

Supplementary Data 19

Details on the analysis of the dataset of *Escherichia coli*

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Section 1 – Supporting data

Section 1 – Supporting data

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

Pipeline	N	QC PASS	QC PASS (%)	Schema size	N partitions	Highest congruence point with ST (ADs)	CS with ST	Highest congruence point with serotype (ADs)	CS with serotype
chewieSnake_HC	2307	2292	99.35	2513	2274	545	2.91	545	2.72
chewieSnake_GT	2307	2292	99.35	2513	2346	609	2.91	609	2.72
INNUENDO-like_HC (INNUENDO wgMLST schema)	2307	2306	99.96	2507/7601	2359	564	2.91	564	2.73
INNUENDO-like_GT (INNUENDO wgMLST schema)	2307	2306	99.96	2507/7601	2447	620	2.91	620	2.73
INNUENDO-like_HC (Enterobase schema)	2307	2292	99.35	2513	2309	553	2.91	553	2.72
INNUENDO-like_GT (Enterobase schema)	2307	2292	99.35	2513	2388	613	2.91	613	2.72
INNUENDO-like_HC (EFSA schema)	2307	2305	99.91	2360	2193	527	2.91	527	2.73
INNUENDO-like_GT (EFSA schema)	2307	2305	99.91	2360	2299	580	2.91	580	2.73
Ridom SeqSphere_HC	2307	2076	89.99	2513	2798	738	2.91	738	2.77
Bionumerics_HC	2307	1067	46.25	2513	2206	-	-	-	-
Mentalist_HC	2307	2274	98.57	1607/7601	1422	-	-	-	-
Mentalist_GT	2307	2274	98.57	1607/7601	1542	-	-	-	-

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

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

Section 1 – Supporting data

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

Serotype	Pipeline	N	QC PASS	QC PASS (%)	N partitions
O157:H7	snippySnake_HC	863	863	100.00	1450
	CSI Phylogeny_HC	863	609	70.57	1972

Section 2 – Comparison of allele-based pipelines

1. chewieSnake 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.

	chewieSnake single-linkage	chewieSnake GrapeTree
Pipeline version	v3.1.1	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2274	2346

Section 2 – Comparison of allele-based pipelines

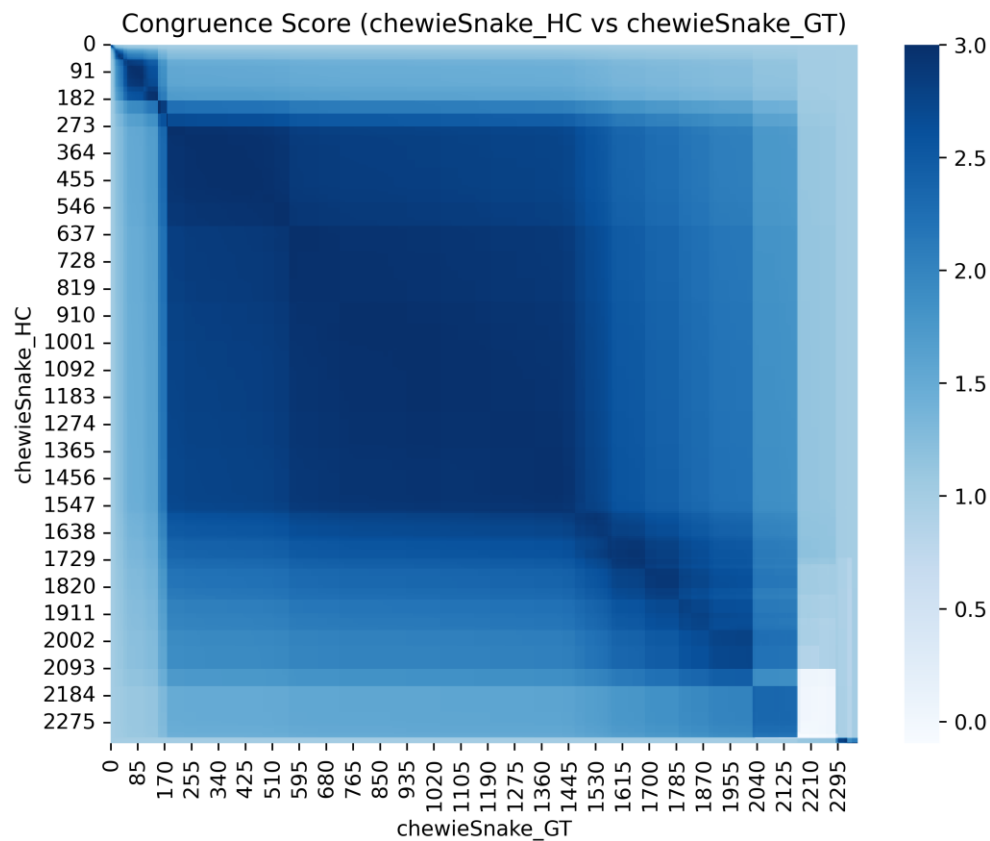


Figure S2.1.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

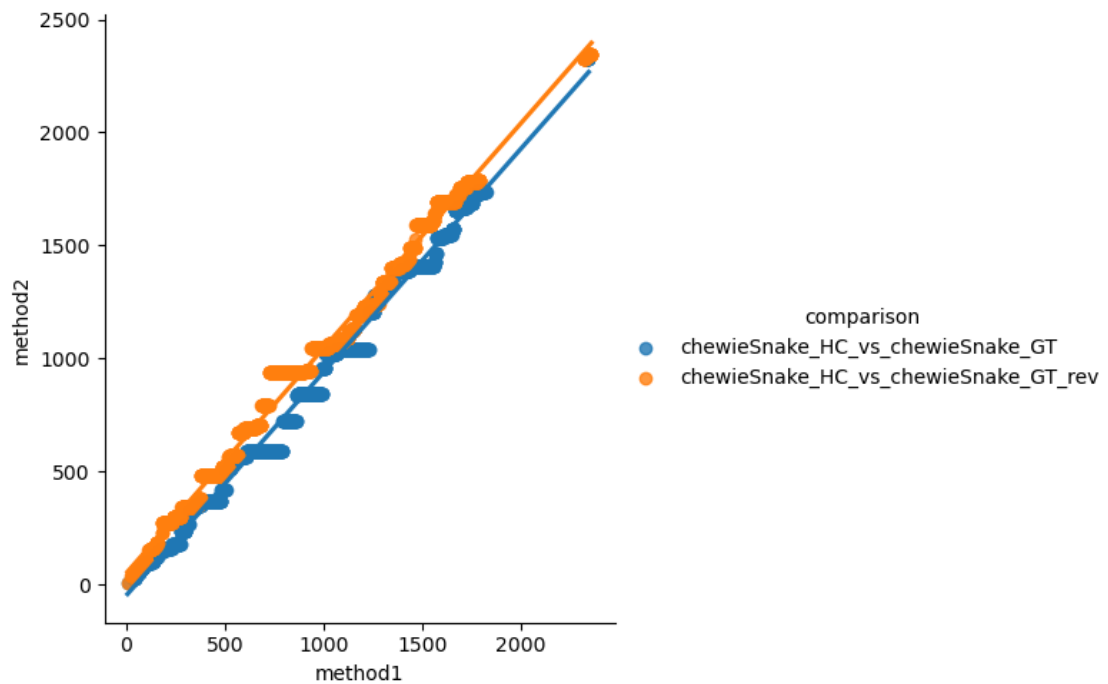


Figure S2.1.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1803 (blue) and 1770 (orange) points is presented.

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

	chewieSnake single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2274	2359

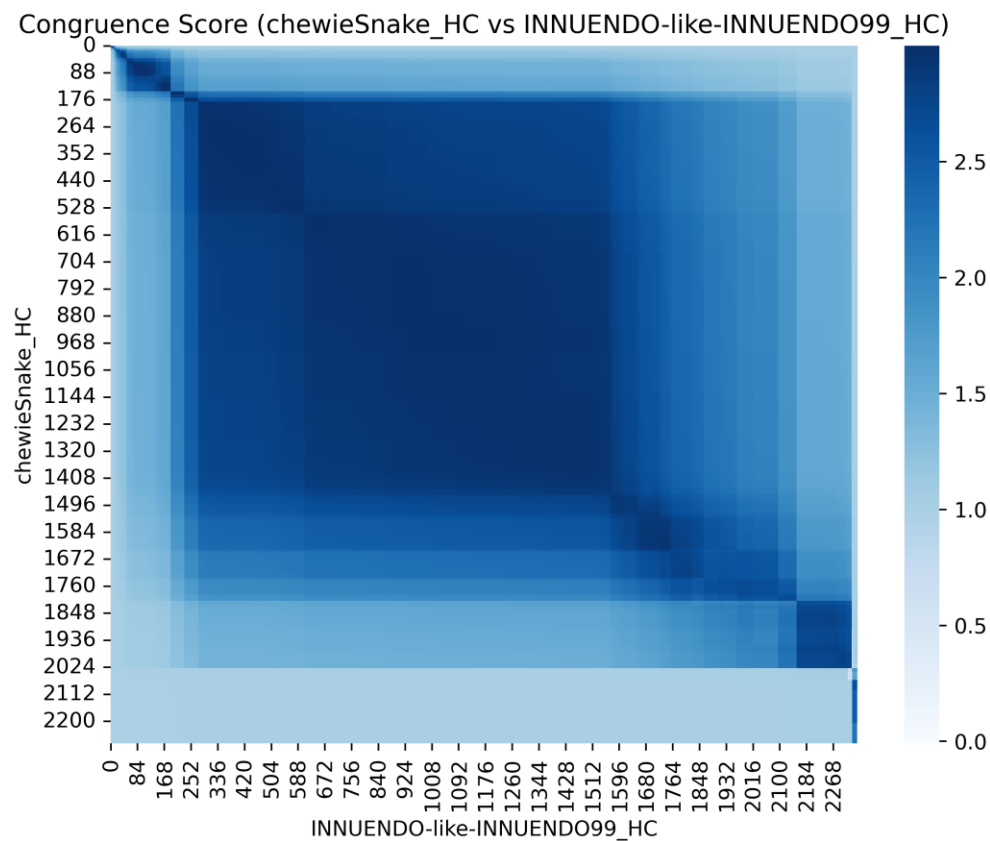


Figure S2.2.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

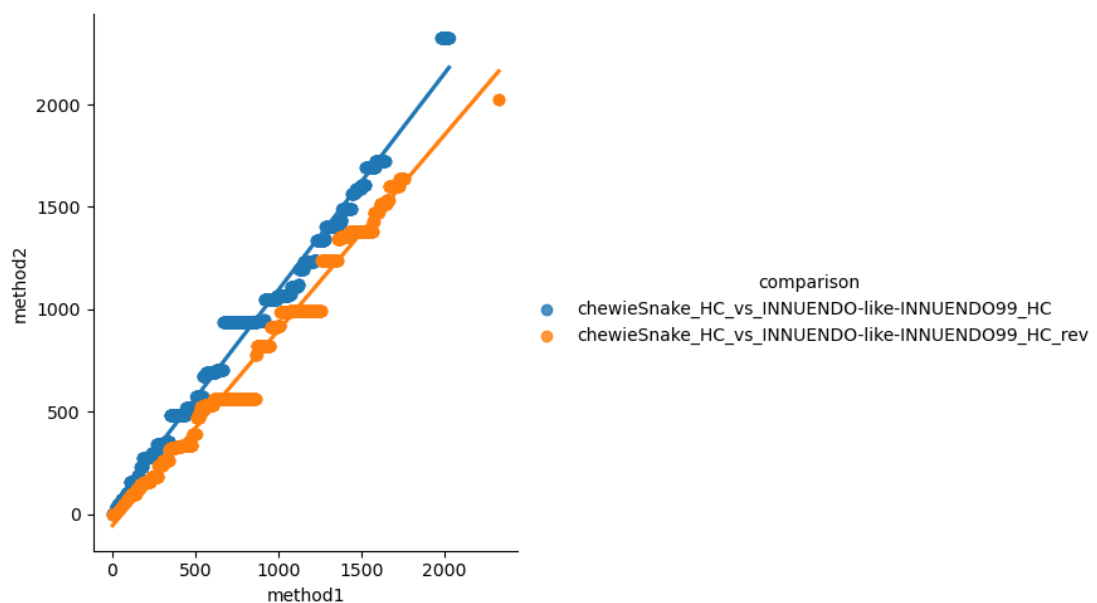


Figure S2.2.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1659 (blue) and 1734 (orange) points is presented.

3. chewieSnake GrapeTree 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.

	chewieSnake GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2346	2359

Section 2 – Comparison of allele-based pipelines

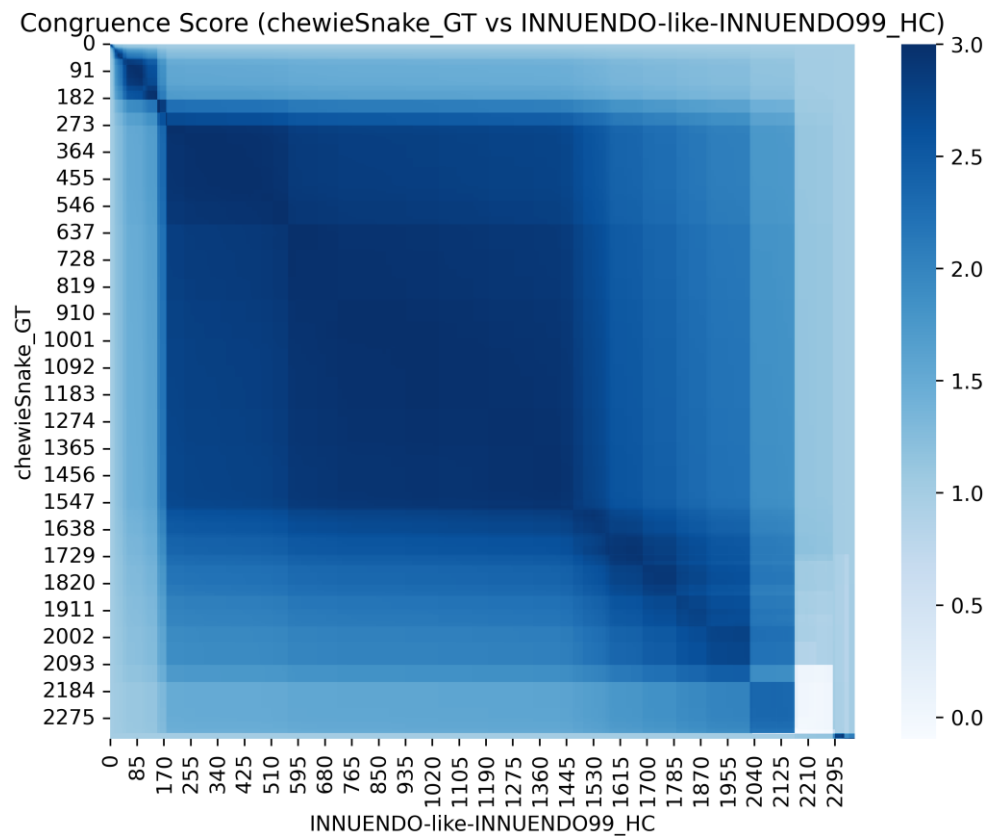


Figure S2.3.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

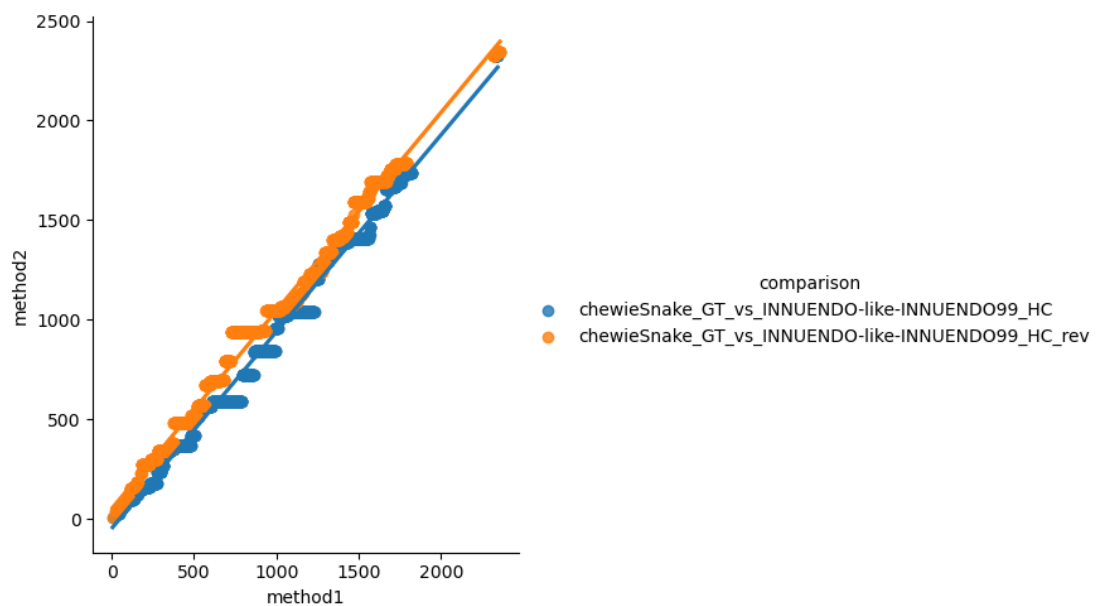


Figure S2.3.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1800 (blue) and 1771 (orange) points is presented.

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

	INNUENDO-like-EFSA GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions		2346

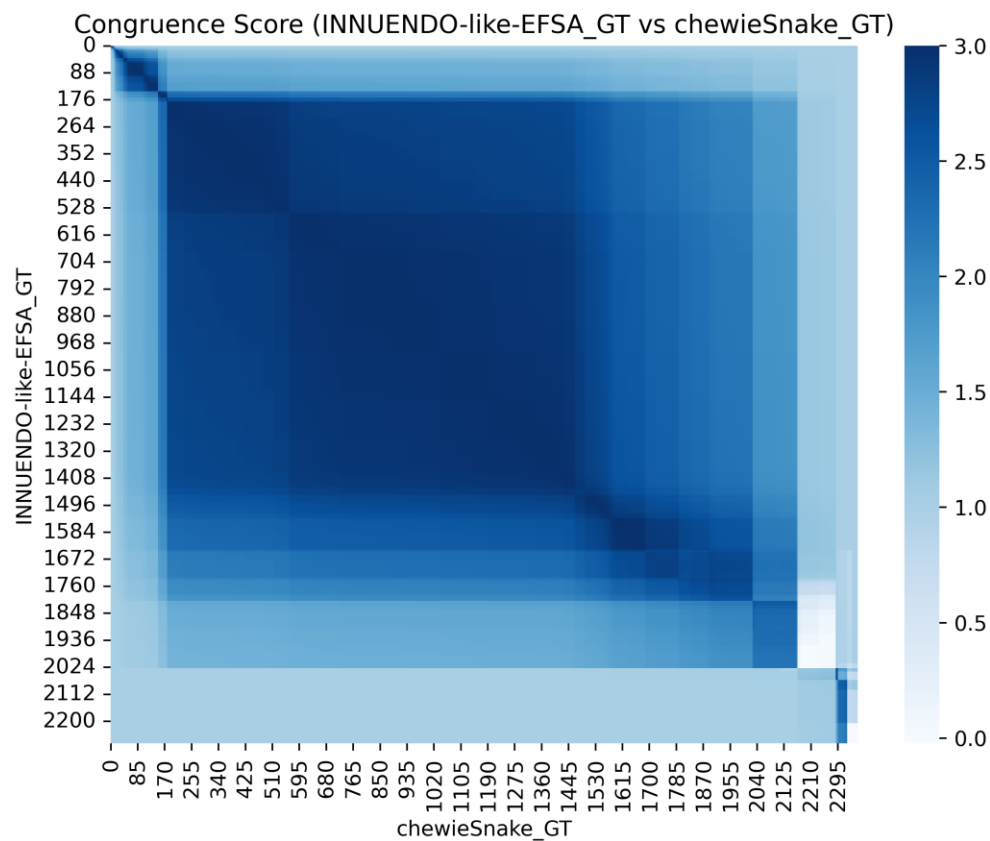


Figure S2.4.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

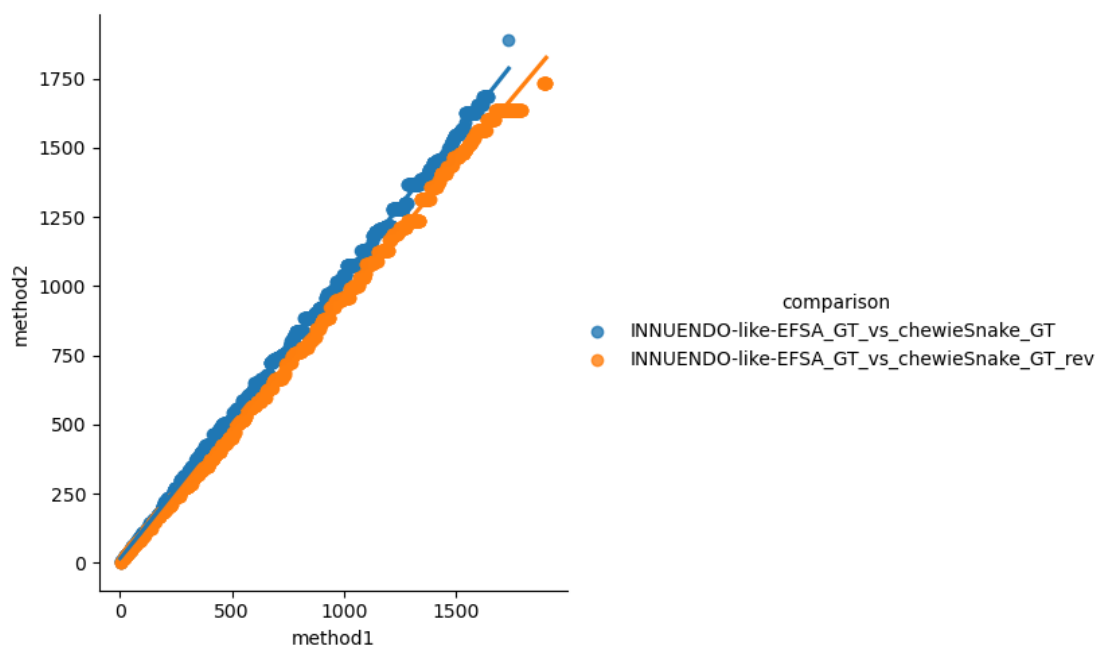


Figure S2.4.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1634 (blue) and 1795 (orange) points is presented.

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

	INNUENDO-like-EFSA GrapeTree	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions		2274

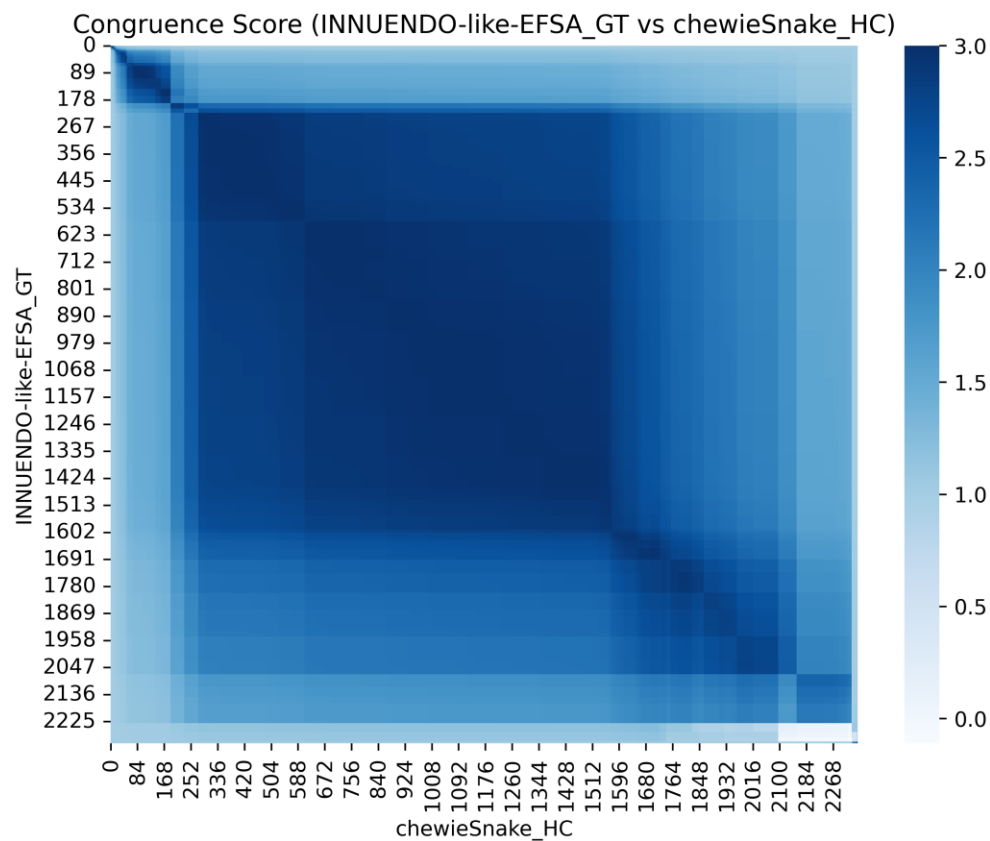


Figure S2.5.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

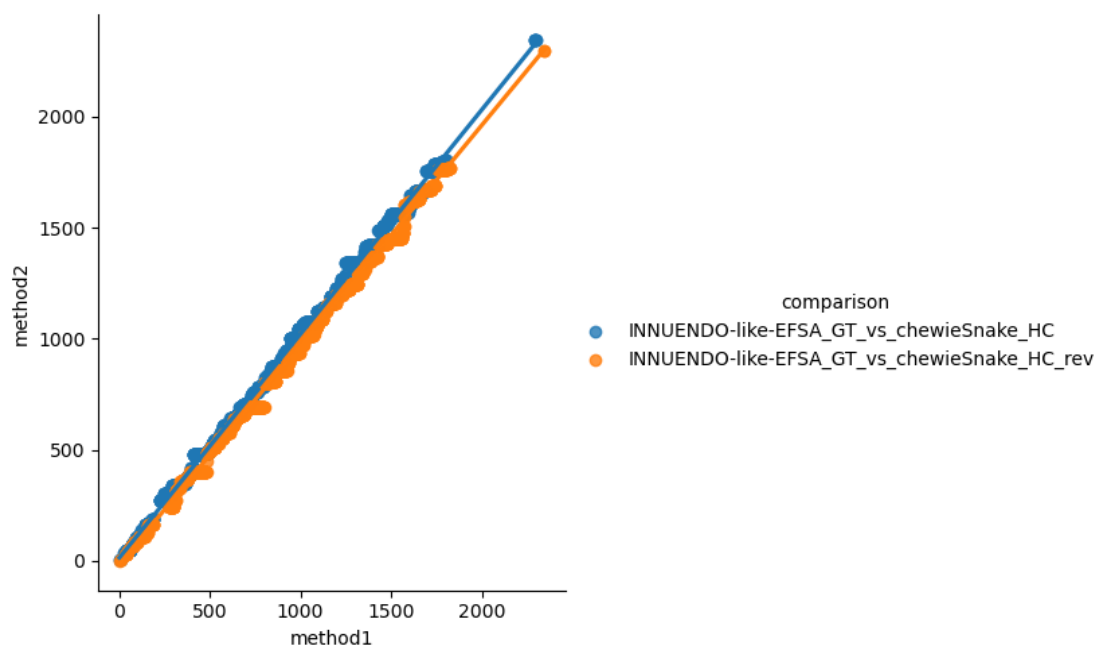


Figure S2.5.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1747 (blue) and 1677 (orange) points is presented.

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

	INNUENDO-like-EFSA GrapeTree	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions		2388

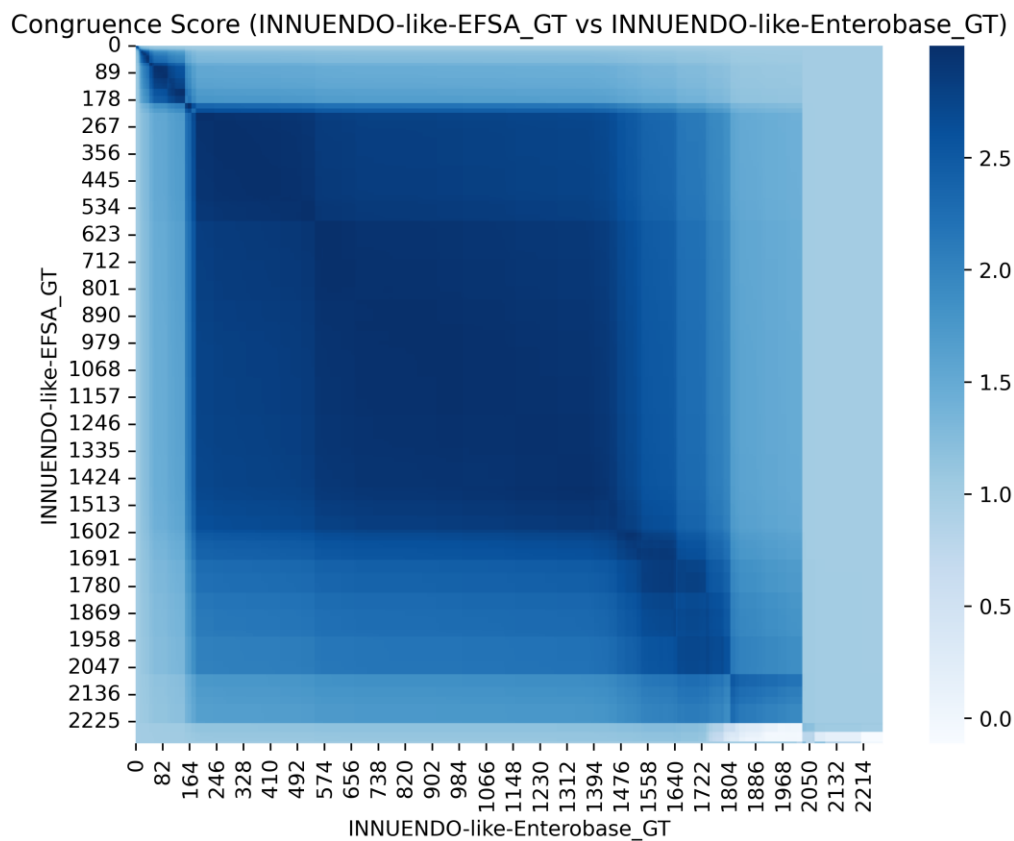


Figure S2.6.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

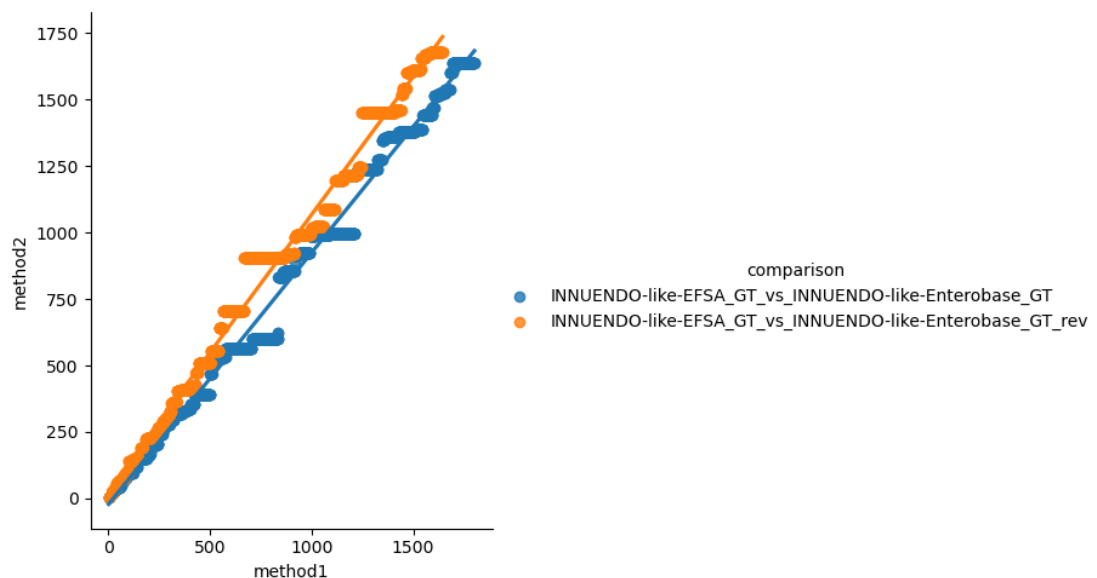


Figure S2.6.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1770 (blue) and 1604 (orange) points is presented.

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

	INNUENDO-like-EFSA GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions		2359

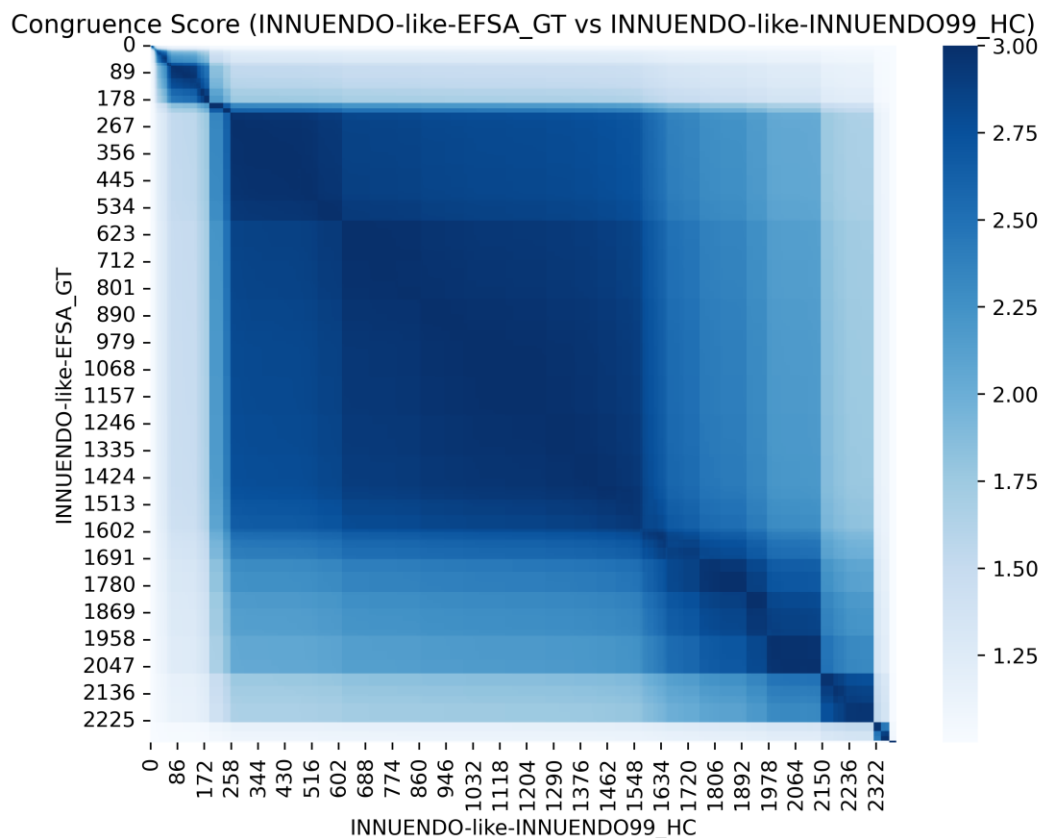


Figure S2.7.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

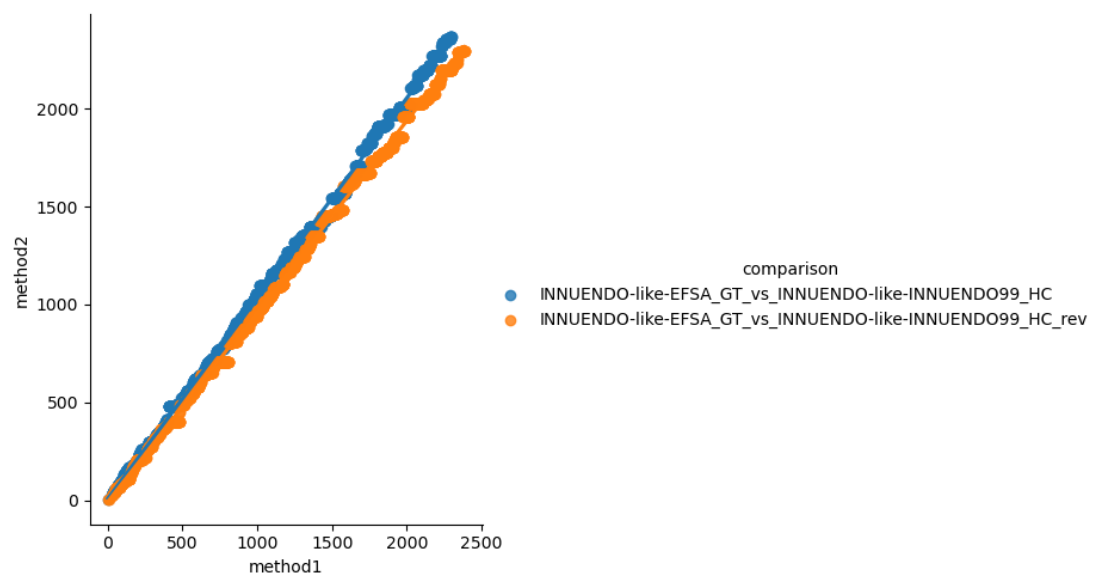


Figure S2.7.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2267 (blue) and 2355 (orange) points is presented.

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

	INNUENDO-like-EFSA single-linkage	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions		2346

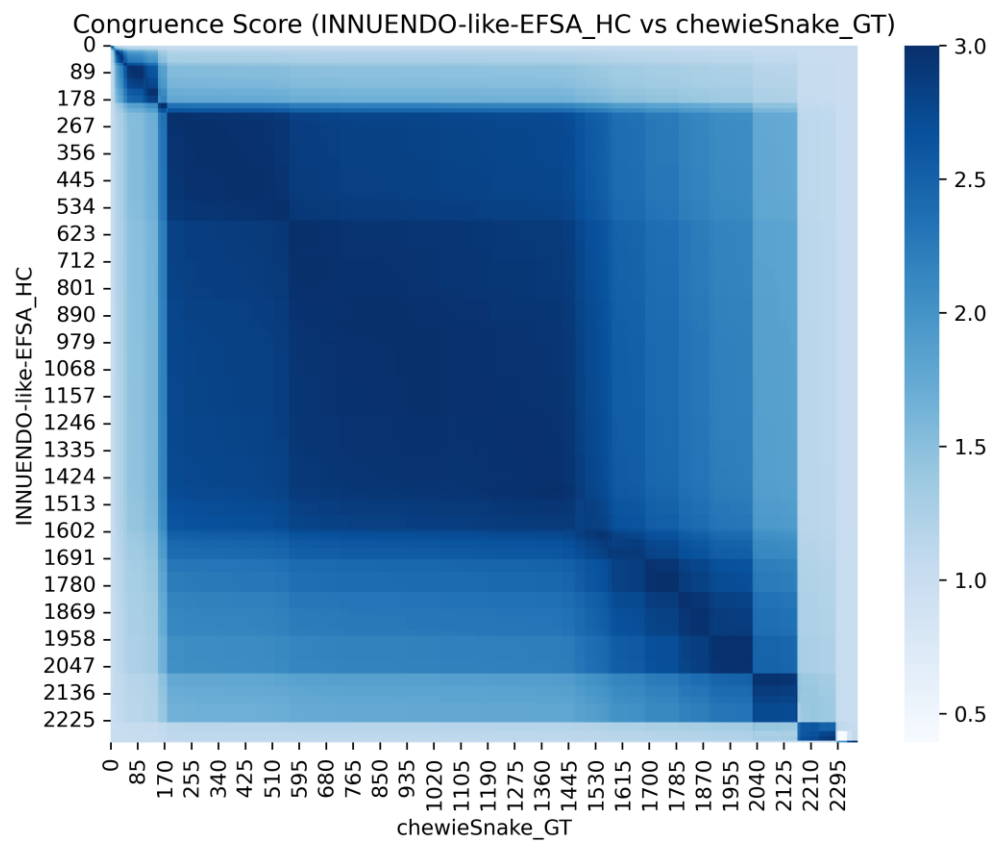


Figure S2.8.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

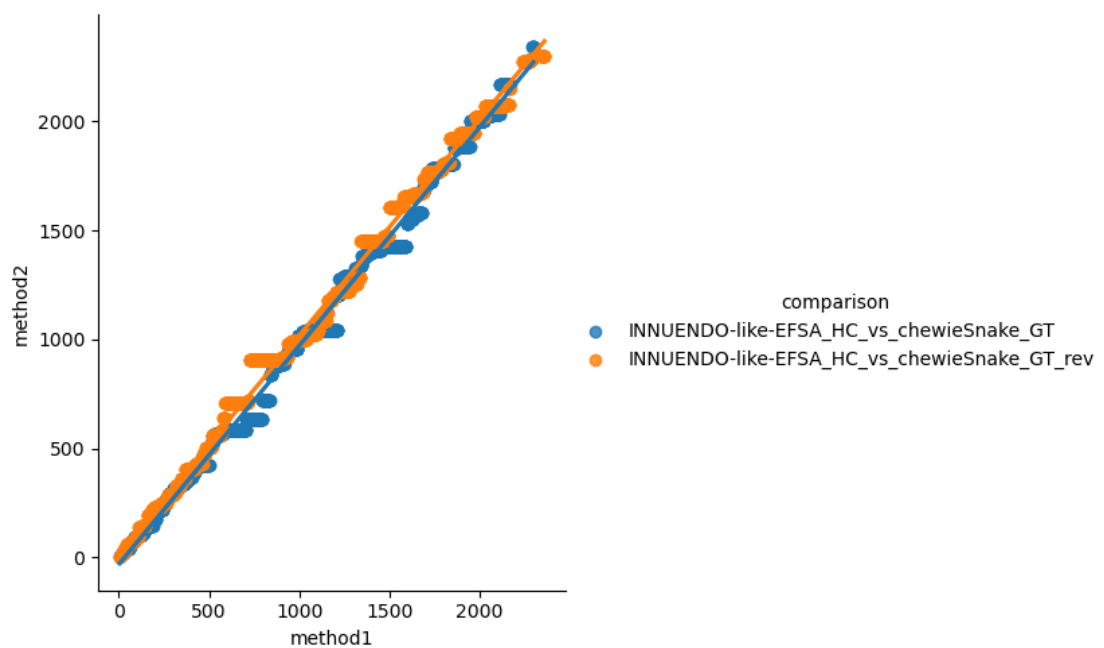


Figure S2.8.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2157 (blue) and 2209 (orange) points is presented.

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

	INNUENDO-like-EFSA single-linkage	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions		2274

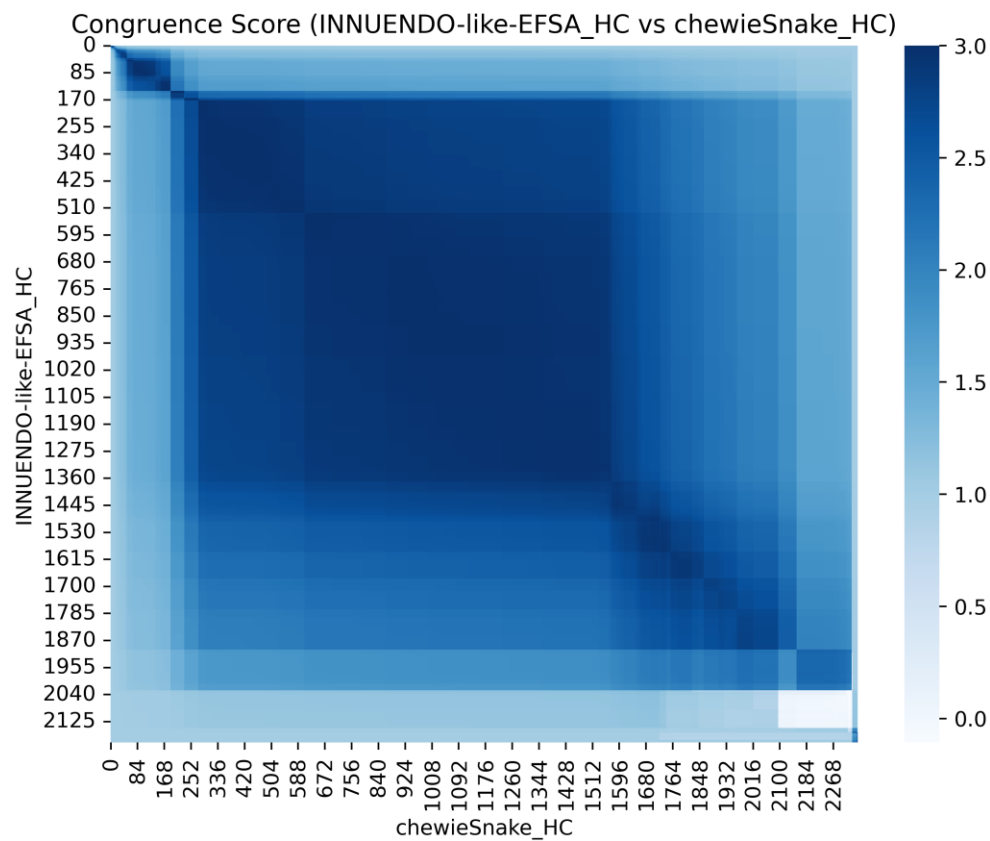


Figure S2.9.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

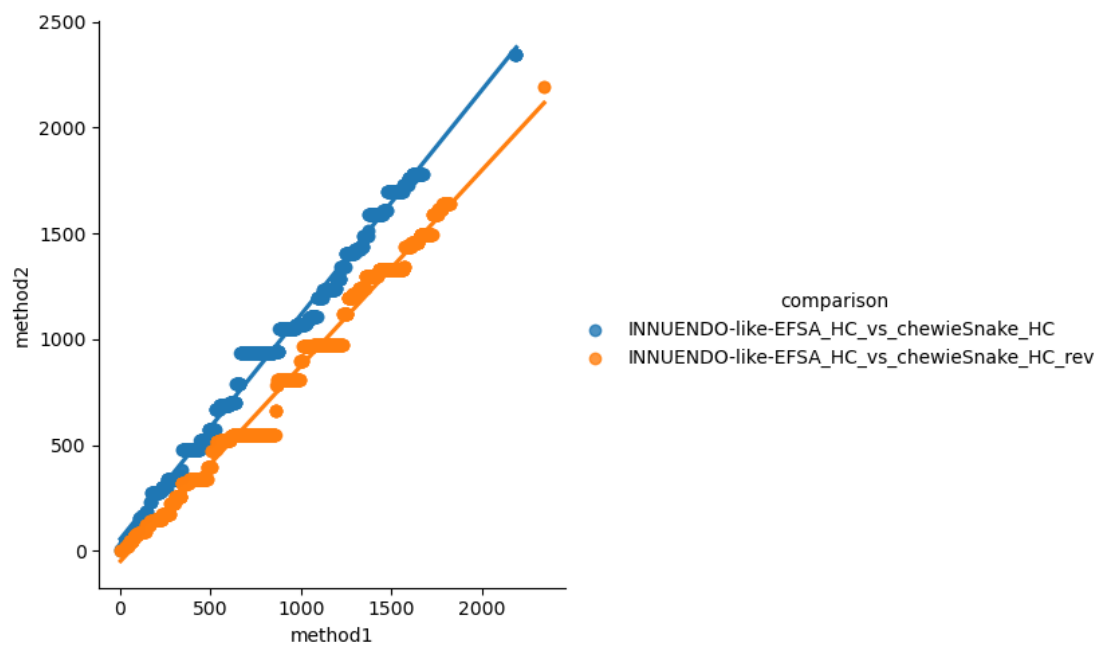


Figure S2.9.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1638 (blue) and 1788 (orange) points is presented.

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

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

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

Section 2 – Comparison of allele-based pipelines

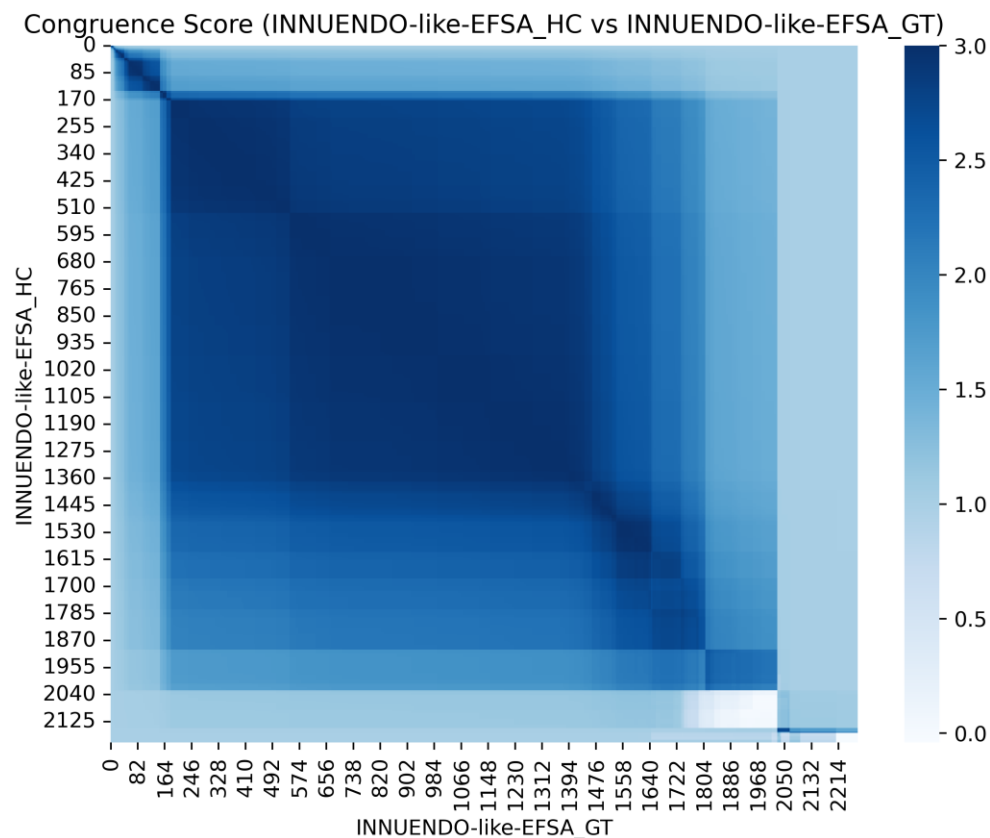


Figure S2.10.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

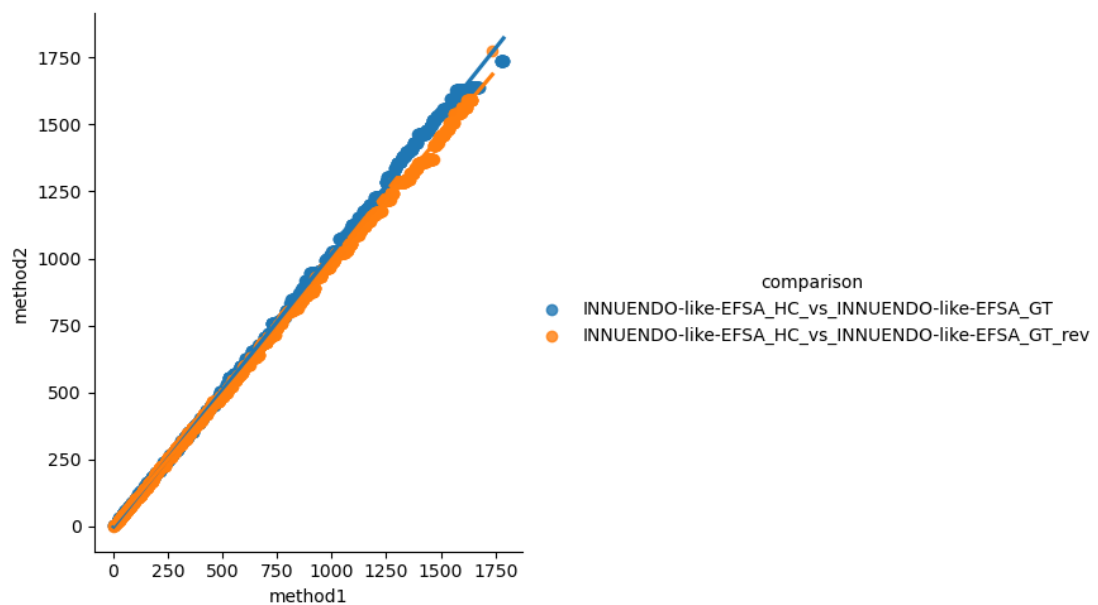


Figure S2.10.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1679 (blue) and 1633 (orange) points is presented.

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

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

	INNUENDO-like-EFSA single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	EFSA	Enterobase
Dataset	All samples	All samples
Number partitions		2388

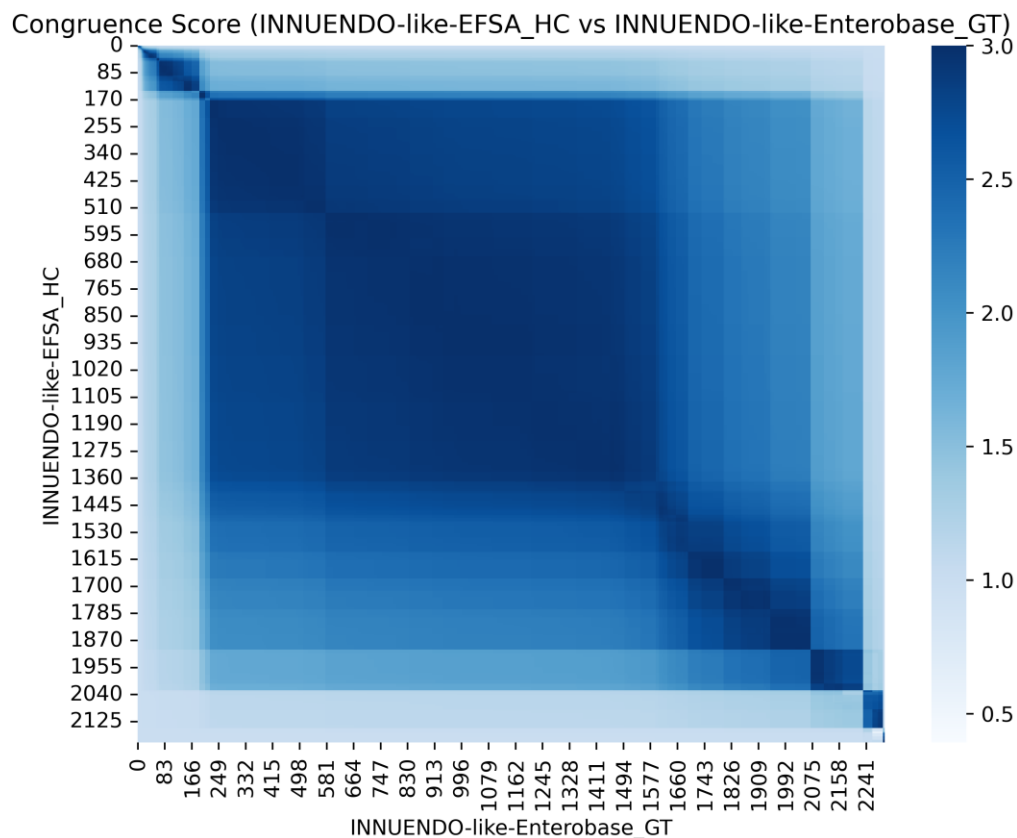


Figure S2.11.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

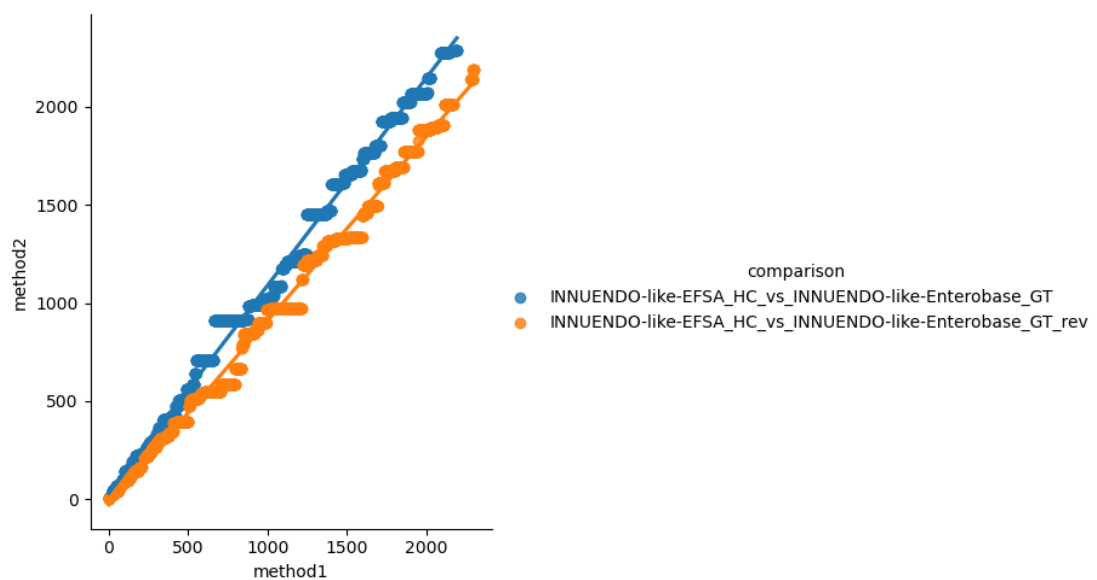


Figure S2.11.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2068 (blue) and 2158 (orange) points is presented.

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

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

	INNUENDO-like-EFSA single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	EFSA	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions		2359

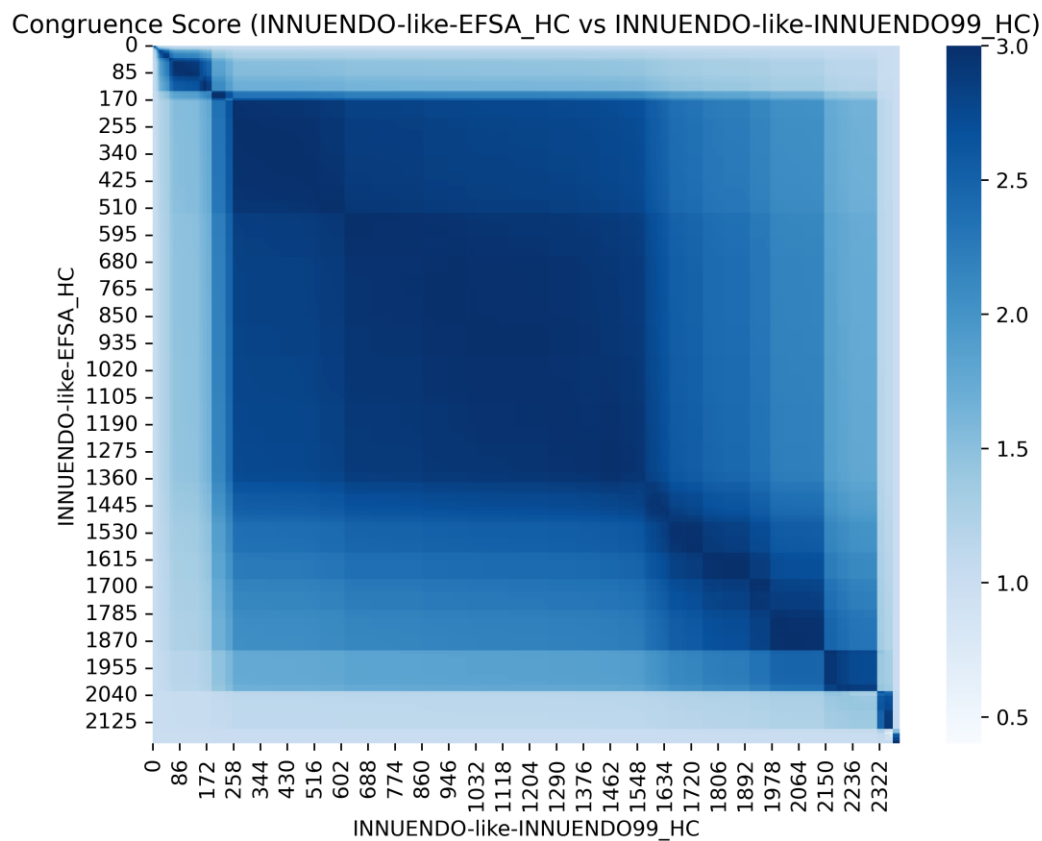


Figure S2.12.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

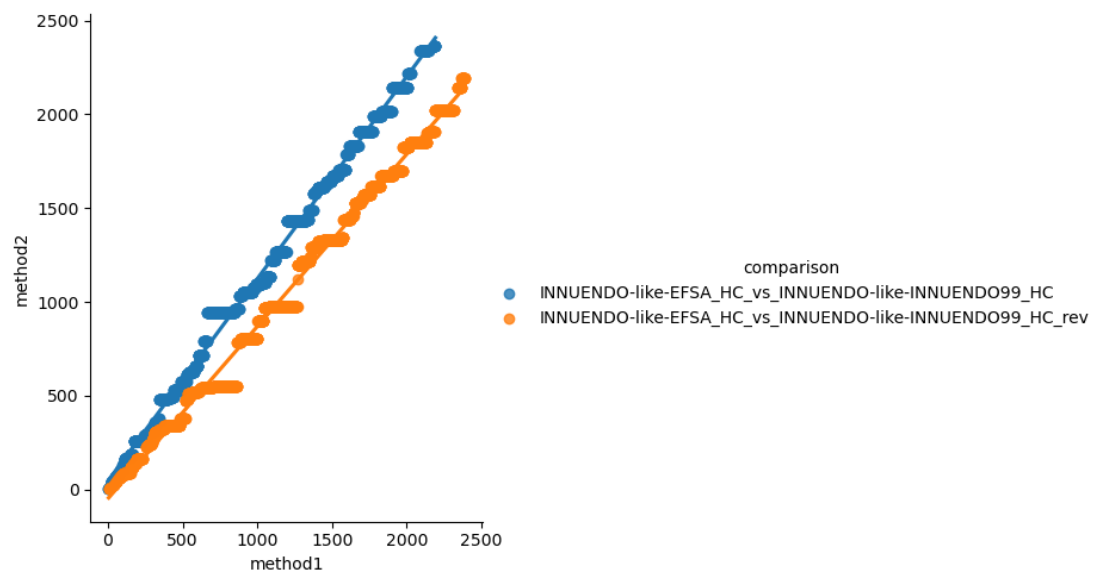


Figure S2.12.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2050 (blue) and 2309 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase GrapeTree	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2388	2346

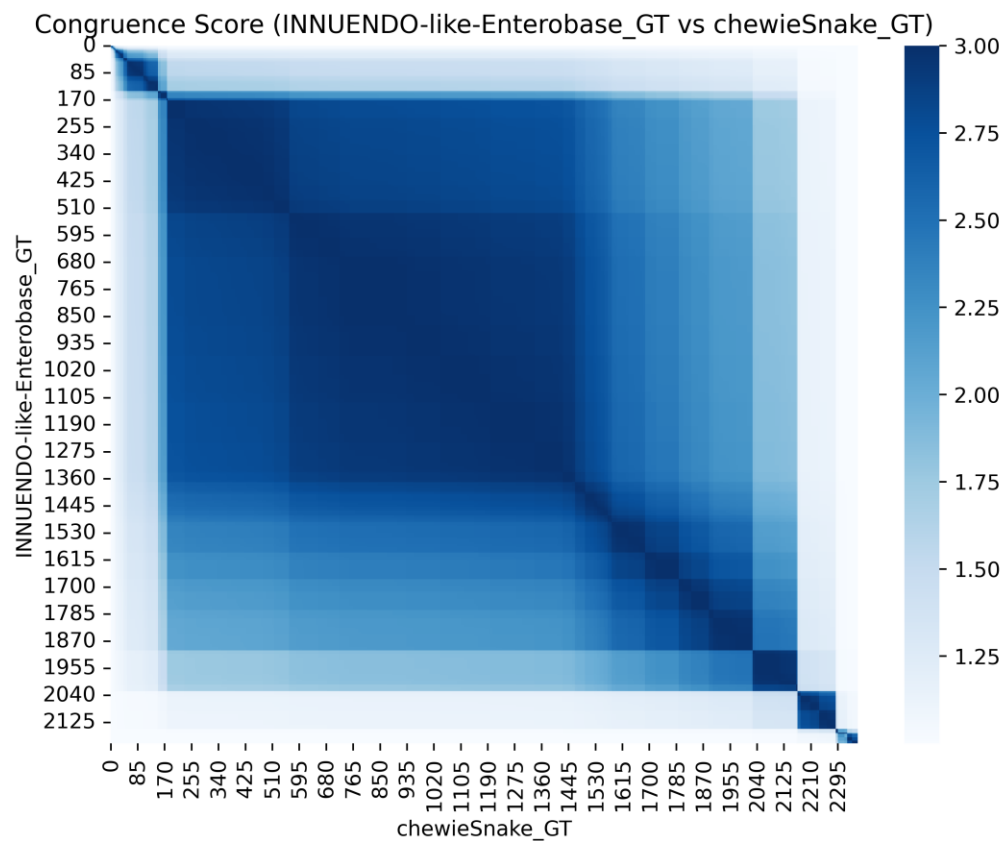


Figure S2.13.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

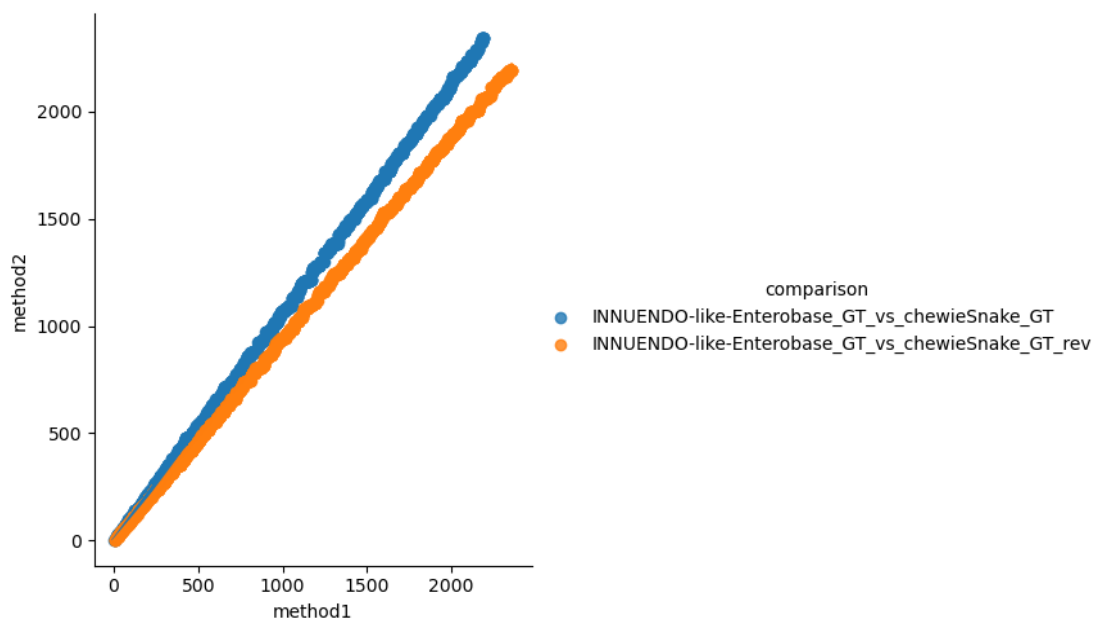


Figure S2.13.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2159 (blue) and 2344 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase GrapeTree	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2388	2274

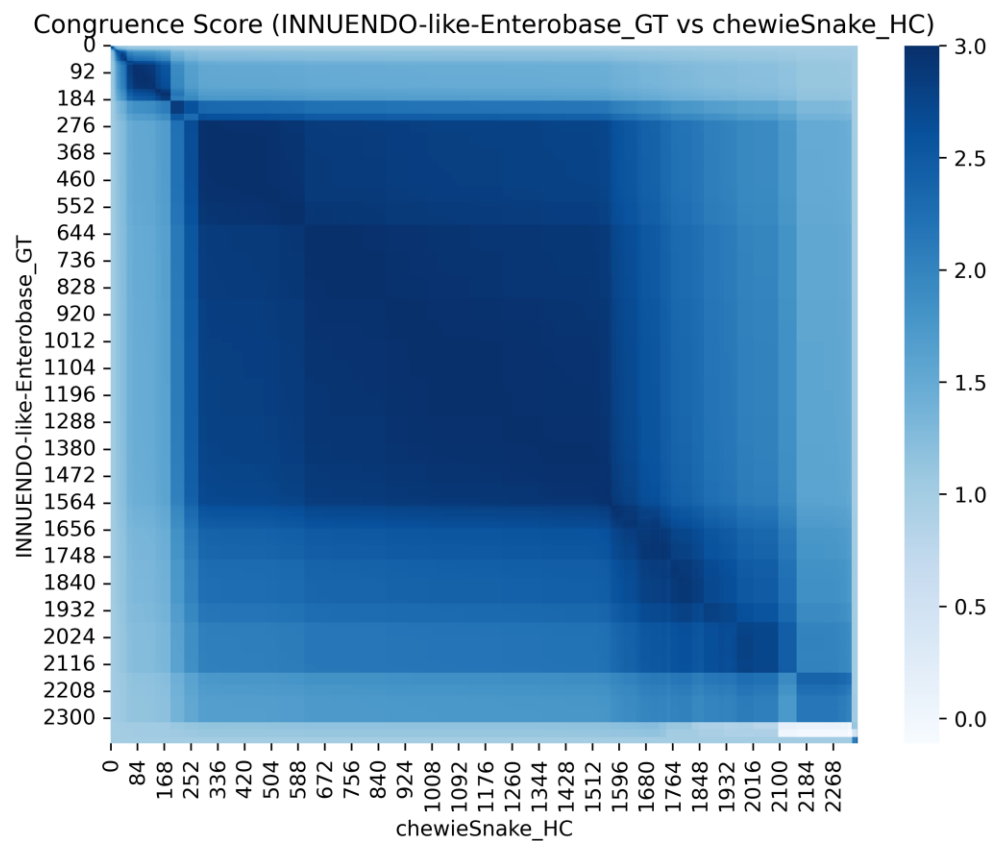


Figure S2.14.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

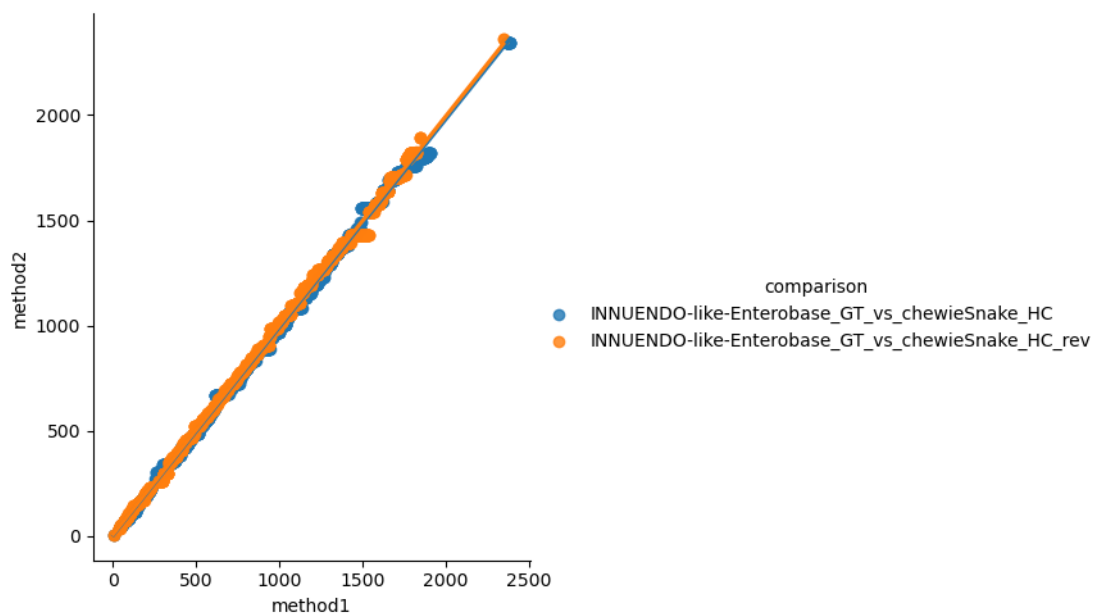


Figure S2.14.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1862 (blue) and 1738 (orange) points is presented.

15. INNUENDO-like-Enterobase GrapeTree 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.

	INNUENDO-like-Enterobase GrapeTree	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2388	2359

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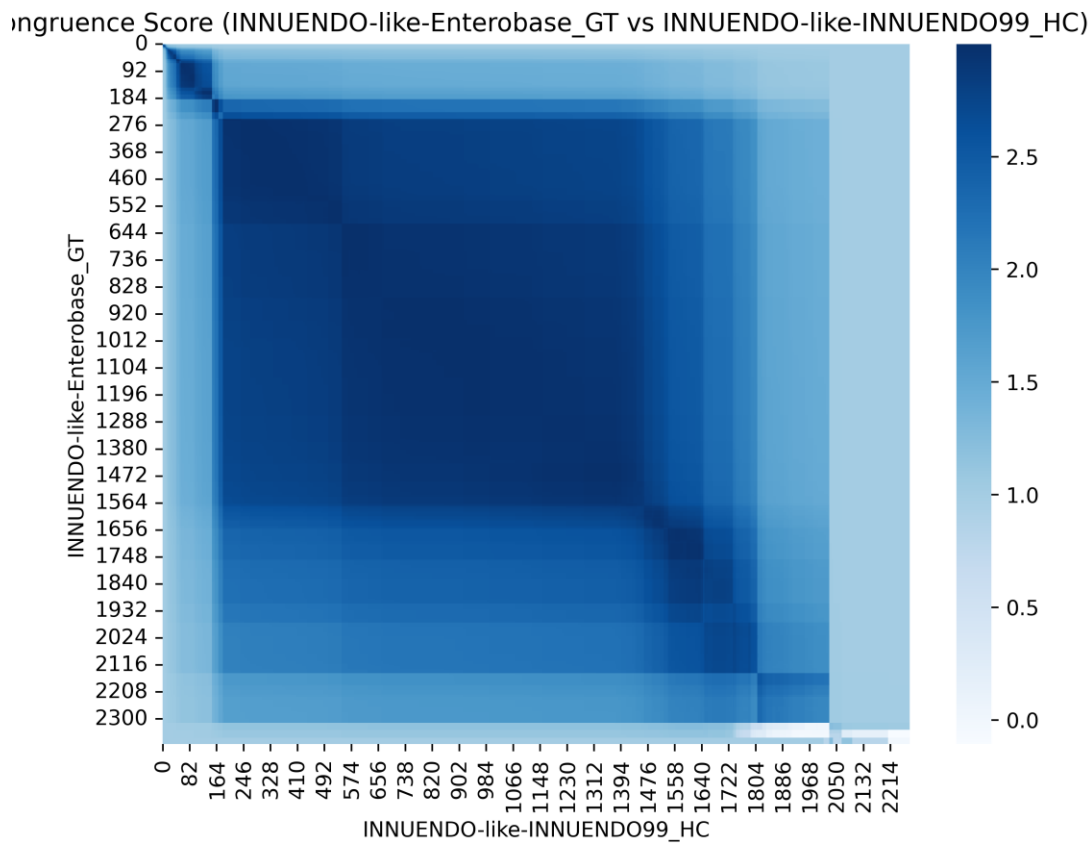


Figure S2.15.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

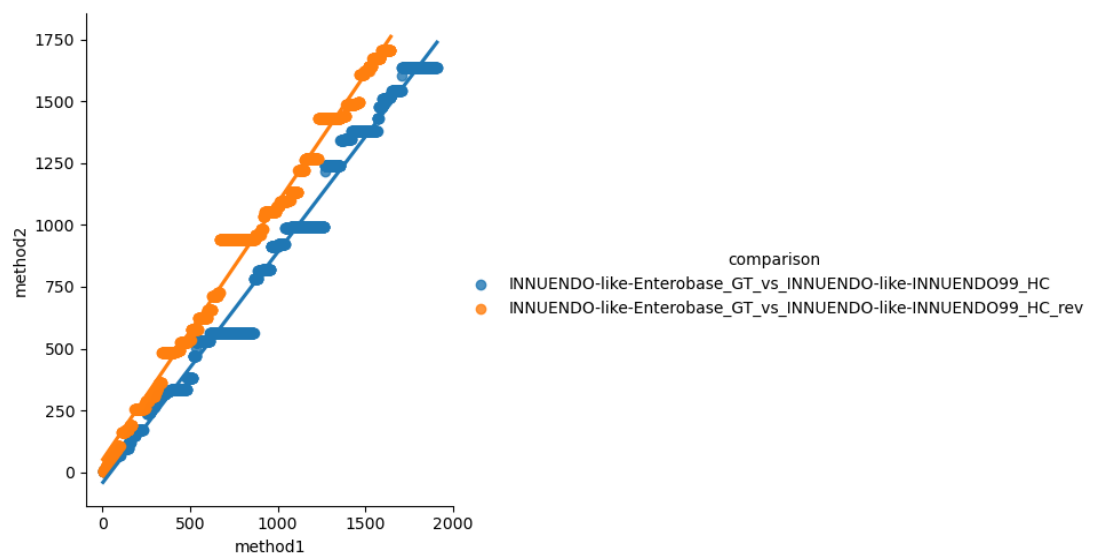


Figure S2.15.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1864 (blue) and 1599 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	chewieSnake GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2309	2346

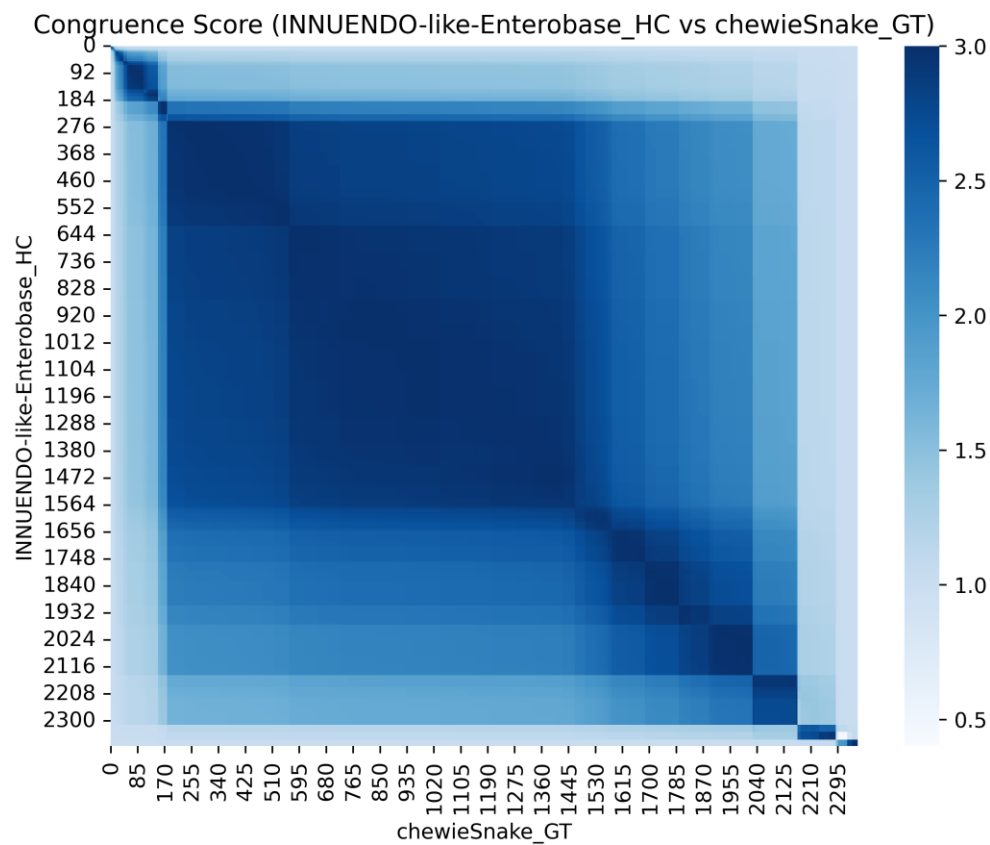


Figure S2.16.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

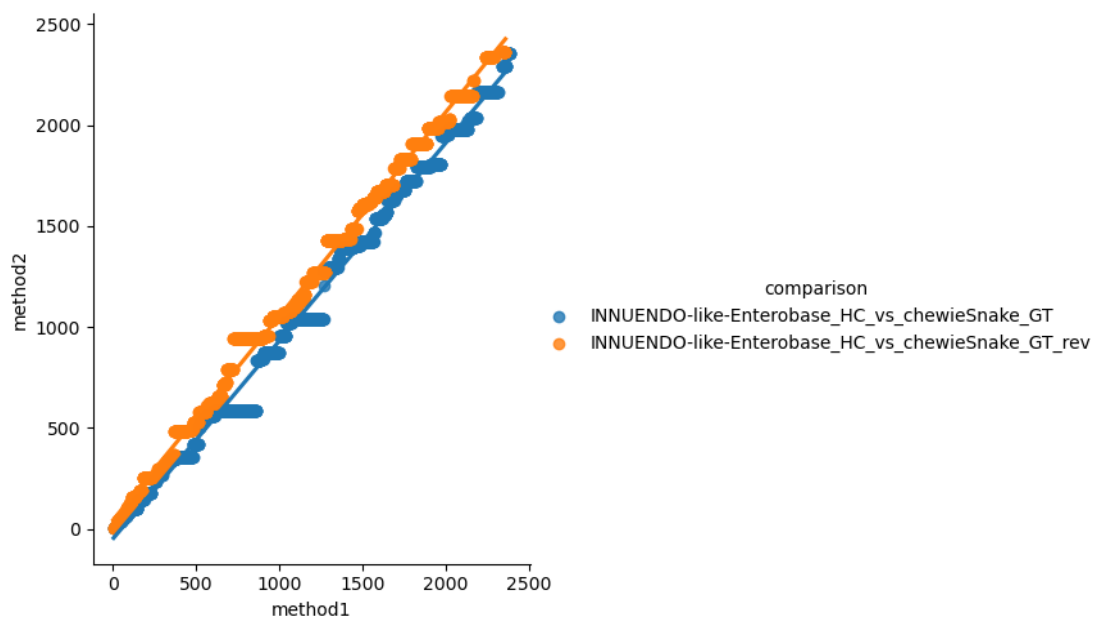


Figure S2.16.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2316 (blue) and 2204 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2309	2274

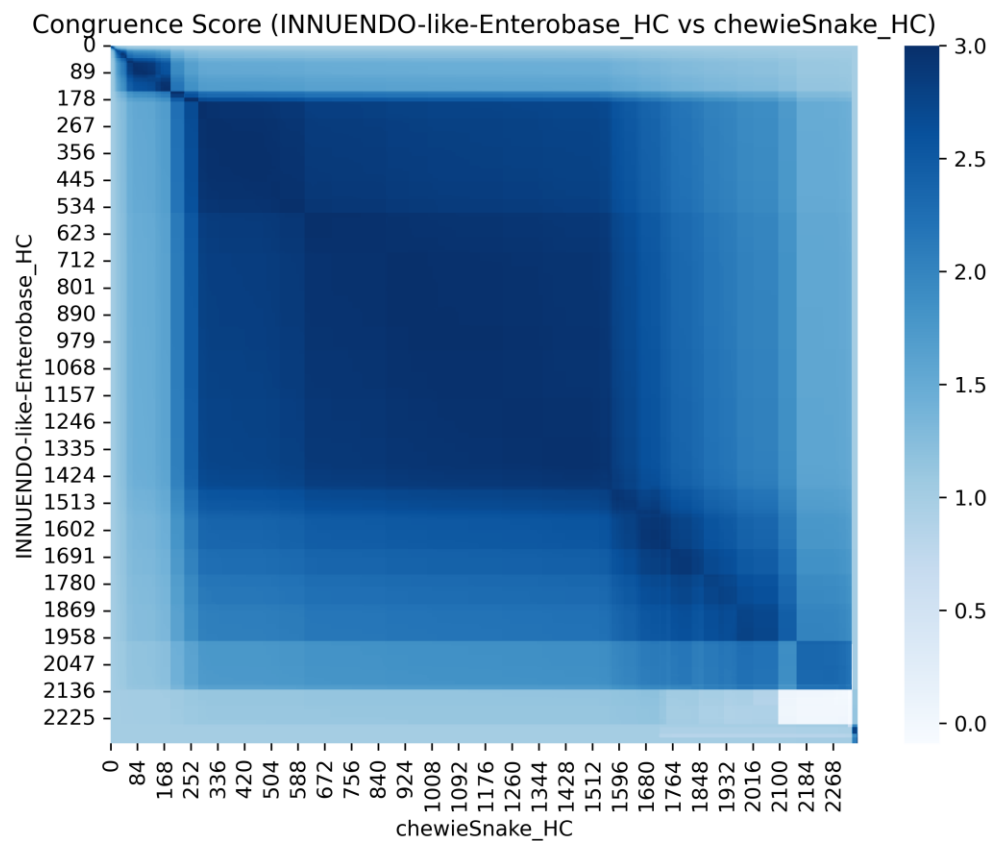


Figure S2.17.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

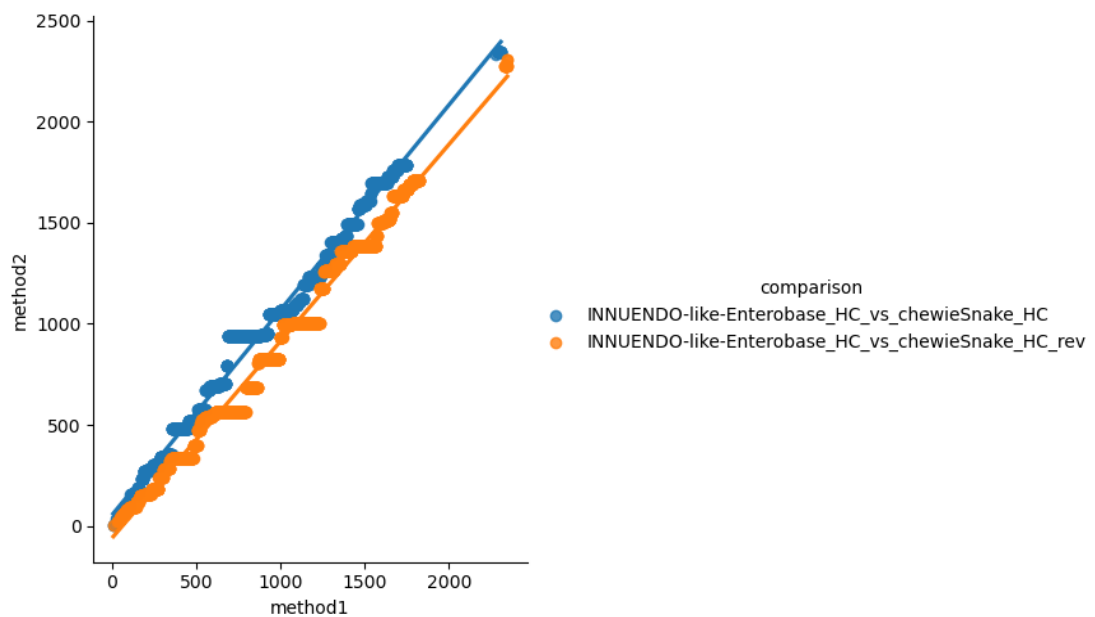


Figure S2.17.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1725 (blue) and 1809 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-EFSA GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2309	

Section 2 – Comparison of allele-based pipelines

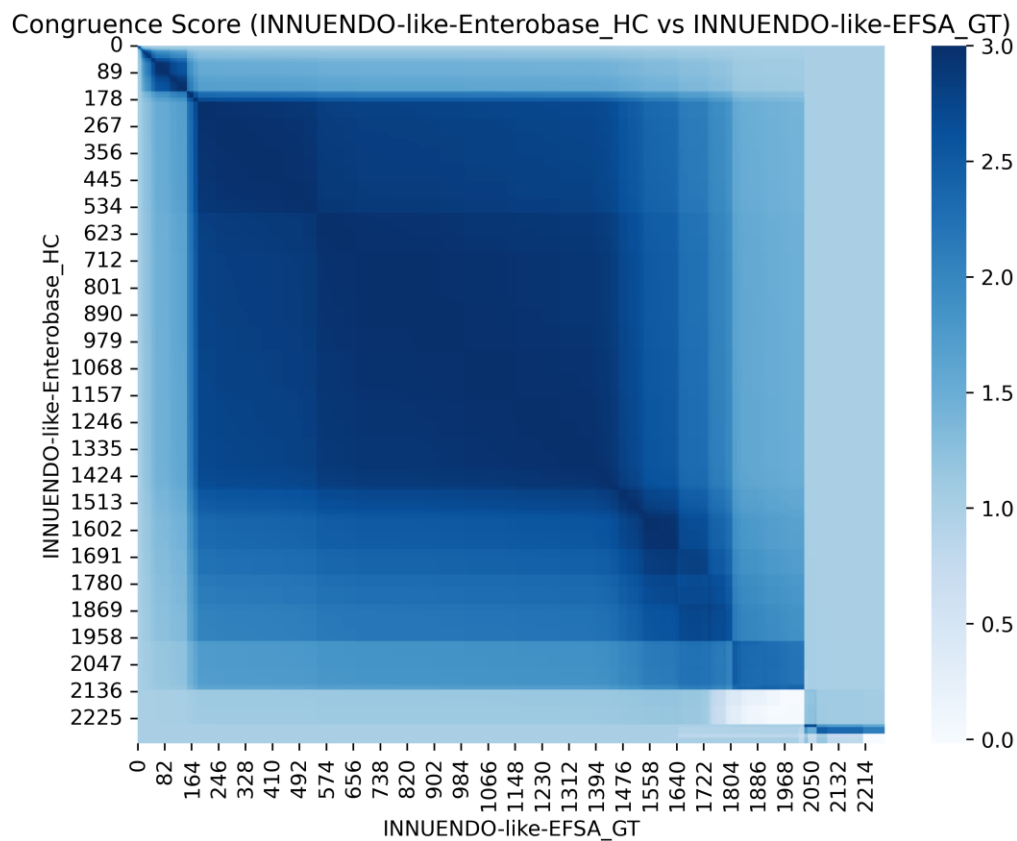


Figure S2.18.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

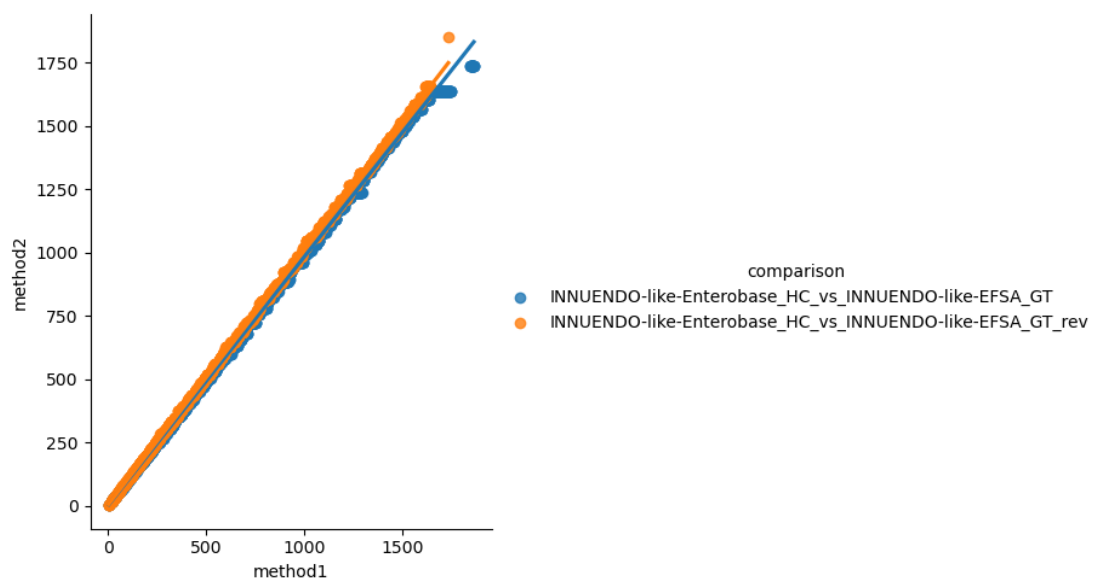


Figure S2.18.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1755 (blue) and 1633 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-EFSA single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2309	

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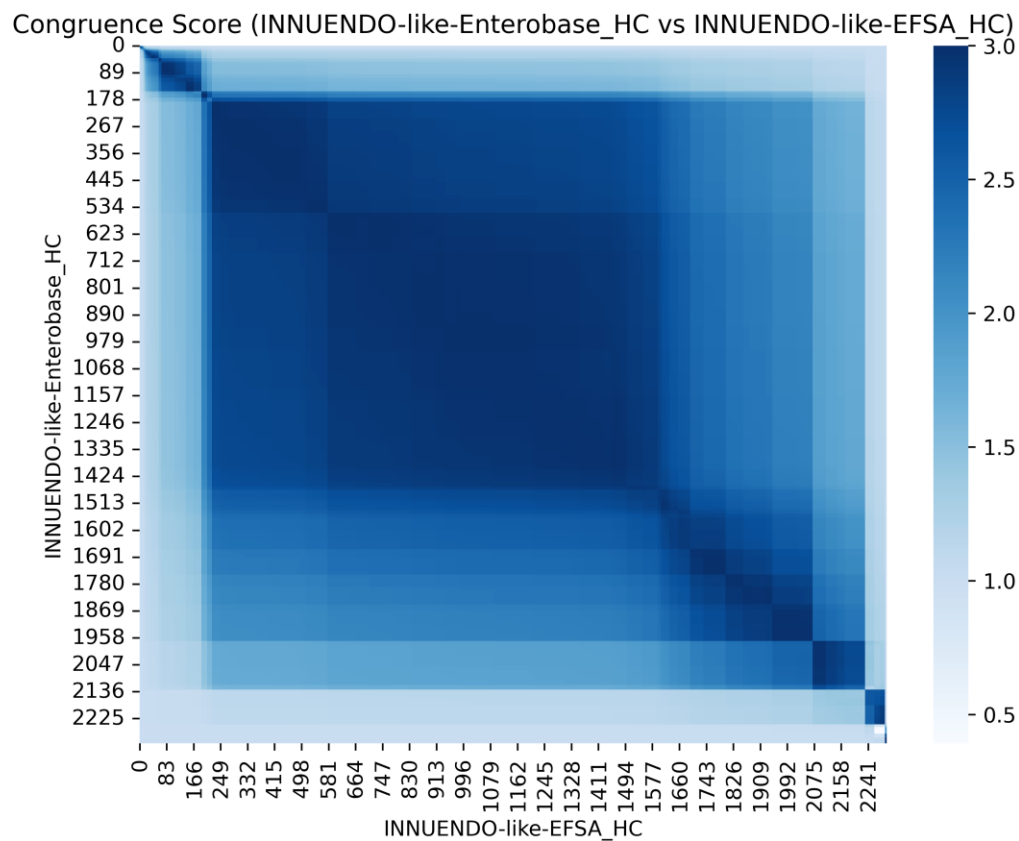


Figure S2.19.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

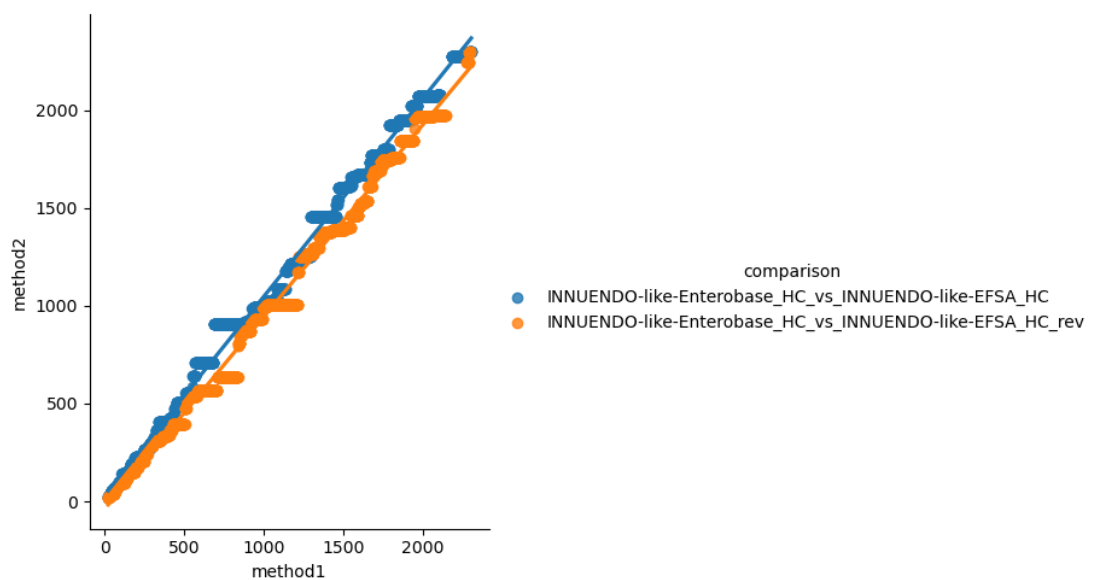


Figure S2.19.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2146 (blue) and 2126 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2309	2388

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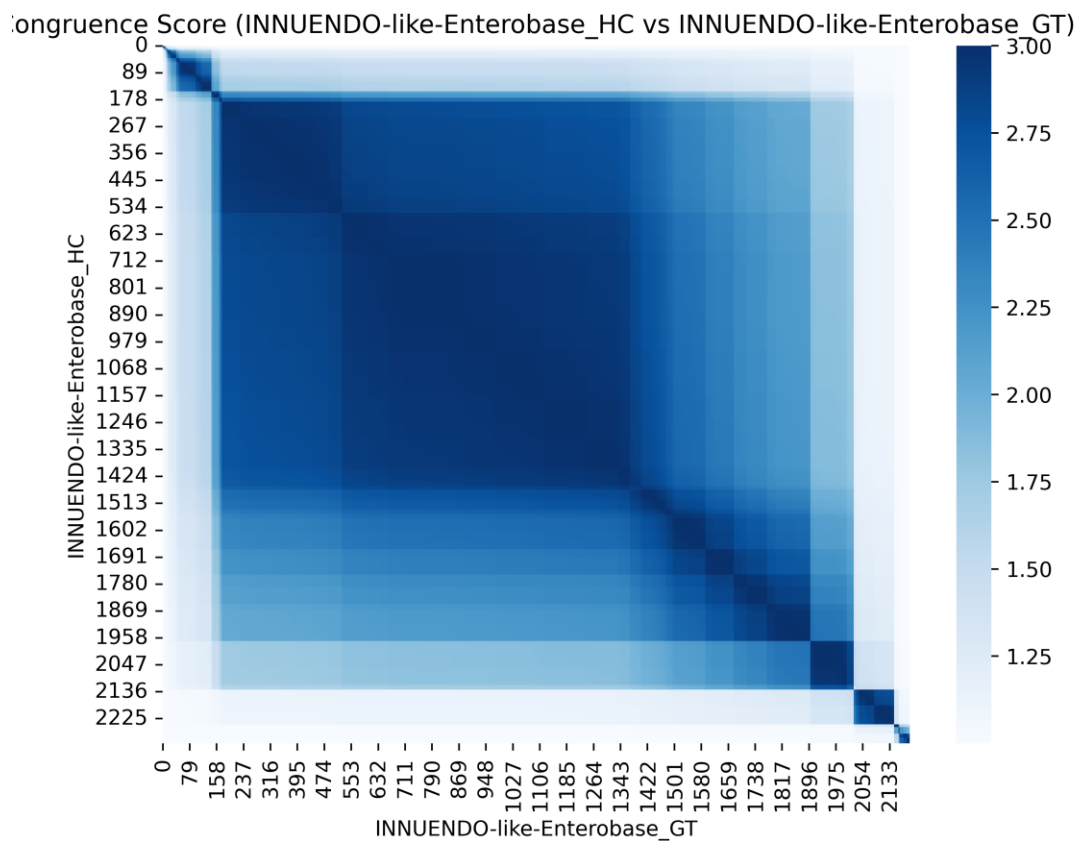


Figure S2.20.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

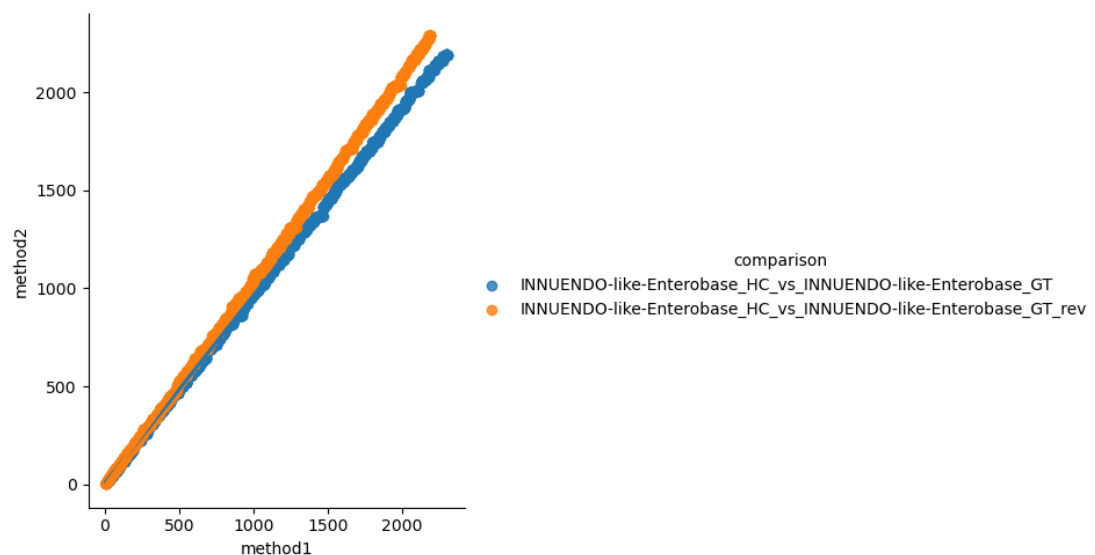


Figure S2.20.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2275 (blue) and 2156 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-INNUENDO99 GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2309	2388

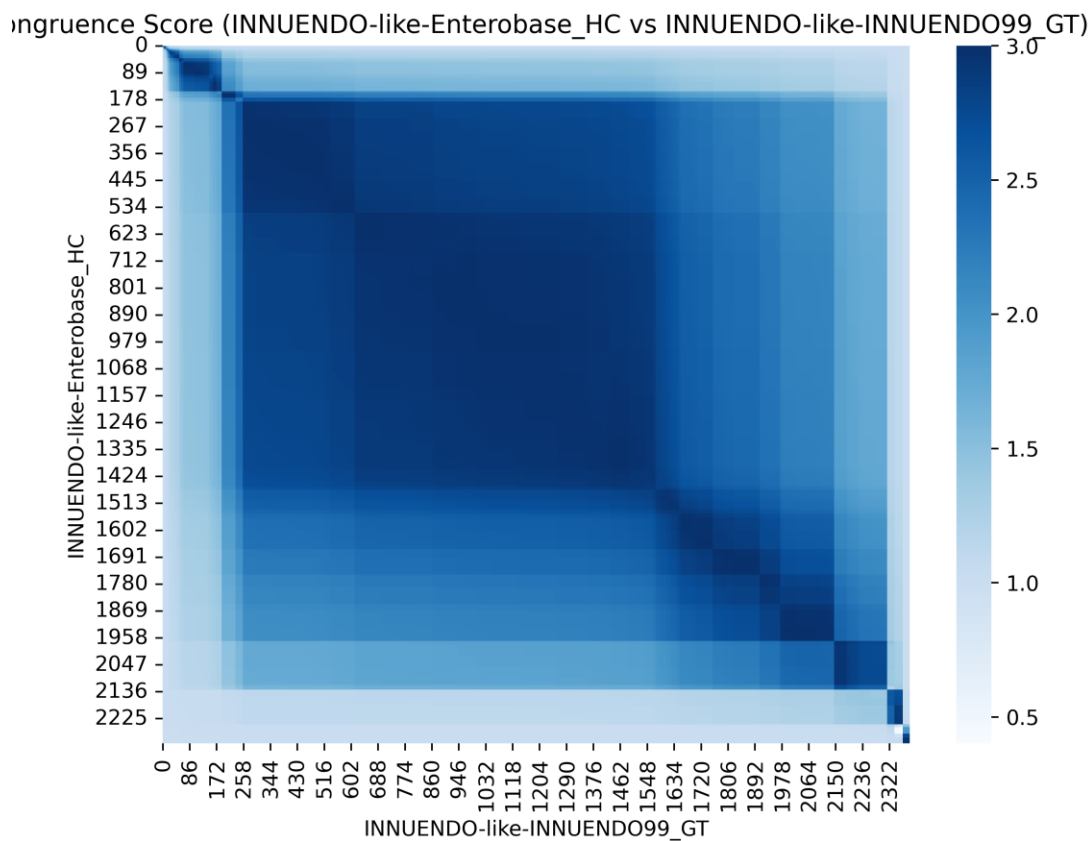


Figure S2.21.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

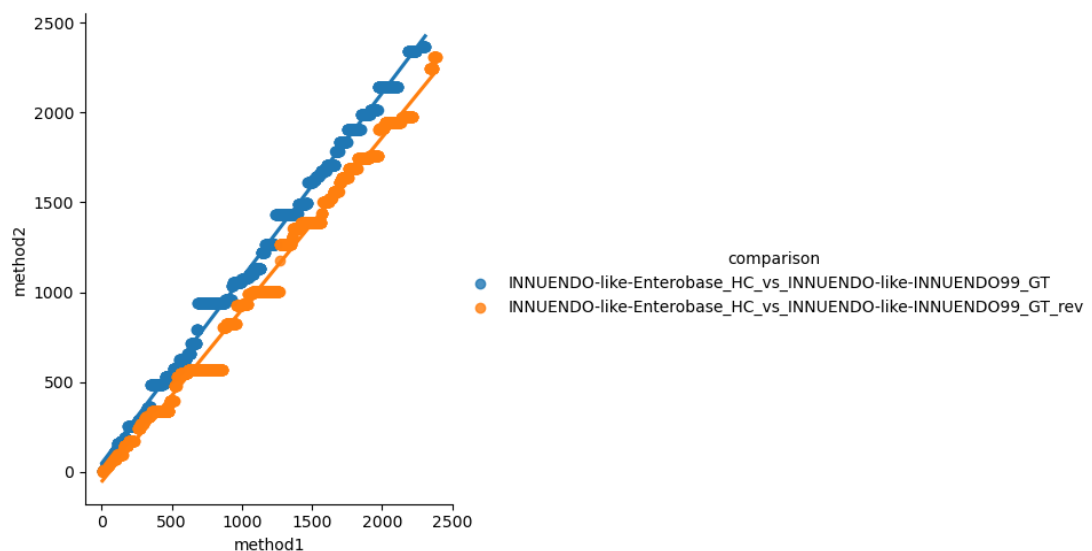


Figure S2.21.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 2153 (blue) and 2221 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2309	2388

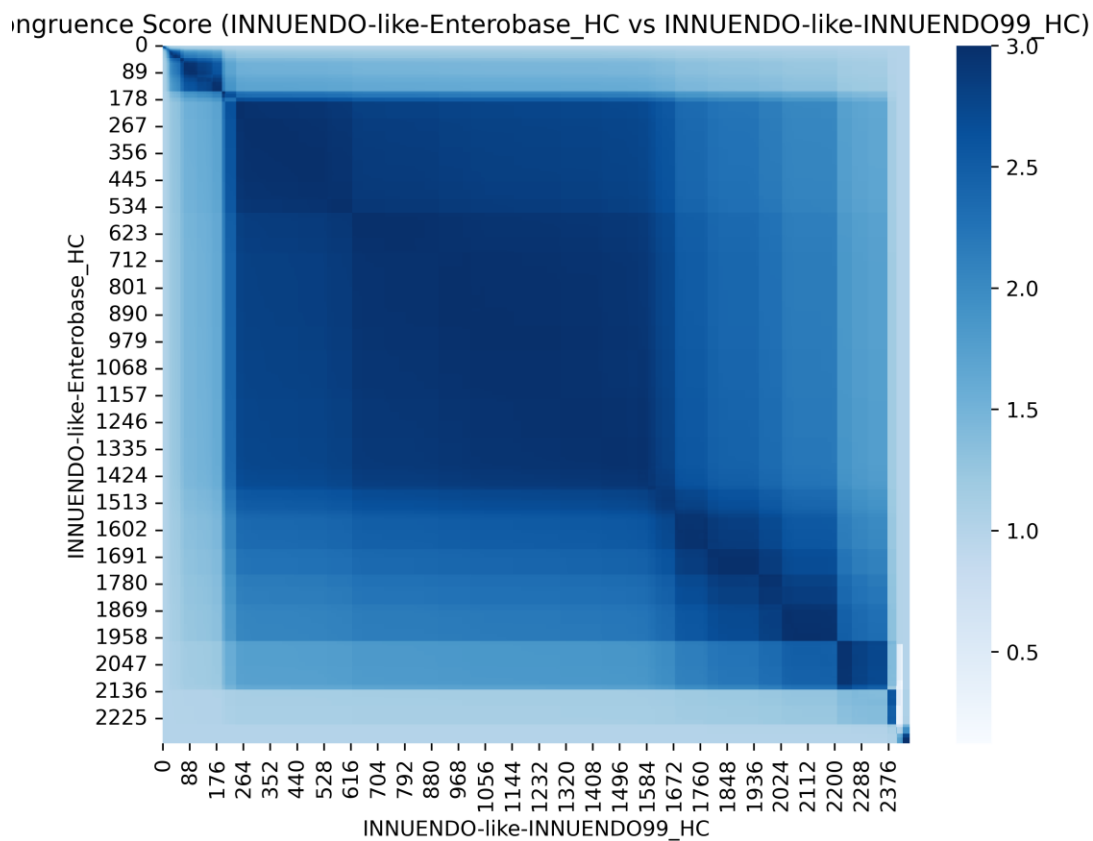


Figure S2.22.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

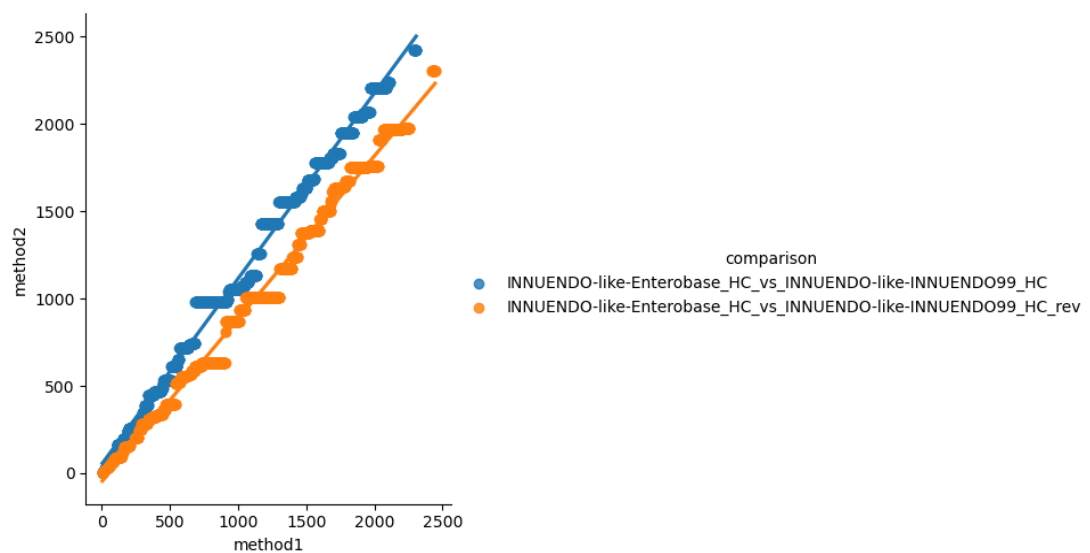


Figure S2.22.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 2086 (blue) and 2210 (orange) points is presented.

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

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 GrapeTree
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2447	2346

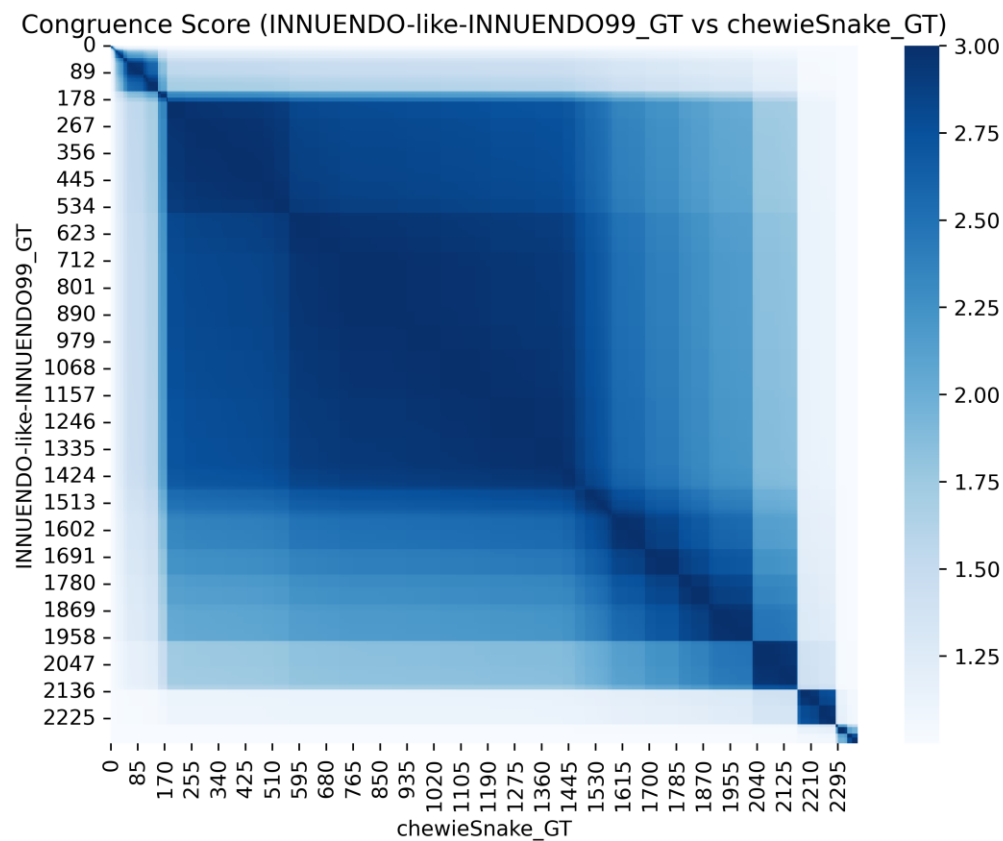


Figure S2.23.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

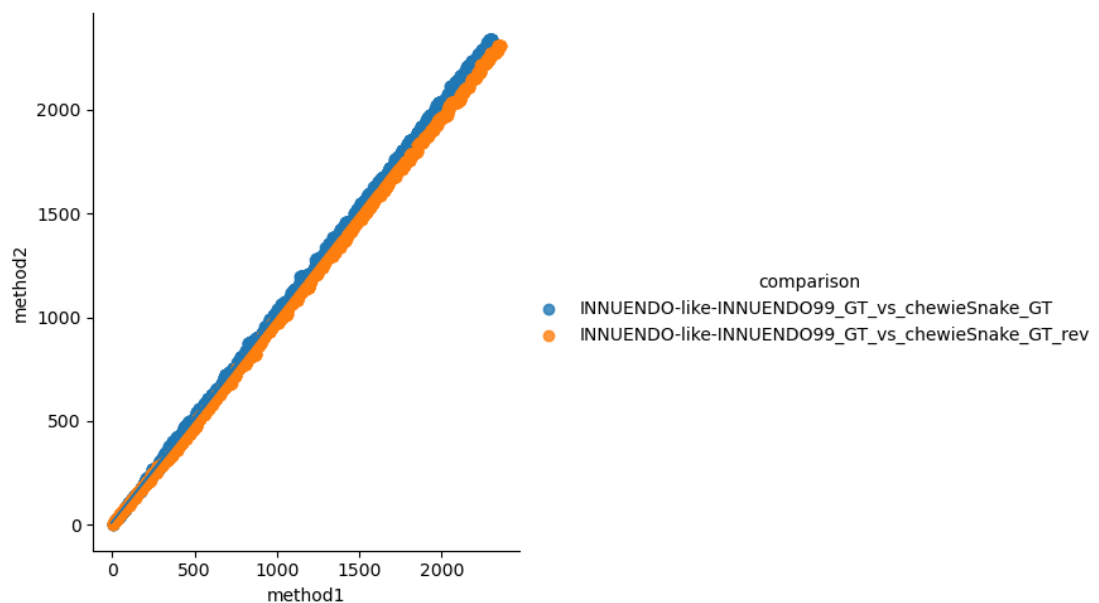


Figure S2.23.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2283 (blue) and 2337 (orange) points is presented.

24. INNUENDO-like-INNUENDO99 GrapeTree vs. chewieSnake 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	chewieSnake single-linkage
Pipeline version	chewBBACA 2.8.5	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2447	2274

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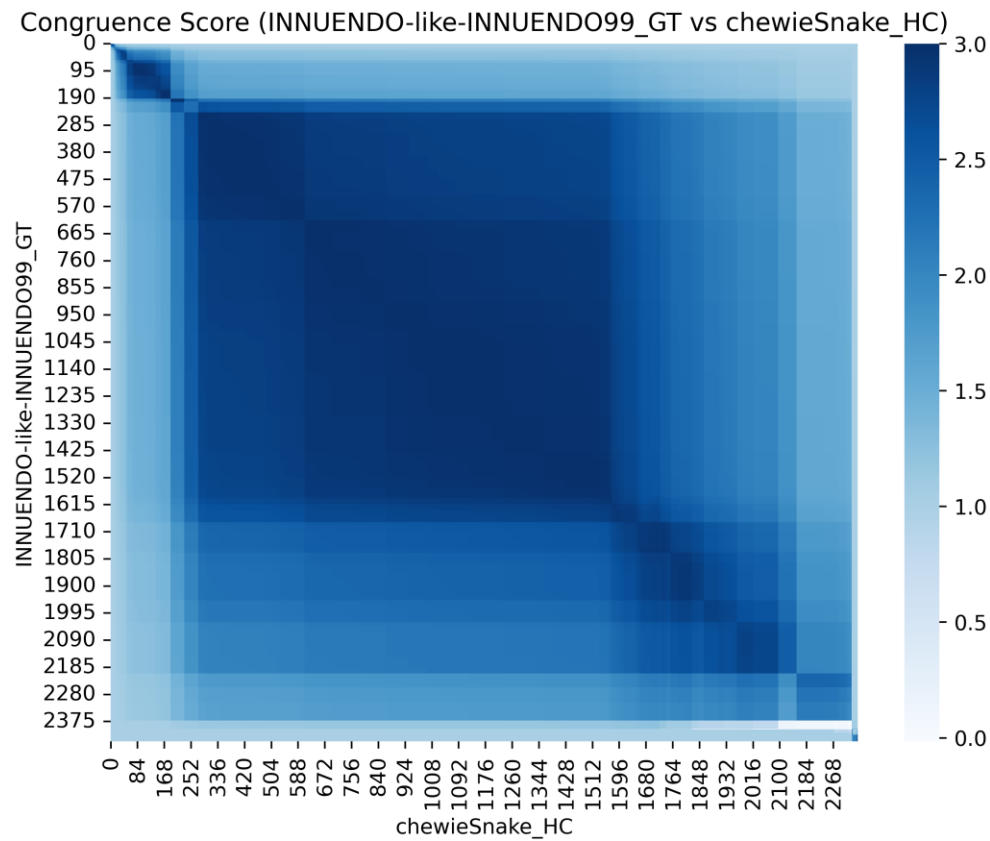


Figure S2.24.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

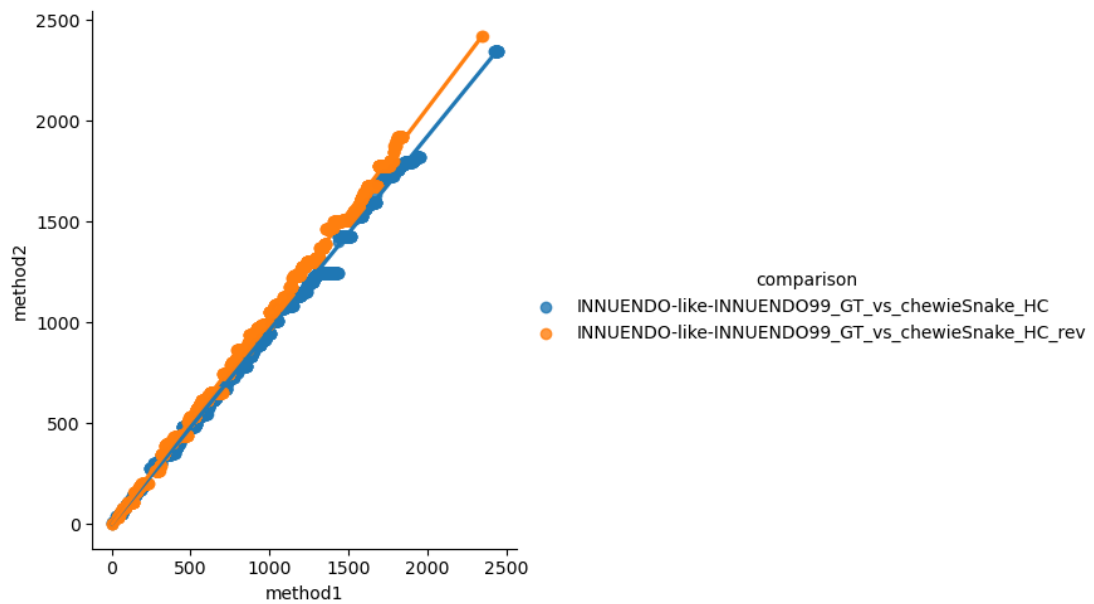


Figure S2.24.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 1905 (blue) and 1751 (orange) points is presented.

25. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-EFSA 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-EFSA GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	EFSA
Dataset	All samples	All samples
Number partitions	2447	

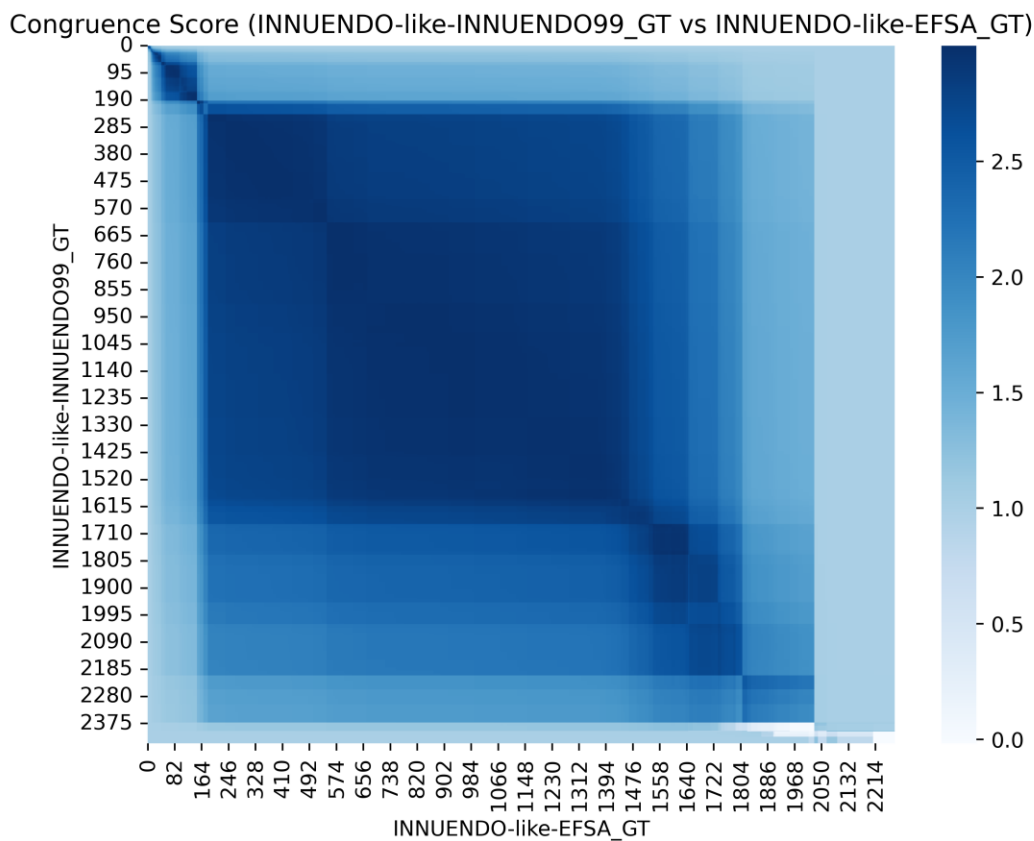


Figure S2.25.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

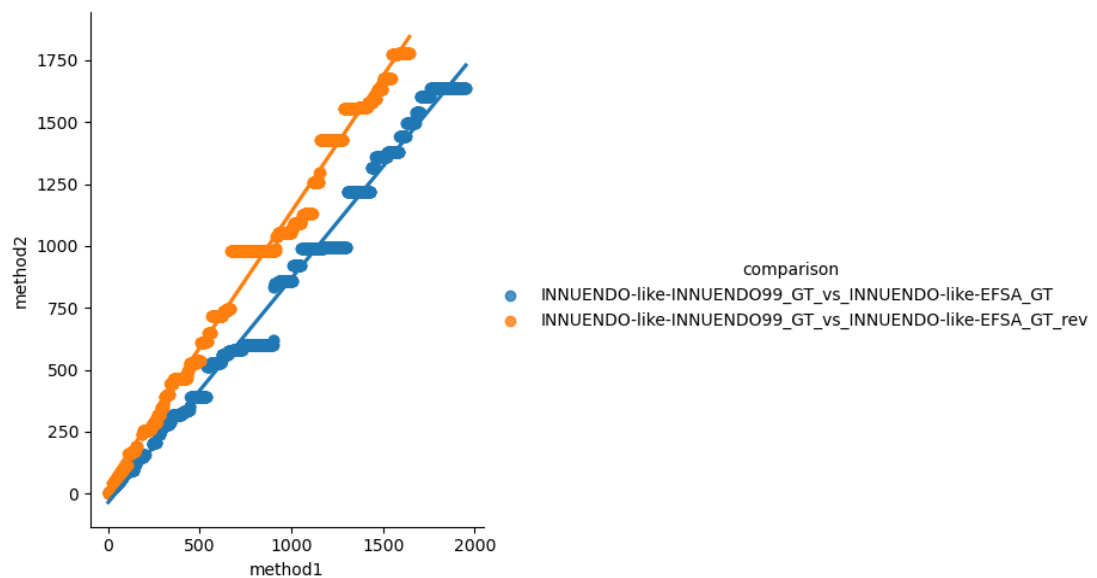


Figure S2.25.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1888 (blue) and 1596 (orange) points is presented.

26. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-EFSA 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-EFSA single- linkage
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	INNUENDO (wgMLST)	EFSA
Dataset	All samples	All samples
Number partitions	2447	

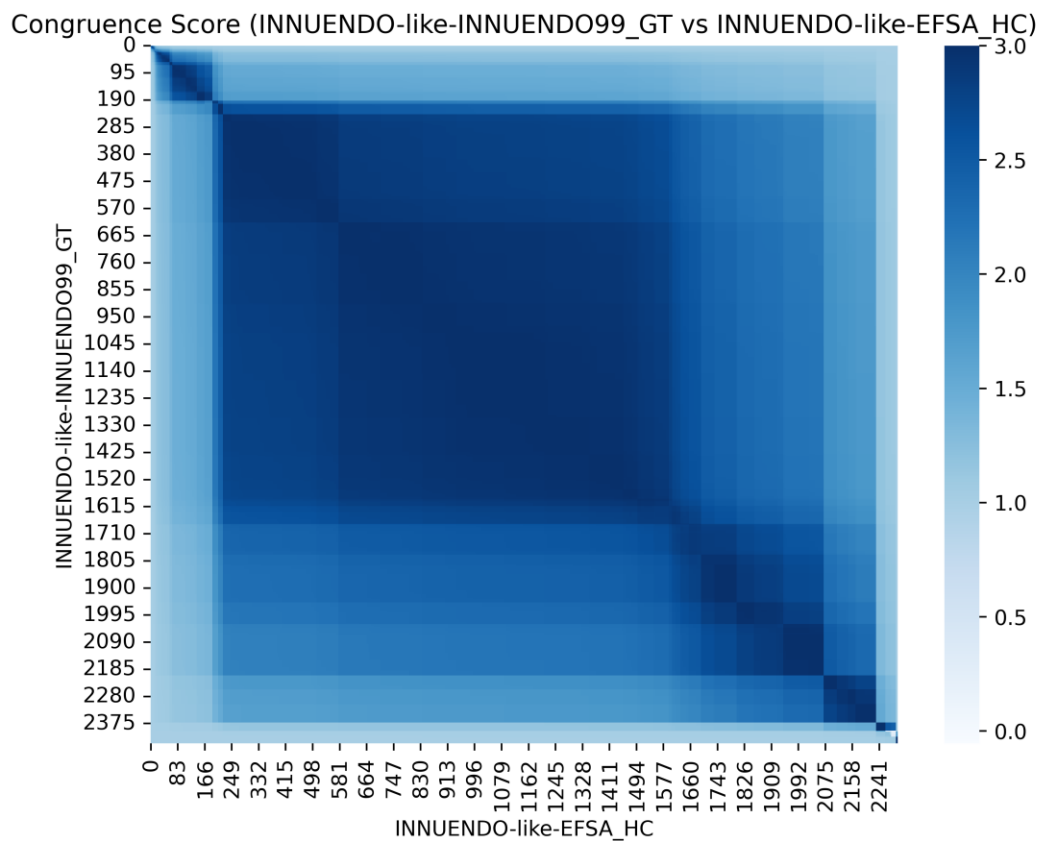


Figure S2.26.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

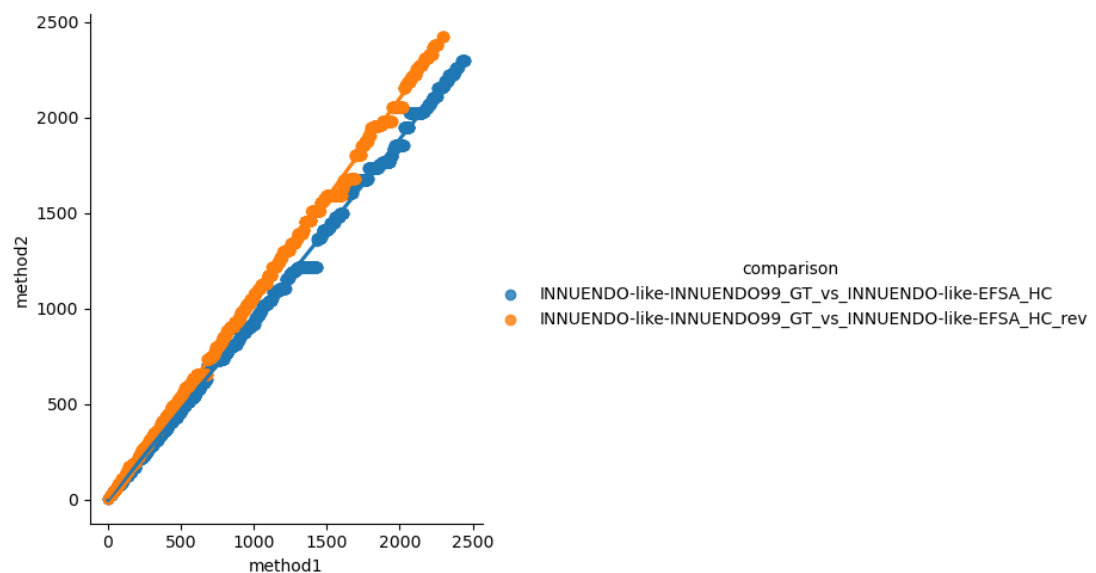


Figure S2.26.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2394 (blue) and 2231 (orange) points is presented.

27. INNUENDO-like-INNUENDO99 GrapeTree vs. INNUENDO-like-Enterobase 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-Enterobase GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	INNUENDO (wgMLST)	Enterobase
Dataset	All samples	All samples
Number partitions	2447	2388

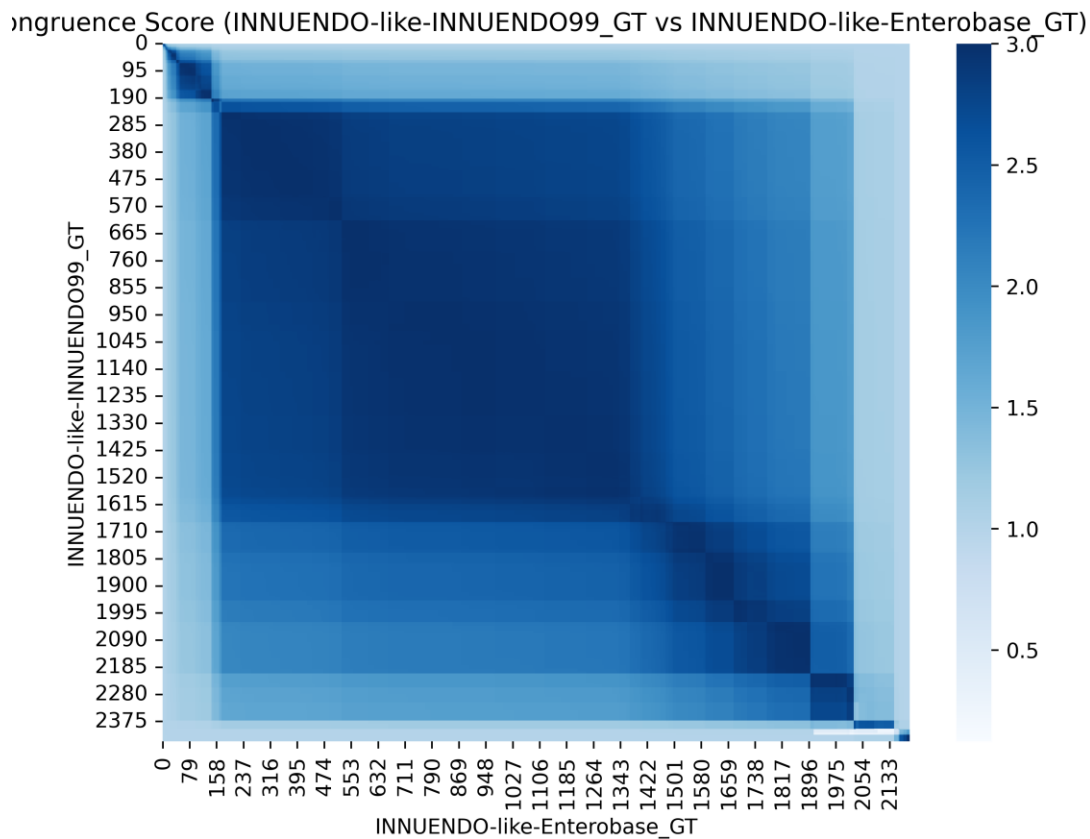


Figure S2.27.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

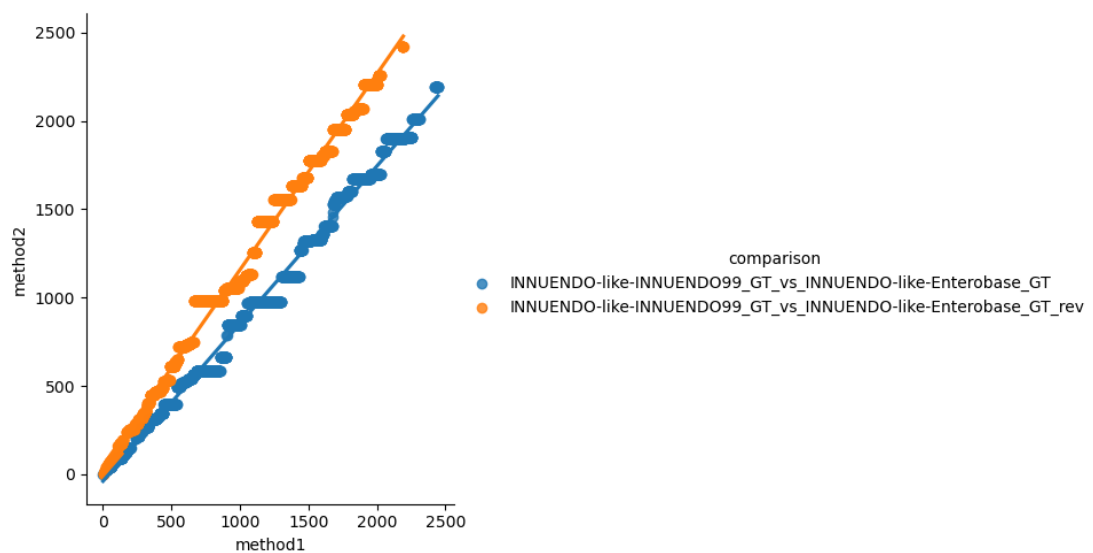


Figure S2.27.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 2275 (blue) and 1998 (orange) points is presented.

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

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

	INNUENDO-like-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	2447	2388

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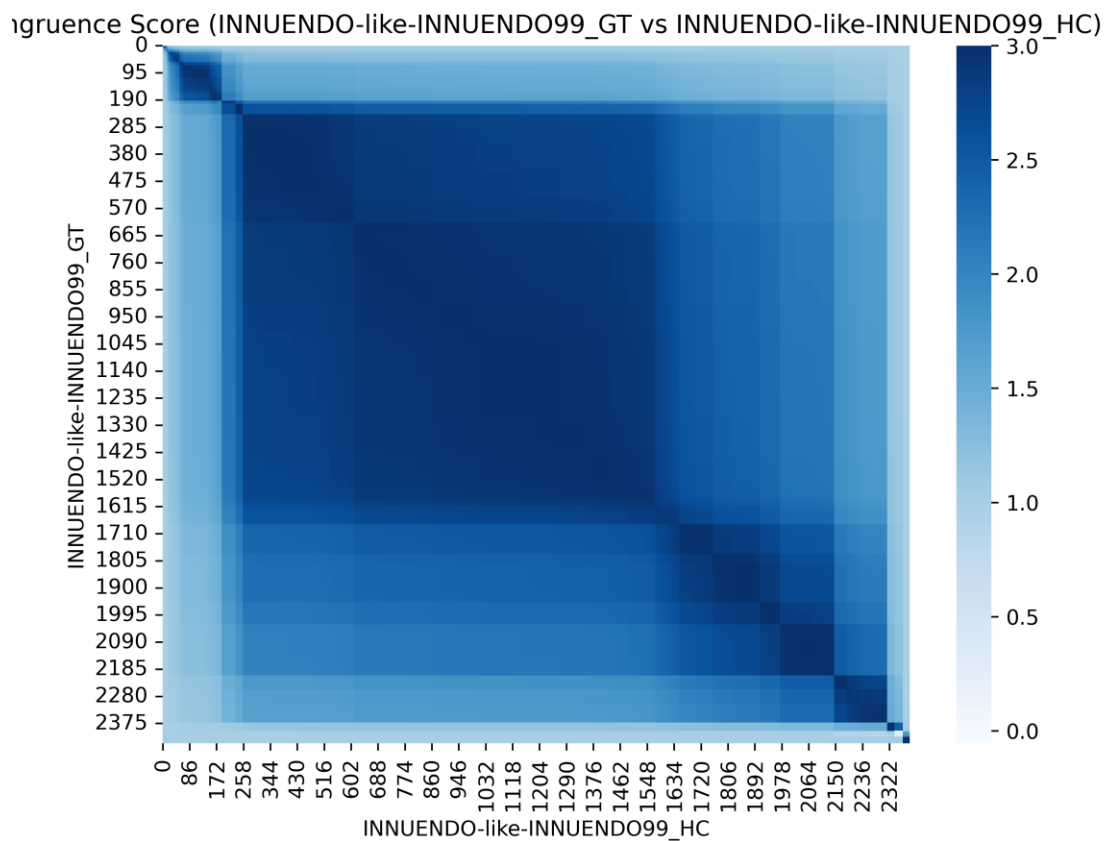


Figure S2.28.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

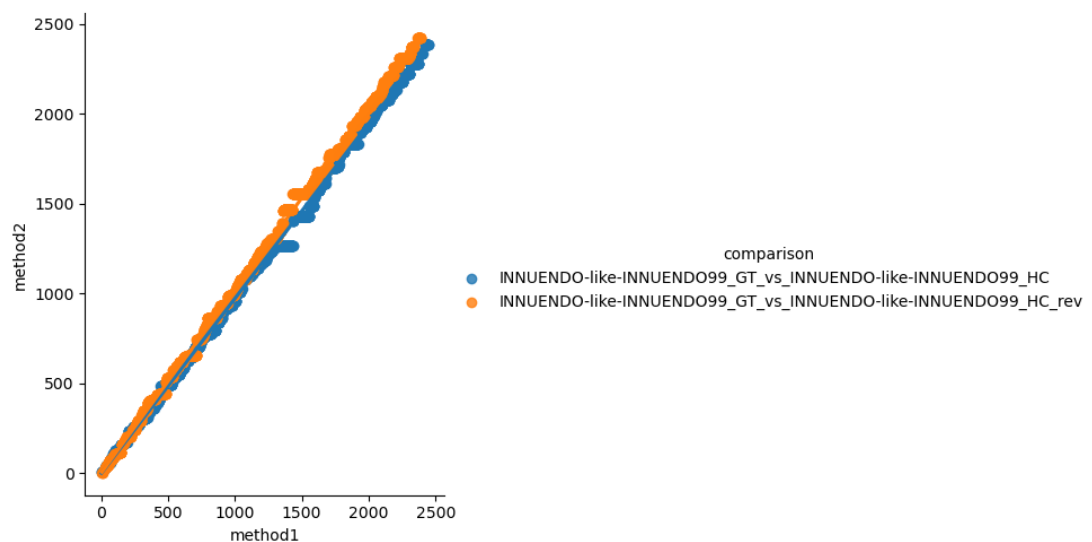


Figure S2.28.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 2398 (blue) and 2322 (orange) points is presented.

29. SeqSphere single-linkage vs. chewieSnake 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.

	SeqSphere single-linkage	chewieSnake GrapeTree
Pipeline version	v8.3.4	v3.1.1
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2798	2346

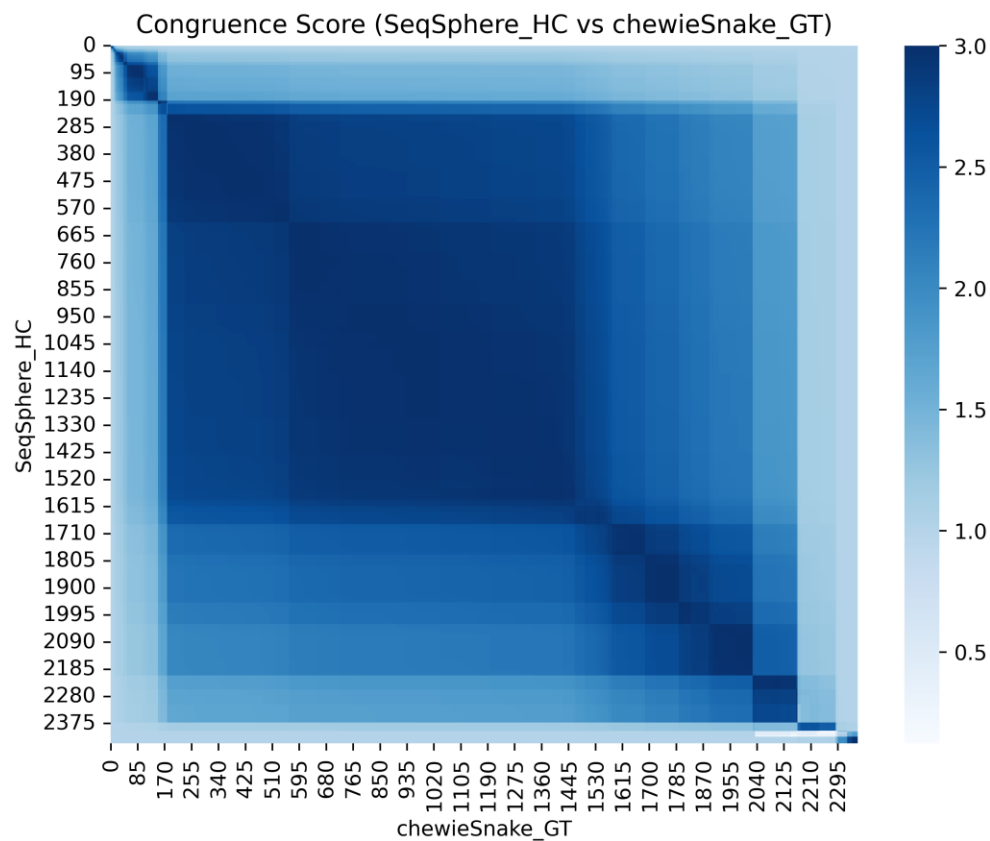


Figure S2.29.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

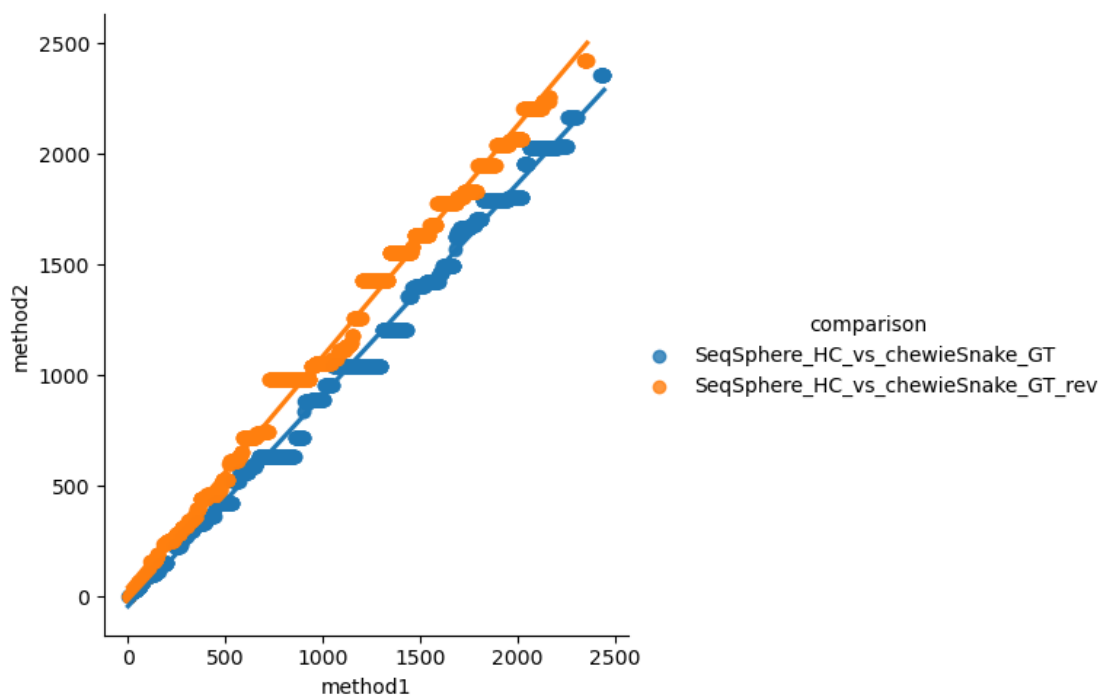


Figure S2.29.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2276 (blue) and 2151 (orange) points is presented.

30. SeqSphere single-linkage vs. chewieSnake 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.

	SeqSphere single-linkage	chewieSnake single-linkage
Pipeline version	v8.3.4	v3.1.1
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2798	2274

Section 2 – Comparison of allele-based pipelines

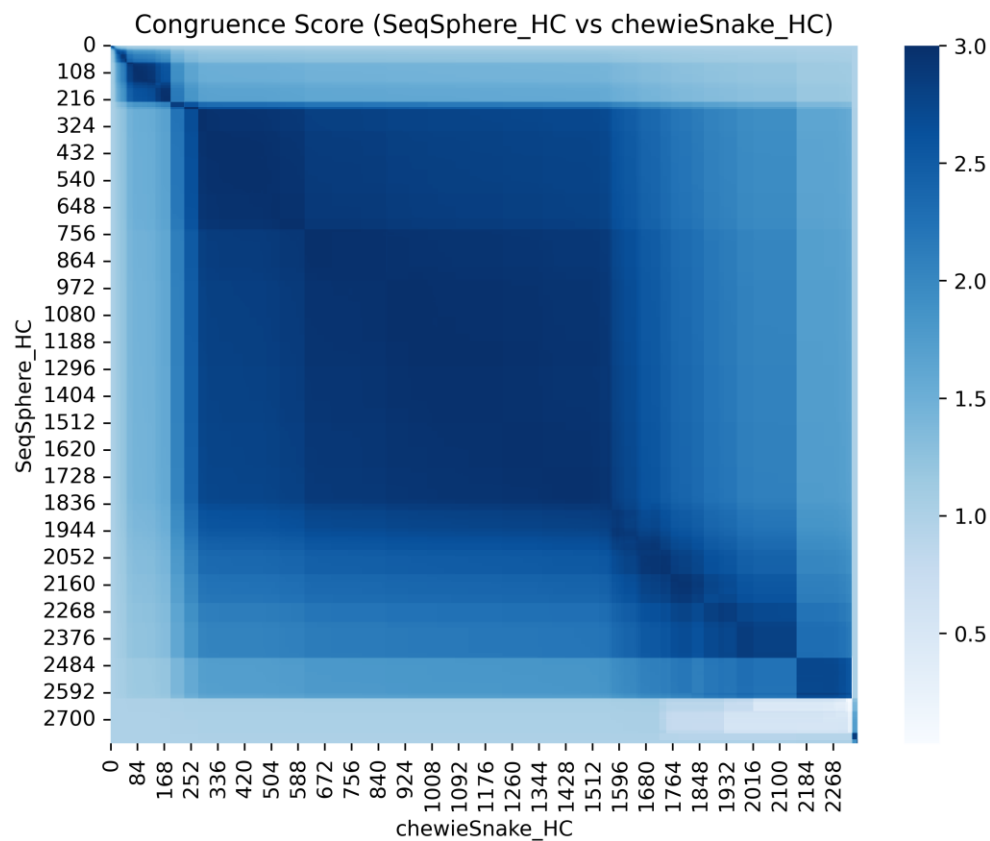


Figure S2.30.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

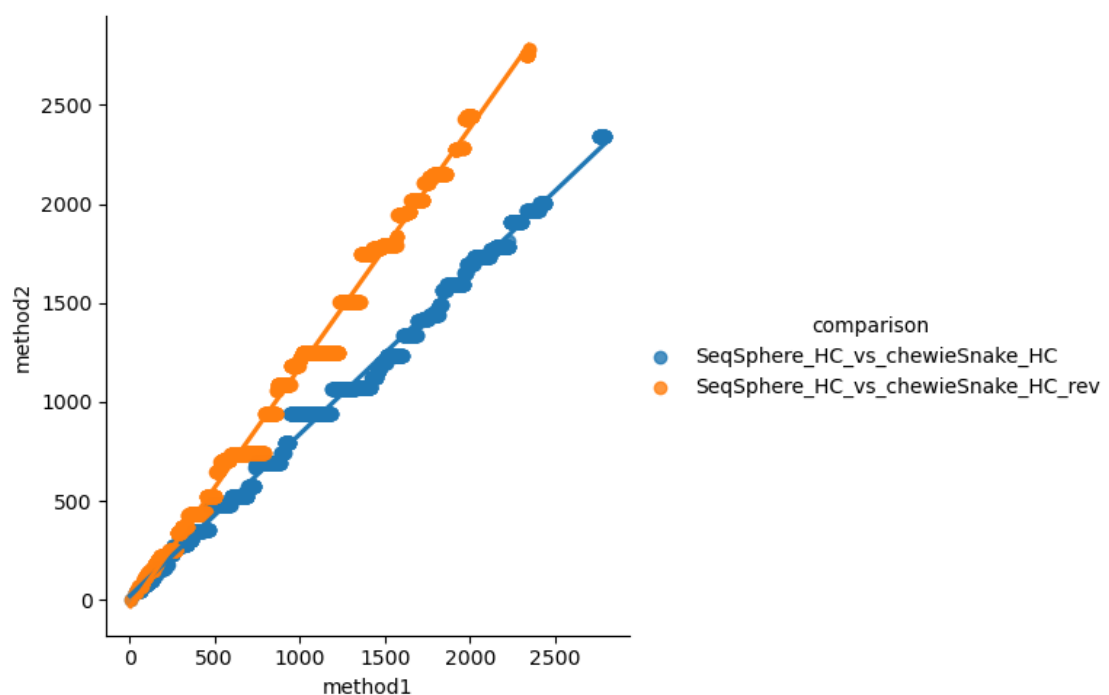


Figure S2.30.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85). A linear tendency line supported by 2405 (blue) and 1876 (orange) points is presented.

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

	SeqSphere single-linkage	INNUENDO-like-EFSA GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2798	

Section 2 – Comparison of allele-based pipelines

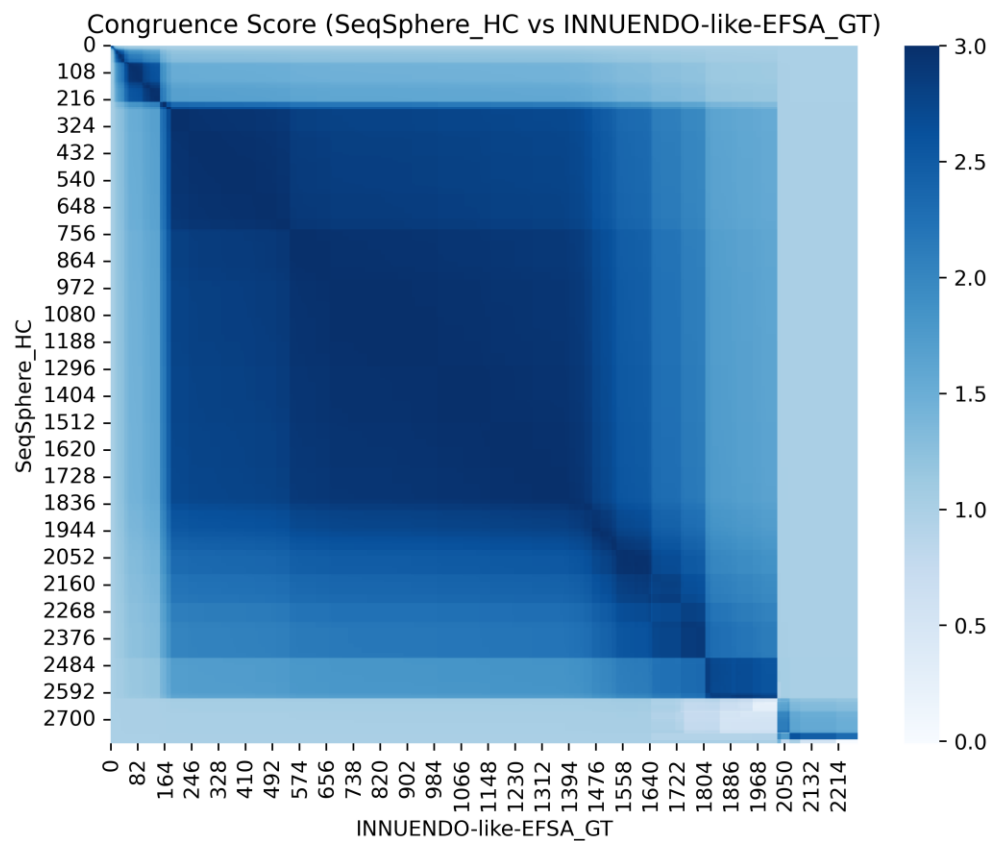


Figure S2.31.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

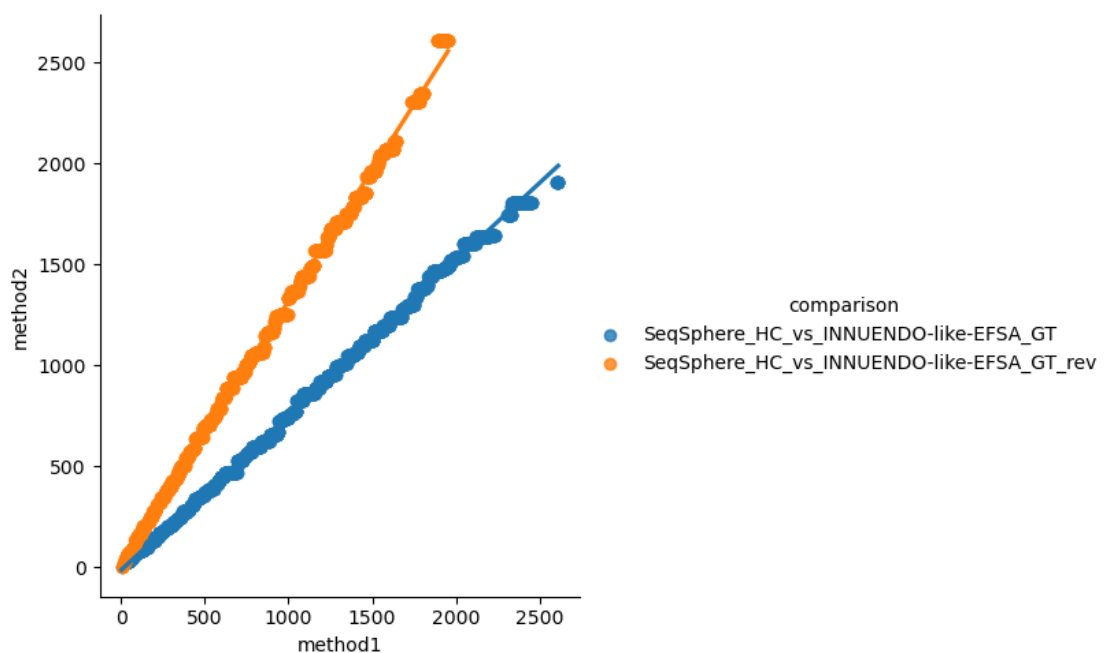


Figure S2.31.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2365 (blue) and 1758 (orange) points is presented.

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

	SeqSphere single-linkage	INNUENDO-like-EFSA single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	EFSA
Dataset	All samples	All samples
Number partitions	2798	

Section 2 – Comparison of allele-based pipelines

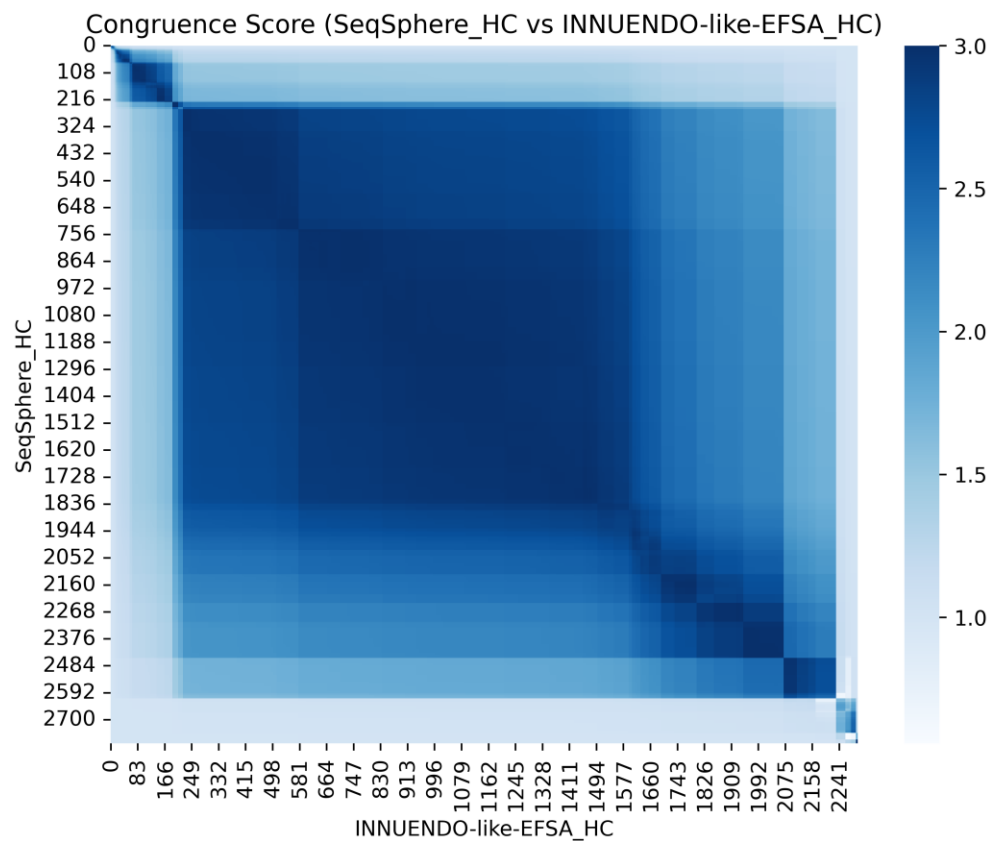


Figure S2.32.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

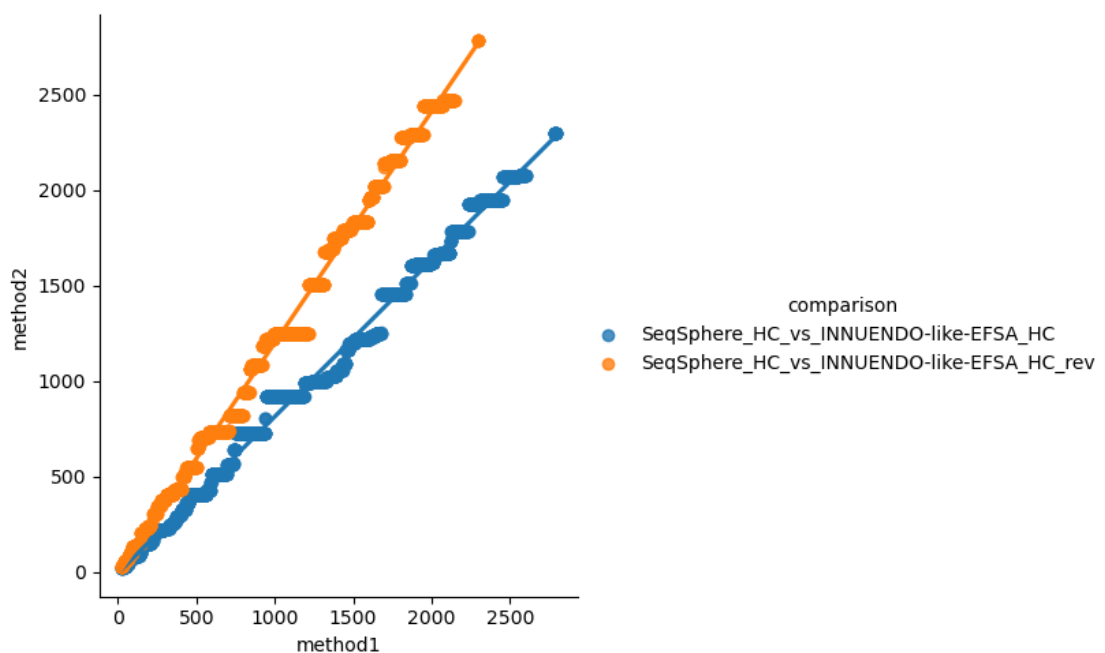


Figure S2.32.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2581 (blue) and 2113 (orange) points is presented.

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

	SeqSphere single-linkage	INNUENDO-like-Enterobase GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2798	2388

Section 2 – Comparison of allele-based pipelines

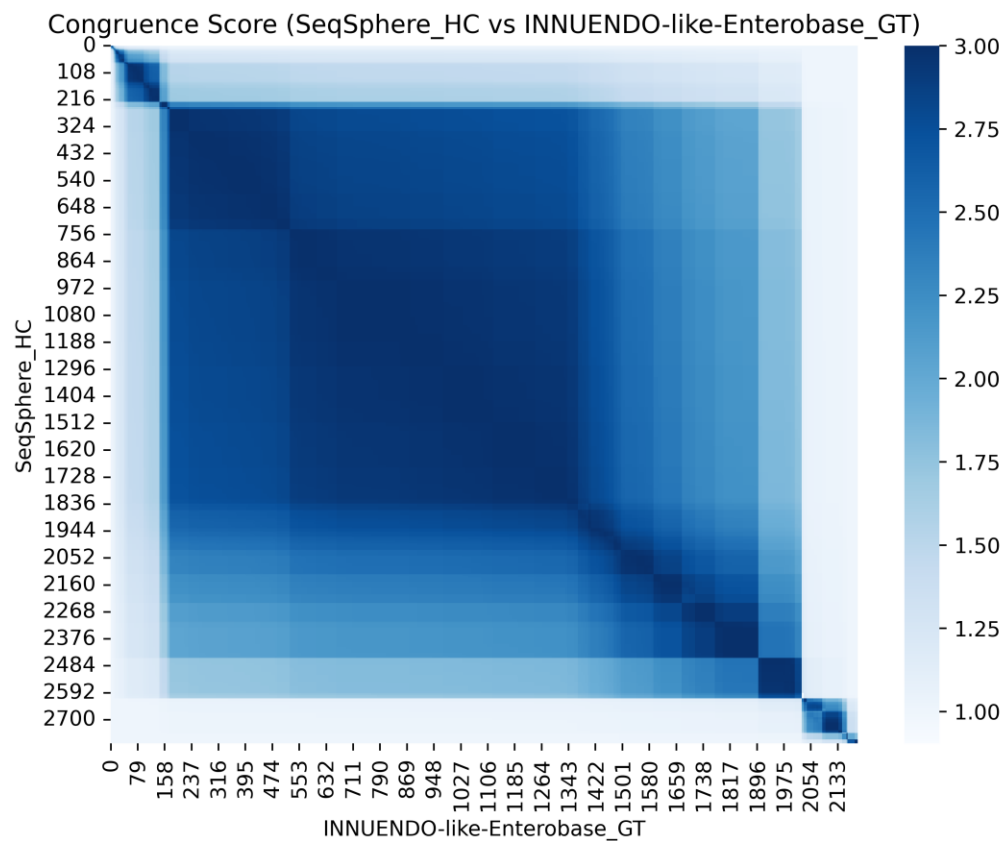


Figure S2.33.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

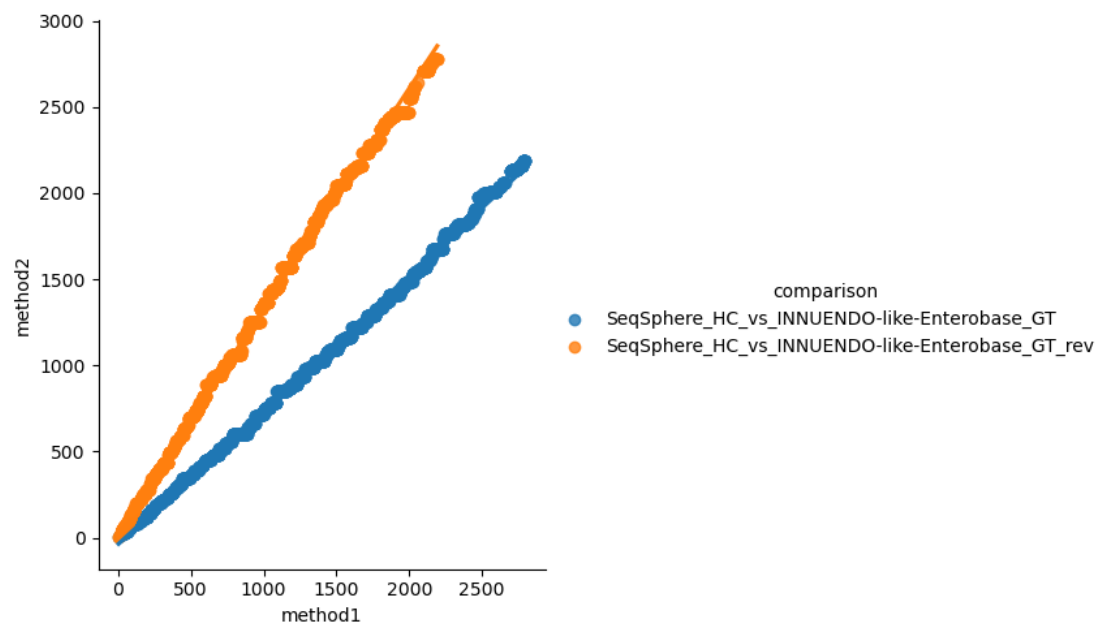


Figure S2.33.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2712 (blue) and 2103 (orange) points is presented.

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

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.

	SeqSphere single-linkage	INNUENDO-like-Enterobase single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	Enterobase
Dataset	All samples	All samples
Number partitions	2798	2309

Section 2 – Comparison of allele-based pipelines

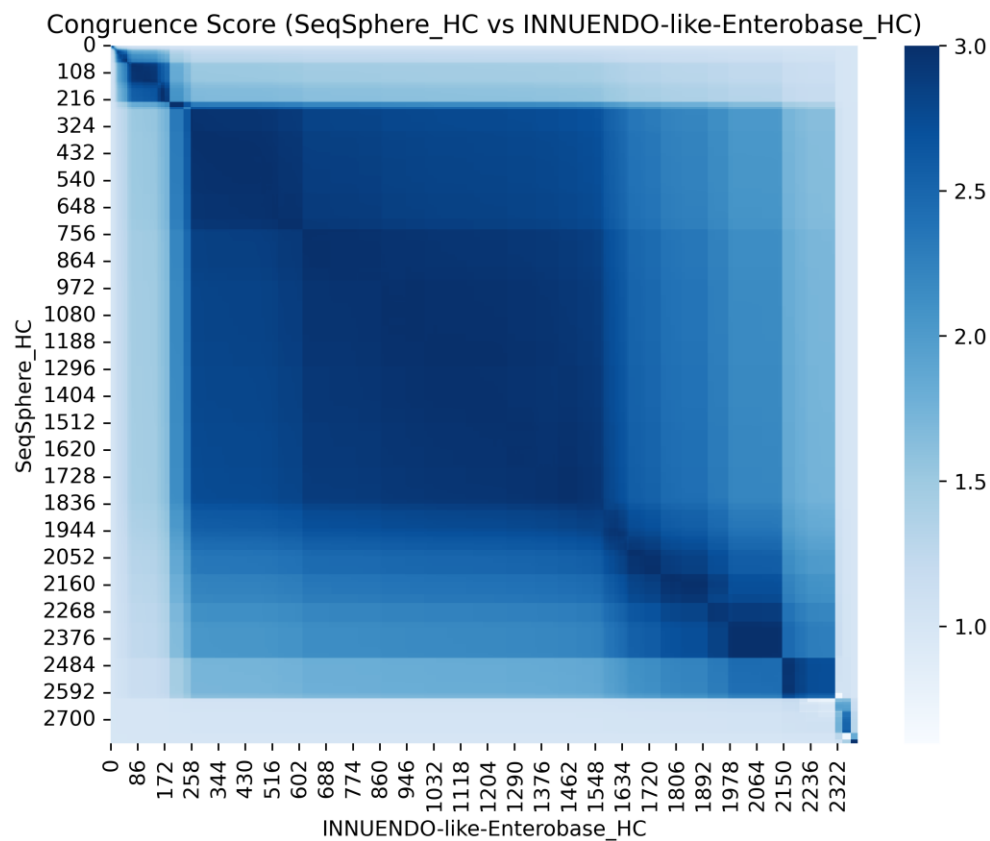


Figure S2.34.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

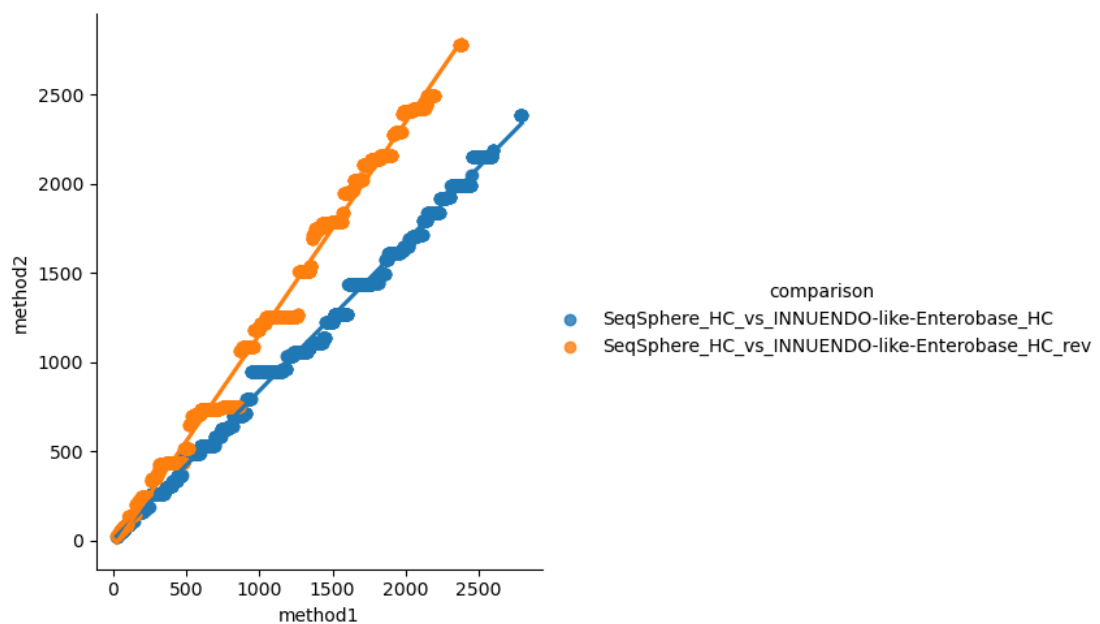


Figure S2.34.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2552 (blue) and 2162 (orange) points is presented.

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

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.

	SeqSphere single-linkage	INNUENDO-like-INNUENDO99 GrapeTree
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2798	2447

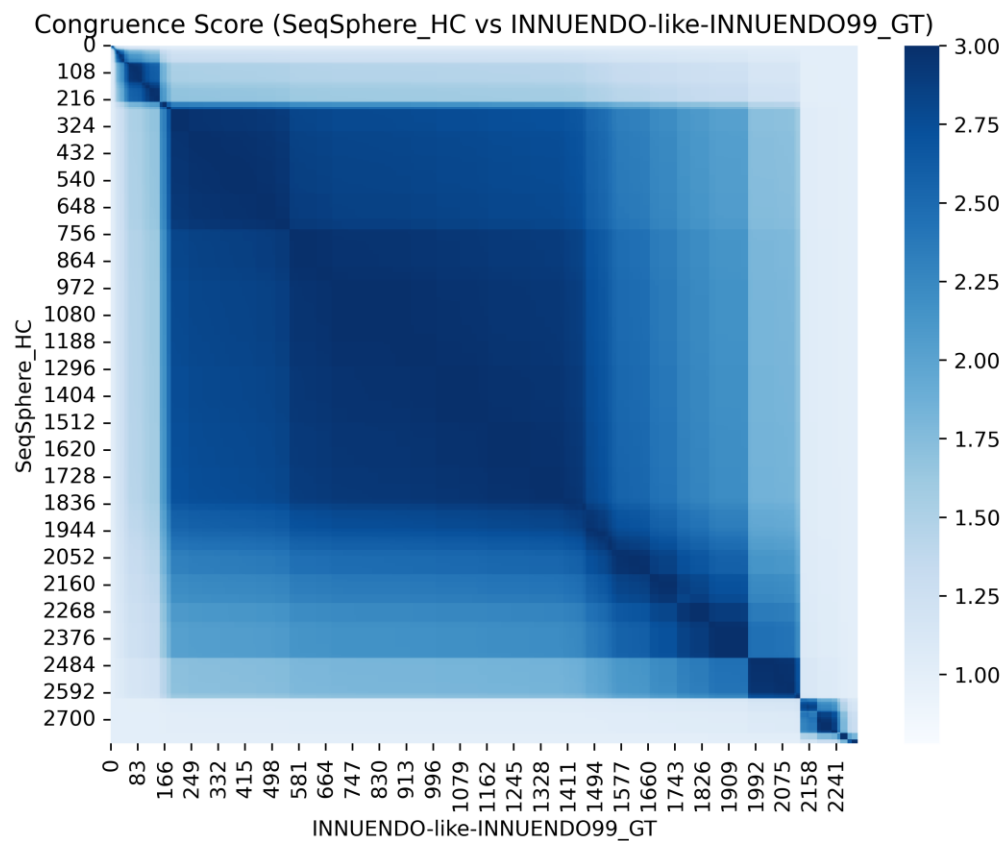


Figure S2.35.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

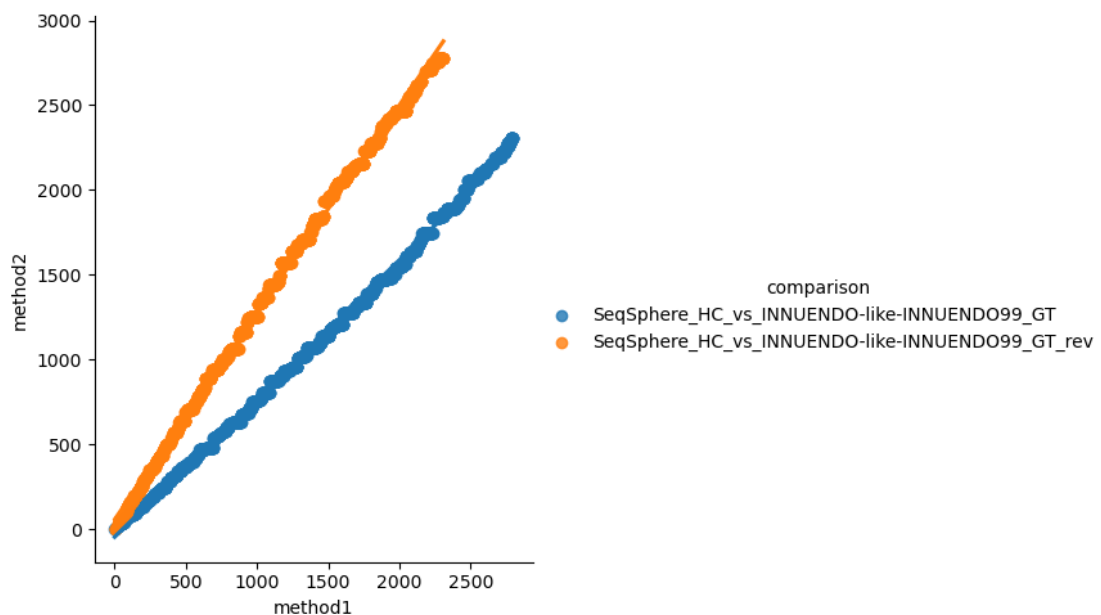


Figure S2.35.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2731 (blue) and 2227 (orange) points is presented.

36. SeqSphere single-linkage 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.

	SeqSphere single-linkage	INNUENDO-like-INNUENDO99 single-linkage
Pipeline version	v8.3.4	chewBBACA 2.8.5
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Enterobase	INNUENDO (wgMLST)
Dataset	All samples	All samples
Number partitions	2798	2359

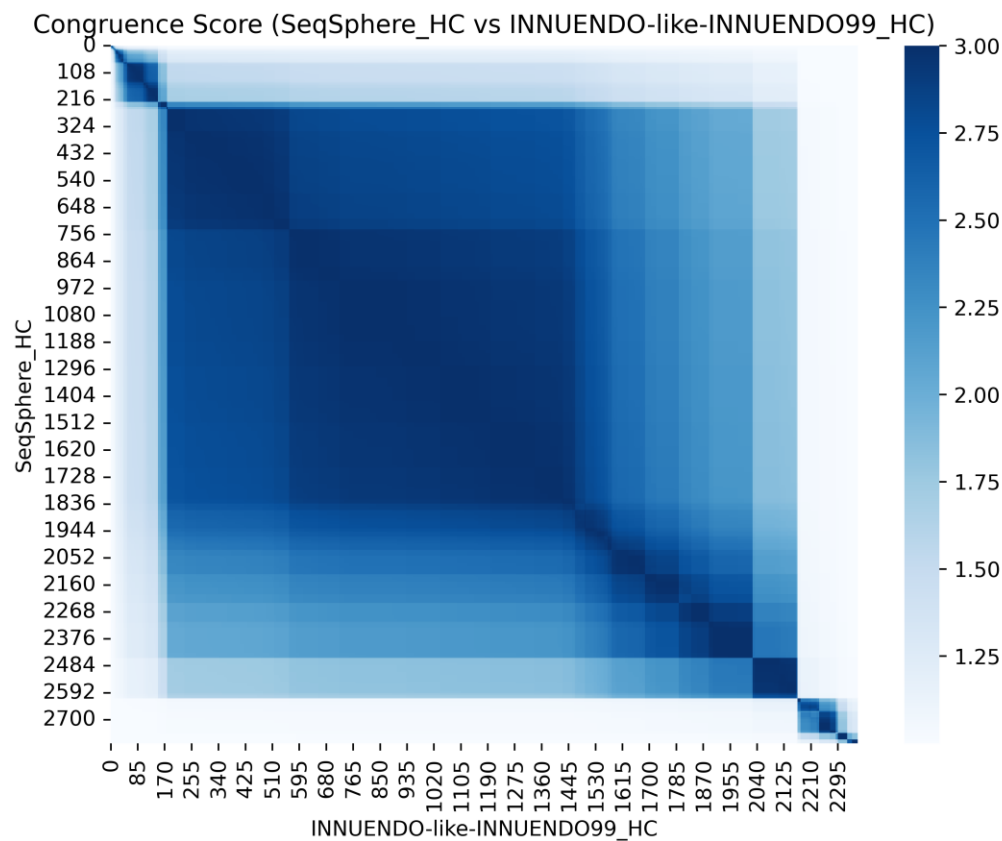


Figure S2.36.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

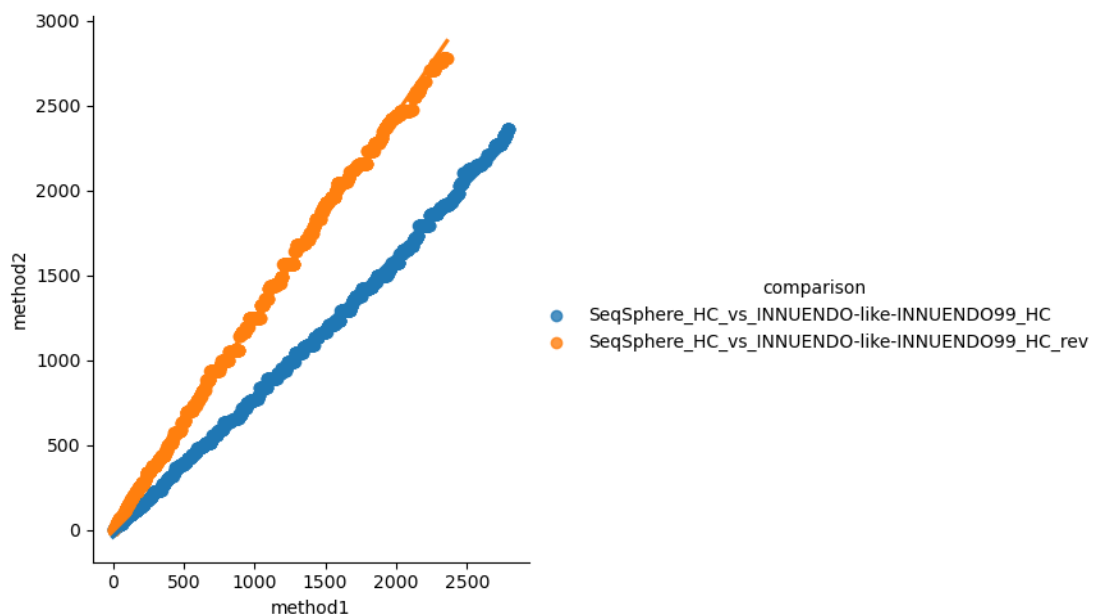


Figure S2.36.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 2710 (blue) and 2270 (orange) points is presented.

Section 3 – Comparison of SNP-based pipelines

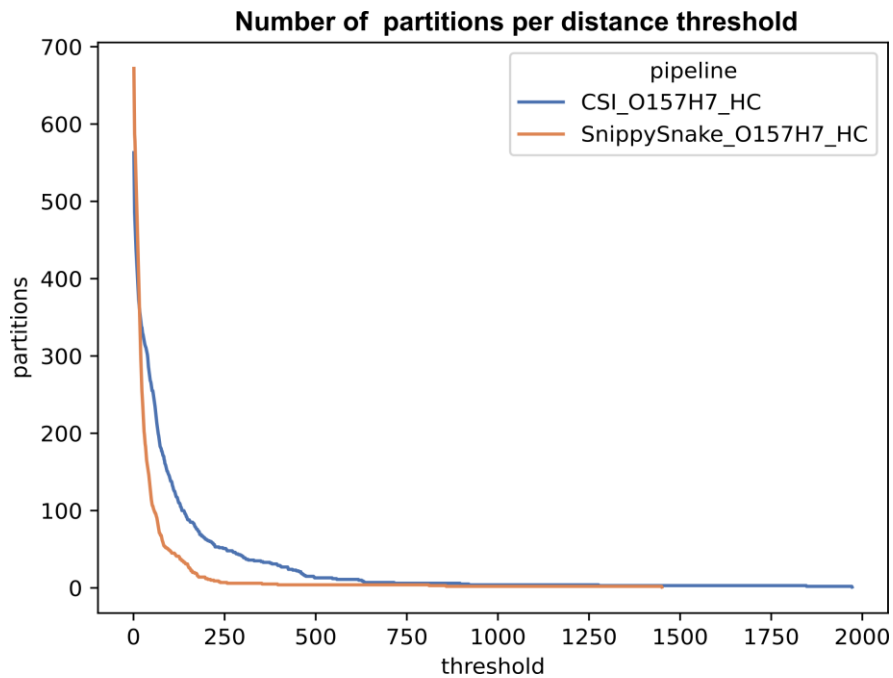


Figure S3. Number of partitions determined by each SNP-based pipeline at each possible distance threshold

1. CSI Phylogeny single-linkage vs. snippySnake single-linkage (O157H7)

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

	CSI Phylogeny single-linkage	snippySnake single-linkage
Pipeline version	v1.4	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Sakai (NC_002695)	Sakai (NC_002695)
Dataset	O157H7	O157H7
Number partitions		

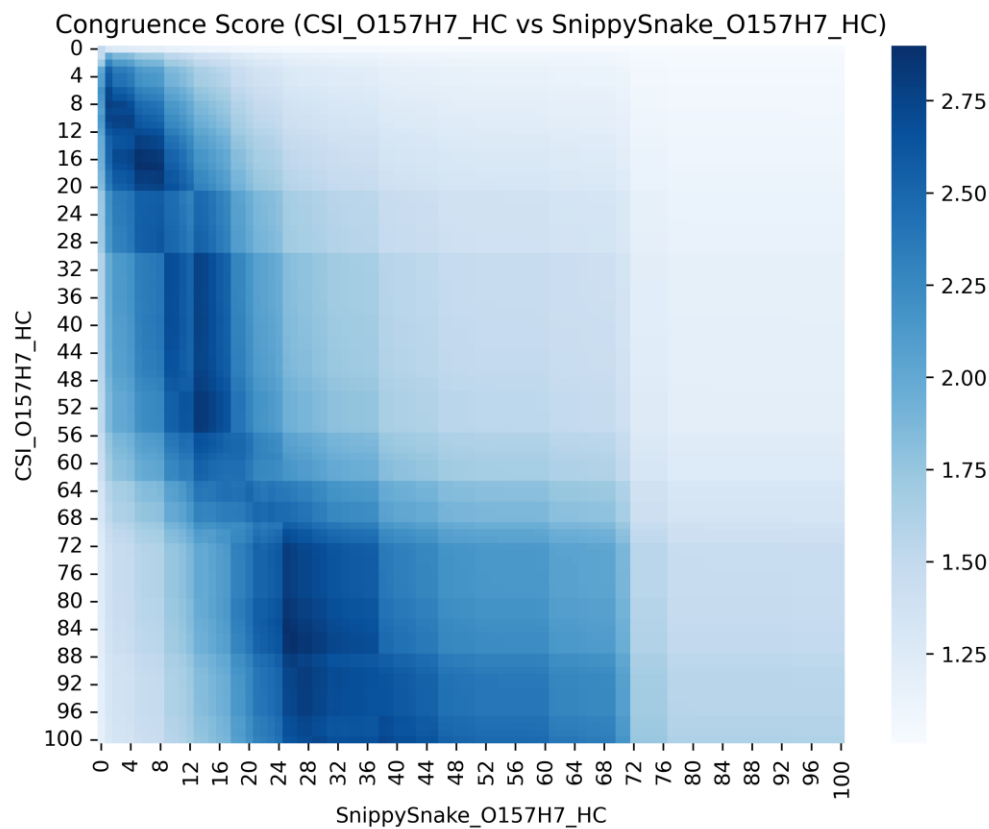


Figure S3.1.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

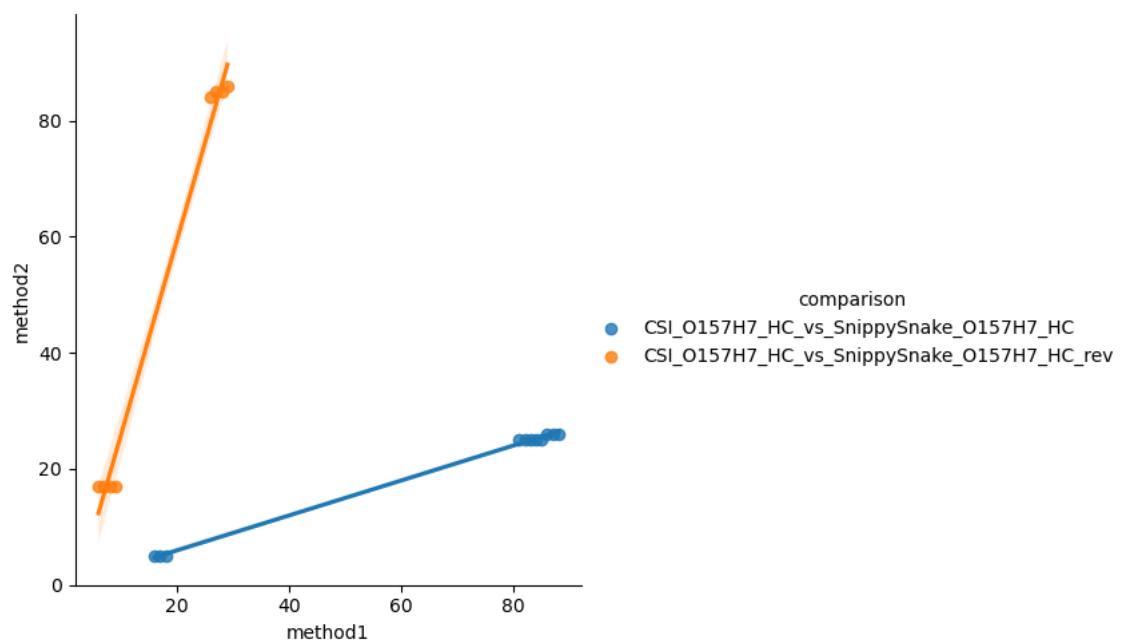


Figure S3.1.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 11 (blue) and 8 (orange) points is presented.

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

1. chewieSnake GrapeTree 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.

	chewieSnake GrapeTree	CSI Phylogeny single-linkage
Pipeline version	v3.1.1	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

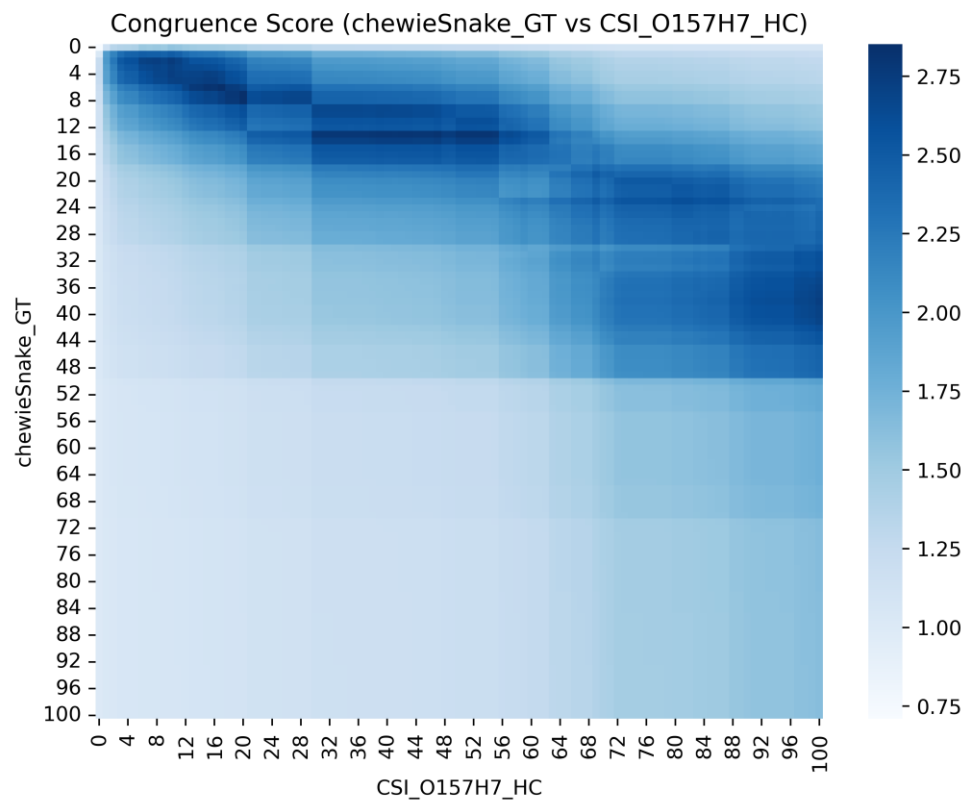


Figure S4.1.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

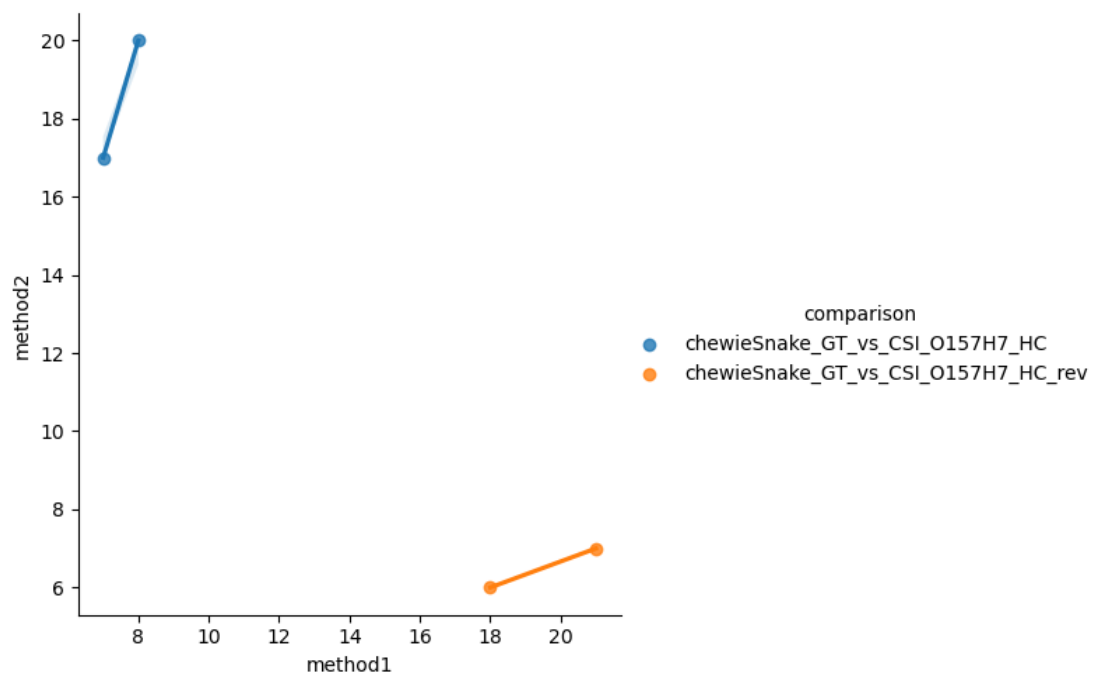


Figure S4.1.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 2 (blue) and 2 (orange) points is presented.

2. chewieSnake GrapeTree vs. snippySnake 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	snippySnake single-linkage
Pipeline version	v3.1.1	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

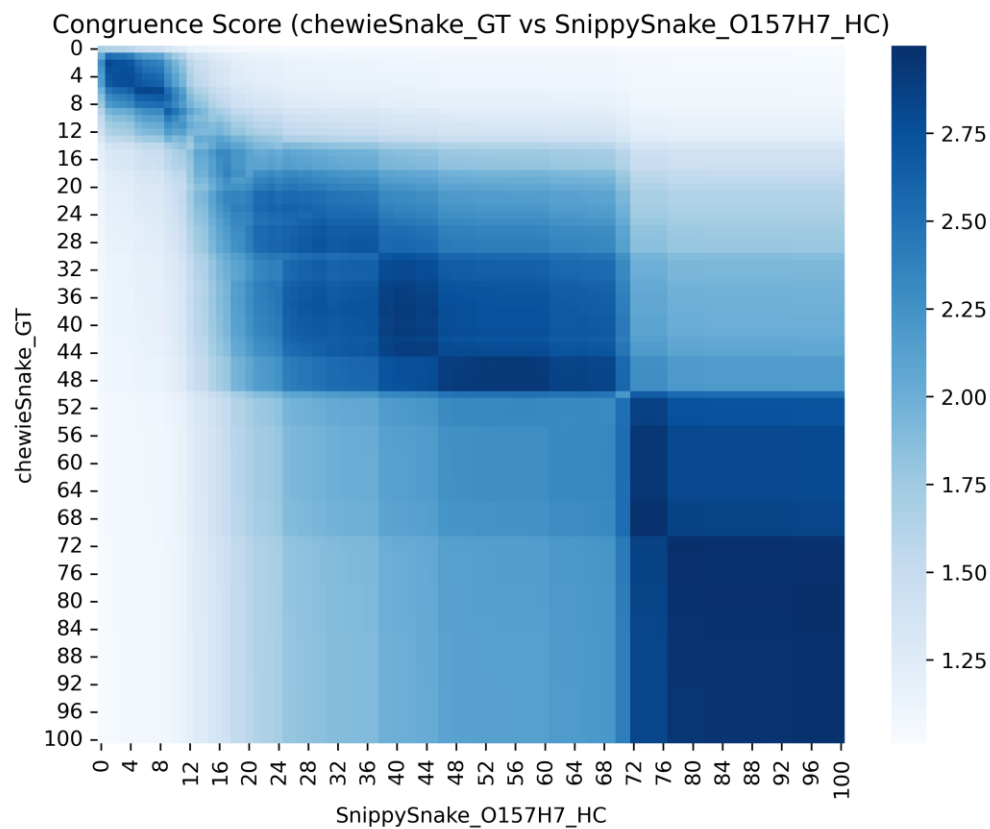


Figure S4.2.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

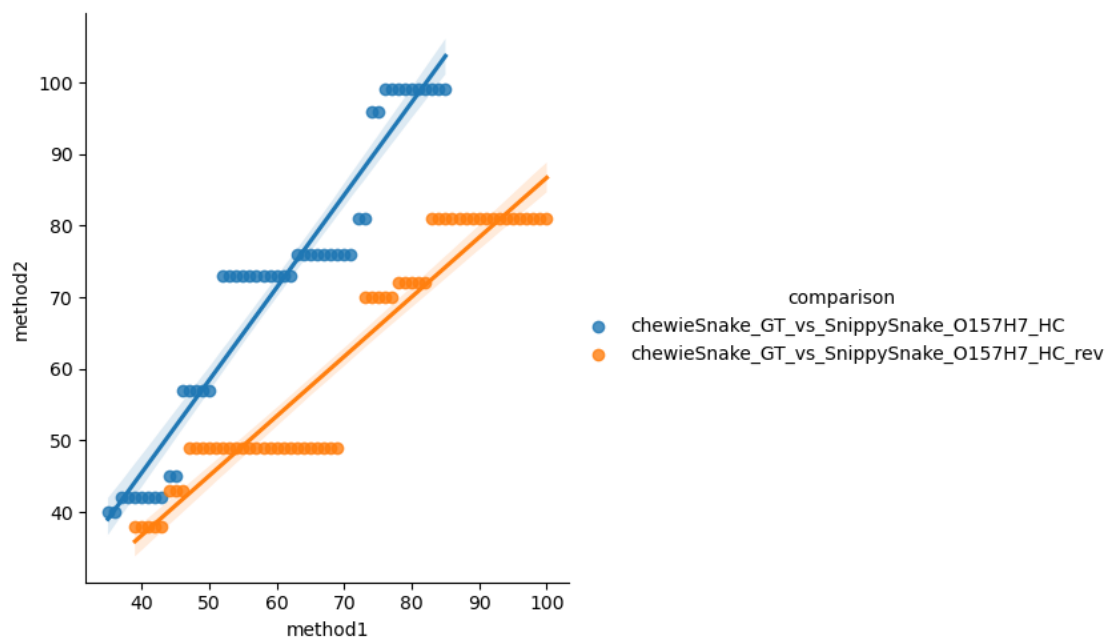


Figure S4.2.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for O157H7. A linear tendency line supported by 50 (blue) and 59 (orange) points is presented.

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	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

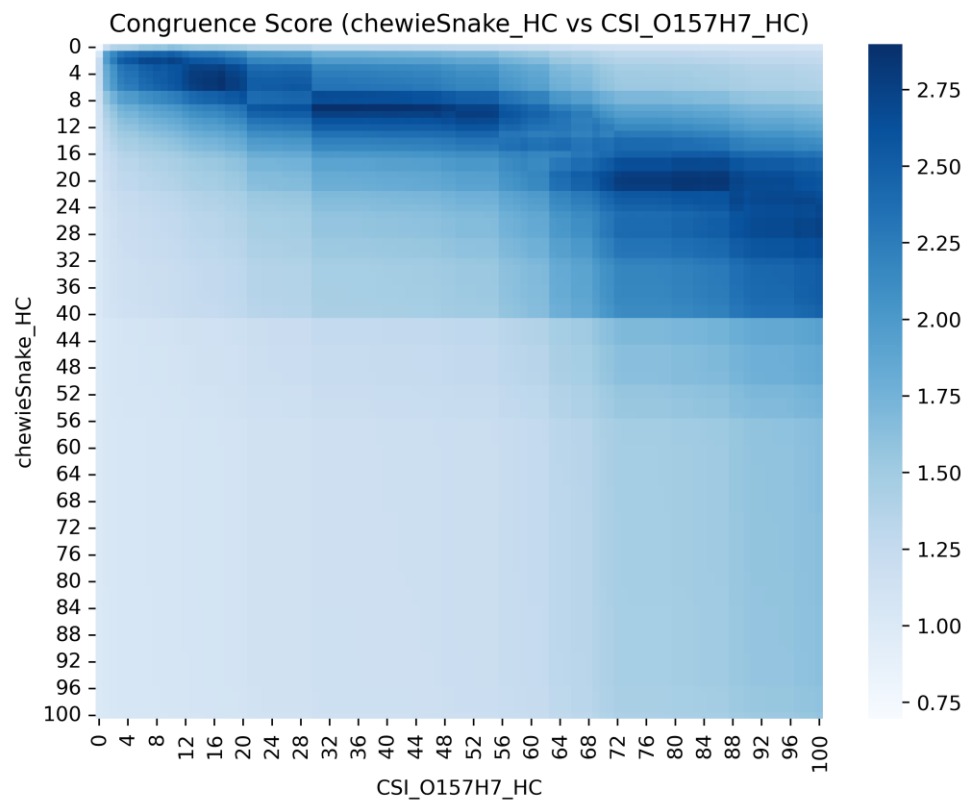


Figure S4.3.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

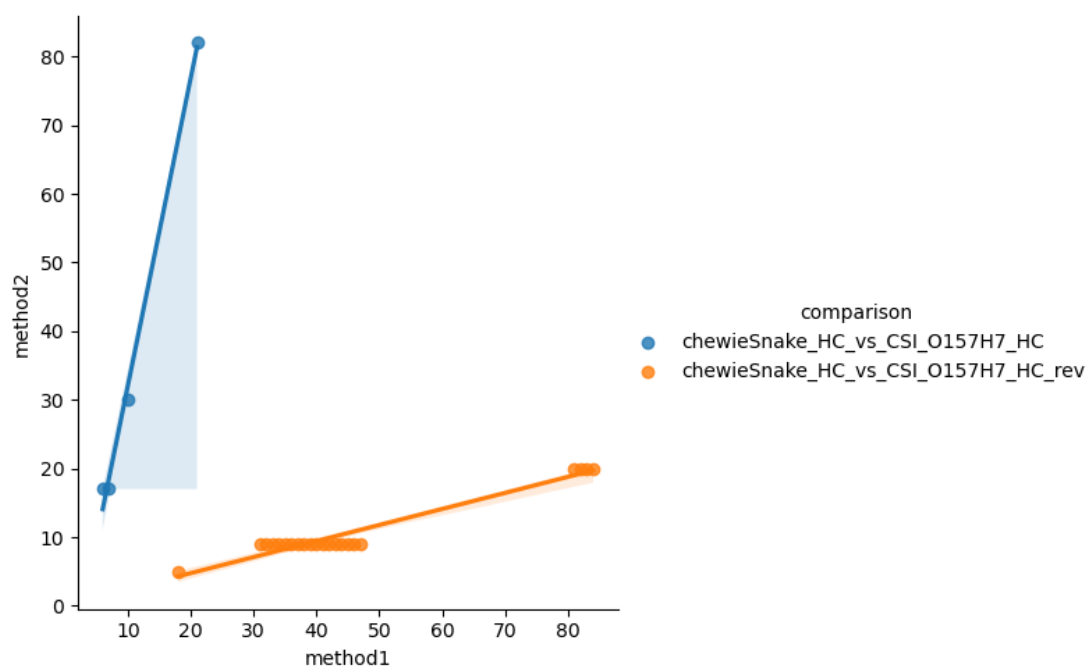


Figure S4.3.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 4 (blue) and 22 (orange) points is presented.

4. chewieSnake single-linkage vs. snippySnake single-linkage

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

	chewieSnake single-linkage	snippySnake single-linkage
Pipeline version	v3.1.1	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

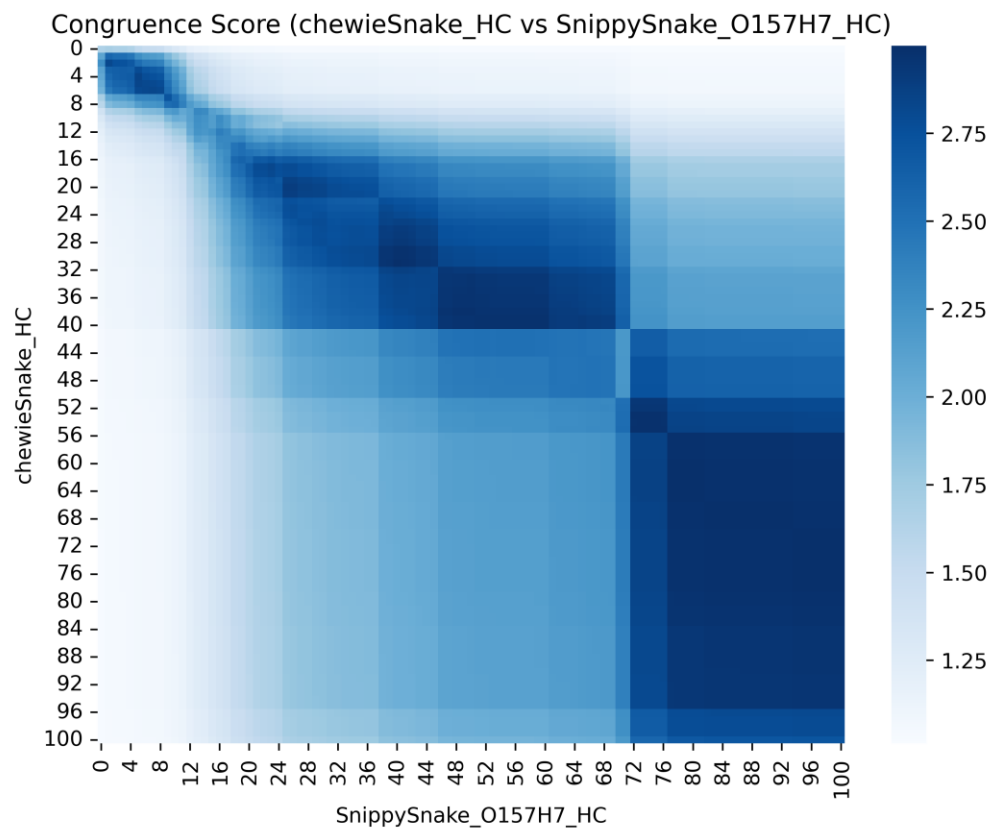


Figure S4.4.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

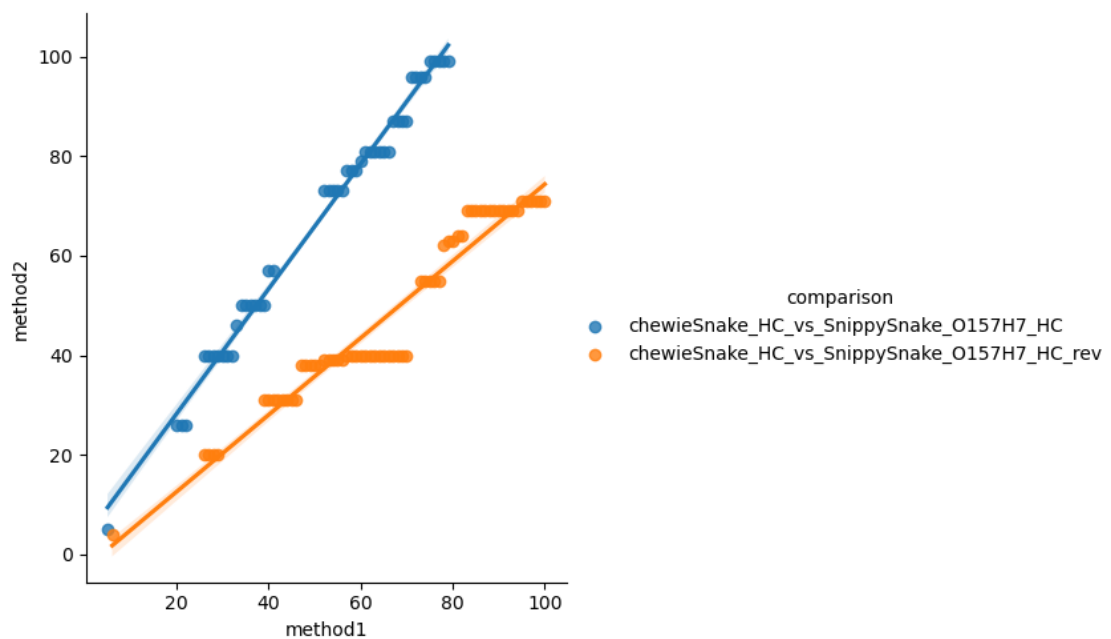


Figure S4.4.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for O157H7. A linear tendency line supported by 48 (blue) and 65 (orange) points is presented.

5. INNUENDO-like-EFSA GrapeTree 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-EFSA GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	Sakai (NC_002695)
Dataset	All Samples	O157H7

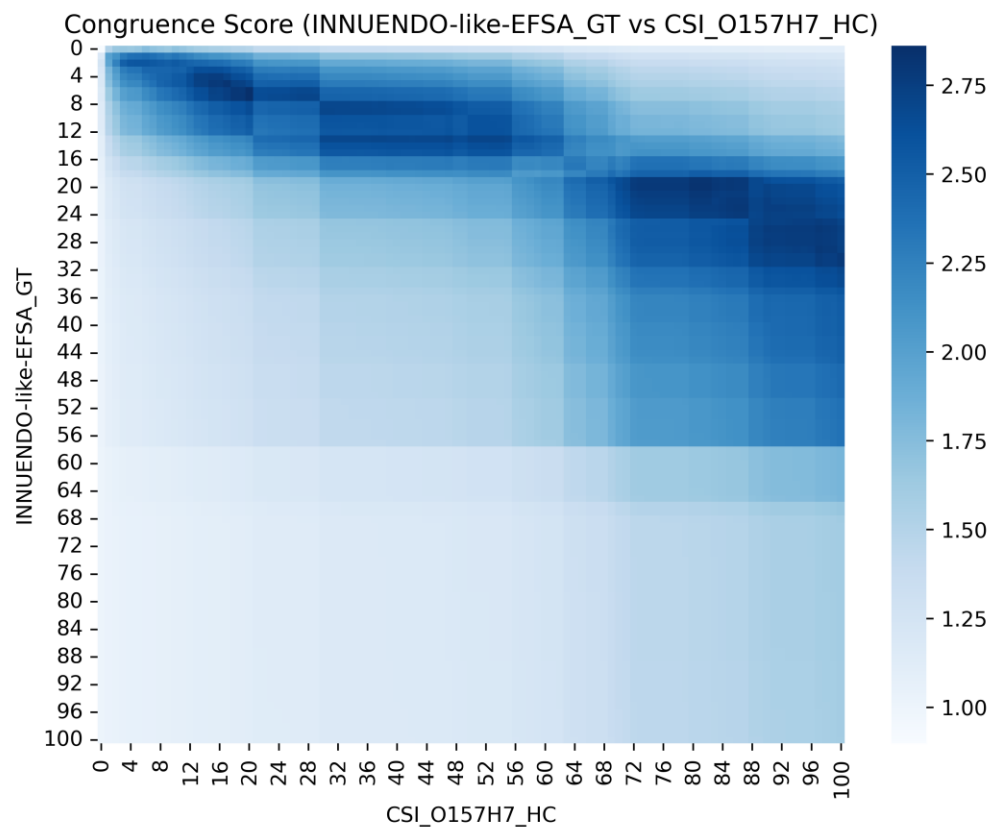


Figure S4.5.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

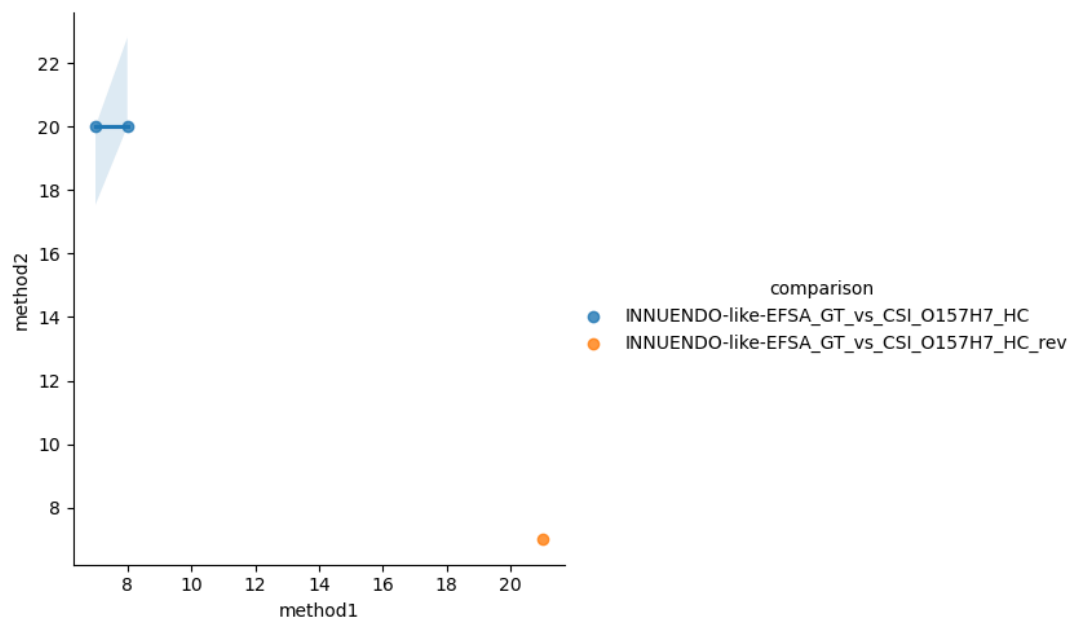


Figure S4.5.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for O157H7. No linear tendency was observed. The 2 (blue) and 1 (orange) points are presented.

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

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

	INNUENDO-like-EFSA GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	Sakai (NC_002695)
Dataset	All Samples	O157H7

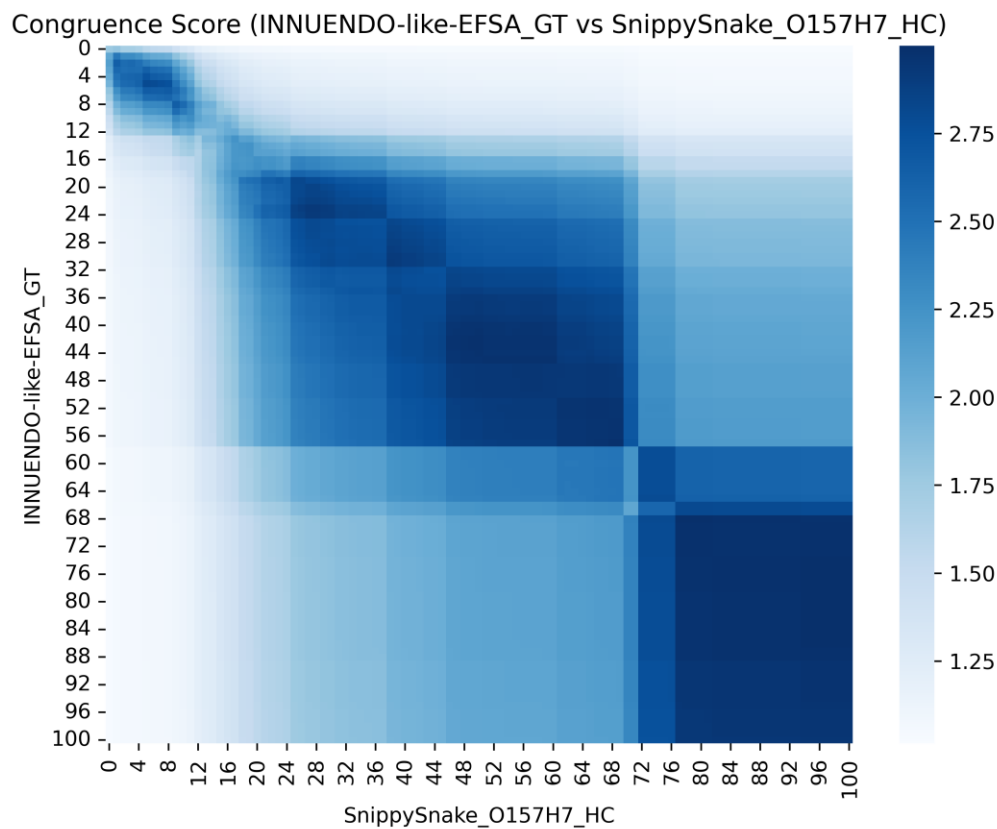


Figure S4.6.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

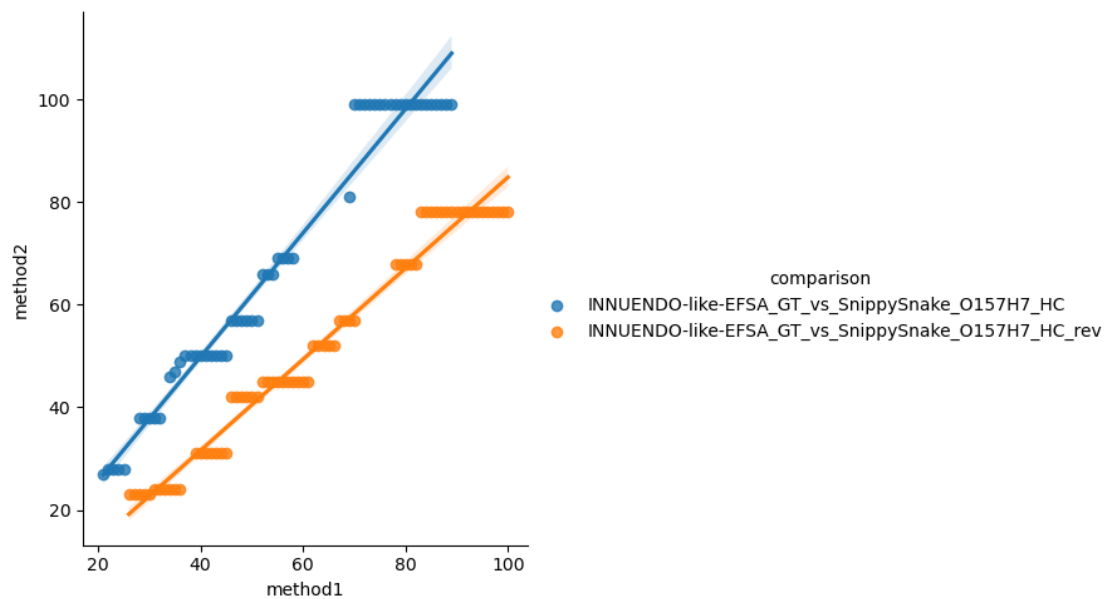


Figure S4.6.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for O157H7. A linear tendency line supported by 56 (blue) and 66 (orange) points is presented.

7. INNUENDO-like-EFSA 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-EFSA single-linkage	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	Sakai (NC_002695)
Dataset	All Samples	O157H7

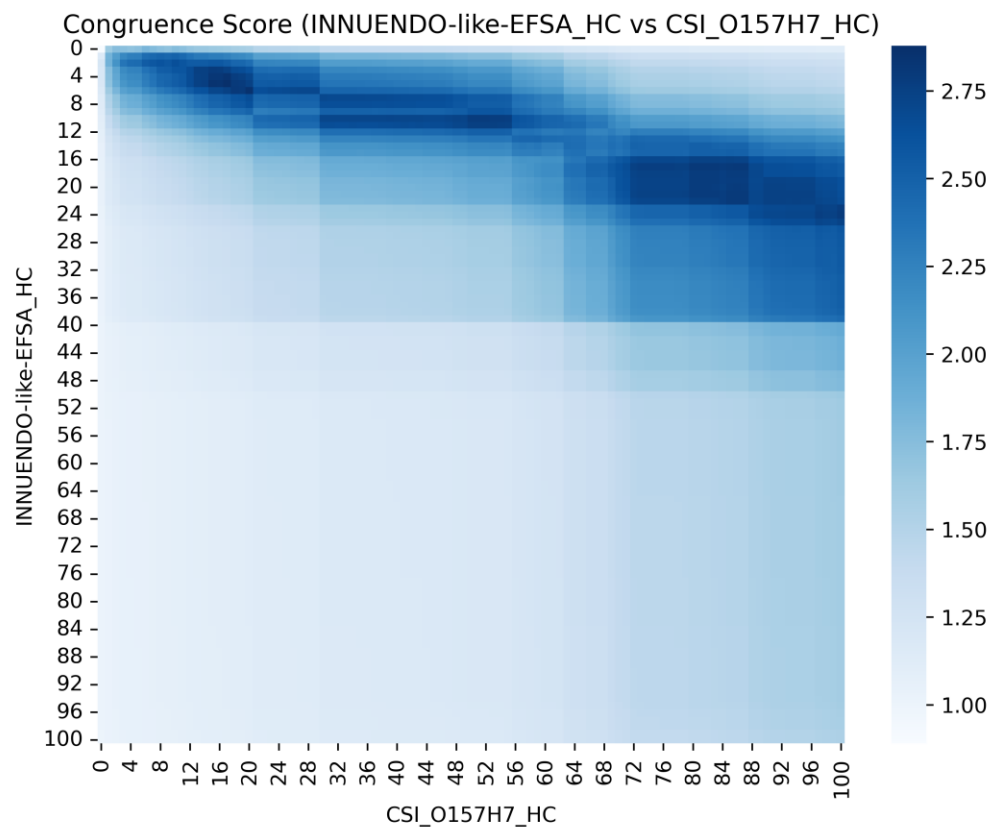


Figure S4.7.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

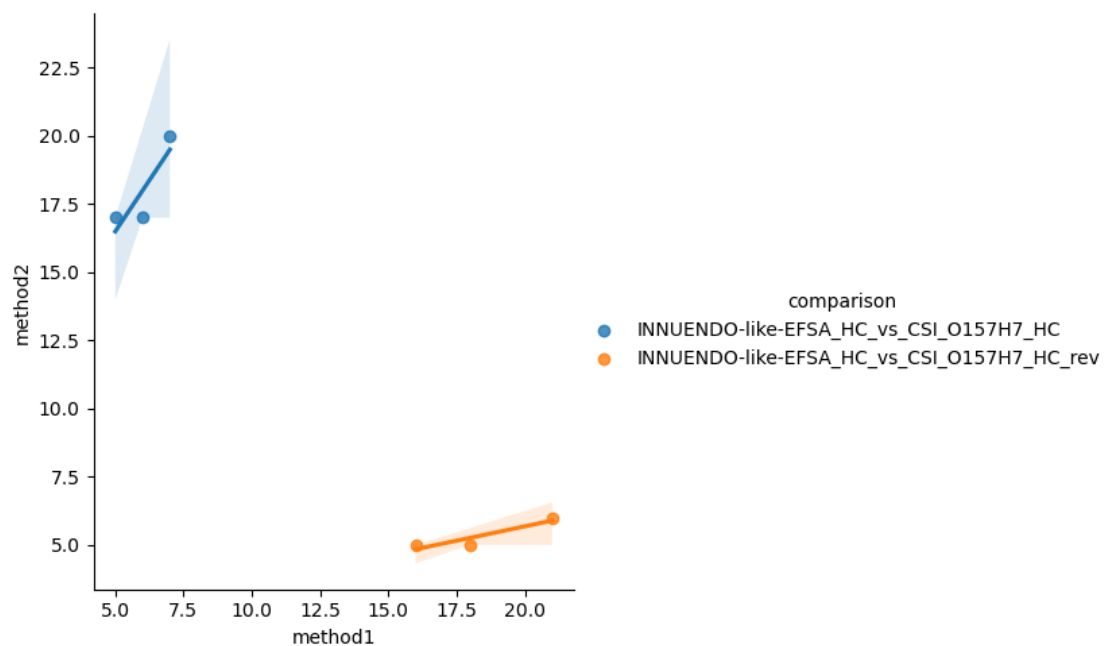


Figure S4.7.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for O157H7. A linear tendency line supported by 3 (blue) and 3 (orange) points is presented.

8. INNUENDO-like-EFSA single-linkage vs. snippySnake 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-EFSA single-linkage	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	EFSA	Sakai (NC_002695)
Dataset	All Samples	O157H7

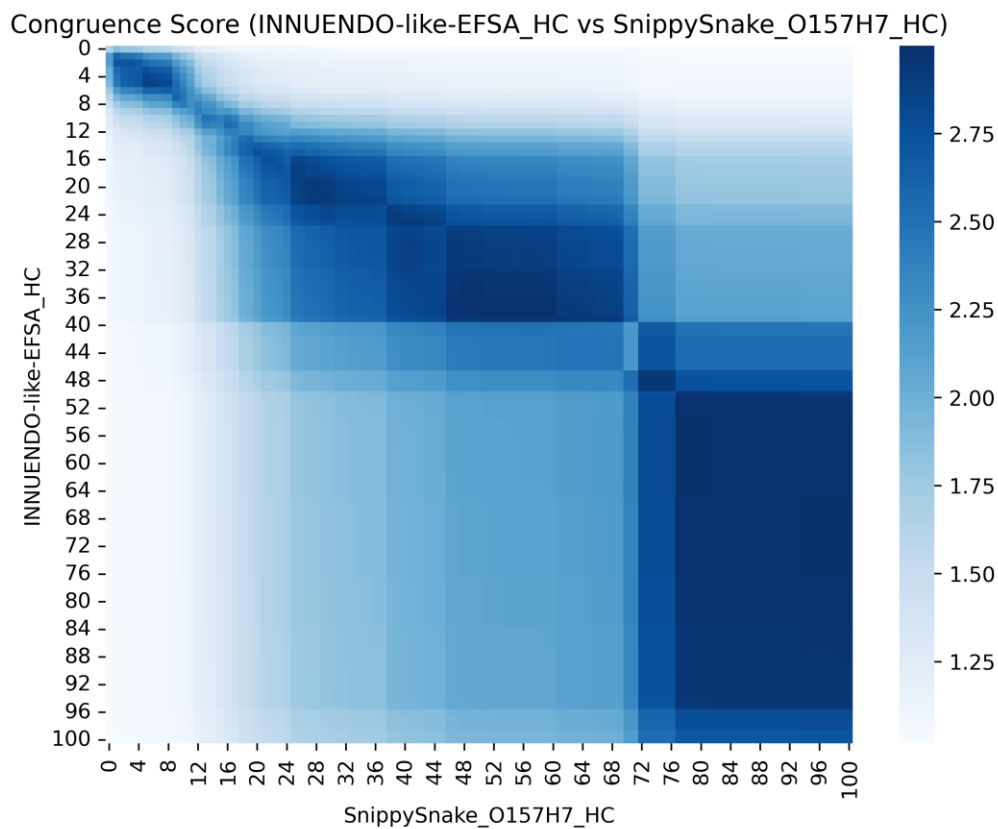


Figure S4.8.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

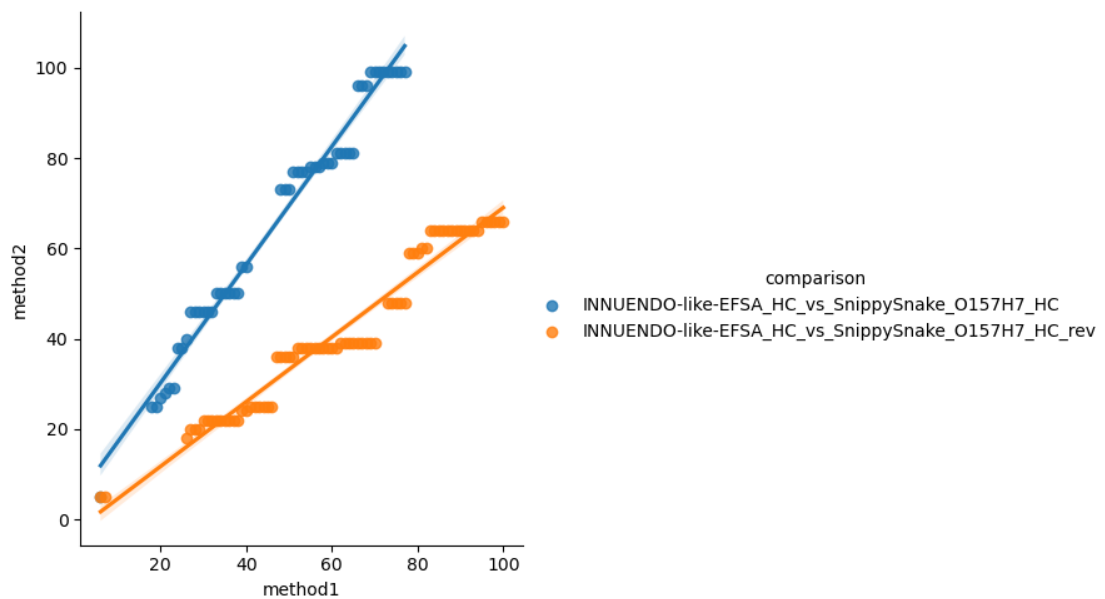


Figure S4.8.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for O157H7. A linear tendency line supported by 54 (blue) and 75 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

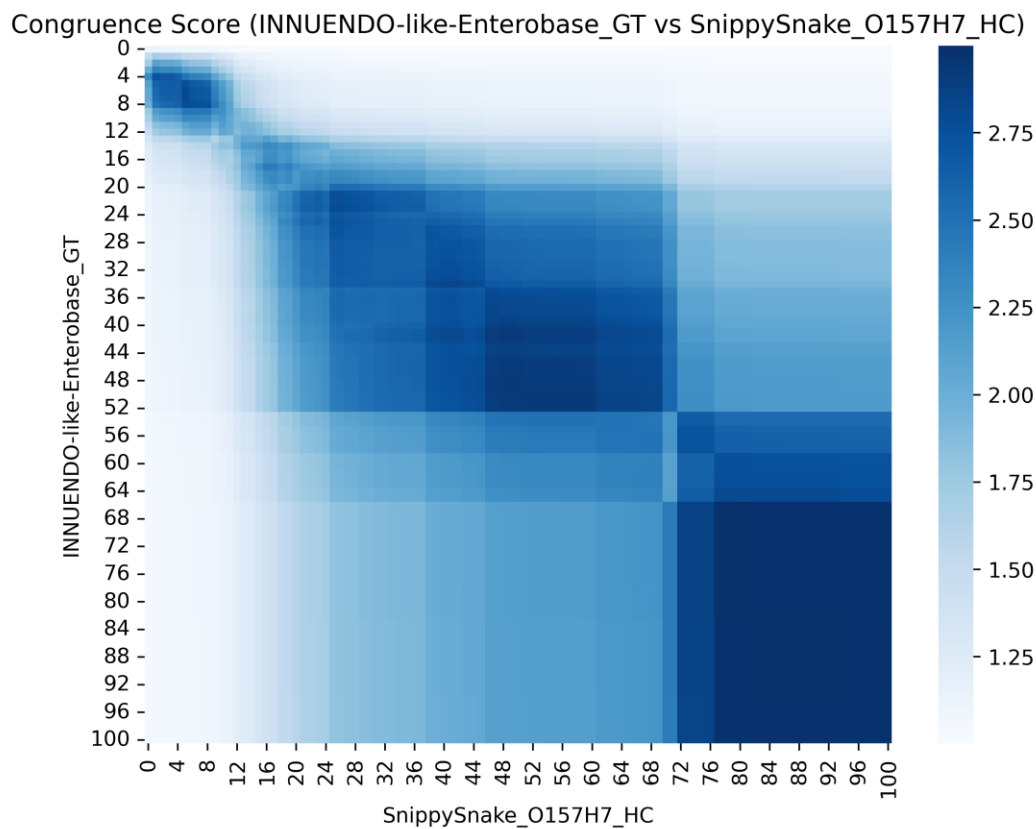


Figure S4.9.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

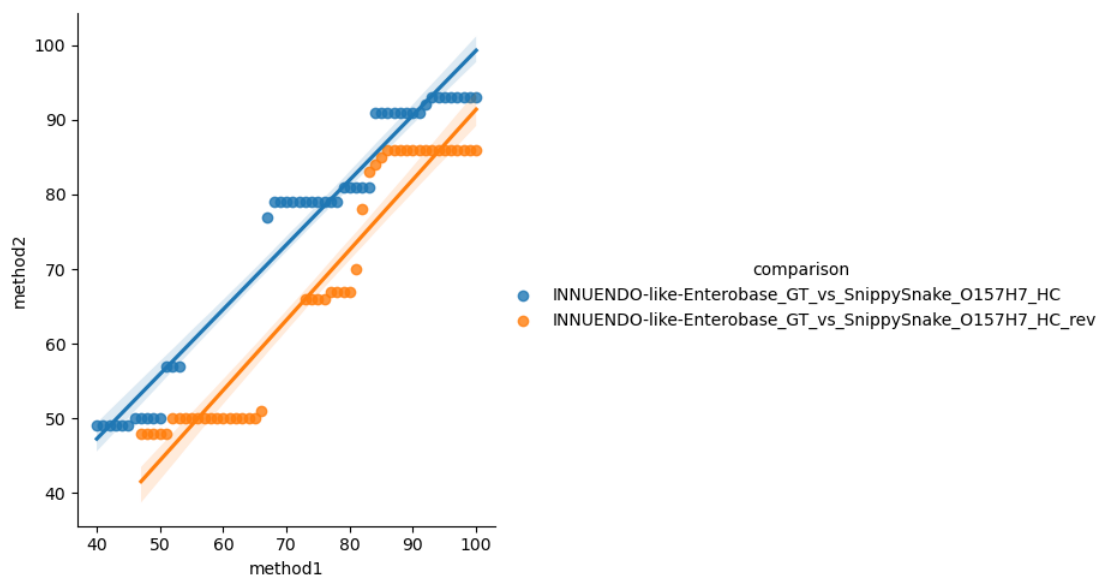


Figure S4.9.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for O157H7. A linear tendency line supported by 48 (blue) and 48 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

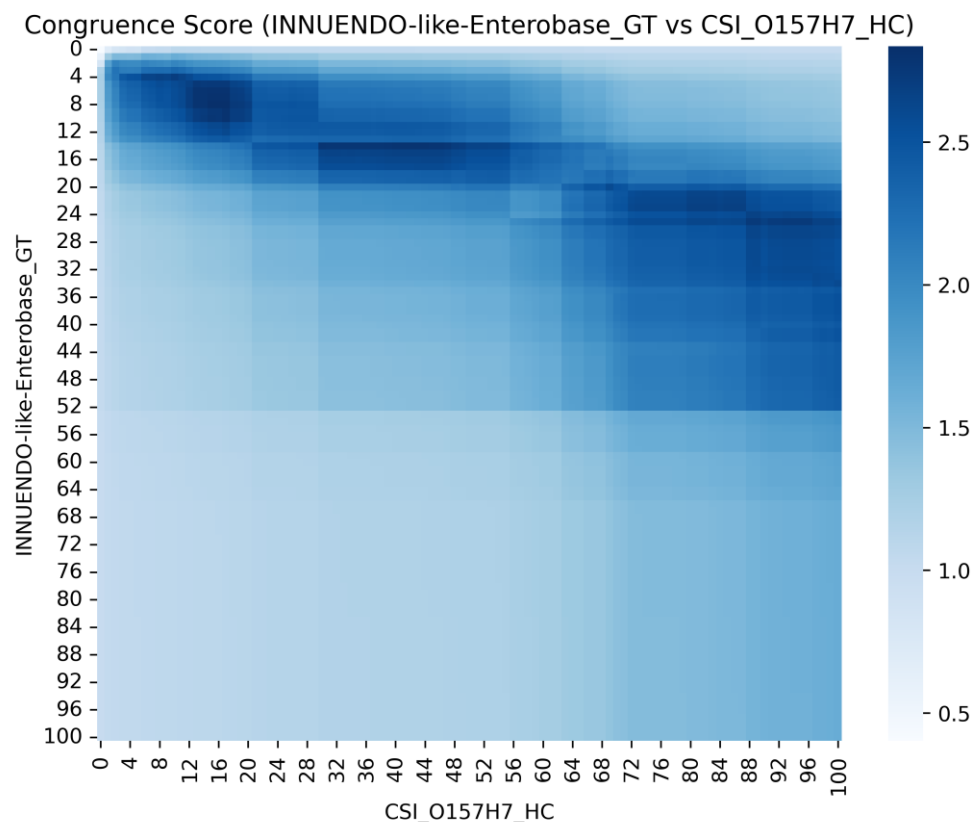


Figure S4.10.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

NOTE: No congruence points with $CS \geq 2.85$ were obtained up to threshold 100 when comparing the partitions of the two pipelines for O157H7.

11. INNUENDO-like-Enterobase 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.

	INNUENDO-like-Enterobase single-linkage	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

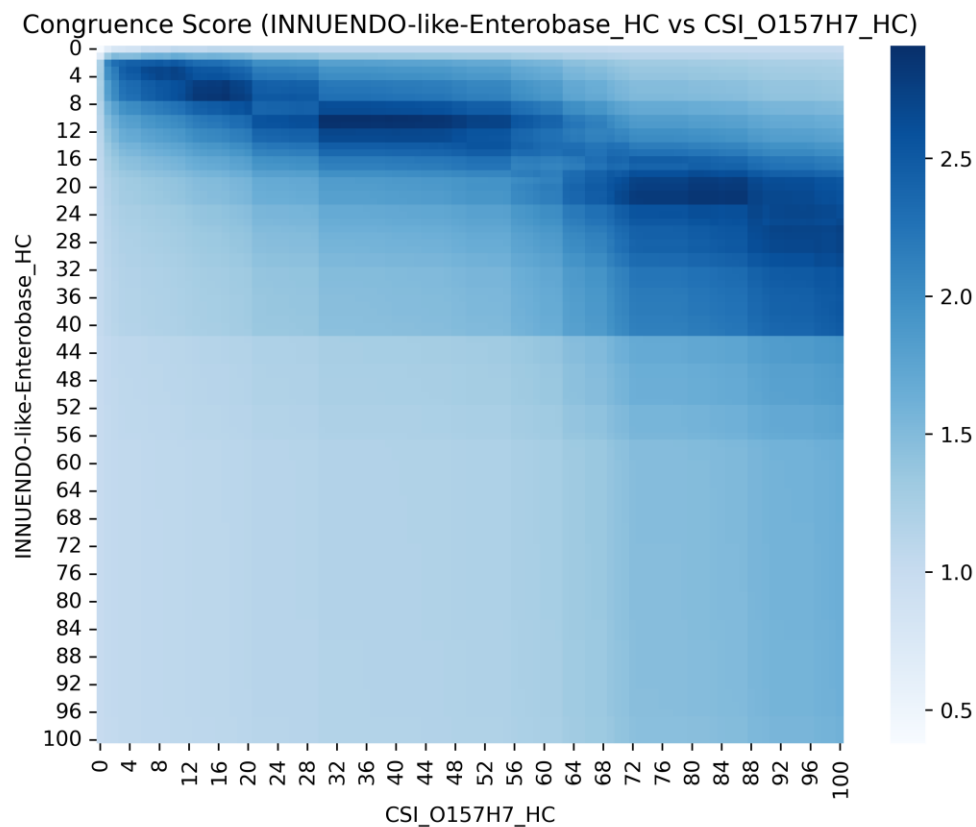


Figure S4.11.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

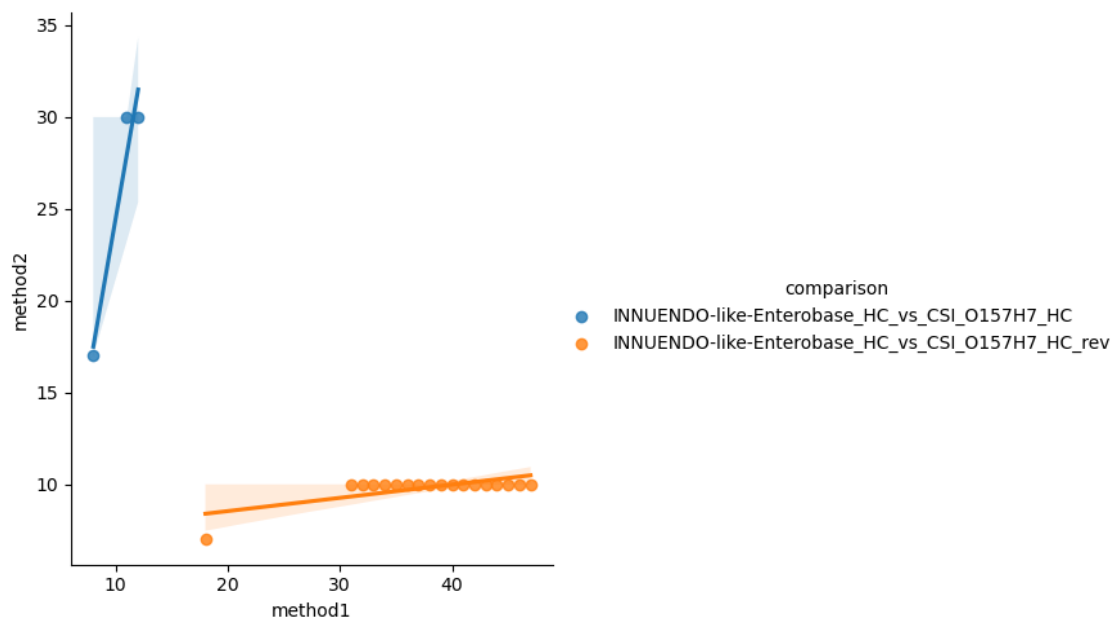


Figure S4.11.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for O157H7. A linear tendency line supported by 3 (blue) and 18 (orange) points is presented.

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

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

	INNUENDO-like-Enterobase single-linkage	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

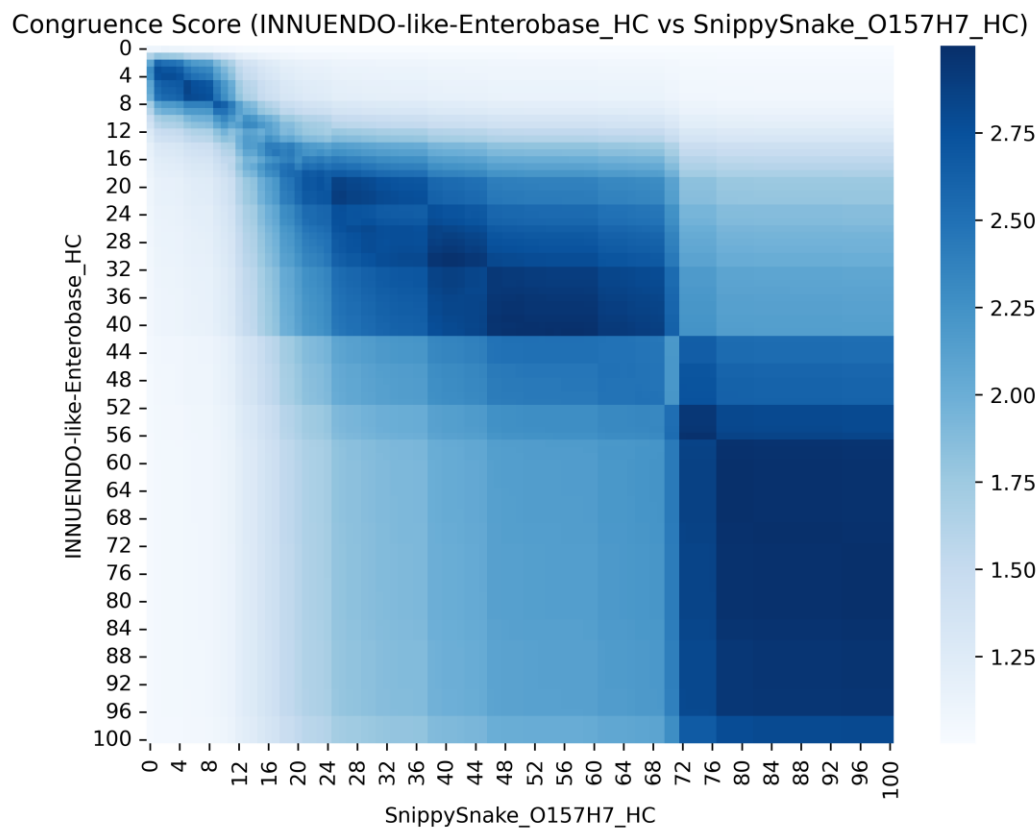


Figure S4.12.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

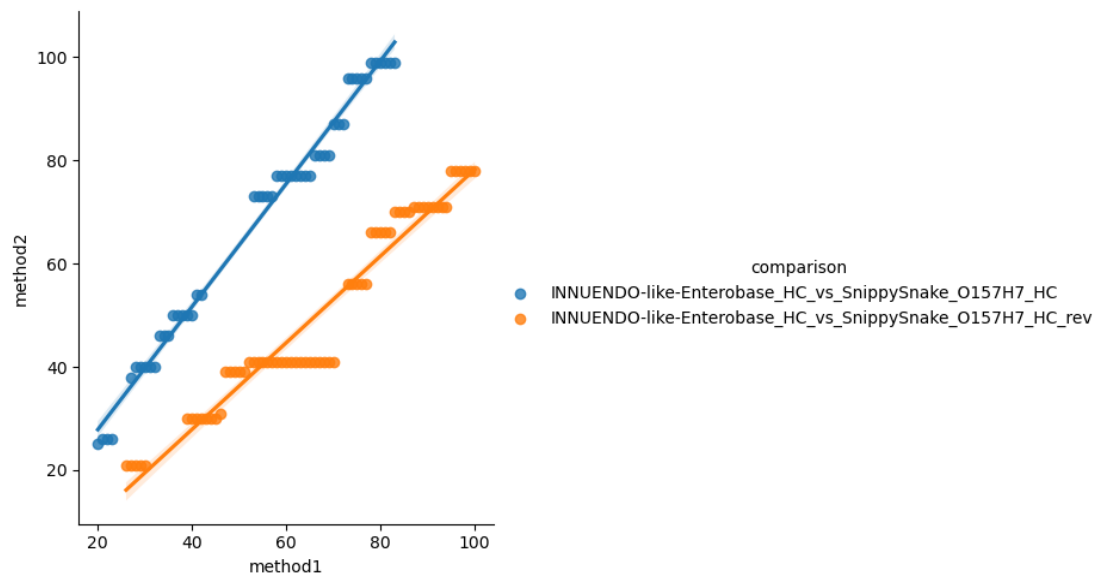


Figure S4.12.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for O157H7. A linear tendency line supported by 51 (blue) and 65 (orange) points is presented.

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

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

	INNUENDO-like-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)	Sakai (NC_002695)
Dataset	All Samples	O157H7

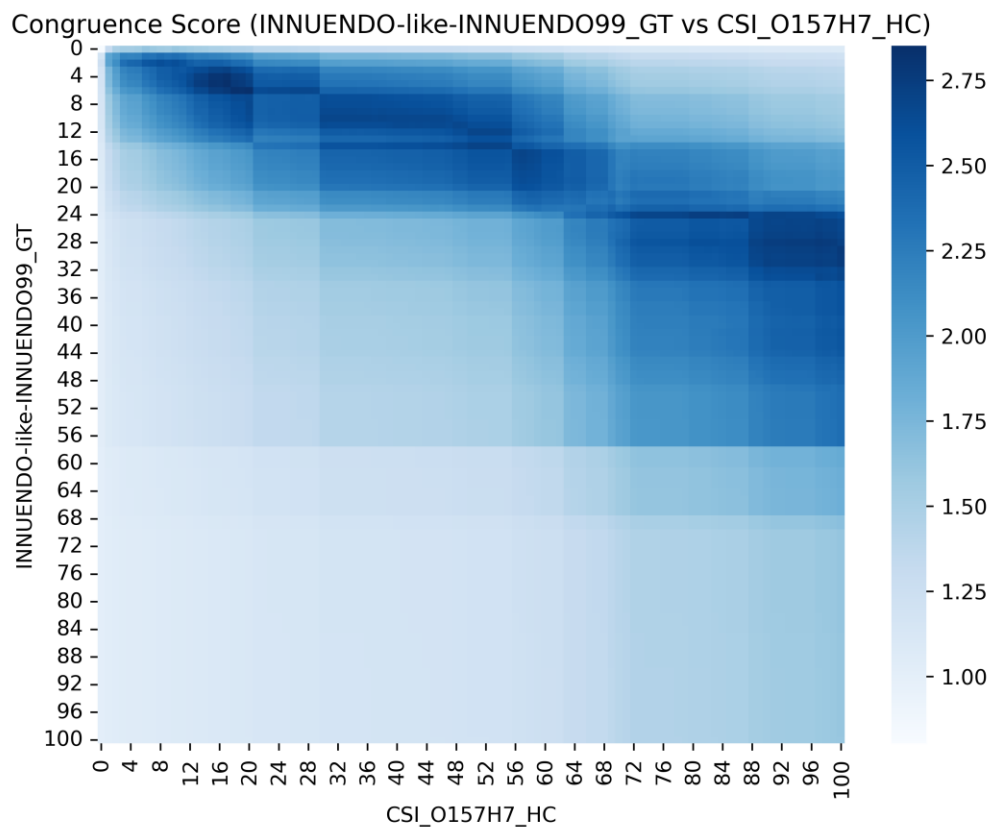


Figure S4.13.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

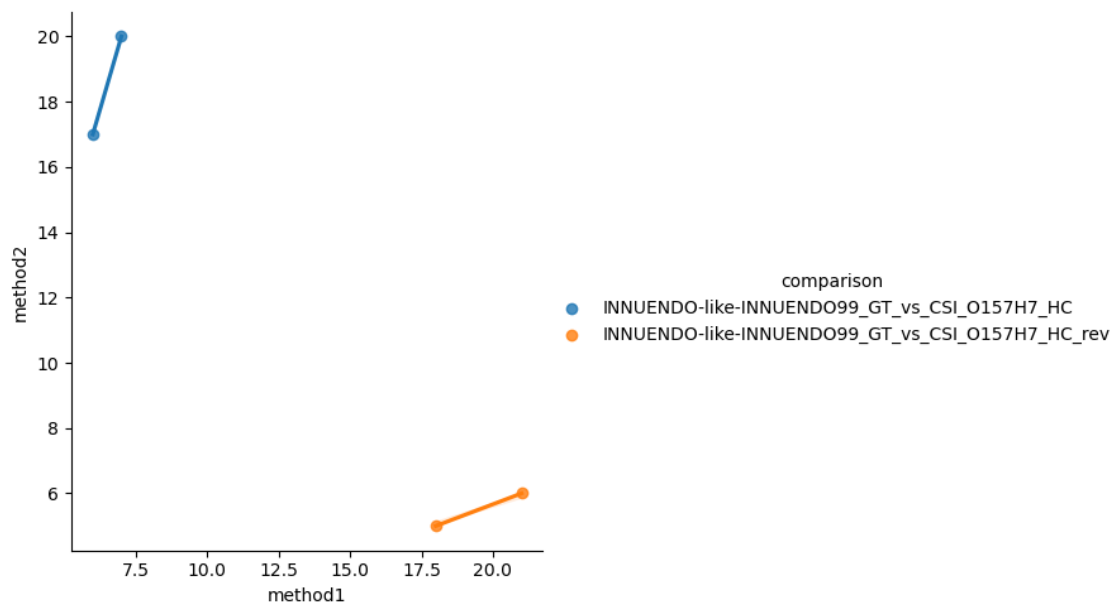


Figure S4.13.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 2 (blue) and 2 (orange) points is presented.

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

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

	INNUENDO-like-INNUENDO99 GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	Sakai (NC_002695)
Dataset	All Samples	O157H7

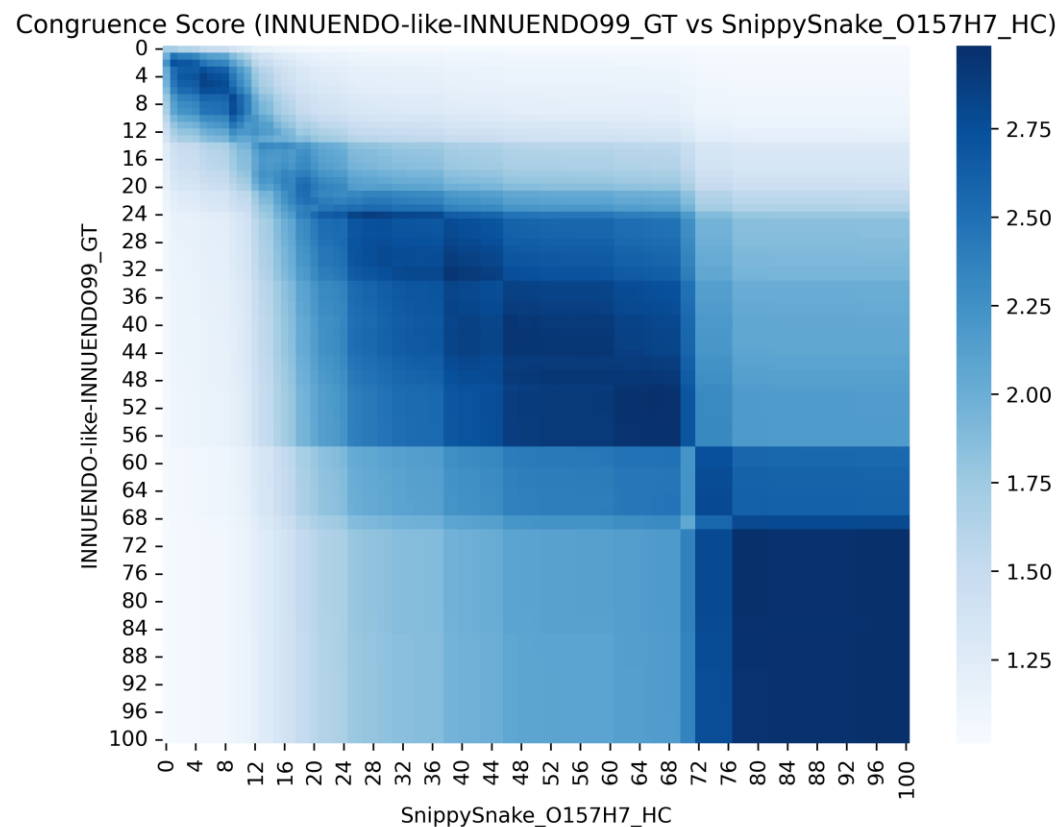


Figure S4.14.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

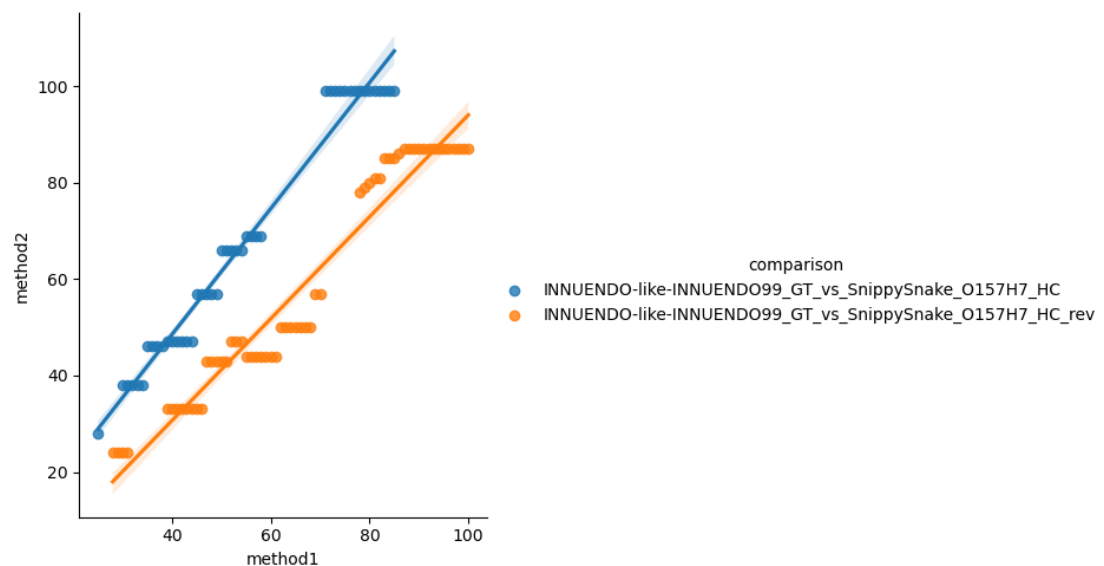


Figure S4.14.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 45 (blue) and 59 (orange) points is presented.

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

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

	INNUENDO-like-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)	Sakai (NC_002695)
Dataset	All Samples	O157H7

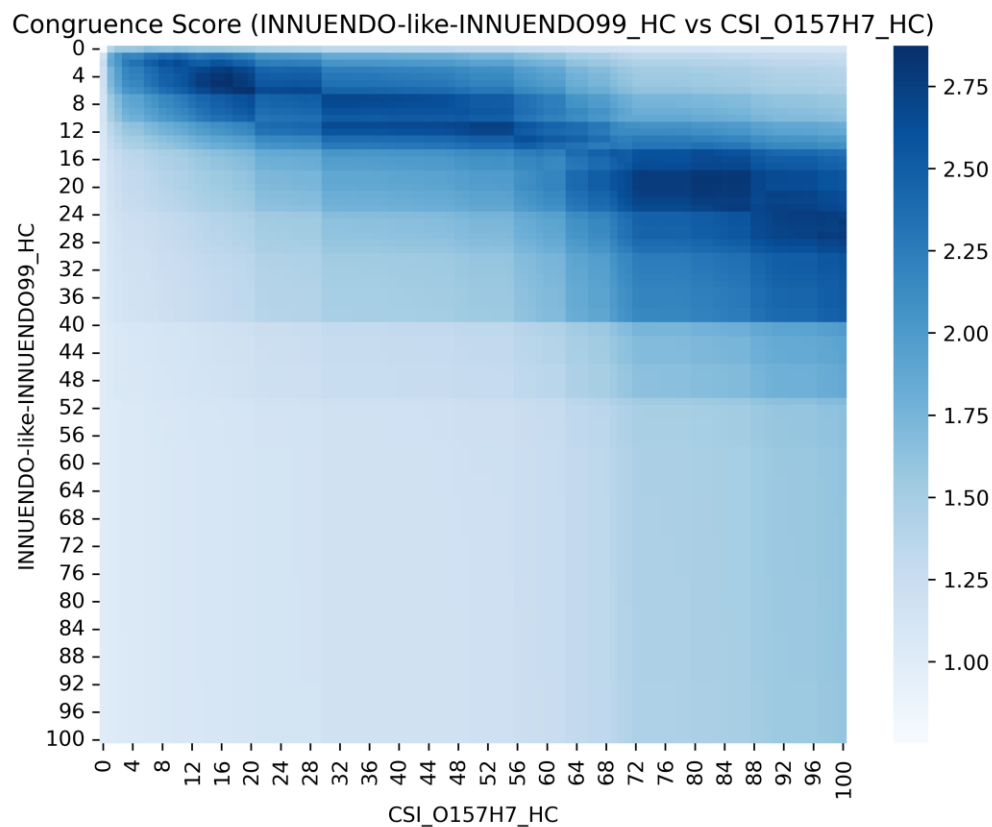


Figure S4.15.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

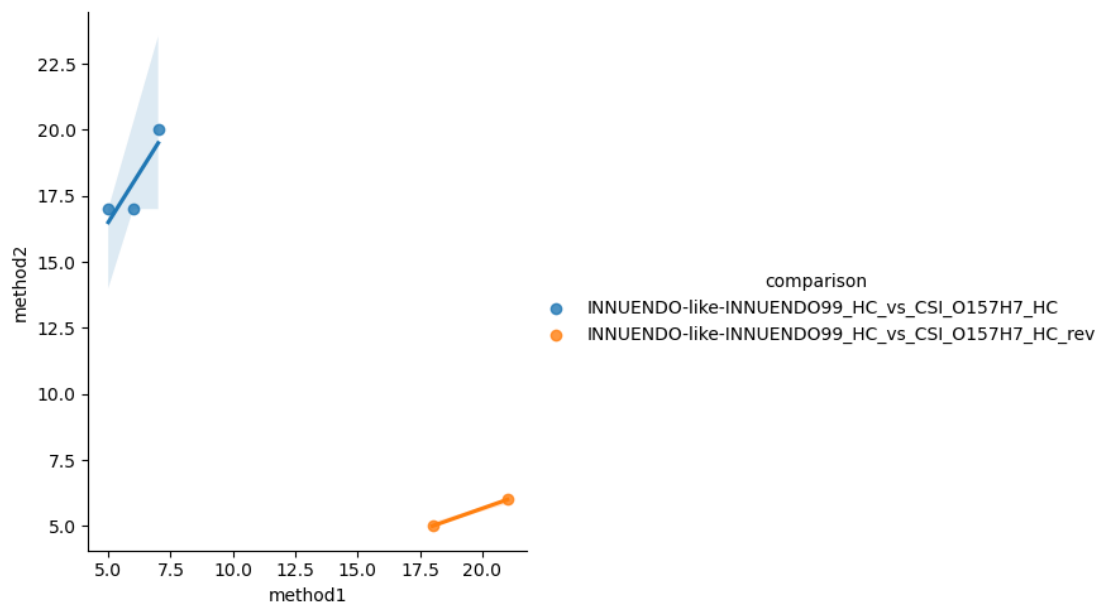


Figure S4.15.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 3 (blue) and 2 (orange) points is presented.

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

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

	INNUENDO-like-INNUENDO99 single-linkage	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	INNUENDO (wgMLST)	Sakai (NC_002695)
Dataset	All Samples	O157H7

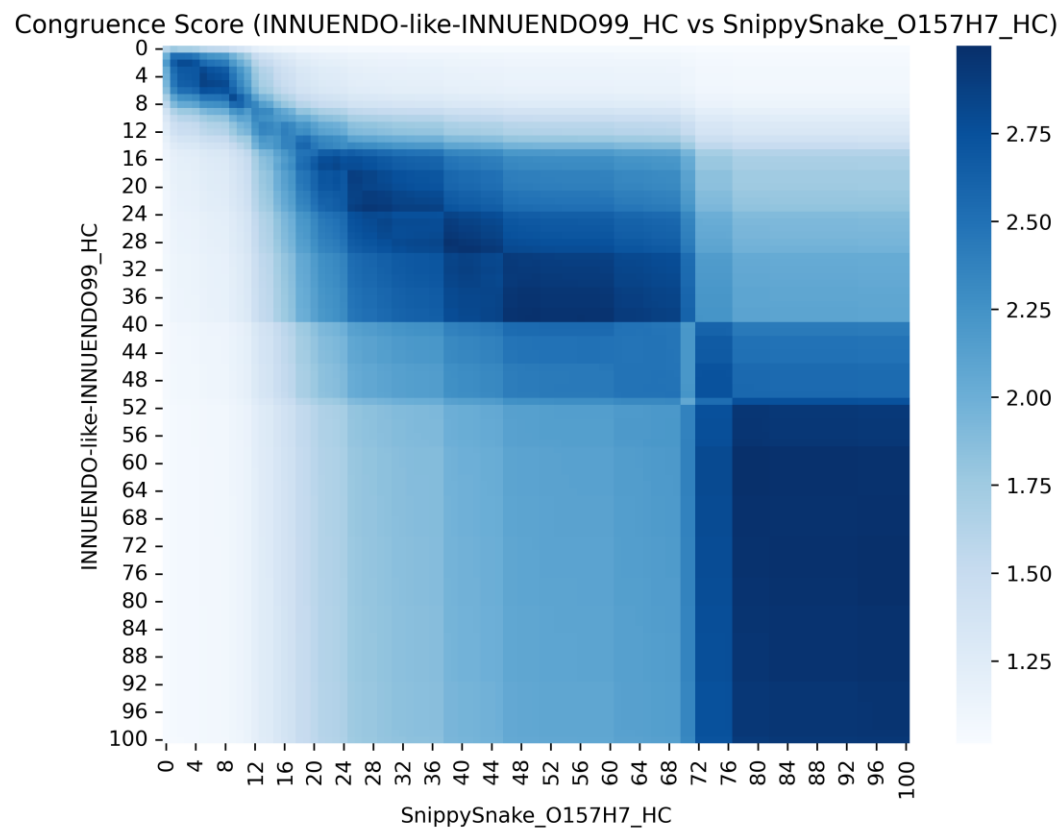


Figure S4.16.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

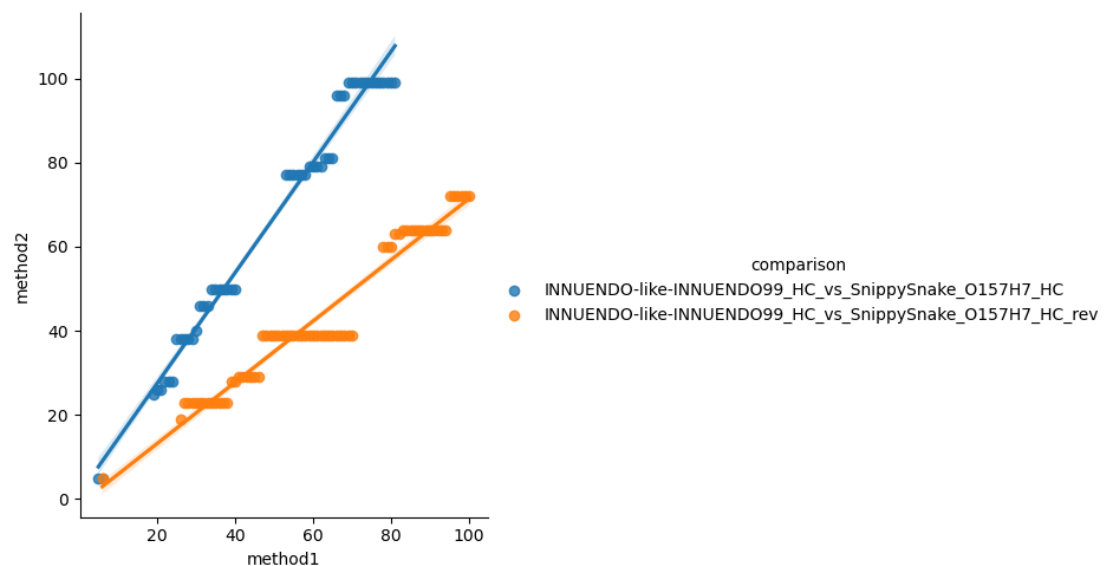


Figure S4.16.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 53 (blue) and 69 (orange) points is presented.

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

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

	SeqSphere single-linkage	CSI Phylogeny single-linkage
Pipeline version	v8.3.4	v1.4
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

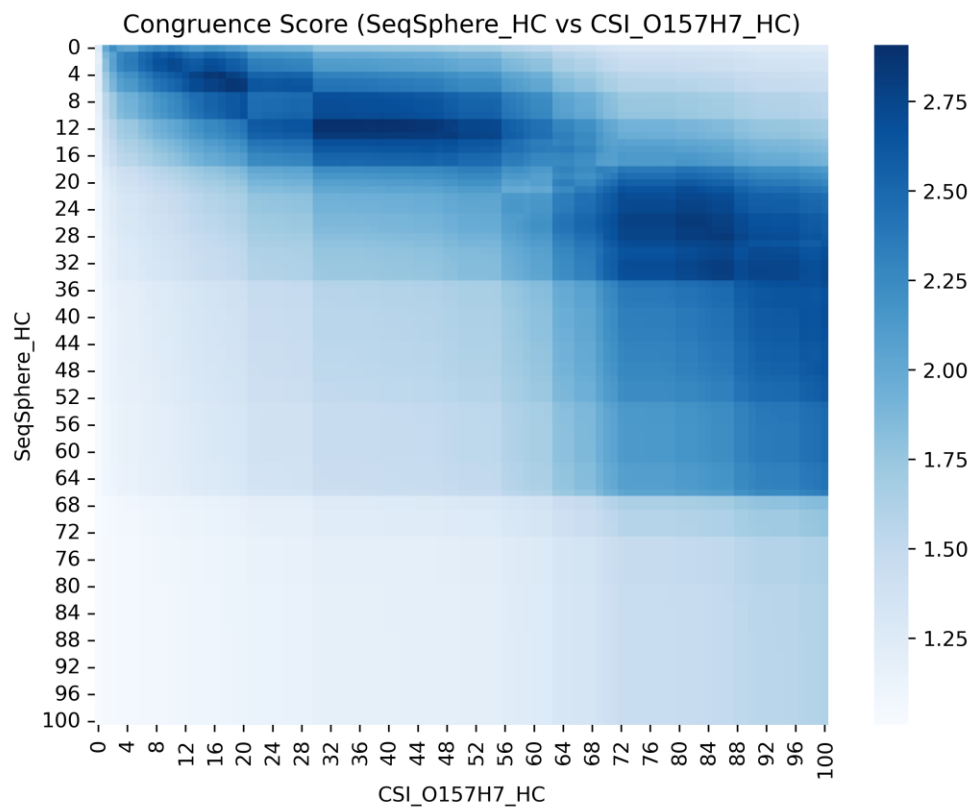


Figure S4.17.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

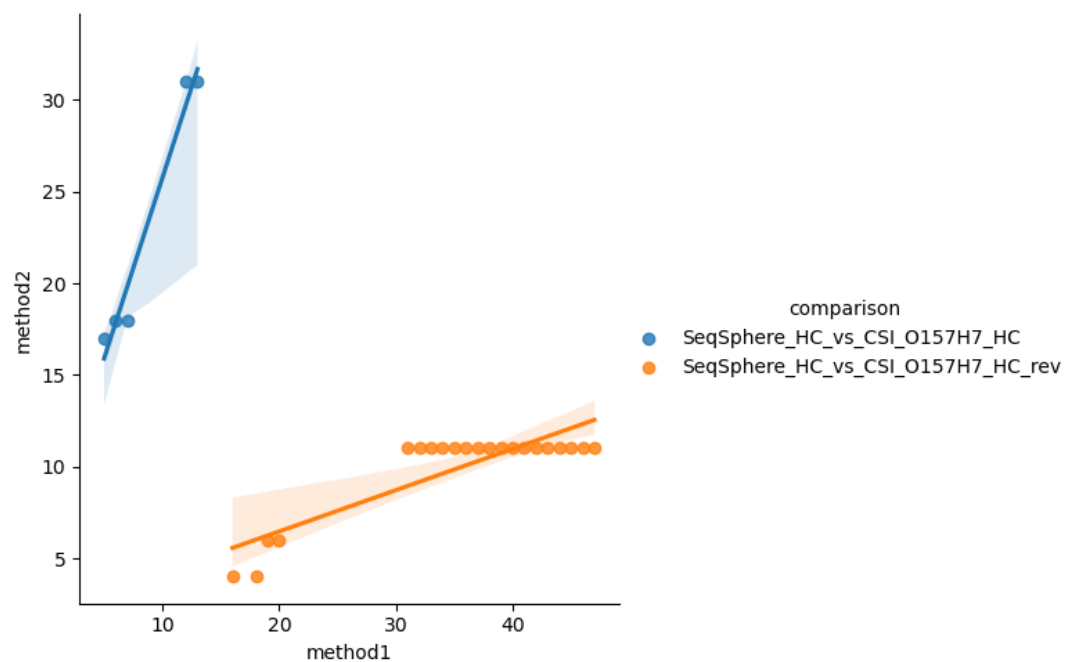


Figure S4.17.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for O157H7. A linear tendency line supported by 5 (blue) and 21 (orange) points is presented.

18. SeqSphere single-linkage vs. snippySnake single-linkage

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

	SeqSphere single-linkage	snippySnake single-linkage
Pipeline version	v8.3.4	v1.1.0
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema / Reference	Enterobase	Sakai (NC_002695)
Dataset	All Samples	O157H7

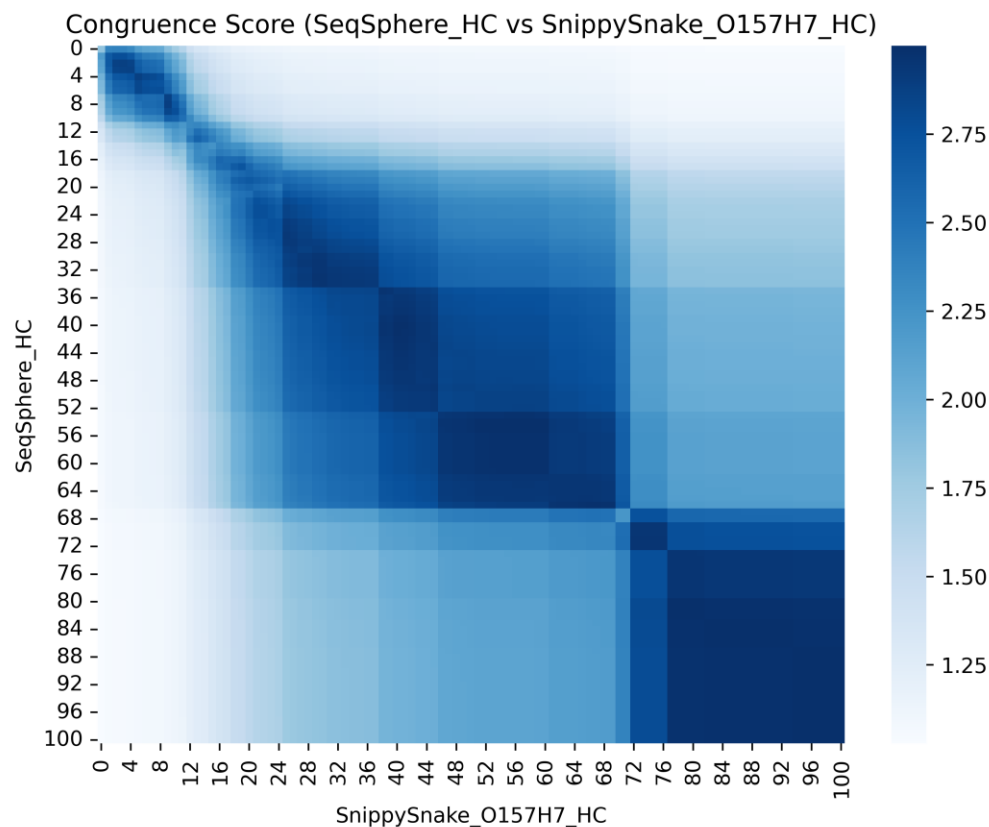


Figure S4.18.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for O157H7. Axis represent the different allele/SNP distance thresholds.

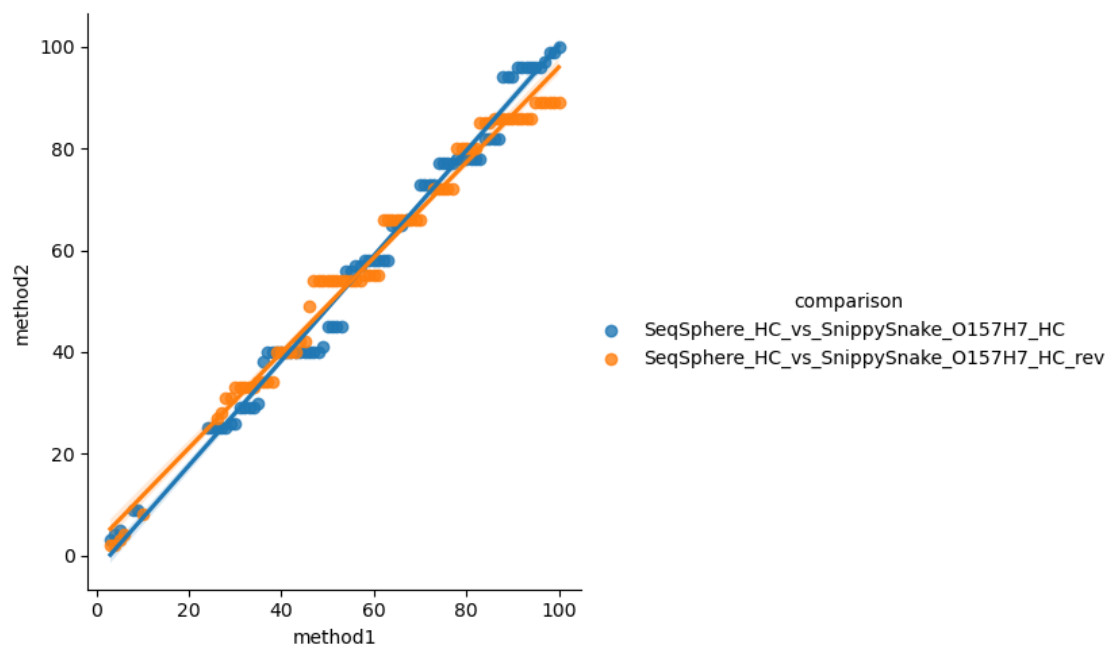


Figure S4.18.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for O157H7. A linear tendency line supported by 80 (blue) and 78 (orange) points is presented.