Resource Summary Report

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CITE-seq and Cell Hashing

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Protocol Information

URL: https://dx.doi.org/10.17504/protocols.io.nhqdb5w

Authors: Marlon Stoeckius, Peter Smibert

Group: Human Cell Atlas Method Development Community

Summary: This protocol is for performing CITE-seq and Cell Hashing in parallel. 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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