CELLECTA

Single-Cell Screening. Simplified.

Single-Cell CRISPR Screening Service

CRISP-Seq, Perturb-Seq, CROP-Seq and more

Study the effect of CRISPR-based perturbations on mRNA expression in thousands of cells using single-cell RNA sequencing (scRNA-Seq) on the 10X Chromium system with **Cellecta's Single-Cell CRISPR Screening Service.** This powerful technique can provide important insights into the transcriptional response resulting from genetic mutations and other perturbations that affect gene function.

- Investigate transcriptional changes associated with 100+ genes in a single experiment
- Combine pooled CRISPR knockout (KO), CRISPR inhibition (CRISPRi) or CRISPR activation (CRISPRa) screening with single-cell expression analysis
- Identify genes affecting gene and pathway activation that are missed with conventional arrayed screens to learn how these genes depend and interact on each other

Cellecta offers its **Single-Cell CRISPR Screening Service** on the 10X Chromium Controller Platform, which allows for screening of multiple genes in a single experiment and enables the identification of transcriptional profiles linked to specific gene perturbations (Fig.1).

We carry out all the services required to run most screens onsite, including:

- Expert design, construction, and packaging of custom pooled sgRNA libraries
- Single-cell RNA-Seq runs on the 10X Chromium and Illumina sequencing instruments
- Bioinformatics workflow to align reads, identify hits, and provide post-screening analysis

Single-Cell CRISPR Screening workflow

Step 1: Clone sgRNA library

Step 2: Cells transduced with pooled sgRNA libraries are loaded in the 10X Chromium instrument

Step 3: Beads are co-encapsulated with unique barcodes and the cells are dispersed in discrete droplets

Step 4: The sgRNA and mRNAs labelled with bead barcodes are used to construct libraries. This is followed by the scRNA-Seq step, generating single-cell transcriptional profiles.

Step 5: Data analysis identifies changes in gene expression associated with gene-specific knockouts

Representative data is shown in Fig. 2.

Related Products

In addition to the full-service screening service, you may be interested in off-the shelf ready-to-use CRISP-Seq barcoded sgRNA libraries for anti-cancer targets as well as Cellecta custom sgRNA pooled library or construct service.

For more information on Cellecta's Single-Cell CRISPR Screening service, visit cellecta.com/services or email info@cellecta.com

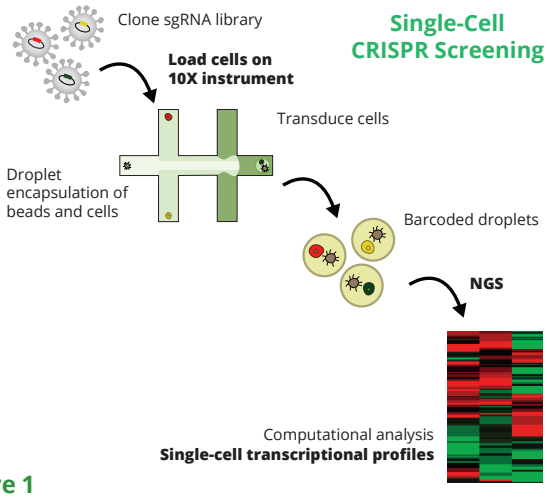

Figure 1

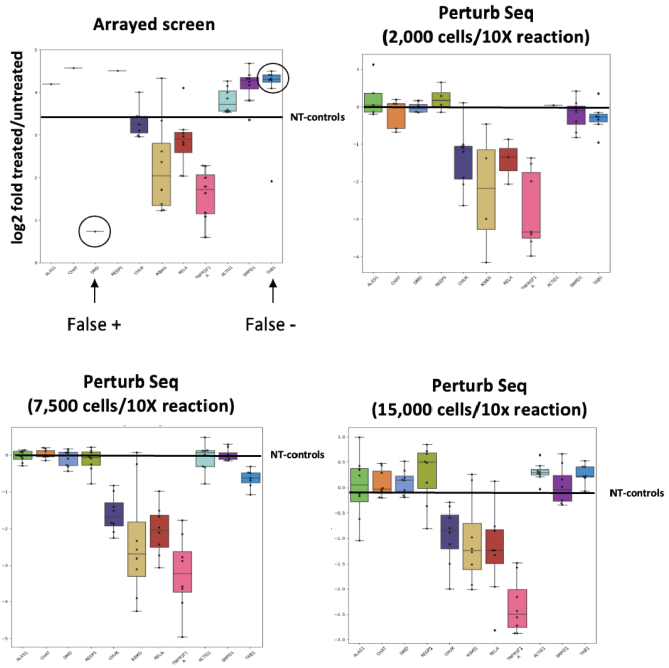

Figure 2

Comparison data obtained from Perturb-Seq screen of IL32 induced HEK293-Cas9 cells transduced with a small library of 85 guides targeting genes in the pathway for TNFα-induced transcriptional activation. Perturb-Seq were run with different numbers of cells and compared with a reference Arrayed screen with individual constructs from the same library. All three Perturb-Seq screens demonstrated better sensitivity than the arrayed screen and had lower false -ve and false +ve gene hits. Increasing the number of cells per 10X reaction from 2,000 (2 reactions: 4,000 cells total) to 7,500 and 15,000 (corresponding to 47 cells/sgRNA, 90 cells/sgRNA, and 180 cells/ sgRNA ratios, respectively) showed a positive effect on sgRNA library coverage and 90 cells/sgRNA proved to be adequate to cover the full complexity of the library.