

SUPPLEMENTARY TABLES

Supplementary Table 1. The clinical characteristics of the participants (Mean \pm SD).

	Control n = 71	EOPE n = 34	LOPE n = 55
Age (years)	31. 15 \pm 4. 99	31. 71 \pm 4. 52	30. 02 \pm 4. 35
Gestational Weeks	37. 82 \pm 1. 35	31. 68 \pm 0. 85	42. 67 \pm 18. 71
Hb (g/L)	117. 61 \pm 17. 50	112. 40 \pm 18. 12	104. 5 \pm 26. 42
BMI (kg/m ²)	24. 47 \pm 4. 21	26. 73 \pm 4. 08	26. 61 \pm 4. 72
D-DIC (mg/L)	0. 54 \pm 0. 19	1. 97 \pm 0. 82	1. 95 \pm 0. 78
FIB (g/L)	4. 34 \pm 1. 01	5. 20 \pm 1. 64	5. 32 \pm 1. 45
Neonatal Weight (kg)	3. 16 \pm 0. 65	1. 35 \pm 0. 37	2. 90 \pm 0. 63
24UPro (mg/24 h)	133. 71 \pm 73. 74	1006 \pm 556. 4	870. 5 \pm 598. 2
Scr (umol/L)	50. 96 \pm 12. 21	55. 24 \pm 17. 67	60. 67 \pm 18. 35
PLT (10 ⁹ /L)	185. 30 \pm 50. 75	175. 60 \pm 60. 72	153. 70 \pm 71. 04
ALT (U/L)	16. 14 \pm 6. 93	51. 62 \pm 14. 64	53. 09 \pm 14. 92
AST (U/L)	22. 07 \pm 7. 05	40. 82 \pm 13. 02	42. 58 \pm 13. 56
SBP (mmHg)	109. 80 \pm 10. 89	163. 80 \pm 14. 88	178. 60 \pm 17. 28
DBP (mmHg)	66. 79 \pm 7. 83	83. 00 \pm 9. 58	85. 96 \pm 17. 08
WBC (* 10 ⁹ /L)	9. 38 \pm 2. 49	11. 28 \pm 1. 94	12. 08 \pm 2. 52
PMN(* 10 ⁹ /L)	5. 85 \pm 1. 59	8. 46 \pm 1. 62	9. 04 \pm 2. 05
Total Ca ²⁺ (mmol/L)	2. 35 \pm 0. 21	2. 03 \pm 0. 089	2. 05 \pm 0. 12

Supplementary Table 2. The primer sequences for PCR.

Gene name	Primer orientation	Sequences
ZNF516	Forward	5'-GGACCCGGTCAACAGCTAC-3'
	Reverse	5'-GGCCCCGTACTTGAGGTACT-3'
	Forward	5'-GGAGCGAGATCCCTCCAAAAT-3'
GAPDH	Reverse	5'-GGCTGTTGTCATACTTCTCATGG-3'
	Forward	5'-ACACTCCAGCTGGGAACTGGCCCTCAAAGT-3'
hsa-miR-193b	Reverse	5'-CTCAACTGGTGTCTCGTGGAGTCGGCAATTCAGTTGAG AGCGGGAC-3'
	Forward	5'-ACACTCCAGCTGGGCTGTGCGTGTGACAGC-3'
hsa-miR-210-3p	Reverse	5'-CTCAACTGGTGTCTCGTGGAGTCGGCAATTCAGTTGAGTCAGCCGC-3'
	Forward	5'-ACACTCCAGCTGGGAACTGGCCCTACAAAGT-3'
hsa-miR-193a-3p	Reverse	5'-CTCAACTGGTGTCTCGTGGAGTCGGCAATTCAGTTGAGACTGGGAC-3'
	Forward	5'-ACACTCCAGCTGGGACTCAAACGTGGG-3'
hsa-miR-371-5p	Reverse	5'-CTCAACTGGTGTCTCGTGGAGTCGGCAATTCAGTTGAG AGTGCCCC-3'
	Forward	5'-ACACTCCAGCTGGGACAGGTGAGGTTCTTG -3'
hsa-miR-125a-3p	Reverse	5'-CTCAACTGGTGTCTCGTGGAGTCGGCAATTCAGTTGAGGGCTCCCA-3'
	Forward	5'-CTCGCTTCGGCAGCACA-3'
U6snRNA	Reverse	5'-AACGCTTCACGAATTTGCGT-3'

Supplementary Table 3. The binding site of ZNF516 to hsa-miR-371-5p through the use of TargetScan (https://www.targetscan.org/vert_80/).

Conserved								
	Predicted consequential pairing of target region (top) and miRNA(bottom)	Site type	Context ++ score	Context+ + score percentile	Weighted Context++ score	Conserved branch length	PC T	Predicted relative Kp
Position 350-357 of ZNF5163'UTR	5'...UCUUAUUCAAGACAAGUUUGA GA..	8mer	-0.03	82	-0.03	2.049	N/A	-4.864
hsa-miR-371a-5p	3'...UCACGGGGGUGUCAAAACUCA..							