Supplemental Material

Title: Secondhand Tobacco Smoke Exposure Associations with DNA Methylation of the Aryl Hydrocarbon Receptor Repressor

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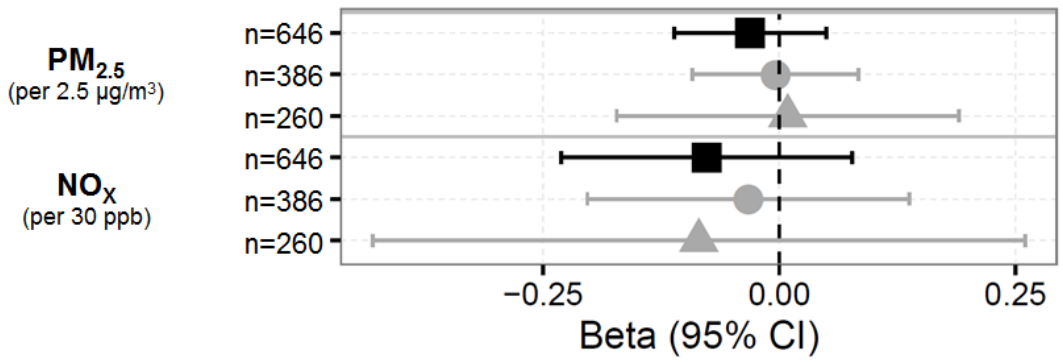
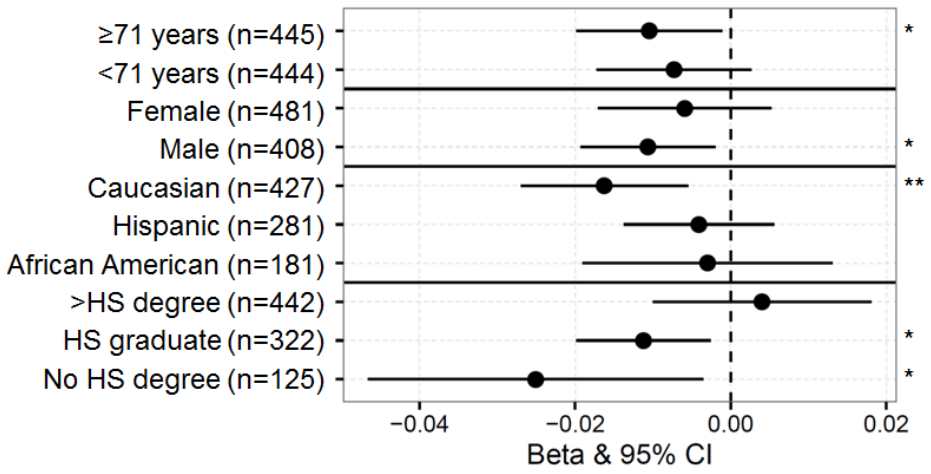


Figure S1. Estimated effects of $PM_{2.5}$, and NO_X on cg05575921 methylation in non-smokers. Forest plots shows effect sizes (Beta) and 95% confidence intervals (CI) of air pollution (fine particulate matter, $PM_{2.5}$ per 2.5 µg/m^3, and oxides of nitrogen, NO_x per 30 ppb) on cg05575921 methylation (x-axis) measured in monocyte samples; effect sizes on methylation are shown overall and stratified by smoking status (never and former smokers). Covariates included age, sex, race/ethnicity, education level, smoking status, pack-years, time since quitting smoking (former smokers only), hours per week of SHS exposure, site of data collection, and estimates of residual sample contamination with non-monocyte cell types. Significance indicated as follows: ***p < 0.001; ** 0.001 ≤ p <0.01; * 0.01 ≤ p< 0.05

A



B

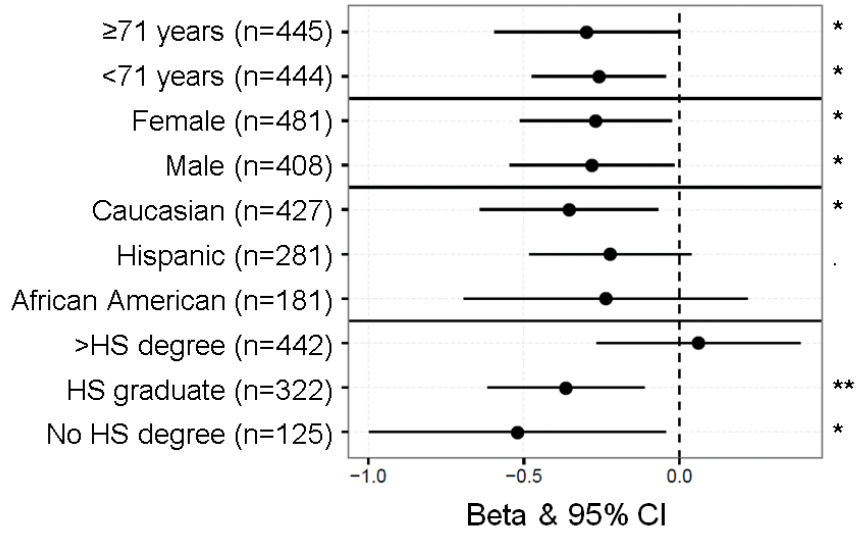


Figure S2. Effect sizes between recent indoor SHS exposure and cg05575921 methylation in non-smokers. Forest plots shows the effect sizes (Beta) and 95% confidence intervals (CI) of **A)** recent SHS exposure and **B)** high levels (≥10 hours per week) vs. no recent SHS exposure on cg05575921 methylation (x-axis) in CD14+ monocyte samples, subset by age (<71 years and ≥ 71 years), sex, race/ethnicity, and education (>high school (HS) degree\diploma, HS degree\diploma, and no HS degree\diploma). Significance indicated as follows: '***' $p < 0.001$; '**' $0.001 \leq p < 0.01$; '*' $0.01 \leq p < 0.05$; '.' $0.05 \leq p < 0.10$; ' ' $p \geq 0.10$