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Transgenerational epigenetics in quail: whole genome DNA methylation analysis

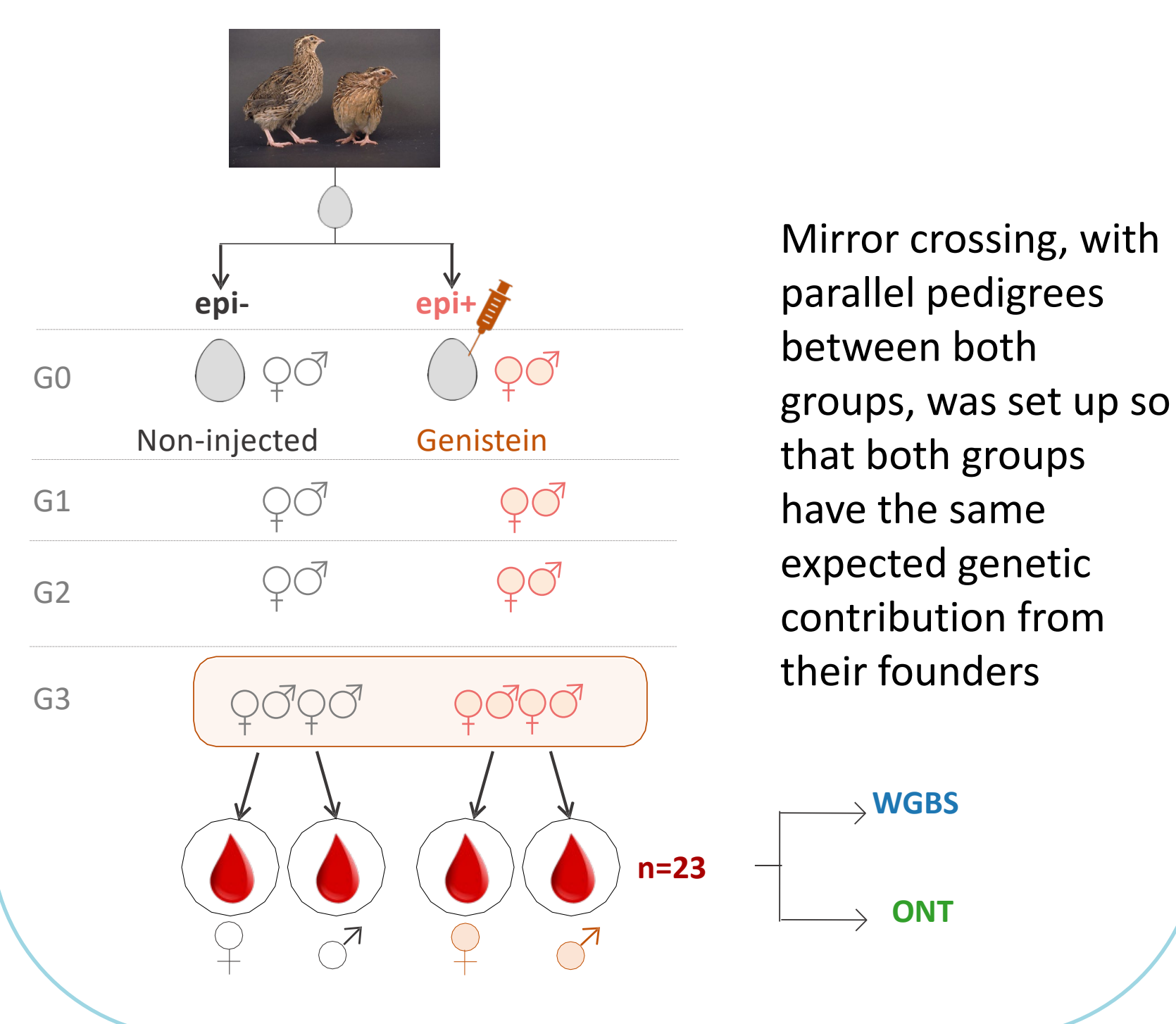
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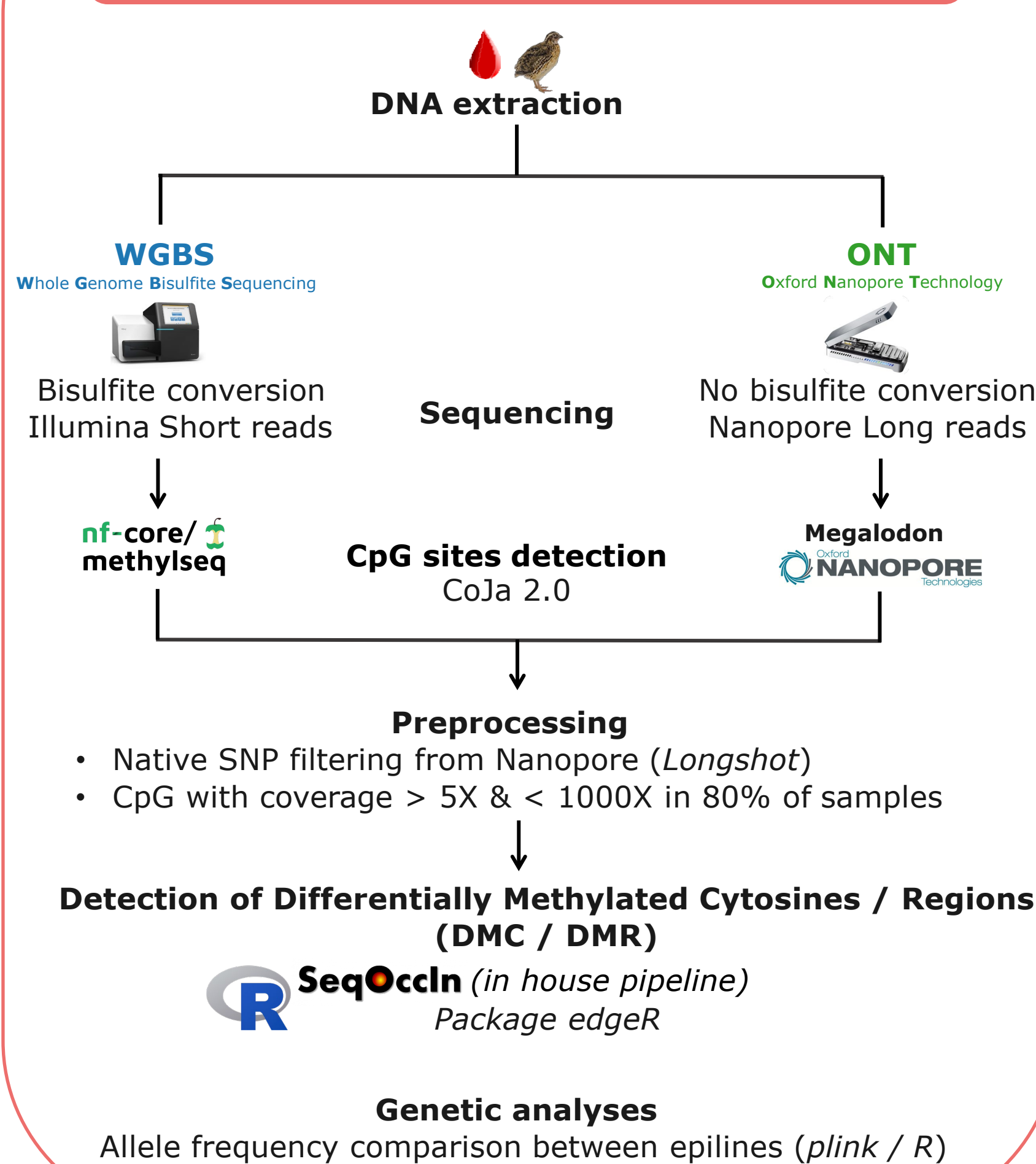
Introduction

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, several traits were impacted by the ancestor treatment such as the reproduction and the behavior. Here we analyse the DNA methylation between control and treated lines of the third generation.

Experimental design



Methods



Conclusion

ONT vs WGBS: comparable results but best detection of differential methylation from ONT data

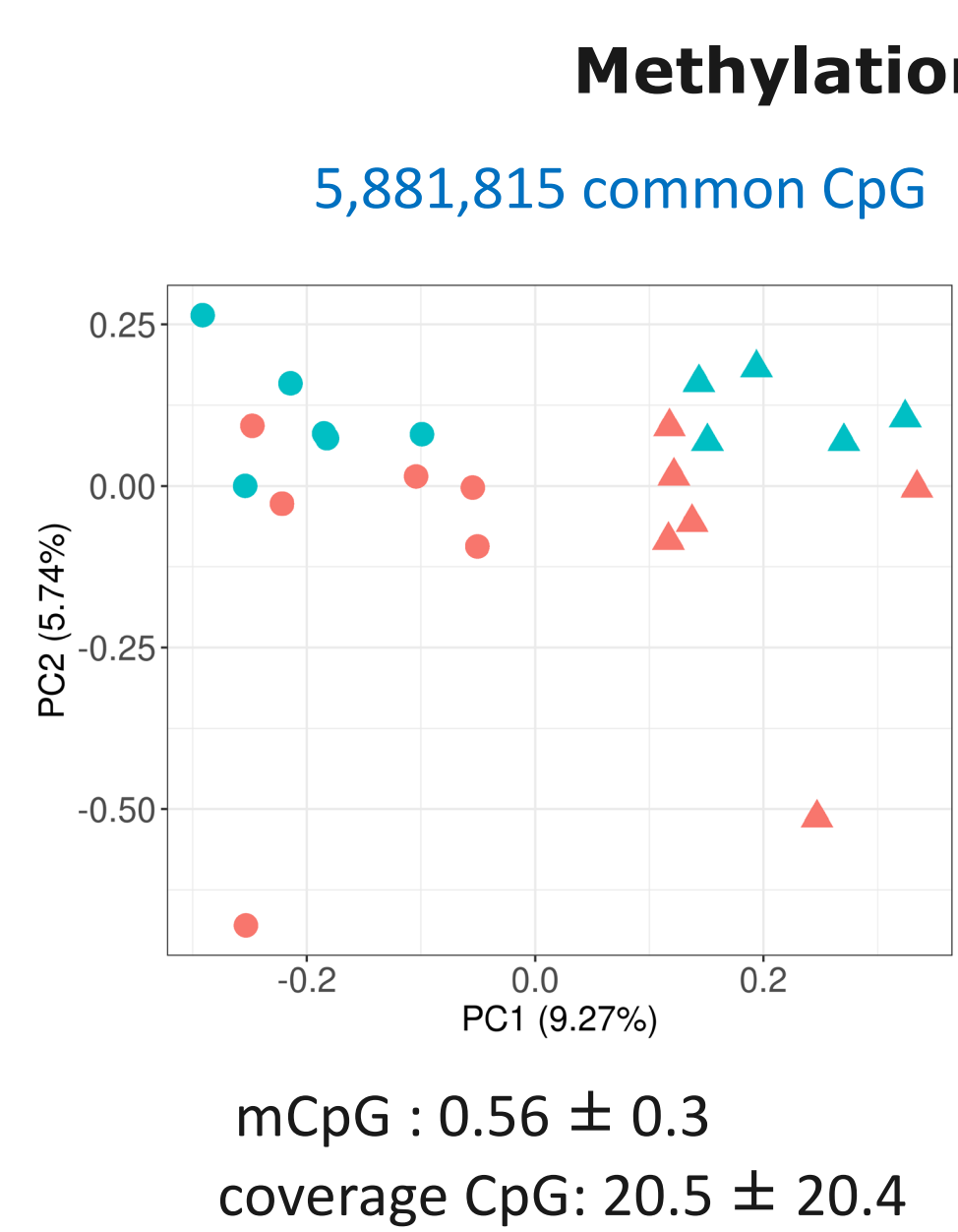
Thousands of DMCs detected between epilines: **transgenerational effects of genistein on DNA methylation level**

Most of the **methylation level variability** seems to be **correlated with genetic variability**

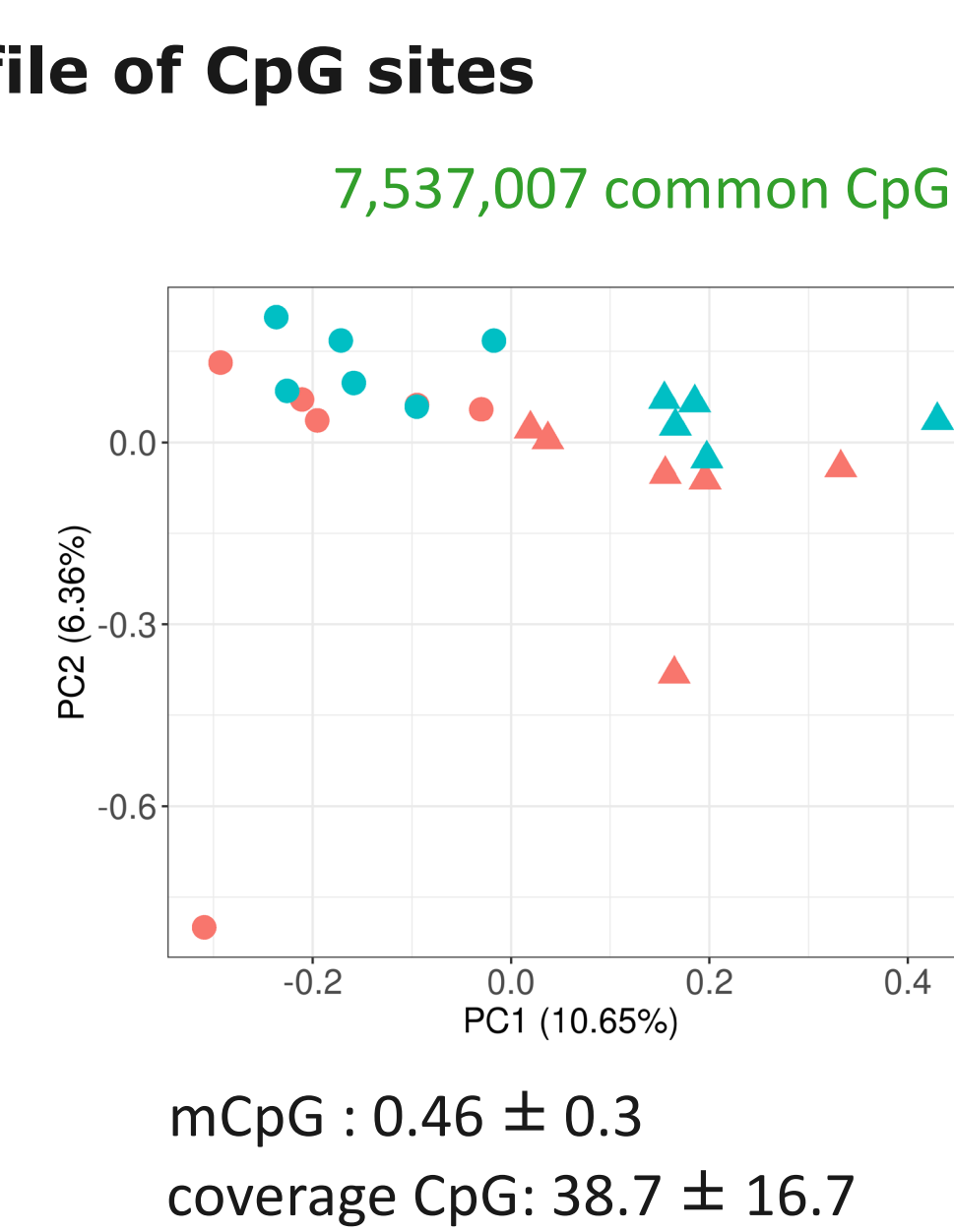
Several candidate regions will be further analysed

Results

WGBS

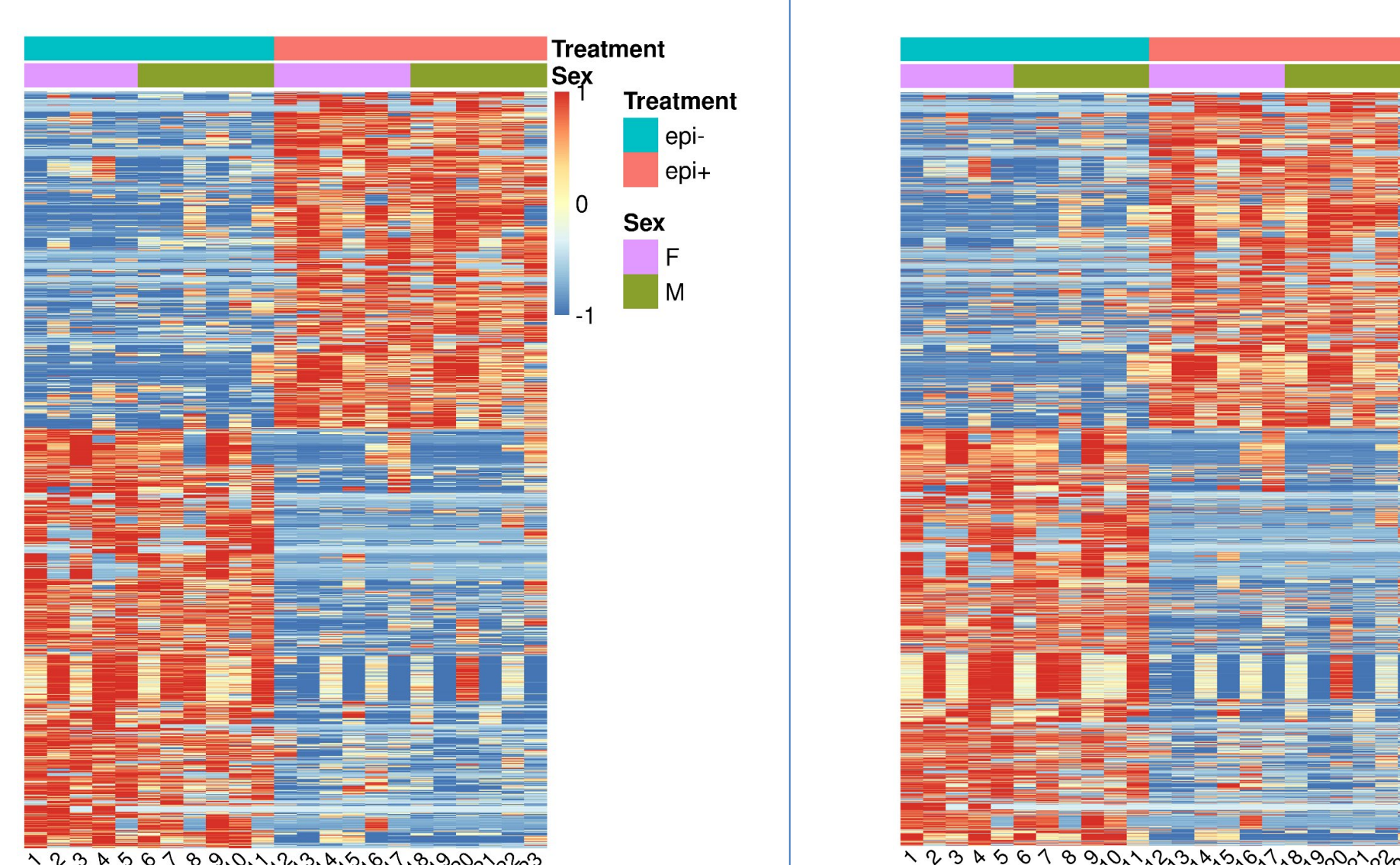


ONT

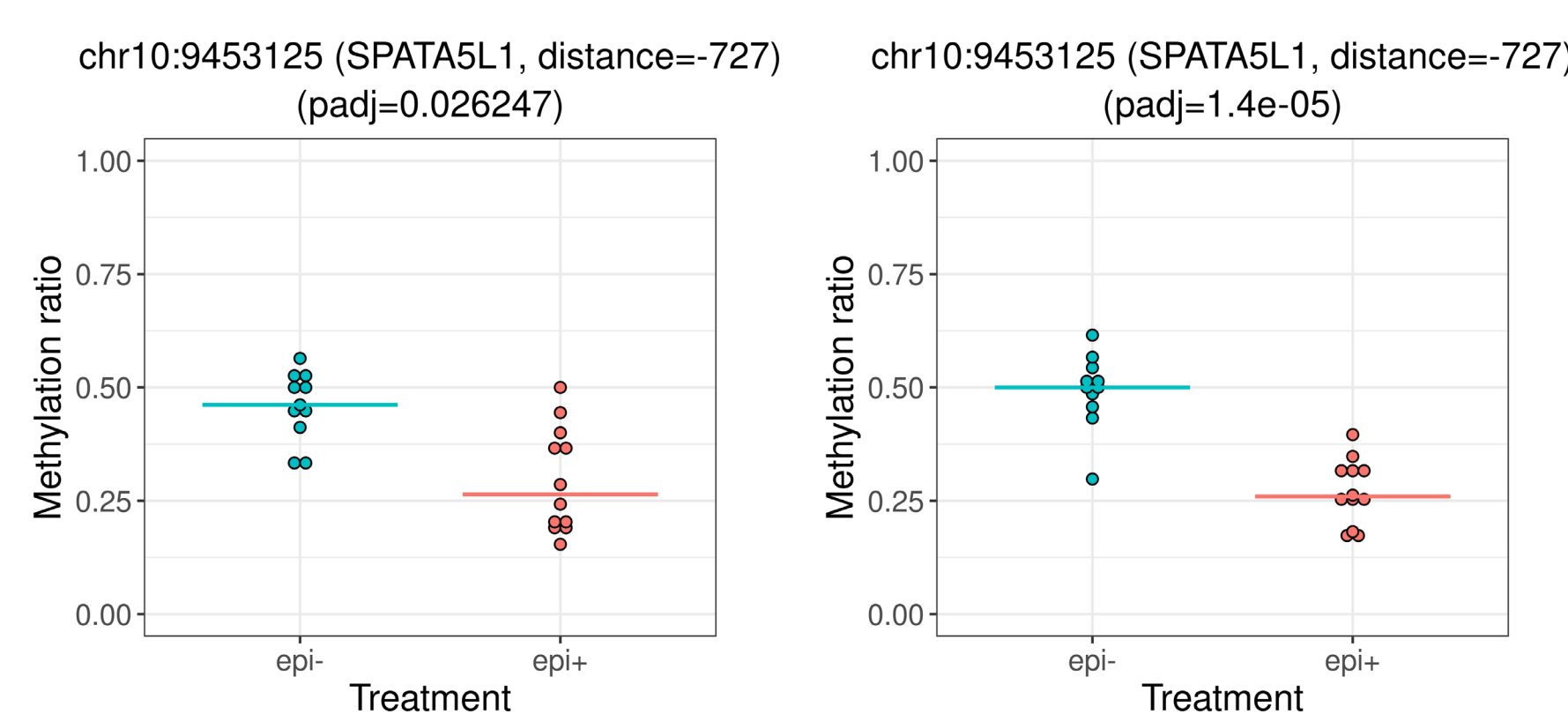
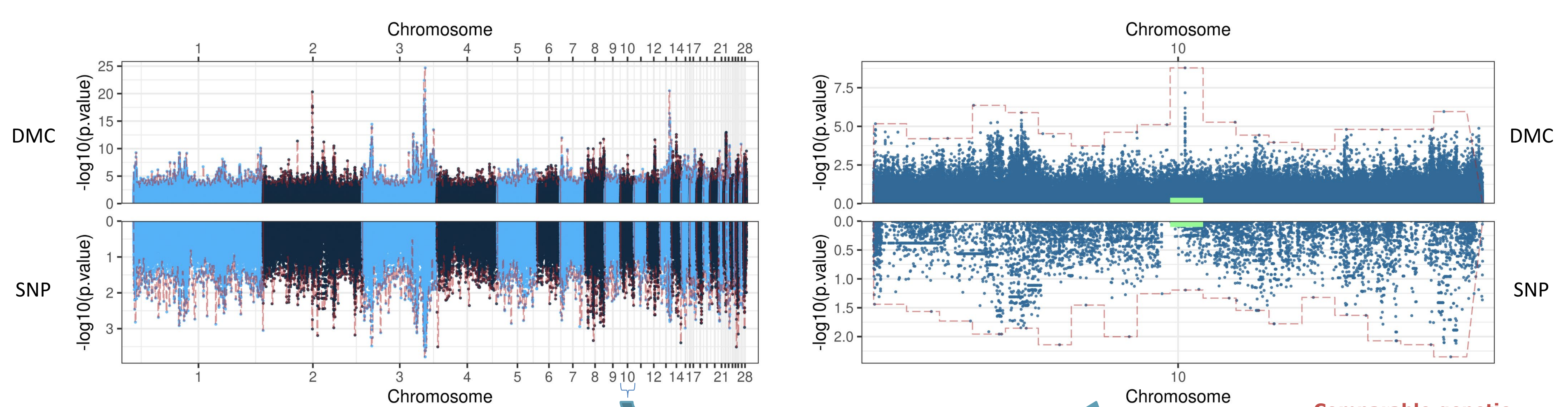


Methylation level: separation per sex and epilines

Heatmap of methylation rate of 10,000 DMCs epilines



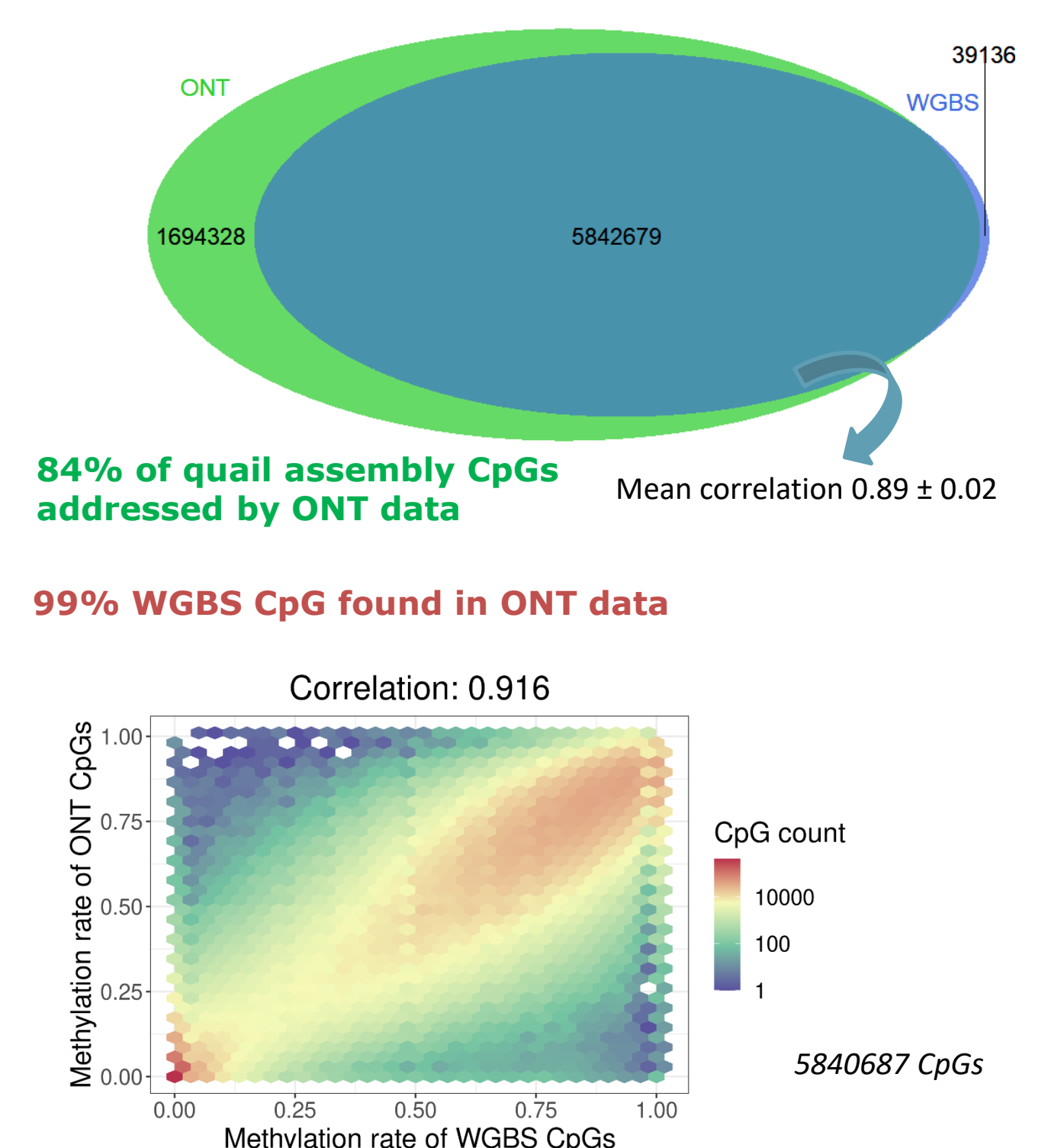
Taking SNPs into account



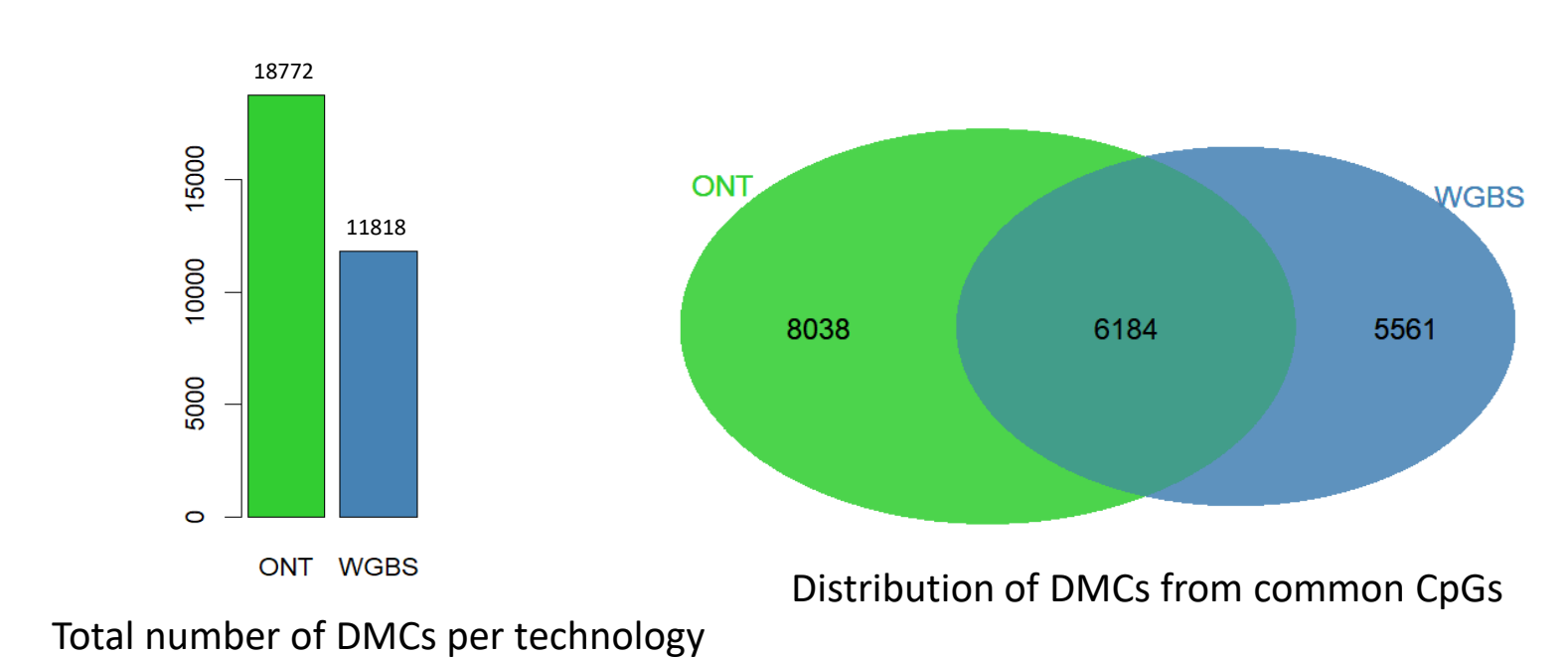
WGBS

ONT

Number of CpG sites measured



Number of significant DMCs observed



Thousands DMCs detected by both technologies

Comparable genetic and epigenetic differential patterns between epilines, but several interesting regions



SPATA5L1 (Spermatogenesis-Associated Protein 5-Like Protein 1) = AFG2B (AFG2 AAA ATPase Homolog B), involved in ribosome biogenesis