**Detailed Laboratory methods**

The *emm* type of each isolate was first determined using a sequential quadriplex real-time PCR-based method.11 Isolates with the outbreak *emm* type were then subject to whole genome sequencing (WGS) using methods reported previously.12 Briefly, GAS strains were cultured on Trypticase soy agar (TSA) supplemented with 5% sheep blood and incubated overnight at 37°C in 5% CO2. Genomic DNA for short read WGS was extracted on QIAcube HT using a modified QIAamp DNA QIAcube HT Kit protocol (Qiagen, Inc., Valencia, CA). Nucleic acid concentration was quantified by Invitrogen™ Qubit™ assay (Thermo Fisher Scientific Inc., USA) and samples were sheared using Covaris LE220 ultrasonicator (Covaris, Inc., Woburn, MA) programmed to generate 500bp fragments. Libraries were constructed on the SciCloneG3 (PerkinElmer Inc., Waltham, MA) using sparQ DNA Library Prep kit (Quantabio, Beverly, MA) with dual indexes (Illumina Inc., San Diego, CA) and quantified by KAPA qPCR library quantification method (Kapa Biosystems Inc., Wilmington, MA). WGS was performed by Illumina Next Generation Sequencing technology using MiSeq v3 600 cycle kit. Sequences were analyzed using the Streptococcus Laboratory bioinformatics pipeline and pairwise single nucleotide polymorphism (SNP) distances were generated for the core genome shared between isolates, employing kSNP3.0 with a kmer size of 19, and the MEGA7 program.12,13,14

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