

Supplementary Data 28

Details on the analysis of the dataset of *Campylobacter jejuni*

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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 clonal complex (CC). 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 CC (ADs)	CS with CC
chewieSnake_HC	3686	3498	94.90	1343	1128	328	2.32	644	2.69
chewieSnake_GT	3686	3498	94.90	1343	1229	460	2.32	796	2.66
INNUENDO-like_HC (INNUENDO wgMLST schema)	3686	3638	98.70	899/2794	852	226	2.32	425	2.69
INNUENDO-like_GT (INNUENDO wgMLST schema)	3686	3638	98.70	899/2794	897	261	2.27	495	2.65
INNUENDO-like_HC (cgMLST schema)	3686	3625	98.35	678	644	168	2.32	315	2.69
INNUENDO-like_GT (cgMLST schema)	3686	3625	98.35	678	677	196	2.27	388	2.69
INNUENDO-like_HC (Enterobase schema)	3686	3496	94.85	1343	1224	351	2.33	681	2.69
INNUENDO-like_GT (Enterobase schema)	3686	3496	94.85	1343	1286	463	2.31	839	2.66
Ridom SeqSphere_HC	3686	3668	99.51	637	116	-	-	-	-
Ridom SeqSphere_HC (wgMLST schema)	3686	3637	98.67	860/1595	806	203	2.33	389	2.69
Ridom SeqSphere_GT (wgMLST schema)	3686	3637	98.67	860/1595	848	234	2.38	522	2.62
Bionumerics_HC	3686	3535	95.90	1343	1202	354	2.33	676	2.69
Mentalist_HC	3686	3581	97.15	209/2794	196	-	-	-	-
Mentalist_GT	3686	3581	97.15	209/2794	207	-	-	-	-

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.

ST	Pipeline	N	QC PASS	QC PASS (%)	N partitions
21	CSI Phylogeny	361	361	100.00	2669
45	CSI Phylogeny	165	165	100.00	2523
48	CSI Phylogeny	173	173	100.00	996
50	CSI Phylogeny	218	218	100.00	1677
257	CSI Phylogeny	110	100	100.00	1382

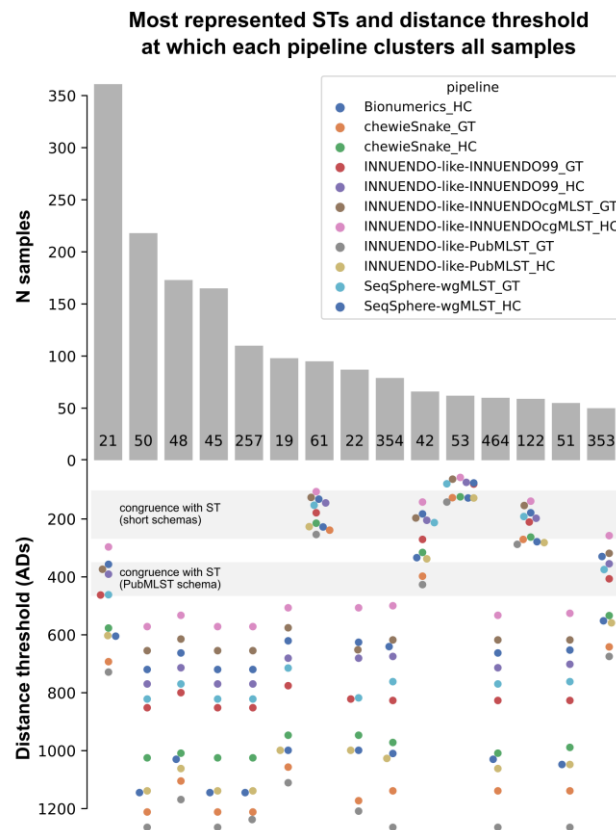


Figure S1. Allele-based clustering congruence with ST. Barplot (top) with the number of samples of the top represented STs (≥ 50 samples) present in the *C. jejuni* dataset, with a swarmplot (bottom) indicating the ADs at which each pipeline clusters together all samples of each of these STs.

Section 2 – Comparison of allele-based pipelines

1. Bionumerics single-linkage vs. chewieSnake GrapeTree

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 GrapeTree
Pipeline version	v8.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1202	1229

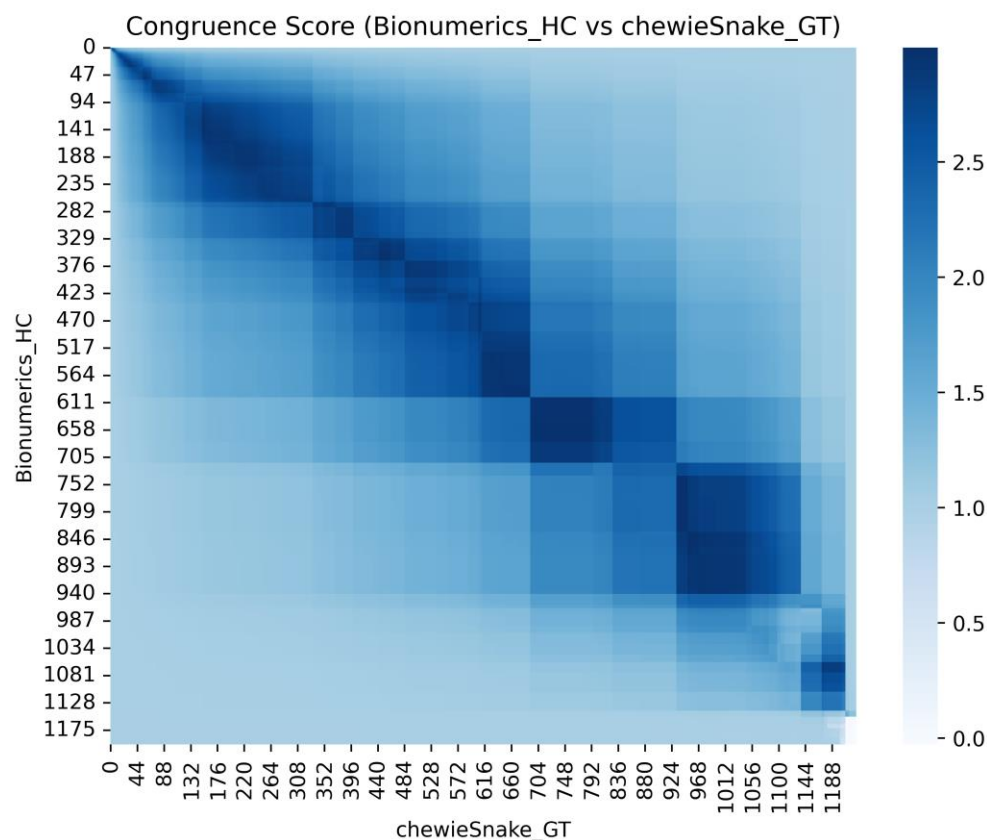


Figure S2.1.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

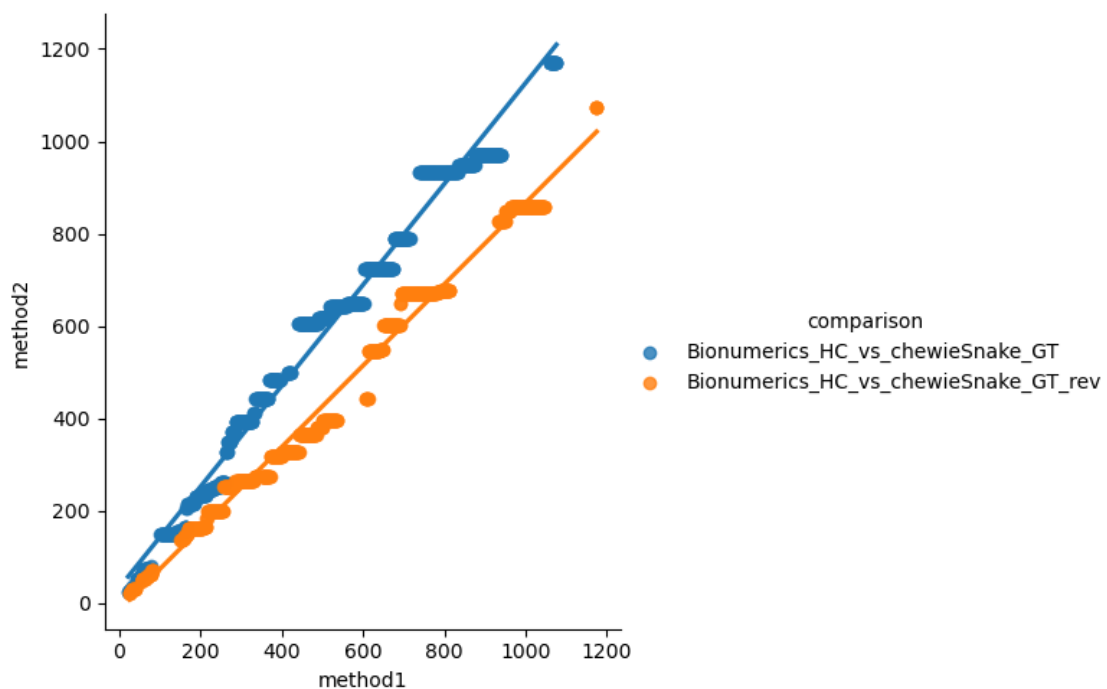


Figure S2.1.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 848 (blue) and 739 (orange) points is presented.

2. Bionumerics single-linkage vs. chewieSnake single-linkage

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	chewieSnake single-linkage
Pipeline version	v8.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1202	1128

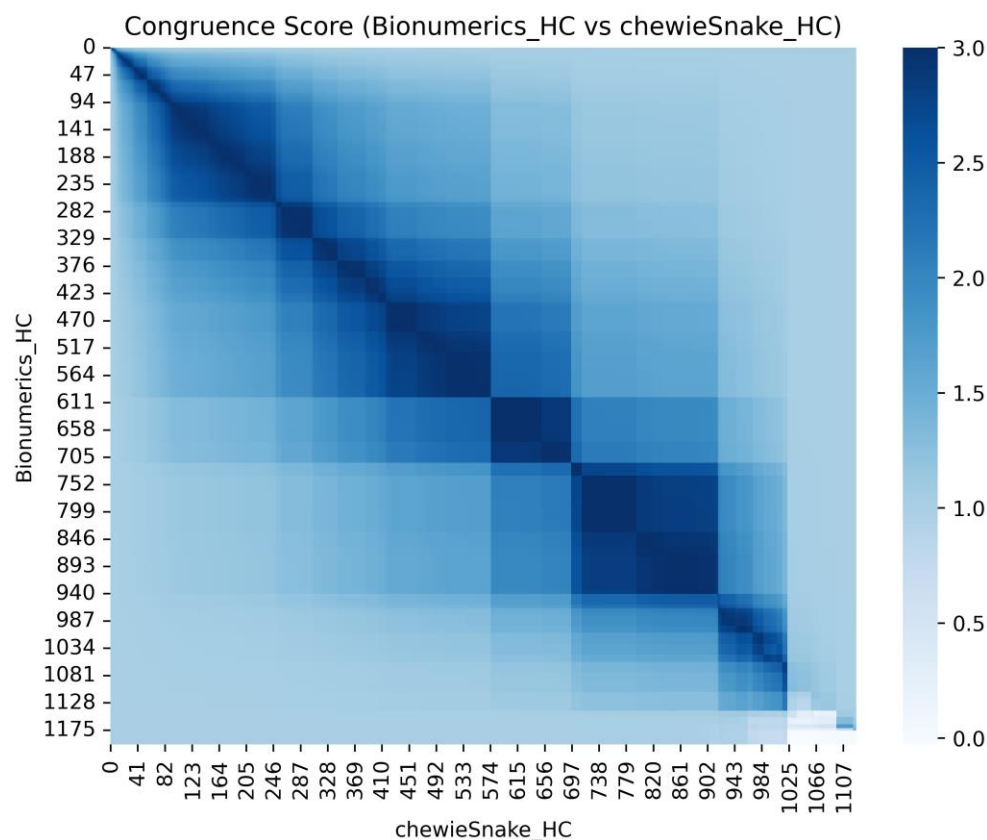


Figure S2.2.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

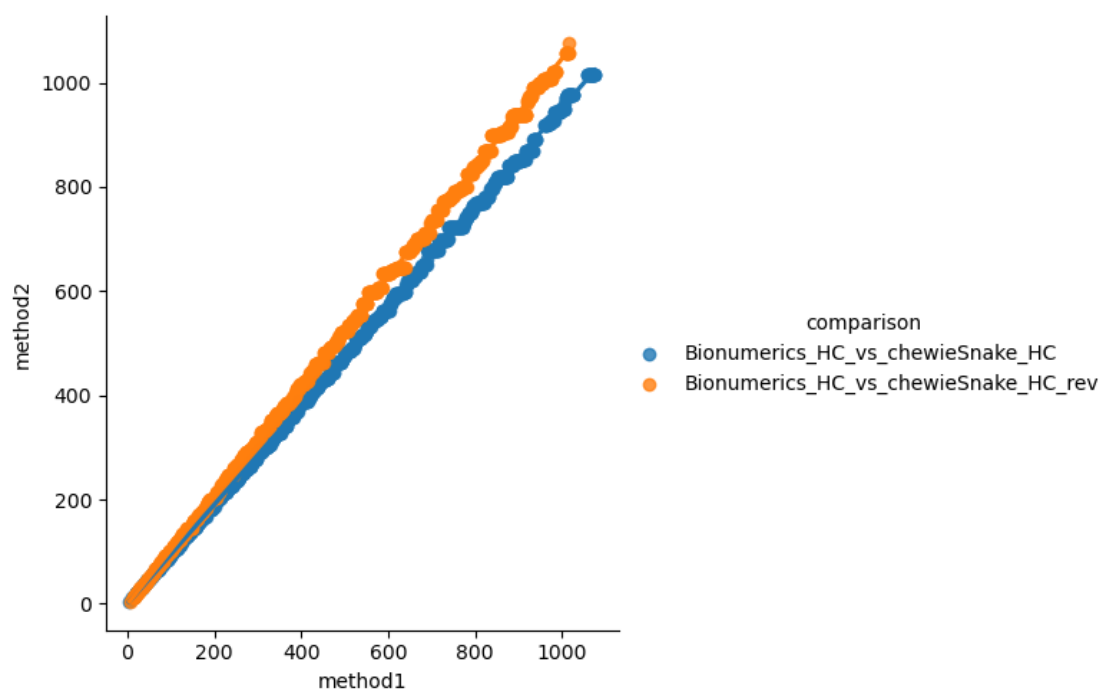


Figure S2.2.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1019 (blue) and 986 (orange) points is presented.

3. **Bionumerics single-linkage vs. INNUENDO-like-INNUENDO99 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-INNUENDO99 single-linkage
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	1202	852

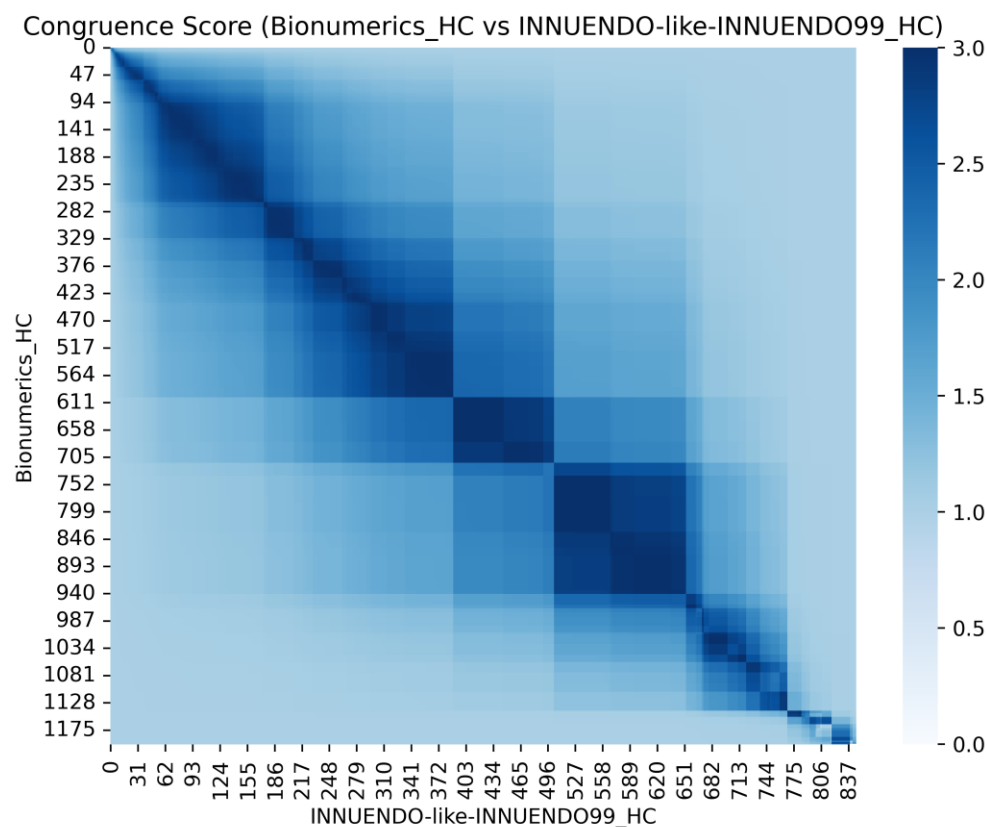


Figure S2.3.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

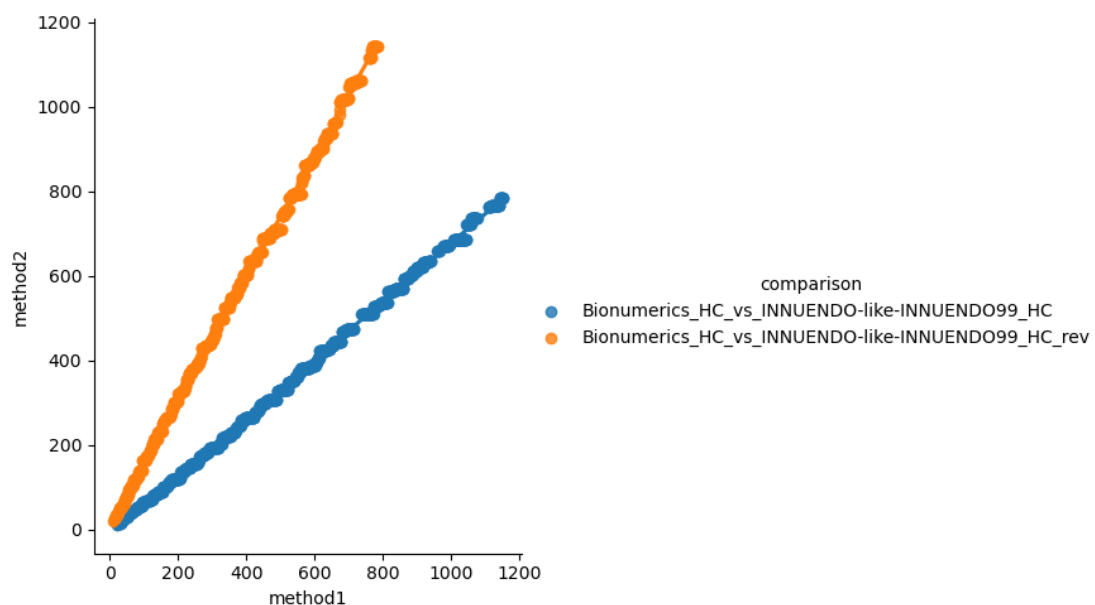


Figure S2.3.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1024 (blue) and 742 (orange) points is presented.

4. **Bionumerics single-linkage vs. INNUENDO-like-INNUENDOCgMLST 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- INNUENDOCgMLST GrapeTree
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1202	677

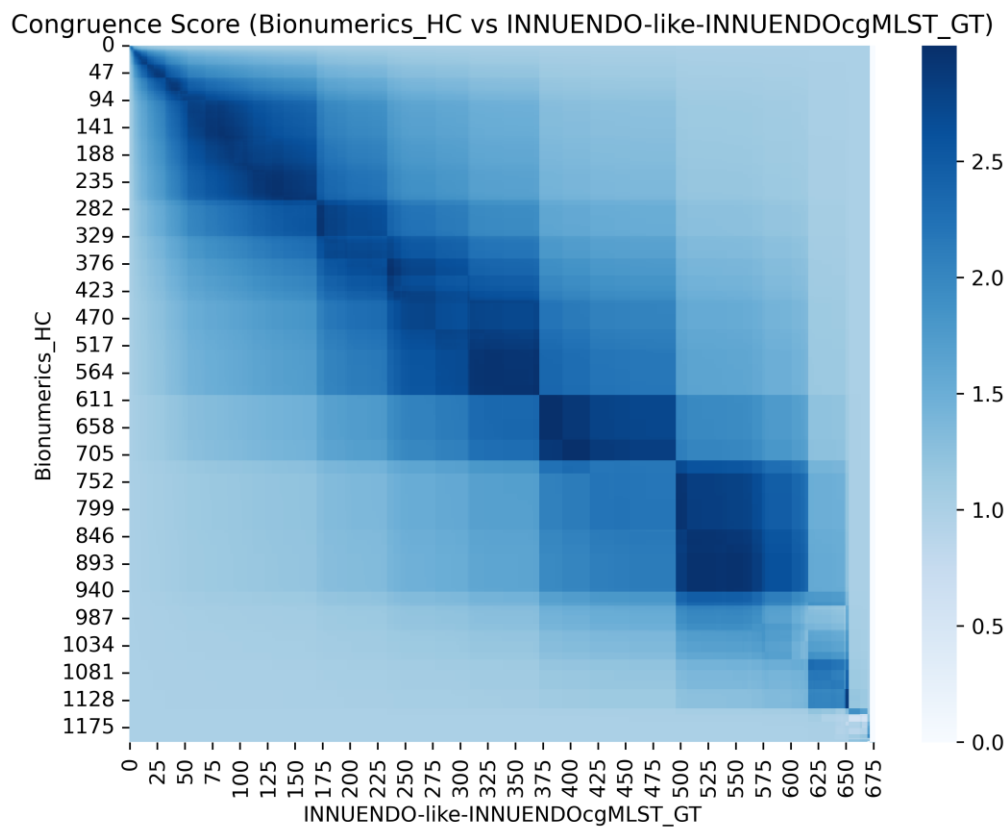


Figure S2.4.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

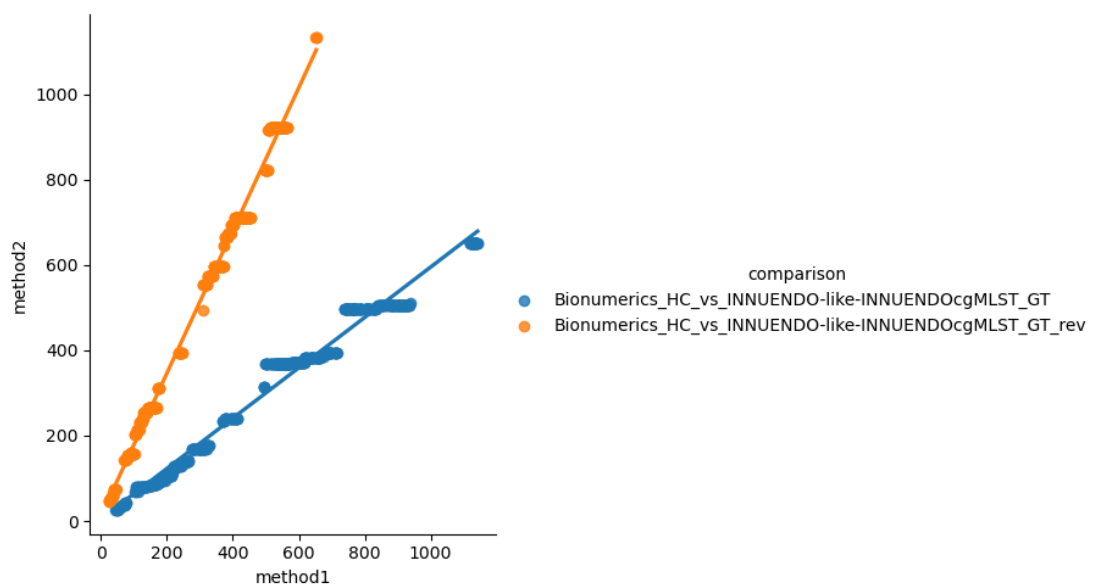


Figure S2.4.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 529 (blue) and 362 (orange) points is presented.

5. Bionumerics single-linkage vs. INNUENDO-like-INNUENDOCgMLST 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-INNUENDOCgMLST single-linkage
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1202	644

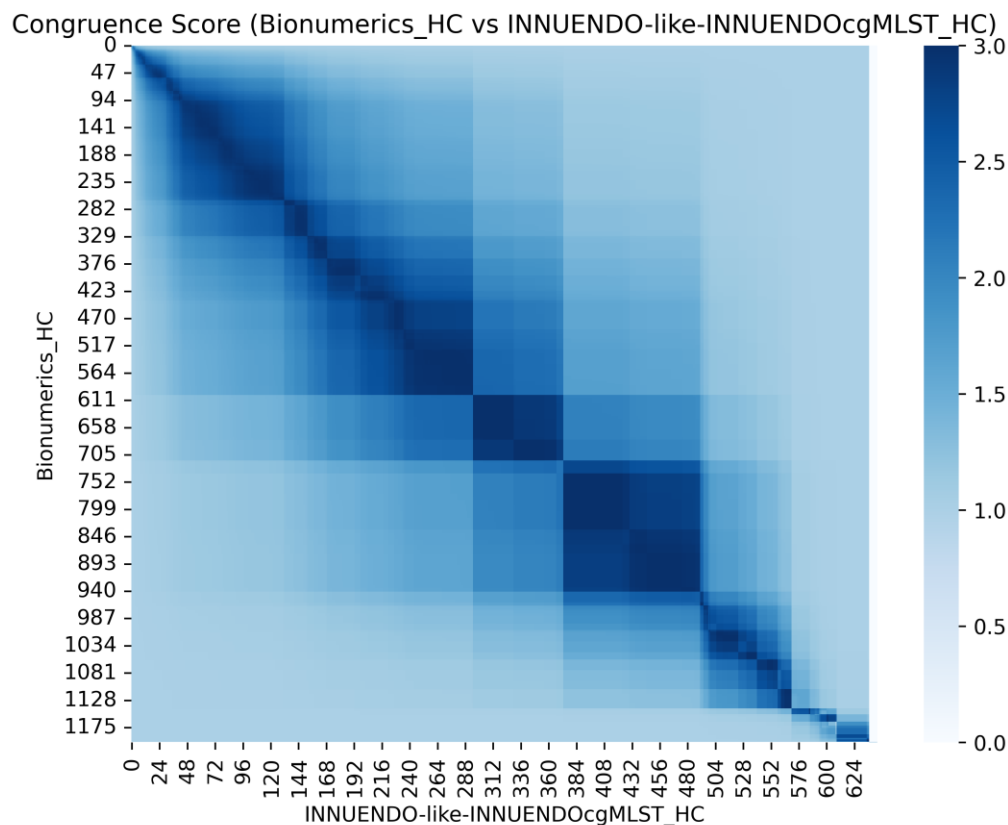


Figure S2.5.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

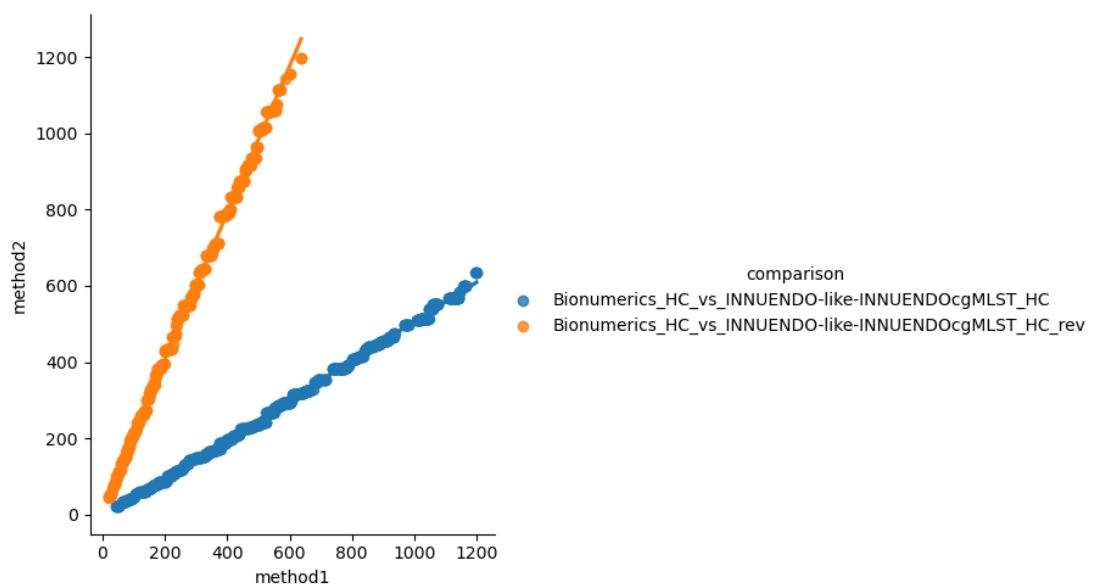


Figure S2.5.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 756 (blue) and 550 (orange) points is presented.

6. Bionumerics single-linkage vs. INNUENDO-like-PubMLST GrapeTree

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.

	Bionumerics single-linkage	INNUENDO-like-PubMLST GrapeTree
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1202	1286

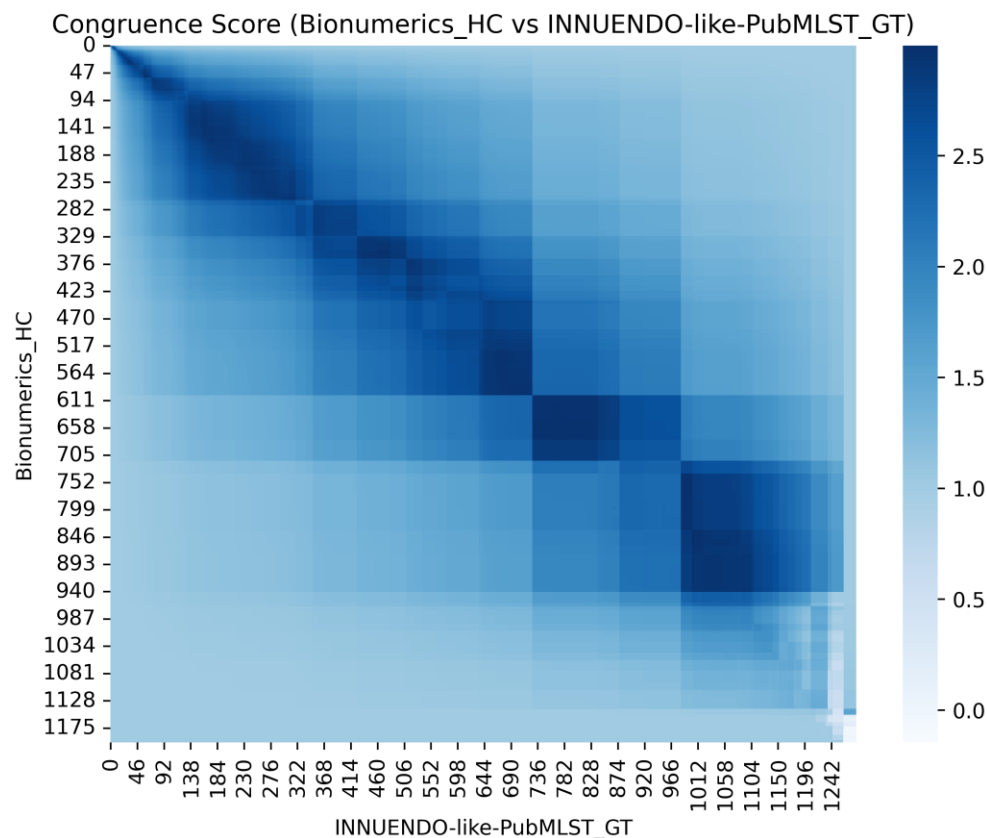


Figure S2.6.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

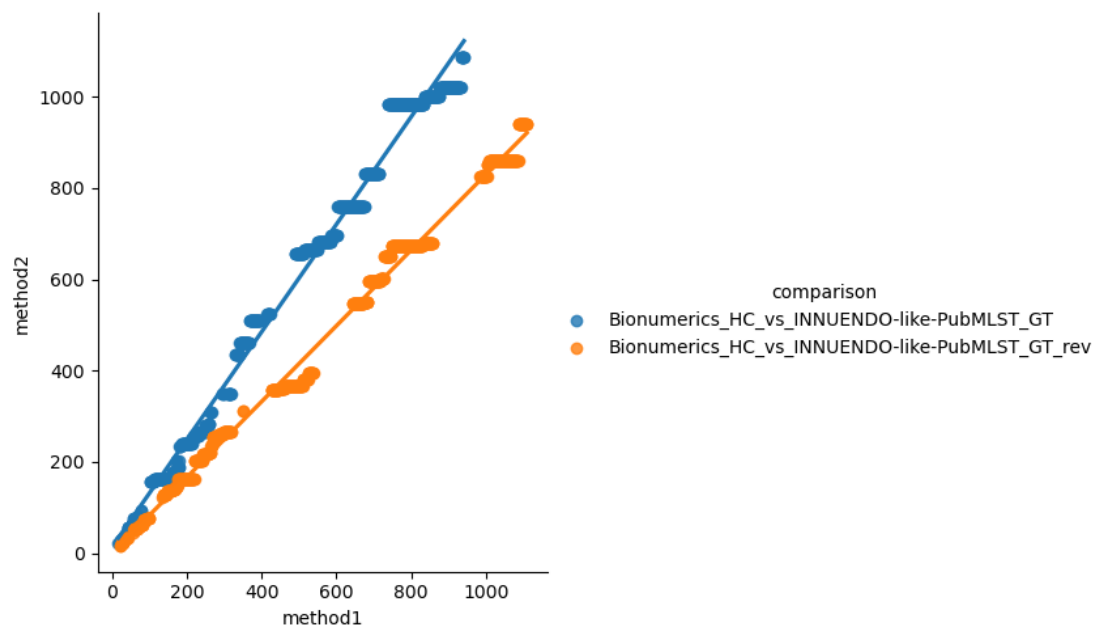


Figure S2.6.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 734 (blue) and 700 (orange) points is presented.

7. Bionumerics single-linkage vs. INNUENDO-like-PubMLST single-linkage

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.

	Bionumerics single-linkage	INNUENDO-like-PubMLST single-linkage
Pipeline version	v8.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1202	1224

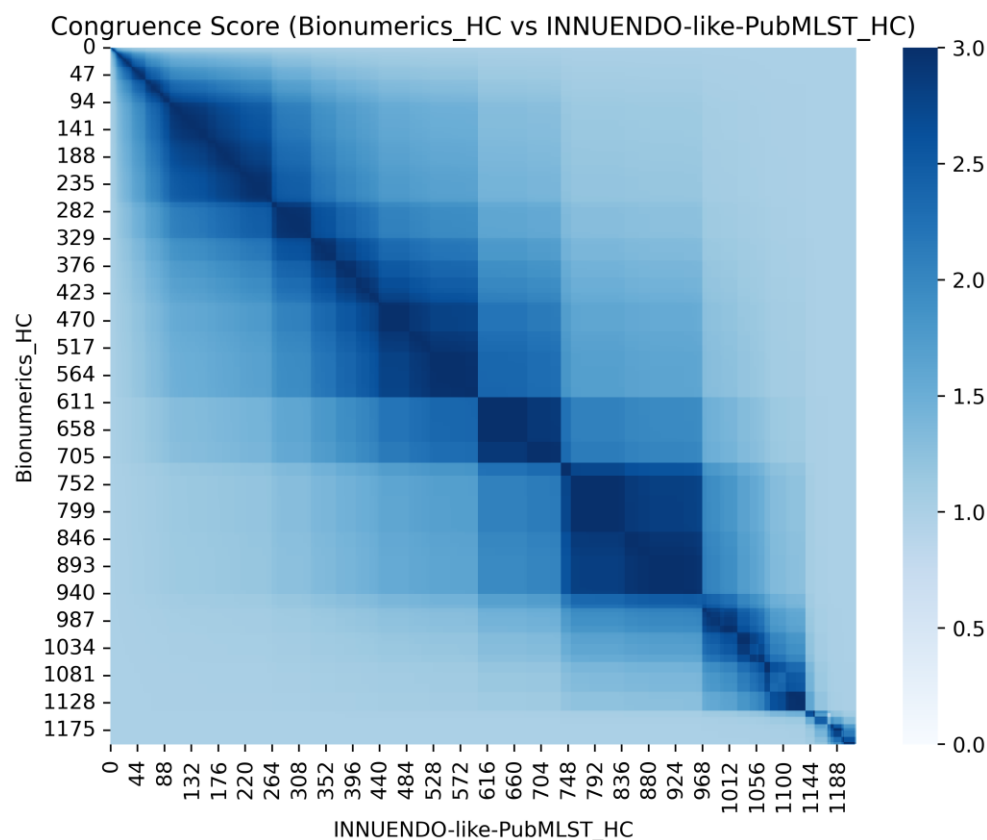


Figure S2.7.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

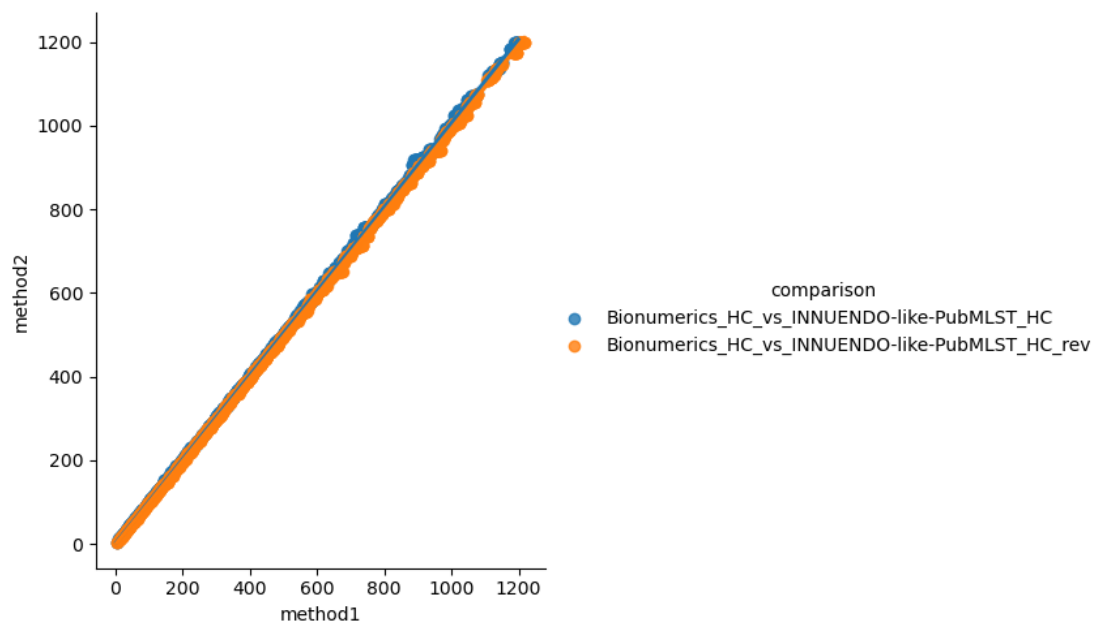


Figure S2.7.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1103 (blue) and 1136 (orange) points is presented.

8. **Bionumerics single-linkage vs. SeqSphere-wgMLST GrapeTree**

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.

	Bionumerics single-linkage	SeqSphere-wgMLST GrapeTree
Pipeline version	v8.1	v8.3.4
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1202	848

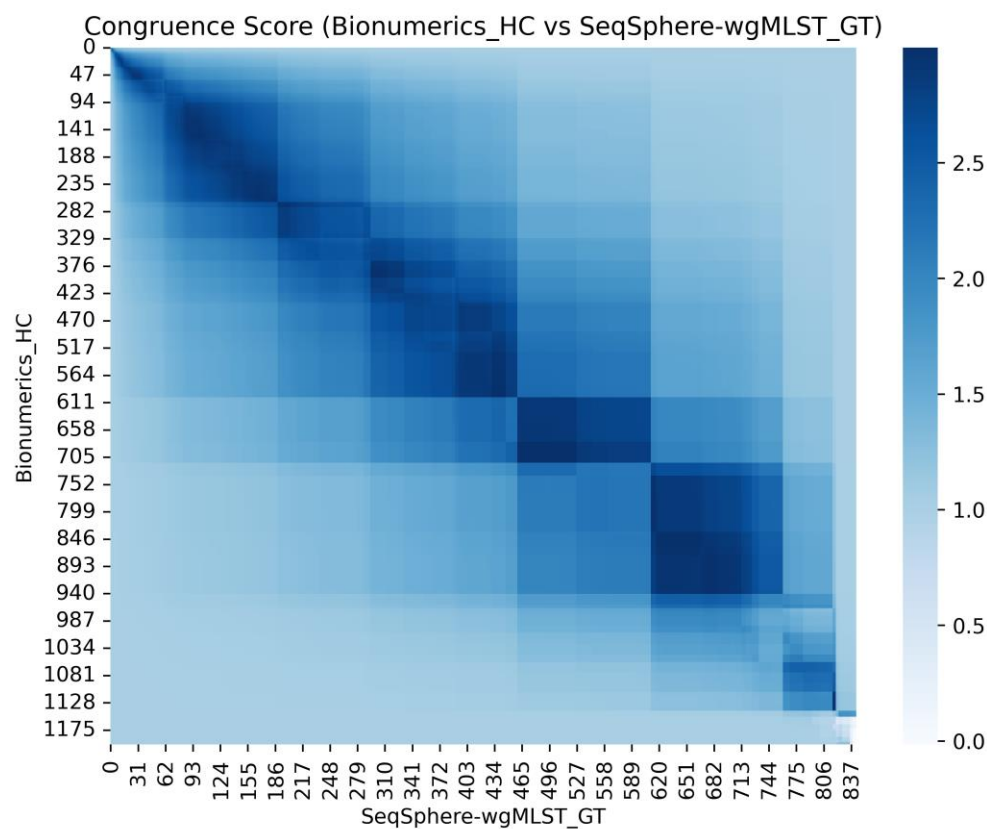


Figure S2.8.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

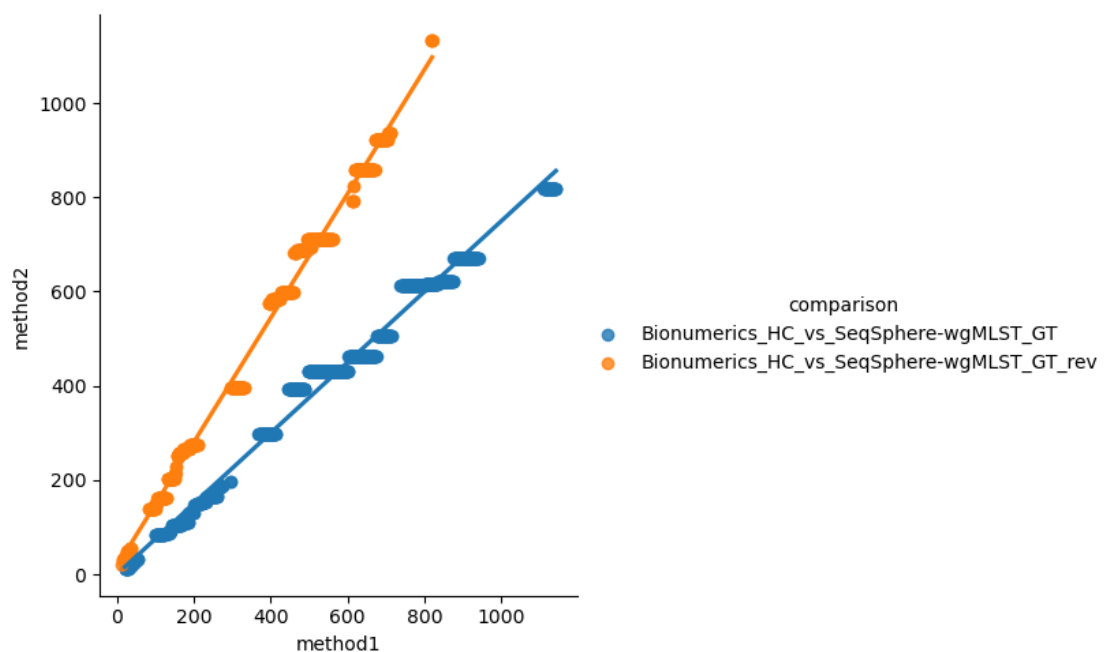


Figure S2.8.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 759 (blue) and 464 (orange) points is presented.

9. Bionumerics single-linkage vs. SeqSphere-wgMLST single-linkage

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.

	Bionumerics single-linkage	SeqSphere-wgMLST single-linkage
Pipeline version	v8.1	v8.3.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1202	806

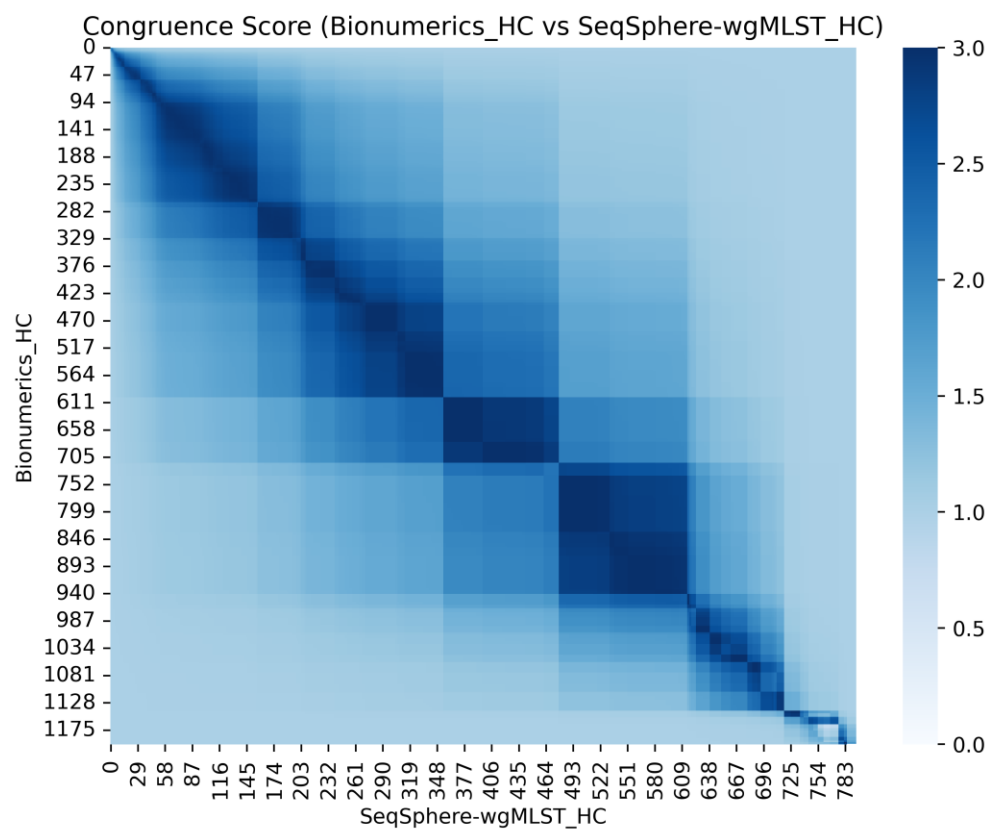


Figure S2.9.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

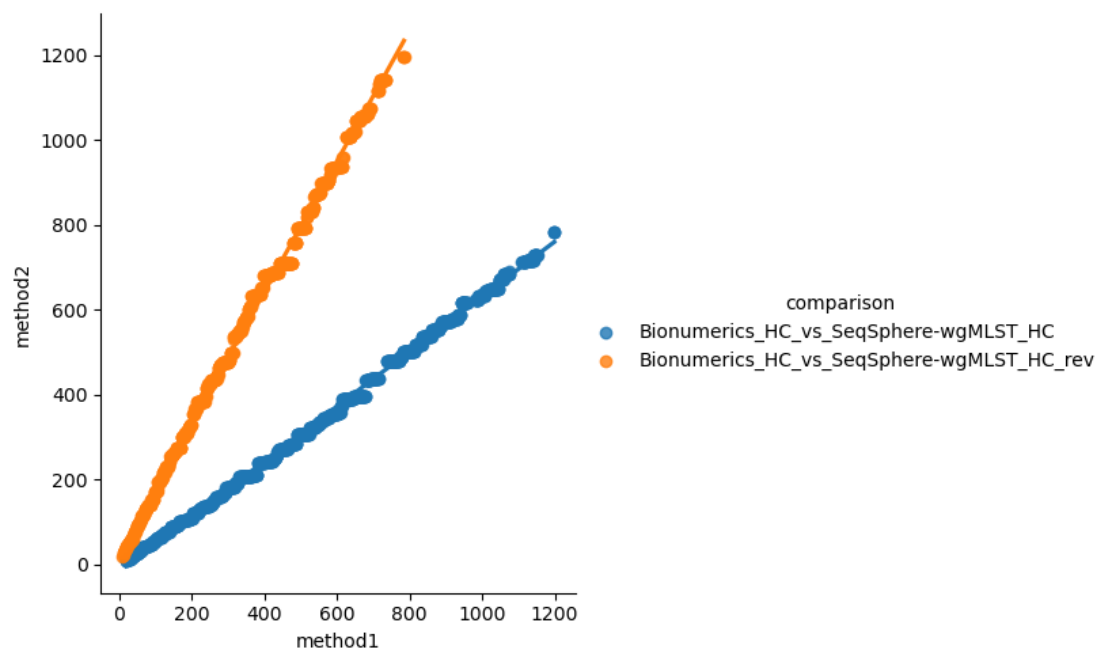


Figure S2.9.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1059 (blue) and 699 (orange) points is presented.

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

	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	PubMLST	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	1229	852

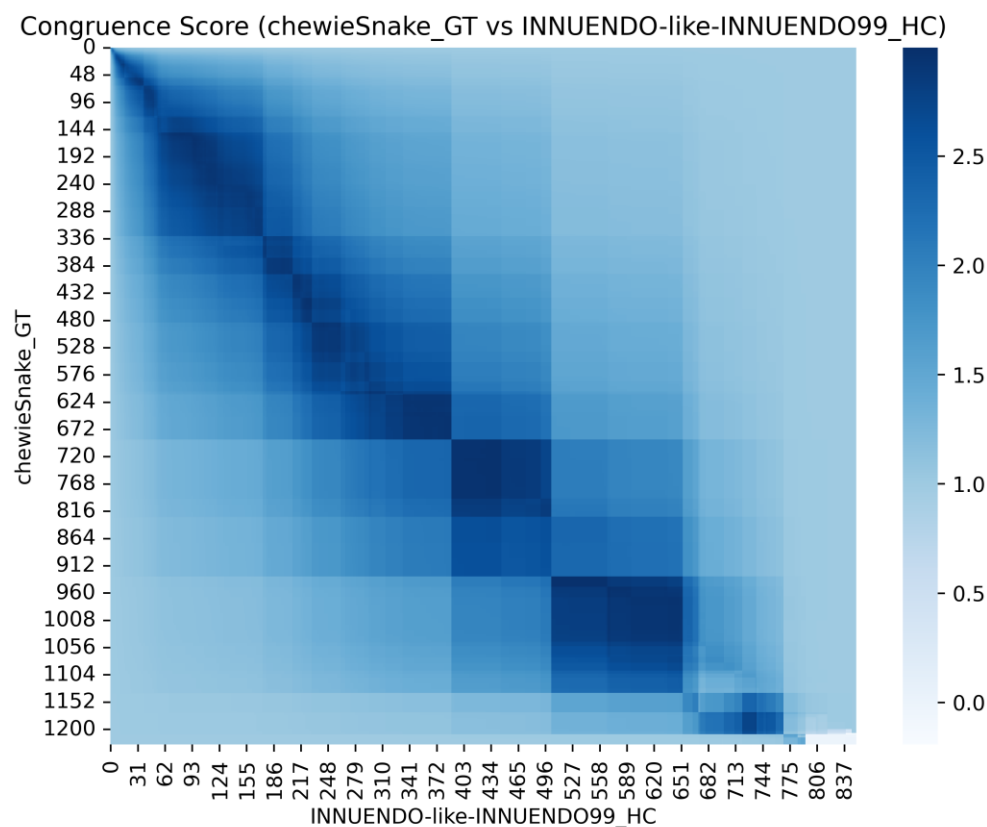


Figure S2.10.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

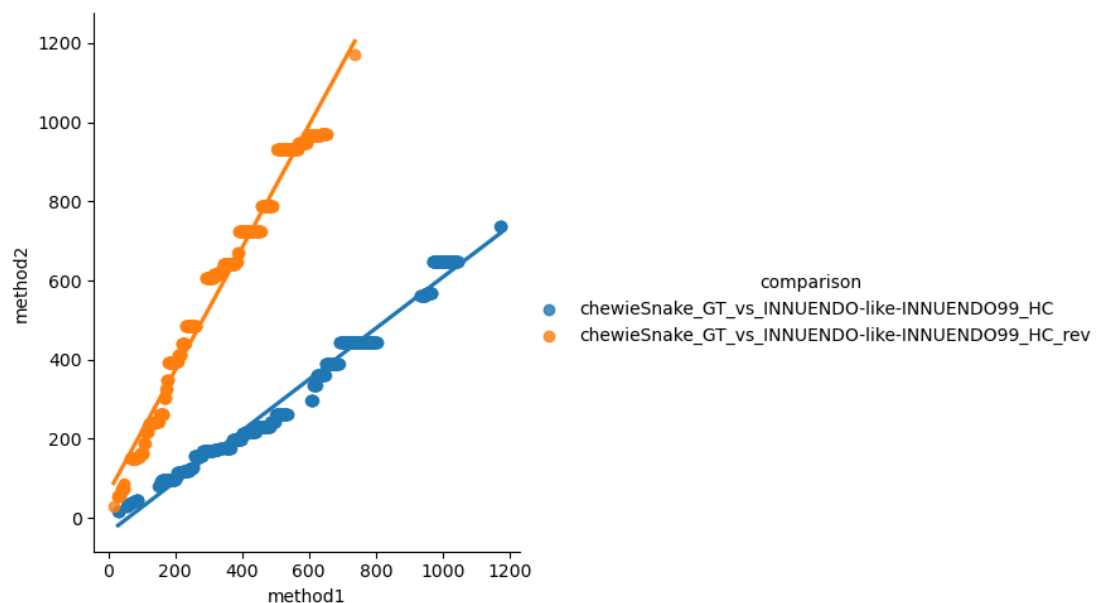


Figure S2.10.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 723 (blue) and 570 (orange) points is presented.

11. chewieSnake GrapeTree vs. INNUENDO-like-INNUENDOCgMLST 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.

	chewieSnake GrapeTree	INNUENDO-like-INNUENDOCgMLST GrapeTree
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1229	677

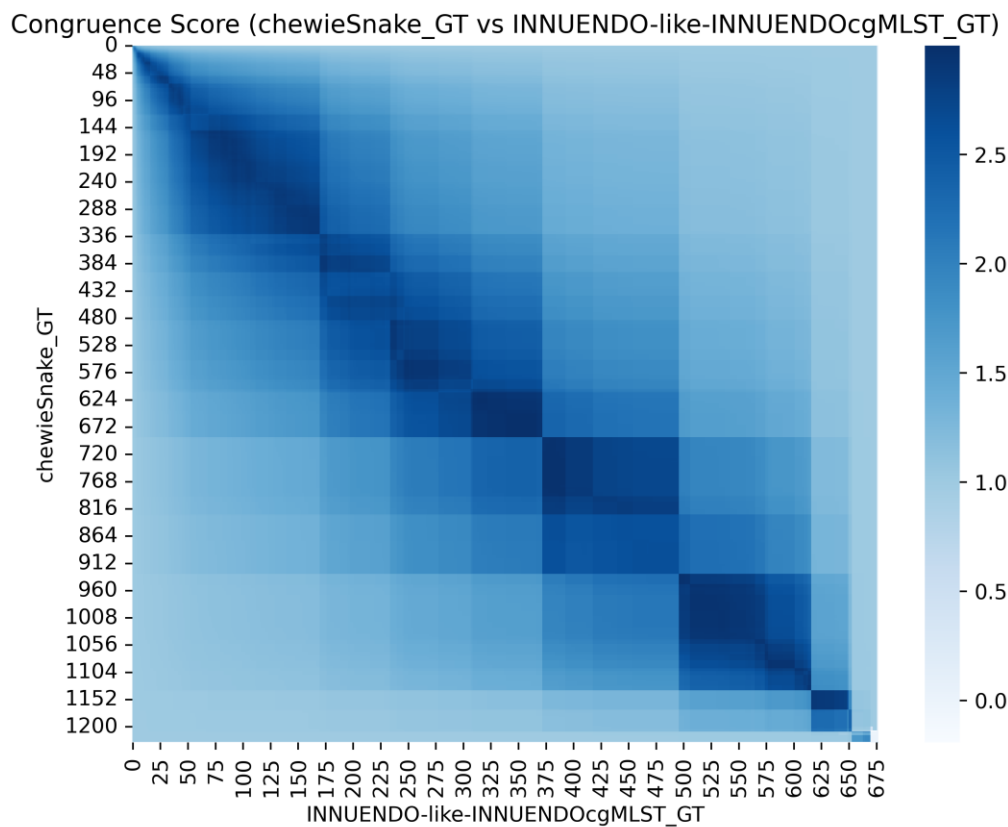


Figure S2.11.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

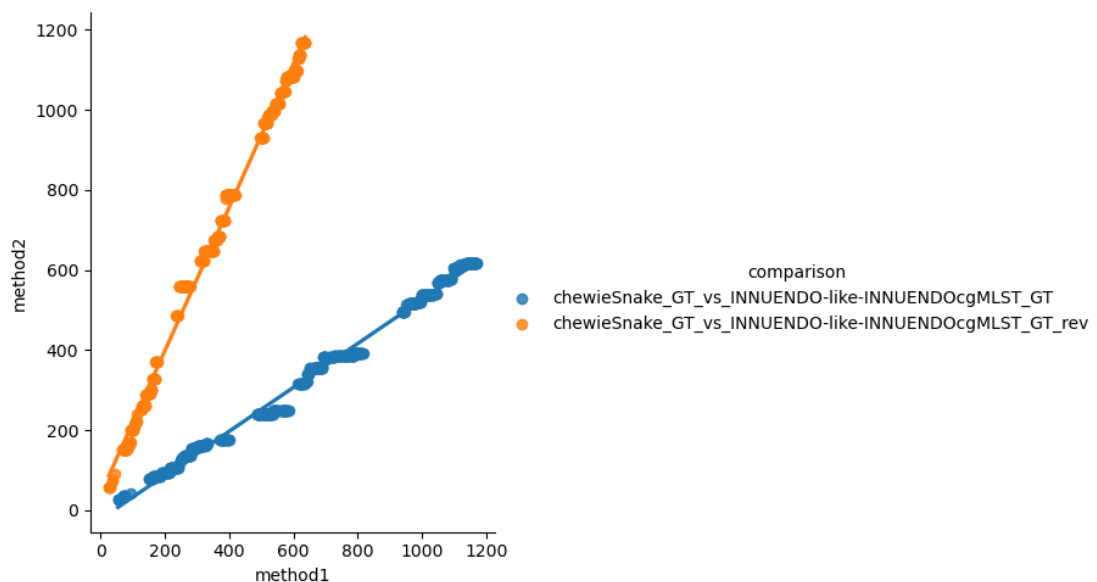


Figure S2.11.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 533 (blue) and 397 (orange) points is presented.

12. chewieSnake GrapeTree vs. INNUENDO-like-INNUENDOccgMLST 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.

	chewieSnake GrapeTree	INNUENDO-like- INNUENDOccgMLST single- linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1229	644

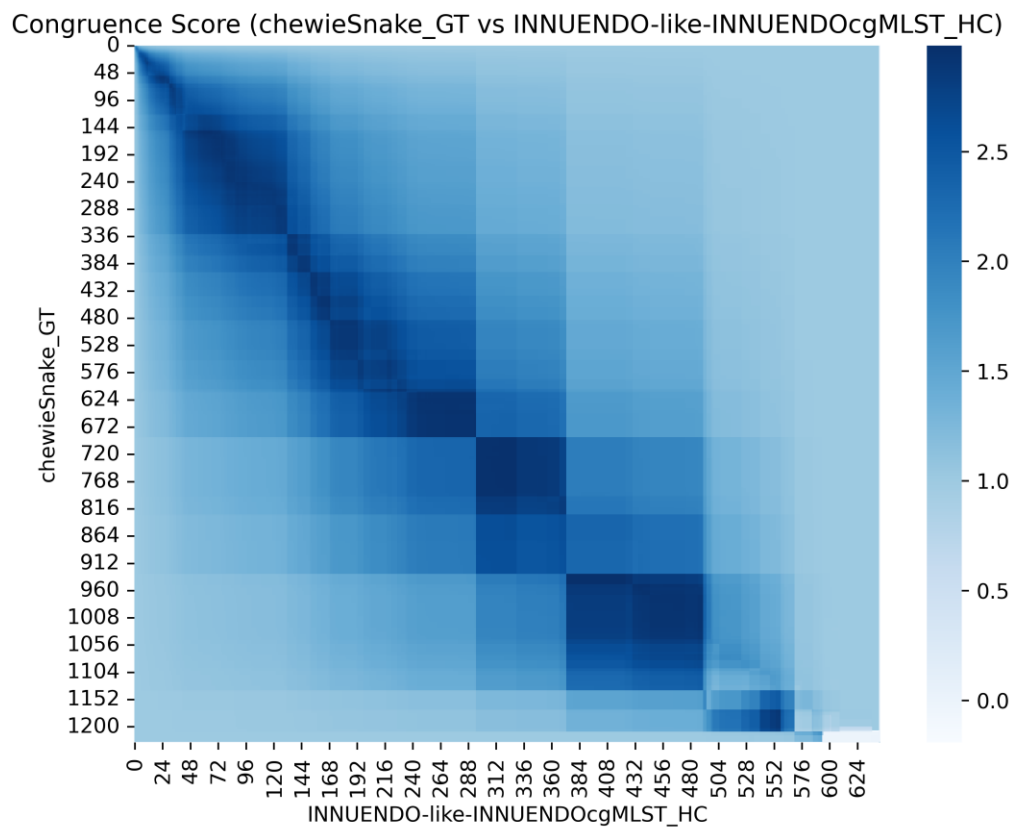


Figure S2.12.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

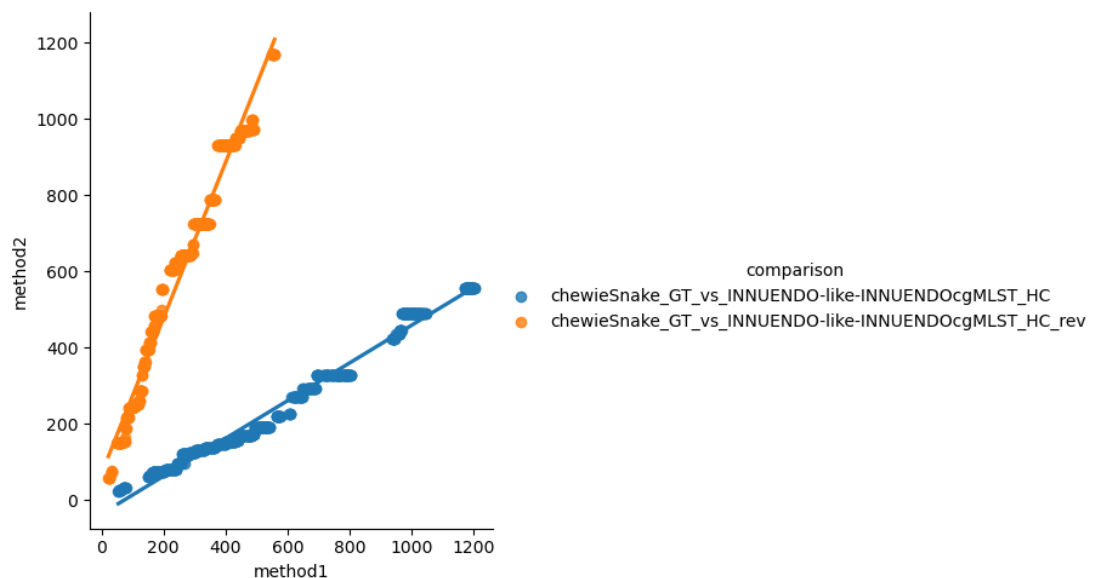


Figure S2.12.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 554 (blue) and 429 (orange) points is presented.

13. chewieSnake GrapeTree vs. SeqSphere-wgMLST 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.

	chewieSnake GrapeTree	SeqSphere-wgMLST GrapeTree
Pipeline version	v3.1.1	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1229	848

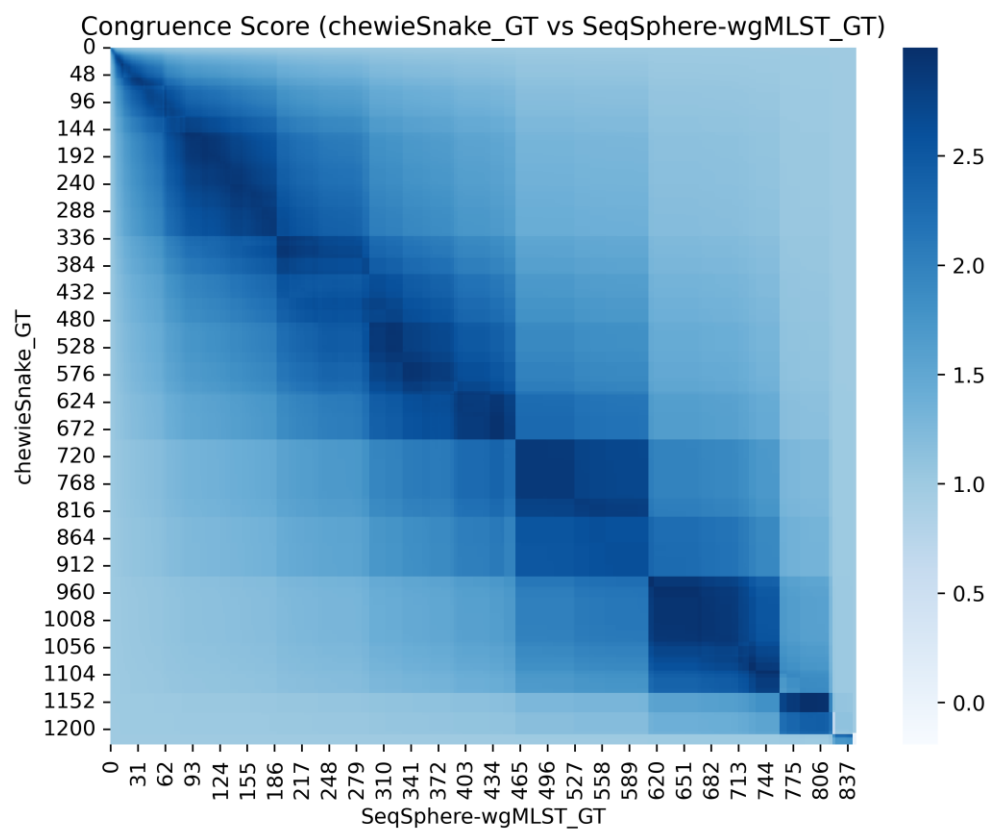


Figure S2.13.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

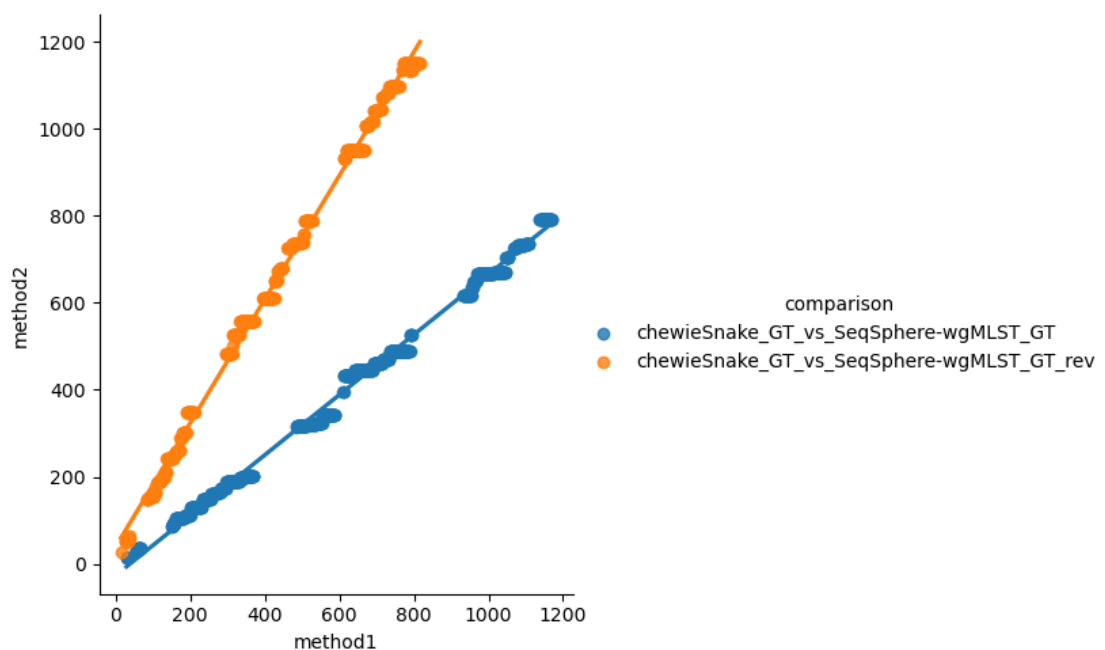


Figure S2.13.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 726 (blue) and 530 (orange) points is presented.

14. chewieSnake single-linkage vs. chewieSnake GrapeTree

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.

	chewieSnake single-linkage	chewieSnake GrapeTree
Pipeline version	v3.1.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1128	1229

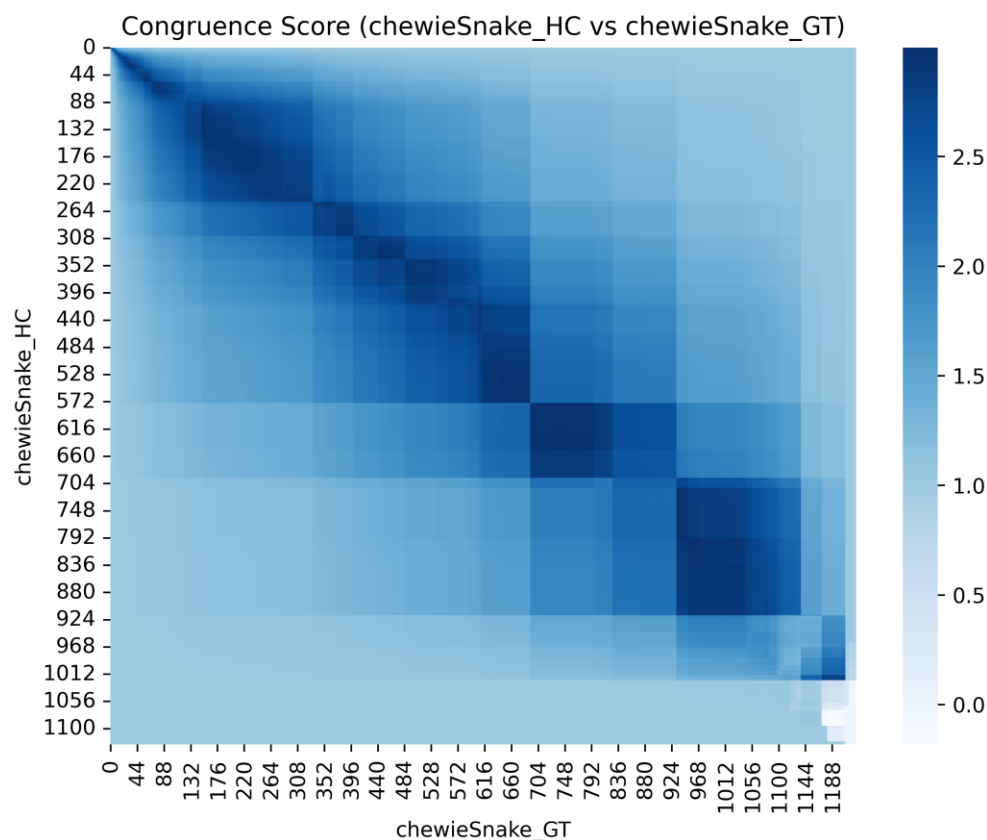


Figure S2.14.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

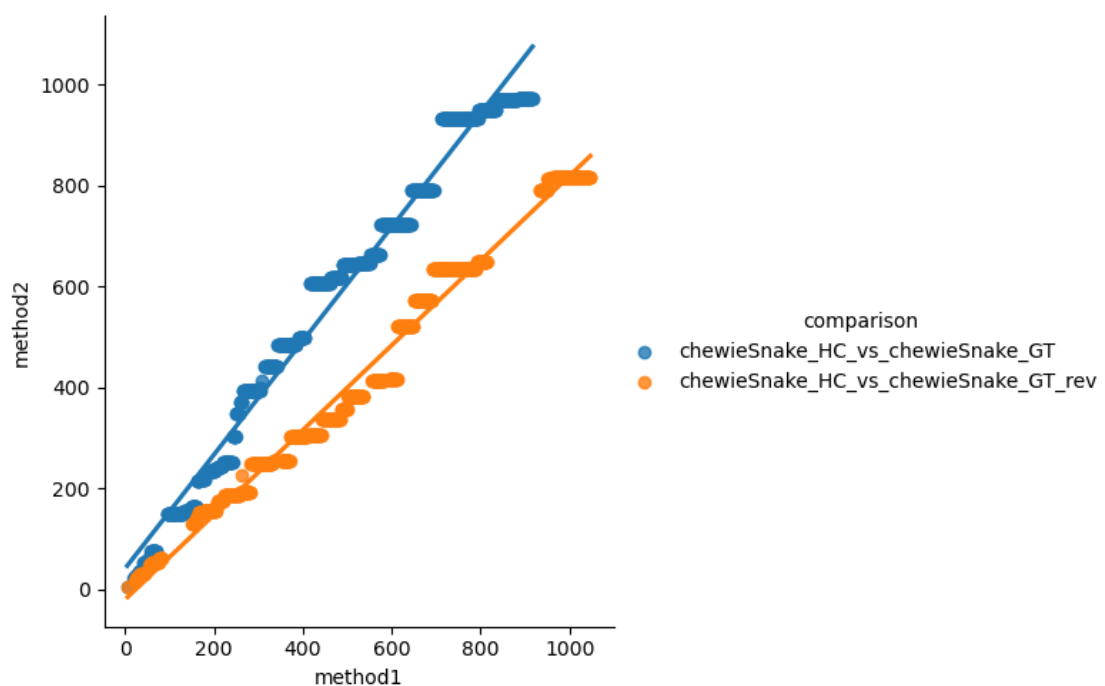


Figure S2.14.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 832 (blue) and 791 (orange) points is presented.

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

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.

	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	PubMLST	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	1128	852

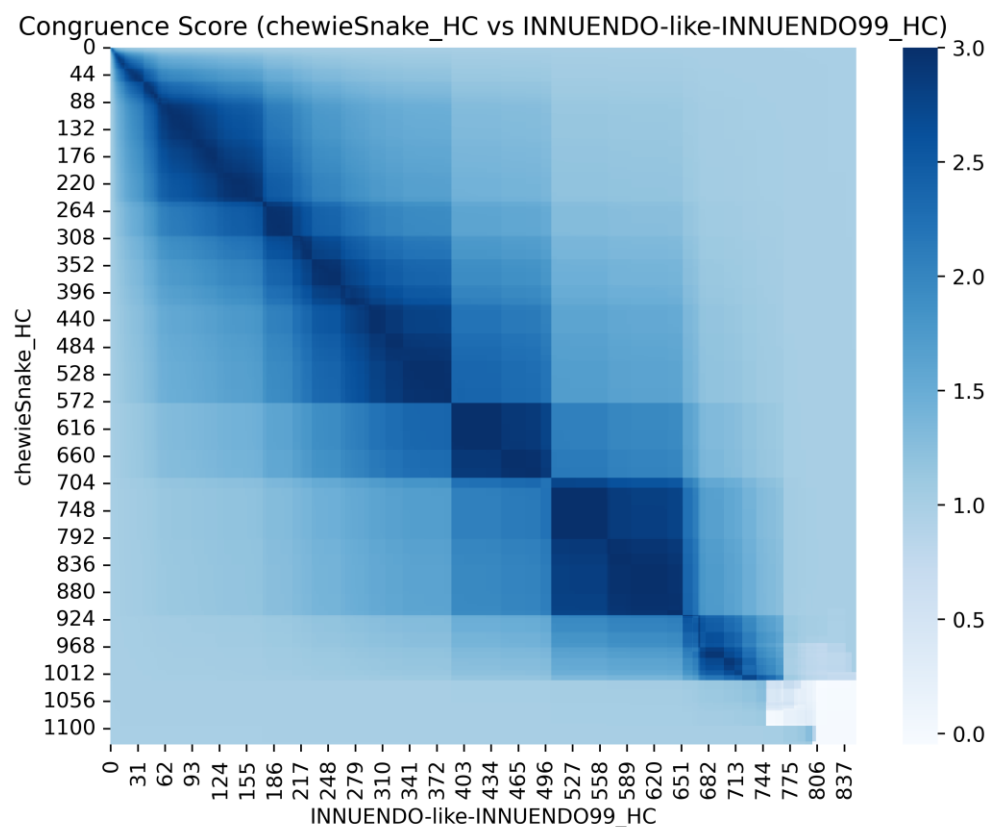


Figure S2.15.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

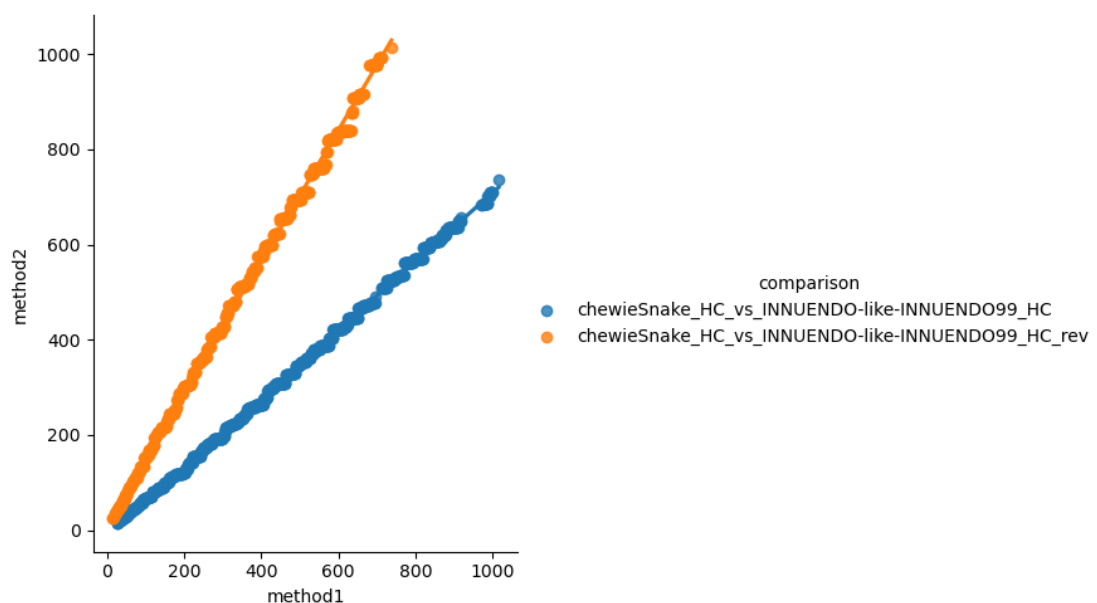


Figure S2.15.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 896 (blue) and 683 (orange) points is presented.

16. chewieSnake single-linkage vs. INNUENDO-like-INNUENDOccgMLST 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.

	chewieSnake single-linkage	INNUENDO-like-INNUENDOccgMLST GrapeTree
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1128	677

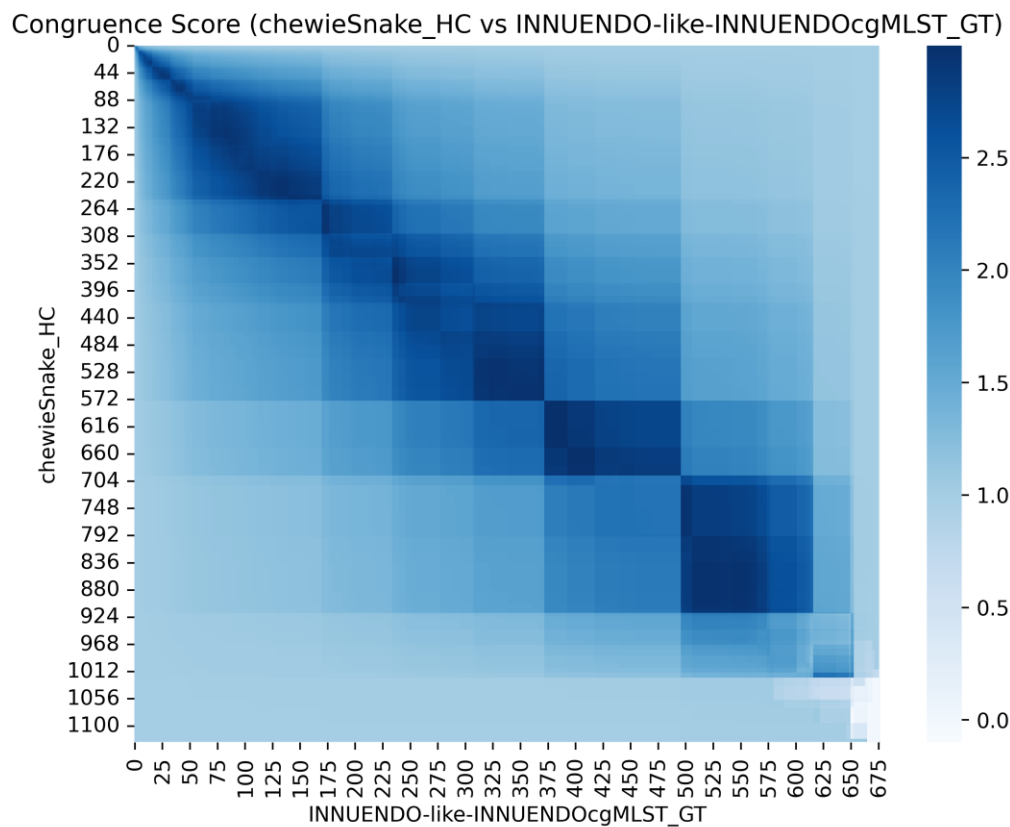


Figure S2.16.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

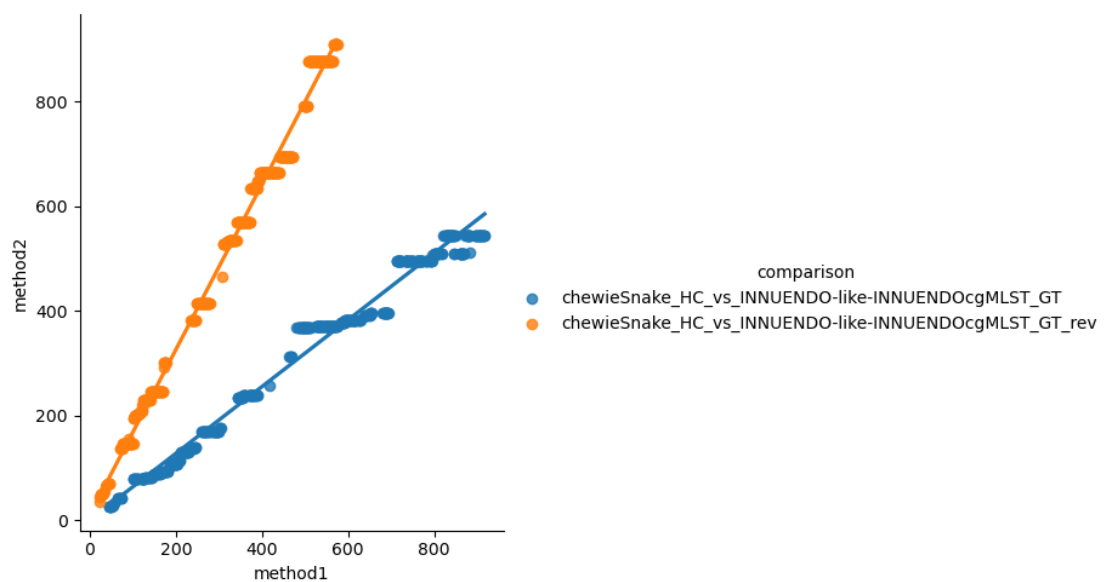


Figure S2.16.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 464 (blue) and 414 (orange) points is presented.

17. chewieSnake single-linkage vs. INNUENDO-like-INNUENDOcgmLST 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.

	chewieSnake single-linkage	INNUENDO-like-INNUENDOcgmLST single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1128	644

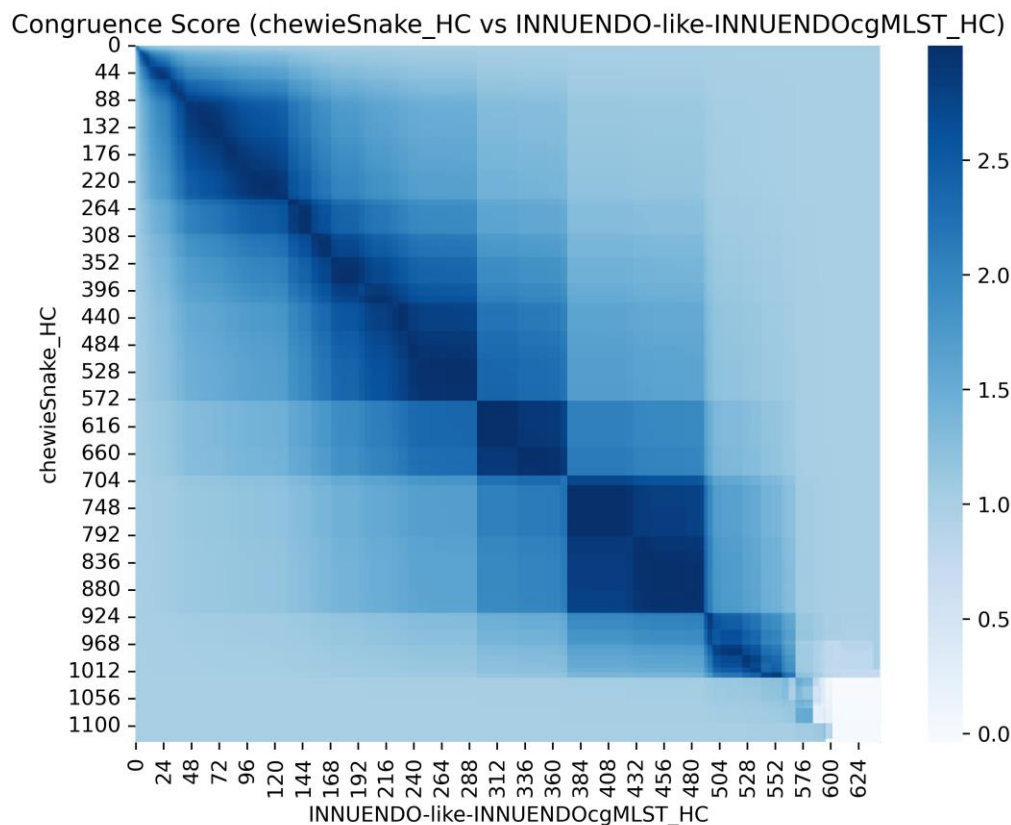


Figure S2.17.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

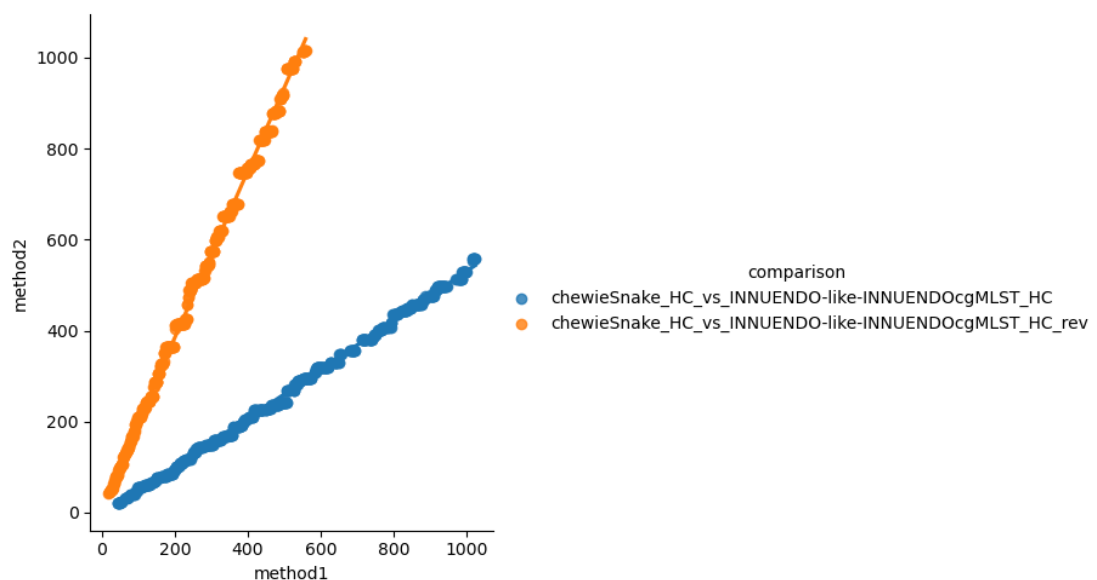


Figure S2.17.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 623 (blue) and 514 (orange) points is presented.

18. chewieSnake single-linkage vs. INNUENDO-like-PubMLST single-linkage

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.

	chewieSnake single-linkage	INNUENDO-like-PubMLST single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1128	1224

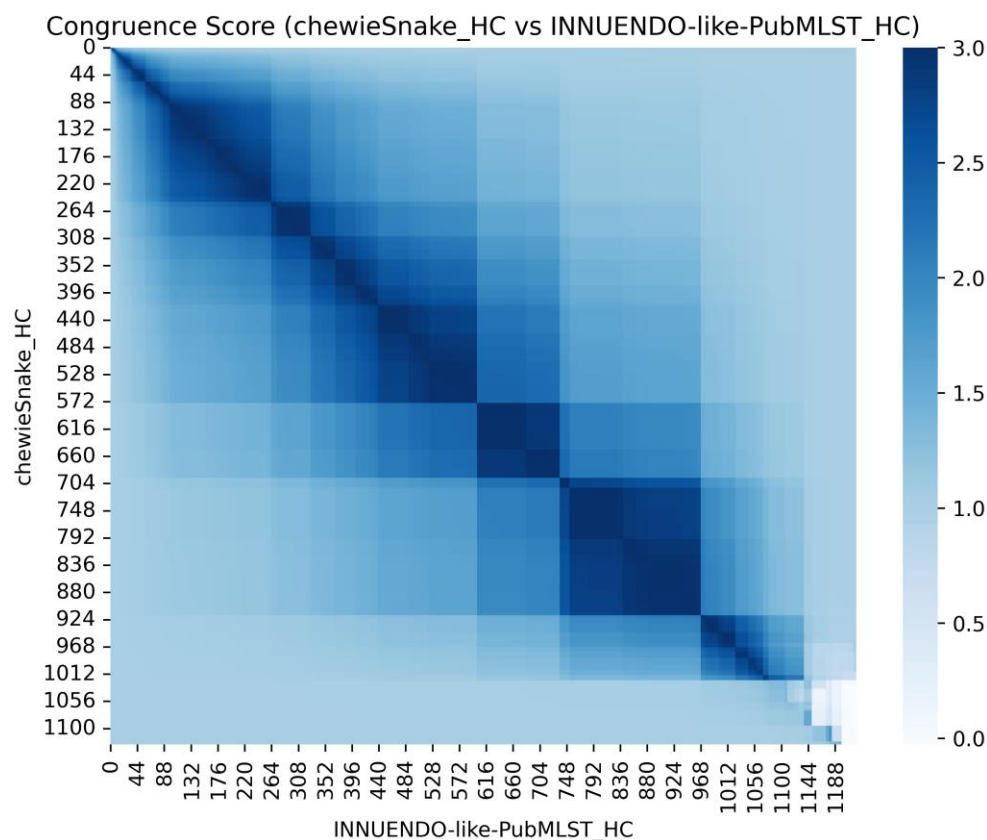


Figure S2.18.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

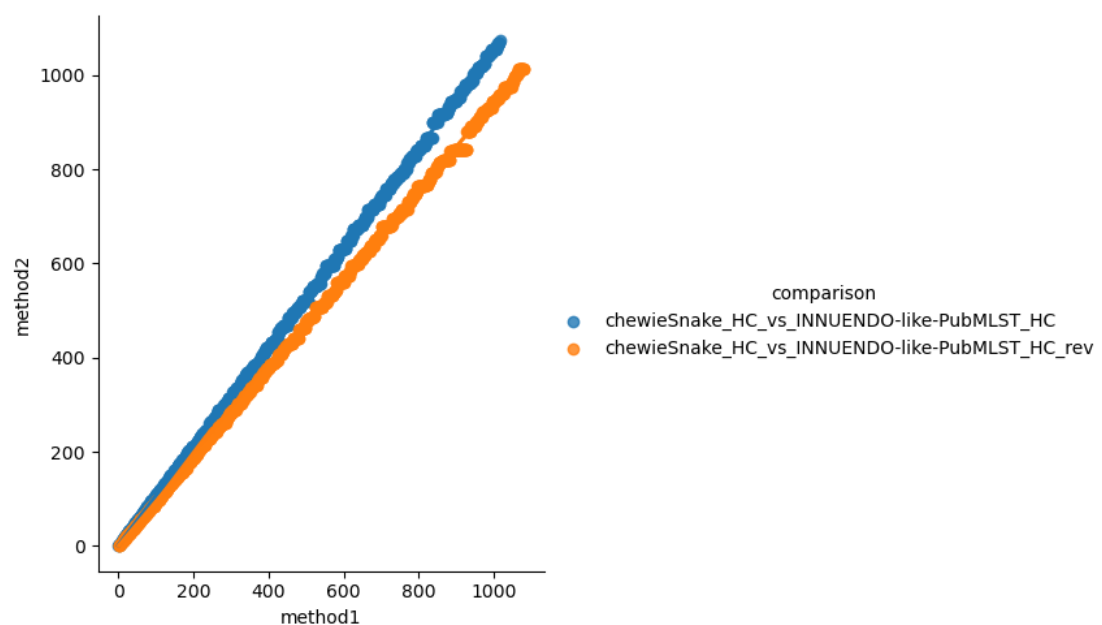


Figure S2.18.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1009 (blue) and 1073 (orange) points is presented.

19. chewieSnake single-linkage vs. SeqSphere-wgMLST GrapeTree

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.

	chewieSnake single-linkage	SeqSphere-wgMLST GrapeTree
Pipeline version	v3.1.1	v8.3.4
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1128	848

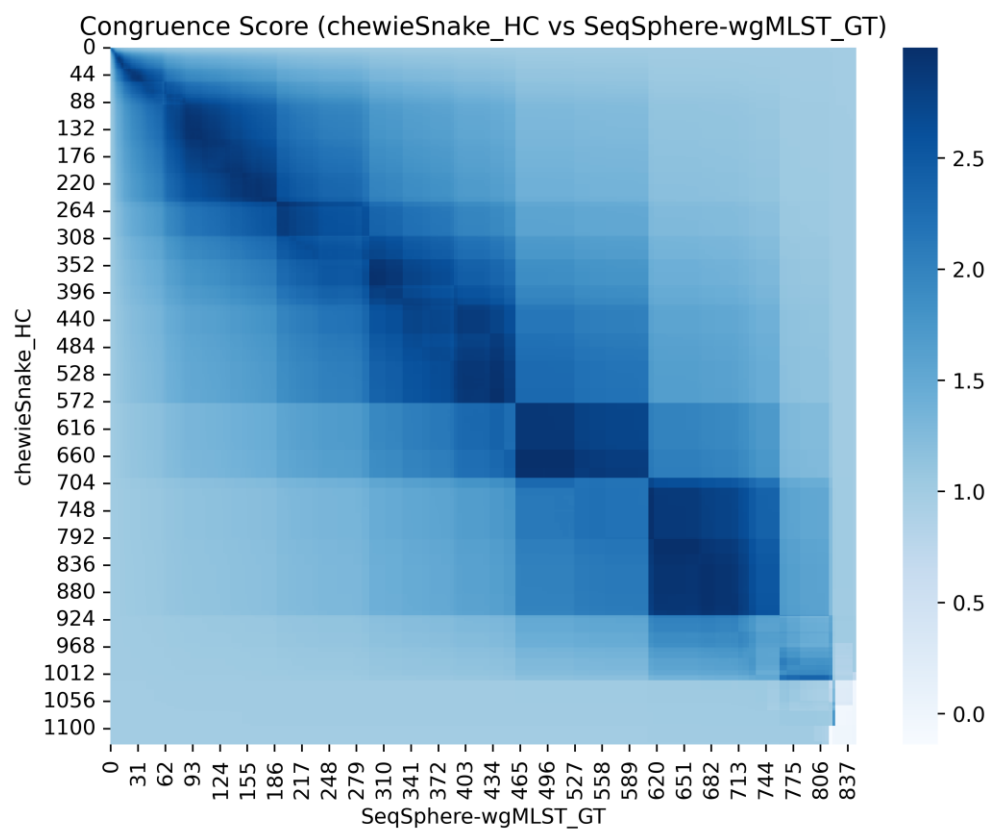


Figure S2.19.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

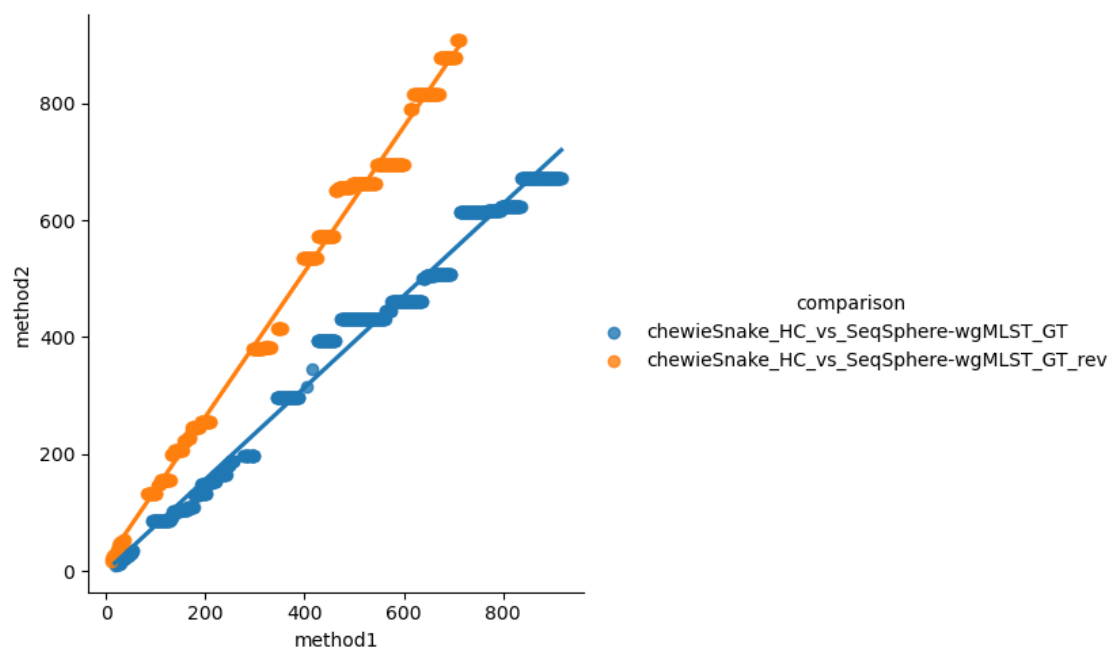


Figure S2.19.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 728 (blue) and 507 (orange) points is presented.

20. chewieSnake single-linkage vs. SeqSphere-wgMLST 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.

	chewieSnake single-linkage	SeqSphere-wgMLST single-linkage
Pipeline version	v3.1.1	v8.3.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1128	806

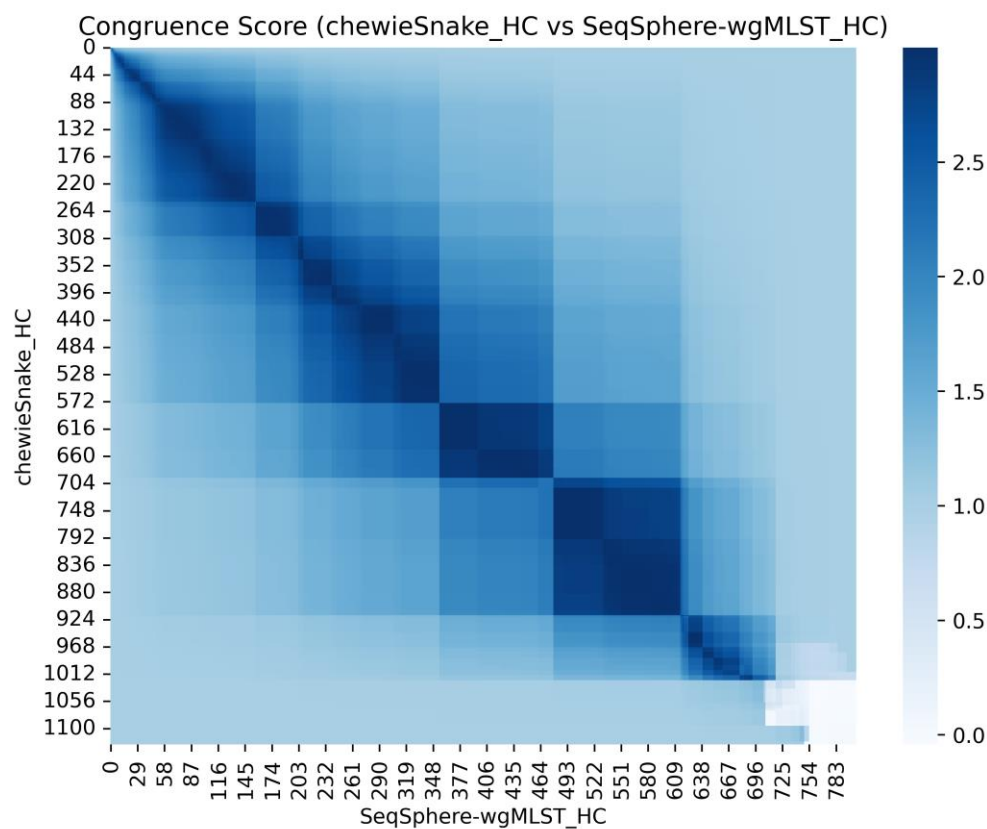


Figure S2.20.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

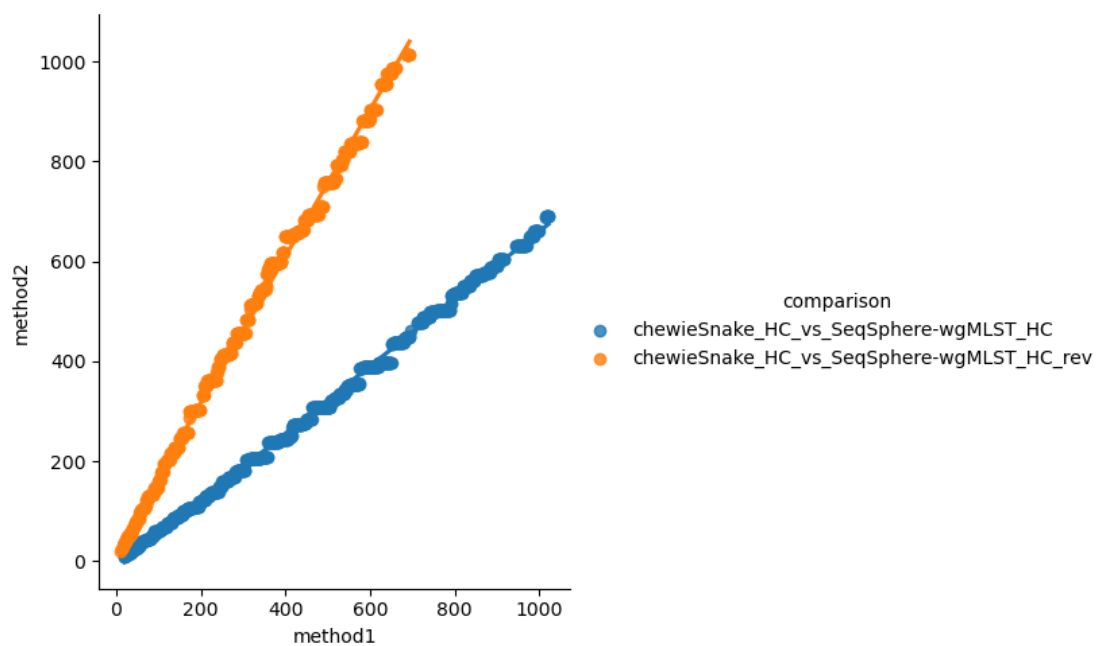


Figure S2.20.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 929 (blue) and 642 (orange) points is presented.

21. INNUENDO-like-INNUENDO99 GrapeTree 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-INNUENDO99 GrapeTree	Bionumerics single-linkage
Pipeline version	chewBBACA 2.8.5	v8.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	PubMLST
Dataset	All samples	All samples
Number partitions	897	1202

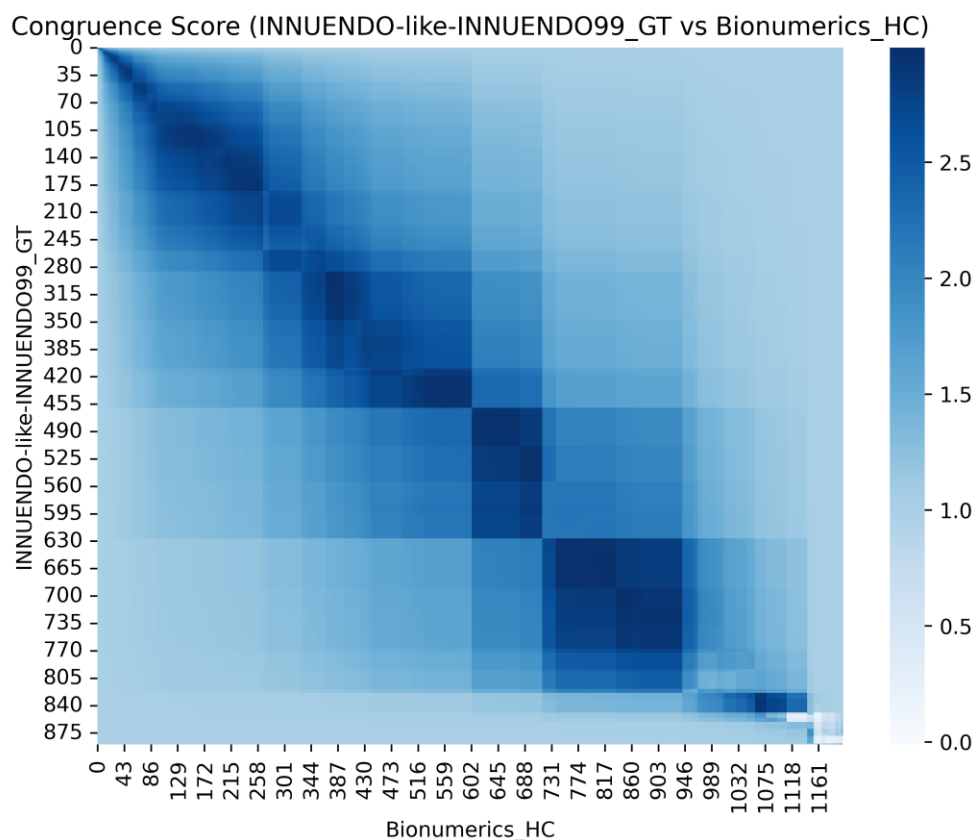


Figure S2.21.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

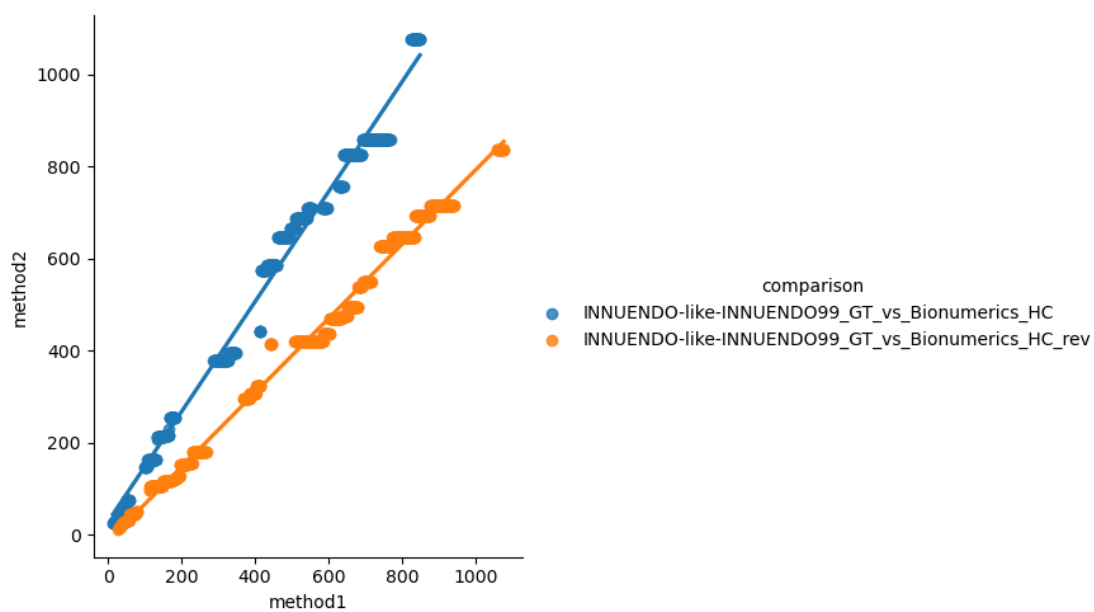


Figure S2.21.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 510 (blue) and 685 (orange) points is presented.

22. INNUENDO-like-INNUENDO99 GrapeTree 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-INNUENDO99 GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	PubMLST
Dataset	All samples	All samples
Number partitions	897	1229

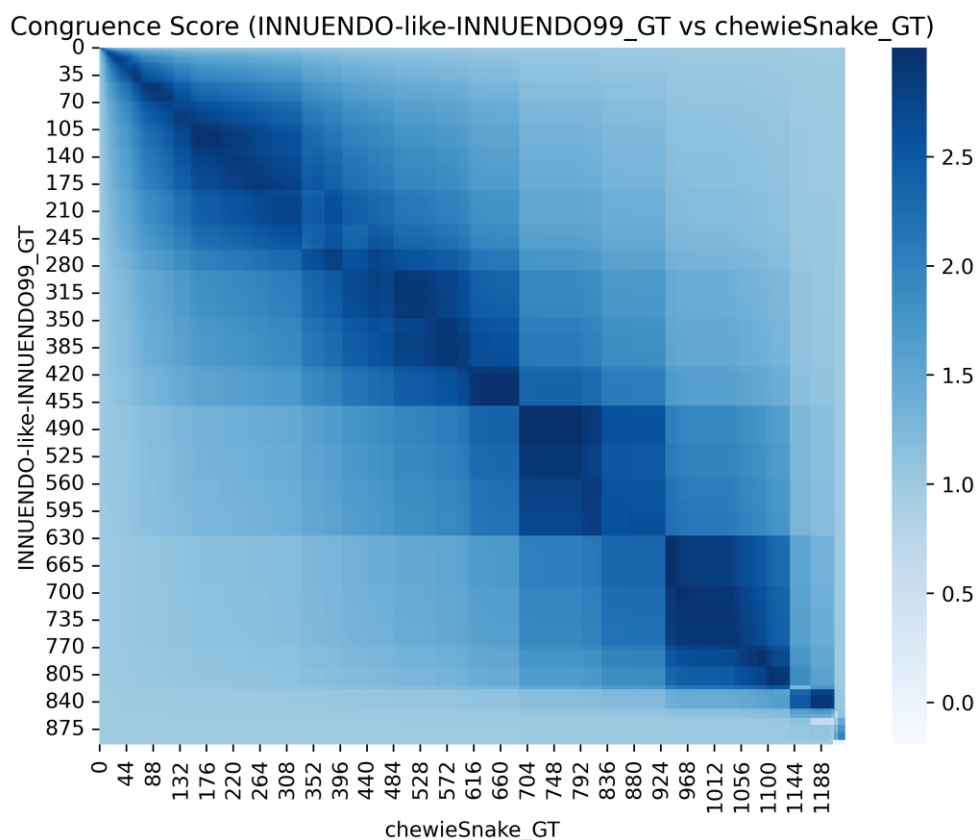


Figure S2.22.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

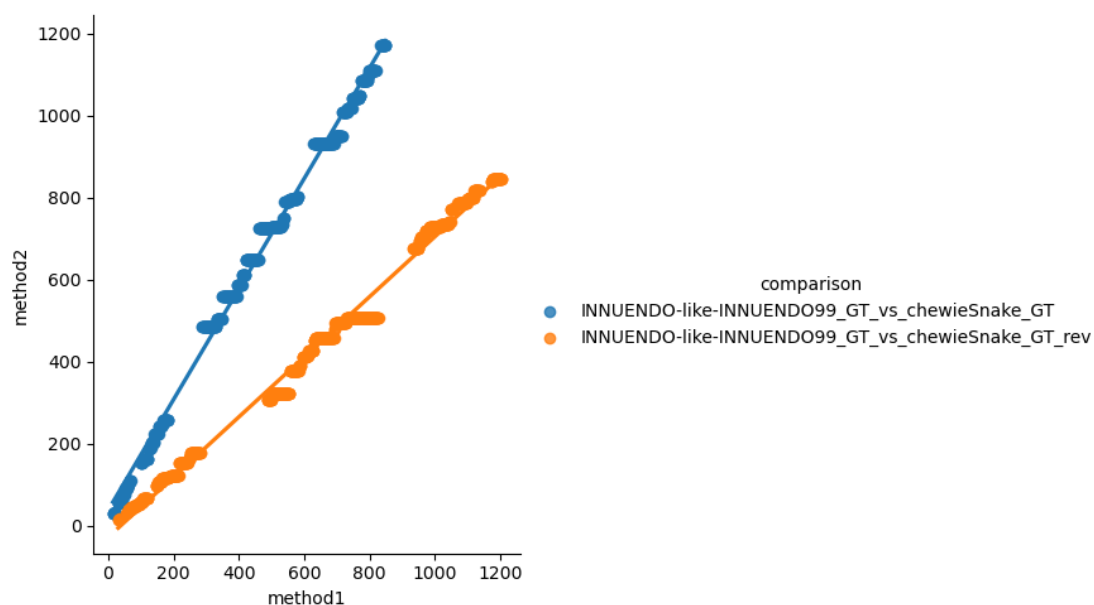


Figure S2.22.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 633 (blue) and 769 (orange) points is presented.

23. INNUENDO-like-INNUENDO99 GrapeTree 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-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)	PubMLST
Dataset	All samples	All samples
Number partitions	897	1128

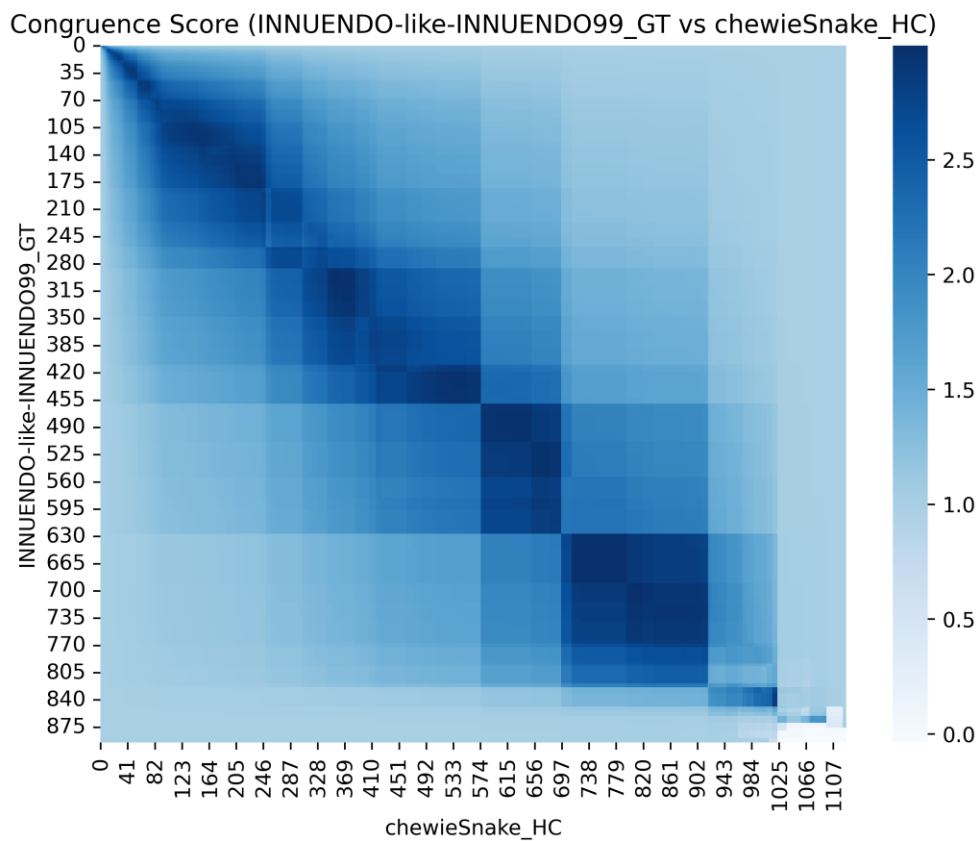


Figure S2.23.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

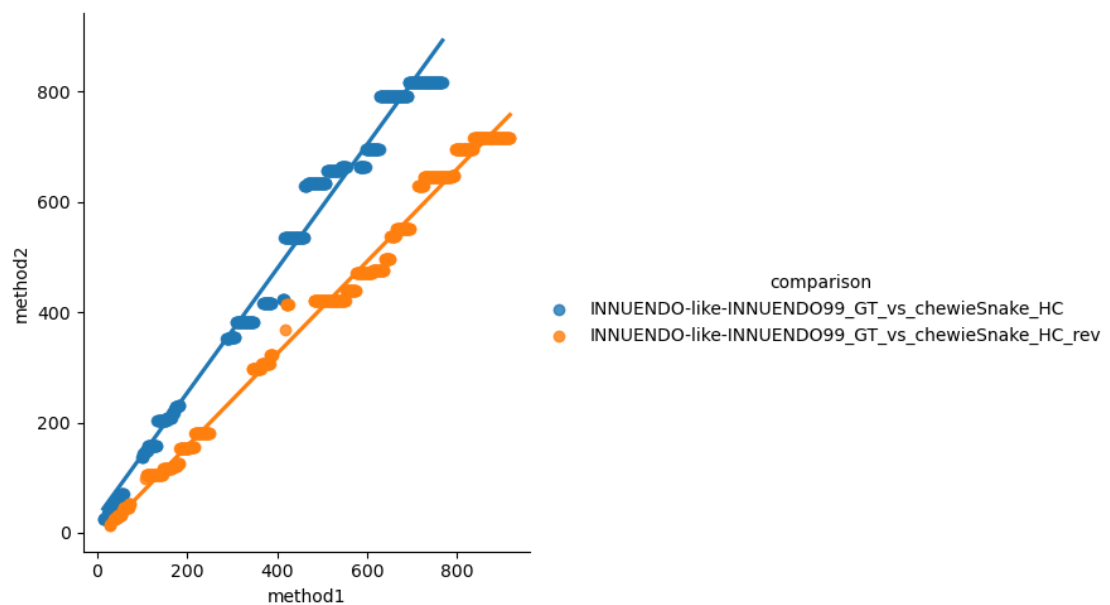


Figure S2.23.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 538 (blue) and 660 (orange) points is presented.

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

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-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	897	852

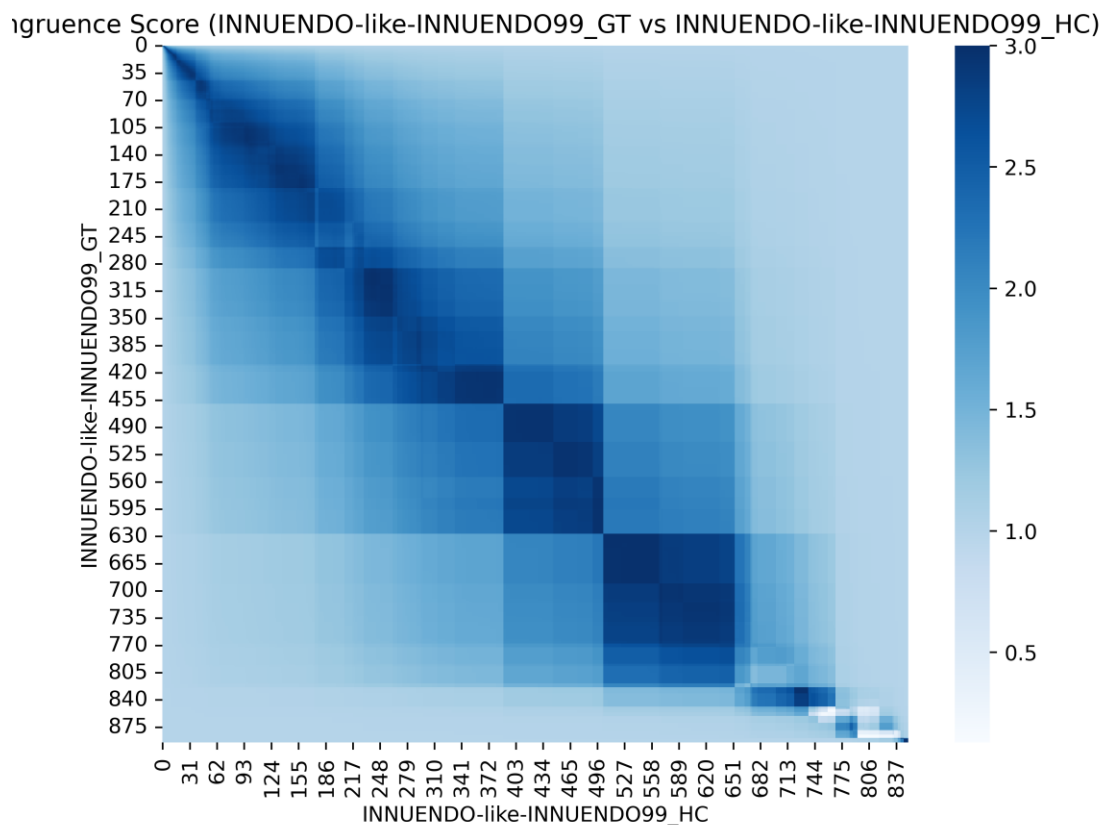


Figure S2.24.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

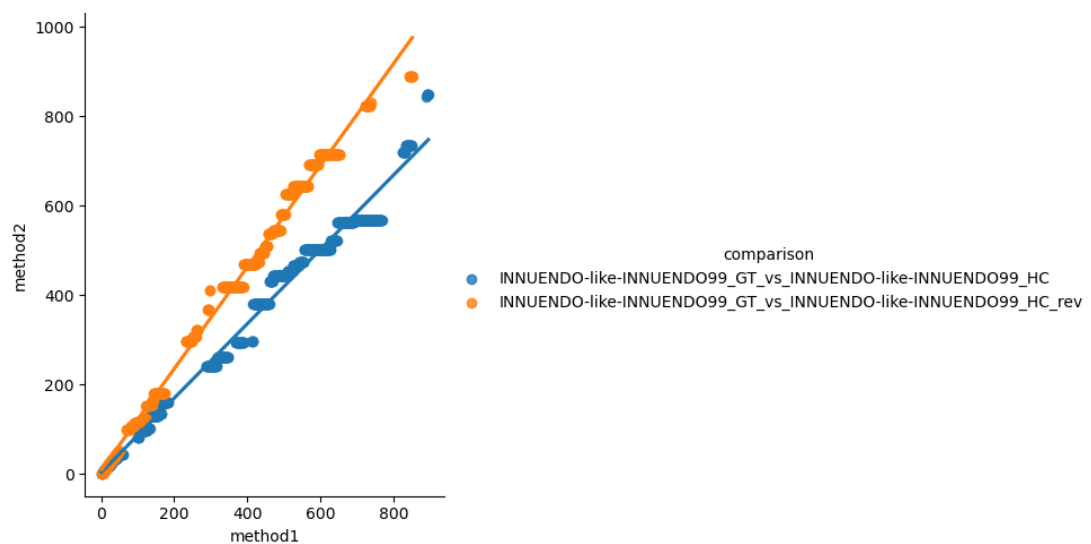


Figure S2.24.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 615 (blue) and 543 (orange) points is presented.

25. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-INNUENDOcgmLST GrapeTree

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-INNUENDO99 GrapeTree	INNUENDO-like- INNUENDOcgmLST GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	897	677

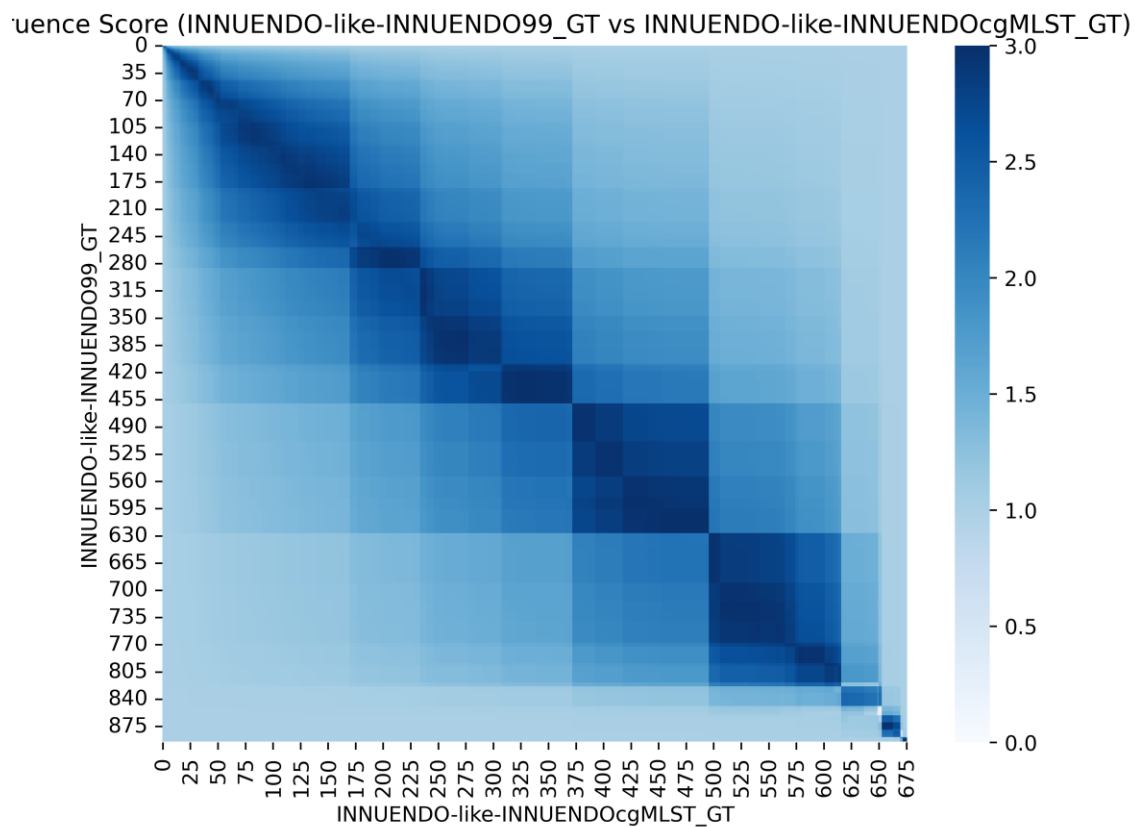


Figure S2.25.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

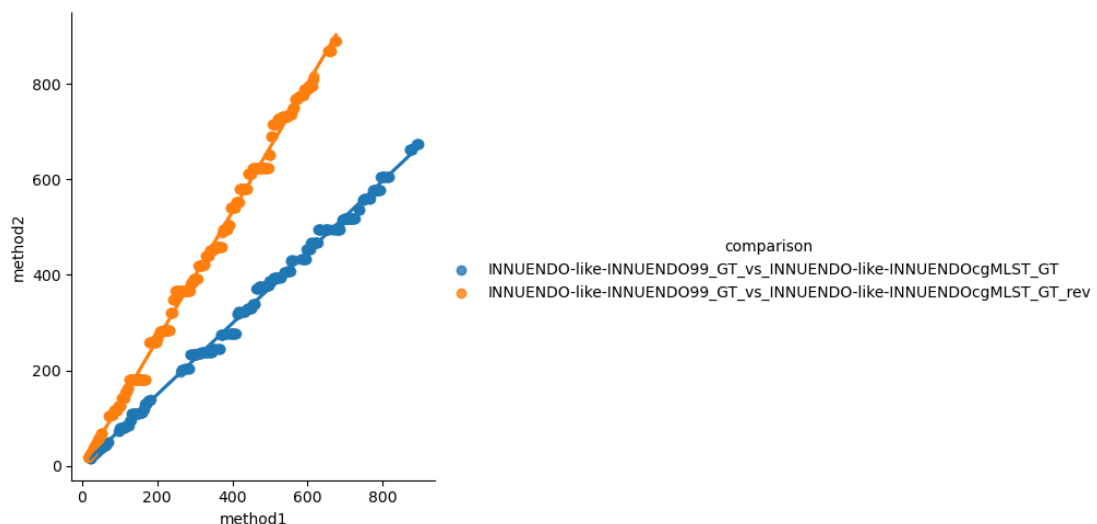


Figure S2.25.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 470 (blue) and 589 (orange) points is presented.

26. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-INNUENDOCgMLST single-linkage

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-INNUENDO99 GrapeTree	INNUENDO-like- INNUENDOCgMLST single- linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	897	644

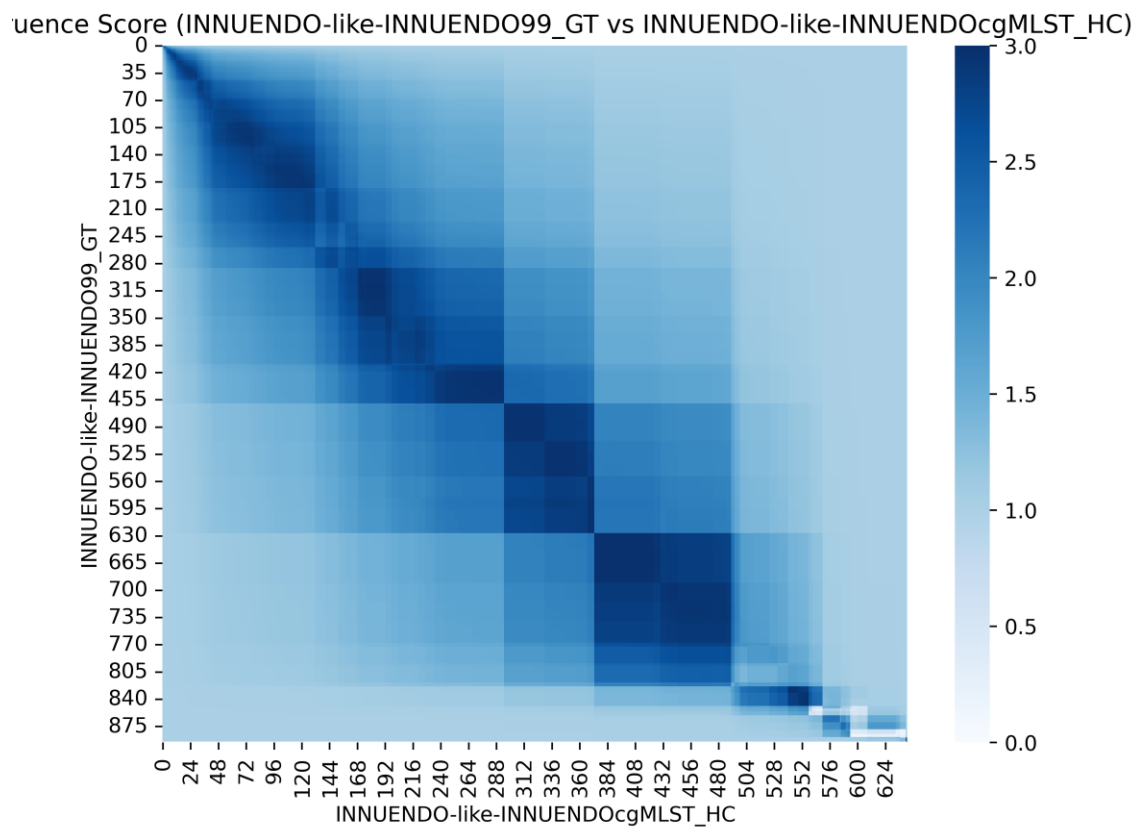


Figure S2.26.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

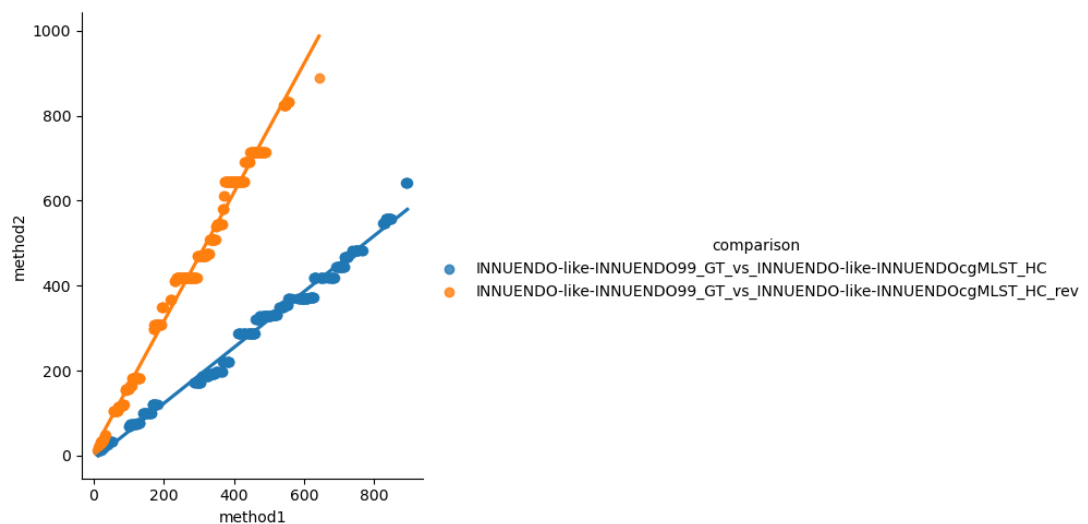


Figure S2.26.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 400 (blue) and 405 (orange) points is presented.

27. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-PubMLST 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-INNUENDO99 GrapeTree	INNUENDO-like-PubMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	PubMLST
Dataset	All samples	All samples
Number partitions	897	1286

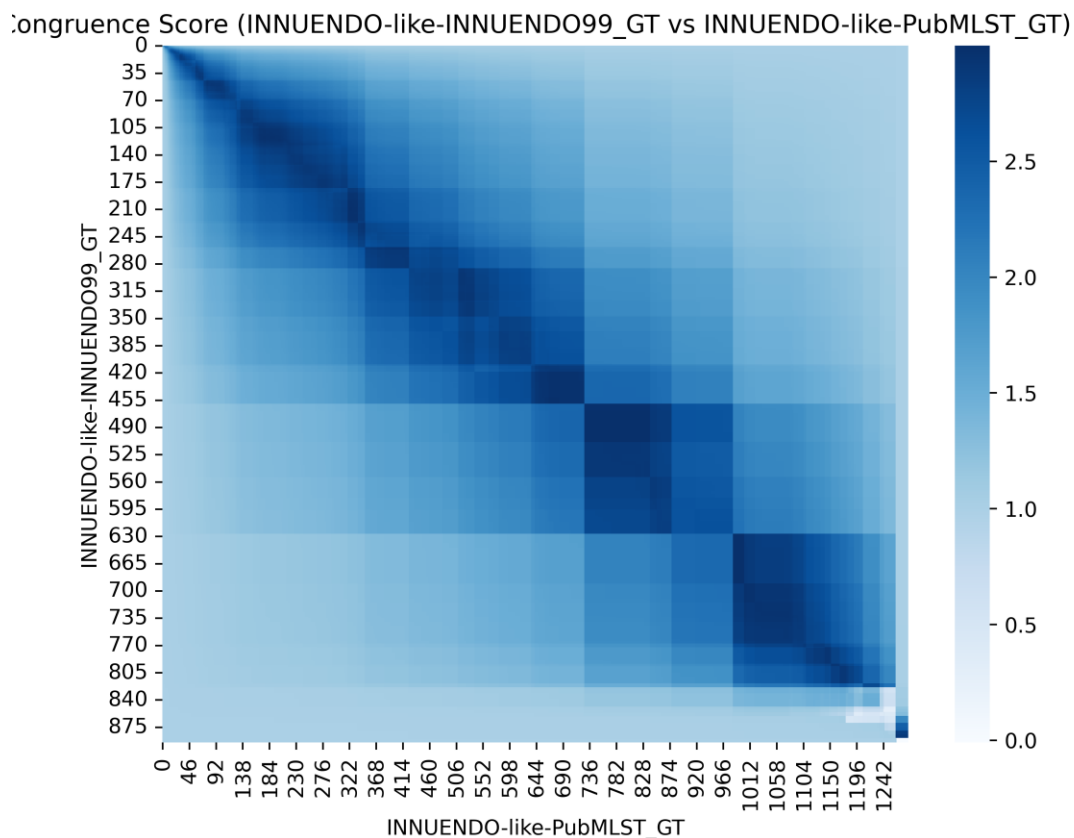


Figure S2.27.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

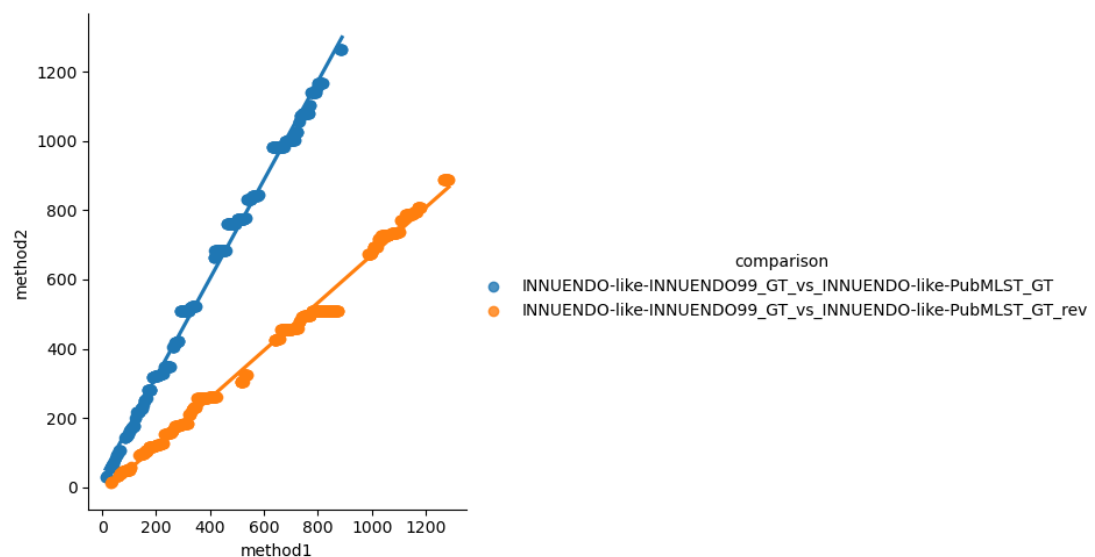


Figure S2.27.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 675 (blue) and 821 (orange) points is presented.

28. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-PubMLST 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-INNUENDO99 GrapeTree	INNUENDO-like-PubMLST single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	PubMLST
Dataset	All samples	All samples
Number partitions	897	1224

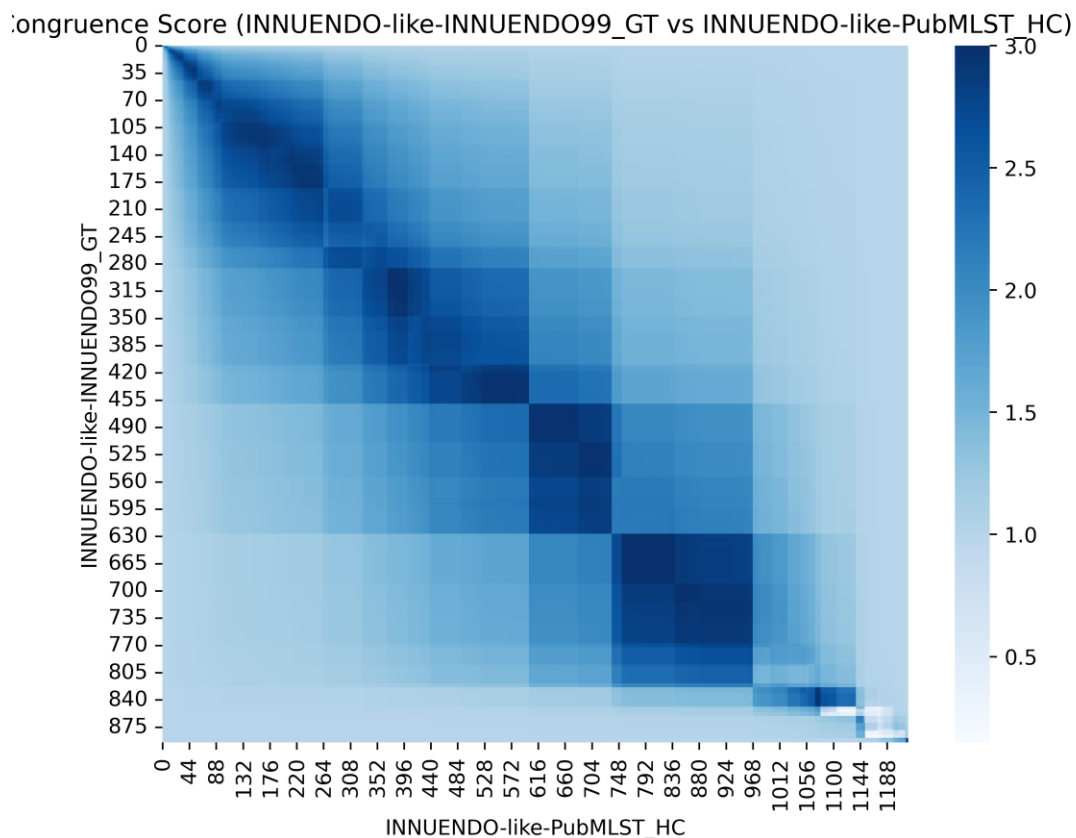


Figure S2.28.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

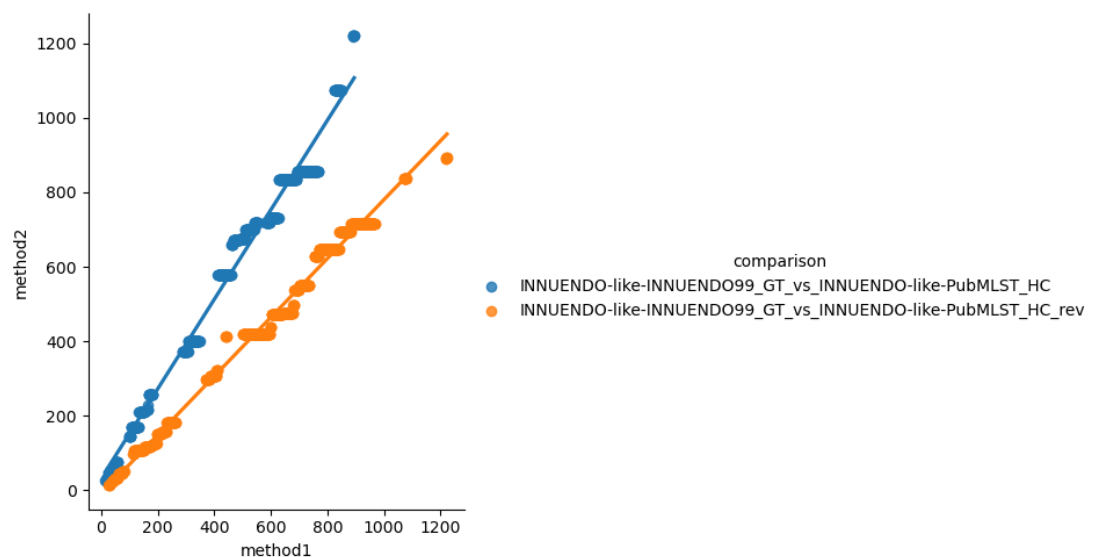


Figure S2.28.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 544 (blue) and 711 (orange) points is presented.

29. INNUENDO-like-INNUENDO99 GrapeTree vs. SeqSphere-wgMLST GrapeTree

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	SeqSphere-wgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	897	848

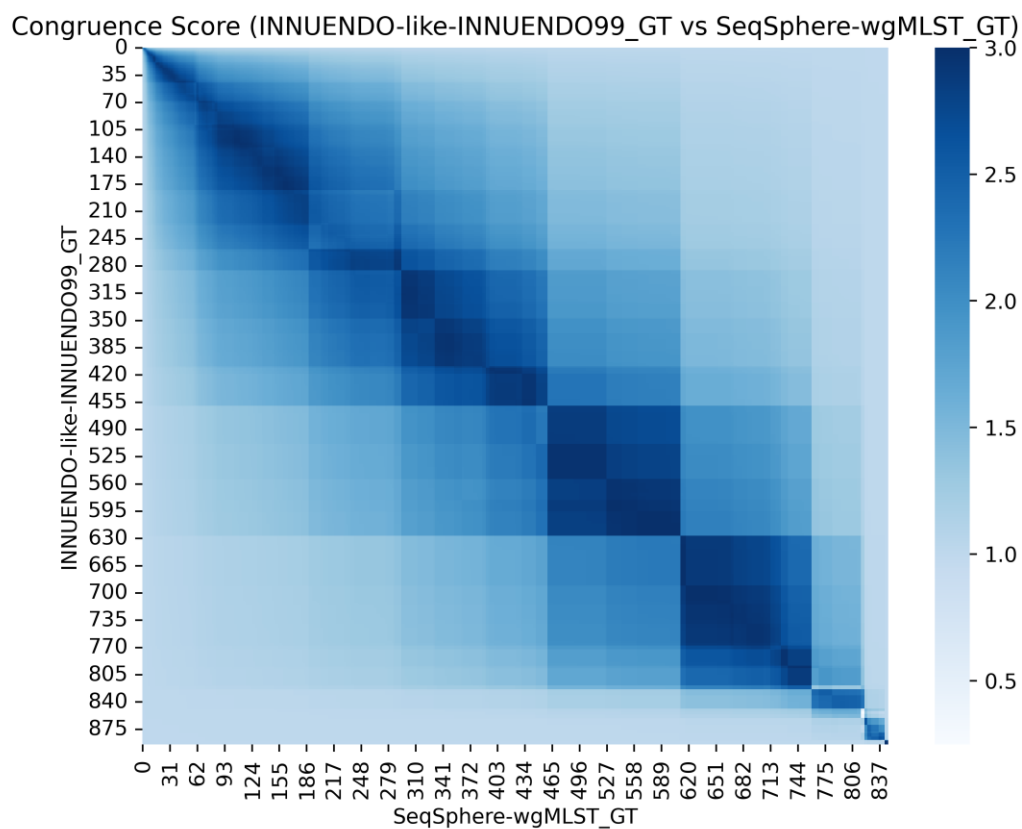


Figure S2.29.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

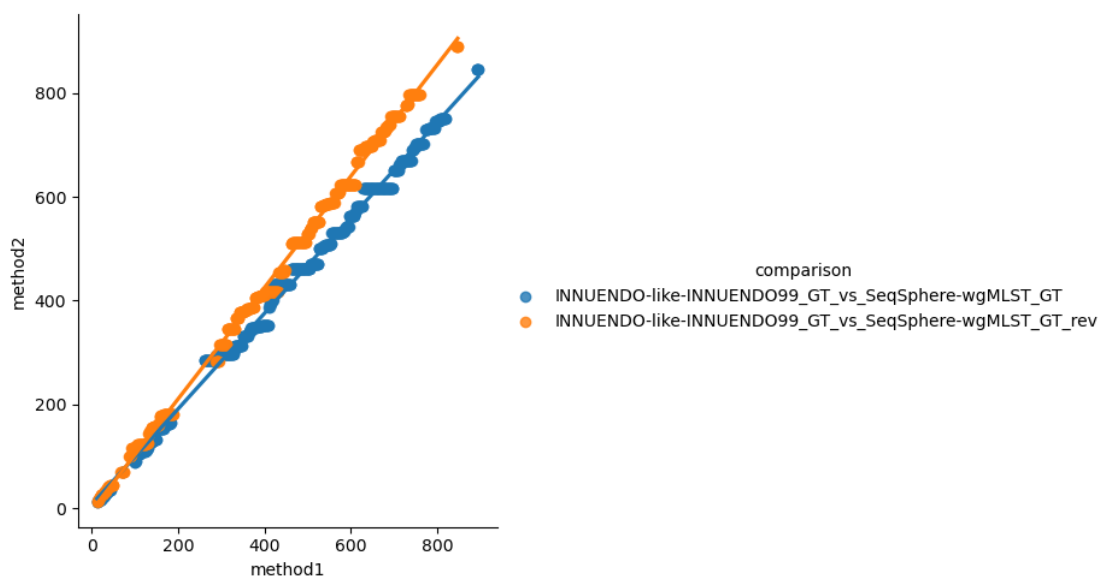


Figure S2.29.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 680 (blue) and 603 (orange) points is presented.

30. INNUENDO-like-INNUENDO99 GrapeTree vs. SeqSphere-wgMLST single-linkage

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	SeqSphere-wgMLST single- linkage
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	INNUENDO (wgMLST)	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	897	806

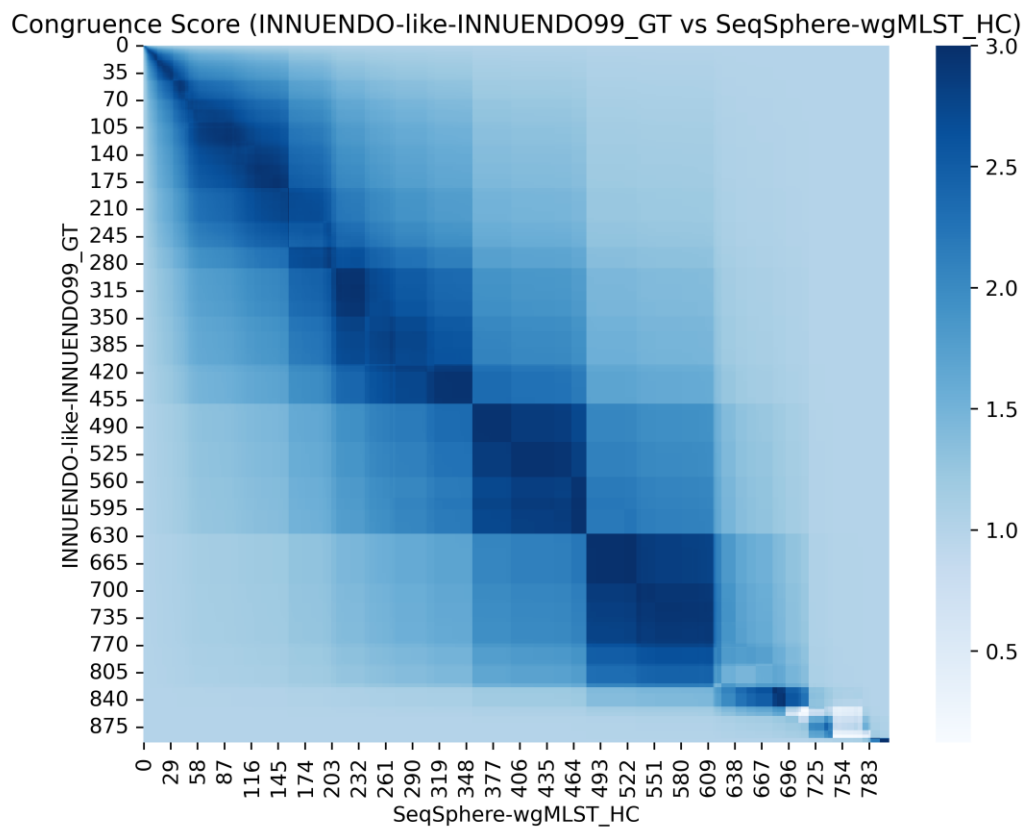


Figure S2.30.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

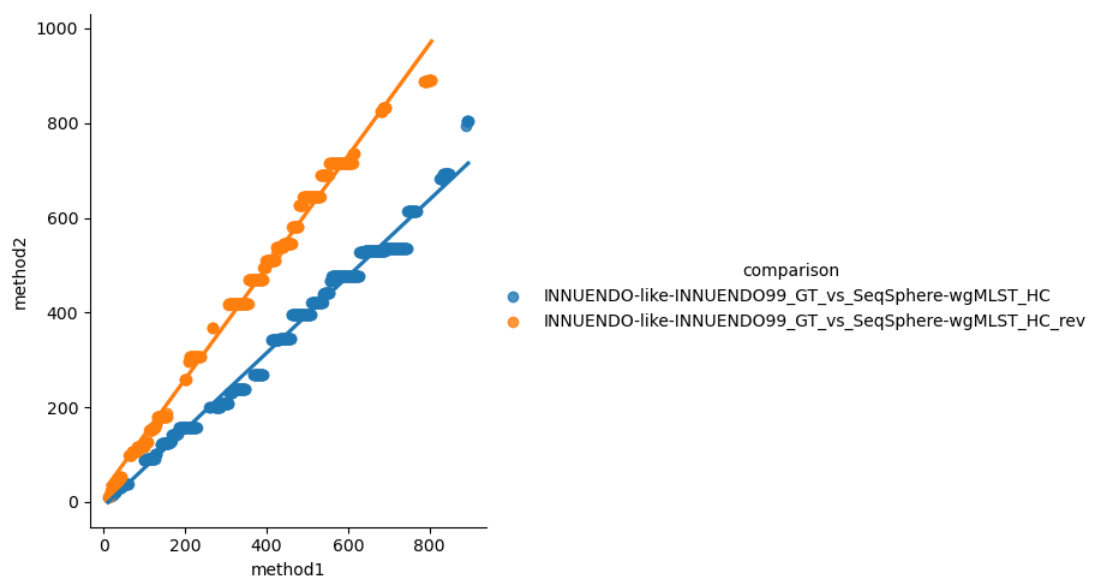


Figure S2.30.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 659 (blue) and 507 (orange) points is presented.

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

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 single-linkage	INNUENDO-like- INNUENDOccgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	852	677

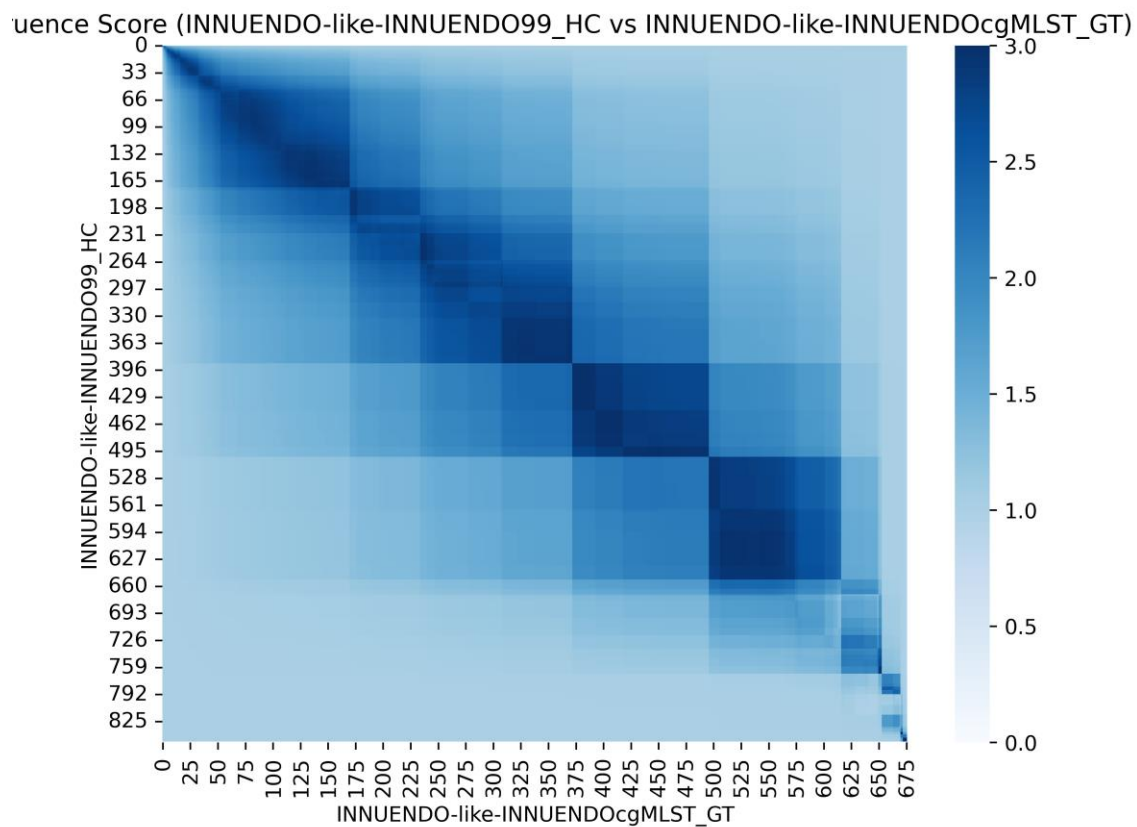


Figure S2.31.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

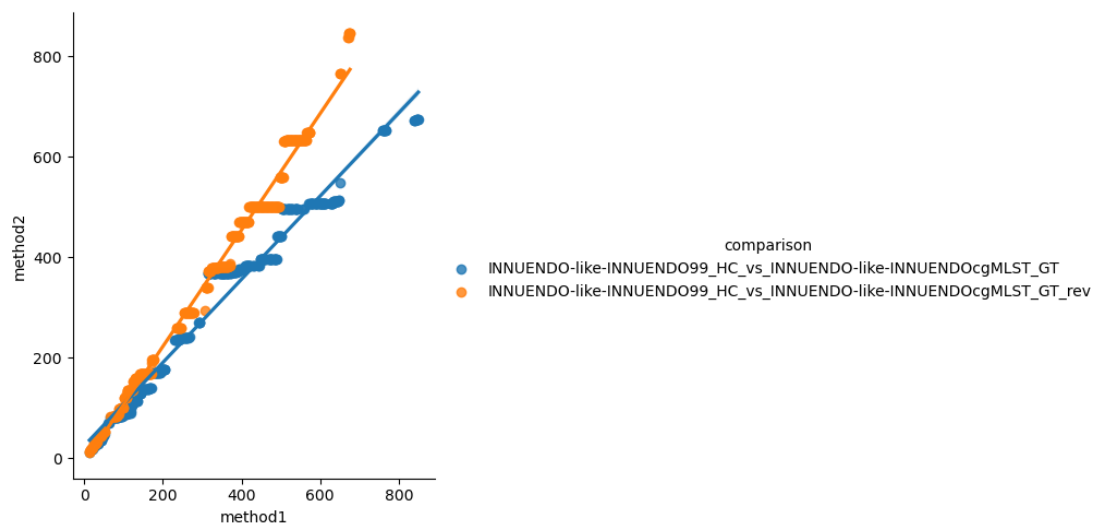


Figure S2.31.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 378 (blue) and 453 (orange) points is presented.

32. INNUENDO-like-INNUENDO99 single-linkage vs. INNUENDO-like-INNUENDOcgmLST single-linkage

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 single-linkage	INNUENDO-like-INNUENDOcgmLST single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	852	644

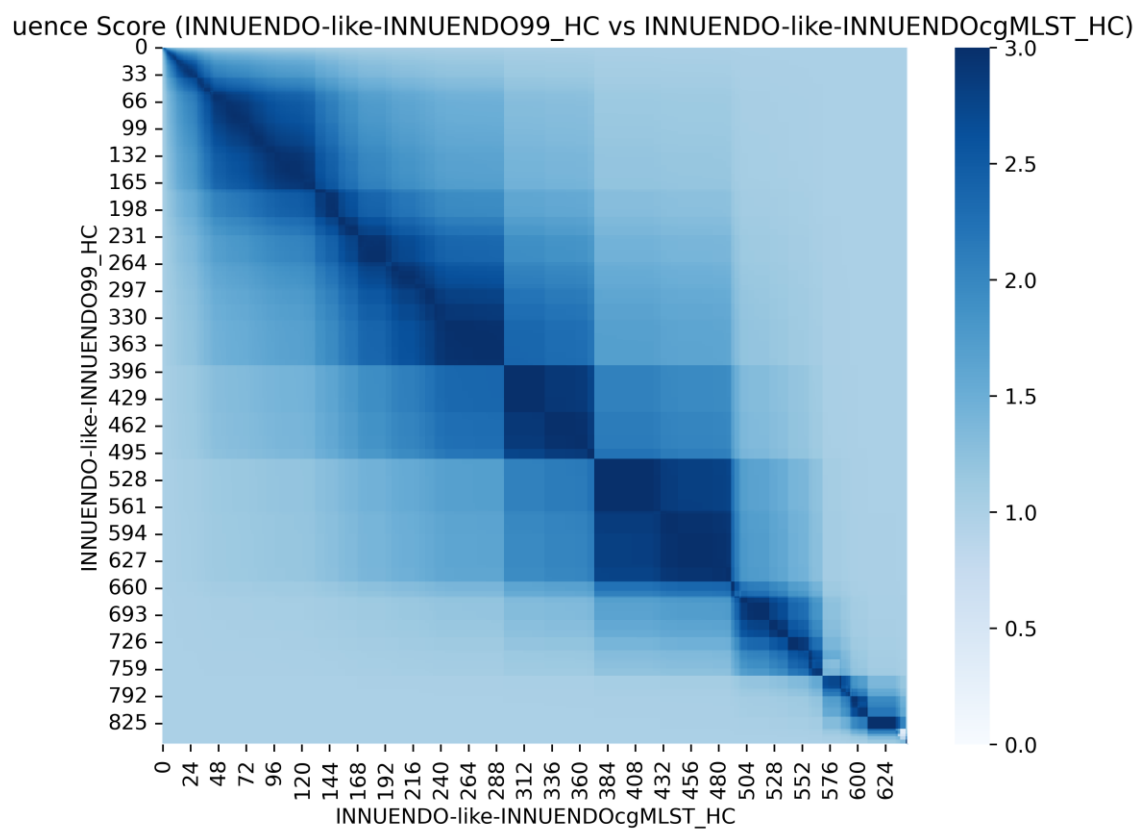


Figure S2.32.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

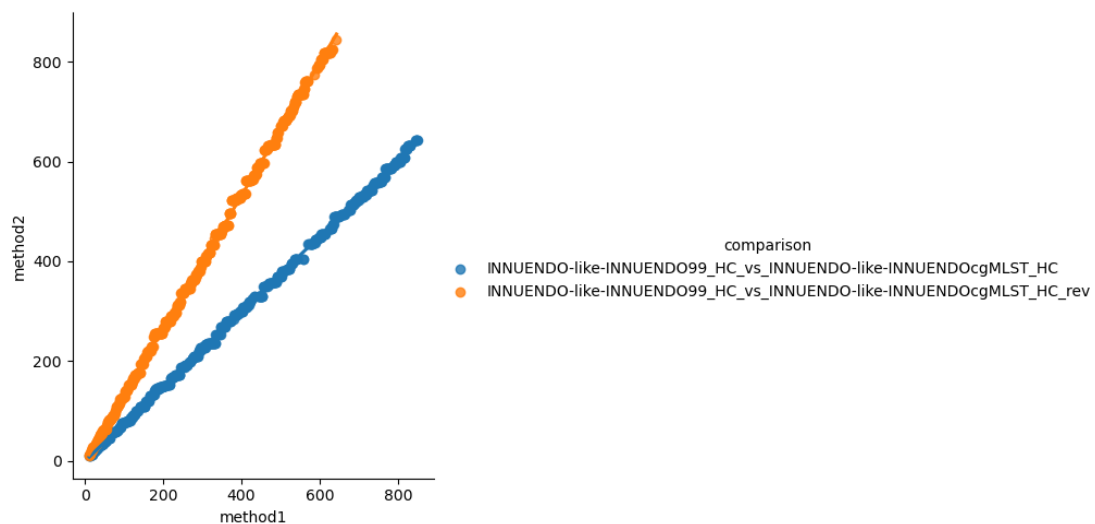


Figure S2.32.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 599 (blue) and 595 (orange) points is presented.

33. INNUENDO-like-INNUENDO99 single-linkage vs. SeqSphere-wgMLST GrapeTree

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 single-linkage	SeqSphere-wgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	852	848

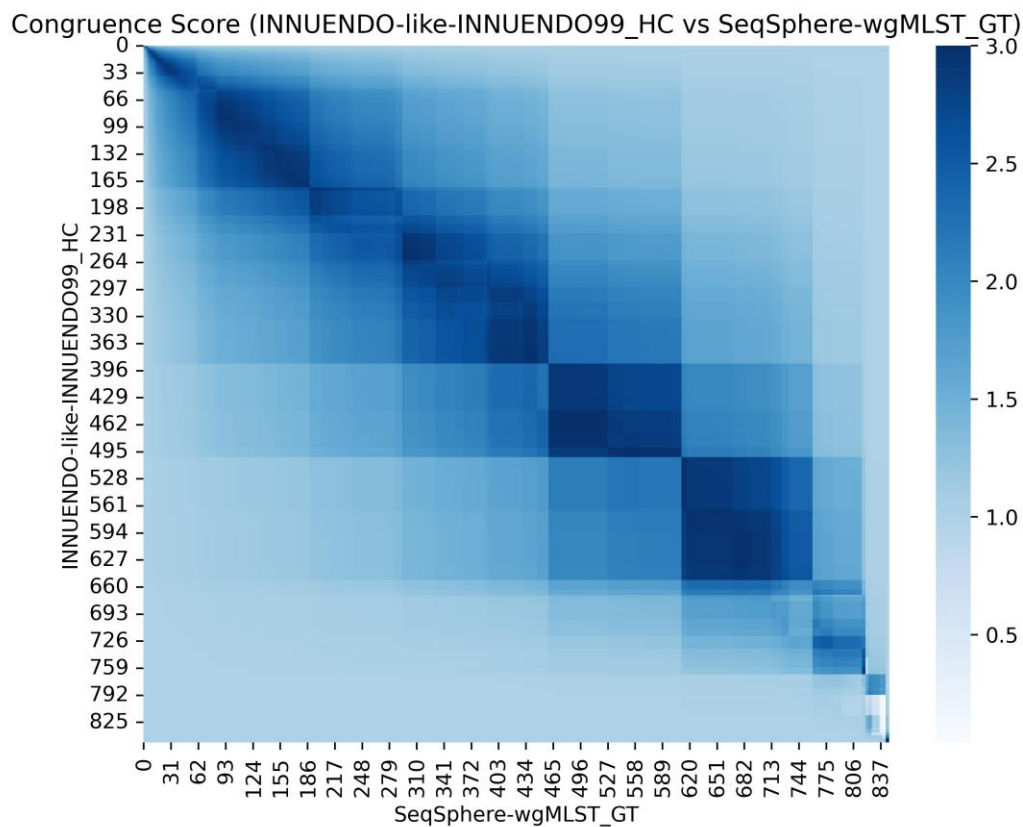


Figure S2.33.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

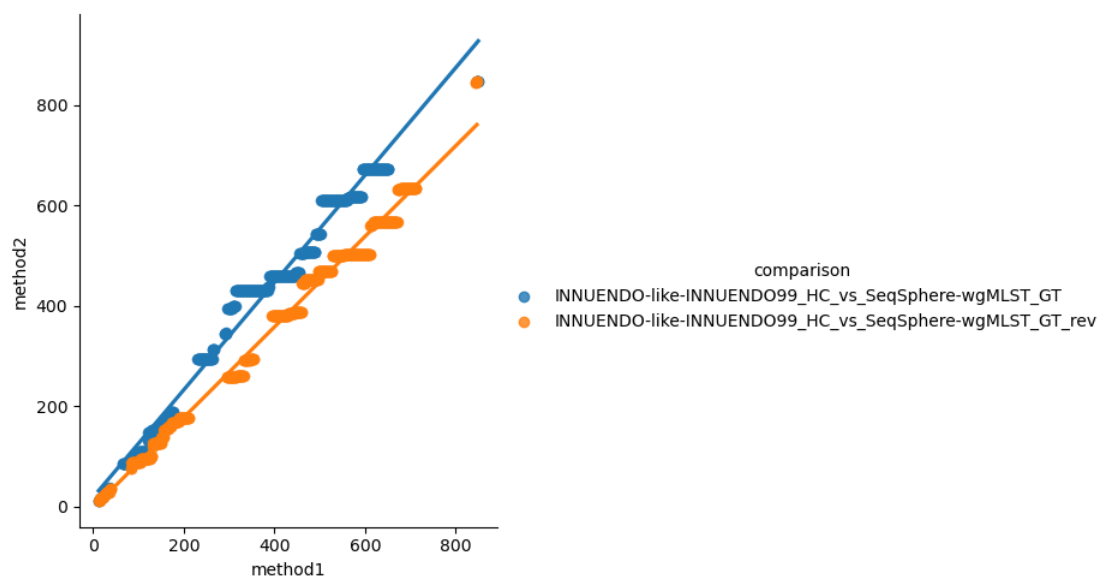


Figure S2.33.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 542 (blue) and 536 (orange) points is presented.

34. INNUENDO-like-PubMLST GrapeTree vs. chewieSnake 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-PubMLST GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1286	1229

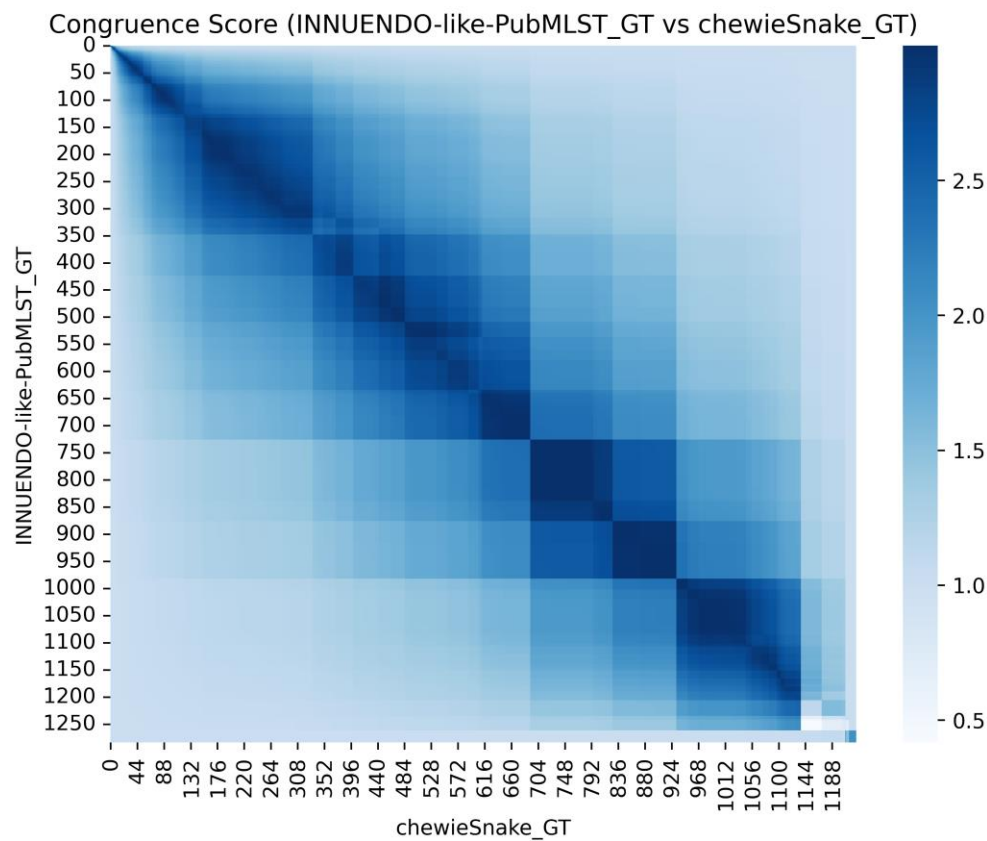


Figure S2.34.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

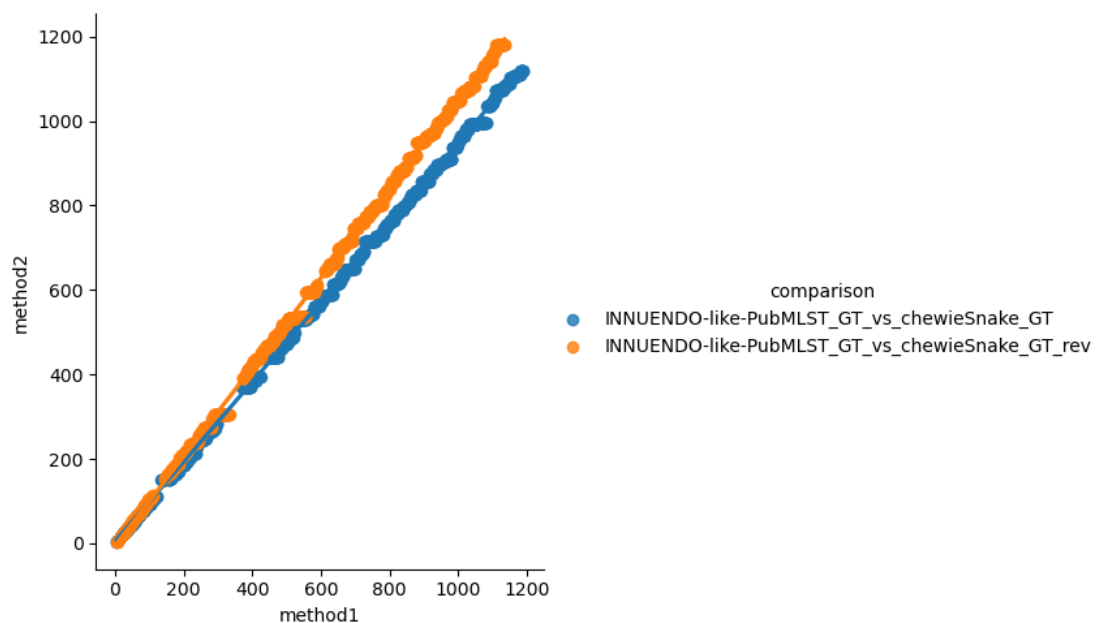


Figure S2.34.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1115 (blue) and 1029 (orange) points is presented.

35. INNUENDO-like-PubMLST GrapeTree vs. chewieSnake 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-PubMLST GrapeTree	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1286	1128

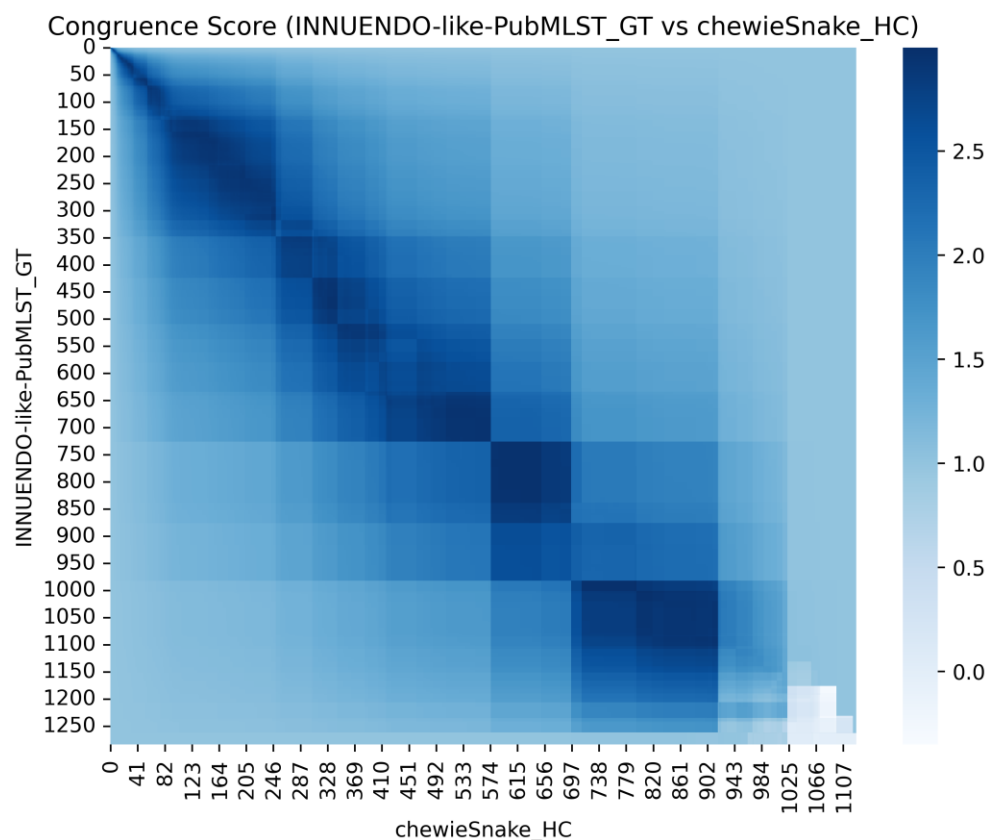


Figure S2.35.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

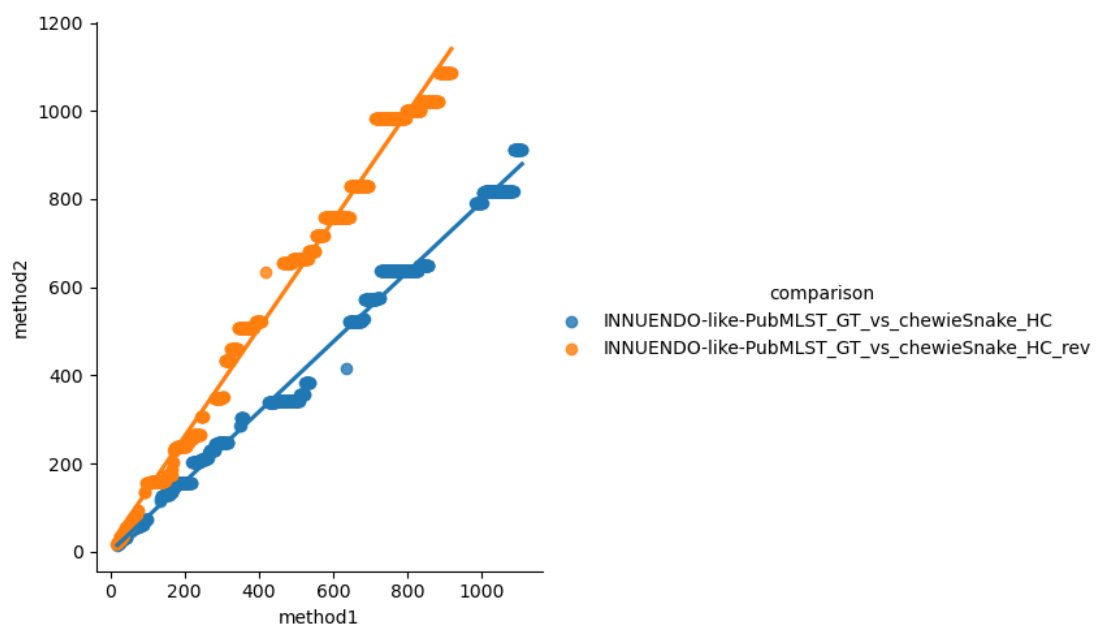


Figure S2.35.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 715 (blue) and 769 (orange) points is presented.

36. INNUENDO-like-PubMLST GrapeTree vs. INNUENDO-like-INNUENDO99 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.

	INNUENDO-like-PubMLST 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	PubMLST	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	1286	852

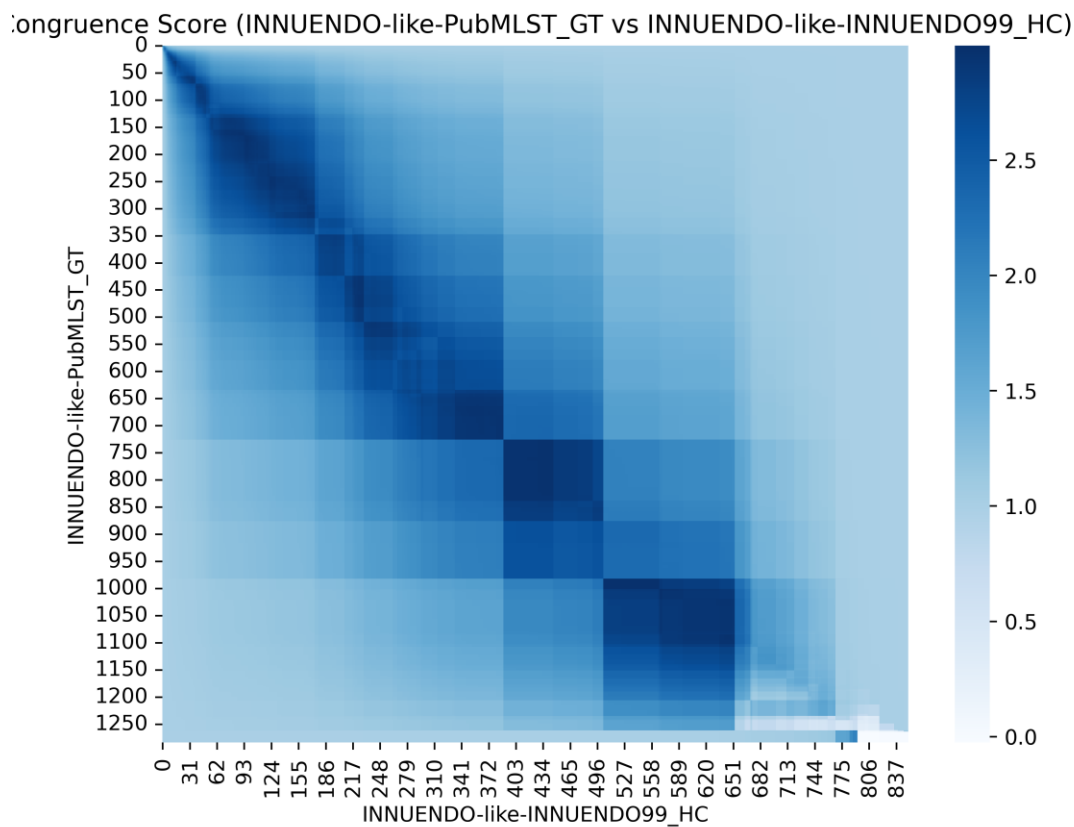


Figure S2.36.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

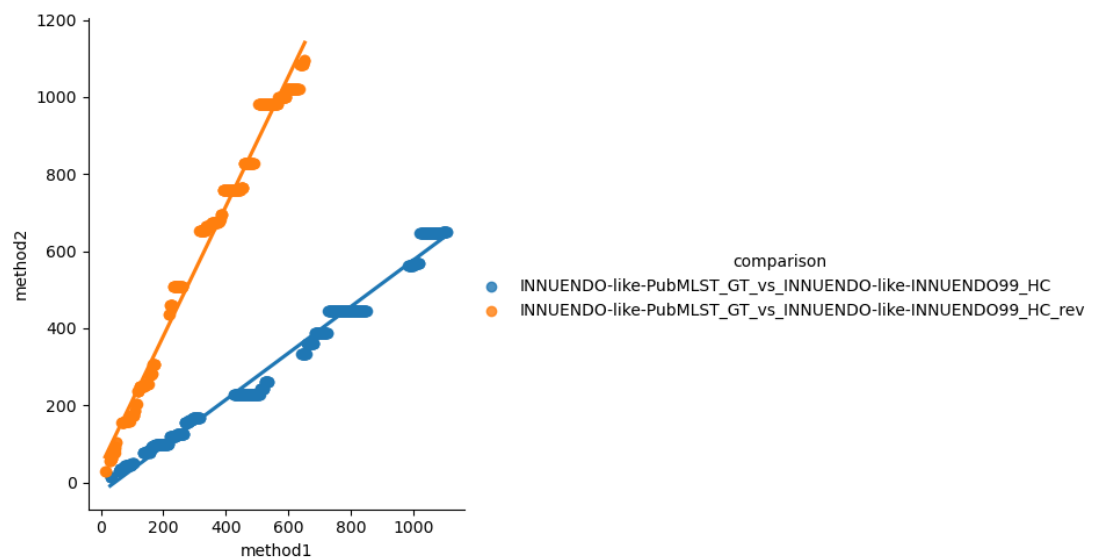


Figure S2.36.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 683 (blue) and 507 (orange) points is presented.

37. INNUENDO-like-PubMLST GrapeTree vs. INNUENDO-like-INNUENDOccgMLST 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.

	INNUENDO-like-PubMLST GrapeTree	INNUENDO-like- INNUENDOccgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1286	677

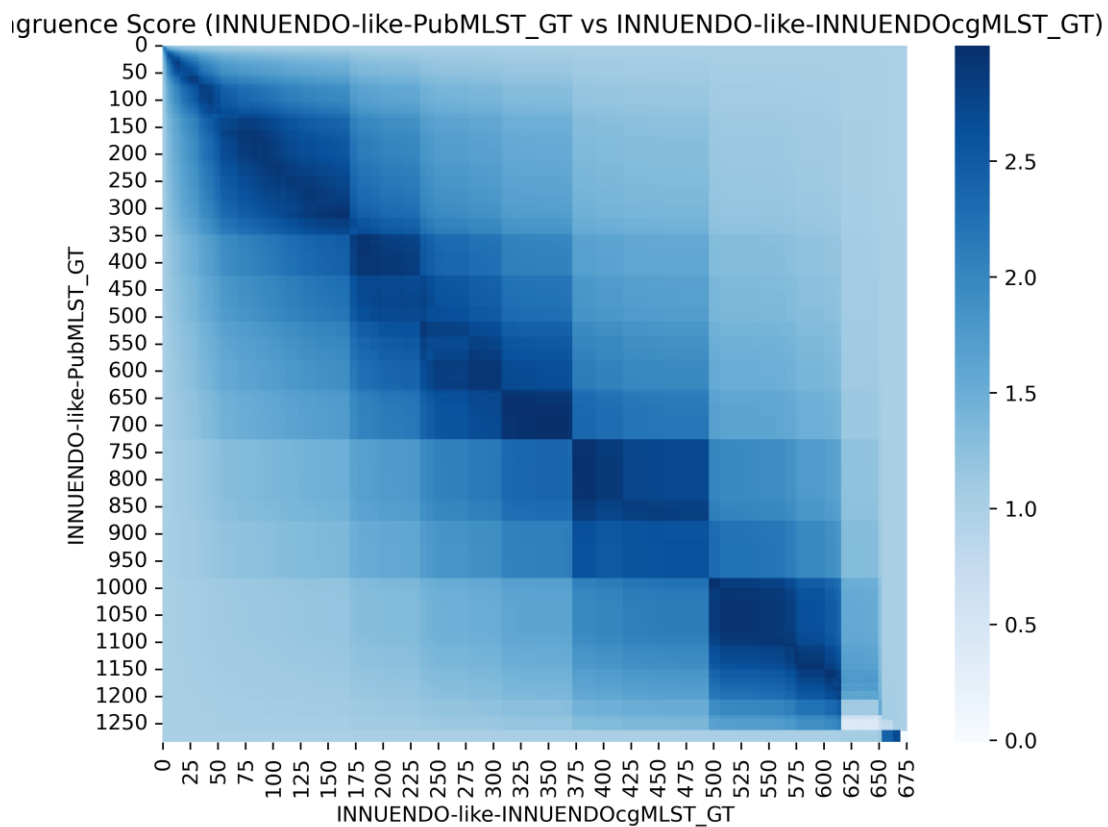


Figure S2.37.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

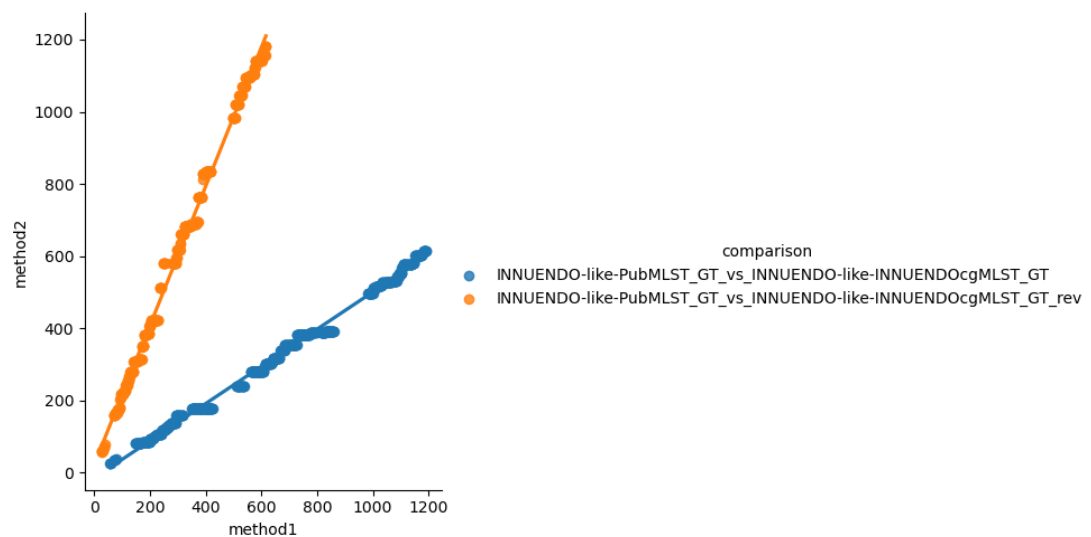


Figure S2.37.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 595 (blue) and 441 (orange) points is presented.

38. INNUENDO-like-PubMLST GrapeTree vs. INNUENDO-like-INNUENDOccgMLST 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.

	INNUENDO-like-PubMLST GrapeTree	INNUENDO-like-INNUENDOccgMLST single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1286	644

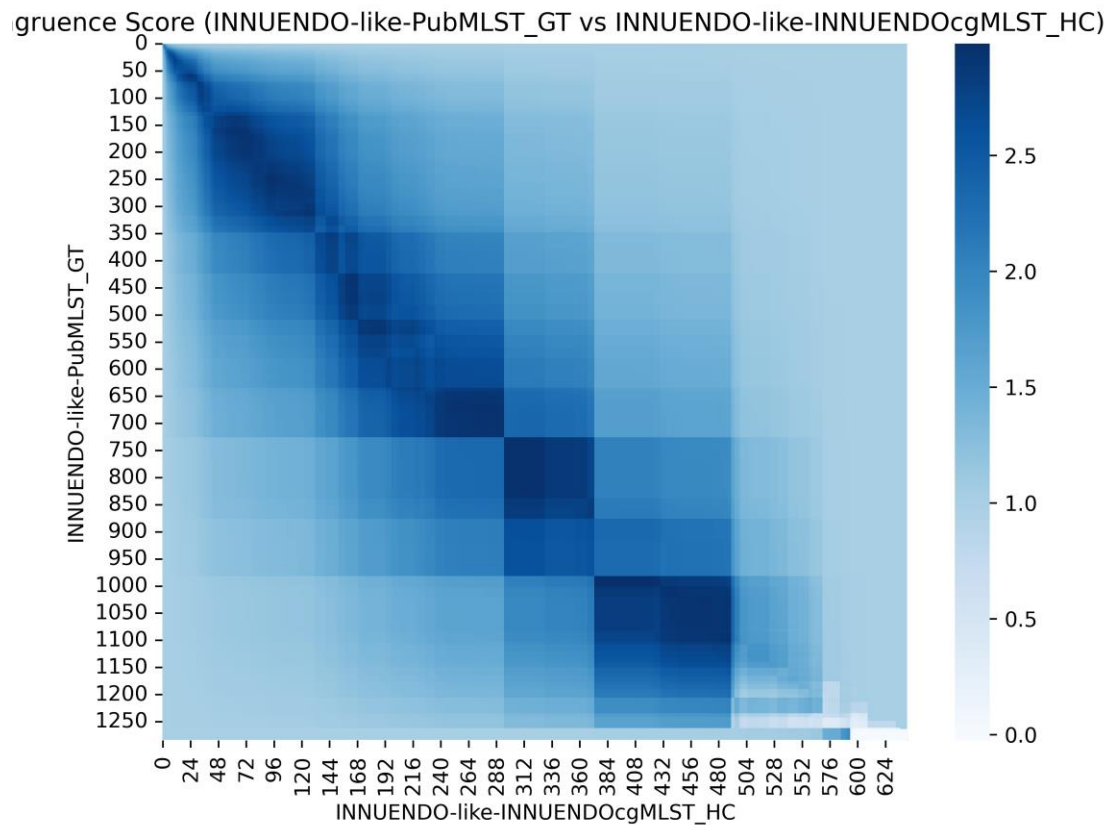


Figure S2.38.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

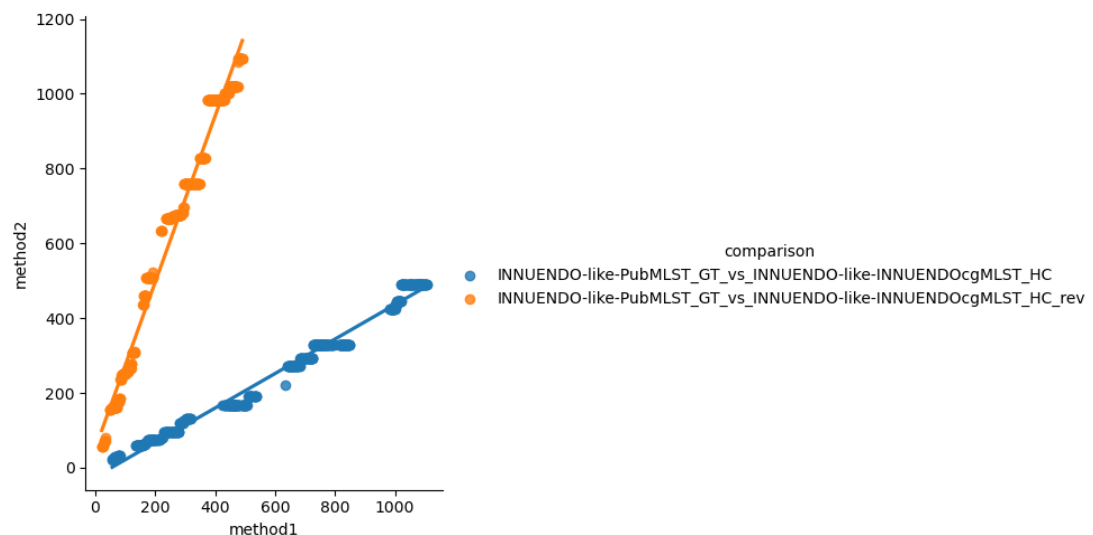


Figure S2.38.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 469 (blue) and 384 (orange) points is presented.

39. INNUENDO-like-PubMLST GrapeTree vs. INNUENDO-like-PubMLST single-linkage

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.

	INNUENDO-like-PubMLST GrapeTree	INNUENDO-like-PubMLST single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1286	1224

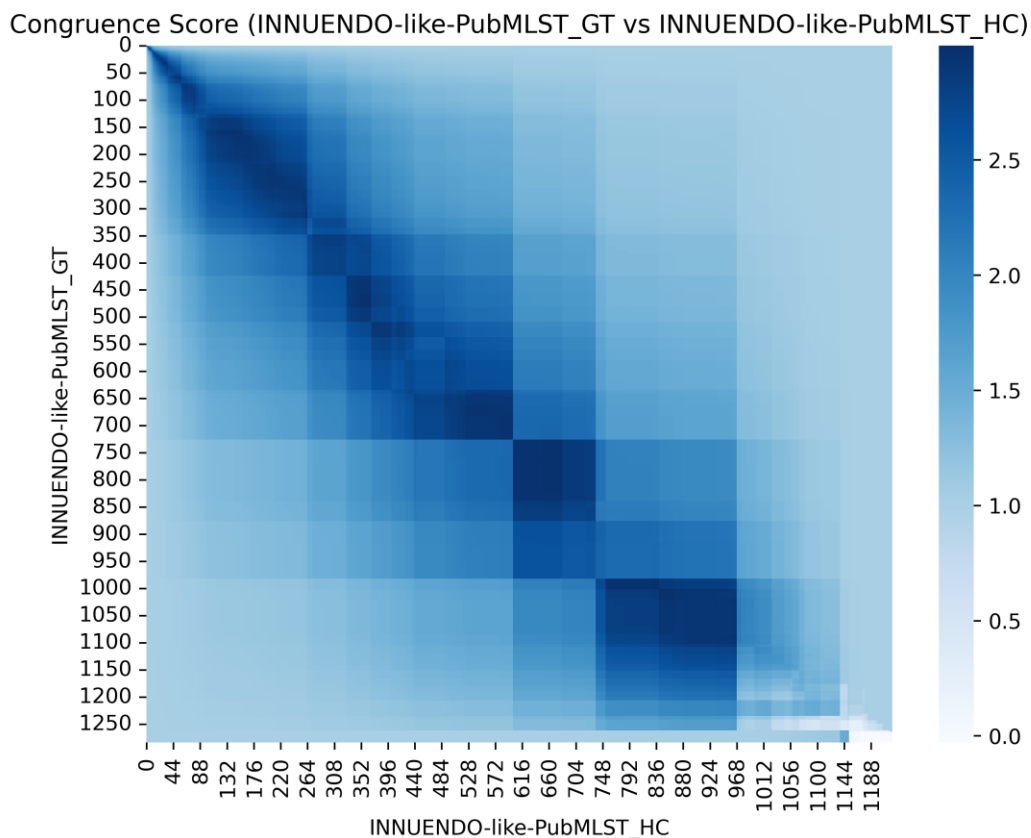


Figure S2.39.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

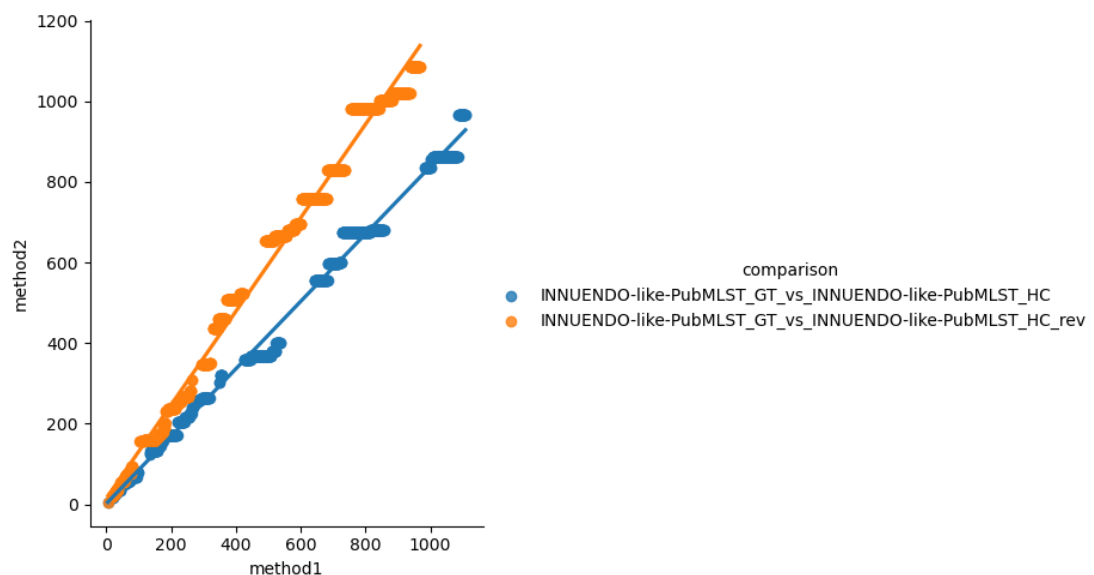


Figure S2.39.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 716 (blue) and 795 (orange) points is presented.

40. INNUENDO-like-PubMLST GrapeTree vs. SeqSphere-wgMLST GrapeTree

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.

	INNUENDO-like-PubMLST GrapeTree	SeqSphere-wgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1286	848

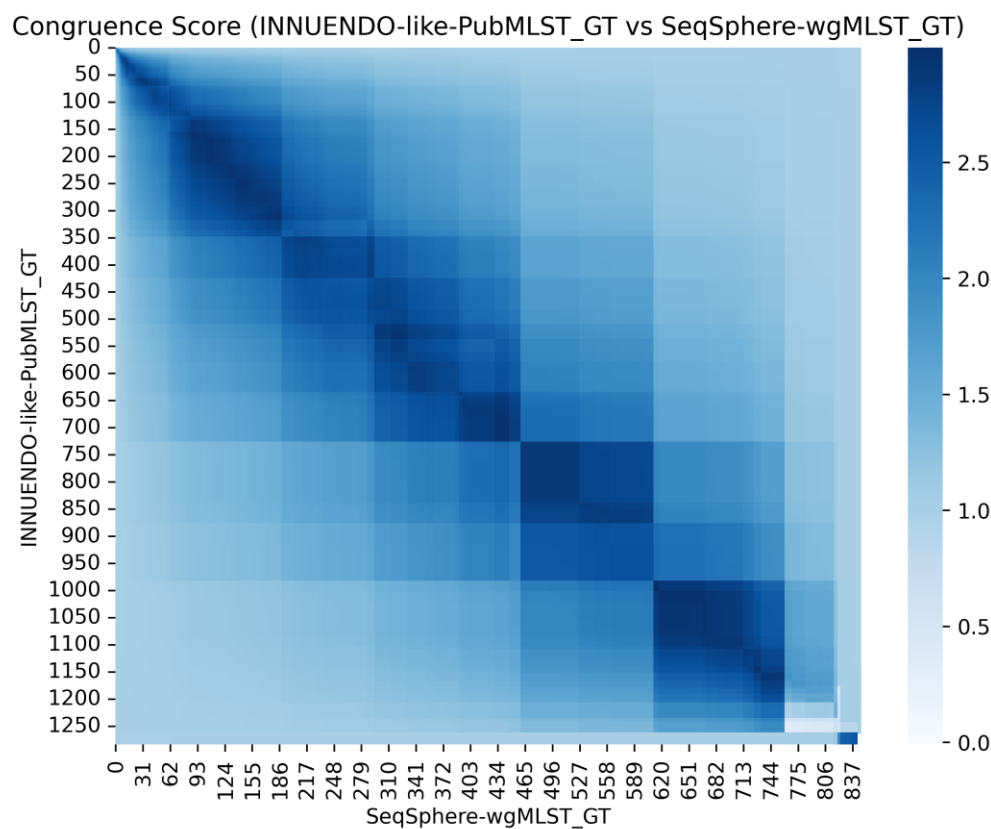


Figure S2.40.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

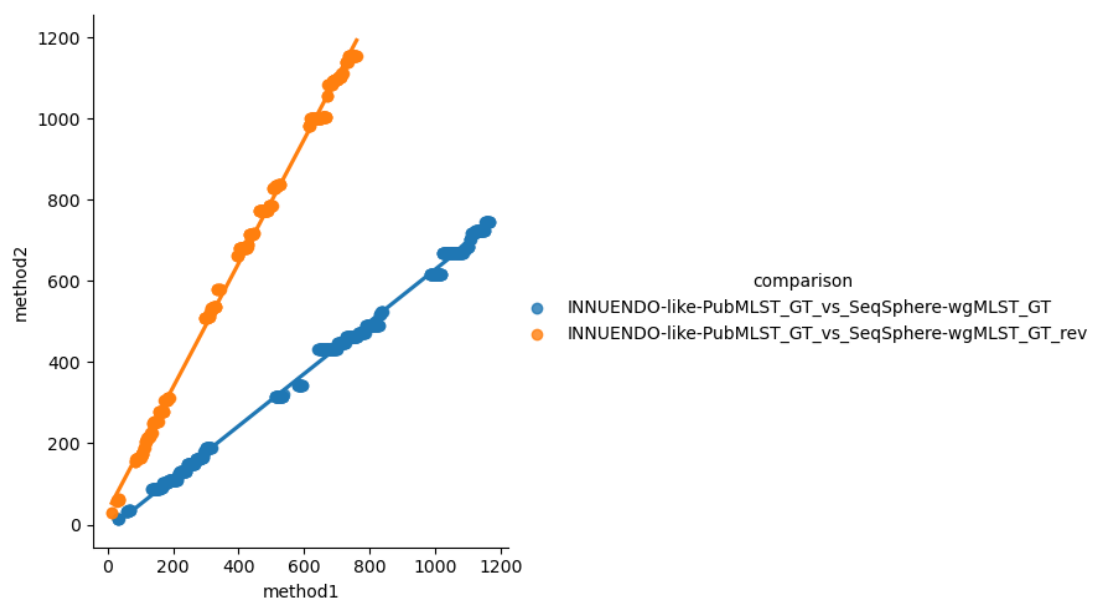


Figure S2.40.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 628 (blue) and 427 (orange) points is presented.

41. INNUENDO-like-PubMLST GrapeTree vs. SeqSphere-wgMLST single-linkage

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.

	INNUENDO-like-PubMLST GrapeTree	SeqSphere-wgMLST single- linkage
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1286	806

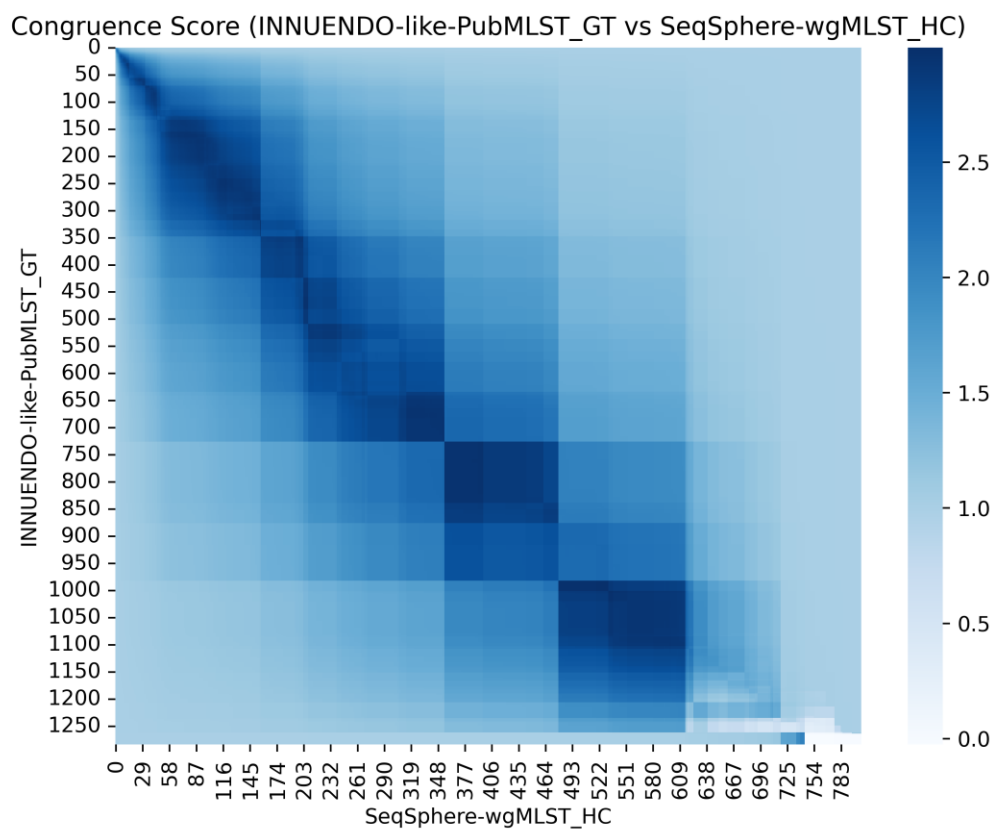


Figure S2.14.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

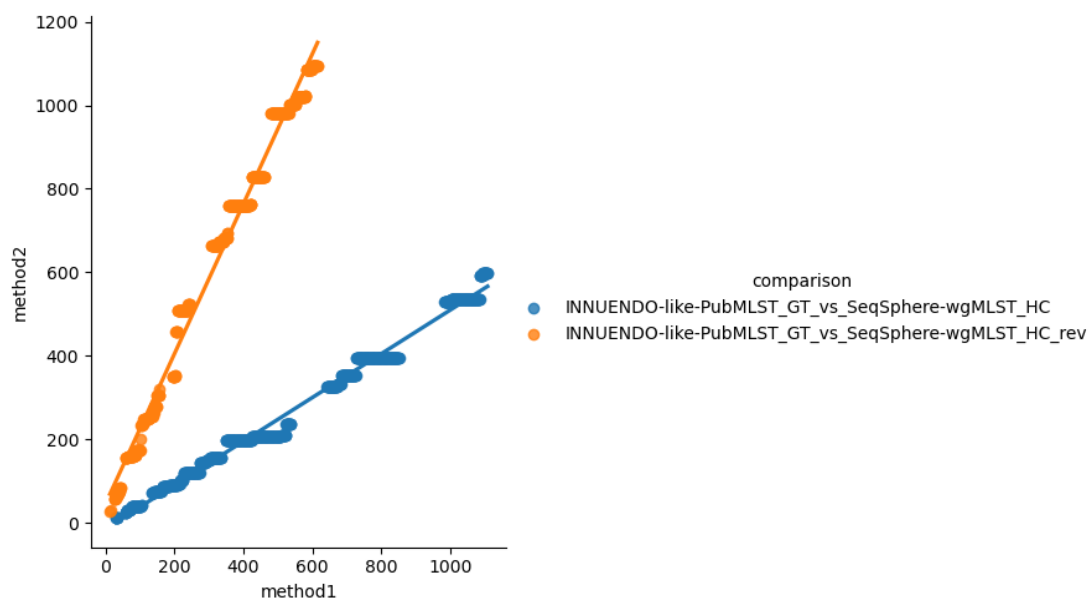


Figure S2.41.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 783 (blue) and 464 (orange) points is presented.

42. INNUENDO-like-PubMLST single-linkage vs. chewieSnake GrapeTree

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.

	INNUENDO-like-PubMLST single-linkage	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	PubMLST
Dataset	All samples	All samples
Number partitions	1224	1229

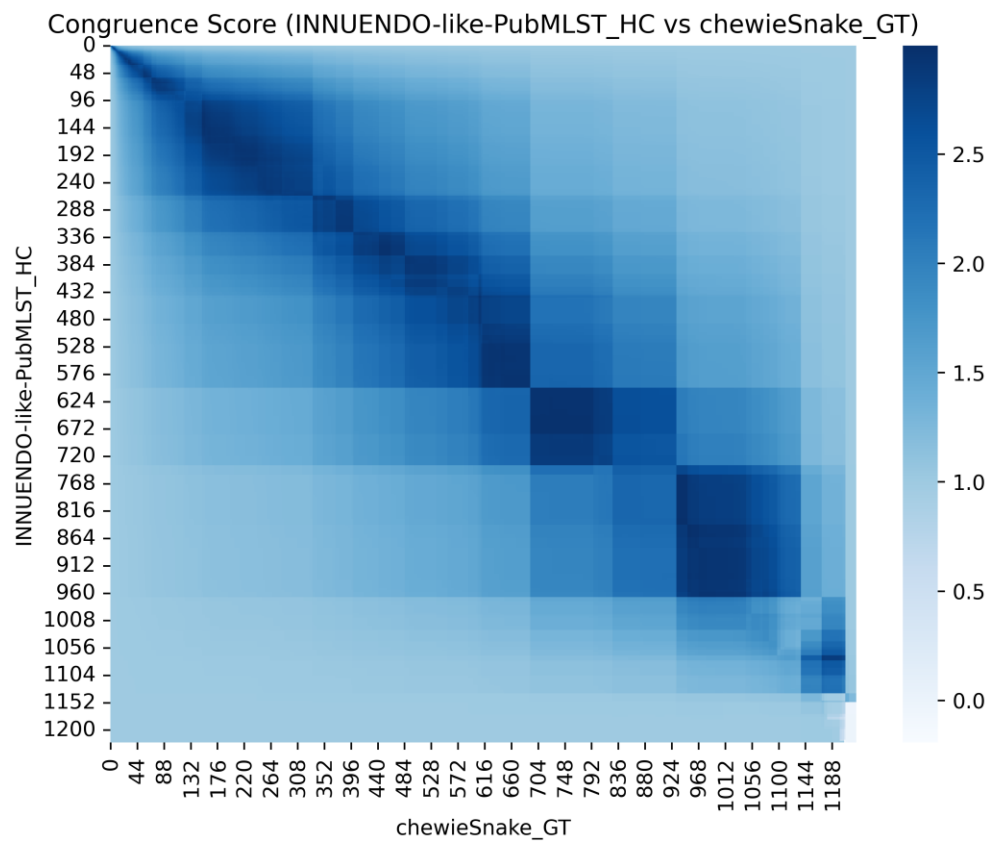


Figure S2.42.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

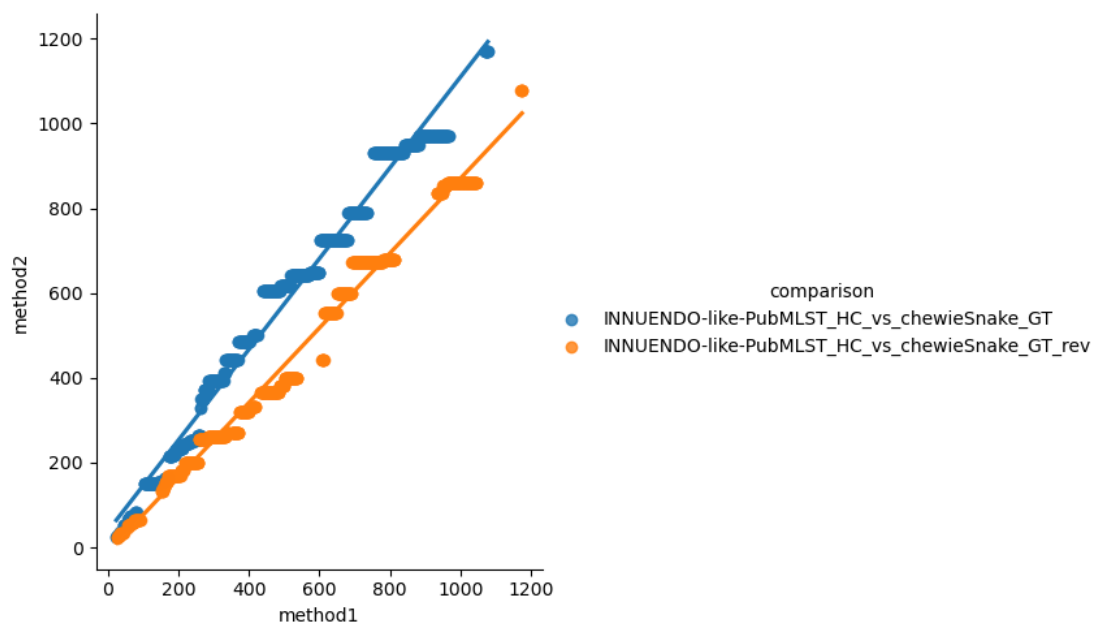


Figure S2.42.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 883 (blue) and 733 (orange) points is presented.

43. INNUENDO-like-PubMLST single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage

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.

	INNUENDO-like-PubMLST 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	PubMLST	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	1224	852

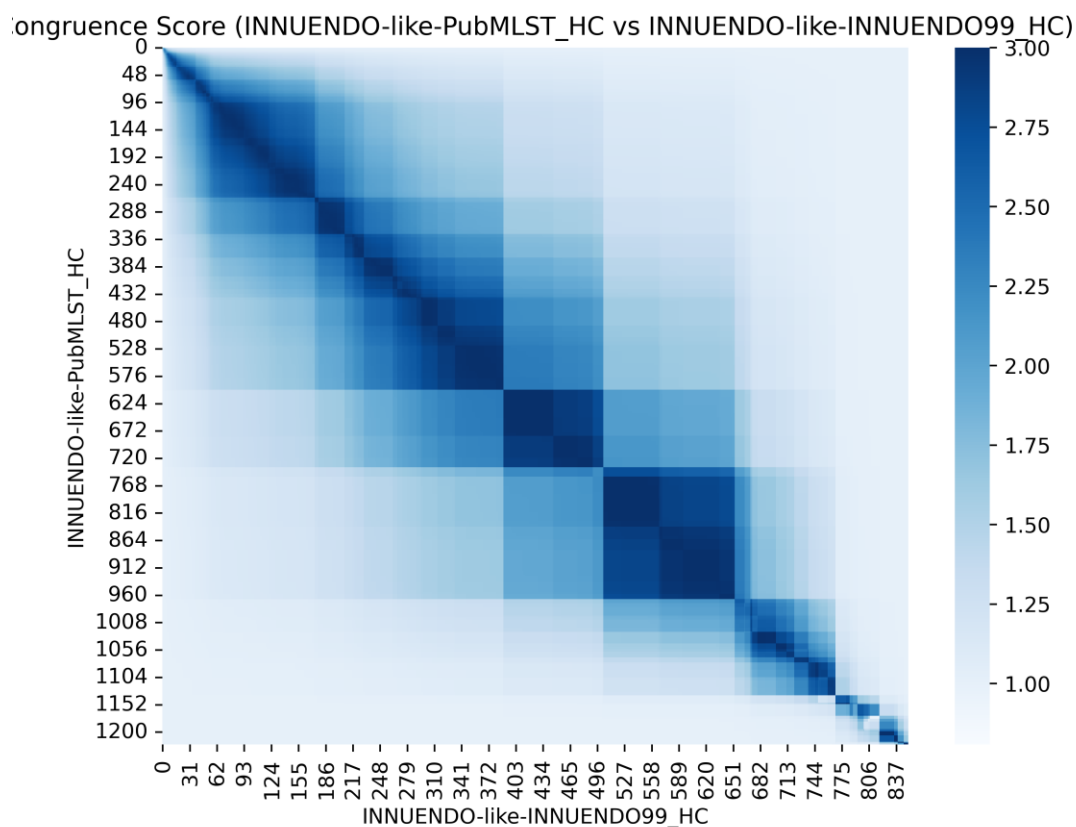


Figure S2.43.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

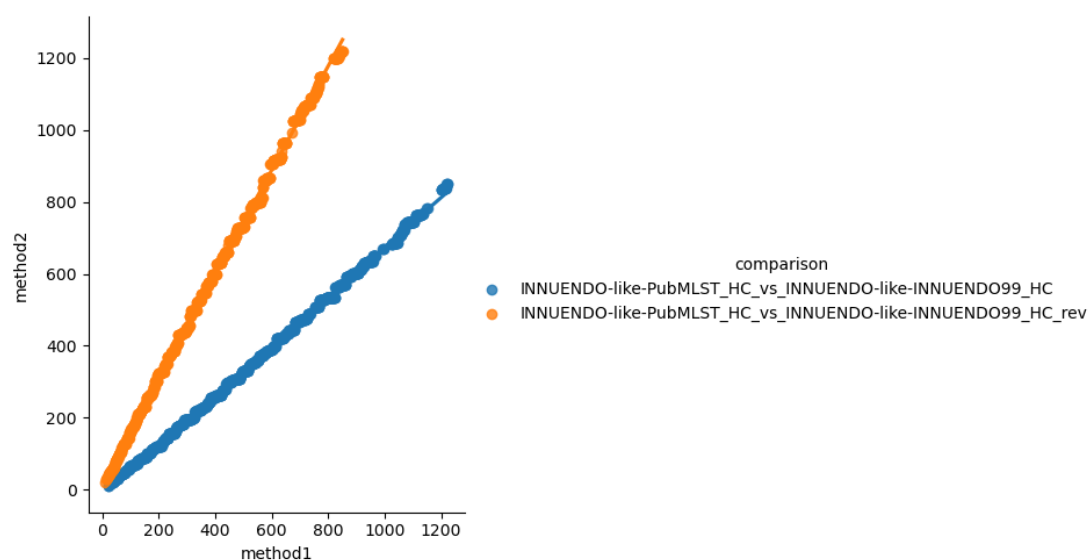


Figure S2.43.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1054 (blue) and 779 (orange) points is presented.

44. INNUENDO-like-PubMLST single-linkage vs. INNUENDO-like-INNUENDOccgMLST GrapeTree

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.

	INNUENDO-like-PubMLST single-linkage	INNUENDO-like-INNUENDOccgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1224	677

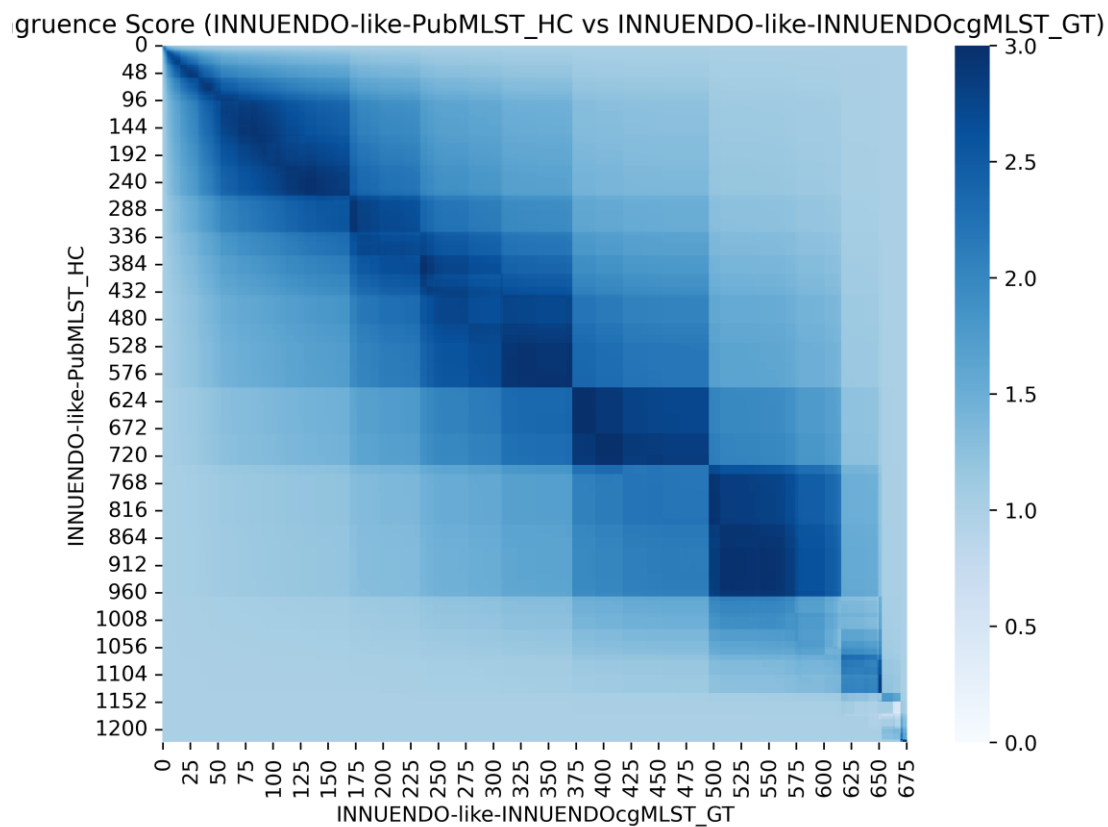


Figure S2.44.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

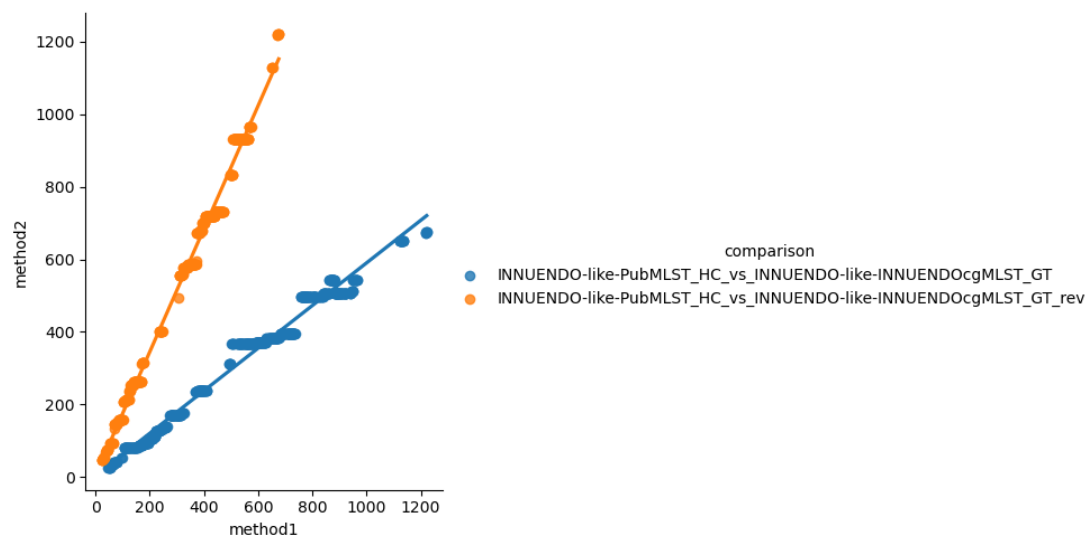


Figure S2.44.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 576 (blue) and 405 (orange) points is presented.

45. INNUENDO-like-PubMLST single-linkage vs. INNUENDO-like-INNUENDOCgMLST single-linkage

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.

	INNUENDO-like-PubMLST single-linkage	INNUENDO-like-INNUENDOCgMLST single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	PubMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	1224	644

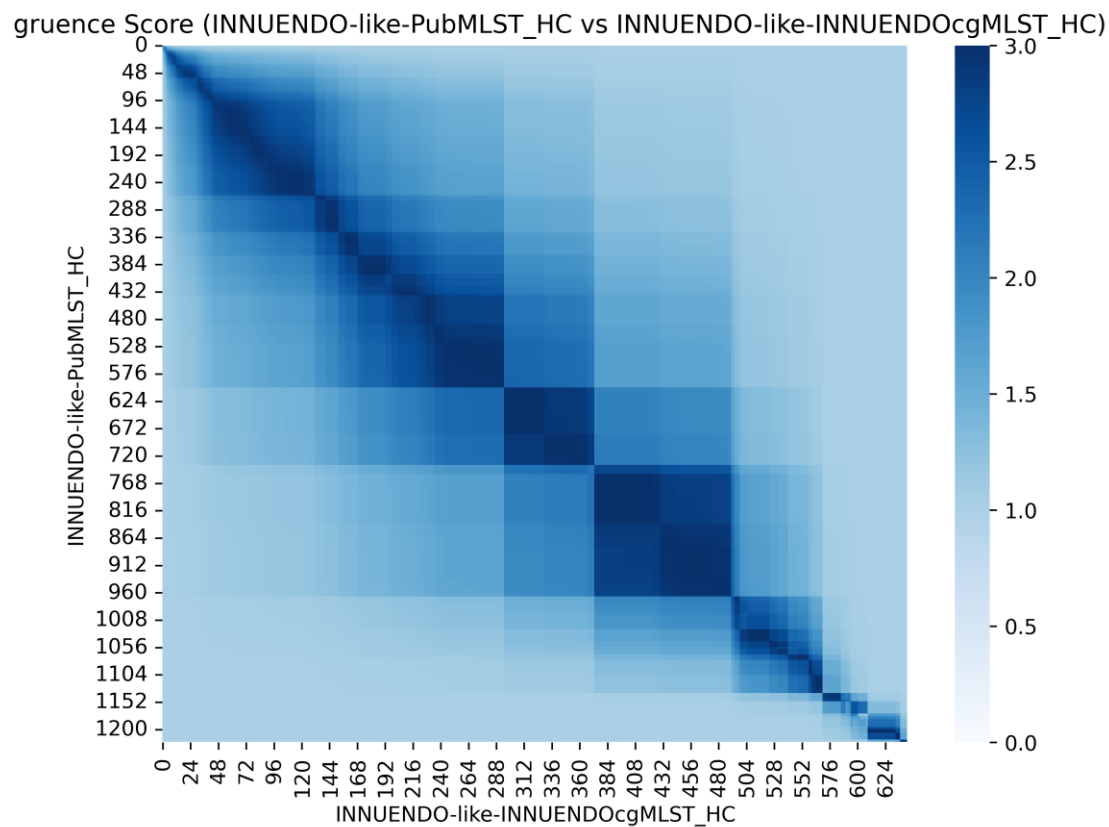


Figure S2.45.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

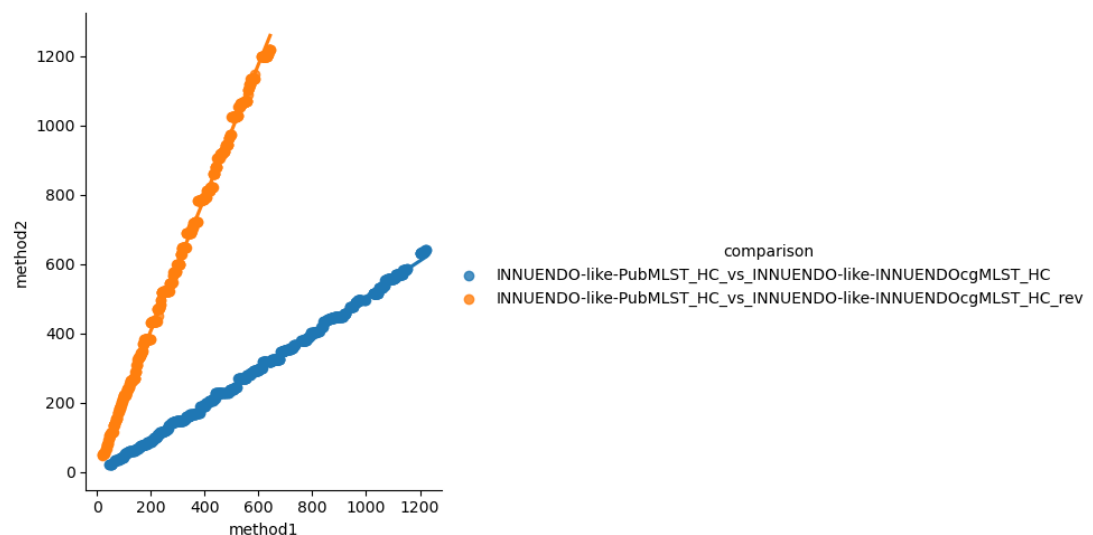


Figure S2.45.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 835 (blue) and 595 (orange) points is presented.

46. INNUENDO-like-PubMLST single-linkage vs. SeqSphere-wgMLST GrapeTree

Table S2.46. 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-PubMLST single-linkage	SeqSphere-wgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1224	848

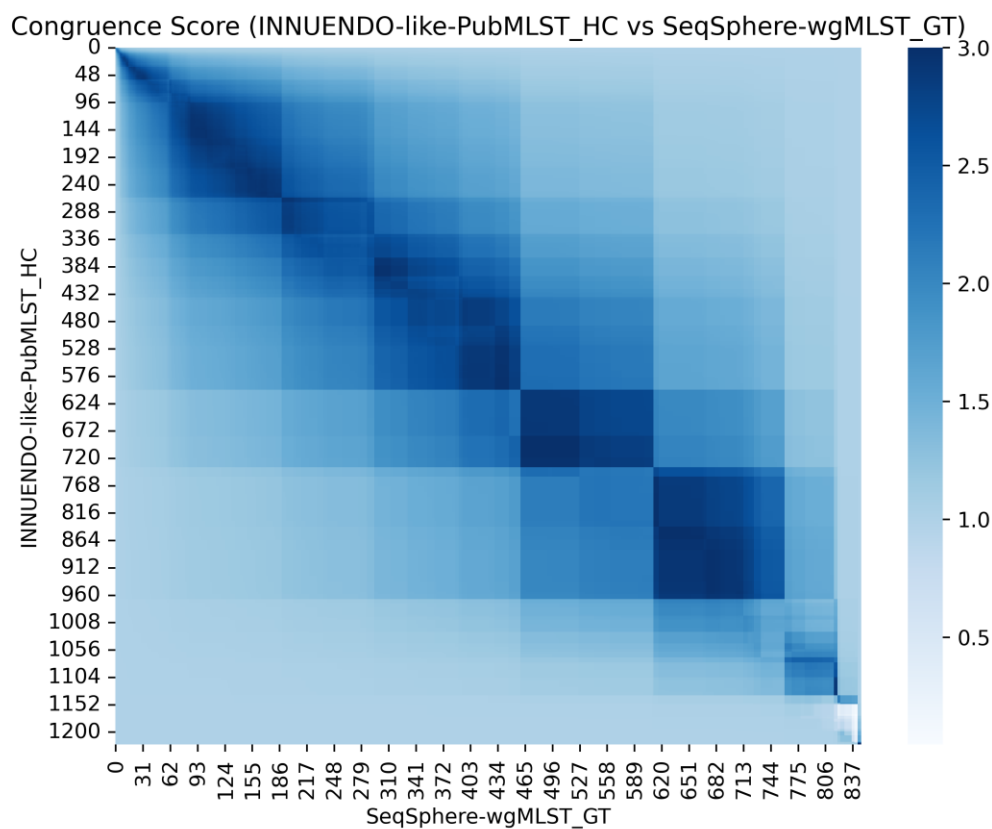


Figure S2.46.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

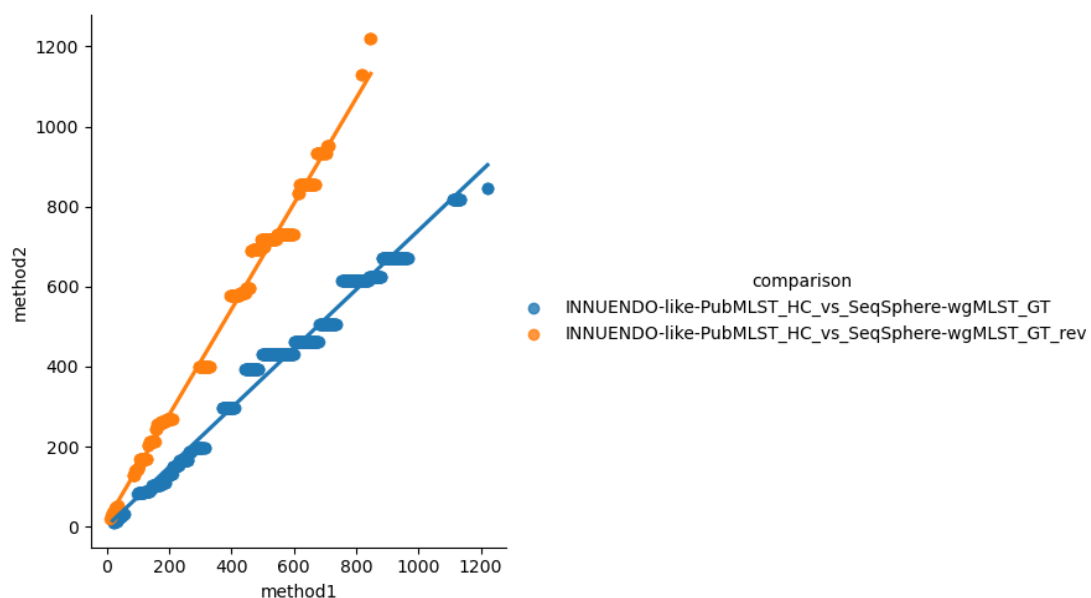


Figure S2.46.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 800 (blue) and 505 (orange) points is presented.

47. INNUENDO-like-PubMLST single-linkage vs. SeqSphere-wgMLST single-linkage

Table S2.47. 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-PubMLST single-linkage	SeqSphere-wgMLST single-linkage
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	PubMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	1224	806

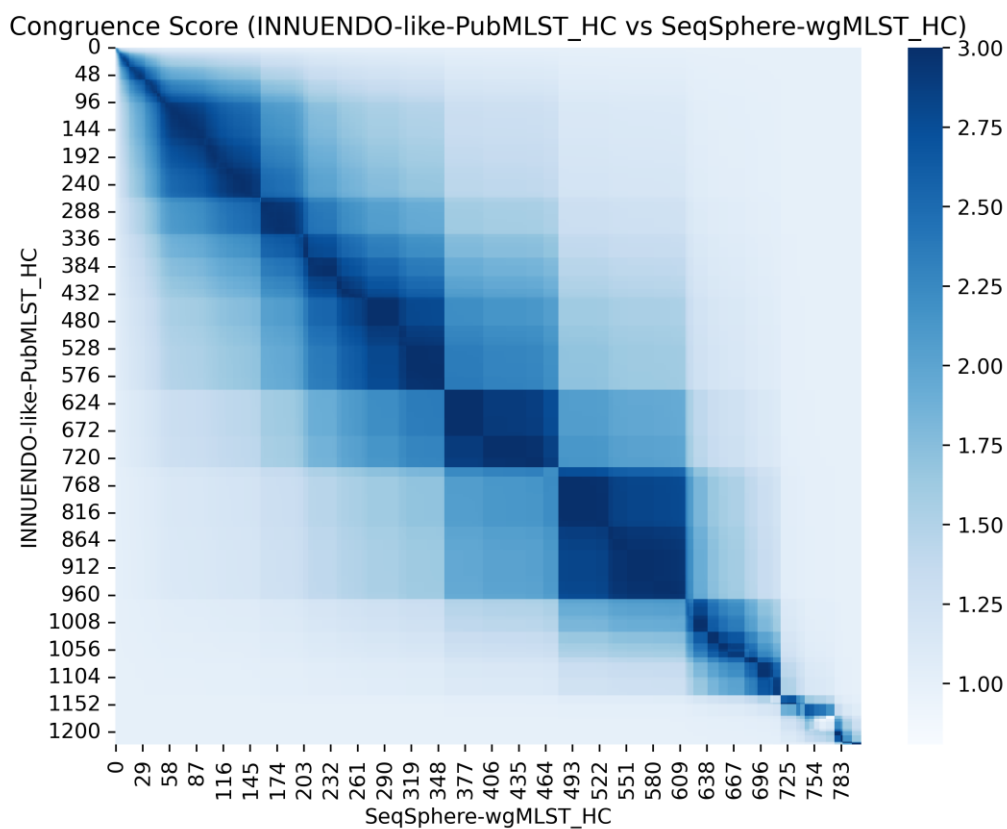


Figure S2.47.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

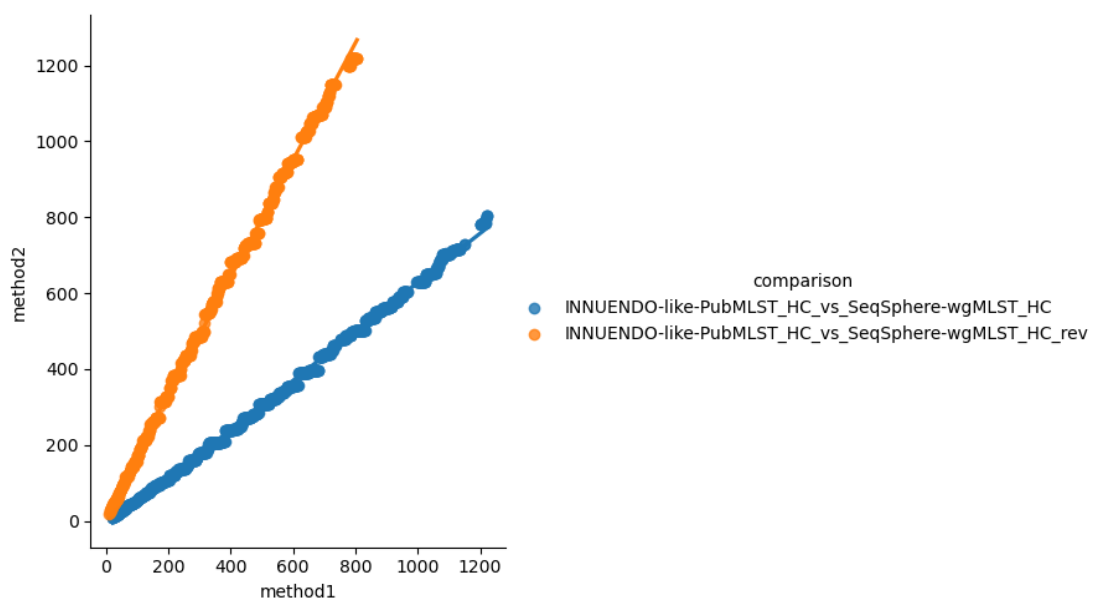


Figure S2.47.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1087 (blue) and 739 (orange) points is presented.

48. SeqSphere-wgMLST GrapeTree vs. INNUENDO-like-INNUENDOcgmLST GrapeTree

Table S2.48. 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-wgMLST GrapeTree	INNUENDO-like-INNUENDOcgmLST GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	SeqSphere wgMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	848	677

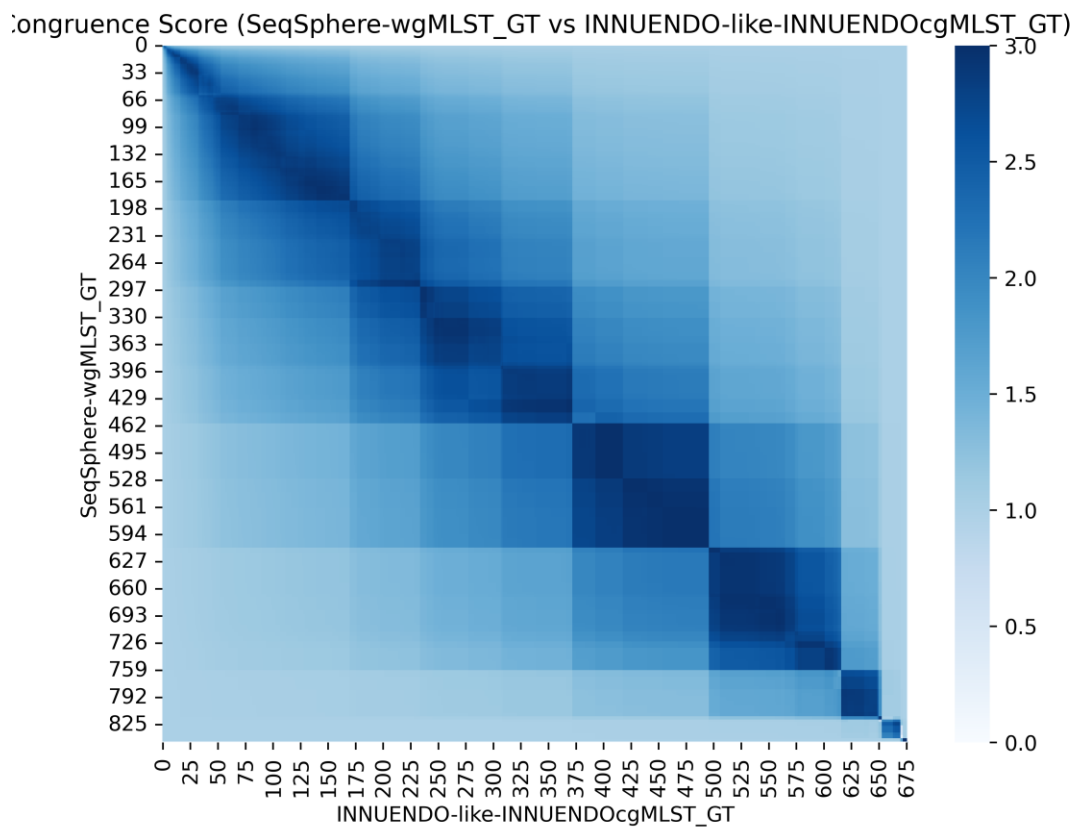


Figure S2.48.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

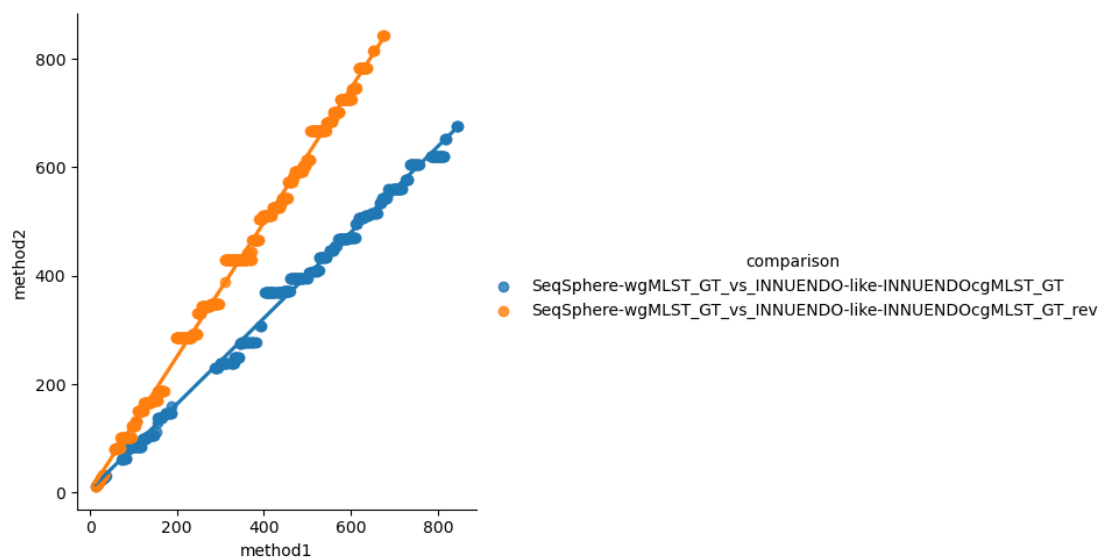


Figure S2.48.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 458 (blue) and 567 (orange) points is presented.

49. SeqSphere-wgMLST GrapeTree vs. INNUENDO-like-INNUENDOcgcMLST single-linkage

Table S2.49. 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-wgMLST GrapeTree	INNUENDO-like-INNUENDOcgcMLST single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	SeqSphere wgMLST	INNUENDO cgcMLST
Dataset	All samples	All samples
Number partitions	848	644

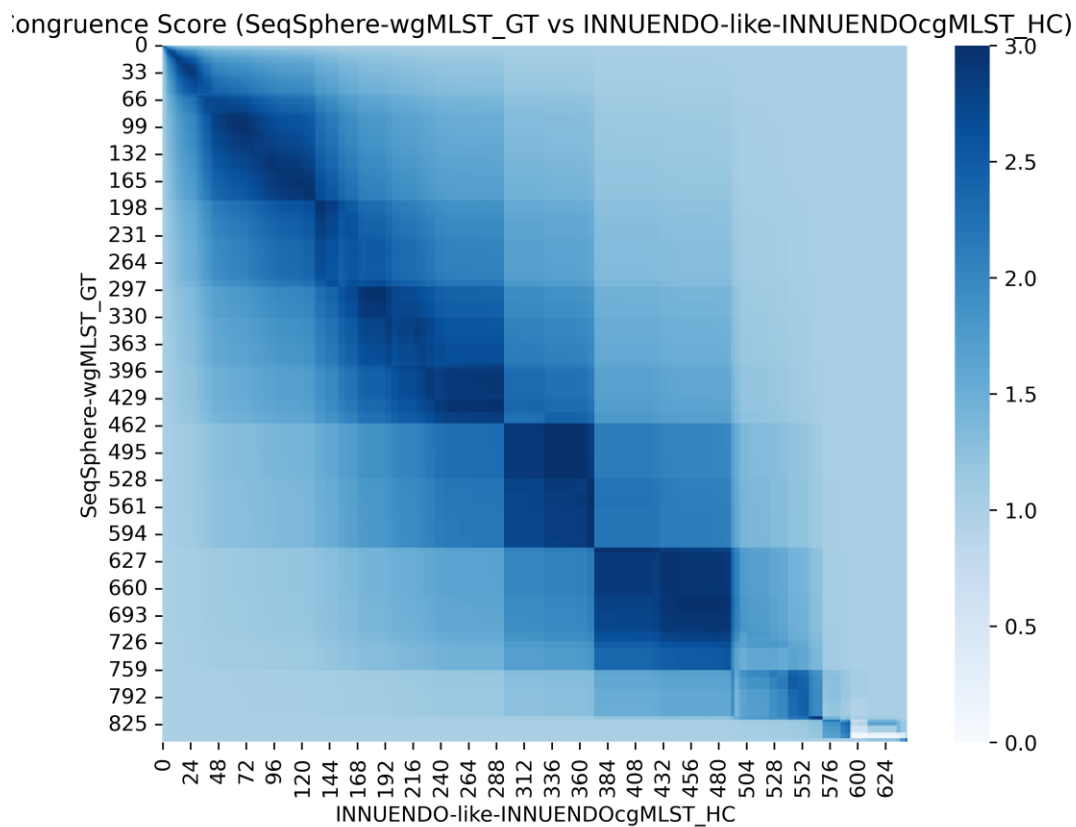


Figure S2.49.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

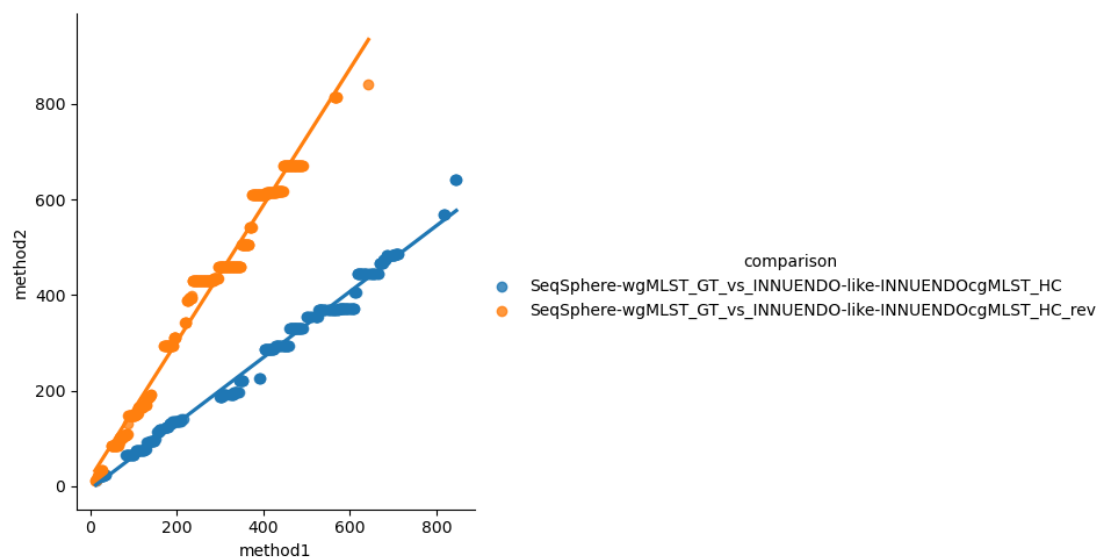


Figure S2.49.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 377 (blue) and 419 (orange) points is presented.

50. SeqSphere-wgMLST single-linkage vs. chewieSnake GrapeTree

Table S2.50. 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-wgMLST single-linkage	chewieSnake GrapeTree
Pipeline version	v8.3.4	v3.1.1
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	SeqSphere wgMLST	PubMLST
Dataset	All samples	All samples
Number partitions	806	1229

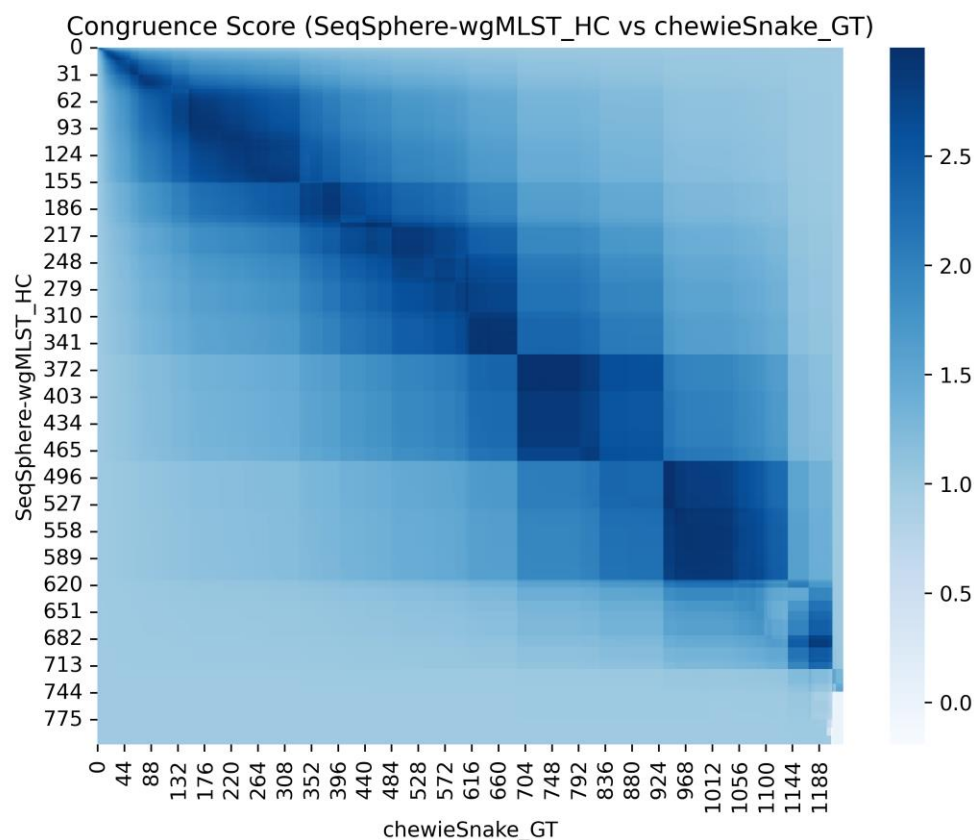


Figure S2.50.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

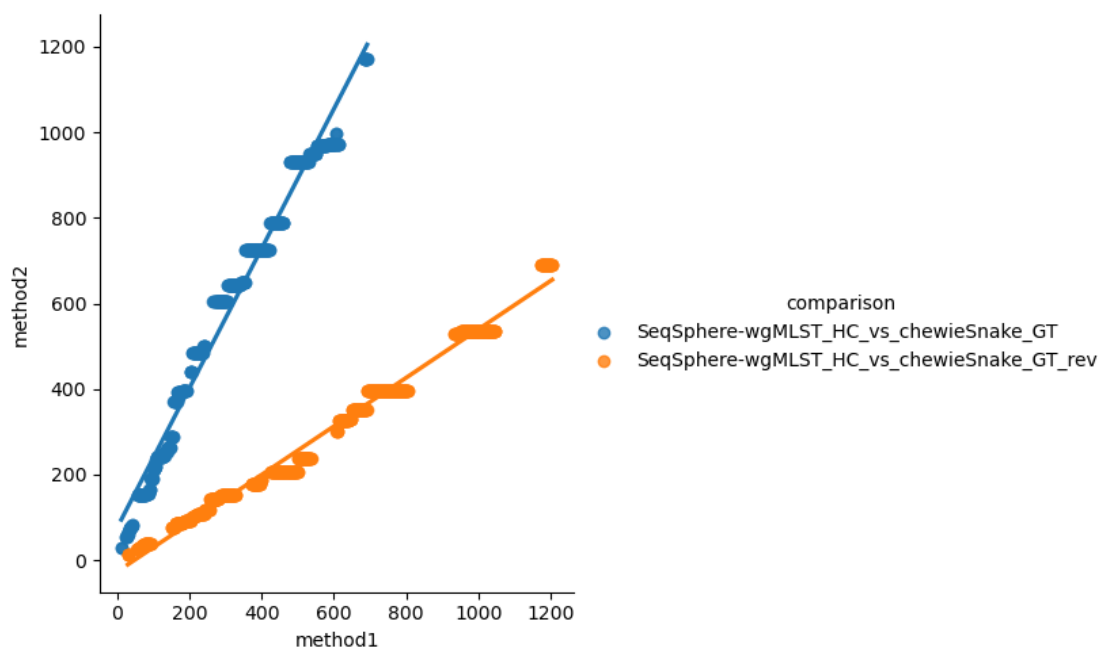


Figure S2.50.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 538 (blue) and 709 (orange) points is presented.

51. SeqSphere-wgMLST single-linkage vs. INNUENDO-like-INNUENDO99 single-linkage

Table S2.51. 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-wgMLST 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	SeqSphere wgMLST	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	806	852

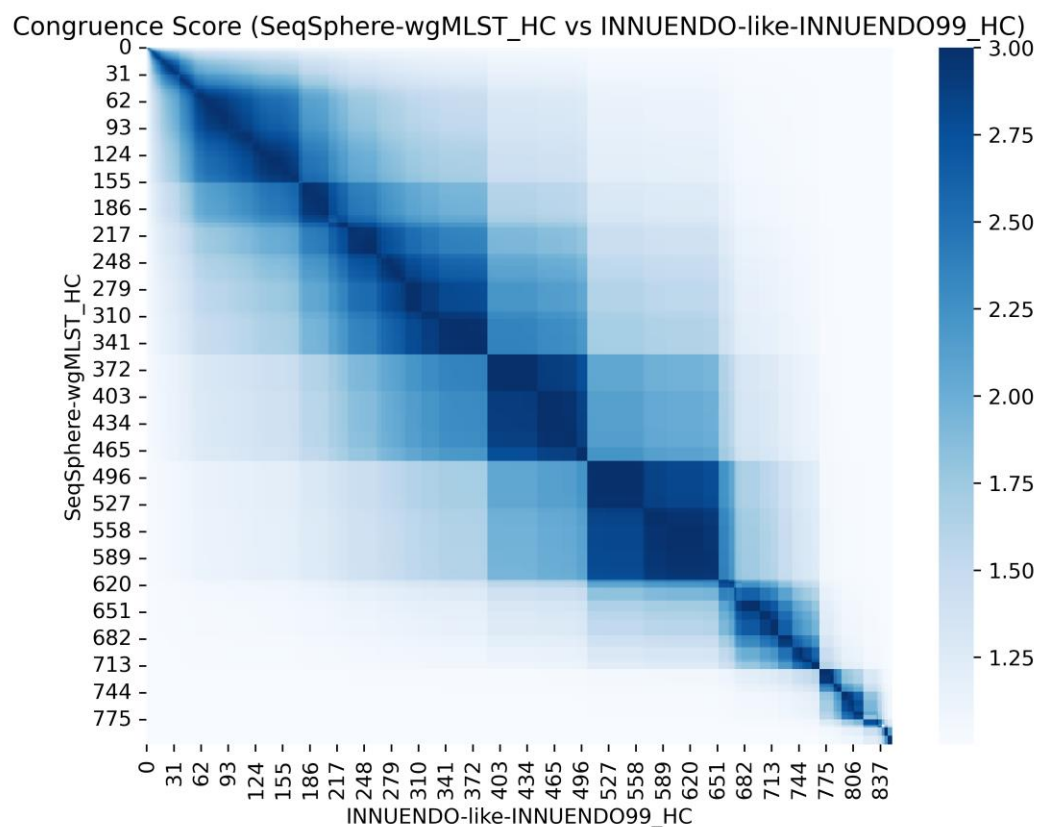


Figure S2.51.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

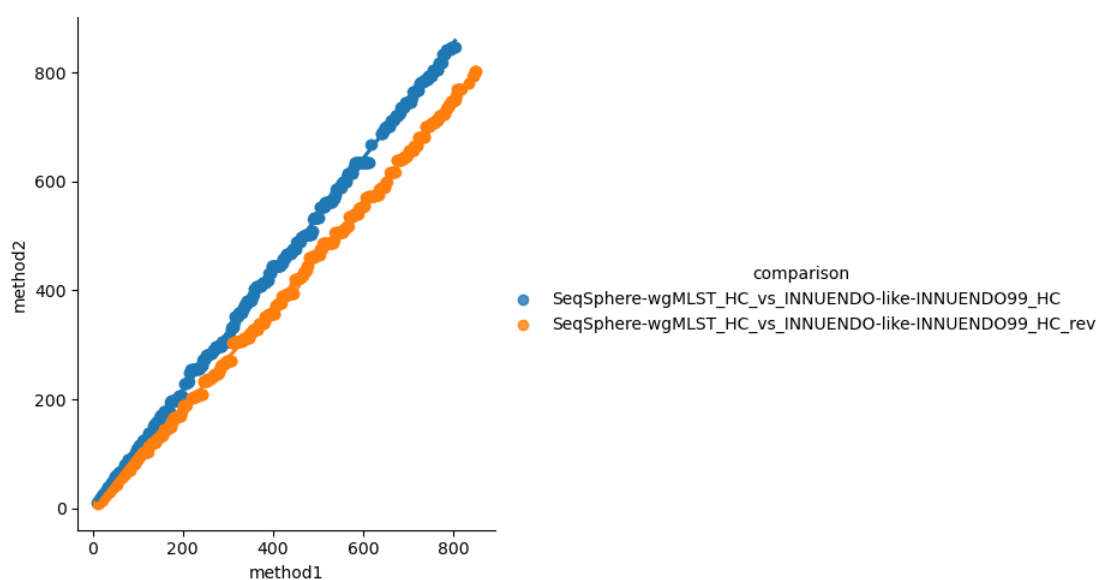


Figure S2.51.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 766 (blue) and 800 (orange) points is presented.

52. SeqSphere-wgMLST single-linkage vs. INNUENDO-like-INNUENDOccgMLST GrapeTree

Table S2.52. 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-wgMLST single-linkage	INNUENDO-like-INNUENDOccgMLST GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	SeqSphere wgMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	806	677

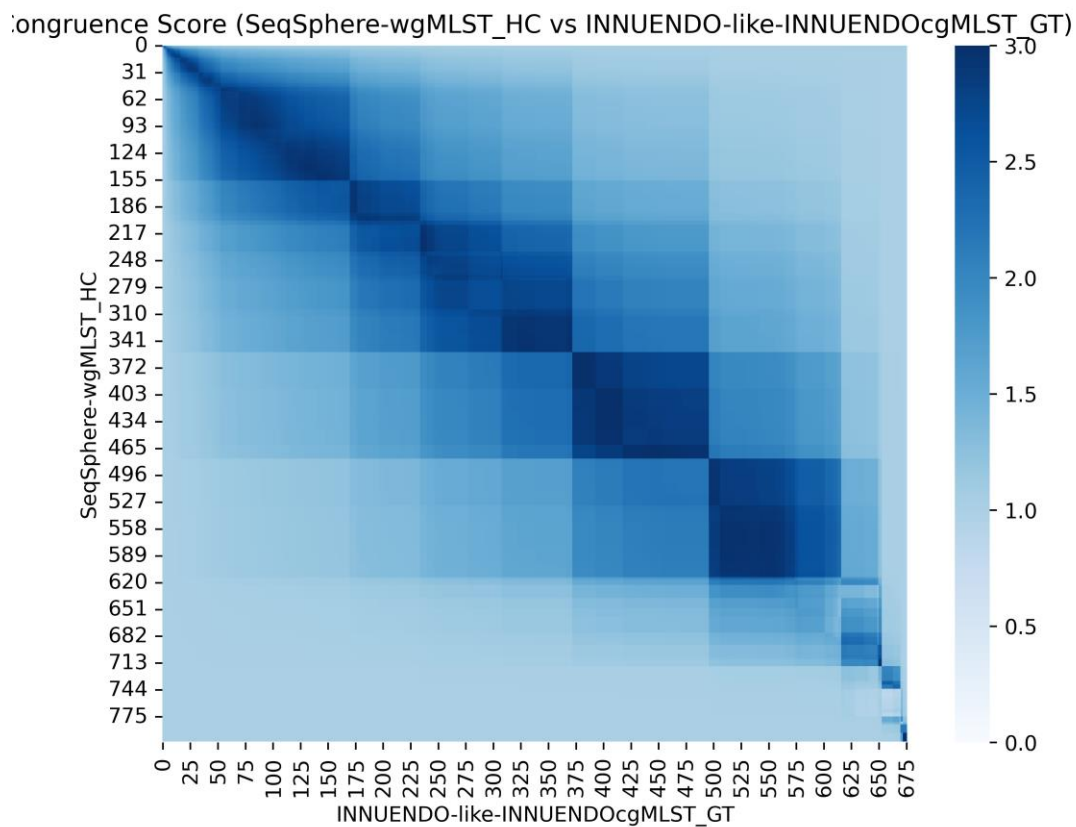


Figure S2.52.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

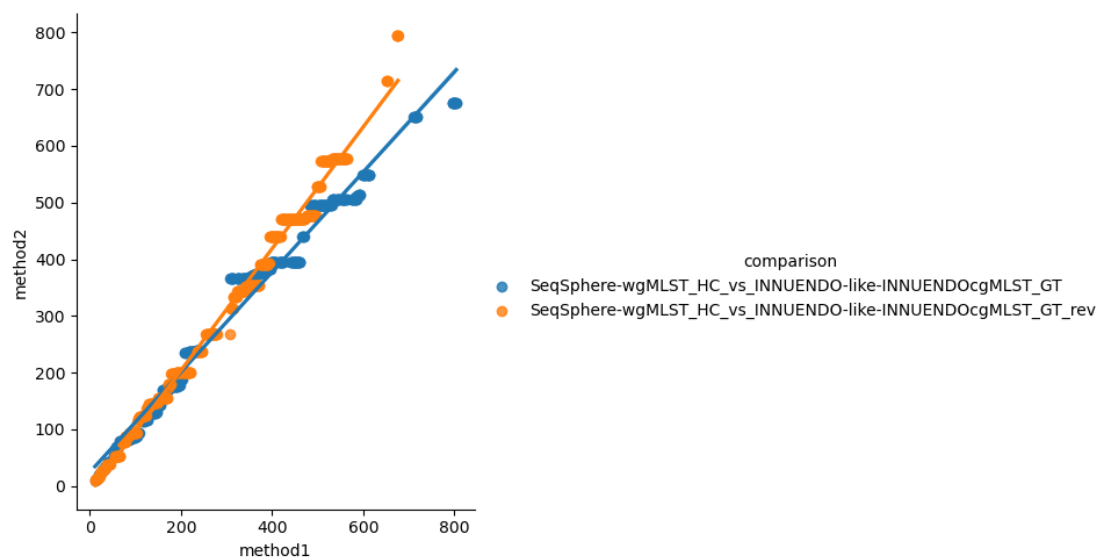


Figure S2.52.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 362 (blue) and 494 (orange) points is presented.

53. SeqSphere-wgMLST single-linkage vs. INNUENDO-like-INNUENDOcgMLST single-linkage

Table S2.53. 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-wgMLST single-linkage	INNUENDO-like-INNUENDOcgMLST single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	SeqSphere wgMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	806	644

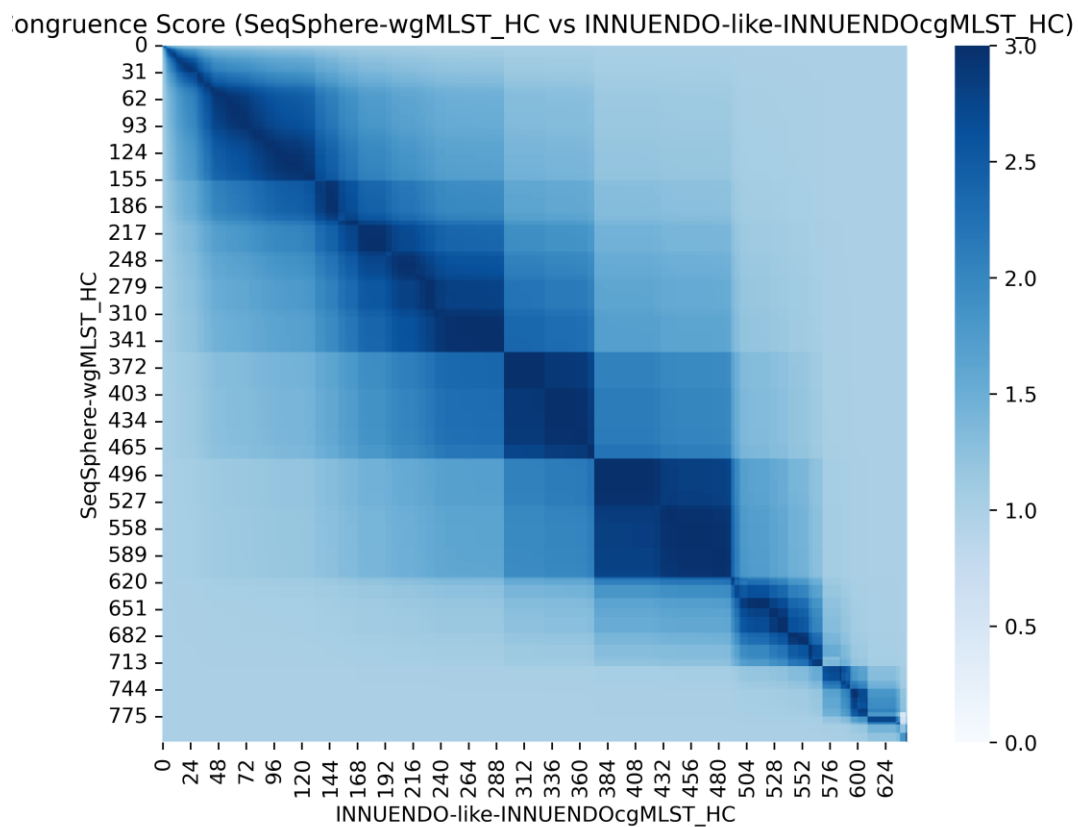


Figure S2.53.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

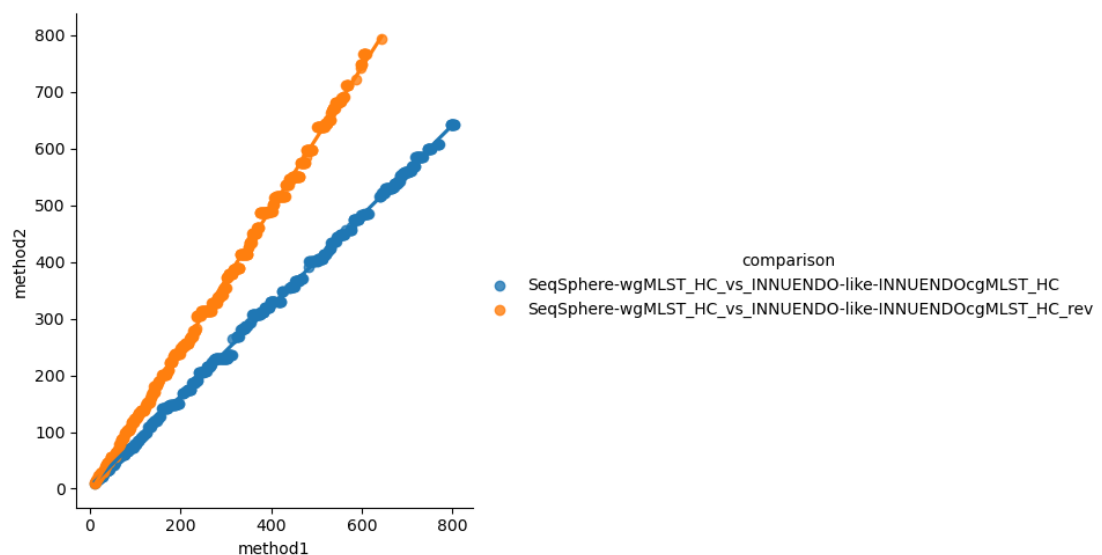


Figure S2.53.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 532 (blue) and 556 (orange) points is presented.

54. SeqSphere-wgMLST single-linkage vs. SeqSphere-wgMLST GrapeTree

Table S2.54. 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-wgMLST single-linkage	SeqSphere-wgMLST GrapeTree
Pipeline version	v8.3.4	v8.3.4
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	SeqSphere wgMLST	SeqSphere wgMLST
Dataset	All samples	All samples
Number partitions	806	848

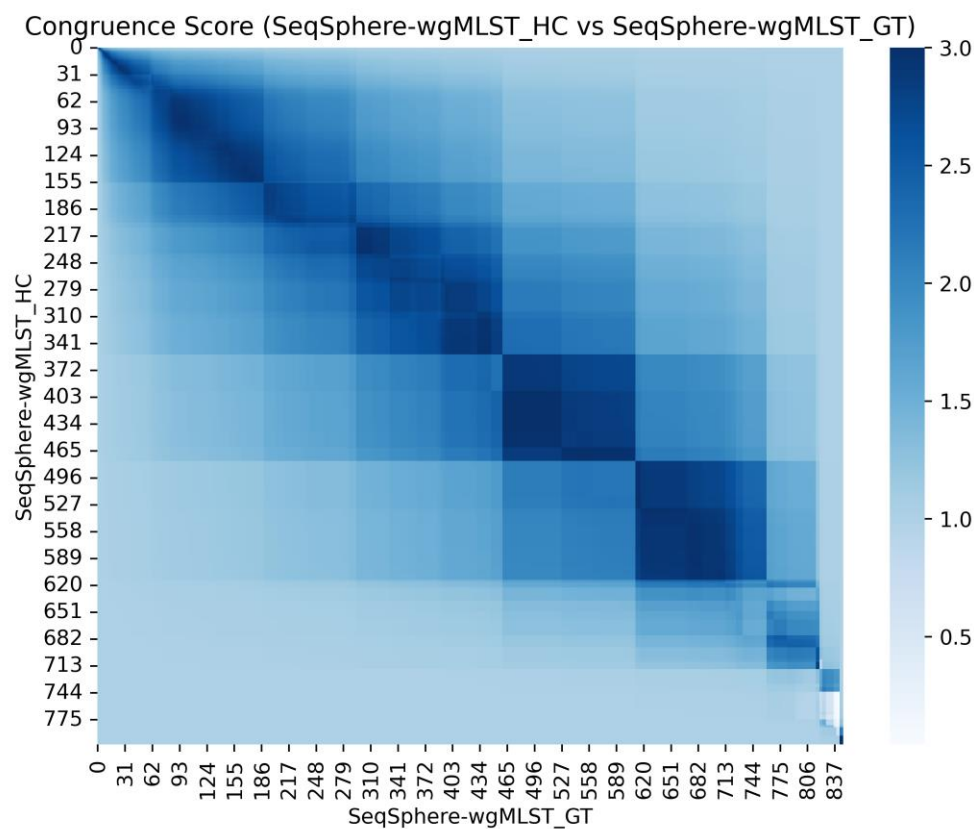


Figure S2.54.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

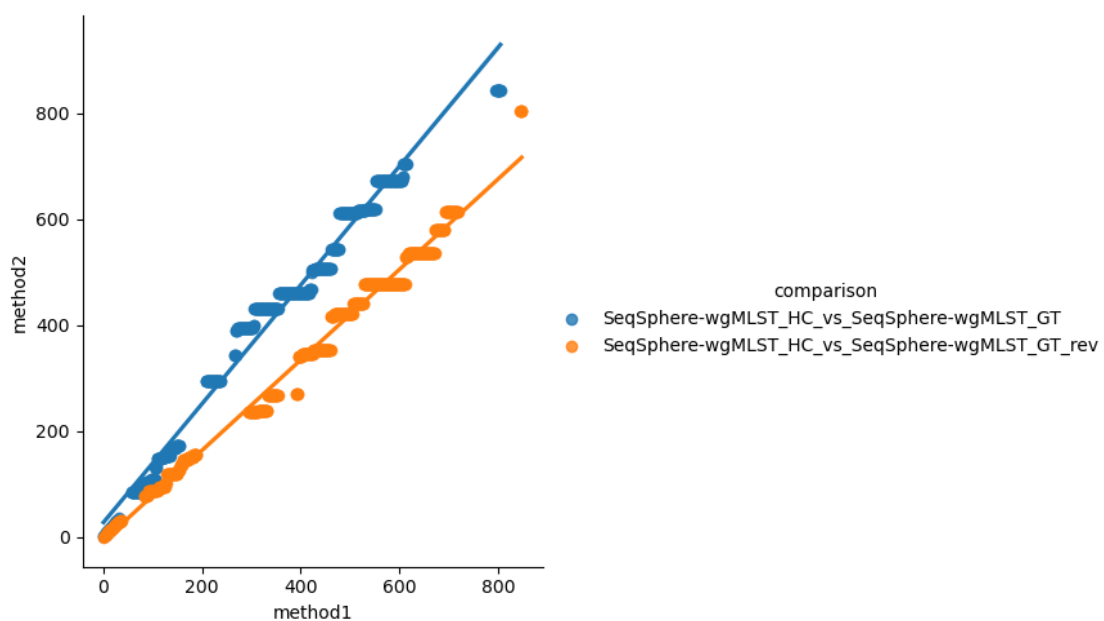


Figure S2.54.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 518 (blue) and 534 (orange) points is presented.

55. INNUENDO-like-INNUENDOccgMLST single-linkage vs. INNUENDO-like-INNUENDOccgMLST GrapeTree

Table S2.55. 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-INNUENDOccgMLST single-linkage	INNUENDO-like-INNUENDOccgMLST GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO cgMLST	INNUENDO cgMLST
Dataset	All samples	All samples
Number partitions	644	677

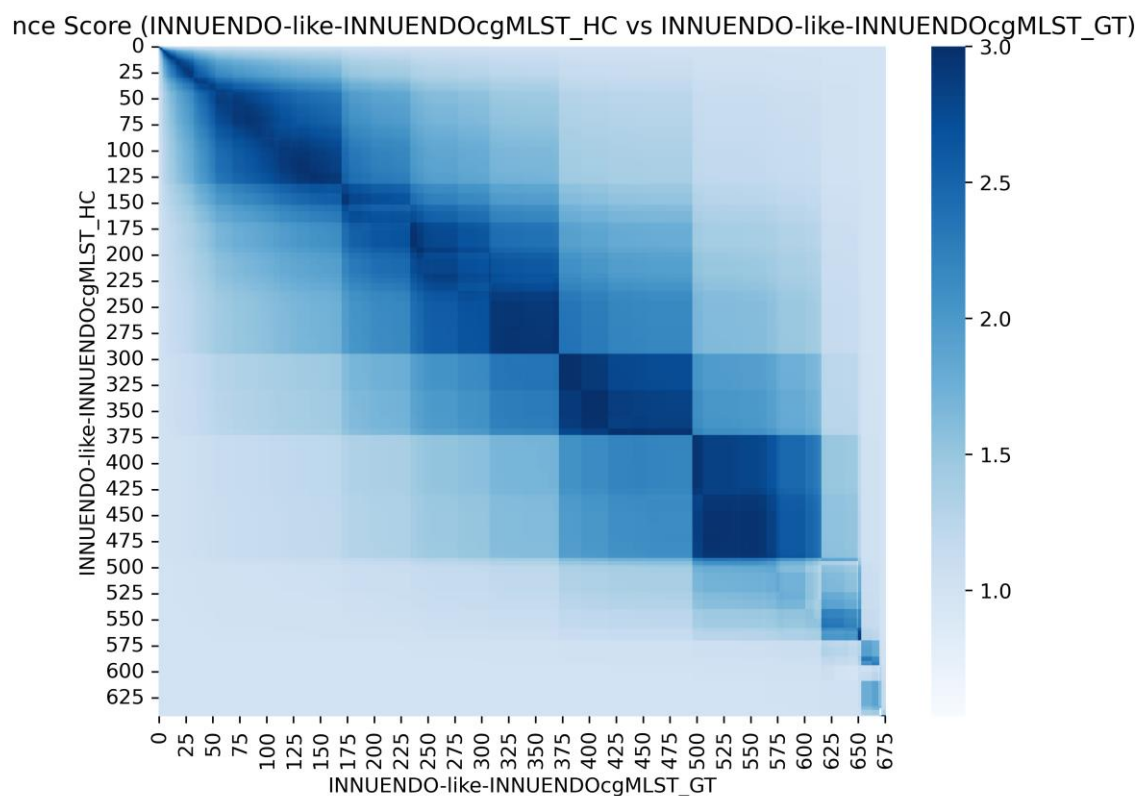


Figure S2.55.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

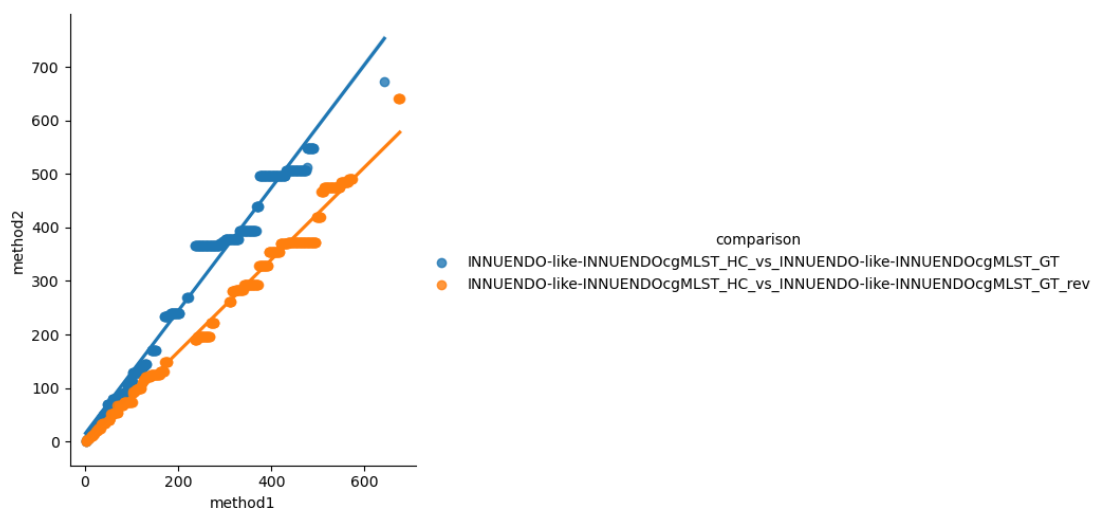


Figure S2.55.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 430 (blue) and 483 (orange) points is presented.

Section 3 – Comparison of SNP-based pipelines

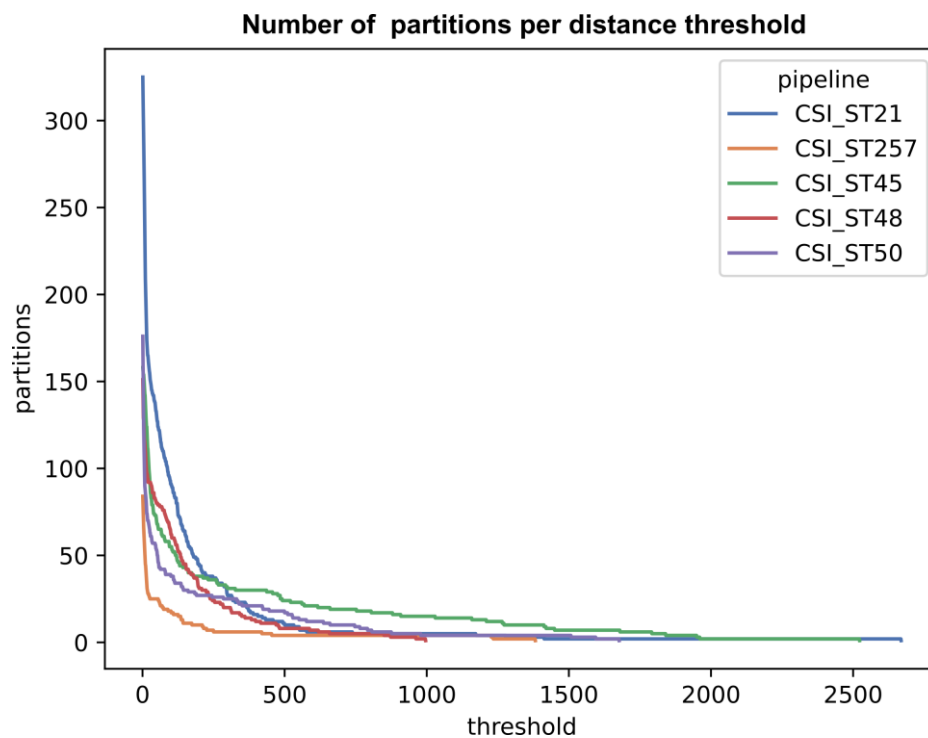


Figure S3. Number of clusters determined by the SNP-based pipeline at each possible distance threshold.

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	PubMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

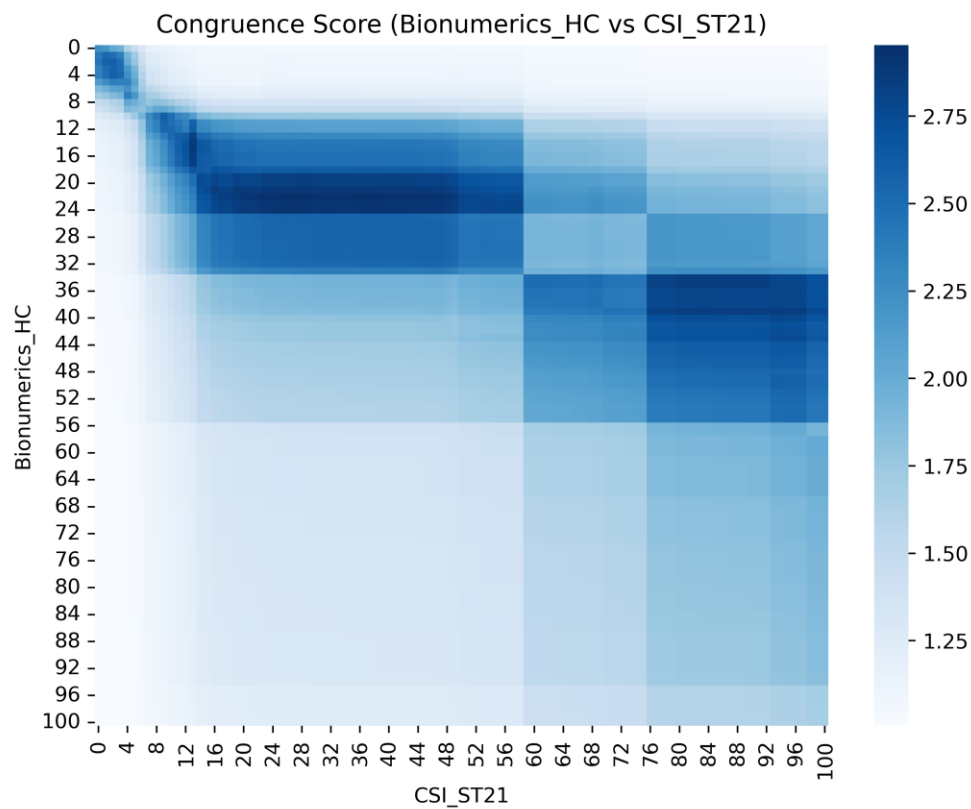


Figure S4.1.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

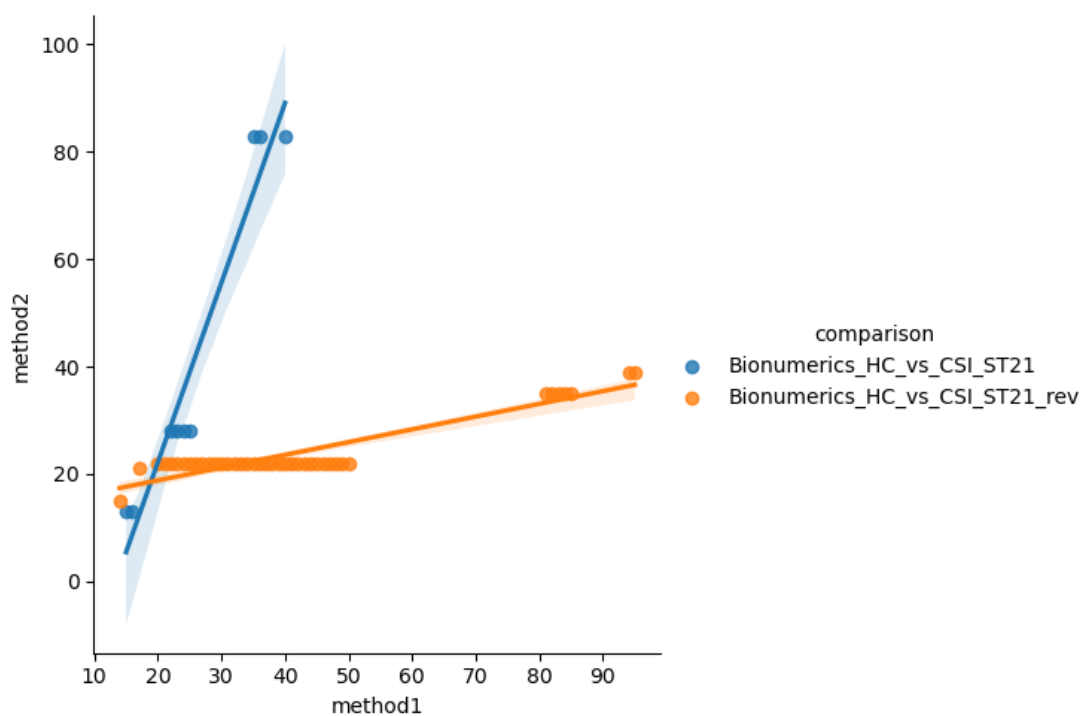


Figure S4.1.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 9 (blue) and 40 (orange) points is presented.

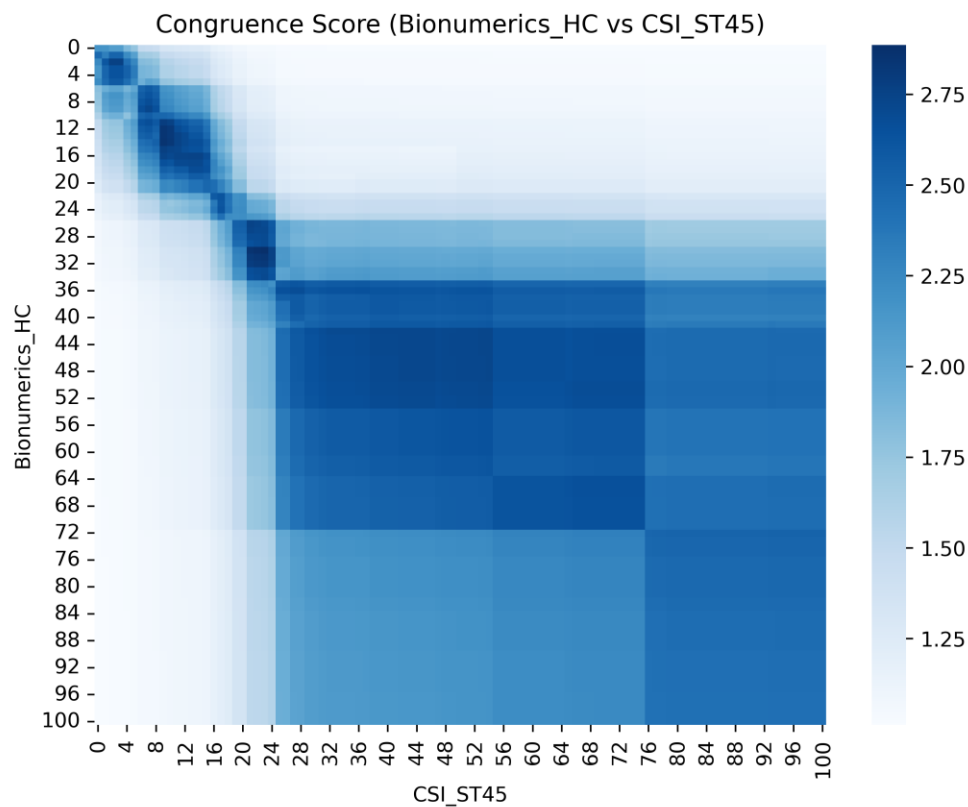


Figure S4.1.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

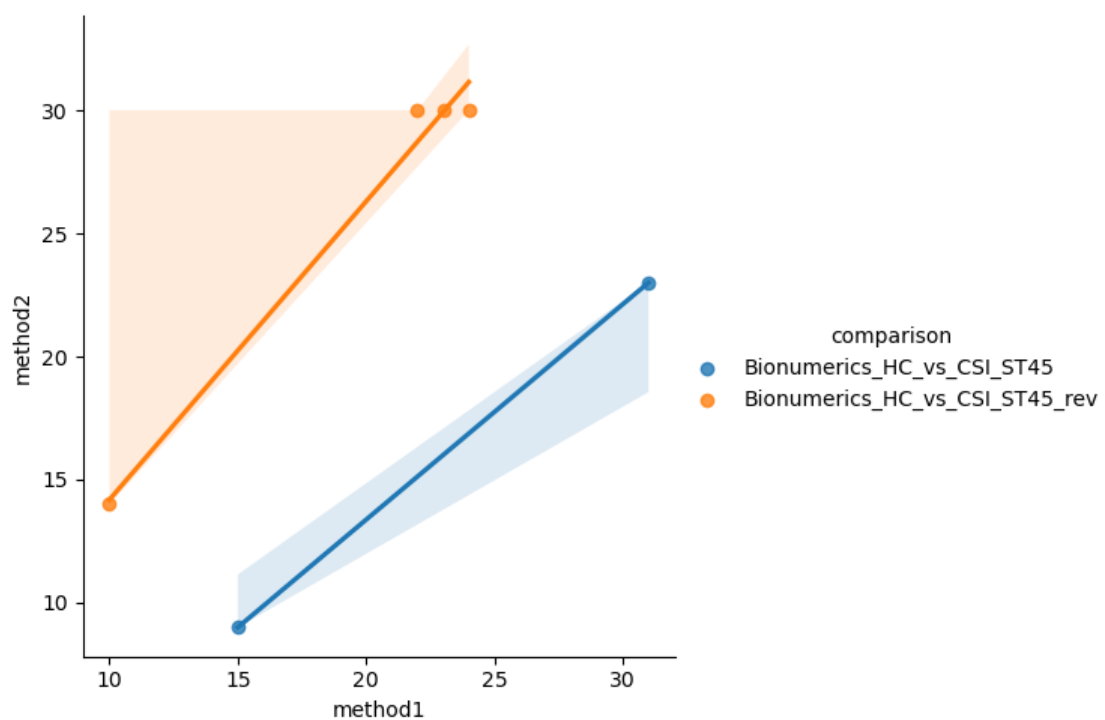


Figure S4.1.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST45. A linear tendency line supported by 2 (blue) and 4 (orange) points is presented.

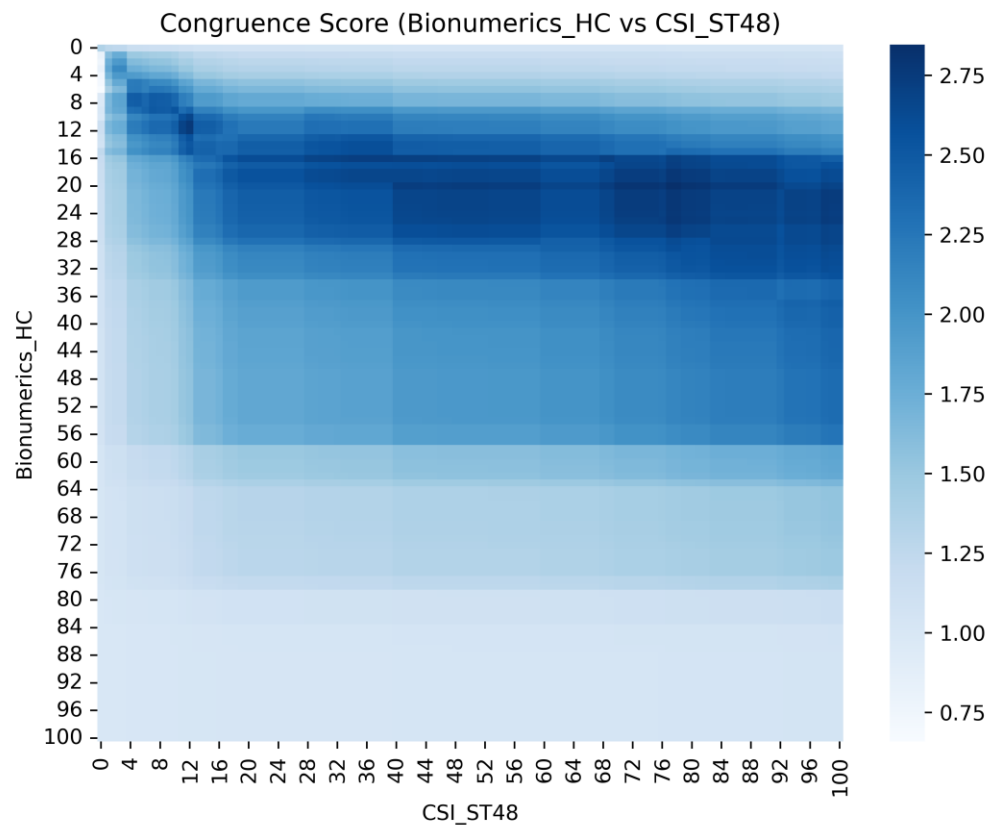


Figure S4.1.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of both pipelines for ST48.

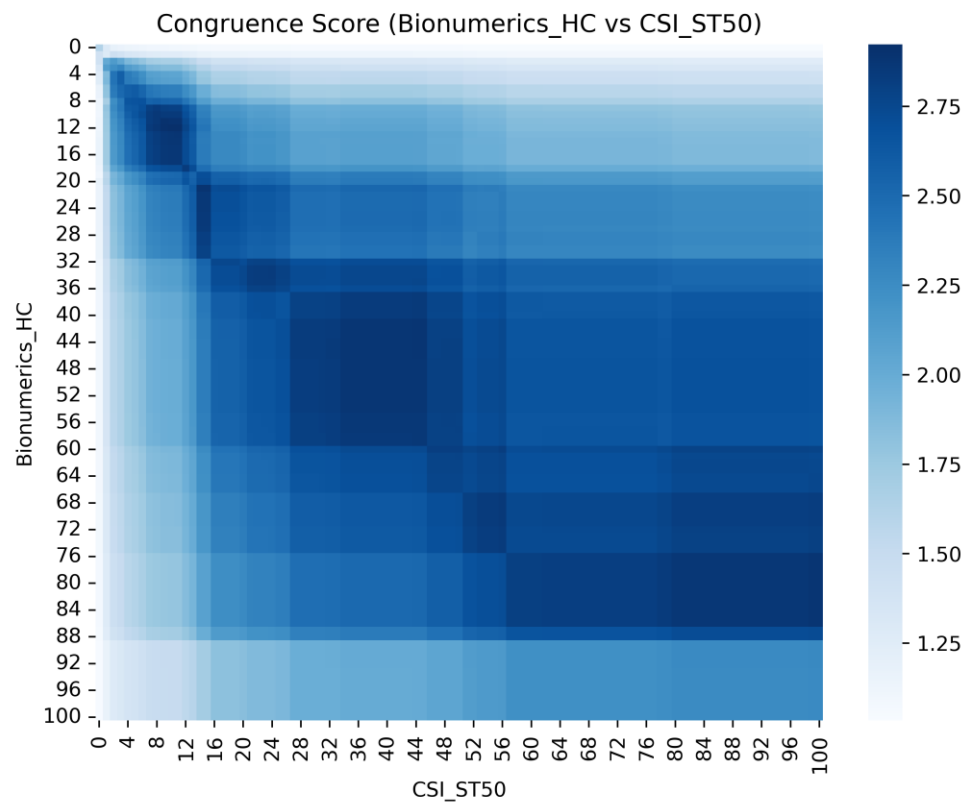


Figure S4.1.6. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

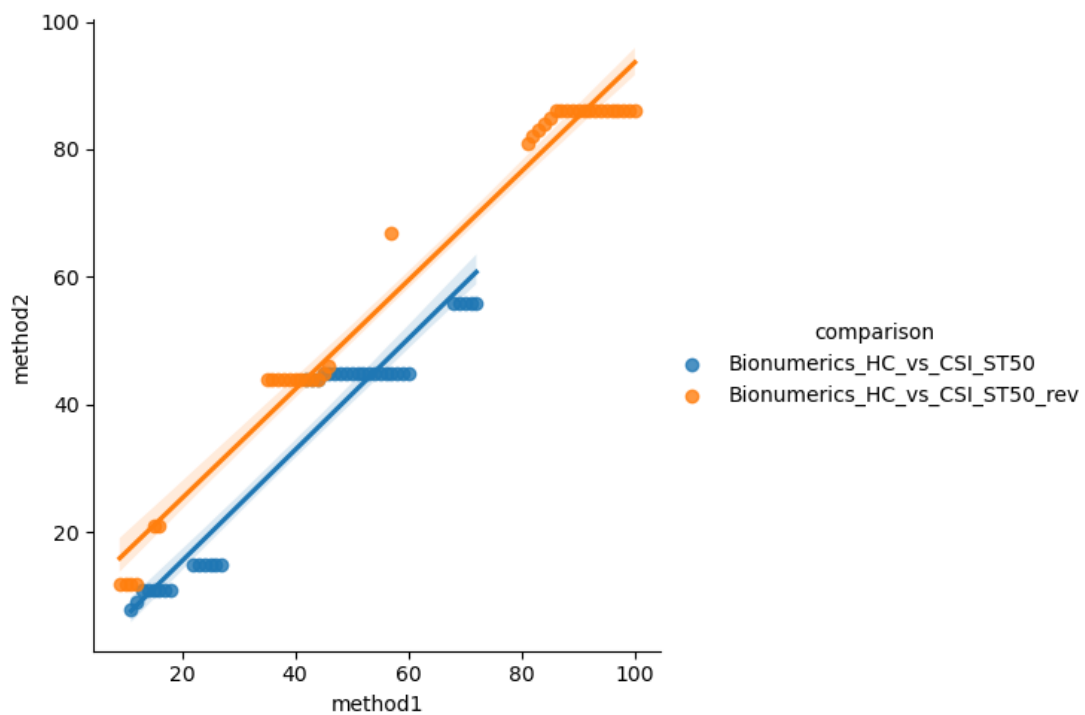


Figure S4.1.7. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST50. A linear tendency line supported by 38 (blue) and 39 (orange) points is presented.

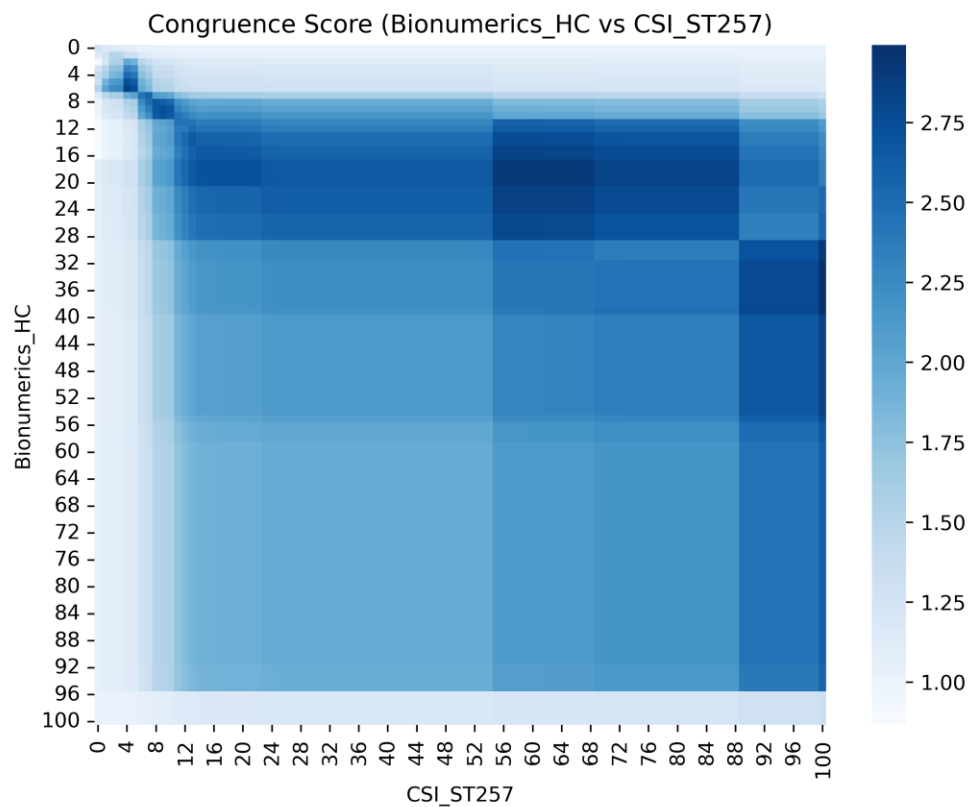


Figure S4.1.8. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

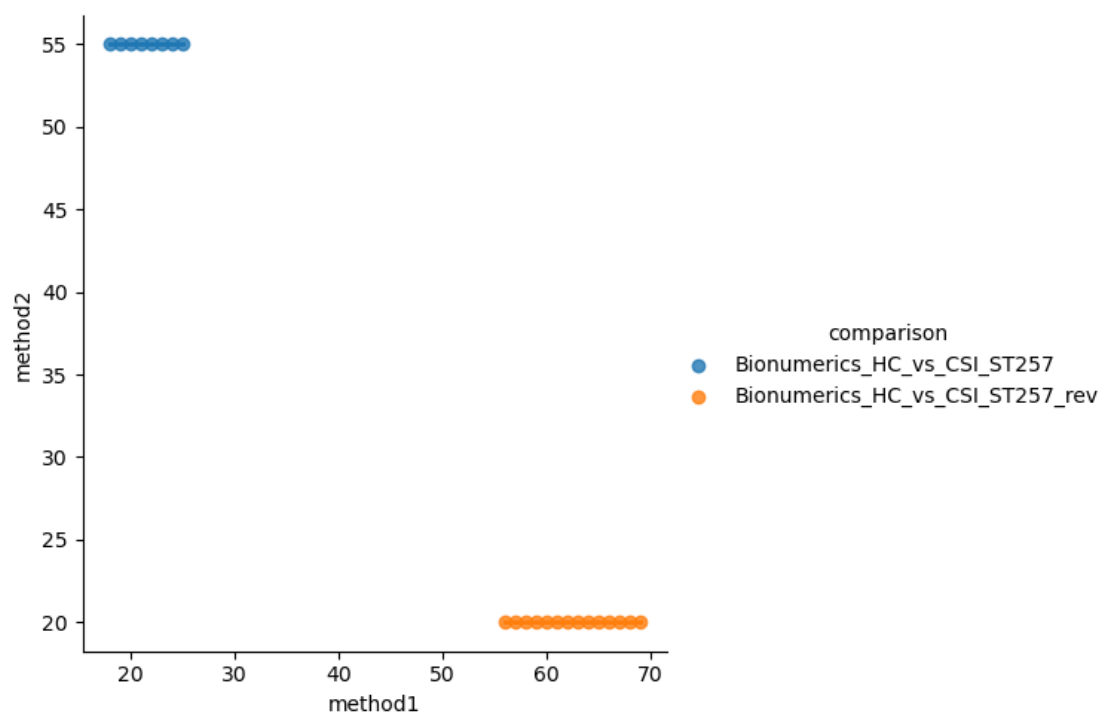


Figure S4.1.9. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST257. No linear tendency was observed. The 8 (blue) and 14 (orange) points are presented.

2. chewieSnake GrapeTree vs. CSI Phylogeny 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.

	chewieSnake GrapeTree	CSI Phylogeny single-linkage
Pipeline version	v3.1.1	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	PubMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

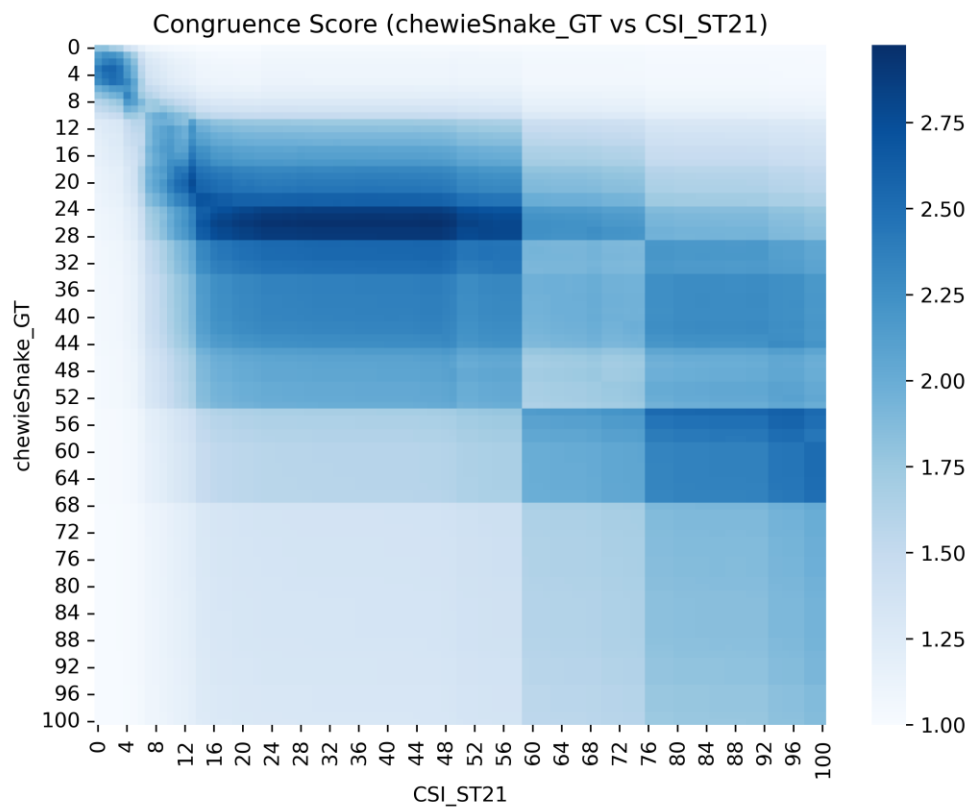


Figure S4.2.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

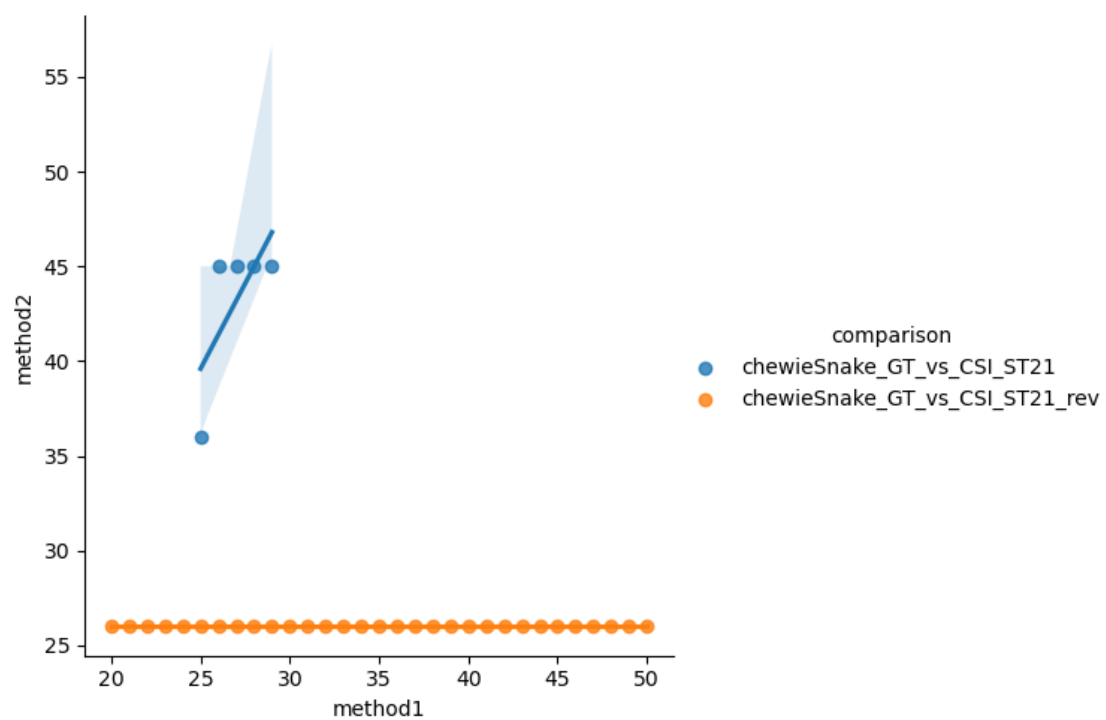


Figure S4.2.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 5 (blue) and 31 (orange) points is presented.

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

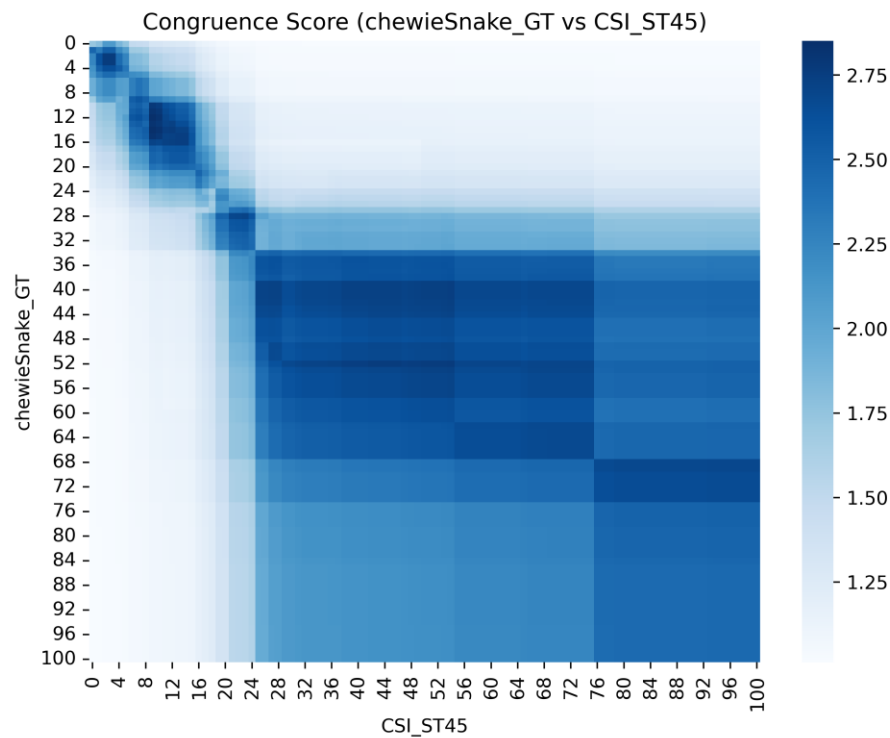


Figure S4.2.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

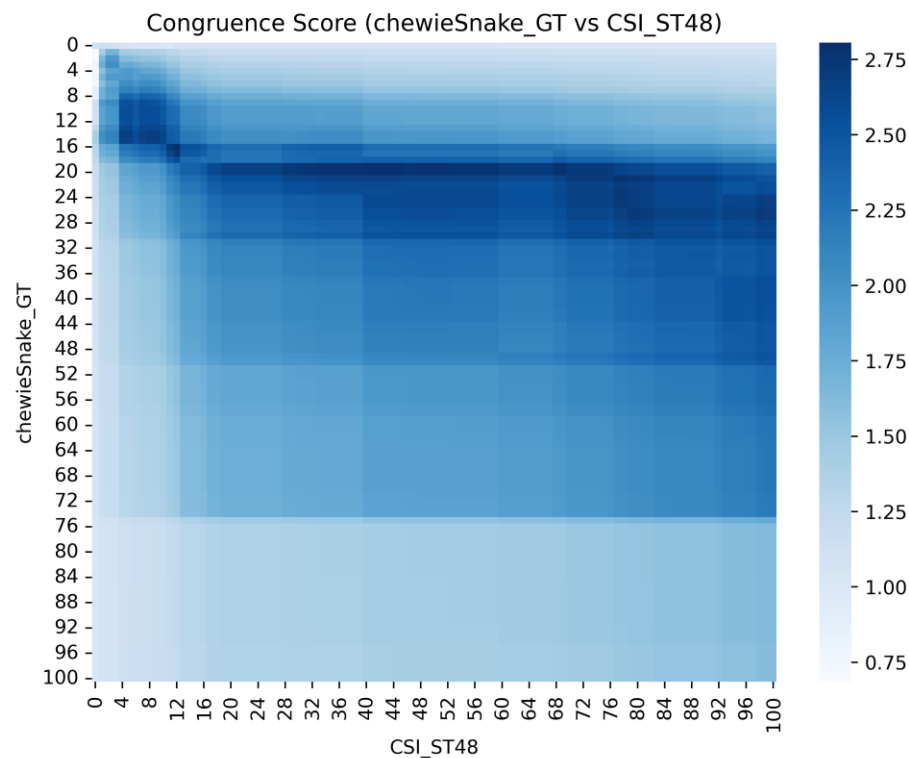


Figure S4.2.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45 and ST48.

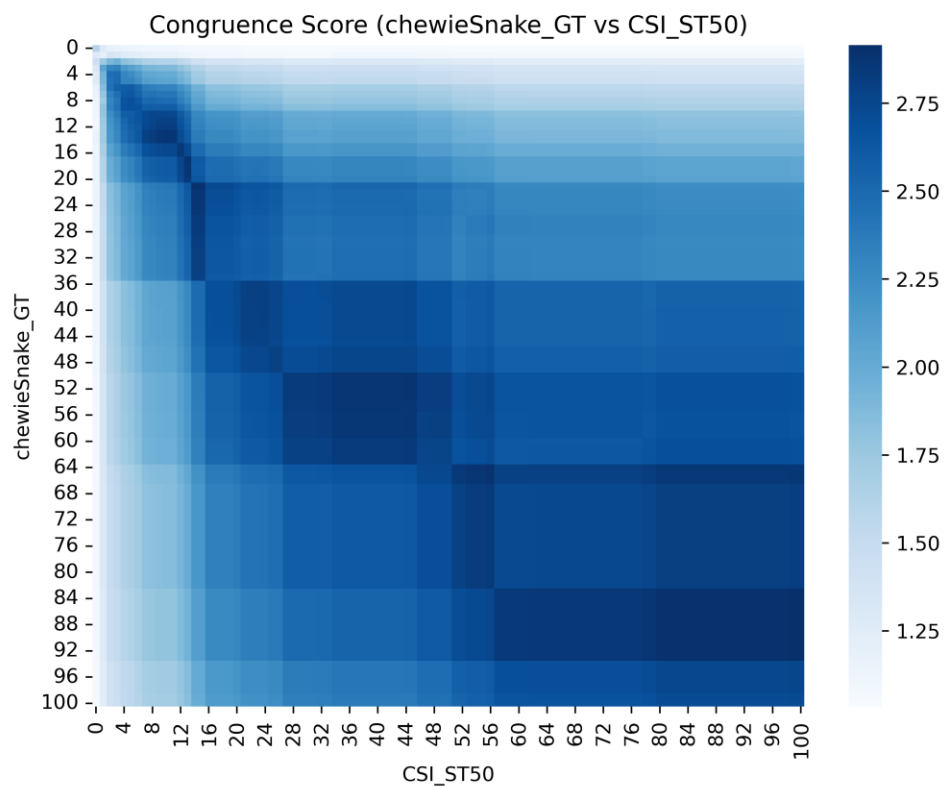


Figure S4.2.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

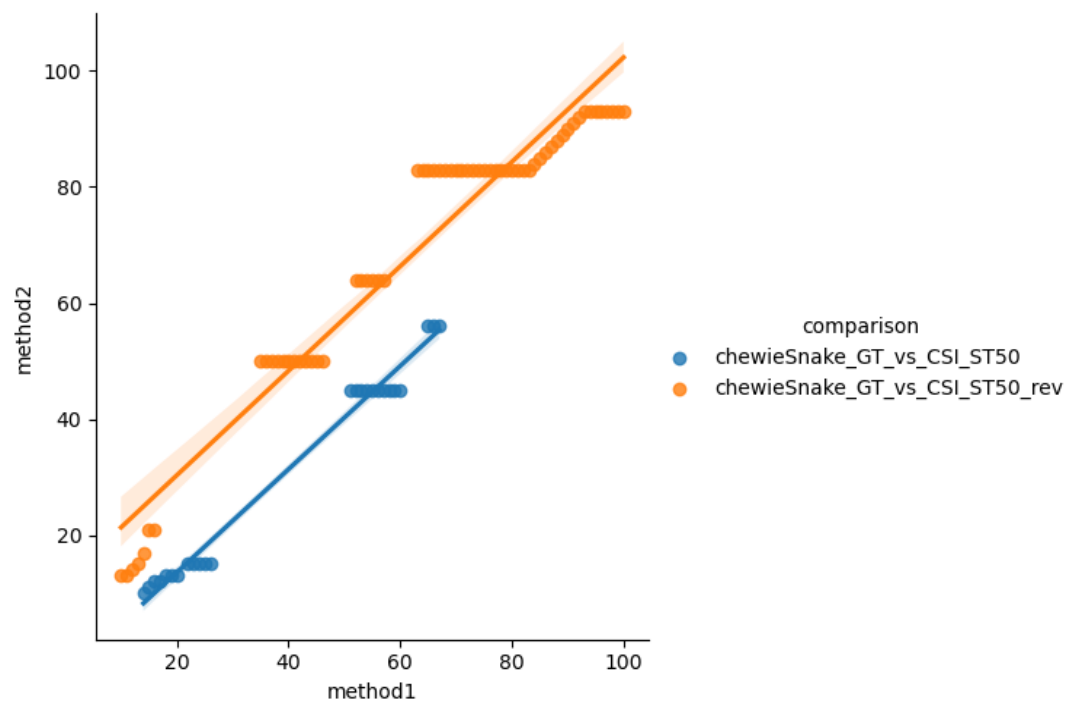


Figure S4.2.6. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST50. A linear tendency line supported by 25 (blue) and 63 (orange) points is presented.

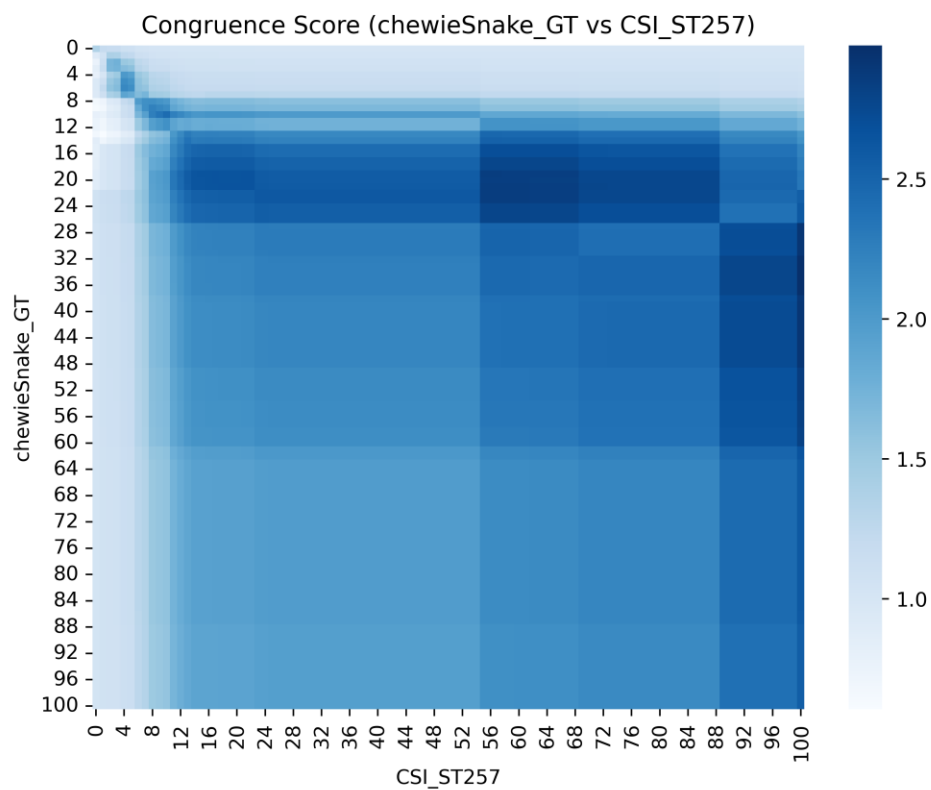


Figure S4.2.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

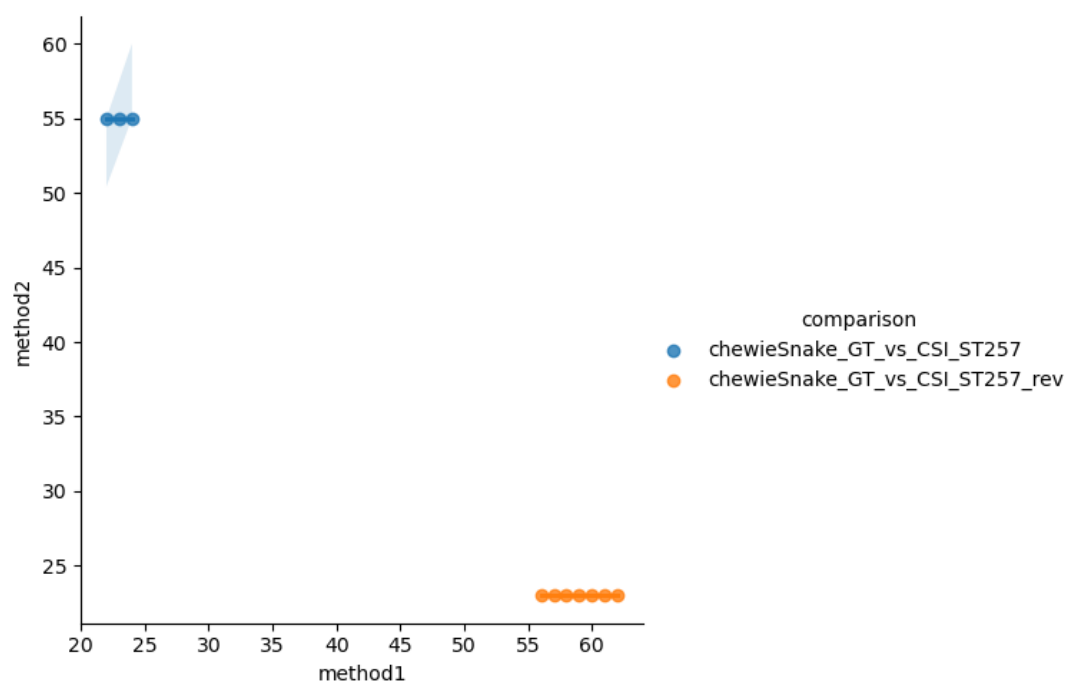


Figure S4.2.8. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST257. No linear tendency was observed. The 3 (blue) and 7 (orange) points are presented.

3. chewieSnake single-linkage vs. CSI Phylogeny 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.

	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	PubMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

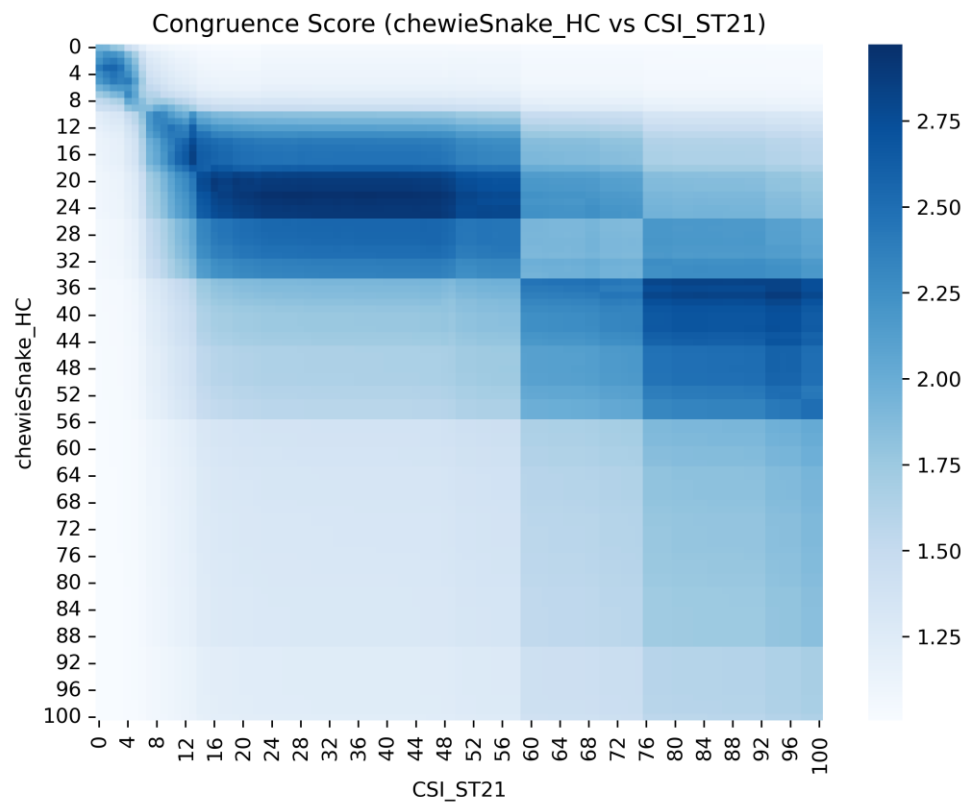


Figure S4.3.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

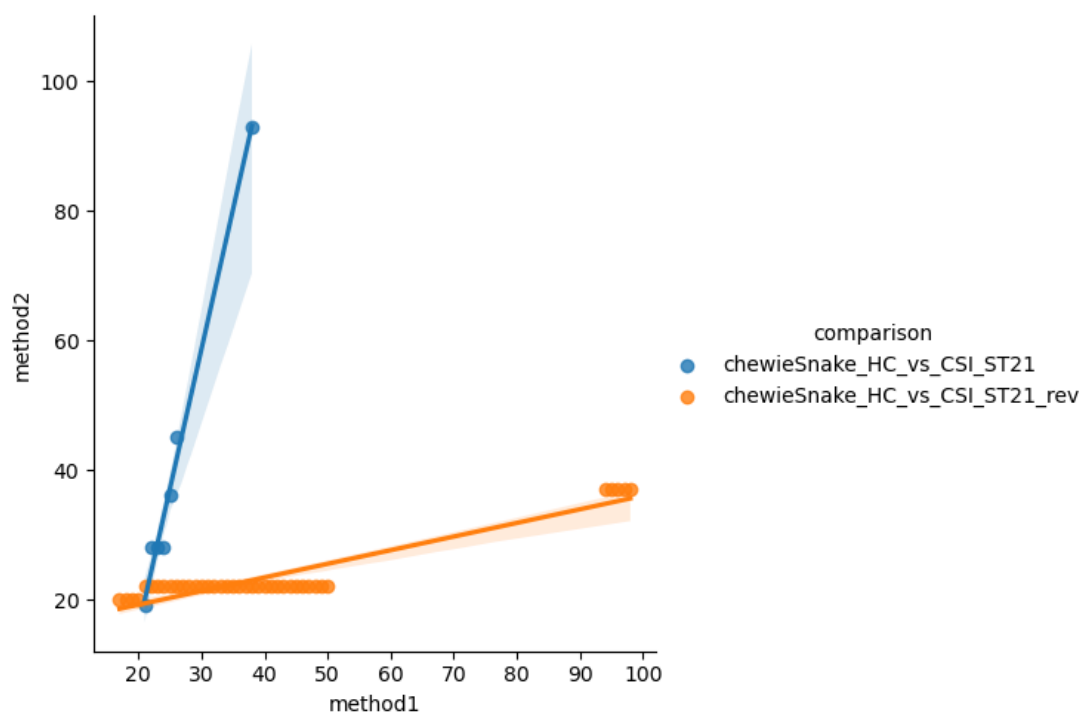


Figure S4.3.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 7 (blue) and 39 (orange) points is presented.

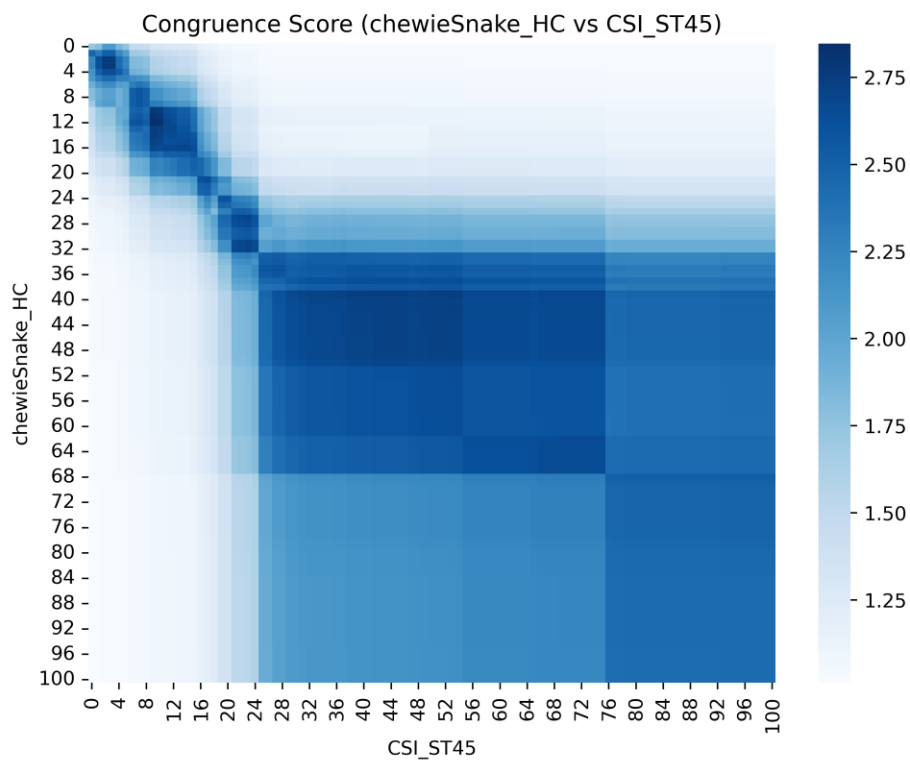


Figure S4.3.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

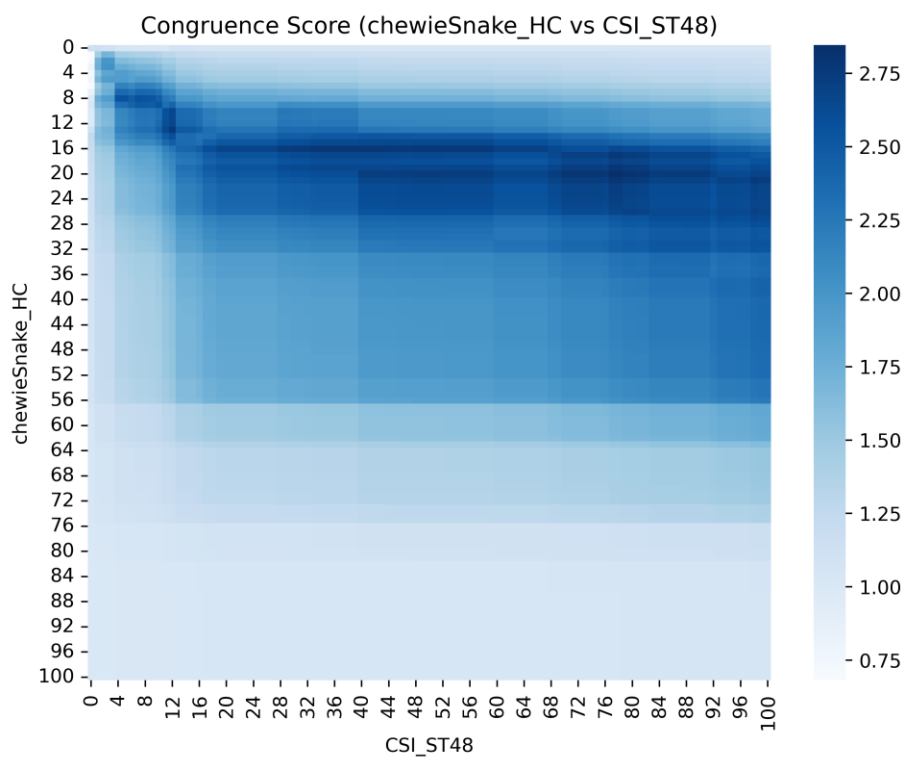


Figure S4.3.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45 and ST48.

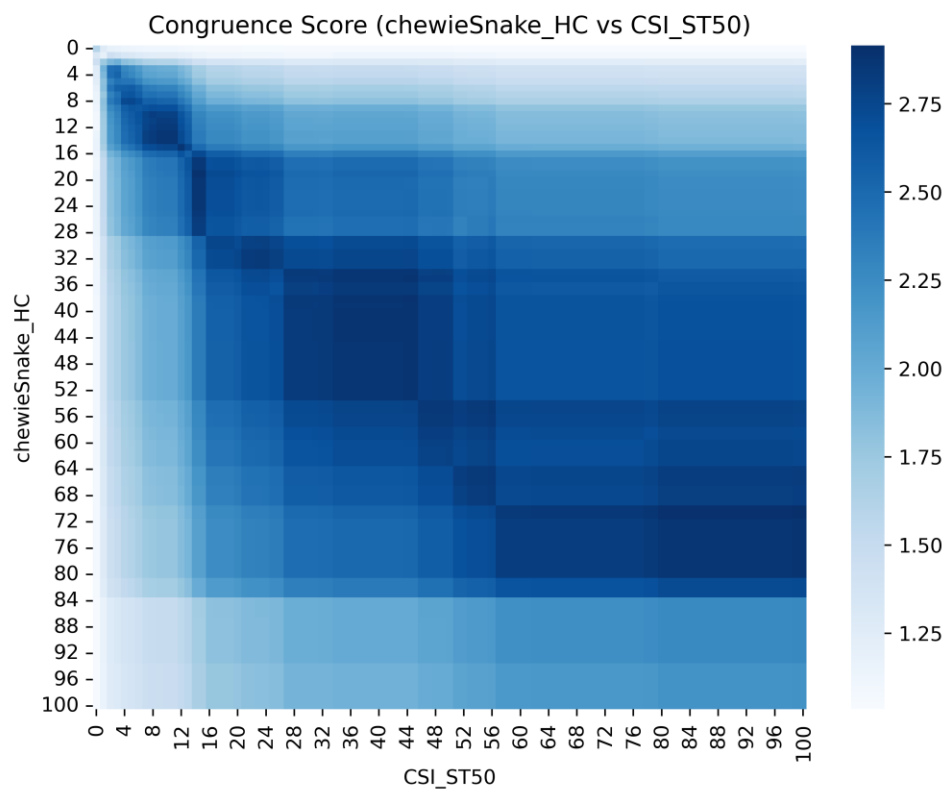


Figure S4.3.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

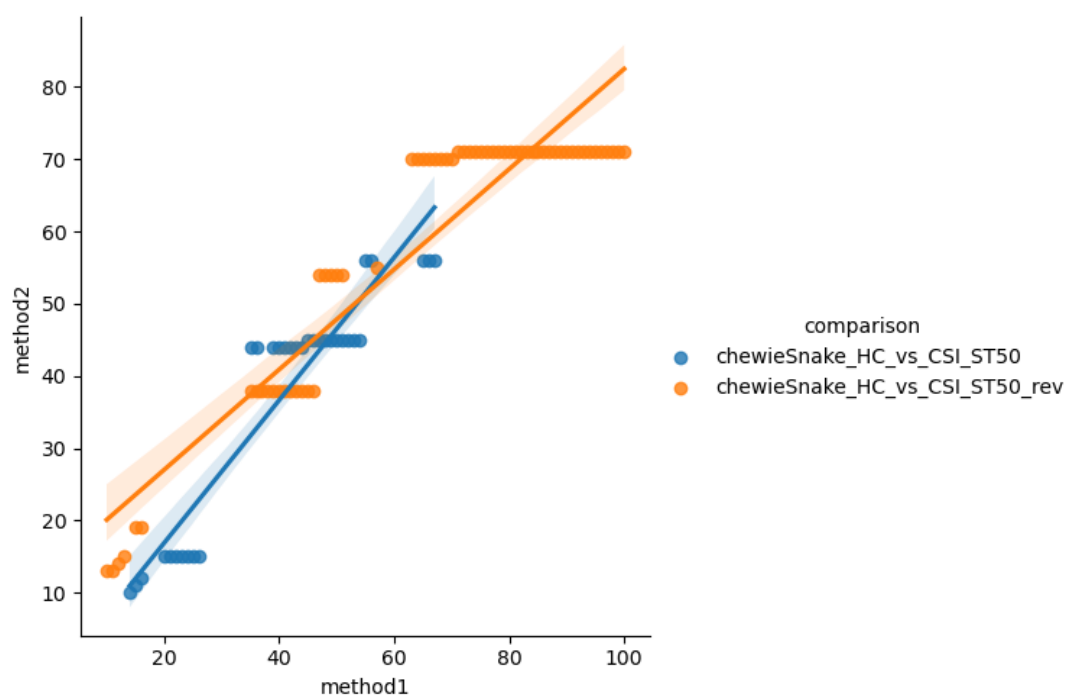


Figure S4.3.6. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST50. A linear tendency line supported by 33 (blue) and 62 (orange) points is presented.

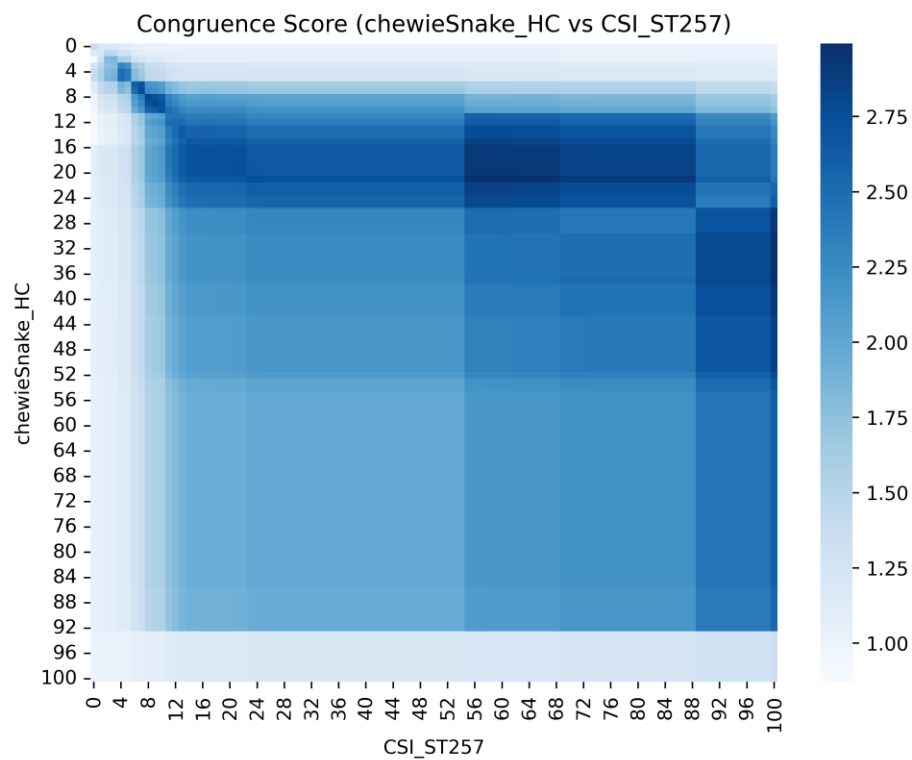


Figure S4.3.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

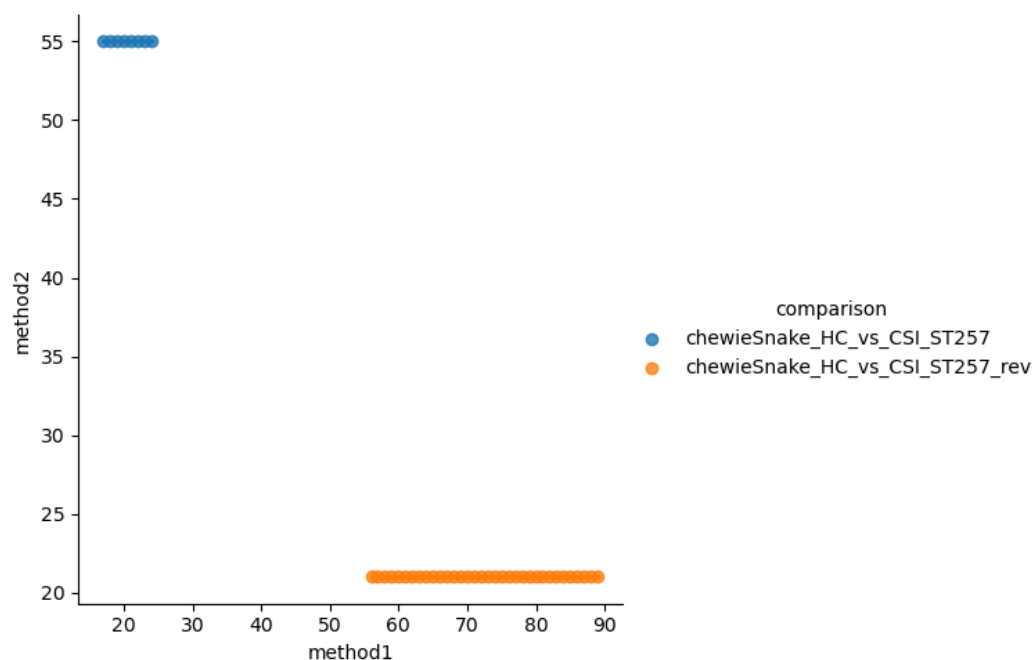


Figure S4.3.8. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST257. No linear tendency was observed. The 8 (blue) and 34 (orange) points are presented.

4. INNUENDO-like-INNUENDO99 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.

	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)	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

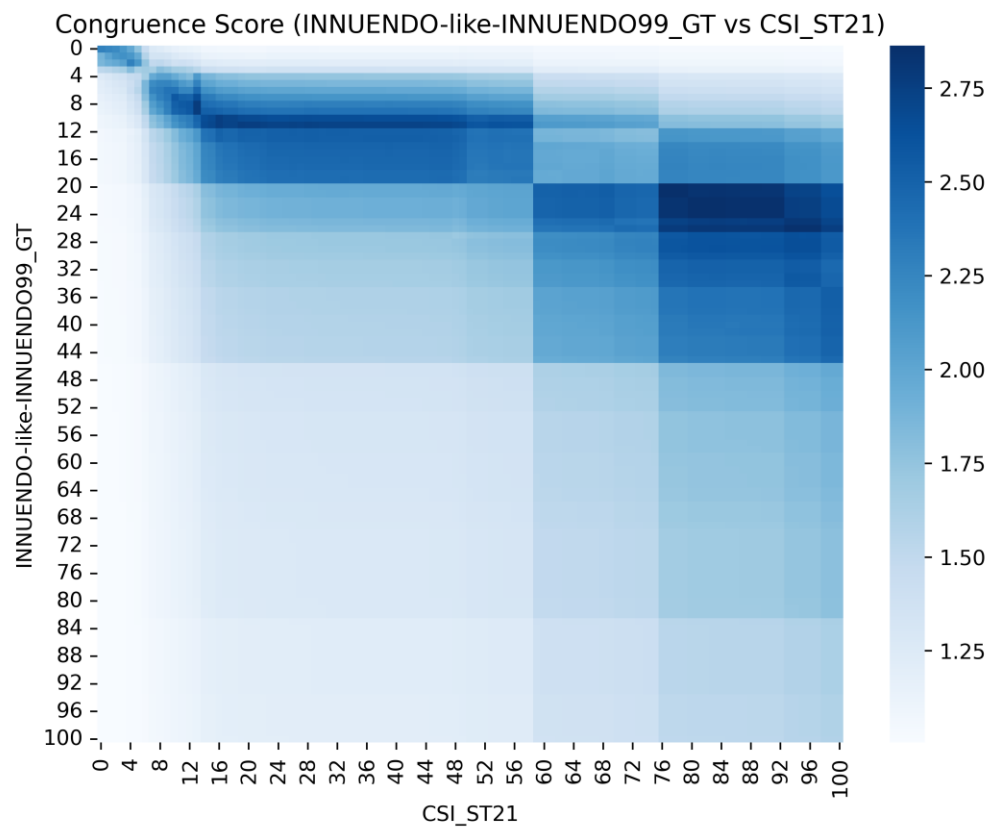


Figure S4.4.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

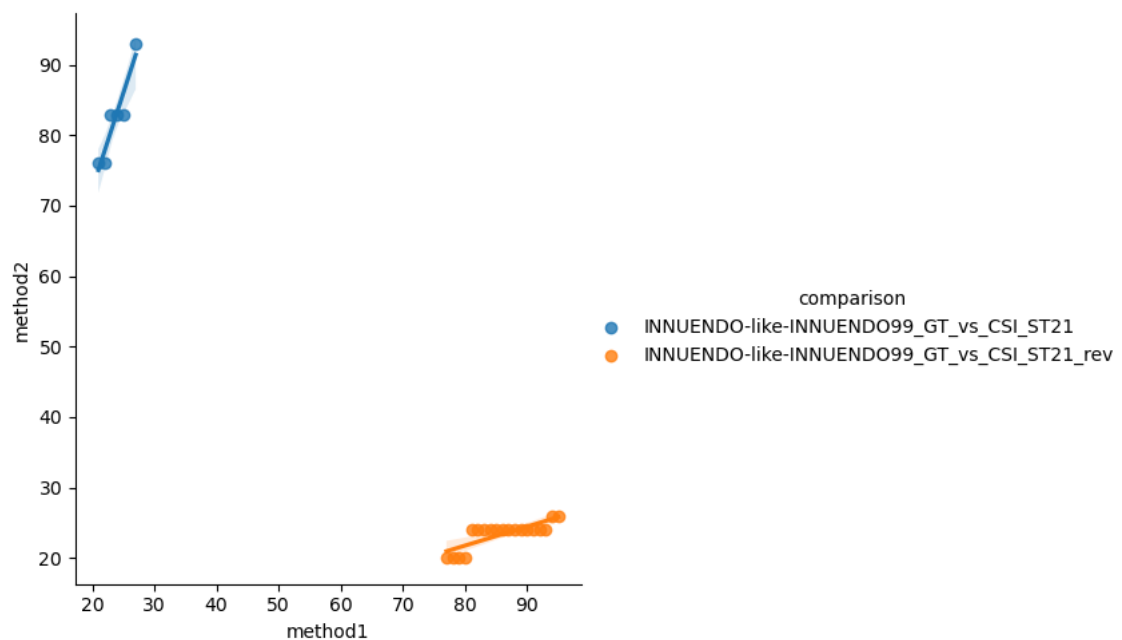


Figure S4.4.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST21. A linear tendency line supported by 6 (blue) and 19 (orange) points is presented.

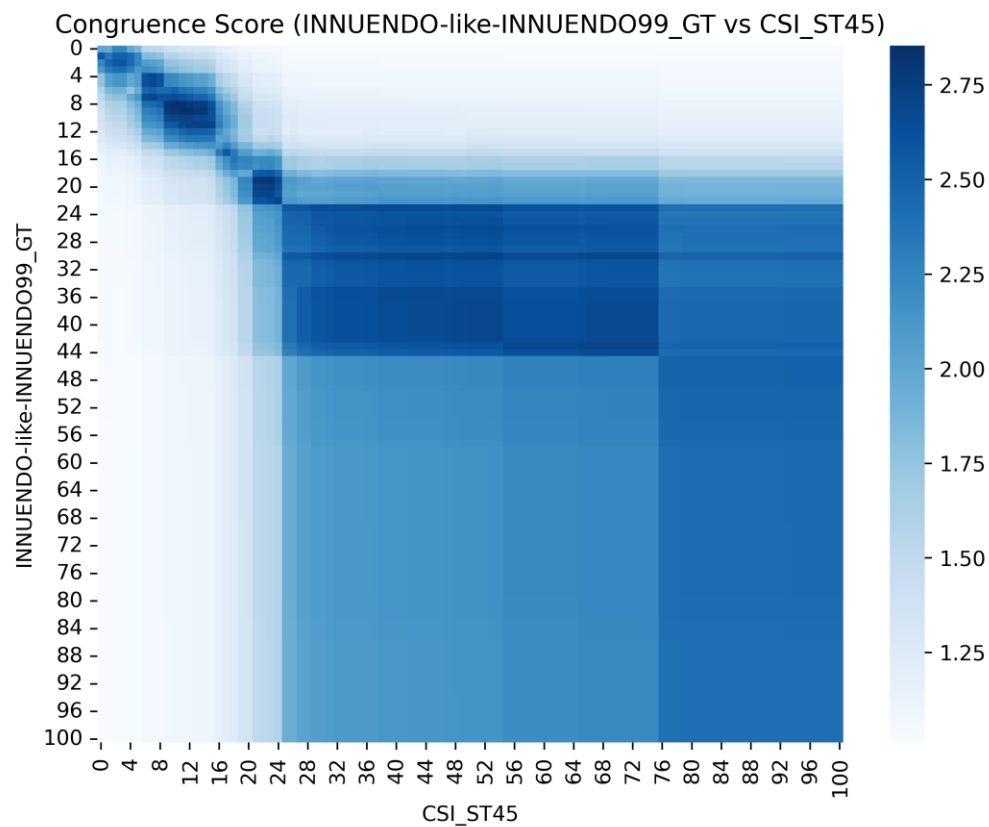


Figure S4.4.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45.

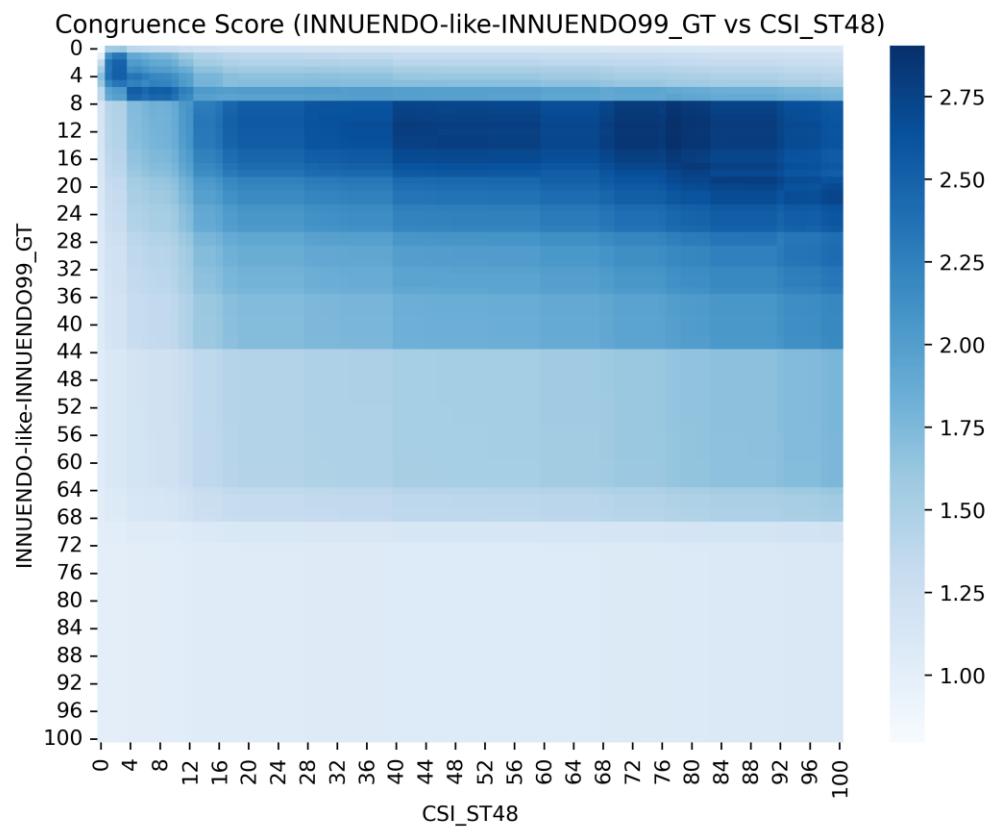


Figure S4.4.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

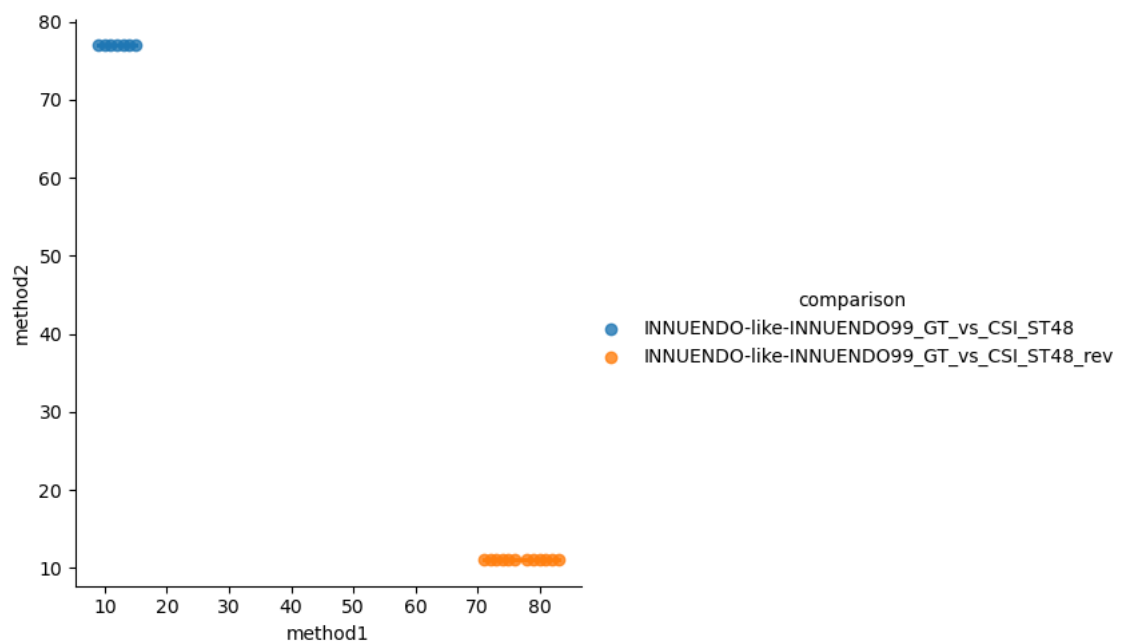


Figure S4.4.5. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST48. No linear tendency was observed. The 7 (blue) and 12 (orange) points are presented.

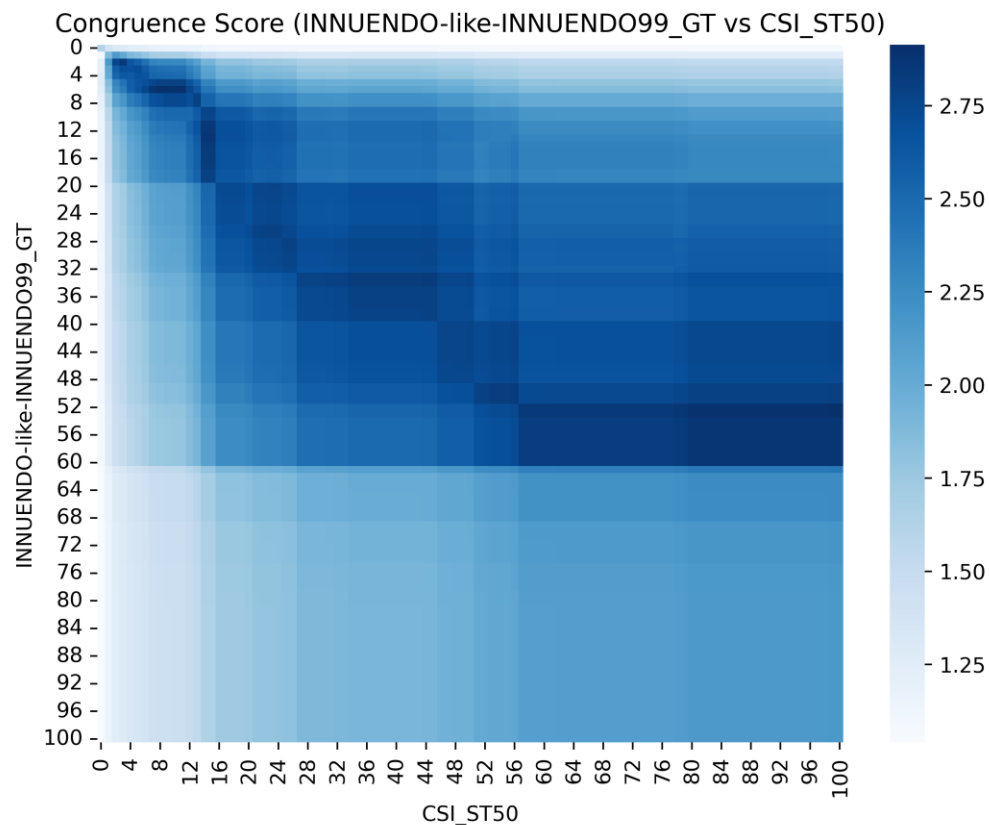


Figure S4.4.6. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

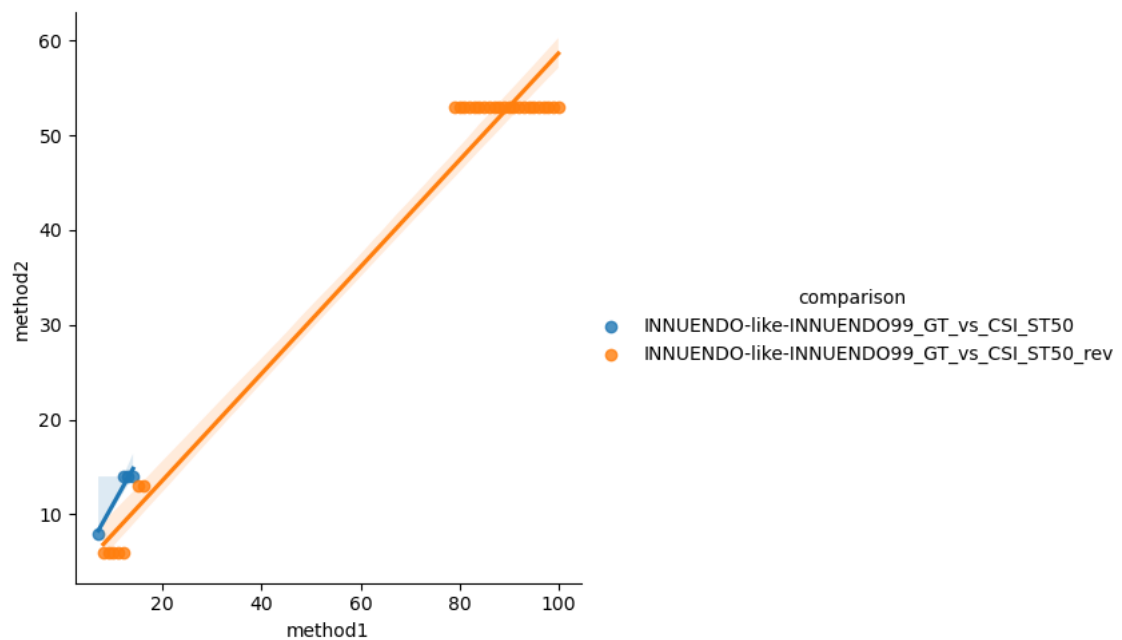


Figure S4.4.7. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST50. A linear tendency line supported by 4 (blue) and 29 (orange) points is presented.

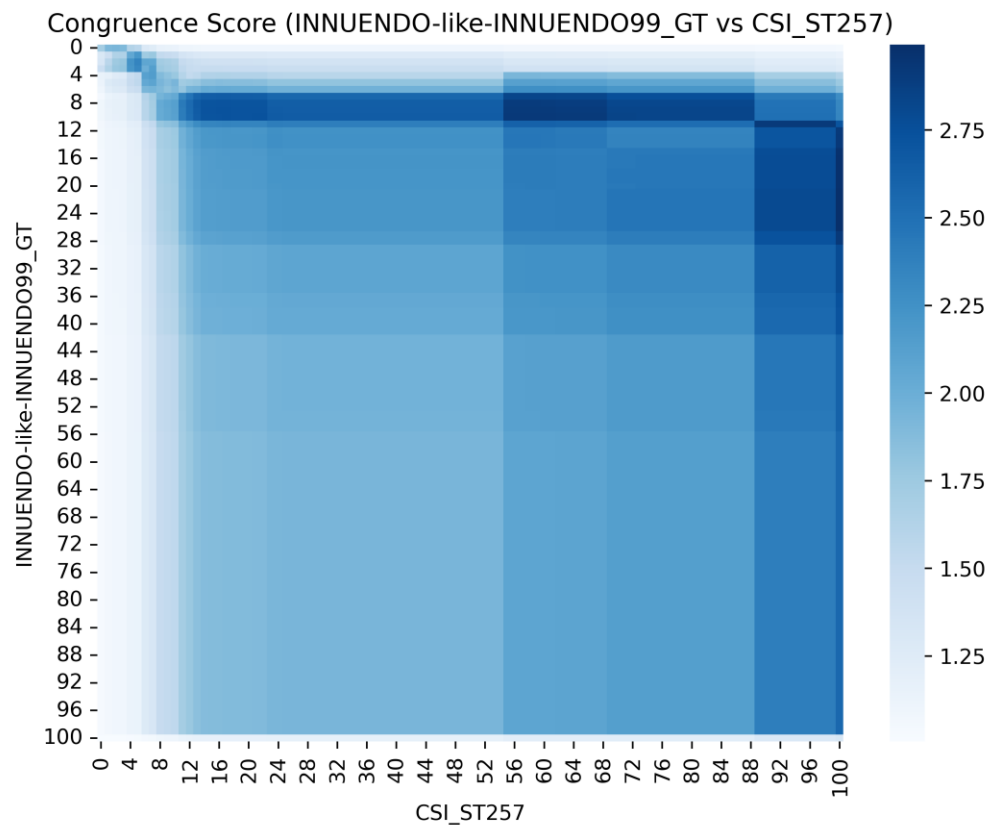


Figure S4.4.8. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

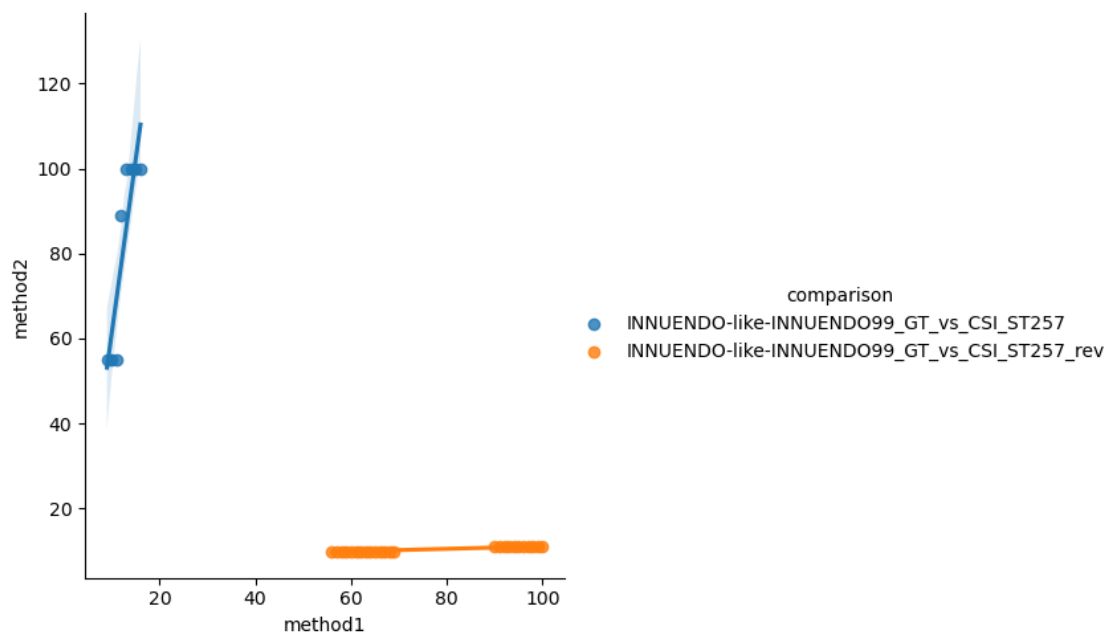


Figure S4.4.9. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST257. A linear tendency line supported by 8 (blue) and 25 (orange) points is presented.

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

	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)	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

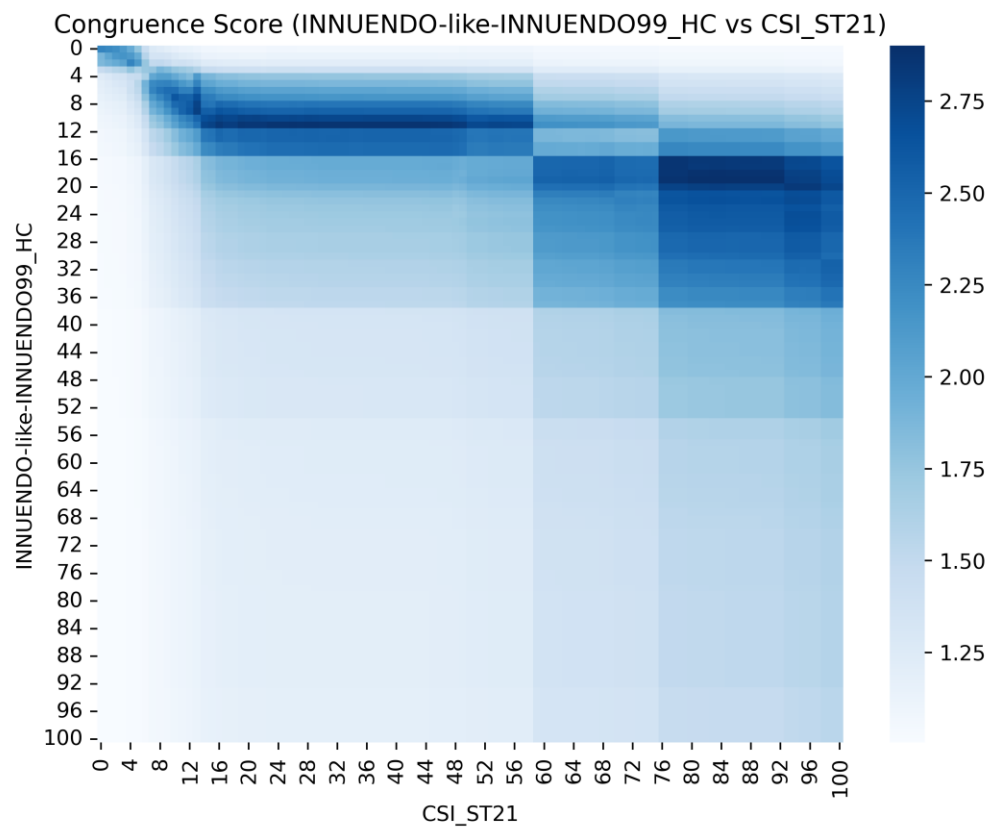


Figure S4.5.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

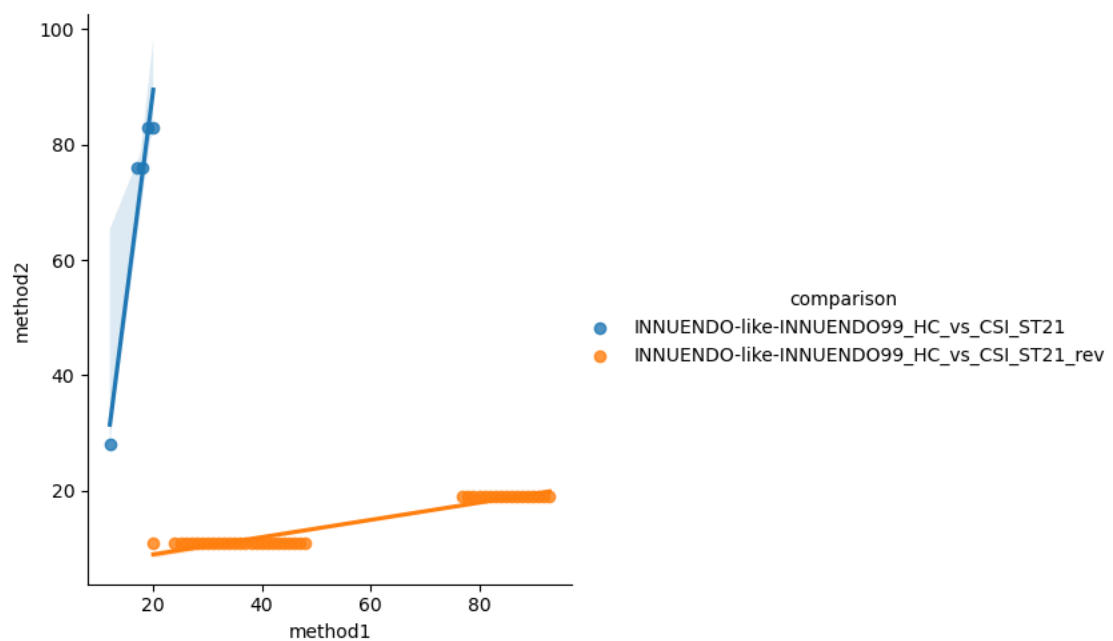


Figure S4.5.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST21. A linear tendency line supported by 5 (blue) and 43 (orange) points is presented.

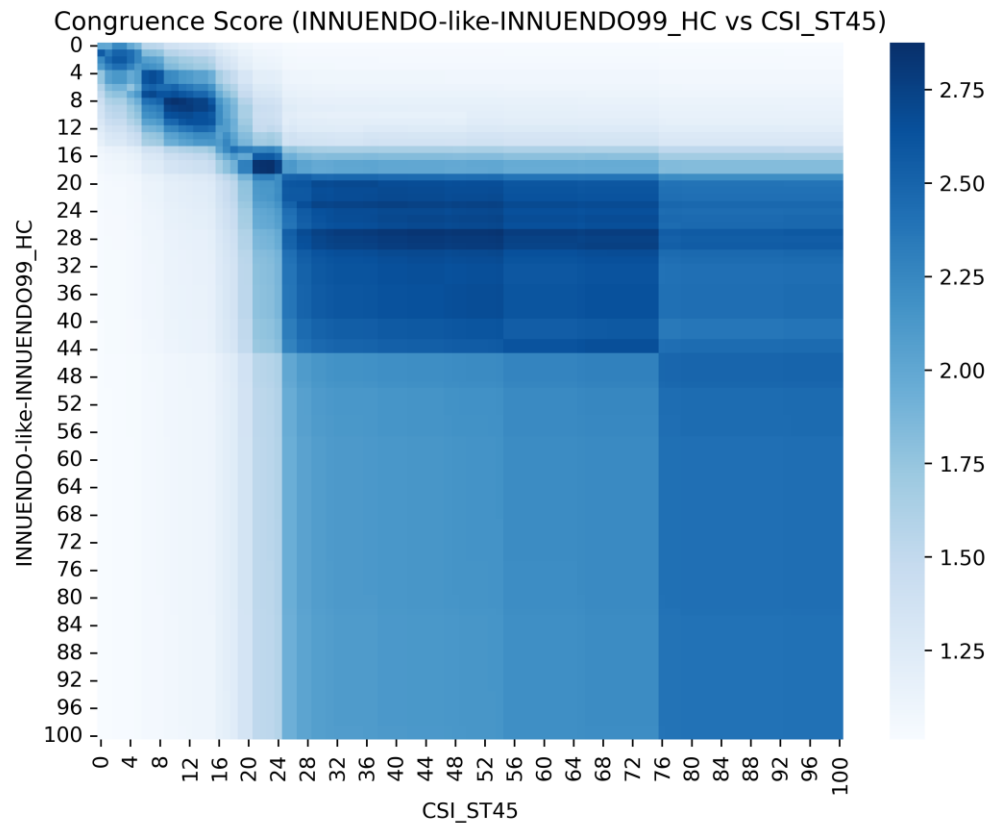


Figure S4.5.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

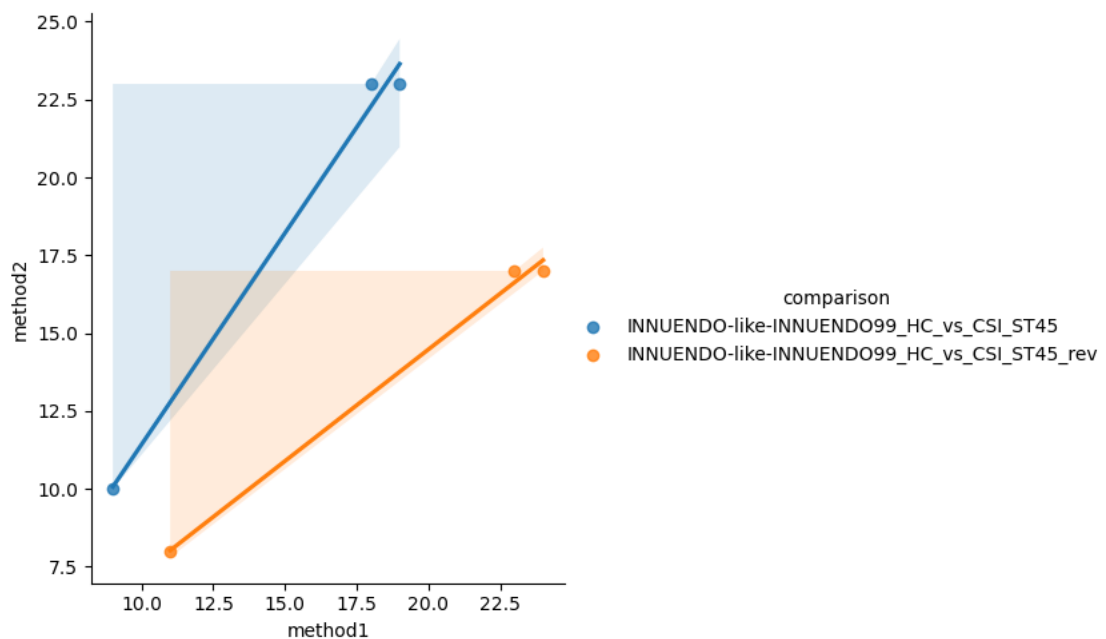


Figure S4.5.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST45. A linear tendency line supported by 3 (blue) and 3 (orange) points is presented.

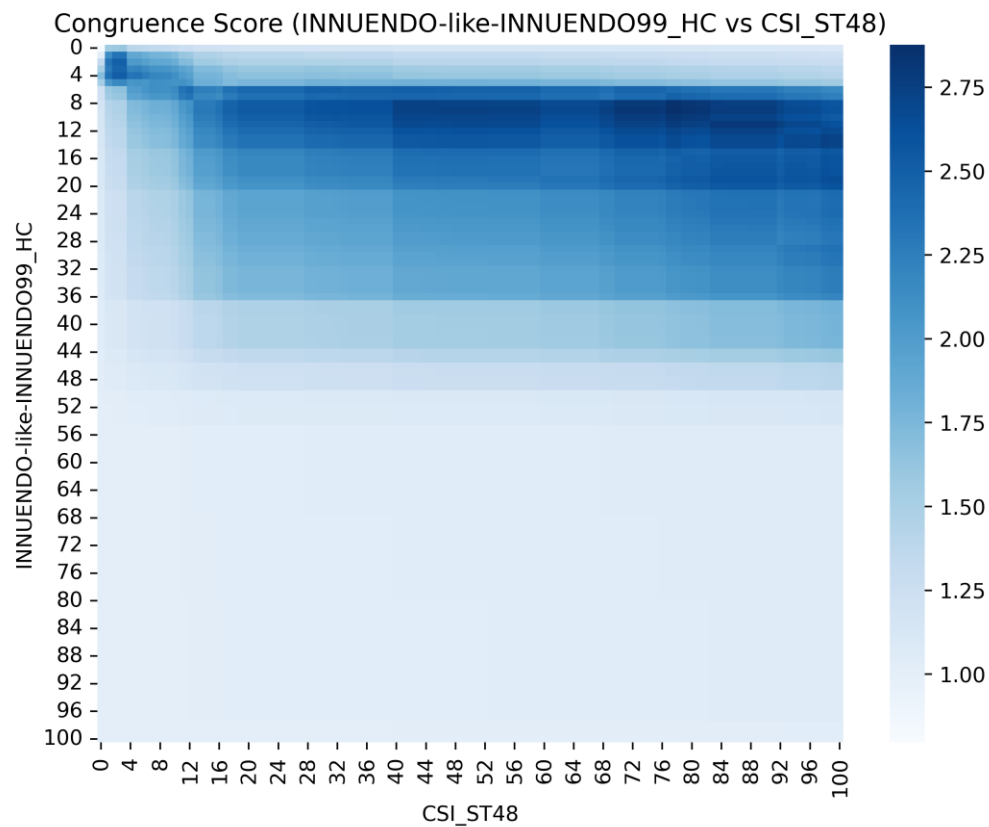
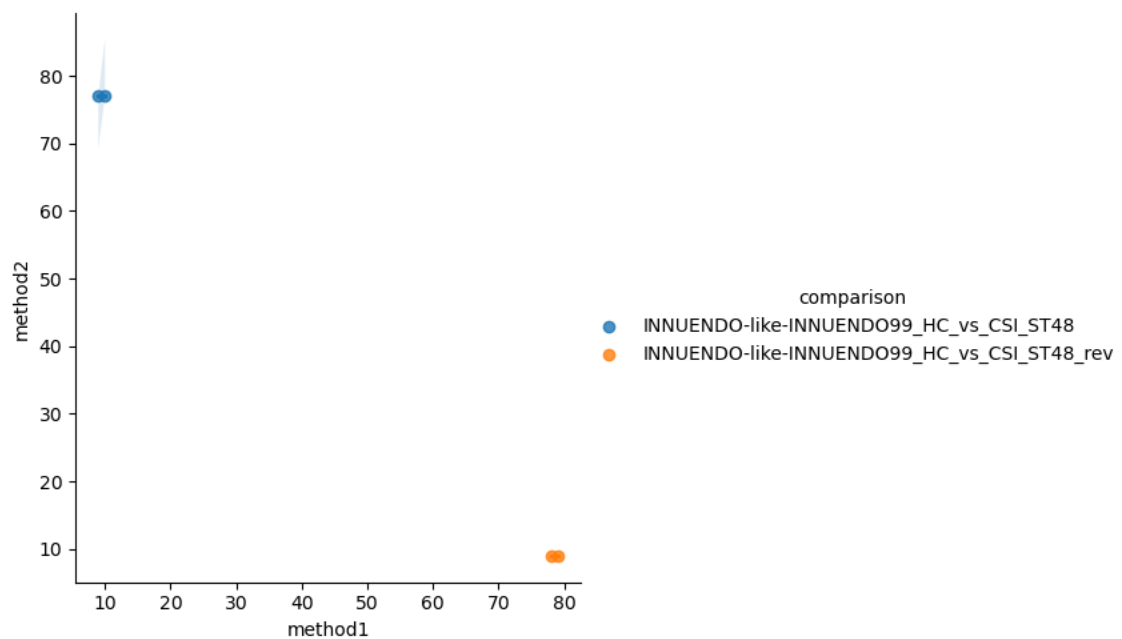


Figure S4.5.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.



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Figure S4.5.6. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST48. No linear tendency was observed. The 2 (blue) and 2 (orange) points are presented

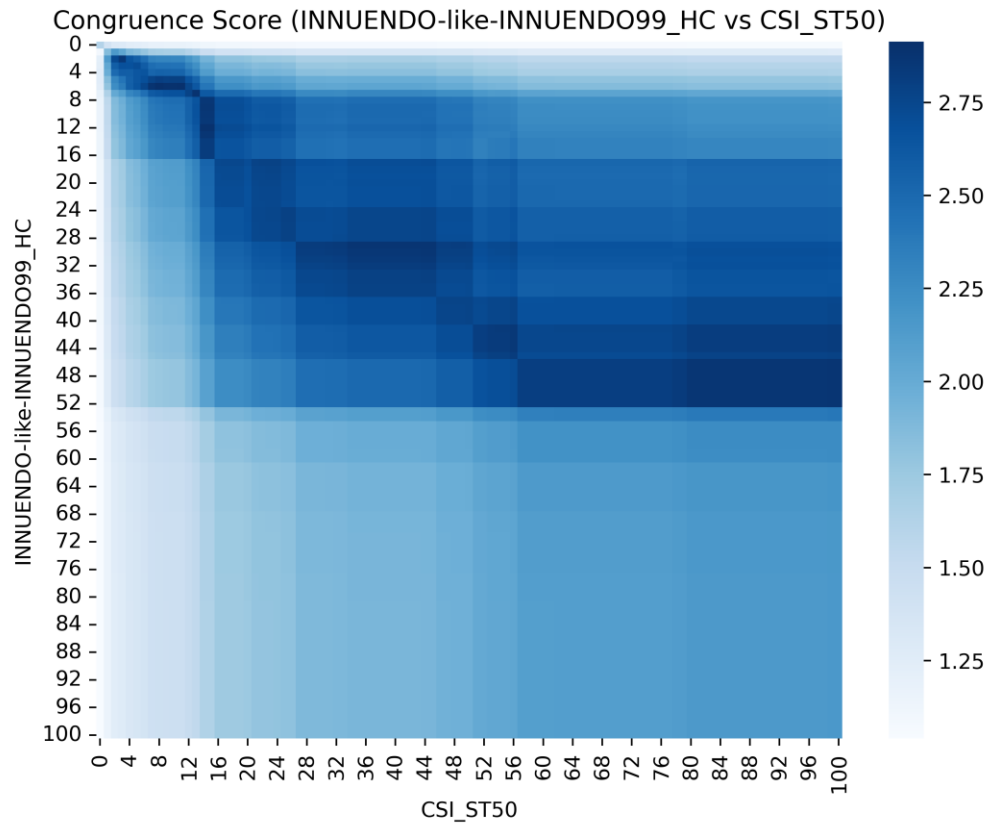


Figure S4.5.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

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

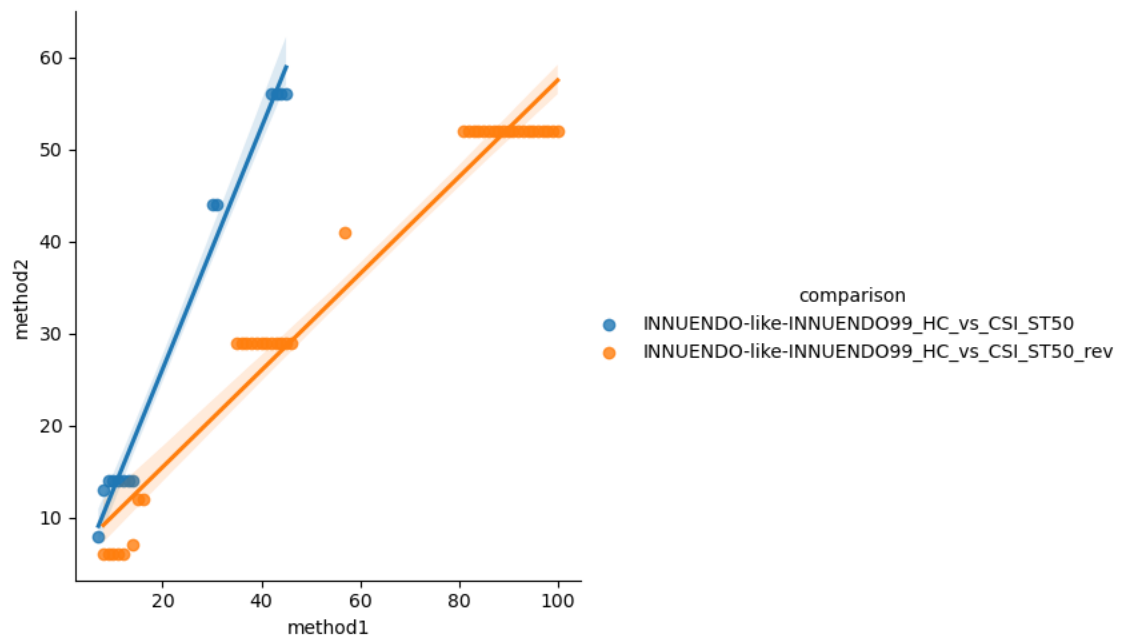


Figure S4.5.8. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST50. A linear tendency line supported by 14 (blue) and 41 (orange) points is presented.

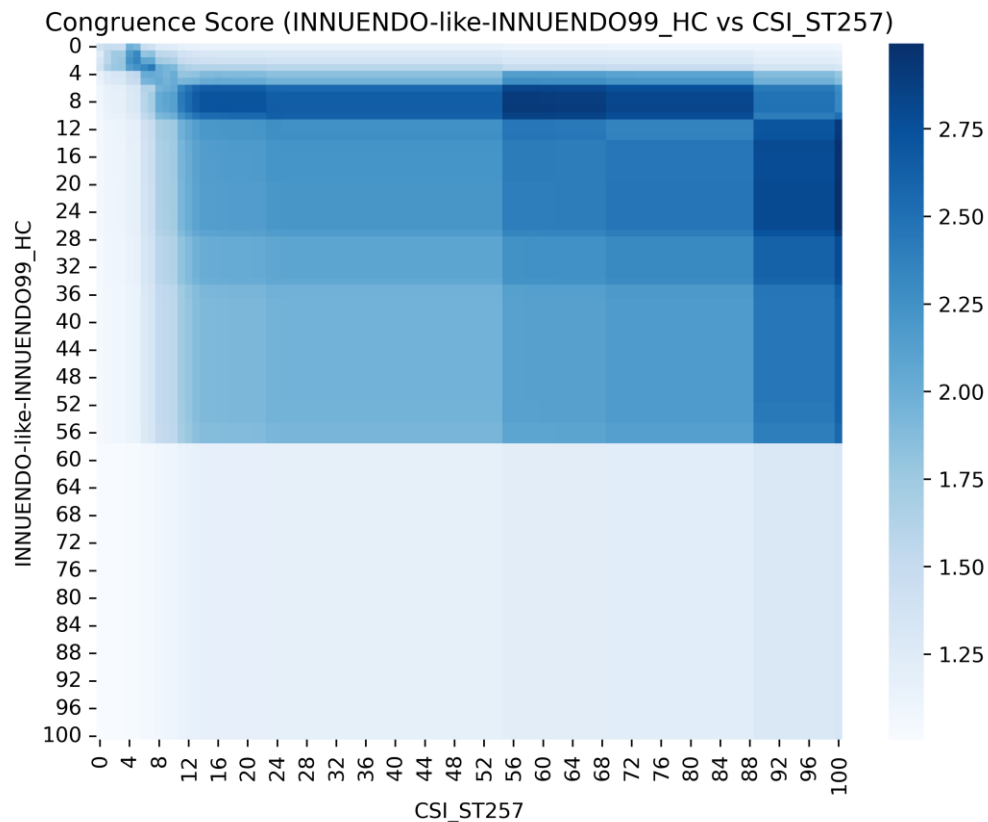


Figure S4.5.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

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

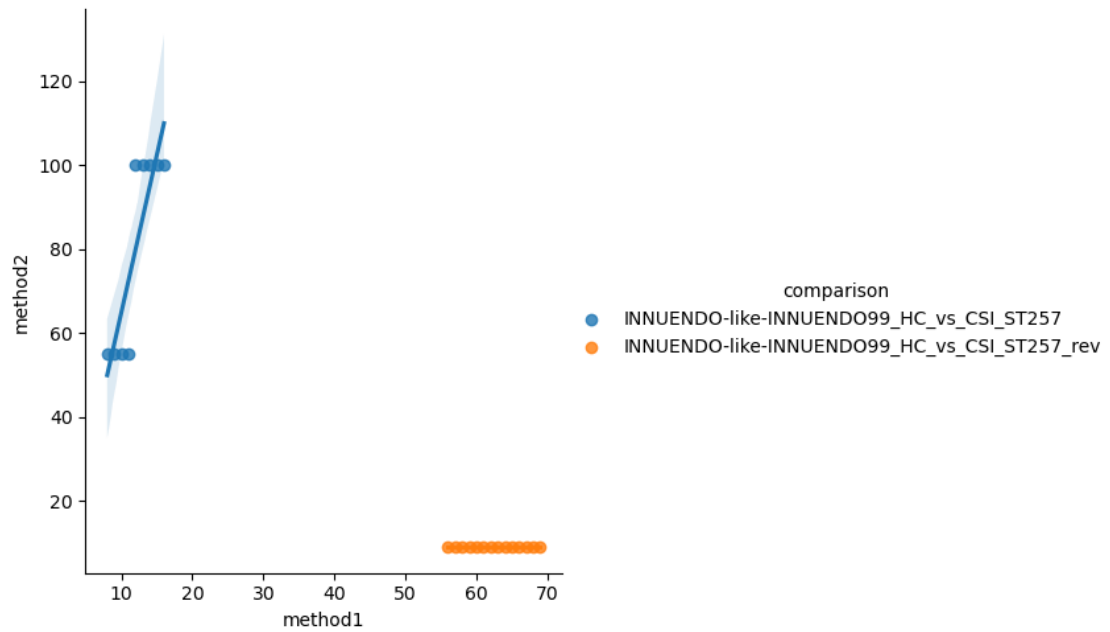


Figure S4.5.10. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST257. A linear tendency line supported by 9 (blue) and 14 (orange) points is presented.

6. INNUENDO-like-INNUENDOCgMLST GrapeTree vs. CSI Phylogeny 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.

	INNUENDO-like-INNUENDOCgMLST GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO cgMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

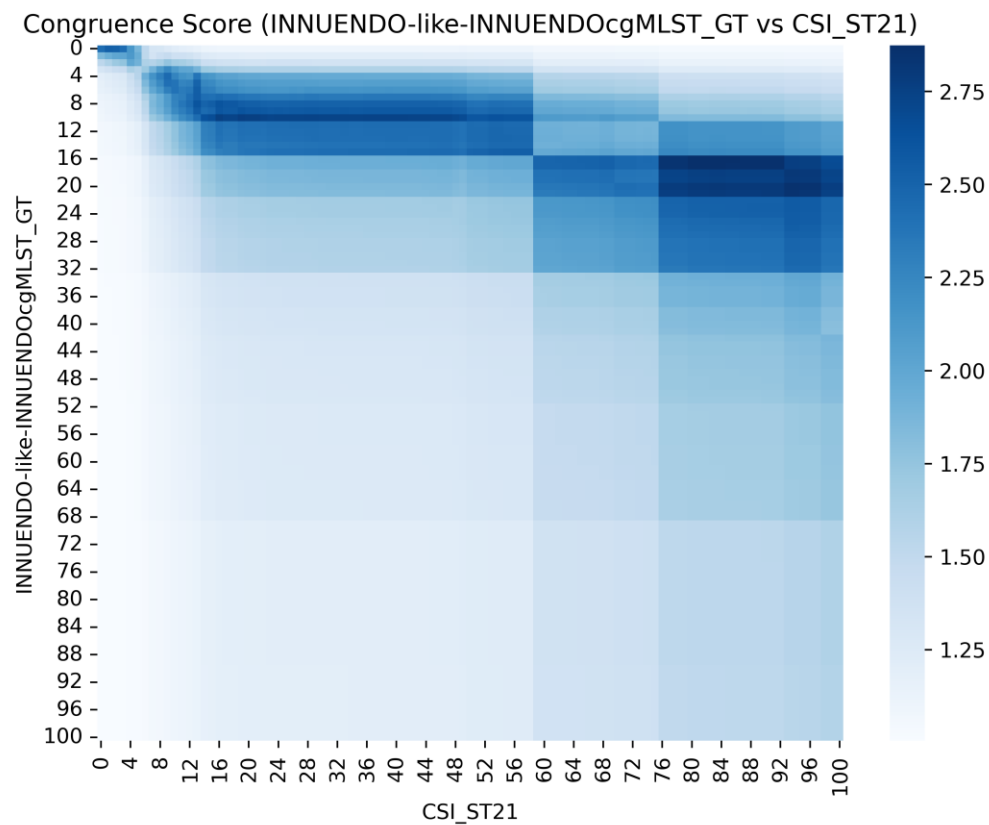


Figure S4.6.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

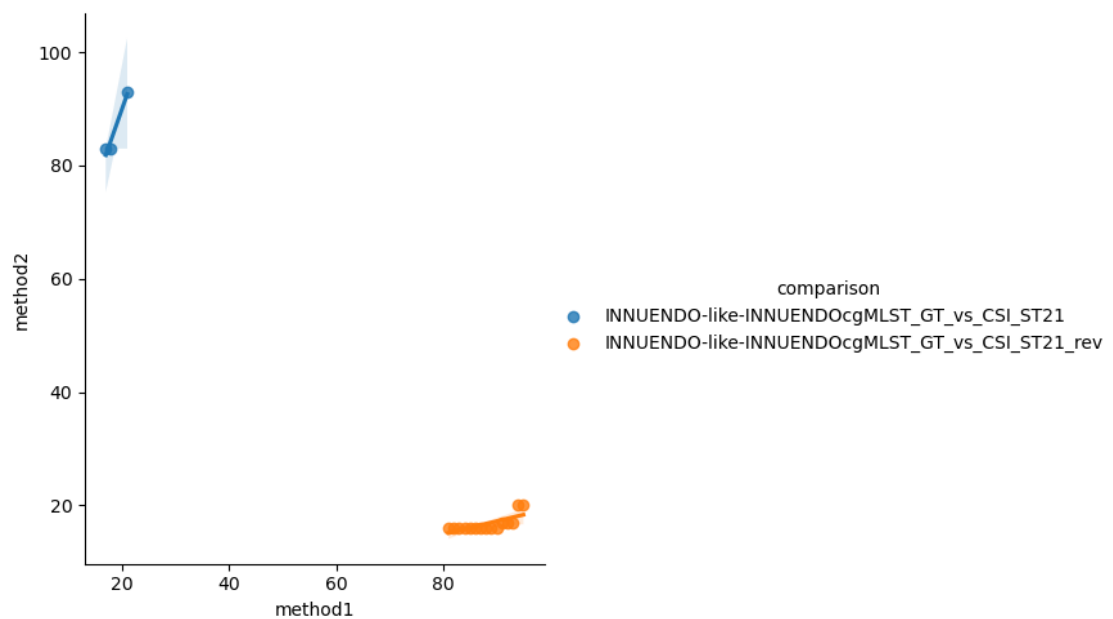


Figure S4.6.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 3 (blue) and 15 (orange) points is presented.

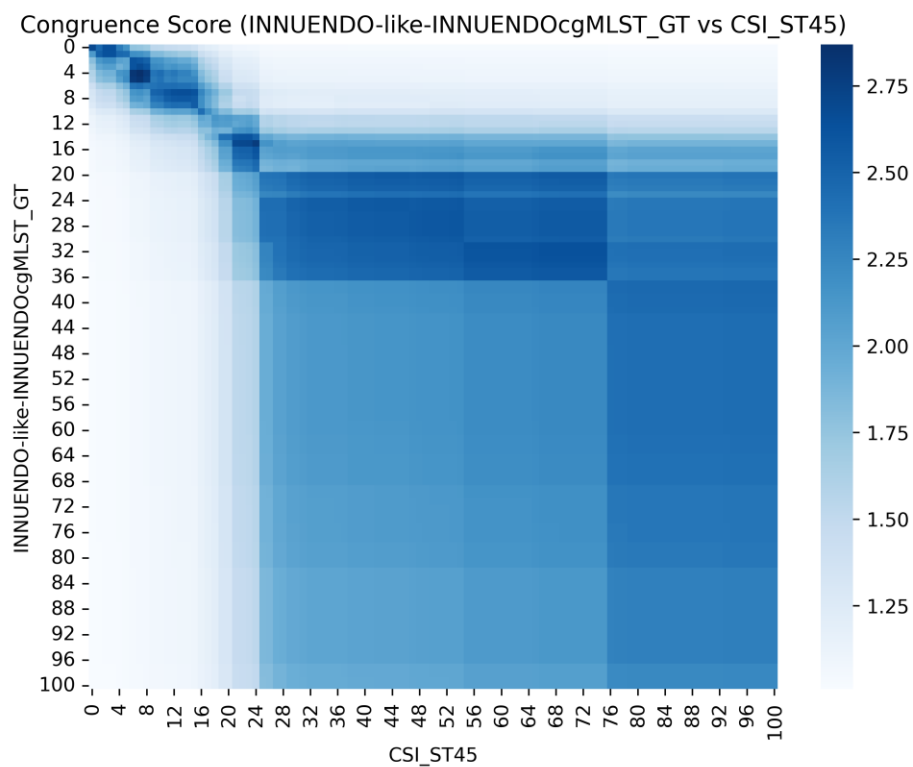


Figure S4.6.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

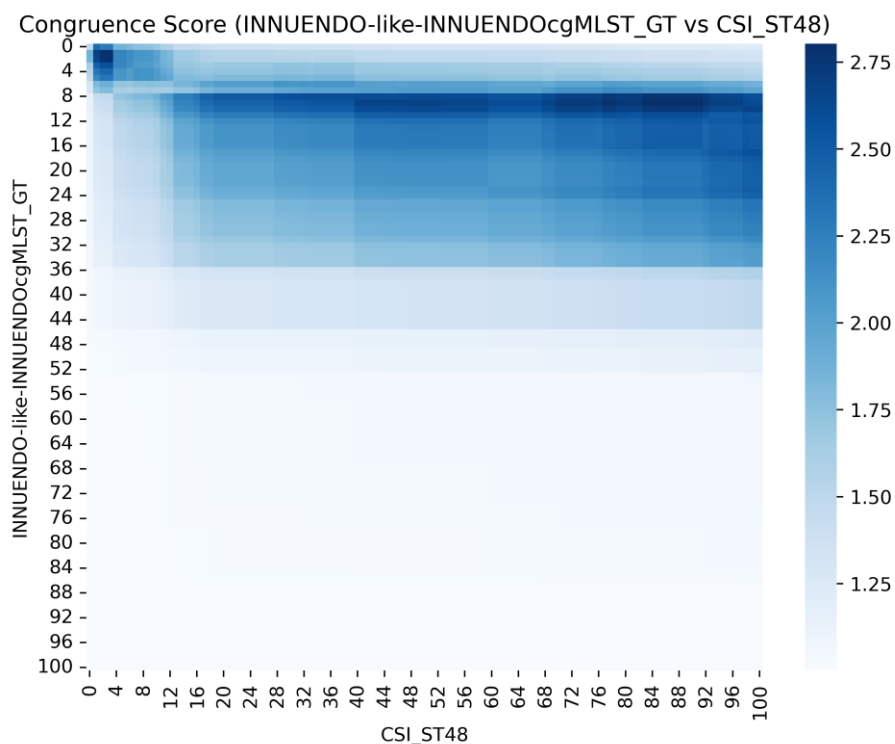


Figure S4.6.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45, ST48 and ST50.

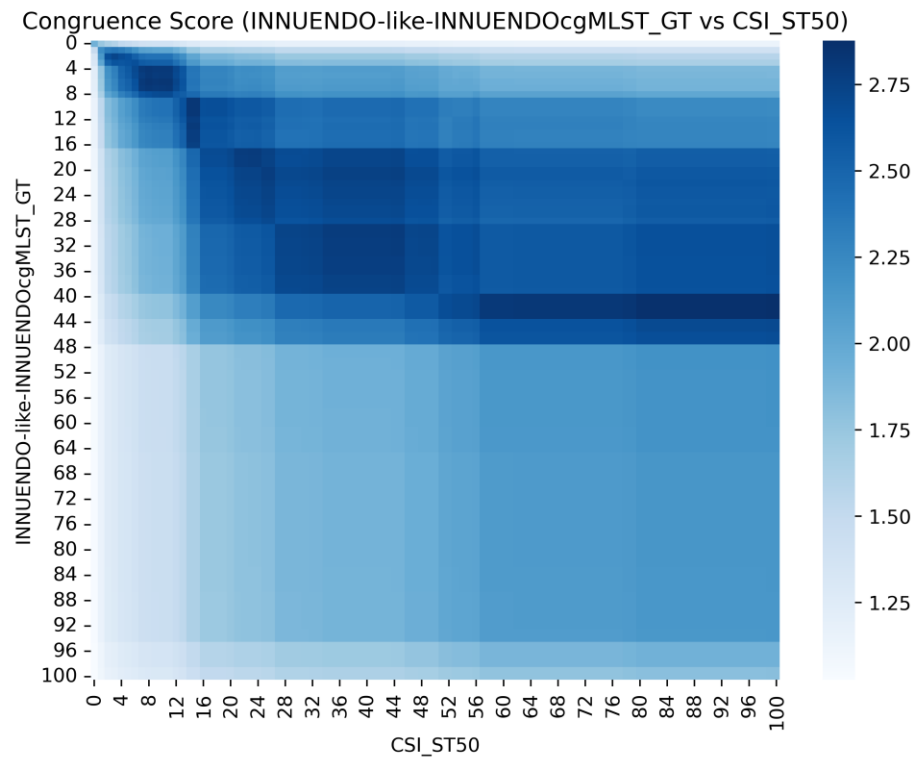


Figure S4.6.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45, ST48 and ST50.

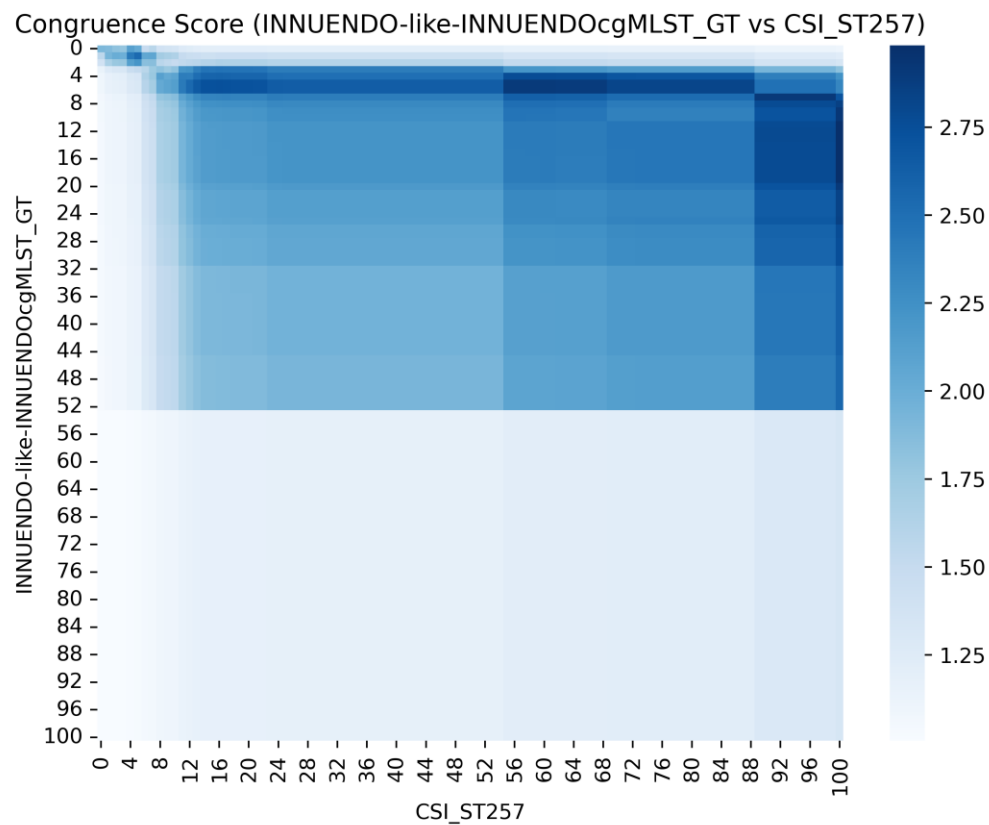


Figure S4.6.6. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

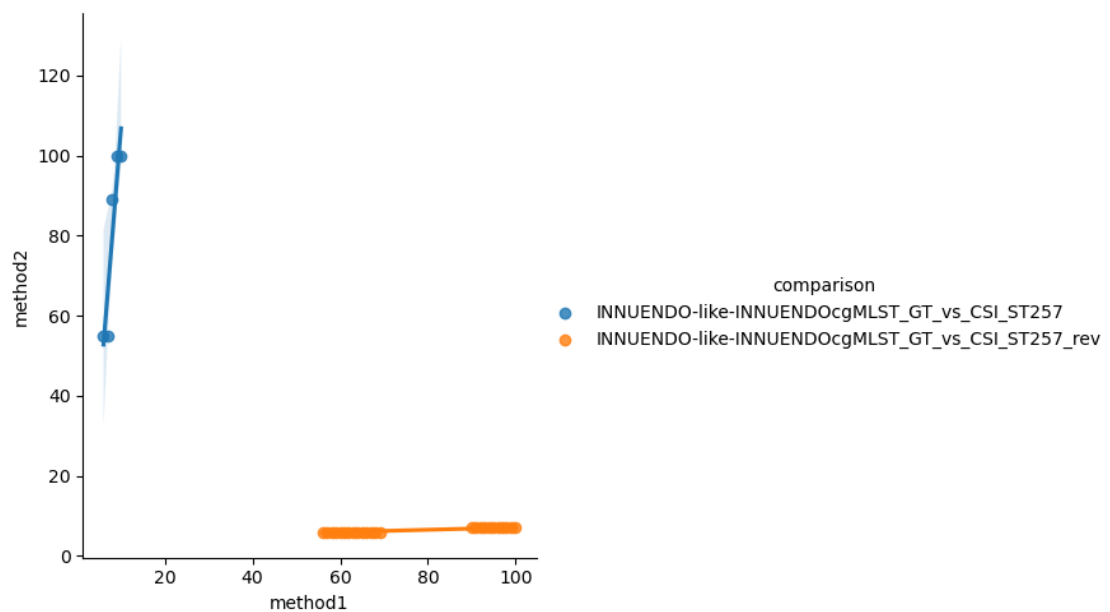


Figure S4.6.7. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST257. A linear tendency line supported by 5 (blue) and 25 (orange) points is presented.

7. INNUENDO-like-INNUENDOCgMLST 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.

	INNUENDO-like-INNUENDOCgMLST 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 cgMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

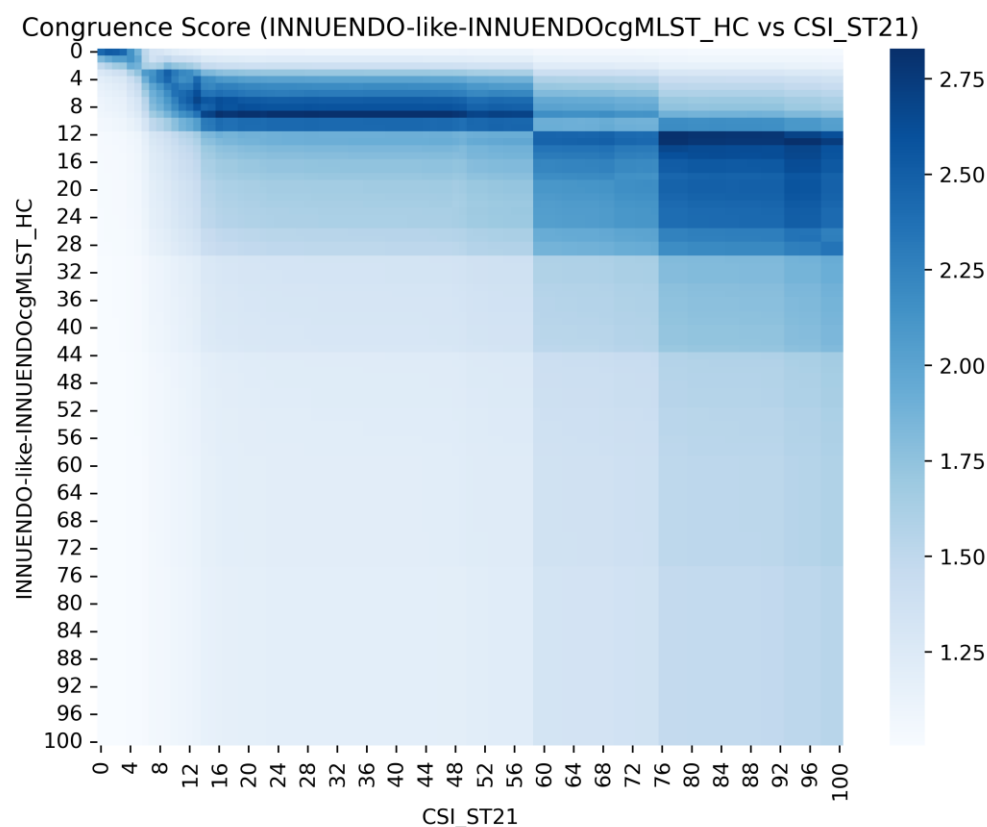


Figure S4.7.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST21, ST45 and ST48.

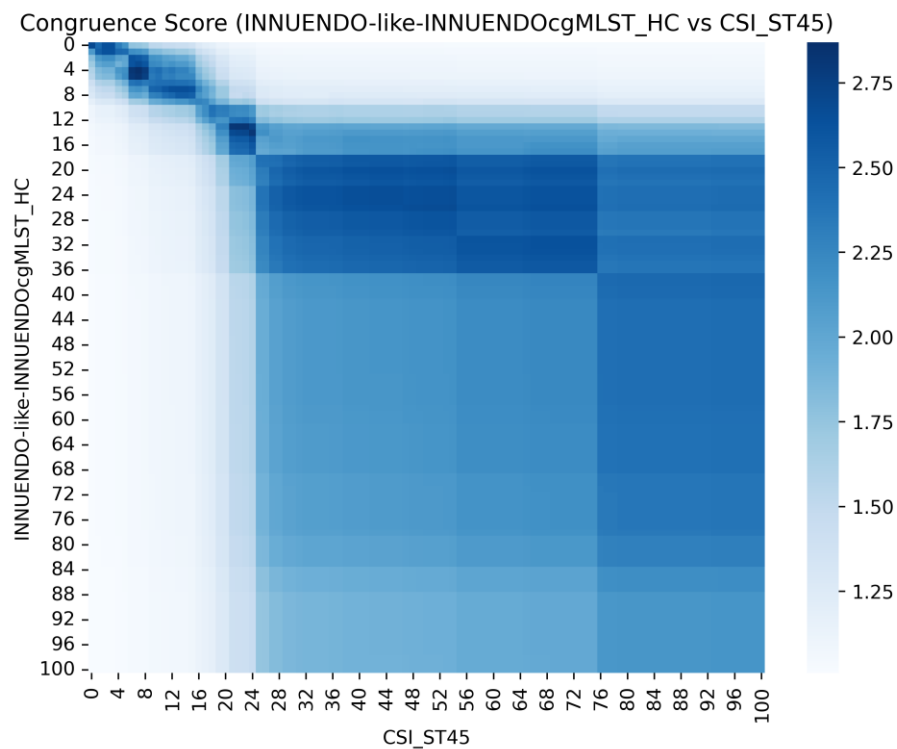


Figure S4.7.2. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

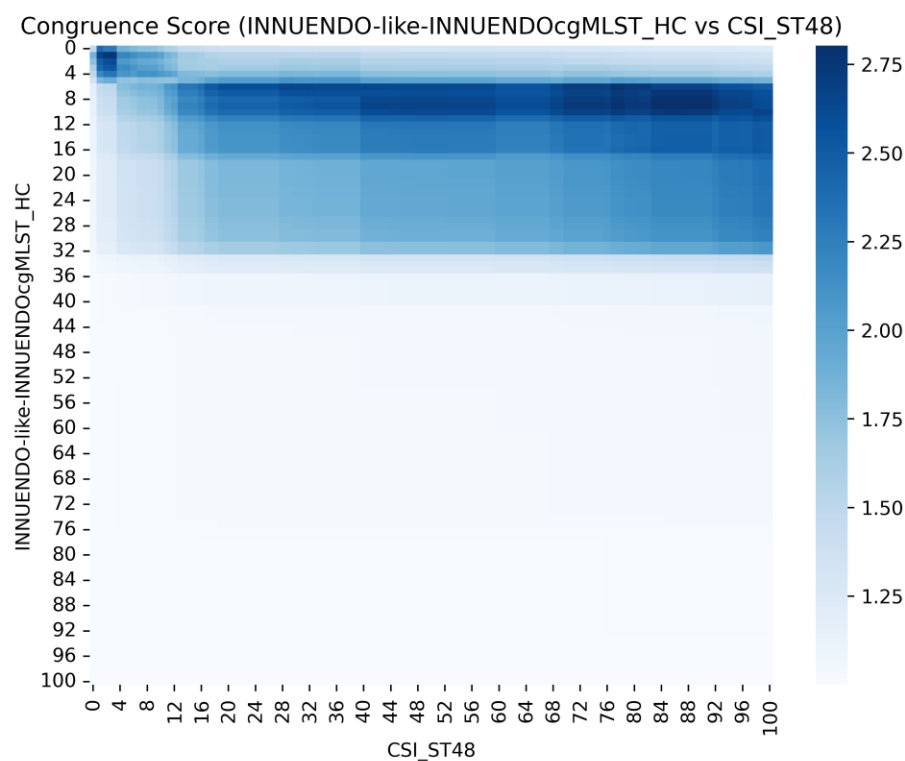


Figure S4.7.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST21, ST45 and ST48.

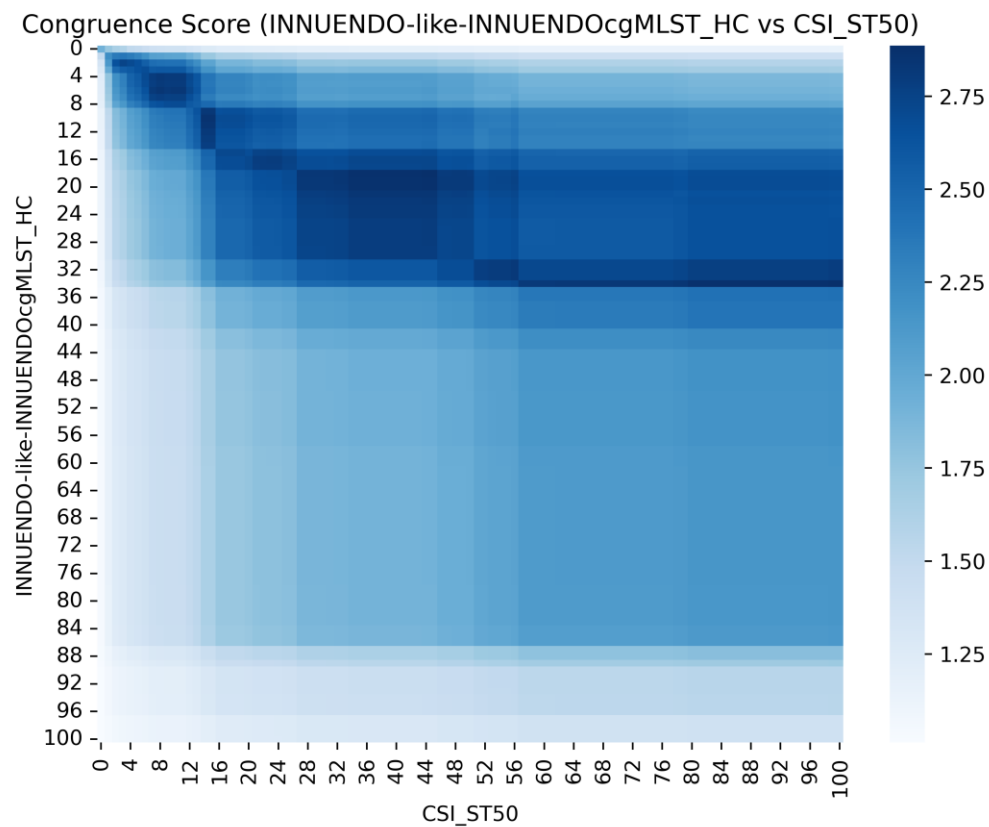


Figure S4.7.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

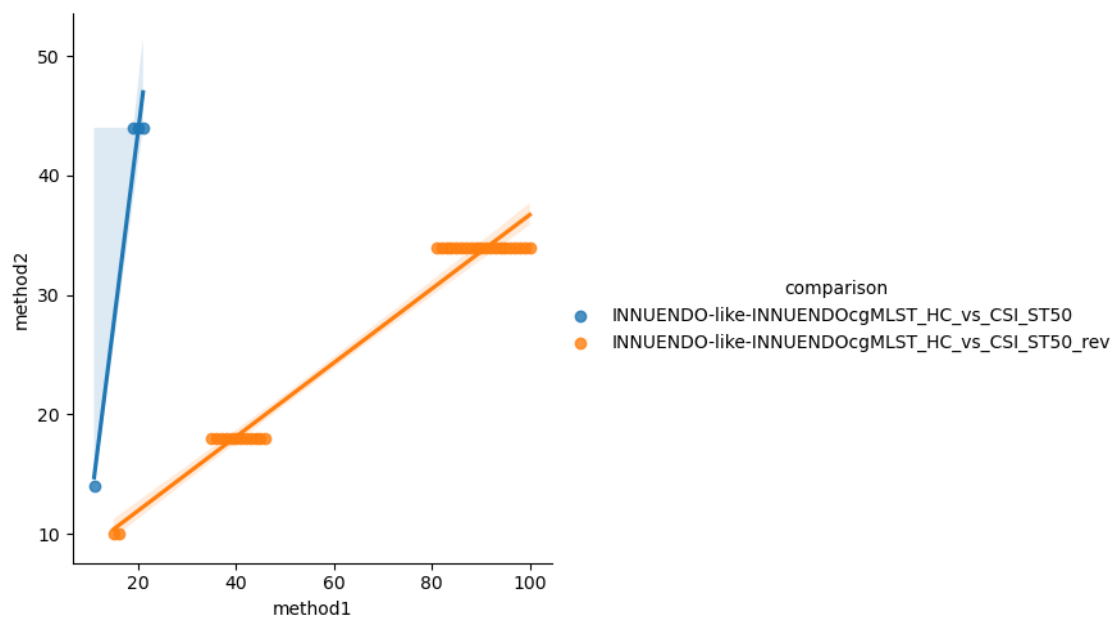


Figure S4.7.5. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST50. A linear tendency line supported by 4 (blue) and 34 (orange) points is presented.

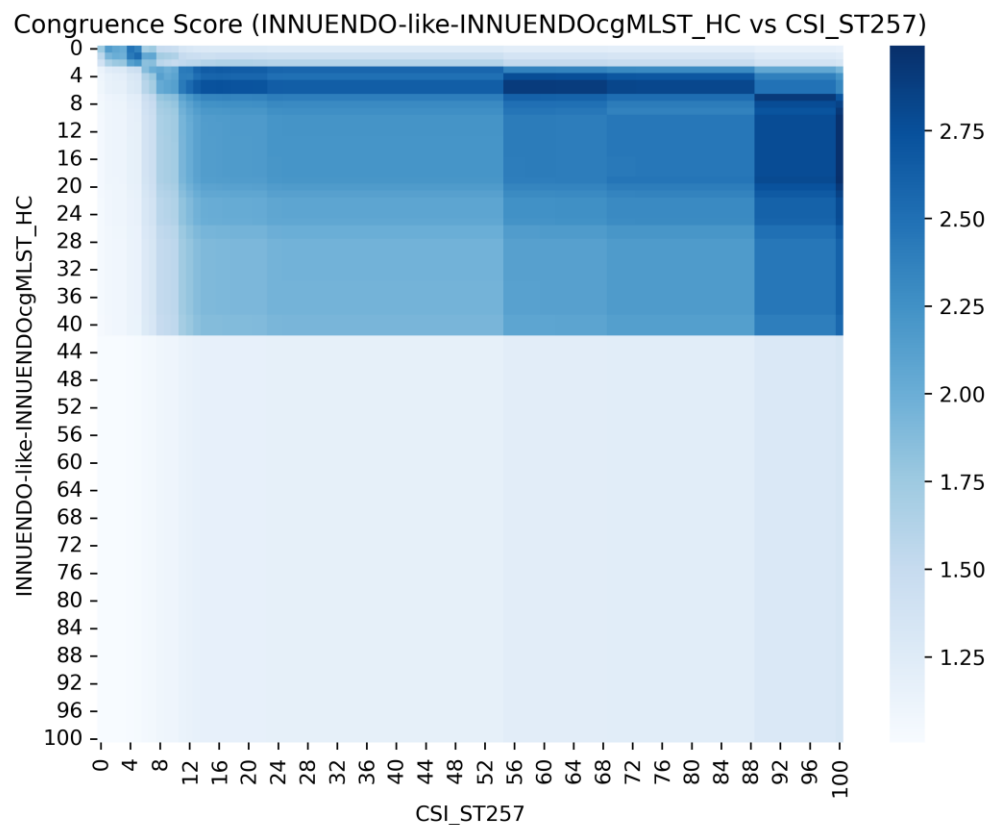


Figure S4.7.6. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

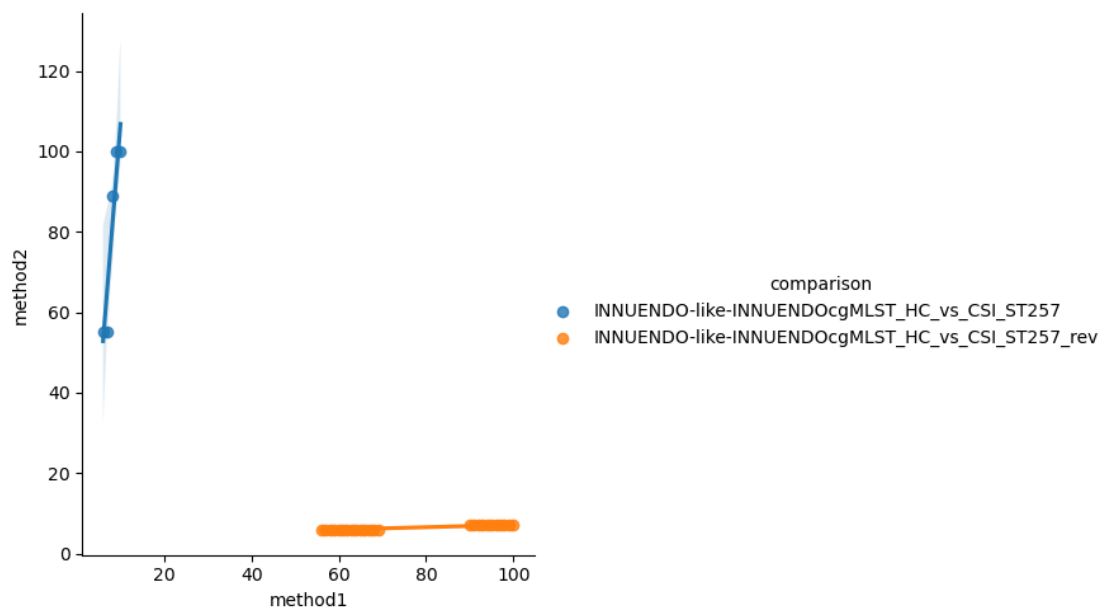


Figure S4.7.7. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST257. A linear tendency line supported by 5 (blue) and 25 (orange) points is presented.

8. INNUENDO-like-PubMLST GrapeTree vs. CSI Phylogeny 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.

	INNUENDO-like-PubMLST GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	PubMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

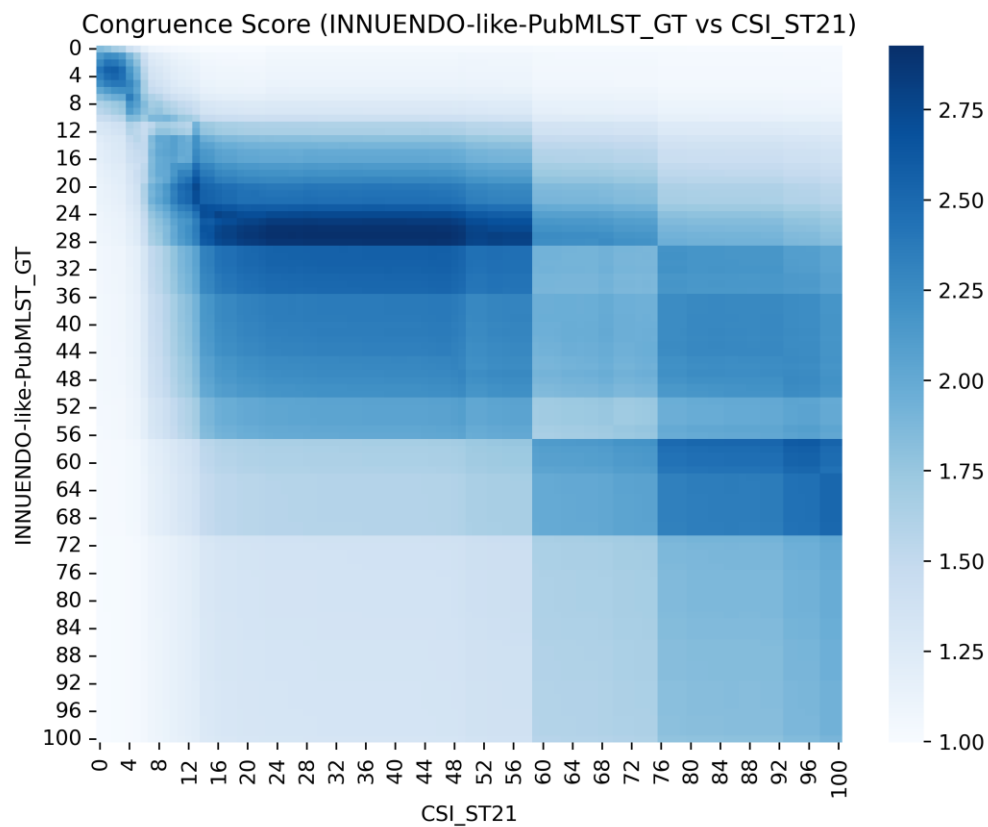


Figure S4.8.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

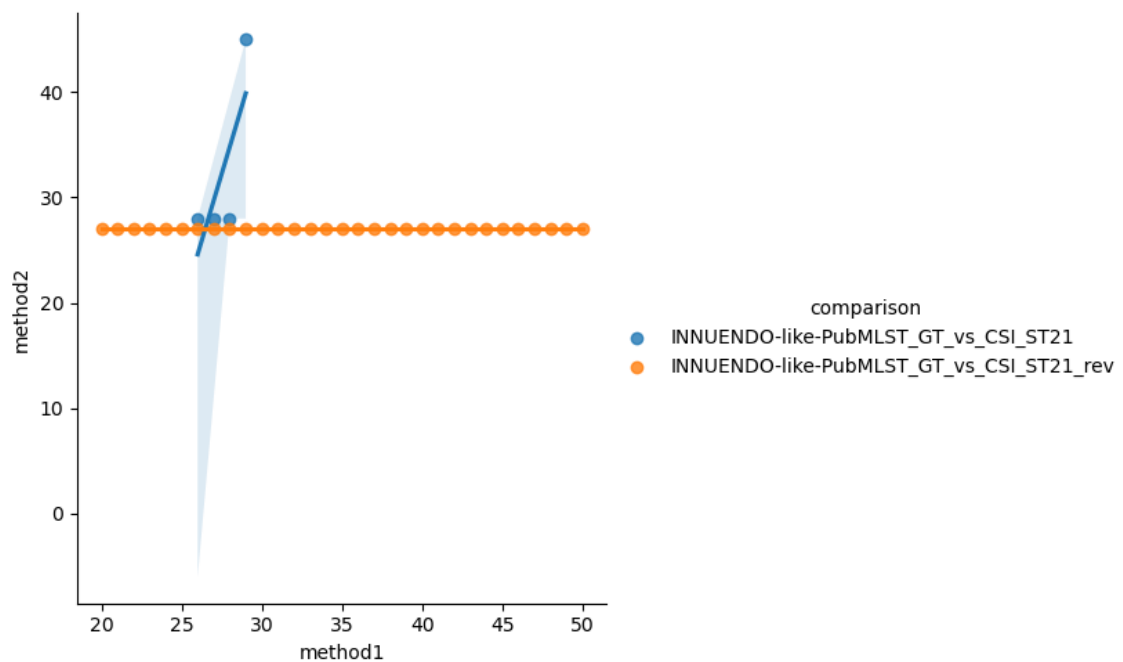


Figure S4.8.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 4 (blue) and 31 (orange) points is presented.

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

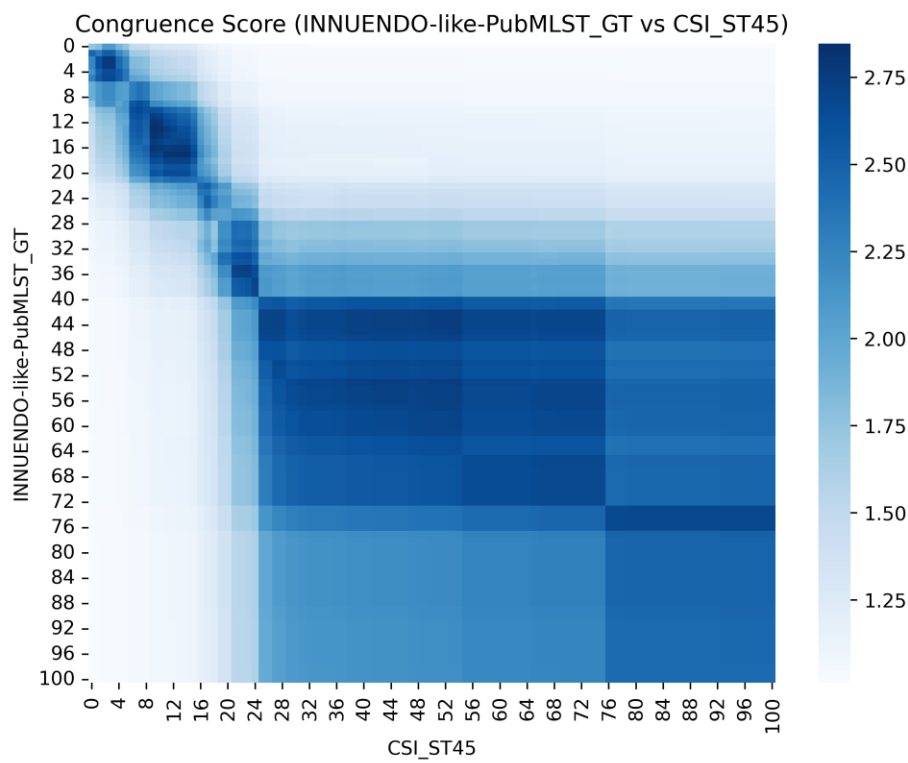


Figure S4.8.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

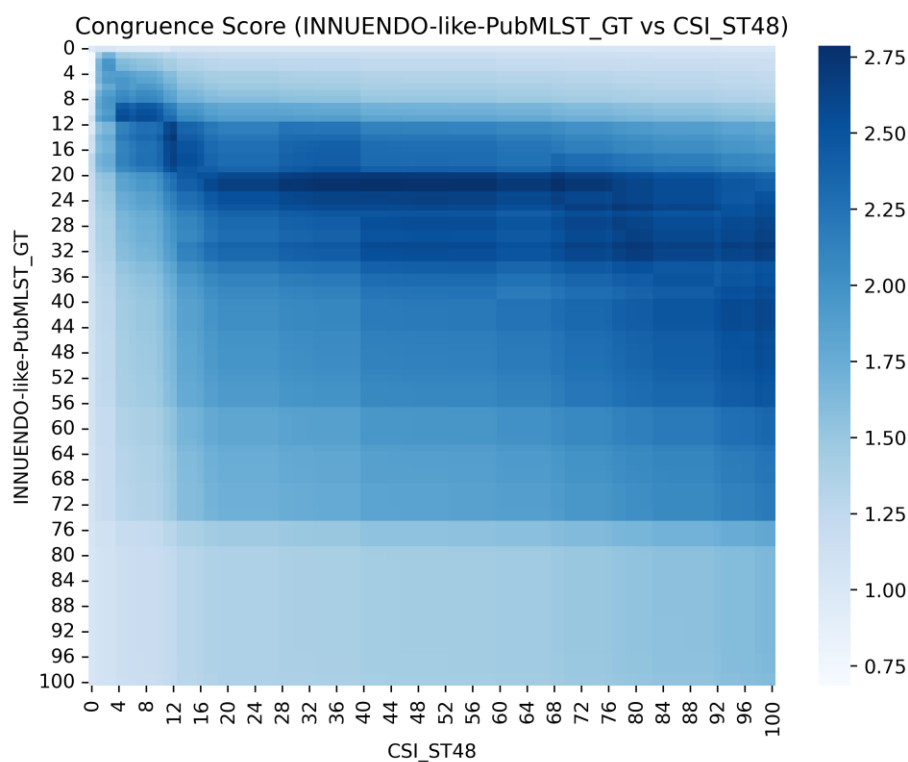


Figure S4.8.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS $\geq$ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45 and ST48.

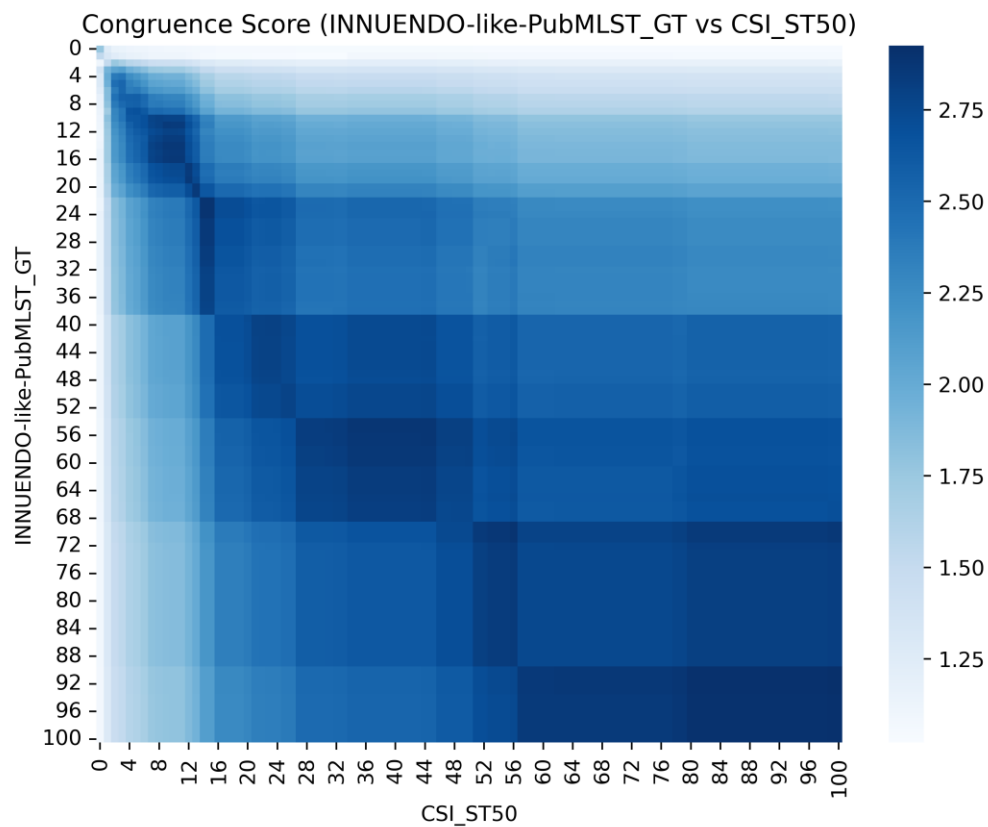


Figure S4.8.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

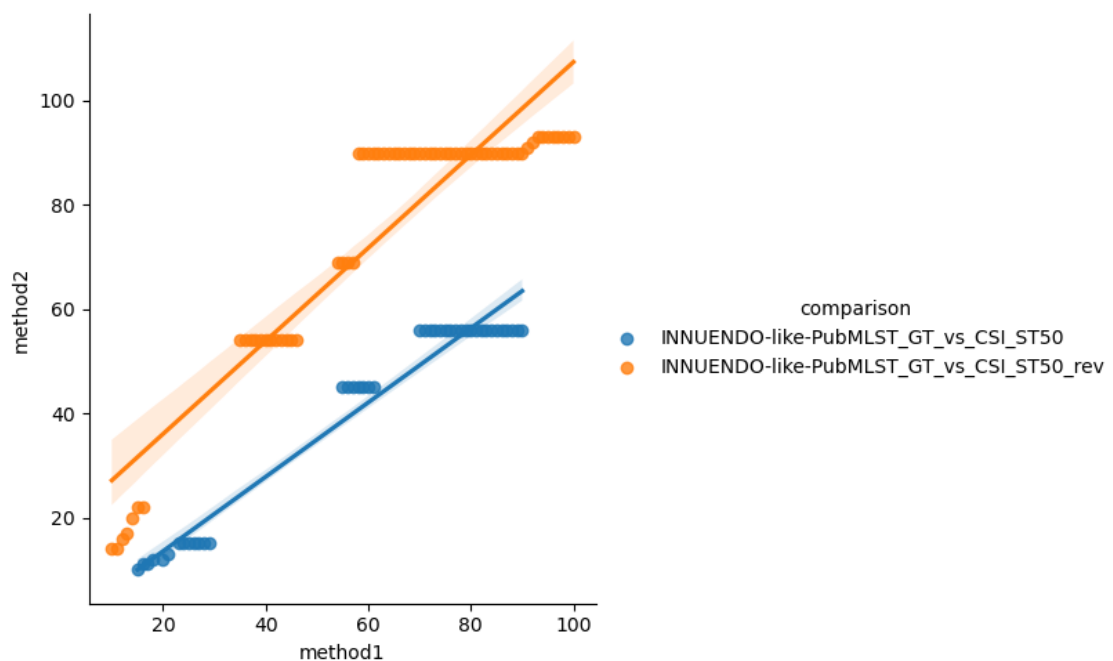


Figure S4.8.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST50. A linear tendency line supported by 41 (blue) and 66 (orange) points is presented.

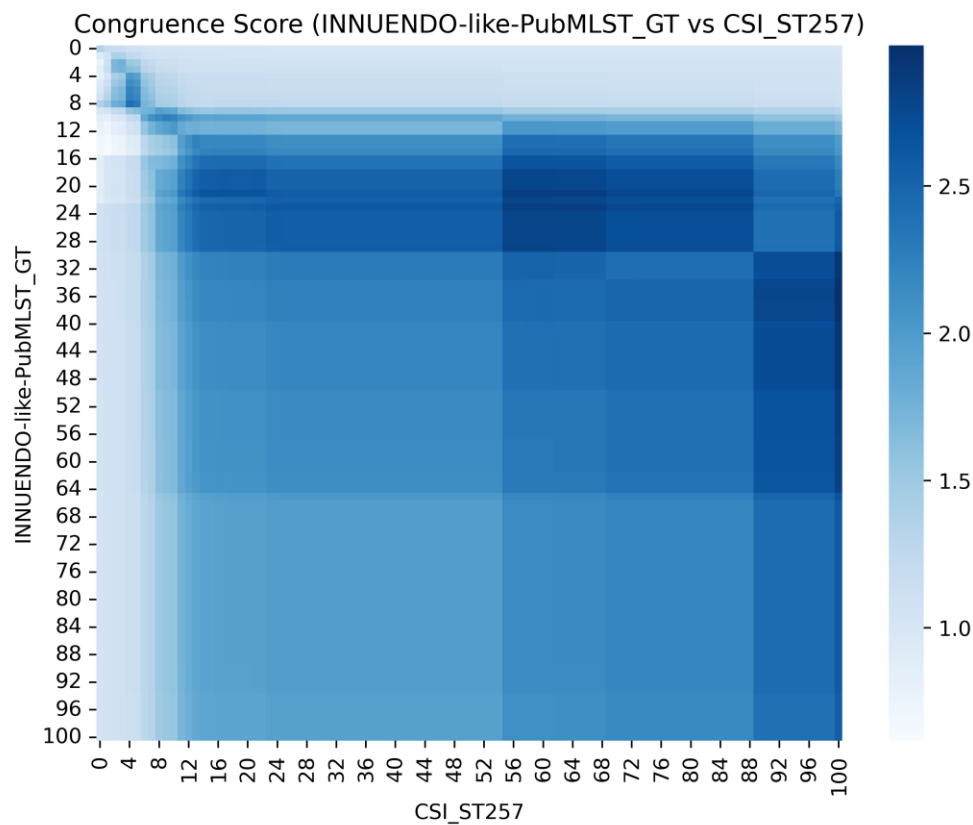


Figure S4.8.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

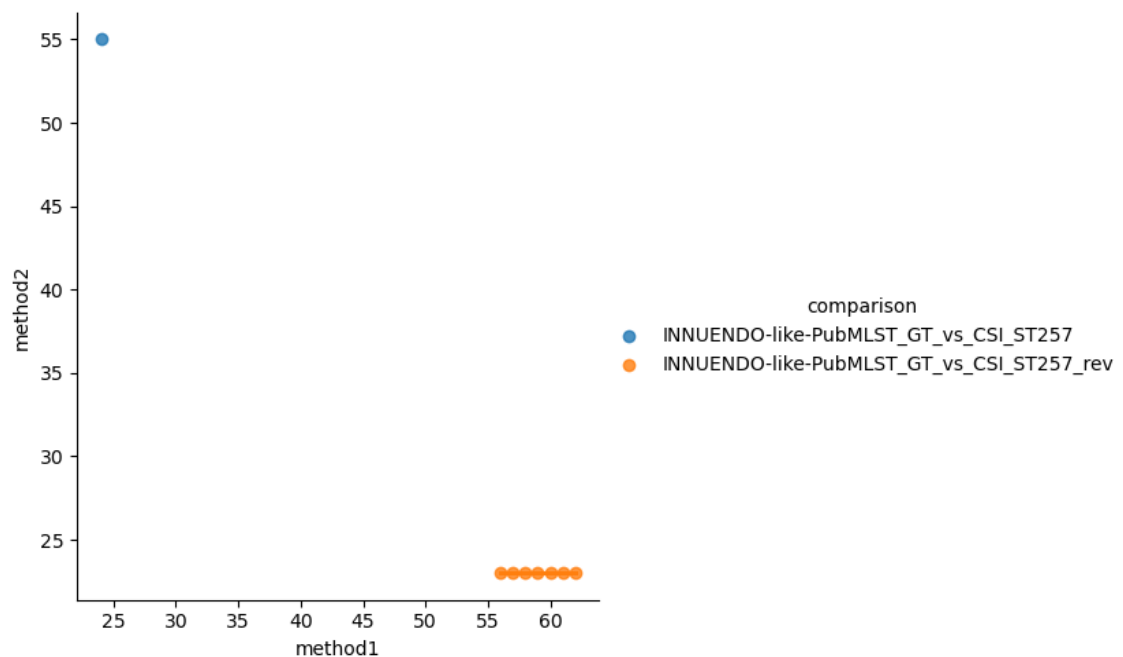


Figure S4.8.8. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST257. No linear tendency was observed. The 1 (blue) and 7 (orange) points are presented.

9. INNUENDO-like-PubMLST single-linkage vs. CSI Phylogeny 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.

	INNUENDO-like-PubMLST 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	PubMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

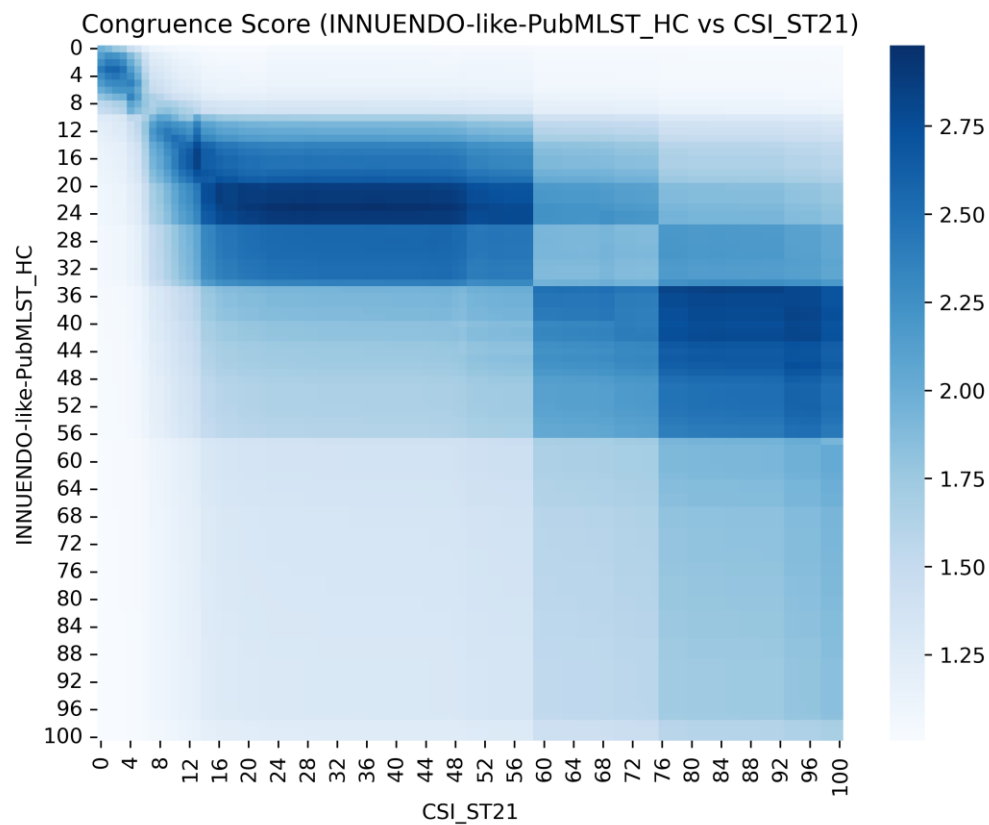


Figure S4.9.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

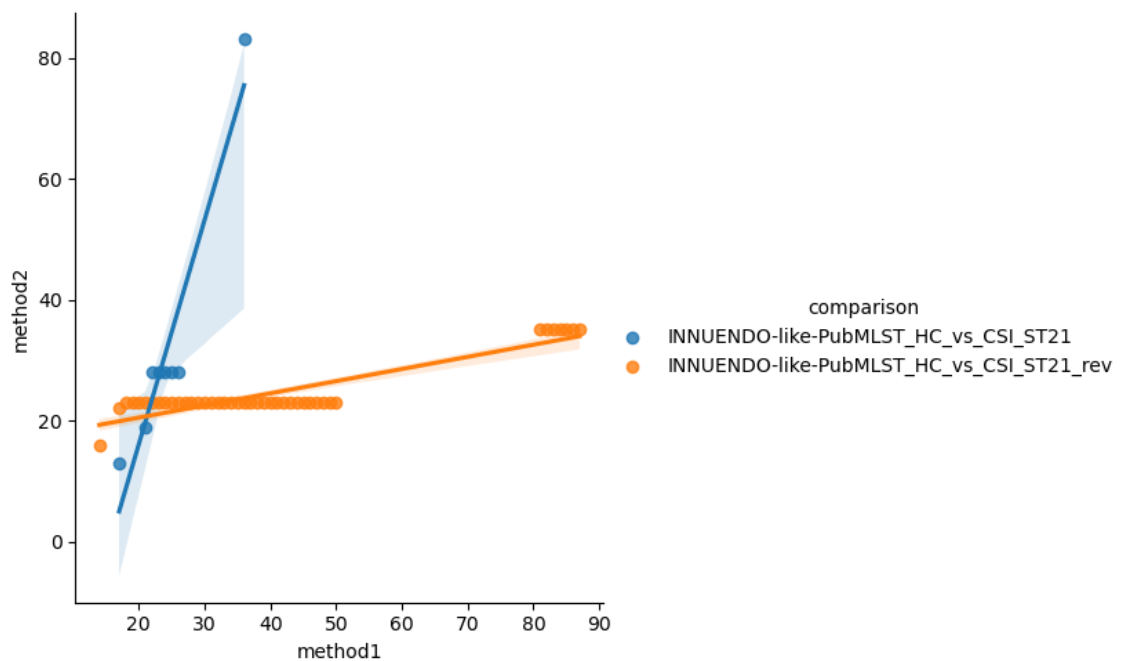


Figure S4.9.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST21. A linear tendency line supported by 8 (blue) and 42 (orange) points is presented.

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

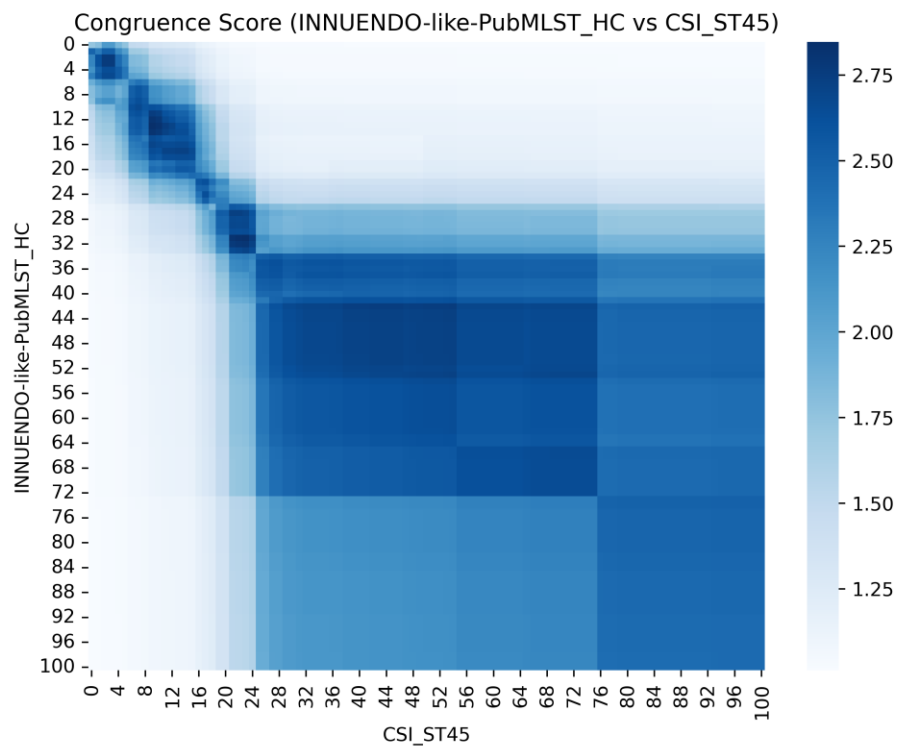


Figure S4.9.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

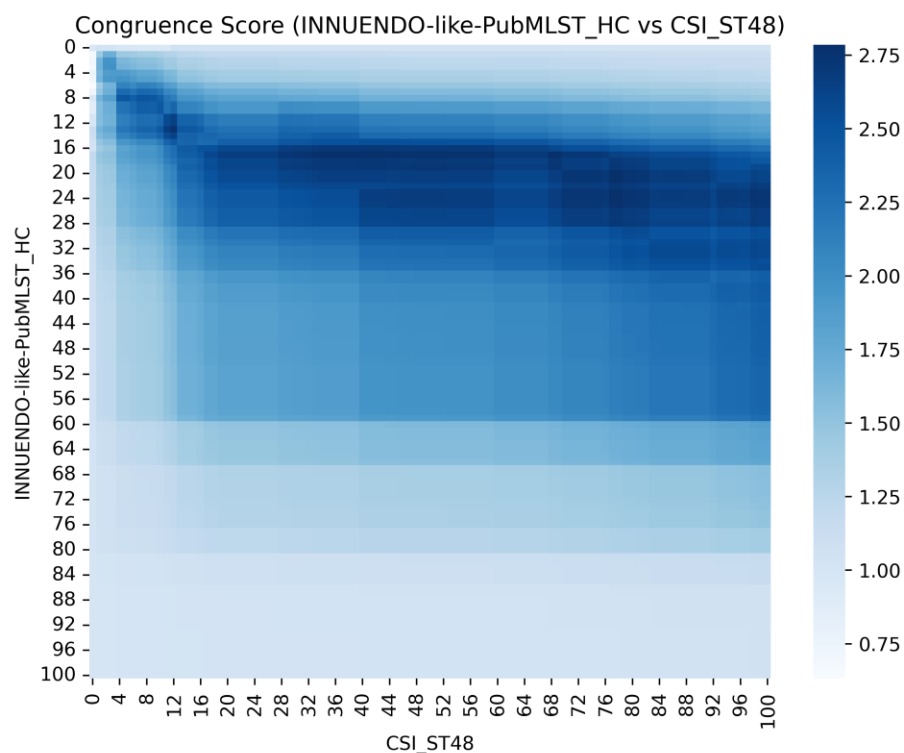


Figure S4.9.4. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45 and ST48.

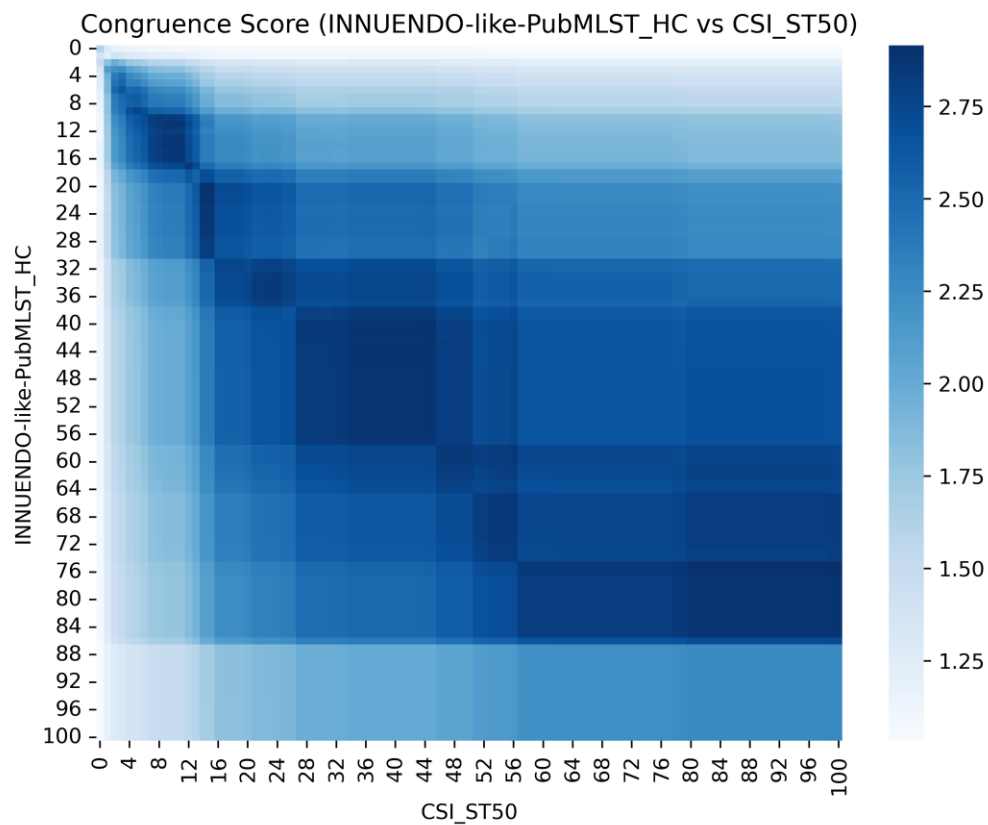


Figure S4.9.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

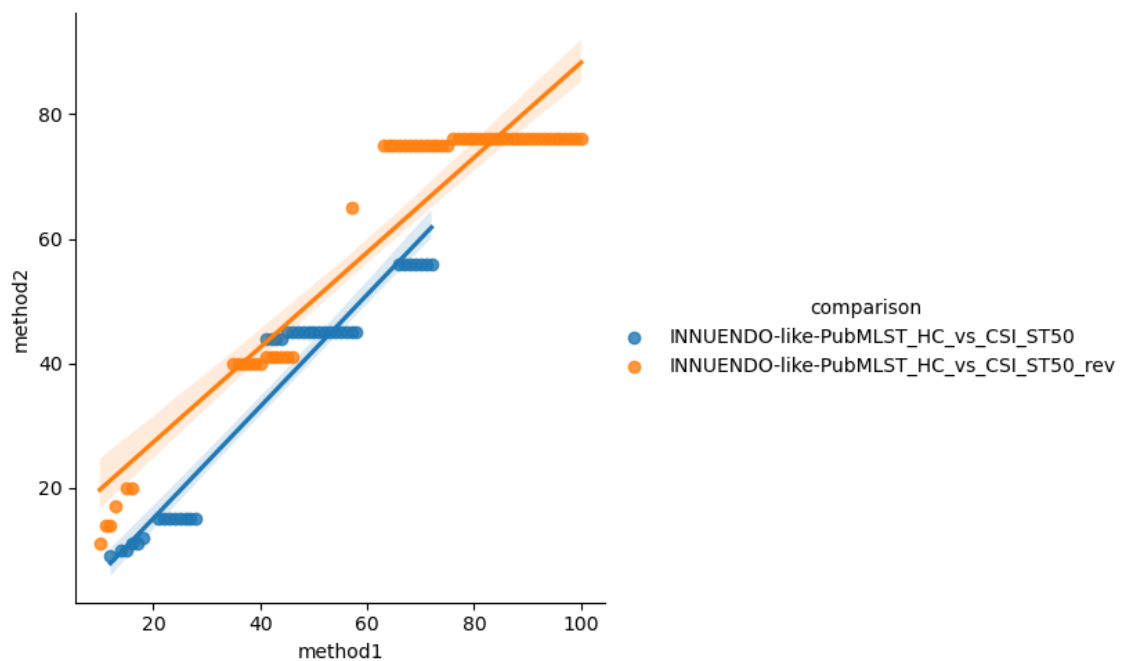


Figure S4.9.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST50. A linear tendency line supported by 39 (blue) and 57 (orange) points is presented.

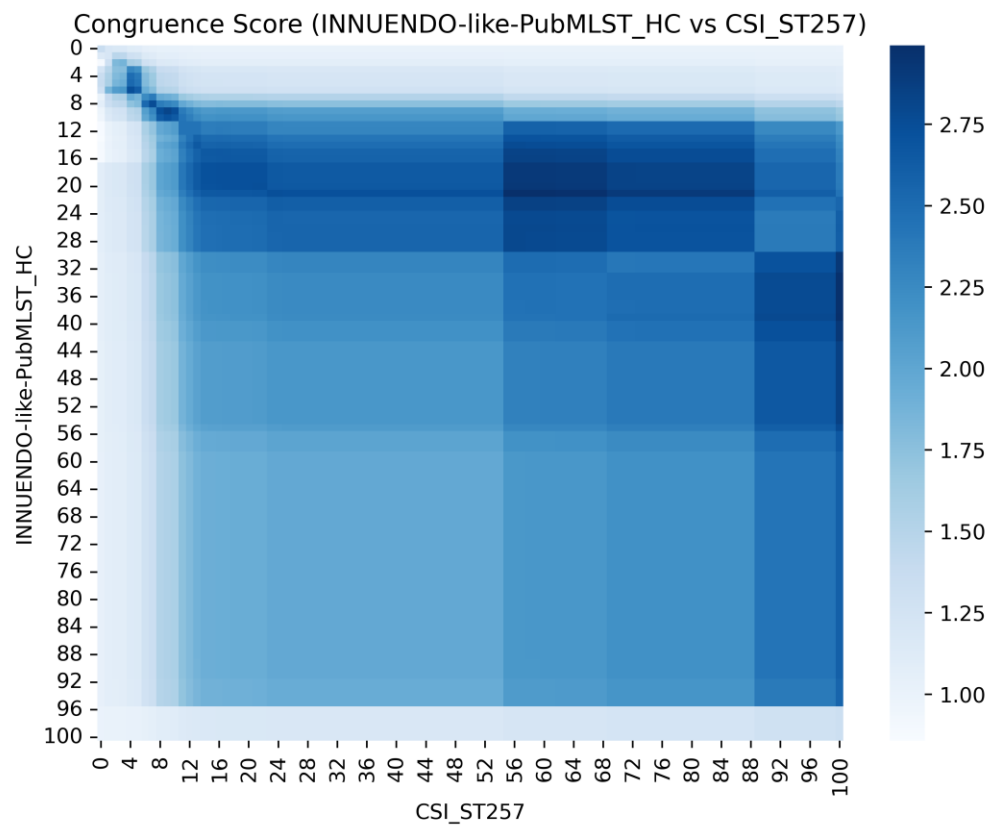


Figure S4.9.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

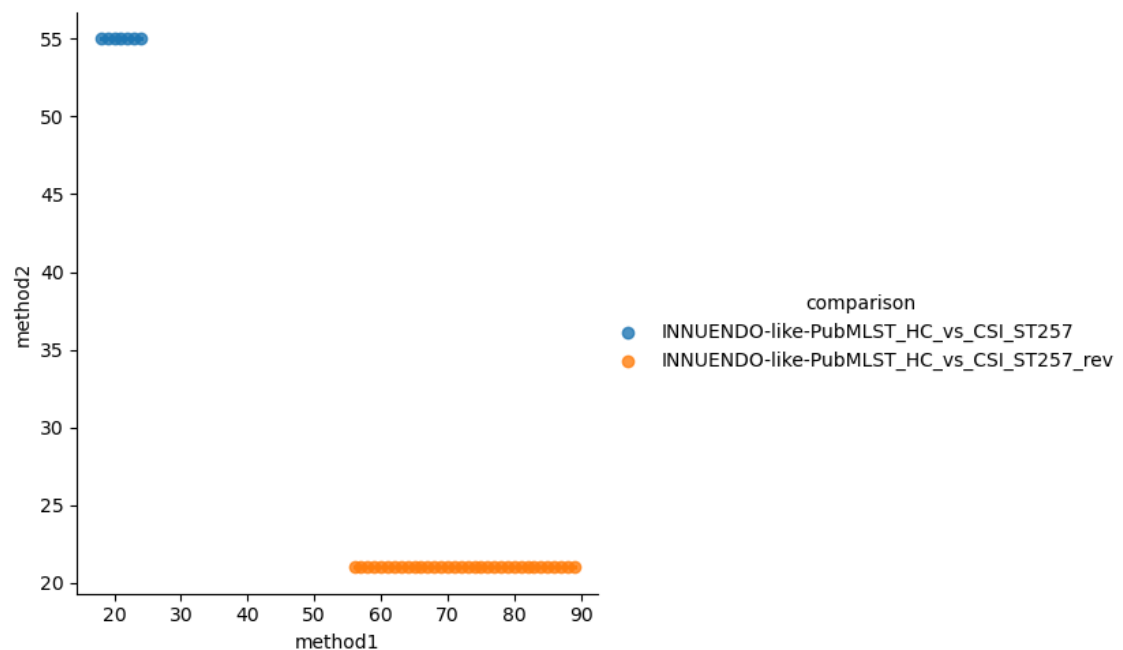


Figure S4.9.8. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST257. No linear tendency was observed. The 7 (blue) and 34 (orange) points are presented

10. SeqSphere-wgMLST 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.

	SeqSphere-wgMLST GrapeTree	CSI Phylogeny single-linkage
Pipeline version	v8.3.4	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	SeqSphere wgMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

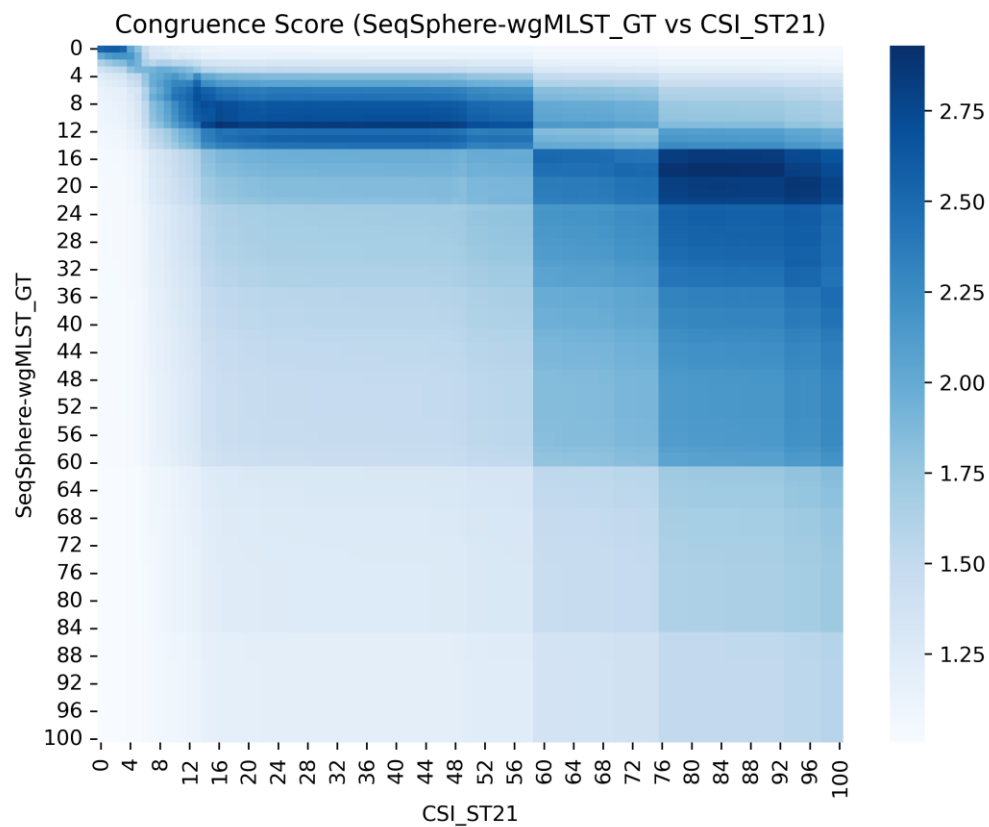


Figure S4.10.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

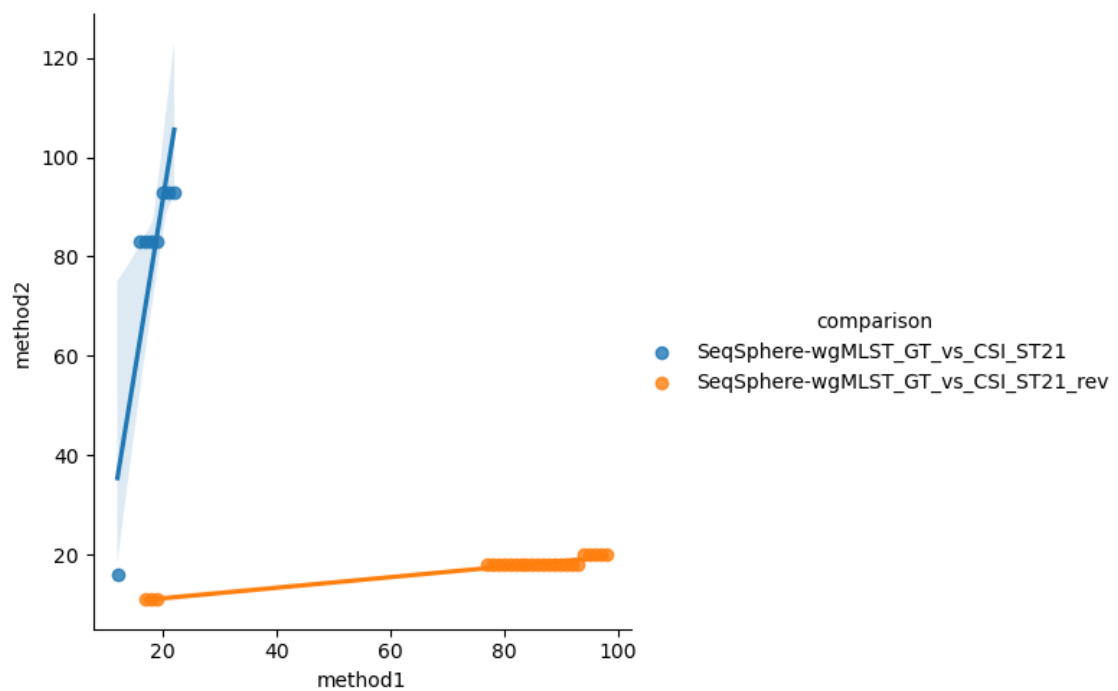


Figure S4.10.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 8 (blue) and 25 (orange) points is presented.

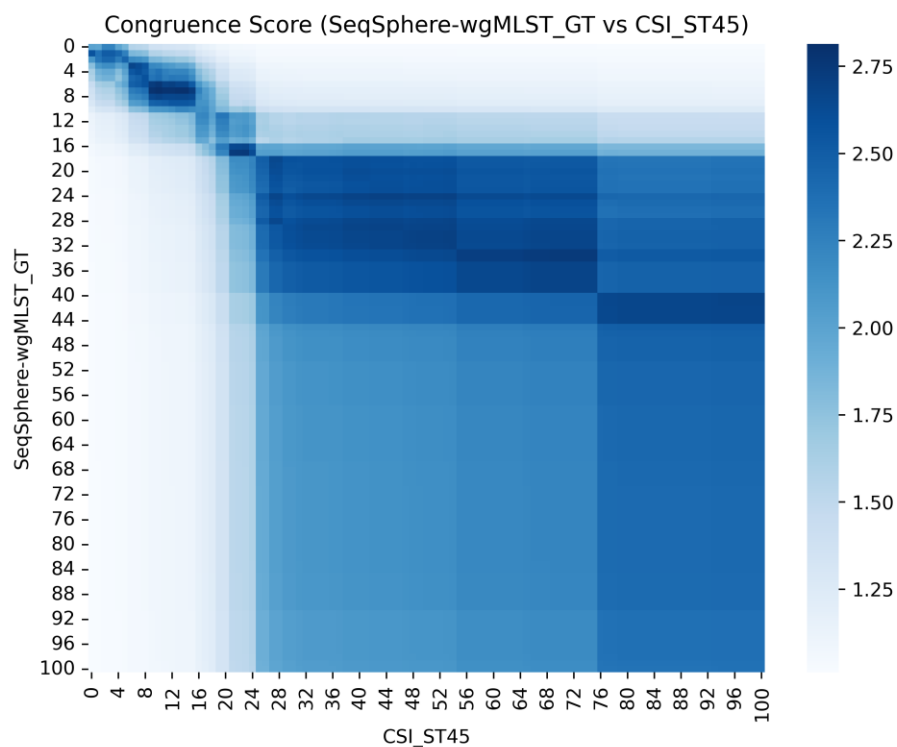


Figure S4.10.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

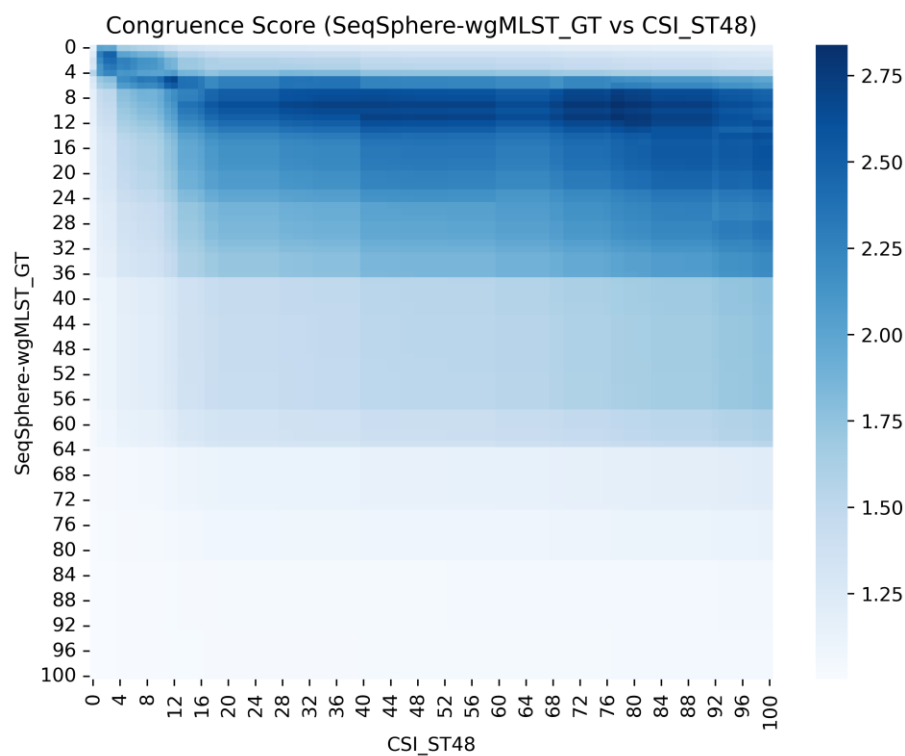


Figure S4.10.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of both pipelines for ST45 and ST48.

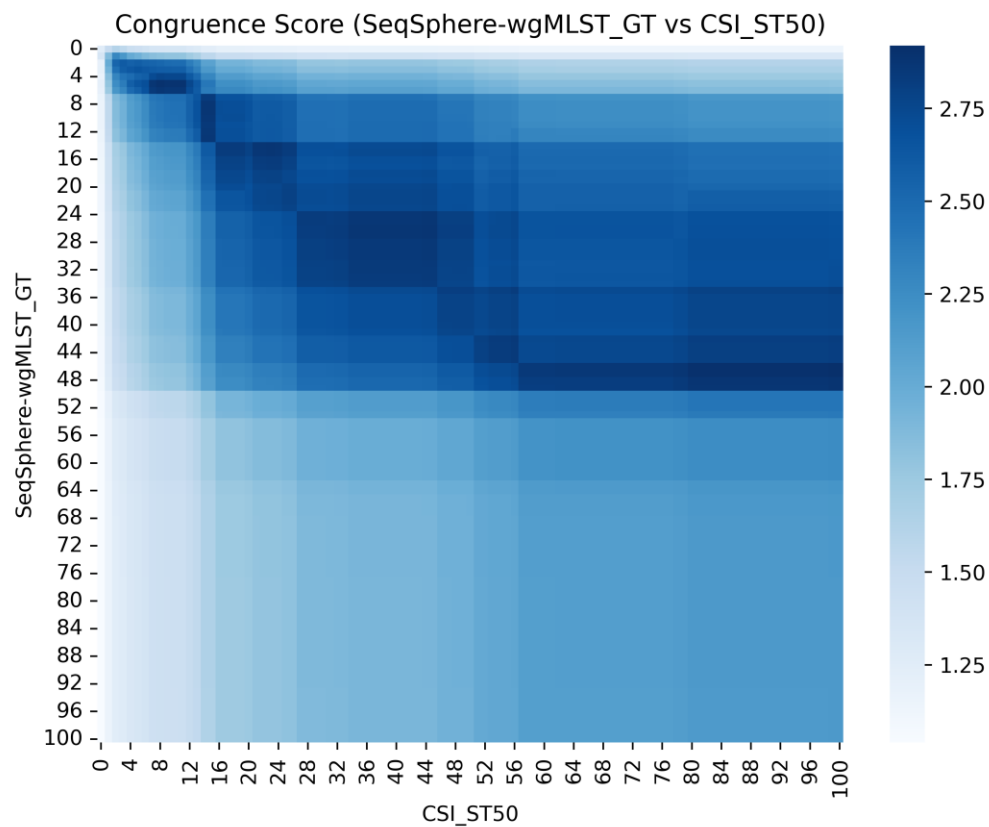


Figure S4.10.5. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST50. Axis represent the different allele/SNP distance thresholds.

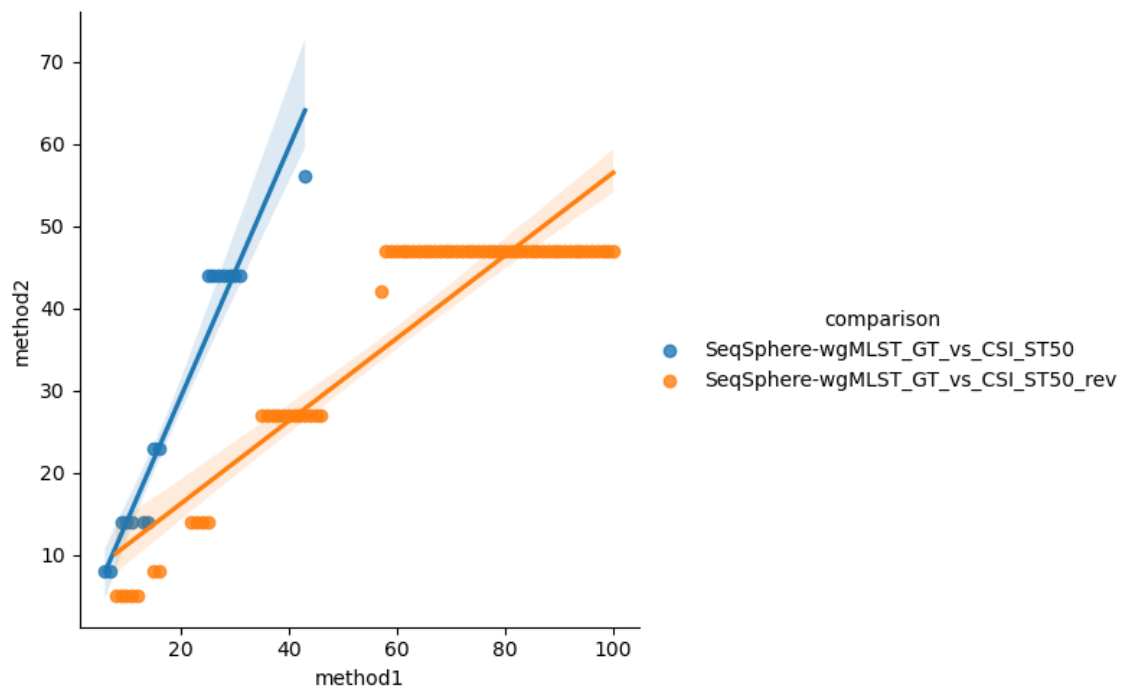


Figure S4.10.6. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST50. A linear tendency line supported by 17 (blue) and 67 (orange) points is presented.

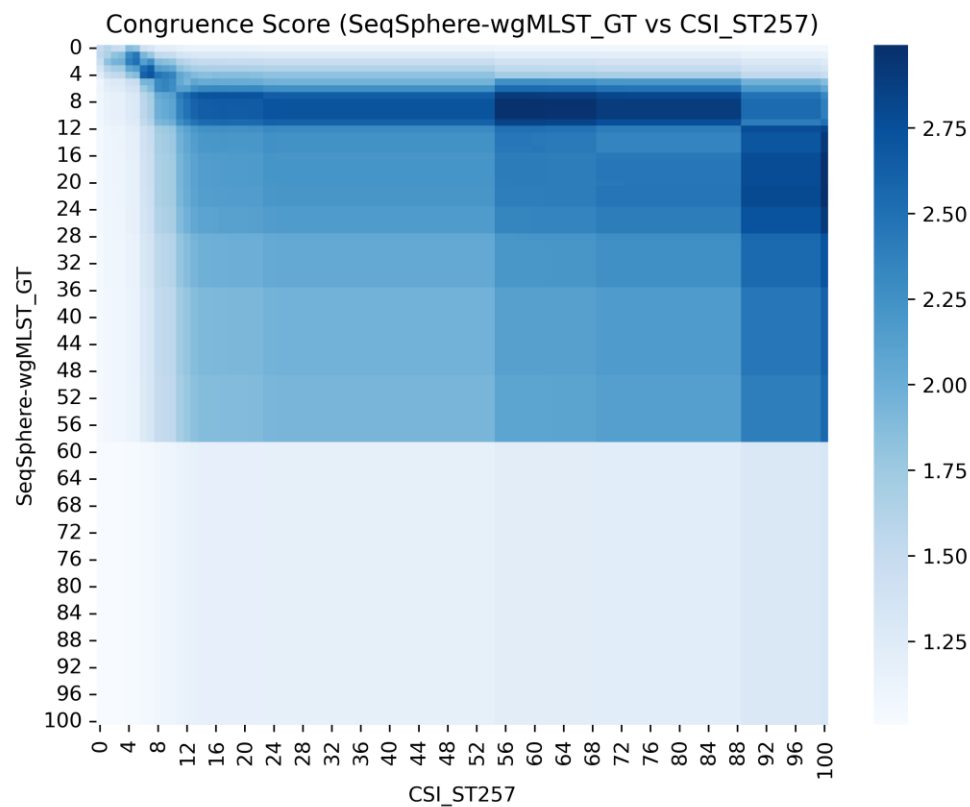


Figure S4.10.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

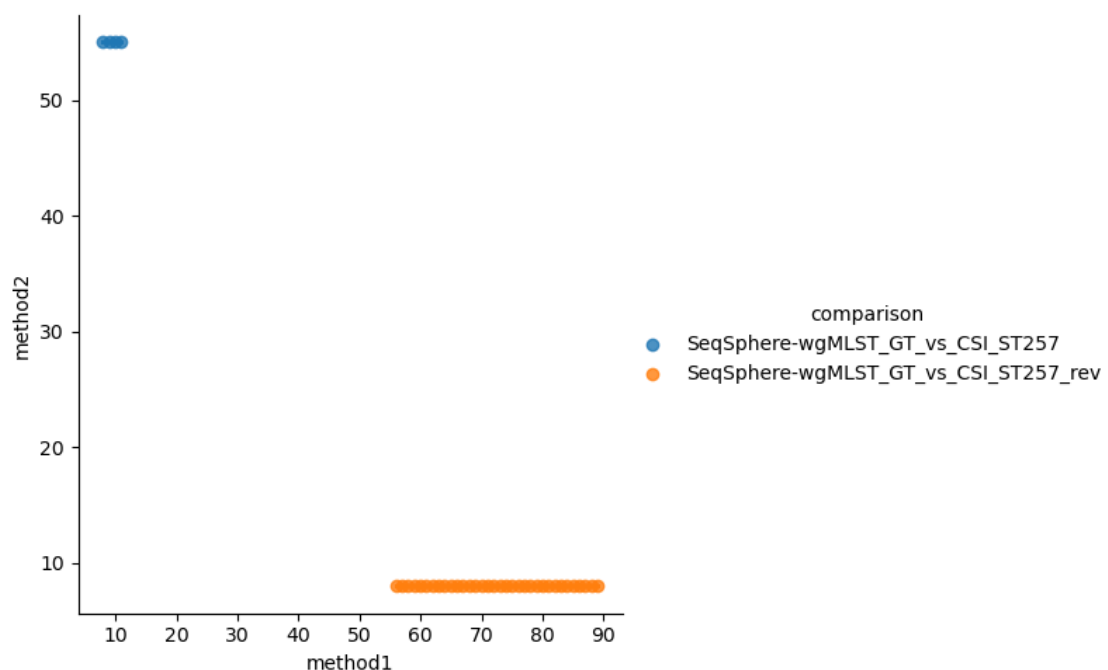


Figure S4.10.8. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST257. No linear tendency was observed. The 4 (blue) and 34 (orange) points are presented.

11. SeqSphere-wgMLST single-linkage vs. CSI Phylogeny 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.

	SeqSphere-wgMLST 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	SeqSphere wgMLST	NCTC_11168 (ST21) / HG428754 (ST45) / CP006006 (ST48) / NCTC_11168 (ST50) / H055140547 (ST257)
Dataset	All samples	ST21 / ST45 / ST48 / ST50 / ST257

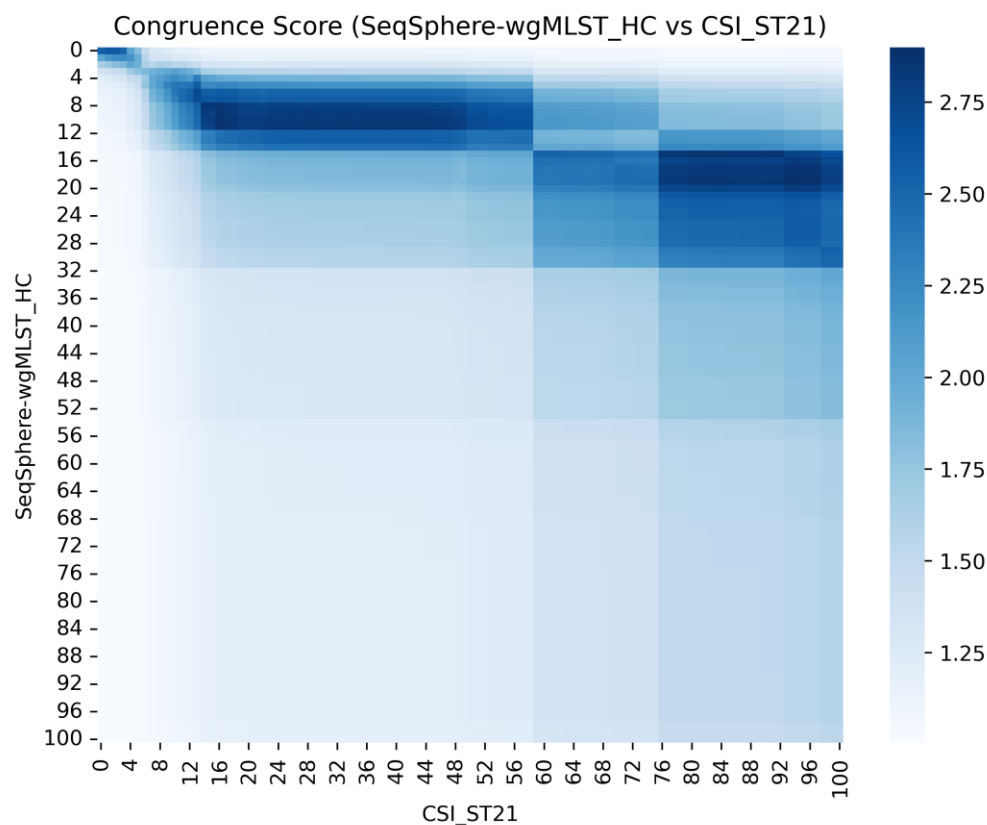


Figure S4.11.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST21. Axis represent the different allele/SNP distance thresholds.

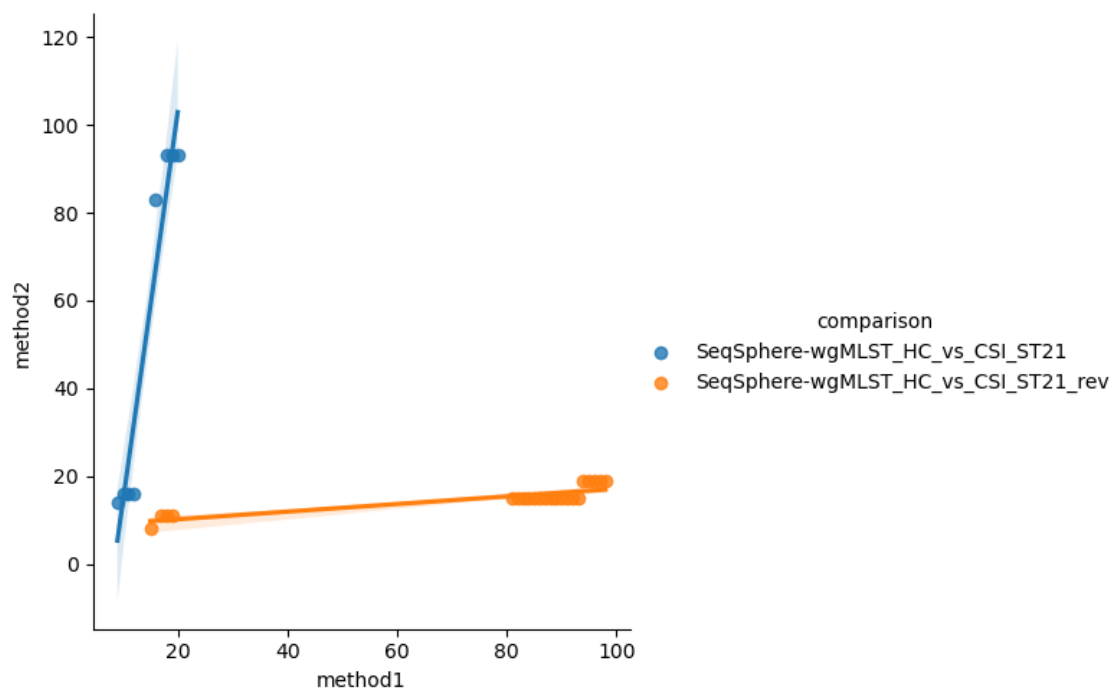


Figure S4.11.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST21. A linear tendency line supported by 8 (blue) and 22 (orange) points is presented.

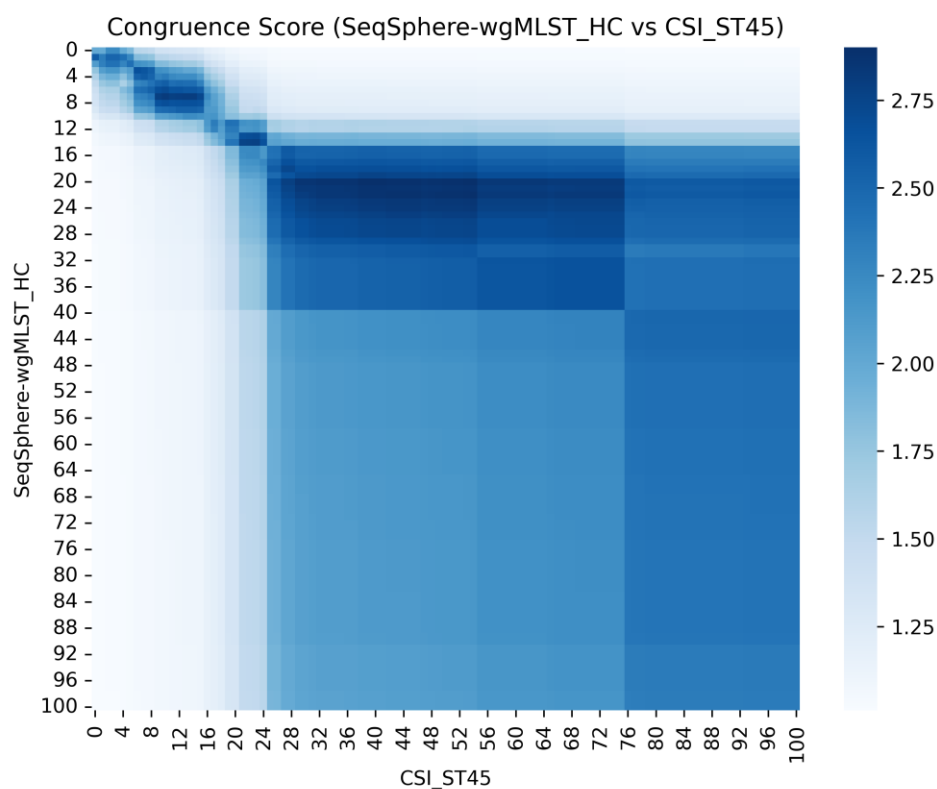


Figure S4.11.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST45. Axis represent the different allele/SNP distance thresholds.

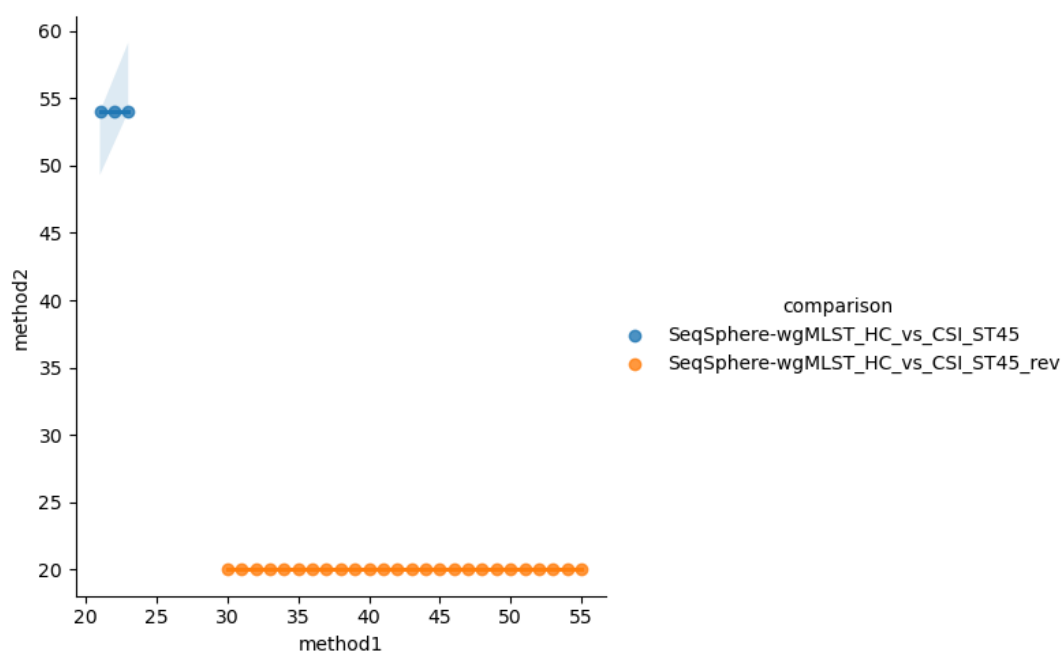


Figure S4.11.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST45. No linear tendency was observed. The 3 (blue) and 26 (orange) points are presented

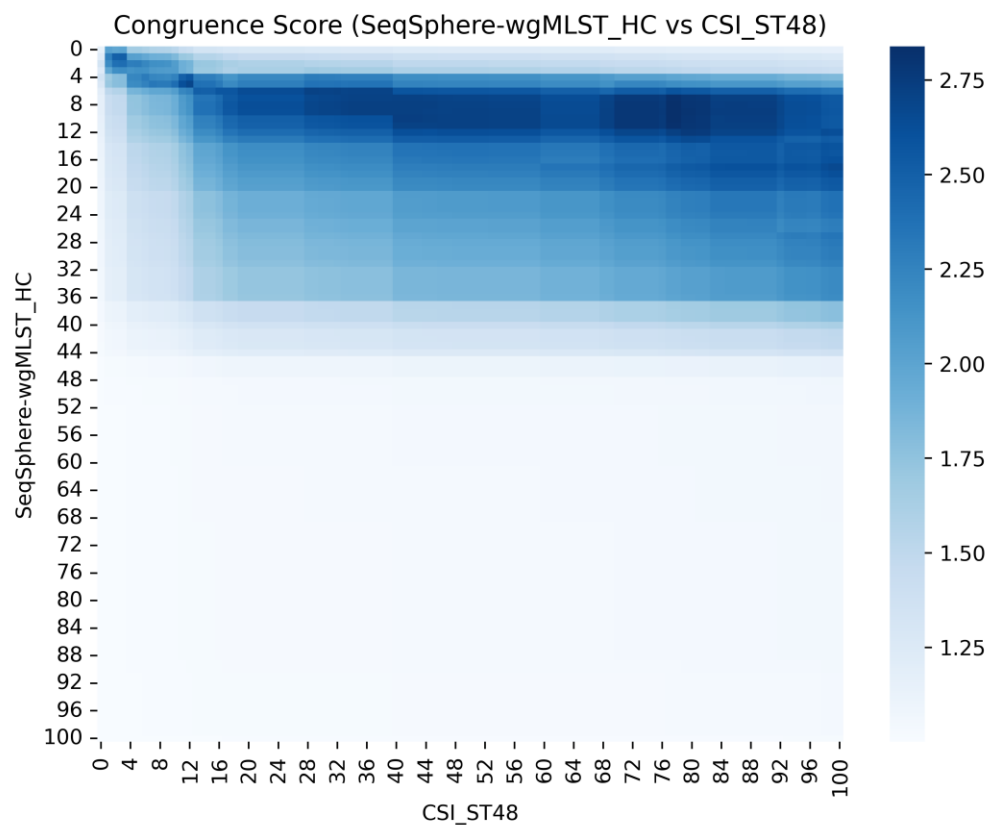


Figure S4.11.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for S48. Axis represent the different allele/SNP distance thresholds.

NOTE: No multiple congruence points with CS ≥ 2.85 were obtained up to threshold 100 when comparing the partitions of both pipelines for ST48.

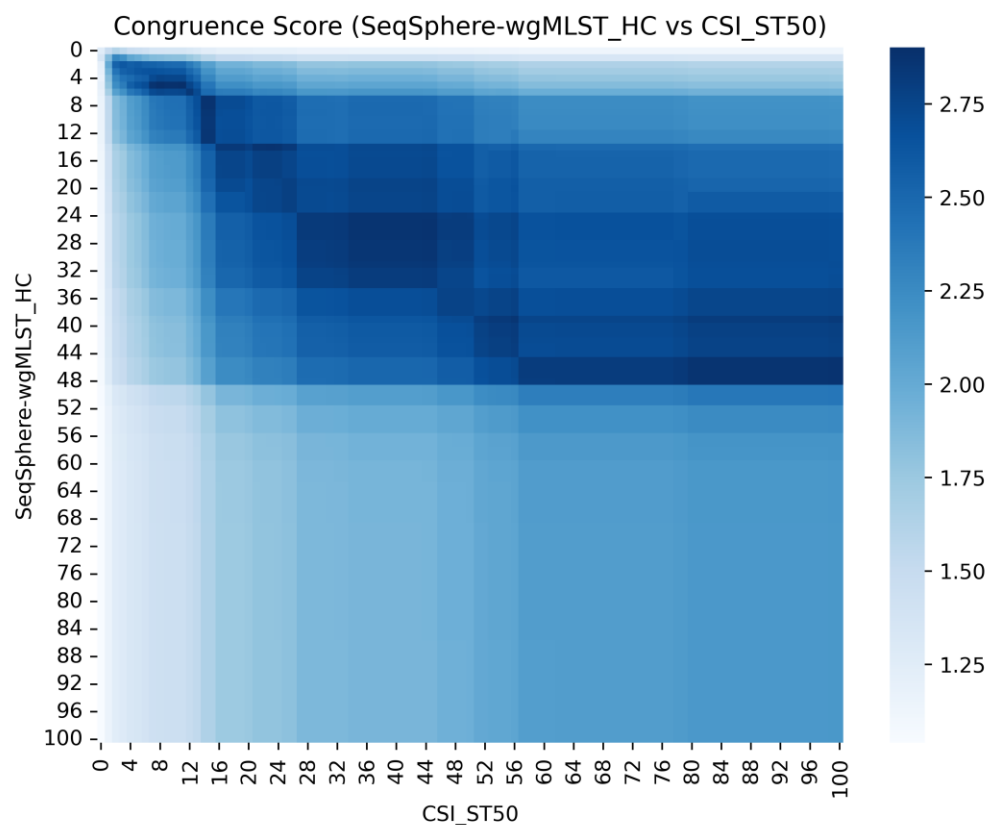


Figure S4.11.6. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST50. Axis represent the different allele/SNP distance thresholds.

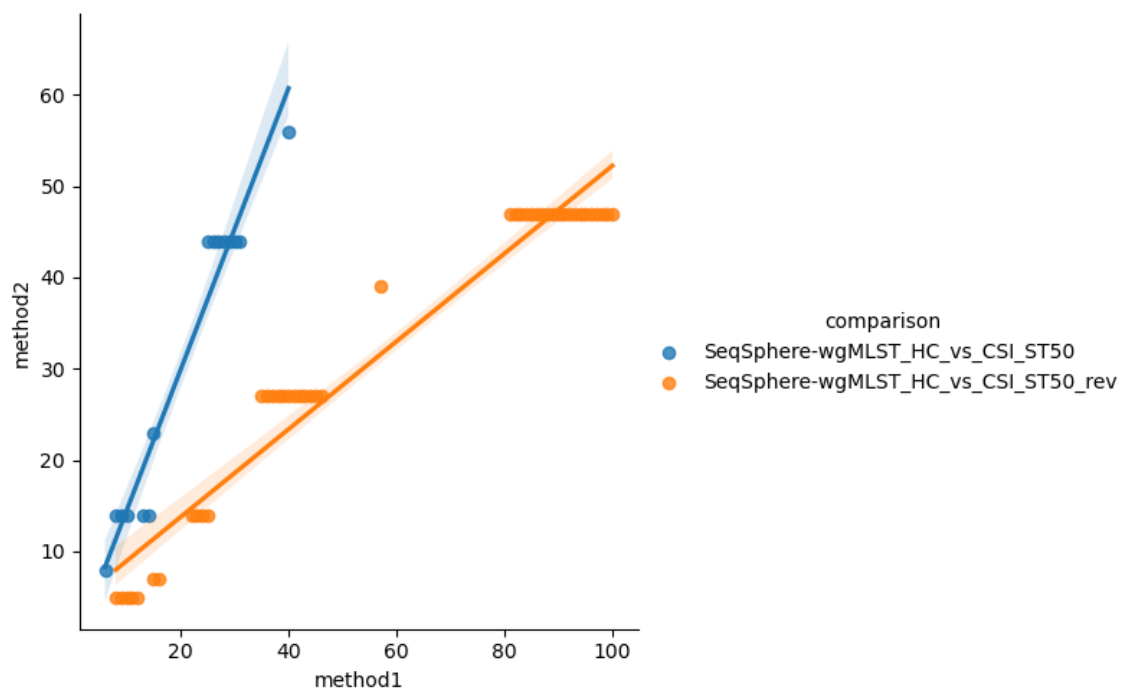


Figure S4.11.7. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST50. A linear tendency line supported by 15 (blue) and 44 (orange) points is presented.

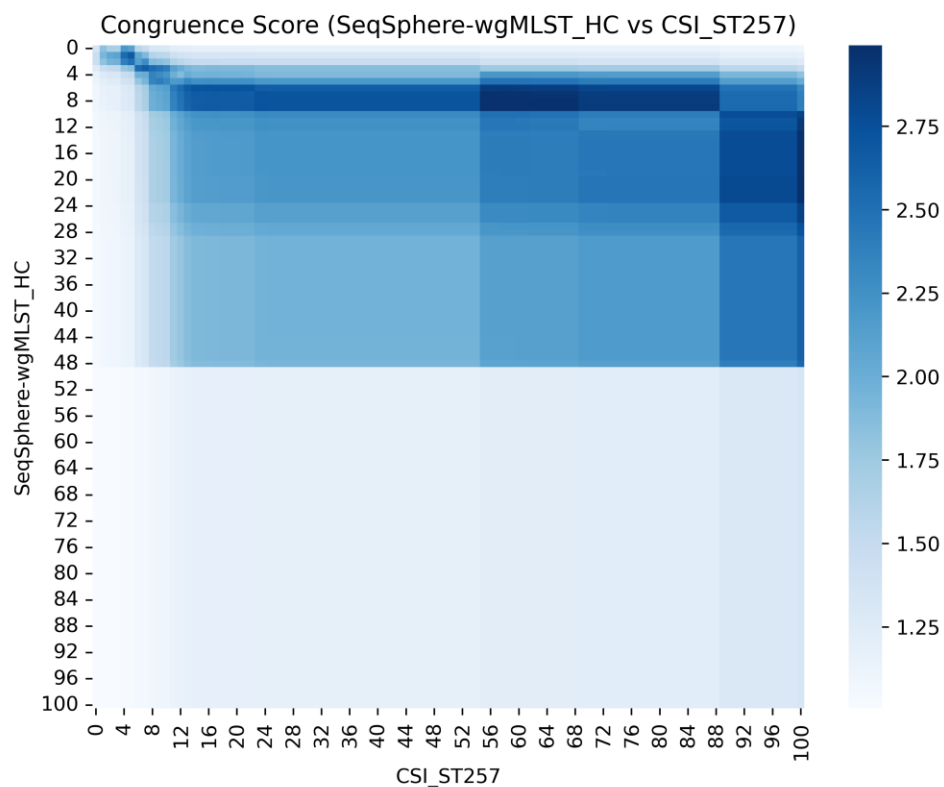


Figure S4.11.8. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST257. Axis represent the different allele/SNP distance thresholds.

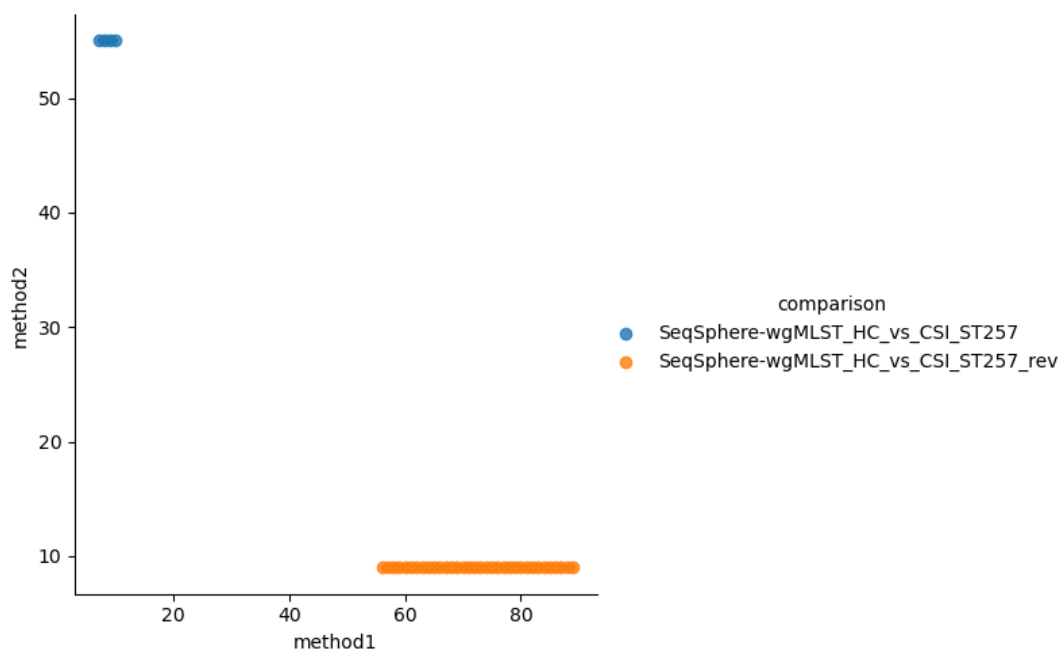


Figure S4.11.9. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST257. No linear tendency was observed. The 4 (blue) and 34 (orange) points are presented