Determining Coverage for Sequencing Single Cell Libraries

The Genomic and RNA Profiling Core is a proud partner with the Single Cell Genomics Core and the Multi-Omics Data Analysis Core at Baylor College of Medicine. Working with the SCG and Multi-Omics Data Analysis Cores, GARP offers quality control, quantification, sequencing and analysis services for single cell based experiments. Most single cell libraries are generated using the 10X Genomics Chromium platform.

10X Genomics offers a variety of applications for Single Cell Sequencing, which include 3' Gene Expression (3' GEX), 5' Gene Expression (5' GEX), 5' V(D)J for paired T-Cell Receptor (TCR) and B-immunoglobulin (Ig) profiling as well as scATAC-seq. The Single Cell Genomics Core will work with users to determine the best approach for the researcher's study. Typically, SCG recommends targeting a standard number of cells when generating libraries for each library application that offers significant coverage for identifying sequences and genes of interest. These standard number of cells are as follows:

10X 3'v3 GX: 15,000 cells targeted

10X 5'GX: 10,000 cells targeted

10X 5'VDJ: 10,000 cells targeted

10X ATAC: 10,000 cells targeted

10X Genomics recommends the following depth of coverage per cell:

10X 3'v3 GX: 20,000 read pairs per cell

10X 5'GX: 20,000 read pairs per cell

10X 5'VDJ: 5,000 read pairs per cell

10X ATAC: 25,000 read pairs per cell

So the following depth of coverage are standard for libraries generated by the Single Cell Genomics Core at BCM. The SCG Core will inform you if more or fewer cells than the standard were targeted during library generation.

10X 3'v3 GX: 15K cells targeted per sample x 20K read pairs per cell = **300M reads per sample**

10X 5'GX: 10K cells targeted per sample x 20K read pairs per cell = **200M reads per sample**

10X 5'VDJ: 10K cells targeted per sample x 5K read pairs per cell = **50M reads per sample**

10X ATAC: 10K cells targeted per sample x 25K read pairs per cell = **250M reads per sample**