A Complete Multiomic Solution: WTA NEXT Powers Deep Immune Profiling Across mRNA, Surface Proteins, and VDJ in One Assay

Poster# 551

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Abstract

- Single-cell profiling now enables simultaneous measurement of mRNA, surface proteins, and immune receptor repertoires, though sensitivity, cost, and background noise remain challenging.
- An updated BD Rhapsody™ Single Cell System workflow featuring BD OMICS-One™ WTA Next Assay markedly improves whole transcript assay (WTA) sensitivity, compared to the previous WTA assay version. These gains improve cell-type resolution, rare transcript detection, and overall assay efficiency.
- BD OMICS-One™ WTA Next workflow is compatible with a number of different multiomic assays including ATAC-seq, TCR/BCR full length profiling, and Cite-seq using oligo-tagged antibodies.
- Together, these data support an assay that achieves enhanced mRNA detection sensitivity while maintaining compatibility with multiomic workflows.

Introduction

We present the BD OMICS-One™ WTA Next Assay, an improved scRNA-seq method that offers greater sensitivity for both molecule and gene detection, while maintaining a streamlined workflow.

Figure 1A. BD Rhapsody™ Single Cell System

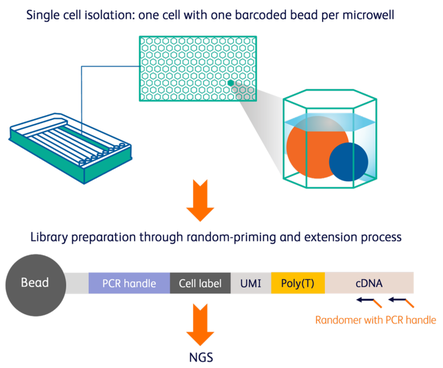


Figure 1B. Compatible Multiomic assays

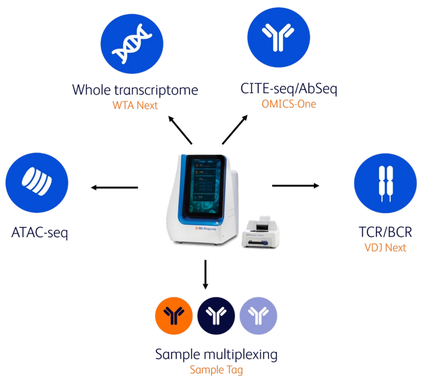
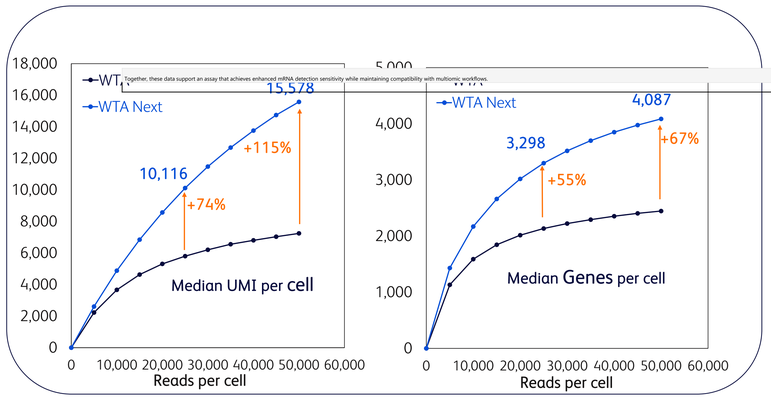


Figure 1: (A) Single cells are isolated into individual microwells together with uniquely barcoded beads, ensuring a one-cell-per-bead configuration. Messenger RNA molecules are captured via poly(T) sequences on the beads, after which cDNA synthesis is performed. Subsequent library preparation is achieved through a random-priming and extension process. (B) The new BD OMICS-One™ WTA Next Assay maintains full compatibility with all multiomic workflows.

Increased assay sensitivity

2A. Increase in molecule and gene detection



2B. Benchmarking shows comparable data to other on-market products

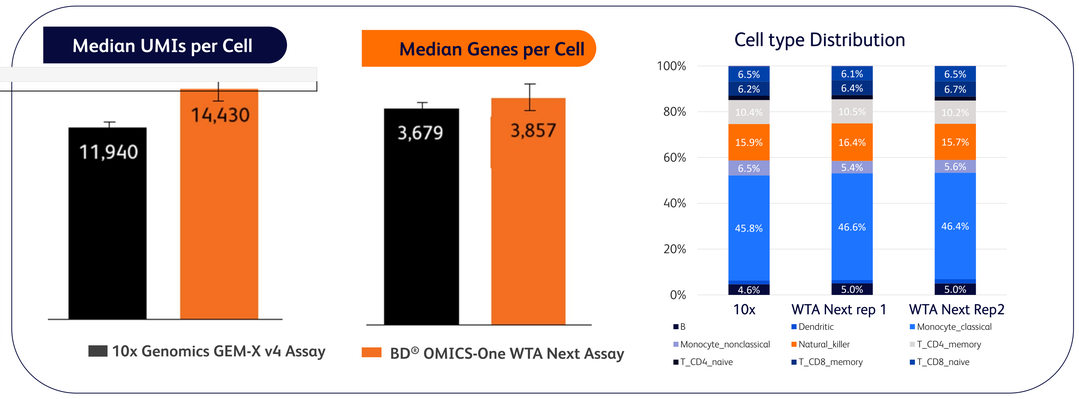


Figure 2: (A) WTA Next showed consistently higher median UMI per cell and median genes per cell than WTA at various read depths. (B) WTA, WTA Next and 10x Genomics GEM-X v4 comparison. Three different PBMC donor samples were tested. WTA and WTA Next were performed in house and 10x GEM-X v4 was performed by an independent NGS vendor. Read depth was 25,000 reads per cell for all samples. WTA Next demonstrates similar sensitivities with 10x v4 and similar cell type distribution.

Compatible with multiomic assays

Figure 3. Increased WTA performance in ATAC-seq, TCR/BCR and Cite-Seq Assays

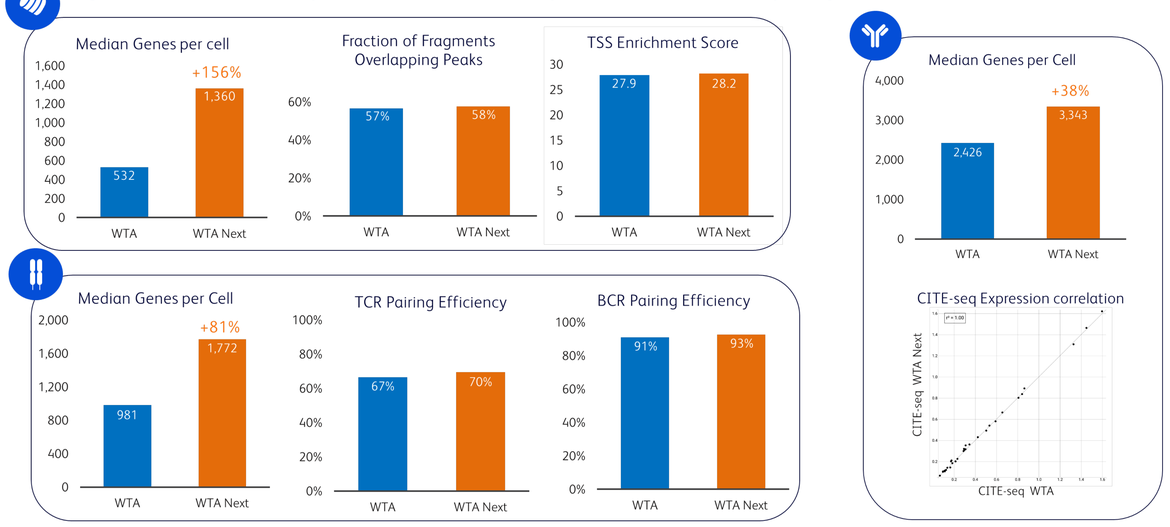


Figure 3: (A) Fresh PBMC samples were tested for multiomic ATAC-seq. At 25,000 reads per cell, WTA Next detected 156% more median genes per cell while showing equivalent ATAC sensitivity (at 53,000 reads per cell) for both assays. (B) Resting PBMC samples were tested for multiomic TCR/BCR Next profiling. At 23,000 reads per cell, WTA Next detected 81% more median genes per cell while showing similar TCR and BCR pairing efficiencies. (C) Resting PBMC samples were tested for CITE-seq using 30-plex Immune Profiler panel. At the read depth of 22,000 reads per cell, WTA Next detected 38% more median genes per cell while showing high CITE-seq expression correlations (R^2=1).

High Reproducibility

Figure 4. Consistent data across all replicates

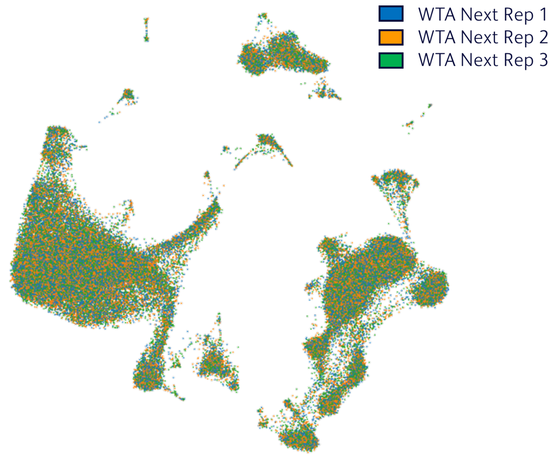
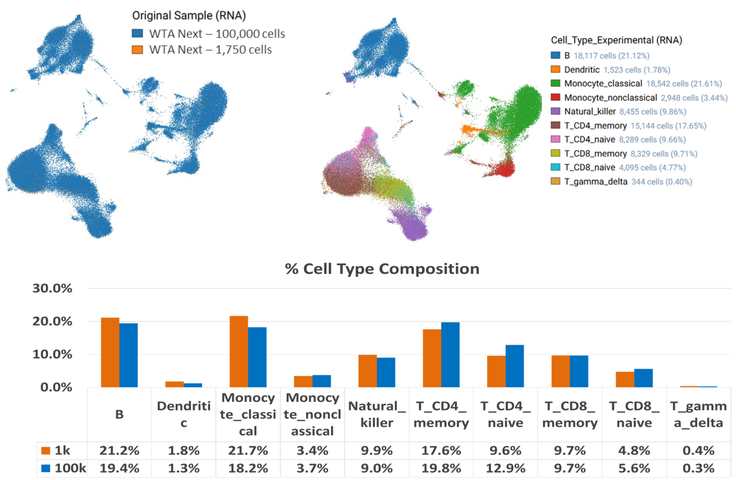


Figure 4: Resting PBMC samples were processed using WTA Next on the same day to generate 3 replicates. UMAP show consistent cell clustering and minimal batch effect for all replicates at a read depth of 25,000 reads per cell. * Note: No batch correction function used in UMAP generation.

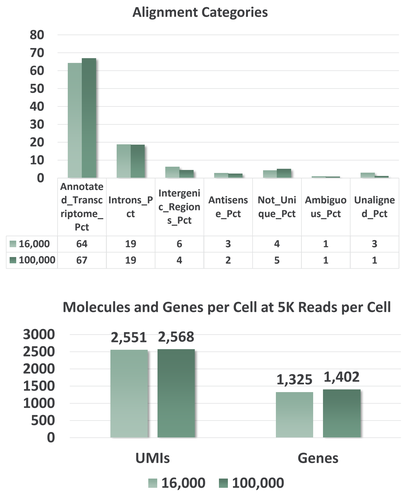
Flexible Cell Input up to 100K cells

Figure 5A. Consistent data across low and high cell input



	B	Dendritic	Monocyte_classical	Monocyte_nonclassical	Natural_killer	T_CD4_memory	T_CD4_naive	T_CD8_memory	T_CD8_naive	T_gamma_delta
1k	21.2%	1.8%	21.7%	3.4%	9.9%	17.6%	9.6%	9.7%	4.8%	0.4%
100k	19.4%	1.3%	18.2%	3.7%	9.0%	19.8%	12.9%	9.7%	5.6%	0.3%

Figure 5B. High data quality and sensitivity



	Annotated_Transcriptome_Pct	Introns_Pct	Intergenic_Regions_Pct	Antisense_Pct	Not_Unique_Pct	Ambiguous_Pct	Unaligned_Pct
16,000	64	19	6	3	4	1	3
100,000	67	19	4	2	5	1	1

Figure 5: (A) Resting PBMC sample was tested using WTA Next. ~ 2000 cells/lane and ~ 100,000 cells/lane cells were loaded onto BD Rhapsody HT cartridges, resulting in ~1.7k and ~84k cells respectively. UMAP shows clear cell clustering of different cell types for both cell inputs and each have similar cell type distributions. (B) Sequencing read alignments and WTA sensitivity remain high irrespective of cell input amounts.

Conclusions

- The BD OMICS-One™ WTA Next Assay shows high sensitivity yielding more than 3,000 median genes per cell at a sequencing depth of 25,000 reads per cell. This performance markedly exceeds that of the previous WTA version and is comparable to 10X Genomics GEM X v4.
- The BD OMICS-One™ WTA Next Assay is compatible with multiomic assays including multiplex CITE-seq, ATAC-seq, multiplex ATAC-seq and TCR/BCR Next assay and enhances gene detection, while maintaining other important metrics specific to these multiomicassays.
- Data generated using the The BD OMICS-One™ WTA Next Assay is highly reproducible and allows for flexible cell inputs up to 100K cells per lane on the BD Rhapsody™ Single Cell System. ~ 800 K cells per cartridge
- This enhanced-sensitivity WTA assay provides a comprehensive solution for scRNAseq profiling