**Supplementary Material 1:** Table detailing the distribution of MLST sequence types across the different datasets. Frequencies are also displayed in percentages. CCOS = Culture Collection of Switzerland

**Supplementary Material 2:** cgMLST MST of CCoS and public repository genomes of MRSA (1960-1992, n = 554), nodes colored by collection country. Clusters are shown with a maximal cluster distance of 24 allele differences and a minimal cluster size of 15.

**Supplementary Material 3:** cgMLST MST of CCoS and public repository genomes of MRSA (1960-1992, n = 554), nodes colored by sequence type and CCs are shaded. Clusters are shown with a maximal cluster distance of 24 allele differences and a minimal cluster size of 15.

**Supplementary Material 4:** cgMLST MST of CCoS, public repository and University Hospital of Basel genomes of MRSA (1960-2022, n = 1761), nodes colored by collection country. Clusters are shown with a maximal cluster distance of 24 allele differences and a minimal cluster size of 15. Clonal complexes are shaded in.

**Supplementary Material 5:** MLST sequence type, clonal complex, collection country and collection year mapped to a maximum likelihood core genome SNP tree of ancient Swiss and international MRSA (1960 -1992, n = 554). Leaves colored by sequence type. Outgroup (*S. epidermis*) line shortened through X-axis break for visualization purposes.

**Supplementary Material 6:** MLST sequence type, clonal complex, collection country and collection year mapped to a maximum likelihood core genome SNP tree of MRSA from the CCoS, public repositories and dereplicated modern Swiss isolates (1960 -2022, n = 777). Leaves colored by sequence type. Outgroup (*S. epidermis*) line shortened through X-axis break for visualization purposes.

**Supplementary Material 7:** Predicted resistance/sensitivity, phenotypical resistance/sensitivity and concordance between the two mapped to a maximum likelihood core genome SNP tree of MRSA from the CCoS, public repositories and dereplicated modern Swiss isolates (1960 -2022, n = 777). Leaves colored by sequence type. Outgroup (*S. epidermis*) line shortened through X-axis break for visualization purposes.

**Supplementary Material 8:** Virulence gene presence/absence heatmap mapped to a maximum likelihood core genome SNP tree of MRSA from the CCoS, public repositories and dereplicated modern Swiss isolates (1960 -2022, n = 777). Leaves colored by sequence type. Outgroup (*S. epidermis*) line shortened through X-axis break for visualization purposes.

**Supplementary Material 9:** SCC*mec* type mapped to a maximum likelihood core genome SNP tree of ancient Swiss and international MRSA (1960 -1992, n = 554). Leaves colored by sequence type. Outgroup (*S. epidermis*) line shortened through X-axis break for visualization purposes.

**Supplementary Material 10:** SCC*mec* type mapped to a maximum likelihood core genome SNP tree of MRSA from the CCoS, public repositories and dereplicated modern Swiss isolates (1960 -2022, n = 777). Leaves colored by sequence type. Outgroup (*S. epidermis*) line shortened through X-axis break for visualization purposes.

**Supplementary Material 11A:** BAPS clusters, collection country and collection year mapped to a maximum likelihood whole genome SNP tree of ST239, ST7844, ST368 and ST241 MRSA (n = 69). Leaves colored by sequence type.

**Supplementary Material 11B:** Maximum likelihood whole genome SNP tree of ST239, ST7844, ST368 and ST241 MRSA (n = 69) adjusted with Bayesian dating of nodes on the left. Root-to-tip distances mapped to sampling date with linear regression shown on the right.

**Supplementary Material 12A:** BAPS clusters, collection country and collection year mapped to a maximum likelihood whole genome SNP tree of ST247 and ST250 MRSA (n = 445). Leaves colored by sequence type.

**Supplementary Material 12B:** Maximum likelihood whole genome SNP tree of ST247 and ST250 MRSA (n = 445) adjusted with Bayesian dating of nodes on the left. Root-to-tip distances mapped to sampling date with linear regression shown on the right.

**Supplementary Material 13A:** BAPS clusters, collection country and collection year mapped to a maximum likelihood whole genome SNP tree of ST22 MRSA (n = 214). Leaves colored by sequence type.

**Supplementary Material 13B:** Maximum likelihood whole genome SNP tree of ST247 and ST22 MRSA (n = 214) adjusted with Bayesian dating of nodes on the left. Root-to-tip distances mapped to sampling date with linear regression shown on the right.

**Supplementary material 14:** Screenshot of the interactive map showing the collection coordinates of ancient Swiss and European isolates.