Scalable and Highly Sensitive Single Cell RNA-seq through Combinatorial Barcoding

Genomics

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Combinatorial barcoding has been demonstrated as a promising approach to scaling up single cell and single nuclei transcriptomics. Here, we present a commercial kit that makes it possible to profile up to 48 different biological samples across 100,000 cells in a single experiment. The kit is based on the Split Pool Ligation-based Transcriptome sequencing (SPLiT-seq) protocol, but includes a streamlined workflow and dramatic improvements in performance. Transcript and gene detection have improved over 5-fold compared to the published method. The rates of doublets in resulting data are low even when profiling 100,000 cells (~3%). The workflow also enables biological samples that are collected on different days to be rapidly fixed, stored, and then later pooled and barcoded in parallel in a single experiment. We will share example data collected from various sample types including cell lines, brain, and PBMCs samples.