FIG S1 Heatmap of pairwise average nucleotide identity (ANI) values for the 33 whole genome sequenced *Campylobacter* spp. by comparison to data from SRA identified as *Campylobacter* spp.

The ANI was calculated using the pyani program after blastn alignment. Only regions present in all genomes were used in the ANI calculation. Values range from 0 (0%) ANI to 1 (100% ANI): Grey represents 0% ANI, clusters of highly similar isolates are highlighted in red. The dendrogram directly reflects the degree of identity between genomes. An ANI above 96% between two genomes is an indication that they belong to the same species and the colored branches represent different clusters.

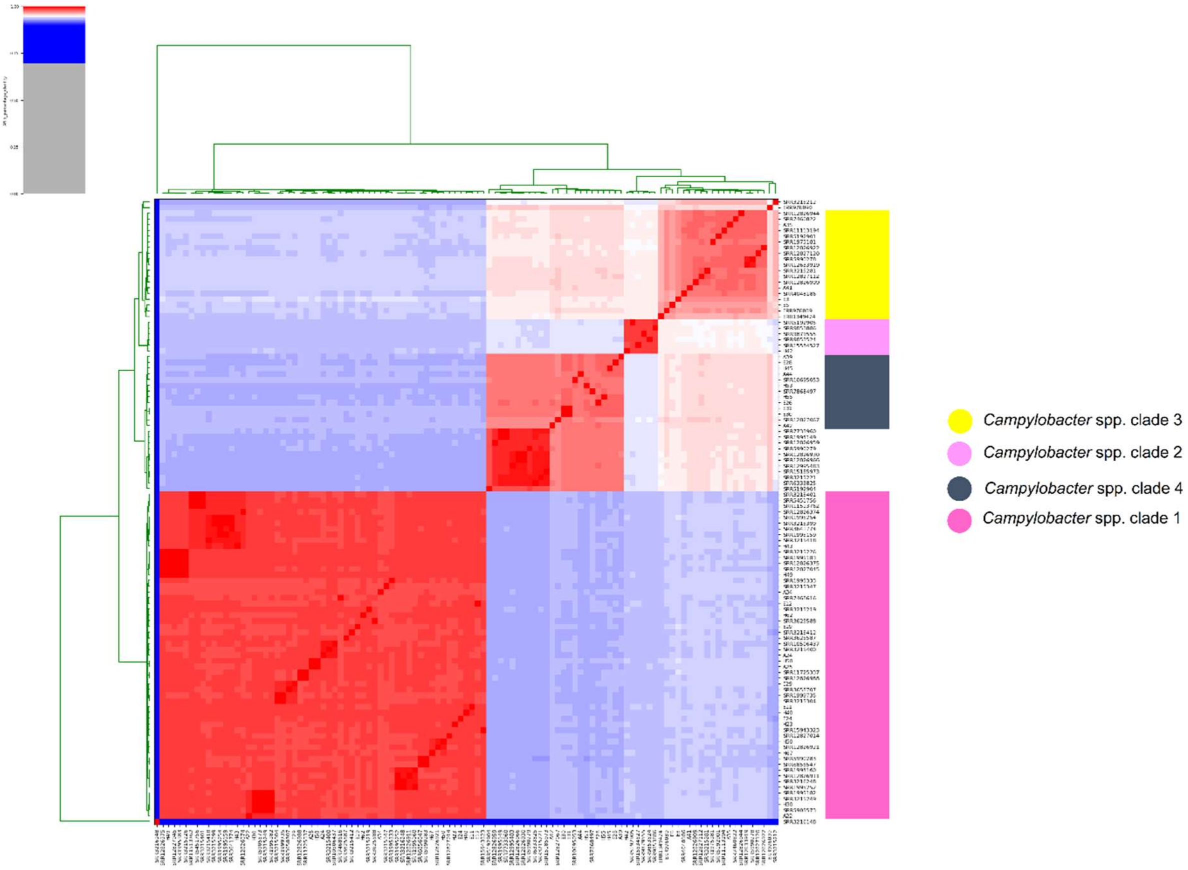

FIG S2 Minimum spanning tree of core genome multilocus sequence typing (cgMLST) with XX targets of 21 *C. lari* isolates from this study and 66 NCBI SRA accession isolates belonging to ST-21. Allelic distances between isolates are indicated, clusters with allele difference <10 are shaded in shade colours (genetically closely related isolates). The numbers given in the circles correspond to the SRA accession numbers and the number of isolates.