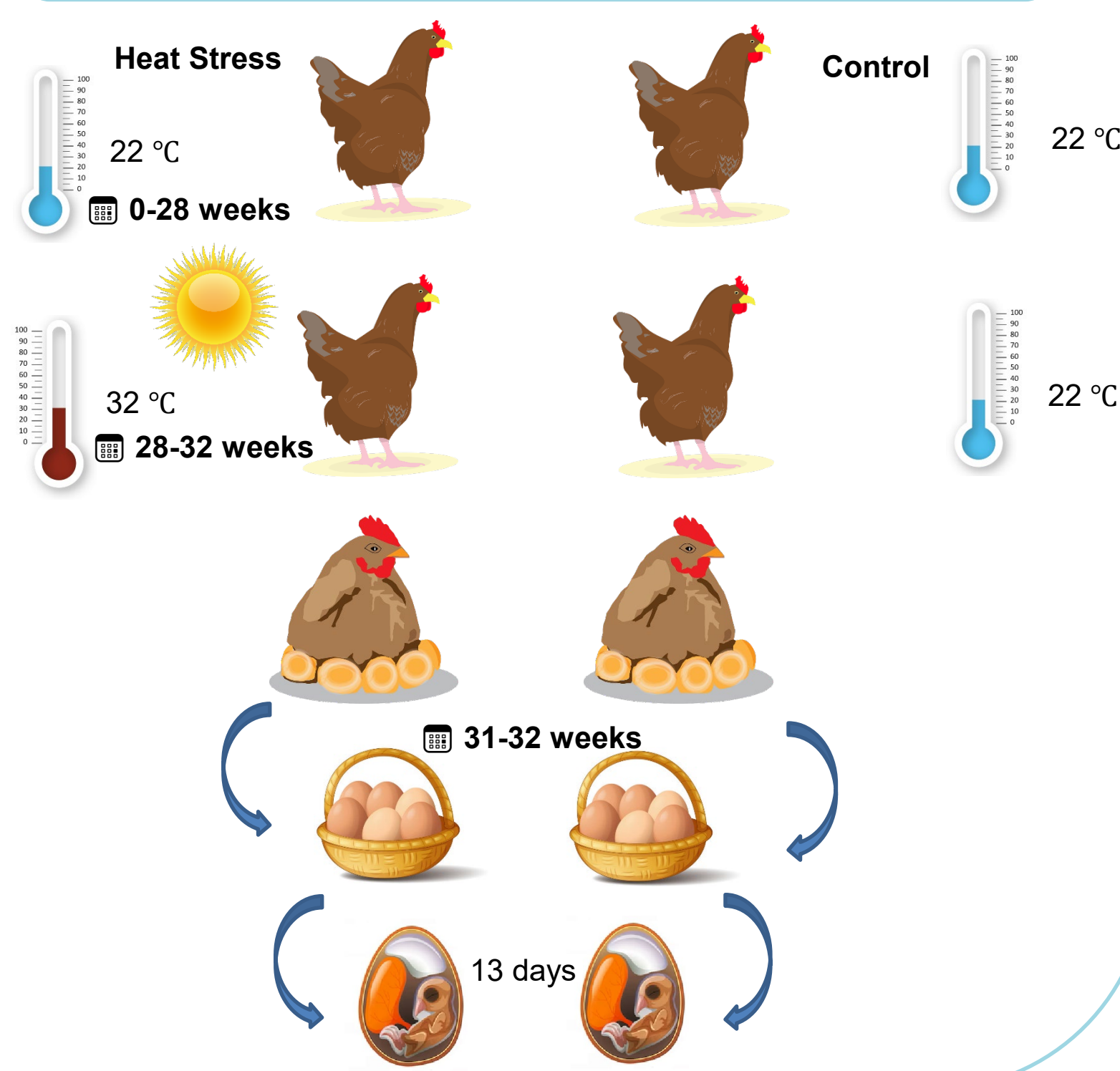


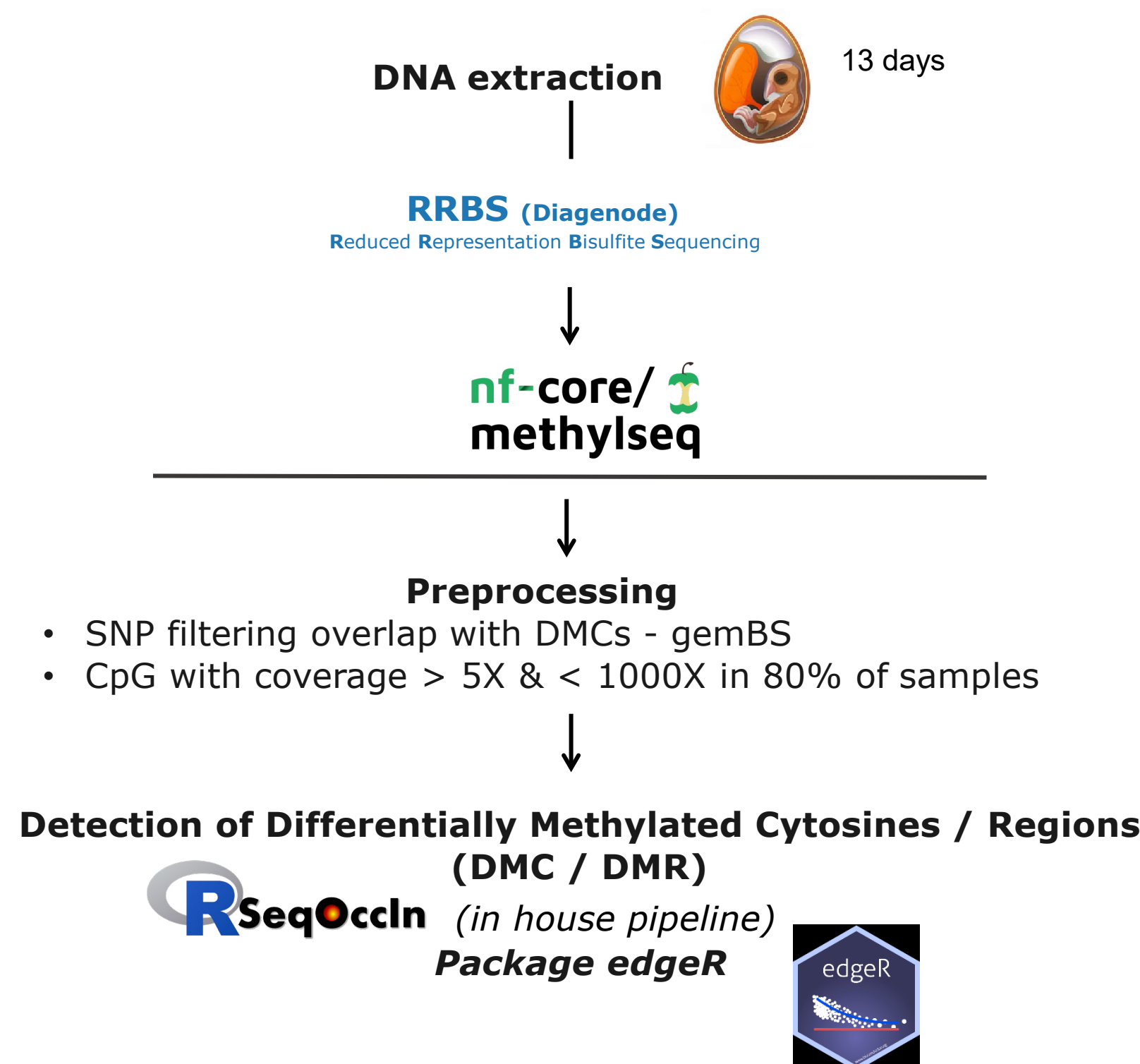
Introduction

Climate change and its impact on the agricultural sector are one of the most important challenges for adaptation especially in livestock production. Increasing social concerns for sustainable agriculture strongly influences animal breeding systems. Poultry production is a major source of proteins for human food worldwide and in a context of growing human population, it is essential to work towards better adaptation of poultry to heat stress and limitations on feed. We propose to address this broad and challenging question from a biological perspective by analyzing the epigenome of chickens, which is known to be modulated in response to environmental variations.

Experimental design



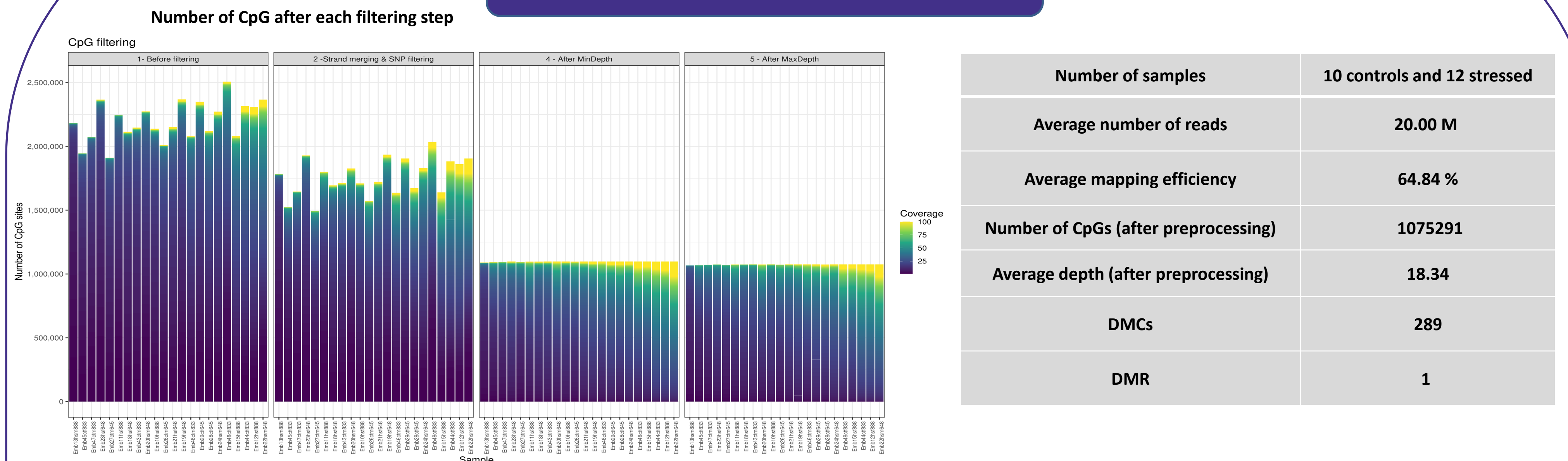
Methods



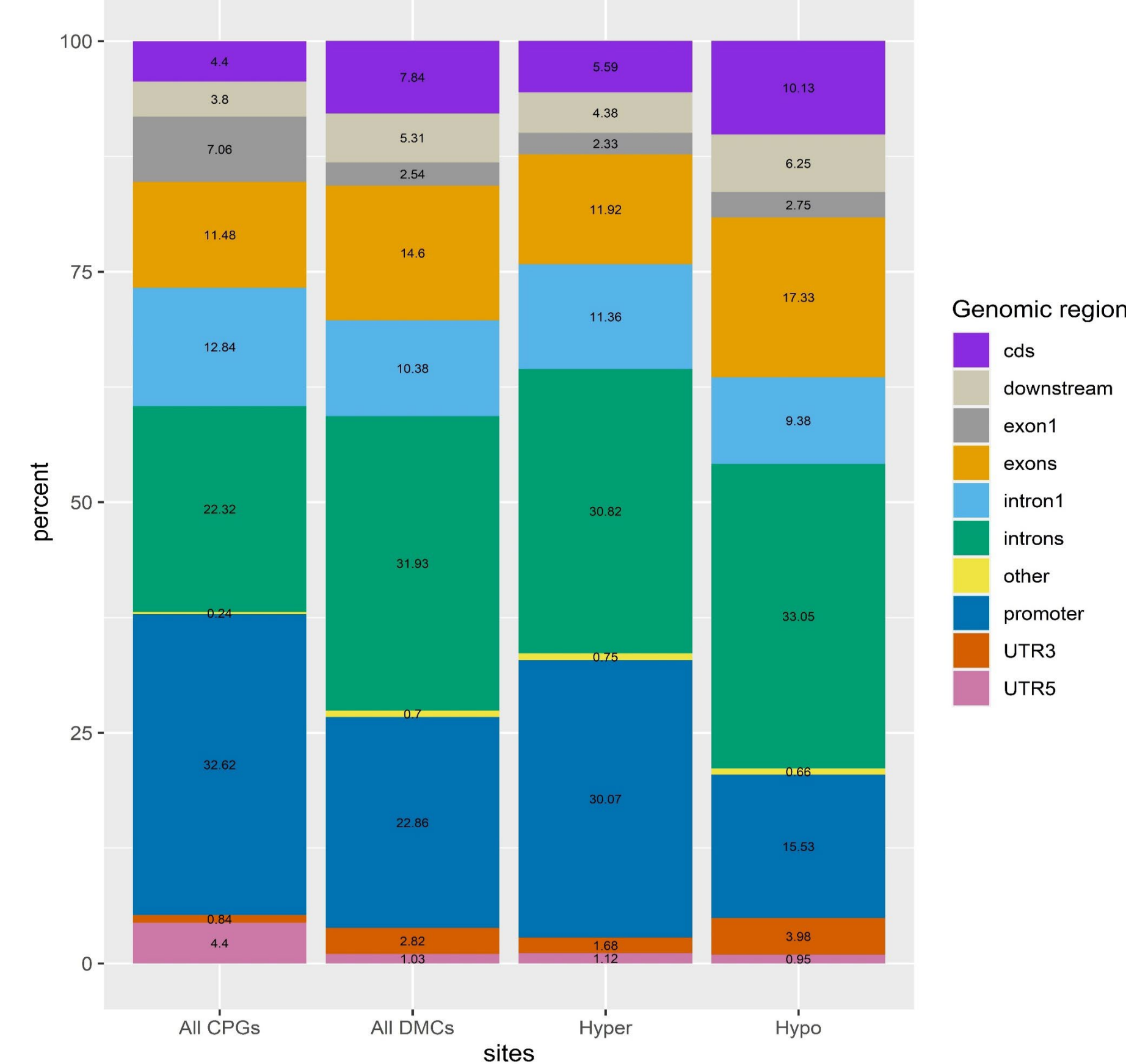
Conclusion

- a total of **289 DMCs** and **one DMR** between offspring of heated stressed mothers and controls.
- These DMCs were associated with **358 genes**, which play an important role in processes such as **cellular response to stimulus** and **developmental processes**.
- Overall, this study provides valuable insights into the **adaptive mechanisms** involved in the response of chicken embryos to heat stress in their mothers.
- These results show that **heat stress of hens can mediate changes in the methylation patterns of offspring during the embryonic stage**, possibly influencing their response to later exposures to heat stress.

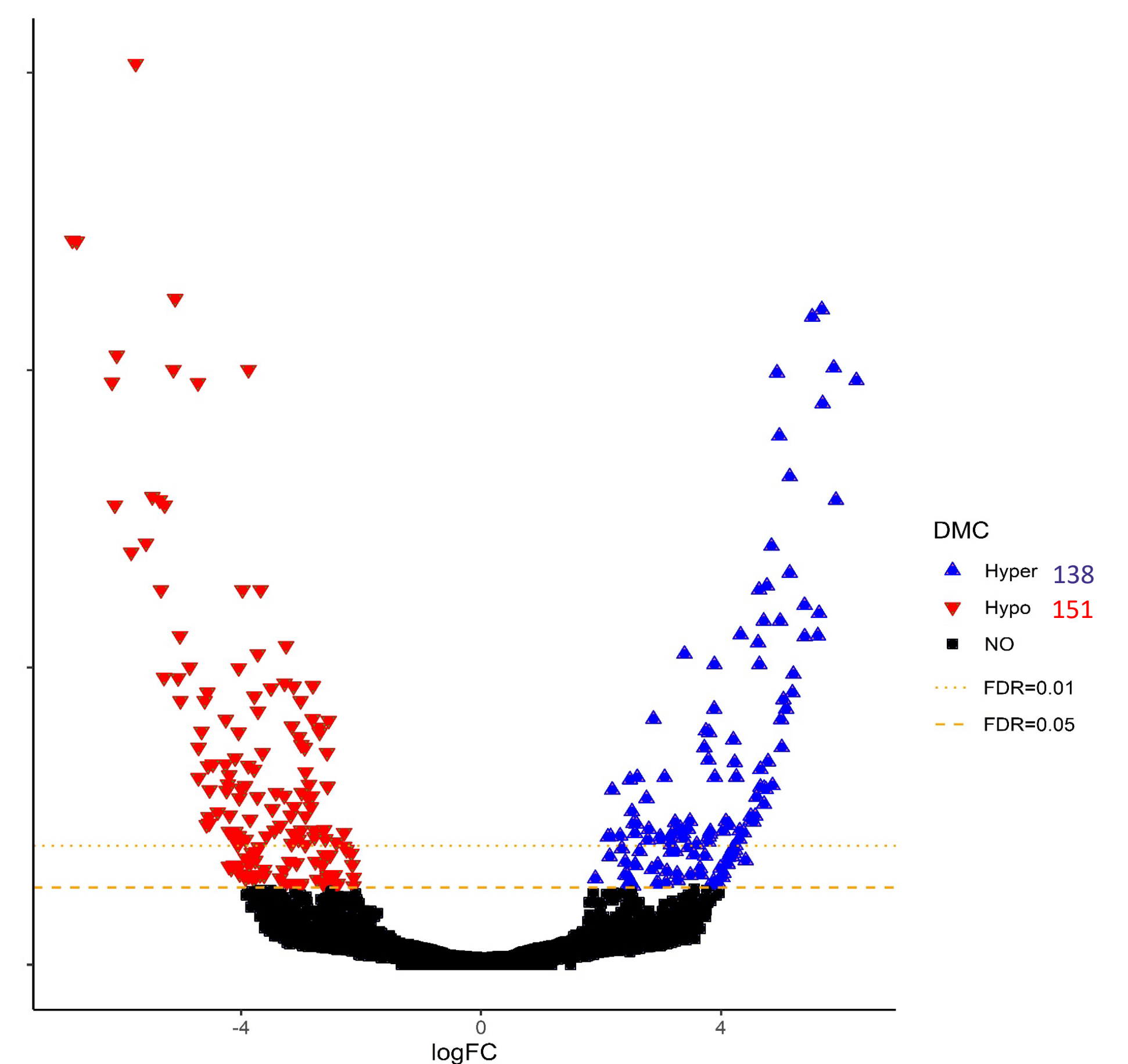
Results



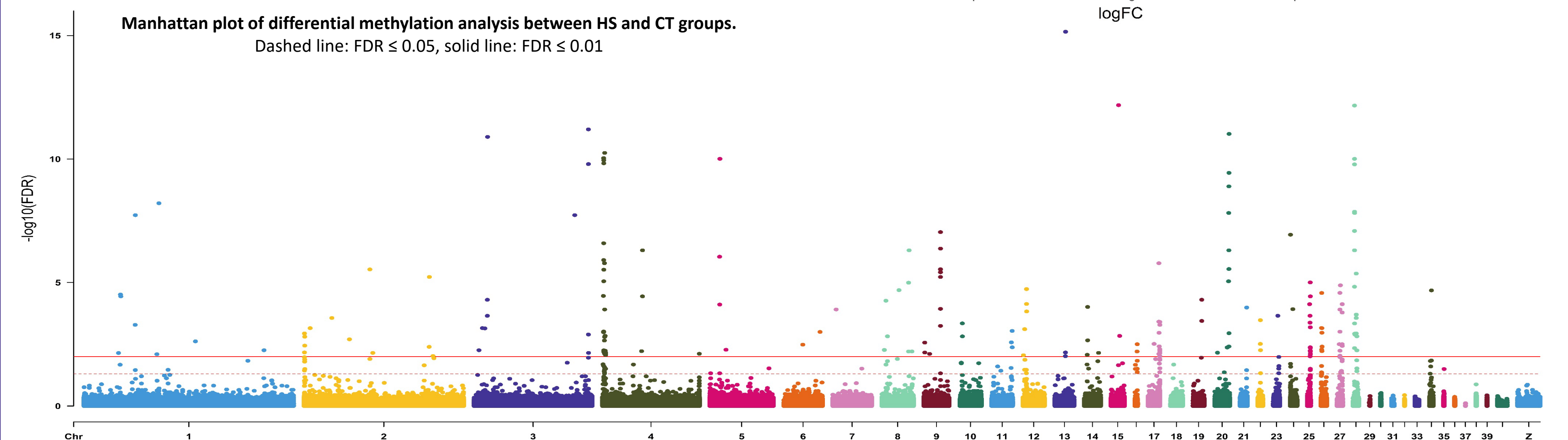
Distribution of total CpGs, DMCs (Hyper and Hypo DMCs) across the different genomic regions



Volcano plot (CpG methylation changes between HS and CT)



Manhattan plot of differential methylation analysis between HS and CT groups. Dashed line: FDR ≤ 0.05, solid line: FDR ≤ 0.01



Clustering plots of the functional sets of gene ontology (GO) terms (obtained using VISEAGO)

