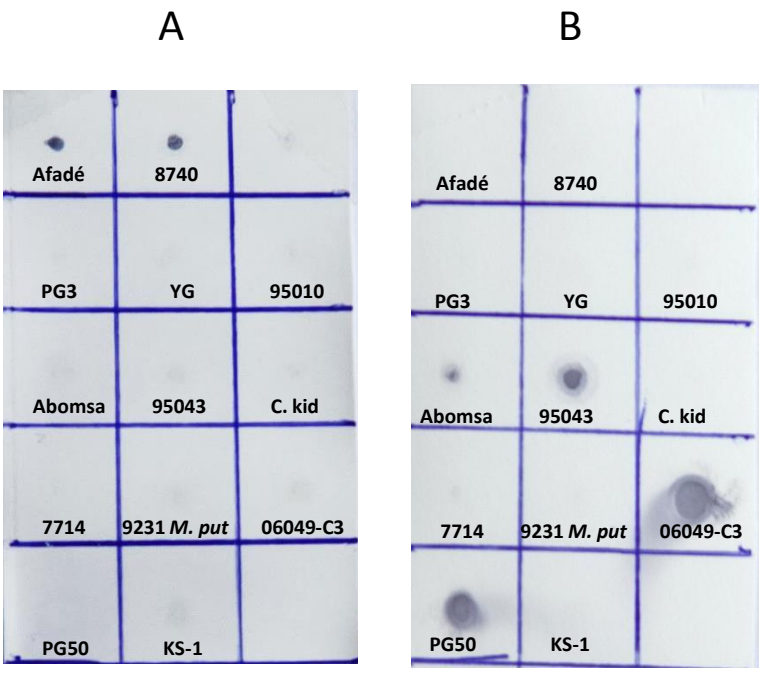


Figure S1: Dot blot analysis of exopolysaccharides extracted from representative strains of the "Mycoplasma mycoides" cluster detected by MAb 2.1.31 (A) and MAb 4.83 (B).

The reactivity of the two selected MAbs was assessed by dot-blot with extracted EPS. MAb 2.1.31 reacted only with MmmSC EPS (strains Afadé and 8740). MAb 4.83 reacted with EPS extracted from Mccp (Abomsa and 95043) and *M. leachii* (PG50, 06049-C3) strains. There was no evidence of any cross-reaction with the two MAbs. An absence of positive reaction signs either an absence of EPS or the presence of an EPS which is not detected by the MAb.

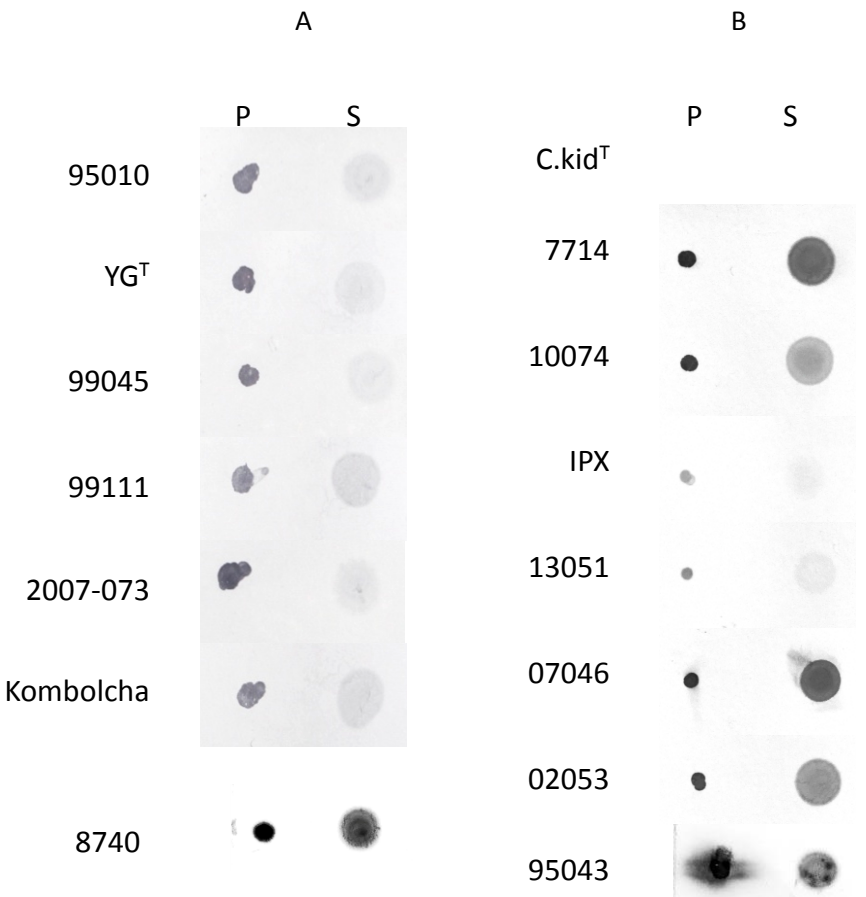
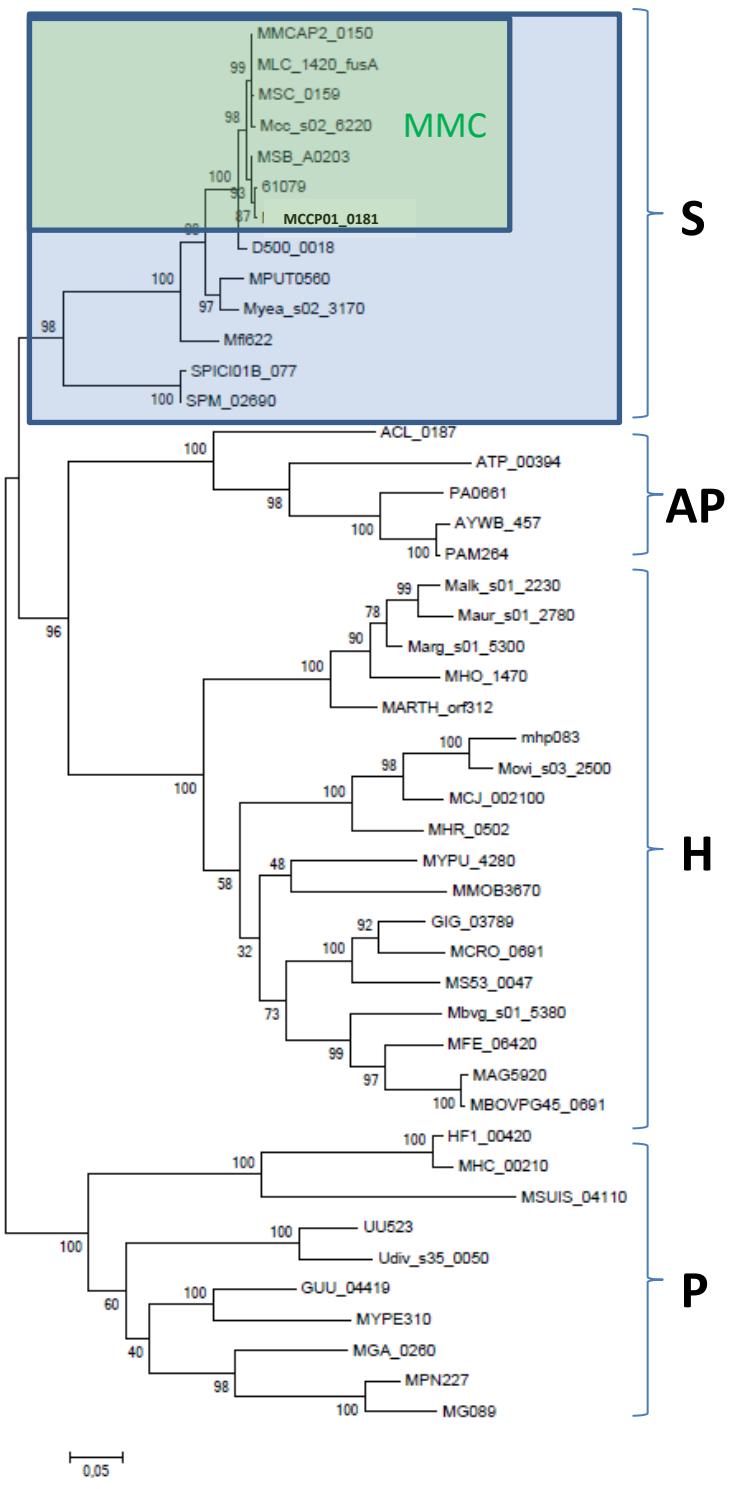


Figure S2: Dot blot analysis of polysaccharides detected in Mmc serovar "LC" strains with MAb 2.1.31 (A) and Mcc strains with MAb 4.83 (B).

The two MAbs were used to detect polysaccharides in mycoplasma cells grown in PPLO medium and washed once in PBS (pellets, P) and corresponding culture supernatants (S). MmmSC 8740 and Mccp 95043 were used as positive controls for each of the MAbs. All Mmc"LC" strain pellets yielded a positive result with MAb 2.1.31 while a faint positivity existed with the supernatants. The detection of Mcc strains with MAb 4.83 was more variable, as the intensity varied among pellets although all cultures were very turbid at the time of harvest. In addition this MAb yielded a positive result for some supernatants.



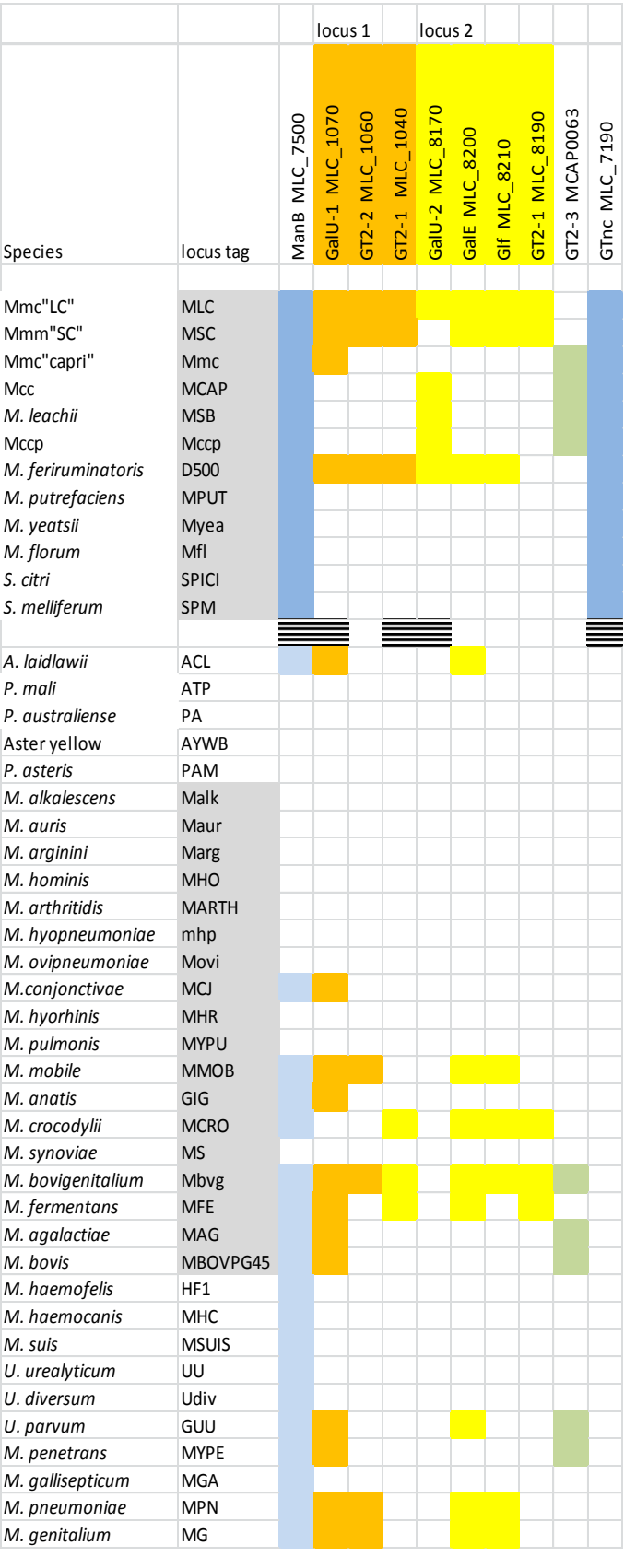


Figure S3: Distribution of polysaccharide-associated genes in the "Mycoplasma mycoides" cluster (MMC) and their homologues in *Mollicutes*.

A: Phylogenetic tree of the *Mollicutes* based on a conserved housekeeping gene, *fusA*. The tree was generated by the Maximum Likelyhood method; bootstrap values are indicated for each node. Phylogenetic groups are indicated: S, *spiroplasma* (boxed in blue); MMC (boxed in green); H, *hominis*; P, *pneumoniae*; AP, *Acholeplasma/Phytoplasma*.

B: Distribution of the polysaccharide-associated genes in *Mollicutes*. Species names and locus tags are mentioned on the left side of the table. Mnemonics for the genes identified in the MMC are indicated on top of the table, using the genome of Mmc"LC" strain 95010 as a reference. Colored dots are indicative of a BLASTP significant result, evalue e^{-8}, for the respective *Mollicutes* species. The blue color was retained for genes found in all MMC members (*manB* and a glycosyltransferase MLC_7190). Orthologs to MLC_7190 were notably absent from all other *Mollicutes* genomes. Orange, yellow and green colors were used for clusters of genes found only in some species of the MMC as defined in figure 4.

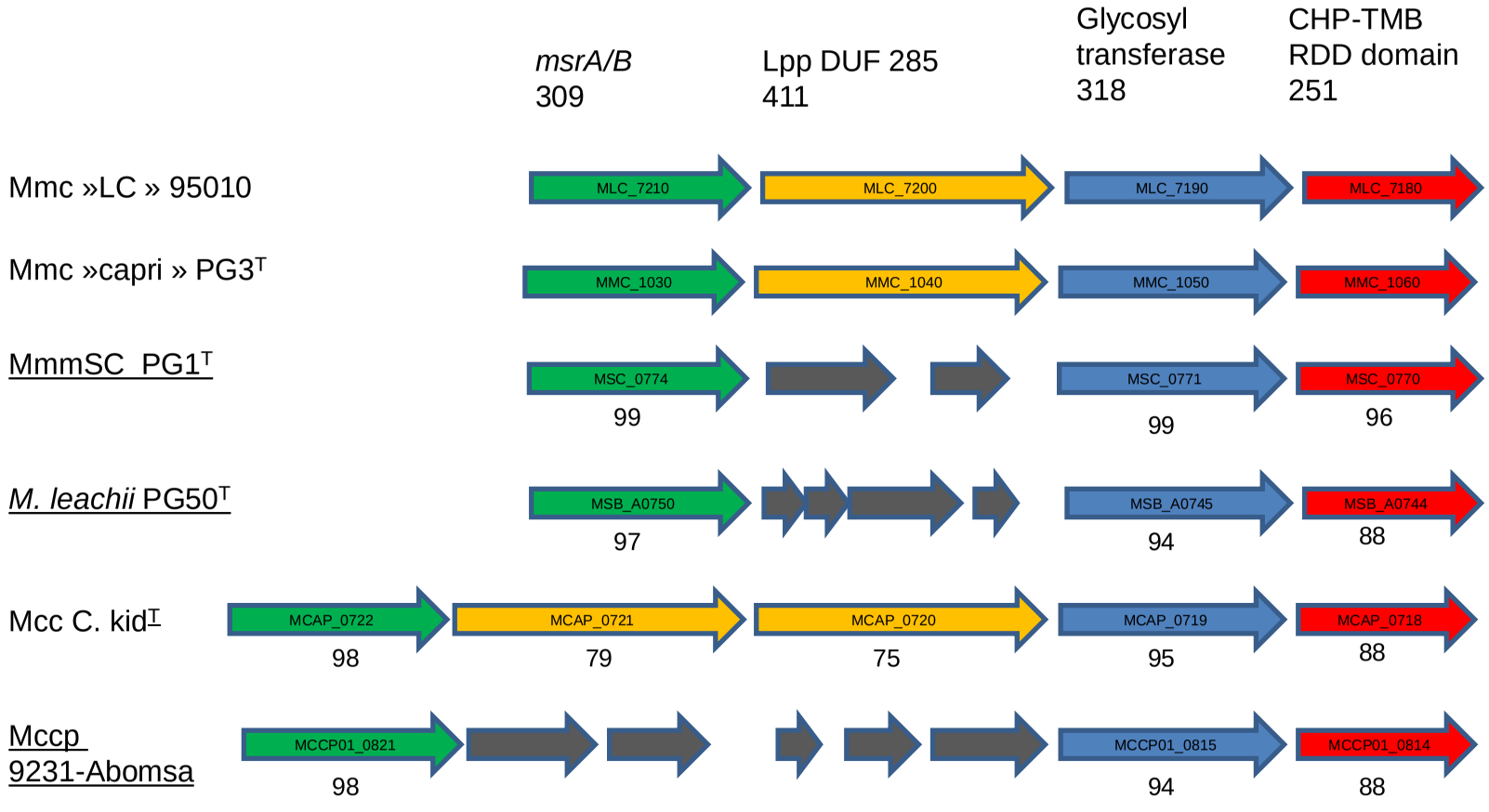


Figure S4: Synteny of the gene cluster surrounding a type 2 glycosyltransferase in the “Mycoplasma mycoides” cluster.
The cluster of genes found in the genome of Mmc serovar"LC" strain 95010 was chosen as reference. Gene names and AA numbers are indicated on the top. The species and names of strains are indicated on the left and underlined names correspond to strains for which EPS was detected. The figures under the genes indicate similarity values to the reference Mmc serovar"LC" genes.
The lipoprotein with a DUF285 motif found upstream of the glycosyltransferase is duplicated in *M. capricolum* subsp. *capricolum* C. kid^T, as well as in *M. capricolum* subsp. *capripneumoniae* 9231-Abomsa. In the latter genome, the two copies are interrupted by frameshift mutations, and are considered pseudogenes. There is a strict correlation between EPS-secreting strains and the presence of a pseudogenized lipoprotein upstream from the glycosyl transferase. The conserved hypothetical protein downstream from the glycosyl transferase possesses an RDD domain that may be associated with transport activity.