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# Probiogenomic pipeline for new promising probiotic *Streptococcus thermophilus* strains

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## ➤ **PROBIOGENOMICS PIPELINE FOR NEW PROMISING PROBIOTIC *STREPTOCOCCUS THERMOPHILUS* STRAINS**

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Société Française  
de Microbiologie

19E CONGRÈS  
NATIONAL DE LA SFM

# MICROBES

7-9 octobre **2024**

**Bienvenue chez les Microbes**



**Lille**  
Grand Palais

## Déclaration de conflit d'intérêt

Pour cette présentation:

- je déclare n'avoir aucun conflit d'intérêt
- j'ai utilisé des images libres de droit

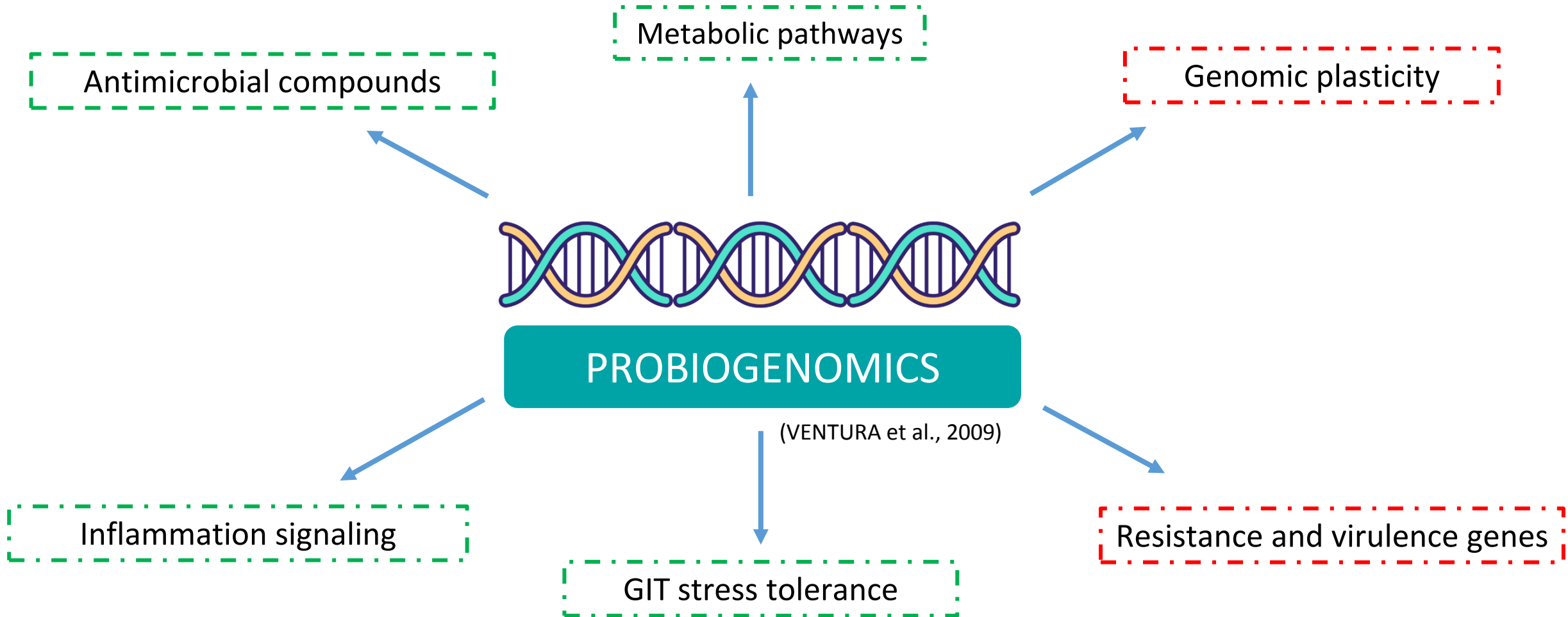


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# Introduction

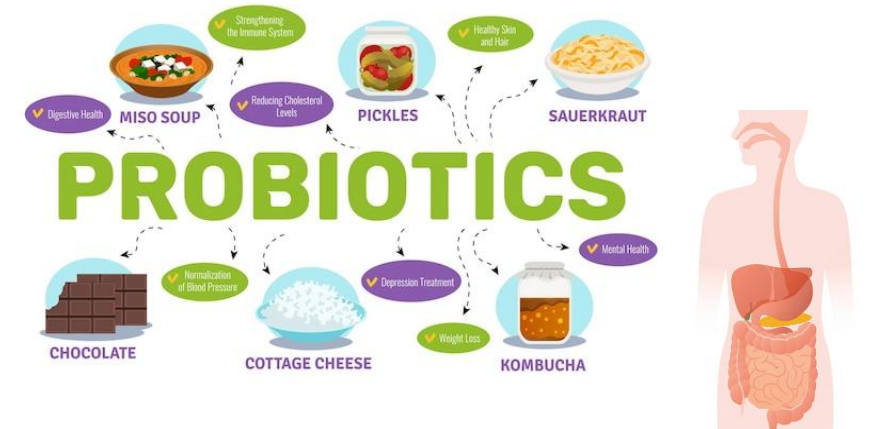
Probiogenomics: what is it for?



# Introduction

*Streptococcus thermophilus*: an underrated probiotic species?

- Gram-positive bacterium;
- Naturally occurs in milk niche;
  - LAB heterogeneous group;
  - **Crucial role in fermentation: commercial relevance**



- Closely related to *S. salivarius* and *S. vestibularis*
- Genomic reshaping
- Health-promoting properties?
  - **ROUX et al., 2022**: ecological and survival traits are universal, while health-promoting properties are strain specific.



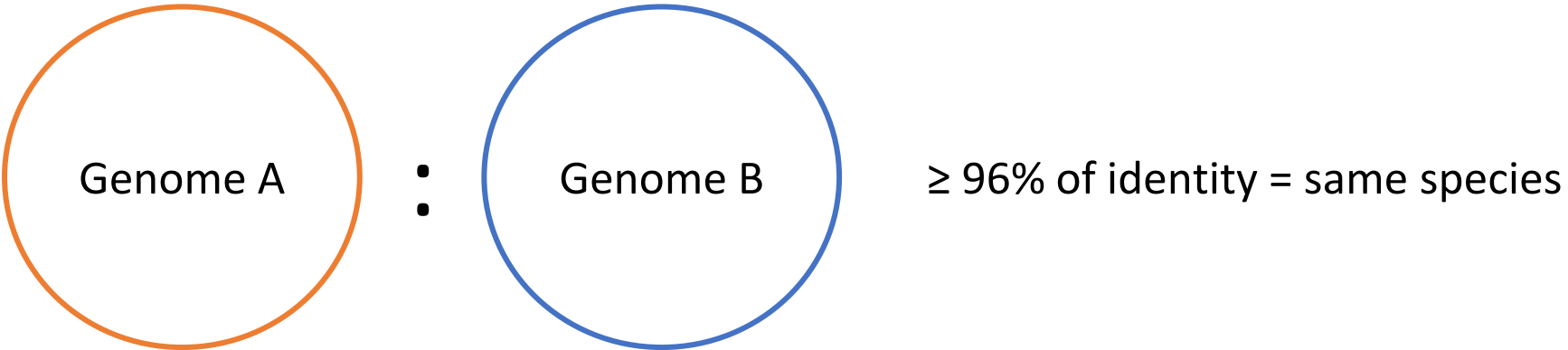
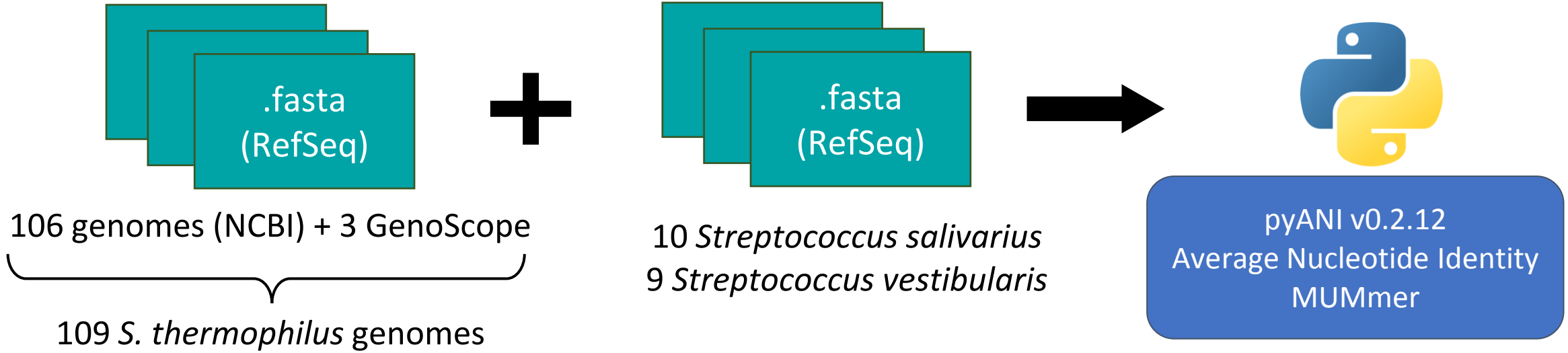
# Objective

To apply a probiogenomics pipeline to *Streptococcus thermophilus* genomes to identify new potential probiotic strains from diverse sources and sites.



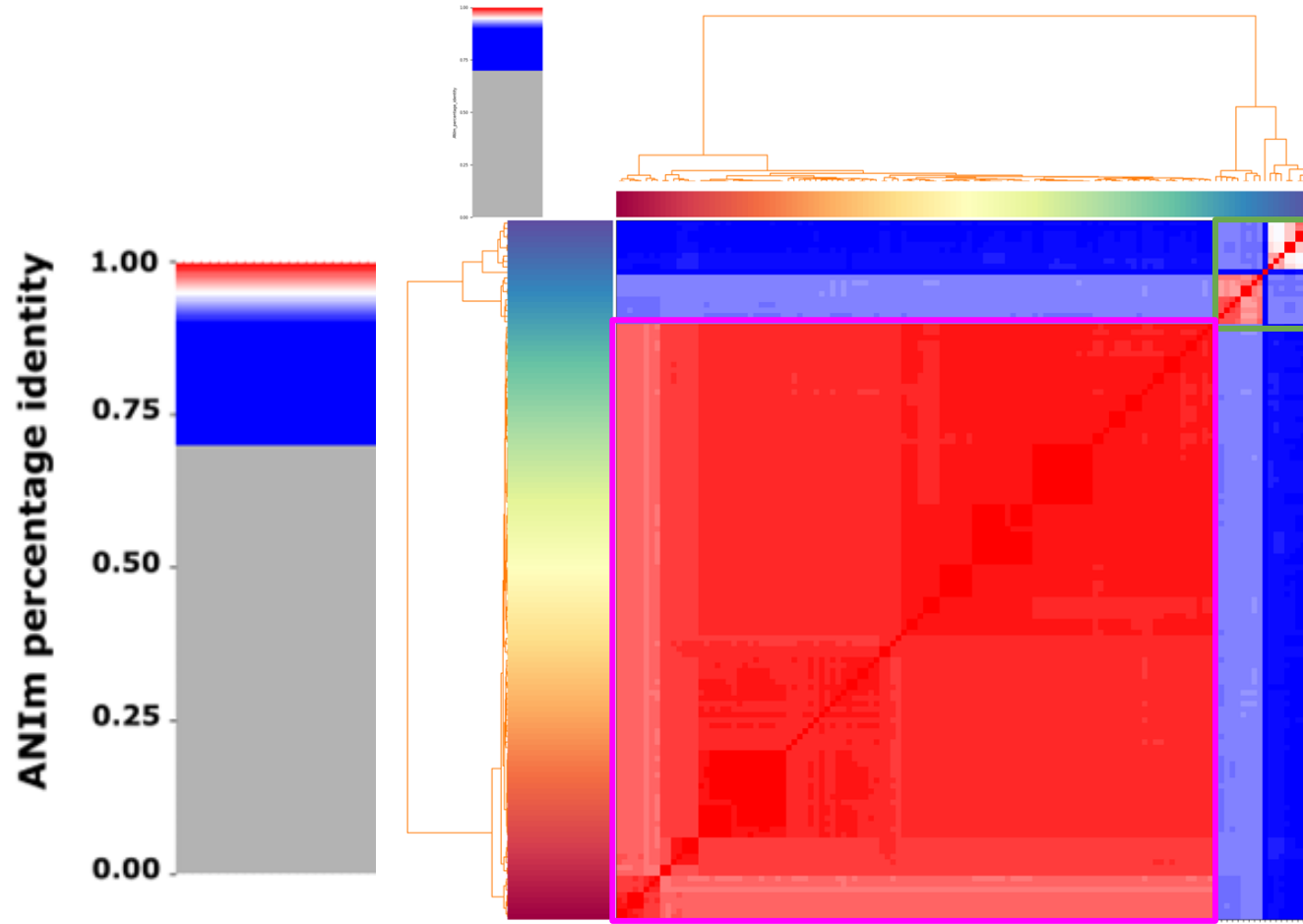
# Methods

Genomes acquisition and taxogenomics



# Results

## Genomes acquisition and taxogenomics



*Streptococcus salivarius*  
*Streptococcus vestibularis*

*Streptococcus thermophilus*



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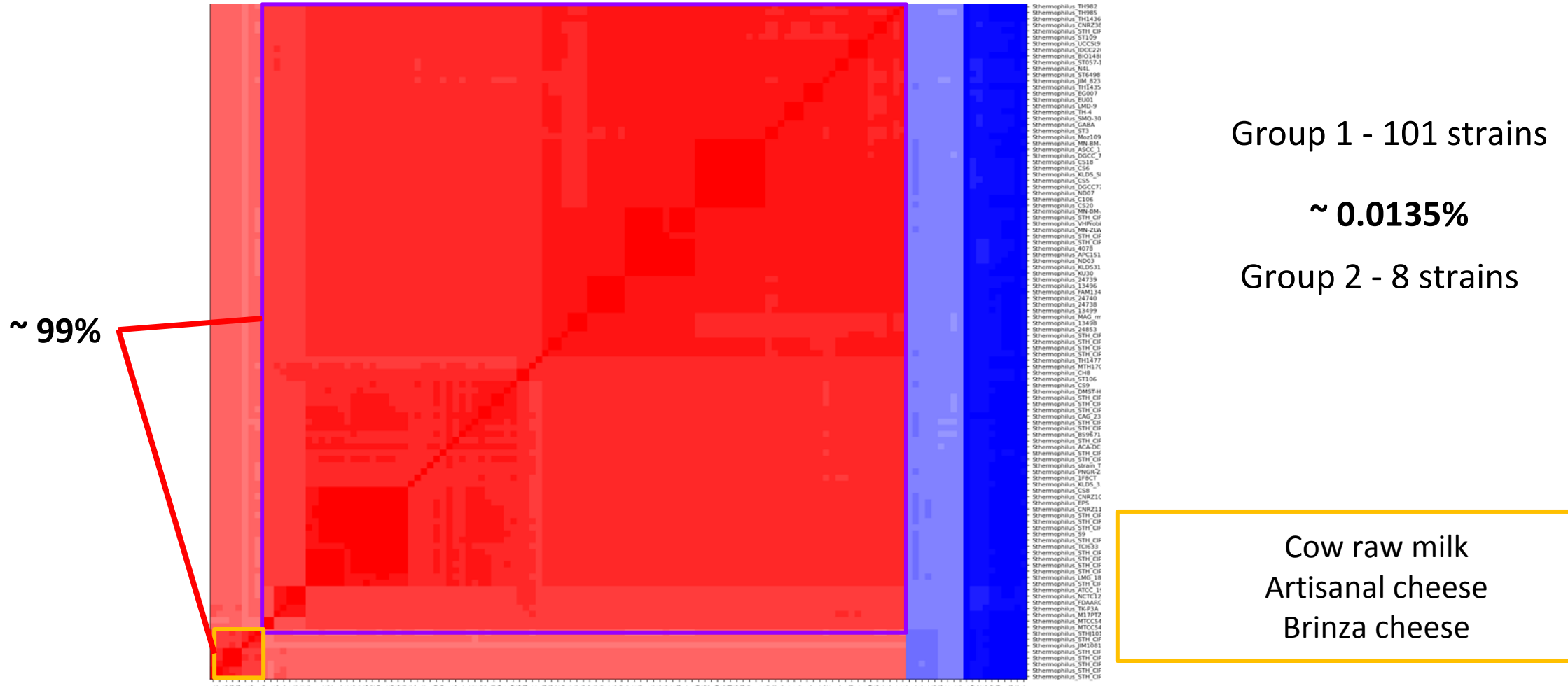
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# Results

## Genomes acquisition and taxogenomics



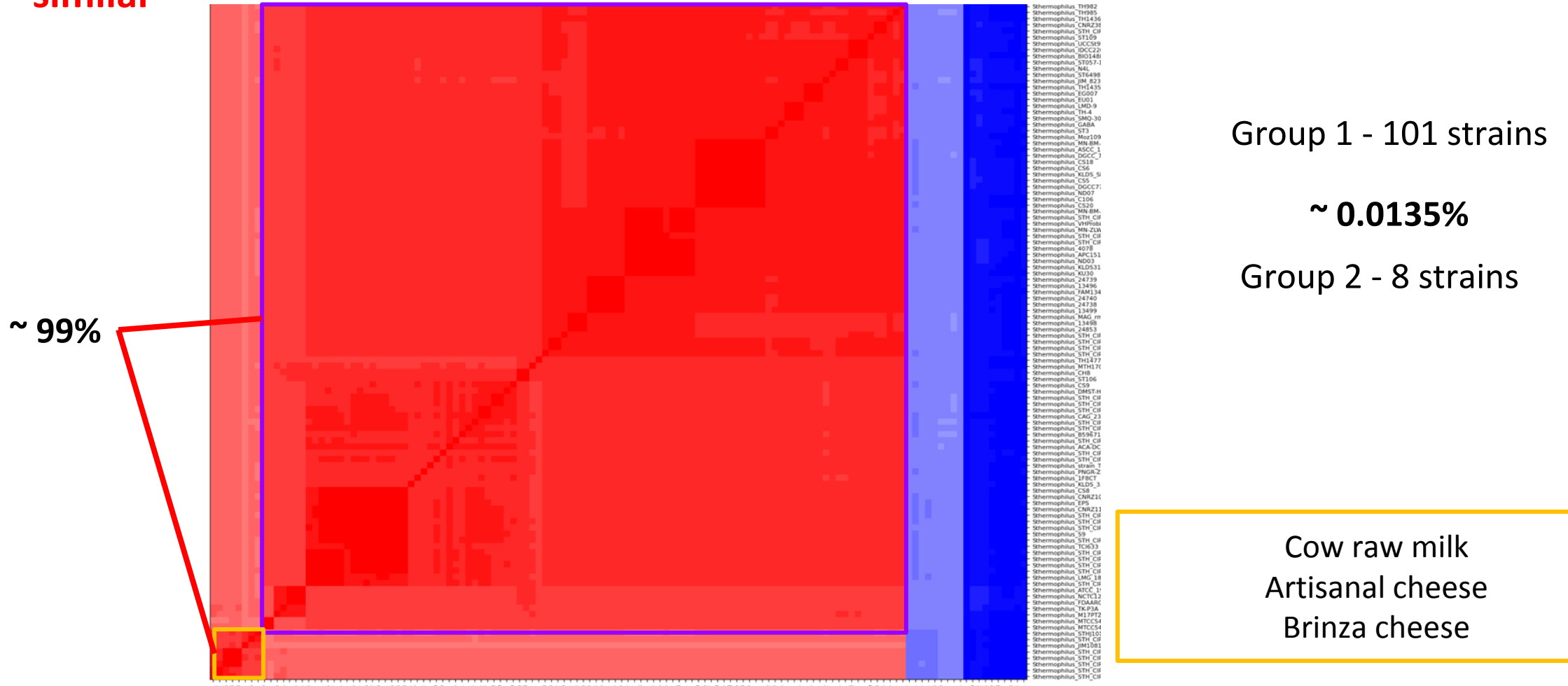
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# Results

Genomes acquisition and taxogenomics - some strains are more genomically similar



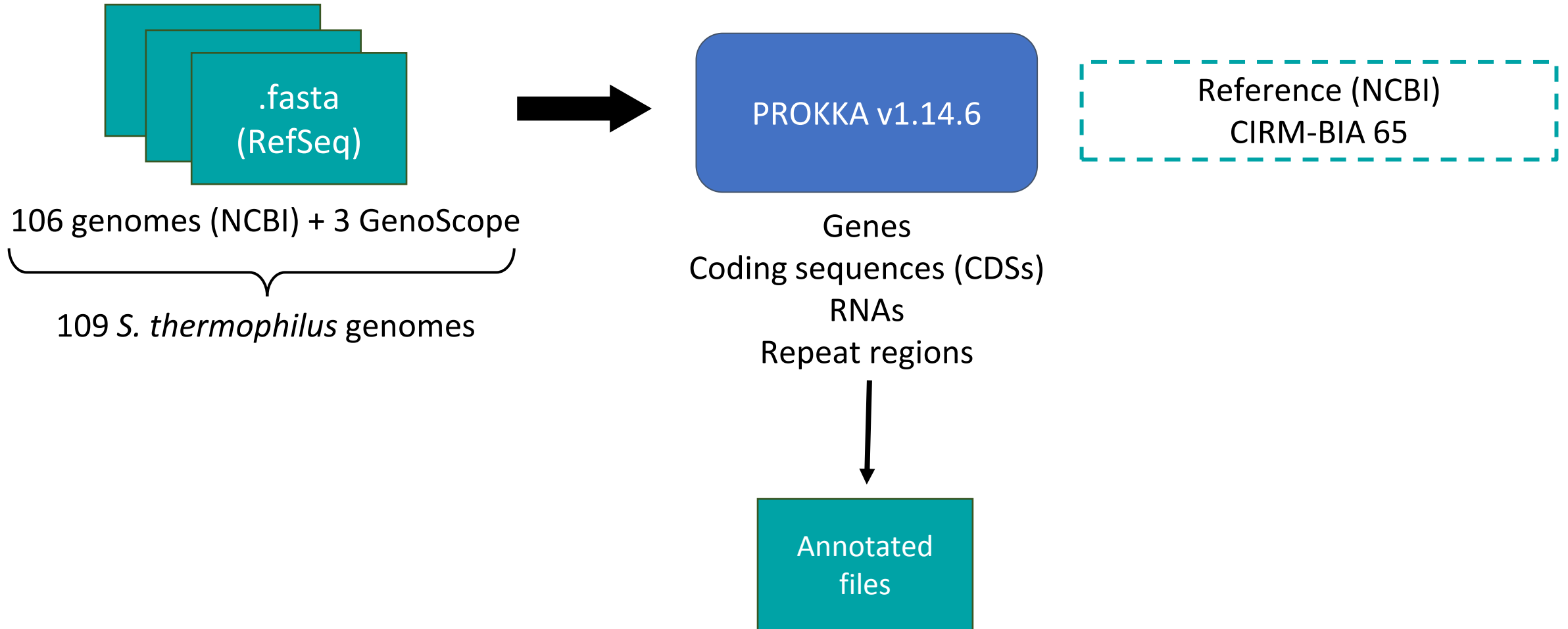
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# Methods

Structural annotation

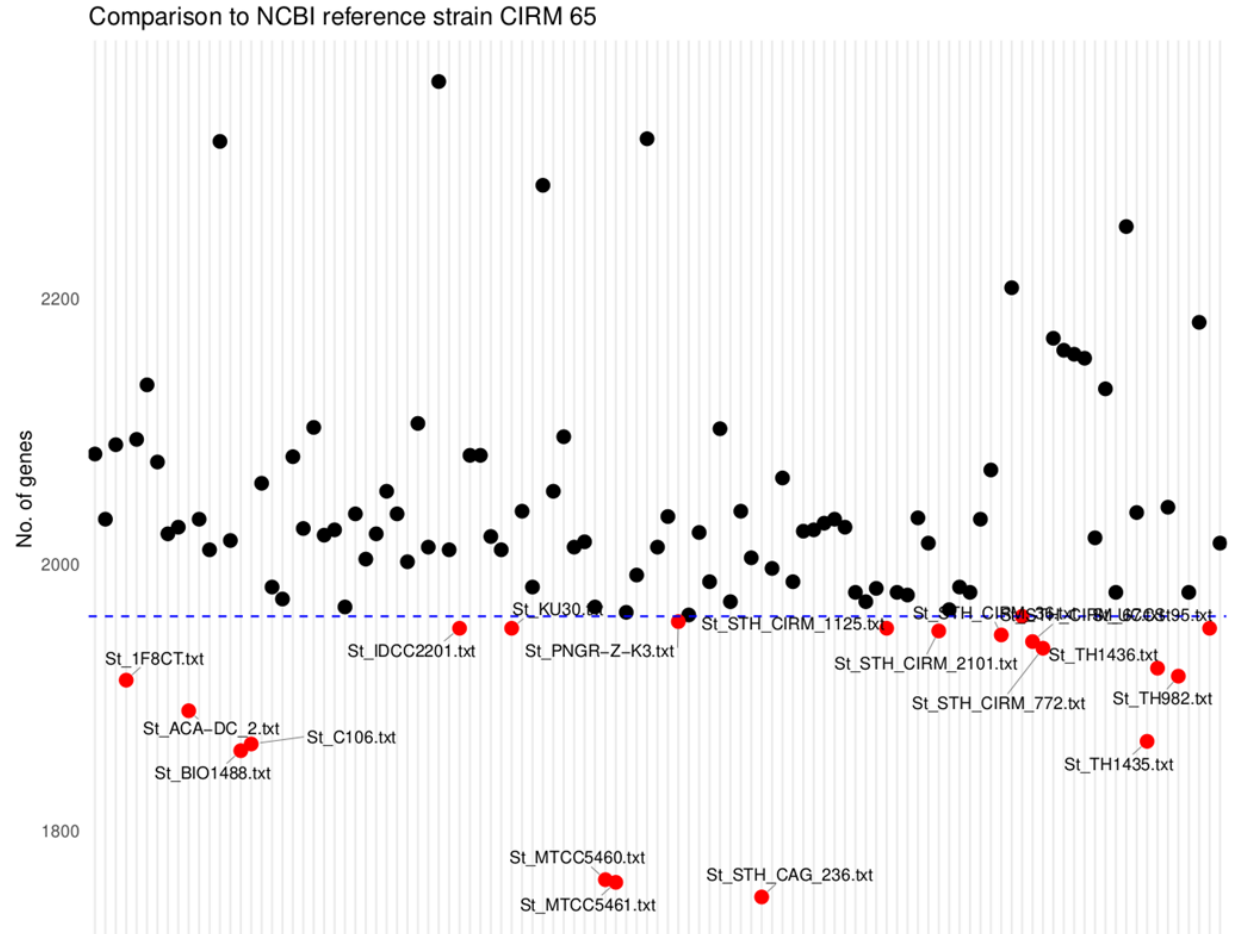


# Results

## Structural annotation

Reference (NCBI): Strain CIRM 65

- No. of genes: 1961
- Coding sequences: 1875
- RNAs: 86
- Lowest no. genes: 1761 (CAG 236)
- Highest no. genes: 2363 (FDAARGOS 1574)

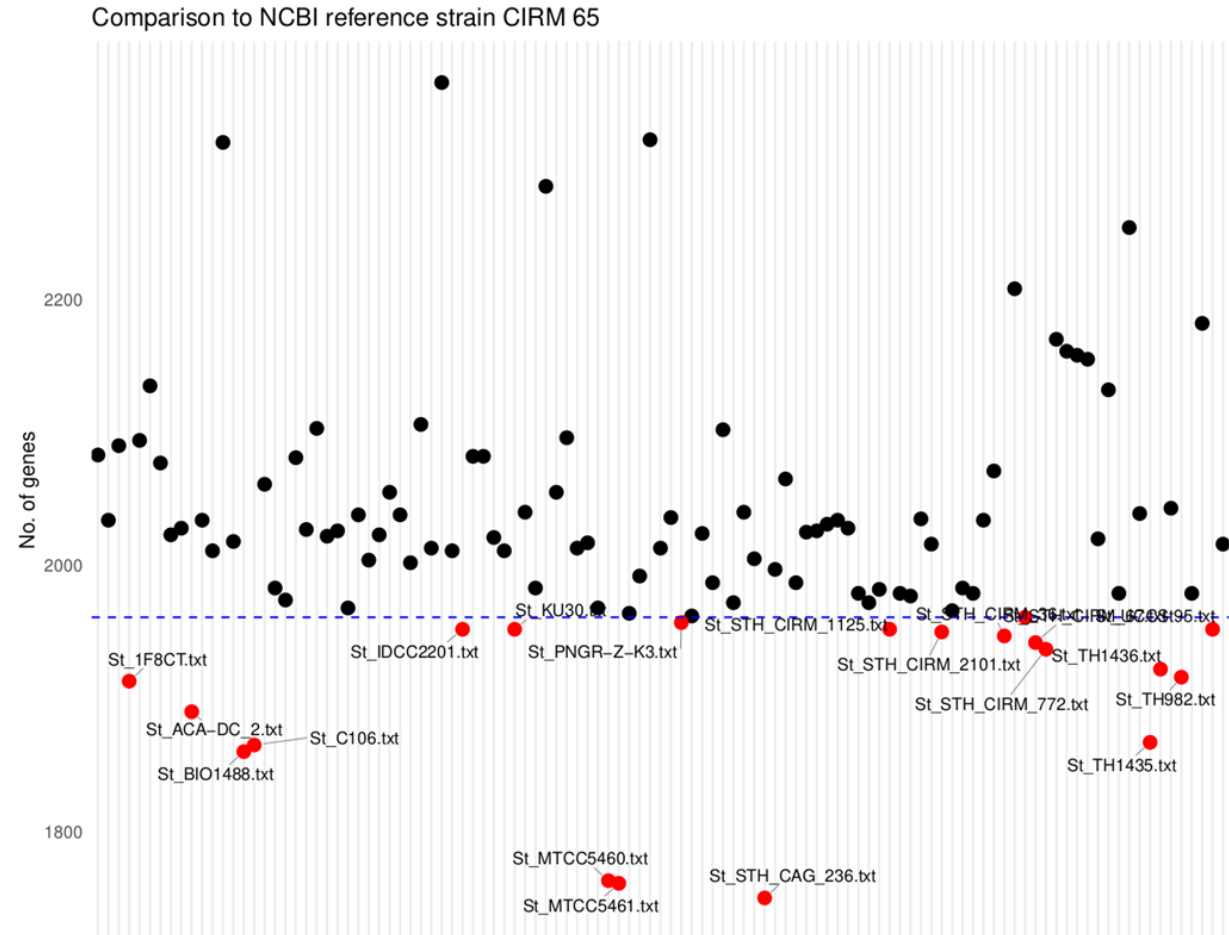


# Results

## Structural annotation - the STH genomes are diverse in size and structure!

Reference (NCBI): Strain CIRM 65

- No. of genes: 1961
- Coding sequences: 1875
- RNAs: 86
- Lowest no. genes: 1761 (CAG 236)
- Highest no. genes: 2363 (FDAARGOS 1574)



# Methods

Prediction of genomic islands



109 *S. thermophilus* genomes



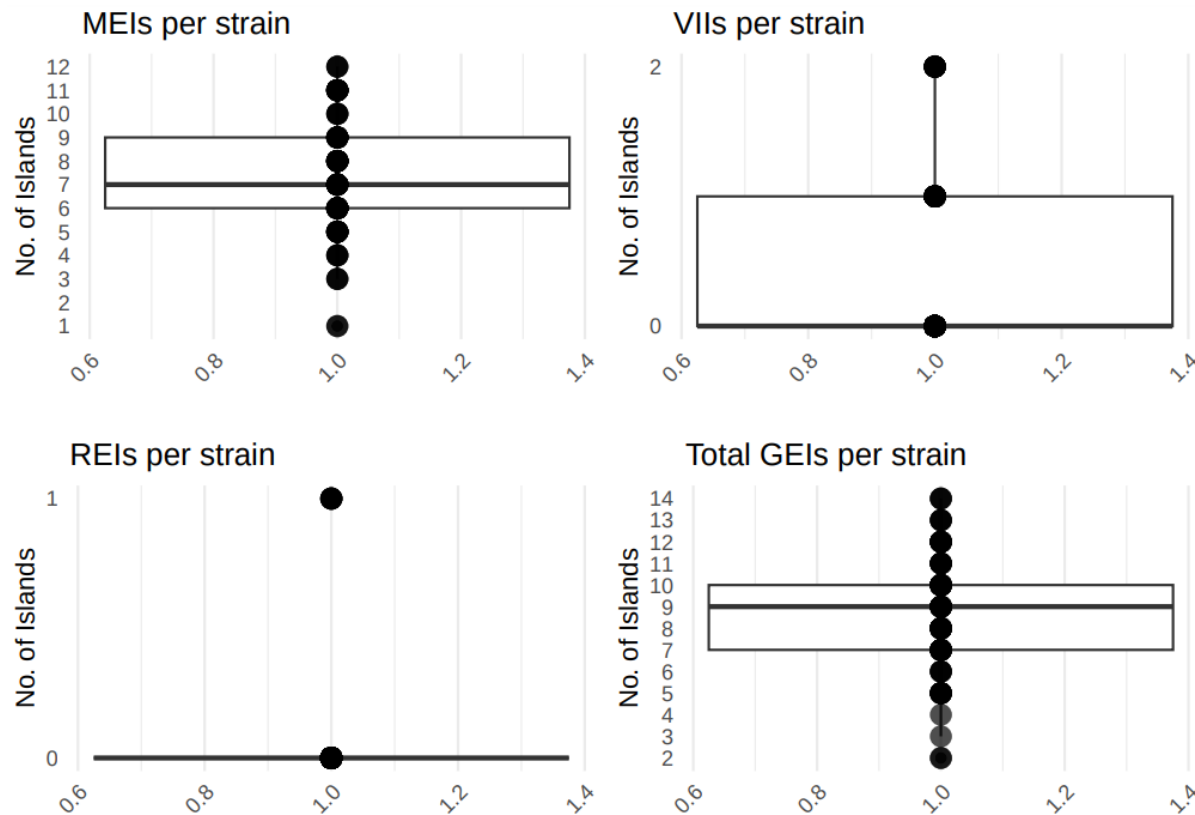
GIPSy v2.0.6  
Fisher

Metabolic islands (MEIs)  
Resistance islands (REIs)  
Symbiotic islands (SYIs)  
Virulence islands (VIIs)

Reference  
APC 151, fish GIT (2015)

# Results

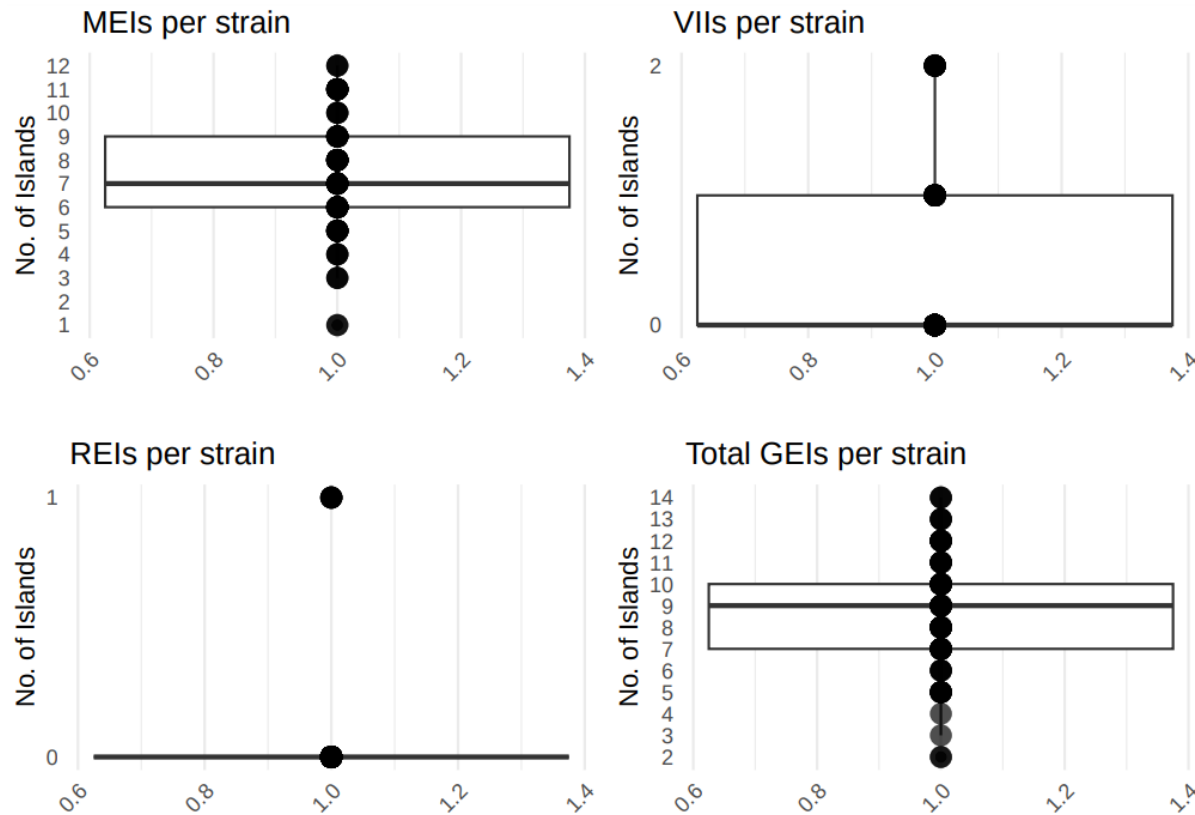
## Prediction of genomic islands



- No. of genomic islands varied greatly
  - MEIs most abundant
  - No SYIs
- VIIs: 49 genomes
- REIs: 7 genomes
- Group 1: 8.5 GEIs
- Group 2: 11.5 GEIs

# Results

## Prediction of genomic islands - some STH genomes are more plastic than others!



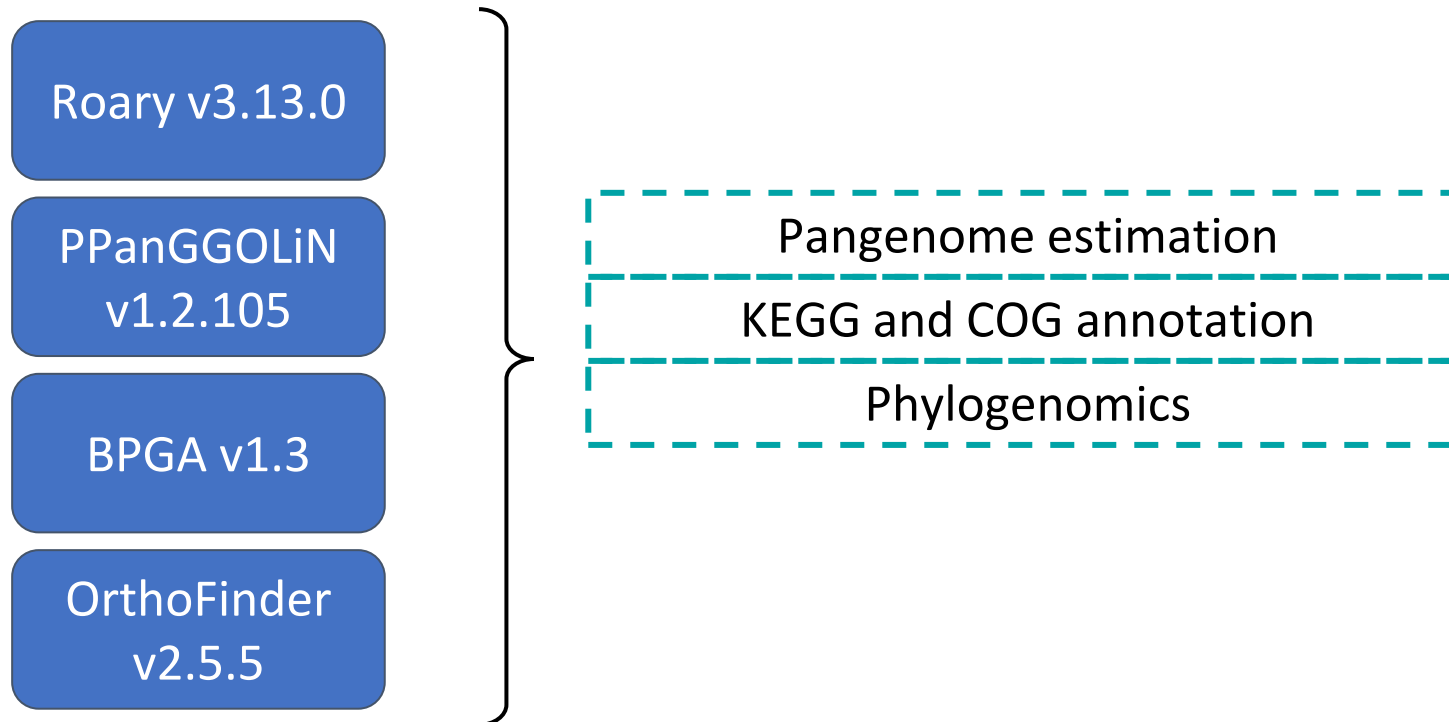
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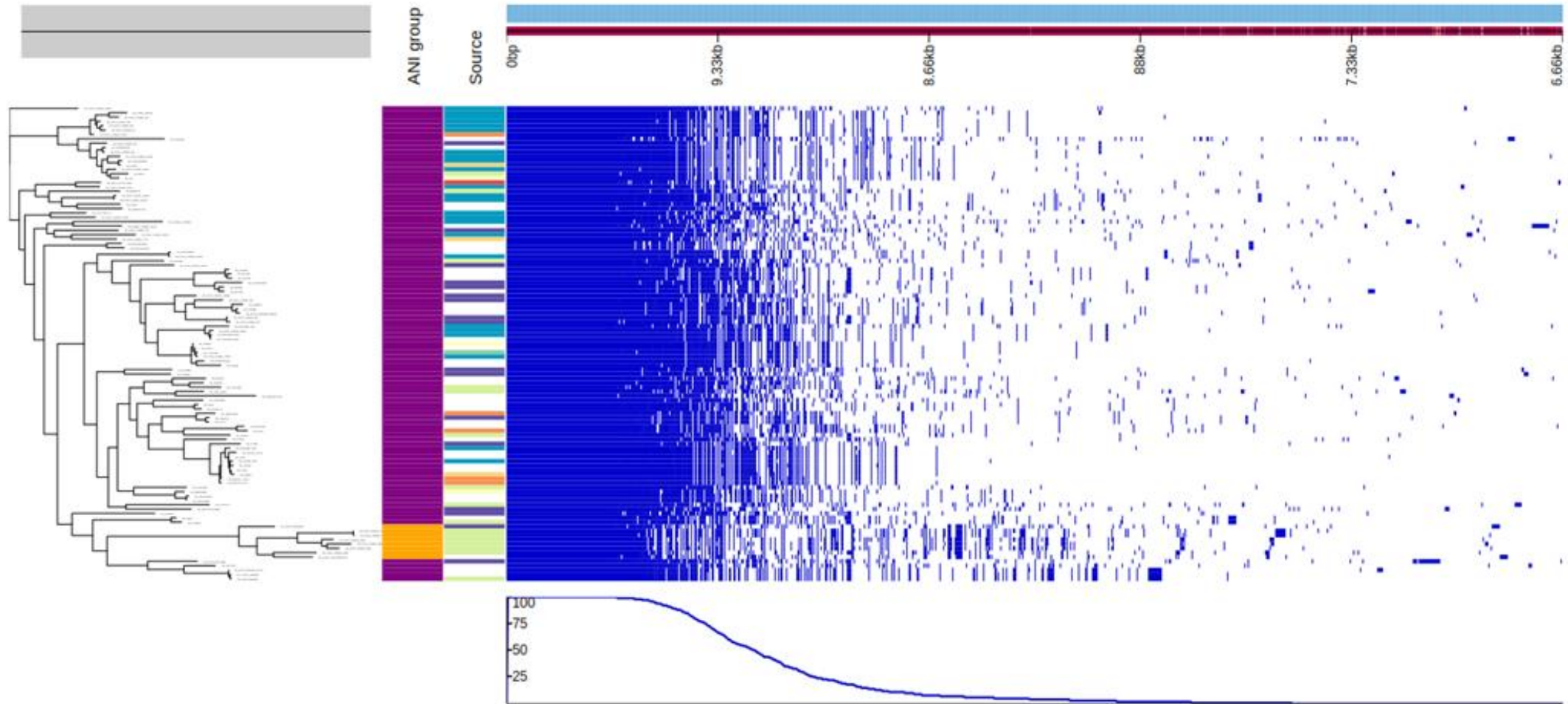
# Methods

Pangenome calculation and functional annotation



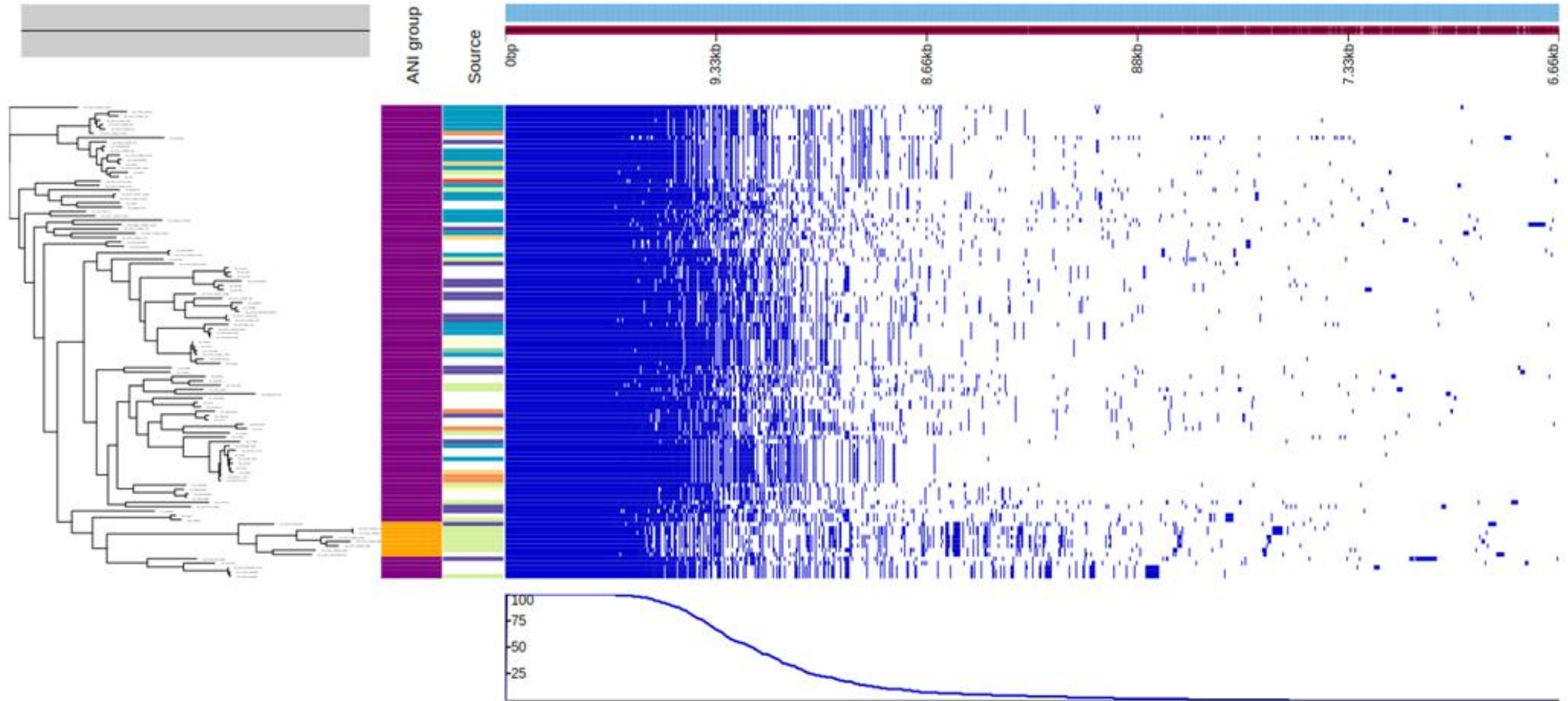
# Results

## Pangenome calculation and functional annotation



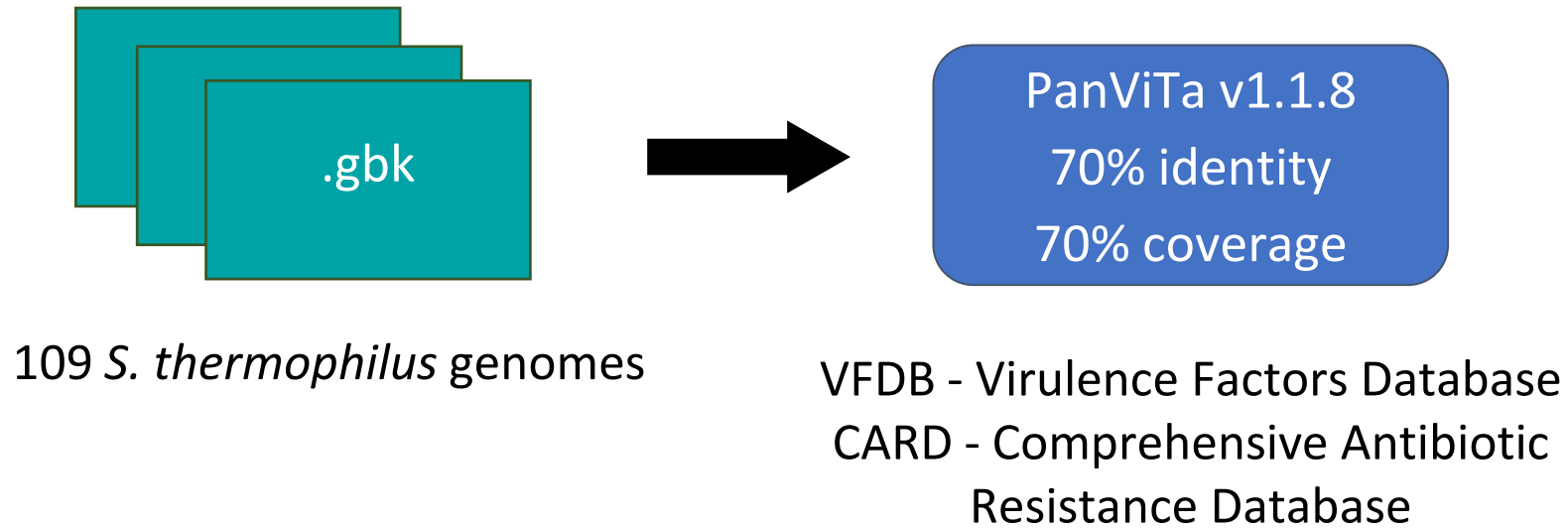
# Results

Pangenome calculation and functional annotation - different functionalities of the genomes!



# Methods

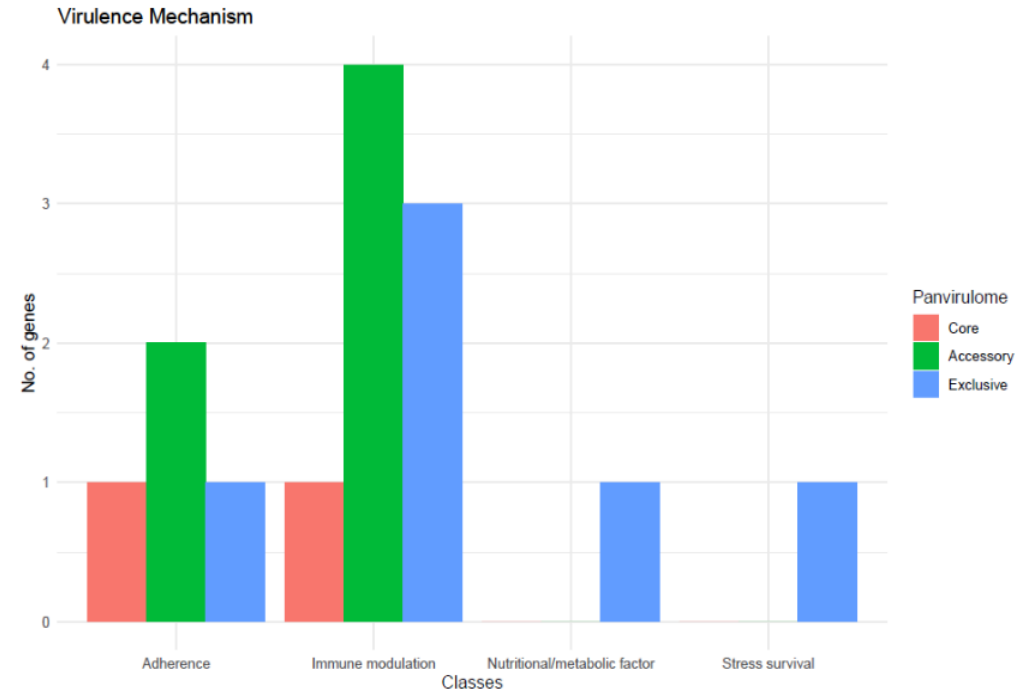
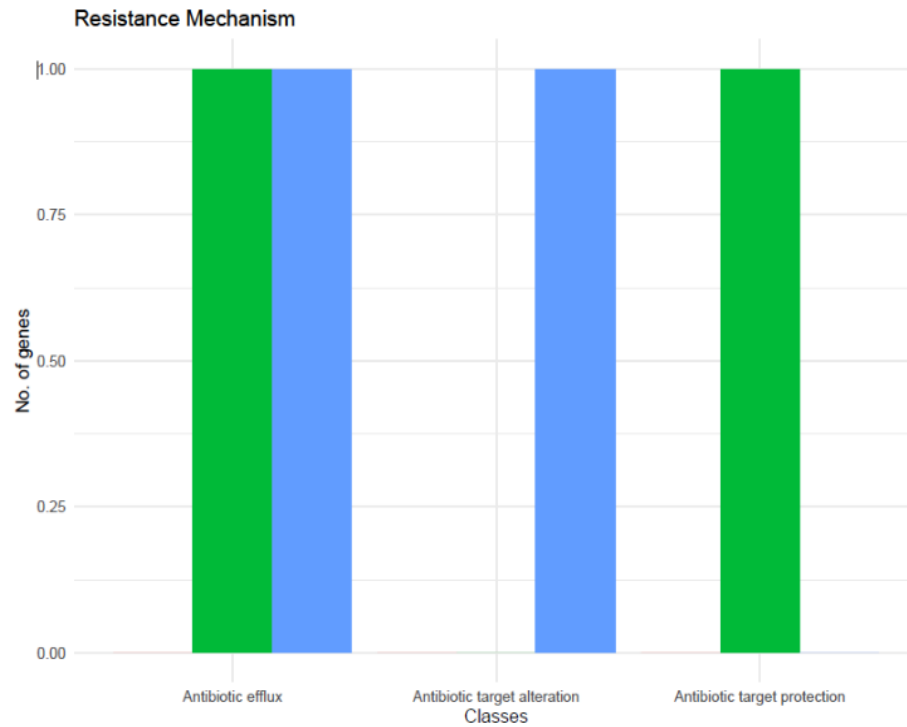
Panvirulome and panresistome prediction



# Results

Panvirulome and panresistome prediction - what's behind the QPS/GRAS status?

- Few genes predicted (4 resistance and 14 virulence)
  - No core resistome
  - Core virulome: Fbp54 and HasC



# Conclusions

More probiotic potential in particular strains!

## Why the disparity in genes amount?

- High level of genomic plasticity (e.g. genomic islands);
- Different sources and times of collection.

## Is it safe for commercial usage?

- Evolution and genomic plasticity;
- Genes might be important in probiosis context.

## Next steps

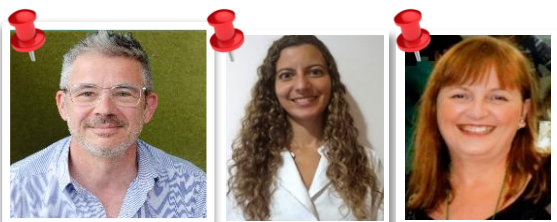
- Pathways - lactose digestion and vitamins;
- Secondary metabolites
- Cell wall characteristics



fish  
milk  
cheese  
commercial  
yoghurt  
fermented\_milk  
human  
dairy



# Acknowledgments



CAPES-COFECUB Scholarship 88887.937879/2024-00



Funding agencies/institutions

## Thank you for your attention!



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