Services
Many types of libraries are sequenced at the core lab however not all are synthesized, please inquire.

**Library Types**
- RNA-Seq
- DNA-Seq
- Small RNA-Seq
- Exome-Seq
- Metagenomics
  - Methyl-Seq
  - ChiP-Seq
  - Small RNA-Seq
  - RAD-Seq.
  - HiC
  - Targeted
  - Mate Pair-End
  - Amplicon
  - Metagenomics

**Sequencing**
- RNA-Seq
- DNA-Seq
- Small RNA-Seq
- Exome-Seq
- Metagenomics
- ChIP
- Targeted
- Mate Pair-End
- Amplicon
- Metagenomics

Running Modes
Two running modes are available. Rapid mode is a shorter turn around time but has lower output.

<table>
<thead>
<tr>
<th>Run Mode</th>
<th>Flow Cell Type</th>
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<tbody>
<tr>
<td></td>
<td>Rapid Mode</td>
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<tr>
<td></td>
<td>High Capacity</td>
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</table>

**Paired End (PE) or Single End (SR)**
- SR 50, 100, 150, 200, 250 bp
- PE2 x 50, 100, 150, 200, 250 bp

High capacity uses an 8 lane flow cell and generally requires additional wait time to fill all lanes.

Experimental Design
The MPS sequencing staff and UVM bioinformatics scientists work closely with investigators to insure project success. We encourage all investigators to take advantage of this consultation service.

Accessing Services
All samples and consults are registered using the MPS core facility iLabs sample management system.

Sample submission must be accompanied by a bioinformatics number issued by the molecular bioinformatics shared resource.

Pricing
Pricing changes every year and has many options including self service for those who prepare their own libraries or full service.

Please see our website or contact the facility by email for pricing information.

Email
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Timothy.Hunter@uvm.edu

Contact
Massively Parallel Sequencing Lab
Advanced Genome Technologies Core
University of Vermont Cancer Center
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802-656-AGTC [2482]
About The Core
The University of Vermont’s Massively Parallel Sequencing (MPS) core lab is a Vermont Cancer Center shared resource facility within the UVM College of Medicine and provides all services related to next generation sequencing using the Illumina HiSeq system to both internal and external customers.

Instrumentation
The facility is equipped with the Illumina HiSeq 1500 System capable of generating 50 gb of DNA sequence per lane with read length from 50bp to 250bp either single or paired end.

Details and Definitions of Next Generation Sequencing

Flow Cell is the device where all sequencing reactions occur. The flow cell is composed of 2 or 8 “lanes” which are microfluidic channels. Sequencing takes place on synthetic genomic “clusters”.

Cluster represents a discrete clonal amplification of a single 400bp DNA fragment from the genome.

Single End vs Paired End Reads
Each DNA fragment can be sequenced in one direction or both directions.

Fold Coverage
Fold coverage represents the depth of coverage. Repetitive sequencing of the same region. Expressed as RPKM (Reads Per Kilobase per Million reads) or FPKM (Fragments Per Kilobase per Million reads).

Number of Reads
The total number of reads per sample type is an important metric and describes the total number of clusters (fragments of the genome) regardless of the read length.

Data Analysis and Storage
All data is processed and stored by the UVM molecular bioinformatics shared resource facility. Data analysis is available as fee for service and is scheduled during the experimental design meeting.

Quality Control
Library and sample QC is performed using Qubit, Agilent Bioanalyzer, and qPCR. All libraries are prepared within a Class 100 HEPA PCR-free Clean Hood. Separate rooms separate PCR and non-PCR areas of the lab.

Contact
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