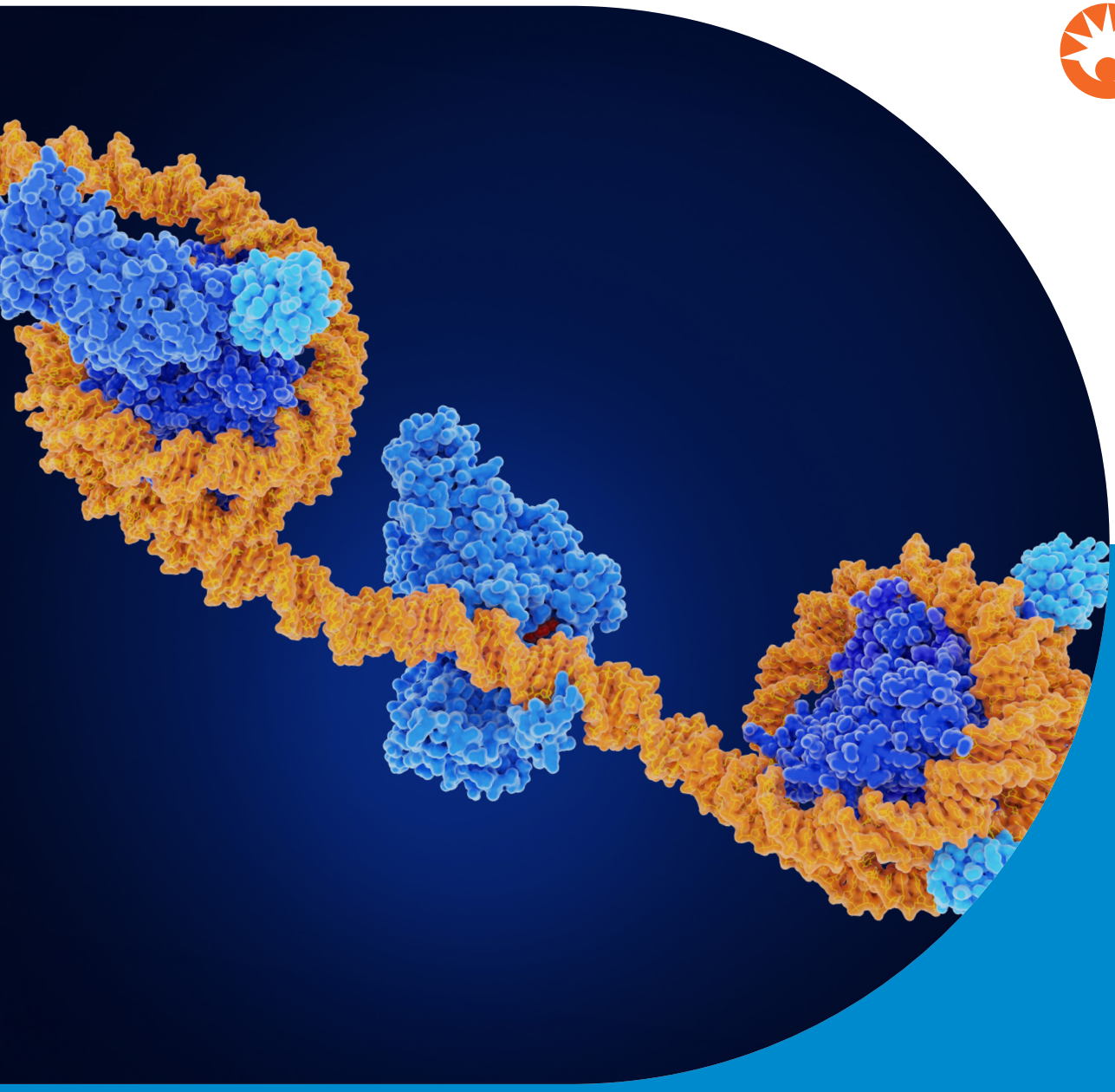

BD Rhapsody™ ATAC-Seq Assay

Genome-wide epigenomic and transcriptomic analysis on the same cell

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Uncover new regulatory connections shaping cellular identity and function

Mapping open chromatin regions at the single-cell level elucidates cell-to-cell variability in regulatory landscapes that drives cell fate decisions and responses to stimuli. Assay for transposase-accessible chromatin using sequencing (ATAC-seq) excels at this by providing an unbiased, genome-wide readout of chromatin accessibility with higher sensitivity than its predecessors.

ATAC-seq utilizes a hyperactive Tn5 transposase to fragment accessible chromatin and insert adapters at the cleaved sites. The adapters permit amplification and sequencing of the captured fragments, the data from which are used to create genome-wide maps of chromatin accessibility, delineating the location of active regulatory elements like promoters, enhancers and transcription factor binding sites.

When combined with single-cell transcriptomic data from the same cells, the resulting multiomic view enables direct associations of the regulatory chromatin state with gene expression output in each cell, affording even deeper mechanistic understanding of cell state in different conditions.

BD Rhapsody™ ATAC-Seq Assays enable you to either reproducibly generate standalone open chromatin profiling data or perform a multiomic analysis of open chromatin accessibility and transcriptome of single cells in one experiment on the BD Rhapsody™ Single-Cell Analysis System.

The BD Rhapsody™ ATAC-Seq Assay workflow: Single nuclei are isolated and tagmented in bulk with Tn5 transposase loaded with sequencing adapters, simultaneously fragmenting the DNA and inserting adapters into regions of open chromatin. The tagmented nuclei are then loaded onto the BD Rhapsody™ Cartridge to capture the tagged DNA fragments on BD Rhapsody™ Beads. Next, beads are retrieved and their captured fragments are PCR-amplified to generate a sequencing library. The library is sequenced, with the resulting reads mapped to the genome to identify accessible chromatin regions across individual nuclei.

Key applications:

- Immunology research: Uncover heterogeneity and dysregulated gene programs driving immunological disease states.
- Cancer research: Reveal regulatory elements driving intra-tumor heterogeneity and therapeutic resistance.
- Developmental biology: Chart chromatin dynamics across cell lineages to pinpoint regulatory elements orchestrating cell fate decisions.
- Neuroscience: Illuminate regulatory landscapes underlying neuronal identities, plasticity and disease states.

Key features:

Reliable performance

High sensitivity and specificity across different experimental conditions.

Multiomic analysis

Integrated epigenomic and transcriptomic characterization on the same cells.

Scalable input

Capable of accommodating a wide range of cell inputs.

Sample tagging enabled

Compatibility with Custom BD® Nuclear Antibody-Oligonucleotide Conjugates.

Unveil epigenomic heterogeneity with great precision

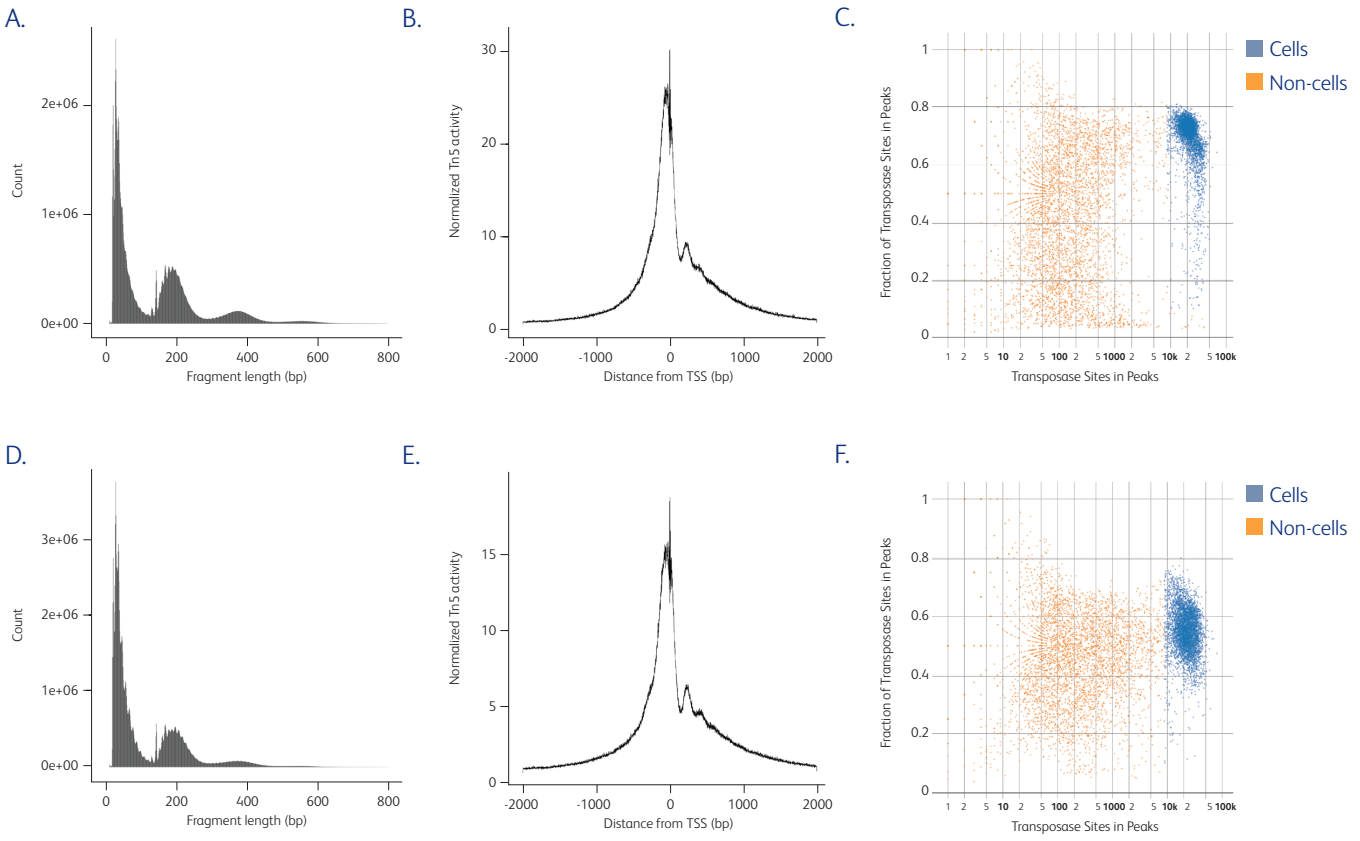


Figure 1. Sensitivity and specificity metrics for the BD Rhapsody™ Single-Cell ATAC-Seq Assay. A) Fragment size distribution from a BD Rhapsody™ ATAC-Seq Assay experiment with human peripheral blood mononuclear cells (PBMCs), demonstrating a preferential transposition of the nucleosome-free regions of open chromatin (large peak at <200 bp) and further peaks reflecting the ~200 bp repeating pattern of nucleosome positioning. **B)** Transcription start site (TSS) enrichment plot, an indicator of signal-to-noise ratio, from the same experiment, showing the aggregated read density around TSS over the genomic background that indicates the preferential accessibility of promoter regions. **C)** Scatter plot from the same experiment, showing the FriP (fraction of reads in peaks) score, a measure of specificity, against the number of transposase sites in peaks, a measure of sensitivity at roughly 50,000 mean raw read pairs per putative cell. **D–F)** The same plots from a BD Rhapsody™ ATAC-Seq Assay experiment with the K562 cell line sequenced to the same depth.

Uncover ties between gene regulation and expression at the single-cell level

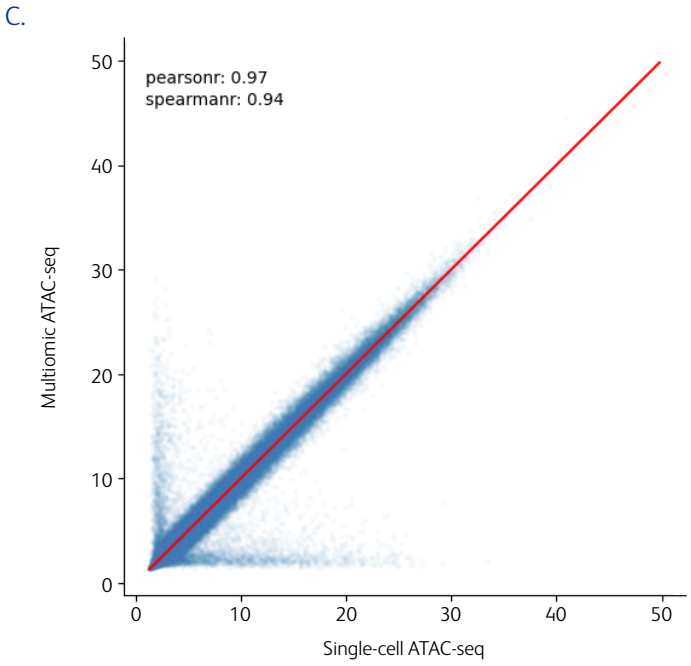
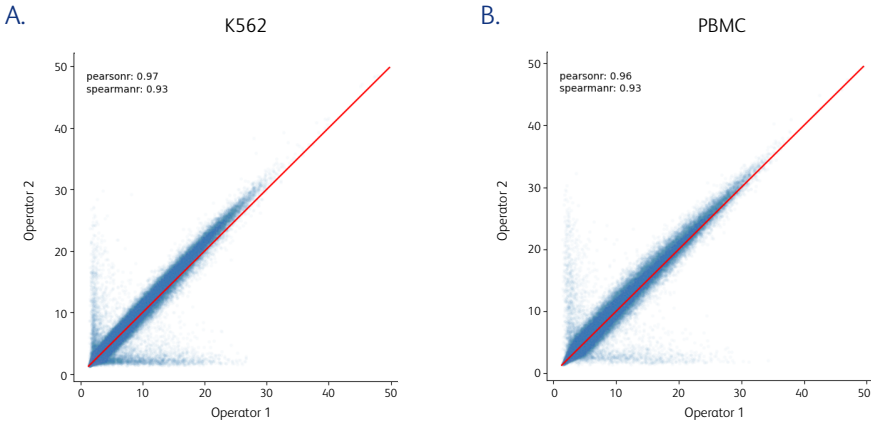
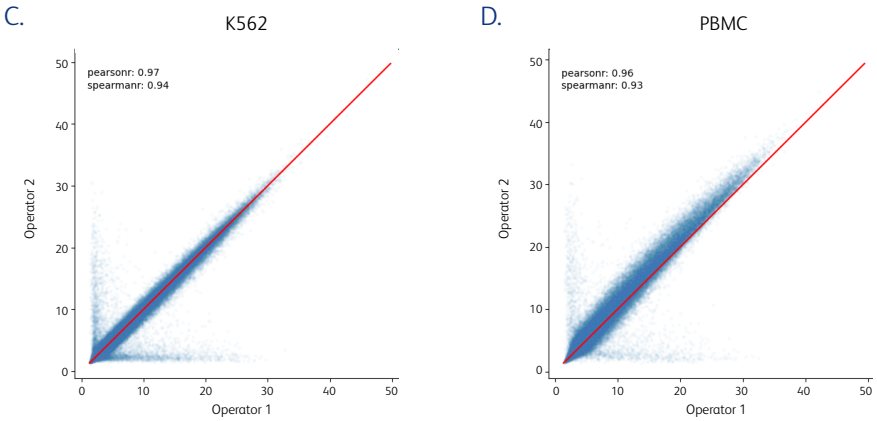


Figure 2. Sensitivity and specificity metrics for the BD Rhapsody™ Single-Cell Multiomic ATAC-Seq Assay. A) Joint calling scatter plot from a multiomic BD Rhapsody™ ATAC-Seq Assay experiment with human PBMCs where each cell is represented as a dot and RNA molecules from each cell are plotted against the ATAC-seq transposition events. **B)** The same plot from a multiomic BD Rhapsody™ ATAC-Seq Assay experiment with the K562 cell line. The clear separation between cell and non-cell events indicates the ability to effectively distinguish real cells from ambient RNA on non-cell barcodes as well as successful co-analysis of the chromatin accessibility and transcriptomic data at the single-cell level. Both samples were sequenced up to roughly 50,000 mean raw read pairs per putative cell. **C)** High correlation between the ATAC-seq data from a standalone BD Rhapsody™ ATAC-Seq Assay experiment vs a multiomic BD Rhapsody™ ATAC-Seq Assay experiment with the K562 cell line as shown by the high peak signal correlation plot.

Generate reproducible results across different samples and studies



ATAC-seq	No. of Peaks	No. of Common	% Common
K562 Exp 1	260,373	227,714	87%
K562 Exp 2	252,839	229,662	91%
PBMC Exp 1	128,983	117,956	91%
PBMC Exp 2	129,136	118,017	91%



Multiomic ATAC-seq	No. of Peaks	No. of Common	% Common
K562 Exp 1	249,702	221,817	89%
K562 Exp 2	246,111	222,865	91%
PBMC Exp 1	122,707	109,687	89%
PBMC Exp 2	120,204	109,924	91%

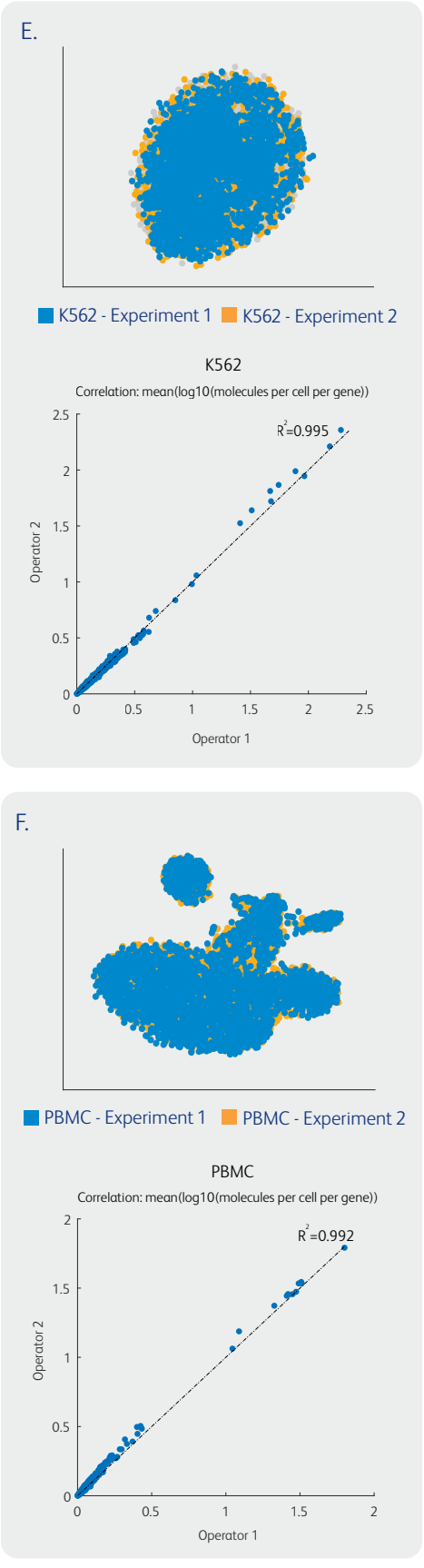


Figure 3. High reproducibility with BD Rhapsody™ ATAC-Seq Assays. The peak signal correlation across two different standalone BD Rhapsody™ ATAC-Seq Assay experiments with the K562 cell line **(A)** and two different standalone BD Rhapsody™ ATAC-Seq Assay experiments with human PBMCs **(B)**. The peak signal correlation across two different multiomic BD Rhapsody™ ATAC-Seq and WTA Assay experiments with the K562 cell line **(C)** and human PBMCs **(D)**. Clustering and gene expression correlation analysis for the WTA samples in the multiomic BD Rhapsody™ ATAC-Seq Assay, indicating no batch effect in WTA libraries made across two different experiments with the K562 cell line **(E)** and human PBMCs **(F)**.

Generate consistent, high-quality data across a wide range of cell input

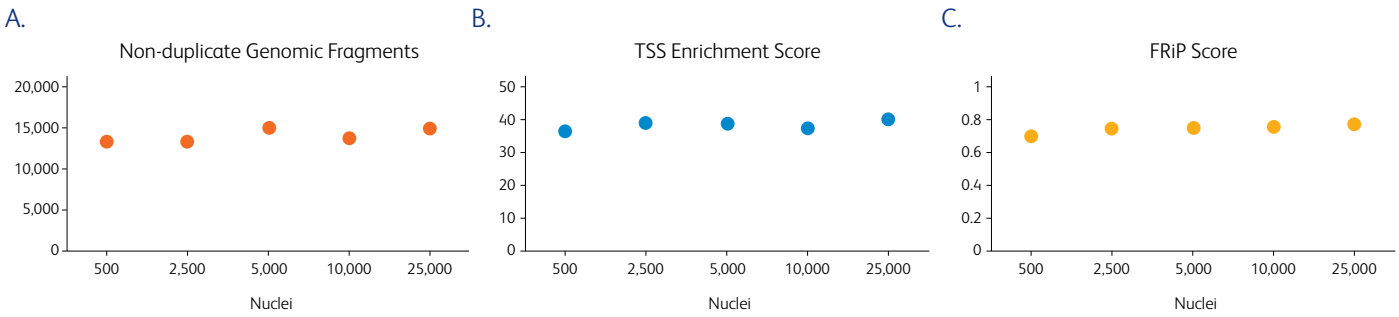


Figure 4. Robust performance across different cell input amounts. BD Rhapsody™ ATAC-Seq Assays enable scalable profiling of open chromatin and gene expression analysis from limited cell inputs to thousands of single cells in one experiment, as demonstrated by the data from a series of BD Rhapsody™ ATAC-Seq Assay experiments with 500, 2,500, 5,000, 10,000, and 25,000 nuclei from human PBMCs captured in a single lane on the BD Rhapsody™ 8-Lane Cartridge. **A)** Median number of nonduplicate fragments per putative cell at roughly 50,000 mean raw read pairs per putative cell. **B)** TSS enrichment plots from the same experiments. **C)** FriP scores from the same experiments, all pointing to a robust and reproducible performance irrespective of the nuclei number.

Gain a comprehensive picture of cellular identities

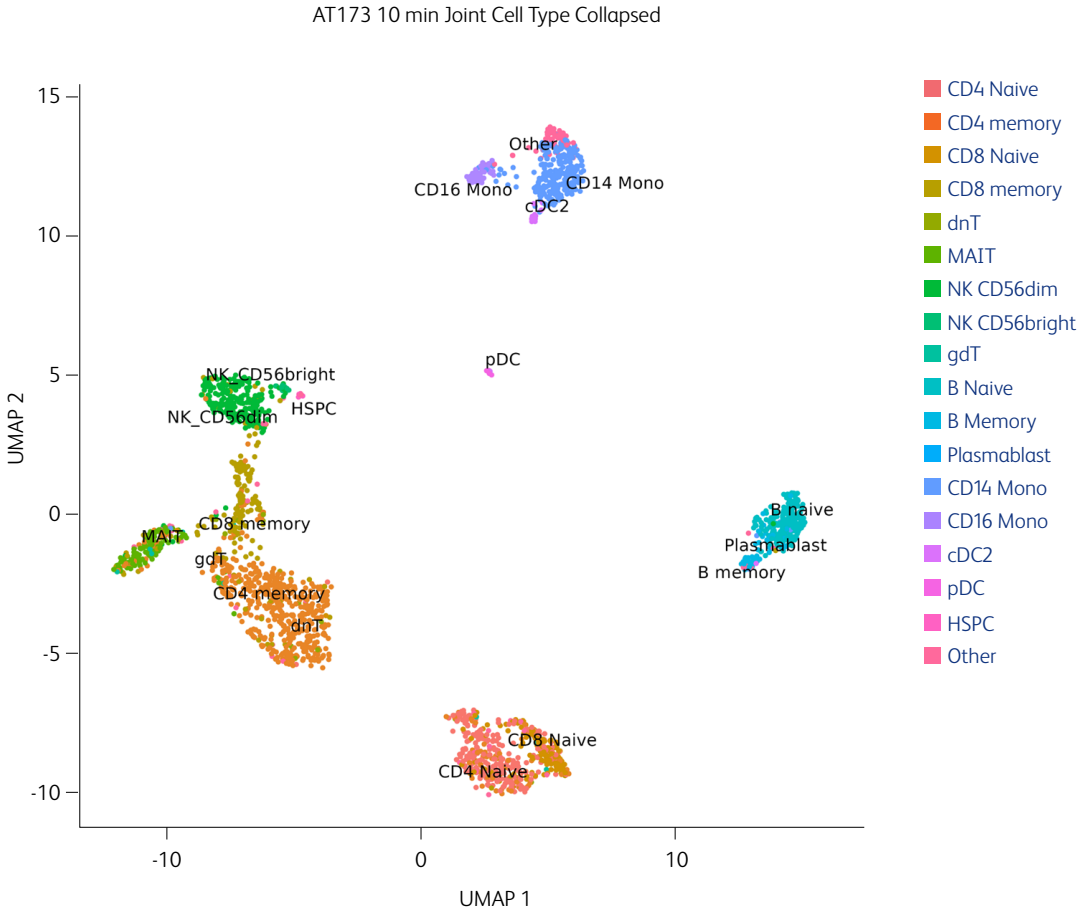


Figure 5. Cell-type annotation using the data from a BD Rhapsody™ Single-Cell Multiomic ATAC-Seq Assay. Representative data from BD Rhapsody™ Single-Cell Multiomic ATAC-Seq and WTA Assays, where 2,190 nuclei from human PBMCs were analyzed, followed by a joint WTA and ATAC-seq dimensionality reduction performed using Uniform Manifold Approximation and Projection (UMAP) and cell type annotation using the WTA data from a PBMC reference atlas.

Enrich cell type-specific transcription factor motifs

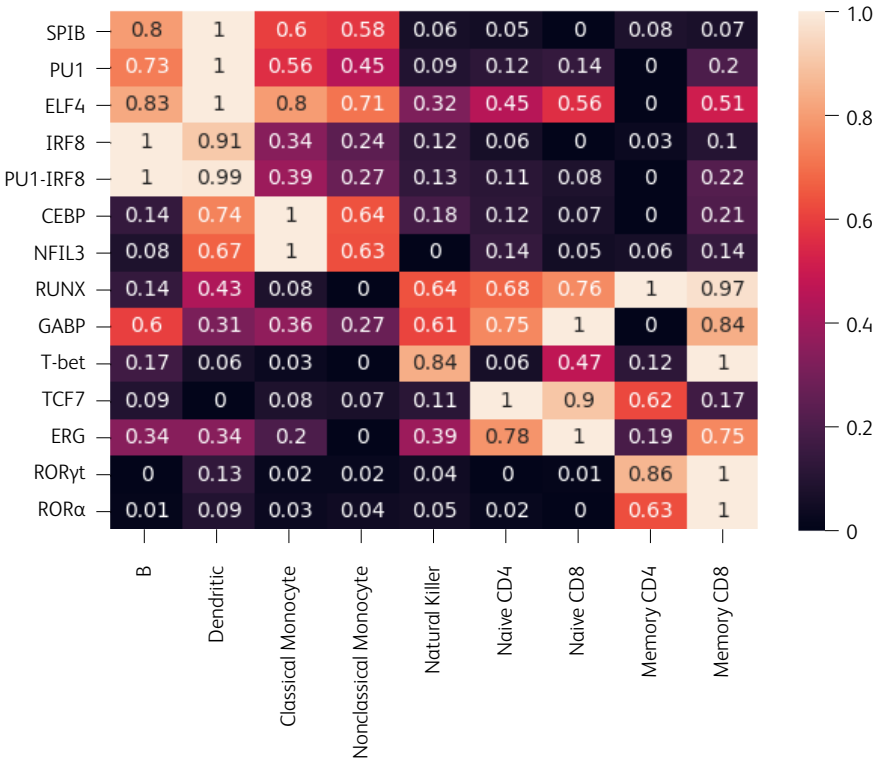


Figure 6. Cell types and their specific motifs revealed using the BD Rhapsody™ Single-Cell Multiomic ATAC-Seq Assay. A heat map showing normalized enrichment scores of cell type–specific transcription factor motifs in PBMCs. Motif scores were calculated using a binomial distribution, determining the relative enrichment of each motif in differentially accessible regions of a given cell type compared to GC-matched background regions. The scores were then normalized across cell types per motif on a 0–1 scale, where 0 indicates least enrichment and 1 indicates highest enrichment of each motif.

Use multiomic epigenomic and transcriptomic data to illuminate epigenetic regulatory landscapes

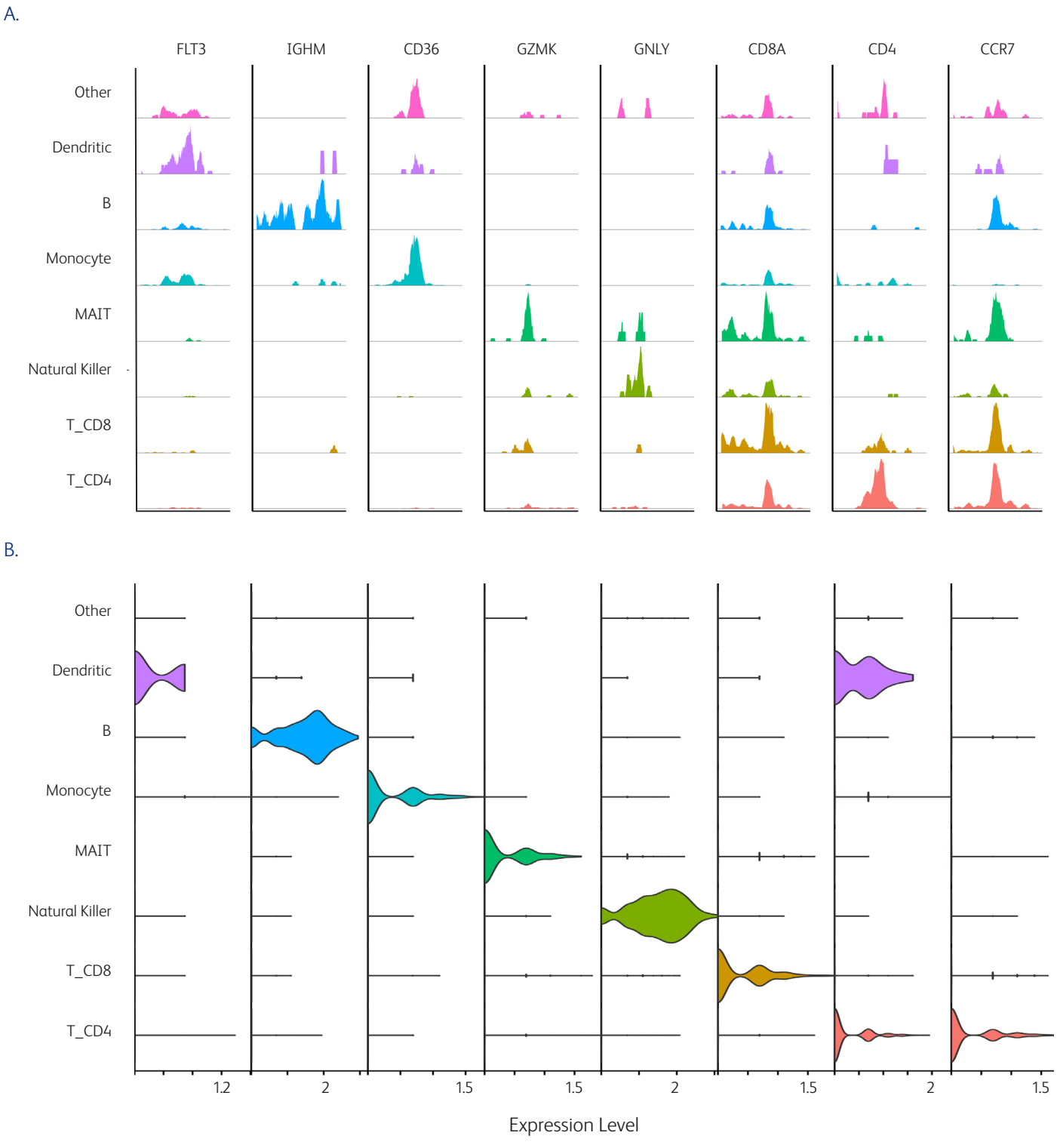


Figure 7. Comparison between single-cell ATAC-seq and WTA data with PBMCs. A) Read density across each ATAC-seq cluster at the transcription start sites of cell type marker genes. **B)** Violin plots showing cell type-specific gene expression in WTA data.

Obtain cell type-specific correlation of ATAC-seq gene activity and gene expression values

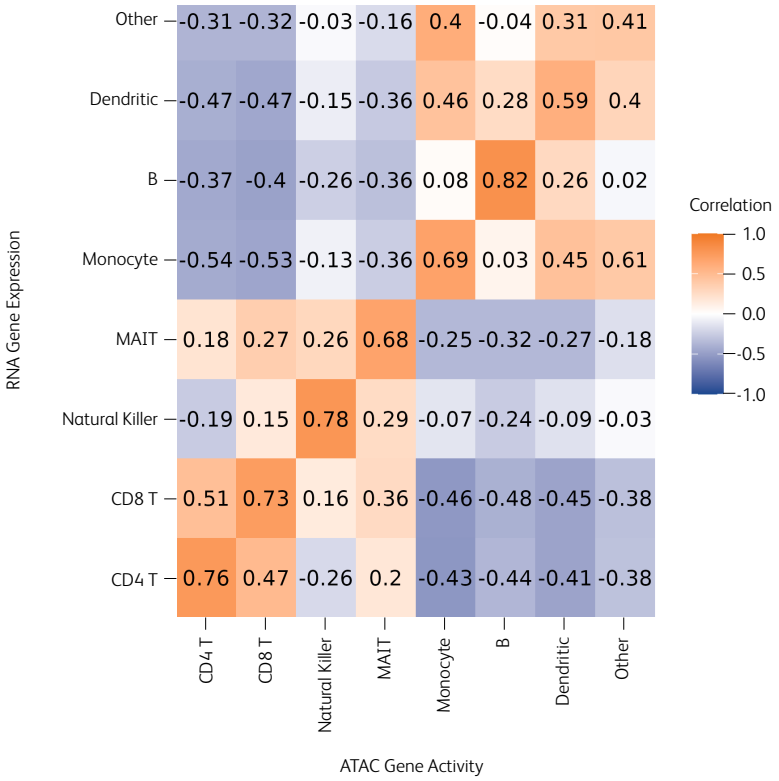
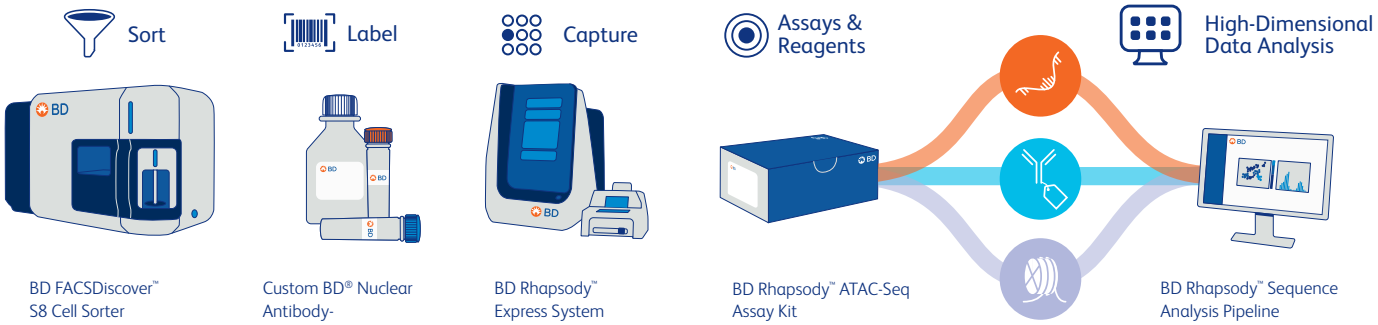


Figure 8. Concordance between gene expression and inferred gene activity score. A heatmap showing Pearson's correlation coefficients between ATAC-seq gene activity scores and gene expression values in PBMCs, with each row representing a cell type in WTA data and each column a cell type in ATAC-seq data.

Complete single-cell multiomics workflow



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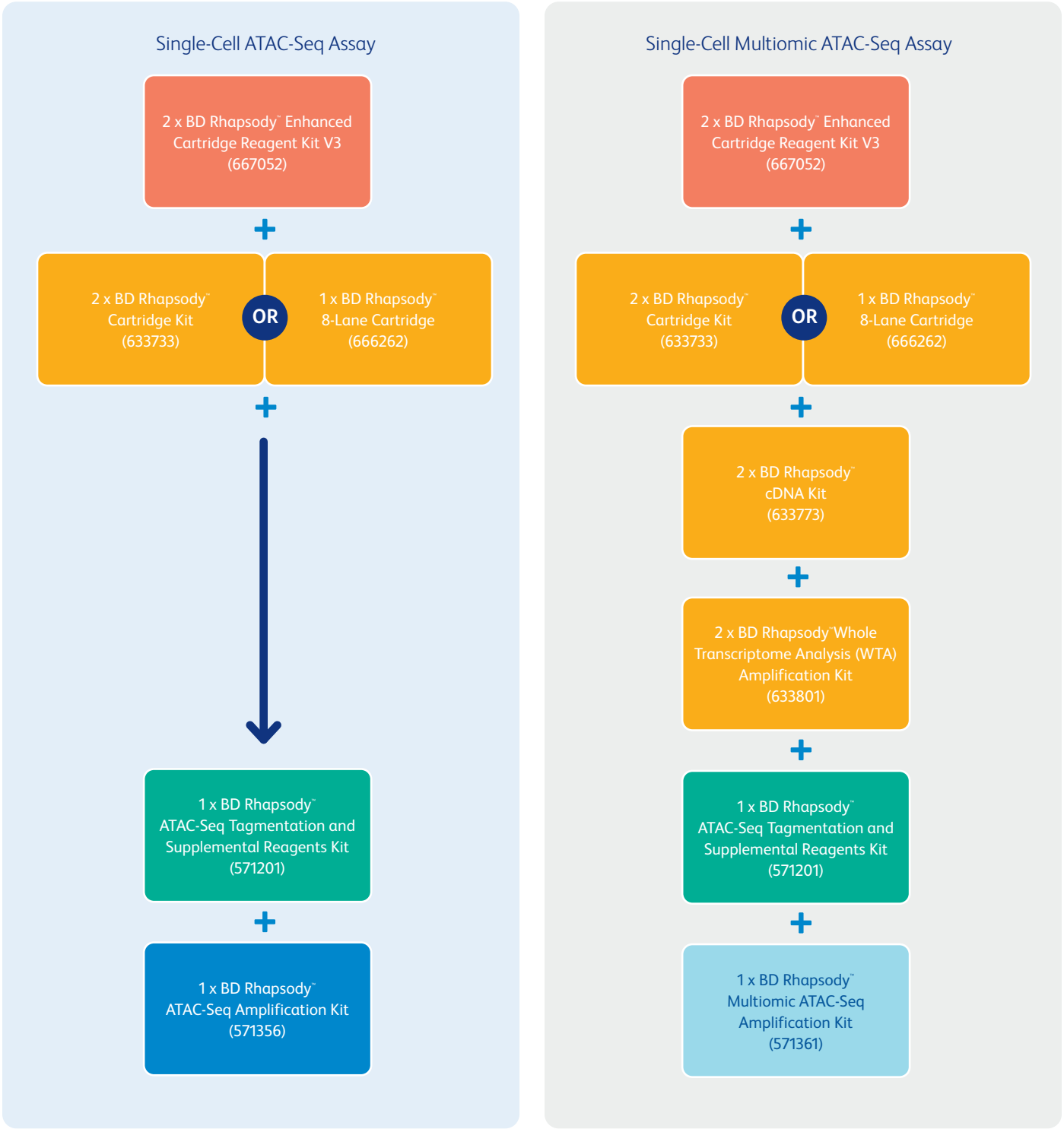
Product purchase guide for BD Rhapsody™ ATAC-Seq Assays

Reagent kits bundle for the BD Rhapsody™ Single-Cell ATAC-Seq Assay and BD Rhapsody™ Single-Cell Multiomic ATAC-Seq Assay. The number in each box represents the number of kits required to enable eight reactions in total with each workflow.



Ordering information

Individual kits	
Description	Fisher Scientific Catalog Number
BD Rhapsody™ ATAC-Seq Tagmentation and Supplemental Reagents Kit	BDB940520
BD Rhapsody™ ATAC-Seq Amplification Kit	BDB940519
BD Rhapsody™ Multiomic ATAC-Seq Amplification Kit	BDB940518
Suggested companion instruments	
Description	Fisher Scientific Catalog Number
BD Rhapsody™ Single-Cell Analysis System	BDB633701
BD Rhapsody™ Express Single-Cell Analysis System Package	BDB633707
BD Rhapsody™ HT Xpress Package	BDB666625
Suggested companion products	
Description	Fisher Scientific Catalog Number
BD Rhapsody™ Cartridge Kit	BDB633733
BD Rhapsody™ 8 Lane Cartridge Kit	BDB666262
BD Rhapsody™ Enhanced Cartridge Reagent Kit V3	BDB940515
BD Rhapsody™ cDNA Kit	BDB633773
BD Rhapsody™ Whole Transcriptome Analysis (WTA) Amplification Kit	BDB633801
BD® OMICS-Guard Sample Preservation Buffer	BDB570911
Nuclear Single-Cell Multiplexing Kit	Contact for more info

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