MAJOR EQUIPMENT
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Major Equipment for Emory Integrated Genomics Core (EIGC) Users

EMORY INTEGRATED GENOMICS CORE (EIGC)

The **Emory Integrated Genomics Core (EIGC)**, one of the **Emory Integrated Core Facilities (EICF)**, is a CLIA-certified (CLIA:11D1086150) laboratory located on the 7th floor of the Woodruff Memorial Research Building, with 2400 square feet of dedicated wet-lab space. The EIGC's laboratory areas include dedicated pre- and post-PCR spaces. Two chemical fume hoods and a biosafty cabinet are also located within the space. Additionally, EIGC has a secondary location on the 4th floor of the Health Sciences Research Building, with 770 square feet of wet-lab space including a biosafety cabinet. The EIGC has 500 square feet of dedicated office adjacent to the laboratory space on the 7th floor of the Woodruff Memorial Research Building, which provides for computational services, meeting customers, and weekly EIGC team meetings. The EIGC is composed of five service divisions: CLIA, Genomics Research, Epigenetics Resarch, Viral Sequencing, and Genome Engineering. Each division provides specialized genomics research services to Emory investigators. A Krishagni Solutions OpenSpecimen Laboratory Information Management System (LIMS) is hosted at Emory and all data is stored on-site in a HIPAA secure zone. This LIMS provides the foundation for EIGC workflows and fosters collaboration across the Emory campus and with external consortia. The EIGC closely coordinates with the Emory Integrated Computational Core (EICC), which is located on the 7th floor of the Woodruff Memorial Research Building adjacent to the EIGC to provide computational and bioinformatics services for Emory investigators. The EIGC infrastructure includes:

DNA/RNA Extraction, Genotyping, and Gene Expression:

10X Genomics Chromium and Chromium X Controllers: An automated system that allows one to encapsulate samples into hundreds to tens of thousands of uniquely addressable partitions in minutes, each containing an identifying barcode for downstream analysis. Supports a wide variety of assays when combined with Illumina sequencing that include: Single Cell Gene Expression, Single Cell Immune Profiling, Single Cell Copy Number Variant Detection, Single Cell ATACseq, Genome sequencing, Exome sequencing, de novo Assembly of genomes.

10x Genomics CytAssist: Provides the means to transfer transcriptome probes from a standard tissue slide to the 10x Genomics Visium slide for spatial transcriptomics experiments.

AirClean PCR Workstation: Provides a clean air environment in order to prevent sample contamination.

Agilent Fragment Analyzer (48/96 wells): A parallel capillary electrophoresis instrument designed to speed nucleic acid fragment analysis and quality control before moving onto downstream applications.

Agilent 2100 Bioanalyzer: Allows for rapid quantification of nucleic and proteomic samples, while providing information about the size distribution of the fragments.

Agilent 2200 TapeStation: Provides simple, fast, and reliable electrophoresis of DNA, RNA, and proteins.

Applied Biosystems SeqStudio Flex: A multi-color fluorescence-based DNA analysis system using the technology of capillary electrophoresis with 8 capillaries operating in parallel. This fully automated system separates amplified fragments of varying sizes for analysis of short tandem repeats (STRs) among individuals and extended pedigrees as well as sequencing.

Applied Biosystems 7900HT: Is a real-time quantitative PCR system that combines 96- and 384-well plate compatibility with fully automated robotic loading. Key applications include gene expression quantitation and the detection of single nucleotide polymorphisms (SNPs) using the fluorogenic 5' nuclease assay.

BioRad QX200 Droplet Digital PCR System: Droplet digital polymerase chain reaction was developed to provide precision quantification of nucleic acid target sequences. ddPCR measures absolute quantities of nucleic acid molecules encapsulated in discrete water-in-oil droplets by measuring the fluorescence generated by binding of gene-specific probes or EvaGreen double-stranded DNA binding dye within each droplet. ddPCR has the ability to detect gene copy number variation, detect rare sequences from tumor cells, measure gene expression levels, and to detect genome edits (HDR and NHEJ).

Bruker/nanoString nCounter FLEX: A highly sensitive, enzyme-free, molecular counting platform for determining gene expression or target enrichment across a predefined panel of genomic regions. The EIGC assists investigators with project planning, sample preparation, and coordination of nCounter services across a number of outside providers.

Bruker/nanoString GeoMx Technology: A high-plex and high-throughput spatial profiling technology which enables researchers to rapidly and quantitatively assess the biological implications of the heterogeneity within tissue samples. The technology allows selection of regions of interest from tissue on a slide and to quantify RNA or protein for the specific region of interest.

Covaris E220 Adaptive Focusing Instrument: Employs ultrasonic pulses to uniformly shear nucleic acids, in a multi-sample format with walk away operation. The instrument can also be used to automate lyses of difficult samples (like mouse tail), shear proteins, and form lipid vesicles.

Eppendorf epMotion 5075t: A liquid handling instrument which is compatible with NGS library preparation used for preparation of NGS libraries and bead cleanup.

Invitrogen Countess: A digital cell counter and viability instrument.

Nanopore Gridion: A sequencing device which provides long-read sequencing capabilities for RNA, cDNA, and DNA.

Nanodrop One Spectrophotometer: A UV-Vis Spectrophotomter which quantifies and qualifies DNA, RNA and protein samples from microliter volumes.

Magnetic Particle Processor: A Kingfisher Flex provides for automated extraction of RNA from FFPE tissue in 96-well format and DNA from FFPE tissue, fresh or frozen tissue, blood, blood products, saliva, urine, and cell cultures in 24-well or 96-well format.

Standard Biotools X9: A liquid handling instrument capable to generate targeted genomic libraries for Illumina sequencing as well as to perform gene expression qPCR in a multiplex system.

Tecan EVO150: Used to perform pre-PCR routine liquid transfers, such as the transfer of nucleic acids from individual vials into the 96-well storage and amplification plates required by downstream applications.

TissueLyser II. Performs tissue homogenization for DNA and RNA isolation.

Tecan Infinite M200 Pro: Quantitates nucleic acids using either PicoGreen or RiboGreen fluorescence protocols.

Qubit: A device which reads fluorescent assays in order to quantify DNA, RNA, and protein.

Nine Thermal Cyclers: Four Applied Biosystems 9700 Peltier-driven thermal cyclers, one MJ BioRad thermal cyclers, one Eppendorf Mastercycler, three BioRad C1000 and one BioRad Tetrad with four 96-well gradient capable blocks.

Non-instrument computers: There are currently two MacBook Pros, two iMacs and thirteen Dell PCs.

Next Generation Sequencing:

One Illumina MiSeq instrument: A fully integrated next generation sequencing platform capable of generating between 540 Mb (~4 hours) up to 8.5 Gb (~39 hours) of raw sequence. Some applications of this platform include targeted sequencing from complex eukaryotic genomes or cancer tumors, microbial whole-genome sequencing, 16S rRNA sequencing for microbiome studies, and sequencing of bisulfite treated DNA for assessing methylation. Samples preparation is rapid and samples can be multiplexed with sequence tags.

One Illumina NextSeq 550 instrument: A fully integrated next generation sequencing platform capable of generating between 16GB to 120GB in instrument runs that range between 11 to 29 hours per experiment. Some applications of this platform include sequencing RNAseq, ATACseq or single cell libraries, targeted sequencing from complex eukaryotic genomes or cancer tumors, microbial whole-genome sequencing, and sequencing of bisulfite treated DNA for assessing methylation. The NextSeq 550 also has array scanning capabilities utilized to read Infinium microarrays, including the Infinium MethylationEPIC array.

One Illumina NextSeq 2000 instrument: A fully integrated next generation sequencing platform capable of generating between 10GB to 540GB in instrument runs that range between 8 to 44 hours per experiment. Some applications of this platform include sequencing RNAseq, ATACseq or single cell libraries, targeted sequencing from complex eukaryotic genomes or cancer tumors, microbial whole-genome sequencing, and sequencing of bisulfite treated DNA for assessing methylation.

Large-Scale Next Generation Sequencing: The EIGC has adopted an innovative business model whereby large-scale next-generation sequencing is outsourced to other academic and commercial entities, with the ultimate goal of obtaining the lowest cost, highest quality, and fastest turn-around for our customers. Academic partners include the Genomic Services Laboratory at HudsonAlpha and genomics core facilities at Yerkes National Primate Research Center, the University of Georgia, Georgia Institute of Technology, and New York University. Commercial companies include: Discovery Life Sciences, Novogene, Omega Bioservices, Genewiz, Tempus, and Otogenetics. We have the flexibility to pursue sequencing projects with any outside provider that provides competitive pricing, rapid turn-around time, and high-quality data. In effect, the EIGC acts as a sequencing service broker, whereby we compete companies against each other to obtain the best pricing and service for Emory investigators.