Altered DNA methylation in human placenta after (suspected) preterm labor

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Aim: The aim of this study was to determine if alterations in DNA methylation in the human placenta would support suspected preterm labor as a pathologic insult associated with diminished placental health. Methods: We evaluated placental DNA methylation at seven loci differentially methylated in placental pathologies using targeted bisulfite sequencing, in placentas associated with preterm labor (term birth after suspected preterm labor [n = 15] and preterm birth [n = 15]), and controls (n = 15). Results: DNA methylation levels at the NCAM1 and PLAGL1 loci in placentas associated with preterm labor did differ significantly (p < 0.05) from controls. Discussion: Specific alterations in methylation patterns indicative of an unfavourable placental environment are associated with preterm labor per se and not restricted to preterm birth.

Graphical abstract: