

Single-cell 10X Genomics Sample Delivery Instructions

RNA-seq

1. Cell/nuclei concentration should be in the range of 700-1200 cell/ul. Please bring at least 30,000 cells (recommended 50,000 cells). See table below for details on expected number of captured cells/nuclei based on sample's input:

Optimal input cell/nuclei concentration	Cell recovery target
700 - 1,200 cells/μl	500 - 10,000 cells
1,300 - 1,600 cells/μl	10,000 - 20,000 cells

2. Cell viability should be >90%. For viability of <70%, dead cell removal must be performed prior to bringing
3. For cell processing, cell counting and dead-cell removal, please follow 10x protocols available on our [website](#).
4. For customized and optimized dissociation protocols please visit- <https://www.worthington-biochem.com/tissuedissociation/>

Multiome ATAC and Gene Expression

1. See table below for details on expected number of captured nuclei based on sample's input. We recommend submitting double the desired amount to account for repeat library prep.

Optimal input nuclei concentration	Nuclei recovery target
500 nuclei/μl	160 - 400 nuclei
1,000 nuclei /μl	320 - 810 nuclei
2,000 nuclei /μl	650 - 1,610 nuclei
3,000 nuclei /μl	970 - 2,420 nuclei

4,000 nuclei / μ l	1,290 - 3,230 nuclei
5,000 nuclei / μ l	1,610 - 4,030 nuclei
6,000 nuclei / μ l	1,940 - 4,840 nuclei
7,000 nuclei / μ l	2,260 - 5,650 nuclei
8,000 nuclei / μ l	2,580 - 6,450 nuclei
9,000 nuclei / μ l	2,900 - 7,260 nuclei
10,000 nuclei / μ l	3,230 - 8,060 nuclei

2. Nuclei isolation for 10x multiome protocols are available on our [website](#).
3. Nuclei quality should be assessed according to [10x guidelines](#).