Supplemental Material

Beyond the Mean: Quantile Regression to Explore the Association of Air Pollution with Gene-Specific Methylation in the Normative Aging Study

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**Figure S1.** Directed Acyclic Graph (DAG) at adjacent visits $j=J$ and $j=J+1$. This DAG illustrates the relationships we assumed between the variables included in the regression models. $A_i^j$ represents the 4-week moving average of air pollutant concentration before the $j^{th}$ visit of participant $i$. $Y_i^j$ represents the $i^{th}$ participant gene-specific DNA methylation at visit $j$. $\psi_p(Y_i^j)$ is the $p^{th}$ quantile of the $Y_{ij}$ distribution. $C_{1i}^j$ and $C_{2i}^j$ correspond to the potential confounding variables and risk factors of DNA methylation for participant $i^{th}$ at visit $j$, respectively. $b_{0i}$ represents the random intercept of participant $i$.

**Figure S2.** Sensitivity analyses restricted to never and former smokers: absolute difference in gene-specific methylation (expressed in %5mC with 95%CI) associated with an IQR increase in exposure (IQR=14,599 number per cm$^3$ for particle number, 0.26 µg/m$^3$ for PM$_{2.5}$ black carbon, and 3.4 µg/m$^3$ for PM$_{2.5}$ mass), according to deciles of the methylation distribution. In this secondary analysis, we considered only never and former smokers based on the time-varying smoking status variable. The analysis included 755 participants and 1,737 individual observations.
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