Toulouse Genomic Core facility

Cécile Donnadieu

GeT Animator

GeT-PlaGe Manager

http://get.genotoul.fr

@GeT_Genotoul

GeT Génome et Transcriptome

The Core facility missions

- **To provide innovating technologies for genome analysis to the scientific community**
  - **identification of genes influencing traits of interests**
  - **study of genetic diversity in all reigns,**
  - **study of gene expression regulation**
  - **sequencing and genomic comparison.**

- **To Develop new protocols, new methodologies, acquire expertise and train in those technologies**

- **To animate workshop for user network**

GeT Génome et Transcriptome

Who are we?

- Genomics and transcriptomics core facility spread on 5 sites GeT in Toulouse
- National Infrastructure within the « France Génomique » program
- IBISA Label
- INRA strategic core-facility
- ISO9001 et NFX0800 Certification

GeT Génome et Transcriptome

Team and Expertise

- **A team of 30 people with:**
  - **Technical Specialty and scientific community by site**
  - **Experts in Agronomy, Environment, Microbiology, Health**
  - **Competence in biology, bioinformatics, biostatistics**

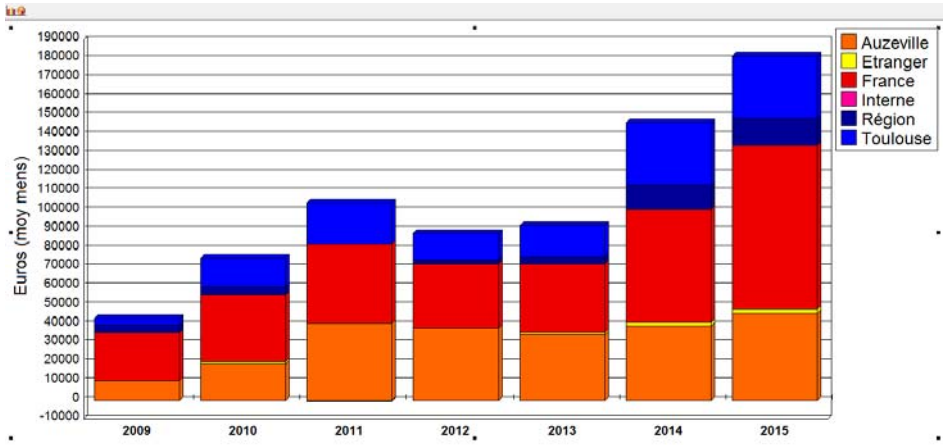
- **Partnership with Genotoul Bioinformatic core-facility (NG6) for:**
  - **Data storage and management**
  - **Data Quality analysis**

ACTIVITY

GeT Génome et Transcriptome

Activity per year

- **15 R&D projects**
  - Mate paired, chipseq, metylation, GBS, 3G NGS, capture, HIC…
- **More than 100 laboratories** (INRA, CNRS, INSA, INSERM, CHU, CIRAD …)
  - More than 160 research teams
  - More than 250 projects
  - 2M€ of activity



Collaboration and partnership

- **17 projects in collaboration (France – Europe)**

  - **CARTOSEQ (2010-2014) INRA : Identification en masse des variants génétiques influençant les caractères d'élevage chez les trois principales races laitières françaises**
  - **FUNHYMAT (2011-2015) Université Pau: Structure et fonctionnement de tapis microbiens contaminés avec des hydrocarbures**
  - **Domestichick (2013-2016) INRA: De la génomique du genre Gallus à l'histoire de la domestication du poulet**
  - **EFFECTOORES (2013-2016) : Exploitation des connaissances sur les effecteurs des Oomycetes pour la recherche de résistances durables aux maladies chez les plantes cultivées**
  - **IMPACT (2014-2016) INRA: Identification of Matrix Proteins Affecting CalciteTexture in chicken and guinea fowls eggshells**
  - **PigLetBiota (2014-2019): Une étude de biologie intégrative de l'influence du microbiote intestinal sur la robustesse des porcelets**
  - **AgENCODE (2015-2016): a French pilot project to enrich the annotation of livestock genomes**
  - **Treasure (2015-2019- H2020): Treatment and Sustainable Reuse of Effluents in semiarid climates**
  - **Bovano (2015-2017): IDENTIFICATION AND FUNCTIONAL STUDY OF CATTLE DELETERIOUS MUTATIONS**
  - **Feed-A-Gene (2015-2020 – H2020) : projet européen pour améliorer l'efficacité alimentaire des monogastriques**
  - **Vaisseaux et Cancer (2013-2016 - INCA) : caractérisation moléculaire des vaisseaux qui contriuent à l'inibition de la croissance tumorale**
  - **SELGEN - GenSSeq: développement et la mise en œuvre des méthodes à haut débit permettant d'estimer la valeur génétique des animaux et végétaux**
  - **Agri-Métatranscriptomique – diversité: Nouvelles perspectives dans l'étude des communautés microbiennes complexes**
  - **HeliOr (2015-2018) : Séquençage du Génome de l'Orobanche et 2ème génotype Tournesol dans le cadre de SUNRISE**
  - **Meta-Pac (2015-2016): Mise au point des analyses de Metagénomique long read**
  - **B-TB (2013 – 2016 ANR) Role of B cells tuberculosis immunity and inflammation.**

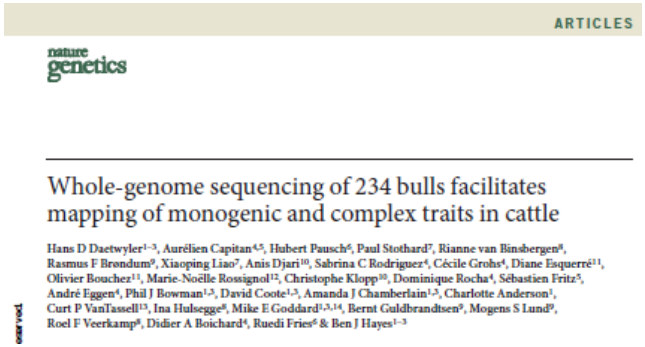
Collaboration and partnership

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

2012 (**14**) : PLoS ONE, NAR, Gene, Current Biology, Developmental and Comparative Immunology, Gene 500, Ecotoxicology, N, Biochimieew Phytologist, FEMS, Ecotoxicology, Nucleic Acids Research, PLOS Genetics, Hepatology

2013 (**13**) : Biotechnology for biofuel, BMC Genomics, Mol Ecol ressources, infection genetics and evolution, PLoS pathogene, BMC, molecular ecology, genome amouncements, molecular phylioenetics and evolution, FEMS, Gastroenterology & Hepatology, Biochem Biophys Res Commun, Front. Microbio

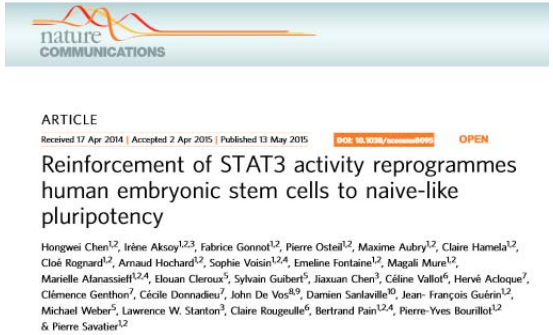
2014 (**19**): nature genetics, BMC Genomics, JAS, Exp and molecular pathology, Gene Nar, Molecular Biology ressources, EMBOJ, Emerging Infectious Diseases, molecular cell, PLoS ONE, PLoS Biol, Poultry science, FEMS, Biochemistry & Molecular Biology, Toxicology, Medecine, Research & Experimental, J Am Soc Nephrol, Pathologie Biologie, Journal of Biotechnology


ARTICLES

nature genetics

Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle

Hans D Daetwyler[1–3], Aurélien Capitan[4,5], Hubert Pausch[6], Paul Stothard[7], Rianne van Binsbergen[8], Rasmus F Brøndum[9], Xiaoping Liao[7], Anis Djari[10], Sabrina C Rodriguez[4], Cécile Grohs[4], Diane Esquerré[11], Olivier Bouchez[11], Marie-Noëlle Rossignol[12], Christophe Klopp[10], Dominique Rocha[4], Sébastien Fritz[5], André Eggen[4], Phil J Bowman[1,3], David Coote[1,3], Amanda J Chamberlain[1,3], Charlotte Anderson[3], Curt P VanTassell[13], Ina Hulsegge[8], Mike E Goddard[1,3,14], Bernt Guldbrandtsen[9], Mogens S Lund[9], Roel F Veerkamp[8], Didier A Boichard[4], Ruedi Fries[6] & Ben J Hayes[1–3]


nature COMMUNICATIONS

ARTICLE

Received 17 Apr 2014 | Accepted 2 Apr 2015 | Published 13 May 2015 OPEN

Reinforcement of STAT3 activity reprogrammes human embryonic stem cells to naive-like pluripotency

Hongwei Chen[1,2], Irène Aksoy[1,2,3], Fabrice Gonnot[1,2], Pierre Osteil[1,2], Maxime Aubry[1,2], Claire Hamela[1,2], Cloé Rognard[1,2], Arnaud Hochard[1,2], Sophie Voisin[1,2,4], Emeline Fontaine[1,2], Magali Muré[1,2], Marielle Afanassieff[1,2,4], Elouan Cleroux[5], Sylvain Guibert[5], Jiaxuan Chen[3], Céline Vallot[6], Hervé Acloque[7], Clémence Genthon[7], Cécile Donnadieu[7], John De Vos[8,9], Damien Sanlaville[10], Jean- François Guérin[1,2], Michael Weber[5], Lawrence W. Stanton[3], Claire Rougeulle[6], Bertrand Pain[1,2,4], Pierre-Yves Bourillot[1,2] & Pierre Savatier[1,2]

TECHNOLOGIES

Tools to improve the activity

- **Sample and library quality controls**



- **Single cell capture (C1 Fluidigm)**

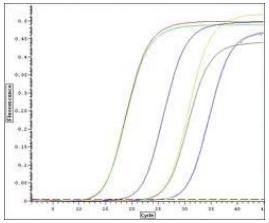

- **Pipetting platforms for sample preparation**
  - **Partnership with Tecan (4 Evo + 1 genesis), Agilent Bravo**
  - **Acces array (fluidigm)**



GeT Génome et Transcriptome

Tools to analyse gene expression and to genotype

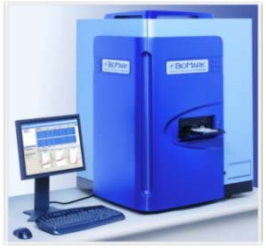
PCR quantitative



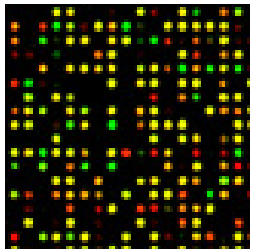
Viia7, QuantStudio, ABI7900HT, …

PCR quantitative microfluidic

BioMark (Fluidigm)



Microarray



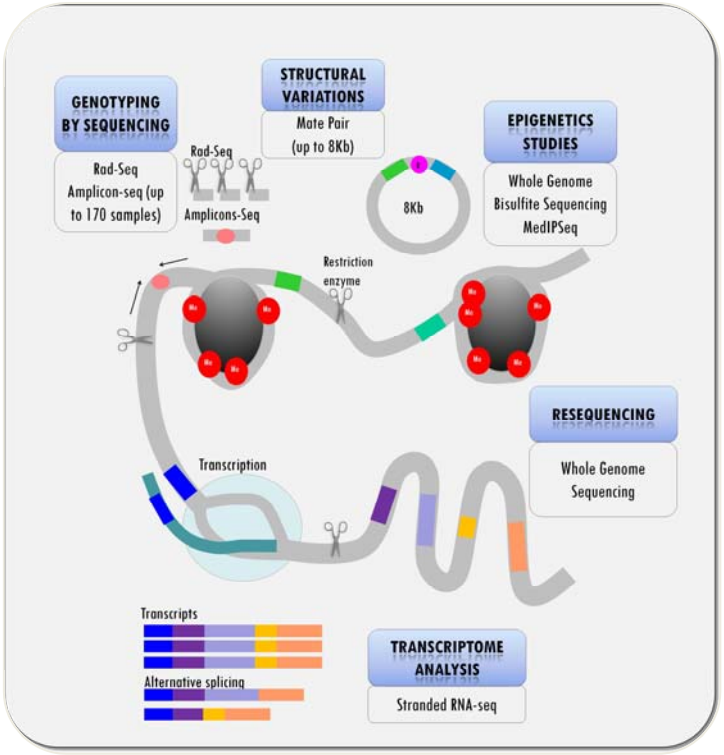
Affymetrix – Agilent iScan

GeT Génome et Transcriptome

From Sanger to short read NGS revolution

400 pb
1Gb

200 pb
13 Gb



2x 300 pb
15 Gb

2x150 pb
700 Gb

From 1 human genome sequencing to....

... « 1000 genomes » projects for all species

GeT Génome et Transcriptome

From NGS short reads to long reads

- **First PACBIO installed in France**

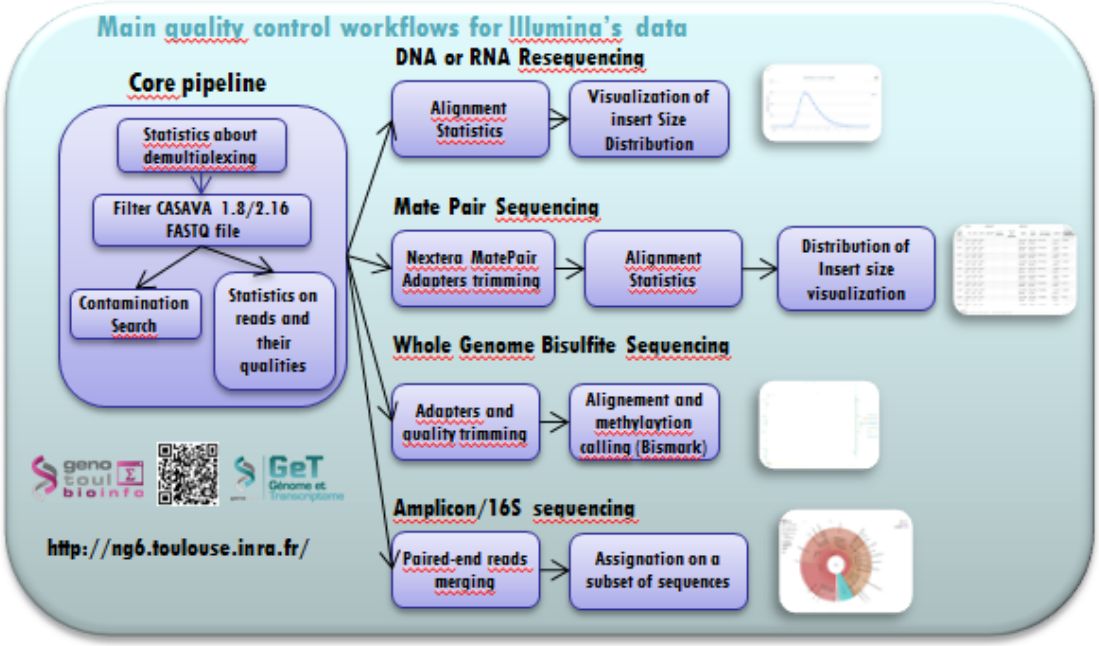
- **SUNRISE project to acquire expertise**
  - To validate quality of DNA
  - To improve librairie preparations
  - To increase the number of reads
  - To increase the length of reads

- **more projects to develop new applications :**
  - Whole genome sequencing on different species
  - Targeted sequencing
  - Complex population
  - RNA sequencing
  - Epigenetic

LIMS

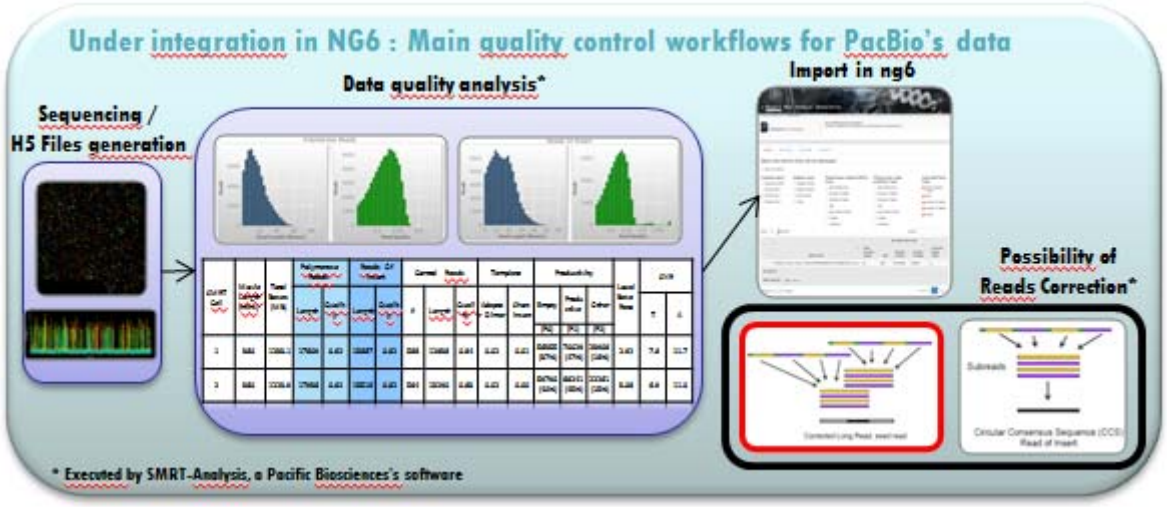
Storage of raw reads and quality control results

- Each step of the process is **tracked** by various modules of our in-house information system.
- Biological samples are uniquely identified using **barcodes**.
- NGS pipelines are provided by **NG6**, an information system built upon the jflow workflow management system



Storage of raw reads and quality control results

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



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

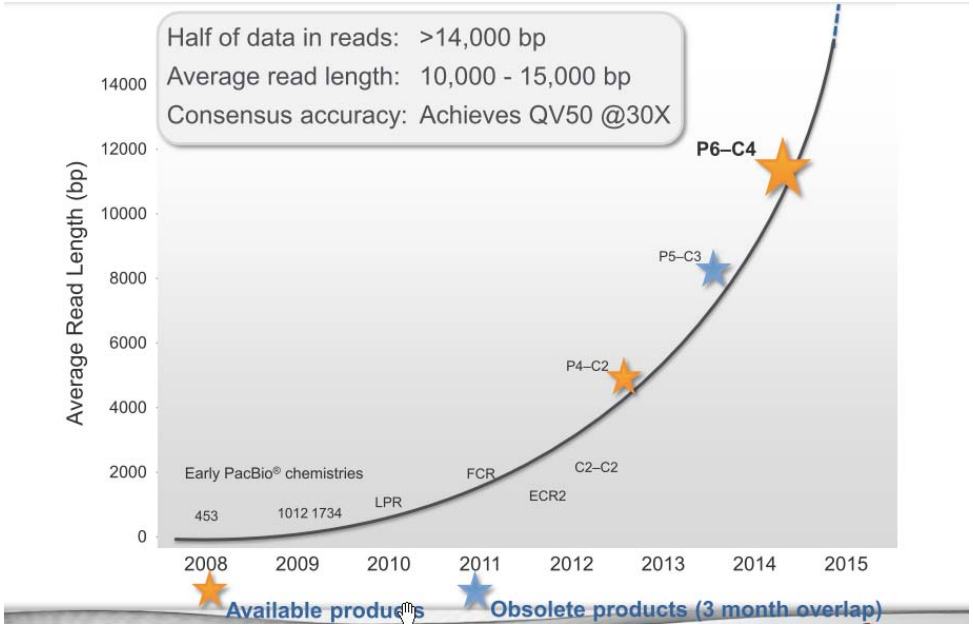
« LONG READ SEQUENCERS»

GeT Génome et Transcriptome

Principle of PACBIO RSII

- No PCR
- Native Enzyme
- Real-Time (SMRT®) technology

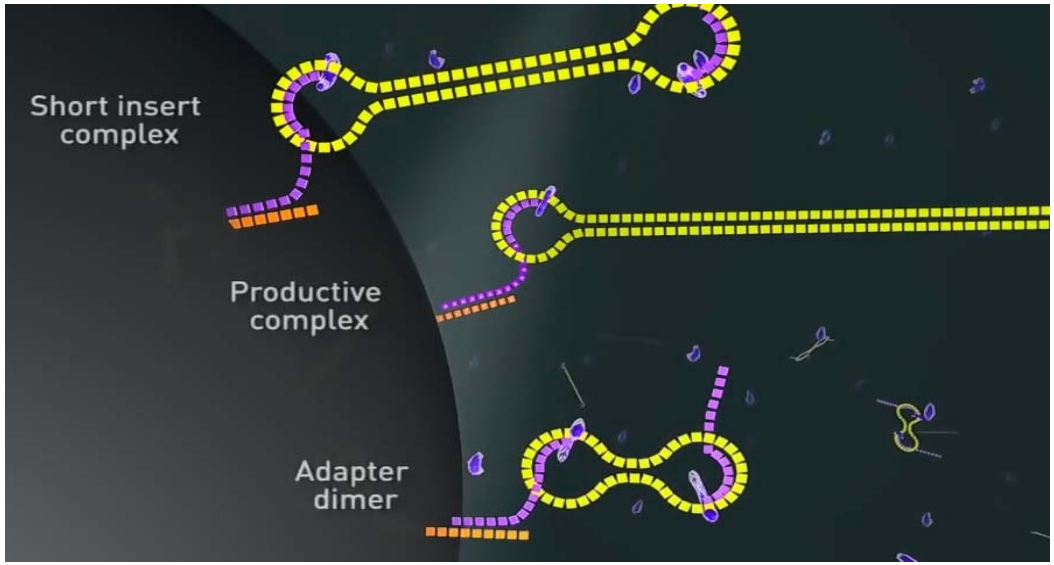
- Phospholinked nucleotides
- A technological revolution with P6-C4 chemistry
  - >10kb, 6h
  - Access to complex genomes



First equipment in France installed in Toulouse in March 2015

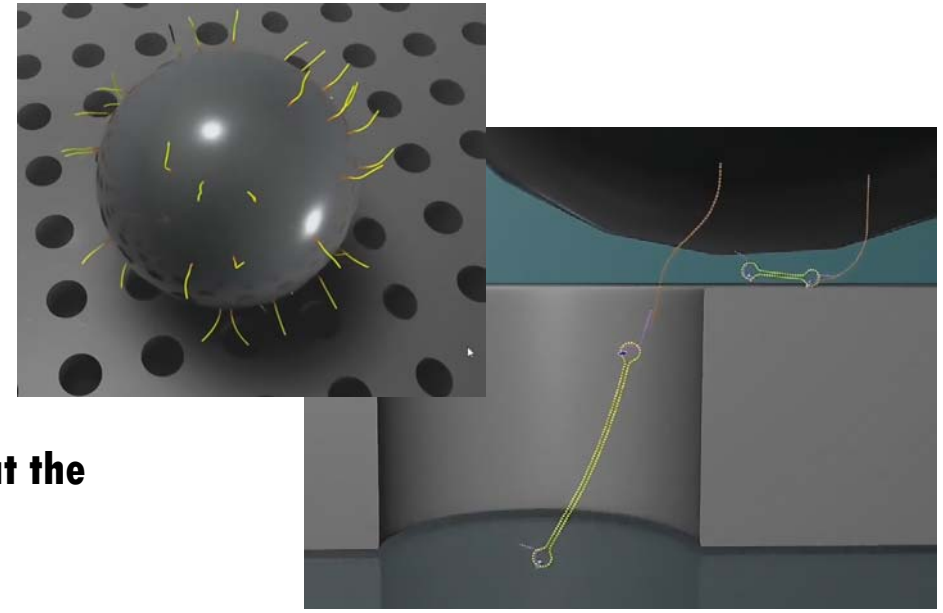
(Europeen and "Midi-Pyrénées" funding program)

Principle of PACBIO RSII



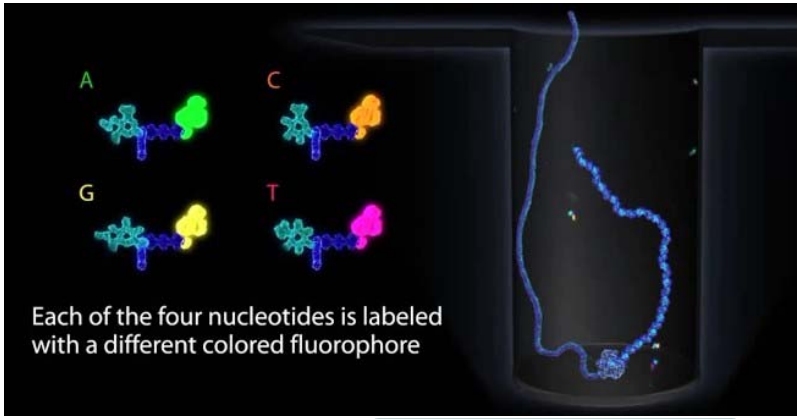
Principle of PACBIO RSII

- 1 SMRTcell
- 150 000 Zero-Mode Waveguides (ZMWs)
- 50 000 to 70 000 usable ZMW

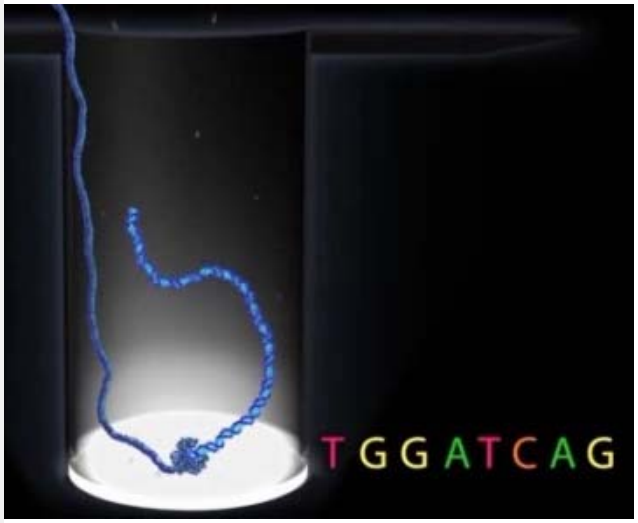


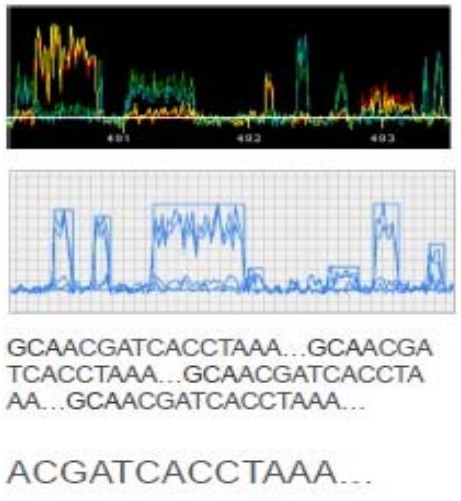
- DNA polymerase complex is immobilized at the bottom of the ZMW

- Nucleotides incorporation and release of the attached fluorophore

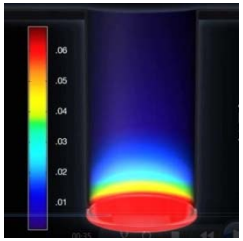


Principle of PACBIO RSII



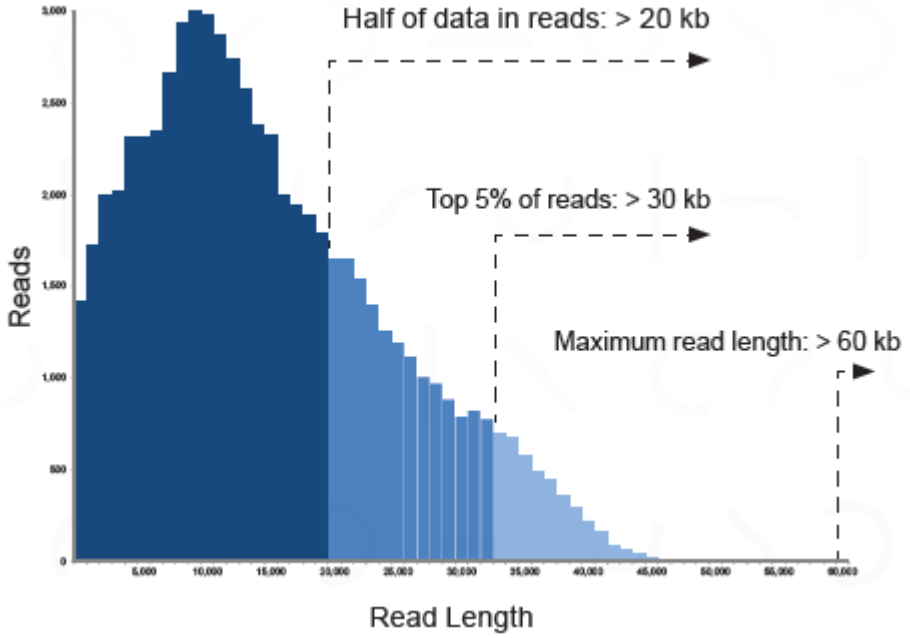


- **Laser illuminates the ZMW from below and capture the fluorophore signal**
- **Read of the sequence in real-time**
- **Translation of the signal according to intensity and length of signal**
- **Format of files H5 and fastq**



Specification of PACBIO RSII

- DNA : 10µg of high molecular weight level *
- Data per SMRT Cell: 500 Mb – 1,2 Gb
- Read length > 15 kb
- Error : 15% random (insertion – deletion)
- Run time : 4 to 6h
- Runs per week : 16 to 32 SMRTcell (mini 8)
- 3,7pb/s
- Reagent Cost : 500€/SMRTcell



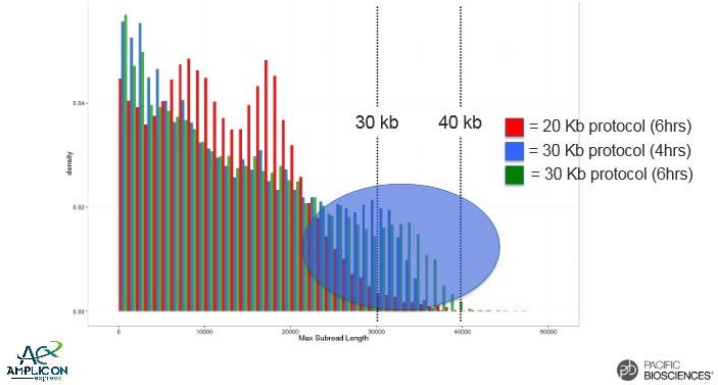
Benefits and Disavantages RSII

- **Benefits**
  - **Good Results : to small genome (Mb) to complex genome >3Gb**
  - **Uniform coverage : high % of GC, repeated sequences, …**
  - **Error : random**
  - **Accuracy : function of coverage**
  - **Variety of analysis methods available through SMRT Software**
  - **No need to combine with short read data**
  - **Simultaneous Epigenetic Characterization**

- **Disadvantages**
  - **High molecular weight level : difficult for some species**
  - **High % of Error : need a high coverage**
  - **Low production : 3Gb 100X =20 week**
  - **High reagent price : 3Gb 100X = 150k€**

2016-2017

- **30% of reads >30kb : new protocol on PACBIO RSII**



- **Sequel system**
  - **System ~2X less : 350k€**
  - **Generates ~7X more reads : 7Gb per SMRTcell**
  - **Reagent coast ~2/4X less / Gb**

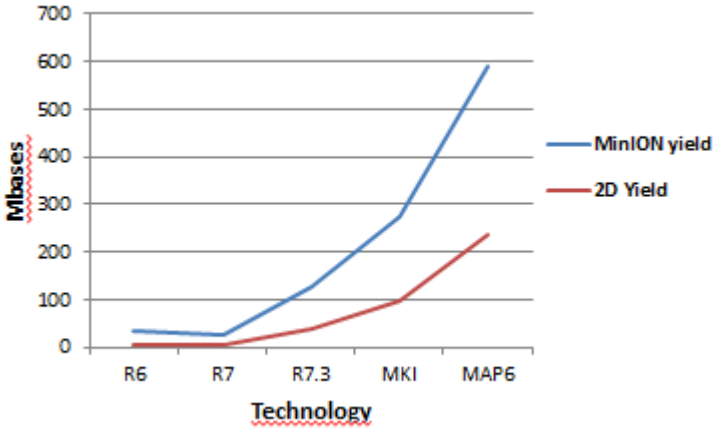
- **In 2016, 5 Sequel systems will be installed in France Genomic core-facilities (France Genomique)**

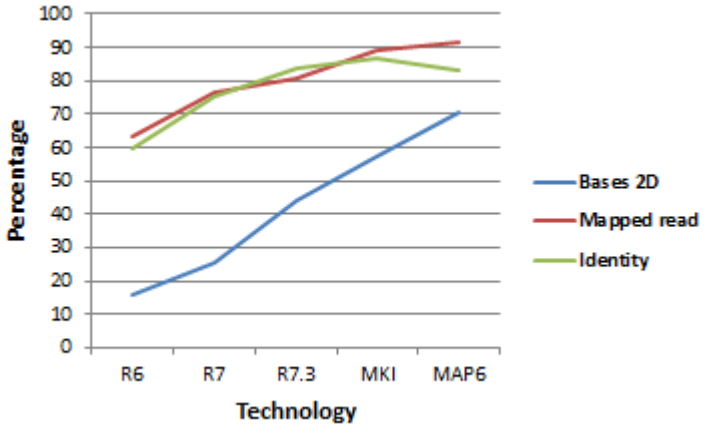
Principle of Oxford nanopore

- A pocket sequencer
- Single strand DNA is passed through a nanopore
- Motrice Enzyme and nanopore reader (transposase)

- Detection of variation of current when DNA moves through the pore

- Fast evolution of the technology





Principle of Oxford nanopore

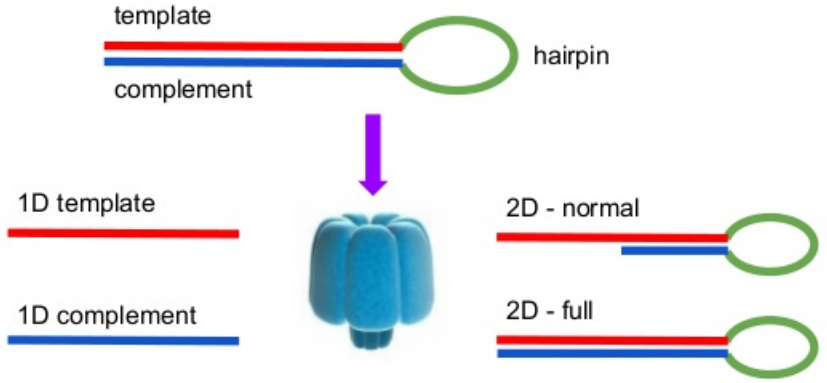
- 1 Minion
- 512 circuits (4 pores/circuits)

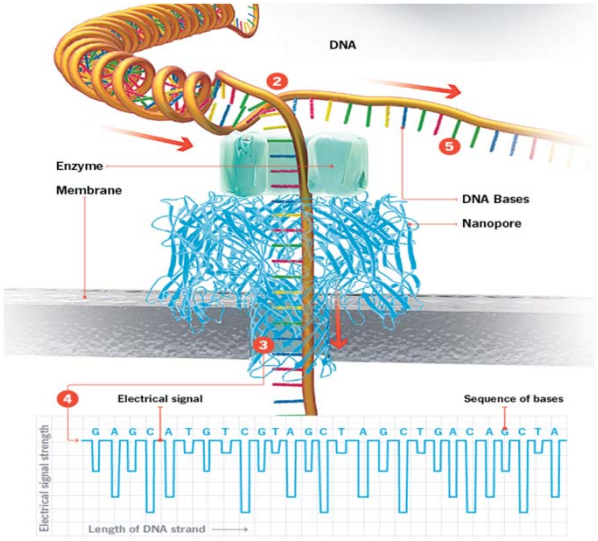
- DNA preparation :1D or 2D
- DNA capture : by motor enzyme

- Run time: 48h it's possible to sequence several samples in the same run

- Signal : measures 6 bases simultaneously
- R7: 70 b/s

- Basecalling : on Oxford cloud
- Files format: H5 and fastq

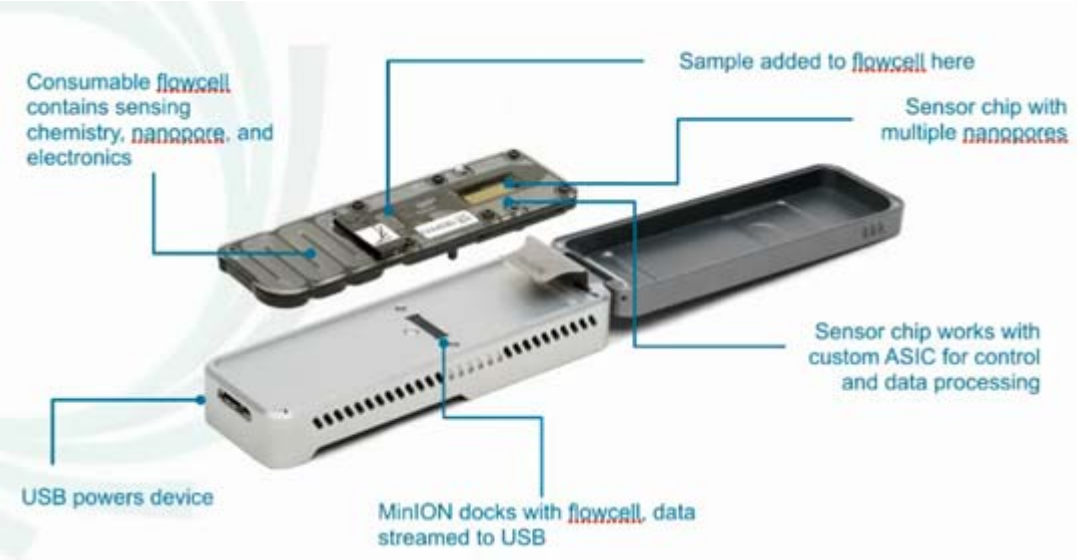




Specification of Oxford nanopore

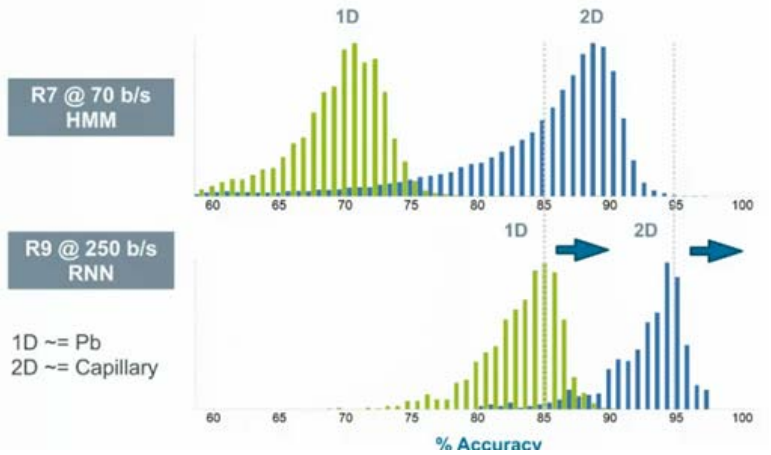
- **DNA : of high molecular weight level ***

- **Data per Minion R7: 600Mb 1D – 250Mb 2D**
- **Read length R7: 8kb**
- **Error R7: 15% D2 not random**
- **Run time : 48h**
- **Run per week : 3**
- **Reagent Cost : 500€/Minion**



Benefits and Disavantages

- **Benefits**
  - **Promising technology… constantly changing**
  - **Interesting for small genome : 12 – 25Mb (Genoscope)**
  - **Easy to install**
  - **Cheap technology**



- **Disadvantages**
  - **No random error**
  - **Basecalling on Oxford cloud**
  - **Unsuitable for complex genome**
  - **Need to be combined with short read data**

Promising technology

	Mk 1 MinION R9	Single PromethION Flow Cell	PromethION (48 Flow Cells)
Number of channels available for sequencing	Up to 512	Up to 3,000	Up to 144,000
Run time[4]	1 minute - 48 hours	1 minute - 48 hours	1 minute - 48 hours
Flow cell lifetime[4]	~72hrs	>= 72hrs	>= 72hrs
Number of reads at 10Kb at standard speed (280bps)[4]	Up to 2.5M	Up to 14.5M	Up to 700M
Number of reads at 10kb in Fast Mode (500bps)[4]	Up to 4.4M	Up to 26M	Up to 1250M
Read Length	8kb	no limit	no limit
1D Yield[5] at 280 bps in 48 hours	2Gb	Up to 145 Gb	Up to 7 Tb
1D Yield[5] at 500 bps in 48 hours	4Gb	Up to 256 Gb	Up to 12 Tb
Base calling accuracy[6]	85% 2D	Up to 96%	Up to 96%
Flow Cell Cost (depending on order type and volume)[8]	$500- $900	POA	POA
Instrument Access Fee	Starter kit $1000	$75K	$75K

GENOSCOPE

genotoul

GET
Génome et
Transcriptome

Sample preparation

Blocking Agents

- Polysaccharides
- Lypopolysaccharides
- Growth media residuals

- Chitin
- Fats
- Proteins
- Pigments

- Chitin
- Protein
- Secondary metabolites
- Pigments
- Growth media residuals

- Polyphenols
- Polysaccharides
- Secondary metabolites
- Pigments

Prerequisite for PACBIO RSII

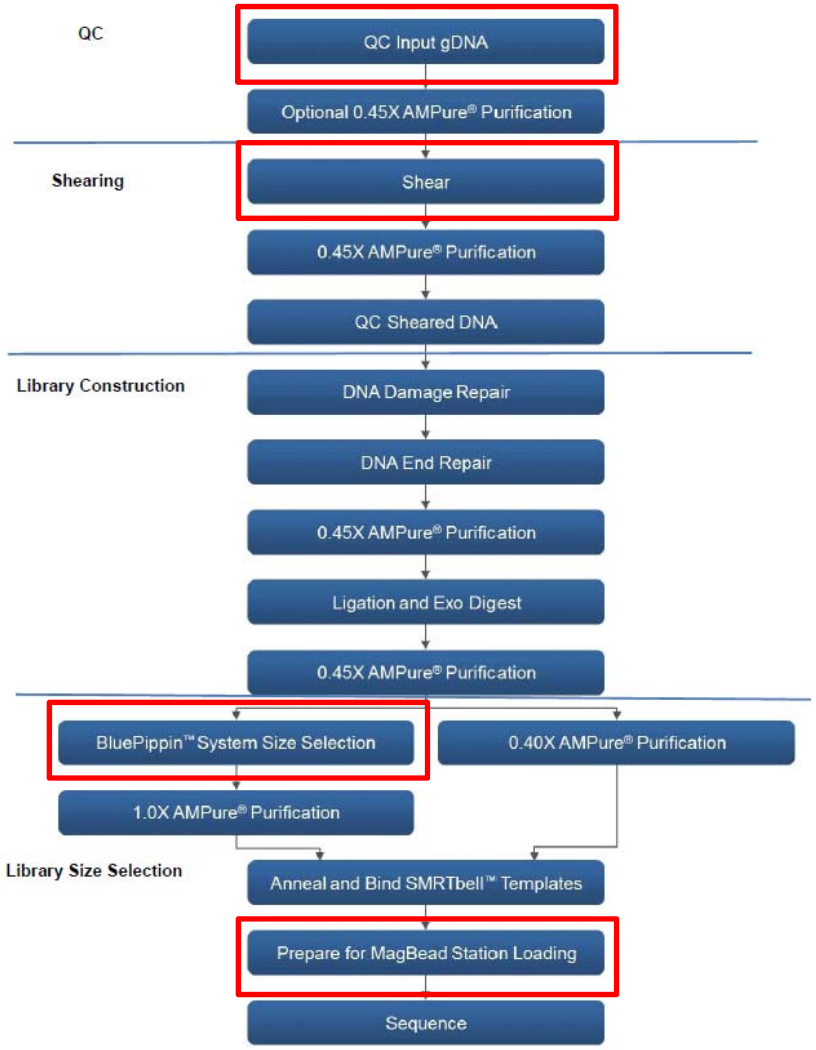
- **Extraction kit advise by Pacific Bioscience**
  - **Qiagen MagAttract HMW kit - Qiagen Genomic-tip kit - Qiagen Gentra Puregene**

- **Quantity (Picogreen/QuBit) : >10 µg DNA for 1 library**
- **Purity (Nanodrop) :**
  - **260/280 : 1.8-2**
  - **260/230 = 2-2,2**

- **Size >50kb perfect**

- **Advice:**
  - **No Freezing – Defreezing**
  - **No temperature >65°C**
  - **No extreme pH (<6 ou>9)**
  - **No vortex**
  - **No fluorescent or ultraviolet**

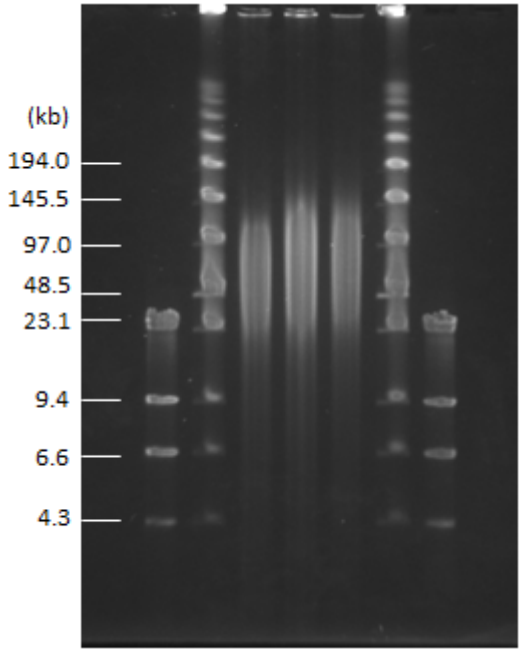
Library process on GeT core facility



- **4 systematic different QC "GeT" core-facility**
  - **Capillary electrophoresis – Fragment Analyser (50kb)**
  - **Pulsed Field – Pippin Pulse**
  - **Spectrometrics based – nanodrop**
  - **Intercalent based – Qubit**
- **Shearing with Megaruptor**
- **Size selection with Blue pippin**
- **DNA is a living element, it will evolve during the process**

Example for Fish – 900Mb – 54X – 48 SMRT

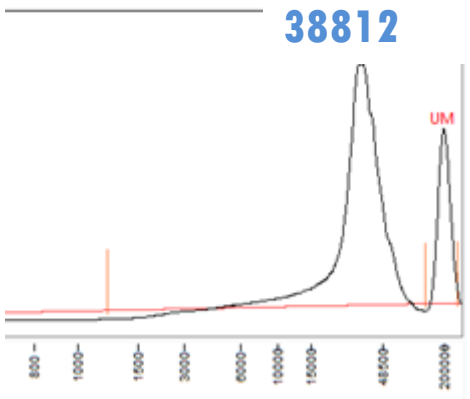
Pulsed Field



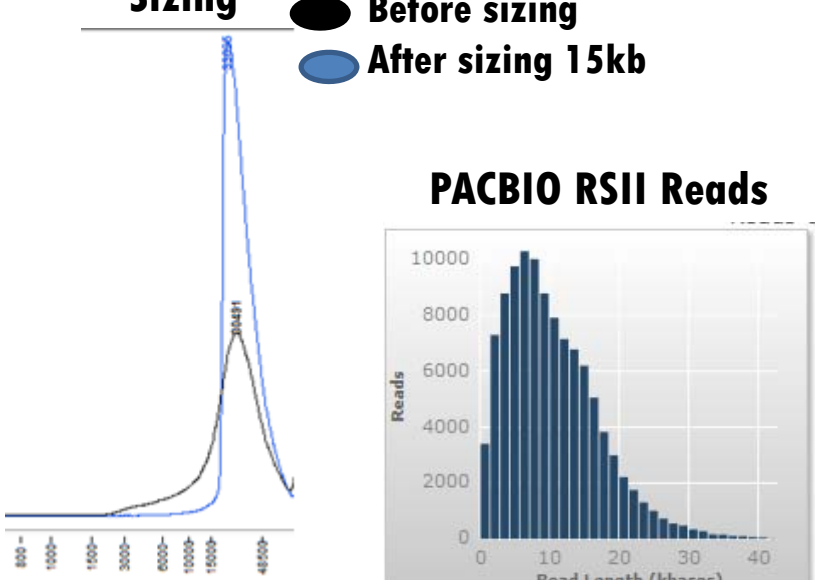
Spectrometrics - Intercalent

Sample ID	Conc.	Units	260/280	260/230	Cursor abs.	Qbit 1/10		Valeur	
javf3	317,7	ng/ul	1,84	1,95	6,354	47,4	ng/ul	474	ng/ul

Fragment Analyser



Sizing



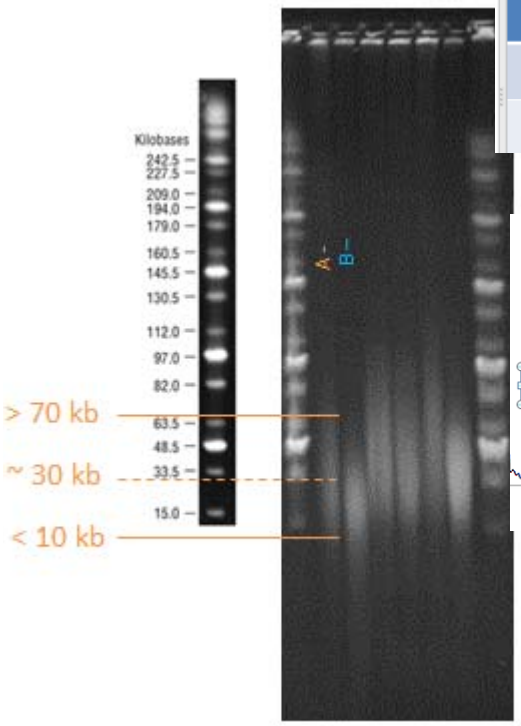
PACBIO RSII Reads

PACBIO RSII Run

Total Bases (MB)	Polymerase Reads		Reads Of Insert		Control Reads			Template		Productivity		
	Length	Quality	Length	Quality	#	Length	Quality	Adapter Dimer	Short Insert	Empty (P0)	Productive (P1)	Other (P2)
1398.82	12990	0.84	10816	0.85	161	21196	0.86	0.03	0.01	12239 (8%)	107685 (72%)	30368 (20%)

Exemple for Phytoplancton – 13Mb – 120X – 3SMRT

Pulsed Field



CNRGV 151014

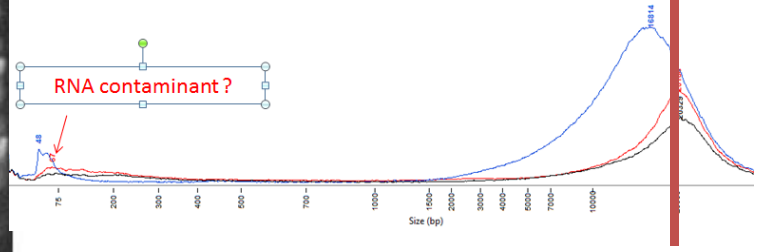
Spectrometrics - Intercalent

RNA contaminant ?

Sample name	Qubit Concentration (ng/µL)	NanoDrop Concentration (ng/µL)	Volume (µL)	Quantity (µg) (Qubit)	A260/280	A260/230	Length (pb) (Fragment analysis)
A	65	116	80	5,2	2,01	2,2	18068
B	100	167	50	5	2,02	1,97	15270

Fragment Analyser

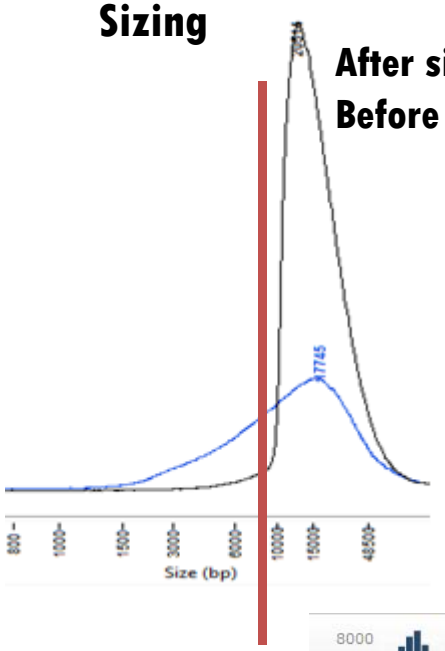
A : 19,1 kb
B : 15,2 kb



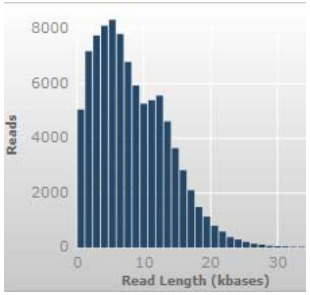
20kb

Sizing

After sizing 9kb
Before sizing



9kb



PACBIO RSII Run

Total Bases (MB)	Polymerase Reads		Reads Of Insert		Control Reads			Template		Productivity		
	Length	Quality	Length	Quality	#	Length	Quality	Adapter Dimer	Short Insert	Empty (P0)	Productive (P1)	Other (P2)
1028.44	11188	0.85	8640	0.86	419	17781	0.85	0.03	0.01	42865 (29%)	91924 (61%)	15503 (10%)

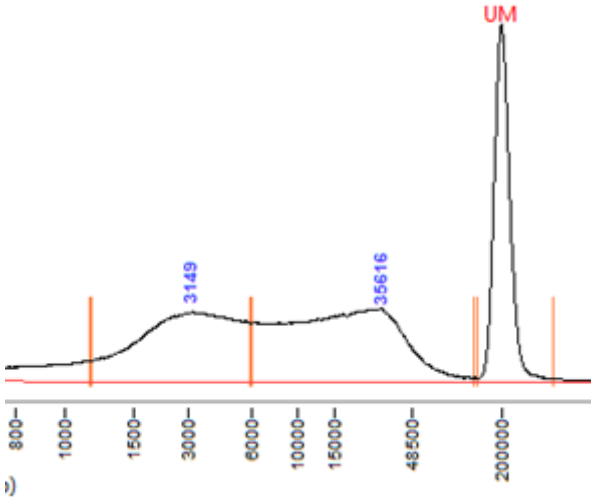
PACBIO RSII Reads

Bouillon of bacterial culture – 5-9Mb - ?- 5SMRT

Spectrometrics - Intercalent

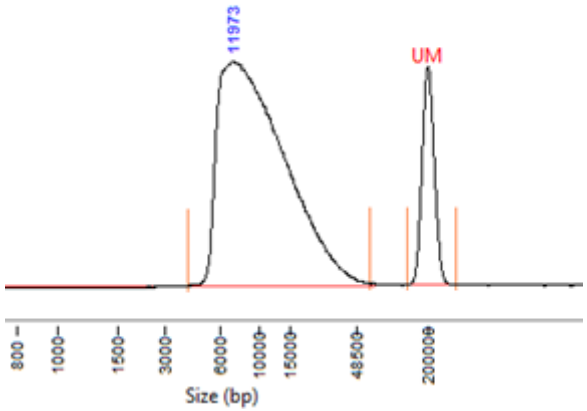
	Nanodrop						Qbit (ng/µl)	
Sample ID	Conc.	Units	A260	A280	260/280	260/230	dil 1/5	Echantillon
[illegible] XI-2013	43,3	ng/ul	0,866	0,416	2,08	0,93	2,42	12,1

Fragment Analyser

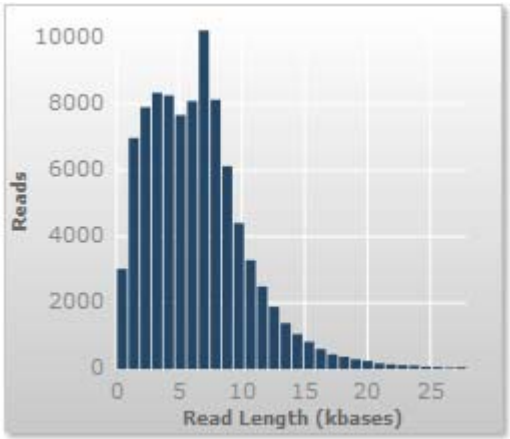


Sizing

After sizing 6kb



PACBIO RSII Reads



PACBIO RSII Run

Total Bases (MB)	Polymerase Reads		Reads Of Insert		Control Reads			Template		Productivity		
	Length	Quality	Length	Quality	#	Length	Quality	Adapter Dimer	Short Insert	Empty (P0)	Productive (P1)	Other (P2)
1135.39	12184	0.84	6775	0.86	180	18681	0.83	0.01	0.00	12961 (9%)	93189 (62%)	44142 (29%)

genotoul

GET
Génome et
Transcriptome

More results on sunflower

Nicolas Langlade, Stephane Munoz, Jérôme Gouzy,
Baptiste Mayjonade,

Lipm
Laboratoire Interactions Plantes Micro-organismes

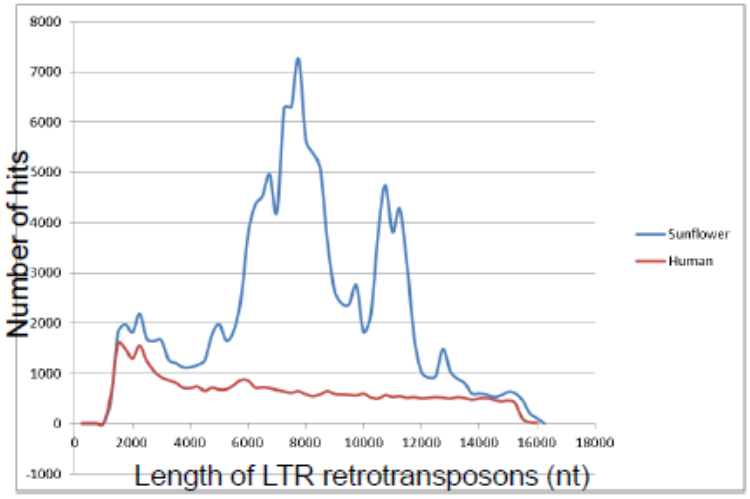
SUNRISE
UNE CULTURE POUR LE FUTUR

SOFIPROTEOL
L'engagement durable

Goals of the project

- **Improve the sunflower genome assembly of the XRQ line by sequencing :100X depth with PacBio sequences only.**
- **Diploid with 2n = 17 chromosome pairs,**
- **3.6Gb,**
- **Lot of repeated sequences : large 9-12kb and highly conserved.**

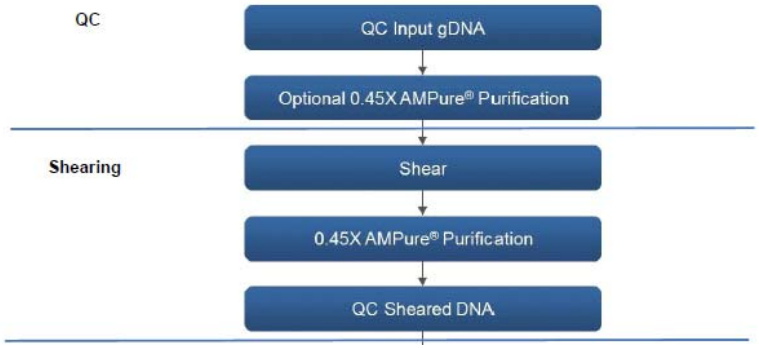
Analysis of the composition ot the LTR retrotransposons with LTRharvest (D. Ellinghaus *et al.* 2008, default parameters)



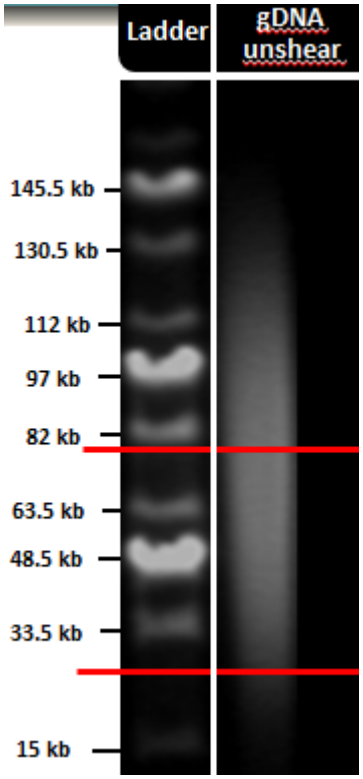
30% of the sunflower genome sequence is composed of LTR retrotransposons.

8.8% of the human genome.

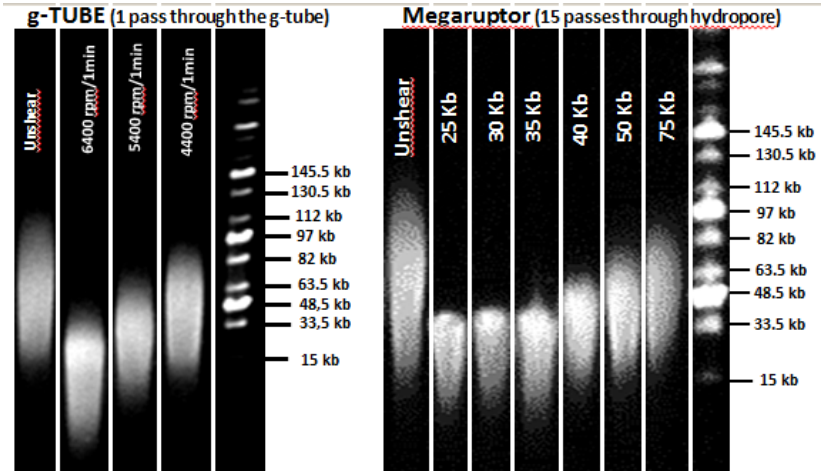
Improvement of large insert library prep



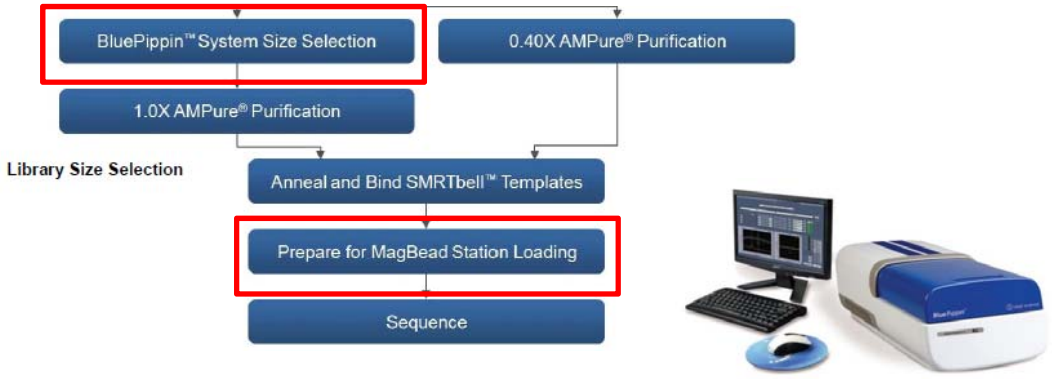
- **High molecular weight DNA (50 to 100kb)**



- **Shearing with megaruptor**

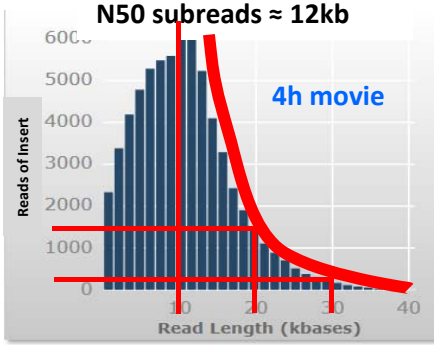


Improvement of large insert library prep

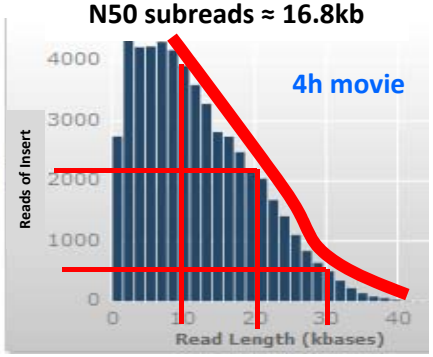


Size selection cutoff	% Recovery (bluepippin input ≈ 4µg)	Migration time
10kb (High pass 6-10kb)	55-65%	2h
15kb (High pass 15-20kb)	40-48%	3-4h
18kb (High pass 15-20kb)	30-35%	4-5h
20kb (High pass 15-20kb)	18-20%	4-5h
30-40kb High pass 30-40kb	????	????

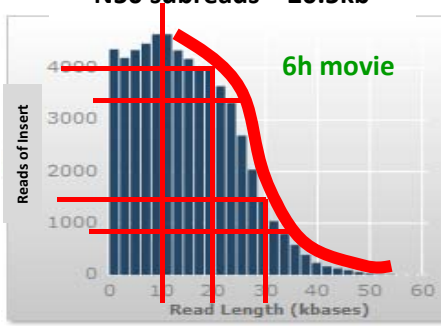
12kb cut off
(loading 0.15nM= 868Mb)
N50 subreads ≈ 12kb



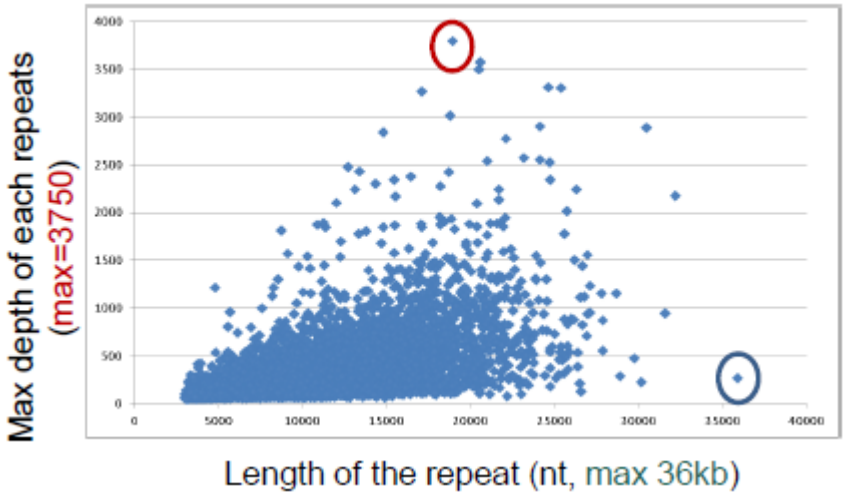
18kb cut off
(loading 0.30nM= 710Mb)
N50 subreads ≈ 16.8kb



20kb cut off
(loading 0.45nM= 1000Mb)
N50 subreads ≈ 20.5kb



Final Results



Top 10 of our longest subreads
80974 bp
79860 bp
79834 bp
78105 bp
77481 bp
76881 bp
76558 bp
76355 bp
75569 bp
75559 bp

- **INRA (Team Sunflower) :**
  Hiseq 127 X → 43 % coverage
- **International project : 454, Hiseq, Genetic and physical map (finger printing of the BAC clones) → 63 % coverage**
- **INRA (Team Sunflower)) :**
  PacBio 107 X (407 SMRT)
  → 84 % coverage
  3,03Gb
  13124 contigs N50 = 498 kb
  +90 % anchored

THANKS

GeT-PlaGe Team

Denis Milan
Gerald Salin
Olivier Bouchez
Diane Esquerre
Anne Fleurbe
Sandra Fourre
Isabelle Hochu
Céline Vendecastel
Dounia Ben Salah
Claire Kuchly
Gaelle Vilchez
Catherine Zanchetta
Marie Vidal
Pauline Heuillard
Céline Jeziorski
Clémence Genthon
Maarten Pirson
Alain Roulet
Céline Roques
Adeline Chaubet
Fréderic Toppan

LIPM Team

Jérôme Gouzy
Nicolas Langlade
Munos Stéphane
Chris Grassa
Sébastien Carrere
Erika Sallet
Ludovic Legrand
Marie-Claude Boniface
Nicolas Pouilly

GeT-BioPuce

Marie-Ange Teste
Lidwine Trouilh
Nathalie Marsaud
Delphine Labourdette
Sophie Lamarre
Matthieu Guionnet

GeT-TRIX Team

Yannick Lippi
Claire Naylies

GeT-TQ Team

Jean-José Maoret
Frédéric Martins

GeT-Purpan Team

Nicolas Borot
Nathalie Jonca
Emeline Lhuillier
Marion Roy

GeT Génome et Transcriptome

Programme de la journée du 27 mai 2016

https://seminaire.inra.fr/pacbio-get-plage

9h Accueil

- 09h20 – 09h30 Evolutions de la plateforme GeT en 2016 - Denis Milan (INRA Directeur Scientifique GeT)
- 09h30 – 09h40 Qualité des matrices et prérequis - Alain Roulet (INRA GeT-PlaGe)

Session De novo

- 09h45 – 10h15 Les génomes complexes du tournesol (3.6Gb) et de sa plante parasite Orobanche cumana (2Gb), assemblés grâce à la technologie PacBio - Jérome Gouzy (INRA Toulouse LIPM)
- 10h15 – 10h45 Chromosome plasticity in the smallest Photosynthetic Eukaryotes Ostreococcus (Chlorophyta) - Gwenaël Piganeau (Observatoire Océanologique de Banyuls sur mer)
- 10h45 - 11h15 Pause
- 11h30 - 12h00 Yann Guigen (INRA Rennes, Fish Physiology and Genomics)
- 12h00 - 12h30 Retour d'expérience sur le séquençage de Bac en PacBio chez la poule et le porc - Valérie Fillon & Yvette Lahbib-Mansais (INRA Toulouse GenPhySE)
- 12h30 - 13h00 Oxford Nanopore Technology : Données et applications - Jean-Marc Aury (Institut de Génomique - Genoscope, Evry)

13h00 – 14h00 Repas sur GeT-PlaGe

Session Meta-genomique

- 14h00 – 14h30 En attente confirmation
- 14h30 - 15h00 De novo assembly of individual bacterial genomes from the seed microbiome - Mathieu Barret (INRA Angers IRHS)

Session Autres applications PACBIO

- 15h00 - 15h30 IsoSeq : transcriptomic analysis using long reads - Christophe Klopp (INRA Toulouse Plateforme Bioinformatique)
- 15h30 – 16h00 En attente confirmation
- 16h00 - 16h15 Pause
- 16h15 - 16h45 En attente confirmation

Ouverture ...

- 16h45 - 17h15 Mise en place d'un nouveau protocole sur la plateforme: le séquençage 3D avec l'Hi-C - Sylvain Foissac (INRA Toulouse GenPhySE)
- 17h15 - 17h45 En attente confirmation

Principle of oxford nanopore