

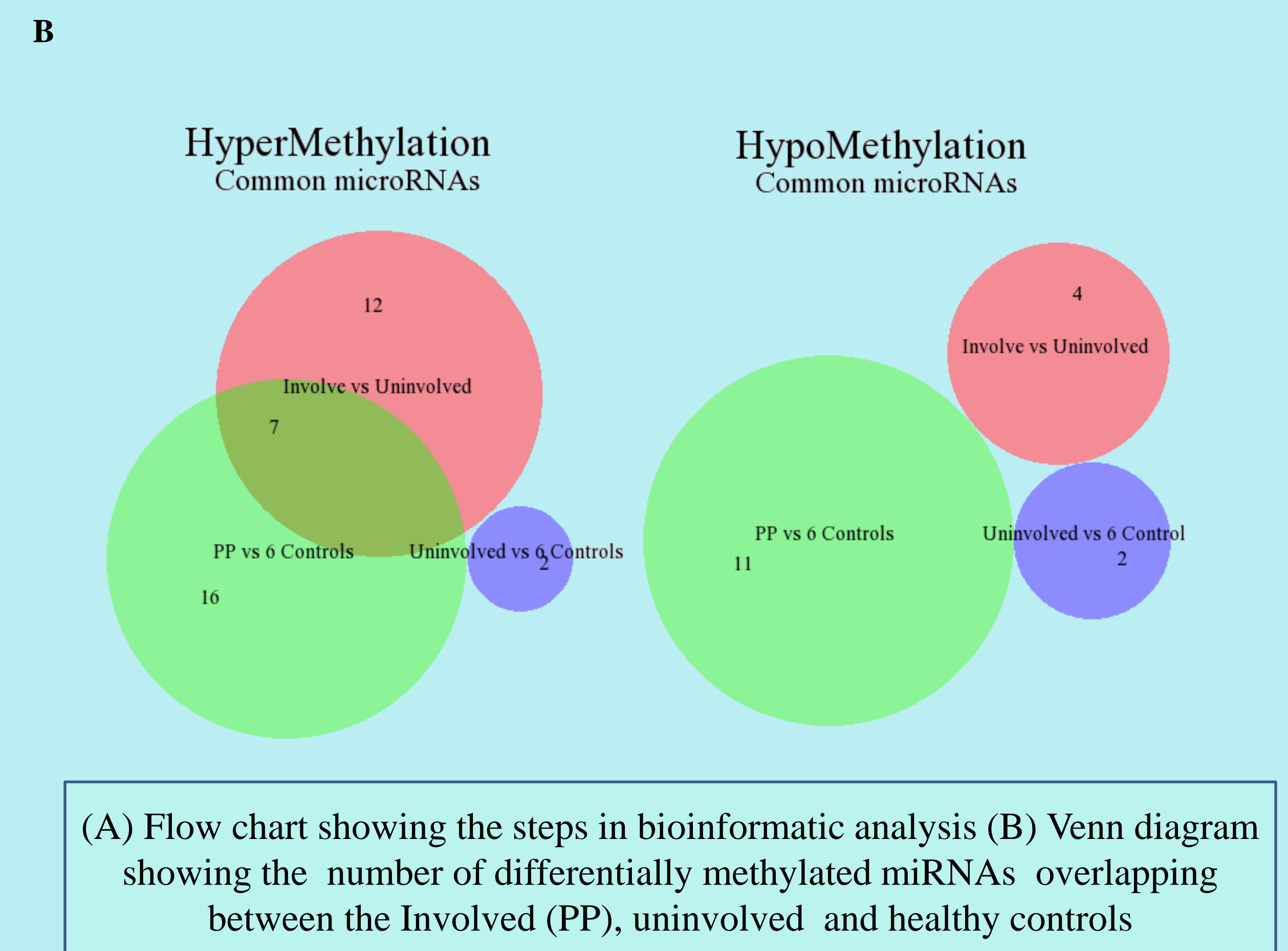
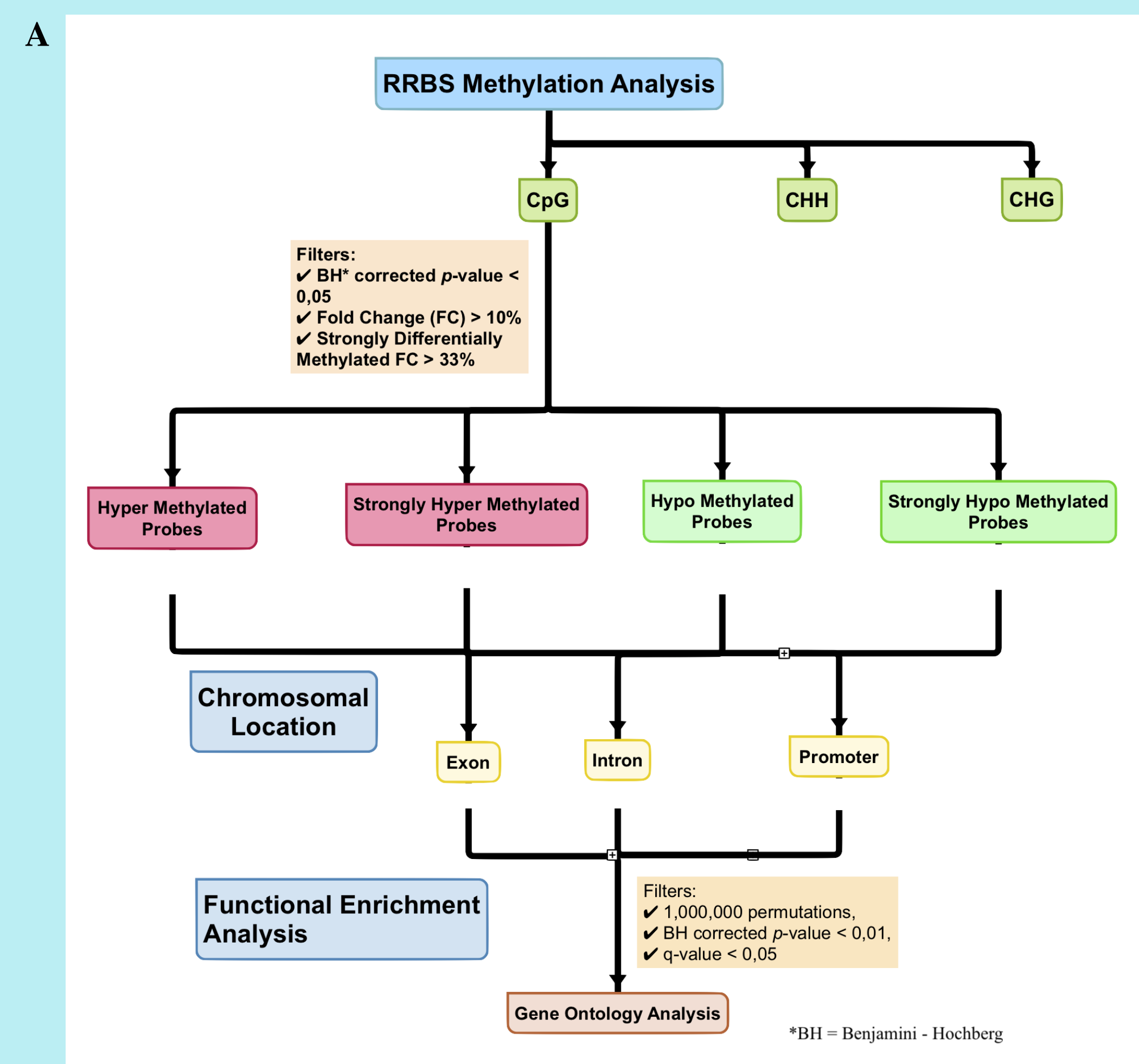
Altered methylation of microRNA (miRNA) in the psoriatic epidermis

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Introduction

MiRNAs are short, single-stranded RNA molecules that regulate gene expression by binding to the target mRNA leading to its degradation. Several miRNAs have been associated with psoriasis susceptibility and disease progression^{1,2}. Although several genome-wide analyses of DNA methylation in psoriasis have been performed, the differential methylation of miRNA in the context of psoriasis is previously unreported. The aim of this study was to explore the existence of epigenetic regulation of miRNA in psoriasis.



Method

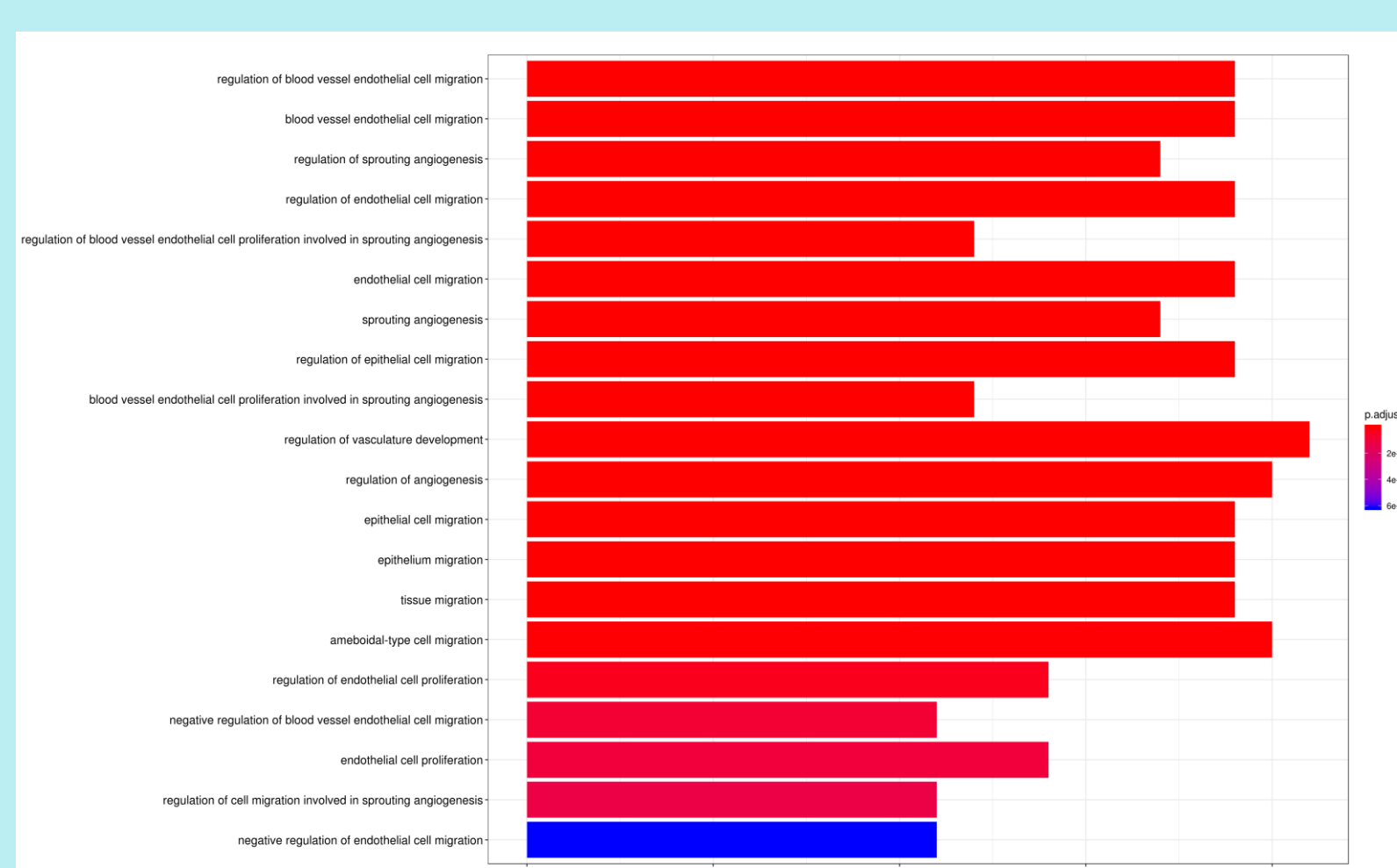
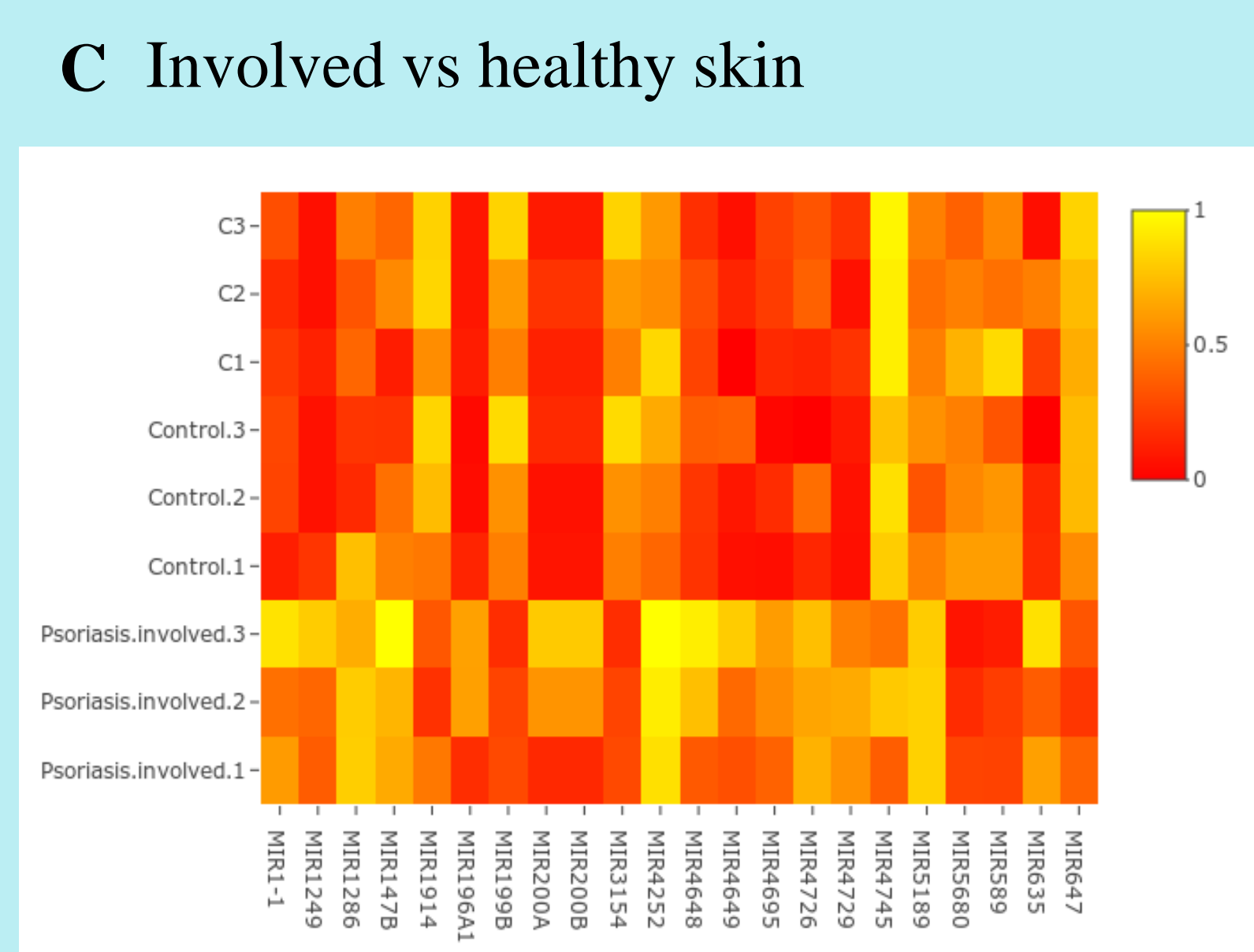
We isolated epidermis from skin punch biopsies and compared the involved and uninvolved epidermis from psoriasis patients with epidermis from healthy controls. We performed an exhaustive genome-wide DNA methylation profiling using reduced representation bisulfite sequencing, which interrogates the methylation status of ~3-4 million CpG sites³. The differentially methylated sites in the miRNAs were analysed as shown in the flowchart.

Results

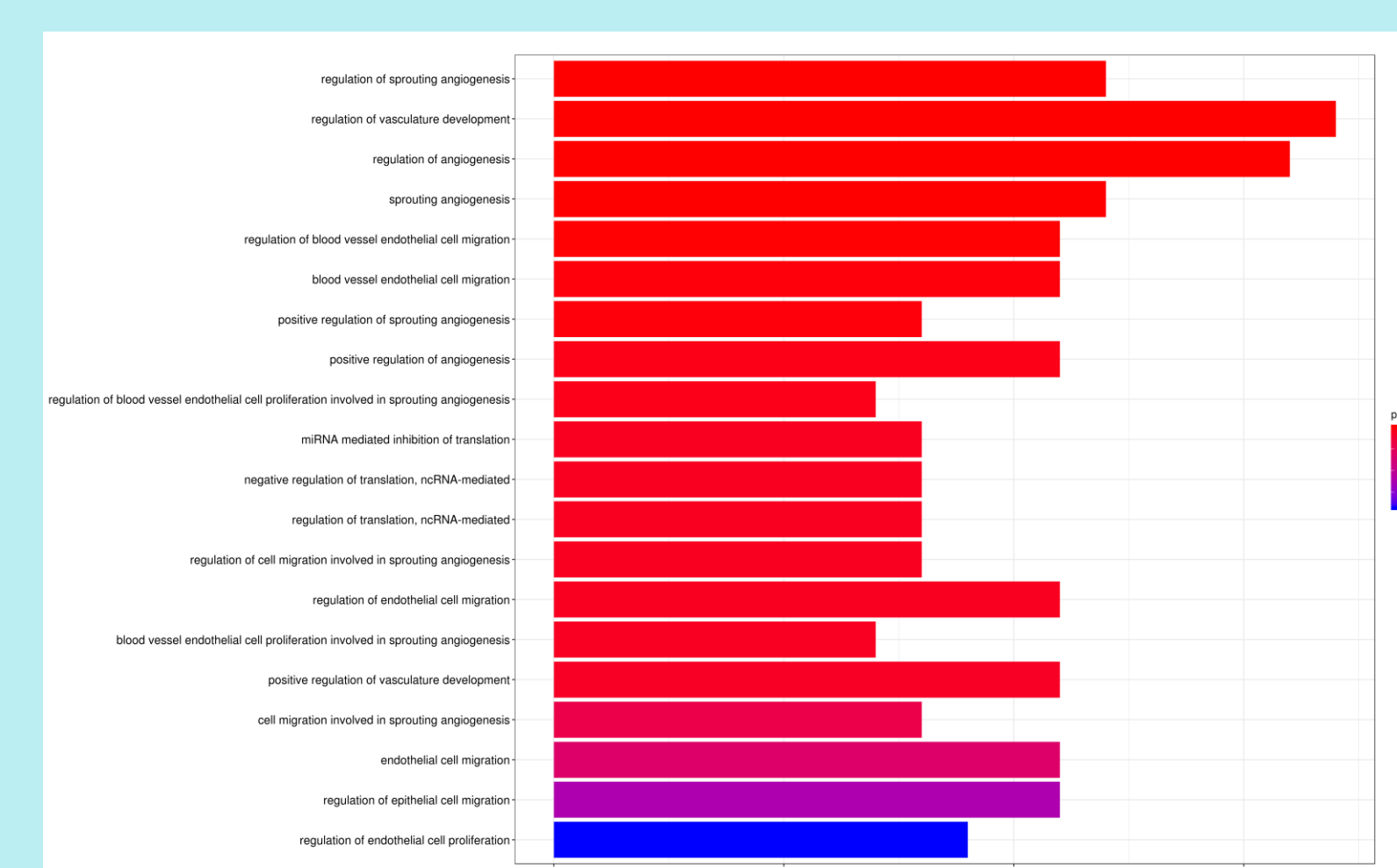
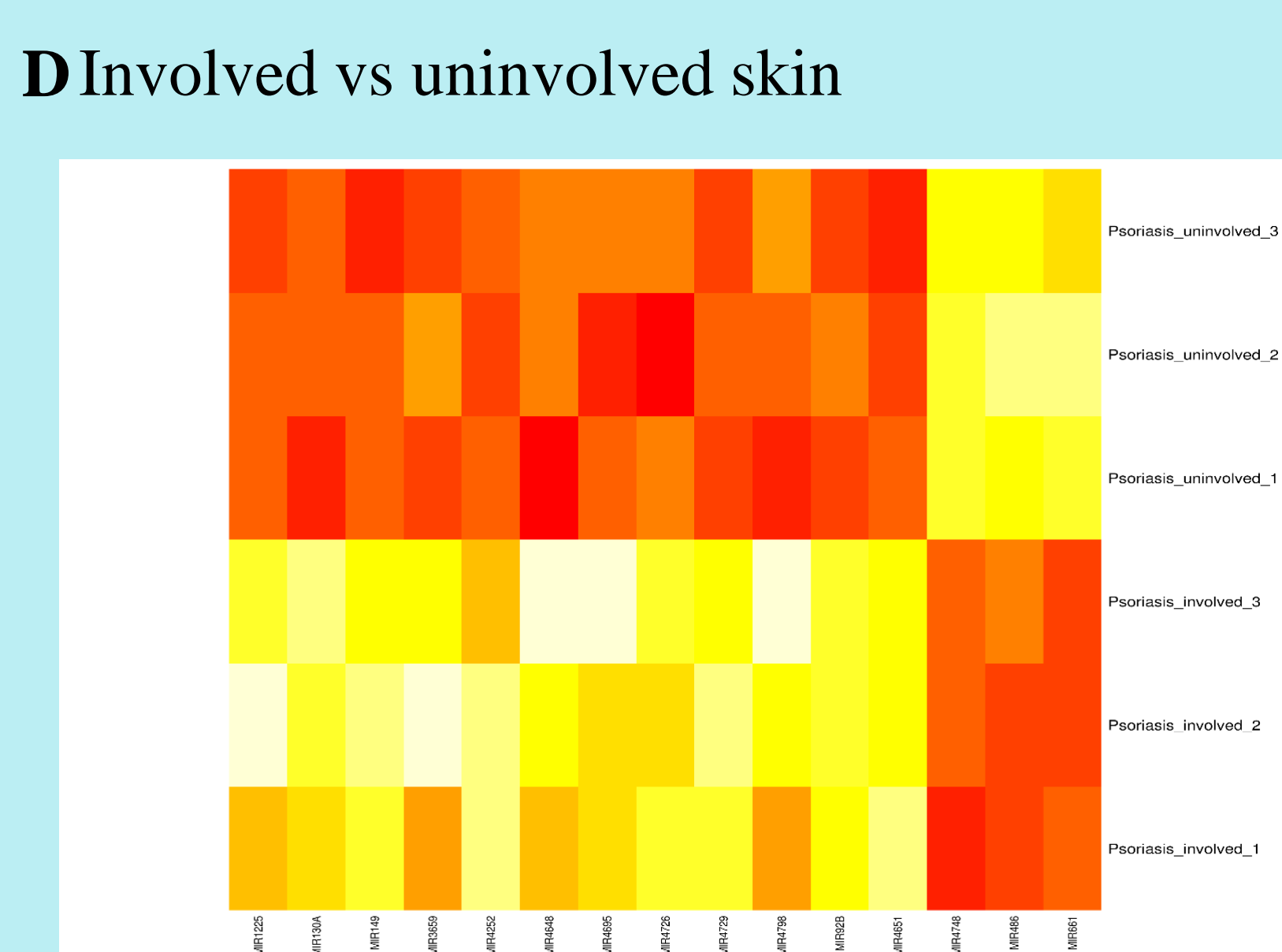
Several strongly differentially methylated sites in the miRNAs were found in the comparisons of psoriasis involved, uninvolved and healthy epidermis.

Conclusions

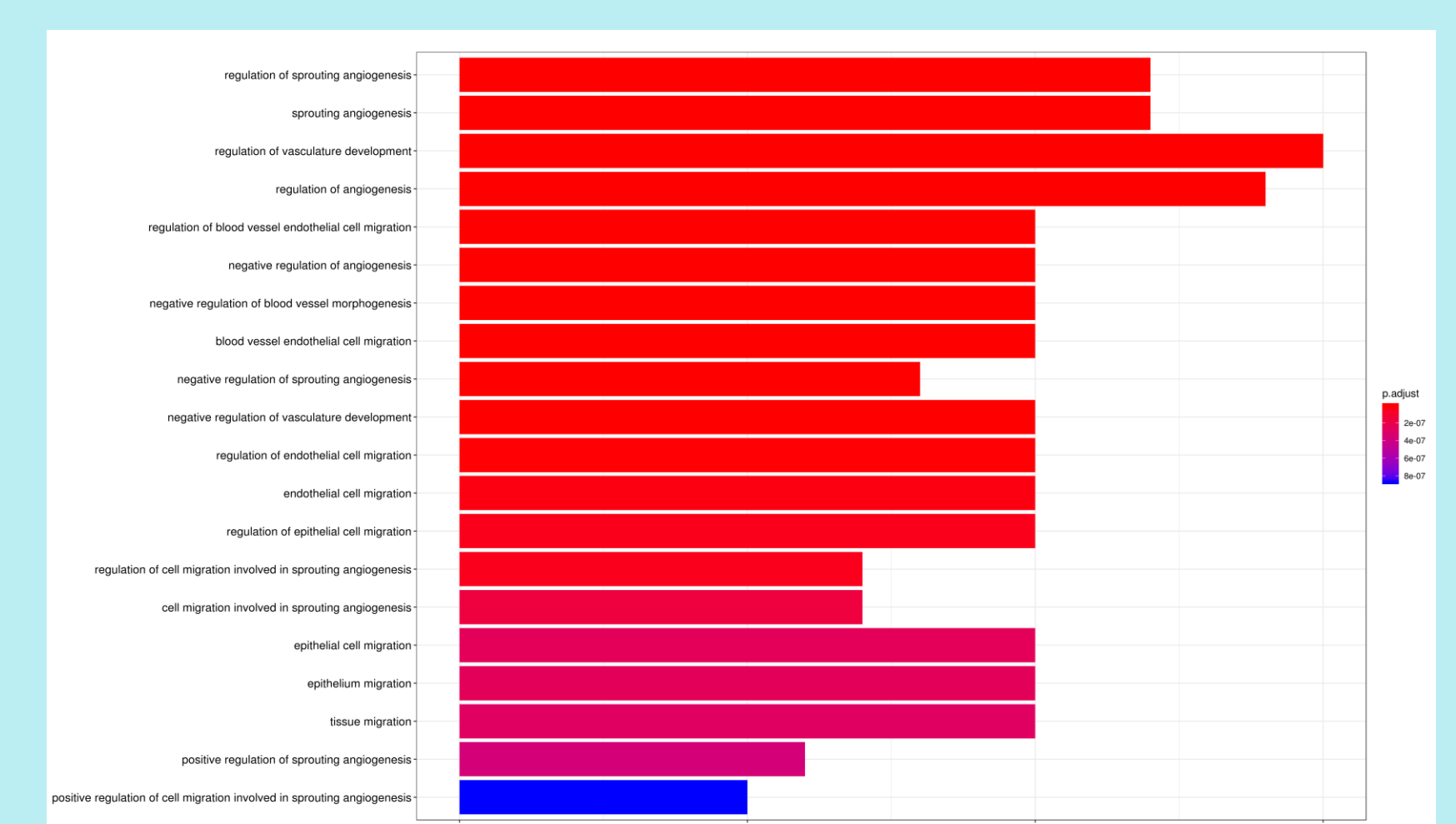
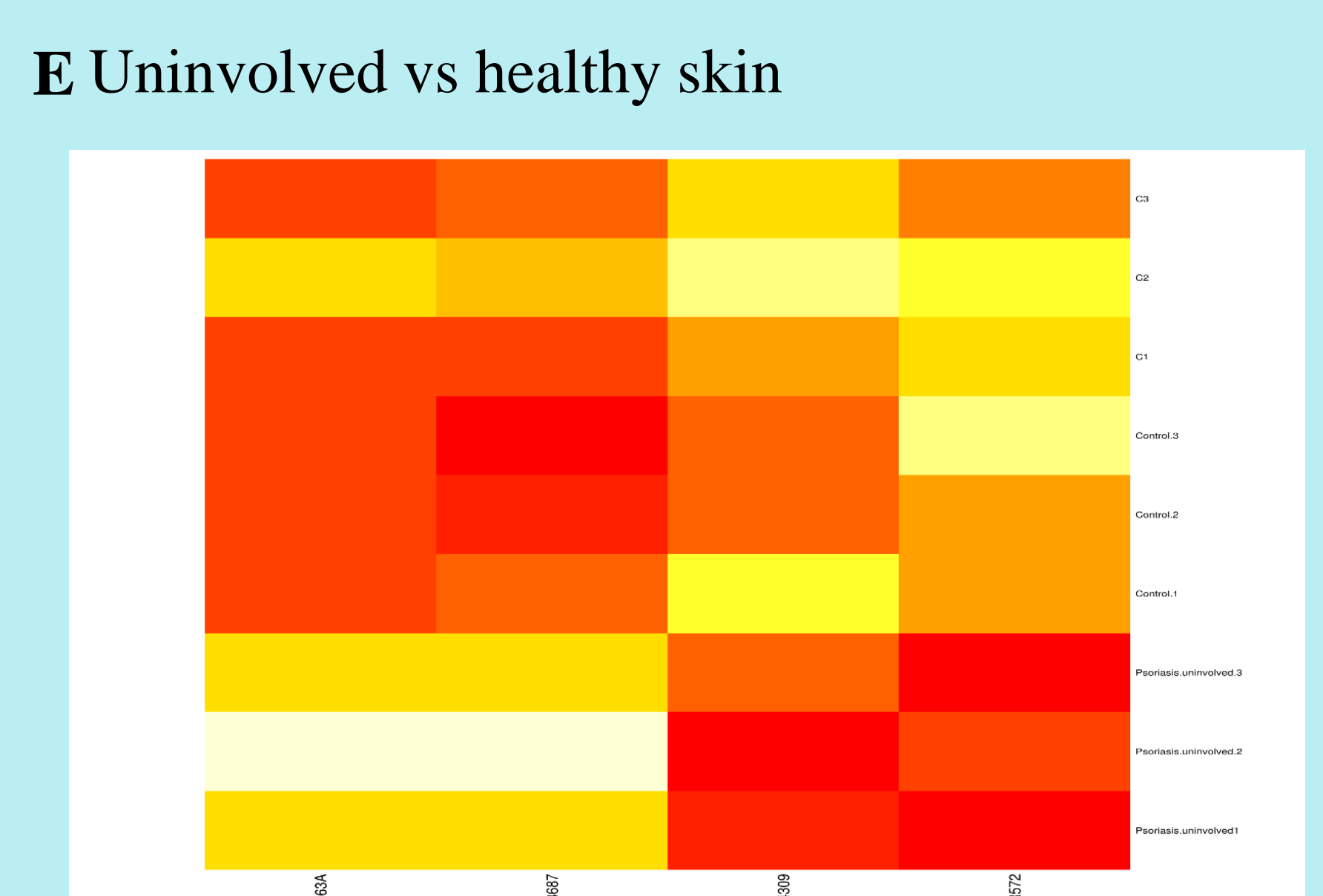
A substantial number of differentially methylated sites present in the psoriatic and healthy epidermis suggests an important regulatory role of miRNA in psoriasis. Further studies elucidating the exact functions of miRNA in psoriasis will help in drawing clinically relevant conclusions.



(C) Heatmap of methylation ratios of the top differentially methylated miRNA genes (top) and the corresponding gene ontology analysis in the comparisons between 3 psoriasis involved vs 6 healthy samples



(D) Heatmap of methylation ratios of the top differentially methylated miRNA genes in the comparisons between 3 psoriasis involved vs uninvolved samples



(E) Heatmap of methylation ratios of the top differentially methylated miRNA genes in the comparisons between 3 psoriasis uninvolved vs 6 healthy samples

References

1. Deep sequencing of small RNAs from human skin reveals major alterations in the psoriasis miRNAome. Joyce et al, Hum Mol Genet. 2011 Oct 15;20(20):4025-40
2. The Role of MicroRNAs in Autoimmune Diseases with Skin Involvement. Deng et al, Scand J Immunol. 2015 Mar;81(3):153-65
3. Genome-Wide DNA methylation profiling identifies Differential Methylation in Uninvolved Psoriatic Epidermis. Verma et al, J Invest Dermatol. 2018 May;138(5):1088-1093