

# Single cell gene expression analysis

## Consultation guidelines

The following guidelines outline a few points you should consider before discussing your project with the Next Generation Sequencing Platform (NGSP) and/or the Interfaculty Bioinformatics Unit (IBU). This will ensure that all important points are discussed and we can provide you with the best possible advice on your project. **Please note that if you require bioinformatics support, it is best to include NGSP and IBU in the same meeting.**

Single-cell RNA-seq experiments are typically aimed at identifying differences in gene expression between (groups of) cells.

### 1. General experimental design

- a) What is the biological question you want to address?
- b) What is your study species?
- c) What experimental design do you have in mind? Specifically, are you interested mostly in identifying cell types within individuals or, additionally, in comparing different samples and/or experimental groups. How many samples in total? **It is generally very helpful to have a schematic representation of the design for discussion.**

### 2. Library preparation and sequencing

- a) Which tissue(s) will be used?
- b) Will you be able to provide a single cell suspension without dead cells, debris or cell clumps?  
→ Perhaps consider a pilot.
- c) Will you be able to provide backup samples?
- d) Do you have any prior information about the heterogeneity of the input cells? Are there any cell types of particular interest? If yes, what is their expected frequency among the input cells?
- e) Do you know the size of your cells?

### 3. Bioinformatic processing

- a) Who will be doing the bioinformatics processing of your data? The following models are possible:
  - i. No bioinformatics. In this case, you will receive fastq files for your samples.
  - ii. Standard analysis as outlined here:  
[https://www.bioinformatics.unibe.ch/services/service\\_mode/single\\_cell\\_rna\\_seq/index\\_eng.html](https://www.bioinformatics.unibe.ch/services/service_mode/single_cell_rna_seq/index_eng.html)

Here, you will receive a basic analysis, and additional downstream analyses will be run by your group. This service is particularly useful for researchers who want to do some downstream analyses on their own, but want to avoid the preprocessing steps which typically require access to a high performance computing infrastructure.

- iii. Custom analysis: Please prepare a description of additional analyses/visualisations you would need. For example, you could refer us to selected publications that include the type of analysis you have in mind.