Introducing: The Genome Analysis & Technology Core (GATC)

The Genome Analysis and Technology Core’s continuous mission is to enable high-throughput Next Generation Sequencing projects for both novice and experienced users alike. The GATC serves as a scientific resource and biotechnology hub enhancing the scope and quality of basic and translational research at UVA by maintaining customer satisfaction, increasing staff accountability, collaboration and quality control. The core staff endeavor to provide timely assistance in all facets of experimentation from project design/execution to data analysis/reporting, stimulating institutional collaborations as well as provide staff/students training and educational opportunities.

The core is a fee-for-service operation that offers instrumentation and expertise in all areas of NGS genomics and transcriptomics, as well as training to access the core shared instrumentation. Current applications supported by the core staff include bulk and single Cell (Sc) RNA Seq, CHIP Seq, ATAC Seq, Amplicon DNA Seq, 16S ribosomal gene sequencing, shot gun sequencing and targeted exome sequencing. The core also provides real time and droplet digital PCR services most suitable for targeted gene expression, SNP genotyping and CNV discovery. The GATC provides free project consultations and support for grant applications.

By opening the doors to new technologies, the core affords investigators at UVA and other partner institutions the tools for a deeper understanding of biological processes. We invite UVA students and researchers to visit us on line (google UVA) GATC or better yet, to come and visit the labs located in Pinn Hall near the Graduate Programs Offices.

List of GATC Services

Scientific Support
Project Design Consultation
Grant Budget Preparation
Grant Letter of Support

NGS Library Preparation
16S and shot gun metagenomics
RNA and total RNA library prep
Low input RNA amplification
Nextera XT and Nextera Flex
Small RNA libraries

Real Time qPCR
NGS Library quantitation
Gene expression/validation
SNP genotyping

Shared instrumentation Access
Digital Droplet PCR
Pippin
Covaris
QIAcube

List of GATC Services

Next Generation Sequencing
MiSeq and Next Seq run set up
Library pooling services Sequencing runs single and paired end

10X Genomics
Single cell RNA seq
Unprocessed sequencing

Qubit and NanoVue
10X linked Read DNA
10X single cell RNA seq
VDJ RNA seq

Sequencing Analysis
Training and Education
Data Analysis
Custom libraries
New Protocol Development

Goal #1: I want to focus on the coding transcriptome and I want to quantify gene expression at the gene level, with one abundance value generated per gene.

Method: Gene expression Profiling – mRNA-seq ≥ 20 Million reads per sample, 1 x 75 bp Library prep: mRNA stranded
Next Seq MO mode: 7 sample pool
Next Seq HO mode: 20 sample pool
MiSeq: 2 samples can be pooled

Goal #2: I want to focus on the RNA exome and I want to quantify gene expression by analyzing abundance values for every transcript isoform from each and identify novel transcript isoforms, SNVs, gene fusions, and/or identify allele-specific expression.

Method: mRNASeq-Seq ≥ 25 Millions reads per sample, 2 x 75 bp Library prep: mRNA stranded
Next Seq MO mode: 5 sample pool
Next Seq HO mode: 15 sample pool
MiSeq: 1 sample per flow cell per run

Goal #3: I want to focus on the abundance values of both coding and multiple forms of noncoding RNA and identify novel transcript isoforms, SNVs, gene fusions, and/or identify allele-specific expression.

Method: Total RNA Sequencing – rRNA depleted ≥ 20 Million reads for QC samples, 2 x 75 bp ≥ 100 Million for degraded samples, 2 x 75 bp Library prep: stranded total RNA ribo-depletion
Next Seq MO mode: 5 sample pool
Next Seq HO mode: 8 sample pool

Goal #4: I want to sequence the known exome at 50X mean coverage

Method: Whole Exome Sequencing WES
Next Seq MO mode: 3 sample
Next Seq HO mode: 12 sample pool

Goal #5: I want to sequence a small genome 130 Mb at 30X coverage 2x150bp

Method: Whole Genome Sequencing
Next Seq MO mode: 10 sample
Next Seq HO mode: 30 sample pool

Goal #6: I want to sequence 12Mb region at 20X

Method: targeted sequencing
Next Seq MO mode: 12 sample
Next Seq HO mode: 36 sample pool

Goal #7: I want to sequence the 16S bacterial ribosomal genes

Method: 16S DNA sequencing
Next Seq MO mode: 3 sample
Next Seq HO mode: 12 sample pool

How to Match Your NGS Research Goal with Core Technologies

RNA Sequencing
RNA-Seq experiments should be performed with at least two or more biological replicates. The first step in any successful sequencing experiment is the preparation of the RNA to be sequenced. The number of RNA samples that can be analyzed on the core’s sequencers will depend on RNA quality, depth of sequencing needed (Goal) and Output of the sequencing kit. The data generated is quantified and analyzed. The results are presented in a format that is easy to interpret.

DNA Sequencing
How to estimate and achieve the desired NGS Coverage for DNA sequencing will depend on the application used and best practice as recommended by the scientific community.

Next Generation Sequencing Instrumentation

The Genome Analysis and Technology Core NGS services located in UVA’s Pinn Hall 1044 include two benchtop Illumina sequencers. Illumina MiSeq Sequencing System

The MiSeq enables automated paired-end reads and up to 15 Gb per lane, delivering over 600 base of sequence data per read. The core provides optimized library prep kits for a variety of applications

Targeted resequencing and CHIP-Seq
16S metagenomics and small genome sequencing
Targeted gene expression profiling

Illumina NextSeq™ 500 Sequencing System

Its flexible configuration (Mid and High output) enables 120Gb of output with 130-400 Million reads per run. Shotgun de novo sequencing RNAseq bulk or single cell
Exome sequencing
Small RNA profiling as well as other custom NGS pipelines

Single Cell Capabilities with 10X Genomics

The GATC’s newest instrument is the 10X Genomics Controller located in Pinn Hall 1076

The GemCode Technology’s flexible throughput enables encapsulation of 500 – 800,000+ cells (8 wells) in 10 minutes and supports processing of (ready to sequence) barcoded CONA libraries in two days.

This technology is compatible with the core’s Illumina NextSeq/MiSeq sequencers and can be used as standalone for library prep or integrated to GATC in house sequencing workflow.

At this time the GATC core enables RNA expression profiling of hundreds to thousands single cells. A typical experimental set up will analyze the expression of 1,000 to 2,000 cell at a depth of 50,000 to 100,000 reads per sample.

- Kits are currently available for haplotype analysis in HMW DNA using barcoded linked reads.
- New protocols are being developed to enable VDJ repertoire typing of B and T cells paralleled with 5’ RNA expression profiling.

See What The Core Can Do For You

The GATC data analysis services include Differential Gene Expression (Panel A), Single Cell 3’ Gene Expression (Panel B), CHIP-Seq Analysis (Panel C), 16S Metagenomics (Panel D).

Panel A: RNA-Seq Volcano plot depicting gene expression resulting from a cell perturbation. Examples of genes that display both large magnitude fold changes and high statistical significance p-values are circled.

Panel B: Gene Expression Visualization of High Dimensional Single Cell RNA-seq: the T-Distribution plot identifying discrete subpopulations of differently expressed Neurons.

Panel C: CHIP-Seq Example of the profiles generated by chromatin immunoprecipitation followed by sequencing (ChIP-seq). The genome browser snapshot shows the mapping quality of reads within the classification results for each taxonomic level.

Panel D: 16S typing This workflow chart shows the number of reads from the classification results within each taxonomic level.

GATC Organizational Chart

Advisory Committee

ORCA Support Team
Jay Fox, PhD
Yuh-Hwa Wang, PhD
Kativa Sol-Church, PhD
Alyson Prorock, MS

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GATC Technology Hub

庆山大学 産業技術領域

BioRad GX200 ddPCR
Qubit Fluorimeter
Nanovue Spectrometer
Copy number Library quant

Agilent Tape Station
DNA and RNA QC

Agilent Bioanalyzer
Real Time PCR System
Glucide Sample prep
Pippin Size Select
Covaris DNA Shearing