Supplementary Materials: Quantification and Application of Potential Epigenetic Markers in Maternal Plasma of Pregnancies with Hypertensive Disorders

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Table S1. Sequences of primers and probes according to assay.

Assay	Target Regions [GenBank ID]		Sequences
Bisulfite sequencing	*SOD1* [NG_008689.1]	Forward	5′- GTAATTTGTTTGTTTTTTTTTTTGTG -3′
		Reverse	5′- CAACAACATCTTATATACAAAAACC -3′
	DSCR3 [NG_009410.1]	Forward	5′- GTAAATATATGTAAAAATAGGAAGTG -3′
		Reverse	5′- CTTTTACTACATATAACTACACCCCC -3′
	C2CD2 [AP001745.1]	Forward	5′- GAGGACGATAAAAGGAATTAGTTTTT -3′
		Reverse	5′- ATTTTTATCTTATTTTTCTCAATTACAC -3′
	UMODL1 [AP001745.1]	Forward	5′- GATTTTTTGGAGGAATTTTTTTT -3′
		Reverse	5′- CAAAAATAAATAATTTACTCTACTCC -3′
	ENST00000433952:-7924—7988 [AL163278.2]	Forward	5′- GAATTGTTTAAGAGGTTTAAGTTTGG -3′
		Reverse	5′- CCTATAATTAAATTACATATAAAACAACC -3′
	RASSF1A [NG_023270.1]	Forward	5′- TAGTTTGGATTTTGGGGGAGG -3′
		Reverse	5′- CCCCAAATAAAATCGCCAC -3′
Real-time PCR	*DSCR3*	Forward	5′- CGTAGCGGCTTCTCGTG -3′
		Reverse	5′- GTTAGCCATCGGCTAGGTGG -3′
		Probe	5′- FAM-CCGAAGCGTCTGGCCTGTGTGCTCT-BHQ1 -3′
		Amplicon (125 bp)	5′-CGTAGCGGCTTCTCGTGGGCGAGTCCCTGTTCGCAGGTGACGTGTGGACCACGCTCTTCCGAAGCGTCTGGCCTGTGTGCTCTCGGGGAGGGGACGCAGGTCAGCCCACCTAGCCGATGGCTAAC -3′
	RASSF1A	Forward	5′- GAGCCTGAGCTCATTGAGCTG -3′
		Reverse	5′- ACCAGCTGCCGTGTGG -3′
		Probe	5′- HEX -CACCCGCTGGGCGCGC-BHQ1 -3′
		Amplicon (131 bp)	5′-GAGCCTGAGCTCATTGAGCTGCGGGAGCTGGCACCCGCTGGGCGCGCTGGGAAGGGCCGCACCCGGCTGGAGCGTGCCAACGCGCTGCGCATCGCGCGGGGCACCGCGTGCAACCCCACACGGCAGCTGGT -3′
	SRY [NG_011751.1]	Forward	5′- AGATCAGCAGGGCAAGTAGT -3′
		Reverse	5′- TGAAACTTGCATTTCTCCGC -3′
		Probe	5′- FAM-CAGGGTACTAGGGGGTAGGCTGGTTG-BHQ1 -3′
	GAPDH [NG_007073.2]	Forward	5′- CCCCACACACATGCACTTACC -3′
		Reverse	5′- GTGGGAAGAGGGGAAGCTG -3′
		Probe	5′- HEX-AAAGAGCTAGGAAGGACAGGCAACTTGGC-BHQ1 -3′

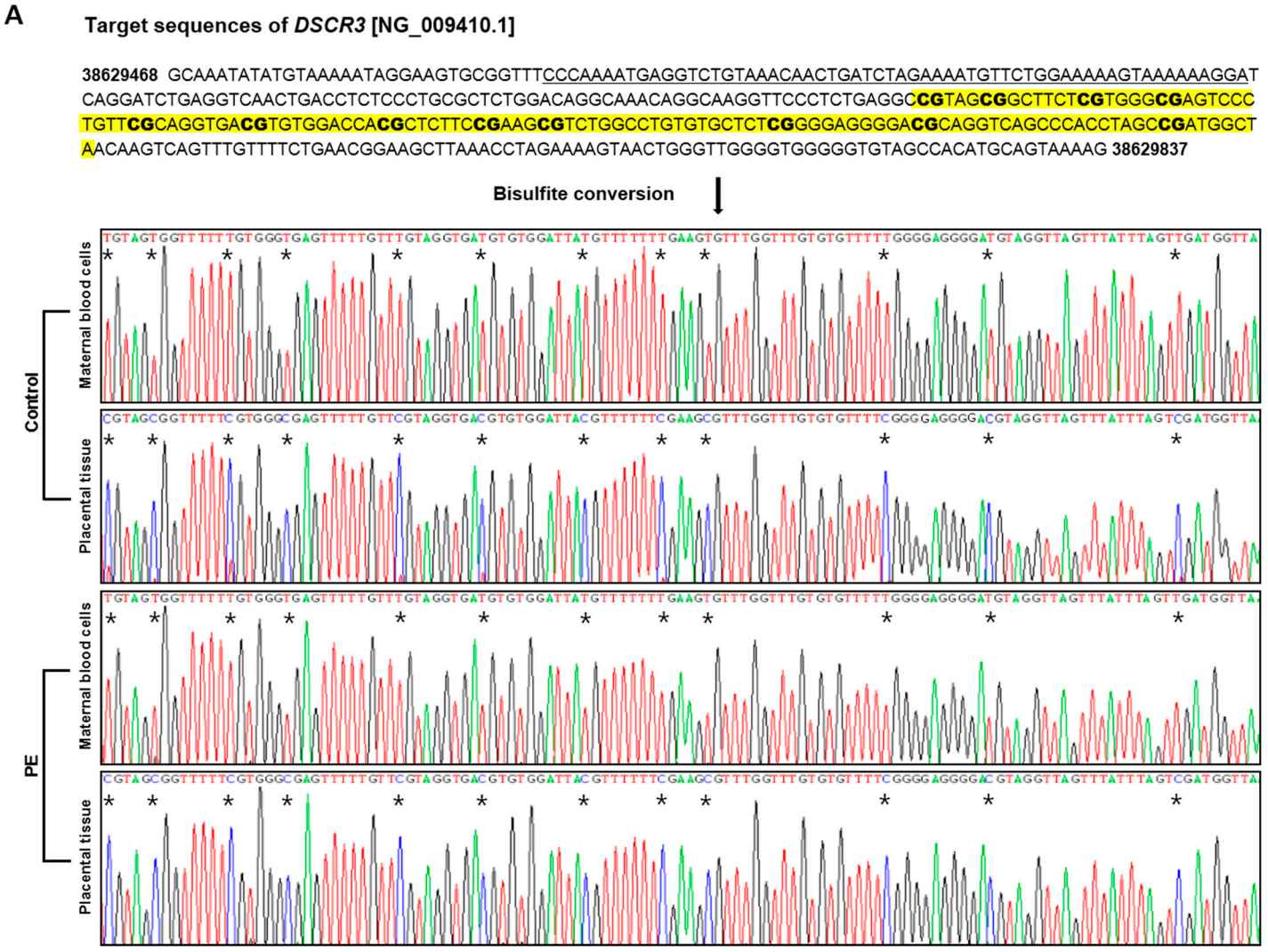

Figure S1. *Cont.*

B

Target sequences of *SOD1* [NG_008689.1]

33037823 GTAACTTGCCTGCCTTTCTCCCTGTGTGGGACTCCTG**CG**GGTGAGAG**CG**TGGCTGAAGACAGC**CG**TGTTATGAAAGGGCCTCCTGTGCTG
T**CG**AGGTTGTGCTCTGTGAATGTCAT CCCCTGGTGCACAGCAGCACCTTCTACACAGGATACAGTTGGAATGCCGCCCCCTCGAGTTGTGTAAGGCA
GCAGCCTTGGCCCTTGCACATAAGATGCTGTTG **33038042**

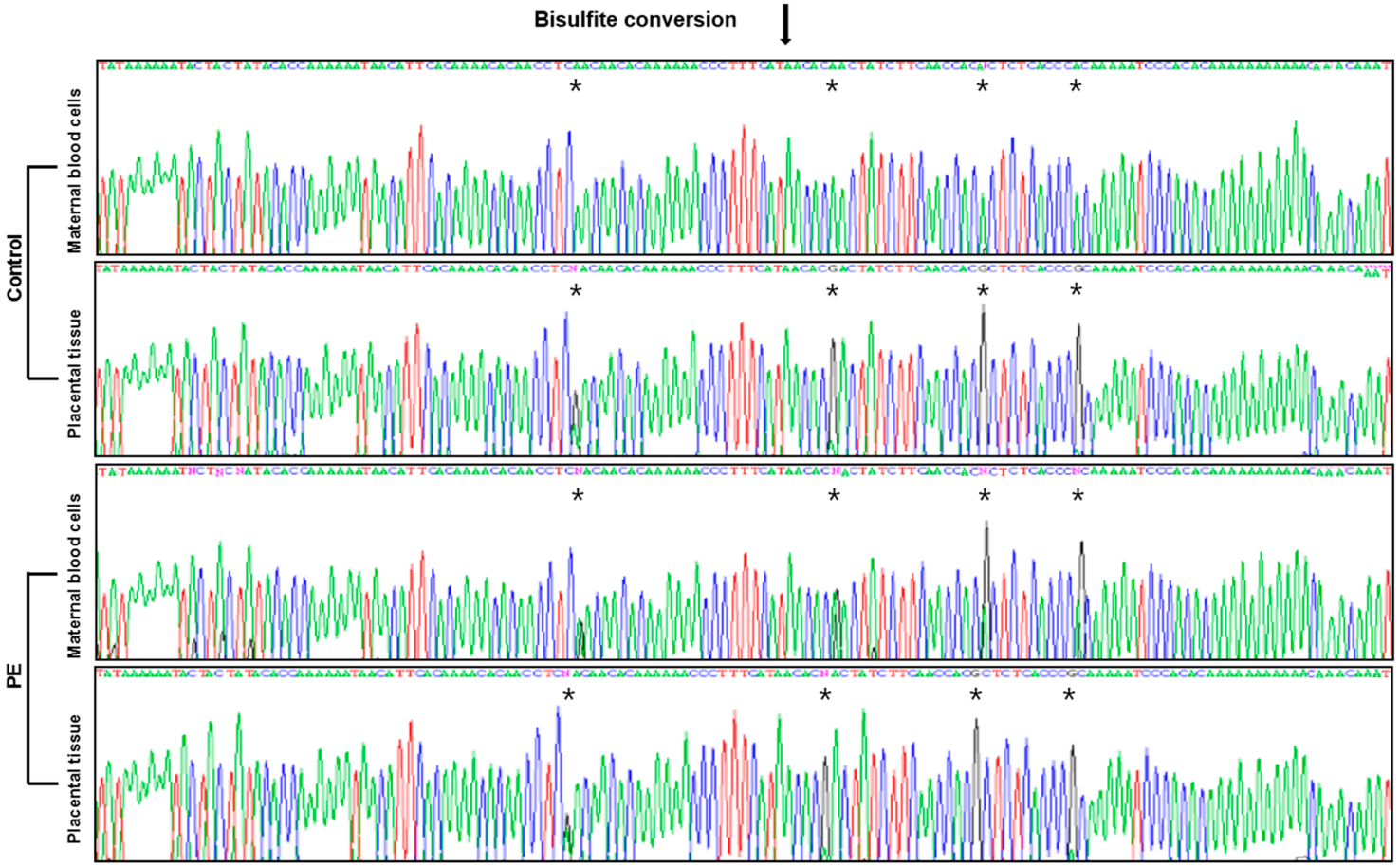

Figure S1. *Cont.*

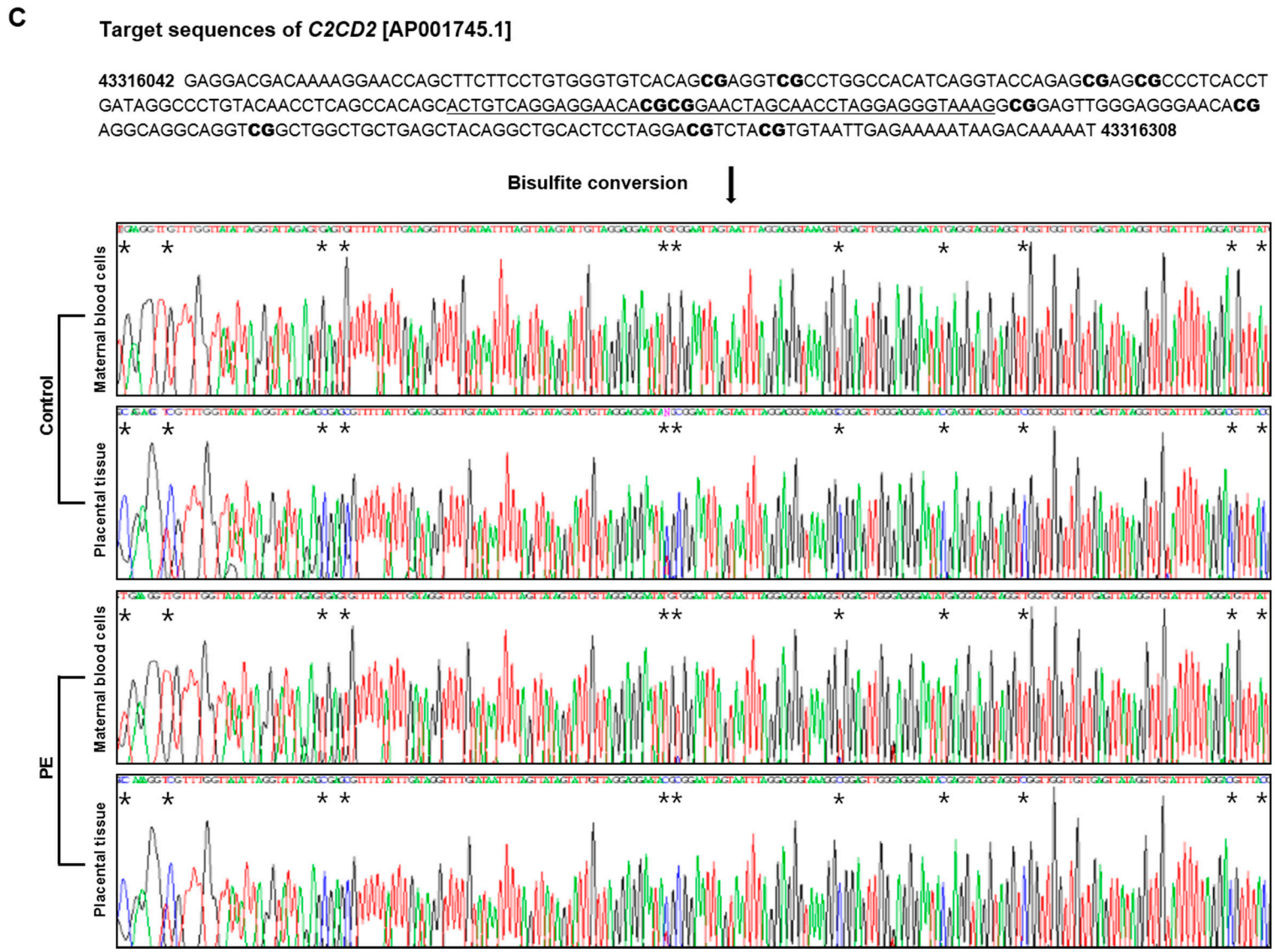

Figure S1. *Cont.*

D

Target sequences of *UMODL1* [AP001745.1]

43483745 GACCCCCTGGAGGAATCCCTCCCTCTAAGACTCTGGGACTGGTGCACGCAAGGAGCTATCGTGAACATTGCTCCCAACTGGC**CG**CTTGCT
TGTCCCC**CG**GCTCCCCTTGGCCCCAGTGG**CG**GCTTTGCCTGAATTAGAGGG**CG**TGAGAGCCACCTGTGTCTCAGCACTGCAATTAAAGCAGGAAGC
CCTTT**CG**GAAGCAGC**CG**TGTGCACCAGCCTCCCATGGGTGGAGCAGAGCAAACCACCCACTTCTGCCCTCTG **43484002**

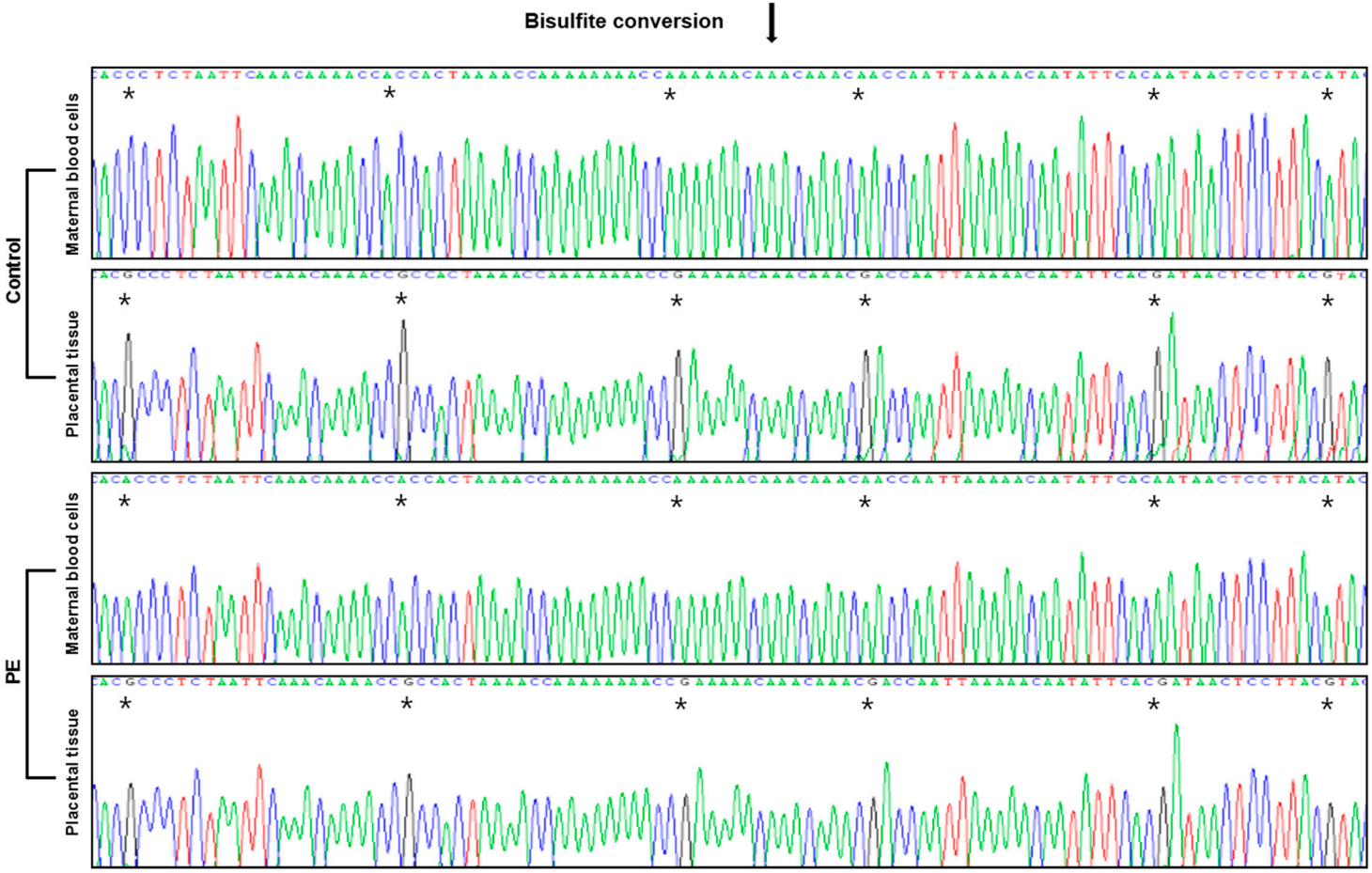

Figure S1. *Cont.*

E

Target sequences of ENST00000433952: -7924 ~ ENST00000433952: -7988 [AL163278.2]

40357575 GAACTGTTCAAGAGGCCCAAGCCTGGTGCTCAGAAACTTGGCAGGATCAAGCATCTCGCCCAGGAATTCATCCCCTGCTTGTCTAAGC**CG**G
CTGGCTCT**CG**TGACTGACT**CG**GAACAACAGAGCAGATGTTTG**CG**TGGGAGGCAAGCCTCACCCAACATCTGTCCTG**CG**G**CG**GGAAGGCCTGGGTGT
TCACAGATAGAGCTGGAGTTCCC**CG**GTGGGTGGCACAGACAATTAGCTGGGGCTGCCTCACATGTAATCTAATTACAGG **40357840**

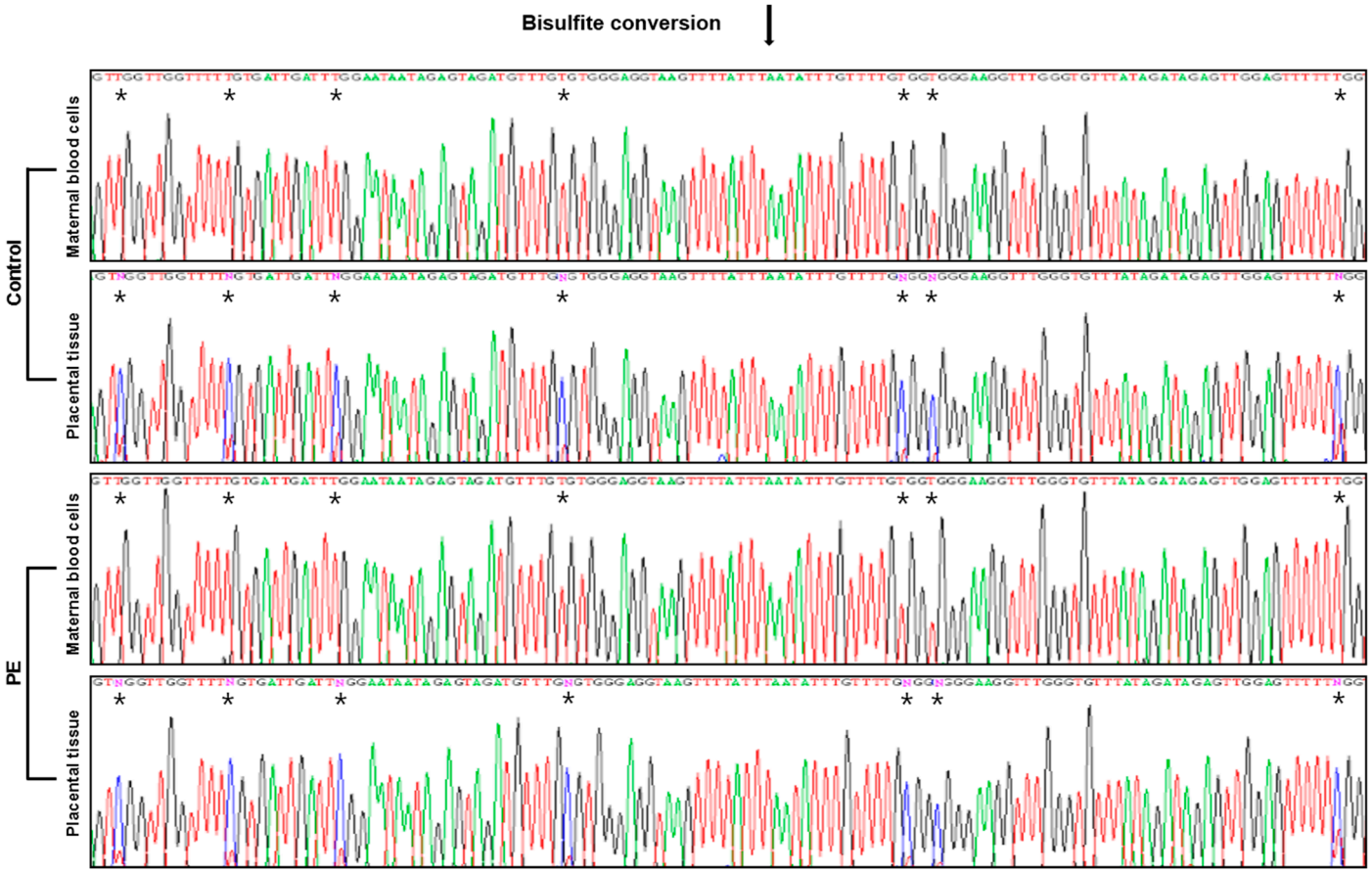

Figure S1. *Cont.*

Figure S1. DNA methylation levels of each CpG site in 6 regions (**A–F**) by bisulfite direct sequencing. The asterisks represent CpG sites in each region. Red and blue peaks in sequences indicate T and C bases, respectively. Probe positions are underlined, and real time PCR regions are highlighted in yellow. The bold characters in the sequences indicate methylation CpG sites of the each region. *SOD1* and *UMODL1* sequences are written in the reverse orientation (3′ to 5′ direction).