

# HiFi Library Preparation Using PacBio® SMRTbell® Prep Kit 3.0 on epMotion®

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## Introduction

The preparation of high-quality SMRTbell® libraries is essential for achieving optimal sequencing performance with PacBio® platforms. Automation of this process enhances reproducibility, minimizes hands-on time, and reduces potential sources of human error.

This application brief summarizes the successful implementation of the PacBio® SMRTbell® prep kit 3.0 on the Eppendorf epMotion automated liquid handling system, demonstrating high efficiency, yield, and quality of prepared libraries.



## User benefits

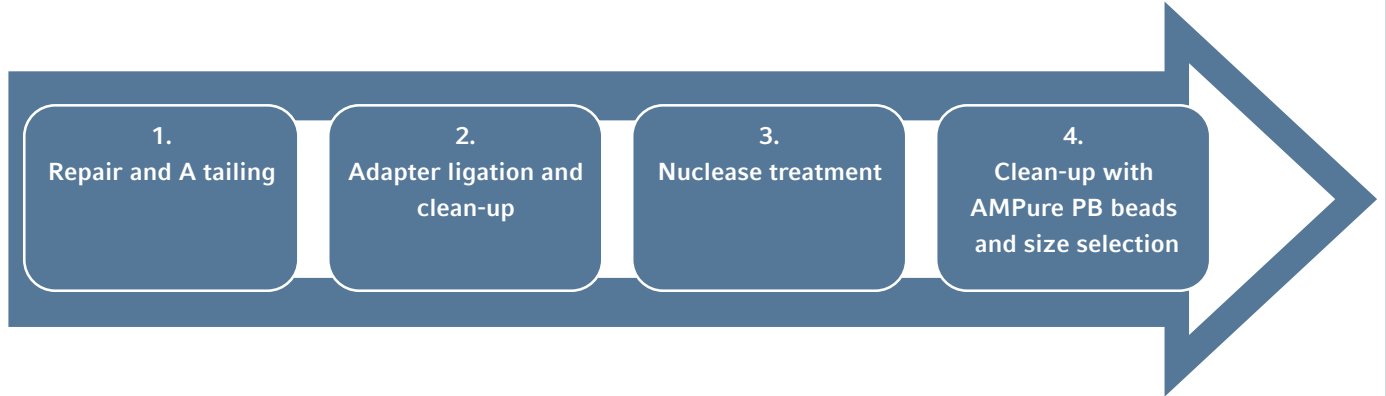
- > High Yield and Consistency – Delivers reproducible library preparation with minimal variability between runs.
- > Suitable for Long-Read Sequencing – Produces high-quality libraries and enhances efficiency for laboratories using PacBio sequencing platforms.
- > Reliable and Automated Solution – Seamless integration of the PacBio® SMRTbell® prep kit with the Eppendorf epMotion system ensures a standardized workflow with improved data accuracy, reliability and reproducibility.
- > Time-Saving Workflow – Reduces hands-on time, allowing researchers to focus on data analysis and other tasks.

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## Workflow

The library preparation workflow on epMotion 5075t for processing 24 samples consisted of the following steps.



Sheared gDNA from *E. coli* (fragment size 8-10 kb) was used as the starting sample for both the manual as well as epMotion runs. The epMotion system was programmed to execute the end-repair, ligation, and bead purification steps with

precision, ensuring consistent and high-quality libraries with no user intervention required during the process. The walk-away time when processing 24 samples was 250 minutes or about 4 hours and 10 minutes.

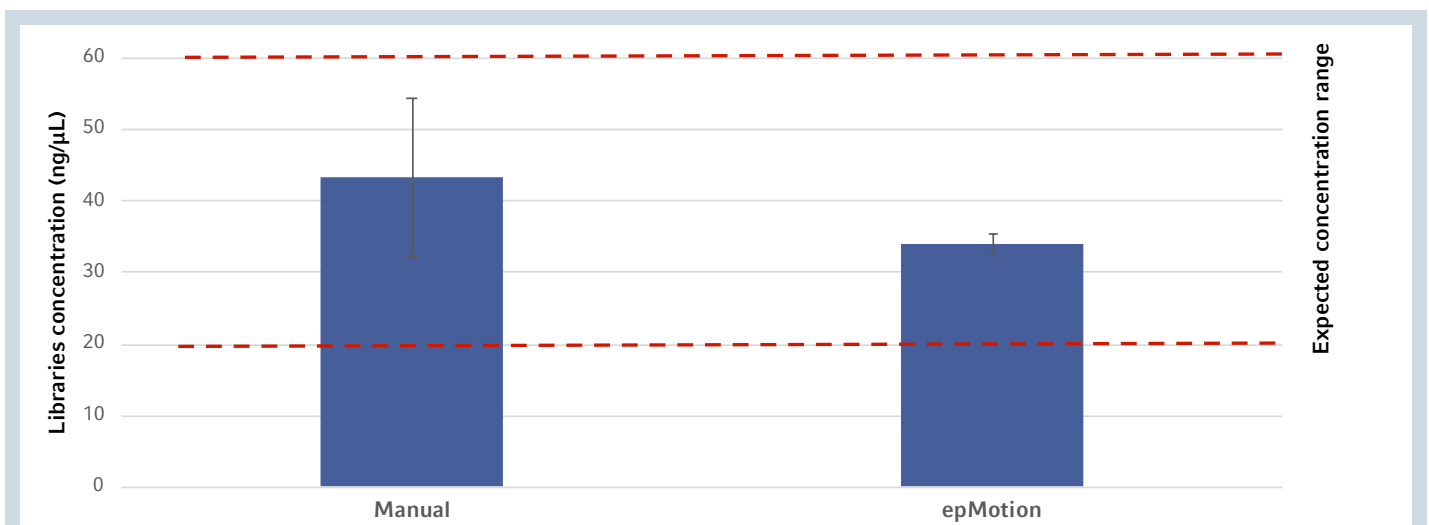
## Results

### Yield and Quality Assessment

The automated workflow on the epMotion system consistently produced SMRTbell® libraries with high yield and quality. The following key metrics were observed:

### > Library Yield:

The library concentrations prepared with the SMRTbell® prep kit 3.0 on the epMotion were within the expected range. The repeatability was improved using an automated process (CV 4%) compared to a manual process (25%)

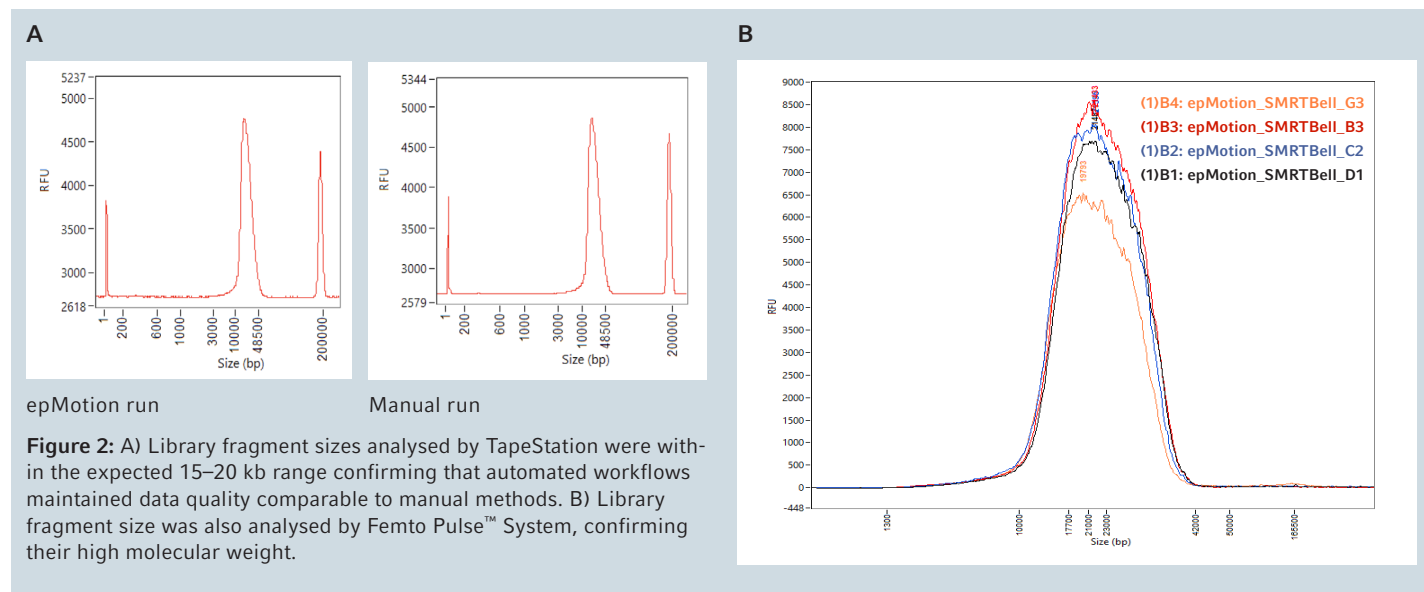


**Figure 1:** Libraries were generated using SMRTbell prep kit 3.0 on the epMotion. Repeatability was improved markedly with automation (CV 4%) compared to manual methods (CV 25%).

### > Library fragment size:

The fragment size of the libraries was checked using the TapeStation and Femto Pulse™ (Agilent Technologies® Inc). The libraries were within the expected range (15-20 kb).

Comparison of the manual workflow data and the automated runs from Tape Station showed that the quality of results when following automated workflow is not compromised.



### > Sequencing Performance:

Initial sequencing runs demonstrated quality of the libraries prepared using the epMotion. The libraries were sequenced on a PacBio Revio® system using Revio v1

chemistry and achieved results that met or exceeded the acceptance specifications.

	Revio sequencing using epMotion for sample prep (plate loading concentration 225pM )		Acceptance criteria – cutoff value
	Mean		
Metric	Femto Peak (kb)	21077	10000-25000
	ABC % Recovery	78.0	60
	P1 loading	0.5	0.5
	HiFi Reads (M)	4.7	1
	HiFi Yields (Gb)	87.4	80 (Revio)
	HiFi Read Length (kb)	18.8	10
	Read Quality	Q33	Q30
	Polymerase Read Length (kb)	76.5	60
	Base Rate (bp/s)	2.5	2
	SMRTBell % recovery	21	20

**Table 1:** Libraries prepared with epMotion demonstrated high quality, as sequencing on the PacBio Revio® system met or exceeded acceptance criteria.

## Summary

Overall, this data shows the automated workflow for SMRTbell® prep kit 3.0 library construction on the Eppendorf epMotion liquid handling system showcases a high-quality, versatile, and robust solution for PacBio® library preparation.

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