[**Sequencing Core Facility**](http://bauercore.fas.harvard.edu/sequencing)

**URL:** <http://bauercore.fas.harvard.edu/sequencing>

**Faculty Director:** Gonzalo Giribet

**Laboratory Manager:** Claire Hartmann (formerly Reardon)

Please contact Claire ([claire@cgr.harvard.edu](mailto:claire@cgr.harvard.edu)) if you plan to submit a grant proposal referencing resources in this core, and she will help you to select instruments and plan your experiments.

**Description:**

*Square Footage:* 2767 sq. ft.

*Facility Location:* Northwest Lab, B239

The Sequencing Core offers high throughput “Next Generation” sequencing by synthesis using Illumina instruments and long read sequencing with Oxford Nanopore. Many instruments from the former “robotics” core facility are now made available through the sequencing core. This Core offers training, support, and fee-for-service work.

**Major Equipment:**

* Illumina NovaSeq 6000: This system offers the lowest cost/base of our fleet of sequencers. Features include: flow cells sizes offering 800 million - 10 billion read pairs; customizable read lengths from 50 to 250 bp long (single or paired end); variable length sample indexing/barcoding reads; custom primers supported.
* Illumina NextSeq 500 and 550: These systems offer our fastest turn-around times. Features include: flow cells sizes offering 130 million – 400 million read pairs; customizable read lengths from 38 to 150 bp long (single or paired end); variable length sample indexing/barcoding reads; custom primers supported.
* Illumina MiSeq: This small-scale sequencer is perfect for small projects or pilot runs. Features include: flow cell sizes offering 1 million – 25 million read pairs; customizable read lengths from 50 to 300 bp long (single or paired-end); variable length sample indexing/barcoding reads; custom primers supported.
* Oxford Nanopore PromethION – Each of the 24 flow cell positions can run independently and generate 50-150 Gb of sequence data with reads lengths up to 100s of Kb. Direct sequencing of DNA or RNA allows for the detection of modified bases.
* 10x Genomics' Chromium: This technology partitions reactions into nanoliter-scale droplets containing uniquely barcoded beads called GEMs (Gel Bead-In EMulsions). This core technology can be used to partition single cells or nuclei to prepare next generation sequencing libraries in parallel. The core provides training and runs samples as a service on the Chromium system.
* Ancillary Equipment including:
  + Liquid handling using Beckman Biomek FX, PE Sciclone, and Formulatrix Mantis.
  + Covaris Shearing
  + Nanodrop and Qubit for small volume spectrophotometry
  + Bioanalyzer and TapeStation to determine nucleic acid size
  + Real Time PCR instruments for superior accuracy of quantification
  + Size selection using convenient gel cassettes on the Sage Pippin Prep and Blue Pippin.
  + Real time PCR using BioRad CFX96 Touch, CFX384 Touch, and Opus, and ABI7900.
  + The BioRad QX200 droplet digital PCR system encapsulates QPCR reactions into up to 20,000 droplets to enable digital readout of the PCR reaction. This allows for increased sensitivity of detection making this system particularly good for absolute quantification of rare genes/transcripts or detection of small fold-changes in expression.
  + Plate readers capable of measuring absorbance, fluorescence, luminescence, and fluorescence polarization.
  + Nanostring nCounter SPRINT for direct detection of RNA, DNA and/or protein (with no amplification required). Multiplexed panel assays enable a variety of experiment sizes. For example, 22 samples x 800 genes or 96 samples x 24 genes.
  + Imaging systems including the Azure Sapphire multimode imager capable of detecting fluorescence, chemiluminescence, visible images, and phosphorimaging.
  + Nucleic Acid isolation on the Autogenprep 965.