**UNMC Genomics Core Facility Resources / Updated October 21, 2020**

**Durham Research Center (DRC) II, Rooms 1010, 1012, 1015, 1017, and 1021 (~ 2200 sq ft).**

The UNMC Genomics Core facility is a comprehensively equipped facility that serves the regional research community. A wide variety of RNA/DNA samples are processed in the core for a number of different applications including RNA sequencing (traditional and single cell), exome, genomic resequencing, metagenomics, methylation, and ChIP sequencing. The core operates the Illumina NovaSeq6000, NextSeq550, and MiSeq systems. (Illumina, San Diego, CA). In addition to NGS systems, the core houses a Nanostring nCounter, ideal for rapid targeted gene expression experiments for pathway profiling and validation of NGS experiments.

**Staff Associated With the Genomics Core**

The laboratory has 5.0 full time research technologists that perform a variety of tasks in the laboratory including the processing of samples for the Illumina NovaSeq6000, NextSeq550, MiSeq systems, and for Sanger Sequencing. These applications include RNA/DNA quality assessment and preparation of samples for gene expression profiling and for genomic sequencing.

**Major Scientific Instruments Located Within the Genomics Core**

**Next Generation DNA Sequencing (NGS) Instruments**

https://emea.illumina.com/systems.html

NovaSeq6000 - The NovaSeq is a high capacity sequencer ideal for projects that benefit from the throughput and capacity: i.e. large RNAseq projects, single cell genomics, exome and whole genome sequencing.

NextSeq550 - The NextSeq Series delivers the power of high-throughput sequencing with the speed, simplicity, and affordability of a benchtop next-generation sequencing (NGS) system. The 550 can also scan Illumina arrays for copy number assessment.

MiSeqV2 - The MiSeq System facilitates your research with a wide range of sequencing applications. It is capable of automated paired-end reads and up to 15 Gb per run, delivering over 600 bases of sequence data per read. The library prep kits that it uses are optimized for a variety of applications, including targeted gene, small genome, and amplicon sequencing, 16S metagenomics, and more.

**Single Cell Genomics Instrumentation**

The Genomics Core Facility at UNMC has the instrumentation necessary to enable single cell genomics experimentation. The instrument used is the 10x Genomics System.

10x Genomics: The 10x genomics system can be used for either single cell RNA expression experiments or generation of single cell DNA libraries. Thousands of individual cells can be captured simultaneously and individually barcoded for RNAseq or DNAseq applications.

<https://www.10xgenomics.com/>

**Targeted Gene Expression Instrumentation**

Nanostring nCounter *MAX* – Nanostring ncounter targeted gene expression panel services. This system is an outstanding system for quickly and efficiently profiling gene expression in pathway specific panels of genes. A wide variety of panels (ranging from 400 to 800 genes per panel) are available including a number of different panels related to oncology, immunology, and neuroscience. Custom panels are available as well. This system is unique in that the color-coded molecular barcodes directly hybridize to nucleic acid, making it ideal for a range of discovery and translational research applications.

https://www.nanostring.com/products/ncounter-systems-overview/ncounter-overview-system-selection-guide

**Robotics / Liquid Handling for NGS Library Construction**

SciClone NGS Library Production Robot (Perkin Elmer): This instrument is used for producing NGS libraries for sequencing. The Sciclone® G3 NGS / NGSx workstations are the most capable automated solution for high-throughput sequencing sample preparation. Built on the Sciclone G3 platform, the NGS / NGSx Workstation is a complete benchtop solution for library prep, sequence capture, and normalization.

http://www.perkinelmer.com/product/sciclone-g3-ngs-workstation-cls145321

Eppendorf 5075 Liquid Handing Robot (Eppendorf North America, Inc., Hauppauge, NY): The EpMotion 5075 automated pipetting system from Eppendorf is used for generating NGS libraries.

**qPCR Instruments**

Applied Biosystems VIIa Real Time PCR Instrument (Life Technologies, Grand Island, NY). The instrument is utilized for real time PCR, quantification of gene expression and validation of gene expression identified by microarrays or NGS. It is also valuable for the quantification of NGS libraries prior to sequencing.

https://www.thermofisher.com/us/en/home/life-science/pcr/real-time-pcr/real-time-pcr-instruments/viia-7-real-time-pcr-system.html

**DNA / RNA Quantification and Sizing Instruments**

Fragment Analyzer Automated CE System: (Advanced Analytical Technologies, Inc. Ames, IA): The Fragment Analyzer™ Automated CE System has been shown to have both better sizing and quantification accuracy/reproducibility than any other analytical methods. This instrument works well for sizing nucleic acids extracted from tissues as well as from single cells in a high throughput fashion. https://www.aati-us.com/instruments/fragment-analyzer/

Agilent Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA): The Bioanalyzer instrument is used in a variety of NGS applications, including initial RNA integrity assessments as well as checking the size distribution of libraries for NGS applications. http://www.genomics.agilent.com/en/Bioanalyzer-System/2100-Bioanalyzer-Instruments/?cid=AG-PT-106

Nanodrop Spectrophotomer Instrument: This instrument is used for measuring the concentration and purity of nucleic acids prior to using them in experiments. https://www.thermofisher.com/order/catalog/product/ND-2000

Qubit Instrument: The Qubit is used for measuring double stranded DNA for use in NGS experiments. https://www.thermofisher.com/us/en/home/industrial/spectroscopy-elemental-isotope-analysis/molecular-spectroscopy/fluorometers/qubit.html

**DNA Shearing Instrumentation**

Covaris S220 Ultrasonicator (Covaris Inc., Woburn, MA): The Covaris S220 Ultrasonicator is used to generate DNA fragments prior to library generation. Next-Gen Sequencing has quickly become one of the most important tools in genomics research and nucleic acid fragmentation is a crucial first step in the sequencing workflow. http://covarisinc.com/applications/dnarna-shearing-for-ngs/

**Bioinformatic Resources at UNMC Campus**

The Genomics Core interfaces extensively with the Bioinformatics and Systems Biology Core at UNMC. This is an important resource for assistance with analysis as PhD and MS level analysts are available for consultation as well as fee for service applications. https://www.unmc.edu/bsbc/

**Bioinformatic Resources Accessible at University of Nebraska at Omaha (UNO)**

The University of Nebraska at Omaha (UNO) is located within three miles of UNMC. Researchers are encouraged to utilize resources at UNO for assistance with NGS data analysis and interpretation as needed. In particular, the Holland Computing Center at UNO allows researchers within the UN network to utilize the supercomputing resource. This resource allows the NGS Core bioinformatician to run computational tasks in a massively parallel fashion, thus providing investigators with analysis in a very timely manner.

**General Resources**

The Genomics Core laboratories are located in rooms 1010, 1012, 1015, 1017, and 1021, comprising approximately 2200 sq ft, located on the first floor of the Durham Research Center (DRC) II building at UNMC. These laboratories contain all the necessary instruments and expertise for an advanced research laboratory, such as a fume hood, gas and water supplies, compressed air, vacuum, benches, microcentrifuges, PH meters, etc.