



Single Cell Genomics Guide

This document provides general information on the following single cell genomic services offered by the Advanced Genomics Technologies (AGT) Laboratory under the direction of Professor Ioannis Ragoussis at the McGill Genome Centre.

Using Single Cell 10X Genomics Platform

- Gene Expression
- Immune Profiling
- Multiome ATAC + Gene Expression Support
- Copy Number Variation (CNV)
- ATAC

Using SMART-Seq

- Single cell RNA-seq
 Single cell RNA-seq by in-house protocol

Make a service request

First create a user account on our website (hercules.genome.mcgill.ca) and follow the service request instructions. Our team will evaluate the pricing and feasibility of your project and will contact you to proceed with the project.

Preparation of samples

The samples should be submitted as

- Cell suspension in PBS (calcium and magnesium free) containing 0.04% weight/volume BSA (400 µg/ml) then kept on ice.
- Single nuclei can be submitted in PBS (calcium and magnesium free) containing 1% weight/volume BSA (10 mg/ml), on ice.
- Cells may be cryopreserved in 15% DMSO in cell culture media containing 20% FBS then shipped on dry ice.

* If you would like to submit samples in any other formats, please contact us in advance to discuss how to proceed.

Below you can find the required volume and concentration of cells/nuclei suspension and the suggested containers for sample submission:

| Sample type | Minimum volume (µL) | Recommended cell concentration | Recommended cell number | Suggested container |
|-------------------|---------------------|--------------------------------|-------------------------|--|
| Dissociated cells | 50 | 1000 cell/ul | 50,000 | 1.5 mL LoBind Tube ¹ on ice |
| Isolated nuclei | 20 | 2000 nuclei/ul | 40,000 | 1.5 mL LoBind Tube ¹ on ice |

¹1.5 mL LoBind Tube - Eppendorf catalog #22431021



The tubes must be clearly identified with sample name. If several tubes are submitted at the same time, please ensure that each of them is labeled legibly. The names on the tubes must match those on the manifest. (See below).

Please note that cell-counting and viability assessment is included in the service in order to ensure satisfactory results.

Sending/delivering the samples

Due to sensitivity of the experiment, it is preferable that single cells are delivered in person, on ice. Samples can be brought directly to the McGill Genome Centre, such shipments must be coordinated with authorized personnel (listed below) prior to delivery.

Cryopreserved samples must be transported either on dry ice in an appropriate container (styrofoam insulating box) or in a cryogenic cylinder for transport in liquid nitrogen. If shipping, make sure the package bears the Class 9 mark and the total weight of dry ice contained in the cooler according to the regulations for the transportation of dangerous goods in Canada. The shipment should be organized so that reception takes place during working days to ensure that the integrity of the sample is preserved.

Samples should be sent to the following address:

***Single Cell Dept.
Room 5500
McGill Genome Centre
740 Avenue du Dr. Penfield, Montréal (Québec), H3A 0G1
Tel: 514-398-3311 ext. 09860***

Transport costs are the responsibility of the customer and the tracking number provided by the transport company must be communicated to us by email at the following addresses:

yc.wang@mcgill.ca

ashot.harutyunyan@mcgill.ca

Confirmation of receipt will be sent to you mentioning the condition of the package on arrival.

Document to be attached to samples

Your shipment must be accompanied by the following sample manifest document (available at <https://www.mcgillgenomecentre.ca/hercules-resources/>), filled with all the information related to your samples. You can contact us if you need to provide more specifications than the model allows. (See contact persons below)

This completed document must be returned to us by email at the same addresses as for the tracking number and a hard copy must be included in your package.

A valid purchase order (PO) corresponding to the statement of work (SOW) must also be received prior to starting the single cell capture experiment.



After sequencing

Following sequencing and fastq generation and raw data release a second level of quality control is performed to verify that high level single cell metrics are within acceptable range. The resulting expression matrices will be made available. Alignment bam files will be made available upon request. For non gene expression applications the appropriate tool will also be run and the output made available.

For more information

For more questions, please contact us by email: agt.genome@mcgill.ca

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