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Transgenerational epigenetics in quail: targeting DNA methylation patterns to address the interplay between genetic and epigenetic mechanisms.

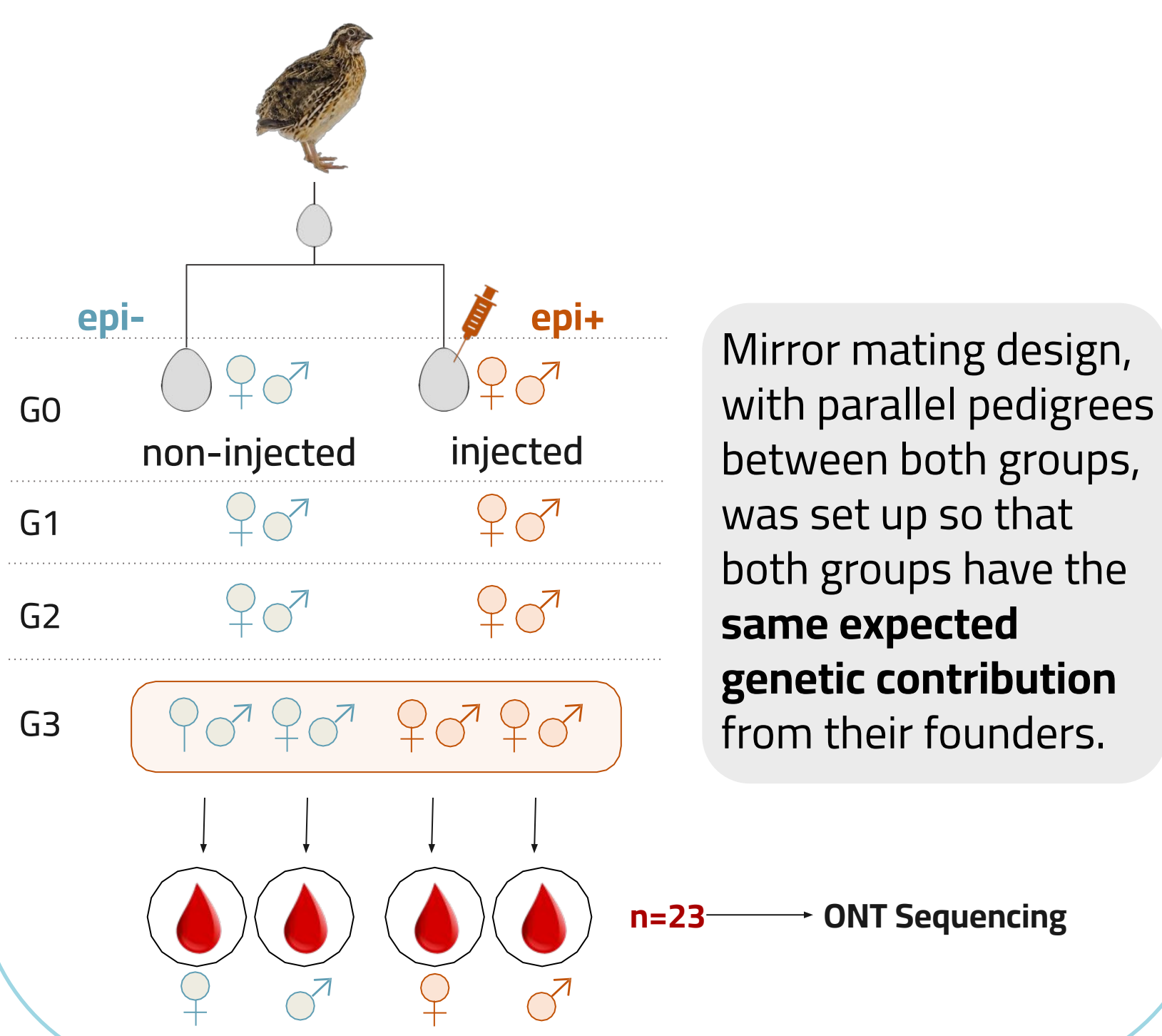
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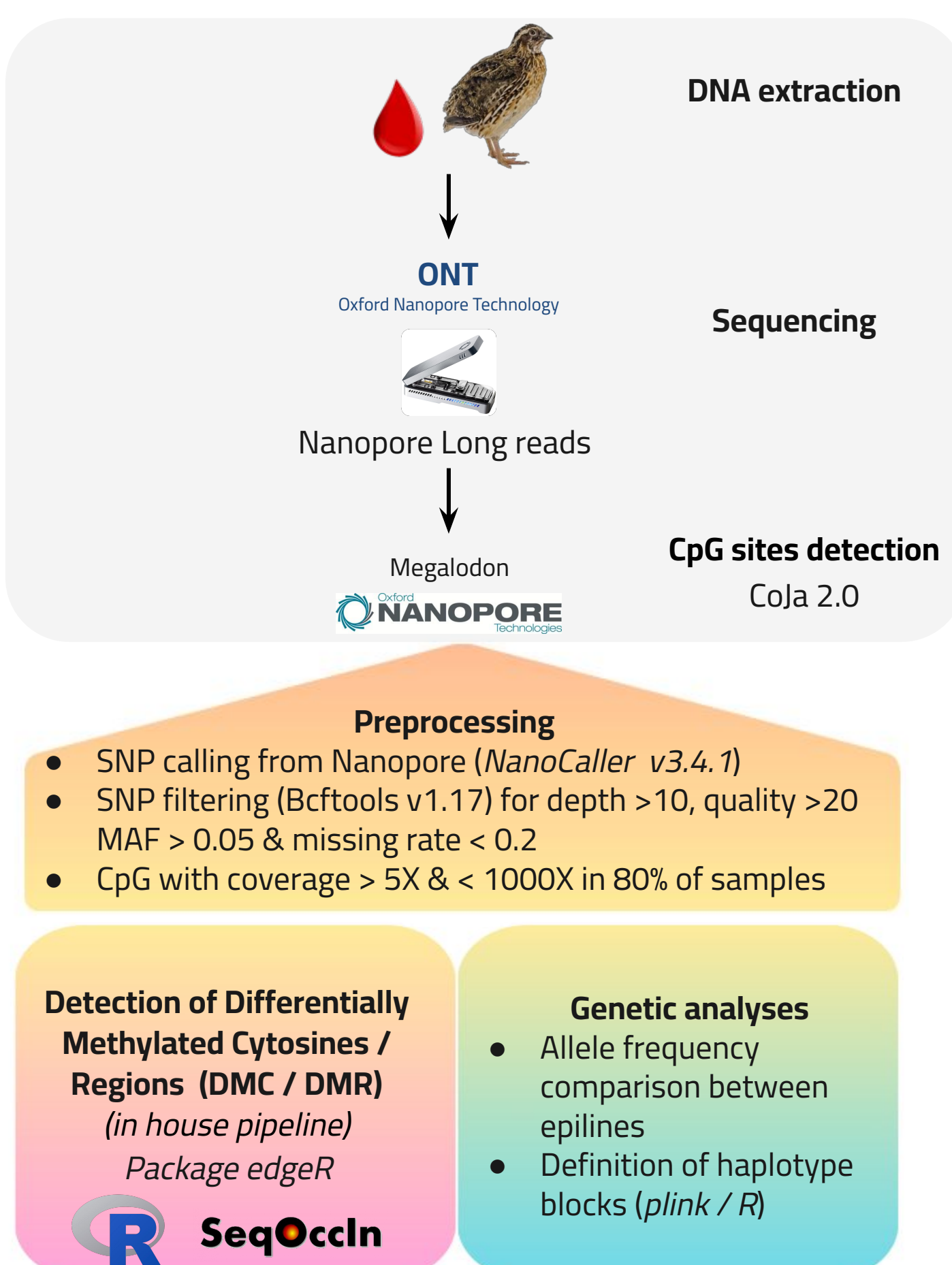
Introduction

The influence of the prenatal environment on the adult phenotype development is partially mediated by epigenetic phenomena. An increasing number of studies highlight the transmission of epigenetic marks between generations following an environmental exposure. However, there is much debate about their acquired transmission beyond the exposed individuals. Recent studies revealed that non-genetic inheritance was probably present in avian species. In one of them, fertilized eggs were injected with an endocrine disruptor (genistein) and after three generations without any other injection, reproduction and behaviour traits of offsprings were impacted by the treatment of the ancestor. Here we analyse the DNA methylation between control and treated lines of the third generation.

Experimental design



Methods



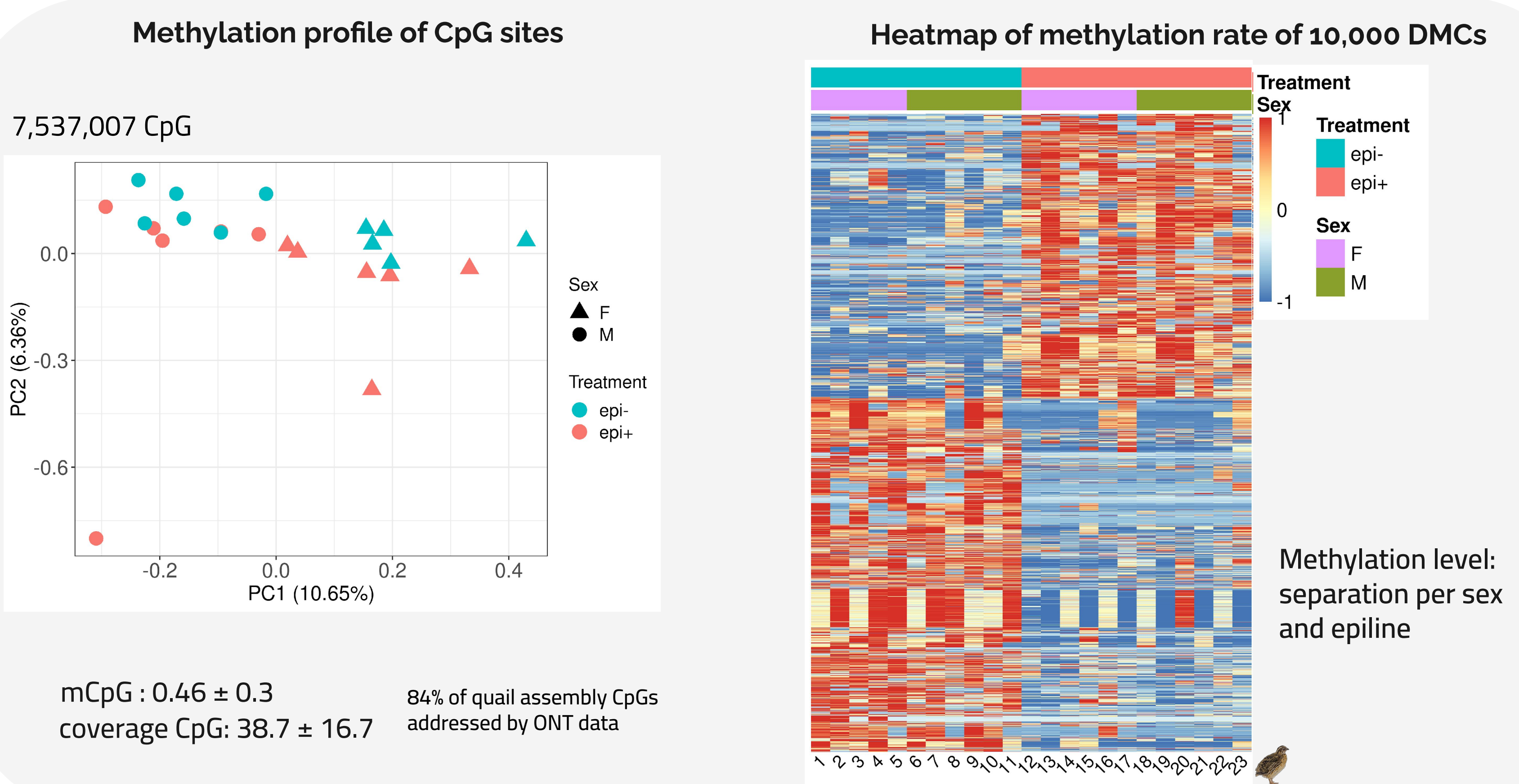
Conclusion

Thousands of DMCs were identified between epilines, supporting the hypothesis that genistein may have **transgenerational effects** on DNA methylation levels.

However, the majority of the variability in methylation levels appears to be associated with **genetic variation**, suggesting that methylation is primarily influenced by genetic factors rather than epigenetic ones.

Candidate regions showing variations between epilines, **observed exclusively in the methylation profile**, will be further analysed to draw conclusions about potential non-genetic inheritance phenomena in quails.

Results



Taking SNPs into account

