APPLICATION NOTE

Automating low throughput Roche® KAPA® HyperPrep™ kit on the BioQule™ NGS System

Key features

- Full walkaway automation
- Easy to use
- Minimize human error
- Open system able to automate different applications

For research use only. Not for use in diagnostic procedures.

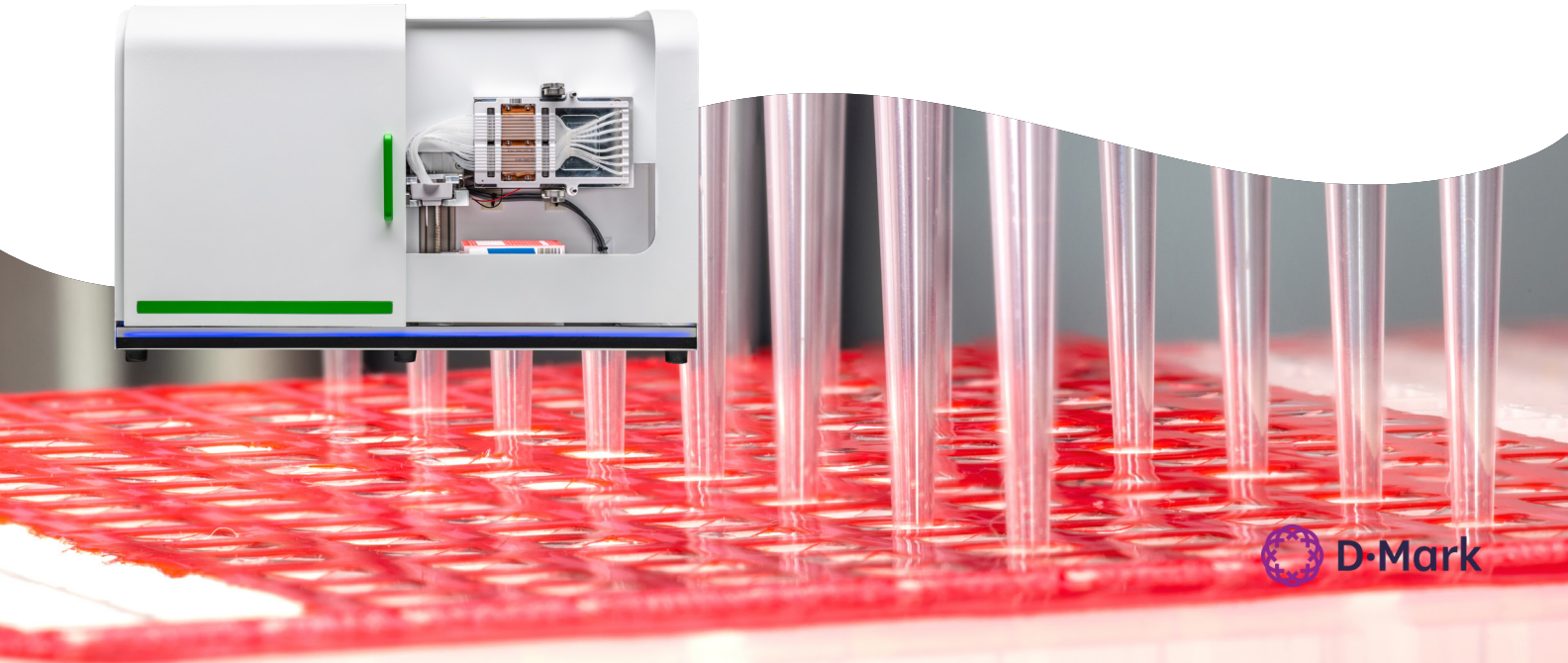
Please note that product labeling (such as kit insert, product label, and kit box) may be different compared to the company branding. Please contact your local representative for further details.

Introduction

The BioQule™ NGS System is a robust, low cost, easy-to-use solution that enables fully walkaway automation and quantitation for low-throughput library preparation. It has the capability to automate most library preparation workflows, resulting in consistent libraries with minimal hands-on time. Here we describe the methods and results obtained when using the BioQule™ NGS System with the Roche® KAPA® HyperPrep™ Kit (Roche) for Whole Genome Sequencing using mechanically fragmented DNA as input. The complete run set up for library prep and quantitation takes 30 minutes of hands-on time.

Methods

WGS libraries were constructed using the Roche® KAPA® HyperPrep™ kit (07962347001) with Roche® KAPA® Unique Dual-Indexed Adapters (08861919702) on the BioQule™ NGS System. 8 samples per run were prepared using 100 ng of mechanically sheared Human Promega® DNA as the starting material. Each run was performed according to the manufacturer's instructions, using 8 cycles of library amplification and a 1:25 dilution of the Roche® KAPA® UDI adapters. Final libraries were automatically quantified during the BioQule™ run and had size determined using a high sensitivity assay. Libraries were manually pooled and sequenced on an Illumina® MiniSeq® or MiSeq® instrument with 2x300 bp read length.



Results

The final volume of library obtained was 23 µL, with an average yield of 10 ng/µL. An average of 1 million reads were generated per sample (0.2x coverage). Libraries produced were a consistent size and showed minimal variability in normalized coverage across 20-60% GC. Sequencing metrics for these WGS libraries can be seen in Figures 1-2.

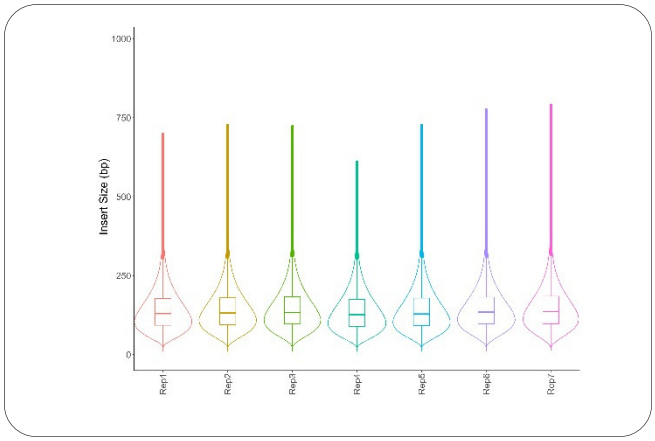


Figure 1. Insert size for a run of libraries prepared on the BioQule™ NGS System

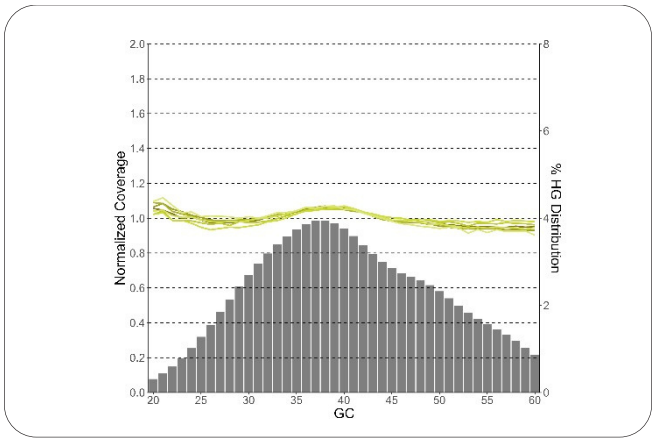


Figure 2. Analysis of GC bias from the libraries obtained with the Roche® KAPA® HyperPrep™ kit. Results show minimal variability in normalized coverage across 20-60% GC, encompassing ~ 95% of the human genome (grey bar)

Conclusions

The BioQule™ NGS System enables low-throughput walkaway automation of the Roche® KAPA® HyperPrep™ workflow from sample to final libraries ready for sequencing. The workflow allows the creation of up to 8 NGS libraries, with minimal set up and hands-on time. The BioQule NGS System has been specifically designed so no automation or prior NGS experience is required to generate libraries.

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DMark
35 Grand Marshall Drive, Toronto, ON, M1B 5W9, Canada
Contact Us - info@dmarkbio.com | 1.800.784.7485 | dmarkbio.com