



# Correction for Quainoo et al., “Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis”

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Volume 30, no. 4, p. 1015–1063, 2017, <https://doi.org/10.1128/CMR.00016-17>. Page 1023, Table 1, “Error rate” column, entry for Oxford Nanopore MinION Mk1 (1D): “12% errors per base” should read “~30% errors per base.”

**Published** 1 November 2017

**Citation** Quainoo S, Coolen JPM, van Hijum SAFT, Huynen MA, Melchers WJG, van Schaik W, Wertheim HFL. 2018. Correction for Quainoo et al., “Whole-genome sequencing of bacterial pathogens: the future of nosocomial outbreak analysis.” *Clin Microbiol Rev* 31:e00082-17. <https://doi.org/10.1128/CMR.00082-17>.

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