

Supplementary Data 2

Details on the analysis of the dataset of *Listeria monocytogenes*

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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 clonal complex (CC). CS – Congruence Score.

Pipeline	N	QC PASS	QC PASS (%)	Schema size	N partitions	Highest congruence point with ST (ADs)	CS	Highest congruence point CC (ADs)	CS
chewieSnake_HC	3300	3288	99.64	1691	1563	144	2.90	388	2.98
chewieSnake_GT	3300	3288	99.64	1691	1623	149	2.90	487	2.97
INNUENDO-like_HC	3300	3283	99.48	1748	1647	161	2.90	428	2.98
INNUENDO-like_GT	3300	3283	99.48	1748	1732	190	2.90	508	2.98
Ridom SeqSphere_HC	3300	3282	99.45	1691	1564	145	2.90	392	2.98
Bionumerics_HC	3300	3164	95.88	1748	1601	159	2.91	414	2.97
Mentalist_HC	3300	3296	99.88	1623/1748	1535	143	2.90	393	2.98
Mentalist_GT	3300	3296	99.88	1623/1748	1595	172	2.90	465	2.98

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

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.

ST	Pipeline	N	QC PASS	QC PASS (%)	N partitions
1	snippySnake_HC	343	343	100.00	145
	CSI Phylogeny_HC	343	343	100.00	136
	WGSBAC_HC	343	343	100.00	145
5	snippySnake_HC	269	269	100.00	138
	CSI Phylogeny_HC	269	269	100.00	147
	WGSBAC_HC	269	269	100.00	138
6	snippySnake_HC	501	501	100.00	57
	CSI Phylogeny_HC	501	500	99.80	60
	WGSBAC_HC	501	501	100.00	57
8	snippySnake_HC	247	247	100.00	63
	CSI Phylogeny_HC	247	247	100.00	50
	WGSBAC_HC	247	247	100.00	63
121	snippySnake_HC	240	240	100.00	1124
	CSI Phylogeny_HC	240	240	100.00	508
	WGSBAC_HC	240	240	100.00	1124
All	CSI Phylogeny_HC	1600	1598	99.88	5839

Section 1 – Supporting data

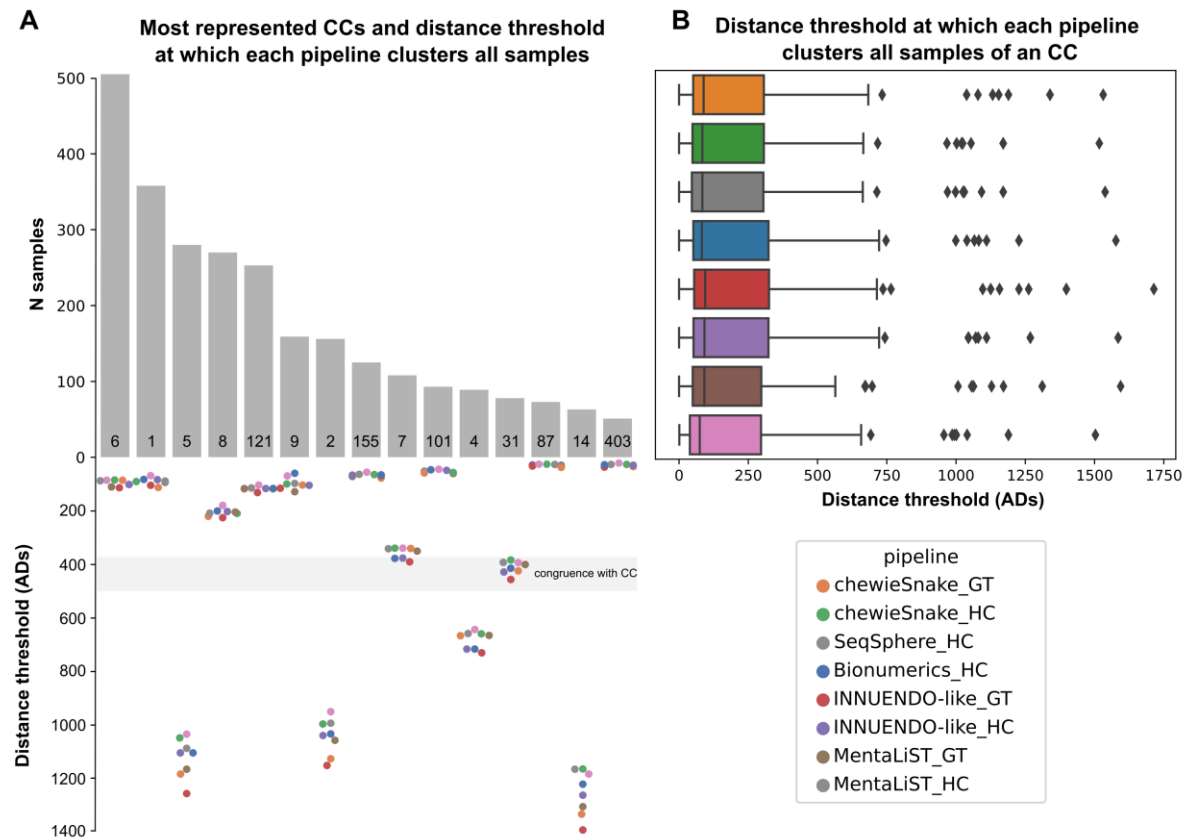


Figure S1. Allele-based clustering congruence with traditional typing (CC). **A)** Barplot (top) with the number of samples of the top represented CCs (≥ 50 samples) present in the *L. monocytogenes* dataset, with a swarmplot (bottom) indicating the ADs at which each pipeline clusters together all samples of each of these CCs. **B)** Distribution of the AD thresholds at which each pipeline clusters together all samples of a given CC.

Section 2 – Comparison of allele-based pipelines

1. chewieSnake GrapeTree vs. Bionumerics single-linkage

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

	chewieSnake GrapeTree	Bionumerics single-linkage
Pipeline version	v3.1.1	v8.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1623	1601

Section 2 – Comparison of allele-based pipelines

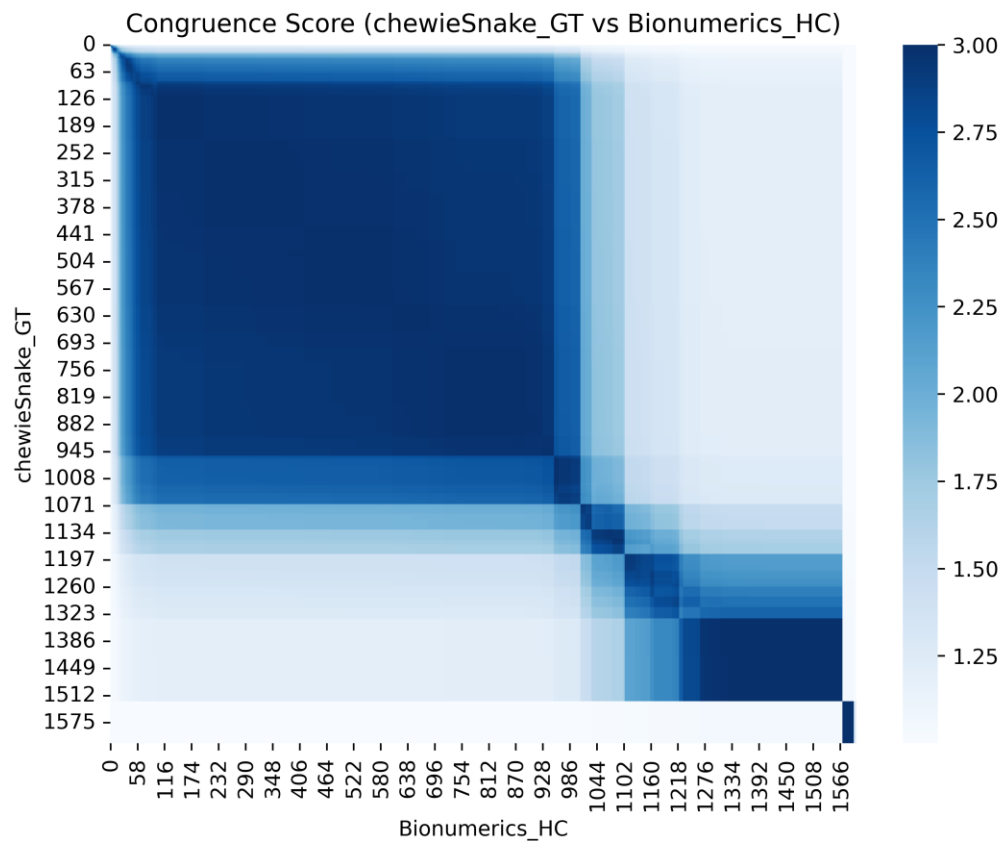


Figure S2.1.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

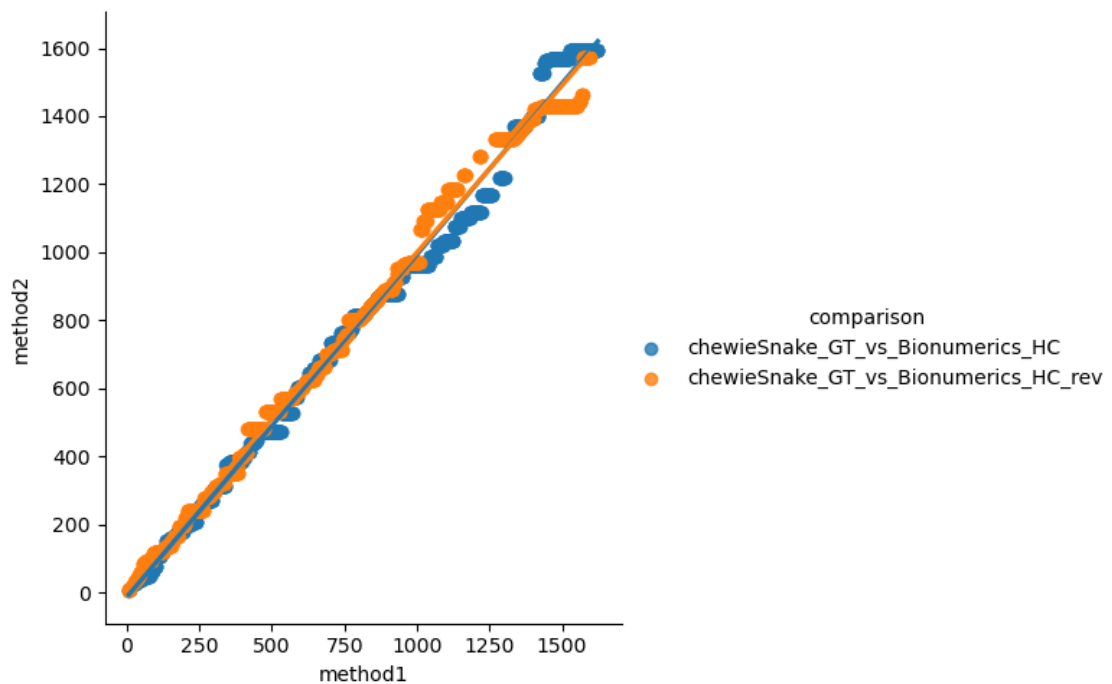


Figure S2.1.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1544 (blue) and 1455 (orange) points is presented.

2. chewieSnake GrapeTree 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.

	chewieSnake GrapeTree	chewieSnake single-linkage
Pipeline version	v3.1.1	v3.1.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Ruppitsch
Dataset	All samples	All samples
Number partitions	1623	1563

Section 2 – Comparison of allele-based pipelines

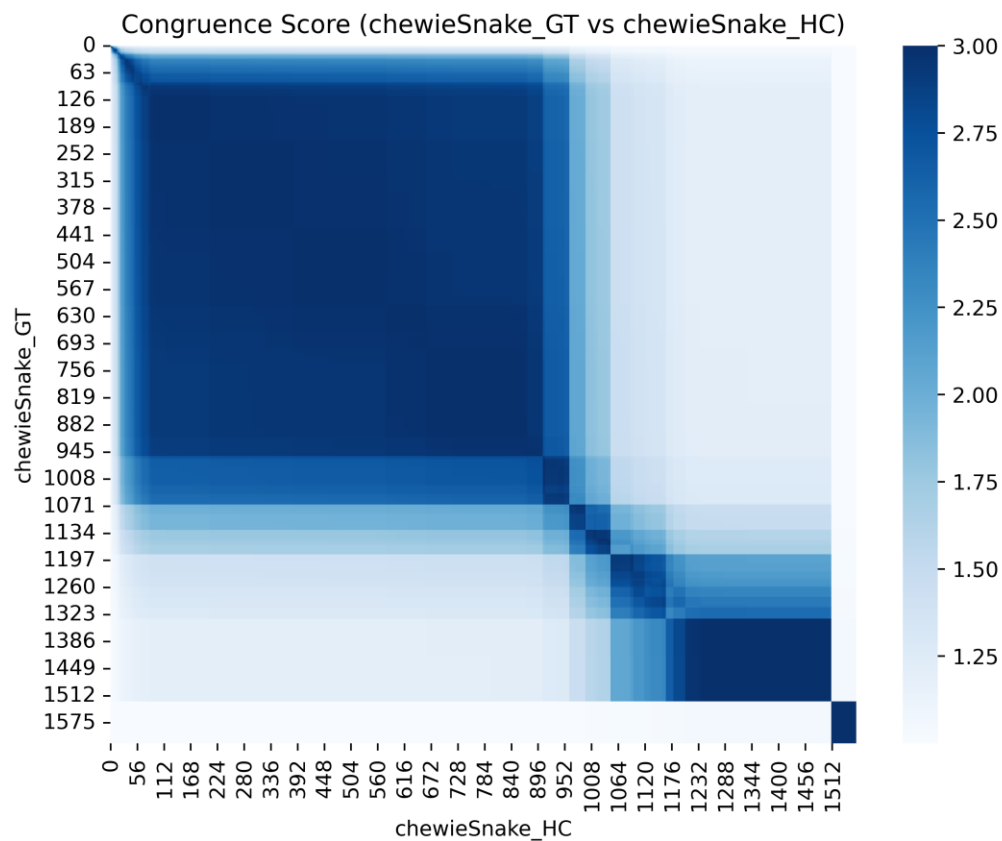


Figure S2.2.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

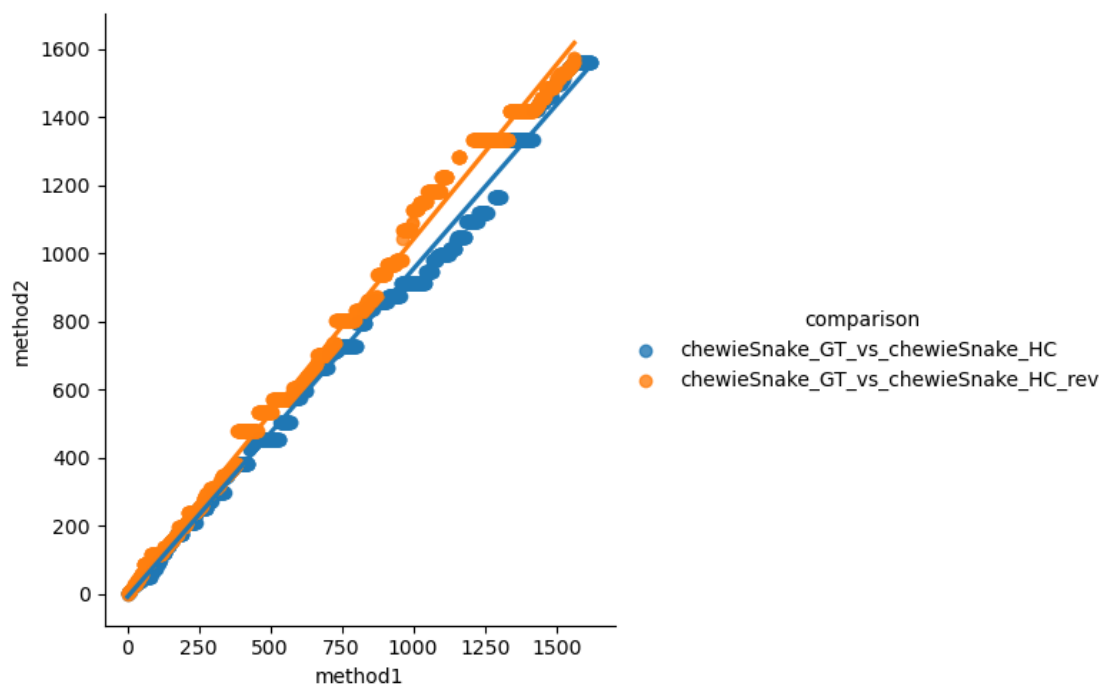


Figure S2.2.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1556 (blue) and 1475 (orange) points is presented.

3. chewieSnake GrapeTree vs. INNUENDO-like GrapeTree

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 GrapeTree
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1623	1732

Section 2 – Comparison of allele-based pipelines

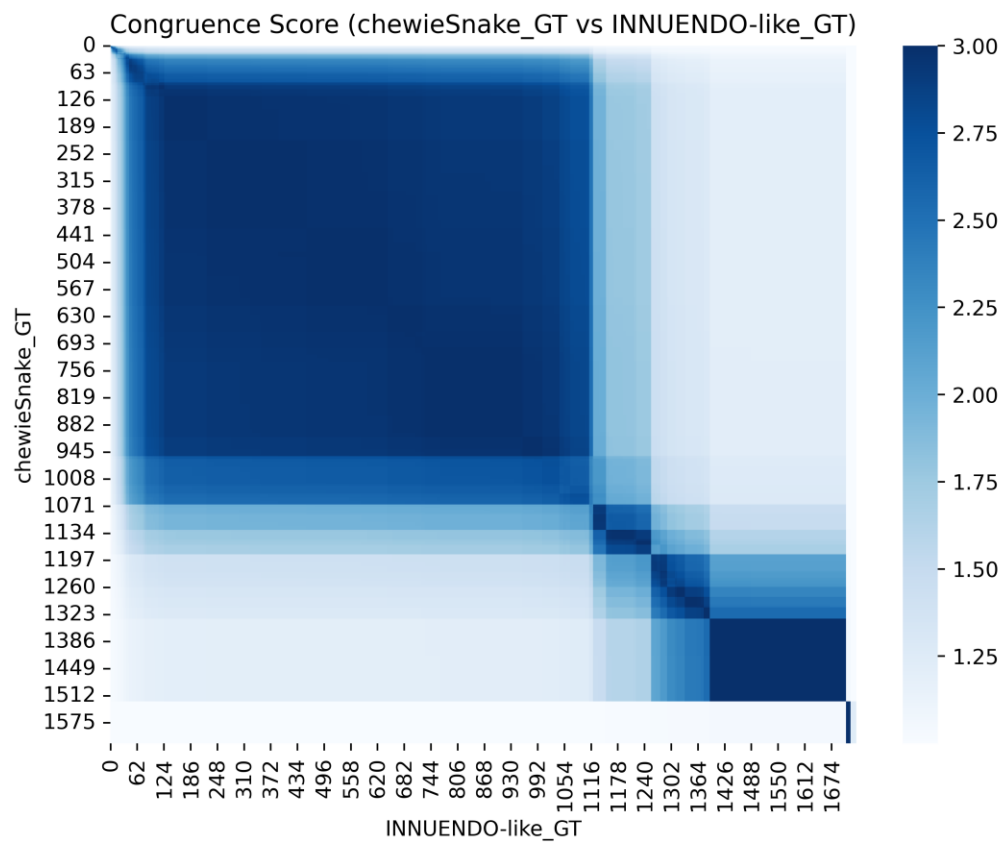


Figure S2.3.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

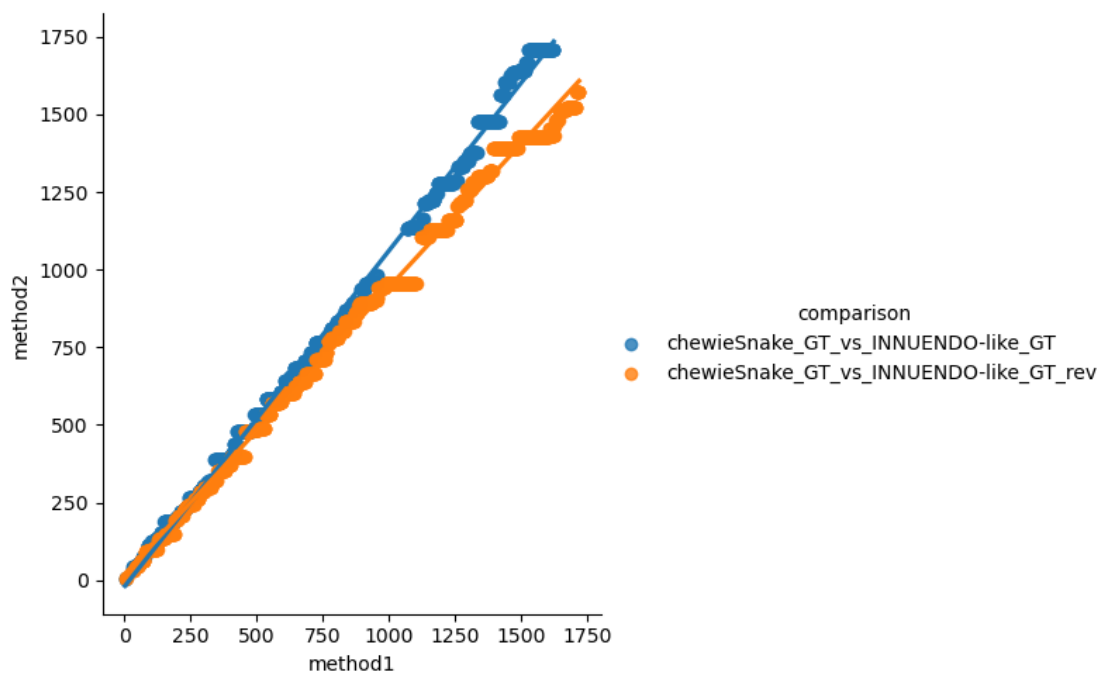


Figure S2.3.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1477 (blue) and 1664 (orange) points is presented.

4. chewieSnake GrapeTree vs. INNUENDO-like single-linkage

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.

	chewieSnake GrapeTree	INNUENDO-like single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1623	1647

Section 2 – Comparison of allele-based pipelines

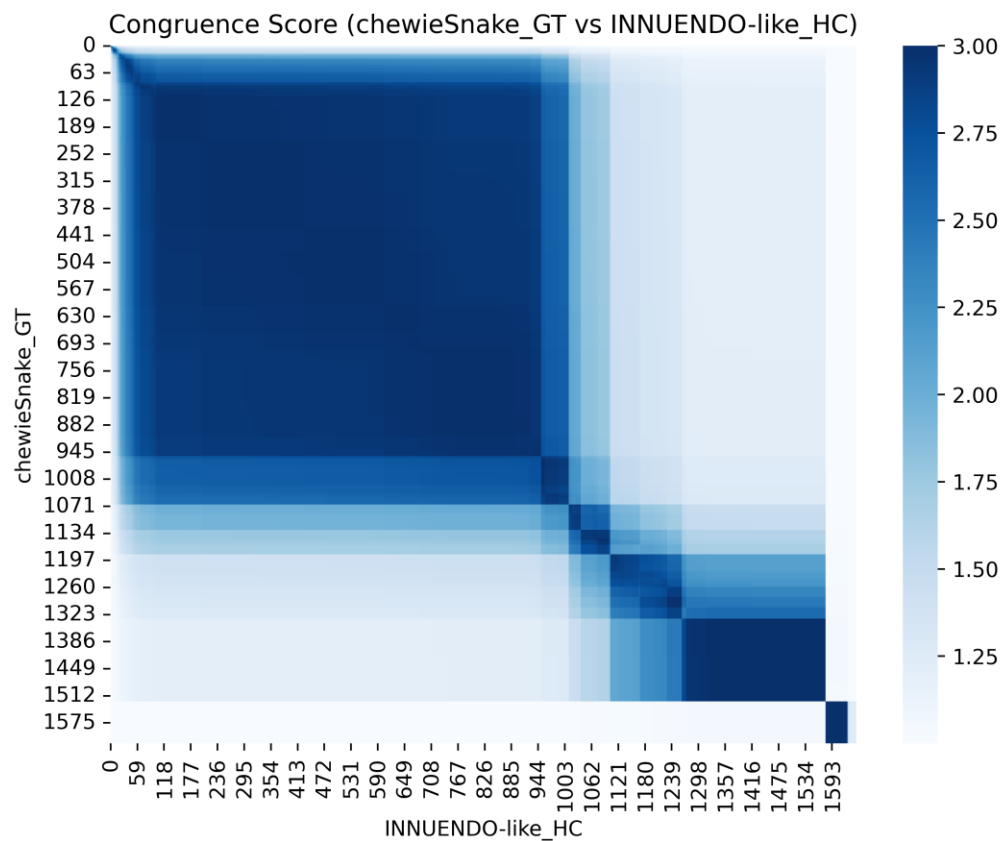


Figure S2.4.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

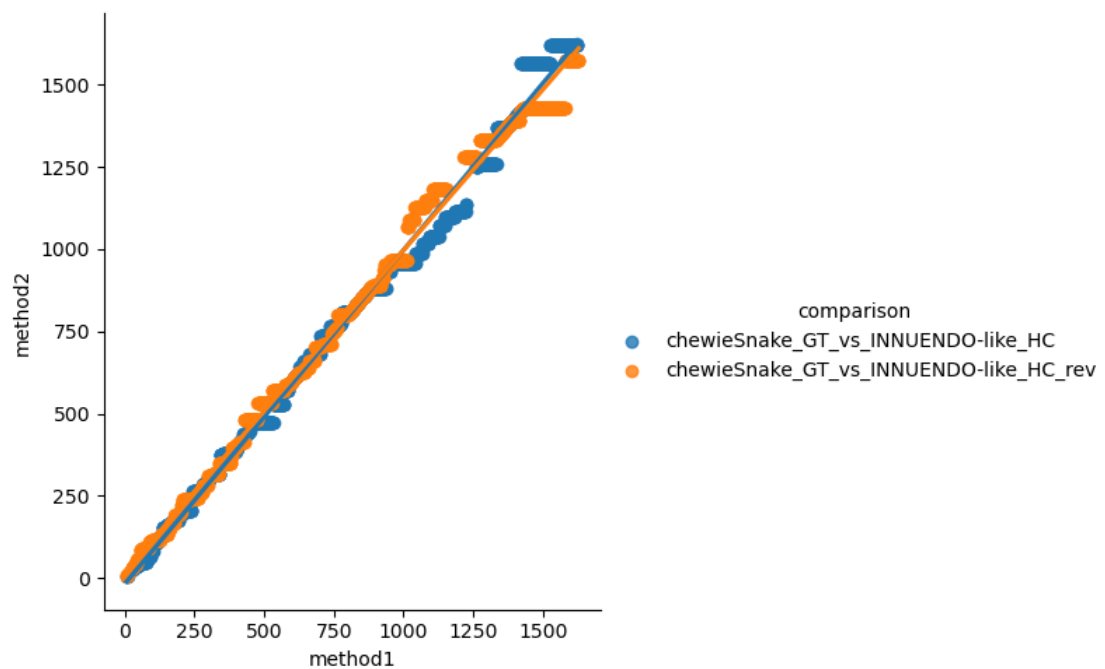


Figure S2.4.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1563 (blue) and 1529 (orange) points is presented.

5. chewieSnake GrapeTree vs. MentaLiST GrapeTree

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.

	chewieSnake GrapeTree	MentaLiST GrapeTree
Pipeline version	v3.1.1	v1.0.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1623	1595

Section 2 – Comparison of allele-based pipelines

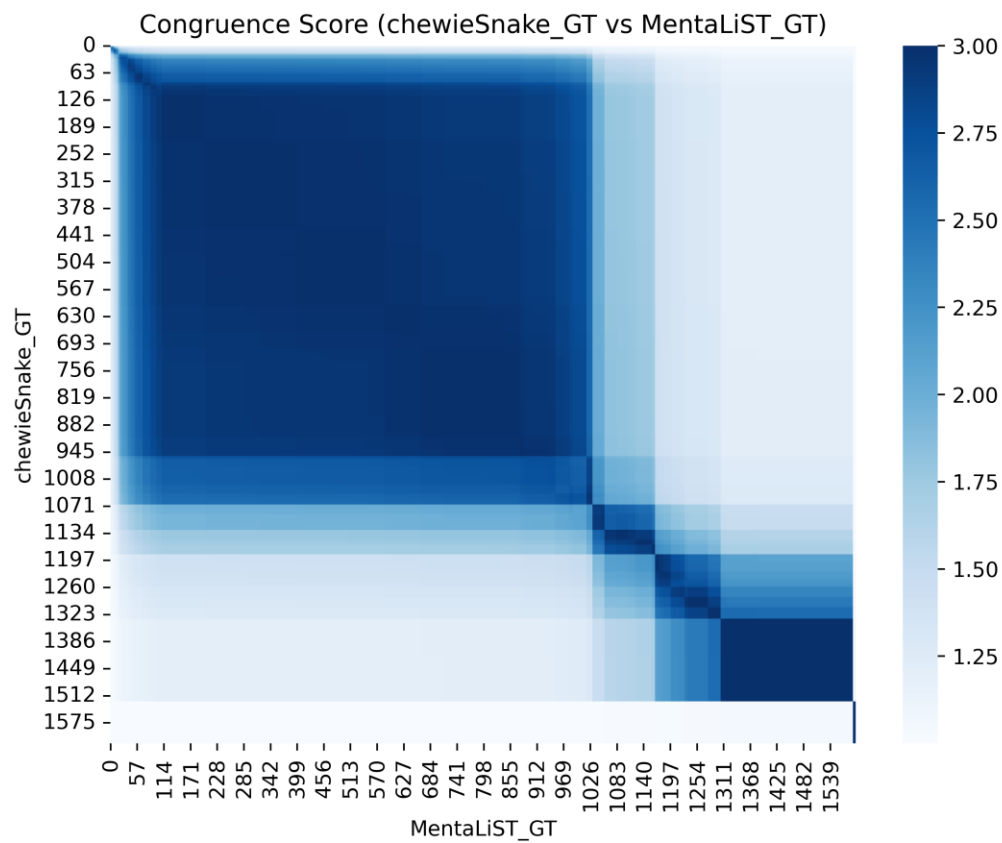


Figure S2.5.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

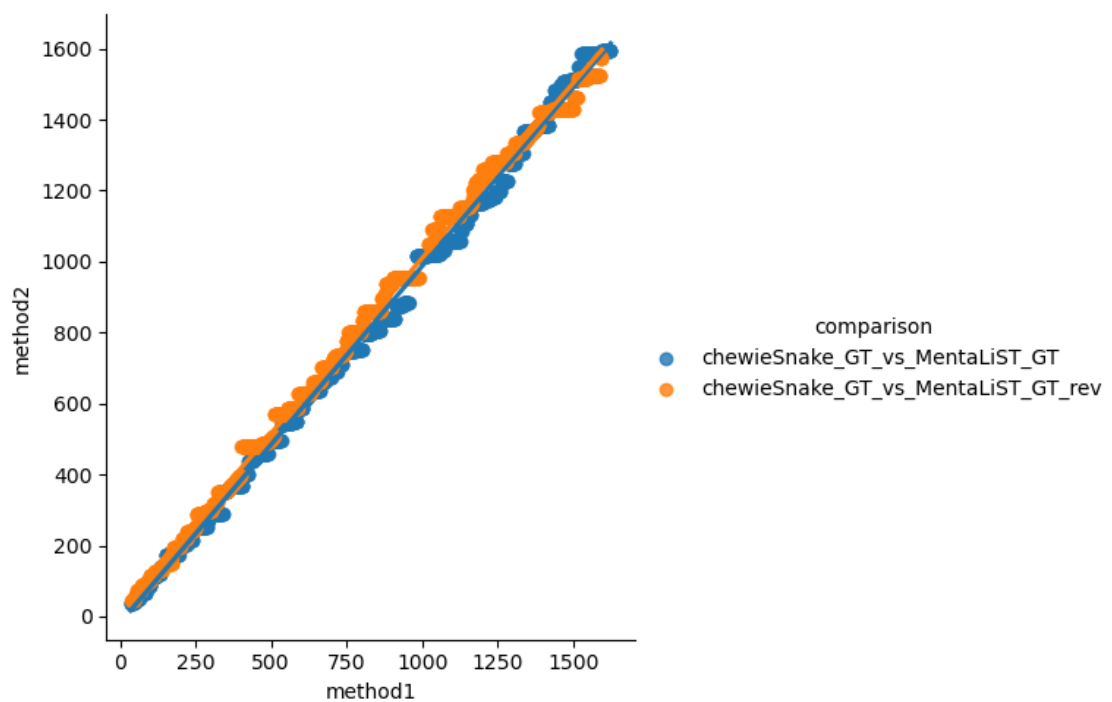


Figure S2.5.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1566 (blue) and 1528 (orange) points is presented.

6. chewieSnake GrapeTree vs. MentaLiST single-linkage

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

	chewieSnake GrapeTree	MentaLiST single-linkage
Pipeline version	v3.1.1	v1.0.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1623	1535

Section 2 – Comparison of allele-based pipelines

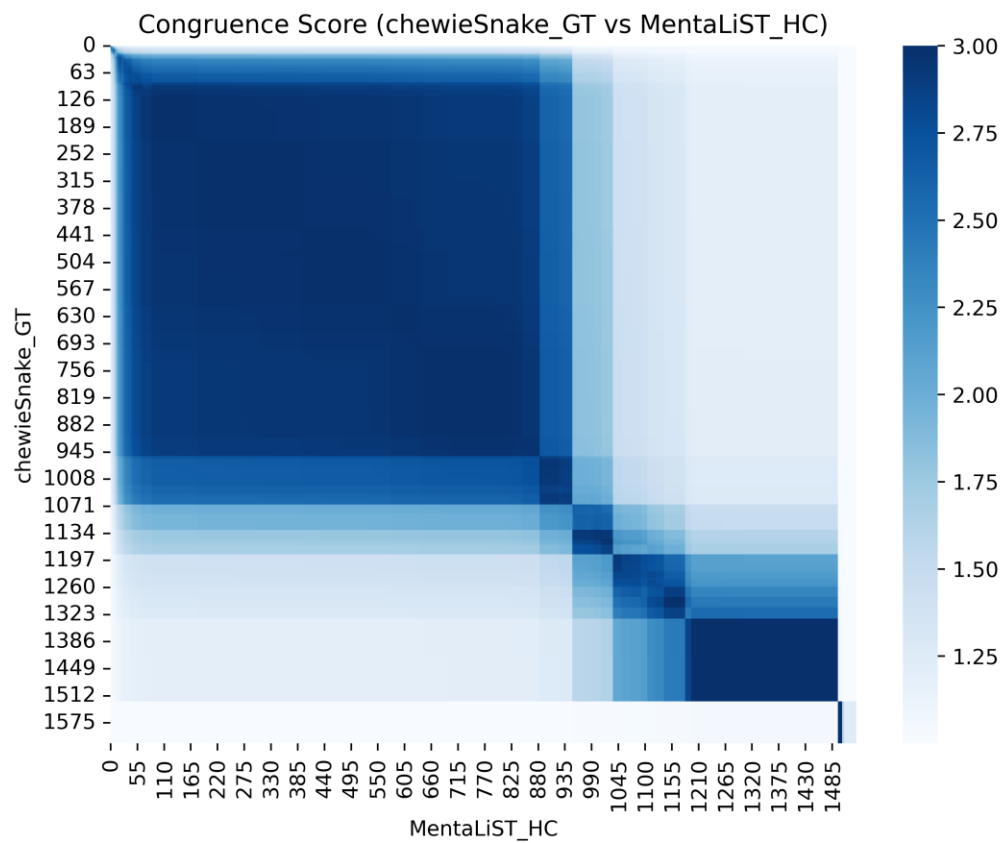


Figure S2.6.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

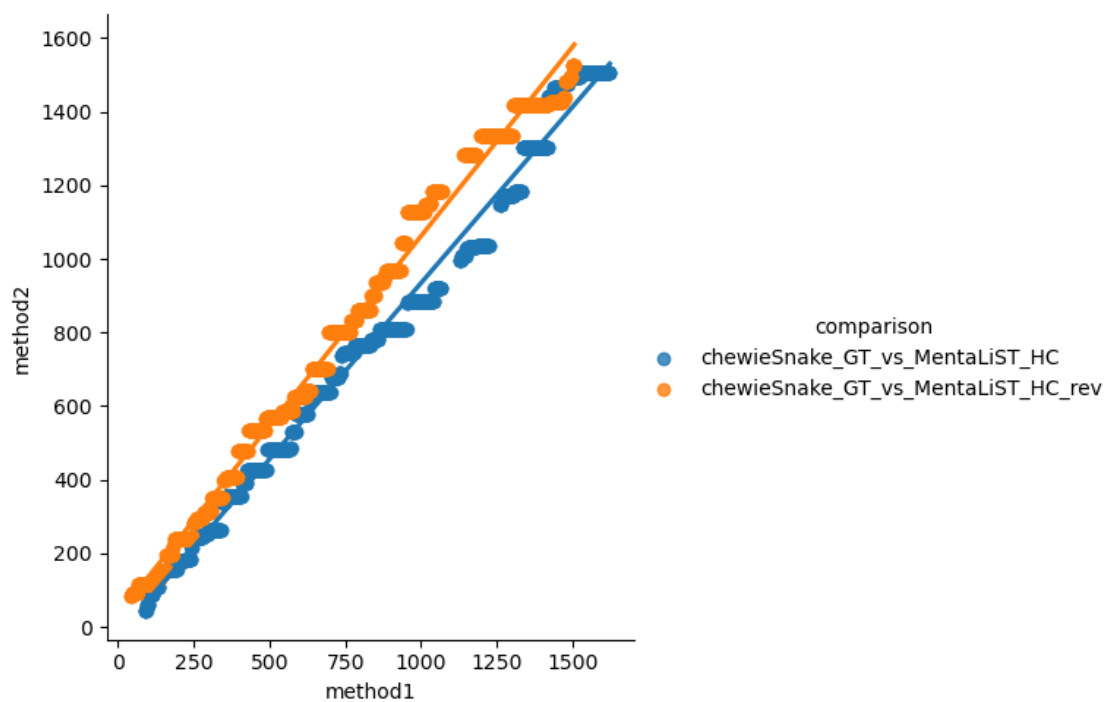


Figure S2.6.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1444 (blue) and 1384 (orange) points is presented.

7. chewieSnake GrapeTree vs. SeqSphere 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.

	chewieSnake GrapeTree	SeqSphere single-linkage
Pipeline version	v3.1.1	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	Ruppitsch	Ruppitsch
Dataset	All samples	All samples
Number partitions	1623	1564

Section 2 – Comparison of allele-based pipelines

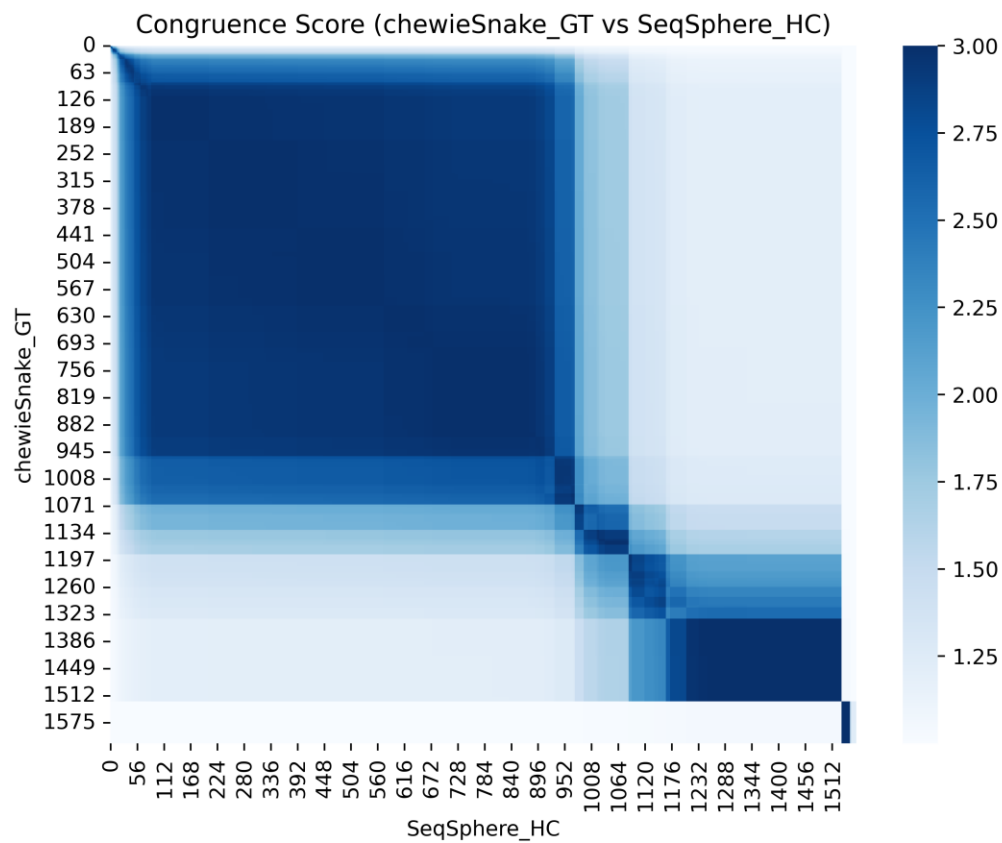


Figure S2.7.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

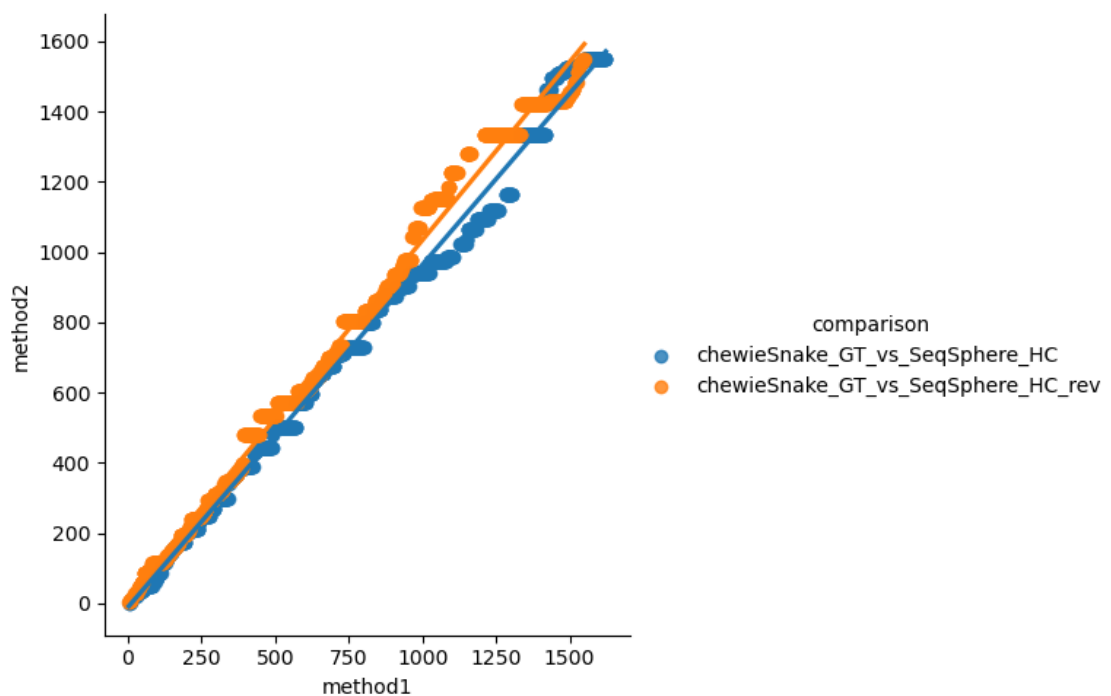


Figure S2.7.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1532 (blue) and 1466 (orange) points is presented.

8. chewieSnake single-linkage vs. Bionumerics single-linkage

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

	chewieSnake single-linkage	Bionumerics single-linkage
Pipeline version	v3.1.1	v8.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1563	1601

Section 2 – Comparison of allele-based pipelines

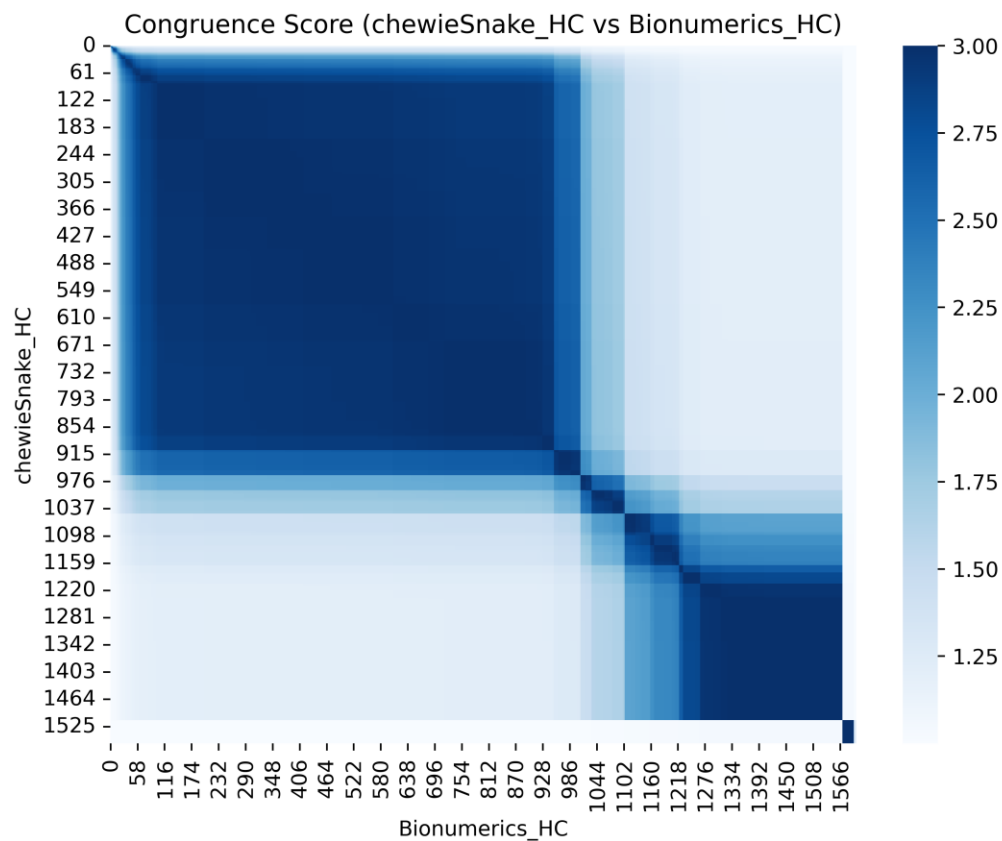


Figure S2.8.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

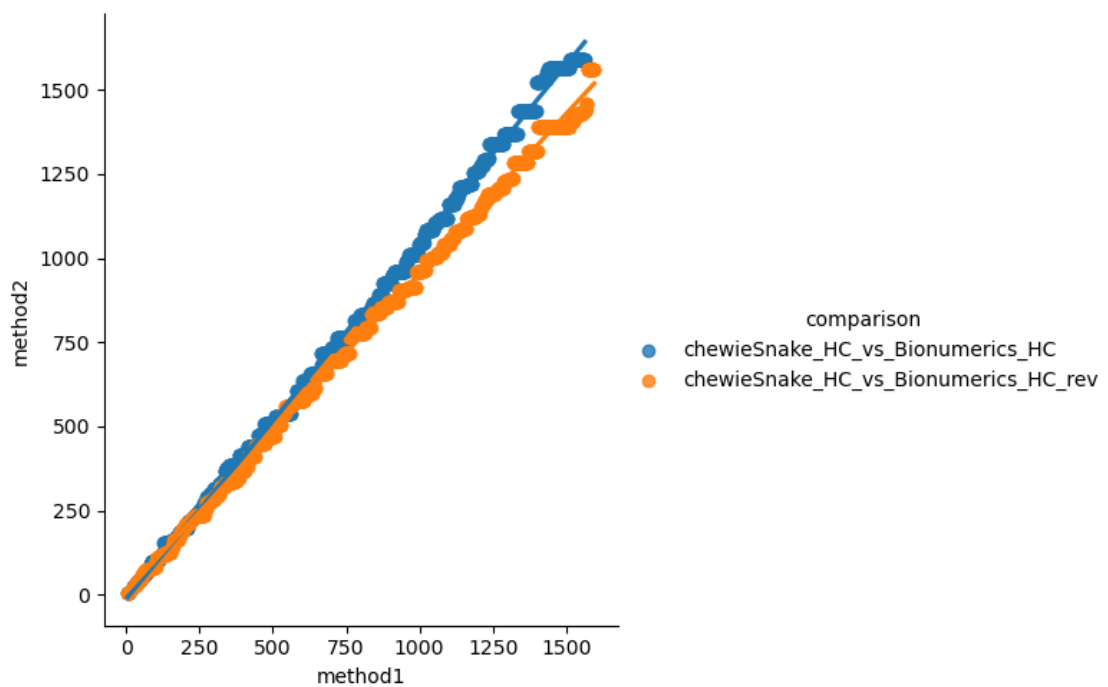


Figure S2.8.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1547 (blue) and 1578 (orange) points is presented.

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

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

	chewieSnake single-linkage	INNUENDO-like GrapeTree
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1563	1732

Section 2 – Comparison of allele-based pipelines

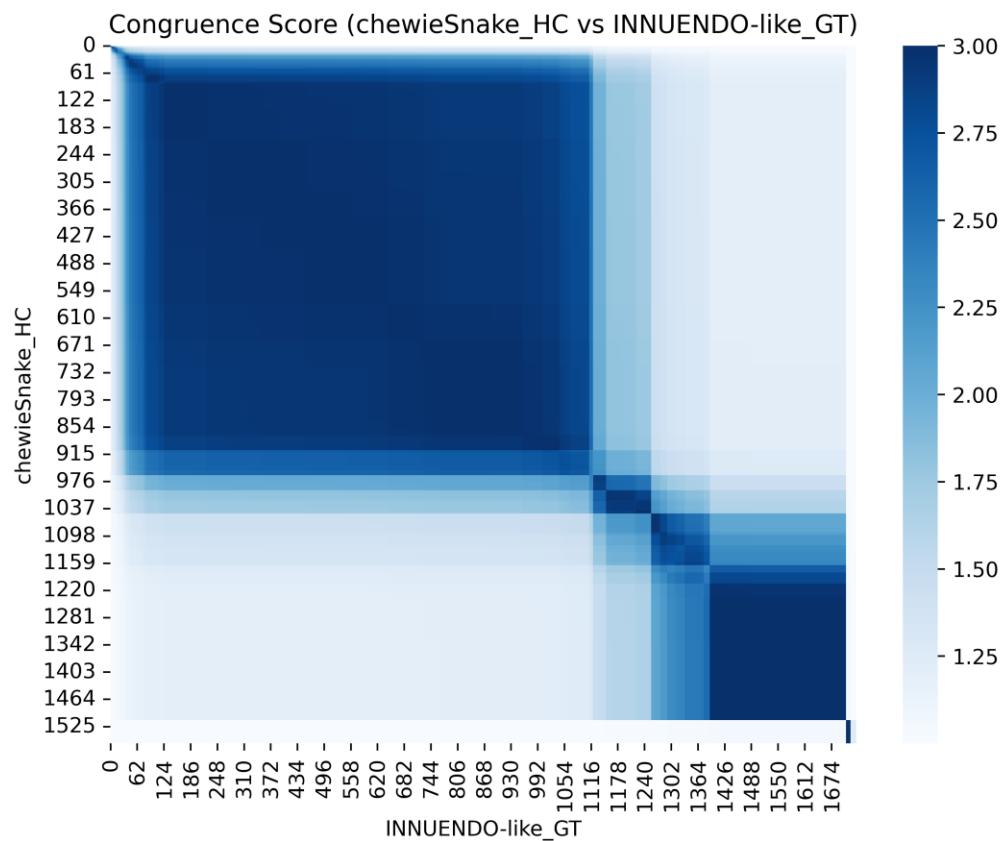


Figure S2.9.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

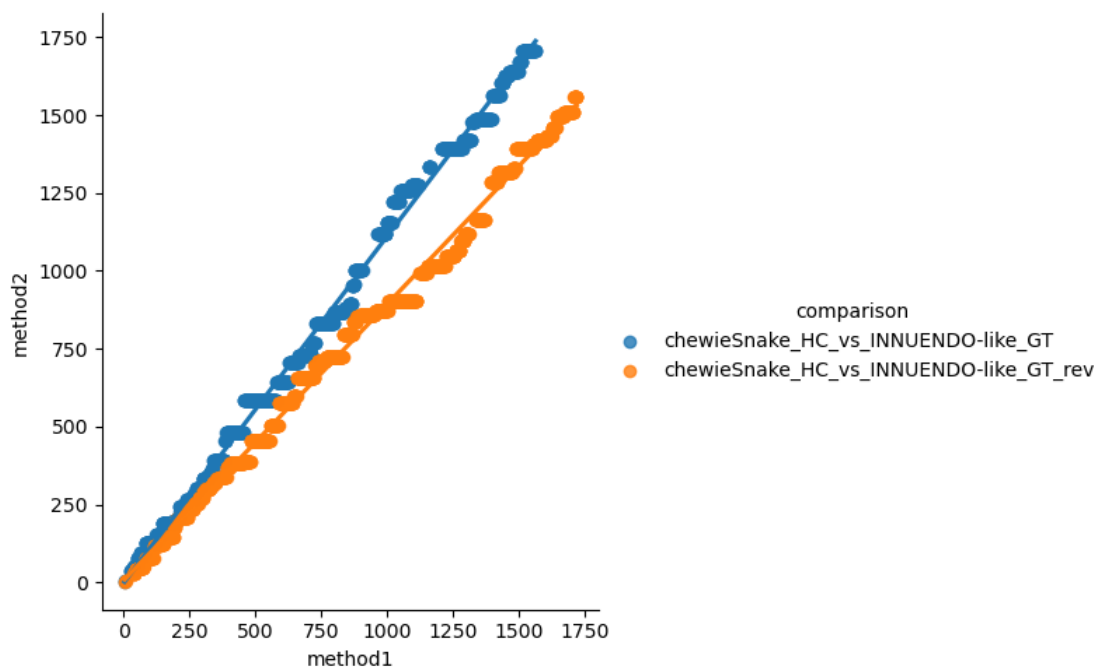


Figure S2.9.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1407 (blue) and 1632 (orange) points is presented.

10. chewieSnake single-linkage vs. INNUENDO-like 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 single-linkage	INNUENDO-like single-linkage
Pipeline version	v3.1.1	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1563	1647

Section 2 – Comparison of allele-based pipelines

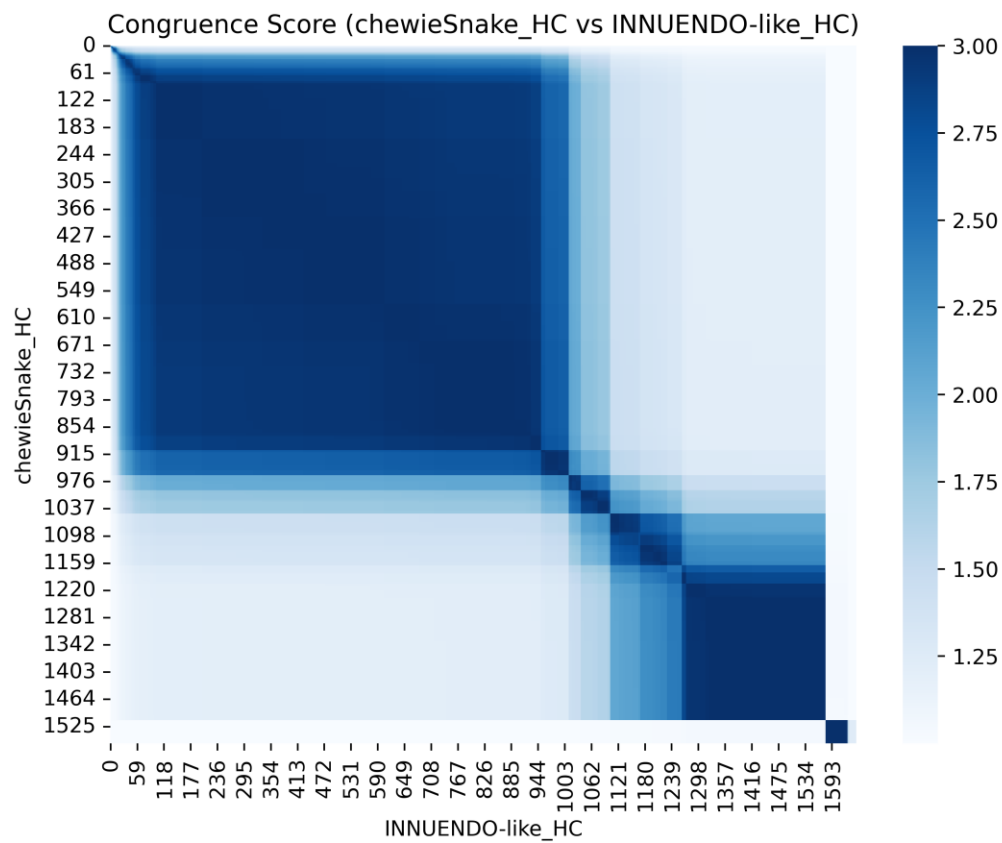


Figure S2.10.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

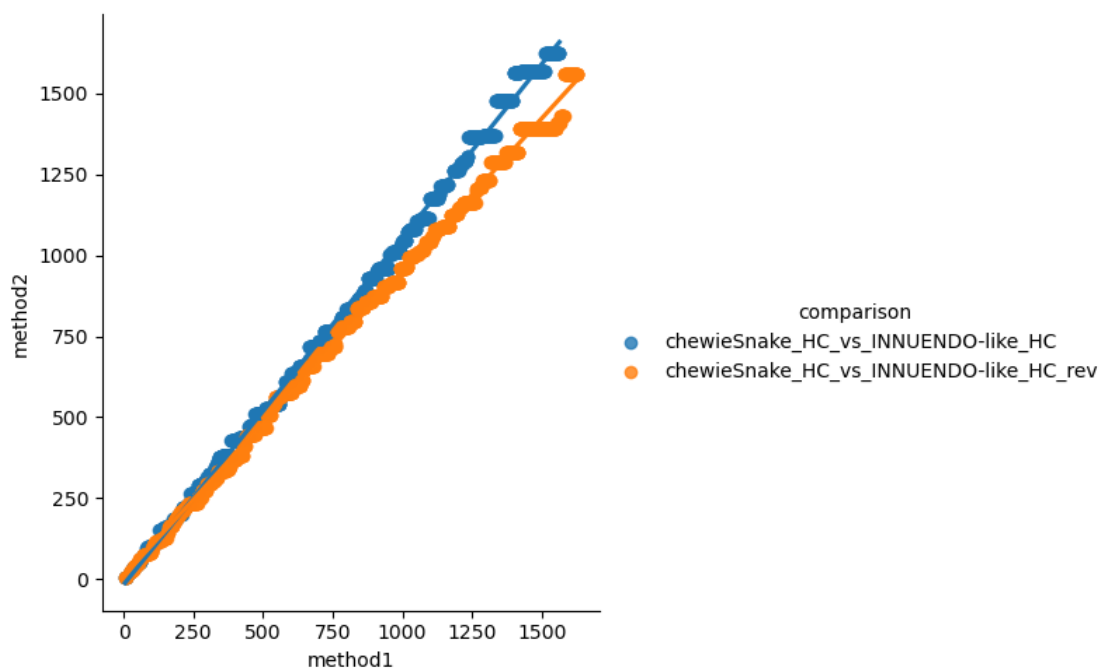


Figure S2.10.2. Corresponding points between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 1531 (blue) and 1612 (orange) points is presented.

11. chewieSnake single-linkage vs. MentaLiST 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 single-linkage	MentaLiST GrapeTree
Pipeline version	v3.1.1	v1.0.0
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1563	1595

Section 2 – Comparison of allele-based pipelines

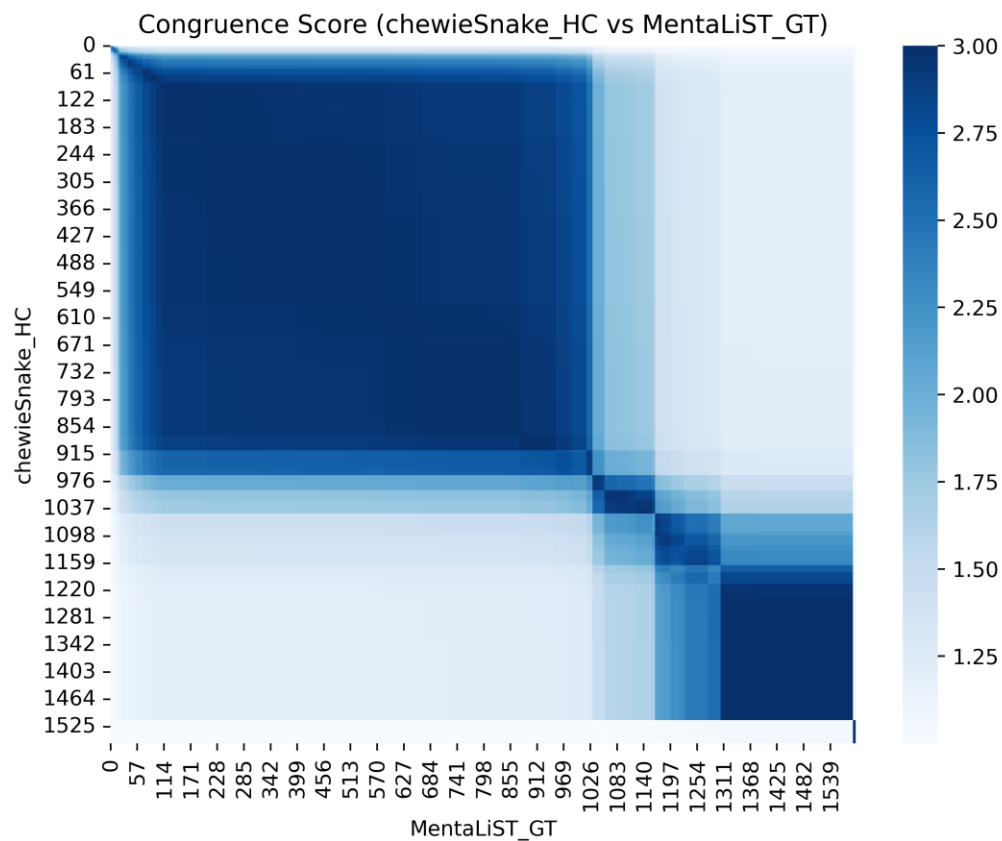


Figure S2.11.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

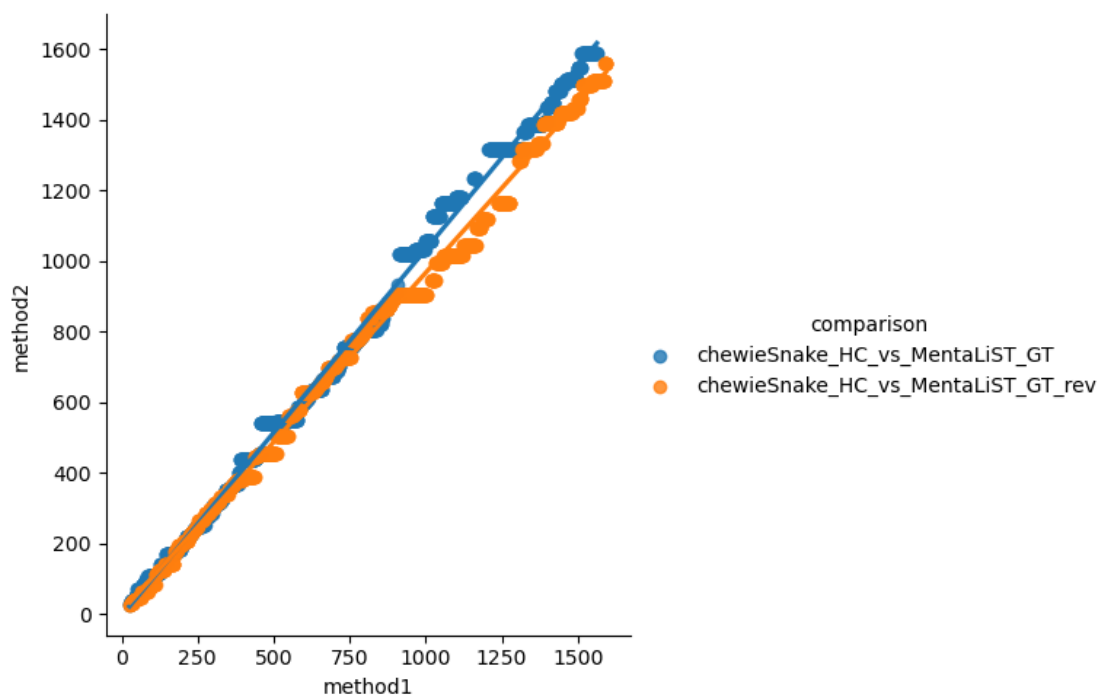


Figure S2.11.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1455 (blue) and 1494 (orange) points is presented.

12. chewieSnake single-linkage vs. MentaLiST 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 single-linkage	MentaLiST single-linkage
Pipeline version	v3.1.1	v1.0.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1563	1535

Section 2 – Comparison of allele-based pipelines

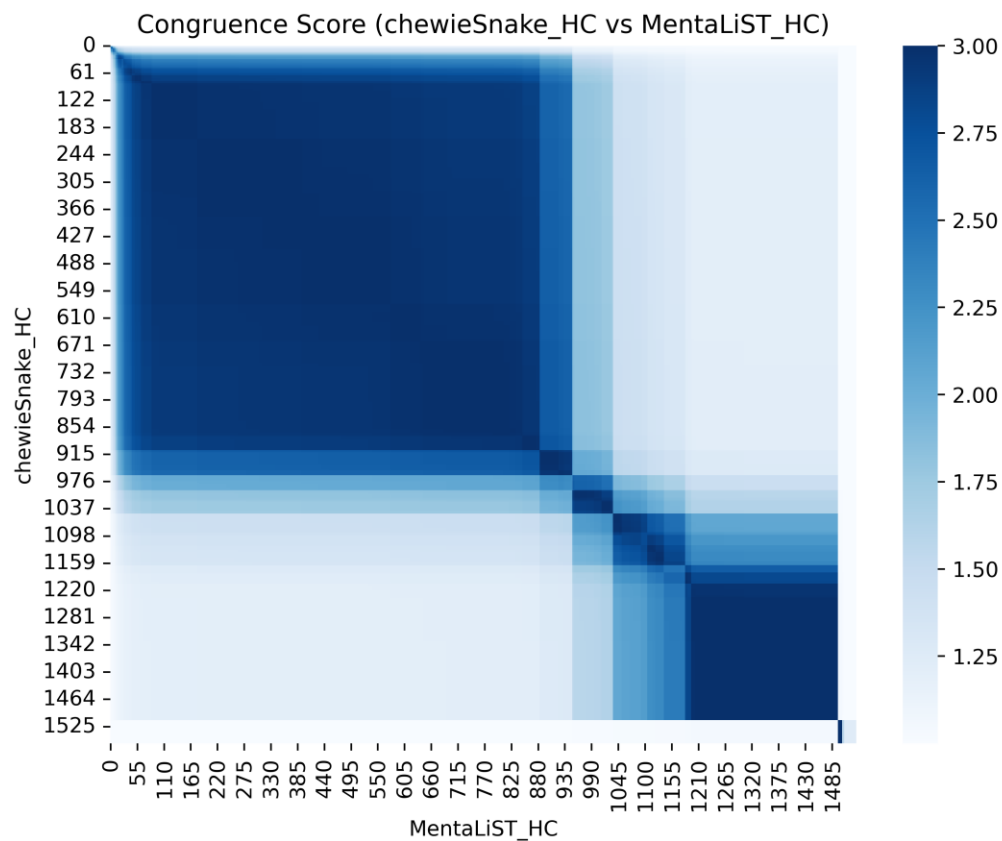


Figure S2.12.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

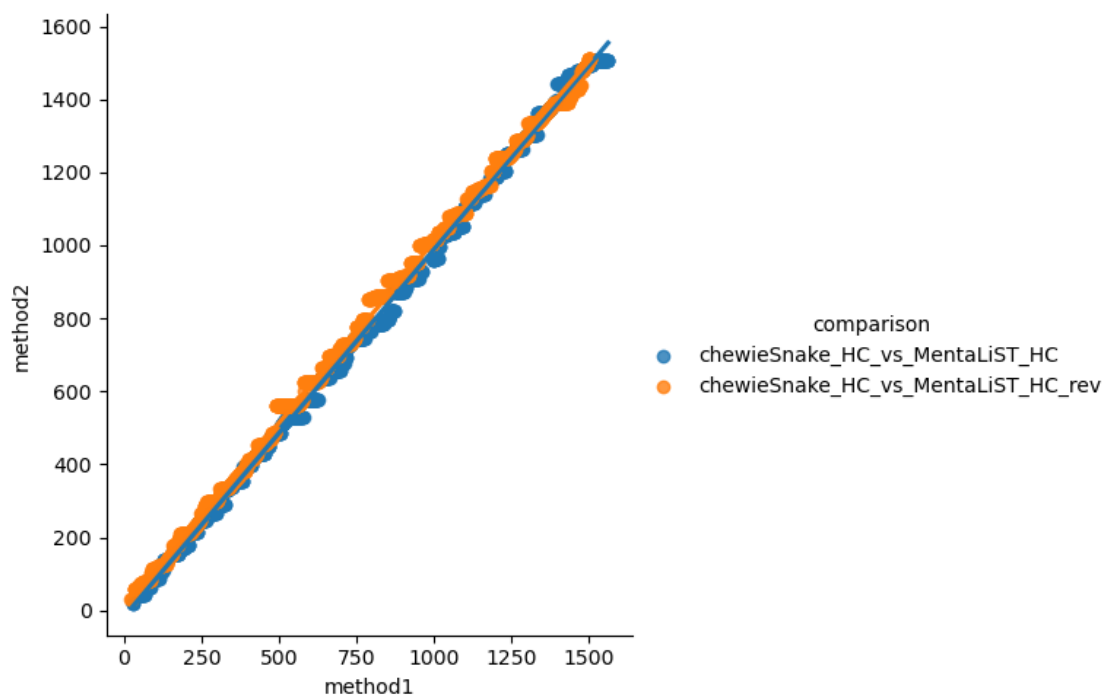


Figure S2.12.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1466 (blue) and 1477 (orange) points is presented.

13. chewieSnake single-linkage vs. SeqSphere single-linkage

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 single-linkage	SeqSphere single-linkage
Pipeline version	v3.1.1	v8.3.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	Ruppitsch	Ruppitsch
Dataset	All samples	All samples
Number partitions	1563	1564

Section 2 – Comparison of allele-based pipelines

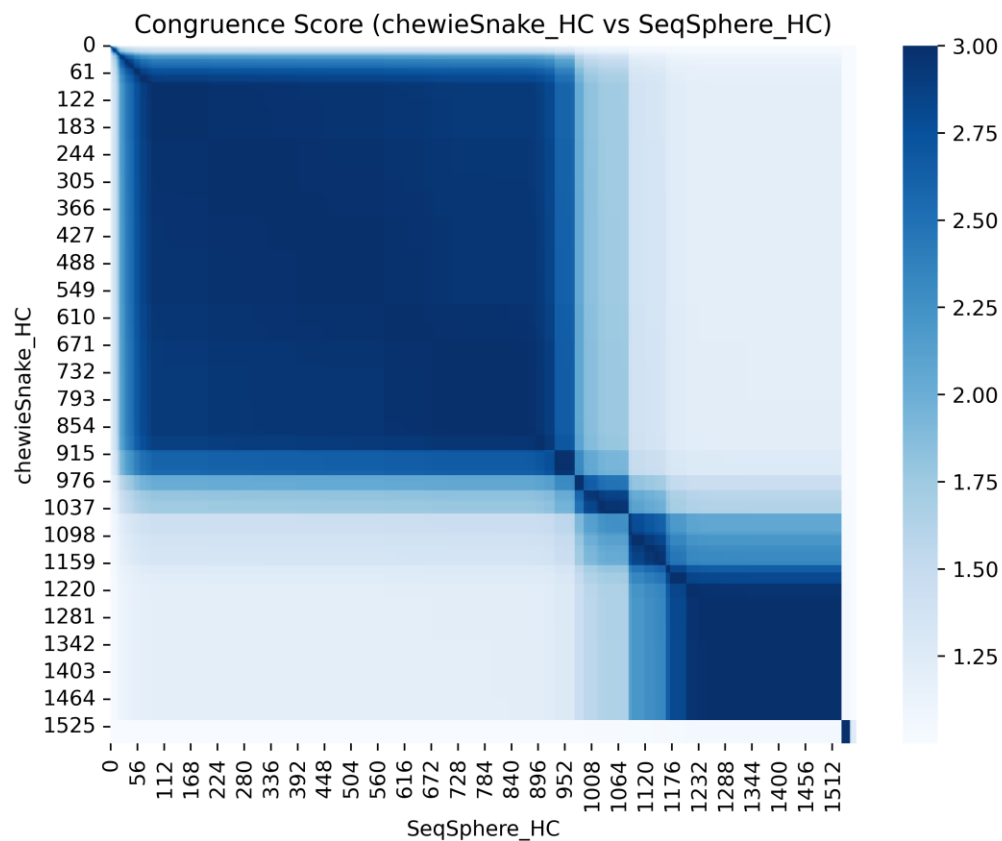


Figure S2.13.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

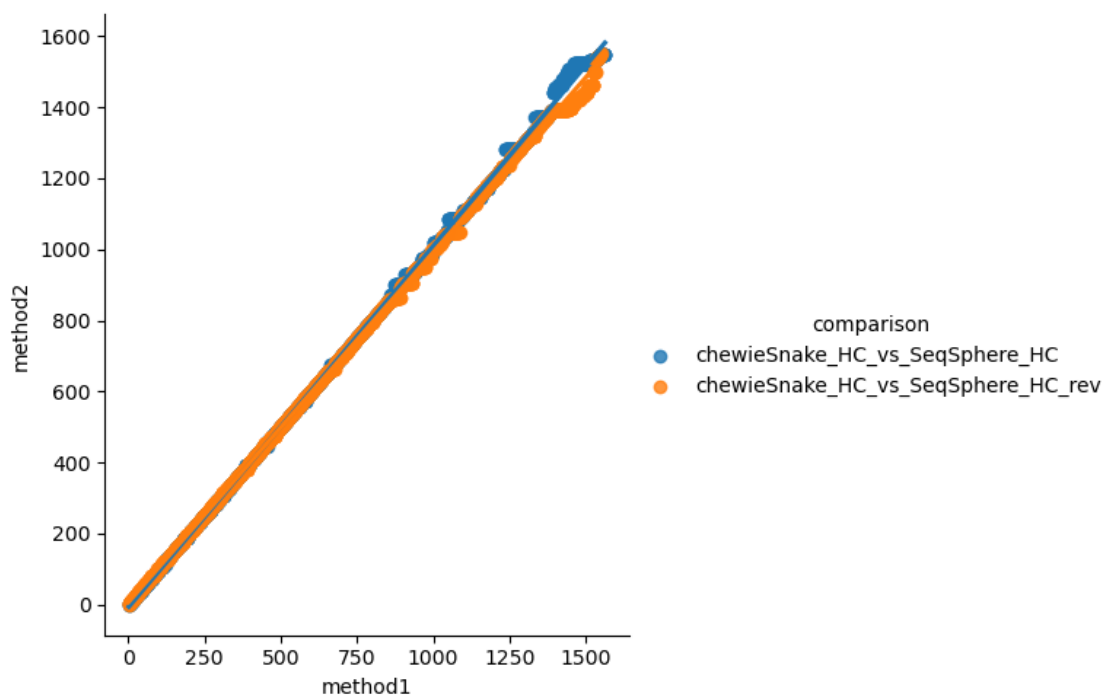


Figure S2.13.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1562 (blue) and 1550 (orange) points is presented.

14. INNUENDO-like GrapeTree vs. Bionumerics 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 GrapeTree	Bionumerics single-linkage
Pipeline version	chewBBACA 2.8.5	v8.1
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1732	1601

Section 2 – Comparison of allele-based pipelines

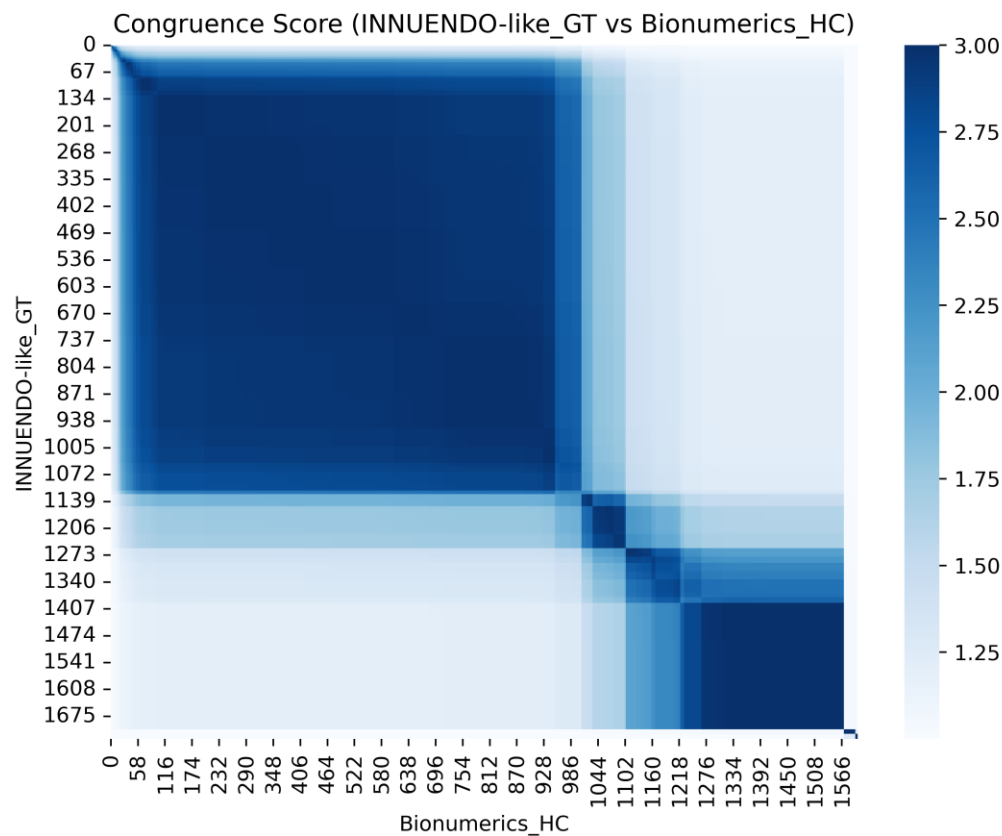


Figure S2.14.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

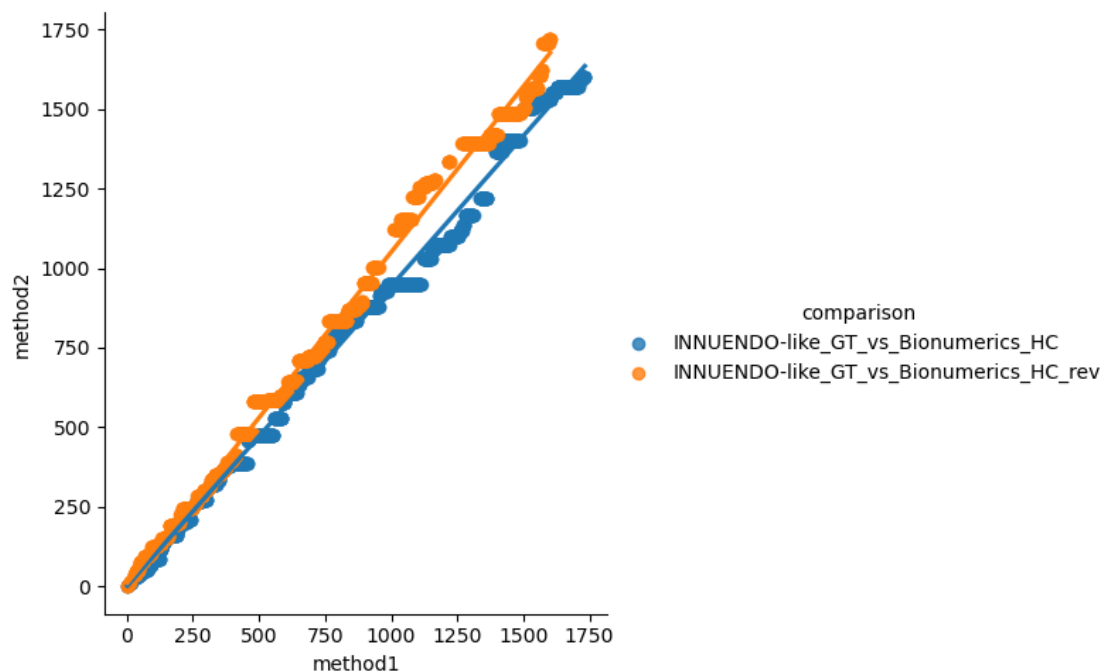


Figure S2.14.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1645 (blue) and 1434 (orange) points is presented.

15. INNUENDO-like GrapeTree vs. MentaLiST GrapeTree

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

	INNUENDO-like GrapeTree	MentaLiST GrapeTree
Pipeline version	chewBBACA 2.8.5	v1.0.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1732	1595

Section 2 – Comparison of allele-based pipelines

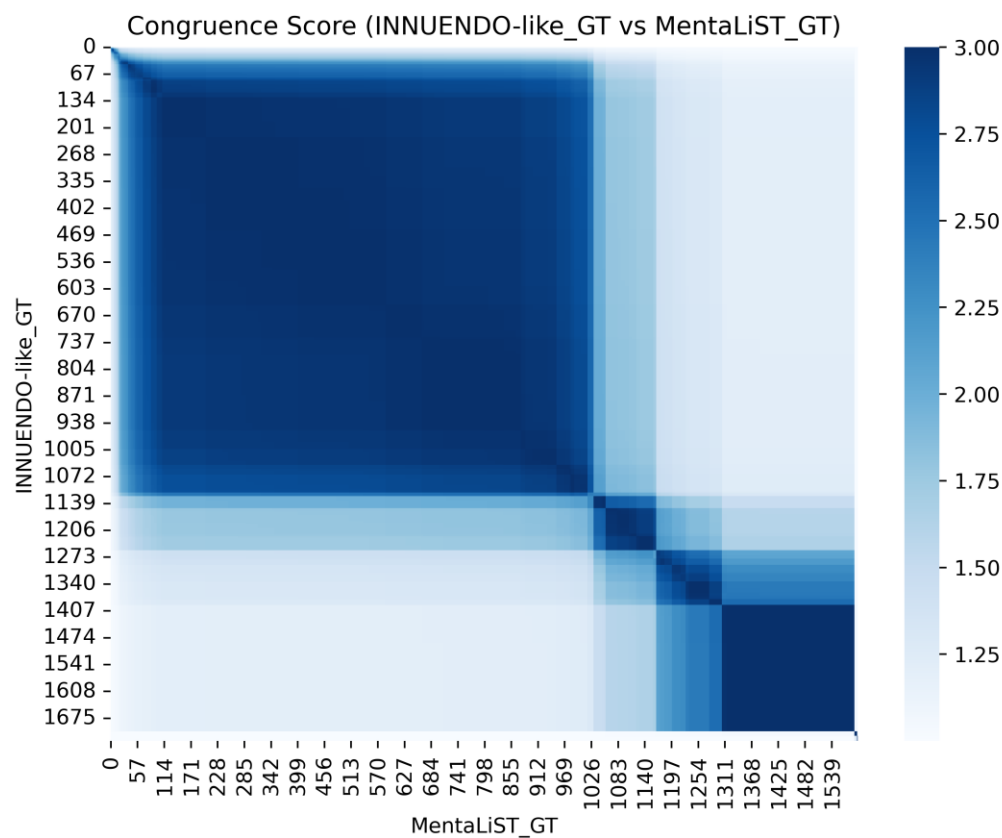


Figure S2.15.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

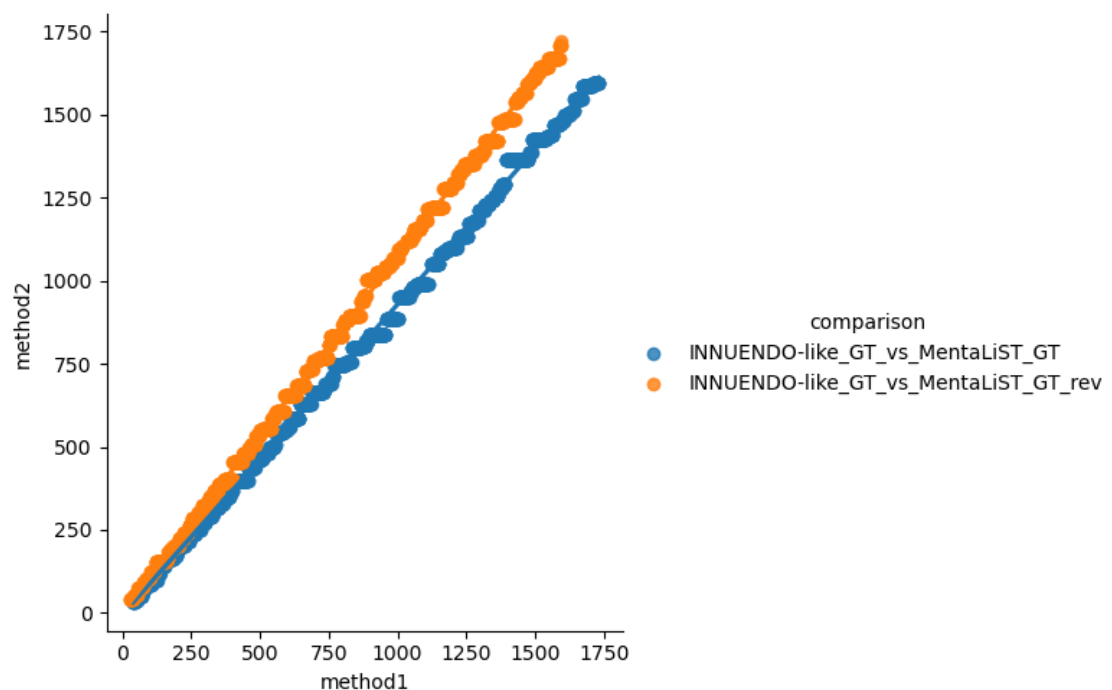


Figure S2.15.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1686 (blue) and 1556 (orange) points is presented.

16. INNUENDO-like GrapeTree vs. MentaLiST single-linkage

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 GrapeTree	MentaLiST single-linkage
Pipeline version	chewBBACA 2.8.5	v1.0.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1732	1535

Section 2 – Comparison of allele-based pipelines

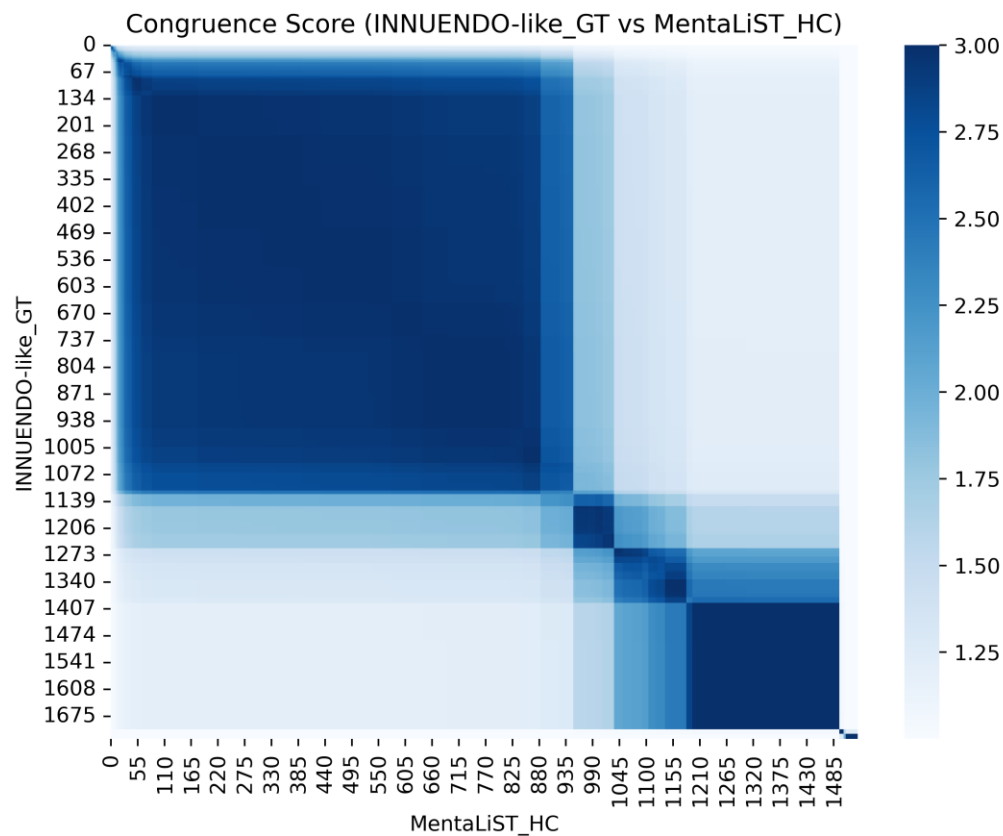


Figure S2.16.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

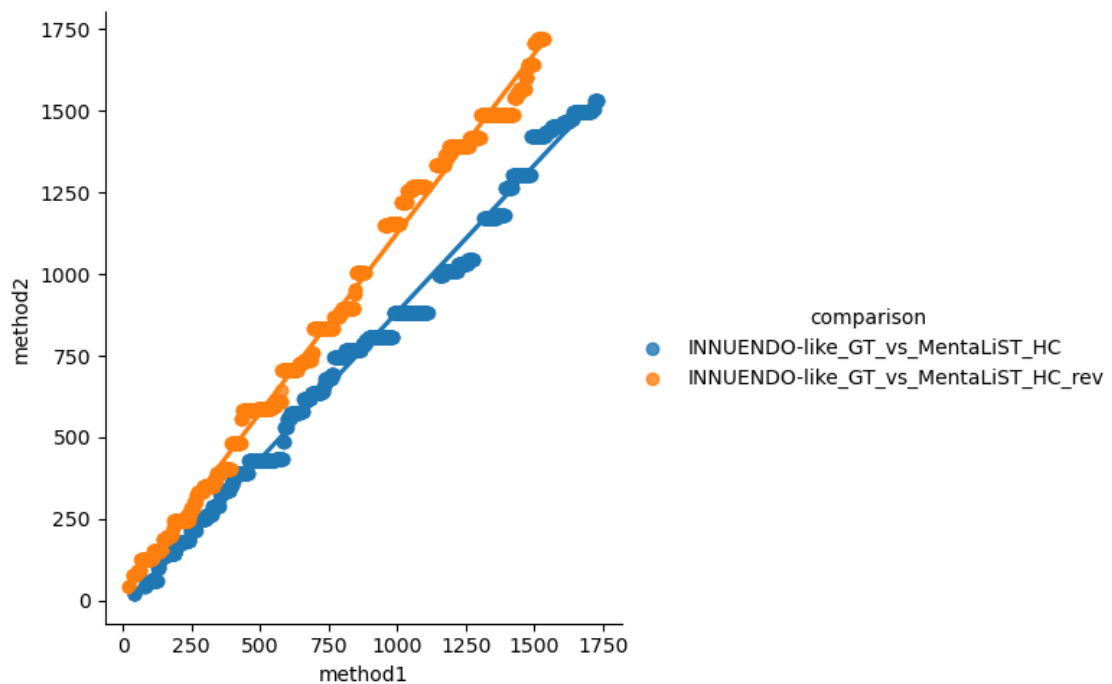


Figure S2.16.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1588 (blue) and 1395 (orange) points is presented.

17. INNUENDO-like GrapeTree vs. SeqSphere 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 GrapeTree	SeqSphere single-linkage
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	Moura	Ruppitsch
Dataset	All samples	All samples
Number partitions	1732	1564

Section 2 – Comparison of allele-based pipelines

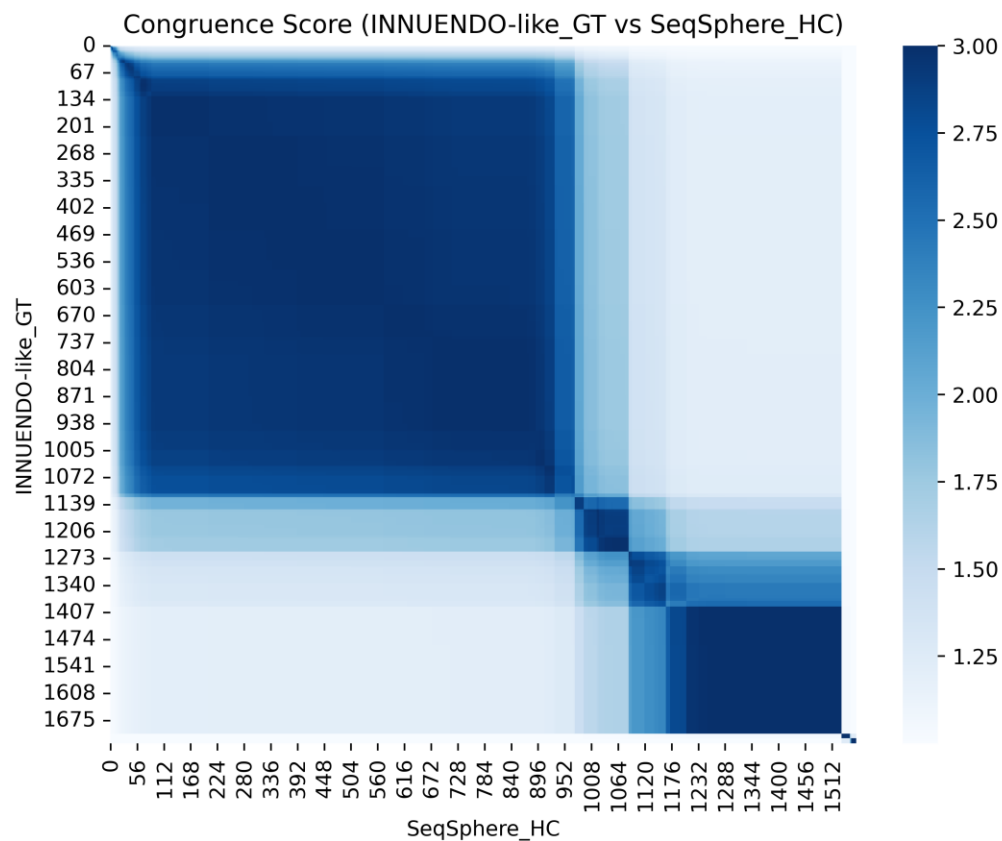


Figure S2.17.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

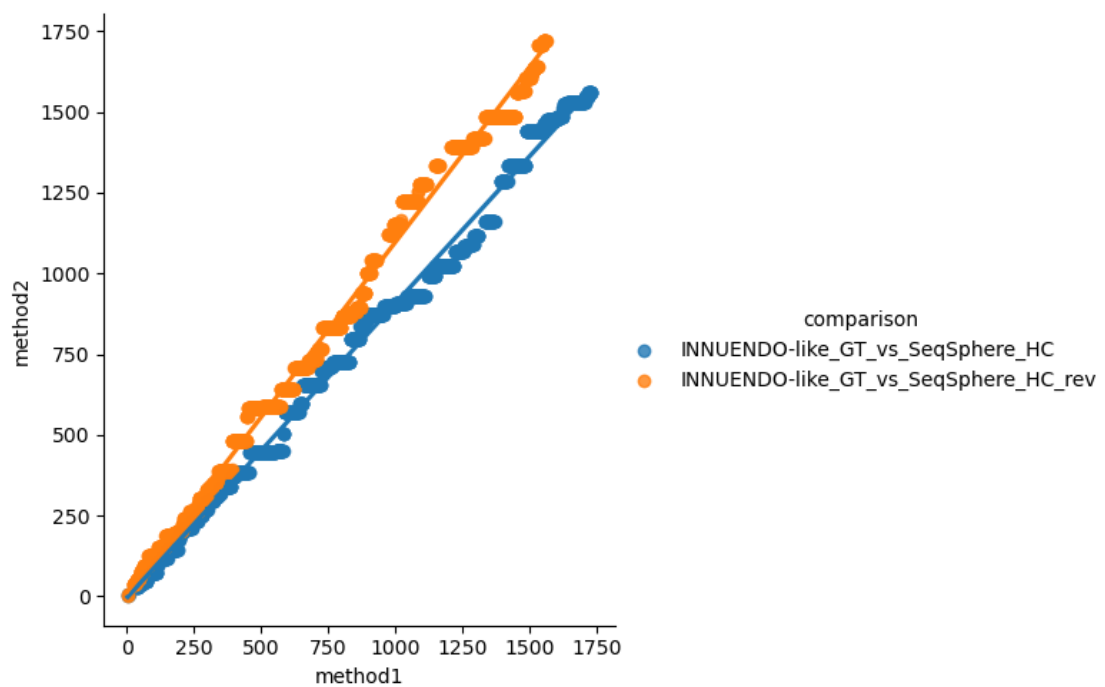


Figure S2.17.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1645 (blue) and 1425 (orange) points is presented.

18. INNUENDO-like single-linkage vs. Bionumerics 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.

	INNUENDO-like single-linkage	Bionumerics single-linkage
Pipeline version	chewBBACA 2.8.5	v8.1
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1647	1601

Section 2 – Comparison of allele-based pipelines

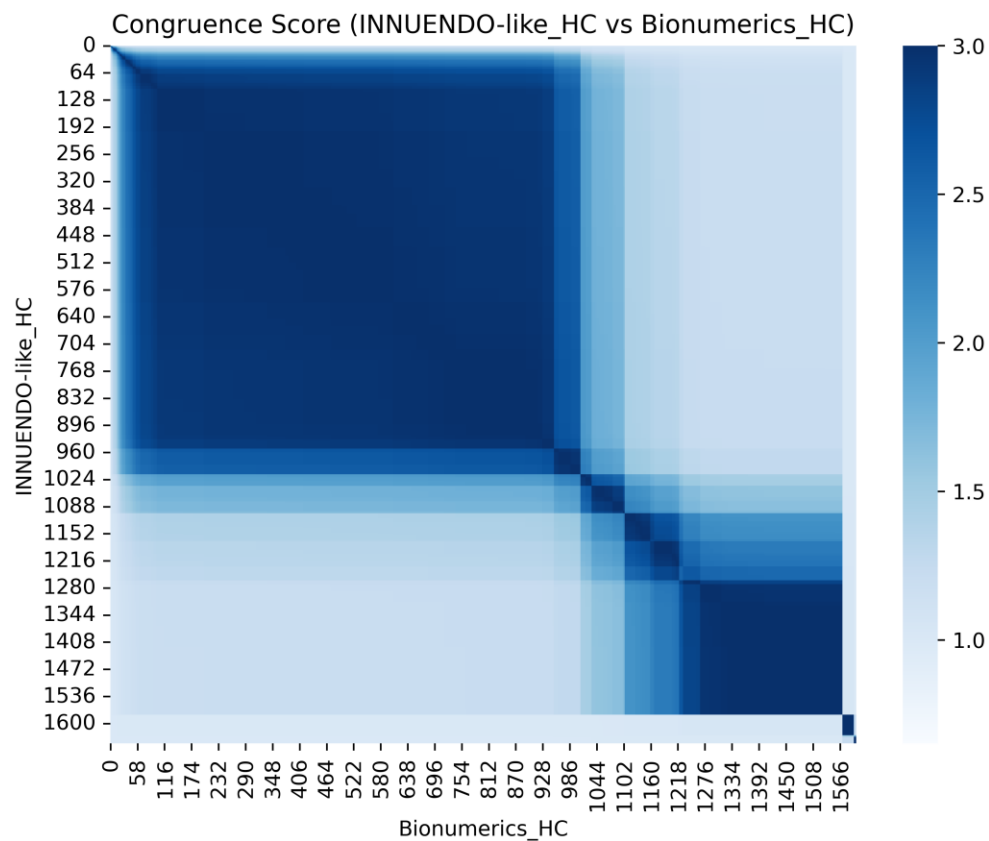


Figure S2.18.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

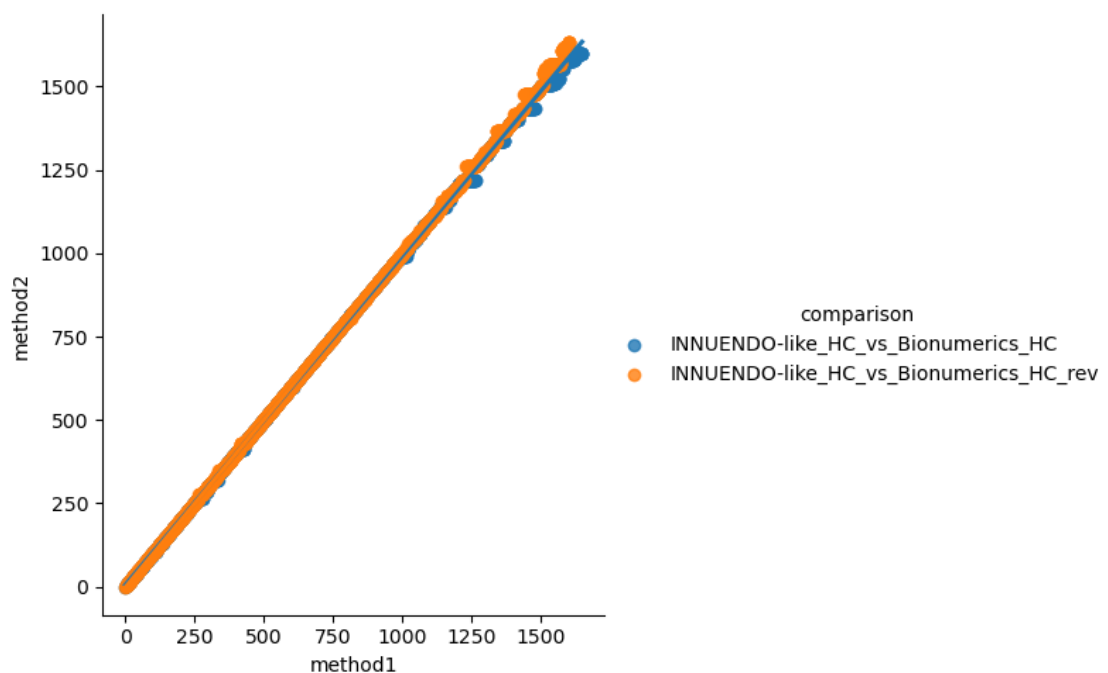


Figure S2.18.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1644 (blue) and 1592 (orange) points is presented.

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

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 single-linkage	INNUENDO-like GrapeTree
Pipeline version	chewBBACA 2.8.5	chewBBACA 2.8.5
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1647	1732

Section 2 – Comparison of allele-based pipelines

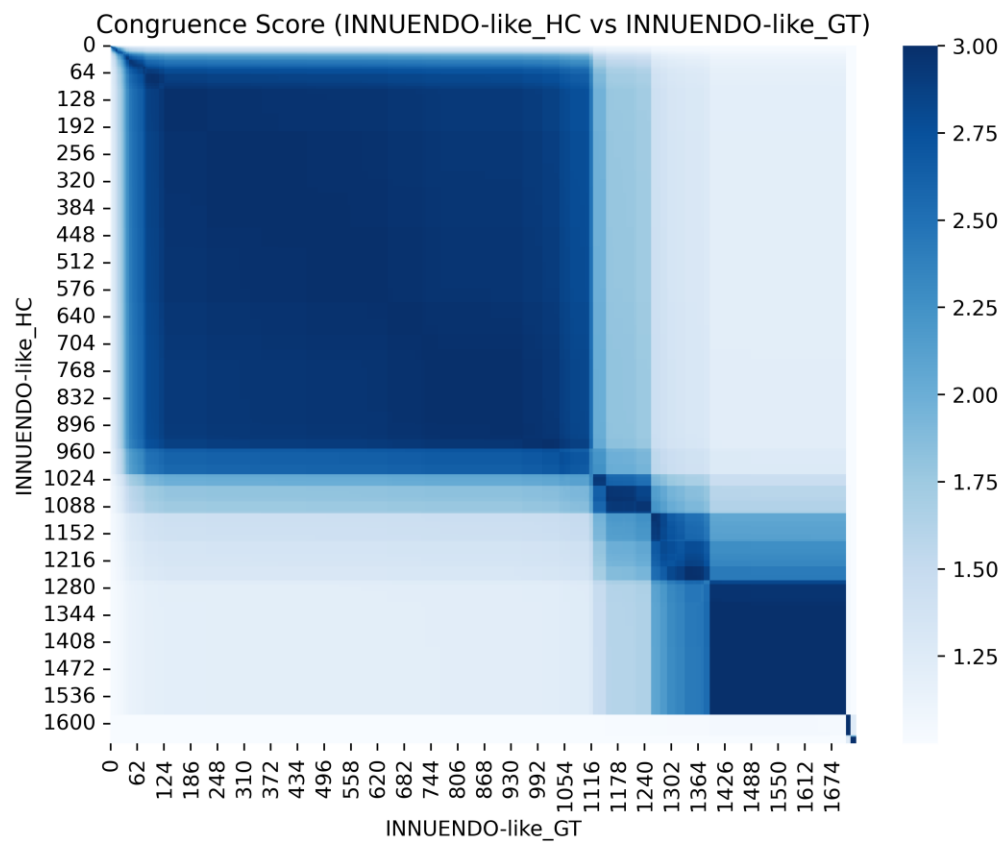


Figure S2.19.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

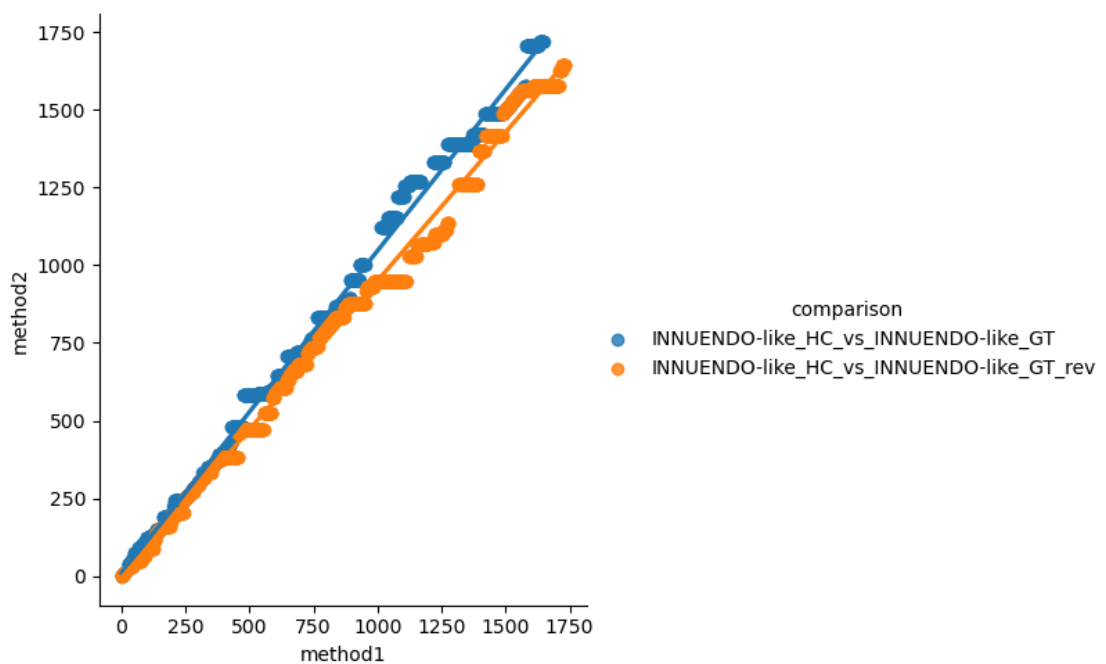


Figure S2.19.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1513 (blue) and 1662 (orange) points is presented.

20. INNUENDO-like single-linkage vs. MentaLiST 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 single-linkage	MentaLiST GrapeTree
Pipeline version	chewBBACA 2.8.5	v1.0.0
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1647	1595

Section 2 – Comparison of allele-based pipelines

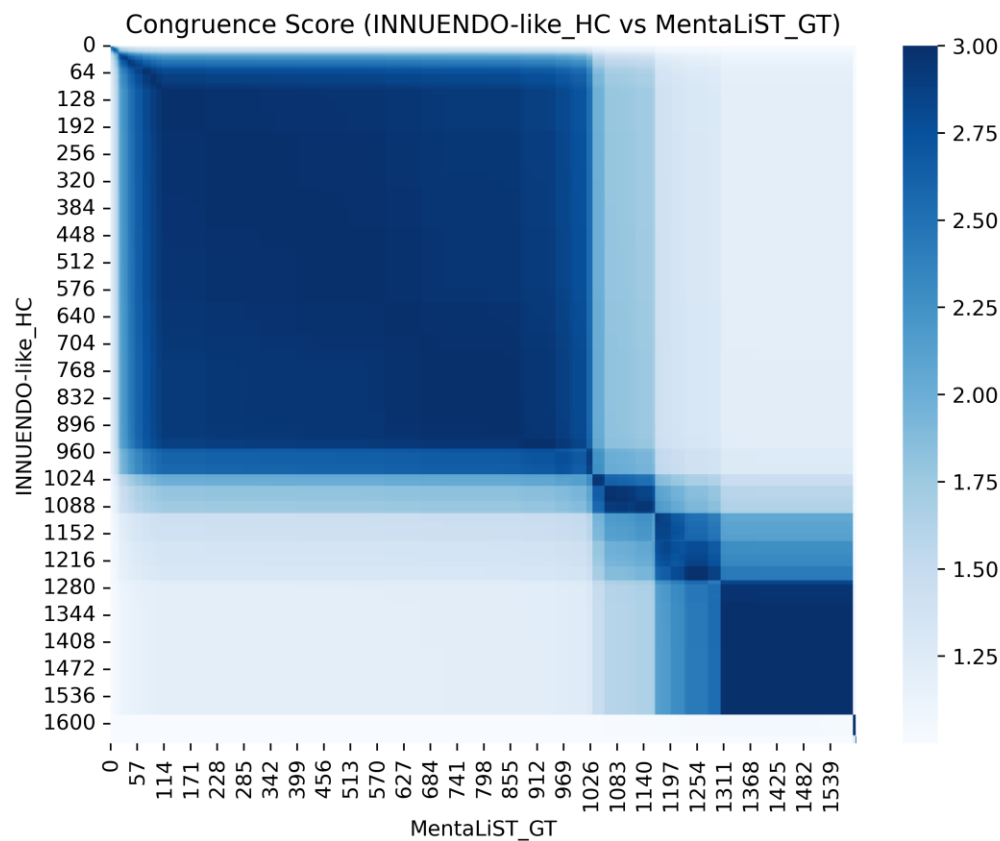


Figure S2.20.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

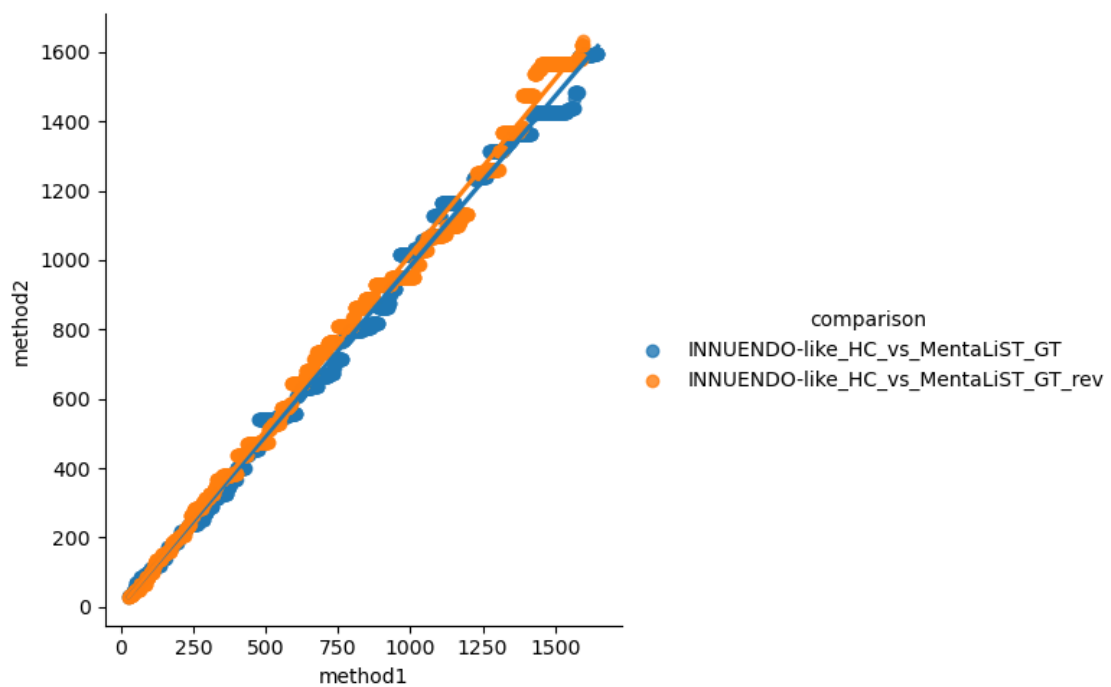


Figure S2.20.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1539 (blue) and 1535 (orange) points is presented.

21. INNUENDO-like single-linkage vs. MentaLiST 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 single-linkage	MentaLiST single-linkage
Pipeline version	chewBBACA 2.8.5	v1.0.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1647	1535

Section 2 – Comparison of allele-based pipelines

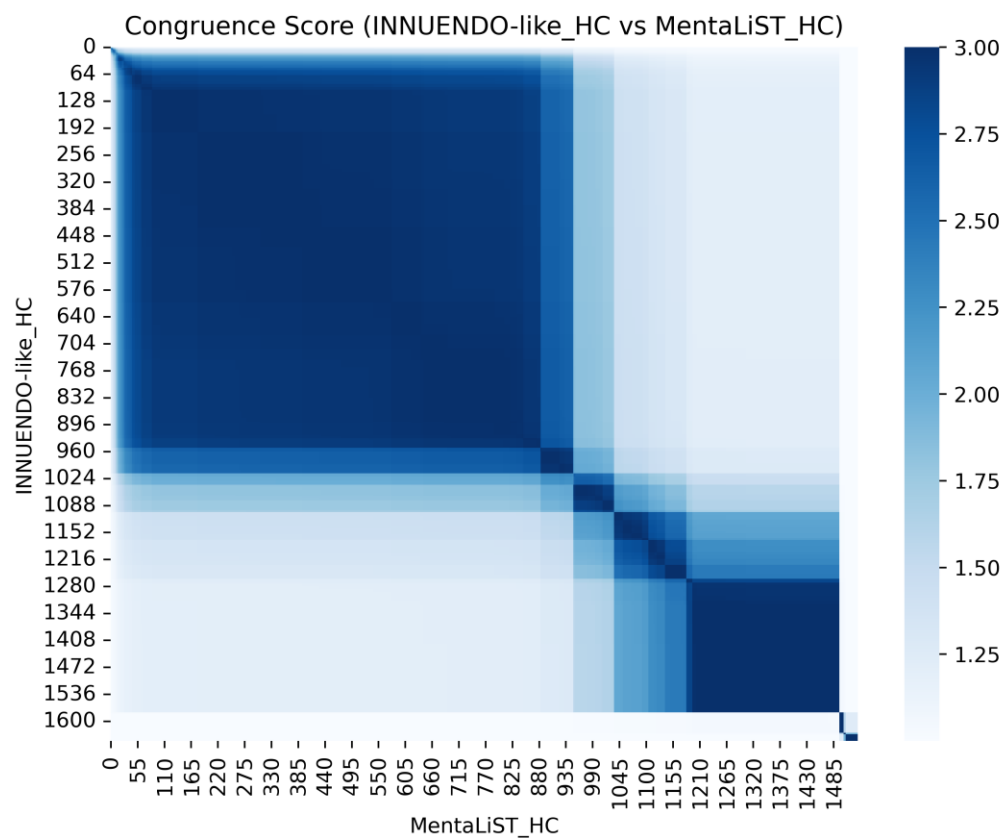


Figure S2.21.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

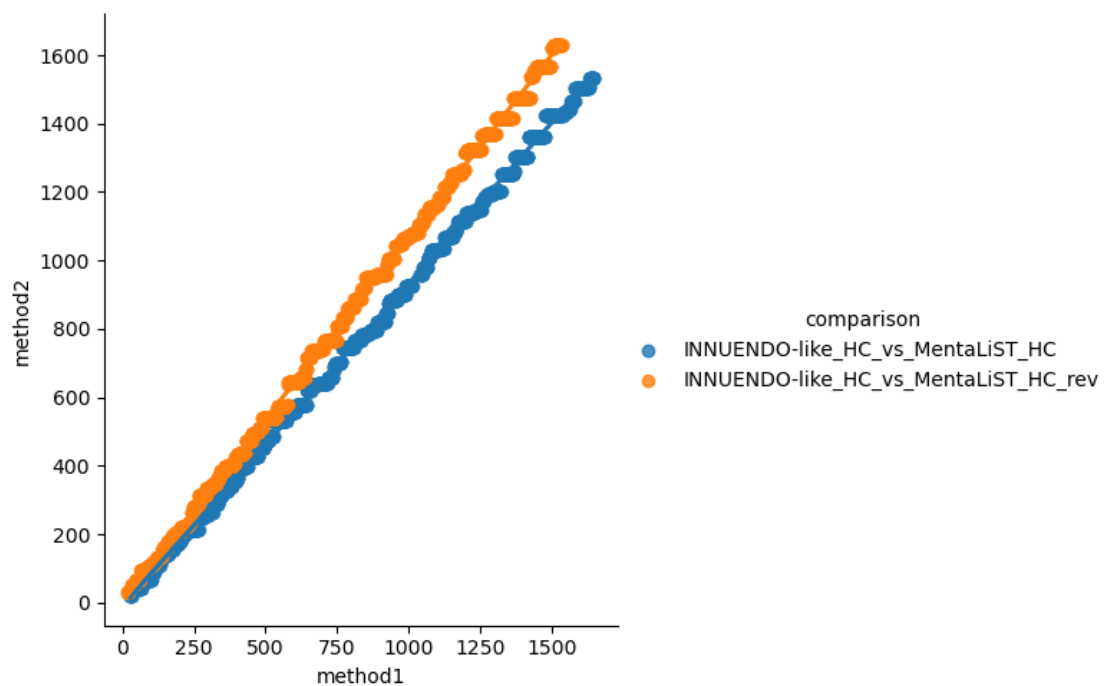


Figure S2.21.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1579 (blue) and 1508 (orange) points is presented.

22. INNUENDO-like single-linkage vs. SeqSphere 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 single-linkage	SeqSphere single-linkage
Pipeline version	chewBBACA 2.8.5	v8.3.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema	Moura	Ruppitsch
Dataset	All samples	All samples
Number partitions	1647	1564

Section 2 – Comparison of allele-based pipelines

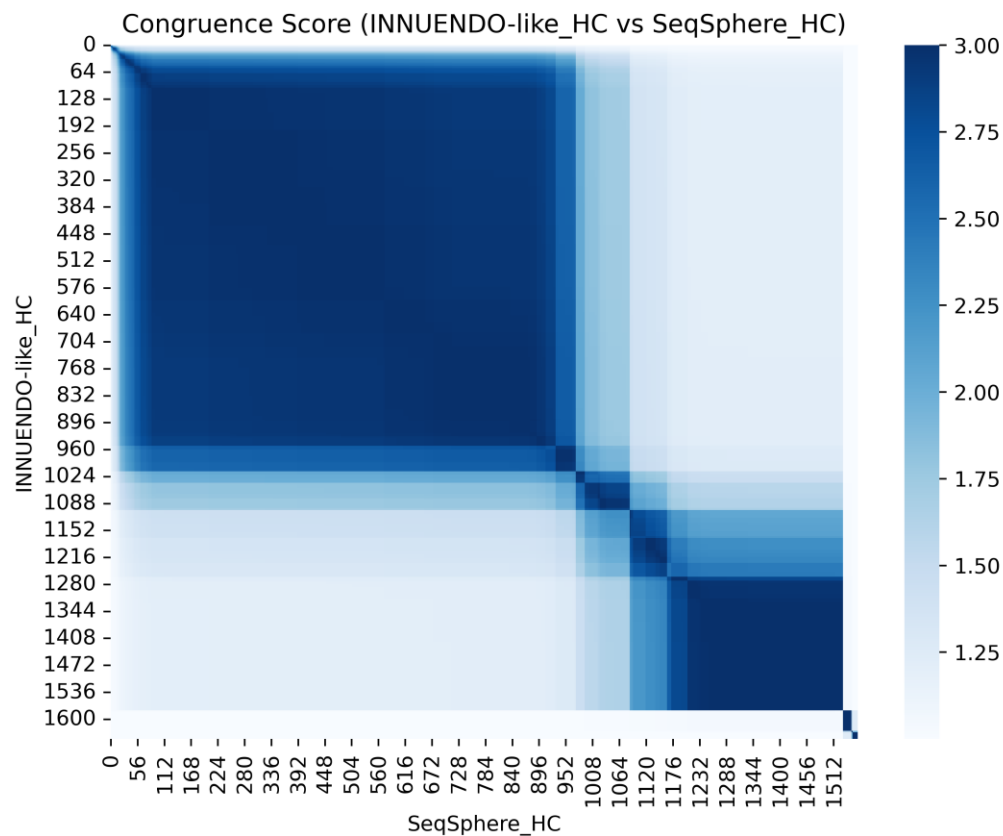


Figure S2.22.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

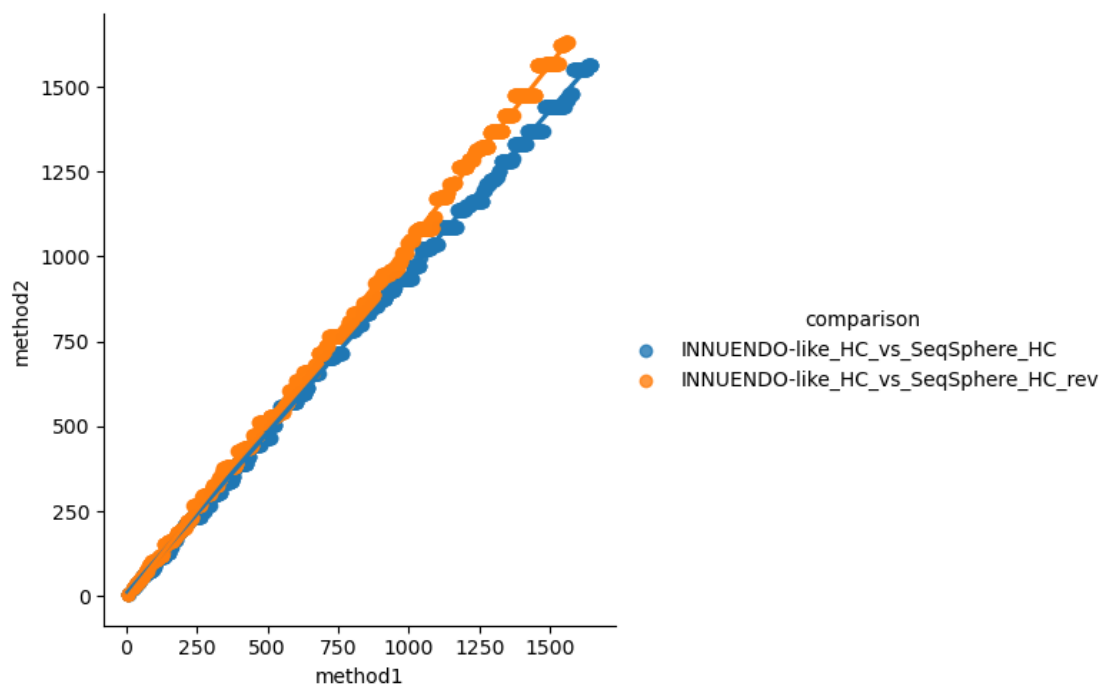


Figure S2.22.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1630 (blue) and 1539 (orange) points is presented.

23. Bionumerics single-linkage vs. MentaLiST 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.

	Bionumerics single-linkage	MentaLiST GrapeTree
Pipeline version	v8.1	v1.0.0
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1601	1595

Section 2 – Comparison of allele-based pipelines

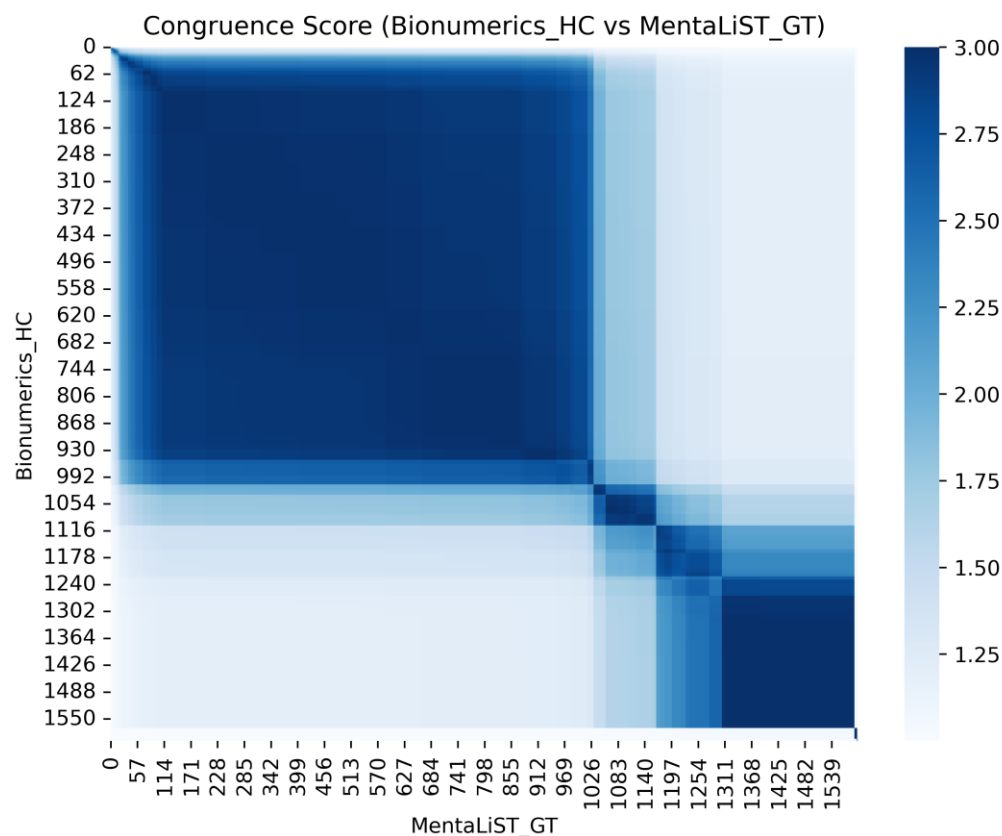


Figure S2.23.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

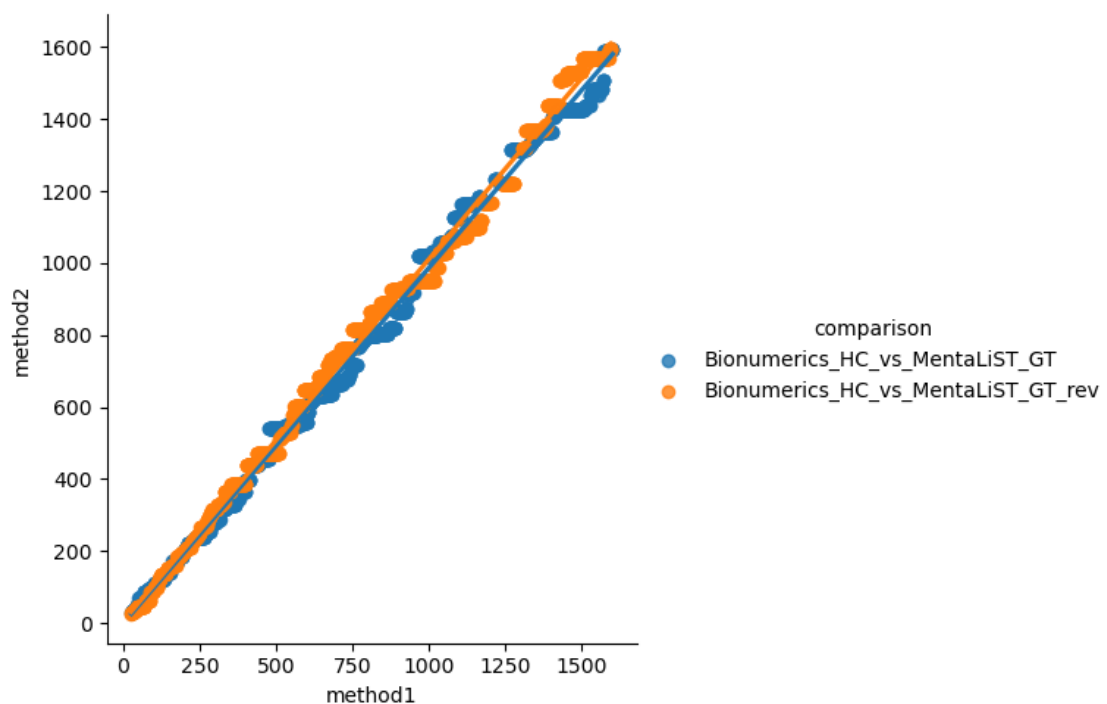


Figure S2.23.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1455 (blue) and 1513 (orange) points is presented.

24. Bionumerics single-linkage vs. MentaLiST 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.

	Bionumerics single-linkage	MentaLiST single-linkage
Pipeline version	v8.1	v1.0.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1601	1535

Section 2 – Comparison of allele-based pipelines

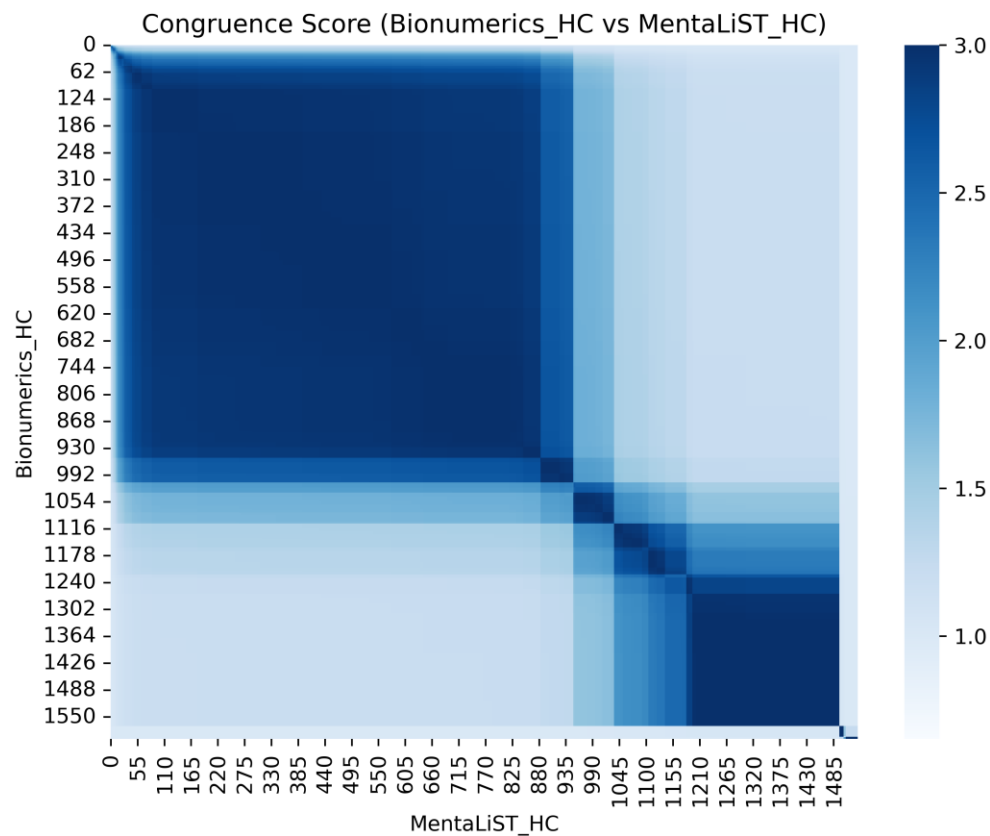


Figure S2.24.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

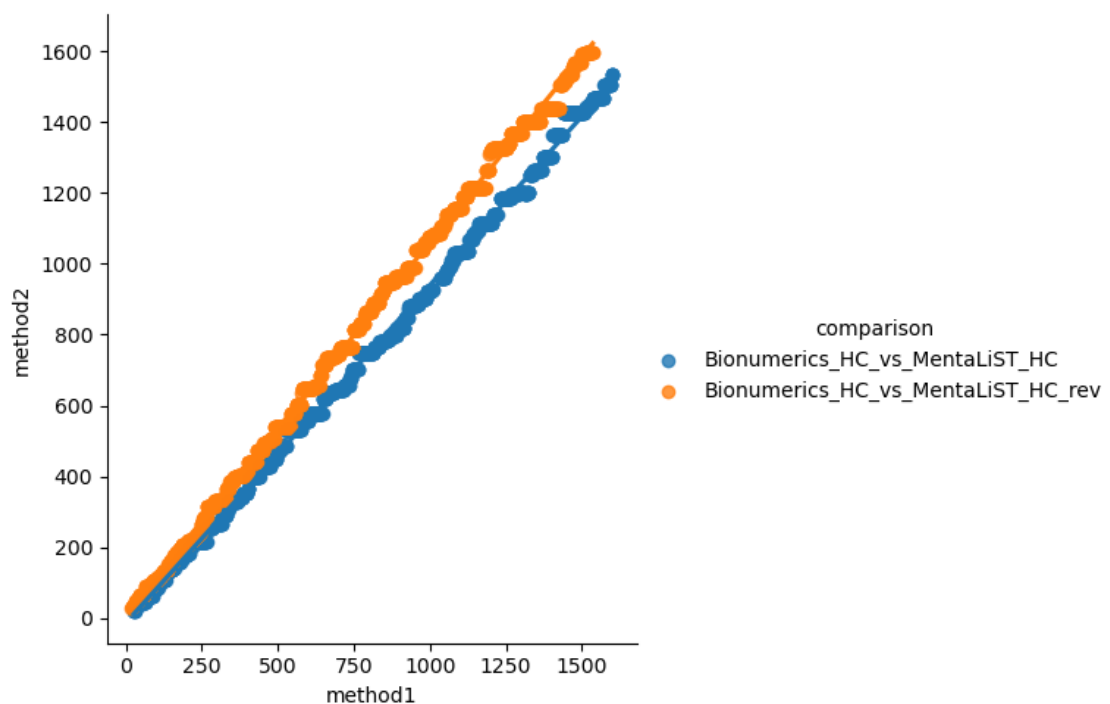


Figure S2.24.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1527 (blue) and 1505 (orange) points is presented.

25. MentaLiST single-linkage vs. MentaLiST 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.

	MentaLiST single-linkage	MentaLiST GrapeTree
Pipeline version	v1.0.0	v1.0.0
Clustering	HC single-linkage (ReporTree)	GrapeTree MSTreeV2 (ReporTree)
Schema	Moura	Moura
Dataset	All samples	All samples
Number partitions	1535	1595

Section 2 – Comparison of allele-based pipelines

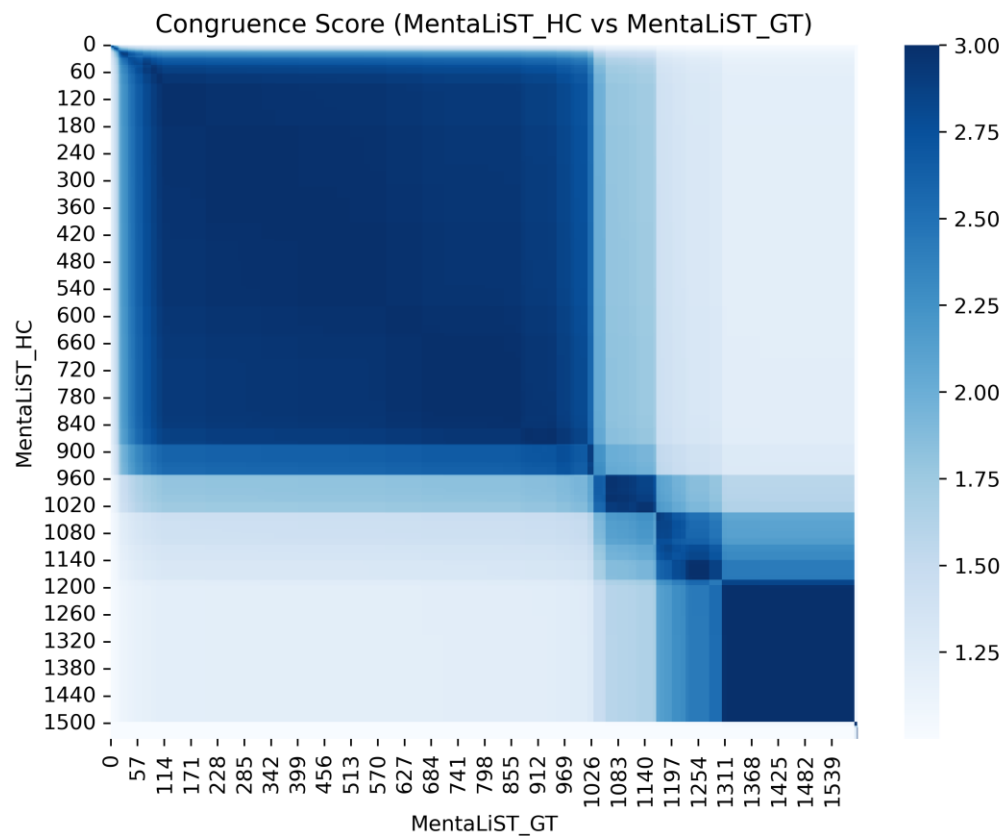


Figure S2.25.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

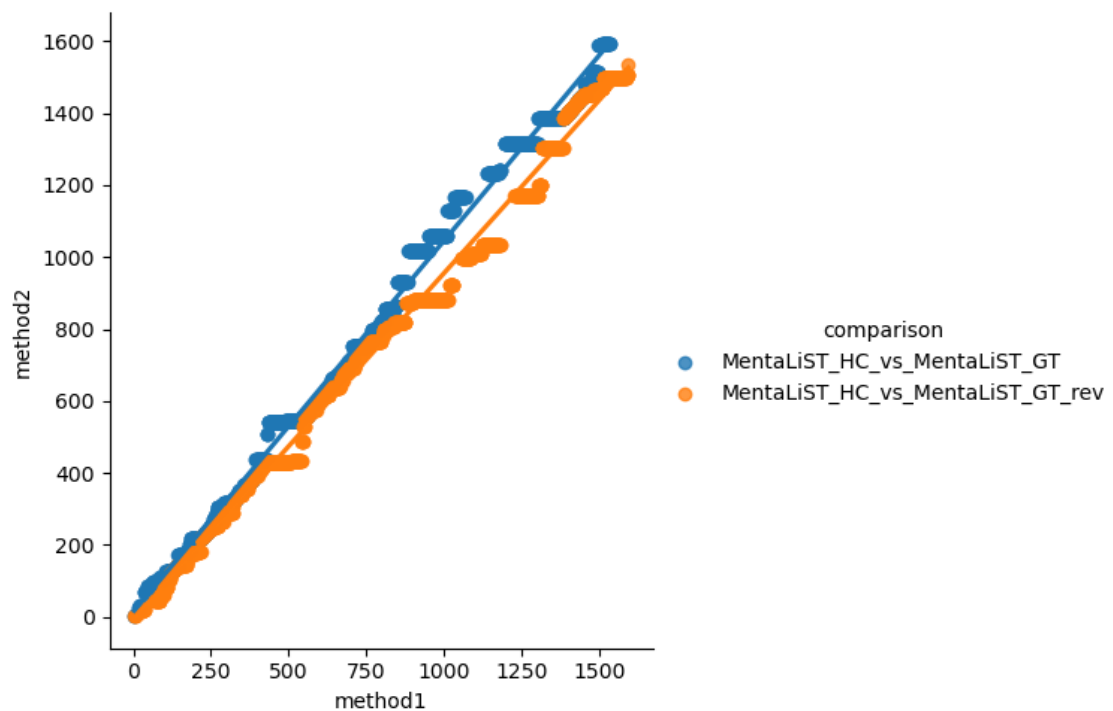


Figure S2.25.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1422 (blue) and 1468 (orange) points is presented.

26. SeqSphere single-linkage vs. Bionumerics 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.

	SeqSphere single-linkage	Bionumerics single-linkage
Pipeline version	v8.3.4	v8.1
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1564	1601

Section 2 – Comparison of allele-based pipelines

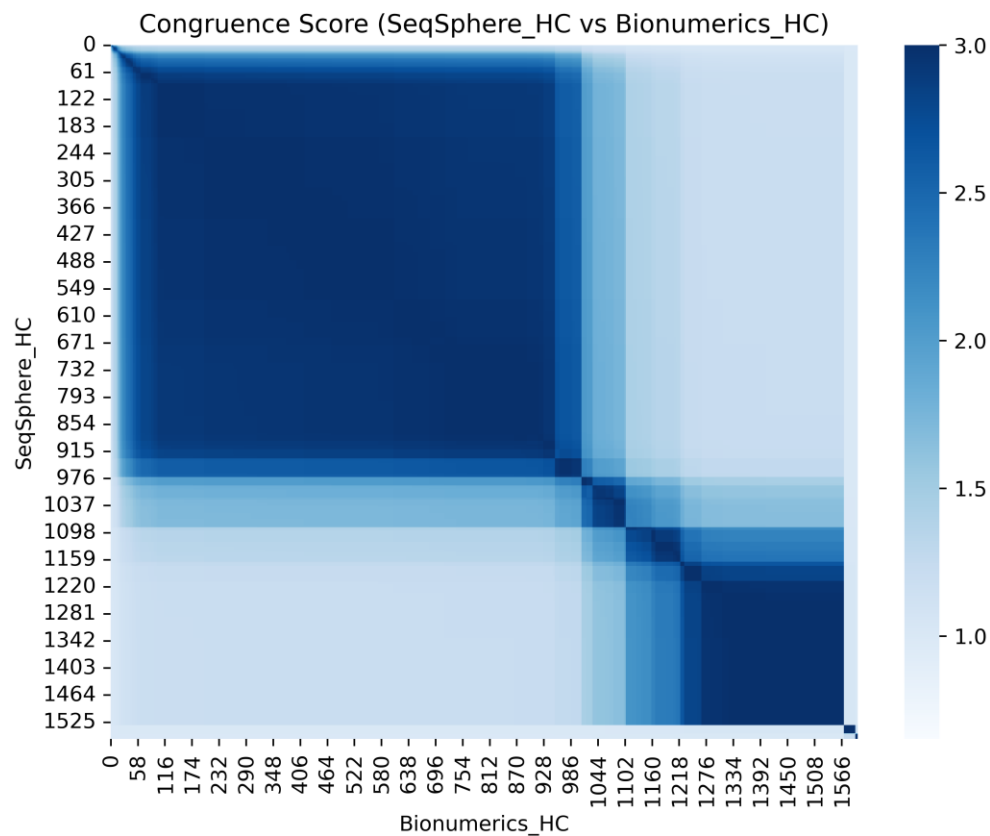


Figure S2.26.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

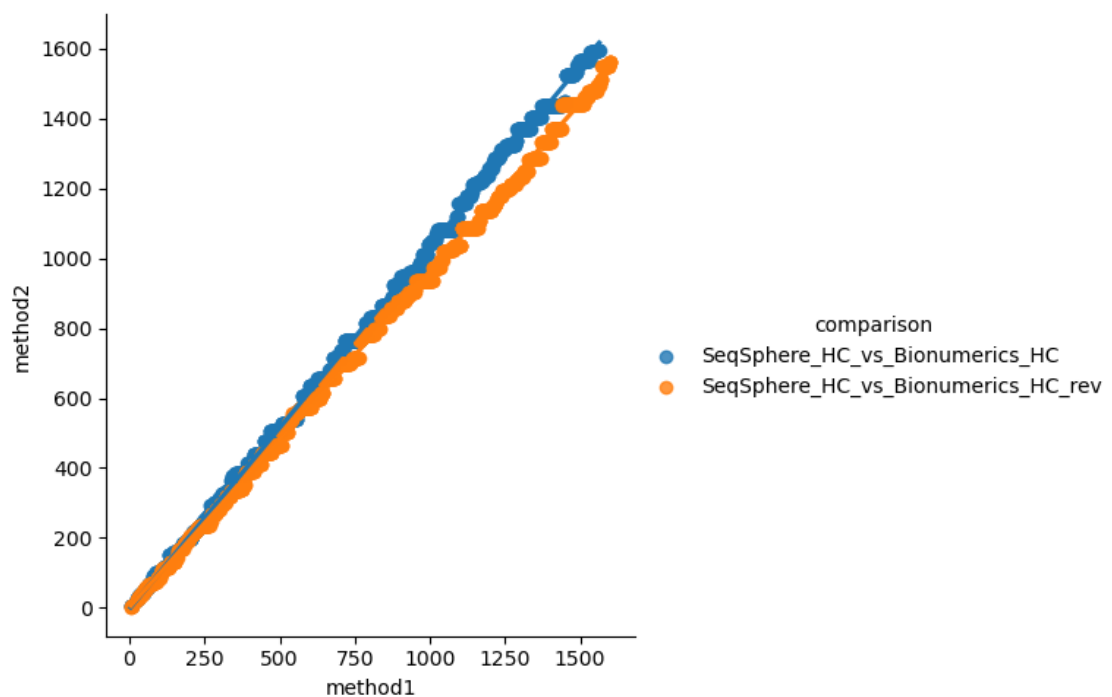


Figure S2.26.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1545 (blue) and 1583 (orange) points is presented.

27. SeqSphere single-linkage vs. MentaLiST 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.

	SeqSphere single-linkage	MentaLiST GrapeTree
Pipeline version	v8.3.4	v1.0.0
Clustering	HC single-linkage (laboratory pipeline)	GrapeTree MSTreeV2 (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1564	1595

Section 2 – Comparison of allele-based pipelines

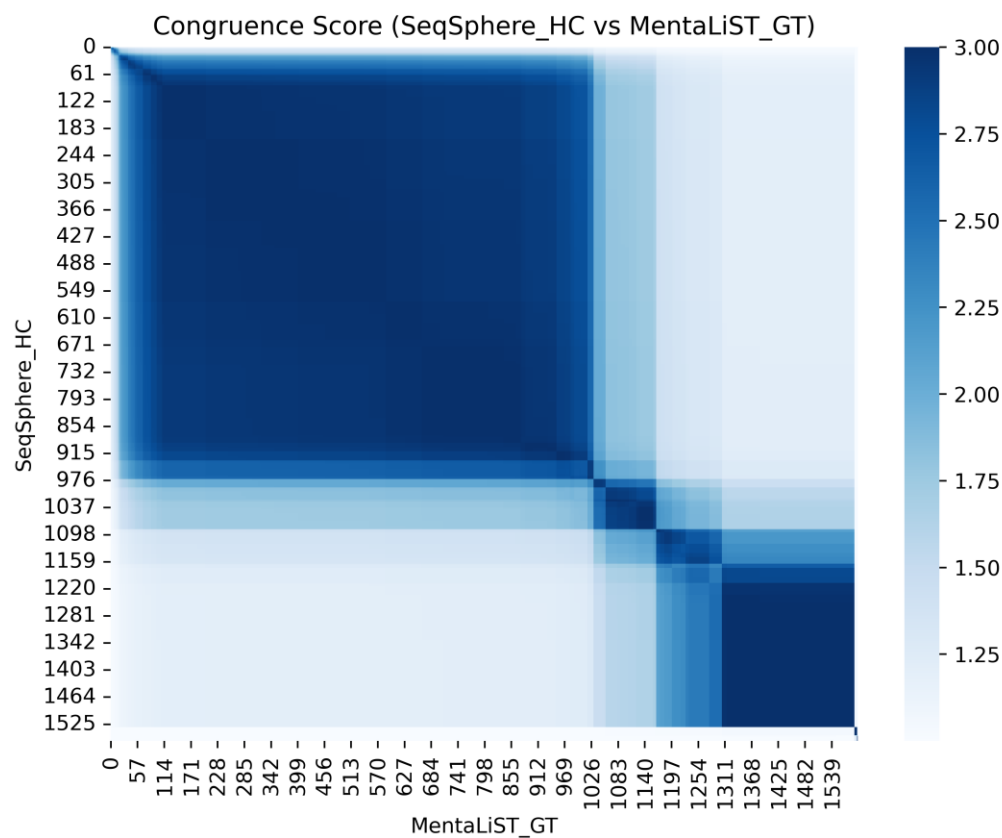


Figure S2.27.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

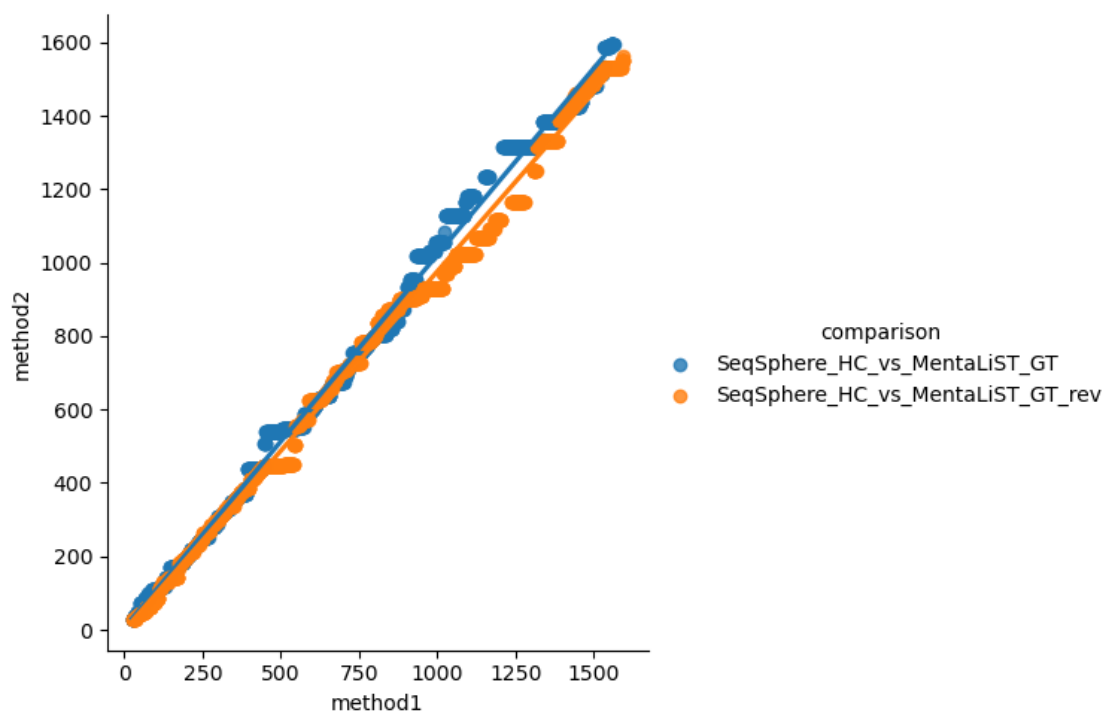


Figure S2.27.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1464 (blue) and 1511 (orange) points is presented.

28. SeqSphere single-linkage vs. MentaLiST 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.

	SeqSphere single-linkage	MentaLiST single-linkage
Pipeline version	v8.3.4	v1.0.0
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (ReporTree)
Schema	Ruppitsch	Moura
Dataset	All samples	All samples
Number partitions	1564	1535

Section 2 – Comparison of allele-based pipelines

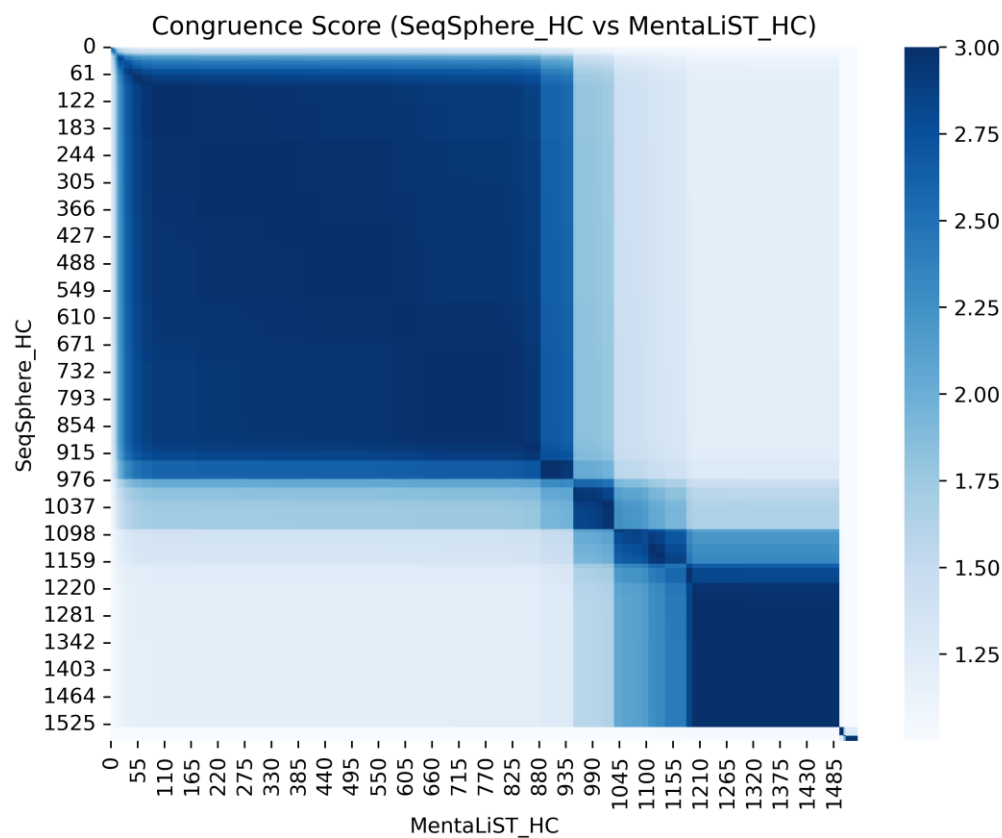


Figure S2.28.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different allele distance thresholds.

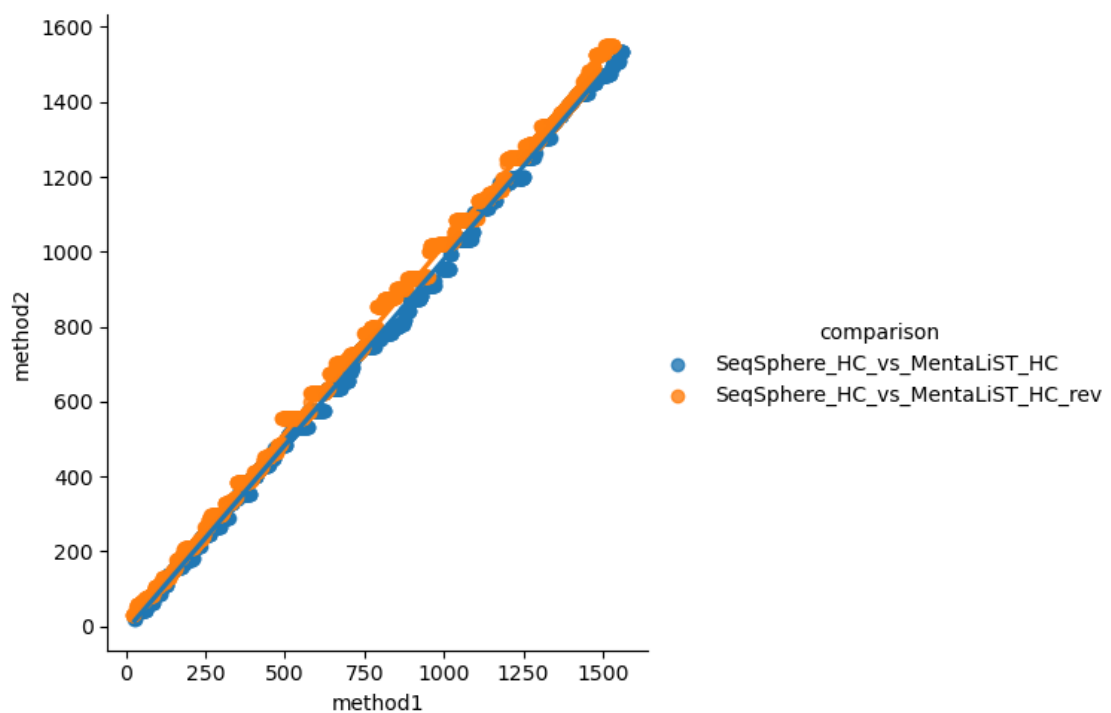


Figure S2.28.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 1490 (blue) and 1509 (orange) points is presented.

Section 3 – Comparison of SNP-based pipelines

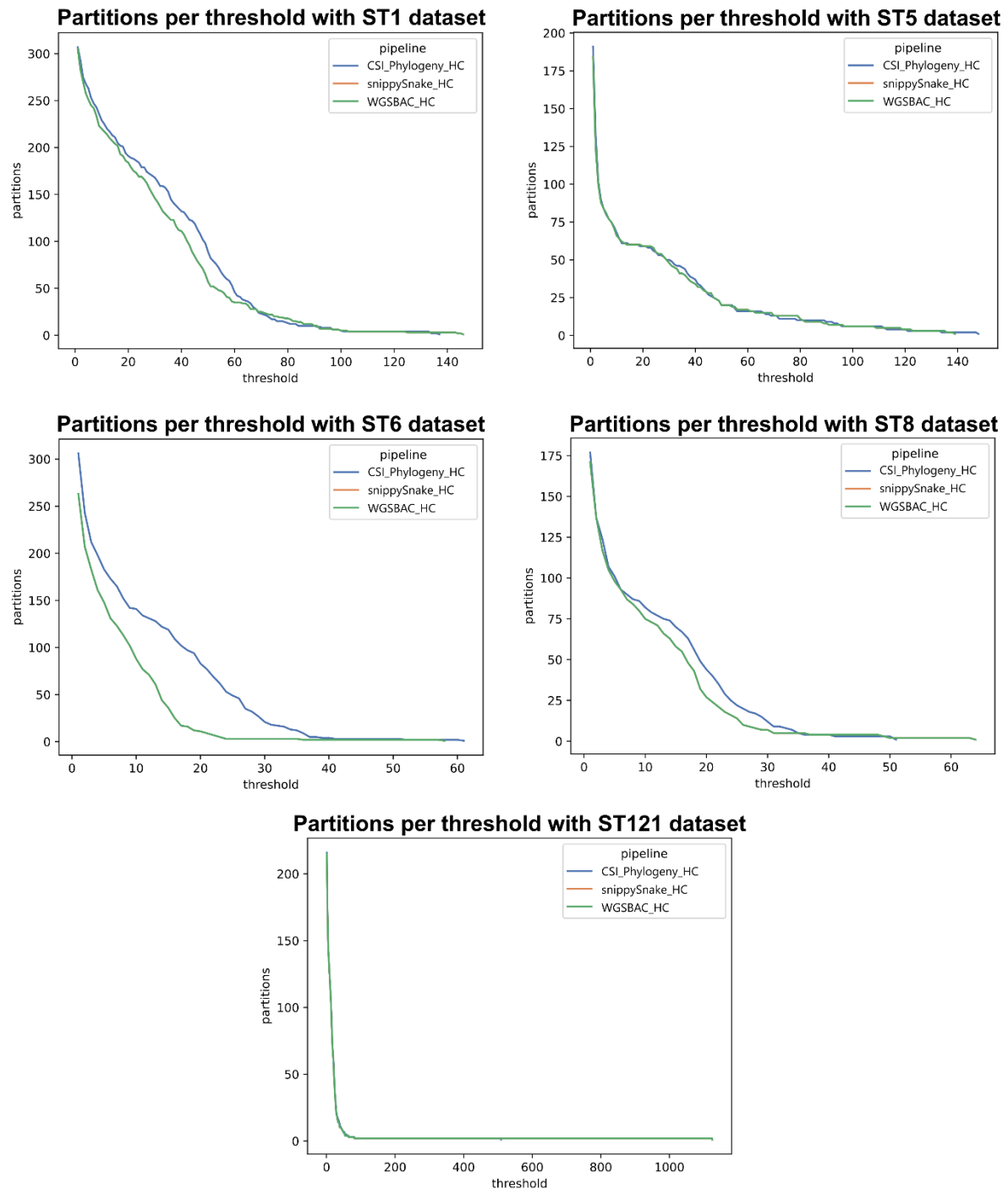


Figure S3. Number of partitions determined by each SNP-based pipeline at each possible distance threshold.

1. CSI Phylogeny single-linkage vs. WGSBAC single-linkage (ST1)

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	WGSBAC single-linkage
Pipeline version	v1.4	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	F2365	F2365
Dataset	ST1	ST1
Number partitions	136	145

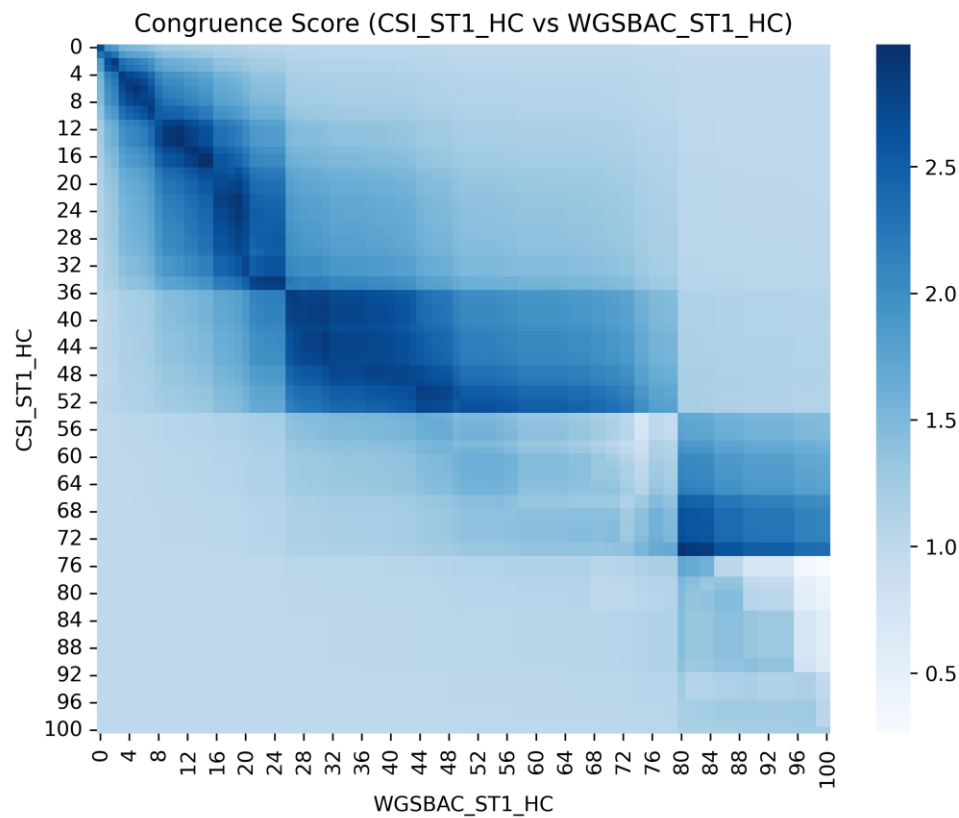


Figure S3.1.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

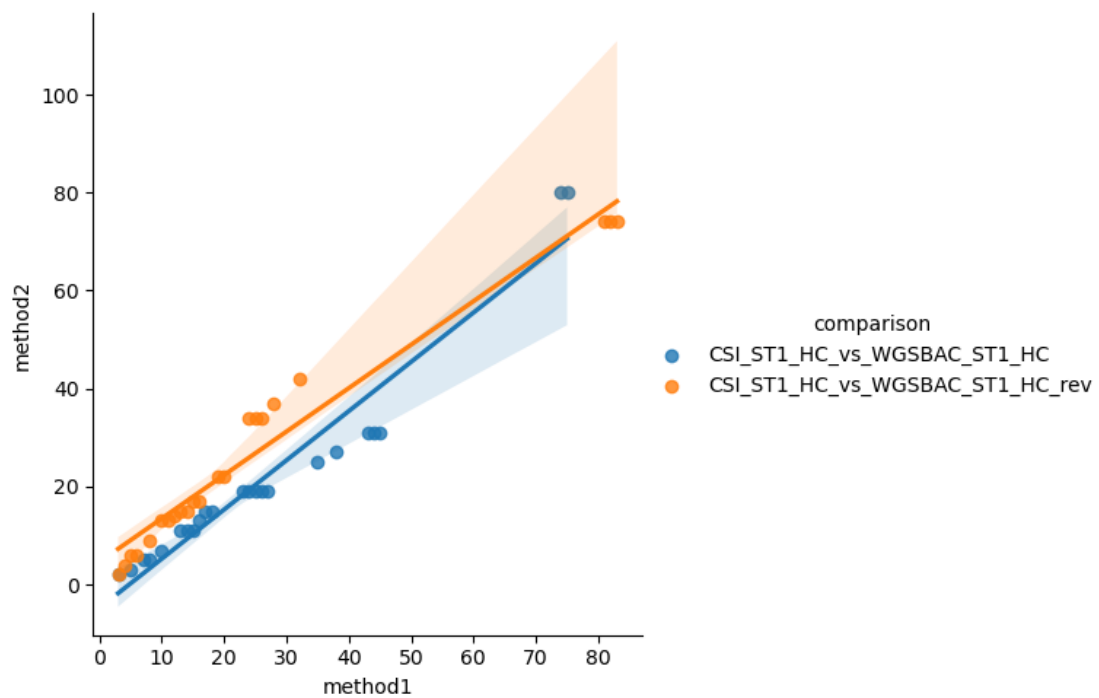


Figure S3.1.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 23 (blue) and 22 (orange) points is presented.

2. CSI Phylogeny single-linkage vs. WGSBAC single-linkage (ST5)

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

	CSI Phylogeny single-linkage	WGSBAC single-linkage
Pipeline version	v1.4	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	CP006592	CP006592
Dataset	ST5	ST5
Number partitions	147	138

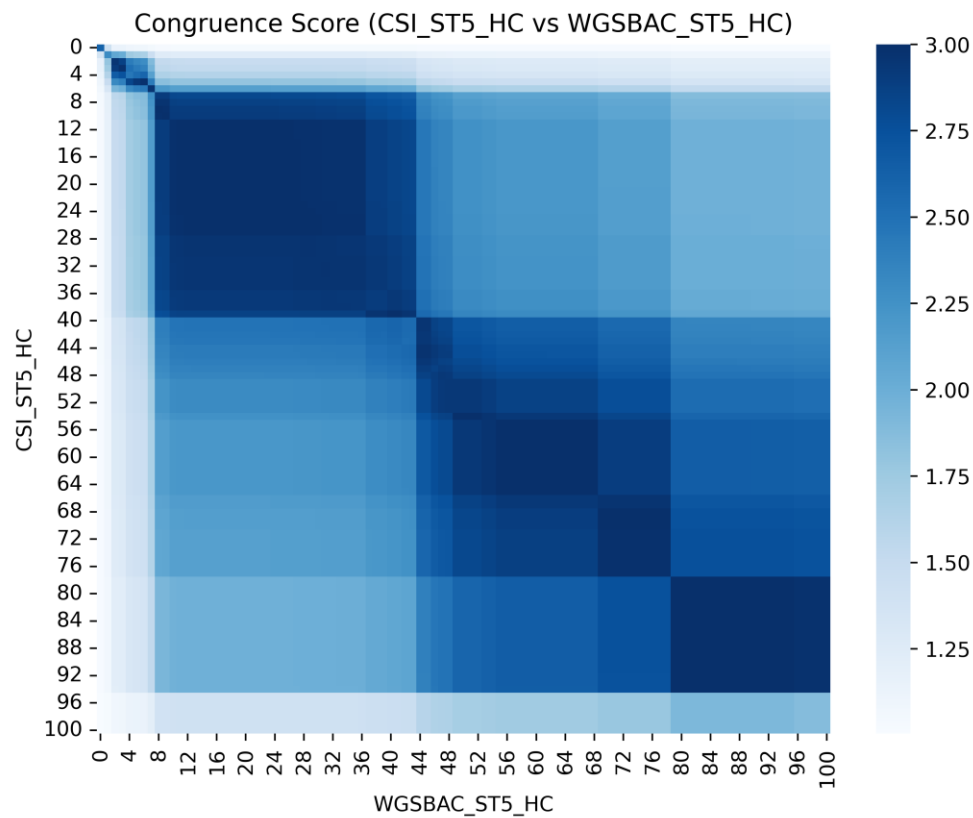


Figure S3.2.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

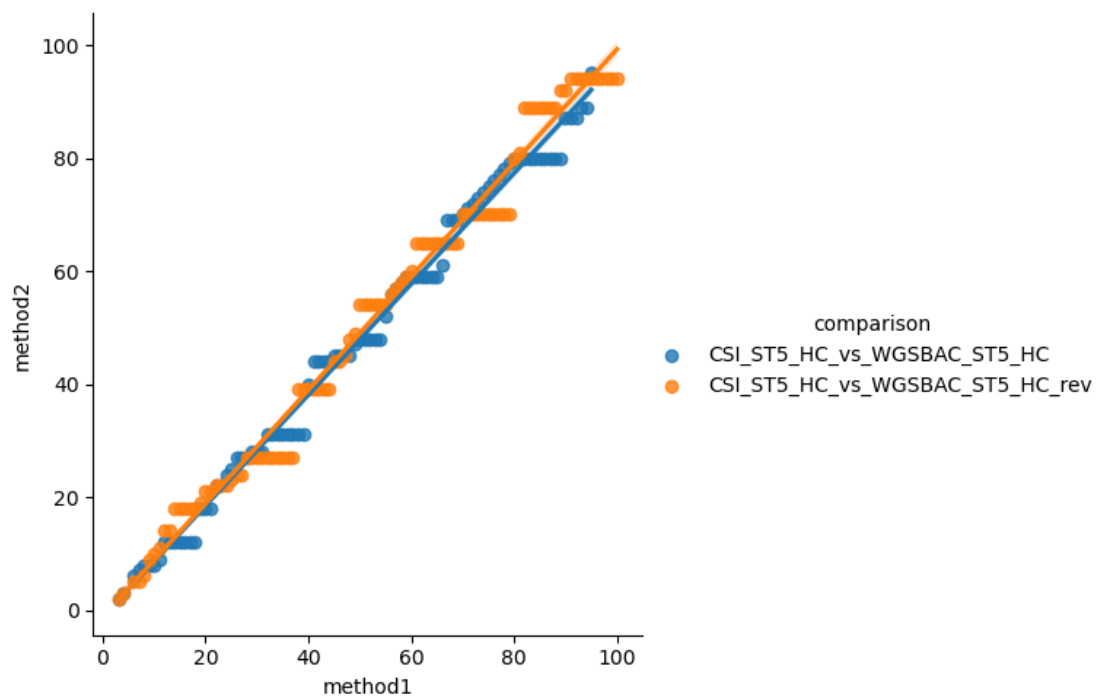


Figure S3.2.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 92 (blue) and 97 (orange) points is presented.

3. CSI Phylogeny single-linkage vs. WGSBAC single-linkage (ST6)

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

	CSI Phylogeny single-linkage	WGSBAC single-linkage
Pipeline version	v1.4	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	CP006046	CP006046
Dataset	ST6	ST6
Number partitions	60	57

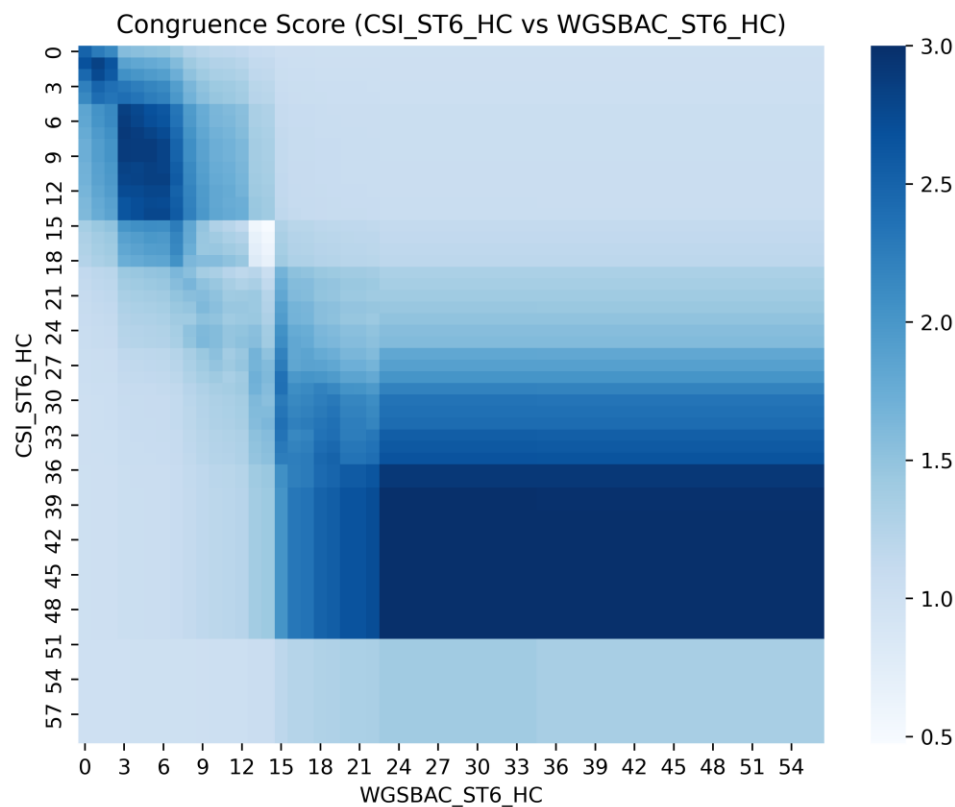


Figure S3.3.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different SNP distance thresholds.

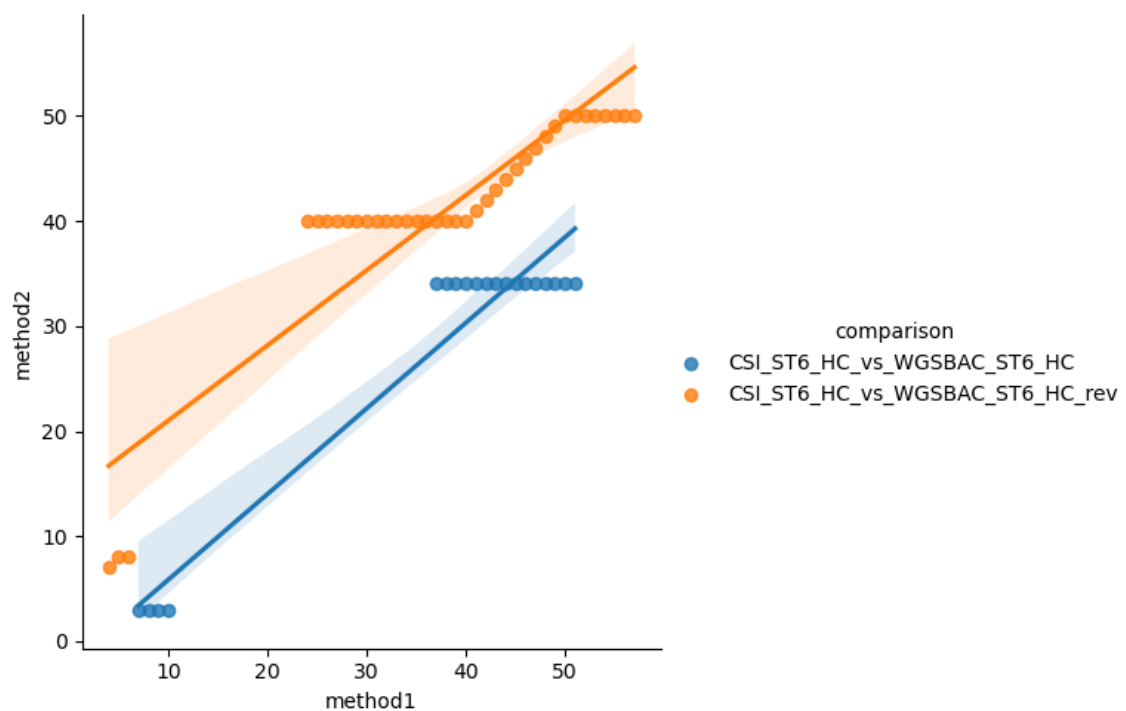


Figure S3.3.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions. A linear tendency line supported by 19 (blue) and 37 (orange) points is presented.

4. CSI Phylogeny single-linkage vs. WGSBAC single-linkage (ST8)

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

	CSI Phylogeny single-linkage	WGSBAC single-linkage
Pipeline version	v1.4	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	CP006862	CP006862
Dataset	ST8	ST8
Number partitions	50	63

Section 3 – Comparison of SNP-based pipelines

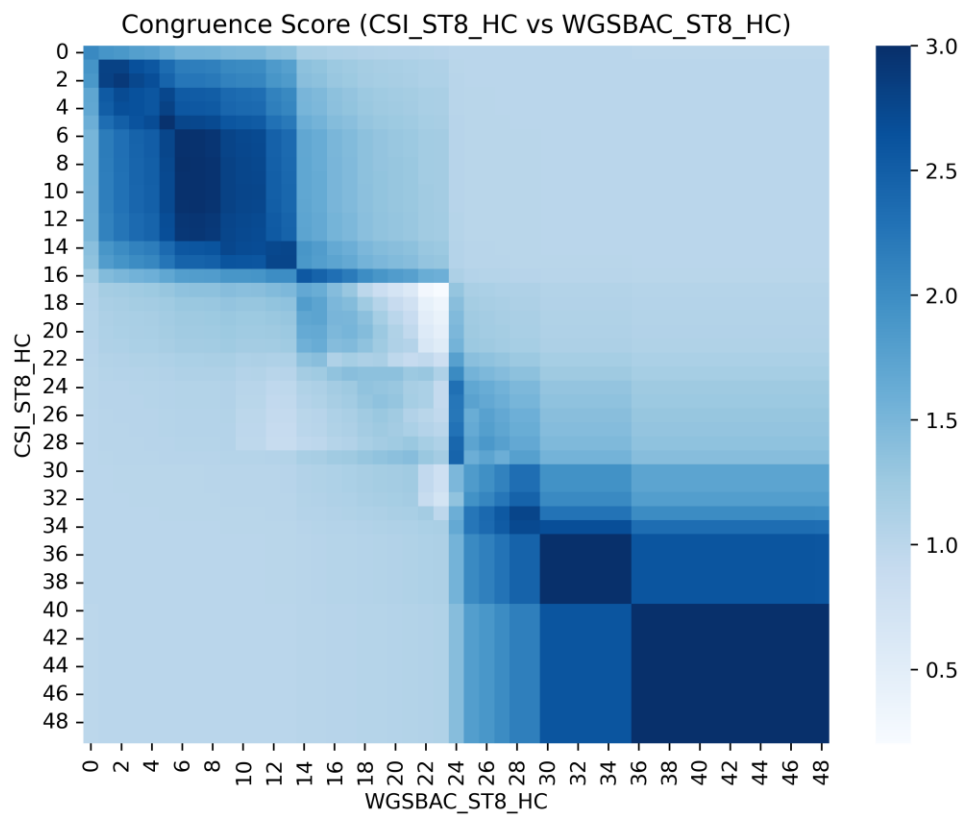


Figure S3.4.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different SNP distance thresholds.

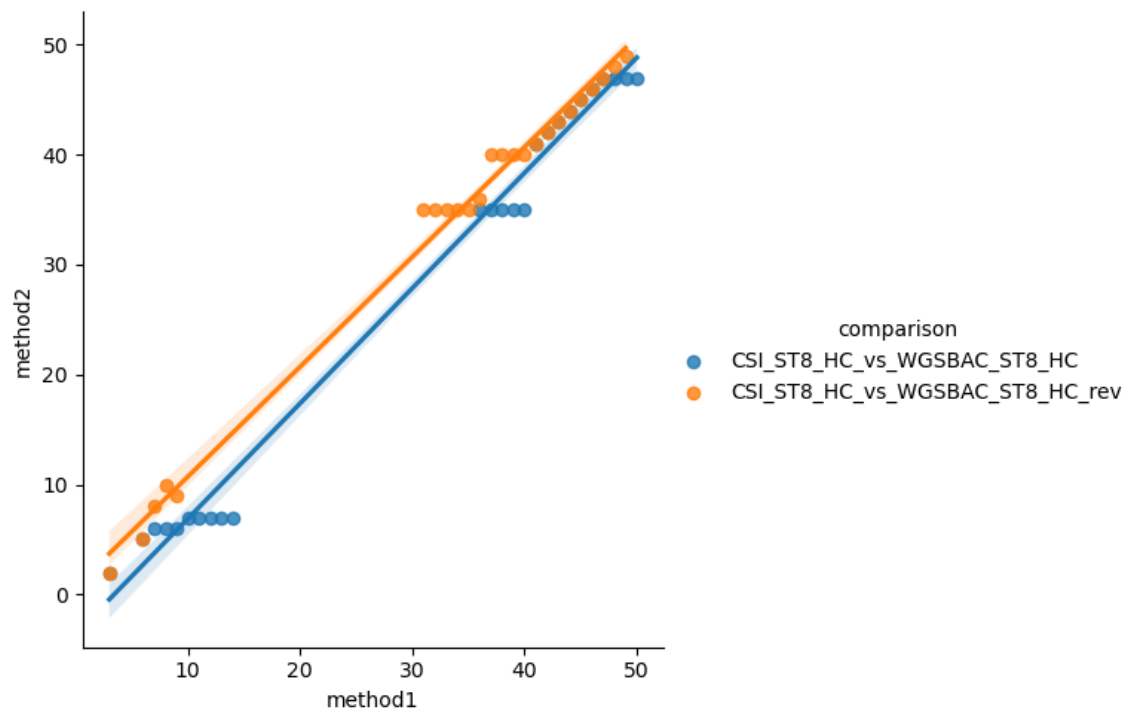


Figure S3.4.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85) of all partitions. A linear tendency line supported by 25 (blue) and 24 (orange) points is presented.

5. CSI Phylogeny single-linkage vs. WGSBAC single-linkage (ST121*)

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

	CSI Phylogeny single-linkage	WGSBAC single-linkage
Pipeline version	v1.4	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	HG813249	HG813249
Dataset	ST121	ST121
Number partitions	508	1124

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution*

Section 3 – Comparison of SNP-based pipelines

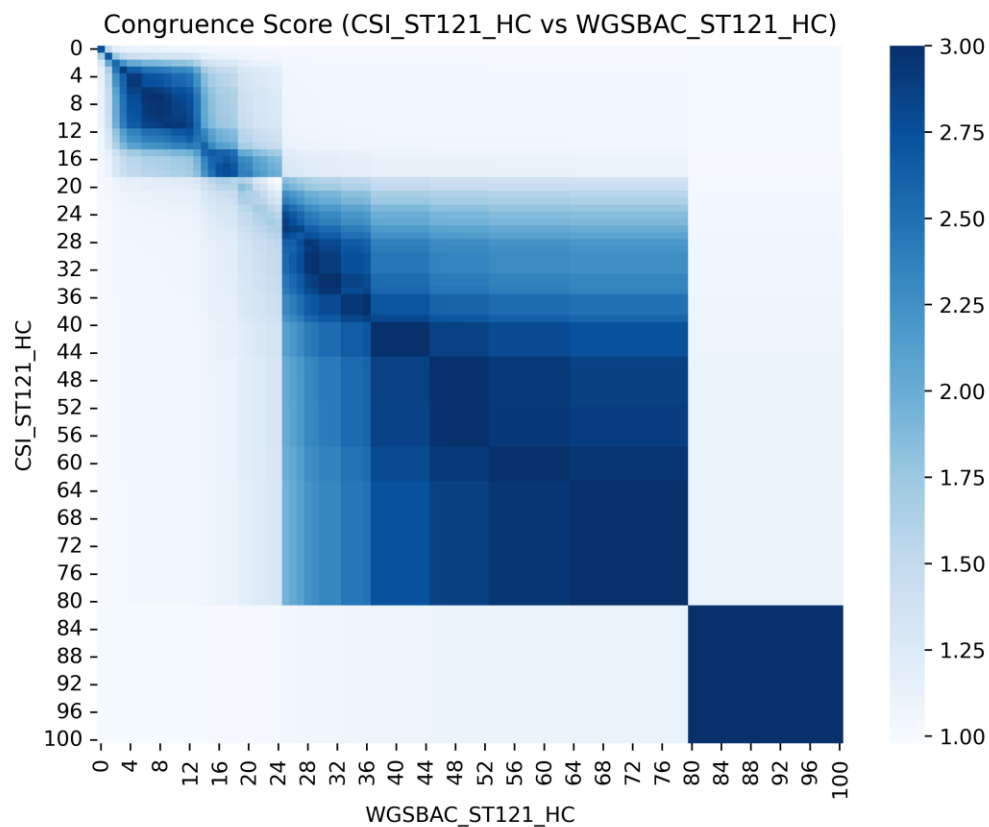


Figure S3.5.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

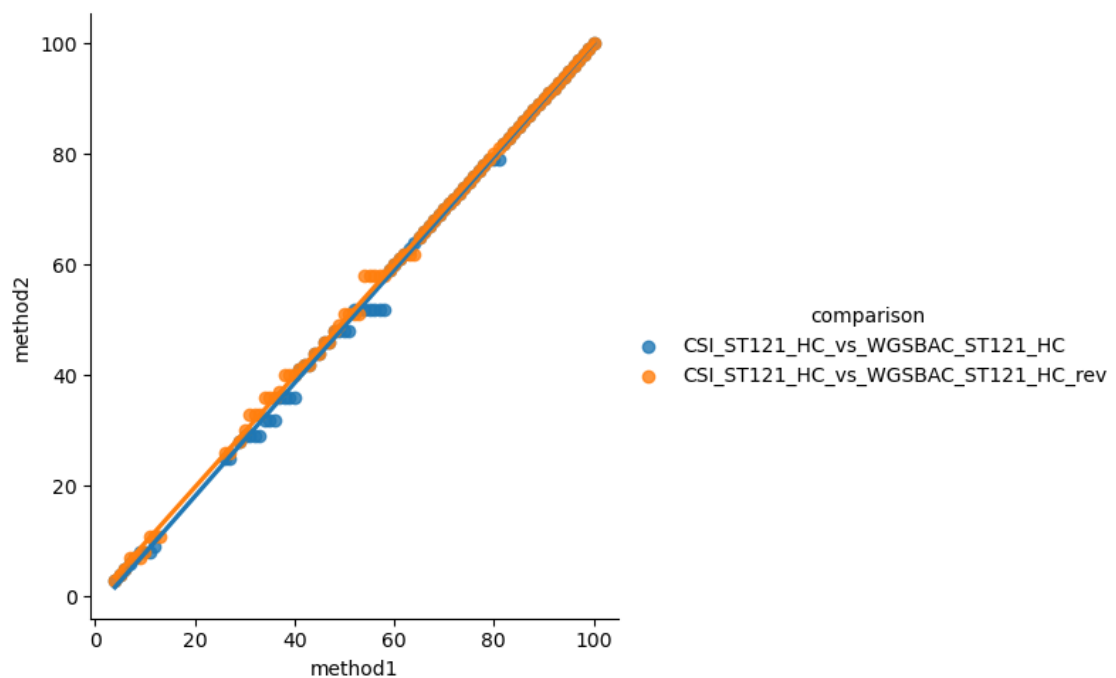


Figure S3.5.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 83 (blue) and 84 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution*

6. snippySnake single-linkage vs. CSI Phylogeny single-linkage (ST1)

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

	snippySnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.1.0	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	F2365	F2365
Dataset	ST1	ST1
Number partitions	145	136

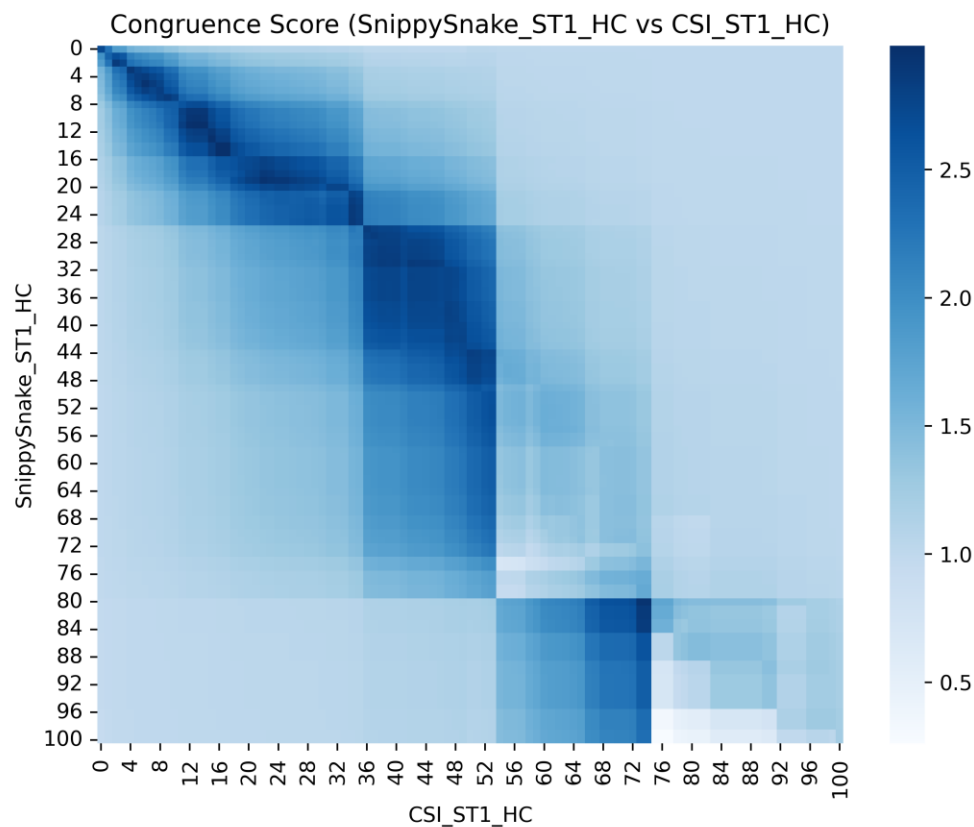


Figure S3.6.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

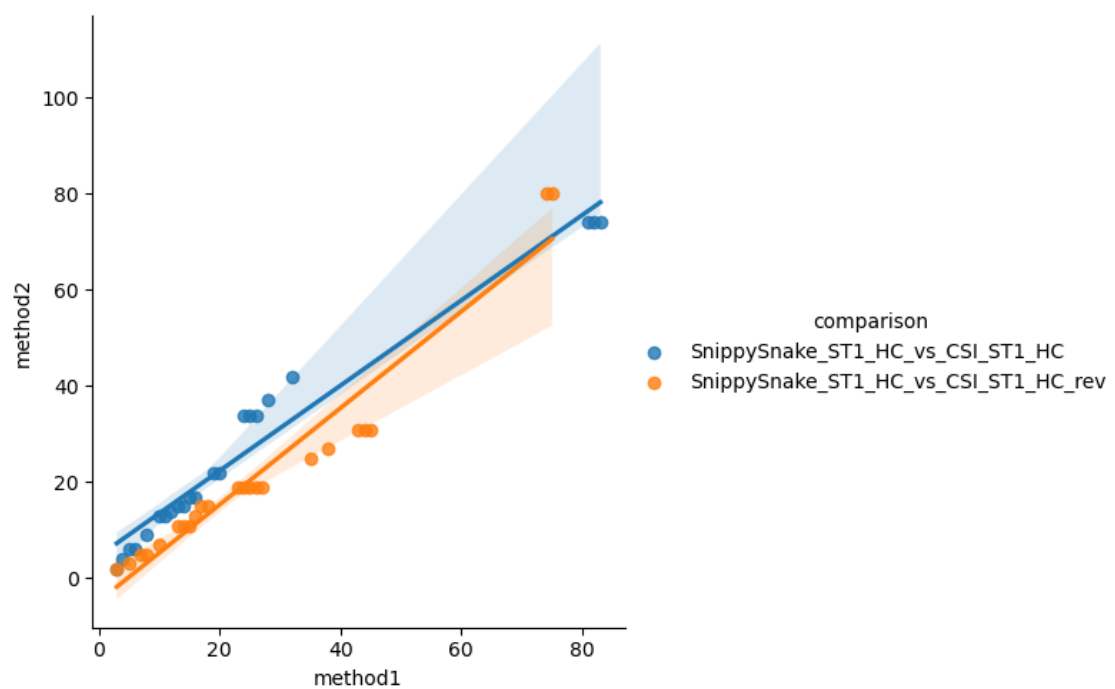


Figure S3.6.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 22 (blue) and 23 (orange) points is presented.

7. snippySnake single-linkage vs. CSI Phylogeny single-linkage (ST5)

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

	snippySnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.1.0	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	CP006592	CP006592
Dataset	ST5	ST5
Number partitions	138	147

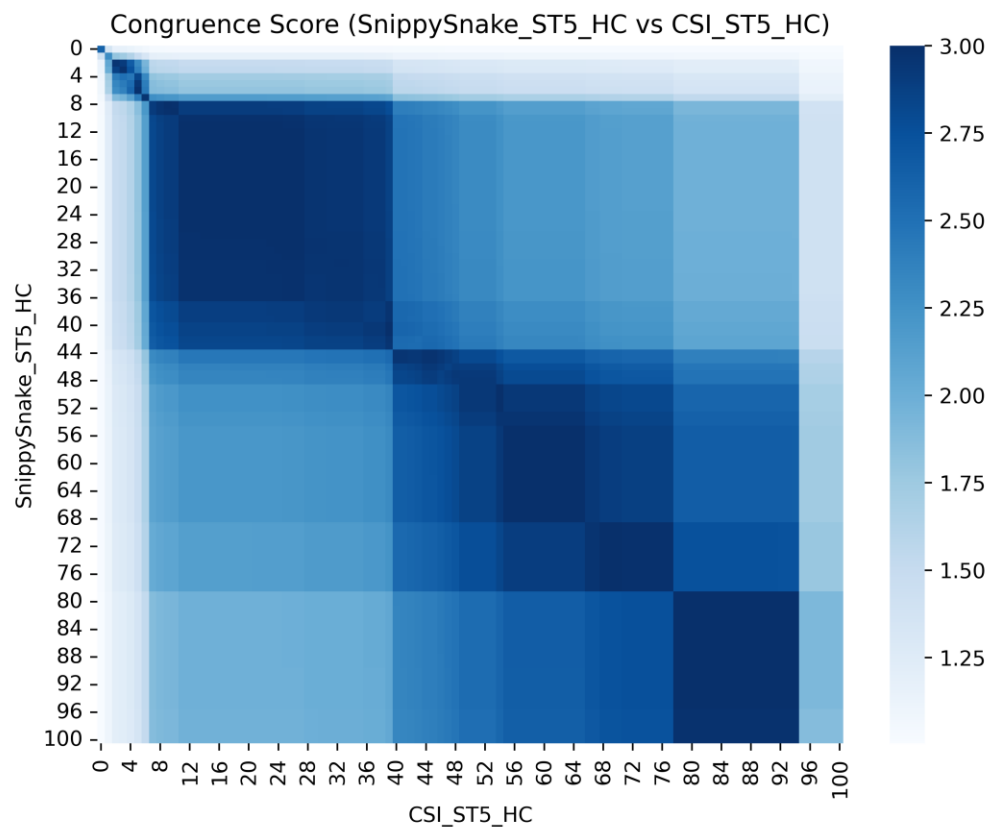


Figure S3.7.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

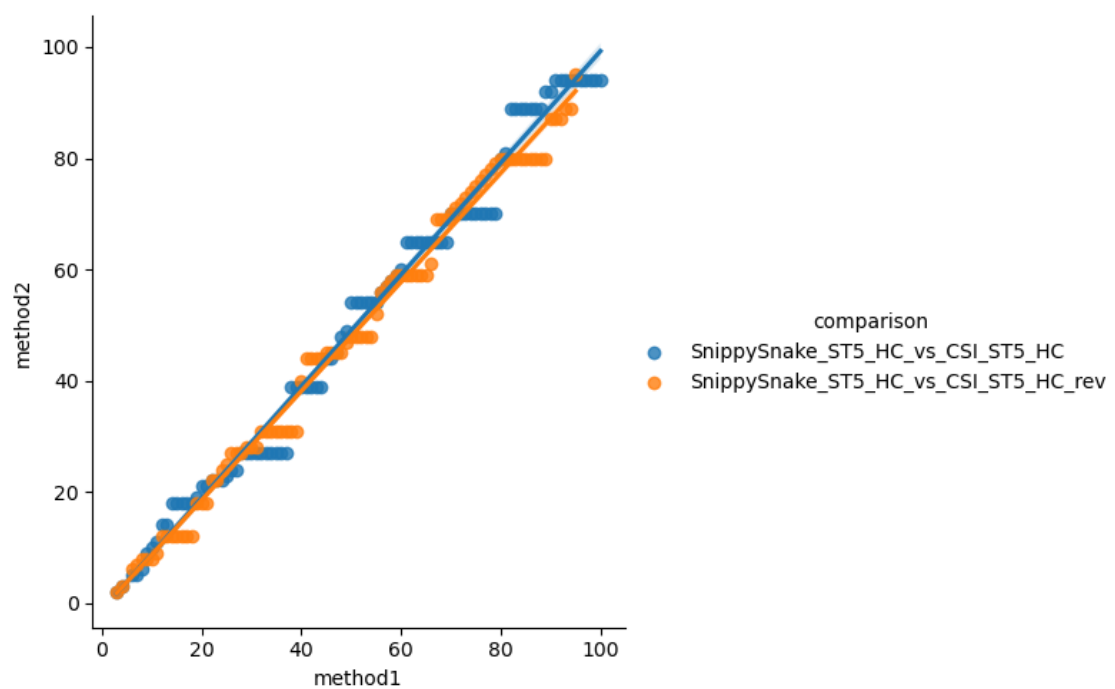


Figure S3.7.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 97 (blue) and 92 (orange) points is presented.

8. snippySnake single-linkage vs. CSI Phylogeny single-linkage (ST6)

Table S3.8. 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.

	snippySnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.1.0	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	CP006046	CP006046
Dataset	ST6	ST6
Number partitions	57	60

Section 3 – Comparison of SNP-based pipelines

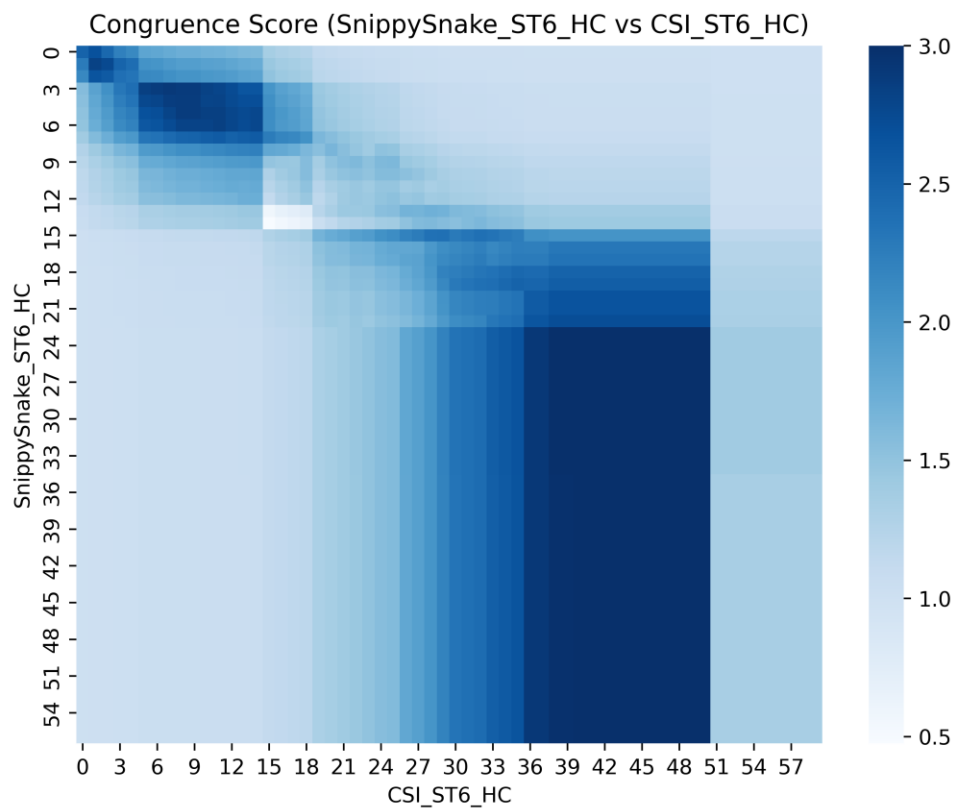


Figure S3.8.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different SNP distance thresholds.

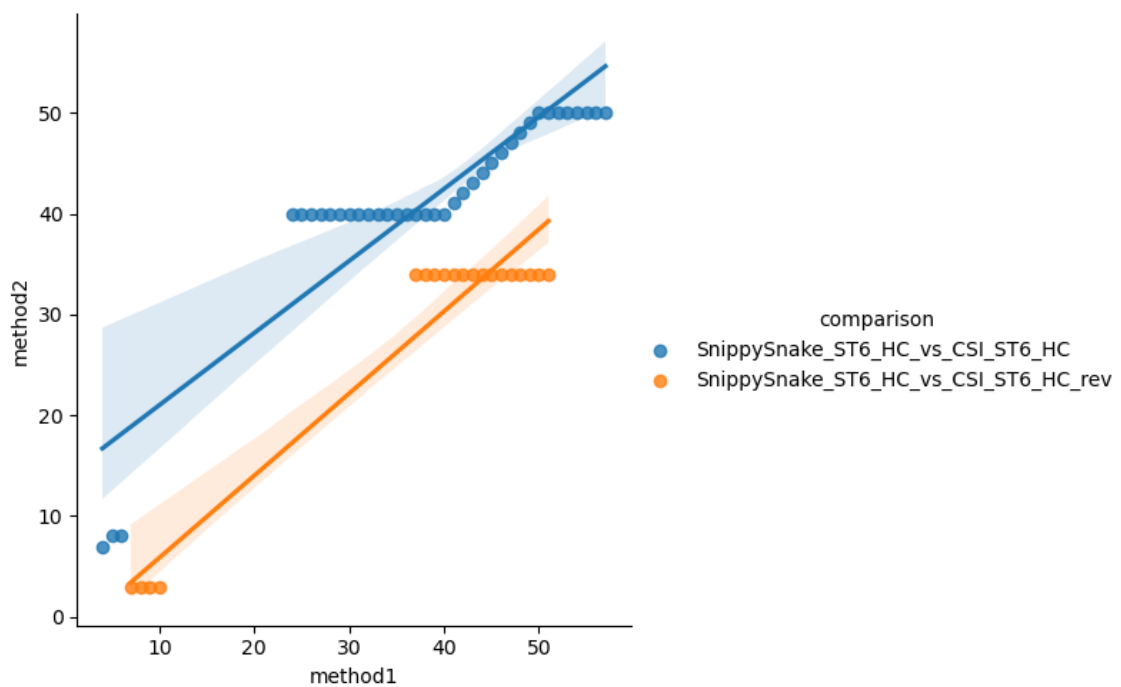


Figure S3.8.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions. A linear tendency line supported by 37 (blue) and 19 (orange) points is presented.

9. snippySnake single-linkage vs. CSI Phylogeny single-linkage (ST8)

Table S3.9. 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.

	snippySnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.1.0	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	CP006862	CP006862
Dataset	ST8	ST8
Number partitions	63	50

Section 3 – Comparison of SNP-based pipelines

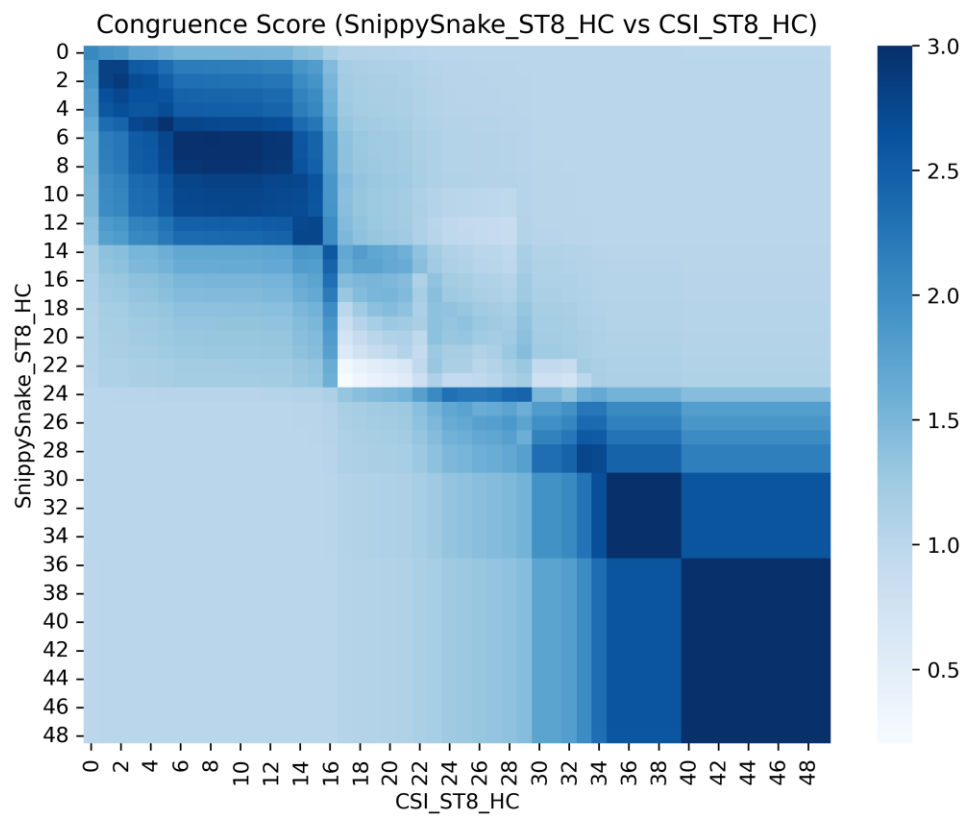


Figure S3.9.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different SNP distance thresholds.

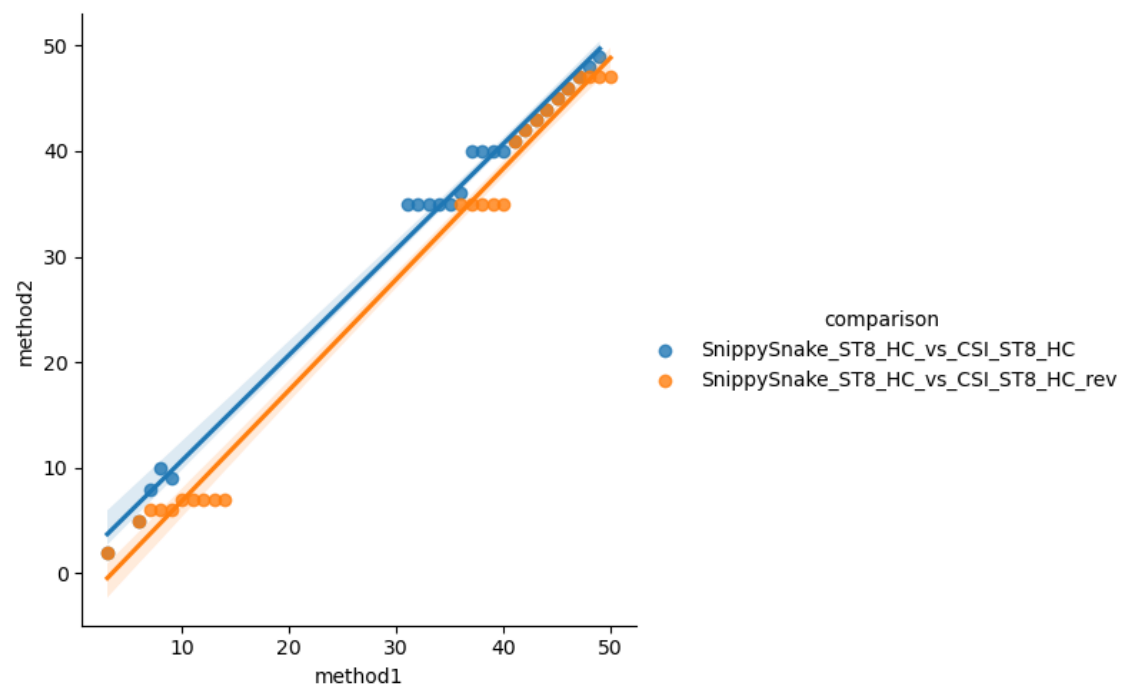


Figure S3.9.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions. A linear tendency line supported by 24 (blue) and 25 (orange) points is presented.

10. snippySnake single-linkage vs. CSI Phylogeny single-linkage (ST121*)

Table S3.10. 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.

	snippySnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.1.0	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	HG813249	HG813249
Dataset	ST121	ST121
Number partitions	1124	508

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

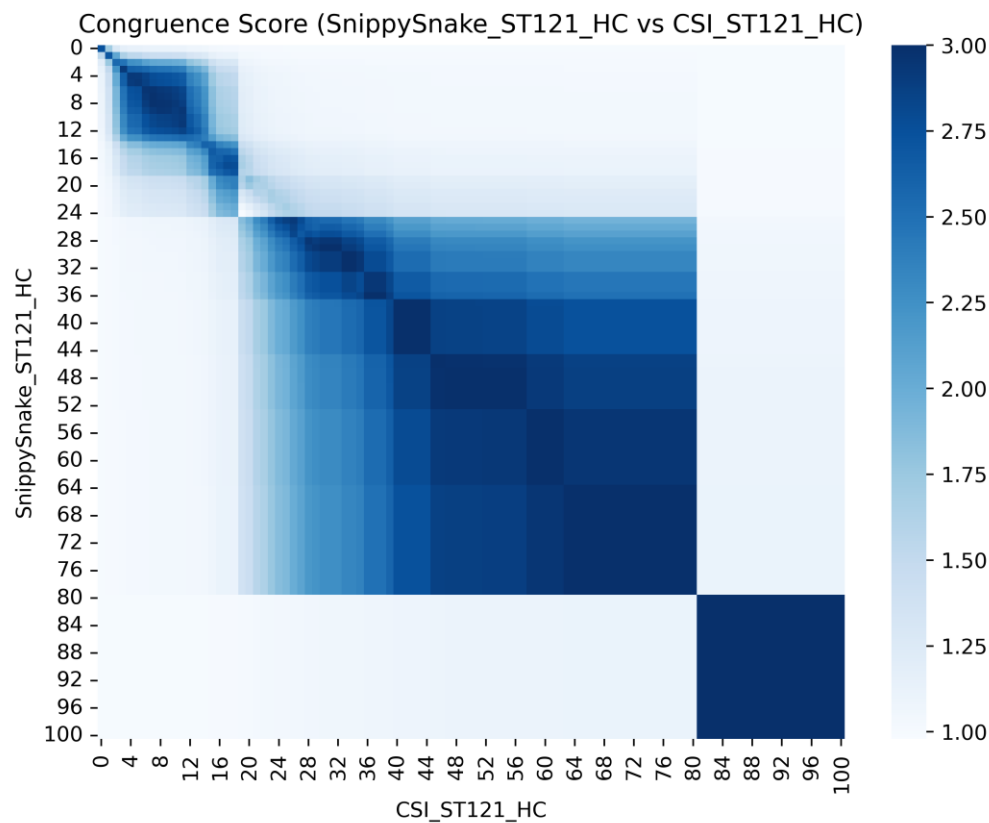


Figure S3.10.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

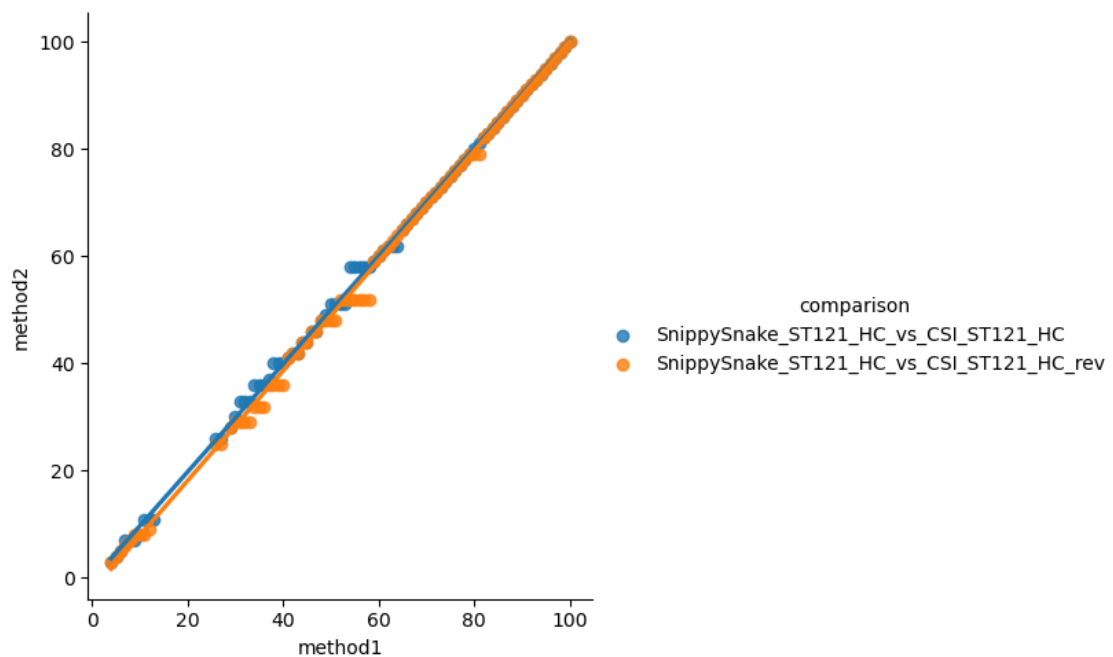


Figure S3.10.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 84 (blue) and 83 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

11. snippySnake single-linkage vs. WGSBAC single-linkage (ST1)

Table S3.11. 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.

	snippySnake single-linkage	WGSBAC single-linkage
Pipeline version	v1.1.0	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	F2365	F2365
Dataset	ST1	ST1
Number partitions	145	145

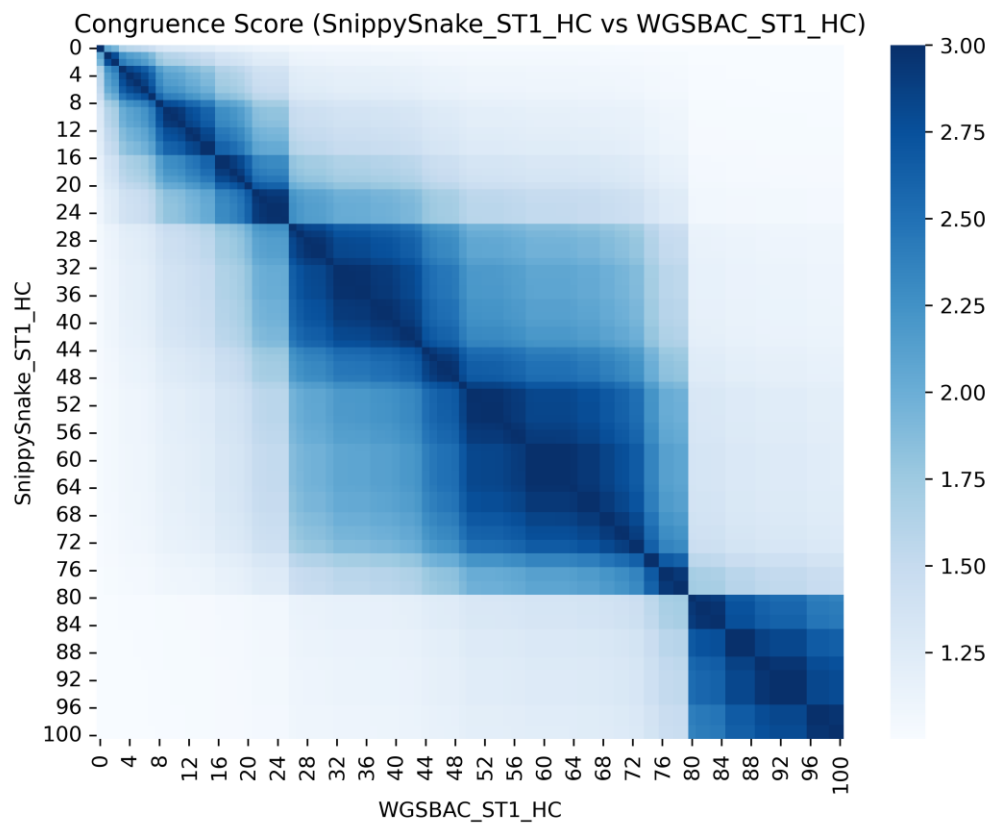


Figure S3.11.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

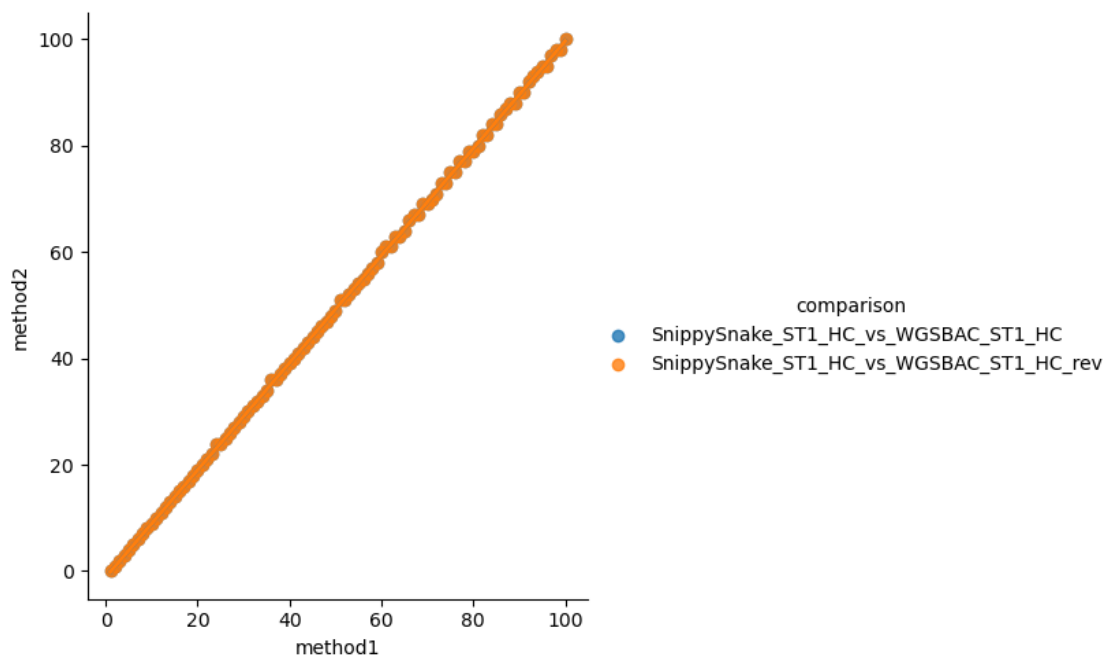


Figure S3.11.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85). A linear tendency line supported by 100 (blue) and 100 (orange) points is presented.

12. snippySnake single-linkage vs. WGSBAC single-linkage (ST5)

Table S3.12. 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.

	snippySnake single-linkage	WGSBAC single-linkage
Pipeline version	v1.1.0	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	CP006592	CP006592
Dataset	ST5	ST5
Number partitions	138	138

Section 3 – Comparison of SNP-based pipelines

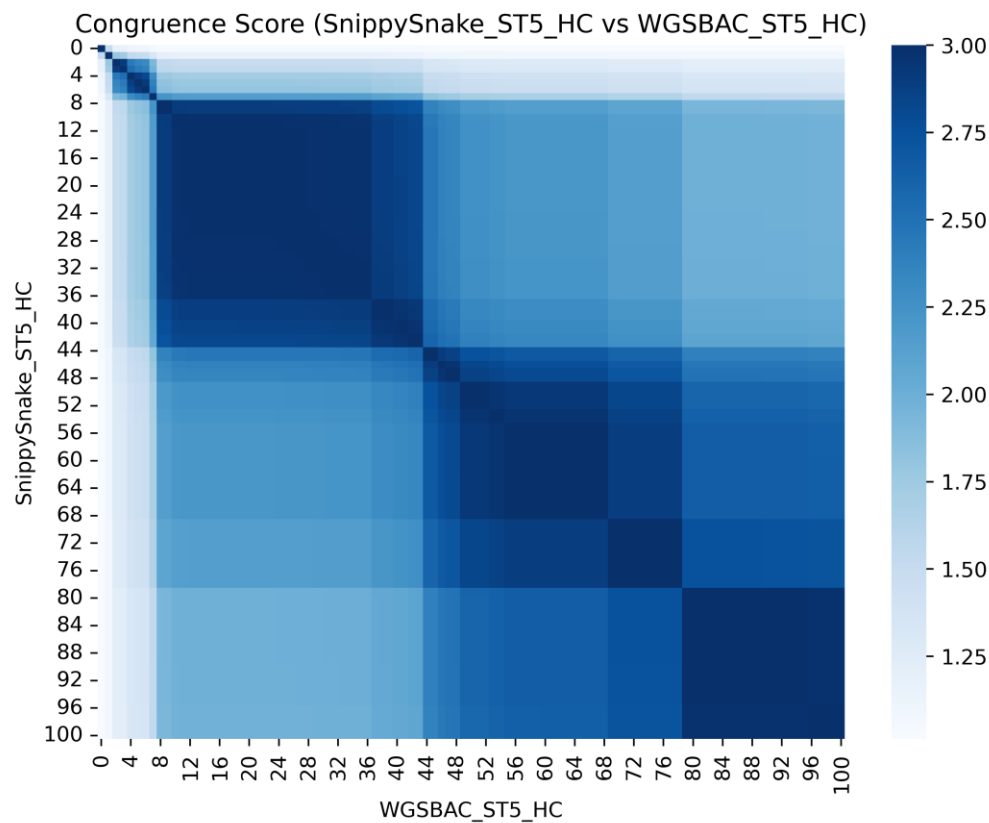


Figure S3.12.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

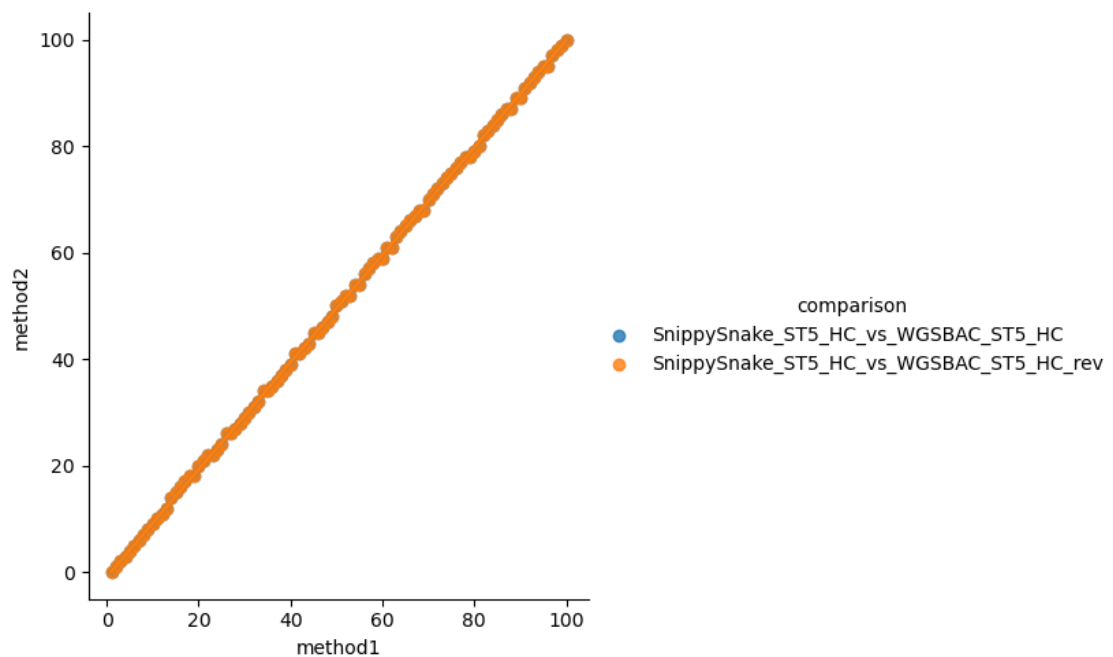


Figure S3.12.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 100 (blue) and 100 (orange) points is presented.

13. snippySnake single-linkage vs. WGSBAC single-linkage (ST6)

Table S3.13. 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.

	snippySnake single-linkage	WGSBAC single-linkage
Pipeline version	v1.1.0	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	CP006046	CP006046
Dataset	ST6	ST6
Number partitions	57	57

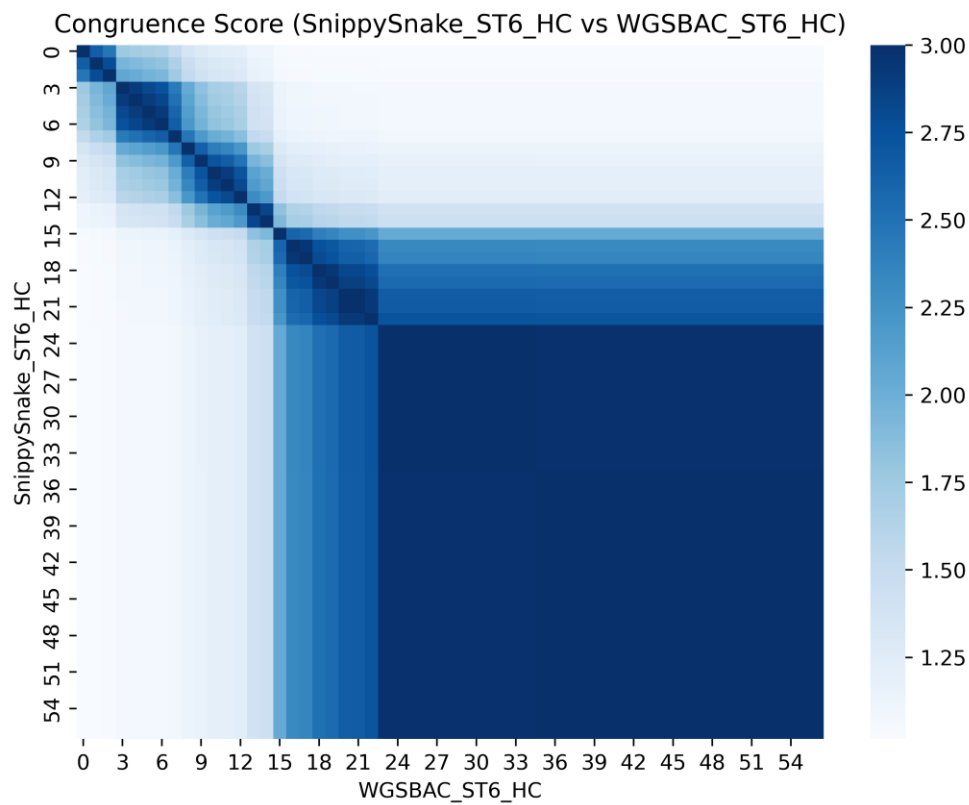


Figure S3.13.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different SNP distance thresholds. Axis represent the different SNP distance thresholds.

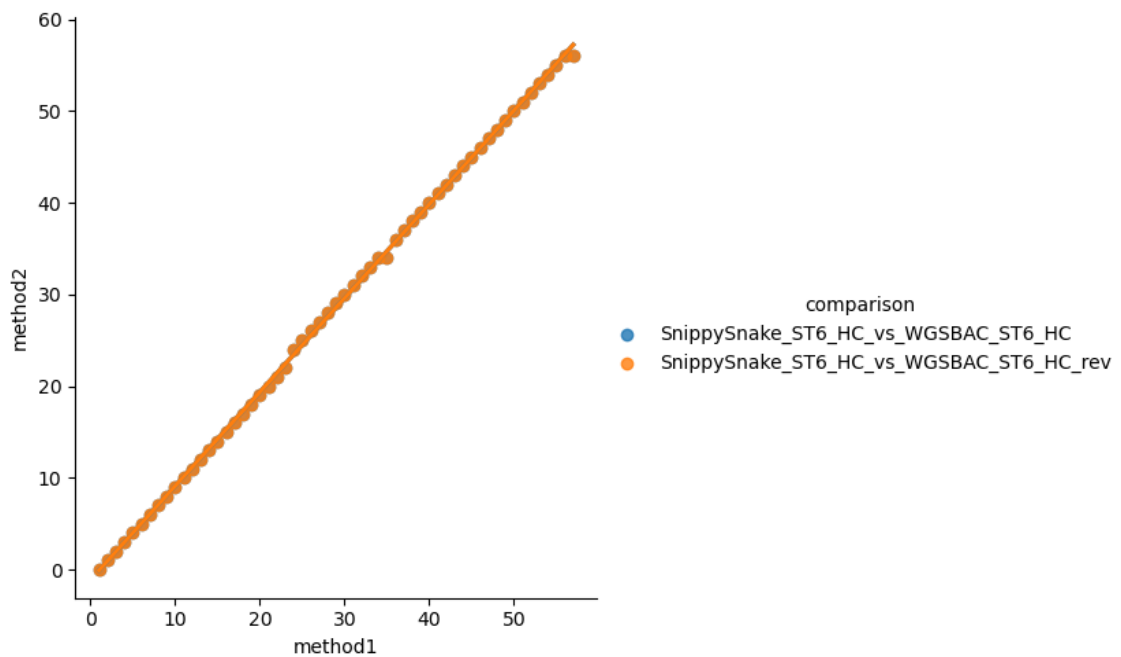


Figure S3.13.2. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions. A linear tendency line supported by 57 (blue) and 57 (orange) points is presented.

14. snippySnake single-linkage vs. WGSBAC single-linkage (ST8)

Table S3.14. 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.

	snippySnake single-linkage	WGSBAC single-linkage
Pipeline version	v1.1.0	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	CP006862	CP006862
Dataset	ST8	ST8
Number partitions	63	63

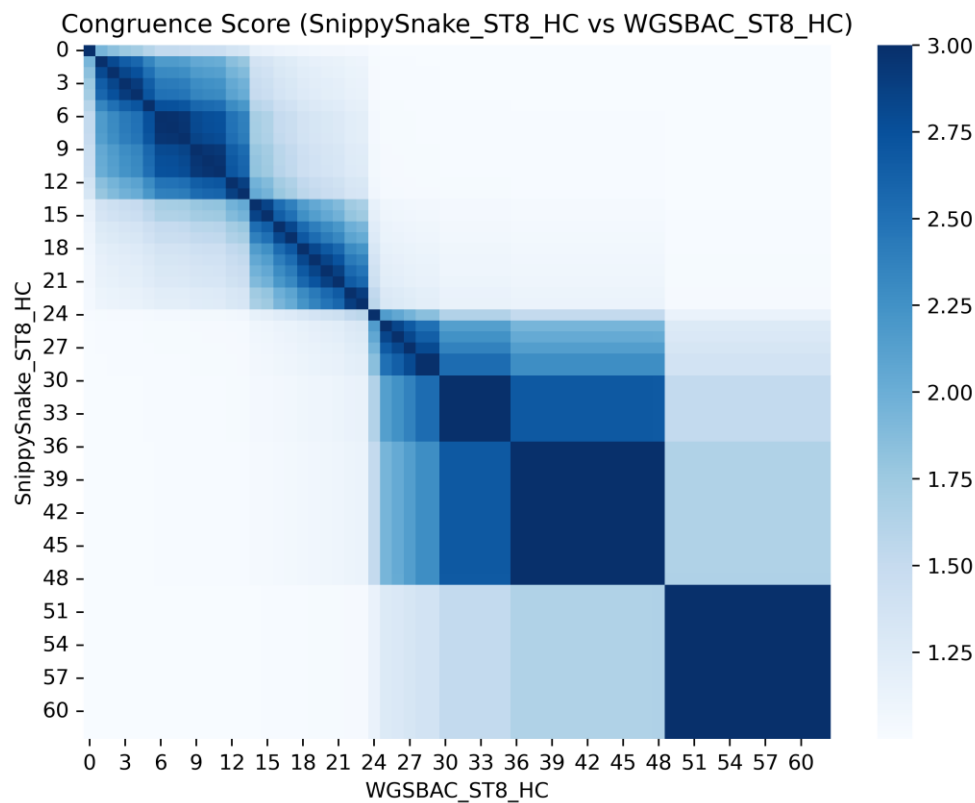


Figure S3.14.1. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines. Axis represent the different SNP distance thresholds.

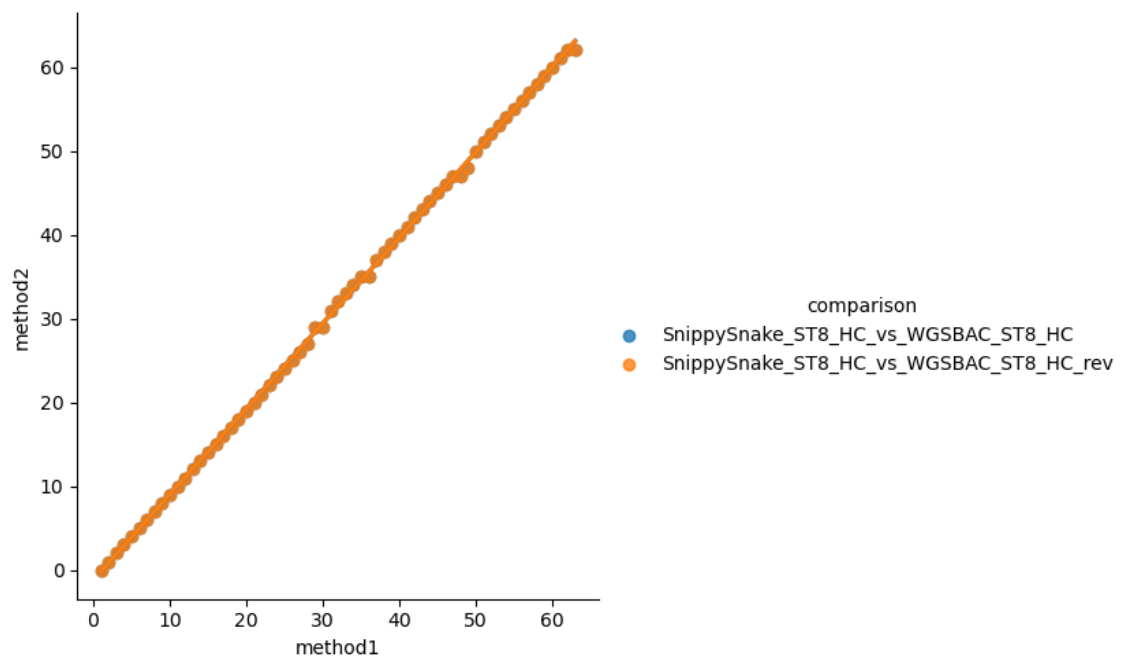


Figure S3.14.2. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85) of all partitions. A linear tendency line supported by 63 (blue) and 63 (orange) points is presented.

15. snippySnake single-linkage vs. WGSBAC single-linkage (ST121*)

Table S3.15. 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.

	snippySnake single-linkage	WGSBAC single-linkage
Pipeline version	v1.1.0	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Reference	HG813249	HG813249
Dataset	ST121	ST121
Number partitions	1124	1124

NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.

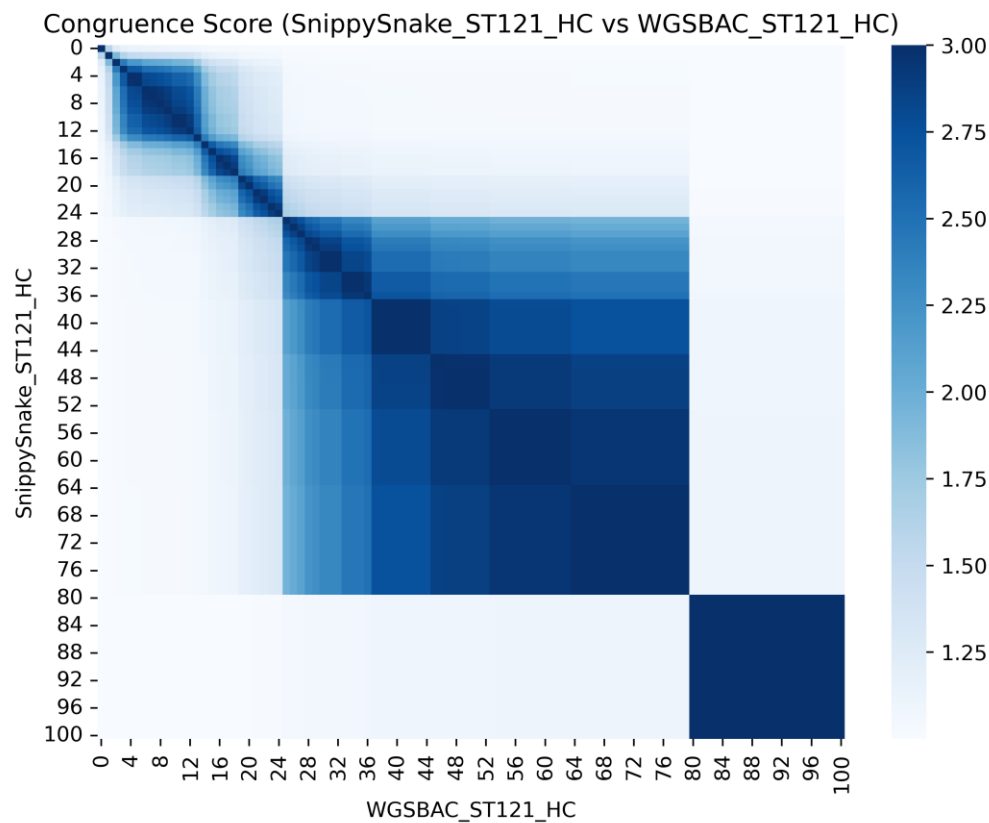


Figure S3.15.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100). Axis represent the different SNP distance thresholds.

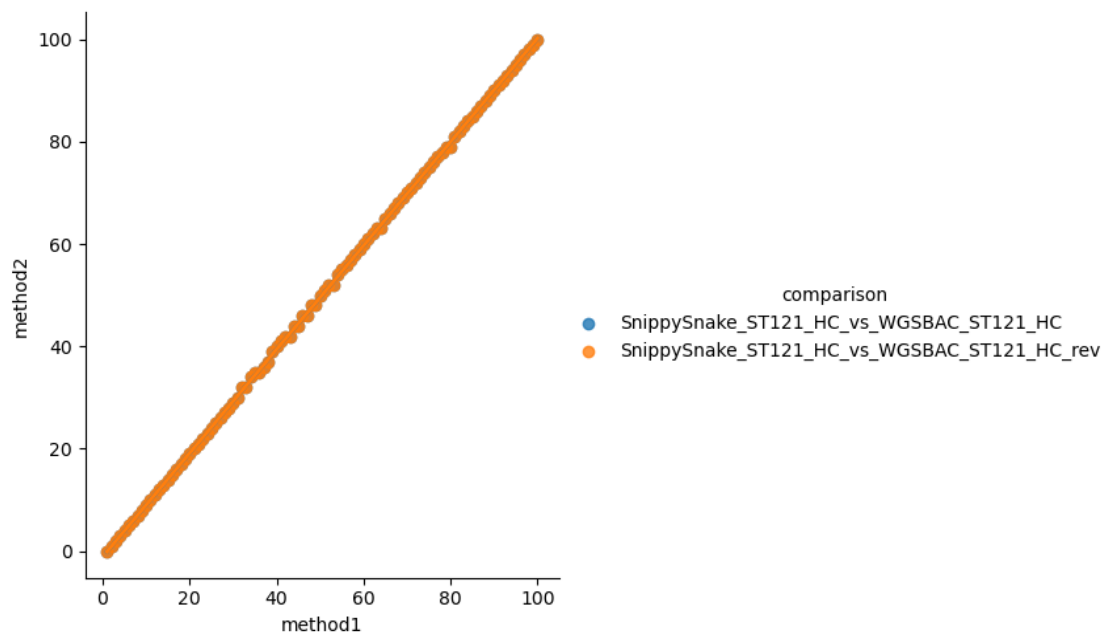


Figure S3.15.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$). A linear tendency line supported by 100 (blue) and 100 (orange) points is presented.

NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.

16. CSI Phylogeny core vs. CSI Phylogeny per ST

Table S3.16. Details on pipeline parameters, with indication of the pipeline version, the clustering method, and reference and the dataset used.

	CSI Phylogeny single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.4	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Reference	CP006046	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	ST1 + ST5 + ST6 + ST8 + ST121	ST1 / ST5 / ST6 / ST8 / ST121

Section 3 – Comparison of SNP-based pipelines

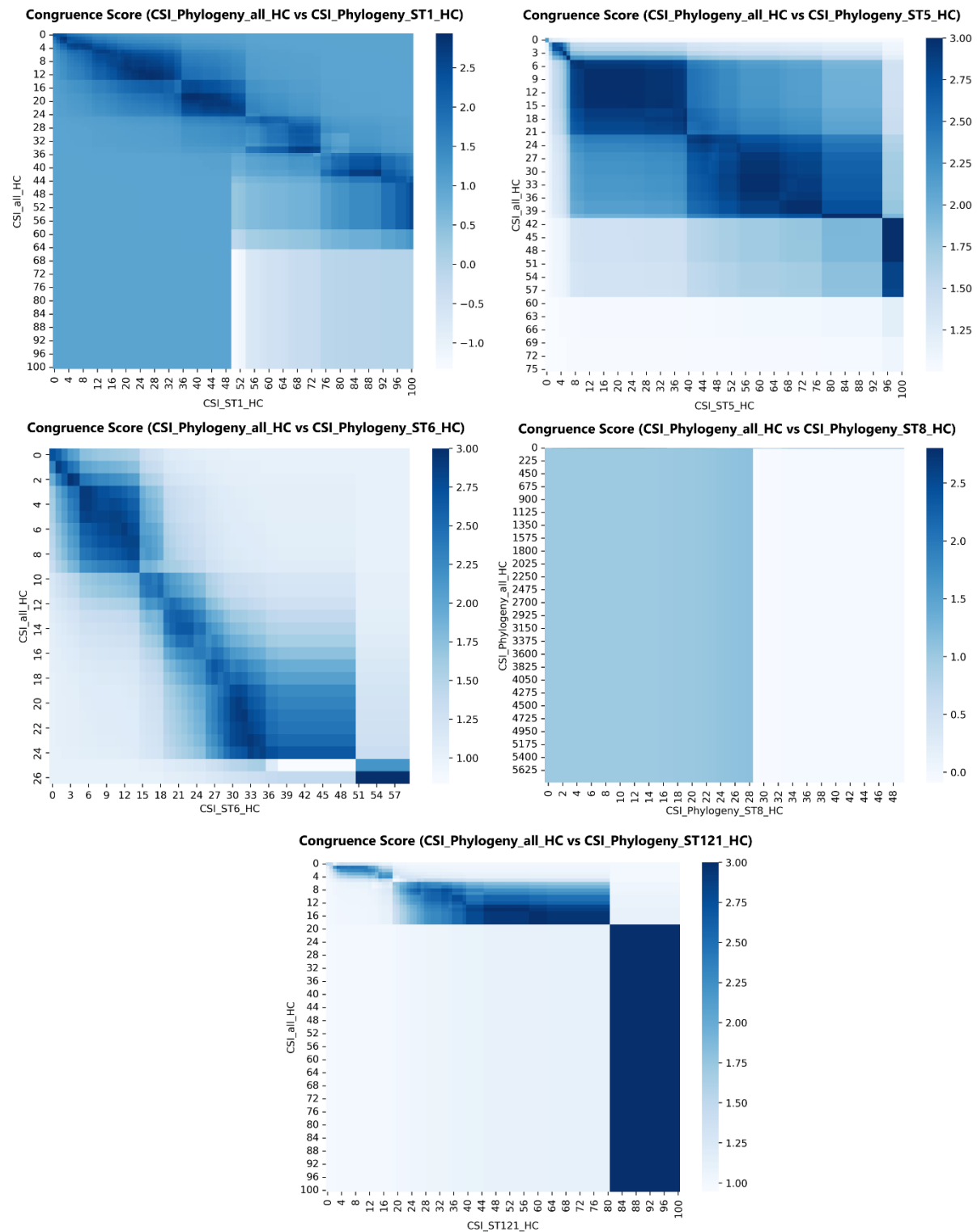


Figure S3.16.1. Heatmap with the congruence score obtained when comparing all the obtained partitions (up to threshold 100) of the CSI Phylogeny pipeline when a dataset per ST and a combined dataset are provided. Axis represent the different SNP distance thresholds.

Section 3 – Comparison of SNP-based pipelines

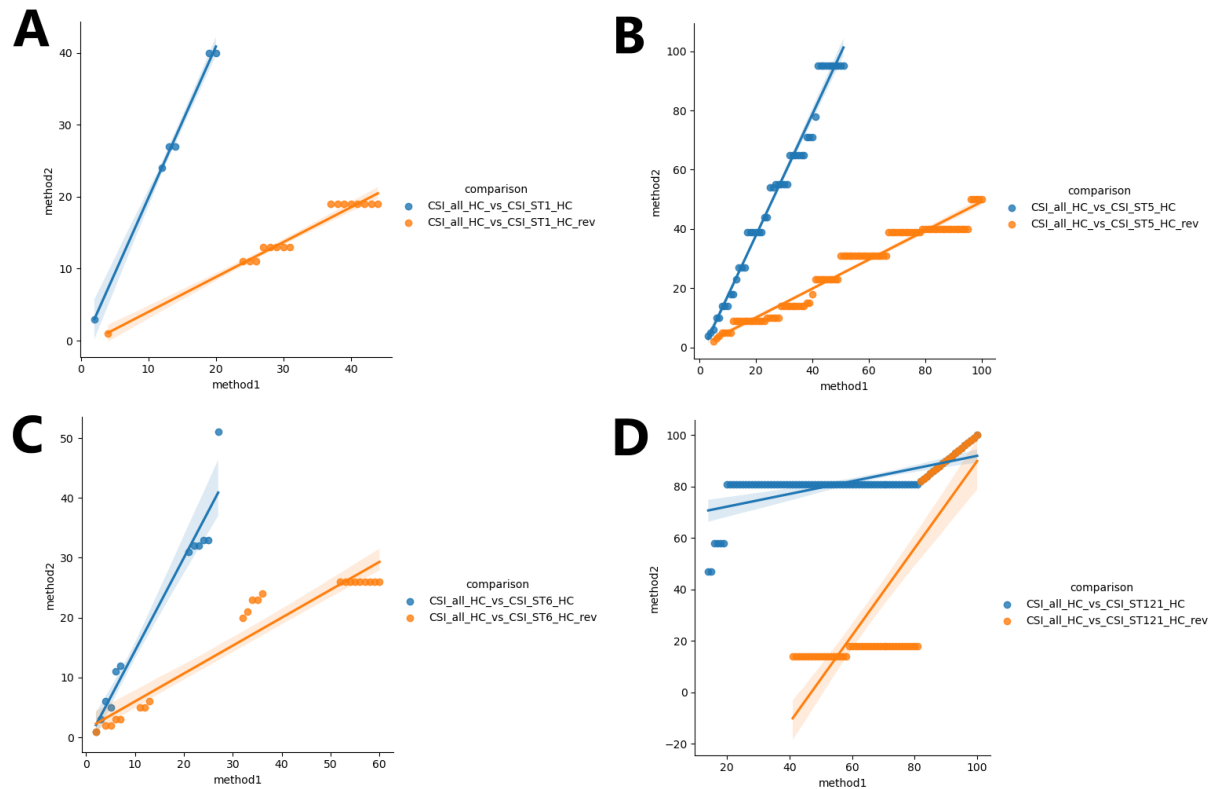


Figure S3.16.2. Corresponding points between CSI Phylogeny clustering when a dataset per ST and a combined dataset are provided ($CS \geq 2.85$) for all the obtained partitions (up to threshold 100). **A)** ST1, a linear tendency line supported by 6 (blue) and 17 (orange) points is presented; **B)** ST5, a linear tendency line supported by 49 (blue) and 96 (orange) points is presented; **C)** ST6, a linear tendency line supported by 12 (blue) and 22 (orange) points is presented; **D)** ST121, a linear tendency line supported by 87 (blue) and 60 (orange) points is presented. Note: For the ST8 dataset, a CS above 2.85 was not observed for any comparison.

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	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

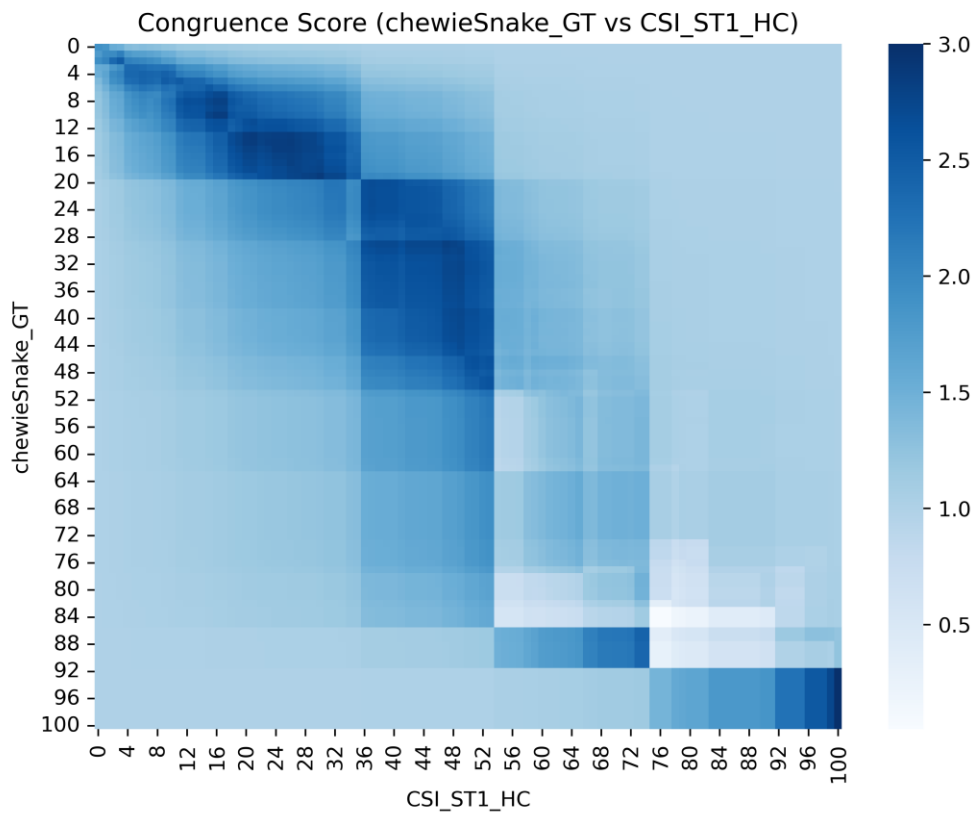


Figure S4.1.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

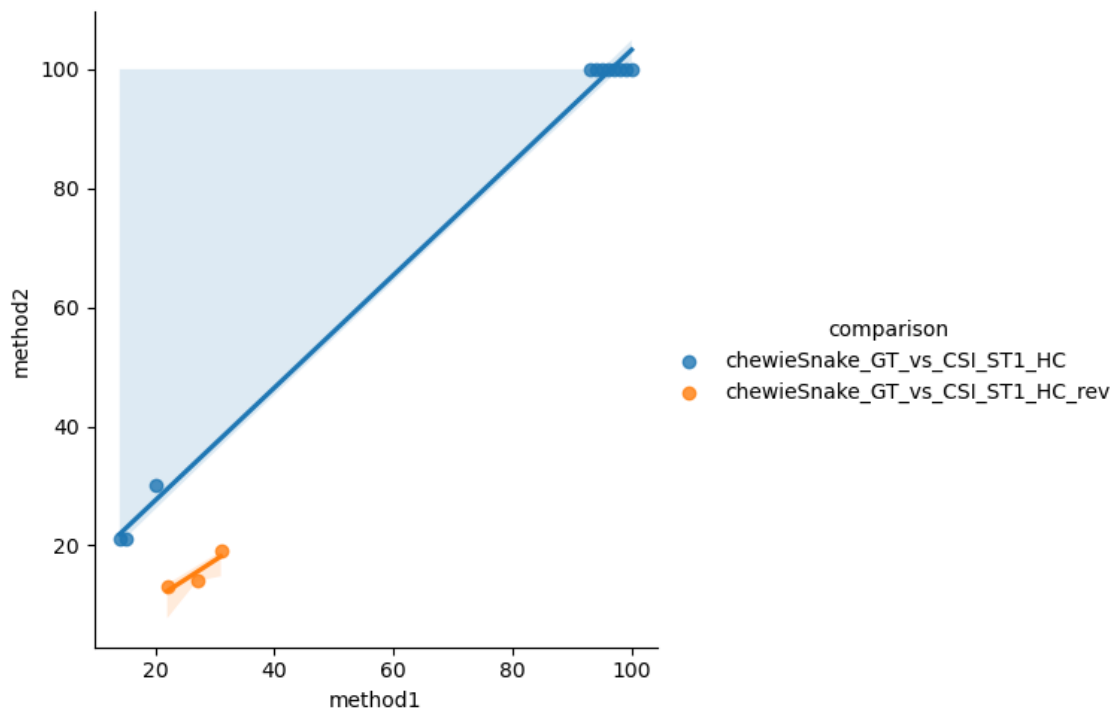


Figure S4.1.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 11 (blue) and 3 (orange) points is presented.

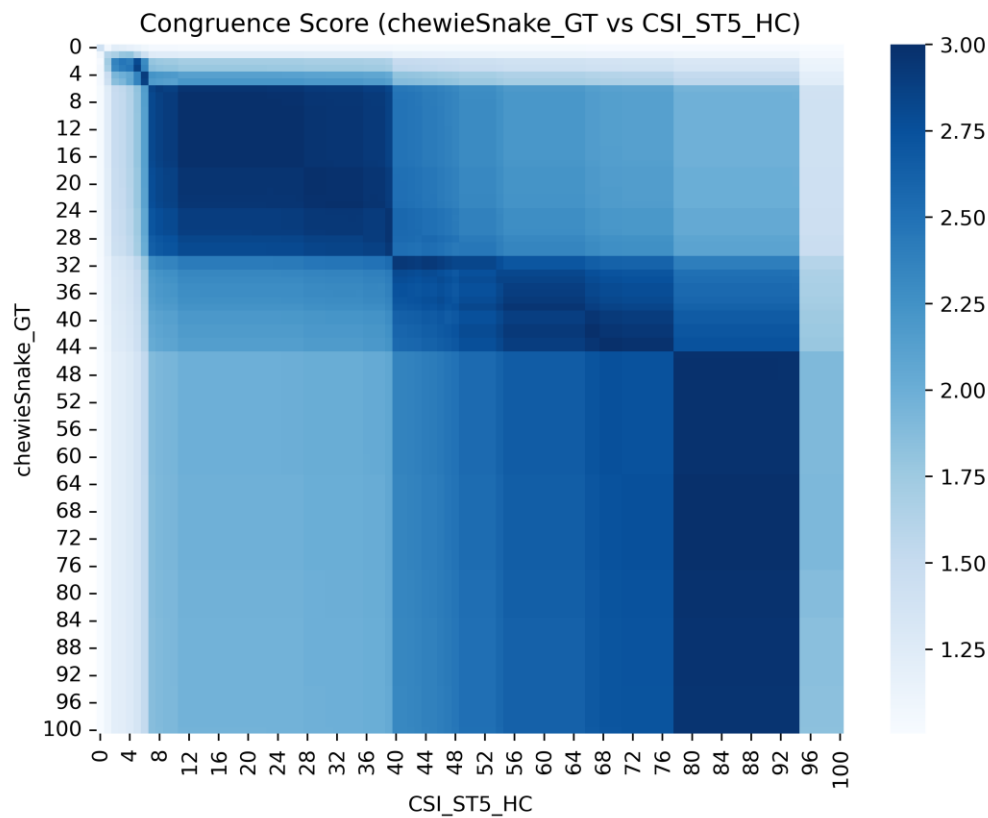


Figure S4.1.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

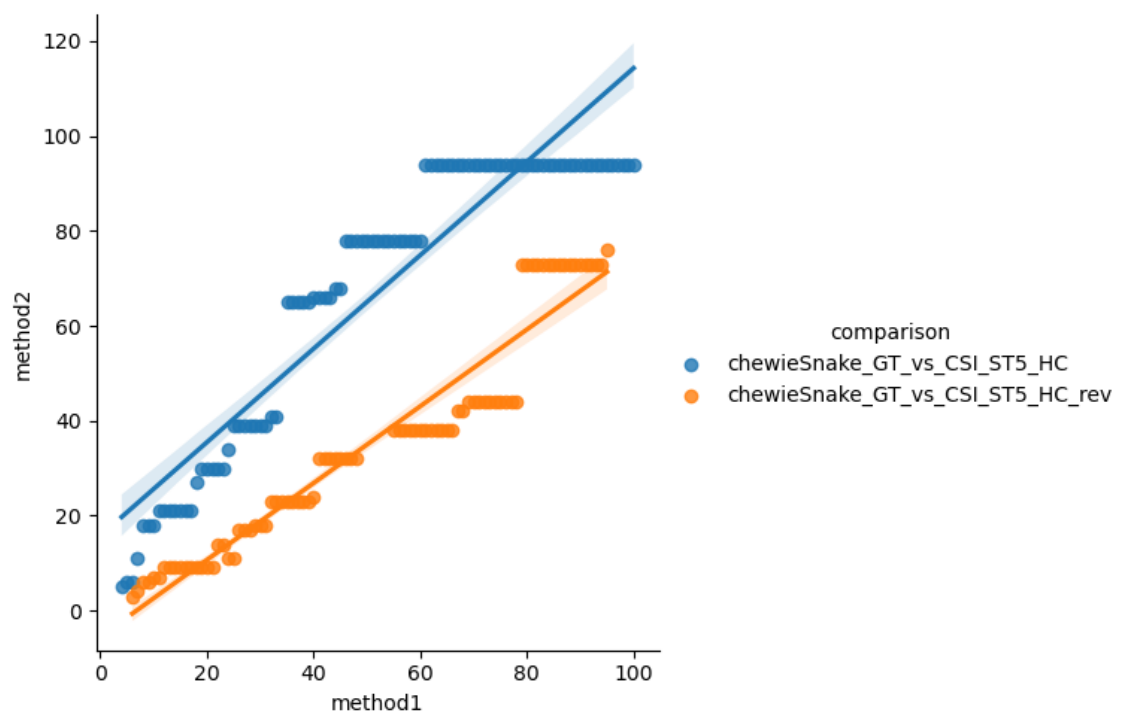


Figure S4.1.6. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 96 (blue) and 84 (orange) points is presented.

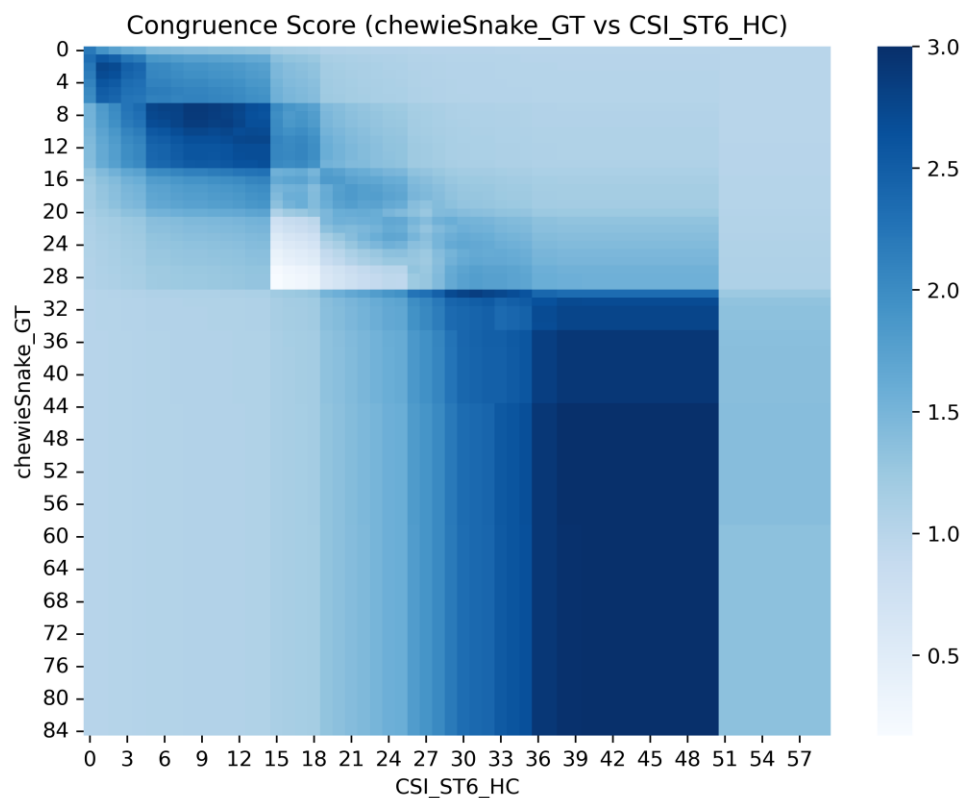


Figure S4.1.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

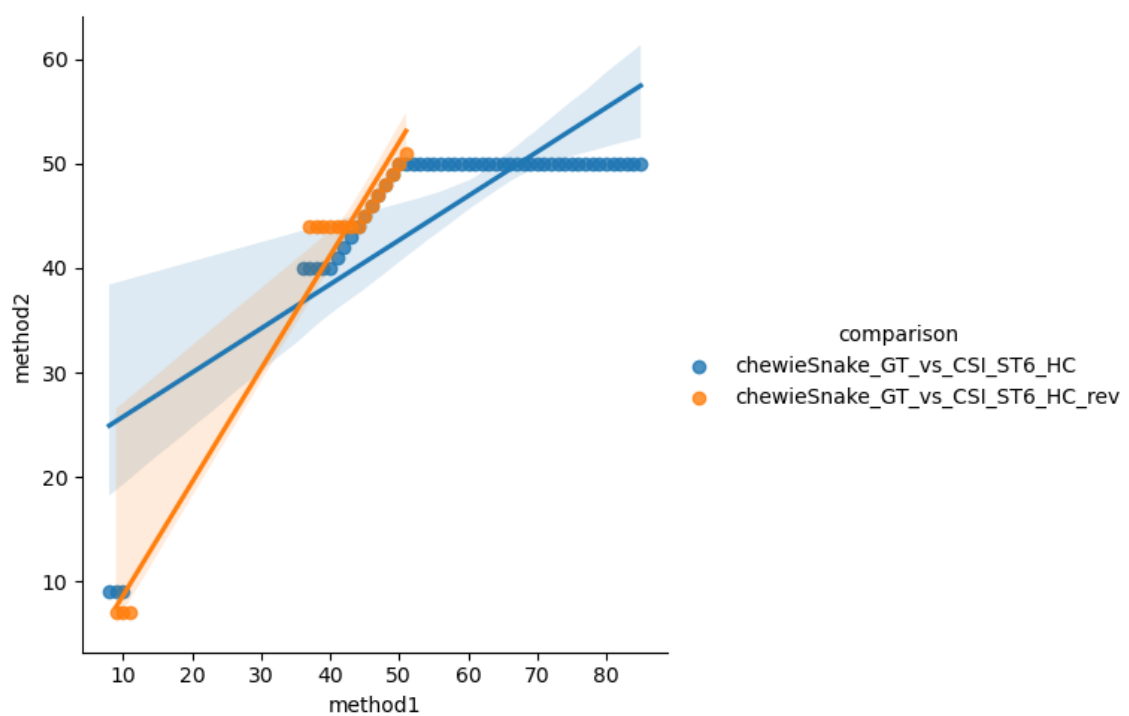


Figure S4.1.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 53 (blue) and 18 (orange) points is presented.

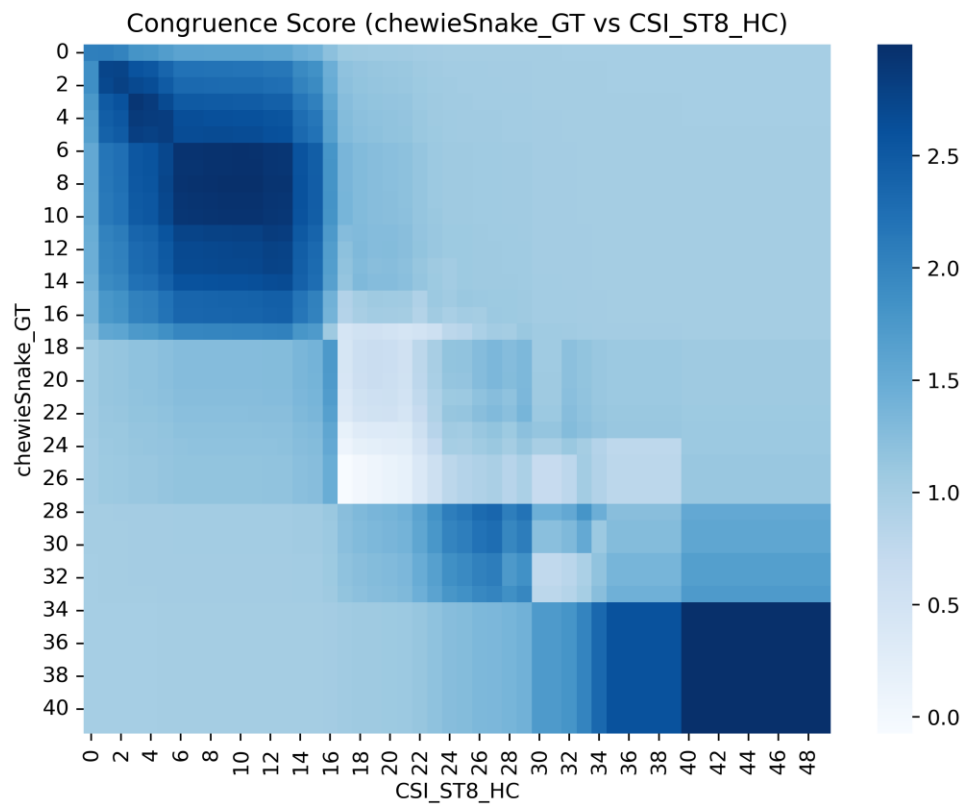


Figure S4.1.9. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

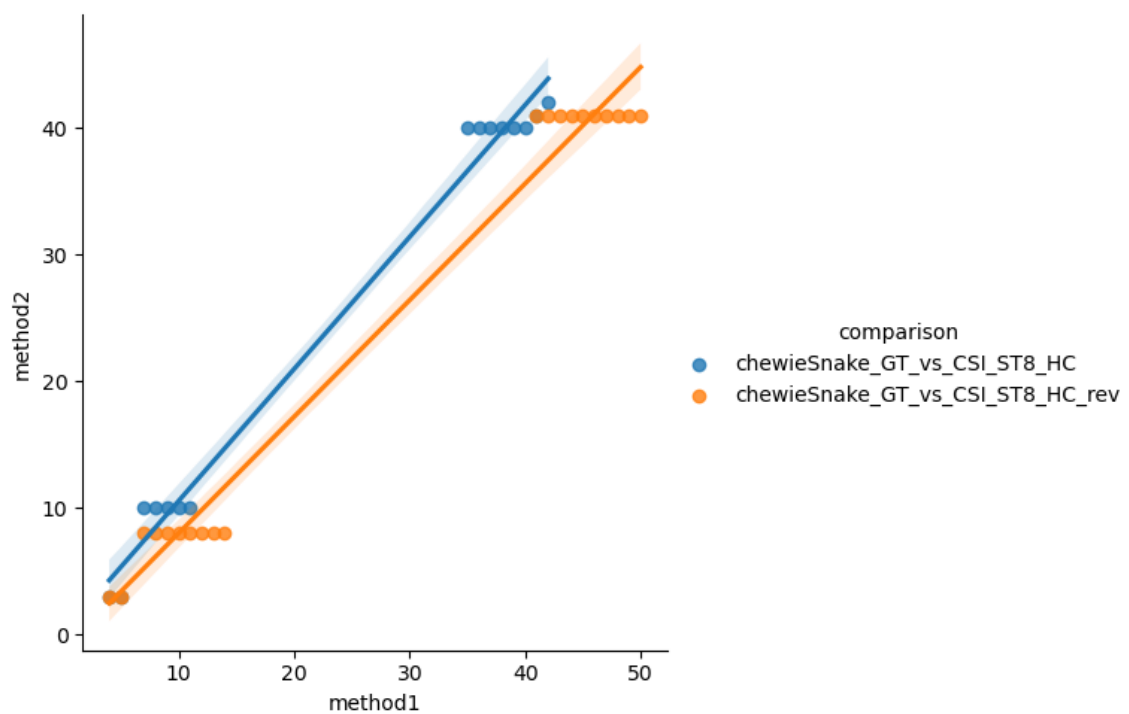


Figure S4.1.10. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 15 (blue) and 20 (orange) points is presented.

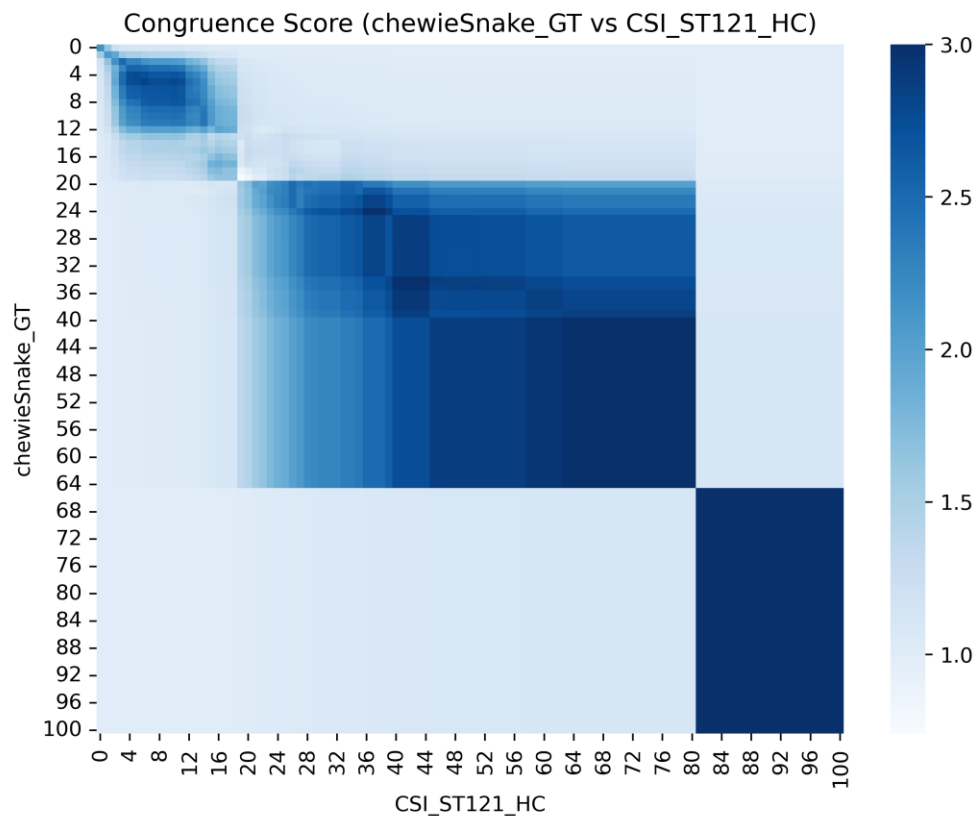


Figure S4.1.11. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

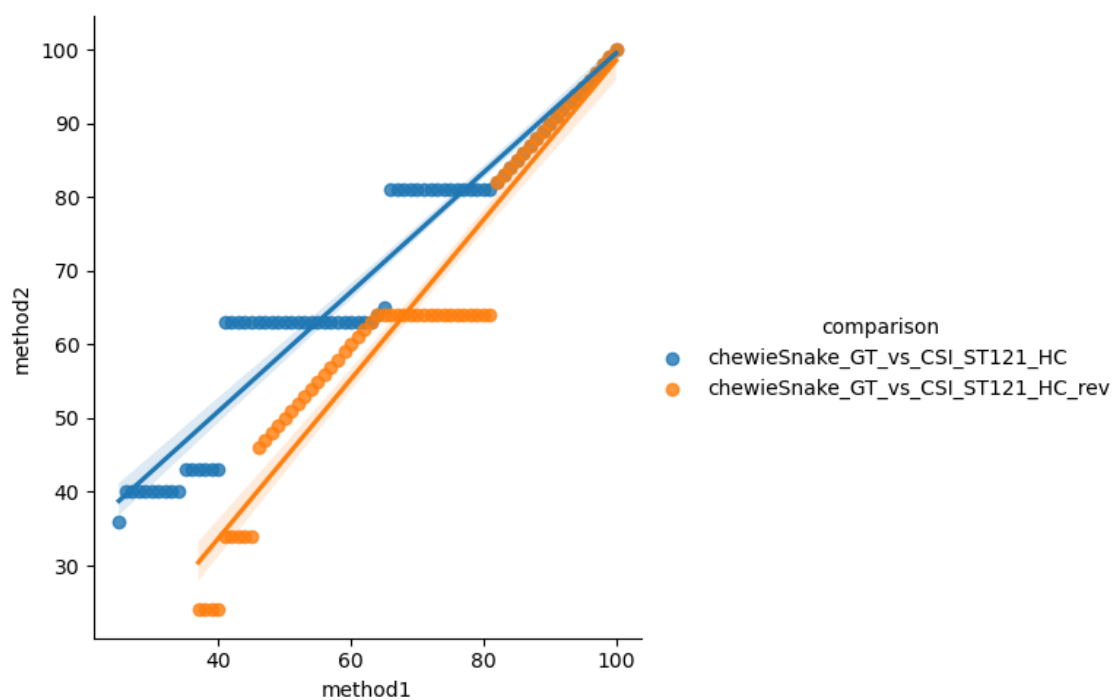


Figure S4.1.12. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 76 (blue) and 64 (orange) points is presented.

NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.

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	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

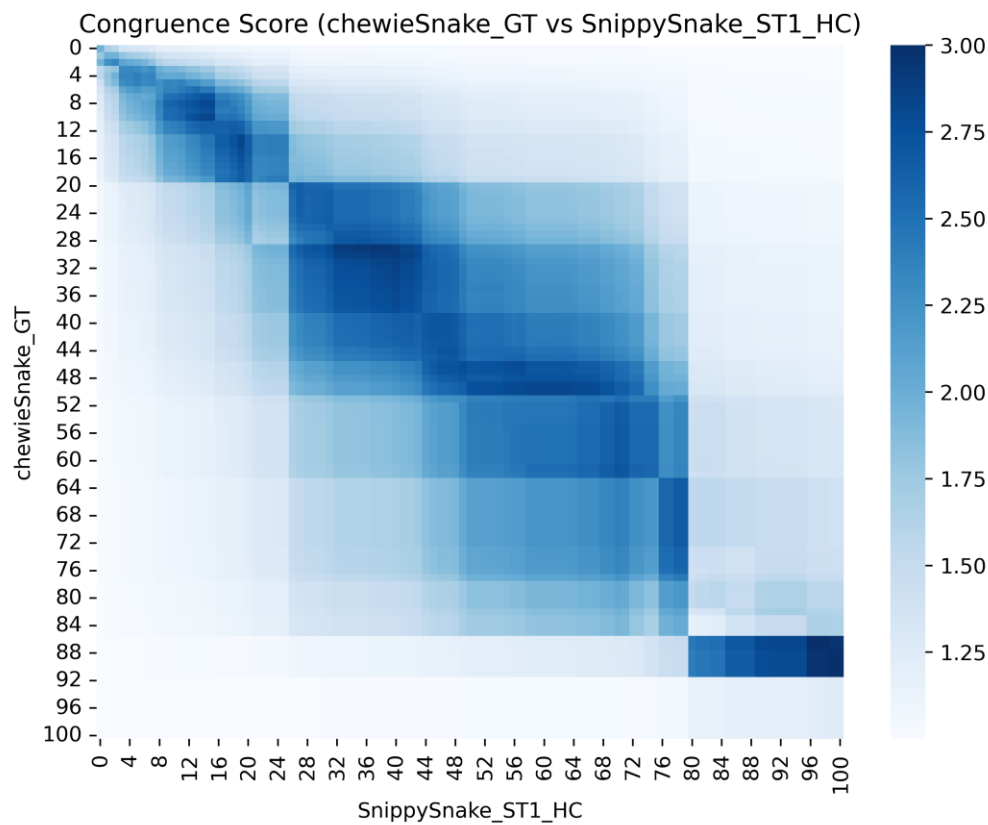


Figure S4.2.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

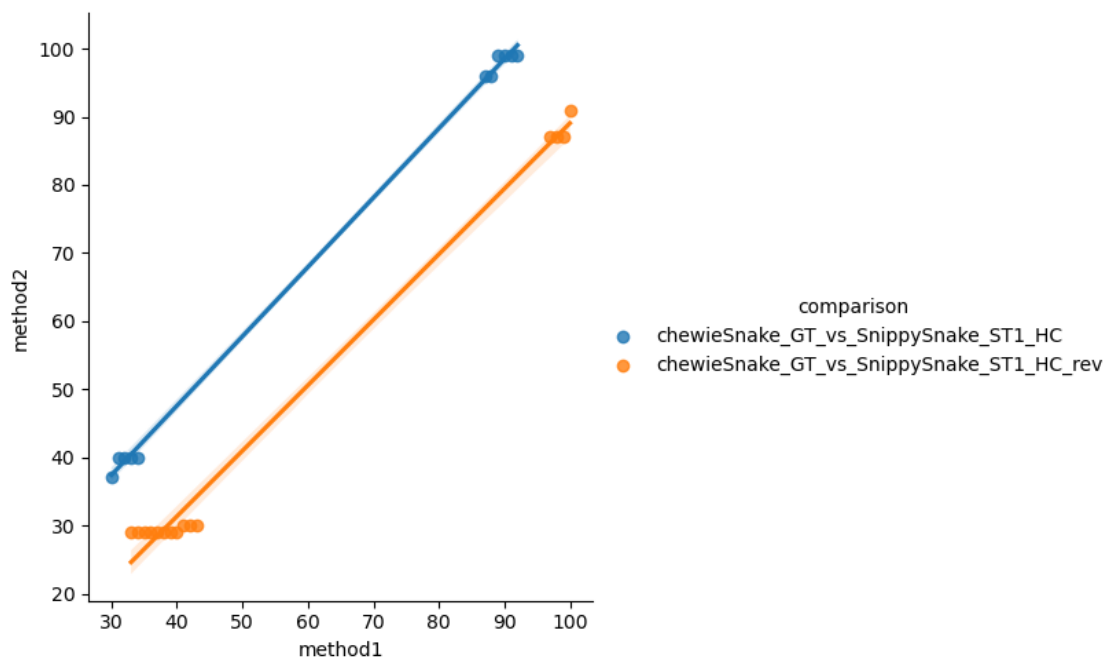


Figure S4.2.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST1. A linear tendency line supported by 11 (blue) and 15 (orange) points is presented.

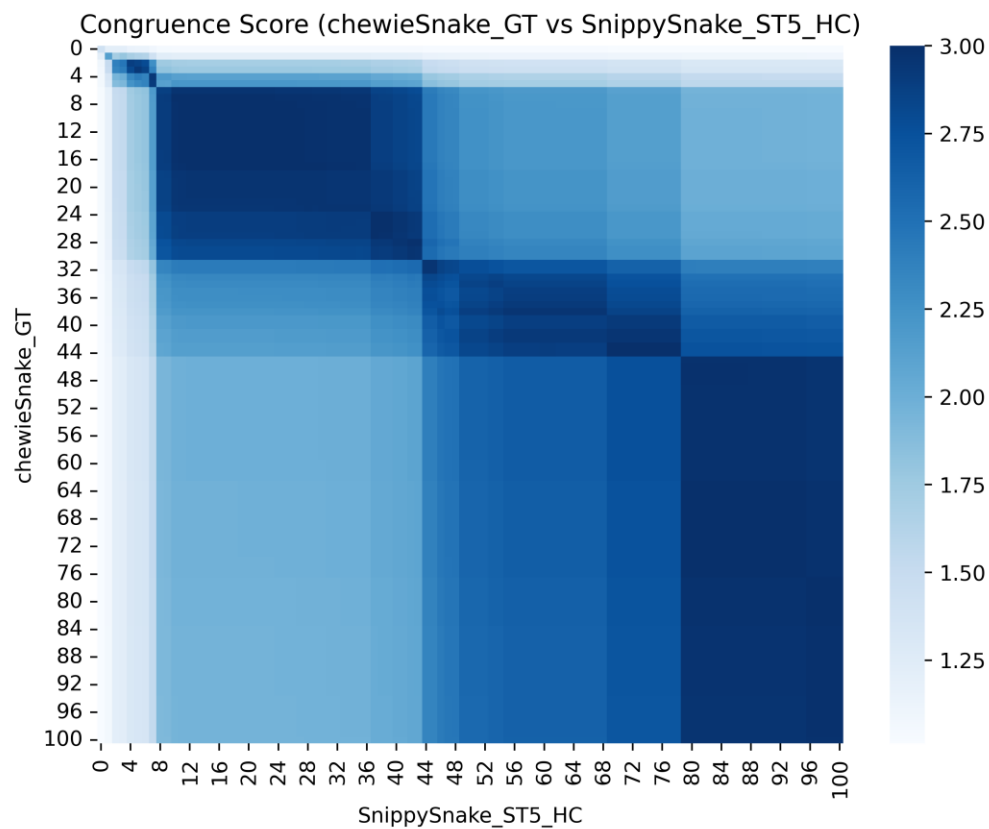


Figure S4.2.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

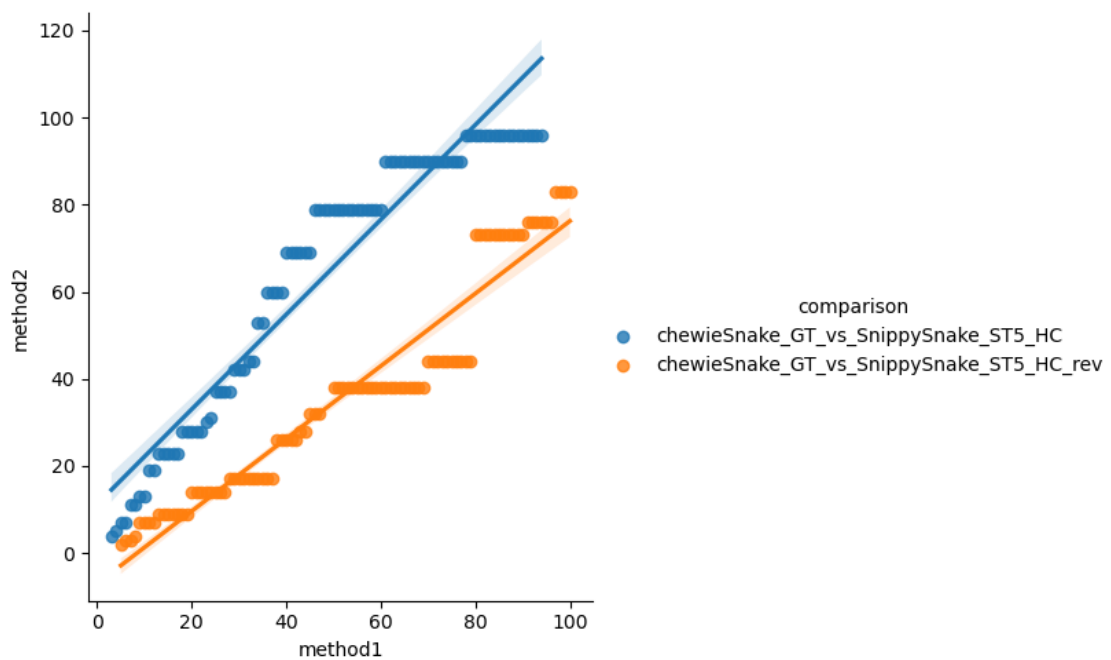


Figure S4.2.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 92 (blue) and 94 (orange) points is presented.

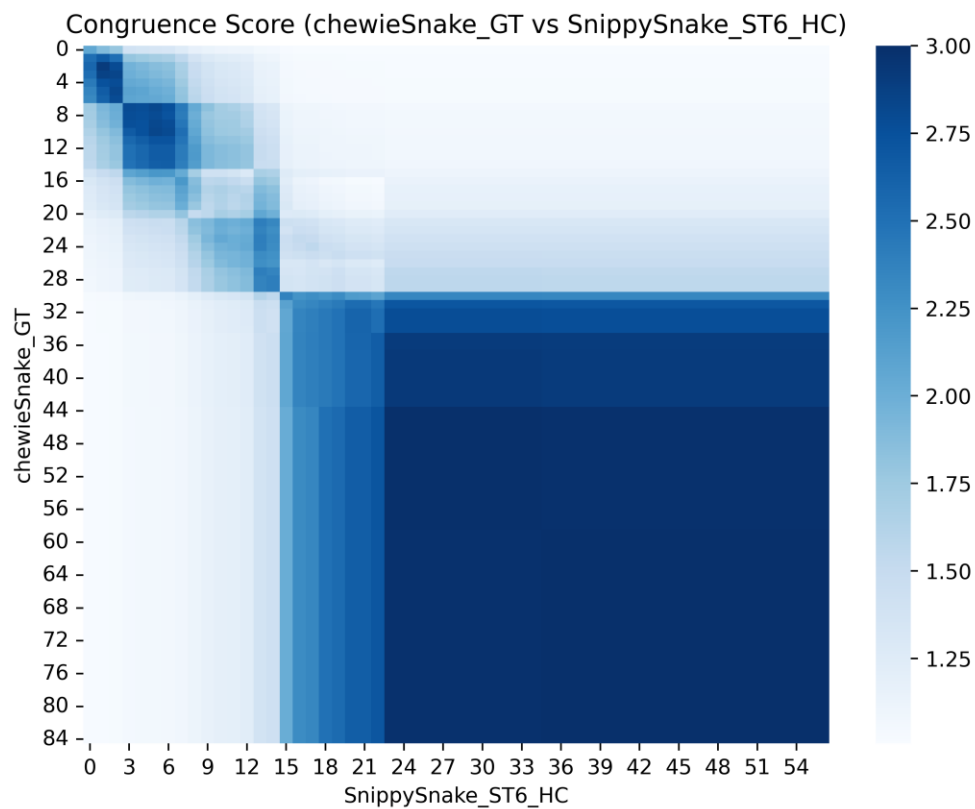


Figure S4.2.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

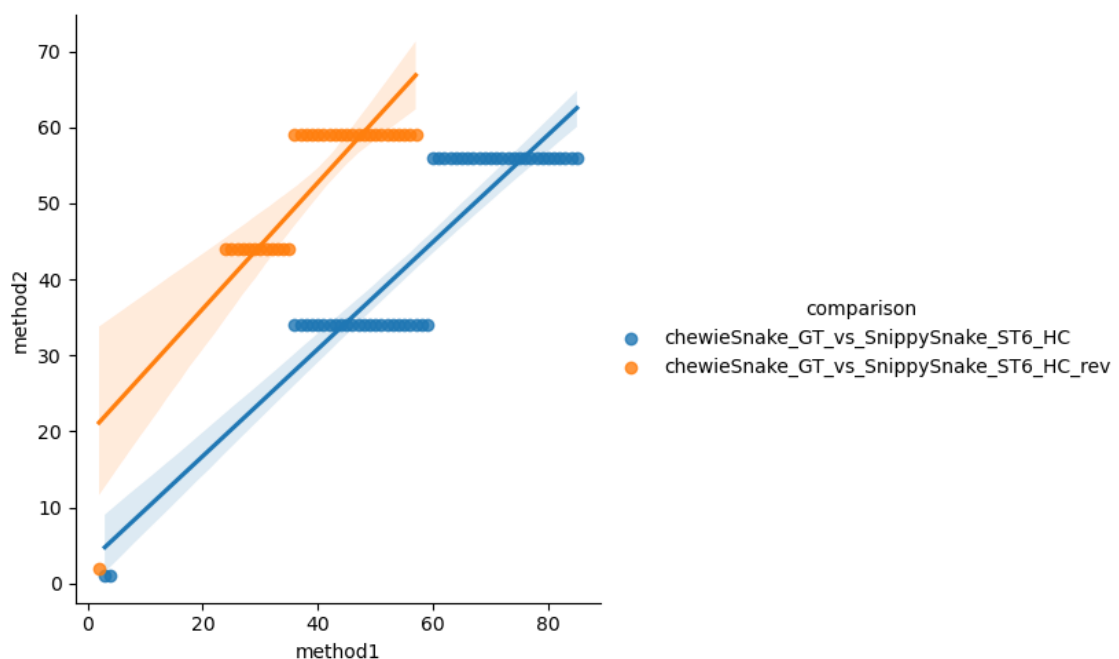


Figure S4.2.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 52 (blue) and 35 (orange) points is presented.

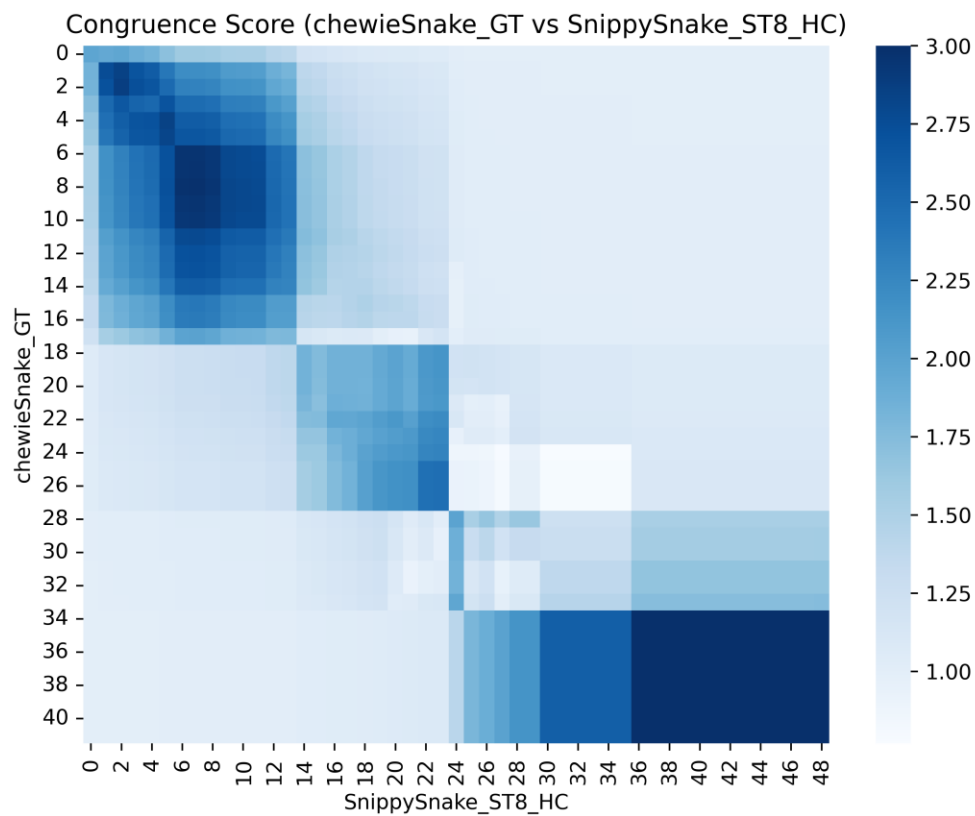


Figure S4.2.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

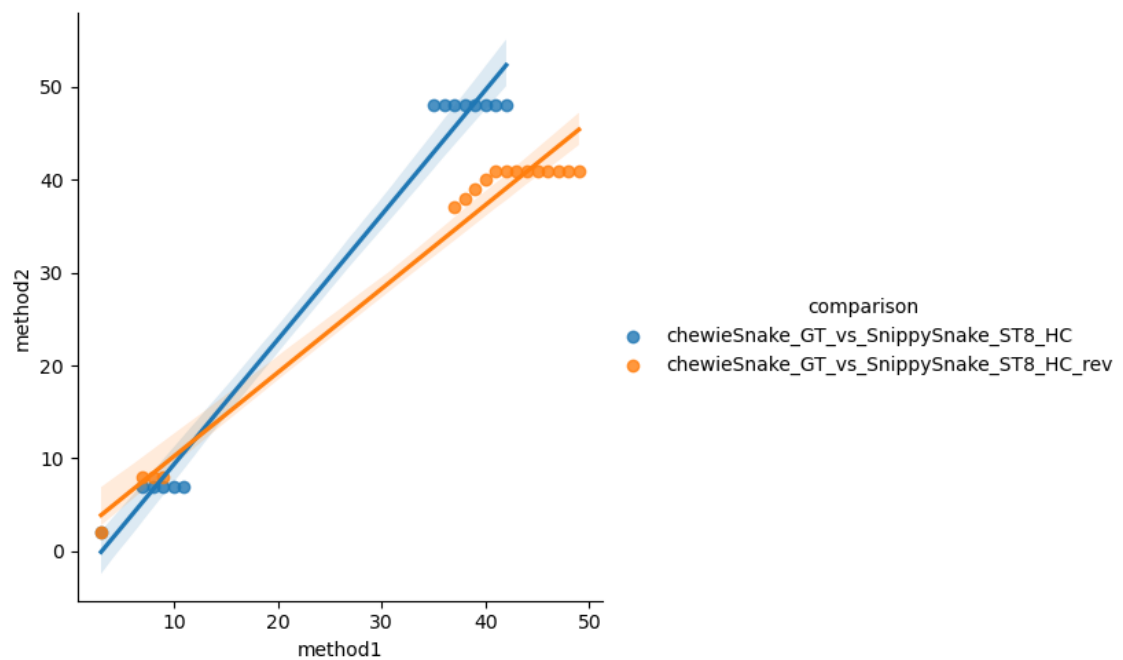


Figure S4.2.8. Corresponding points between the two pipelines in both directions (CS ≥ 2.85) of all partitions for ST8. A linear tendency line supported by 14 (blue) and 17 (orange) points is presented.

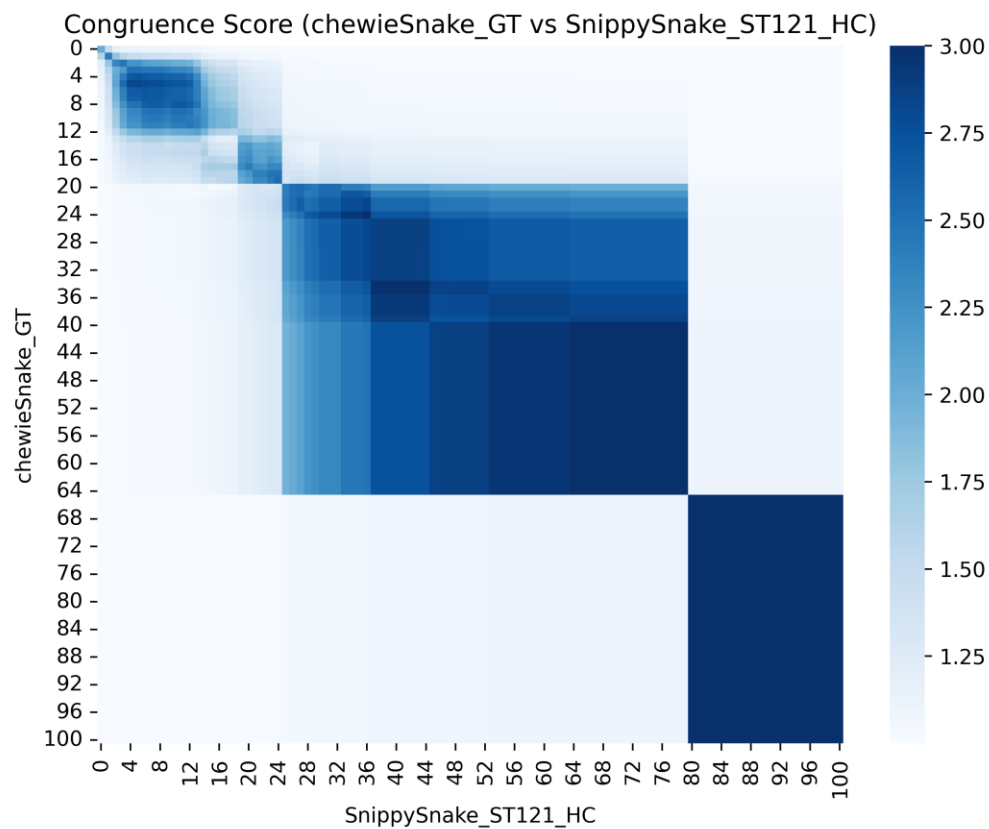


Figure S4.2.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

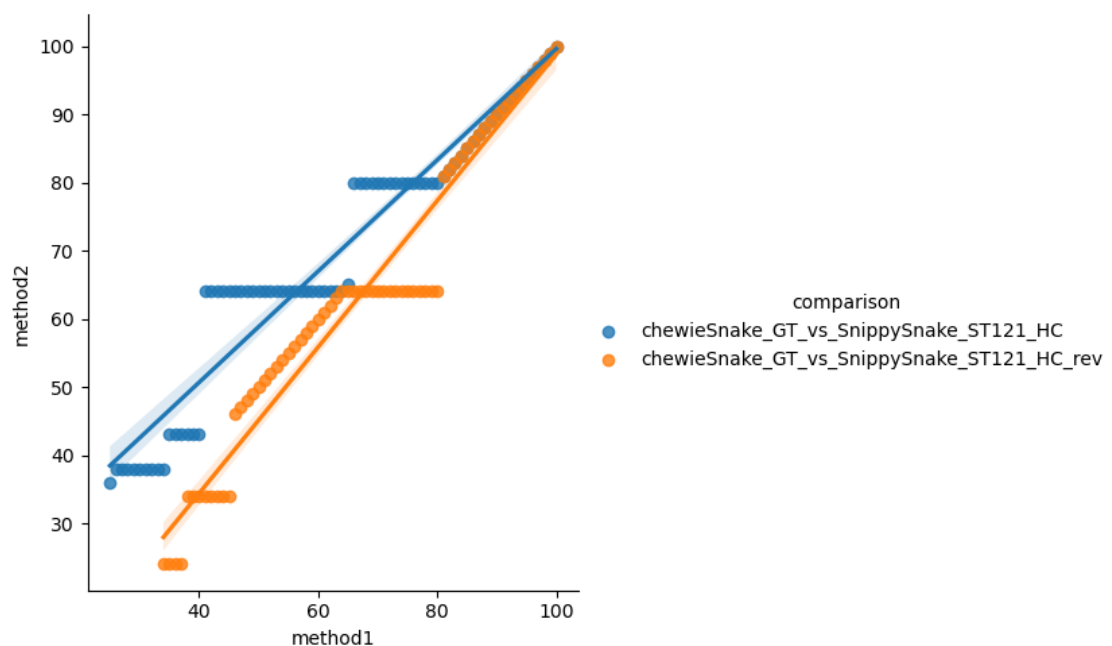


Figure S4.2.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 76 (blue) and 67 (orange) points is presented.

NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.

3. chewieSnake GrapeTree vs. WGSBAC 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 GrapeTree	WGSBAC single-linkage
Pipeline version	v3.1.1	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

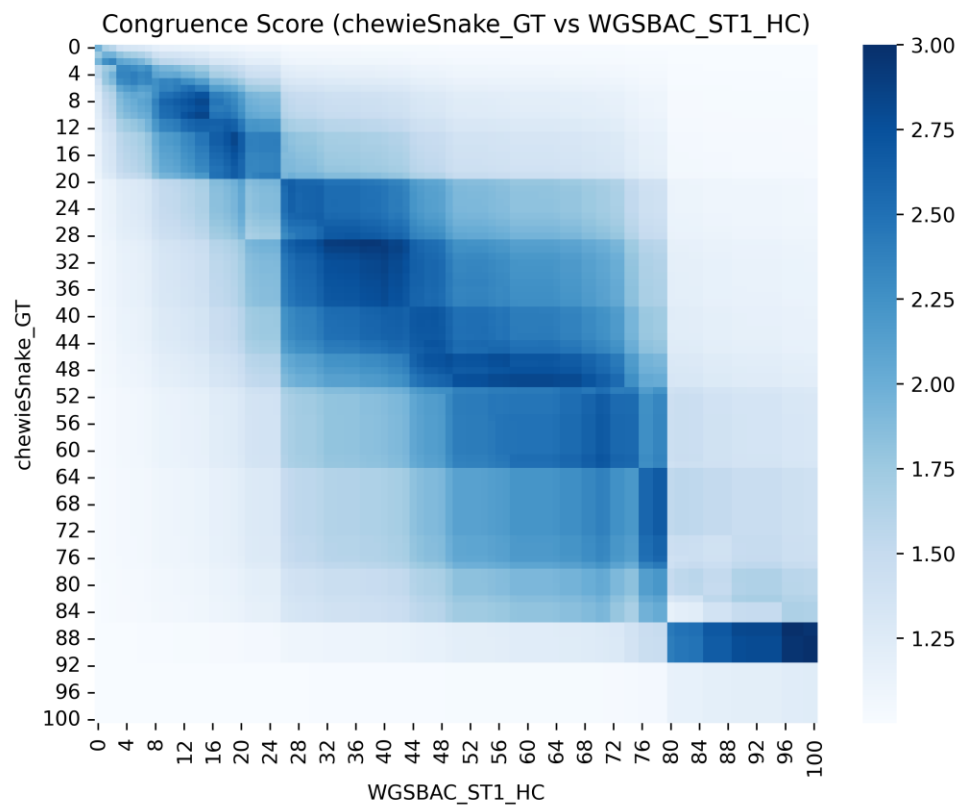


Figure S4.3.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

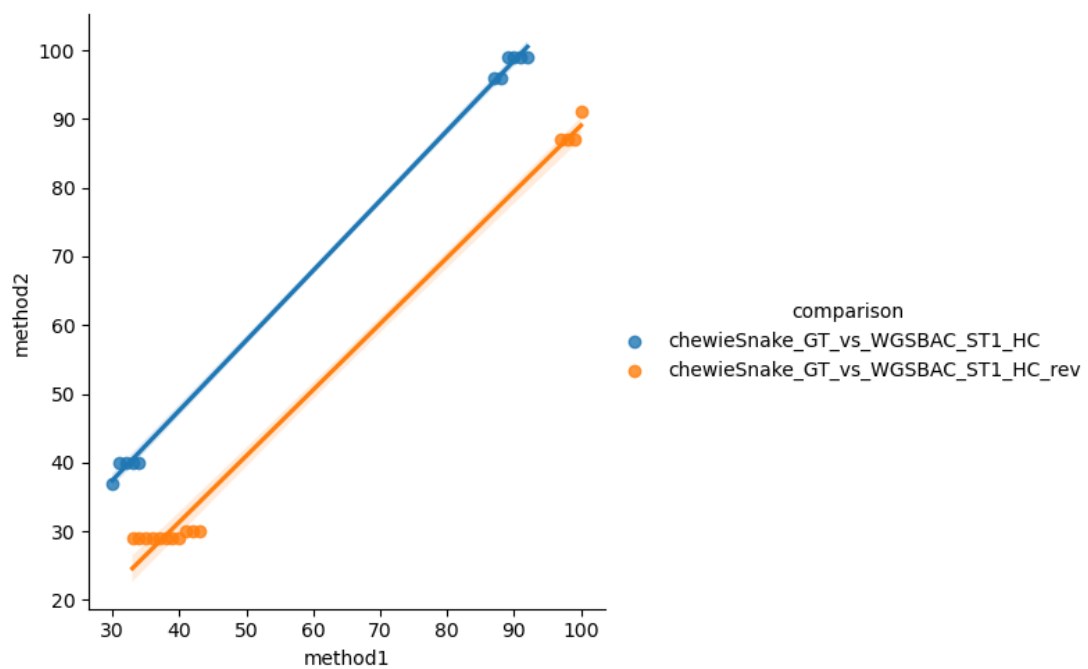


Figure S4.3.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST1. A linear tendency line supported by 11 (blue) and 15 (orange) points is presented.

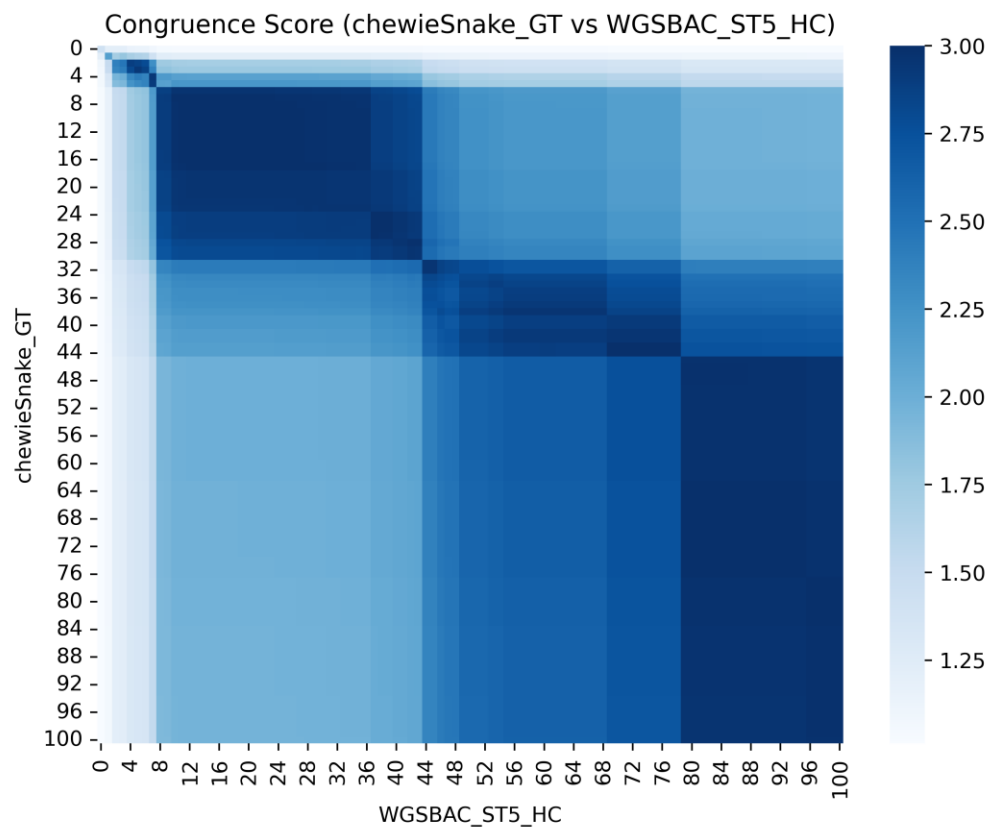


Figure S4.3.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

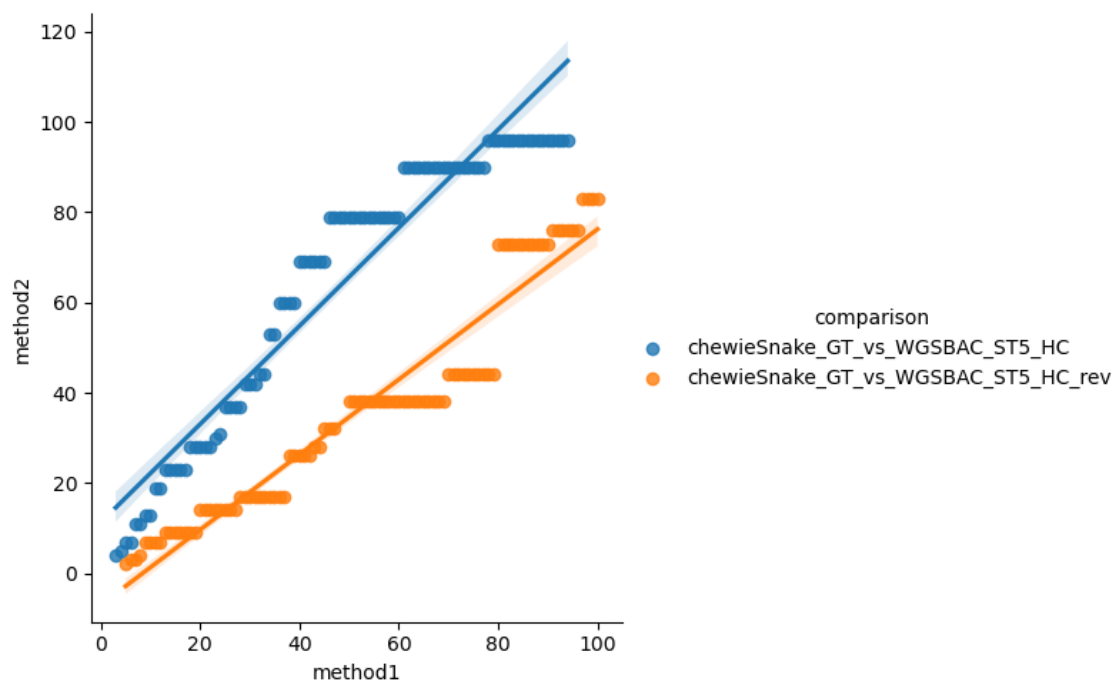


Figure S4.3.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 92 (blue) and 94 (orange) points is presented.

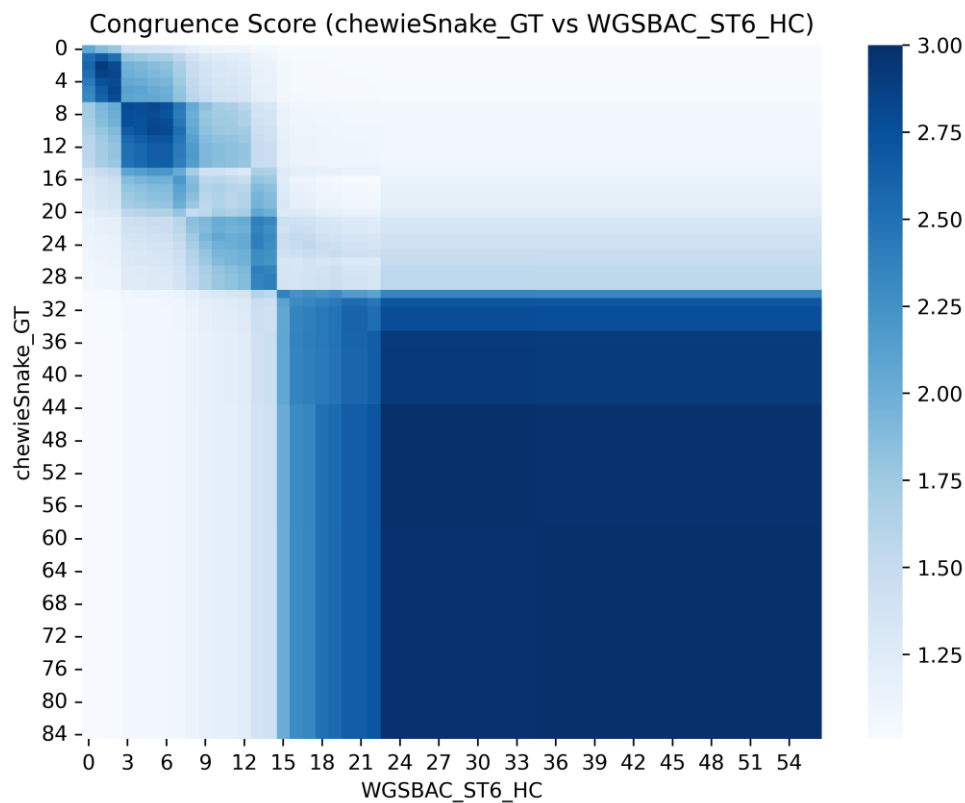


Figure S4.3.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

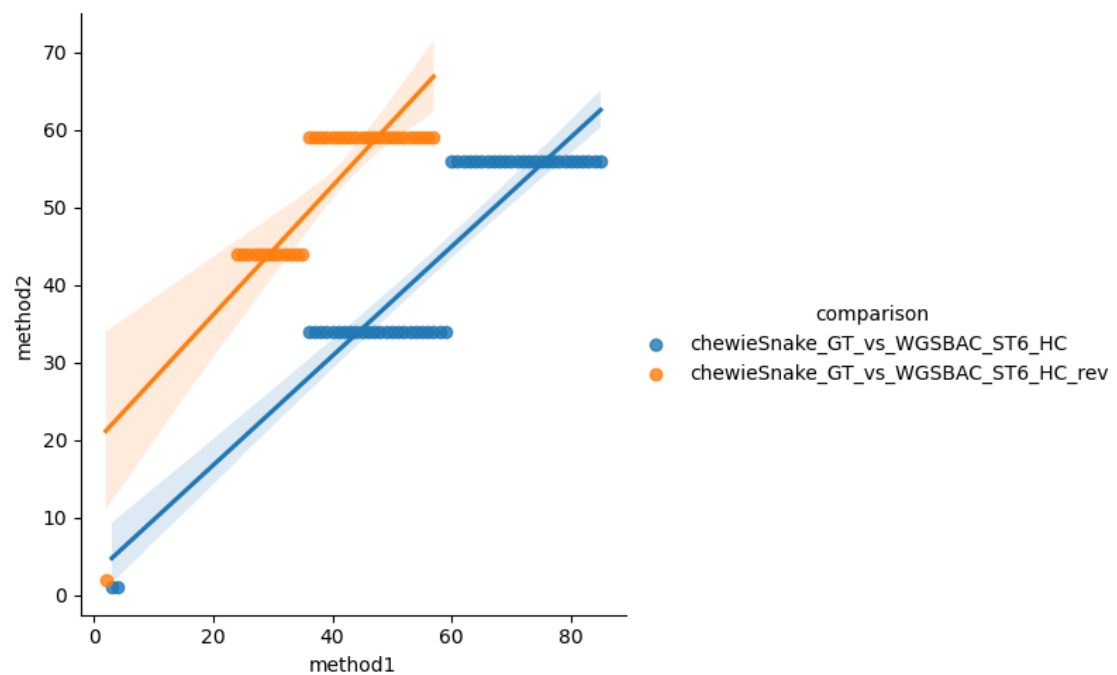


Figure S4.3.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 52 (blue) and 35 (orange) points is presented.

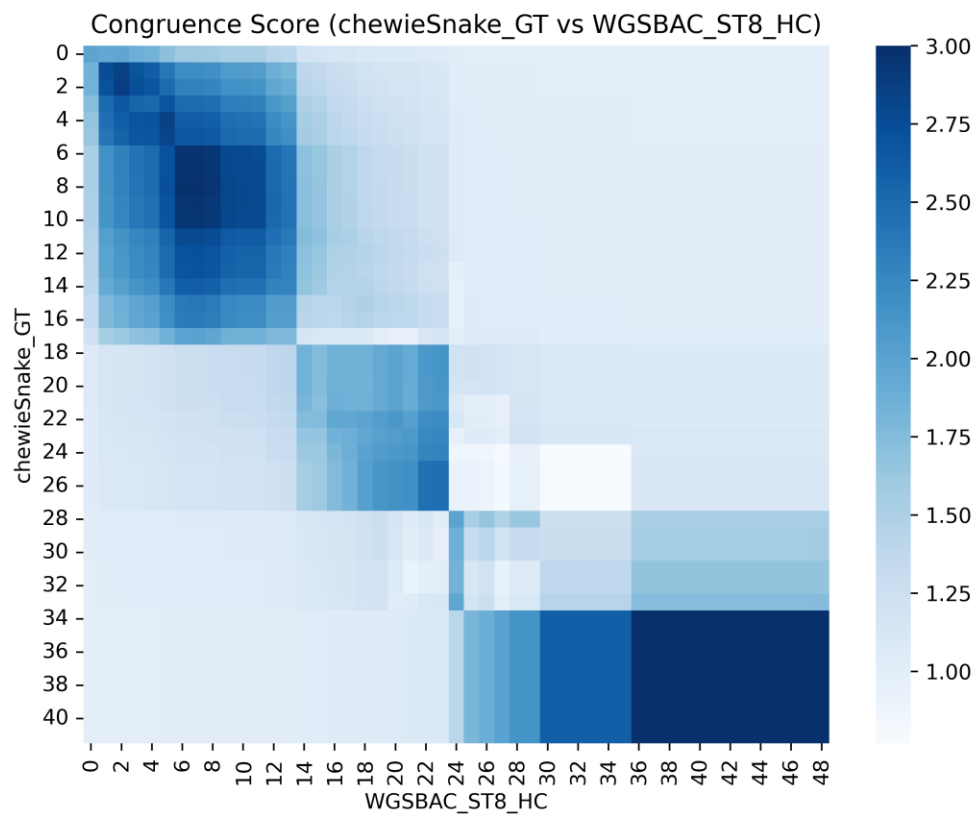


Figure S4.3.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

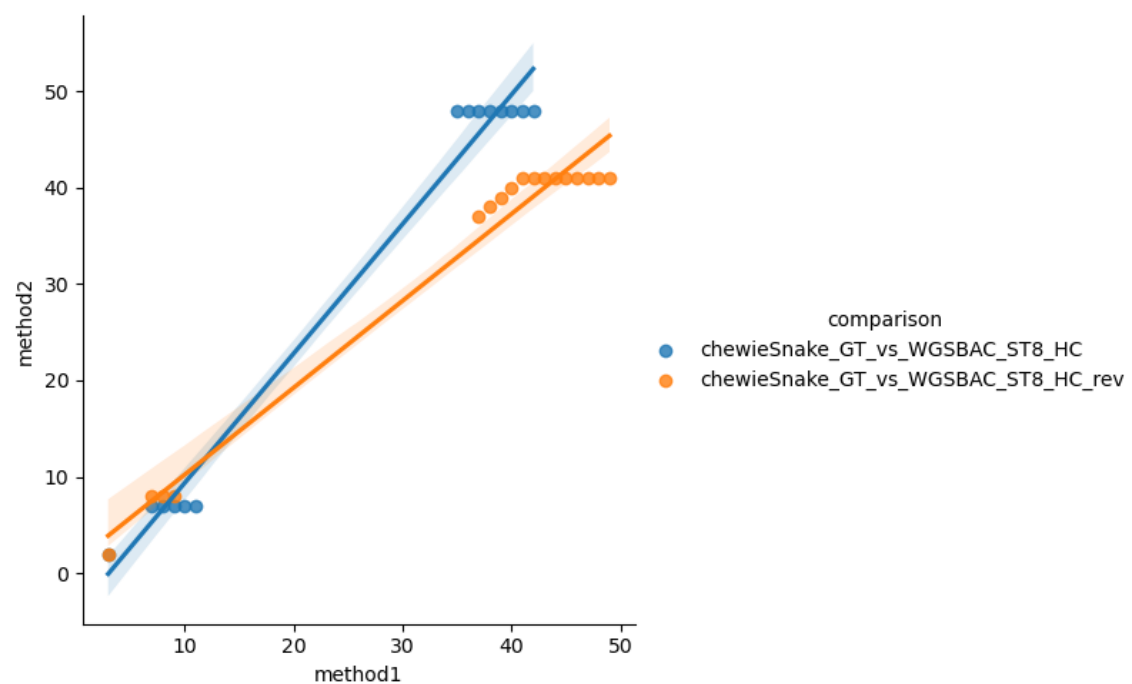


Figure S4.3.8. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85) of all partitions for ST8. A linear tendency line supported by 14 (blue) and 17 (orange) points is presented.

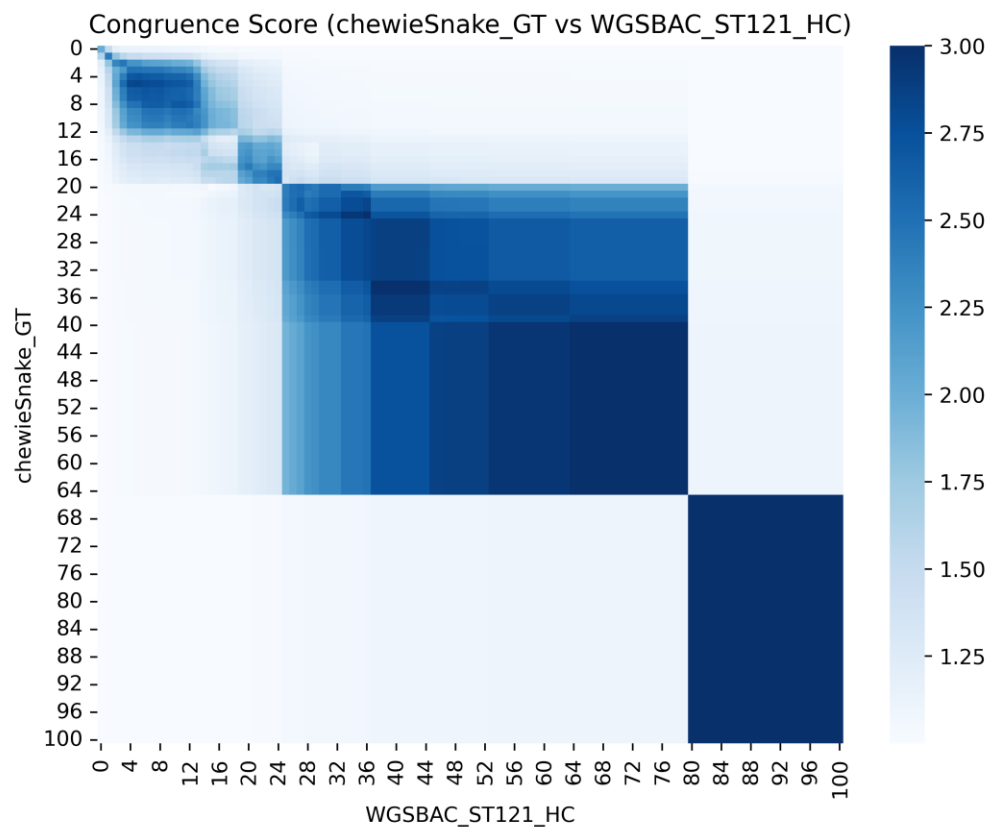


Figure S4.3.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

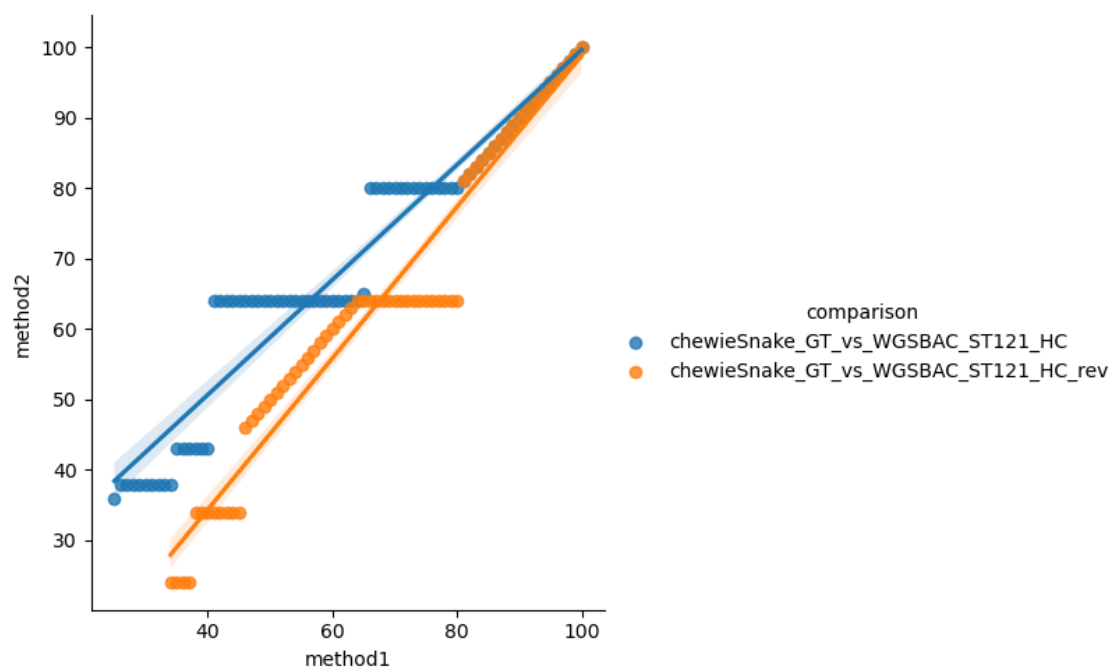


Figure S4.3.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST121. A linear tendency line supported by 76 (blue) and 67 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

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

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

	chewieSnake single-linkage	CSI Phylogeny single-linkage
Pipeline version	v3.1.1	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

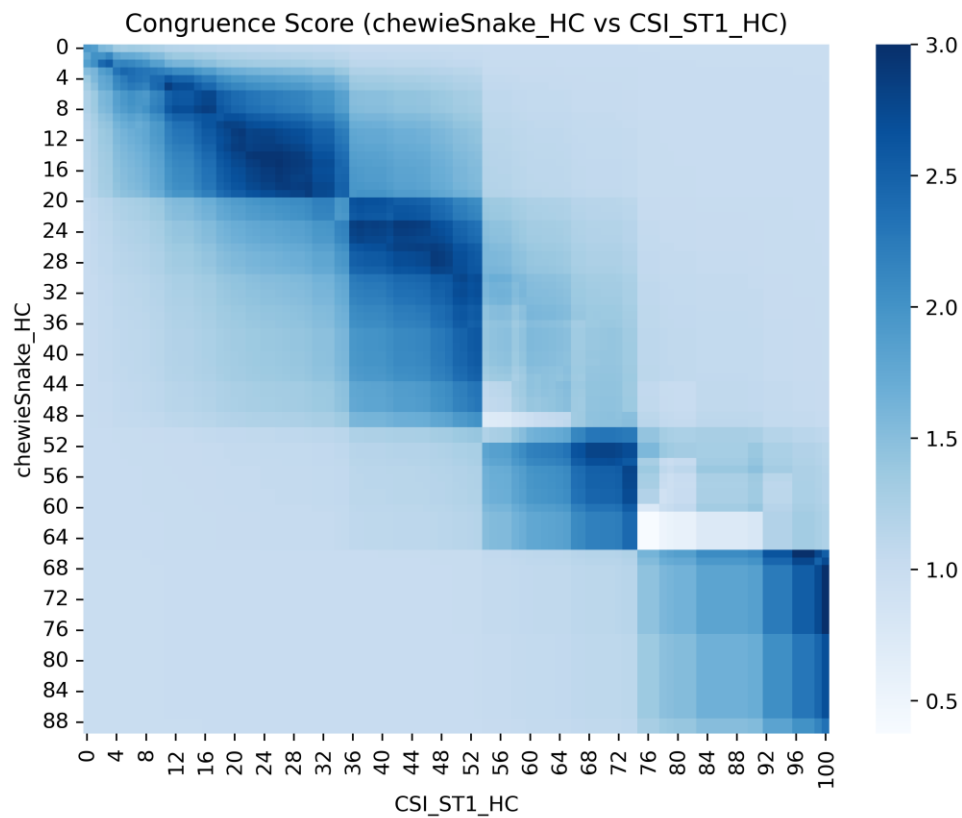


Figure S4.4.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

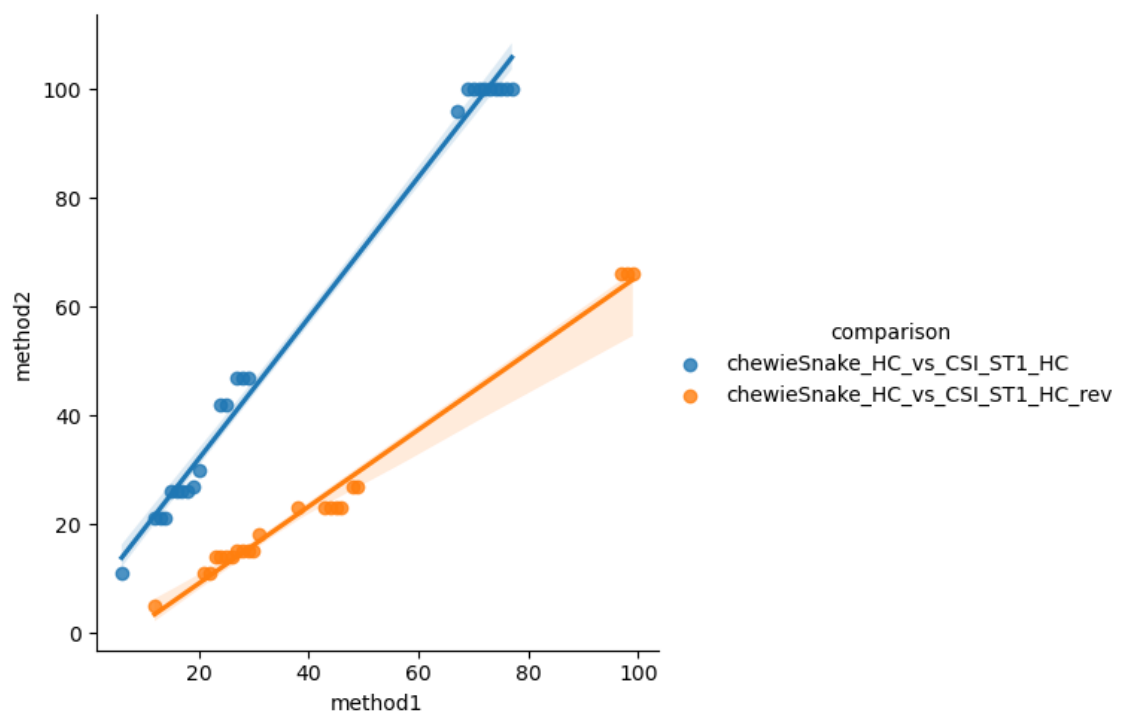


Figure S4.4.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 25 (blue) and 22 (orange) points is presented.

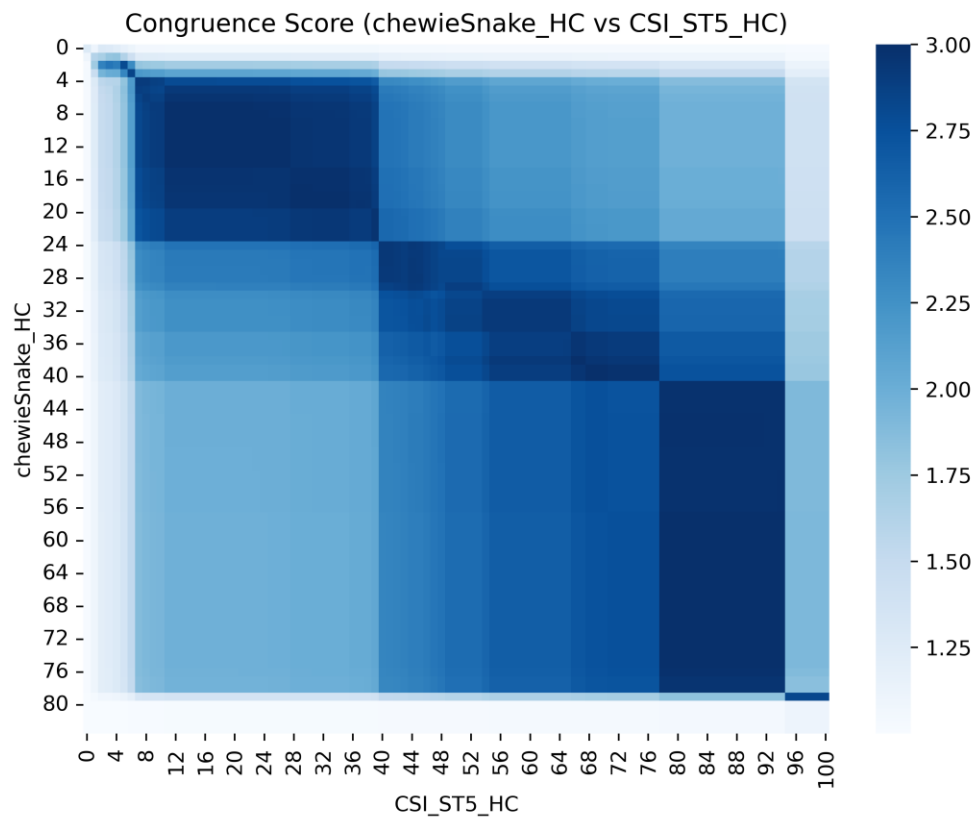


Figure S4.4.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

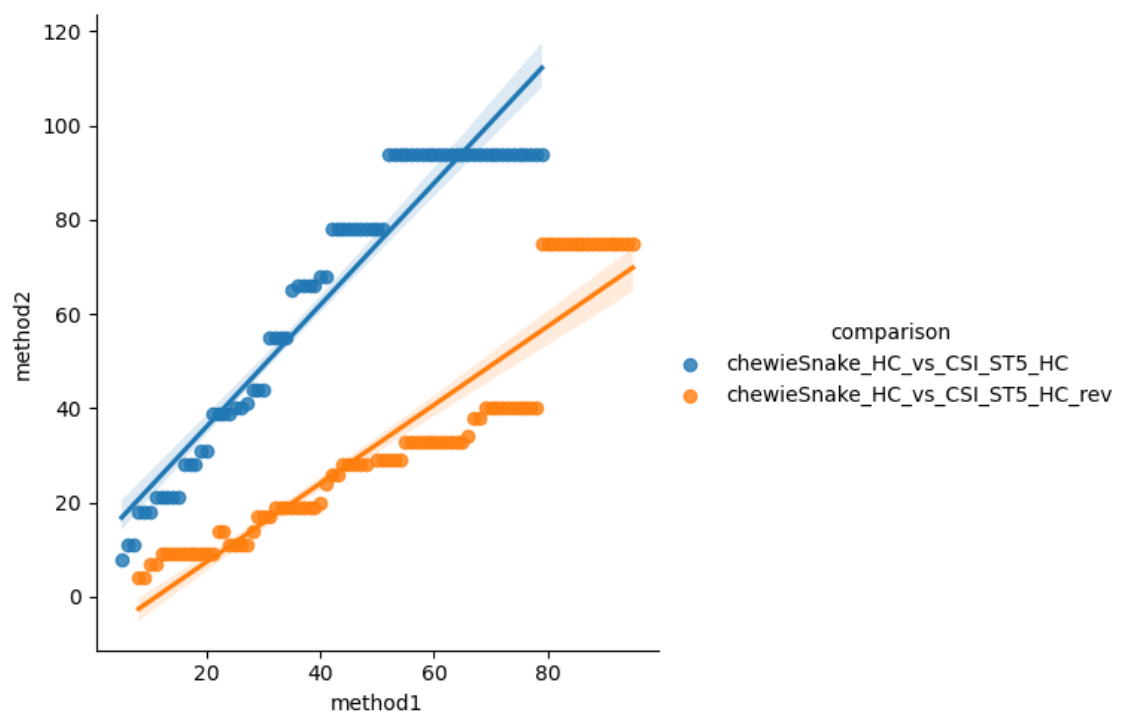


Figure S4.4.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 75 (blue) and 87 (orange) points is presented.

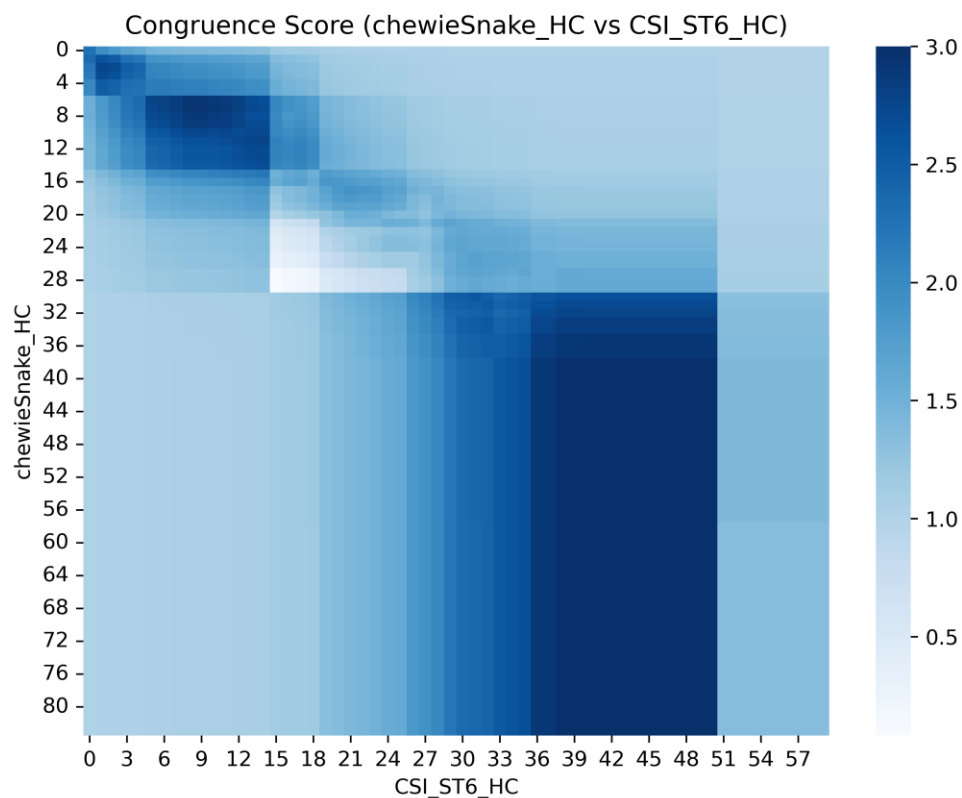


Figure S4.4.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

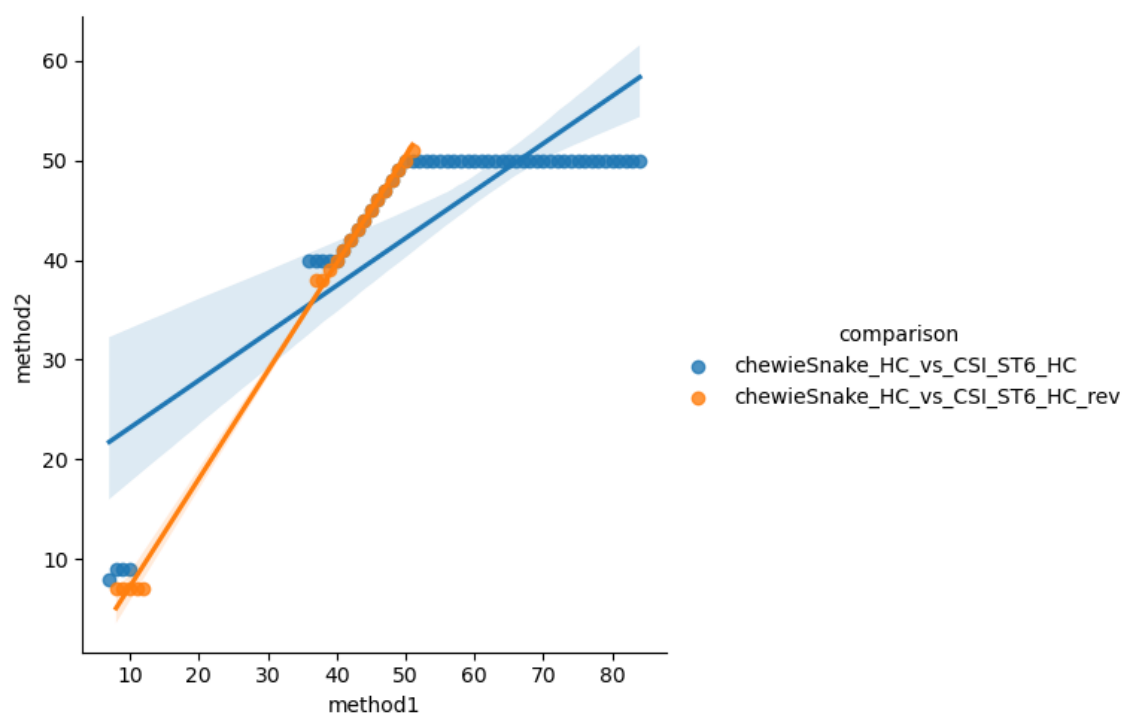


Figure S4.4.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 53 (blue) and 20 (orange) points is presented.

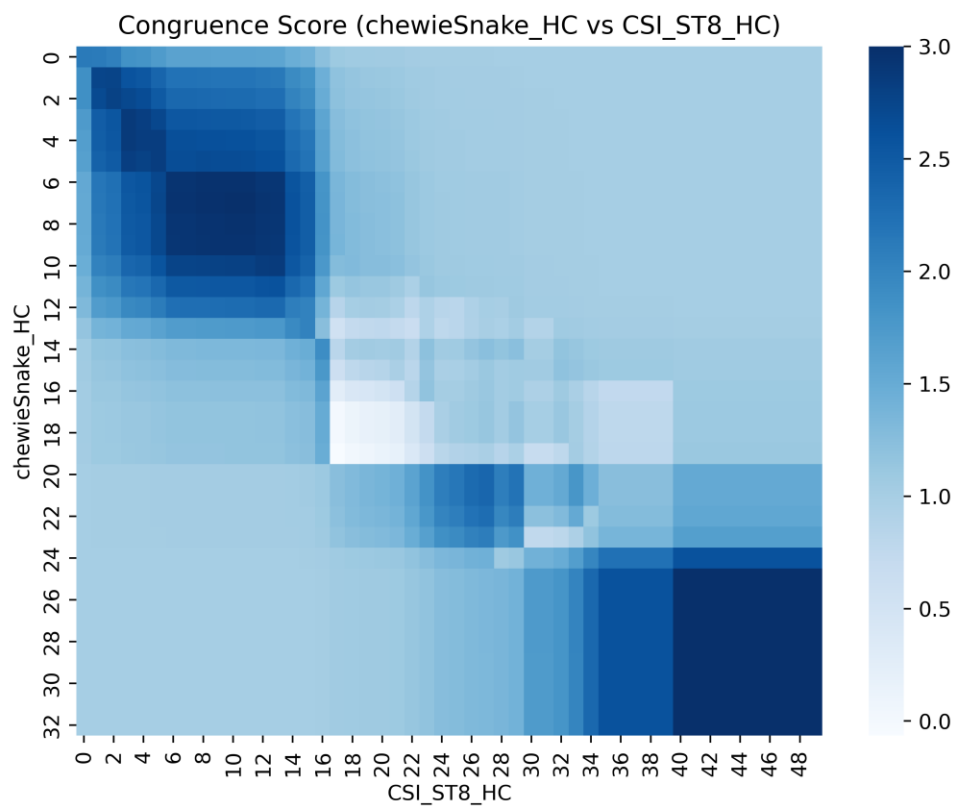


Figure S4.4.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

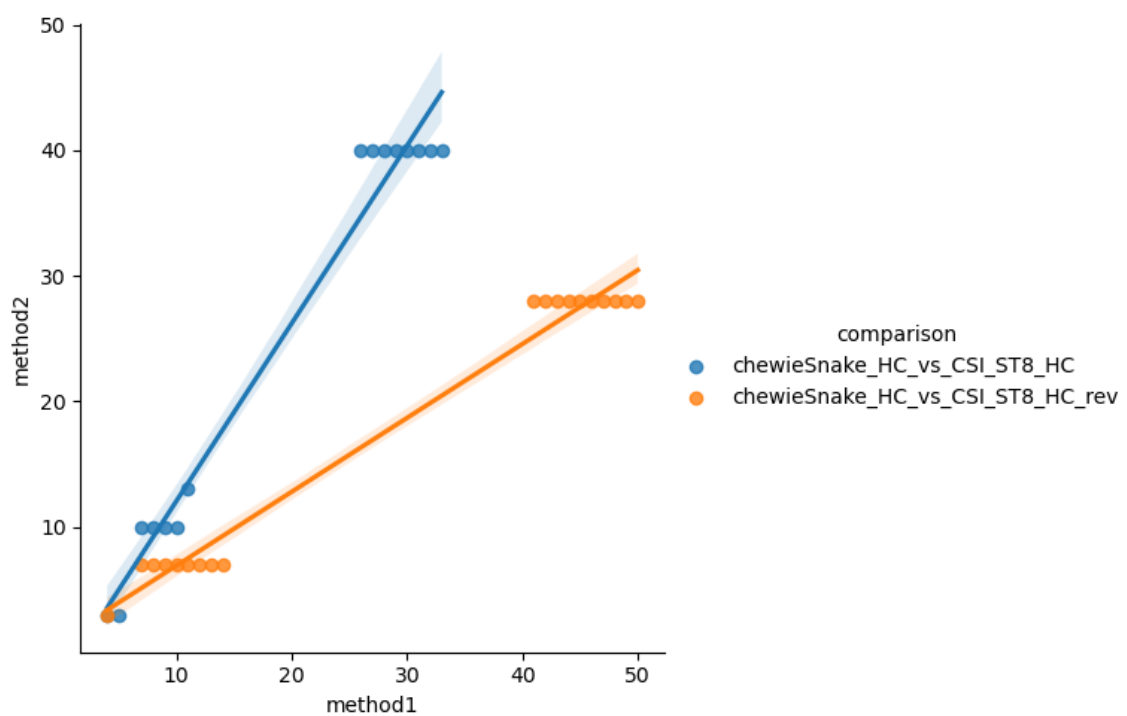


Figure S4.4.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 15 (blue) and 19 (orange) points is presented.

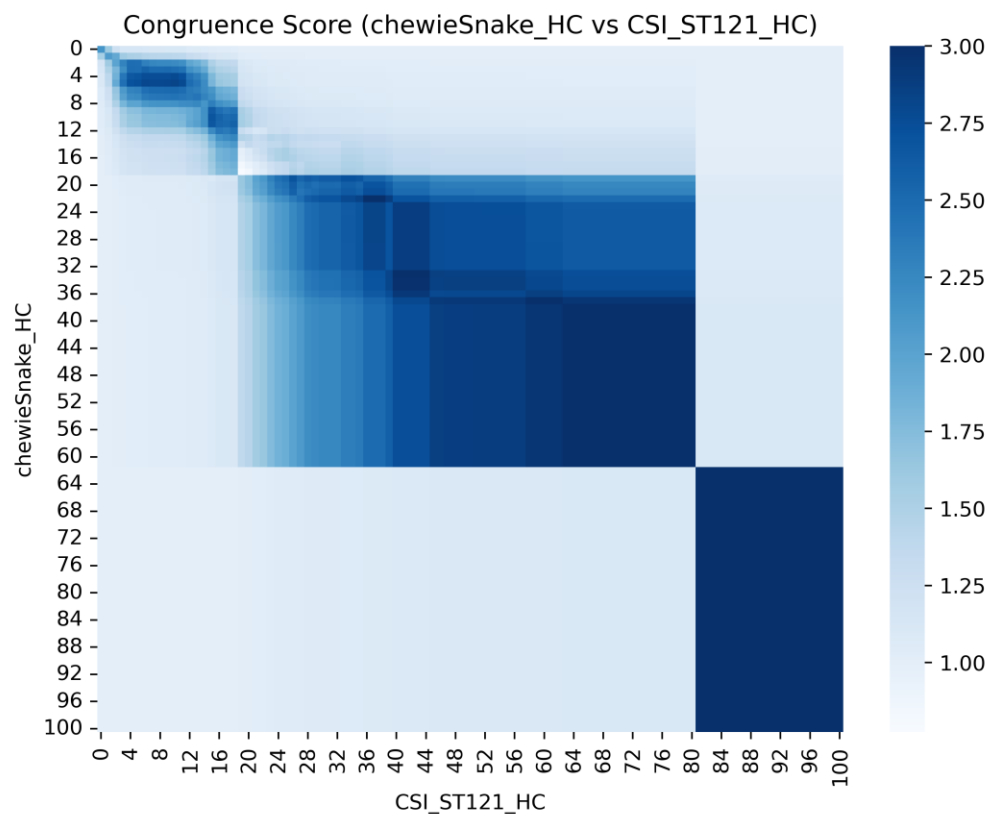


Figure S4.4.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

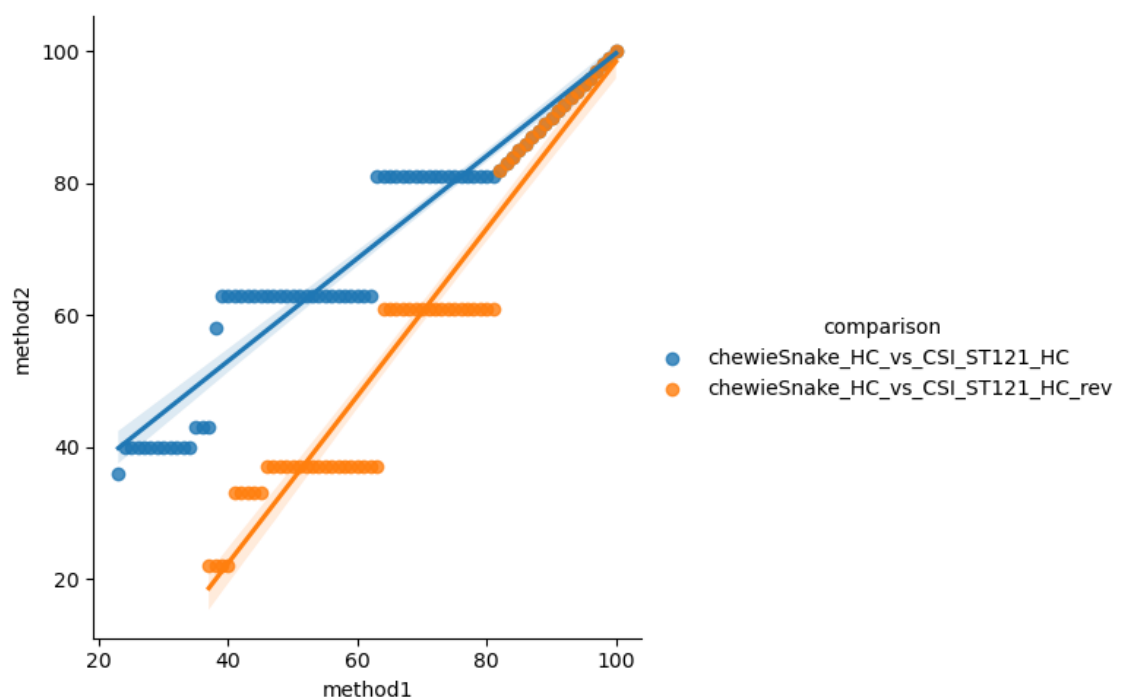


Figure S4.4.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 78 (blue) and 64 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

5. chewieSnake single-linkage vs. snippySnake single-linkage

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

	chewieSnake single-linkage	snippySnake single-linkage
Pipeline version	v3.1.1	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

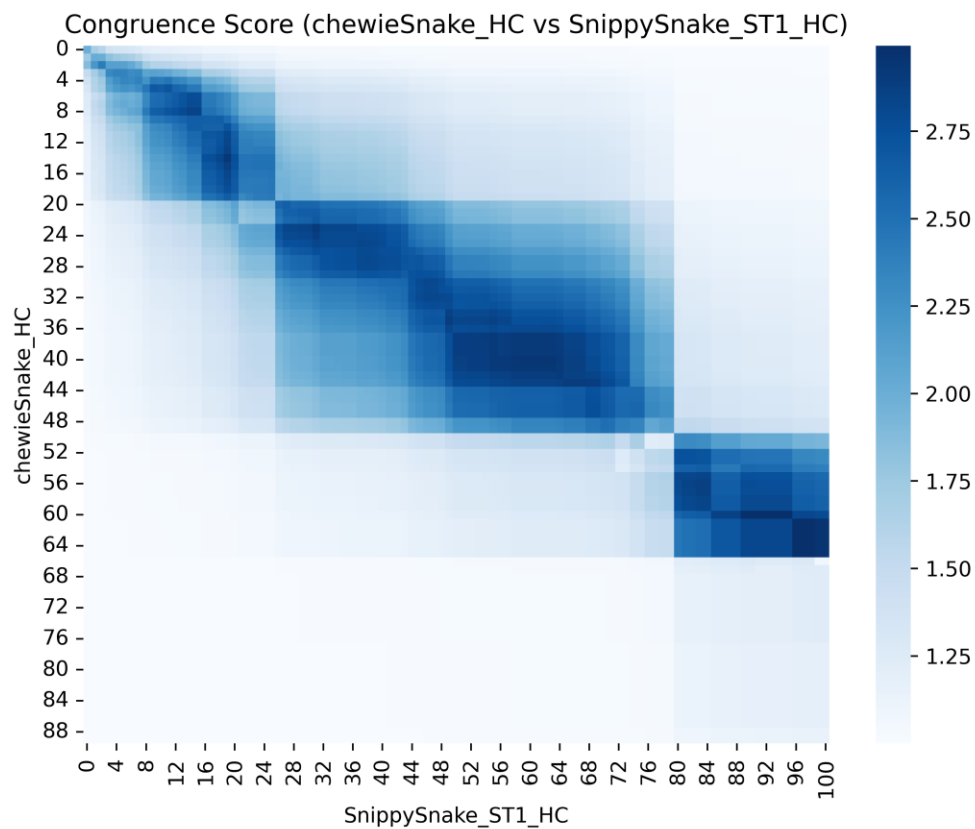


Figure S4.5.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

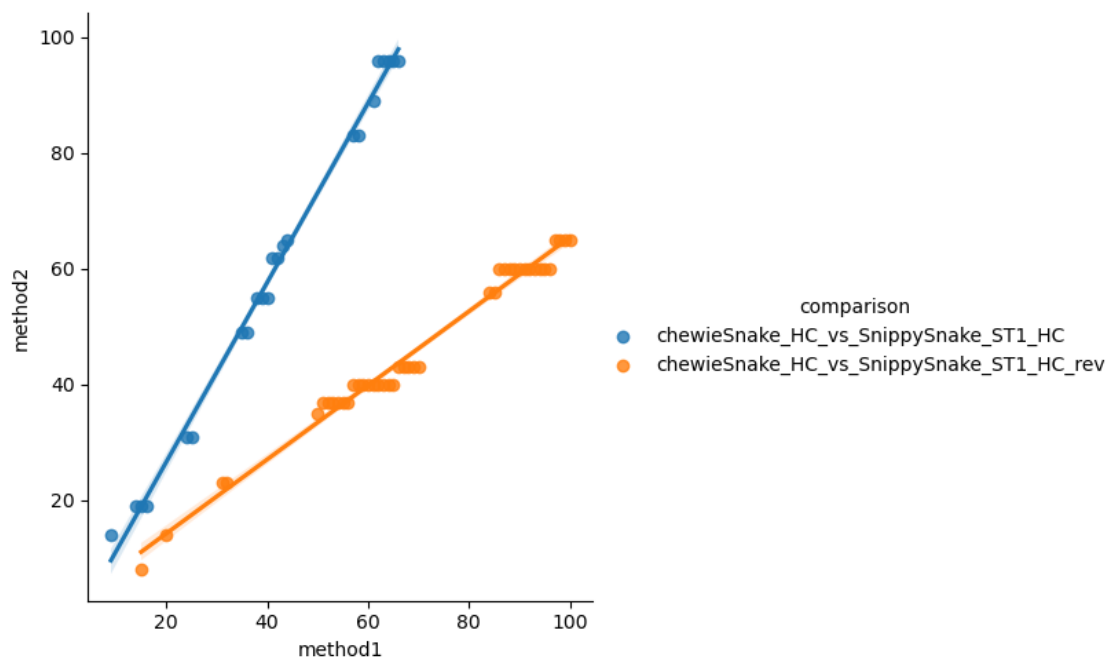


Figure S4.5.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST1. A linear tendency line supported by 23 (blue) and 42 (orange) points is presented.

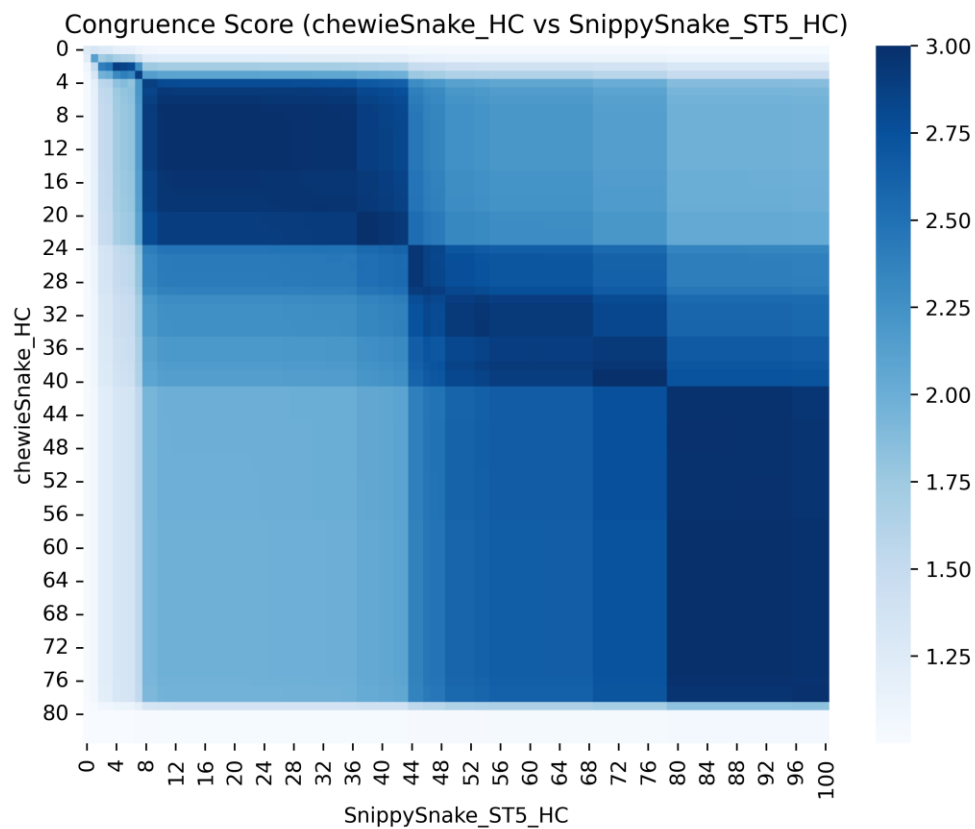


Figure S4.5.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

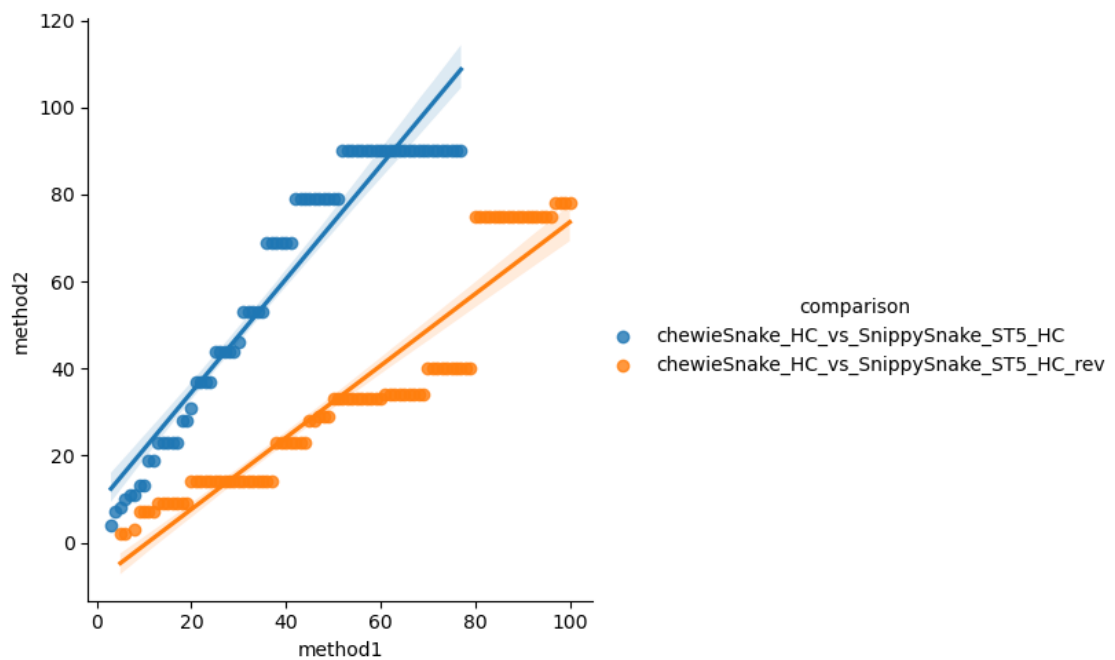


Figure S4.5.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 75 (blue) and 95 (orange) points is presented.

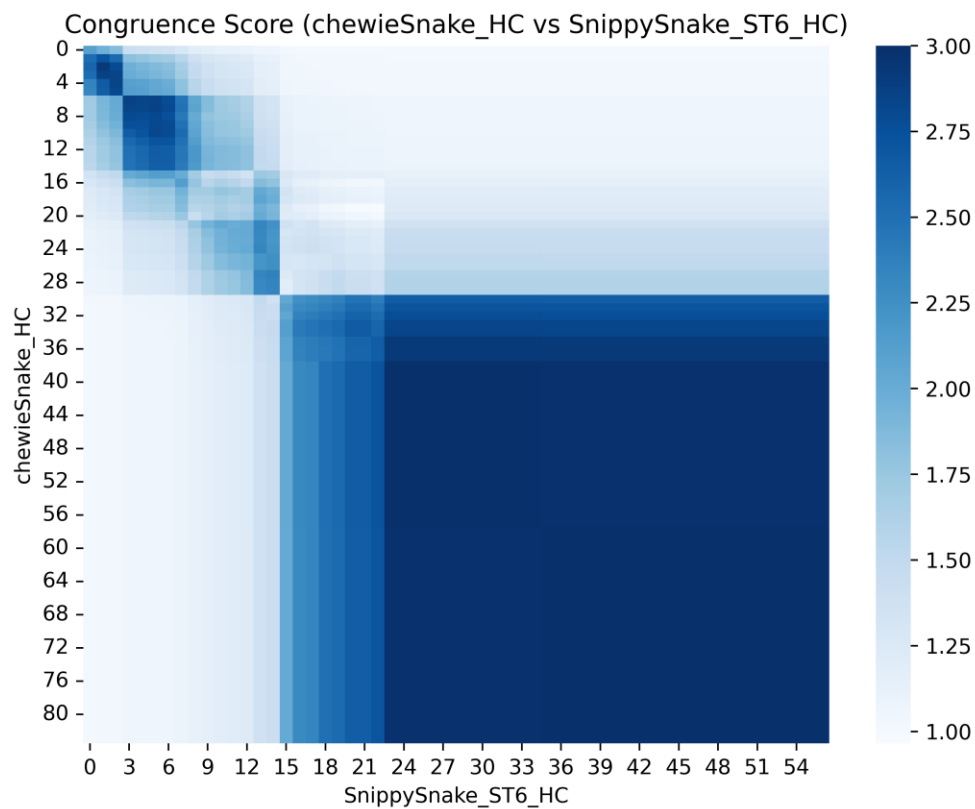


Figure S4.5.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

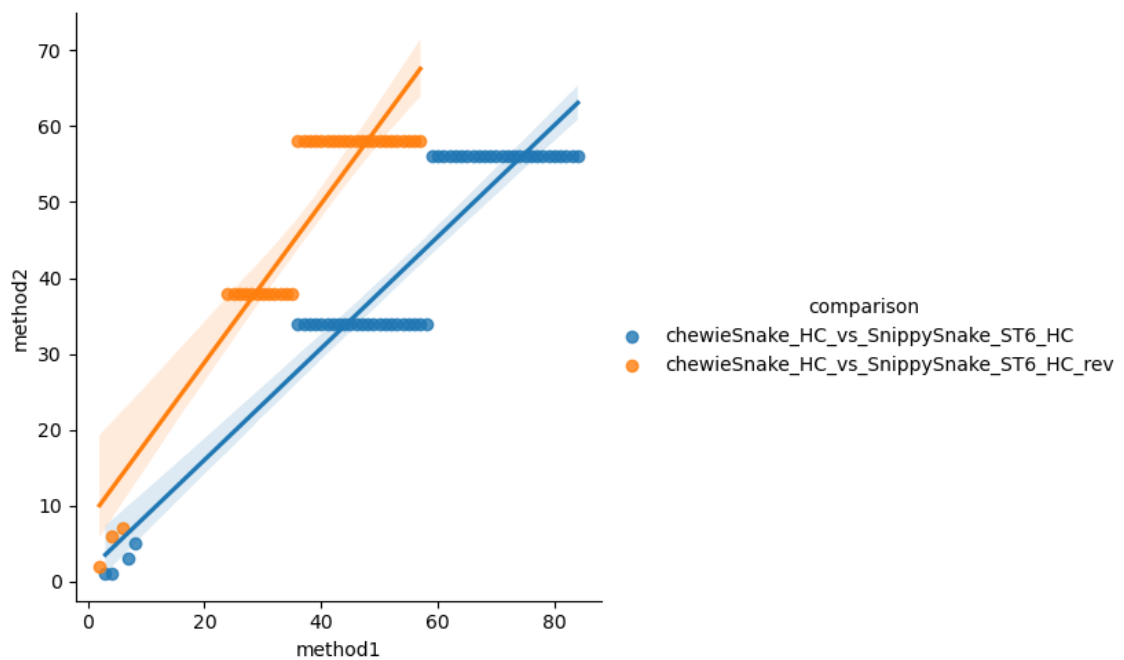


Figure S4.5.6. Corresponding points between the two pipelines in both directions (CS ≥ 2.85) of all partitions for ST6. A linear tendency line supported by 53 (blue) and 37 (orange) points is presented.

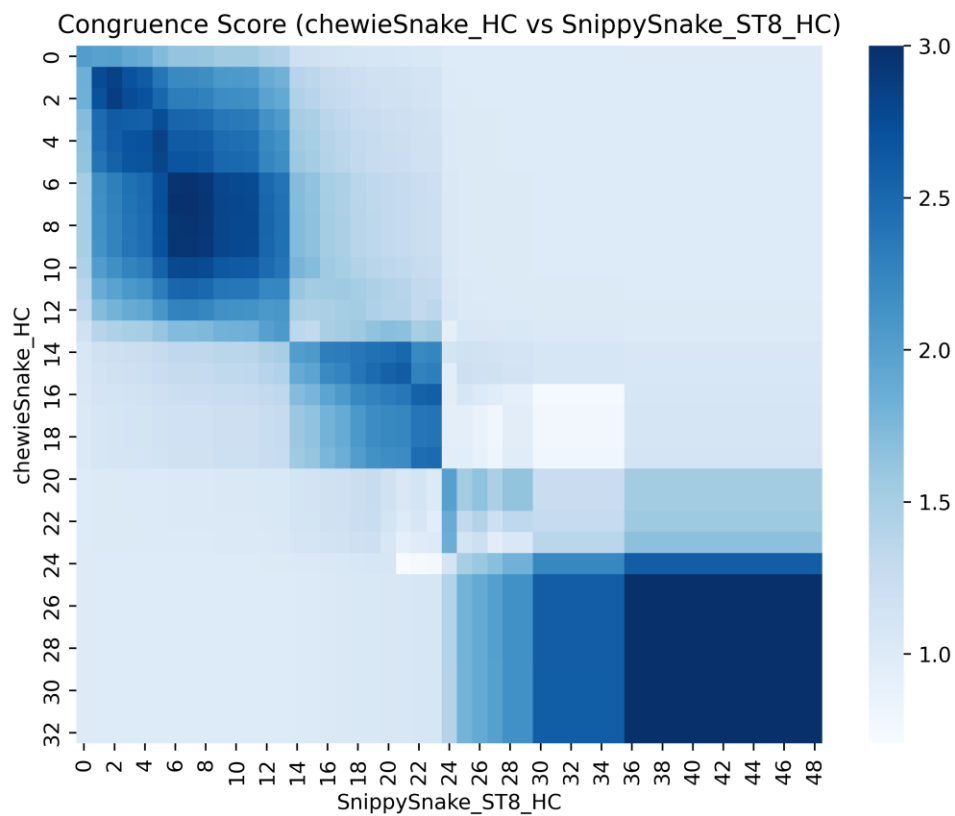


Figure S4.5.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

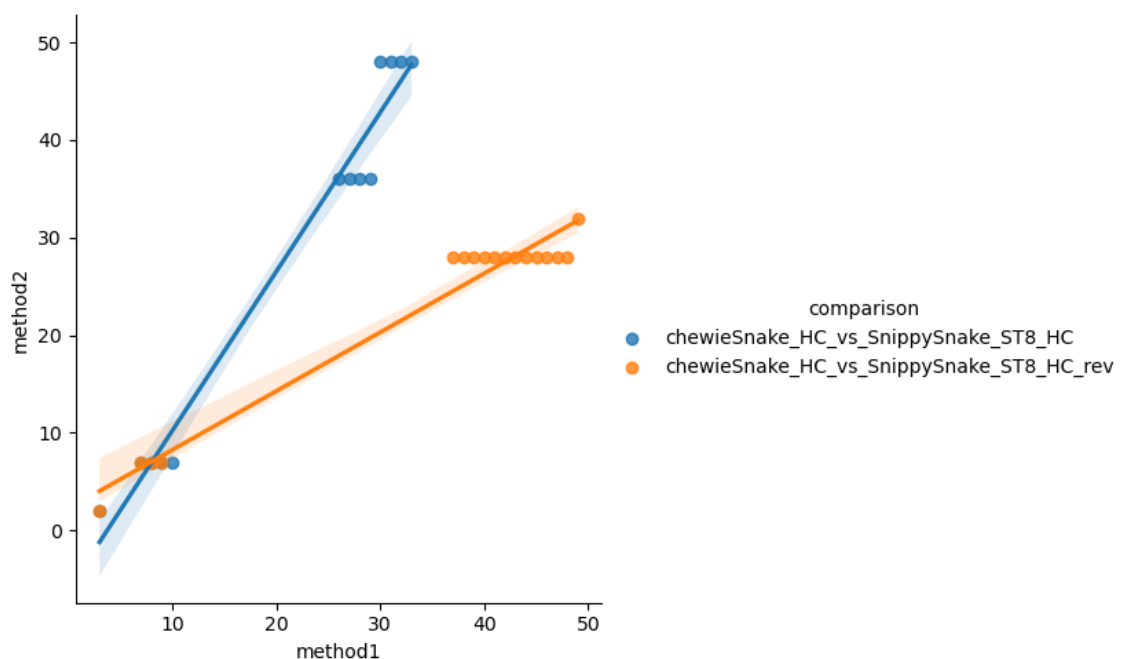


Figure S4.5.8. Corresponding points between the two pipelines in both directions (CS ≥ 2.85) of all partitions for ST8. A linear tendency line supported by 13 (blue) and 17 (orange) points is presented.

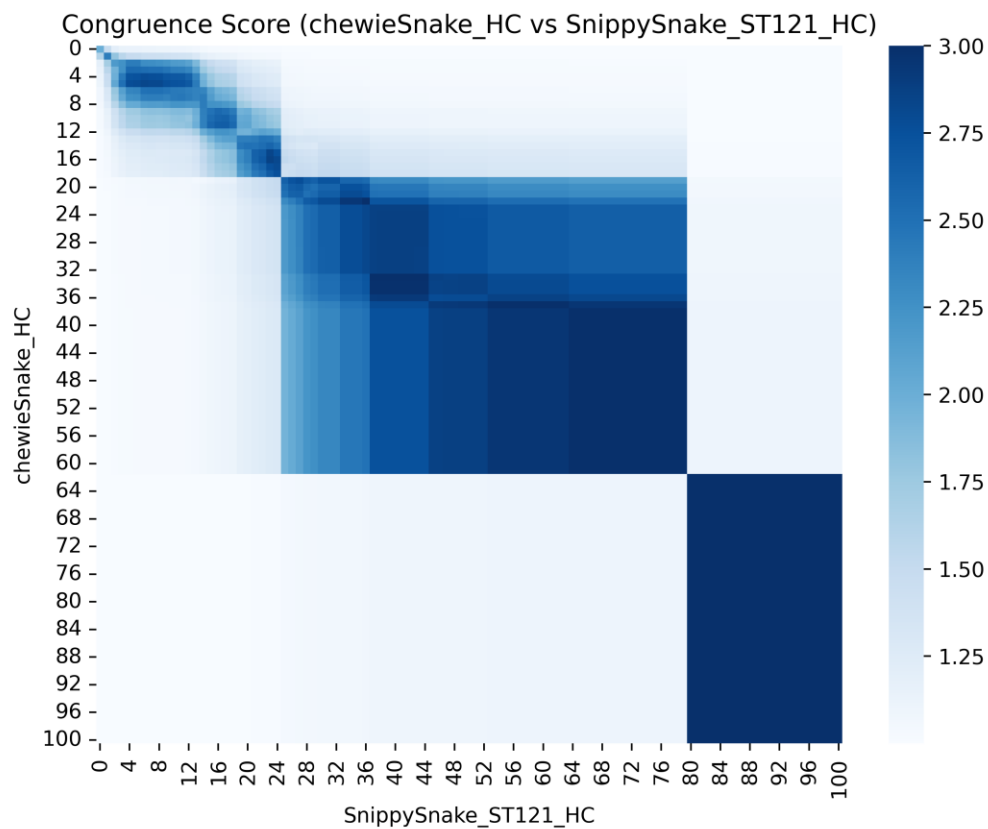


Figure S4.5.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

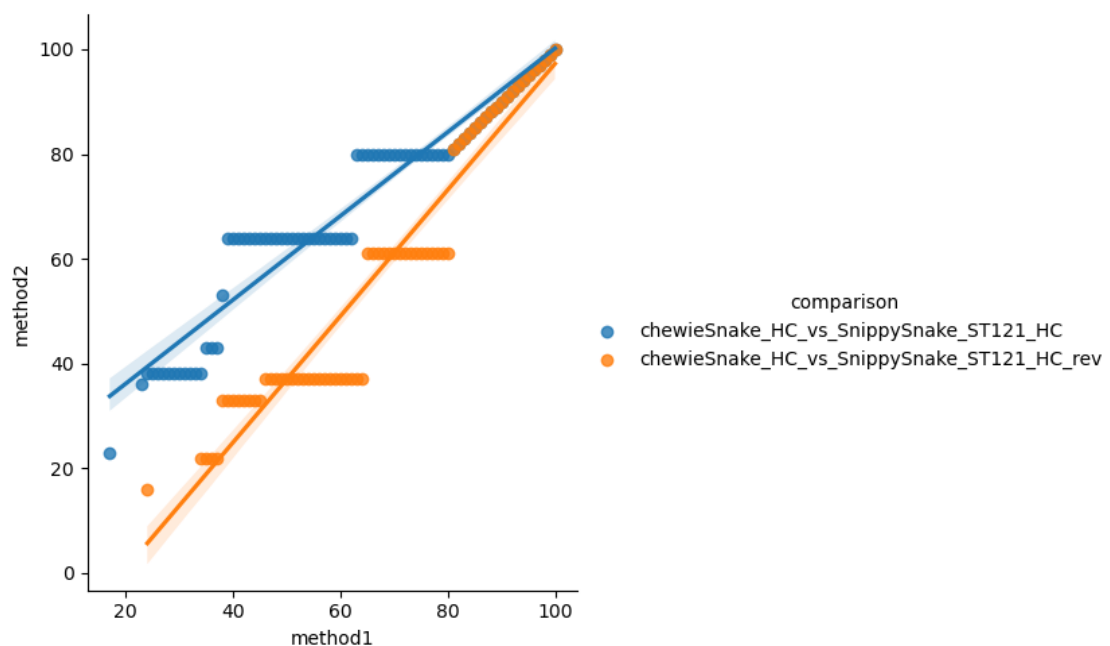


Figure S4.5.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 79 (blue) and 68 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

6. chewieSnake single-linkage vs. WGSBAC single-linkage

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

	chewieSnake single-linkage	WGSBAC single-linkage
Pipeline version	v3.1.1	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

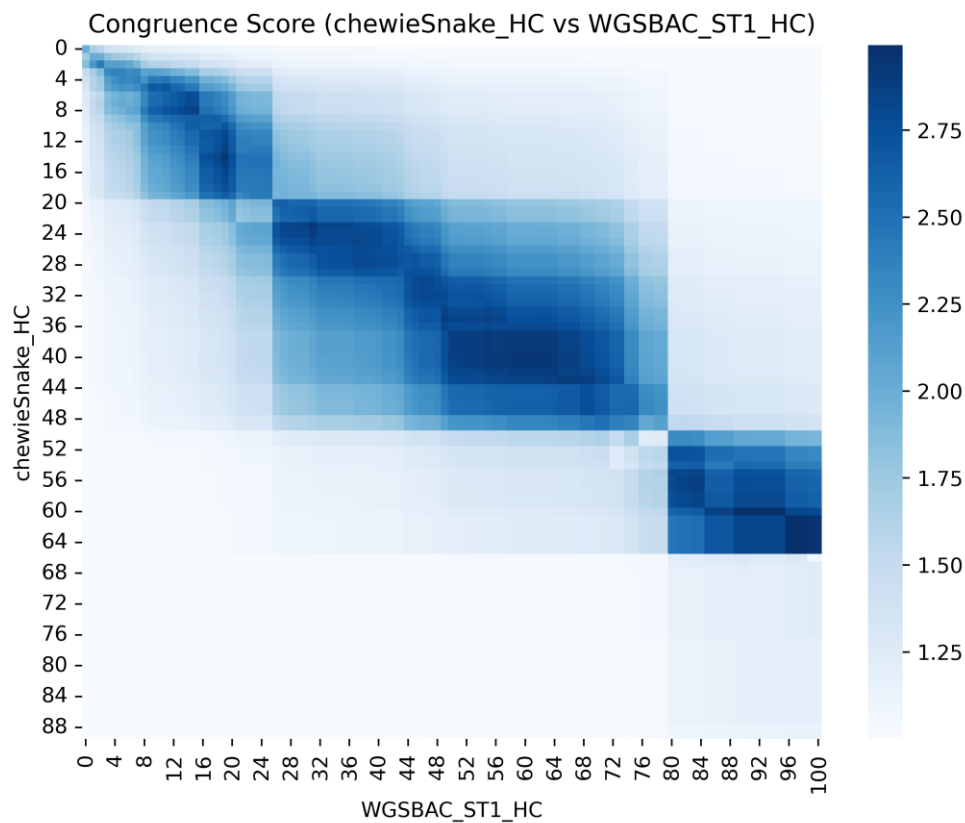


Figure S4.6.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

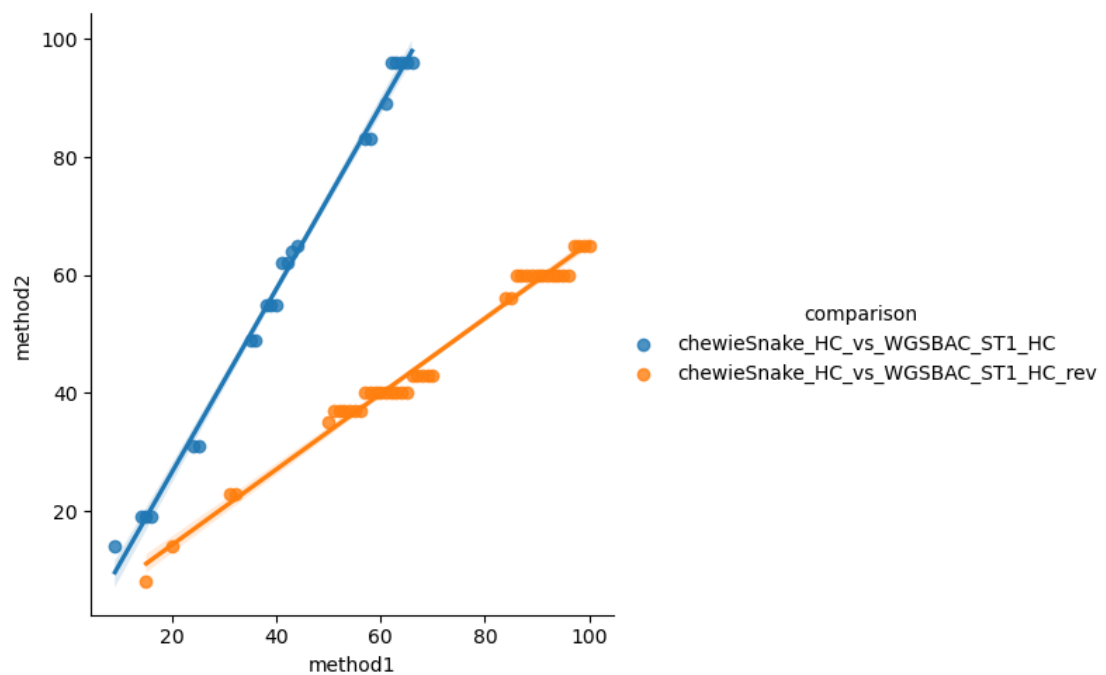


Figure S4.6.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 23 (blue) and 42 (orange) points is presented.

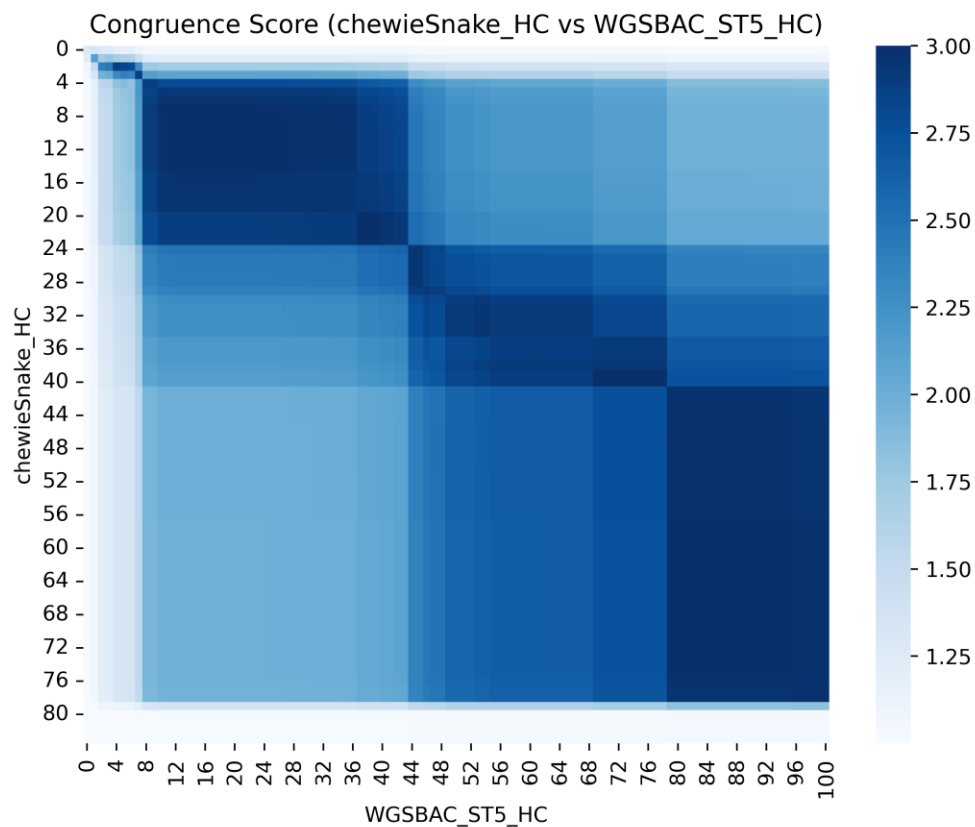


Figure S4.6.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

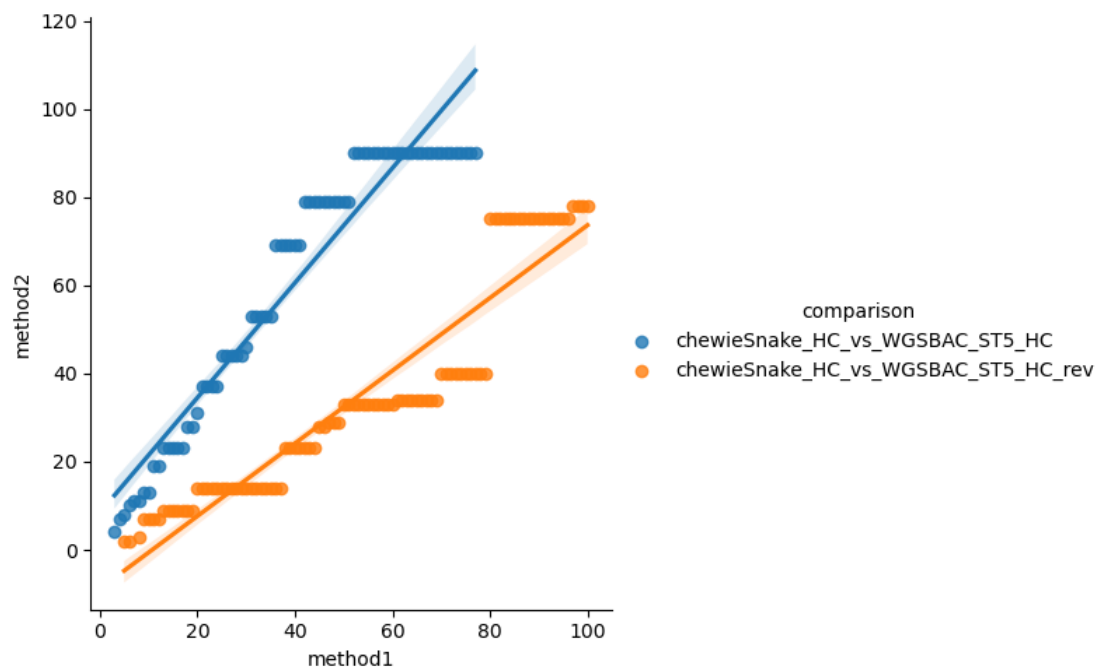


Figure S4.6.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 75 (blue) and 95 (orange) points is presented.

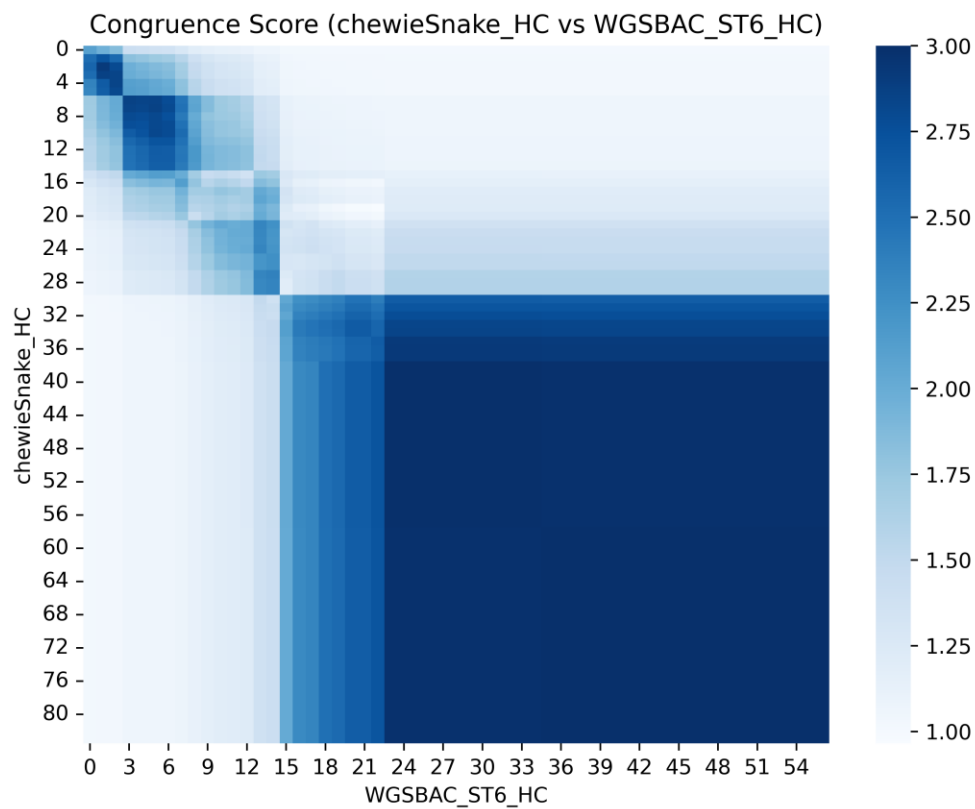


Figure S4.6.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

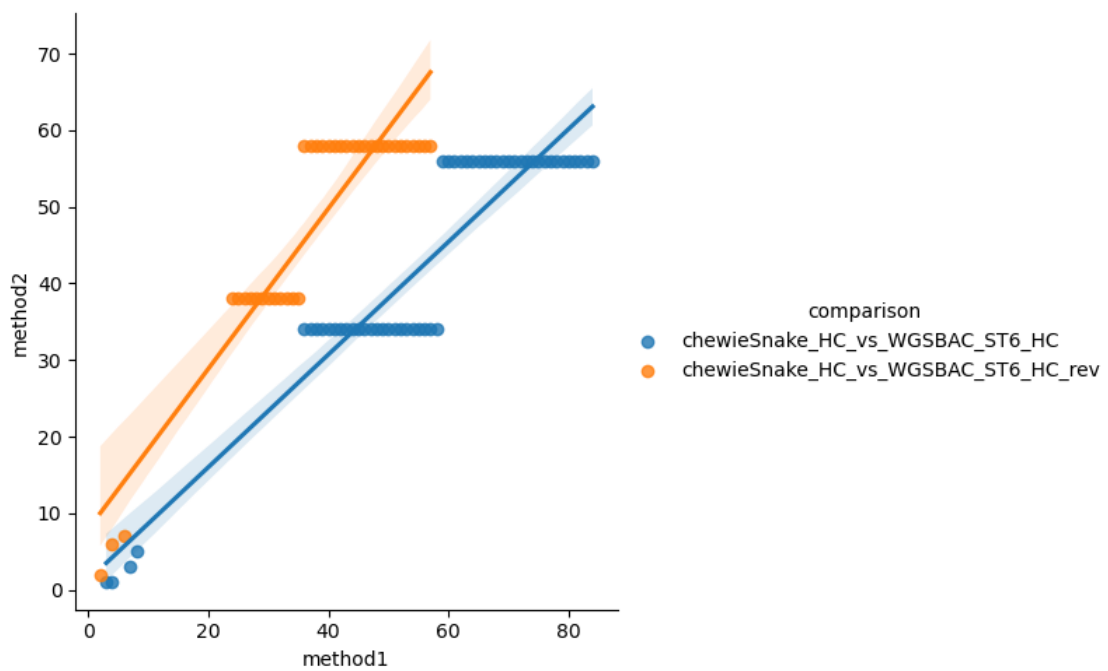


Figure S4.6.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 53 (blue) and 37 (orange) points is presented.

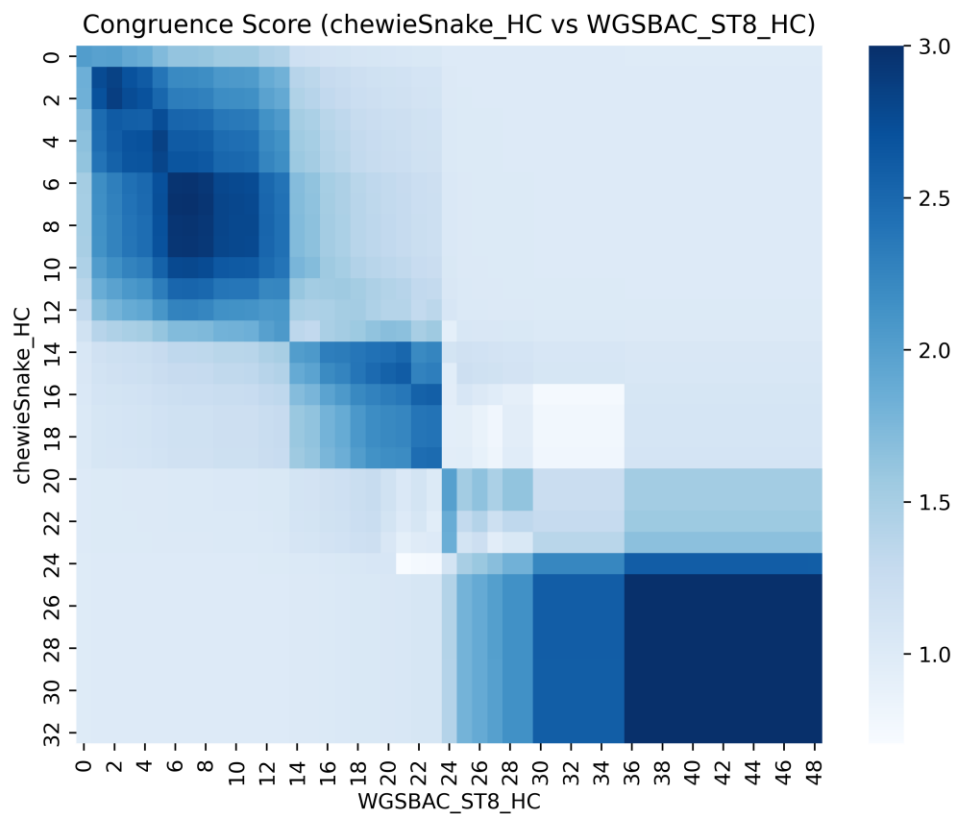


Figure S4.6.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

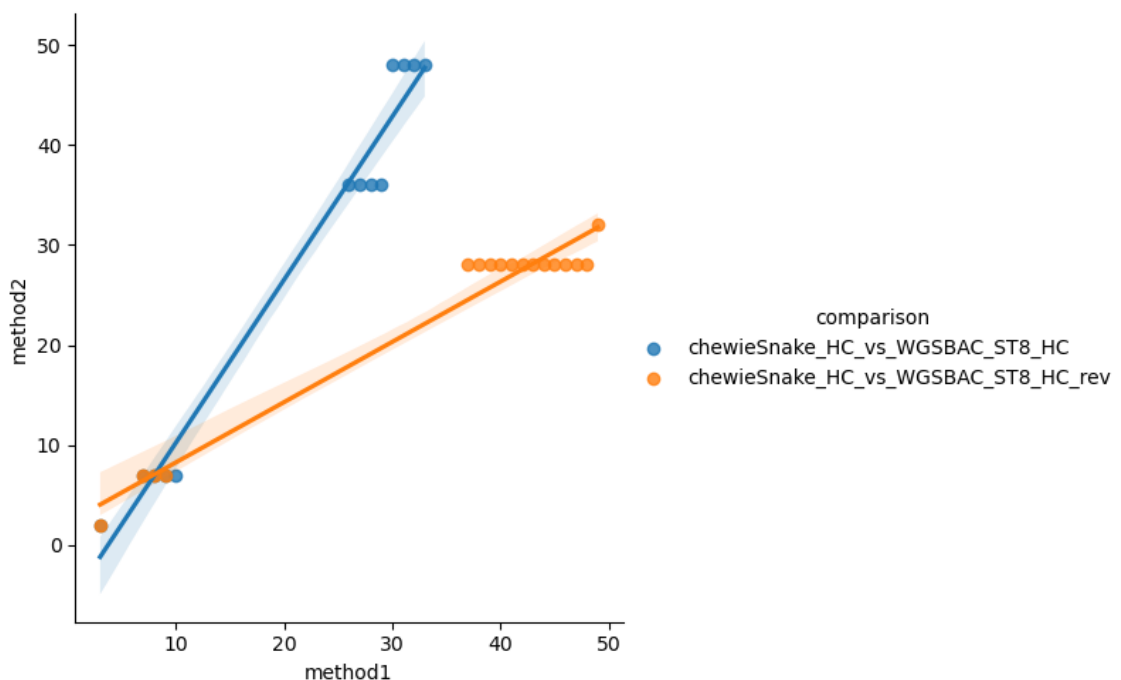


Figure S4.6.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 13 (blue) and 17 (orange) points is presented.

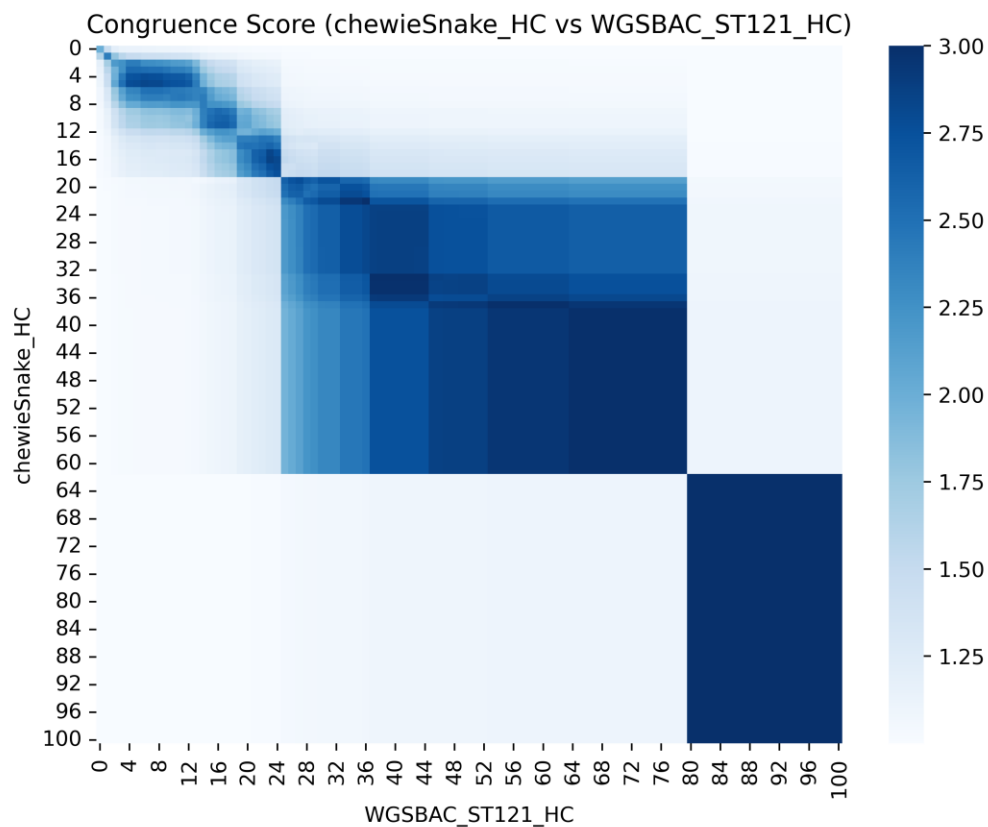


Figure S4.6.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

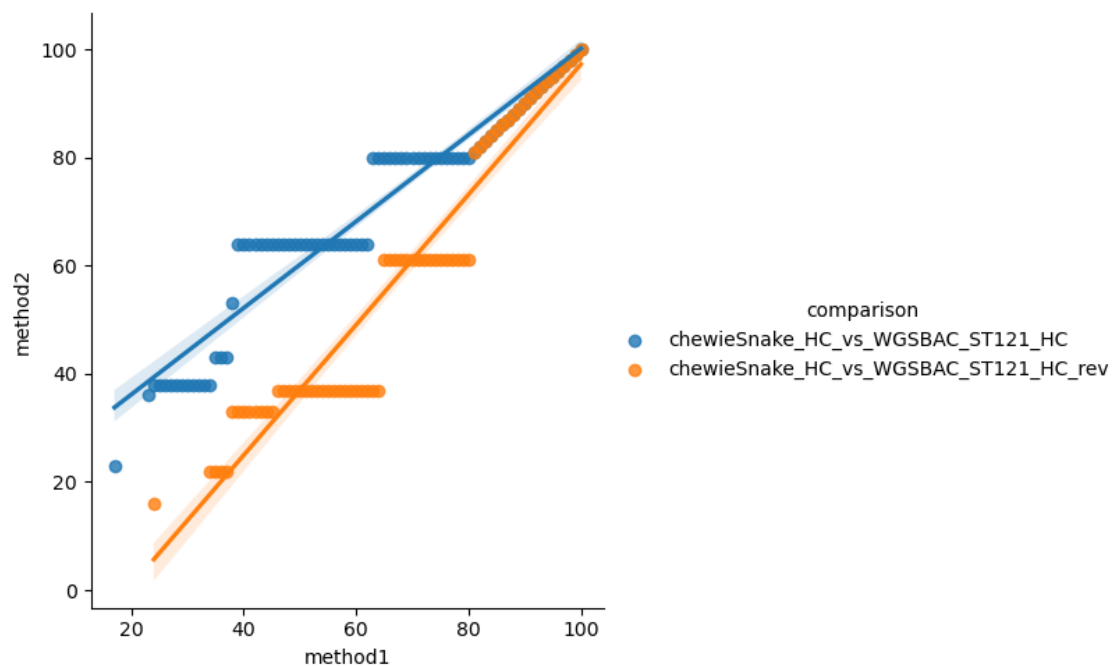


Figure S4.6.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 79 (blue) and 68 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

7. INNUENDO-like GrapeTree 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 GrapeTree	CSI Phylogeny single-linkage
Pipeline version	chewBBACA 2.8.5	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

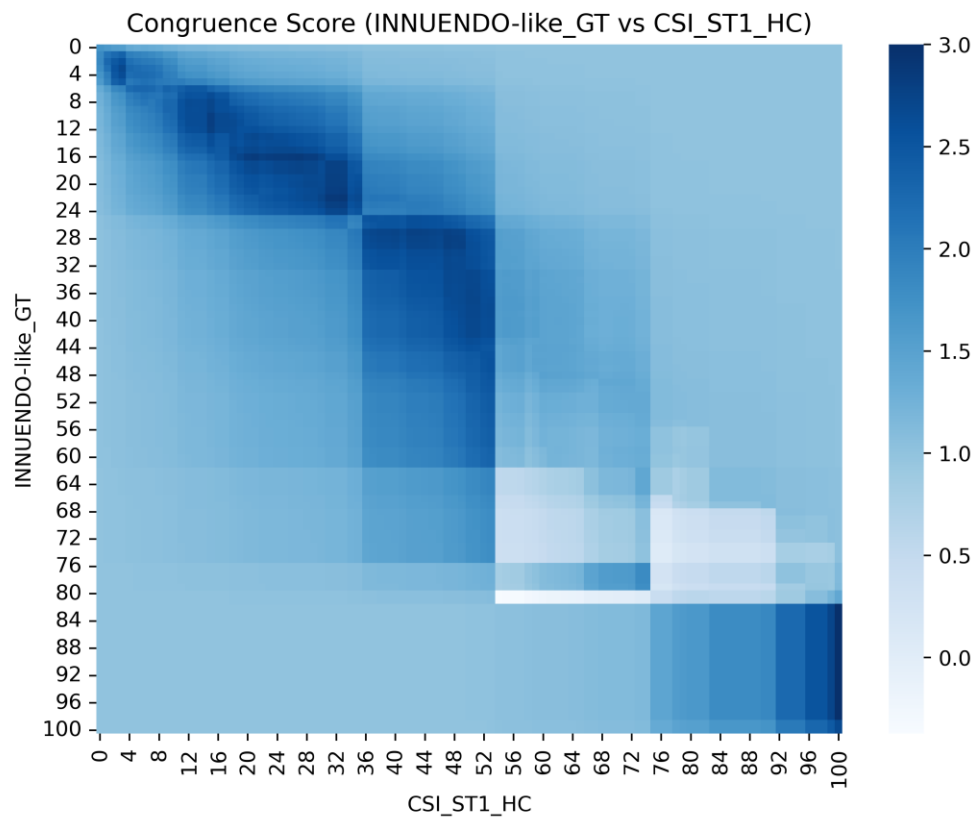


Figure S4.7.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

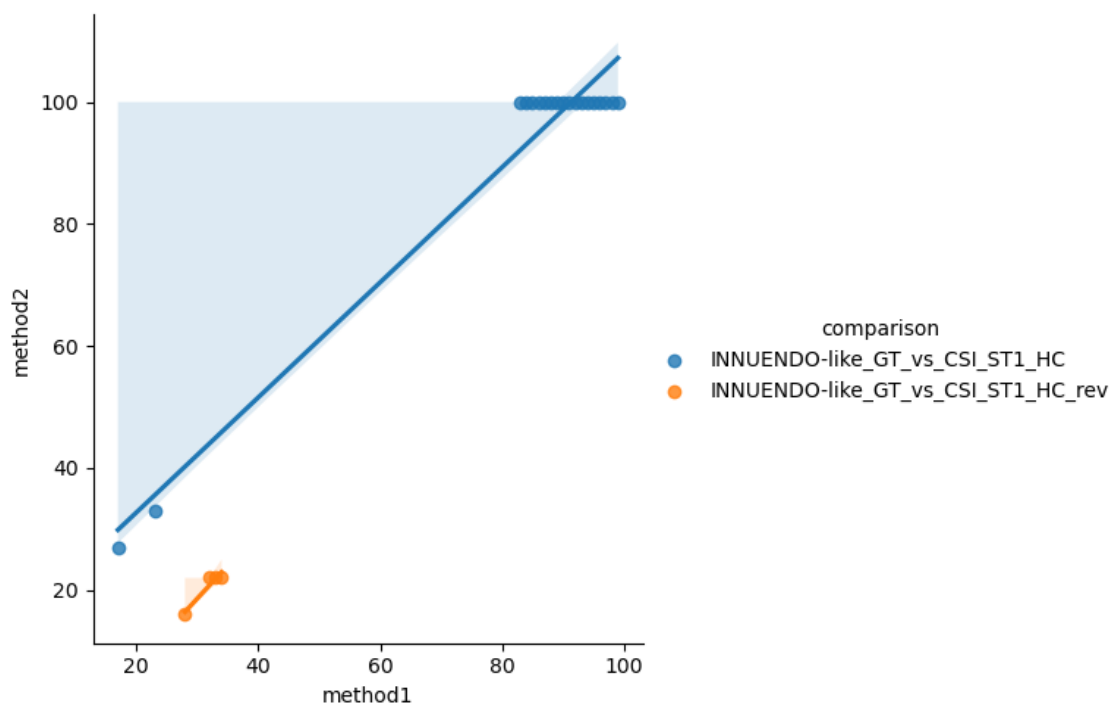


Figure S4.7.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 37 (blue) and 3 (orange) points is presented.

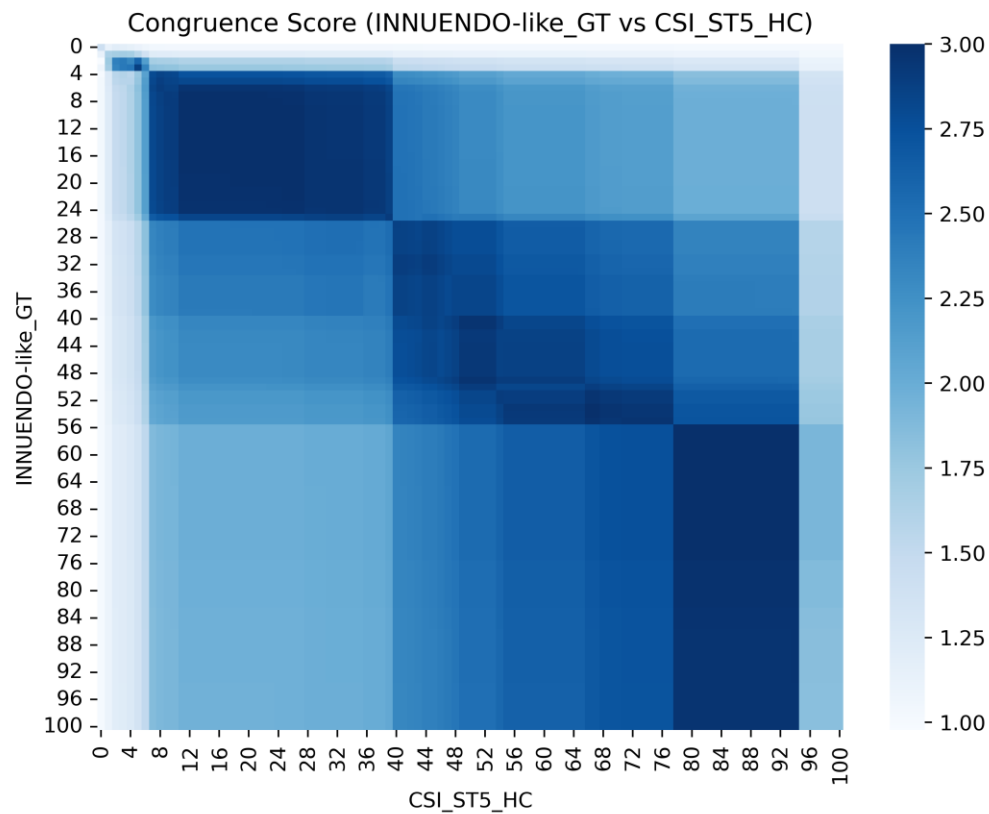


Figure S4.7.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

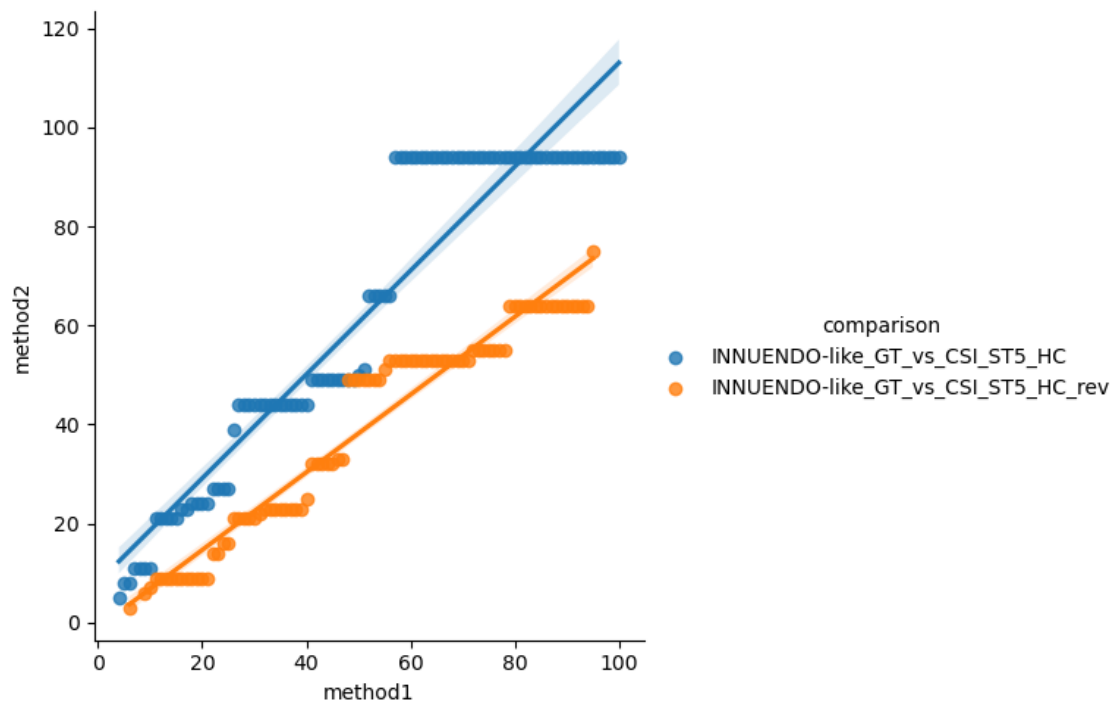


Figure S4.7.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 97 (blue) and 88 (orange) points is presented.

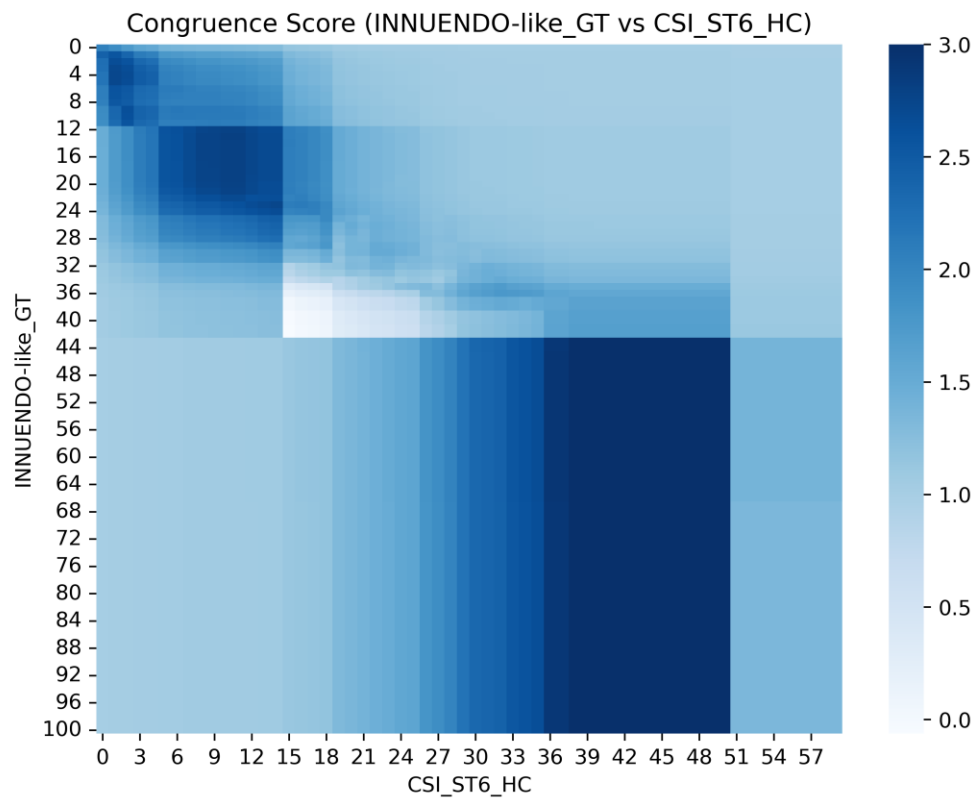


Figure S4.7.5 Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

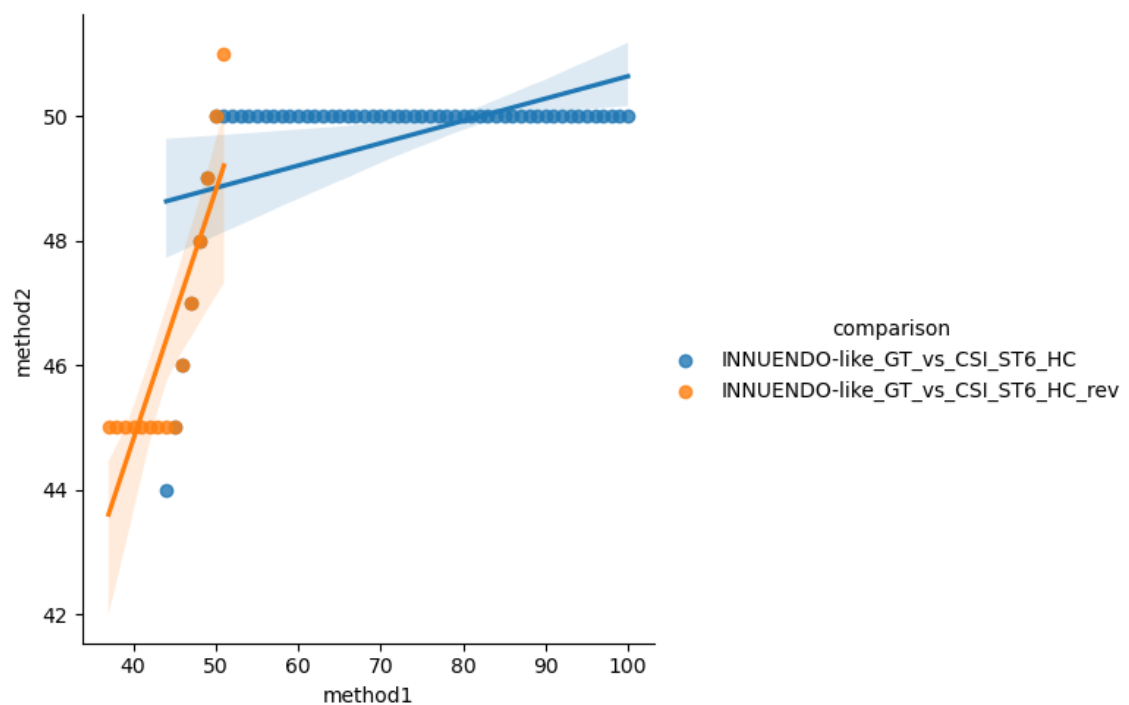


Figure S4.7.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 57 (blue) and 15 (orange) points is presented.

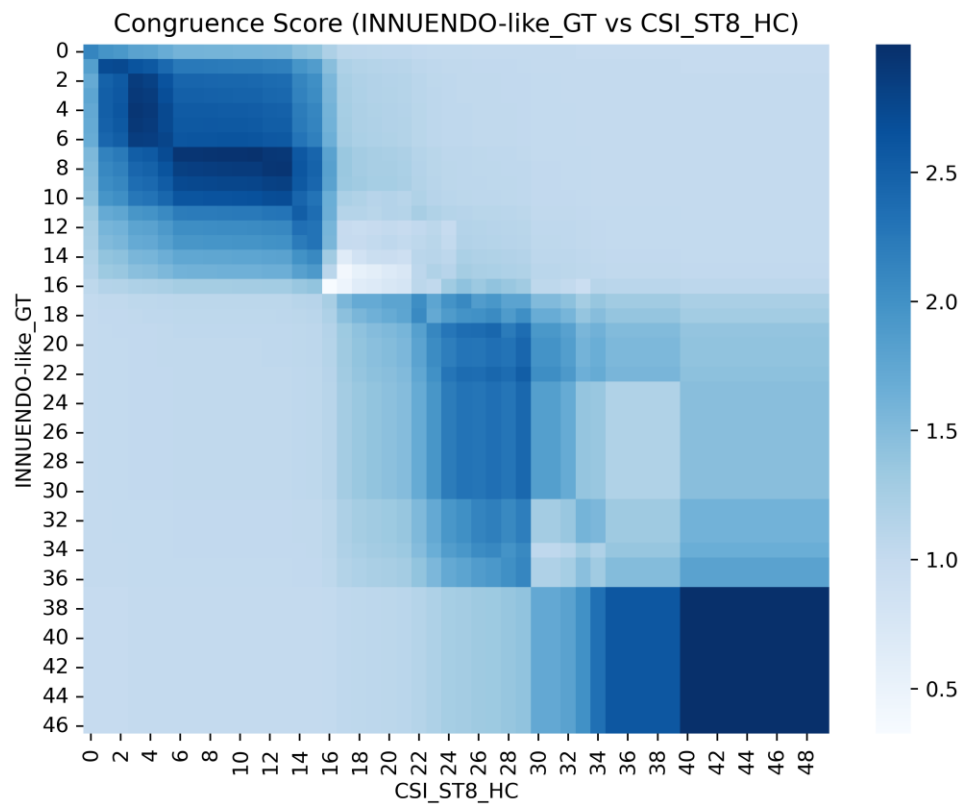


Figure S4.7.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

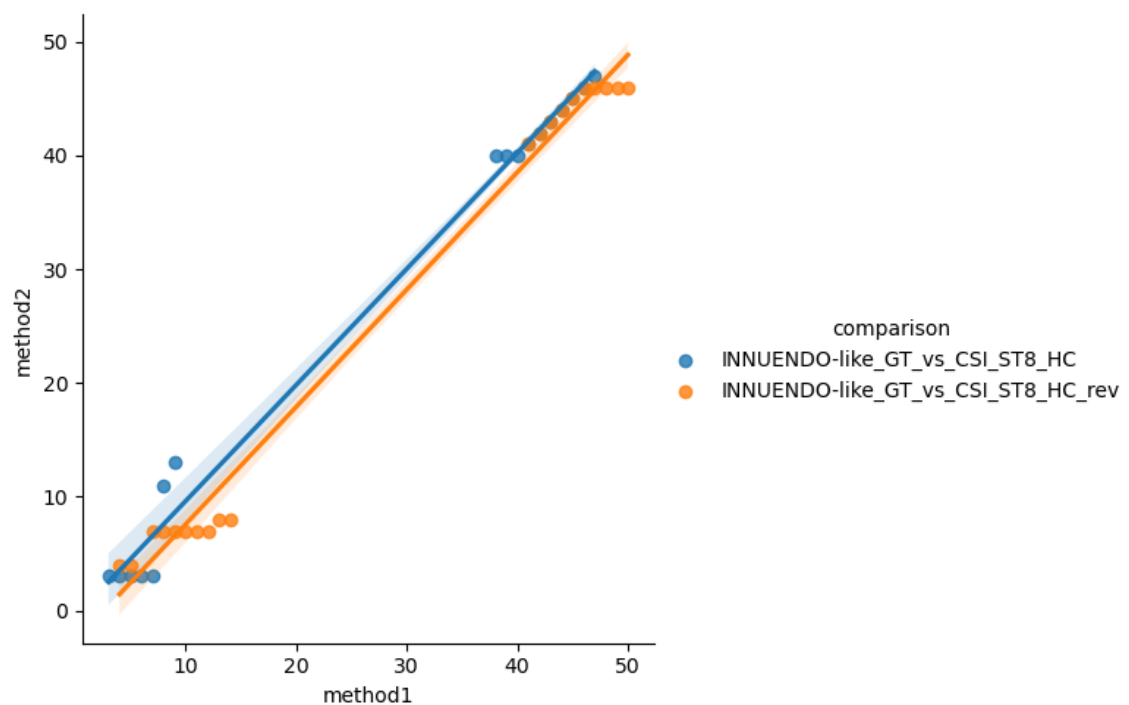


Figure S4.7.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 17 (blue) and 20 (orange) points is presented.

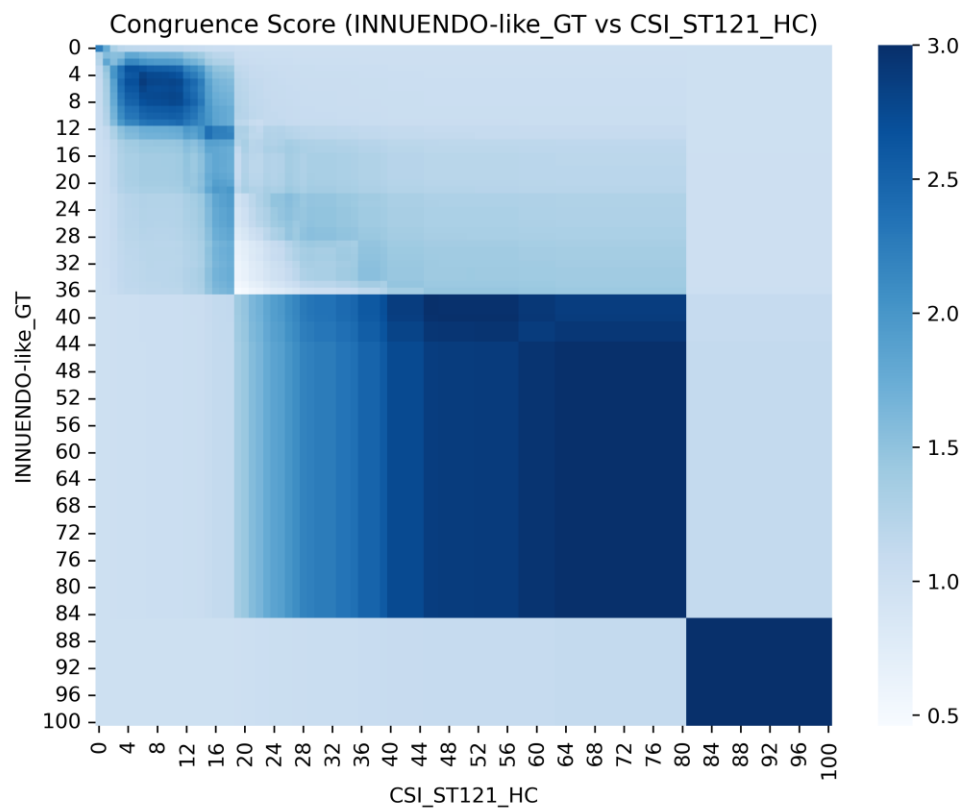


Figure S4.7.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

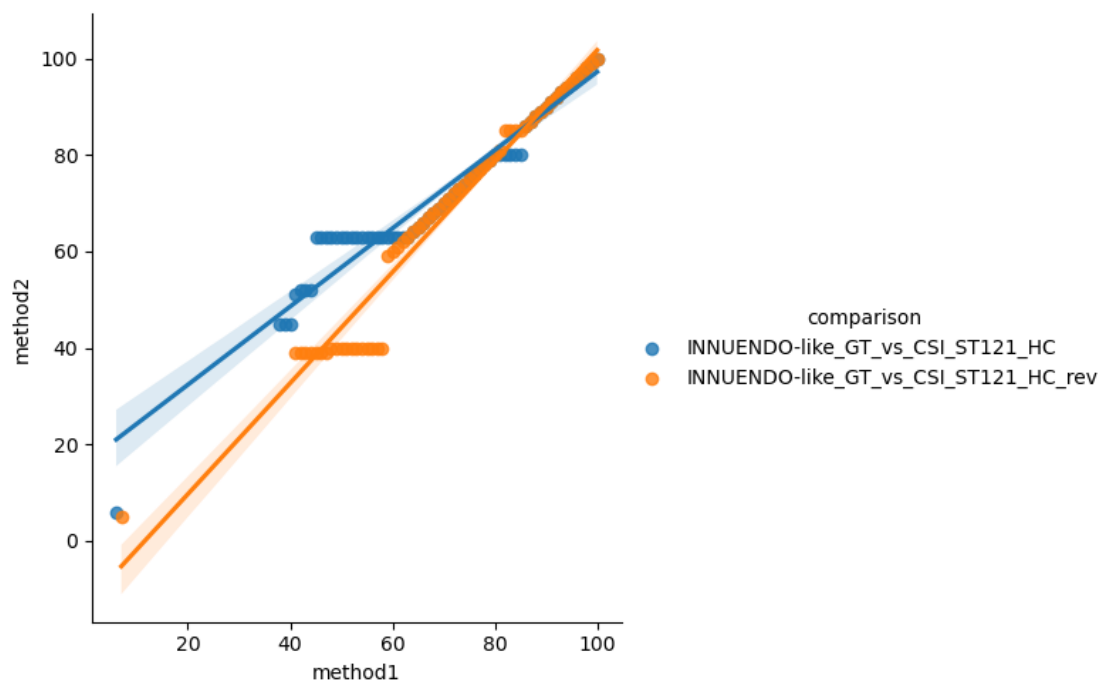


Figure S4.7.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 64 (blue) and 61 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

8. INNUENDO-like GrapeTree 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 GrapeTree	snippySnake single-linkage
Pipeline version	chewBBACA 2.8.5	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

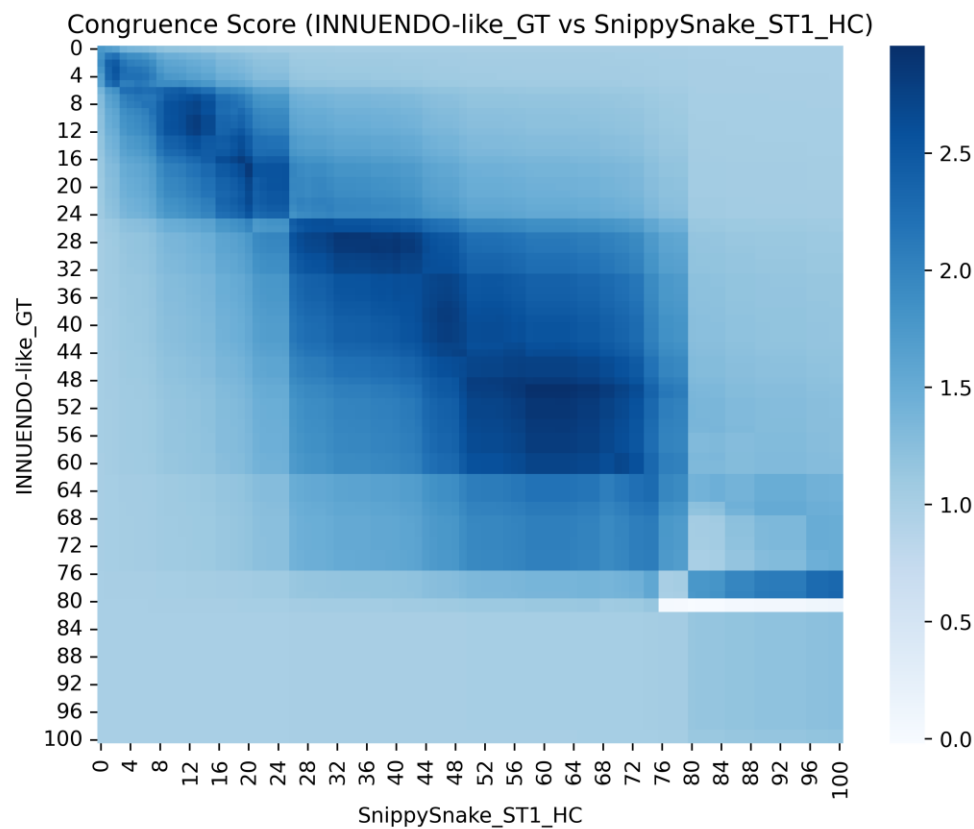


Figure S4.8.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

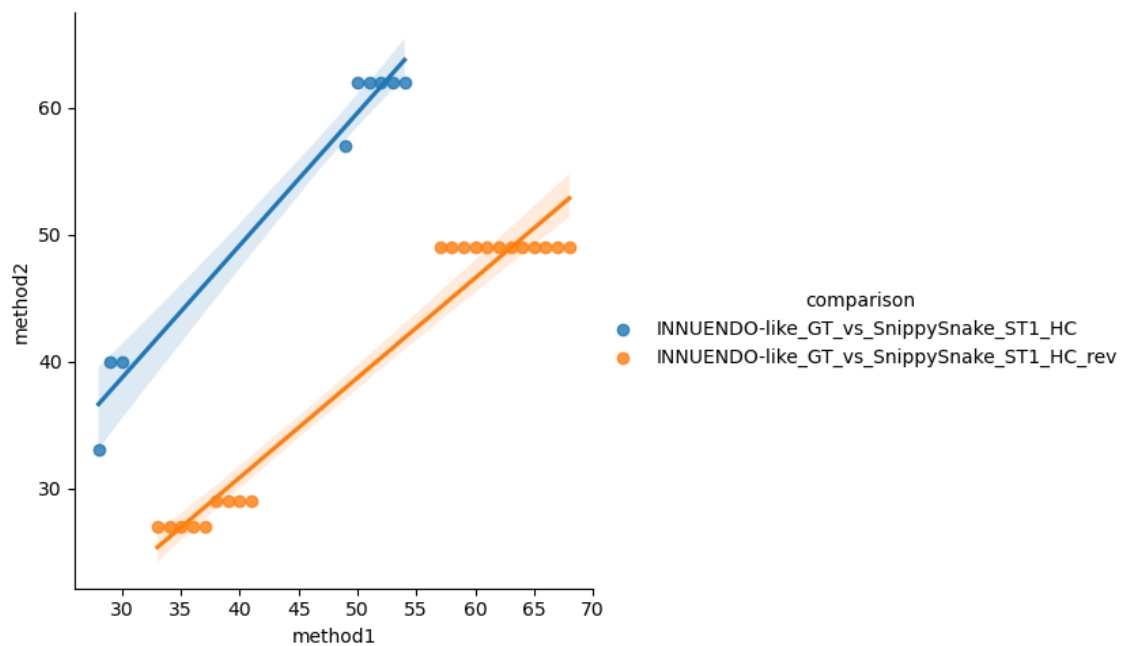


Figure S4.8.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST1. A linear tendency line supported by 9 (blue) and 21 (orange) points is presented.

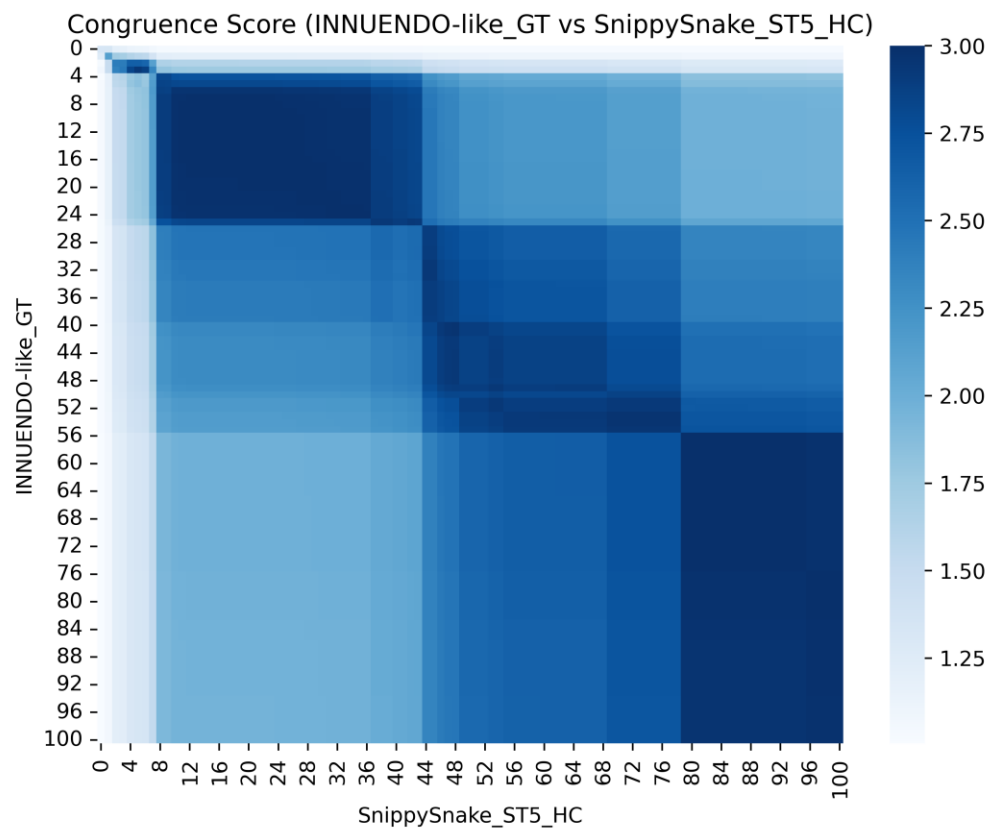


Figure S4.8.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

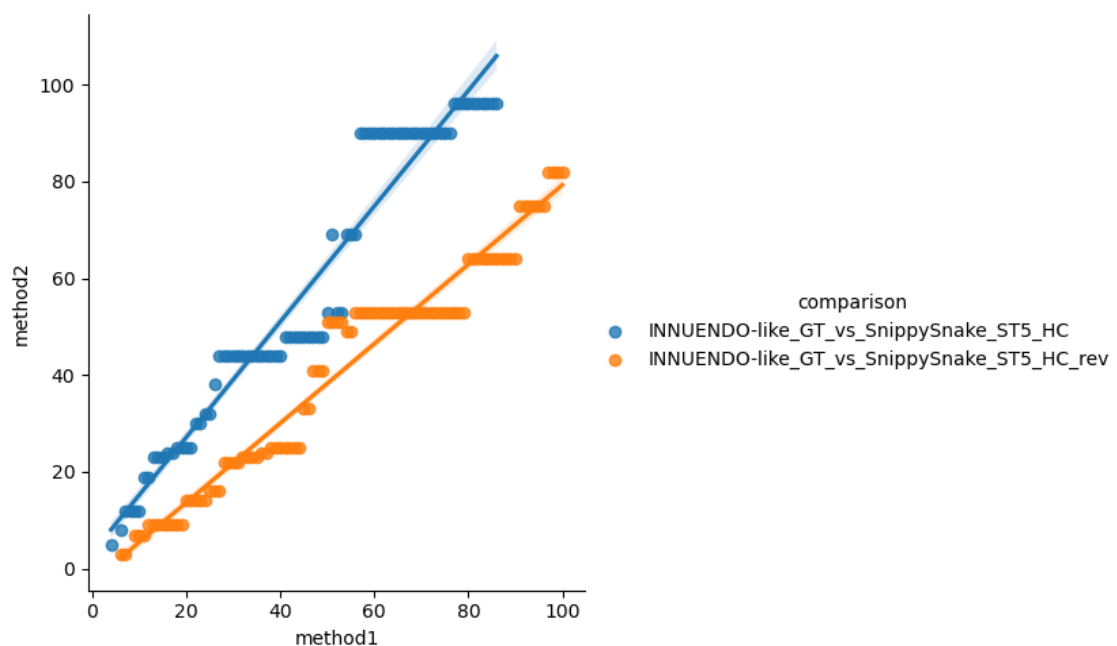


Figure S4.8.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 82 (blue) and 94 (orange) points is presented.

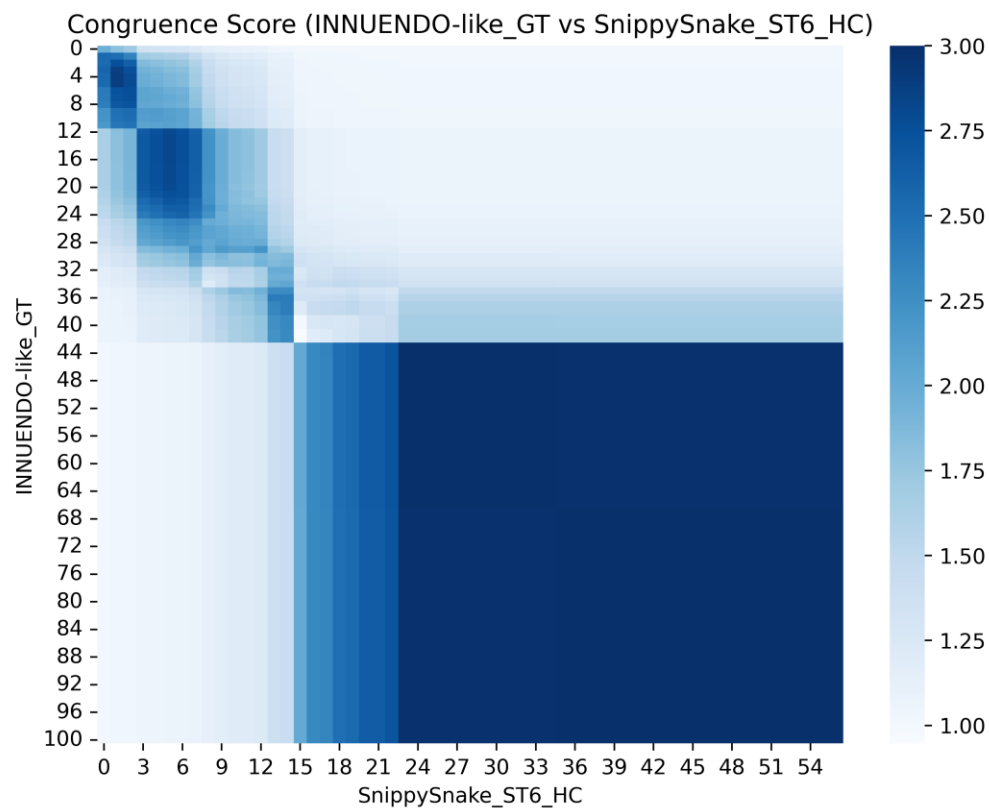


Figure S4.8.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

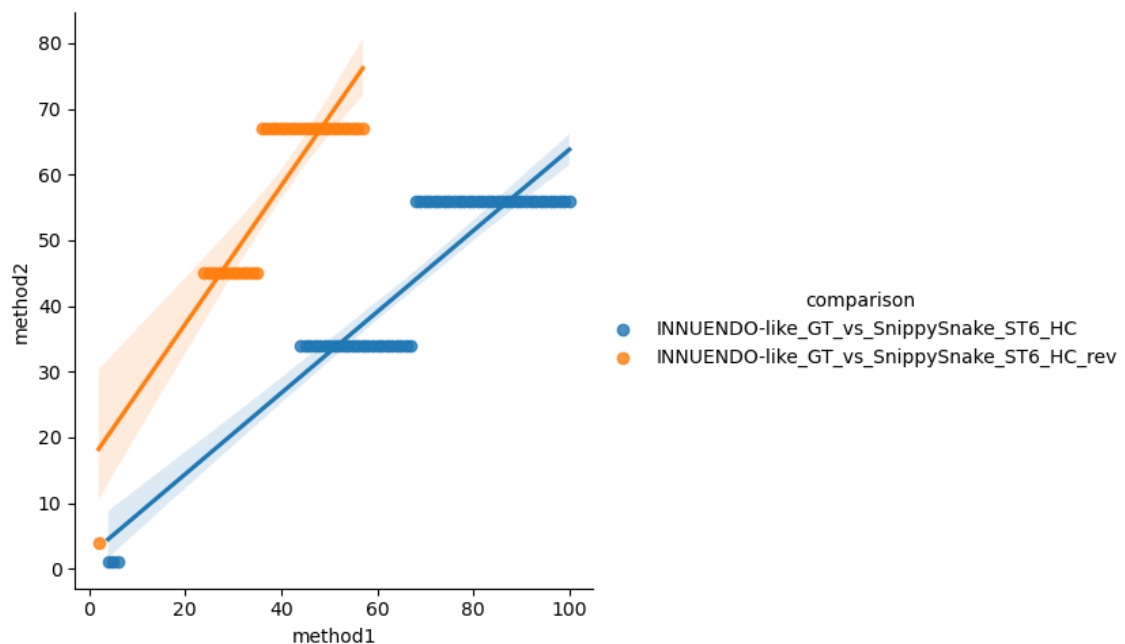


Figure S4.8.6. Corresponding points between the two pipelines in both directions (CS ≥ 2.85) of all partitions for ST6. A linear tendency line supported by 60 (blue) and 35 (orange) points is presented.

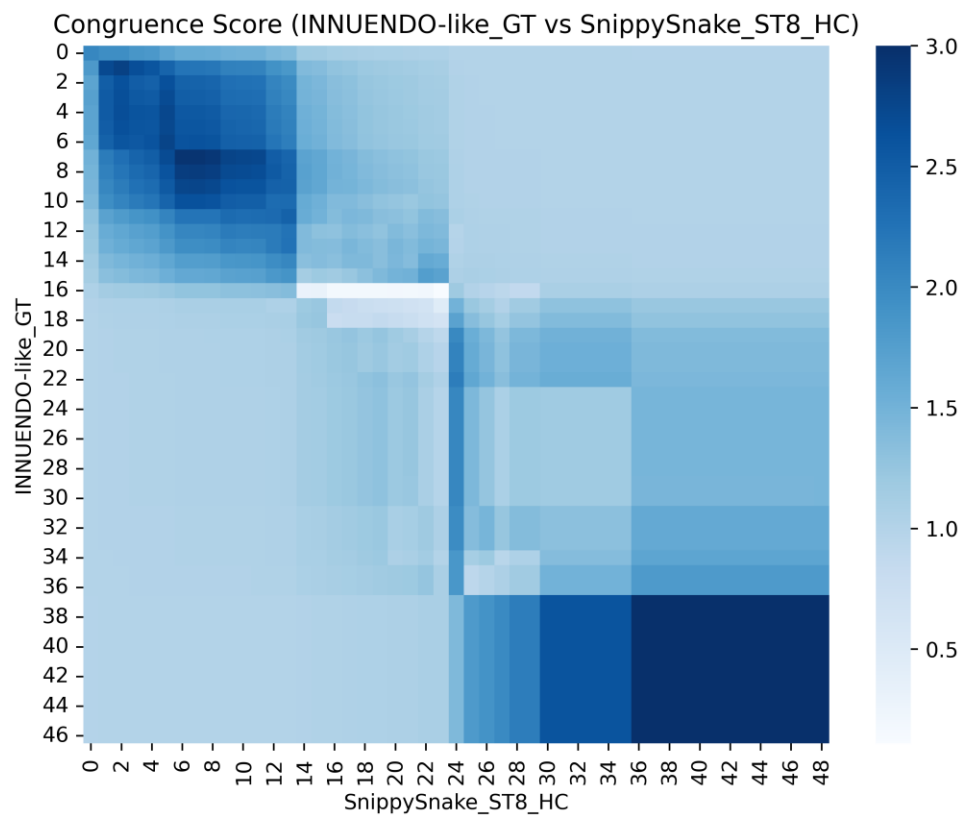


Figure S4.8.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

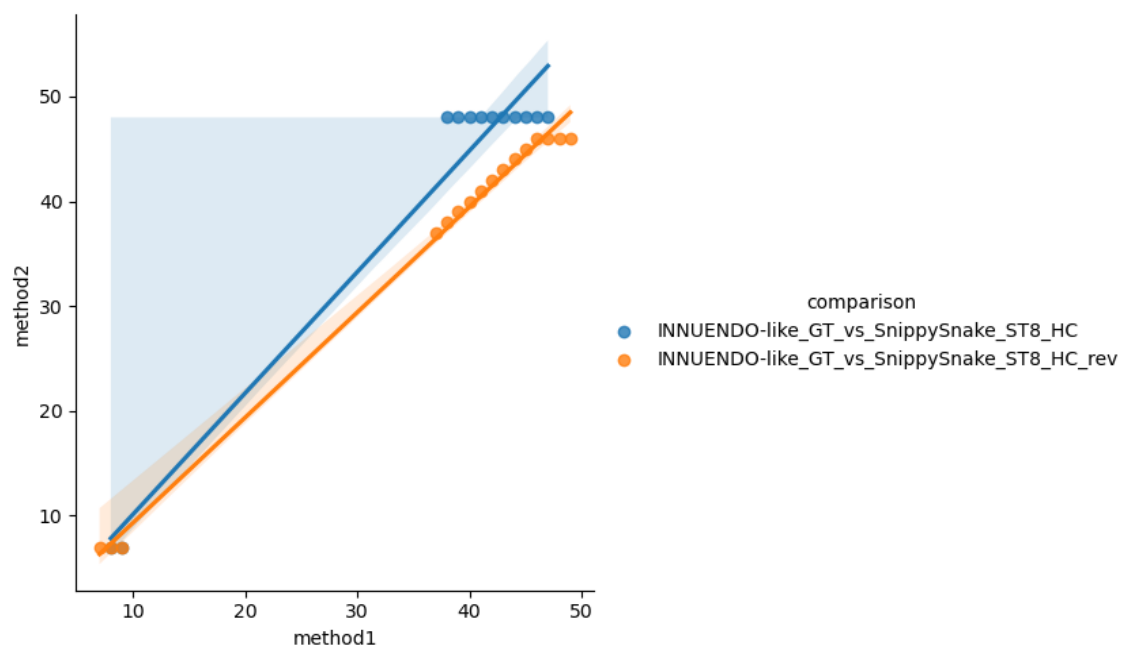


Figure S4.8.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 12 (blue) and 16 (orange) points is presented.

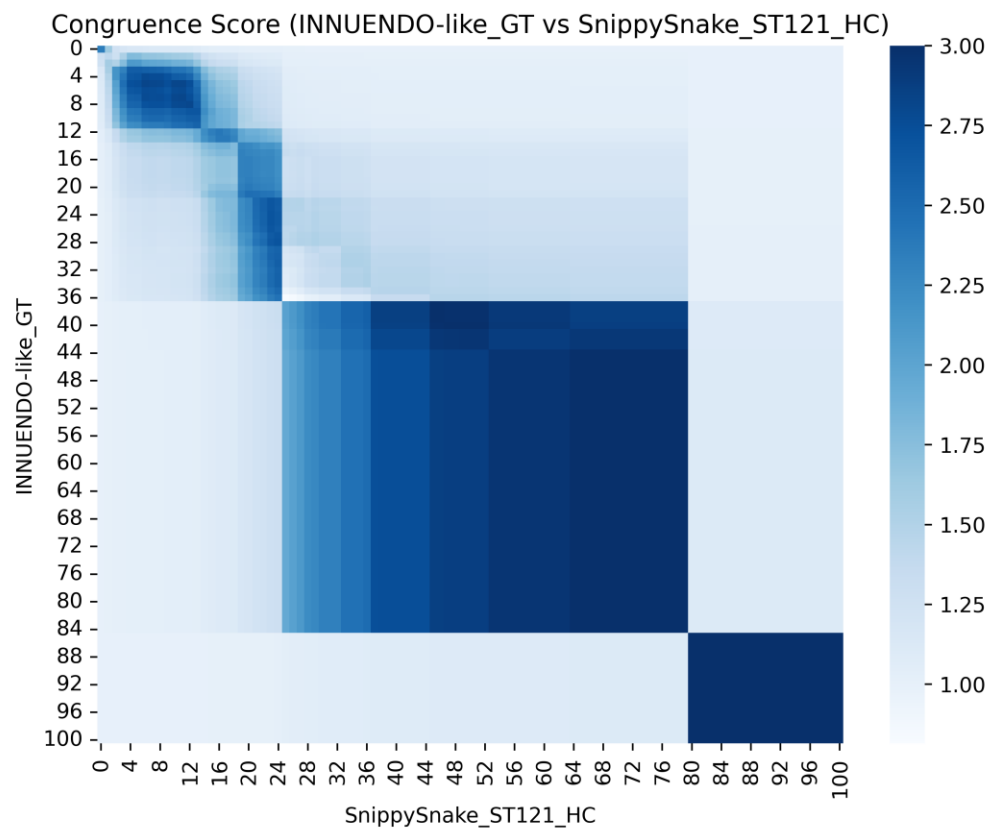


Figure S4.8.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

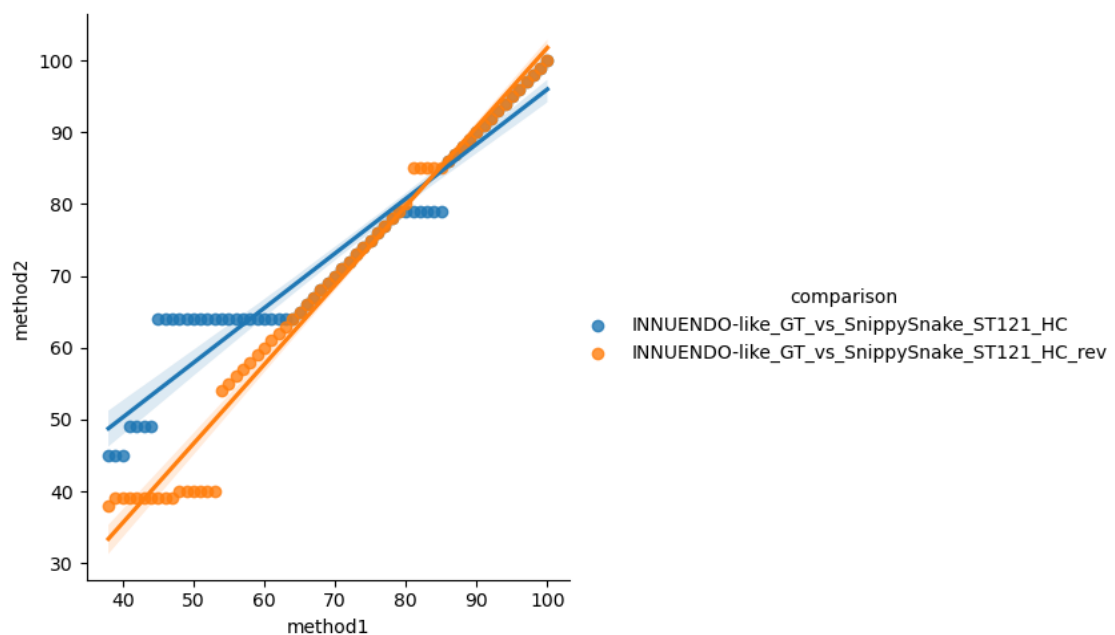


Figure S4.8.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 63 (blue) and 63 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

9. INNUENDO-like GrapeTree vs. WGSBAC 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 GrapeTree	WGSBAC single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

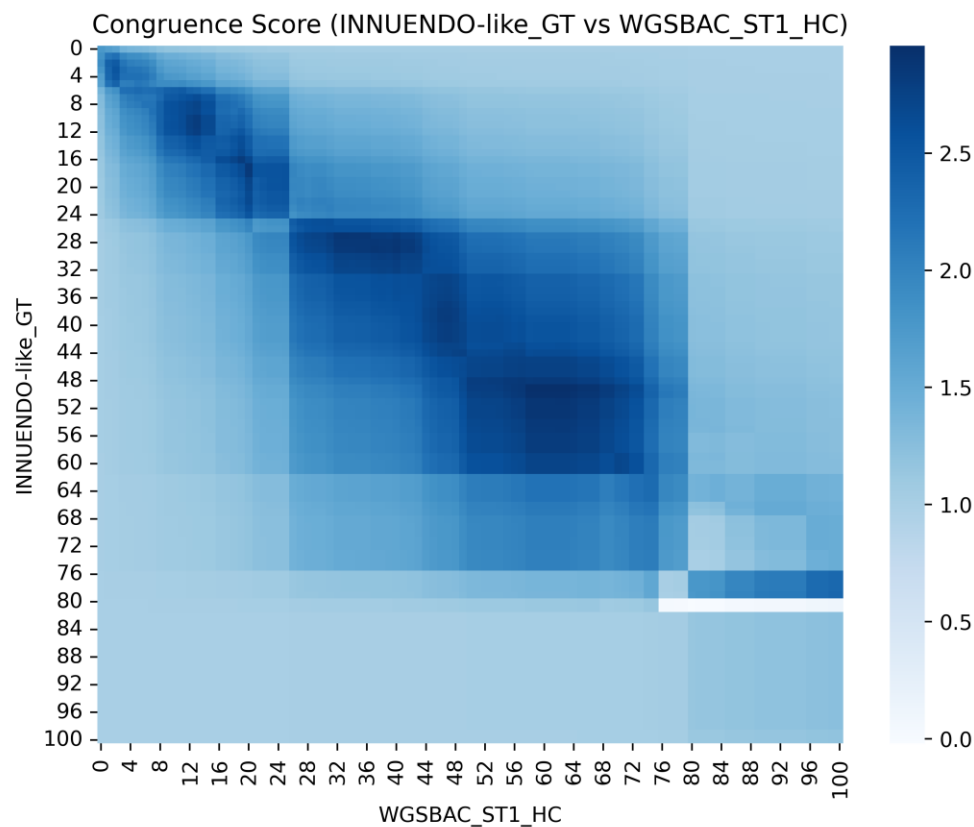


Figure S4.9.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

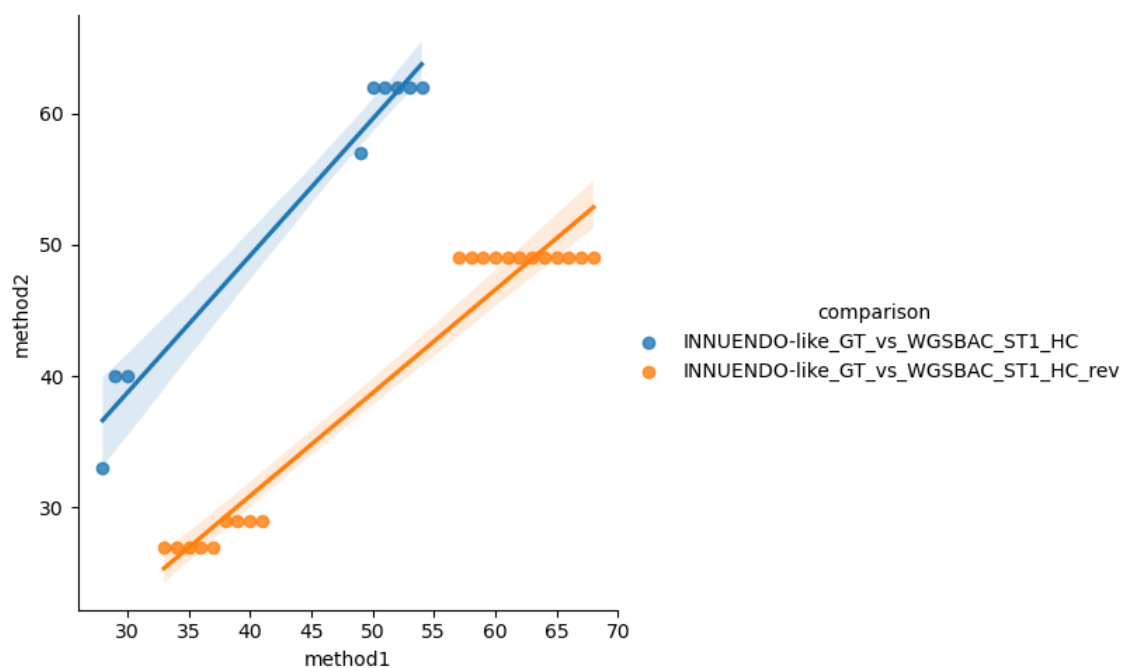


Figure S4.9.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 9 (blue) and 21 (orange) points is presented.

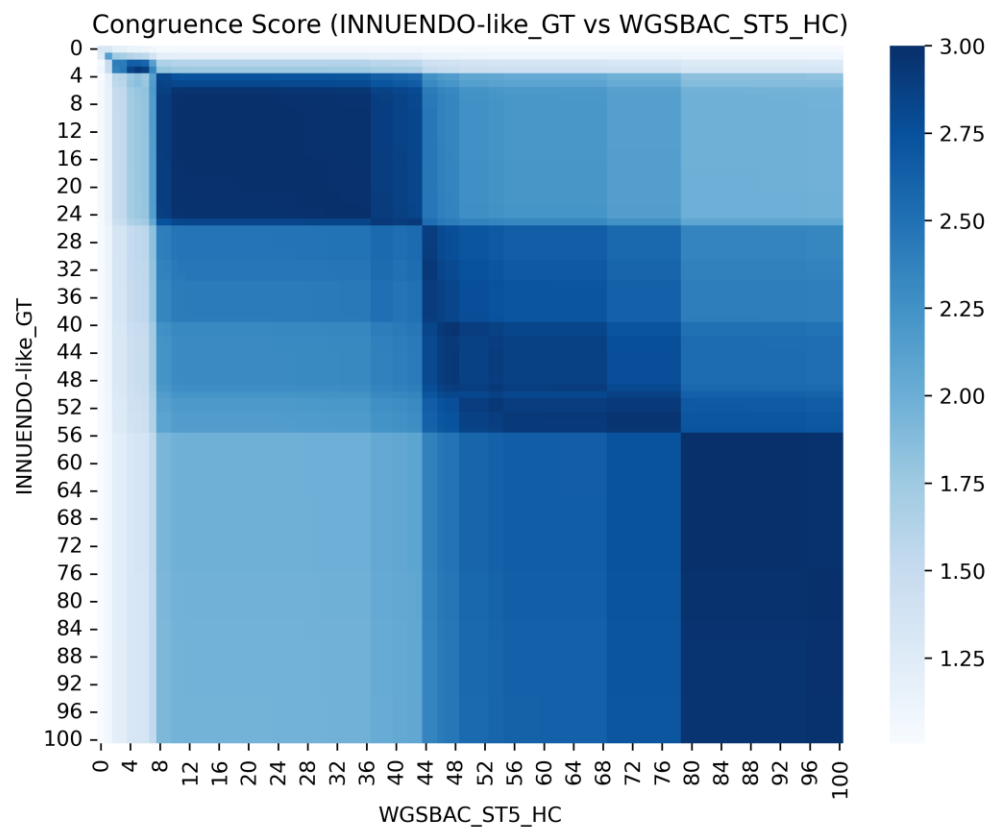


Figure S4.9.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

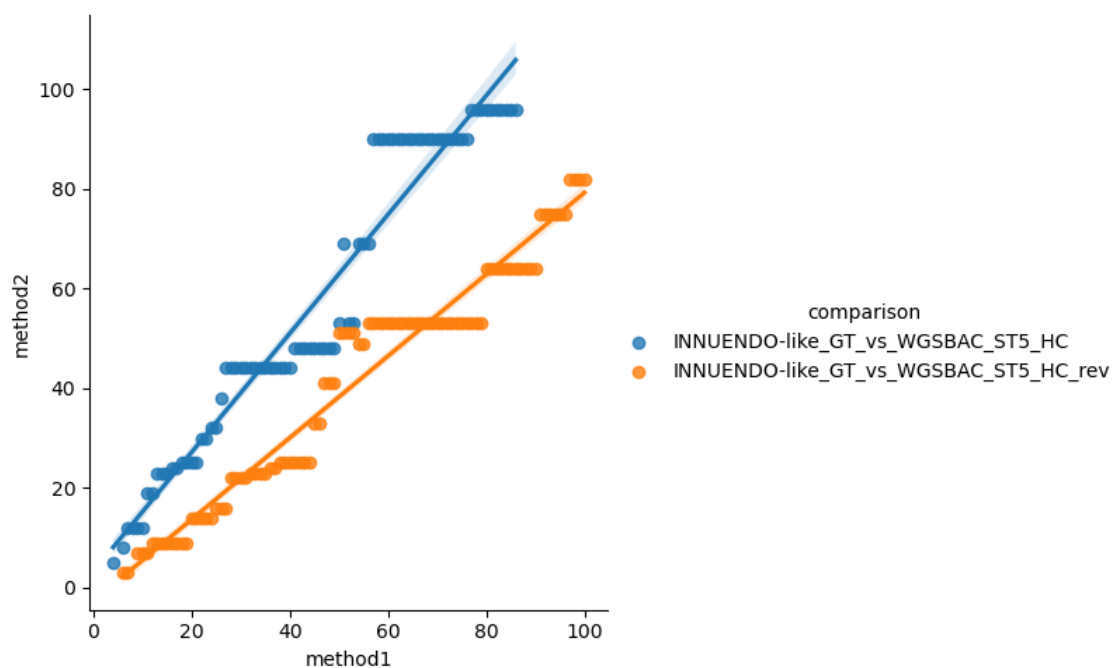


Figure S4.9.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 82 (blue) and 94 (orange) points is presented.

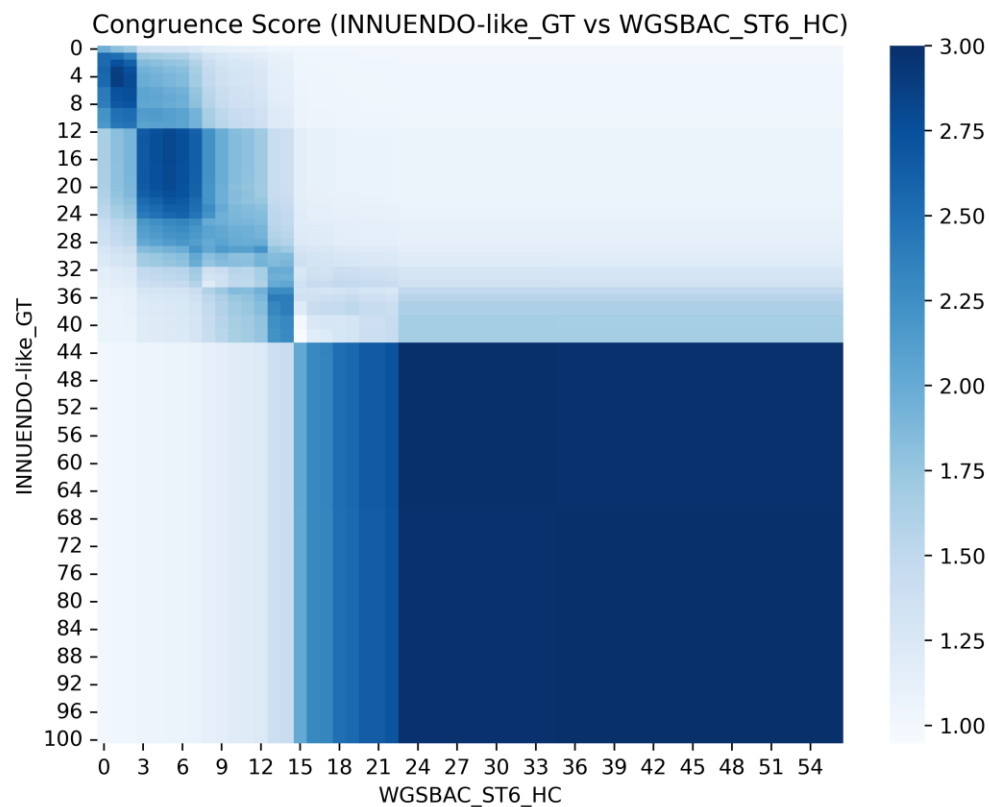


Figure S4.9.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

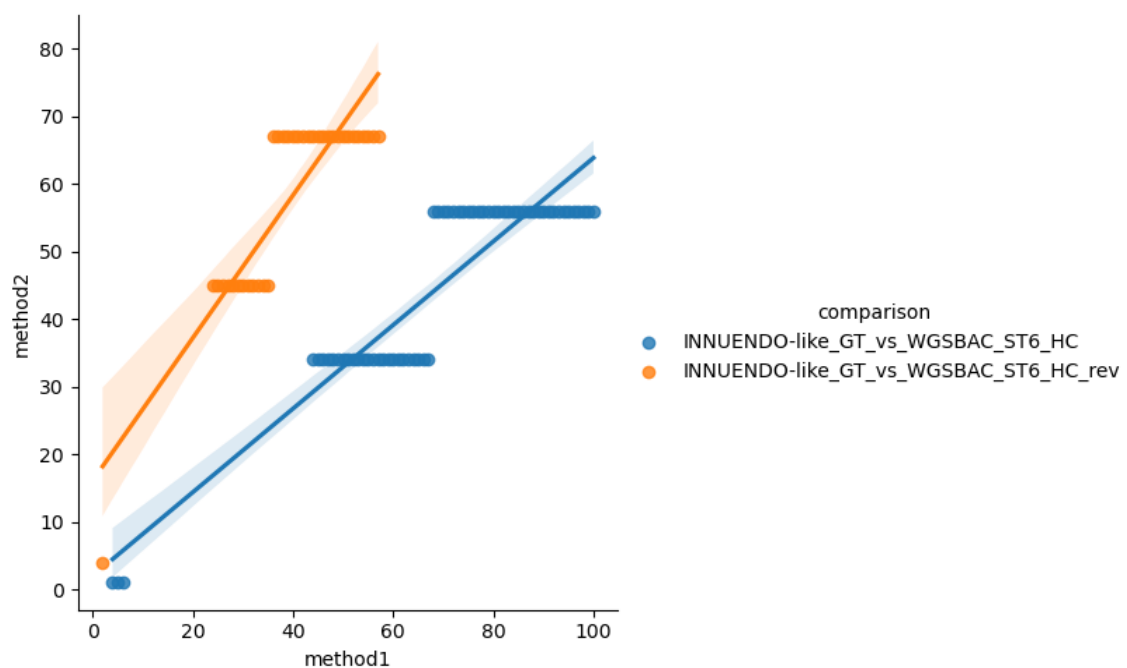


Figure S4.9.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 60 (blue) and 35 (orange) points is presented.

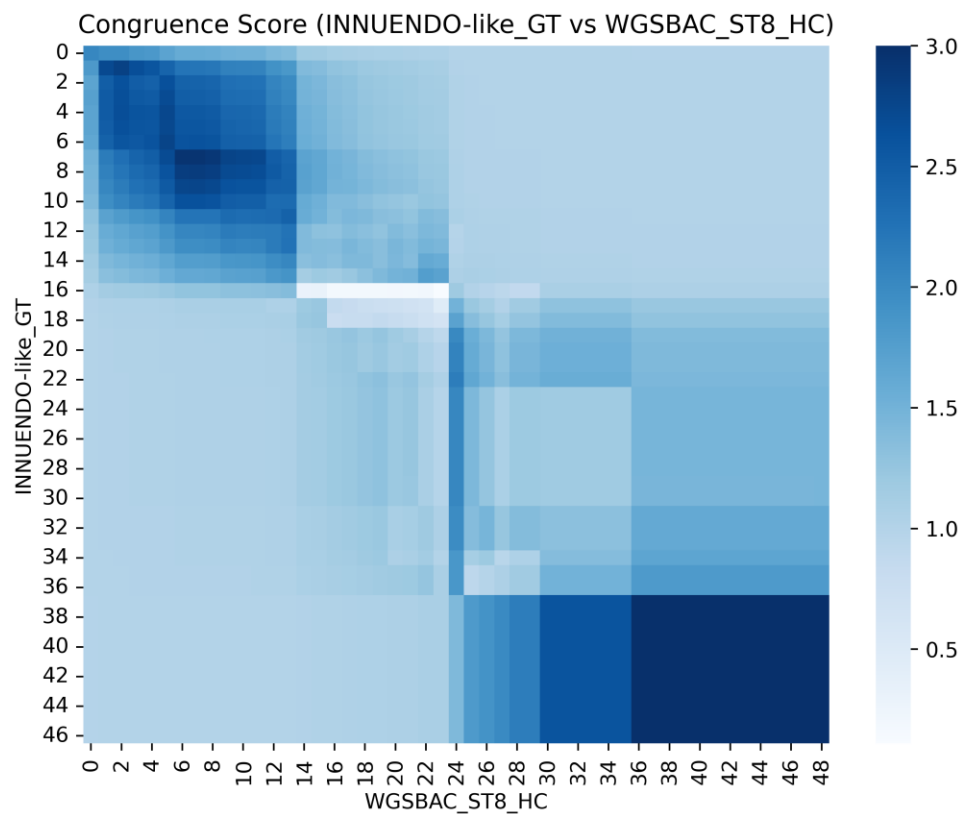


Figure S4.9.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

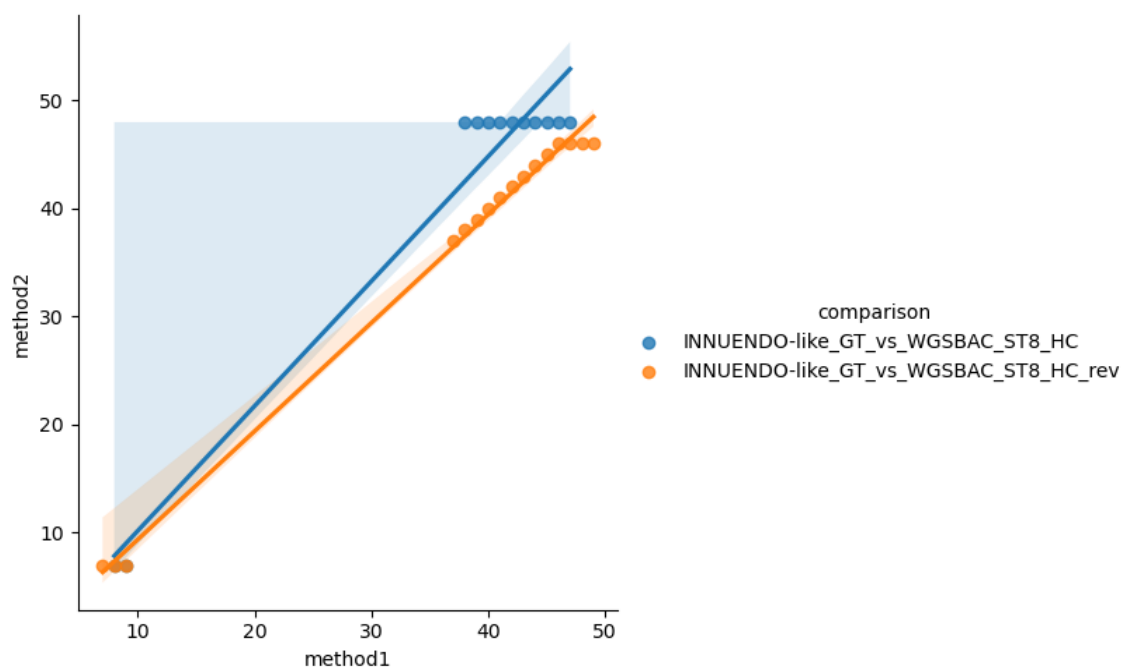


Figure S4.9.8. Corresponding points between the two pipelines in both directions (CS $\geq$ 2.85) of all partitions for ST8. A linear tendency line supported by 12 (blue) and 16 (orange) points is presented.

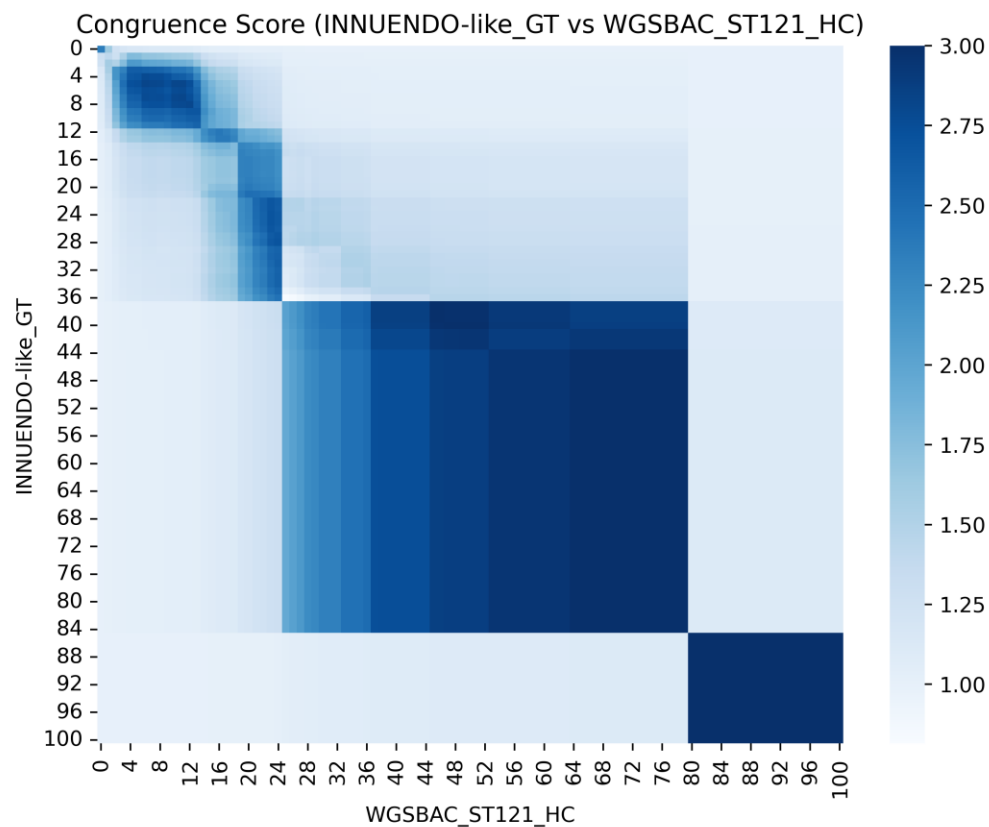


Figure S4.9.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

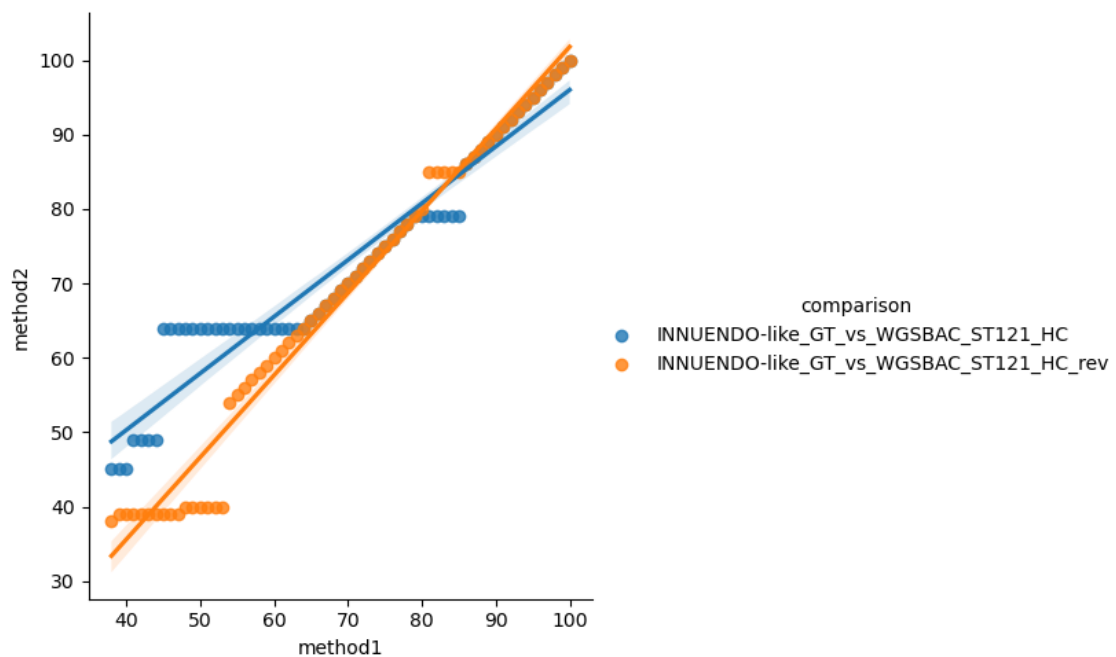


Figure S4.9.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 63 (blue) and 63 (orange) points is presented

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

10. INNUENDO-like single-linkage 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 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	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

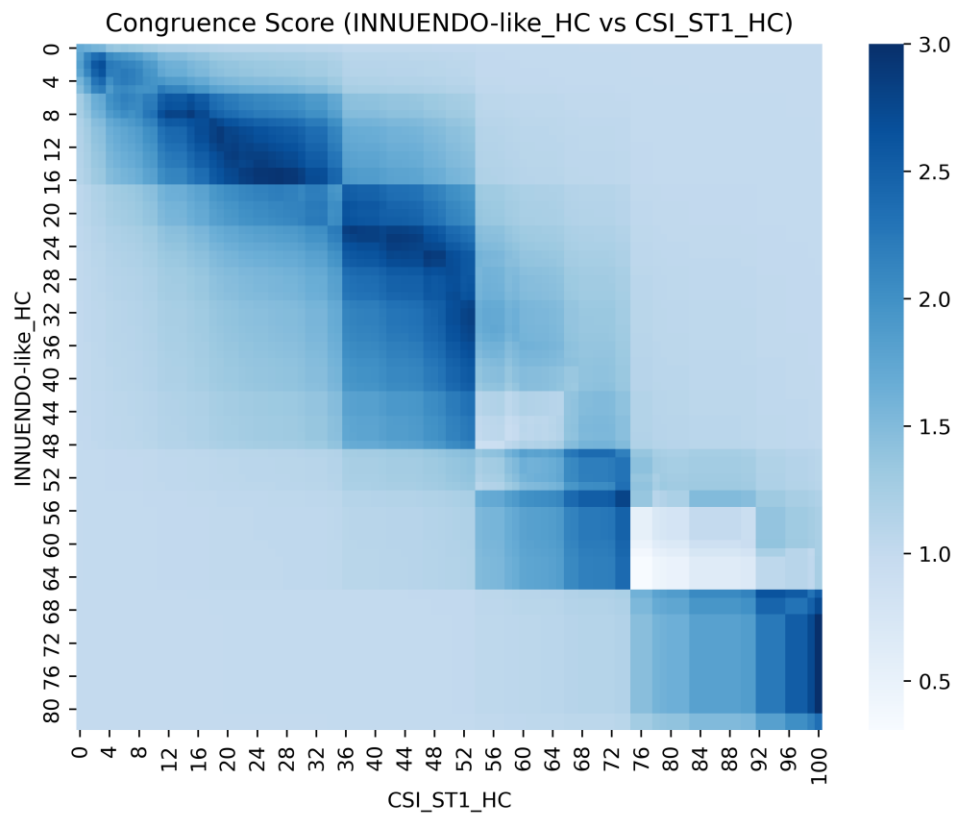


Figure S4.10.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

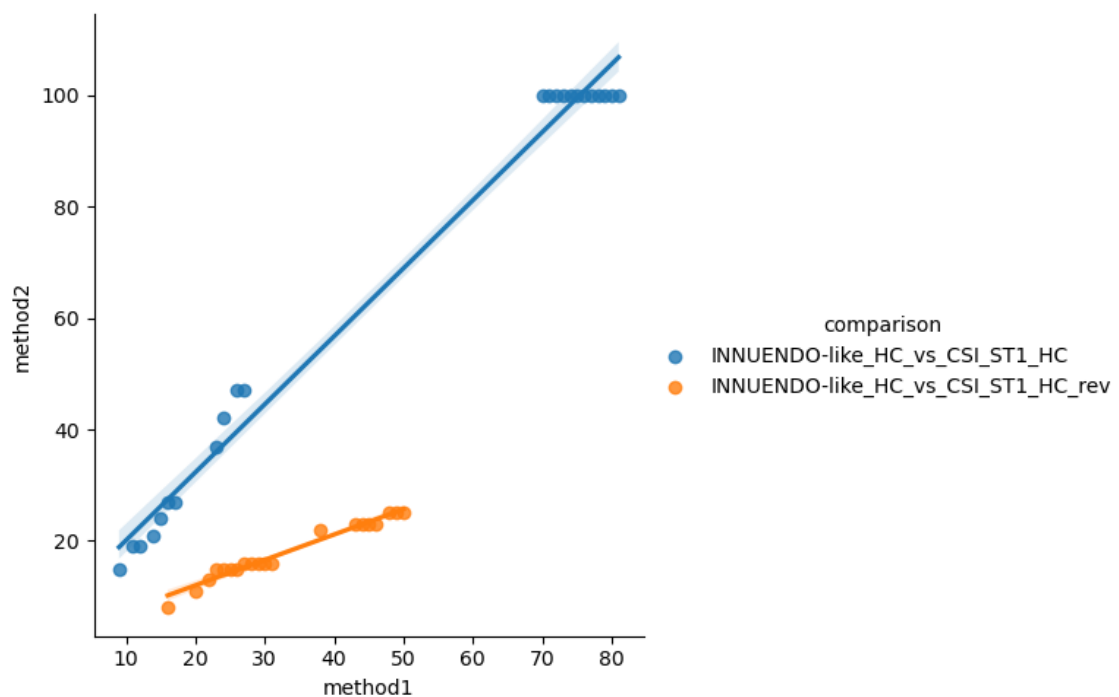


Figure S4.10.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 23 (blue) and 20 (orange) points is presented.

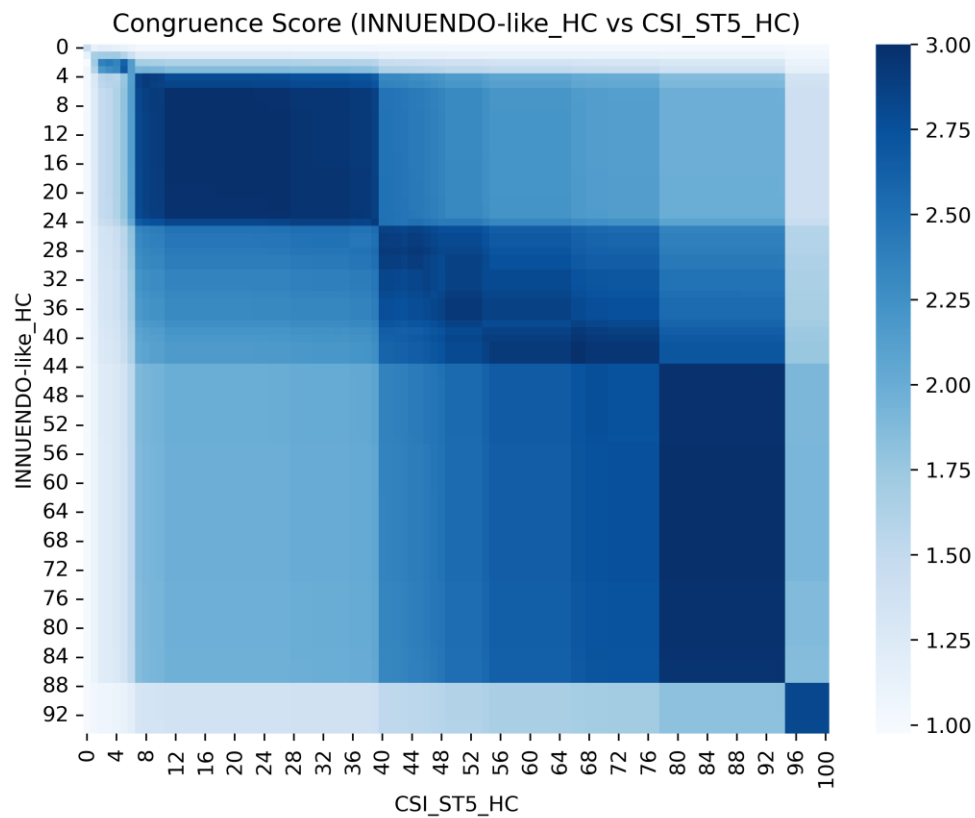


Figure S4.10.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

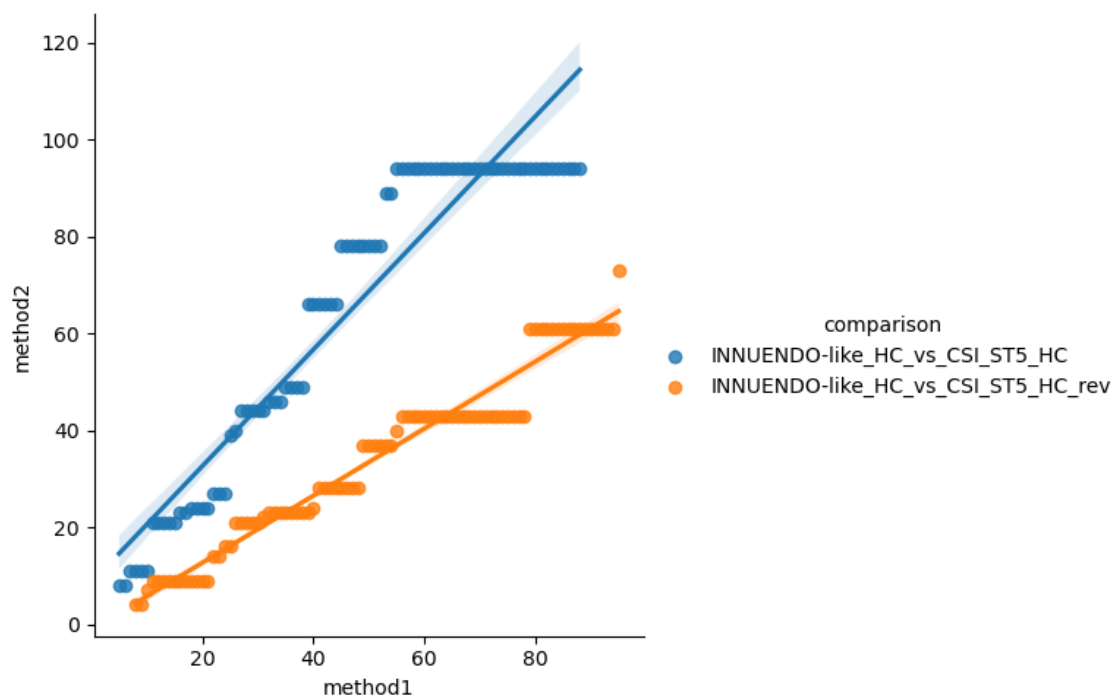


Figure S4.10.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 84 (blue) and 88 (orange) points is presented.

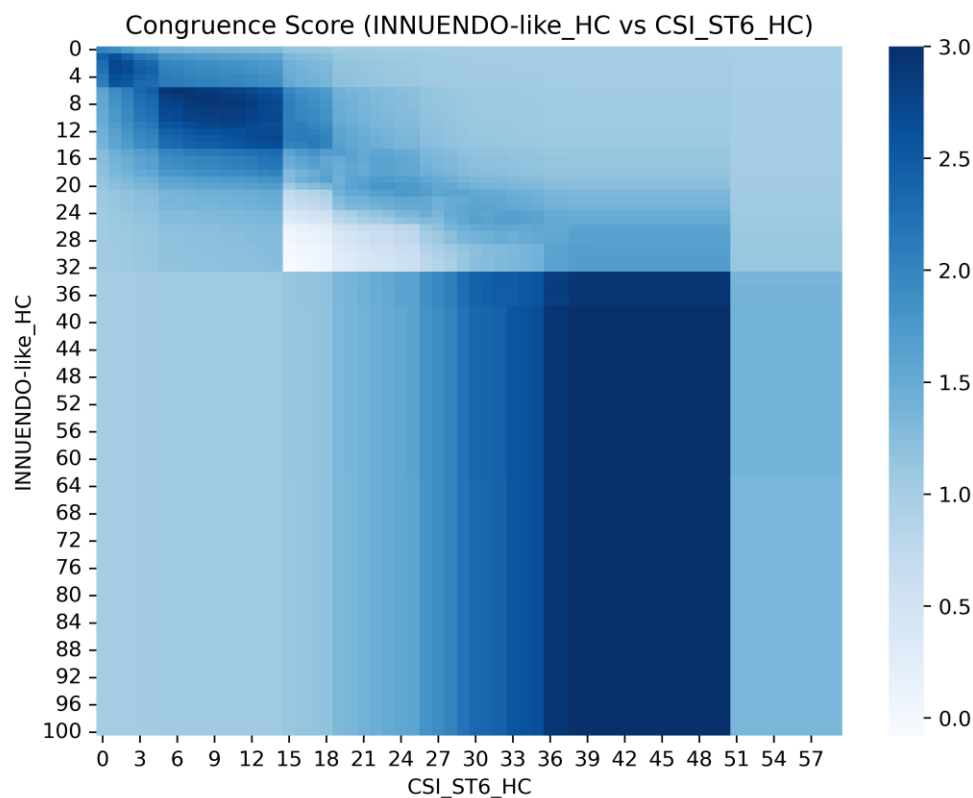


Figure S4.10.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

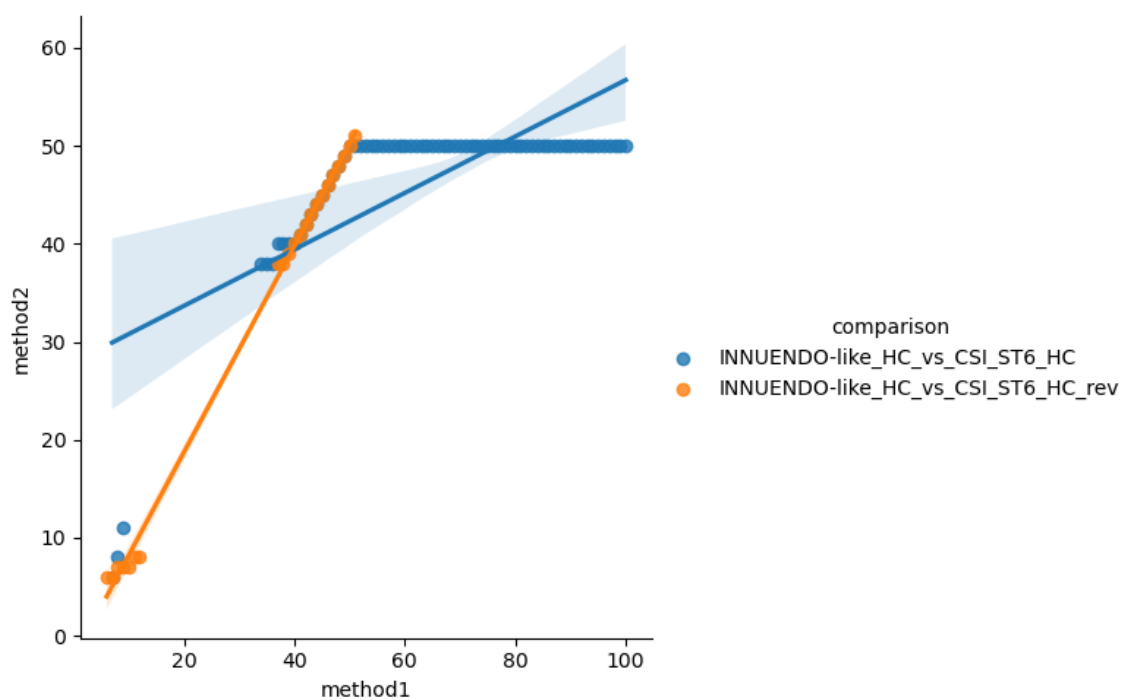


Figure S4.10.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 70 (blue) and 22 (orange) points is presented.

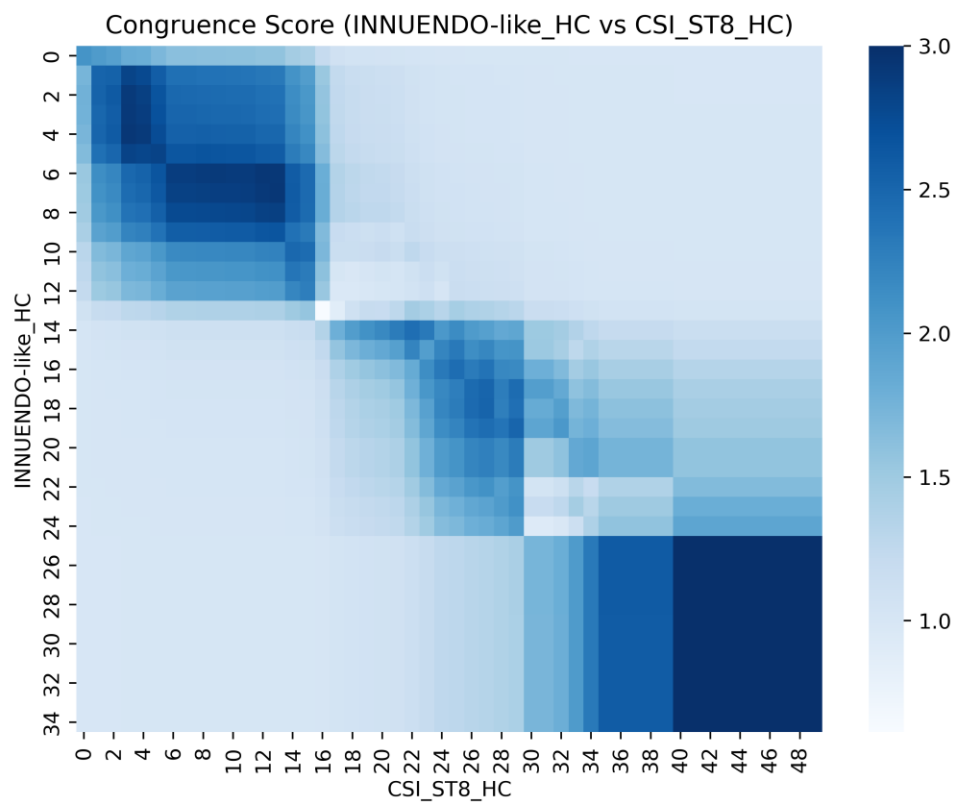


Figure S4.10.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

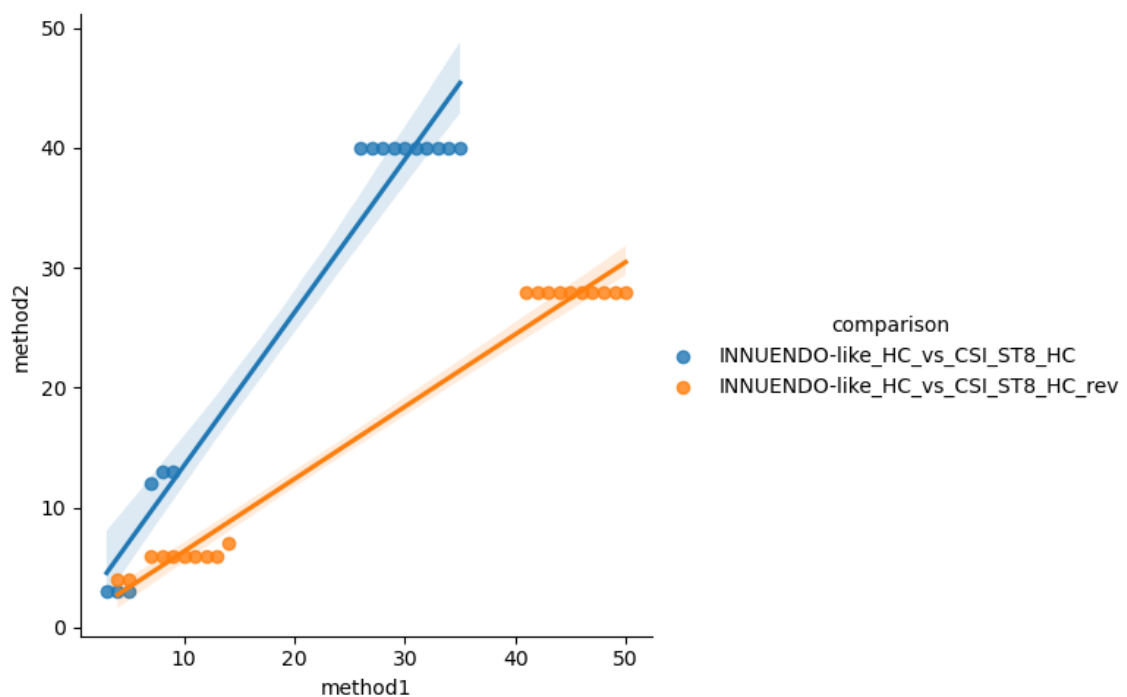


Figure S4.10.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 16 (blue) and 20 (orange) points is presented.

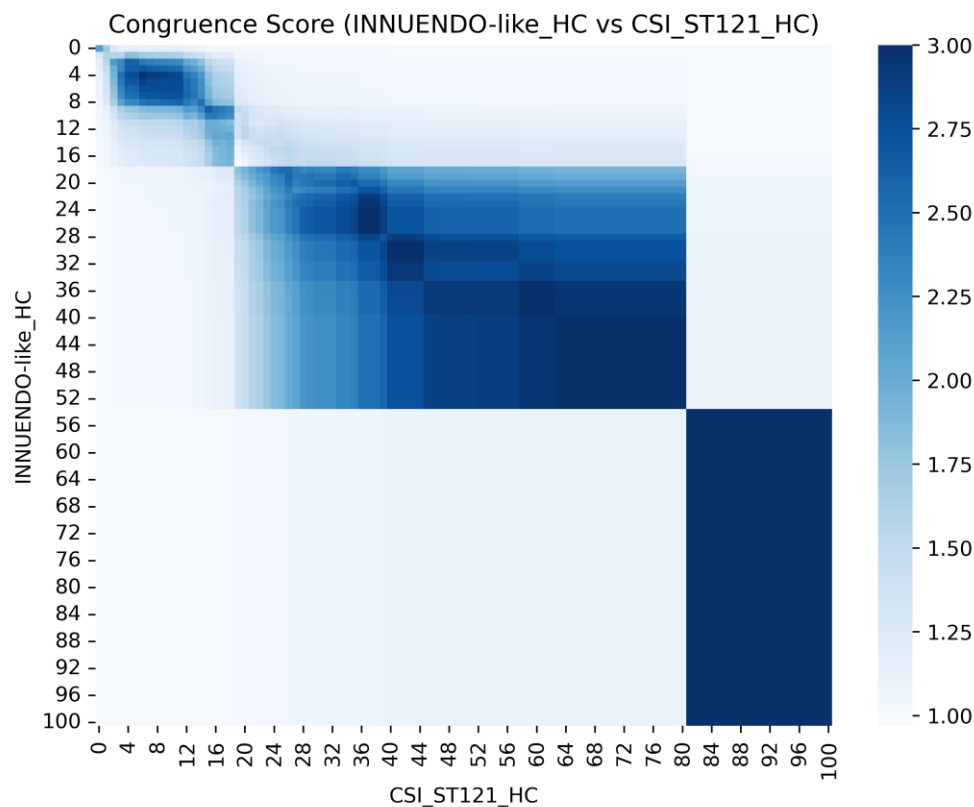


Figure S4.10.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

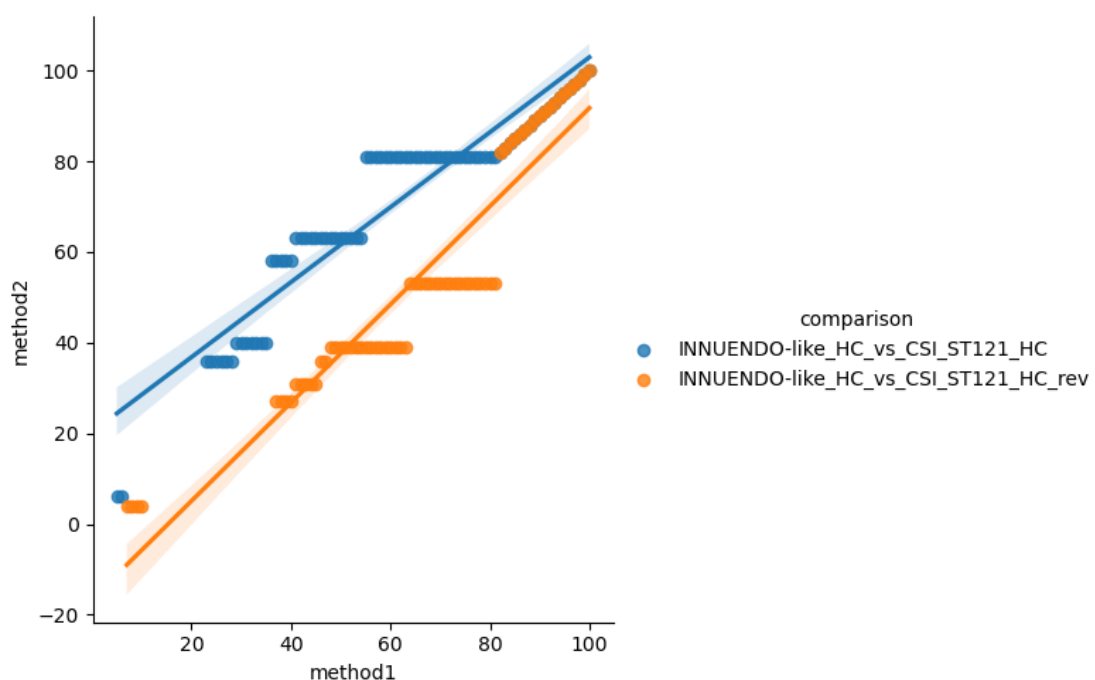


Figure S4.10.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST121. A linear tendency line supported by 80 (blue) and 68 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

11. INNUENDO-like single-linkage vs. snippySnake 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 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	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

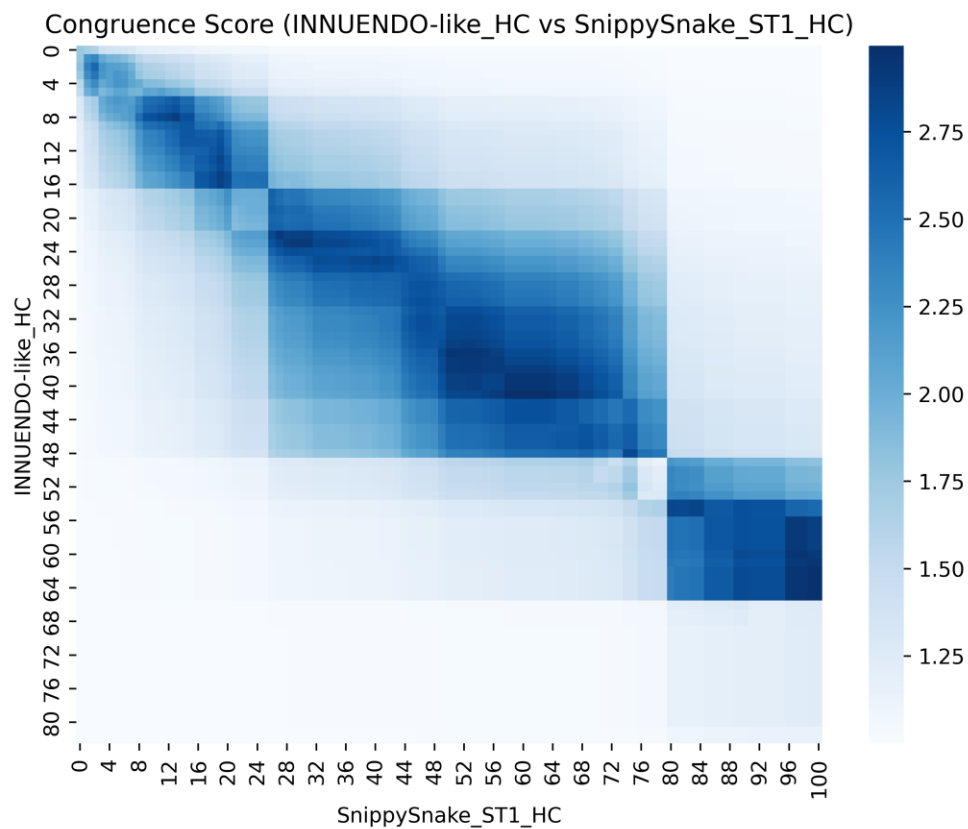


Figure S4.11.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

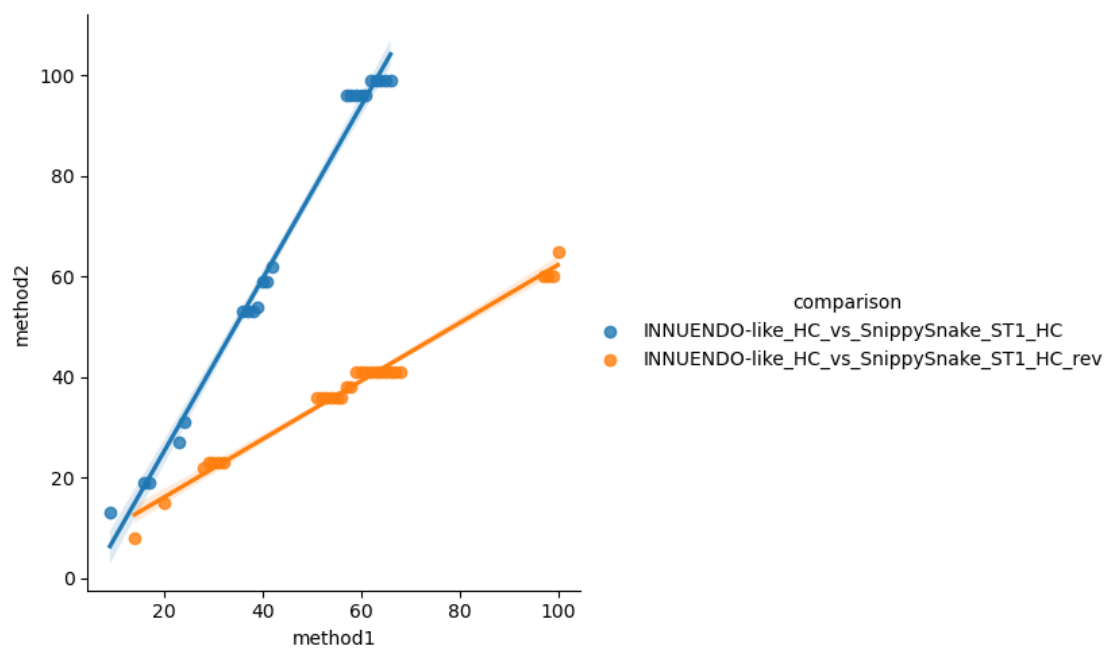


Figure S4.11.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST1. A linear tendency line supported by 22 (blue) and 29 (orange) points is presented.

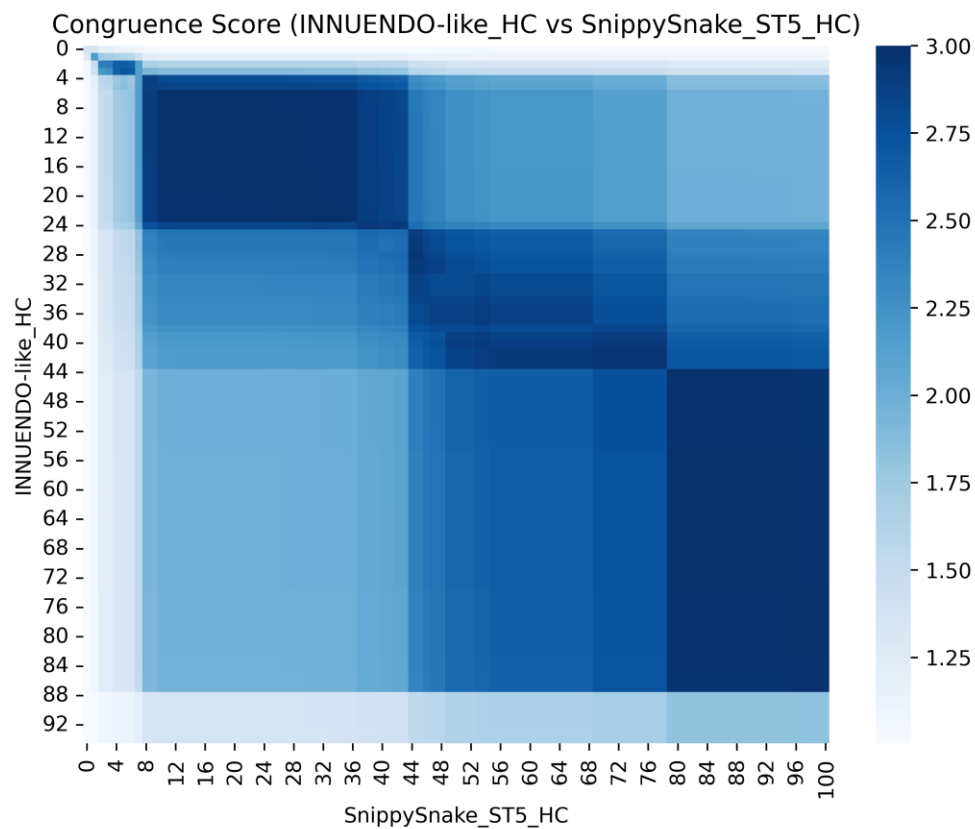


Figure S4.11.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

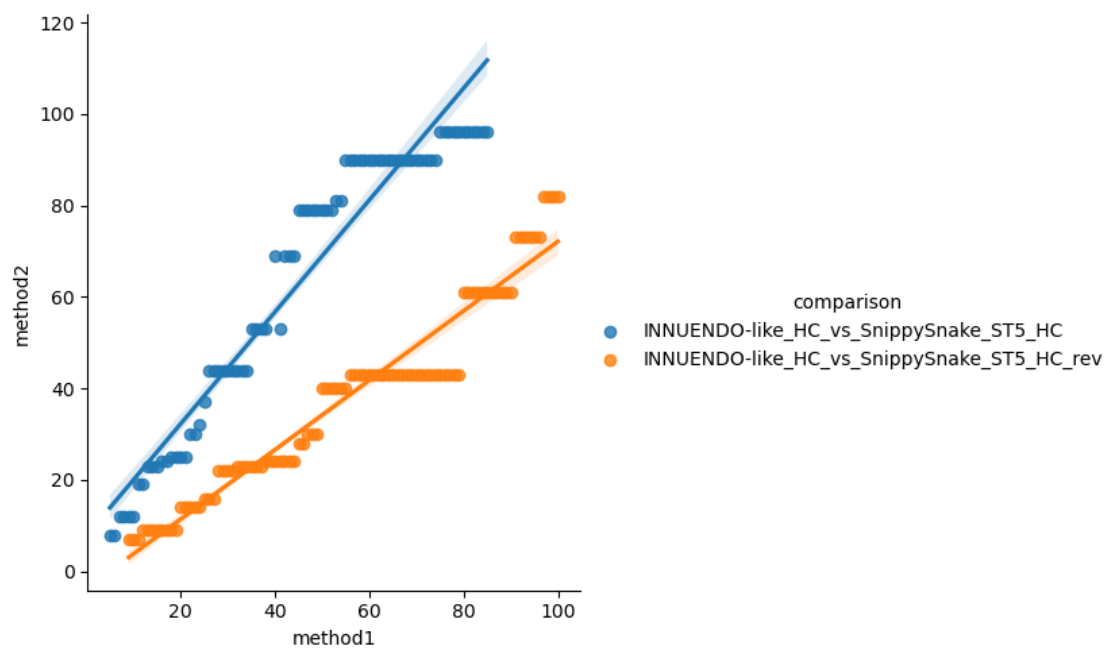


Figure S4.11.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 80 (blue) and 92 (orange) points is presented.

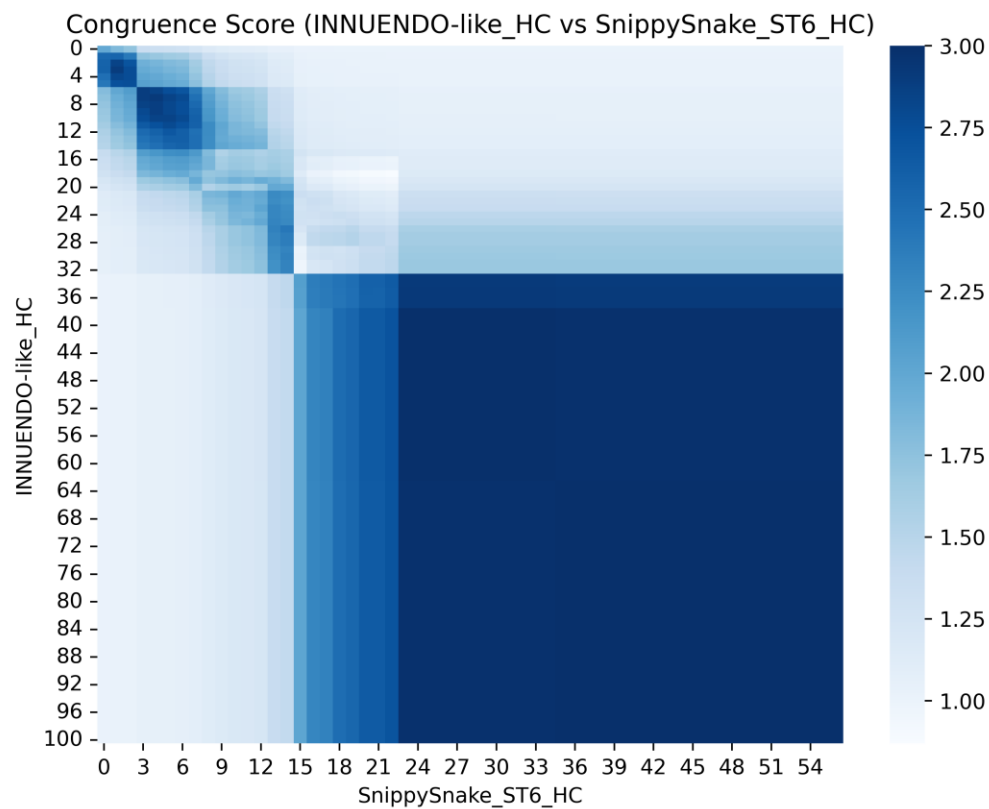


Figure S4.11.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

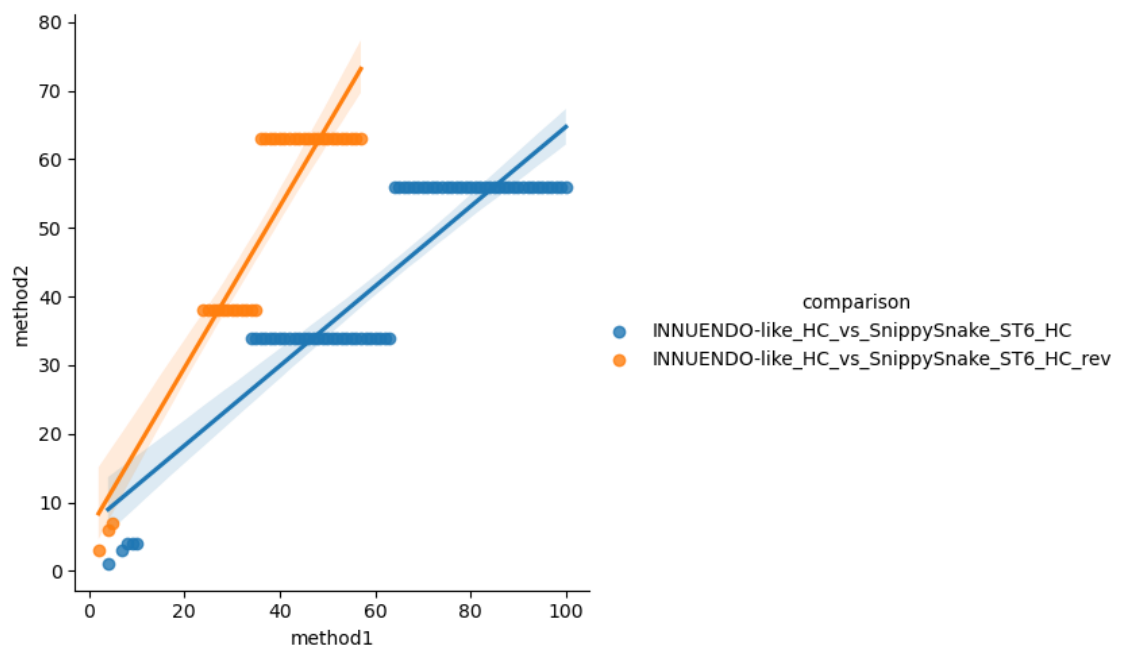


Figure S4.11.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 72 (blue) and 37 (orange) points is presented.

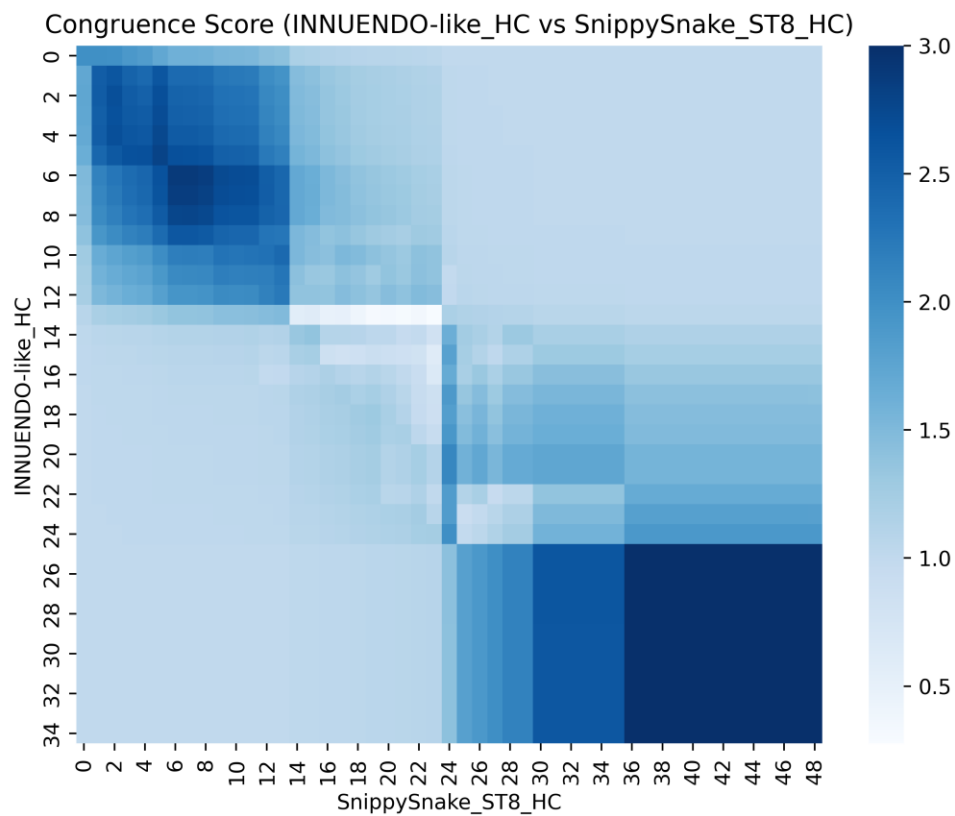


Figure S4.11.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

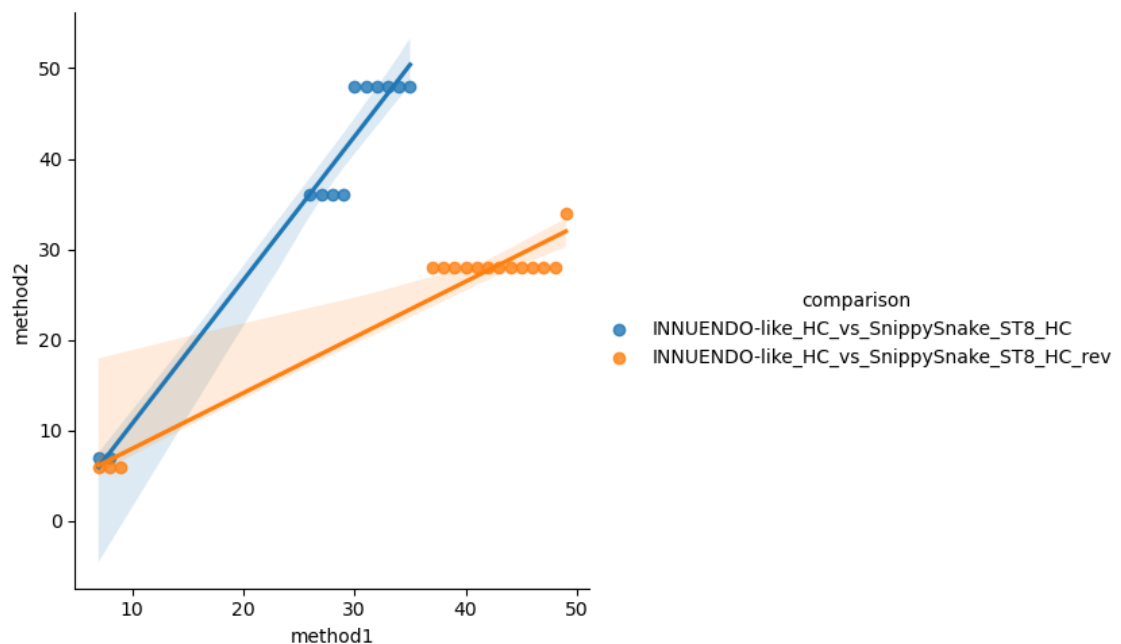


Figure S4.11.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 12 (blue) and 16 (orange) points is presented.

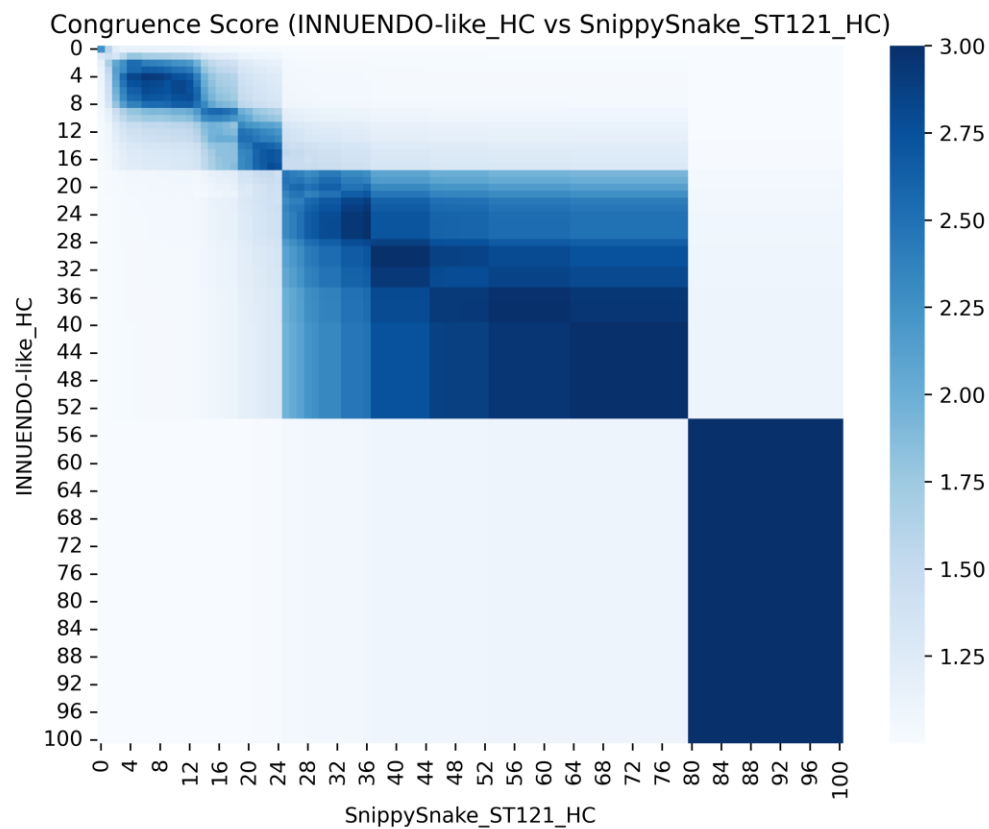


Figure S4.11.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

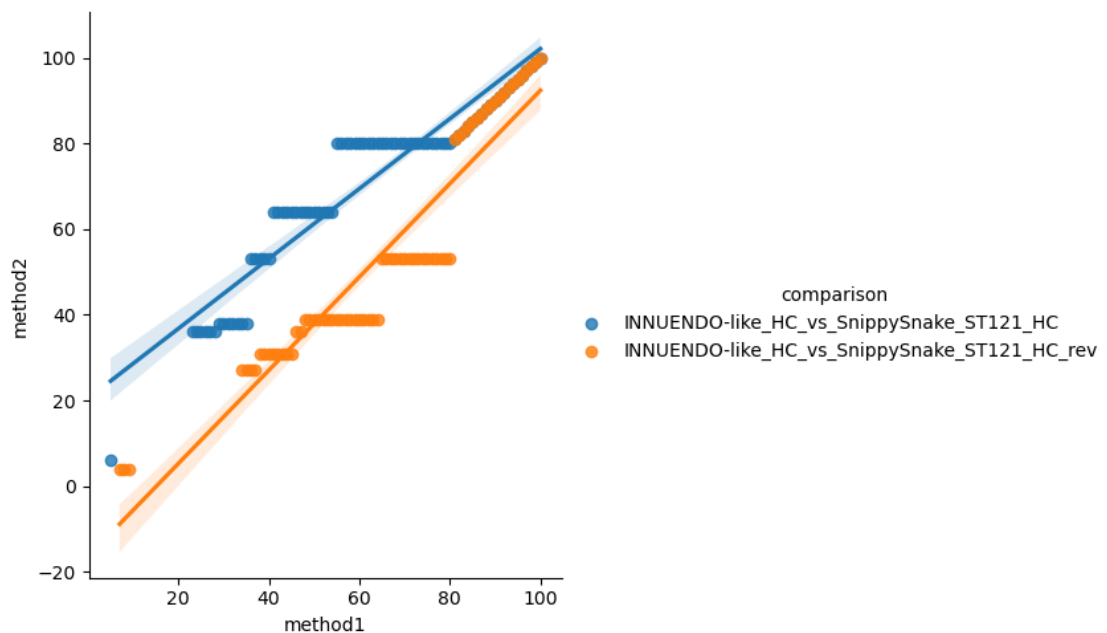


Figure S4.11.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 79 (blue) and 70 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

12. INNUENDO-like single-linkage vs. WGSBAC 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 single-linkage	WGSBAC single-linkage
Pipeline version	chewBBACA 2.8.5	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

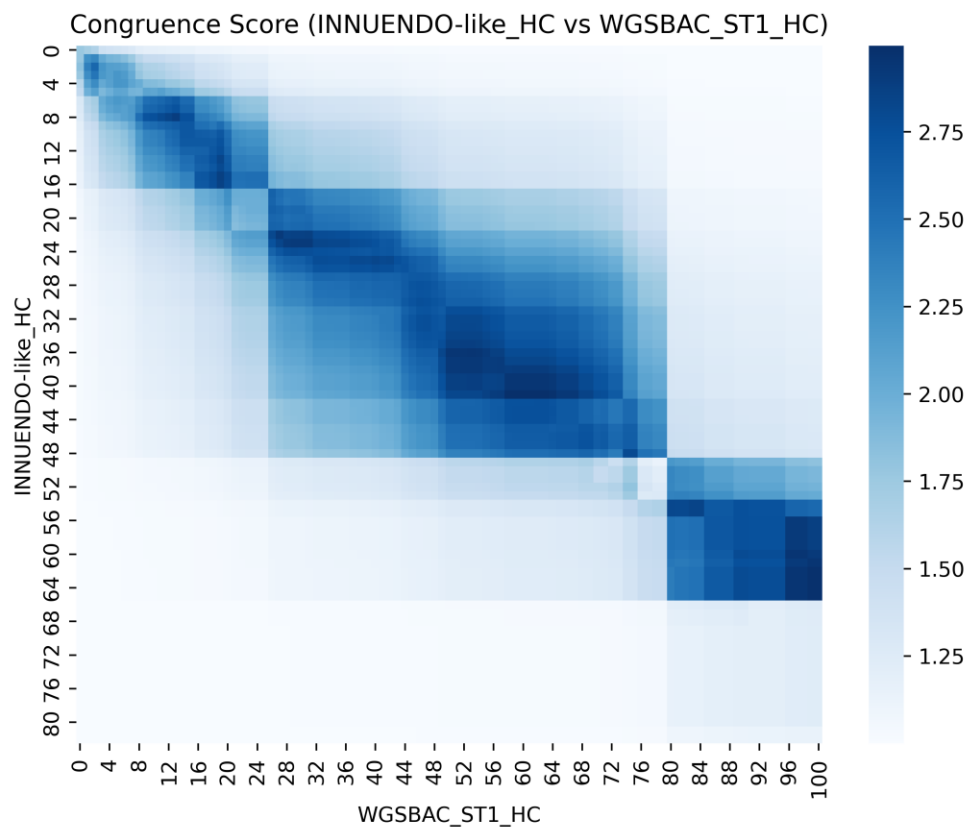


Figure S4.12.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

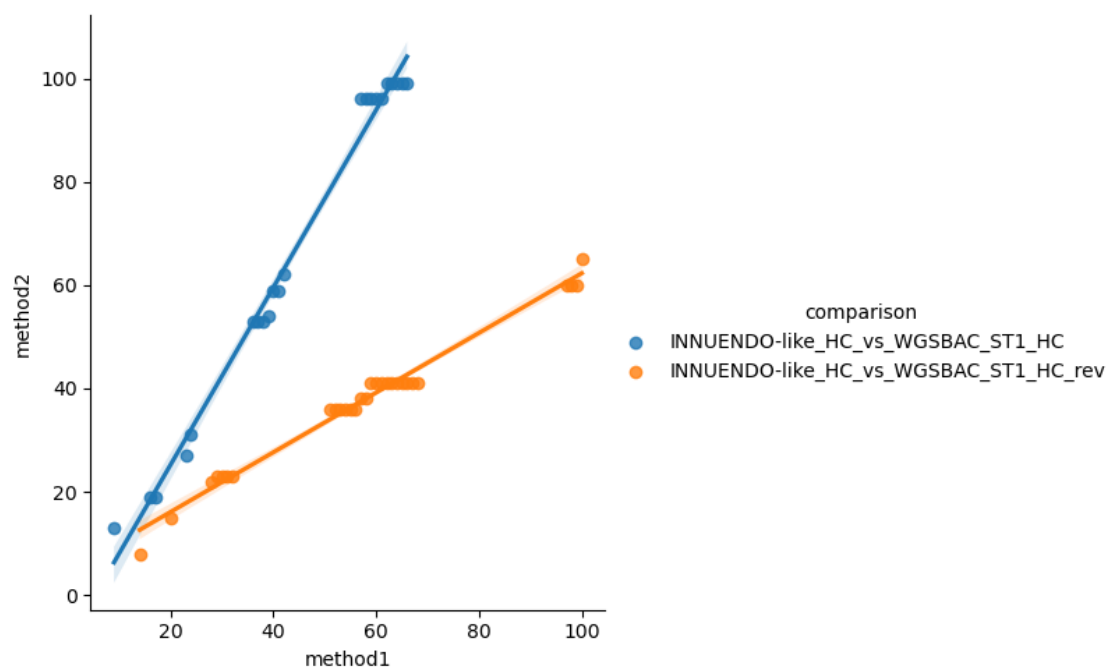


Figure S4.12.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST1. A linear tendency line supported by 22 (blue) and 29 (orange) points is presented.

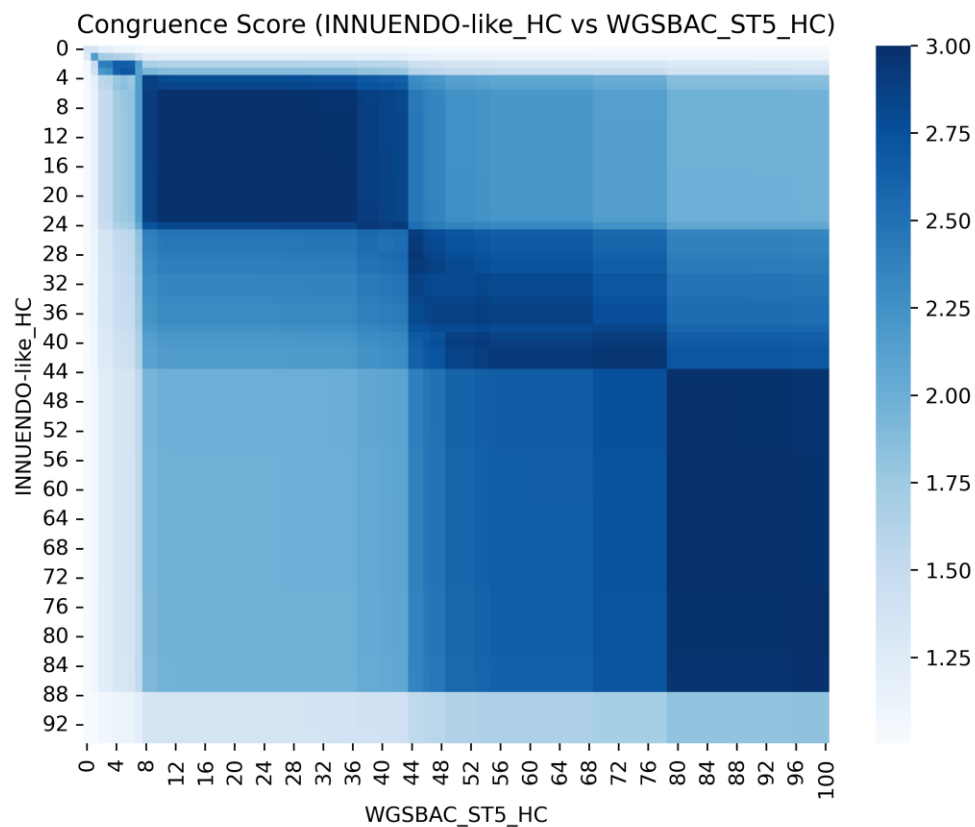


Figure S4.12.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

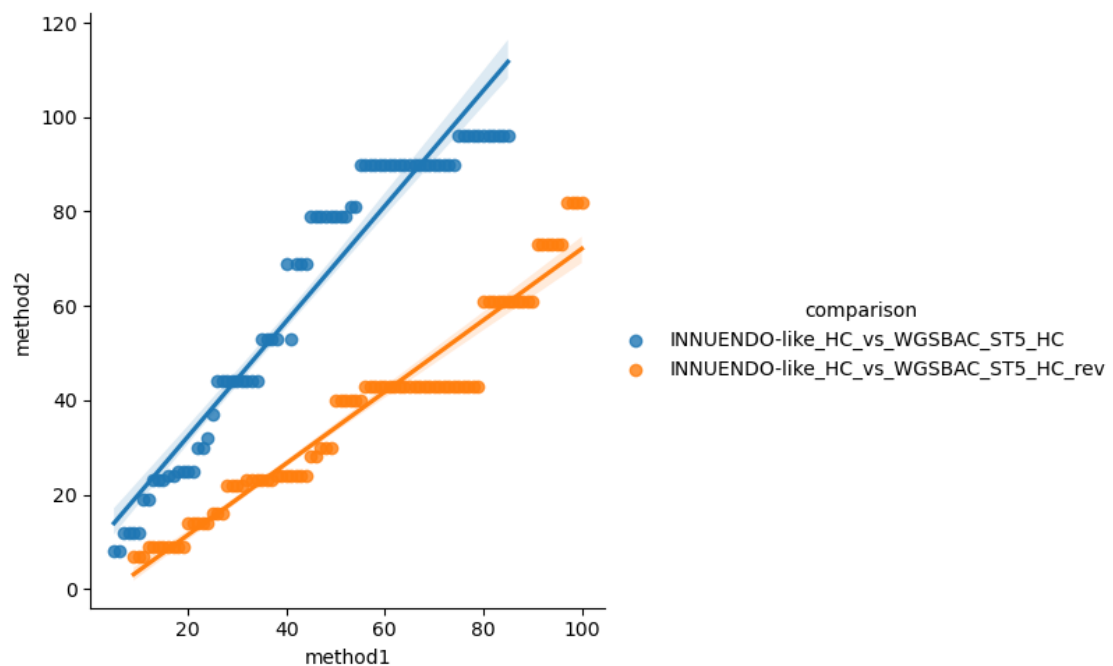


Figure S4.12.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST5. A linear tendency line supported by 80 (blue) and 92 (orange) points is presented.

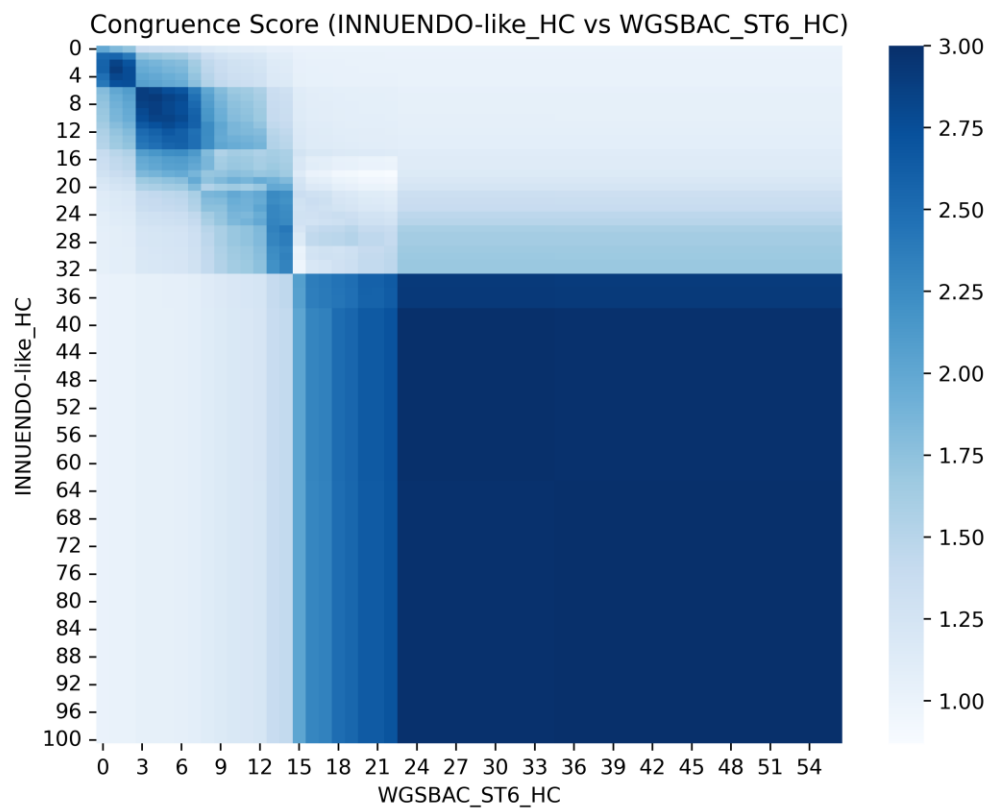


Figure S4.12.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

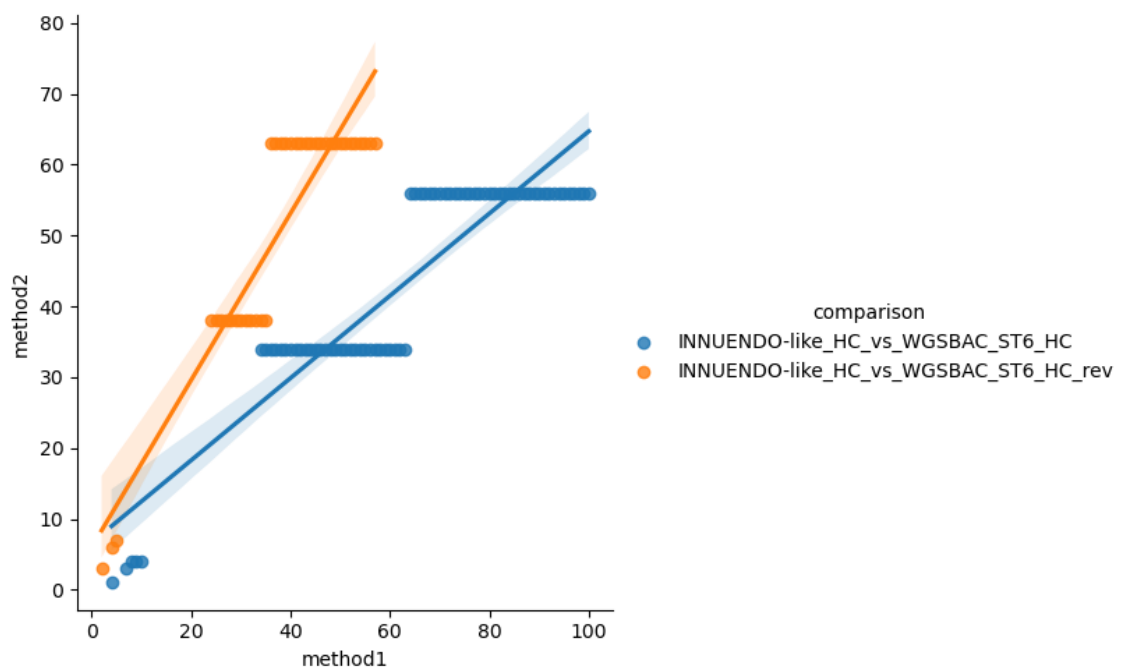


Figure S4.12.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 72 (blue) and 37 (orange) points is presented.

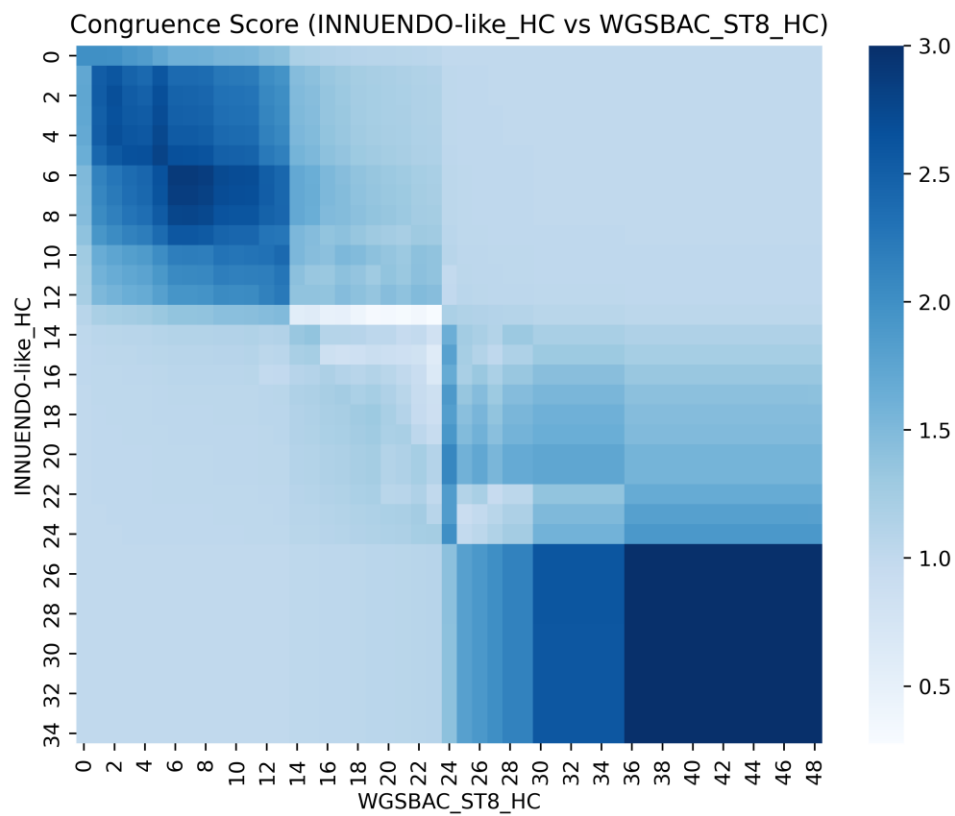


Figure S4.12.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

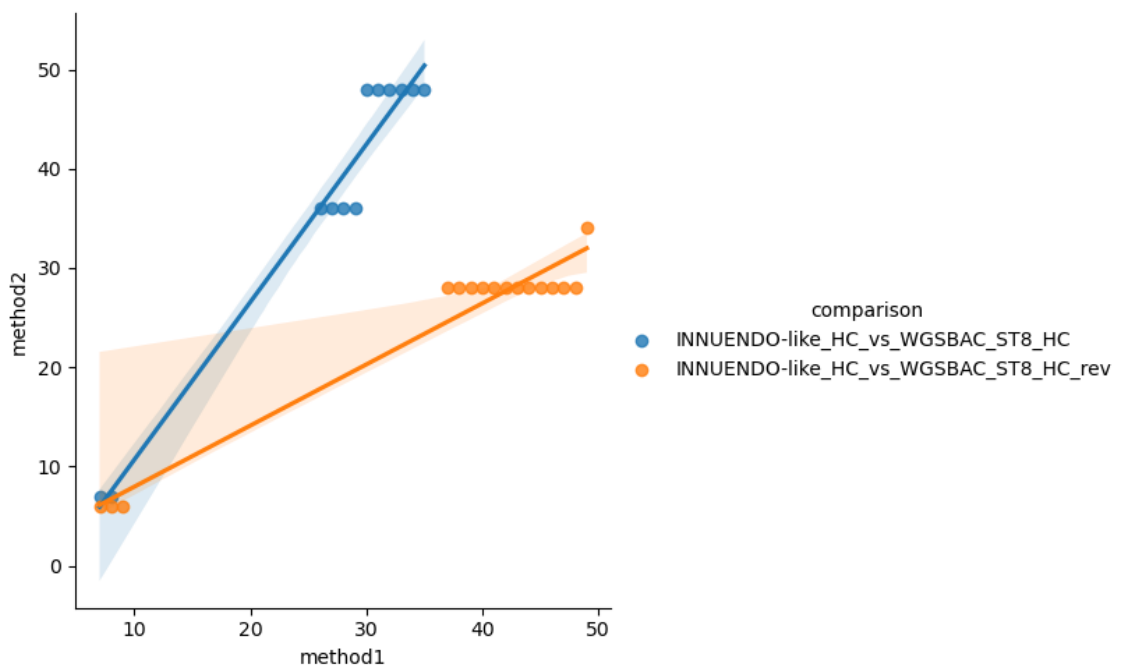


Figure S4.12.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 12 (blue) and 16 (orange) points is presented.

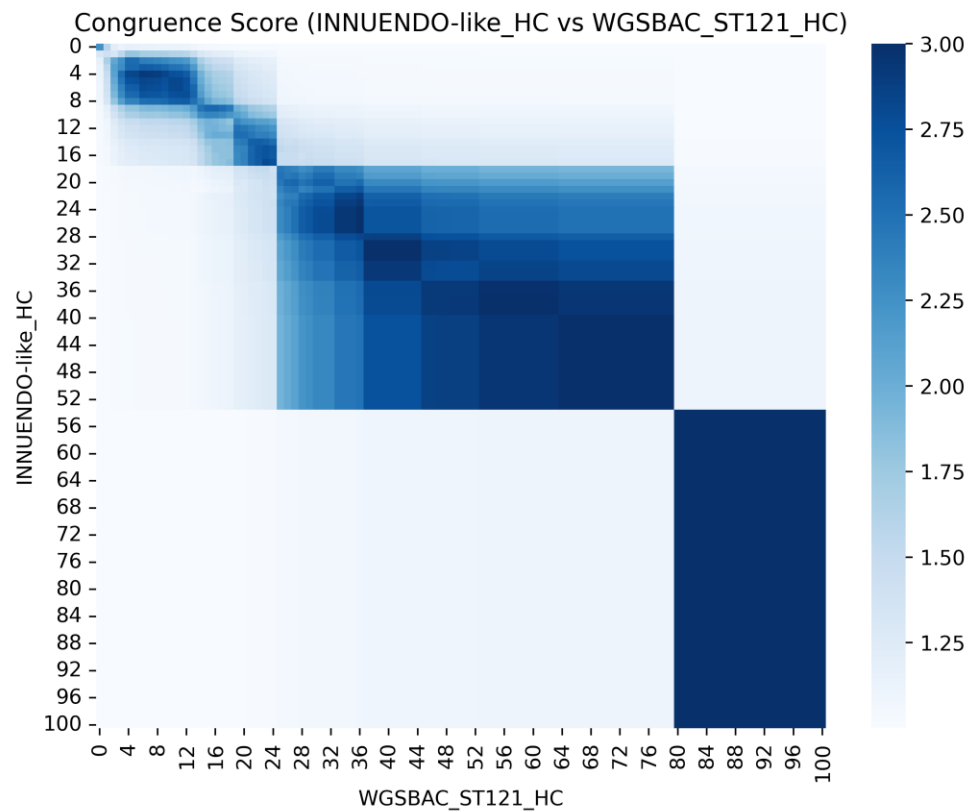


Figure S4.12.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

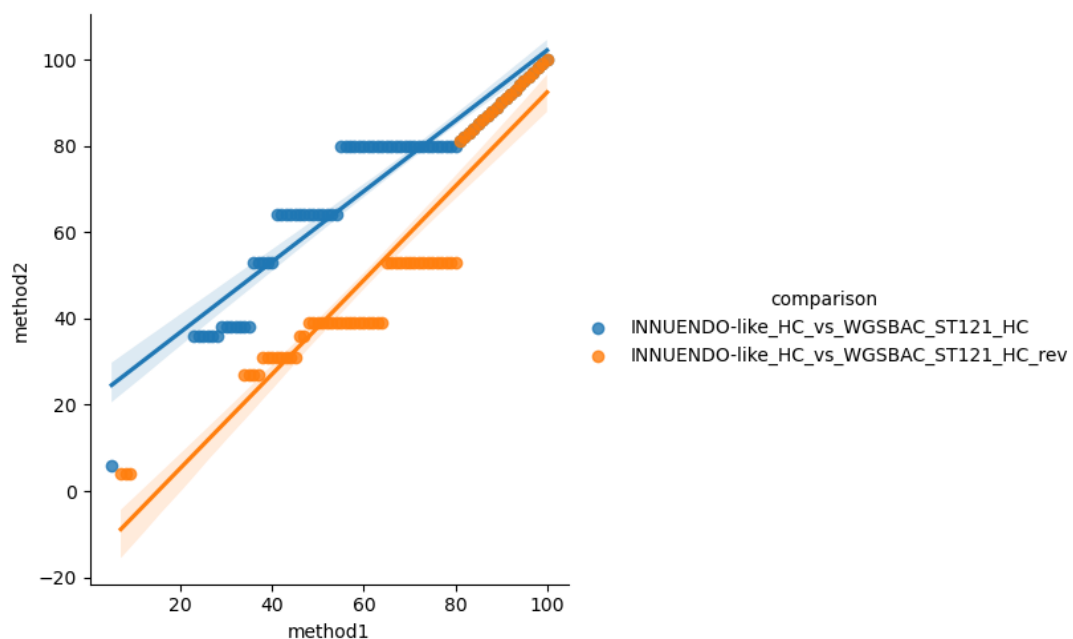


Figure S4.12.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST121. A linear tendency line supported by 79 (blue) and 70 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

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

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

	Bionumerics single-linkage	CSI Phylogeny single-linkage
Pipeline version	v8.1	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

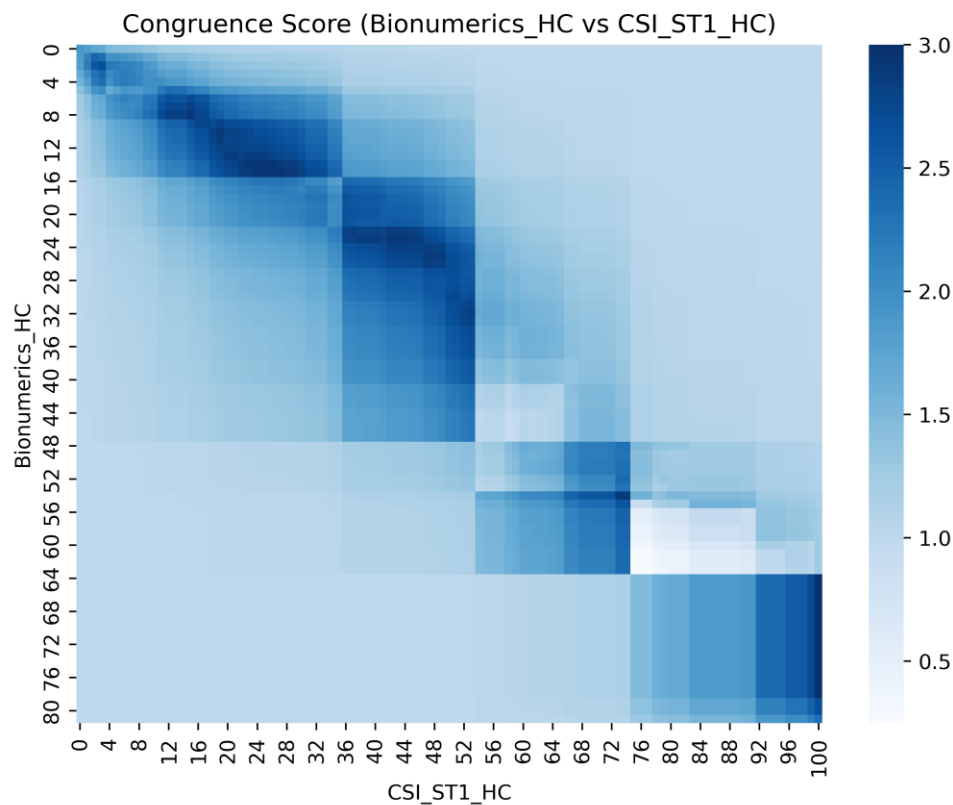


Figure S4.13.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

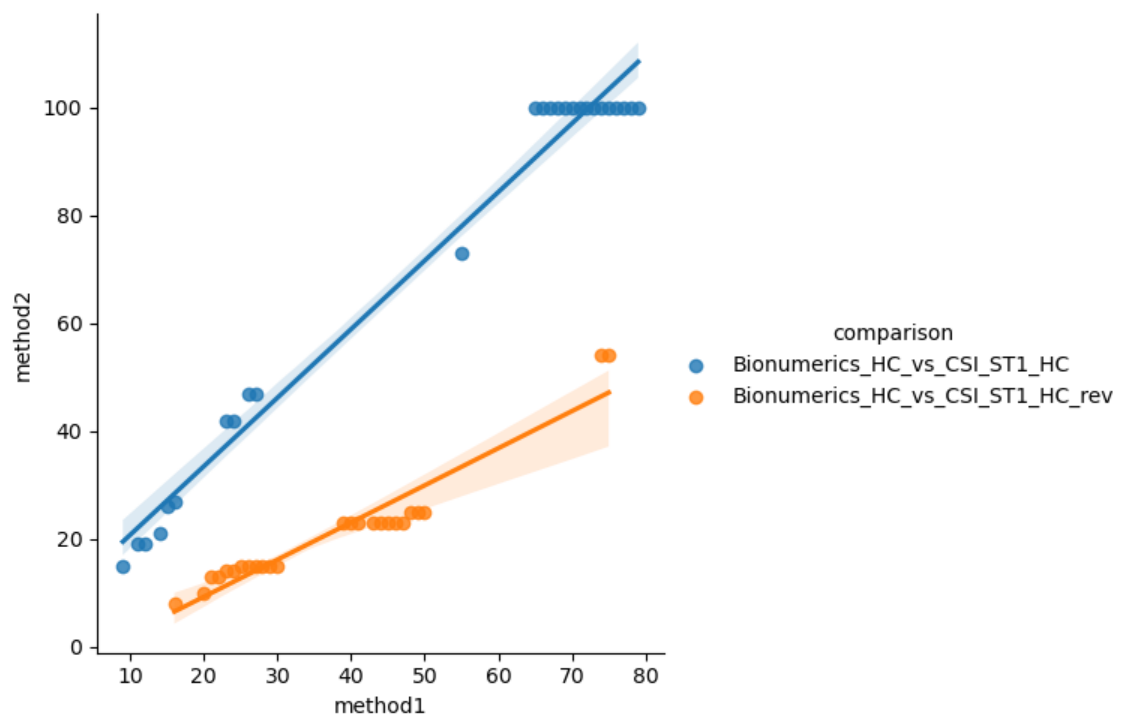


Figure S4.13.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 26 (blue) and 25 (orange) points is presented.

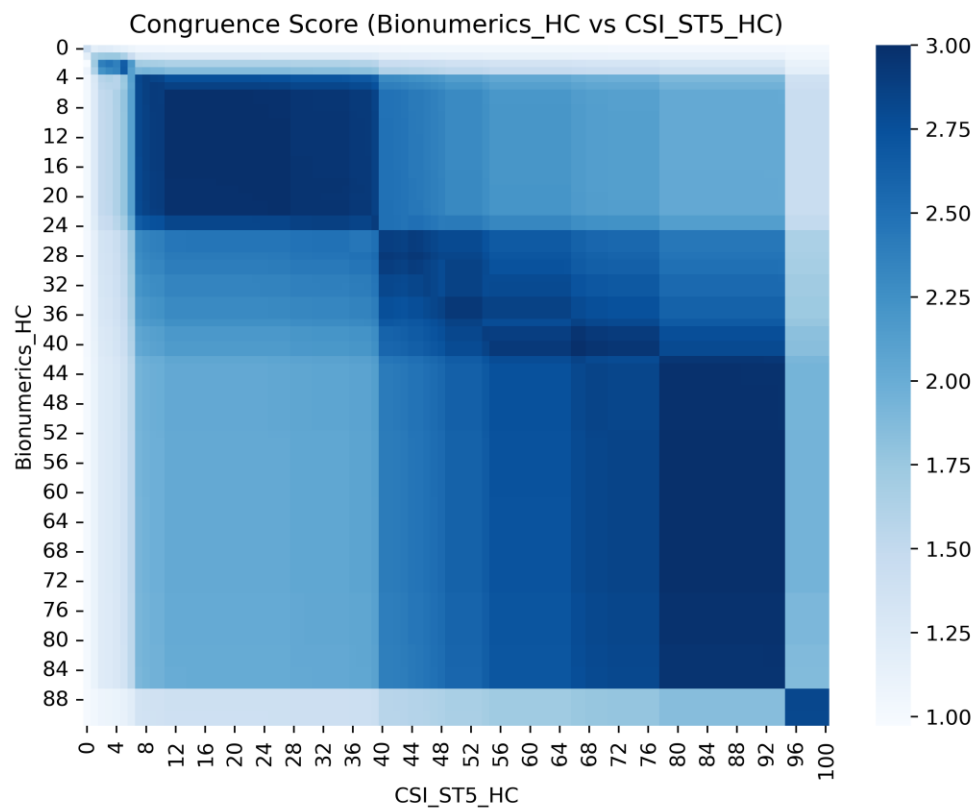


Figure S4.13.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

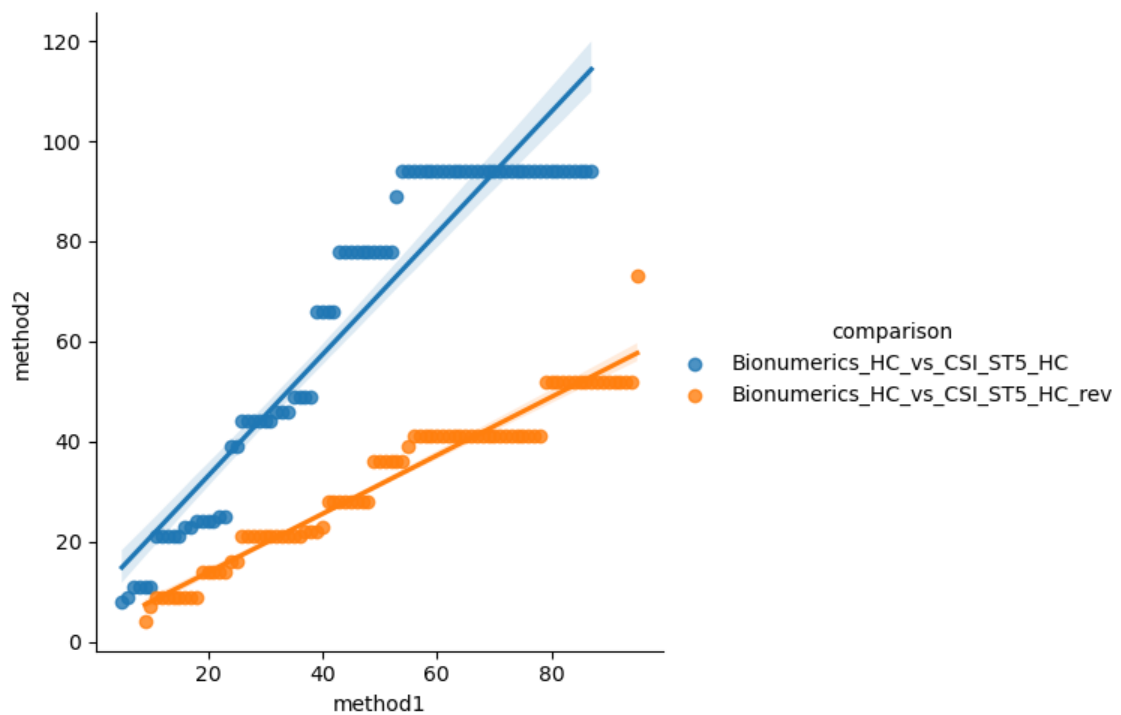


Figure S4.13.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 83 (blue) and 87 (orange) points is presented.

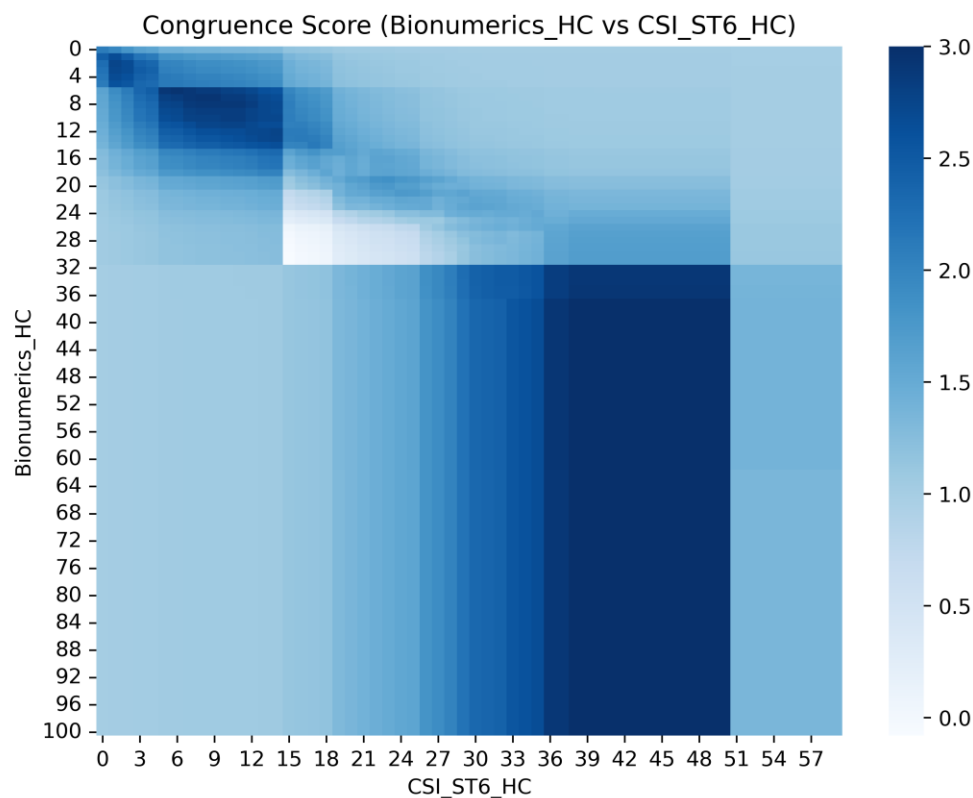


Figure S4.13.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

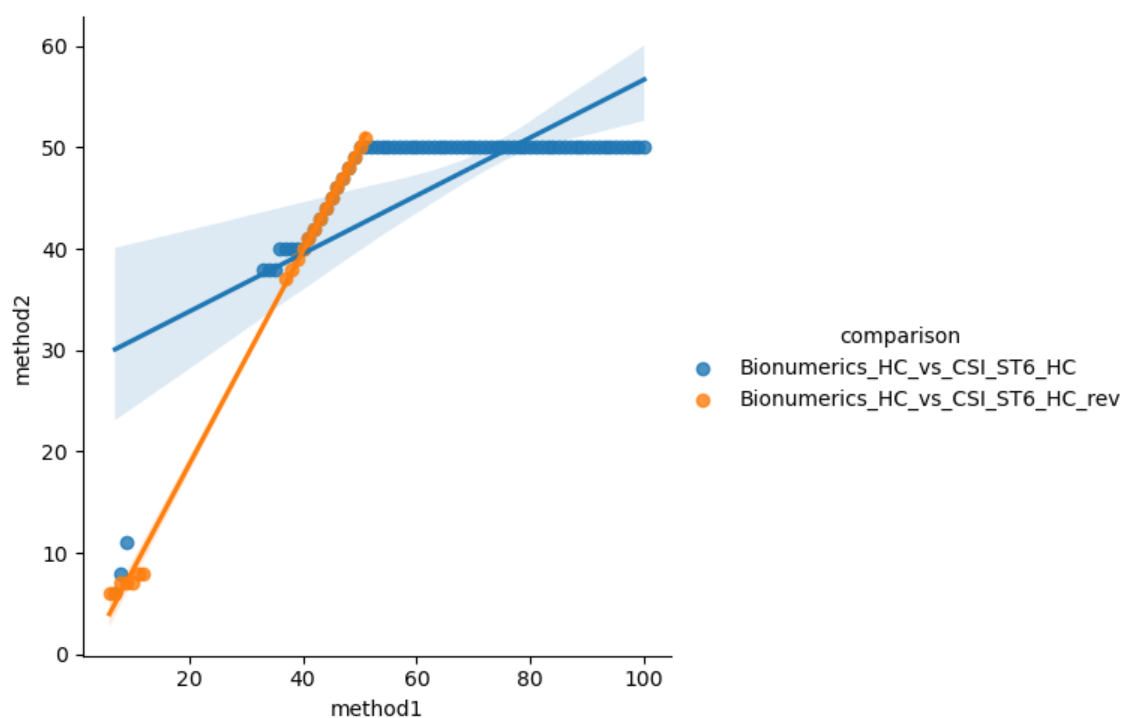


Figure S4.13.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 71 (blue) and 22 (orange) points is presented.

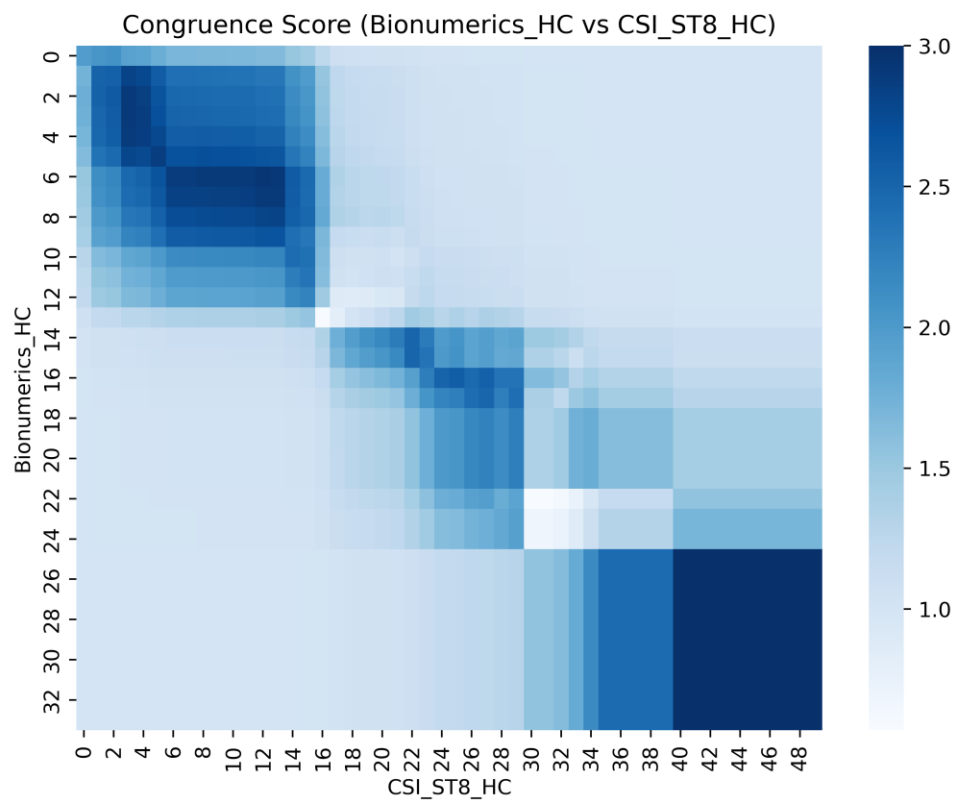


Figure S4.13.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

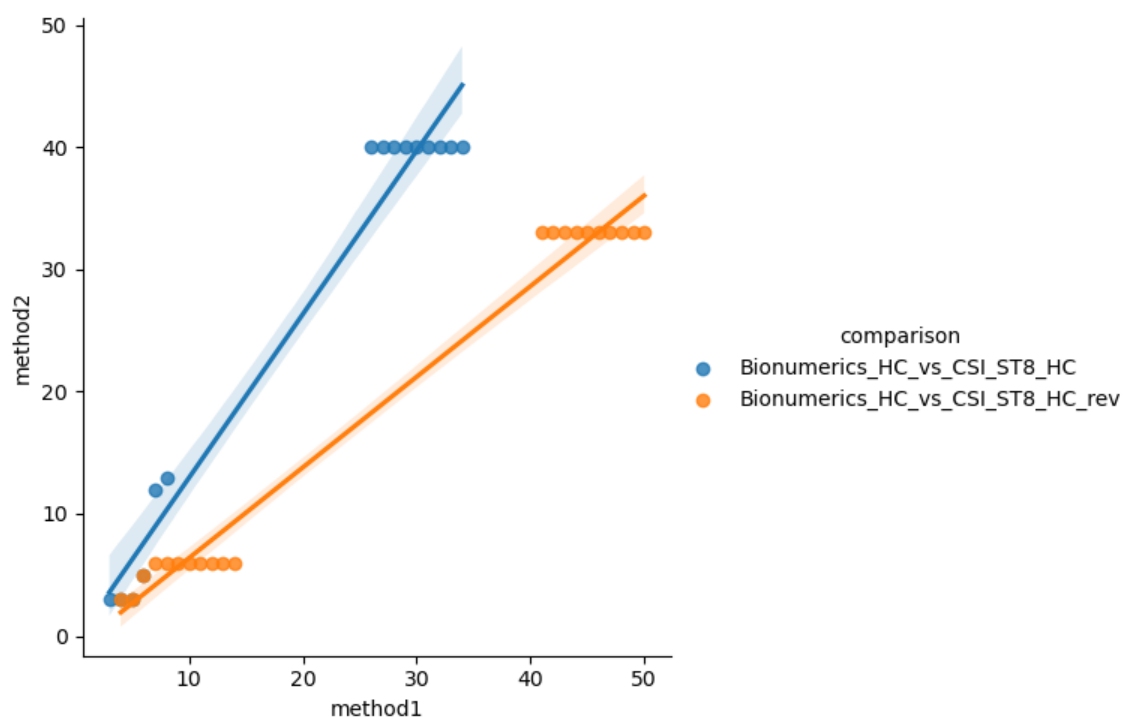


Figure S4.13.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 15 (blue) and 21 (orange) points is presented.

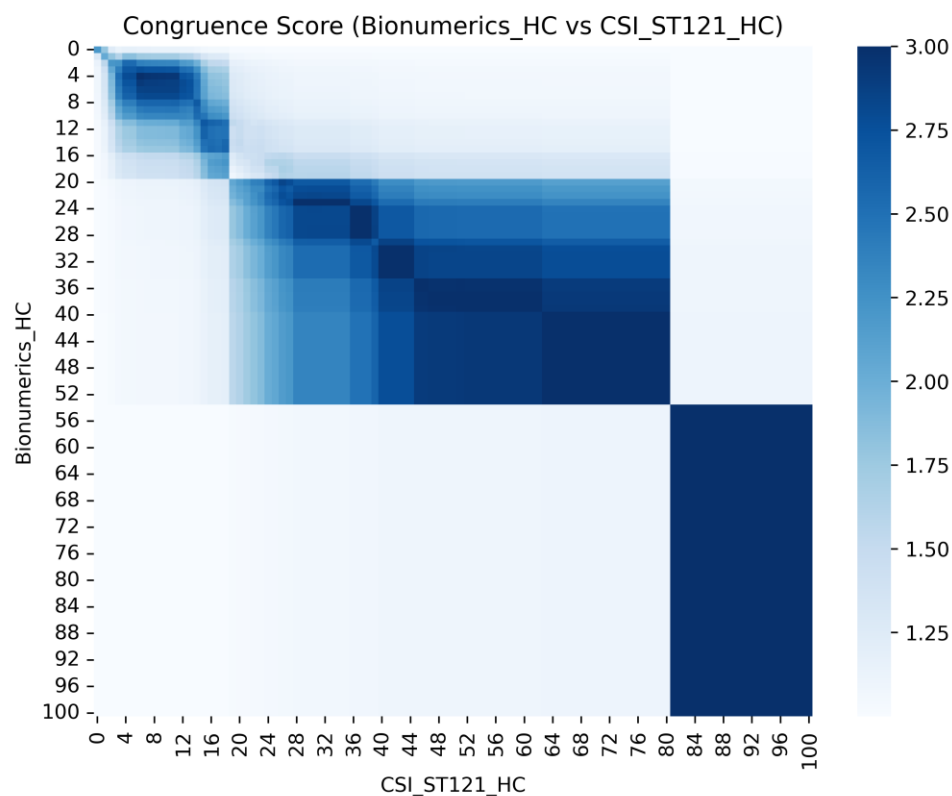


Figure S4.13.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

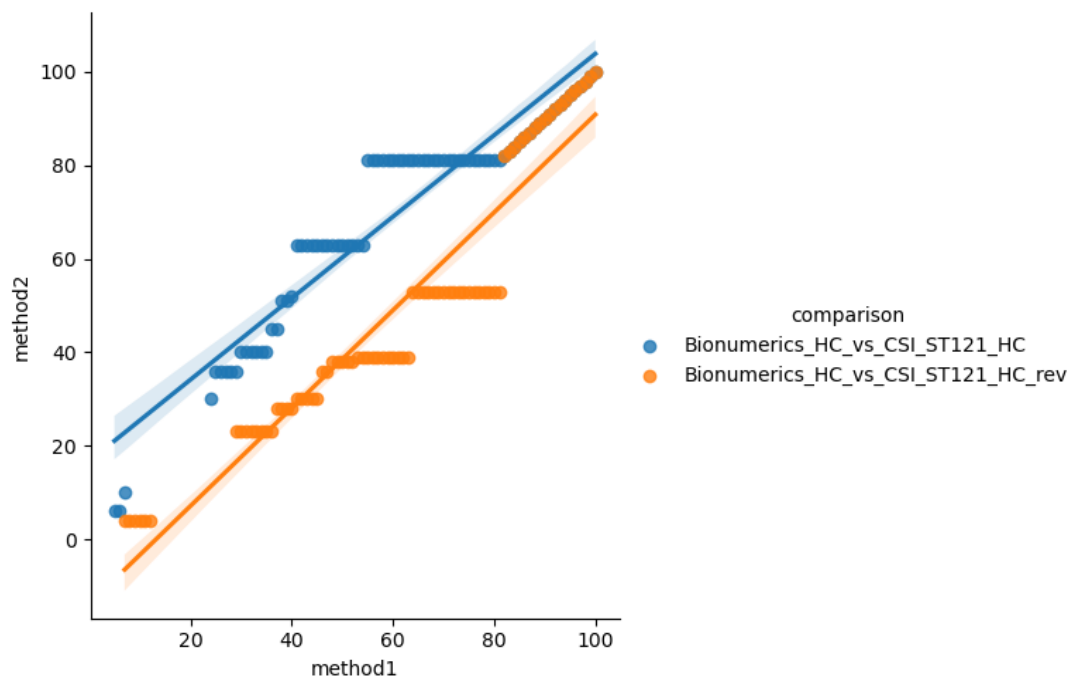


Figure S4.13.10. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST121. A linear tendency line supported by 80 (blue) and 78 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

14. Bionumerics single-linkage 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.

	Bionumerics single-linkage	snippySnake single-linkage
Pipeline version	v8.1	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

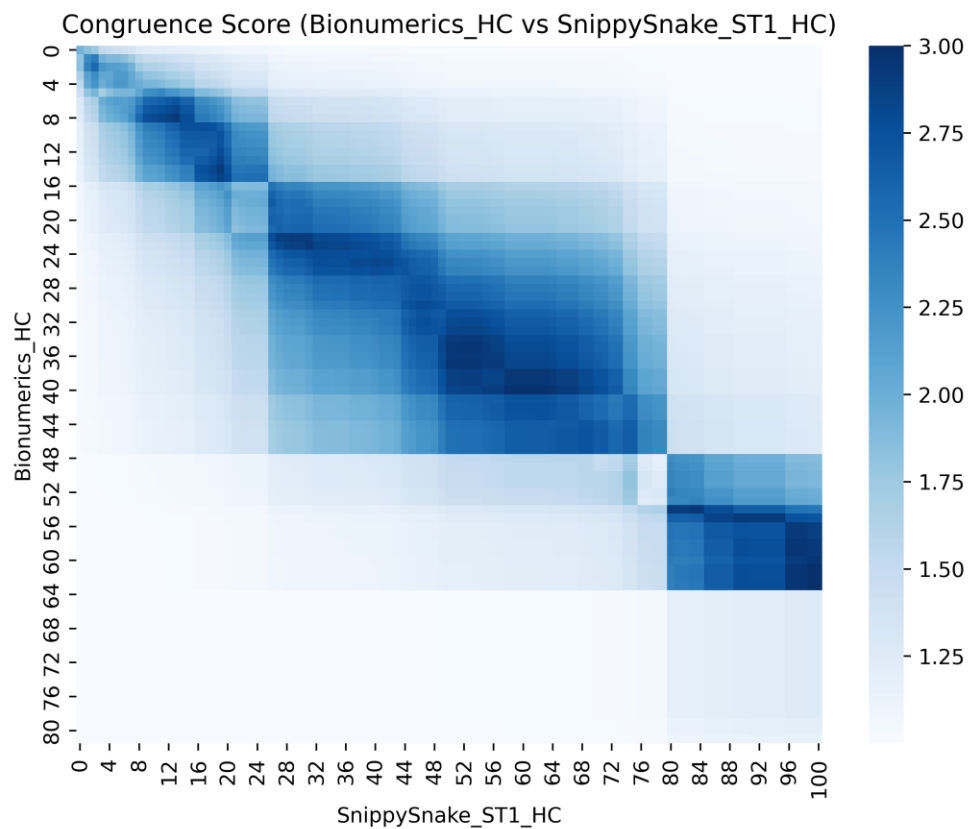


Figure S4.14.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

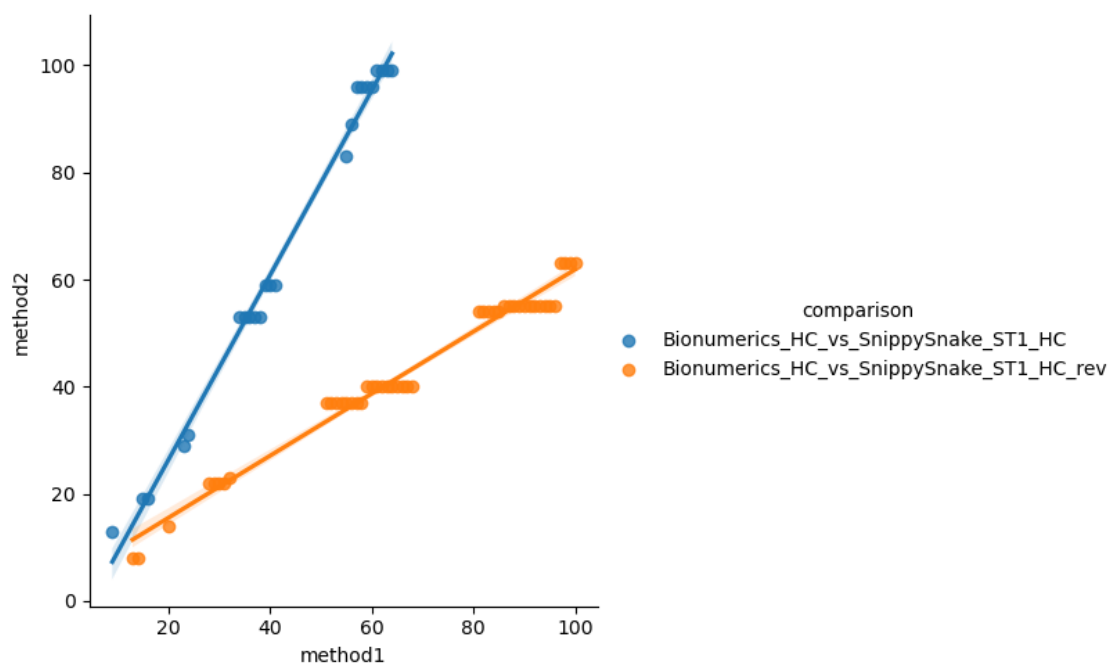


Figure S4.14.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST1. A linear tendency line supported by 23 (blue) and 46 (orange) points is presented.

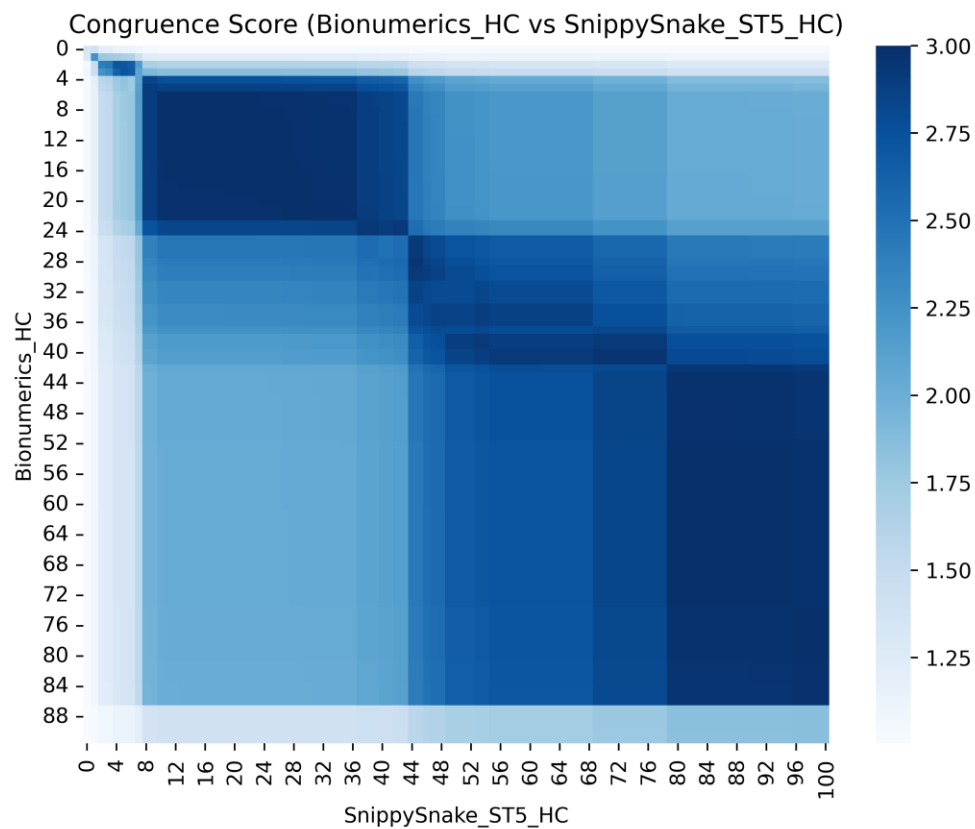


Figure S4.14.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

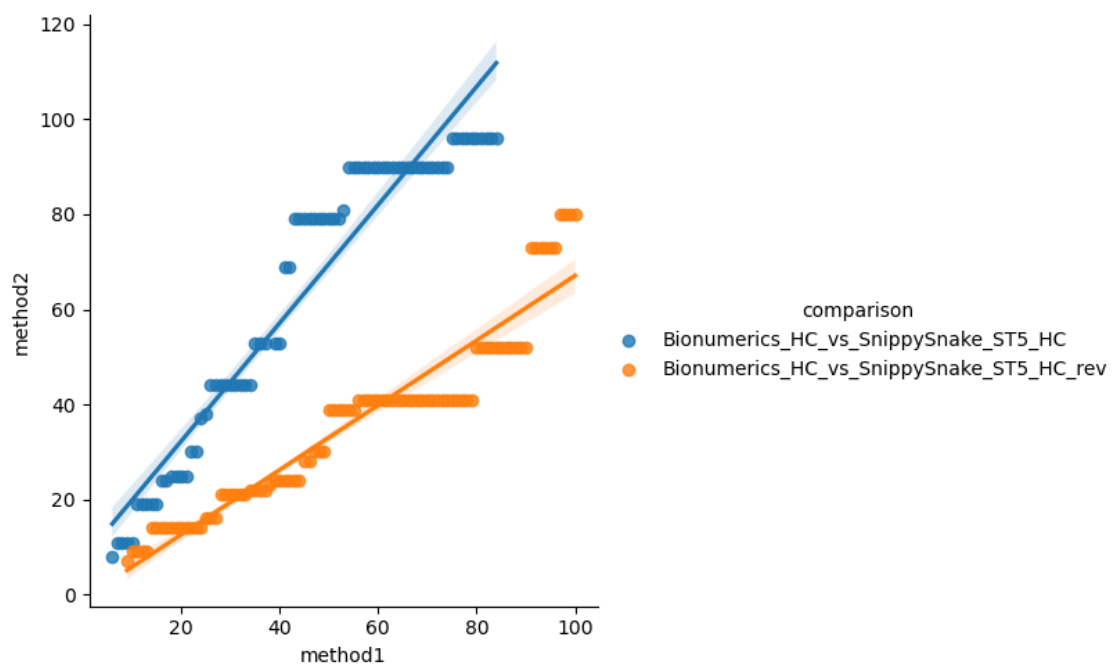


Figure S4.14.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST5. A linear tendency line supported by 78 (blue) and 92 (orange) points is presented.

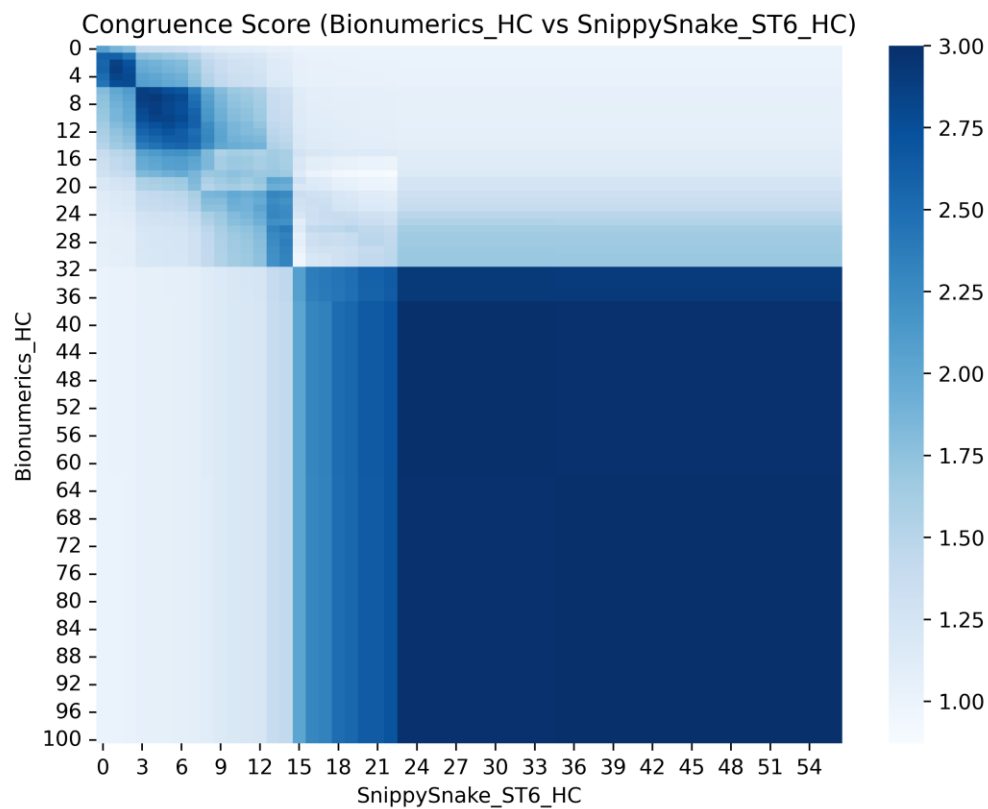


Figure S4.14.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

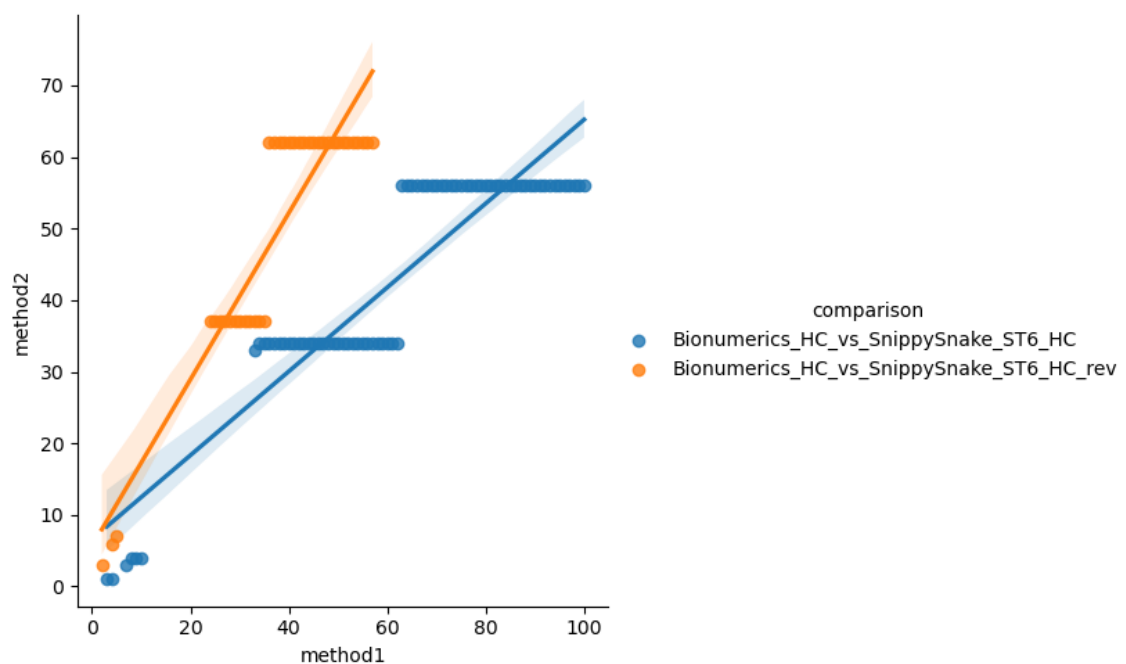


Figure S4.14.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported 74 X (blue) and 37 (orange) points is presented.

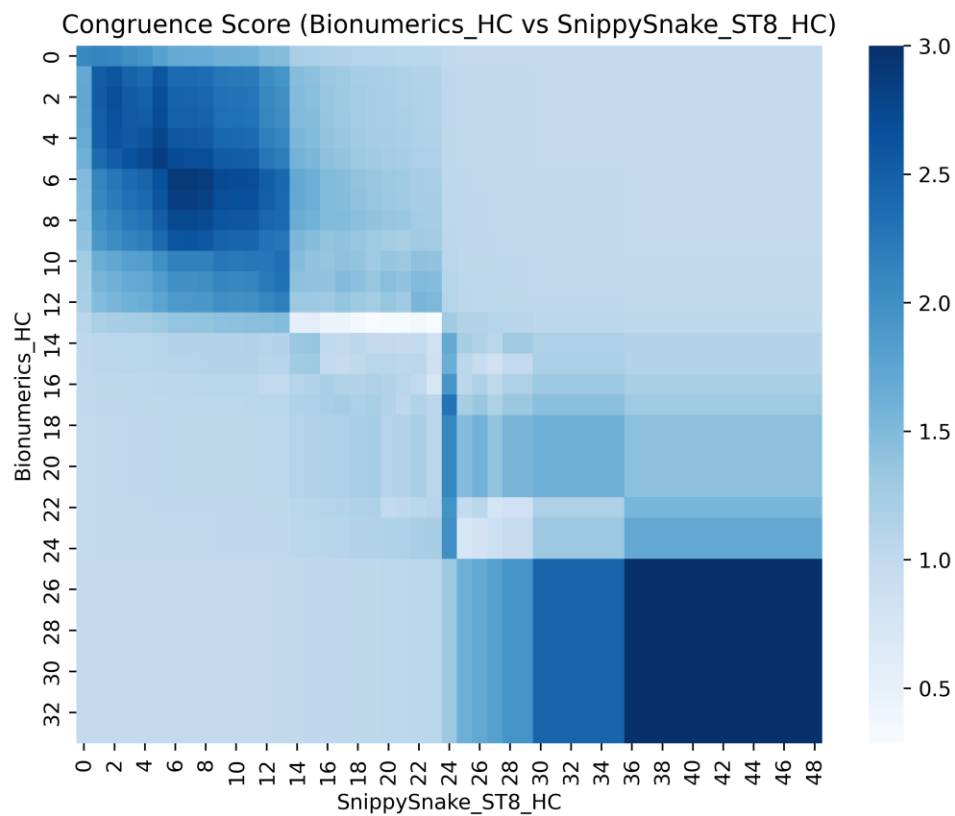


Figure S4.14.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

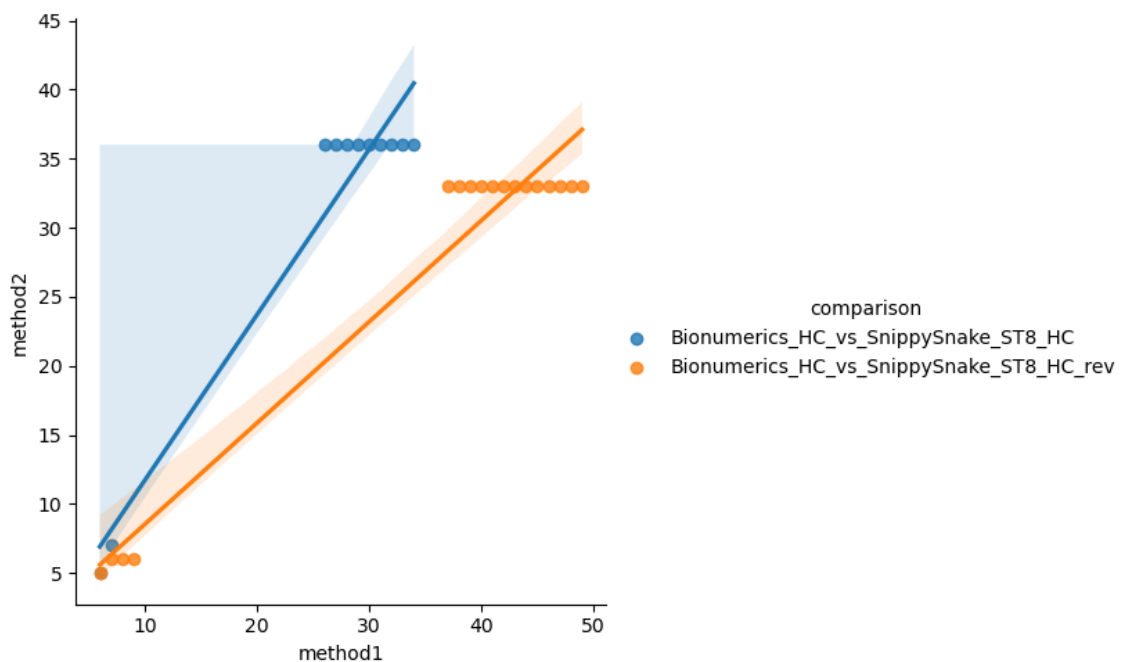


Figure S4.14.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 11 (blue) and 17 (orange) points is presented.

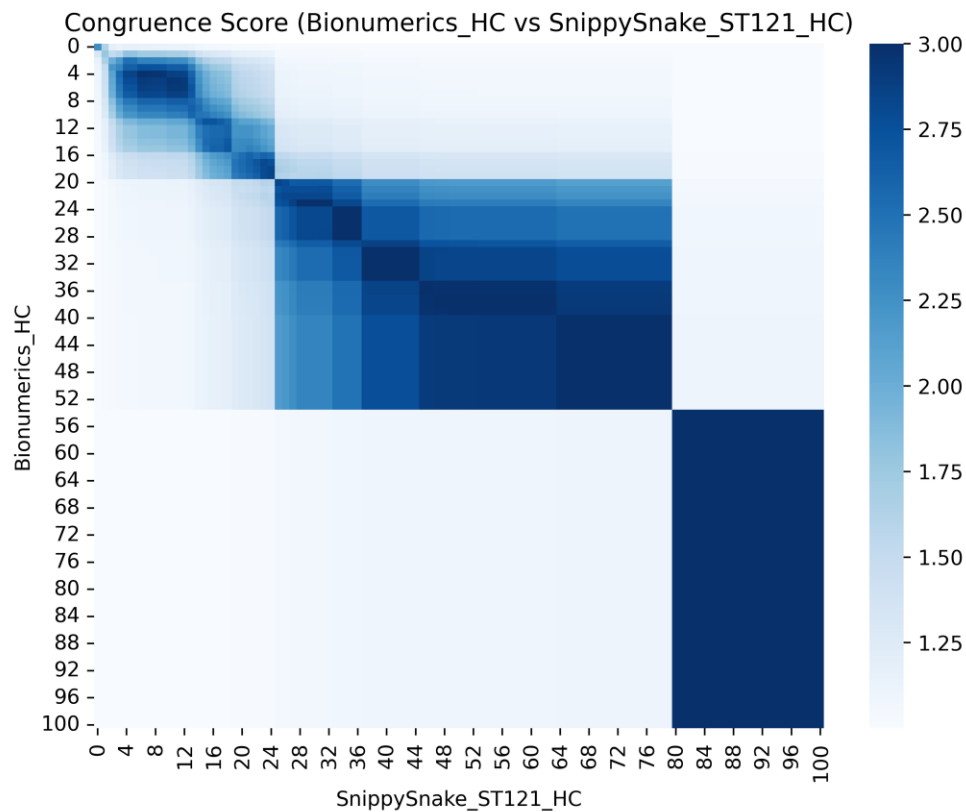


Figure S4.14.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

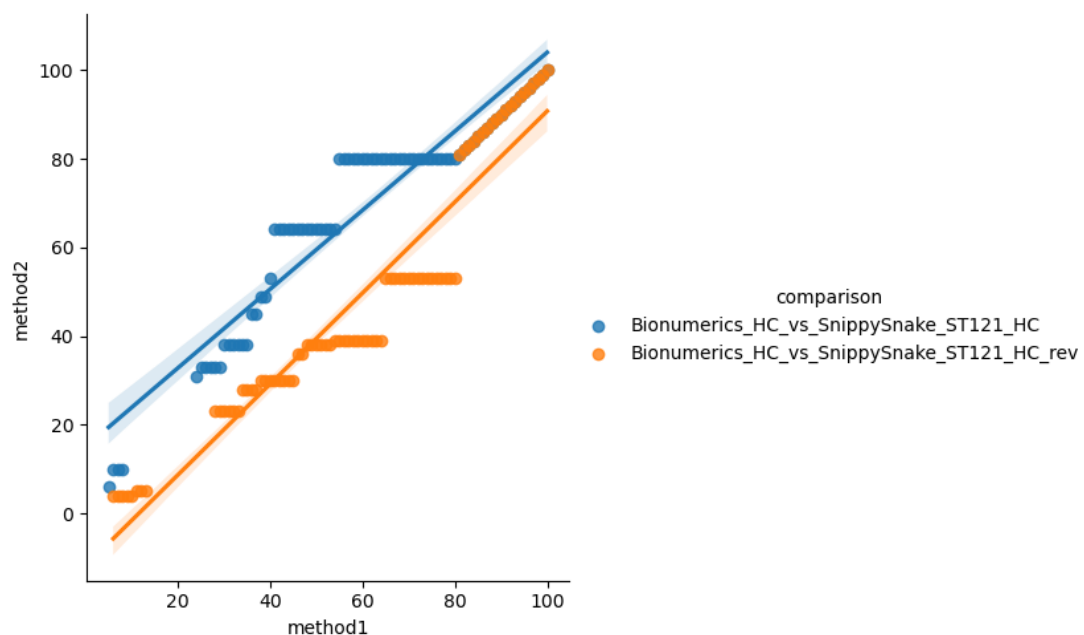


Figure S4.14.10. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST121. A linear tendency line supported by 81 (blue) and 81 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

15. Bionumerics single-linkage vs. WGSBAC 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.

	Bionumerics single-linkage	WGSBAC single-linkage
Pipeline version	v8.1	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

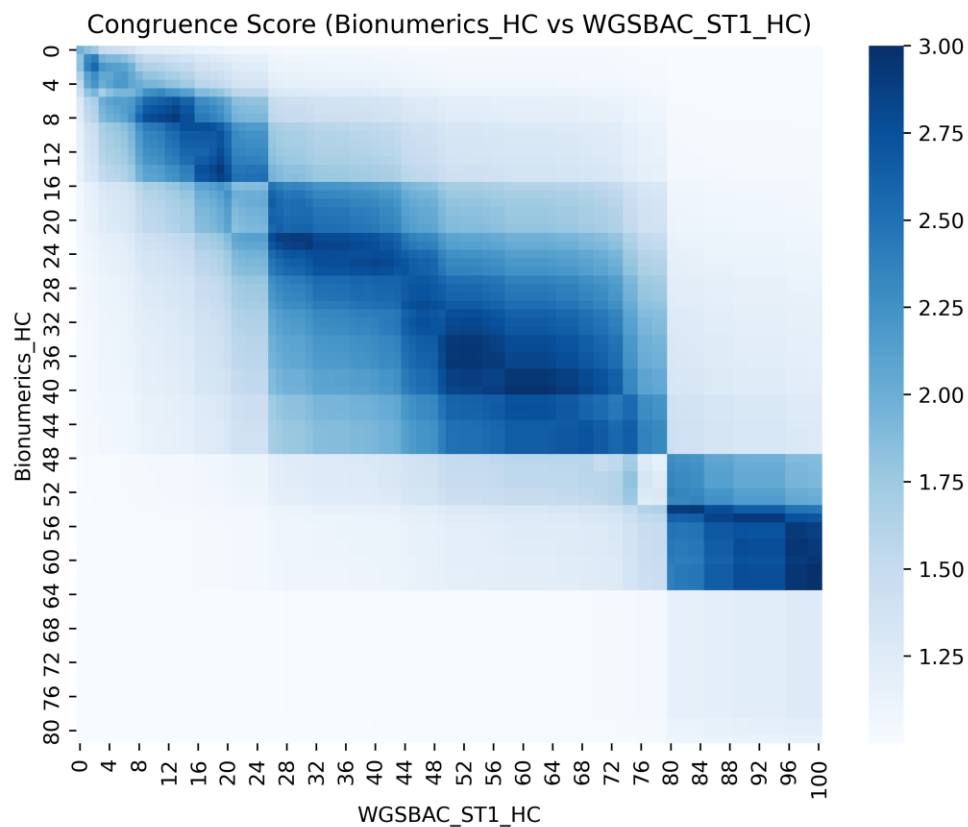


Figure S4.15.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

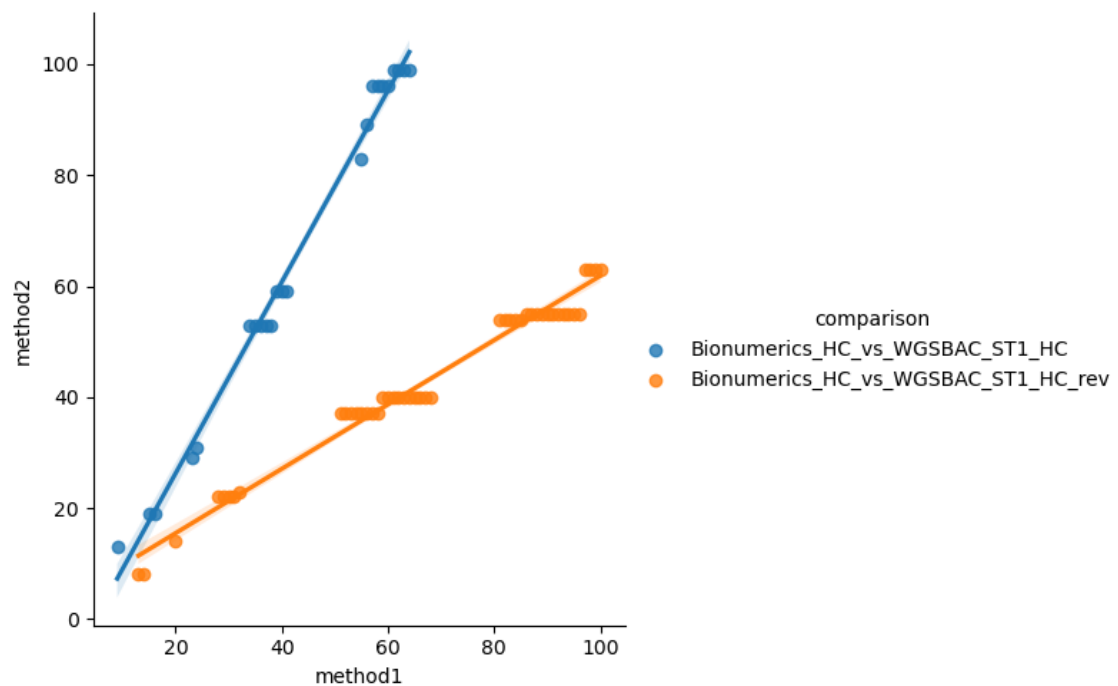


Figure S4.15.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 23 (blue) and 46 (orange) points is presented.

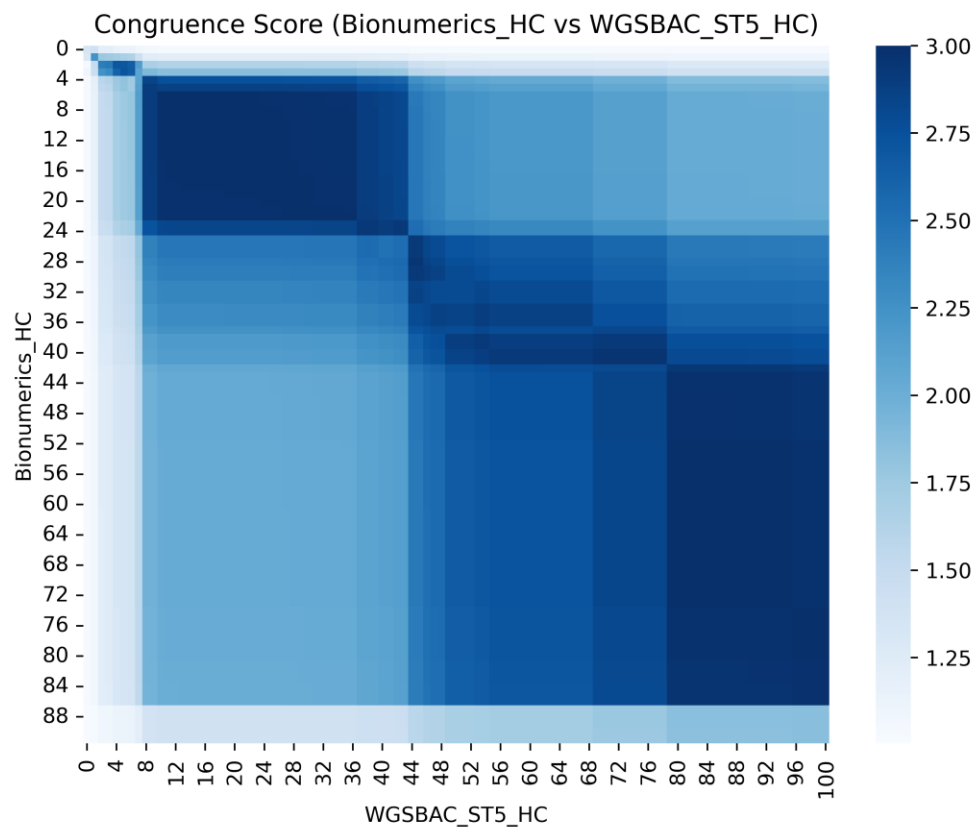


Figure S4.15.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

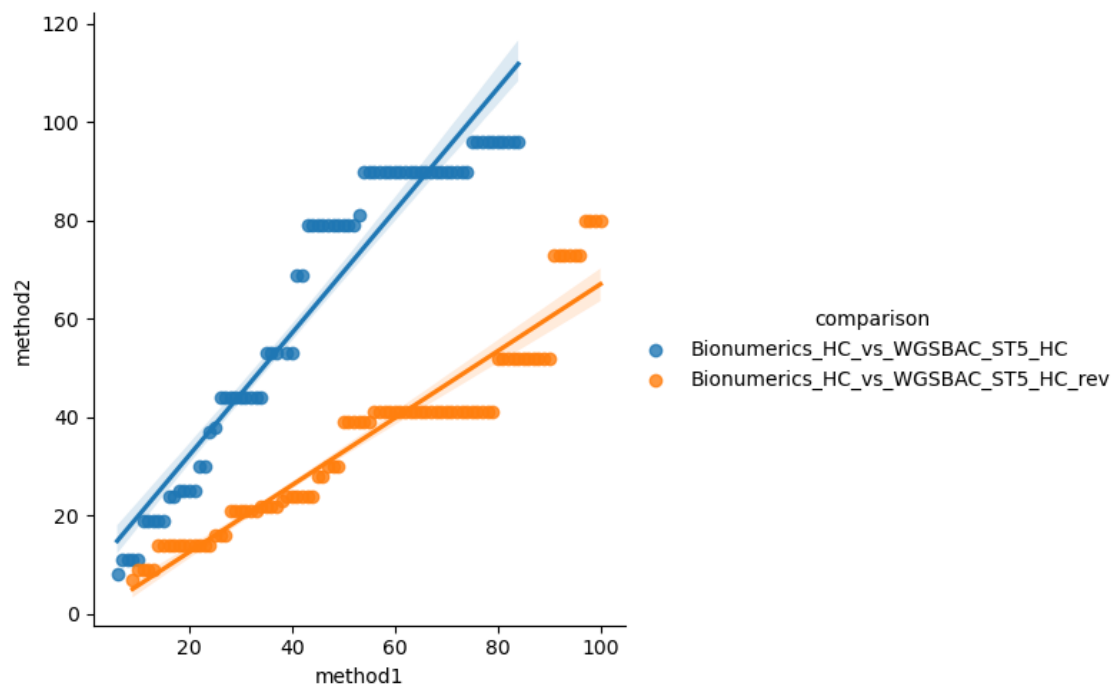


Figure S4.15.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 78 (blue) and 92 (orange) points is presented.

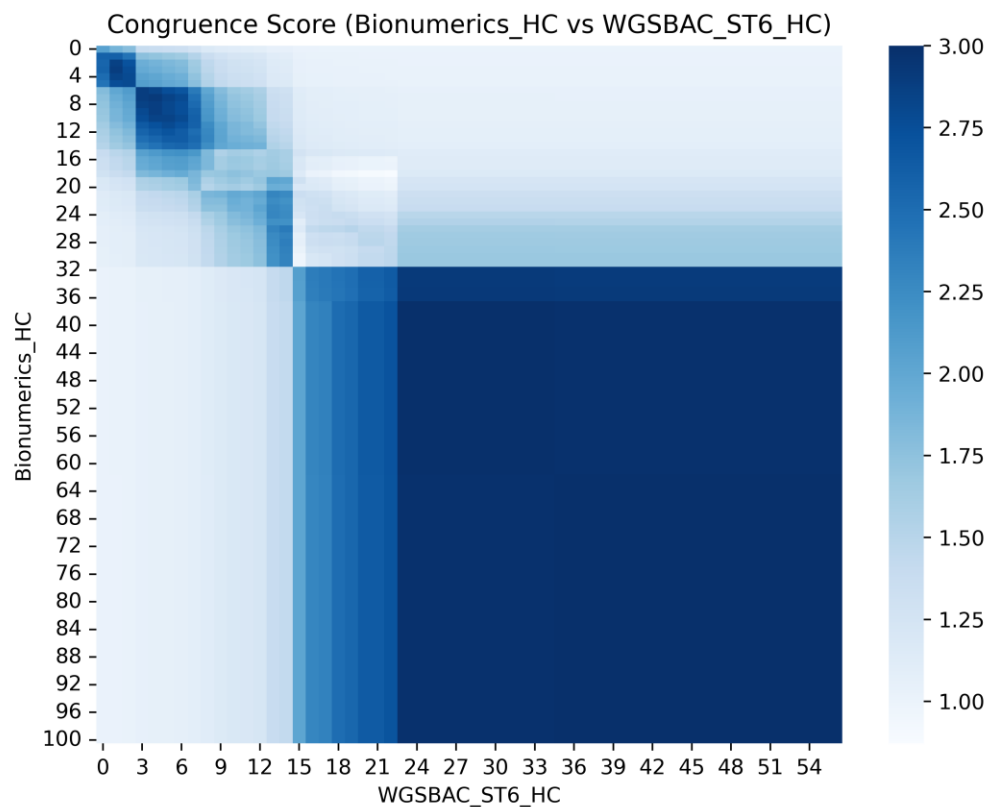


Figure S4.15.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

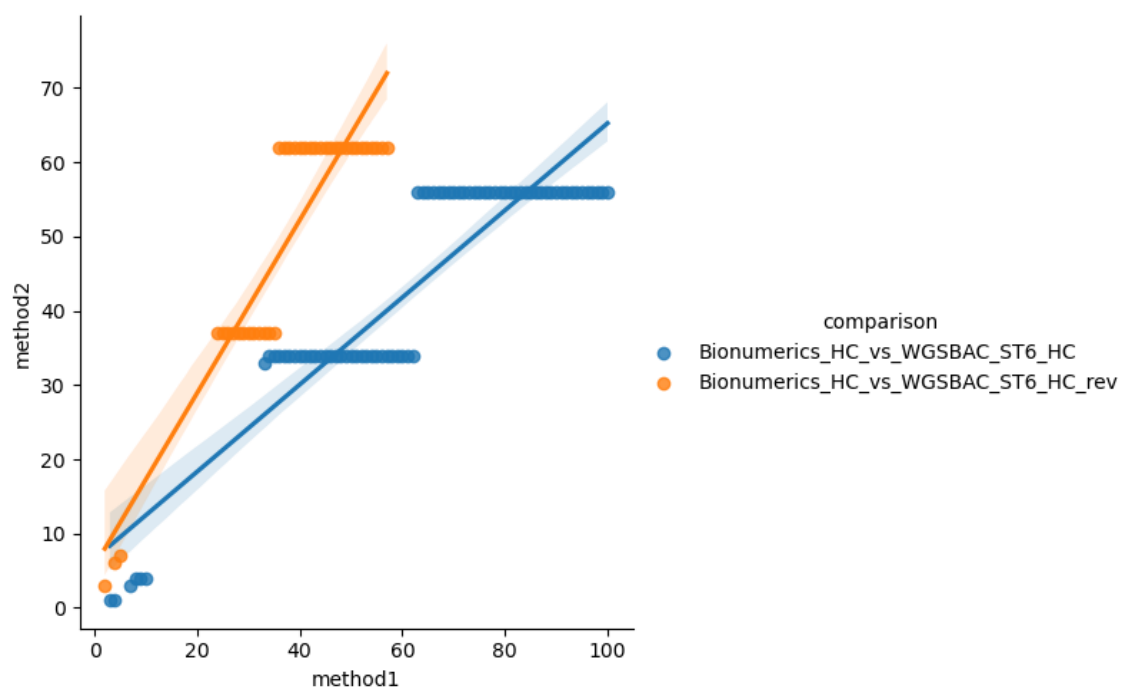


Figure S4.15.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 74 (blue) and 37 (orange) points is presented.

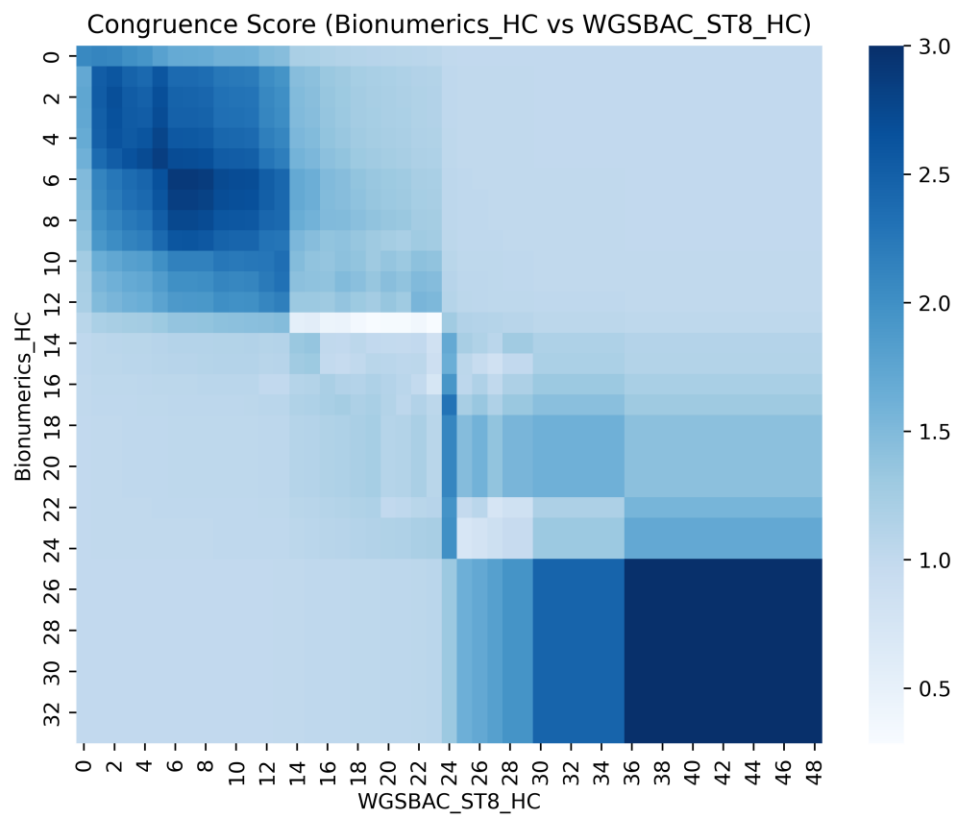


Figure S4.15.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

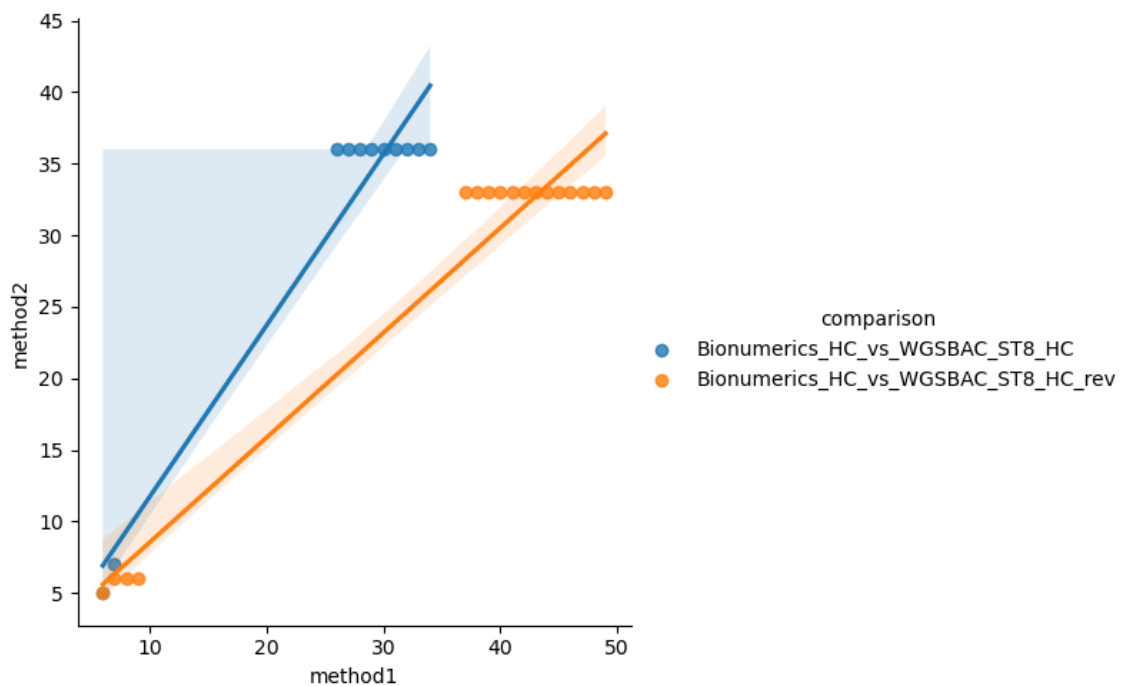


Figure S4.15.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 11 (blue) and 17 (orange) points is presented.

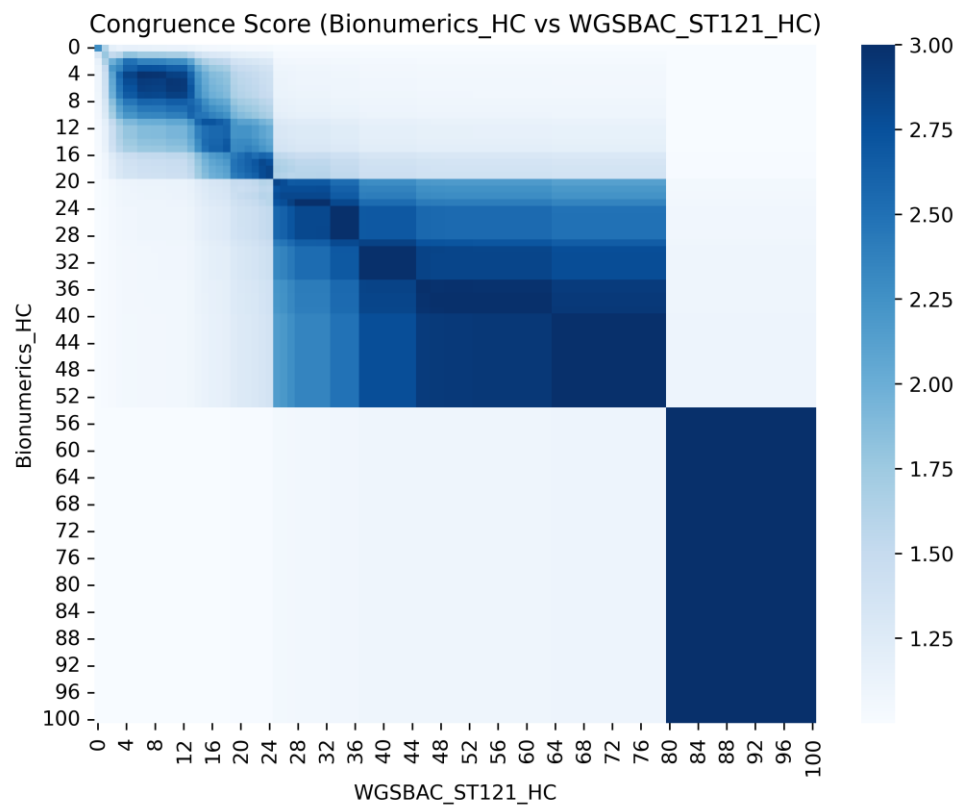


Figure S4.15.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

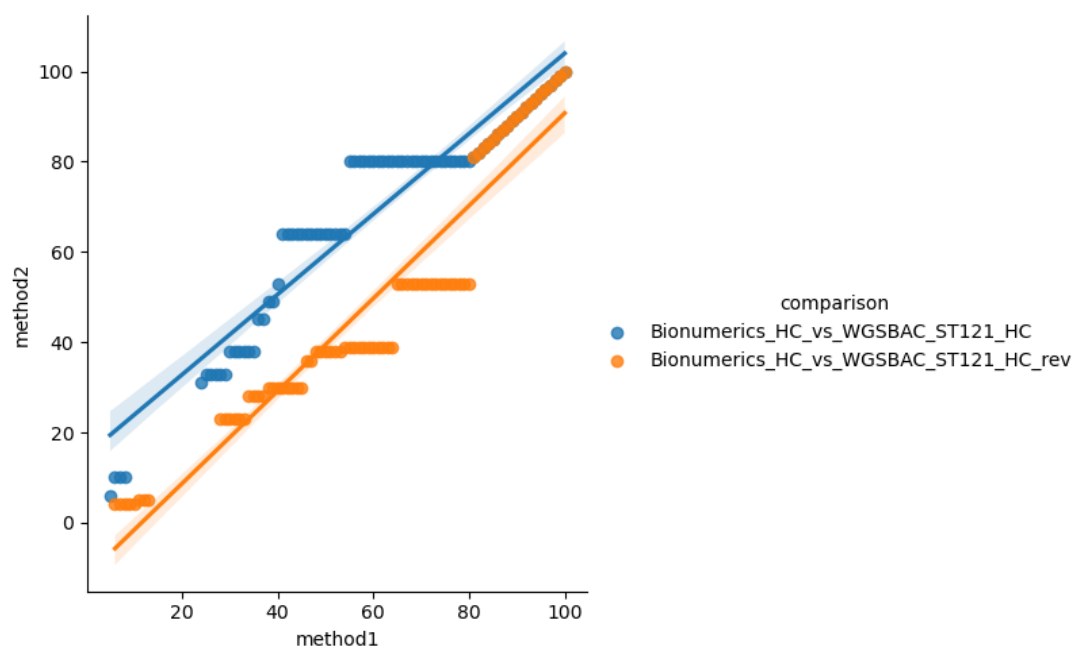


Figure S4.15.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST121. A linear tendency line supported by 81 (blue) and 81 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

16. MentaLiST GrapeTree vs. CSI Phylogeny single-linkage

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

	MentaLiST GrapeTree	CSI Phylogeny single-linkage
Pipeline version	v1.0.0	v1.4
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	CP006592 (ST5) / CP006046 (ST6) / HG813249 (ST121)
Dataset	All samples	ST5 / ST6 / ST121

NOTE: Data for ST1 and ST8 dataset comparisons are not presented as no congruence points with CS ≥ 2.85 were obtained.

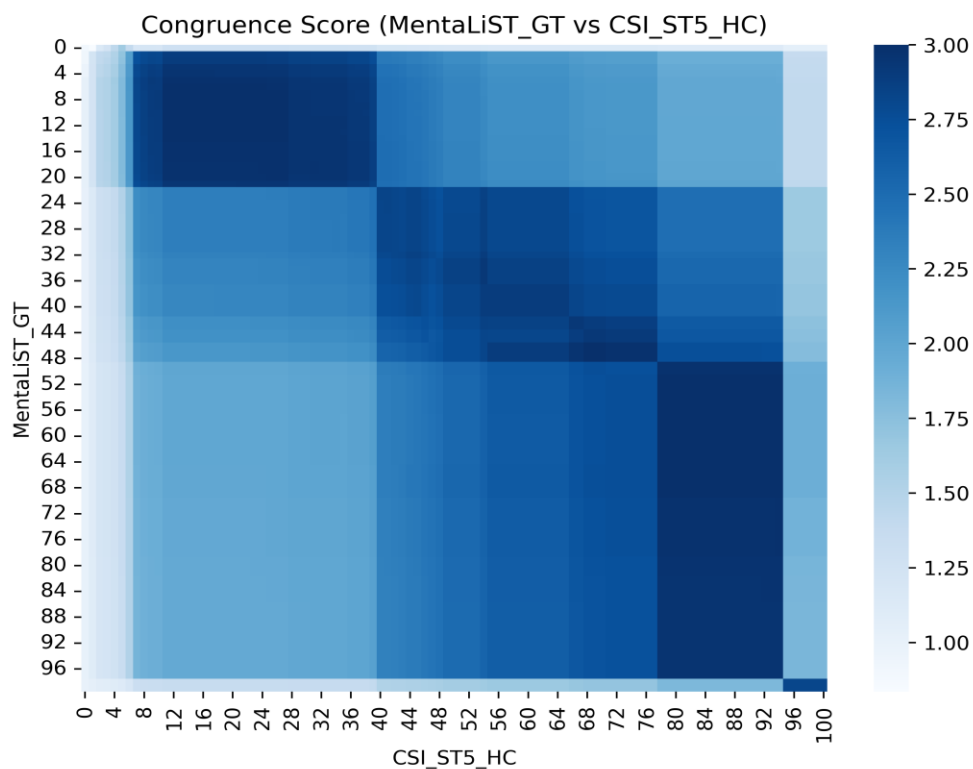


Figure S4.16.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

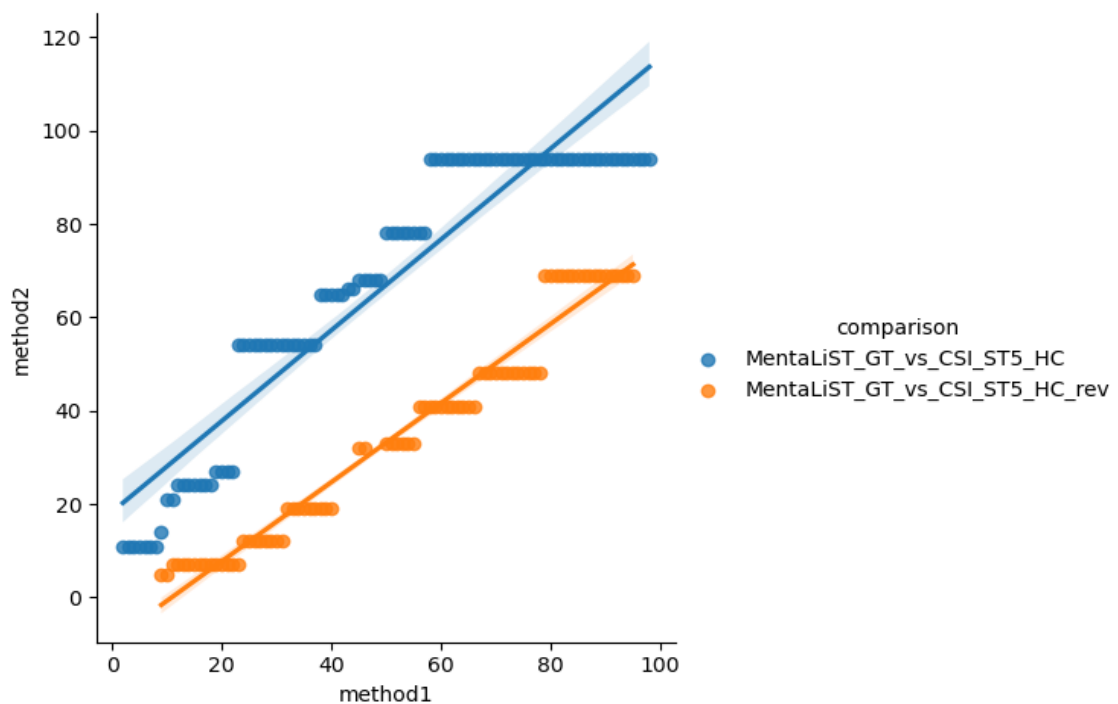


Figure S4.16.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 97 (blue) and 80 (orange) points is presented.

NOTE: Data for ST1 and ST8 dataset comparisons are not presented as no congruence points with $CS \geq 2.85$ were obtained.

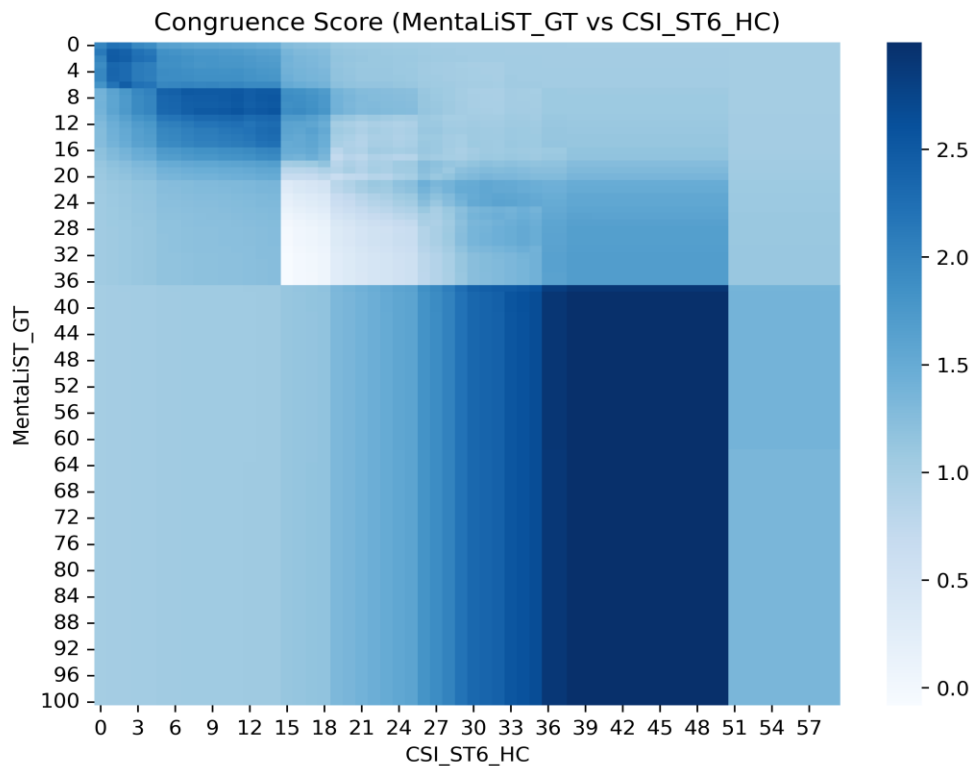


Figure S4.16.3. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

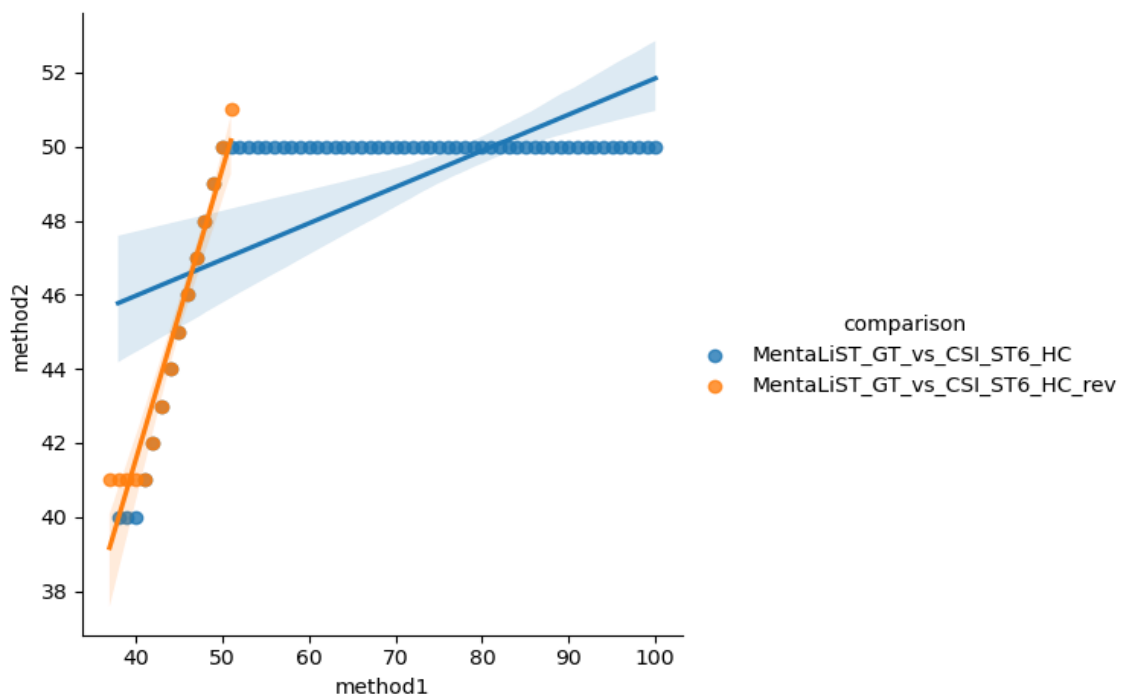


Figure S4.16.4. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 63 (blue) and 15 (orange) points is presented.

NOTE: Data for ST1 and ST8 dataset comparisons are not presented as no congruence points with $CS \geq 2.85$ were obtained.

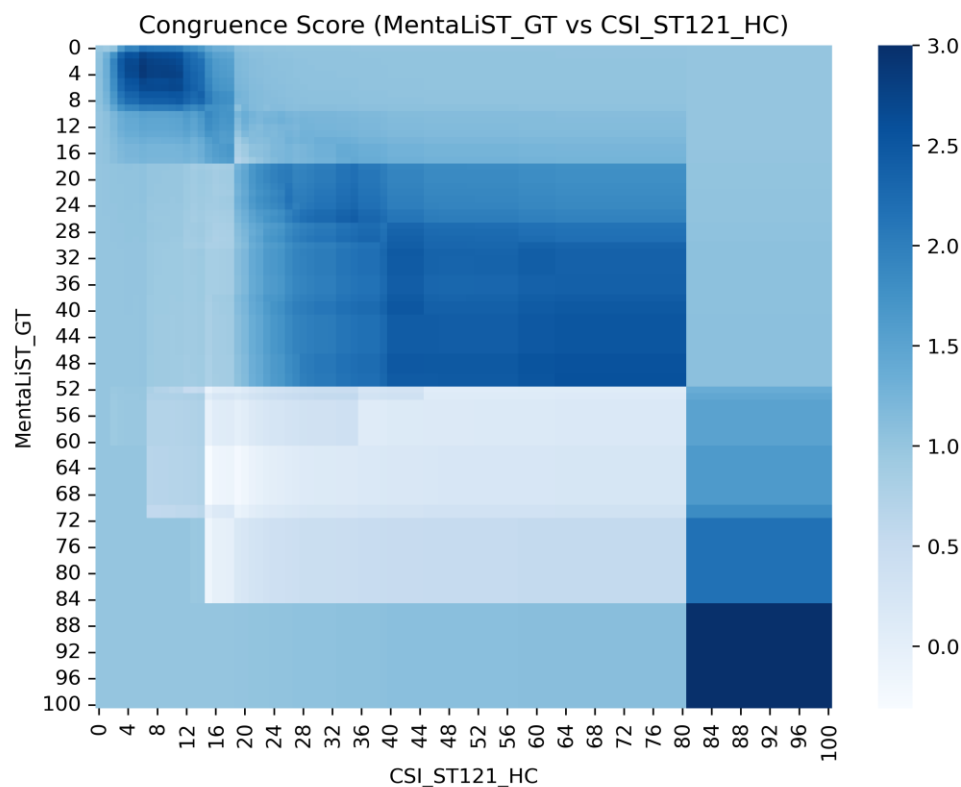


Figure S4.16.5. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

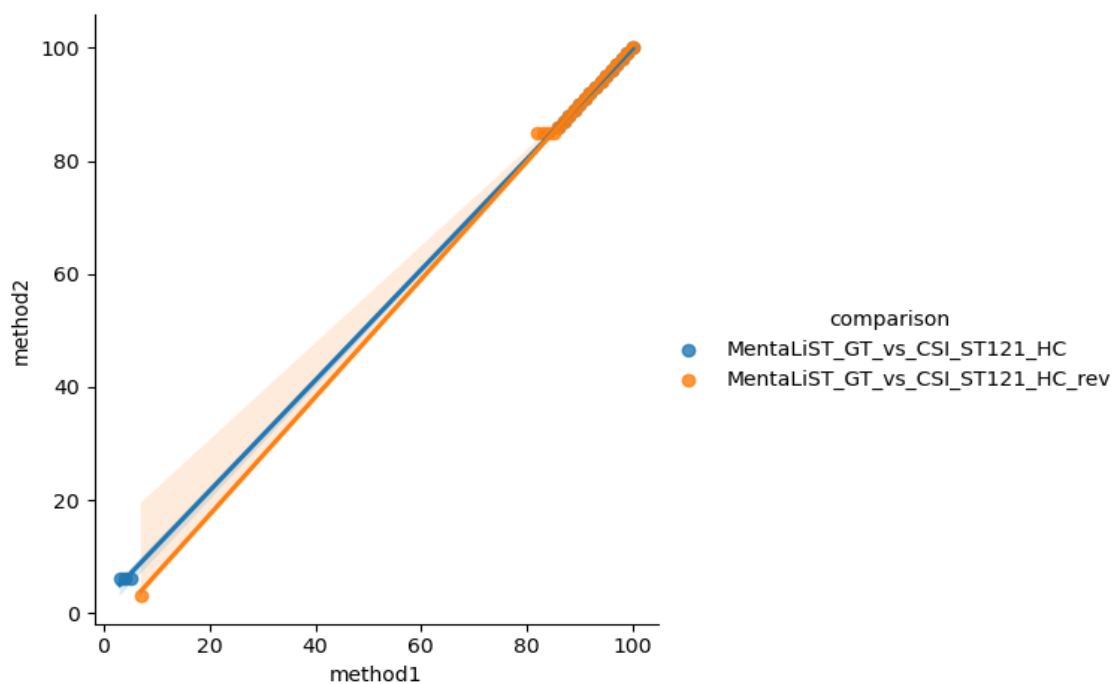


Figure S4.16.6. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 18 (blue) and 20 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

17. MentaLiST GrapeTree vs. snippySnake 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.

	MentaLiST GrapeTree	snippySnake single-linkage
Pipeline version	v1.0.0	v1.1.0
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) // HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST121

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with $CS \geq 2.85$ were obtained.

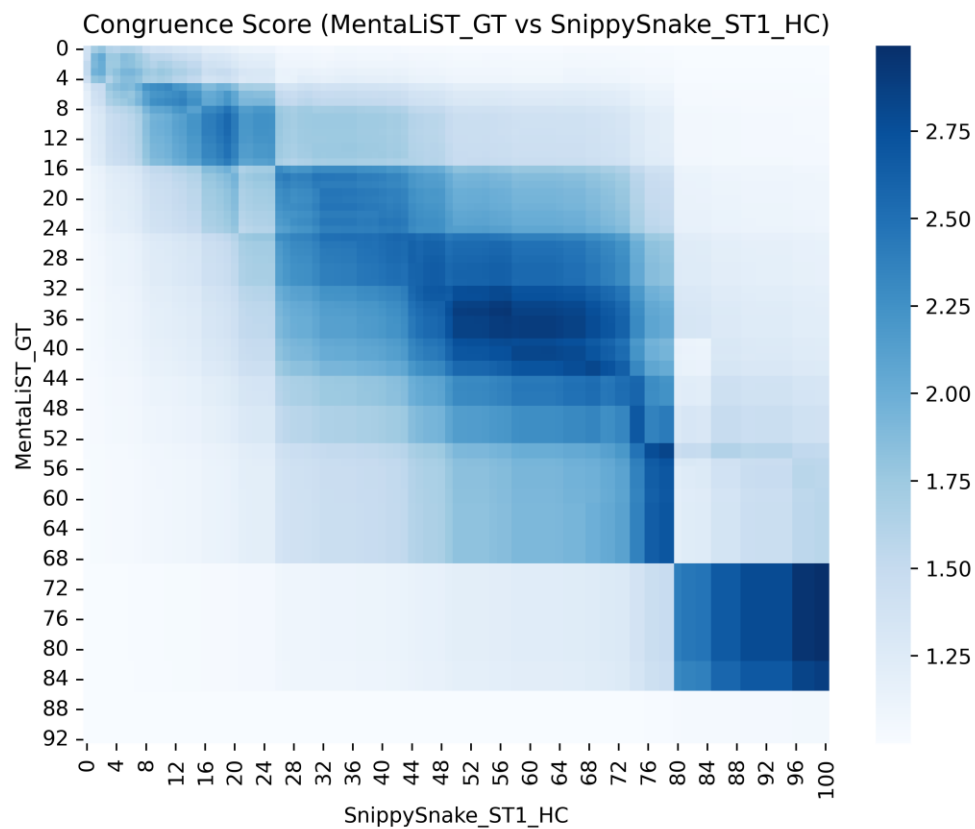


Figure S4.17.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

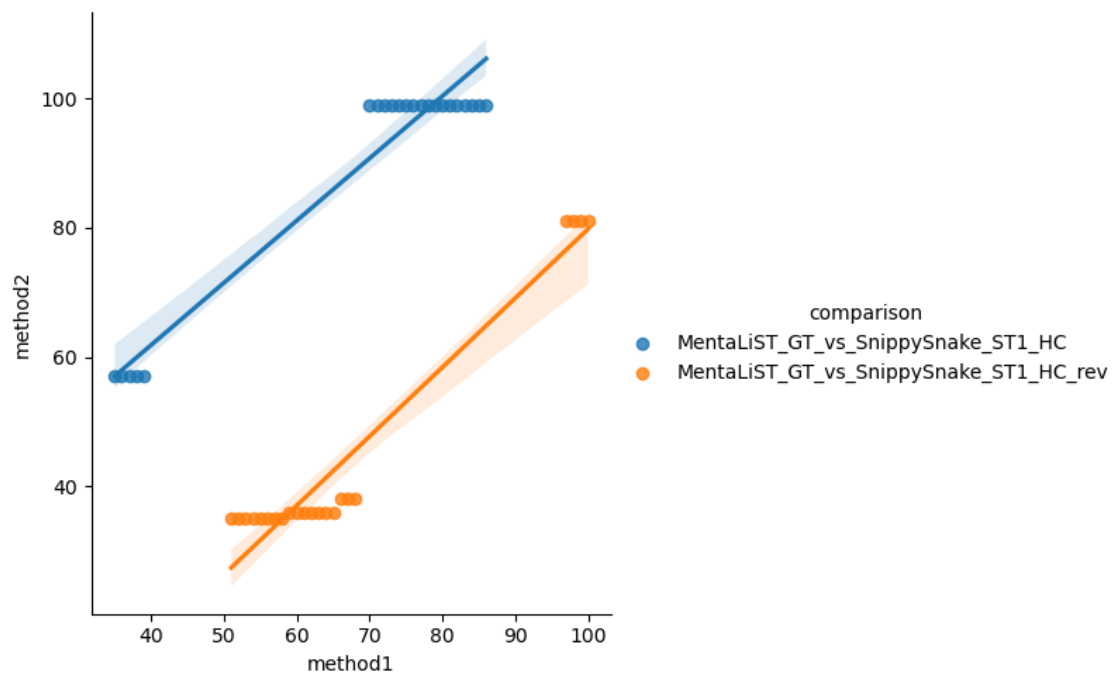


Figure S4.17.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 22 (blue) and 22 (orange) points is presented.

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with $CS \geq 2.85$ were obtained.

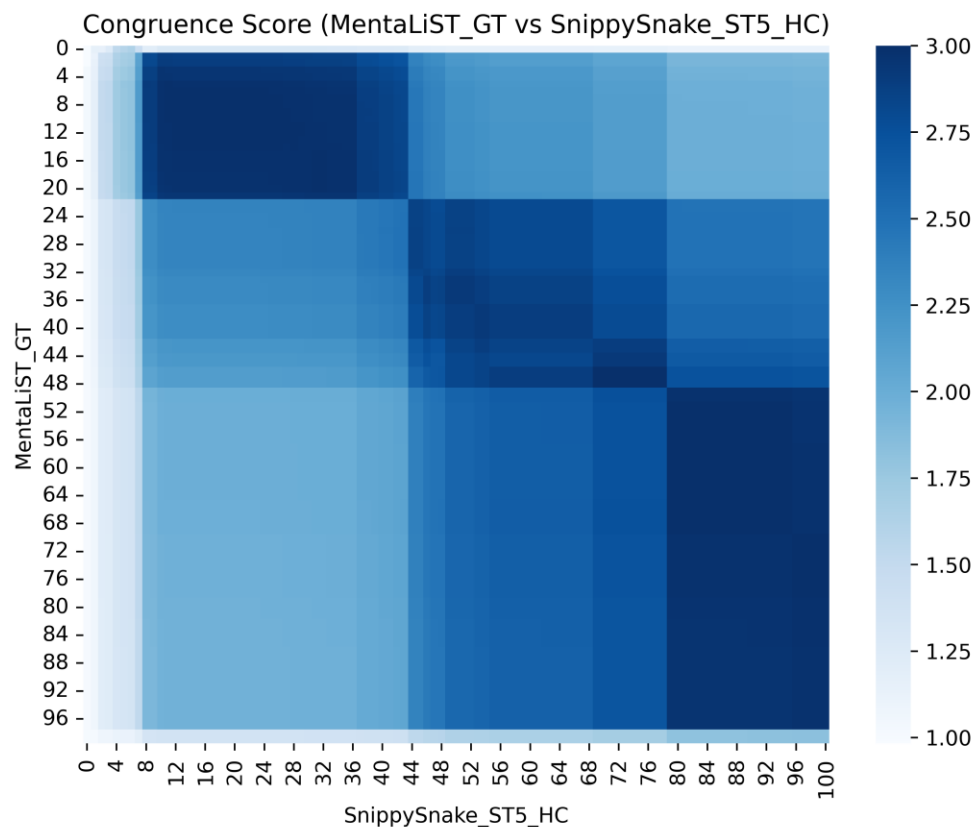


Figure S4.17.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

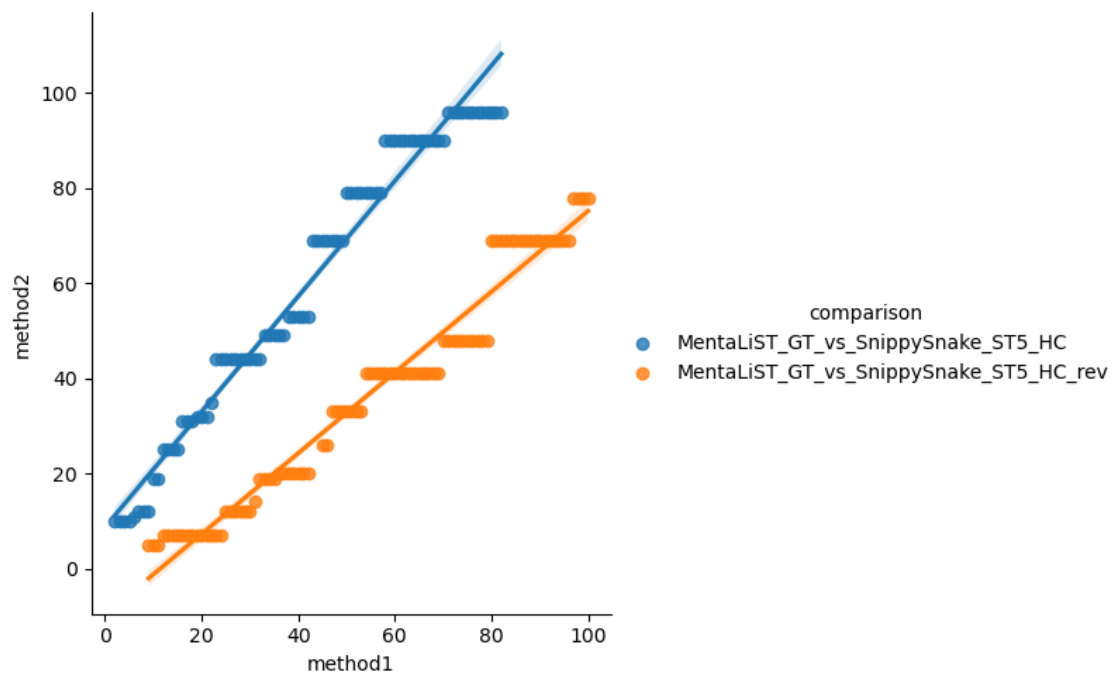


Figure S4.17.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 81 (blue) and 90 (orange) points is presented.

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with CS ≥ 2.85 were obtained.

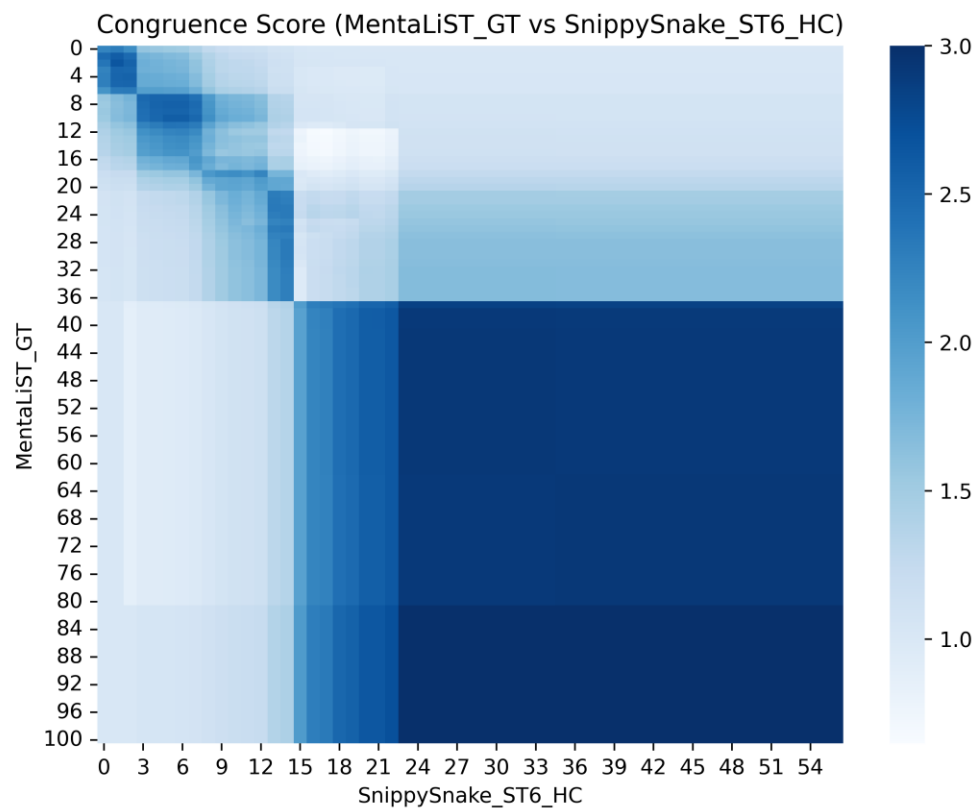


Figure S4.17.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

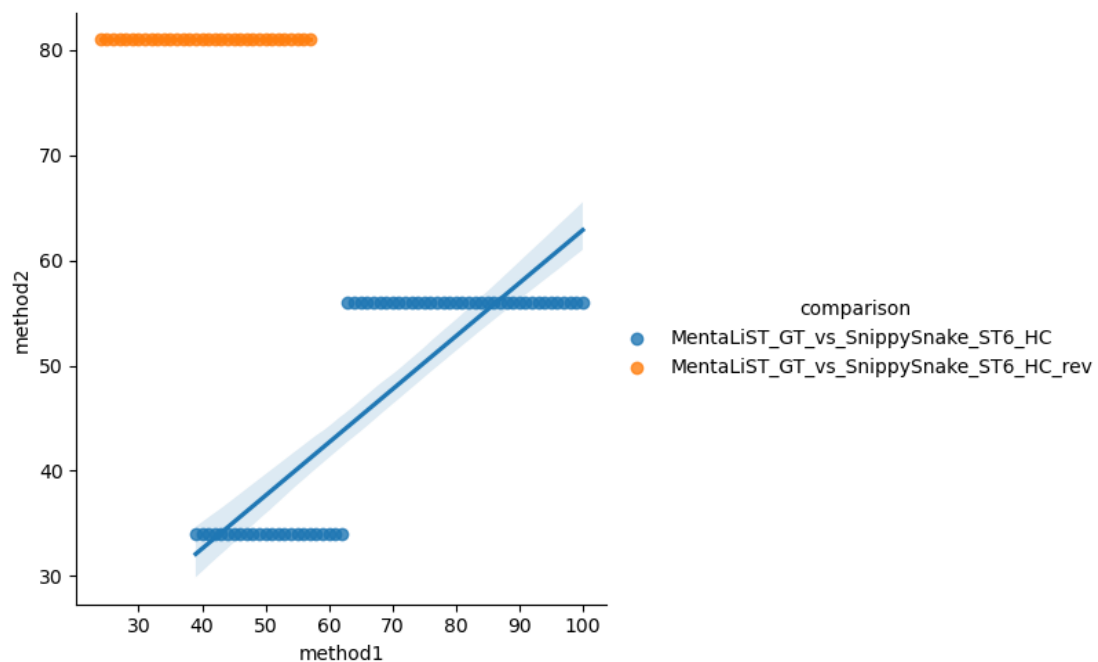


Figure S4.17.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. No linear tendency was observed. The 62 (blue) and 34 (orange) points are presented.

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with $CS \geq 2.85$ were obtained.

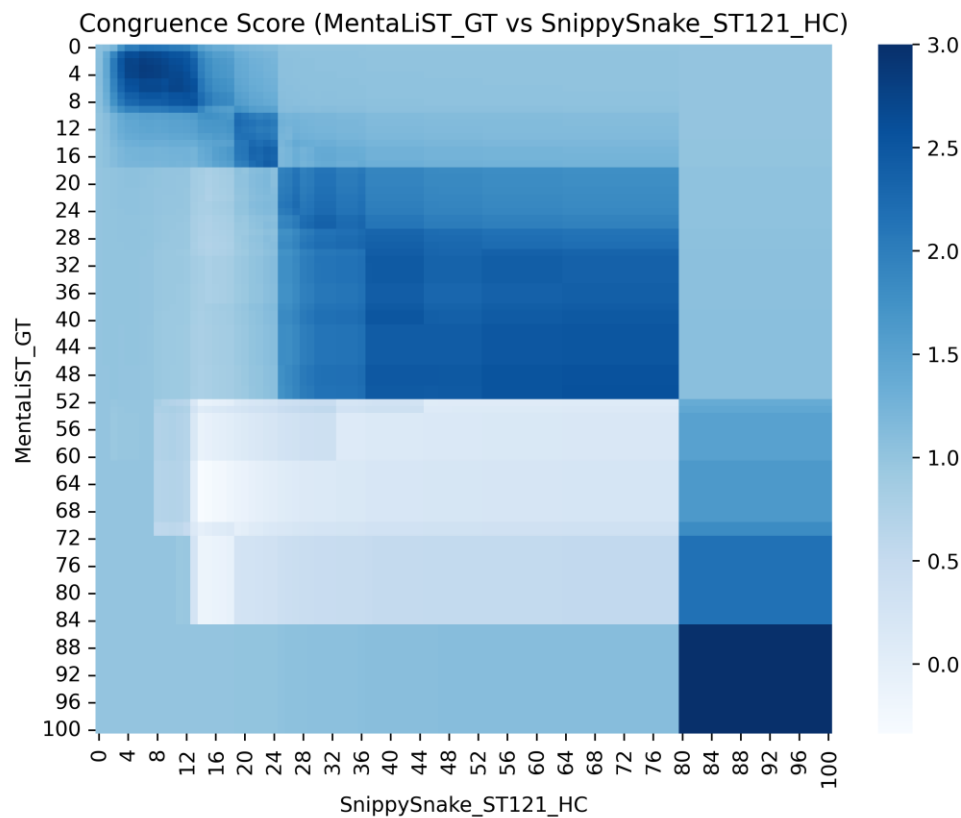


Figure S4.17.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

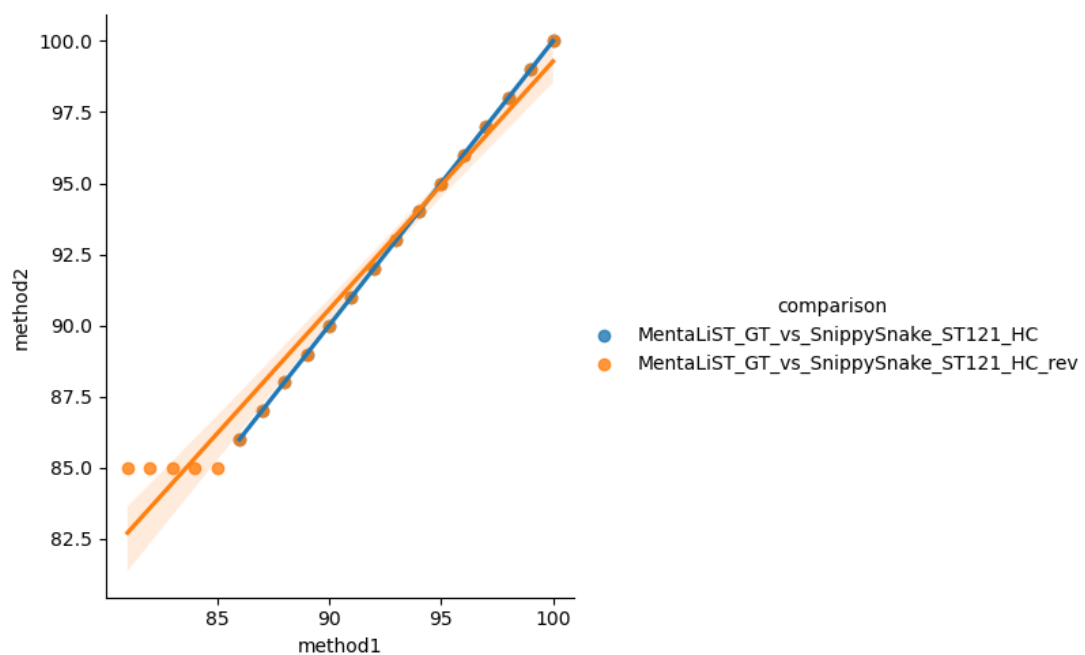


Figure S4.17.8. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 15 (blue) and 20 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

18. MentaLiST GrapeTree vs. WGSBAC 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.

	MentaLiST GrapeTree	WGSBAC single-linkage
Pipeline version	v1.0.0	-
Clustering	GrapeTree MSTreeV2 (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST121

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with $CS \geq 2.85$ were obtained.

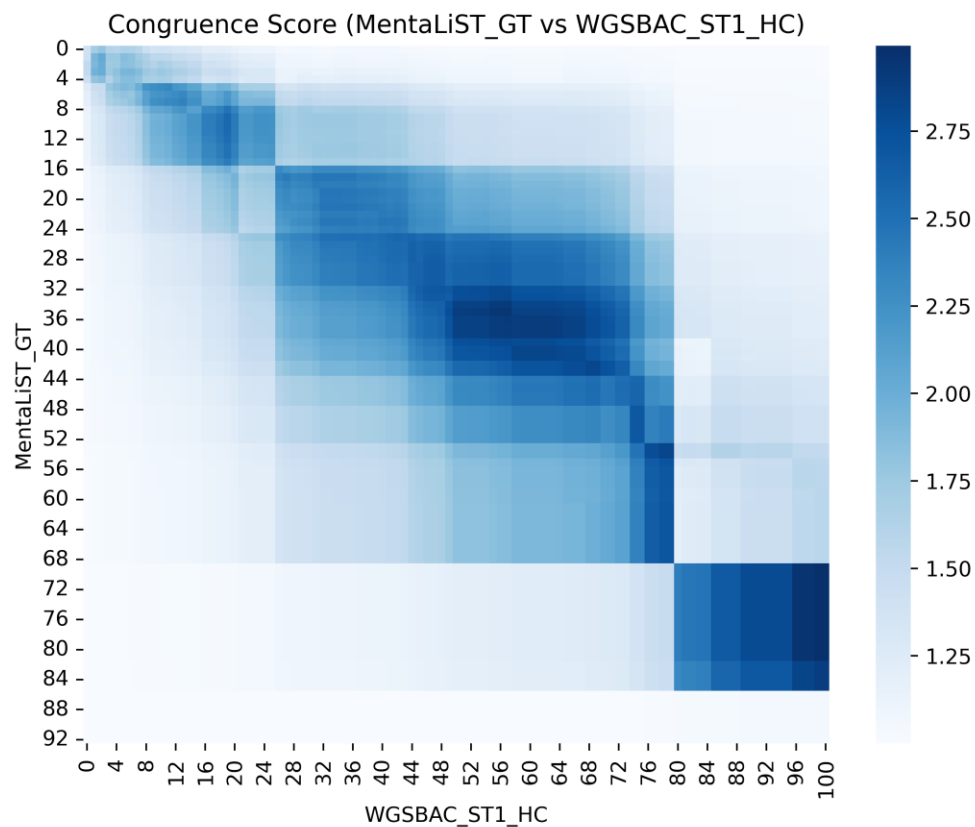


Figure S4.18.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

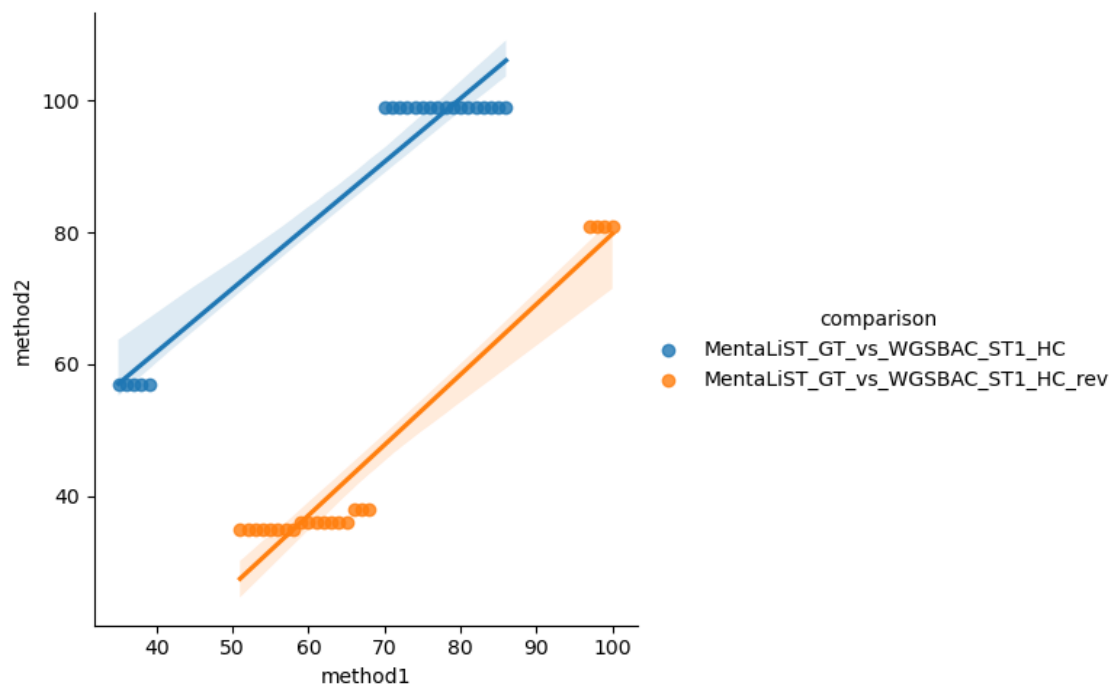


Figure S4.18.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 22 (blue) and 22 (orange) points is presented.

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with $CS \geq 2.85$ were obtained.

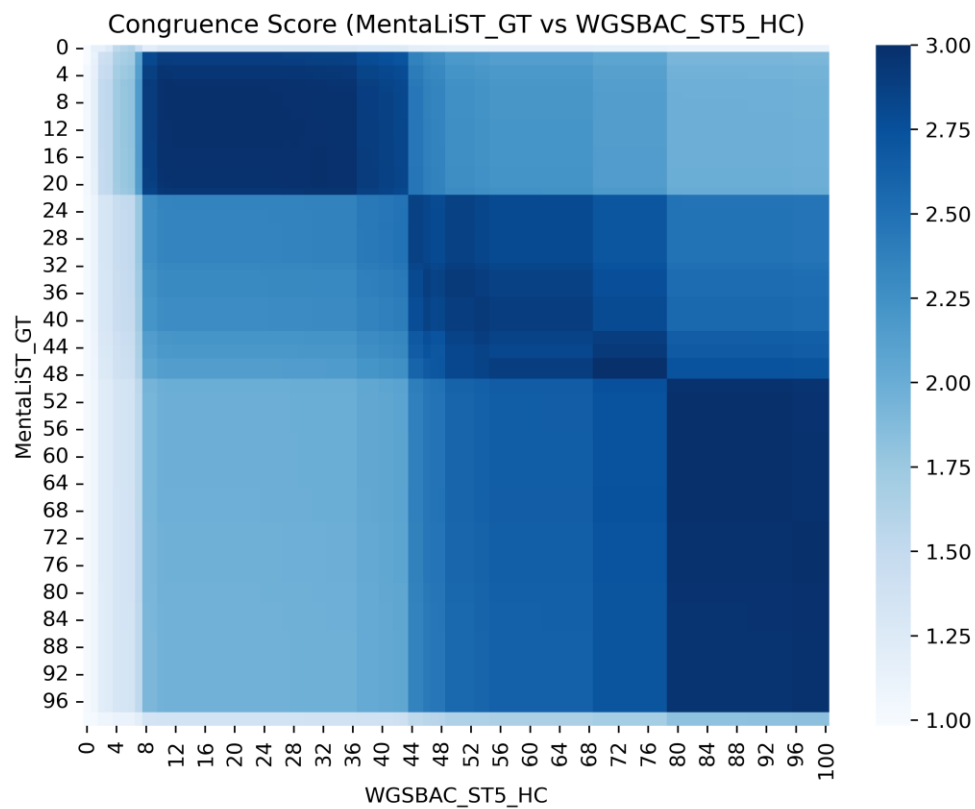


Figure S4.18.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

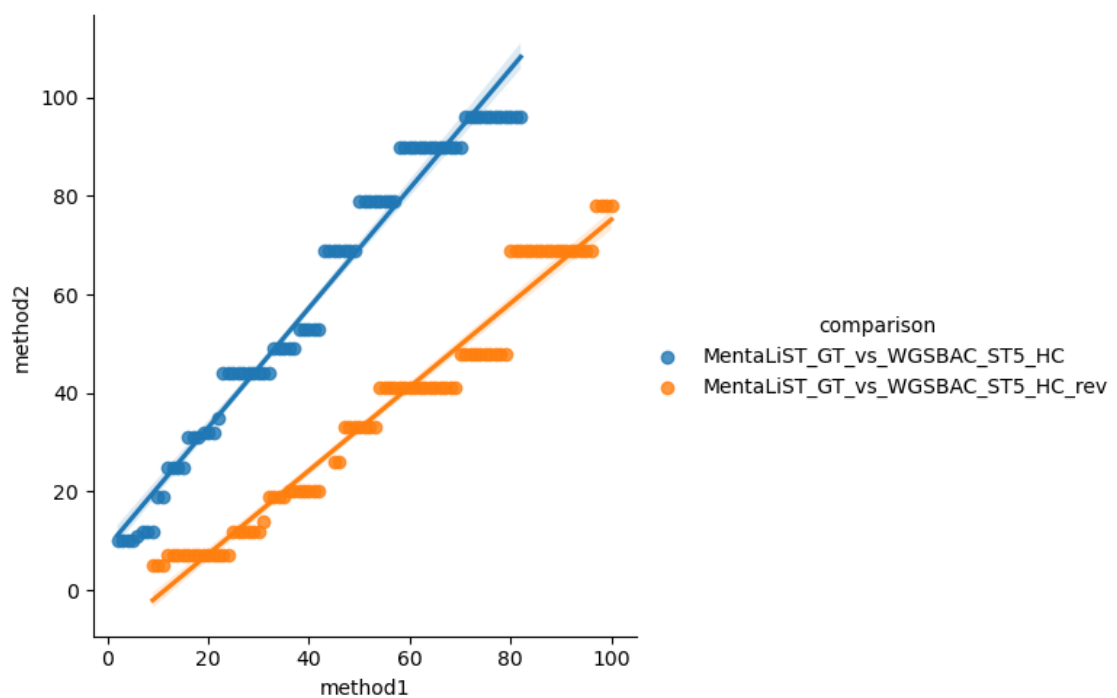


Figure S4.18.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 81 (blue) and 90 (orange) points is presented.

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with CS ≥ 2.85 were obtained.

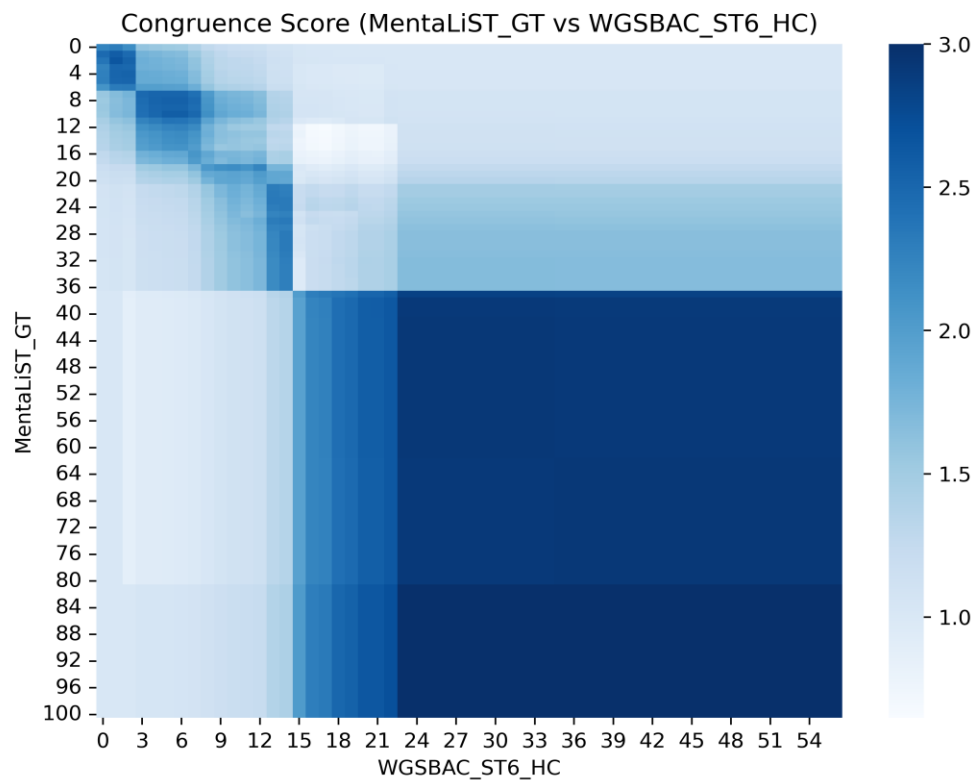


Figure S4.18.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

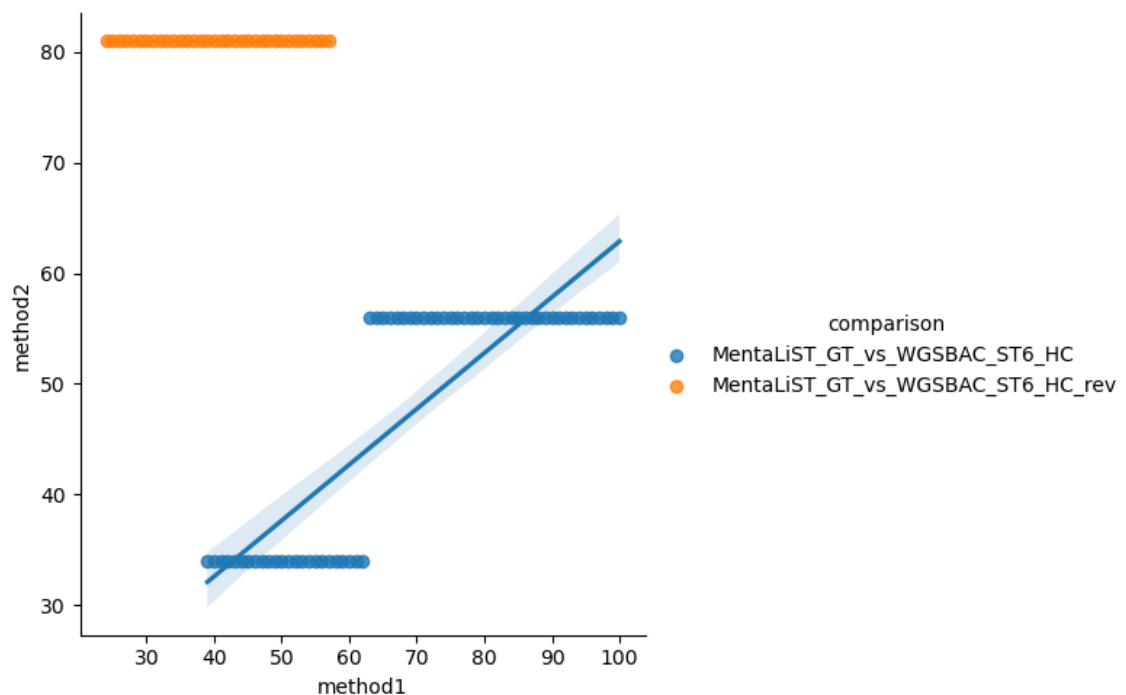


Figure S4.18.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. No linear tendency was observed. The 62 (blue) and 34 (orange) points are presented.

NOTE: Data for ST8 dataset comparisons are not presented no congruence points with $CS \geq 2.85$ were obtained.

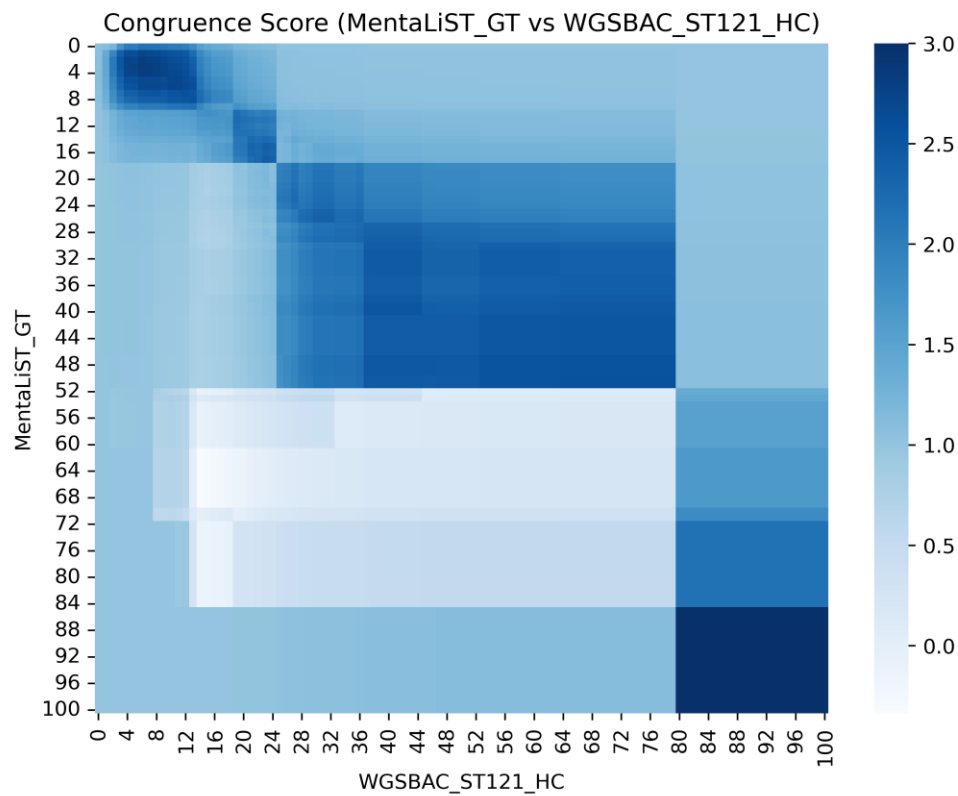


Figure S4.18.7. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

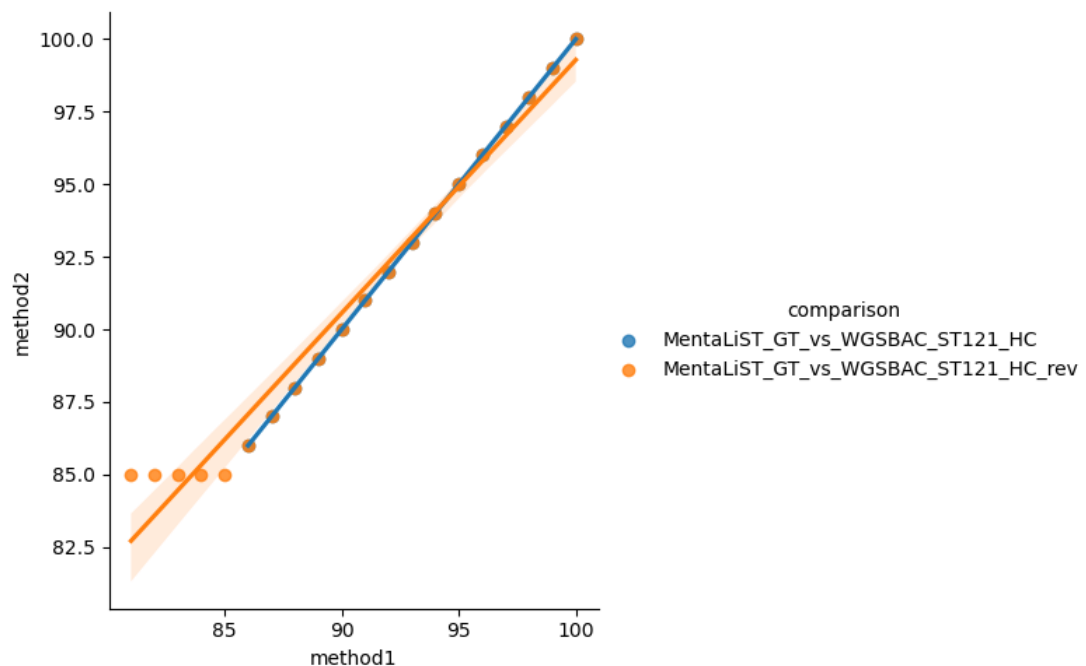


Figure S4.18.8. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 15 (blue) and 20 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

19. MentaLiST single-linkage vs. CSI Phylogeny single-linkage

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

	MentaLiST single-linkage	CSI Phylogeny single-linkage
Pipeline version	v1.0.0	v1.4
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

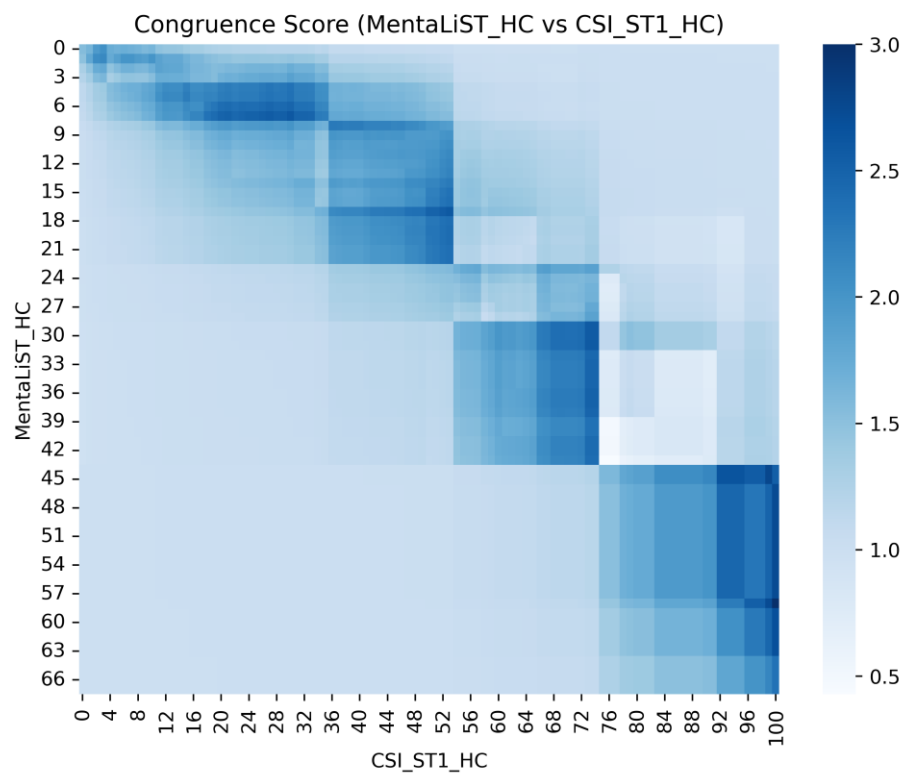


Figure S4.19.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

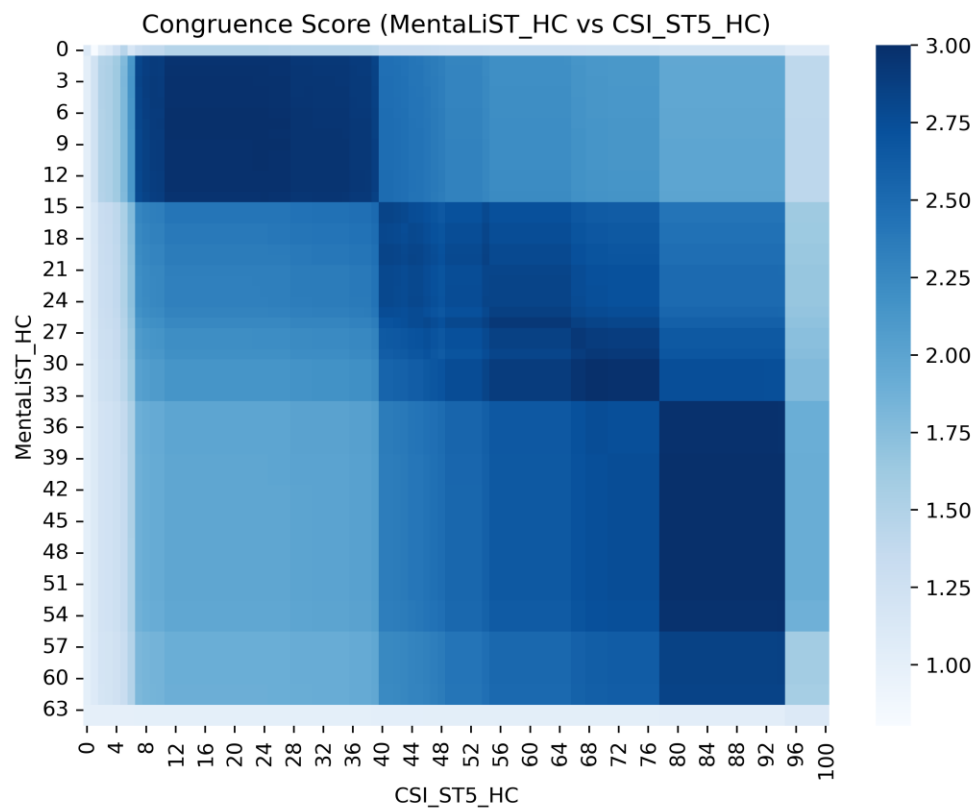


Figure S4.19.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

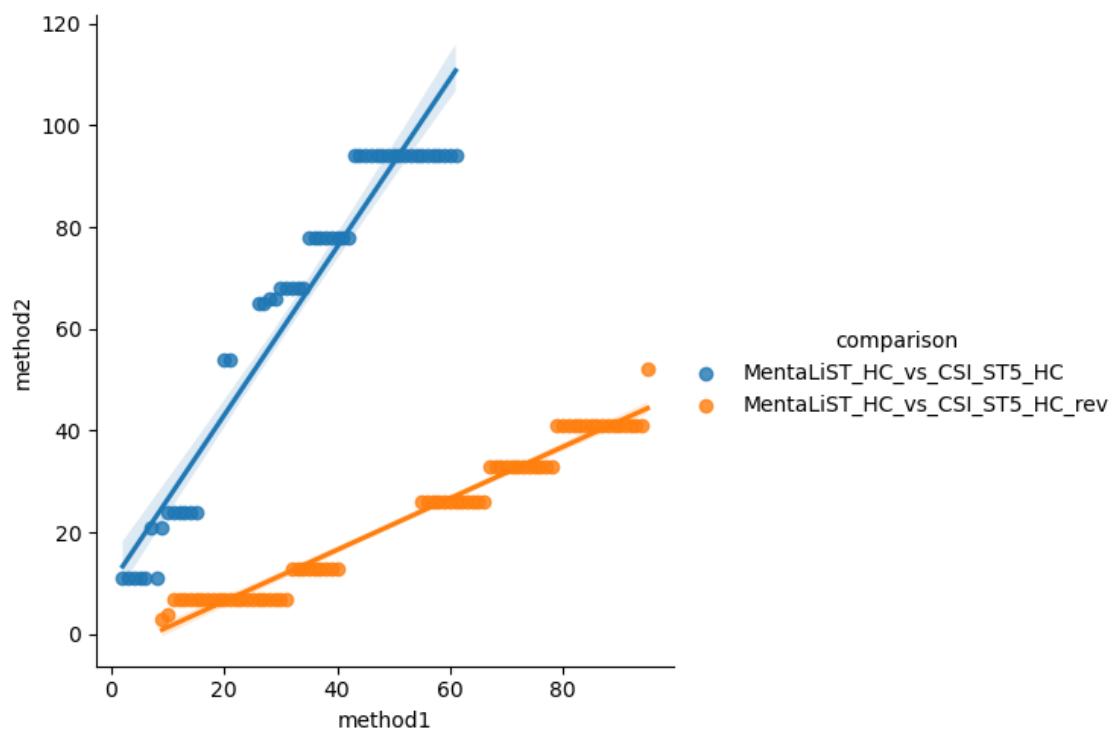


Figure S4.19.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 52 (blue) and 73 (orange) points is presented.

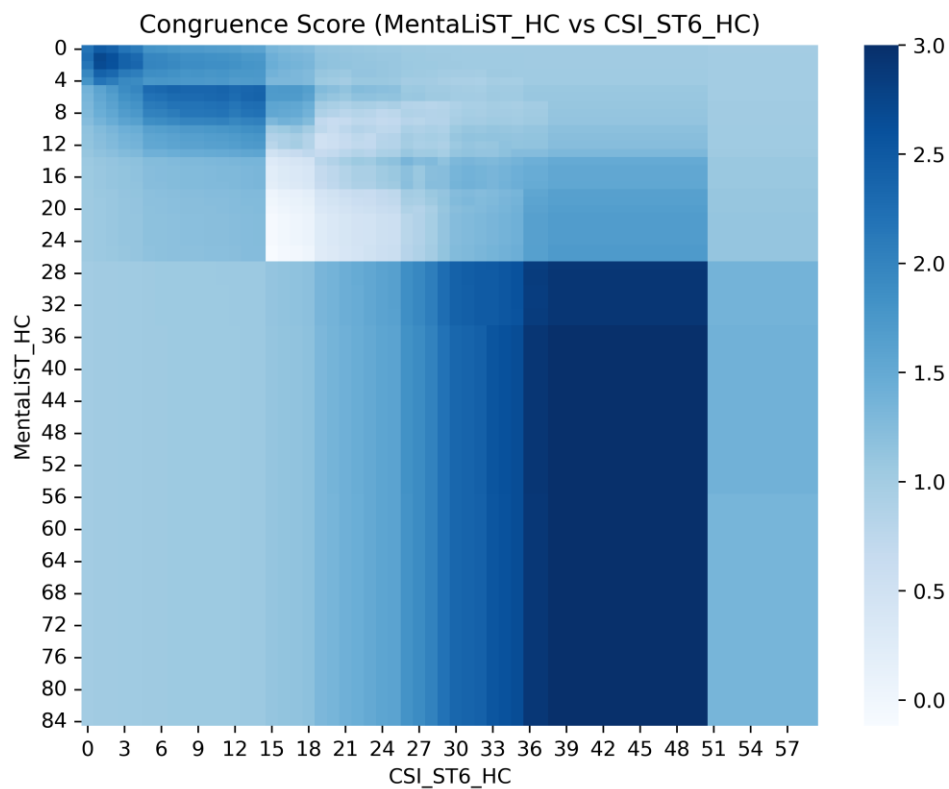


Figure S4.19.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

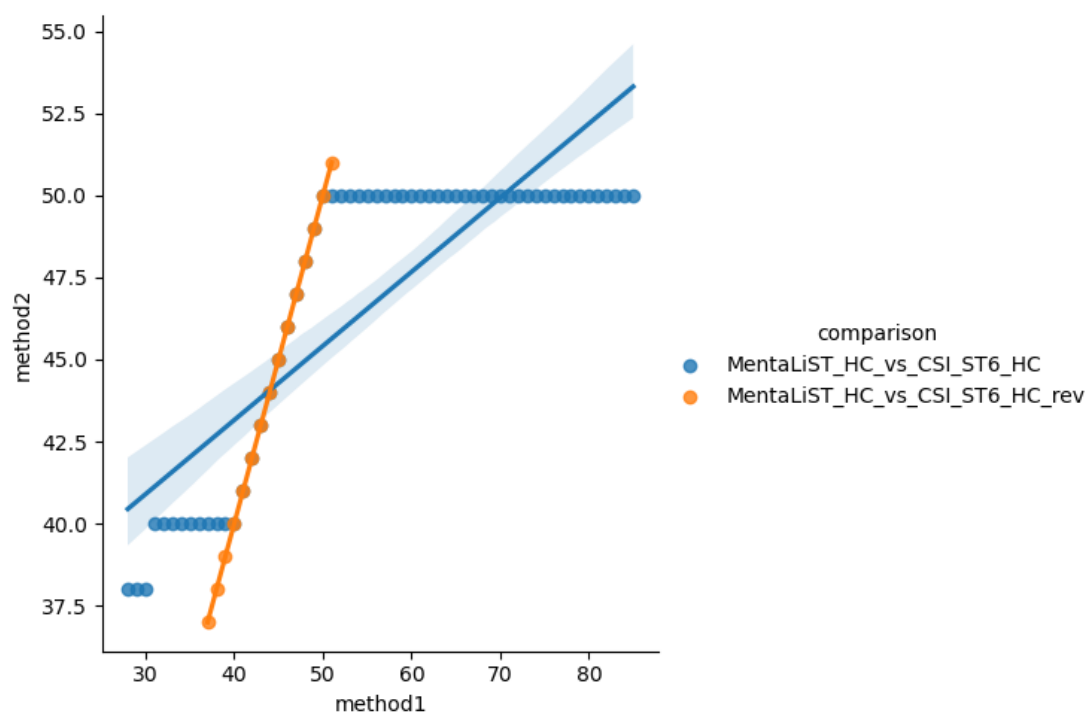


Figure S4.19.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 58 (blue) and 15 (orange) points is presented.

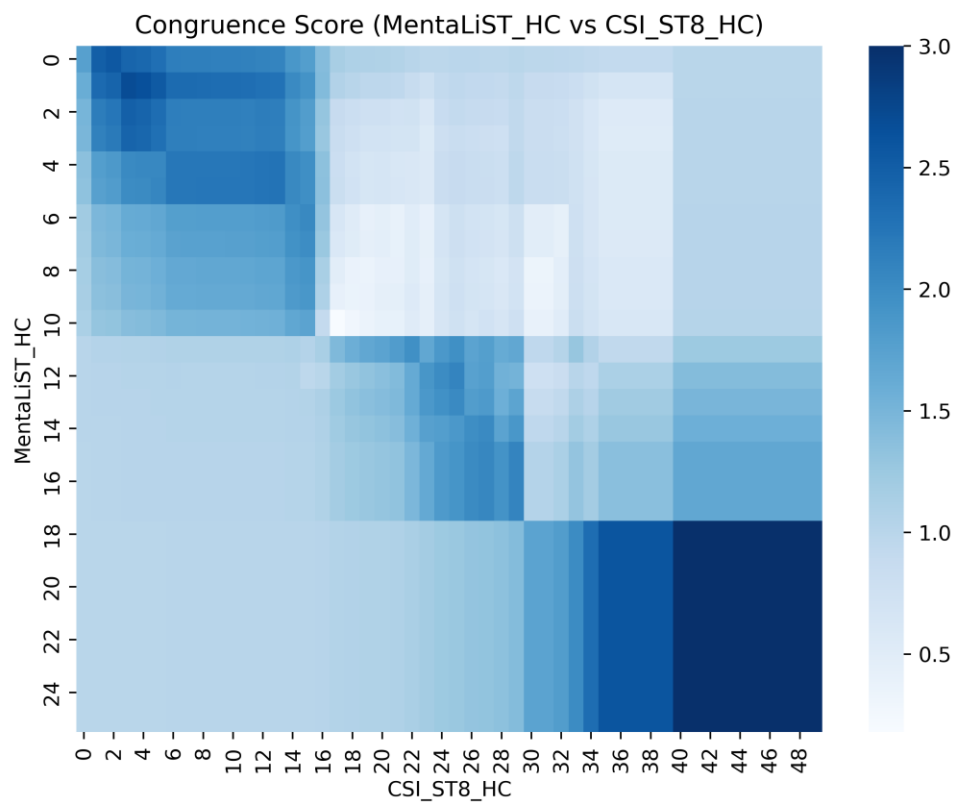


Figure S4.19.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

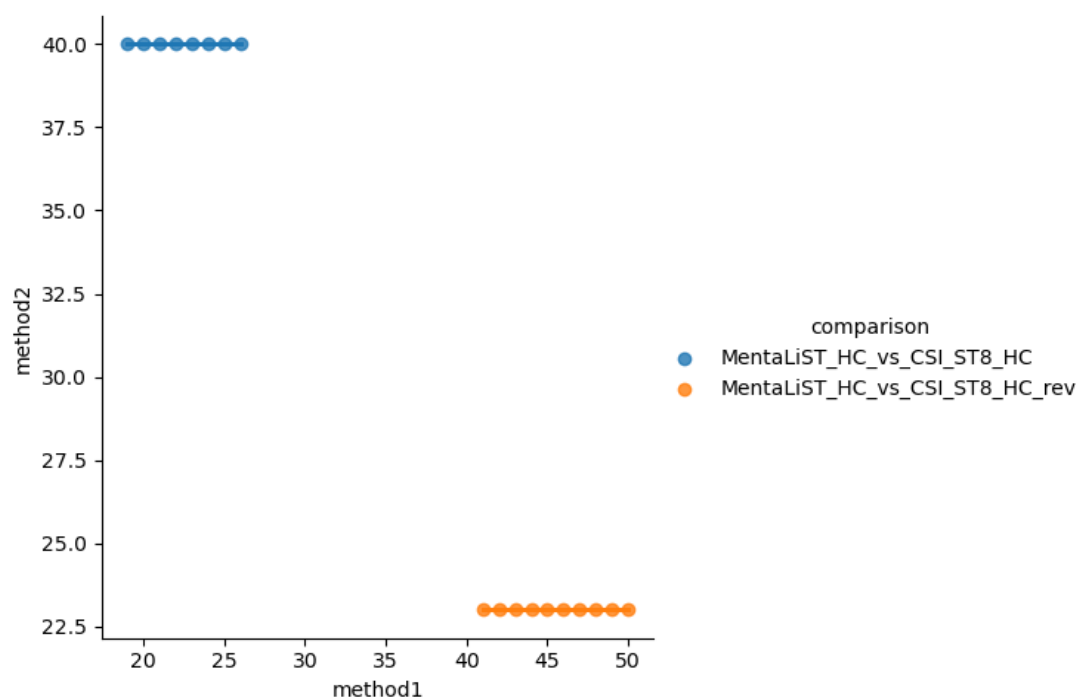


Figure S4.19.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. No linear tendency was observed. The 8 (blue) and 10 (orange) points are presented.

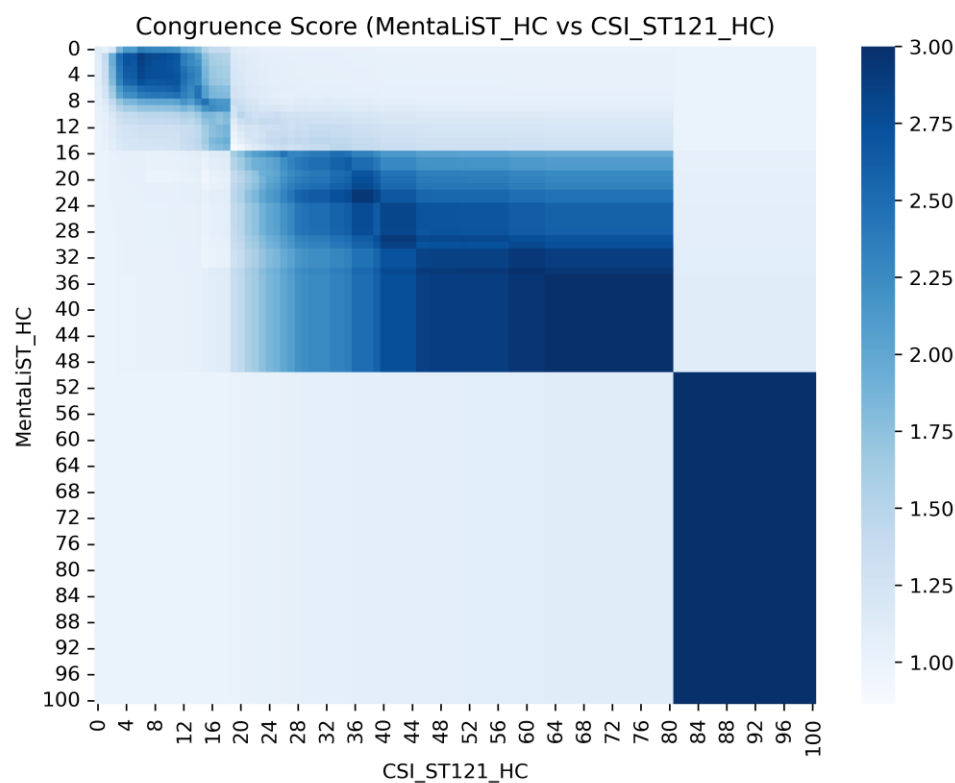


Figure S4.19.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

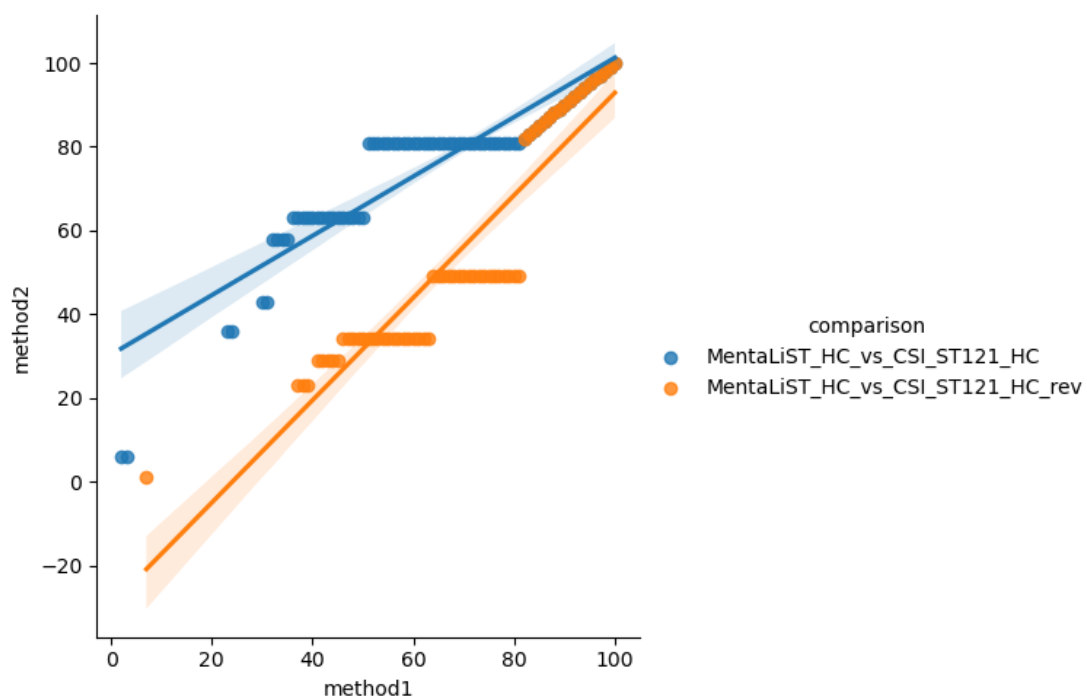


Figure S4.19.10. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST121. A linear tendency line supported by 75 (blue) and 64 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

20. MentaLiST single-linkage vs. snippySnake single-linkage

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

	MentaLiST single-linkage	snippySnake single-linkage
Pipeline version	v1.0.0	v1.1.0
Clustering	HC single-linkage (ReporTree)	HC single-linkage (ReporTree)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

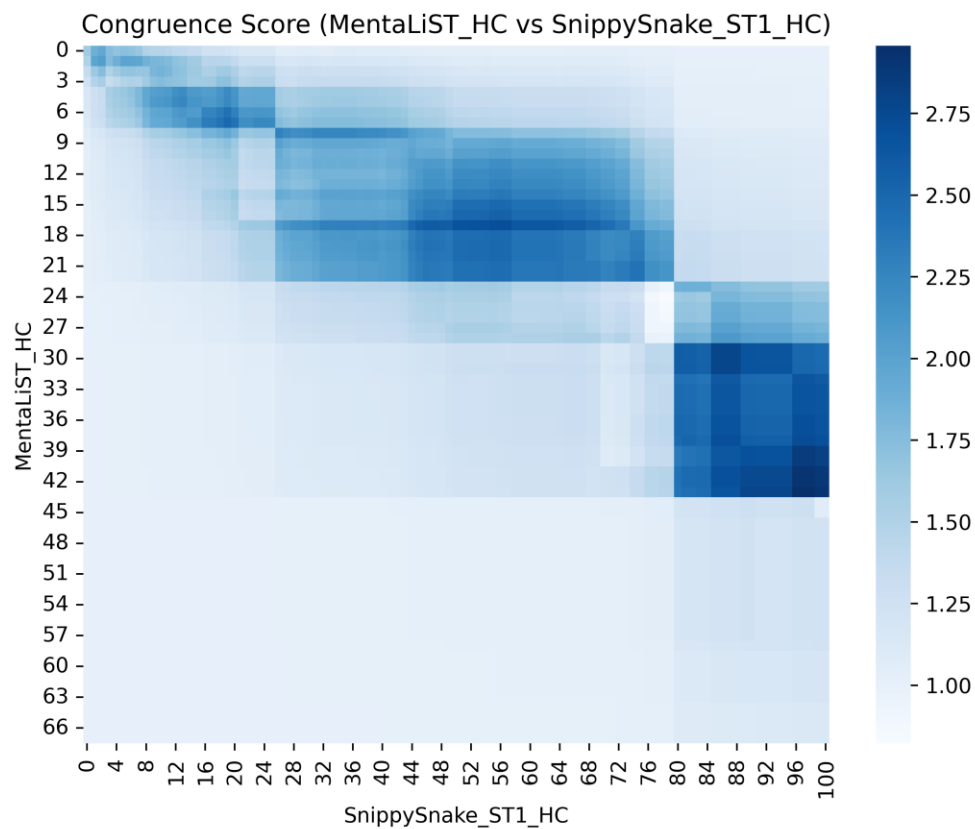


Figure S4.20.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

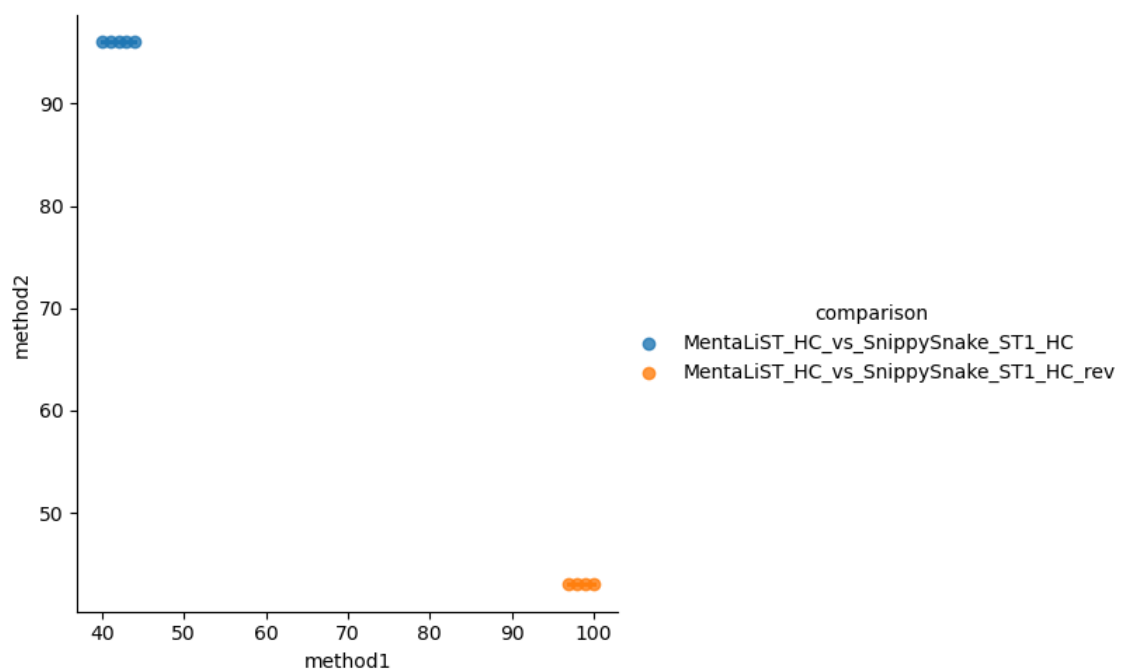


Figure S4.20.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. No linear tendency was observed. The 5 (blue) and 4 (orange) points are presented.

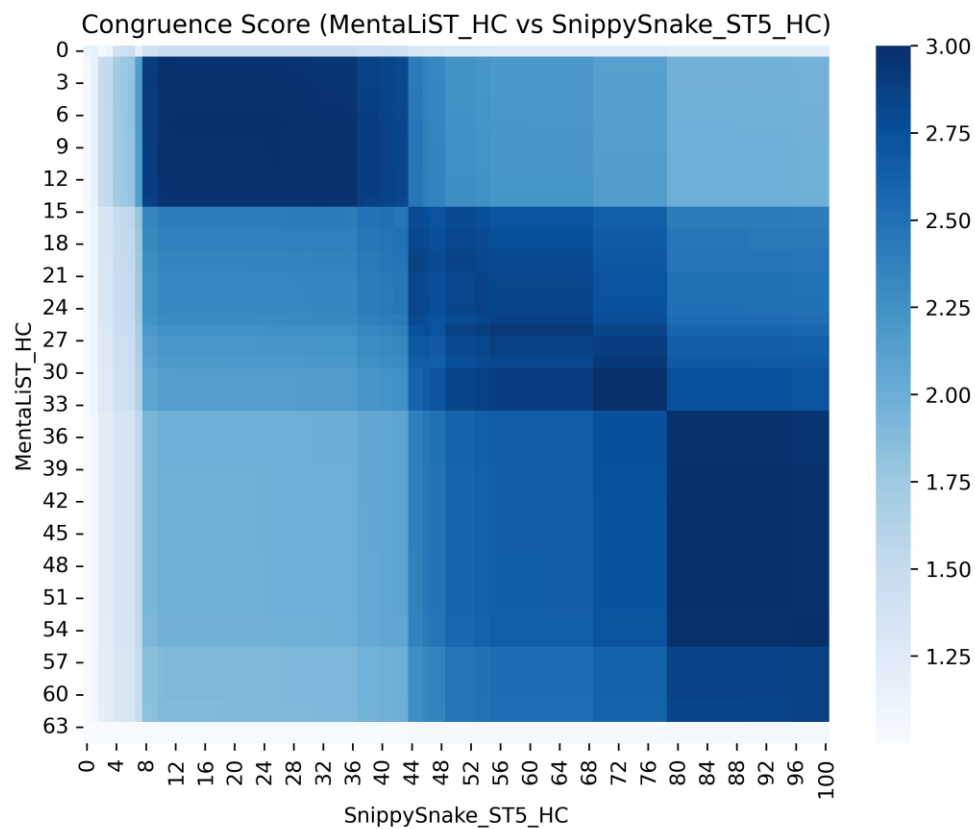


Figure S4.20.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

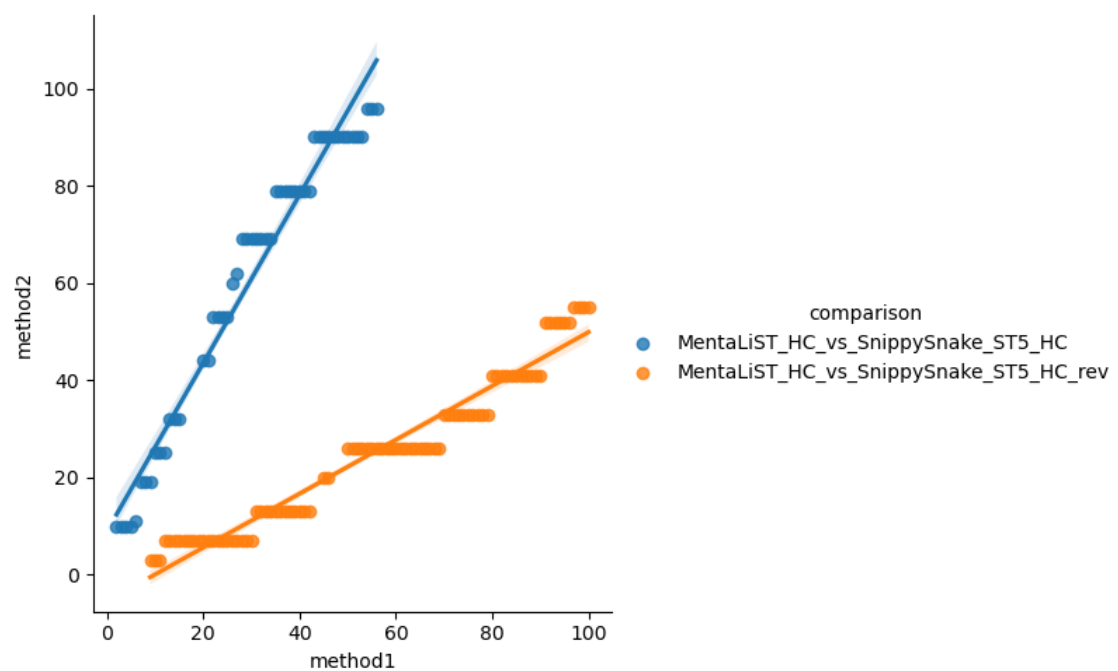


Figure S4.20.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 51 (blue) and 87 (orange) points is presented.

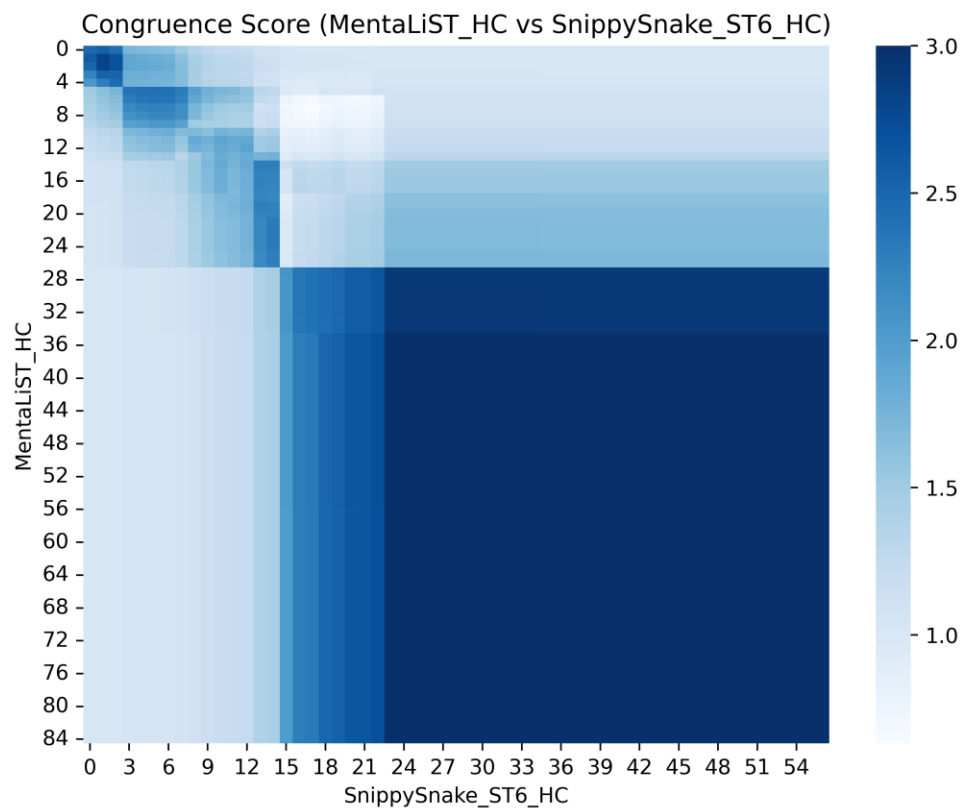


Figure S4.20.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

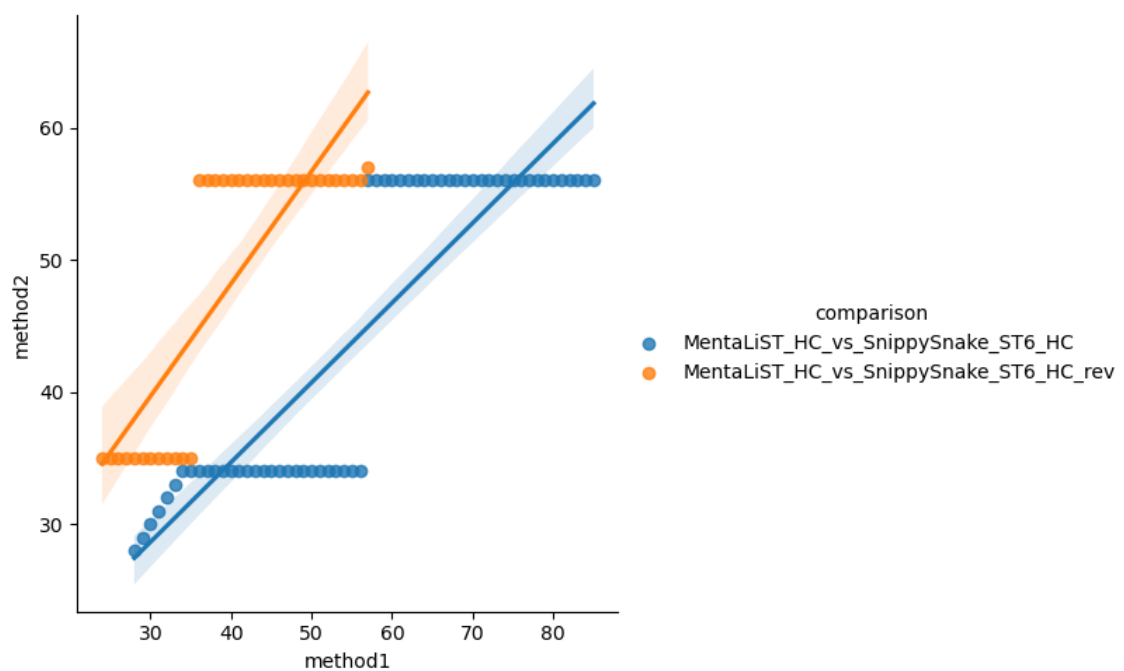


Figure S4.20.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 58 (blue) and 34 (orange) points is presented.

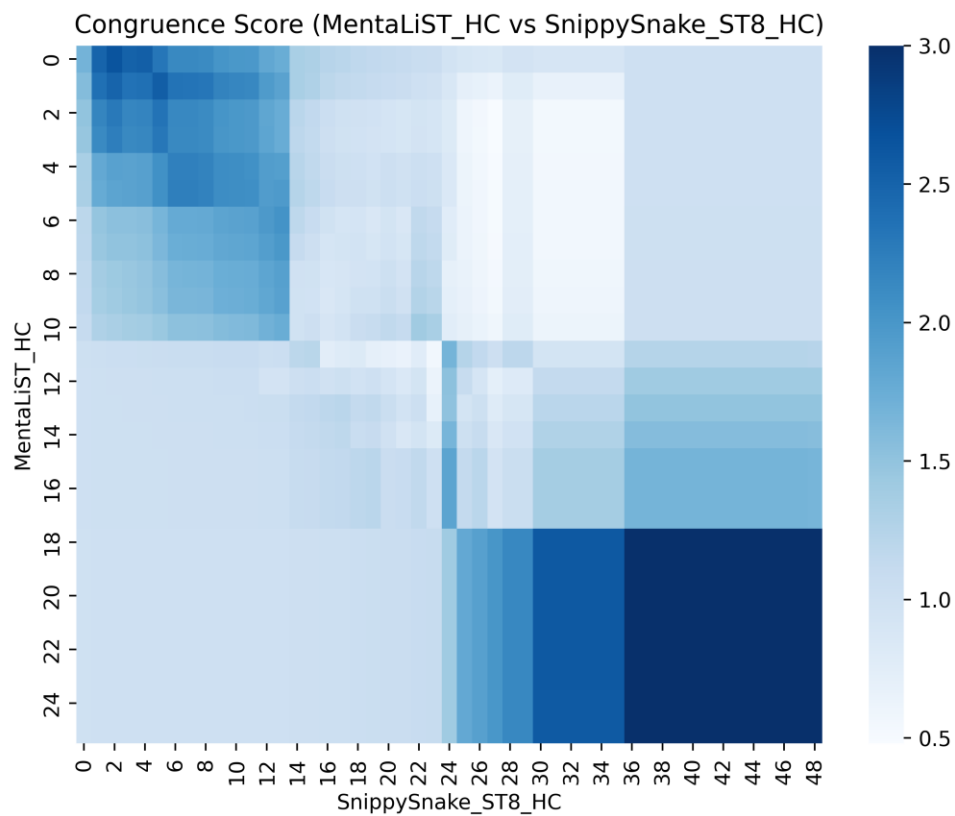


Figure S4.20.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

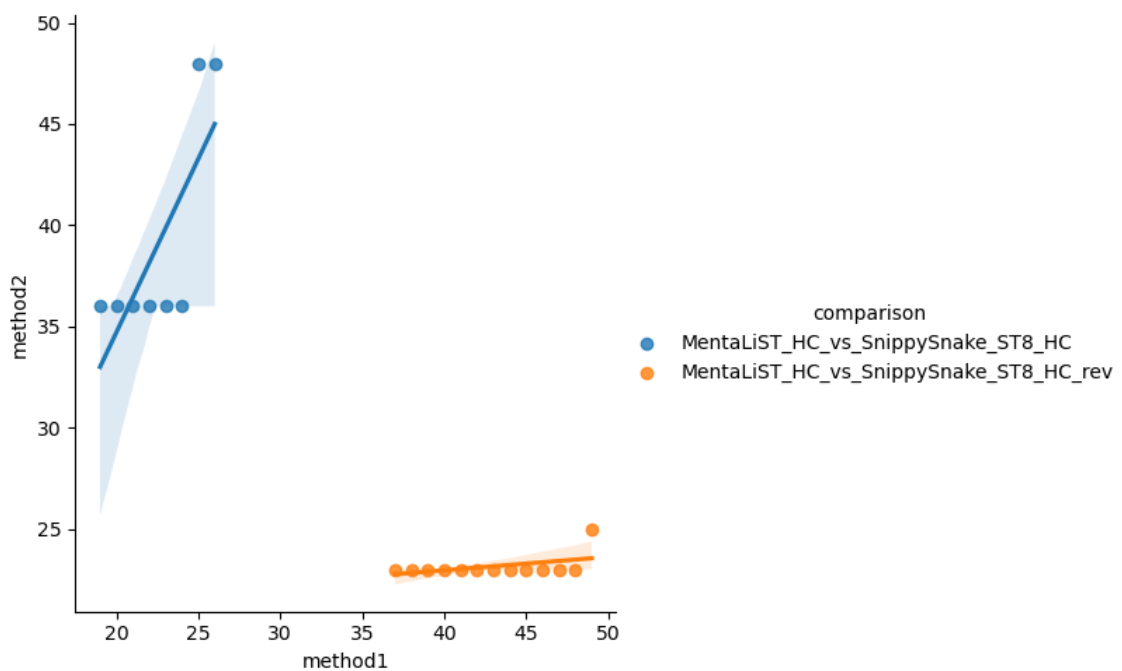


Figure S4.1.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 8 (blue) and 13 (orange) points is presented.

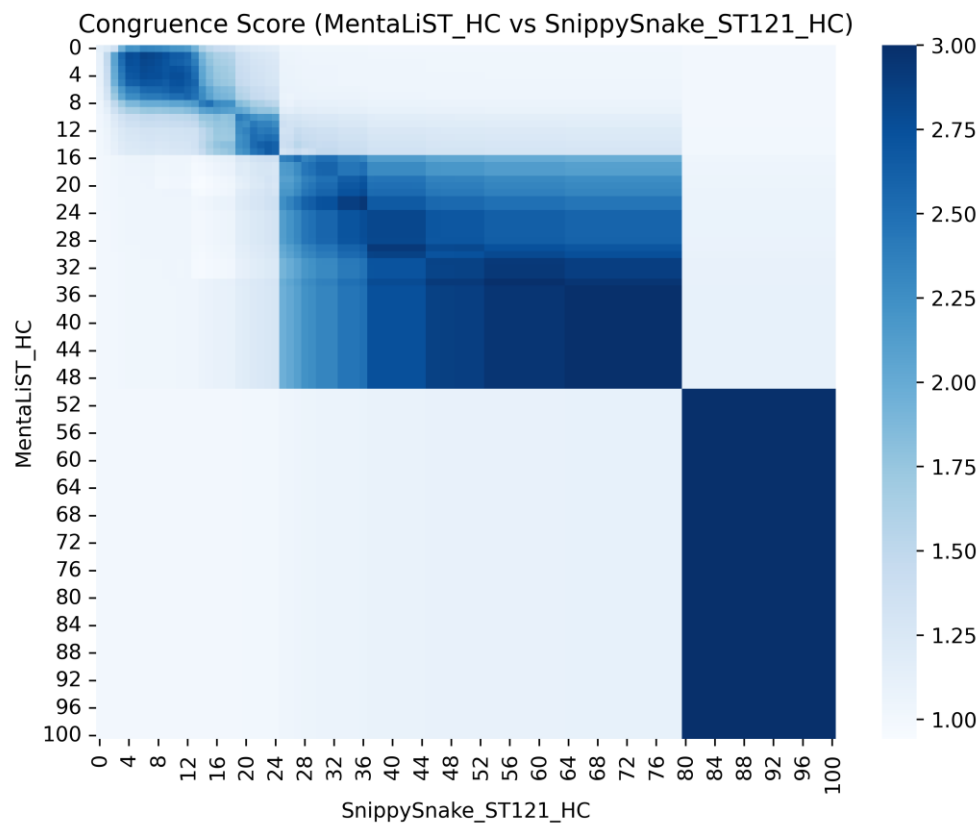


Figure S4.20.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

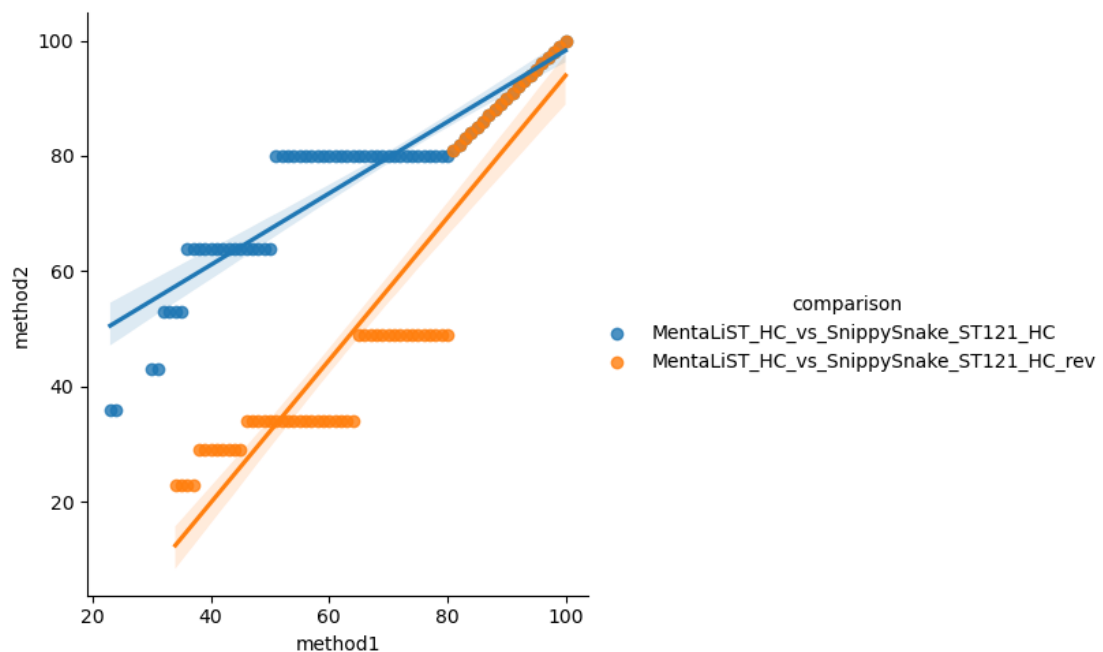


Figure S4.20.10. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST121. A linear tendency line supported by 73 (blue) and 67 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

21. MentaLiST single-linkage vs. WGSBAC single-linkage

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

	MentaLiST single-linkage	WGSBAC single-linkage
Pipeline version	v1.0.0	-
Clustering	HC single-linkage (ReporTree)	HC single-linkage (laboratory pipeline)
Schema / Reference	Moura	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

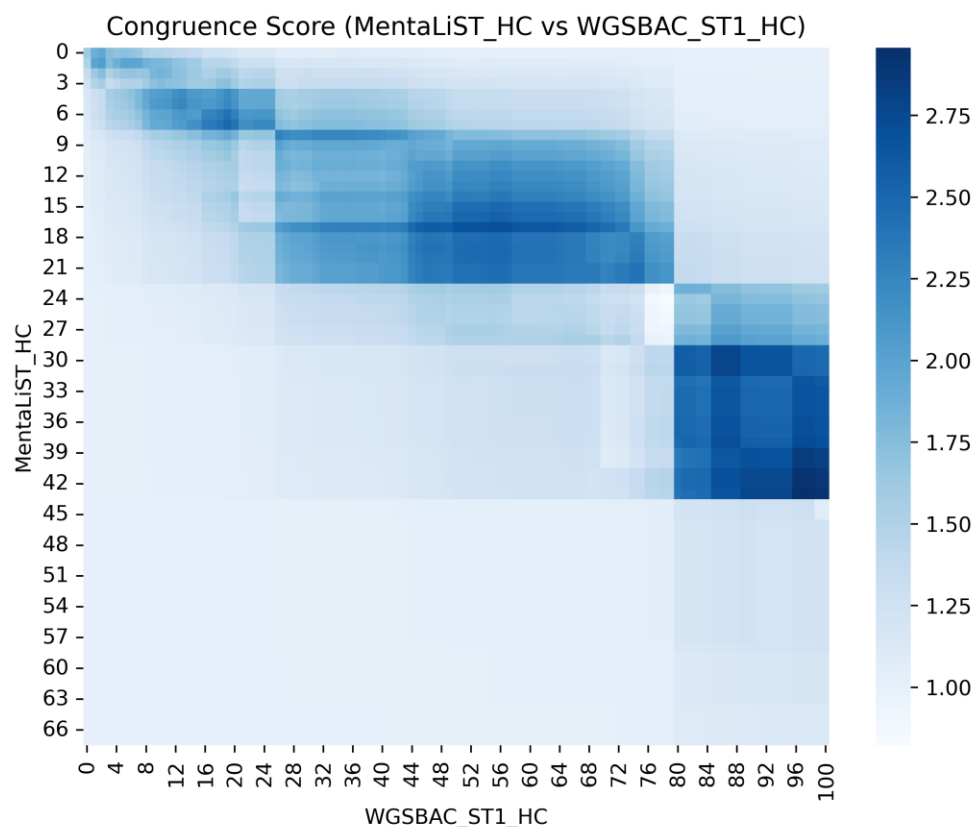


Figure S4.21.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

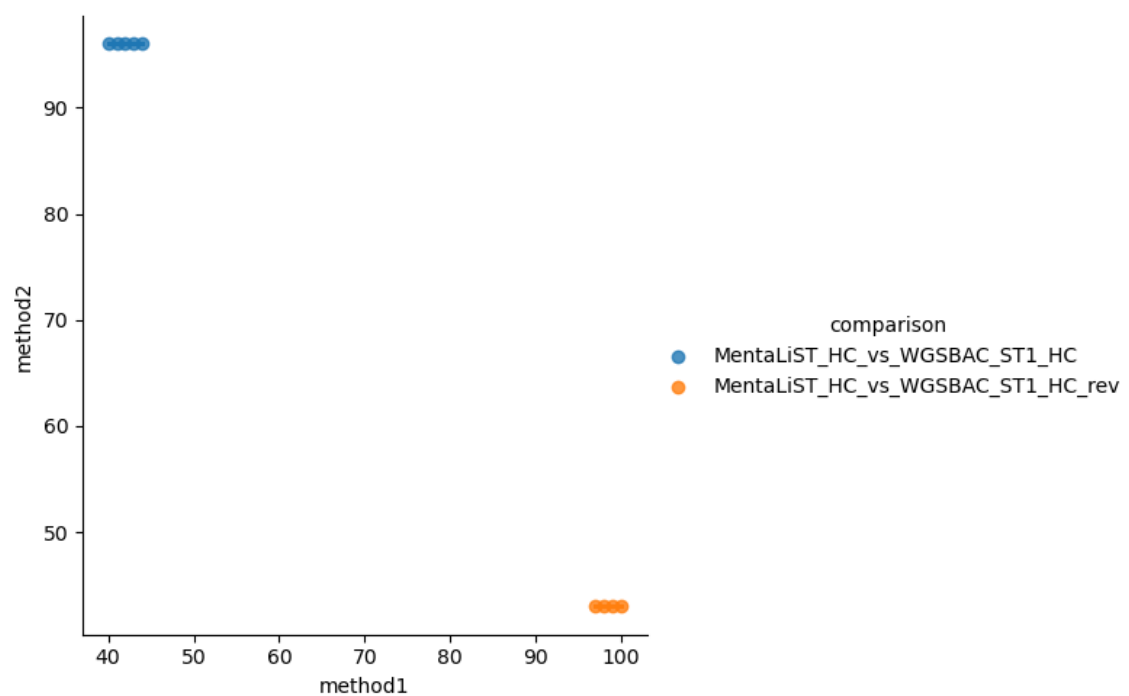


Figure S4.21.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST1. No linear tendency was observed. The 5 (blue) and 4 (orange) points are presented.

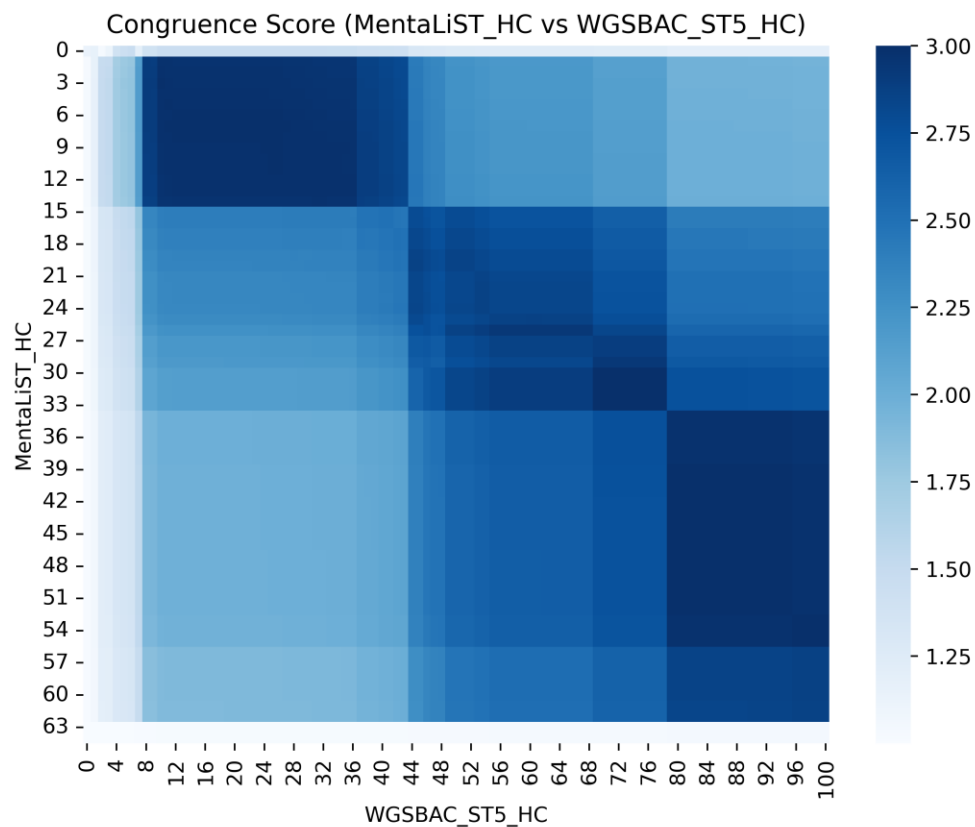


Figure S4.21.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

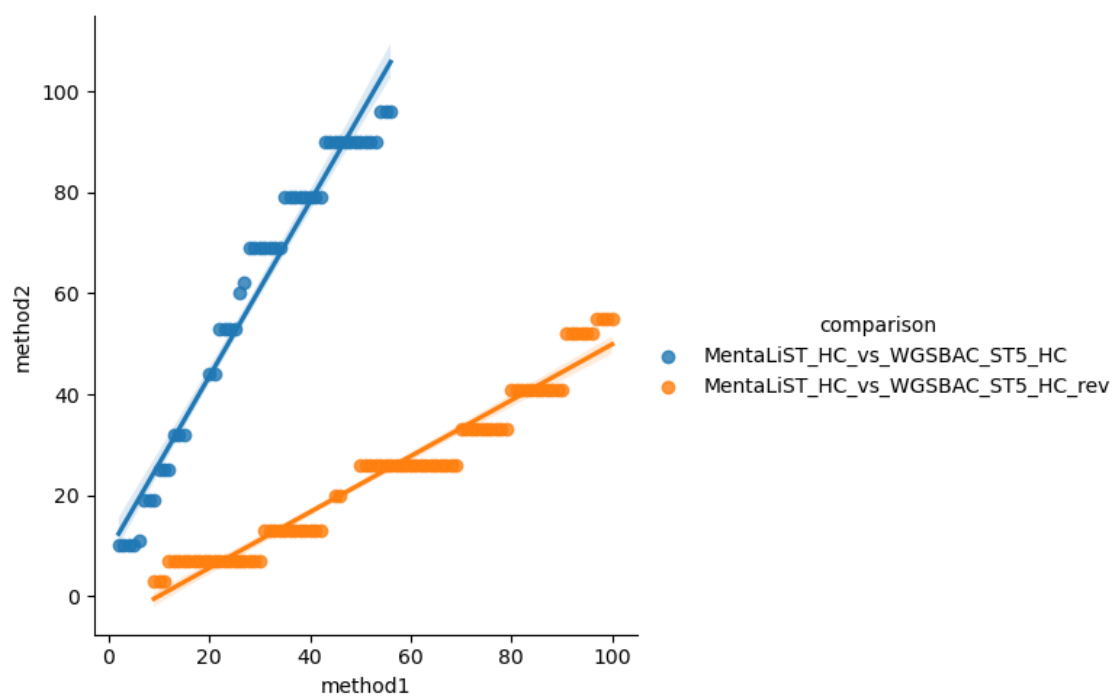


Figure S4.21.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 51 (blue) and 87 (orange) points is presented.

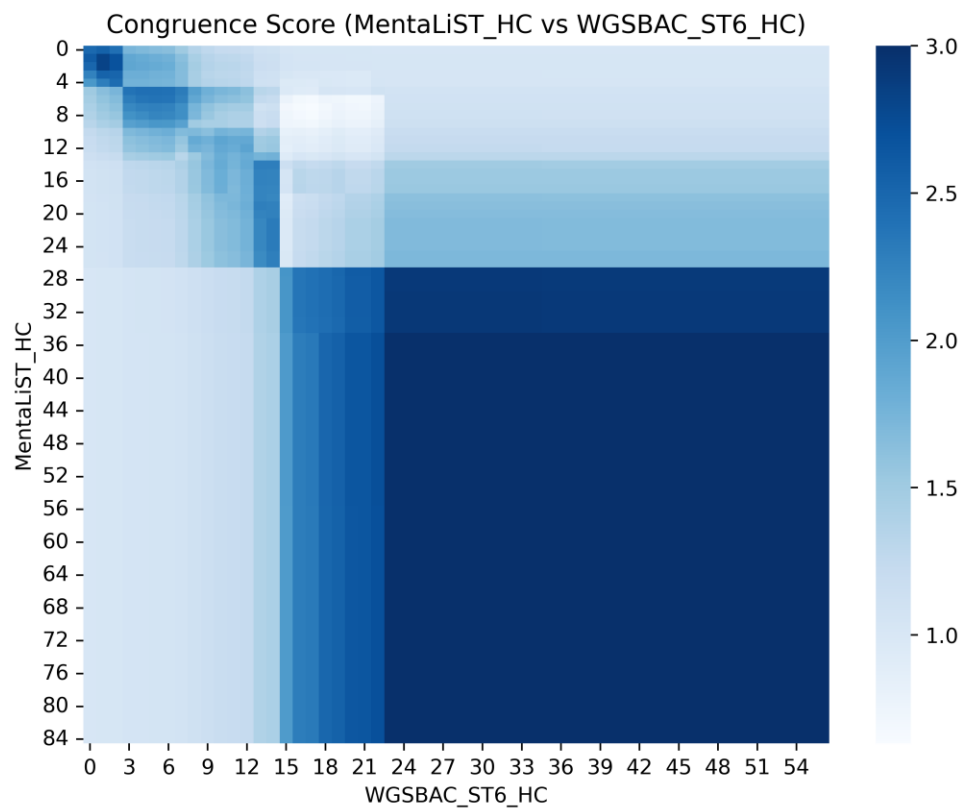


Figure S4.21.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

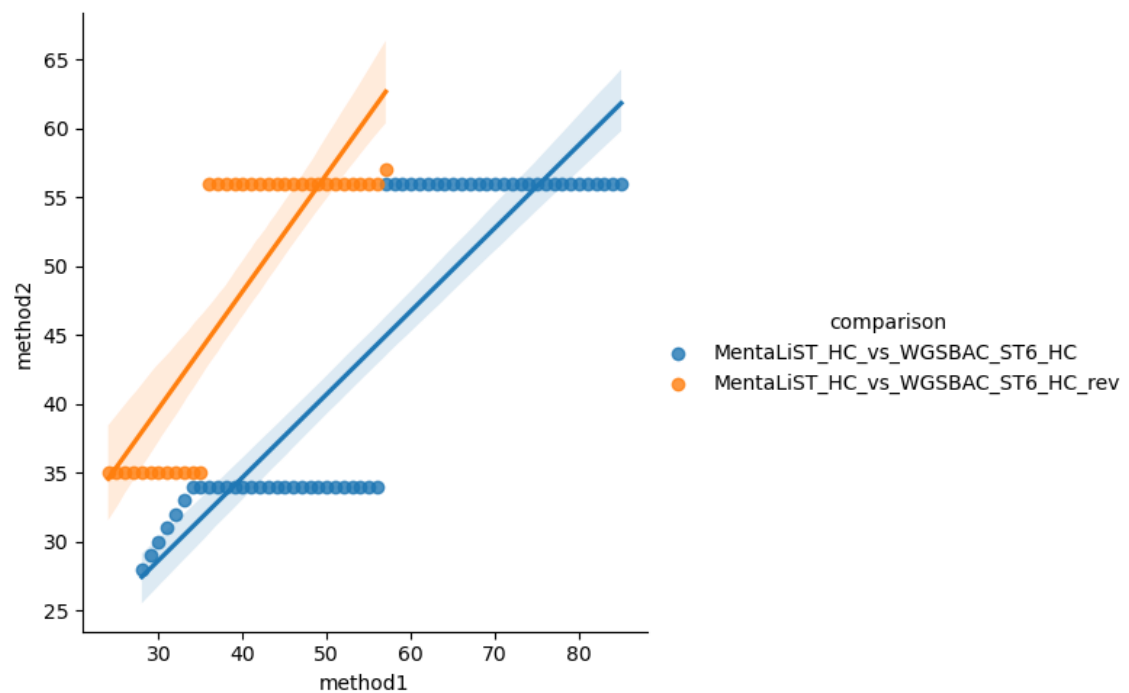


Figure S4.21.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 58 (blue) and 34 (orange) points is presented.

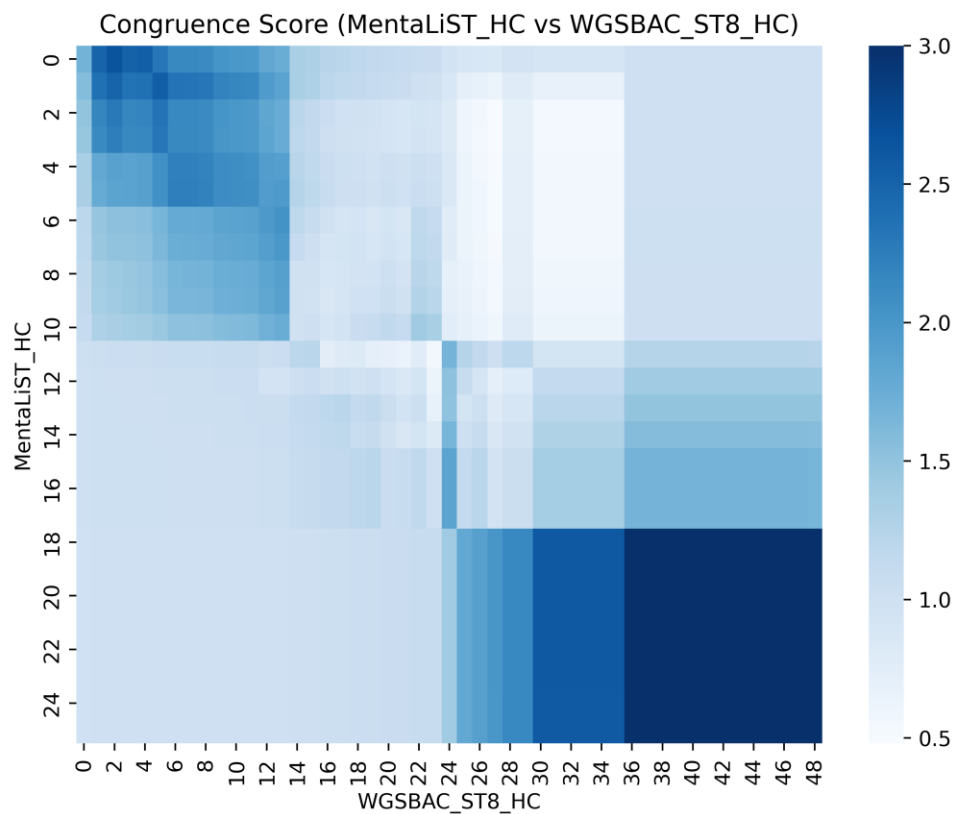


Figure S4.21.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

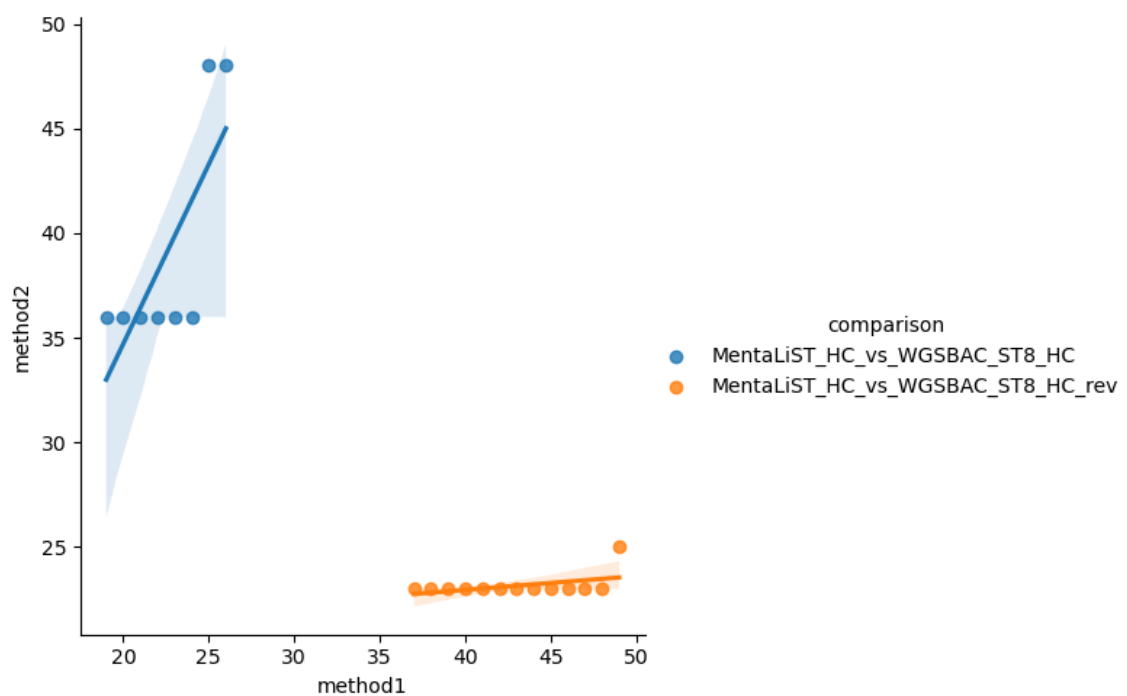


Figure S4.21.12. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 8 (blue) and 13 (orange) points is presented.

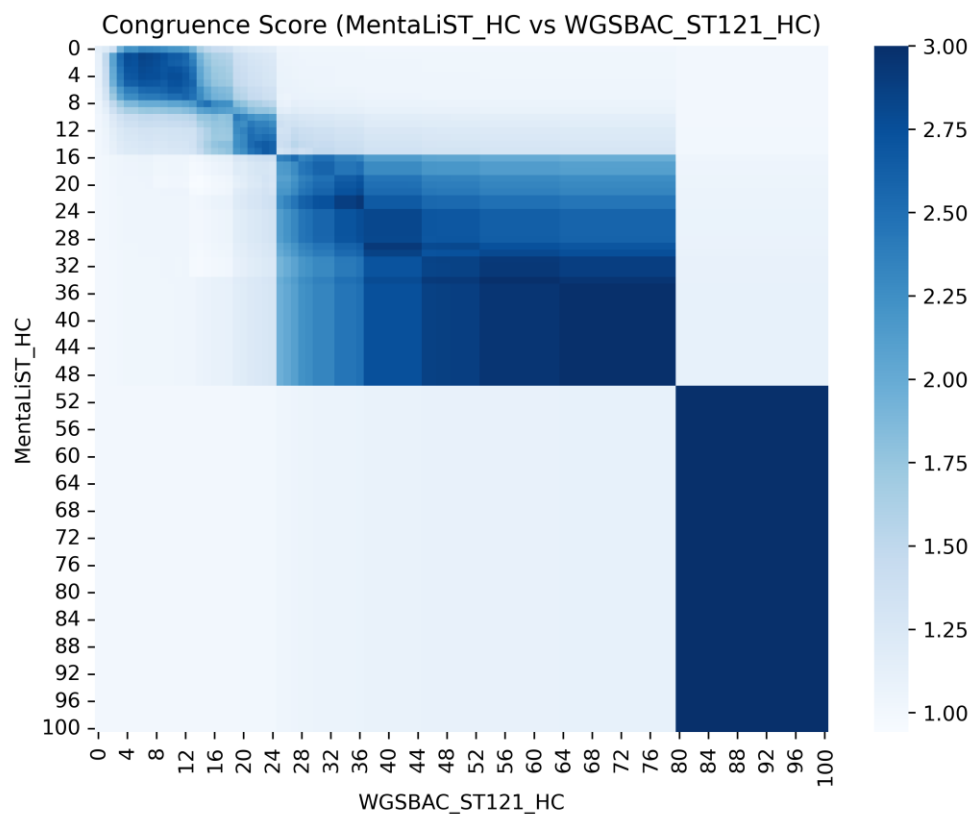


Figure S4.21.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

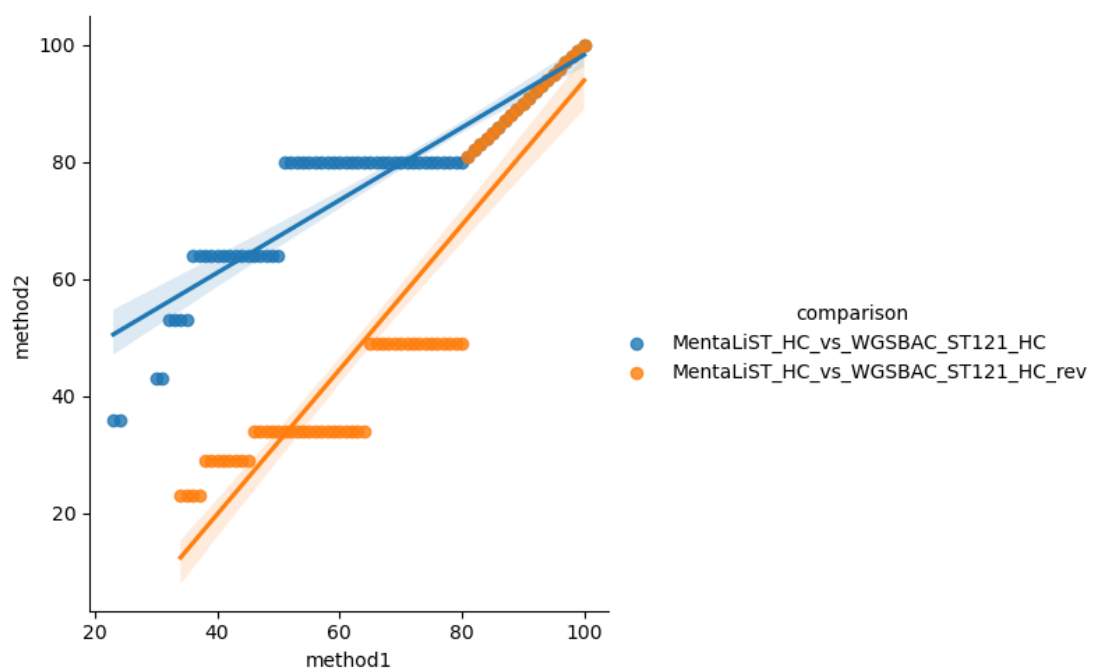


Figure S4.21.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST121. A linear tendency line supported by 73 (blue) and 67 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

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

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

	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	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

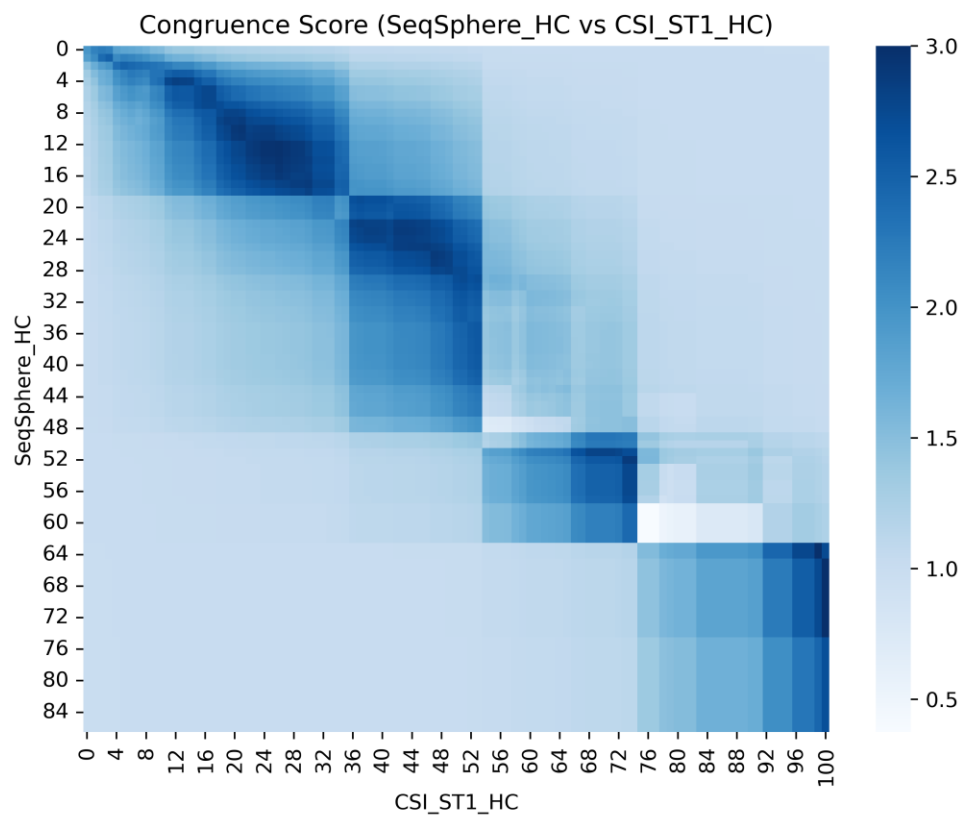


Figure S4.22.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

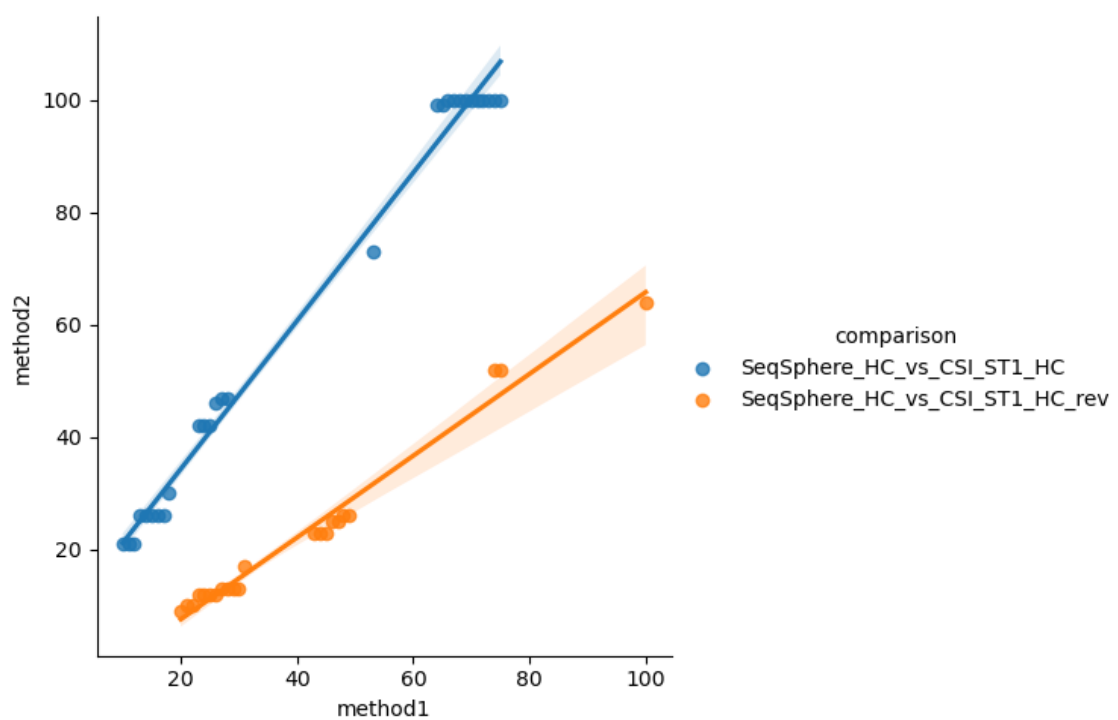


Figure S4.22.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 28 (blue) and 22 (orange) points is presented.

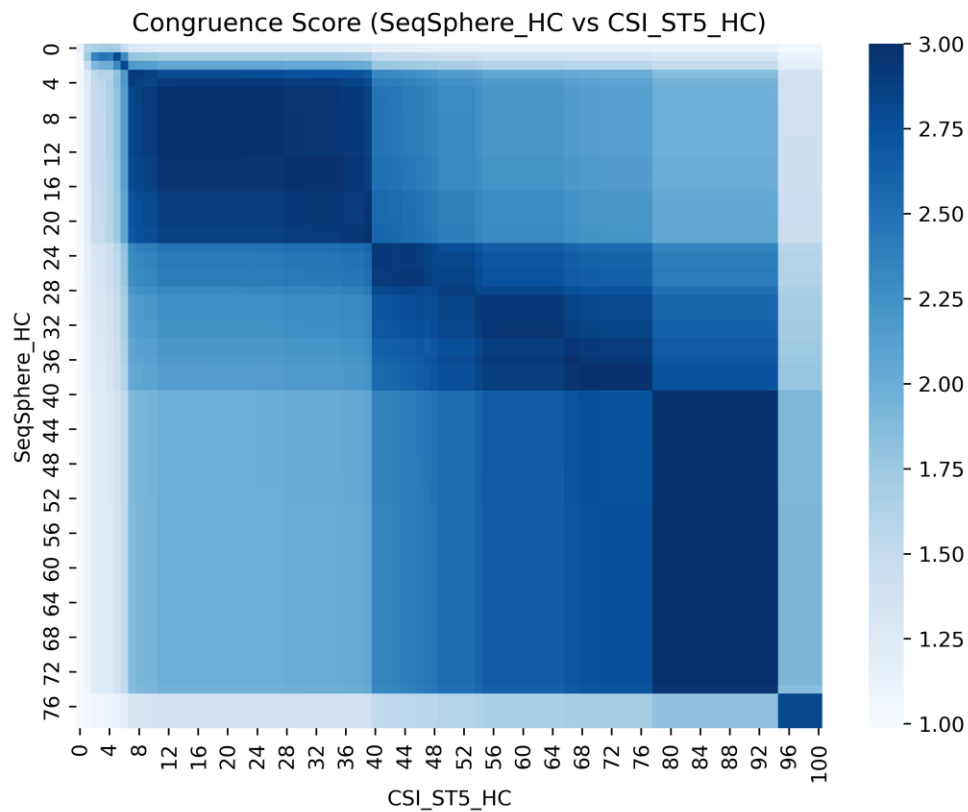


Figure S4.22.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

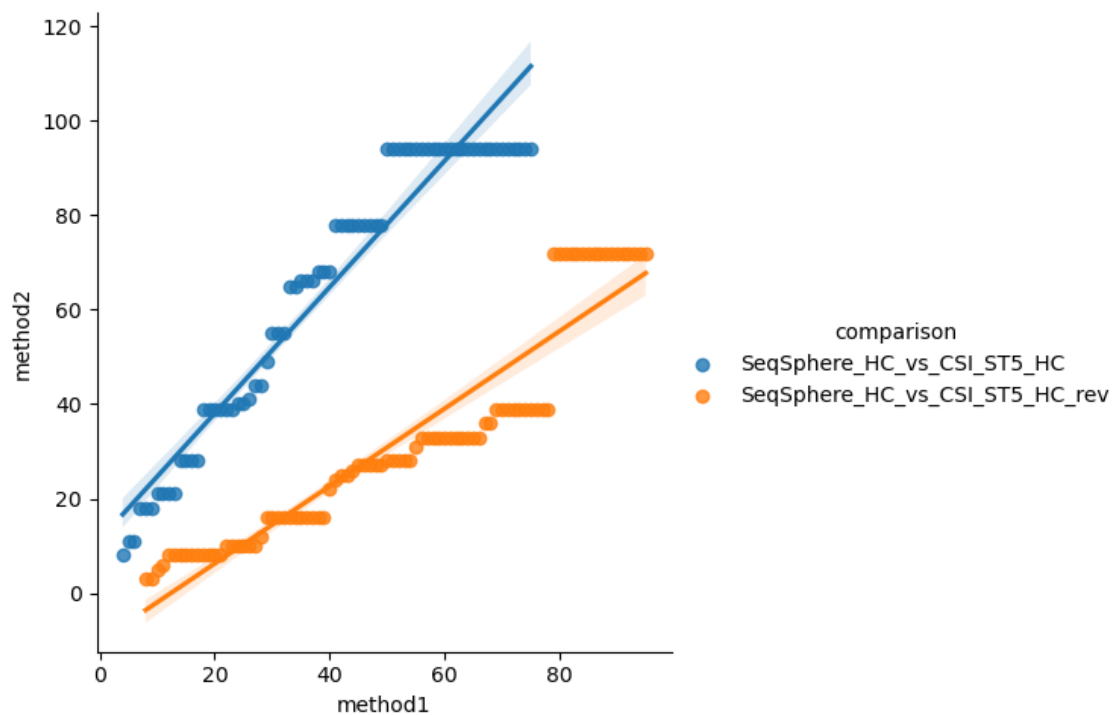


Figure S4.22.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 72 (blue) and 88 (orange) points is presented.

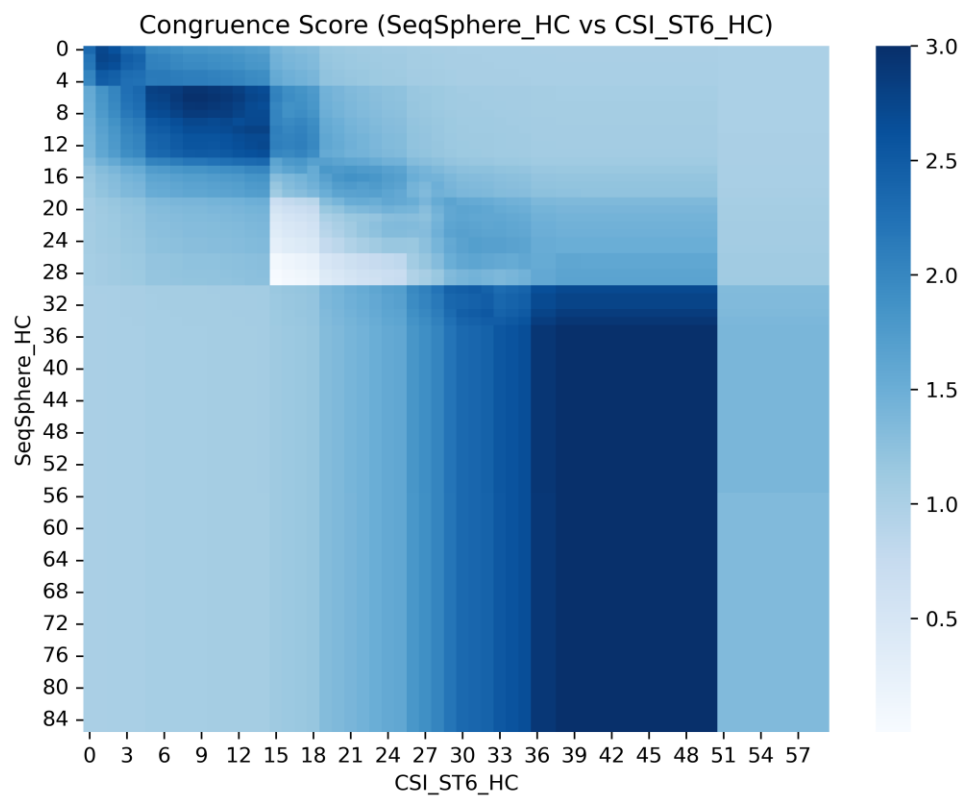


Figure S4.22.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

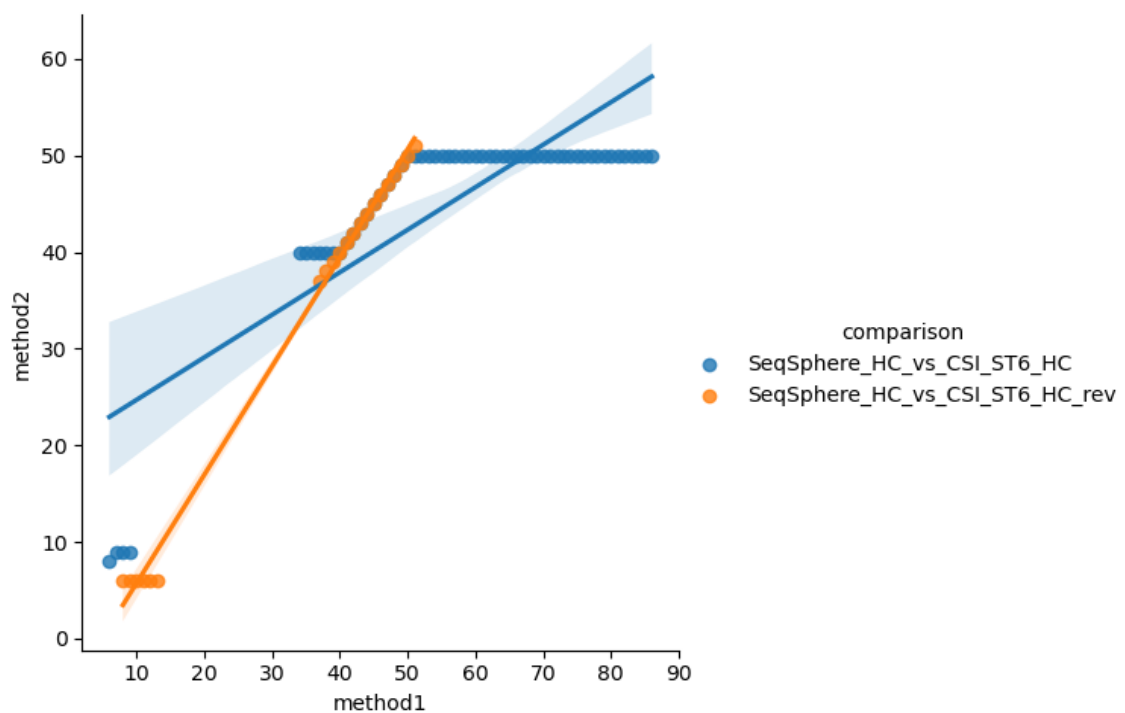


Figure S4.22.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 57 (blue) and 21 (orange) points is presented.

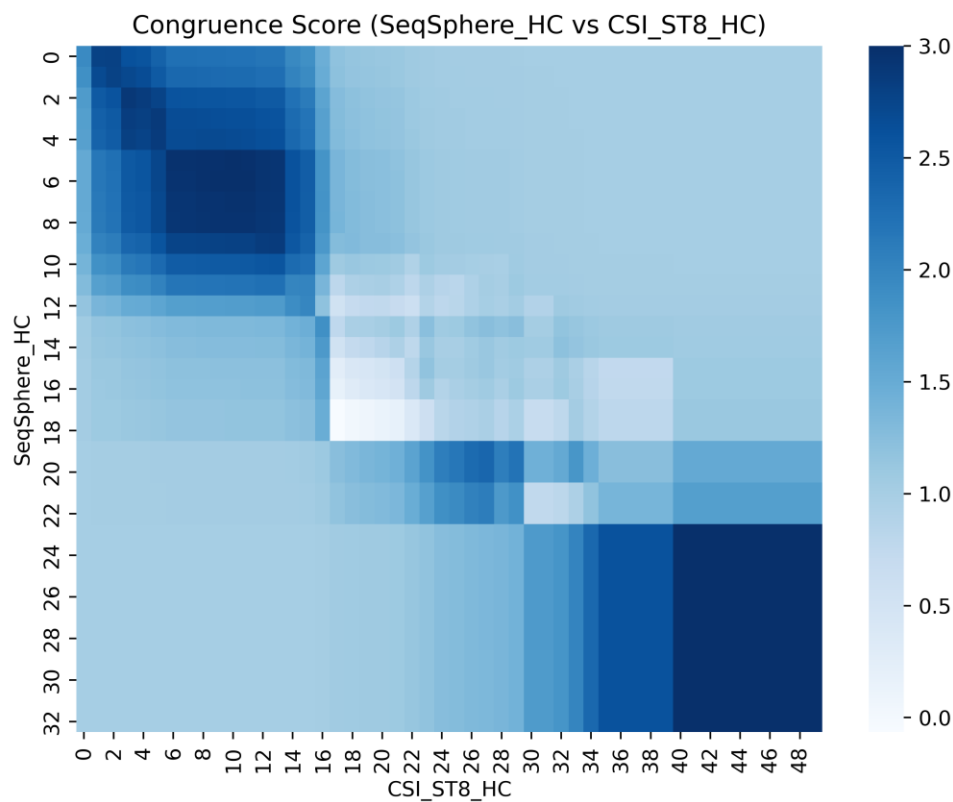


Figure S4.22.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

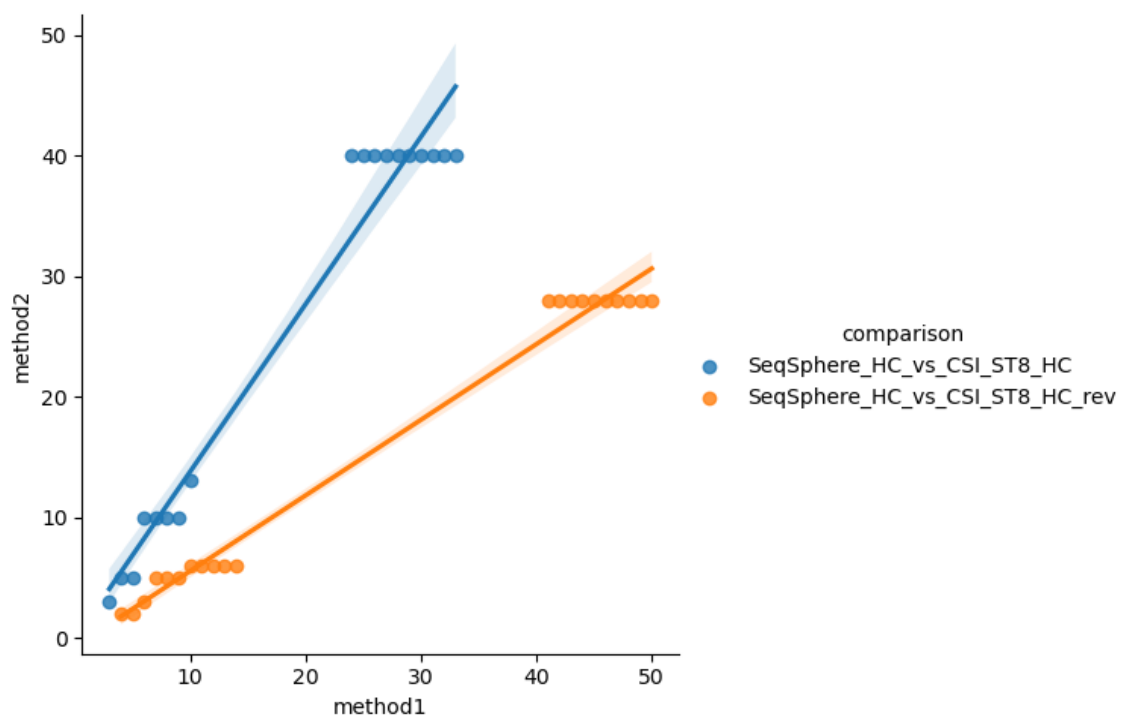


Figure S4.22.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 18 (blue) and 21 (orange) points is presented.

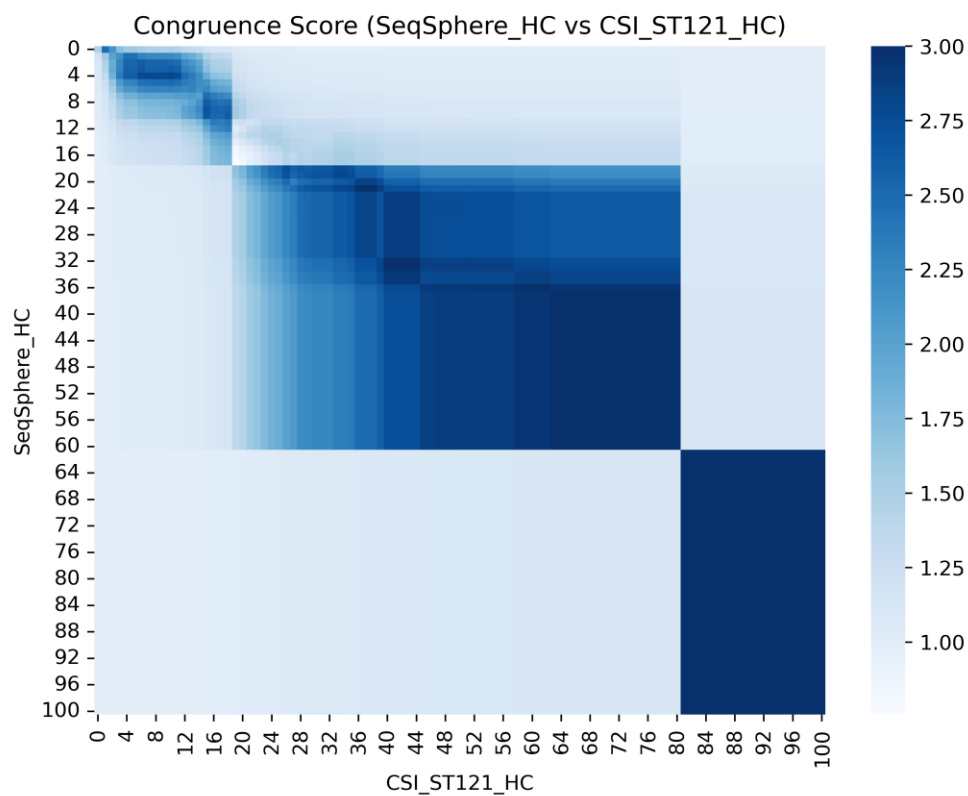


Figure S4.22.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

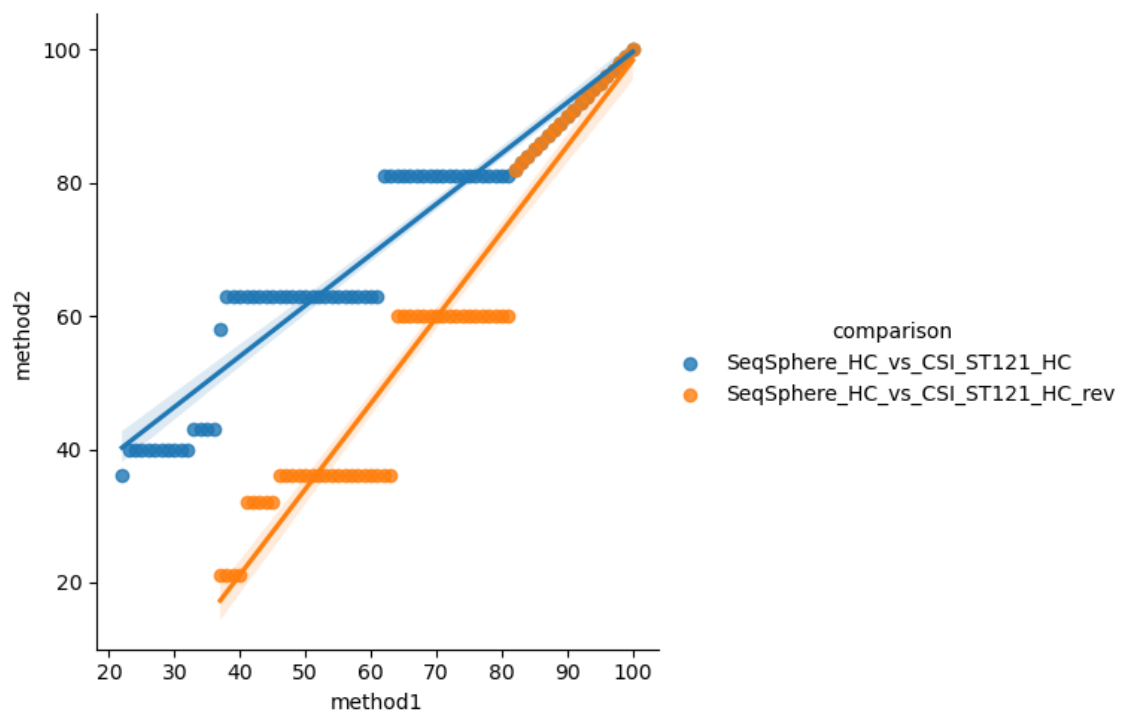


Figure S4.22.10. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST121. A linear tendency line supported by 79 (blue) and 64 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

23. SeqSphere single-linkage vs. snippySnake single-linkage

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

	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	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

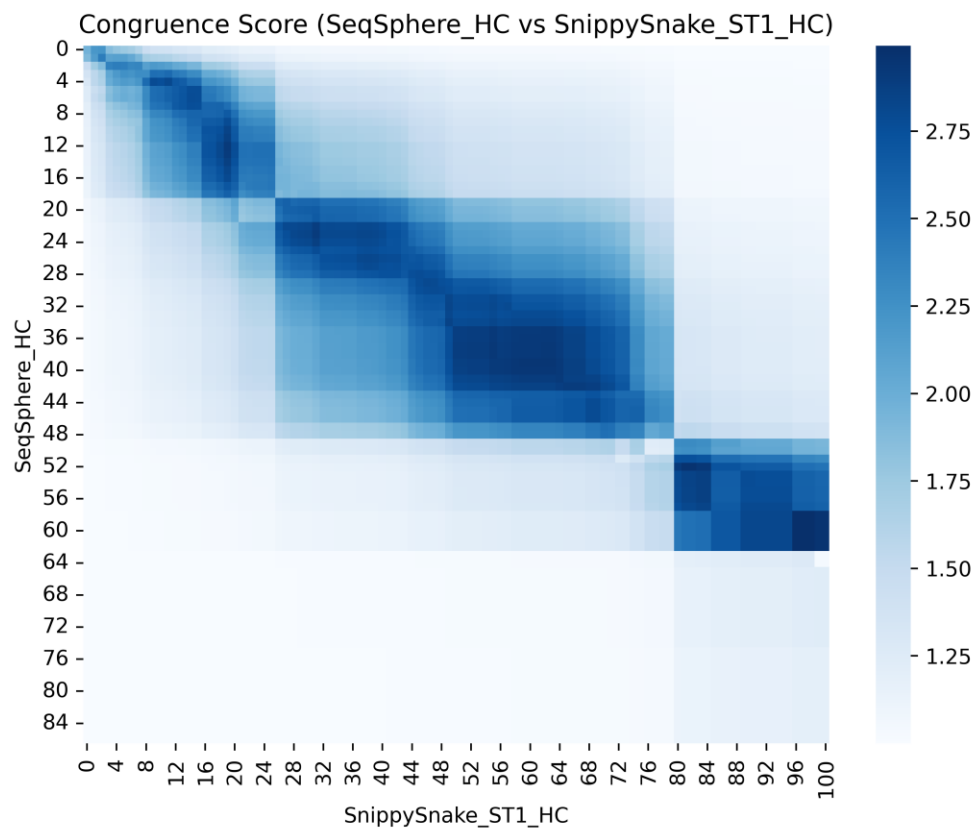


Figure S4.23.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

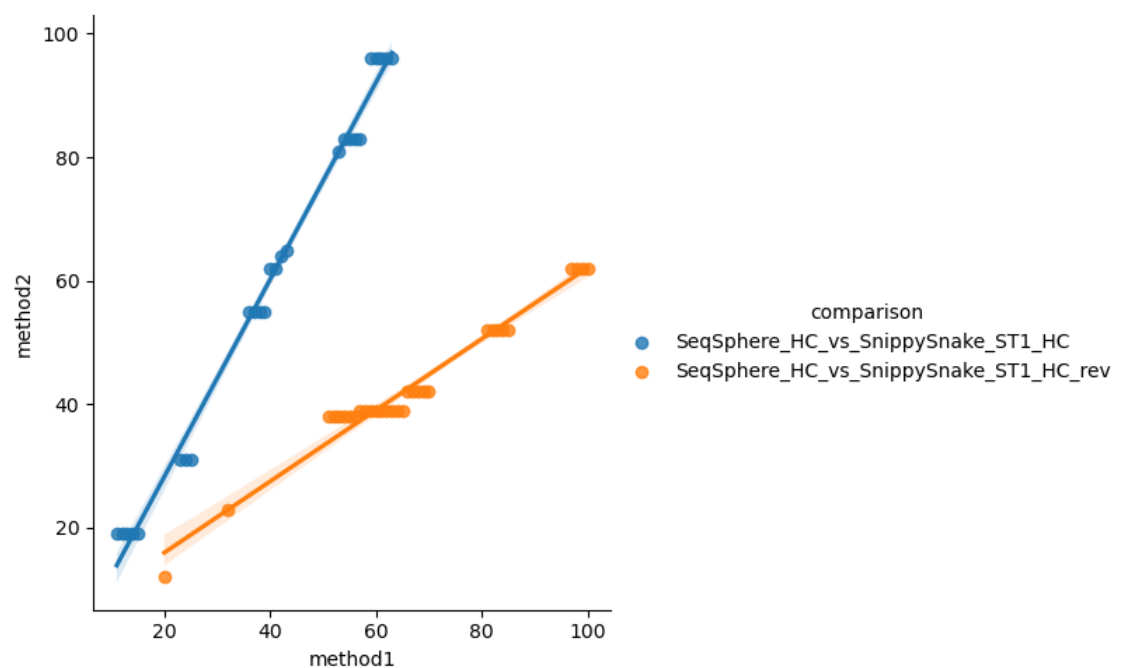


Figure S4.23.2. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST1. A linear tendency line supported by 26 (blue) and 31 (orange) points is presented.

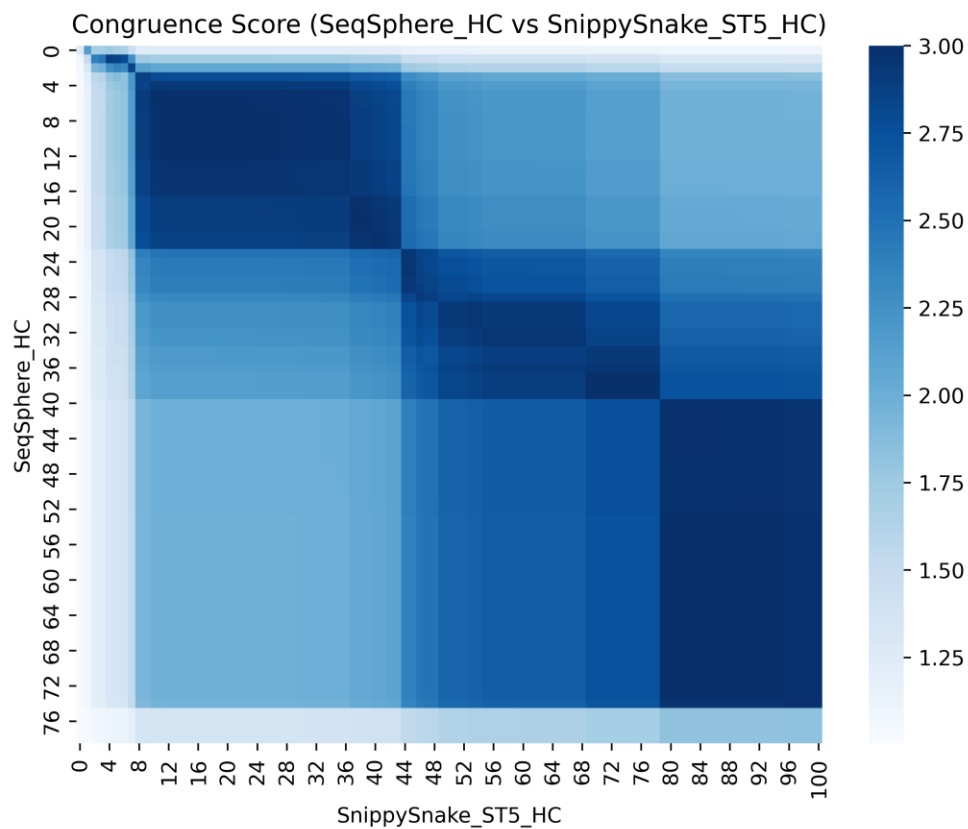


Figure S4.23.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

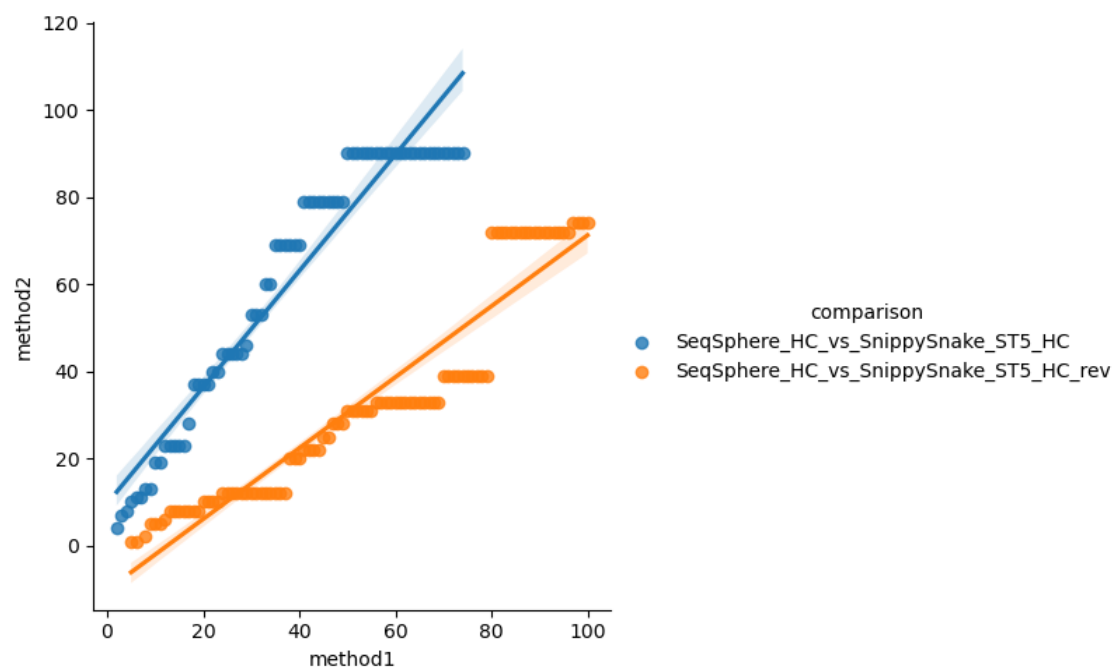


Figure S4.23.4. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS ≥ 2.85) for ST5. A linear tendency line supported by 73 (blue) and 95 (orange) points is presented.

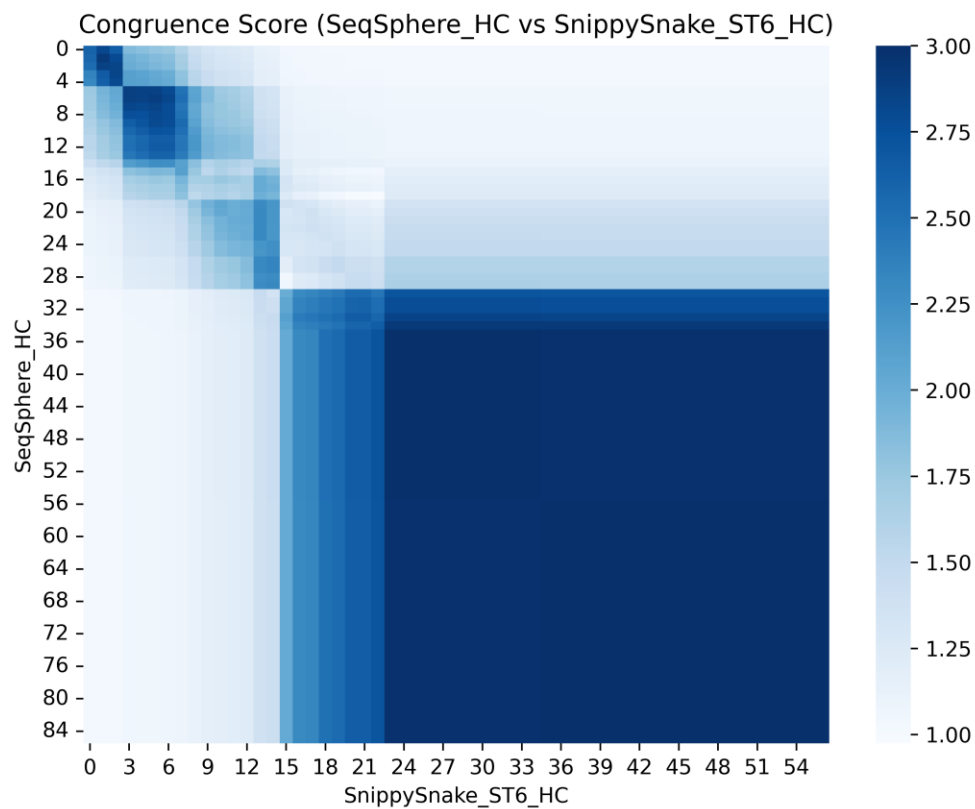


Figure S4.23.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

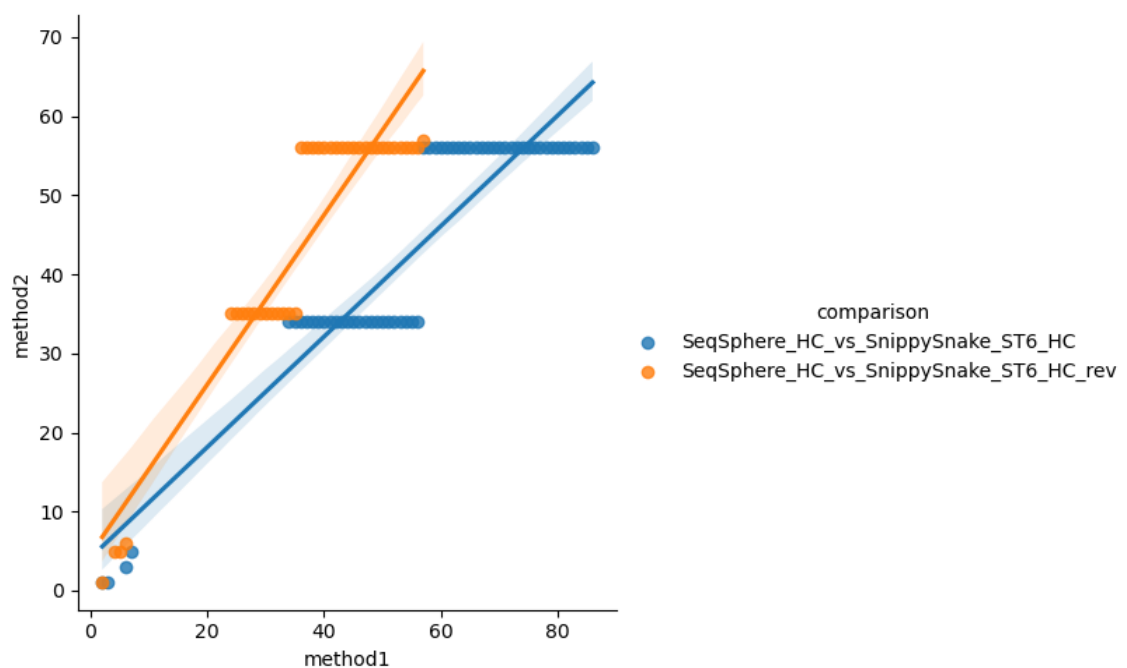


Figure S4.23.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 57 (blue) and 38 (orange) points is presented.

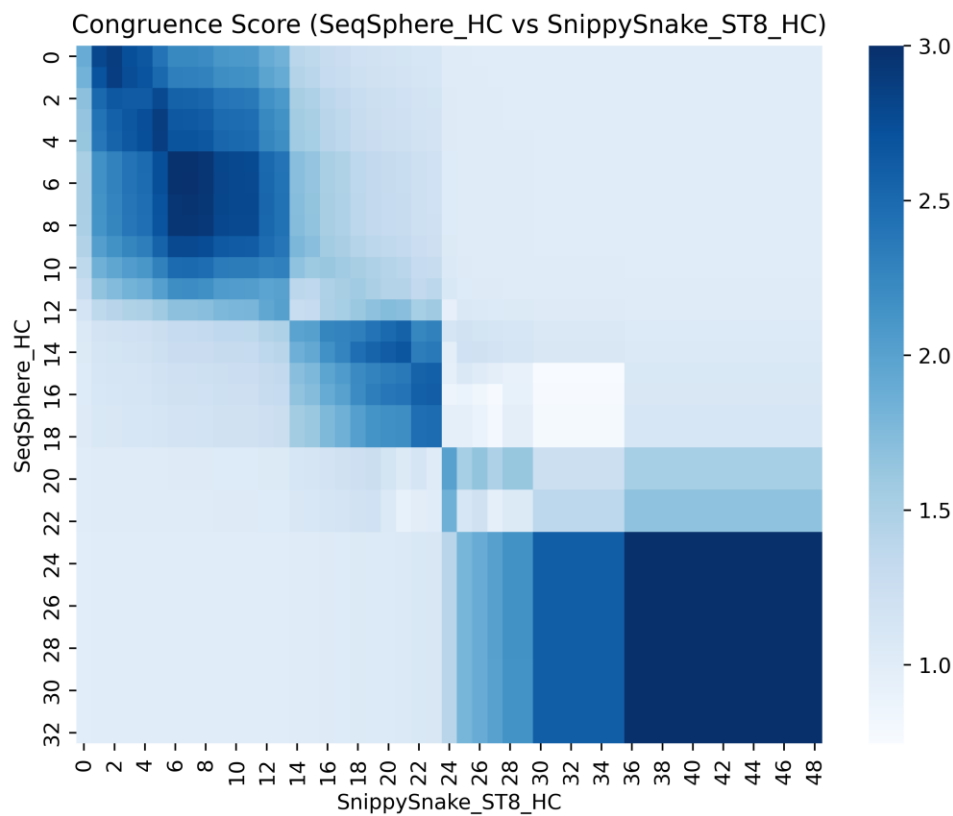


Figure S4.23.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

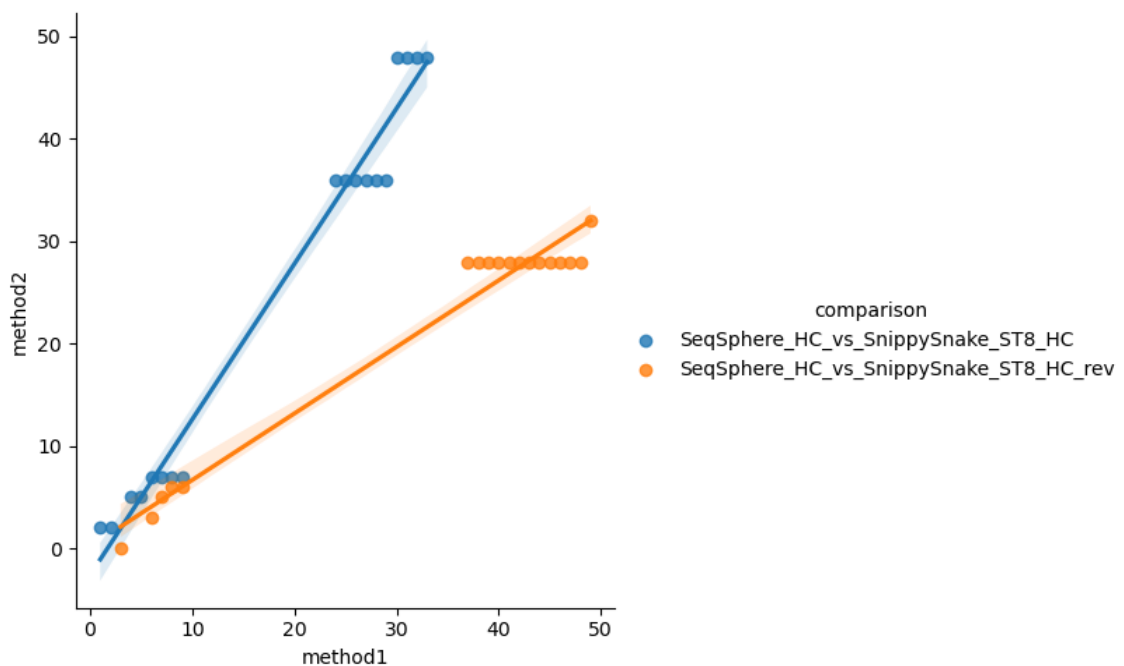


Figure S4.23.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 18 (blue) and 18 (orange) points is presented.

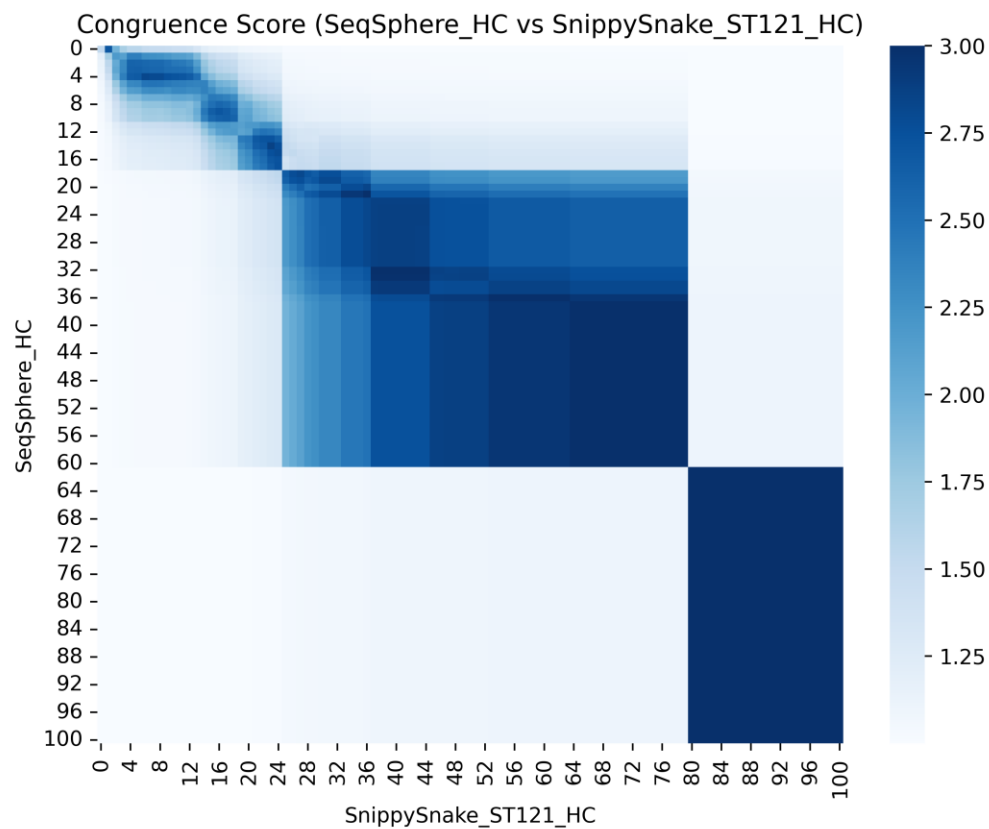


Figure S4.23.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

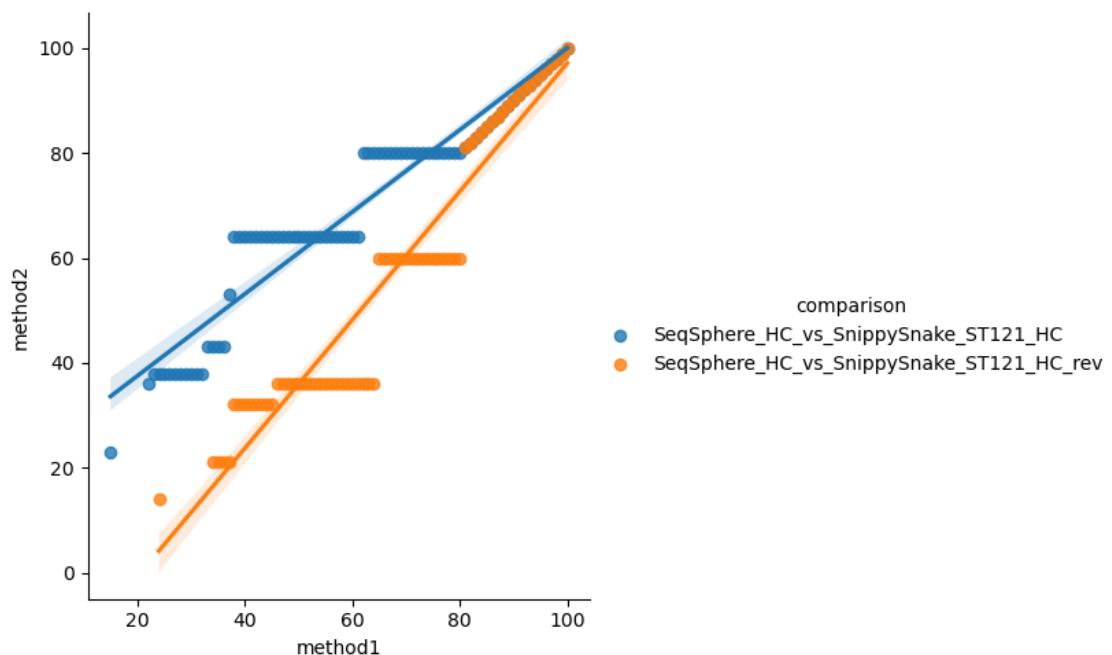


Figure S4.23.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 80 (blue) and 68 (orange) points is presented.

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*

24. SeqSphere single-linkage vs. WGSBAC single-linkage

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

	SeqSphere single-linkage	WGSBAC single-linkage
Pipeline version	v8.3.4	-
Clustering	HC single-linkage (laboratory pipeline)	HC single-linkage (laboratory pipeline)
Schema / Reference	Ruppitsch	F2365 (ST1) / CP006592 (ST5) / CP006046 (ST6) / CP006862 (ST8) / HG813249 (ST121)
Dataset	All samples	ST1 / ST5 / ST6 / ST8 / ST121

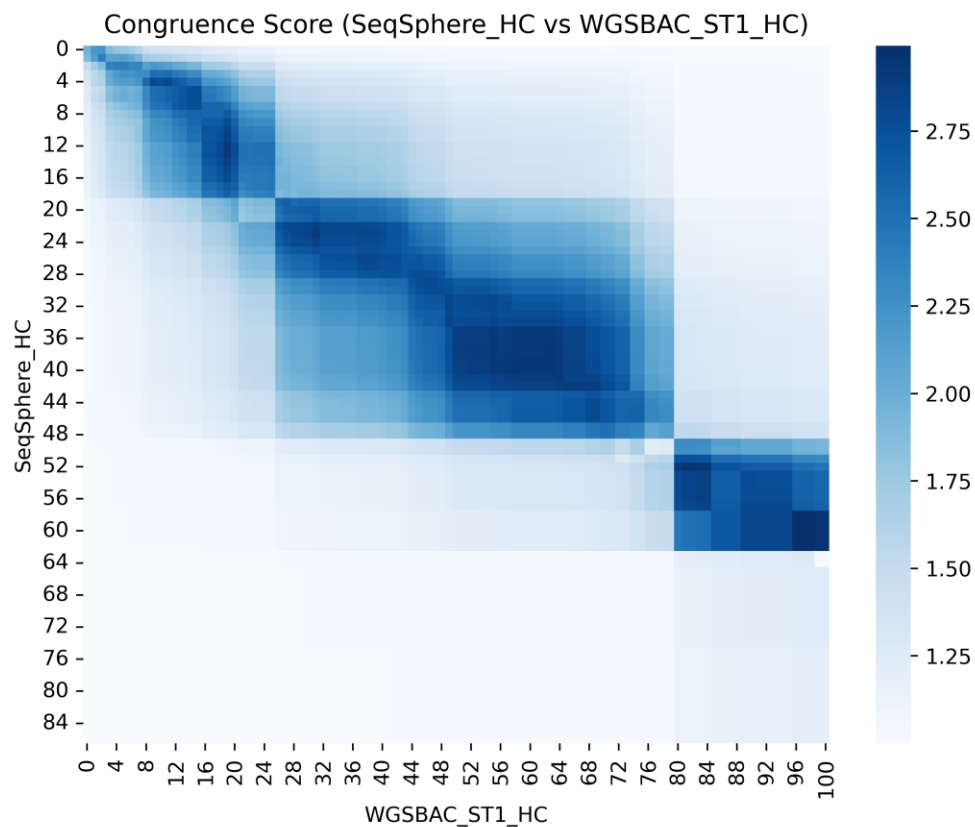


Figure S4.24.1. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST1. Axis represent the different allele/SNP distance thresholds.

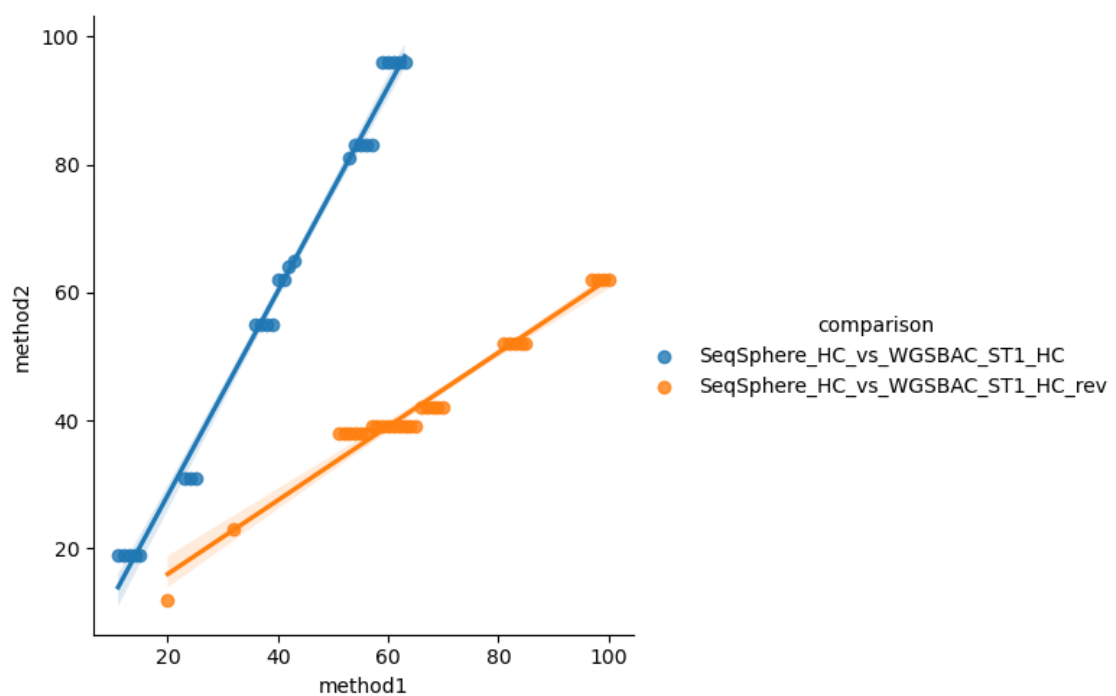


Figure S4.24.2. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST1. A linear tendency line supported by 26 (blue) and 31 (orange) points is presented.

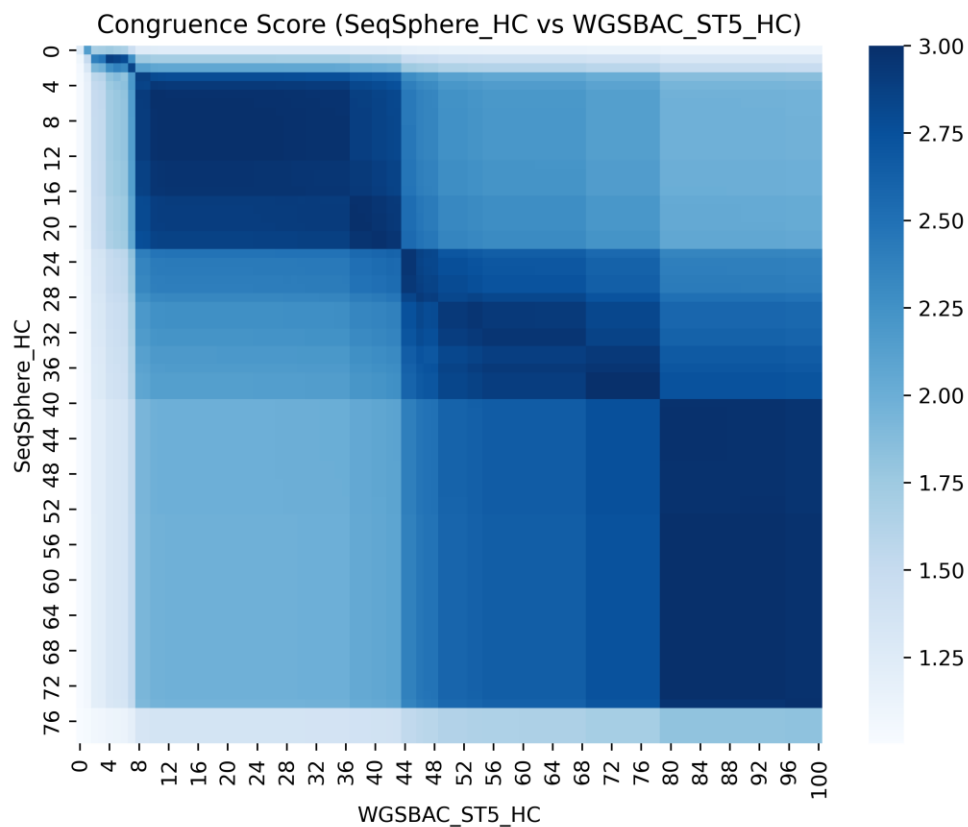


Figure S4.24.3. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST5. Axis represent the different allele/SNP distance thresholds.

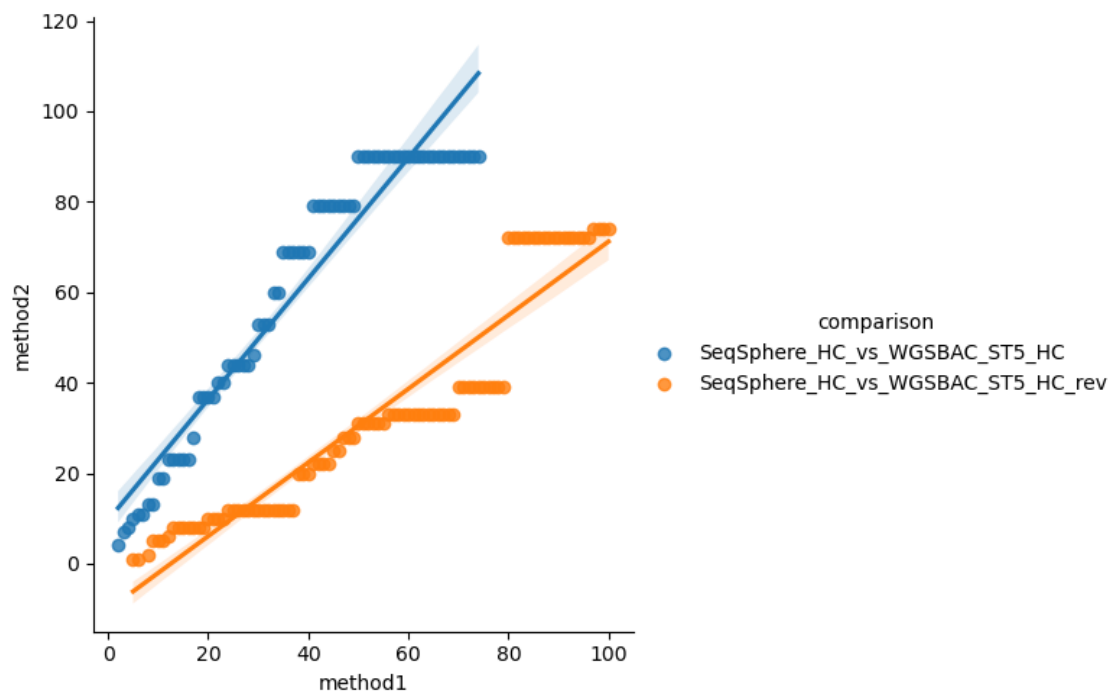


Figure S4.24.4. Corresponding points (up to threshold 100) between the two pipelines in both directions ($CS \geq 2.85$) for ST5. A linear tendency line supported by 73 (blue) and 95 (orange) points is presented.

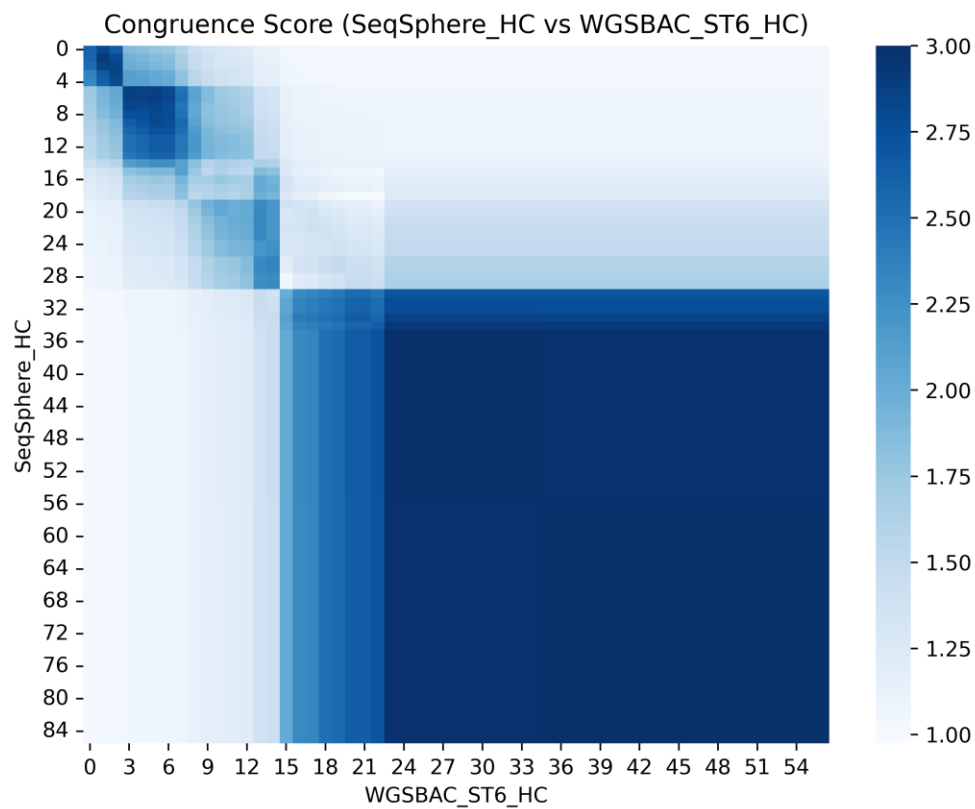


Figure S4.24.5. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST6. Axis represent the different allele/SNP distance thresholds.

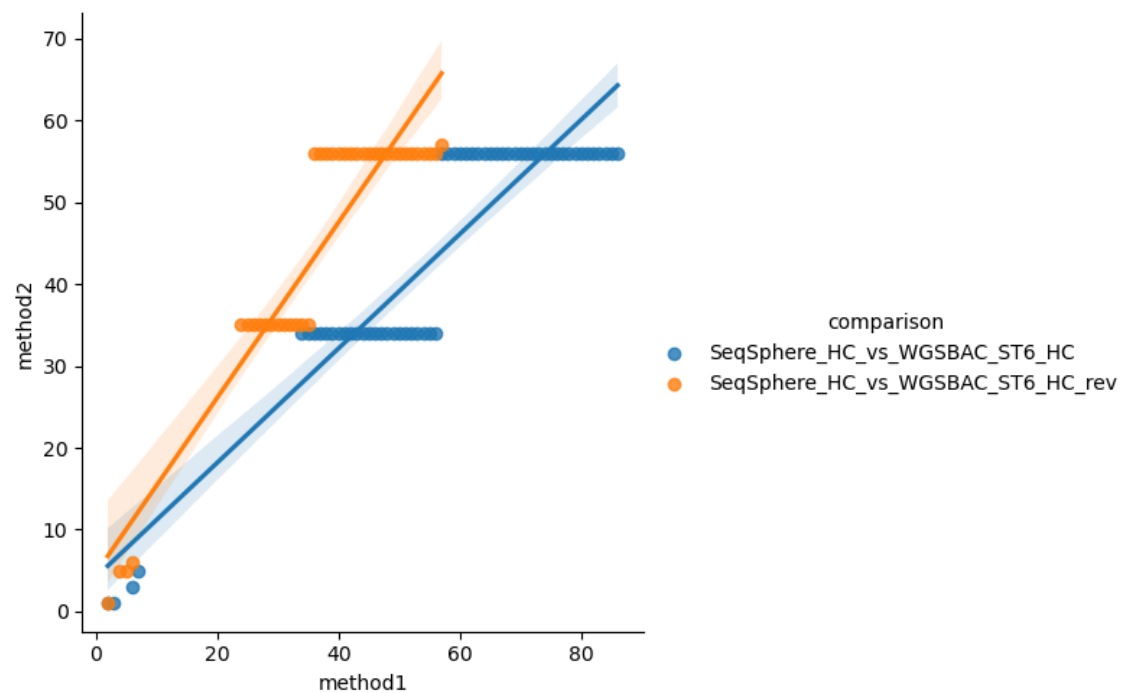


Figure S4.24.6. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST6. A linear tendency line supported by 57 (blue) and 38 (orange) points is presented.

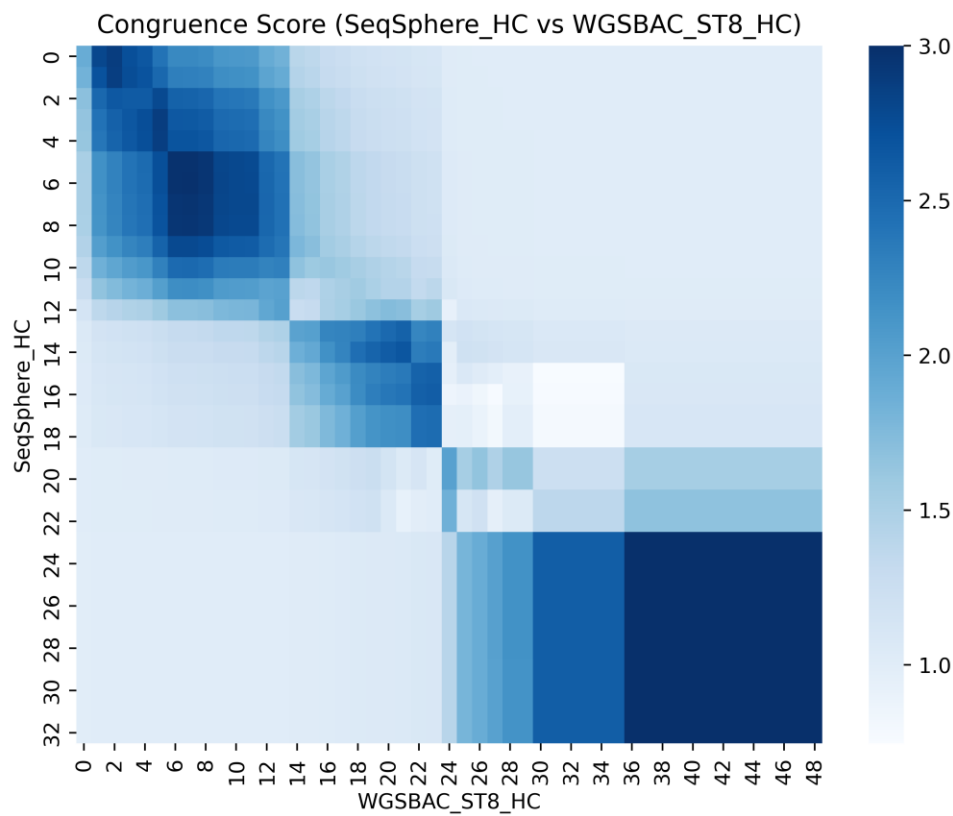


Figure S4.24.7. Heatmap with the congruence score obtained when comparing all partitions of the two pipelines for ST8. Axis represent the different allele/SNP distance thresholds.

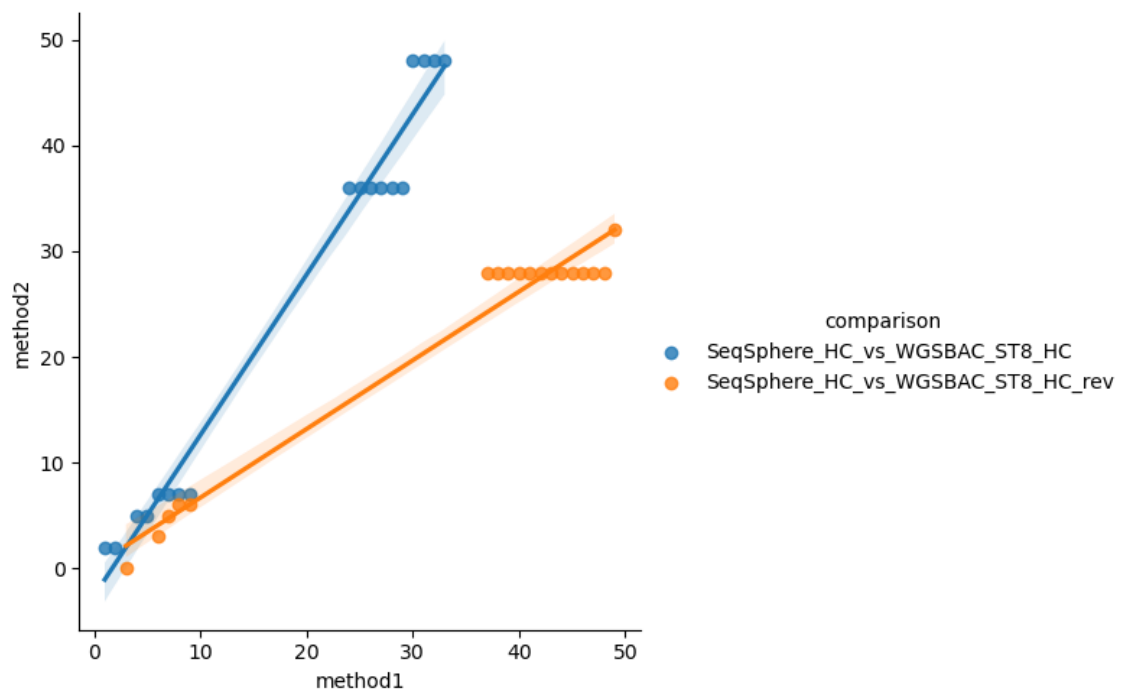


Figure S4.24.8. Corresponding points between the two pipelines in both directions ($CS \geq 2.85$) of all partitions for ST8. A linear tendency line supported by 18 (blue) and 18 (orange) points is presented.

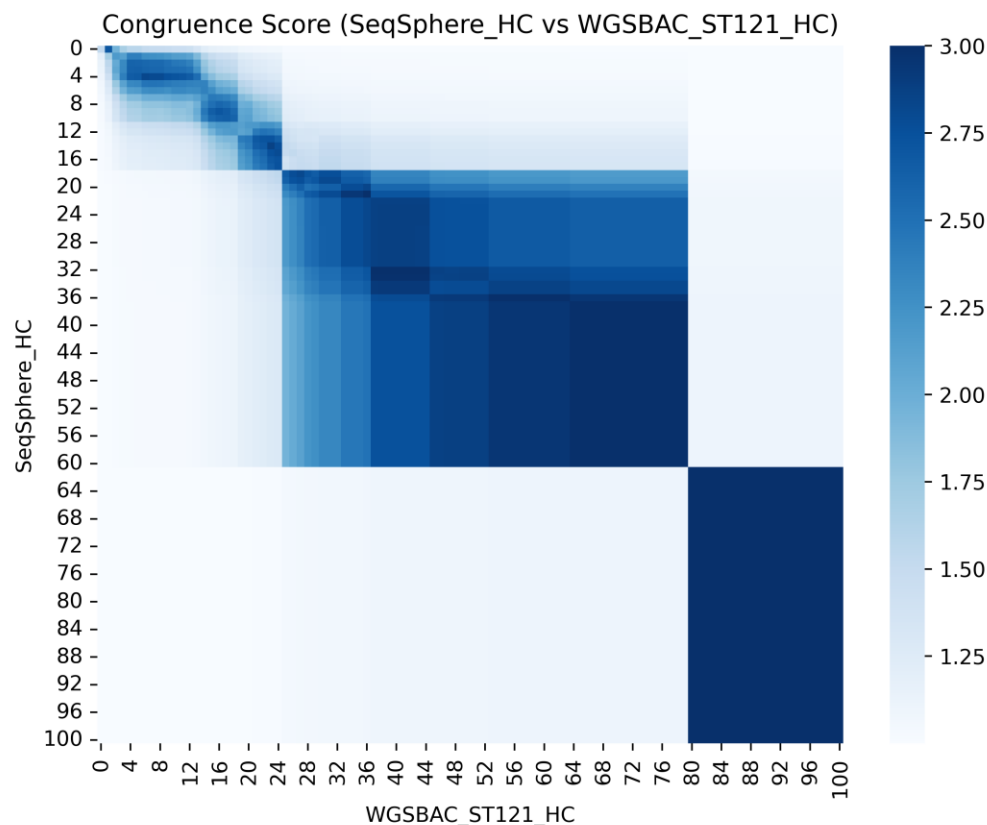


Figure S4.24.9. Heatmap with the congruence score obtained when comparing the partitions of the two pipelines (up to threshold 100) for ST121. Axis represent the different allele/SNP distance thresholds.

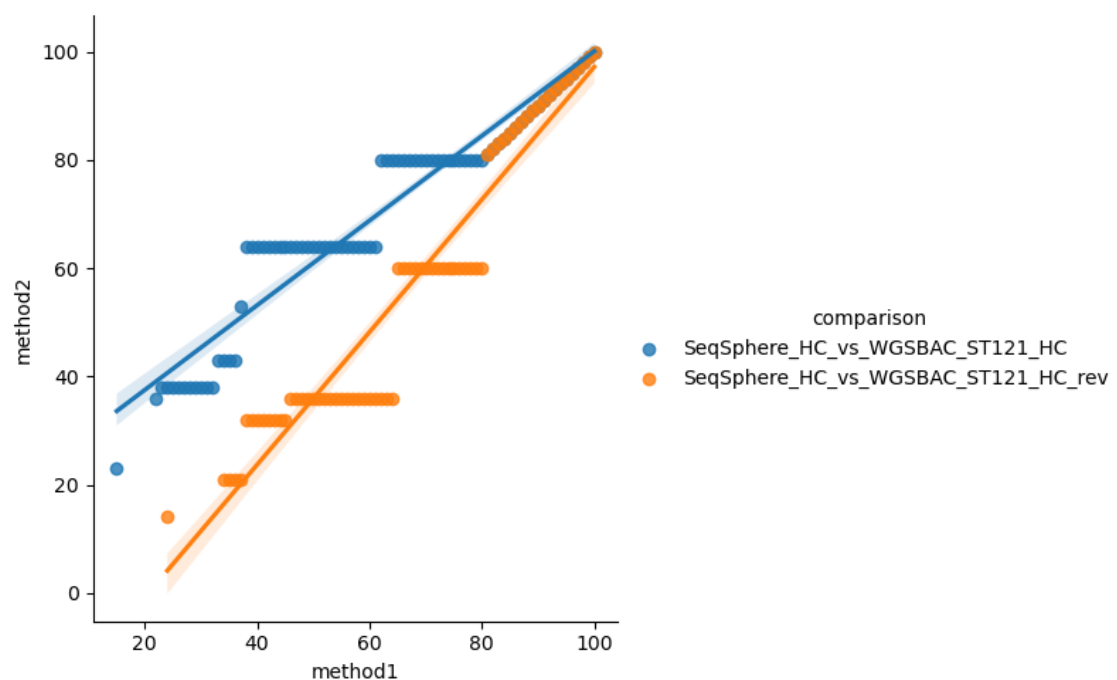


Figure S4.24.10. Corresponding points (up to threshold 100) between the two pipelines in both directions (CS $\geq$ 2.85) for ST121. A linear tendency line supported by 80 (blue) and 68 (orange) points is presented

**NOTE: The results obtained for ST121 are highly influenced by sample SRR7440736, which remains a singleton until the lowest level of resolution.*