# BD OMICS-One™ WTA Next Assay

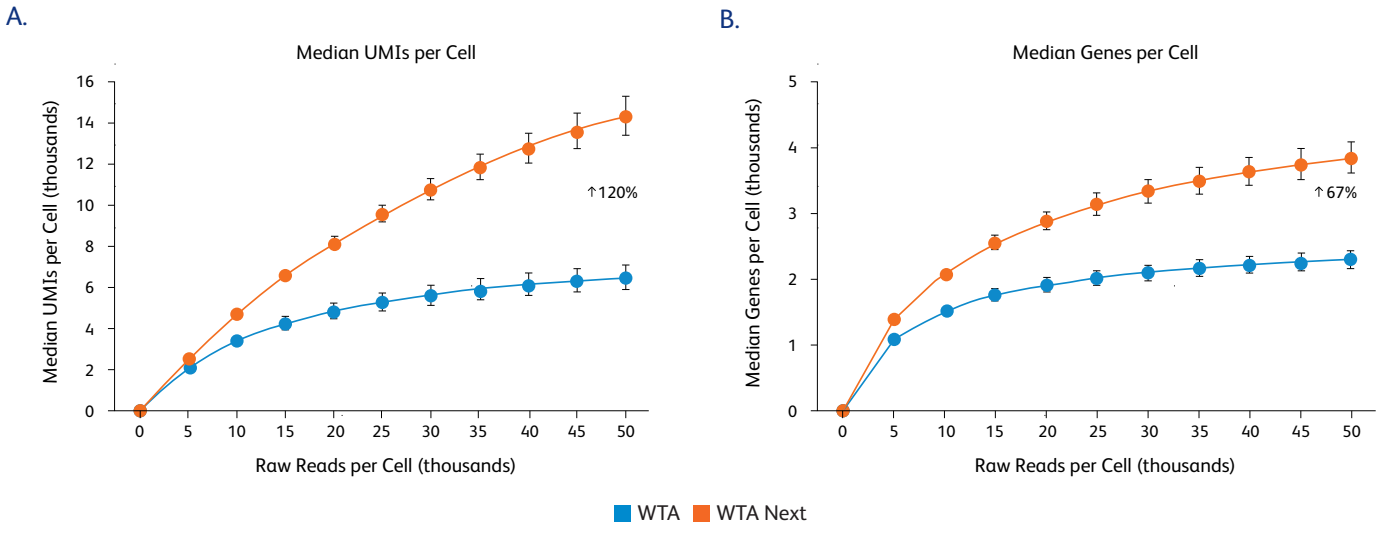
More possibilities. More convenience. More value.

The BD OMICS-One™ WTA Next Assay redefines single-cell RNA-seq on the BD Rhapsody™ Single-Cell Analysis System by delivering unbiased, sensitive transcriptome profiling that captures the complete gene expression landscape without target limitations. This data sheet provides representative performance validation data for the BD OMICS-One™ WTA Next Assay across diverse experimental conditions and workflows:

- **Assay sensitivity**—standalone and multiomics molecule and gene recovery metrics
- **Competitive benchmarking**—head-to-head comparison with the 10x Genomics v4 GEM-X Assay
- **Mitochondrial molecules assessment**—violin plot showing % of reads
- **Sample preservation validation**—performance with short- and long-term storage solutions
- **Robustness**—technical consistency across users and replicates
- **Scalability**—performance across different cell input range
- **Data analysis**—secondary data processing using the BD Cellismo™ Data Visualization Tool

## Unlock cellular heterogeneity with precision

The BD OMICS-One™ WTA Next Assay delivers breakthrough sensitivity to capture rare transcripts and cellular heterogeneity as a standalone assay.




**The BD OMICS-One™ WTA Next Assay captures a significantly higher number of molecules and genes per cell at the same sequencing depth.** Performance comparison of the new BD OMICS-One™ WTA Next Assay (WTA Next) versus the current BD Rhapsody™ Whole Transcriptome Analysis (WTA) Assay using previously frozen PBMC samples from three healthy matched donors processed in standalone WTA experiments. **(A)** Median number of unique molecular identifiers (UMIs) per cell as a function of raw sequencing reads per cell, demonstrating a 120% increase in transcript detection with WTA Next at 50,000 reads per cell. **(B)** Median number of genes detected per cell across varying sequencing depths, showing a 67% improvement with WTA Next at 50,000 reads per cell. Error bars represent standard deviation across three biological replicates. WTA workflow: 20,000 cells targeted with ~16,000 recovered, subsampled to 4,000 for analysis. WTA Next workflow: 30,000 cells targeted with ~30,000 recovered, subsampled to 3,000 cells. All captures were performed on a BD Rhapsody™ 8-Lane Cartridge.

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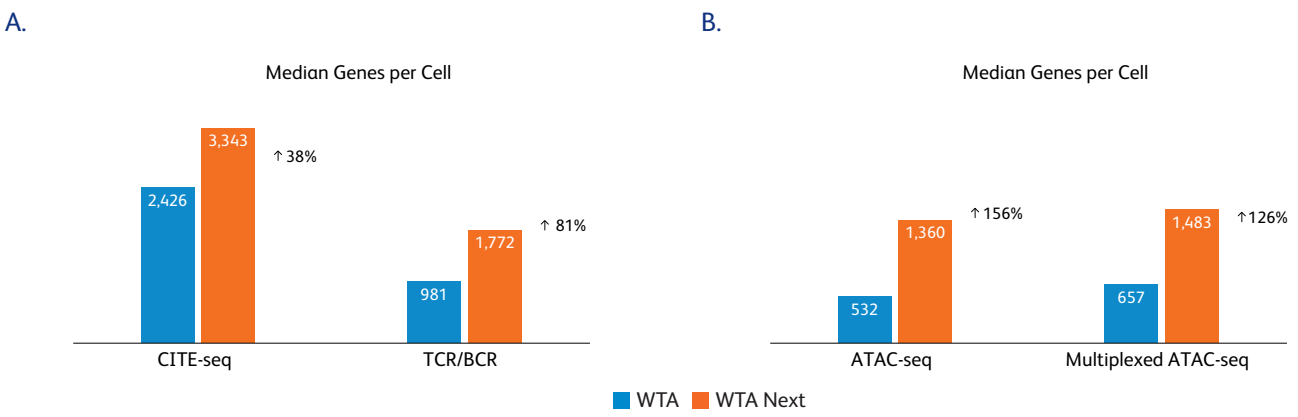
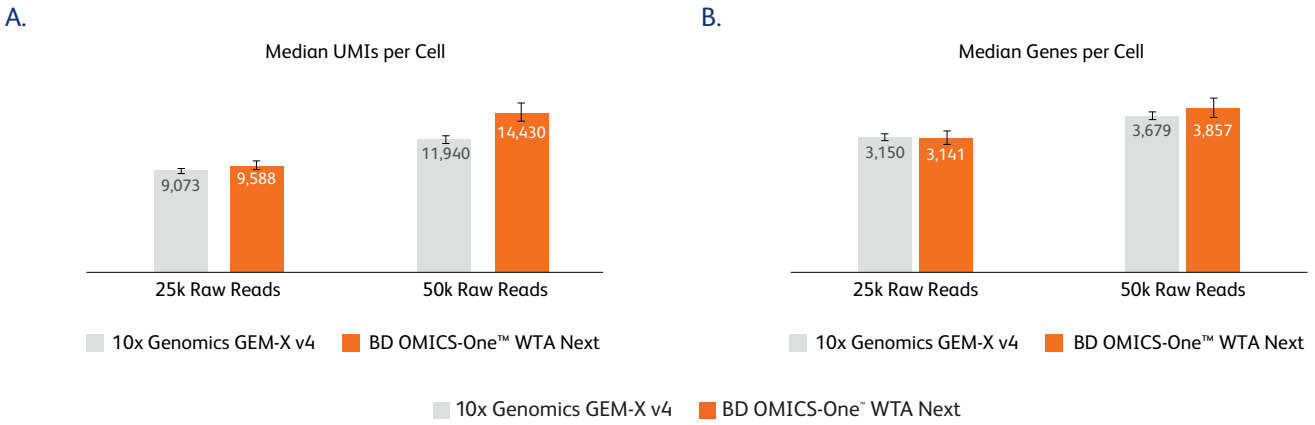
The BD OMICS-One™ WTA Next Assay delivers breakthrough sensitivity to capture rare transcripts and cellular heterogeneity across all supported multiomic workflows.




**The BD OMICS-One™ WTA Next Assay enhances gene expression analysis across all supported multiomic workflows.** Gene recovery comparison between the current BD Rhapsody™ Whole Transcriptome Analysis (WTA) Assay and the new BD OMICS-One™ WTA Next Assay (WTA Next) across different multiomics applications. **(A)** Cell-based workflows using frozen PBMCs. Left: CITE-seq showing 38% increase in median genes per cell with WTA Next at ~23,000 reads per cell. Right: TCR/BCR analysis demonstrating 81% improvement with WTA Next at ~22,700 reads per cell. **(B)** Nuclei-based workflows using fresh PBMCs. Left: ATAC-seq showing 156% increase in median genes per cell with WTA Next at 25,000 reads per cell. Right: Multiplexed ATAC-seq demonstrating 126% improvement with WTA Next at 25,000 reads per cell. WTA Next assay delivers substantial performance gains across all supported multiomic combinations, either in single-cell or single nuclei-based implementations.

# Benefit from industry-leading performance

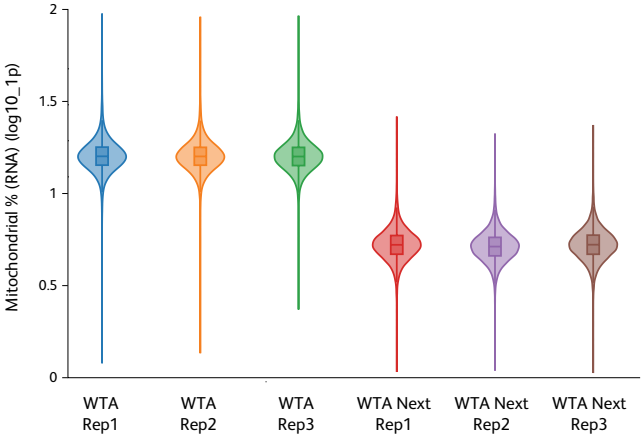
The BD OMICS-One™ WTA Next Assay exceeds the 10x Genomics GEM-X v4 Assay in key performance metrics.




**The BD OMICS-One™ WTA Next Assay delivers superior performance across key sensitivity metrics at different sequencing depths.** Head-to-head comparison of the BD OMICS-One™ WTA Next Assay versus the 10x Genomics Chromium GEM-X Single Cell 3' v4 Gene Expression Assay using matched PBMC samples from three donors processed under identical conditions. Bar graphs show median UMIs **(A)** and median genes per cell **(B)** at 25,000 and 50,000 raw sequencing reads per cell. The BD OMICS-One™ WTA Next Assay achieves higher molecule detection at both representative sequencing depths. Gene detection matches the GEM-X assay at 25,000 reads per cell, with the BD OMICS-One™ WTA Next Assay emerging superior after 25,000 reads per cell with increasingly more genes recovered at higher sequencing depths. Error bars represent standard deviation across three biological replicates.

# Maximize usable data

The BD OMICS-One™ WTA Next Assay delivers cleaner data with significantly reduced mitochondrial background in standalone and multiomic configurations.

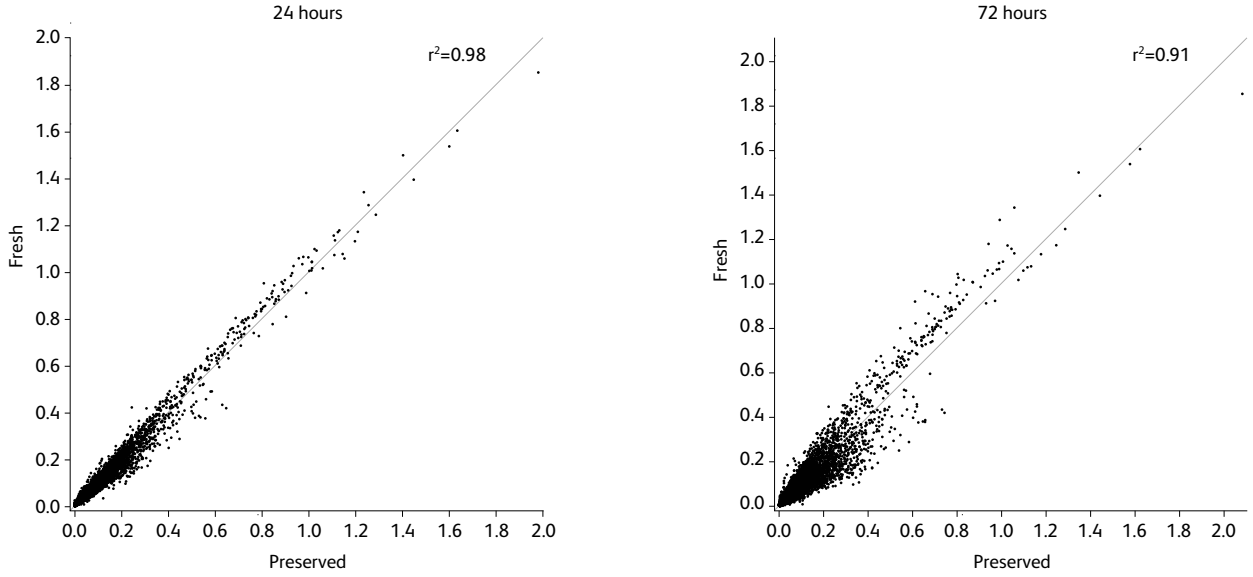



**The BD OMICS-One™ WTA Next Assay reduces mitochondrial background by more than 70% resulting in higher quality data.** Comparison of mitochondrial molecules percentage between the current BD Rhapsody™ Whole Transcriptome Analysis (WTA) Assay and the new BD OMICS-One™ WTA Next Assay across three technical replicates. Violin plots show the distribution of mitochondrial molecules per cell on the logarithmic scale, with the BD OMICS-One™ WTA Next Assay demonstrating a 73% reduction compared to the BD Rhapsody™ WTA Assay. Lower mitochondrial content enhances sequencing efficiency, enabling more informative gene expression analysis without increased sequencing costs. The data from all replicates were down-sampled to 15,000 raw sequencing reads per cell.

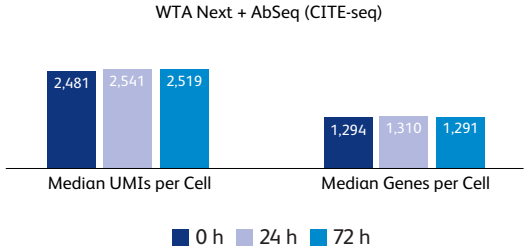
# Adapt workflows to your timeline

The BD OMICS-One™ WTA Next Assay offers workflow flexibility with robust performance across fresh and short-term storage conditions.

A.



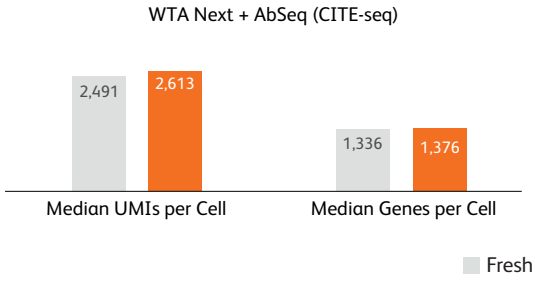

B.




**The BD OMICS-One™ WTA Next Assay maintains high performance with short-term sample preservation using the BD® OMICS-Guard Sample Preservation Buffer. (A)** Gene expression correlation comparing fresh versus preserved PBMC samples in a CITE-seq workflow with the BD OMICS-One™ WTA Next Assay. Left: Fresh versus 24-hour preservation ($R^2$ = 0.98). Right: Fresh versus 72-hour preservation ($R^2$ = 0.91). **(B)** Median UMI and genes per cell from the same experiments showing nearly identical recovery across fresh, 24-hour and 72-hour preserved samples. Samples stored in the BD® OMICS-Guard Sample Preservation Buffer at 4 °C demonstrate robust correlation with freshly processed samples, enabling flexible experimental timelines for multi-site collection, sample batching and workflow optimization without compromising data quality.

The BD OMICS-One™ WTA Next Assay offers workflow flexibility with robust performance under long-term storage conditions.

A.

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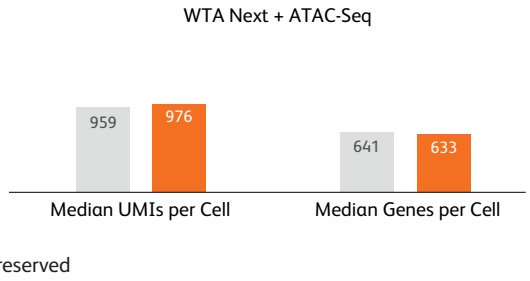


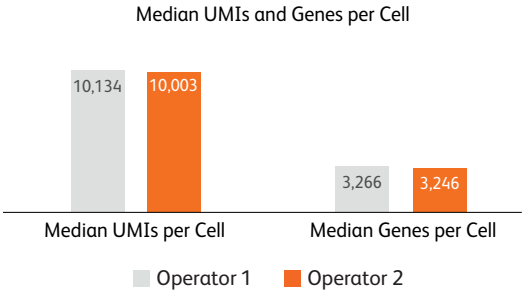

Fresh Long-Term Preserved

**The BD OMICS-One™ WTA Next Assay delivers equivalent performance with long-term cryopreserved samples.** Performance comparison of fresh versus long-term cryopreserved PBMC samples using BD OMICS-One™ WTA Next Assay multiomics workflows. Samples were cryopreserved using a proprietary cryopreservation solution. **(A)** CITE-seq workflow showing median UMIs and genes per cell for fresh versus cryopreserved samples, demonstrating nearly identical recovery. Samples were sequenced at a shallow depth of ~7,000 raw sequencing reads per cell. **(B)** Multiomic ATAC-seq workflow with comparable performance between fresh and cryopreserved samples at 20,000 raw sequencing reads per cell. The results confirm long-term sample storage compatibility, enabling extended study timelines and retrospective analysis without compromising performance.

# Trust your data across experiments

The BD OMICS-One™ WTA Next Assay achieves consistent performance across independent experiments performed by different users.

A.

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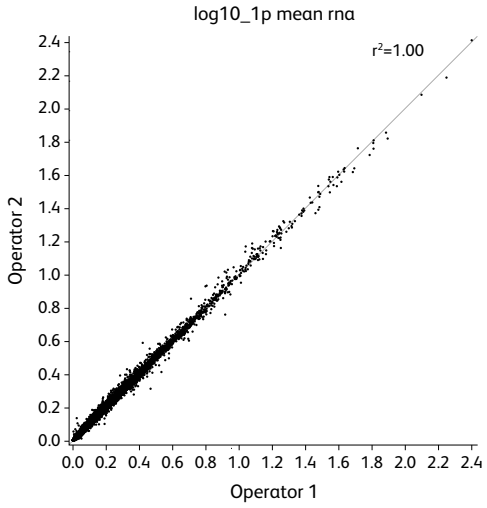
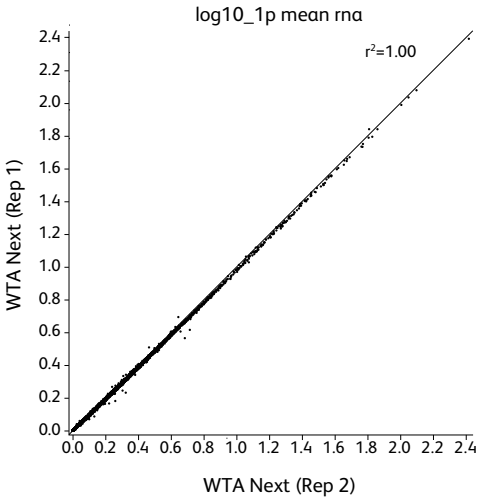
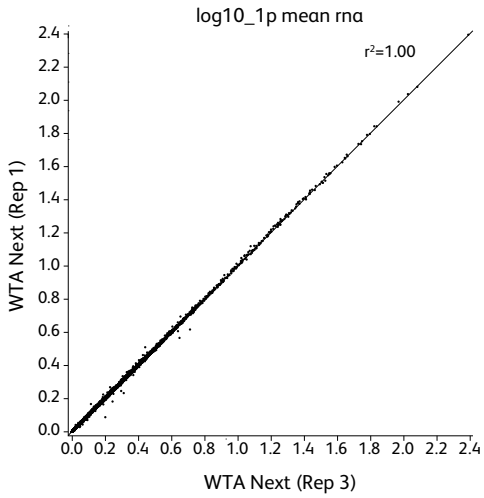


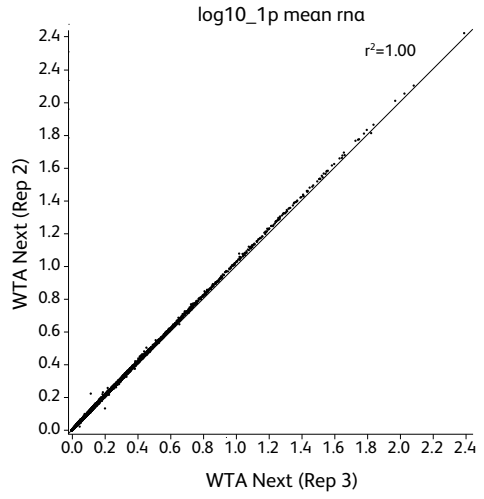

**The BD OMICS-One™ WTA Next Assay delivers consistent results across different users and experiments.** Reproducibility assessment with two independent users processing the same frozen PBMC sample from one donor in separate experiments (with 30,000 cells). **(A)** Bar graphs show nearly identical median UMIs (left) and median genes per cell (right) at 25,000 reads per cell, confirming consistent sensitivity across users. **(B)** Gene expression correlation ($R^2$ = 1.0) demonstrating exceptional inter-user reproducibility, confirming robust assay performance independent of operator variability. Consistent results across users ensure reliable data generation in multi-operator laboratories and collaborative research settings.

The BD OMICS-One™ WTA Next Assay delivers consistent results across replicates within the same experiments.

A.

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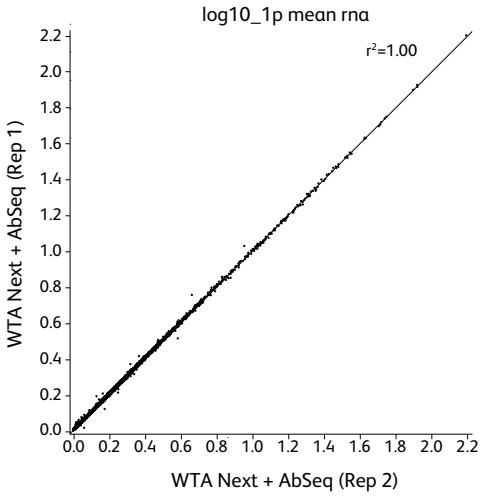
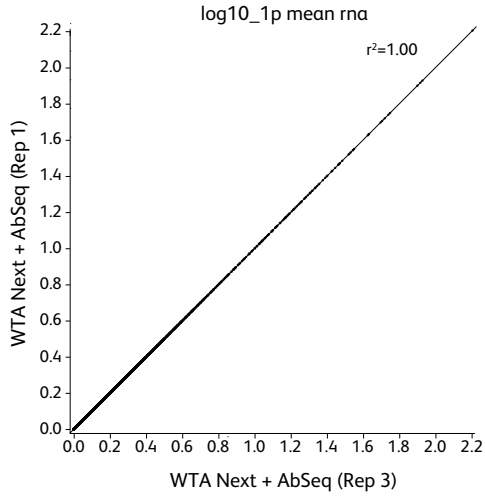
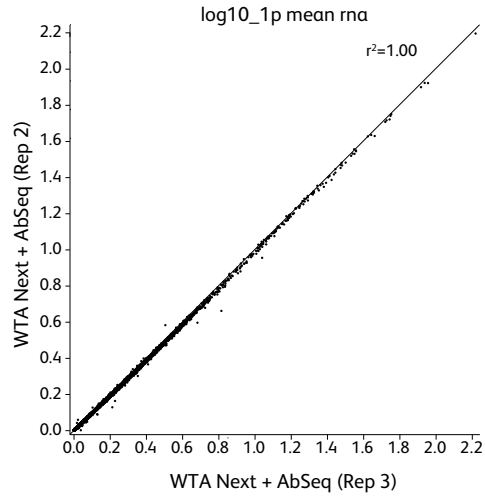


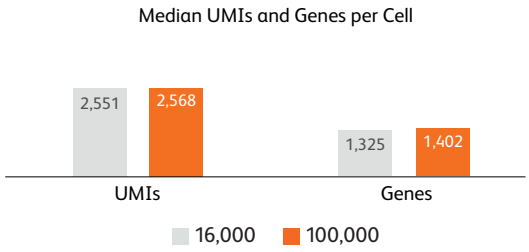




**The BD OMICS-One™ WTA Next Assay generates highly reproducible results across technical replicates.** Gene expression correlation across three technical replicates for a standalone BD OMICS-One™ WTA Next Assay workflow **(A)** and multiomic BD OMICS-One™ WTA Next Assay + BD® AbSeq Antibody-Oligos (CITE-seq) workflow **(B)**. Each scatter plot compares pairwise gene expression levels between technical replicates (Rep 1 vs Rep 2, Rep 1 vs Rep 3, and Rep 2 vs Rep 3) with the high Pearson correlation coefficients ($R^2$) indicating excellent technical repeatability and minimal technical variation in both standalone and multiomic workflows, ensuring robust assay performance and data quality.

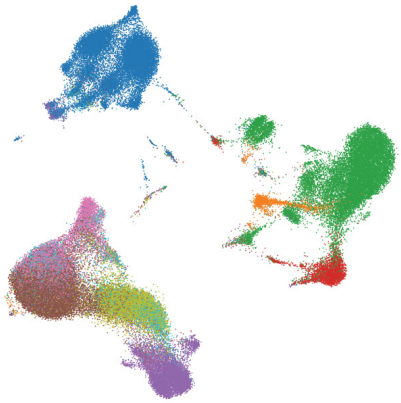
# Scale confidently with high-quality data across a wide range of cell inputs

The BD OMICS-One™ WTA Next Assay delivers reliable results across variable cell loading concentrations. These data demonstrate the BD OMICS-One™ WTA Next Assay's exceptional flexibility—delivering consistent sensitivity, accurate cell type identification and reproducible results across a 100-fold range of cell inputs without requiring reagent optimization, enabling seamless workflow adaptation from pilot studies to large-scale experiments.

A.




B.



**Cell Type Experimental (RNA)**

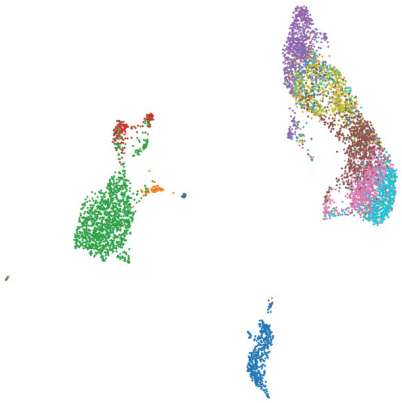
| | |
|---|---|
| B | 18,117 cells (21.12%) |
| Dendritic | 1,523 cells (1.78%) |
| Monocyte_classical | 18,542 cells (21.61%) |
| Monocyte_nonclassical | 2,948 cells (3.44%) |
| Natural_killer | 8,455 cells (9.86%) |
| T_CD4_memory | 15,144 cells (17.65%) |
| T_CD4_naive | 8,289 cells (9.66%) |
| T_CD8_memory | 8,329 cells (9.71%) |
| T_CD8_naive | 4,095 cells (4.77%) |
| T_gamma_delta | 344 cells (0.40%) |

C.

**Original Sample (RNA)**

- WTA Next–Experiment 1 (~100,000 cells)
- WTA Next–Experiment 1 (~2,000 cells)

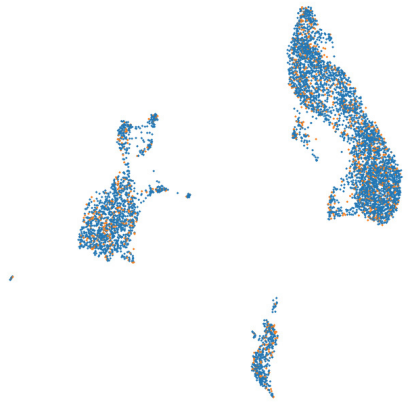
D



**Cell Type Experimental (RNA)**

| | |
|---|---|
| B | 474 cells (8.07%) |
| Dendritic | 60 cells (1.02%) |
| Monocyte_classical | 1,293 cells (22.00%) |
| Monocyte_nonclassical | 156 cells (2.65%) |
| Natural_killer | 796 cells (13.54%) |
| T_CD4_memory | 931 cells (15.84%) |
| T_CD4_naive | 754 cells (12.83%) |
| T_CD8_memory | 538 cells (9.15%) |
| T_CD8_naive | 801 cells (13.63%) |
| T_gamma_delta | 74 cells (1.26%) |

E.



**Original Sample (RNA)**

- WTA Next–Experiment 1 (~5,000 cells)
- WTA Next–Experiment 1 (~1,000 cells)

**The BD OMICS-One™ WTA Next Assay delivers consistent performance across variable cell loading concentrations.** Scalability assessment demonstrating the robustness of the BD OMICS-One™ WTA Next Assay across cell input ranges. **(A)** Median UMIs and genes per cell comparing 16,000 versus 100,000 cell inputs show nearly identical sensitivity metrics using identical reagent volumes per lane, confirming that reagent amounts do not limit performance across input ranges. **(B)** UMAP visualization of 100,000-cell experiment showing clear immune cell type differentiation and proper clustering. **(C)** Integration analysis demonstrating no batch effect between high-throughput (~100,000 cells) and low-input (~2,000 cells) experiments processed on different days by different operators. **(D)** UMAP of 5,000-cell experiment maintaining robust immune cell type resolution. **(E)** Batch integration confirming no systematic variation between 5,000-cell and 1,000-cell experiments.

# Transform raw data into biological insights

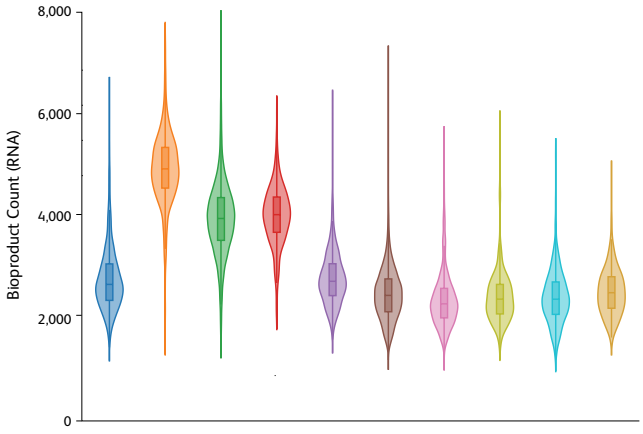
The BD OMICS-One™ WTA Next Assay seamlessly integrates with the BD Cellismo™ Data Visualization Tool for streamlined secondary data analysis and visualization, with no coding required. The integrated analysis pipeline enables researchers to move rapidly from raw sequencing data to publication-quality visualizations and biological interpretation, providing a complete solution from sample processing through data exploration and cell type characterization.

A.

**Cell Type Experimental**

| | |
|---|---|
| B | 1,290 cells (6.01%) |
| Dendritic | 636 cells (2.96%) |
| Monocyte_classical | 11,091 cells (51.63%) |
| Monocyte_nonclassical | 493 cells (2.29%) |
| Natural_killer | 716 cells (3.33%) |
| T_CD4_memory | 3,894 cells (18.13%) |
| T_CD4_naive | 1,127 cells (5.25%) |
| T_CD8_memory | 480 cells (2.23%) |
| T_CD8_naive | 1,572 cells (7.32%) |
| T_gamma_delta | 183 cells (0.85%) |

B.

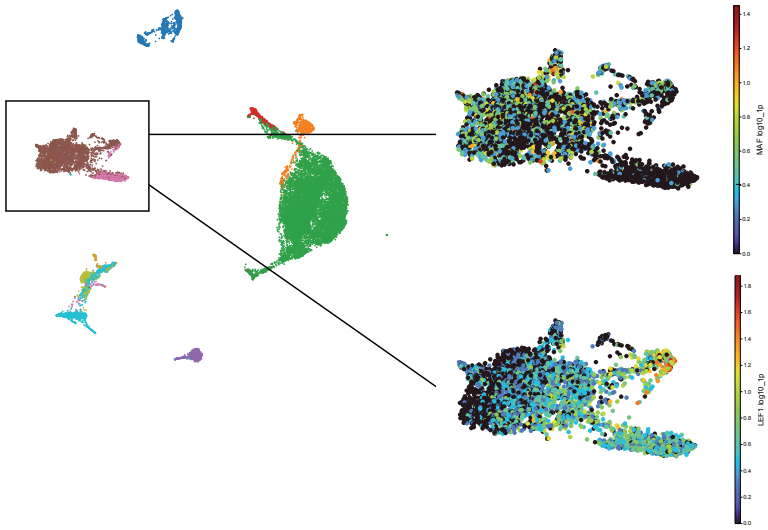



- B
- Dendritic
- Monocyte_classical
- Monocyte_nonclassical
- Natural_killer
- T_CD4_memory
- T_CD4_naive
- T_CD8_memory
- T_CD8_naive
- T_gamma_delta

**The BD OMICS-One™ WTA Next Assay integrates seamlessly with the powerful BD Cellismo™ Data Visualization Tool for rapid biological insights.** End-to-end workflow demonstration using the BD Cellismo™ Data Visualization Tool for BD OMICS-One™ WTA Next Assay data analysis. **(A)** UMAP projection from an experiment (20,000 frozen PBMCs targeted, ~21,000 cells retrieved, no subsampling) showing distinct immune cell populations with clear cluster separation. **(B)** Violin plots displaying RNA count distributions across identified immune cell types from the same experiment, revealing expression patterns and population-specific transcriptional signatures.

The BD OMICS-One™ WTA Next Assay enables detailed characterization of cellular subpopulations.

A.




**Cell Type Experimental**

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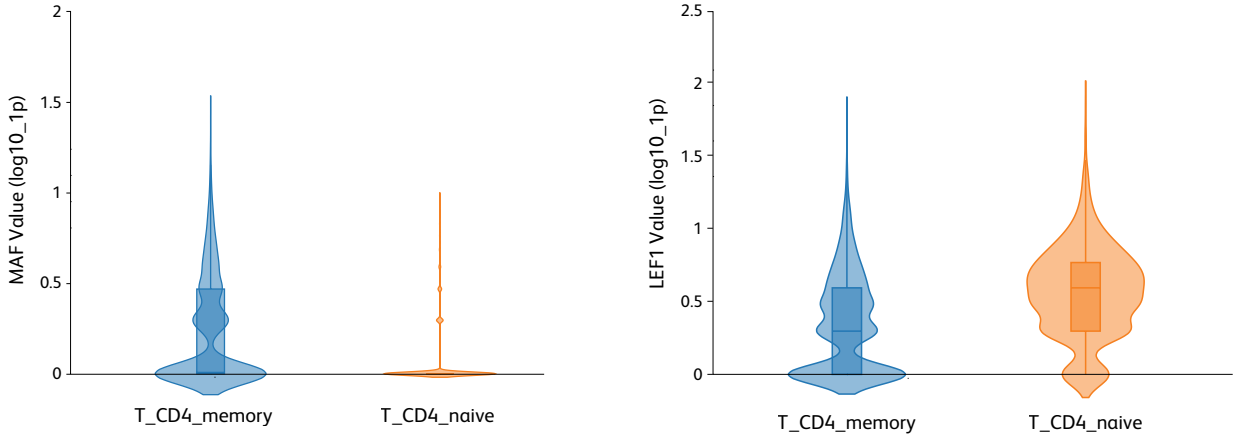


**The BD OMICS-One™ WTA Next Assay enables deeper immune profiling ability to resolve functional subpopulations within major cell types. (A)** UMAP showing distinct immune cell populations in a PBMC sample from the same experiment in the preceding figure. Right panels: Magnified CD4+ T cell cluster with expression overlay for *MAF* (top) and *LEF1* (bottom) genes. *MAF* expression enriches in memory T cell subsets, reflecting differentiation into memory phenotypes including Tph and Tfh populations. *LEF1* expression localizes to naive T cells, where this transcription factor maintains cellular homeostasis and stemness. **(B)** Violin plots quantifying differential expressions of *MAF* (left) and *LEF1* (right) across CD4+ T cell subsets, confirming distinct transcriptional programs between naive and memory populations. This resolution enables functional subset identification and characterization critical for immunology research, demonstrating how the BD OMICS-One™ WTA Next Assay's sensitivity translates to biologically meaningful insights at the subpopulation level.

Visit **bdbiosciences.com/WTANext** to learn more.

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

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