MRC Laboratory
of Medical
Sciences

Imperial College
London

LMS Genomics Laboratory

MRC Laboratory of Medical Sciences, Imperial College,
ICTEM Building 2ndfloor, Hammersmith Campus, London

NGS –Illumina Sequencing Platforms

NextSeq2000

P1, P2 or P3 runs

- 100, 400 million or 1.2 billion reads
- 50-300bp reads, single or paired end
- 11-48 hours run time
- Patterned high density flow cells

Applications

Single-cell sequencing, RNA-seq, ChIP-seq, Whole genome, Whole exome, Whole methylome, Targeted re-sequencing

MiSeq

- up to 25 million reads per run
- 50-300bp reads, single or paired end
- 5 to 24 hours run time

Applications

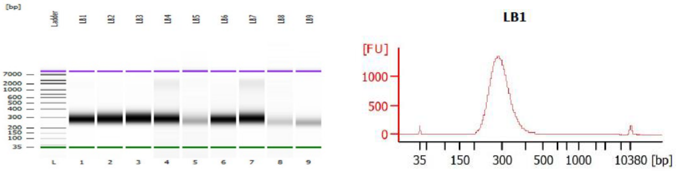
- Library QC
- Small genomes re-sequencing
- Small RNA sequencing
- Amplicon and targeted sequencing

Nextseq cartridge and flow cell

MiSeq flow cell

NGS Library Preparation

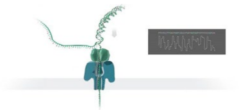
- RNA-seq library prep using NEB kits
- DNA-seq and ChIP-seq library prep using NEB kits
- Single-cell library prep
- Amplicon-seq using PCR
- Other applications on demand

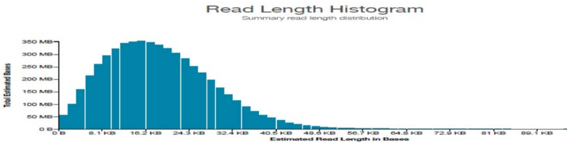


Bioanalyser profiles of RNA-seq libraries

Nanopore Sequencing – P2 Solo and MinION

- Long read genomic DNA sequencing
- Native methylation marks
- Full length cDNA
- Direct RNA
- Other applications on demand





Open access equipment

- Agilent 5200 Fragment Analyser
- Agilent 2100 Bioanalyser
- Agilent Tapestation
- Nanodrop 2000
- Qubit
- Covaris S220
- Mosquito HV nanolitre robot

Short-hairpin RNA library clone picking service

We host the **Dharmacon GIPZ Lentiviral short-hairpin RNA (shRNA) libraries for Human and Mouse.**

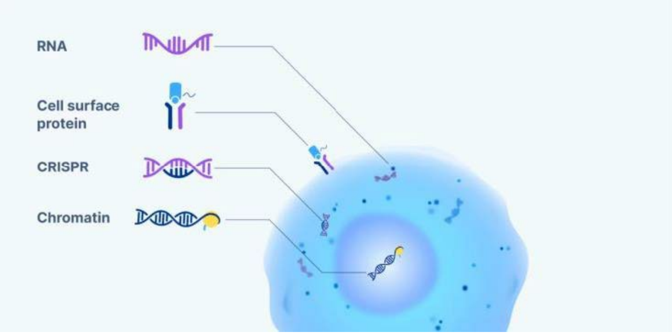
The libraries provide a RNA tool capable of producing RNA interference with powerful viral delivery for targeting highly

Single-cell Genomics

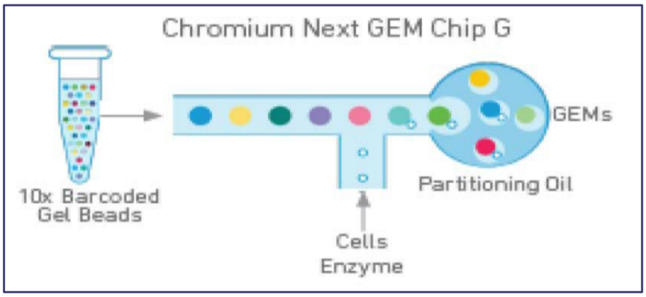
Chromium droplet system

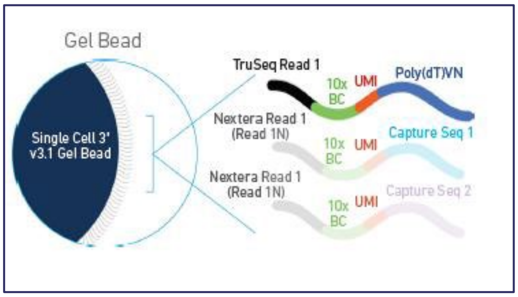
- For targeting up to 10,000 cells
- Sequencing based
- Single cell/nuclei RNA-seq
- Single Cell Multiome ATAC + Gene Expression from the same cell/nuclei
- Feature Barcoding technology for cell surface protein expression and CRISPR perturbations

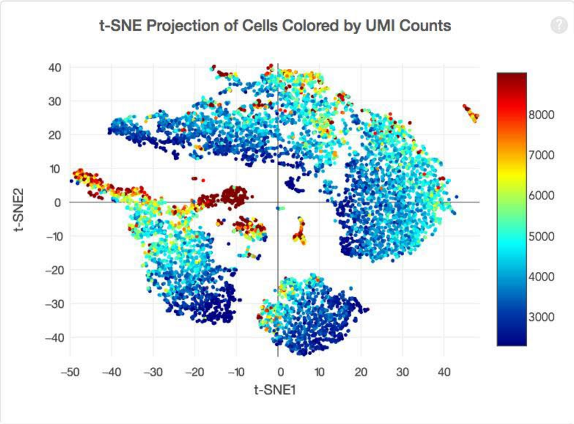
10x GENOMICS

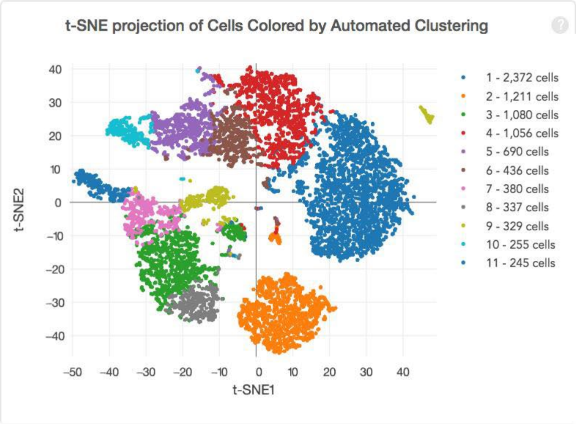


Gel Beads in Emulsion (GEMs)






t-SNE Projection of Cells Colored by UMI Counts


t-SNE projection of Cells Colored by Automated Clustering

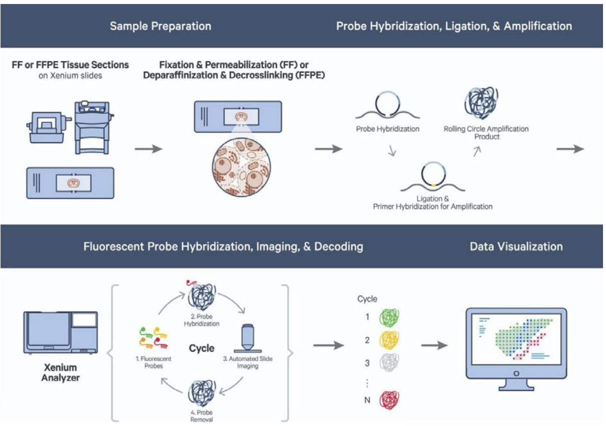
Spatial Genomics

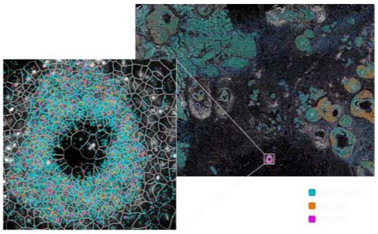
Visium CytAssist

- Whole Transcriptome Analysis
- Sequencing-based
- 2µm resolution

Xenium In Situ

- Targeted In Situ Analysis – up to 5000 genes
- Padlock probe-based chemistry for high sensitivity
- Sub-cellular resolution





Spatial Genomics

We work closely with the LMS Computing and Bioinformatics groups for data management and analysis

- NGS and single-cell data processing and analysis –QC, demultiplexing, alignment and downstream analysis
- Dedicated Isilon File store for NGS/single cell data storage and data archiving
- LMS Bioinformatics: Dr George Young (Head), Marian Dore, Sanjay Khadayate, Jesus Urtasun

Contact details

Head: Laurence Game
Lab staff: Ivan Andrew, Ka Lok Choi

https://lms.mrc.ac.uk/research-facility/genomics-laboratory

Recent Publications

- Simpson Ragdale H. et al. (Parrinello'sgroup) **Injury primes mutation-bearing astrocytes to later life de-differentiation**. *CurrBiol.* 2023 Mar 27;33(6):1082-1098
- Ho KwongLi et al. (Sriskandan'sgroup) 2023 **Characterisationof emergent toxigenic M1UKStreptococcus pyogenesand associated sublineages** *MicrobGenom*. Apr;9(4):mgen000994
- Page N. et al. (Galizi'sgroup) **Single-cell profiling of Anopheles gambiaespermatogenesis defines the onset of meiotic silencing and premeioticoverexpression of the X chromosome**. *CommunBiol.* 2023 Aug 15;6(1):850
- Ceire J.Wincottet al. (Matthew Child's group) **Cellular barcoding of protozoan pathogens reveals the within-host population dynamics of Toxoplasma gondiihost colonization.** *Cell Reports Methods* 2022 Volume 2, Issue8, 100274
- RedhaiS. et al. (Miguel-Aliaga'sgroup) 2020 **An intestinal zinc sensor regulates food intake and developmental growth**. *Nature*. 580(7802):263-268. doi: 10.1038/s41586-020-2111-5.