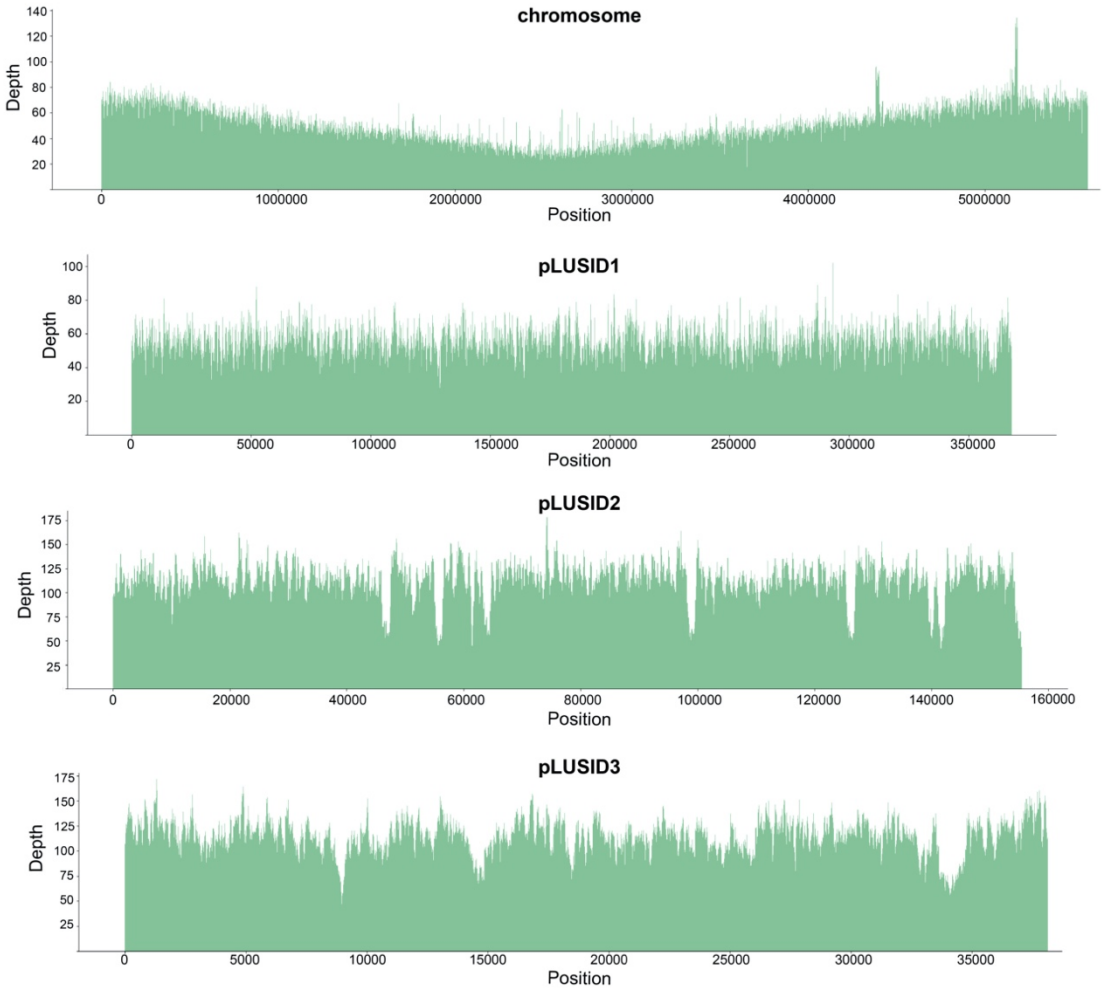
Completed genomic sequence of *Bacillus thuringiensis* HER1410 reveals a *cry*-containing chromosome, two megaplasmids & an integrative plasmidial prophage.

Ana Lechuga[*,1], Cédric Lood[†,‡,1], Margarita Salas[*,2], Vera van Noort, V.[‡,§], Rob Lavigne[†], and Modesto Redrejo-Rodríguez[*,**]

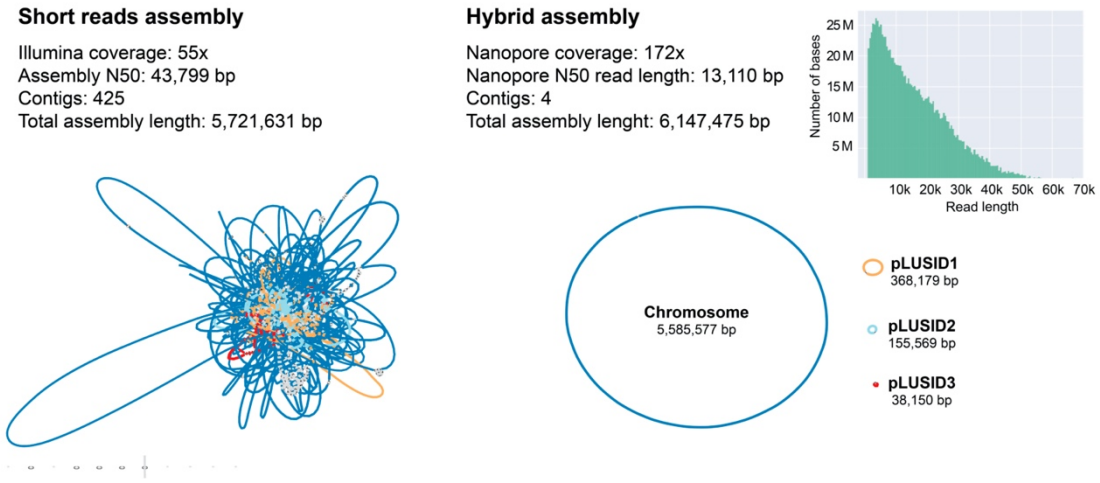
[*]Centro de Biología Molecular Severo Ochoa (CSIC-UAM) Madrid, Spain.
[†]Department of Biosystems, Laboratory of Gene Technology, KU Leuven, Leuven, Belgium.
[‡]Department of Microbial and Molecular Systems, Centre of Microbial and Plant Genetics, Laboratory of Computational Systems Biology, KU Leuven, Leuven, Belgium.
[§]Institute of Biology, Leiden University, Leiden, The Netherlands.
[**]Departamento de Bioquímica, Universidad Autónoma de Madrid (UAM) and Instituto de Investigaciones Biomédicas Alberto Sols (CSIC-UAM), Madrid, Spain.

[1]These authors contributed equally to this work

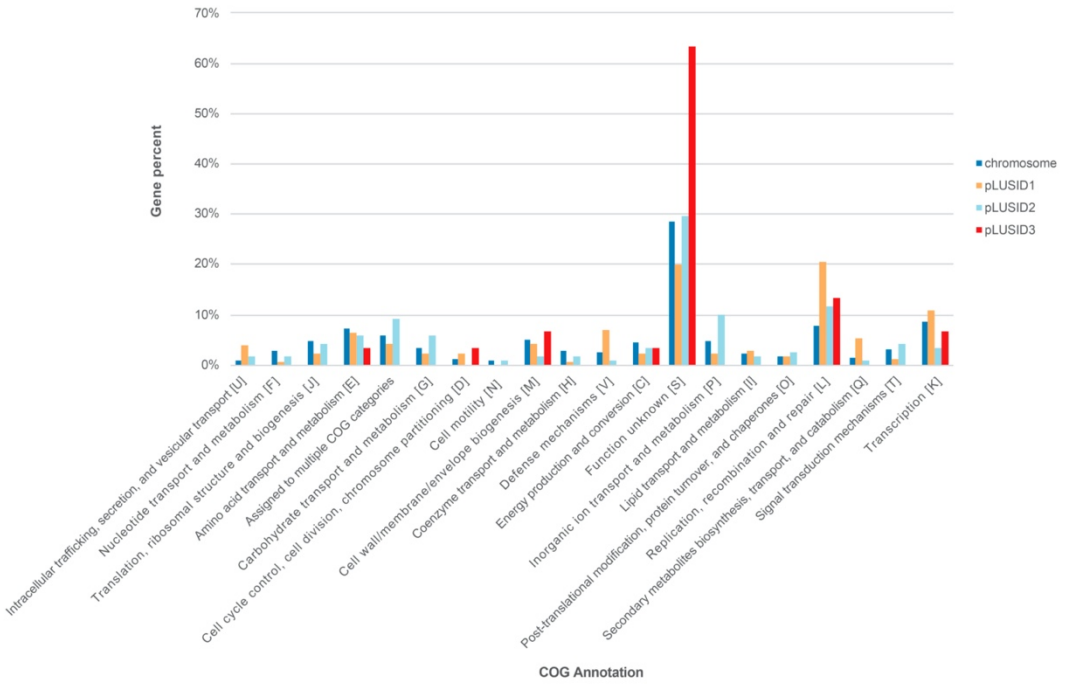
SUPPLEMENTAL FIGURES



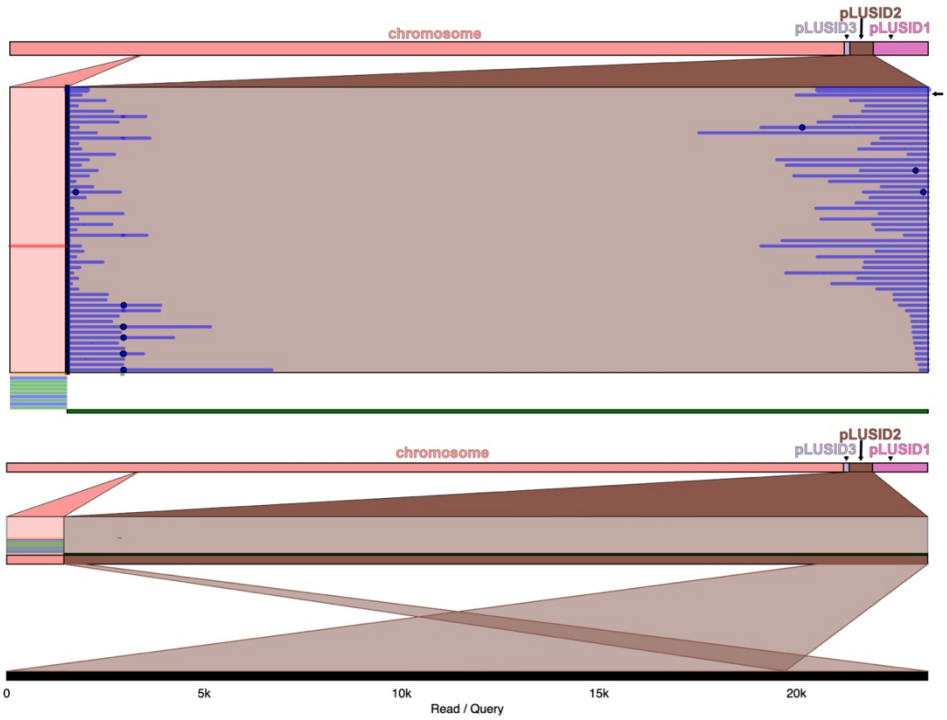
Supplemental Figure 1. Mapping of short-reads to the resolved components of HER1410. Coverage plots represent sequence depth along each element sequence. Plots were generated with weeSAM pipeline (available at https://github.com/centre-for-virus-research/weeSAM).



Supplemental Figure 2. Comparative metrics of short reads assembly using Illumina sequences and hybrid assembly using Illumina and Nanopore sequences. Representation of assemblies was created with Bandage where chromosome=dark blue, pLUSID1=orange, pLUSID2=light blue, pLUSID3=red.



Supplemental Figure 3. Bar plot of COG categories proportions for the elements of HER1410 genome. Ratio of genes belonging to each COG category, relative to the total number of genes in each element is shown (Supplemental Table 2).



Supplemental Figure 4. Structural variation analysis of pLUSID2. Long reads from Nanopore sequencing show evidence for pLUSID2 in HER1410 genome as a closed circular element. The only structural variation detected shown above resulted from the linearization of the circular molecule sequence (upper panel). One of the reads is indicated by an arrow and represented in the lower panel. Variants are visualized