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

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From Beyond the Genome 2012  
Boston, MA, USA. 27-29 September 2012

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.

Published: 1 October 2012

doi:10.1186/1753-6561-6-S6-P26

Cite this article as: Liu et al.: A fast solution to NGS library preparation with low nanogram DNA input. *BMC Proceedings* 2012 **6**(Suppl 6):P26.

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