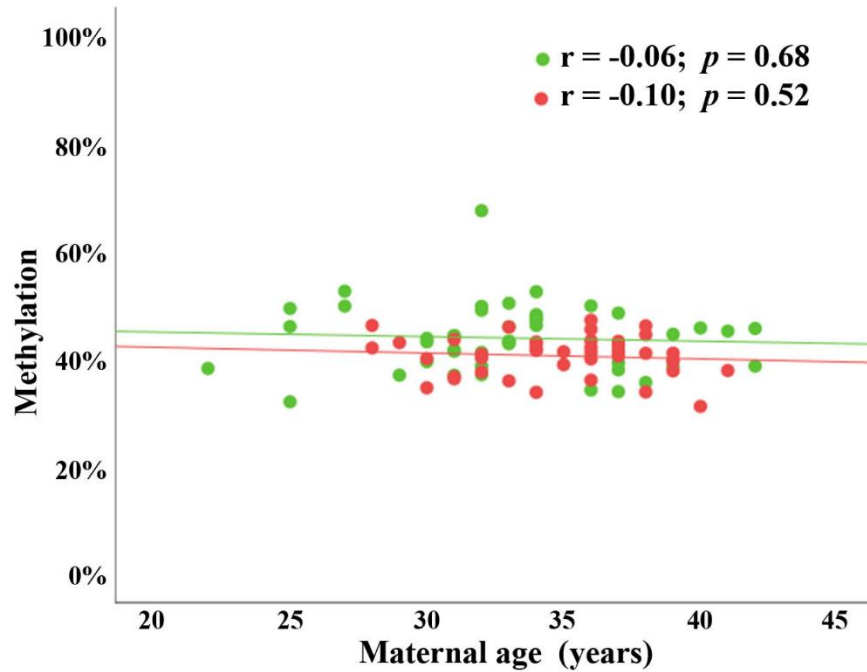
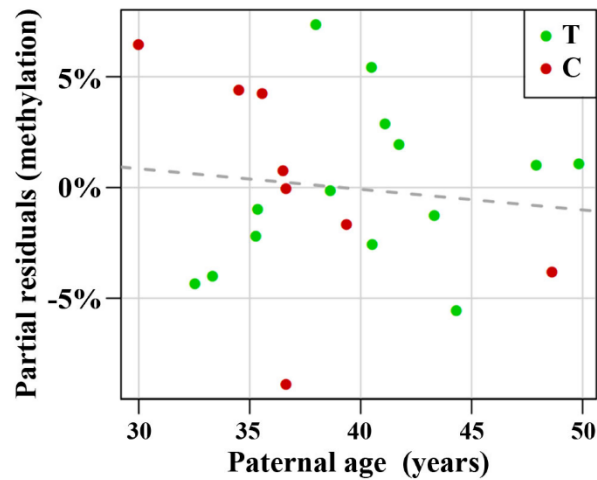


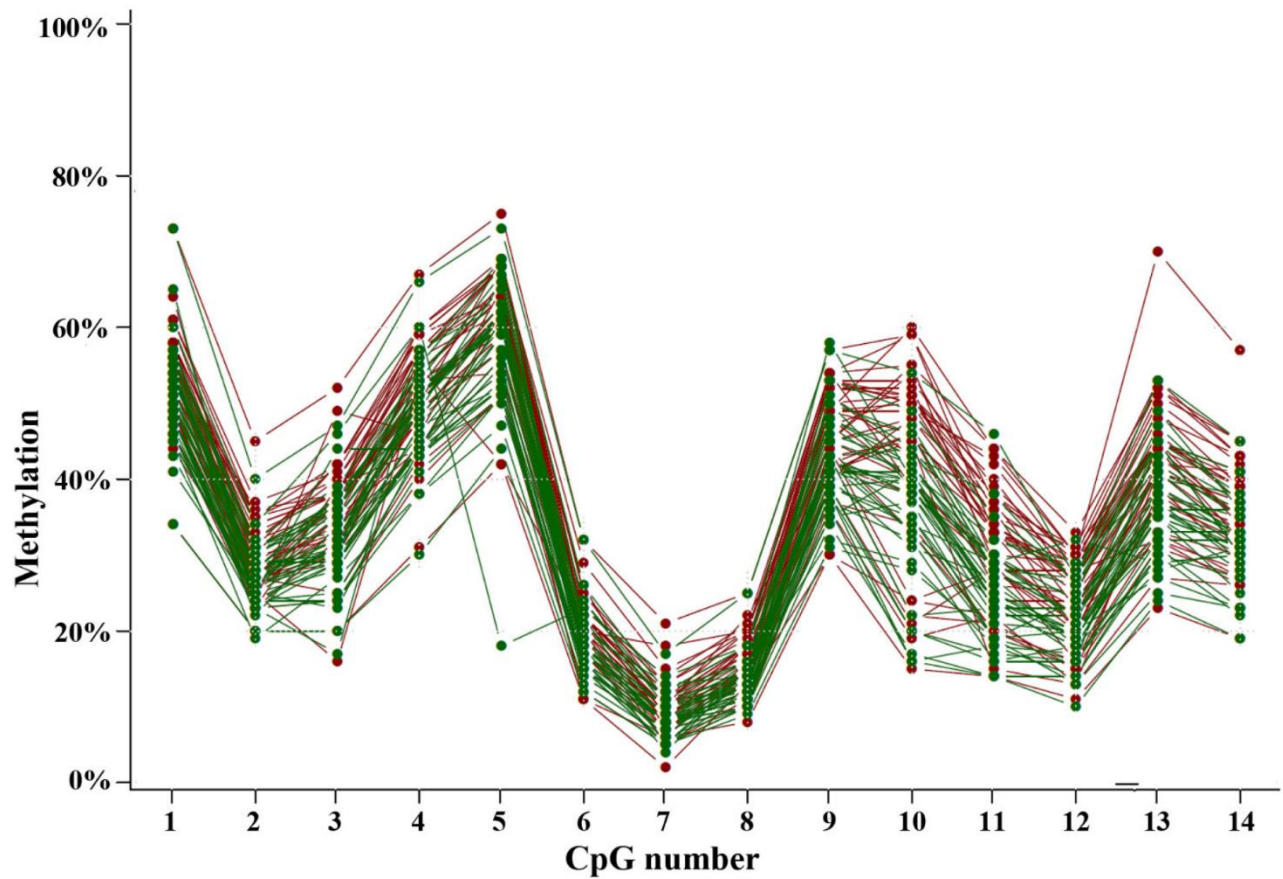
SUPPLEMENTARY FIGURES



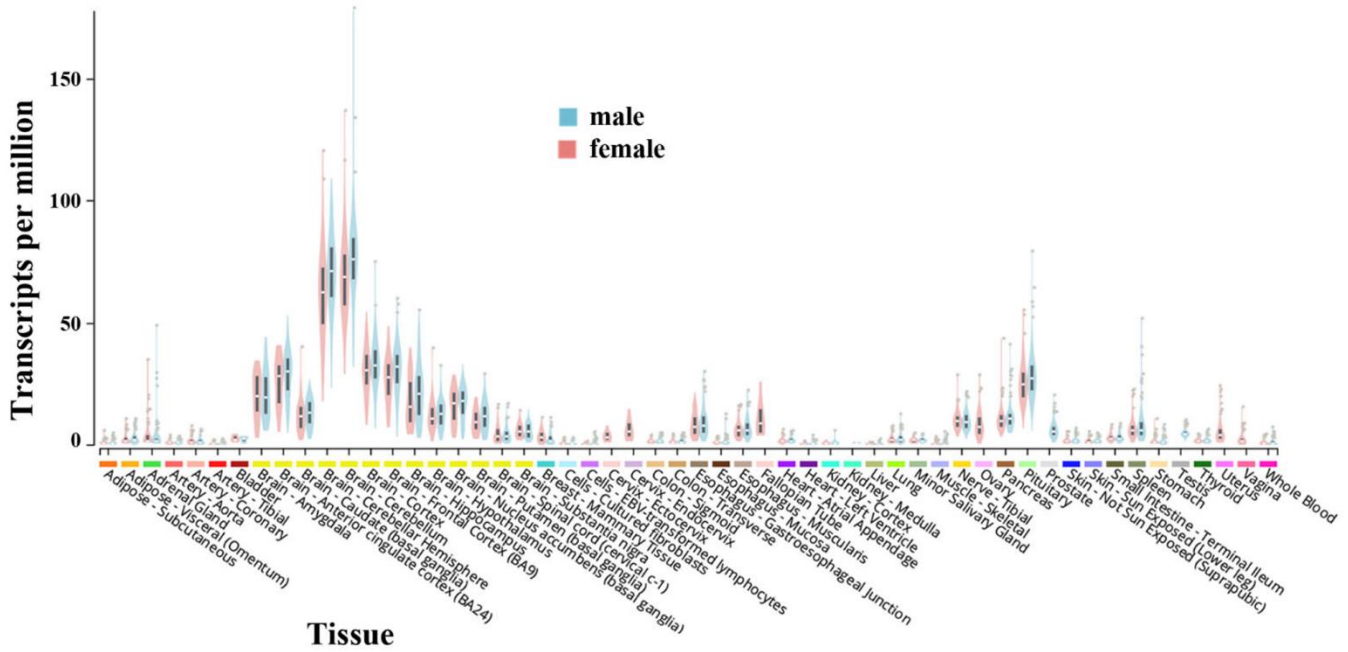
**Supplementary Figure 1. No detectable maternal age effect on cord blood methylation.** Methylation of the human *BEGAIN* promoter (y-axis in %) is not affected by maternal age (x-axis in years). Red dots represent 43 male and green dots 46 female FCB samples.



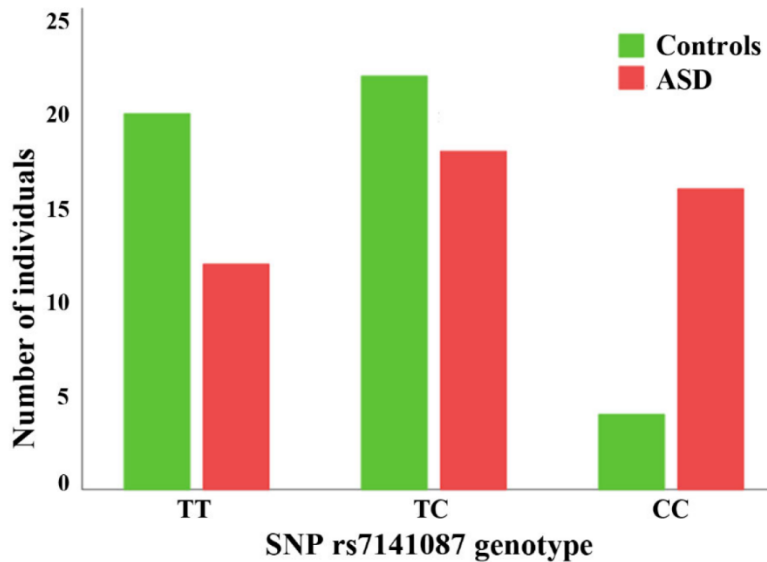
**Supplementary Figure 2. Paternal allele methylation of the human *BEGAIN* promoter in male cord bloods.** The component and residual plot shows a negative association (coefficient of regression model = -0.09;  $p = 0.62$ ) between paternal age (x-axis in years) and mean methylation of 14 CpGs (y-axis in %) of the paternal allele in FCB samples. Green dots represent FCBs with a paternal T and red dots samples with a paternal C allele. The partial residuals are adjusted for the base effects of SNP rs7141087.



**Supplementary Figure 3. No evidence for parent-specific *BEGAIN* methylation in FCBs.** The x-axis indicates 14 contiguous CpG sites in the *BEGAIN* promoter region studied by DBS, the y-axis the methylation level at a given site. Thin colored lines represent methylation profiles of individual alleles. Green lines represent the maternal and red lines the paternal alleles of 38 informative samples.



**Supplementary Figure 4. *BEGAIN* gene expression across different human tissues using the GTEx data set.** The y-axis displays the expression values in transcripts per million (TPM). The box plots are displayed as 25<sup>th</sup> and 75<sup>th</sup> percentile with the horizontal white line indicating the median. Outliers above or below 1.5 times the interquartile range are displayed as points. *BEGAIN* is widely expressed in the brain with the highest expression in cerebellum and cerebellar hemisphere. Please note that in most brain regions *BEGAIN* expression is somewhat higher in males (light blue bars), compared to females (pink bars).



**Supplementary Figure 5. Genotype distribution of SNP rs7141087.** Bar diagrams showing the number of TT, TC, and CC genotypes in 40 individuals with ASD (red bars) and 40 age- and sex-matched controls (green bars). Please note that the CC genotype is overrepresented in the ASD group.