Single Cell Sequencing

GENERAL DETAIL REPORT

Go beyond averages and get the most accurate picture of your cells' transcriptomes with single cell sequencing. Using state-of-the-art 10x Genomics Chromium technology, we offer accurate, reliable data – including immune cell profiling – at various throughput levels to suit your requirements.

INTRODUCTION

Single-cell sequencing, named Method of the Year for 2013 by *Nature*, is a powerful tool for understanding gene expression at the individual cell level.

Single-cell methods offer a way to dissect heterogeneity in tissue samples or cell populations, allowing for better predictions of disease progression, identification of new drug targets, measurement of efficacy, determination of unknown or rare cell types or states, study of immune profiling, and more. These methods hold enormous potential for tackling diseases such as cancer and neurodegeneration. Another advantage of single-cell sequencing is its ability to make rare cells more accessible for analysis, provided that effective methods are available to isolate or enrich these cells from their heterogeneous environments.

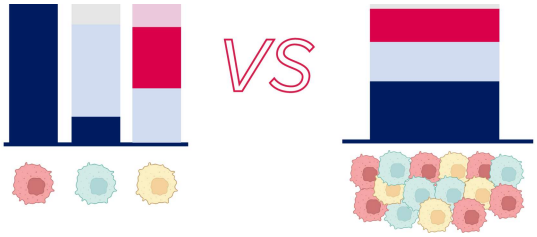
SINGLE-CELL ANALYSIS VS BULK ANALYSIS

Both technologies have their advantages, and the choice largely depends on what you are trying to achieve in your research. Let's have a look!

With bulk RNA sequencing, you get an overview of the average differences in gene expression between samples (e.g., cancer patients versus healthy individuals). This can be sufficient if your goal is to discover biomarkers for cancer or to study the biology of diseases.

Single-cell sequencing offers the potential to uncover molecular differences that are specific to certain cell types. Sometimes the key lies in specific cell types, and in that case, it's necessary to look at gene expression in individual cells rather than an average representation.

It does not have to be an either/or decision. Integrating data from both bulk and single-cell sequencing experiments can bring you valuable insights!



would evolve, identify new drug targets and efficacy, determine unknown cell types and study immune profiling

It makes rare cells more accessible to analysis. This method allows to isolate or enrich these cells from their heterogeneous environments.

FIELD OF RESEARCH

Oncology

Single-cell transcriptome profiling can identify biologically relevant differences in cells, even when they may not be distinguishable by marker genes or cell morphology. A tumor is never a homogeneous mass of cells but rather a mixture of different tumor cell types, each influencing the tumor in a unique way. This complexity makes it challenging to identify the precise molecular mechanisms at work when analyzing bulk RNA-seq expression data. However, **the enhanced resolution of single-cell sequencing enables the assessment of tumor heterogeneity and a deeper understanding of how tumors behave within their microenvironment.**

Development Biology

Stem cells develop and differentiate into progenitor and mature cells by following specific differentiation pathways. In some species, these developmental processes can be reactivated to regenerate tissues, offering significant potential for treating congenital diseases and advancing regenerative medicine. Single-cell sequencing is a powerful tool for studying these developmental patterns at the level of individual stem or progenitor cells, enabling the precise determination of cell lineage. **This technology allows for the identification of the stages of differentiation and the corresponding cell types, from stem cell to mature cell, across any species and cell type.**

Immunology

The immune system is highly complex, consisting of various cell types and sub-types, each involved in different immune responses. Studying this field at high resolution with single-cell sequencing can deepen our understanding of these intricate processes. This approach enables the identification and characterization of immune cell types in your sample, including their cell surface markers. Additionally, **single-cell sequencing can identify antigen specificity, aiding in the further characterization of immune cell populations and facilitating antibody discovery.**

Neuroscience

The field of neuroscience greatly benefits from the high-resolution data provided by single-cell sequencing. The central nervous system is a complex structure composed of various cell types and signaling pathways. By

References:

https://www.nature.com/articles/nmeth.2801

https://www.nature.com/articles/s41368-021-00146-0