Single-Cell Perturb and TAP Sequencing

Product overview

Perturb-seq is a high-throughput pooled CRISPR screen that combines CRISPR technology for precise gene manipulations with single-cell RNA sequencing (10x Genomics) allowing for whole transcriptome profiling of perturbation effects.

TAP-seq (TArgeted Perturb-seq) has a similar approach but focuses on a subset of genes, selected by the user, using gene-targeting primer pools. TAP-seq is cost effective and is more sensitive for lowly expressed genes.

Sequencing will be performed on the NovaSeq X Plus platform (Illumina) with tailored sequencing settings based on the project design and the user's needs.

What is included

- GEM generation
- Single-cell library preparation
- Quality control of cDNA and library
- Library pooling and sequencing on Illumina NovaSeq X Plus
- FASTQ files
- Standard data processing, QC, and basic bioinformatics analysis (optional).

Input and quality requirements

Isolation of cells or nuclei

Preparation and thawing of perturbed cells as well as cell counting is the responsibility of the user. Contact SCOP to consult.

Quality

The quality of the cells will reflect the downstream process – poor quality leads to poor data.

- > 90% cell viability (a cell viability between 70-80% can be accepted but data quality may be compromised)
- Intact cell membranes
- No to minimal debris and cells aggregates.

SCOP strongly recommends performing a pilot experiment to assess both sample and data quality.

Sample drop-off

Perturbed cells should be delivered at a specific concentration which depends on the assay type and the desired number of cells. Contact SCOP for more information.

Data deliverables

SCOP's preprocessing workflow includes:

- FASTQ files.
- Preprocessed data stored in Seurat objects.
- Output from Sceptre.