EQUIPMENT

Linda T. and John A. Mellowes Center for Genomic Sciences and Precision Medicine (Mellowes Center)

The Mellowes Center provides modern laboratory space, state-of-the-art instrumentation, and expert technical personnel to support the efficient execution of genomic, transcriptomic, epigenomic, and molecular pathology studies across cancer, non-cancer clinical genomics, pharmacogenomics, and rare disease research. Sequencing infrastructure includes the Illumina NovaSeq 6000 for high-throughput short-read sequencing and Oxford Nanopore platforms (GridION, P2 Solo, and P2 Integrated) for long-read sequencing applications, enabling studies ranging from whole-genome and transcriptome analysis to structural variant detection and isoform characterization. Additional capabilities include NanoString platforms for targeted gene expression and transcriptomic profiling.

To enhance throughput, reproducibility, and experimental consistency, the Center maintains automated instrumentation for nucleic acid extraction, liquid handling, library preparation, chromatin fractionation, ChIP-based workflows, and 10x Genomics single-cell and Visium CytAssist spatial transcriptomic sample processing. These systems support a wide range of applications, including RNA-seq, ATAC-seq, ChIP-seq, CUT&RUN, CUT&Tag, single-cell sequencing, and spatial transcriptomics.

Comprehensive quality control and sample characterization instrumentation is available throughout the workflow, including the NanoDrop 2000 and Agilent BioTek Synergy LX for nucleic acid quantification, the Diagenode Bioruptor® Pico for controlled chromatin shearing and DNA fragmentation, and the Agilent Fragment Analyzer for library quality assessment and fragment size analysis prior to sequencing.

The major instrumentation available for applications include:

Equipment	Company	Description
Maxwell RSC	Promega	Nucleic Acid (RNA/DNA) Extractions
Chemagic 360	Revvity	Nucleic Acid (RNA/DNA) Extractions
Tissue Lyser II	Qiagen	Sample disruption and preparation
Nanodrop 2000	ThermoFisher	DNA/RNA quantification, spectrophotometer quality assessment
Qubit	ThermoFisher	DNA/RNA quantification
Synergy LX Multimode Reader	BioTek	DNA/RNA quantification, fluorescence intensity, luminescence
Bioruptor Pico and Bioruptor Plus	Diagenode	DNA shearing, sonication
Fragment Analyzer	Agilent	QC, fragment analysis, 3x96 well plates
SciClone G3, Zephyr	Revvity	Automated library preparation and liquid handling robotics
CFX384	Bio-Rad	Thermocycling and real time, quantitative PCR
Blue Pippin	Sage Sciences	High molecular weight size selection
Chromium iX	10x Genomics	Single cell transcriptomics, epigenomics

Visium CytAssist	10x Genomics	Spatial transcriptomic profiling in standard and high definition
NovaSeq 6000 and MiSeq	Illumina	Next generation sequencer, short reads
GridION, P2 Solo and P2 integrated	Oxford Nanopore Technologies	Next generation sequencer, long reads
nCounter Loader and Scanner suite	Bruker Spatial Biology	FFPE sample transcriptomics and miRNA expression panels

Concurrent to next generation sequencing capabilities, the Mellowes Center utilizes high-end bioinformatic and molecular modeling software to apply advanced analytic methodologies to high-throughput data. The Center regularly performs primary, secondary, and tertiary analyses of the available genome-wide methodologies, as well as high-level integrative modeling of multiparametric data, using mathematical and statistical methods, including Ordinary Differential Equations, Hidden Markov Models, Monte Carlo, Random Forest, Machine Learning, and Neurolinguistics Processing approaches. Suites and tools offered include GeneString, Qiagen Ingenuity Suite (IVA, IPA, and QCI-I), BIOVIA Discovery Studio: Comprehensive Modeling and Simulation for Life Sciences Research, as well as custom made, proprietary pipelines and tools. The suite of software and tools runs in a high-performance computing environment including 79 computational nodes, 4,200 processor cores, and 96 graphical processing units (GPUs), all of which are administered by MCW's **Research Computing Center (RCC)**. The RCC's managed data center securely stores the generated data.