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 optical mapping, 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 were 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. A collaboration with Predilife (company developing innovative solutions predicting the risk of diseases to facilitate personalized medicine), has been signed in 2019 and allows the genetic analysis of the new generation MammoRisk breast cancer prediction test.
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, optical mapping based on Bionano genomics tools)
- 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 2020**


**PLK1 inhibition exhibits strong anti-tumoral activity in CCND1-driven breast cancer metastases with acquired palbociclib resistance.**

*Nature communications*: 4053 : [DOI: 10.1038/s41467-020-17697-1](https://doi.org/10.1038/s41467-020-17697-1)


**BRCAness, SLFN11, and RB1 loss predict response to topoisomerase I inhibitors in triple-negative breast cancers**
Reference-free transcriptome exploration reveals novel RNAs for prostate cancer diagnosis.

*Science Translational Medicine*: DOI: 10.1126/scitranslmed.aax2625

Year of publication 2019


The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist.

*Nature genetics*: 51: 1024-34, DOI: 10.1038/s41588-019-0412-0

Year of publication 2017

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

Year of publication 2015

Sylvie Maubant, Bruno Tesson, Virginie Maire, Mengliang Ye, Guillem Rigail, David Gentien, Francisco Cruzalegui, Gordon C Tucker, Sergio Roman-Roman, Thierry Dubois (2015 Apr 8)

Transcriptome analysis of Wnt3a-treated triple-negative breast cancer cells.

*PloS one*: e0122333, DOI: 10.1371/journal.pone.0122333