

Supplementary material

A retrospective whole-genome-based study of the epidemiology of *Salmonella* Dublin in cattle and humans in Denmark 1996-2016

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Figure legends

FIG S1 The networks of closely related *S. Dublin* isolates drawn based on isolate similarity of <10 SNPs, and the year of the isolation in a specific herd. The boxes with the same colour represent different isolates from the same herd, belonging to a different network. The herds connected with a green line share at least one isolate collected in the same year with <10 SNP difference. Herds connect with the orange lines share at least one isolate, but one year apart, blue – two years apart, and black – more than two years apart. The numbers on the lines indicate a number of SNPs found between the isolates (min.-max.). When the herd ID is given without a number, it means that all isolates from the herd had a SNP different indicated on the line. When the number is given along with the herd ID, it means that only that specific isolate was similar by given SNP between the herds, and the rest differed by >10 SNPs. Dashed line show herds connected indirectly, with no isolates differing by <10 SNPs between these herds.

FIG S2 A map of possible regions of recombination detected in the core gene alignment of 197 *S. Dublin* isolates from cattle. The phylogenetic tree on the left is a final tree generated by Gubbins from the alignment and with the predicted recombinant regions excluded. The scale bar on the top of the map shows the length of the alignment. Red regions indicate the recombinant regions that were found in multiple isolates, and blue regions those found only in single isolates. White areas indicate the absence of recombination events.

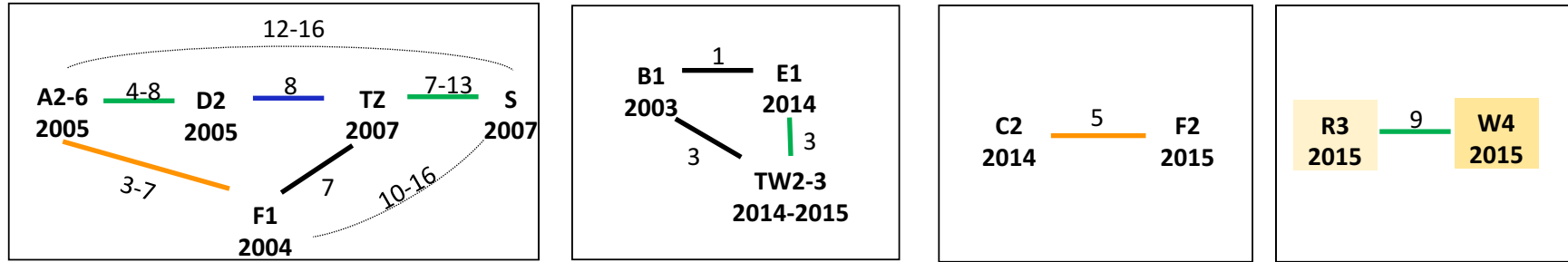
FIG S3 Plasmid profiles of selected *S. Dublin* isolates out of 64 analysed. Lines labelled as M represent plasmid size markers (shown on the left) *E. coli* 39R61 and *E. coli* V517. Lanes 1, 2, 5, 7, 11, 12 are *S. Dublin* isolates containing a plasmid of 83 kb. Lanes 3, 4, 6, 8, 9, 10 are *S. Dublin* isolates containing plasmids of 49kb, 83 kb, and 87 kb. Lanes 13 and 14 are *S. Dublin* isolates containing plasmids of 83 kb and 87 kb.

FIG S4 BLAST ring of IncN plasmid homolog of *Salmonella* Dublin and reference *S. enterica* serovar Stanleyville plasmid CP017725. Blast ring was created with GView. The middle ring is a reference plasmid, around which BLAST lanes are shown. Every lane corresponds to plasmid in each genome. The location of type IV secretion and antibiotic resistance genes are indicated outside the ring.

FIG S5 BLAST ring of IncFII/IncFIB plasmid homolog of *Salmonella* Dublin and reference *Escherichia coli* plasmid KJ484628. Blast ring was created with GView. The middle ring is a reference plasmid, around which BLAST lanes are shown. Every lane corresponds to plasmid in each genome.

FIG S6-S9 Contain information and the results on additional phylogenetic analyses of two *S. Dublin* sample sets from the study using alternative approaches and pipelines.

Networks within clade II



Networks within clade III

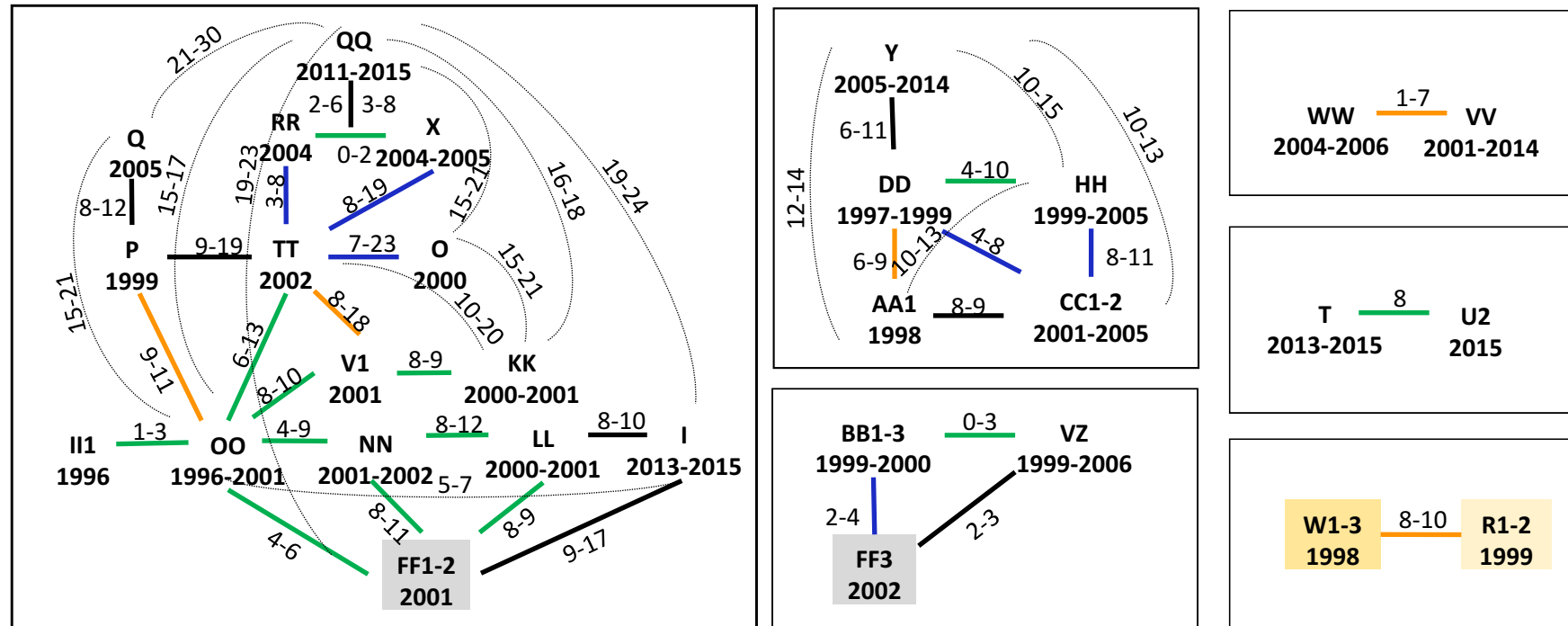


Figure S1 The networks of closely related *S. Dublin* isolates drawn based on isolate similarity of <10SNPs, and the year of the isolation in a specific herd

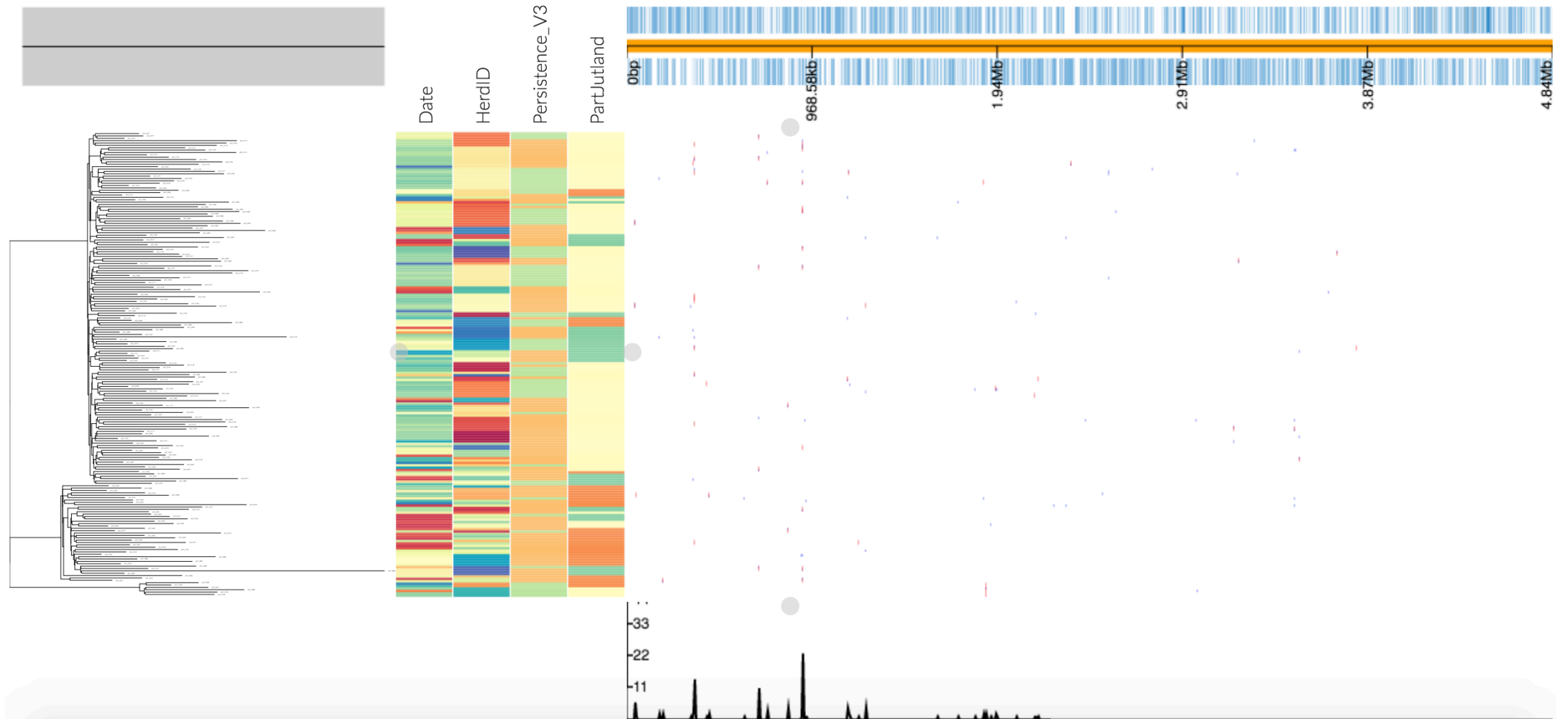


Figure S2 A map of possible regions of recombination detected in the core gene alignment of 197 *S. Dublin* isolates from cattle

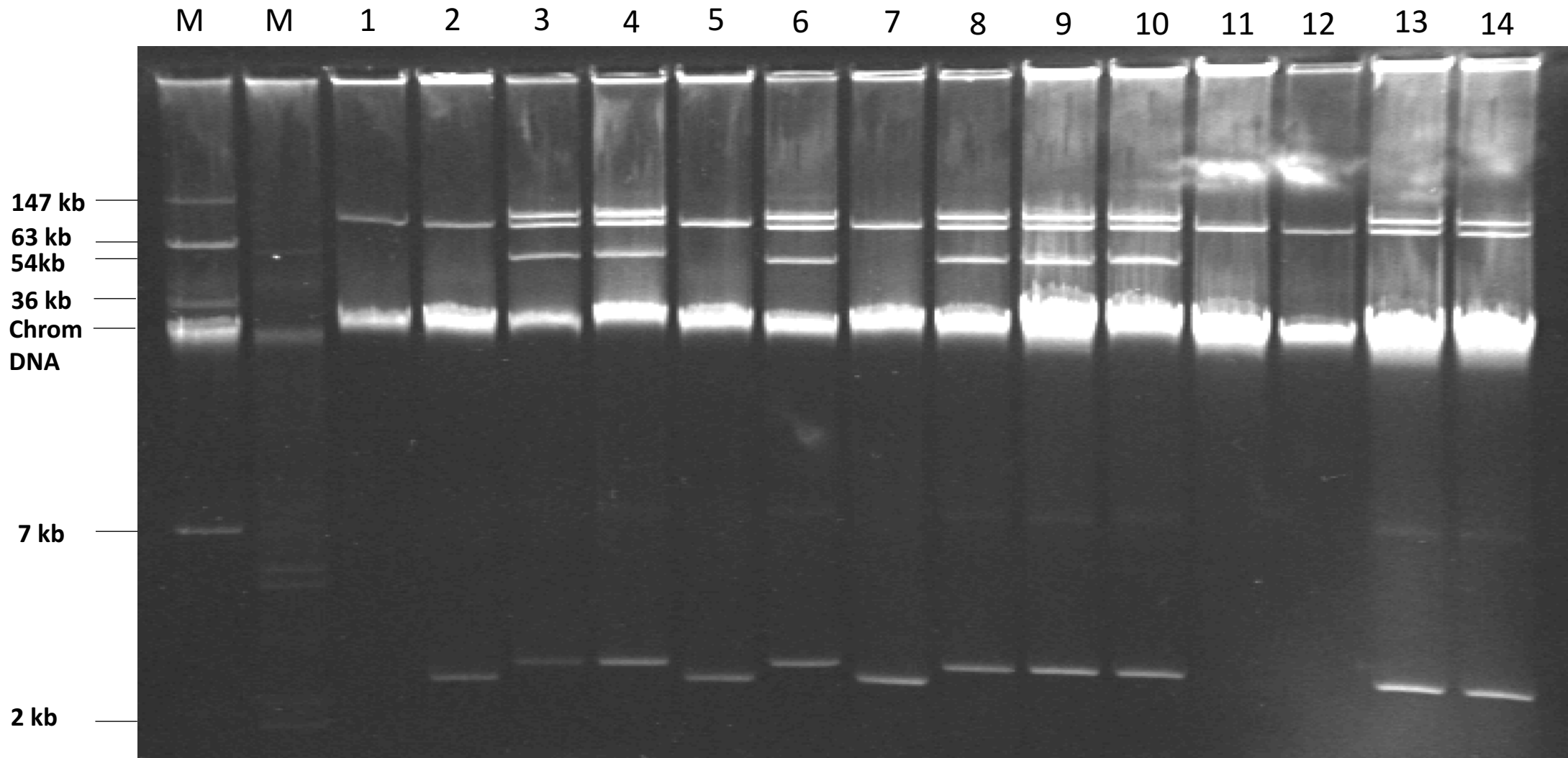


Figure S3 Plasmid profiles of selected *S. Dublin* isolates out of 64 analysed

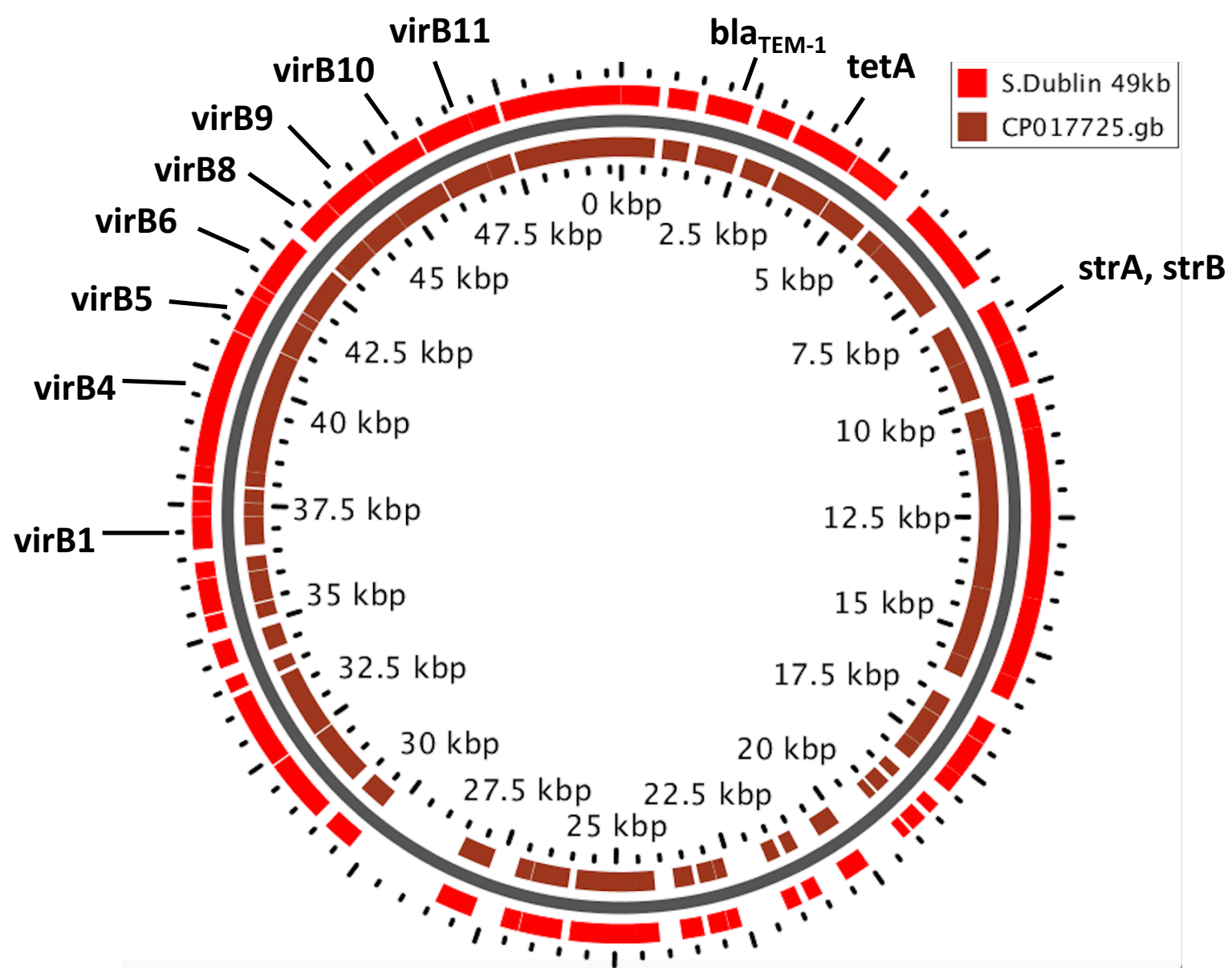


Figure S4 BLAST ring of IncN plasmid homolog of *Salmonella* Dublin and reference *S. enterica* serovar Stanleyville plasmid CP017725

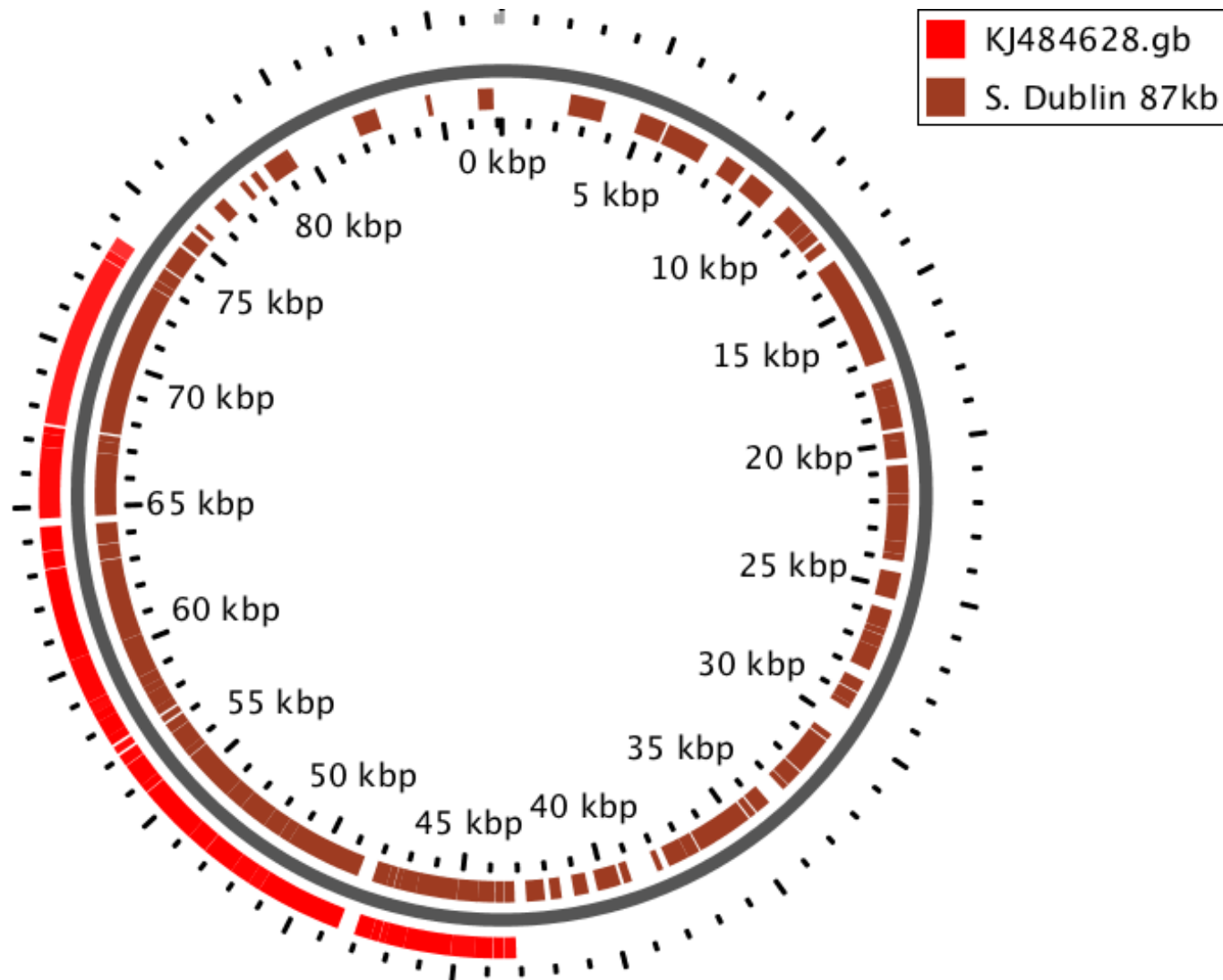


Figure S5 BLAST ring of IncFII/IncFIB plasmid homolog of *Salmonella* Dublin and reference *Escherichia coli* plasmid KJ484628

Phylogenetic analysis with alternative pipelines

Materials and methods

- Datasets:
 - *S. Dublin* from Danish cattle, n=197 (Fig. S6 and Fig. S7)
 - *S. Dublin* from Denmark and global isolates, n=288 (Fig. S8 and Fig. S9)
- Methods applied to both datasets:
 - Core genome SNP analysis using NASP pipeline (Fig. S6 and Fig. S8)
 - wgMLST analysis (Fig. S7 and Fig. S9)

Salmonella Dublin from
Danish cattle

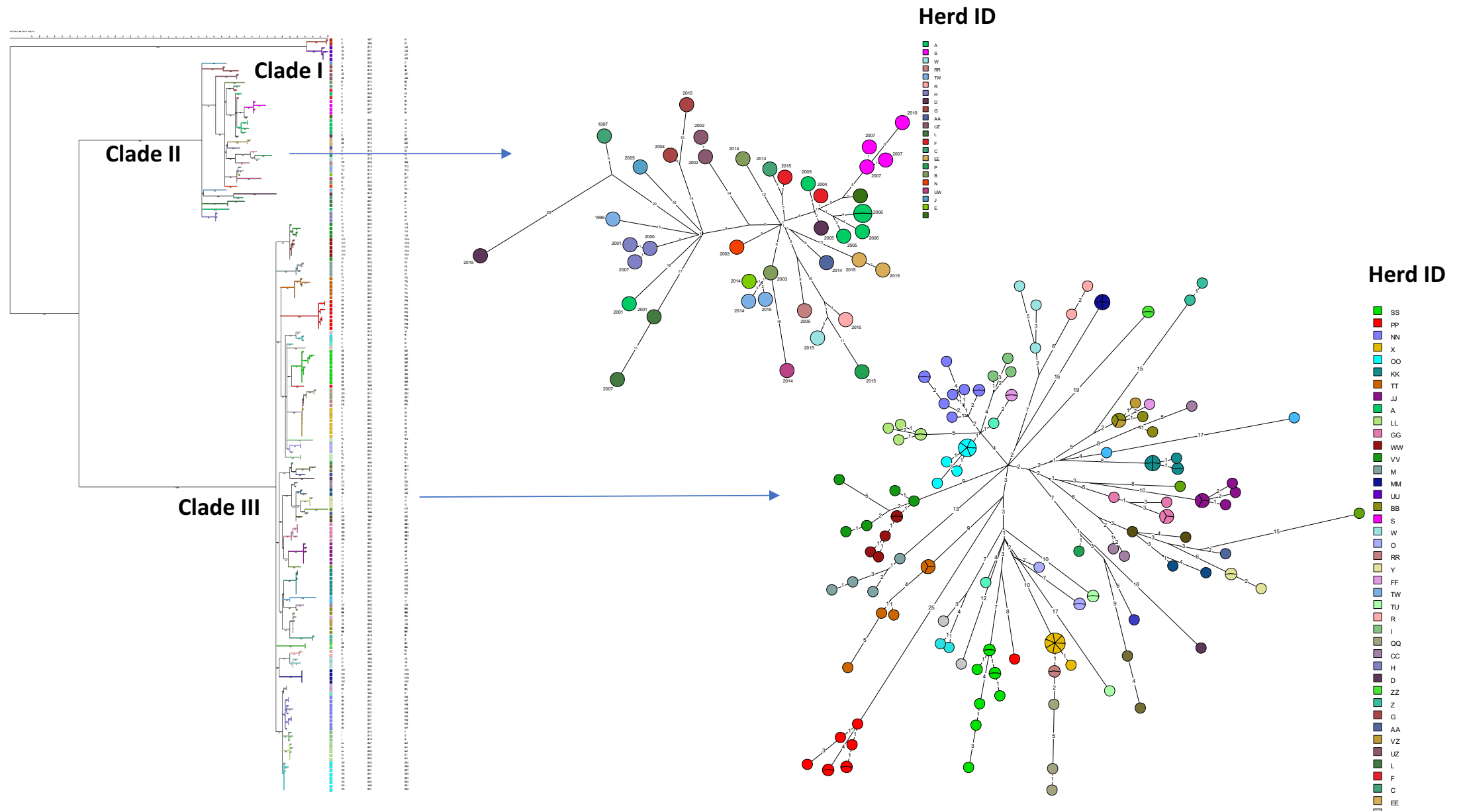


Figure S6 cgSNP maximum parsimony tree of 197 isolates of *S. Dublin* from Danish cattle, generated with NASP pipeline

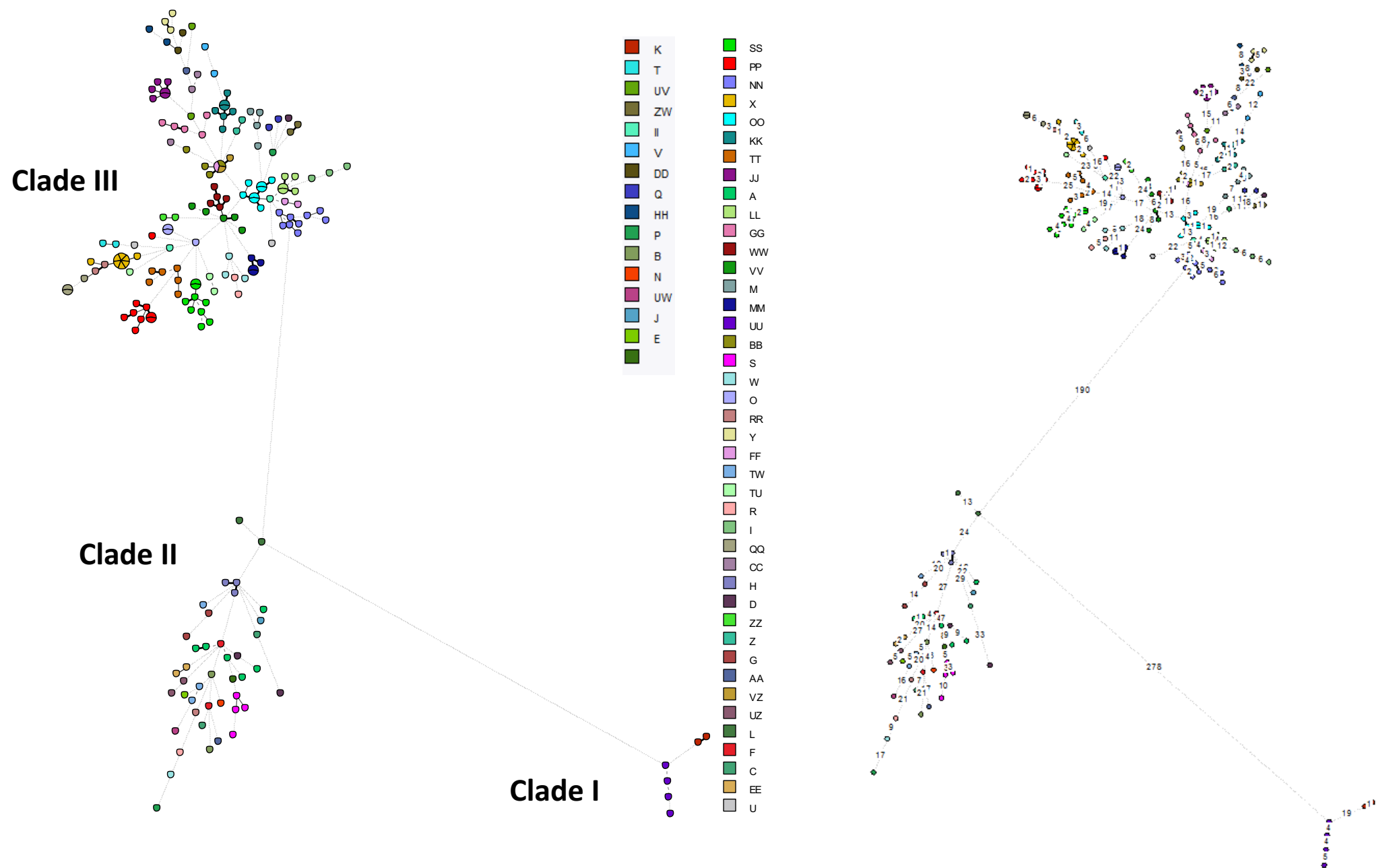


Figure S7 wgMLST MST tree of 197 isolates of *S. Dublin* from Danish cattle. On the right, the allelic differences between the isolates are displayed

Comparison of *S. Dublin* from
Denmark with global isolates
from the period 2001 - 2016

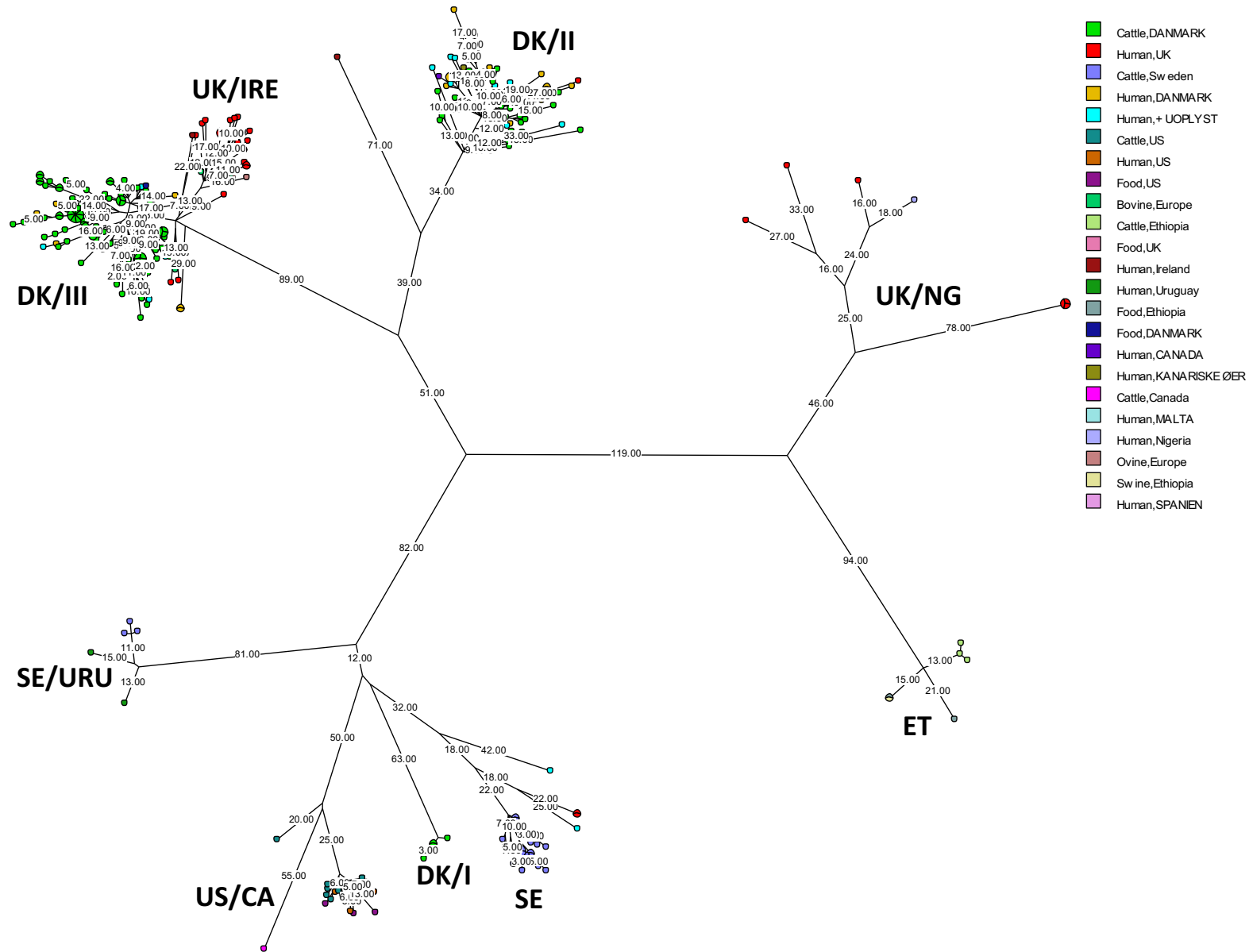


Figure S8 cgSNP maximum parsimony tree of 185 Danish and 103 global *S. Dublin* isolates, generated with NASP pipeline

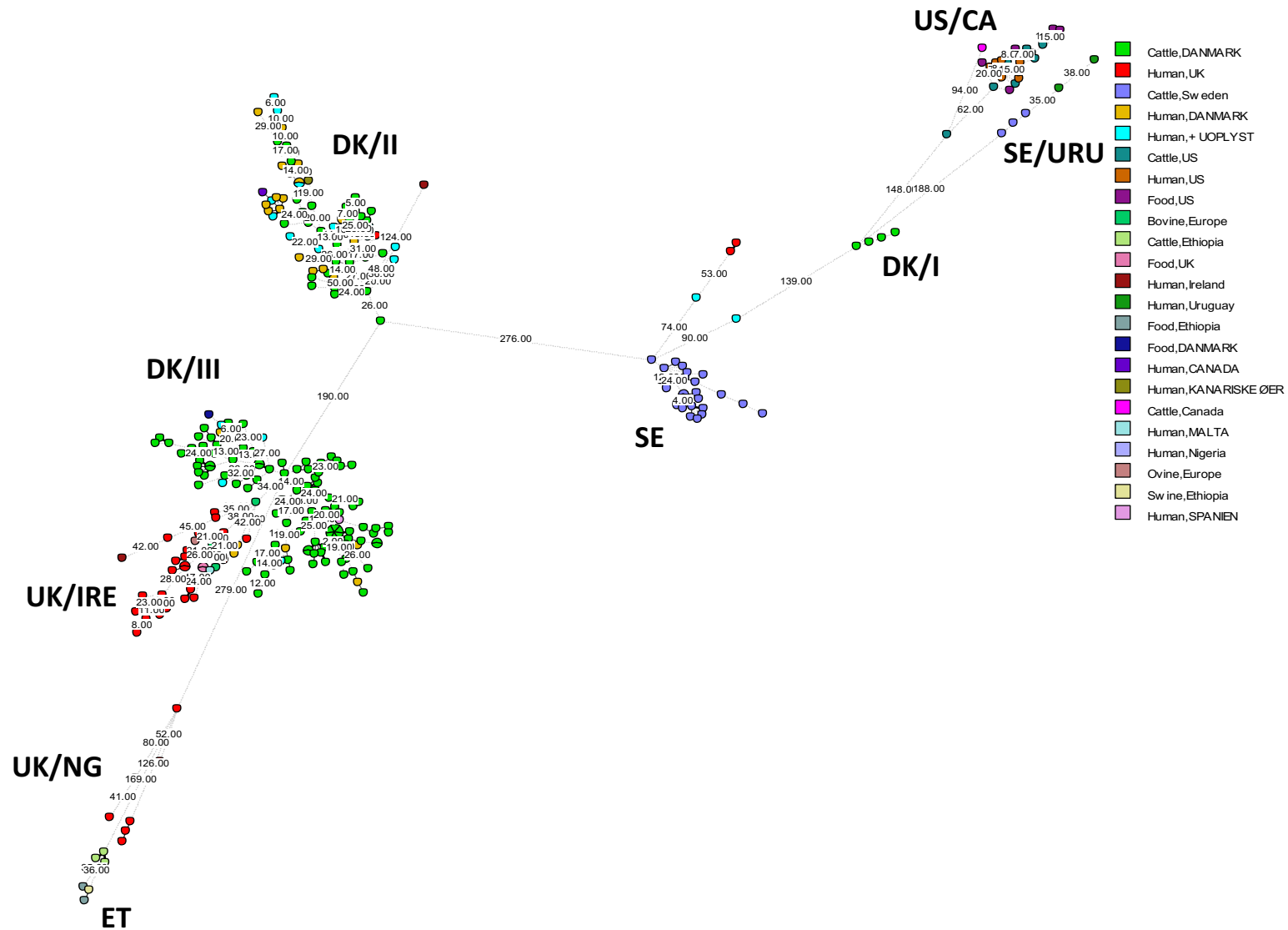


Figure S9. wgMLST MST tree of 185 Danish and 103 global *S. Dublin* isolates. On the branches, the allelic differences between the isolates are displayed