

## Mission Statement

The mission of the Genomics Core Laboratory is to provide state-of-the-art genomic services to UTHSCSA and the local scientific community in an economical and timely manner.

## Services Provided

- Illumina custom SNP genotyping (48-384plex)
- Illumina whole genome genotyping
- Genotyping of length polymorphisms
  - custom assays
- TaqMan allelic discrimination genotyping
- Illumina whole genome gene expression
  - Human (HT12) and mouse (WG6)
- Illumina mouse medium density linkage panel analysis
  - speed congenics
- Quantitative real-time PCR analysis
  - gene expression and copy number
  - processing of low density microfluidics cards
- Bioanalyzer analysis of DNA and RNA
- Ion Torrent PGM Microbiome sequencing
  - 16S rRNA gene
- Ion Torrent PGM MicroRNA sequencing
- Biological specimen banking
  - DNA and RNA isolation
  - Human cell line authentication

## Contact Information

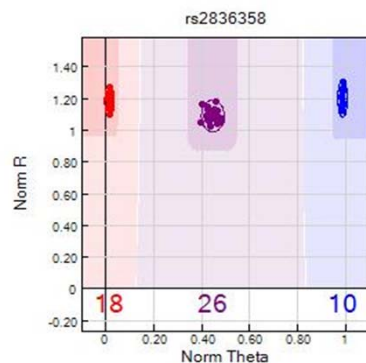
Phone: 567-0950  
 Locations: MED 571C, 573C 540E, 542E  
 Website: <http://www.uthscsa.edu/csb/genomics.asp>  
 Also find us on science exchange.

## Key Equipment

- Illumina BeadXpress reader
- Illumina iScan array scanner
- ABI 7900HT Sequence Detection System
- ABI microfluidics card block
- Ion Torrent Personal Genome Machine
- Ion OneTouch System
- Agilent Bioanalyzer
- NanoDrop spectrophotometer
- Qubit fluorometer

## Research Supported

### Illumina Custom SNP Genotyping



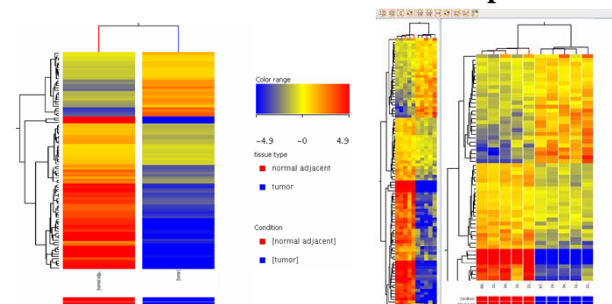
Validation of Genome-Wide Prostate Cancer Associations in Men of African Descent  
 Chang et al. (2011) *Cancer Epidemiology, Biomarkers & Prevention* 20:23-32.

### Real Time qPCR Analysis

Reduced Expression of Fumarate Hydratase in Clear Cell Renal Cancer Mediates HIF-2 $\alpha$  Accumulation and Promotes Migration and Invasion  
 Sudarshan et al. (2011) *PLoS One* 6:e21037

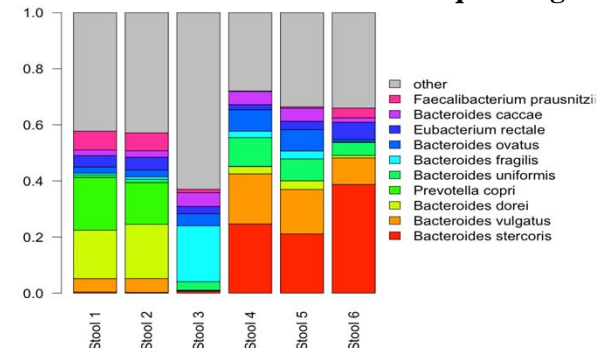
## Research Supported

### Illumina Whole Genome Gene Expression



Differentially expressed genes between normal adjacent and tumor tissue. Heatmaps of significantly differentially expressed genes identified using paired T-test (GeneSpring software, Agilent). Normalized values are represented by color ranges with red as higher expression and blue with lower expression compared to mean values. In the first the tissue median value is shown while in the second non-averaged values are shown.

### Ion Torrent PGM Microbiome Sequencing



Sequencing of the bacterial 16S rRNA gene hypervariable region demonstrates variation in the microbial populations found in stool specimens from subjects in the San Antonio Family Heart Study. CTSA pilot project: Charles Leach, M.D.