



# GeT

Génome et  
Transcriptome

# GeT

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<http://get.genotoul.fr>

@GeT\_Genotoul 

# Who are we?

- **Genomics and Transcriptomics (GeT) core facility of Genotoul located on 5 sites**
- **Regional node of National Infrastructure within the « France Génomique » PIA program**



- **Labels :**

- **IBISA Label**
- **INRA strategic core-facility**



- **Quality Certification :**

- **ISO9001 (GeT-PlaGe, GeT-Biopuces)**
- **NFX 50 900 (GeT-PlaGe)**



# Team and Expertise

- **A team of 30 people with:**

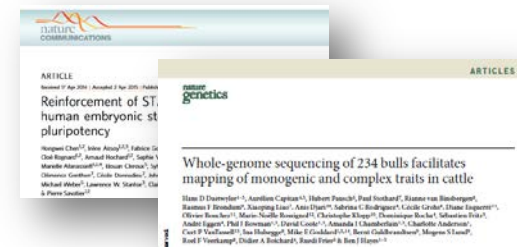
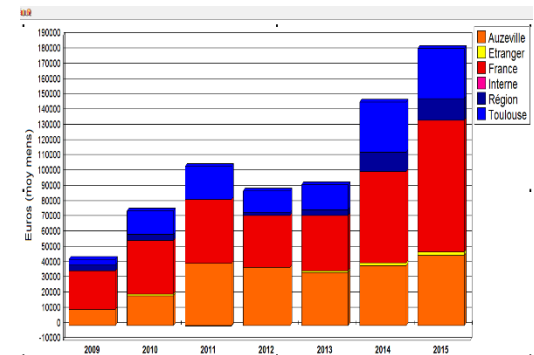
- **Technological Specialty and Scientific community by site**
- **Experts in Agronomy, Environment, Microbiology, Health**
- **Competence in biology, bioinformatics, biostatistics**



- **Partnership with Genotoul Bioinformatic core-facility (NG6) for:**

- **Data storage and management**
- **Data Quality analysis**

- **15 R&D projects**
  - Mate paired, chipseq, metylation, GBS, 3G NGS, capture, long fragments, HIC...
- **More than 100 laboratories (INRA, CNRS, INSA, INSERM, CHU, CIRAD ...)**
  - More than 160 research teams
  - More than 250 projects
  - 2M€ of activity
- **17 Research projects (ANR, INCA, H2020 ...)**
- **46 Publications as co-author since 2012**



**WHAT IS NEW ?**

# Organization : The new GeT

- **NEW** : From “a network of platforms” to

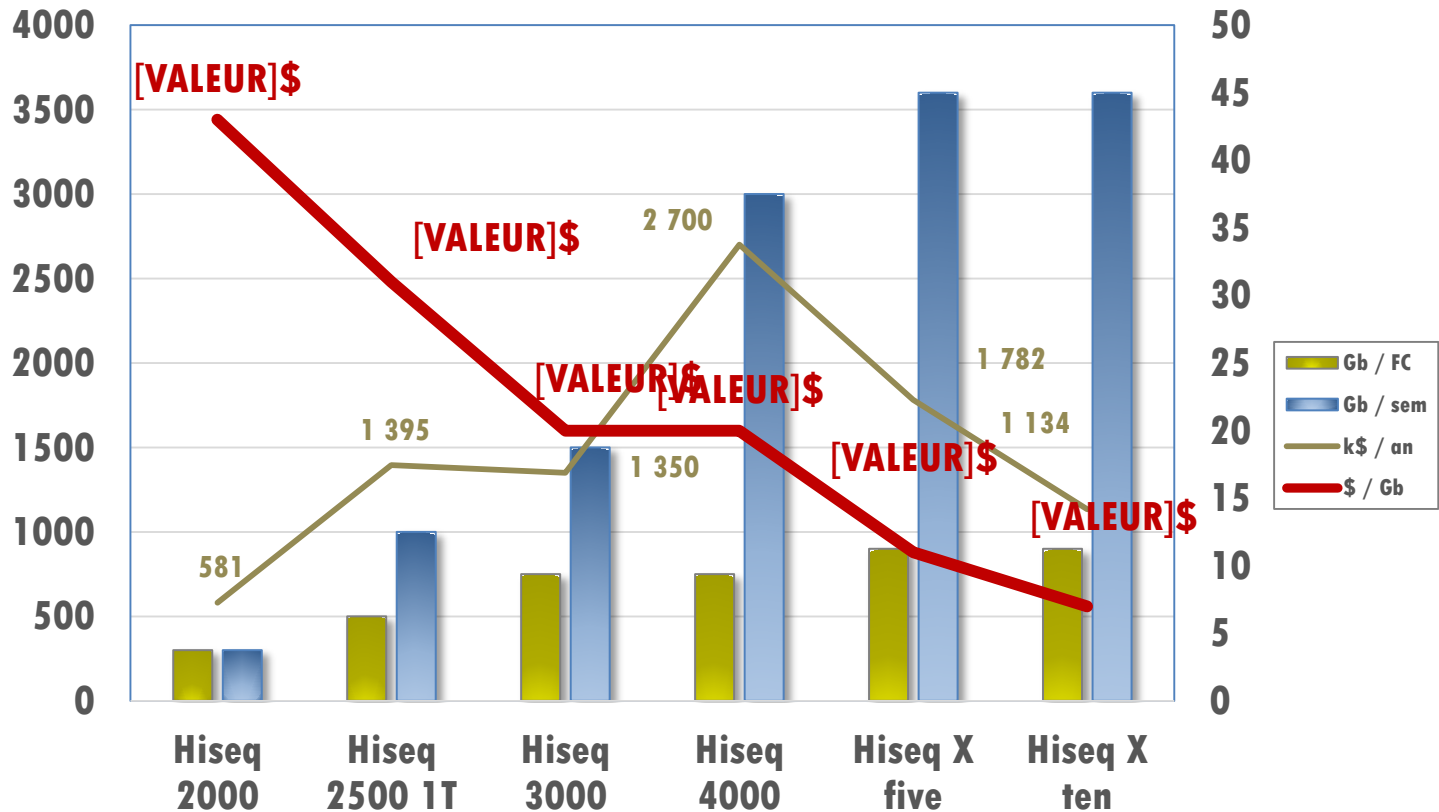
“a **ONE** multi-sites more integrated core facility”

- A **closer** management



- **GeT Ambassadors** in the different scientific communities
- **GeT Engineers** can work on different sites if needed

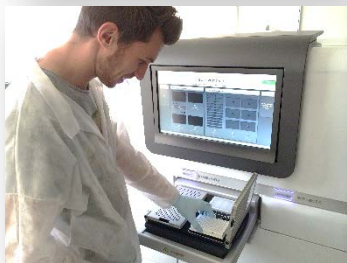
# Evolution of Hiseq sequencers family



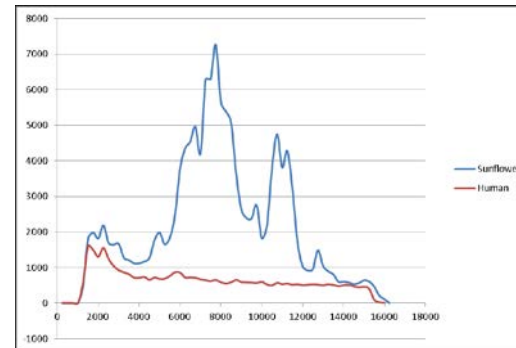
**October 2015 : Non human DNA can be sequenced on HiSeq X (at 30x)**  
**(sold by 5 or more)**

# Evolution of Long Fragments sequencers

- January 2015 :**
  - P6/C4 chemistry of **PacBio** permits sequencing of **longer fragments** (at the same error rate)
  - **Oxford Nanopore** is ever in **development**
- Investment in a PacBio RSII with Region MP/FEDER funding, at first**



**Sunflower : 30 % of repeated sequences (LTR)**  
**Human : 8.8 % of repeated sequences**



libragen

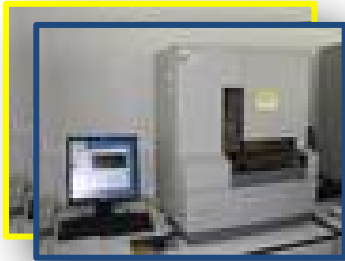


# From NGS short reads to long reads

- **First PACBIO installed in France**
- **SUNRISE project to acquire expertise**
  - **To validate quality of DNA**
  - **To improve library preparation**
  - **To increase the number of reads**
  - **To increase the length of reads**
- **More projects to develop new applications :**
  - **Whole genome sequencing on different species**
  - **Targeted sequencing**
  - **Complex population**
  - **RNA sequencing**
  - **Epigenetic**



# A complete portfolio of sequencers at GeT



400 pb  
1Gb



200 pb  
13 Gb



Waiting for  
Promethion  
Sequel



2x 300 pb  
15 Gb



2x150 pb  
700 Gb

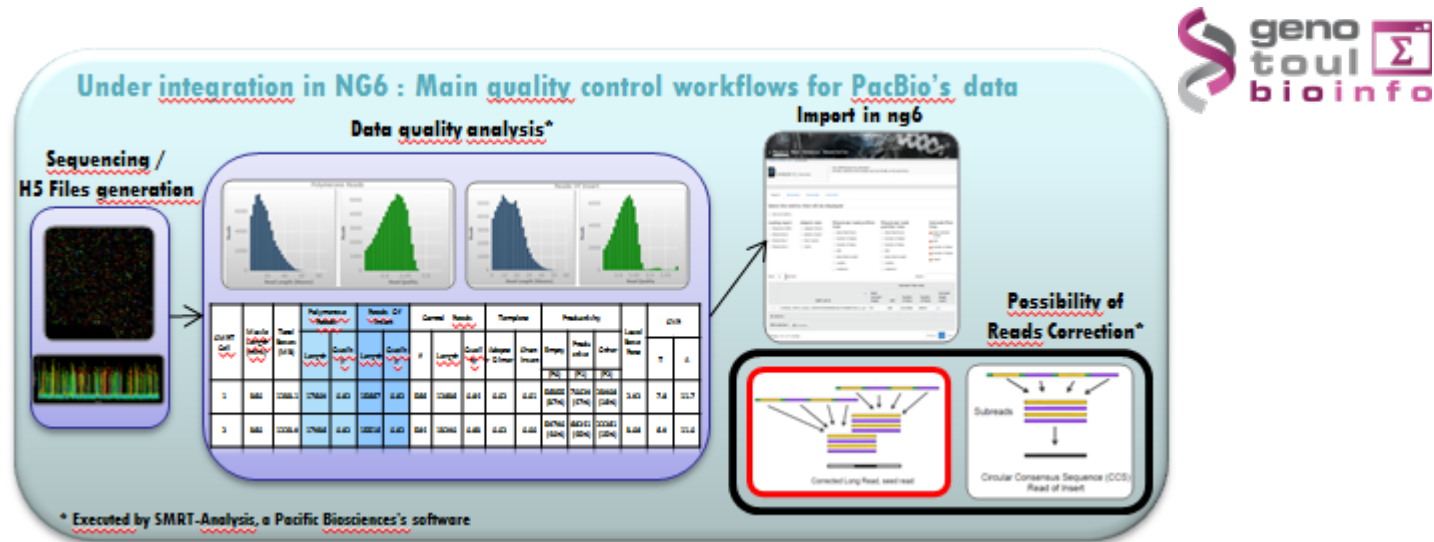


15 000 pb  
1.2 Gb (6h)



# LIMS development

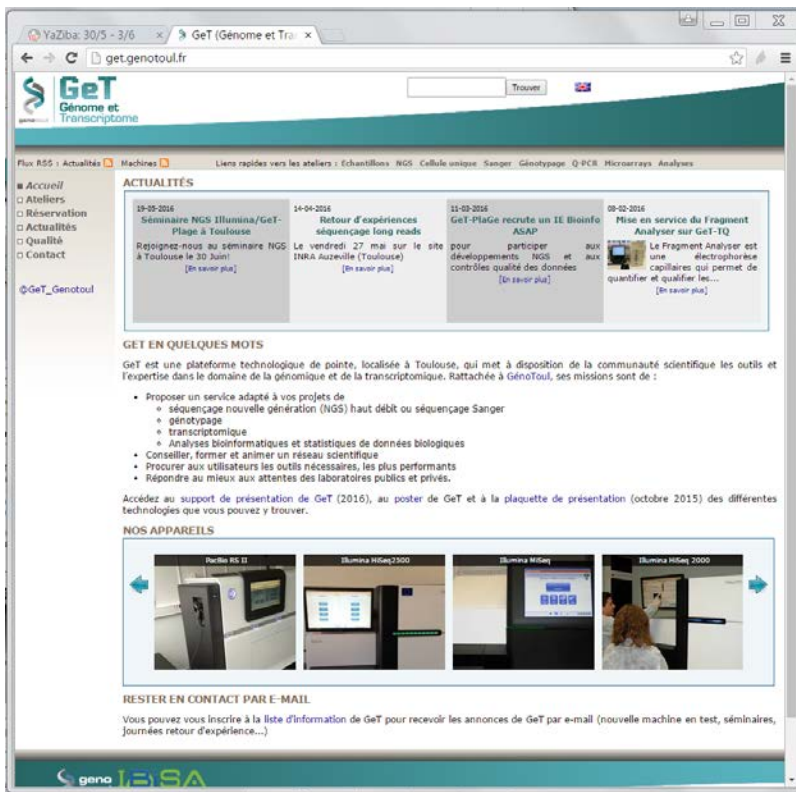
- **Current integration in NG6 : Main quality control workflows for PacBio's data**



- **Upcoming : A new LIMS for NGS samples, sequencing and analysis tracking**



- Website



The screenshot shows the website's homepage with a navigation menu on the left, a search bar, and a main content area with news articles and technical specifications.

**ACTUALITÉS**

- 19-05-2016: Séminaire NGS Illumina/Get-PlaGe à Toulouse. Rejoignez-nous au séminaire NGS à Toulouse le 30 Juin! [En savoir plus]
- 14-01-2016: Retour d'expériences séquençage long reads. Le vendredi 27 mai sur le site INRA Auzouville (Toulouse) [En savoir plus]
- 11-03-2016: Get-PlaGe recrute un IE Bioinfo ASAP. pour participer aux développements NGS et aux contrôles qualité des données [En savoir plus]
- 09-02-2016: Mise en service du Fragment Analyser sur Get-T2. Le Fragment Analyser est une électrophorese capillaire qui permet de quantifier et qualifier les... [En savoir plus]

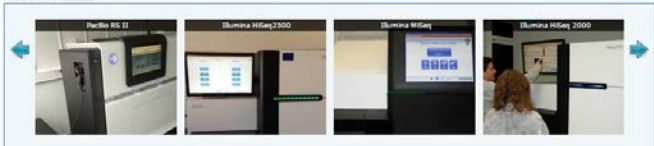
**GET EN QUELQUES MOTS**

Get est une plateforme technologique de pointe, localisée à Toulouse, qui met à disposition de la communauté scientifique les outils et l'expertise dans le domaine de la génomique et de la transcriptomique. Rattachée à GenoToul, ses missions sont de :

- Proposer un service adapté à vos projets de
  - séquençage nouvelle génération (NGS) haut débit ou séquençage Sanger
  - génomique
  - transcriptomique
- Analyses bioinformatiques et statistiques de données biologiques
- Conseiller, former et animer un réseau scientifique
- Procureur aux utilisateurs les outils nécessaires, les plus performants
- Répondre au mieux aux attentes des laboratoires publics et privés.

Accédez au support de présentation de Get (2016), au poster de Get et à la plaquette de présentation (octobre 2015) des différentes technologies que vous pouvez y trouver.

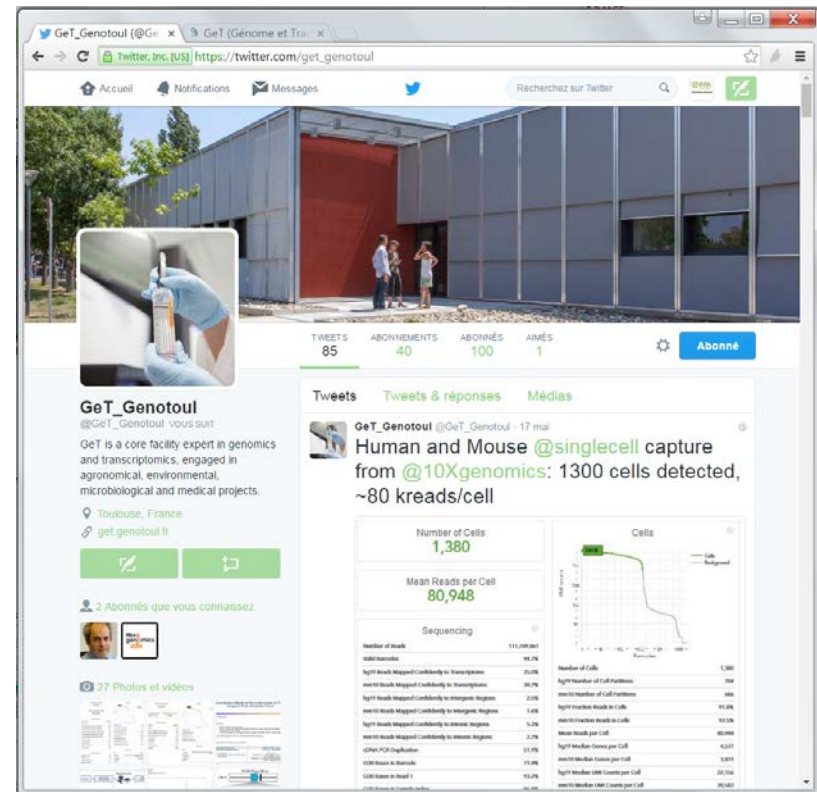
**NOS APPAREILS**



**RESTER EN CONTACT PAR E-MAIL**

Vous pouvez vous inscrire à la liste d'information de Get par e-mail (nouvelle machine en test, séminaires, Journées retour d'expérience...)

- Twitter account : @Get\_Genotoul

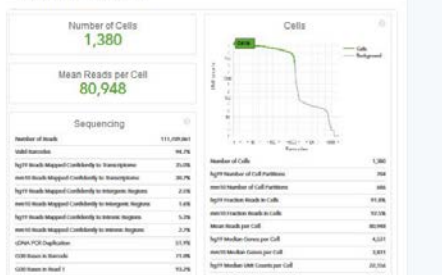



The screenshot shows the Twitter profile page for @Get\_Genotoul. The profile bio states: "Get is a core facility expert in genomics and transcriptomics, engaged in agronomical, environmental, microbiological and medical projects." The location is listed as "Toulouse, France" and the website as "get.genotoul.fr".

**Tweets & réponses Médias**

**Get\_Genotoul @Get\_Genotoul · 17 mai**

Human and Mouse @singlecell capture from @10Xgenomics: 1300 cells detected, ~80 kreads/cell



Sequencing		Number of Cells	
Number of Reads	111,000,000	Number of Cells	1,380
10X Genomics	98.7%	Human	1,380
10X Single-Cell	20.7%	Mouse	1,380
10X Single-Cell	39.7%	Human	1,380
10X Single-Cell	2.5%	Mouse	1,380
10X Single-Cell	1.2%	Human	1,380
10X Single-Cell	5.2%	Mouse	1,380
10X Single-Cell	2.7%	Human	1,380
10X Single-Cell	11.7%	Mouse	1,380
10X Single-Cell	11.2%	Human	1,380
10X Single-Cell	11.2%	Mouse	1,380
10X Single-Cell	11.2%	Human	1,380
10X Single-Cell	11.2%	Mouse	1,380