**[RESEARCH](https://health.ucdavis.edu/cancer/research/sharedresources/)**

Cancer Center Shared Resources

Genomics Shared Resource (GSR)

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[](https://ppms.us/ucdavis/login/?pf=11)

[**Request Services (PPMS Required)**](https://ppms.us/ucdavis/login/?pf=11) correct link so that it goes to GSR section of PPMS

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The GSR serves the cancer research community with centralized, cost-effective services and comprehensive expertise in genomics and bioinformatics. Investigators have access to contemporary genomic applications and state-of-the-art instrumentation for next-generation sequencing (NGS) and spatial transcriptomics. We regularly prepare sequencing libraries for RNA-seq, whole exome, whole genome, ChIP-seq, Hi-C, CUT&RUN, single-cell transcriptomics, spatial transcriptomics, spatial proteomics, and a variety of other NGS applications. The GSR also provides ancillary genomic services for nucleic acid isolation, quality assessments, DNA shearing, and quantitative PCR.

Our unique features include:

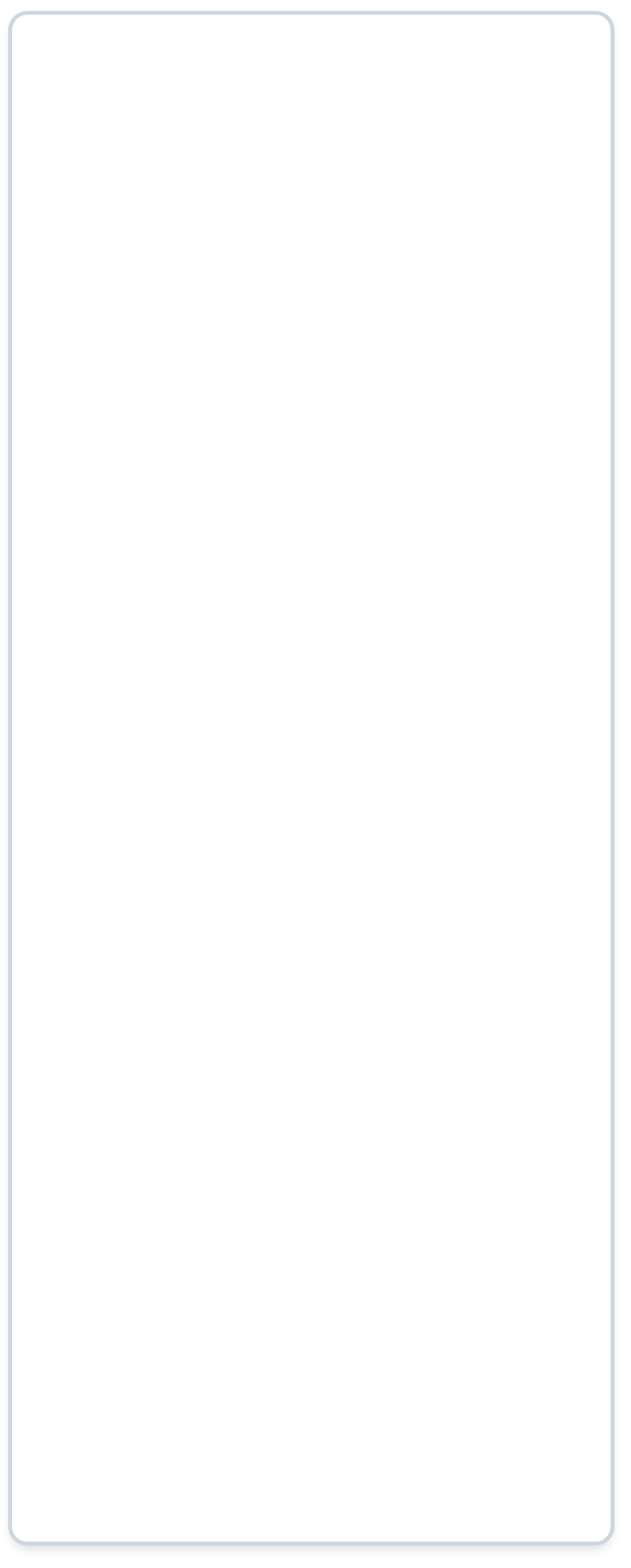
 Complete repertoire of high-resolution genomics services  Development of customized protocols

 Specialization in translational genomics and analysis of clinical specimens

The GSR offers hands-on specialized training, mentorship, and monthly workshops to support cancer studies. We provide consultation for experimental design, project logistics and management, and manuscript and grant proposal preparation. Our faculty have expertise in bioinformatics, cancer genomics, DNA sequencing, and epigenomics.

Services

We provide a comprehensive suite of genomics services to support your cancer research, as well as grant writing support, assistance with manuscript preparation, and letters of support.



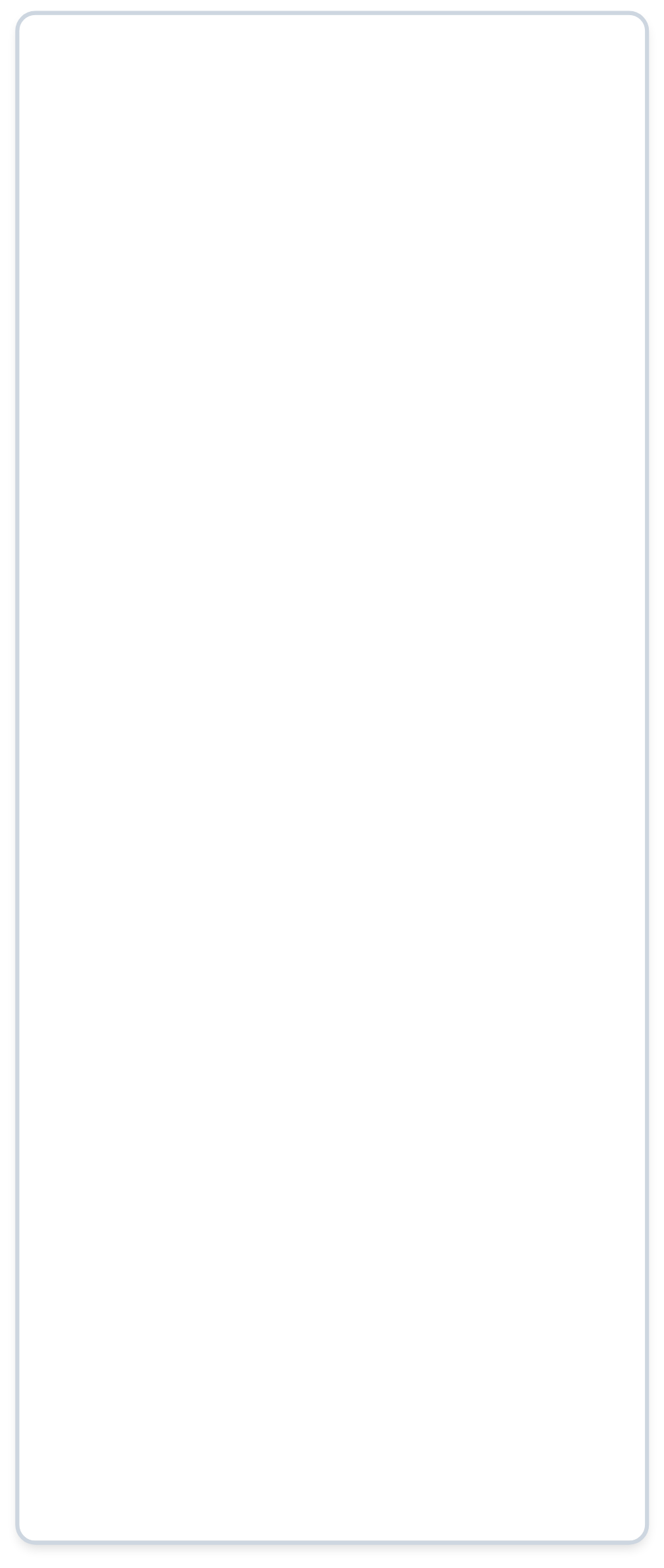
Use DNA double-helix icon here instead

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Genomic Services

The GSR provides comprehensive support for genomic research, specializing in RNA-seq, whole- exome sequencing (WES), whole- genome sequencing (WGS), and ChIP-seq analysis. We assist researchers with library preparation, quality control, and bioinformatics, enabling insights into gene expression, genetic variation, and epigenetic regulation.

Our team offers expert consultation and customized data analysis to ensure high-quality, reproducible results. Whether studying human health, model organisms, or non- model species, we tailor our services to meet diverse research needs, helping scientists extract meaningful insights from complex genomic data.



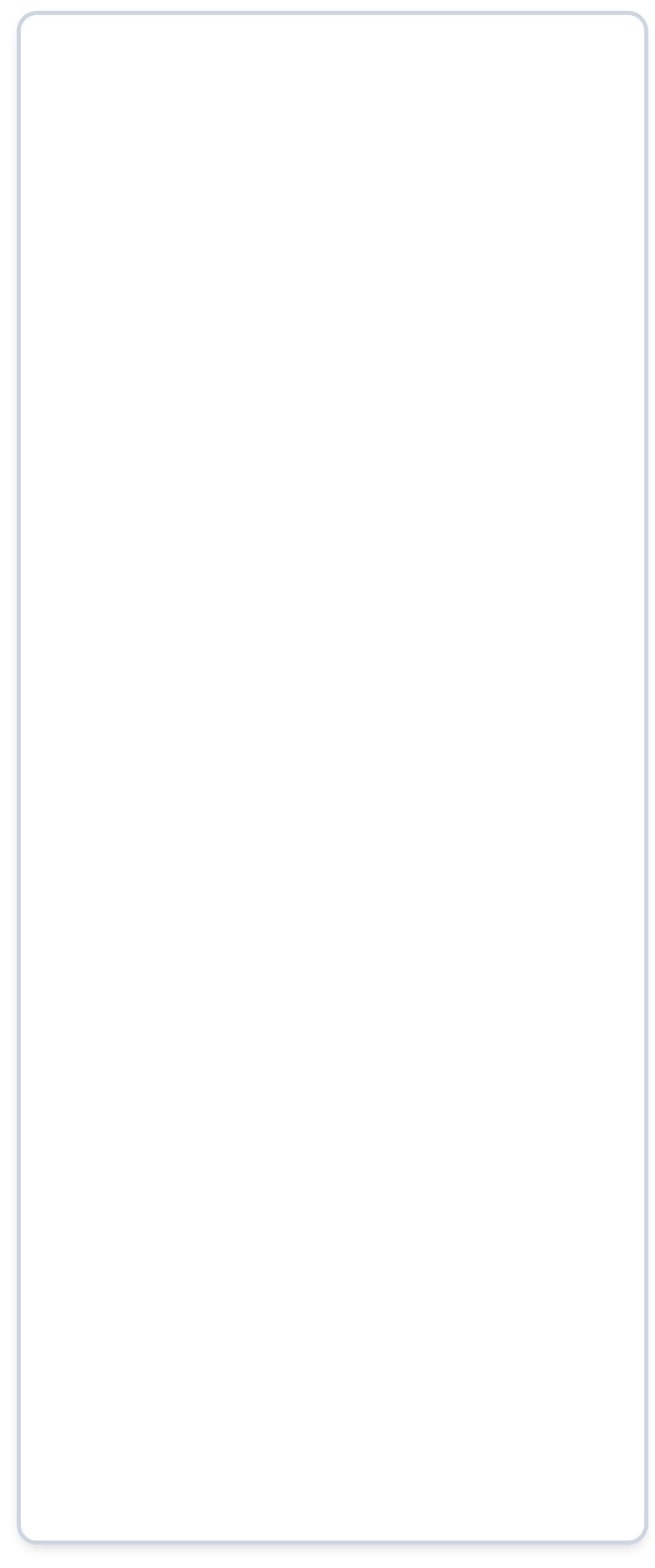
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High-Resolution

Genomics

We offer cutting-edge single-cell RNA sequencing (scRNA-seq) and spatial biology services to explore gene expression at unprecedented resolution. Using the 10x Genomics Chromium platform, we provide high- throughput single-cell transcriptomics, enabling researchers to study cellular heterogeneity and dynamic gene expression in complex tissues.

For spatial biology, we support NanoString GeoMx Digital Spatial Proﬁling and 10x Genomics Visium, allowing precise.





Translational Genomics

Sample Support

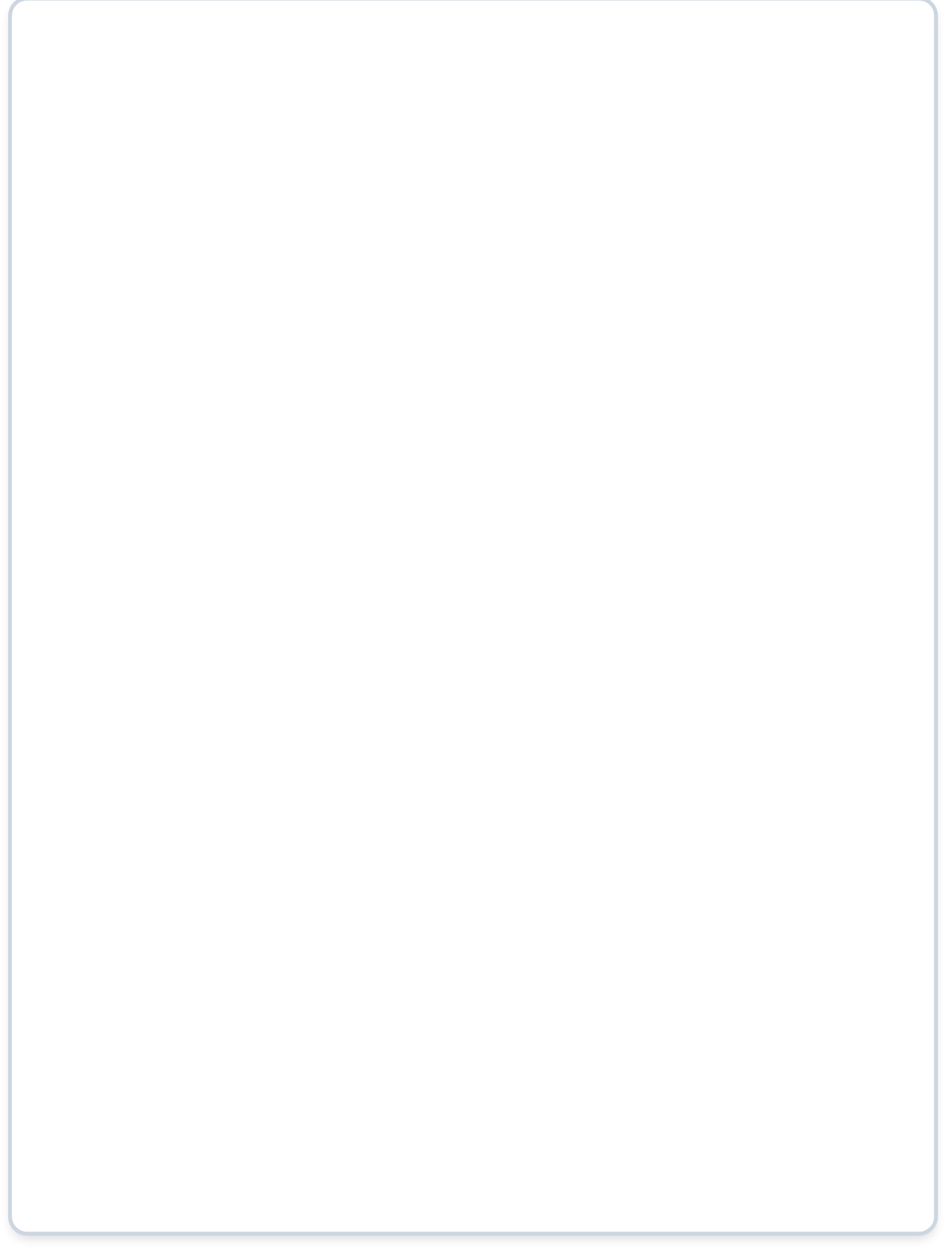
The GSR provides a wide range of services for the collection, preservation and molecular analysis of multiple types of clinical specimens, including:

Flash-frozen tissue FFPE tissue Saliva Serum

Whole blood

We apply specialized protocols to isolate high-quality nucleic acids from challenging samples and analyze very small specimens, like needle biopsies. Our expertise with in vivo tumor models enables us to support preclinical drug studies and research on genetic mechanisms of tumorigenesis.





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Customized Protocols

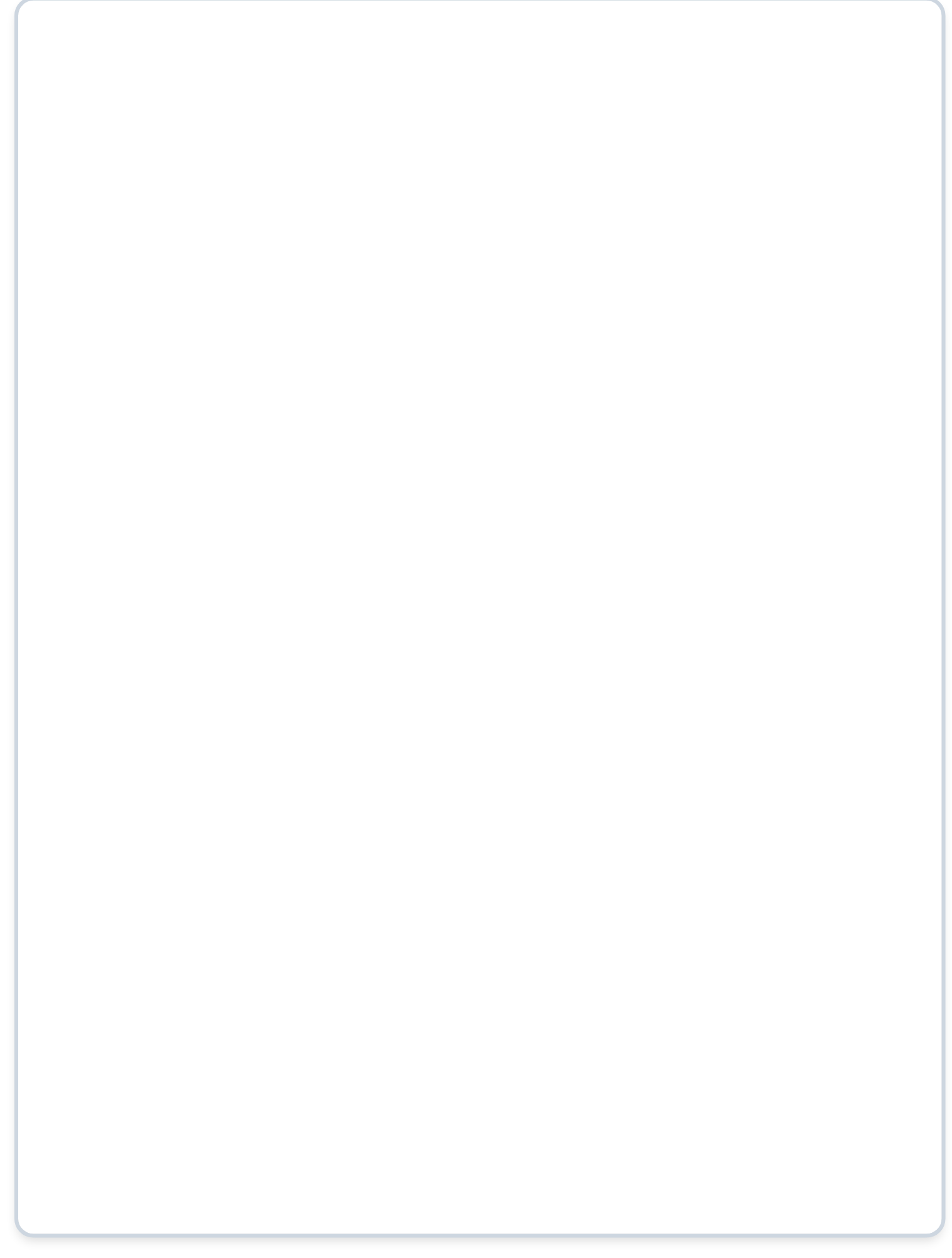
We support investigator-driven projects with the ability to develop protocols for specialized genomics applications, including:

Chromatin & Epigenomics Assays – Hi-C for chromatin conformation and CUT&RUN for targeted protein-DNA interactions

Long-Read & Targeted Sequencing – ONT adaptive sampling for real-time enrichment and targeted capture or amplicon-based panels

Liquid Biopsy Applications – Circulating tumor DNA (ctDNA) and exosomal miRNA for minimally invasive cancer research

Viral Genomics – High-sensitivity sequencing of viral genomes for pathogen detection and surveillance



Use graph or puzzle piece icon here instead

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Bioinformatics and Data Analysis

The GSR provides comprehensive bioinformatics support, ensuring that your genomics data is both interpretable and actionable. Our specialized computational infrastructure, including high-performance servers and advanced analytical tools, enables the processing of complex datasets with eﬃciency and precision.

We offer a range of customized analysis pipelines, including:

Advanced data interpretation, such as functional analysis of expression signatures

Integration of large-scale public NGS datasets for comparative and meta-analyses

Multimodal data integration, combining diverse genomic, transcriptomic, and epigenomic data for deeper insights

With our expertise, you can conﬁdently extract meaningful biological insights from your genomics research.

Rate

Below are the rates for a sampling of the GSR's most commonly requested services. For genomics services not listed here, please contact the GSR. Please note that some services have a complex pricing structure and require project consultation in order to determine accurate pricing.

[**View GSR rate car**](https://health.ucdavis.edu/media-resources/cancer/documents/xl/gsr-rate-card.xlsx)**d** [</media-resources/cancer/documents/xl/gsr-rate-card.xlsx>](https://health.ucdavis.edu/media-resources/cancer/documents/xl/gsr-rate-card.xlsx)

Subsidized Rates for Cancer Center Members

Members of the cancer center receive priority access and subsidized rates for Shared Resources services. Not yet a member? Learn about the beneﬁts and privileges of [**cancer center membership**](https://preview.ucdavis.edu/cancer/research/membership/)[<https://preview.ucdavis.edu/cancer/research/membership/>](https://preview.ucdavis.edu/cancer/research/membership/).

 Request GSR Services

Our team looks forward to providing a solution for your complex genomics and bioinformatics-related research.

We highly recommend [setting up a planning meeting](https://gsr.youcanbook.me/) with us so that you can get the most out of your genomics project.

Email the completed form(s) as an attachment to [**gsr@ucdavis.ed**](mailto:gsr@ucdavis.edu)**u** [<mailto:gsr@ucdavis.edu>](mailto:gsr@ucdavis.edu). A member of our staff will follow up with you by email regarding your request.

**NOTE:** A PPMS account is required. [**View our quick start guid**](https://health.ucdavis.edu/media-resources/cancer/documents/pdfs/stratocore-ppms-customer-guide-grs.pdf)**e** [</media-resources/cancer/documents/pdfs/stratocore-ppms-customer-guide-](https://health.ucdavis.edu/media-resources/cancer/documents/pdfs/stratocore-ppms-customer-guide-grs.pdf) [grs.pdf>](https://health.ucdavis.edu/media-resources/cancer/documents/pdfs/stratocore-ppms-customer-guide-grs.pdf) for creating an account or [**set up an accoun**](https://ppms.us/ucdavis/areq/?pf=2)**t** [<https://ppms.us/ucdavis/areq/?pf=2>](https://ppms.us/ucdavis/areq/?pf=2).

call Contact the GSR

For questions about our services, please contact:

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# GSR staff

To reach GSR staff, please call the laboratory at **916-703-0366** <tel:916-703-0366> or [**email u**](email%20u)**s** [<mailto:gsr@ucdavis.edu>](mailto:gsr@ucdavis.edu).

# Location

The GSR facility is located at:

UC Davis Medical Center

[**4645 2nd Avenu**](https://maps.app.goo.gl/kFosxkFwxBgcoEcS6)**e** [<https://maps.app.goo.gl/kFosxkFwxBgcoEcS6>](https://maps.app.goo.gl/kFosxkFwxBgcoEcS6) [**Research III, Room 240**](https://maps.app.goo.gl/kFosxkFwxBgcoEcS6)**0** [<https://maps.app.goo.gl/kFosxkFwxBgcoEcS6>](https://maps.app.goo.gl/kFosxkFwxBgcoEcS6) [**Sacramento, CA 9581**](https://maps.app.goo.gl/kFosxkFwxBgcoEcS6)**7** [<https://maps.app.goo.gl/kFosxkFwxBgcoEcS6>](https://maps.app.goo.gl/kFosxkFwxBgcoEcS6)

quick\_reference Policies and Procedures

Please read our policies and procedures below to ensure the GSR runs smoothly and eﬃciently.

By submitting samples to the GSR, the primary investigator and all researchers involved agree to the following:

 Some processes consume samples. As a result, the GSR may not return every sample you send to us. We discard remaining samples three months after notifying a client about completion of an order.

 The user must cite UC Davis Comprehensive Cancer Center Genomics Shared Resource (NCI P30 CA93373) in the acknowledgements section of any published work (manuscript, poster, presentation, etc.) that uses data obtained through work done by the GSR. The user must also notify the GSR of any potential and actual publication(s) that use data obtained through work done by the GSR. This condition of use is vital for the success of the shared resource and of UC Davis Comprehensive Cancer Center. It plays a crucial role in helping us earn a competitive renewal of the Cancer Center Support Grant and to retain our NCI designation.

 The GSR reserves the right to use any data from services performed by the GSR. We use data to assess the quality of data generated by our facility and to develop technical protocols and analysis tools. We keep all details pertaining to the data, samples and treatments conﬁdential. The GSR will never exploit the biological relevance of a user's experiment.

 The GSR is not responsible for animal or human subject assurances pertaining to the samples submitted. By submitting samples, the user assures the GSR that they have obtained all the appropriate animal subjects or human subjects protocol approvals for their study. Users will not submit samples to the GSR unless they have met all the requirements for animal or human studies.

 We require 24-hour notice of cancellation for instrument bookings. Cancellations made less than 24 hours in advance are subject to fees. The fees will cover the GSR's costs for setting up the instrument and reserving the time slot.

 We charge for costs associated with damage to instrumentation due to user error. Charges apply to the account provided by the user at the time of instrument booking.

**Recommended Protocols & Helpful Tips**

## Cell harvesting

 For RNA: Scrape cells directly into desired lysis buffer (Qiagen RLT or Thermo TRIzol recommended) as per manufacturer’s recommendations. Triturate to ensure lysis, and store at -80°C. Avoid unnecessary cell manipulation such as trypsin, centrifugation, resuspension, etc.

 For DNA: Pellet cells, wash with cold PBS, remove as much supernatant as possible, and freeze. Store at -80°C.

## Flash-frozen tissue collection

***Remove extra line-break***

Always use clean, nuclease-free tools and tubes, and avoid cross-contamination between samples. Immediately after tissue harvest, dissect out a desired piece no larger than 4mm x 4mm x 4mm (for fatty tissues, cartilage, tendon, ligament, bone, or eye, contact the GSR for special instructions). Remove any excess blood and necrotic tissue. Carefully place the tissue piece on the sidewall of a microfuge tube or cryovial and snap-freeze in liquid nitrogen. Store at -80°C. Transport on dry ice only.

## FFPE tissue

***Remove extra line-break***

FFPE scrolls should be provided in 2mL microfuge tubes. Sections should be cut fresh and stored at -20°C, preferably no longer than a week. For guidance on the quantity of scrolls for various applications, please contact the GSR.

## Blood collection

 For RNA: Use PAXgene Blood RNA Tubes for blood collection as per manufacturer’s instructions. Freeze tubes on their sides and store at -20°C or -80°C.

 For DNA: Use purple-top EDTA tubes for blood collection and store at 4°C no more than 3 days before delivering to the GSR. Please schedule with the GSR before scheduling blood draws to ensure sample integrity and yield.

## Saliva collection

***Remove extra line-break***

Collect saliva using an appropriate kit from DNA Genotek (Oragene).

## RNA isolation

***Remove extra line-break***

For RNA from ﬂash-frozen tissue, we highly recommend following our Combined TRIzol-RNeasy method <attached PDF>. For RNA from cells and other sources, we strongly recommend QIAGEN RNA isolation kits. For all RNA isolations, we require that the samples be DNased, preferably using an on-column DNase protocol.

## DNA isolation

We recommend QIAGEN DNA isolation kits and require that an RNase A step be included during isolation.

Publications Using GSR Services

Sample GSR Acknowledgement: The authors wish to acknowledge the support of the UC Davis Comprehensive Cancer Center Genomics Shared Resource, supported by the National Cancer Institute (award number P30CA093373). Disclaimer: The content is solely the responsibility of the authors and does not necessarily represent the oﬃcial views of the National Institutes of Health.

info

This resource is funded by the Cancer Center Support Grant (CCSG) awarded by the National Cancer Institute (NCI P30CA093373). Publications that have utilized facility resources, services, or consultation, or that include scientiﬁc data generated by the resource should acknowledge the resource and the assistance provided by resource staff and cite the NCI CCSG. An electronic copy of the publication should also be sent to the resource directors.

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