

Three beads were washed with extraction buffer containing lysozyme (or lysostaphin for *Staphylococcus* sp.) and RNase A, incubated for 25 min at 37°C. Proteinase K and RNaseA were added and incubated for 5 min at 65°C. Genomic DNA was purified using an equal volume of SPRI beads and resuspended in EB buffer.

DNA was quantified in triplicates with the Quantit dsDNA HS assay in an Eppendorf AF2200 plate reader. Genomic DNA libraries were prepared using Nextera XT Library Prep Kit (Illumina, San Diego, USA) following the manufacturer's protocol with the following modifications: two nanograms of DNA instead of one were used as input, and PCR elongation time was increased to 1 min from 30 seconds. DNA quantification and library preparation were carried out on a Hamilton Microlab STAR automated liquid handling system. Pooled libraries were quantified using the Kapa Biosystems Library Quantification Kit for Illumina on a Roche light cycler 96 qPCR machine. Libraries were sequenced on the Illumina HiSeq using a 250bp paired end protocol.

Reads were adapter trimmed using Trimmomatic 0.30 with a sliding window quality cutoff of Q15 [1]. De novo assembly was performed on samples using SPAdes version 3.7 [2], and contigs were annotated using Prokka 1.11 [3].

1. Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*, 30(15), 2114–2120. <http://doi.org/10.1093/bioinformatics/btu170>

2. Bankevich, A., Nurk, S., Antipov, D., Gurevich, A. A., Dvorkin, M., Kulikov, A. S., ... Pevzner, P. A. (2012). SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. *Journal of Computational Biology*, 19(5), 455–477. <http://doi.org/10.1089/cmb.2012.0021>

3. Seemann T (2014) Prokka: rapid prokaryotic genome annotation. *Bioinformatics*. 30(14):2068-9