



**HAL**  
open science

## The evolution of epigenetics across multiple generations

Sonia E Eynard, Cécile Donnadiou, Loïc Flatres-Grall, Carole Iampietro, Sandrine Lagarrigue, Sophie Leroux, Joanna Lledo, Juliette Riquet, Bertrand Servin, Céline Vandecasteele, et al.

### ► To cite this version:

Sonia E Eynard, Cécile Donnadiou, Loïc Flatres-Grall, Carole Iampietro, Sandrine Lagarrigue, et al.. The evolution of epigenetics across multiple generations. Epigenetic inheritance symposium, Aug 2023, Zurich, Switzerland. 2023. hal-04195749

**HAL Id: hal-04195749**

**<https://hal.science/hal-04195749>**

Submitted on 4 Sep 2023

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



# The evolution of epigenetics across multiple generations



Sonia E. Eynard<sup>1</sup>, Cécile Donnadieu<sup>2</sup>, Loïc Flatres-Grall<sup>3,4</sup>, Carole Iampietro<sup>2</sup>, Sandrine Lagarrigue<sup>5</sup>, Sophie Leroux<sup>1</sup>, Joanna Lledo<sup>2</sup>, Juliette Riquet<sup>1</sup>, Bertrand Servin<sup>1</sup>, Céline Vandecasteele<sup>2</sup>, Frédérique Pitel<sup>1</sup>

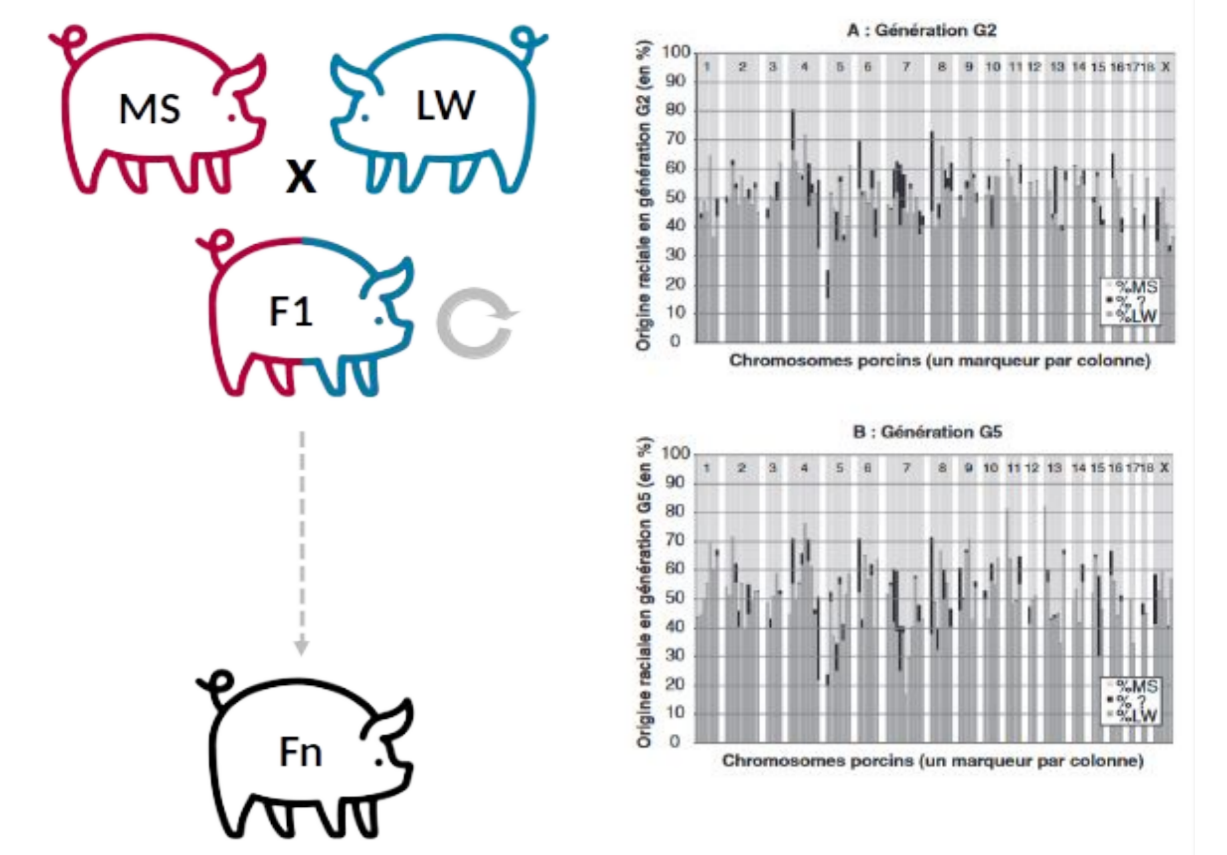
<sup>1</sup> GenPhySE, Université de Toulouse, INRAE, INPT, INP-ENVIT, 31326 Castanet Tolosan, France; <sup>2</sup> INRAE, US1426, GeT-PlaGe, Genotoul, France Génomique, Université de Toulouse, 31326 Castanet Tolosan, France; <sup>3</sup> AXIOM, 37310 Azay sur Indre, France; <sup>4</sup> Alliance R&D, 35650 Le Rheu, France; <sup>5</sup> PEGASE, INRAE, Institut Agro, 35590, Saint Gilles, France

Epigenetic Inheritance  
Symposium Zurich, 2023

## Introduction

**Context:** Remaining missing heritability in animal breeding can be partly explained by factors other than solely genetics, e.g. epigenetics.

**Question:** How does epigenetic patterns evolve through time across multiple generations of selection in a commercial pig breed? Can we link this pattern with selection decisions?



## Methods

### Animals:

- 15 generations
- Each generation 1 pool of n = 4 to 16 boars
- Sperm

### Genomics and Epigenomics:

- Oxford Nanopore Technology - PromethION
- Long read sequences + methylation
- 30M CpGs covered
- Average 30X
- Focus on chromosome 7

### Evolution of allele frequencies:

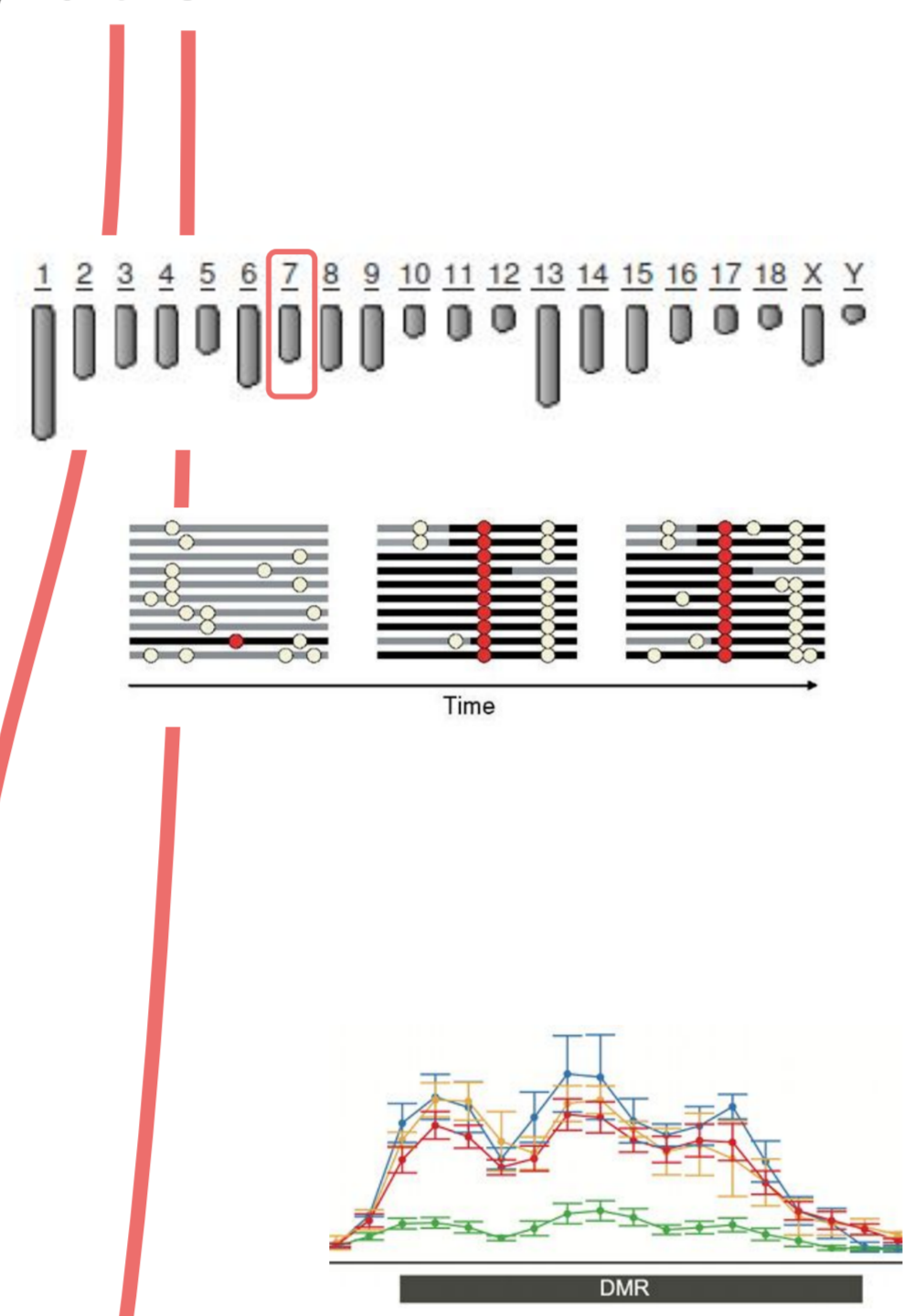
- Fst
- Signature of selection

### DMC and DMR analysis:

- DSS (R, Hao et al. 2013)
- edgeR (R, Robinson et al. 2010)

### Evolution of methylation rate:

- Poisson lognormal models (PLNmodels, Chiquet et al. 2021)



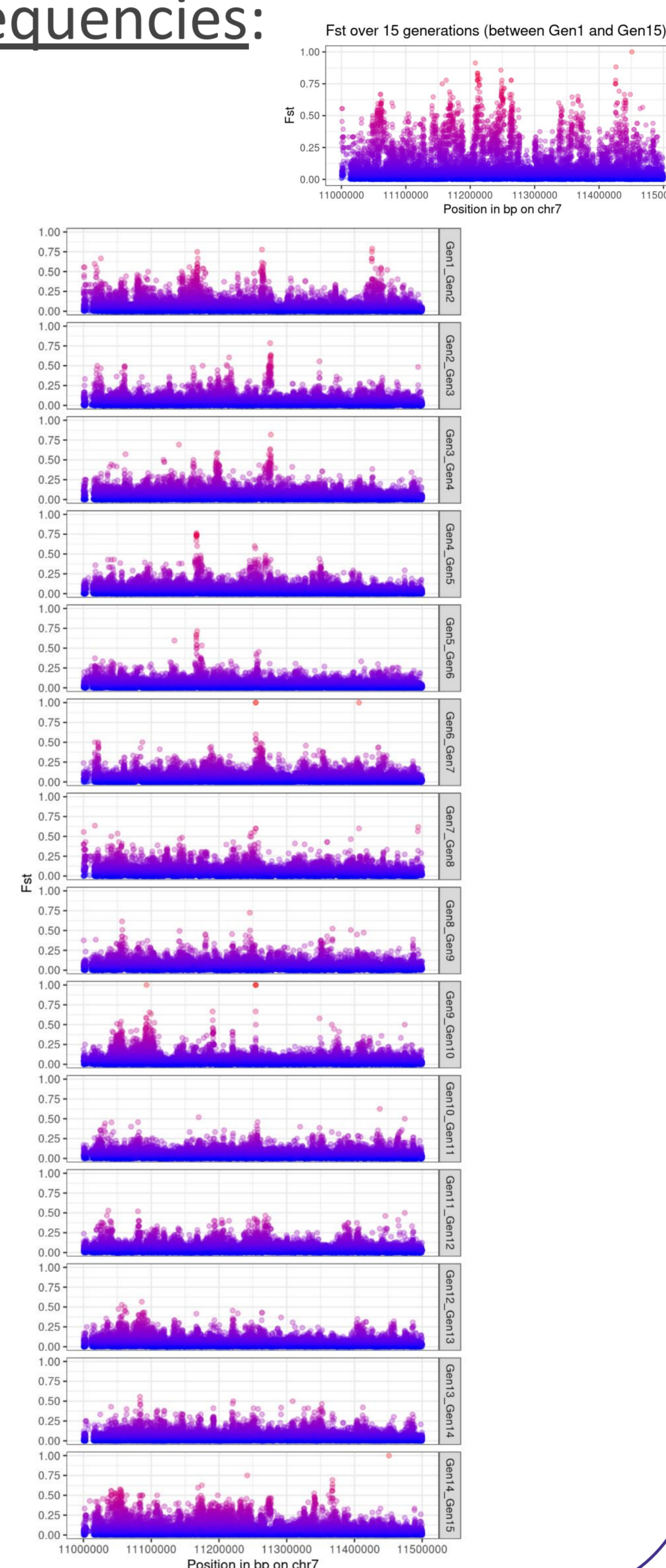
## Results

For the region between 11 to 11.5Mb on chromosome 7

### Why this region:

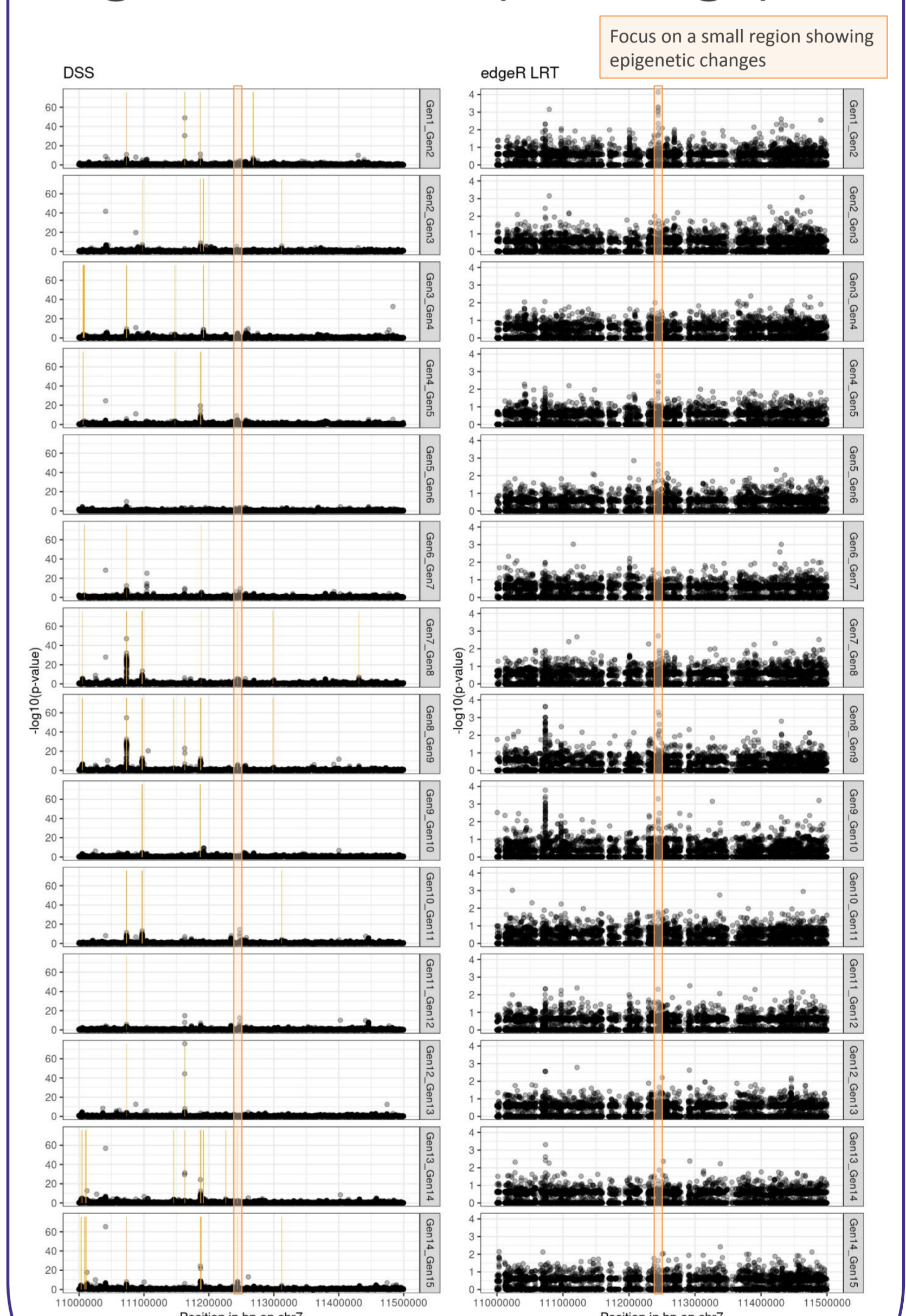
Contains QTLs identified in our breed of interest

### Evolution of allele frequencies:



### DMC and DMR analysis:

P-value of DMC and significant DMR (in orange)



## Conclusions and perspectives

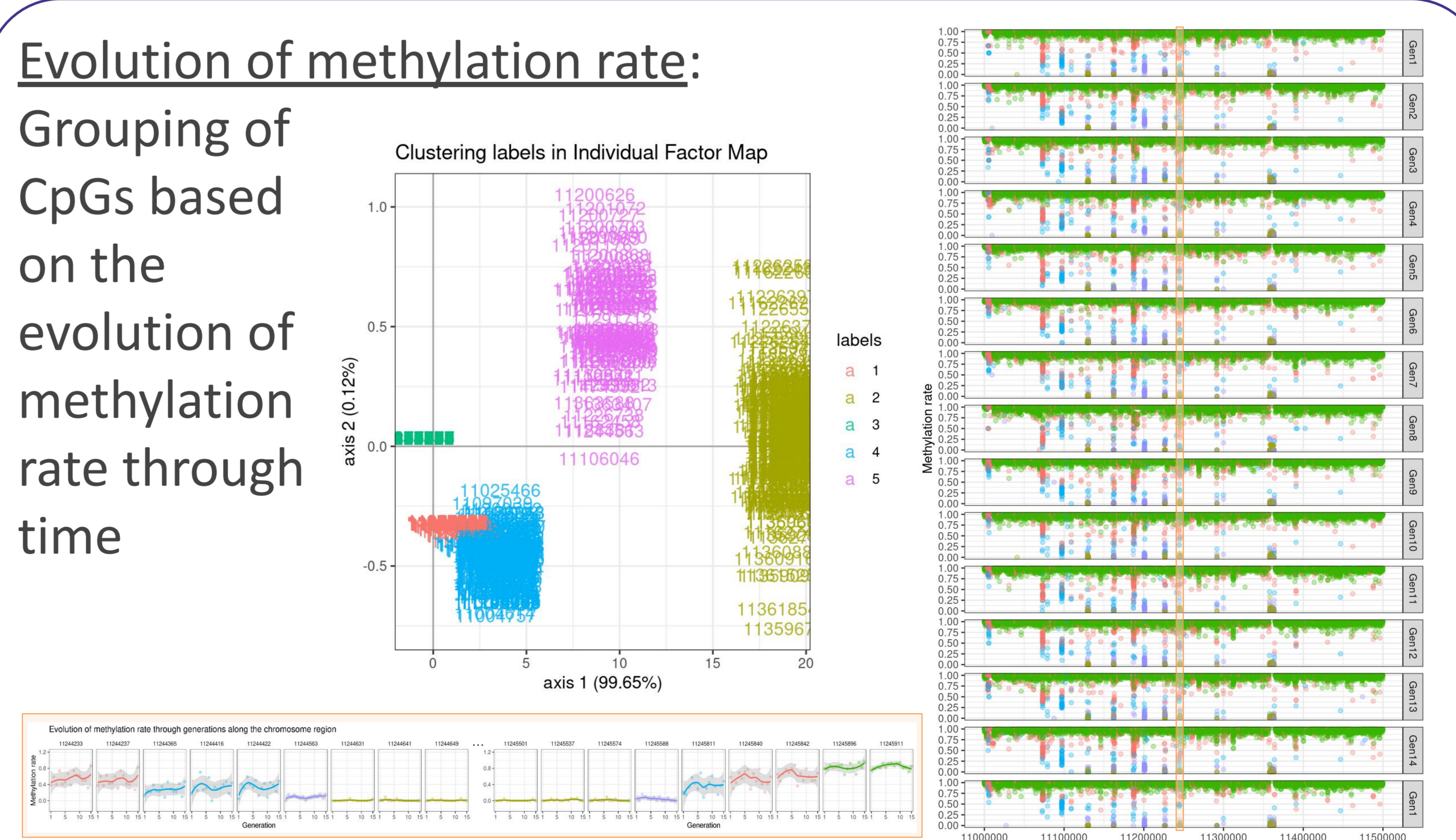
- Chromosome 7 carries a lot QTLs on which we can identify allele frequency and methylation rate changes through time
- Possible link with selection decision on the breed
- Evolution of methylation can be linked or not to genetics

### Perspectives:

- Same analysis on the whole genome
- Link signal to genome features
- Correlated changes with breed selection decisions

### Evolution of methylation rate:

Grouping of CpGs based on the evolution of methylation rate through time



H2020 grant GEroNIMO 101000236  
FEDER-FSE Midi-Pyrénées et Garonne 2014-2020 SeqOccin