S. aureus is a Gram-positive, clinically important pathogen, and it is one of the leading causes of blood sepsis (1–3). Preterm neonates are a highly susceptible patient group for bacterial infections (3–5), and rapid detection of blood sepsis and identification of the causative agent are critical to enable proper treatment (6–8). The ClouDx-i project aims to extend current knowledge of circulating pathogenic strains linked with blood sepsis in neonates to help inform the development of new and improved molecular diagnostics. Herein, we present the draft genome of a S. aureus strain, isolated from a preterm neonate at the Royal Infirmary in Edinburgh in 2013. Positivity for blood sepsis and species were confirmed by classical microbiological identification and characterization 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 agar, and genomic DNA was isolated using Qiagen genomic tips.

Herein, we report the draft genome sequence of S. aureus ED-NGS-1006, cultivated from a blood sample taken from a neonatal sepsis patient at the Royal Infirmary in Edinburgh, Scotland, United Kingdom.

**REFERENCES**