

Supplemental Information

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Within-host genomic evolution of methicillin-resistant *Staphylococcus aureus* in long-term carriers

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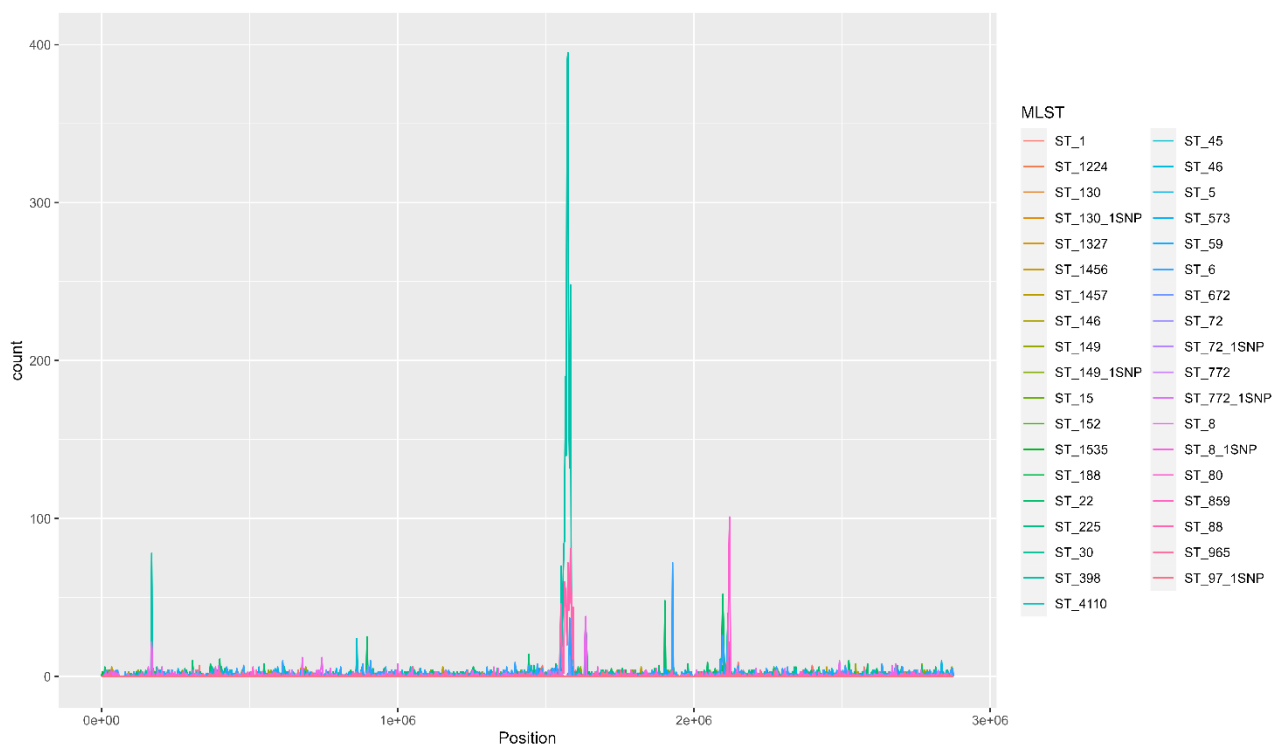


Figure S1

The plot shows the number of SNPs across the genome grouped by MLST before removing "recombination regions" using Gubbins. The highest peak represents isolates belonging to ST398.

X-axis: Position in the genome. Y-axis: Number of SNPs

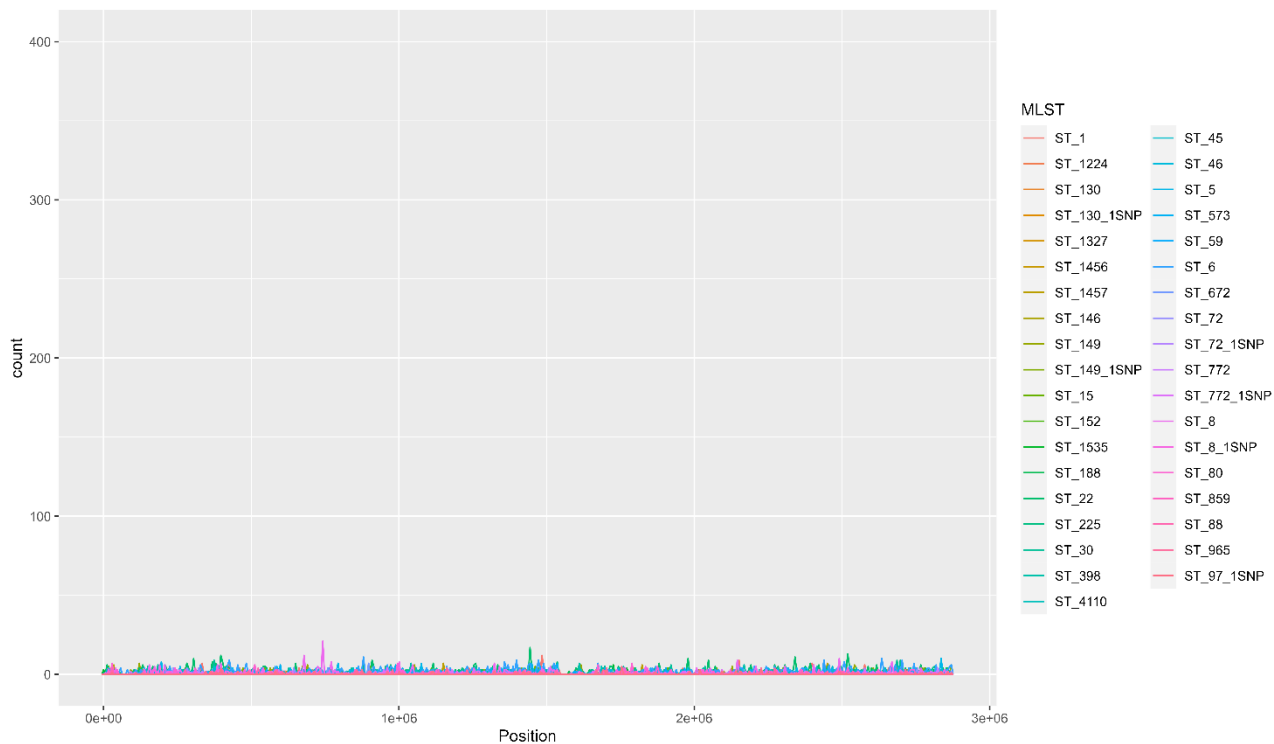


Figure S2

The plot shows the number of SNPs across the genome grouped by MLST after removing "recombination regions" using Gubbins. The high peaks seen in Figure S1 have disappeared. X-axis: Position in the genome. Y-axis: Number of SNPs