Compatibility of BD Rhapsody™ System Single-Cell Libraries with the Ultima Genomics UG 100® Sequencing Platform

Introduction

Advances in both single-cell capture and next-generation sequencing are converging to enable multiomic studies at unprecedented scale. The BD Rhapsody™ Single-Cell Analysis System employs microwell-based technology to efficiently isolate cells and barcode RNA and protein content, while the Ultima Genomics UG 100® Sequencing Platform delivers high sequencing throughput at substantially reduced cost. Together, these platforms offer a workflow that makes large-scale single-cell experiments economically feasible, expanding opportunities for studies with the statistical power and sample depth required for meaningful research insights

However, as new sequencing platforms emerge, assessment of their compatibility and data consistency with earlier studies and established single-cell library formats remains essential. In this technical note, we compare sequencing quality, cell-level metrics and data reproducibility between the Ultima UG 100® Platform and other sequencing platforms. Our analysis provides a framework for researchers considering the Ultima platform to support million-cell BD Rhapsody™ System studies with the scale and depth demanded by translational research.

Methods

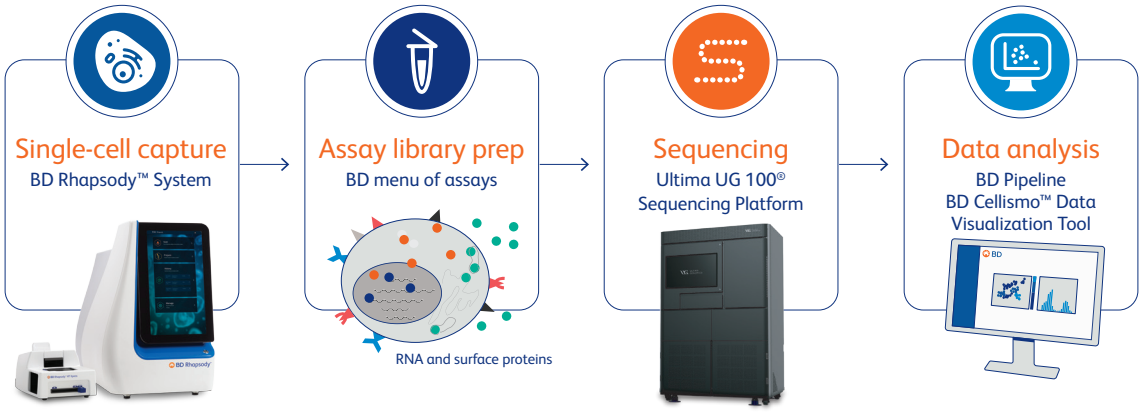

Figure 1. Ultima UG 100® Platform sequencing is seamlessly integrated into the existing BD Rhapsody™ System workflow.

The BD Rhapsody™ Whole Transcriptome Analysis (WTA) Assay, BD® AbSeq Antibody-Oligos and BD® Single-Cell Multiplexing Kit (SMK) were evaluated for compatibility with the Ultima UG 100® Sequencing Platform. Using Ultima's Indexing PCR Library Preparation Protocol (Rev. 02, 2025), Illumina™-compatible BD Rhapsody™ System libraries were converted into Ultima-compatible libraries and sequenced. Converted libraries were benchmarked against internal BD datasets previously generated on the Element AVITI™ Sequencer, and analyses of read quality, cell recovery, UMI/molecule counts and clustering performance demonstrated strong concordance across platforms. These findings support the Ultima UG 100® Platform as a viable alternative NGS readout for BD Rhapsody™ System single-cell workflows.

ULTIMA GENOMICS

BD

Results

The sequencing outcomes demonstrated strong interoperability between the platforms and yielded robust, reproducible data for every library configuration tested.

WTA + AbSeq + Sample Tag (ST) profile and quality metrics

Library type	WTA	AbSeq	Sample Tag
Putative cell count	10.764	10.764	10.764
Raw reads per cell	564,924	267,415	218.768
% Sequencing saturation	90	95	N/A
Median molecules per cell	4,223	19,311	N/A
Median bioproducts per cell	1,530	120	N/A
% Reads assigned to cell labels	100	100	100
% Reads filtered out	19	1	14
% Q30 bases in filtered R2	54	85	100
% Aligned to transcriptome/AbSeq	67	100	100

Table 1. Key performance metrics for WTA, AbSeq and sample multiplexing libraries sequenced on the platform, highlighting consistent cell recovery, high saturation, strong sensitivity and the platform's capacity to generate billions of reads per run—as reflected by the hundreds of thousands of reads produced per cell.

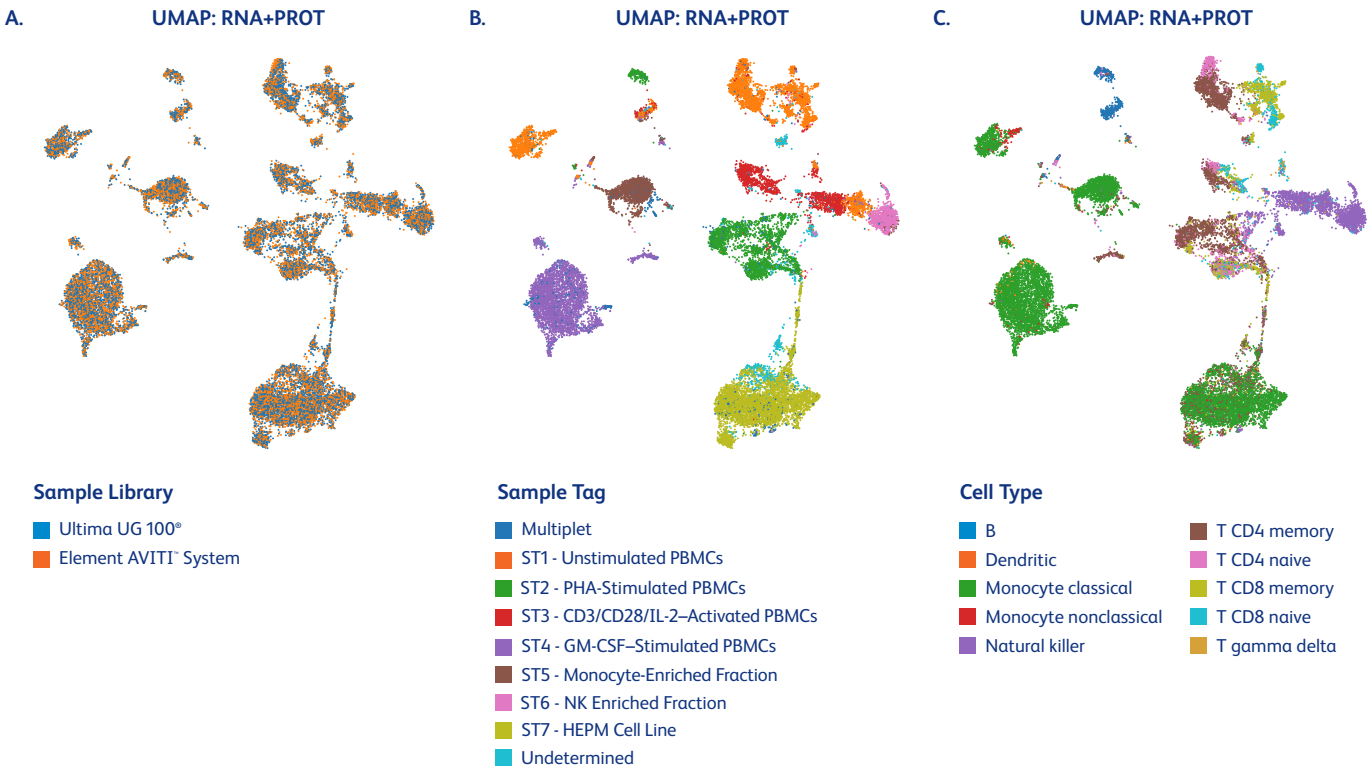

Figure 2. Multimodal UMAP analysis demonstrates consistent performance across sequencing platforms and reliable sample and cell-type resolution using the BD Rhapsody™ System's WTA + AbSeq + ST workflow. (A) Integrated RNA + protein profiles generated from samples sequenced on the Ultima UG 100® Platform and the Element AVITI™ System align closely, illustrating strong cross-platform concordance with no observable batch effect. **(B)** Multiplexed sample tags enable clear differentiation of unstimulated, stimulated and enriched PBMC samples, while **(C)** multimodal cell type annotations reveal well-resolved immune populations, supporting confident downstream interpretation in diverse single-cell applications.

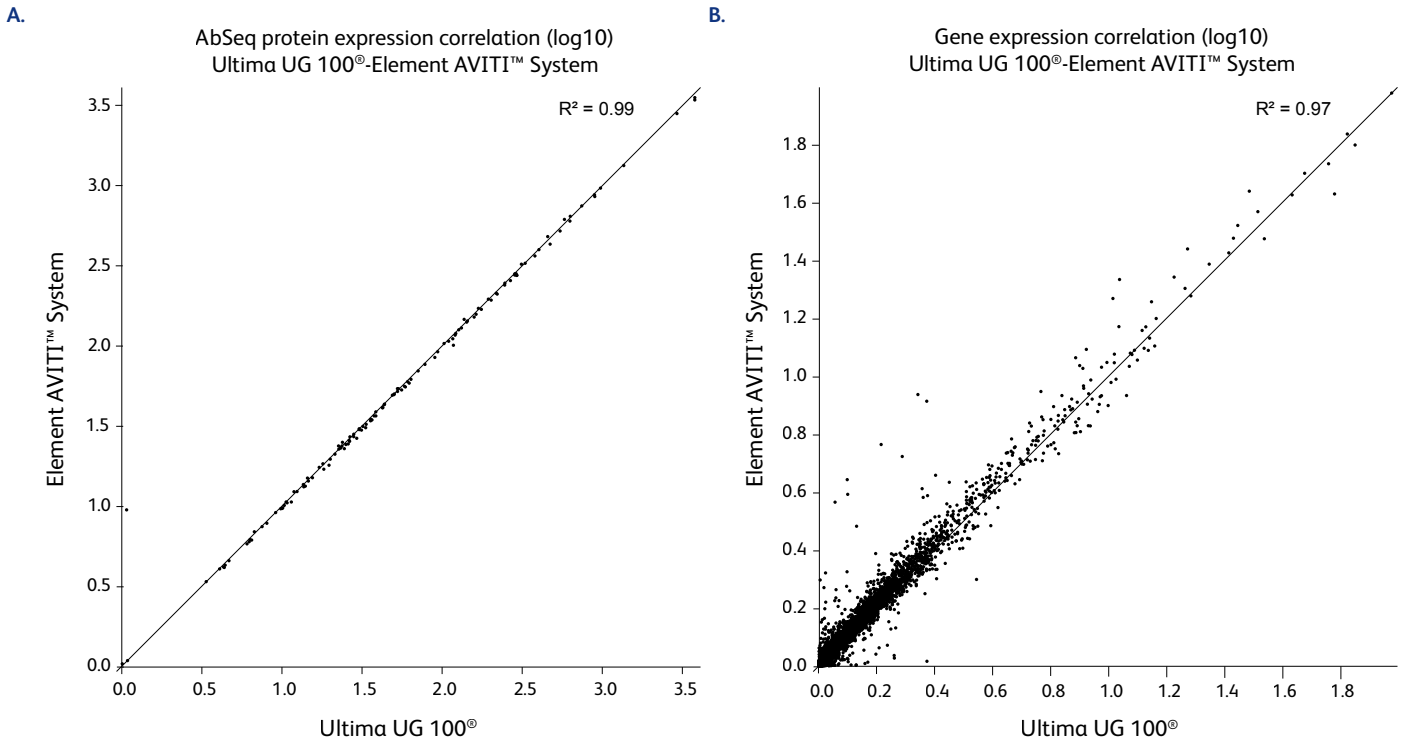

Figure 3. The BD Rhapsody™ System's multimodal single-cell workflow delivers consistent, high-quality protein and mRNA measurements across sequencing platforms. (A) AbSeq correlation analysis demonstrates tightly aligned protein expression signals between datasets sequenced on the Ultima UG 100® Platform and the Element AVITI™ System, highlighting reliable detection of surface marker profiles across platforms. **(B)** mRNA correlation analysis shows similarly strong agreement in gene expression measurements, supporting confident interpretation of transcriptomic data regardless of sequencing system. Together, these results illustrate how the BD Rhapsody™ System's integrated WTA+AbSeq workflow provides stable, reproducible insights that enable clear biological discovery across diverse sequencing environments.

Conclusions

These results highlight the strong compatibility of BD Rhapsody™ System WTA, AbSeq and sample multiplexing libraries with the Ultima UG 100® Sequencing Platform and demonstrate how the BD Rhapsody™ System fits seamlessly into emerging high-throughput sequencing ecosystems. By delivering consistent single-cell resolution across RNA, protein and Sample Tag modalities—with no observable batch effects and highly reproducible expression profiles—the Ultima UG 100® Platform provides a compelling option for laboratories looking to scale their BD Rhapsody™ System workflows to larger studies, deeper profiling or expanded assay menus.

As multiomic experiments grow in size and complexity, this interoperability gives researchers more flexibility in how they design and execute their studies. The combination of the proven BD single-cell barcoding architecture with Ultima's high-capacity sequencing technology enables streamlined, cost-effective data generation without compromising quality, helping accelerate discovery across immunology, oncology and translational applications.

BD Rhapsody™ System users can confidently adopt the Ultima UG 100® Platform as an alternative sequencing solution—empowering high resolution science at new scales.

Converting BD Rhapsody™ System libraries for use on the Ultima UG 100® Sequencing Platform

1. Prepare standard BD Rhapsody™ System libraries (e.g., WTA, AbSeq, Sample Tag).
2. Quantify the library using the Qubit™ dsDNA High Sensitivity Assay.
3. Set up the UG Indexing PCR using compatible primers according to the UG Indexing PCR Library Preparation Protocol for Solaris Flex (D1001055).

Reagent	IDT Part Number	Storage	Reaction Size	Container
xGen™ UG-tR1 Indexing Primer v2 for Ultima, P1	10028412	–20 °C	1 rxn x 96 wells	96-well plate
xGen™ UG-tR1 Indexing Primer v2 for Ultima, P2	10028413	–20 °C	1 rxn x 96 wells	96-well plate
xGen™ UG-tR1 Indexing Primer v2 for Ultima, P3	10028414	–20 °C	1 rxn x 96 wells	96-well plate
xGen™ UG-tR1 Indexing Primer v2 for Ultima, P4	10028415	–20 °C	1 rxn x 96 wells	96-well plate
xGen™ UG-tR2 Universal Primer v2 for Ultima	10028399	–20 °C	96 reactions	1 tube

4. Run the UG-recommended PCR cycling program.
5. Purify the PCR product with AMPure beads using the application specific bead ratio (e.g., 0.9× for WTA/AbSeq/ST).
6. Perform final QC using the Agilent Bioanalyzer with DNA High Sensitivity Reagent Kit and Qubit™ Fluorometer.
7. Sequence on the Ultima UG 100® Platform using the recommended loading concentration (600 µL at 600–800 pM).

References and Resources

1. Ultima Genomics conversion protocol guide: https://www.ultimagenomics.com/resources/?category=protocols
2. Ultima Genomics Solaris™ Flex: https://www.ultimagenomics.com/products/solaris-free-and-solaris-flex/
3. IDT xGen™ PCR-Free Adapters for Ultima Genomics conversion: https://www.idtdna.com/pages/products/next-generation-sequencing/workflow/xgen-ngs-library-preparation/ngs-adapters-indexing-primers/xgen-for-ultima-genomics

BD Life Sciences, Milpitas, CA 95035, U.S.

bdbiosciences.com