

**Supplemental Figure S1.** PFOS and PFOA levels by sample plates for 450K DNA methylation analysis.



**Supplemental Figure S2.** Distribution of PFOS (A) and PFOA (B) levels in maternal serum. PFOS levels were detected in all samples. For the 12 samples with PFOA levels below the detection limit (0.50 ng/mL), we assigned a value of half the detection limit (0.25 ng/mL). Median (25th to 75th percentiles) of PFOS and PFOA concentrations in maternal blood were 5.2 ng/mL (3.8 to 7.1) and 1.4 ng/mL (0.9 to 2.1), respectively.



**Supplemental Figure S3.** Quantile-quantile plots of the log10(P-values) for epigenome-wide analysis of the association between PFASs exposure during pregnancy and cord blood DNA methylation. Adjusted for maternal age, parity, maternal educational levels, maternal blood sampling period, maternal pre-pregnancy BMI, maternal smoking during pregnancy, gestational age, infant sex, and cord blood cell estimates.



**Supplemental Figure S4**. Location of the differentially methylated CpGs (*P* < 0.001) compared to all CpGs on the methylation array.

Χ2 test: (A) PFOS (*P* = 0.0005), PFOA (*P* = 0.06); (B) Χ2 test: PFOS (*P* = 0.0004), PFOA (*P* = 0.09)



**Supplemental Figure S5**. Beta coefficients for each site contained in DMRs in discovery and replication cohorts.





**Supplemental Figure S6.** Significantly enriched pathways among the genes with differentially methylated CpGs associated with the exposures to PFOS (A) and PFOA (B).

White bars, observed number of genes; black bars, expected number of genes in each pathway. *P* < 0.001 vs. the expected number of genes.