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."