**Massively Parallel Sequencing Facility:**

The AGTC Massively Parallel Sequencing Facility was initiated by the Vermont Cancer Center and the Lake Champlain Cancer Research Organization, and established in 2011 in collaboration with the College of Medicine and College of Agriculture and Life Sciences to provide genome-scale DNA sequencing. The facility employs the use of massively paralleled sequencing (MPS) technology of the Illumina HiSeq system which is sequencing by synthesis approach (SBS).

Next generation sequencing (also known as deep sequencing or high throughput sequencing) enables researchers to sequence as much as an entire human or mouse genome with greater than 50 fold coverage. A single run on the Illumina HiSeq 1000 can sequence over 350 billion bases of DNA. It can be used for genome wide DNA sequencing, RNA-seq, ChIP-Seq, methylation sequencing, metagenomics, exome sequencing, amplicon sequencing, and microRNA sequencing. All Massively Parallel Sequencing projects are reviewed using an integrated approach to experimental design, workflow, and sample collection in collaboration with the UVM Bioinformatics Core Facilities to ensure high quality, statistically relevant results.

**Staffing:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Email</th>
<th>Phone</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tim Hunter</td>
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<td>656-AGTC</td>
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</tbody>
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**Services Offered:**

- Experimental Design Consultation

- Single End, Paired End, or Mate Paired End Library Construction for the following applications:
  - RNA-seq (prokaryote or eukaryote)
  - Whole Genome DNA Sequencing
  - Methyl-Seq
  - ChIP-Seq
  - Metagenomics
  - Amplicon Sequencing

- Sequencing by Synthesis
Ability to multiplex 16 samples/lane via indexing for prokaryotes and up to 48 for the standard Illumina TruSeq protocols (multiplex number dependent on coverage/depth required for each sample)

**Access Guidelines:**

**Step I:** **Consultation:** Consulting on experimental design is mandatory to discuss sample requirements, sequence coverage desired, library construction best approaches, insure appropriate number of replicates for statistical significance, and to draft a project design file in support of downstream bioinformatics analysis.

**Step II:** **Quantification and Qualitative assessment of Nucleic Acid:** All RNA submitted for sequencing must be tested for integrity and for gDNA contamination (extremely important for prokaryotes). It is highly recommended that all nucleic acids are quantified using a fluorometric approach to insure accuracy.

**Step III:** **Submit Nucleic Acid(s) for library construction:** This should be done in combination with submitting appropriate order form online. Samples can be dropped off in the -20°C Freezer in 303 HSRF that is marked “drop MPS samples here”.

**Step IV:** **Data Upload:** All data will be transferred to a server at the VACC and stored on the College Of Medicine Shared Drive

**Sample Requirements:**

<table>
<thead>
<tr>
<th>Application</th>
<th>Input concentration required</th>
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<tbody>
<tr>
<td>Whole Genome Sequencing</td>
<td>500 ng</td>
</tr>
<tr>
<td>RNA-Seq</td>
<td>1 ug</td>
</tr>
<tr>
<td>Methyl-Seq</td>
<td>see facility staff</td>
</tr>
<tr>
<td>ChIP-Seq</td>
<td>&gt;20 ng (Purified ChIP DNA)</td>
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</table>

**FAQ’s: Still in development**

**Acknowledging the Core Facility:**

**Citing the VCC-COM Massively Parallel Sequencing Facility**

Please remember to cite the VCC-COM Massively Parallel Sequencing Facility in your abstracts and publications. These citations demonstrate to the NCI and other funding organizations (as well as the UVM administration) the importance of this facility to UVM researchers and thereby encourage their continued support. We try to keep a current list of all publications that cite the facility, so please let us know as when your papers are published! Below is an example of how to cite the facility:
"The next-generation sequencing was performed in the Advanced Genome Technologies Core Massively Parallel Sequencing Facility and was supported by the Vermont Cancer Center, Lake Champlain Cancer Research Organization, UVM College of Agriculture and Life Sciences, and the UVM College of Medicine."

**Links of Interest:**

SeqAnswers Home(forum for next-gen sequencing community): http://seqanswers.com/

ABRF DNA Sequencing Research Group:
http://www.abrf.org/index.cfm/group.show/DNASequencing.28.htm

Illumina, Inc.: http://www.illumina.com/

ABRF Genomics Research Group: http://www.abrf.org/index.cfm/group.show/Microarray.30.htm

ABRF Next-generation Sequencing:
http://www.abrf.org/index.cfm/group.show/NextGenerationSequencing(NGS).75.htm

NuGEN Technologies, Inc.: http://www.nugeninc.com/nugen/