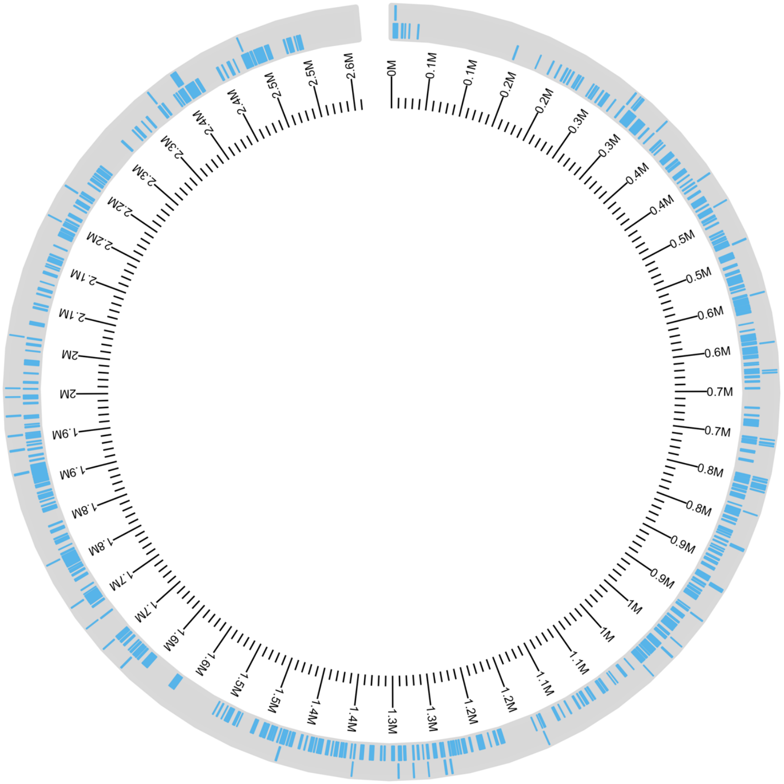
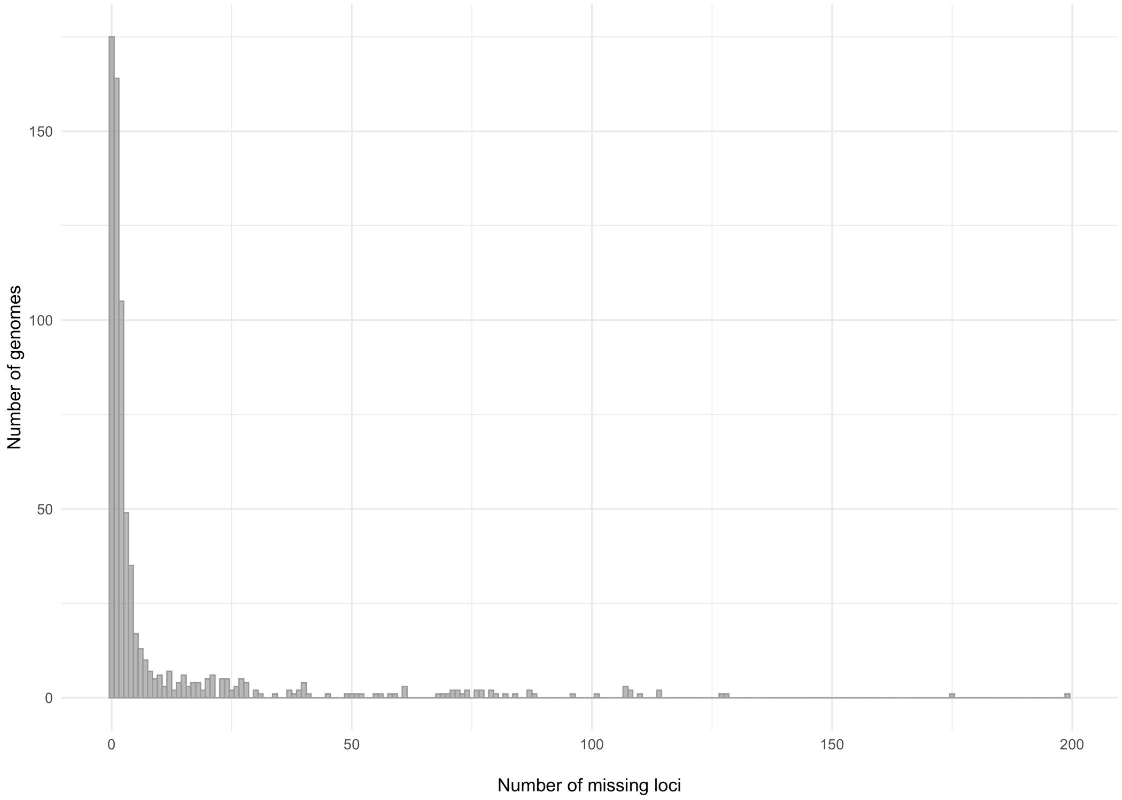


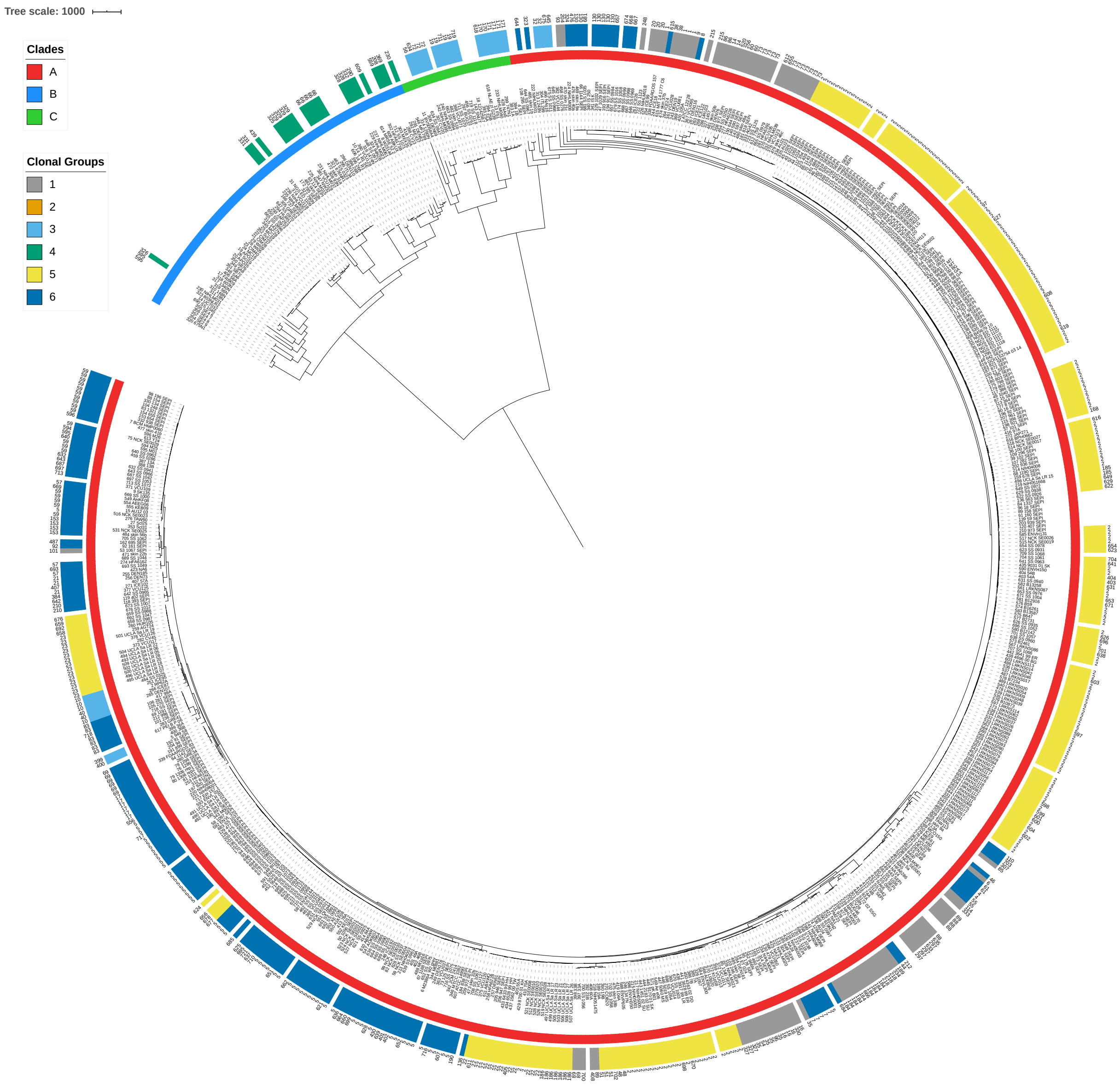
Supplementary Figure S1. Location of the 699 loci of the cgMLST scheme along the ATCC 12228 reference genome.

Blue lines on the 2 external circles indicate location of the core genes along the ATCC 12228 reference genome (the most outer circle is used to show overlapping genes). The inner circle represents the genomic positions (in Mb).

The graphical representation was generated with the ggbio R package (1).



Supplementary Figure S2. Distribution of the number of missing loci per genome.
The number of isolates (Y-axis) with each number of missing loci (X-xis) among the 699 core genes among genomes in the entire database (N=703) is given.



Supplementary Figure S3. Maximum likelihood phylogenetic tree of 703 isolates. Recombination regions were identified using Gubbins v2.2.0 with default parameters resulting in an alignment of 703 isolates and 31,385 sites. RAxML v8.2.8 was used for the phylogenetic inference under the GTRCAT model (final tree optimized under the GTRGAMMA model). The tree was drawn using iTOL. The inner color strip corresponds to the 3 clades A, B and C as defined by Meric and colleagues (2). The outer color strip represents the clonal groups as defined previously (3, 4). Missing clonal groups correspond to isolates for which no MLST sequence type (ST) has been identified. Outer numbers correspond to the ST. The tree is rooted using the midpoint method.

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