ATAC Sequencing

Product Overview

The Assay for Transposase-Accessible Chromatin (ATAC) sequencing provides a simple and scalable way to profile chromatin accessibility across the genome. ATAC-seq can be used to uncover gene regulation and transcription factor binding during perturbations or disease.

The ATAC-seq protocol, Omni-ATAC, is robust and can be used on a variety of mammalian cells and tissue types. Isolated cells or nuclei are lysed, and accessible chromatin is captured using Tn5 transposase. Fragments are amplified, purified and their quality is controlled. Libraries are sequenced on the NovaSeq X Plus platform (Illumina) with tailored sequencing settings based on the project design and the user's needs.

What is Included

- Library preparation
- Quality control of library
- Library pooling and sequencing on Illumina NovaSeq X Plus
- FASTQ files
- Standard data processing and QC (optional).

Input and quality requirements

Input

In general SCOP recommends:

- 50.000 freshly cultured cells (or nuclei) per sample in a total volume of 100µl
- 60.000 cryopreserved cells (or nuclei) per sample in a total volume of 100µl (cryopreserved samples may have reduced quality).

Quality

The quality of the samples will reflect the downstream process – poor quality may lead to compromised data.

- If using cells as input: > 90% cell viability)
- If viability is <90%, pretreat with DNase.

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

Data Deliverables

The data will be processed with the NF-core pipeline. The data will be transferred to the project folder including:

- FASTQ files
- Output files from pipeline
- Data upload to repository prior publication.

Disclaimer

SCOP does not offer services such as:

- Cell culturing
- Cell or nuclei isolation.