

# Comparative genomic analysis between *Lactobacillus delbreuckii* subsp. *lactis* and *Lactobacillus delbreuckii* subsp. *bulgaricus* of dairy origin

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## Abstract

*Lactobacillus delbreuckii* subsp. *lactis* and *Lactobacillus delbreuckii* subsp. *bulgaricus* are lactic acid bacteria commonly exploited by the dairy industry as starter cultures, mainly for the production of cheese and yogurt. In this work, we present the comparative genomic analysis between the recently sequenced genomes of *L. lactis* ACA-DC 178 and *L. bulgaricus* ACA-DC 87, isolated from Kasser cheese and yogurt, respectively. The genome of *L. lactis* ACA-DC 178 is larger than that of *L. bulgaricus* ACA-DC 87, containing 2,048 and 1,928 protein coding genes, respectively. Full chromosome alignments revealed strain specific differences, although a high degree of synteny between the two strains was also observed. The core genome of the two strains contained about 1,300 genes while the unique genes of the two strains were also identified. The two genomes contained several genomic islands, indicating that a number of genes have been acquired through horizontal gene transfer. We also predicted one CRISPR system in each genome, three potential antimicrobial peptides in total and also prophage sequences integrated into the genomes of the two strains. Overall, our analysis provides useful insights into the technological potential of the ACA-DC 178 and ACA-DC 87 strains.

## Results

Figure 1 - Circular maps of the genome of *L. lactis* ACA-DC 178 (A) and *L. bulgaricus* ACA-DC 87 (B). Genomic features appearing from the periphery to the center of the map: 1. Forward CDSs (cyan); 2. Reverse CDSs (red); 3. tRNA genes (blue); 4. rRNA genes (green); 5. %GC plot; 6. GC skew.

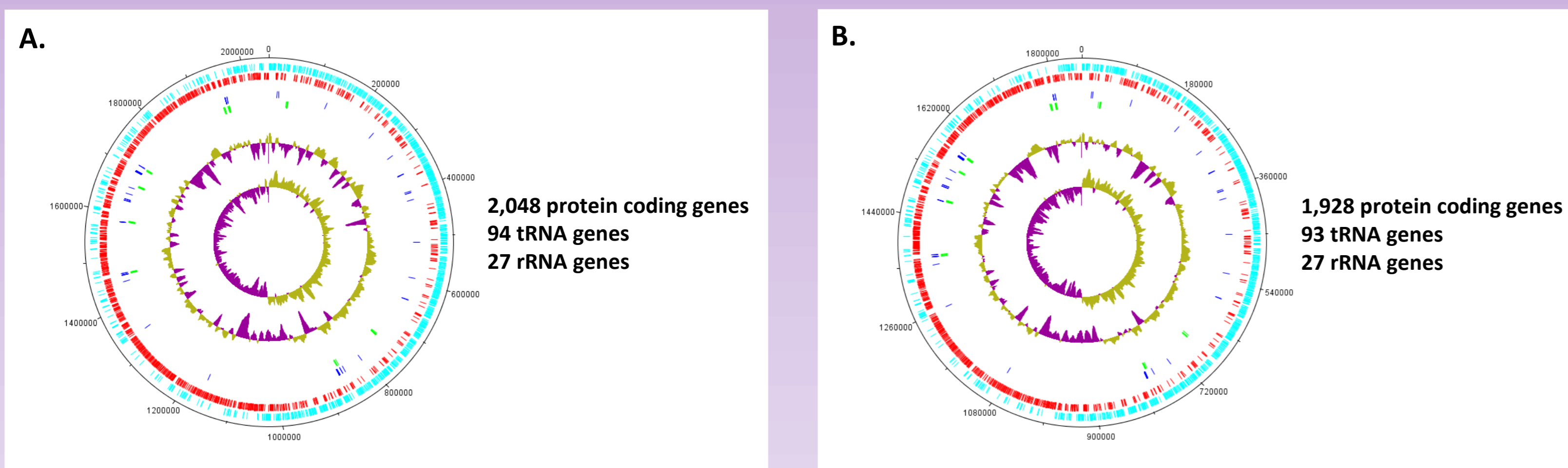


Figure 2 – Chromosome alignments of the strains as calculated by progressiveMauve. The *L. bulgaricus* ATCC BAA-365 and the *L. bulgaricus* ND02 strains were used as the reference genomes for the *L. bulgaricus* ACA-DC 87 and the *L. lactis* ACA-DC 178 strains, respectively. Although the ND02 strain is deposited in NCBI as *Lactobacillus delbreuckii* subsp. *bulgaricus*, Kafsi et al. 2014 suggested that the ND02 is a *Lactobacillus delbreuckii* subsp. *lactis* strain. Local collinear blocks (LCBs) of conserved sequences among the strains are represented by rectangles of the same colour. Connecting lines can be used to visualize synteny or rearrangement. LCBs positioned above or under the chromosome (black line) correspond to the forward and reverse orientation, respectively. The level of conservation is equivalent to the level of vertical colour filling within the LCBs (e.g. white regions are strain-specific). Sequences not placed within an LCB are unique for the particular strain.

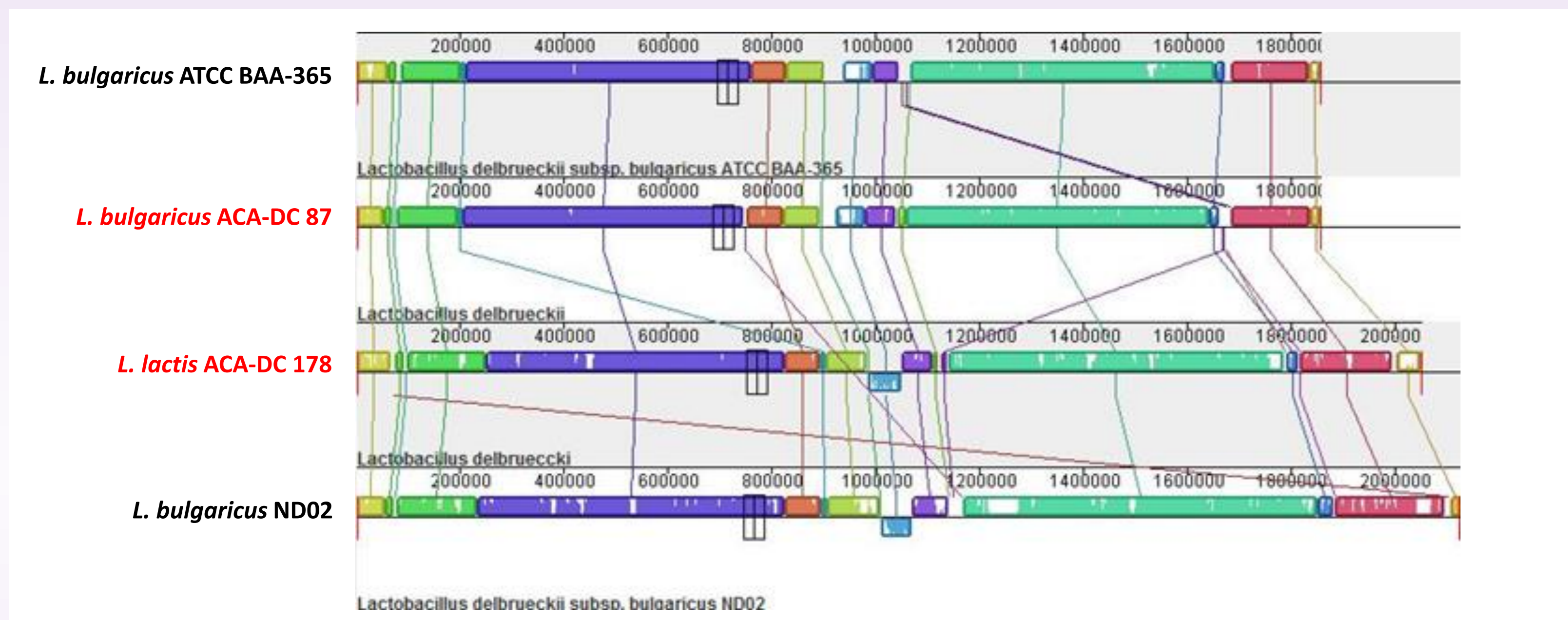


Figure 3 –The pangenome, the core genome, the accessory and the unique genes as obtained through the analysis of each set of genomes sequences with progressiveMauve. Genome sequences of *L. bulgaricus* strains (A). Genome sequences of *L. lactis* strains (B). Genome sequences of *L. bulgaricus* ACA-DC 87 and *L. lactis* ACA-DC 178 strains (C).

A. <i>L. delbreuckii</i> subsp. <i>bulgaricus</i>		B. <i>L. delbreuckii</i> subsp. <i>lactis</i>		C. <i>L. lactis</i> ACA-DC 178 vs <i>L. bulgaricus</i> ACA-DC 87	
Pangenome	2956	Pangenome	2558	Pangenome	2670
Core genome	1267	Core genome	1502	Core genome	1306
Accessory genes	551	Unique genes	ACA-DC 178: 546 ND02: 510	Unique genes	ACA-DC 178: 742 ACA-DC 87: 622
Unique genes	ACA-DC 87: 270 ATCC BAA-365: 235 ATCC 11842: 440 2038: 193				

Figure 4 – CRISPR systems in the genome sequences of *L. lactis* ACA-DC 178 (A) and *L. bulgaricus* ACA-DC 87 (B) as predicted by CRISPRfinder

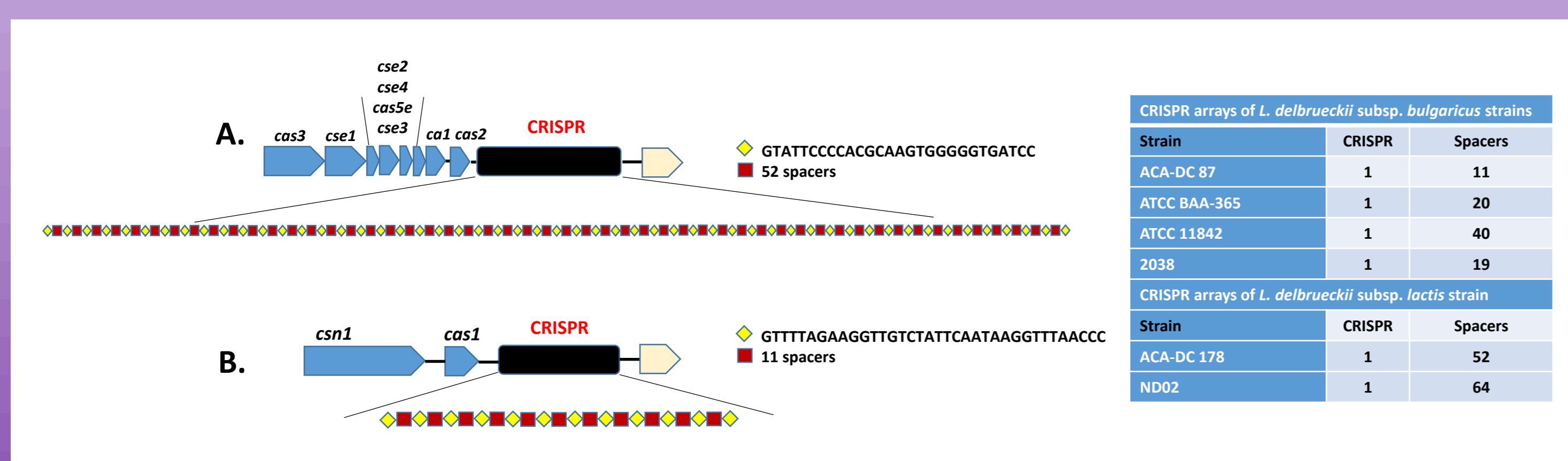


Figure 5 – Circular maps of the genome of *L. lactis* ACA-DC 178 (A) and *L. bulgaricus* ACA-DC 87 (B) genomes. Highlighted regions correspond to genomic islands (GIs). GIs are colored within the circular maps according to the tool that predicted each one: orange and blue were predicted with SIGI-HMM and IslandPath-DIMOB, respectively. The integrated GIs are presented on the periphery in red. The black line plot represents the GC content (%) of the genomic sequences. Numbering of the GIs for each genome starts from the first GI found after position 0 of the genome and going clockwise.

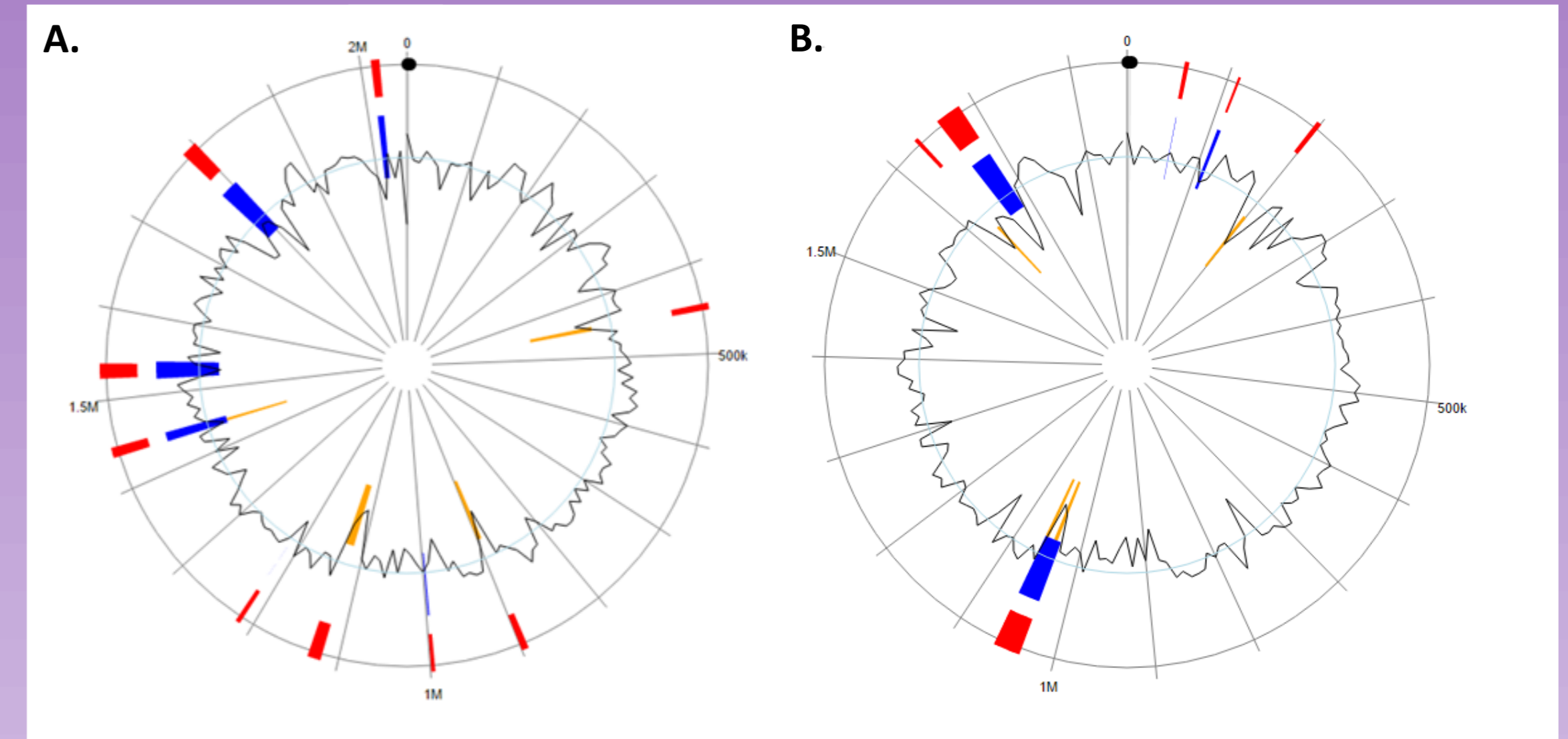


Figure 6 – Genes encoding for antimicrobial peptides in the genome sequences of *L. lactis* ACA-DC 178 (A,B) and *L. bulgaricus* ACA-DC 87 (C), as predicted by BAGEL3.

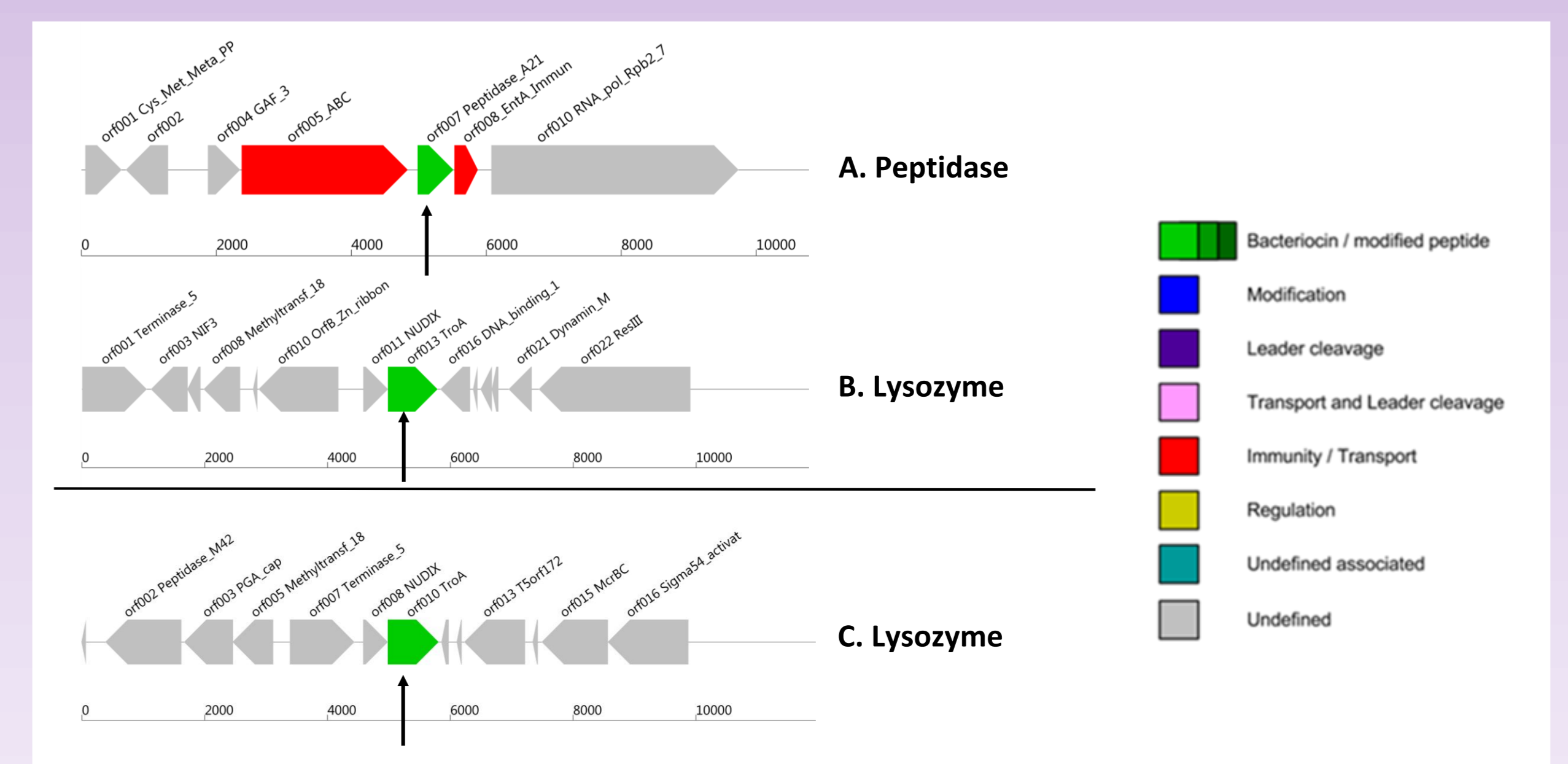
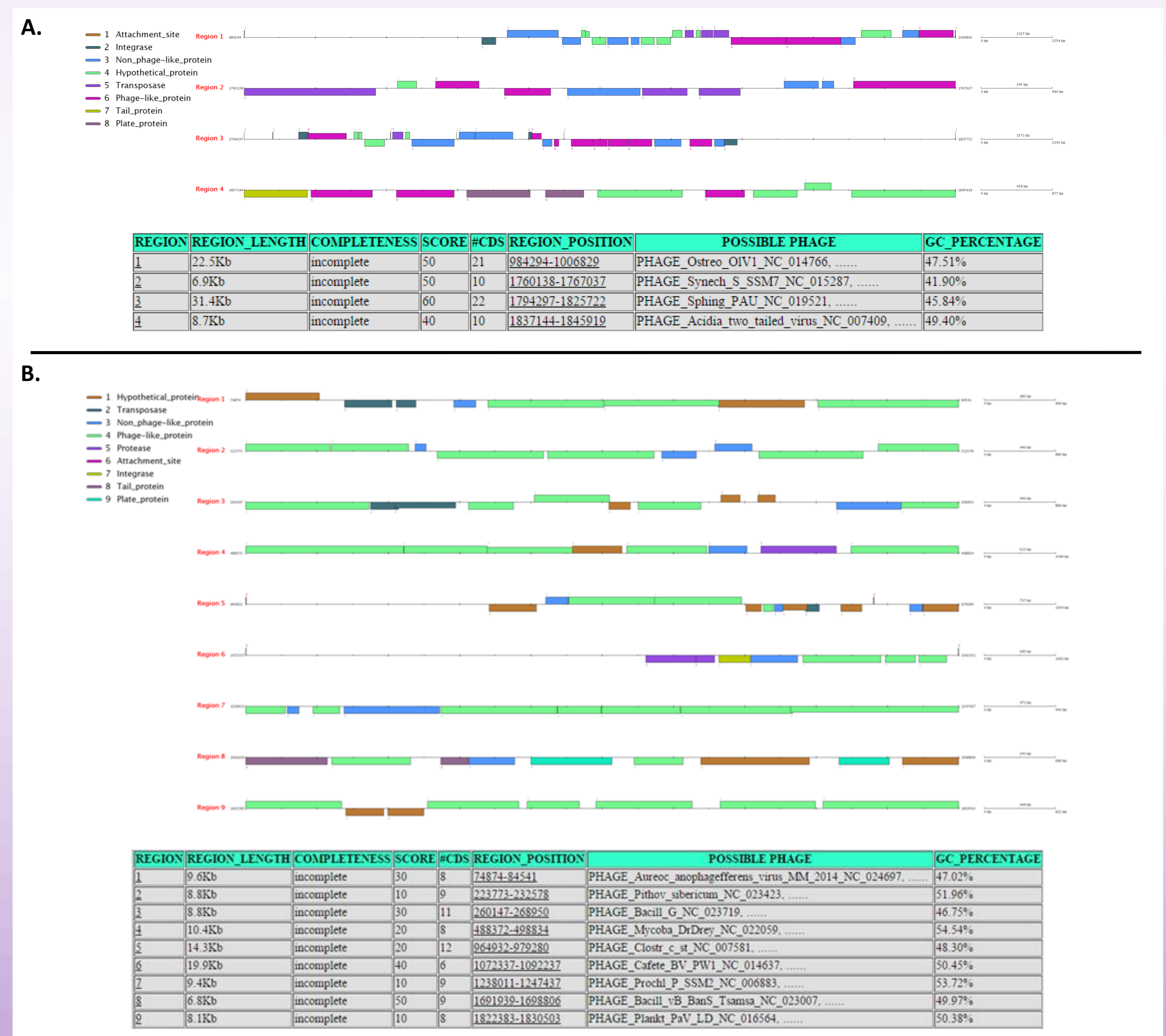


Figure 7 – Prophage sequences of *L. lactis* ACA-DC 178 (A) and *L. bulgaricus* ACA-DC 87 (B) as predicted by PHAST.



## Bibliography

Hela El Kafsi, Johan Binesse, Valentin Loux, Julien Buratti, Samira Boudebouze, Rozenn Dervyn, Sean Kennedy, Nathalie Galleron, Benoit Hingault, Jean-Michel Batto, Bouziane Moumen, Emmanuelle Maguin and Maarten van de Guchte (2014). *Lactobacillus delbreuckii* ssp. *lactis* and ssp. *bulgaricus*: a chronicle of evolution in action. BMC Genomics, 15:407.

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