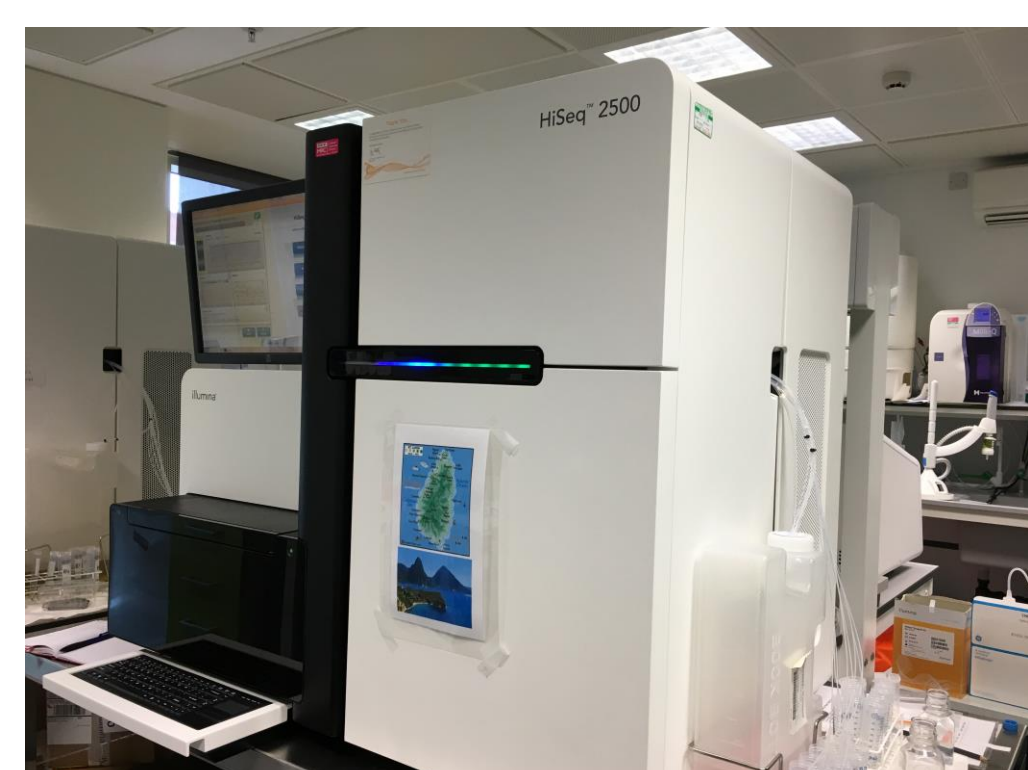


MRC London Institute of Medical Sciences, Imperial College, ICTEM Building 2nd floor, Hammersmith Campus, London

High Throughput Sequencing – Illumina platforms

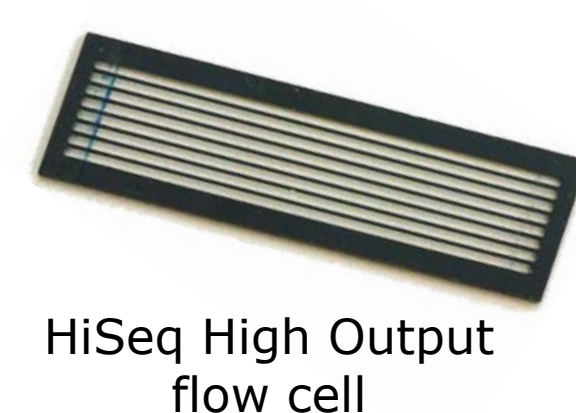
HiSeq2500



Specifications

High Output mode – v4

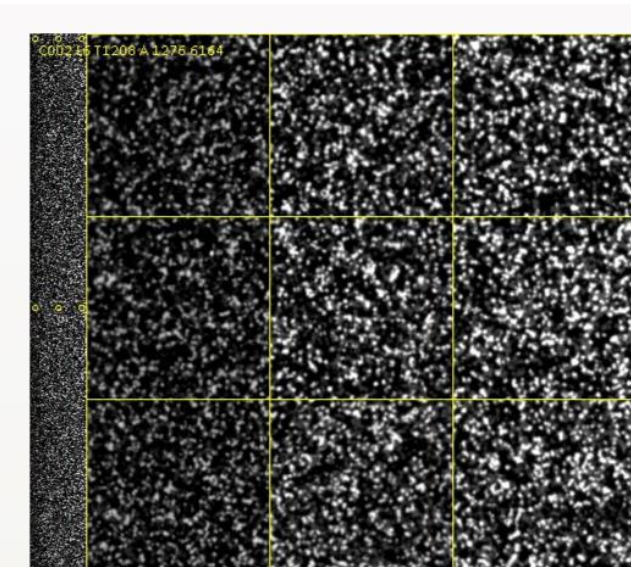
- 50-125bp reads
- Single read or paired end
- 8 lanes per flow cell
- up to 400 Gigabases per run (v4)
- up to 250 millions reads per lane
- 5 days per run (2x100bp)
- £1,600 per lane (2x100bp – v4)*
- £750 per lane (1x50bp)



HiSeq Rapid Flow cell

Rapid mode

- 50-250bp reads
- Single read or paired end
- 2 lanes per flow cell
- up to 50 Gigabases per run
- up to 150 millions reads per lane
- 3 days per run (2x250bp)
- £2,650 per lane (2x250bp)*
- £2,200 per lane (2x150bp)

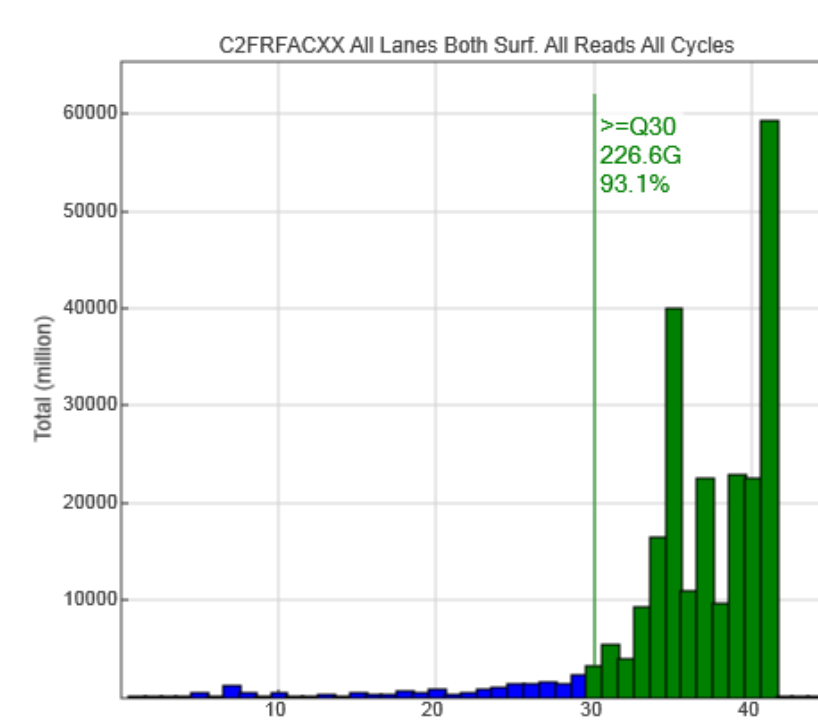


HiSeq Thumbnail images

Applications

- Whole genome re-sequencing
- Whole methylome sequencing
- RNA-seq
- ChIP-seq
- Exome sequencing
- Targeted re-sequencing

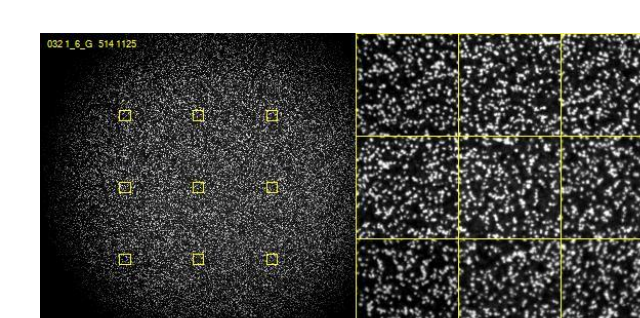
Quality score distribution for a 2x100bp High Output HiSeq run of TruSeq Illumina RNA-seq libraries.



MiSeq



MiSeq flow cell



MiSeq Thumbnail images

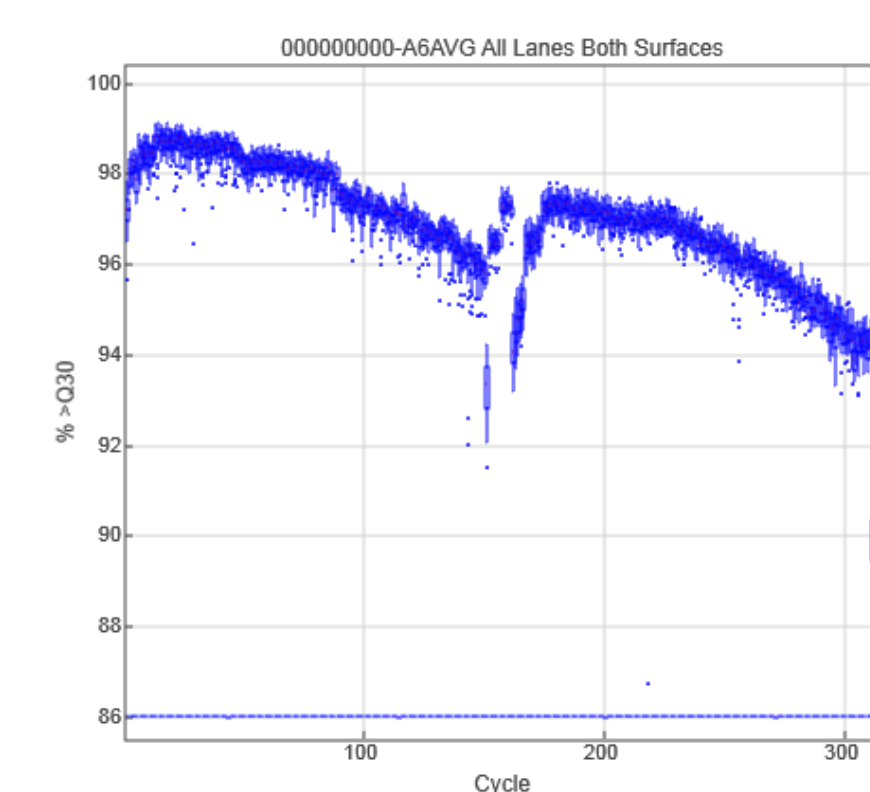
Specifications

- 50-300bp reads
- Single read or paired end
- 1 lane per flow cell
- up to 7 Gigabases per run
- up to 20 million reads per run
- 48hours run (2x300bp)
- £800-1000 per run*

Applications

- Small genomes re-sequencing
- Small RNA sequencing
- Amplicon sequencing
- Targeted re-sequencing

Run Quality Metrics			Total Yield 5.6 Gb			
Read	Density (K/mm2)	Clusters PF (%)	Phas/Prephas (%)	Reads PF (Million)	%reads >= Q30	Yield Total (Gb)
Read 1	976 +/- 23	95.4 +/- 0.4	0.111 / 0.085	18.07	97.7	2.7
Index Read	976 +/- 23	95.4 +/- 0.4	0.227 / 0.094	18.07	96.9	0.2
Read 2	976 +/- 23	95.4 +/- 0.4	0.086 / 0.063	18.07	96.1	2.7



Run quality metrics and Q30 quality plot for a MiSeq 2x150bp run of a pool of 96 amplicons prepared by Fluidigm multiplexed PCR method.

* Prices accurate in 2017, subject to changes

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 characterized genes in the human and mouse genomes. Selected clones can be picked and cultured on demand.

\$ Restricted to LMS users



High Throughput Sequencing – Library prep service\$

- **RNA-seq** library prep using Truseq or NEB kits ~£45 per sample*
- **DNA-seq** libraries using Truseq kit ~£45 per sample* **Other applications on demand**
- **Amplicon-seq** using PCR * Prices accurate in 2017, subject to changes \$ Restricted to LMS users

Single-cell analysis

- **Fluidigm microfluidics C1 System and Biomark** 
- **Chromium 10X Genomics** 
- **FACS sorted single cells and SCR-seq** library preparation with Nextera

Open access equipment

- **Bioanalyser** DNA and RNA quality assessment
- **Nanodrop and Qubit** nucleic acid quantitation
- **Quantitative PCR machines** ABI 7500Fast and ABI 7900HT 
- **Biomek Fx robot** Automated liquid handling
- **Covaris** DNA shearing 
- **Fluidigm Access Array system** multiplexed amplicon PCR preparation for high throughput sequencing

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 Group contacts: Marian Dore, Gopu Dharmalingam, Sanjay Khadayate, Yi-Fang Wang

Contact details

Facility Head: Laurence Game

Lab staff: Ivan Andrew, Katerina Rekopoulou

Admin support: Christine Greig

Web: <http://genomics.lms.mrc.ac.uk>

Recent Publications

- **Complex multi-enhancer contacts captured by genome architecture mapping**
Beagrie RA, Scialdone A, Schueler M, Kraemer DC, Chotalia M, Xie SQ, Barbieri M, de Santiago I, Lavitas LM, Branco MR, Fraser J, Dostie J, Game L, Dillon N, Edwards PA, Nicodemi M, Pombo A. **2017**. *Nature* 534; 519-524.
- **Kenn4 is a regulator of macrophage multinucleation in bone homeostasis and inflammatory disease**
Kang H, Kerloch A, Rotival M, Xu X, Zhang Q, D'Souza Z, Kim M, Scholz JC, Ko JH, Srivastava PK, Genzen JR, Cui W, Altman TJ, Game L, Melvin JE, Hanidu A, Dimock J, Zheng J, Souza D, Behera AK, Nabozny G, Cook HT, Bassett JH, Williams GR, Li J, Vignery A, Petretto E, Behmoaras J. *Cell Reports* **2014** 8(4):1210-24.
- **Genome sequencing reveals loci under artificial selection that underlie disease phenotypes in the laboratory rat**
S. S. Atanur, A. G. Diaz, K. Maratou, A. Sarkis, M. Rotival, L. Game, H. R. Tschannen, P. J. Kaisaki, G. W. Okto, M. C. John, M. T. M. Keane, O. Hummel, K. Saas, W. Chen, V. Guryev, K. Gopalakrishnan, M. R. Garrett, B. Joe, L. Citterio, G. Bianchi, M. McBride, A. Dominiczak, D. J. Adams, T. Serikawa, P. Flicek, E. Cuppen, N. Hubner, E. Petretto, D. Gauguier, A. Kwitek, H. Jacob, T. J. Altman. *Cell*. **2013** Aug 1;154(3):691-703.