CANCER GENOMIC PLATFORM

Expertise

- Advice and establishment of optimal experimental design
- Nucleic acid extraction and QC
- Constitution of sample cohorts (DNA/RNA preparation and quality validation)
- Transcriptional analysis
- Primary data analysis
- Biological interpretation of sequence variations or copy number alterations

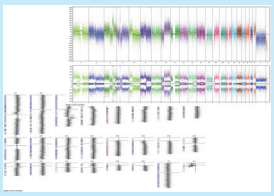
Applications

- High Throughput Sequencing (Targeted re-sequencing, exome sequencing)
- Genotyping-Arrays
- Array Comparative Genomic Hybridization (CGH)
- Clinical genomic alterations detection (tumor or other tissues)
- Single/multiple amplicons approach (Sanger sequencing)
- Detection of copy number alterations (CNA) in tumor or other tissues (NGS, CGH, Microarrays)
- Transcriptome analysis (RNA-Seq, microarrays)
- Targeted transcription analysis (HTG EdgeSeq)
- Targeted miRNA analysis (HTG EdgeSeq)

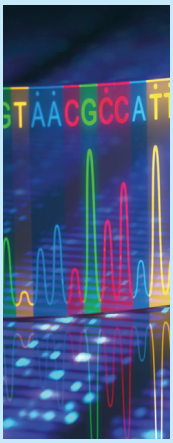
Instrumentation

- NGS: Novaseq6000 (Illumina)
- NGS: Nextseq500 (Illumina)
- NGS: Miseq system (Illumina)
- HTG EdgeSeq system
- Affymetrix Microarray station
- Agilent CGH station

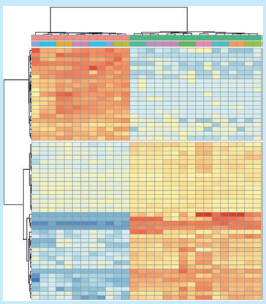
The **Cancer Genomic Platform** is a technological facility dedicated to **molecular biology in cancer research**. This platform encompasses state-of-the-art technologies to enable you to successfully conduct clinical and/or basic research projects. The latest innovation is comprised of The Nova 6000 Sequencing System that opens research possibilities to new dimensions.



Biologists, engineers and technical staff of the platform are at your disposal to **provide assistance to your research projects**: to suggest appropriate technical approaches, to conduct experiments using methodologies/equipment of your choice, to interpret biological significance of results generated.



With the next generation of sequencing systems, in particular to advanced high-capacity NovaSeq sequencer, we offer a wide field of applications from high-throughput sequencing (whole genome sequencing, whole exome sequencing, RNAseq, Chip-sequencing) to panel-based sequencing in DNA or RNA (HTG) in response to investigator's requirement, as well as conventional approaches such as Array CGH or Microarrays. These powerful technologies provide useful tools for **the detection of genomic alterations including mutations and copy number and structural changes** for the analysis of gene expressions and epigenetic modifications and other related studies.



The platform has been implicated in many projects involving basic, translational research or clinical studies, either through collaborations with local, national and international research teams. For instance, **the platform plays an essential role in the ProfiLER project** dedicated to precision medicine which was initiated in 2012 at the CLB. Our contribution to different projects has been acknowledged in a number of scientific publications.

Access details

- Basic science projects
- Translational projects
- Preclinical projects
- Animal samples
- Human samples

Advice for sample preparation

- Primary samples
- DNA / RNA and nucleotide quality control

D.I.Y.?

There is no free access to platform equipment.

Mention us in your publications!

To allow our platform to pursue its objectives, we need you to mention our work in your publications as follows:
Plateforme de génomique des cancers, Département de recherche translationnelle et d'innovations, Centre Léon Bérard, Lyon, France

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Project workflow

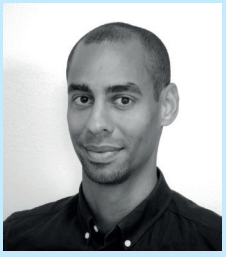
1. *Initial consultation (phone, e-mail Qing Wang)*
2. *Request form filling*
3. *Validation of the project design by the « project coordinating committee »*
4. *Sample registration and processing*
5. *Result transmission to PI and to bioinformatics platform if required in the project design*

Qing Wang
– Scientific director

Qing Wang is responsible for submitting your project to the « coordinating committee », and after acceptance for managing the execution of the project by the different technical platform managers.

Sandrine Boyault
– Platform manager

With her expertise in CNA detection, transcriptomic analysis and other associated methodologies, as well as her active involvement in national and international collaborations, Sandrine Boyault will provide you with suggestions and guidance when conducting experimental processes and interpreting your results.



Valéry Attignon
– Platform manager

With his experience and expertise in NGS, Valéry Attignon is the best suited to advise you on the detection of genomic mutations or transcriptional abnormalities using NGS technologies: from panel design to technical processing. He can also help you with the biological interpretation of certain results.

Submission form and more infos:
www.cancer-research-lyon.com