



CANADA'S MICHAEL SMITH
GENOME SCIENCES CENTRE

From Nobel roots.

NANOPORE ADAPTIVE SAMPLING



USER GUIDE

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CANADA'S MICHAEL SMITH
GENOME SCIENCES CENTRE

ABOUT US

Our [CAP](#), [DAP](#), [ISO 15189](#), 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 at GSC_Submissions@bcgsc.ca if you have any questions about the services we provide.

ABOUT THIS GUIDE

This user guide is for the submission of DNA samples for [Nanopore Adaptive Sampling](#) experiments. It describes how to validate and submit the FASTA reference and BED files required for completion of the [Sample Submission Form](#).

For general instructions on submitting DNA samples, please refer to the [DNA Guide](#) available in the [Guides Section](#) of the [Sample Submissions Interface](#).

If you are submitting samples, please refer to the other user guides at bcgsc.ca/services.

CONTACTS

Submissions

GSC_submissions@bcgsc.ca

Statements of Work

SOW@bcgsc.ca

Data Support and Access

data_support@bcgsc.ca

Shipping

GSC_submissions@bcgsc.ca

General

info@bcgsc.ca



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1. ADAPTIVE SAMPLING

Adaptive Sampling is a software-based enrichment and depletion method that targets regions of interest during Nanopore sequencing with no additional library preparation or PCR steps.

Adaptive Sampling experiments at the GSC typically use a **FASTA** reference file (.fa) and a **BED** file (.bed) to specify the regions of interest in the reference to be enriched.

Please refer to Nanopore's Adaptive Sampling Documentation for an overview of adaptive sampling, and how to generate the necessary files (<https://nanoporetech.com/document/adaptive-sampling>).

Although adaptive sampling can be used to deplete regions, our production pipeline currently only offers enrichment sampling, which our online submission forms assume to be the only option.

If you require depletion sampling, we may be able to set up a bespoke protocol. This would fall under our technology development platform and would require different SOWs and specific arrangements.



2. BEFORE STARTING A SAMPLE SUBMISSION

The steps outlined in this guide require that you coordinate with our staff — in particular, our Laboratory Information Management System (LIMS) team.

At any point if you have questions, please email LIMS@bcgsc.ca, and copy GSC_Submissions@bcgsc.ca and SOW@bcgsc.ca.

2.1. PREPARE THE REFERENCE AND BED FILES

Before your [Sample Submission Form](#) can be accepted and samples can be submitted to the GSC, you will need to provide both the reference to use (a **FASTA** file), and a **BED** file containing the regions of interest within that reference.

If you are using a reference already published by NCBI, then the GSC may already have it ready for use, or may install it at your request. If it is an unpublished reference, then you may need to send us the **FASTA** file by **SFTP**.

Similarly, the experiment will require a **BED** file, specifying the regions of interest within that reference.

We recommend following Nanopore's adaptive sampling documentation for finding and creating **FASTA** and **BED** files:

<https://nanoporetech.com/document/adaptive-sampling#where-to-find-create-and-modify-fasta-and-bed-files>

It is the responsibility of the project to choose or generate reference and bed files that are suitable for the adaptive sampling experiment.

2.2. VALIDATE THE FILES WITH “BED BUGS” ONLINE TOOL

Nanopore has an online tool to check the validity of a **BED** file against a specific reference (<https://epi2me.nanoporetech.com/bed-bugs/>) which will prompt you to enter both files and then validate them. If there are any formatting or consistency problems raised by this tool, it may cause delays in the adaptive sampling experiment or for the experiment to fail.

Please let us know before sample submission if **Bed Bugs** has raised any errors with your reference and **BED** file.



2.3. SUBMIT YOUR FILES

Once you have the reference file and the **BED** file ready, you are ready to submit them.

If your experiment uses an already-published reference, then we may already have it installed and ready to use. Otherwise, we will install it on our filesystem.

If your experiment uses a novel reference, then you will need to provide us with the **FASTA** reference file prior to submitting your samples. Since **FASTA** files are typically too large to send by email, submit them using **Secure File Transfer Protocol (SFTP)**. Please email us at LIMS@bcgsc.ca to confirm those details *before you submit your sample*.

Typically, **BED** files are much smaller and you can email them directly to us at LIMS@bcgsc.ca.



3. FILL OUT THE SAMPLE SUBMISSION FORM

Once you have prepared and submitted the necessary [FASTA](#) reference and [BED](#) files to the GSC, you will be able to complete a [Sample Submission Form](#).

Please refer to our [DNA Sample Submission Guide](#) for the general instructions for filling out the DNA Submission form, but note these three extra steps required to enter the adaptive sampling information:

1. From the [Create a New Submission](#) page, after you enter [DNA](#) into the [Type of Submission](#) field, you will be prompted to select any additional [Sample Options](#) that apply to your samples. Select [Nanopore Adaptive Sampling](#) from this list, in addition to any other options that are relevant to your samples.

Sample Options

Please select all that apply to your samples

- ☐ Amplicons
- ☐ Canadian Precision Health Initiative (CPHI)
- ☐ cDNA
- ☐ Cell Lines
- ☐ ChIP
- ☒ Nanopore Adaptive Sampling
- ☐ Xenograft

2. While filling out the [Sample Information](#) section, you will be prompted to select on a per-sample basis whether the sample is for adaptive sampling. Select [Yes](#) for any samples that should undergo adaptive sampling.



3. For each row where you select **Yes**, you will be prompted to enter the **BED File Path** and **FASTA File Location**. Both of these fields are mandatory and are used to specify a location on our filesystem. This step depends on you having provided (or otherwise specified) the reference and bed file according to the instructions above. Please reach out to LIMS@bcgsc.ca to confirm this information if you are unsure.

Adaptive Sampling <

Adaptive Sampling* ⓘ	Bed File Path* ⓘ	Fasta File Location* ⓘ
Yes ▼		
Yes ▼		
No ▼		



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Bringing genomics to life.