GeT

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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
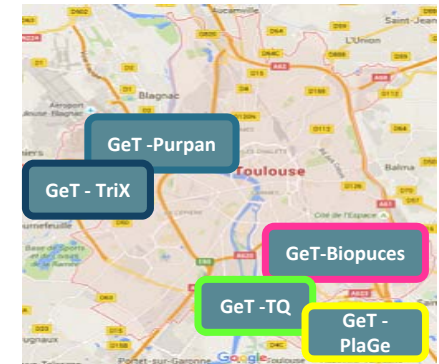 - INRA strategic core-facility

- 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**

http://get.genotoul.fr

Activity

- **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**

- **19 Research projects (ANR, INCA, H2020 …)**

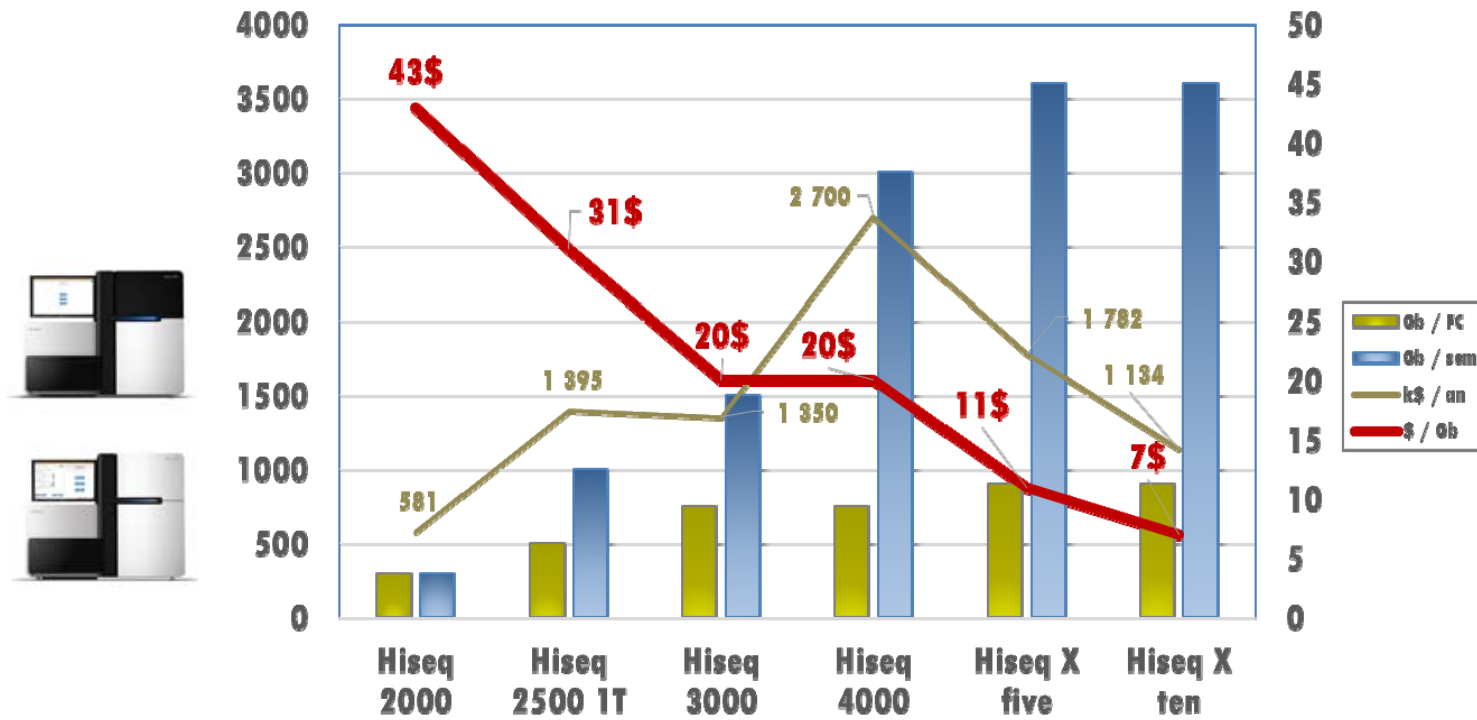- **46 Publications as co-author since 2012**

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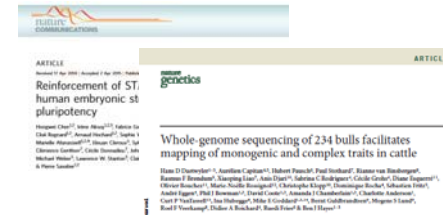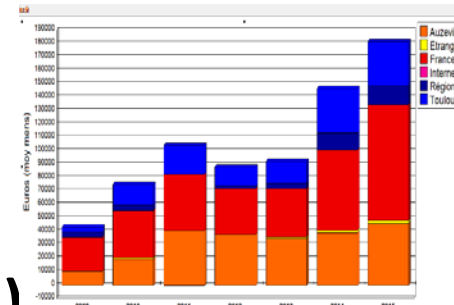
What is NEW ?

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**

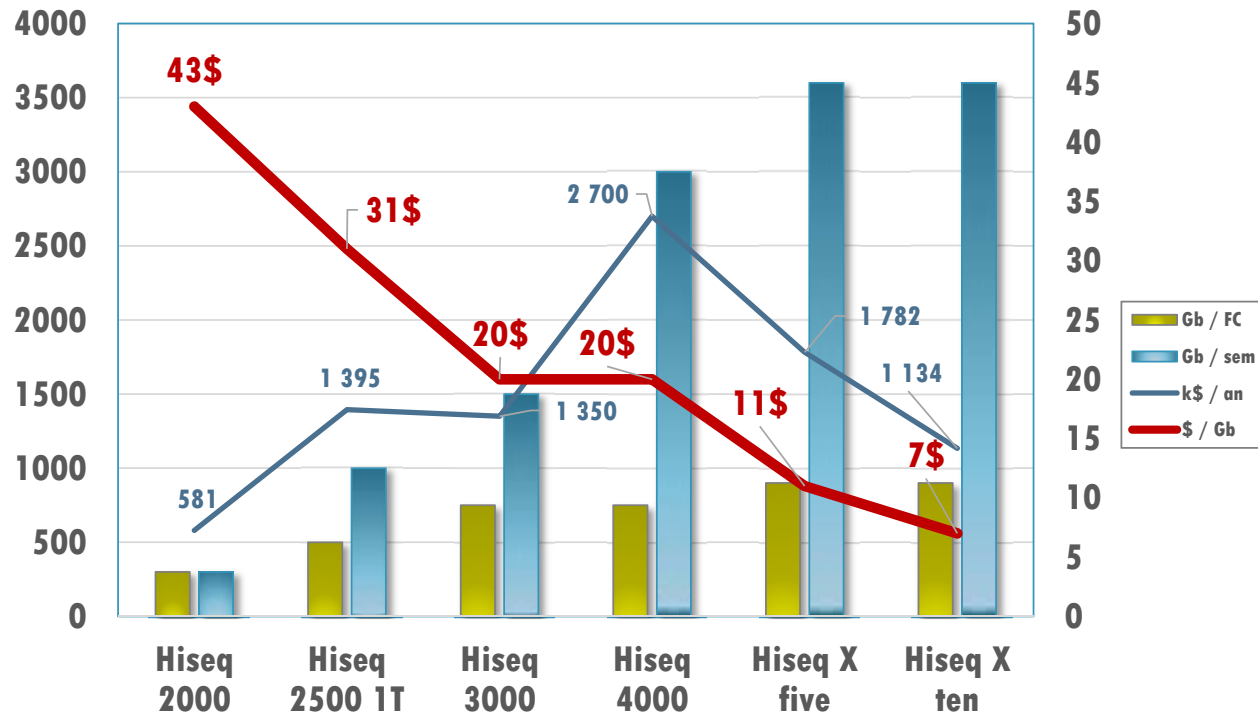⊚ **GeT Engineers can work on different sites if needed**

Evolution of Hiseq sequencers family

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

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# 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 for plant genomes**

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


SUNRISE
UNE CULTURE POUR LE FUTUR

libragen

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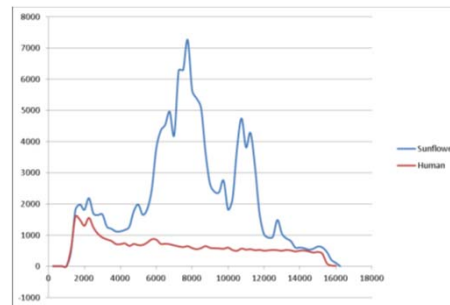
From NGS short reads to long reads

- **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**
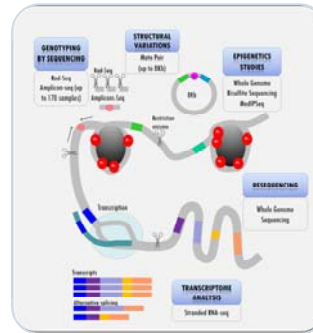 - **Complex population**
  - **RNA sequencing**
  - **Epigenetic**

A complete portfolio of sequencers at GeT
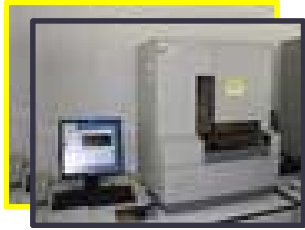
400 pb
1Gb

200 pb
13 Gb

2x 300 pb
15 Gb

2x150 pb
700 Gb

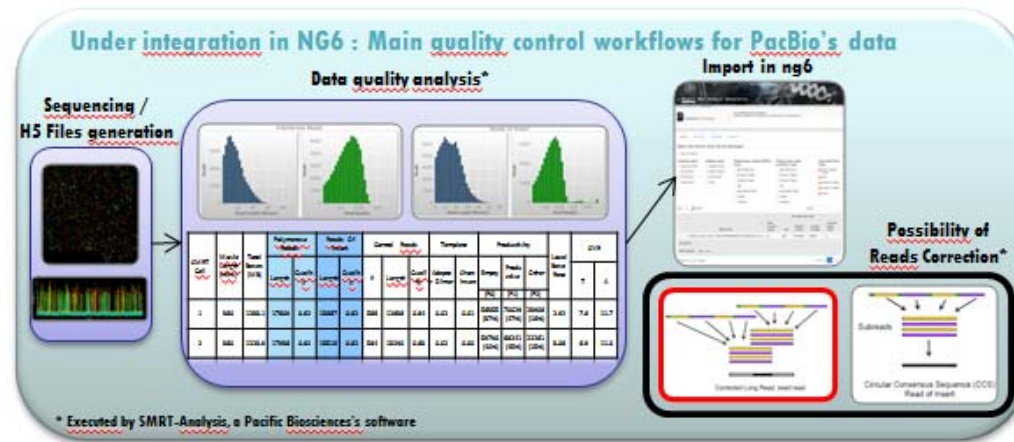15 000 pb
1.2 Gb (6h)

25 000 pb
7 Gb (48h)

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LIMS development

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

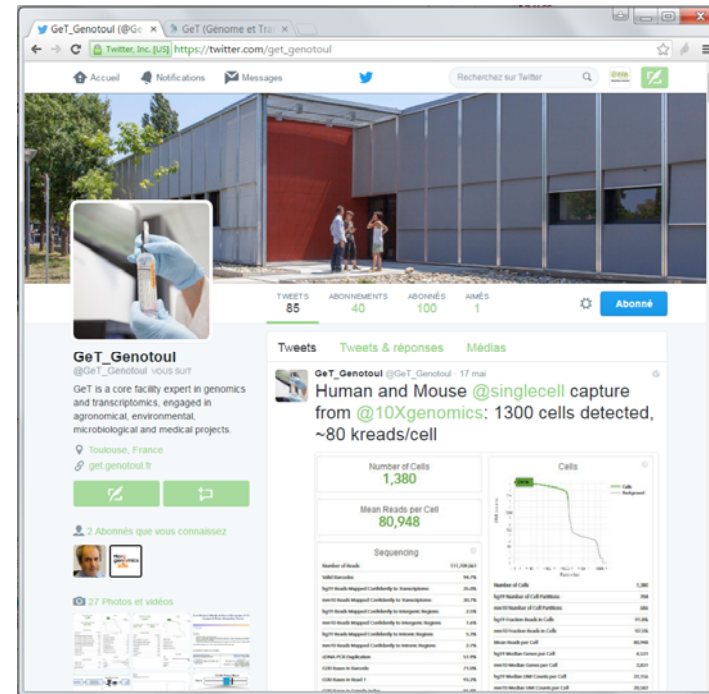- **Upcoming : A new LIMS for NGS samples, sequencing and analysis tracking**

Communication

Website

Twitter account :@GeT_Genotoul

http://get.genotoul.fr

GeT in a mapmind