Herein, we report the draft genome sequence of *Enterococcus faecalis* ED-NGS-1009, cultivated from a blood sample taken from a neonatal sepsis patient at the Royal Infirmary in Edinburgh, Scotland, United Kingdom.

**Enterococcus faecalis** is a nosocomial, opportunistic pathogen showing resistance to antibiotics, specifically vancomycin (1–4). Preterm neonates are a highly susceptible patient group for bacterial infections (1, 5, 6) and rapid detection of blood sepsis and the causative pathogen are critical steps to enable proper treatment (7–9). Therefore, in the ClouDx-i project, we are aiming to extend our existing knowledge of currently circulating pathogenic strains linked with blood sepsis in neonates to inform the development of new molecular diagnostic assays. Herein, we present the draft genome sequence of an *Enterococcus faecalis* strain isolated from a preterm neonate at the Royal Infirmary in Edinburgh, in 2013. Positivity for blood sepsis and species identification were confirmed by classical microbiological techniques.

The isolate was grown overnight at 37°C on Luria broth (LB) agar, and genomic DNA was isolated using Qiagen genomic tips (Venlo, Limburg, Netherlands). Genomic DNA was fragmented (fragments 2 to 10 kb) using sonication and a non–size selected shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JPWN00000000. The version described in this paper is version JPWN01000000.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JPWN00000000. The version described in this paper is version JPWN01000000.

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**REFERENCES**


