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LONDON
CENTRE

Genomics TTP



SEQUENCING SERVICES
GENOME MODIFICATION
SINGLE CELL GENOMICS
SPATIAL TECHNOLOGY
HAMILTON NGS


Genome engineering services

The UCL Cancer Institute Genomics Translational Technology Platform is staffed by experienced specialists who can offer their expertise and support at all stages of your research project. We can help with experimental design, providing technical services and training to facilitate your research projects across a range of genomics and genome engineering technologies.

We provide comprehensive sequencing services. Our state-of-the-art Illumina MiSeq 500 sequencer provides high output next generation sequencing, enabling scientists to generate vast amounts of data in a fraction of the time it would take with traditional sequencing methods.




Image: Illumina



The MiSeq 500 is a benchtop sequencer that is perfect for a wide variety of applications, including small genome sequencing, targeted resequencing, small RNA sequencing and metagenome sequencing. With its highly automated workflow, the MiSeq is both fast and cost-effective, offering short sequencing run times, long reads up to 600bp, while still maintaining an exceptionally high level of data quality. A standard MiSeq run can routinely produce anywhere from 1 - 25 million reads

In addition to our sequencing capabilities, we have in-depth experience with a comprehensive range of commercial library preparation techniques and can guide sample isolation, reagent selection and budgetary considerations. Our team of experts is dedicated to supporting scientists throughout their research from sample preparation, sequencing and data analysis, ensuring that your results are accurate, reliable and reproducible.



For researchers that are interested in genome modification, including gene knockdown, knockout and knock in, our service provides support for CRISPR Cas9 project and shRNA assays, including the provision of CRISPR plasmids and the Open Biosystems, pGIPZ based, human and mouse whole genome lentiviral shRNA libraries. These powerful tools will enable you to explore the intricate mechanisms of genome expression and regulation.

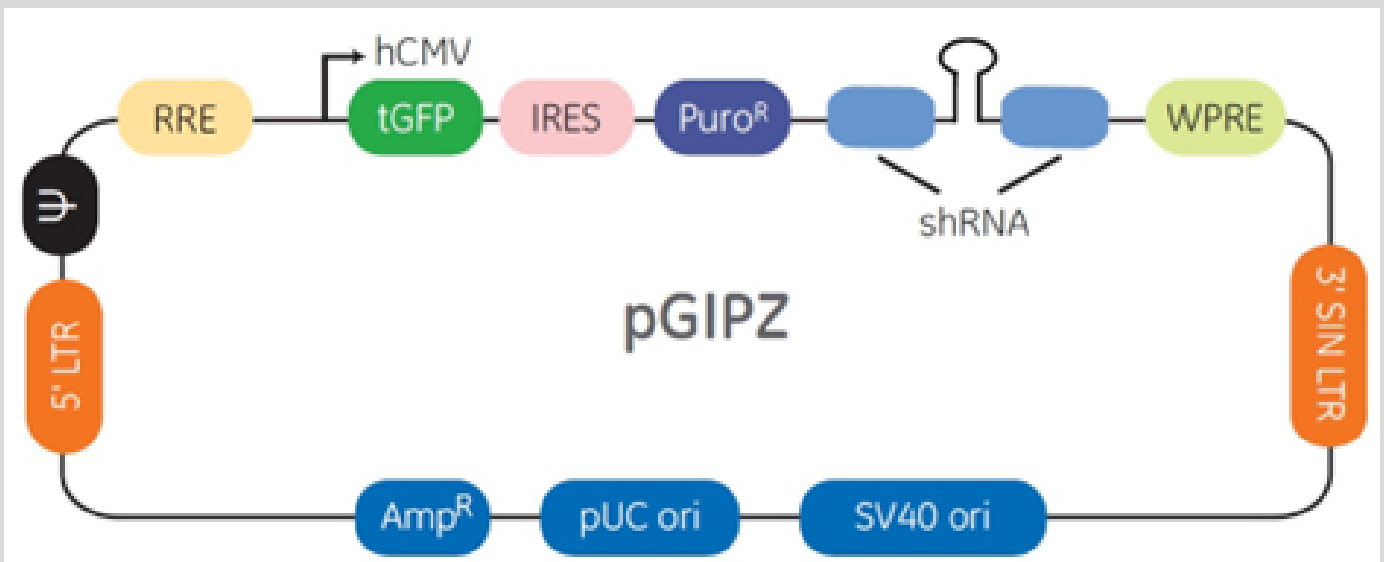


Image: Horizon discovery

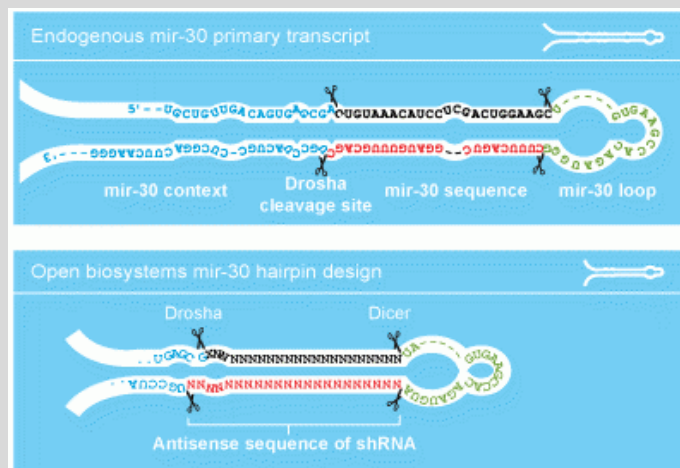
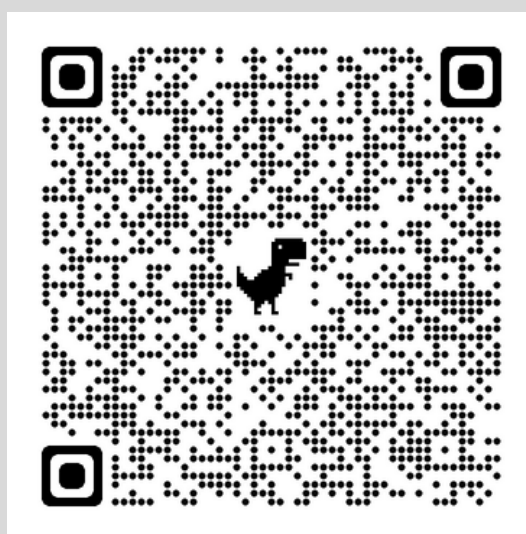


Image: Open Biosystems

By utilizing our state-of-the-art technology, experience and expertise the UCL Cancer Institute Genomics Translational Technology Platform is committed to providing you as a researcher with the tools, support and solutions that you need to make a difference, do not hesitate to contact us today to learn more about how we can help you achieve your research goals

Please contact ci.genomics@ucl.ac.uk for more information



Single Cell Genomics Facility

Single Cell technologies



Image: Chromium Controllers by Uddin, Imran

Chromium Single Cell products enable you to obtain gene expression, chromatin accessibility, cell surface proteins, immune clonotype, antigen specificity, and CRISPR screens from a given sample.

With the Chromium iX you are able to conduct pilot studies, early stage research, and everyday single cell experiments. Cells can also be fixed before processing and FFPE samples can also be run on the instrument

Sample Prep GEM Generation Library Construction Sequencing Data Processing Data Visualization



*Experimental timeline. From cell submission to visualisation of data
(Image: 10X Genomics)*

User supplied cells or nuclei are submitted to the facility which are loaded on the chromium controller or Chromium iX. GEM's produced by the instruments are amplified and library construction is conducted on the sample enabling them to be sequenced on a Illumina platform

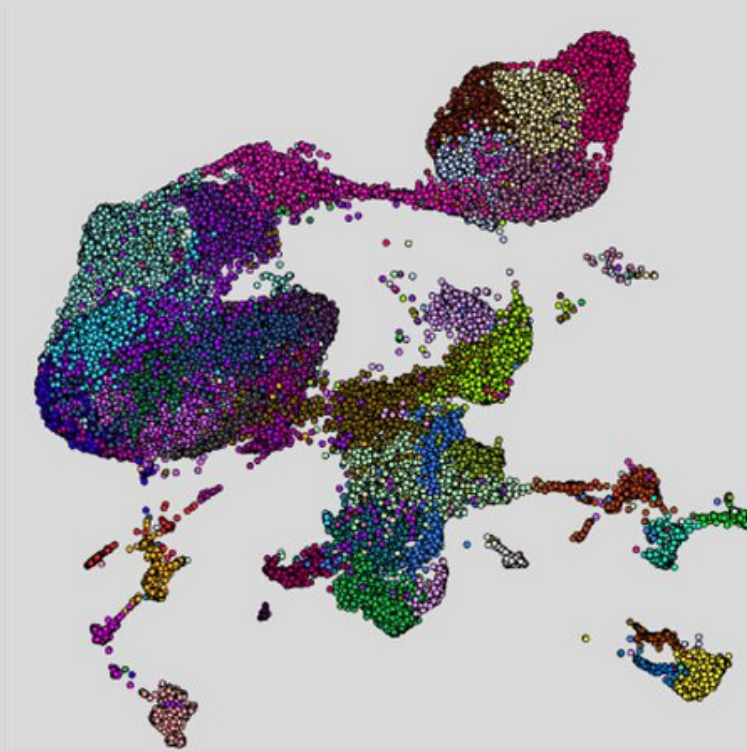
What 10X experiments can the facility perform?

- Single Cell Gene Expression (3'GEX kit)
- Single Cell Immune Profiling (5'GEX kit with TCR/BCR sequencing)
- Single Cell Multiome ATAC + Gene Expression (nuclei optimisation is required beforehand by user)
- Single Cell ATAC
- CITE-Seq (quantification of proteins with RNA) on both 3'GEX and 5'GEX kits. Antibody optimisation may be required by the user
- CellPlex (multiplexing samples – currently only available on the 3'GEX kit)
- Single Cell Gene Expression Flex (fixation and also processing FFPE using the Chromium iX)



Single Cell Bioinformatics Service

All researchers eligible for access to the CoL Single Cell Facility also have access to its bioinformatics services. We provide a full bioinformatics pipeline, from mapping and QC to downstream analyses that are most suited to your data and biological questions.



Beattie G. UCL CoL single cell genomics facility. 2024

Contact:

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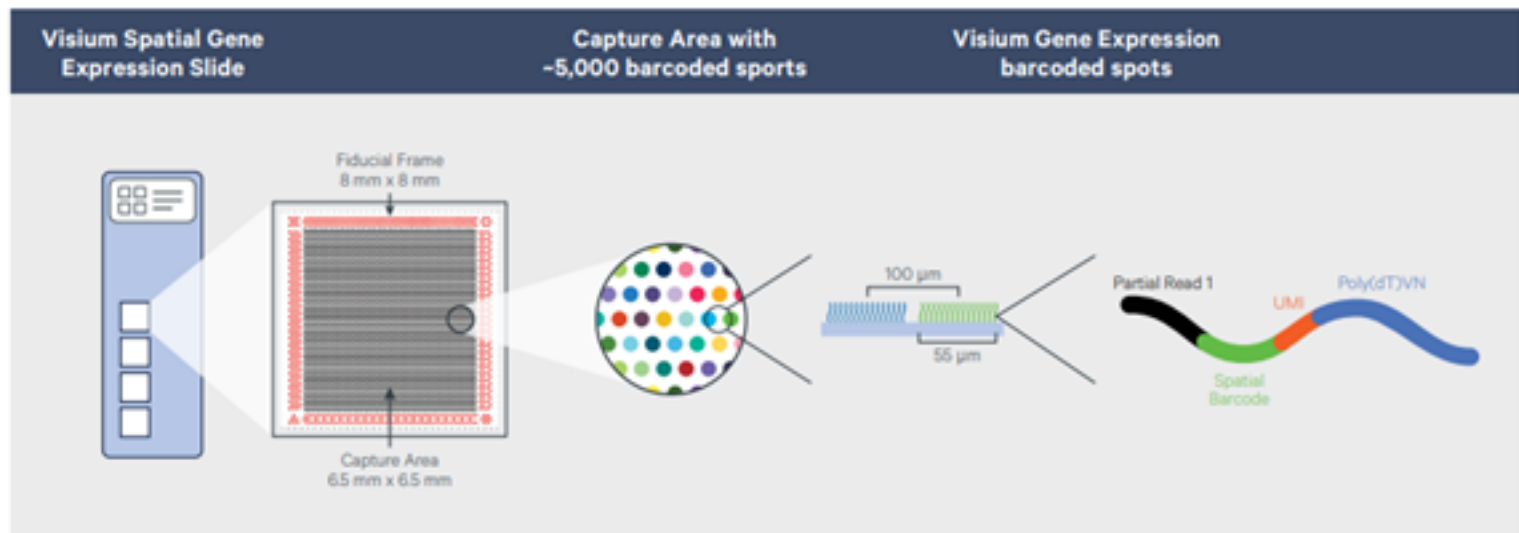


Spatial Technologies

With Visium Spatial Gene Expression, you are able to conduct whole transcriptome analysis from tissue sections with a morphological context.

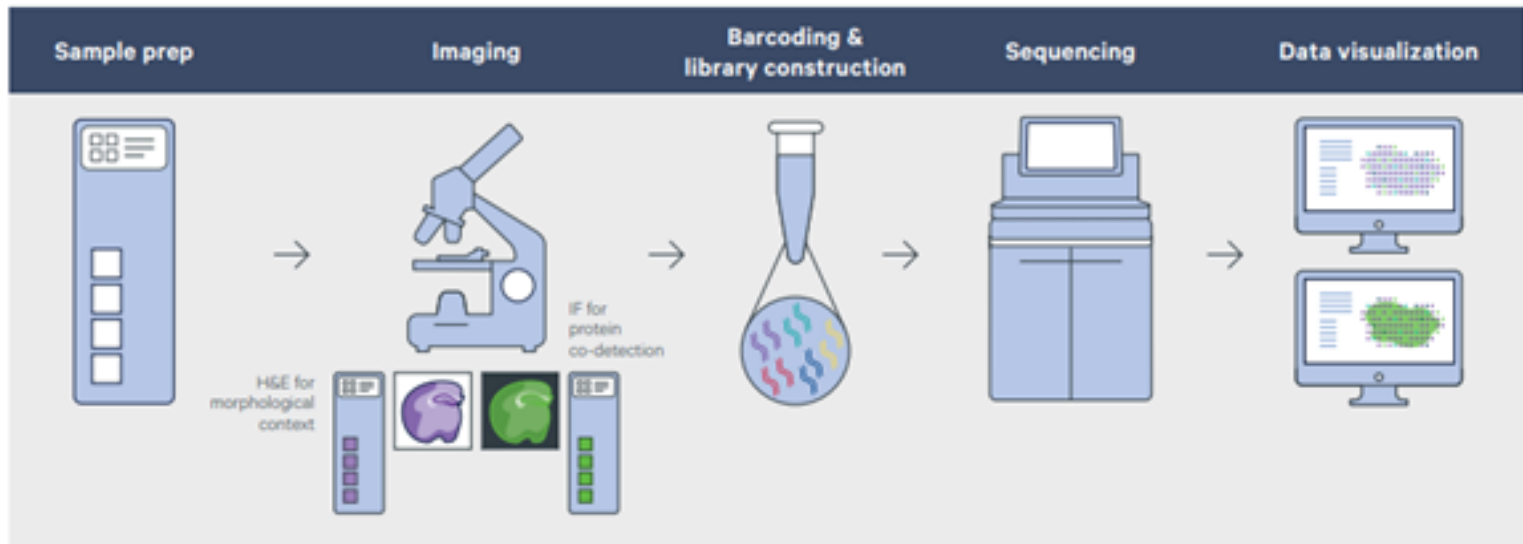
Tissue sections are fixed, stained and imaged on the slide before novel spatial barcodes on the slide utilize poly(A) capture technology to generate a library. To capture gene expression information in fresh frozen tissue, mRNA is released from processed tissue sections allowing it to bind to capture oligos from a proximal location on the tissue.

To capture gene expression in formalin-fixed paraffin embedded (FFPE) tissue, the tissue is permeabilized to release ligated probe pairs which bind to capture probes on the slide. The probe pairs are extended to generate a library that incorporates complements of the spatial barcodes and preserves spatial information.



Composition of Visium Gene Expression Slide. Each slide can contain either two or four Capture Areas with Approximately 5000 barcoded spots, containing millions of spatially barcoded capture oligos. Released tissue mRNA binds to each oligo, enabling the capture of gene expression information (Image: 10X Genomics).

Barcoded libraries are mapped back to a specific spot on the Capture Area. This gene expression data is subsequently layered over a high-resolution microscope image of the tissue section, making it possible to visualize the expression of any mRNA, or combination of mRNAs, within the morphology of the tissue in a spatially resolved manner.



Workflow diagram from Visium Spatial Gene Expression. Fresh frozen FFPE tissue is sectioned, placed onto a library preparation slide, then fixed, stained with either H&E or immunofluorescence (IF) and imaged, followed by spatial barcoding and library construction. The libraries are then sequenced and data visualized (Image: 10X Genomics).

What Spatial experiments can the facility perform?

- Spatial Gene Expression for FFPE (Visium)
- Spatial Gene Expression for Fresh Frozen (Visium)

Want to find out more about single cell and spatial transcriptomics techniques? Why not contact us to find out more.

Imran Uddin

Single Cell Genomics Facility Manager

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HAMILTON NGS STAR LIQUID HANDLING SYSTEM

- High-throughput NGS Libraries
- Minimal human intervention
- Includes an On-Deck Thermal Cycler for enzymatic fragmentation
- Workflows in operation for:
 1. WGS (including FFPE samples)
 2. Exome_seq (including FFPE samples)
 3. mRNA capture
 4. Total RNA by rRNA depletion

Available at CI Genomics TTP. Please contact Ramin Sadri at r.sadri@ucl.ac.uk

