**SUPPLEMENTARY FIGURES**

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**Fig S1: Effect size estimates of DEmiRs are highly robust to various suspected technical and biological covariates.** Bar plot showing effect size estimates for all DEmiRs after correction for suspected technical and biological covariates not included in the original (base) model. RIN = RNA integrity, Lane = Flow cell lane, Smoke = maternal smoking status, BWG = birth weight group, Race = maternal race, Sex = offspring sex, YOB = year of birth, BWP = birth weight percentil



**Fig S2: Effect size estimates of placental miRNAs are highly robust on a transcriptome-wide scale to various suspected technical and biological covariates**. Scatter plots displaying the coefficient of determination (R2) to emphasize the relationship between the estimates produced by the original (base) model and estimates of various models which correct for additional, suspected technical and biological covariates across all miRNAs analyzed. (A) RIN = RNA integrity, (B) Lane = Flow cell lane, (C) Smoke = maternal smoking status, (D) Race = maternal race, (E) BWG = birth weight group, (F) Sex = offspring sex, (G) YOB = year of birth, (H) BWP = birth weight percentile.