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## **Mission and activity**

The genomics platform provides to basic, translational, and medical research teams with high throughput technological tools for analyzing gene structure and expression in various organisms, cellular models, and tumors.

Structural alterations in genomes, such as mutations, gains, amplifications, loss of genomic regions, polymorphisms, allelic imbalances, loss of heterozygosity are identified using SNP arrays, Nanostring analysis, Sanger sequencing, or qPCR.

Gene expression is complex and may be addressed at multiple levels. Coding and non-coding transcript for proteins can be quantified using Affymetrix chip for a pangenomic analysis, or using NanoString tools, or via qPCR depending on the number of samples and markers to quantify. The platform analyses the regulation of gene expression by quantifying microRNA, non-coding functional RNA, and other specific types of RNA, which modulate gene expression at various levels (transcription and translation). Such quantifications are performed by using Affymetrix chips or via NanoString multiplexing tools. Technics for quantifying certain epigenetic markers are currently being tested to meet internal demand (OxBS method developed by Cambridge Epigenetix). Other technics to analyse the chromatin conformation are being setup (in situ HiC, Uveal Melanoma project, with Pr. E. Heard) to enrich our portfolio of activities

In addition, the platform is analysing samples in the frame of several clinical trials or upon biologist request, in the field of cancer and rare diseases. DNA and RNA are daily analysed on dedicated tools (Oncoscan, Cytoscan from Affymetrix, and Prosigna Pam50 test). Very recently an agreement was setup with Nanostring to become a Backup Platform in Europe for Prosigna tests.

The platform is also participating in international projects and collaborations with partner from industry.

Finally other complementary approaches are proposed to teams who require the preparation of samples or enrichment by laser microdissection. New genomics activities can be evaluated and implemented according to the needs of the teams.

## Services

- Advises in Genomics
- Sample preparation (cryo-sectioning, laser microdissection, nucleic acid purification)
- Genome analysis (genome wide, based on arrays, or specific to hotspots, Sanger sequencing,)
- Transcriptome analysis: genome wide, or customized up to 800 targets (Nanostring approaches)
- Regulome analyses: miRNA and ncRNA, analysed with arrays or using Nanostring tools, methylation analysis (OxBS library preparation), chromosome conformation analysis (in situ HiC).

## Key publications

### Year of publication 2017

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Roman Rouzier, Aurelie Roulot, Arthur H Jeiranian, Namratha Ram, Jean Marc Guinebretiere, Anne Vincent Salomon, David Gentien (2017 Jan 11)

**Denaturing fixatives are compatible with the NanoString nCounter(®) platform and the Prosigna(®) assay.**

*New biotechnology* : 37-41 : [DOI : S1871-6784\(16\)32312-3](https://doi.org/10.1016/j.nbt.2017.01.003)

### Year of publication 2016

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Alejandra Urrutia, Darragh Duffy, Vincent Rouilly, Céline Posseme, Raouf Djebali, Gabriel Illanes, Valentina Libri, Benoit Albaud, David Gentien, Barbara Piasecka, Milena Hasan, Magnus Fontes, Lluís Quintana-Murci, Matthew L Albert, (2016 Aug 30)

**Standardized Whole-Blood Transcriptional Profiling Enables the Deconvolution of Complex Induced Immune Responses.**

*Cell reports* : 2777-91 : [DOI : 10.1016/j.celrep.2016.08.011](https://doi.org/10.1016/j.celrep.2016.08.011)

### Year of publication 2014

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D Gentien, O Kosmider, F Nguyen-Khac, B Albaud, A Rapinat, A G Dumont, F Damm, T Popova, R Marais, M Fontenay, S Roman-Roman, O A Bernard, M-H Stern (2014 Jan 17)

**A common alternative splicing signature is associated with SF3B1 mutations in malignancies from different cell lineages.**

*Leukemia* : 1355-7 : [DOI : 10.1038/leu.2014.28](https://doi.org/10.1038/leu.2014.28)



## Genomics Platforms