S2 File: Supplementary Data:

Sample Q/C analysis. Erythrocyte lysis is an important source of miRNA contamination in plasma samples [1, 2]. Therefore, as published previously [3], we assessed the quality of the plasma samples and derived RNA in four ways. Firstly, we assessed plasma samples for free hemoglobin content as well as bound oxy- and de-oxy hemoglobin by spectrometric analysis. We found no evidence for whole erythrocyte contamination (i.e., no detectable oxy and deoxyhemoglobin **S1 Fig., a**) in plasma samples, and minimal hemolysis (spectral absorbance at 414nm), equal to or less than previously published [3]. There was no significant effect of recruitment site (P=0.88) or exposure group (P=0.76) on hemolysis. Interestingly, there was a small but statistically significant decline in free hemoglobin at the end of pregnancy compared to the mid-pregnancy period (ANOVA, $F_{(1,125)}$=6.67, P<0.01, **S1 Fig., b**), indicative perhaps of pregnancy-associated anemia in this cohort. Secondly, none of the assessed plasma samples amplified the mRNA transcript for Band-3 protein (SLC4A1, **S1 Fig., c**) which is abundent in erythrocytes. Thirdly, the mean sample ΔCq for $_{plasma_stable}$miR23a-$_{erythrocyte_abundent}$miR451a, -0.88 ± 0.677 (Mean ± SEM), was below the identified threshold for hemolysis (ΔCq>7, [4], and was not significantly altered due to recruitment site (P=0.94), pregnancy stage (P=0.71) or exposure group (P=0.65) indicating that there was not a systematic variable-dependent effect on hemolysis. These data collectively eliminate hemolysis as a signifciant contributor to sample miRNA content.

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