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Supplemental Material

First-Trimester Urine Concentrations of Phthalate Metabolites and Phenols and Placenta miRNA Expression in a Cohort of U.S. Women

Jessica LaRocca, Alexandra M. Binder, Thomas F. McElrath, and Karin B. Michels

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Figure S1. Study population for women eligible for analysis of first-trimester urinary phthalate and phenol concentrations with miRNA alterations in the placenta. Urinary phthalate and phenol concentrations were analyzed in 196 women who were enrolled in both the Predictors of Preeclampsia Study (POPS) and Epigenetic Birth Cohort (EBC) and had a first-trimester urine sample. Women without available placenta for RNA extraction were excluded from relevant analyses (N=17), giving a total population of N=179. The participants for the original pilot project were nested in this population (N=48).

Table S1. Estimates and p values for pilot project results comparing miRNA expression with grouped phthalate and phenol categories.

Table S2. List of analyzed miRNAs and accession numbers

Figure S2. Coefficient of variation (CV) for a subset of samples run in triplicate for all miRNAs analyzed.

Figure S3. Distribution of phenols and phthalates among the samples chosen for the pilot study and the full sample.

Figure S4. Pearson correlation (r) between the miRNA levels estimated from the pilot and the full study. *p<0.001.

Table S3. Associations between Placental miRNA Expression and Grouped Maternal Phenol Urine Concentrations. Estimated change in ΔCt for a one unit increase in $\log(\text{mol/L})$ EDC burden in multivariable models.

Table S4. Associations between Placental miRNA Expression and Additive Maternal Phthalate Urine Concentrations. Estimated change in ΔCt expression for a one unit increase in $\log(\text{mol/L})$ EDC burden in multivariable models.

Figure S5. Association between miRNA Expression and each EDC Metabolite Independently. Each cell corresponds to a test for the association between an individual metabolite (columns) and the expression of a specific miRNA (rows). The cell color corresponds to the change in ΔCt miRNA expression with a one $\log(\text{mol/L})$ increase in metabolite adjusting for maternal age, maternal ethnicity, and self-reported maternal smoking (Yes/No), and infant-sex; dots indicate $p < 0.05$ for the association between metabolite and EDC in the multivariable model; green=non-paraben phenol, orange=paraben; pink=LMW phthalate; turquoise=HMW non-DEHP phthalate; purple=HMW DEHP phthalate.

Figure S6. MicroRNA and gene expression levels among the subset of significant pairwise Spearman correlations identified among a subset of samples run on Affymetrix GeneChip® Human Gene 2.0 ST Array after adjusting for multiple testing.

Table S5. Correlations between birth outcomes and miRNAs significant among EDC profiles.