

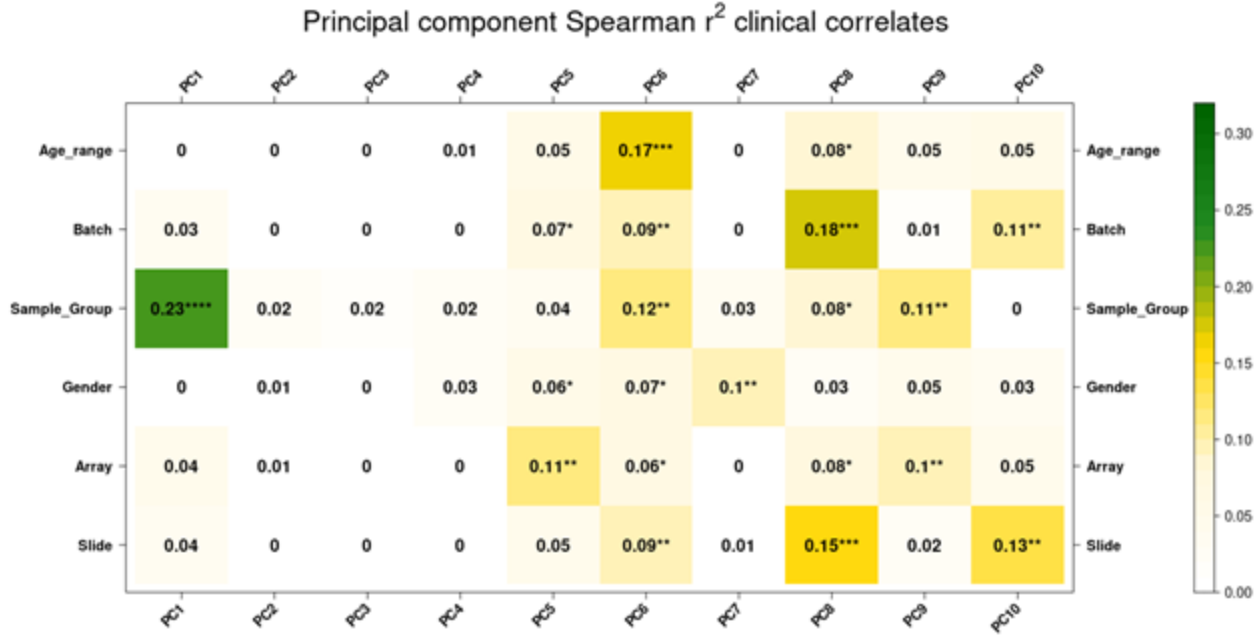


Fig. S1 SVD plot showing the Spearman correlation among the Principal Components and the variables in the metadata. The plot showed a high statistical significance for the Sample_Group (Case vs Control) while no significance for the other variables.

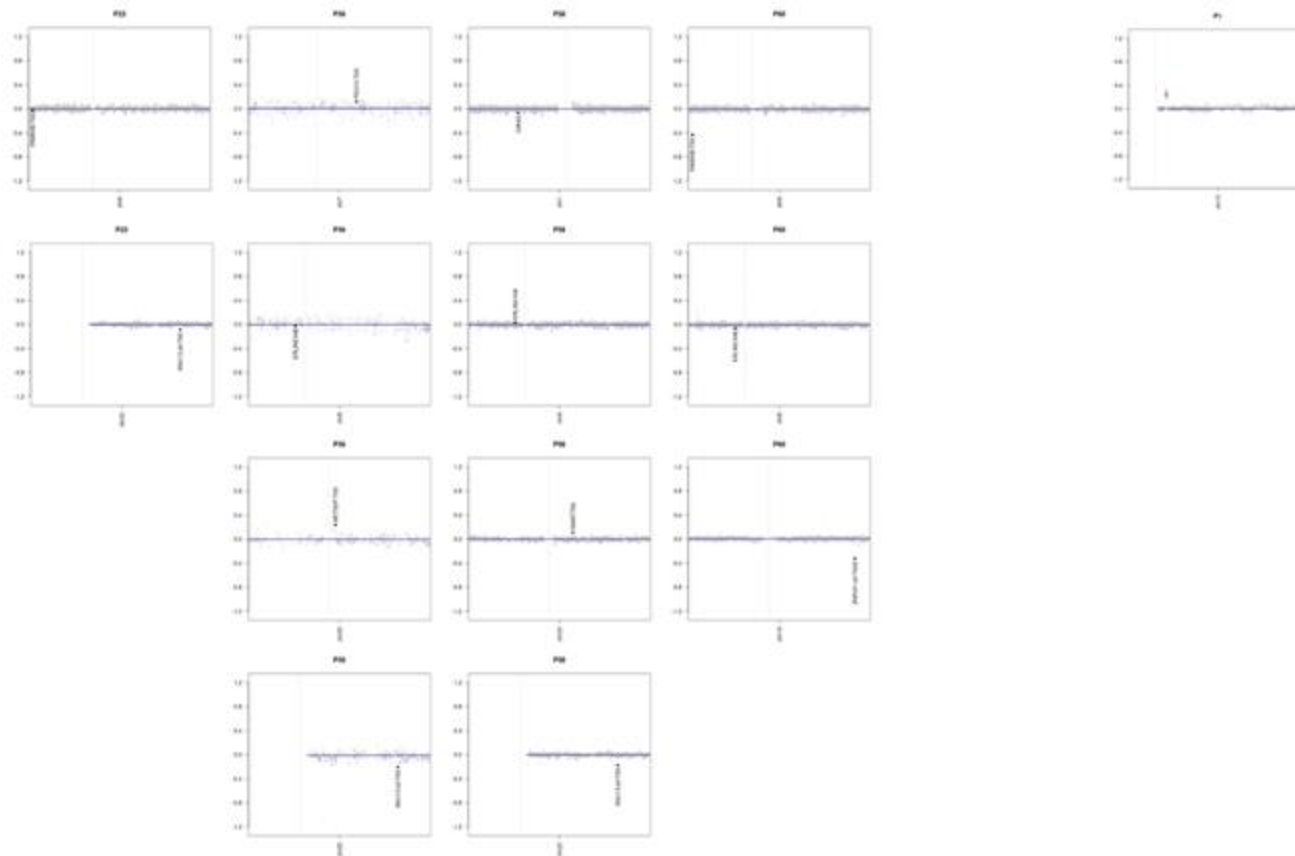


Fig. S2 Plot displaying the CNV status of the chromosome regions containing the iDMRs with abnormal methylation identified by EPIC array analysis in patients 23, 56, 58 and 60.

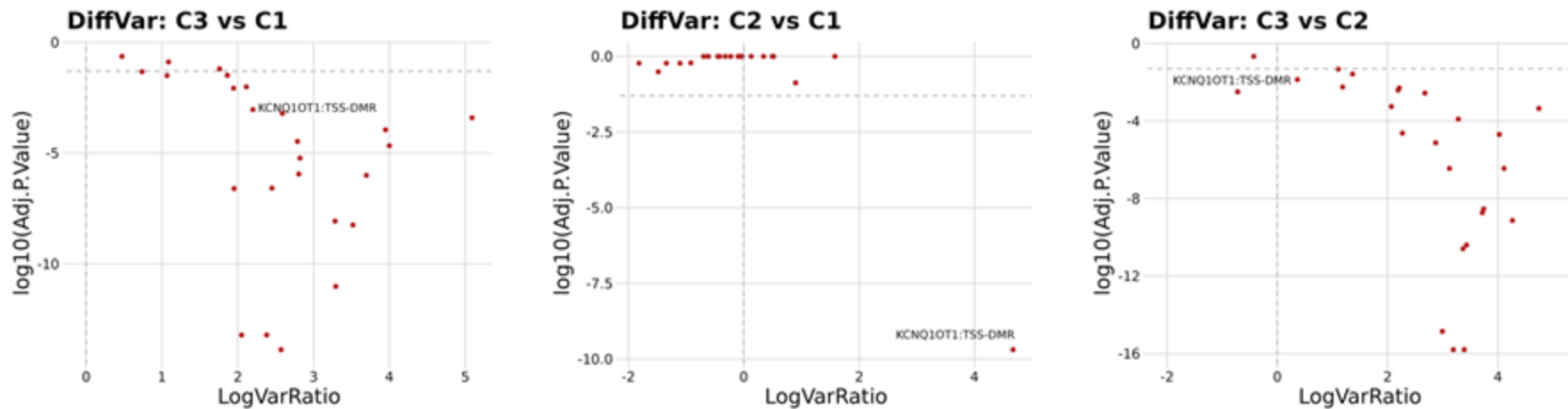
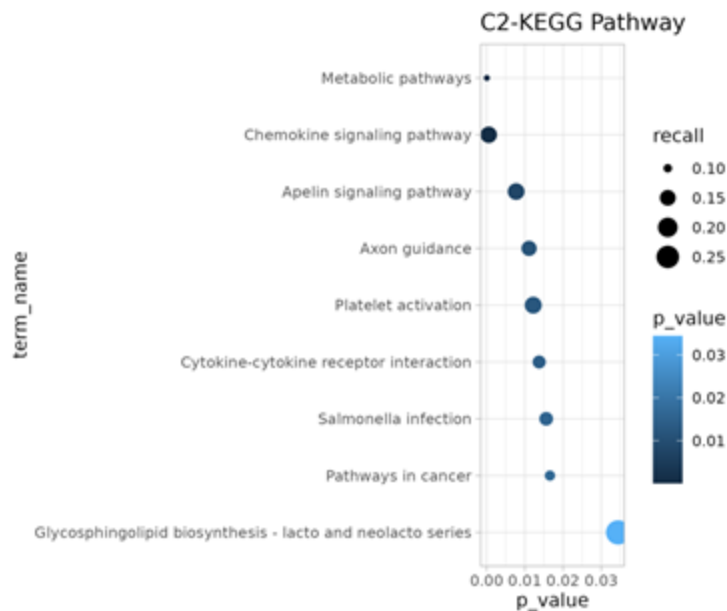


Fig. S3 Scatterplots displaying the differentially variable iDMRs between the C3 patient group and controls (C1, left panel), C2 patient group and controls (middle panel) and the C3 and C2 patient groups (right panel). The significance ($\log_{10}(\text{adj.p.value})$) is indicated on the Y-axis, fold difference (LogVarRatio) on the X-axis.

A



B

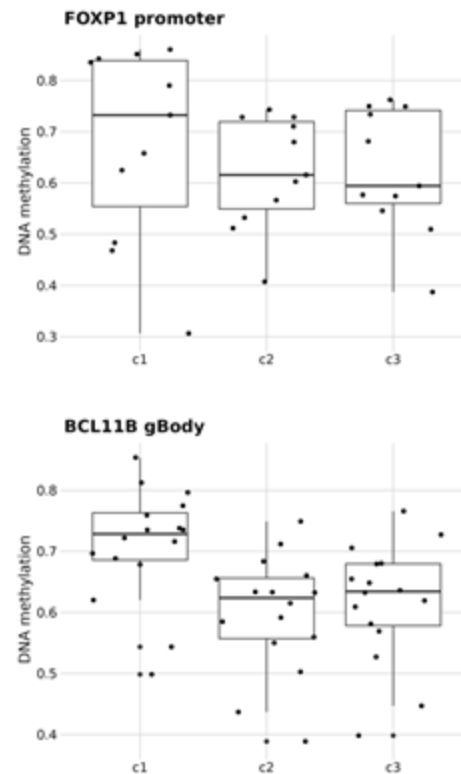


Fig. S4 Pathways and genes associated with DMPs. **A** KEGG pathway enrichment analysis of genes associated with DVPs in the C2 patient group, represented as in Fig. 4C. **B** Boxplot showing the methylation level (beta-values) of the FOXP1 promoter and BCL11B gene body in the C2 and C3 patient groups and controls (C1). Each dot represents a CpG.

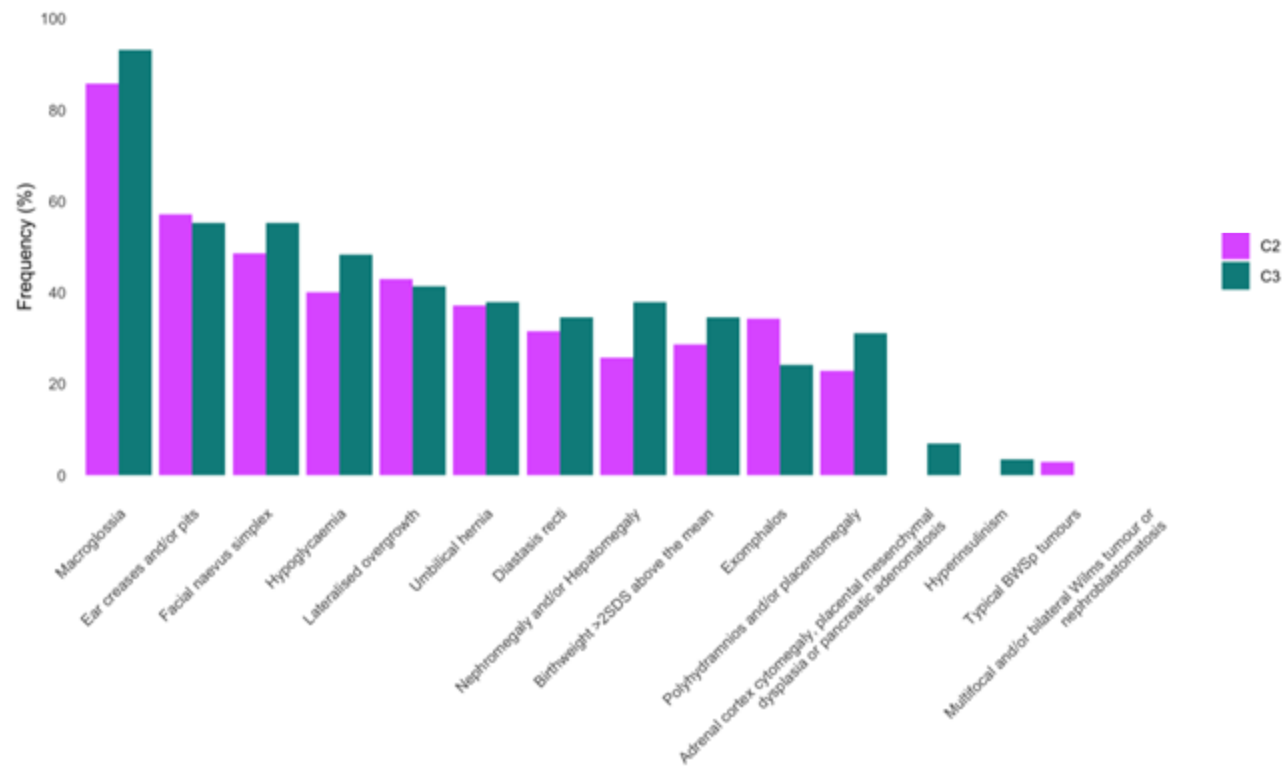


Fig. S6 Frequency of BWS clinical features in C2 (pink) and C3 (green) patient groups.