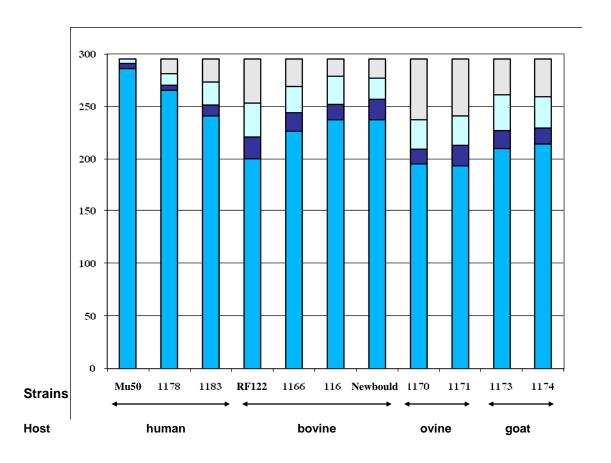
Supplementary data, Figure 1: Success rates of LR-PCR experiments on the 12 *S. aureus* strains. The y-axis gives the number of LR-PCR fragments (a total of 295 fragments for each strain). The colors correspond to fragments amplified with a size similar to that in N315 (blue), with a bigger size (dark blue), a smaller size (light blue) or non-amplified (grey).



Supplementary data, Figure 2: Phylogenetic tree based on the PFGE analysis on the additional strains. The tree was constructed using UPGMA method and a Dice coefficient (with a tolerance limit of 1.1%). Using a similarity cut-off value of 50%, four groups are identified.

