Vermont Integrative Genomics Resource (VIGR)

**Overview**

The Vermont Integrative Genomics Resource is a multi-faceted facility that offers a full range of genomics and bioinformatics services. The facilities primary goals include consultation for experimental design, data generation, troubleshooting assays, full service to bioinformatics analyses, and support for data management and publication. VIGR employs three full time dedicated analytical staff and three full time bioinformatics staff that have over 30 years of combined experience in advanced genomics, molecular and microbiology, and bioinformatics analysis, with over 50 publications and numerous national and internationals presentations.

**Personnel**

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|  | **Julie A. Dragon, Ph.D., Director** |  |
| **Wet lab**  |  | **Dry lab** |
| Scott Tighe, B.S. |  | Korin Eckstrom, M.S. |
| Jess Hoffman, B.S. |  | John Hanley, Ph.D. (0.5 FTE) |
| Pheobe Kehoe, M.S. |  | Ramiro Barrantes, Ph.D. (0.3 FTE) |
| Lab Tech, TBN  |  | Marni Slavik, Ph.D. (0.2 FTE) |

**Facilities and equipment**

The facility is located in the UVM College of Medicine complex in the heart of the UVM Health Sciences complex, and occupies 2019 sf of contiguous wet lab space, and 507 sf of discontinuous dry lab space.

Massively Parallel Sequencing (MPS): MPS includes single-cell genomic analysis, chromosome conformation capture techniques, RNA-Seq, Exome-Seq, ChIP-Seq, Methyl-Seq, whole genome sequencing, metagenomics and microbiome, and small RNA sequencing to name a few.

Major equipment includes:

* Illumina HiSeq 1500 Sequencer, MiSeq Sequencer, and MiniSeq Sequencer
* Oxford Nanopore GridION X5 MK2, and 3 Oxford Nanopore MinION MK1B
* 10x Single Cell Genomics System
* Eppendorf epMotion 5073 liquid handler
* Covaris AFA Hydroshear

General Genomic Services (GGS): GGS provides a vast array of analysis services including DNA/RNA extraction, PCR and PCR troubleshooting, primer design, Sanger sequencing, (SNP/MSI/AFLP), human cell line authentication, quantitative PCR, nucleic acid and protein quantification, and microarrays. Major equipment includes:

* ABI Prism 3130 and 3130xl (4 & 16 cap) Genetic Analyzers
* ABI Quant Studio 6 RTqPCR system and Prism 7500 Fast RTqPCR
* BioRad QX200 Digital Droplet qPCR
* BioRad PharosFX & QRS+ ChemiDoc imagers
* Agilent 2100 Bioanalyzer
* NanoDrop (ND-1000) Spectrophotometer
* Quantas Spectrofluorometers, and 3 Qubit spectrofluorometer
* Logo Quantum Microbial imager
* Zeiss digital AxioScope with DIC and full spectrum fluorescence
* Benchmark Beadbug6 Homogenizer
* 4 PCR free Clean Air HEPA cabinets
* 1 Biosafety II hood
* Savant SpeedVac
* Thermo Omni Bead Ruptor 24 Elite
* 2 Biometra TAdvanced 60 Thermal Cyclers with Exchangeable Blocks
* Affymetrix Microarray - 7G scanner, hybridization oven, fluidics station

Bioinformatics Shared Resource (BSR): The wide range services offered include experimental design for genomics-based research, and analysis of all types of next-generation sequencing data including metagenomics. In addition, the BSR supports microarray and other array-based assays.

The BSR provides cutting edge bioinformatics analysis that includes data processing, visualization, archival storage, and deposition in public repositories. Services also include data quality assessment, calculation of probe set statistics, sequence reads, alignment to a reference genome, variant calls, linear modeling, and multivariate analysis. Resource staff can provide text describing methodology, figures for manuscripts, and can deposit data into public databases. In addition to providing established resources, staff assist in implementing new bioinformatics tools to provide innovative solutions for bioinformatics challenges as they occur. Resource personnel also support use of tools associated with the Vermont Advanced Computing Cluster (VACC), a multi-core cluster that will run computational intensive applications.

The BSR has infrastructure to support analyses of multiple and integrated data types and leverages the VACC for high performance computing and data storage. Major equipment includes:

**10 dedicated multi-core processing nodes** (2-20-core (256 GB RAM) and 8-12-core (32GB RAM), and **30 TB storage** in the Vermont Advanced Computing Core cluster (VACC).

An **independent VIGR queue** on the high performance compute cluster so our jobs start immediately and are not interrupted by smaller, lower memory requiring jobs.

**50 TB of secure long-term archival storage** provided by ETS. The entire 50 TB is backed up on a three-month rotating schedule to provide archival backup capability.

**8 TB local external storage**, configured as a RAID array providing 3.25TB mirrored working space for project files, and a 1.5 TB hourly desktop backup.

The VACC provides access to two HPCs

* “Bluemoon,” a **multi-thousand-core**, high-performance computing cluster, supporting large-scale computation, low-latency networking for MPI workloads, large memory systems, and high performance parallel file systems.
* “Big Green,” a **massively parallel cluster composed of over 70 GPUs** capable of over 8 petaflops of mixed precision calculations based on the NVIDIA Tesla V100 architecture. Its hybrid design and parallelism can expedite and support high-throughput artificial intelligence and machine learning workflows.