

Figure S1. Comparison of the functional categories of genes lost in selected groups of *Lactobacillus* spp. and *Pediococcus*. Functional COG categories are abbreviated as follows (bottom up): **K**, Transcription; **G**, Carbohydrate transport and metabolism; **S**, Function unknown; **R**, General function prediction only; **V**, Defense mechanisms, **E**, Amino acid transport and metabolism; **H**, Coenzyme transport and metabolism; **M**, Cell wall/membrane/envelope biogenesis; **T**, Signal transduction mechanisms; **X**, Mobilome: prophages, transposons; **I**, Lipid transport and metabolism; **F**, Nucleotide transport and metabolism; **C**, Energy production and conversion; **O**, Posttranslational modification, protein turnover, chaperones; **J**, Translation, ribosomal structure and biogenesis; **L**, Replication, recombination and repair; **P**, Inorganic ion transport and metabolism; **Q**, Secondary metabolites biosynthesis, transport and catabolism; **Others**: A, RNA processing and modification; B, Chromatin structure and dynamics; D, Cell cycle control, cell division, chromosome partitioning; Y, Nuclear structure; N, Cell motility; Z, Cytoskeleton; W, Extracellular structures; U, Intracellular trafficking, secretion, and vesicular transport.

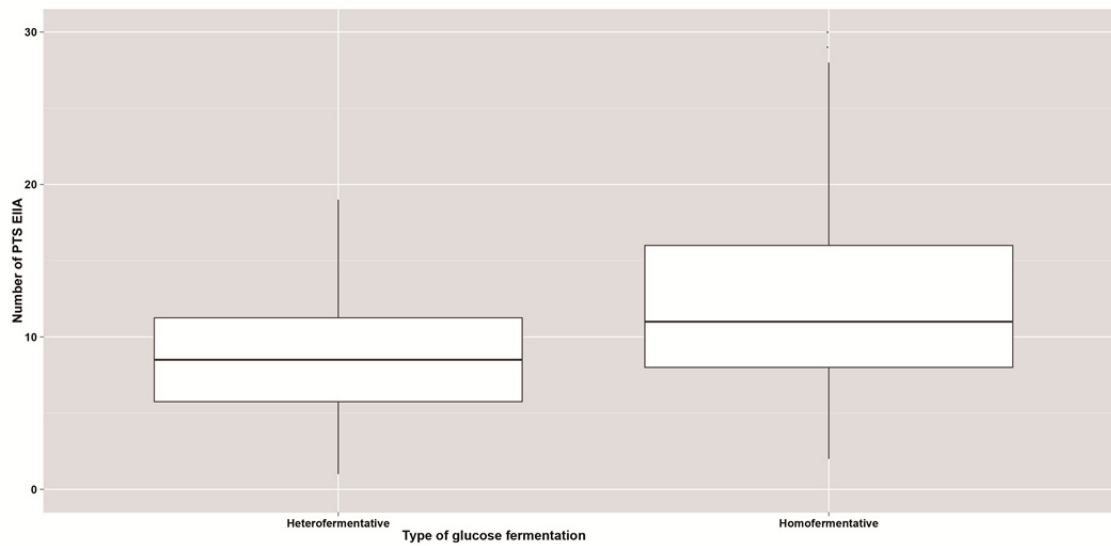
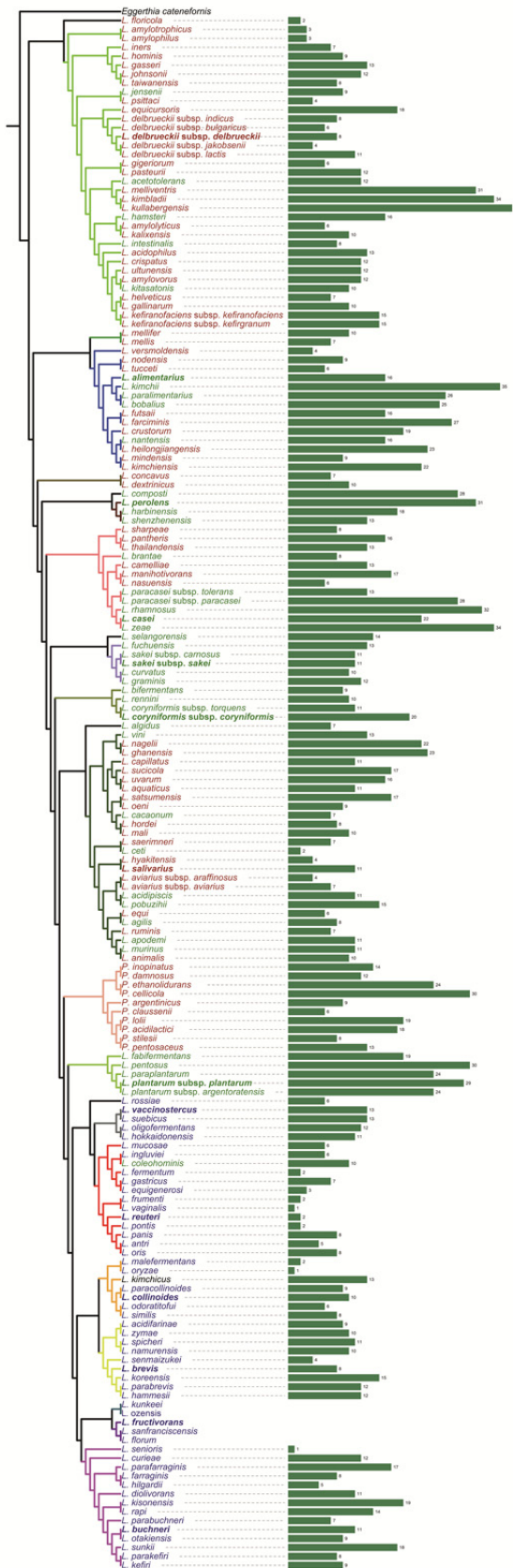


Figure S2.

Panel A. Comparison of the number of genes coding for the EIIA component of PTS systems per genome in heterofermentative lactobacilli and homofermentative lactobacilli. The horizontal line indicates the median; the boxes indicate the 25% and 75% percentiles, the vertical lines indicate the 10% and 90% percentiles, respectively. The number of PTS systems per genome of heterofermentative lactobacilli was significantly (6.71×10^{-5} , Mann–Whitney test) lower when compared to the number of PTS systems per genome in homofermentative lactobacilli.



Panel B. Number of genes coding for the EIIA component of PTS systems for each genome analysed in this study. The topology of the phylogenetic tree to the left matches the topology of the trees shown in Figure 1 and 4. ⁶