

# USER GUIDE



## RNA SEQUENCING AT THE GSC



Bringing Genomics to Life.

# ABOUT US

The GSC's CAP, DAP and ISO 27001 certified technology platform is a high-throughput, large-scale DNA and RNA sequencing and analysis facility that has been designed to maximize analytical capacity, diversity, efficiency, scalability and flexibility. Our state-of-the-art clinical, sequencing, bioinformatics and proteomics platforms are ready to be put to use for your research or clinic.

We partner with researchers, guide experimental design, execute high quality processing of complex and valuable biological samples and provide extensive bioinformatics analyses with the aim of making genomics research accessible to our partners and collaborators within the scientific community.

Please feel free to [contact us](#) if you have any questions about the services we provide.



[www.bcgsc.ca](http://www.bcgsc.ca) | [info@bcgsc.ca](mailto:info@bcgsc.ca) | [@BCCancer\\_GSC](https://twitter.com/BCCancer_GSC)

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# | THIS GUIDE

This user guide is for the preparation of samples for RNA extraction at the GSC or RNA extracted in your laboratory. If you are submitting constructed libraries, please refer to our [Constructed Libraries User Guide](#).



# 1 SAMPLE PREPARATION

## Submitting samples for RNA extraction at the GSC

We accept a variety of samples for RNA extraction and sequencing at the GSC including blood, fresh or frozen tissues, formalin-fixed paraffin-embedded (FFPE) tissues, and saliva and buccal (cheek) swabs. Tissue and cell samples are accepted in tube format.

All samples must be frozen at -80°C immediately after sectioning. The following starting material guidelines work well for human and mouse samples. If working with other organisms, please [contact us](#).

SAMPLE TYPE	PIPELINE	SUBMISSION REQUIREMENTS
FFPE	Ribodepletion	Scrolls: min 120 mm <sup>2</sup> x 10 µm. For tissue surface area ≤ 120 mm <sup>2</sup> up to 3 scrolls per 1.0 mL matrix tube. Cores: 2.5 mm x 1-3 mm. Up to 2 cores per matrix tube.
OCT	RNA	Sections: 50 µm x 10 mm x 1 mm, minimum of 4 sections supplied in 2 mL tubes.
Fresh Frozen	RNA	Sections: 50 µm x 10 mm x 1 mm, minimum of 4 sections supplied in 2 mL tubes.

**\*Note** that we currently are not accepting tissue samples for nucleic acid extraction via online sample submission. Instructions for sample submission will be provided to you.

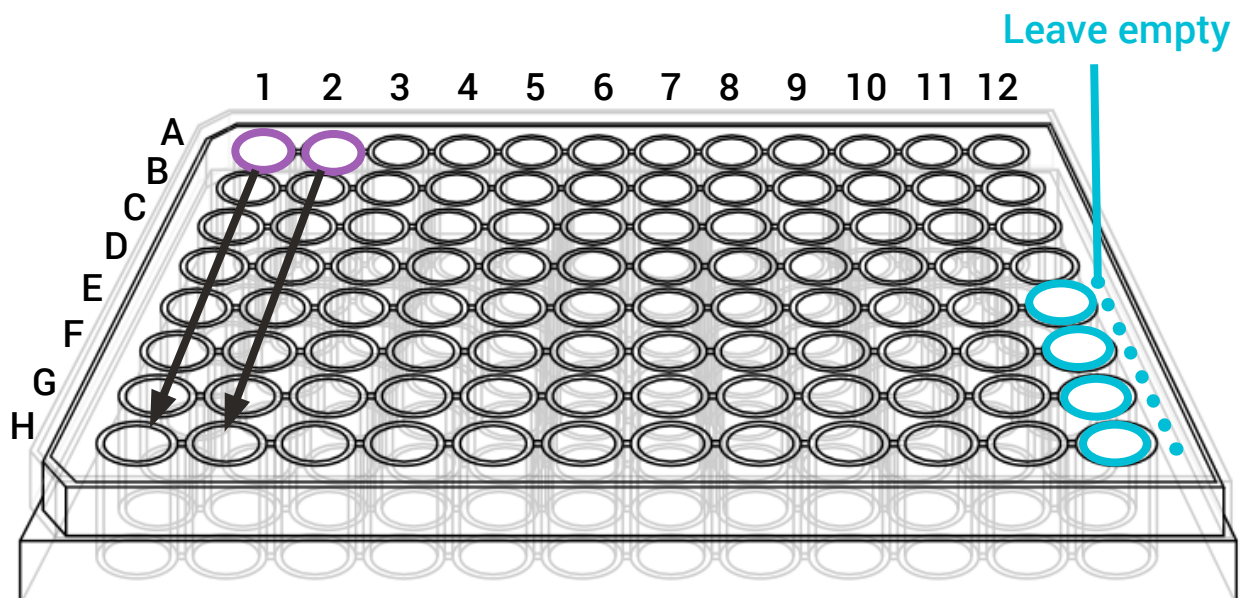
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## Submitting extracted RNA for library construction

Extracted RNA samples must be submitted frozen, and samples must be normalized by concentration. RNA samples are accepted in the following formats:

- Less than 24 samples: 1.5 mL snap-top Eppendorf tubes (or equivalent). Screw cap tubes are not accepted.
- 24 or more samples: Samples to be submitted in Axygen 96 FS-C plates, or equivalent. If these are not available in your lab, contact us at [GSC\\_submissions@bcgsc.ca](mailto:GSC_submissions@bcgsc.ca) and we will supply one.

If submitting in a 96-well plate format, arrange samples in columns (eg. A1 to H1; A2 to H2). Wells E12, F12, G12 and H12 must be left empty for internal controls.



For best library construction results please submit the recommended amount of starting material or more. The recommended starting materials work well for human or mouse derived nucleic acids. Please enquire if you are working with other species.

LIBRARY TYPE	STARTING MATERIAL	SUBMISSION REQUIREMENTS
mRNA using strand specific protocols (ssRNA-Seq)	Total RNA	<b>Recommended:</b> 750 ng <b>Minimum:</b> 250 ng (enquire for non-mammalian) <b>Concentration:</b> >12.5 ng/μL (in 20-35 μL) <b>Quantification:</b> Agilent Bioanalyzer RNA nano chip <b>Quality assessment:</b> Agilent Bioanalyzer RNA nano chip <b>Quality value:</b> RIN > 7 (not applicable for FFPE) <b>Additional assessment:</b> A260/280, A260/230
Low input RNA (ribodepletion)	Total RNA	<b>Recommended:</b> 50 ng <b>Minimum:</b> 40 ng <b>Concentration:</b> >4 ng/μL (in 10 μL) <b>Quantification:</b> Agilent Bioanalyzer RNA pico chip <b>Quality assessment method:</b> Agilent Bioanalyzer RNA pico chip <b>Quality value:</b> RIN > 7 (not applicable for FFPE) <b>Additional assessment:</b> A260/280, A260/230
Ribodepleted strand specific RNA-Seq	Total RNA	<b>Recommended:</b> 200 ng (1 μg for FFPE RNA) <b>Minimum:</b> 125 ng (800 ng for FFPE RNA) <b>Concentration:</b> >12.5 ng/μL (>80 ng/μL for FFPE) (in 10 μL) <b>Quantification:</b> Agilent Bioanalyzer RNA nano chip <b>Quality assessment method:</b> Agilent Bioanalyzer RNA nano chip <b>Quality value:</b> RIN > 7 (not applicable for FFPE) <b>Additional assessment:</b> A260/280, A260/230
miRNA	Total RNA	<b>Recommended:</b> 1 μg <b>Minimum:</b> 700 ng <b>Concentration:</b> >70 ng/μL (in >4 μL) <b>Quantification:</b> Agilent Bioanalyzer RNA nano chip <b>Quality assessment method:</b> Agilent Bioanalyzer RNA nano chip <b>Quality value:</b> RIN > 7 (not applicable for FFPE) <b>Additional assessment:</b> A260/280, A260/230

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## 2

# SAMPLE SUBMISSION

Our guide to online submissions will provide helpful information that will assist you in navigating our online submission website. Please contact us at [GSC\\_Submissions@bcgsc.ca](mailto:GSC_Submissions@bcgsc.ca) if you have any questions.

Online Submissions webpage: <https://www.bcgsc.ca/samplesubmissions>

**\*The online submission form must be completed and approved prior to submitting your samples to the GSC.**

This guide is for the submission of **extracted RNA**. If you are submitting samples for nucleic acid extraction at the GSC, submission instructions will be provided.

### OVERVIEW

Please read this entire section prior to starting your submission. This section will describe all information that is required to successfully fill out your submission form. We recommend ensuring all required information is gathered prior to starting your submission.

**To start a new submission**, click on the **Dashboard** or **Submissions** tab on the left side panel, and then the “Start New Submission” button. Please note that an active Statement of Work (SOW) is required to start a new submission and each SOW requires a new submission.

**To continue working on an existing submission**, click “Submissions” on the left side panel. This is the central location from which you can view all of your current and past submissions, as well as your submission status.



## Questionnaire

There are three tabs to complete in this section, corresponding to three categories of information required. Please note that all the fields in the three tabs are mandatory. You need to complete each field in order to proceed to the next page.

1. SOW Selection
2. Sample Details
3. Work Request

## Sample Information

There are ten mandatory tabs to complete by providing information about your samples. If submitting one of the following sample types, there will be additional tab(s) to complete: Xenograft and Cell Lines.

We recommend that you complete all the fields relevant to your samples. Some fields are mandatory (denoted by \*) and other fields are optional (but recommended for tracking purposes).

1. Sample Information
2. Tissue Information
3. Pathology Information
4. Pathology Information Continued
5. Analyte Information
6. Analyte Information Continued
7. Work Request Assignment
8. Work Request Pooling
9. Comments and Extra Information
10. Submission Review

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## QUESTIONNAIRE

### SOW section

- Submission Name: create a submission name that is complex enough to easily and uniquely identify each submission. For example, "Doe Lab ABC cell-line transcriptomes."
- Statement of Work (SOW): select a SOW from the drop-down menu provided. If your SOW is not listed, please contact GSC Projects at [SOW@bcgsc.ca](mailto:SOW@bcgsc.ca). If a SOW has a revision associated, please select the parent SOW. Once selected, options for revisions will appear in a separate drop-down list. Please select the appropriate revision for the sample submission.
- Once the SOW is selected, PI and Dissemination Recipients(s) will be displayed on the right. To edit the dissemination recipients list, please return to the SOW homepage in the SOWs section. Only the PI or a designated Dissemination Editor can edit this list.

### Sample details

- Sample Type: only one sample type is allowed per submission.
- Sample Number: a maximum of 92 samples, corresponding to one plate, are allowed per submission. Unless otherwise instructed, 1-23 samples need to be submitted in 1.5 mL Eppendorf tubes (or equivalent) and 24-92 samples need to be submitted in an Axygen 96 FS-C plate or equivalent. If this plate is not available in your lab, the GSC can supply one. Please click the "Request a Plate" checkbox, and we will contact you to confirm whether you want to pick up the plate from the GSC or have it shipped. If the latter, you will need to provide your shipping address and FedEx account number.
- Taxonomy: you may enter multiple taxonomy IDs per submission. You may search by typing NCBI taxonomy ID (e.g. 9606) or name (e.g. human). Only selected taxonomy IDs will be available later in your submission.

- Additional Sample Information: select any that apply. There are additional fields you need to complete for these sample types listed.
- Unused sample: indicate what you want us to do with any unused samples upon completion of your project. If you select "Destroy unused sample," we will discard your samples six months following data dissemination.

### **Work request**

- Please refer to your SOW to obtain the work request information that will be required in this section.
- If the samples you are submitting have different library protocol and/or sequencing goals, you will need to click "Add Additional Work Request" to be able to enter different goals for each sample.
- Once the sample information is completed and before the form is submitted, you will assign one of the work requests to each sample. At this point, you can also edit or add work request details.
- You will also be able to enter any additional comments regarding your work request such as specific pooling strategy, should extra or clarifying information be required.

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## SAMPLE INFORMATION

### Overview

There are at least ten tabs to complete in this section. Note that mandatory fields are denoted by \*. Certain field selections will grey out mandatory fields. In these situations field entry is not required.

For additional information on any given field, click the column heading (Figure 1, Arrow A).

Under each column heading are tools to help you complete each field more conveniently (Figure 1, Arrow B). Please refer to the tool tips on the top right corner to find out how each tool can help (Figure 2).

	#	Pool ID*
		▼ 📄 ✏️ ☰
-	1.	Sample 1
-	2.	Sample 2


FIGURE 1

<u>Column Options</u>
(Click icon for usage examples)
▼ - Fill Down
📄 - Paste Into Column
✏️ - Clear Column
☰ - Increment Row Values

FIGURE 2

For each tab, you need to complete all the accessible mandatory fields before you can proceed to the next page. When you click the “Next” button, the webpage will validate each field to make sure all the cells meet our requirements. If there are any errors, cells will display red or orange error message(s). Please edit all the errors before proceeding to the next page. Please note that fields with warnings will be highlighted yellow for your review. It is not necessary to resolve warnings before proceeding.

Your draft submission will be saved when you click “Next”. Note that a submission can be saved at any step using the “Save as Draft” button at the bottom of the page.

You may add or remove a sample by clicking the  icon located on the top left corner, next to your submission name. Note that if you decrease the sample number by one, the last row will be deleted. If you decrease the sample number by two, the last two rows will be deleted.

### **Sample Information (fields vary slightly for non human samples)**

- Sample ID\*
- Alternate Sample ID
- Taxon\*
- Tube Label\* (when submitting 1-23 samples)
- Plate Location\* (when submitting 24-92 samples): samples must be sorted by column, so they are A1, B1, C1, etc. instead of A1, A2, A3, etc.
- Anonymous Patient ID\*: provide a minimum of five characters, recommended eight characters, with no symbols or spaces. Samples from a same patient must have the same Anonymous Patient ID. This is the only way to link samples collected from the same patient (e.g. normal/tumour samples).
- Family Information

- 
- Strain (for non-human samples)
  - Developmental Stage
  - Sex\*
  - Sample Collection Date

### **Tissue Information**

- Anatomic Site\*: this is a type-ahead search field. Please enter three or more characters to search and select the best option. If there are no appropriate matching selections, you may enter free text.
- Tissue Disease Status\*: this field pertains to the tissue, not the patient. Please select from the drop-down menu provided. If “Normal” is selected, provide Disease Status of Patient (for Normal Samples) in the next column. If “Diseased” is selected, provide the Pathology of the sample in the next page.
- Disease Status of Patient (for Normal Samples): this is a type-ahead search field. Please enter three or more characters to search and select the best option.
- Tissue Type\*
- Cell Type
- Cell Line (for cell line samples)

### **Xenotransplant Recipient Information** (For xenograft samples only)

- Xenograft\*
- Recipient Taxonomy\*
- Recipient Strain

## **Pathology Information**

- Pathology\*: this is a type-ahead search field. Please enter three or more characters to search and select the best option.
- Additional Pathology Information
- Pathology Occurrence\*

## **Pathology Information - continued**

- Grade
- Stage
- Tumour Content
- Treatment Status

## **Analyte Information**

- Nucleic Acid Isolation Date
- Tissue Fixation Process\*: this information is important for QC purposes. If FFPE is used, select "FFPE" under Tissue Fixation Process and the appropriate FFPE RNA selection under Nature of Analyte.
- Nature of Analyte\*
- Nucleic Acid Isolation Method
- DNase Treatment Method Applied\*


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## Analyte Information - continued

Prior to preparing your samples, review the table on [page 7](#) to ensure that your samples meet the requirements of amount, volume, and concentration for submission.

- Volume ( $\mu\text{L}$ )\*
- Concentration ( $\text{ng}/\mu\text{L}$ )\*
- RNA Amount (ng)
- Storage Medium\*
- Quantification Method\*
- RNA Quality Test\*
- RNA Quality Test Value\*

## Work request assignment

Assign a work request to each sample. You may edit the Work Request by clicking , located on the top right corner of the Work Request summary box. The required amount, volume and concentration are validated based on the library protocol selected. If you are submitting less than the minimum amounts, you will be asked to accept the risks of failure.

## Work request pooling

Enter the number of samples per pool.

## Comments and extra information (optional)

Use this field to provide any extra information or details regarding your submission or sample.

## Submission review



## **AFTER SAMPLE SUBMISSION**

The submission form will be reviewed for completeness and accuracy within two business days. You will then receive a notification of approval or a request for edits.

Once your submission has been approved, you will receive an email with detailed instructions for shipping your samples.

You can retrieve the submission info at any time from the submissions page under the Accepted tab.

**If you have any questions during this process please contact the GSC submissions team at [GSC\\_Submissions@bcgsc.ca](mailto:GSC_Submissions@bcgsc.ca).**

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# SAMPLE SUBMISSION BY COURIER

Once the sample submission form is approved, samples must be shipped on dry ice and should be addressed to:

Dr. Andrew Mungall - Biospecimen Core, Room 508

Genome Sciences Centre BC Cancer

Suite 100 - 570 West 7th Avenue

Vancouver, BC Canada

V5Z 4S6

email: [amungall@bcgsc.ca](mailto:amungall@bcgsc.ca)

Tel: 604-707-5900 ext 3251

When samples have been shipped, we ask that you please email [sampleshipments@bcgsc.ca](mailto:sampleshipments@bcgsc.ca) to notify us of your shipment and the associated tracking number, so we can monitor the progress during transit.

Please ensure that there is sufficient dry ice for a couple of days. We recommend shipping Monday to Wednesday, as we cannot accept packages on weekends.

## 4 SAMPLE DROP-OFF

The sample submission form must be reviewed and approved by GSC personnel prior to submitting samples to the GSC.

### **Regular hours for sample drop-off and plate pick-up:**

Monday – Friday: 9:30-11:30 am and 1:30-3:30 pm

### **Location:**

Suite 100-570 West 7th Avenue, Vancouver, BC V5Z 4S6

To enter the building, dial #100 on the intercom and the receptionist will let you in. The reception is on the ground floor (past the elevators and on the left). Go through to reception and ask the receptionist to call or page anyone from the Biospecimen Core group. We'll come down to reception to meet you.



## Technology platform

Echelon Innovation Centre  
570 West 7th Avenue  
Vancouver, B.C. V5Z 4S6  
Phone: 604-707-5900



## Research department

BC Cancer Research Centre  
675 West 10th Avenue  
Vancouver, B.C. V5Z 1L3  
Phone: 604-675-8000