**Methods Methylation QC**

Preprocessing of all methylation samples was conducted using the same pipeline (Maksimovic, Phipson, & Oshlack, 2017). Scan intensity signals as stored in .idat files were loaded into R and transformed into beta-values within the R package *minfi* (Aryee et al., 2014). Samples with a mean detection p-value > 0.05 were excluded (n = x). Additionally, we excluded samples presenting with distribution artefacts in raw beta-values (n = x), as well as samples showing sex mismatches between estimated sex from methylation data and confirmed phenotypic sex (n = x).

Beta-values were normalized using stratified quantile normalization (Touleimat & Tost, 2012), followed by BMIQ (Teschendorff et al., 2013).

Probes on X or Y chromosomes, probes containing SNPs, cross-hybridizing and polymorphic probes according to Chen et al. (2013) and McCartney et al. (2016), and probes with a detection p-value of > 0.01 in one or more samples were removed.

Afterwards beta-values were transformed into M-values, and batch-effects were removed using Combat (Leek, Johnson, Parker, Jaffe, & Storey, 2012). For this, we computed a principal component analysis (PCA) on the M-values and checked which batches were most strongly associated with the principal components. The strongest batches for the respective data set were iteratively removed. Corrected m-values were re-transformed into beta-values.

In a next step, we applied Mixup Mapper (Westra et al., 2011) to the genotype and methylation data to check for possible sample mix-ups. No/X mix-ups were detected.

For cord blood samples, contamination with maternal blood was tested (Morin et al., 2017) and samples identified as contaminated were excluded from further analyses.

Cell type composition into seven cell types in cord blood was estimated in *minfi* based on the algorithm proposed in Bakulski et al. (2016) / was estimated using the approach proposed in Salas et al. (2018).

For CVS and placenta, we estimated cell types using the R-package *RefFreeEWAs* (Houseman et al., 2016) which led to x estimated cell-types.

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