

Supplementary Figures

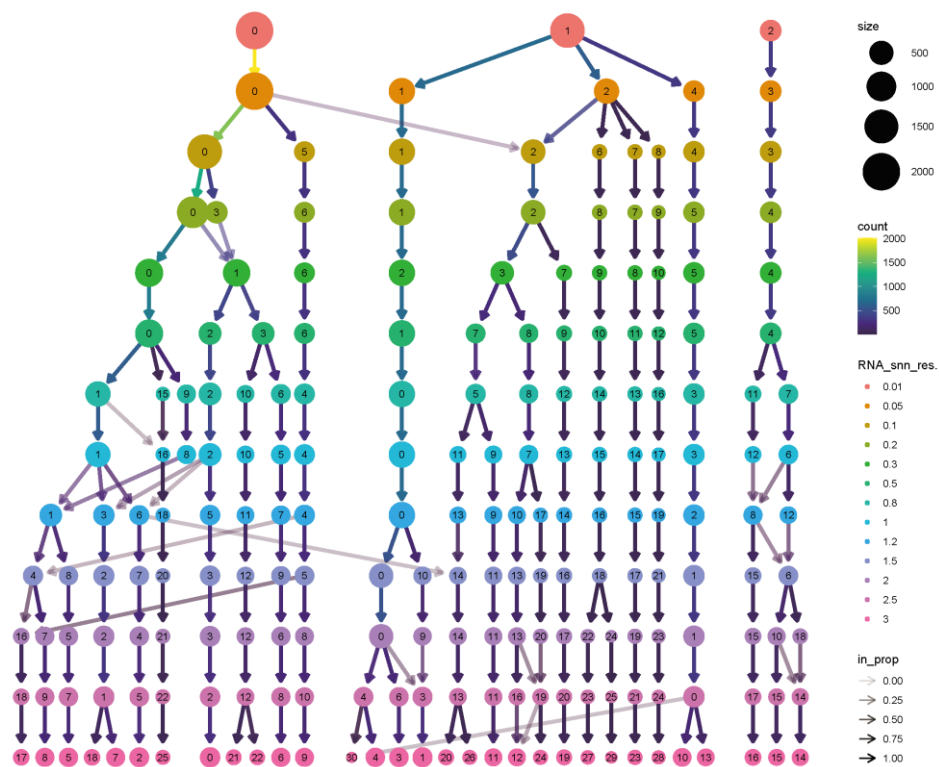


Figure S1. Cluster tree of this analysis and resolution was set as 1.2

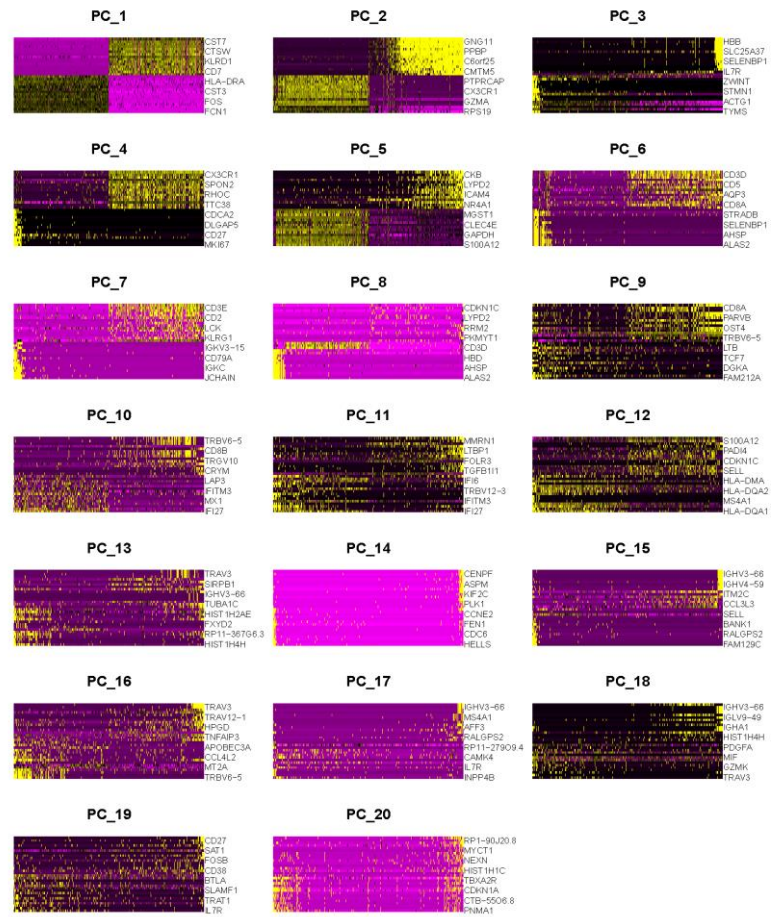


Figure S2. The heatmap shows the expression of the top 8 marker genes in PC

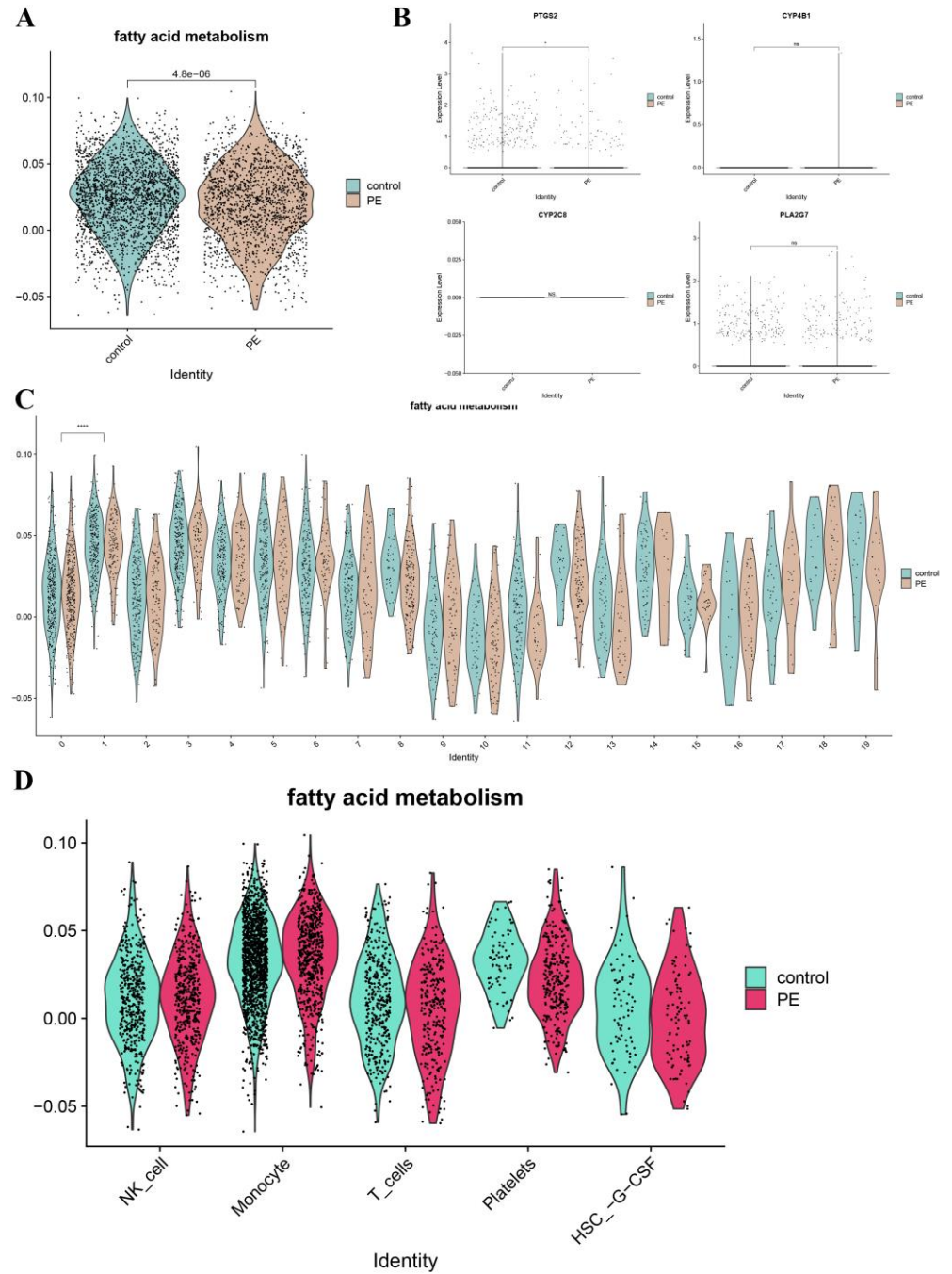


Figure S3. Difference analysis of fatty acid metabolism-related genes between the PE and control groups. **(A)** The differential expression of fatty acid metabolism-related genes between the PE and control groups. **(B)** The differential expression of PTGS2, PLA2G7, CYP2C8, and CYP4B1. **(C)** The differential expression of fatty acid metabolism-related genes between the PE and control groups across 20 clusters. **(D)** The differential expression of fatty acid metabolism-related genes between the PE and control groups across 5 cell types

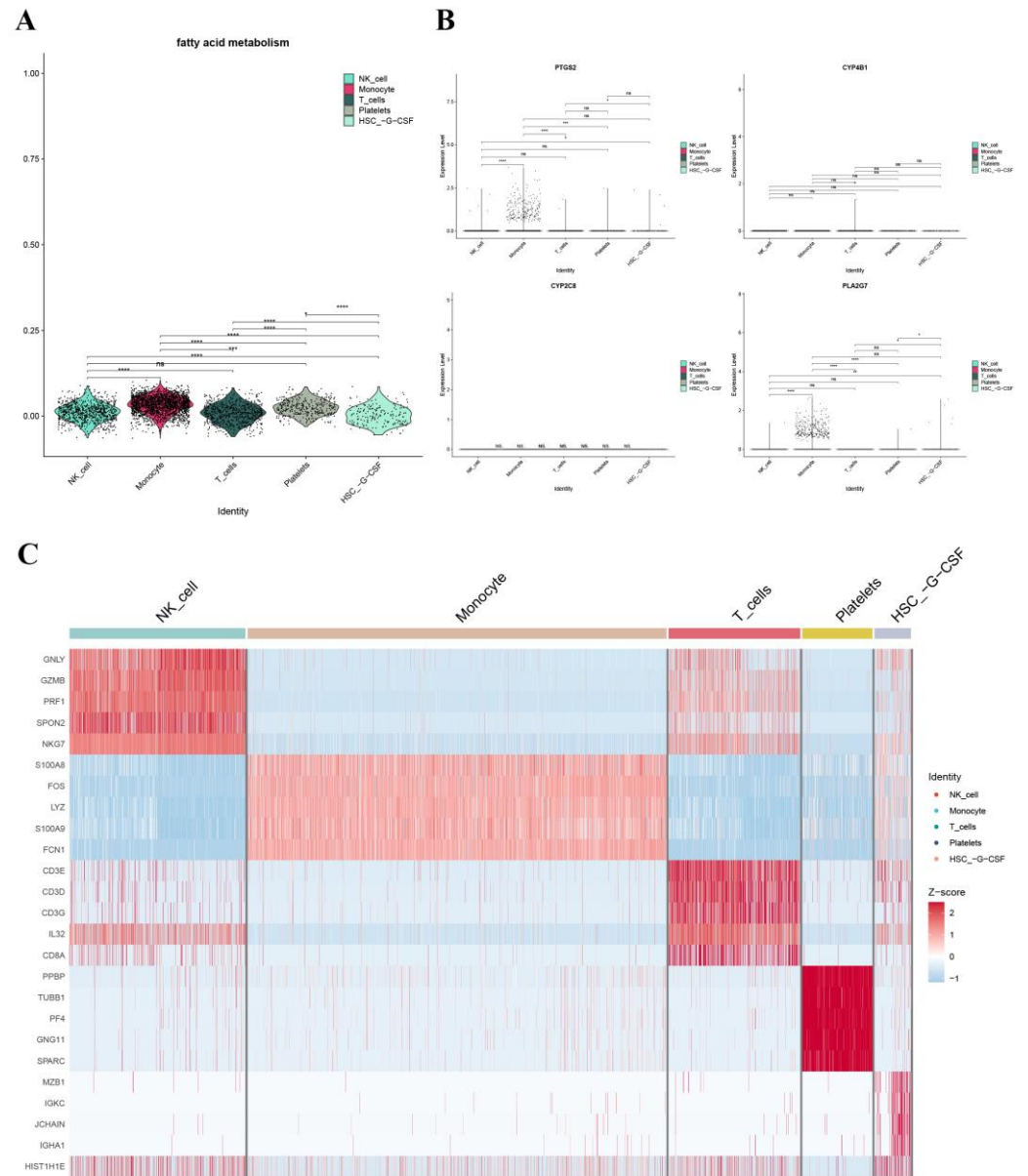


Figure S4. (A) The violin plot illustrates the expression of fatty acid metabolism-related genes in each cell type. (B) The violin plot illustrates the expression of PTGS2, PLA2G7, CYP2C8, and CYP4B1 in each cell type. (C) The heatmap shows the expression of the top 5 marker genes in different cell clusters.

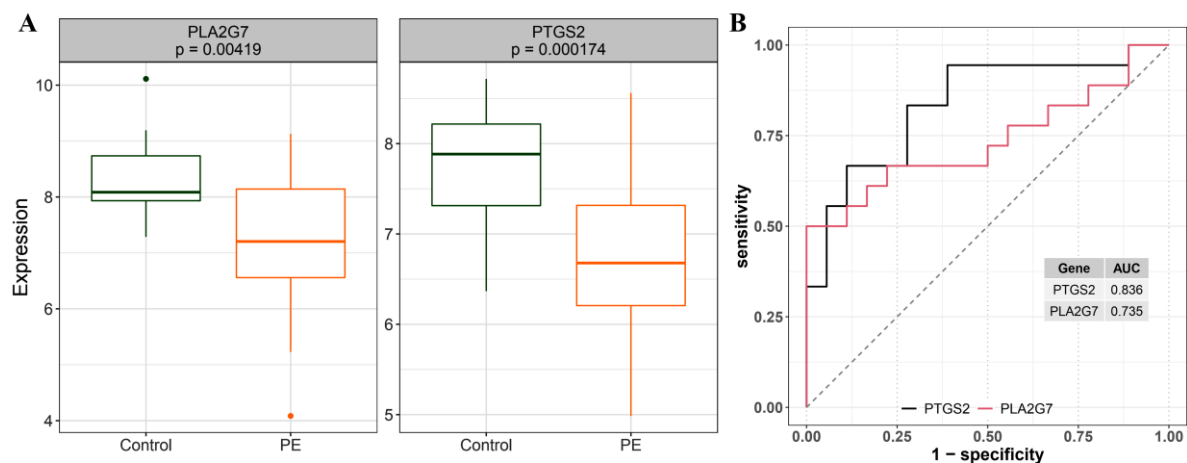


Figure S5. (A) Expression of hub genes (B) ROC of hub genes.

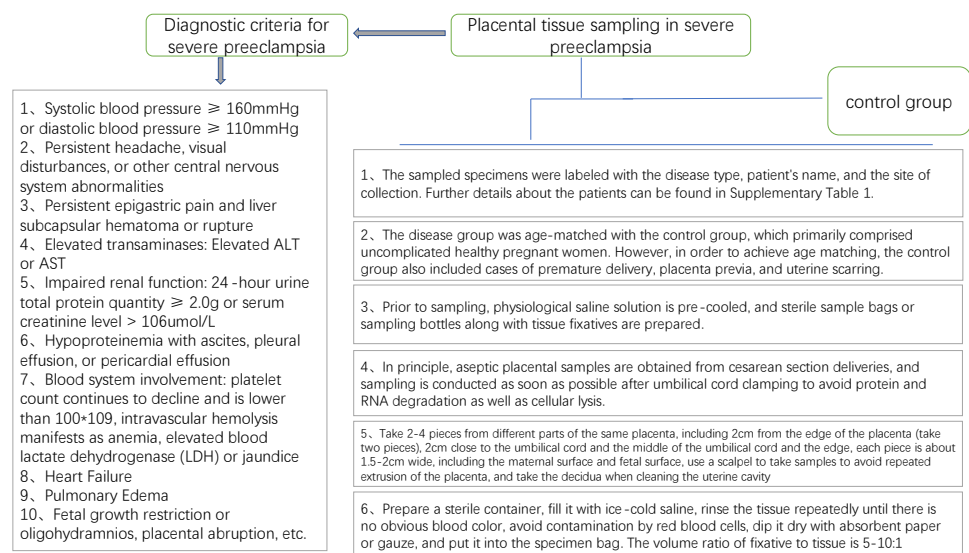


Figure S6. Inclusion criteria for sample collection.

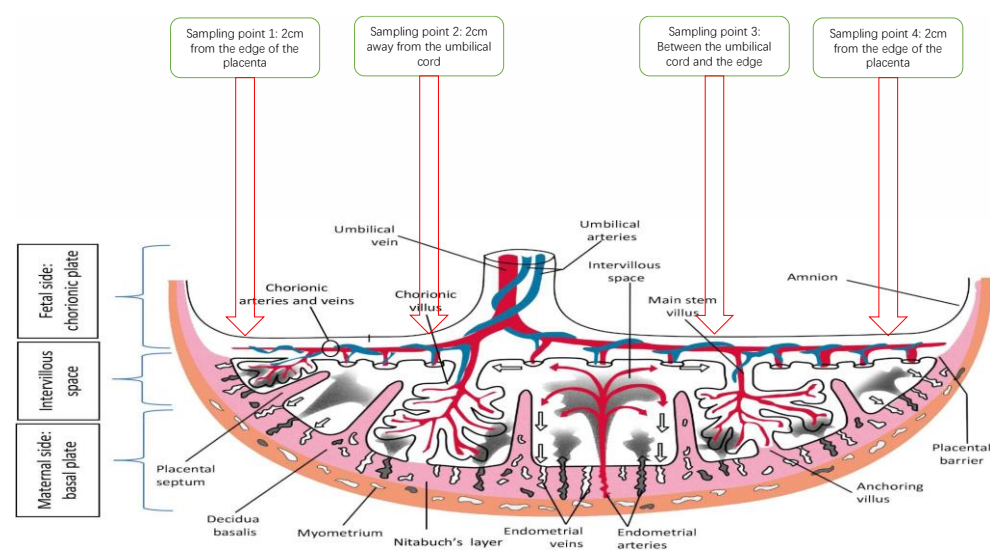


Figure S7. The location where the sample was taken during sample collection.