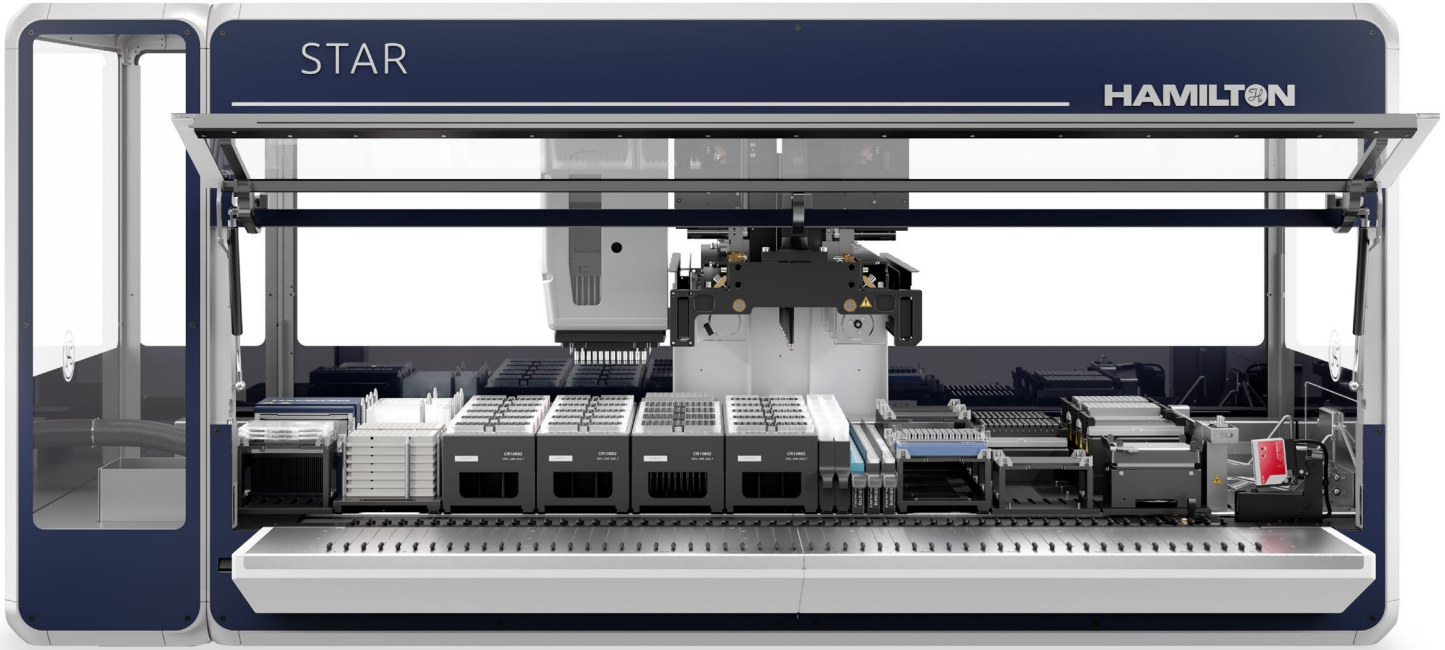
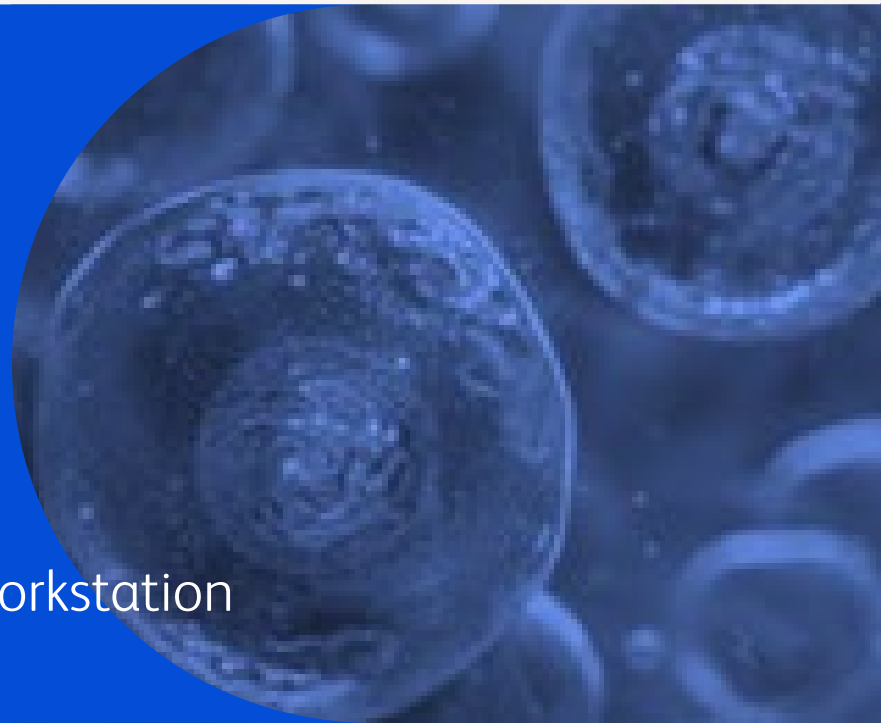



BD

# BD® OMICS-One XT WTA Assay

Automated on the Hamilton™ Microlab™ NGS STAR Assay Ready Workstation



# Contents

- Overview
- Workflow and automated process
- System description
- Chemistry
- Application performance
- BOM and pricing
- Support

# Overview

# Overview

## Single-cell analysis

Obtaining high-quality libraries from single cells to evaluate transcriptomic heterogeneity at the single-cell level is complicated for many reasons, including:

### Manual library prep is time consuming

Hours spent on library prep take away from data analysis and interpretation

### Manual prep is error prone

Variability and mistakes can occur at any step, impacting data quality

### Scaling is difficult

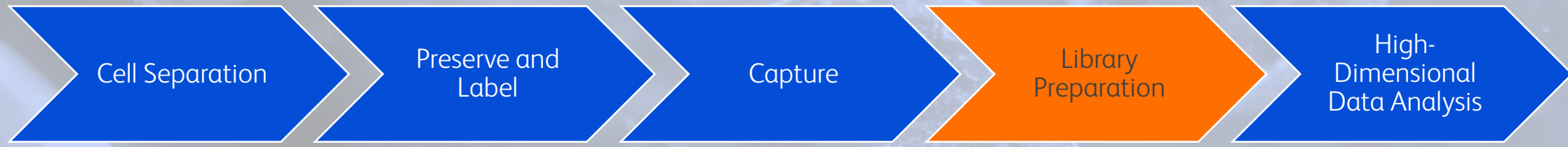
Manual methods struggle to keep pace with increasing sequencing demands

The automated BD® OMICS-One XT WTA Assay minimizes hands-on time and technical variability caused by human error, increases throughput to keep pace with sequencing demands and ensures consistent and quality libraries using robust reagents and pre-optimized methods.

# Workflow and automated process

# Workflow

## BD Rhapsody™ Single-Cell Analysis System workflow




BD Cell Sorters

BD Rhapsody™ Single-Cell Multiplexing Kits

CITE-seq using BD® AbSeq Ab-Oligos

BD® OMICS-Guard Sample Preservation Buffer

BD Rhapsody™ HT Xpress System

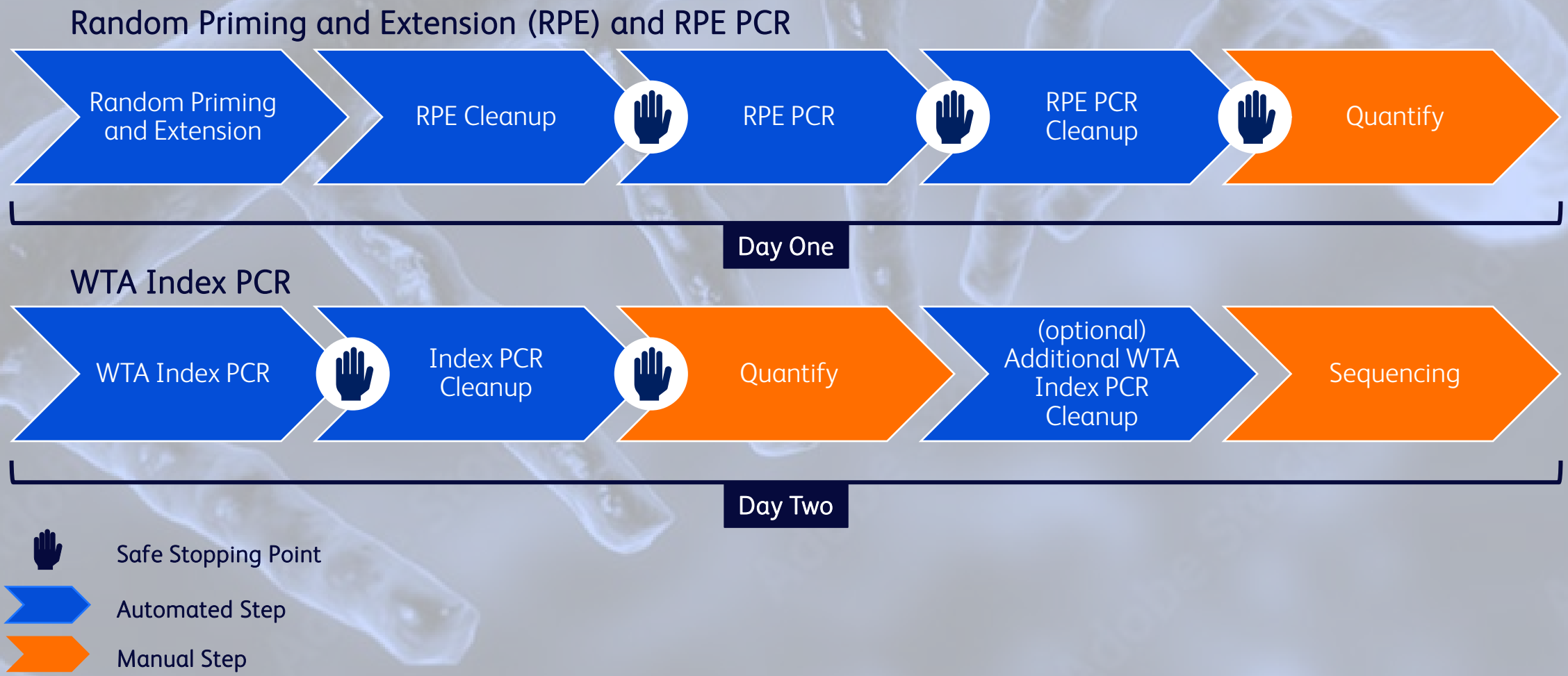
BD Rhapsody™ HT Single-Cell Analysis System

BD® OMICS-One XT Automation Kits

BD Rhapsody™ Sequence Analysis Pipeline

# Workflow

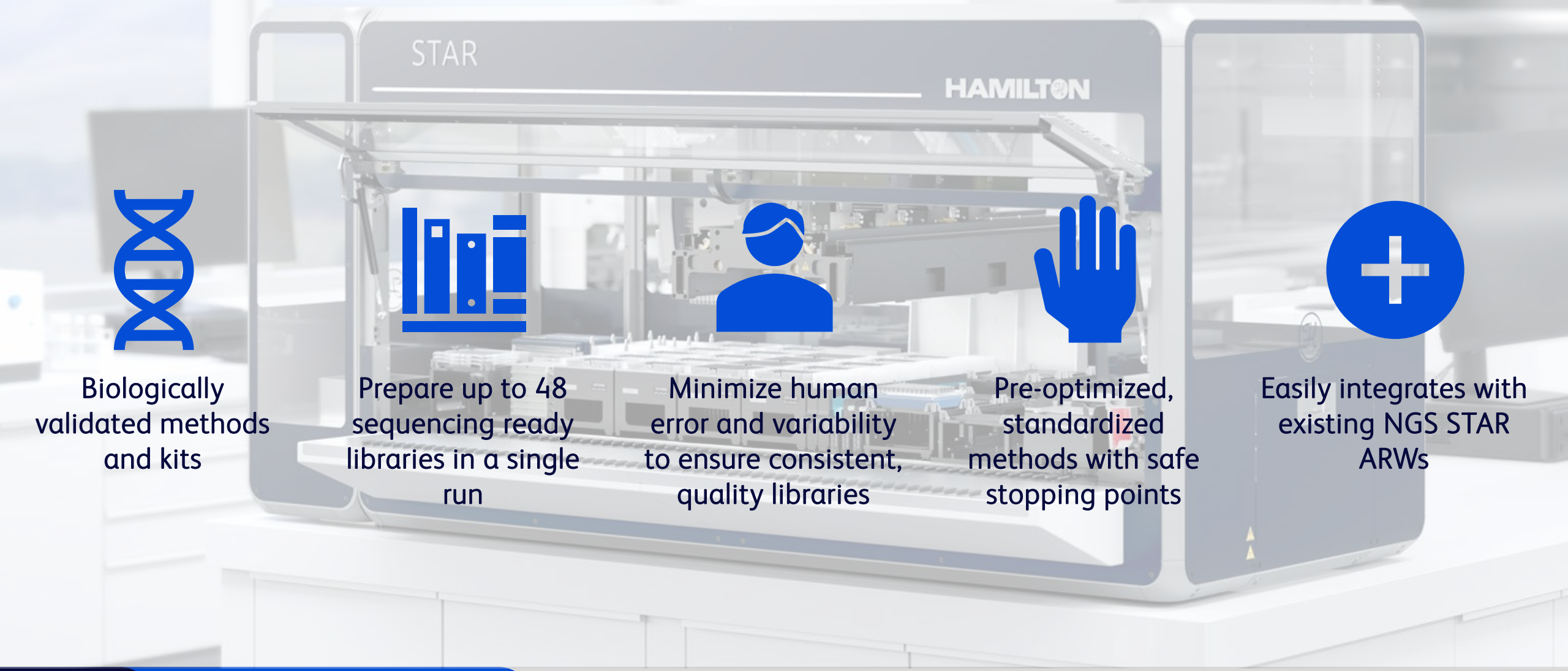
WTA library prep workflow on the Hamilton™ Microlab™ NGS STAR Assay Ready Workstation (ARW)



# System description

# Features

WTA library prep from single cells on the Hamilton™ Microlab™ NGS STAR Assay Ready Workstation (ARW)




Biologically validated methods and kits

Prepare up to 48 sequencing ready libraries in a single run

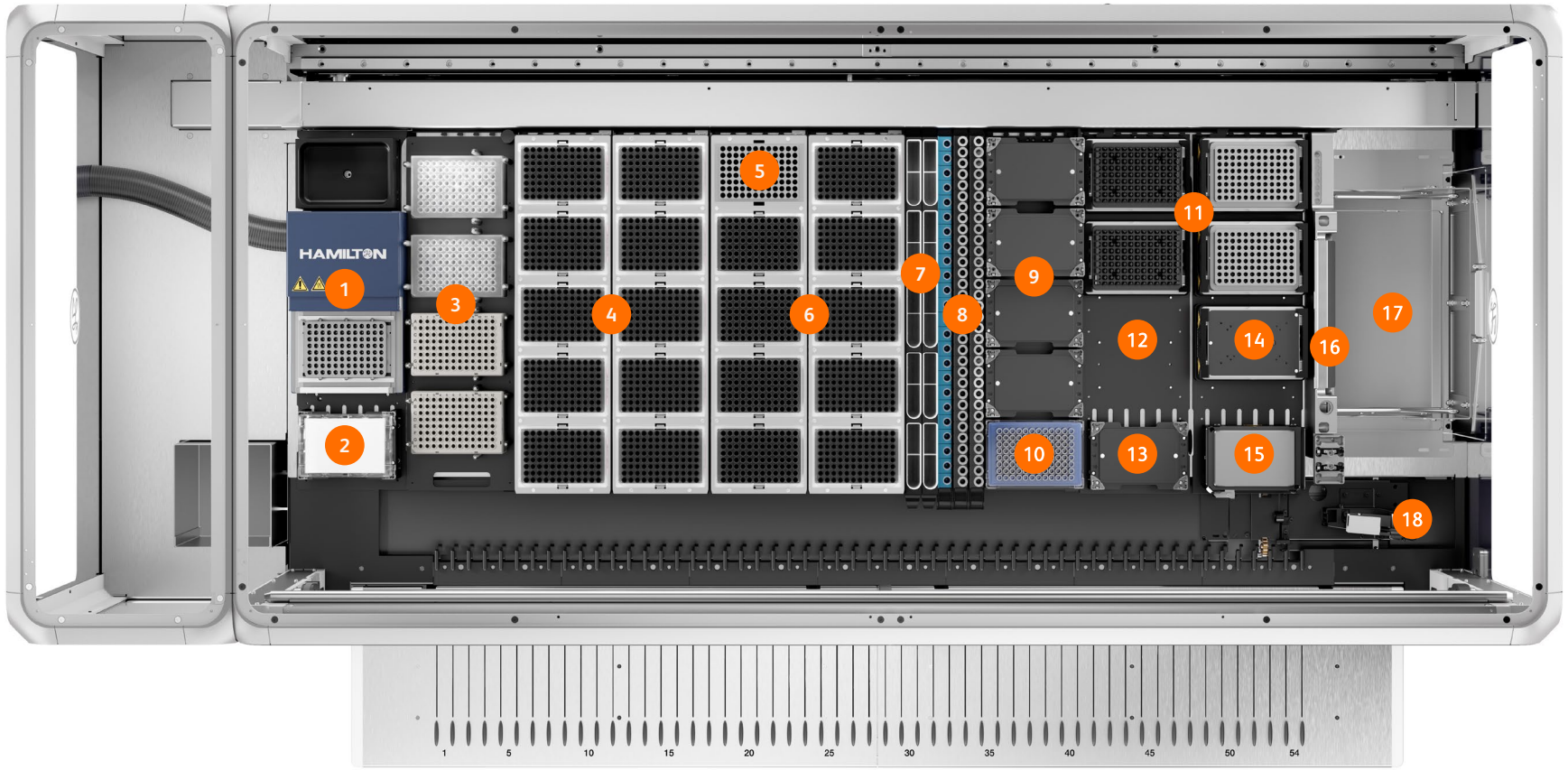
Minimize human error and variability to ensure consistent, quality libraries

Pre-optimized, standardized methods with safe stopping points

Easily integrates with existing NGS STAR ARWs

# Deck layout

## WTA library prep from single cells on the Hamilton™ Microlab™ NGS STAR Assay Ready Workstation (ARW)




1. 96-Well On-Deck Thermal Cycler*
2. Stacked Plate Lids
3. Stacked Plates
4. 50-µL and 1,000-µL Conductive Tips
5. Tip Adapter*
6. 300-µL Conductive Tips
7. 60-mL Reagent Troughs
8. Microtubes
9. Plate Positions
10. Plate Magnet
11. Heater Shakers
12. Cold Plate (Air Cooled)
13. Cold Plate (Air Cooled)
14. Heater Shaker
15. Cold Plate (Air Cooled)
16. CO-RE® Paddles
17. Channel Waste
18. Autoload

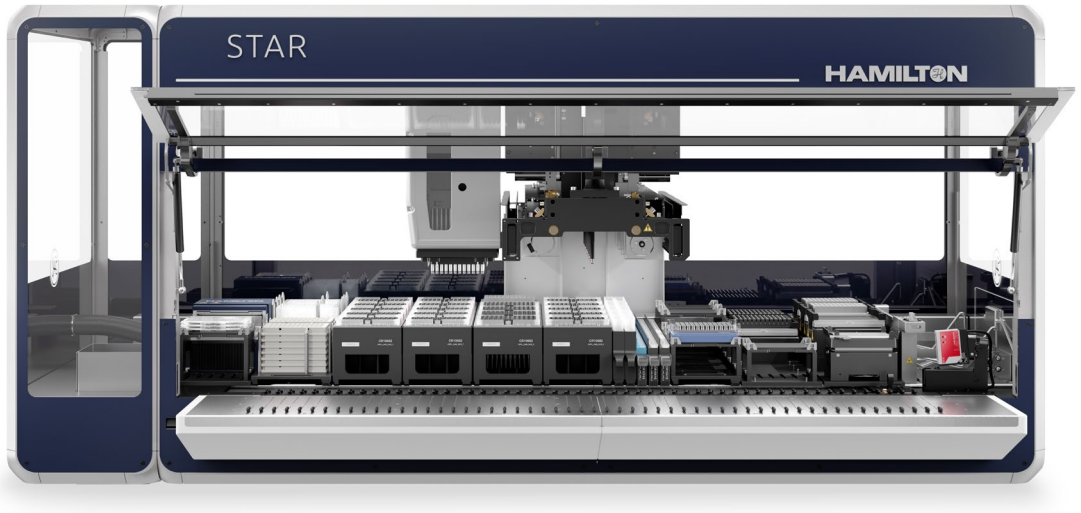
*On-Deck Thermal Cycling and 96 Multi-Probe Head are optional

# Timing and consumables requirements

## WTA library prep from single cells on the Hamilton™ Microlab™ NGS STAR ARW

This solution can process 24 libraries from single cell cDNA in under 2 days

| Labware | BD® OMICS-One XT WTA Assay Kit | | |
|---|---|---|---|
| | **8 samples/run** | **24 samples/run** | **48 samples/run** |
| 60-mL reagent reservoir | 6 | 6 | 6 |
| 50-µL filtered tips | 120 | 360 | 720 |
| 300-µL filtered tips | 224 | 672 | 1344 |
| 1,000-µL filtered tips | 192 | 528 | 1032 |
| 96-well PCR plate | 4 | 4 | 4 |
| 96-well midi plate | 5 | 5 | 5 |
| 2-mL screw cap tubes | Up to 23 | Up to 23 | Up to 23 |
| Comfort lid | 2 | 2 | 2 |
| *Estimated hands on time | 30 min | 30 min | 30 min |
| Estimated instrument processing time | 7 h 17 min | 9 h 17 min | 14 h 50 min |
| Estimated total workflow time | 7 h 47 min | 9 h 47 min | 15 h 20 min |




Note: Max throughput is 48 samples
*Hands on time includes loading the instrument with consumables and reagents, not manual reagent prep time

# Chemistry

# Chemistry
## BD® OMICS-One XT WTA Assay

**Streamline your library prep workflow with the BD® OMICS-One XT WTA Assay and make automation set up easier.**

- Optimized and consolidated reagents for single-cell library preparation
- Tailored for compatibility with liquid handling automation systems
- Modular workflow with safe stopping points
- Compatible with Illumina™ and Element™ sequencing platforms

# Chemistry
## BD® OMICS-One XT WTA Assay Kits

| BD® OMICS-One XT WTA Products | Cat. No. | List Price (USD) |
|---|---|---|
| BD® OMICS-One XT WTA Amplification Kit (48 Rxns) | 667246 | $11,502 |
| BD® OMICS-One XT Dual Index Kit A (48 Rxns) | 571973 | $450 |
| BD® OMICS-One XT Magnetic Baseplate | 667393 | $1,400 |

| Companion Products | Cat. No. | List Price (USD) |
|---|---|---|
| BD Rhapsody™ HT Xpress Package | 666625 | $15,000 |
| BD Rhapsody™ Scanner | 633701 | $54,450 |
| BD Rhapsody™ 8-Lane Cartridge | 666262 | $2,000 |
| BD Rhapsody™ Enhanced Cartridge Reagent Kit V2 | 664887 | $3,210 |
| BD Rhapsody™ Enhanced Cartridge Reagent Kit V3 | 667052 | $3,210 |
| BD Rhapsody™ cDNA Kit | 633773 | $1,550 |



For Research Use Only. Not for use in diagnostic or therapeutic procedures.

Pricing is current as of August 2024.

# Application performance

# WTA NGS data from single cells in PBMC samples

## Library DNA yield and QC metrics

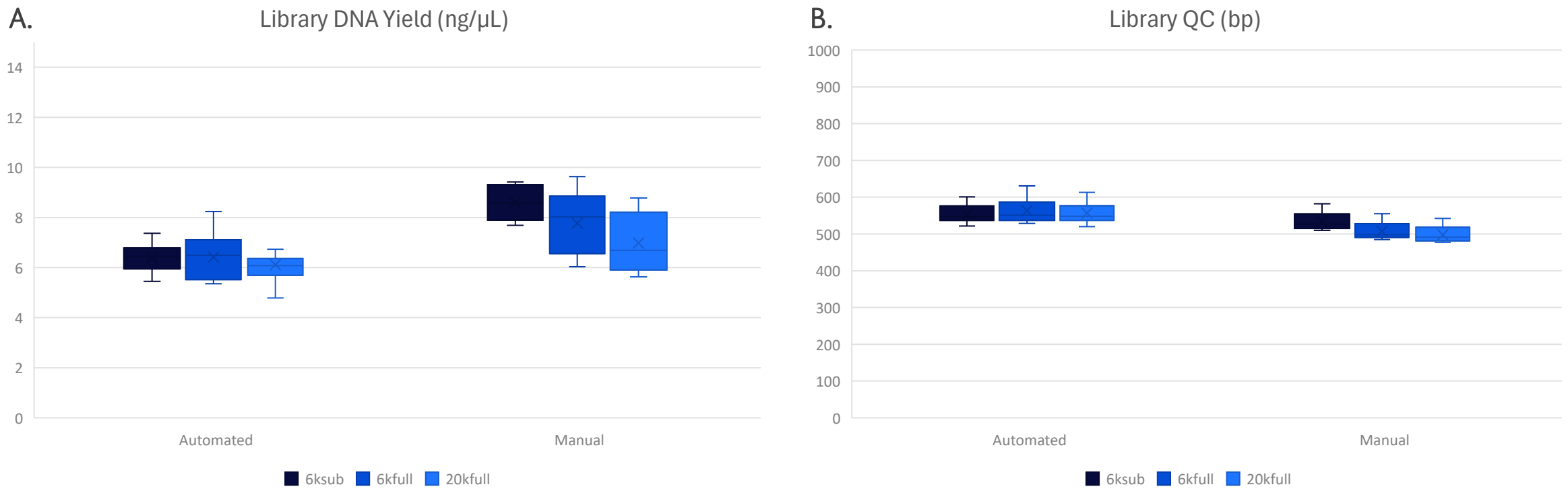
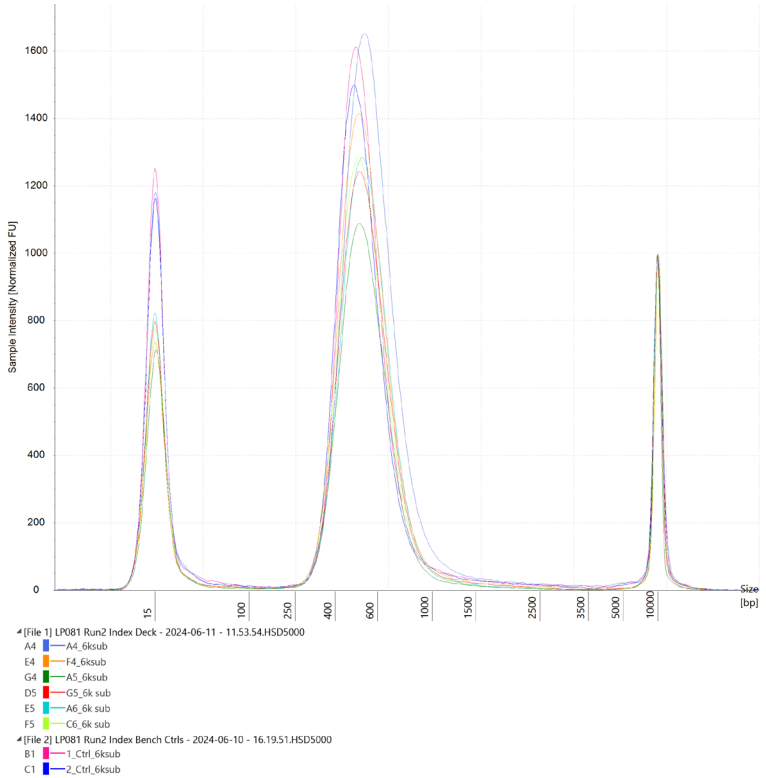



**Figure legend:** Three runs of 18 libraries (six each of 6K subsampled beads, 6K full sampled beads and 20K full sampled beads from the same pool of cellular transcripts captured on the BD Rhapsody™ Enhanced Cell Capture Beads) were prepared on the Hamilton™ Microlab™ NGS STAR ARW along with five manual bench controls of each condition. Shown are sequenced libraries of 15 libraries total for 6K sub and 6K full each and nine libraries total for 20K full sampled beads. **A)** Final quality control of indexed libraries show automated libraries was comparable to manual bench controls for Qubit concentration (ng/µL). **B)** Final quality control by TapeStation analysis shows similar average bp size distribution between 200–1,000bp.

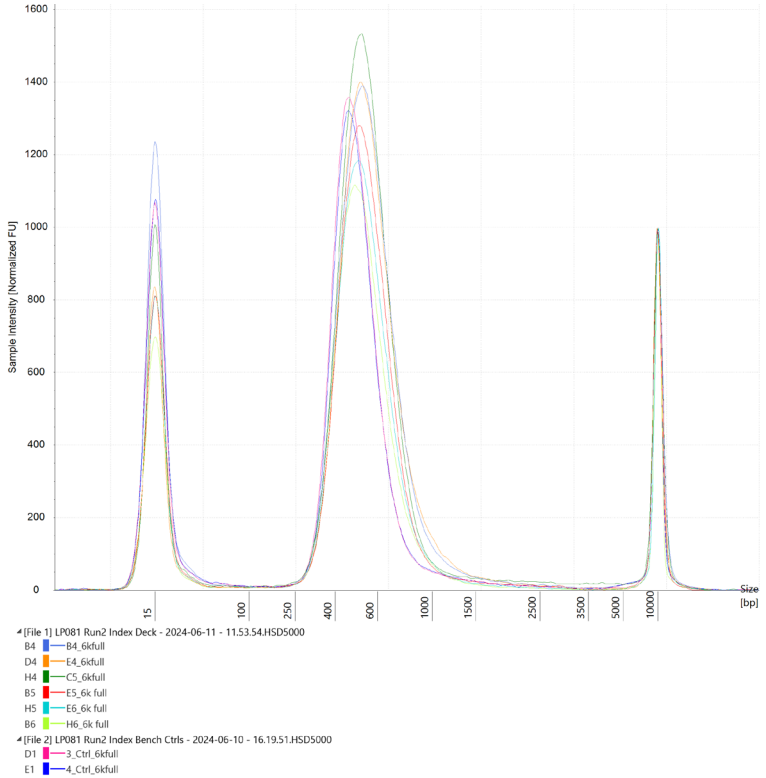
# WTA NGS data from single cells in PBMC samples

## Final library QC TapeStation traces

### 6K sub




### 6K full




### 20K full

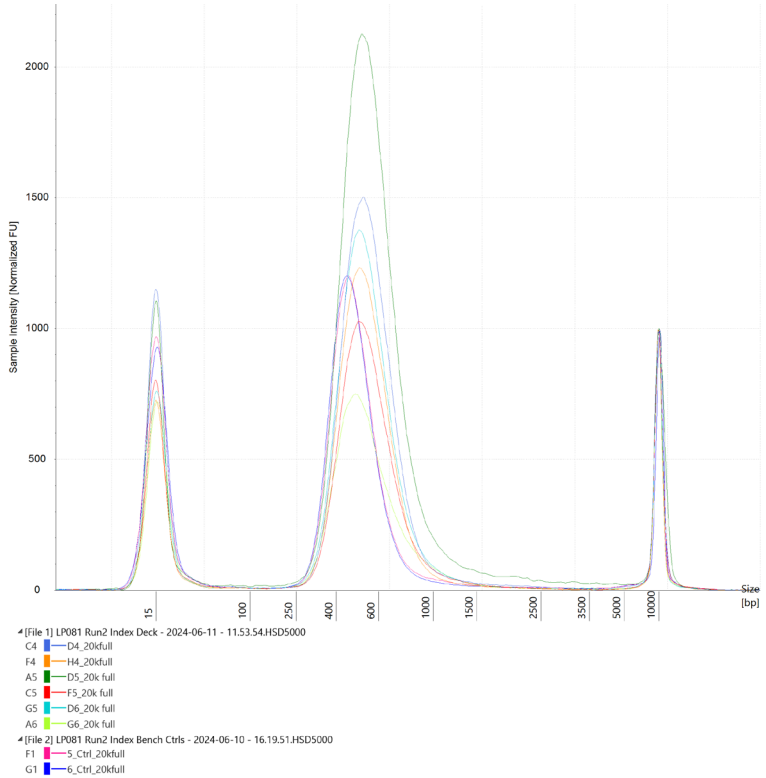



**Figure legend:** At the end of Index PCR purification, libraries were quantified via Qubit and normalized to 1 ng/µL prior to running on TapeStation for size analysis. All cell inputs prepped on the Hamilton™ Microlab™ NGS STAR ARW were comparable in bp size distribution against manual bench controls.

# WTA NGS data from single cells in PBMC samples

## Sequencing QC metrics

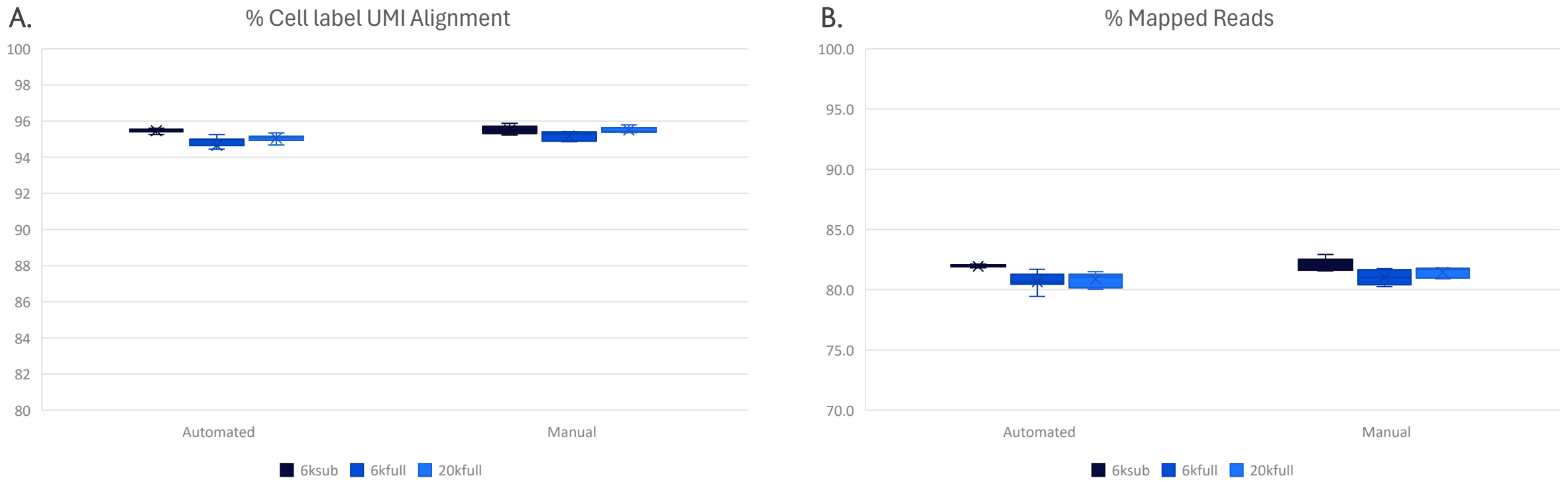



**Figure legend:** Three runs of 18 libraries (six each of 6K subsampled beads, 6K full sampled beads and 20K full sampled beads from the same pool of cellular transcripts captured on the BD Rhapsody™ Enhanced Cell Capture Beads) were prepared on the Hamilton™ Microlab™ NGS STAR ARW along with five manual bench controls of each condition. After sequencing, all automated and manual libraries were down sampled to between 7,600–8,000 raw reads per cell. **A)** The percentage of reads identified with a cell label UMI and align uniquely generated from libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW are comparable to manually prepped libraries. **B)** Percentage of mapped reads that align to a known gene generated on the automated system are like those libraries generated manually.

# WTA NGS data from single cells in PBMC samples

## Cells retrieved by sequencing

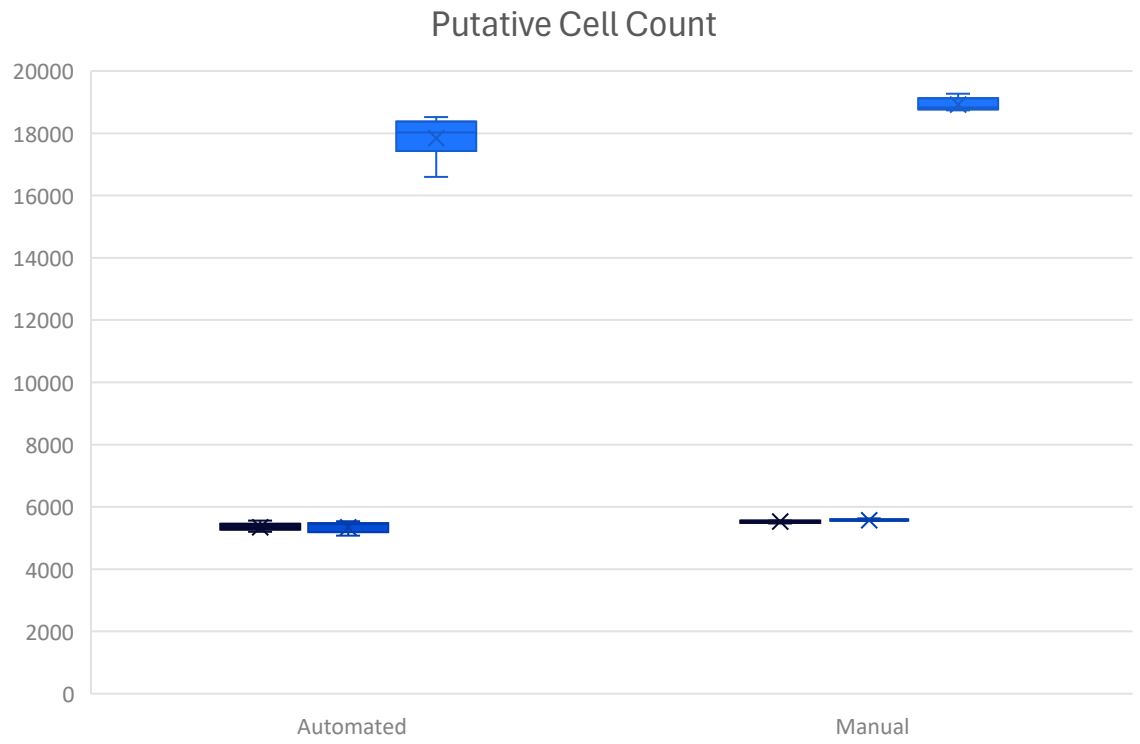



**Figure legend:** Putative cell detection is similar between automated library preparation and manual library preparation. The expected cell inputs of 6,000 cells and 20,000 cells were approximately detected.

# WTA NGS data from single cells in PBMC samples

## Assay sensitivity

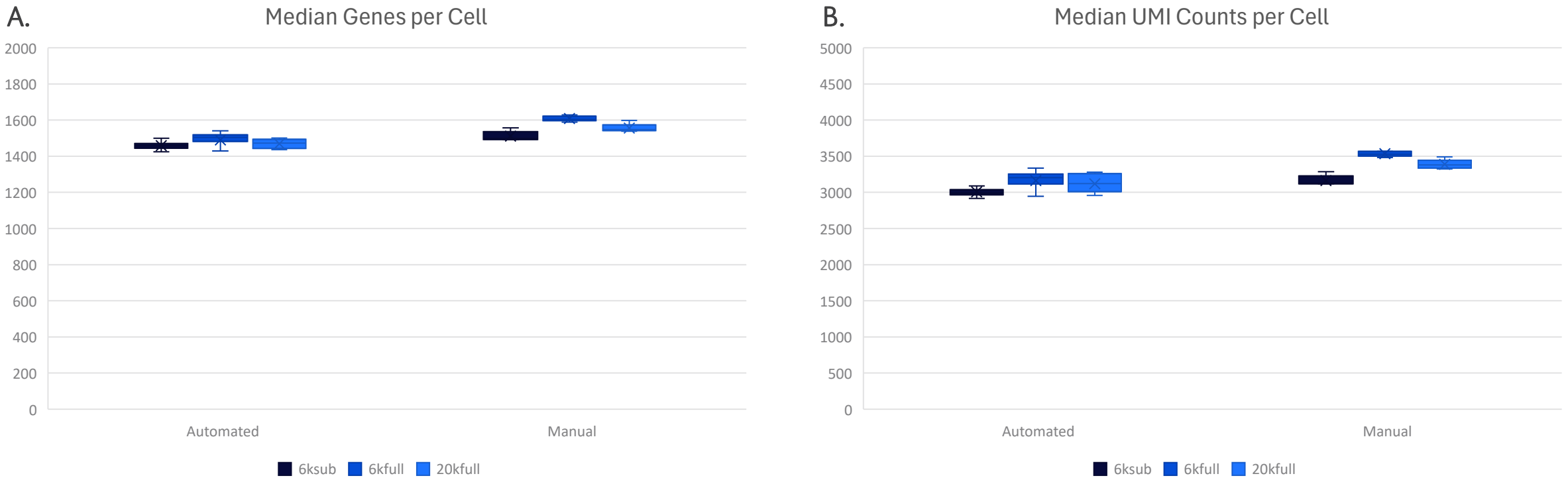
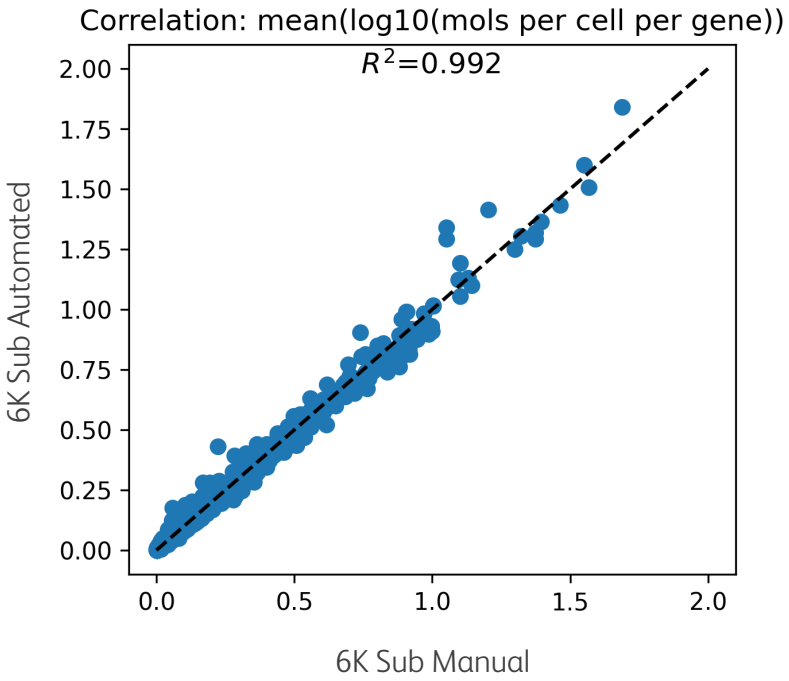
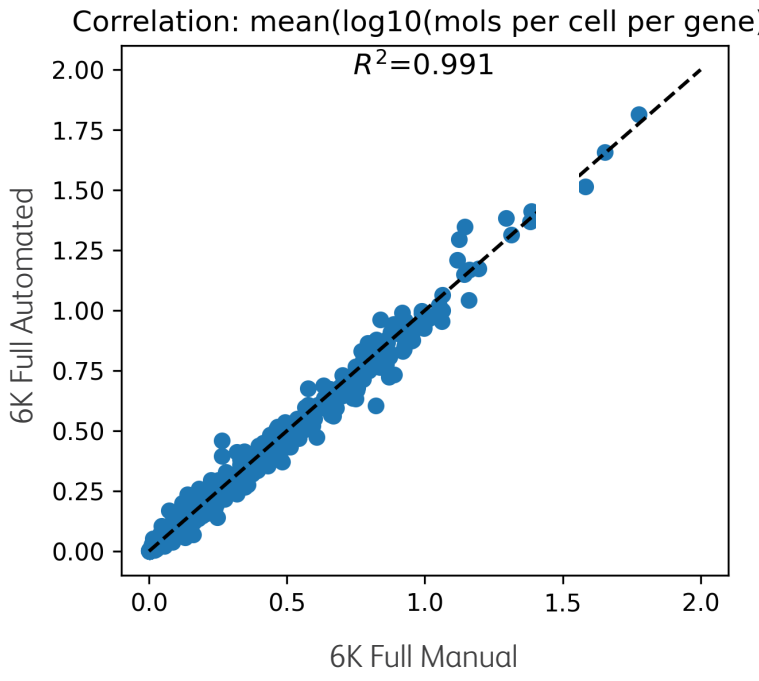



**Figure legend:** Three runs of 18 libraries (six each of 6K subsampled beads, 6K full sampled beads and 20K full sampled beads from the same pool of cellular transcripts captured on the BD Rhapsody™ Enhanced Cell Capture Beads) were prepared on the Hamilton™ Microlab™ NGS STAR ARW along with five manual bench controls of each condition. Shown are sequenced libraries of 15 libraries total for 6K sub and 6K full each and nine libraries total for 20K full sampled beads. After sequencing, all automated and manual libraries were down sampled to between 7,600–8,000 raw reads per cell. **A)** Median genes per cell generated from libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW are comparable to manually prepped libraries. **B)** Median UMI counts per cell generated on the automated system are like those libraries generated manually.

# WTA NGS data from single cells in PBMC samples

## Assay sensitivity



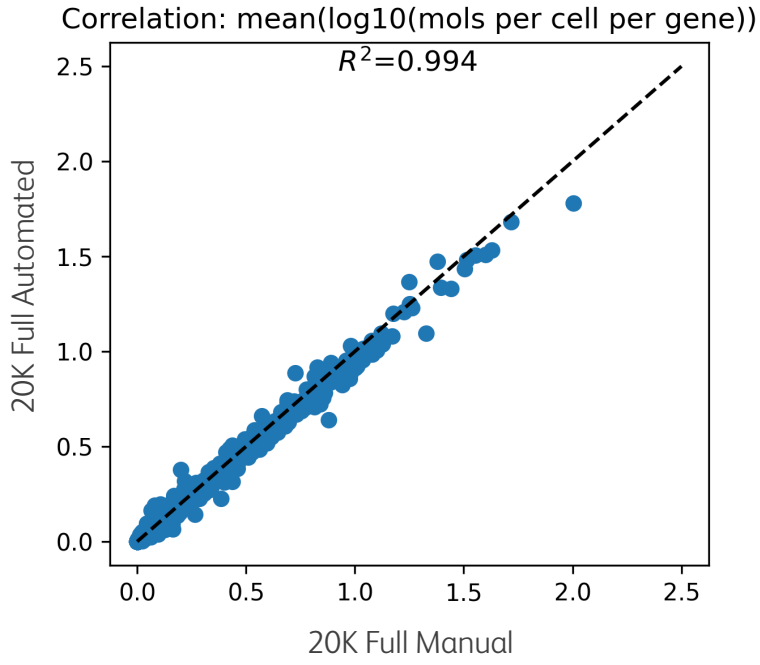




**Figure legend:** Gene expression correlation plots for 6K subsampled, 6K full sampled and 20K full sampled beads show a correlation greater than 0.99 when automated library prepped samples are compared to manually prepared samples. Here all genes containing greater than 50 total molecules are analyzed, where 6K subsampled library contains approximately 18,000 genes and both 6K and 20K full libraries contain approximately 14,000 genes when sequenced at 8,000 raw reads per cell.

# WTA NGS data from single cells in PBMC samples

## Cell type identification

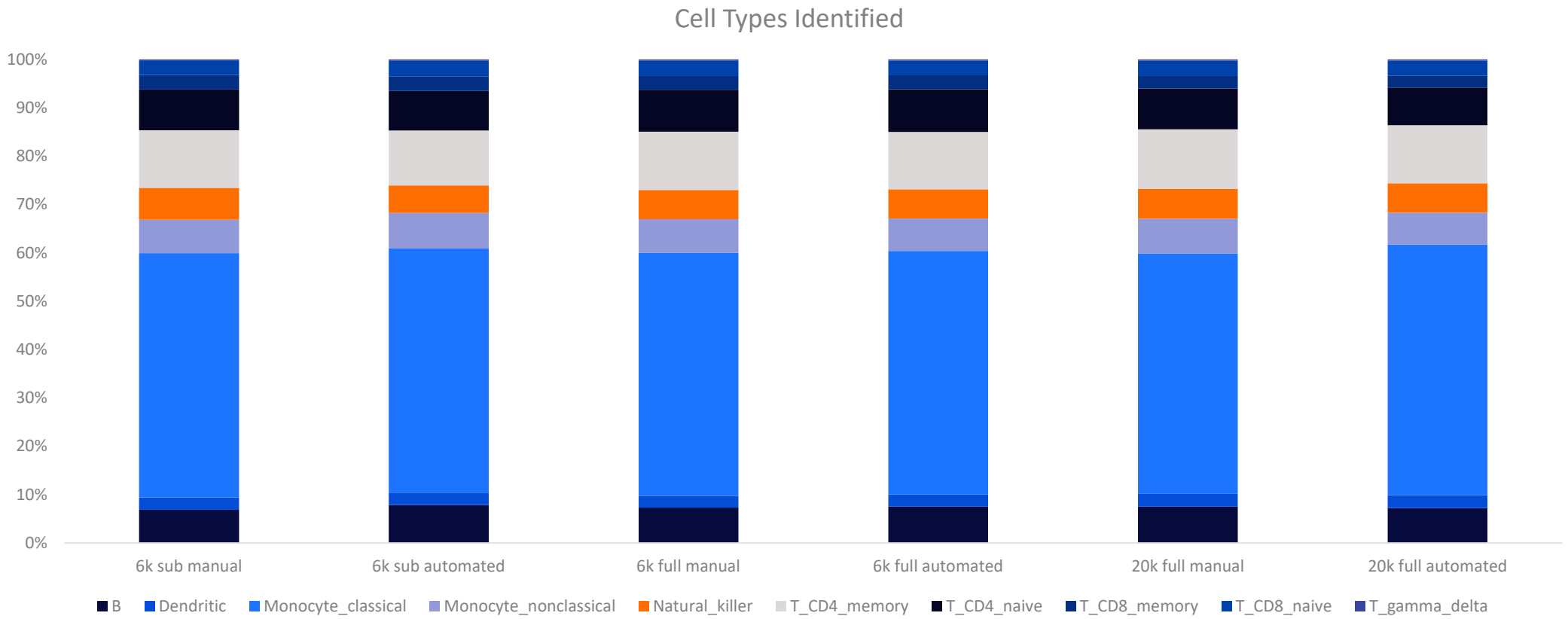



**Figure legend:** Similar percentages of cell types were identified with automated libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW compared to manual bench controls.

# WTA NGS data from single cells in PBMC samples

## Cell type identification

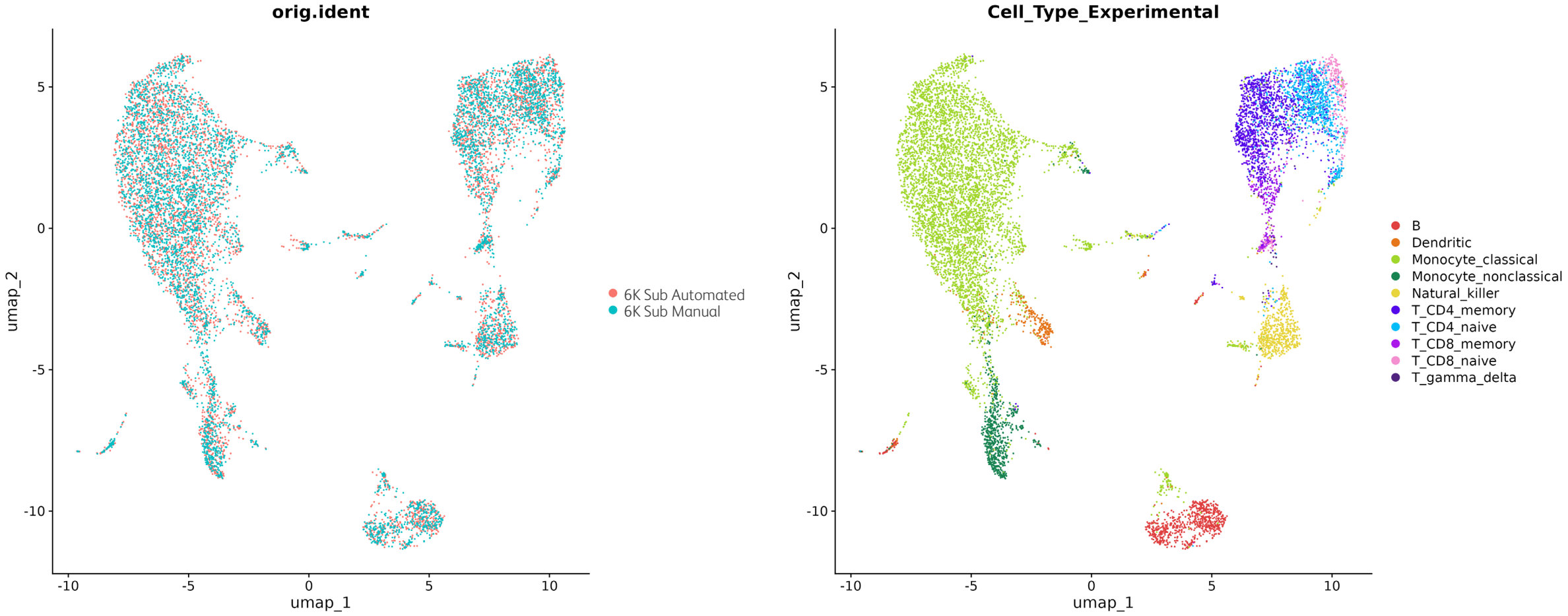



**Figure legend:** UMAP of 6K subsamples beads shows cell types were identified and no batch effects between manual and automated library prep.

# WTA NGS data from single cells in PBMC samples

## Cell type identification

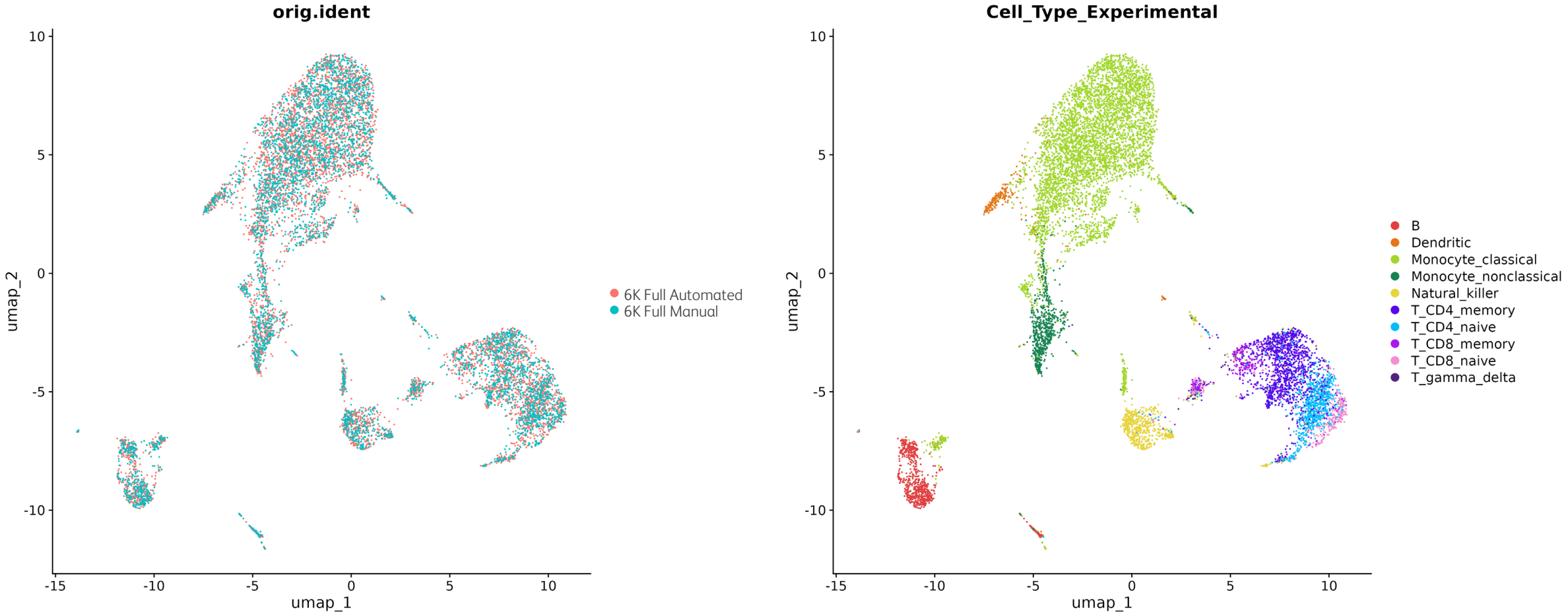



**Figure legend:** UMAP of 6K full beads shows cell types were identified and no batch effects between manual and automated library prep.

# WTA NGS data from single cells in PBMC samples

## Cell type identification

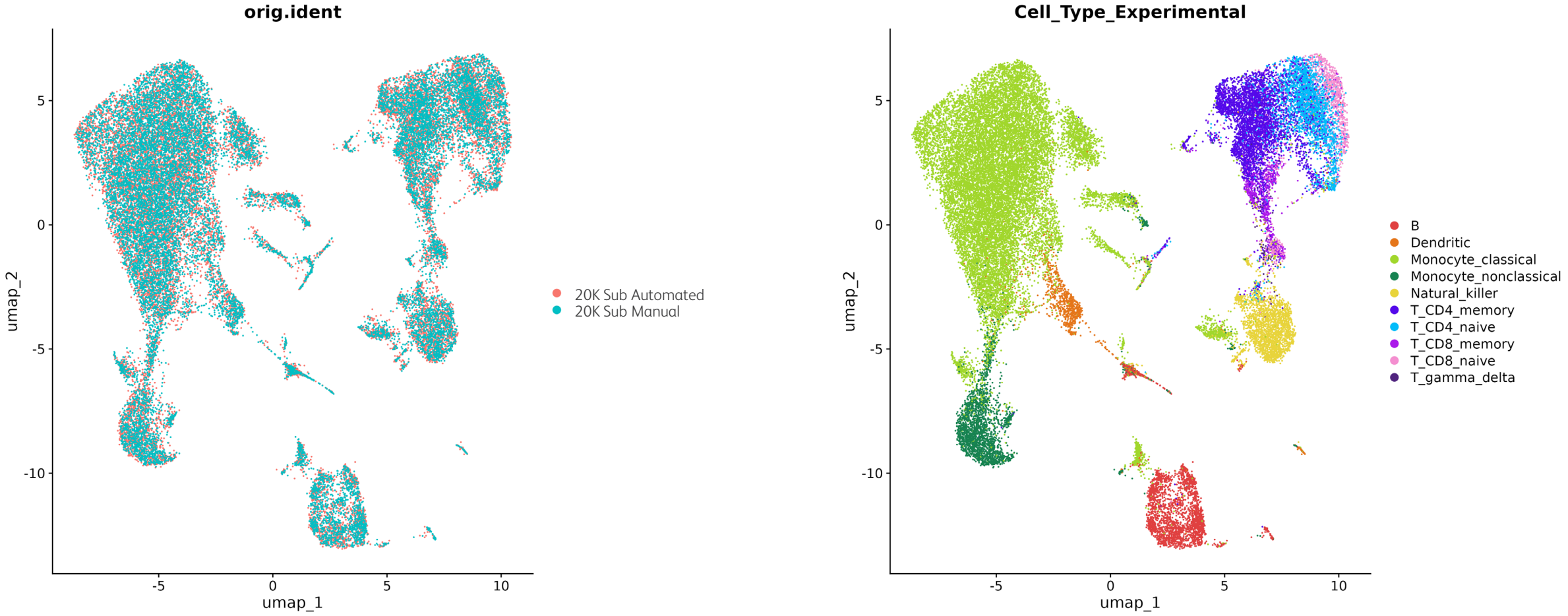



**Figure legend:** UMAP of 20K full beads shows cell types were identified and no batch effects between manual and automated library prep.

# WTA NGS data from single cells in PBMC samples

## Reproducibility across instruments

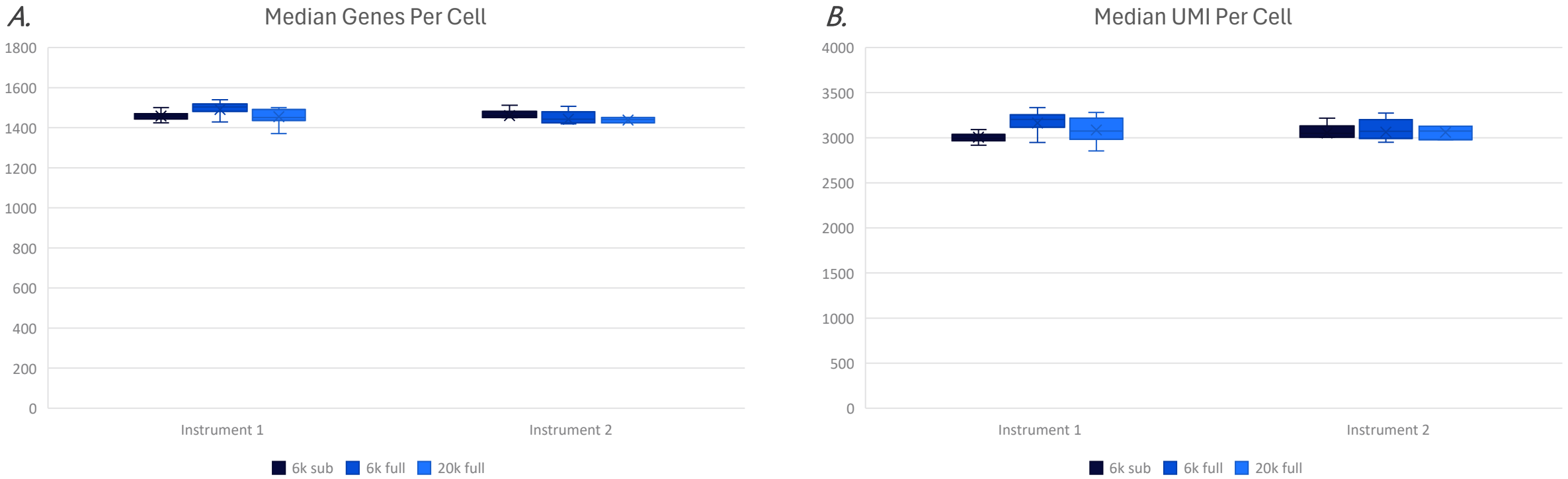



**Figure legend:** Three runs of 18 libraries (six each of 6K subsampled beads, 6K full sampled beads and 20K full sampled beads from the same pool of cellular transcripts captured on the BD Rhapsody™ Enhanced Cell Capture Beads) were prepared on the Hamilton™ Microlab™ NGS STAR ARW 1 and 2. Shown are sequenced libraries of 15 libraries total for 6K sub and 6K full each and nine libraries total for 20K full sampled beads. After sequencing, all automated and manual libraries were down sampled to between 7,600–8,000 raw reads per cell. **A)** Median genes per cell generated from libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW 1 are comparable to Hamilton™ Microlab™ NGS STAR ARW 2. **B)** Median UMI counts per cell generated on the automated system are comparable across different instruments.

# WTA NGS data from single cells in PBMC samples

## Reproducibility across instruments

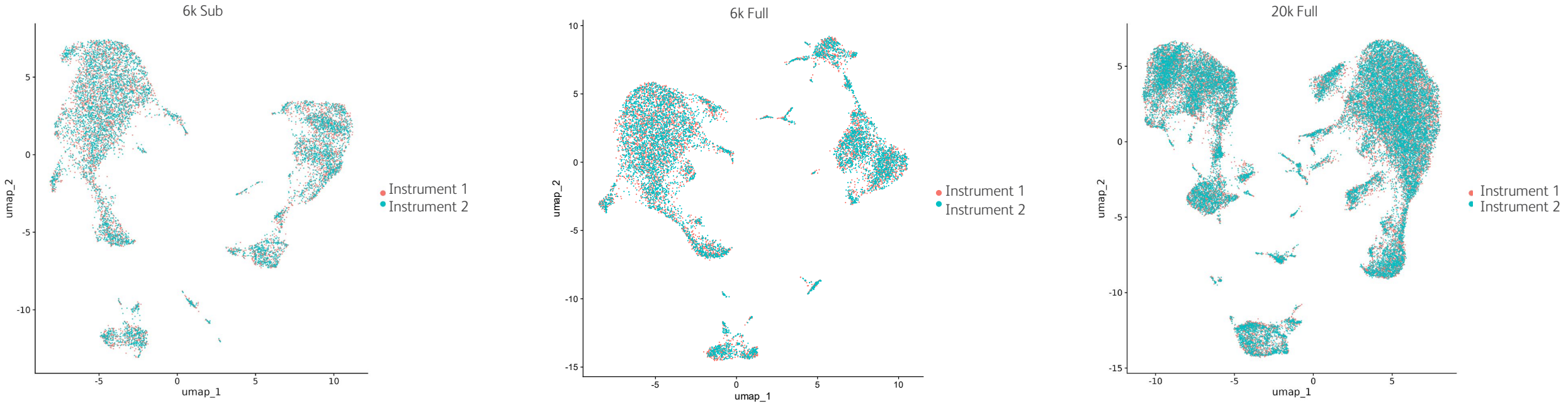
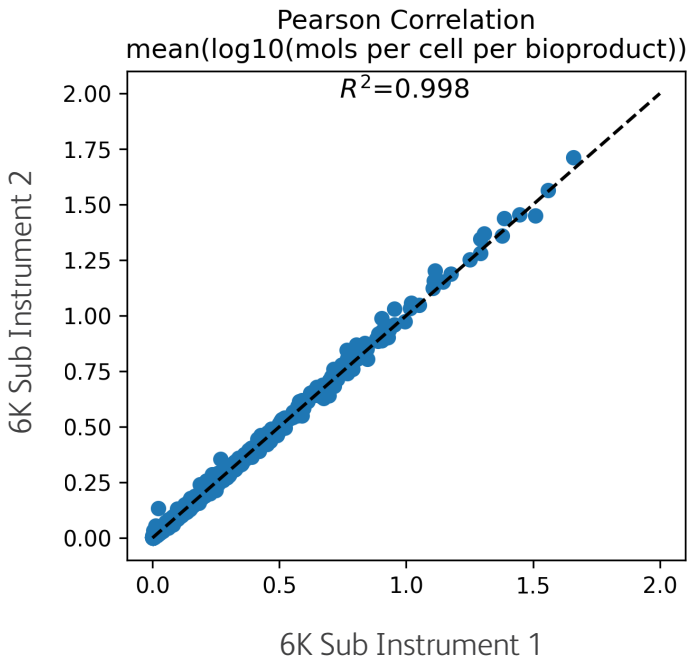
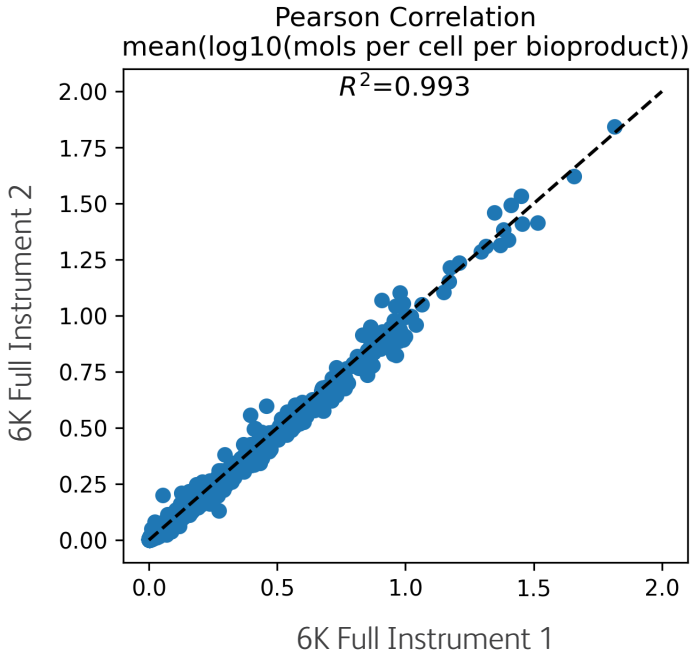



**Figure legend:** Wells across instruments with the same cell input were compared on UMAP and no batch effects were observed between Hamilton™ Microlab™ NGS STAR ARW 1 and Hamilton™ Microlab™ NGS STAR ARW 2.

# WTA NGS data from single cells in PBMC samples

## Reproducibility across instruments



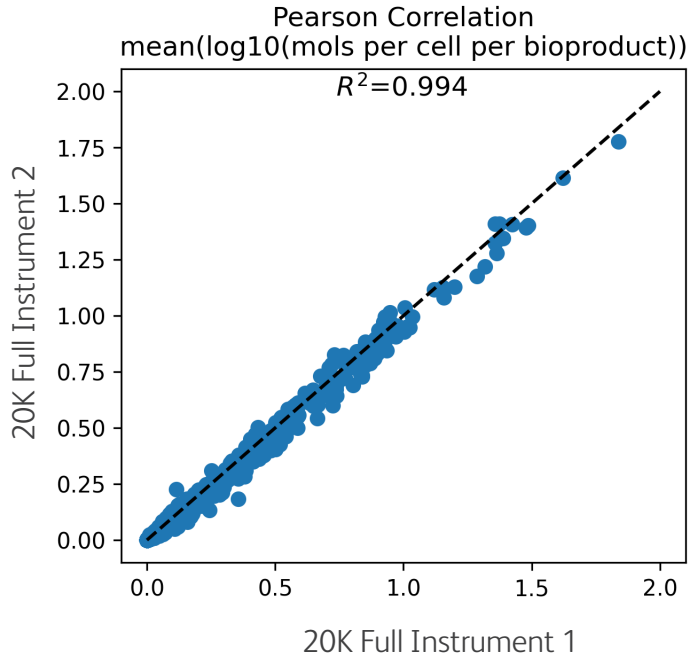




**Figure legend:** Wells across instruments with the same cell input were compared on a gene expression correlation and the $R^2$ is greater than 0.99, indicating there was no difference between Hamilton™ Microlab™ NGS STAR ARW 1 and Hamilton™ Microlab™ NGS STAR ARW 2.

# 100,000 cell input

# 100,000 cell input experimental design for automated library prep:

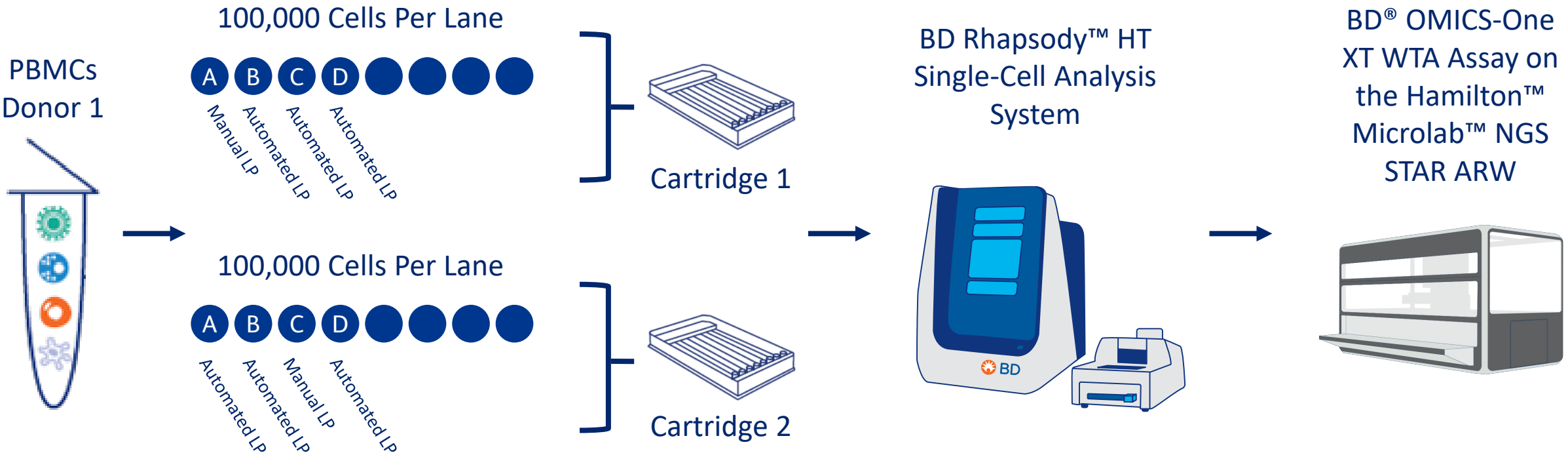



**Figure legend:** 100,000 PBMCs each were loaded into Lanes A-D on two BD Rhapsody™ HT Xpress Cartridge, for a total of 8 lanes. After retrieval, approximately 68,000 to 75,000 cells per lane were retrieved for library preparation. Cartridge 1 (lanes B, C, D) were set for automated library preparation for Run 1 and Cartridge 2 (lanes B, C, D) were set for automated library preparation for Run 2. Lane A (Cartridge 1) and lane A (Cartridge 2) were prepared manually on bench.

# BD Rhapsody™ Scanner metrics

| Sample (Cartridge-Lane) | 1-A | 1-B | 1-C | 1-D | 2-A | 2-B | 2-C | 2-D |
|---|---|---|---|---|---|---|---|---|
| Number of wells with viable cells and a bead | 71242 | 71651 | 72884 | 73014 | 74932 | 68851 | 73459 | 74473 |
| Number of viable cells captured in wells with a bead | 84391 | 84862 | 86916 | 87097 | 89335 | 81561 | 86960 | 88723 |
| Cell multiplet rate | 16.7% | 16.7% | 17.4% | 17.5% | 17.4% | 16.7% | 16.7% | 17.3% |
| Cell retention rate | 99.4% | 98.9% | 98.3% | 99.5% | 97.3% | 95.2% | 96.4% | 97.9% |
| **Number of retrieved beads with 1+ viable cells** | **71028** | **71436** | **72665** | **72795** | **74707** | **68644** | **73239** | **74250** |
| Run | Manual | Run 1 | Run 1 | Run 1 | Run 2 | Run 2 | Manual | Run 2 |
| Library Prep Location | Ctrl-1 | E4 | A4 | B4 | A4 | B4 | Ctrl-2 | E4 |

**Figure legend:** 100,000 PBMCs each were loaded into Lanes A-D on two BD Rhapsody™ HT Xpress Cartridge, for a total of 8 lanes. After retrieval, approximately 68,000 to 75,000 cells per lane were retrieved for library preparation. Cartridge 1 (lanes B, C, D) were set for automated library preparation for Run 1 and Cartridge 2 (lanes A, B, D) were set for automated library preparation for Run 2. Lane A (Cartridge 1) and lane C (Cartridge 2) were prepared manually on bench.

# WTA NGS data from single cells in PBMC samples

## Library DNA yield and QC metrics

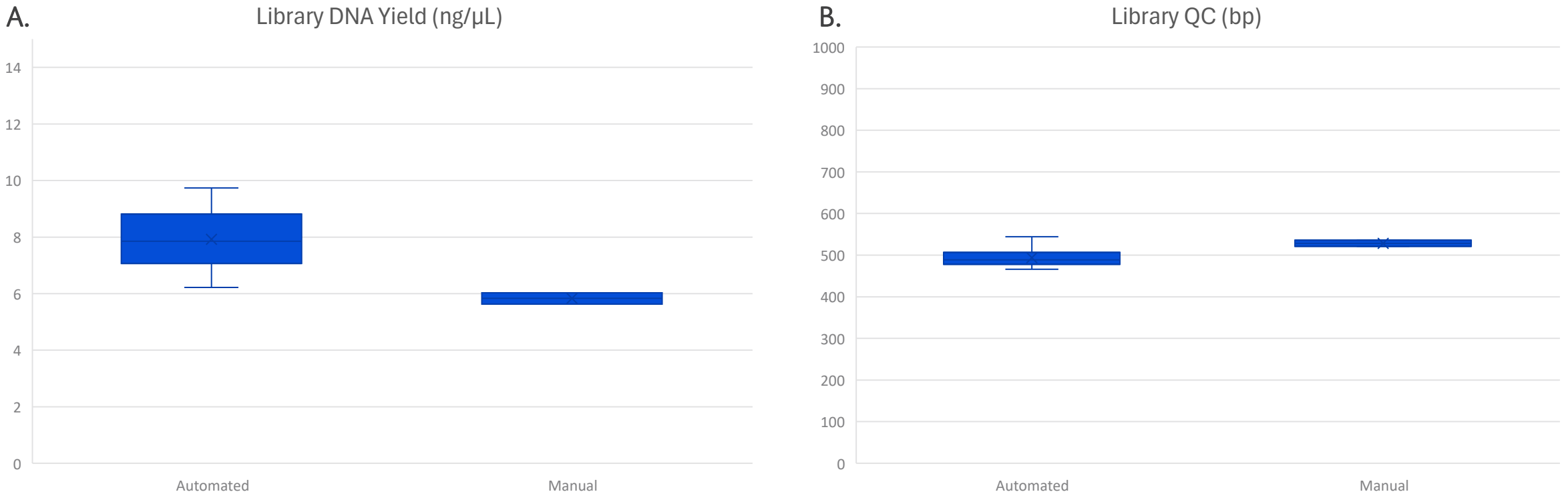



**Figure legend:** Two runs of 3 libraries each of 100K full sampled beads of cell-captured BD Rhapsody™ Enhanced Cell Capture Beads were prepared on the Hamilton™ Microlab™ NGS STAR ARW for a total of 6 automated libraries along with two manual bench controls. **A)** Final quality control of indexed libraries show automated libraries were comparable to manual bench controls for Qubit concentration (ng/µL). **B)** Final quality control by TapeStation analysis shows similar average bp size distribution between 200–1,000bp.

# WTA NGS data from single cells in PBMC samples

## Final library QC TapeStation traces

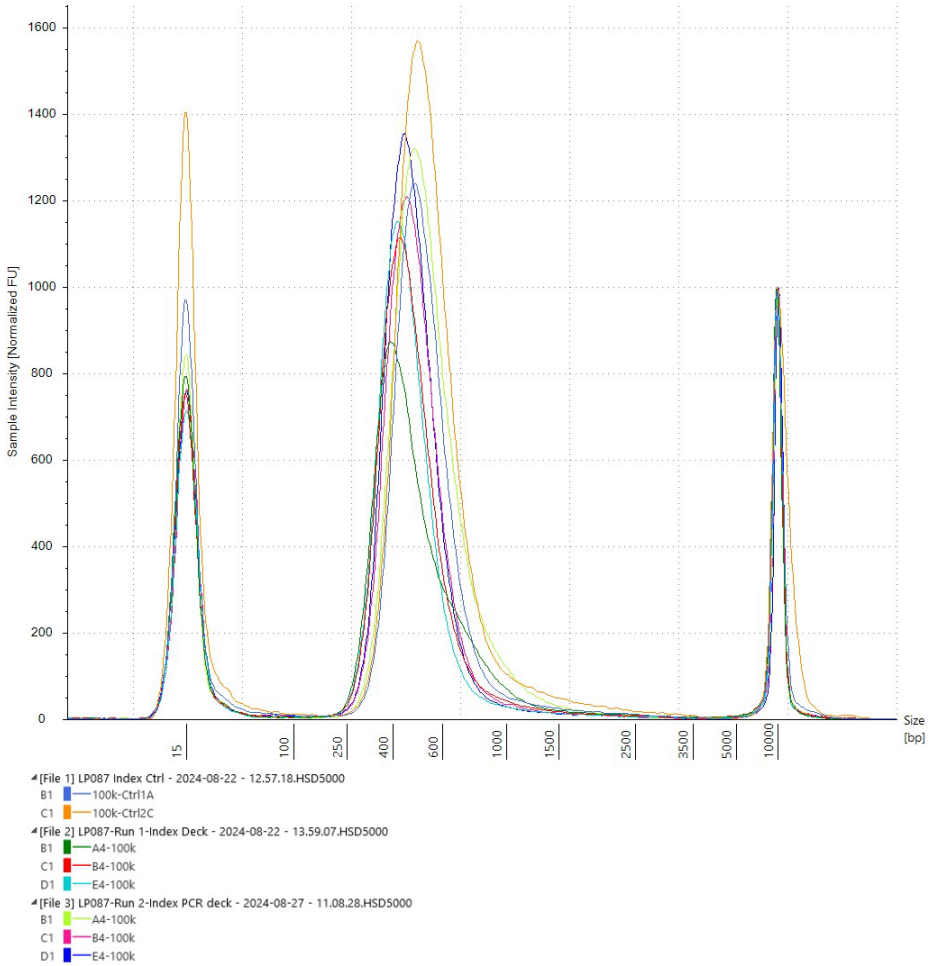



**Figure legend:** At the end of Index PCR purification, libraries were quantified via Qubit and normalized to 1 ng/µL prior to running on TapeStation for size analysis. All libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW were comparable in bp size distribution against manual bench controls.

# WTA NGS data from single cells in PBMC samples

## Sequencing QC metrics

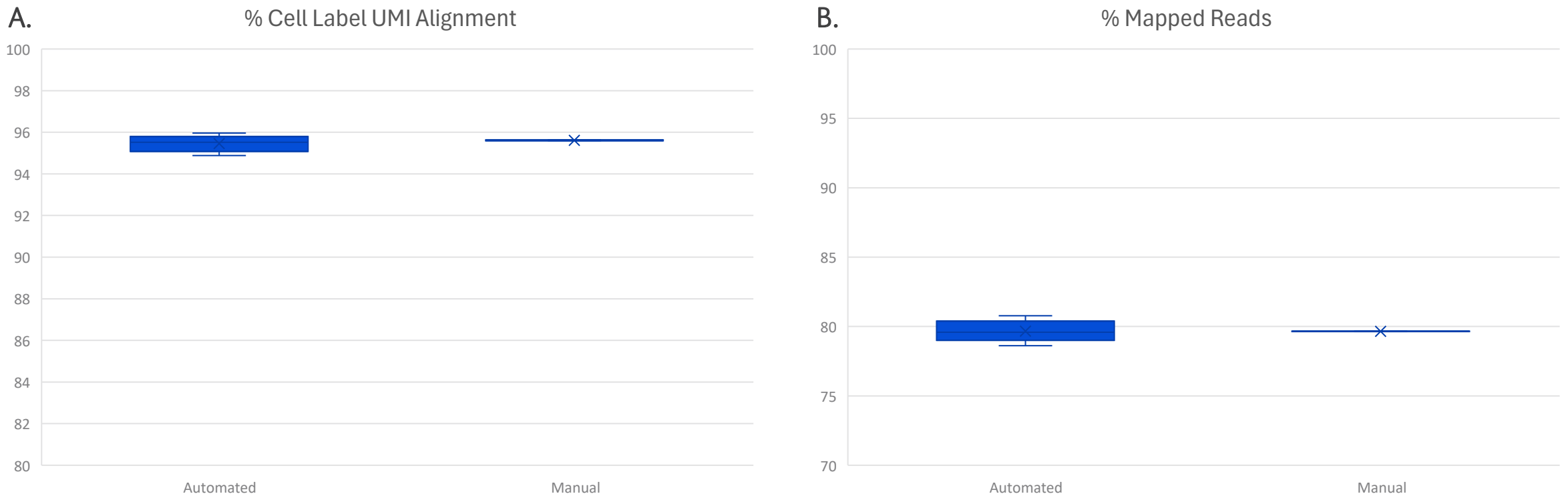



**Figure legend:** Two runs of 3 libraries each of 100K full sampled beads of cell-captured BD Rhapsody™ Enhanced Cell Capture Beads were prepared on the Hamilton™ Microlab™ NGS STAR ARW for a total of 6 automated libraries along with two manual bench controls. After sequencing, all automated and manual libraries were down sampled to approximately 10,500 raw reads per cell. **A)** The percentage of reads identified with a cell label UMI and align uniquely generated from libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW are comparable to manually prepped libraries. **B)** Percentage of mapped reads that align to a known gene generated on the automated system are like those libraries generated manually.

# WTA NGS data from single cells in PBMC samples

## Cell retrieved by sequencing

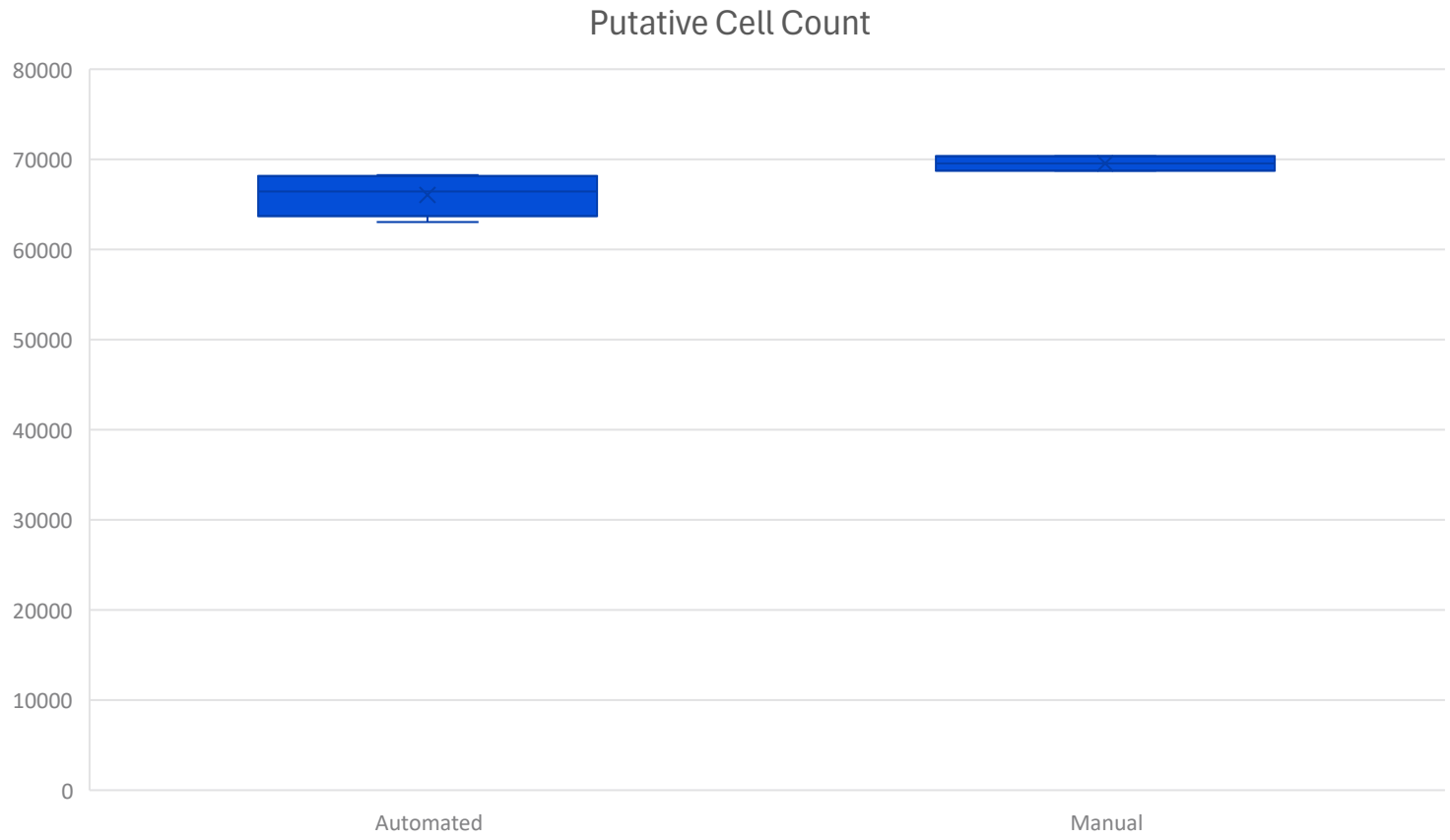



**Figure legend:** Putative cell detection, automated library preparation vs. manual library preparation. The expected cell inputs of 100,000 cells were approximately detected.

# WTA NGS data from single cells in PBMC samples

## Assay sensitivity

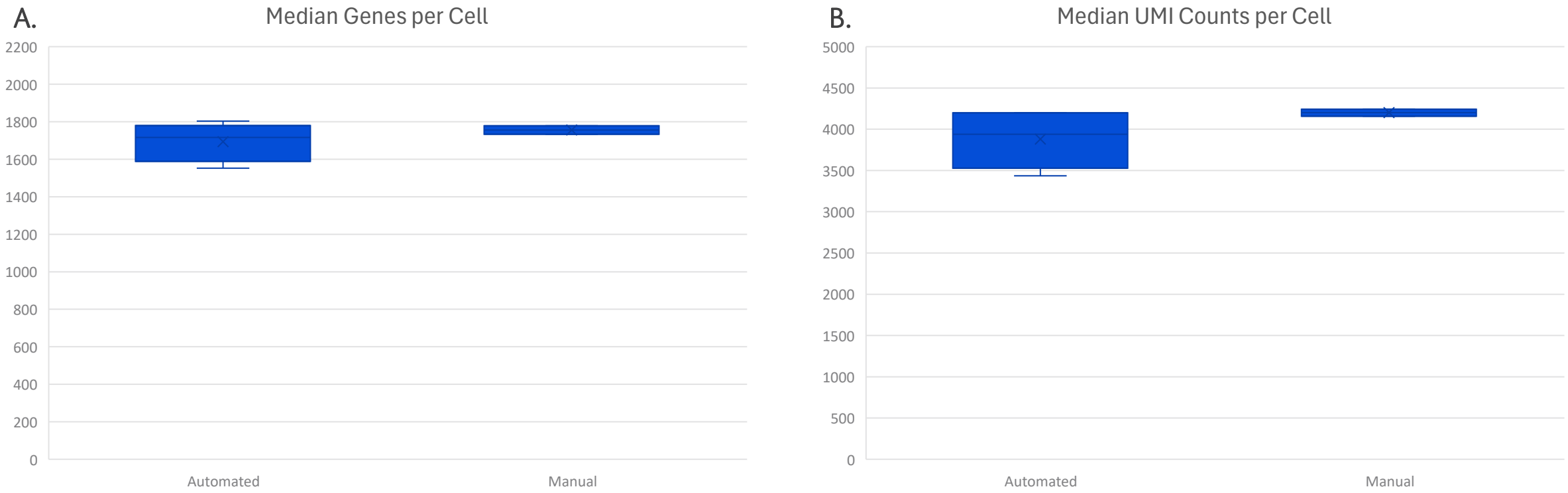



**Figure legend:** Two runs of 3 libraries each of 100K full sampled beads of cell-captured BD Rhapsody™ Enhanced Cell Capture Beads were prepared on the Hamilton™ Microlab™ NGS STAR ARW for a total of 6 automated libraries along with two manual bench controls. After sequencing, all automated and manual libraries were down sampled to approximately 10,500 raw reads per cell. **A)** Median genes per cell generated from libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW are comparable to manually prepped libraries. **B)** Median UMI counts per cell generated on the automated system are like those libraries generated manually.

# WTA NGS data from single cells in PBMC samples

## Assay sensitivity

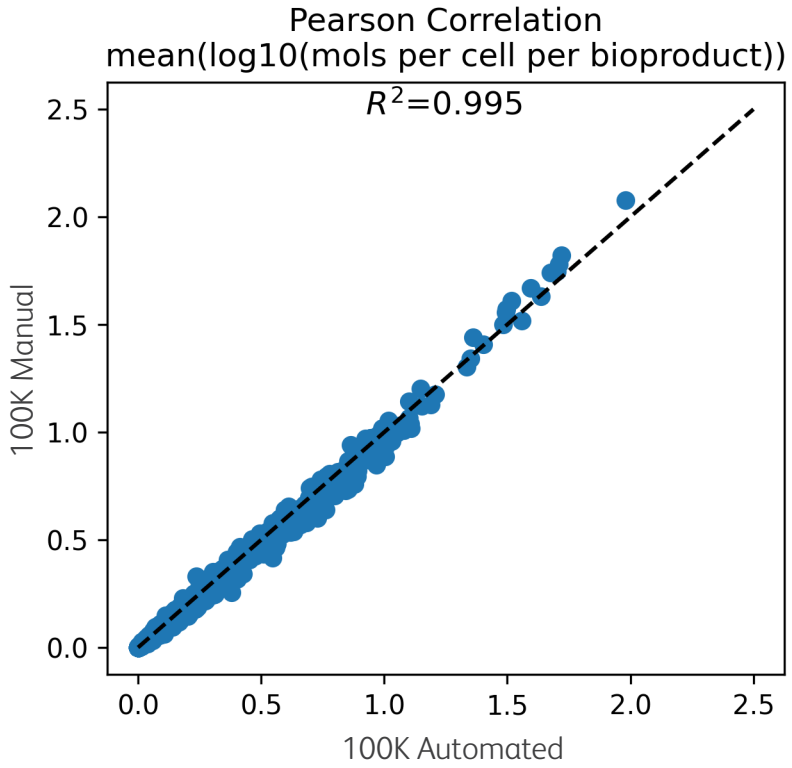



**Figure legend:** Gene expression correlation plot 100K full sampled beads show a correlation greater than 0.99 when automated library prepped samples are compared to manually prepared samples. Here all genes containing greater than 50 total molecules are analyzed, each library contains approximately 23,360 genes when sequenced at 10,500 raw reads per cell.

# WTA NGS data from single cells in PBMC samples

## Cell type identification

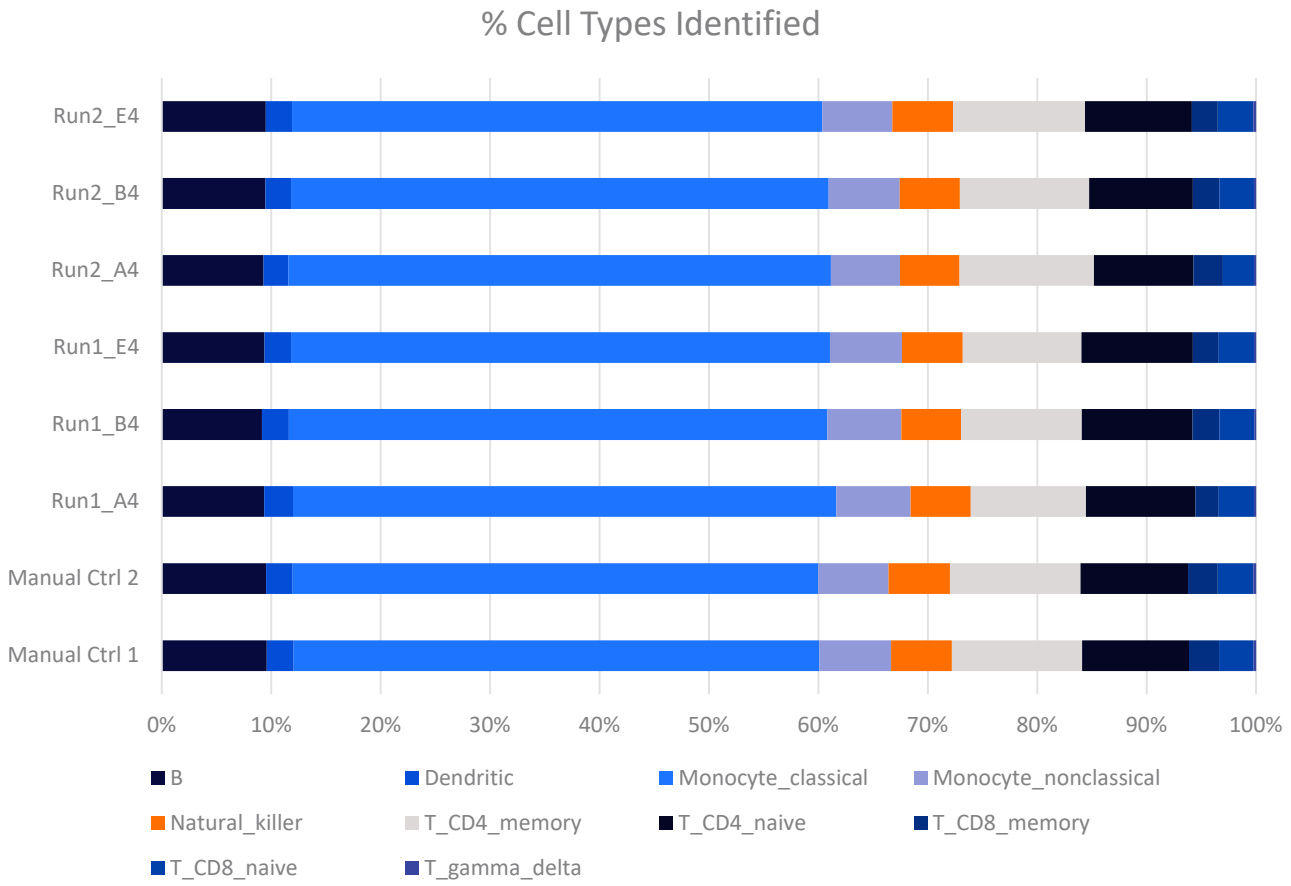
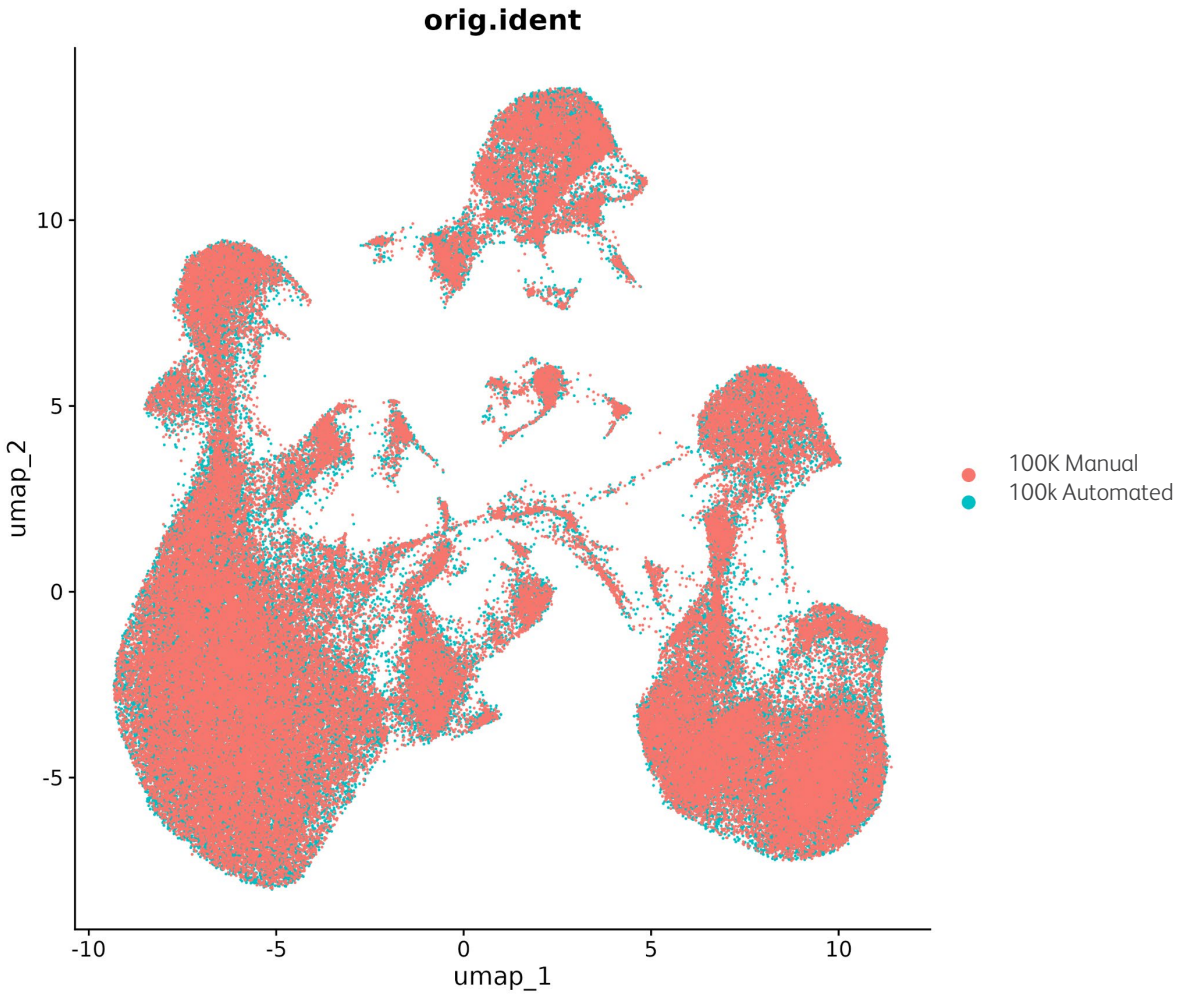



**Figure legend:** Similar percentages of cell types were identified with automated libraries prepped on the Hamilton™ Microlab™ NGS STAR ARW compared to manual bench controls.

# WTA NGS data from single cells in PBMC samples

## Cell type identification



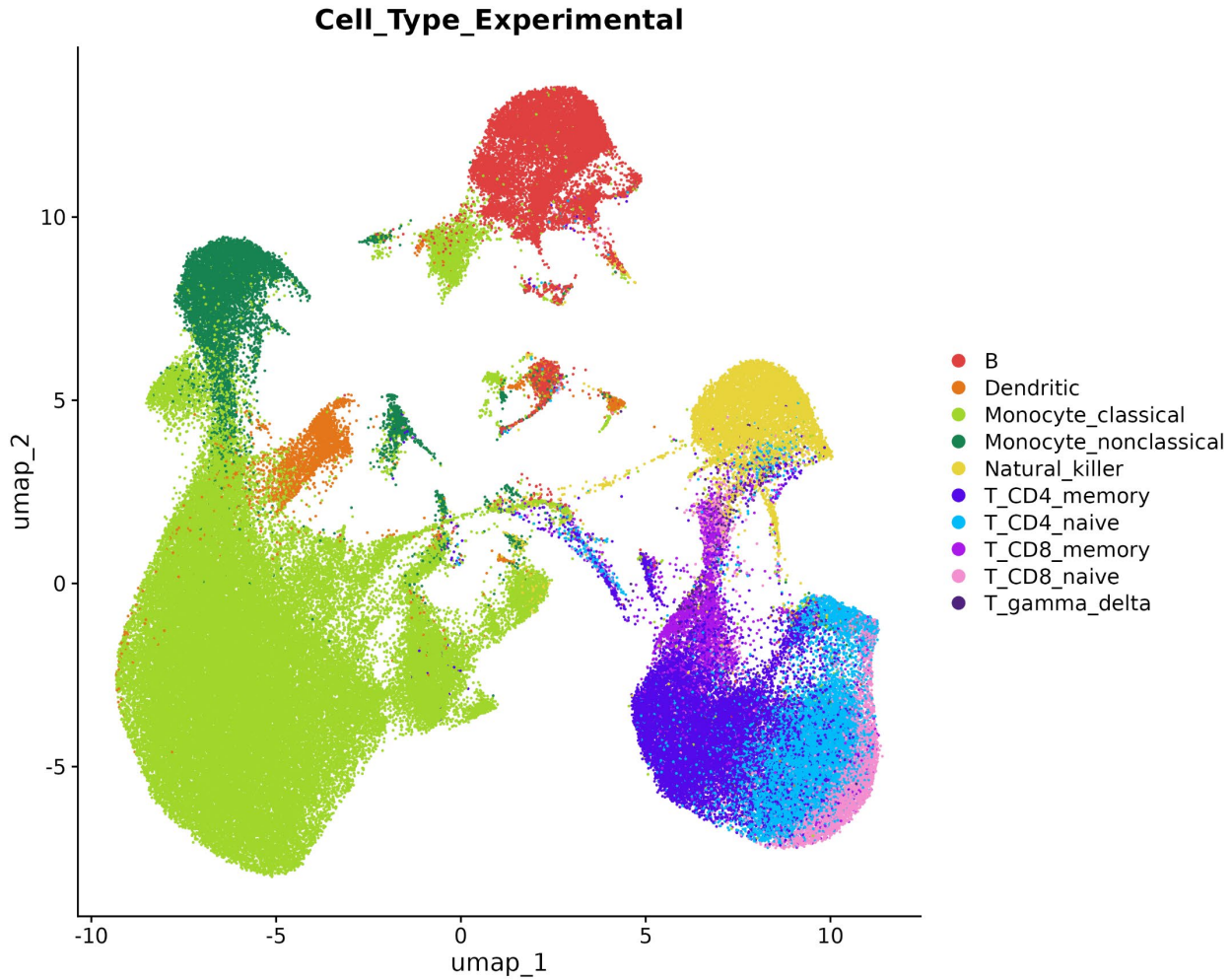




**Figure legend:** UMAP of 100K full beads shows cell types were identified, and no batch effects were seen between manual and automated library prep.

# Hamilton™ Microlab™ NGS STAR ARW pricing

# NGS STAR pricing (NA Territory)
## with MOA (MPH and ODTC add-on) deck configuration


| Base Items | List Price |
|---|---|
| NGS STAR with 8x 1 mL Channels and iSWAP (MOA Deck) | $160,055 |
| NGS STAR with 8x 1mL Channels, 96 MPH, and iSWAP (MOA Deck) | $202,233 |

| Options | List Price |
|---|---|
| 96 MPH Upgrade | $42,178 |
| On-Deck Thermal Cycler for NGS STAR (MOA Deck) | $16,022 |
| On-Deck Thermal Cycler for NGS STAR, 96 MPH (MOA Deck) | $16,022 |



For Research Use Only. Not for use in diagnostic or therapeutic procedures.

Pricing is current as of August 2024.

# Other required materials

## Ordered separately

| Manufacturer | Cat. No. | Description |
|---|---|---|
| Hamilton | 194051 | 60-mL reagent reservoir |
| Hamilton | 235948 | 50-µL filtered tips |
| Hamilton | 235903 | 300-µL filtered tips |
| Hamilton | 235905 | 1,000-µL filtered tips |
| Beckman Coulter | A63880 | Agencourt AMPure XP Magnetic Beads |
| Fisher Scientific | BP2818100 | Absolute ethyl alcohol |
| Invitrogen | 10-977-015 | Nuclease-free water |
| Bio-Rad | HSP9601 | Hard-Shell™ 96 Well PCR Plates<br>(low profile, thin wall, skirted, white/clear) |
| Thermo Fisher Scientific | AB0859 | Abgene™ 96 Well 0.8 mL Polypropylene DeepWell™ Storage Plate (midi plate) |

# Support

# Support

Supporting you with your BD® OMICS-One XT Automation Kit experiments

## Getting help from single-cell experts

Visit us at scomix.bd.com to view our resource library, learning center and FAQs or to file a ticket for help or contact your local BD application specialist

## In need of technical support

BD technical service support is here to help with assay support. Contact us **by phone** at 877.232.8995, prompt 2, then prompt 2, 6:30 a.m. to 5 p.m. PT or by **email** at ResearchApplications@bd.com.

## Ordering BD® OMICS-One XT Assay Kits

To request a quote or place an order, visit bdbiosciences.com or contact your local BD sales representative

# Support

Supporting you with your Hamilton™ Microlab™ NGS STAR ARW (NA Territory)

## Getting help from automation experts

Hamilton technical support is available for your automation questions. Contact **by phone** at 1.775.858.3000, **by email** at tech@hamiltoncompany.com or contact your local Hamilton application specialist

## In need of service support

Hamilton service support is here to help with instrument support. Contact **by phone** at 1.800.527.5269 or by **email** at roboticservice@hamiltoncompany.com.

## Ordering the Hamilton™ Microlab™ NGS STAR ARW

To request a quote or place and order, **visit** hamiltoncompany.com/robotics, **by phone** at 1.800.646.2871, **by email** at roboticsales@hamiltoncompany.com or contact your local Hamilton sales representative

BD flow cytometers are Class 1 Laser Products.

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