

## Real Time Quantitative PCR



ABI 7900 HT DNA Detection System

### Applications

- Gene expression Quantification
- SNP Characterization and Screening
- MicroRNA Quantification
- DNA Copy Number Determination
- Viral Titration

### Features

Barcode reading Capacity  
Fast Block to adopt  
Multiple dye capability  
Automation adoptability of high throughput  
QC measure: [reference RNA/housekeeping](#)

### Auxiliary Services

- Nanodrop quantitation of small samples
- Agilent Bioanalyzer for RNA Integrity
- Assay design and validation
- Assay design to validate microarray data

## Other Services via Core Storefront with Commercial Ventures

**Oligosynthesis** can be ordered through the UVA-Invitrogen SupplyCenter program.

**PCR arrays** can be ordered via a soon coming UVA-supperArray program. The special application for this array type is to validate the pathway discovery in microarray experiments.

### Staff Members



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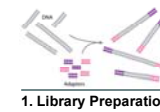
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## DNA SCIENCES CORE

### Inauguration of next-generation DNA Sequencing



1. Library Preparation



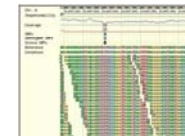
2a. Cluster Generation



2b. Flow Cell



3. Sequencing & Imaging



4. Data Analysis

### Applications offered by Illumina Genome Analyzer

Genome DNA sequencing using single or paired-end reads

- Discover and confirm SNPs
- Identify chromosomal rearrangements, including Copy Number Variations (CNVs)
- Map break points
- Detect rare variants

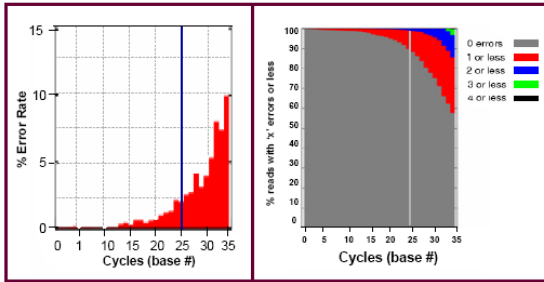
Digital gene expression

- Novel RNA discovery
- Accurate quantification of low abundance RNA
- Orthogonal microarray validation

ChIP-Seq supports genome-wide study

- Transcription factors
- Proteins
- Polymerases and transcriptional machinery
- Structural proteins such as histones and histone variants
- Protein modifications such as methylated histones and phosphorylated proteins

**Typical throughput and quality of an Illumina Genome Analyzer run**



Lane	Clusters per tile: Average 1 <sup>st</sup> Cycle Intensity	% Intensity After 20 Cycles	% Error Rate (raw)	Perfect Clusters per Tile (raw)	% Align (PF)	% Error Rate (PF)	
1	27587 +/- 1860	2057	94.19	1.63	16444	83.24	0.69
2	32781 +/- 2208	2172	92.19	1.54	19045	79.34	0.6
3	35372 +/- 2002	2206	86.54	1.69	21513	81.11	0.82
4	36257 +/- 2110	2123	79.55	3.49	21274	81.79	2.7

**Conventional Sanger DNA Sequencing**



**Applications**

- Plasmid DNA
- PCR amplicons
- BAC/PAC/Cosmid DNA
- Gene walking

**Features**

- Current instrument—ABI 3730 DNA Analyzer, 48 capillary array
- Sanger DNA sequencing with BigDye 3.1 terminator chemistry
- Average read length—750 bp
- Capacity—1.2 Mbp/day
- DNA Fragment Analysis
- Microsatellite Genotyping (STR)
- SNP Genotyping
- ALFP Analysis
- QC measure: control plasmid/Phred score

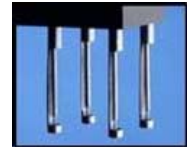
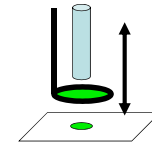
**Microarrays on Various Platforms**



**Affymetrix GeneChip Arrays**

- 3' Expression arrays
- Whole genome-wide expression arrays
- Whole genome-wide exon arrays
- SNP arrays
- Chromosome tiling arrays
- Resequencing arrays

**Custom spot arrays**



Services include:

- Other commercial arrays
- Protein arrays
- microRNA arrays

**Auxiliary and post –microarray Services**

- All steps of microarray analysis starting from cell or tissues.
- All standard Affymetrix GeneChip analysis.
- Any type of commercially available slide arrays (DNA or protein).
- Integrated projects: microarray analysis and qPCR validation of the genes found regulated by microarray analysis.
- Data analysis and consultation
- Meta data analysis
- Data mining on facility-generated data or outside data
- QC measure: spiked-in genes and 3':5' ratios