

Sample Submission Guidelines (for sc/snRNA-seq)

Successful library preparation for single-cell and single-nuclei RNA sequencing is highly dependent on sample quality, viability, and proper handling. Please review the following requirements carefully prior to submission. The optimal input depends on the platform (e.g. 10x Genomics, BD Rhapsody, etc.), but typical recommendations are:

Single-cell suspensions:

- $\geq 50,000$ – $1,000,000$ cells total (preferred range depends on target recovery)
- Cell viability should be $\geq 85\%$ (measured by Trypan Blue or equivalent)
- Minimal debris and cell aggregates
- Cells should be **intact and not lysed**
- Doublets/multiplets should be minimized

Single-nuclei suspensions:

- $\geq 100,000$ nuclei total
- Nuclei should be **intact with clearly defined borders**
- Minimal cytoplasmic contamination
- Low clumping and debris
- DAPI staining (or similar) recommended to confirm integrity

Final concentration:

- 700–1,200 cells or nuclei/ μL (platform-dependent; please confirm with the core prior to sample submission)