# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

# UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility

RRID:SCR_022620
Type: Tool

## Proper Citation

UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility (RRID:SCR_022620)

## Resource Information

**URL:** https://www.med.unc.edu/genomics/about/

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**Description:** Full service sequencing facility to assist with genetic and genomic research. Part of Integrated Genomics Cores. Offers comprehensive library services, NextGen sequencing and alternative technologies including long reads. Offers library preparations and multiple sequencing platforms including MiSeq, HiSeq, NovaSeq, NextSeq, BioNano, Oxford Nanopore. Services also include using techniques and data analyses via sister core BARC.

**Abbreviations:** HTSF

**Synonyms:** UNC School of Medicine Integrated Genomics Cores HighThroughput Sequencing Facility, University of North Carolina at Chapel Hill School of Medicine Integrated Genomics Cores High-Throughput Sequencing Facility, UNC School of Medicine HighThroughput Sequencing Facility

**Resource Type:** access service resource, core facility, service resource

**Keywords:** NextGen sequencing, library preparations, Illumina kits, non Illumina kits, novel R&D, Oxford Nanopore, BioNano, MiSeq, HiSeq, NovaSeq, NextSeq, BioNano, Oxford Nanopore, sequencing platforms, ABRF, USEDit

**Availability:** open

**Resource Name:** UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility

**Resource ID:** SCR_022620

**Record Creation Time:** 20220803T050137+0000

**Record Last Update:** 20260905T133428+0000

## Ratings and Alerts

No rating or validation information has been found for UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility.

No alerts have been found for UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at PRECISE-TBI .

Laughery MF, et al. (2026) Genome-wide mutation spectra of canonical and atypical UV photoproducts in S. cerevisiae. Nucleic acids research, 54(10).

Avila TU, et al. (2026) Repeat expansions in C9orf72 rewire the 3D chromatin landscape in ALS. bioRxiv : the preprint server for biology.

Wu S, et al. (2026) Persistence of large mtDNA rearrangements linked to premature aging in Pol ? exonuclease-deficient mice. Nucleic acids research, 54(12).

Pantazis JC, et al. (2025) Integrating functional genomics and proteomics identifies Folate Carrier SLC19A1 as a predictor of pralatrexate sensitivity in T-cell lymphoma. bioRxiv : the preprint server for biology.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.