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A fast solution to NGS library preparation with low nanogram DNA input

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Next-generation sequencing (NGS) has significantly impacted human genetics, enabling a comprehensive characterization of human genome as well as better understanding of many genomic abnormalities. By delivering massive DNA sequences at unprecedented speed and cost, NGS promises to make personalized medicine a reality in the foreseeable future. To date, library construction with clinical samples has been a challenge, primarily due to the limited quantities of sample DNA available. To overcome this challenge, we have developed a fast library preparation method using novel NEBNext reagents and adaptors, including a new DNA polymerase that has been optimized to minimize GC bias. This method enables library construction from an amount of DNA as low as 5 ng, and can be used for both intact and fragmented DNA. Moreover, the workflow is compatible with multiple NGS platforms.

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