

Nucleic Acid Extraction Services

NYGC may offer nucleic acid extraction as an **add-on service to sequencing projects**, depending on laboratory capacity, sample requirements, and project timelines. Extraction services are not offered as a standalone service and must be coupled with downstream sequencing or genomic analysis performed by NYGC.

When available, NYGC provides automated nucleic acid extraction workflows using both **Qiagen QIAcube** and **Thermo Fisher KingFisher** platforms to support a variety of sample types and sequencing applications. Our extraction workflows are optimized to generate high-quality DNA, RNA, and cell-free DNA (cfDNA) suitable for downstream genomic and transcriptomic studies.

Available extraction workflows include:

- DNA extraction
 - Whole blood or peripheral blood mononuclear cells (PBMCs)
 - Fresh frozen tissue or OCT-embedded tissue
 - Buccal swabs and saliva
- RNA extraction
 - Whole blood
 - Fresh frozen tissue
 - PBMCs
- Combined DNA and RNA extraction
 - Fresh frozen tissue
 - OCT-embedded tissue
 - Bone marrow
 - FFPE tissue (using an internally developed workflow)
- Cell-free DNA (cfDNA) extraction
 - Blood plasma

Extraction workflows are selected based on sample type, available input material, and downstream sequencing requirements. Our team will work with you during project planning to determine the most appropriate extraction approach for your study.

Extraction Sample Submission Requirements

The following guidelines represent NYGC's standard minimum input requirements to support successful nucleic acid extraction and maximize sequencing performance and data quality. If your samples do not meet these specifications, please contact our Project Management team prior to submission. In many cases, our team can recommend alternative workflows or evaluate samples on a project-specific basis.

Whole Blood for DNA Extraction

- Minimum **2 mL of whole blood** collected in **EDTA (lavender-top) tubes**

Whole Blood for RNA Extraction

- Minimum **2.5 mL of whole blood** collected in **PAXgene Blood RNA tubes**

Peripheral Blood Mononuclear Cells (PBMCs)

- Submit a **cell pellet with cell count provided**

Fresh Frozen Tissue or OCT-Embedded Tissue

- Minimum input:
 - **2 × 2 × 2 mm** tissue sample (optimal size: **0.5 × 0.5 × 0.5 cm**), or
 - At least **10 tissue sections (scrolls)**, each **5–10 µm thick**
- Maximum recommended tumor tissue input: **30 mg**
- Please provide **collection date and time** with the sample submission
- Tissue may be submitted in cryogenic tubes or as snap-frozen tissue stored at **–80°C**
- Frozen specimens must be shipped overnight on **dry ice** using an insulated container to maintain frozen conditions during transport
- Samples that have thawed during storage or shipment are not suitable for analysis. If a thawed specimen is received, resubmission of an appropriate sample may be required

FFPE Tissue

- Preferred input:
 - **100 µm total tissue**, provided as either:
 - 10 sections of 10 µm, or
 - 5 sections of 20 µm
- Minimum input:
 - **40 µm total tissue**, submitted together in a single tube
- NYGC does not scrape slides or perform pathology review to distinguish tumor from normal tissue. Tissue sections should be prepared prior to submission according to project requirements.

Blood Plasma for cfDNA Extraction

- Minimum input: **500 µL–1 mL of plasma**

Buccal Swab or Saliva for DNA Extraction

- Minimum input: **2 mL of saliva**

Frequently Asked Questions – Extraction

How should samples be submitted?

Materials submitted for nucleic acid extraction, including blood, tissue, and cell samples, can be shipped directly to NYGC. Your Project Manager will provide the appropriate shipping address and an electronic sample manifest to complete prior to shipment. Please provide at least 24 hours' advance notice before shipping samples to ensure proper receipt and processing. To maintain sample integrity and ensure successful delivery, samples should arrive during NYGC business hours, as the laboratory is closed on weekends and holidays.

Can you perform extraction from a sample type not listed above?

NYGC may be able to support extraction from additional sample types not listed above, depending on sample characteristics, project requirements, and laboratory capacity. Please contact our Project Management team at ProjectManagement@nygenome.org to discuss your sample type and determine the most appropriate workflow for your project.

Are pathology services offered?

No, we do not offer pathology services. When submitting slides for extraction, the full sample will be used.

How is nucleic acid extracted from FFPE tissue?

For FFPE tissue samples, NYGC uses an internally developed extraction workflow optimized for recovery of high-quality nucleic acids from archived and often highly processed tissue specimens. This specialized approach is designed to support downstream sequencing applications by maximizing nucleic acid yield and quality from FFPE samples.

Can DNA and RNA be extracted from the same sample?

Yes. NYGC can support parallel DNA and RNA extraction from the same biological sample for several sample types, including fresh frozen tissue, OCT-embedded tissue, FFPE tissue, bone marrow, and cell samples. For whole blood samples, extraction requirements depend on the intended nucleic acid type and sample collection method. DNA extraction is performed from whole blood collected in EDTA tubes, while RNA extraction is performed from whole blood collected in PAXgene Blood RNA tubes to support RNA preservation and quality. At this time, NYGC offers DNA extraction only for buccal swabs and saliva samples. Please discuss your sample type and downstream sequencing goals with our Project Management team to determine the most appropriate extraction workflow for your project.