

Figure S1

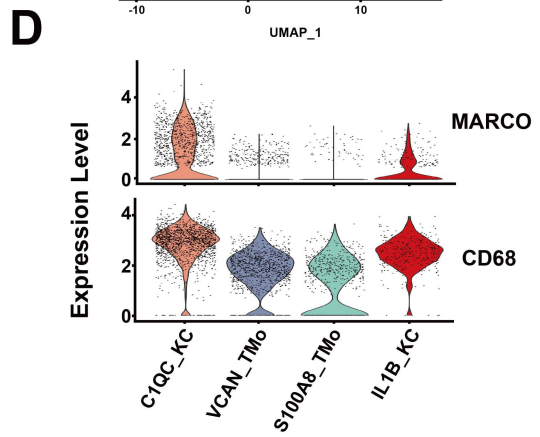
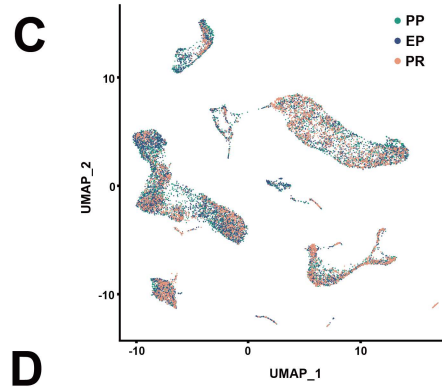
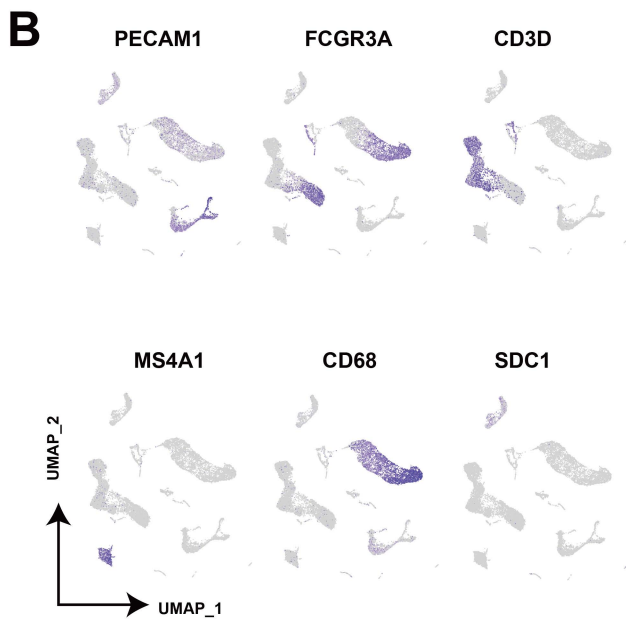
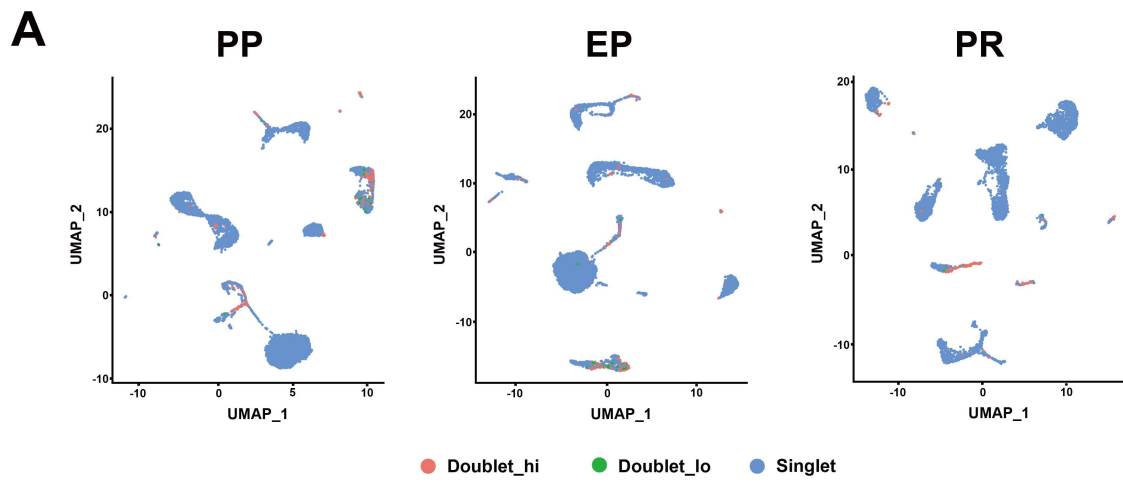
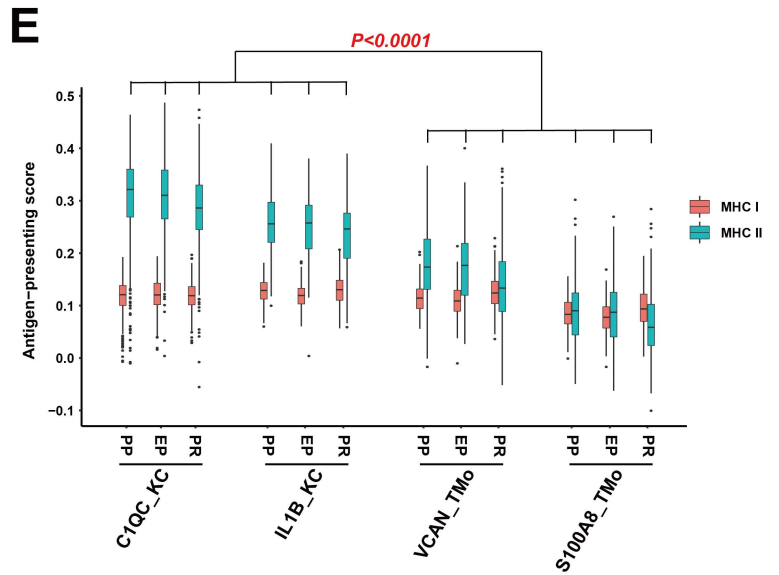
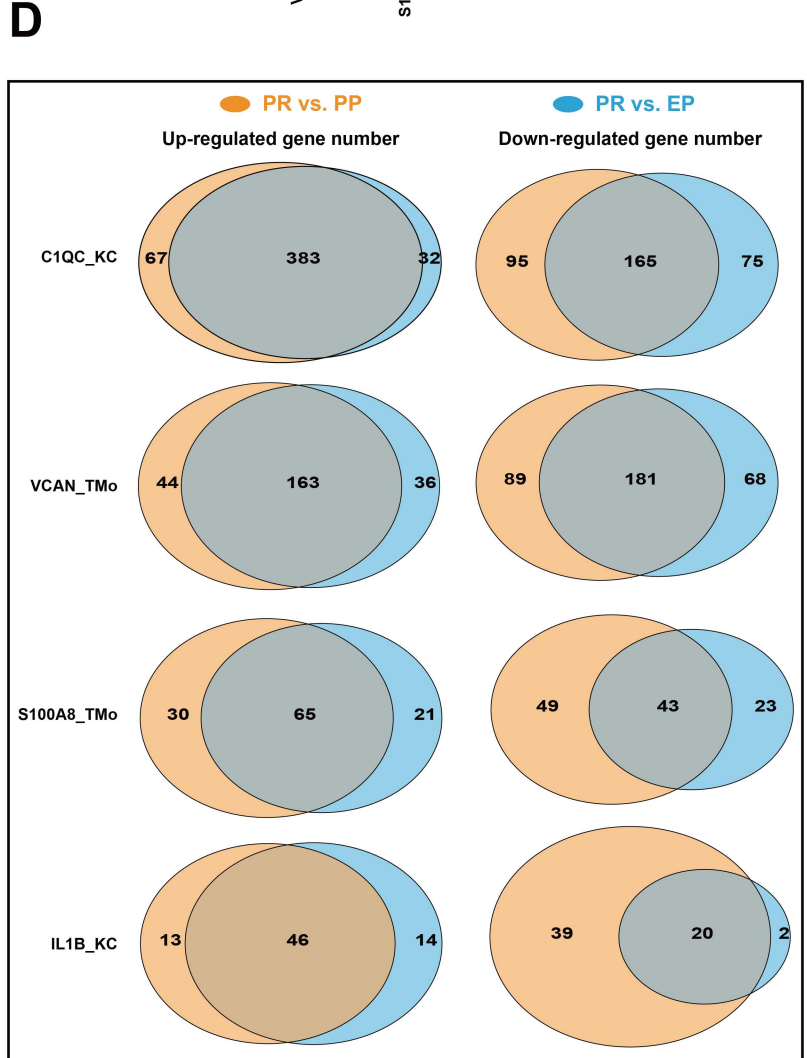
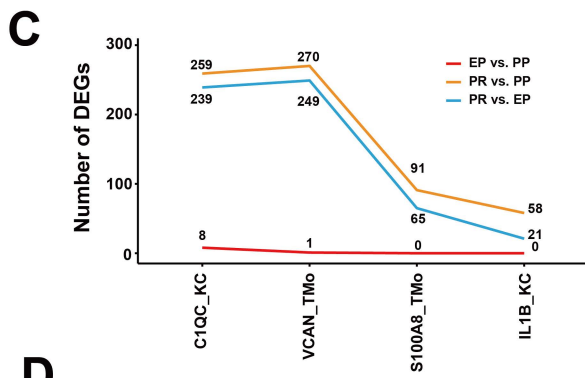
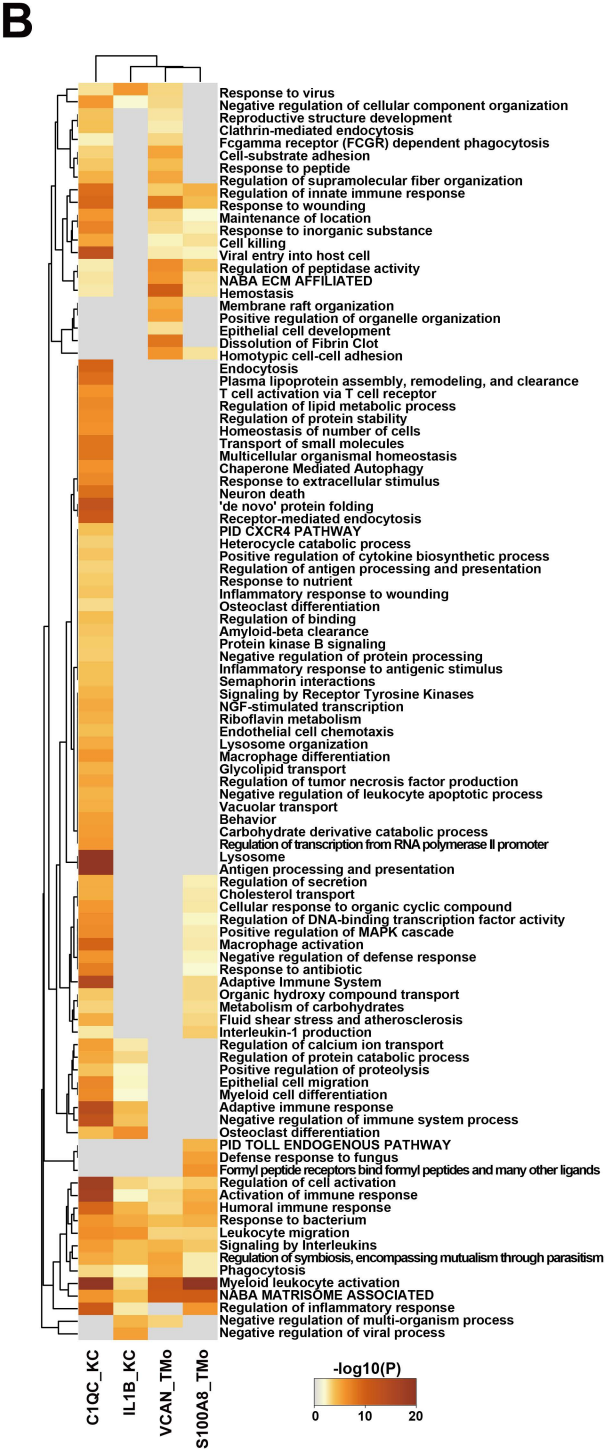
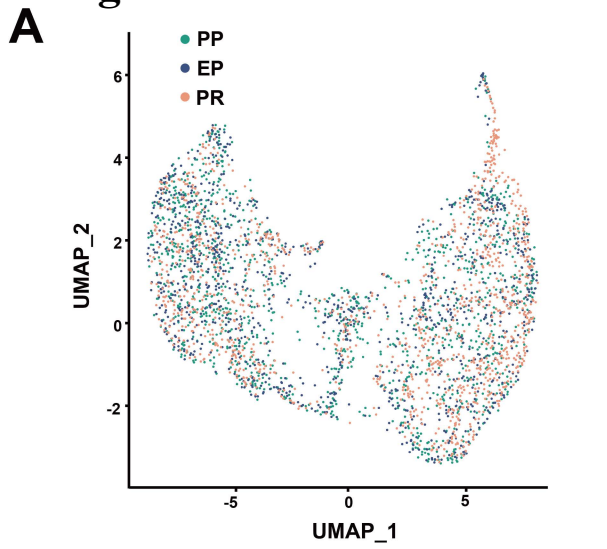


Figure S2

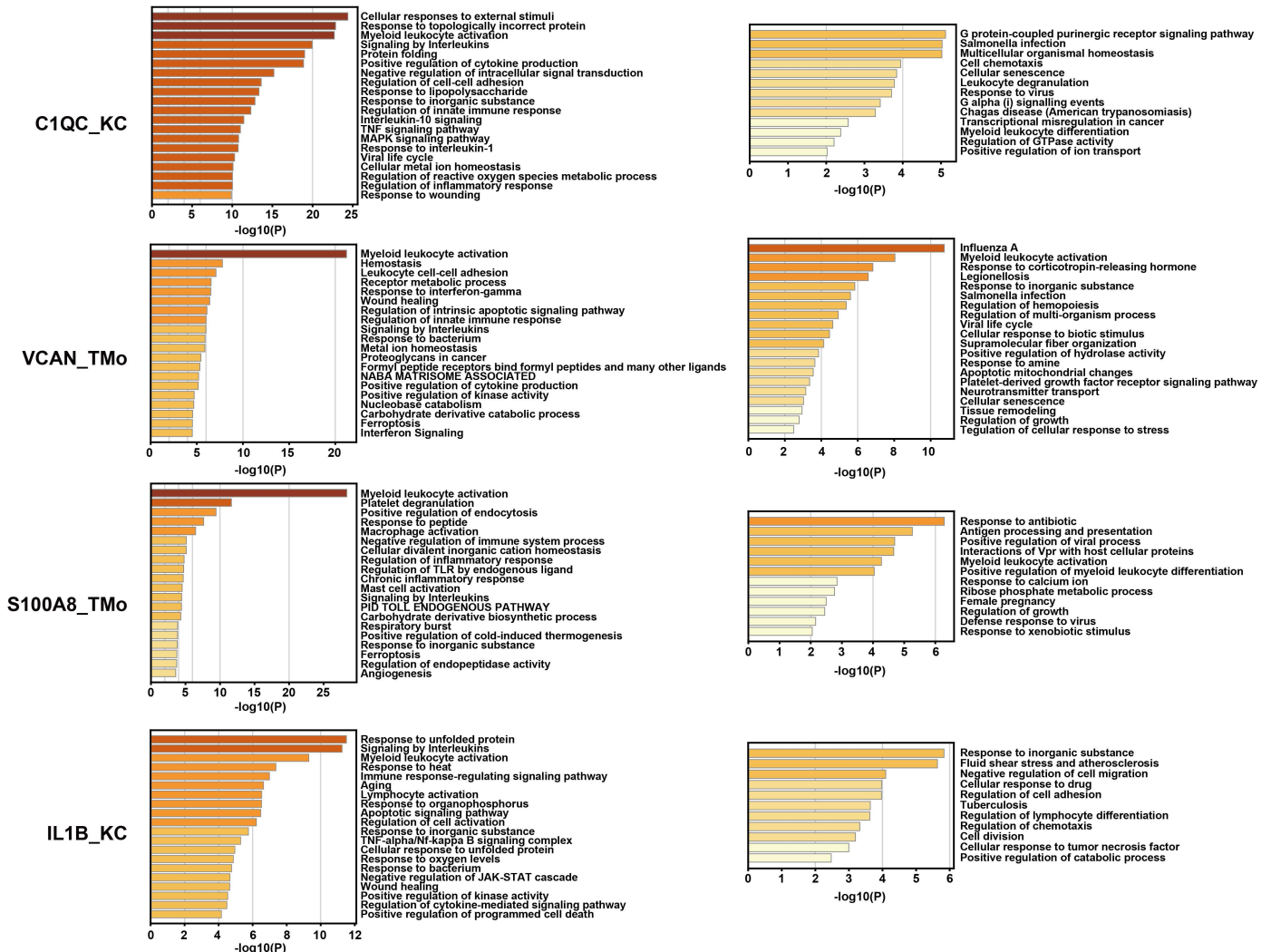


A

PR vs. EP up-regulated pathways

Figure S3

PR vs. EP down-regulated pathways

**B**

PR vs. PP up-regulated pathways

PR vs. PP down-regulated pathways

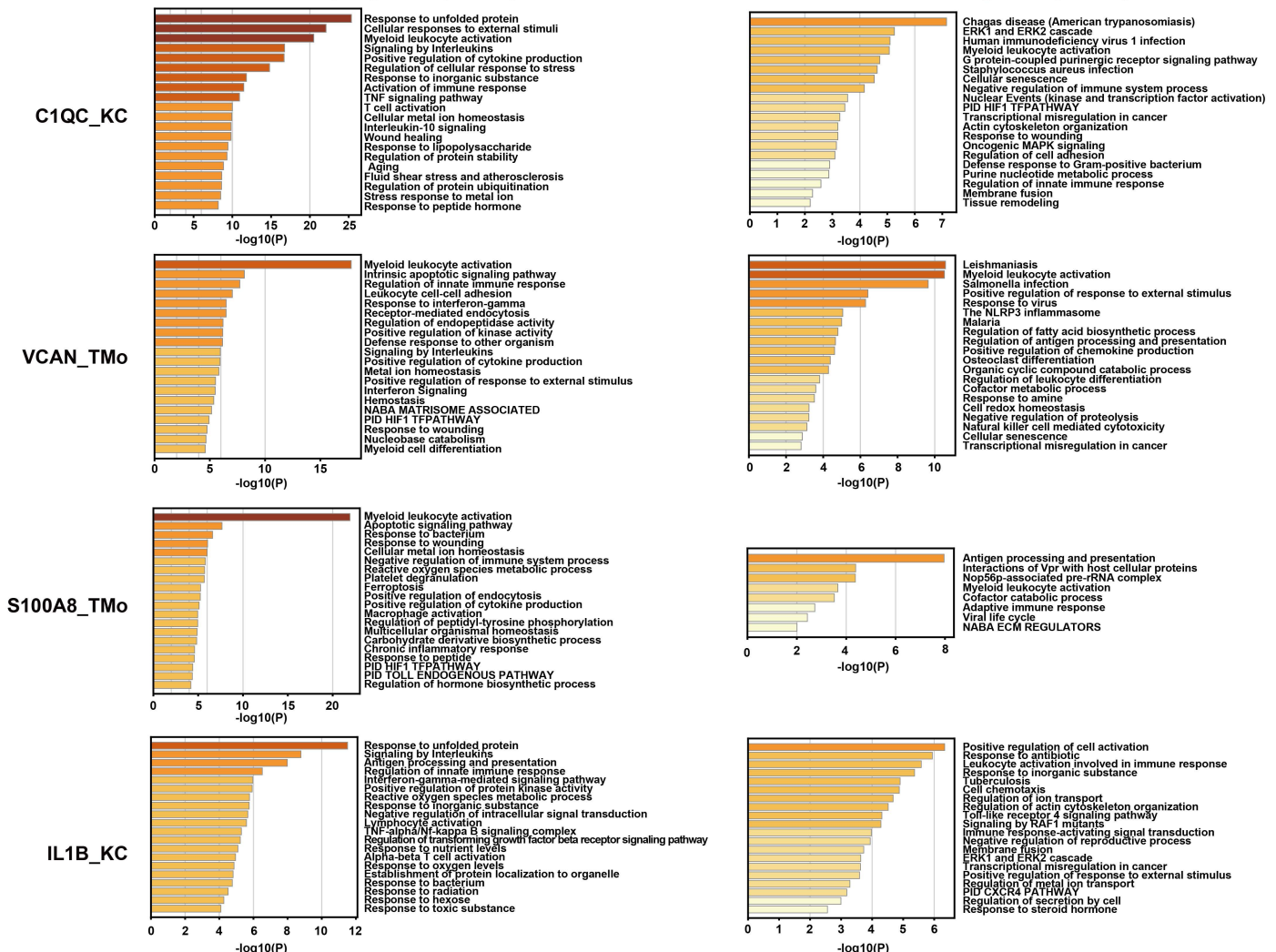
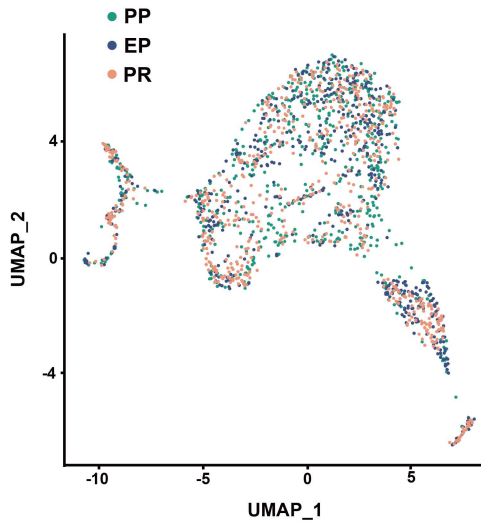
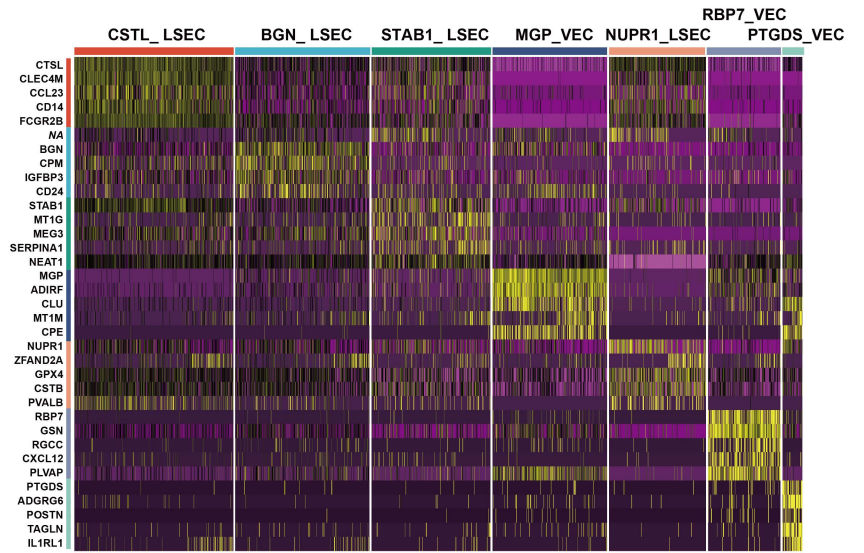


Figure S4

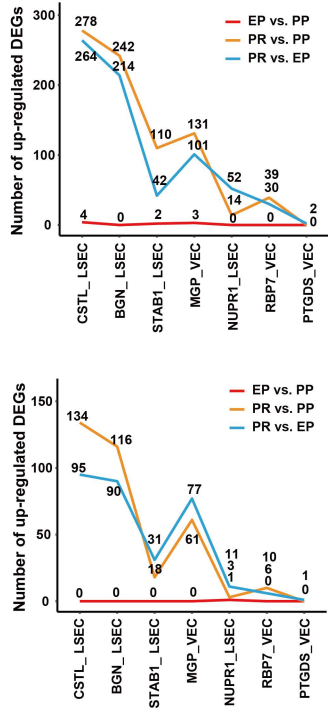
A



B



C



D

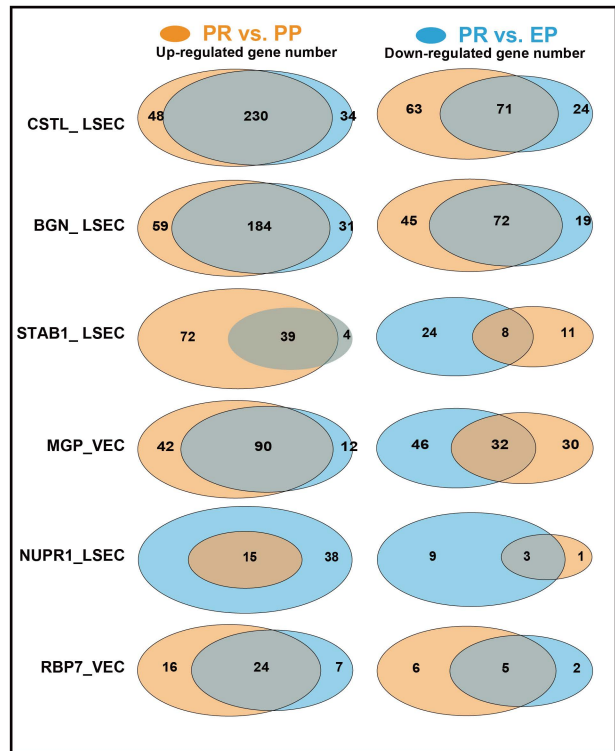
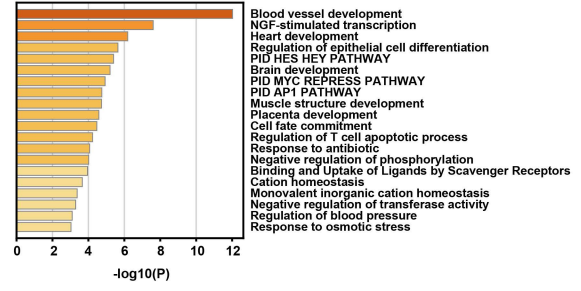
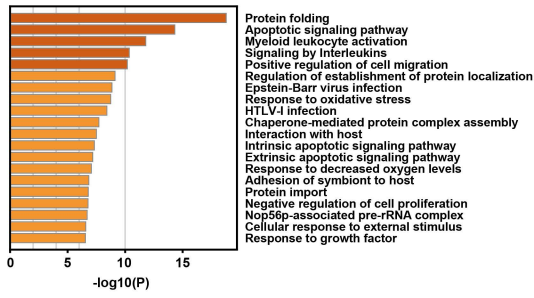


Figure S5

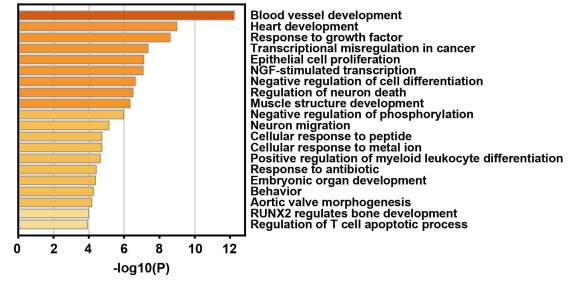
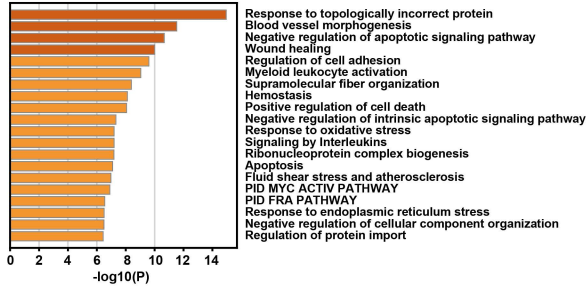
PR vs. EP up-regulated pathways

PR vs. EP down-regulated pathways

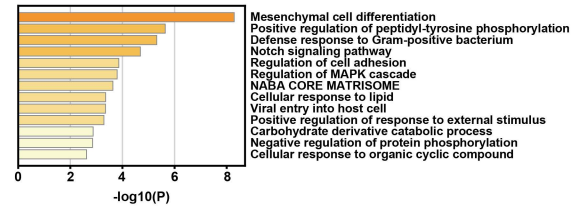
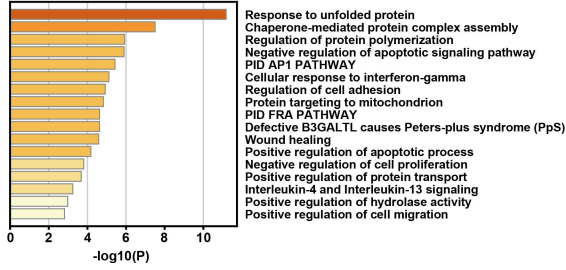
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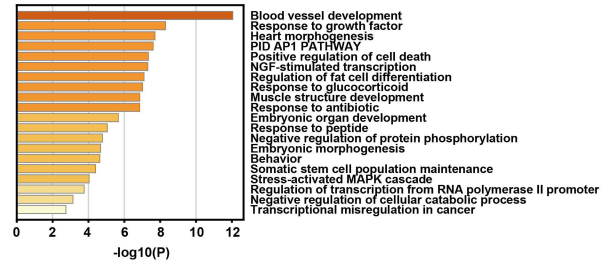
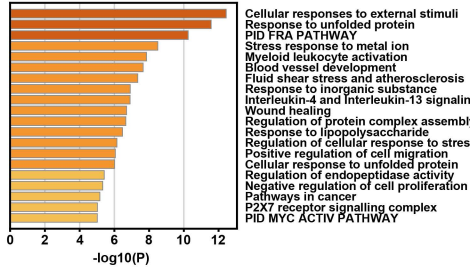
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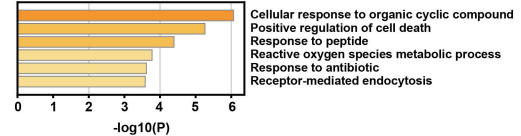
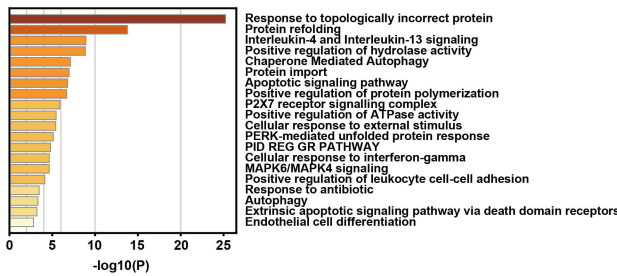
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MGP_VEC



NUPR1_LSEC



RBP7_VEC

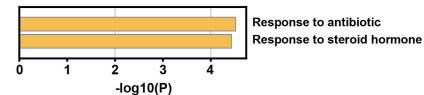
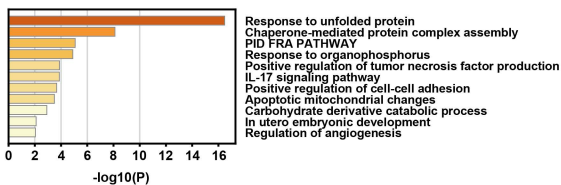
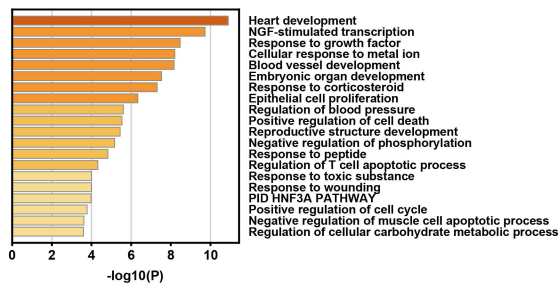
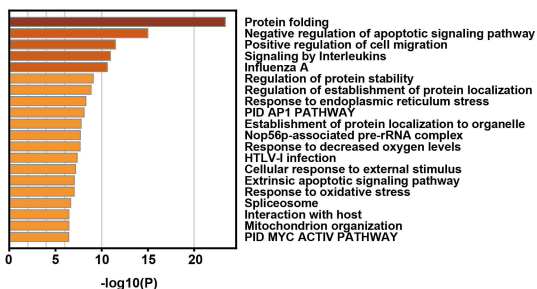


Figure S6

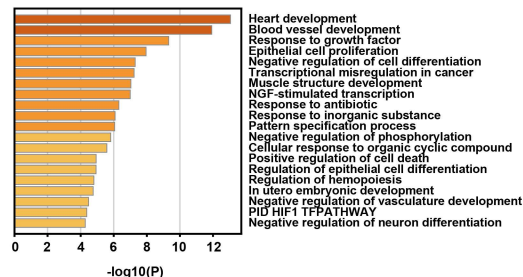
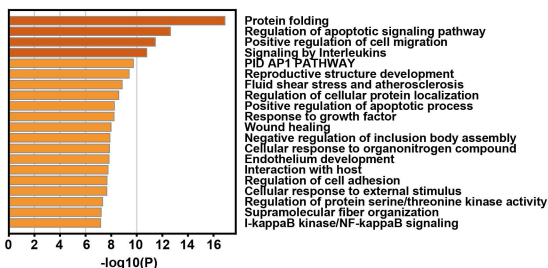
PR vs. PP up-regulated pathways

PR vs. PP down-regulated pathways

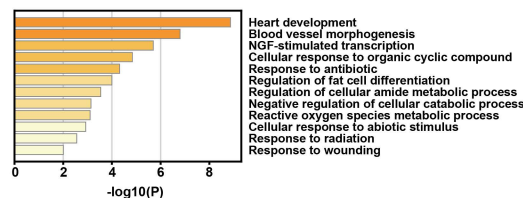
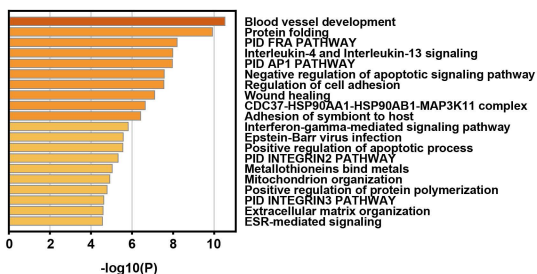
CSTL_LSEC



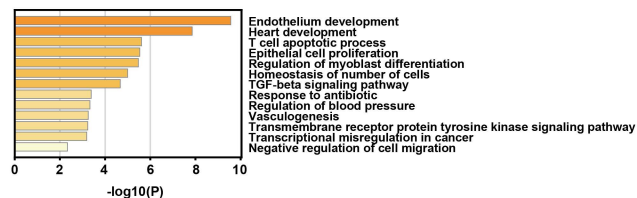
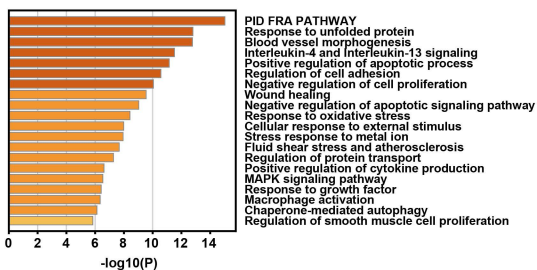
BGN_LSEC



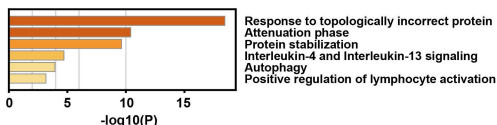
STAB1_LSEC



MGP_VEC



NUPR1_LSEC



RBP7_VEC

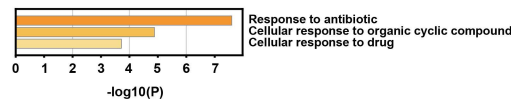
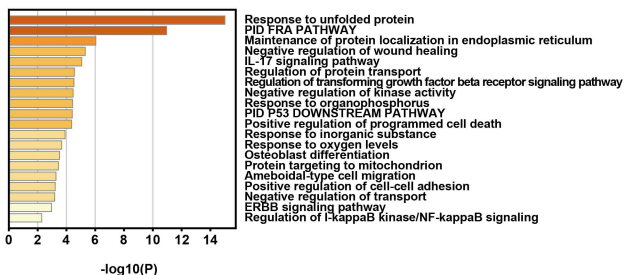
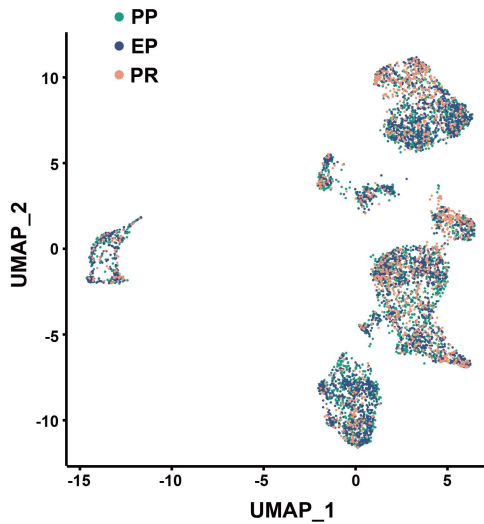
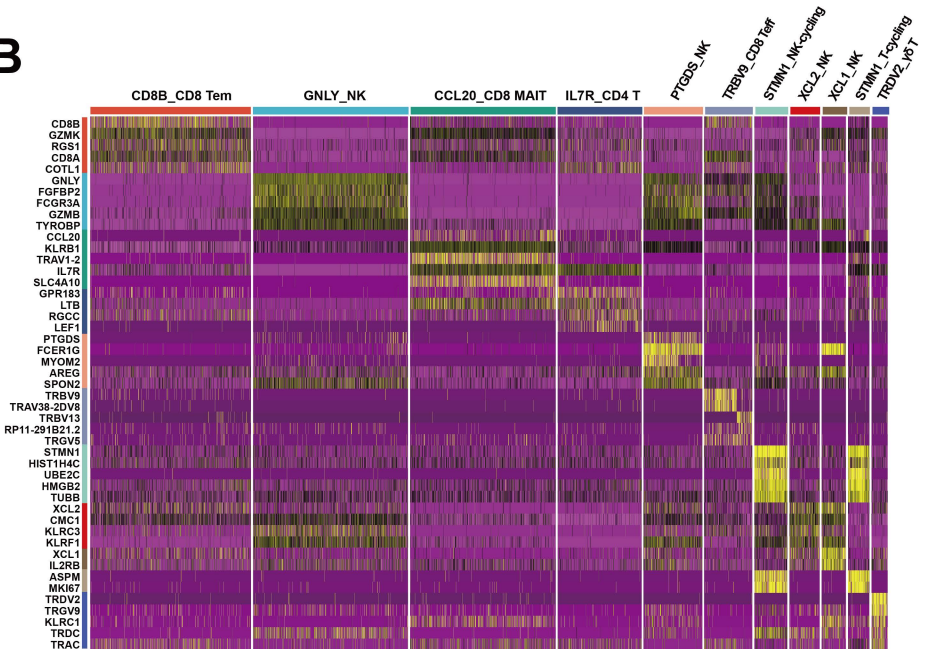


Figure S7

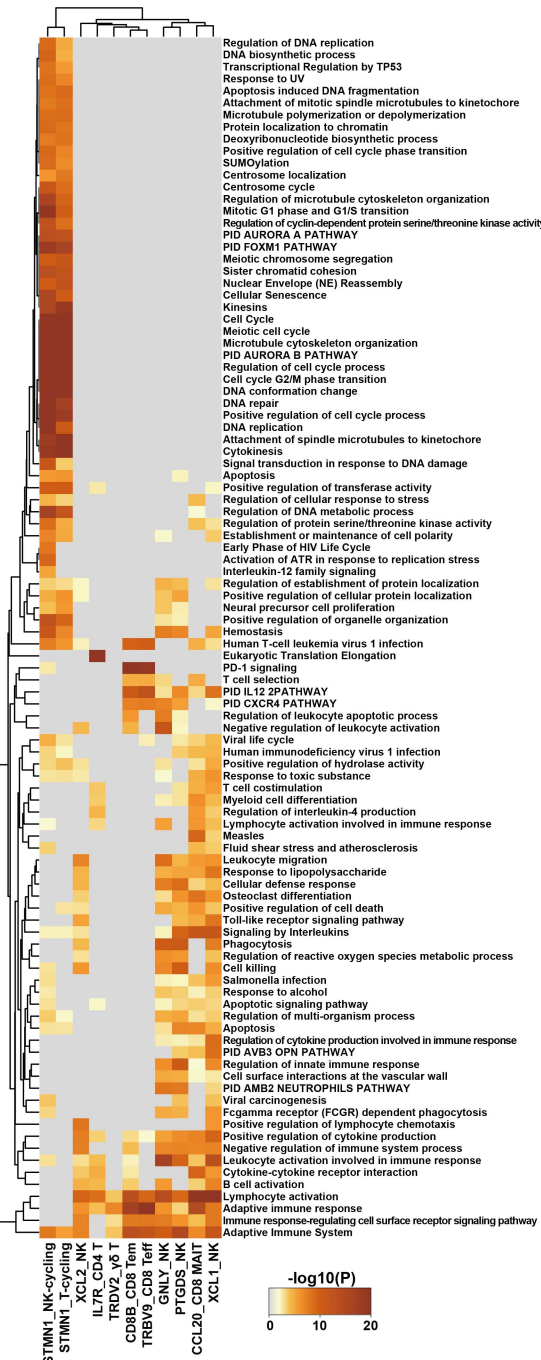
A



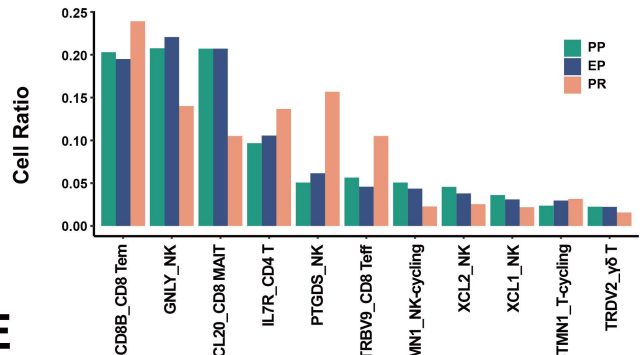
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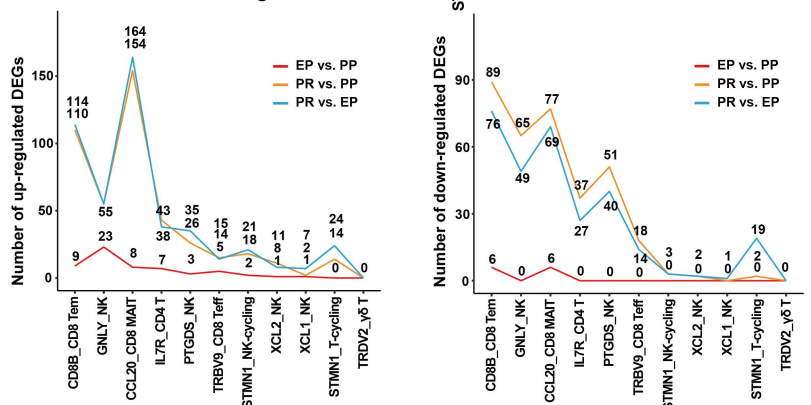
C



D



E



F

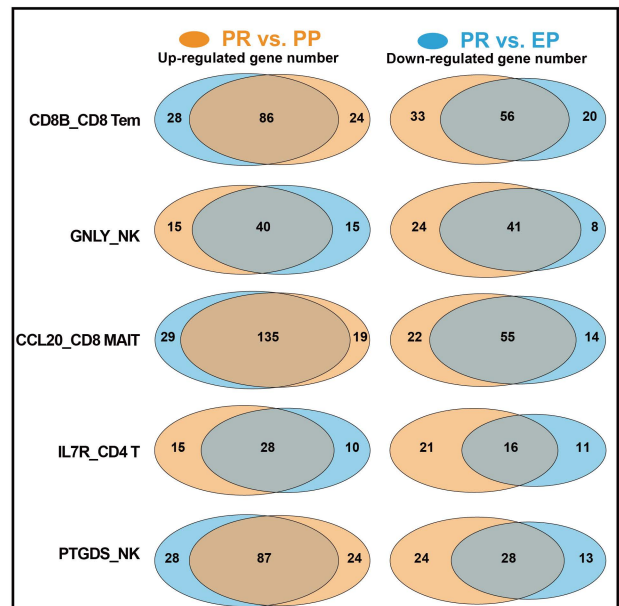
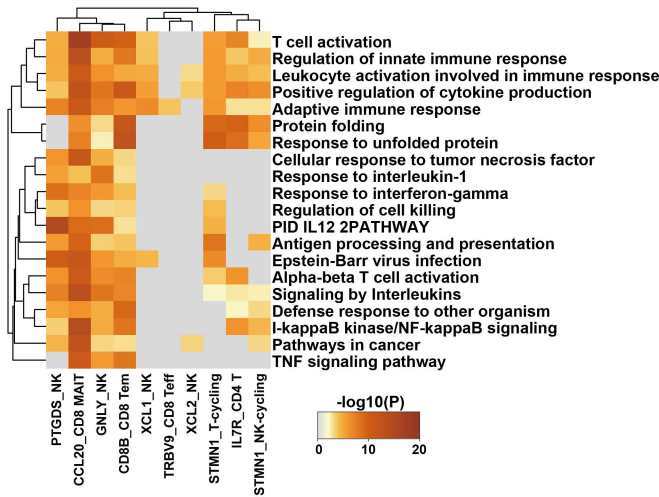


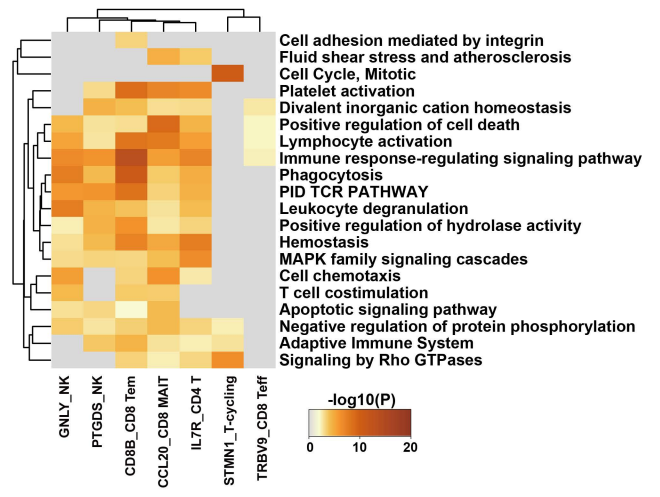
Figure S8

A

PR vs. EP up-regulated pathways

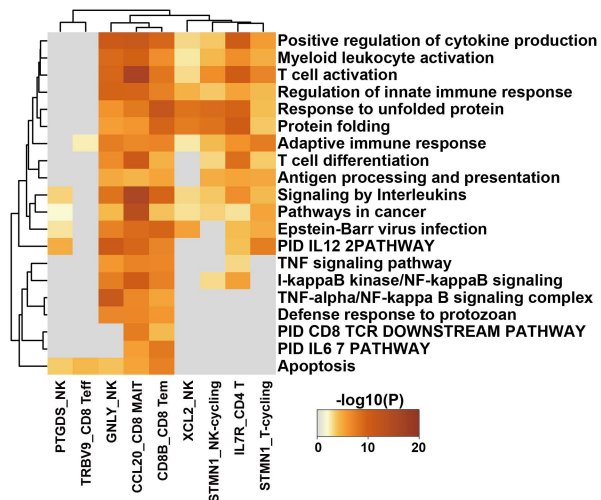


PR vs. EP down-regulated pathways



B

PR vs. PP up-regulated pathways



PR vs. PP down-regulated pathways

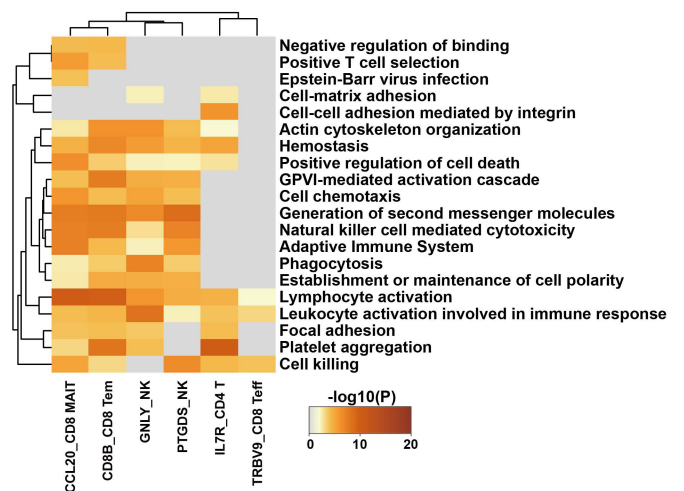


Figure S9

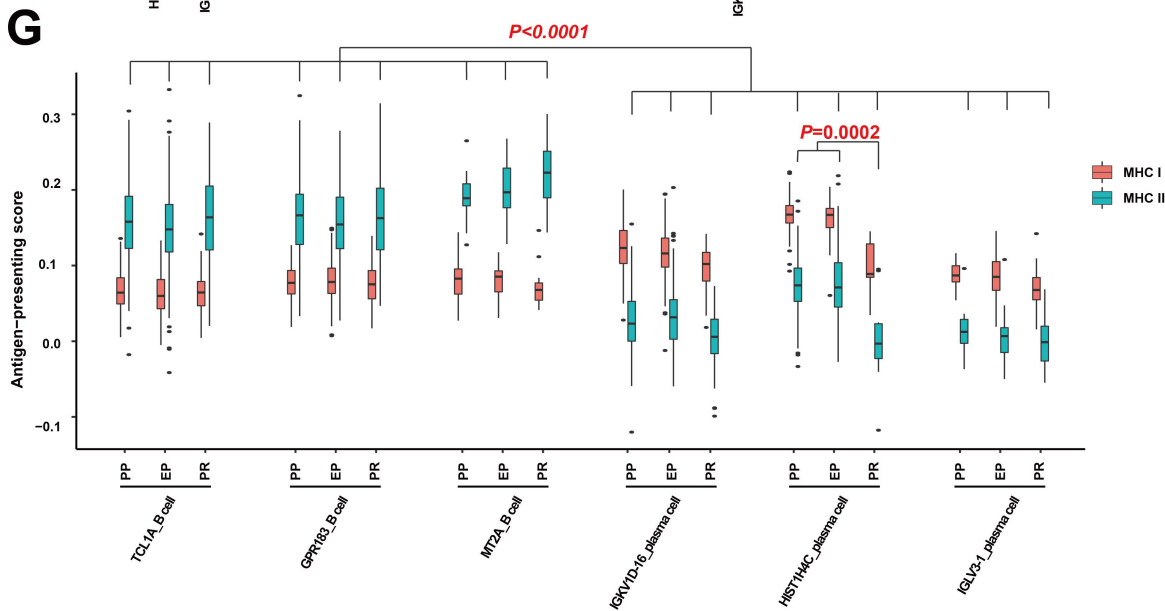
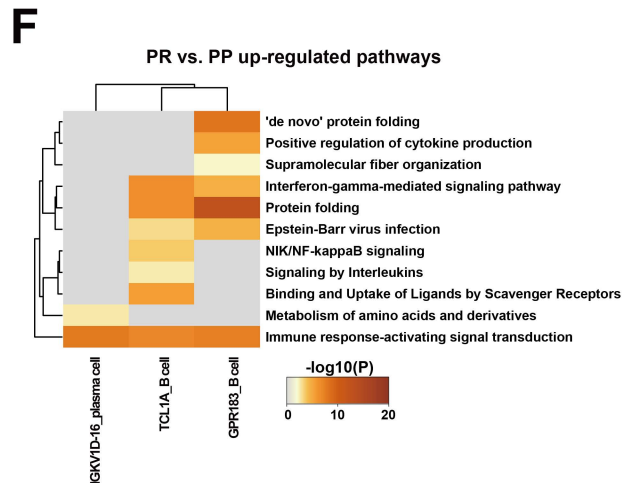
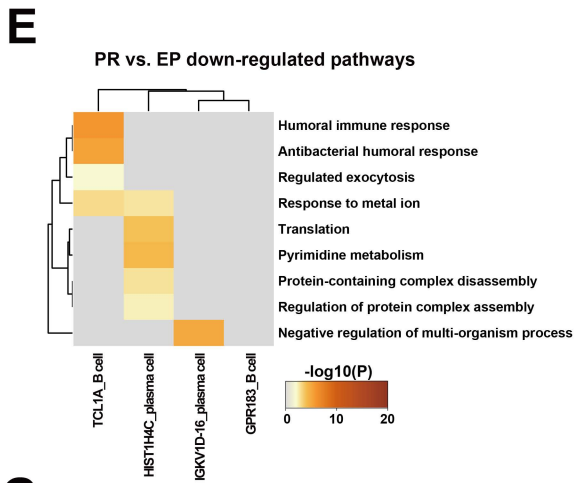
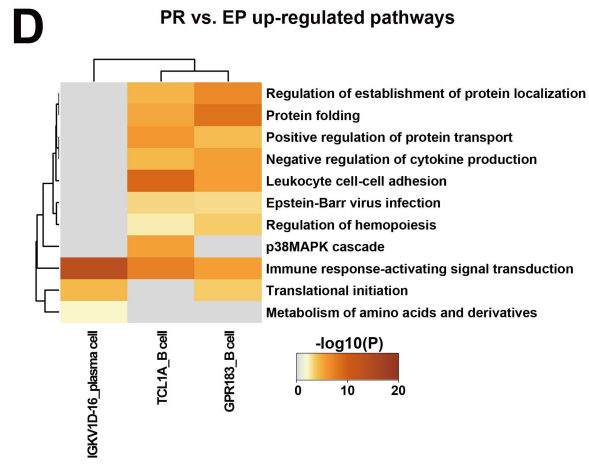
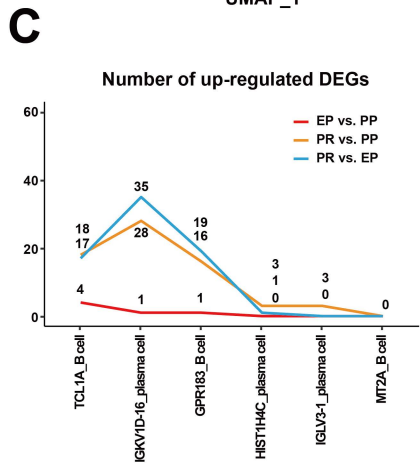
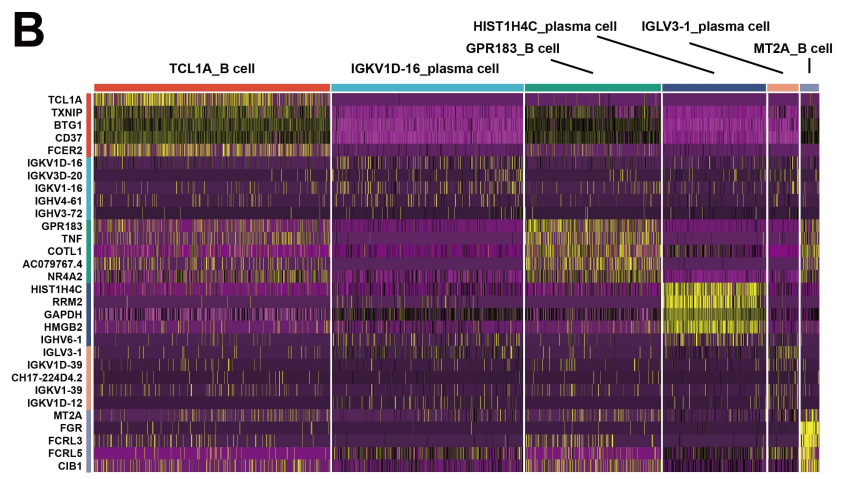
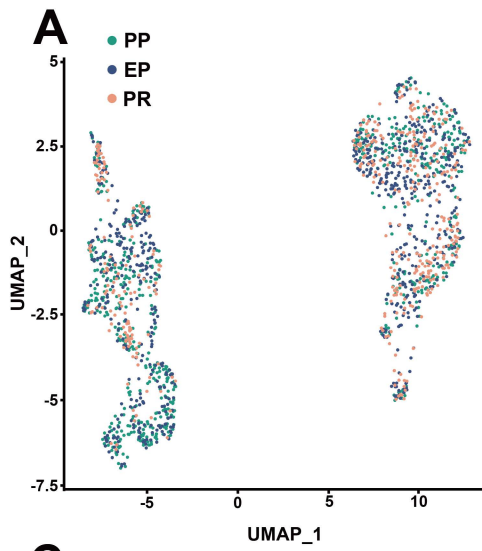


Figure S1:

A: “DoubletFinder” software identified 1160 doublet cells in PP, EP and PR. Red dots represent high expression level doublets, green dots represent low level doublets, and blue dots represent singlet.

B: Feature plots showing the normalized expression of marker genes in different cell lineage.

C: UMAP visualization of all cell clusters by PP, EP and PR samples.

D: Violin plots showing the normalized expression of *MARCO* and *CD68* genes (y axis) for mononuclear phagocyte clusters (x axis).

Figure S2:

A: UMAP visualization of mononuclear phagocyte clusters by PP, EP and PR samples.

B: Gene Ontology enrichment analysis results of mononuclear phagocyte clusters. The top 100 most significant GO terms (P -value < 0.05) are shown in rows.

C: Number of down-regulated DEGs between different samples in different mononuclear phagocyte clusters.

D: The Venn diagram shows the overlap gene number of DEGs in PR vs. PP (yellow) and DEGs in PR vs. EP (blue) of different mononuclear phagocyte clusters. The left column shows the number of up-regulated genes while the right column shows the number of down-regulated genes.

E: Antigen presentation ability of MHC class I genes (red) and MHC class II genes (green) in different mononuclear macrophage clusters. The antigen-presenting score (y axis) of MHC class II genes of KC clusters is higher than that of TMO clusters (x axis, $P < 0.0001$).

Figure S3:

A-B: Gene Ontology enrichment analysis results of up-regulated (left column) and down-regulated DEGs (right column) in different mononuclear phagocyte clusters

from PR vs. EP (**Figure S3A**) and PR vs. PP (**Figure S3B**). Only the top 20 most significant GO terms (P -value < 0.05) are shown in rows.

Figure S4:

A: UMAP visualization of endothelial cell clusters by PP, EP and PR samples.

B: Heatmap of top five differentially expressed genes between different endothelial cell clusters. The line is colored according to clusters in **Figure 4A**.

C: Number of up-regulated (left panel) and up-regulated (right panel) DEGs between different samples in different endothelial cell clusters.

D: The Venn diagram shows the overlap gene number of DEGs in PR vs. PP (yellow) and DEGs in PR vs. EP (blue) of different endothelial cell clusters. The left column shows the number of up-regulated genes while the right column shows the number of down-regulated genes.

Figure S5:

Gene Ontology enrichment analysis results of up-regulated (left column) and down-regulated DEGs (right column) in different endothelial cell clusters from PR vs. EP. Only the top 20 most significant GO terms (P -value < 0.05) are shown in rows.

Figure S6:

Gene Ontology enrichment analysis results of up-regulated (left column) and down-regulated DEGs (right column) in different endothelial cell clusters from PR vs. PP. Only the top 20 most significant GO terms (P -value < 0.05) are shown in rows.

Figure S7:

A: UMAP visualization of NK/T cell clusters by PP, EP and PR samples.

B: Heatmap of top five differentially expressed genes between different NK/T cell clusters. The line is colored according to clusters in **Figure 5A**.

C: Gene Ontology enrichment analysis results of NK/T cell clusters. Only the top 100 most significant GO terms (P -value < 0.05) are shown in rows.

D: Cell ratio of different NK/T cell clusters in PP, EP and PR samples.

E: Number of up-regulated (left panel) and up-regulated (right panel) DEGs between different samples in different NK/T cell clusters.

F: The Venn diagram shows the overlap gene number of DEGs in PR vs. PP (yellow) and DEGs in PR vs. EP (blue) of different NK/T cell clusters. The left column shows the number of up-regulated genes while the right column shows the number of down-regulated genes.

Figure S8:

A-B: Gene Ontology enrichment analysis results of up-regulated (left panel) and down-regulated DEGs (right panel) in different NK/T clusters from PR vs. EP (**Figure S8A**) and PR vs. PP (**Figure S8B**). Only the top 20 most significant GO terms (P -value < 0.05) are shown in rows.

Figure S9:

A: UMAP visualization of B and plasma cell clusters by PP, EP and PR samples.

B: Heatmap of top five differentially expressed genes between different B and plasma cell clusters. The line is colored according to clusters in **Figure 6A**.

C: Number of up-regulated DEGs between different samples in different B and plasma cell clusters.

D-E: Gene Ontology enrichment analysis results of up-regulated pathways (**Figure S9D**) and down-regulated (**Figure S9E**) in different B and plasma cell clusters from PR vs. EP.

F: Gene Ontology enrichment analysis results of up-regulated pathways in different B and plasma cell clusters from PR vs. PP.

G: Antigen presentation ability of MHC class I genes (red) and MHC class II genes (green) in different B and plasma cell clusters. The antigen-presenting score (y axis)

of MHC class II genes of B cell clusters is higher than that of plasma cell clusters (x axis, $P < 0.0001$), and decrease after reperfusion in HIST1H4C_plasma ($P = 0.0002$).