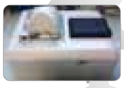
Making Our Lives Easier: NGS Goes Automatic

Olivier Bouchez[1], **Diane Esquerré**[1], Emeline Lhuillier[1], Johanna Barbieri[1], Céline Jeziorski[1], Sophie Valière[1], Clémence Genthon[1], Marie Vidal[1], Cemile Ant[2], David Rodarie[2], David Rengel[3], Gérald Salin[1], Frédéric Escudié[1], Claire Kuchly[1], Cécile Donnadieu[1] and Denis Milan[1].
1 : INRA, UMR444 LGC, GeT-PlaGe Genomics Facility, Castanet-Tolosan. France. 2 : TECAN SASU, Lyon, France. 3 : INRA, UMR441 LIPM, Castanet-Tolosan, France.

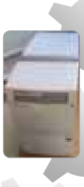
With the standardization of Next Generation Sequencers, such as Illumina HiSeq2000 and MiSeq, for genomics, transcriptomics and epigenetics and their growing output, the challenge is in the sequencing at the same time, in a single run, of more and more samples of any kind. If we want to benefit from this very high throughput and the many related applications, we have to achieve a high multiplexing level, the bottleneck being the manual preparation of the libraries. To get rid of this time-consuming task, we developed at the INRA GeT-PlaGe facility an automated process to produce in parallel more libraries on an automated line composed by 3 TECAN liquid handling robots: an EVO200 for pre PCR library preparation, an EVO150 for post PCR processing and pooling and a TECAN150 for library quantification. Currently, several protocols are completely automated allowing library preparation for Whole Genome sequencing, Rad-seq, Amplicon sequencing (e.g. 16S sequencing on MiSeq in metagenomic studies) and stranded RNA seq. Some applications such as Mate-Pair and Whole Genome Bisulfite sequencing are partially automated at the moment.

Template QC



Nanodrop ND8000

Picogreen on ABI7900HT or QuBit



Agilent BioAnalyzer

Library preparation

Pre PCR steps TECAN EVO200

Post PCR purifications TECAN EVO150

Library QC

Agilent BioAnalyzer

QPCR controls TECAN Genesis 150 & ABI7900 HT

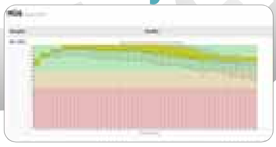
Sequencing

Automatic Sample Sheet generation

HiSeq 2000/2500 x2

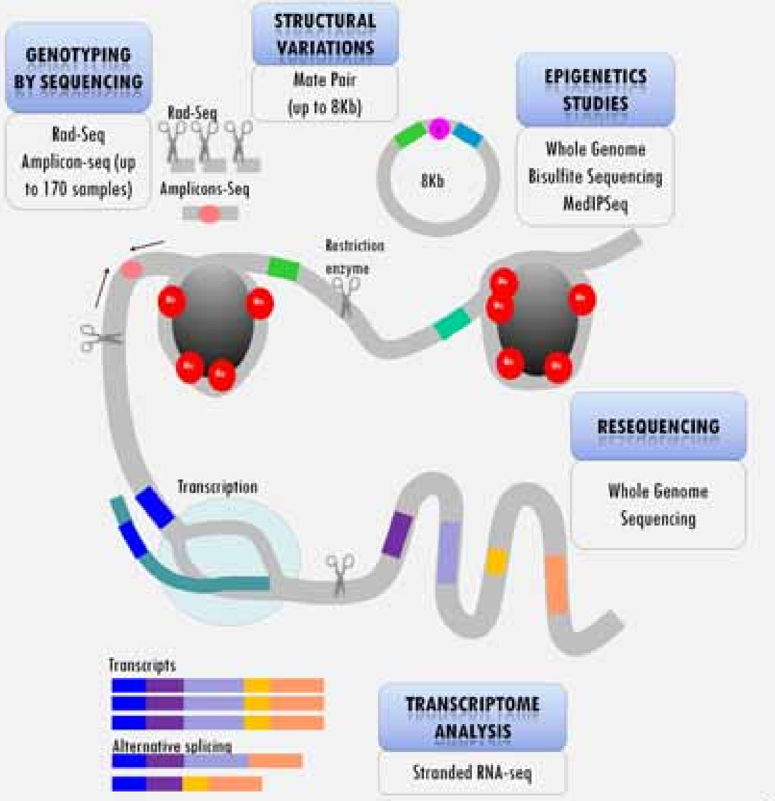
MiSeq x 1

Data quality analysis



Data available on a common website with Genotoul Bioinformatics Platform http://ng6.toulouse.inra.fr/

Automated or semi-automated applications



GENOTYPING BY SEQUENCING
Rad-Seq
Amplicon-seq (up to 170 samples)

STRUCTURAL VARIATIONS
Mate Pair (up to 8Kb)

EPIGENETICS STUDIES
Whole Genome Bisulfite Sequencing
MedIPSeq

RESEQUENCING
Whole Genome Sequencing

TRANSCRIPTOME ANALYSIS
Stranded RNA-seq

http://get.genotoul.fr/