

## UB Genomics and Bioinformatics Core Illumina Sequencing Sample Submission Form

Please print both pages of this form and send a completed copy with your samples when they are dropped-off or shipped to the UB Genomics and Bioinformatics Core (UB - GBC) for sequencing services. We will not accept samples unless accompanied by this signed and completed form.

### Lab Contact Information

PI Name \_\_\_\_\_  
 Institution/Business \_\_\_\_\_  
 Address \_\_\_\_\_  
 City/State/Zip \_\_\_\_\_  
 Phone \_\_\_\_\_  
 Email \_\_\_\_\_

Technician Name \_\_\_\_\_  
 Phone \_\_\_\_\_  
 Email \_\_\_\_\_

#### All State University of New York Researchers:

How will you be paying, please circle one?

RF Account      State Account      Other: \_\_\_\_\_

#### University at Buffalo Researchers Only:

Is this a NYSTEM project?      Yes      No

### Experimental Design Information

1) How many samples are you submitting? \_\_\_\_\_

5) Are the samples being multiplexed?

Yes      No

(If yes, please provide multiplexing instructions)

2) What organism are you sequencing?  
 \_\_\_\_\_

6) How many lanes on the flow cell do you plan to use? \_\_\_\_\_

(standard flow cells have 8 lanes and rapid flow cells have 2 lanes)

3) Is GBC preparing the libraries?

Yes      No

(If yes, please fill section # 4. If no, please attach a copy of your library prep protocol.)

7) What type of sequencing run are you requesting?

4) What type of library prep do you require?  
(circle one below)

Small RNA Seq      RNA Seq      DNA Seq

ChIP-Seq      Mate Pair      Exome

Other: \_\_\_\_\_

#### Sequencing Options

Circle One Below

Standard 50-Cycle Single Read	Standard 50-Cycle Paired End
Standard 100-Cycle Single Read	Standard 100-Cycle Paired End
Rapid 50-Cycle Single Read	Rapid 50-Cycle Paired End
Rapid 100-Cycle Single Read	Rapid 100-Cycle Paired End
Rapid 150-Cycle Single Read	Rapid 150-Cycle Paired End

Provide a brief description of your experimental design and any bioinformatics requests. Please include multiplexing plans and sample pooling strategy (if applicable). If more space is needed for the description, you may attach additional pages to this form.

## Sample Information

The following information is required for each sample that you are bringing to the UB Genomics and Bioinformatics Core for illumina sequencing services. For all sample types, confirm that each sample name is unique and that the name written on this form matches the name written on the sample tube. Provide the sample volume, concentration, and measurement method. Attach a Bioanalyzer or agarose gel image of the samples to this form and make sure to clearly label the sample wells and ladder sizes. Please provide the 260/280 ratio (when applicable) and identify the method that was used for sample preparation. Please attach a copy of your sample prep protocol. **If you are unable to provide any of the required information for your samples you must contact us prior to dropping off samples to discuss alternative options.**

Please check the appropriate boxes below:

- Bioanalyzer or agarose gel image attached (all sample types)?  
 Copy of your sample preparation protocol attached?

<u>Sample Name</u>	<u>Volume (<math>\mu</math>L)</u>	<u>Concentration (ng/<math>\mu</math>L)</u>	<u>260/280 Ratio</u>	<u>Measurement Method (NanoDrop, Spec, etc.)</u>	<u>Method of Sample Preparation</u>
_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____

\* Please attach another sample sheet if more space is needed. If you have a spreadsheet with sample info, you can e-mail it to [cbi-ubnextgencore@buffalo.edu](mailto:cbi-ubnextgencore@buffalo.edu)

## Sample Drop-Off

The UB GBC is open for sample drop-off Monday-Friday 10:00am-4:00pm. Please call ahead or schedule an appointment to make sure that a technician will be available to accept your samples as we are often busy working on other projects. Samples should be brought to the UB Genomics and Bioinformatics Core Facility (B3-123) at the New York State Center of Excellence in Bioinformatics and Life Sciences Building (COE) located at 701 Ellicott Street, Buffalo, NY 14203. There is a receptionist at the entrance of the COE who will be able to let you into the building and contact us to let us know that there is a researcher dropping off samples. Alternatively, samples can be shipped overnight on dry ice to the below address, but please email or call to let us know to expect the sample shipment.

## Required Signatures

Please have both the Principle Investigator (PI) that will be paying for the illumina sequencing services and the Research Technician/Student/Post-Doc preparing the samples sign below acknowledging that all of the information provided on the form is correct. Signature of this form acknowledges that the PI and Technician/Student/Post-Doc agree to all sample submission, quality, quantity, project scheduling, and researcher financial responsibility requirements. Signature of this form authorizes the UB Genomics and Bioinformatics Core to order all consumables necessary for the researcher's sequencing project and confirms that the PI is financially responsible for items ordered for their project and all labor cost associated with the project.

## Acknowledgement

All services performed by the UB GBC should be acknowledged in publications, scholarly reports, presentations, and posters. Proper acknowledgment provides a visible measure of the impact of the UB GBC and is essential for our future funding efforts.

**Principle Investigator Signature** \_\_\_\_\_ **Date** \_\_\_\_\_

**Technician/Student/PostDoc Signature** \_\_\_\_\_ **Date** \_\_\_\_\_

## Contact Information

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New York State Center of Excellence in Bioinformatics and Life Sciences  
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Buffalo, NY 14203  
phone: (716) 881-7514  
**email: [cbi-ubnextgencore@buffalo.edu](mailto:cbi-ubnextgencore@buffalo.edu)**

### UB GBC Use Only

Technician receiving samples:  
Date Received:  
# of Samples:  
Sample Location:  
Comments: