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POSTER

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High-Throughput, Single Cell Whole Transcriptome Sequencing Analysis of Cancer Cells with the New BD FACSMelody™ Cell Sorter and BD™ Precise assay

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Abstract

Gene expression studies performed on bulk samples might obscure the understanding of complex samples. Gene expression analyses performed on single cells, however, can offer a powerful method to resolve sample heterogeneity andreveal hidden biology. Optimal sample preparation is critical to obtain high quality gene expression data from single cells.

Historically, single cells or small numbers of cells were isolated and prepared by limiting dilutions, laser capture microdissection, or microfluidics technologies, or fluorescence-activated cell sorting (FACS). FACS sorting enables highthroughput processing of a heterogeneous mixture of cells and ensures the delivery of single cells or a small number ofcells into a chosen receptacle to meet the selection criteria at a purity level that is unmatched by other approaches.Furthermore, by FACS, the single cell selection criteria can be based on surface marker expression, cell size, and granularity(represented by scatter). Sorted cells can be used for any downstream application including next generation sequencing(NGS).

In this study, the new, easy-to-use BD FACSMelody™ sorter was applied to sort individual cancer cells. Jurkat cells (a Tleukemia cell line), and T47D cells (a breast cancer cell line) were mixed, stained, analyzed, and sorted on a BD FACSMelody system. The individual cell's whole transcriptome was interrogated using BD™ Precise Single Cell WTA (wholetranscriptome amplification) Assay. Principal component analysis was applied to cluster the sorted Jurkat and T47D-cell populations.

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