

# Sample requirements for single-cell applications on 10x Genomics Chromium System

## General remarks:

- 1) Fresh or cryopreserved cells can be used for single-cell applications.
- 2) For snap-frozen samples nuclei have to be prepared.
- 3) The system requires a single cell / single nuclei suspension.
- 4) Clumps will cause clogging and failure in droplet formation.
- 5) Please filter cells / nuclei with a regular FACS filter if necessary.

## Sample preparation:

- 1) Cryopreserved samples have to be washed to remove any freezing buffer.
- 2) Free RNA / DNA will cause severe contamination and the detection of single cells in the data analysis will fail.
- 3) Please remove any debris / dead cells with appropriate methods (e.g. gradient centrifugation, apoptosis separation kit, washing, etc.).
- 4) Cells / nuclei should be counted to achieve optimal loading of the chip.
- 5) If the samples were processed by FACS, please use the total count after sorting divided by 1.5 as a cell number estimate.
- 6) Typically 50% of the input number of cells are captured. Input cell number may range from 500 to 20.000 cells.
- 7) Please provide the cell / nuclei suspension in 35  $\mu$ l with the total cell numbers as stated above (500 – 20.000). Buffer may contain FCS, BSA or sucrose. Do NOT exceed 35  $\mu$ l as this is the maximal volume that can be loaded on the Chromium machine.
- 8) If you wish to provide larger volumes / higher cell number / higher cell concentration due to sample stability please count the cells (and provide the cell concentration as number of cells /  $\mu$ l).
- 9) Processing should be done as quickly as possible – please let us know at least 30 min prior to the start of the run as the chemistry has to be thawed and prepared.
- 10) Eight samples can be loaded on one chip. Fewer samples are possible however – please state the number of samples in the 10X check list below.

## Cost estimates for consumables:

Library preparation/sample: 1,500 €

Lab:

# 10x check list

Cell type:

Method:  *scRNA-seq*     *sc-V(D)J*

Date:

## Single cell suspension:

*Fresh cells*

*FACS*

*filtered*

*Cryopreservation*

*dissociated tissue*

*snap-frozen*

*Nuclei*

## Buffer:

*PBS*

*+ medium / FCS*

*+ BSA*

*other, please specify:* \_\_\_\_\_

## Source:

*cell culture*

*primary samples*

## Species:

*Human*

*Mouse*

*Other*

## Cell number:

sample								
# cells / $\mu$ l								
# cells loaded *								

\* will be filled out in the sc-open lab