



Figure S1. Genetic environment of *pbp5* and distribution of isolates according to clades and ampicillin susceptibility. The physical maps represent the five patterns described by Montealegre *et al.* (A to E) and the four newly described patterns (F to I). The name of a representative strain is shown for each pattern. Genes and insertion sequences are indicated by arrows of different colors. The links between physical maps are coloured according to the protein identity between sequences. *The hybrid genomes EnGen0002 and 1_231_408 were not considered. **Isolates without ampicillin susceptibility data were ignored. ***The isolate EnGen0052 was considered as pattern A based on whole genome sequence analysis.