

Library Sequencing

In addition to our library preparation services, NYGC accepts client-prepared libraries for sequencing across our available platforms, including the Illumina NovaSeq X+, Ultima Genomics UG100, Oxford Nanopore Technologies PromethION 24, and PacBio Revio. Our scientific project management team will work with you to confirm library compatibility, sequencing requirements, and project specifications prior to submission. Libraries must be pooled before shipment. Sequencing of client-prepared libraries includes data generation and delivery of standard sequencing files. Bioinformatics analysis is not included as part of the standard sequencing-only service.

If you would like your data processed through one of NYGC's analysis pipelines or require a customized bioinformatics workflow, our Computational Biology team can provide analysis solutions tailored to your research objectives. Please discuss your analysis needs with your Project Manager during project planning.

Illumina NovaSeq X+

NYGC offers flexible sequencing options on the Illumina NovaSeq X+ platform. We accept submissions for full flow cells across all available flow cell formats and cycle configurations. Depending on your project needs, a single library pool may be sequenced across an entire flow cell, or separate library pools may be submitted for individual lanes. Additionally, NYGC also accepts submissions for individual lanes on the NovaSeq X+ 25B 300-cycle flow cell. Our Project Management team will work with you to determine the most appropriate flow cell configuration and pooling strategy based on your sequencing goals, desired output, and project design.

Library Pool Submission Requirements

- **3 nM** in a minimum volume of **300 µL**
- Pool concentration and quality verified using **PicoGreen** (or equivalent fluorescence-based assay) and **BioAnalyzer** (or equivalent), and traces shared with NYGC

Standard Deliverables

- **FASTQ** file containing all pass filter reads and quality scores
- For library sequencing, expected read number and sequence quality is application dependent

Ultima UG100

NYGC accepts both native Ultima libraries (**Solaris Free**) and converted libraries (**Solaris Flex**) for sequencing on the Ultima Genomics UG100 platform. Solaris Free is designed for libraries prepared with Ultima-compatible adapters. Solaris Flex supports libraries originally prepared with Illumina or other non-Ultima barcodes and converted for compatibility with the UG100

platform. *NYGC does not provide conversion services.* Our team will review your library preparation method and recommend the appropriate sequencing workflow. Solaris Flex submissions are accepted in two-wafer batches, while Solaris Free libraries can be submitted in a wider range of wafer sizes. Partial wafer submissions are not available. To ensure optimal sequencing performance and data processing, please provide your Project Manager with the library preparation kit and indexing strategy used to generate your libraries. This information allows NYGC to configure the appropriate sequencing and bioinformatics parameters for your project.

Library Pool Submission Requirements

- **5 nM in 100 µL**
- pool concentration and quality verified using **PicoGreen** (or equivalent fluorescence-based assay) and **BioAnalyzer** (or equivalent), and traces shared with NYGC
- **Converted Libraries:** A minimum of 2 wafers per submission

Standard Deliverables

- Depending on library type, either **CRAM** or **FASTQ** files

ONT PromethION24

NYGC accepts compatible client-prepared libraries for sequencing on the Oxford Nanopore Technologies (ONT) PromethION 24 platform, subject to project review and instrument availability. During project planning, our scientific team will review your library preparation method, sequencing objectives, and desired data outputs to ensure compatibility and recommend the optimal sequencing strategy.

As part of our ONT sequencing service, NYGC offers multiple basecalling options, including **Fast, High Accuracy (HAC)**, and **Super Accuracy (SUP)**, allowing researchers to balance sequencing speed and accuracy based on the needs of their project. Our team will help determine the most appropriate basecalling model during project planning, and discuss any additional computational charges associated with the options.

For studies investigating epigenetic modifications, NYGC also offers **modified base detection**, including DNA methylation calling, as part of the data processing workflow. These analyses can provide additional biological insight without requiring separate library preparation.

Library Pool Submission Requirements

- Because optimal loading conditions vary by library type and sequencing application, specific library requirements will be confirmed with your NYGC Project Manager before submission. Please provide library QC information, including library preparation kit, quantification method, and fragment size assessment, to support successful sequencing.

Standard Deliverables

- **uBAM** or **FASTQ** files

- POD5 files are available for an additional cost

PacBio Revio

NYGC accepts compatible client-prepared libraries for sequencing on the PacBio Revio platform, subject to project review and instrument availability. Both SPRQ and SPRQ-Nx chemistries are supported. During project planning, our scientific team will review your library preparation method, sequencing objectives, and desired data outputs to ensure compatibility and recommend the optimal sequencing strategy.

Library Pool Submission Requirements

- Because optimal loading conditions vary depending on library type, insert size, and sequencing application, specific submission requirements will be confirmed during project planning. Please provide library QC information to ensure successful sequencing and high-quality HiFi data generation.

Standard Deliverables

- **BAM** or **FASTQ** files

Frequently Asked Questions – Library Sequencing

What information is needed to start a project?

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

- Desired sequencing platform
- Desired total number of reads
- Number of pools
- Library prep type
- 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.

What is the expected turnaround time?

All turnaround times can be found on our '[main research services page](#)'.

How should library pools 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.

Will you check library quality and quantity before sequencing?

Yes. All projects include an initial quality control (QC) assessment to confirm pool quantity and evaluate quality for optimal loading. If any concerns are found during QC, the QC will be shared prior to sequencing to ensure that we should move forward.

Do you offer downstream alignment and analysis services?

Depending on the library type and species, yes, for an additional cost. See more about Bioinformatics and Data Analysis Services on '[main research services page](#)'.

Will my libraries be pooled with other projects?

No. Client libraries are processed as project-specific pools and are not pooled with libraries from other projects. This ensures clear sample tracking, accurate data attribution, and consistent sequencing performance throughout the workflow.

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.