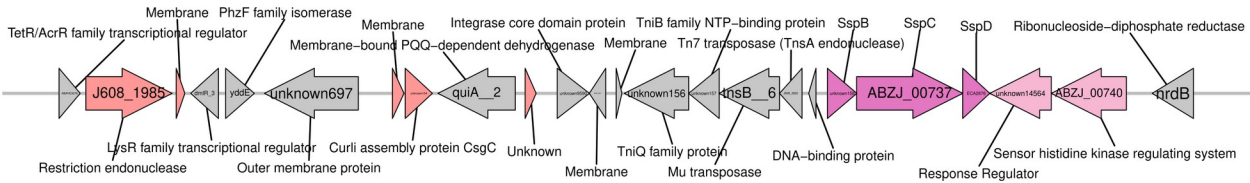
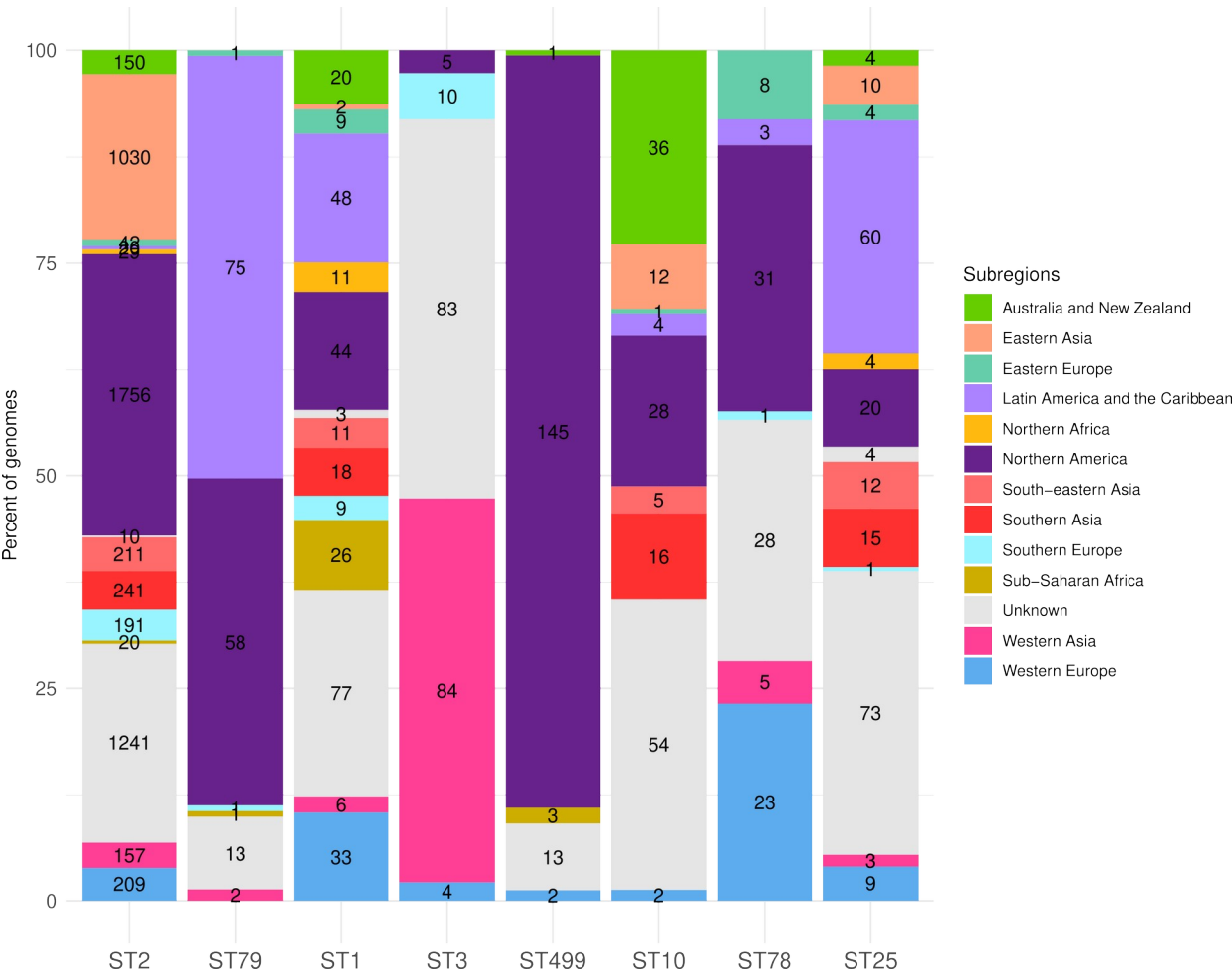


Innate antiviral systems are major defensome components that drive prophage distribution in *Acinetobacter baumannii*

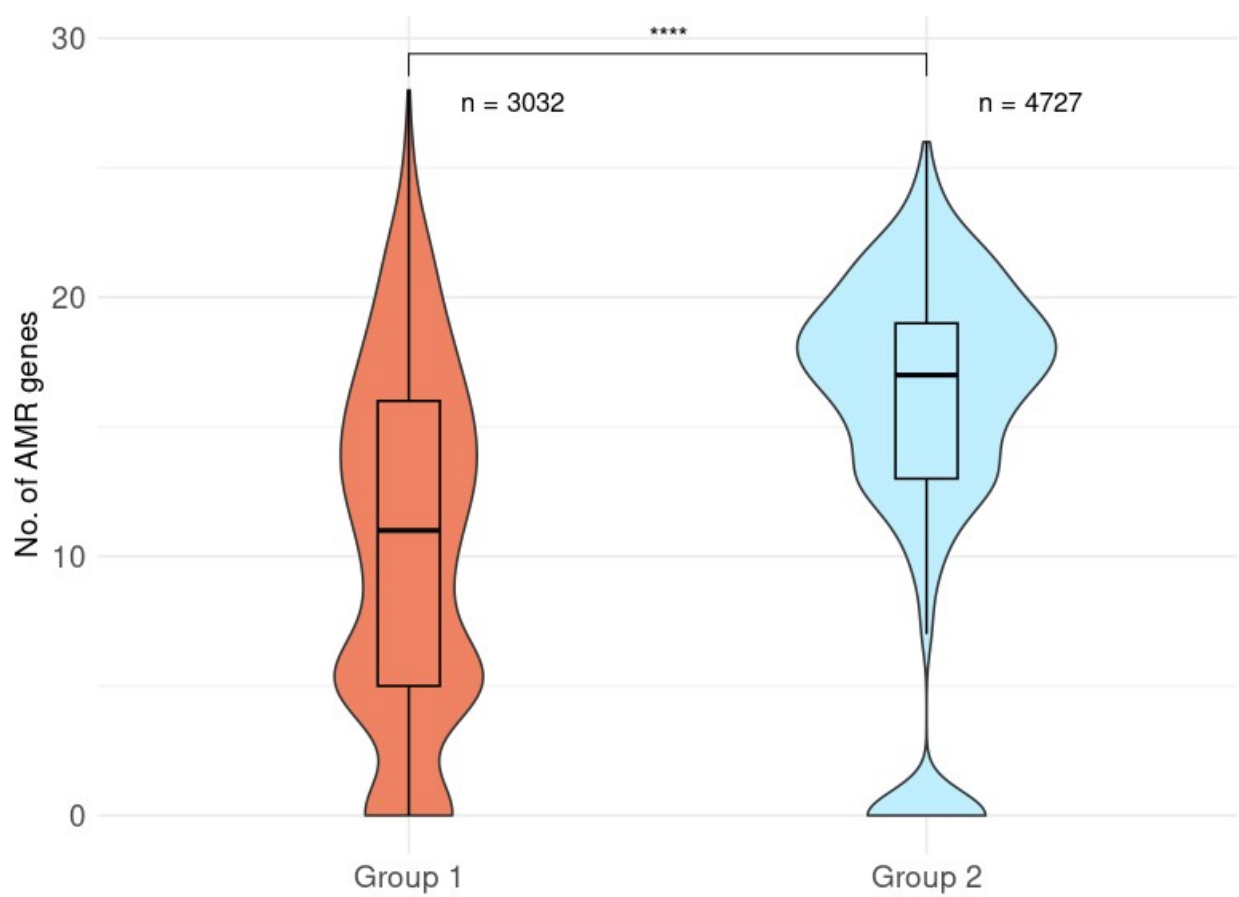
Supplementary Files



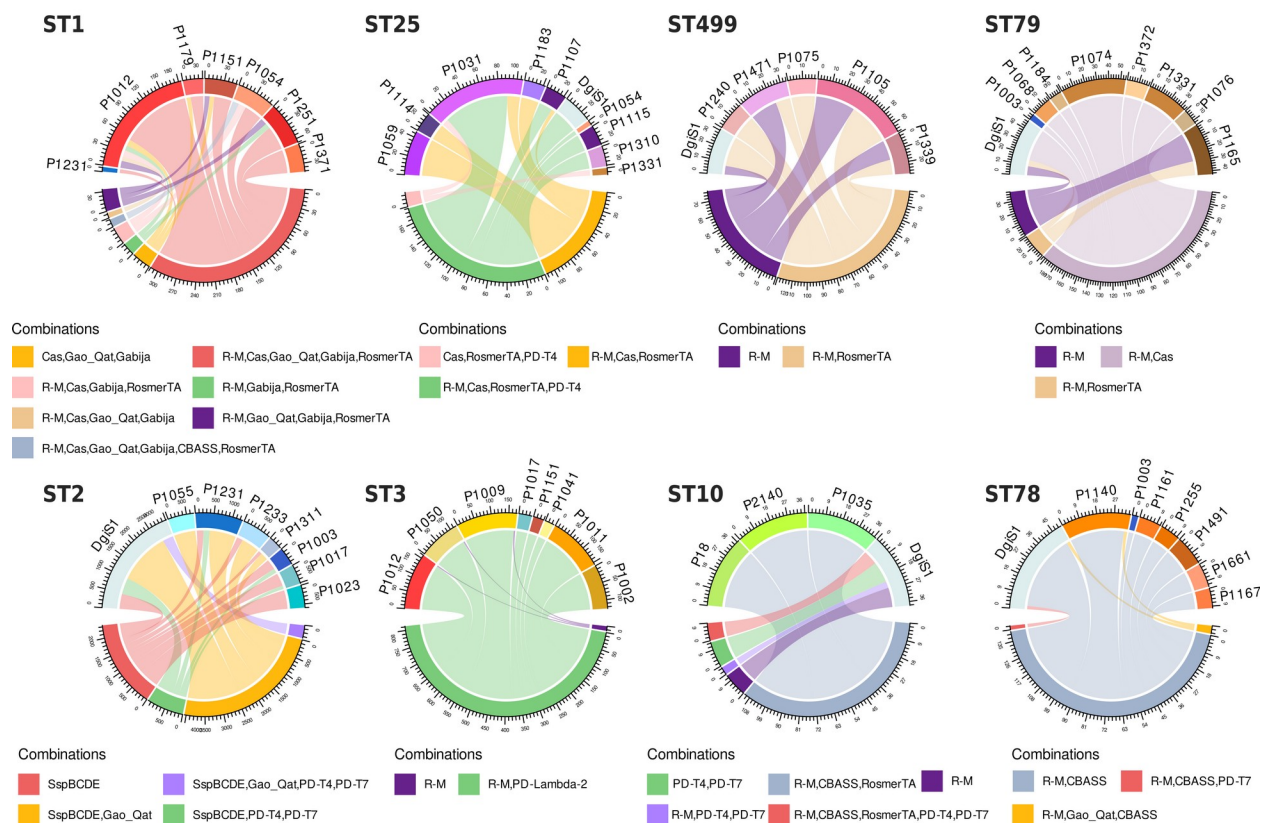
**Suppl. Fig. S1.** Locus where the Ssp system is mostly found. Genes highlighted in colors other than gray appear in more than 90% of strains in group 2 and in less than 1% of strains in group 1.



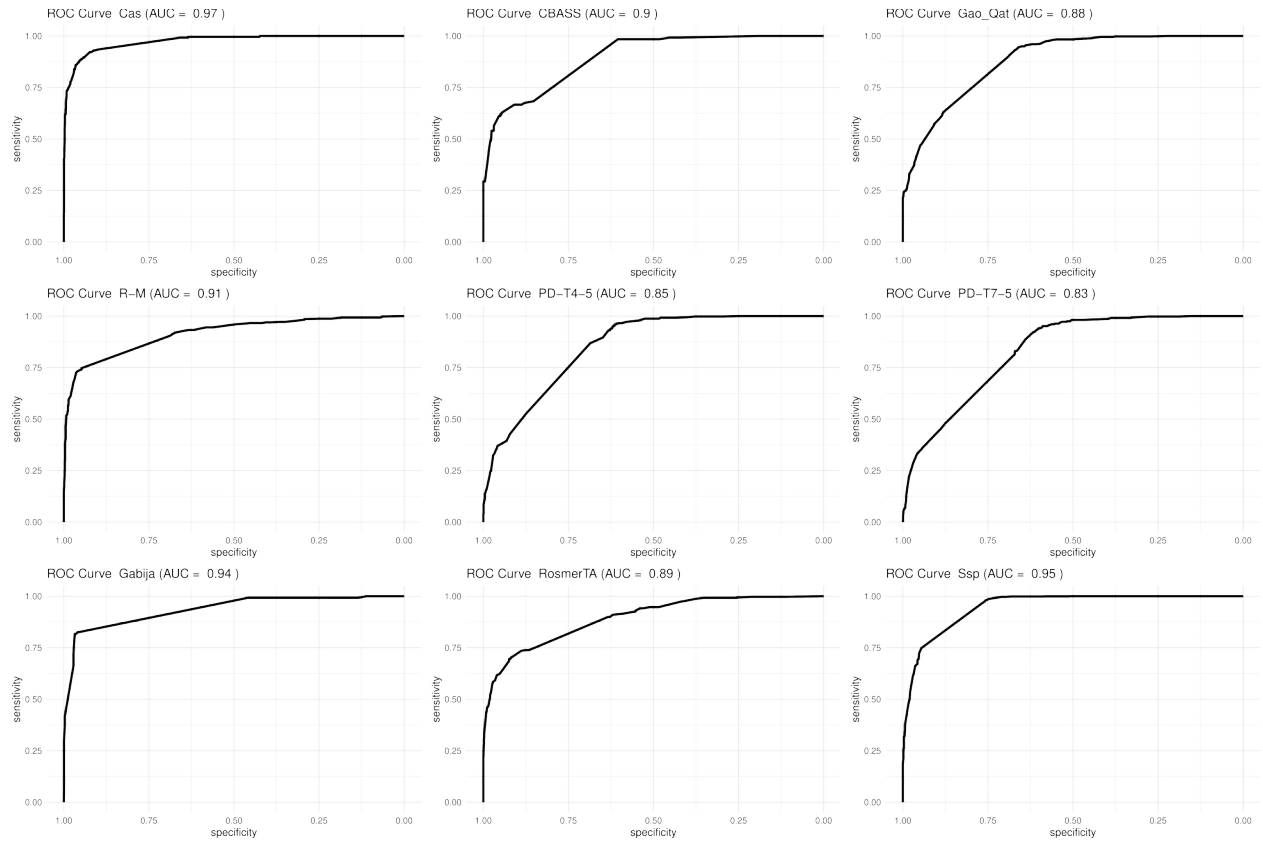
**Suppl. Fig. S2.** Distribution by subcontinent of the different MLST groups.



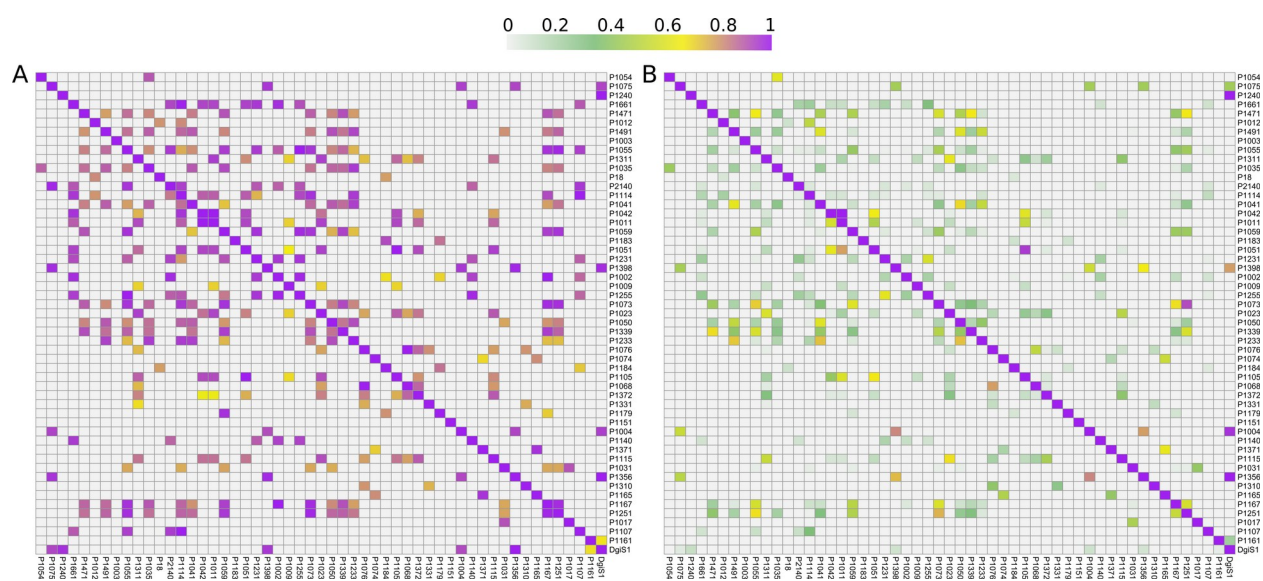
**Suppl. Fig. S3.** Distribution of the number of genes involved in antibiotic resistance in groups 1 and 2. Wilcoxon, p-value =  $2.32 \times 10^{-219}$ .



**Suppl. Fig. S4.** Specific prophages occurring in bacterial genomes with specific combinations of defense systems (clonal groups missing in Fig. 4C).



**Suppl. Fig. S5.** ROC curves for each of the models used for each defense system. The models with the best performance are those associated with the CRISPR-Cas, Ssp, Gabija and R-M systems.



**Suppl. Fig. S6.** Average nucleotide identity (ANI) of the prophages found in the bacterial genomes.