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# Transgenerational epigenetics in quail: whole genome DNA methylation analysis

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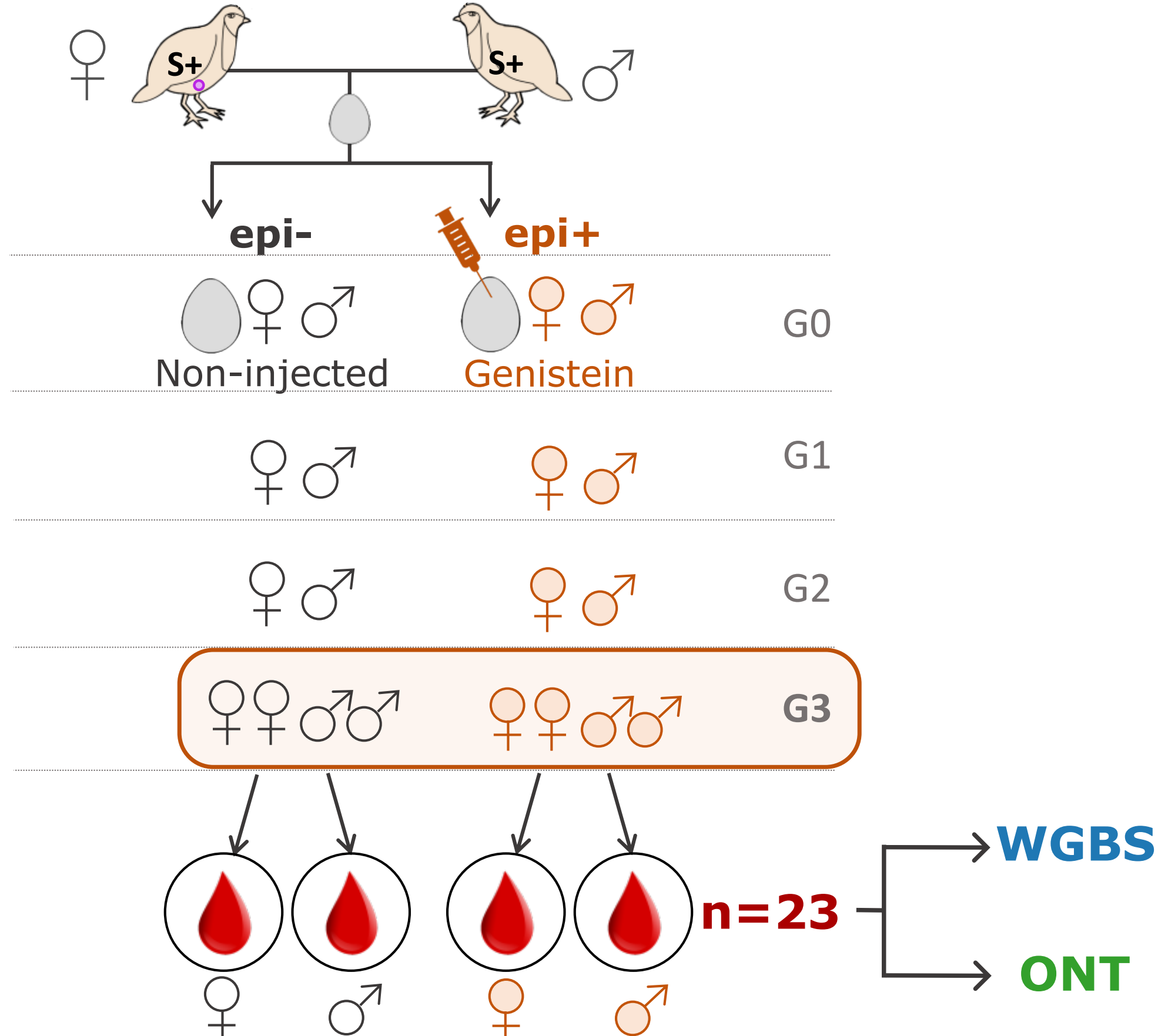
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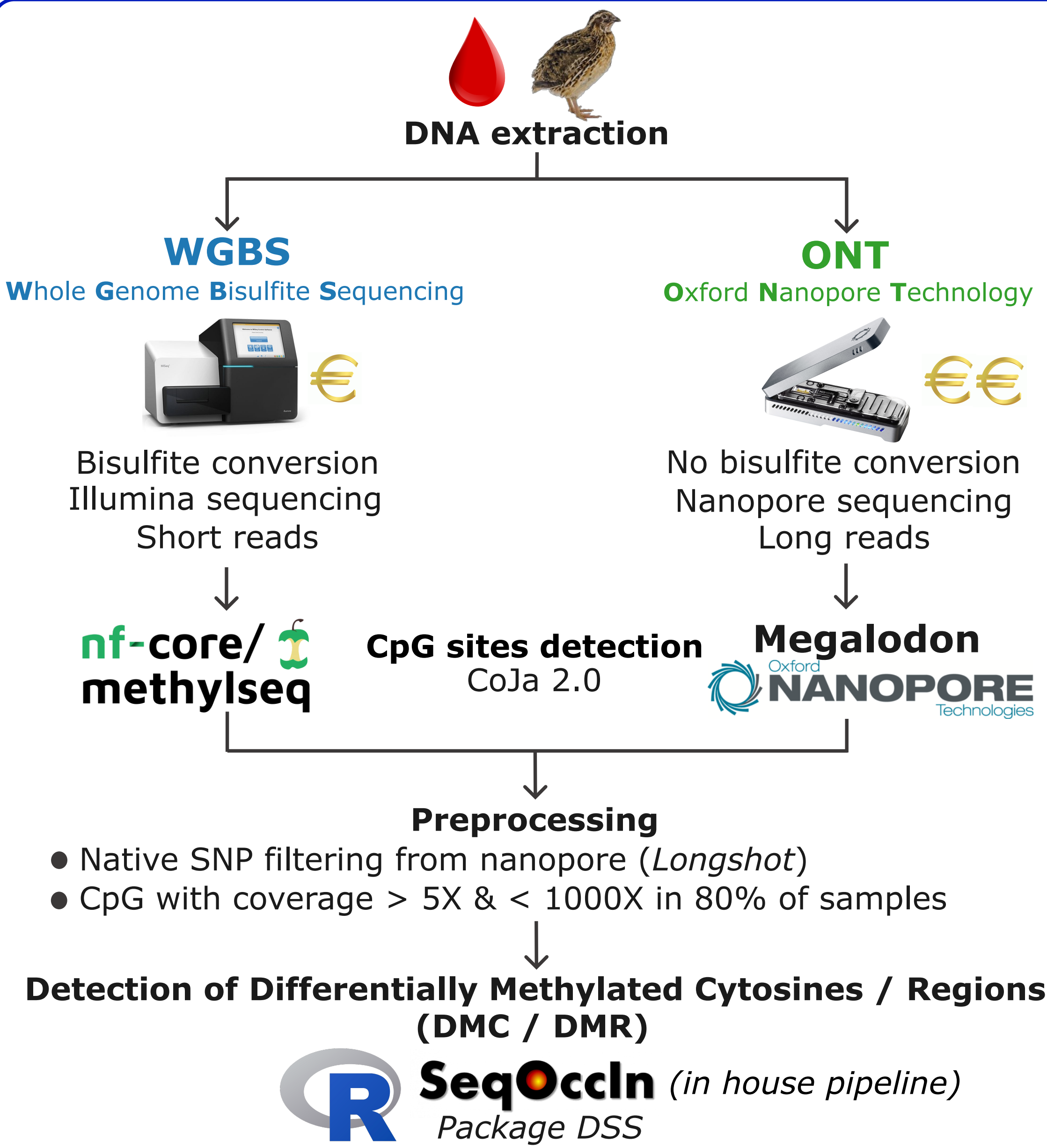
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The influence of the **prenatal environment** on the adult **phenotype development** is partially mediated by **epigenetic phenomena**. Recently, an increasing number of studies highlighted the **transmission of epigenetic marks between generations**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



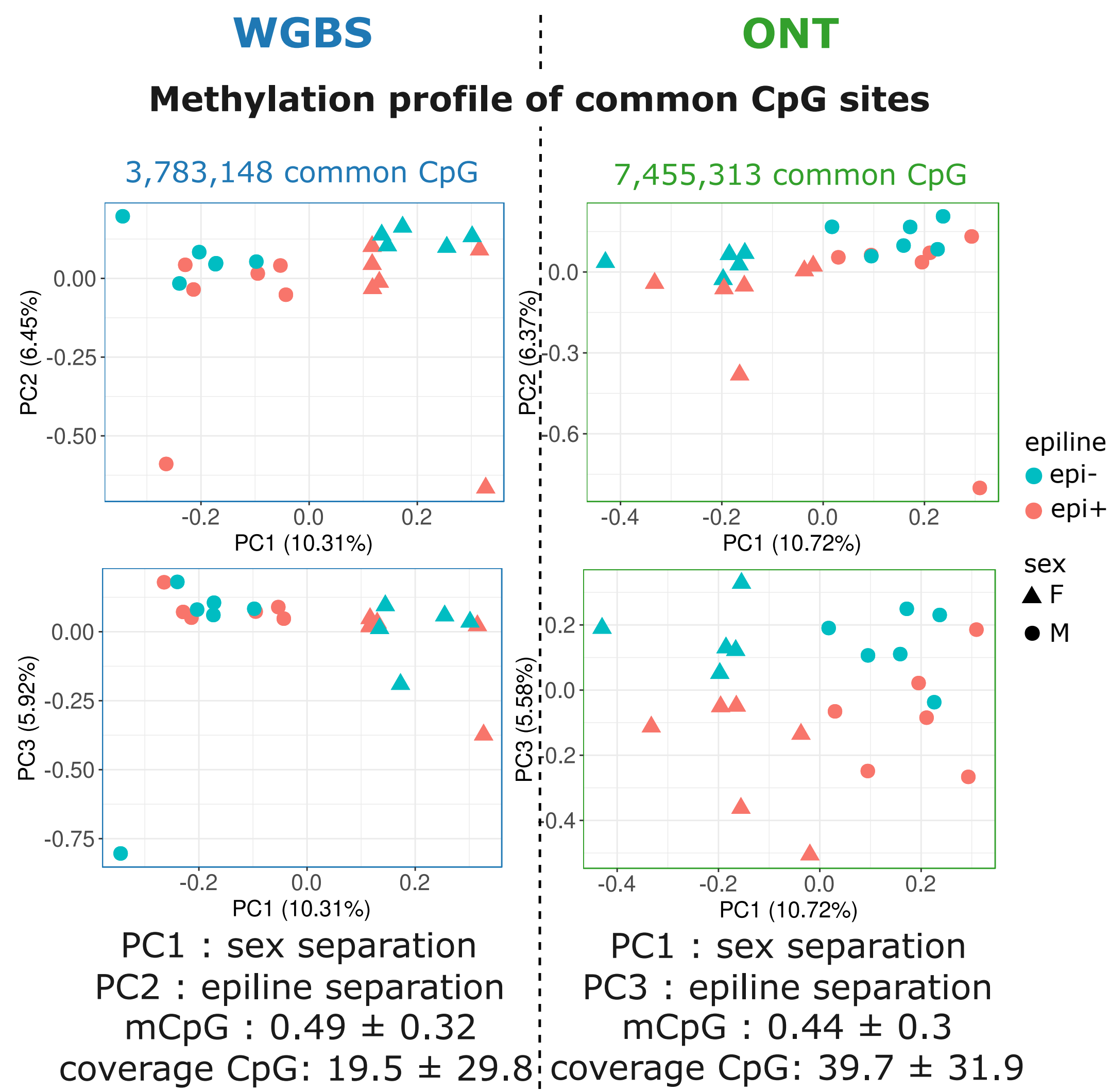
## Conclusion

- 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

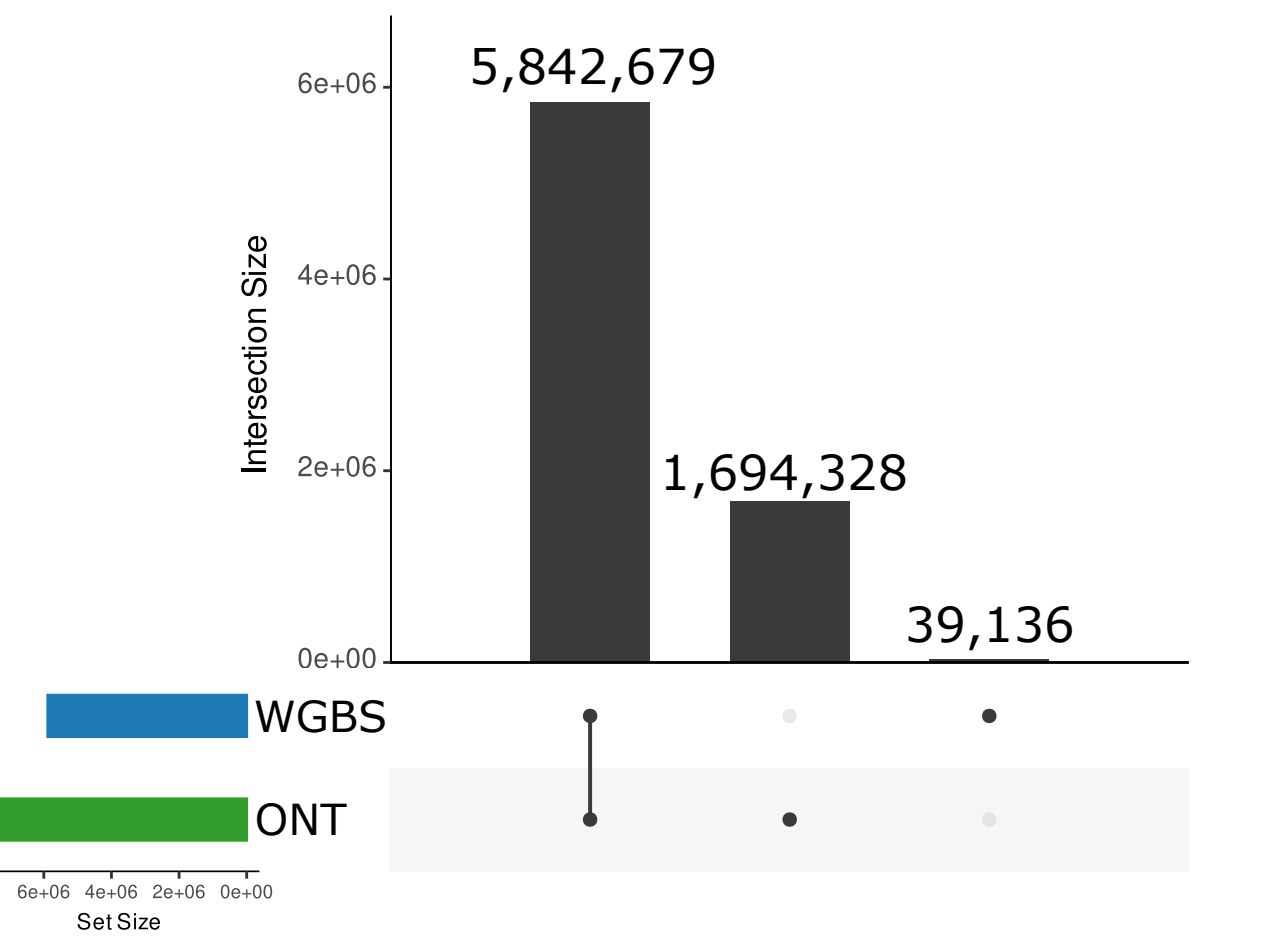
## Perspectives

- 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

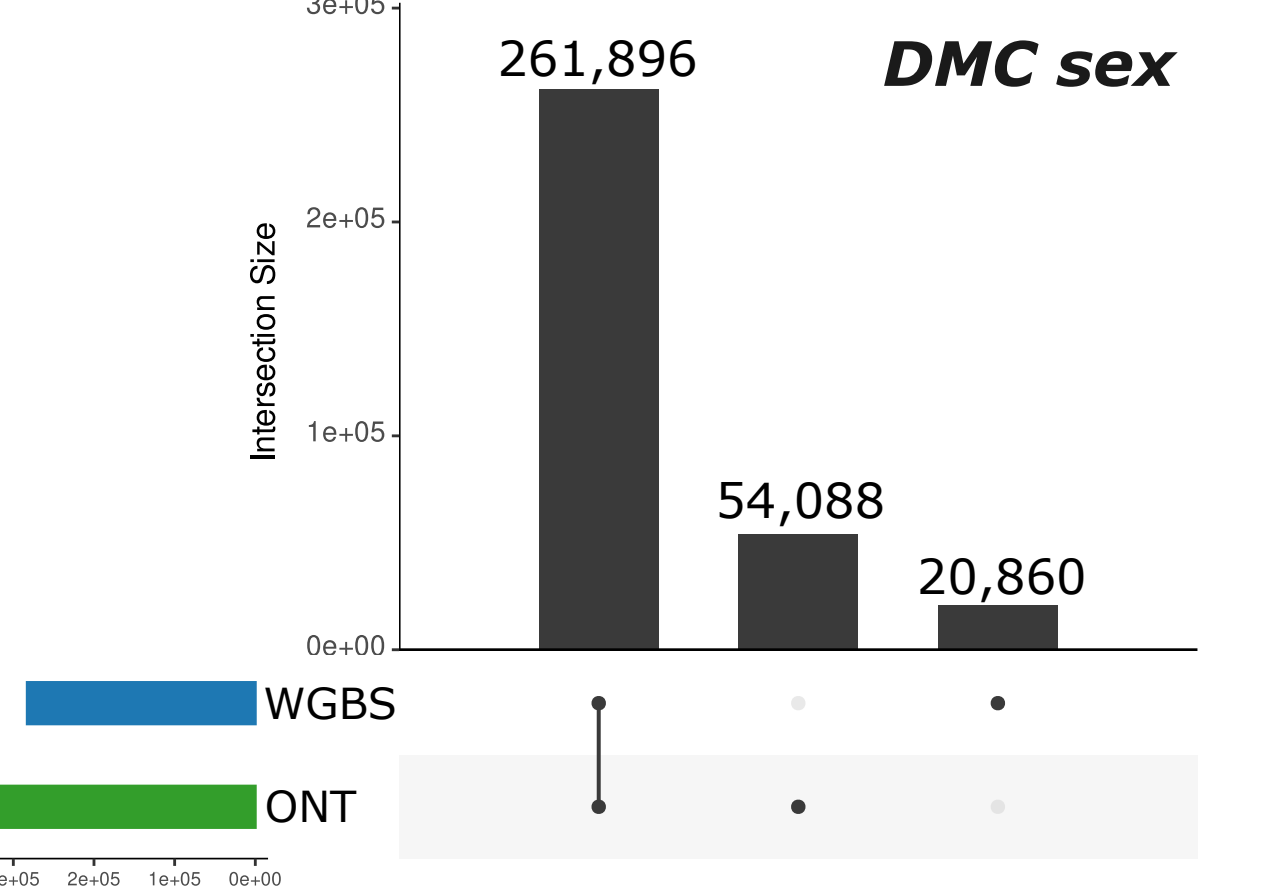
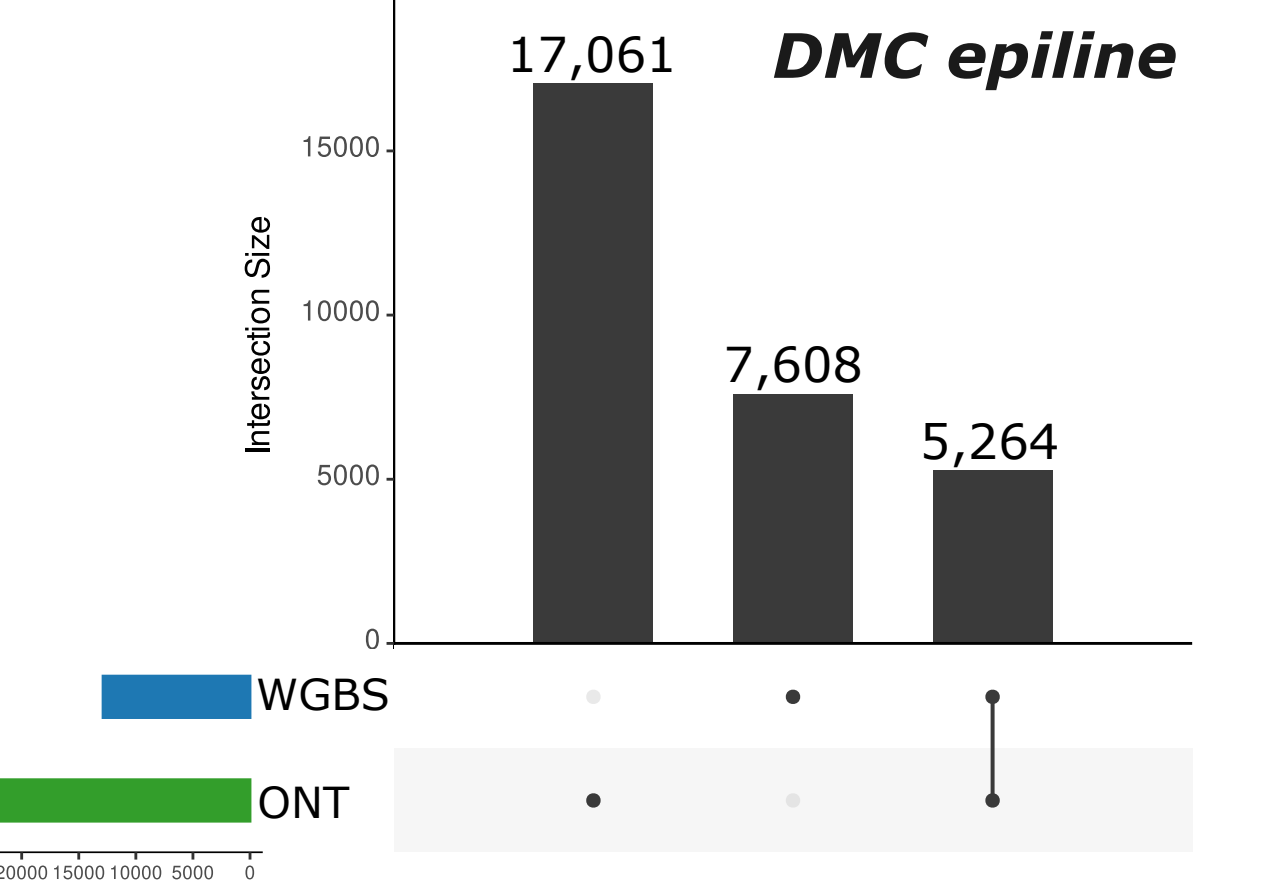


### Number of CpG sites measured



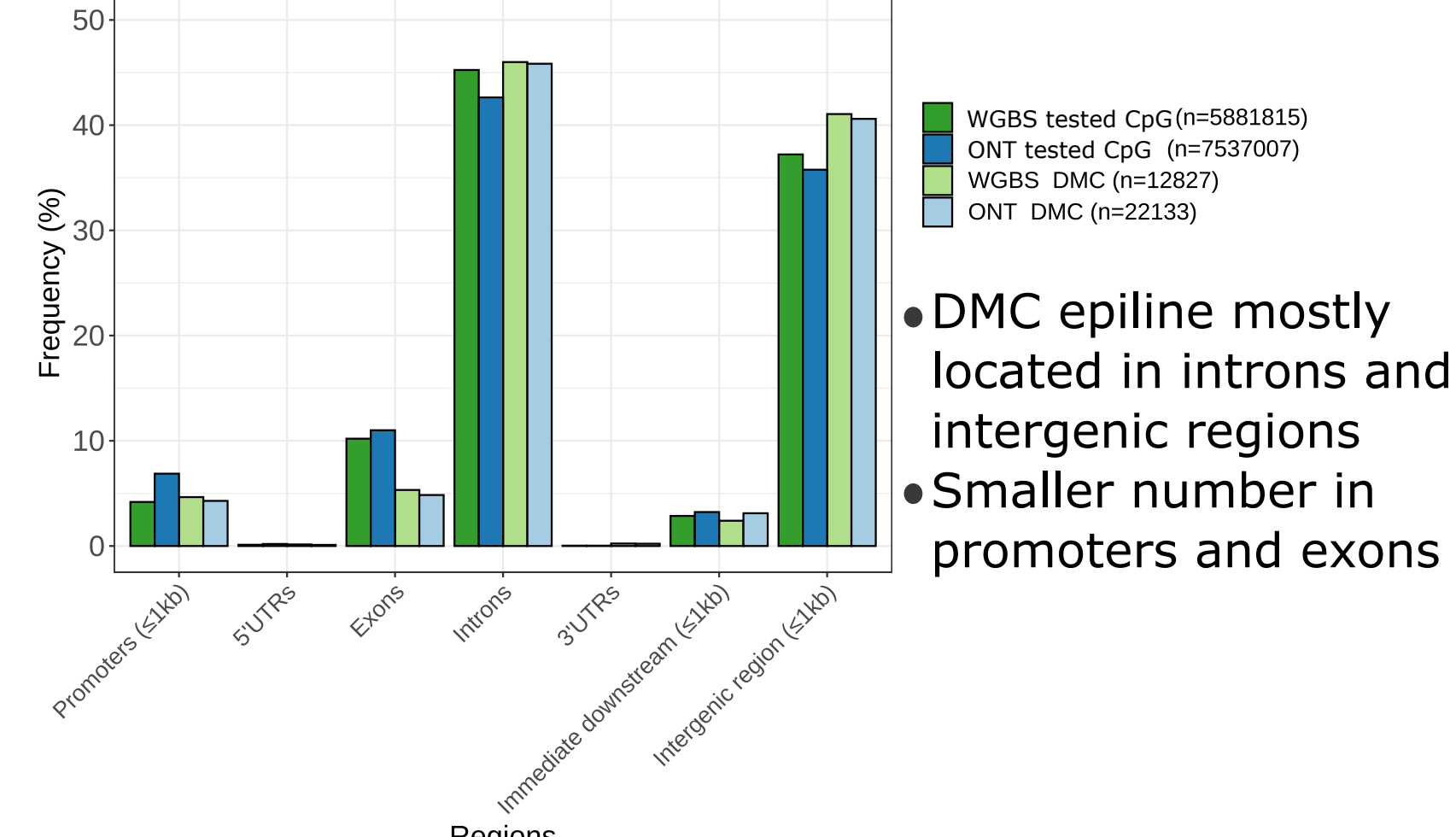
99% WGBS CpG found in ONT (from 8,974,565 CpG in quail assembly)

### Number of DMC epilines/sex detected



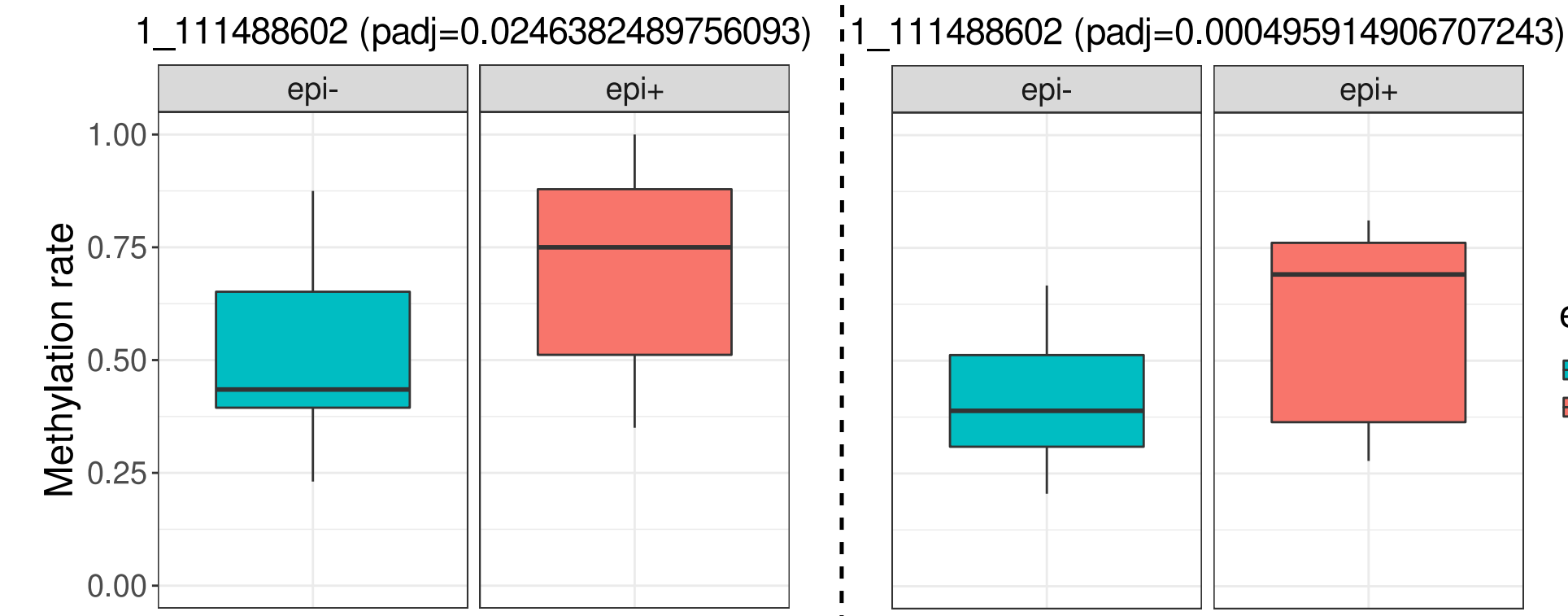
Greater number of DMC detected with ONT than WGBS

### Distribution of CpG sites and DMC epilines by genomic region

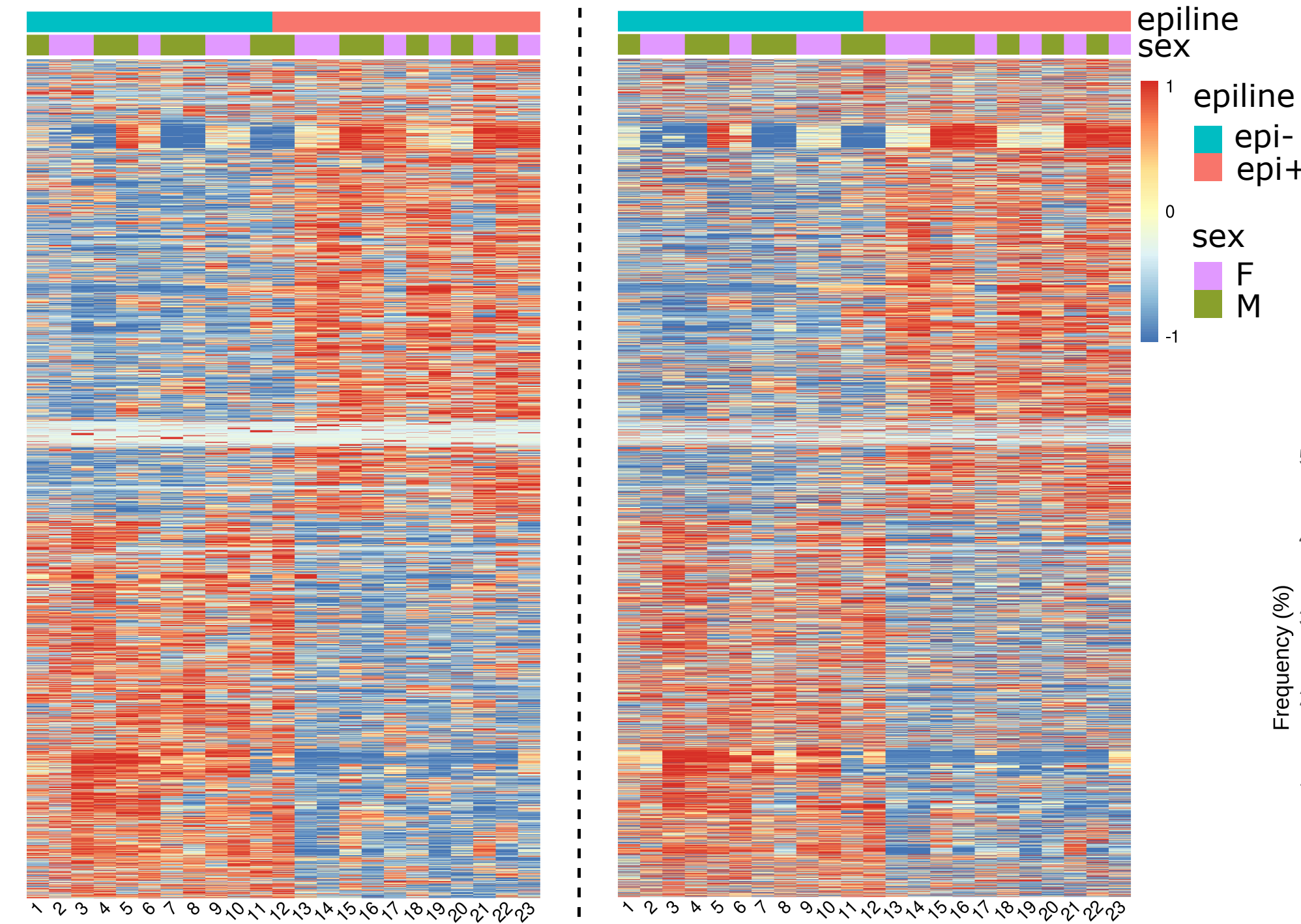


- DMC epilines mostly located in introns and intergenic regions
- Smaller number in promoters and exons

### Mean methylation rate of one DMC epiline

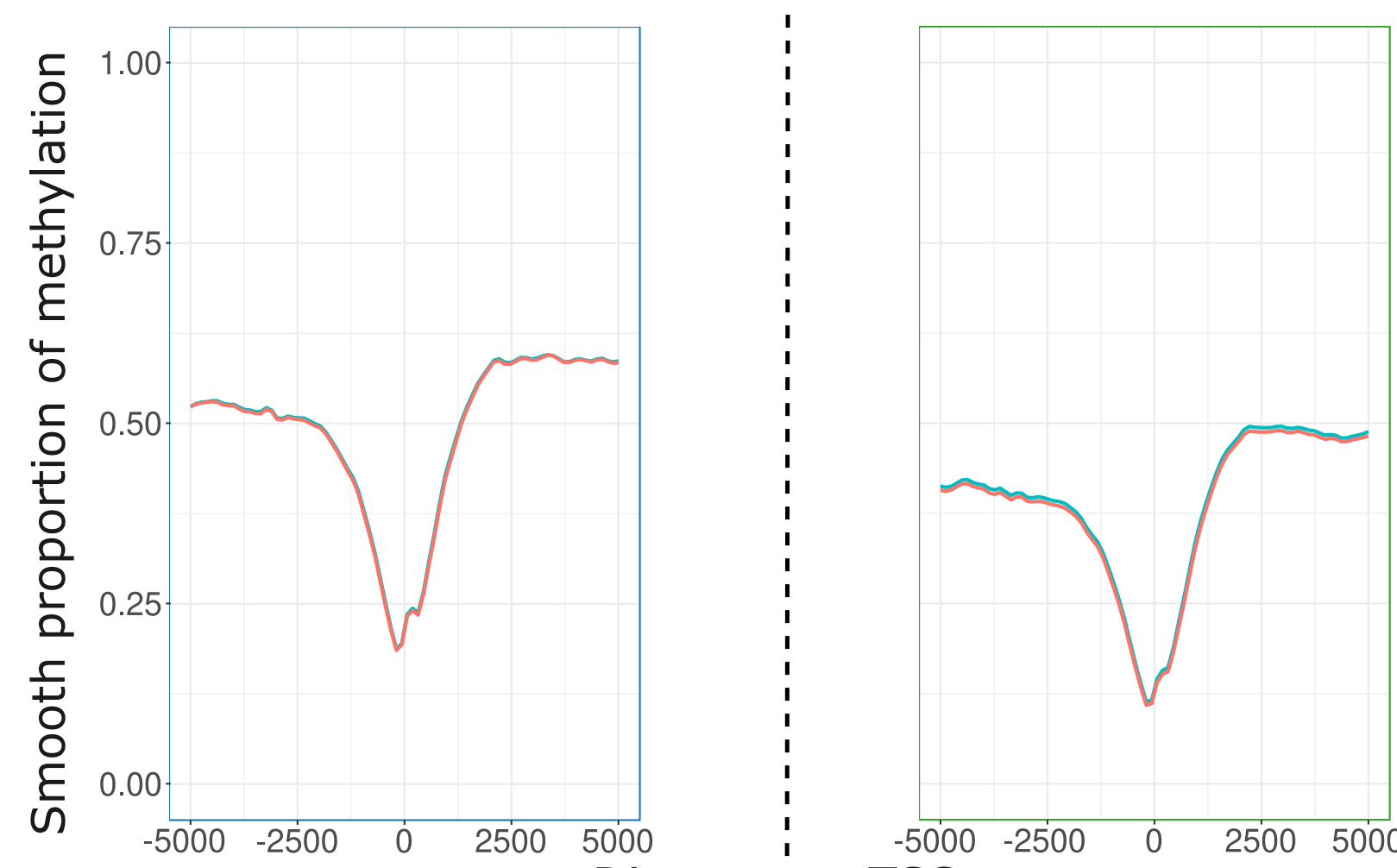


### Heatmap of methylation rate of 10,000 DMC epilines



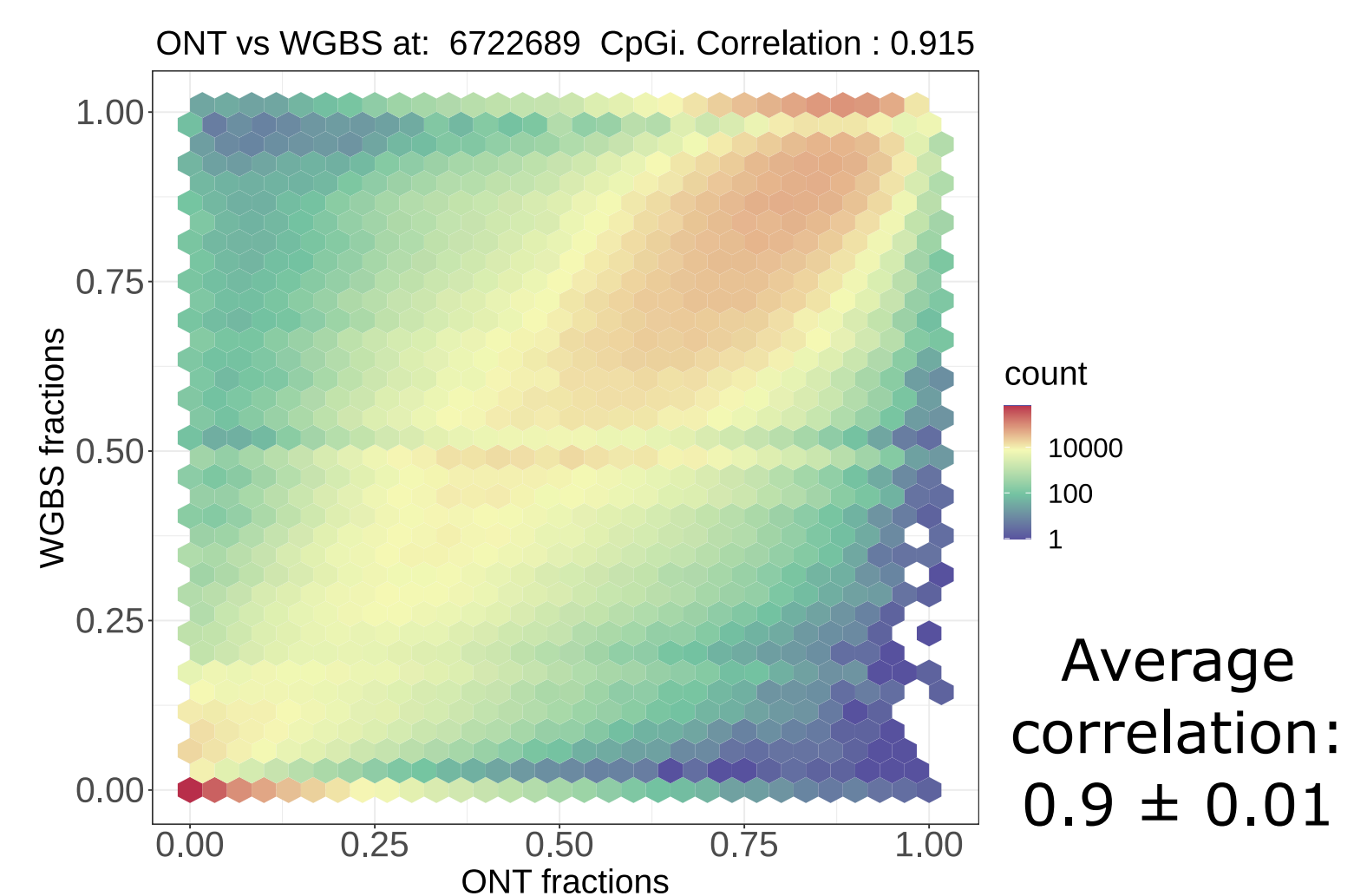
Similar methylation profile between WGBS and ONT  
Significant difference between epi-/epi+

### 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)



Average correlation: 0.9 ± 0.01