The Genomics Core (a combined Genomics and Bioinformatics Core) at the University of North Dakota is a shared resource providing state of the art genomics resources to investigators at UND, institutions across the northern Midwest, as well as external commercial clients. The Core facility is a COBRE funded operation intended to help regional researchers utilize next-generation sequencing technologies in basic and translational genomic research. The Core provides services, training, and genomics resources to the scientific research community here at UND, NDSU, USDA and nearby colleges. Core staffs are available to design, analysis, and visualize sequencing data based on the needs of individual investigators and research projects. The emphasis in the Genomics Core operation is to enable investigators with little experience in genomics-based tools to design and prepare experiments utilizing NGS based technologies. The Genomics Core group provides services in data analysis standard analysis pipelines as well as project-specific analysis, which is free of charge. The Core's primary function is to help researchers analyze, interpret, visualize, and store the massive amount of data produced in next-generation sequencing experiments.

The Genomics Core group has a well-equipped lab for various type of library preparation and to support sequencing needs of investigators. Core provides Poly-A selected and Ribo-depleted library (directional or non-directional) preparation services for RNA-Sequencing. The Genomics Core also prepares DNA libraries for whole-genome sequencing based on the request from the various research group. Genomics Core recently started library preparation service for long read platform using VolTrax system. The Core staff train and help investigators in library preparation for ChIP-Seq, ATAC-Seq, and Sodium Bisulfite sequencing. The Core Lab has an Illumina MiSeq short-read sequencer and Nanopore GridIon X5 long-read sequencing platform along with a variety of instrumentation to support sequencing and quality control needs for NGS based experiments. The Genomics Core facility also have 10X chromium system (10X genomics) for single-cell genomics and optimized protocol for spatial transcriptomics. Quality control for nucleic acid and NGS libraries are performed either on a Tapestation 4200 or an Agilent Bioanalyzer 2100. The Core facility provides automated bead-based extraction of nucleic acid (DNA/ RNA) using Maxwell RSC system (Promega). BravoA system and SureCycler thermal cycler (Agilent technologies) are used for automated NGS library preparation and library are quantified using AriaMx Real-Time PCR System (Agilent technologies) with five filters (SYBR/FAM, ROX, HEX, CY3, and CY5) or with a BioRad QX200 Droplet Digital PCR system. The lab also offers a variety of instrumentation for shared use to trained, qualified users within the university. Patrons of the Core may sign up for access to a Covaris S220 Focused-ultrasonicator, a Bio-Rad CFX384 Touch Real-Time PCR Detection System, a Li-Cor. Biosciences' Odyssey Fc Dual-Mode Imaging System, an Aplegen OmegaLum C Imaging System, BioRad NGC Quest 10 Chromatography system, Thermo Scientific Sorvall MTX 150 micro Ultracentrifuge, and a BioRad Personal Molecular Imaging System.

The UND Genomics Core has ample computing resources for analysis and storage, including workstations for handling the analysis of large datasets that complement the UND high-performance computational cluster. Submission scripts to streamline data analysis have been developed to utilize both the core workstations as well as the UND cluster. All labs have high-speed, at least 1Gbs or more access channels to the network via WiFi and wired LAN.

- Two Dell Precision T7610 Tower Workstations each equipped with Intel Xeon E5-2687W v2 Eight-core 3.4 GHz Turbo, 25 MB CPU, 256 GB 1866MHz DDR3 RAM, 1GB NVIDIA Quadro K600 Video card, 256 GB Solid-state drive, six 4 TB SATA drives, 10 Gb network adapter, and a Nvidia Tesla K20C GPU. Both workstations run Red Hat Enterprise Linux with authentication via NDUS ID and password.
- One Dell Precision T5610 Tower Workstation equipped with an Intel Xeon E5-2687W v2 Eight-core 3.4 GHz Turbo, 25 MB processors (capable of 16 independent three processes), 64 GB 1866MHz DDR3 RAM, 1 GB NVIDIA Quadro K600 Video card, 256 GB Solid-state drive, two 1 TB SATA drives, DVD-RW drive, and a 10 Gb network adapter.
- Four Dell PowerEdge FC360 Server nodes are running on VMWare Vshpere 6 virtualization software capable of running multiple operating systems. Each server node has two sockets containing Intel Xeon E5-2660 v4 2.0 GHz HT CPUs with 14 dual-threaded cores and 512GB total onboard RAM. The environment encompasses a total of 224 virtual compute cores and 2 TB of total RAM. Computer hardware is connected via two 10 GB iSCSI ports to the SAN housing core storage. All access to these computing resources is integrated into the NDUS identification management system for ease of access and security.

Data Storage: Data collected by the core and UND epigenetic investigators is being stored redundantly on the High-Availability NSS Dell storage appliance (110 TB usable space with weekly backups, located at the UND-CRC) and on a Dell PowerEdge R720xd (6 core Intel Xeon processor) with a dedicated NIC setup with 4 TB SATA hard drive platters configured for file versioning configured with RAID 6 Disk Redundancy to protect from disk failure. The server's data is replicated to a second (off-site) server via DFS Replication, and VSS shadow copies of the data have been implemented to allow restoration of any folder or file, back to a previous state. This asset was created to allow for requisite storage and sharing of a large amount of data generated by sequencing experiments. Permission is administered by the Core, in conjunction with Medical School IT, and set up to provide all investigators and their lab members storage space as well as provide them access to other group's data to facilitate and encourage collaboration.