

Resource Summary Report

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A step-by-step beginner's protocol for whole genome sequencing of human bacterial pathogens

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Protocol Information

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Summary: Bacterial whole genome sequencing (WGS) is becoming a widely-used technique in research, clinical diagnostic, and public health laboratories. It enables high resolution characterization of bacterial pathogens in terms of properties that include antibiotic resistance, molecular epidemiology, and virulence. The introduction of next-generation sequencing instrumentation has made WGS attainable in terms of costs. However, the lack of a beginner's protocol for WGS still represents a barrier to its adoption in some settings. Here, we present detailed step-by-step methods for obtaining WGS data from a range of different bacteria (Gram-positive, Gram-negative, and acid-fast) using the Illumina platform. Modifications have been performed with respect to DNA extraction and library normalization to maximize the output from the laboratory consumables invested. The protocol represents a simplified and reproducible method for producing high quality sequencing data. The key advantages of this protocol include simplicity of the protocol for users with no prior genome sequencing experience and reproducibility of the protocol across a wide range of bacteria.

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