

The complete genome of *Pedobacter lusitanus* NL19: a comprehensive genomic analysis

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OBJECTIVES

- Assemble the complete genome of *Pedobacter lusitanus* NL19 for further annotation and comprehensive genomic analysis.
- Identification and *in silico* characterisation of biosynthetic gene clusters (BGCs) encoding new natural products (NP), namely ribosomal (RiPPs) and non-ribosomal peptides (NRPs) with predicted features, for their future expression using synthetic biology approaches.

BACKGROUND

Pedobacter lusitanus NL19 exhibits strong bioactivity against Gram-positive and Gram-negative bacteria, and yeasts with relevance in the clinic, food industry and aquaculture [1].

The draft genome revealed the presence of 16 BGCs encoding secondary metabolites NPs, including RiPPs and NRPs [2].

Except for the BGC encoding the pedopeptins [3], most of the BGCs are cryptic or are weakly expressed in the laboratory condition tested, making it difficult to characterize the compounds encoded.

High-quality genome sequence will allow future molecular manipulations which are fundamental to unravel the full biotechnological potential of the microorganism.

RESULTS

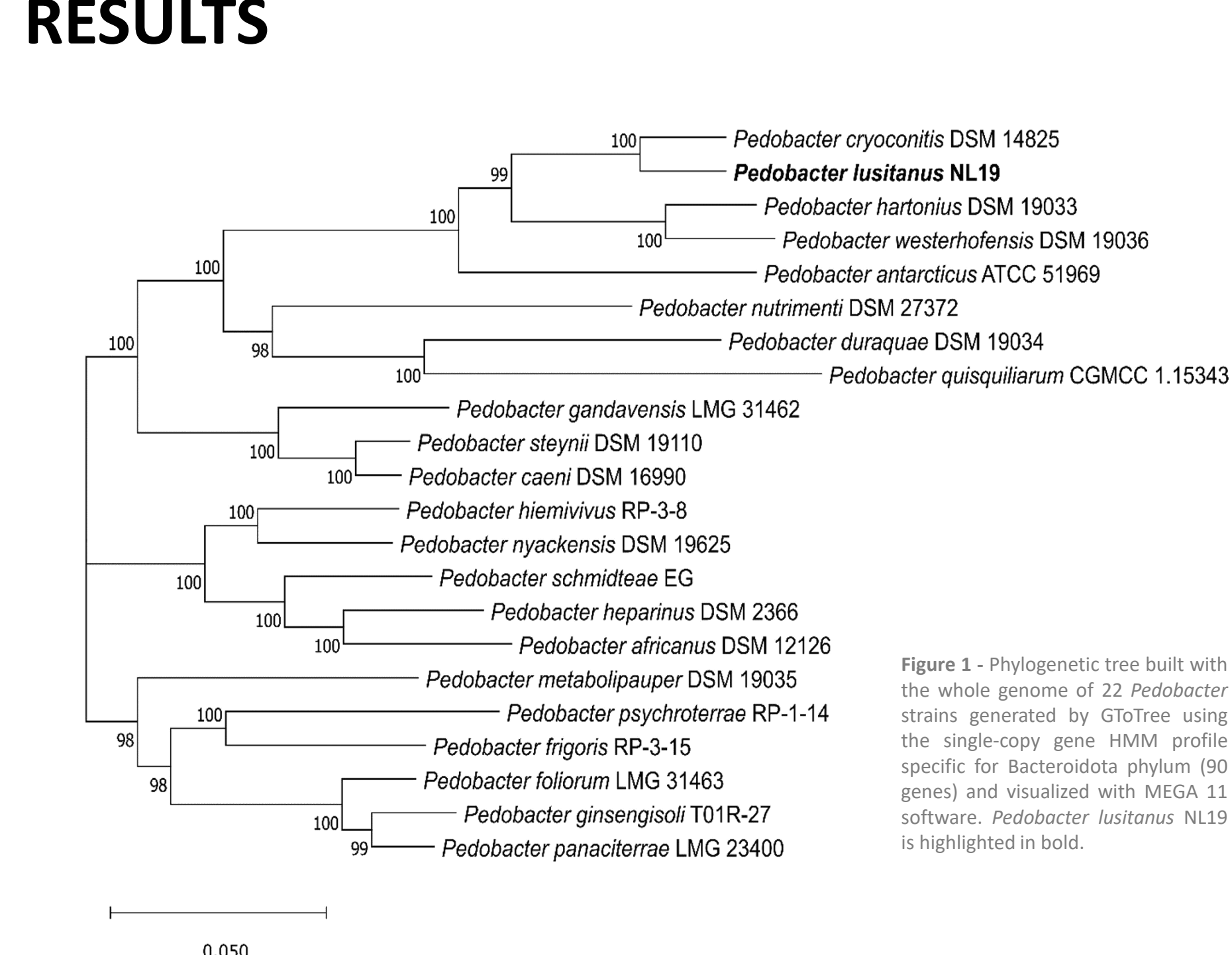


Figure 1 - Phylogenetic tree built with the whole genome of 22 *Pedobacter* strains generated by GToTree using the single-copy gene HMM profile specific for Bacteroidota phylum (90 genes) and visualized with MEGA 11 software. *Pedobacter lusitanus* NL19 is highlighted in bold.

Table 1 - Genomic features from the genome of *Pedobacter lusitanus* NL19

Characteristic	Value
Genome size (bp)	6,049,699
G+C content (%)	39.1
Genes (total)	5193
CDS (total)	5103
Genes (coding)	5078
CDS (protein)	5078
Genes (RNA)	90
rRNA (5S, 16S, 23S)	7, 6, 6
tRNA	68
ncRNA	3
Number of BGCs	18

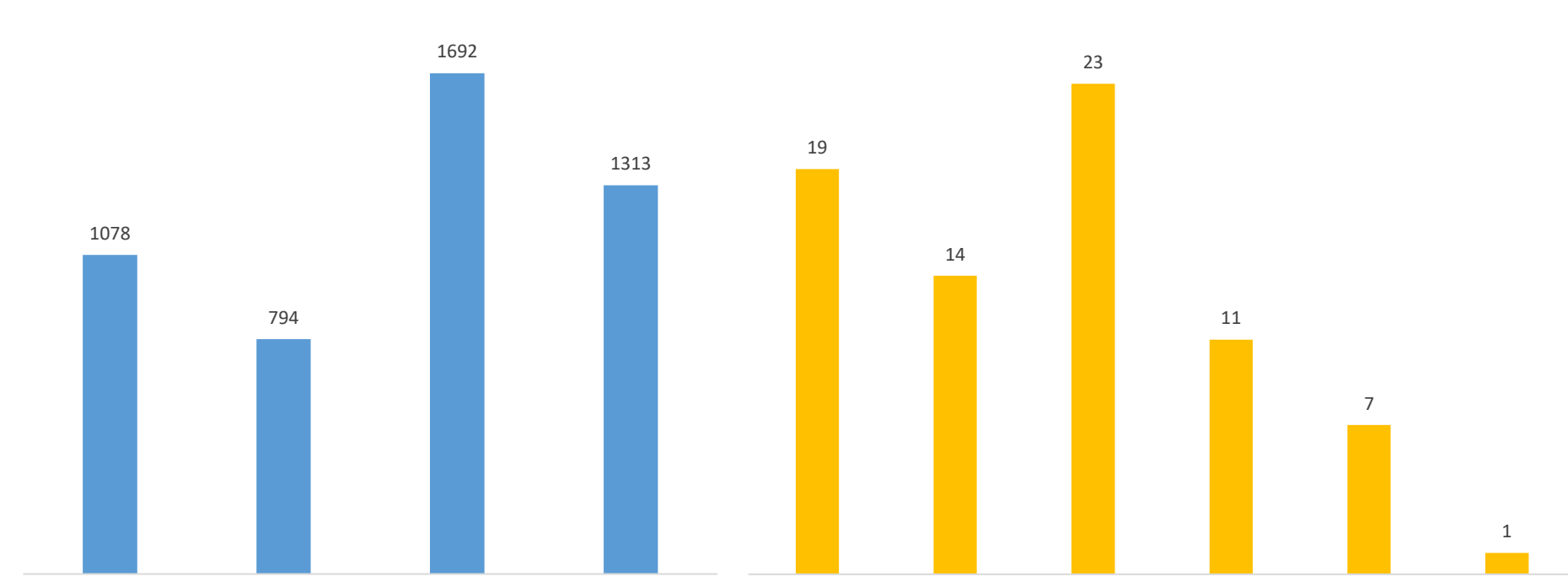


Figure 2 - Number of clusters of orthologous groups produced by eggNOG-mapper. Each category has a hit number that corresponds to the number of proteins associated.

Figure 3 - Putative genes implicated in metal resistance distributed according to function. The possible function is indicated in the x axis and the number of putative genes is indicated in the top of the bars.

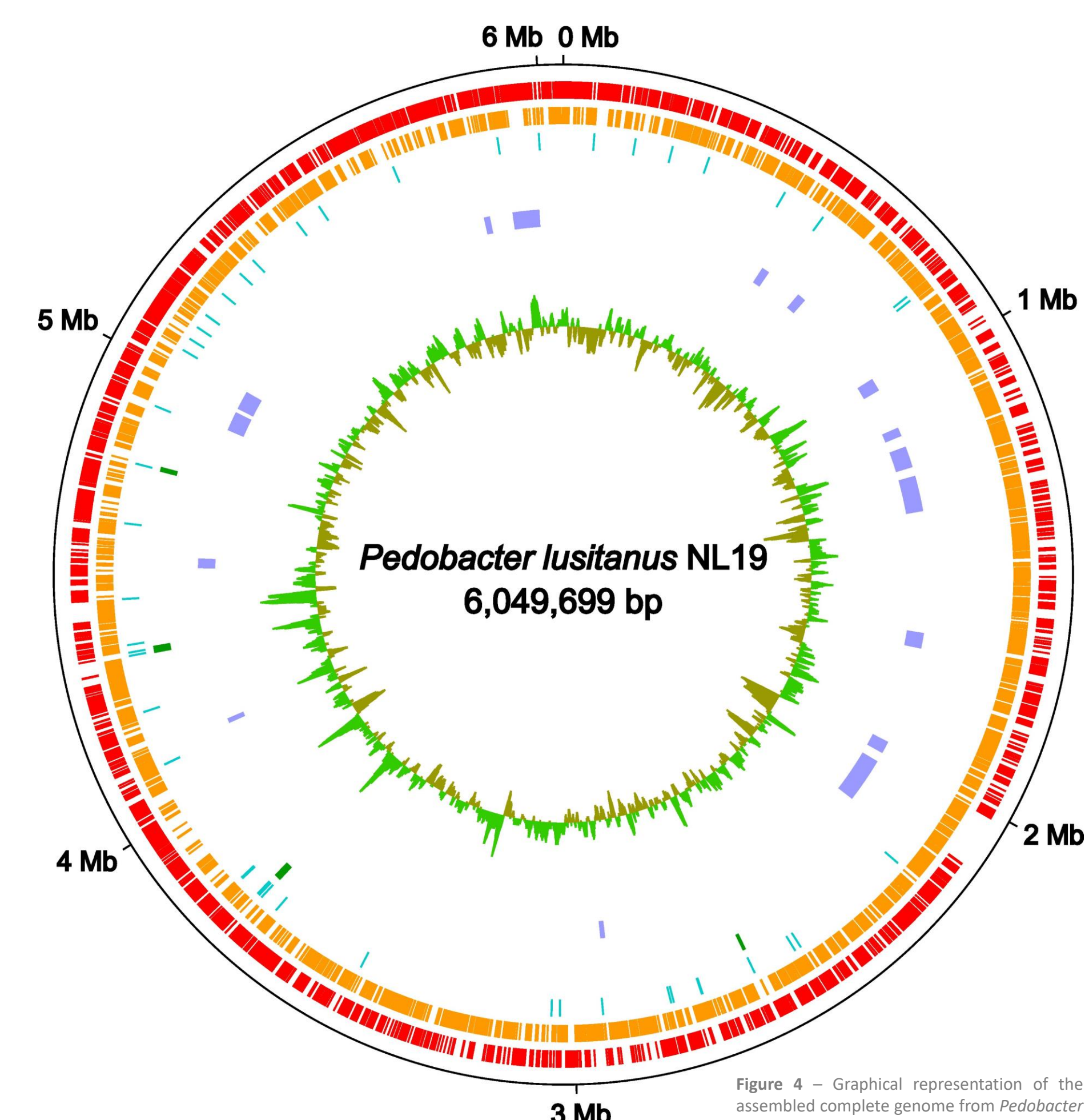
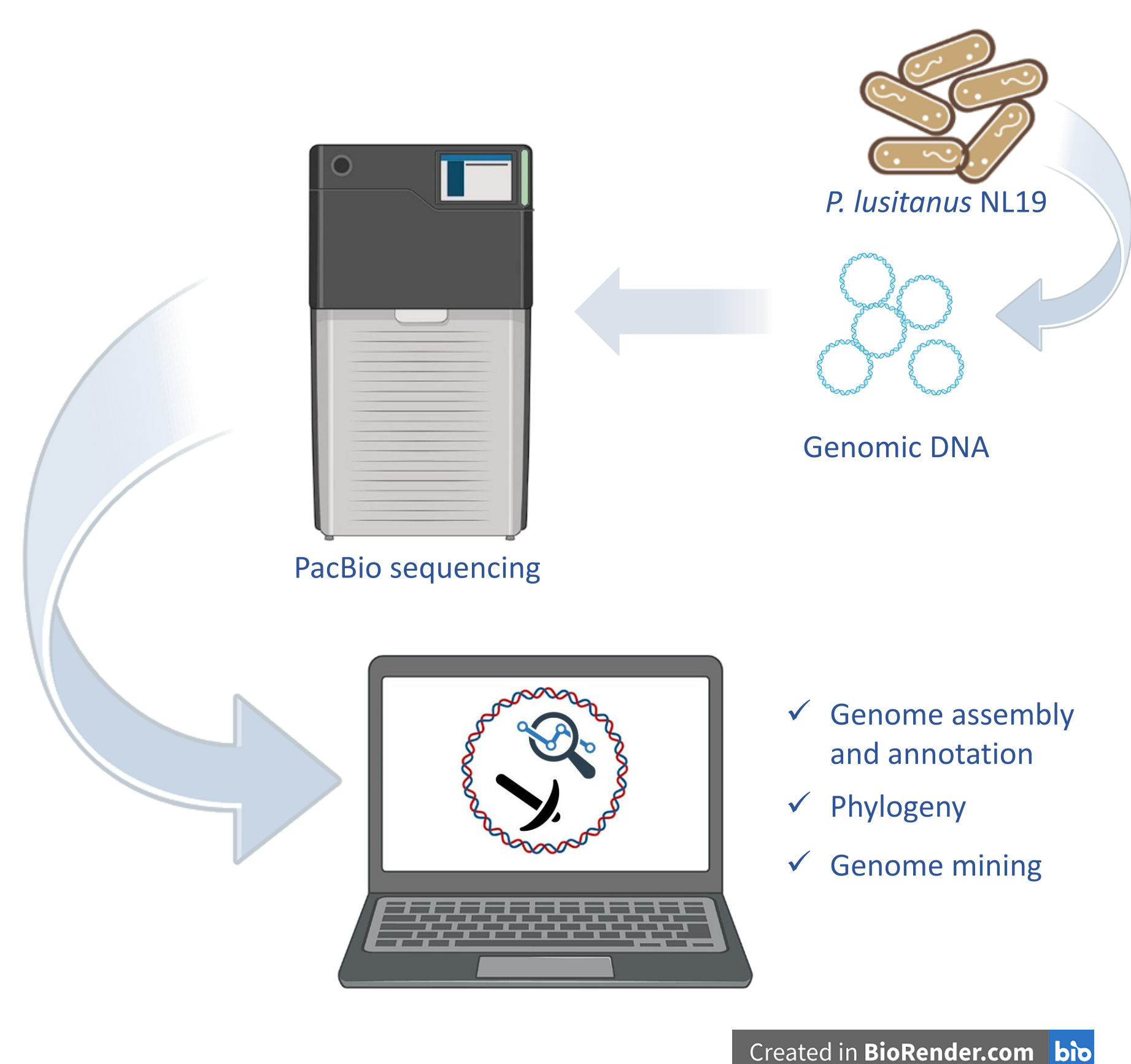


Figure 4 - Graphical representation of the assembled complete genome from *Pedobacter lusitanus* NL19. Genomic coordinates (black), forward strand (red) and reverse strand (orange) coding sequences, tRNA genes (blue), rRNA genes (green), biosynthetic gene clusters (purple), interior circle light (above average) and dark green (below average) corresponds to the GC percentage.

METHODS



CONCLUSIONS

- The genome of *P. lusitanus* NL19 is rich in BGCs that encode new NPs, including RiPPs and NRPs, with promising biotechnological potential;
- The use of specific bioinformatic tools made it possible to predict that some of these NPs have new chemical structures;
- Information gathered on the full genome will allow to proceed with experimental work involving the expression and characterization of these promising novel NPs.

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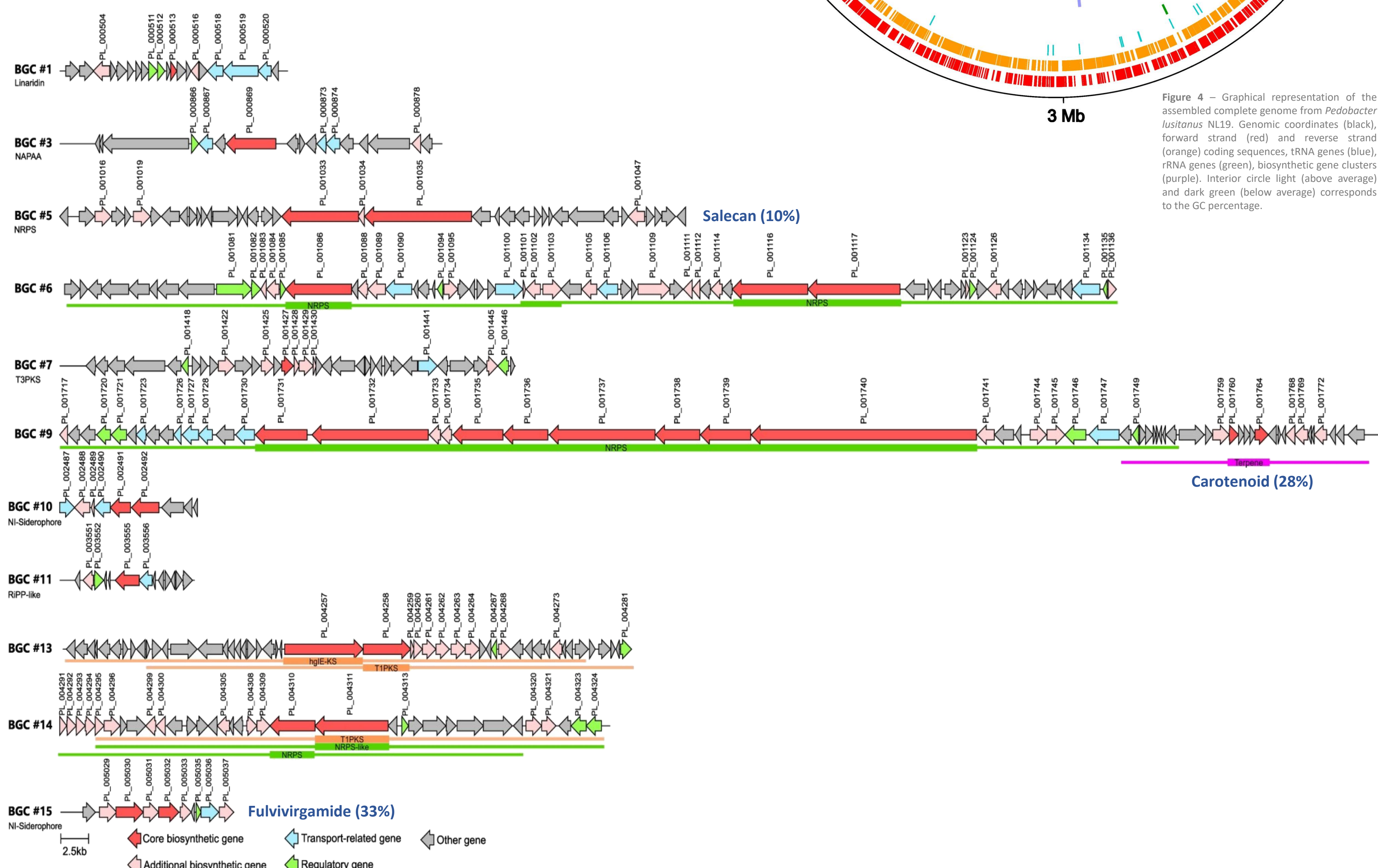


Figure 5 - Graphic representation of the predicted BGCs and associated BGC classes, by antiSMASH 7.0. Also, the locus tag of the relevant genes (core biosynthetic genes, additional biosynthetic genes, transport-related genes and regulatory genes) is displayed. The BGCs with more than one class are clearly identified.