Next Generation Sequencing Facility

ACRI's next-generation sequencing core facility (**NGS Core**), located in the New Brunswick Center for Precision Medicine (**NBPCM**) is well-positioned to contribute to significant advances in genomics studies, cancer research, and precision medicine. Our NGS core consists of the latest technologies to provide high quality data at competitive prices. We work with our clients to tailor the sequencing requests according to the project requirements with a four week turnaround time.

Our expertise includes clinical consultants, research associates, and bioinformaticians. NGS Core has developed a proprietary custom Laboratory information management system (LIMS) software to effectively manage samples and associated data. The team is currently moving towards providing CLIA certified sequencing.

NGS Core's sequencing platform is comprised of the following key technologies:

- **Novaseq 6000** from Illumina (paired-end sequencing)
- **Ion Proton** from Thermo Fisher
- **iSeq 100** from Illumina
- **MinION** from Oxford Nanopore (long-read sequencing)
- **Fragment Analyzer from Advanced Analytical** (nucleic acid quality control)
- **Agilent 2200 Tape Station** (nucleic acid quality control)
- **Kingfisher Duo** (automated nucleic acid extraction).
- **Other automation tools for increased reliability and reproducibility**

NGS Core's computational capabilities include AI-ready workstations and several redundant data storage servers. Additionally, the bioinformatics team has expertise in high-throughput data analysis, including clinical research sequencing panels, RNA-Seq (protein-coding and non-coding RNAs), DNA-Seq, Single Cell sequencing and proteomics on different types of samples. Multi-omics studies including machine learning strategies can be also performed. The bioinformatics team has analyzed data from human source (tissue and liquid biopsy samples from different types of genetic diseases, such

as different types of cancer and ALS) and non-human source (e.g. pigs, salmon, zebra fish, and different insects).

Ion Torrent Platform-Proton/S5

- This platform is suitable for low throughput transcriptome sequencing studies, small RNA sequencing and ampliseq panels (FFPE and liquid biopsies). For poly-A sequencing we sequence two samples per chip with 25 million aligned reads. Output obtained might vary depending on the quality of the library and project requirements. Small RNA sequencing can be performed from as low as 5ng of RNA. We can work with low quality small RNA from plasma and extracellular vesicles and deliver 50-70% miRNA alignment. We also work with non-human RNA samples like salmon, beetles, locusts and zebra fish.

Illumina Platform- Novaseq 6000/iSeq 100

Novaseq 6000 is routinely used for high throughput projects, whole exome sequencing, whole genome sequencing, DNA methylation, and for clients specifically requesting paired end sequencing. Due to high sample input requirement for whole transcriptome sequencing, clients have the option to purchase one full flow cell or opt for flow cell sharing when available. We also work with non-model organisms for whole genome and transcriptome sequencing. iSeq is routinely used for quality control purposes.

Oxford nanopore: MinION

MinION sequencer is ideal for long read sequencing, direct RNA sequencing and CRISPR Cas9 mediated studies for repeat expansion, and long structural variants.