

Epigenetics Core at Advanced Science Research Center  
Sample Submission Guidelines

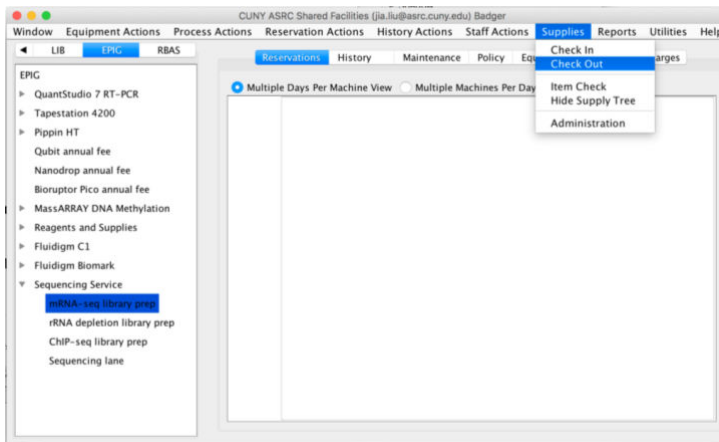
**Shipping Address:**

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Email: [JLIU1@GC.CUNY.EDU](mailto:JLIU1@GC.CUNY.EDU)

**Sample Submission Guidelines Submission Guidelines**

1. User registration and sample submission:

- (i) Please follow the [instruction](#) on the Core's Website to register as a user for the Epigenetics Core Facility
- (ii) Once access request has been approved on our end, you can select the service of your choice to submit a service request to our core. To do so, please check out the service through [Badger](#).



- (iii) Please fill out appropriate sample submission forms and email the forms to [JLIU1@GC.CUNY.EDU](mailto:JLIU1@GC.CUNY.EDU).

2. Sample Volume and Concentration Guidelines

(i) Quality Control Volume Requirements: All extracted DNA or RNA samples will be evaluated for quantity and quality with NanoDrop Spectrophotometer or Qubit Fluorometer, and Agilent TapeStation4200. The QC results or the issues with sample quality and quantity will be reported to the users via email before sample library construction.

For quality control, please provide at least 3  $\mu\text{L}$  of sample volume plus 1  $\mu\text{L}$  or more to allow for pipetting errors:

- TapeStation: 1-2  $\mu\text{L}$
- NanoDrop: 1  $\mu\text{L}$
- Qubit: 1-2  $\mu\text{L}$

(ii) Submit your samples in 0.5 ml or 1.5 ml microcentrifuge tubes. The tubes must be clearly labeled on the lid. We suggest using low-retention tubes.

### 3. Sample shipment:

We suggest to ship all samples (DNA or RNA) on dry ice. Please only ship with courier services (FedEx, UPS, DHL). Please do not ship samples on Fridays to avoid potential delay due to the weekend.

### 4. RNA-Seq sample submission:

(i) For RNA sample library preparation, please provide the following (with Qubit measurement):

(ii) mRNA-seq selection: 200 to 500 ng of DNase-digested total RNA in 10 -30  $\mu\text{L}$  water, RNA integrity number (RIN) > 8

(iii) rRNA depletion: 200 to 500 ng of DNase-digested total RNA in 10  $\mu\text{L}$  water, RNA integrity number (RIN) 5 –8

### 5. ChIP-Seq sample submission:

Please submit 10-50ng of ChIP DNA in nuclease-free water. We will check the fragment size and the quality / quantity of the sample before library construction. We strongly recommend ChIP DNA be fragmented to 200-600bp in size for optimal library performance and reduced background noise levels.

#### 6. MassArray Epityper sample submission:

- (i) Genomic DNA: please submit 500ng – 1µg of genomic DNA in a concentration of  $\geq 50\text{ng}/\mu\text{l}$  (based on Nanodrop measurements).
- (ii) Primers: If users request the core to perform PCR amplification, please submit the primers either lyophilized or in 100µM dissolved in H<sub>2</sub>O. Please submit the primer sequence and amplicon size in sample submission forms.
- (iii) PCR amplicons: please submit  $>11\mu\text{l}$  gel-verified PCR products along with samples to confirm a specific PCR amplicon.

#### 7. Single-cell sequencing and targeted gene expression analysis:

The Fluidigm C1 and Biomark systems have been installed in our core lab. We provide the services including RNA-Seq and Deltagene assays. Please contact us if you would like to initiate single-cell projects.

#### 8. RNAscope/Basescope sample submission:

- (i) Please submit sections with a thickness of 7-15 µm, within 2 cm x 2 cm in size, mounted on SuperFrost Plus slides (Fisher Scientific #12-550-15). Mount sections on other types of slide may result tissue loss during sample processing.
- (ii) We recommend air dry the slides for 2 HR at -20°C and overnight at -80°C after cryostat sectioning.
- (iii) We recommend using slides which are sectioned within 3 months.
- (iii) Please include 1-2 additional slides to be used for control probes.
- (iv) Fill out the sample submission form.