Scalable and Flexible Single Cell RNA-seq

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In scRNA-sequencing, sample size is critical to confidently detect rare cell types and low-expressed transcripts. Accommodating large sample sizes enables multi-sample and time-course experiments. But with a large sample size come technical concerns, such as storing multiple samples until use without compromising their integrity and avoiding batch effect.

Parse Evercode™ Whole Transcriptome (WT) Mega can profile up to 96 samples across up to 1 million cells in a single experiment. A fixation procedure separates sample preparation from cell barcoding, enabling the pooling of different samples into one experiment. The Parse combinatorial barcoding strategy yields hundreds of thousands of uniquely labeled cells with a verified low doublet rate.

For this study, we collected 24 PBMC samples from donors over a three-week period, fixed them using the Evercode Fixation kit, and stored at -80C until use. We processed all 24 samples with a single Evercode WT Mega kit and generated more than 1 million individually barcoded cells that were used to generate a sequencing library. The FASTQ files resulting from sequencing were analyzed using the Parse data analysis pipeline.

After sequencing the transcriptome for 1 million cells, we could detect distinct sub-types of cells in each sample. With > 27,000 cells captured from each sample, we were able to generate gene expression profiles for low-frequency cell types such as classical and plasmacytoid dendritic cells.

Parse Evercode WT Mega showed high-resolution immune cell profiling and low-frequency cell subtypes identification.