### NGS – Illumina sequencing platforms

<table>
<thead>
<tr>
<th>Platform</th>
<th>Flow Cell</th>
<th>Description</th>
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</table>
| **HiSeq2500** | ![](image1.png) | High Output v4 mode or Rapid  
- 50-125bp reads, single or paired-end  
- 8 lanes per flow cell  
- 2 lanes for Rapid flow cell  
- up to 400 Gigabases per run  
- up to 250 millions reads per lane  
**Applications**  
- RNA-seq, ChIP-seq, Whole genome, exome seq, Whole methylome seq, Targeted re-sequencing |
| **NextSeq500** | ![](image2.png) | High or Mid Output  
- 50-150bp reads, single or paired-end  
- up to 130 or 400 millions reads per mid or high output run  
**Applications**  
- RNA-seq, ChIP-seq, Whole genome, exome seq, Whole methylome seq, Targeted re-sequencing |
| **MiSeq** | ![](image3.png) | 50-300bp reads, single or paired-end  
- up to 7 Gigabases per run  
- up to 25 million reads per run  
**Applications**  
- Small genomes re-sequencing  
- Small RNA sequencing  
- Amplicon sequencing  
- Targeted re-sequencing |

### NGS – Library prep service

- **RNA-seq** library prep using NEB kits  
- **DNA-seq** library prep using NEB kits  
- **ChIP-seq** library prep using NEB kit  
- **Amplicon-seq** using PCR  
- Other applications on demand

### Nanopore sequencing - MinION

- Native DNA and RNA sequencing  
- Long reads 10-100 kilobases  
- Bacterial strain sequencing  
- Native methylation marks

### Single-cell analysis

**Chromium 10X Genomics droplet system**  
- For targeting 10,000 cells  
- Single-cell RNA-seq  
- scATAC-seq  
- Feature Barcoding technology for cell surface protein expression and CRISPR perturbations  
- Visium Spatial transcriptomics

**FACS sorted single cells analysis** in 96- or 384-well plates and library preparation using nanoliter volumes on Mosquito HV robot

**Fluidigm microfluidics C1 System and Biomark**

### Open access equipment

- Bioanalyser & Tapestation  
- Nanodrop and Qubit  
- Covaris  
- qPCR machines  
- Mosquito HV nanolitre robot  
- Biomek Fx robot  
- Fluidigm Access Array system

### Short-hairpin RNA library clone picking service

We host the Dhharmacon GIPZ Lentiviral short-hairpin (shRNA) libraries for Human and Mouse. The libraries provide a RNA tool capable of producing RNA interference with powerful viral delivery for targeting highly characterized genes in the human and mouse genomes. Selected clones can be picked and cultured on demand.

### Bioinformatics and Computing Support

We work closely with the LMS Computing and Bioinformatics group for data management and analysis.  
- NGS data processing and analysis – QC, demultiplexing, alignment and downstream analysis.  
- Dedicated Isilon File store for NGS data storage and data archiving at Imperial HPC  
- LMS Bioinformatics contacts: Mahdi Karimi, Marian Dore, Gopu Dharmalingam, Sanjay Khadayate, Yi-Fang Wang

### Recent Publications

- Single-cell imaging and RNA sequencing reveal cellular patterns of gene expression heterogeneously during cancer cell growth and adaptation.  
- Endogenous selector expression identifies known cancer loci and suggests novel candidates.  
- Proc Natl Acad Sci U S A. 2018 115(13), 3383-3388.
- Complex multi-exon enhancer patterns captured by genome architecture imaging.  

### Contact details

**Head:** Laurence Game  
**Lab staff:** Ivan Andrew, JP Haywood  
**Email:** laurence.game@imperial.ac.uk

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