

DNA Methylation Profiling

NYGC offers comprehensive DNA methylation profiling services, primarily using the Illumina Infinium MethylationEPIC v2.0 array. With approximately 930,000 CpG sites, the EPIC v2.0 array provides high-resolution, genome-wide methylation profiling across well-characterized regulatory regions and methylation hotspots. Workflows are available for both human and mouse samples, including FFPE-derived DNA.

In addition to array-based profiling, NYGC offers methylation analysis through select long-read sequencing workflows, enabling direct detection of DNA methylation alongside sequence information. Please see our Long-Read Sequencing page for additional details.

Additional arrays and alternative profiling approaches may also be available depending on your research objectives, sample type, and project requirements. Our Project Management team can help you select the most appropriate methylation profiling strategy for your study.

Illumina Infinium MethylationEPIC v2.0 Array

The following guidelines represent NYGC's standard DNA input requirements for methylation profiling and are intended to maximize assay performance and data quality. If you have questions about sample quality, quantity, or compatibility, our team is happy to review your samples before submission. In many cases, we can recommend alternative approaches or evaluate samples on a project-specific basis.

Submission Requirements:

- **Minimum input:** 500 ng of unamplified, RNase-treated, high molecular weight DNA
- **Submission volume:** 20–25 µL in Elution Buffer (EB)
- **DNA quantification:** Concentration should be measured using **PicoGreen** or an equivalent fluorescence-based assay

Standard Analysis & Deliverables

NYGC provides standard data processing and quality control for projects performed using the Illumina Infinium MethylationEPIC v2.0 array. Arrays are scanned on the Illumina iScan platform, and initial data processing is performed using GenomeStudio. Standard analysis results are included with data delivery. For projects requiring advanced statistical analyses, differential methylation analysis, integrative multi-omics analysis, or customized bioinformatics workflows, additional support from NYGC's Computational Biology team is available and can be discussed during project planning.

Our **standard analysis** workflow includes:

- Comprehensive quality control, including assessment of control probes, bisulfite conversion efficiency, hybridization performance, probe specificity, beta-value distributions, batch effects, and sample sex concordance
- Probe intensity preprocessing, including background correction and normalization using control probes
- Generation of processed methylation values suitable for downstream analysis

Standard data deliverables include:

- Raw IDAT files
- Per-sample quality control plots illustrating the effects of normalization on beta-value distributions
- Processed and filtered β -values and M-values for each probe across all samples

Frequently Asked Questions

What information is needed to start a project?

To begin planning a library sequencing project, we typically request:

- Number and type of samples
- Sample source and preservation method
- Required timeline
- Data delivery requirements
- Any planned downstream analyses

How are projects initiated?

Once project scope and service requirements have been finalized with your NYGC Project Manager, NYGC will provide a formal service quote outlining the agreed-upon deliverables, pricing, and project details. To begin project execution and submit samples, NYGC requires a signed copy of the quote and an approved purchase order (PO). For large-scale projects, additional discussions regarding customized terms and conditions may be accommodated.

How should DNA be submitted?

For U.S.-based submissions, once a project has been quoted and a purchase order has been received, we provide NYGC-barcoded tubes in a matrix rack, an electronic sample manifest, and an overnight return shipping label for sample submission. Note that the provided tube orientation is critical, and tubes should not be rearranged.

Your Project Manager will coordinate international submissions, including shipping requirements and documentation.

What DNA input requirements do you recommend?

We recommend submitting high-quality genomic DNA that meets our standard quantity and quality requirements. Specific requirements may vary depending on sample type and requested

sequencing depth. Our team will review your sample information during project planning to confirm suitability before submission.

Will you check DNA quality and quantity before library preparation?

Yes. All projects include an initial quality control (QC) assessment to confirm DNA quantity and evaluate DNA quality. QC results, including DNA integrity metrics, will be shared with you for review before proceeding with library preparation.

How is data returned?

We support data delivery to a variety of client-managed endpoints and storage environments. Before delivery, we can perform a test transfer to confirm connectivity and ensure efficient transfer of large sequencing datasets.