**Analysis pipeline.**All the genomes were meticulously screened for the presence of antimicrobial resistance (AMR), virulence, and metal resistance genes by leveraging the AMRFinder Plus (version: 3.12.8 , database version: 2024-07-22.1 ) [1] command line tool.Furthermore, the plasmid analysis pipeline consisted of a combination of tools used to analyze bacteria plasmids. Plasflow (v1.1) [2] was employed for the detection of plasmids within the WGS data while The plasmids were annotated using Prokka (v1.14.5) [3]. BRIG (v0.95) [4] was used for plasmid visualization and comparison (with S\_aureus\_plasmid\_pPR9 as the reference plasmid for comparisons). AMRFinder Plus [1] was utilized for antimicrobial resistance gene detection. Abricate (v1.0.0; Torsten Seemann, <https://github.com/tseemann/abricate>) with the plasmidfinder database [5] and Copla [6,7] were used to determine the replicon type and plasmid taxonomic unit (PTU). The relaxase MOB families of the mupA carrying plasmids were determined using MOBSCAN [8].

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