

FACILITIES AND RESOURCES – Molecular Genomics Core

The USC Norris Molecular Genomics Core (MGC) is a full-service facility that houses state-of-the-art instrumentation and provides access to advanced genomic technologies. Located within the Norris Tower (NOR) at the University of Southern California Health Sciences Campus, the MGC is a Norris Comprehensive Cancer Center (NCI–subsidized) data production core facility, offering discounted services to Cancer Center members.

The MGC maintains a strong commitment to staying at the forefront of genomic innovation by continually expanding its capabilities to include cutting-edge technologies such as single-cell, spatial transcriptomics, and long-read sequencing. These additions enable comprehensive multi-omic and high-resolution analyses that support a wide range of translational and basic research studies.

MGC served as the primary data production site for DNA methylation assays for The Cancer Genome Atlas (TCGA) and remains one of the largest Illumina single nucleotide polymorphism (SNP) and DNA methylation array production facilities in the U.S.

Laboratory:

The Molecular Genomics Core Facility occupies ~3,000 sq. ft of space within NOR. The MGC houses a microarray production Illumina BeadLab System, including a BeadExpress Reader, with automation equipment (including two Tecan EVO robotic workstations), iScan Readers, and GenomeStudio data analysis software for the generation of millions of genotypes per day or hundreds of thousands of gene expression profiles. All samples are tracked using internal electronic laboratory management systems.

For next generation sequencing, the core facility now houses one Illumina NextSeq 2000 and two Illumina MiSeq sequencer. RNA and DNA samples for next-generation sequencing are library prepared in-house using Illumina and NEB assays. In addition, the MGC now supports long-read sequencing with an Oxford Nanopore PromethION 2i system.

The core also features advanced single-cell and spatial transcriptomics capabilities, including a 10x Genomics CytAssist for Visium Spatial Transcriptomics and a 10x Genomics Xenium system for in situ spatial analysis. For pre-imaging and quality control, the core also houses the Keyence VHX 7000 microscope.

Additionally, the core has several liquid handling robots, including a Hamilton NGS STAR 8/96 iSWAP with on deck thermal cycler and a Tecan Freedom EVO-100 liquid handler. The facility houses four ThermoFisher SimpliAmp thermal cyclers, four ThermoFisher MiniAmp thermal cyclers and one Bio-Rad C1000 thermal cycler as well as a Thermo QuantStudio 7 qPCR instrument. The core also includes two Agilent BioAnalyzers and one Agilent TapeStation for library and sample QC, and several general bench-top items of laboratory equipment.

The MGC includes appropriate sample storage systems including two 4°C refrigerators, four -20°C freezers, and three large-capacity -80°C freezers. These freezer systems are managed by a departmental alarm system.

Computational Resources:

Computers are on the USC medical network, which has special security provisions for patient privacy, anti-virus software, and appropriate firewalls. Computational resources are deployed in a two-tiered structure with equipment located both on site and at the USC Advanced Research Computing service site.

Resources on-site at the Norris building are primarily used for data acquisition and image processing and comprise a hybrid of dedicated HPC integrated to leverage and access cloud-based environments (e.g., Amazon and Google) through 10Gbit connectivity. Dedicated computing consists of six (6) 64-bit Dell Xeon dual core processing workstations and a Puget Systems Peak Dual Xeon 8-core tower running Linux Ubuntu operating system. Finally, the core utilizes Synology 84TB redundant storage for project data.

Other:

Library:

Large and diverse libraries exist at USC and are accessible by high-speed internet connections. All project investigators have inter-library privileges, so rapid access to timely journals and scientific information is readily available.

CHLA CAP/CLIA Certified Services:

The Molecular Genomics Core's CAP/CLIA certified service environment is housed within the Molecular Pathology Genomics Core located within Children's Hospital Los Angeles' Department of Pathology and Laboratory Medicine and Center of Personalized Medicine. Please see the CHLA Genomics Core Facilities and Resources page for more specifics.

- Single Cell
 - 10X Genomics scRNAseq 3'
 - 10X Genomics scRNAseq 5'
 - 10X Genomics Multiome
 - 10X Genomics scATACseq
 - 10X Genomics FLEX
 - Parse Evercode scRNAseq 3'
 - Illumina PIPseq scRNAseq 3'
 - Long Read single cell via Oxford Nanopore
- Bulk NGS
 - DNA Sequencing
 - RNA Sequencing
 - Whole Exome Sequencing
 - Amplicon Sequencing
 - Metagenomic Sequencing

- Oxford Nanopore Long-reads DNaseq
 - Oxford Nanopore Long-reads RNAseq
- Spatial
 - 10X Genomics Visium v2 CytAssist
 - 10X Genomics Visium HD CytAssist
 - 10X Genomics Xenium Prime
 - 10X Genomics Xenium w/ Custom Panel
- Proteomics
 - Illumina Protein Prep 9.5K targets
 - Olink Reveal 1K targets
- Epigenetic
 - Illumina EPIC array
 - Oxford Nanopore Methylation sequencing
- SNP Genotyping
 - Illumina Global Diversity Array
 - Illumina OncoArray
 - Illumina Omni Array
 - Illumina Screening Array
 - Illumina Array with Custom Content
- Instrument
 - Illumina Nextseq2000 Sequencer
 - Illumina Miseq
 - 10X Genomics Chromium X
 - 10X Genomics CytAssist
 - 10X Genomics Xenium
 - Oxford Nanopore PromethION
 - ThermoFisher QuantStudio 7
 - Illumina Infinium Beadlab
 - Keyence VHX 7000
 - ThermoFisher SimpliAmp
 - ThermoFisher MiniAmp