Epigenome-Wide Association of Neonatal Methylation and Prenatal PM2.5 Exposure Suggests Timing-Specific Effects

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# Supplementary Materials

#### Average Prenatal PM2.5 Exposure

##### Trimester 1

Analyzing average PM2.5 concentrations over trimester 1 generated a genomic control factor of 0.941 and a QQ plot showing minimal deviation of the observed p-value distribution from the expected under the null hypothesis (eFigure 1). The SVA was not included in the model as it negatively impacted the QQ plot.



**eFigure 1.** QQ plot for the analysis between DNA methylation at each studied CpG site and PM2.5 averaged over trimester 1 of pregnancy with observed and expected p-values transformed on a negative log10 scale.



**eFigure 2.** Manhattan plots for the association between DNA methylation at each studied CpG site and PM2.5 averaged over trimester 1 of pregnancy adjusted for specified covariates. The vertical axis plots the negative log10 p-value for each association. The Bonferroni cutoff for significance is denoted by the horizontal red line.

##### Trimester 2

Analyzing average PM2.5 concentrations over trimester 2 generated a genomic control factor of 1.01 and a QQ plot with minimal deviations from expected (eFigure 3). This model was additionally adjusted for SVA as its inclusion greatly improved the QQ plot and the genomic control factor.



**eFigure 3.** QQ plot for the analysis between DNA methylation at each studied CpG site and PM2.5 averaged over trimester 2 of pregnancy with observed and expected p-values transformed on a negative log10 scale.



**eFigure 4.** Manhattan plots for the association between DNA methylation at each studied CpG site and PM2.5 averaged over trimester 2 of pregnancy adjusted for specified covariates. The vertical axis plots the negative log10 p-value for each association. The Bonferroni cutoff for significance is denoted by the horizontal red line.

##### Combined

Analyzing average PM2.5 concentrations across the first two trimesters generated a genomic control factor of 0.881 and a QQ plot with minimal deviations from expected (eFigure 5). The SVA was not included in the model as it negatively impacted the QQ plot.



**eFigure 5.** QQ plot for the analysis between DNA methylation at each studied CpG site and PM2.5 averaged over trimesters 1 and 2 of pregnancy with observed and expected p-values transformed on a negative log10 scale.