APPLICATION NOTE

Automating low throughput Illumina® DNA Prep 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.

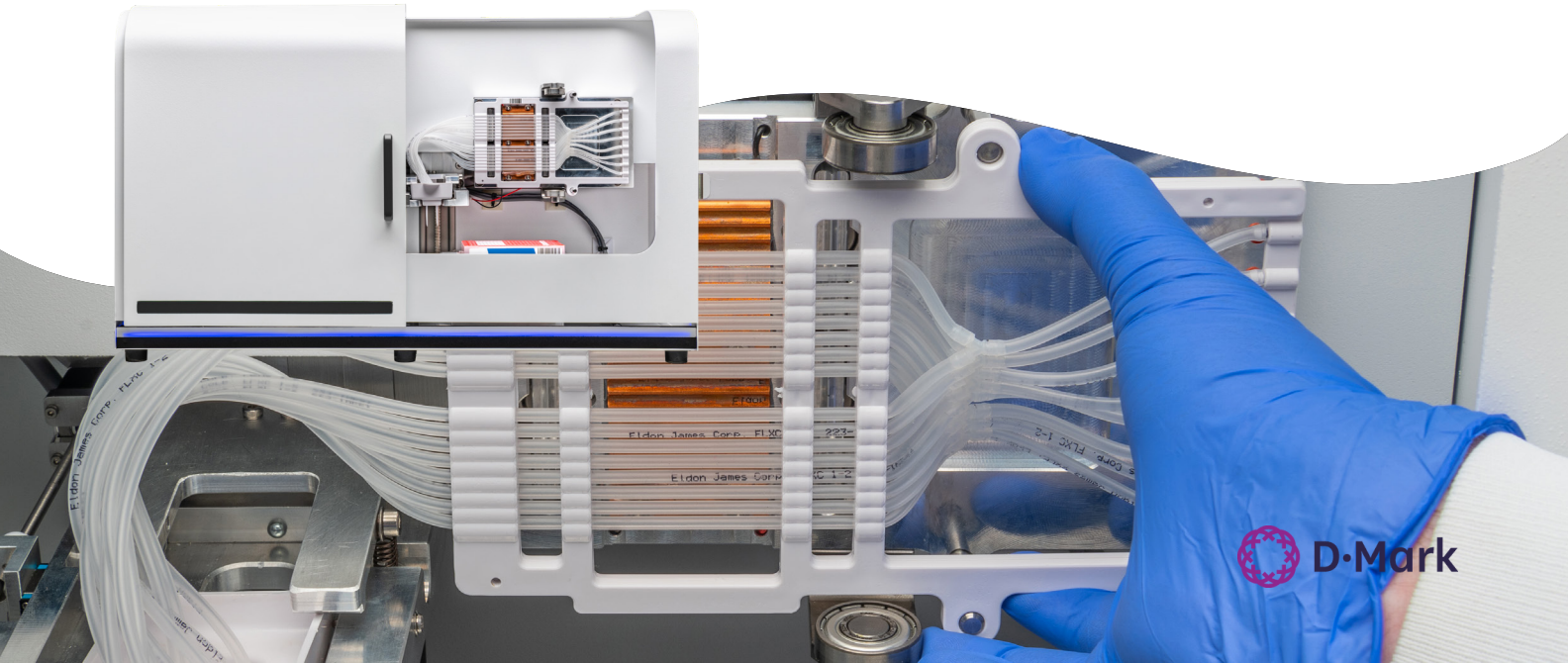
Please note that product labeling (such as kit insert, product label, and kit box) may be different compared to the company branding. Please contact your local representative for further details.

Introduction

The BioQule™ NGS System is a robust, open, easy-to-use solution that enables walkaway automation and quantitation for low-throughput library preparation. It has the capability to automate most library preparation workflows, resulting in the generation of consistent libraries with minimal hands-on time. Here we describe the results obtained when using the BioQule™ NGS System with the Illumina® DNA Prep for Whole Genome Sequencing. The complete run set up takes only 30 minutes of hands-on time.

Methods

WGS libraries were constructed using the Illumina® DNA Prep kit, (M) Tagmentation (20018704) with Illumina® Index Adapters (20027213) on the BioQule™ NGS System. 8 samples per run were prepared using 100 ng of Human Promega® genomic DNA as the starting material. Each run was performed according to the manufacturer's instructions. 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

Sequencing metrics for these WGS libraries can be seen in Figures 1-3. 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. Figure 3 shows the reproducibility of libraries obtained on two different instruments by looking at the alignment rate to the human genome.

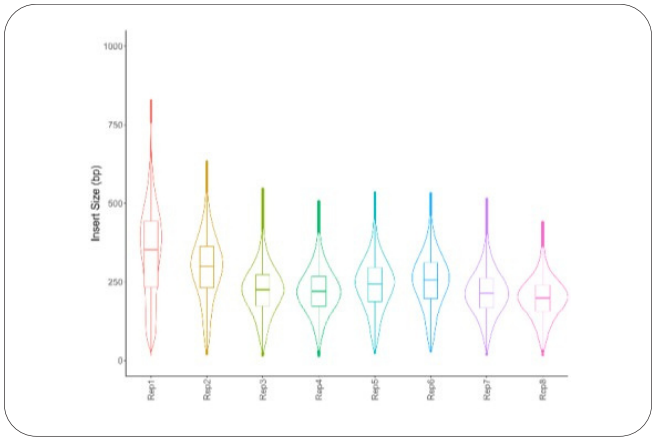


Figure 1. Insert size for a run of libraries prepared on the BioQule™ NGS System

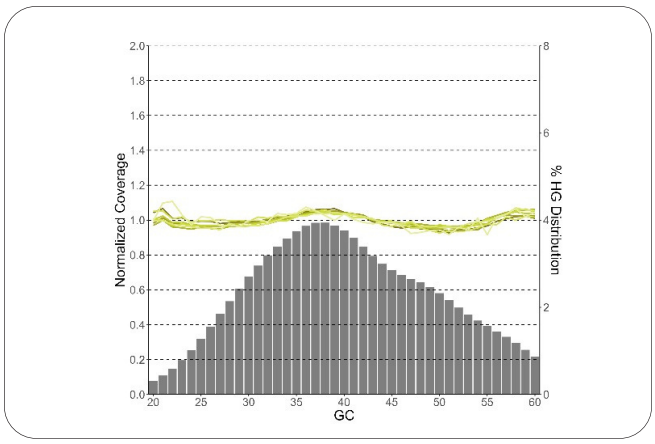


Figure 2. Analysis of GC bias from the libraries obtained with Illumina® DNA Prep kit. Results show minimal variability in normalized coverage across 20-60% GC, encompassing ~ 95% of the human genome (grey bar)

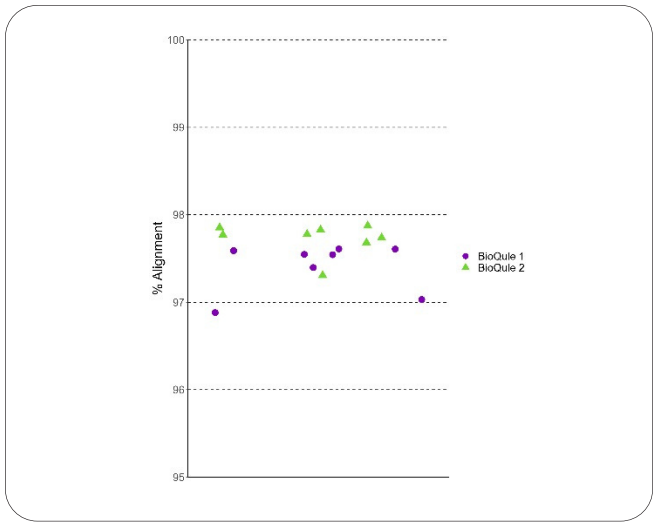


Figure 3. Consistent percentage of alignment to human genome of sample replicates run in two different BioQule™ instruments

Conclusions

The BioQule™ NGS System is an open platform that can be used in combination with the Illumina® DNA Prep kit to automate the complete library preparation protocol 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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