**Supplemental Material Legend**

**Supplemental Figure S1. USA100 classification using cognac tree.** Sequences used in this study and three publicly available reference genomes were assembled using an internal assembly pipeline that can be found on Github: [https://github.com/Snitkin-Lab-Umich/assembly_umich](https://github.com/Snitkin-Lab-Umich/assembly_umich).

After assemblies were aligned with cognac (1), a maximum likelihood phylogeny was made with FastTree (2). Scale bar indicates substitutions per site. MLST was generated by ARIBA (3) and overlayed on the tree with ggtree (4). For the purposes of this analysis, all isolates on this tree were considered USA100 on the basis that they clustered with either of the 2 USA100 reference genomes or were ST5.

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Supplemental Dataset S1. Analytic dataset of MRSA isolates used for analysis. Information includes strain type by whole genome sequencing (USA300 or USA100) and predicted strain type based on phenotypic prediction rule. MLST designations are also included.