

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



Nextseq cartridge
and flow cell

MiSeq

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

Applications

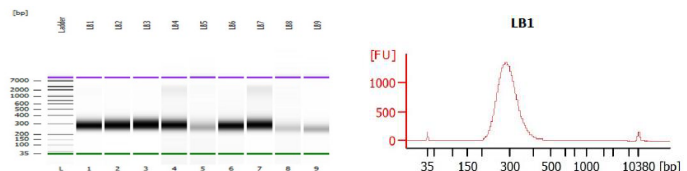
- Library QC
- Small genomes re-sequencing
- Small RNA sequencing
- Amplicon and targeted sequencing



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

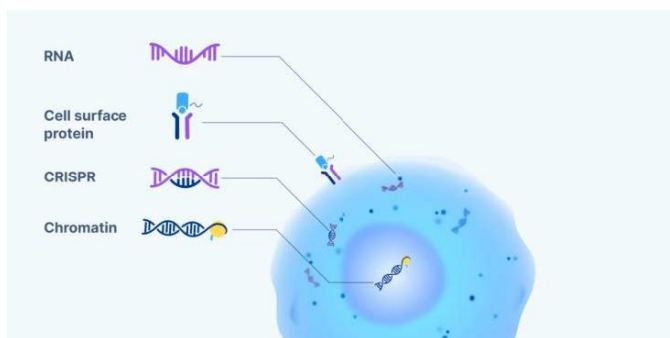
We host the **Dharmacon GIPZ Lentiviral short-hairpin RNA (shRNA) libraries for Human and Mouse.**

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

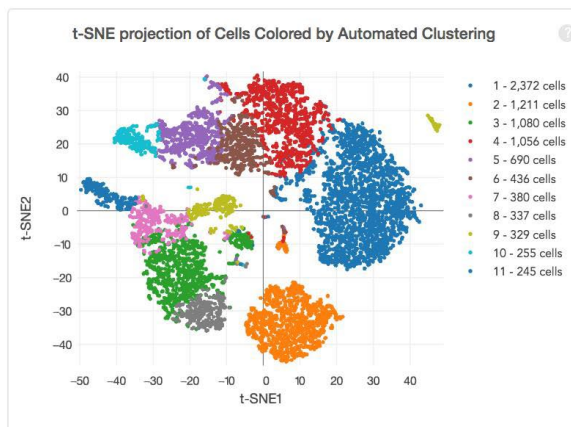
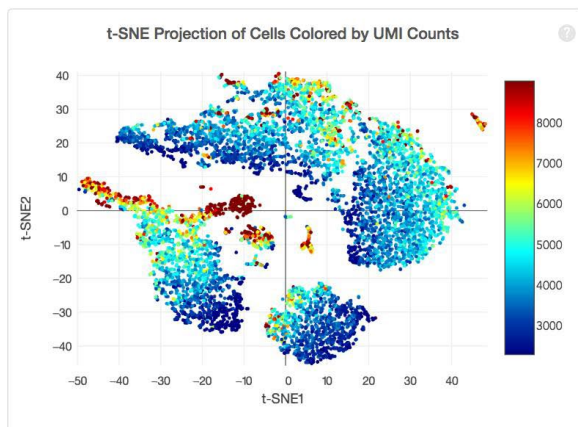
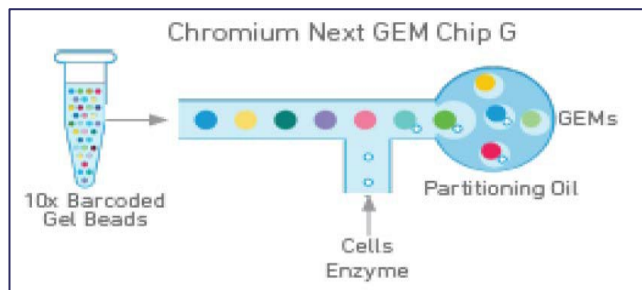
Single-cell Genomics

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



Gel Beads in Emulsion (GEMs)



Spatial Genomics

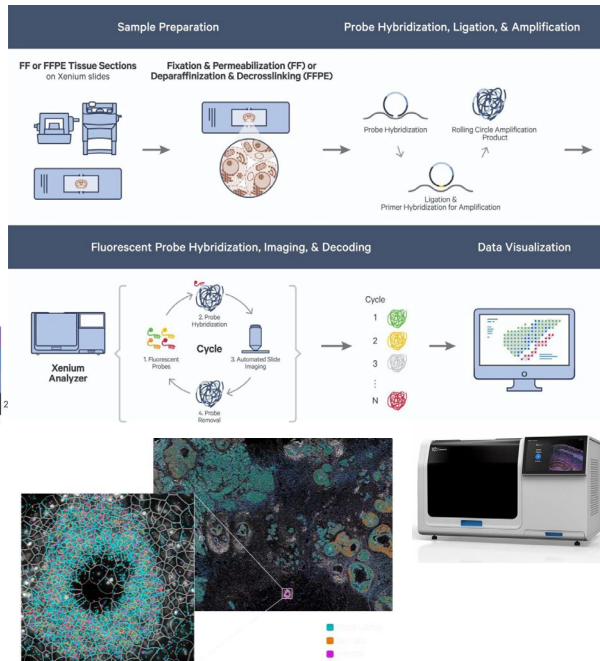
Visium CytAssist

- 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

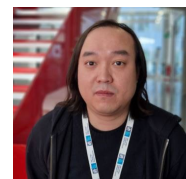
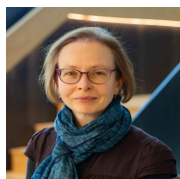
We work closely with the LMS Computing and Bioinformatics groups for data management and analysis

- 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 **Characterisation of emergent toxigenic M1UKStreptococcus pyogenes and associated sublineages** *MicrobGenom.* Apr;9(4):mgen000994
- Page N. et al. (Galizi'sgroup) **Single-cell profiling of Anopheles gambiae spermatogenesis defines the onset of meiotic silencing and premeiotic overexpression of the X chromosome.** *CommunBiol.* 2023 Aug 15;6(1):850
- Ceire J.Wincott et al. (Matthew Child's group) **Cellular barcoding of protozoan pathogens reveals the within-host population dynamics of Toxoplasma gondii host colonization.** *Cell Reports Methods* 2022 Volume 2, Issue 8, 100274
- Redhai S. 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.