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# The evolution of epigenetics across multiple generations



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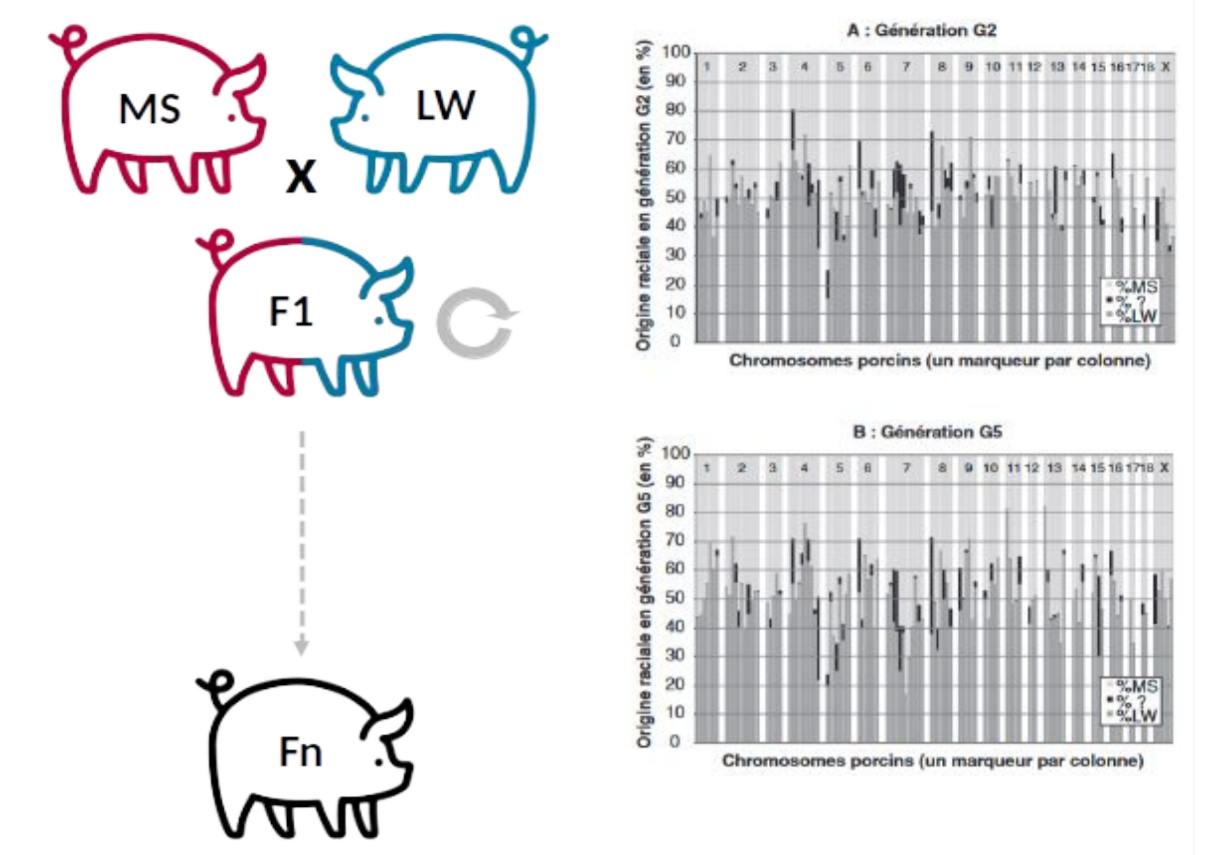
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Epigenetic Inheritance  
Symposium Zurich, 2023

## 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

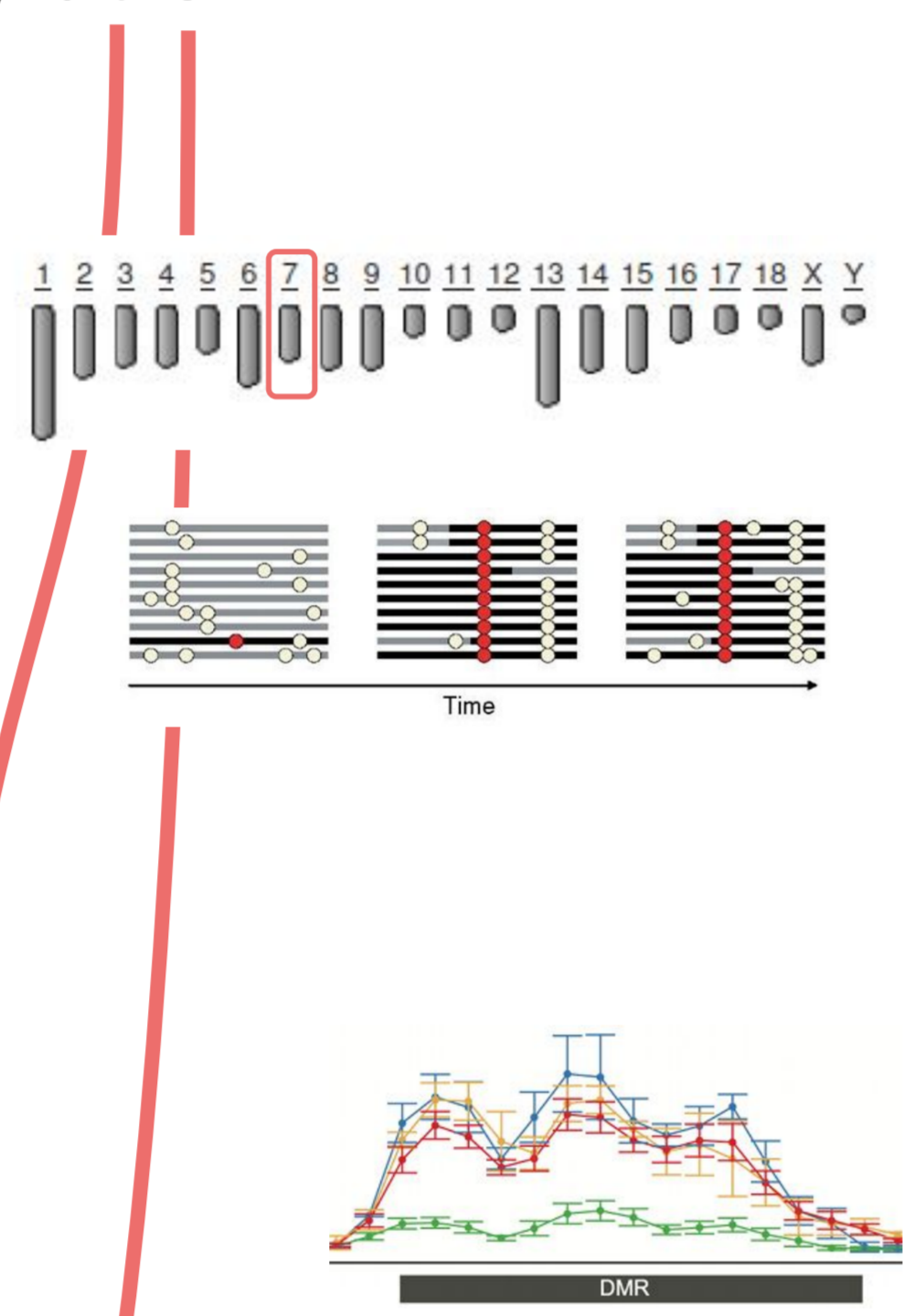
### DMC and DMR analysis:

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

### Evolution of methylation rate:

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

<https://what-when-how.com/genetics/genetic-signatures-of-natural-selection/>  
<http://www.iefbio.com/methylation/>



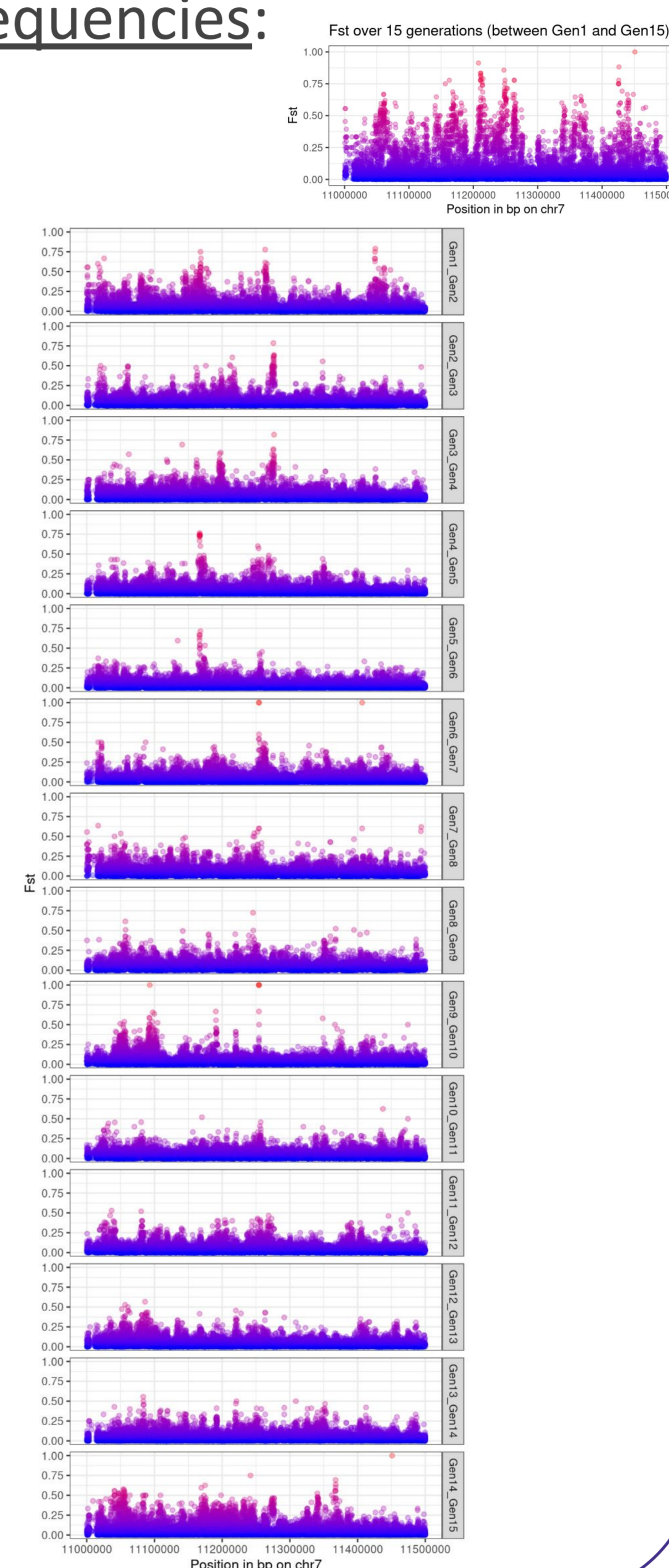
## Results

For the region between 11 to 11.5Mb on chromosome 7

### Why this region:

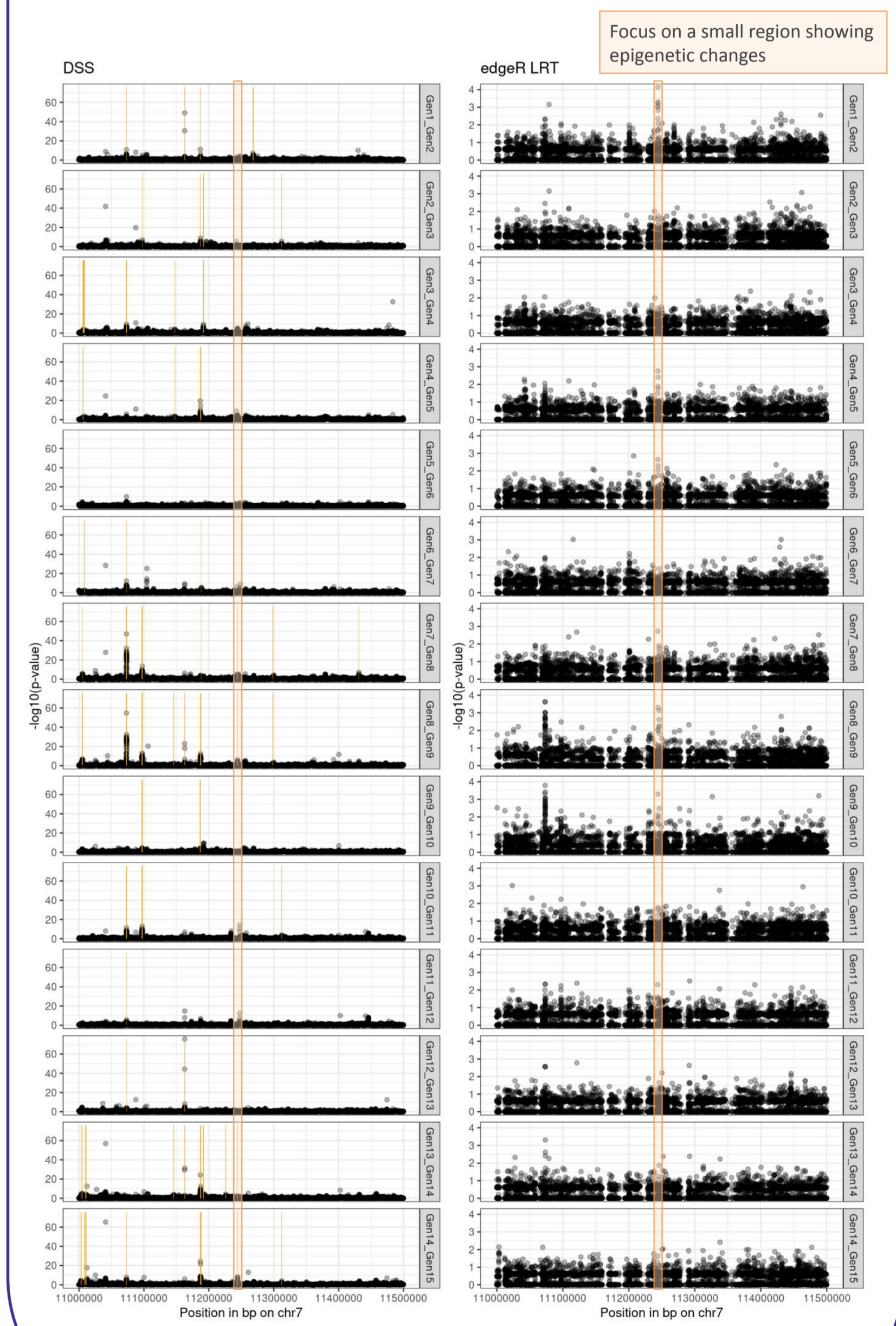
Contains QTLs identified in our breed of interest

### Evolution of allele frequencies:



### DMC and DMR analysis:

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



## Conclusions and perspectives

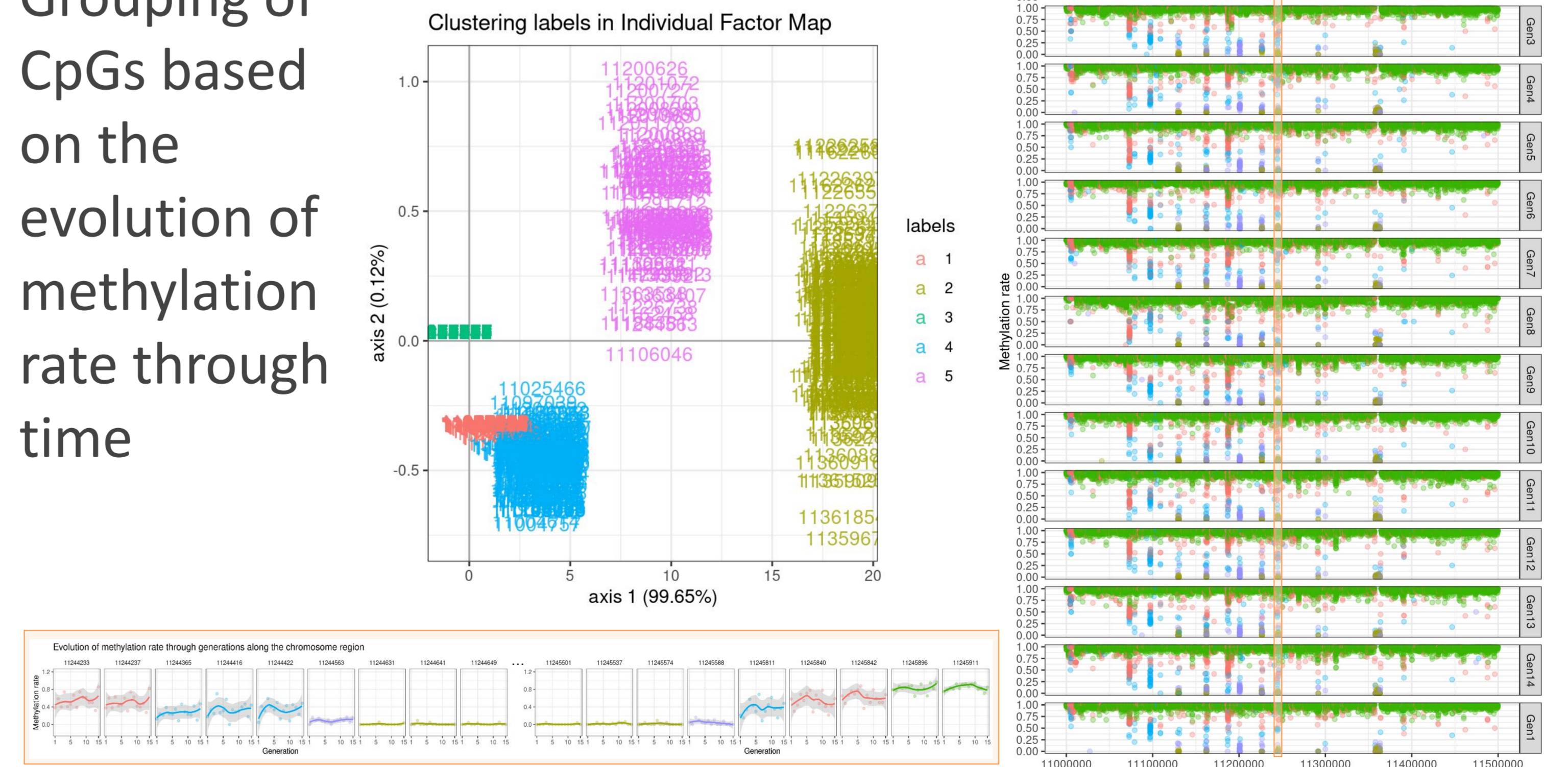
- Chromosome 7 carries a lot QTLs on which we can identify allele frequency and methylation rate changes through time
- Possible link with selection decision on the breed
- Evolution of methylation can be linked or not to genetics

### 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



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