Center for Cellular Profiling: Cytometry and Single-Cell Multiomics

Brigham & Women's Hospital

New User or New Project Introductory Questionnaire

Thank you for your interest in our core. For new users or new project requests, we ask that you please create a Power Point slide or two addressing the following questions and send the attachment to SingleCell@bwh.harvard.edu:

1. Please state basic experimental design, questions, and project goals. *(Note: when designing experiment, take into account batch effects which can often confound biological signal. Here is a blog post with best practices.)*

2. If you plan to submit multiple samples, what is the total number of samples you expect to submit in the next 3 months?

3. What is the species of origin & cell type you wish to submit?

4. When was your sample collected?

5. If your samples were collected after 01/01/2020 and are any of the following: respiratory samples, saliva, stool, or tissues of the lung, gut, heart, liver, brain, and kidney, can you provide written documentation of COVID status?

6. If isolating cells from tissue, has the tissue dis-aggregation/digestion protocol been optimized?

7. What is the cell yield and viability of your sample?

8. What is your method of cell isolation: Flow Sorting, MACS, etc? (*Note: If requesting CITE-seq service and using flow sorting as isolation method, please provide list of antibodies used in each panel)*

Note: we require the viability to be at least 85% for optimal sequencing results. In most cases, some form of live cell purification, either by FACS or MACS column, is required. We therefore request that prior to scheduling a consult with us, you undertake necessary optimization to ensure adequate cell yield and viability. If applicable, we can offer to perform a QC check of your technique on our automated cell counter.

9. For Nuc-Seq/ATAC-Seq projects, has cell lysis protocol for nuclei isolation from your cells of interest been optimized? See the cell lysis protocols here.

10. What is the expected size of your cells? *(Note: According to 10X, the microfluidics chip used to capture cells has a cell size maximum of ~ 60um)*

11. How many different condition(s) are you interested in comparing?

12. Does your lab have experience with bulk- or single-cell RNAseq of these cells?

13. What is your bioinformatic capacity?

14. For billing purposes, do you plan to use an internal MGB Peoplesoft Fund or an external non-MGB source of funding? *(Note: if external, please provide more details)*