Infections caused by vancomycin-resistant Enterococcus (VRE) are increasingly difficult to treat and often cause prolonged hospital outbreaks (1). In the case of E. faecium, these challenges appear to be caused by the expansion and dissemination of strains belonging to the clonal complex (CC) 17 (2). In Brazil, E. faecium strains belonging to sequence type (ST) 412 (part of CC17) are often found in hospitalized patients (3–6). Recently, vanA-containing E. faecium ST412 was found in urban rivers (Tietê River and Pinheiros River) in Sao Paulo, the largest and most populous metropolitan area in Brazil, underscoring the importance of this lineage as a major public health threat (7).

E. faecium VRE16 is an ST412 strain, isolated from a perianal swab collected from a male patient on 3 September 2009, during a surveillance program in the Intensive Care Unit of Risoleta Tolen- tino Neves Hospital–MG/Brazil. It is representative of the endemic VRE E. faecium strains found within this hospital in that year. VRE16 is resistant at high levels to vancomycin, teicoplanin, erythromycin, ampicillin, penicillin, and streptomycin (3).

Genomic DNA of VRE16 was extracted using a DNeasy blood and tissue kit (Qiagen, USA). DNA libraries were prepared using an Illumina Nextera XT DNA sample preparation kit (Illumina Inc., USA), with recommended modifications for 2 × 250-bp paired-end sequencing. Samples were multiplexed and sequenced on an Illumina MiSeq machine (Illumina Inc., USA). CLC Genomics Workbench version 8.0.2 (CLCBio, Denmark) was used for genome assembly, using default parameters. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (8). The entire vancomycin resistance-encoding transposon Tn1546 (10.8 kb) was amplified by long-range PCR, as described by Woodford et al. (9). Overlapping PCR was performed following the protocol of Arthur et al. (10), and the fragments were sequenced to identify the insertion sequences present in them. IS16, exclusively prev-
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