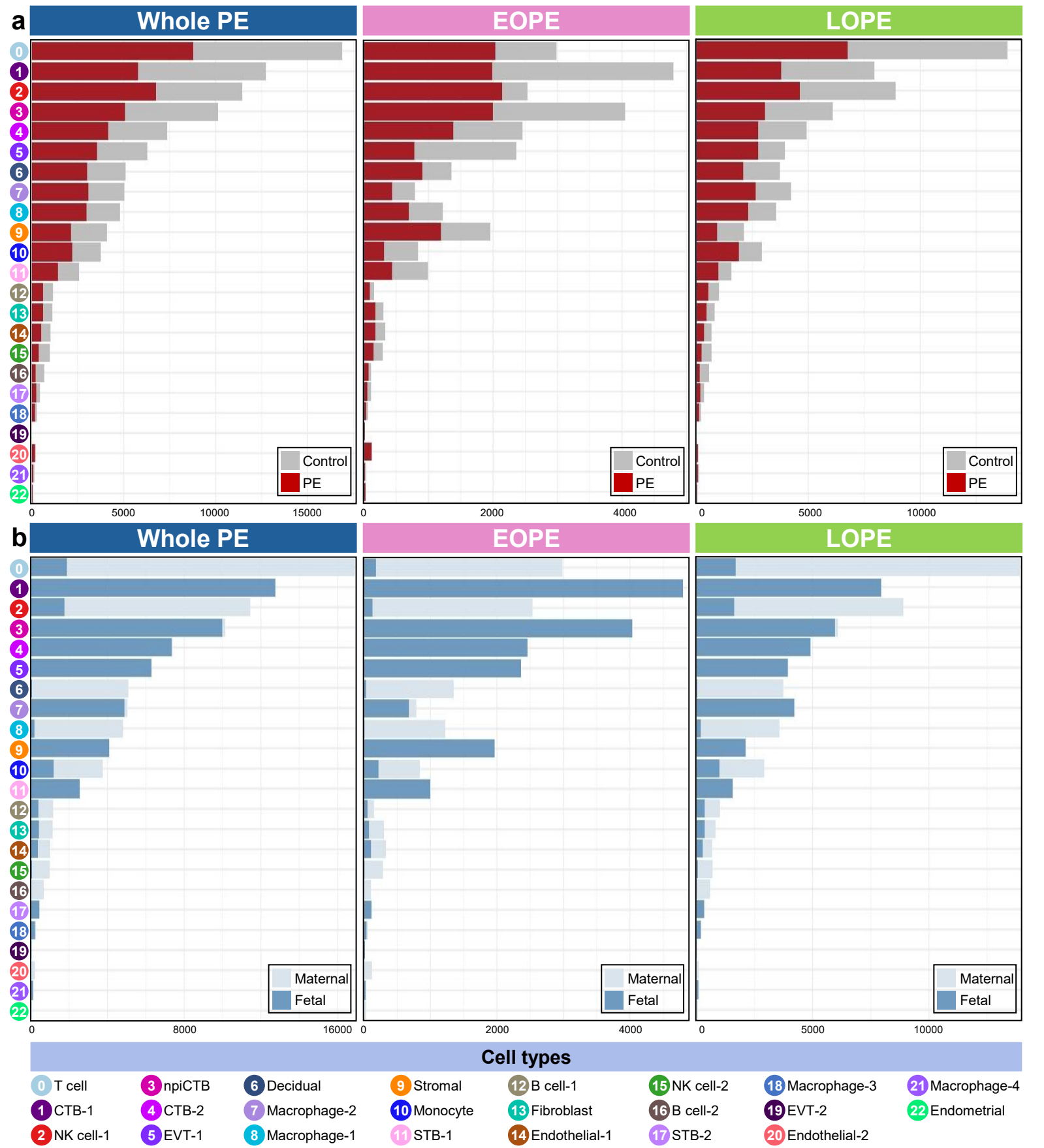


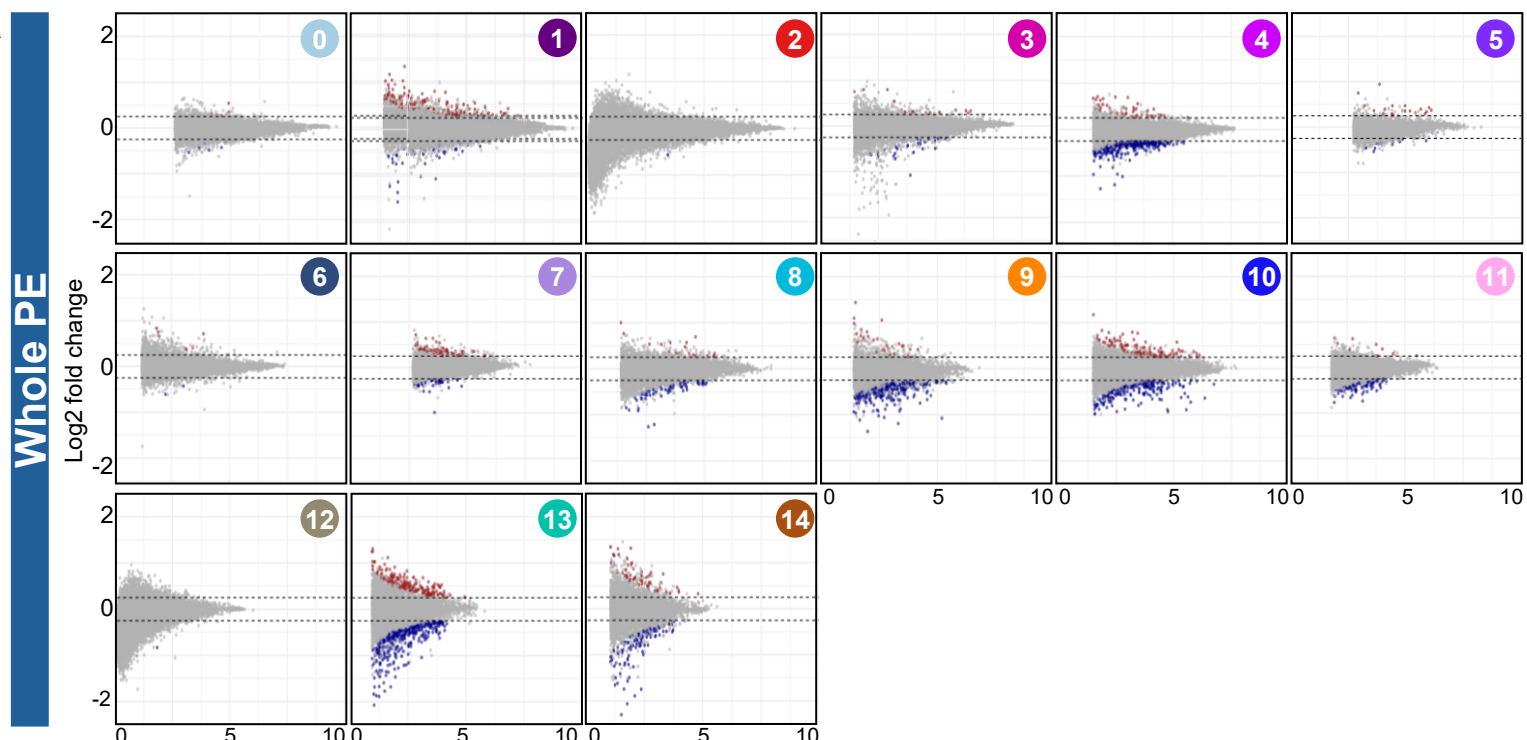
Supplementary Fig. 1



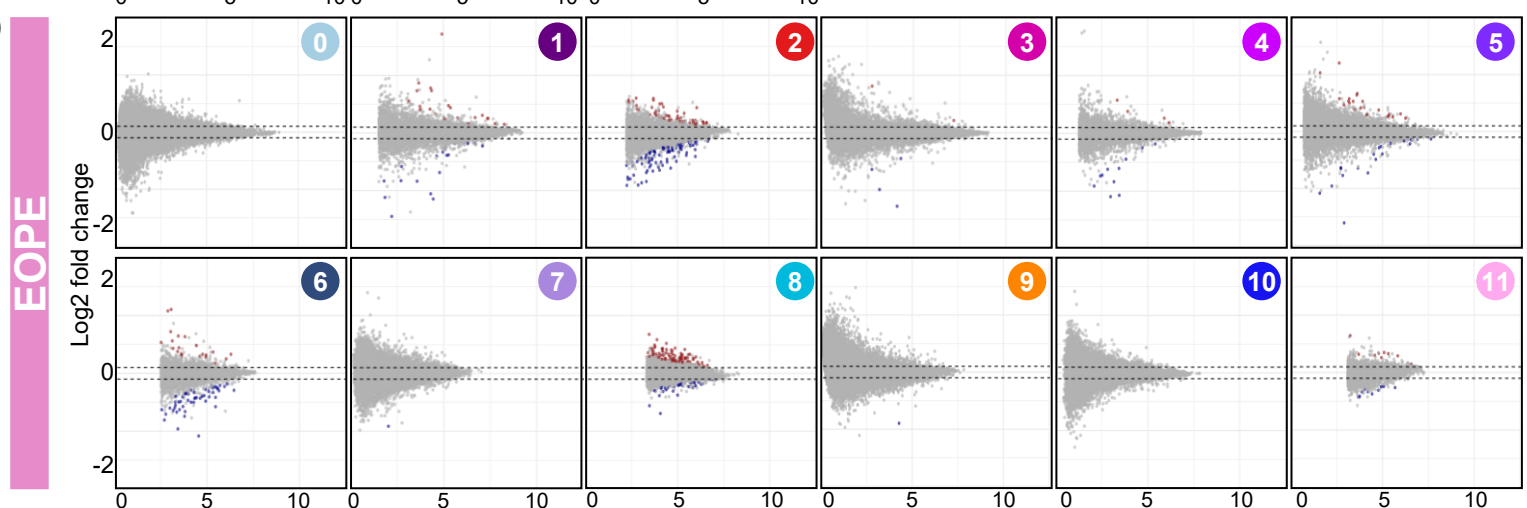
Supplementary Fig. 1. Cell counts in each cell type. Bar plots represent the numbers of each cell type with (a) women with PE (red bars) and controls (grey bars) and with (b) maternal (light blue) or fetal (dark blue) origin in the whole PE, EOPE, and LOPE.

Supplementary Fig. 2

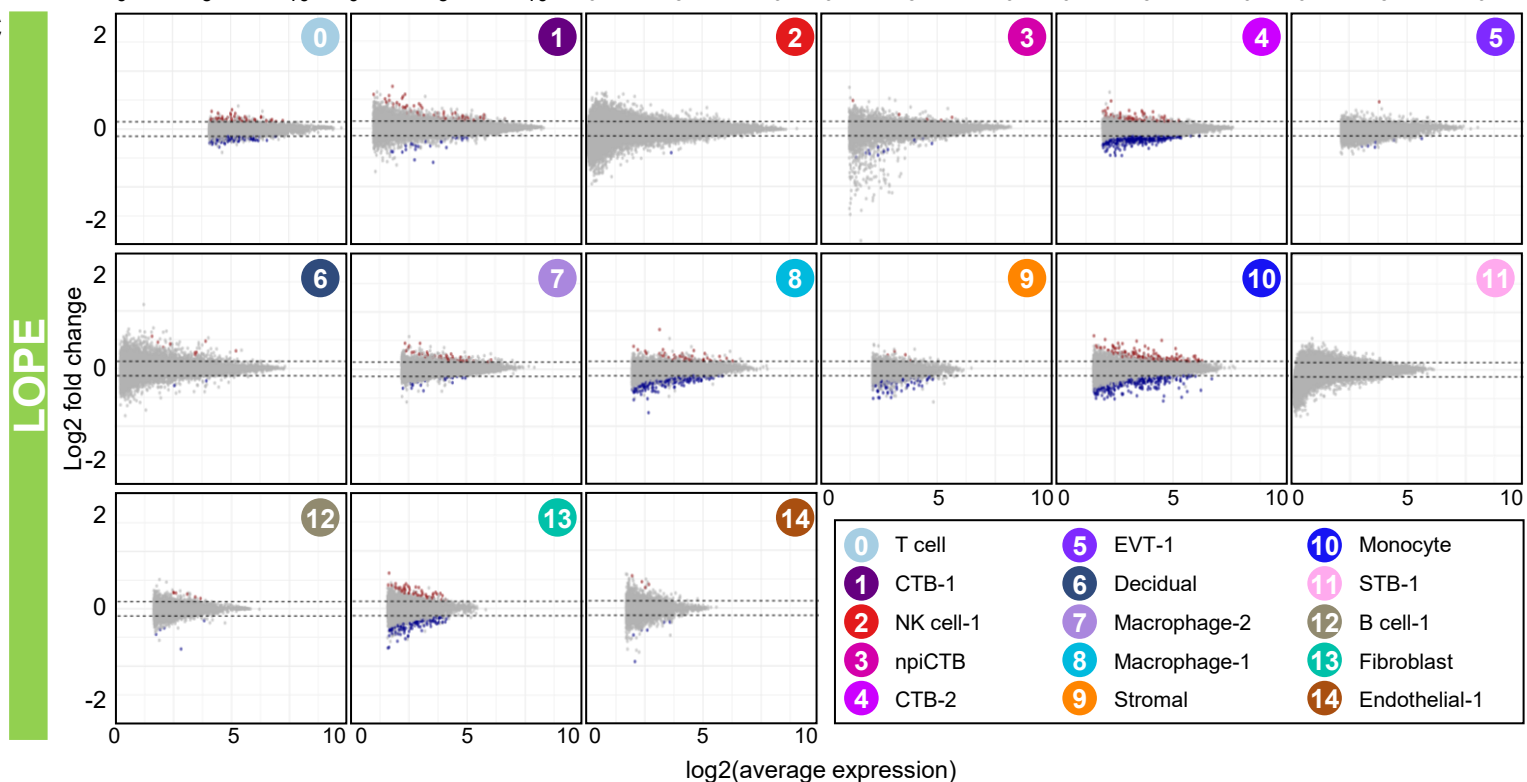
a



b

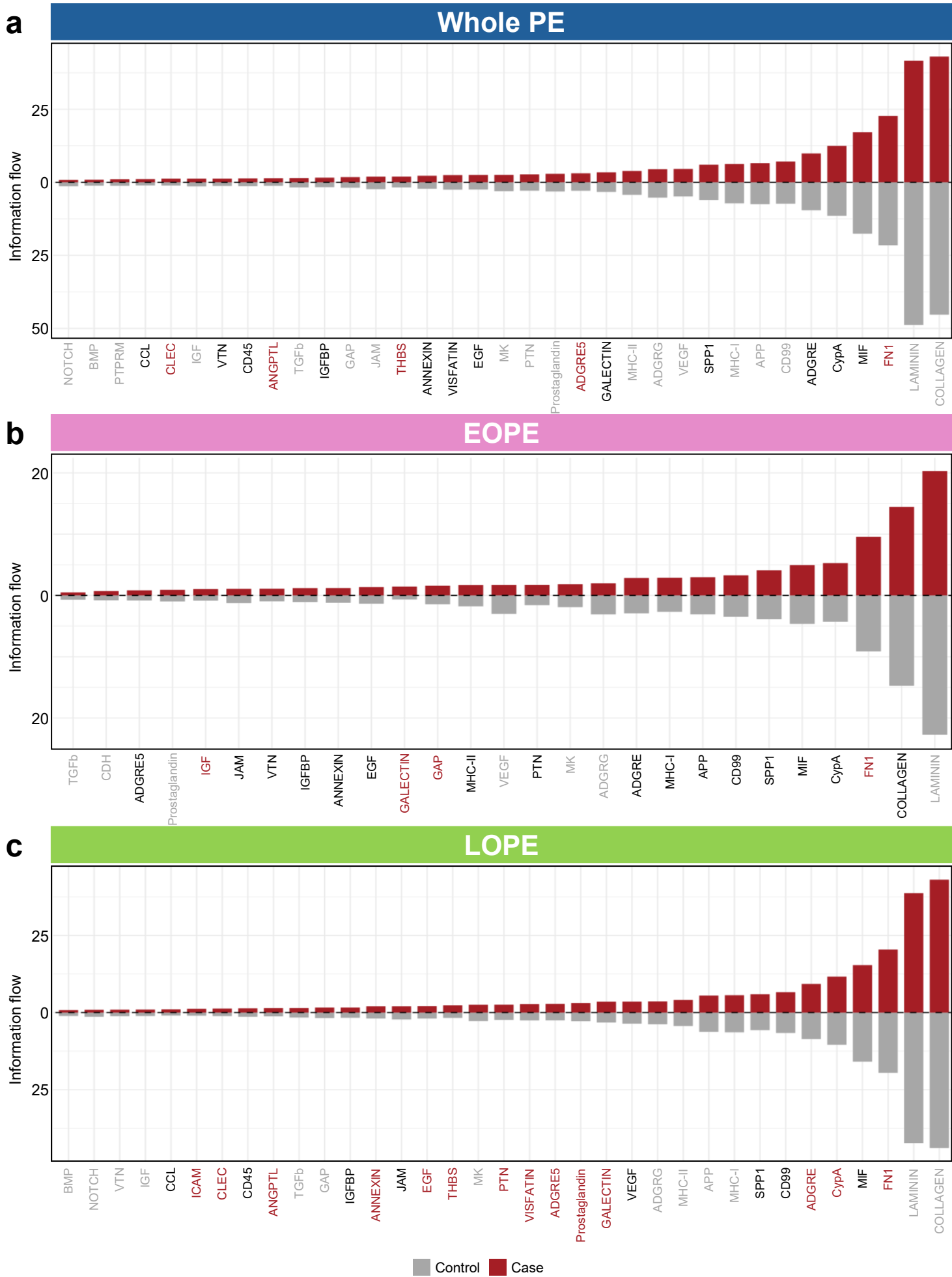


c



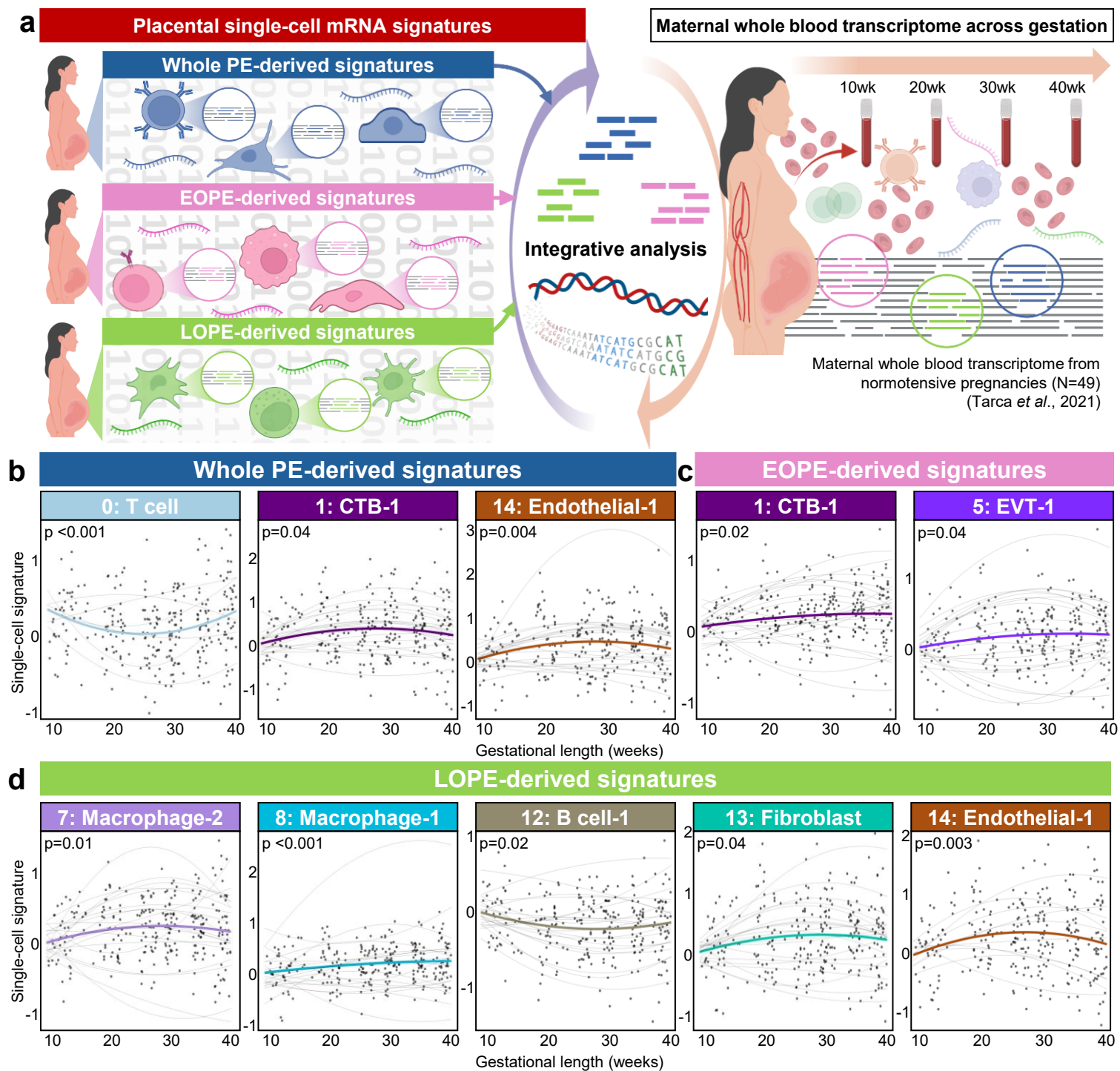
Supplementary Fig. 2. MA plot of all detected genes. MA-plot showing the log₂ fold changes and average expression values of differentially expressed genes (DEGs). Significant genes after p-value adjustment are displayed in red when they are upregulated and blue when they are down regulated in PE cases compared to controls.

Supplementary Fig. 3



Supplementary Fig. 3. Top 25% aggregated interaction. Bar plots represent information flow of each pathway in women with PE and controls in (a) whole PE, (b) EOPE, and (c) LOPE. The top 25% signaling pathways colored red are more enriched in PE, the ones colored black are equally enriched in PE and controls, and the ones colored grey are more enriched in controls.

Supplementary Fig. 4.



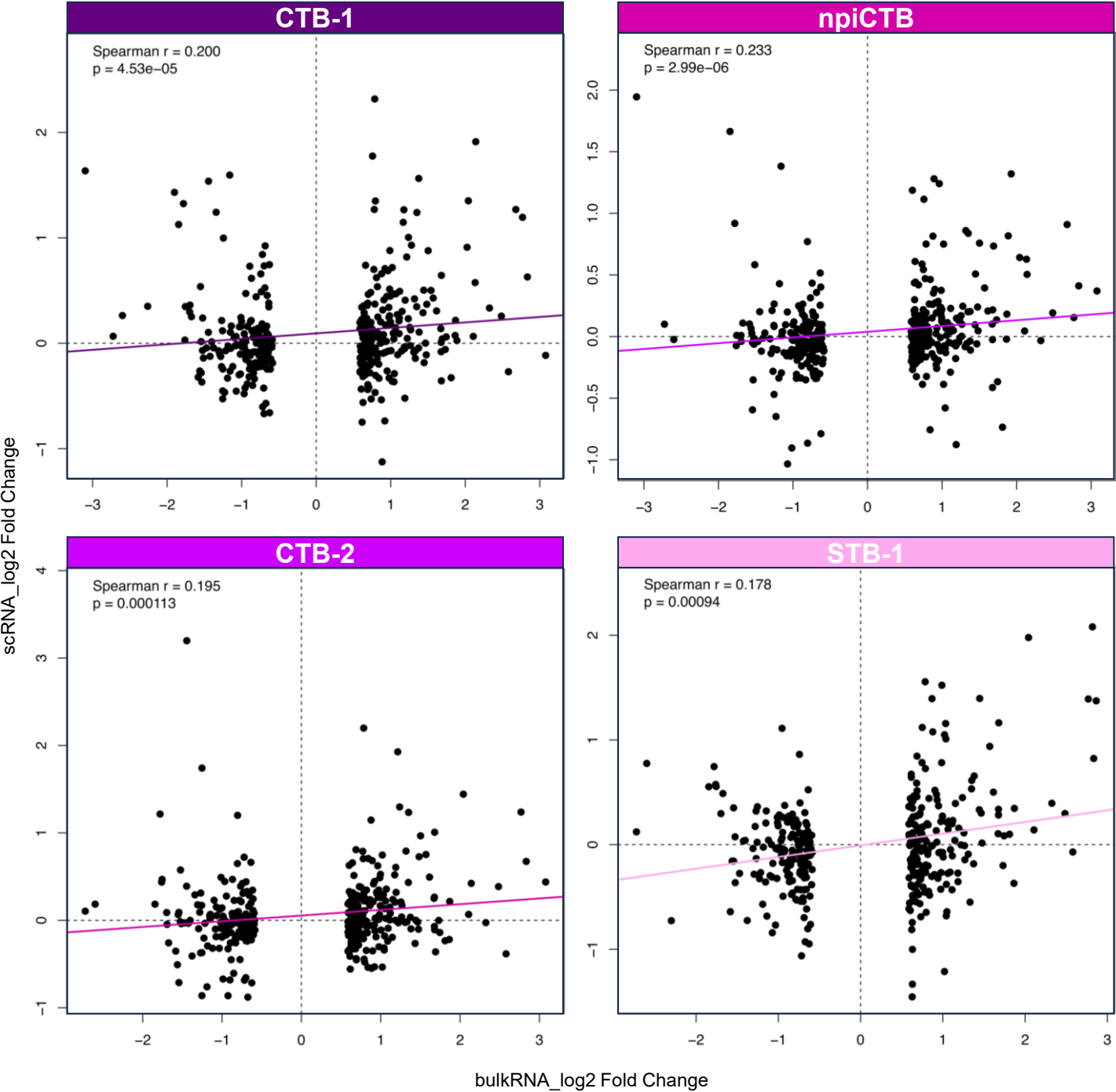
Supplementary Fig. 4. Placental single-cell signatures detected in the maternal circulation of normotensive pregnant women. (a) Schematic overview of the integrative analysis between placental single-cell signatures and whole blood transcriptomic profiles from maternal peripheral blood collected throughout normal pregnancy (n=49). Line plots show the longitudinal trajectories of single-cell signatures derived from (b) whole PE, (c) EOPE, and (d) LOPE in the maternal circulation. Dots represent gene expression values detrended for gestational age, and colored lines indicate the average trajectories of the aggregated signatures for each cell type.

Supplementary Fig. 5



Supplementary Fig. 5. Placental single-cell signatures detected in maternal circulation at PE diagnosis. (a) Schematic overview of the integrative analysis between placental single-cell signatures and whole blood transcriptomic profiles from maternal peripheral blood collected at the time of EOPE (n=25) and LOPE diagnosis (n=47). ROC curves of (b) whole PE, (c) EOPE, and (d) LOPE-derived signatures evaluated for their performance in differentiating EOPE and LOPE cases from matched controls. AUC values with 95% confidence intervals are reported for each signature. An AUC lower bound >0.5 indicates significant discriminatory performance.

Supplementary Fig. 6.



Supplementary Fig. 6. Correlation of DEGs between bulk and scRNA-seq analyses. Correlation coefficient (r) and statistical significance (p) were calculated via spearman correlation analysis. Each dot represents DEGs identified in both bulk and scRNA-seq analyses.

Supplementary Tables

Supplementary Table 1. Previous studies for human placental scRNA-seq studies in PE

Reference	Year	Samples	Sample size
Tsang (26)	2017	Placenta	8 PE, 4 Healthy pregnancies
Zhang (27)	2021	Placenta	3 EOPE, 3 Healthy pregnancies
Zhou (28)	2022	Placenta	2 severe PE, 2 Normal controls
Liu (29)	2023	Placenta	8 PE, 8 Healthy pregnancies
Yang (30)	2023	Placenta	3 LOPE, 3 Normal pregnancies
Luo (31)	2023	Placental decidua	2 PE, 2 Normal controls
Admati (32)	2023	Placenta	12 EOPE, 9 LOPE, 6 Healthy pregnancies
Tsuda (33)	2024	Decidua	3 PE, 3 Normal controls
Li (34)	2024	Decidual basalis	6 PE, 4 Normal controls
Wei (35)	2025	Chorioamniotic membranes	2 EOPE, 2 LOPE, 4 Healthy pregnancies
		Placental villous	
		Basal plate	
Xiao (36)	2025	Placenta	3 PE, 3 Normal controls

PE; preeclampsia, EOPE; early-onset preeclampsia, LOPE; late-onset preeclampsia

Supplementary Table 2. Clinical characteristics of early-onset preeclampsia (EOPE) and late-onset preeclampsia (LOPE) patients and non-preeclamptic controls

	No Preeclampsia (<34 weeks)	Early-onset preeclampsia (<34 weeks)	p- value	No Preeclampsia (≥34 weeks)	Late-onset preeclampsia (≥34 weeks)	p- value
N	10	10		29	29	
Maternal age (years; median [IQR]) ^a	24.0 (21.8-29.8)	29.0 (23.5-34.5)	0.190	29.0 (24.0-32.5)	29.0 (24.5-35.0)	0.714
Body mass index (kg/m ² ; median [IQR]) ^a	29.3 (25.6-33.4)	33.9 (26.5-42.3)	0.247	33.0 (23.0-37.7)	35.9 (28.3-43.0)	0.039
Primiparity ^b	30% (3/10)	20% (2/10)	1.0	10.3% (3/29)	24.1% (7/29)	0.149
Race/Ethnicity ^b			0.171			0.801
African-American	70% (7/10)	100% (10/10)		79.3% (23/29)	79.3% (23/29)	
White	20% (2/10)	0% (0/10)		13.8% (4/29)	17.2% (5/29)	
Asian	10% (1/10)	0% (0/10)		0% (0/29)	0% (0/29)	
Not provided	0% (0/10)	0% (0/10)		6.9% (2/29)	3.4% (1/29)	
Systolic blood pressure (mmHg) ^a	133.0 (125.8-143.0)	177.0 (160.3- 184.0)	<0.001	126.0 (115.0- 136.0) ^c	168.0 (158.5-177.5)	<0.001
Diastolic blood pressure (mmHg) ^a	74.0 (73.0-84.5)	102.5 (99.0-112.0)	<0.001	78.0 (73.0-82.0) ^c	103.0 (97.5-111.0)	<0.001
Gestational age at delivery (weeks; median [IQR]) ^a	30.5 (29.6-32.5)	30.1 (26.8-32.9)	0.631	36.9 (35.7-38.2)	36.9 (35.8-39.0)	0.618
Birthweight (grams; median [IQR]) ^a	1670 (1278.3- 2126.3)	1220 (760.0- 1482.5)	0.019	2680.0 (2185.0- 3055.0)	2655.0 (2232.5- 3212.5)	0.646
Fetal sex ^b			0.185			0.50
Female	40% (4/10)	70% (7/10)		55.2% (16/29)	58.6% (17/29)	
Male	60% (6/10)	30% (3/10)		44.8% (13/29)	41.4% (12/29)	

Data are given as median (interquartile range, IQR) and percentage (n/N).

^aMann-Whitney U-test, ^bFisher's exact test, ^cMissing data for two late-onset preeclampsia controls