# CANCER GENOMICS & BIOINFORMATICS CORE (CGBC)

Paolo Fortina, MD, PhD

Director

215-955-0683

Melanie Kelly,

Manager

215-955-9572

Kimmel Cancer Center

233 South, 10th Street

BLSB, Room 1009

Philadelphia, PA 19107

http://www.jefferson.edu/jmc/departments/cancer-biology/research/cancer-genomics/services.html

|  |  |
| --- | --- |
| Mission, Goals, Capabilities | The goal of the NCI-funded and CLIA-certified Cancer Genomics and Bioinformatics Core is to provide genomics and bioinformatics leadership to clinicians and research scientists to facilitate projects in basic, translational and clinical research. By serving as a centralized resource with a full array of services from Sanger sequencing, genotyping, gene expression analysis to next-generation sequencing and with a significant computational infrastructure for data analysis and storage, and experienced professionals in genomics-based methods, the Cancer Genomics and Bioinformatics Core provides assistance in all facets of experimentation from design to data analysis, including grant and manuscript preparations. It strives to service the research community in a cost-effective and efficient manner to enable to conduct the best research possible at cost-effective prices to investigators for DNA and RNA analysis. |
| Major Equipment | * Chemagen Magnetic Separation Module I Chemagic * Agilent 2100 Bioanalyzer * Agilent 2200 Tape Station * Applied Biosystems 3730 DNA Sequencer * Applied Biosystems-SOLiD 5500xl System Automated Sequencer (X2) * Ion Torrent PGM System (X2) * Applied Bioystem EZ-Bead System * Affymetrix GeneChip System * Affymetrix GeneChip System DX2 * Applied Biosystems 7900HT Real-Time Quantitative PCR Systems * Applied Biosystems 7500 Real-Time Quantitative PCR Systems * TaqMan® QuantStudioTM 12K Flex Real-Time PCR System * Beckman Coulter Biomek FXP (dual pods) * Bioinformatics: Computational expertise for generation, management, analysis and delivery of information derived from the research setting. Areas include nucleic acid, genomic, and functional genomic data analysis; large data set manipulation and management; data visualization; high performance computing; database design and implementation; Internet-based data dissemination solutions. * Software applications: * Affymetrix Expression Console, * Affymetrix Genotyping Console, * Sequencher, * GeneSpring GX 11 * Ingenuity Pathways Analysis * Applied Bioystem BioScope, * GenePattern |
| Services | All projects are required to be discussed with the resource Director, Dr. P. Fortina, the laboratory manager, Ms. M. Kelly and the project manager for bioinformatics, Dr. A. Ertel, to ensure that experimental design, genomics technology options, bioinformatics challenges and budget can be considered. This is essential for all projects and ensures users are fully informed about technology available, suitability, costs and data analyses.  The Cancer Genomics and Bioinformatics Core offers services for:   * Nucleic acid isolation and purification, and related molecular biological services including PCR, cloning, sub-cloning and site-directed mutagenesis; * Cost-effective, reliable, long-read, automated Sanger sequencing; * Microsatellite-based genotyping and fragment analysis; * Genome-wide SNP genotyping (GWAS), copy number variation (CNV), aCGH and loss of heterozygosity (LOH); * CytoScan High Density Cytogenetics (coverage of all 36,000 RefSeq genes including 12,000 OMIM, all ISCA constitutional regions and Sanger cancer genes) * Genome-wide mRNA and microRNA expression profiling on Affymetrix microarrays and/or custom made disease- and/or pathway-targeted arrays; * Independent validation of candidate loci/genes by quantitative PCR; * Whole exome and targeted resequencing of human and model organisms; * OncoScan FFPE assay for genome-wide copy number and (LOH) in ~900 cancer genes; * Chromatin-IP sequencing (ChIP-, RIP- and CLIP-seq); * RNA expression by RNA-sequencing (whole transcriptome) including short and long non-coding RNA; * Genome-wide DNA methylation sequencing; * Whole genome sequencing; * Assisting investigators with experimental design and analyzing results providing web-based pathway analysis software * Bioinformatics including management and delivery of information derived from genomic and functional genomic data analysis, large data set manipulation and management, data visualization, high performance computing, database design and implementation, and internet-based data dissemination solutions. A web-based delivery mechanism for result files   **CLIA certified:**   * Sanger sequencing, * K-RAS, * BRAF, * EGFR, * AmpliSeq Cancer panel (50 oncogenes and TS genes) resequencing, * Whole exome sequencing |