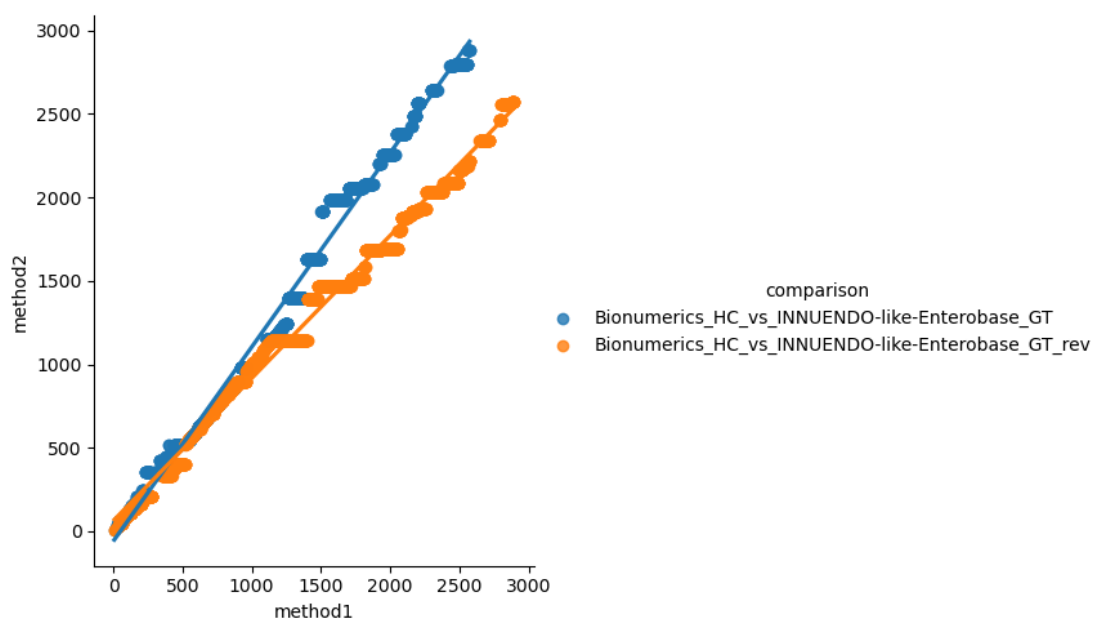


Figure S2.4.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1890 (blue) and 2779 (orange) points is presented.

5. **Bionumerics single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage**

Table S2.5. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	Bionumerics single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2844	2881

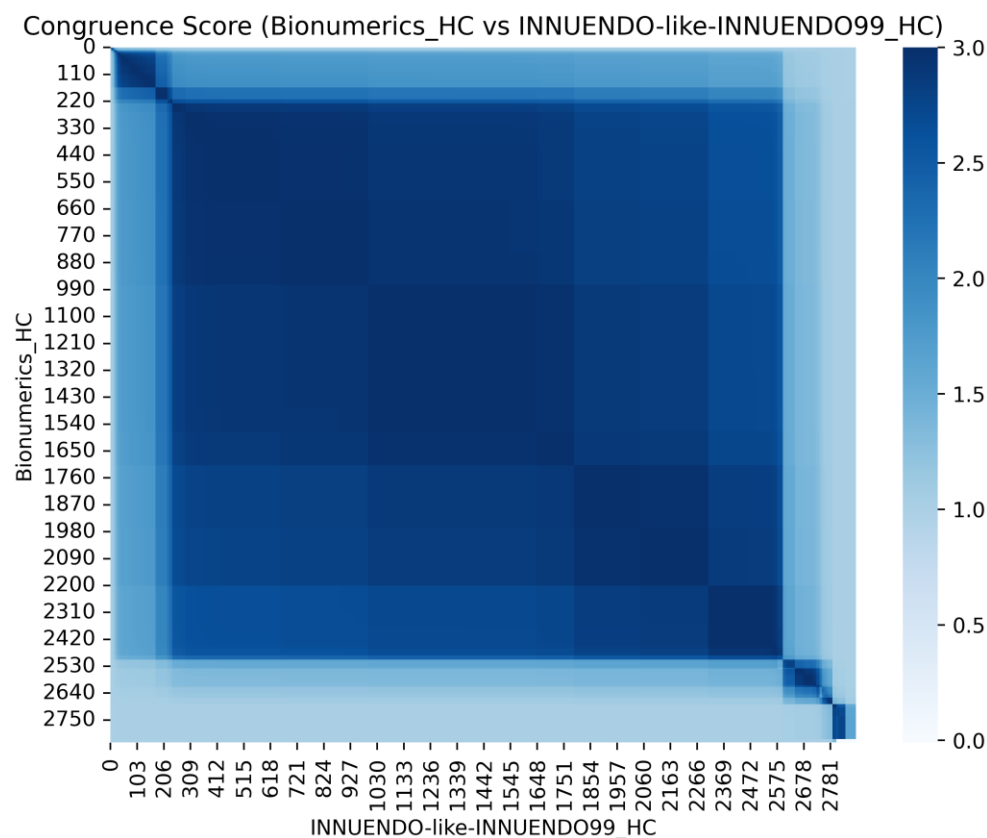


Figure S2.5.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

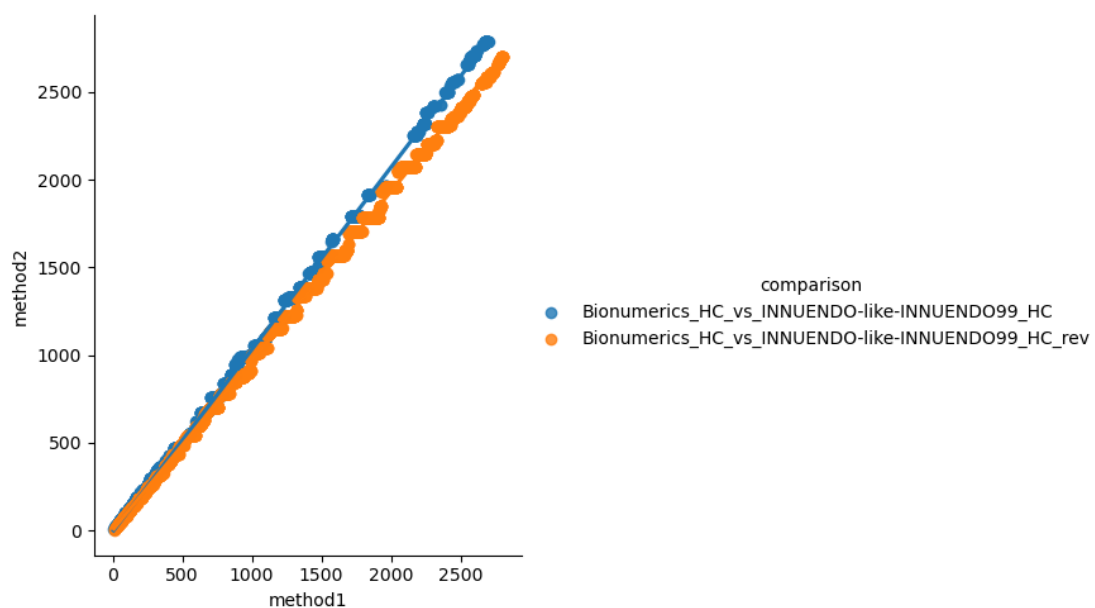


Figure S2.5.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1726 (blue) and 2643 (orange) points is presented.

6. chewieSnake GrapeTree vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.6. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	chewieSnake GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2801	2881

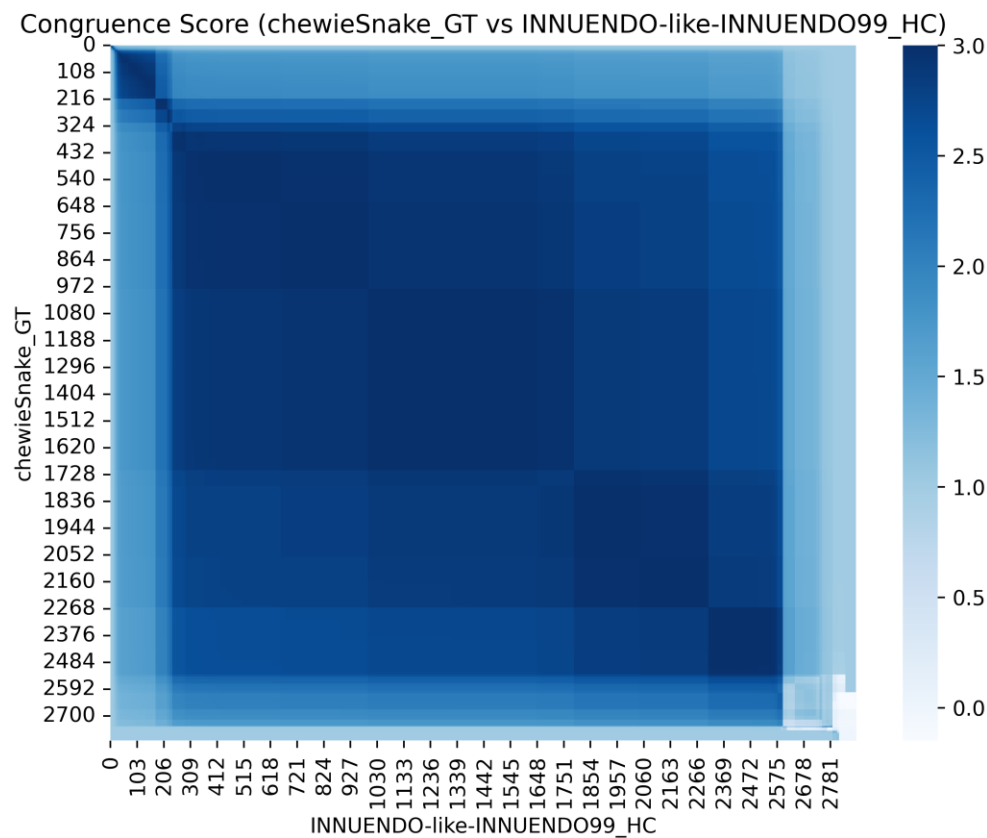


Figure S2.6.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

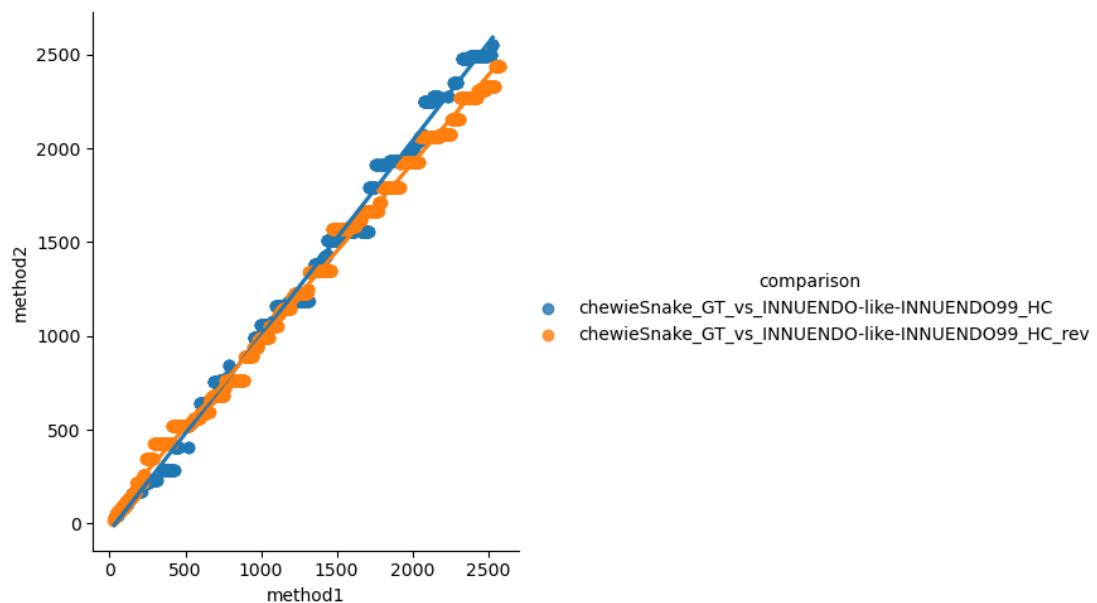


Figure S2.6.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1607 (blue) and 2703 (orange) points is presented.

7. chewieSnake single-linkage vs. chewieSnake GrapeTree

Table S2.7. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	chewieSnake single-linkage	chewieSnake GrapeTree
Pipeline version	v3.1.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2615	2801

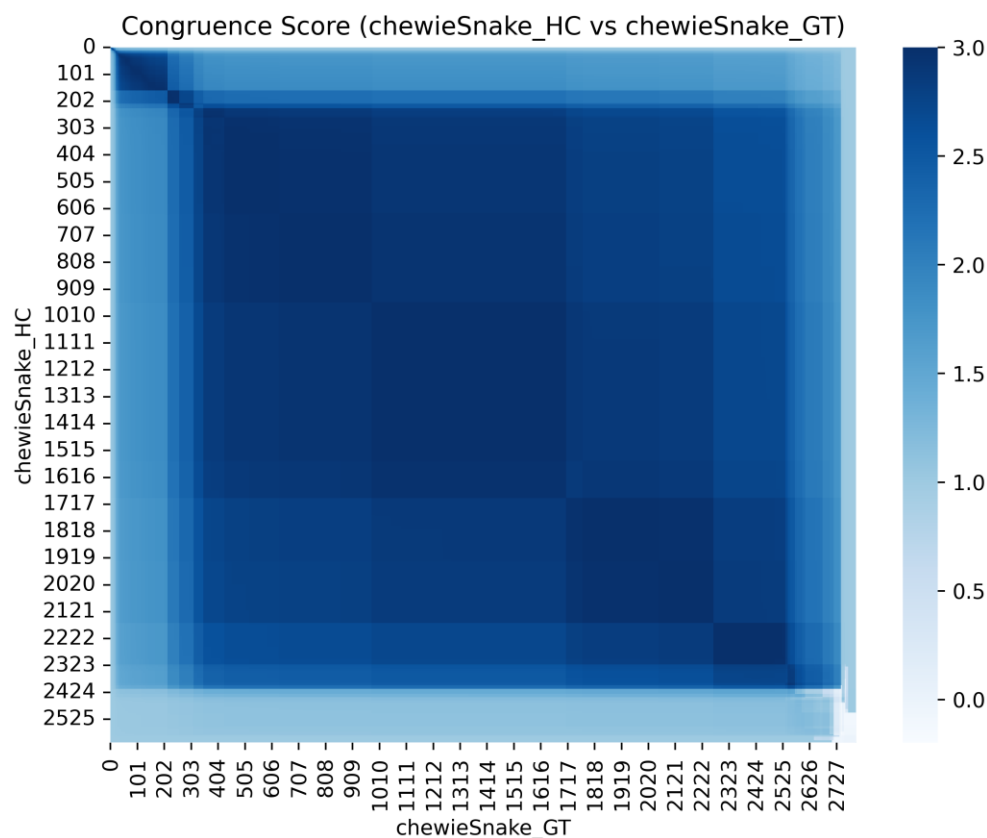


Figure S2.7.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

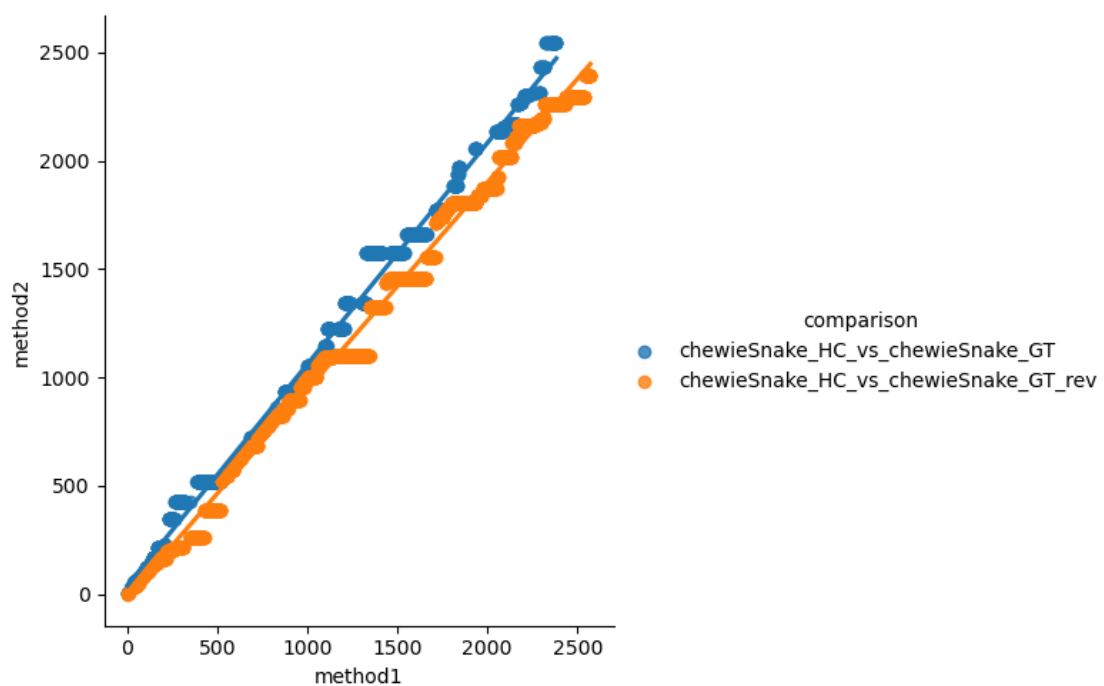


Figure S2.7.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1666 (blue) and 2539 (orange) points is presented.

8. chewieSnake single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.8. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	chewieSnake single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2615	2881

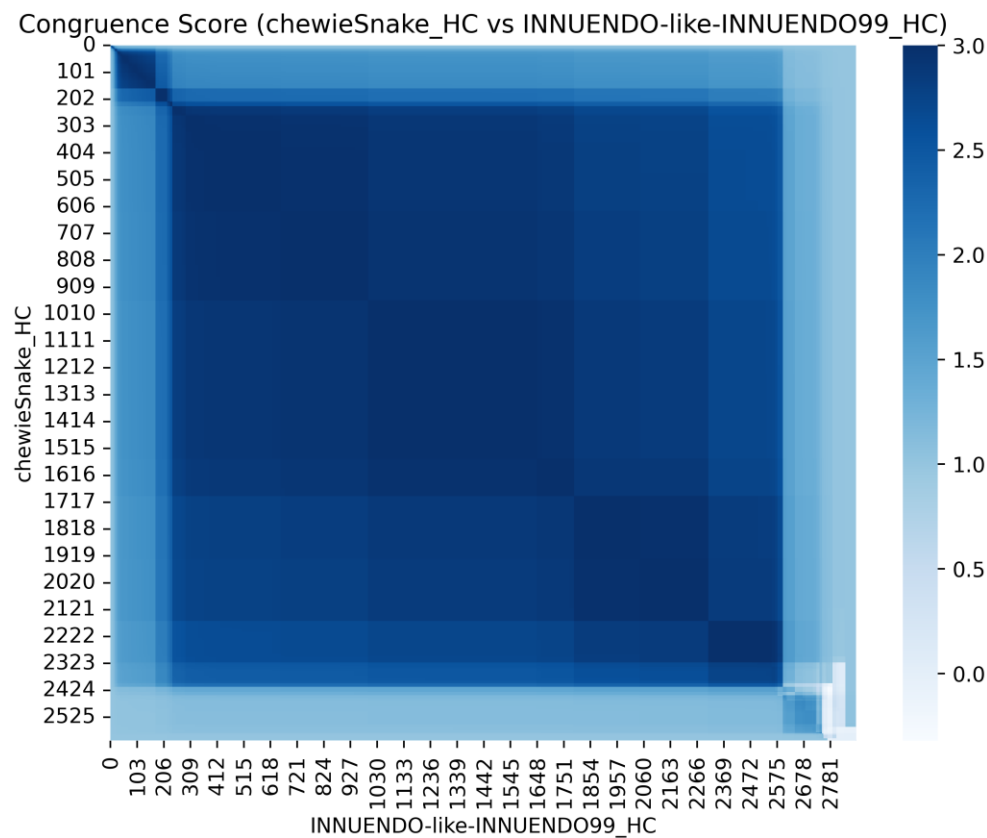


Figure S2.8.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

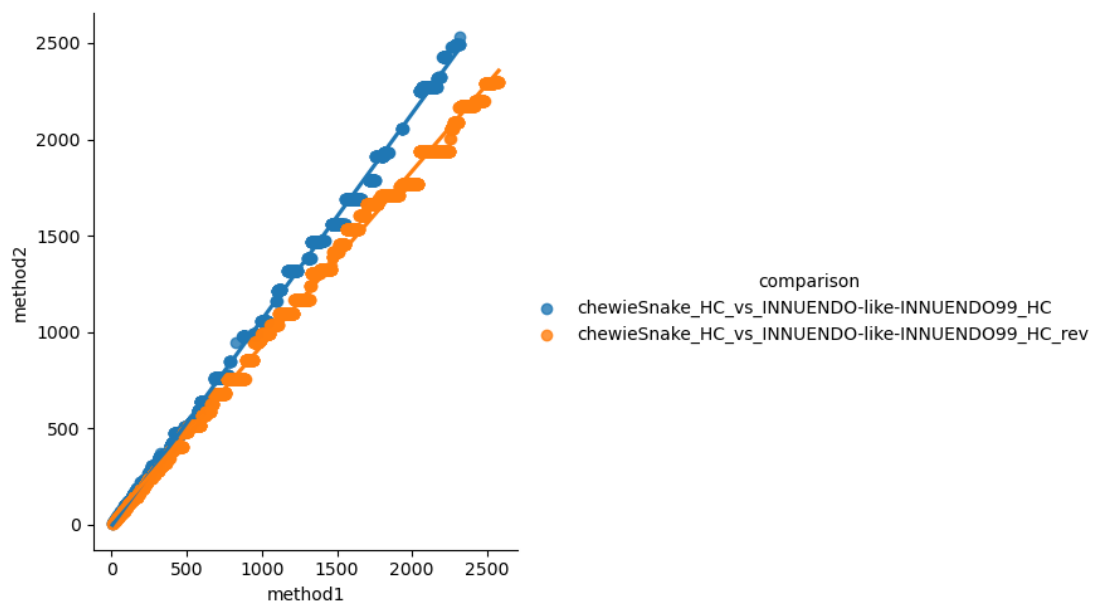


Figure S2.8.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1330 (blue) and 2502 (orange) points is presented.

9. INNUENDO-like-EFSA GrapeTree vs. chewieSnake GrapeTree

Table S2.9. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2801

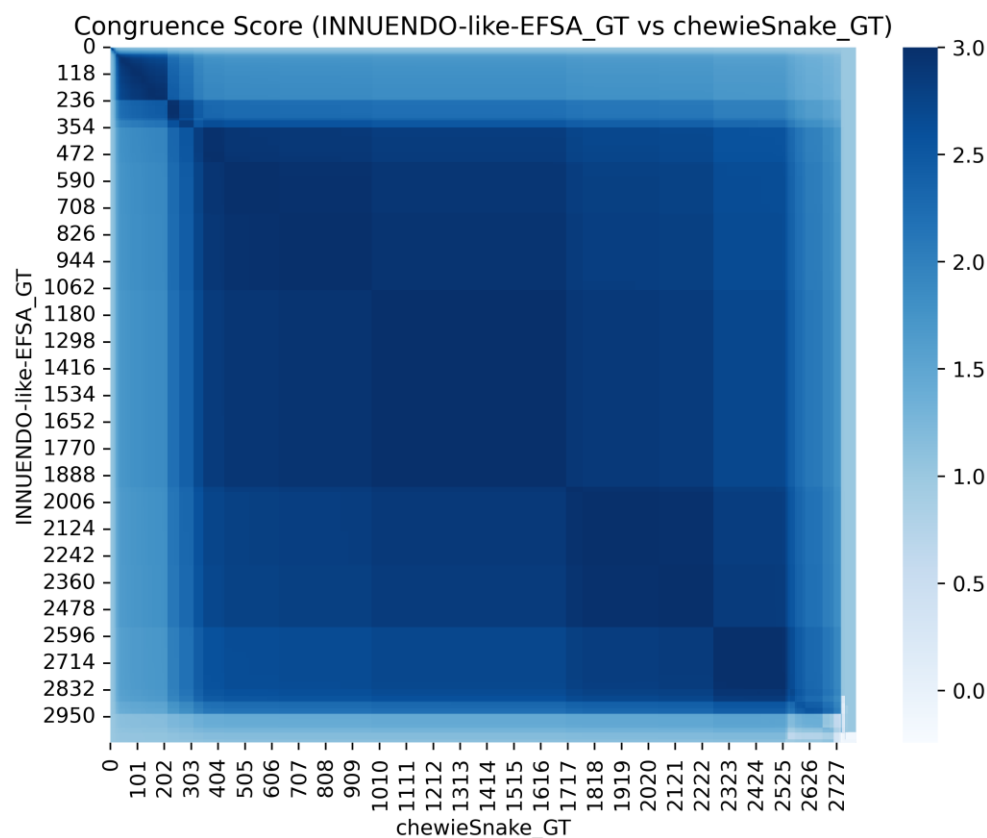


Figure S2.9.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

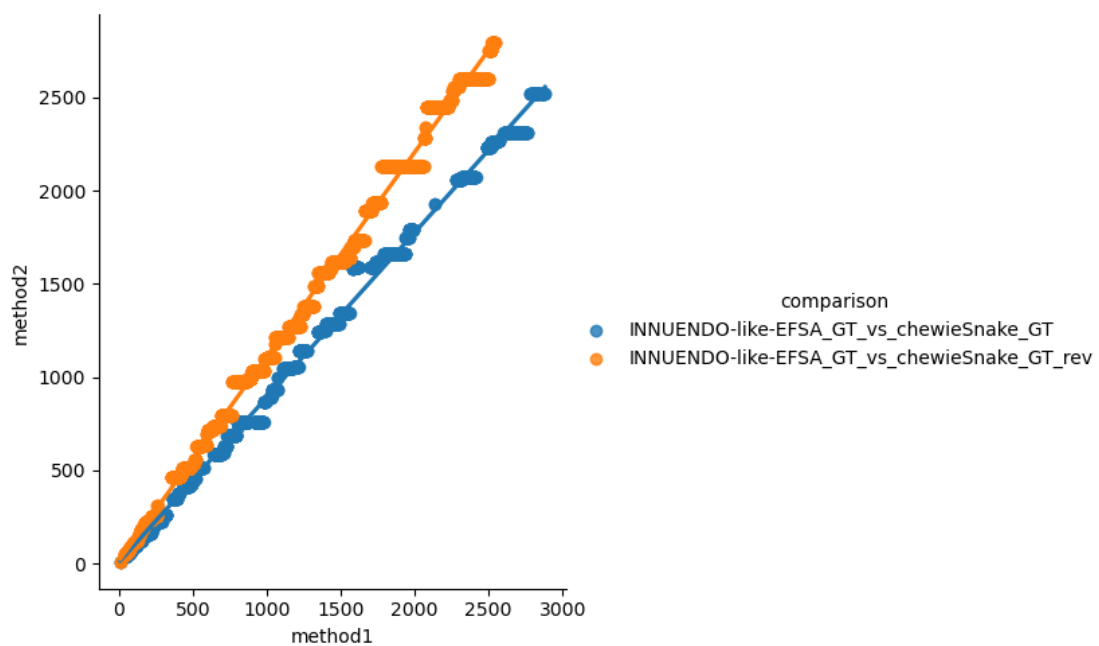


Figure S2.9.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1308 (blue) and 2563 (orange) points is presented.

10. INNUENDO-like-EFSA GrapeTree vs. chewieSnake single-linkage

Table S2.10. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA GrapeTree	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2615

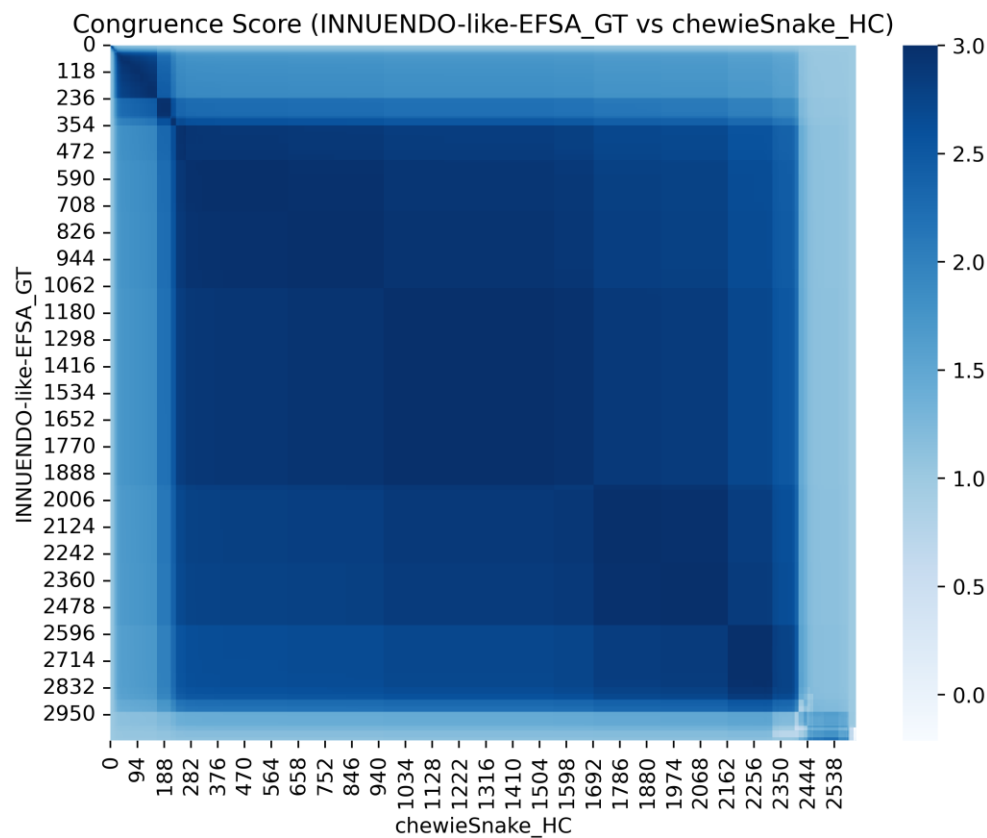


Figure S2.10.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

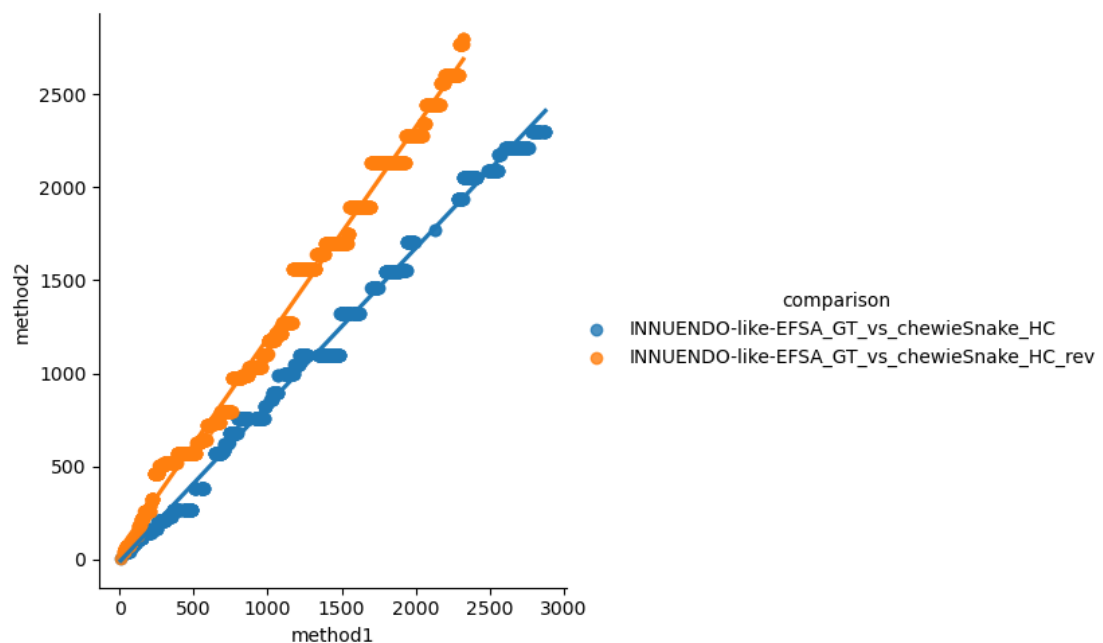


Figure S2.10.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1751 (blue) and 2422 (orange) points is presented.

11. INNUENDO-like-EFSA GrapeTree vs. INNUENDO-like-Enterobase GrapeTree

Table S2.11. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA GrapeTree	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2895

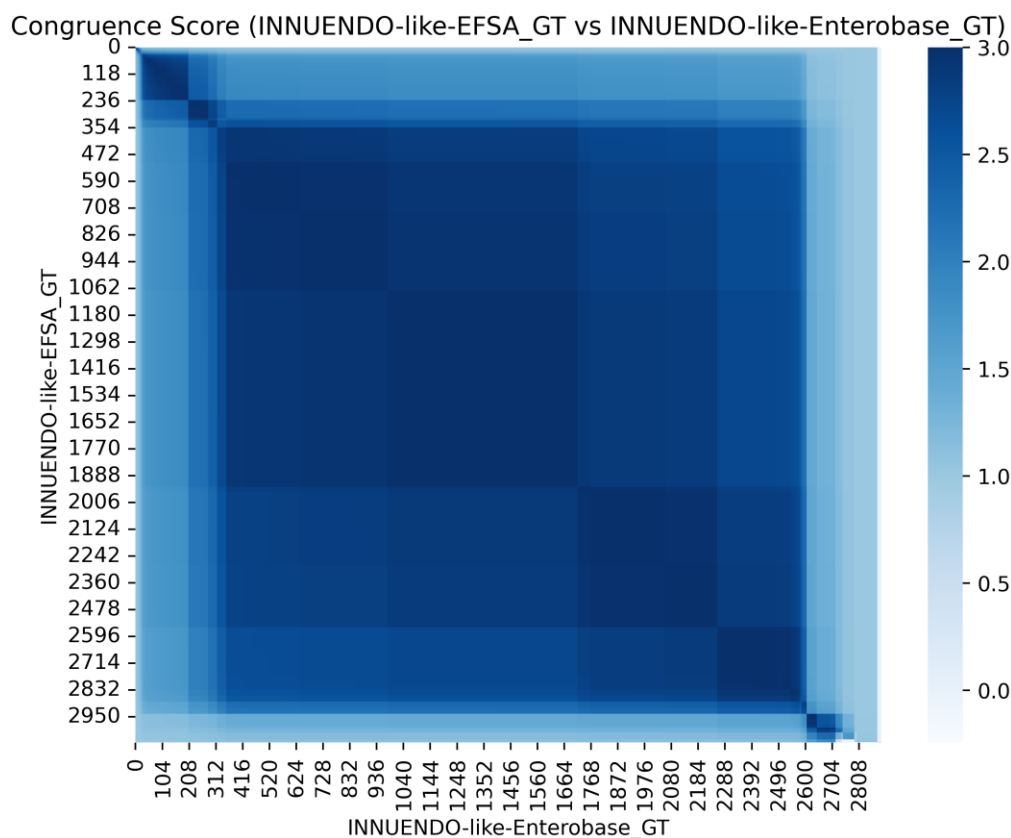


Figure S2.11.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

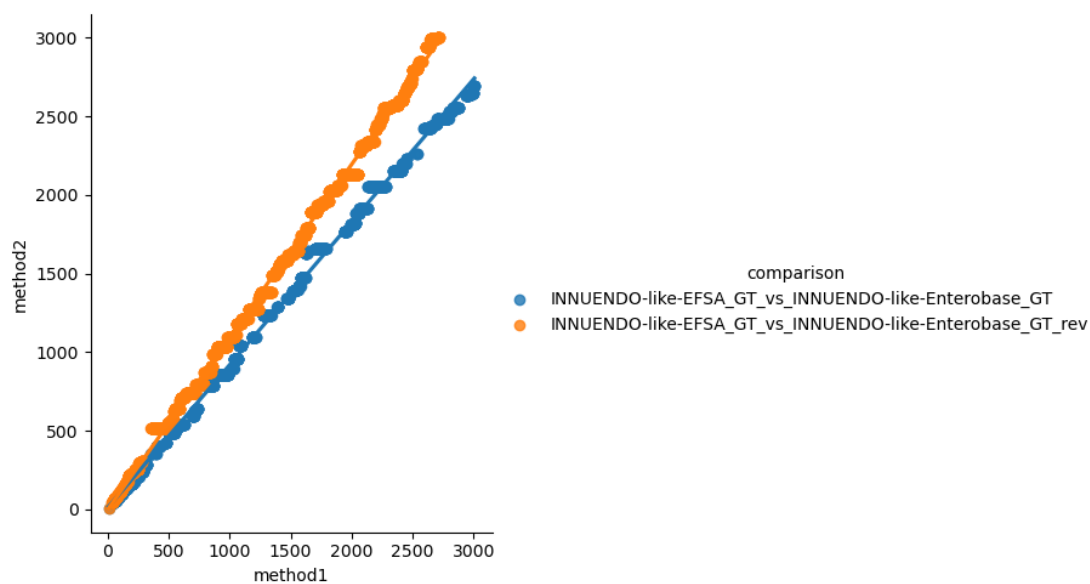


Figure S2.11.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1769 (blue) and 2292 (orange) points is presented.

12. INNUENDO-like-EFSA GrapeTree vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.12. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2998	2881

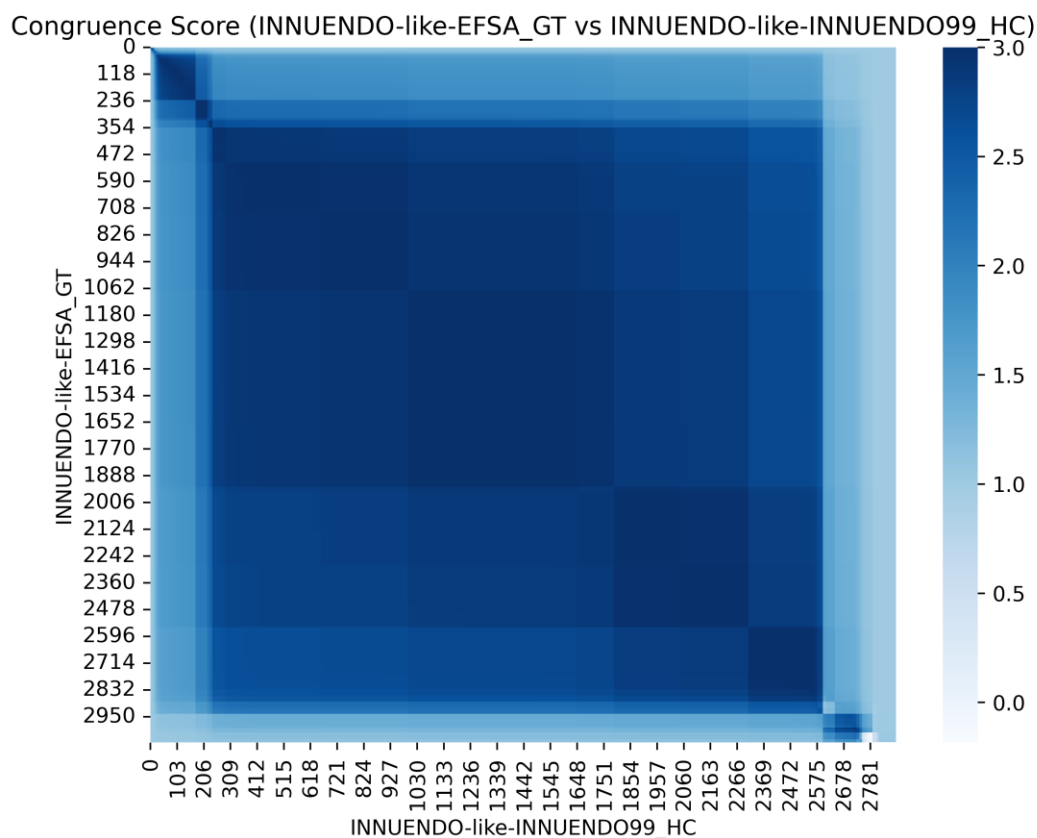


Figure S2.12.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

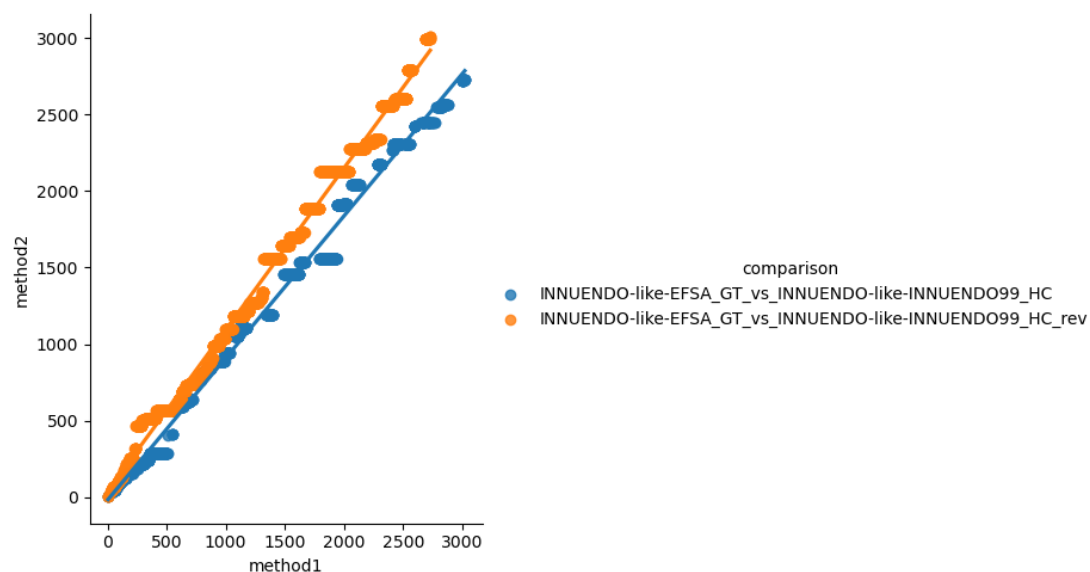


Figure S2.12.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1710 (blue) and 2586 (orange) points is presented.

13. INNUENDO-like-EFSA single-linkage vs. chewieSnake GrapeTree

Table S2.13. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA single-linkage	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions	2948	2801

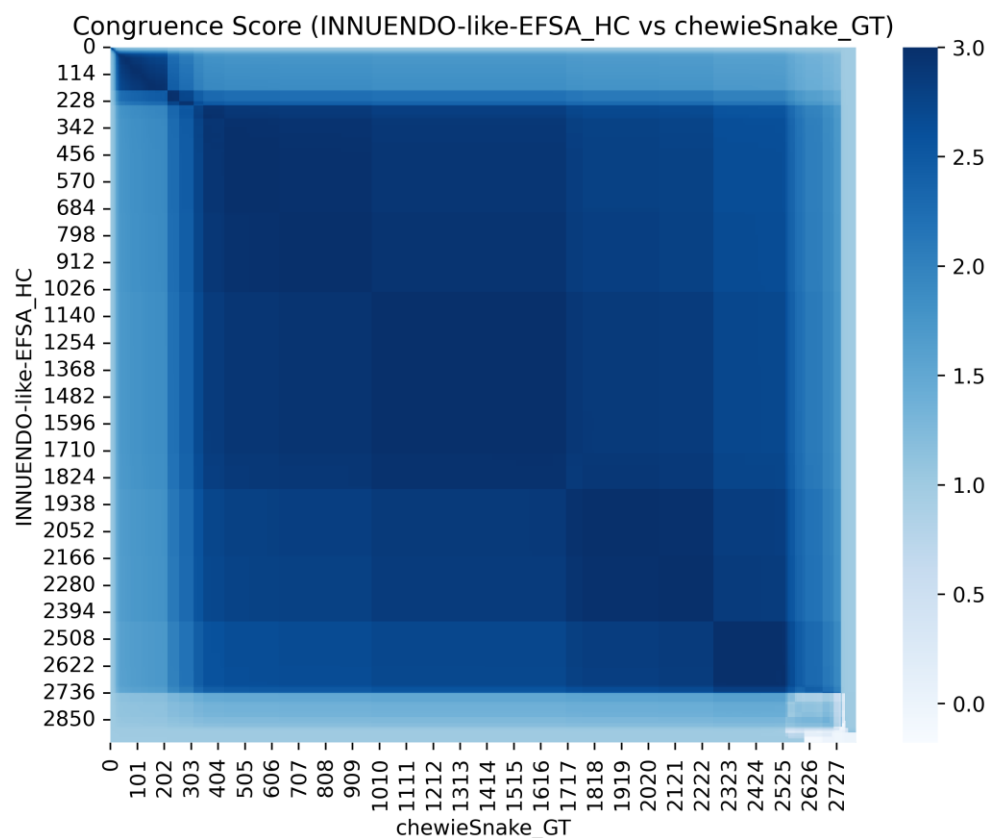


Figure S2.13.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

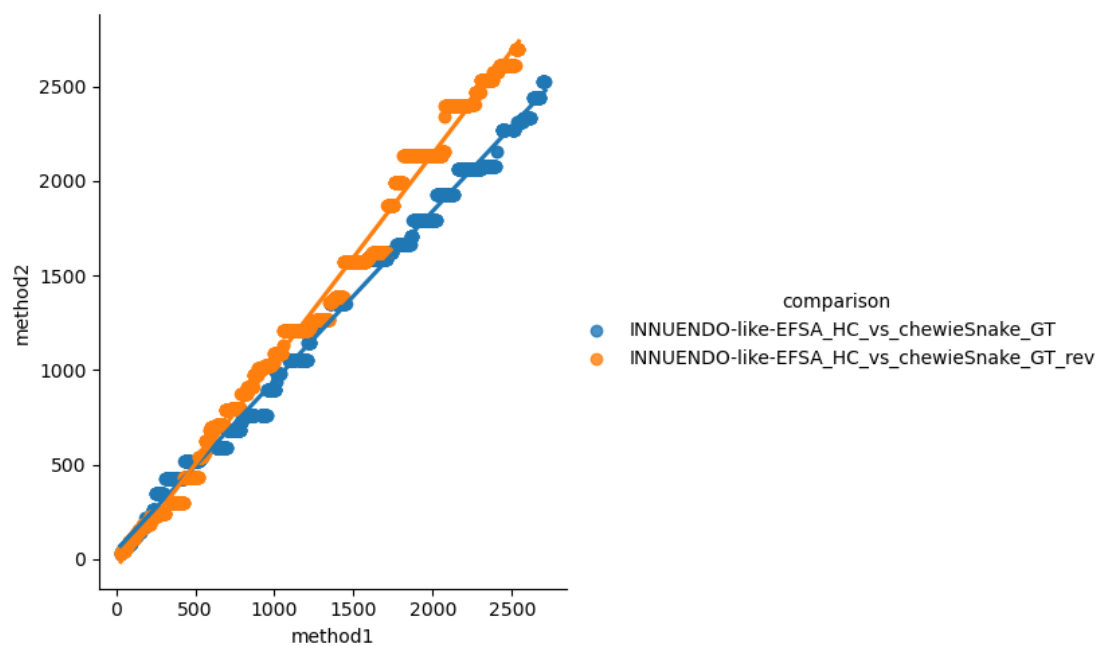


Figure S2.13.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1603 (blue) and 2588 (orange) points is presented.

14. INNUENDO-like-EFSA single-linkage vs. chewieSnake single-linkage

Table S2.14. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA single-linkage	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions	2948	2615

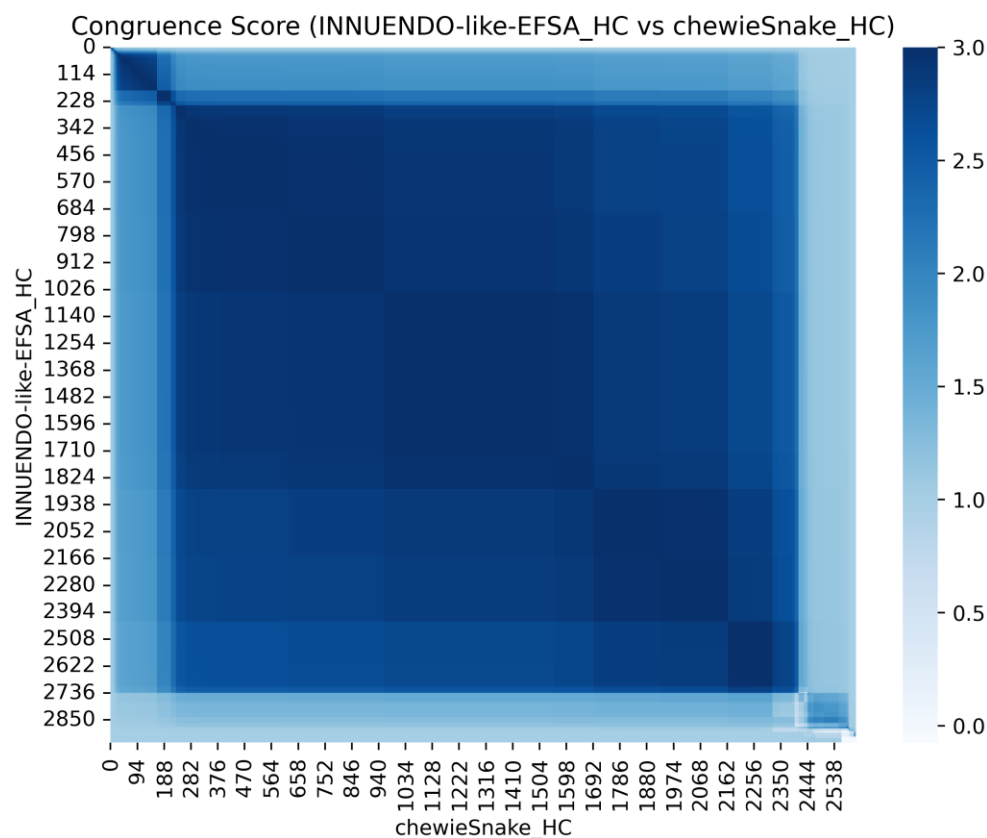


Figure S2.14.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

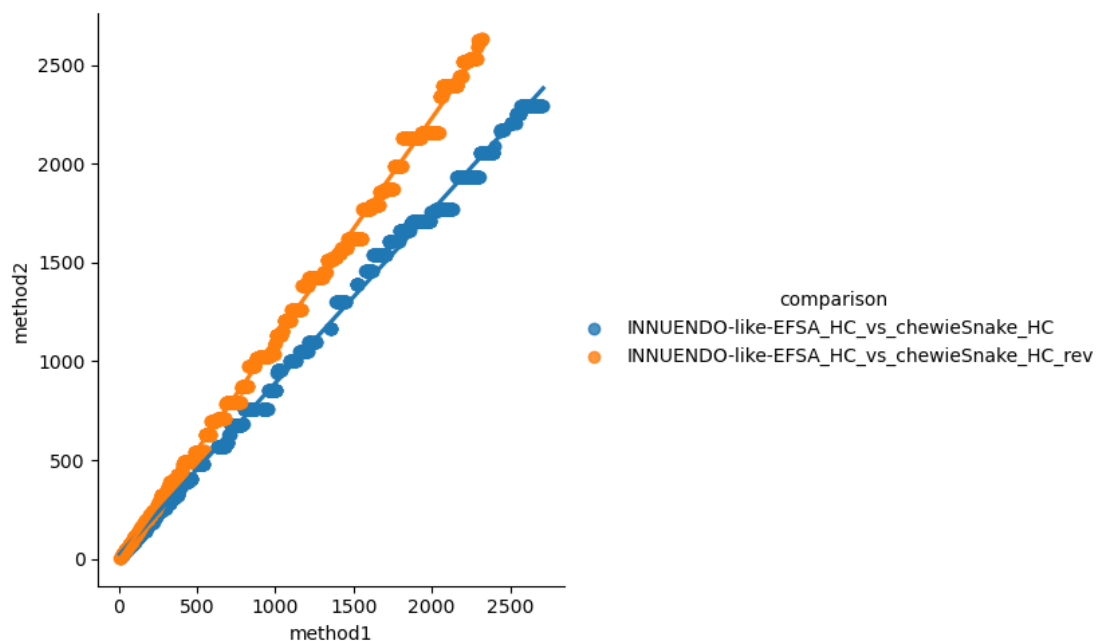


Figure S2.14.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1914 (blue) and 2478 (orange) points is presented.

15. INNUENDO-like-EFSA single-linkage vs. INNUENDO-like-EFSA GrapeTree

Table S2.15. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA single-linkage	INNUENDO-like-EFSA GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	EFSA
Dataset	All samples	All samples
Number partitions	2948	2998

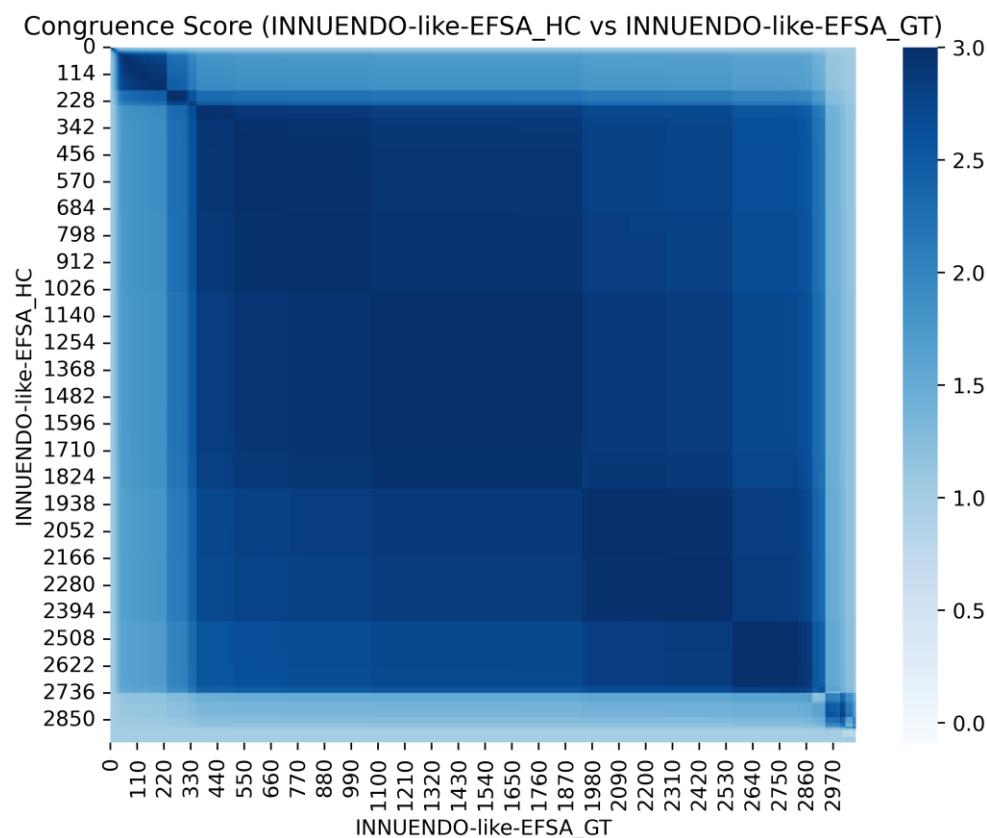


Figure S2.15.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

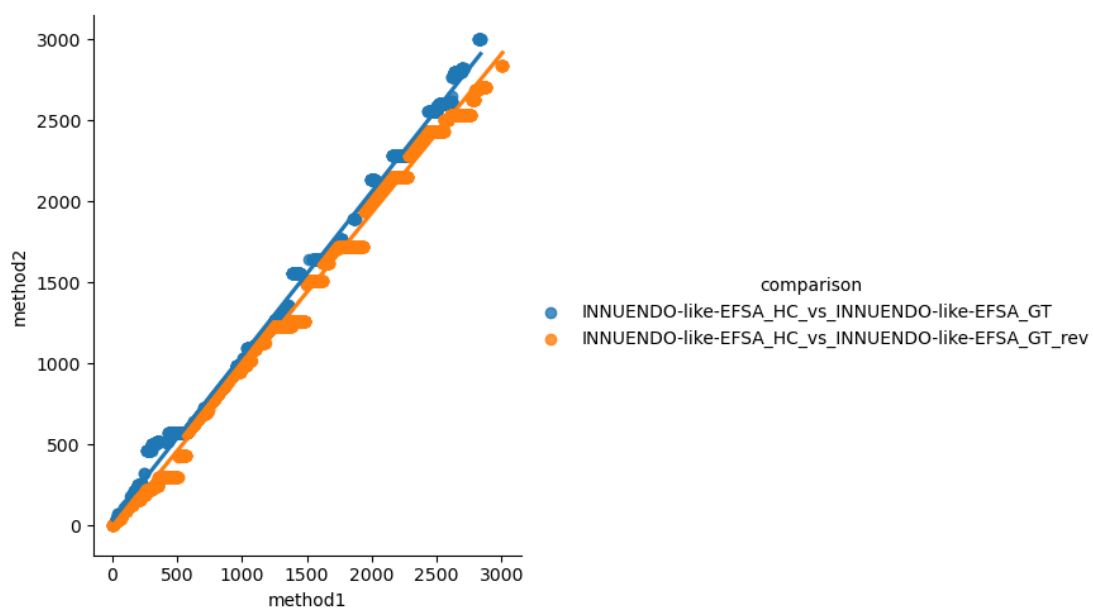


Figure S2.15.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1925 (blue) and 2308 (orange) points is presented.

16. INNUENDO-like-EFSA single-linkage vs. INNUENDO-like-Enterobase GrapeTree

Table S2.16. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions	2948	2895

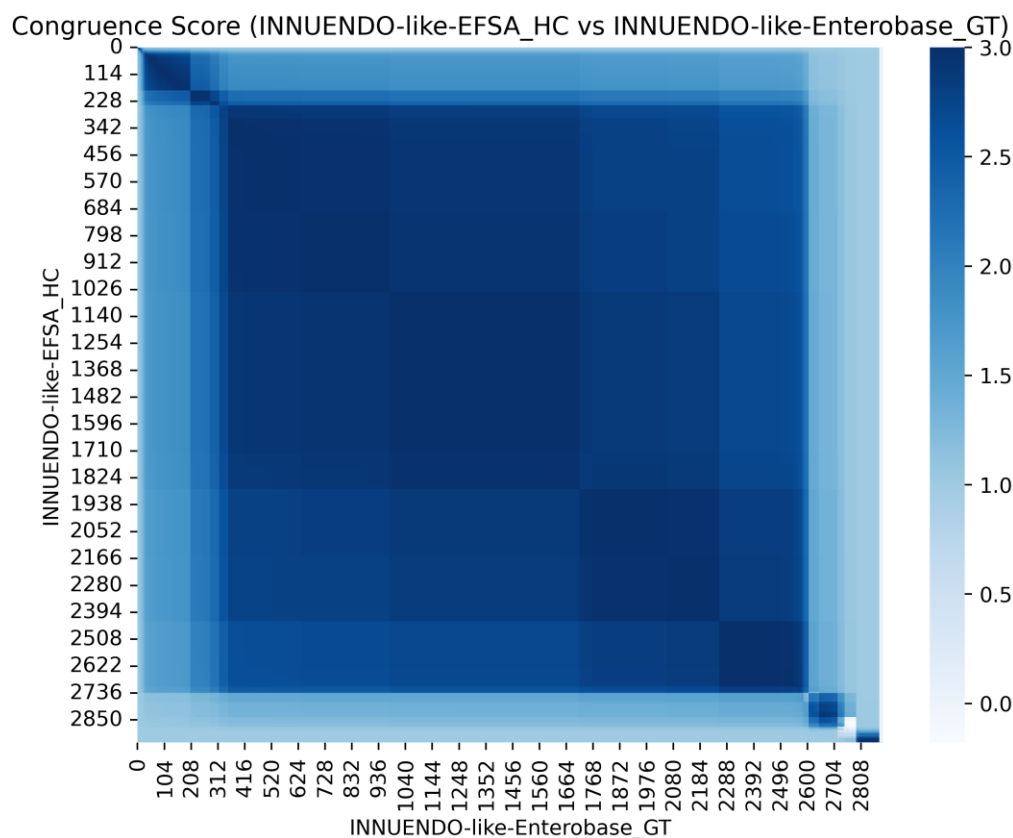


Figure S2.16.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

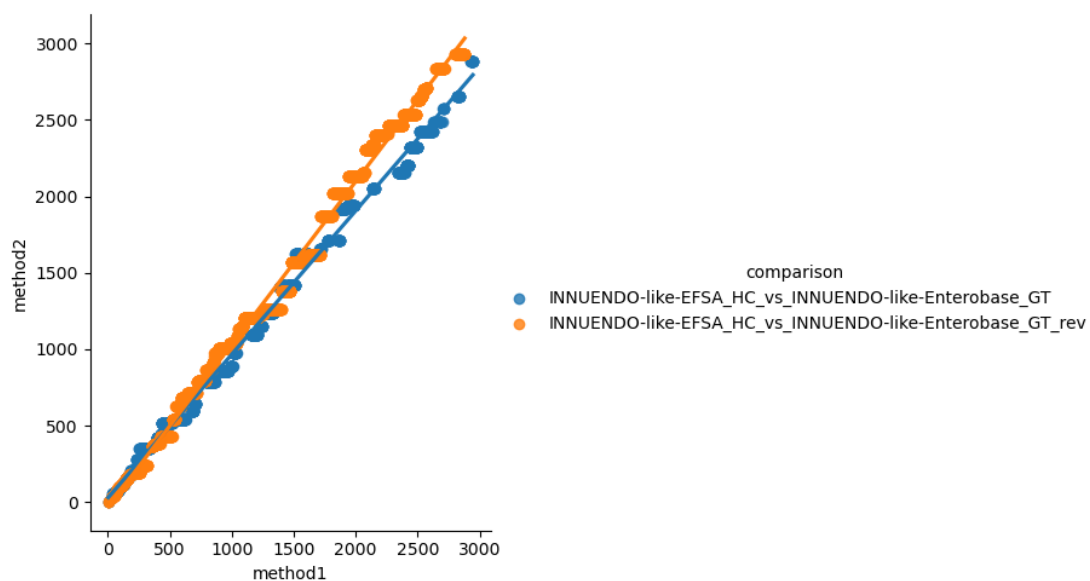


Figure S2.16.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1555 (blue) and 2856 (orange) points is presented.

17. INNUENDO-like-EFSA single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.17. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-EFSA single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2948	2881

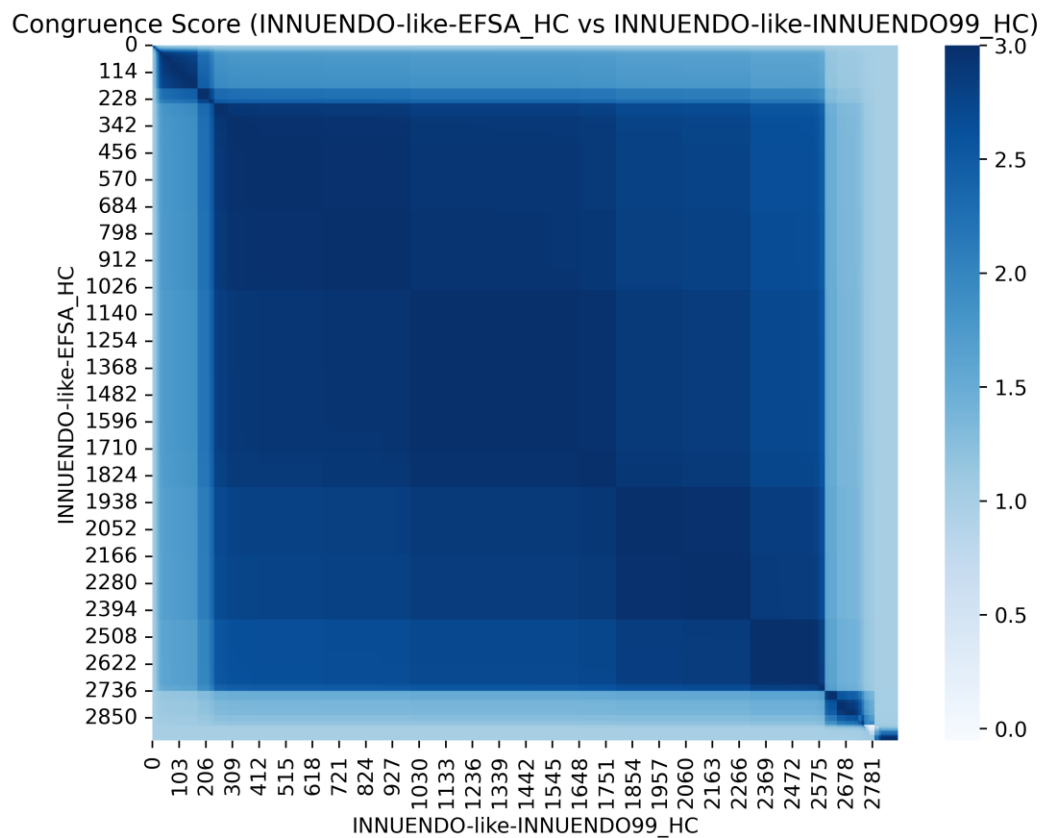


Figure S2.17.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

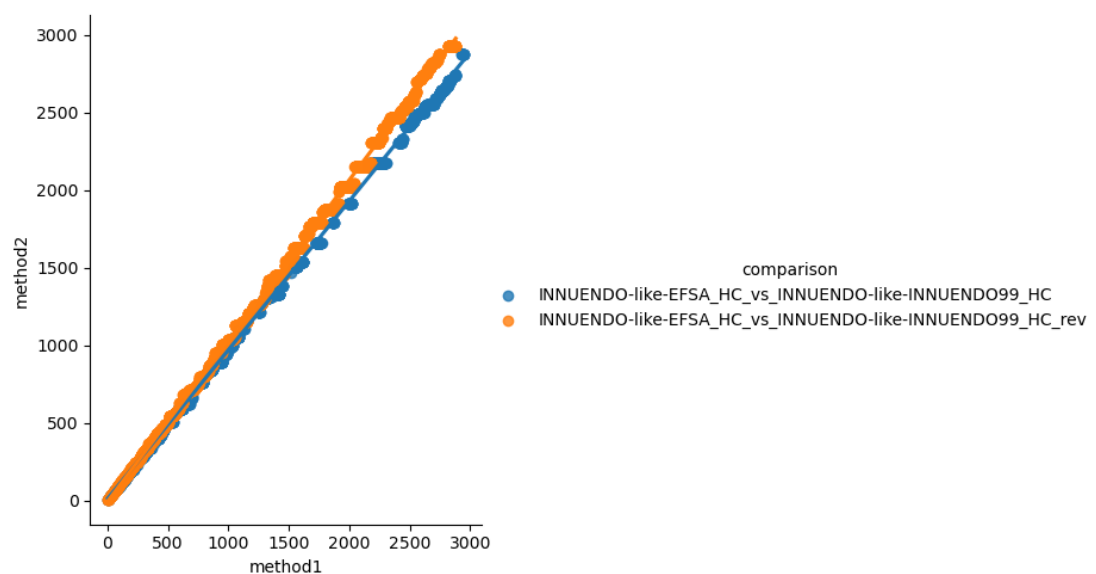


Figure S2.17.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1471 (blue) and 2666 (orange) points is presented.

18. INNUENDO-like-Enterobase GrapeTree vs. chewieSnake GrapeTree

Table S2.18. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2895	2801

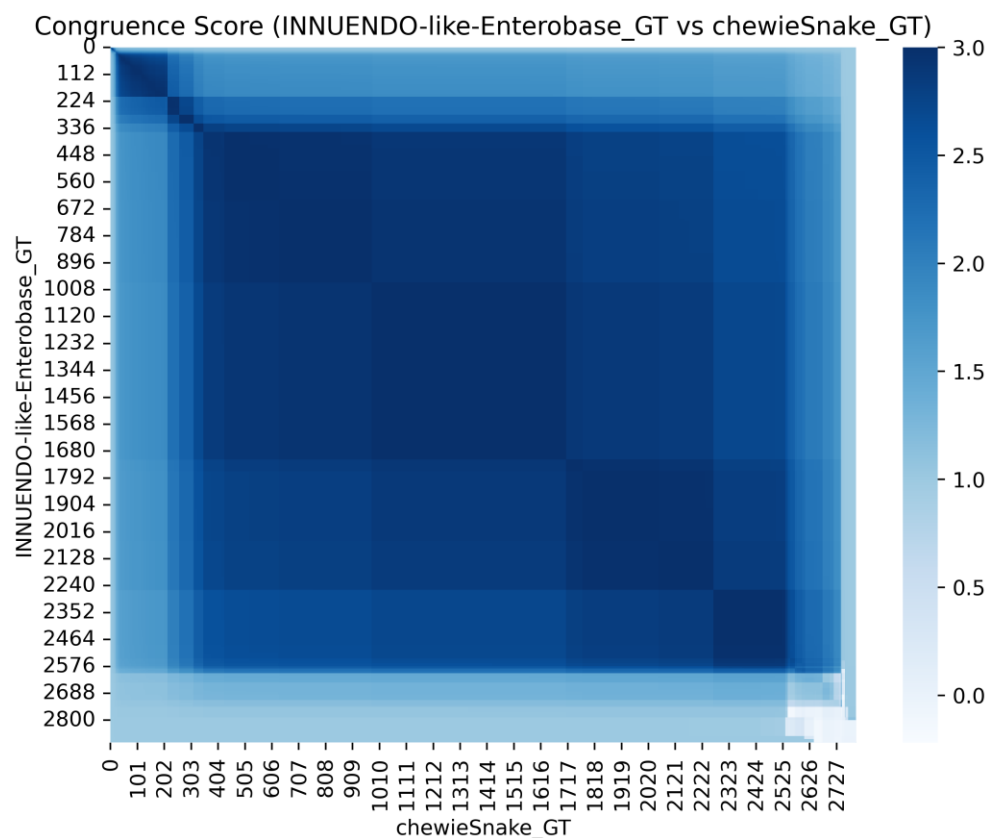


Figure S2.18.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

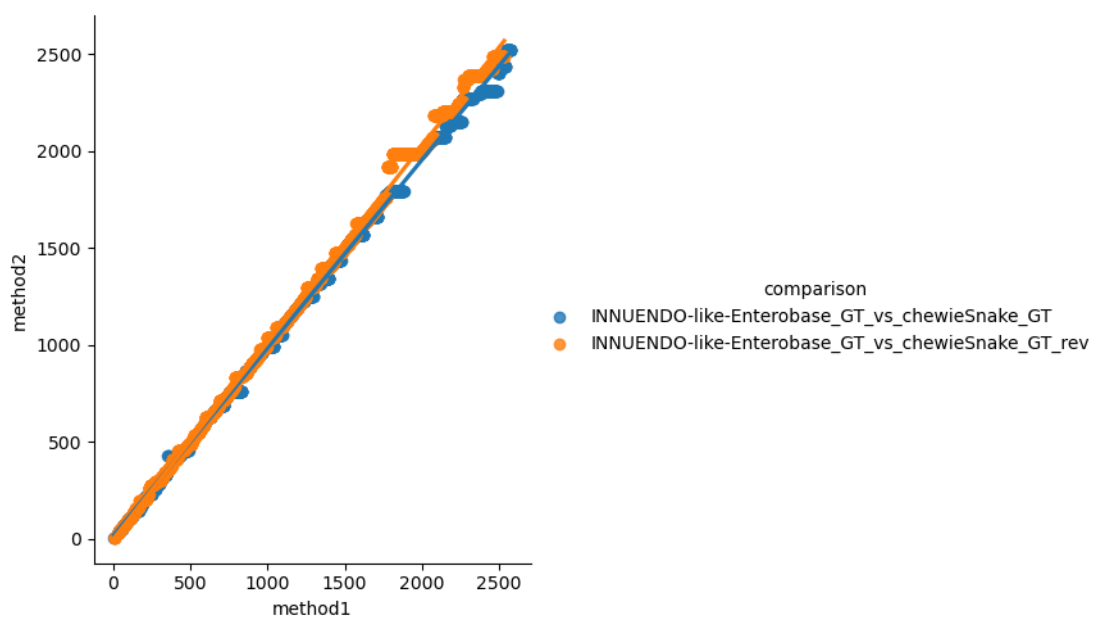


Figure S2.18.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1700 (blue) and 2791 (orange) points is presented.

19. INNUENDO-like-Enterobase GrapeTree vs. chewieSnake single-linkage

Table S2.19. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase GrapeTree	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2895	2615

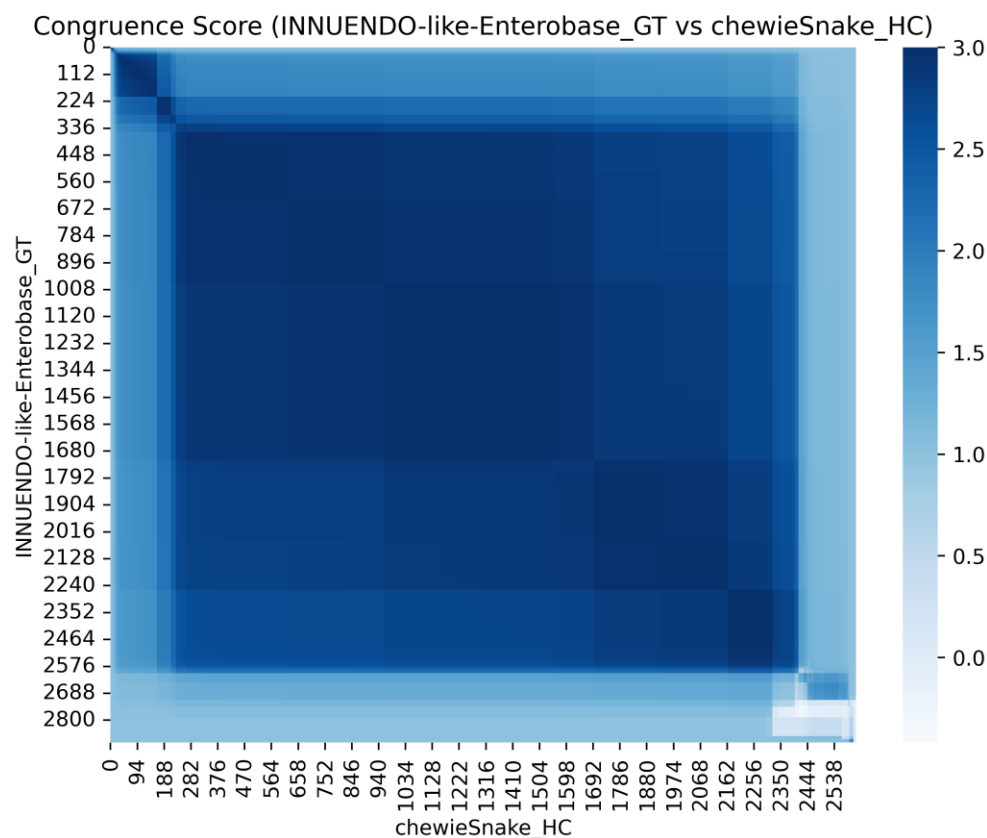


Figure S2.19.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

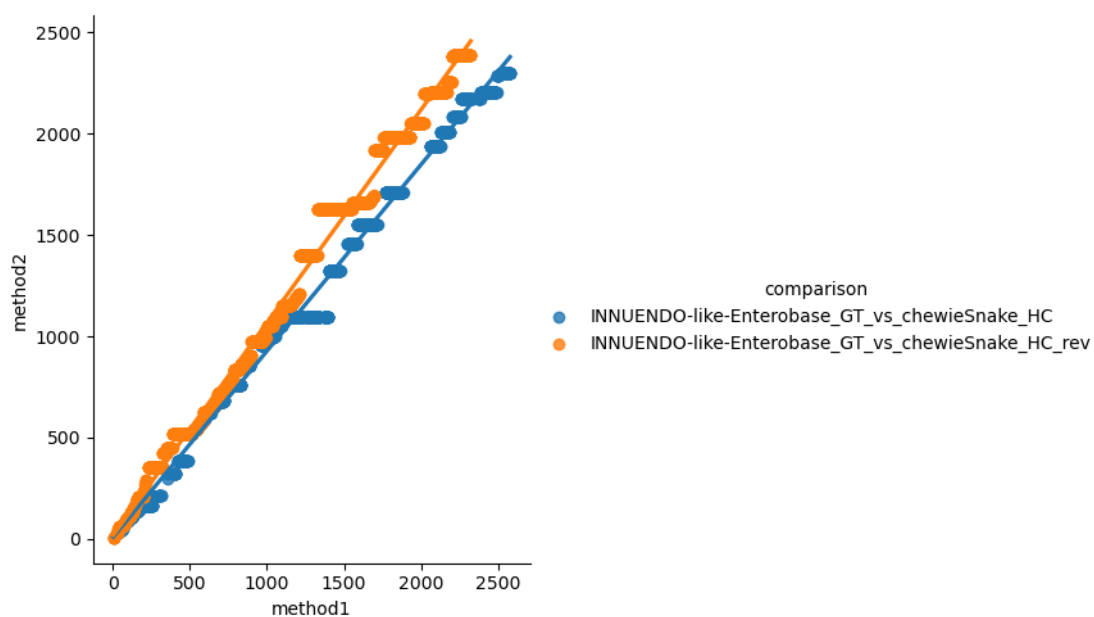


Figure S2.19.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1755 (blue) and 2510 (orange) points is presented.

20. INNUENDO-like-Enterobase GrapeTree vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.20. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2895	2881

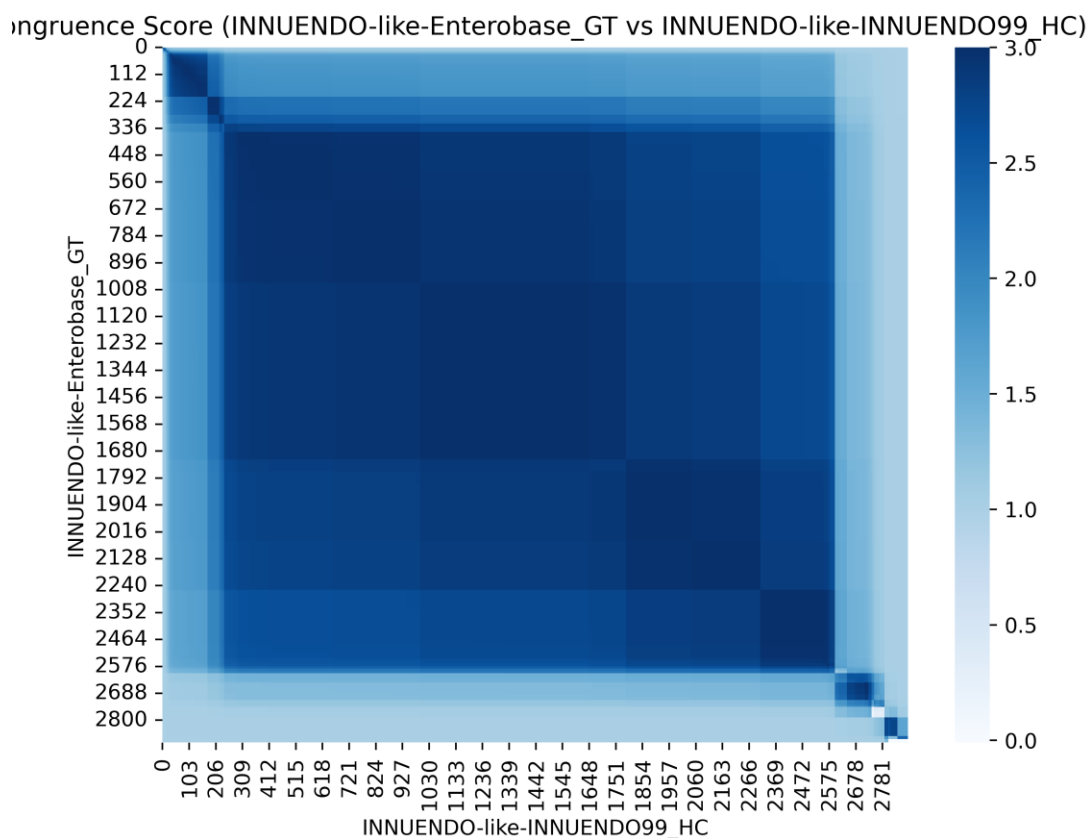


Figure S2.20.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

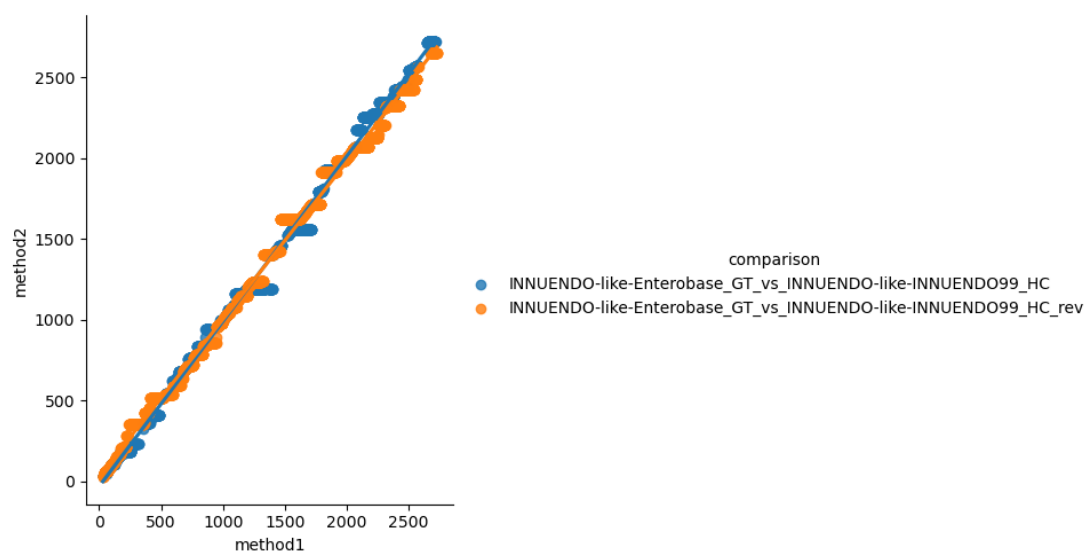


Figure S2.20.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1728 (blue) and 2283 (orange) points is presented.

21. INNUENDO-like-Enterobase single-linkage vs. Bionumerics single-linkage

Table S2.21. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	Bionumerics single-linkage
Pipeline version	chewBBACA 2.8.5	v8.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2800	2844

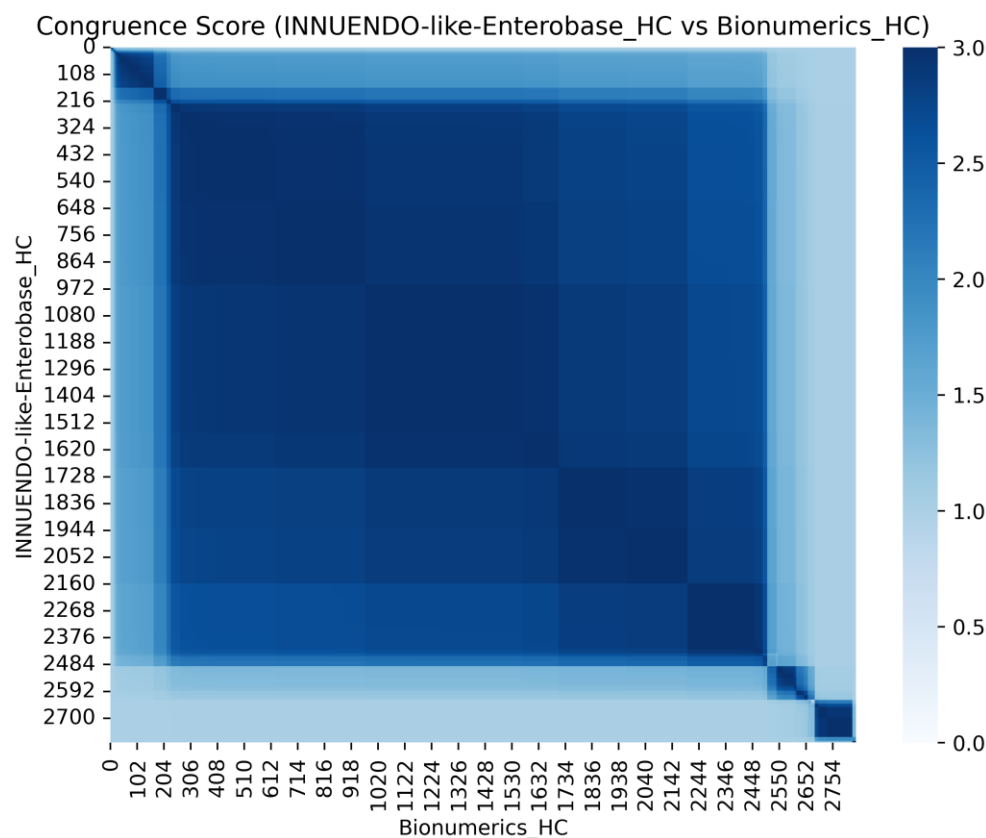


Figure S2.21.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

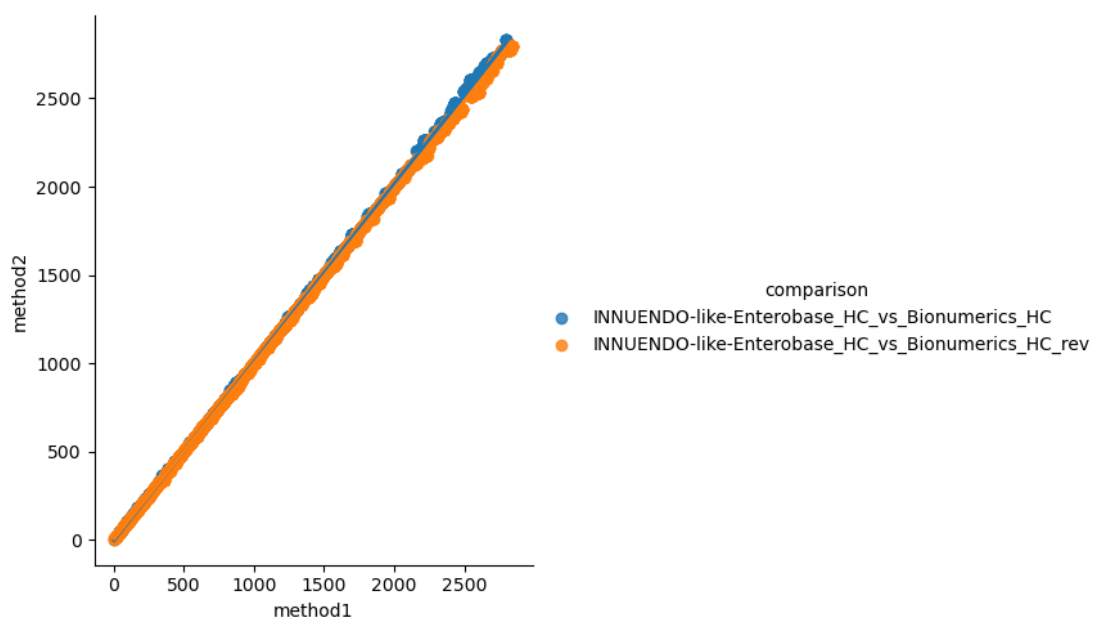


Figure S2.21.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 1798 (blue) and 2592 (orange) points is presented.

22. INNUENDO-like-Enterobase single-linkage vs. chewieSnake GrapeTree

Table S2.22. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2800	2801

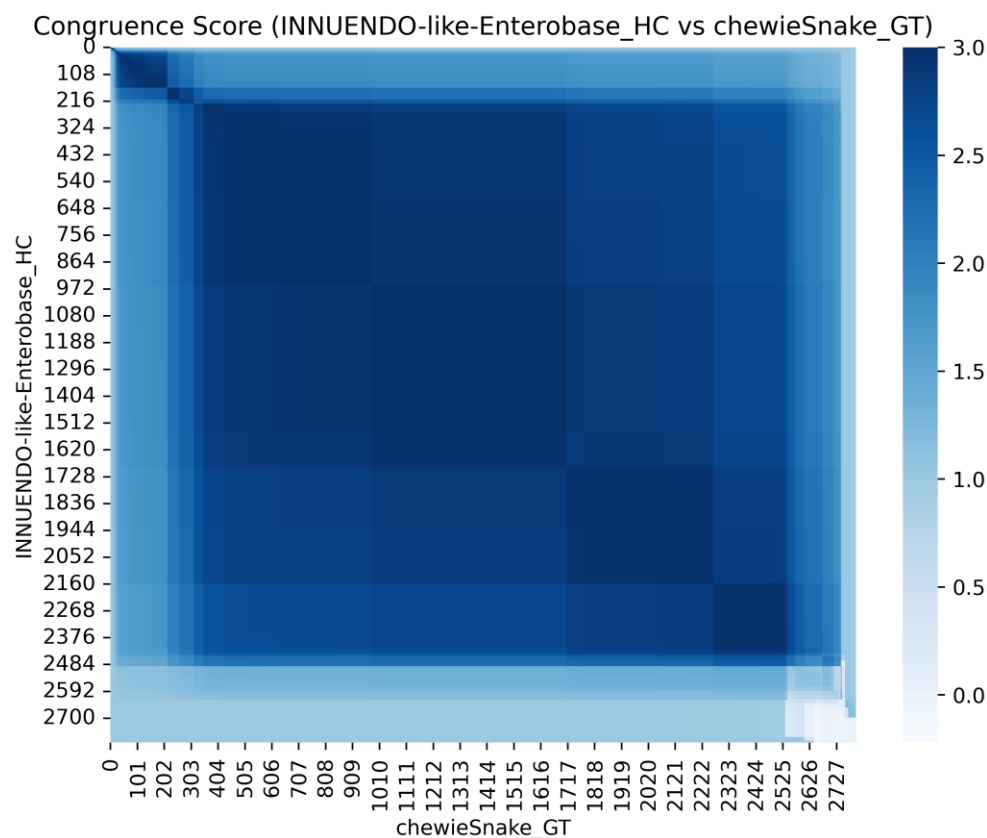


Figure S2.22.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

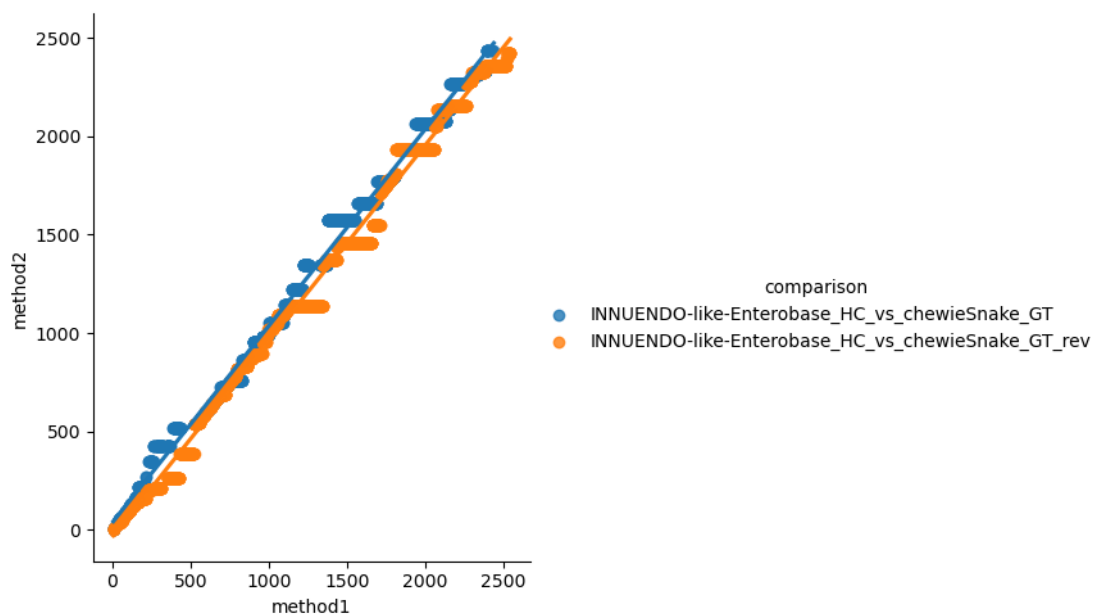


Figure S2.22.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 2079 (blue) and 2749 (orange) points is presented.

23. INNUENDO-like-Enterobase single-linkage vs. chewieSnake single-linkage

Table S2.23. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2800	2615

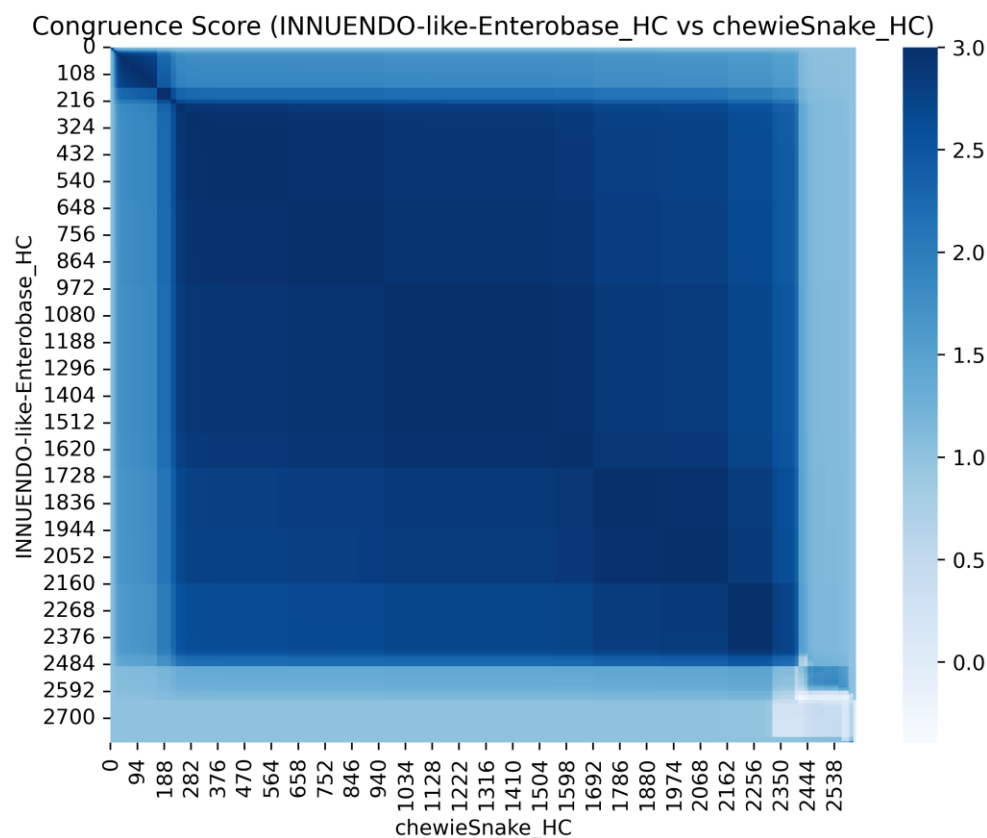


Figure S2.23.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

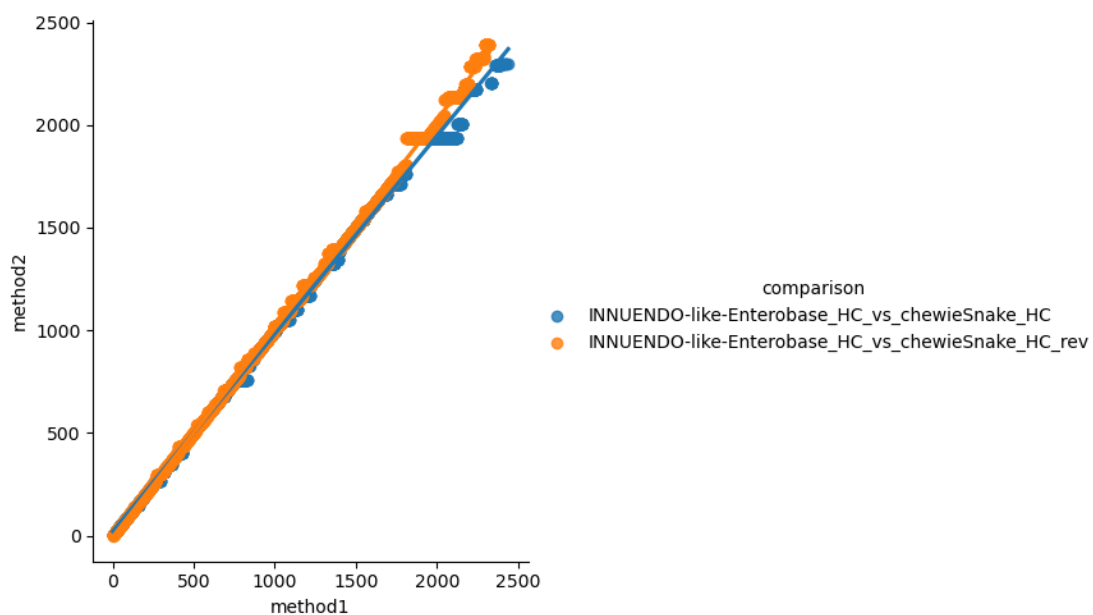


Figure S2.23.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1687 (blue) and 2482 (orange) points is presented.

24. INNUENDO-like-Enterobase single-linkage vs. INNUENDO-like-EFSA GrapeTree

Table S2.24. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-EFSA GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2800	2998

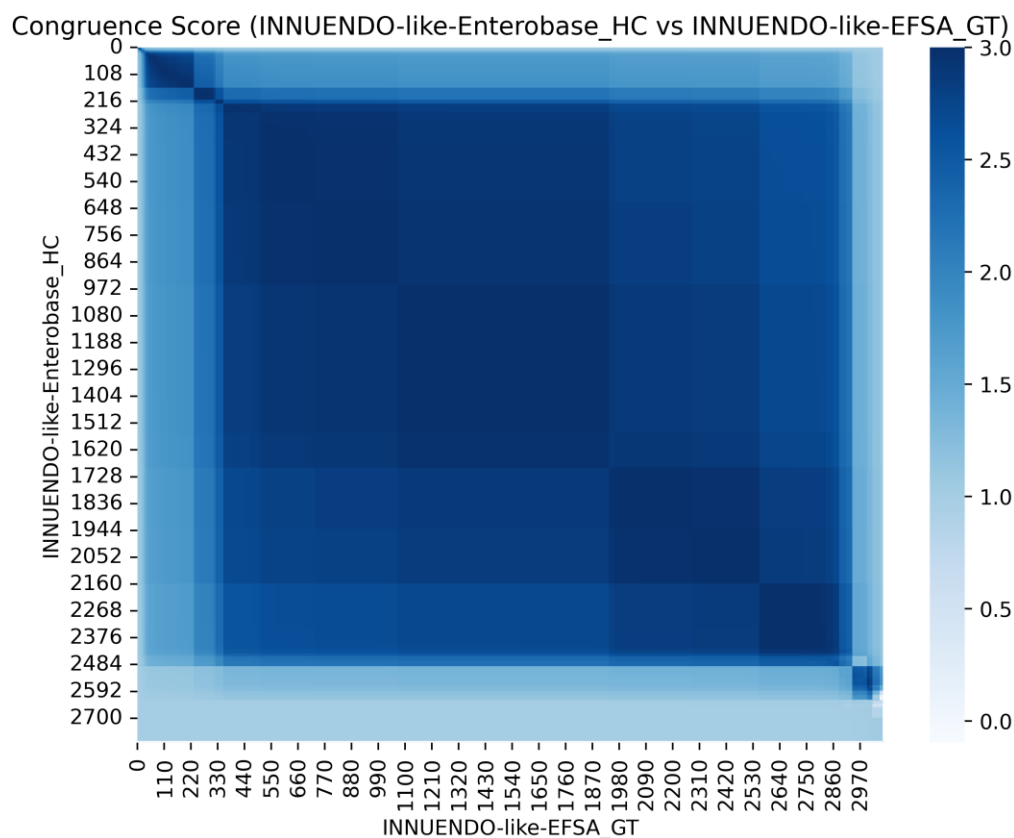


Figure S2.24.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

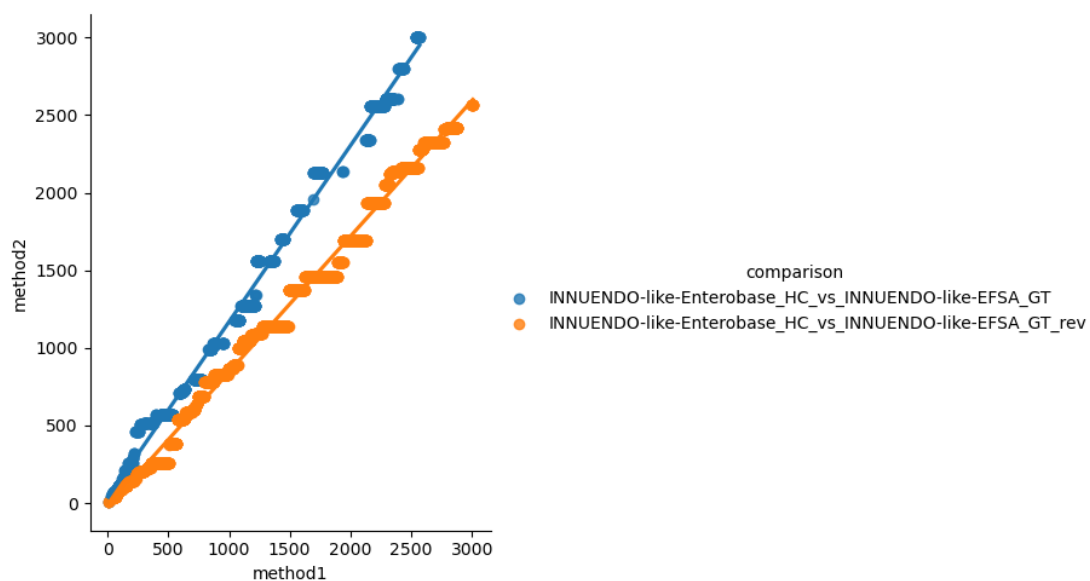


Figure S2.24.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1712 (blue) and 2318 (orange) points is presented.

25. INNUENDO-like-Enterobase single-linkage vs. INNUENDO-like-EFSA single-linkage

Table S2.25. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-EFSA single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2800	2948

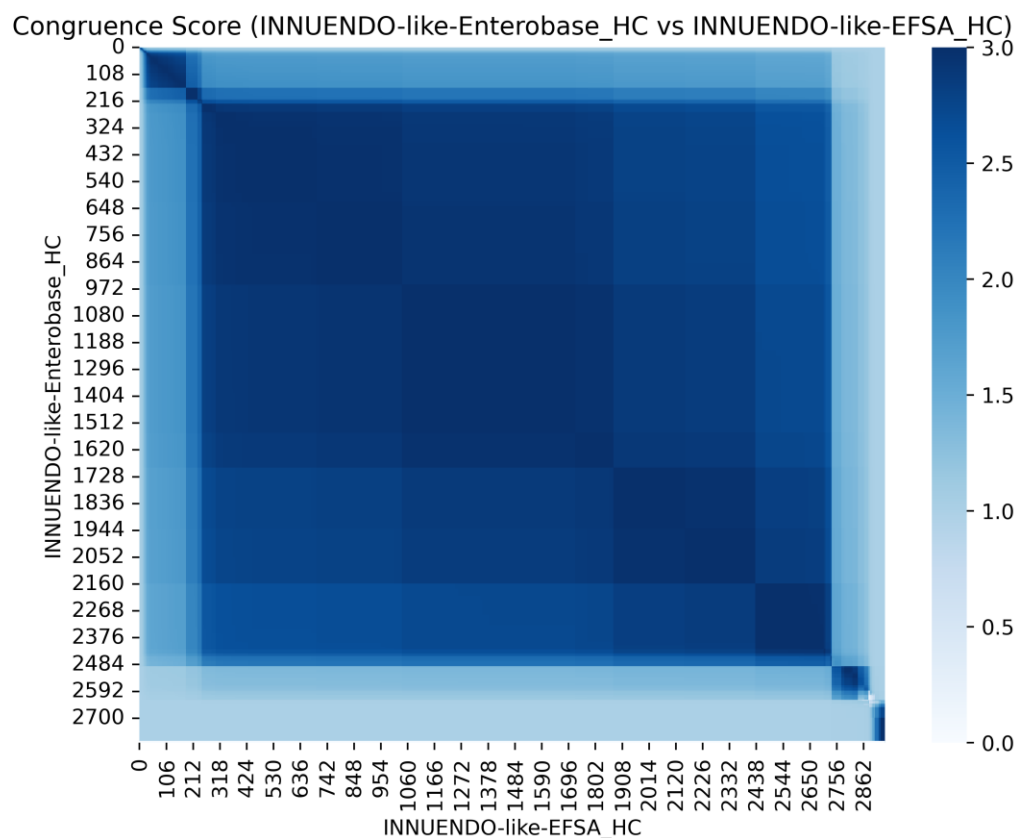


Figure S2.25.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

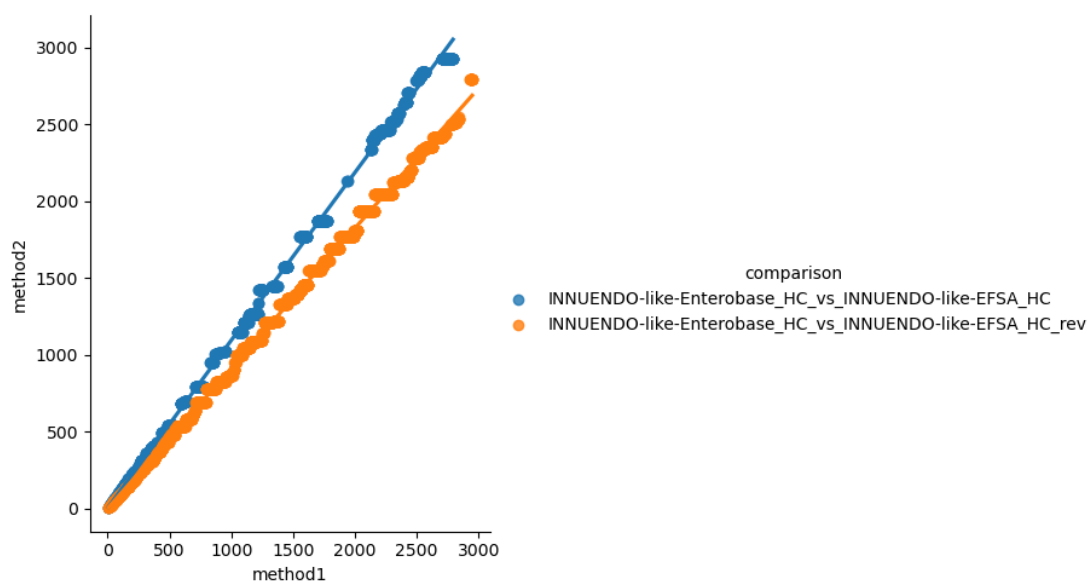


Figure S2.25.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1243 (blue) and 2842 (orange) points is presented.

26. INNUENDO-like-Enterobase single-linkage vs. INNUENDO-like-Enterobase GrapeTree

Table S2.26. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2800	2895

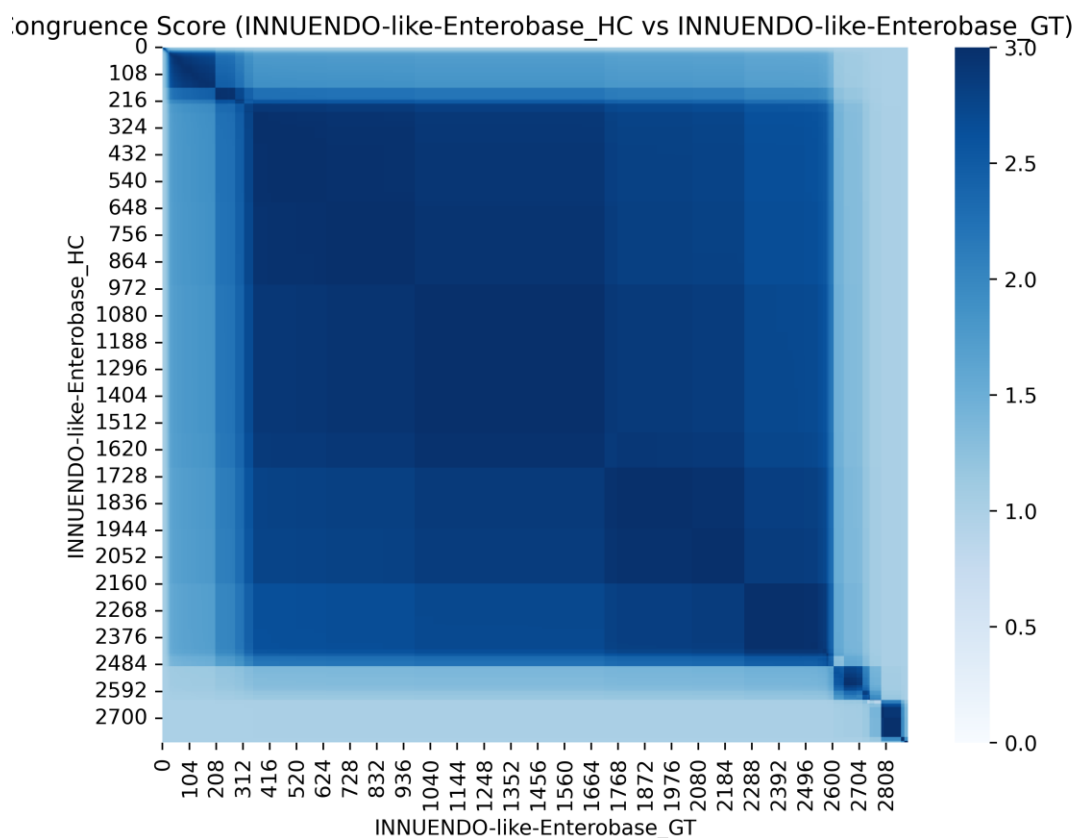


Figure S2.26.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

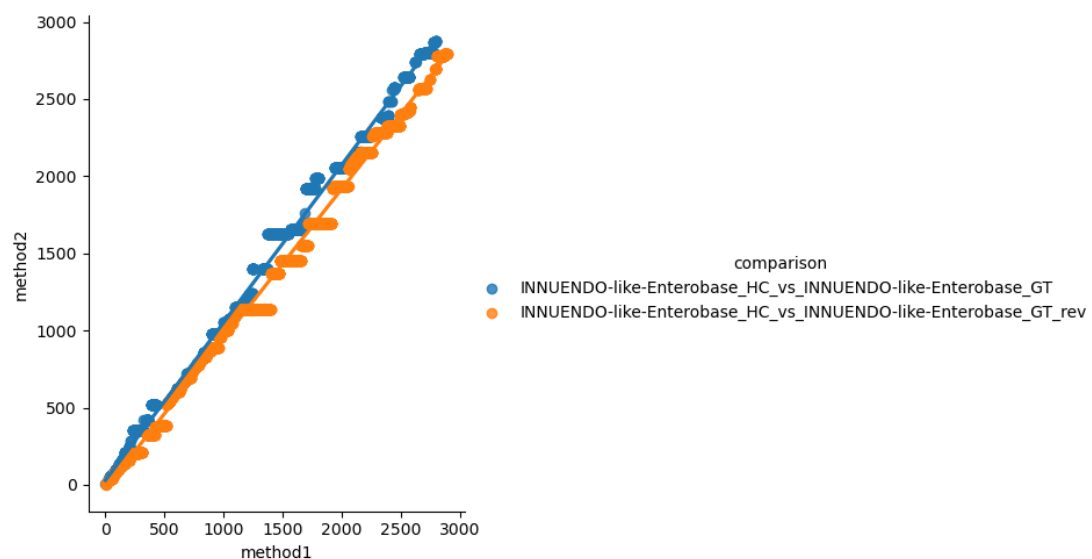


Figure S2.26.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1391 (blue) and 2795 (orange) points is presented.

27. INNUENDO-like-Enterobase single-linkage vs. INNUENDO-like-INNUENDO99 GrapeTree

Table S2.27. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-INNUENDO99 GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2800	2998

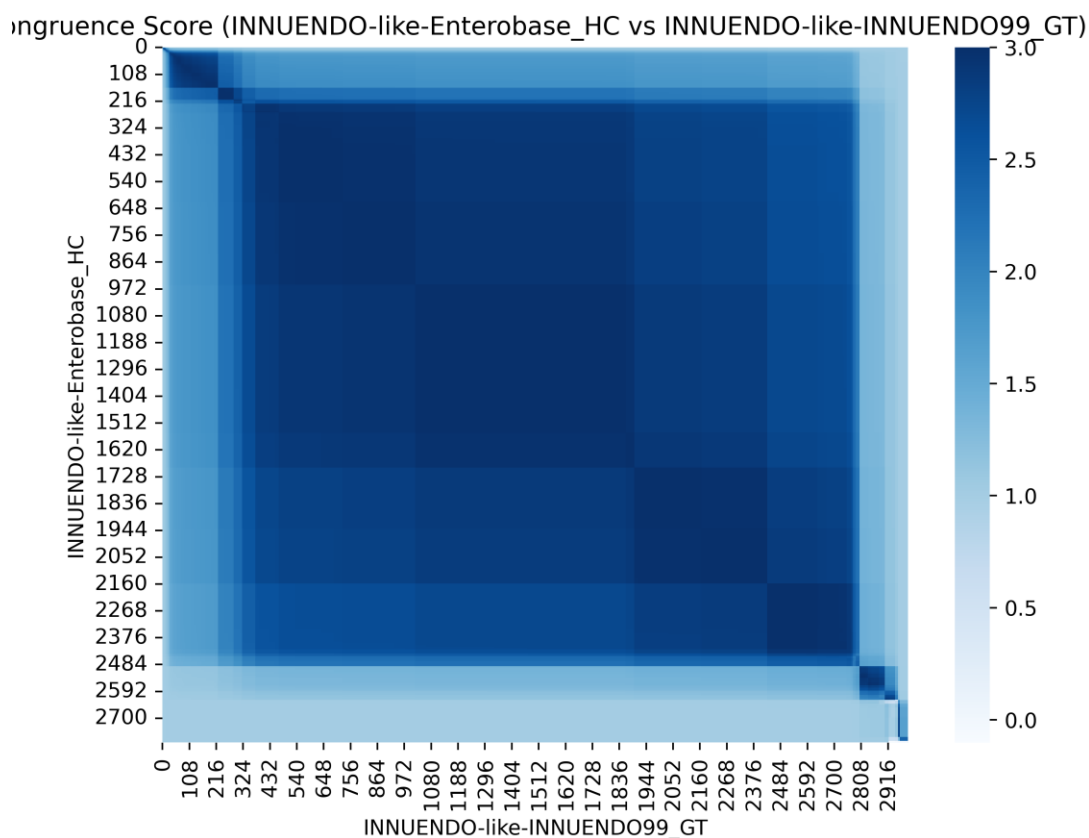


Figure S2.27.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

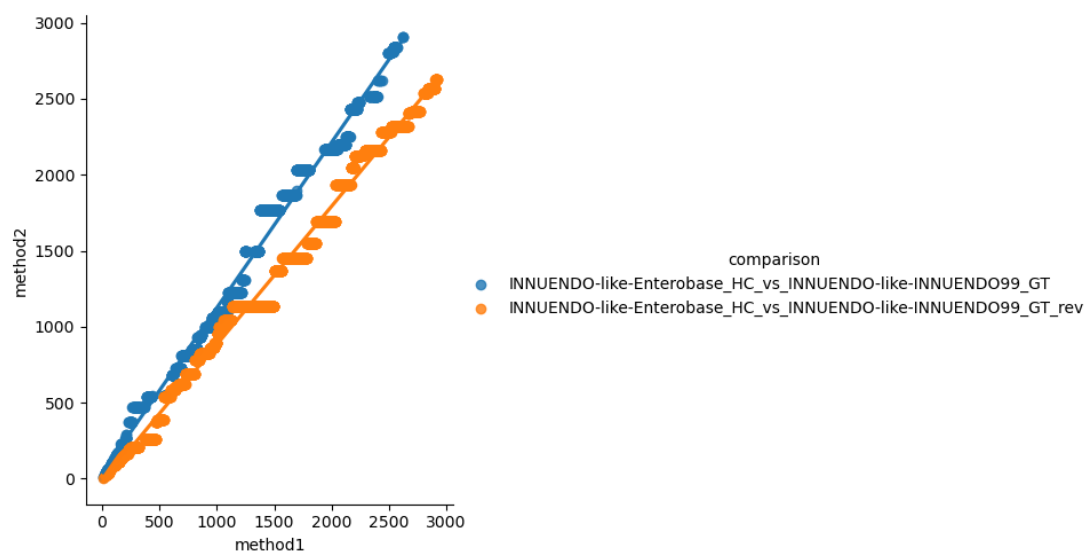


Figure S2.27.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1900 (blue) and 2706 (orange) points is presented.

28. INNUENDO-like-Enterobase single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.28. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2800	2881

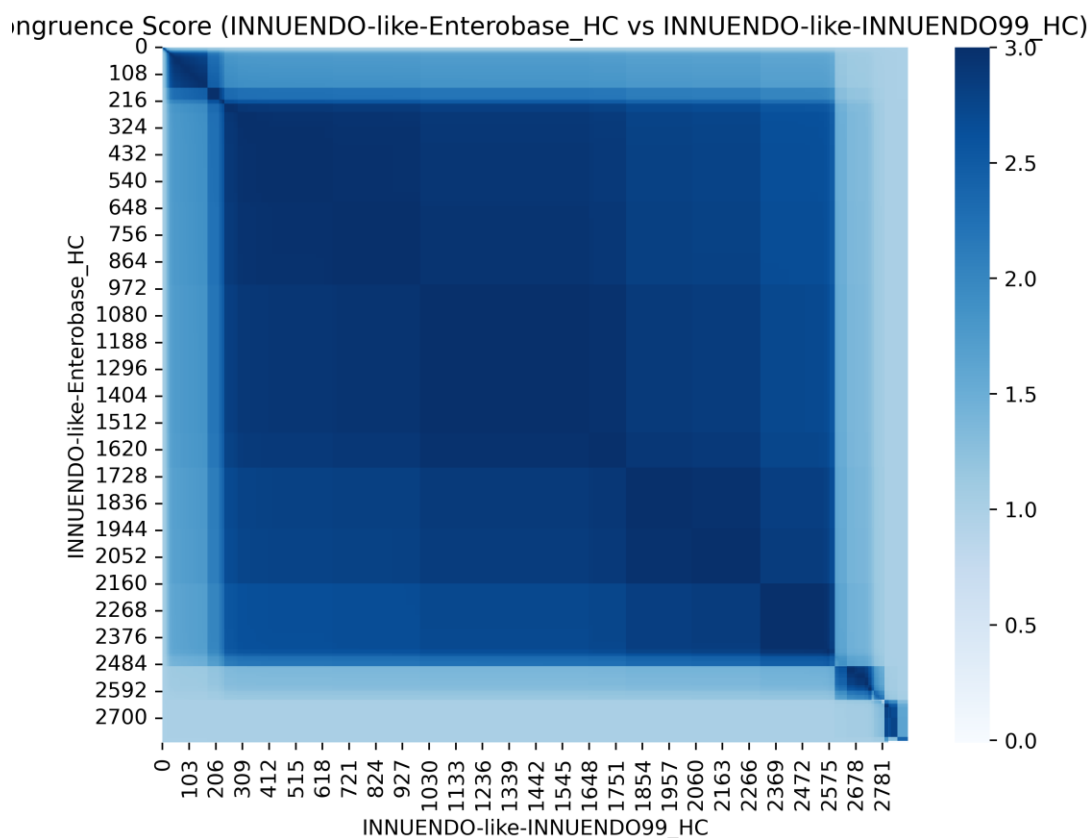


Figure S2.28.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

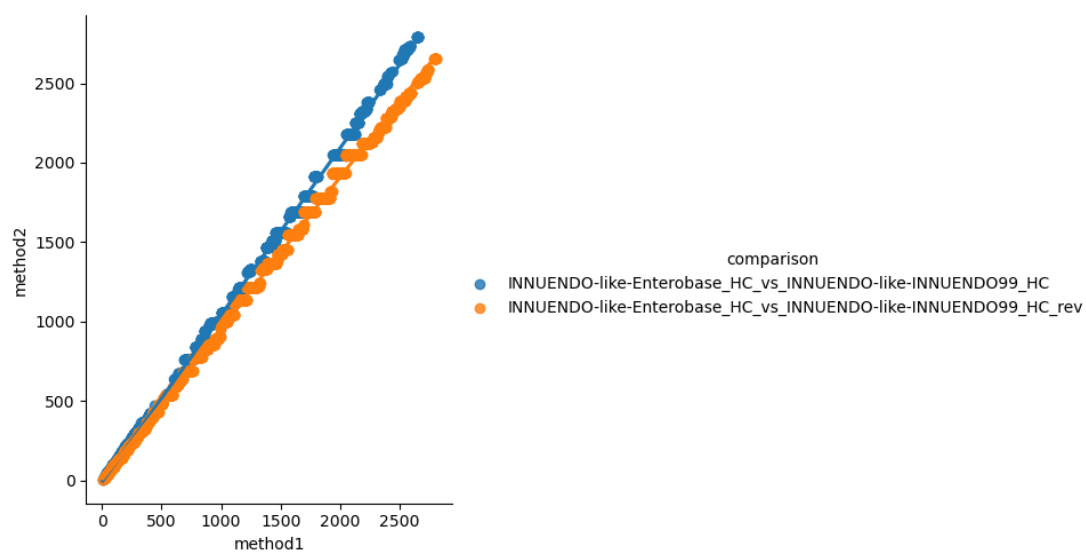


Figure S2.28.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1765 (blue) and 2800 (orange) points is presented.

29. INNUENDO-like-INNUENDO99 GrapeTree vs. Bionumerics single-linkage

Table S2.29. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	Bionumerics single-linkage
Pipeline version	chewBBACA 2.8.5	v8.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2844

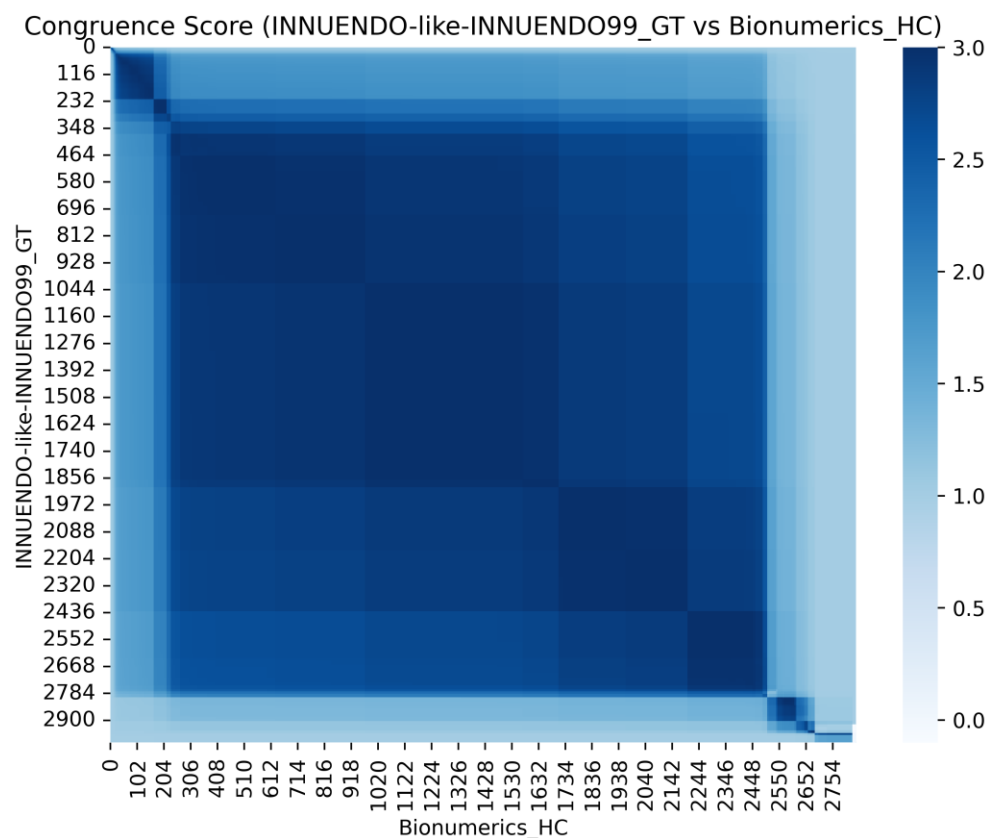


Figure S2.29.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

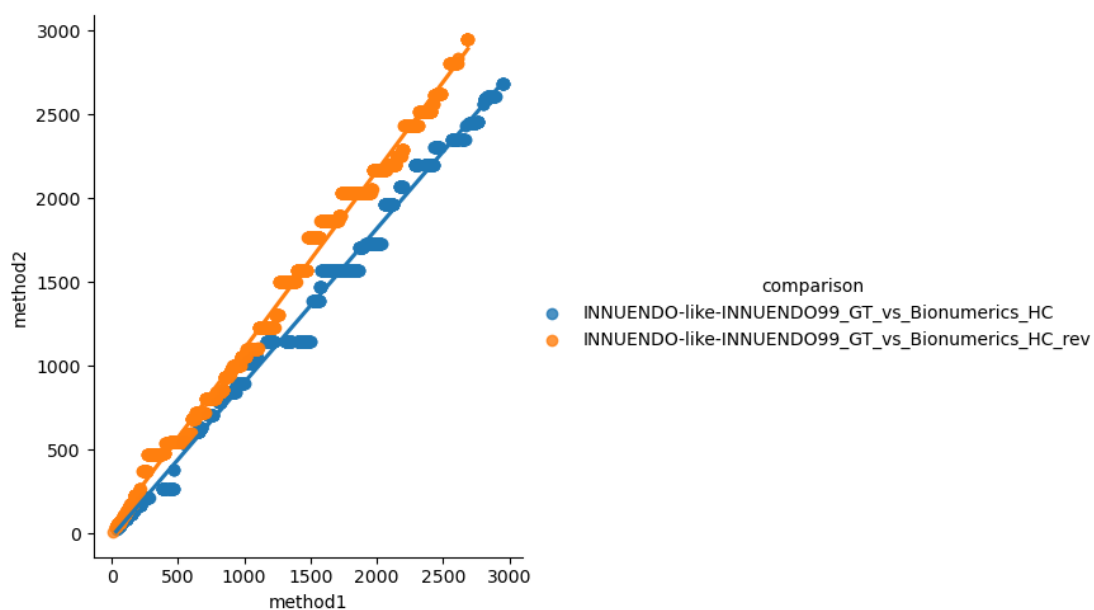


Figure S2.29.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1813 (blue) and 2690 (orange) points is presented.

30. INNUENDO-like-INNUENDO99 GrapeTree vs. chewieSnake GrapeTree

Table S2.30. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2801

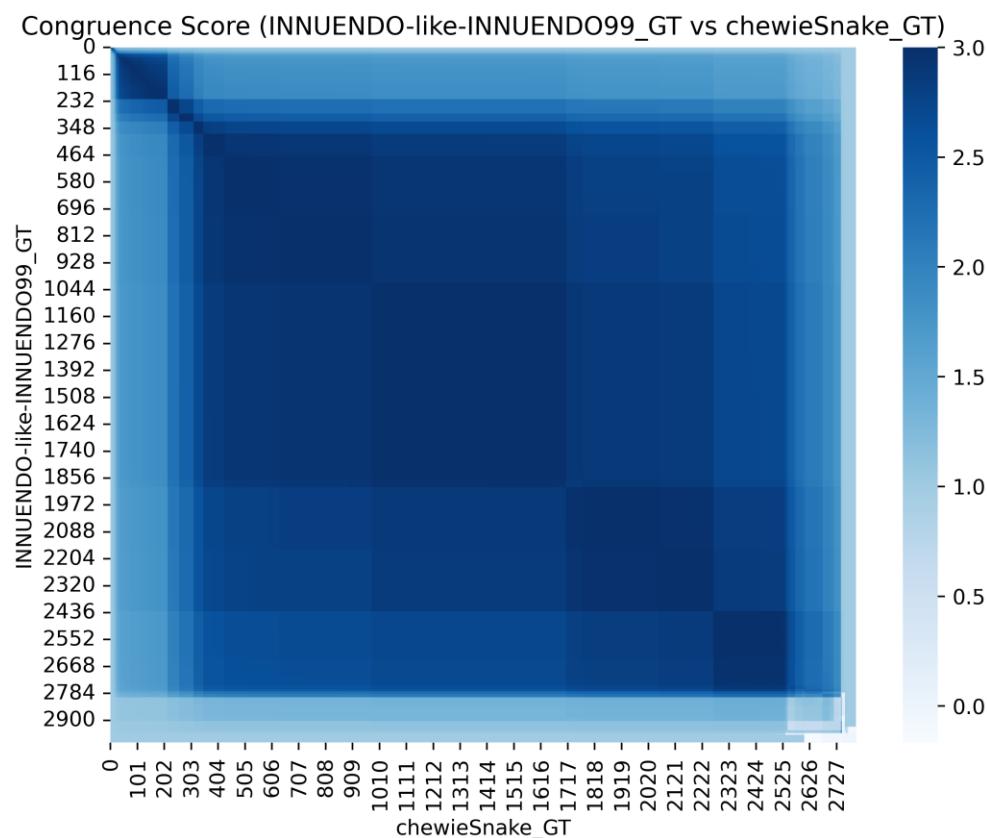


Figure S2.30.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

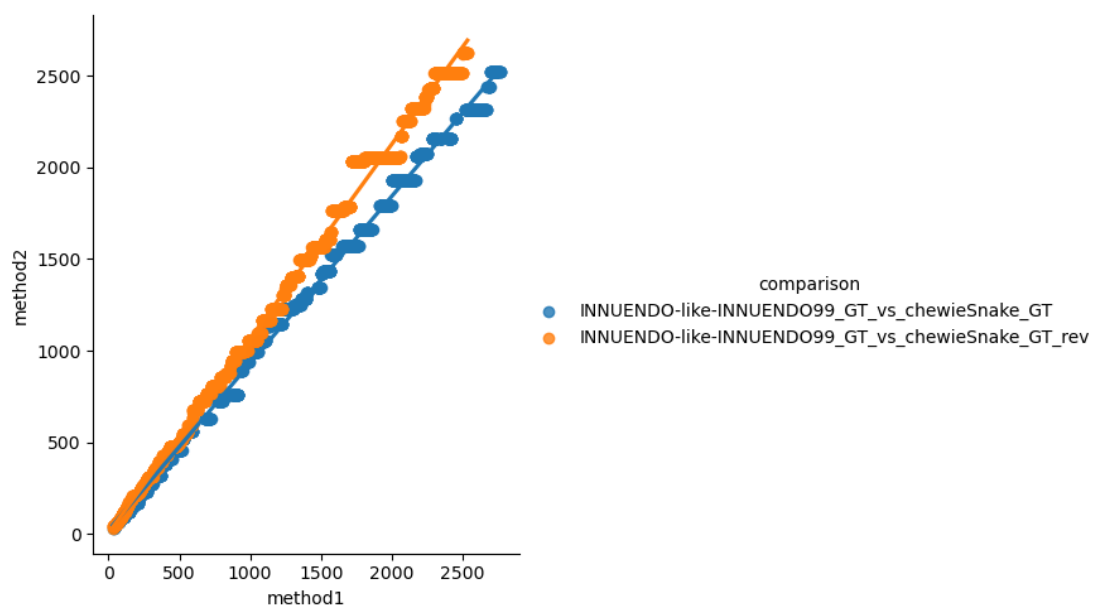


Figure S2.30.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1797 (blue) and 2526 (orange) points is presented.

31. INNUENDO-like-INNUENDO99 GrapeTree vs. chewieSnake single-linkage

Table S2.31. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2615

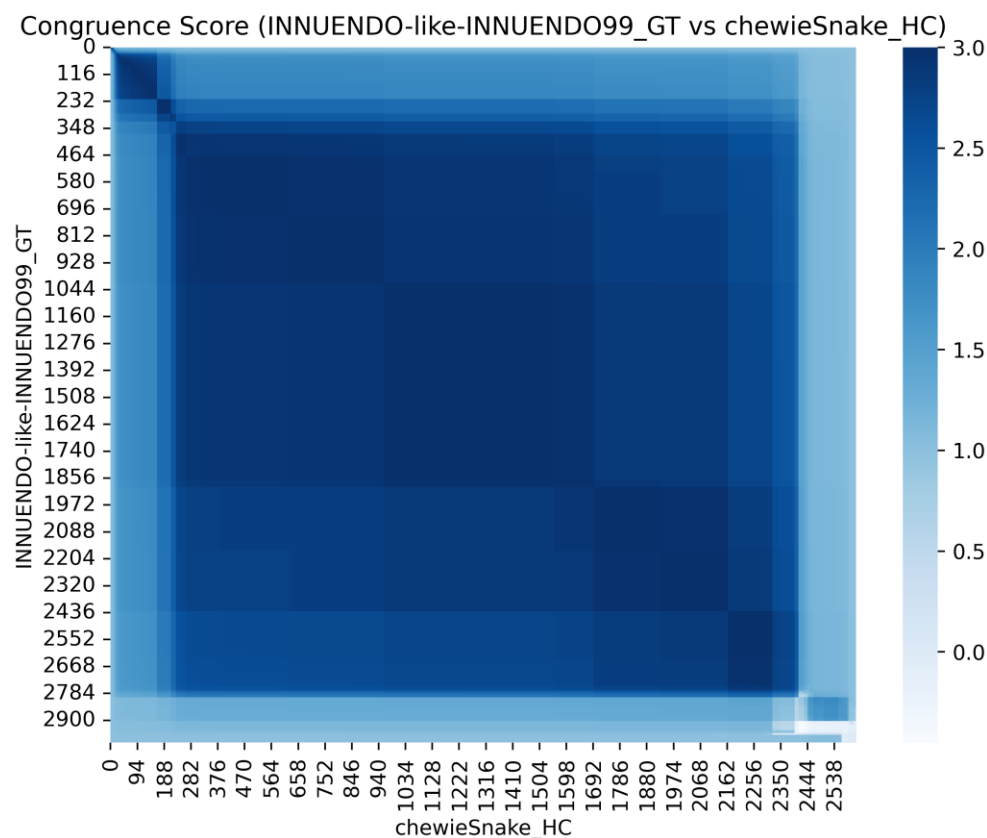


Figure S2.31.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

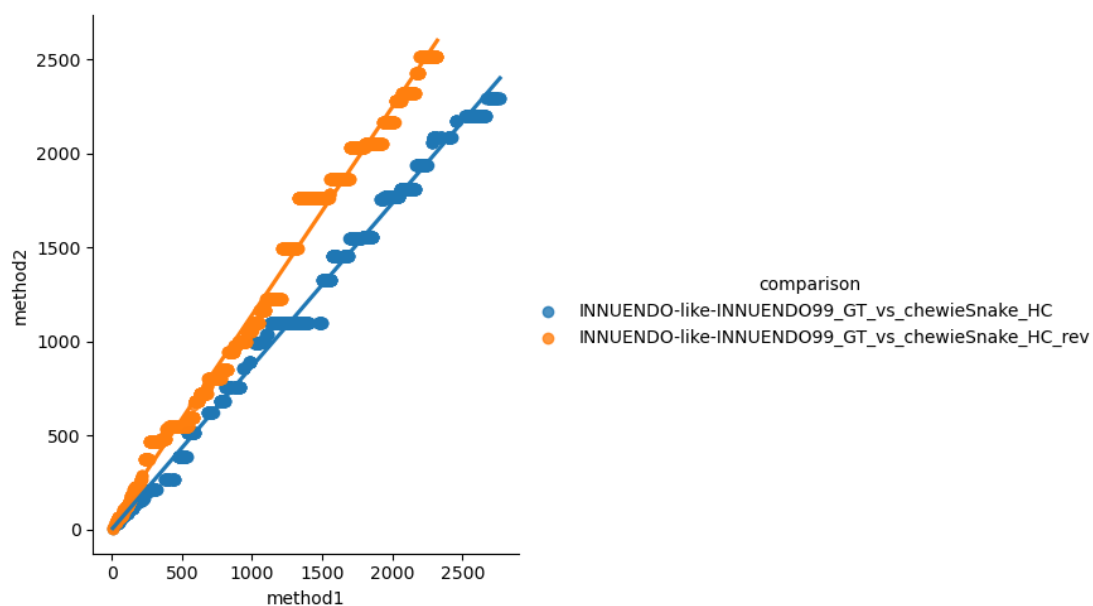


Figure S2.31.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1956 (blue) and 2503 (orange) points is presented.

32. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-EFSA GrapeTree

Table S2.32. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	INNUENDO-like-EFSA GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	EFSA
Dataset	All samples	All samples
Number partitions	2998	2998

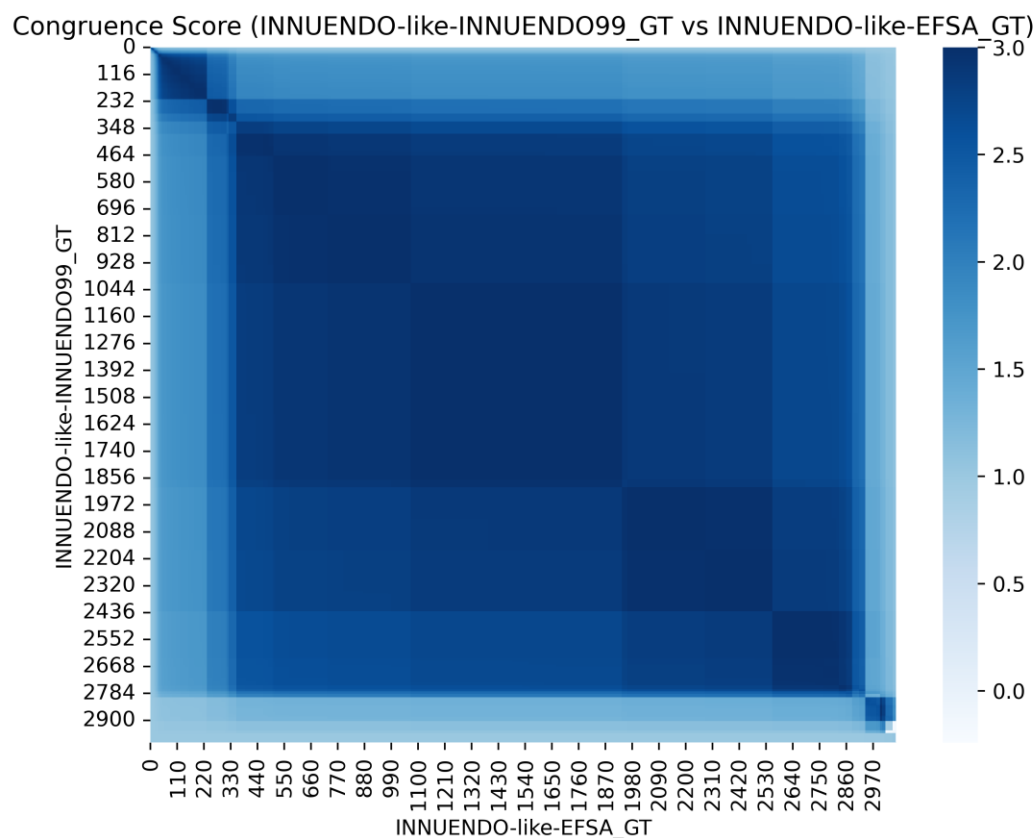


Figure S2.32.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

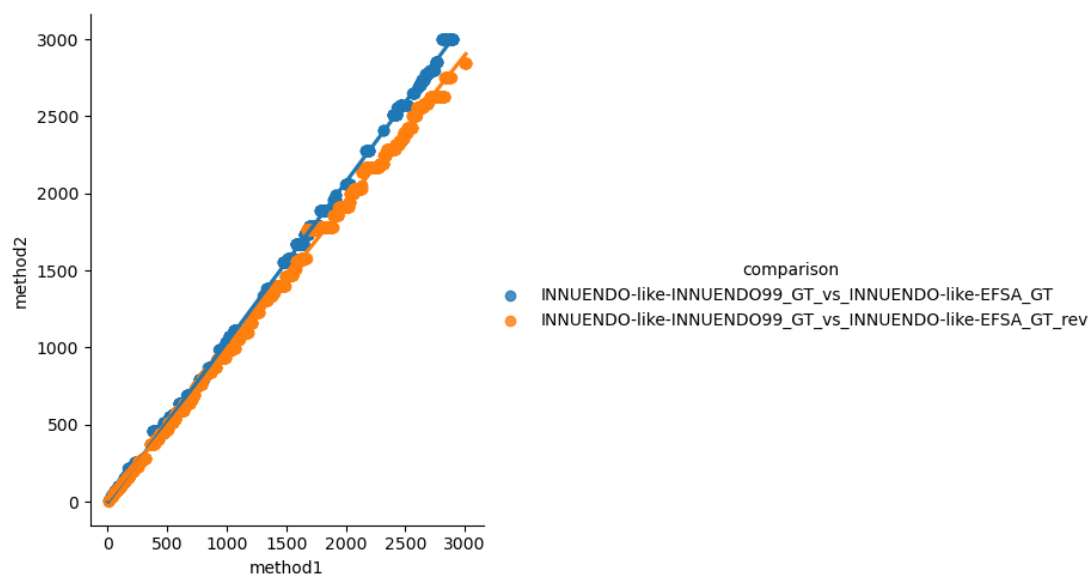


Figure S2.32.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1928 (blue) and 2284 (orange) points is presented.

33. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-EFSA single-linkage

Table S2.33. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	INNUENDO-like-EFSA single- linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	EFSA
Dataset	All samples	All samples
Number partitions	2998	2948

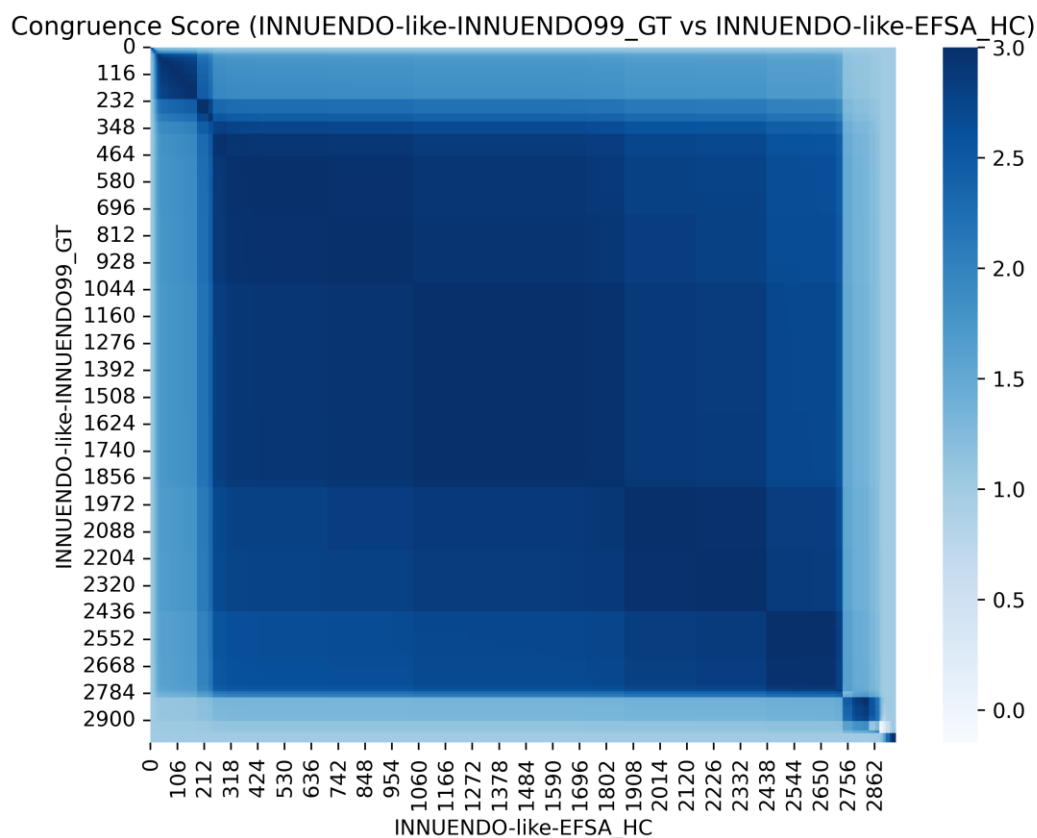


Figure S2.33.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

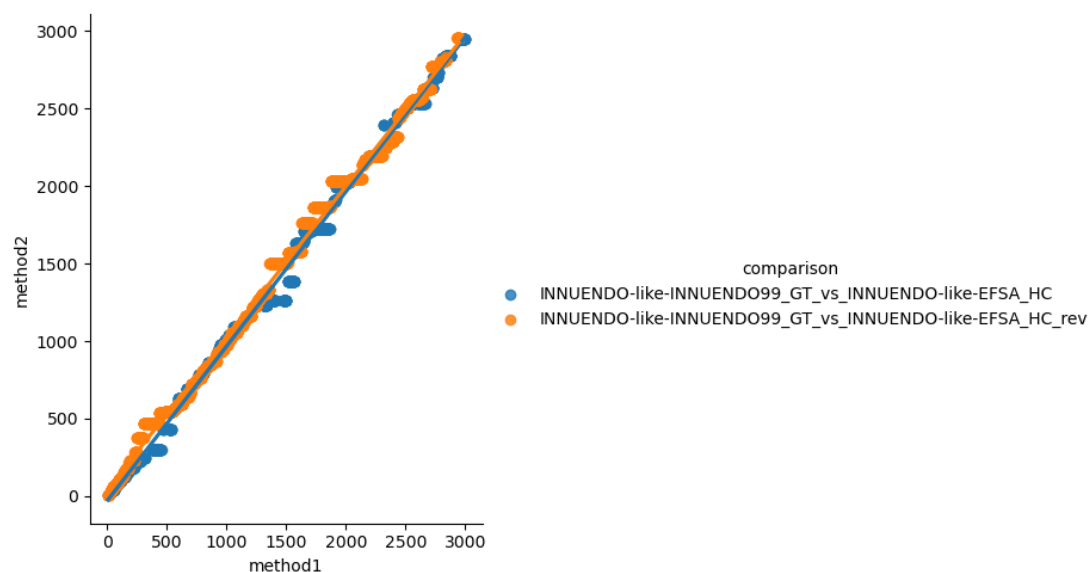


Figure S2.33.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1524 (blue) and 2830 (orange) points is presented.

34. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-Enterobase GrapeTree

Table S2.34. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2998	2895

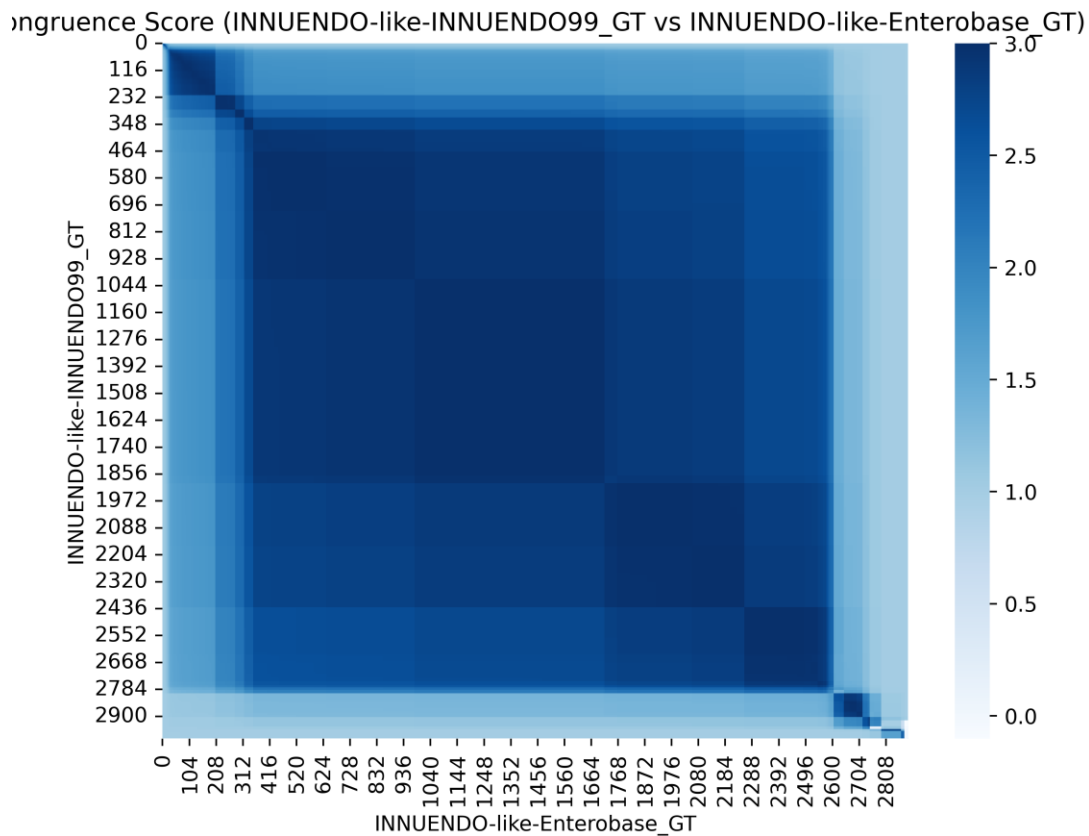


Figure S2.34.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

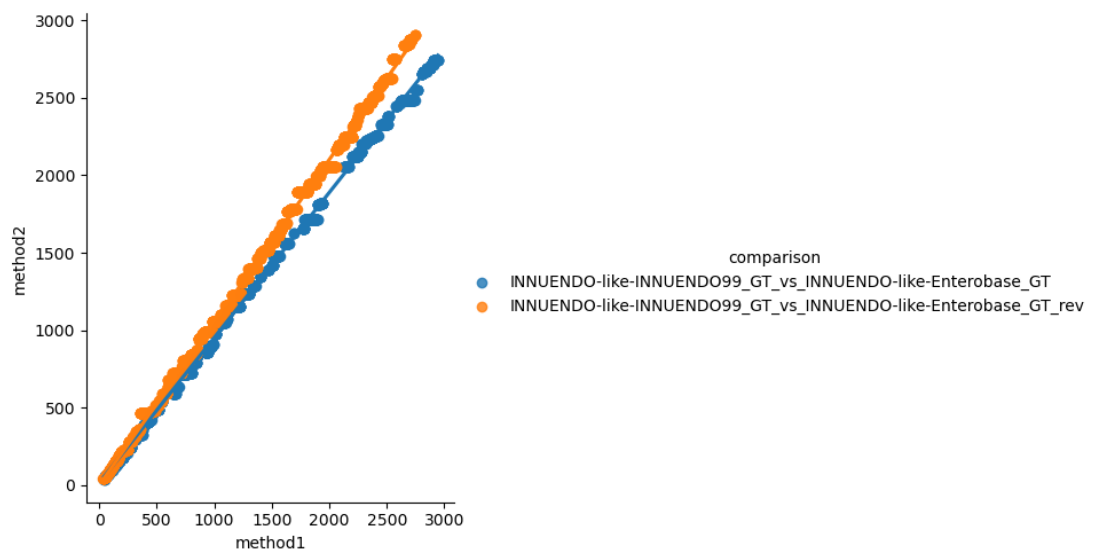


Figure S2.34.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1576 (blue) and 2778 (orange) points is presented.

35. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.35. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	INNUENDO-like-INNUENDO99 GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2998	2881

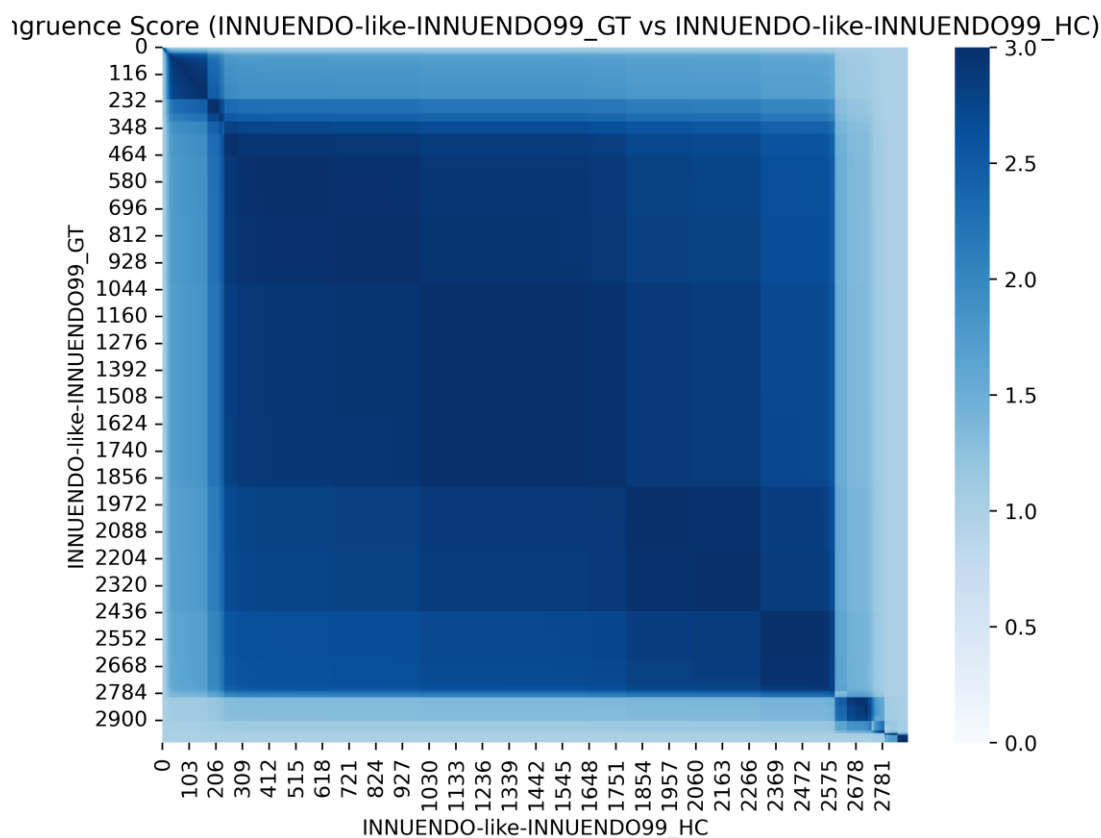


Figure S2.35.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

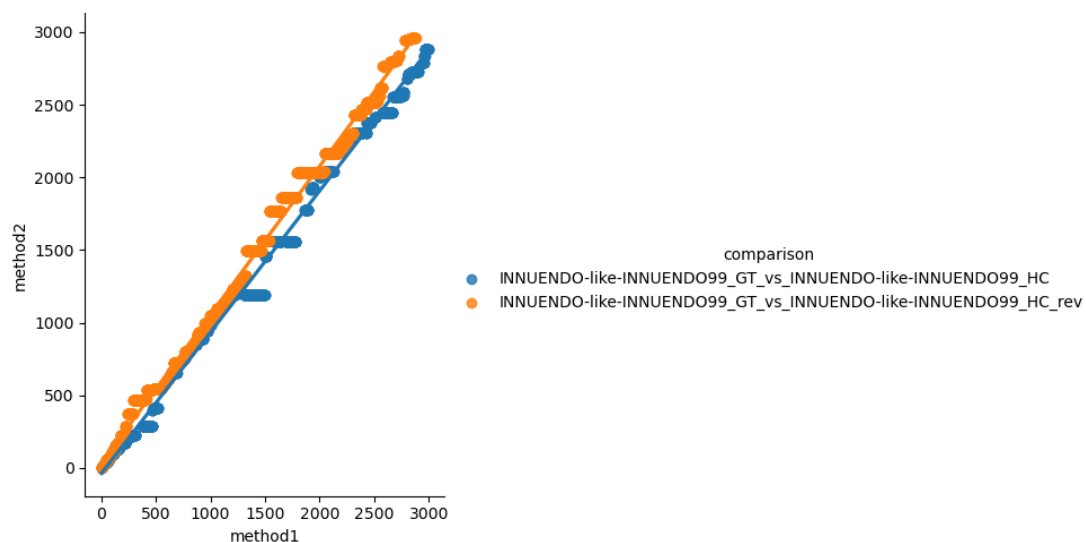


Figure S2.35.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1825 (blue) and 2622 (orange) points is presented.

36. SeqSphere single-linkage vs. Bionumerics single-linkage

Table S2.36. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	Bionumerics single-linkage
Pipeline version	v8.3.4	v8.1
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2602	2844

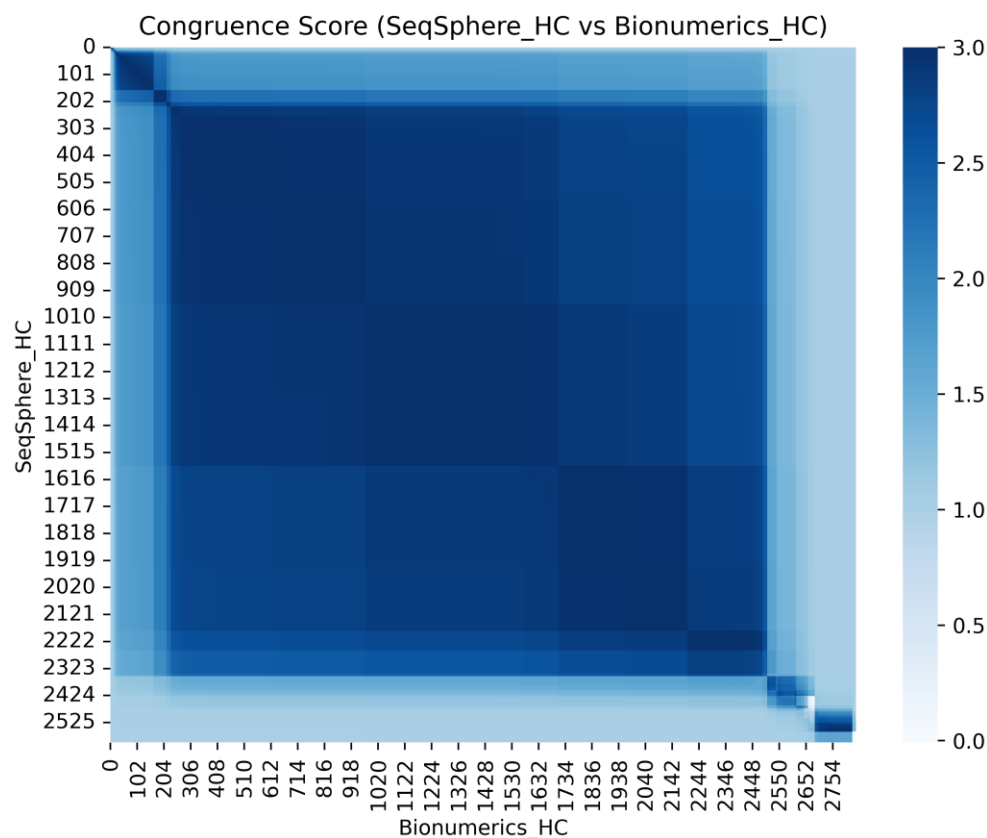


Figure S2.36.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

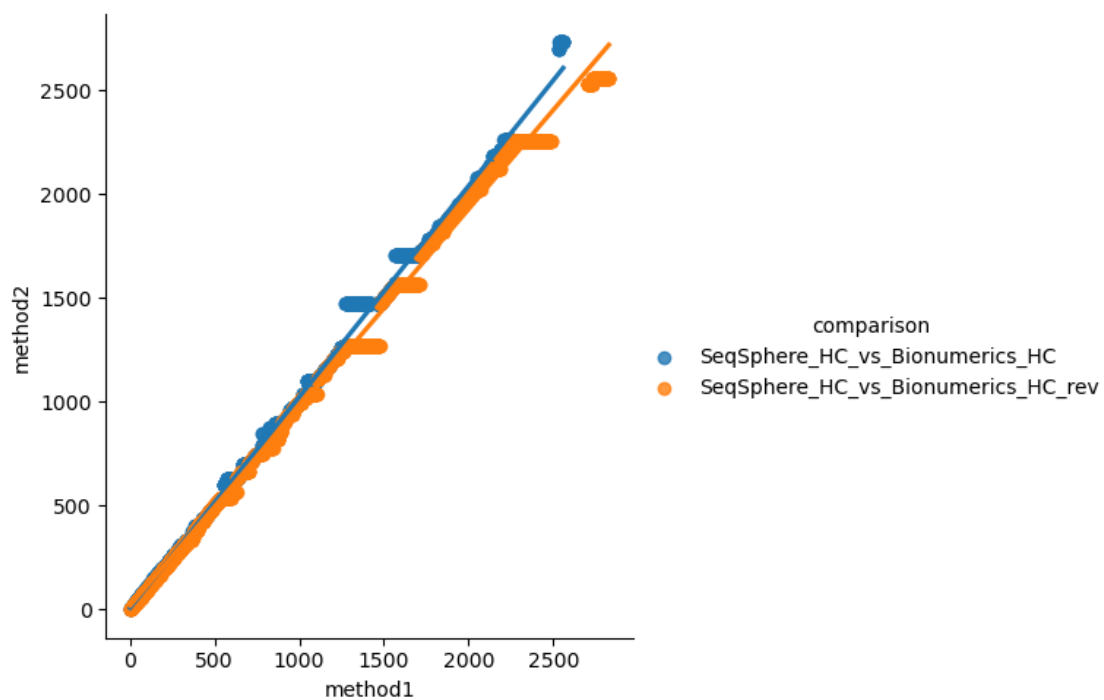


Figure S2.36.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1825 (blue) and 2736 (orange) points is presented.

37. SeqSphere single-linkage vs. chewieSnake GrapeTree

Table S2.37. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	chewieSnake GrapeTree
Pipeline version	v8.3.4	v3.1.1
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2602	2801

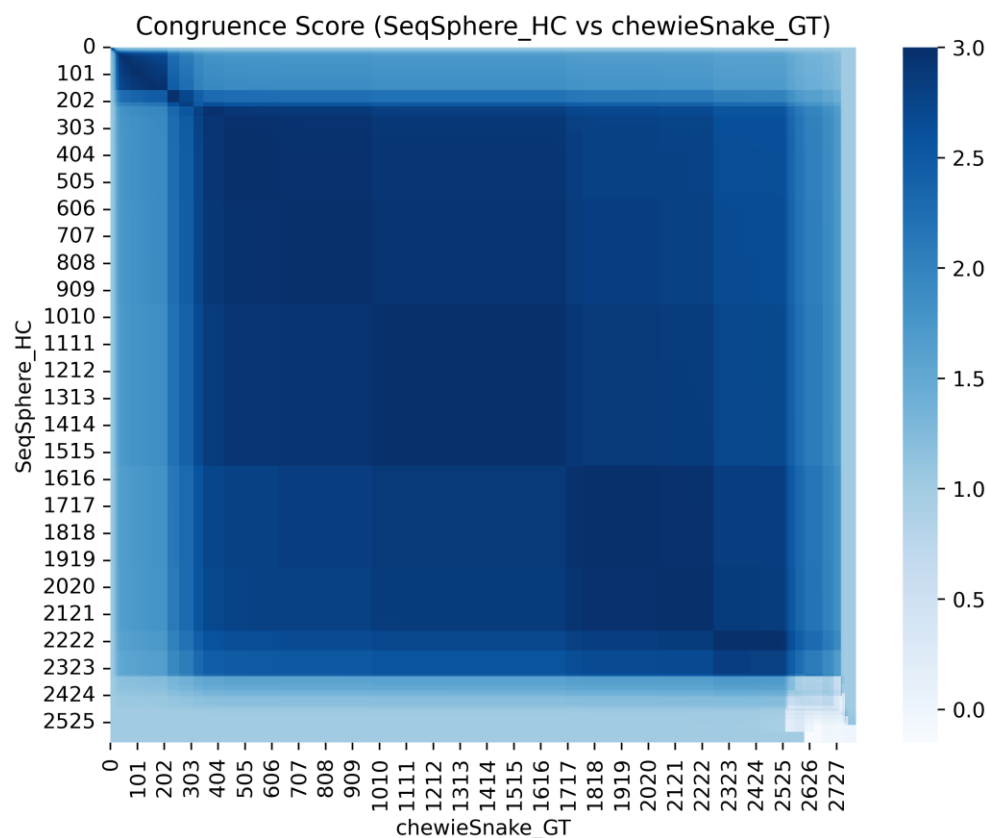


Figure S2.37.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

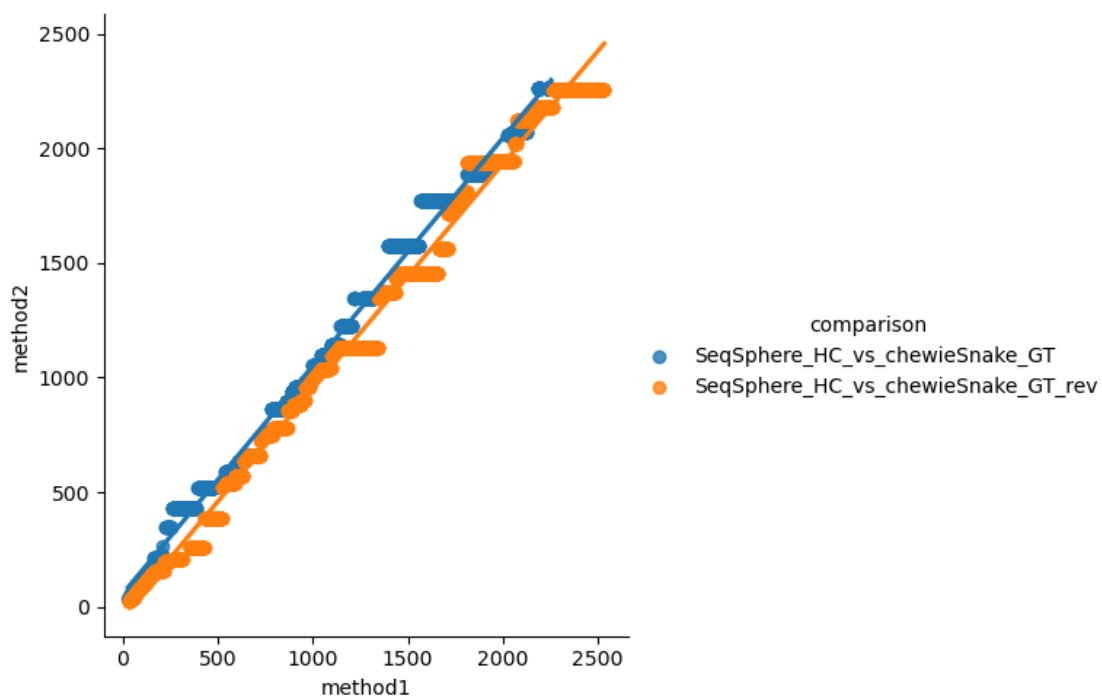


Figure S2.37.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1731 (blue) and 2613 (orange) points is presented.

38. SeqSphere single-linkage vs. chewieSnake single-linkage

Table S2.38. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	chewieSnake single-linkage
Pipeline version	v8.3.4	v3.1.1
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2602	2615

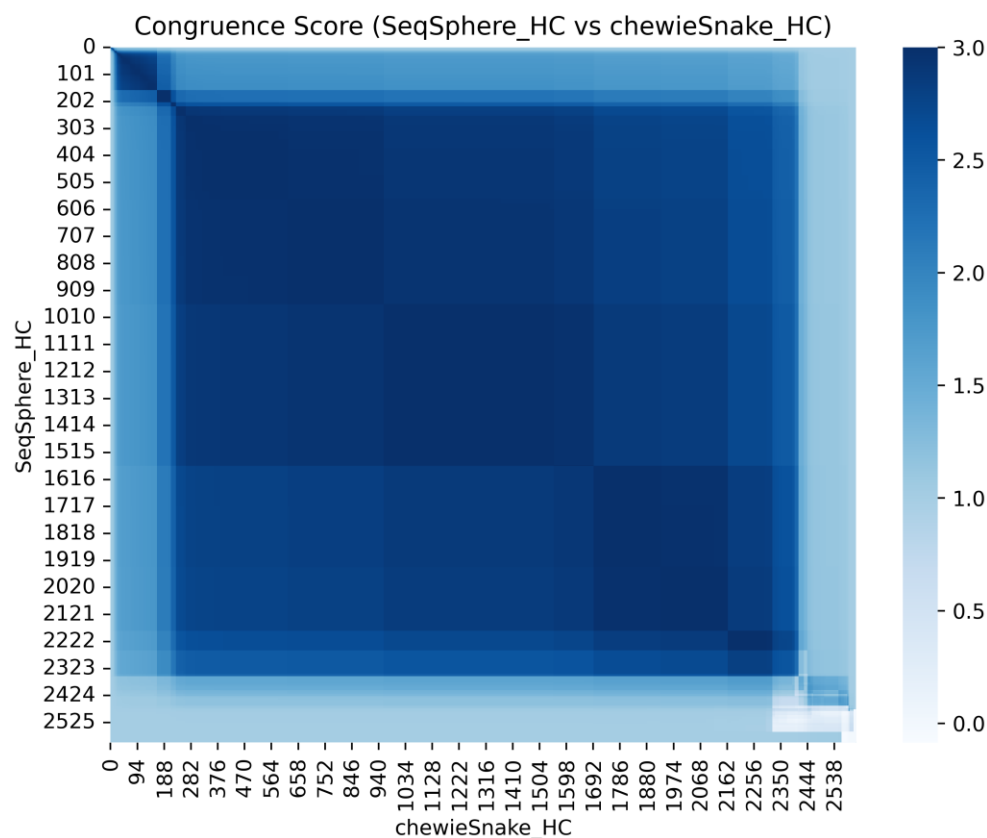


Figure S2.38.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

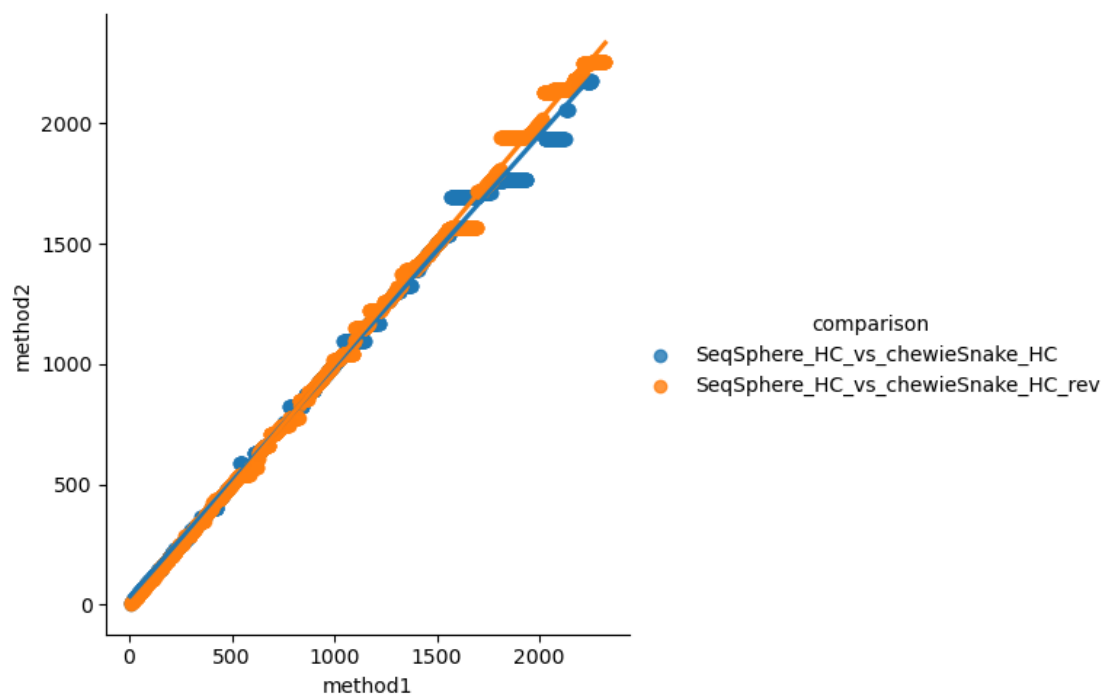


Figure S2.38.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1619 (blue) and 2467 (orange) points is presented.

39. SeqSphere single-linkage vs. INNUENDO-like-EFSA GrapeTree

Table S2.39. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	INNUENDO-like-EFSA GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2602	2998

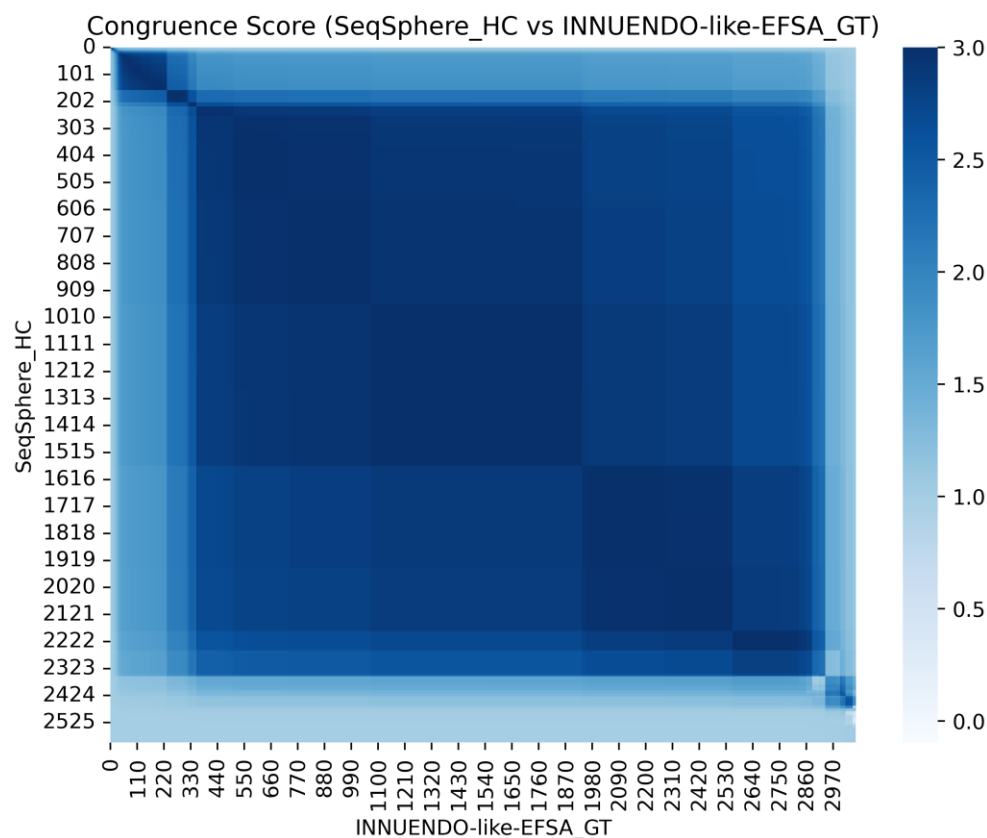


Figure S2.39.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

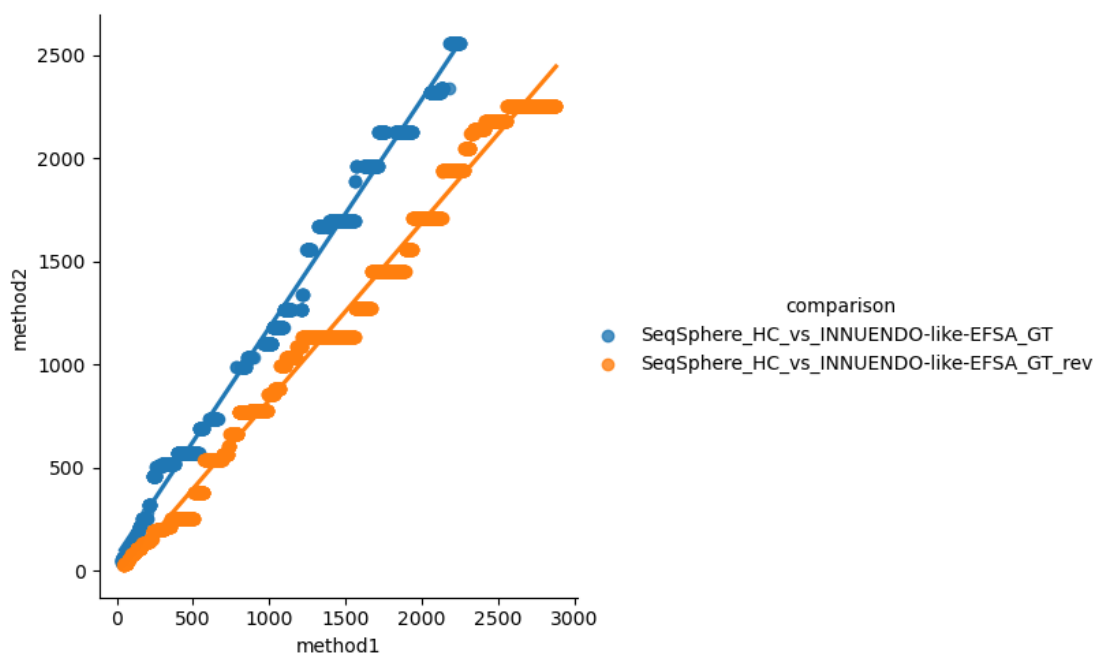


Figure S2.39.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1640 (blue) and 2311 (orange) points is presented.

40. SeqSphere single-linkage vs. INNUENDO-like-EFSA single-linkage

Table S2.40. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	INNUENDO-like-EFSA single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2602	2948

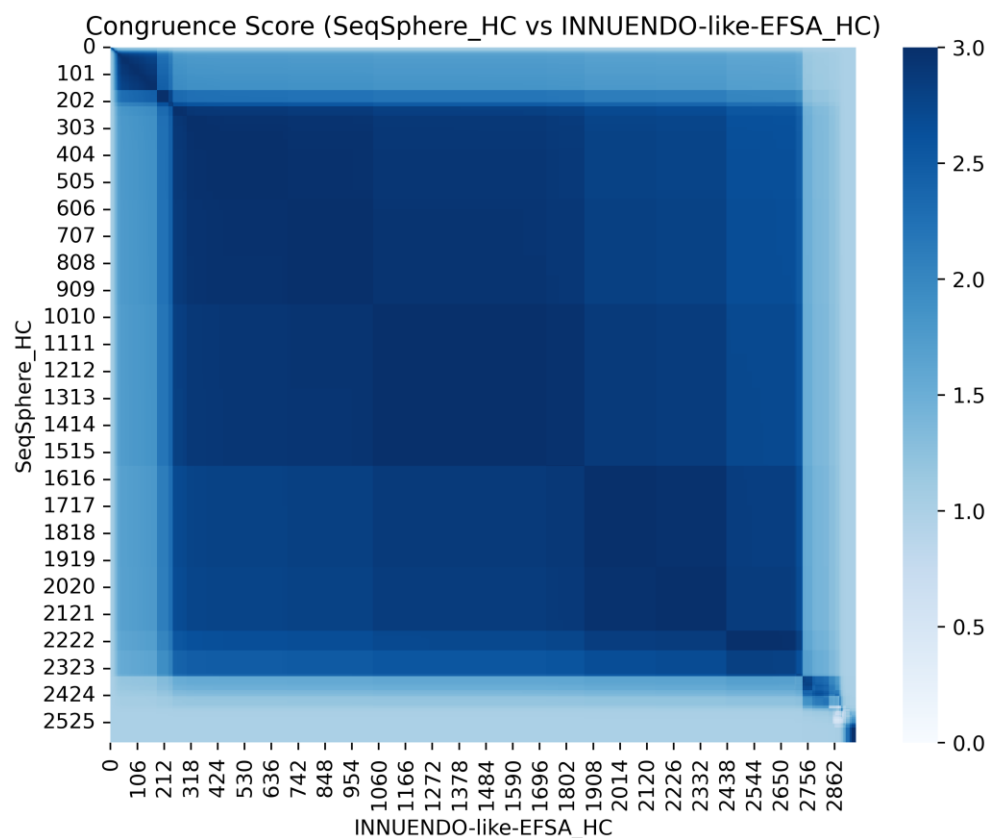


Figure S2.40.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

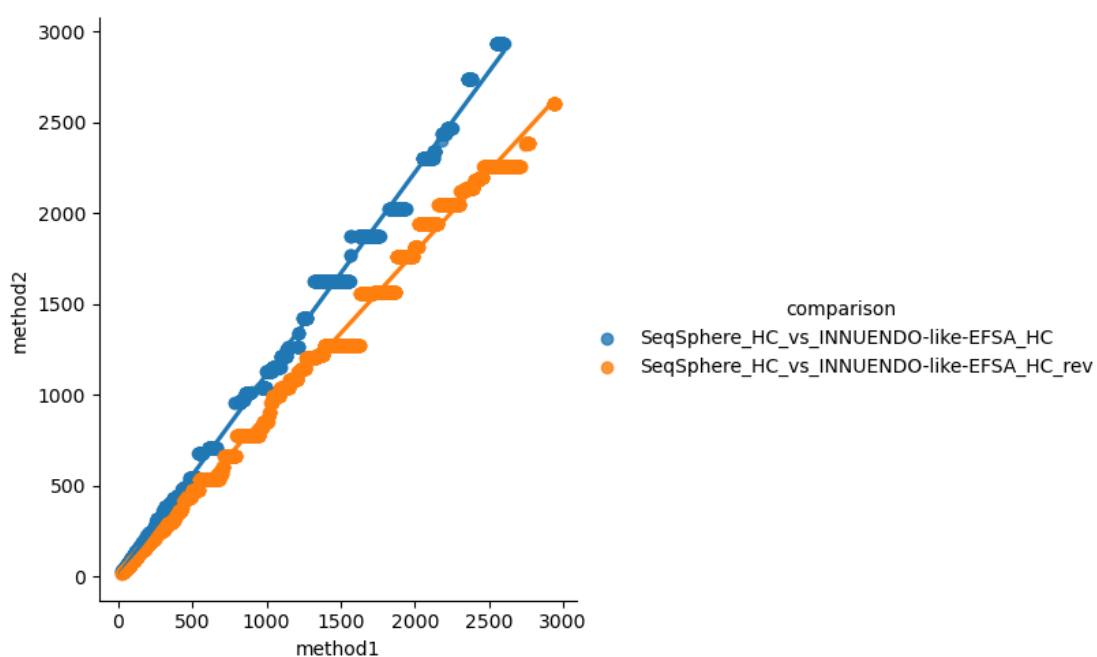


Figure S2.40.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1425 (blue) and 2829 (orange) points is presented.

41. SeqSphere single-linkage vs. INNUENDO-like-Enterobase GrapeTree

Table S2.41. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2602	2895

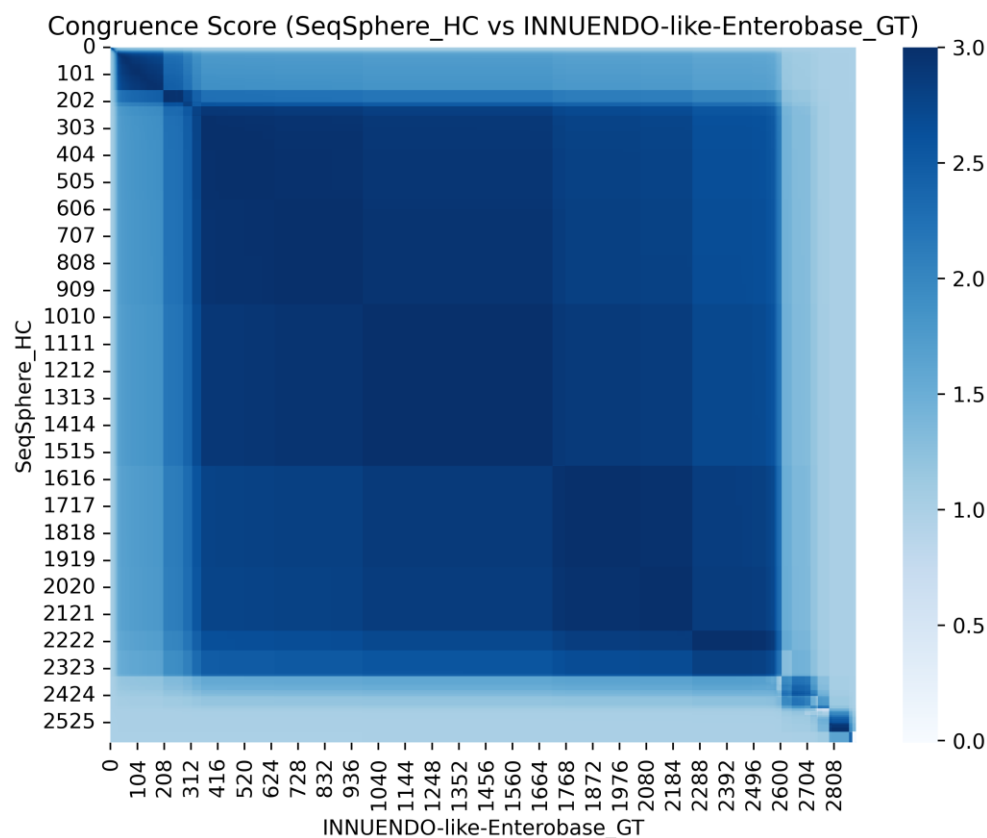


Figure S2.41.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

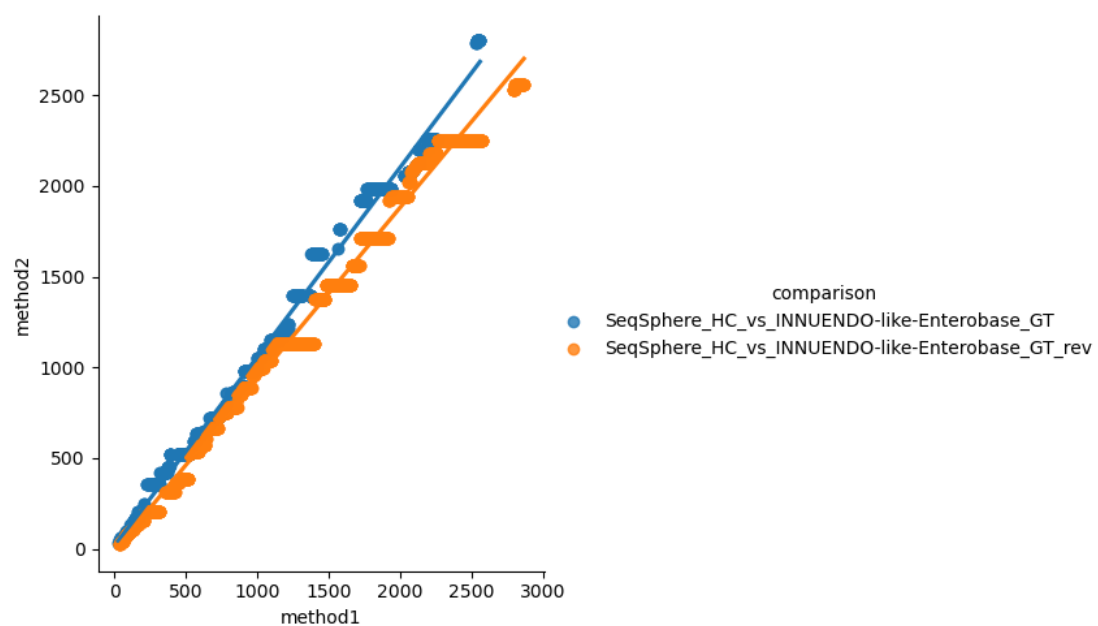


Figure S2.41.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1519 (blue) and 2732 (orange) points is presented.

42. SeqSphere single-linkage vs. INNUENDO-like-Enterobase single-linkage

Table S2.42. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	INNUENDO-like-Enterobase single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2602	2800

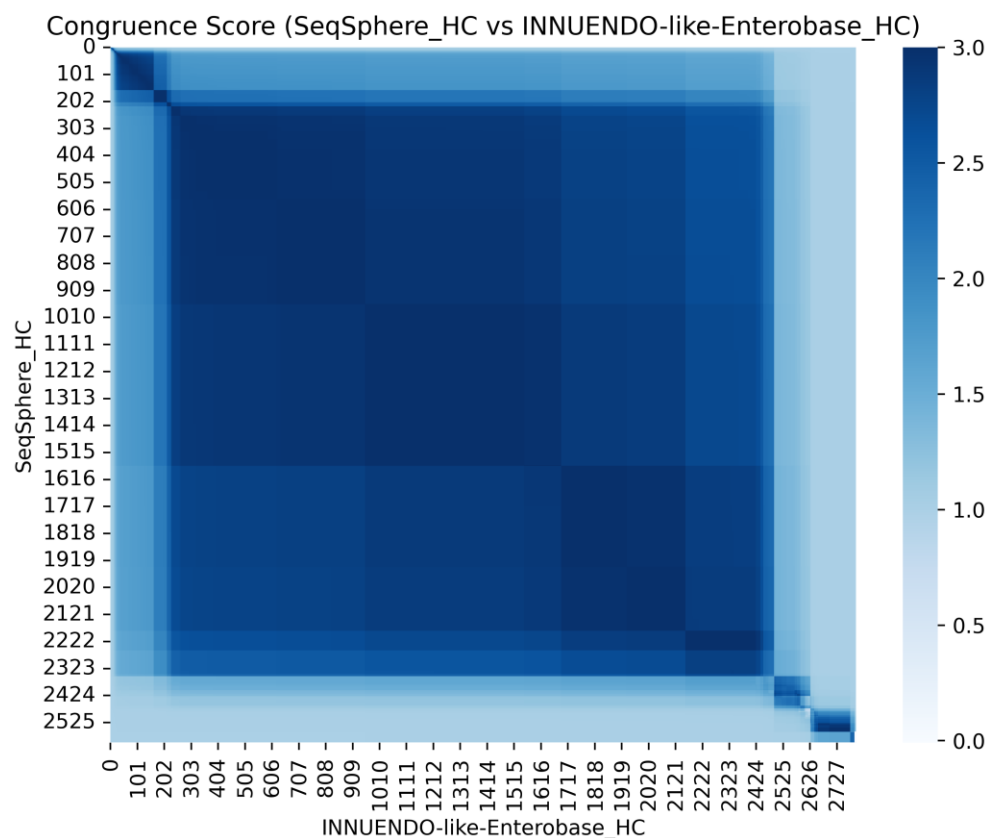


Figure S2.42.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

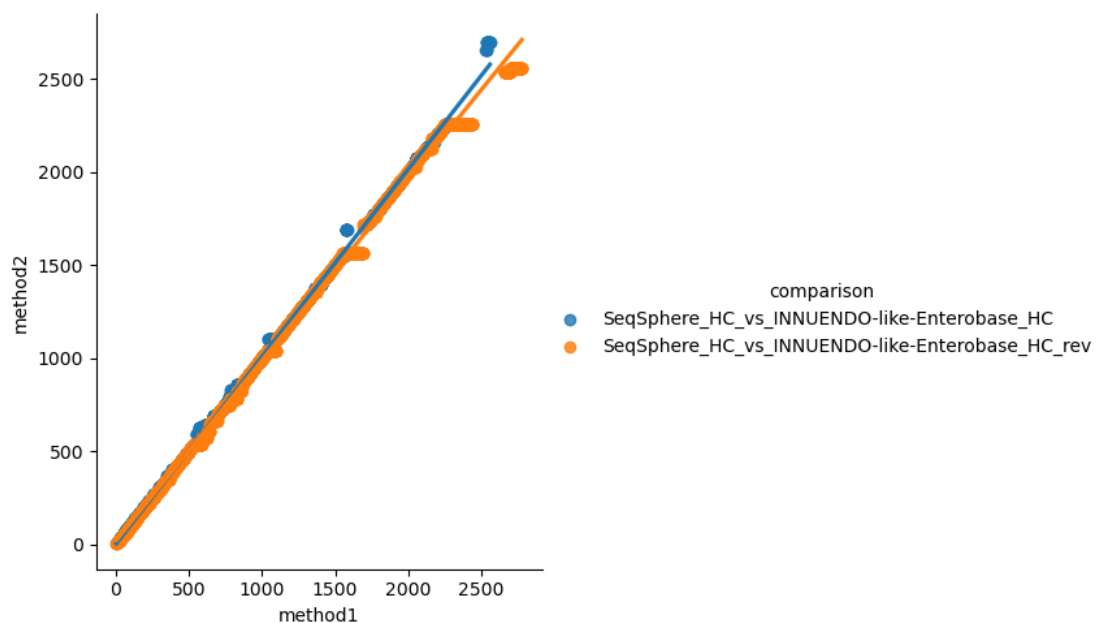


Figure S2.42.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1489 (blue) and 2588 (orange) points is presented.

43. SeqSphere single-linkage vs. INNUENDO-like-INNUENDO99 GrapeTree

Table S2.43. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	INNUENDO-like-INNUENDO99 GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2602	2998

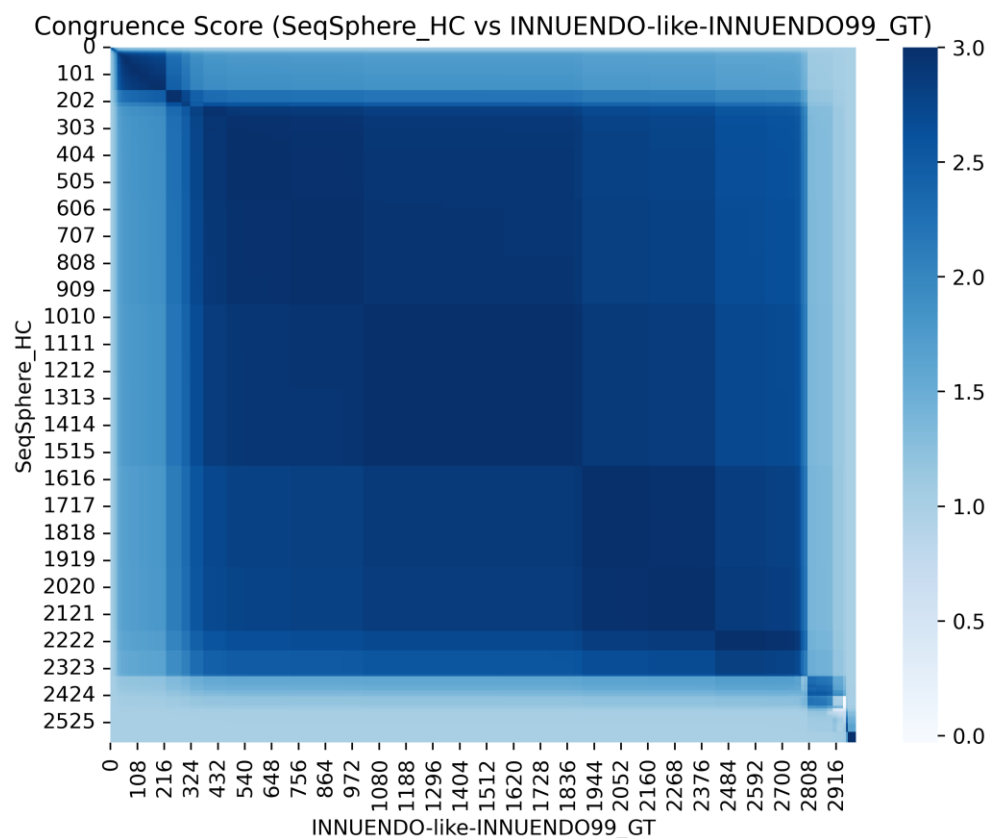


Figure S2.43.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

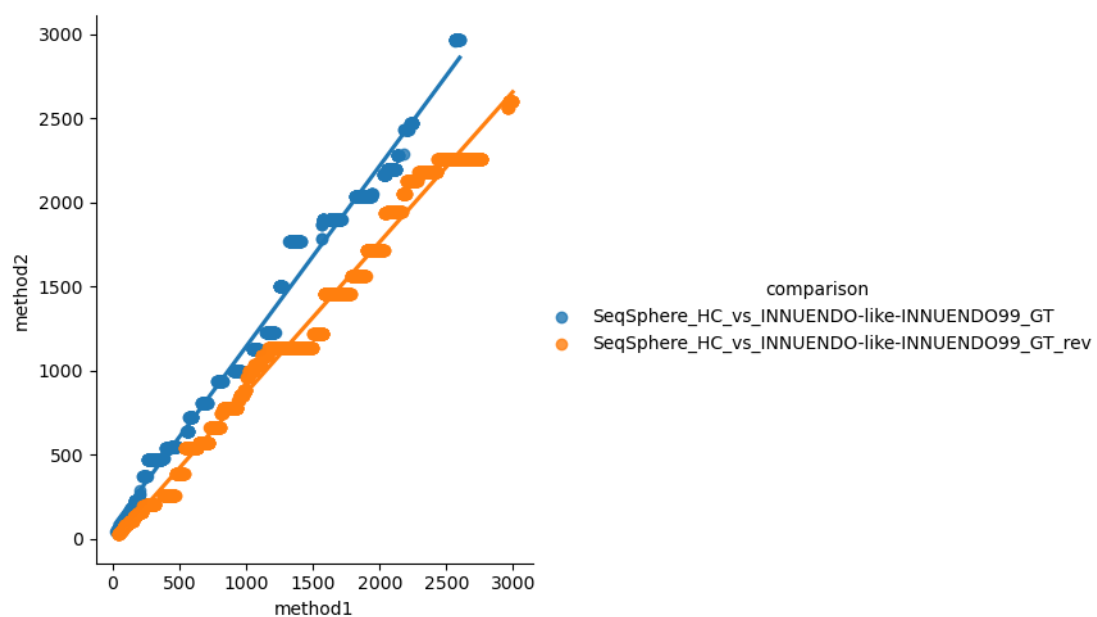


Figure S2.43.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1512 (blue) and 2549 (orange) points is presented.

44. SeqSphere single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.44. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SeqSphere single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2602	2881

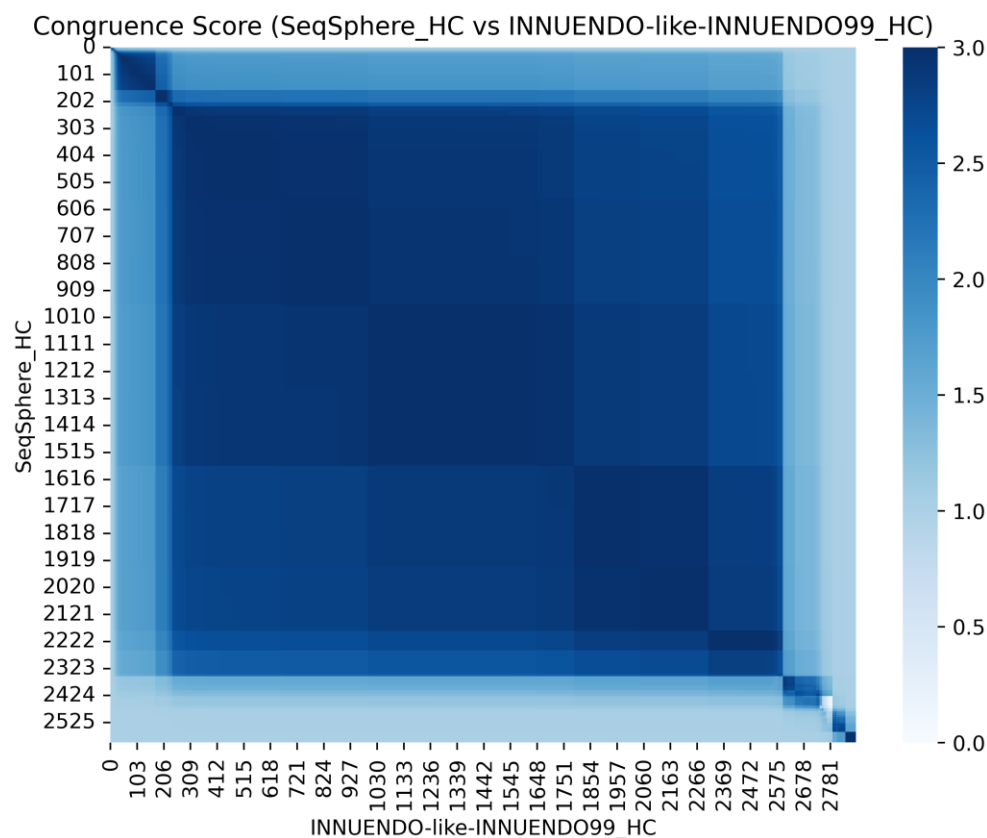


Figure S2.44.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

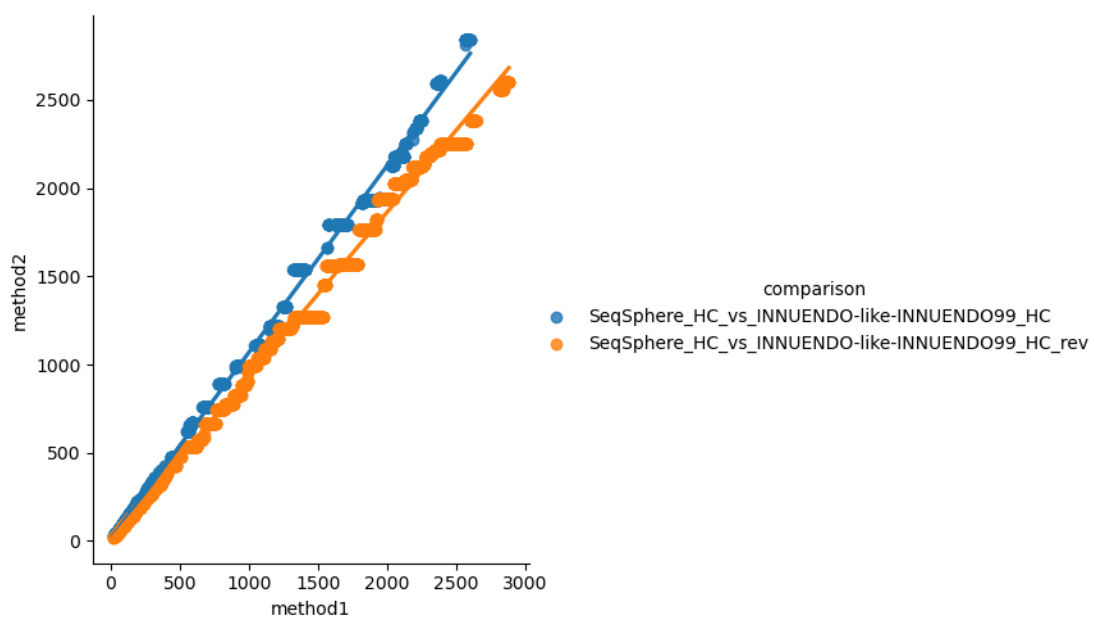


Figure S2.44.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1276 (blue) and 2672 (orange) points is presented.

45. Bionumerics single-linkage vs. chewieSnake GrapeTree

Table S2.45. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	Bionumerics single-linkage	chewieSnake GrapeTree
Pipeline version	v8.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2844	2801

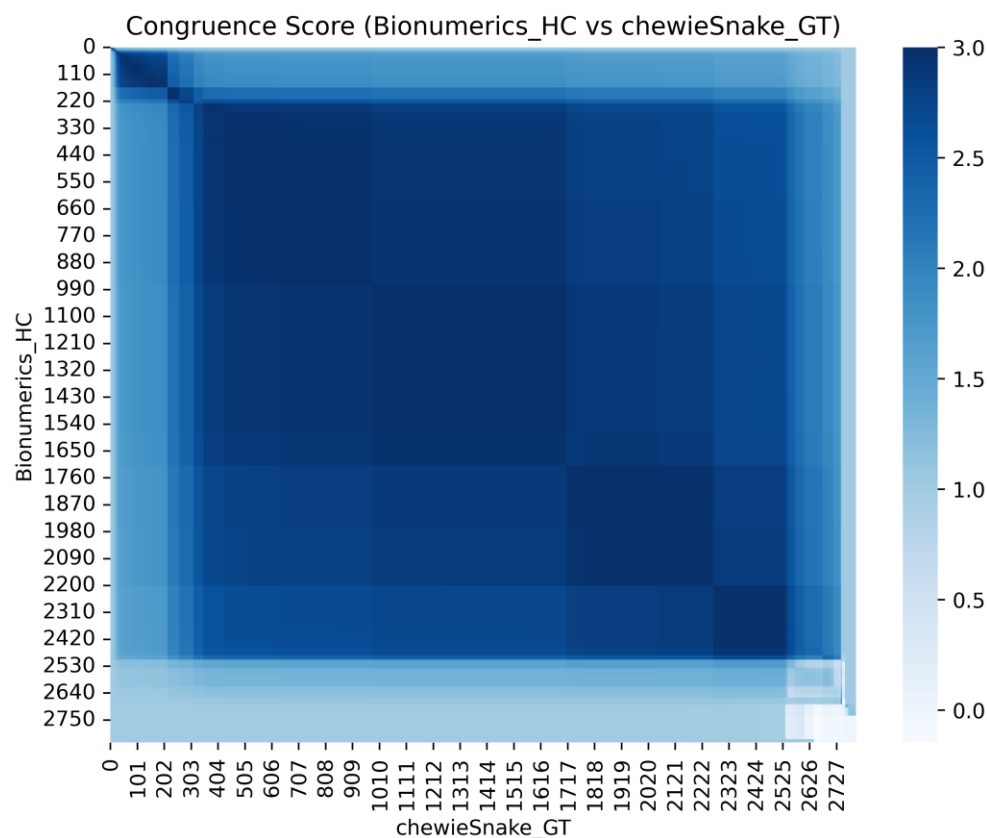


Figure S2.44.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

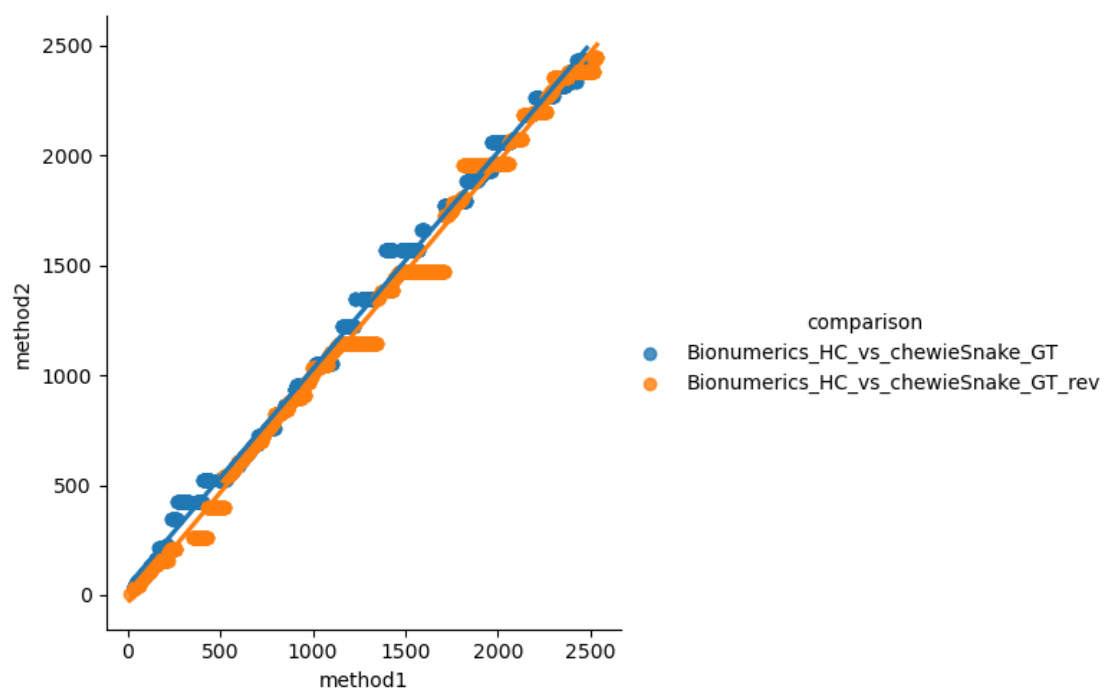


Figure S2.44.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 1561 (blue) and 2415 (orange) points is presented.

Section 3 – Comparison of SNP-based pipelines

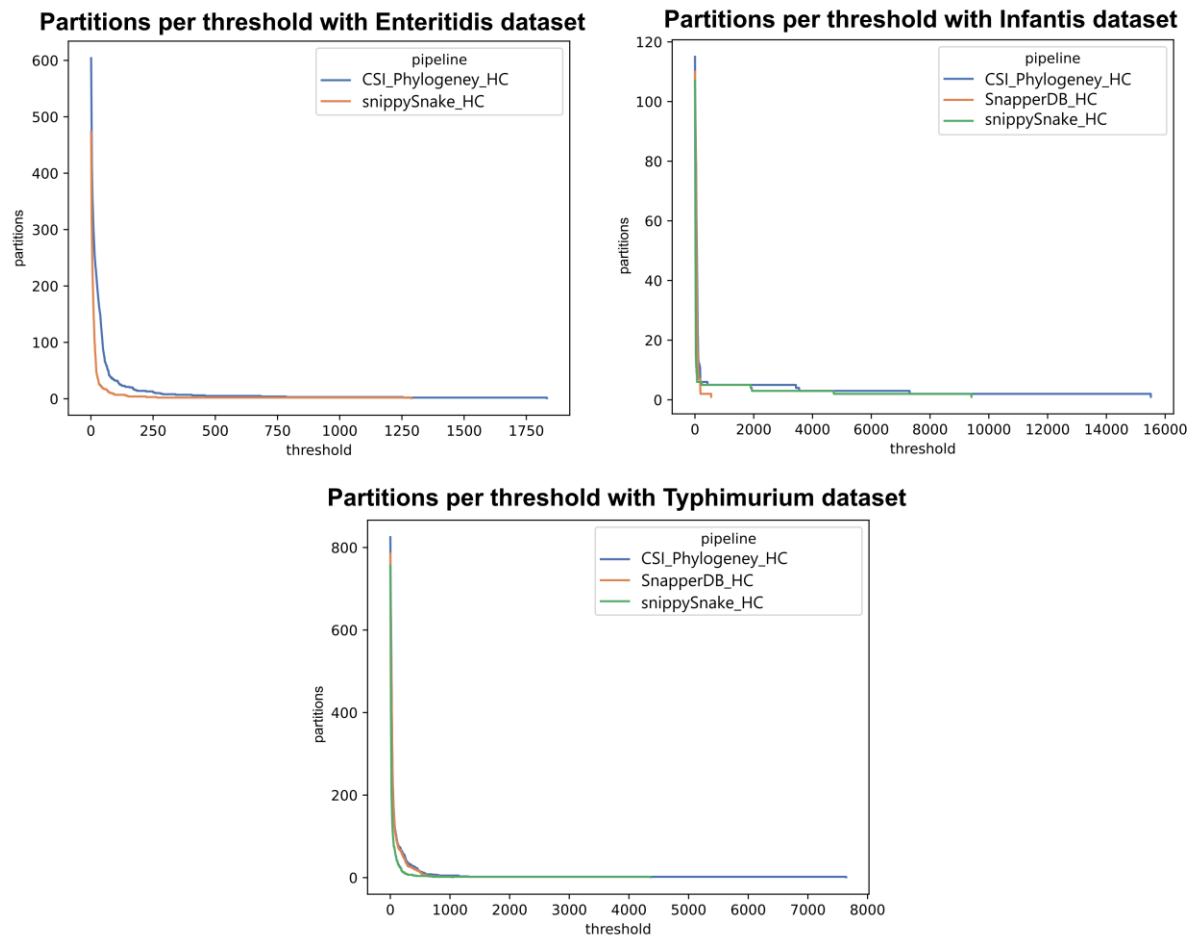


Figure S3. Number of clusters determined by each SNP-based pipeline at each possible distance threshold.

1. CSI Phylogeny single-linkage vs. snippySnake single-linkage (Enteritidis)

Table S3.1. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	CSI Phylogeny single-linkage	snippySnake single-linkage
Pipeline version	v1.4	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	AM933172	AM933172
Dataset	Enteritidis	Enteritidis
Number partitions	1833	1289

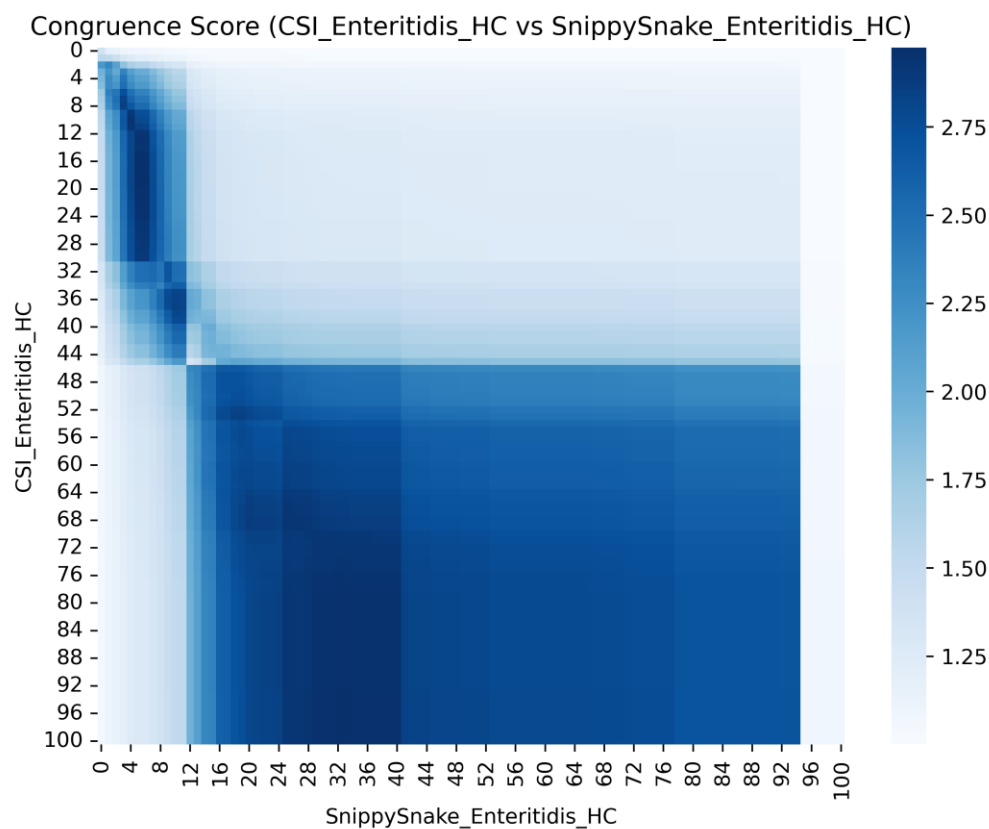


Figure S3.1.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

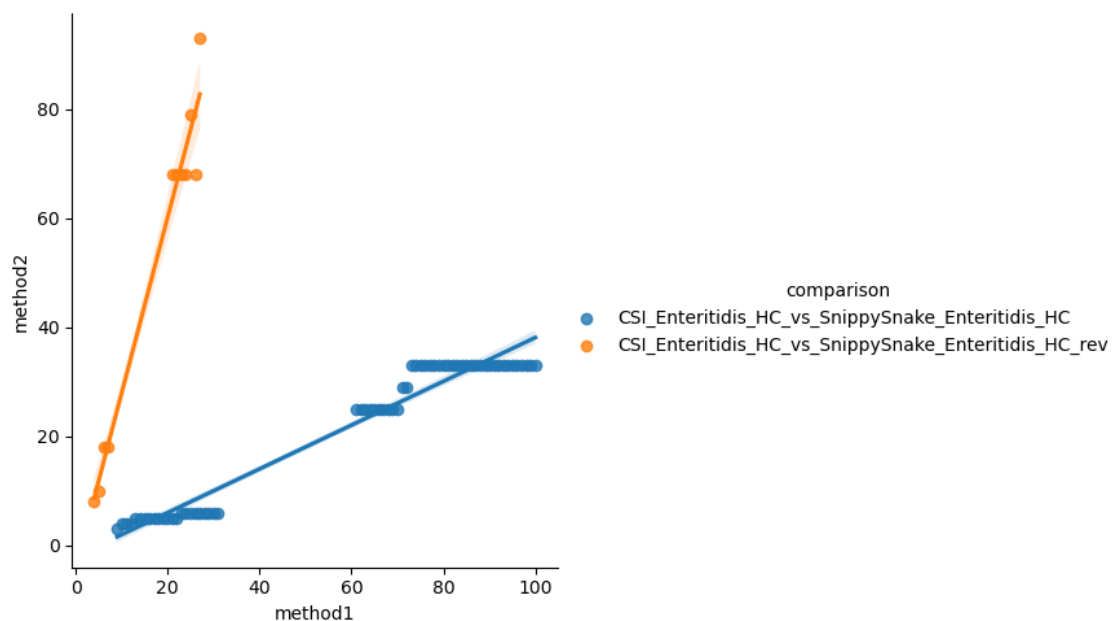


Figure S3.1.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 61 (blue) and 11 (orange) points is presented.

2. CSI Phylogeny single-linkage vs. snippySnake single-linkage (Infantis)

Table S3.2. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	CSI Phylogeny single-linkage	snippySnake single-linkage
Pipeline version	v1.4	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	H15092067901-2	H15092067901-2
Dataset	Infantis	Infantis
Number partitions	15512	9409

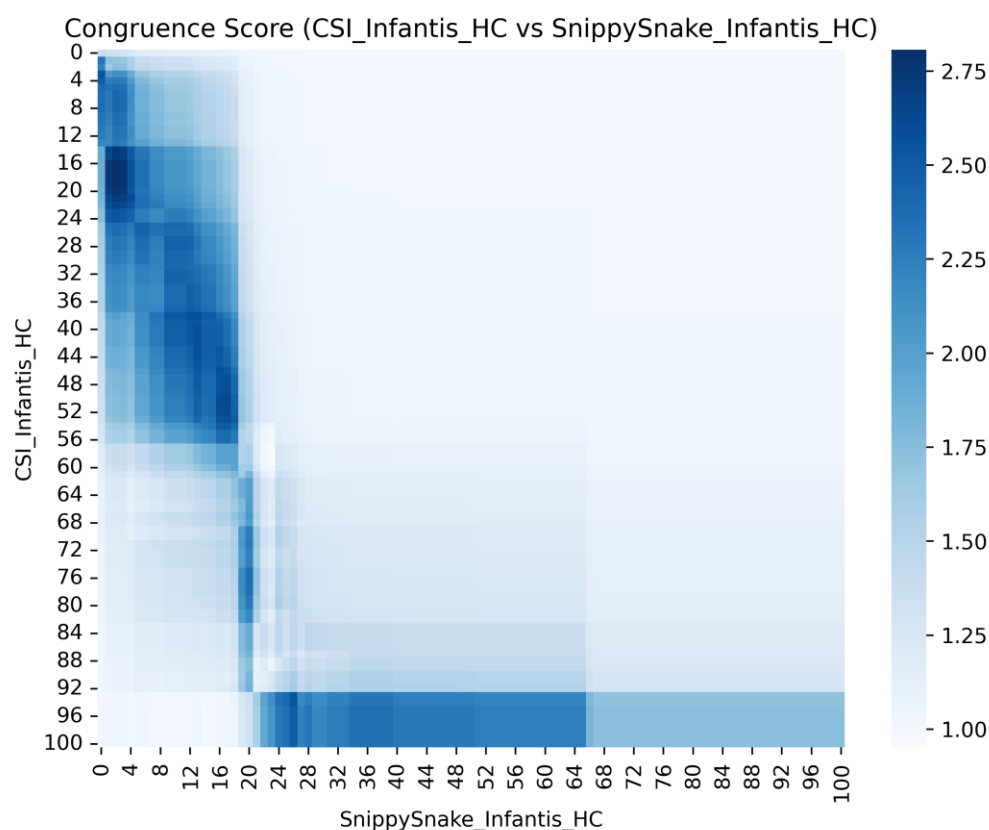


Figure S3.2.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

NOTE: No congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of the two pipelines.

3. CSI Phylogeny single-linkage vs. snippySnake single-linkage (Typhimurium)

Table S3.3. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	CSI Phylogeny single-linkage	snippySnake single-linkage
Pipeline version	v1.4	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	AE006468	AE006468
Dataset	Typhimurium	Typhimurium
Number partitions	7642	4369

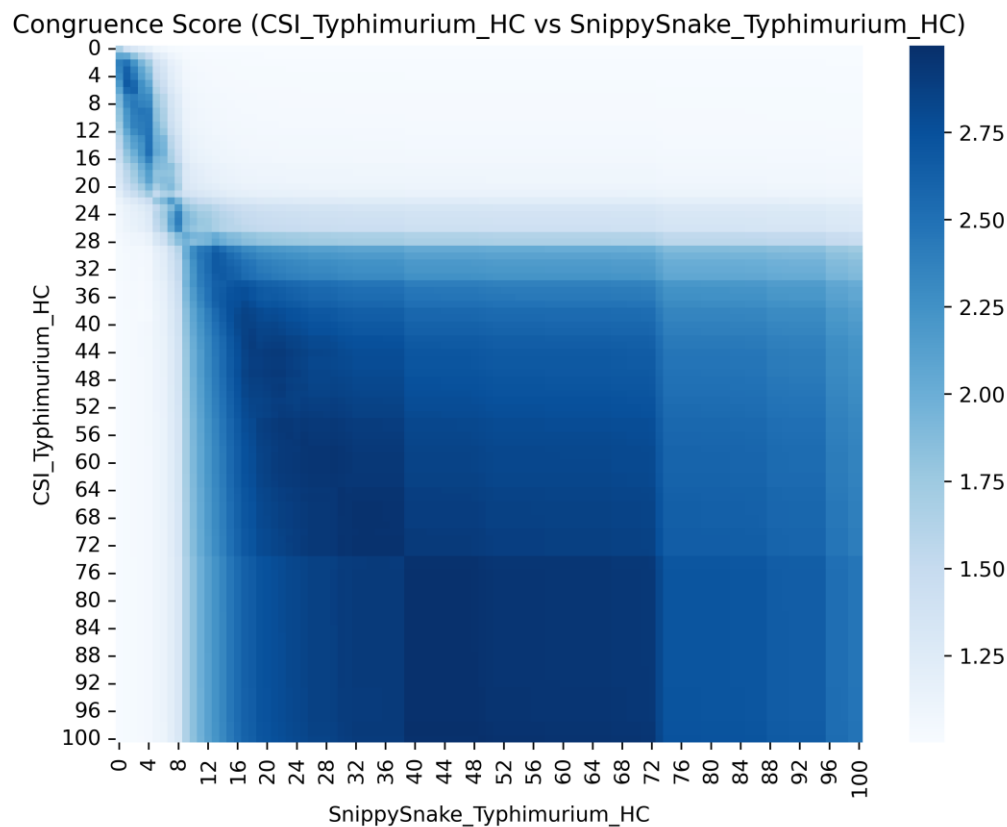


Figure S3.3.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

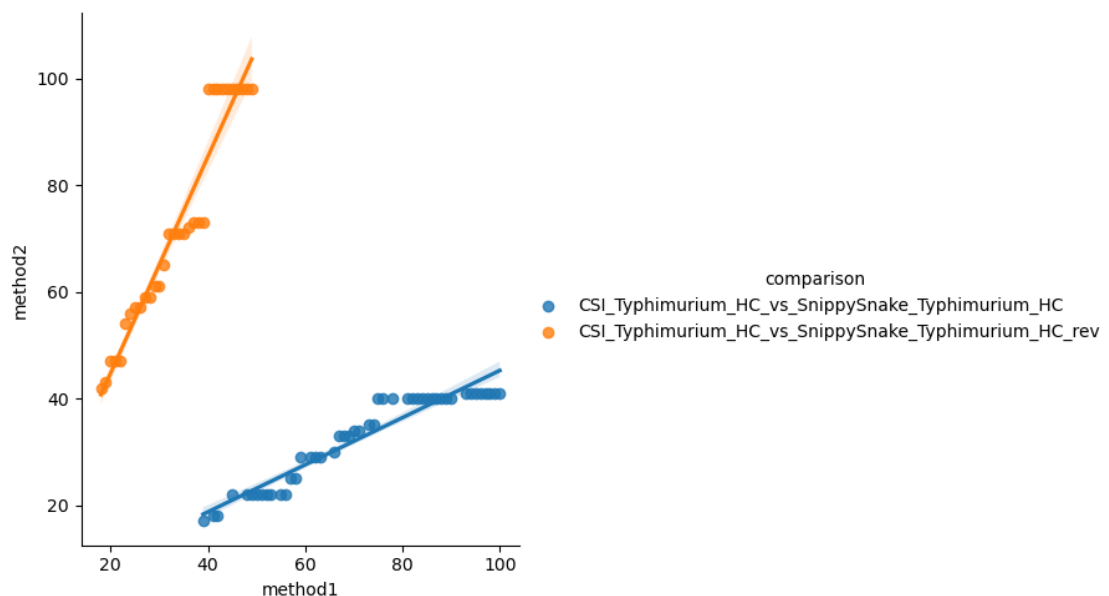


Figure S3.3.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 47 (blue) and 32 (orange) points is presented.

4. SnapperDB single-linkage vs. CSI Phylogeny single-linkage (Infantis)

Table S3.4. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SnapperDB single-linkage	CSI Phylogeny single-linkage
Pipeline version	-	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	H15092067901-2	H15092067901-2
Dataset	Infantis	Infantis
Number partitions	553	15512

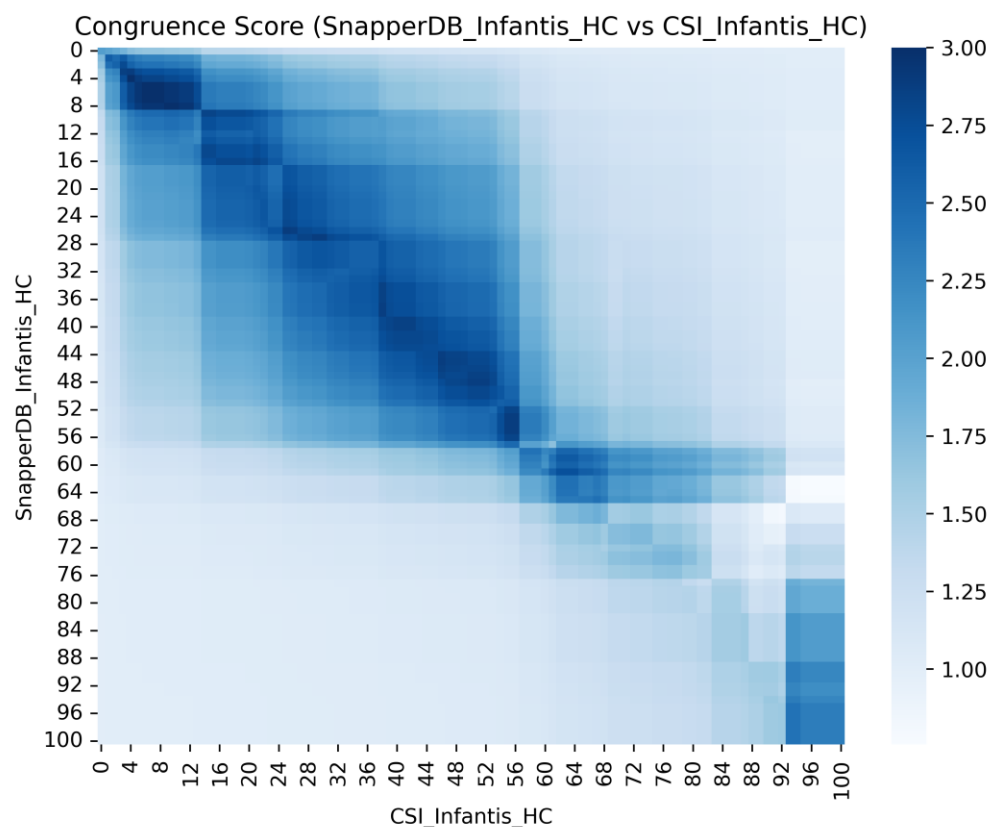


Figure S3.4.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

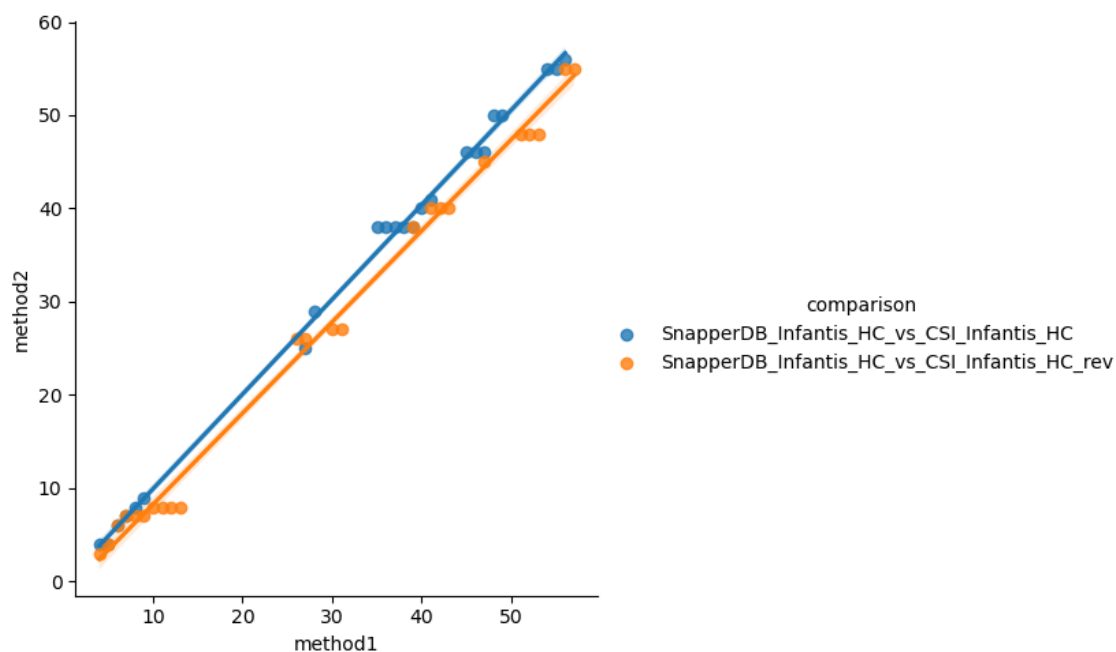


Figure S3.4.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 23 (blue) and 24 (orange) points is presented.

5. SnapperDB single-linkage vs. snippySnake single-linkage (Infantis)

Table S3.5. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SnapperDB single-linkage	snippySnake single-linkage
Pipeline version	-	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	H15092067901-2	H15092067901-2
Dataset	Infantis	Infantis
Number partitions	553	9409

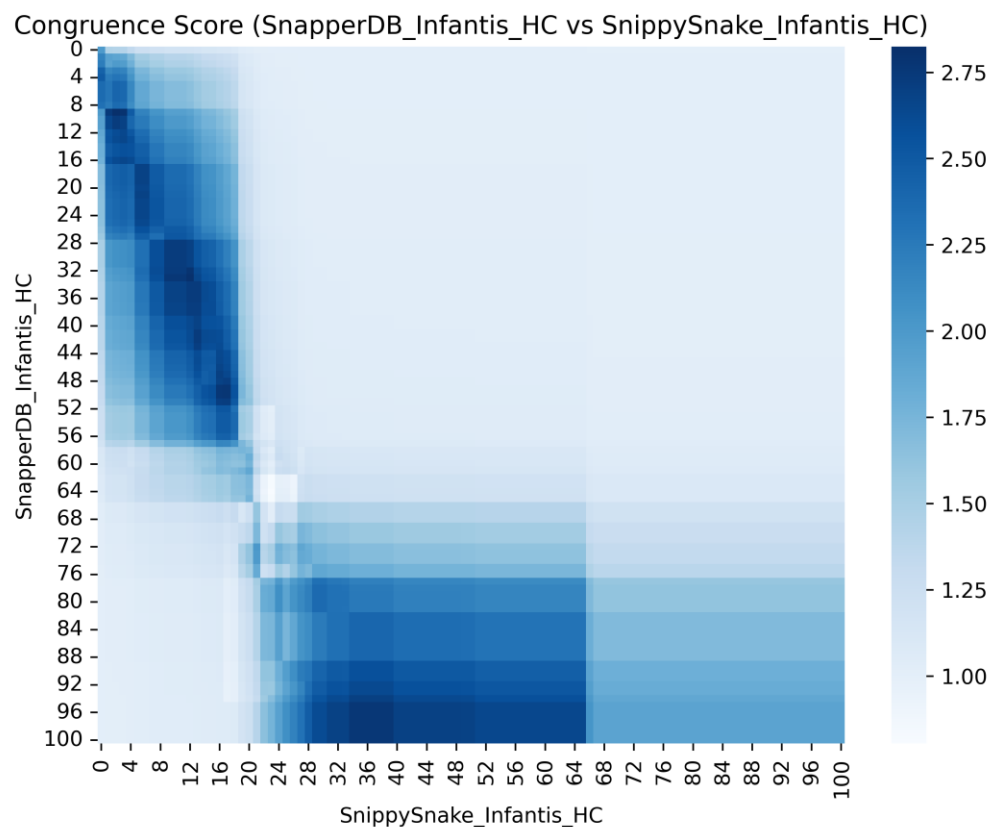


Figure S3.5.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

NOTE: No congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of the two pipelines

6. SnapperDB single-linkage vs. CSI Phylogeny single-linkage (Typhimurium)

Table S3.6. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SnapperDB single-linkage	CSI Phylogeny single-linkage
Pipeline version	-	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	AE006468	AE006468
Dataset	Typhimurium	Typhimurium
Number partitions	1045	7642

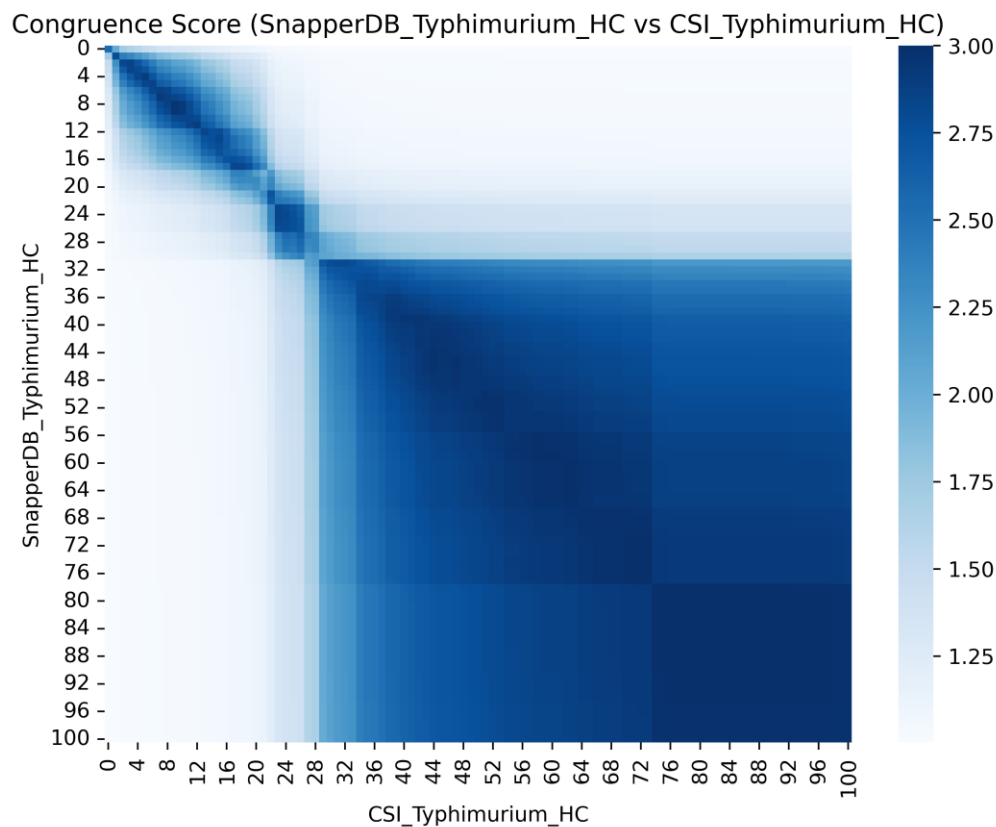


Figure S3.6.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

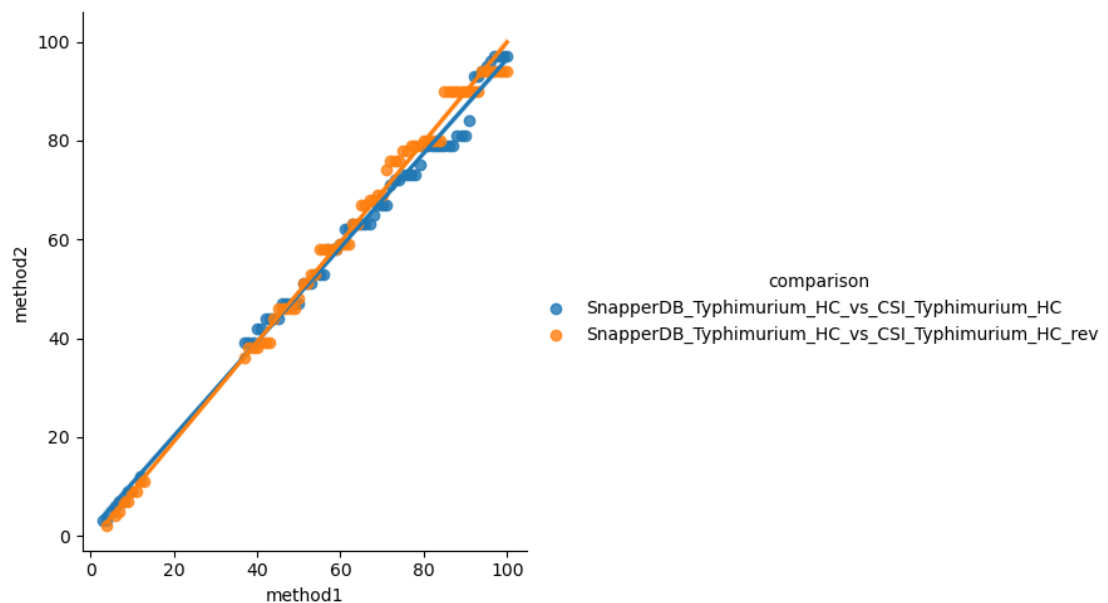


Figure S3.6.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 73 (blue) and 73 (orange) points is presented.

7. SnapperDB single-linkage vs. snippySnake single-linkage (Typhimurium)

Table S3.7. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used. Information about the total number of partitions (i.e., the maximum sample distance obtained with each pipeline) is also shown.

	SnapperDB single-linkage	snippySnake single-linkage
Pipeline version	-	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	AE006468	AE006468
Dataset	Typhimurium	Typhimurium
Number partitions	1045	4369

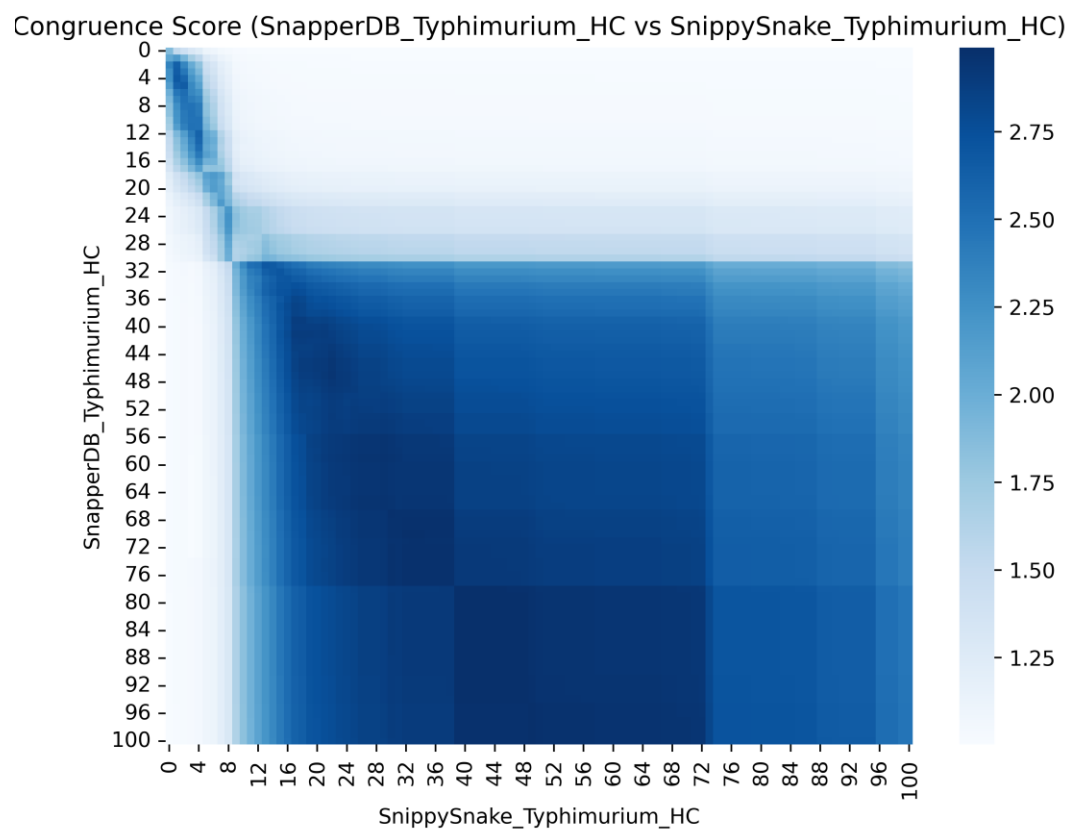


Figure S3.7.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

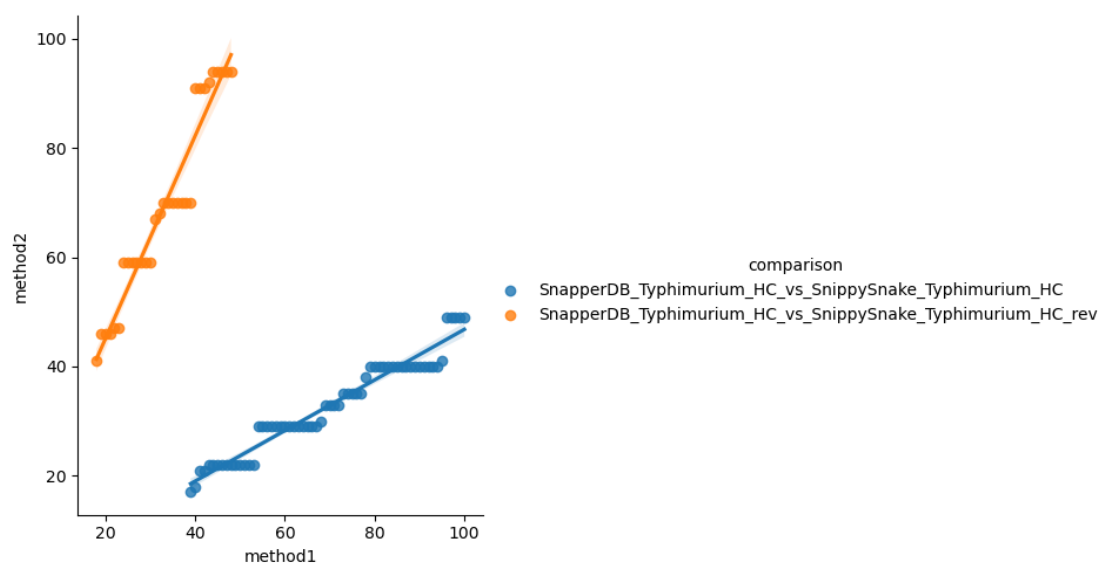


Figure S3.7.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 62 (blue) and 31 (orange) points is presented.

Section 4 – Comparison of allele- and SNP-based pipelines

1. Bionumerics single-linkage vs. CSI Phylogeny single-linkage

Table S4.1. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	Bionumerics single-linkage	CSI Phylogeny single-linkage
Pipeline version	v8.1	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

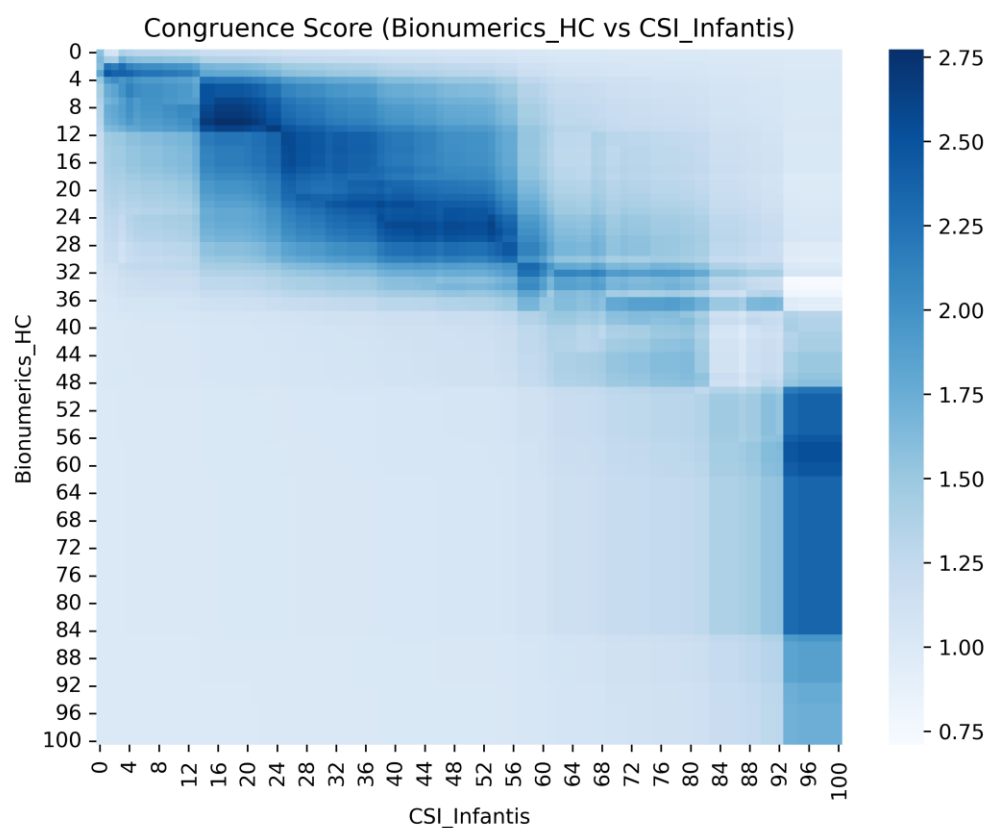


Figure S4.1.1 Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

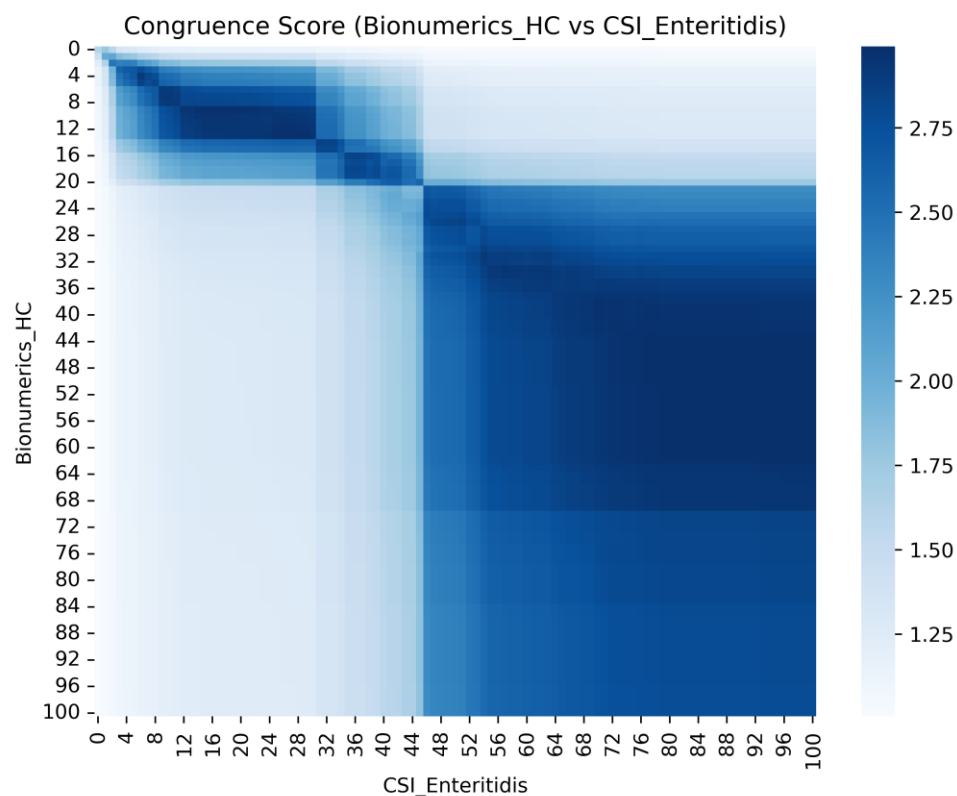


Figure S4.1.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

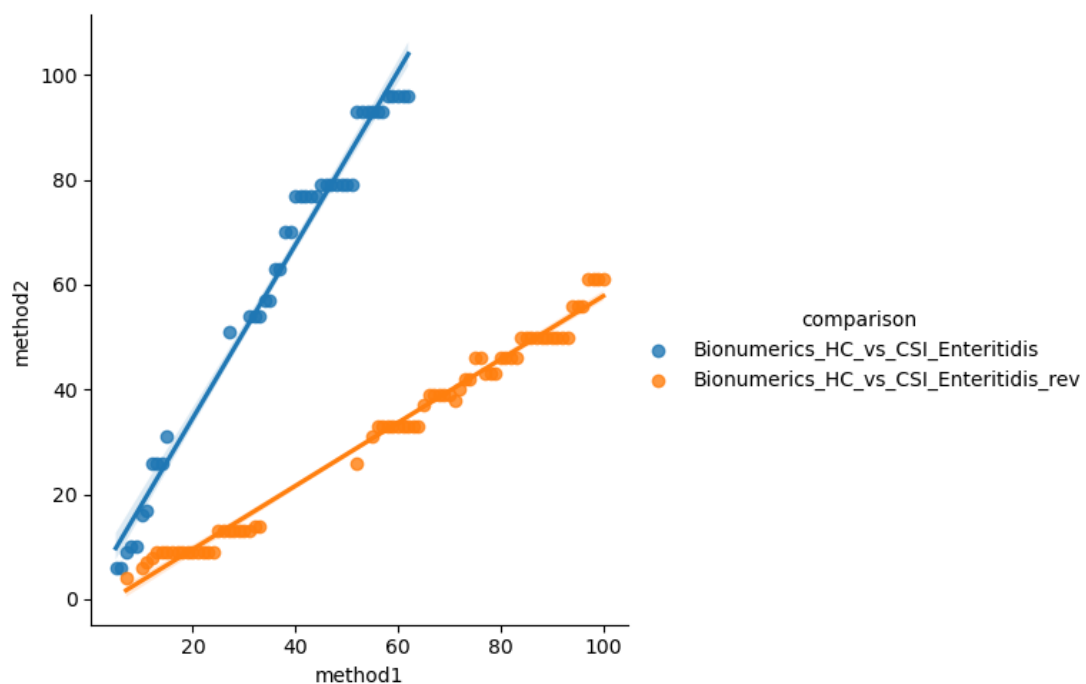


Figure S4.1.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 44 (blue) and 72 (orange) points is presented.

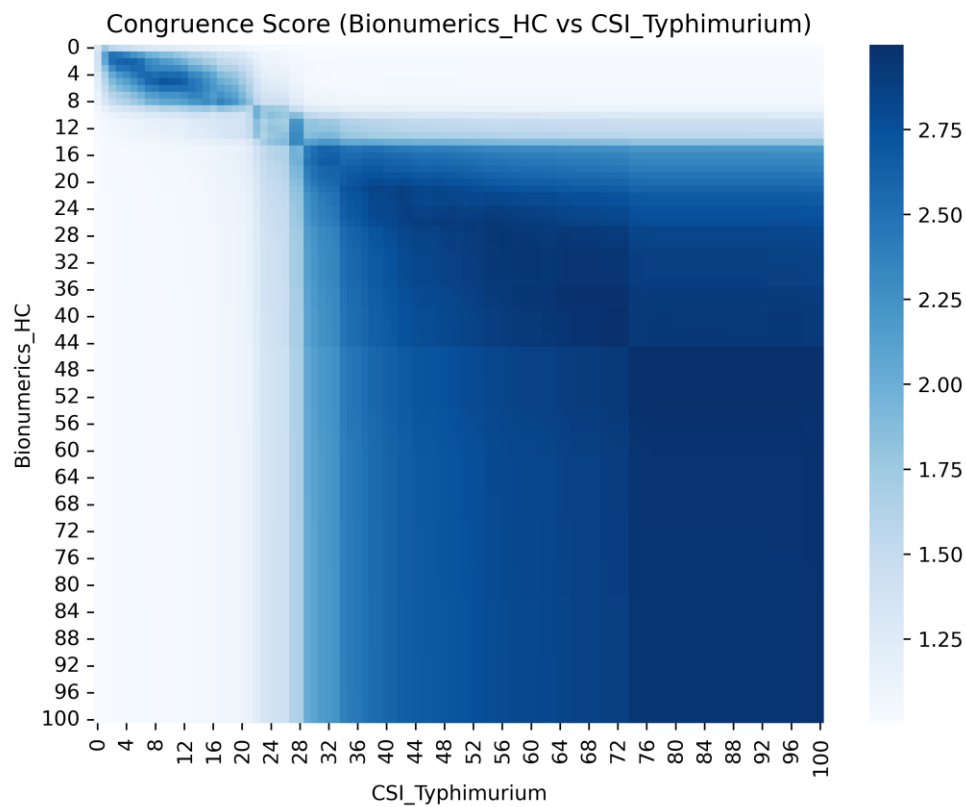


Figure S4.1.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

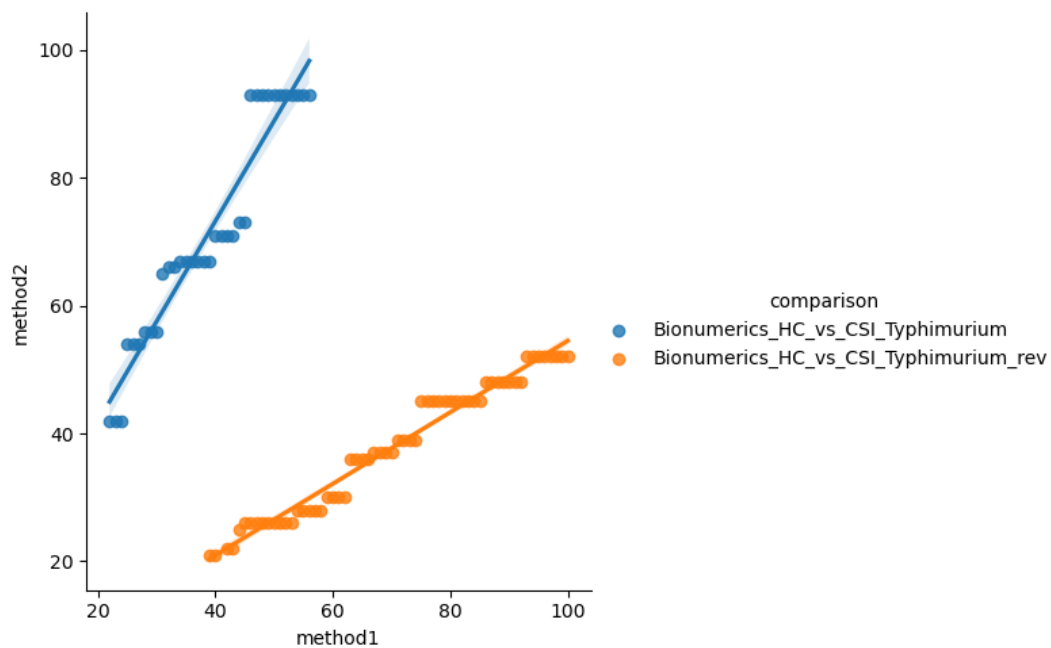


Figure S4.1.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 35 (blue) and 61 (orange) points is presented.

2. Bionumerics single-linkage vs. SnapperDB single-linkage

Table S4.2. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	Bionumerics single-linkage	SnapperDB single-linkage
Pipeline version	v8.1	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

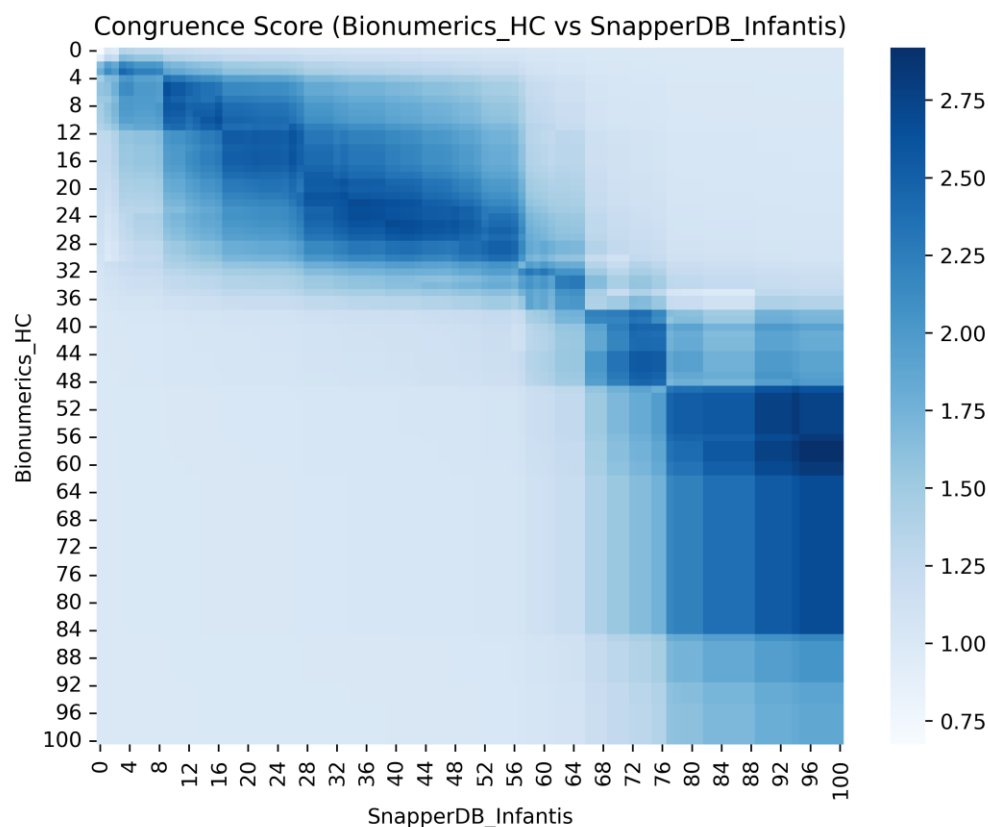


Figure S4.2.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

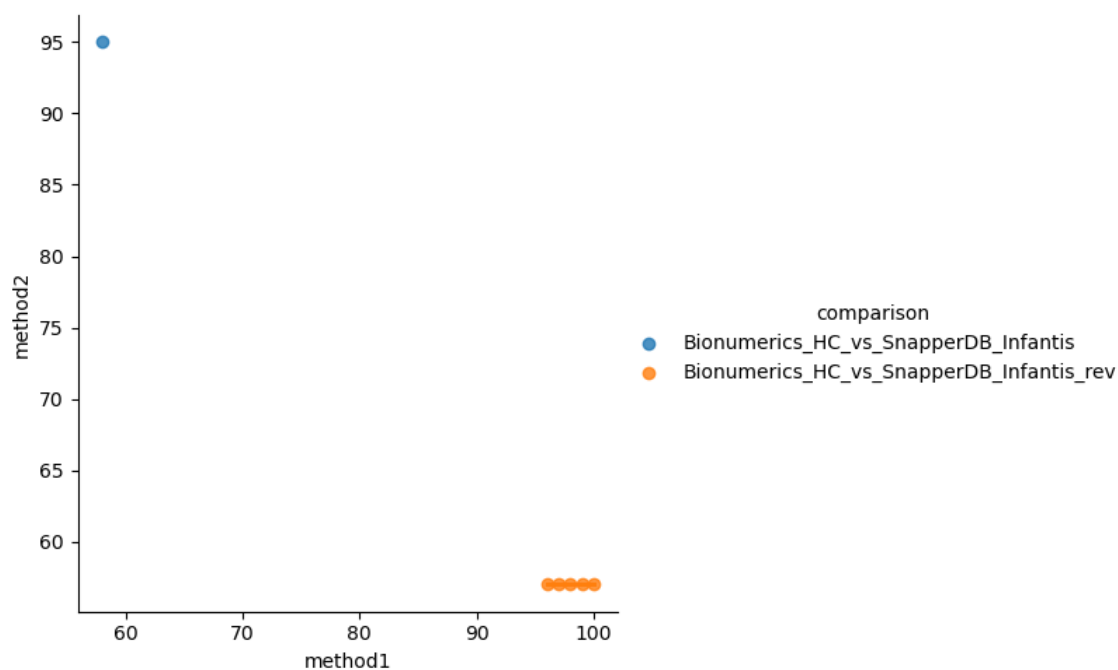


Figure S4.2.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Infantis. No linear tendency was observed. The 1 (blue) and 5 (orange) points are presented.

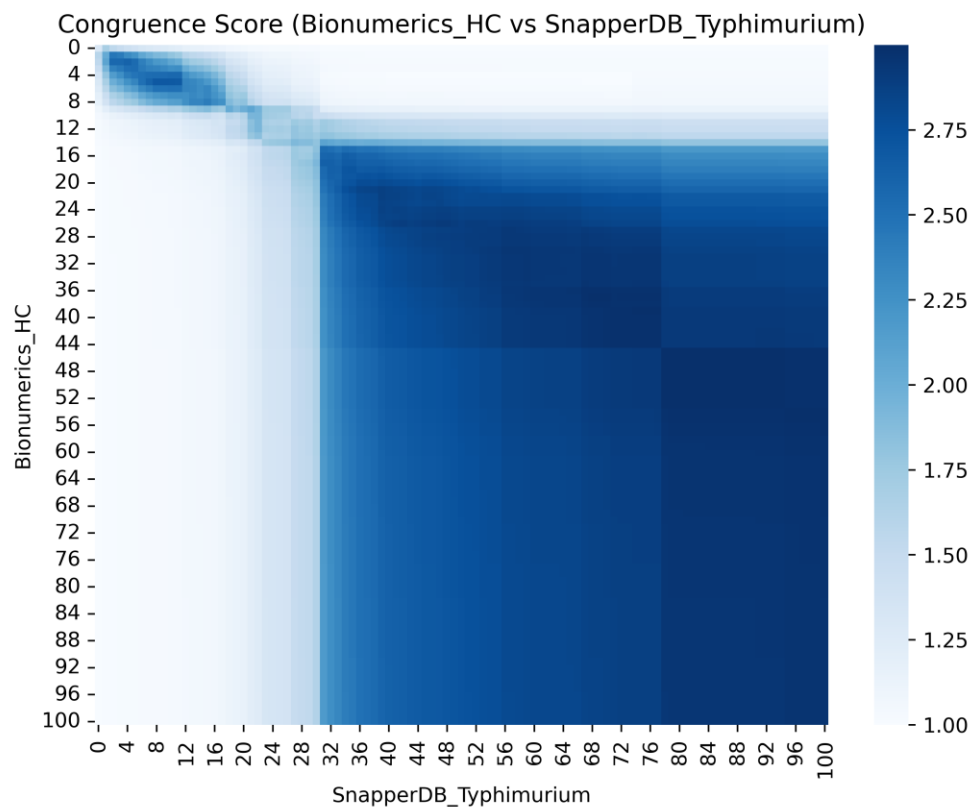


Figure S4.2.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

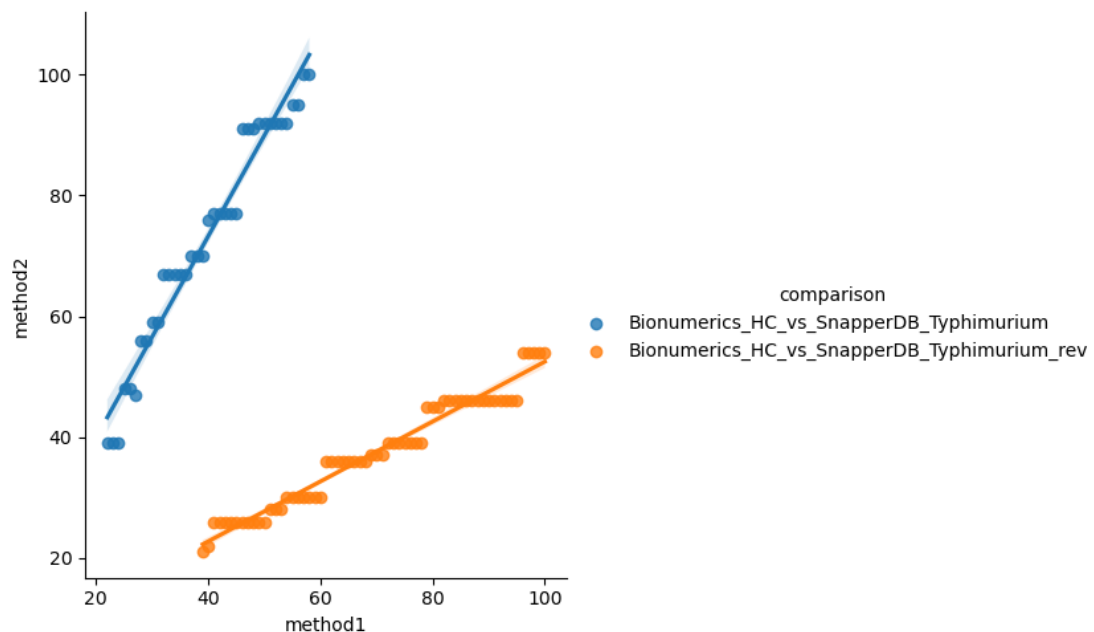


Figure S4.2.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 37 (blue) and 62 (orange) points is presented.

3. Bionumerics single-linkage vs. snippySnake single-linkage

Table S4.3. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	Bionumerics single-linkage	snippySnake single-linkage
Pipeline version	v8.1	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

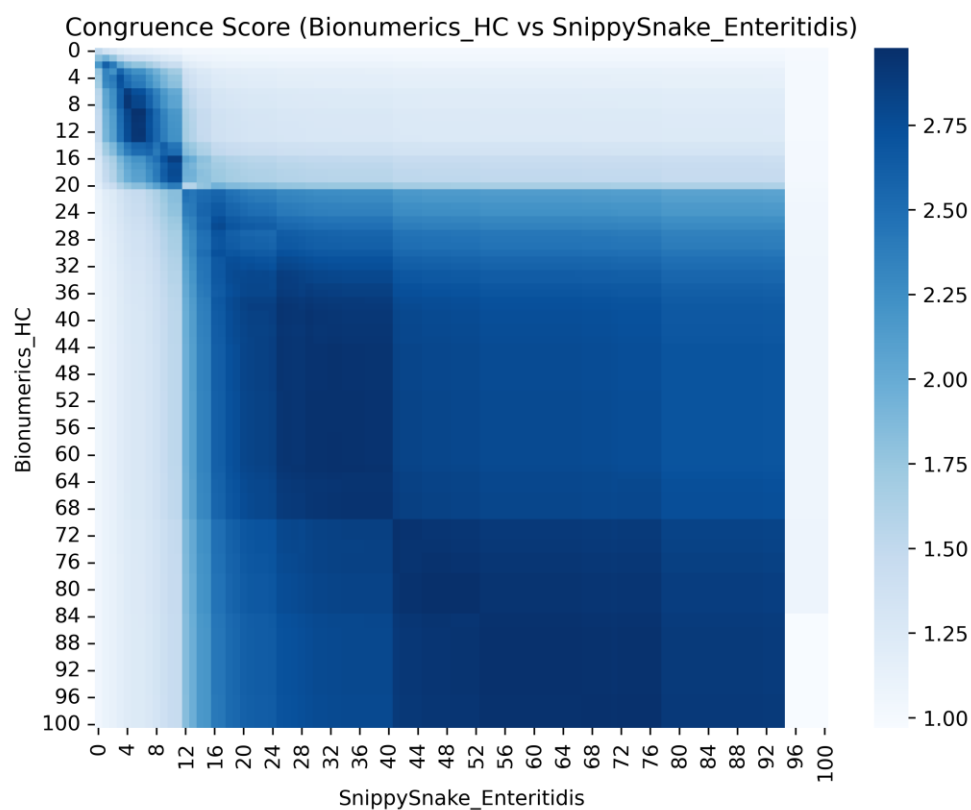


Figure S4.3.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

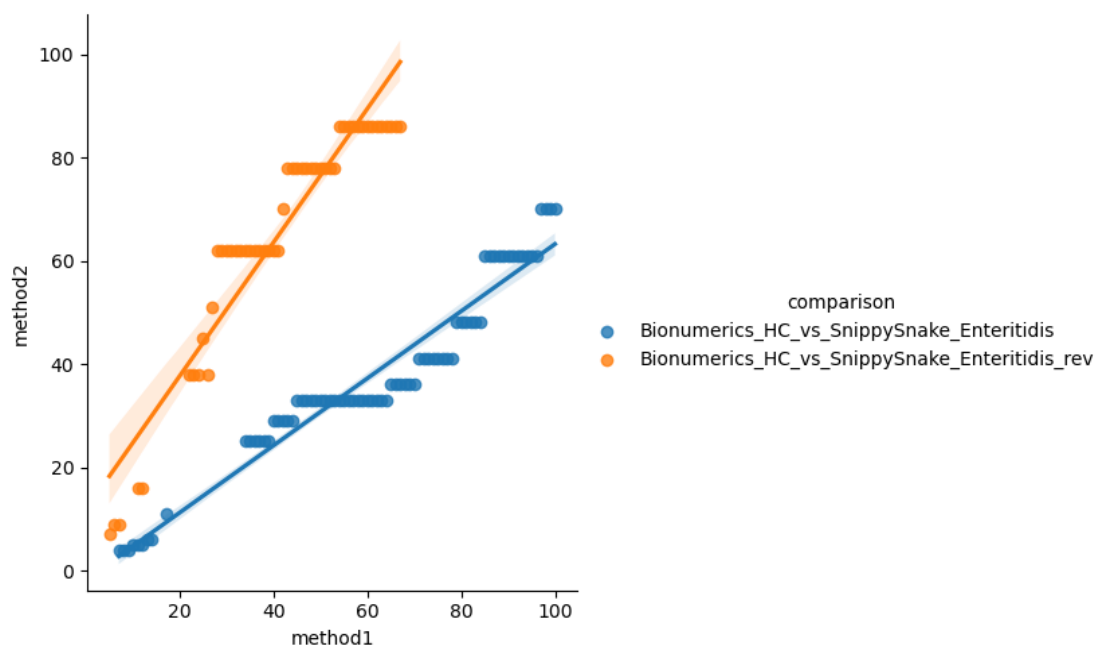


Figure S4.3.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 76 (blue) and 51 (orange) points is presented.

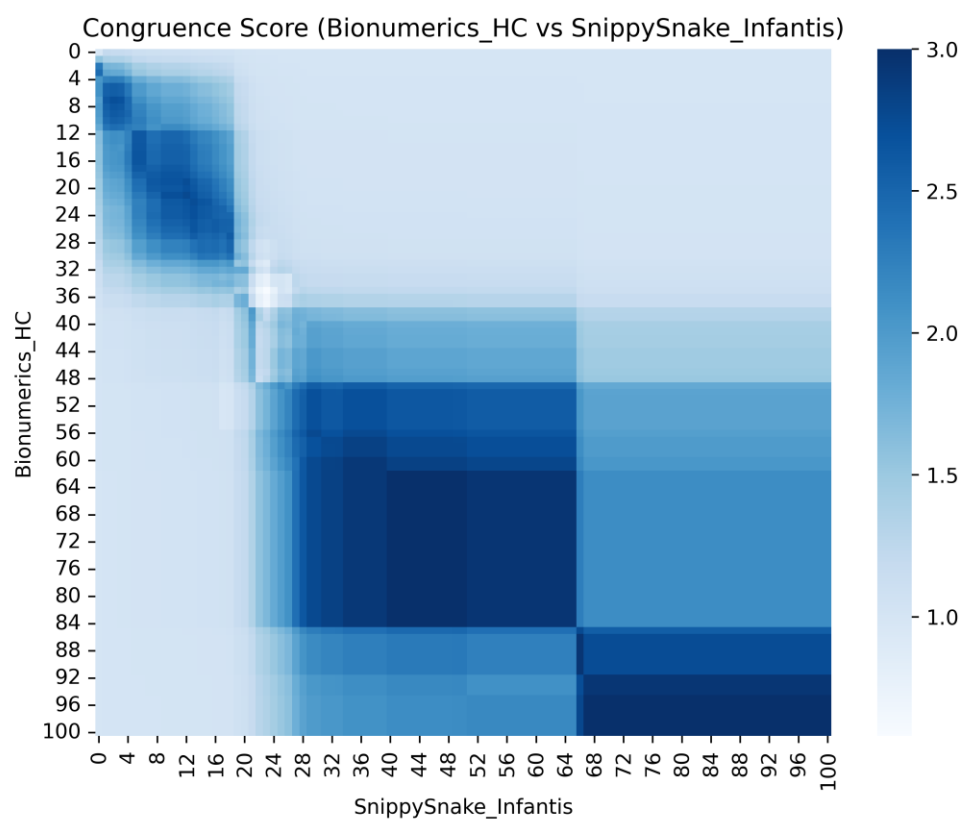


Figure S4.3.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

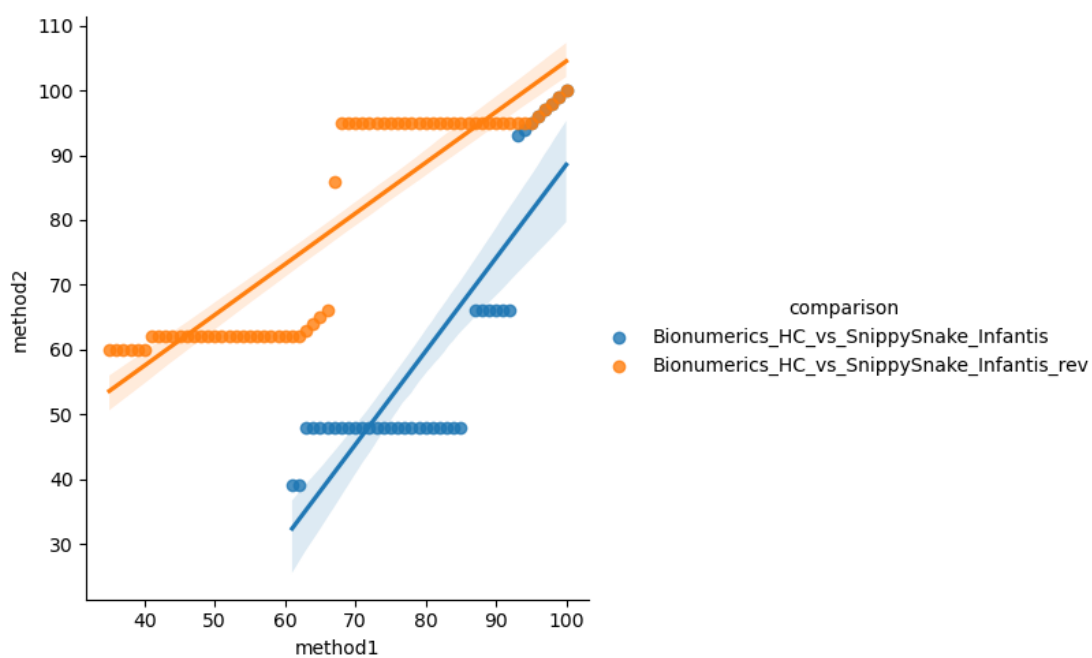


Figure S4.3.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Infantis. A linear tendency line supported by 39 (blue) and 66 (orange) points is presented.

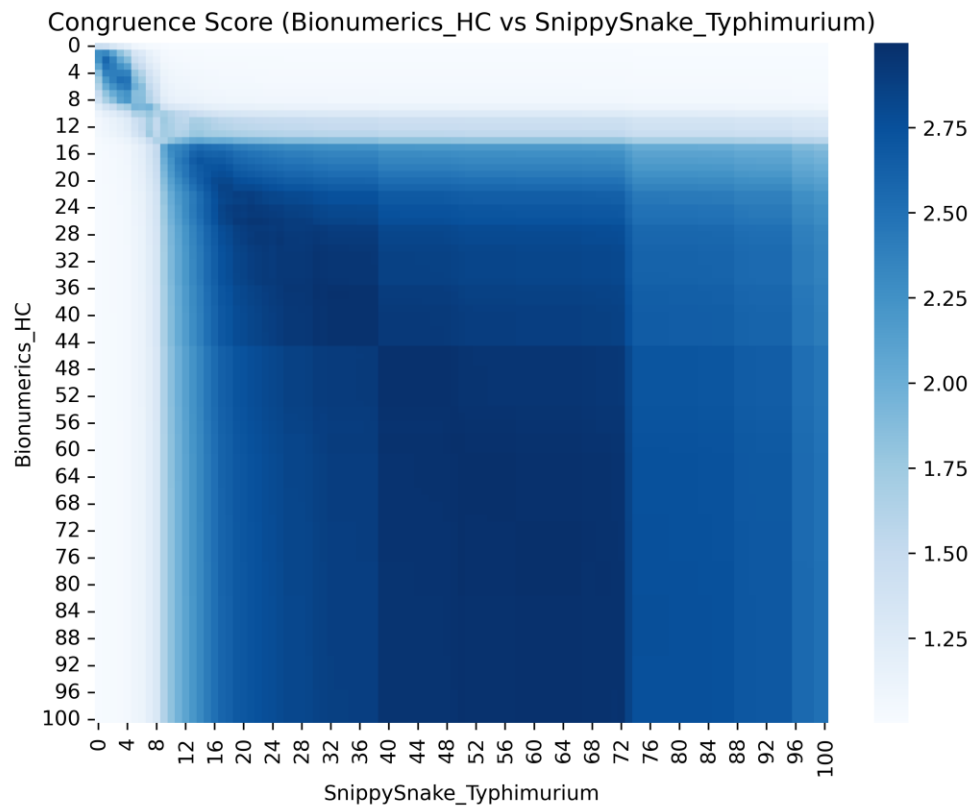


Figure S4.3.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

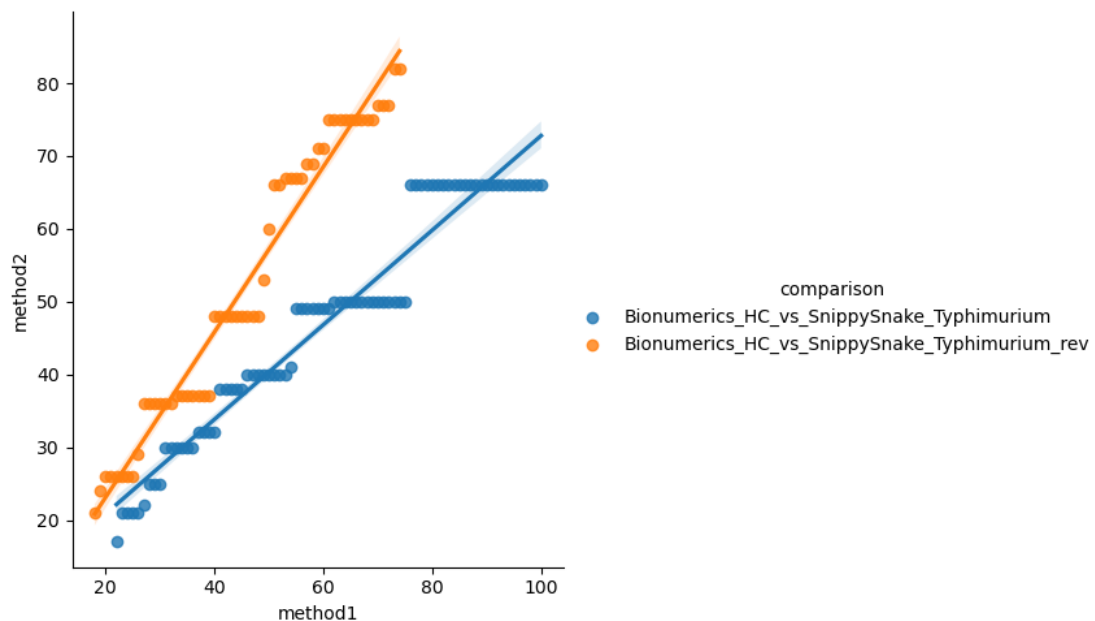


Figure S4.3.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 79 (blue) and 57 (orange) points is presented.

4. chewieSnake GrapeTree vs. CSI Phylogeny single-linkage

Table S4.4. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	chewieSnake GrapeTree	CSI Phylogeny single-linkage
Pipeline version	v3.1.1	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

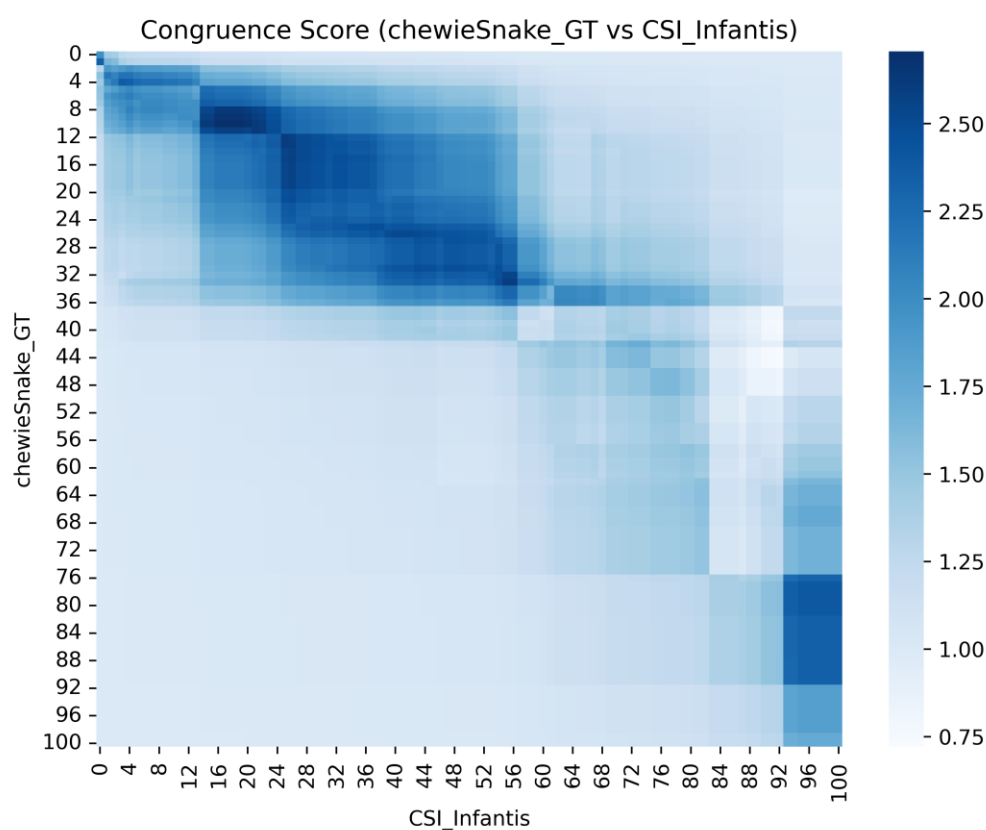


Figure S4.4.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

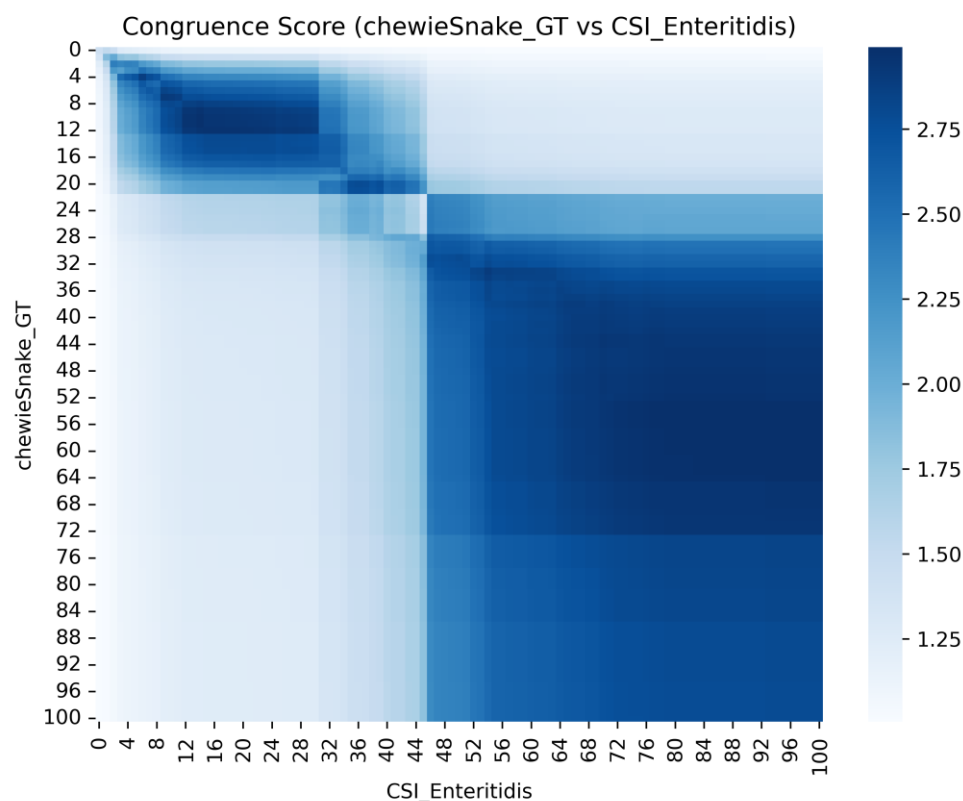


Figure S4.4.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

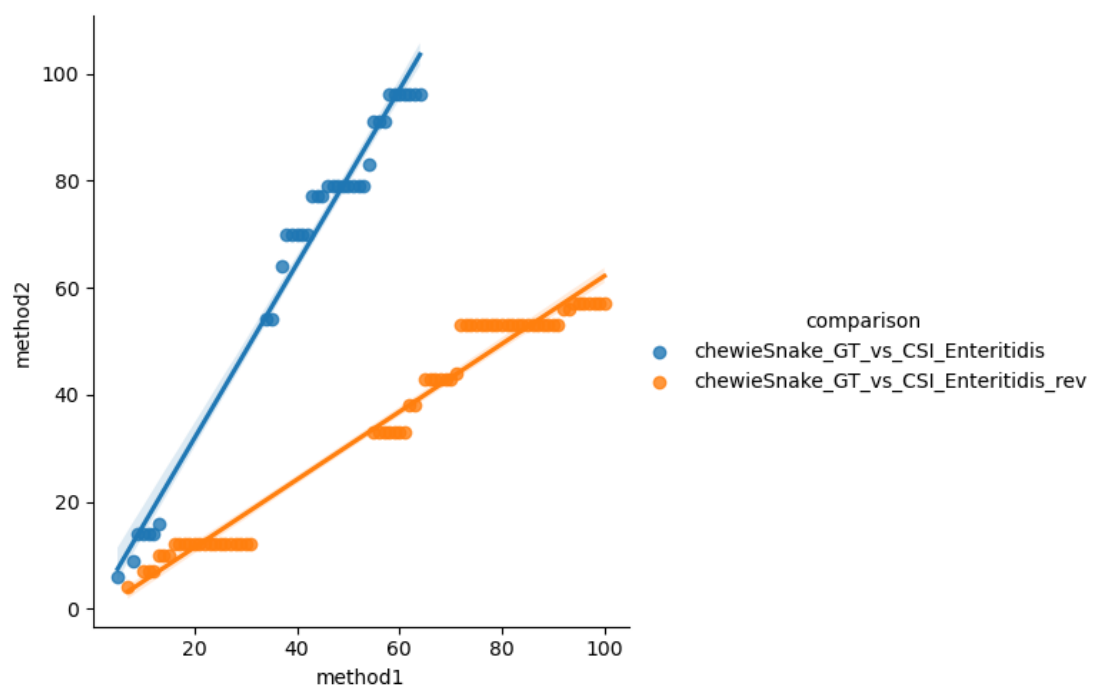


Figure S4.4.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Enteritidis. A linear tendency line supported by 37 (blue) and 68 (orange) points is presented.

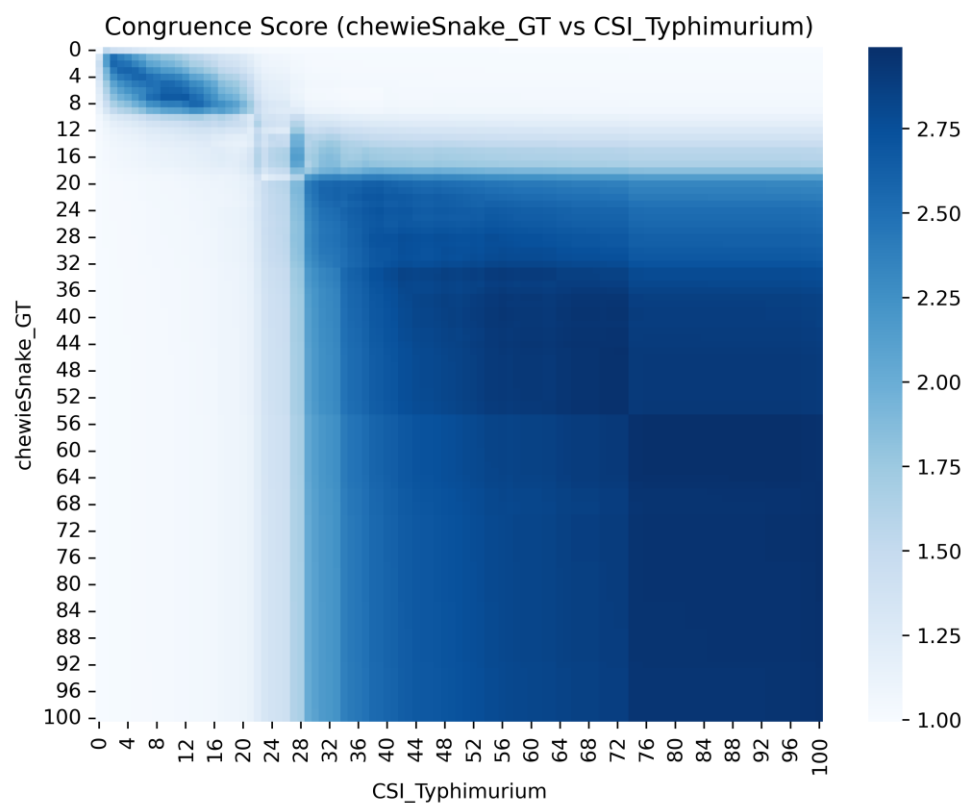


Figure S4.4.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

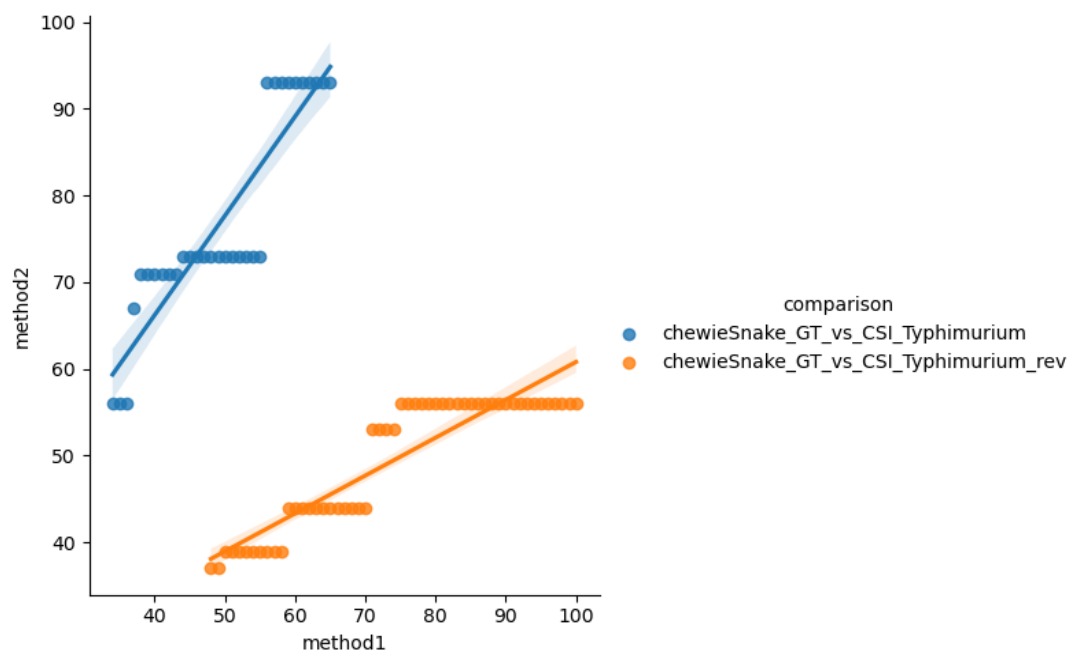


Figure S4.4.5. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Typhimurium. A linear tendency line supported by 32 (blue) and 53 (orange) points is presented.

5. chewieSnake GrapeTree vs. SnapperDB single-linkage

Table S4.5. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	chewieSnake GrapeTree	SnapperDB single-linkage
Pipeline version	v3.1.1	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

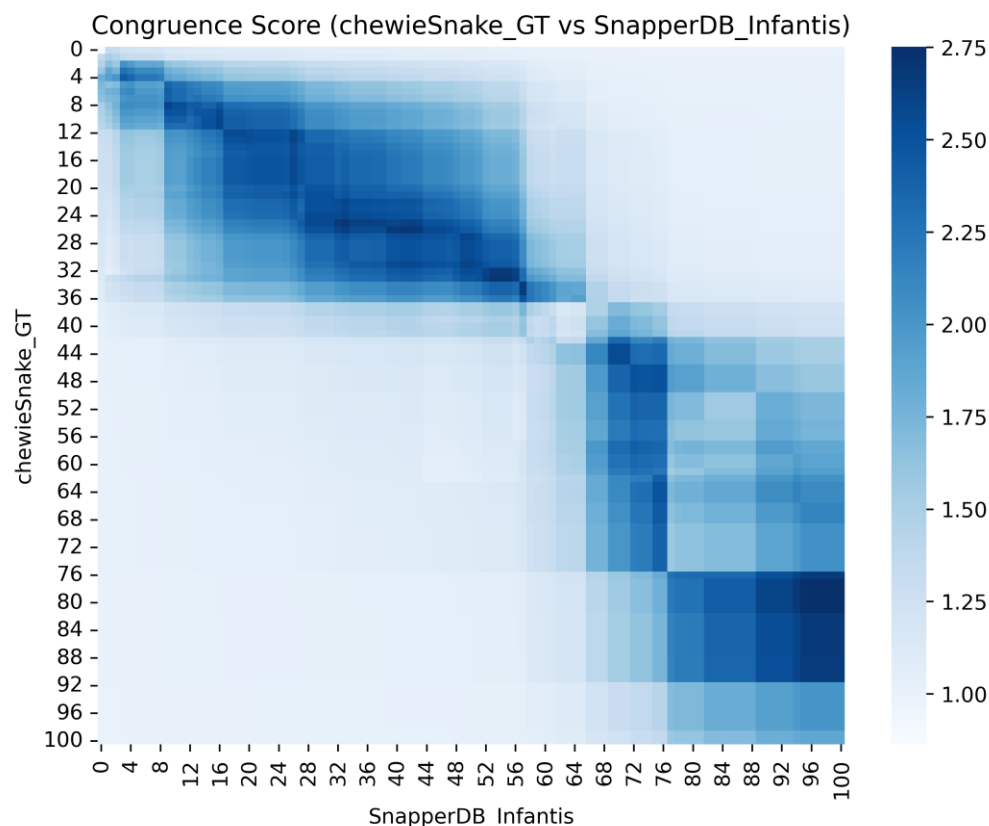


Figure S4.5.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds

NOTE: No congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

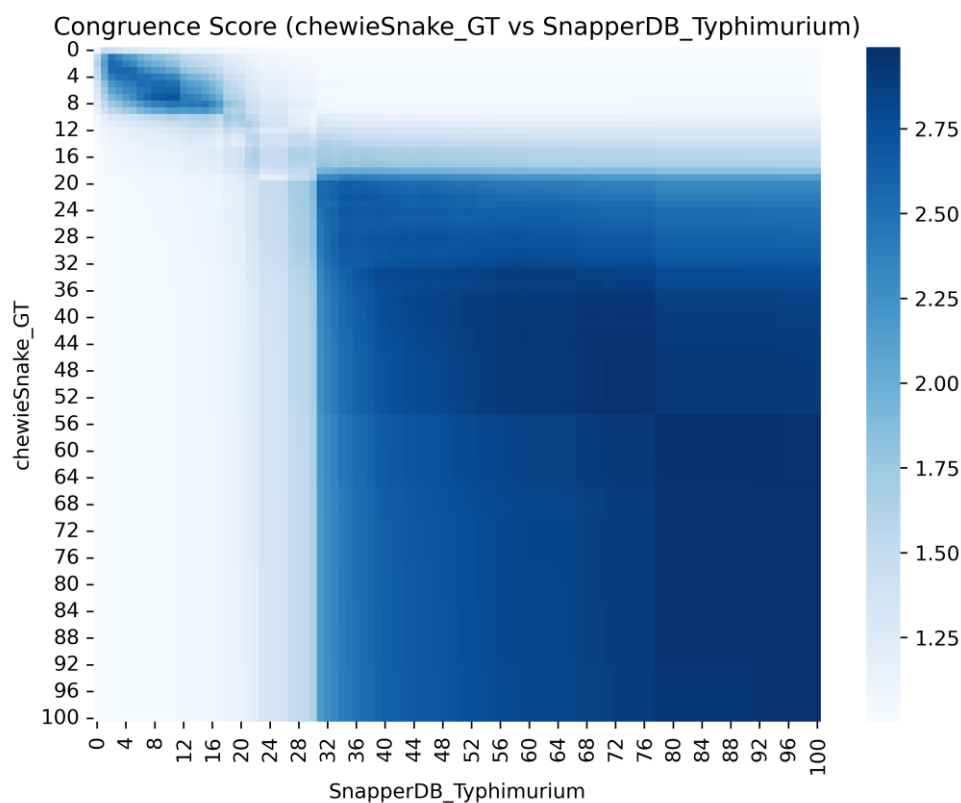


Figure S4.5.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

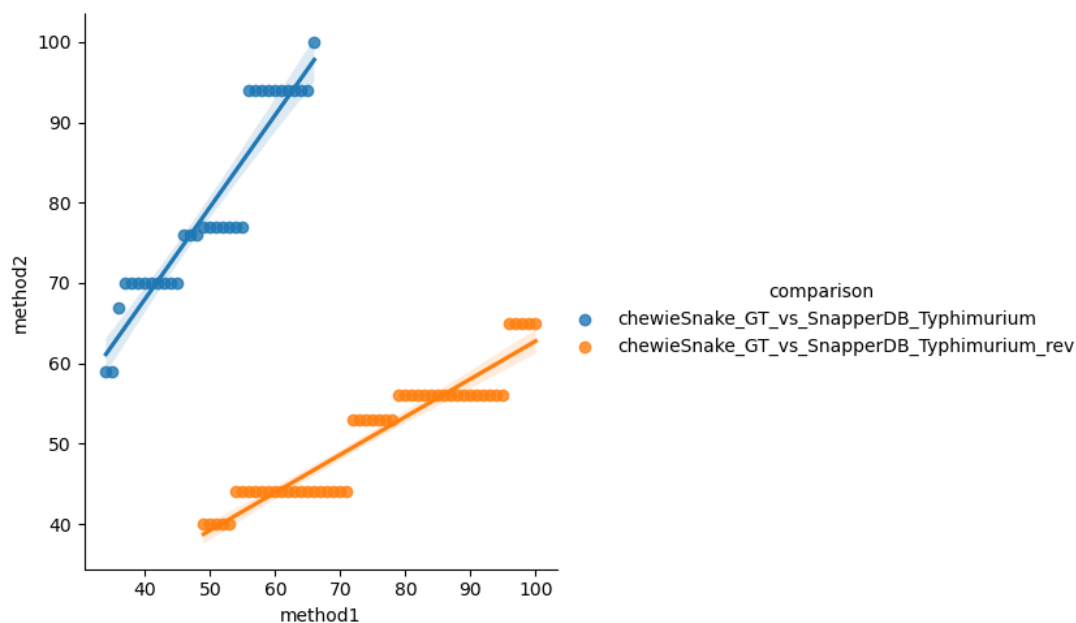


Figure S4.5.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 33 (blue) and 52 (orange) points is presented.

6. chewieSnake GrapeTree vs. snippySnake single-linkage

Table S4.6. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	chewieSnake GrapeTree	snippySnake single-linkage
Pipeline version	v3.1.1	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

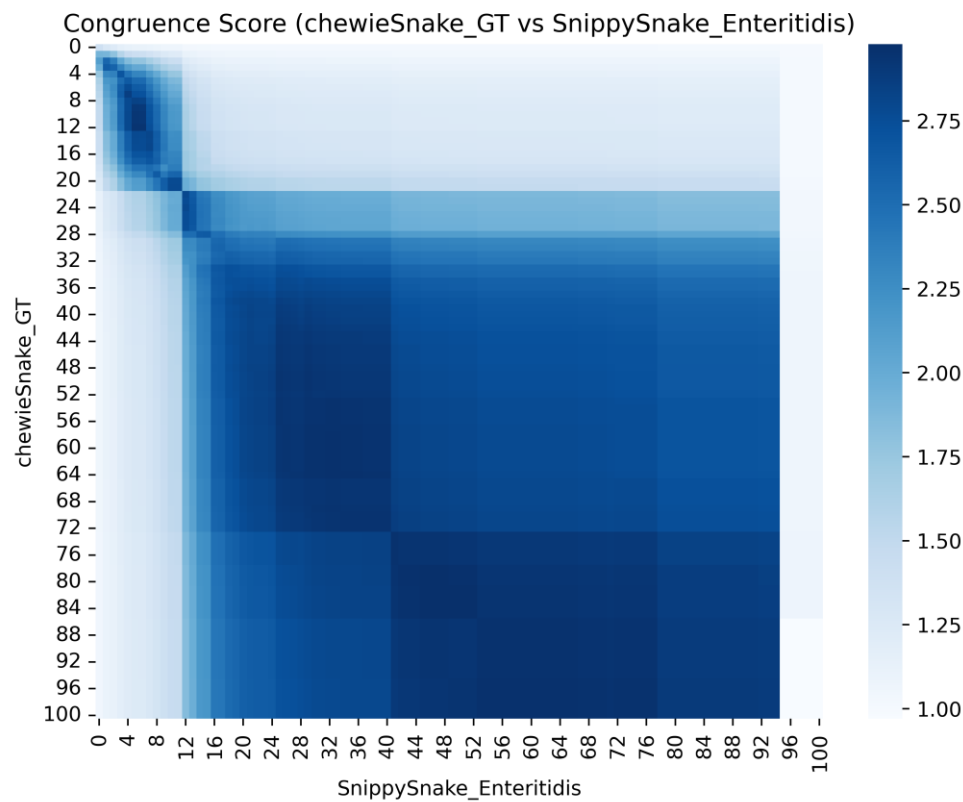


Figure S4.6.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

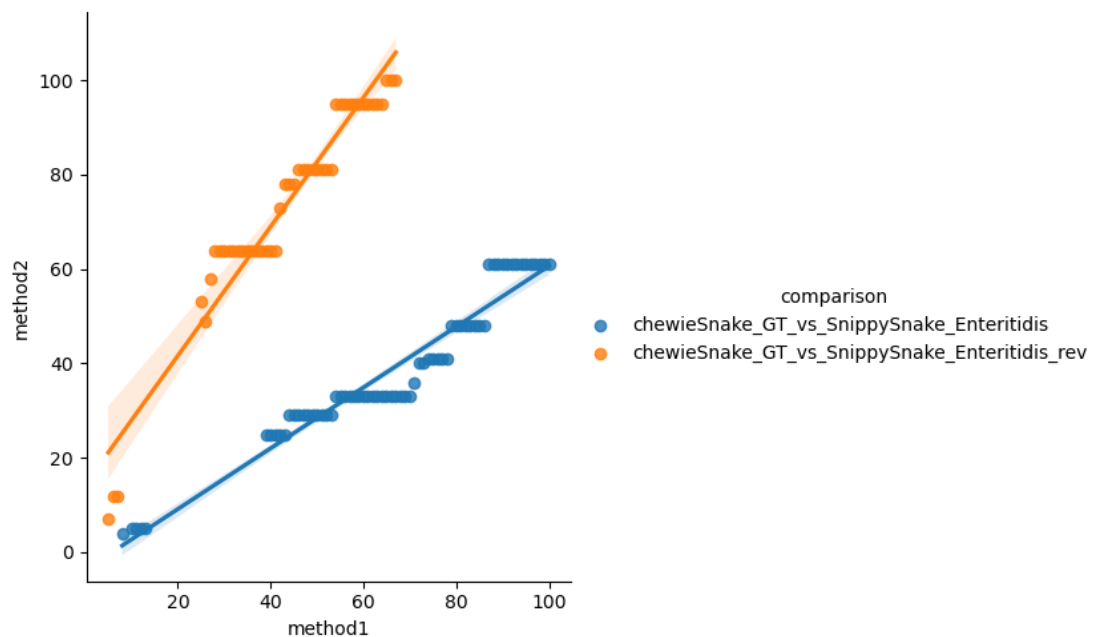


Figure S4.6.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 67 (blue) and 46 (orange) points is presented.

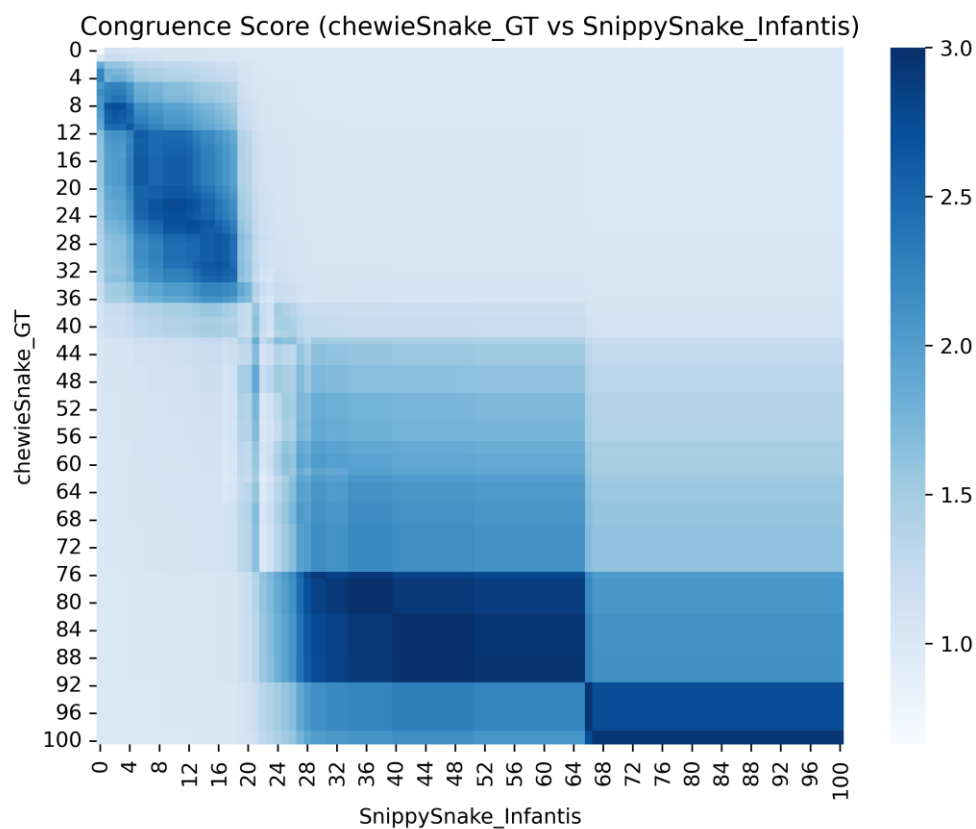


Figure S4.6.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

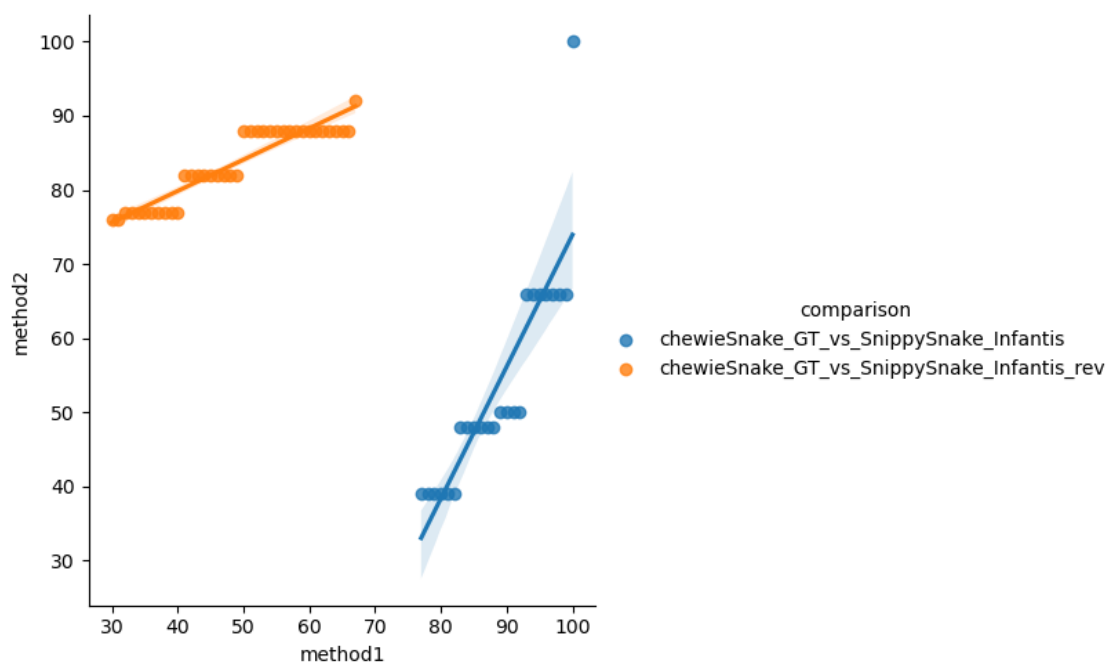


Figure S4.6.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Infantis. A linear tendency line supported by 24 (blue) and 38 (orange) points is presented.

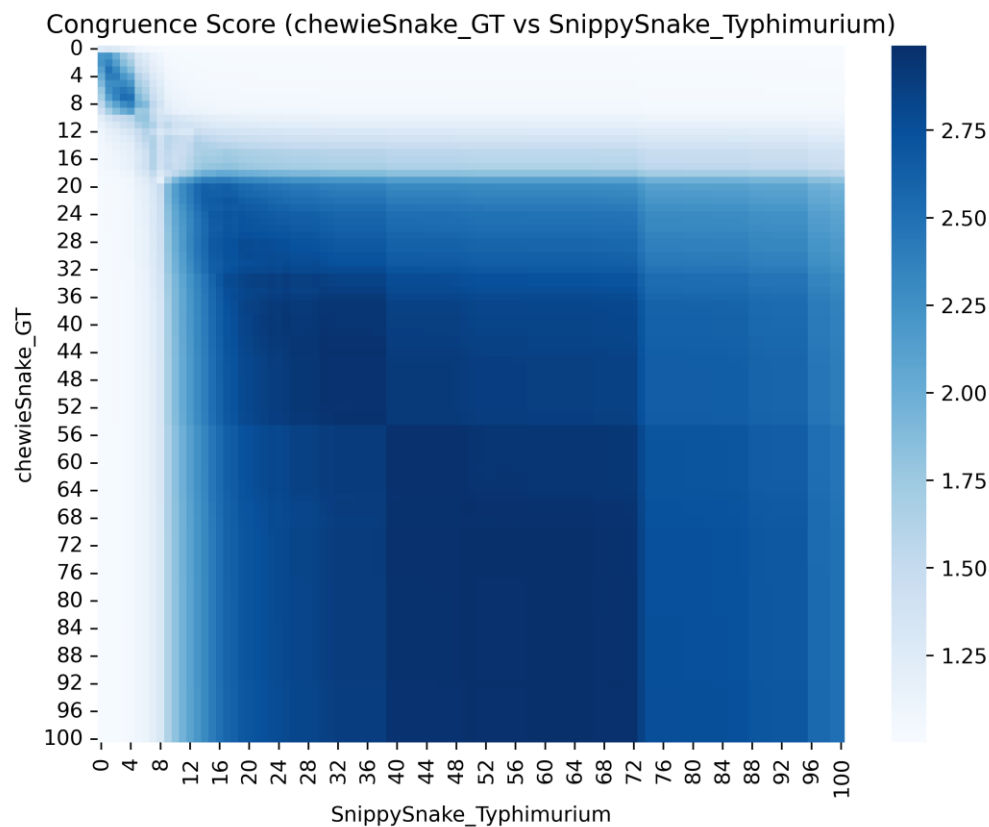


Figure S4.6.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

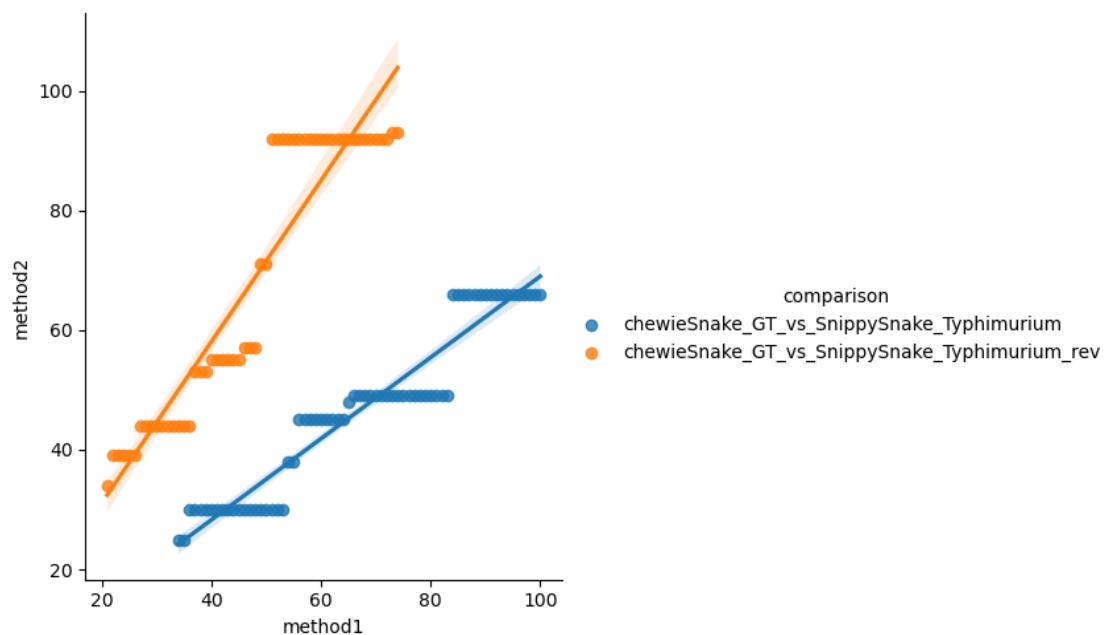


Figure S4.6.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 67 (blue) and 54 (orange) points is presented.

7. chewieSnake single-linkage vs. CSI Phylogeny single-linkage

Table S4.7. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	chewieSnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v3.1.1	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

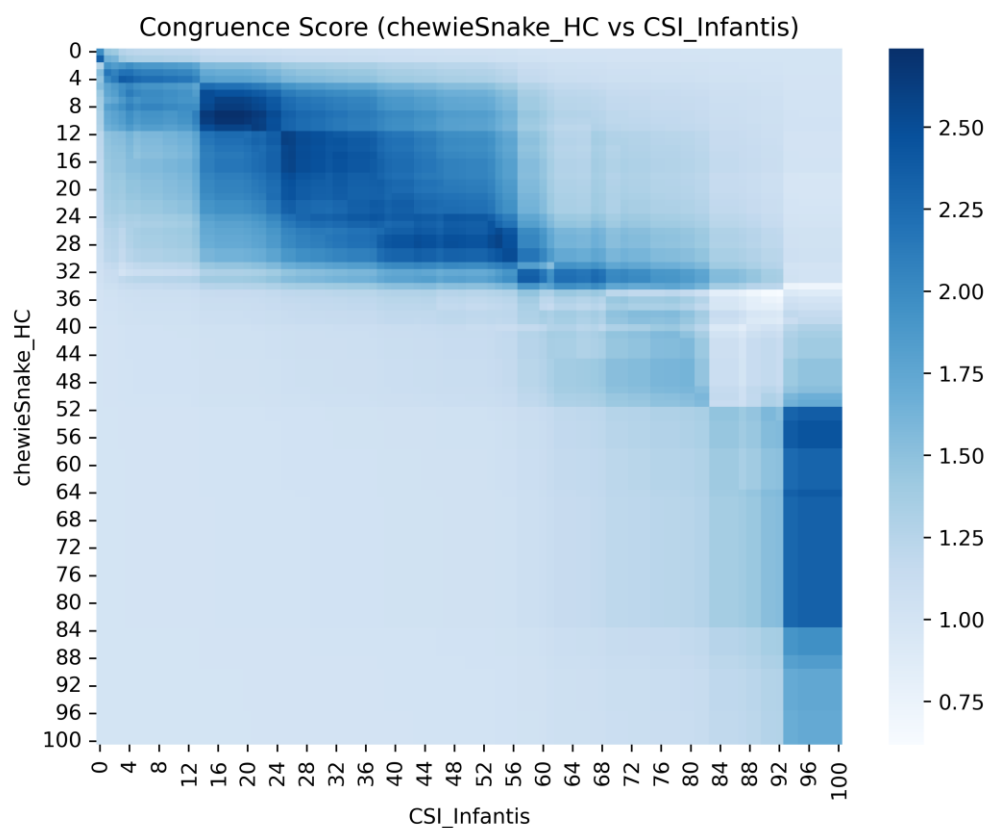


Figure S4.7.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

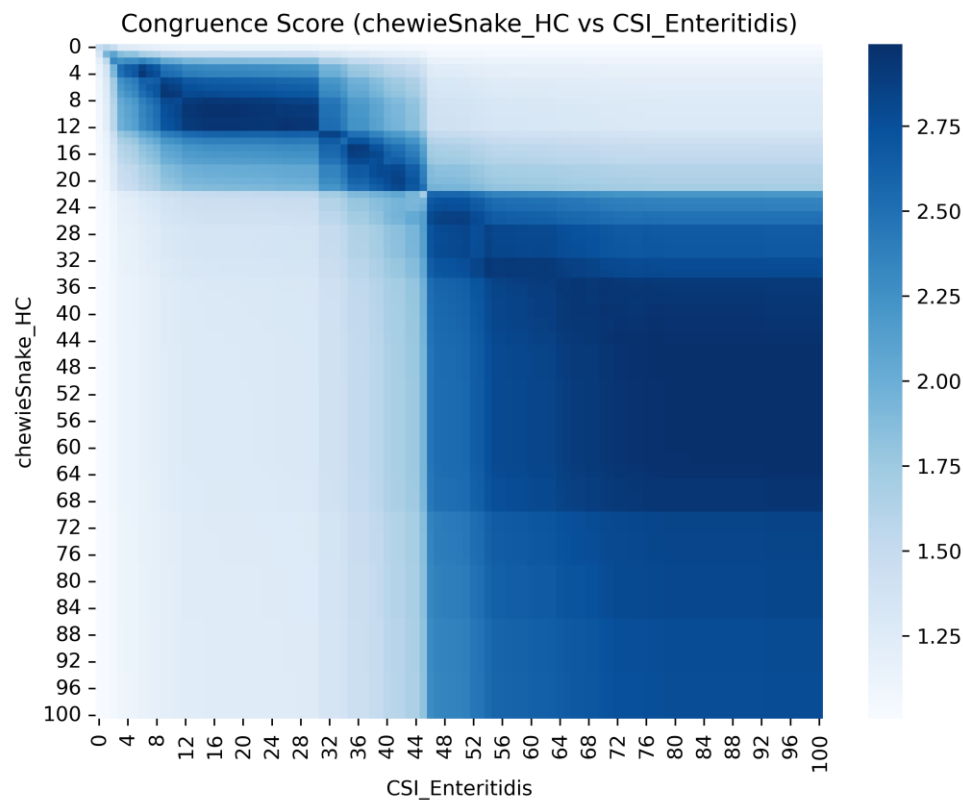


Figure S4.7.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

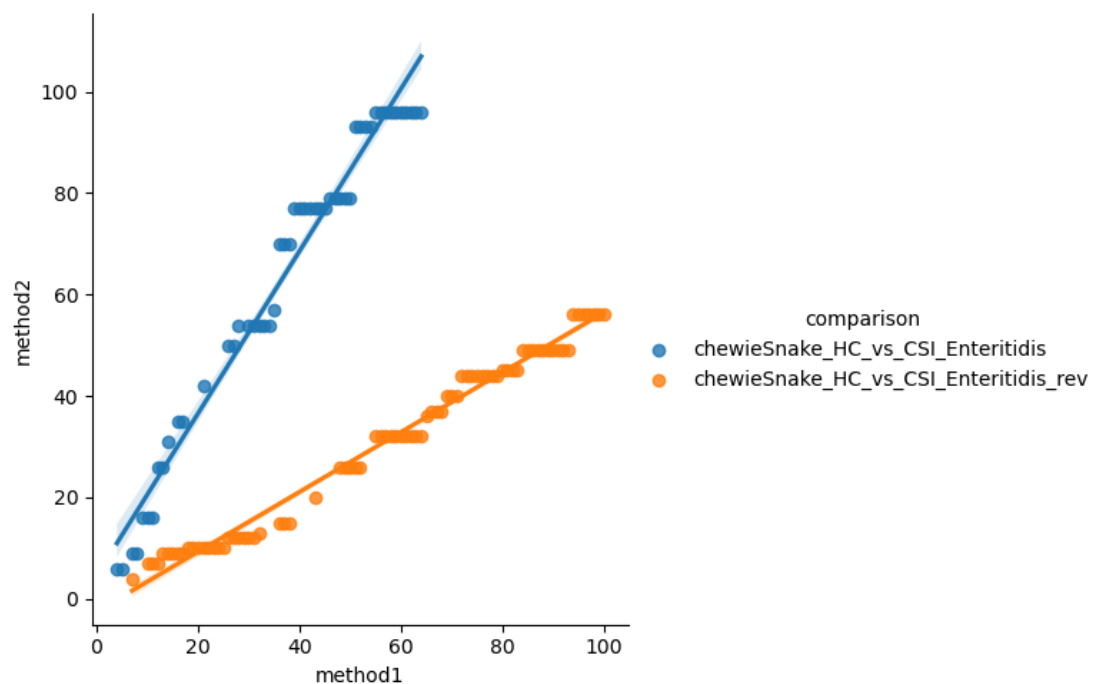


Figure S4.7.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 51 (blue) and 79 (orange) points is presented.

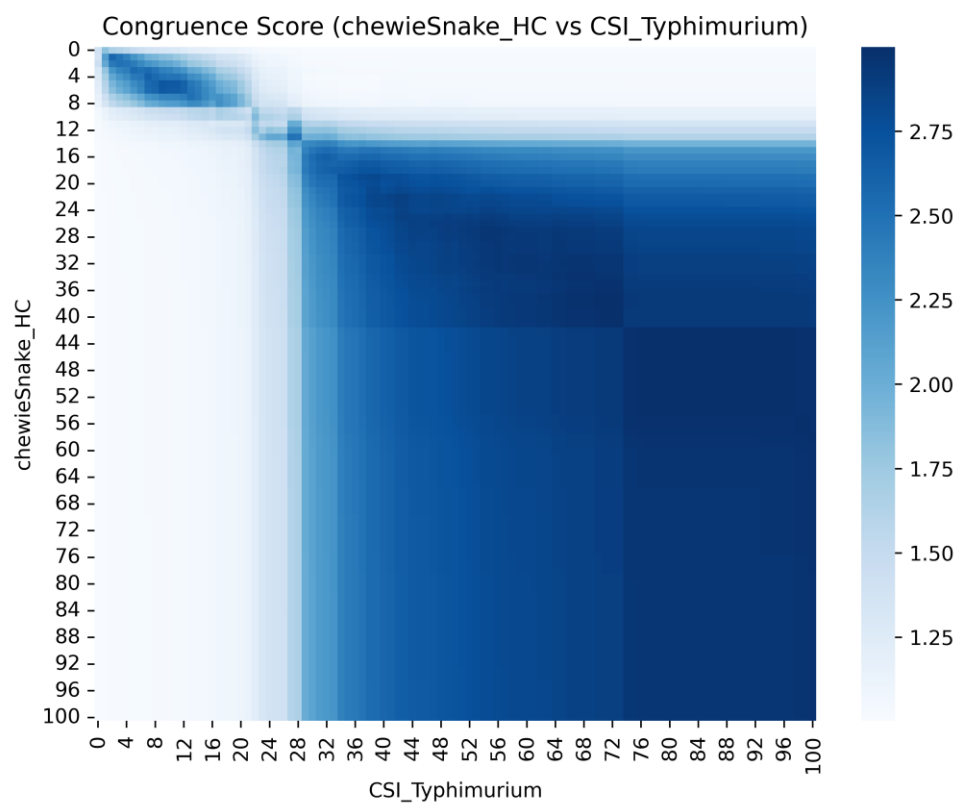


Figure S4.7.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

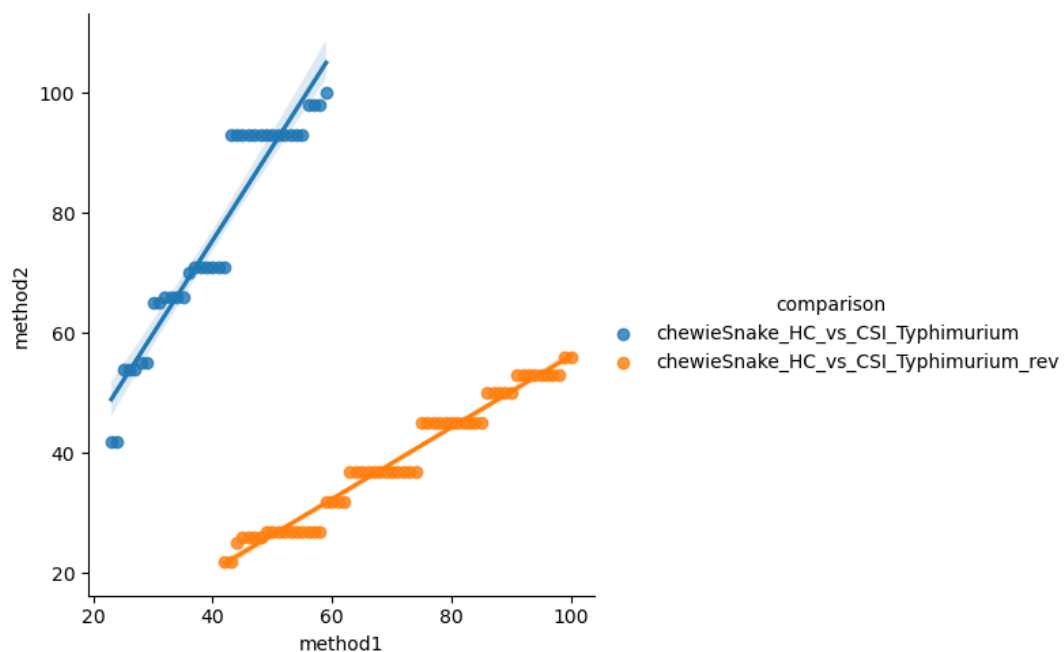


Figure S4.7.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 37 (blue) and 59 (orange) points is presented.

8. chewieSnake single-linkage vs. SnapperDB single-linkage

Table S4.8. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	chewieSnake single-linkage	SnapperDB single-linkage
Pipeline version	v3.1.1	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

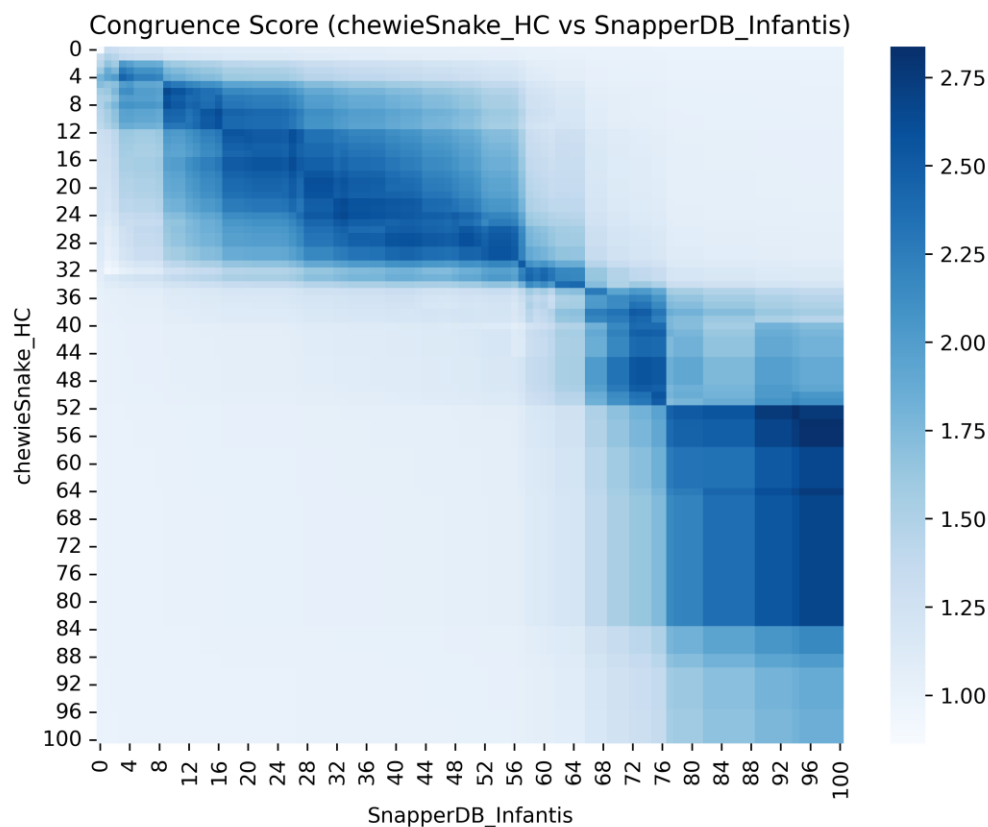


Figure S4.8.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

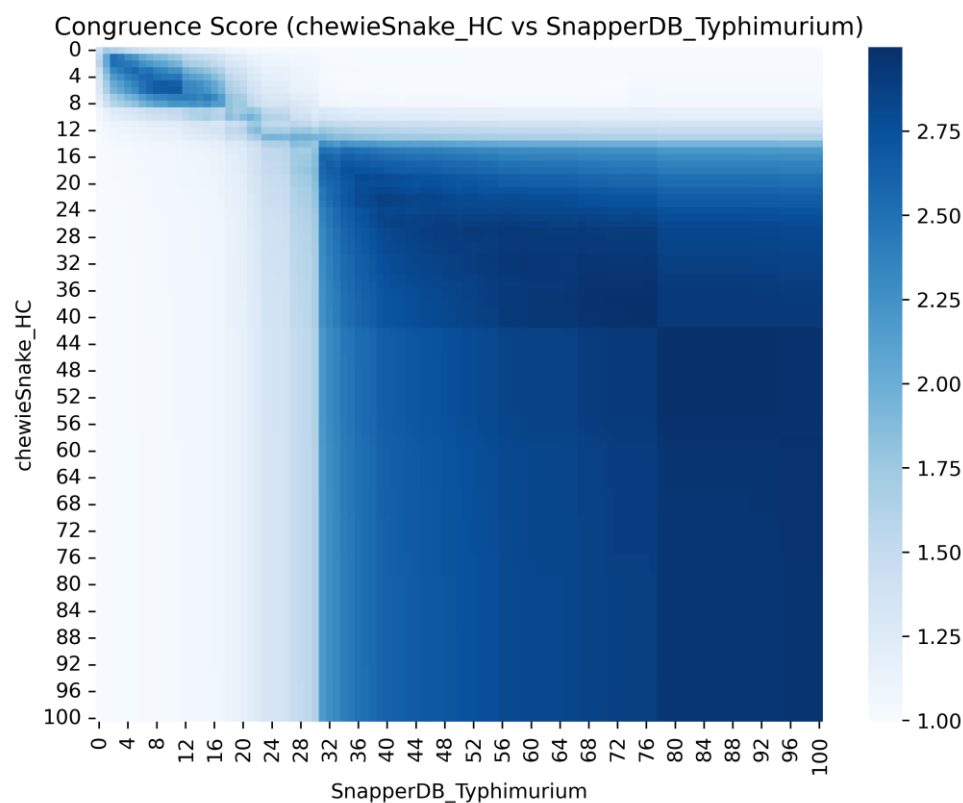


Figure S4.8.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

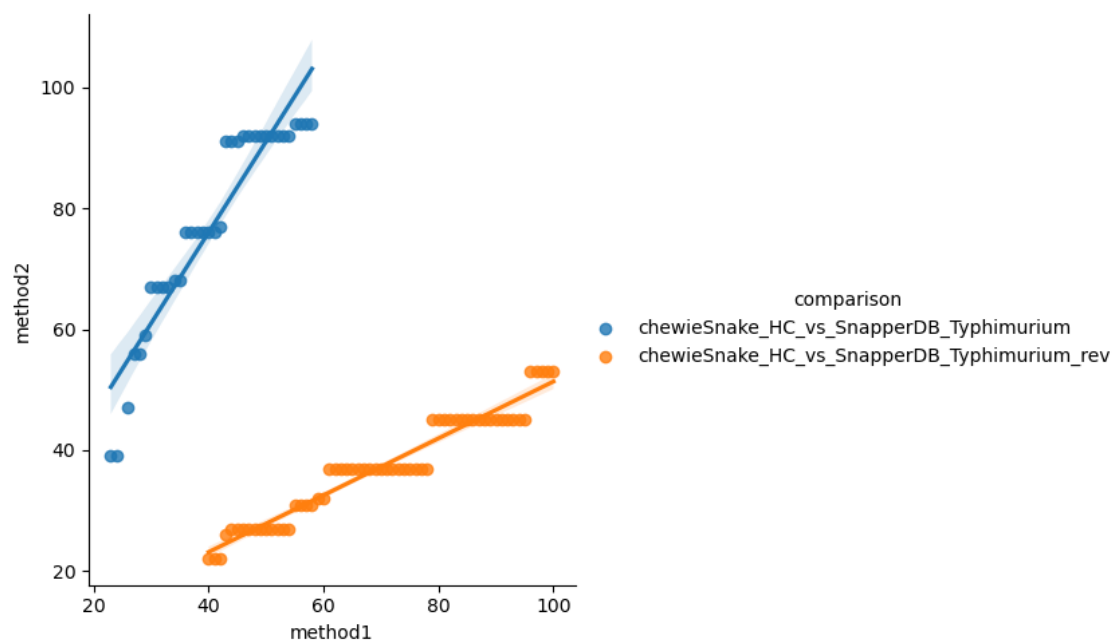


Figure S4.8.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 35 (blue) and 61 (orange) points is presented.

9. chewieSnake single-linkage vs. snippySnake single-linkage

Table S4.9. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	chewieSnake single-linkage	snippySnake single-linkage
Pipeline version	v3.1.1	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

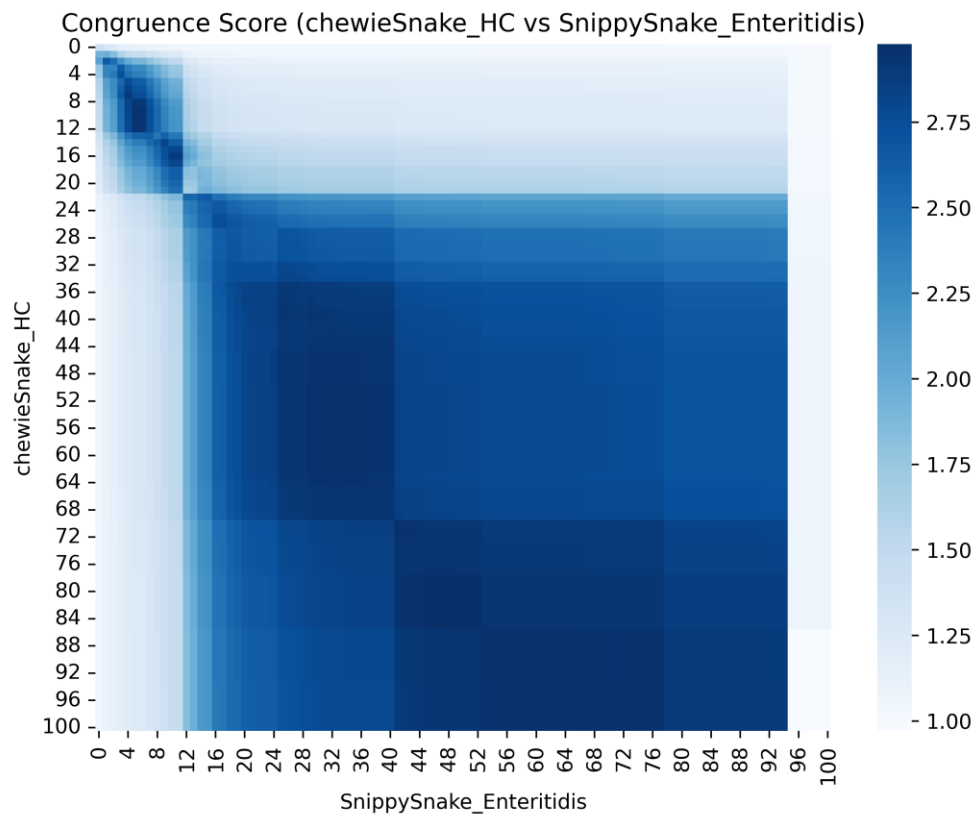


Figure S4.9.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

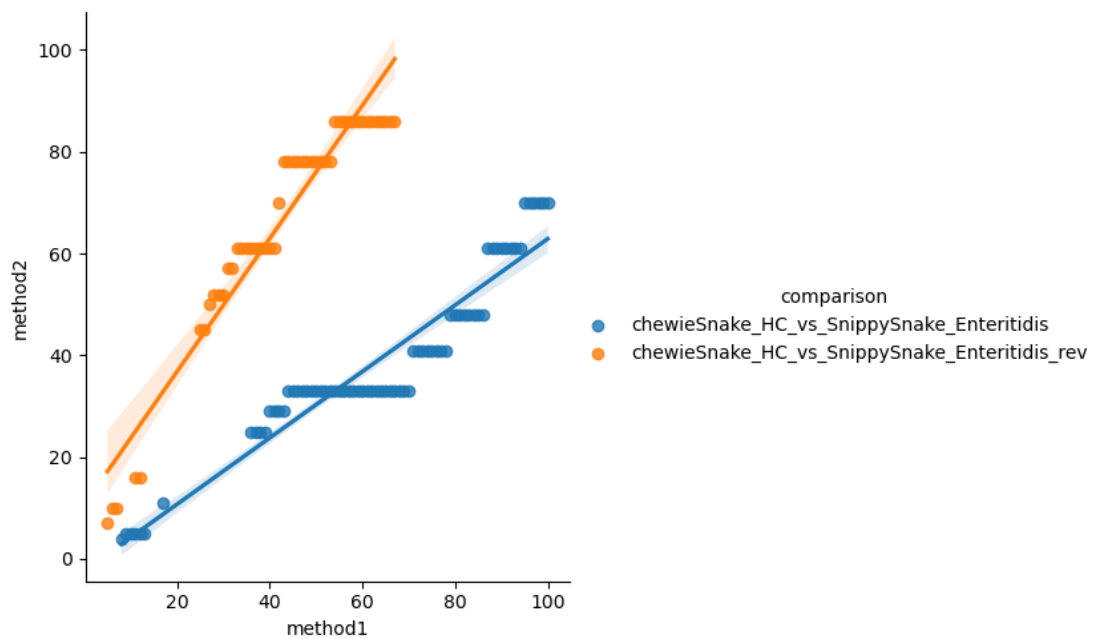


Figure S4.9.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 78 (blue) and 48 (orange) points is presented.

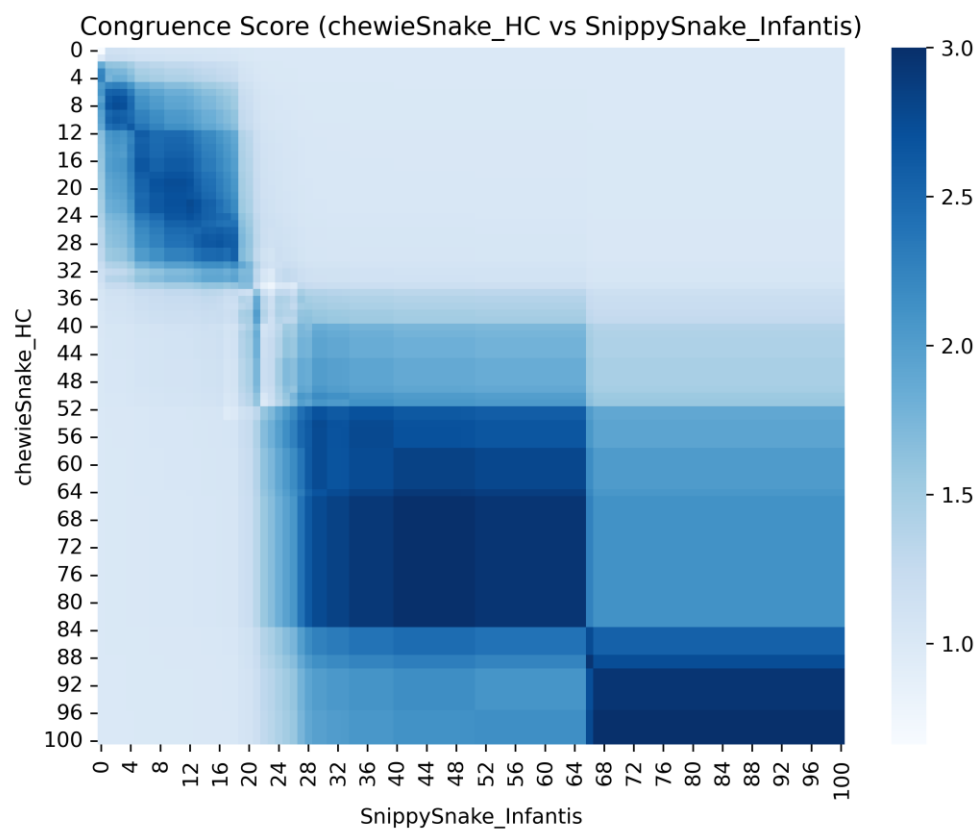


Figure S4.9.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

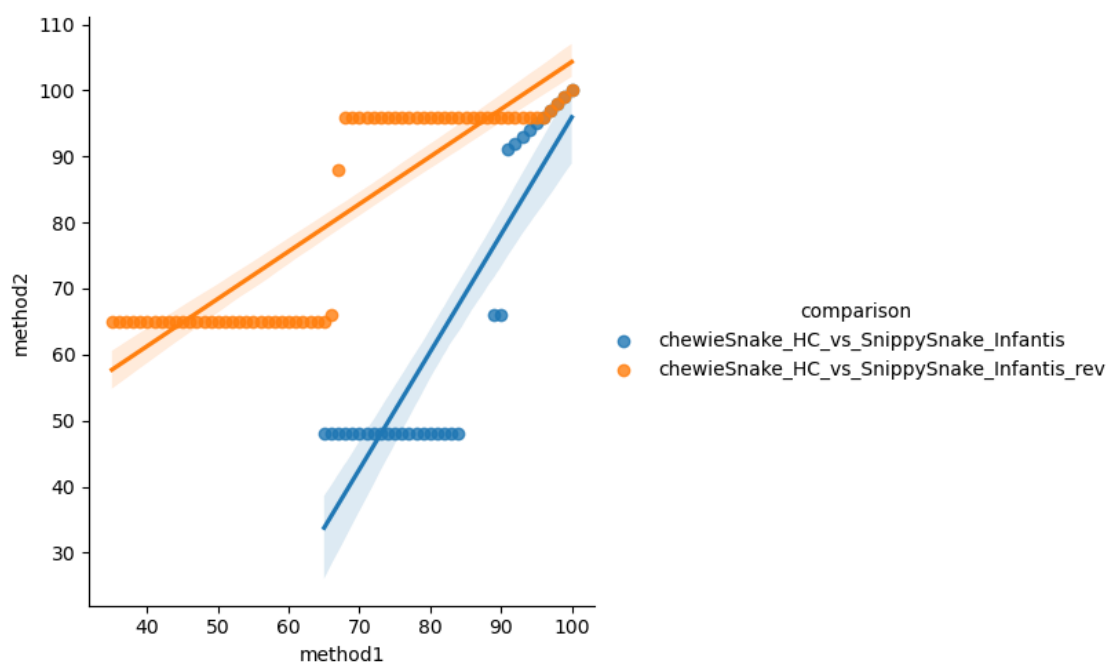


Figure S4.9.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Infantis. A linear tendency line supported by 32 (blue) and 66 (orange) points is presented.

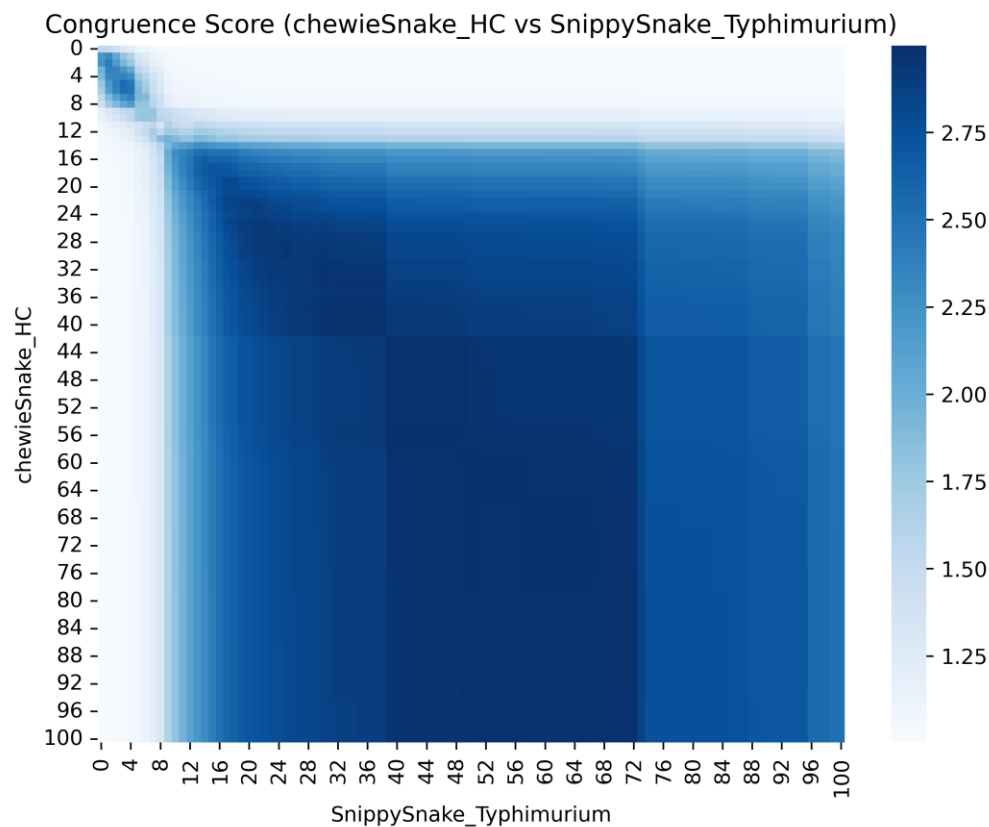


Figure S4.9.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

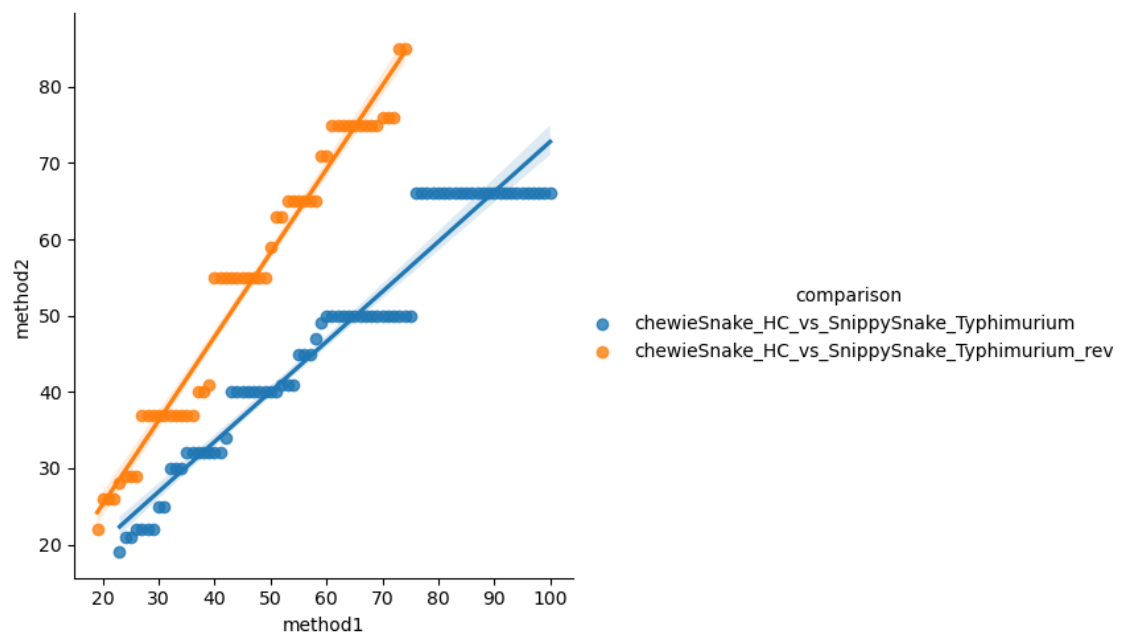


Figure S4.9.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 78 (blue) and 56 (orange) points is presented.

10. INNUENDO-like-EFSA GrapeTree vs. CSI Phylogeny single-linkage

Table S4.10. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-EFSA GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

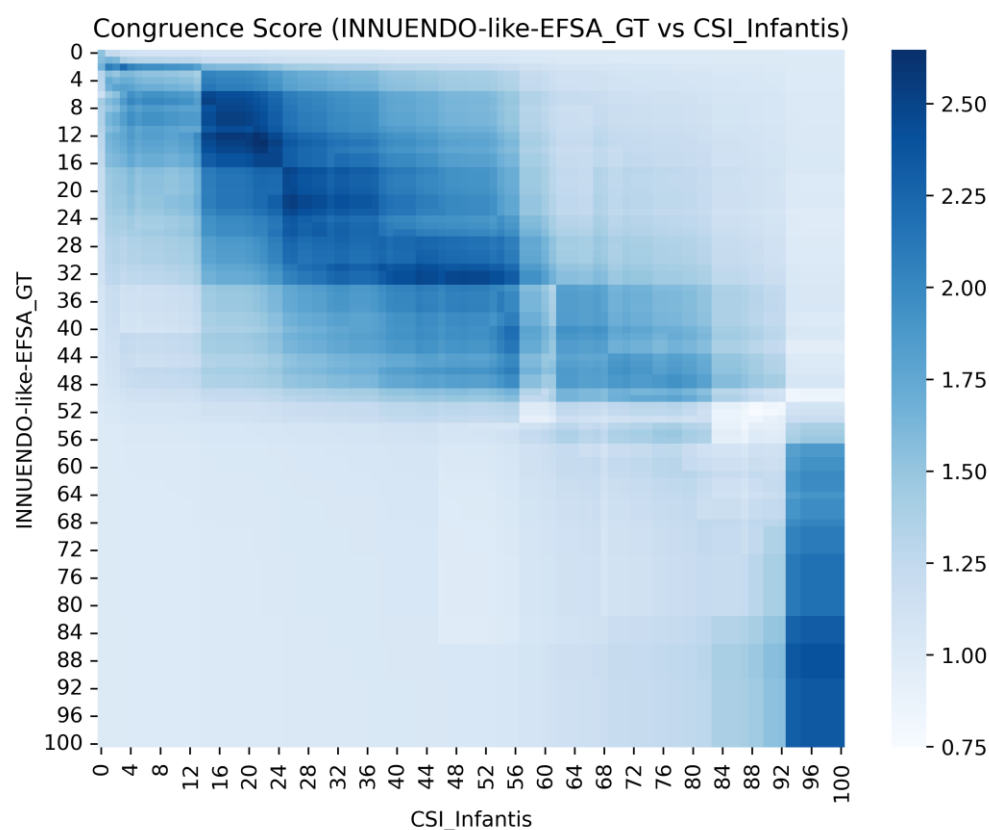


Figure S4.10.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

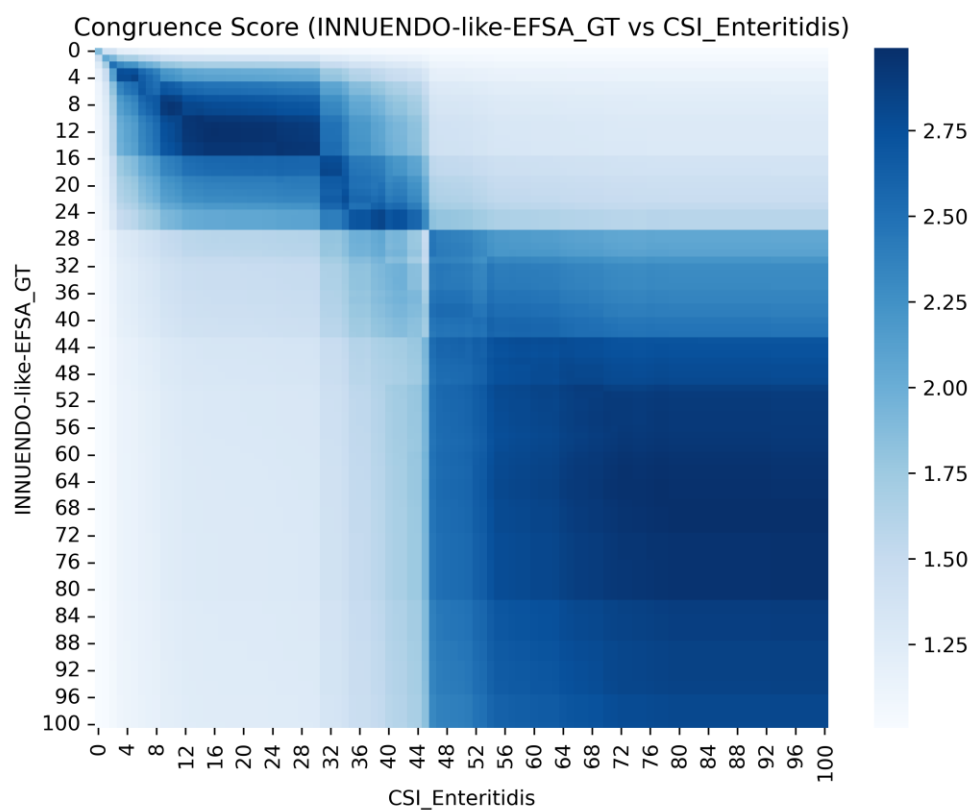


Figure S4.10.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

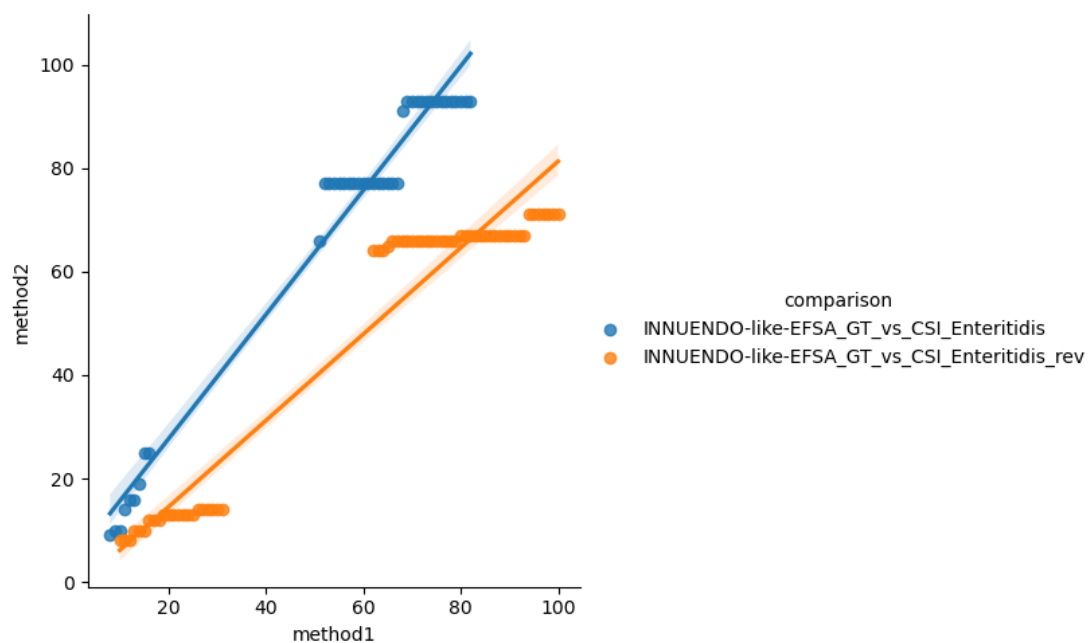


Figure S4.10.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 41 (blue) and 61 (orange) points is presented.

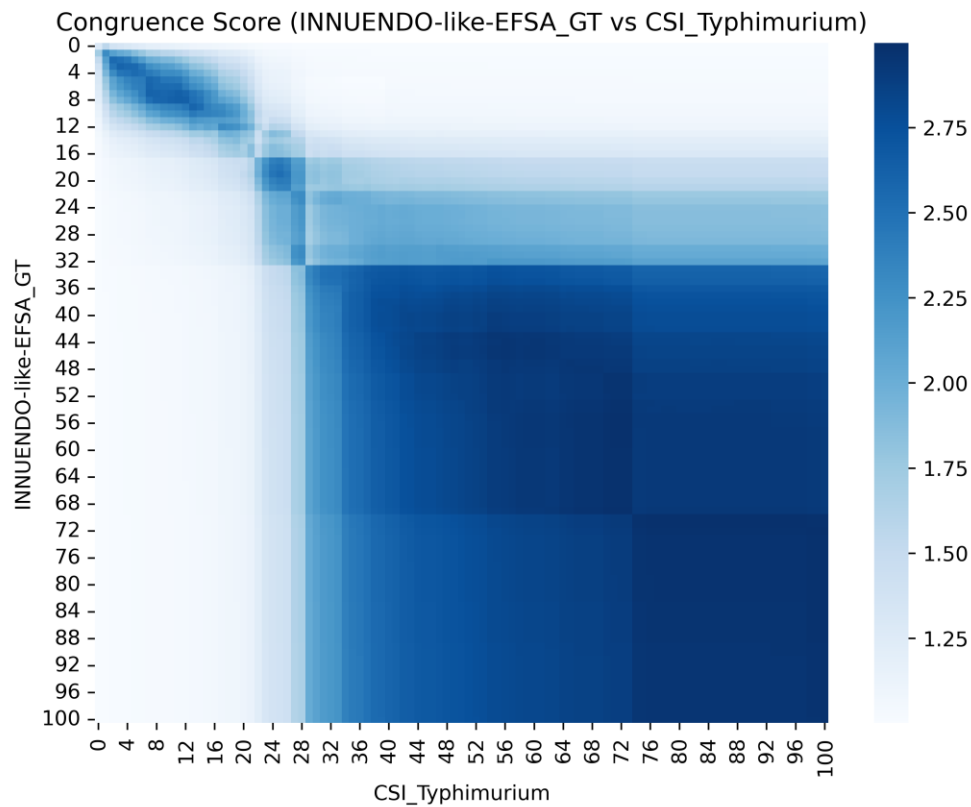


Figure S4.10.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

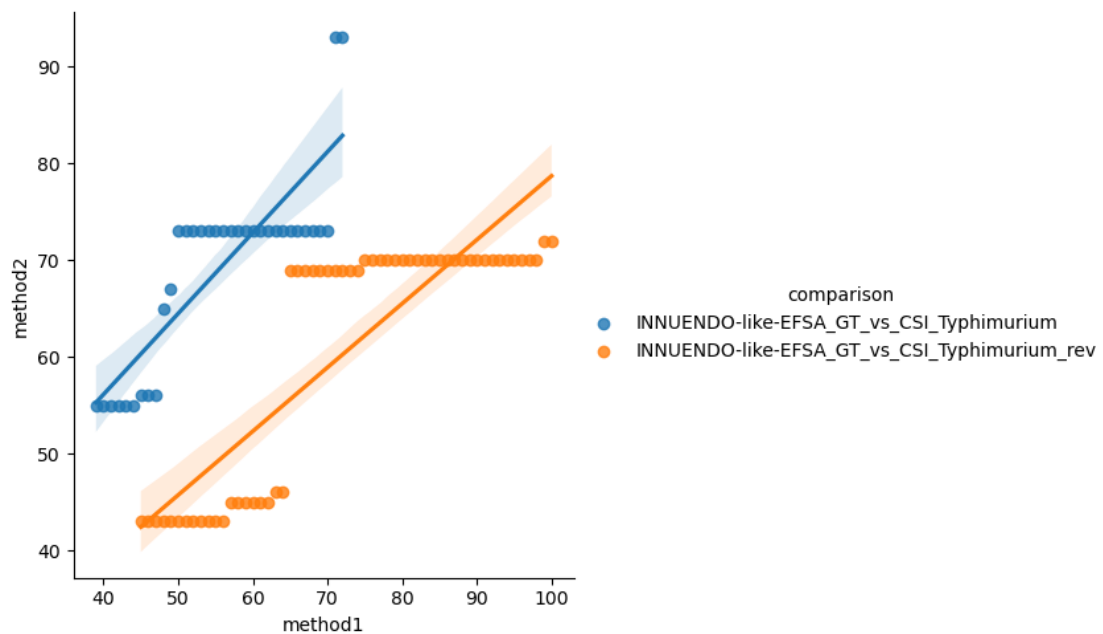


Figure S4.10.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 34 (blue) and 56 (orange) points is presented.

11. INNUENDO-like-EFSA GrapeTree vs. SnapperDB single-linkage

Table S4.11. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-EFSA GrapeTree	SnapperDB single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

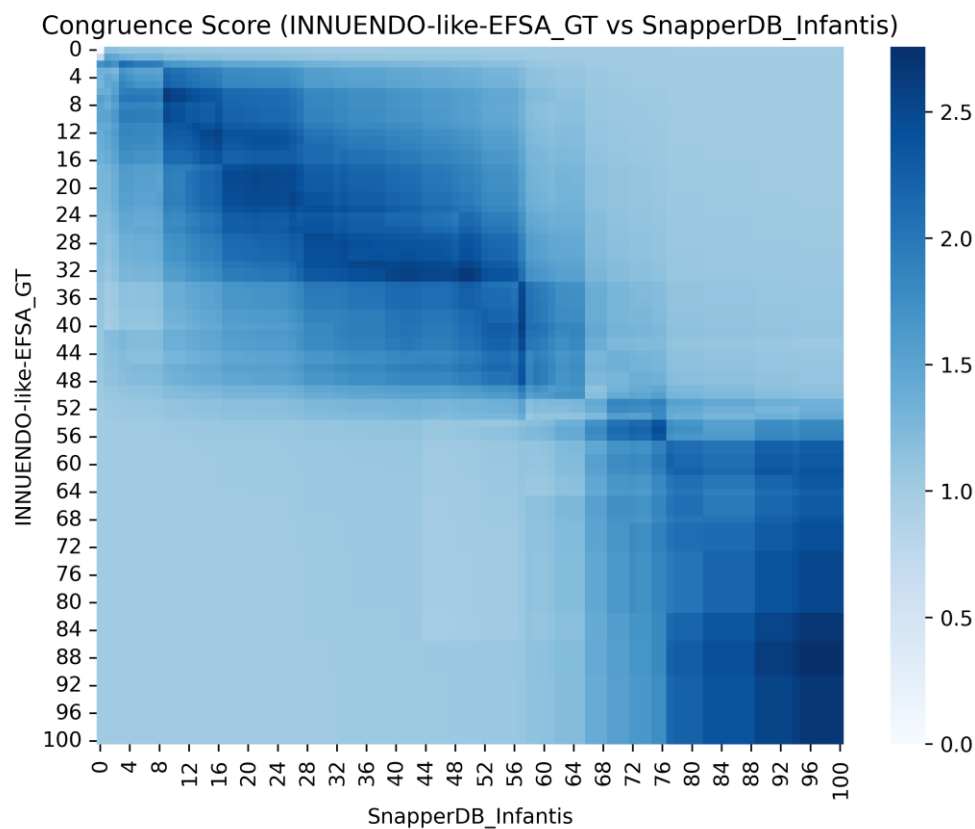


Figure S4.11.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

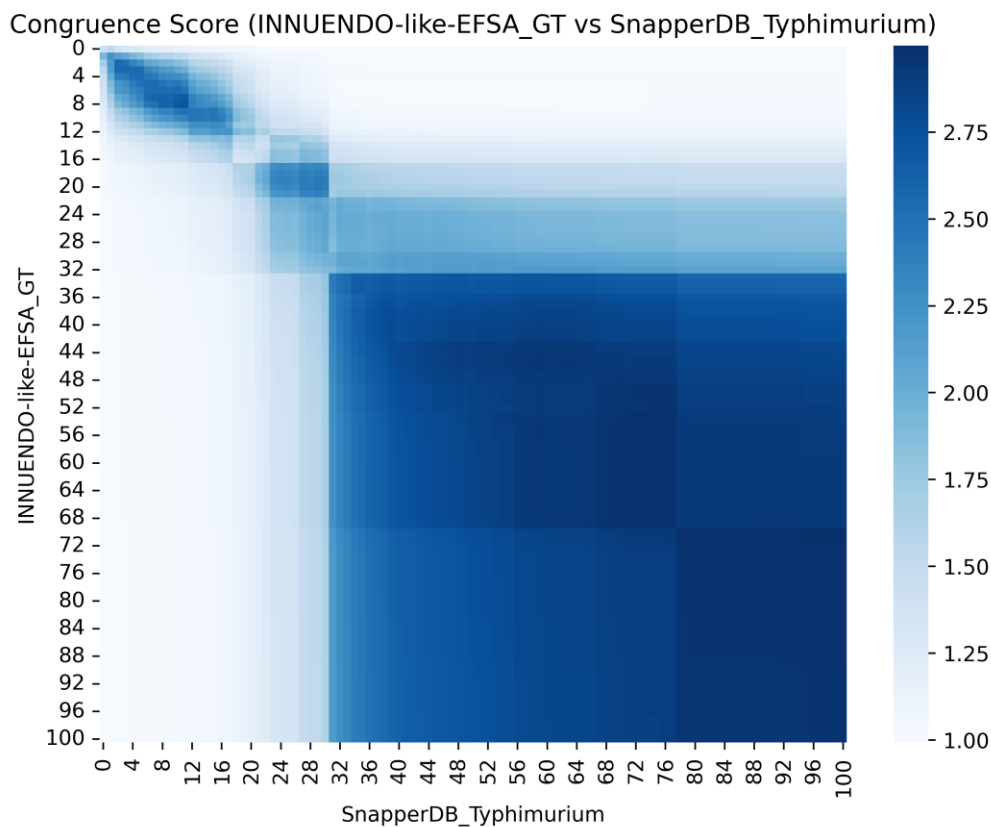


Figure S4.11.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

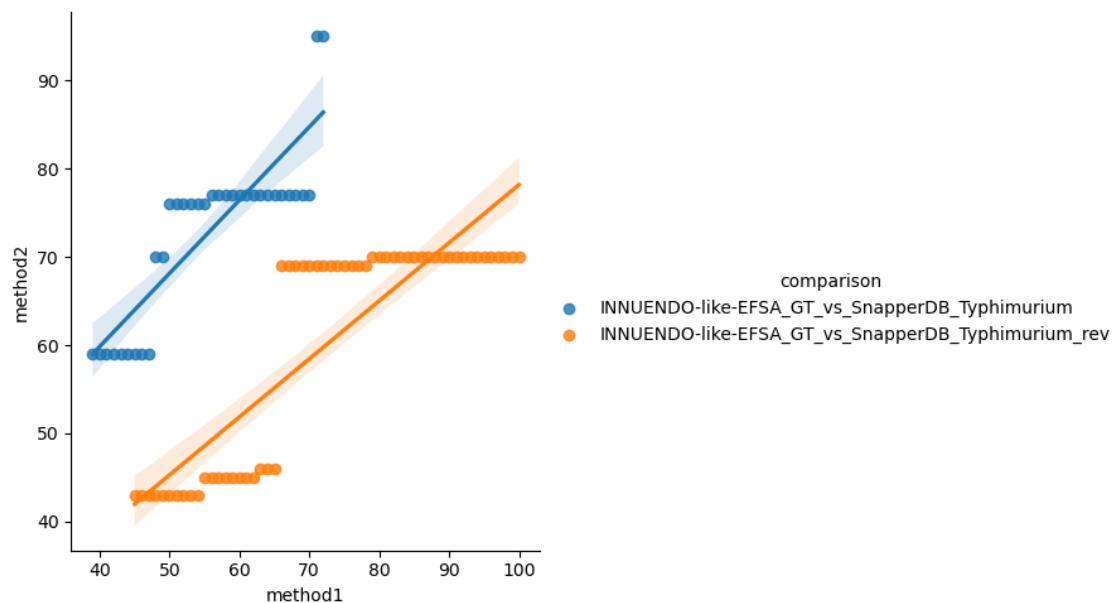


Figure S4.11.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 34 (blue) and 56 (orange) points is presented.

12. INNUENDO-like-EFSA GrapeTree vs. snippySnake single-linkage

Table S4.12. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-EFSA GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

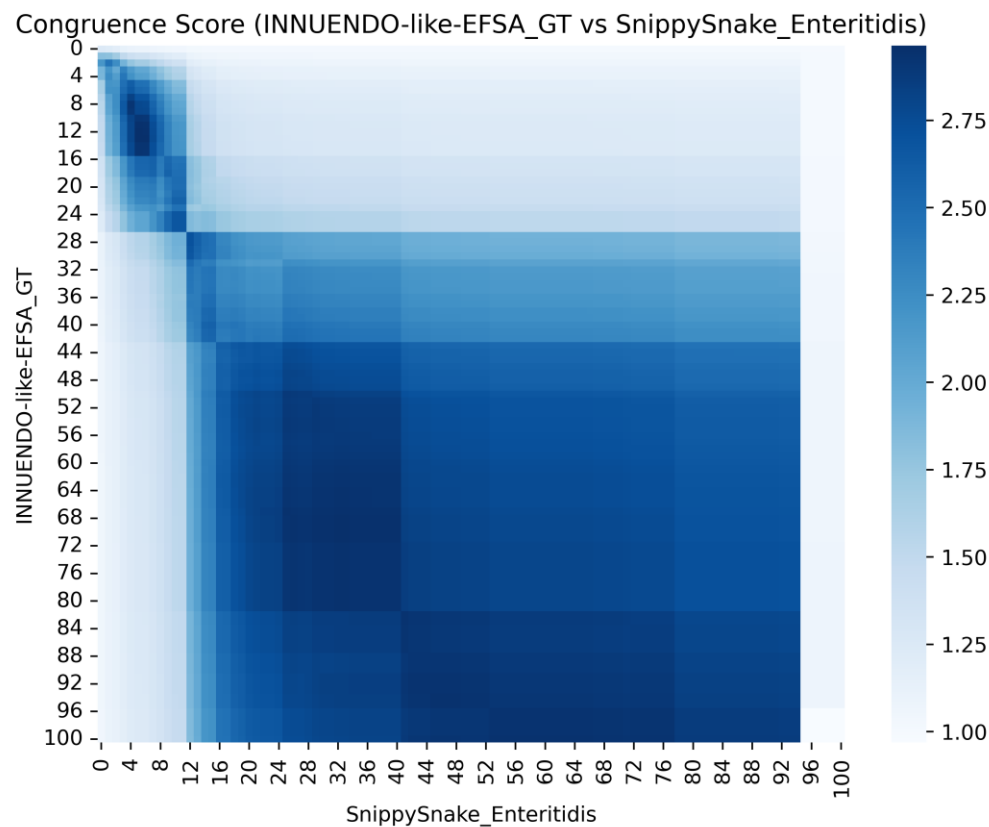


Figure S4.12.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

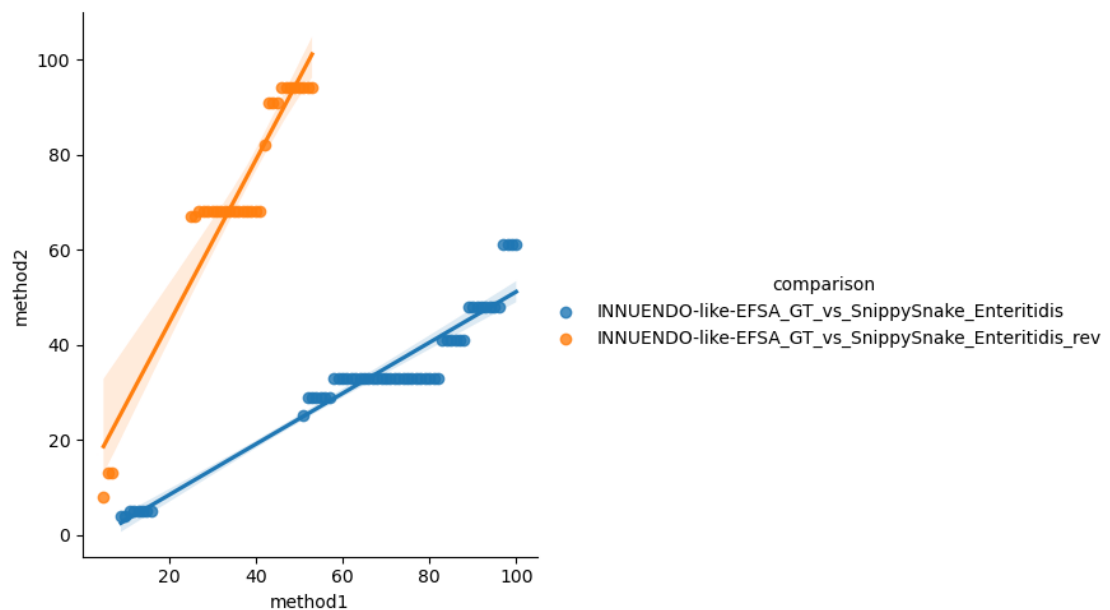


Figure S4.12.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 58 (blue) and 32 (orange) points is presented.

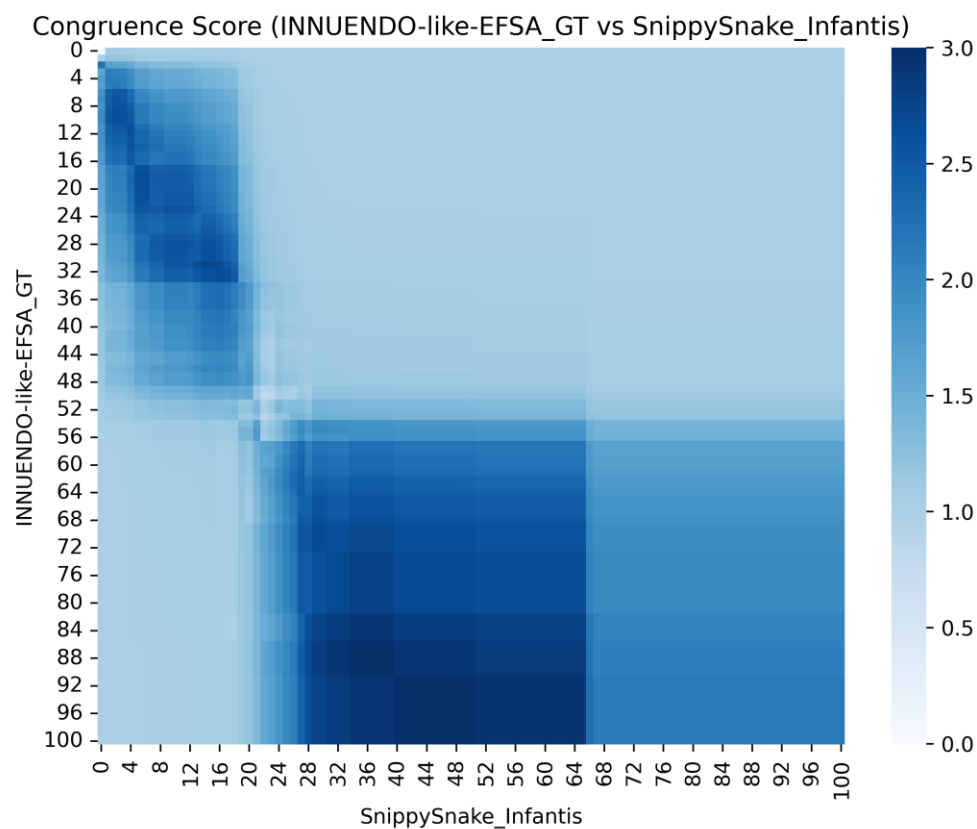


Figure S4.12.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

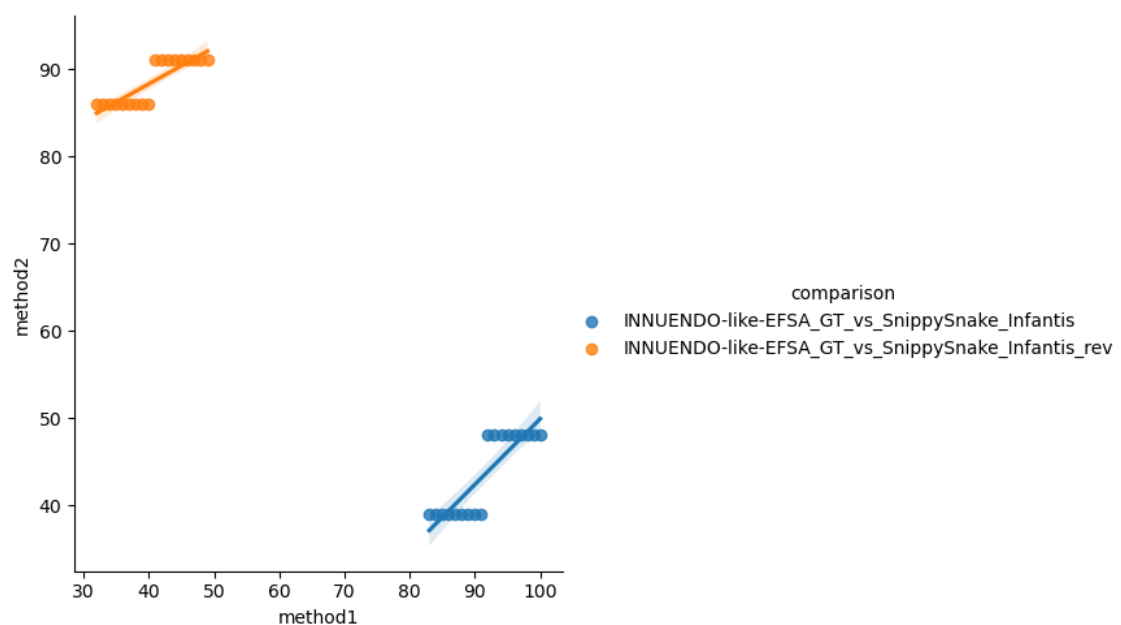


Figure S4.12.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Infantis. A linear tendency line supported by 18 (blue) and 18 (orange) points is presented.

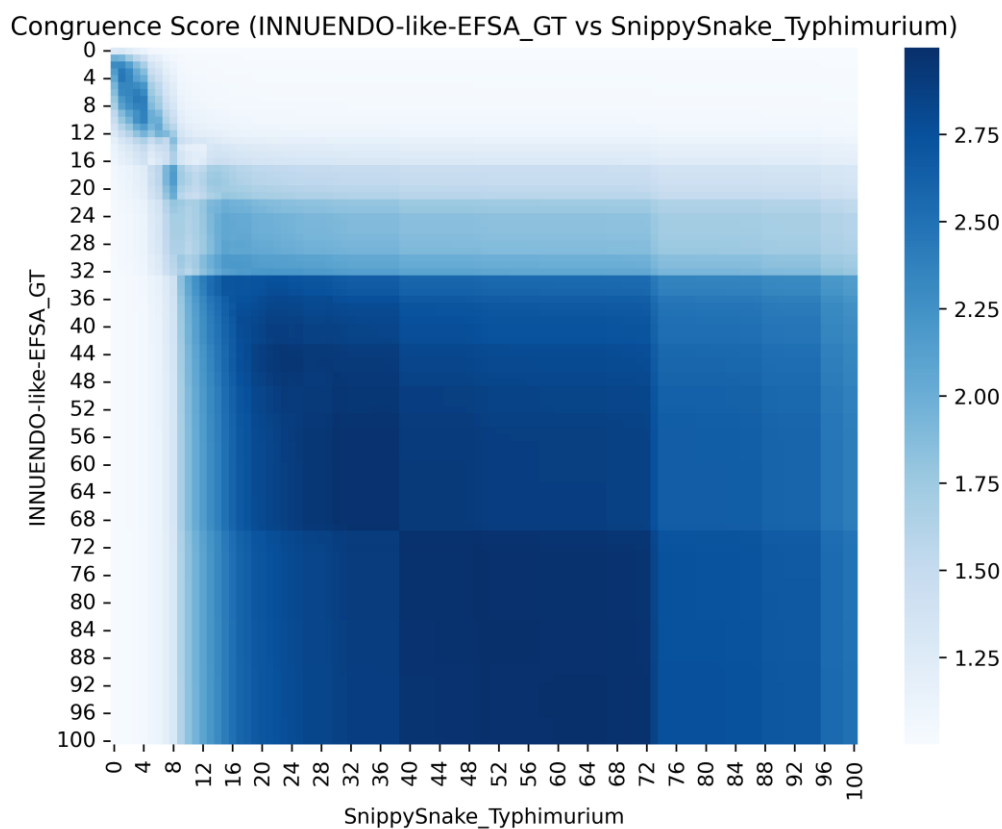


Figure S4.12.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

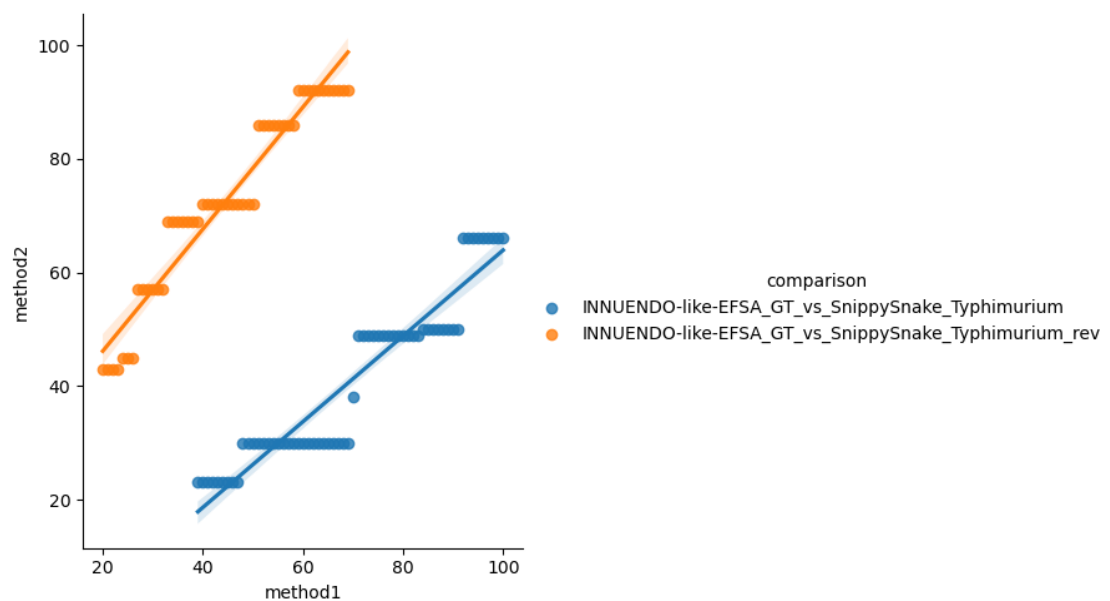


Figure S4.12.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 62 (blue) and 50 (orange) points is presented.

13. INNUENDO-like-EFSA single-linkage vs. CSI Phylogeny single-linkage

Table S4.13. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-EFSA single-linkage	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

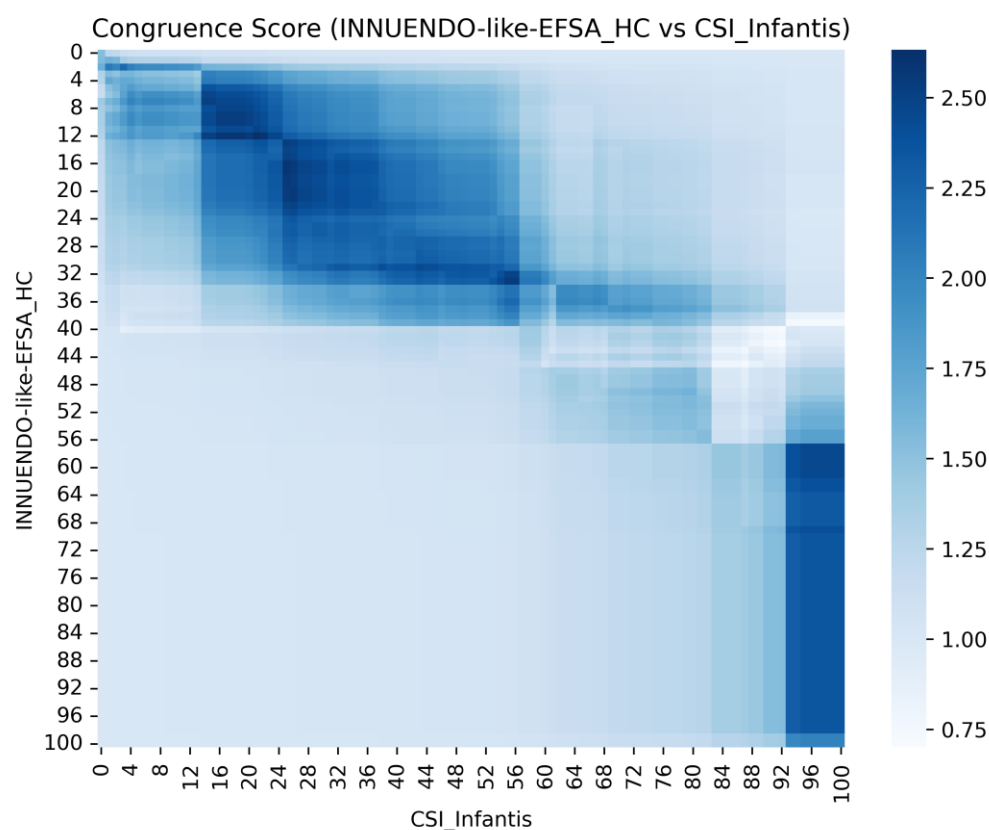


Figure S4.14.1 Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

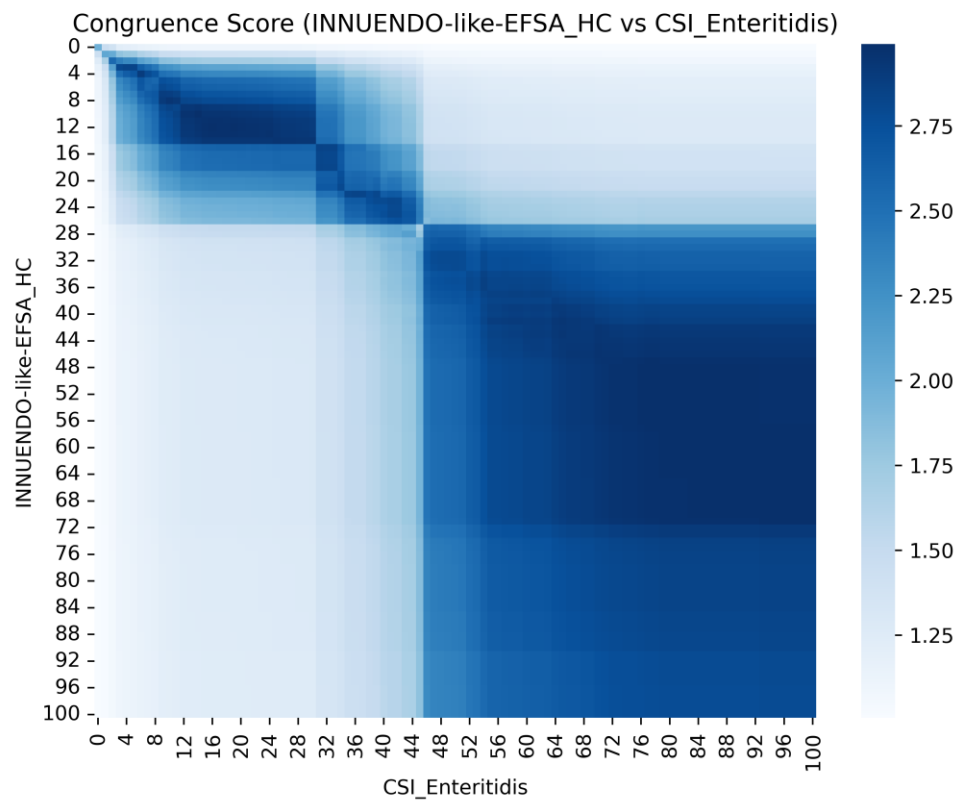


Figure S4.13.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

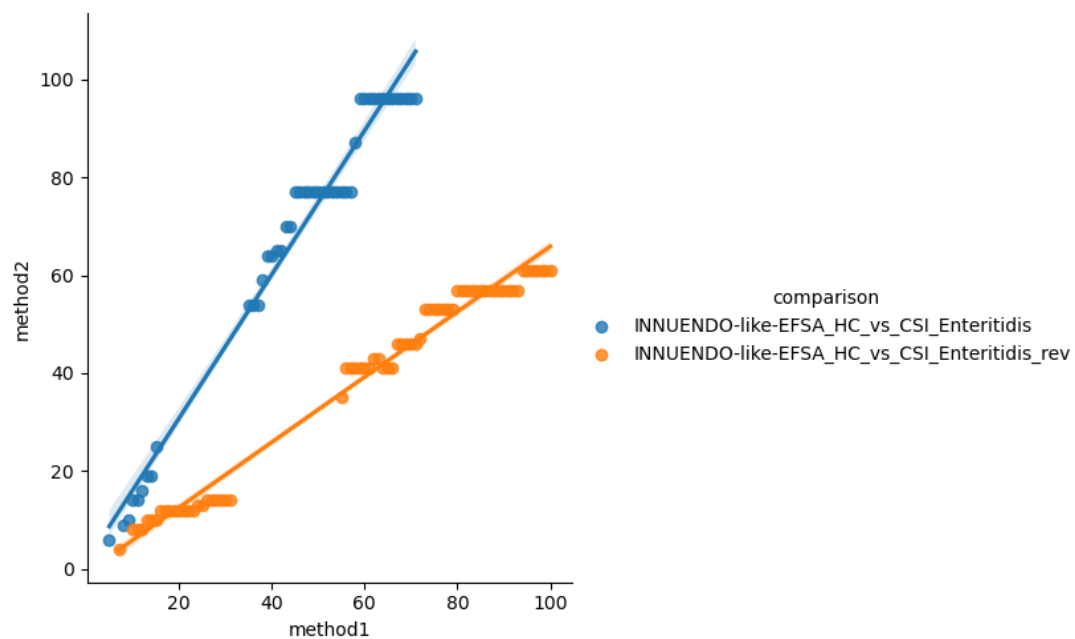


Figure S4.13.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 46 (blue) and 69 (orange) points is presented.

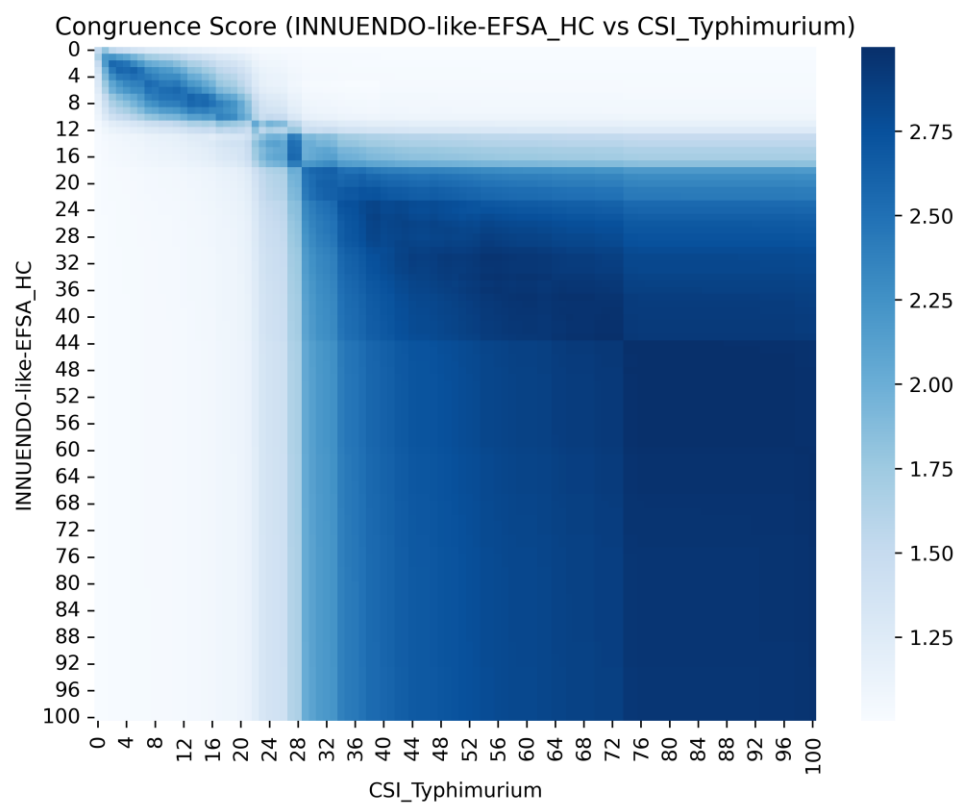


Figure S4.14.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

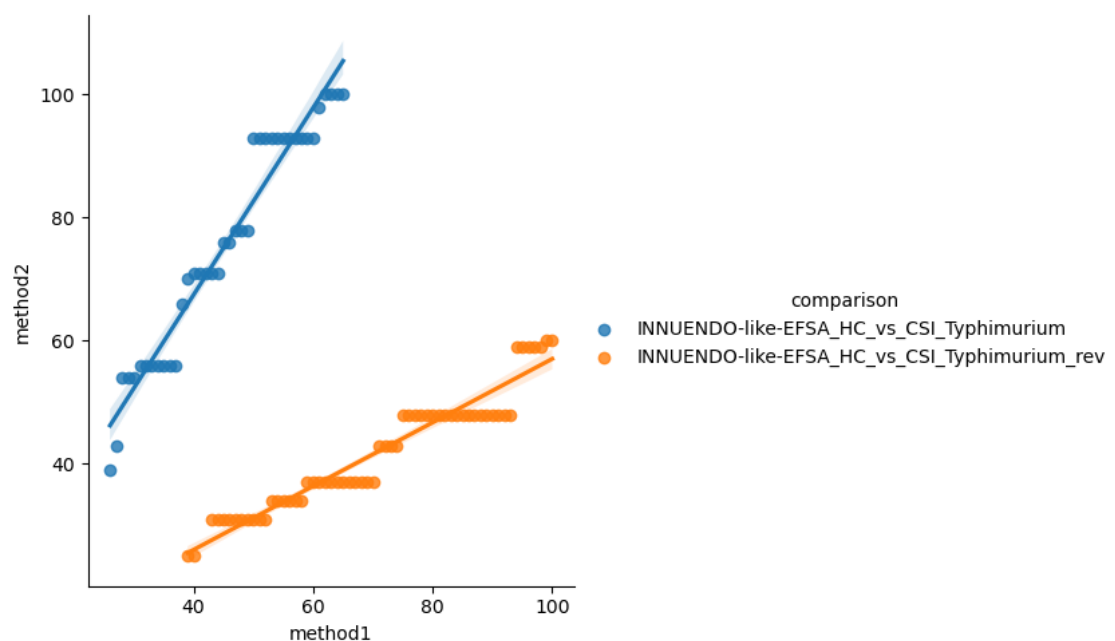


Figure S4.14.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 40 (blue) and 60 (orange) points is presented.

14. INNUENDO-like-EFSA single-linkage vs. SnapperDB single-linkage

Table S4.14. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-EFSA single-linkage	SnapperDB single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

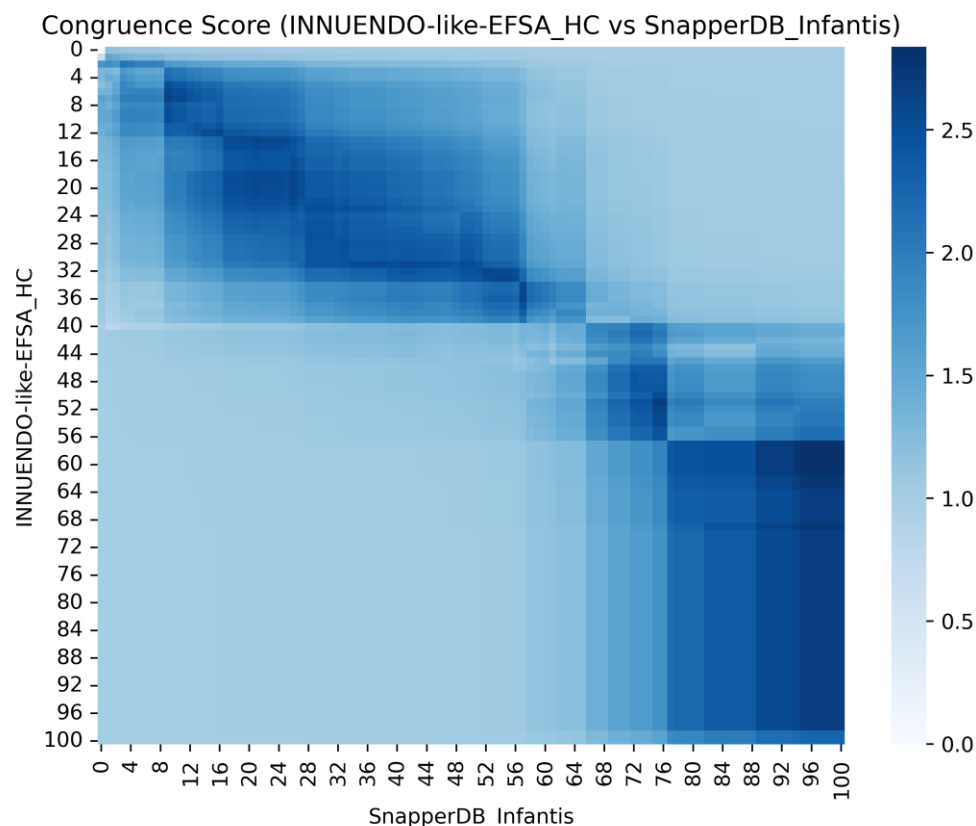


Figure S4.14.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

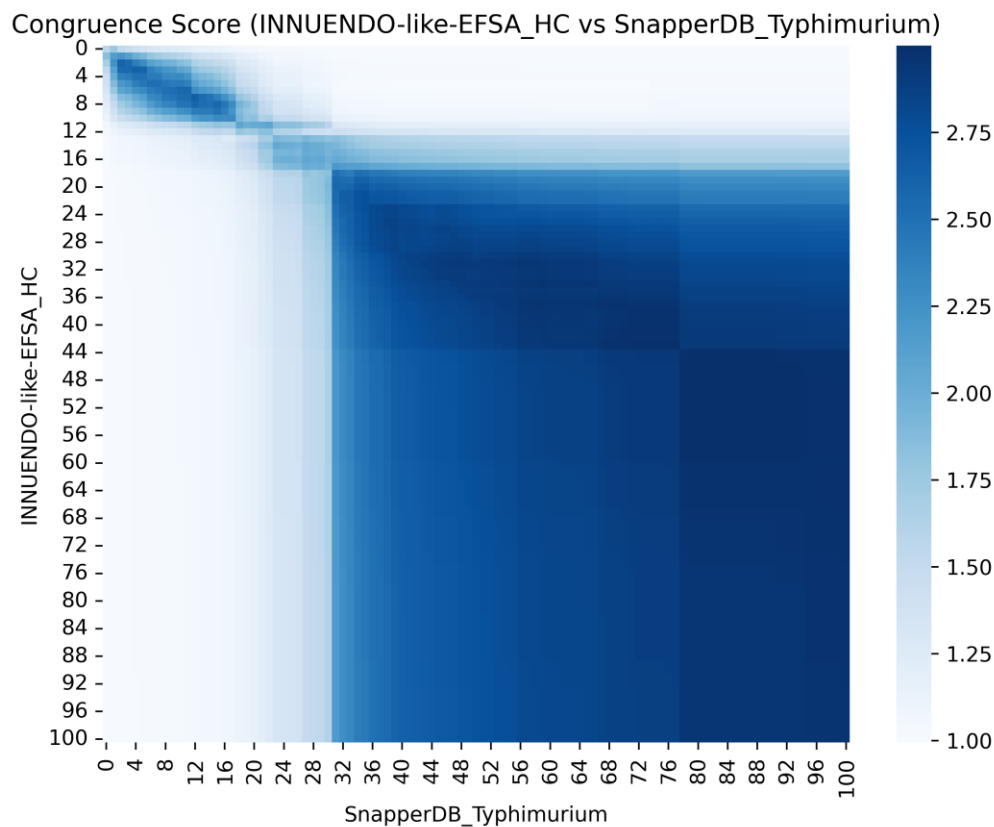


Figure S4.14.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

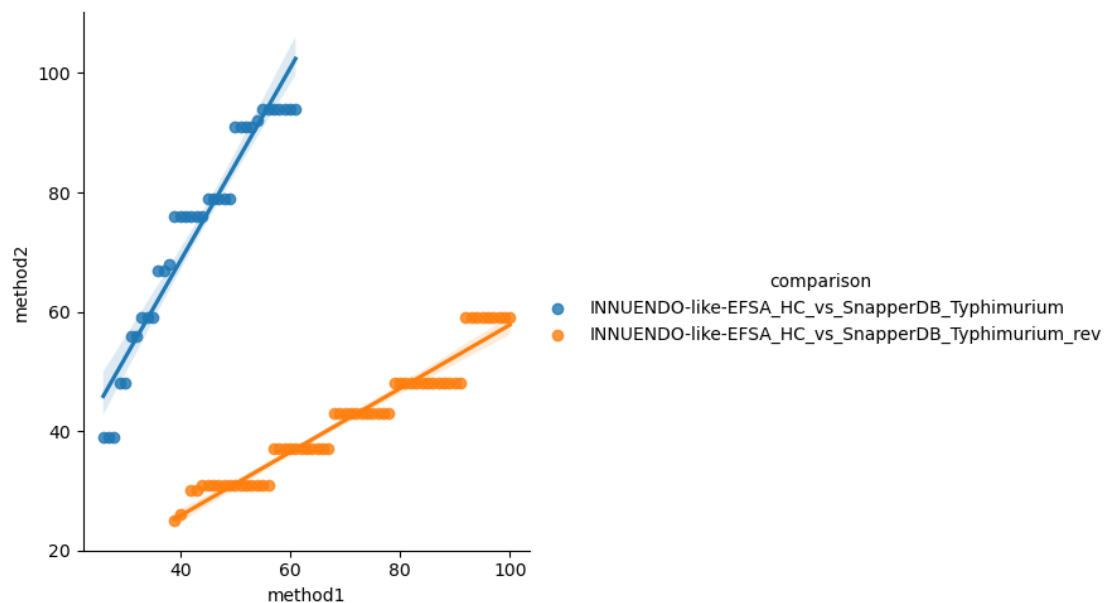


Figure S4.14.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 36 (blue) and 61 (orange) points is presented.

15. INNUENDO-like-EFSA single-linkage vs. snippySnake single-linkage

Table S4.15. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-EFSA single-linkage	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

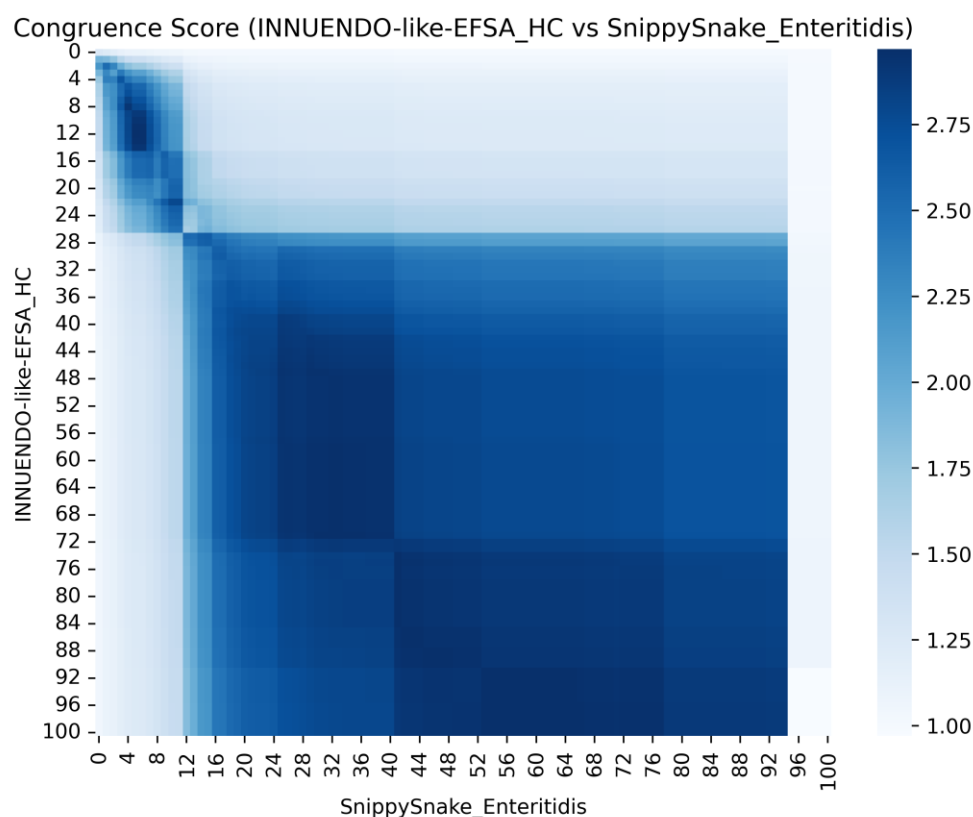


Figure S4.15.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

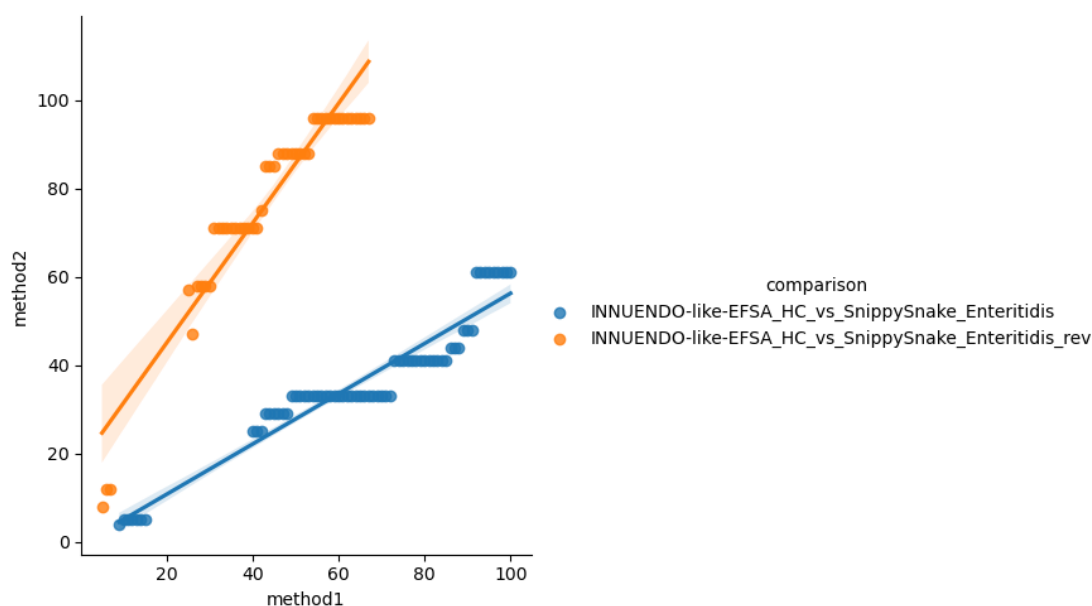


Figure S4.15.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 68 (blue) and 46 (orange) points is presented.

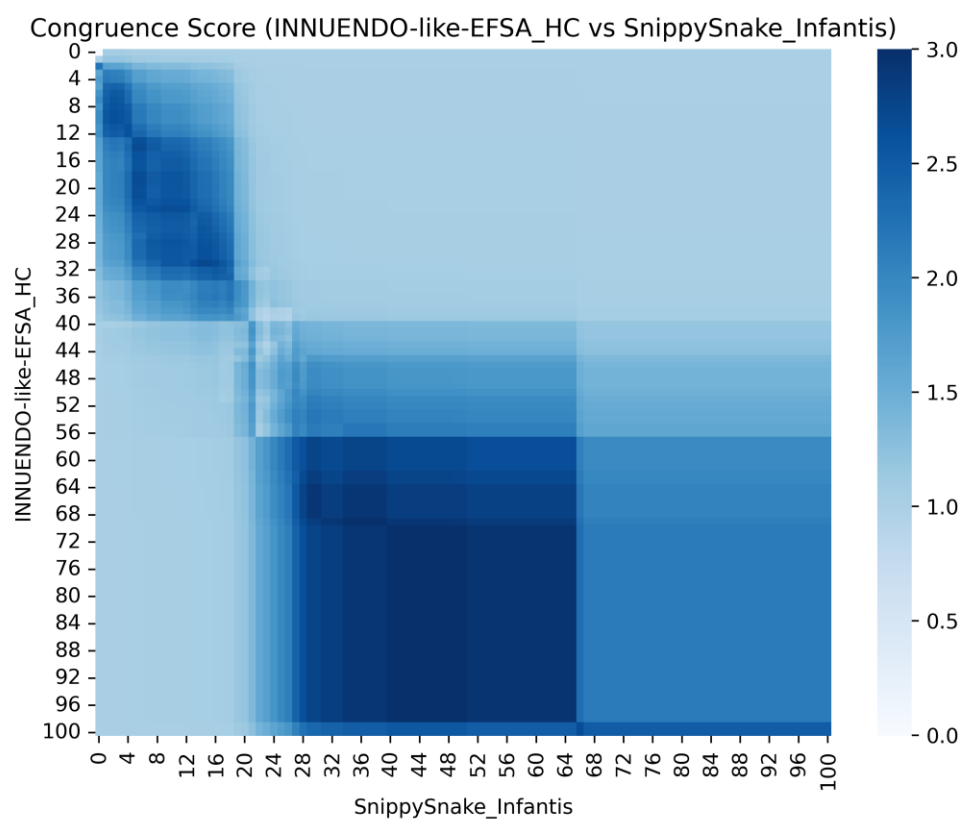


Figure S4.15.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

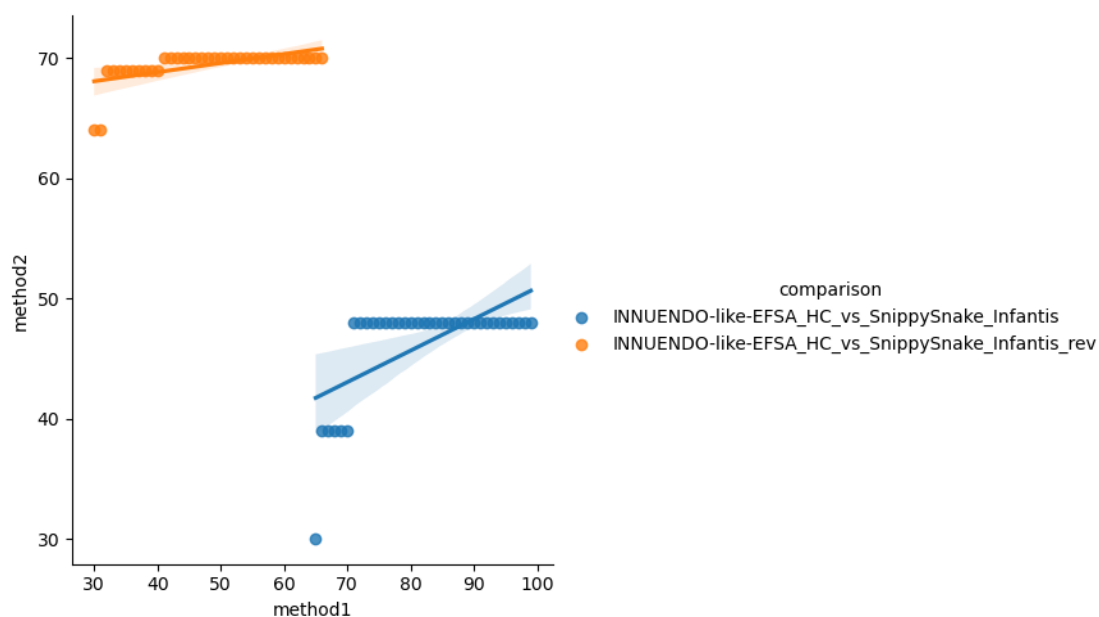


Figure S4.15.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Infantis. A linear tendency line supported by 35 (blue) and 37 (orange) points is presented.

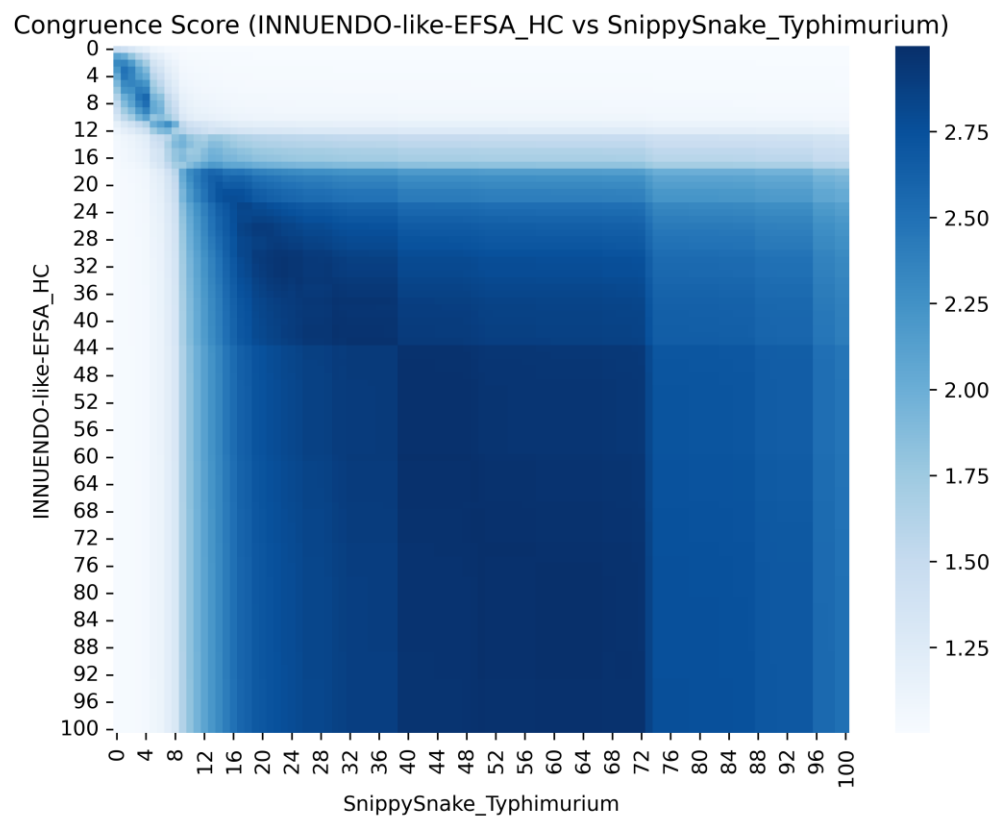


Figure S4.15.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

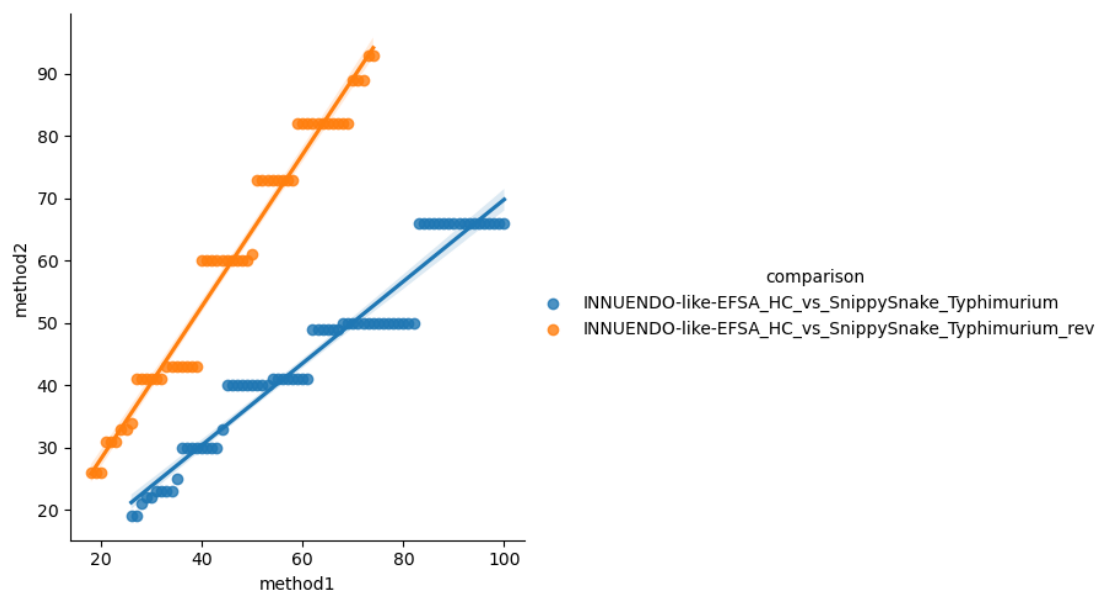


Figure S4.15.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 75 (blue) and 57 (orange) points is presented.

16. INNUENDO-like-Enterobase GrapeTree vs. CSI Phylogeny single-linkage

Table S4.16. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-Enterobase GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage(ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

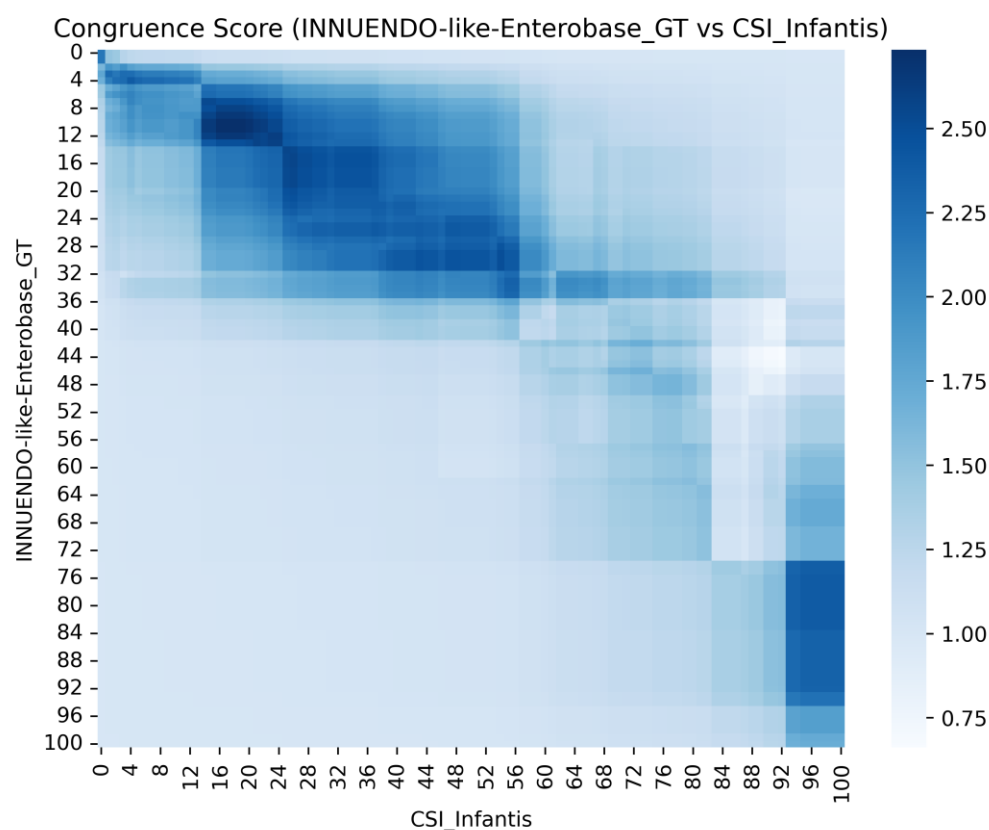


Figure S4.16.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

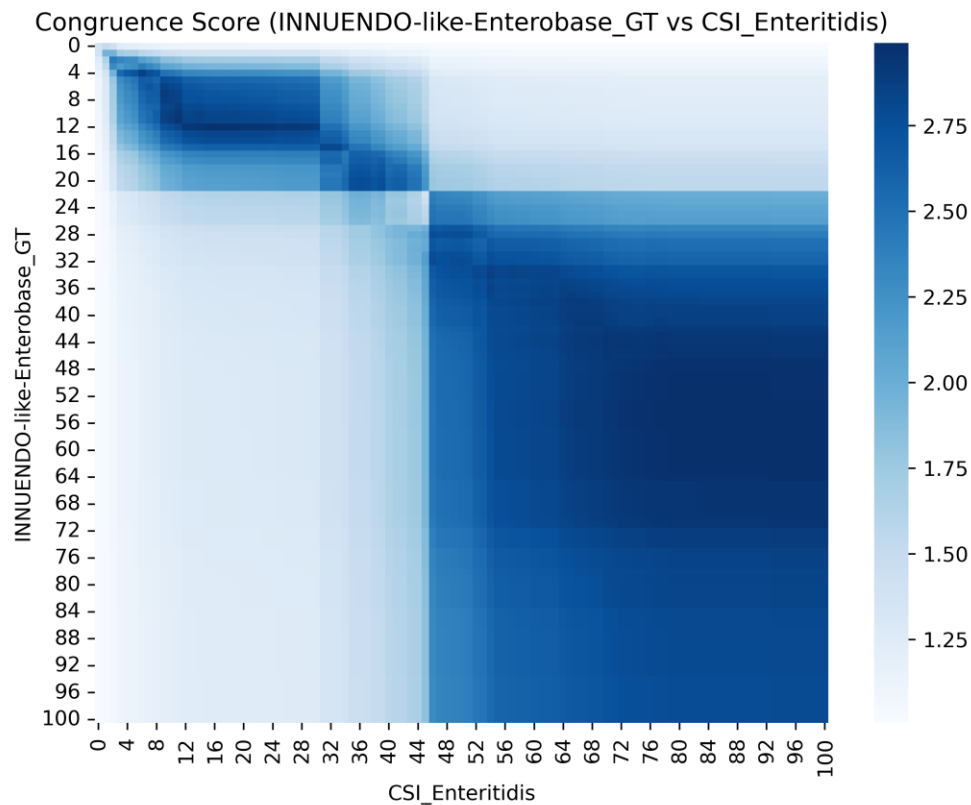


Figure S4.16.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

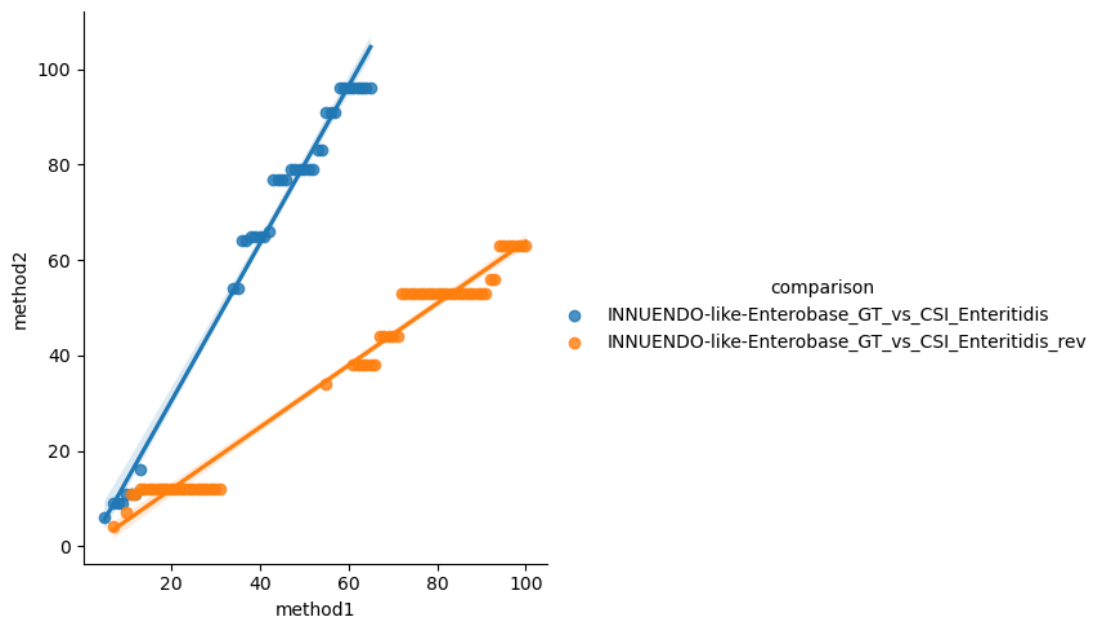


Figure S4.16.3. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Enteritidis. A linear tendency line supported by 40 (blue) and 64 (orange) points is presented.

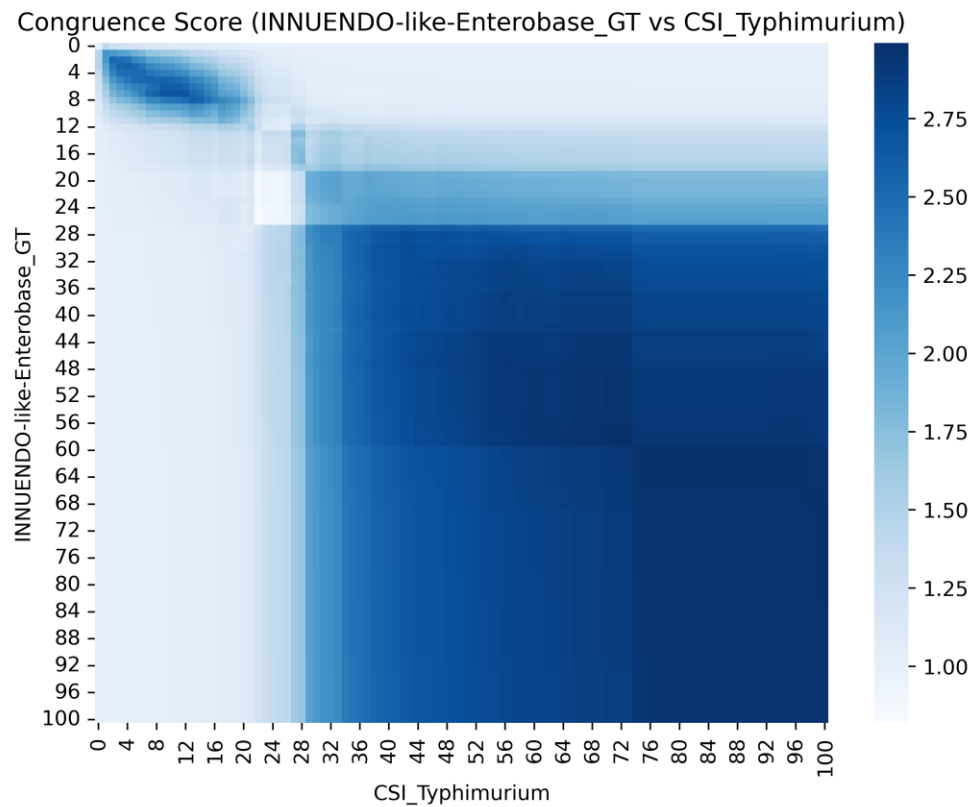


Figure S4.16.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

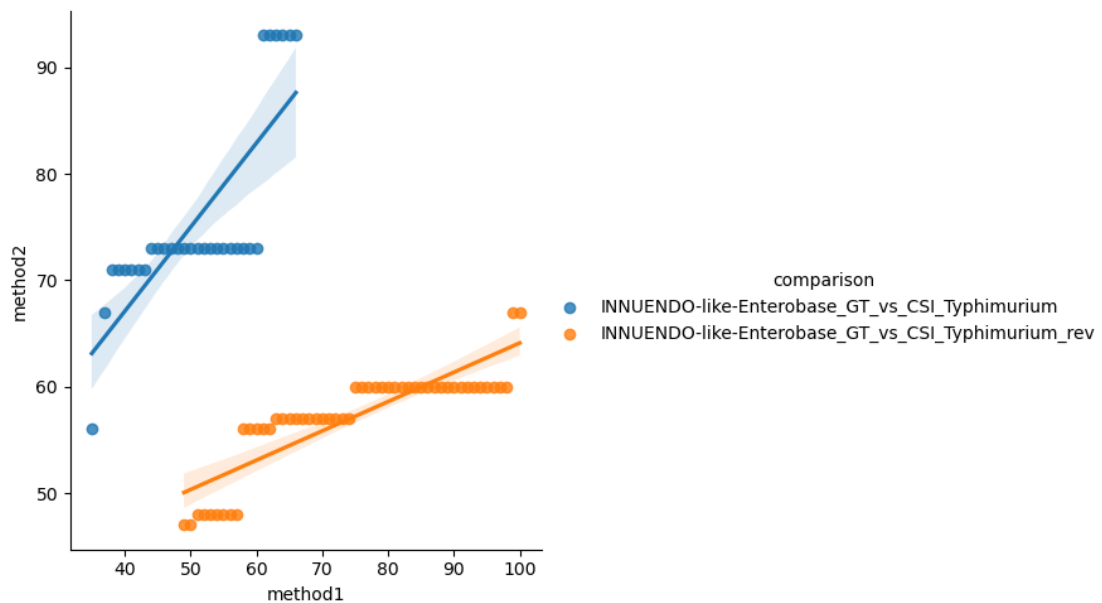


Figure S4.16.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 31 (blue) and 52 (orange) points is presented.

17. INNUENDO-like-Enterobase GrapeTree vs. SnapperDB single-linkage

Table S4.17. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-Enterobase GrapeTree	SnapperDB single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

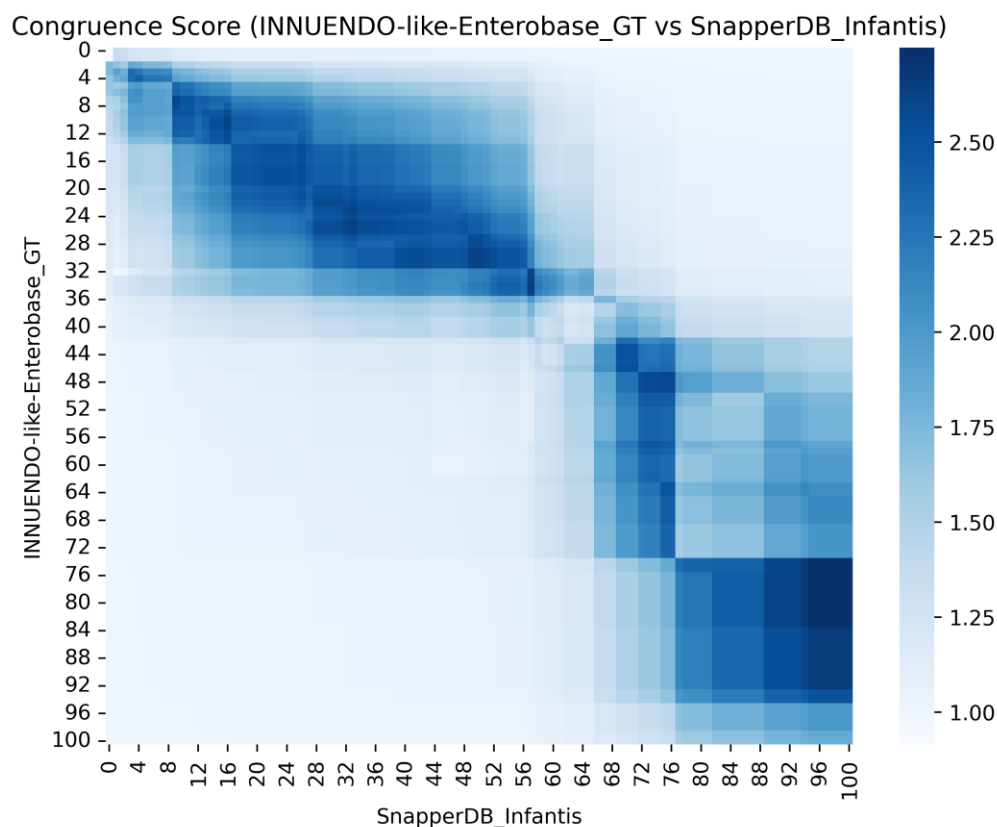


Figure S4.17.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

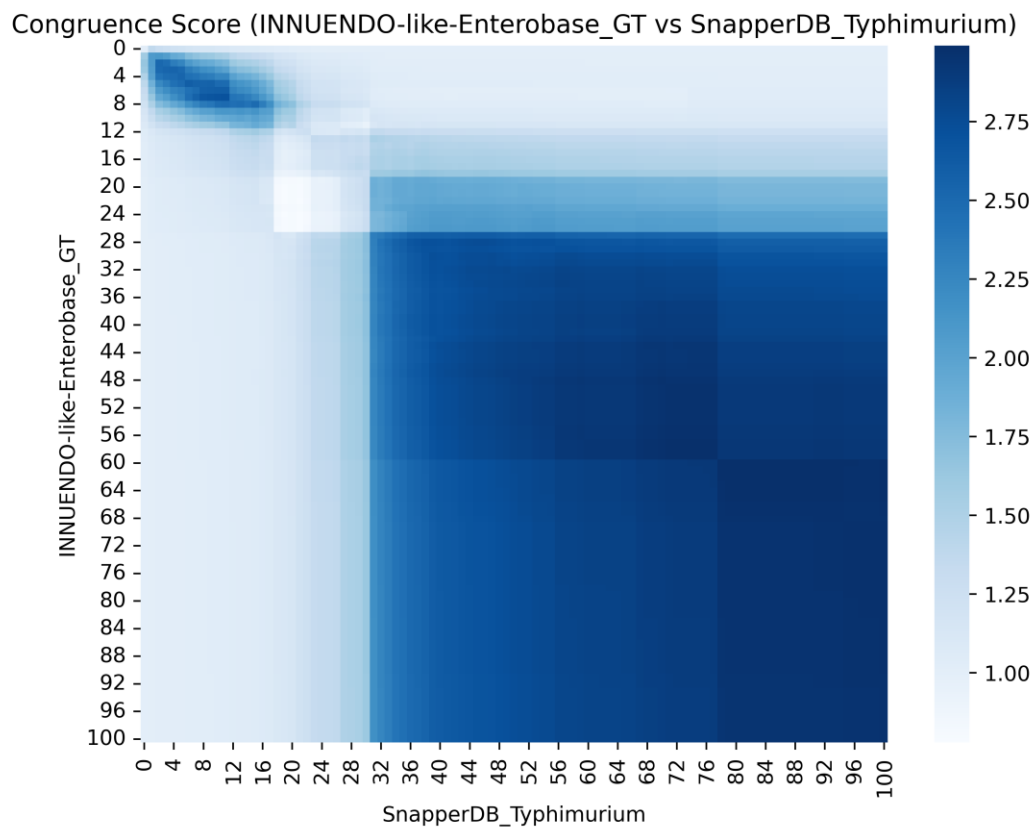


Figure S4.17.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

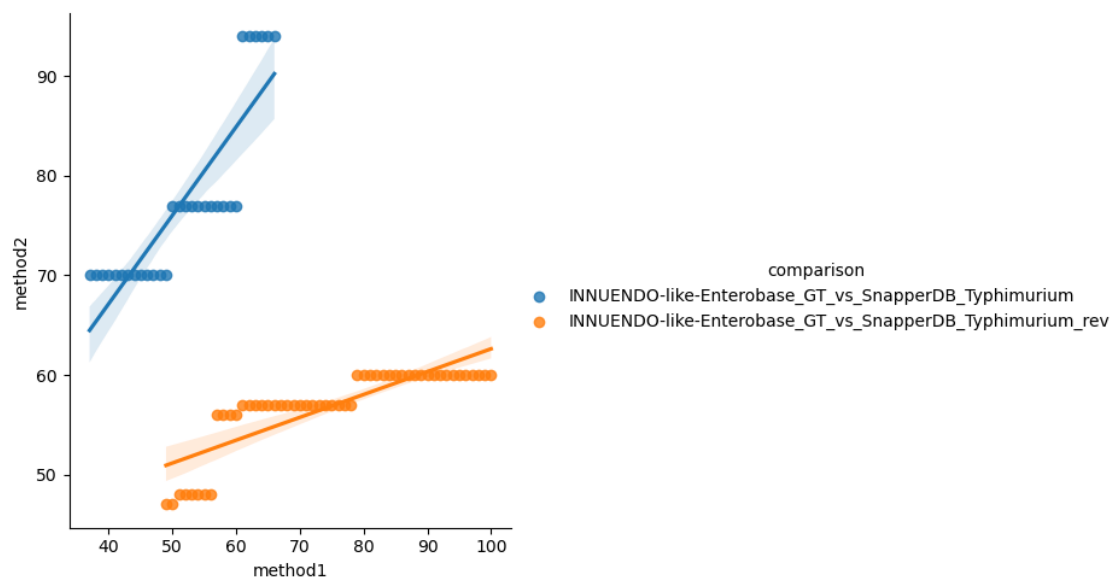


Figure S4.17.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 30 (blue) and 52 (orange) points is presented.

18. INNUENDO-like-Enterobase GrapeTree vs. snippySnake single-linkage

Table S4.18. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-Enterobase GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

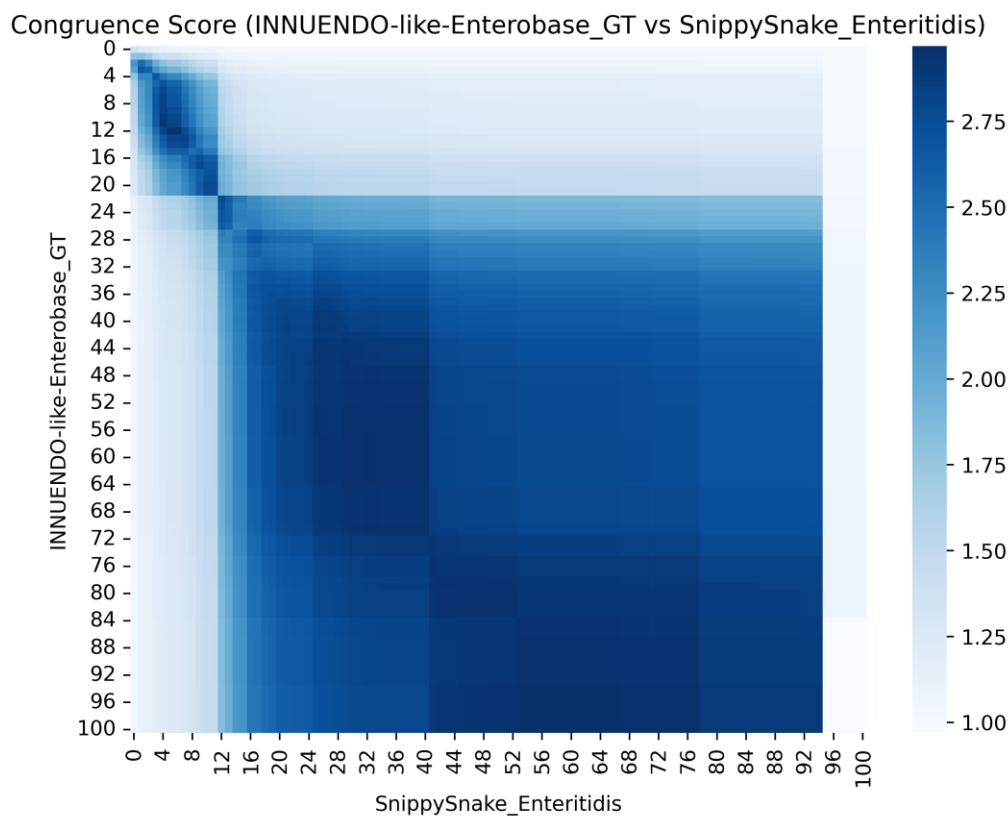


Figure S4.18.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

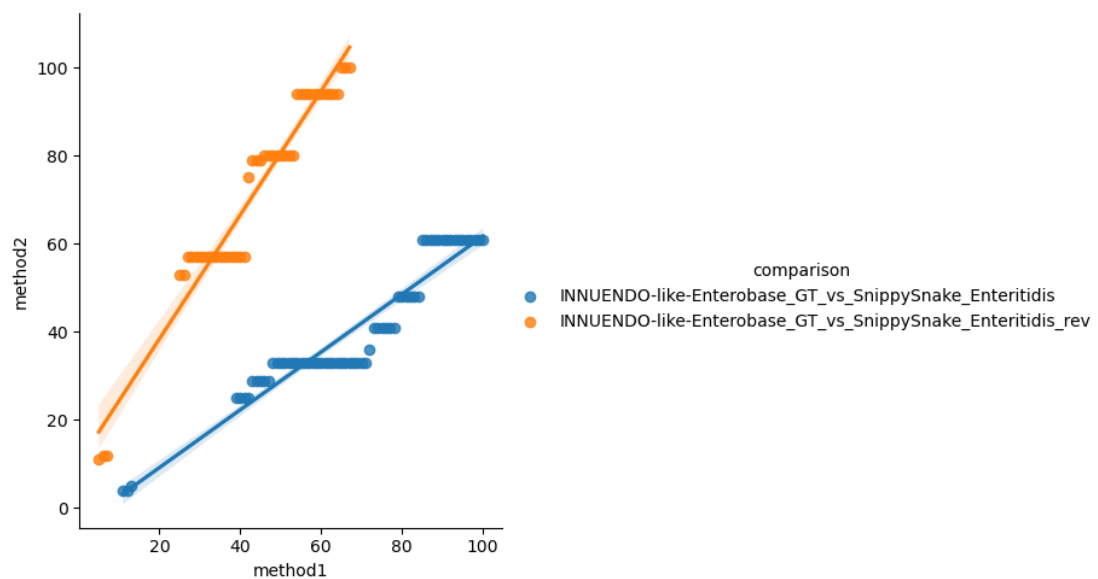


Figure S4.18.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 65 (blue) and 46 (orange) points is presented.

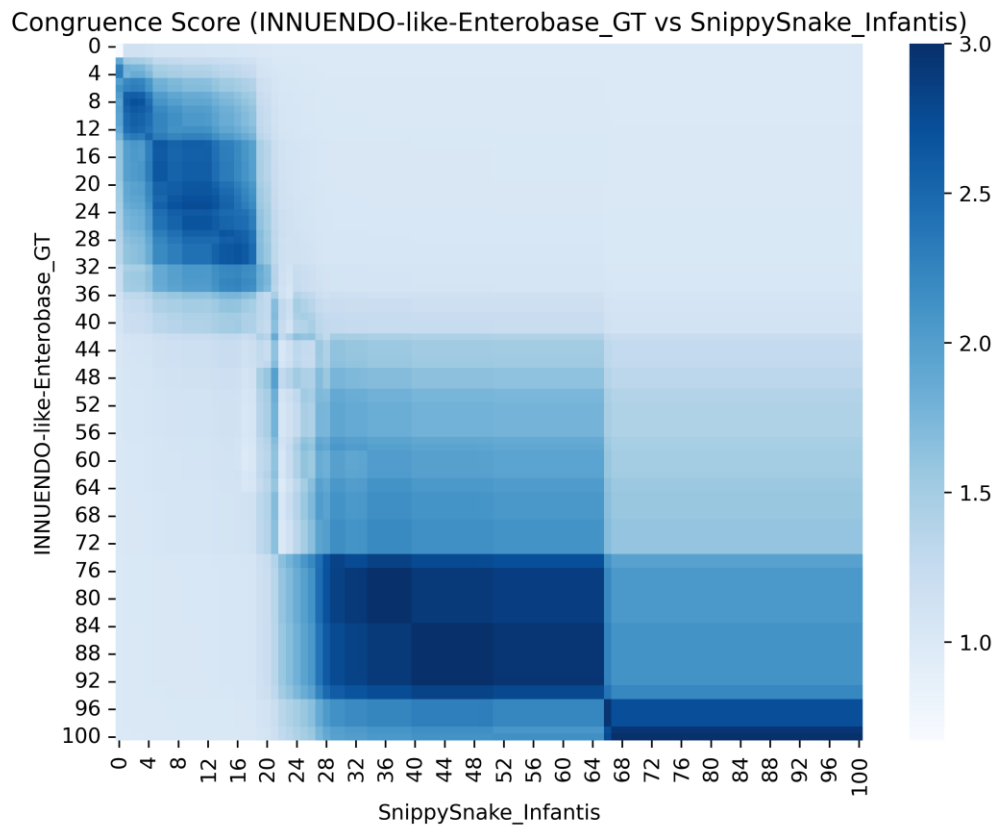


Figure S4.18.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

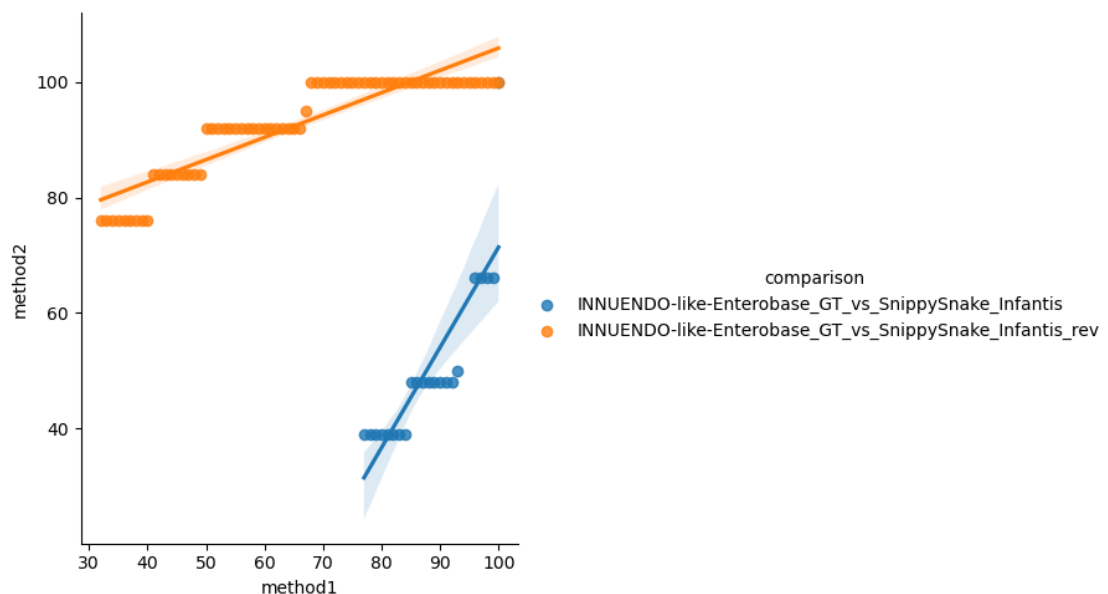


Figure S4.18.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Infantis. A linear tendency line supported by 22 (blue) and 69 (orange) points is presented.

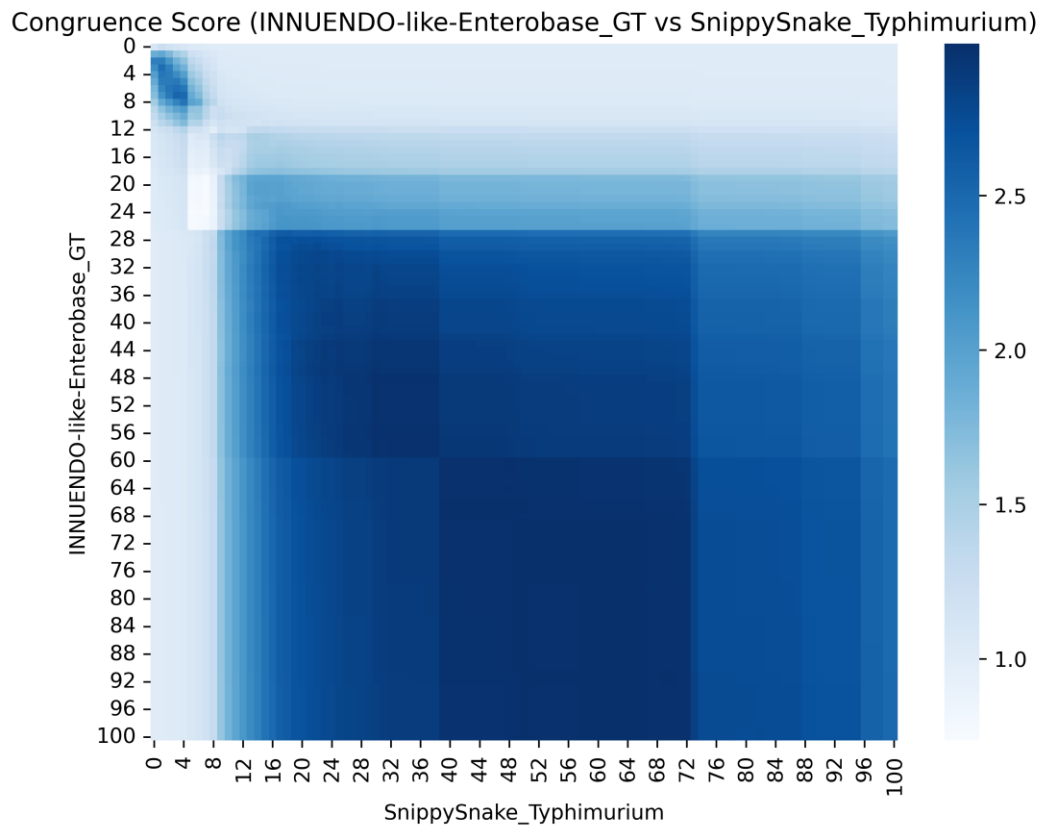


Figure S4.18.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

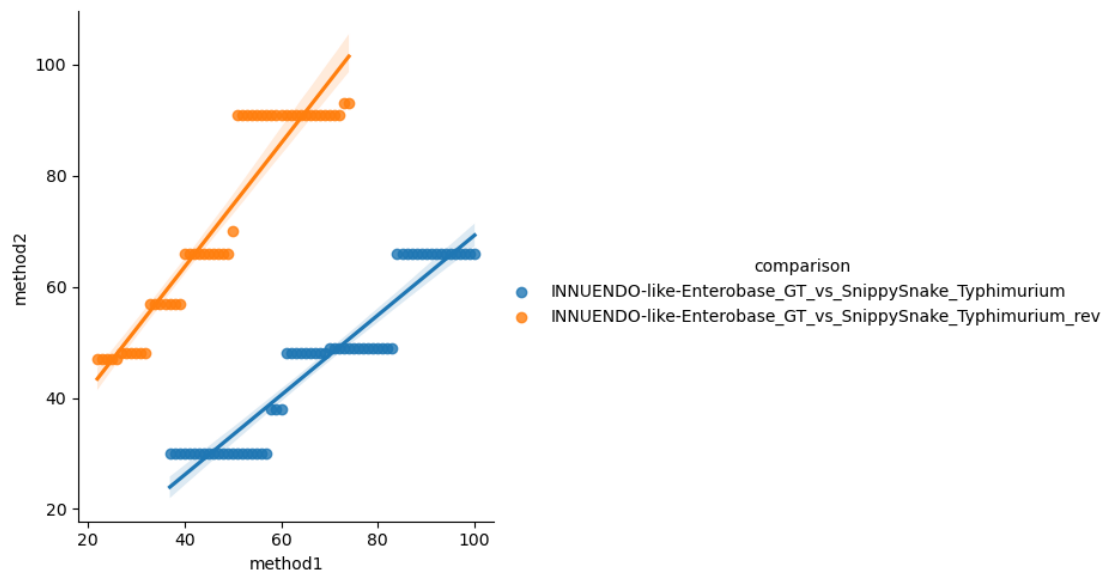


Figure S4.18.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 64 (blue) and 53 (orange) points is presented.

19. INNUENDO-like-Enterobase single-linkage vs. CSI Phylogeny single-linkage

Table S4.19. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-Enterobase single-linkage	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

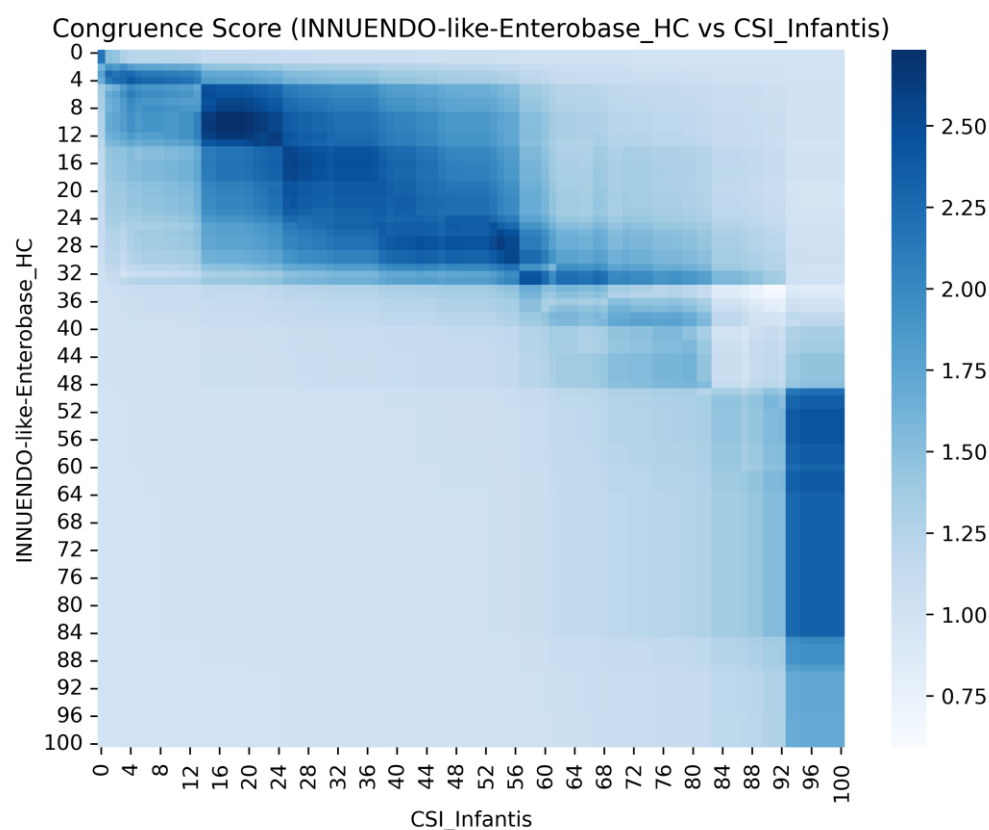


Figure S4.19.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

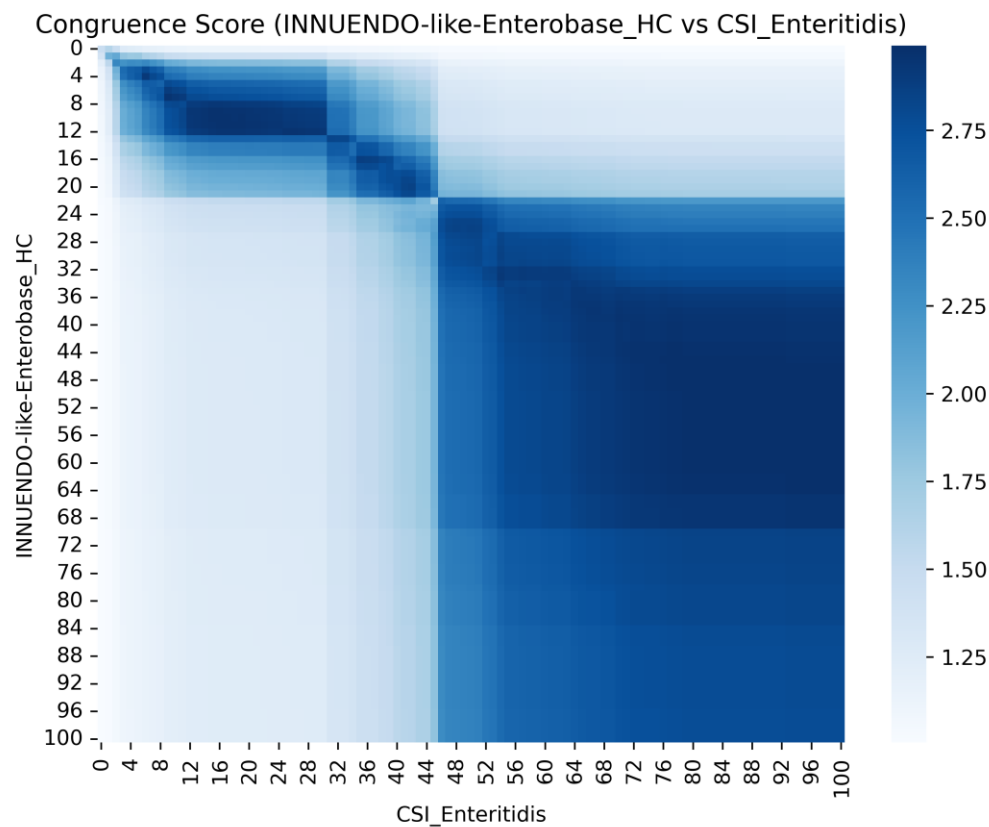


Figure S4.19.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

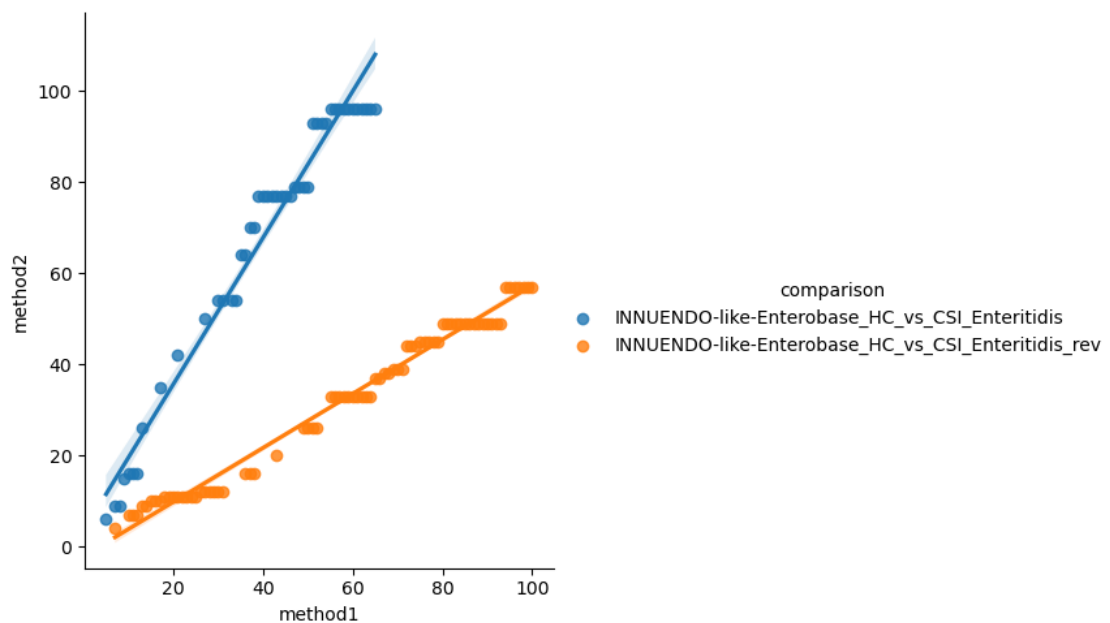


Figure S4.19.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 46 (blue) and 77 (orange) points is presented.

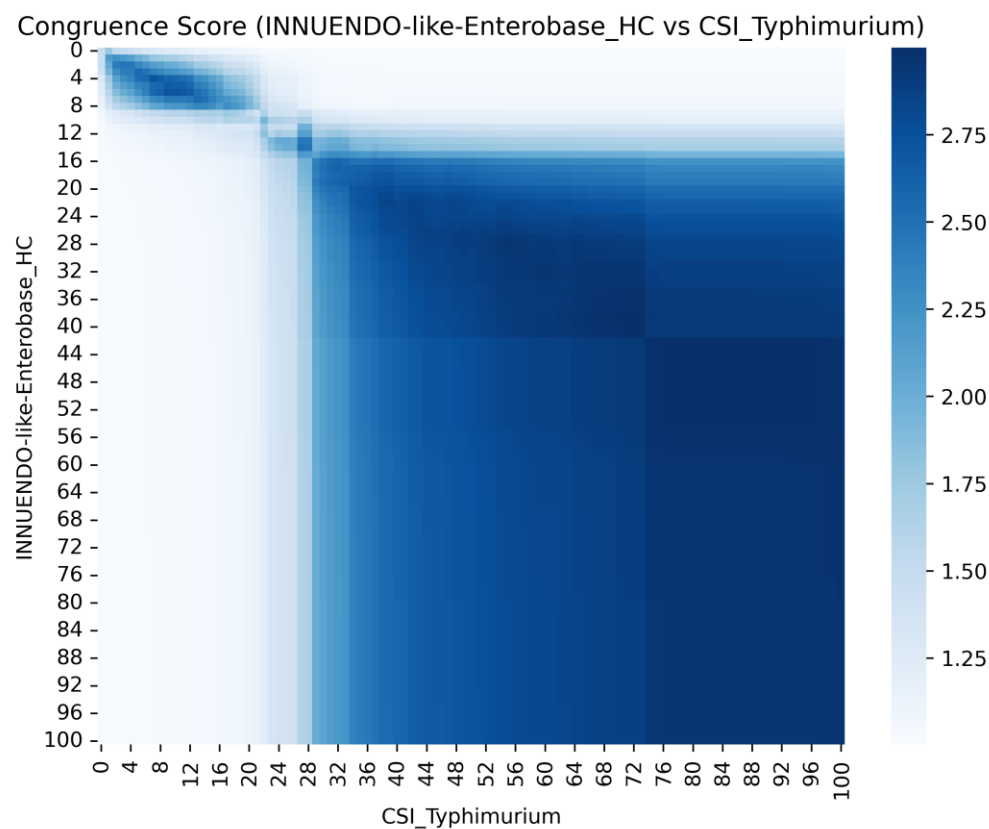


Figure S4.19.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

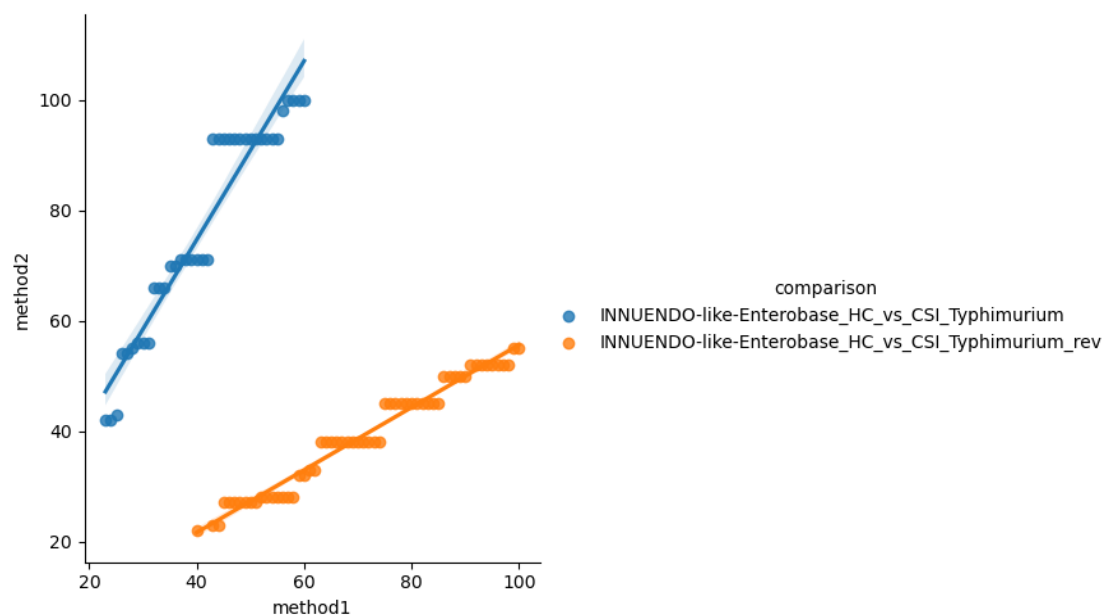


Figure S4.19.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 38 (blue) and 59 (orange) points is presented.

20. INNUENDO-like-Enterobase single-linkage vs. SnapperDB single-linkage

Table S4.20. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-Enterobase single-linkage	SnapperDB single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

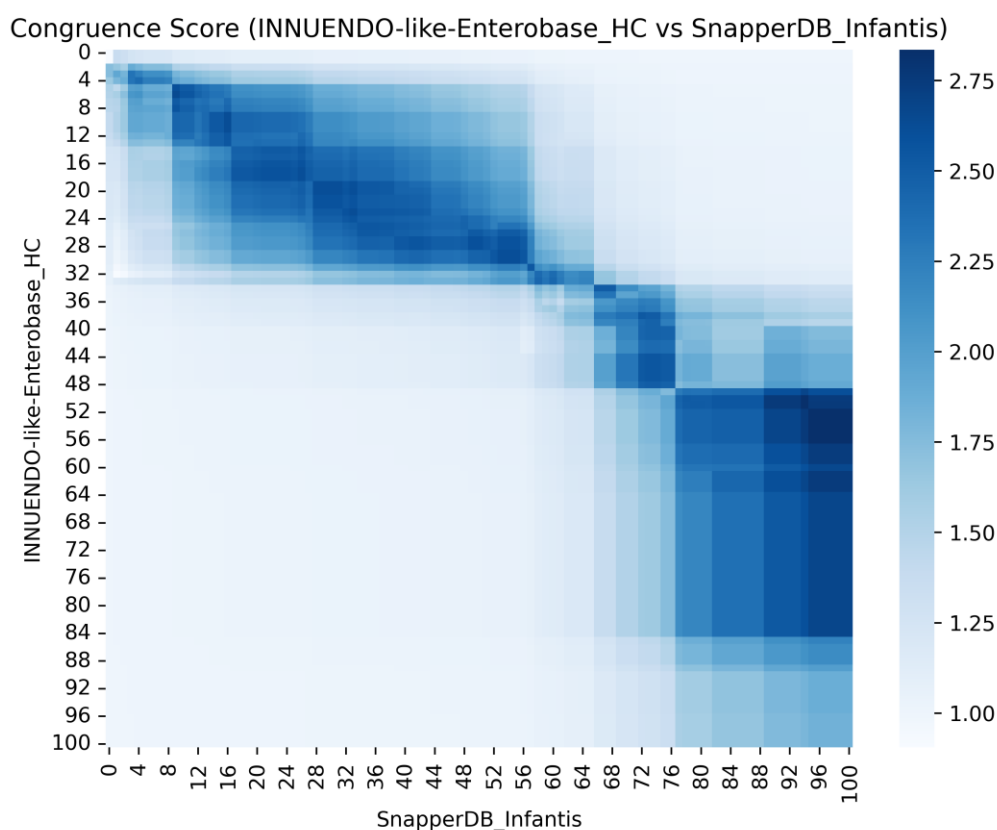


Figure S4.20.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

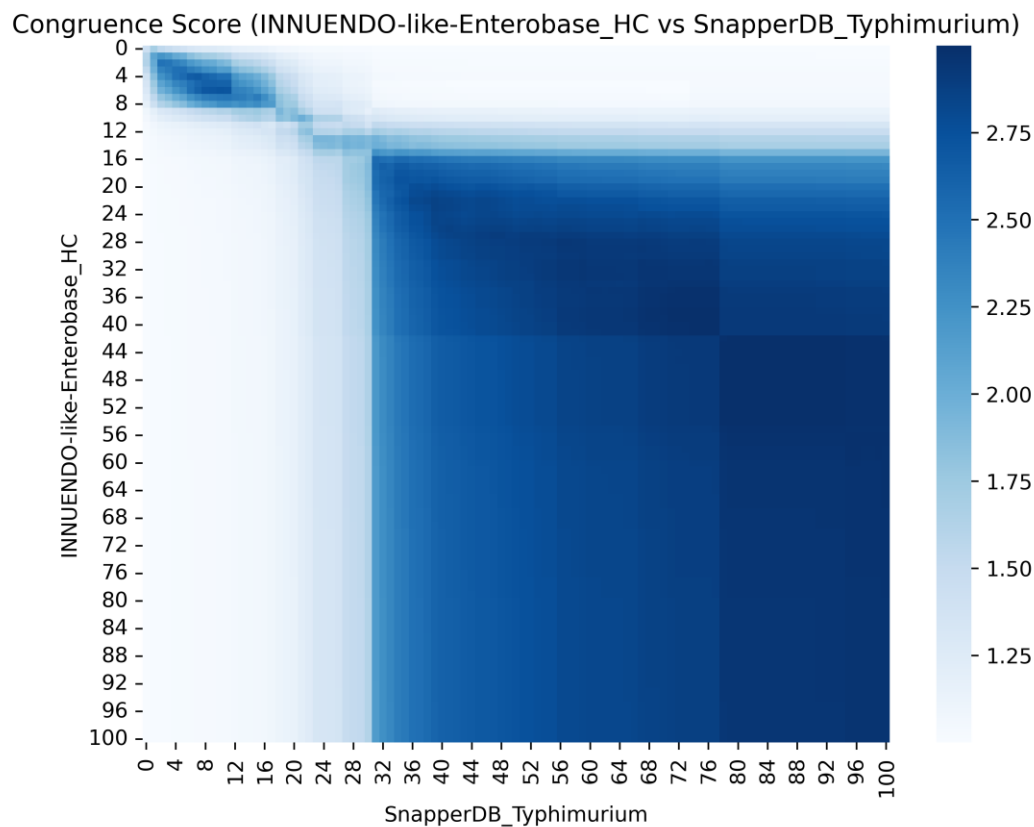


Figure S4.20.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

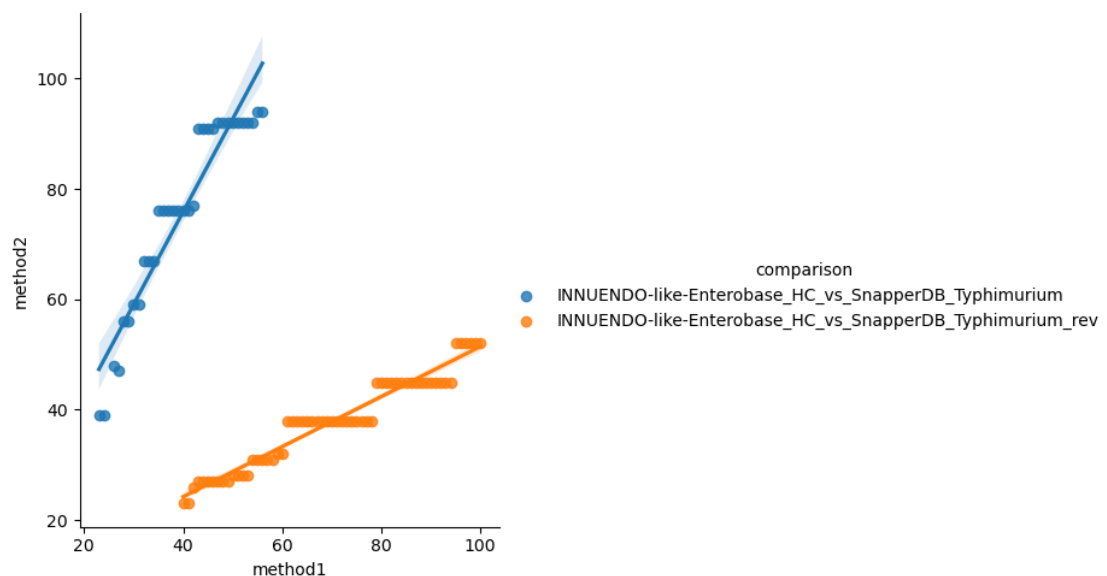


Figure S4.20.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 33 (blue) and 61 (orange) points is presented.

21. INNUENDO-like-Enterobase single-linkage vs. snippySnake single-linkage

Table S4.21. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-Enterobase single-linkage	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

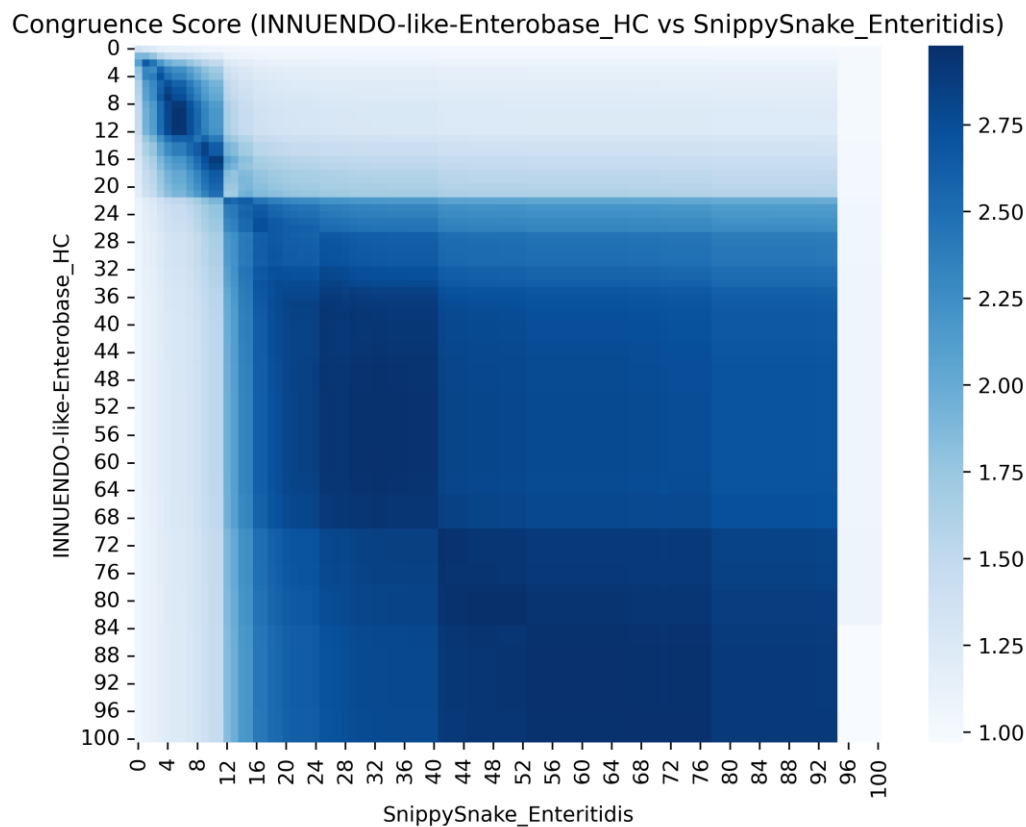


Figure S4.21.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

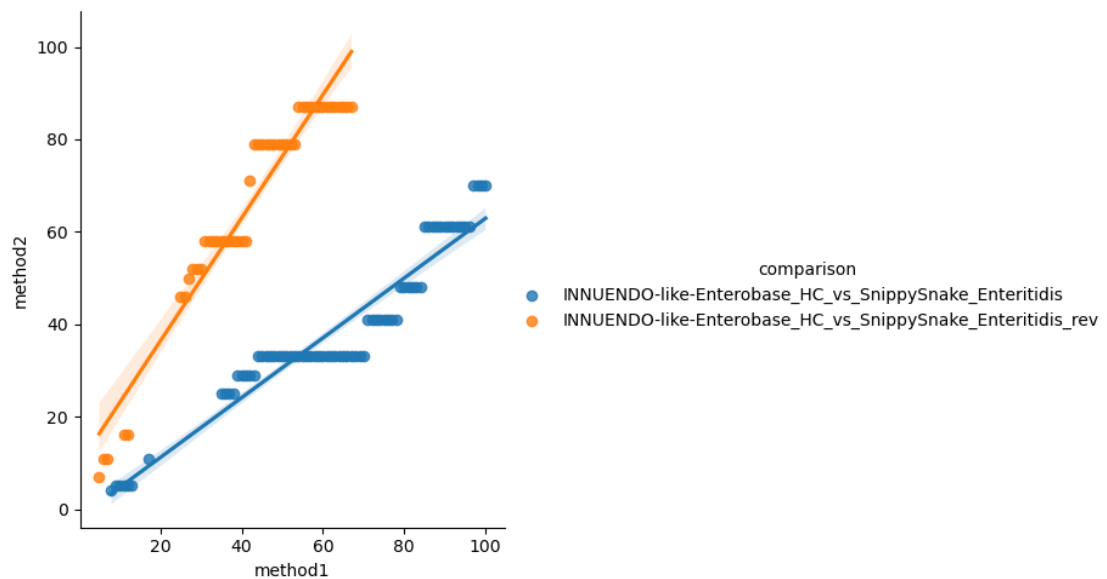


Figure S4.21.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 73 (blue) and 48 (orange) points is presented.

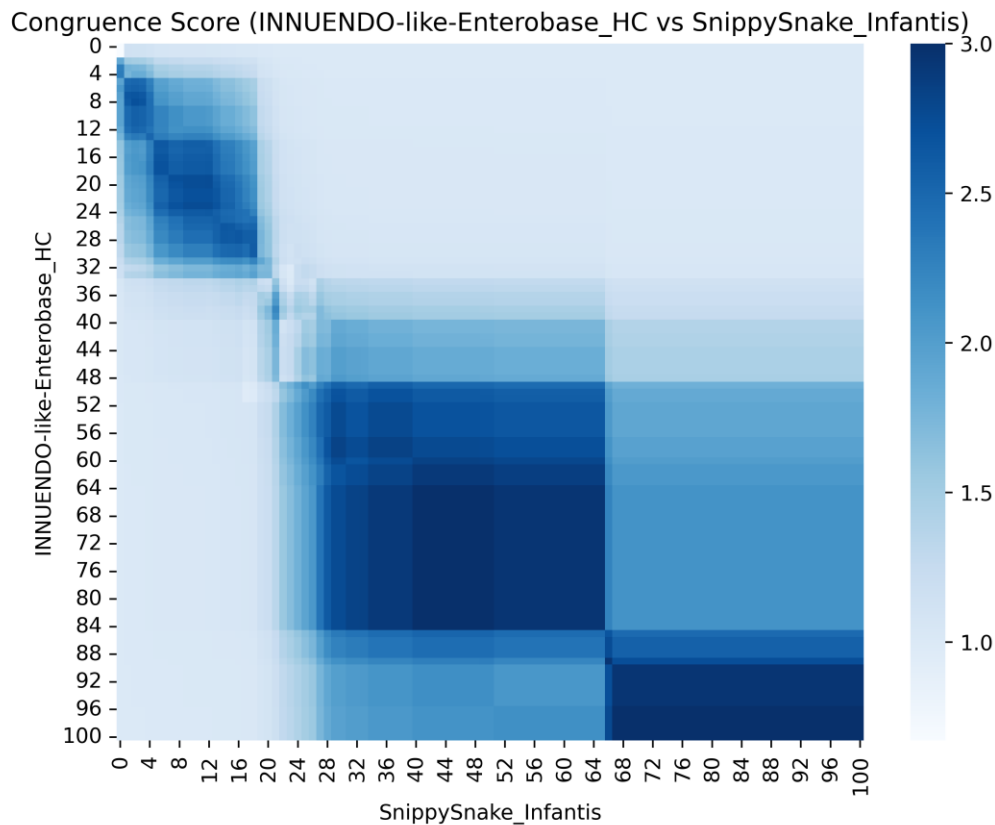


Figure S4.21.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

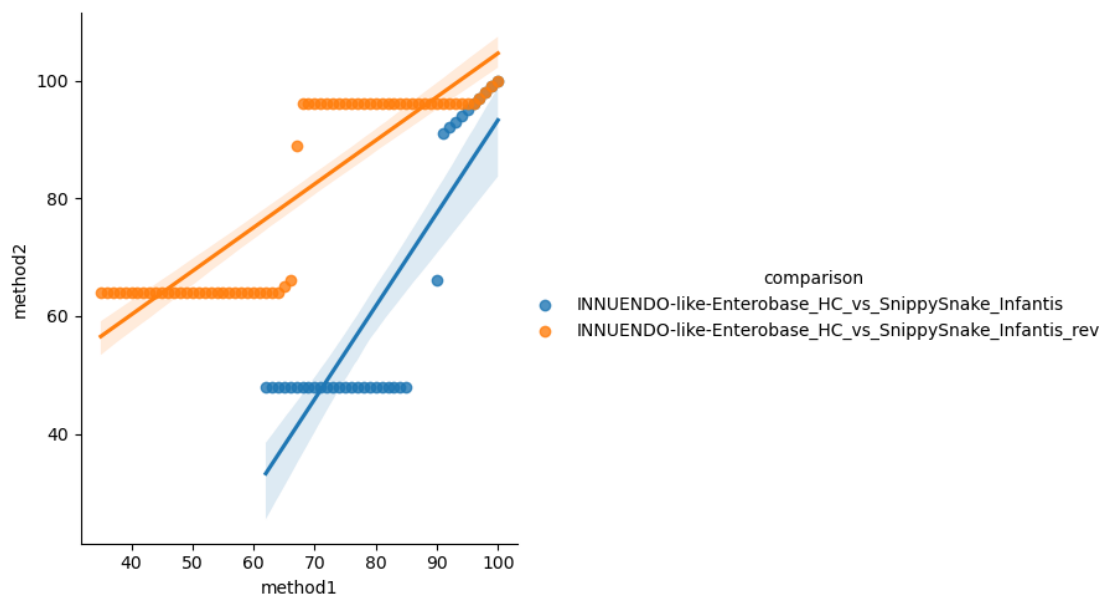


Figure S4.21.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Infantis. A linear tendency line supported by 35 (blue) and 66 (orange) points is presented.

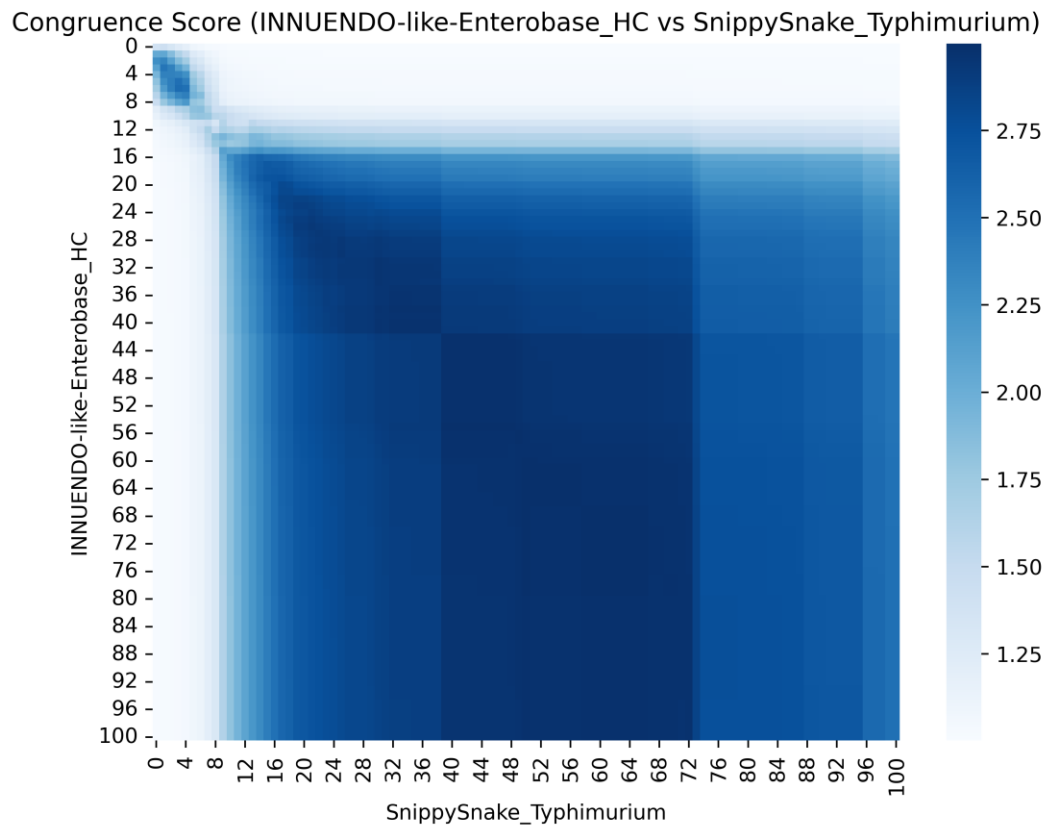


Figure S4.21.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

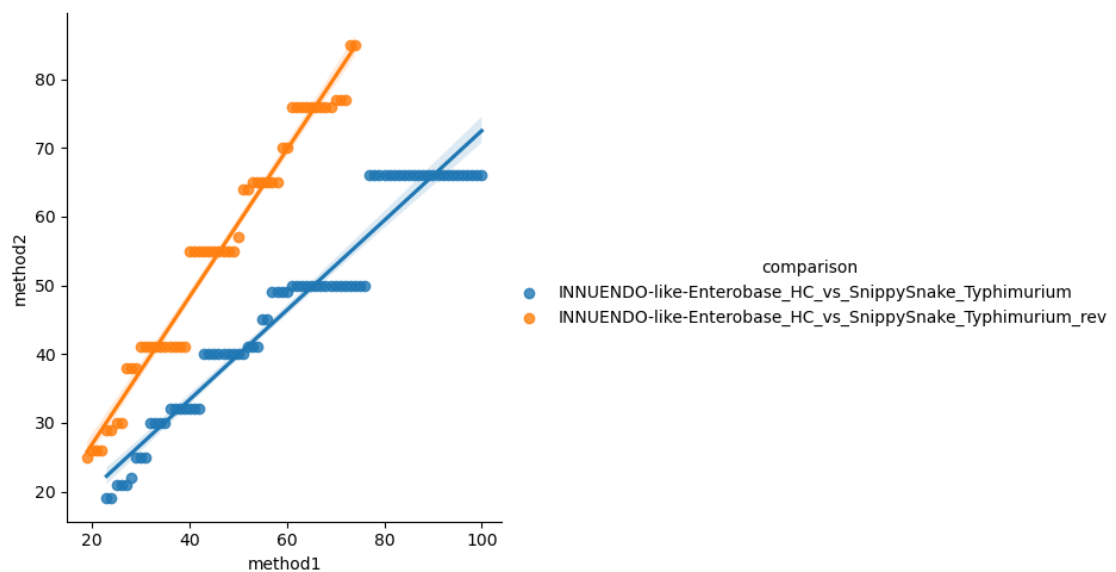


Figure S4.21.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 78 (blue) and 56 (orange) points is presented.

22. INNUENDO-like-INNUENDO99 GrapeTree vs. CSI Phylogeny single-linkage

Table S4.22. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-INNUENDO99 GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

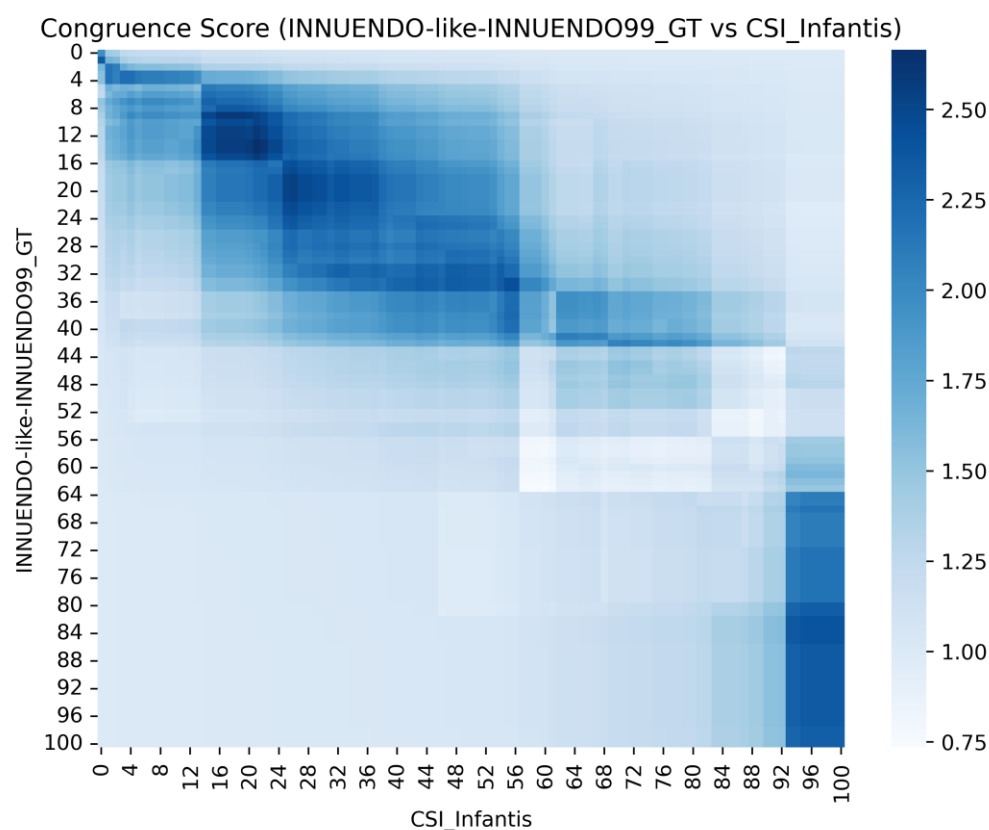


Figure S4.22.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

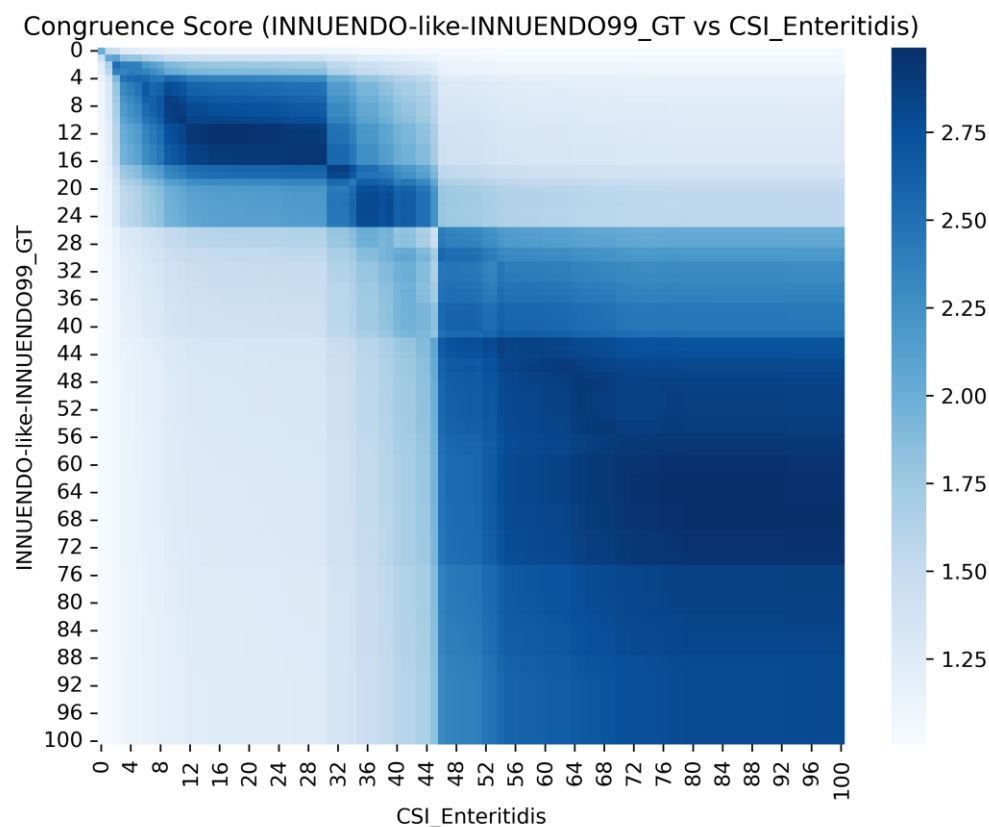


Figure S4.22.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

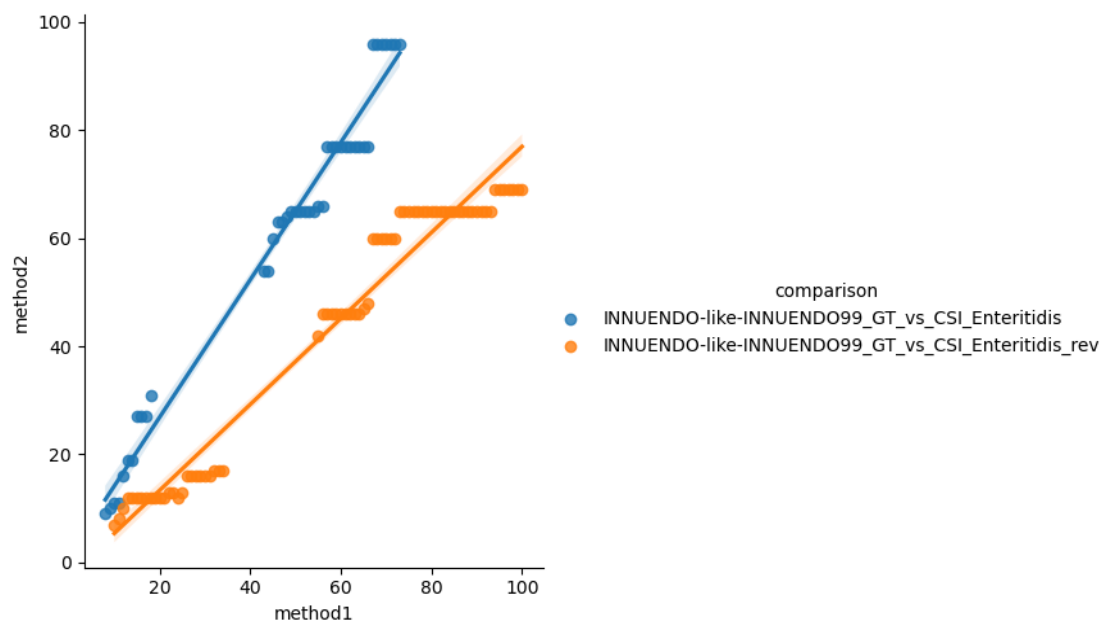


Figure S4.22.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 42 (blue) and 71 (orange) points is presented.

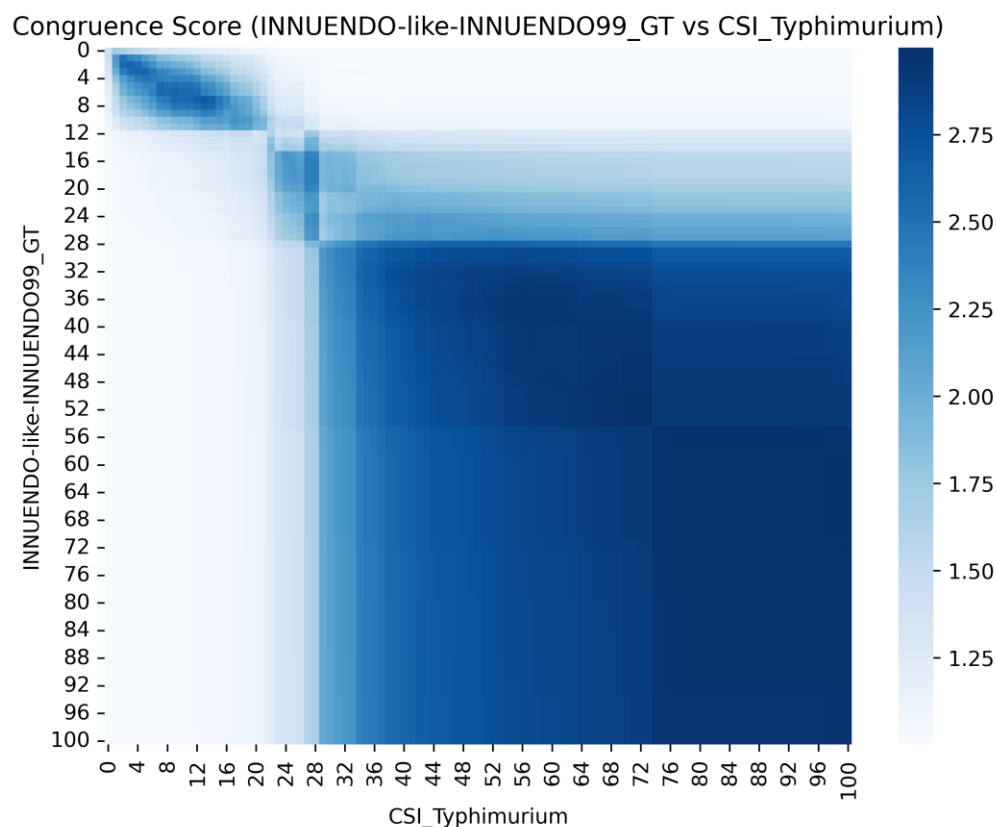


Figure S4.22.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

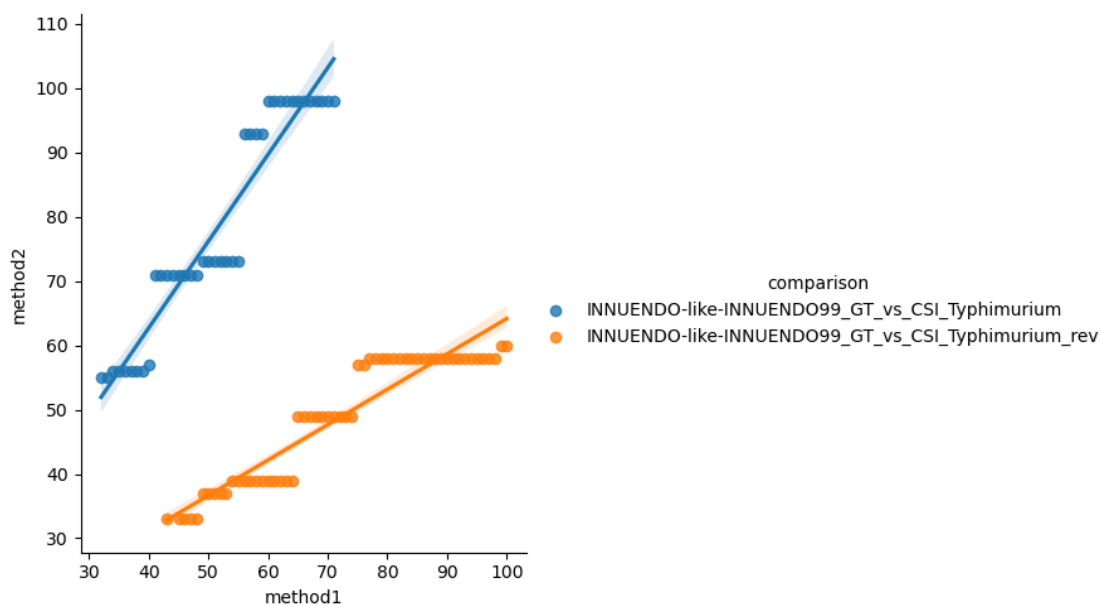


Figure S4.22.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 40 (blue) and 57 (orange) points is presented.

23. INNUENDO-like-INNUENDO99 GrapeTree vs. SnapperDB single-linkage

Table S4.23. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-INNUENDO99 GrapeTree	SnapperDB single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

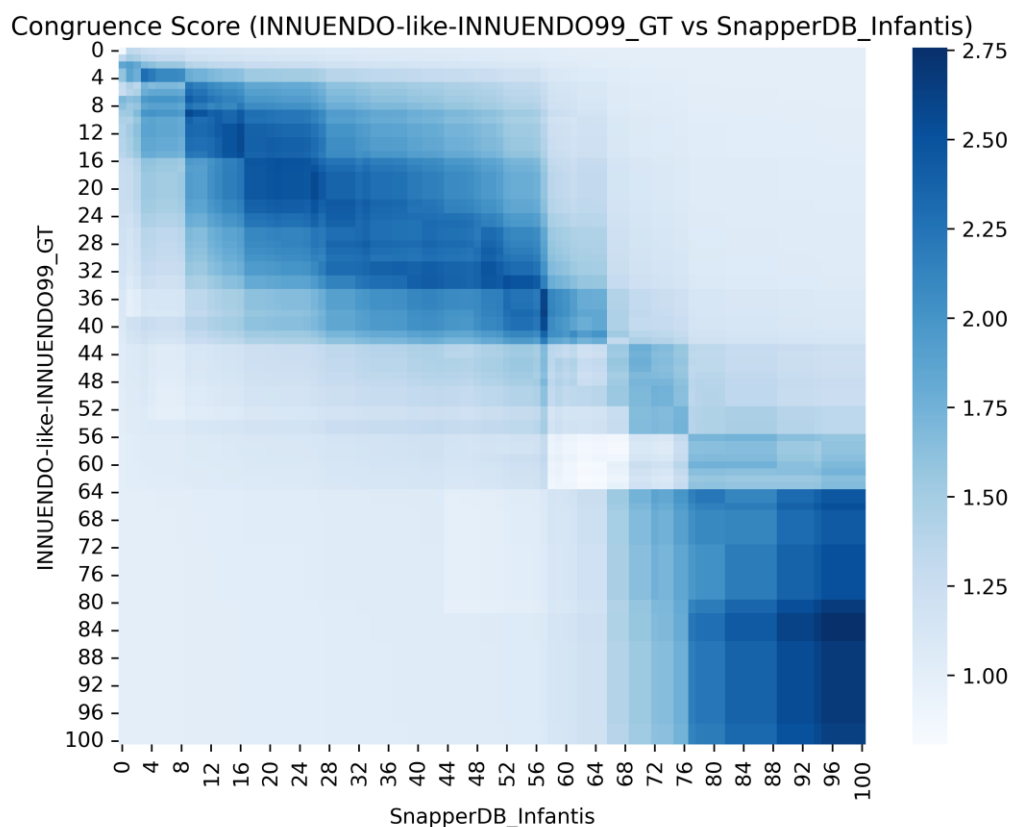


Figure S4.23.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

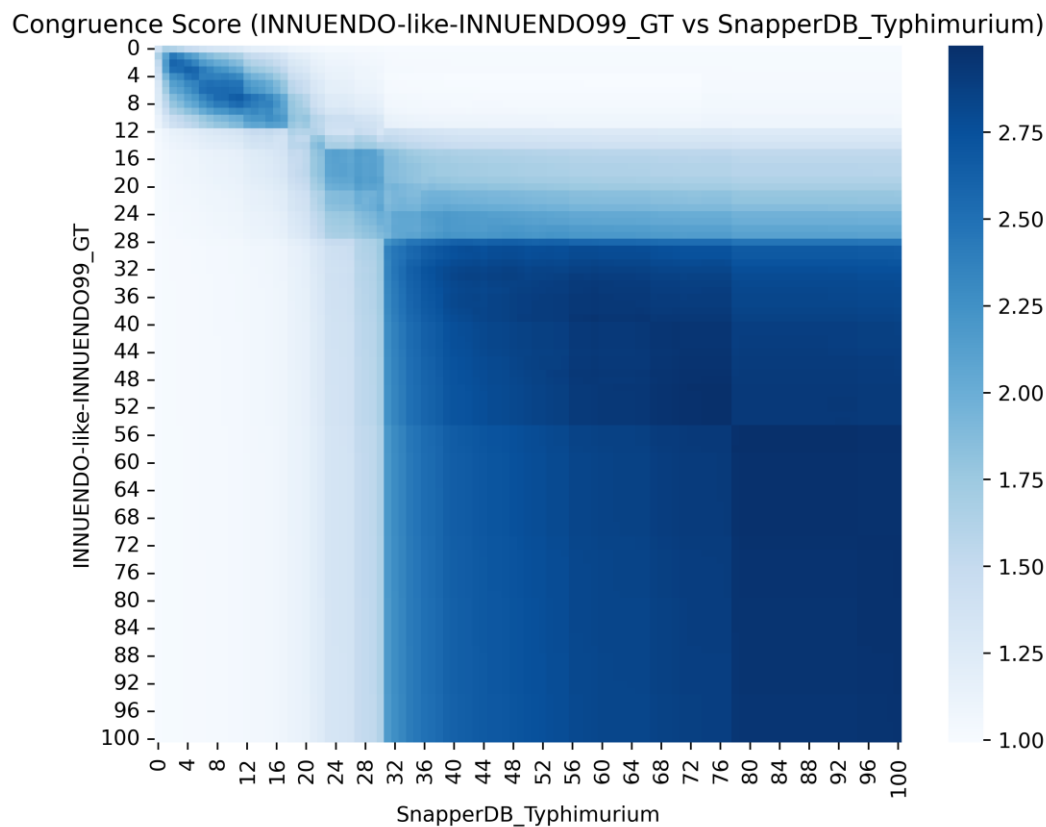


Figure S4.23.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

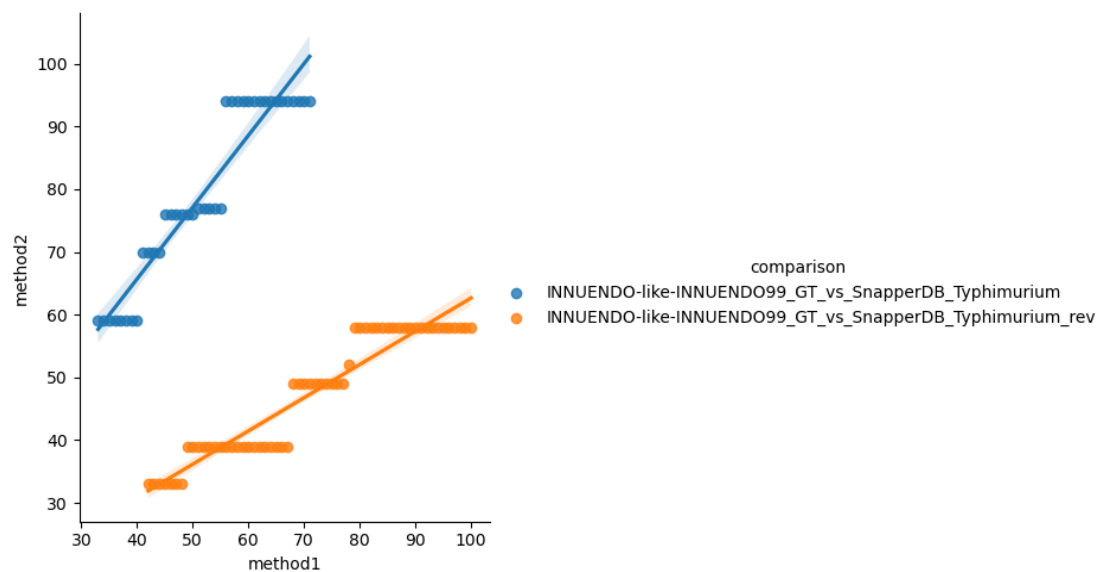


Figure S4.23.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 39 (blue) and 59 (orange) points is presented.

24. INNUENDO-like-INNUENDO99 GrapeTree vs. snippySnake single-linkage

Table S4.24. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-INNUENDO99 GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

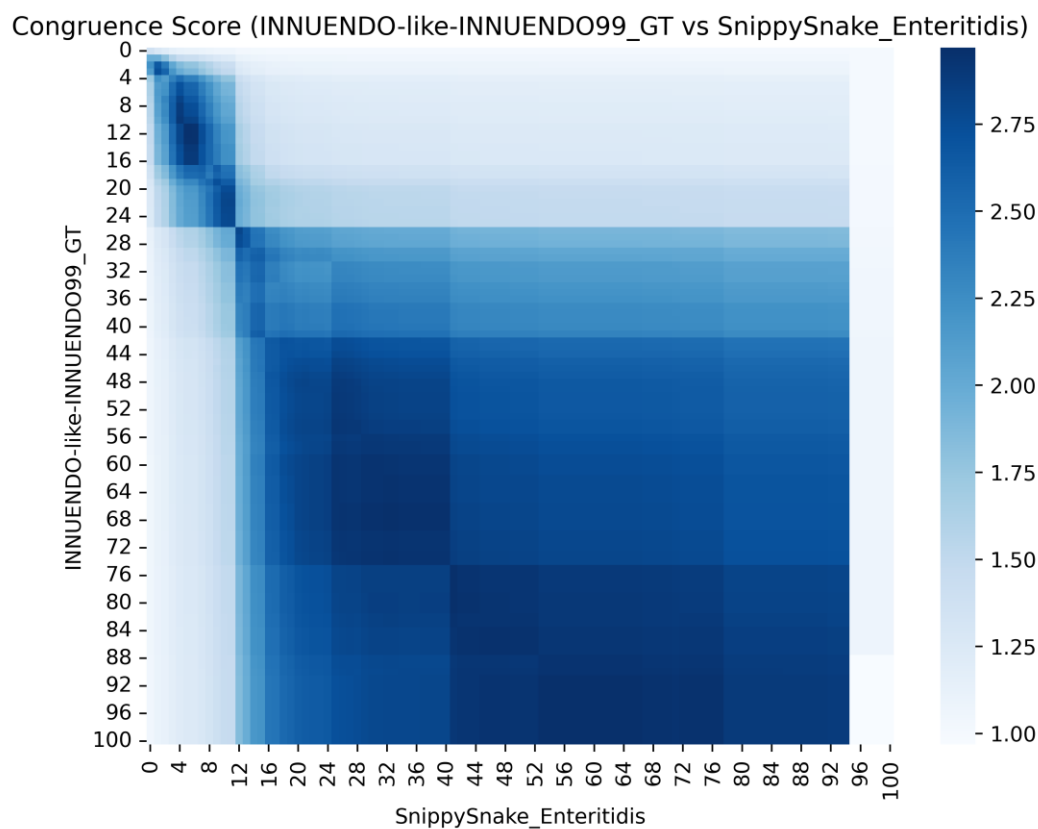


Figure S4.24.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

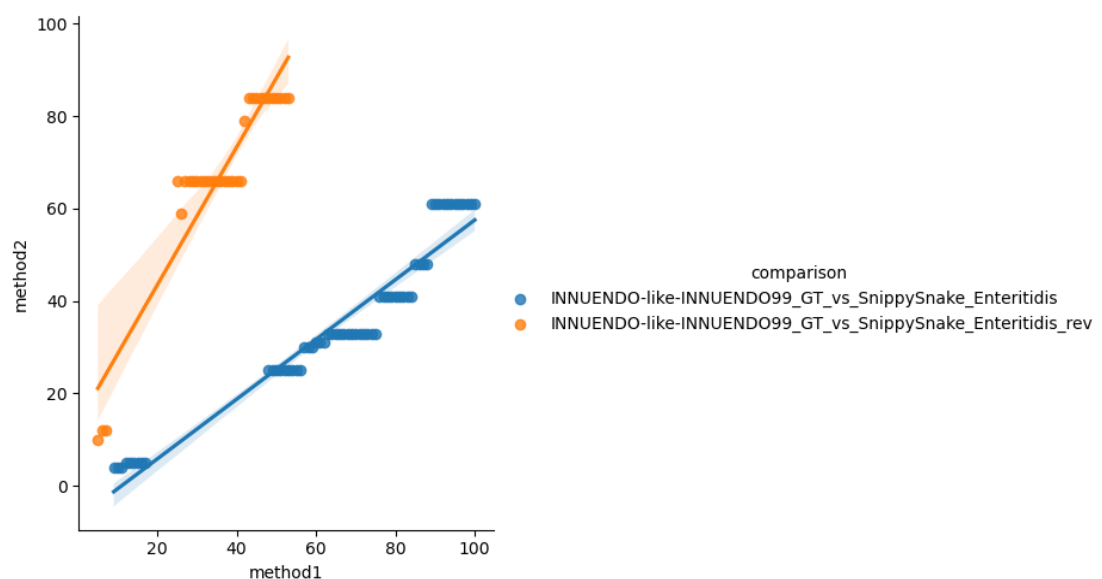


Figure S4.24.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Enteritidis. A linear tendency line supported by 62 (blue) and 32 (orange) points is presented.

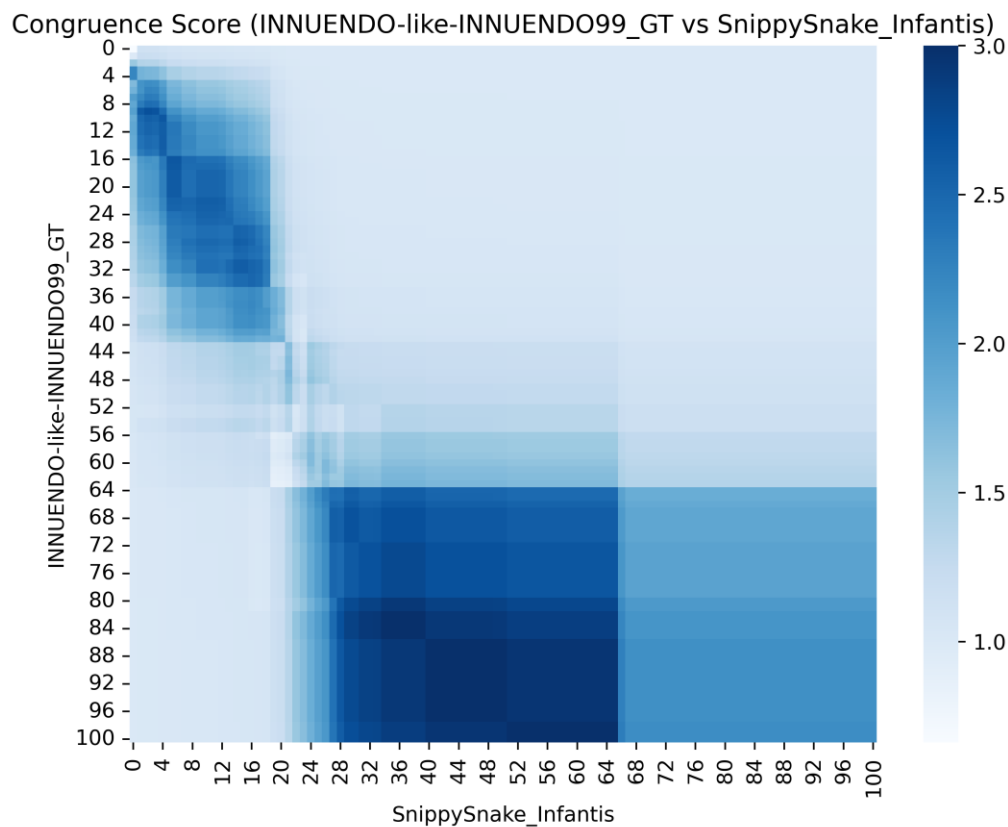


Figure S4.24.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

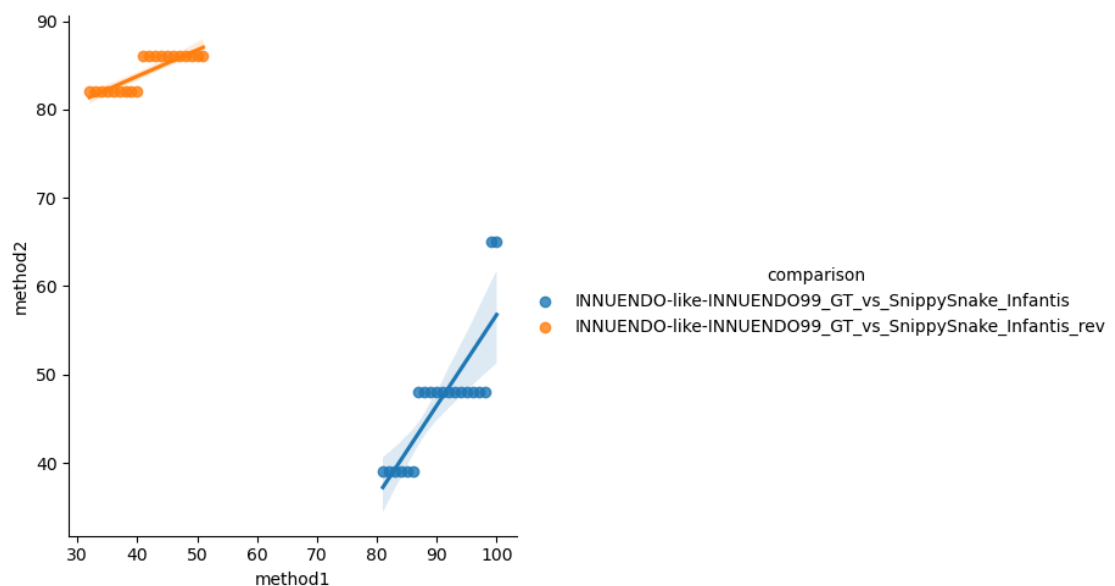


Figure S4.24.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Infantis. A linear tendency line supported by 20 (blue) and 20 (orange) points is presented.

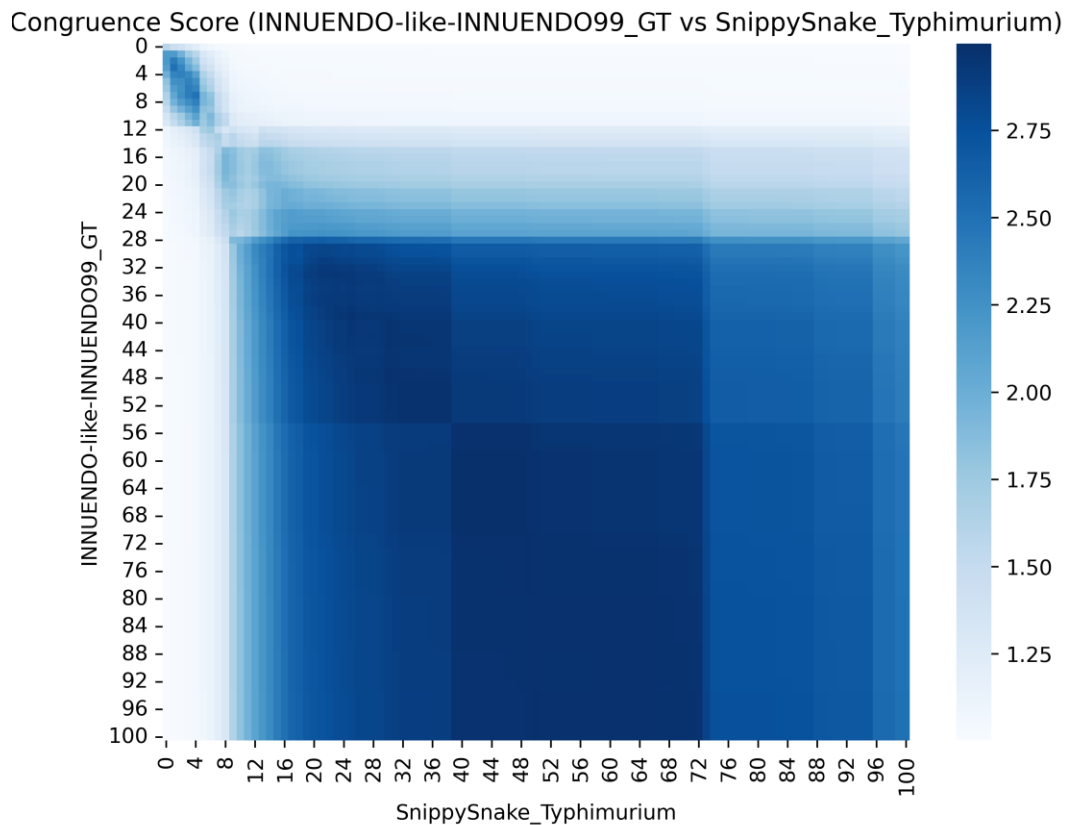


Figure S4.24.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

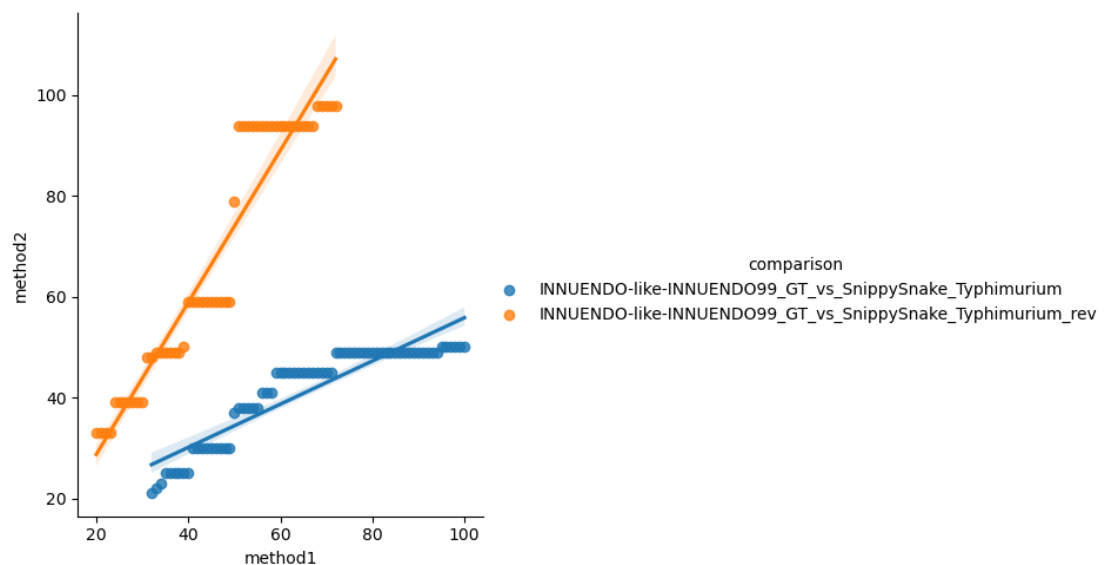


Figure S4.24.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 69 (blue) and 53 (orange) points is presented.

25. INNUENDO-like-INNUENDO99 single-linkage vs. CSI Phylogeny single-linkage

Table S4.25. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-INNUENDO99 single-linkage	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

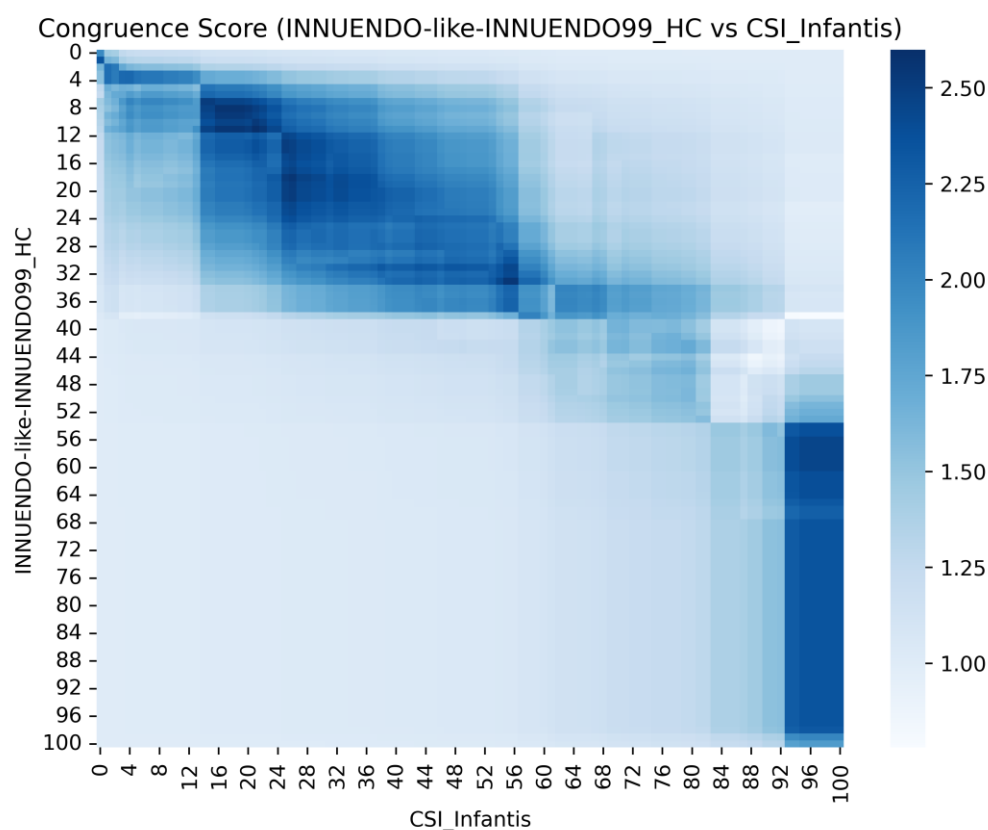


Figure S4.25.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

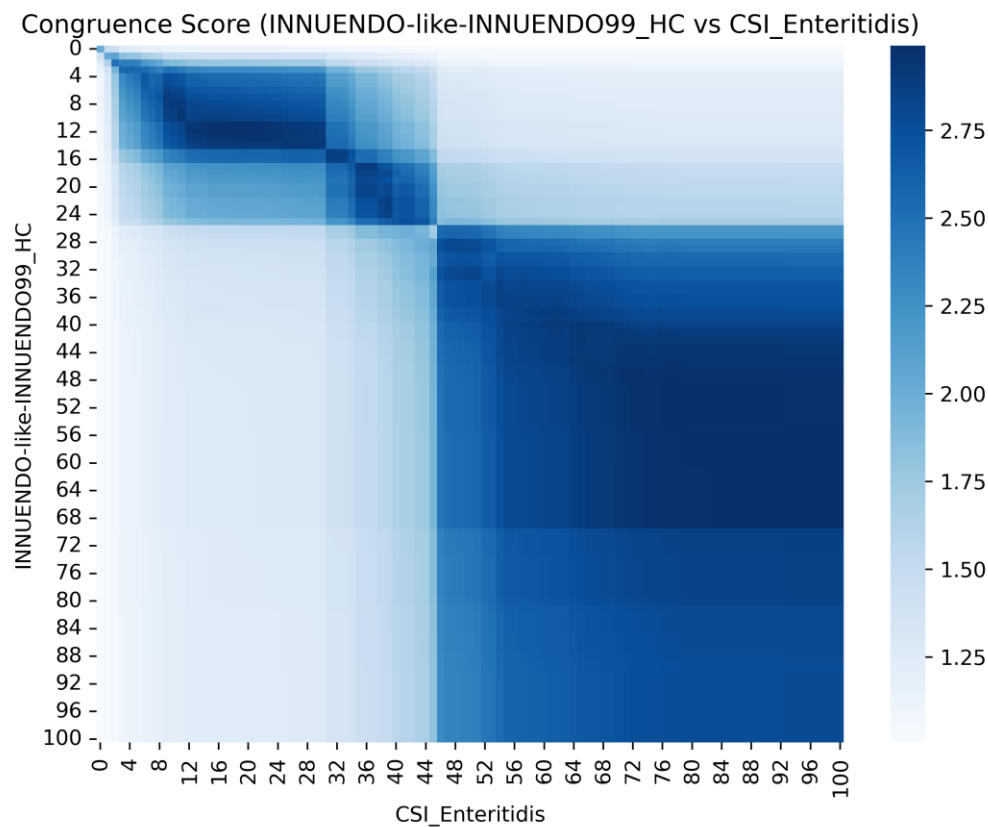


Figure S4.25.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

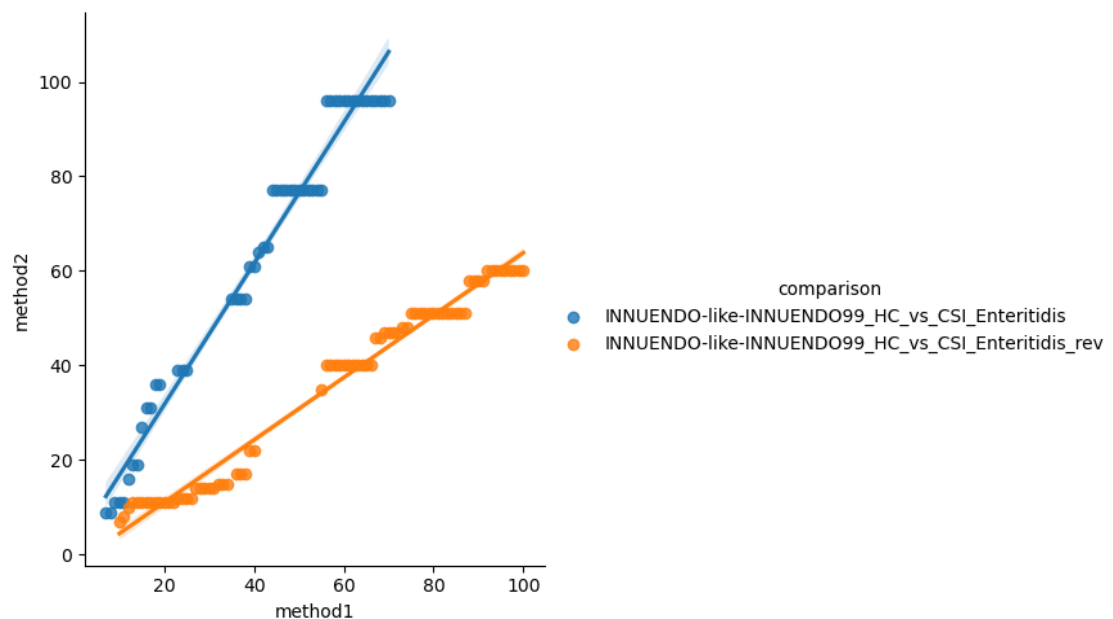


Figure S4.25.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 52 (blue) and 76 (orange) points is presented.

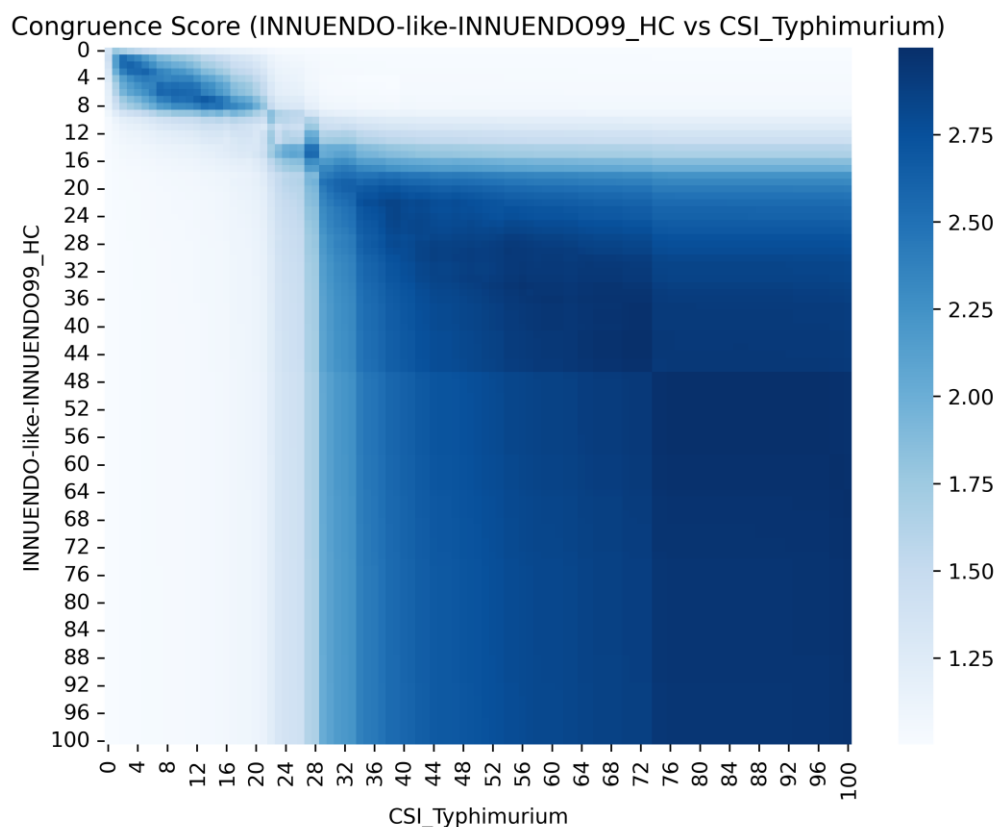


Figure S4.25.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

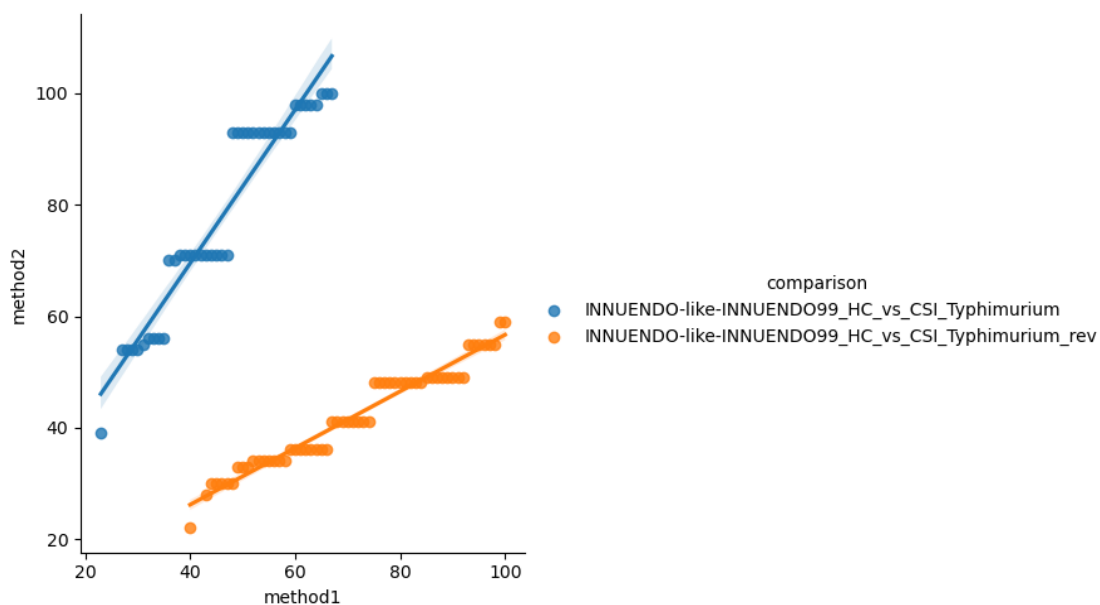


Figure S4.25.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 42 (blue) and 59 (orange) points is presented.

26. INNUENDO-like-INNUENDO99 single-linkage vs. SnapperDB single-linkage

Table S4.26. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-INNUENDO99 single-linkage	SnapperDB single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

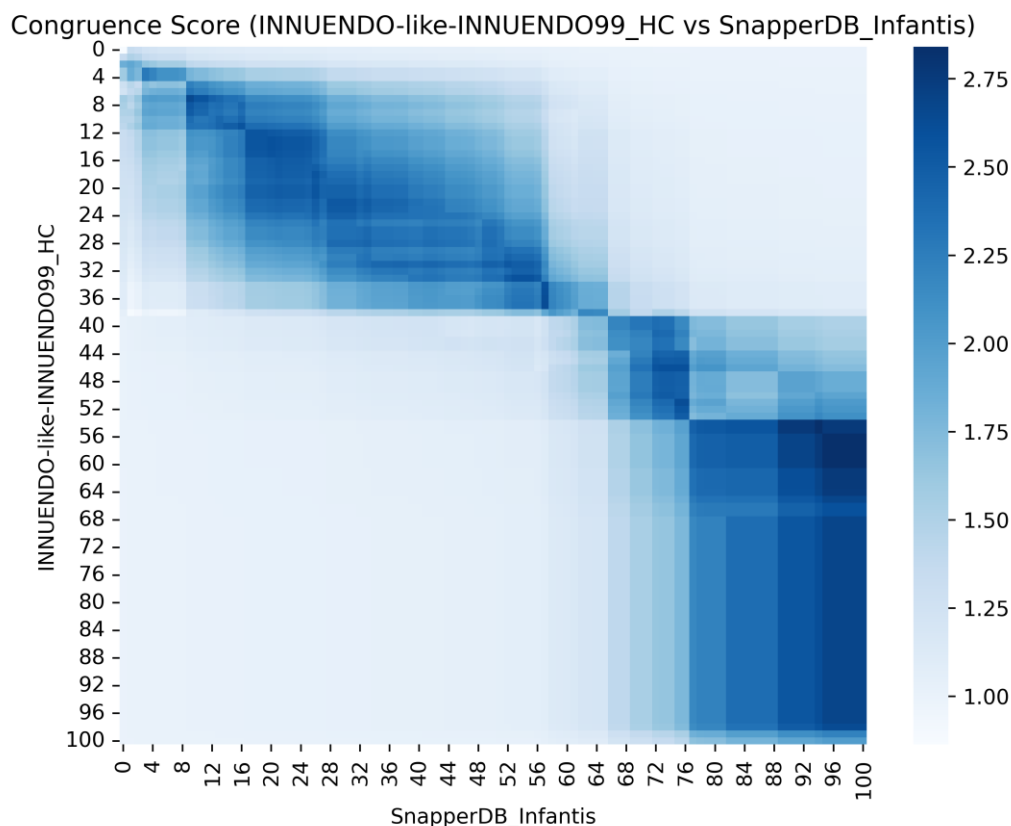


Figure S4.26.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

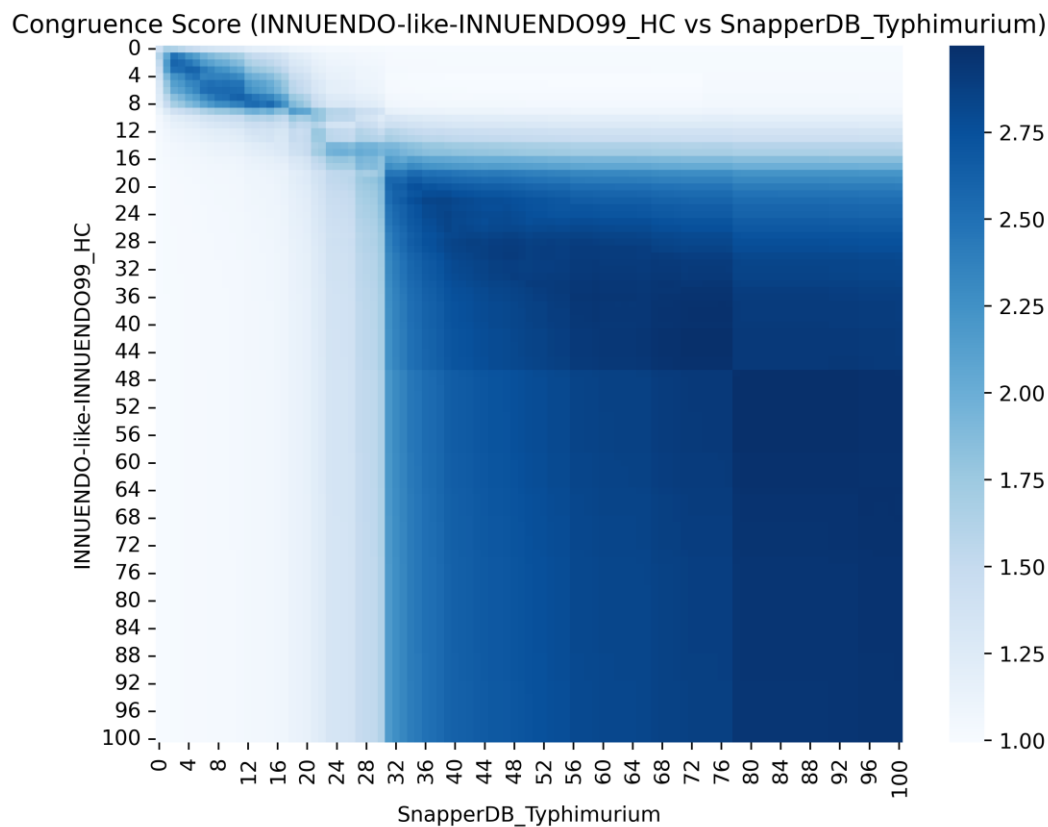


Figure S4.26.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

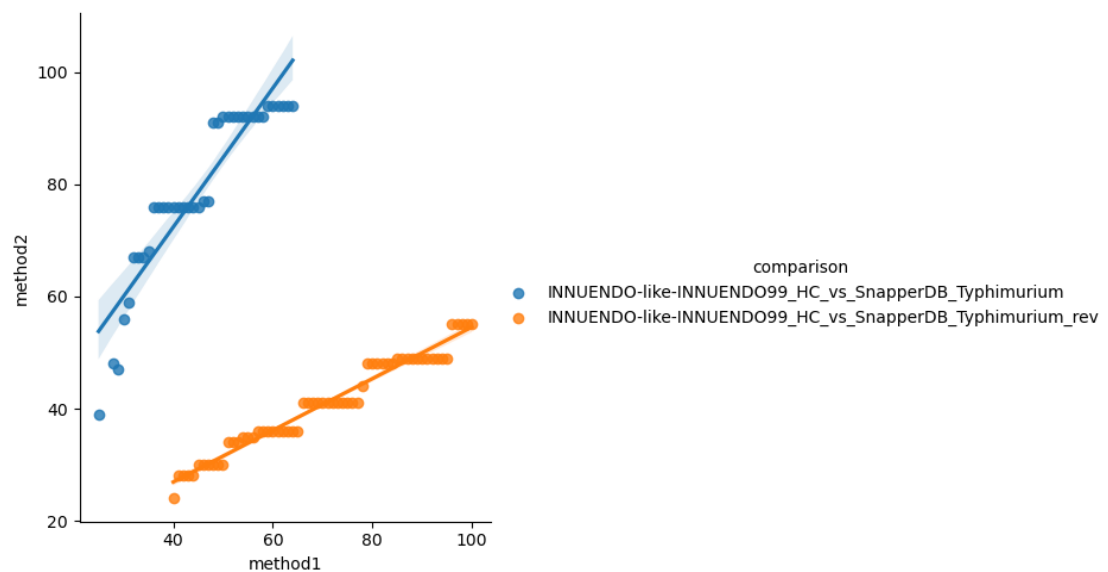


Figure S4.26.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 38 (blue) and 61 (orange) points is presented.

27. INNUENDO-like-INNUENDO99 single-linkage vs. snippySnake single-linkage

Table S4.27. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	INNUENDO-like-INNUENDO99 single-linkage	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

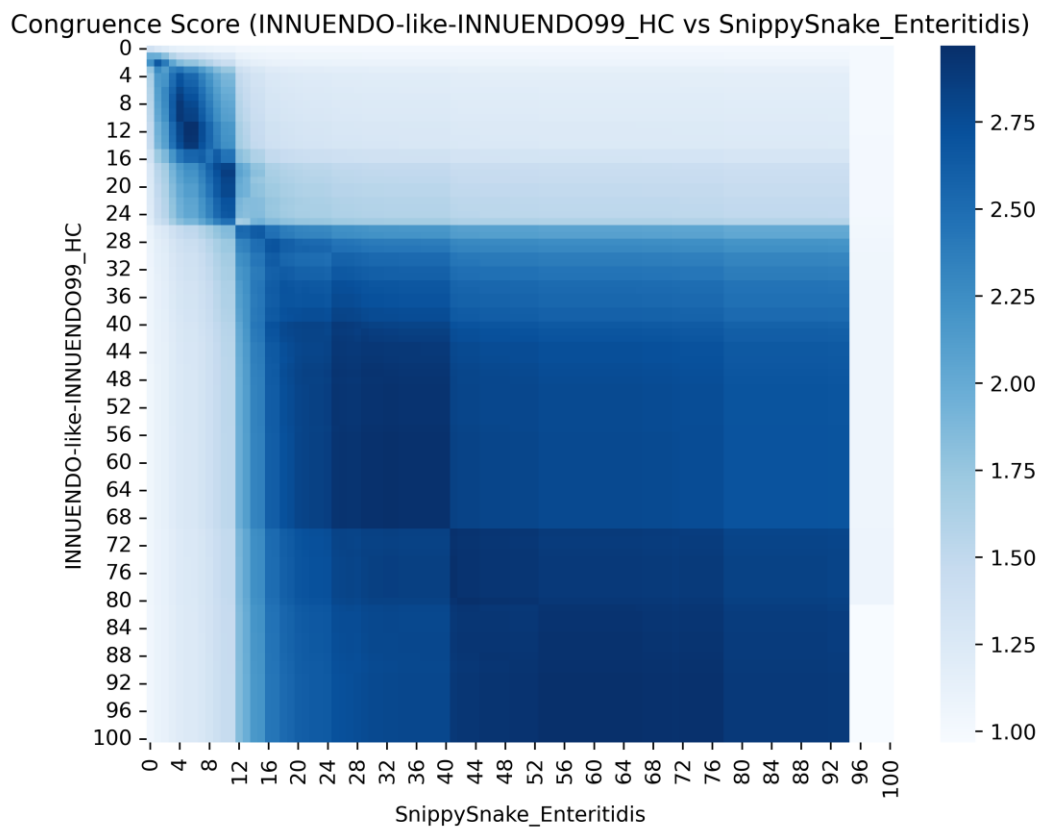


Figure S4.27.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

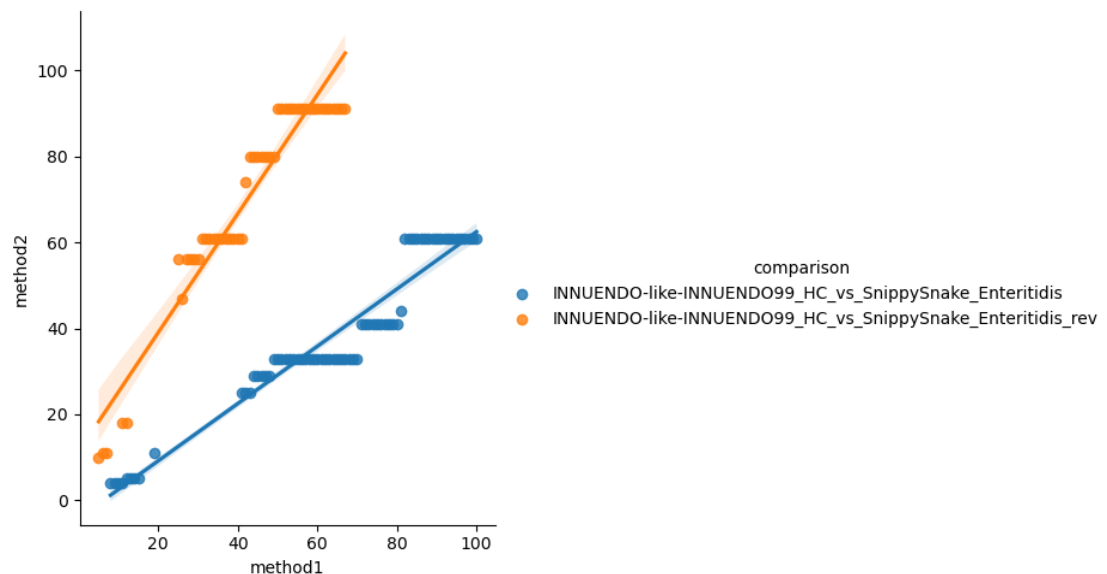


Figure S4.27.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Enteritidis. A linear tendency line supported by 69 (blue) and 48 (orange) points is presented.

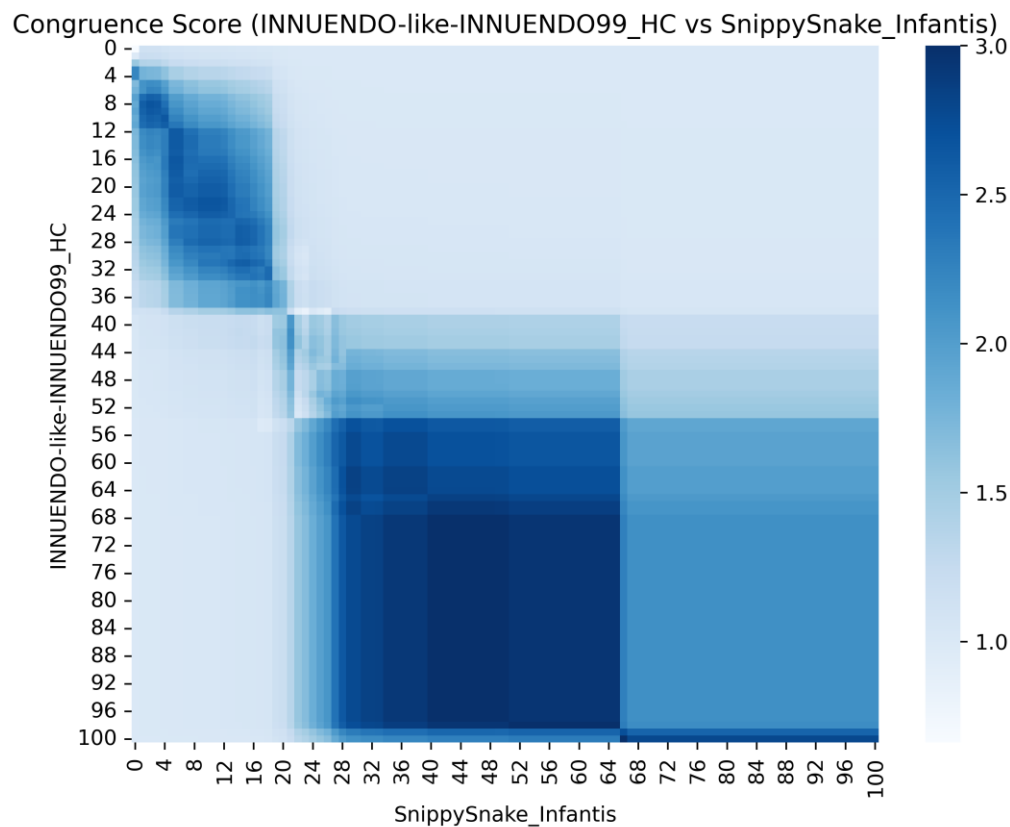


Figure S4.27.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

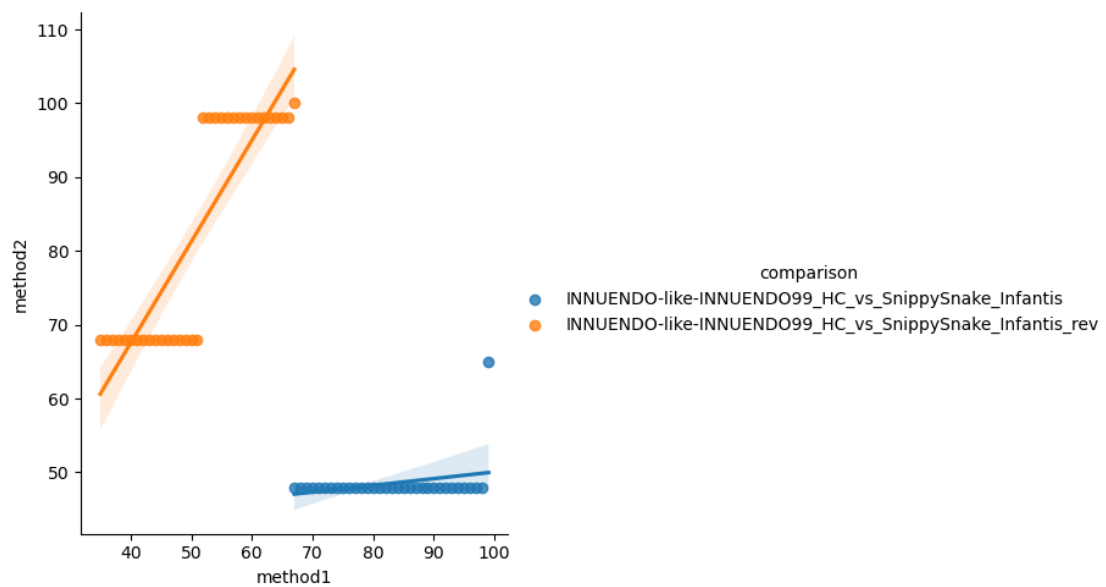


Figure S4.27.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for Infantis. A linear tendency line supported by 33 (blue) and 33 (orange) points is presented.

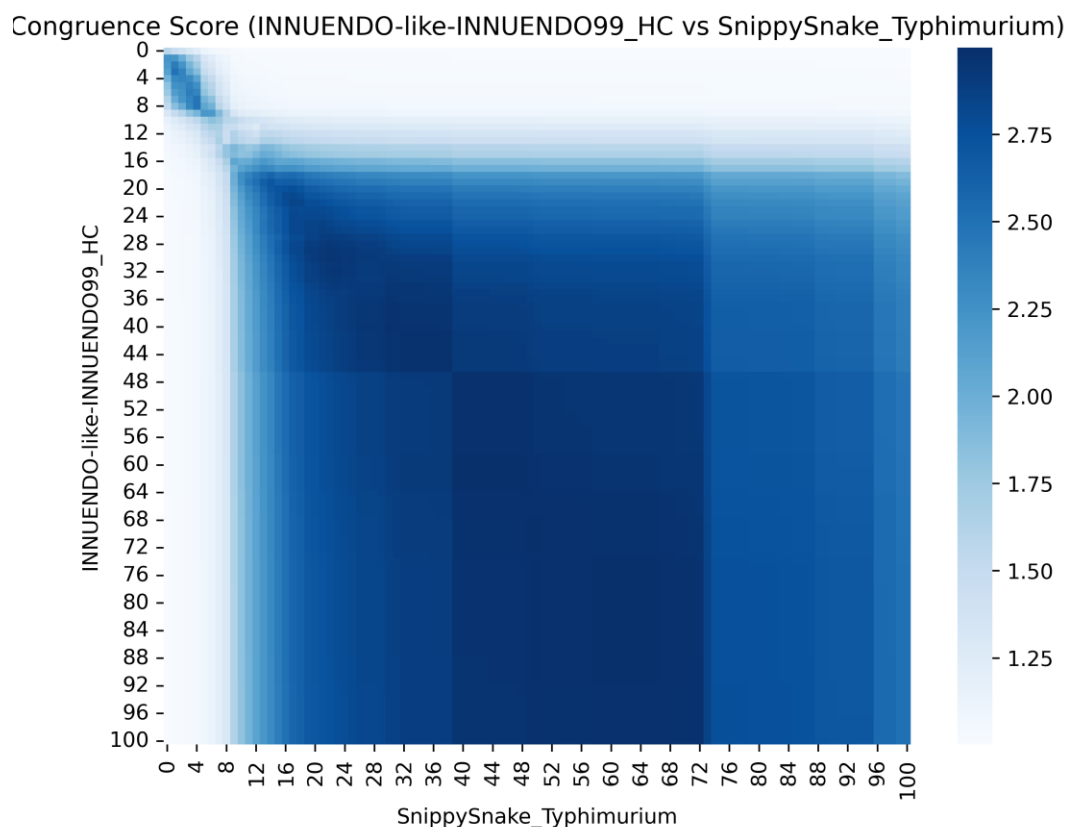


Figure S4.27.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

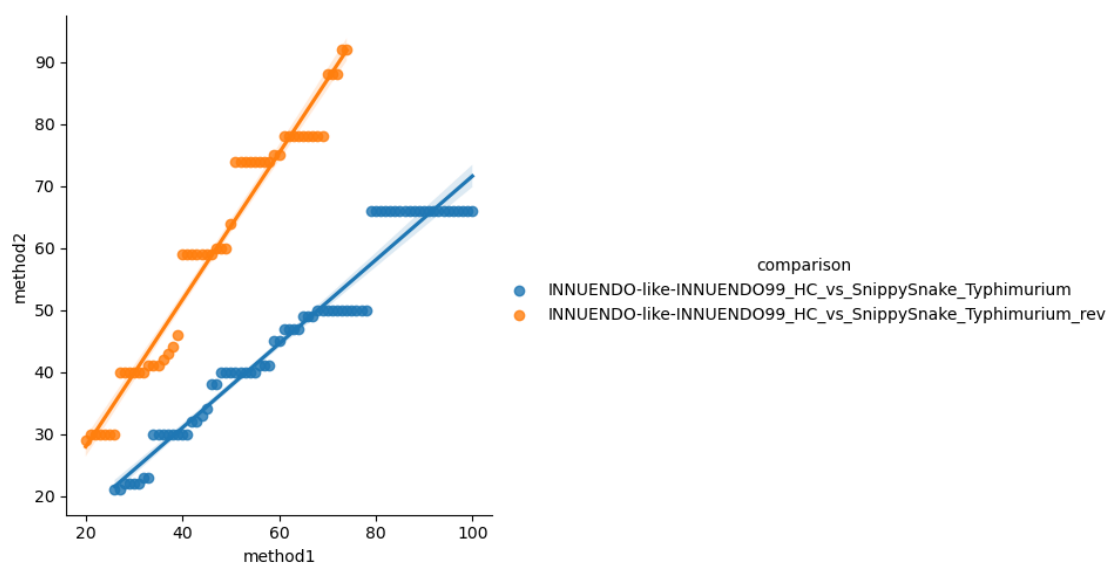


Figure S4.27.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 75 (blue) and 55 (orange) points is presented.

28. SeqSphere single-linkage vs. CSI Phylogeny single-linkage

Table S4.28. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	SeqSphere single-linkage	CSI Phylogeny single-linkage
Pipeline version	v8.3.4	v1.4
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

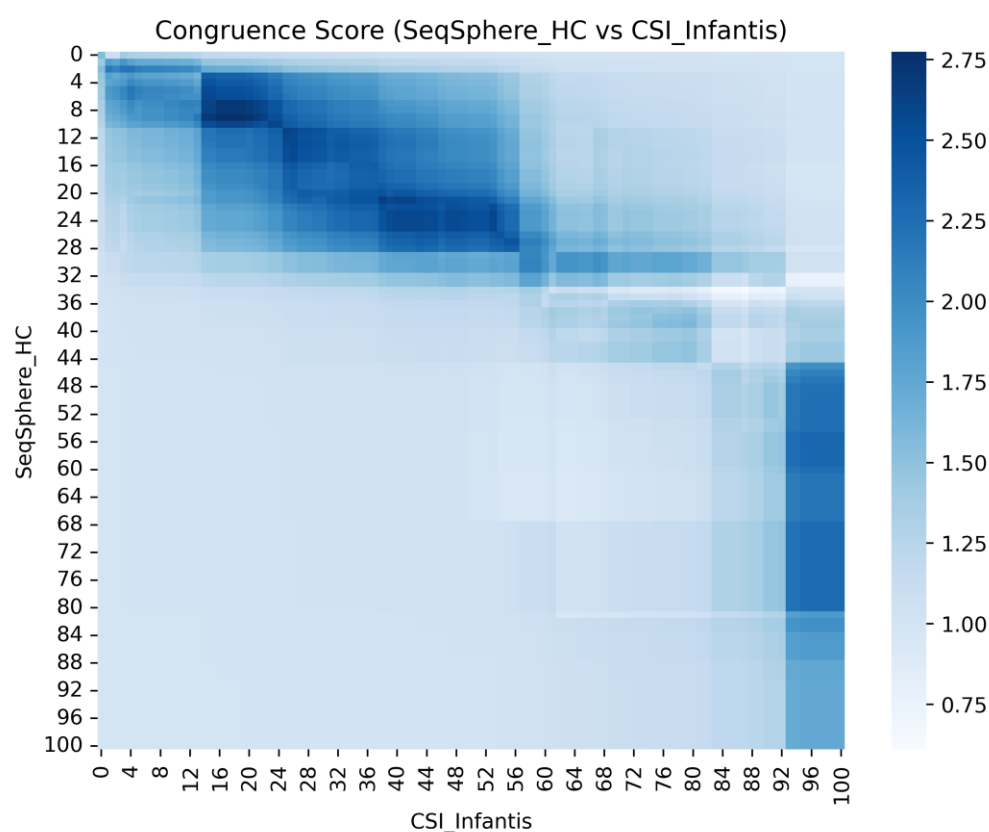


Figure S4.28.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

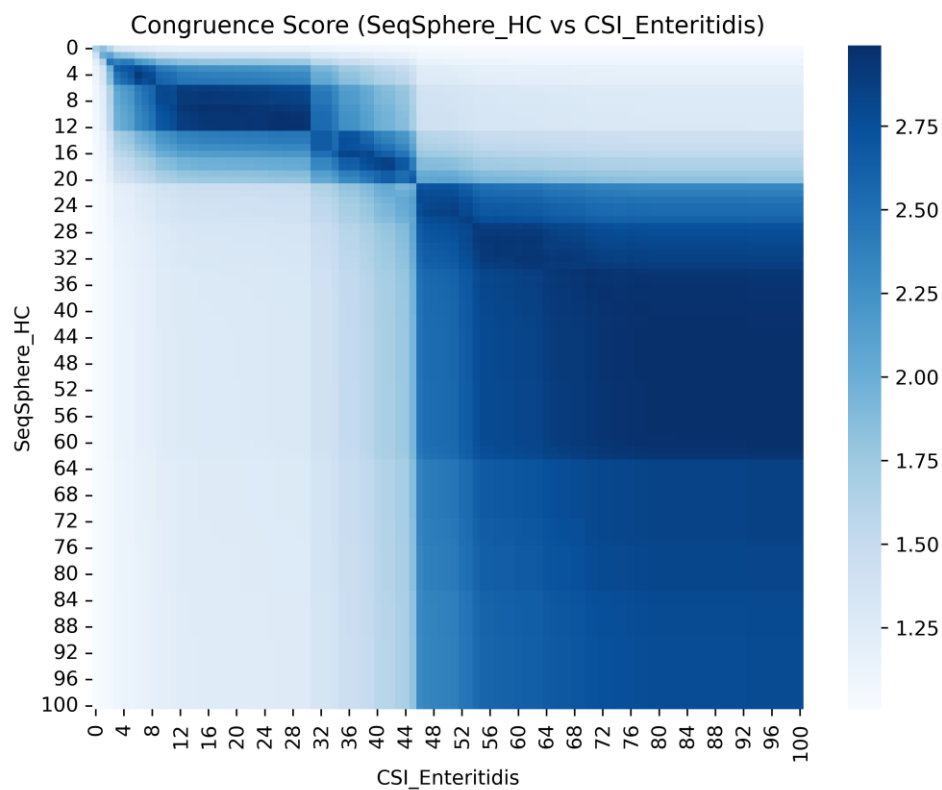


Figure S4.28.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

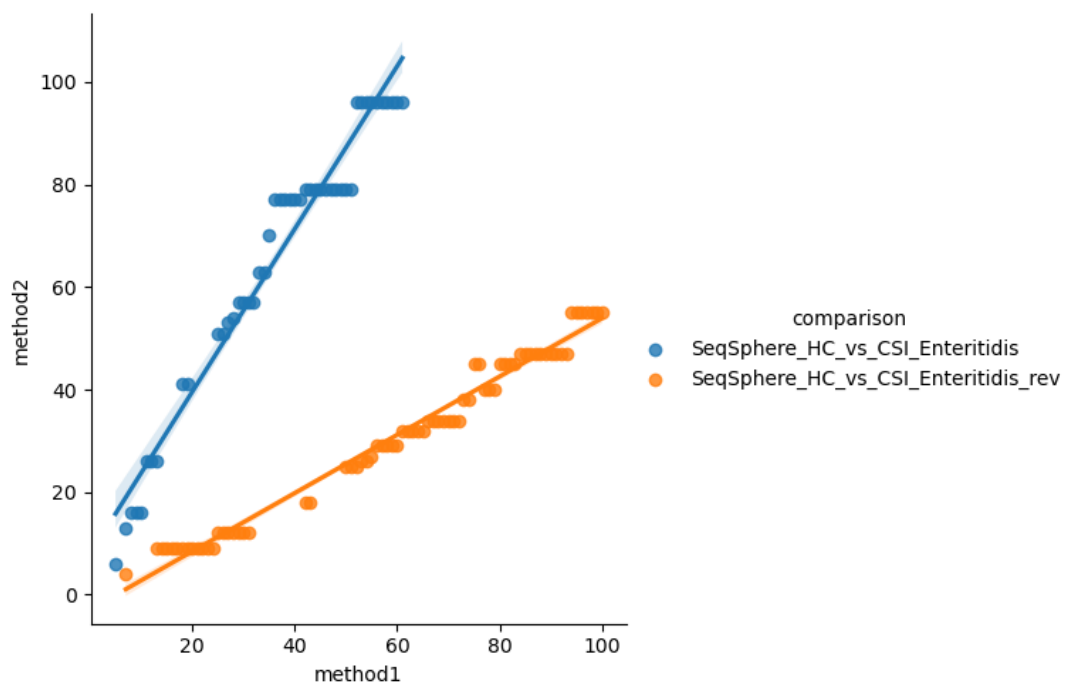


Figure S4.28.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 47 (blue) and 73 (orange) points is presented.

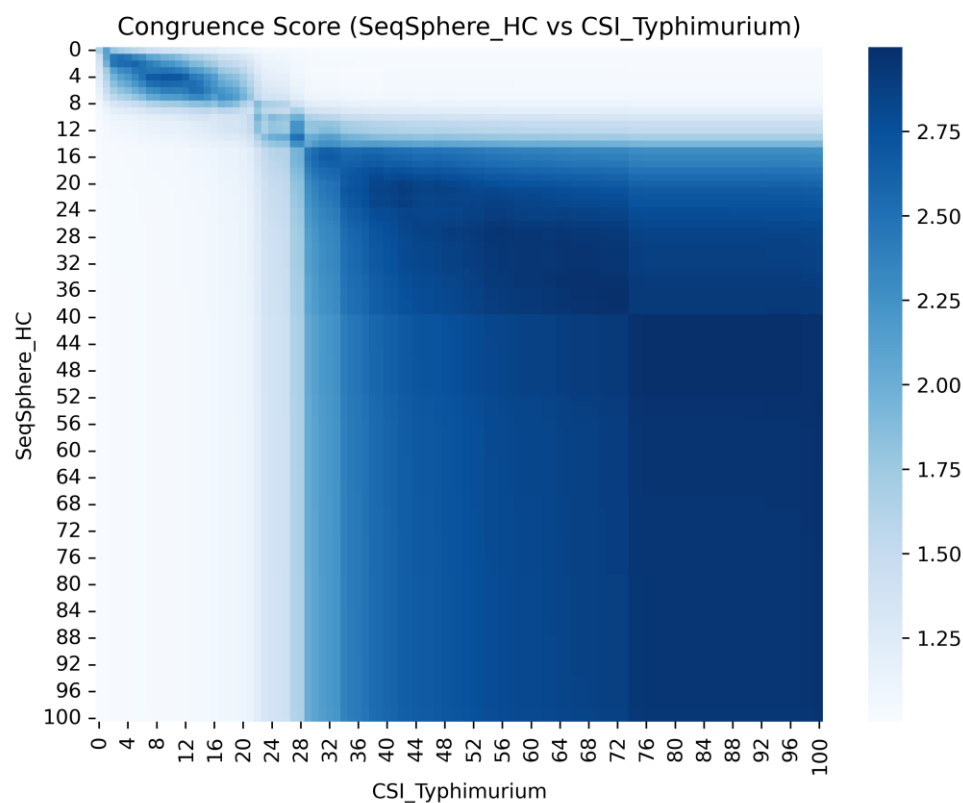


Figure S4.28.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

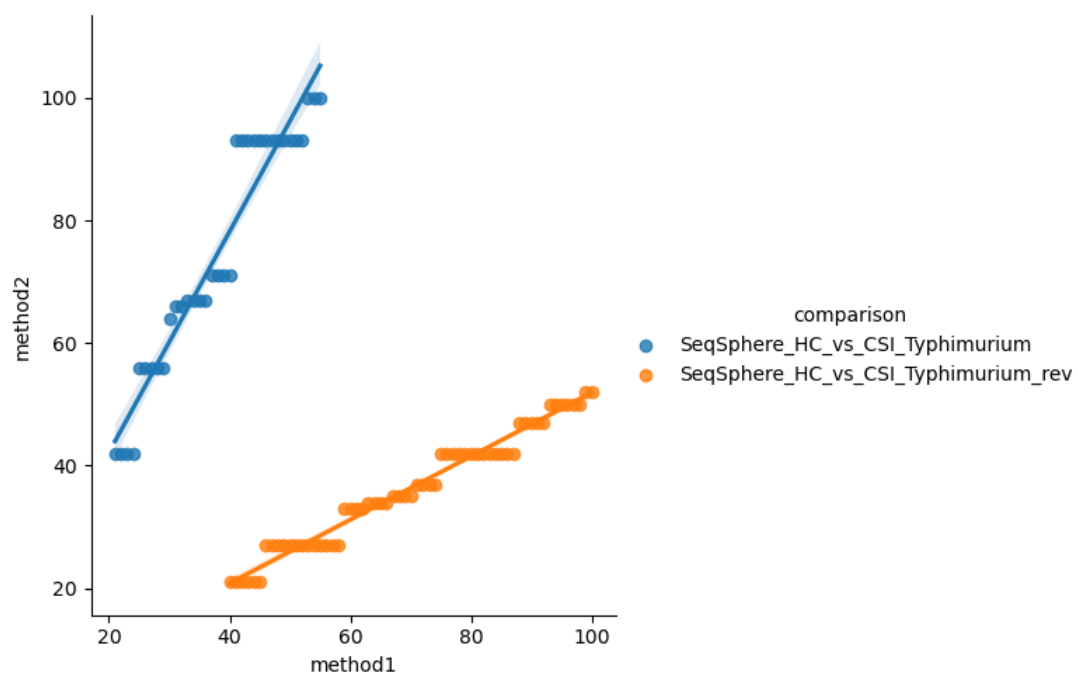


Figure S4.28.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for Typhimurium. A linear tendency line supported by 35 (blue) and 61 (orange) points is presented.

29. SeqSphere single-linkage vs. SnapperDB single-linkage

Table S4.29. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	SeqSphere single-linkage	SnapperDB single-linkage
Pipeline version	v8.3.4	-
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Typhimurium

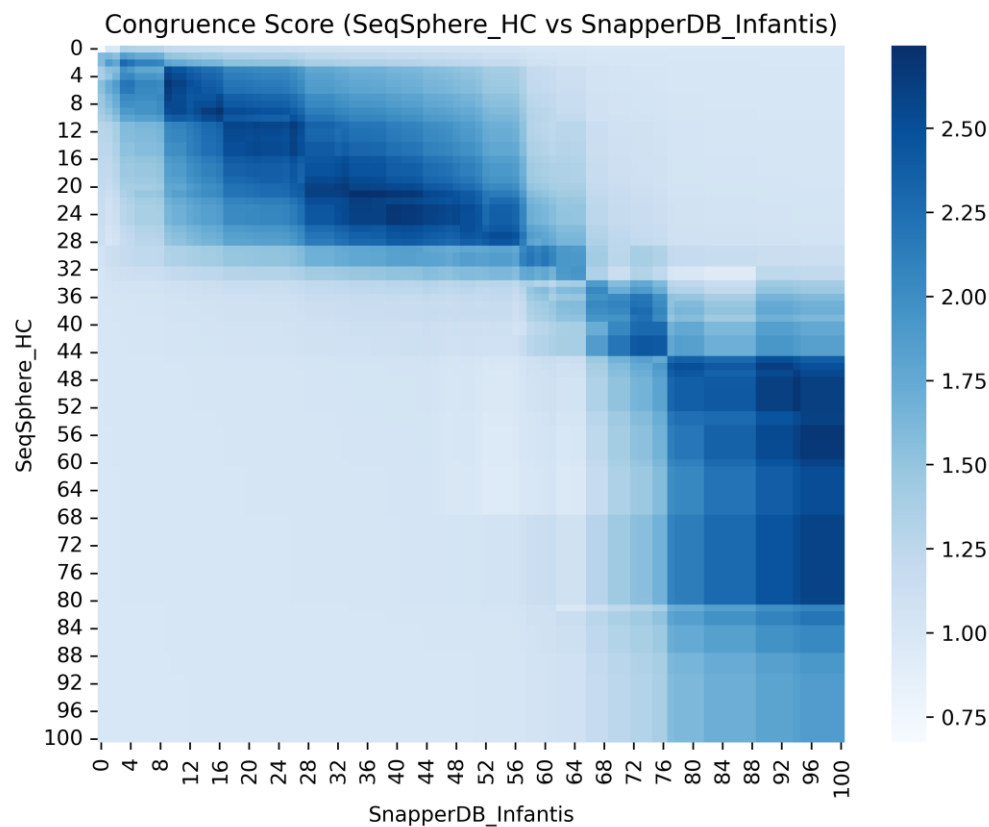


Figure S4.29.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of the two pipelines for Infantis.

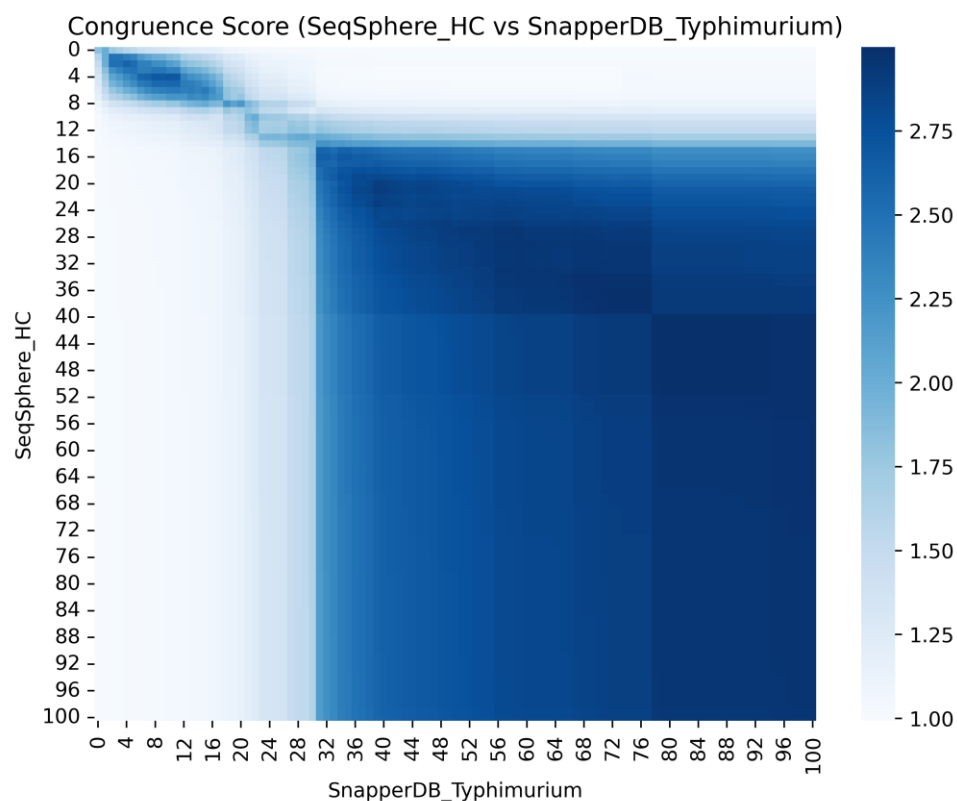


Figure S4.29.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

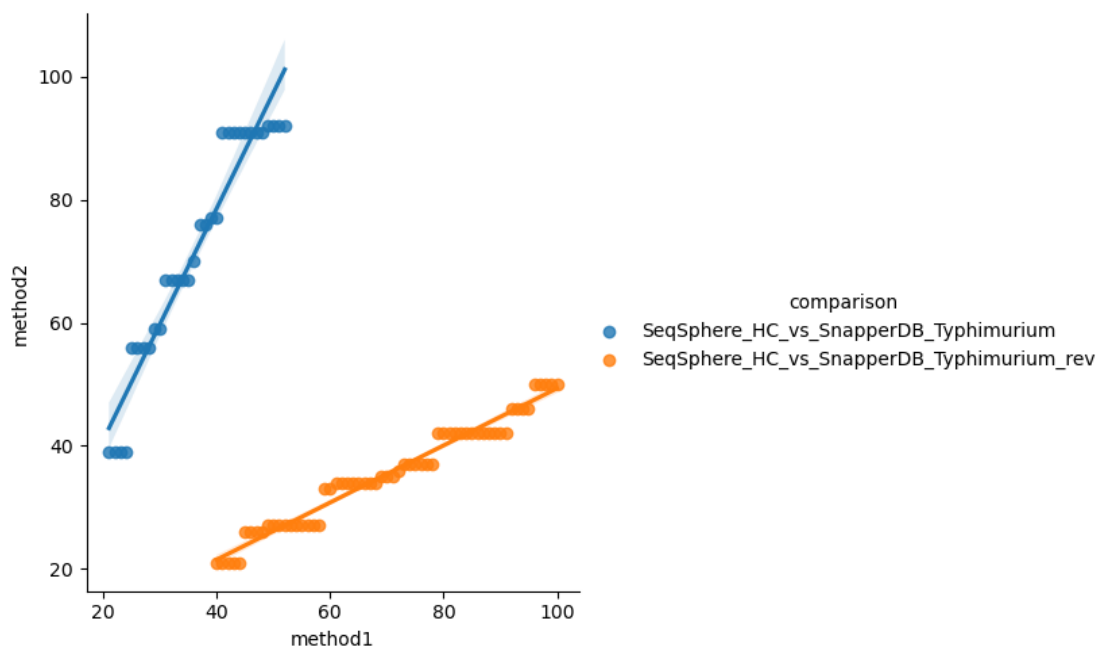


Figure S4.29.3. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 32 (blue) and 61 (orange) points is presented.

30. SeqSphere single-linkage vs. snippySnake single-linkage

Table S4.30. Details on pipeline parameters, with indication of the pipeline version, the clustering method, the schema (for allele-based pipelines) and reference (for SNP-based pipelines), and the dataset used.

	SeqSphere single-linkage	snippySnake single-linkage
Pipeline version	v8.3.4	v1.1.0
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage(ReporTree)
Schema / Reference	Enterobase	H15092067901-2 (Infantis) / AM933172 (Enteritidis) / AE006468 (Typhimurium)
Dataset	All samples	Infantis / Enteritidis / Typhimurium

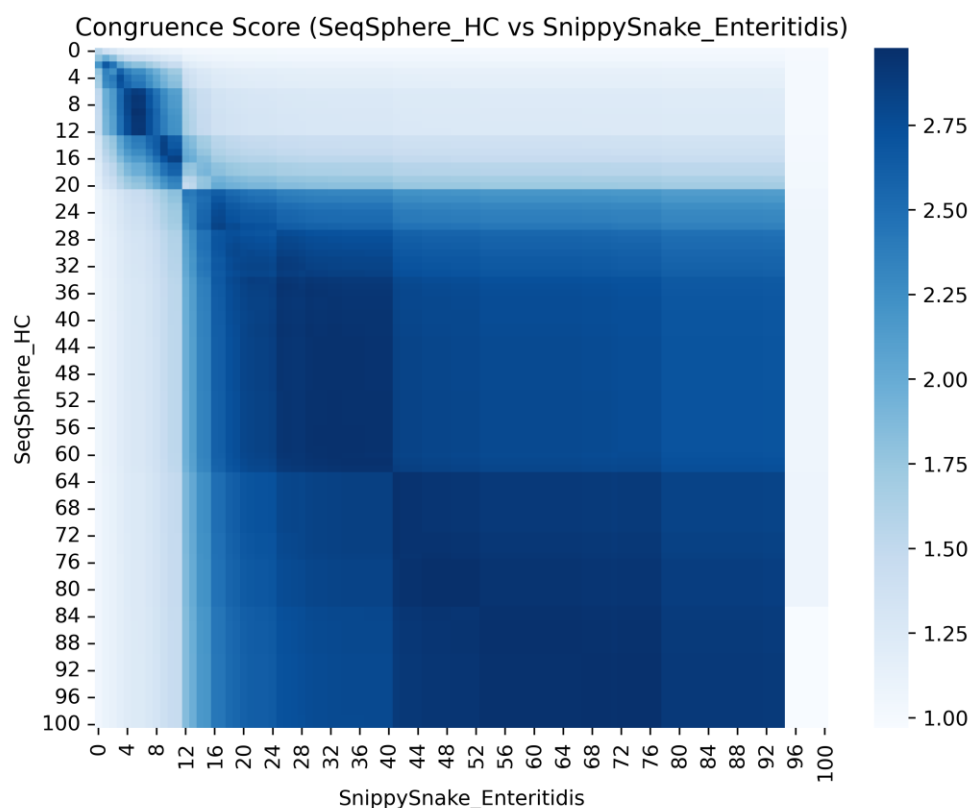


Figure S4.30.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Enteritidis. Axis represent the different allele/SNP distance thresholds.

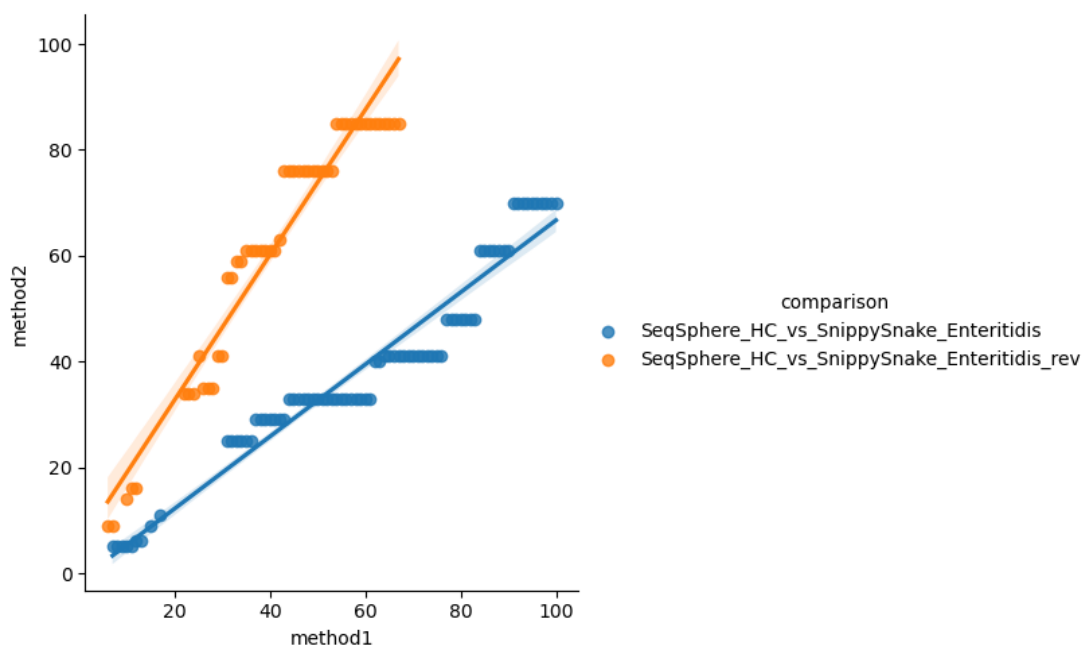


Figure S4.30.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Enteritidis. A linear tendency line supported by 32 (blue) and 61 (orange) points is presented.

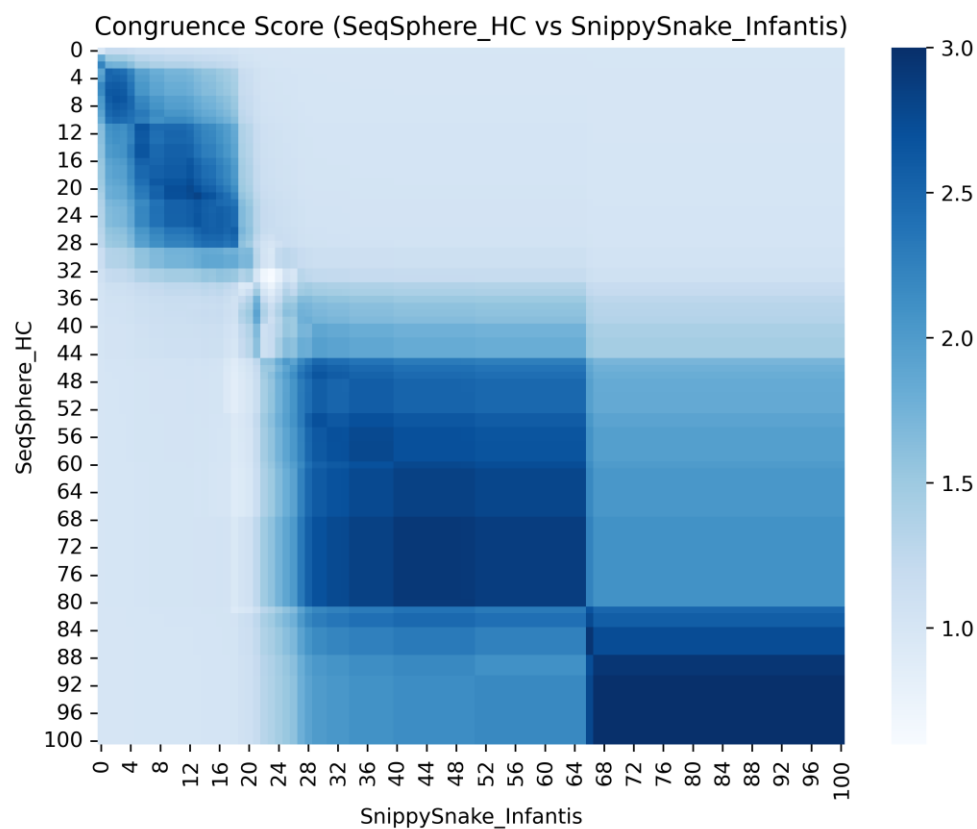


Figure S4.30.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Infantis. Axis represent the different allele/SNP distance thresholds.

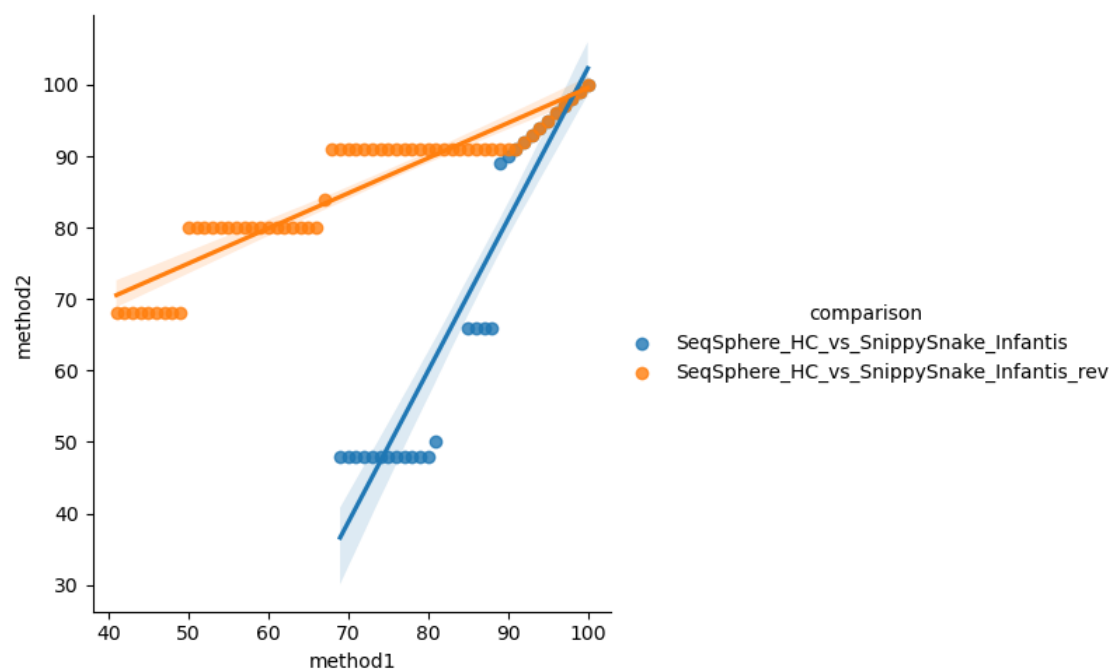


Figure S4.30.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Infantis. A linear tendency line supported by 79 (blue) and 51 (orange) points is presented.

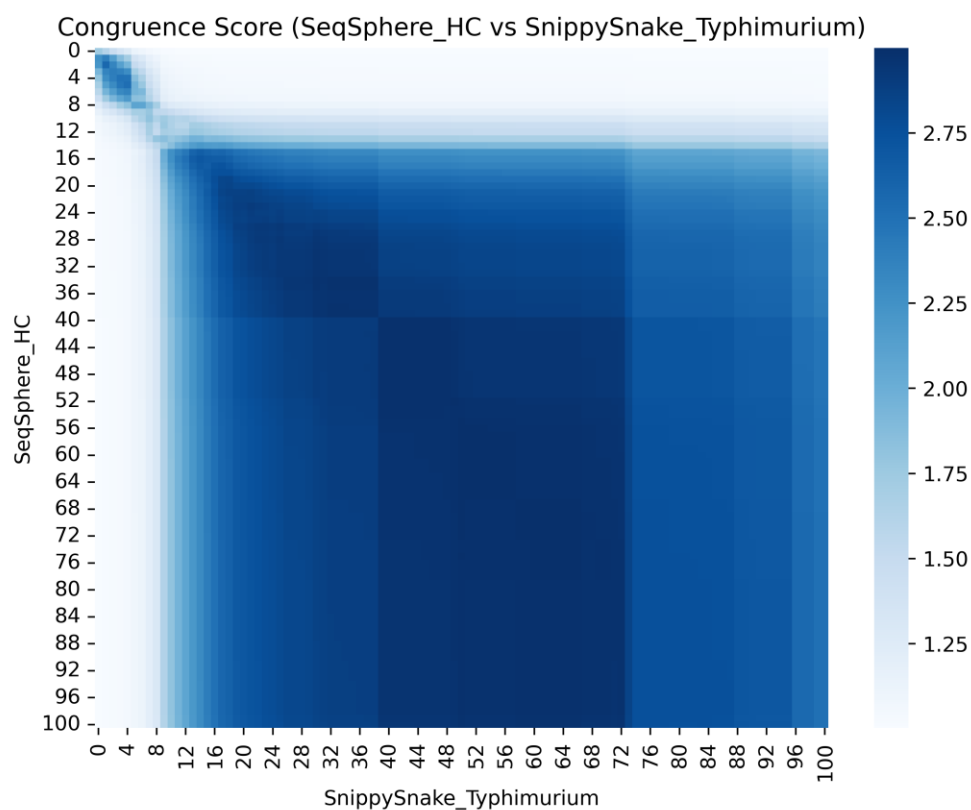


Figure S4.30.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for Typhimurium. Axis represent the different allele/SNP distance thresholds

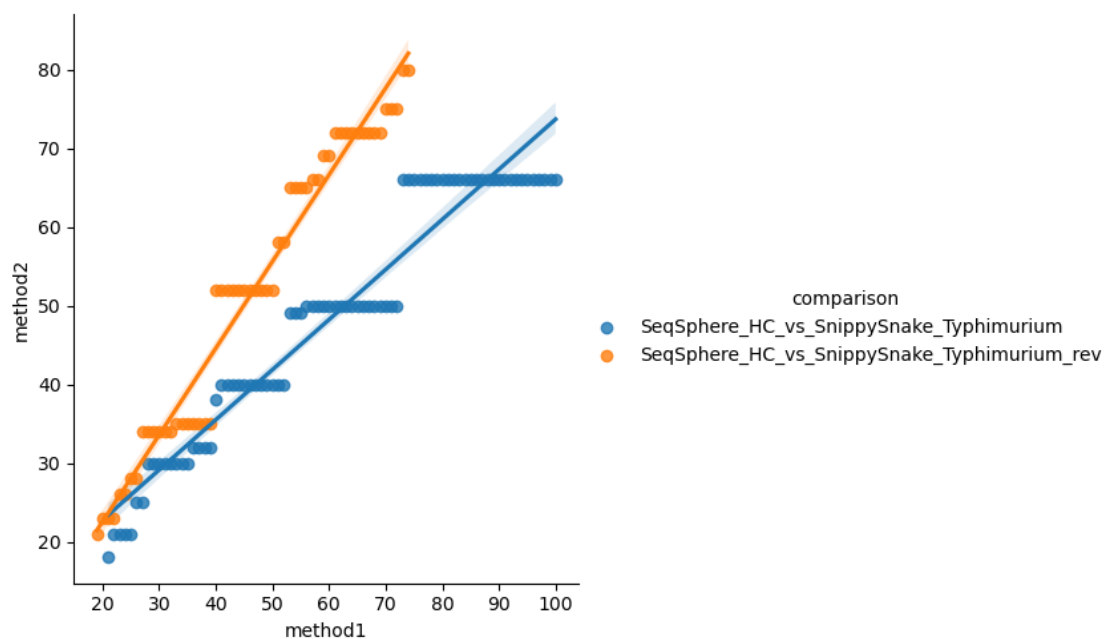


Figure S4.30.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for Typhimurium. A linear tendency line supported by 80 (blue) and 56 (orange) points is presented.