CORRIGENDUM

Acetaminophen use during pregnancy and DNA methylation in the placenta of the extremely low gestational age newborn (ELGAN) cohort

Kezia A. Addo, Catherine Bulka, Radhika Dhingra, Hudson P. Santos Jr, Lisa Smeester, T. Michael O’Shea and Rebecca C. Fry

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Corrigendum

It has come to the attention of the authors that an error occurred during sample processing. Placental DNA samples on 96-well plate were misoriented to their matching barcodes. This resulted in a mismatch of methylation and phenotype data. These errors influenced results published in Environmental Epigenetics: Kezia A Addo, Catherine Bulka, Radhika Dhingra, Hudson P. Santos Jr, Lisa Smeester, T. Michael O’Shea and Rebecca C. Fry. Acetaminophen use during pregnancy and DNA methylation in the placenta of the extremely low gestational age newborn (ELGAN) cohort. Once correctly aligned, we identified a small number of samples for which the reported infant sex and methylation-predicted sex (using the minfi R package) differed. Correction for these errors resulted in changes in beta estimates, p-values, and the CpG probes identified as significant.

For this re-analysis, we excluded five placentas with an apparent sex mismatch (two infants reported to be female and three reported to be male), decreasing our sample size from n=286 to n=281. Previously, a total of 42 CpG sites were identified as differentially methylated comparing placental tissues from mothers who reported acetaminophen use during pregnancy and those who did not (FDR < 0.05). Upon re-analysis, 17 (40.5%) of the previously identified 42 CpG sites remained significant. We identified an additional seven FDR-significant probes for a total of 24 FDR-significant hits. With respect to interaction by fetal sex, we previously identified six CpGs ($P_{interaction} < 0.2$); none of these remained significant upon re-analysis. However, we identified nine different probes that showed evidence of interaction by fetal sex ($P_{interaction} < 0.2$).