Washington University in St. Louis
Office of Technology Management

SINGLE CELL MASSIVELY PARALLEL REPORTER ASSAYS

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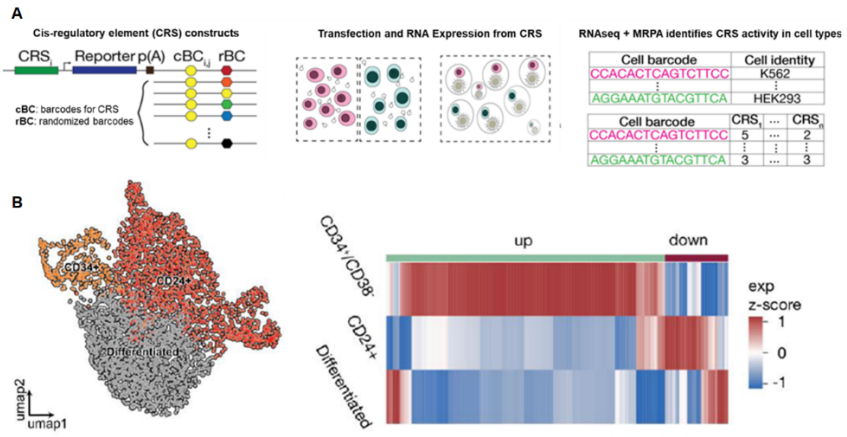
Technology Description

Researchers in Barak Cohen's lab at Washington University have developed a method for single cell massively parallel reporter assay (scMPRA) to preserve cell type-specific information. This technology is scalable and sequencing platform agnostic.

Massively parallel reporter assay (MPRA) is a powerful technique that allows high-throughput analysis of libraries of *cis*-regulatory sequences (CRSs). However, a major limitation of MRPAs is that they are generally performed in monocultures, or as bulk assays across heterogenous cultures and tissues, where the transcriptional information pertaining to any given cell type is lost. This technology overcomes the limitation by simultaneously measuring the activities of reporter genes in single cells and the identities of those cells using their transcriptomic readout. This technology should be of interest to anyone wishing to identify CRSs with cell-type specific activities or anyone wishing to create transgenes that drive cell-type specific activity



A) *Summary of the scMRPA workflow: The CRS library includes a novel 5' UTR dual bar-coded system. The library is transfected into cells/tissue of interest, followed by expression of constructs. scRNAseq and MRPA are carried out to identify the cell type as well as the activities of CRS within a given cell type.* ***B)*** *Detection of cellular subsets and their CRS profiles in the K562 (leukemia) line.*

Stage of Research

Researchers have successfully tested this technology on multiple human cell and tissue samples, including live explanted retinas.

Publications

Zhao S, Hong CKY, Granas DM, Cohen BA. (2021). A single-cell massively parallel reporter assay detects cell type specific cis-regulatory activity. *bioRxiv*.

Applications

- Assessing cell type-specific CRS activity in a large heterogenous biological sample, without *a priori* knowledge of the sample's cellular composition
- Discovering CRS activities in rare cells such as cancer stem cells without special enrichment or isolation procedures

Key Advantages

- Scalable and sequencing platform agnostic
- Provides granular information on CRS activity not possible with other MRPA methods

Patents: Pending

Related Web Links: Cohen Profile & Lab