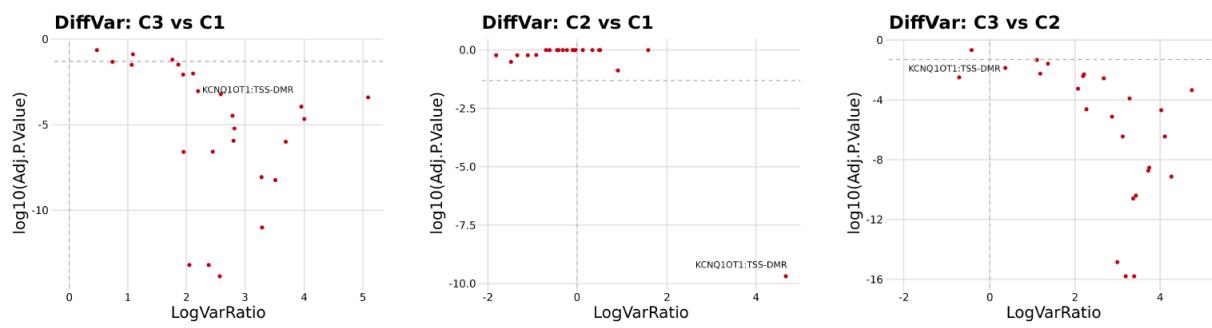


1

2 **Fig. S1** Plot displaying the CNV status of the chromosome regions containing the iDMRs with abnormal
 3 methylation identified by EPIC array analysis in the patients 23, 56, 58 and 60.

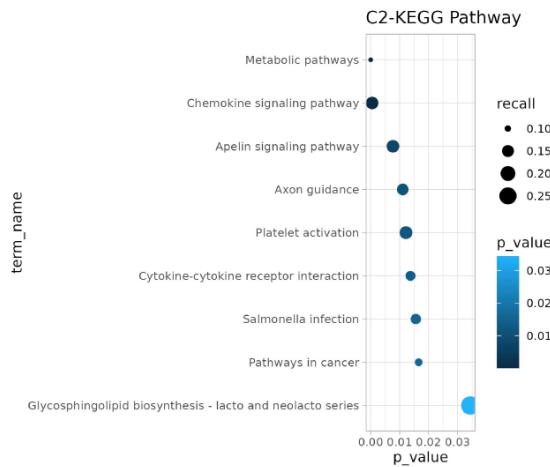


4

5 **S2** Scatterplots displaying the differentially variable iDMRs between the C3 patient group and controls
 6 (C1, left panel), C2 patient group and controls (middle panel) and the C3 and C2 patient groups (right
 7 panel). The significance ($\log_{10}(\text{adj.p.value})$) is indicated on the Y-axis, fold difference (LogVarRatio) on
 8 the X-axis.

Fig.

A



B

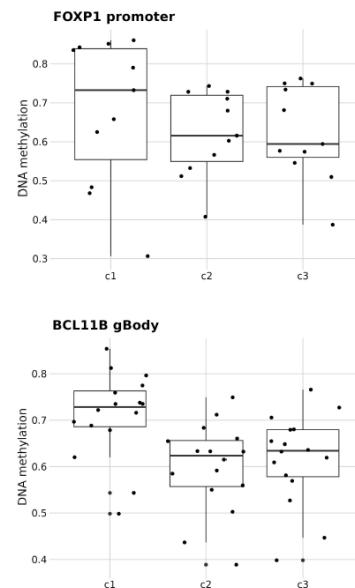
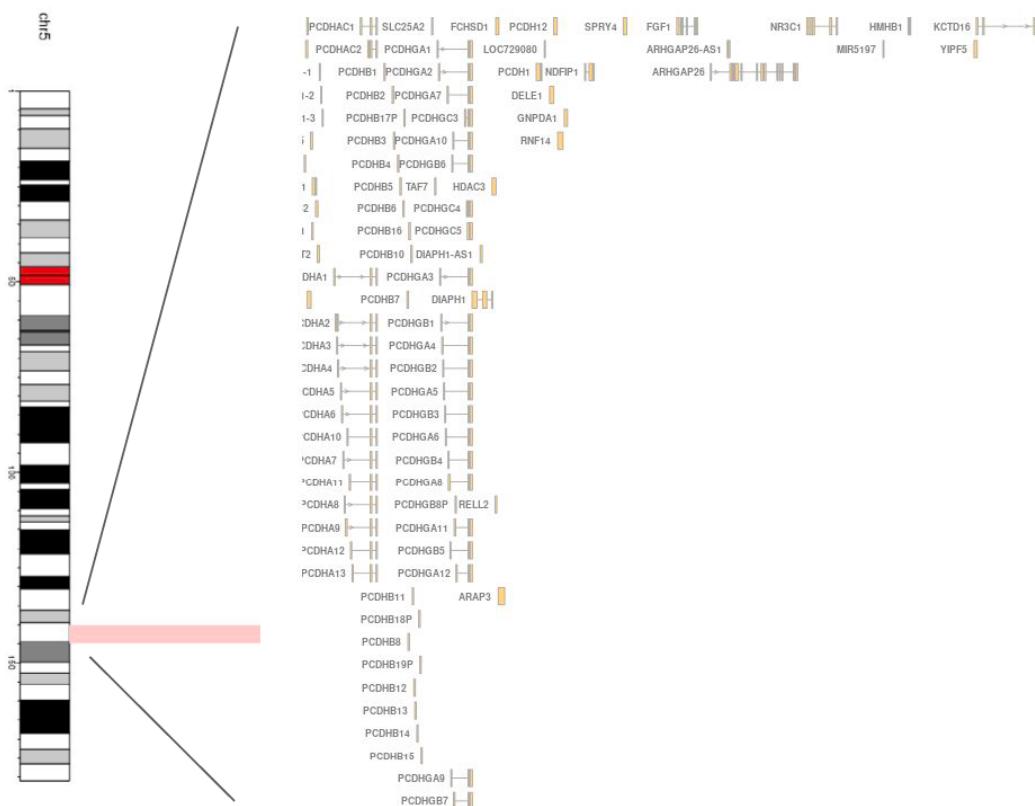


Fig.

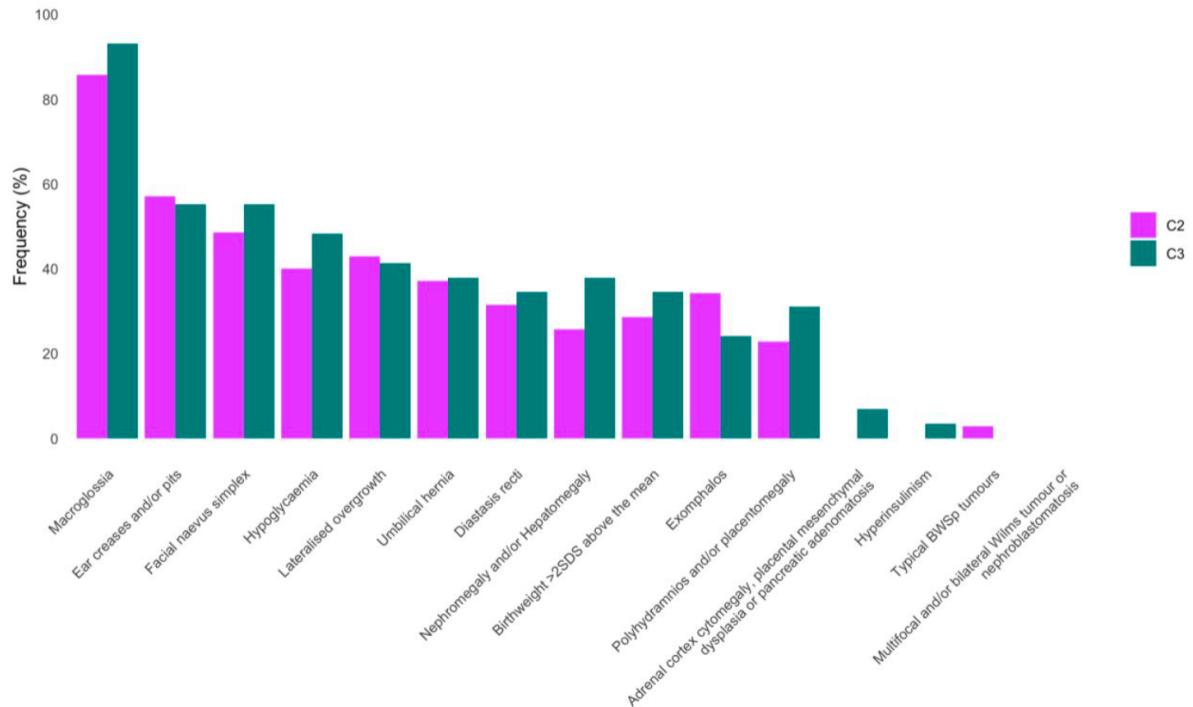
9

10 **S3** Pathways and genes associated with DMPs. **A** KEGG pathway enrichment analysis of genes associated
 11 with DVPs in the C2 patient group, represented as in Fig. 4C. **B** Boxplot showing the methylation level
 12 (beta-values) of the FOXP1 promoter and BCL11B gene body in the C2 and C3 patient groups and controls
 13 (C1). Each dot represents a CpG.

14



15 **Fig. S4** Ideogram representing the chr5q31.3 band and the genes affected in by DVPs in the C3 patient
 16 group.



17

18 **Fig. S5** Frequency of BWS clinical features in C2 (pink) and C3 (green) patient groups.