**Supplementary Methods & Materials**

**Revival of *E. faecium* LR13, DNA isolation, Genome sequencing, assembly and annotation**

*E. faecium* LR13preserved as glycerol stock (50% v/v) at -80ºC in our laboratory was revived by incubating overnight in deMan, Rogosa and Sharpe (MRS) broth at 37°C, 200 rpm. Bacteria were grown up to the exponential phase (OD600=0.8) and harvested by centrifugation at 8000 rpm for 8 minutes at 4ºC. Genomic DNA was extracted using Nucleospin Microbial DNA kit (Takara Bio, USA) following the manufacturer's instructions. DNA was quantified by Qubit 4 fluorometer (Thermo Fisher Scientific, USA).

**Genome sequencing and assembly**

The sequencing DNA library wasprepared by QIASeq FX DNA Library Kit (Qiagen, USA). Quantitative and qualitative library QC was done by Qubit 4 fluorometer (Thermo Fisher Scientific, USA) and tapestation 4150 (Agilent technologies, USA), respectively. The libraries were sequenced on Novaseq 6000 (Illumina, USA) by using 2X150 bp paired end sequencing chemistry. The quality of the raw reads was assessed using FastQC v0.11.8 (1) and BLAST against NCBI Nucleotide Database (NT) at e-value 1e-6. The reads were trimmed using Trimmomatic v0.39 (2) at default parameters to remove Illumina adaptors, low-quality bases and/or reads less than 36bp. The trimmed short overlapped paired-end reads were merged using Flash (v1.2.11) (3) at default parameters to create longer reads (single-end). The merged single-end reads along with the remaining trimmed pair-end reads were used to perform *de novo* genome assembly using SPAdes v3.13.0 (4) and Unicycler v0.4.8 (5). From the assembled contigs, all contigs with length ≤ 200bp were discarded using SeqKit v0.16.1 (6). The quality of the assembled genome was further assessed using QUAST v5.0.2 (7) and checkM v1.1.3 (8) .

**Genome annotation**

The assembled genome was annotated using prokaryotic genome annotation pipeline PGAP (2021-07-01) (9), Prokka v1.14.6 (10), KAAS server with BBH (bi-directional best hit) (11) and PATRIC RAST tool kit (RASTtk) v3.6.12 (12). The protein coding genes, tRNA and rRNA genes were predicted using Glimmer version v3.02 (13), tRNAscan-SE v2.0.9 (14), and RNAmmer v1.2, (15) respectively.

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