UB Next-Generation Sequencing and Expression Analysis Core
Roche/454 GS FLX Titanium Sequencing Sample Submission Form

Please print both pages of this form and bring a completed and signed copy with you when you drop-off or ship samples to the UB Next-Gen Sequencing and Expression Analysis Core for GS FLX Titanium 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 _____

SUNY at Buffalo Researchers Only – How will you be paying for your GS FLX Titanium Sequencing Services (Research Foundation Account, State Account, etc.)?

_____

Experimental Design Information

What type of GS FLX Titanium Run will you be doing (circle one)?

Shotgun 3kb Paired End 8kb Paired End 20 kb Paired End Amplicon

How many sequencing runs? _____ **How many samples?** _____

Do you want to use MIDs (circle one)? Yes No

How many regions should the sequencing plate be divided into (circle one)? 2 4 6 8

Provide a brief description of your experimental design in the space below. Please include your multiplexing plans making sure to describe how you want to use MIDs and which samples should be pooled, 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 Next-Gen Sequencing and Expression Analysis Core for GS FLX Titanium 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 an agarose gel image of the samples to this form and make sure to clearly label the sample wells and ladder sizes. For shotgun and paired end samples only; provide the 260/280 ratio and identify the method that was used for DNA extraction or indicate that you would like the UB Next-Gen Sequencing Core to extract DNA from bacterial pellets provided by the researcher. If you used a method other than the recommended Qiagen Genomic Buffers Set in conjunction with the Qiagen Genomic-Tip Protocol, attach a copy of your protocol and confirm that your samples have been RNase treated. For amplicon samples only; attach a description of your PCR amplification conditions and list all of your primer sequences. Indicate which amplicons were amplified with which primers, the exact amplicon size (base pairs), and which samples should be pooled together. 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.

- ☐ **Agarose gel image attached (all sample types)?**
- ☐ **Copy of your extraction protocol attached if you are not using the Qiagen Genomic-Tip Protocol or our bacterial DNA extraction services (shotgun and paired end only)?**
- ☐ **Description of PCR amplification conditions and fusion primers attached (amplicon only)?**

Sample Name	Volume (µL)	Concentration (ng/µL)	260/280 Ratio	Measurement Method (NanoDrop, Spec, etc.)	Method of Extraction (Qiagen Genomic-Tip, Phenol-Chloroform, UB Core Extraction, etc.)

***** *Please attach another sample sheet if more space is needed*

Sample Drop-Off

The UB Next-Gen Sequencing and Expression Analysis Core is open for sample drop-off Monday-Friday 9:00am-3:00pm. 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 University at Buffalo Next-Generation Sequencing and Expression Analysis Core Facility (B3-123) at the New York State Center of Excellence in Bioinformatics and Life Sciences Building (COE) located at 701 Ellicott Street in Buffalo, NY 14203. There is a receptionist at the entrance of the COE who will be able to let you in 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 GS FLX Titanium 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 have read the UB Next-Gen Sequencing and Expression Analysis Core GS FLX Titanium Sequencing Services Document and agree to all sample submission, quality, quantity, project scheduling, and researcher financial responsibility requirements. Signature of this form authorizes the UB Next-Gen Sequencing and Expression Analysis 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.

Principle Investigator Signature _____ **Date**_____

Technician/Student/PostDoc Signature _____ **Date**_____

Contact Information

UB Next-Generation Sequencing and Expression Analysis Core Facility (B3-123)
State University of New York at Buffalo
New York State Center of Excellence in Bioinformatics and Life Sciences
701 Ellicott Street
Buffalo, NY 14203
phone: (716) 881-7514
email: cbi-ubnextgencore@buffalo.edu

UB Next-Gen Sequencing Core Use Only

Technician receiving samples:

Date Received:

# of Samples:

Sample Location:

Comments: