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Transgenerational epigenetics in quail: whole genome DNA methylation analysis

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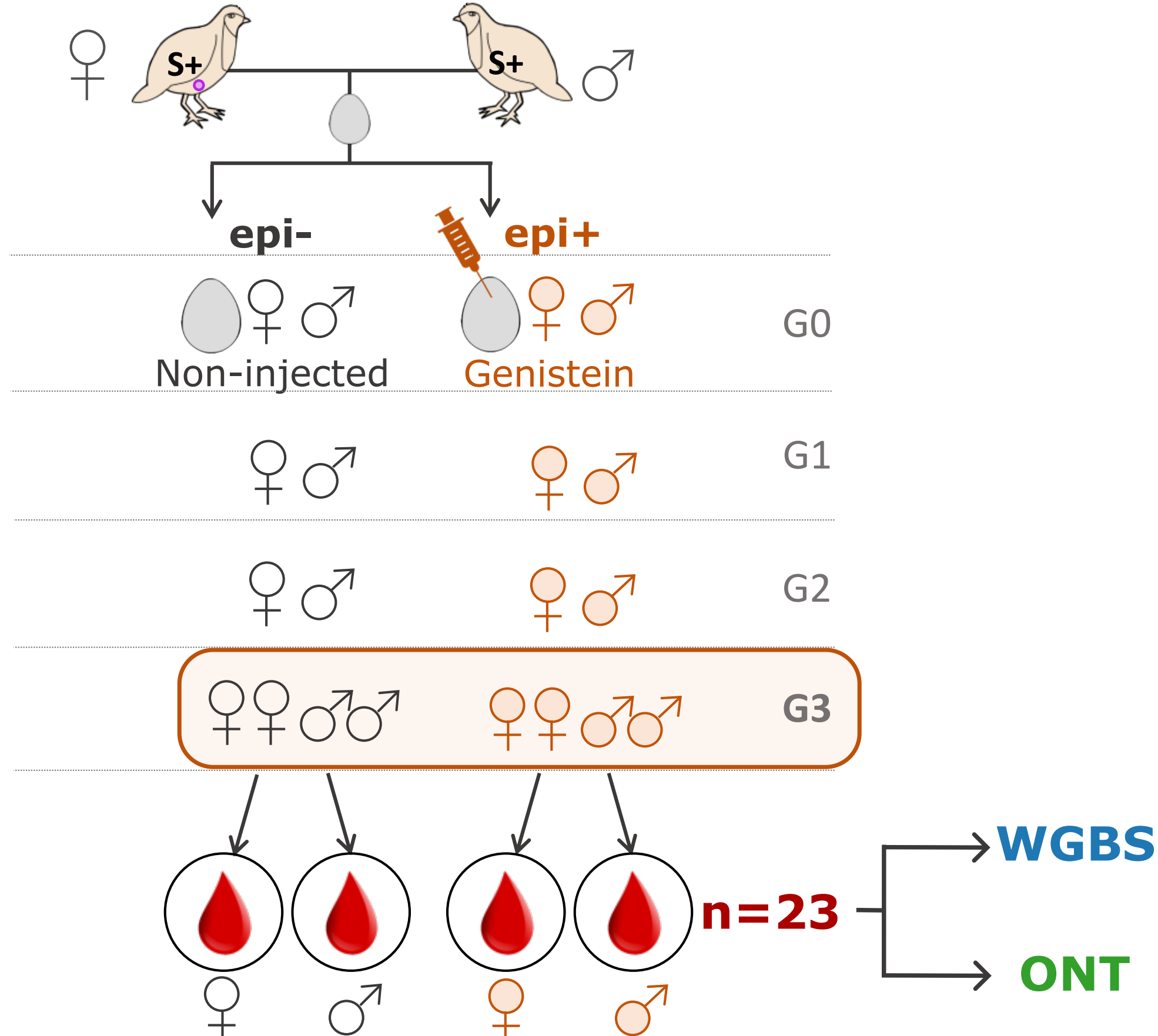
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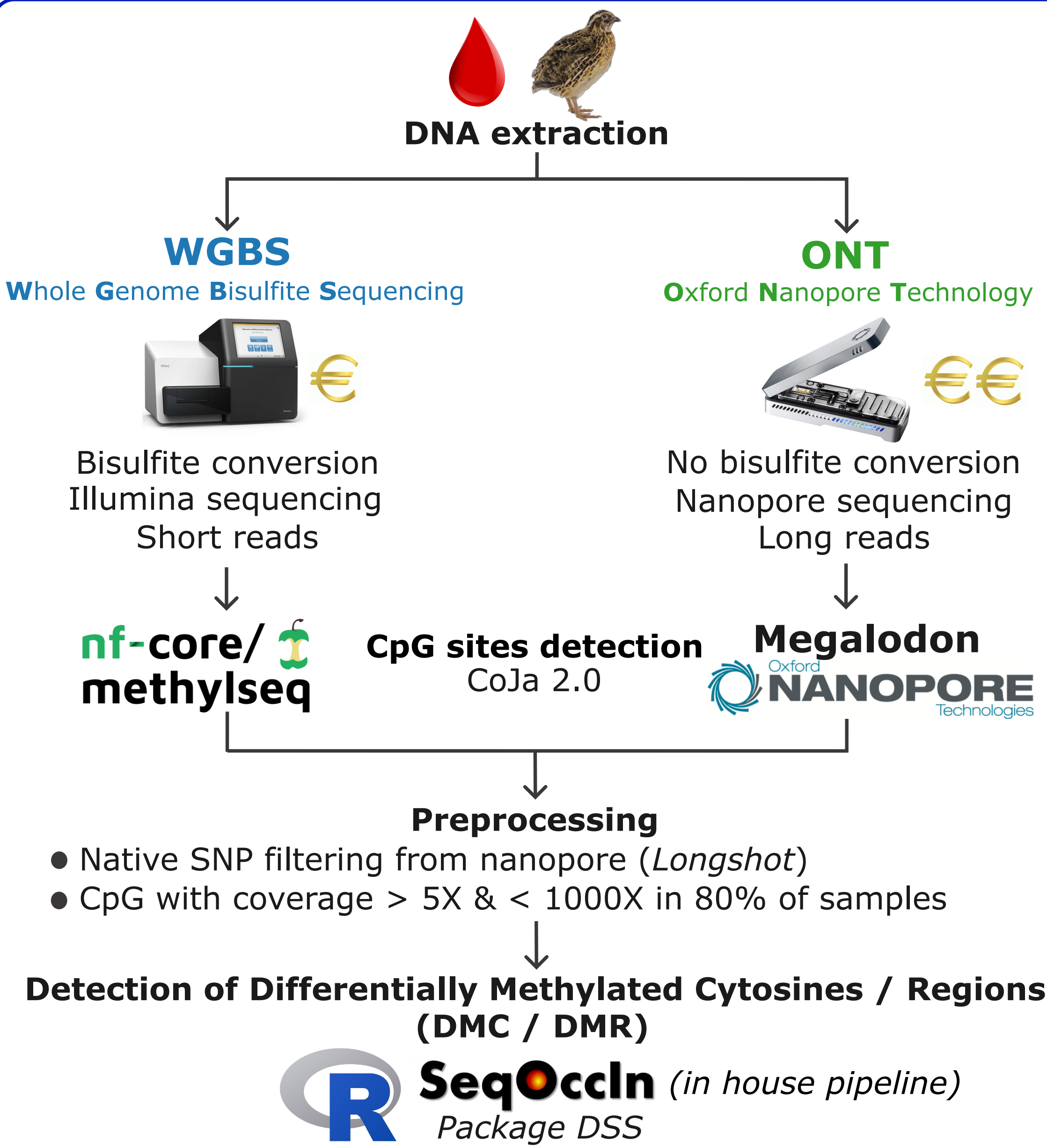
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The influence of the **prenatal environment** on the adult **phenotype development** is partially mediated by **epigenetic phenomena**. Recently, an increasing number of studies highlighted the **transmission of epigenetic marks between generations** 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**.

1 - Experimental design



2 - Methods



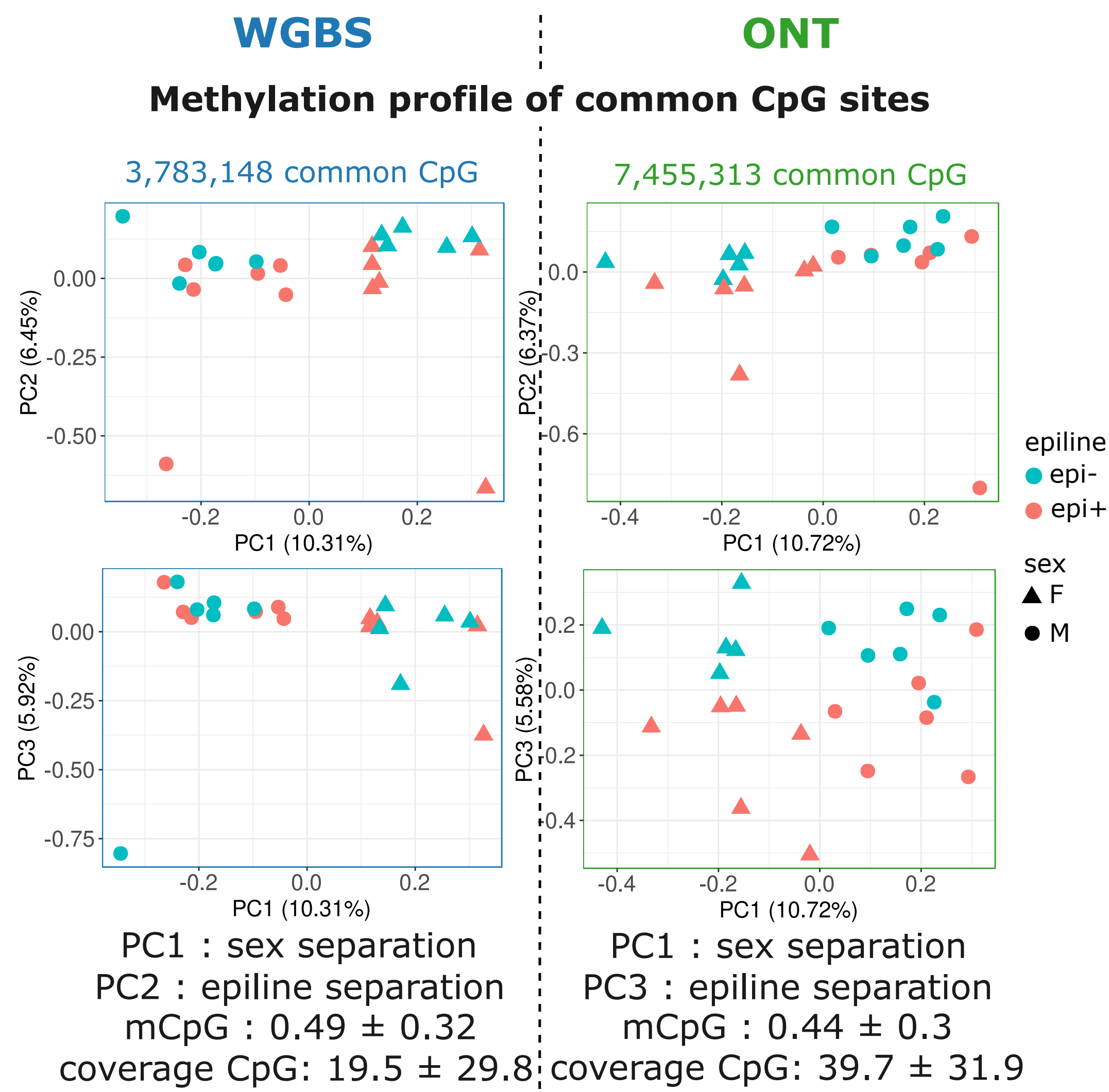
Conclusion

- Thousands of DMC detected between epilines
- Transgenerational effects of genistein on the DNA methylation
- ONT vs WGBS: comparable results and best detection of transgenerational effects from ONT data

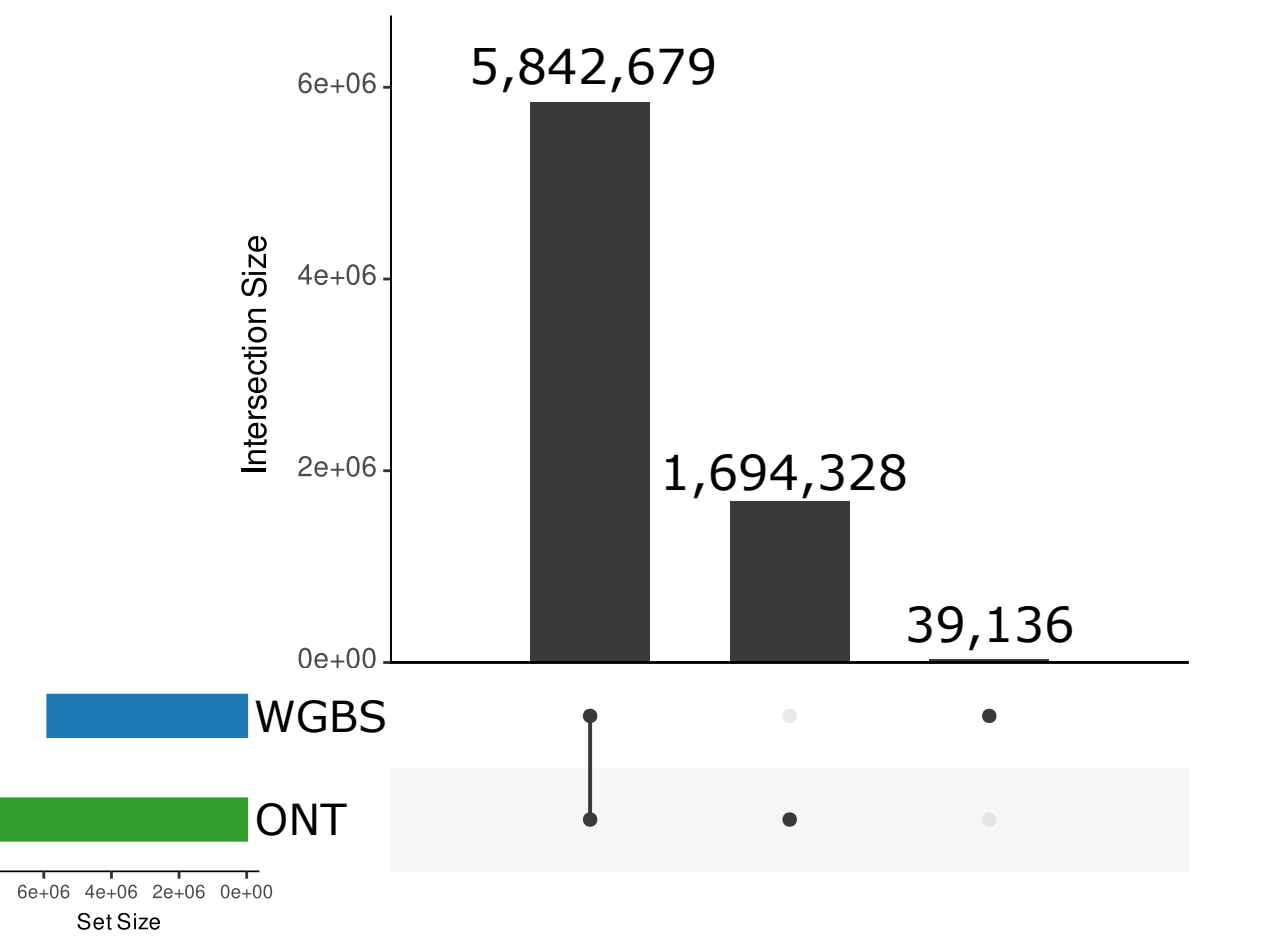
Perspectives

- Optimising SNP filtering and minimising false positives:
 - SNP calling with GemBS for WGBS data
- Gene Ontology (GO) analysis to be finalised:
 - ViSEAGO
- Exclude the genetic causes for the observed differences between epilines
- Identification of the biological mechanisms involved

3 - Results

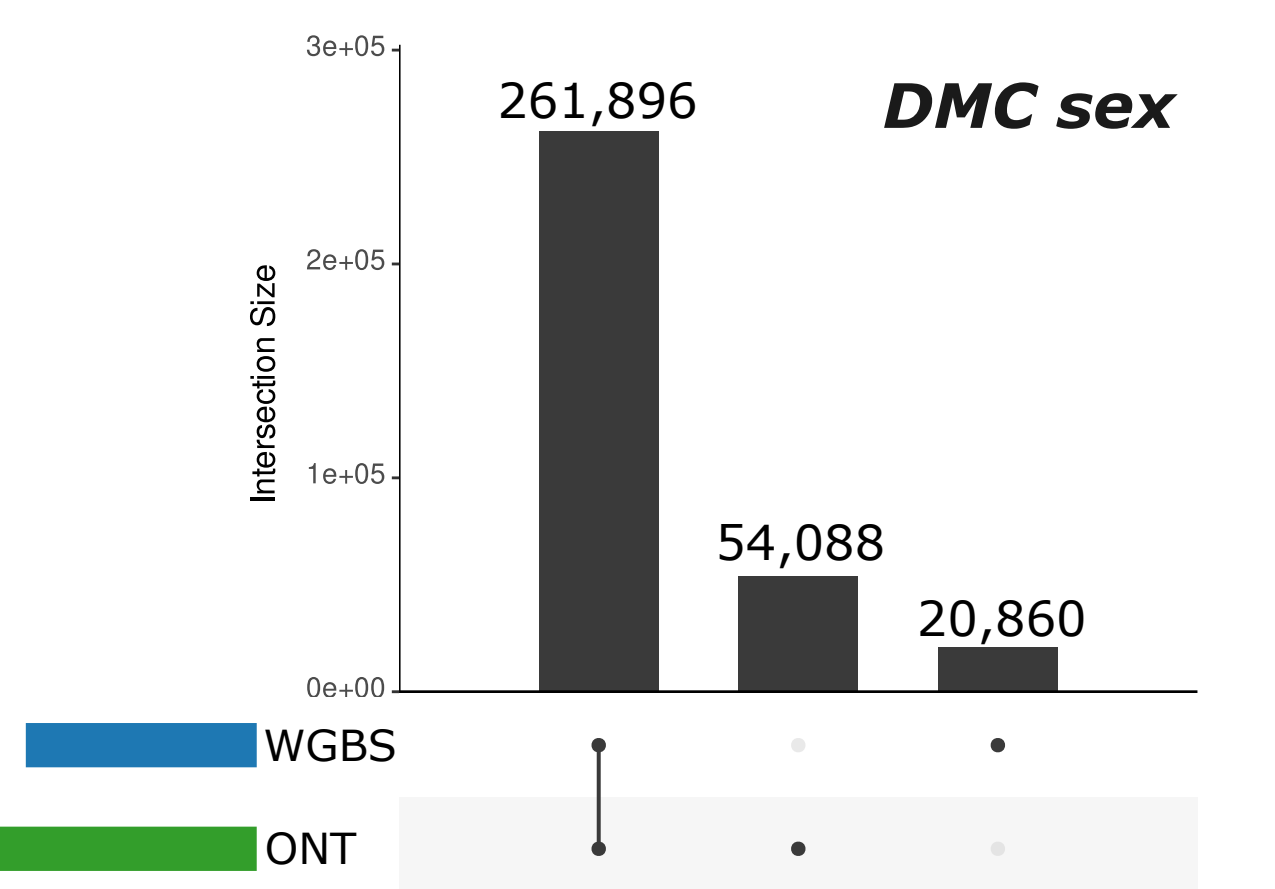
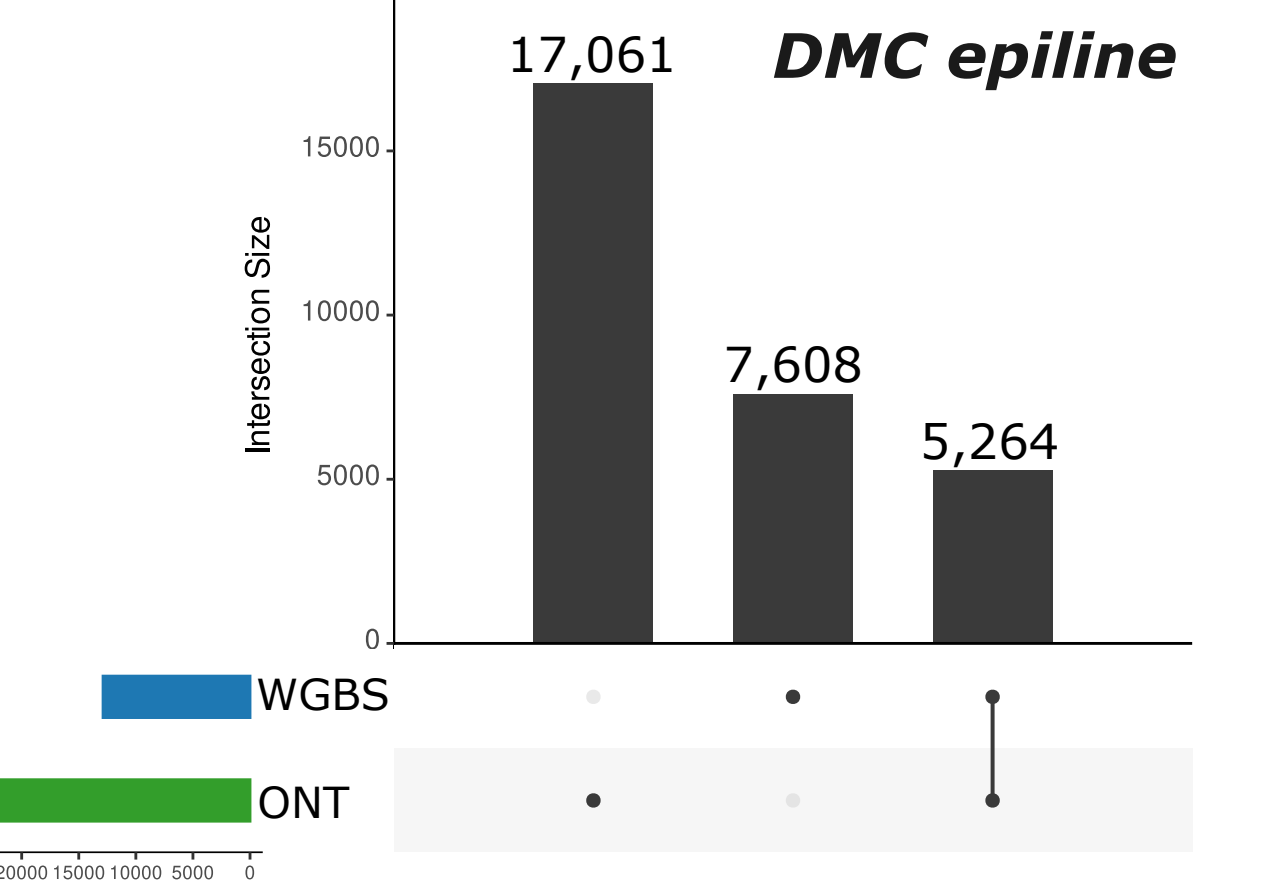


Number of CpG sites measured



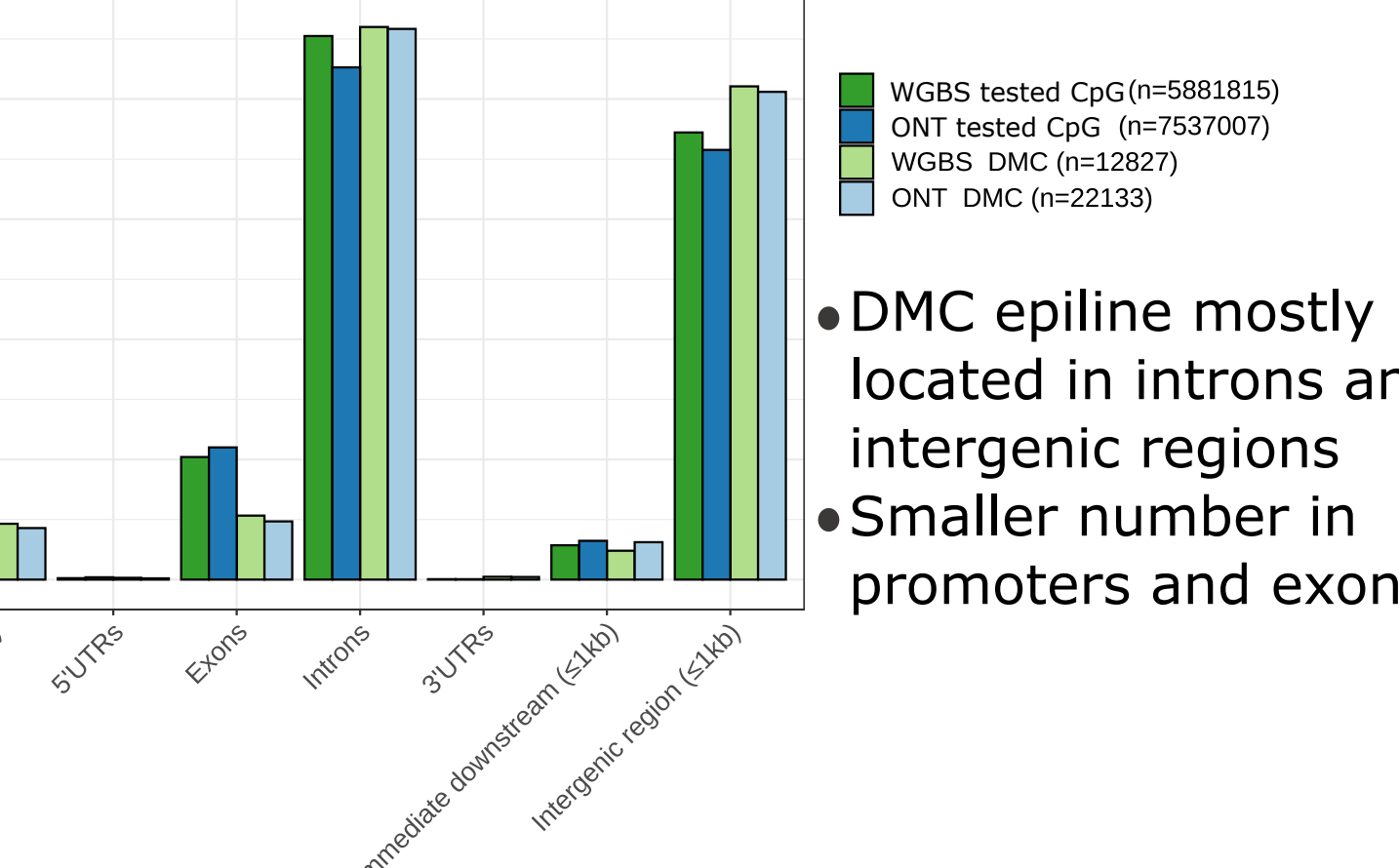
99% WGBS CpG found in ONT (from 8,974,565 CpG in quail assembly)

Number of DMC epilines/sex detected



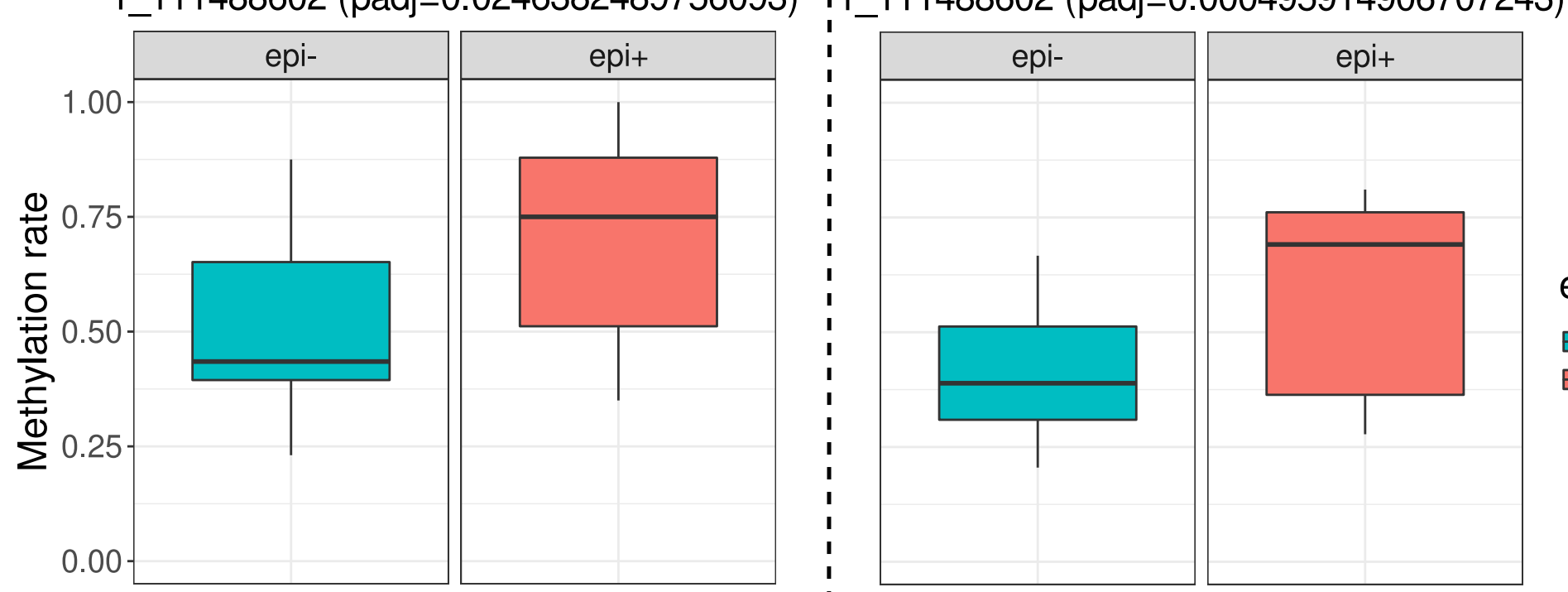
Greater number of DMC detected with ONT than WGBS

Distribution of CpG sites and DMC epilines by genomic region

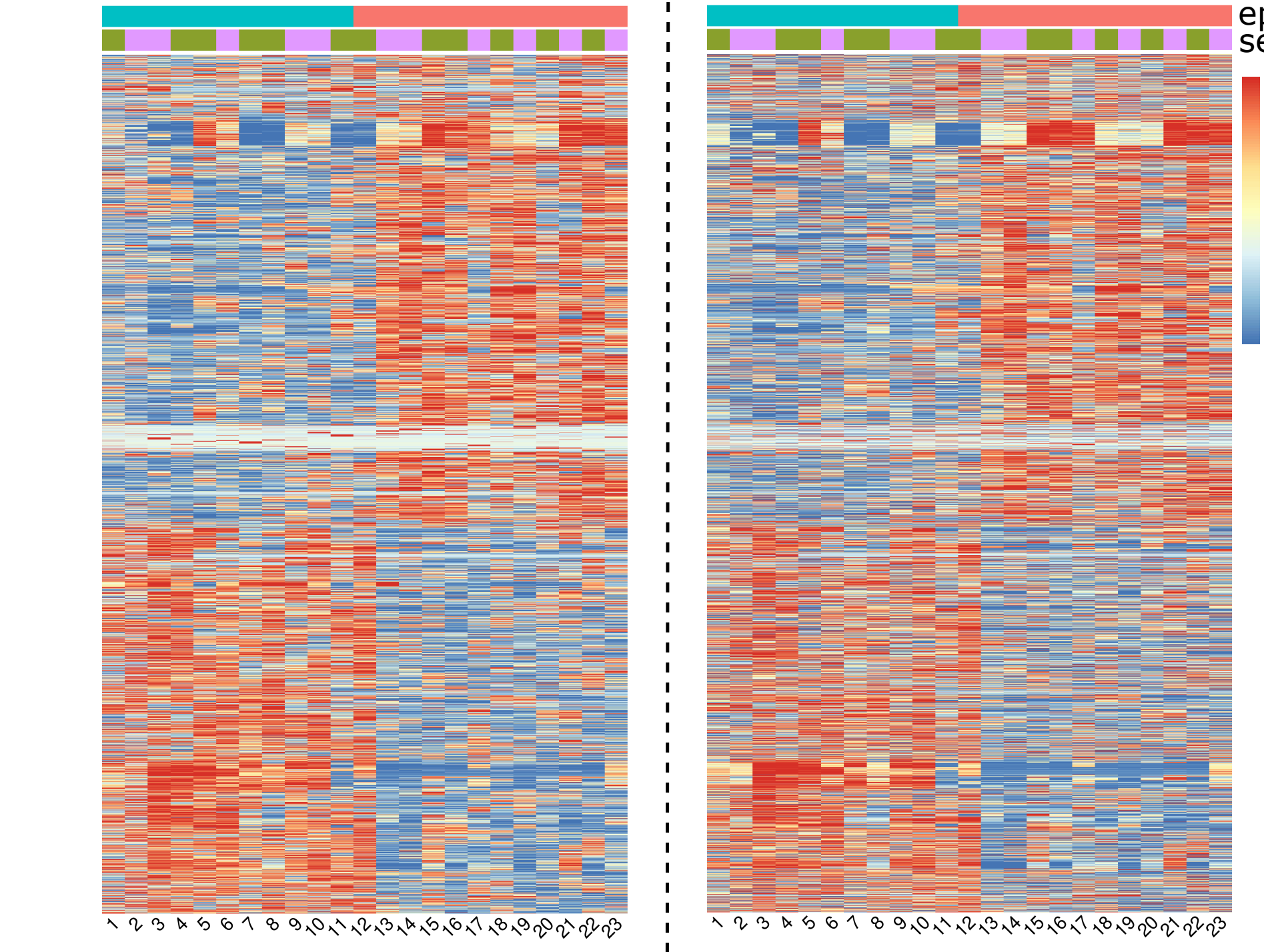


• DMC epilines mostly located in introns and intergenic regions
• Smaller number in promoters and exons

Mean methylation rate of one DMC epiline

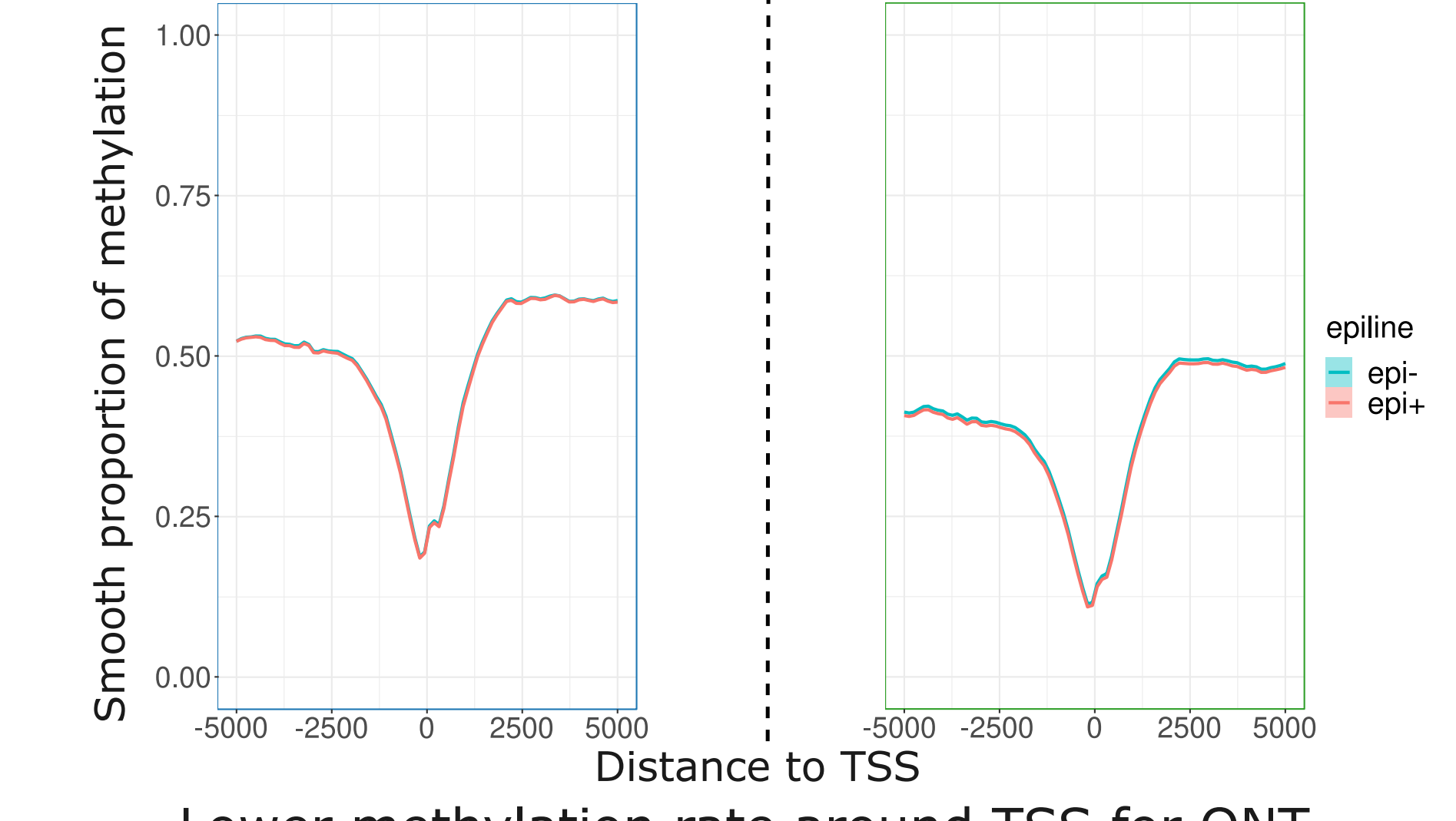


Heatmap of methylation rate of 10,000 DMC epilines



Similar methylation profile between WGBS and ONT
Significant difference between epi-/epi+

Smooth proportion of methylation by distance to TSS



Lower methylation rate around TSS for ONT

Correlation of the methylation rate between WGBS and ONT (1 sample)

