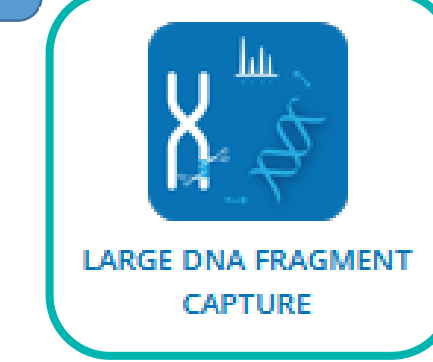
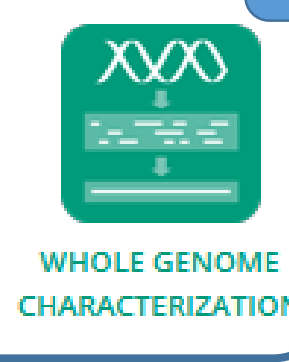
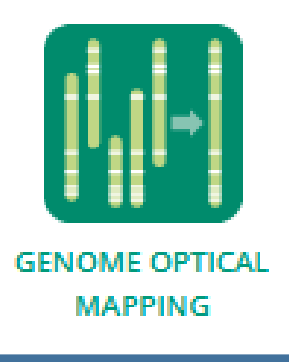
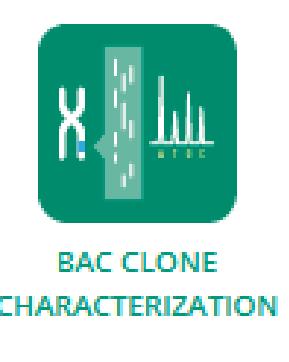
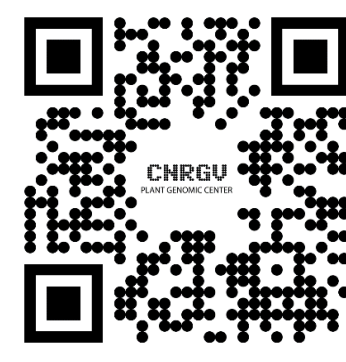


# Genetic Diversity Analysis using Targeted sequencing : Tools and Strategies

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Poster  
#53420



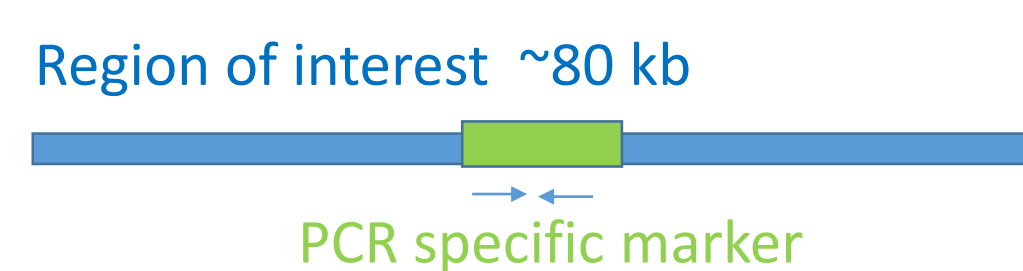
Gaining access to **plant genome assemblies** enhances our comprehension of the **diversity** within plant species. The large cost reduction of a genome sequence production enables the access to biodiversity, but the **exploration of intra-species variability within a region of interest** and even more for large genome is **still costly**. Therefore the utilization of **targeted enrichment methods** stands out as a strategic approach for **biodiversity analysis of larger panel**. This method offers precise and reliable information to link a genomic region to a trait of interest carried by a specific genotype.

The french genomic center (**CNRGV**), offers **two new strategies** for efficiently **targeting large regions of interest in complex plant genomes**. The first one is based on a microfluidic-based system, Xdrop from **Samplix®**, that allows the enrichment of targeted long DNA molecules starting from only a few nanograms and one PCR marker.

We explore this technology by screening a diversity of sunflowers for a large locus (150kb) implicated in the resistance of broomrape.

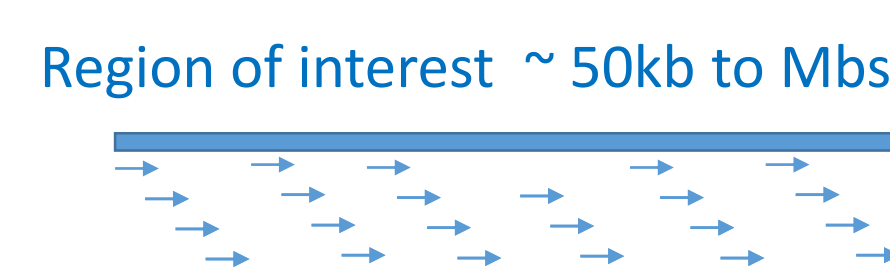
In a second hand, we investigate the potential of **Twist BIOSCIENCE** target enrichment solution. A panel of 90 probes was designed to cover the locus KTR 2/3 (size of 63 kb) involved in the resistance of anthracnose (*Colletotrichum lindemuthianum*) on common bean.

Samplix

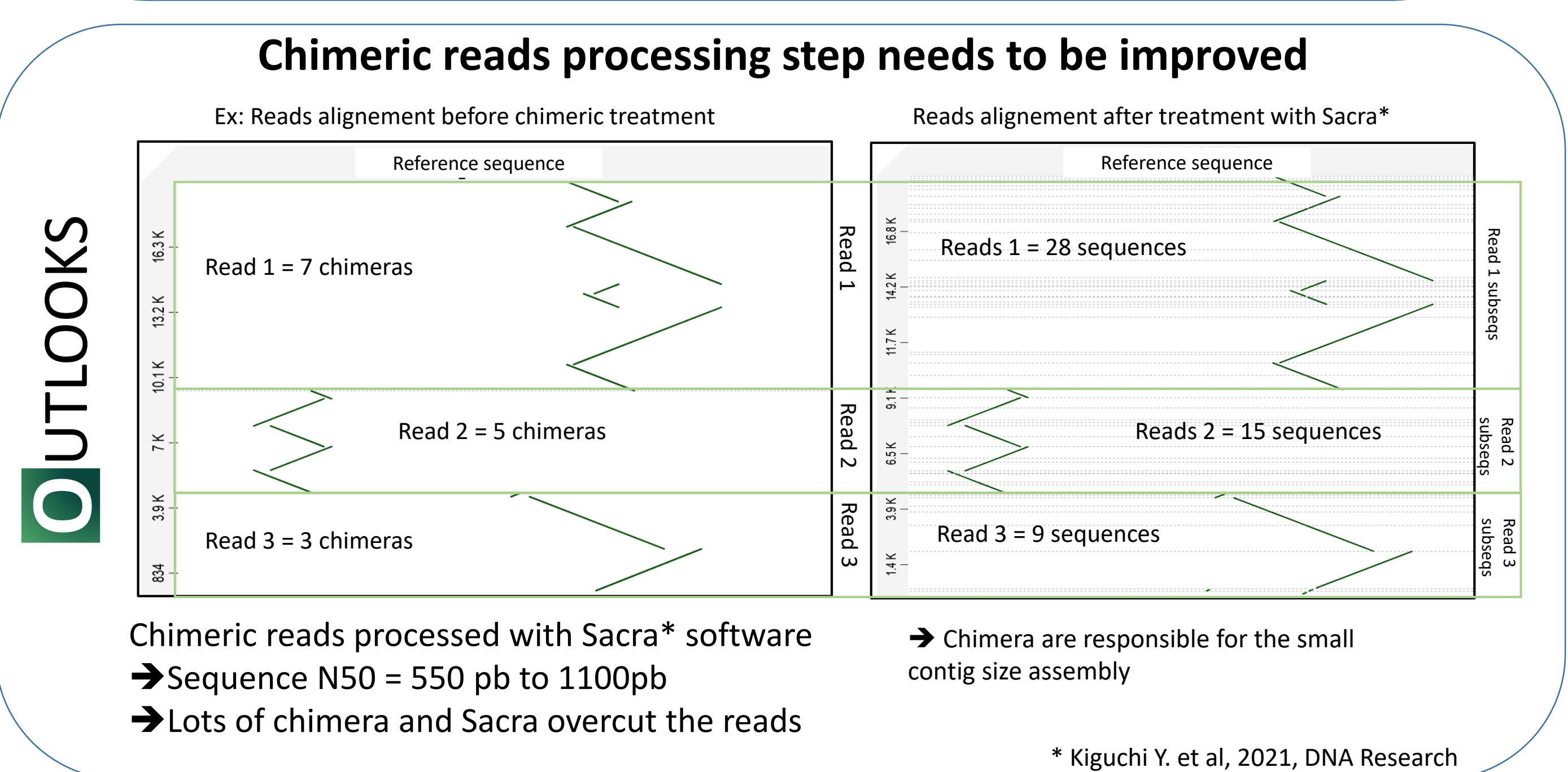
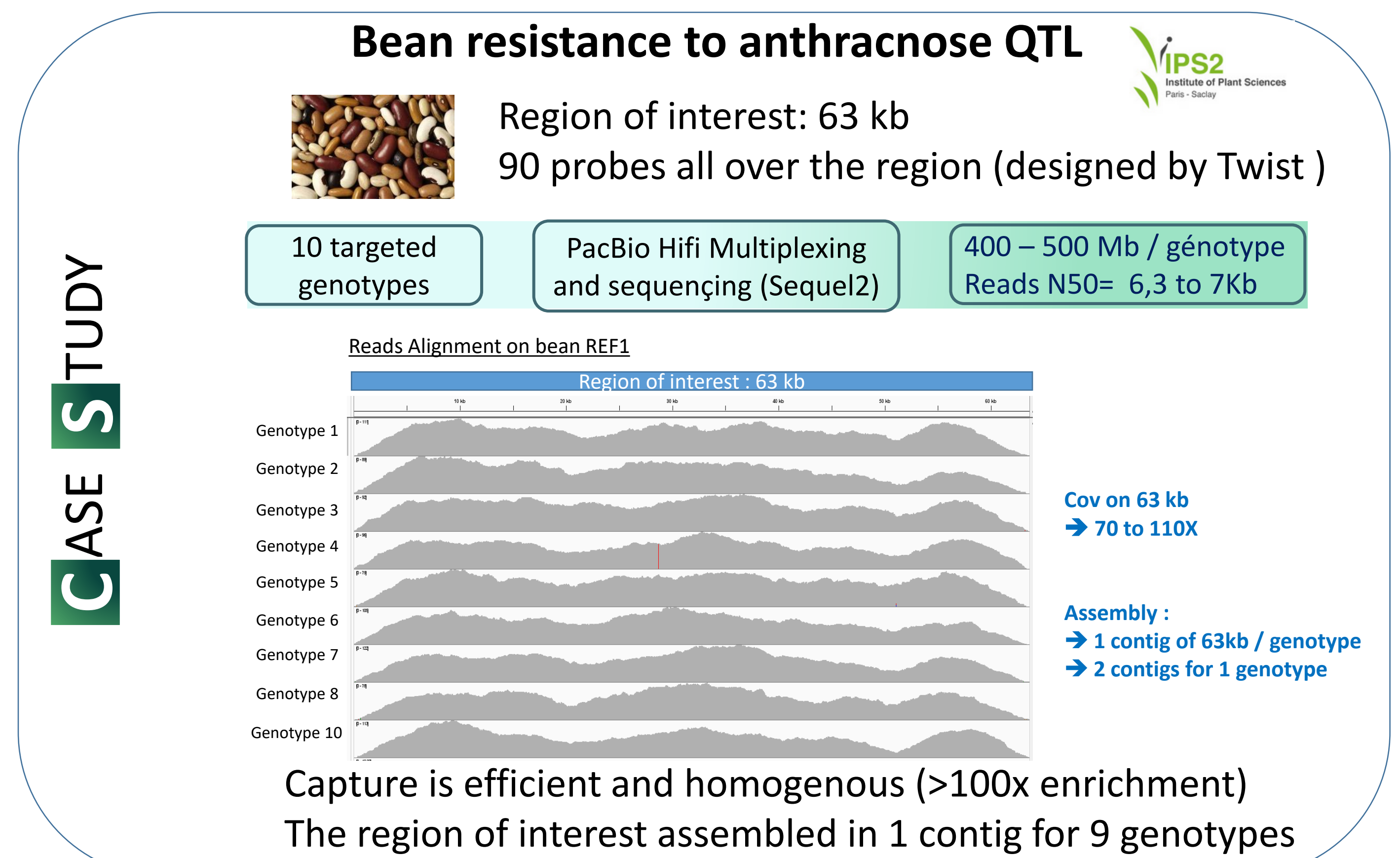
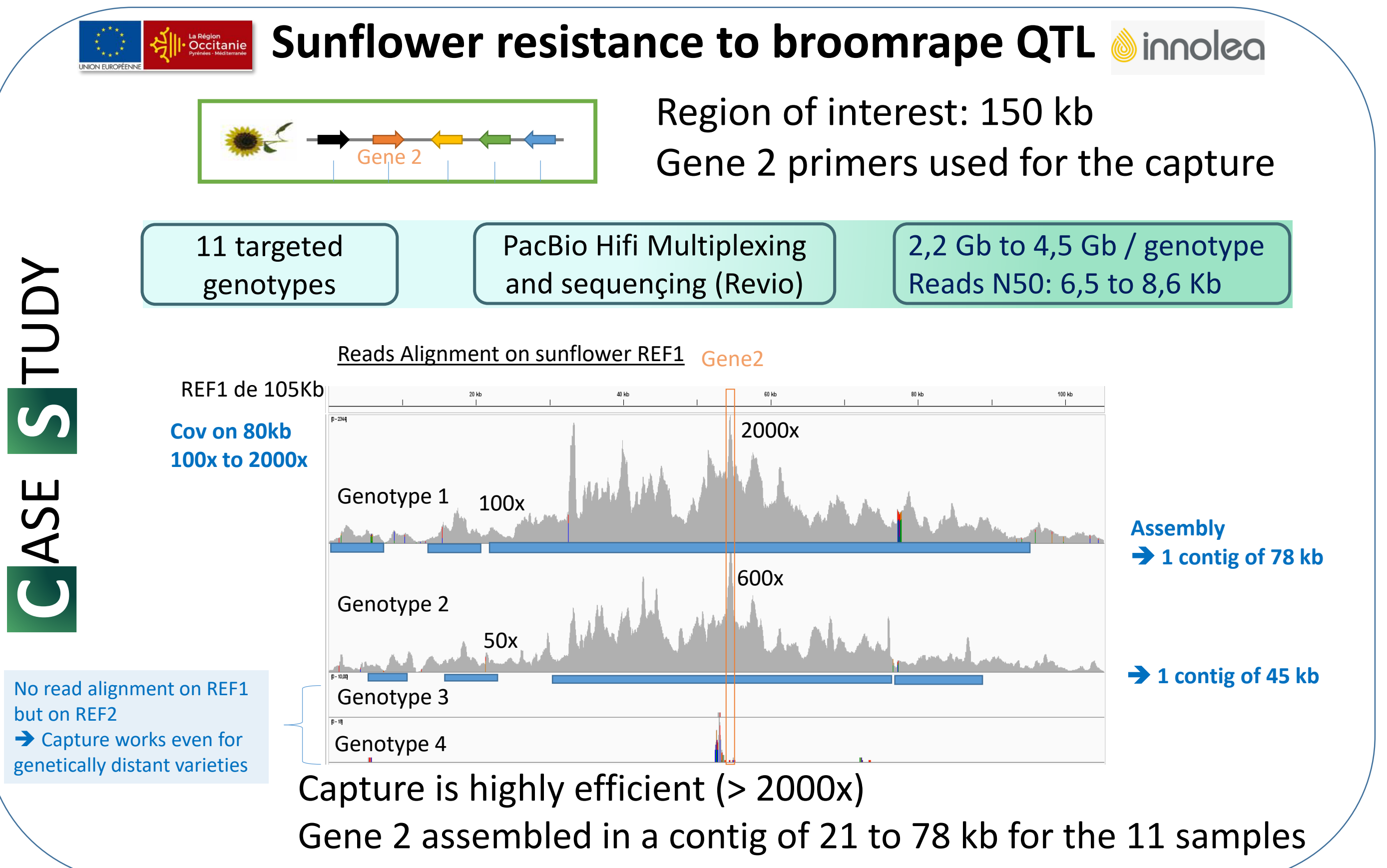
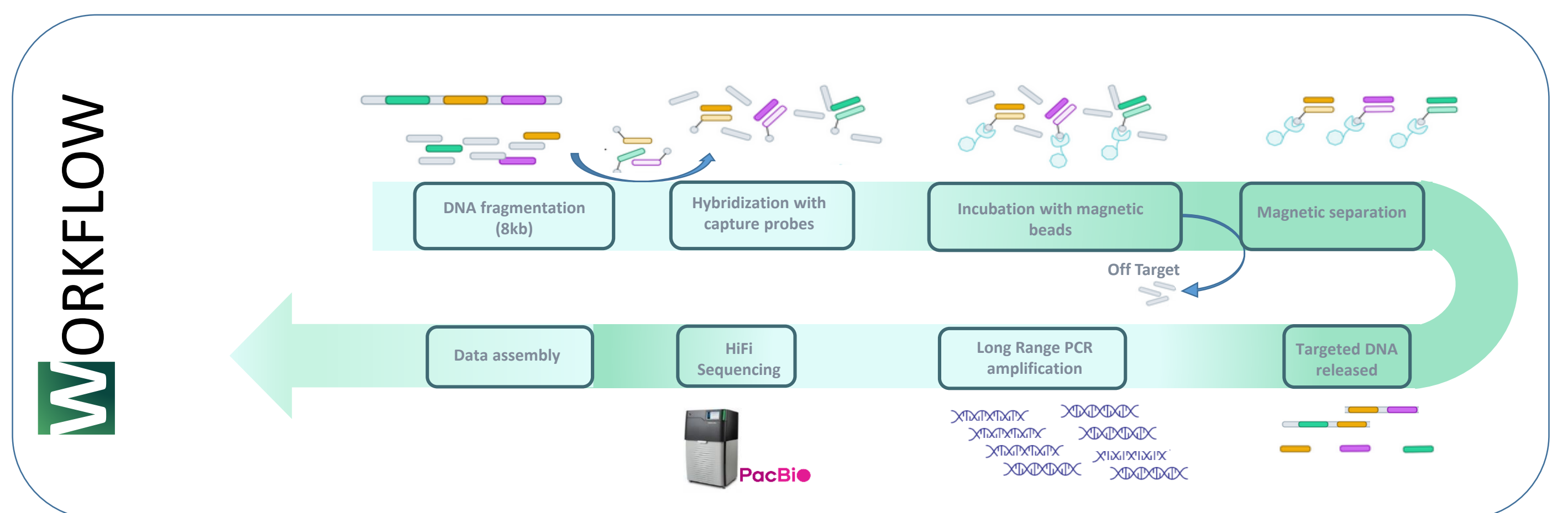
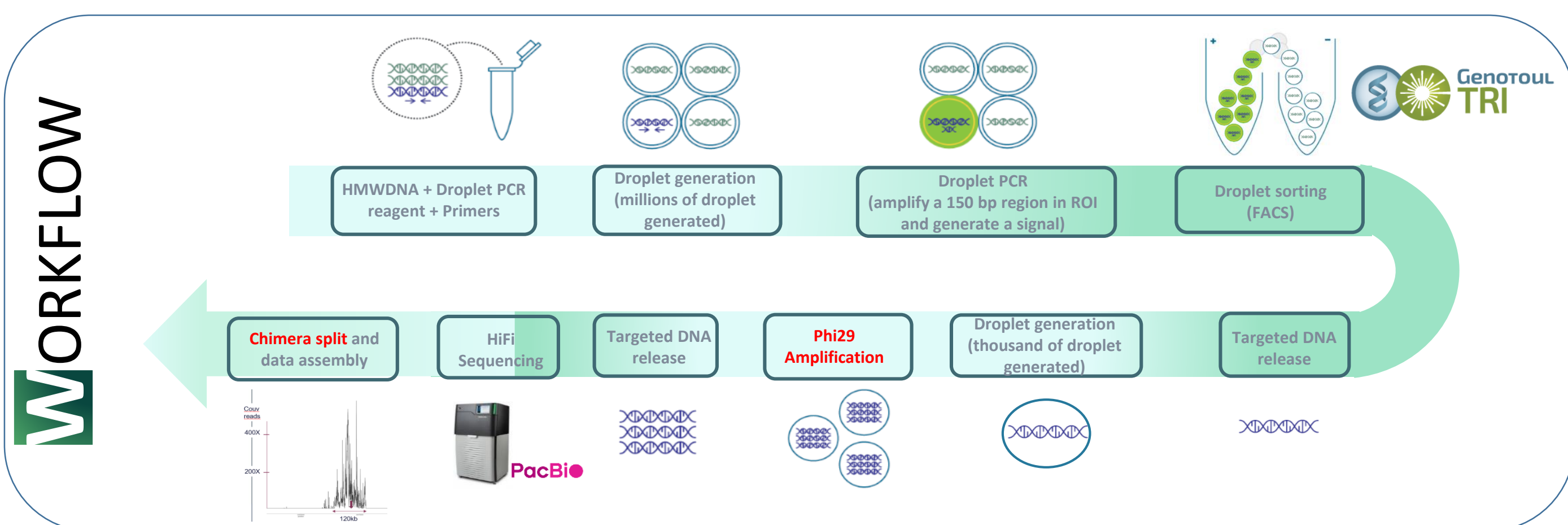


- Project that requires little knowledge
- 1 specific PCR marker conserved in diversity
- 100ng HMW DNA
- Region variability is not a limitation
- Possibility of multiplexing / 30 samples

TWIST  
BIOSCIENCE



- Project that requires a reference genome
- Probes are designed all over the region of interest
- 200ng HMW DNA
- Large structural variation may be a limitation
- Possibility of multiplexing / 96 samples



- OUTLOOKS**
- **Sequencing yield improvement**  
→ Cleaning test before sequencing in progress (sequencing production is better)
  - **Method ready for more complex projects**  
Maize project with 10 genotypes and 2 regions of 150 kb  
Wheat project with 20 genotypes and 1 region of 700 kb

**What's Next?**

**Adaptive Sampling: Targeted sequencing method based on a software controlled enrichment. No need for upfront sample preparation.**

- CONCLUSION**
- ❖ The presented capture methods offer efficient solutions to target large genomic region of interest in complex plant genomes
  - ✓ Need **Low-input amount DNA** for the capture
  - ✓ Provide an **accurate and reliable genomic information** for the region of interest
  - ✓ Allow a **rapid comparison** of a region of interest between several genotypes

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