**2022 Preterm Birth Scientific Reports**

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**Publication**

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**Summary**

Preterm birth is the major cause of newborn and infant mortality affecting nearly one in every ten live births. The current study was designed to develop an epigenetic biomarker for susceptibility of preterm birth using buccal cells from the mother, father, and child (triads). An epigenome-wide association study (EWAS) was used to identify differential DNA methylation regions (DMRs) using a comparison of control term birth versus preterm birth triads. Epigenetic DMR associations with preterm birth were identified for both the mother and father that were distinct and suggest potential epigenetic contributions from both parents. The mother (165 DMRs) and female child (136 DMRs) at p < 1e−04 had the highest number of DMRs and were highly similar suggesting potential epigenetic inheritance of the epimutations. The male child had negligible DMR associations. The DMR associated genes for each group involve previously identified preterm birth associated genes. Observations identify a potential paternal germline contribution for preterm birth and identify the potential epigenetic inheritance of preterm birth susceptibility for the female child later in life. Although expanded clinical trials and preconception trials are required to optimize the potential epigenetic biomarkers, such epigenetic biomarkers may allow preventative medicine strategies to reduce the incidence of preterm birth.