UC Davis DNA Technologies Core -- 11/2023

FACILITIES

The UCD Genome Center is a world class facility with a combination of cutting-edge research facilities. Among these the DNA Technologies Core provides comprehensive sequencing, genotyping, single-cell multi-omics, and spatial transcriptomics services. The DNA Technologies Core operates in four adjacent rooms of the UC Davis Genome Center encompassing 3000 square feet of lab space including a dedicated pre-PCR room. The Core is staffed by a total of ten personnel, including four PhD level scientists.

MAJOR EQUIPMENT

PacBio Sequel ***Revio***	Sequencer
PacBio Sequel ***II***	Sequencer
Oxford Nanopore PromethION	Sequencer
Oxford Nanopore MinION Mk1C	Sequencer
Element Biosciences AVITI	2 sequencers
Bionano Saphyr	Optical genome mapper
Illumina HiSeq 4000	Sequencer
Illumina MiSeq	3 sequencers
Illumina NextSeq 500	Sequencer
Illumina cBot	Sequencing Cluster Generator (**2**)
10X Genomics Chromium **X** Controller	Single-cell RNA-seq and ATAC-seq preparation
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10X Genomics Visium CytAssist	Spatial transcriptomics processor
Pippin Pulse	Pulsed-Field Electrophoresis System
Blue Pippin	Automated DNA Size-Selection
Pippin HT	High-Throughput Automated DNA Size-Selection
Luna-FL (Logosbio)	Automated Dual Fluorescence Cell Counter
Countess *II* (Invitrogen)	Automated Cell Counter
Perkin Elmer Sciclone G3 NGS	Liquid handling robot (8 channel & 96-channel)
CyBio FeliX	Liquid handling robots (single, 8 & 96-channel) (**2**)
Opentrons OT-2	Liquid handler (single channel & 8 channel)
Integra Assist Plus	Liquid handler robot (8 & 12-channel)
Integra Viaflo96	Semiautomated 96-channel pipettor
Formulatrix Mantis	Automated nanoliter reagent dispenser (**2**)
QuantStudio 5, RT-qPCR Thermocycler	qPCR quantifications, genotyping
Covaris E220 Focused-Ultrasonicator	DNA sonication, 96 sample, fragmentation, ChIP-seq
Diagenode Megaruptor V3	Large fragment DNA shearing
Agilent Femto Pulse	Large fragment DNA analyzer (Field Invers. MCE)
Agilent Tapestation 4200	DNA/RNA fragment analyzers
Agilent Bioanalyzer 2100	DNA/RNA fragment analyzers (**2**)

Perkin Elmer LabChip Gx Touch	96 well, Microcapillary fragment analyzer
FilterMax F5 Plate Reader (Molecular Devices) Luminescence, DNA RNA quantification	96 well/384-well, absorbance, fluorescence,
Boreal Genomics Aurora	Nucleic acid purification and extraction
Fludigm EP1	High throughput SNP genotyping; end-point reader
Fludigm AX Access Array	Highly multiplexed amplicon sequencing library prep.
Nanodrop Micro Volume Spectrophotometer	Single-channel & 8-channel; nucleic acid purity
Qubit and Quantus Fluorometers	Precise nucleic acid quantification
Eppendorf Vacufuge Plus	Concentrator

MINOR EQUIPMENT

Thermocyclers, thermomixers, ultra-low temperature freezers, centrifuges, plate sealers, biological safety cabinet, fume hoods, freezers, microscope, cold room.

COMPUTATION

- High Performance Computing: The DNA Technologies Core acesses the biggest HPC cluster on campus, the Genome Center cluster, for data processing
- Sequencing data are delivered via a secure web portal (BioShare) enabling fast downloads and convenient data sharing among collaborators.
- The sequencing data are stored and delivered via a 400 TB HDD array.

DNA TECHNOLOGIES CORE SERVICES:

- High-throughput-sequencing (HTS) and genotyping services: Long-read (PacBio, Nanopore) and short-read sequencing (Illumina. This includes full services for all standard DNA and RNA-sequencing protocols as well as custom sequencing.
- Single-cell RNA-seq and multi-omics
- Genotyping: Illumina Infinium, Fluidigm, and genotyping by targeted sequencing
- Free consultations (frequently in collaboration with the Bioinformatics Core)
- Training in HTS technology (e.g. sequencing library preparation workshops)

The core laboratory provides short-read sequencing services on a range of in-house Illumina sequencers (Element Biosciences AVITI, NextSeq 500, and three MiSeqs) as well as on a NovaSeq 6000 and X (UCSF). Long-read sequencing is provided one PacBio Revio and one PacBio Sequel ***II*** sequencer, one Oxford Nanopore Technologies PromethION and several MinION sequencers. The core generates sequencing libraries for a wide range of analyses for all sequencers and offers the development of custom sequencing solutions. The core will also sequence client submitted sequencing libraries on all types of sequencers. High throughput library construction employs Perkin Elmer Sciclone NGS, two Cybio FeliX, Opentrons OT-2, and Integra Assist Plus robotic liquid handlers. The core offers all technologies relevant for *de novo* genome assemblies and structural variant genome analyses including both long-read sequencing technologies, linked-read sequencing, optical genome mapping (Bionano Saphyr) as well as Hi-C sequencing.

Single-cell RNA, DNA and multiomics experiments are processed on a 10X Genomics Chromium system and with Parse Biosystems protocols. The Core also provides high

throughput Single Nucleotide Polymorphism (SNP) genotyping analyses using a Tecan liquid handler and the Illumina Iscan system. Bioinformatics support includes demultiplexing, sequencing data QC, as well as data access through a secure web portal. Additional data analyses are available through the neighboring Bioinformatics Core.

The DNA Technologies Core maintains a range of instruments available for use by members of the UC Davis research community following training. These include an Agilent Bioanalyzer and Tapestation, a Perkin Elmer Labchip GX Touch analyzer, Agilent FemtoPulse, Covaris E2 sonicator, Sage Science BluePippin and BluePippin HT preparative electrophoresis platforms, Nanodrop spectrophotometer, a Molecular Devices plate reader, and several robotic liquid handlers.

During the SARS-CoV2 pandemic, the DNA Technologies Core has performed over 2 million clinical RT-PCR COVID19 tests.

OTHER RESOURCES

The UC Davis Genome Center:

The UC Davis Genome Center integrates experimental and computational approaches to address questions at the forefront of genomics. The Center is housed in a new research building with state-of-the-art computational and laboratory facilities. The Center has made major investments in contemporary instrumentation and has recruited experienced staff to manage and run its five campus resource core facilities. There are five service Cores including DNA Technologies and Expression Analysis (sequencing and genotyping), Proteomics, Metabolomics, and Bioinformatics. All services are recharged at-cost providing researchers with cost-effective access to the latest technologies on an as-needed basis.

Bioinformatics Core in the Genome Center

The Bioinformatics Core (http://bioinformatics.ucdavis.edu/) in the Genome Center provides researchers at the University of California, Davis access to experience, expertise, and computational infrastructure in “omics” data analysis needed to analyze and visualize data generated from the high throughput technologies commonly used in genomics, proteomics and metabolomics research. Core staff includes 6 PhD level researchers, 4 highly skilled individuals and 1 undergraduate across two groups: data analysis and research computing. The computing infrastructure of the Bioinformatics Core includes low and high memory nodes totaling more than 150 nodes, 12,000 CPU cores, 60 TB RAM, and 7 PB of disk storage, including 20 GPU nodes each with 448 cores and 6 GB of memory (to provide a total of 65,100 GPU cores) as well as large memory servers with 128, 256, 512, 1,000 and 2,000 GB of RAM. There is a 10 Gbit/s network connection to Corporation for Education Network Initiatives in California (CENIC). In addition to Bioinformatics analysis and computational infrastructure, the Bioinformatics Core produces a series of internationally renowned week-long workshops, with participants from across the U.S. as well as from overseas. The workshop topics include genome assemblies, RNA-seq data analysis and single-cell RNA-seq data analysis. The Core offers bioinformatic data analysis support through staff bioinformaticians and can perform a full

range of analysis tasks to address biological questions in areas such as population genetics, genomics, microbial community dynamics, functional genomics, proteomics, metabolomics, and systems biology.

The Bioinformatics Core has developed strong expertise in *de novo* genome assemblies, genome annotations, and single-cell transcriptomics. Thus, the DNA Technologies and Bioinformatics Cores offer complete solutions from sample preparation and sequencing to the assembly of high-quality annotated genomes.

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