A Brief Description of
UCLA Technology Center for Genomics & Bioinformatics

UCLA Technology Center for Genomics & Bioinformatics (UCLA TCGB) is a high-throughput and fully automated genomics center located in the Center for Health Sciences (CHS) building and equipped with all major state-of-the-art instruments for genomics analyses including a range of next generation sequencers, single cell 10X Genomics Chromium Controller and Chromium Connect, 10X Visium transcriptomics and Nanostring GeoMx DSP technologies. The UCLA TCGB, directed by Dr. Xinmin Li, has 8 Ph.D. level scientists and a total staff of fourteen, who together have 76 years combined genomics experience. TCGB has following major instruments, bioinformatics tools and big data management systems:

- Nucleic acids isolation & QC
  - MagNa pure compact automated nucleic acid isolation system
  - Biochain AnaPrep automated nucleic acid isolation system
  - Qiagen QIAcube HT automated nucleic acid isolation system
  - Tape station, Agilent 2100 Bioanalyzer, Fragment Analyzer, NanoDrop 8000, Qubit 2.0 Fluorometer, Plate Reader
  - Applied Biosystems 7500 Fast Real Time PCR System
- NGS
  - Oxford NANOPORE GriDIONx5 Sequencing System
  - Illumina NovaSeq™ 6000 Sequencing System
  - Illumina HiSeq3000 sequencing system
  - Illumina HiSeq2500 sequencing system
  - Illumina NextSeq500
  - Illumina MiSeq sequencing system
  - 10X genomics Single cell sequencing system
  - 10X Visium Spatial gene expression system
  - Nanostring GeoMx DSP system
  - 10X Chromium Connect system
  - IntegenX Apollo 324 system (for Automated NGS library construction)
  - Beckman Biomek Fx (for Automated NGS library construction)
- Bioinformatics
  - Falcon Automated Genomic Analysis System
  - Hoffman2 Linus clusters equipped with various genomic data analysis tools including Galaxy server
  - Lab-hosted data analysis server and data analysis tools including Partek Flow, Ingenuity.
  - Hoffman2 data storage server
  - Amazon S3 unlimited data storage server & AWS

With the state of the art instruments and well established data analysis and management systems, the UCLA TCGB offers a wide range of genomic services including:

- Automated DNA/RNA isolation & quality evaluation
- RNA-Seq
- miRNA-Seq
- Methy-Seq
- ChIP-Seq
- CLIP-Seq
- ATAC-seq
- Single cell sequencing (3’ GEX, ATAC, V(D)J, 5’GEX+ FB, 5’GEX+V(D)J, Multiome 3’GEX+ ATAC)
- Whole exon sequencing
- Targeted DNA resequencing
- Whole genome sequencing
- Visium spatial gene expression profiling
- GeoMx spatial RNA & protein assays
- NGS Data analysis
- Data analysis consultation & software tutorial
- Online data delivery & long-term data storage

These state-of-the-art genomic services are offered at a cost-effective and timely manner to serve basic science, translational and clinical researchers. The TCGB clientele include researchers generally unfamiliar with whole genome and bioinformatics approaches as well as experts seeking more sophisticated solutions. In addition to providing comprehensive genomic services, the UCLA TCGB provides “beyond service” assistance in science and technology which includes fostering new ideas, facilitating project collaboration and integration across biomedical disciplines and developing new applications to advance the quality of the science. The UCLA TCGB also provides educational training to faculty, staff and students and strives to raise awareness of new directions and major discoveries in the areas of genomics and bioinformatics.

By providing the above services, the UCLA TCGB has supported a wide range of translational investigations, including:

- Evaluation of drug effect
- Optimization of drug dose
- Identification of drug targets
- Identification of expression signature for disease classification
- Identification of gene expression markers for disease diagnosis/prognosis
- Identification of SNV/CMV markers for disease diagnosis/prognosis
- Evaluation of host response to pathogen infection

- Identification of disease-associated SNPs
- Identification of pathogenic copy number variations
- understanding molecular mechanisms of pathogenesis and evolution

In summary, the UCLA TCGB provides next-generation sequencing (NGS) platforms, integrated bioinformatics pipelines and technical/intellectual expertise to support basic, translational and clinical researches, which has significantly facilitated scientific findings and yielded numerous high impact publications including:

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