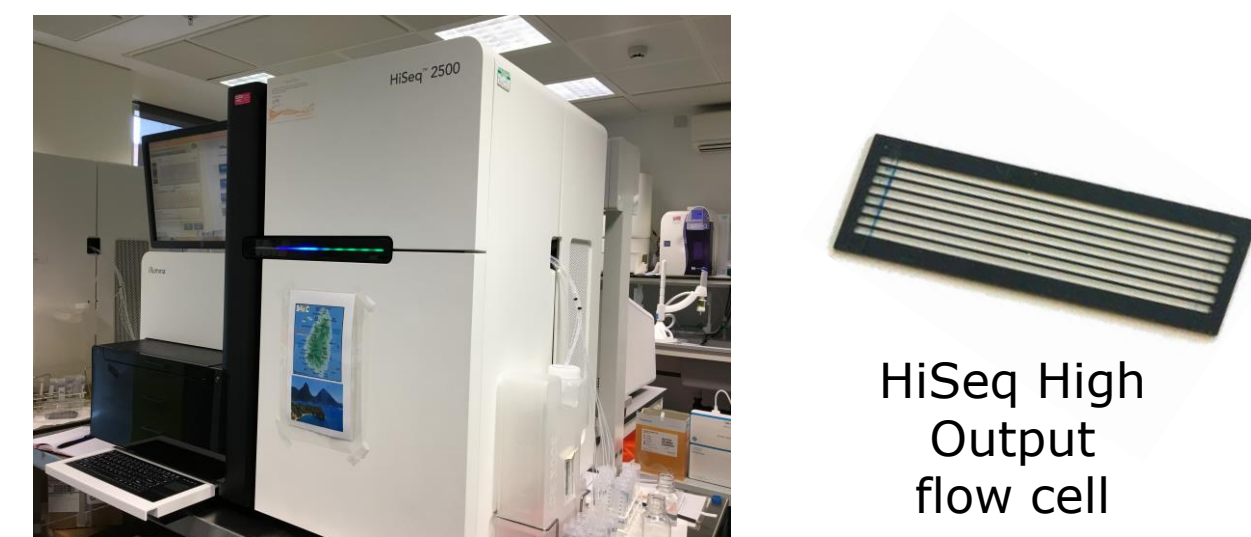# LMS Genomics Laboratory

MRC London Institute of Medical Sciences, Imperial College, ICTEM Building 2nd floor, Hammersmith Campus, London - Web: **http://genomics.lms.mrc.ac.uk**

NGS – Illumina sequencing platforms
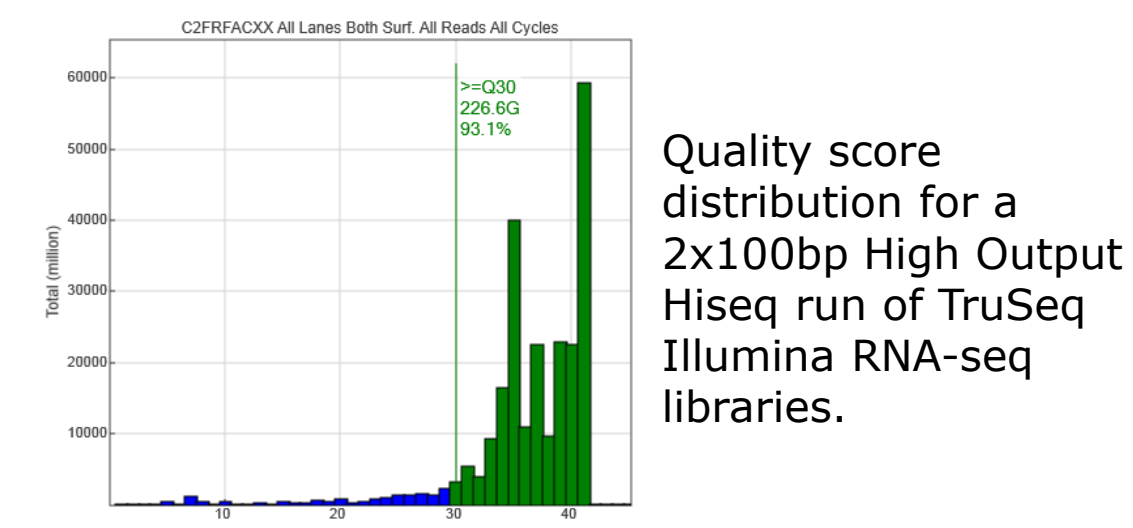
HiSeq2500

HiSeq High Output flow cell

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

Quality score distribution for a 2x100bp High Output Hiseq run of TruSeq Illumina RNA-seq libraries.
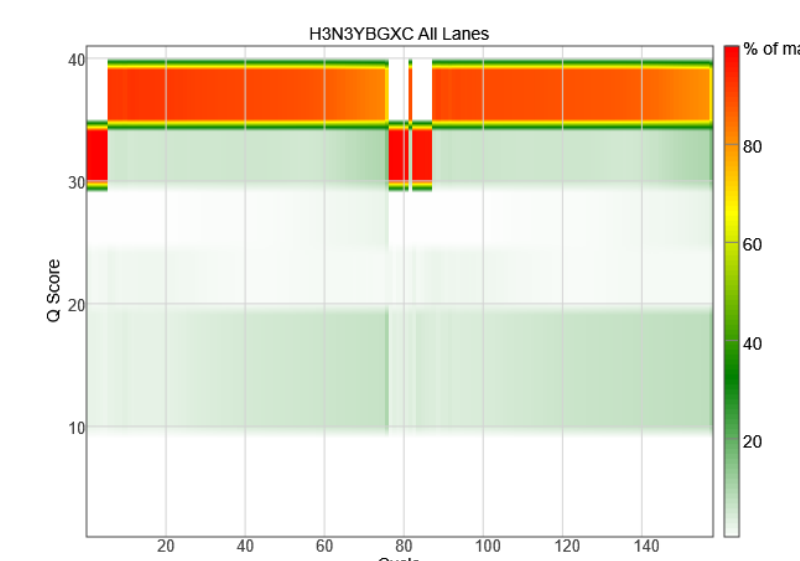
NextSeq500

NextSeq flow cell

High or Mid Output
• 50-150bp reads, single or paired-end
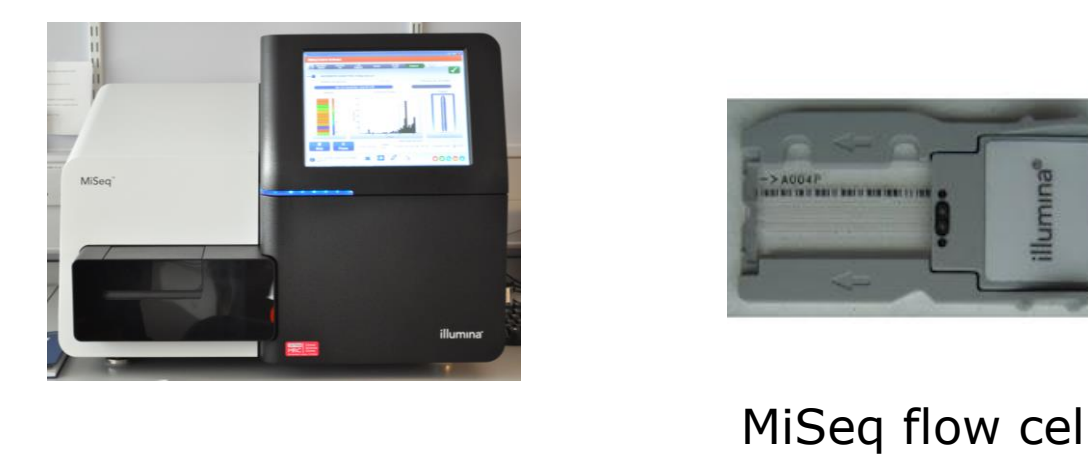• up to 130 or 400 millions reads per mid or high output run

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

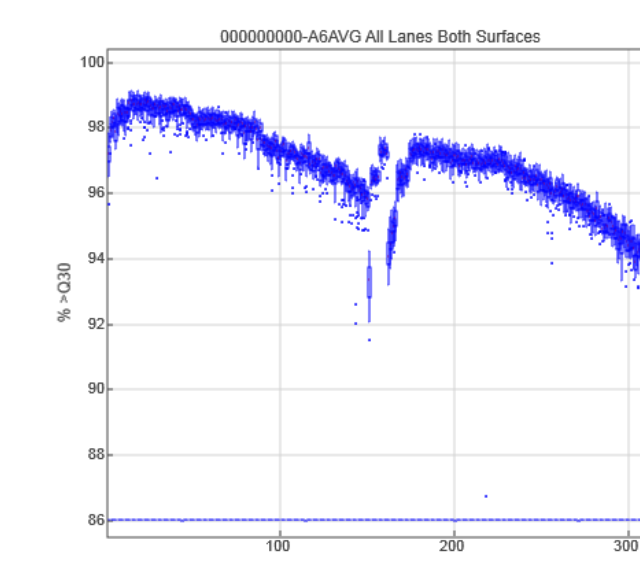Qscore heatmap of a Nextseq 2x75bp run of a RNA-seq pool of 12 libraries.

MiSeq

MiSeq flow cell

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

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

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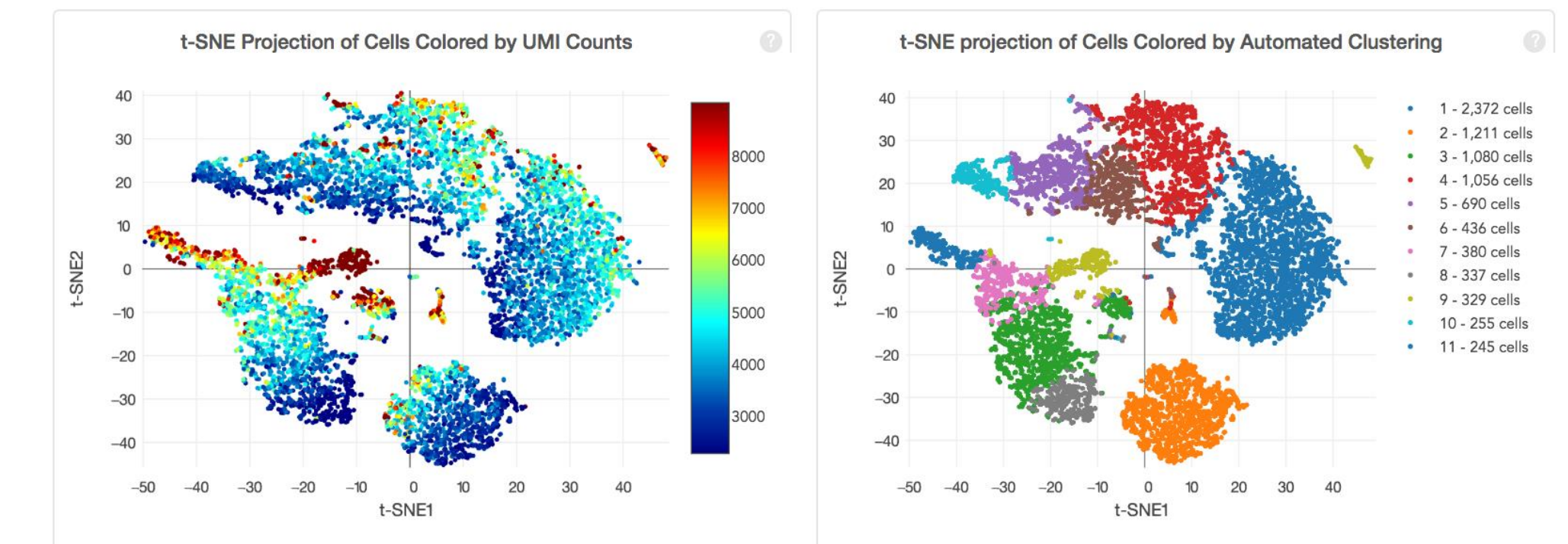
FACS sorted single cells analysis in 96- or 384-well plates and library preparation using nanoliter volumes on Mosquito HV robot

Fluidigm microfluidics C1 System and Biomark

Open access equipment

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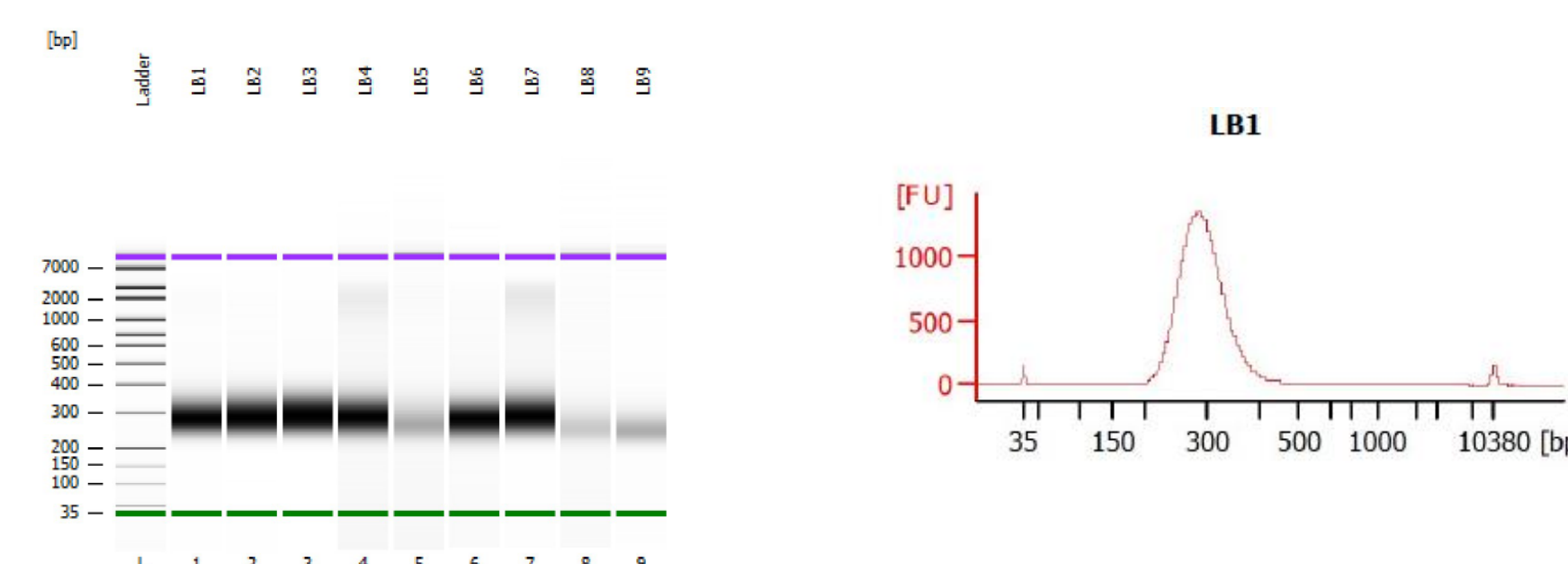• **Fluidigm Access Array system**

Short-hairpin RNA library clone picking service

We host the **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.

NGS – Library prep service

Restricted to LMS users

• **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

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

Nanopore sequencing - MinION

Read Length Histogram
Summary read length distribution

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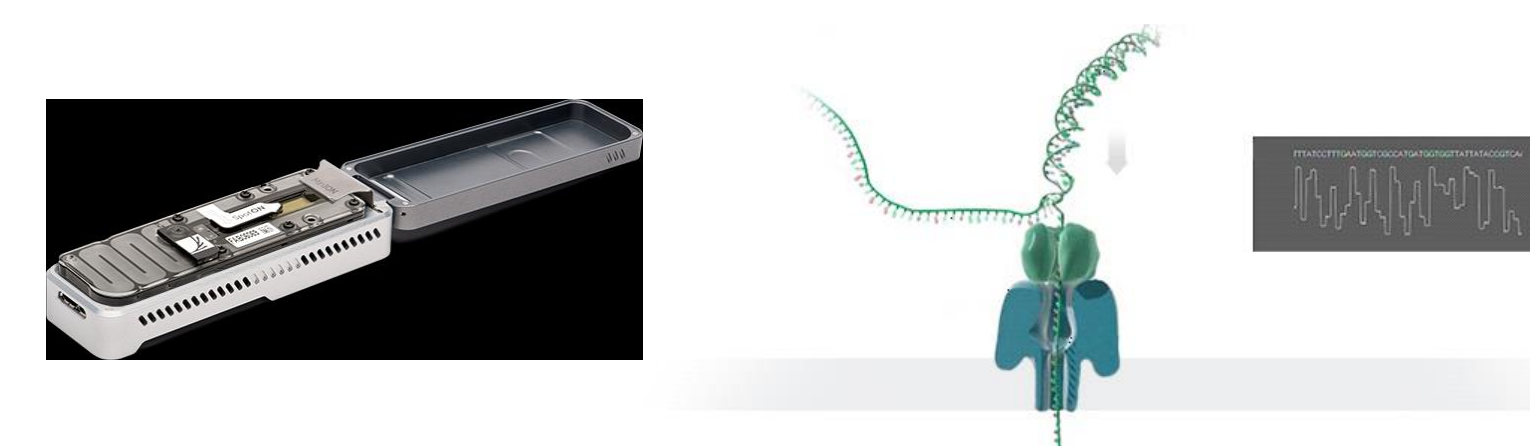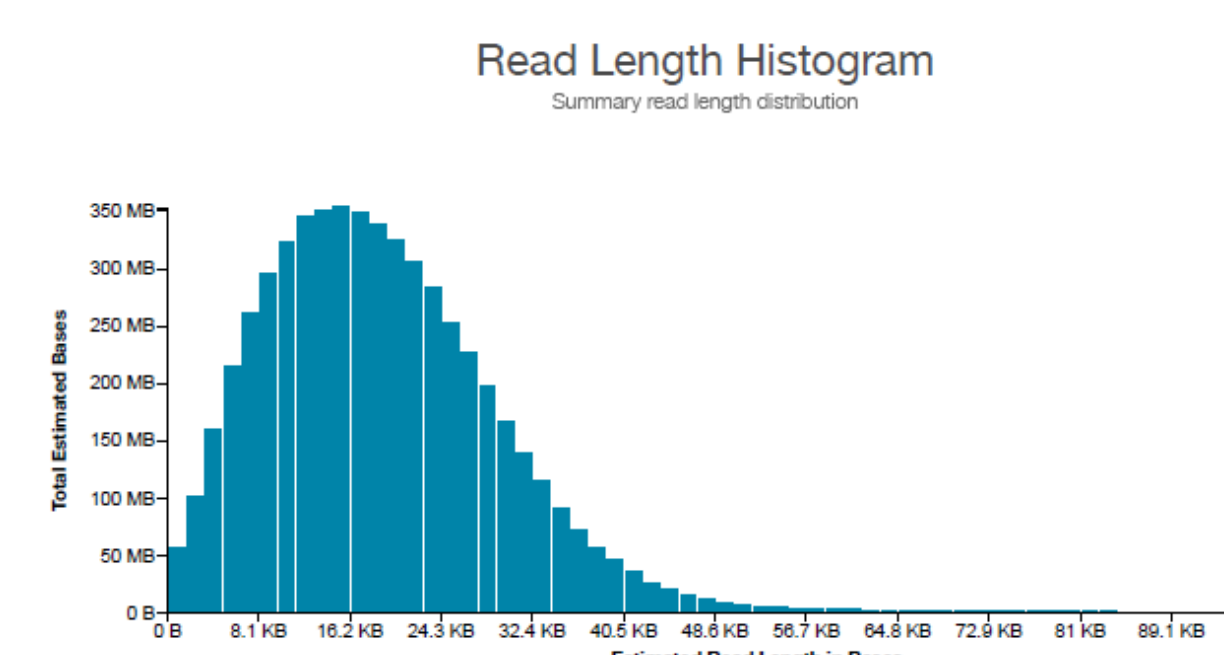
Contact details

Head: Laurence Game - Lab staff: Ivan Andrew, JP Haywood

Email: laurence.game@imperial.ac.uk

Recent Publications

• **Single-cell imaging and RNA sequencing reveal patterns of gene expression heterogeneity during fission yeast growth and adaptation.**
Saint M, Bertaux F, Tang W, Sun XM, Game L, Köferle A, Bähler J, Shahrezaei V, Marguerat S. **Nat Microbiol. 2019** Mar;4(3):480-491

• **Subclonal mutation selection in mouse lymphomagenesis identifies known cancer loci and su suggests novel candidates.**
Webster P, Dawes JC, Dewchand H, Takacs K, Iadarola B, Bolt BJ, Caceres JJ, Kaczor J, Dharmalingam G, Dore M, Game L, Adejumo T, Elliott J, Naresh K, Karimi M, Rekopoulou K, Tan G, Paccanaro A, Uren AG. **Nat Commun. 2018** 9(1):2649.

• **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. **Nature 2017** 534; 519-524.