

USC Norris Molecular Genomics Core

Illumina Methylation (EPIC) Array Project Workflow

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Consultation and Cost Estimation

- To start the submission process, please email Stephanie Tring at tring@med.usc.edu
- An in-person or Zoom meeting will be scheduled to discuss your project.
- Based on the information provided, a formal quote will be emailed to you.

Please prepare the following information prior to the meeting:

- Sample type (blood, cell lines, tissue, FFPE, etc.) and number of samples.
- Do you already have DNA extracted, or will extraction be required?
- Do you anticipate low-input or FFPE samples that may require the **Infinium Restore option**?

Scheduling and Submitting

- After you have reviewed the quote and are ready to start, please email Stephanie and submit the **MGC Microarray Submission Form**.
- MGC can assist in ordering reagents/arrays. We will need confirmation from you with your **USC Worktag and Cost Center** to place the array order.
- DNA samples should be submitted in 1.5–2 mL tubes or 96-well plates, properly labeled.

Pre-EPIC Array Quality Control

DNA quality and quantity requirements:

- Standard samples: ≥ 250 ng total DNA at ≥ 20 ng/ μ L
- Low input/FFPE samples: ≥ 100 ng total DNA (Infinium Restore option available)
- DNA purity: OD_{260/280} ~ 1.8 ; OD_{260/230} > 1.8
- DNA should be intact; degraded samples may be eligible for Restore treatment.
- MGC will assess DNA QC and determine if **Restore** treatment is needed prior to bisulfite conversion.

Infinium EPIC Array Run

- Samples passing QC will be scheduled for the Infinium Methylation workflow.
- Arrays will be processed according to Illumina protocols (bisulfite conversion, amplification, fragmentation, hybridization, staining, and imaging.)
- Turnaround time is approximately **15-20 working days** for < 96 samples.
- Final deliverables include raw IDAT files and Methylation QC calls.
- Data will be delivered via **CARC** or external hard drive.