CITE-seq Protocols

Marlon Stoeckius,Peter Smibert

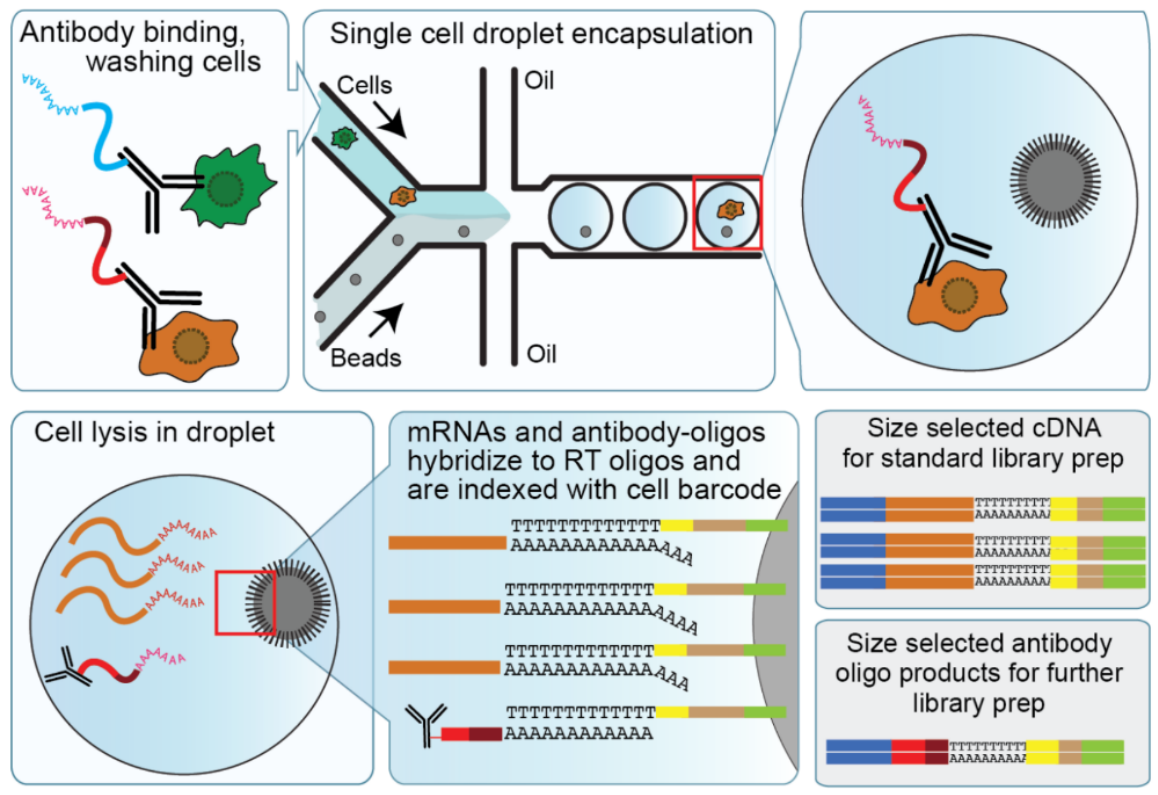
Abstract

This collection contains our main protocols for performing CITE-seq and Cell Hashing, specifically on Drop-seq or 10x Genomics single cell 3′ v2 chemistry.

CITE-seq:

Cellular Indexing of Transcriptomes and Epitopes by Sequencing (CITE-seq) is a multimodal single cell phenotyping method developed in the Technology Innovation lab at the New York Genome Center in collaboration with the Satija lab.

CITE-seq uses DNA-barcoded antibodies to convert detection of proteins into a quantitative, sequenceable readout. Antibody-bound oligos act as synthetic transcripts that are captured during most large-scale oligodT-based scRNA-seq library preparation protocols (e.g. 10x Genomics, Drop-seq, ddSeq).

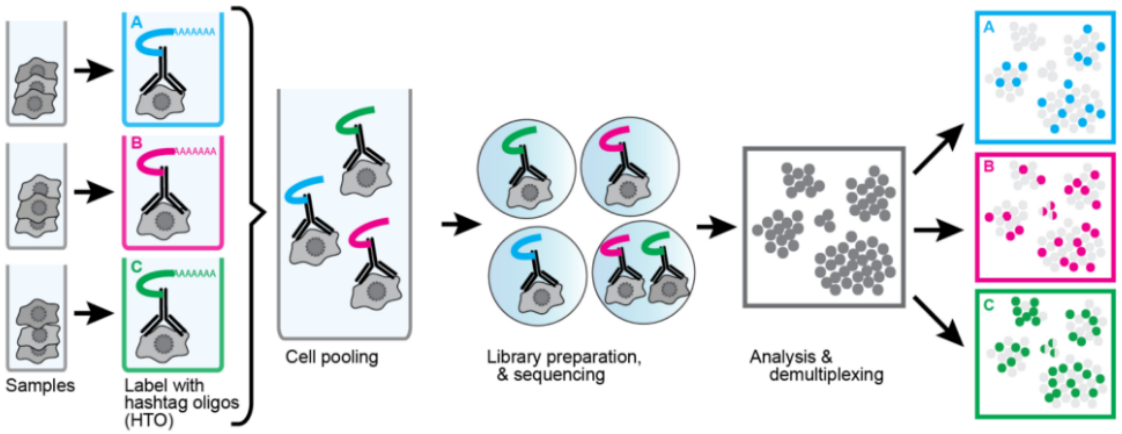


This allows for immunophenotyping of cells with a potentially limitless number of markers and unbiased transcriptome analysis using existing single-cell sequencing approaches.

Cell Hashing:

Sample multiplexing and super-loading on single cell RNA-sequencing platforms.

Cell Hashing uses a series of oligo-tagged antibodies against ubiquitously expressed surface proteins with different barcodes to uniquely label cells from distinct samples, which can be subsequently pooled in one scRNA-seq run. By sequencing these tags alongside the cellular transcriptome, we can assign each cell to its sample of origin, and robustly identify doublets originating from multiple samples.



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Collection

PROTOCOLS

1. CITE-seq

CONTACT: Peter Smibert

2. Cell Hashing

CONTACT: Peter Smibert

3. CITE-seq and Cell Hashing

CONTACT: Peter Smibert