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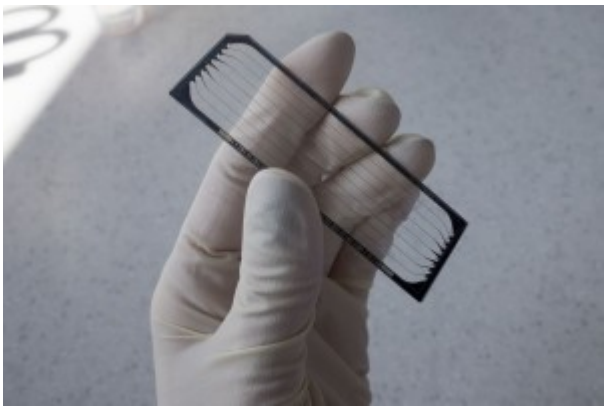
Next generation sequencing technology has now reached tremendous throughput and accuracy that enable researchers to conduct large-scale genomic projects at affordable cost and less time.

The NGS Platform of the Institut Curie has greatly evolved since 2012 mainly with the financial support of ICGEx grant obtained in the frame of the EQUIPEX « investissement d'avenir » competitive call. This grant allowed to purchase high throughput NGS sequencers, to fully equip a dedicated lab at the 7th floor of the hospital and expand the staff in charge of running sequencing projects.

Aims

- Provide state of the art services in sequencing for the different research teams of the Institut Curie.
- Offer technical and scientific support in experimental design and sequencing strategies
- Be flexible to best respond to scientific needs (technical development and implementation)

Activity



Under the supervision of Olivier Delattre and Alain Nicolas, the NGS platform provides state of the art services in sequencing. This includes the organization of pre-run meetings where the choice of the most appropriate technical strategy is defined in order to best address the biological question of collaborators. Multiple sequencing protocols have been developed and routinely used in the platform to cover most commonly used applications in genetics and epigenetics (Genome, Exome and targeted resequencing, RNA sequencing, DNA methylation sequencing, ChIP-seq ...). Furthermore, we are also willing to co-develop more specific protocols according to the need of research teams of the Institute.

Once the technical aspects are defined, samples are provided by collaborators and libraries compatible to the dedicated sequencing devices (Illumina or Ion Torrent) are then prepared by the NGS team. After sequencing, raw data are transferred to the bioinformatics team (U900) for quality controls and basic analysis. At the end, sequence data are provided to research teams under a Galaxy user-friendly interface and a bioinformatics support is available to help in data analysis.

The platform is not restricted to fundamental research, we are also involved in multiple translational research projects in collaboration with U830, the translational research department and the Hôpital Curie (SHIVA, SAFIR02 ...). The molecular characterization of clinical samples within few days is used by clinician to evaluate the best therapeutic options for patient care during MTB (Molecular Tumor Board).

Networking

- Active member of France Génomique, a French consortium of NGS platforms dedicated to the mutualisation of NGS resources that benefit to French research teams
- Collaboration with Cambridge Epigenetix Company to improve epigenetic tools with benefits for the Institute

Training

- Organisation of a genomic module from Paris VII Master degree « Ingénieur de plateforme »
- Oral presentation in « International Courses » organized by the training unit of the Institute

Services

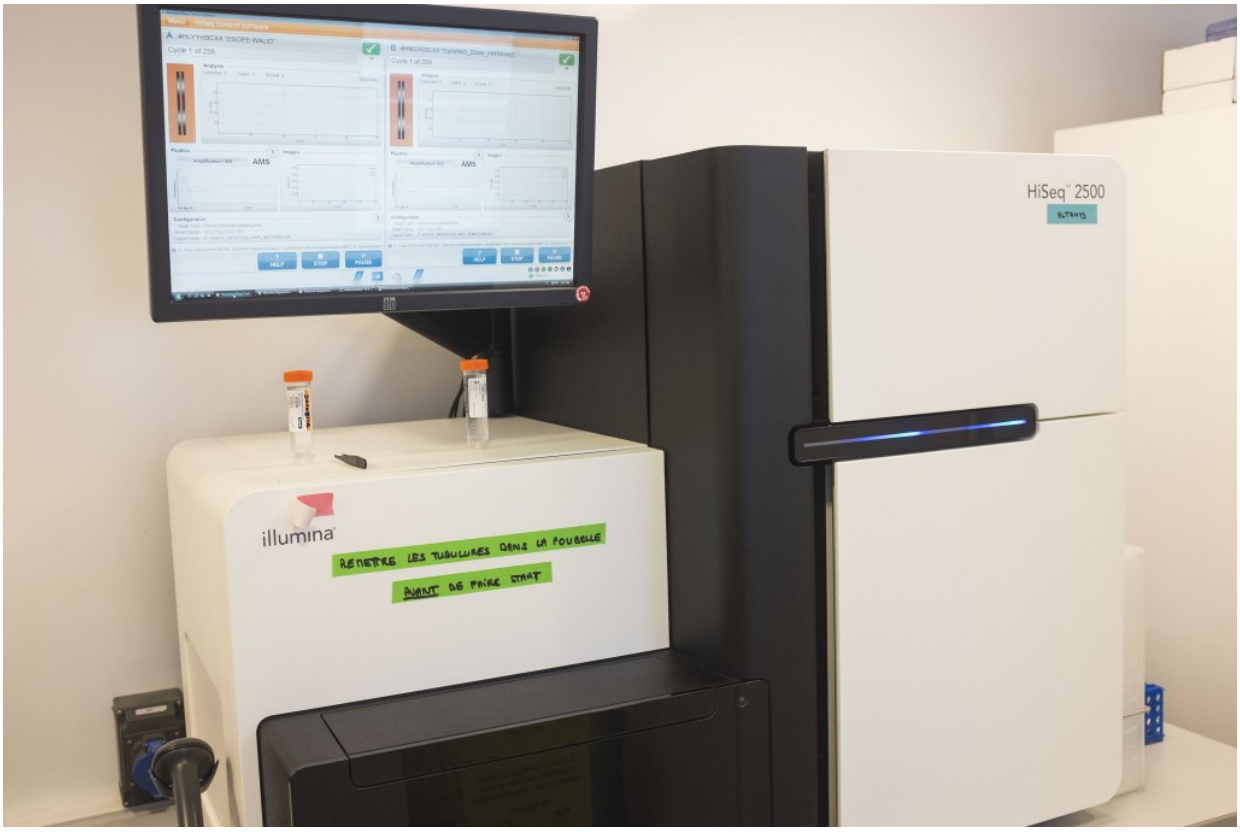
Quality control assessment of samples and library preparations for multiple sequencing applications:

- Whole genome, whole exome and targeted resequencing
- Transcriptome analysis (RNAseq for mRNA, total RNA and small RNA)
- Epigenetics with DNA methylation, ChIP-seq for histone modifications or protein binding analysis
- Single cell DNA and RNA sequencing
- Bioinformatics supports through a Galaxy user-friendly interface (U900)

Equipment

- Two high throughput sequencers from Illumina : 1 HiSeq 2500 and 1 HiSeq 2000 dedicated to applications requiring a huge amount of data (human genome and exome sequencing, transcriptome analysis ...).
- Five benchtop sequencers: 2 IonTorrent PGM, 1 IonProton (Life Tech) and 2 MiSeq (Illumina). These devices are dedicated to routine patients clinical diagnosis from Hôpital Curie and for small research projects such as sequencing of gene panels.
- One C1 single-cell auto-prep system that enables the analysis of transcriptome and genome of individual cells since the heterogeneous nature of tumors point to the need to analyse their biology to a much finer resolution.
- A motorized fluorescent LEICA microscope to assess single cell capture efficiency
- A LabChip, a BioAnalyzer, a Nanodrop, a Qubit fluorometer; a CFX96 real-time PCR system used to assess sample quality and concentration.

All equipments have been funded by ICGex (except the IonProton cofunded by ICGex and France Génomique and the LEICA microscope exclusively funded by France Génomique).



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Key publications

Year of publication 2015

María Elena Fernández-Sánchez, Sandrine Barbier, Joanne Whitehead, Gaëlle Béalle, Aude Michel, Heldmuth Latorre-Ossa, Colette Rey, Laura Fouassier, Audrey Claperon, Laura Brullé, Elodie Girard, Nicolas Servant, Thomas Rio-Frio, Hélène Marie, Sylviane Lesieur, Chantal Housset, Jean-Luc Gennisson, Mickaël Tanter, Christine Ménager, Silvia Fre, Sylvie Robine, Emmanuel Farge (2015 Jul 2)
Mechanical induction of the tumorigenic β-catenin pathway by tumour growth pressure.
Nature : 92-5 : DOI : 10.1038/nature14329

Angela Bellini, Virginie Bernard, Quentin Leroy, Thomas Rio Frio, Gaelle Pierron, Valérie Combaret, Eve Lapouble, Nathalie Clement, Herve Rubie, Estelle Thebaud, Pascal Chastagner,

Anne Sophie Defachelles, Christophe Bergeron, Nimrod Buchbinder, Sophie Taque, Anne Auvrignon, Dominique Valteau-Couanet, Jean Michon, Isabelle Janoueix-Lerosey, Olivier Delattre, Gudrun Schleiermacher (2015 Feb 20)
Deep Sequencing Reveals Occurrence of Subclonal ALK Mutations in Neuroblastoma at Diagnosis.
Clinical cancer research : an official journal of the American Association for Cancer Research : 4913-21 : DOI : 10.1158/1078-0432.CCR-15-0423

Thomas F Eleveld, Derek A Oldridge, Virginie Bernard, Jan Koster, Leo Colmet Daage, Sharon J Diskin, Linda Schild, Nadia Bessoltane Bentahar, Angela Bellini, Mathieu Chicard, Eve Lapouble, Valérie Combaret, Patricia Legoix-Né, Jean Michon, Trevor J Pugh, Lori S Hart, JulieAnn Rader, Edward F Attiyeh, Jun S Wei, Shile Zhang, Arlene Naranjo, Julie M Gastier-Foster, Michael D Hogarty, Shahab Asgharzadeh, Malcolm A Smith, Jaime M Guidry Auvil, Thomas B K Watkins, Danny A Zwijnenburg, Marli E Ebus, Peter van Sluis, Anne Hakkert, Esther van Wezel, C Ellen van der Schoot, Ellen M Westerhout, Johannes H Schulte, Godelieve A Tytgat, M Emmy M Dolman, Isabelle Janoueix-Lerosey, Daniela S Gerhard, Huib N Caron, Olivier Delattre, Javed Khan, Rogier Versteeg, Gudrun Schleiermacher, Jan J Molenaar, John M Maris (2015 Jan 15)
Relapsed neuroblastomas show frequent RAS-MAPK pathway mutations.
Nature genetics : 864-71 : DOI : 10.1038/ng.3333

Year of publication 2014

Ronald Lebofsky, Charles Decraene, Virginie Bernard, Maud Kamal, Anthony Blin, Quentin Leroy, Thomas Rio Frio, Gaëlle Pierron, Céline Callens, Ivan Bieche, Adrien Saliou, Jordan Madic, Etienne Rouleau, François-Clément Bidard, Olivier Lantz, Marc-Henri Stern, Christophe Le Tourneau, Jean-Yves Pierga (2014 Aug 14)
Circulating tumor DNA as a non-invasive substitute to metastasis biopsy for tumor genotyping and personalized medicine in a prospective trial across all tumor types.
Molecular oncology : 783-90 : DOI : 10.1016/j.molonc.2014.12.003