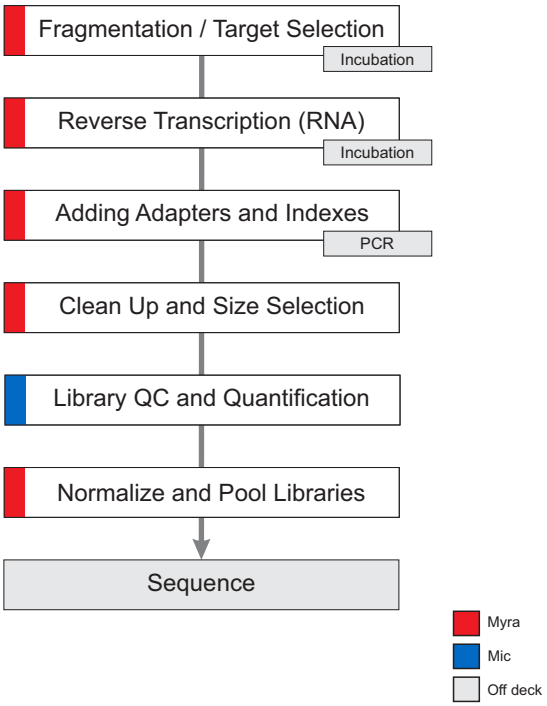
Myra Liquid Handling System

NGS Library Prep

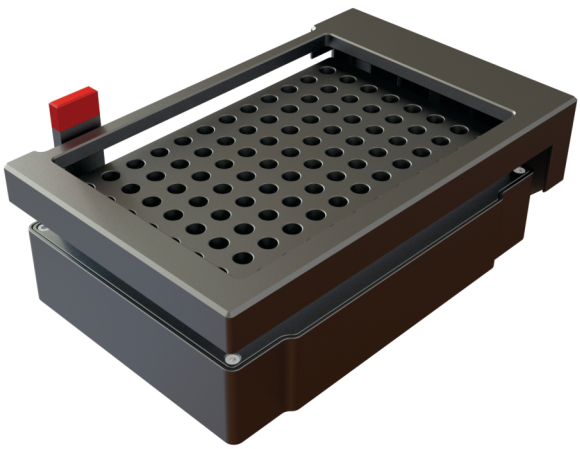
Automated Library Prep

Myra offers semi-automated library preparation - streamlining the workflow, significantly reducing manual errors, increasing reproducibility all while minimizing hands-on time.



Key Features

Capable of handling up to 24 libraries, Myra incorporates a 96 Well Magnetic Station for bead clean-up steps, with off-deck heating to reduce robotic downtime. The workflow is split into manageable runs, with safe stopping points after the various library preparation steps including bead clean up.



Library Prep Kits

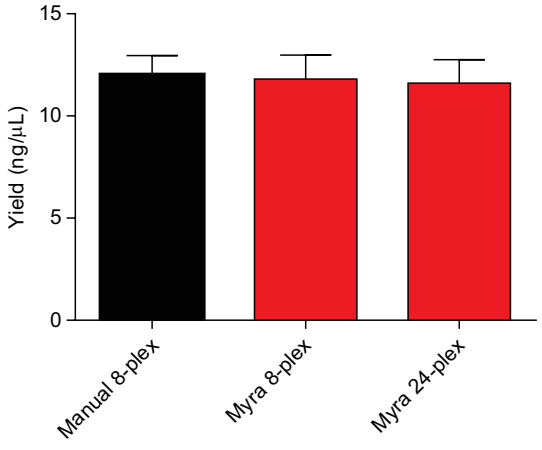
- Illumina DNA Prep
- NEBNext Ultra II FS DNA Library Prep Kit for Illumina
- Oxford Nanopore Technologies - Rapid Barcoding Kit
- Oxford Nanopore Technologies - Native Barcoding Kit
- Zymo Quick - 16S Plus NGS Library Prep Kit (V3/V4, UDI)
- Watchmaker DNA Library Prep kit with Fragmentation
- seqWell plexWell Lp384

Full list available at
www.biomolecularsystems.com/myra/myra-script

Ask us to automate your NGS protocol.

Consistency and Reproducibility

In NGS, repeatability and reproducibility are paramount. The Myra Liquid Handling System can successfully generate high-quality DNA libraries, with performance comparable to manual methods. Sequencing runs show high Q30 scores and consistent barcode balance. Sequencing coverage exhibits uniformity across the prepared libraries, resulting in low library variability and reliable performance. Thus, Myra not only reduces manual labour but also ensures high-quality sequencing results.



Summary

Myra offers a cost-effective and reliable solution for NGS library prep. Myra ensures that you spend less time on library prep and more on what truly matters – groundbreaking research.

Intuitive Software

Affordable Automation

Case Study: Illumina DNA Prep Kit

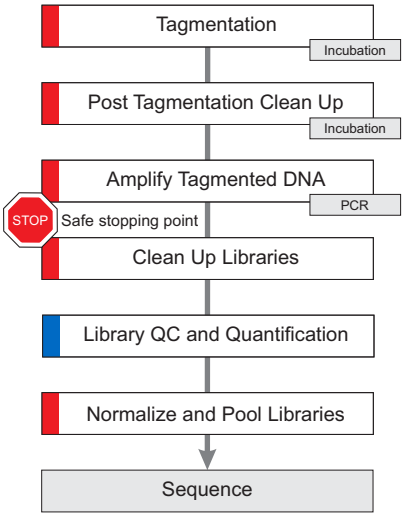
We validated up to 24 samples using the Illumina DNA Prep kit. Libraries displayed low variability across replicates, even barcode balance, and high coverage of sequence alignments.

Experimental Setup

To demonstrate capability, 8-sample and 24-sample plates of 150 ng of input DNA (48 kB genome Lambda DNA and Human Genomic DNA) were prepared on the Myra Liquid Handling System. Manual preparation of an 8-sample plate of 150 ng of input DNA (48 kB genome Lambda DNA) was also performed as a comparison method.

The quality of these libraries were checked with BiOptic Qsep1-Plus bio-fragment analyser. The libraries were quantified using NEBNext Library Quant Kit for Illumina with reaction setup on the Myra Liquid Handling System and amplification on the Mic qPCR Cycler. Libraries were simultaneously normalised and pooled to 2 nM using the Myra Liquid Handling System, then sequenced on a 2x 150 bp flow cell on an iSeq 100 System for whole genome sequencing. Q30 and percentage PF were used to show the quality of the libraries.

Sequencing data was demultiplexed using Illumina's BaseSpace Sequence Hub and coverage maps of the Lambda genome were analysed using Geneious Prime 2022.2.2.



Results

We were able to successfully generate high-quality 8-plex and 24-plex DNA libraries on the Myra, with comparative performance to the manual method (**Table 1**).

	Final Yield Produced (ng/µL)			
	8-plex Lambda Manual	8-plex Lambda Myra	24-plex Lambda Myra	8-plex Human Myra
Mean	12.0	11.8	11.6	9.4
%CV	8	10	10	9

Table 1. Mean library yield after Illumina DNA Prep was processed.

Fragment analyzer results show consistent fragment sizes across all 24 DNA libraries (**Figure 1**).

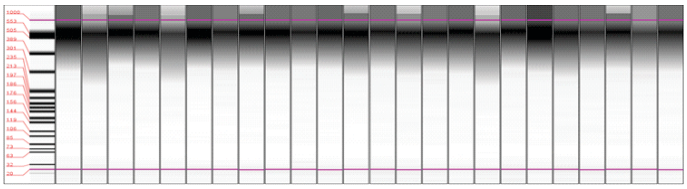


Figure 1. Capillary electrophoresis gel of library quality analysed on BiOptic Qsep1-Plus with S2 Cartridge for 24-plex Lambda libraries.

The quality of the sequencing runs were comparative with Q30 score >90% for all methods (**Table 2**).

Method	Q30 (%)	PF (%)	Yield (GB)	Barcode Balance
8-plex Lambda Manual	92	71	1.7	25
8-plex Lambda Myra	91	72	1.8	11
24-plex Lambda Myra	91	65	1.6	18
8-plex Human Myra	91	71	1.7	10

Table 2. The sequencing quality data produced for all methods.

Barcode balance was also accurate, with variability less than the manual method (**Figure 2**).

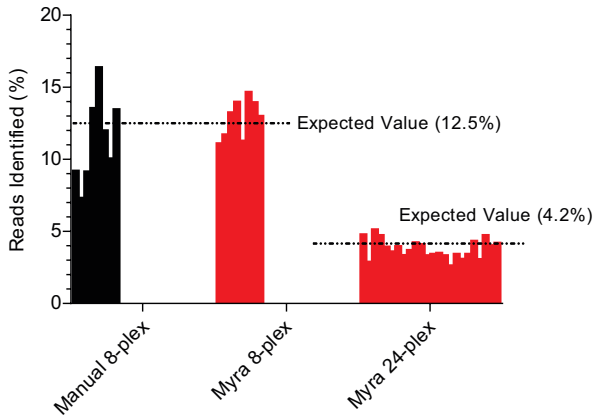


Figure 2. Barcode balance for 8-plex Manual Lambda DNA, 8-plex Myra Lambda DNA and 24-plex Myra Lambda DNA.

Sequencing coverage of the Lambda genome also showed consistent uniformity across 8-plex and 24-plex DNA prep libraries constructed on the Myra. The sequence data showed low sample variability and reliable uniformity for libraries prepared using Illumina DNA Prep.

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