

Supplementary Information

Supplementary figures

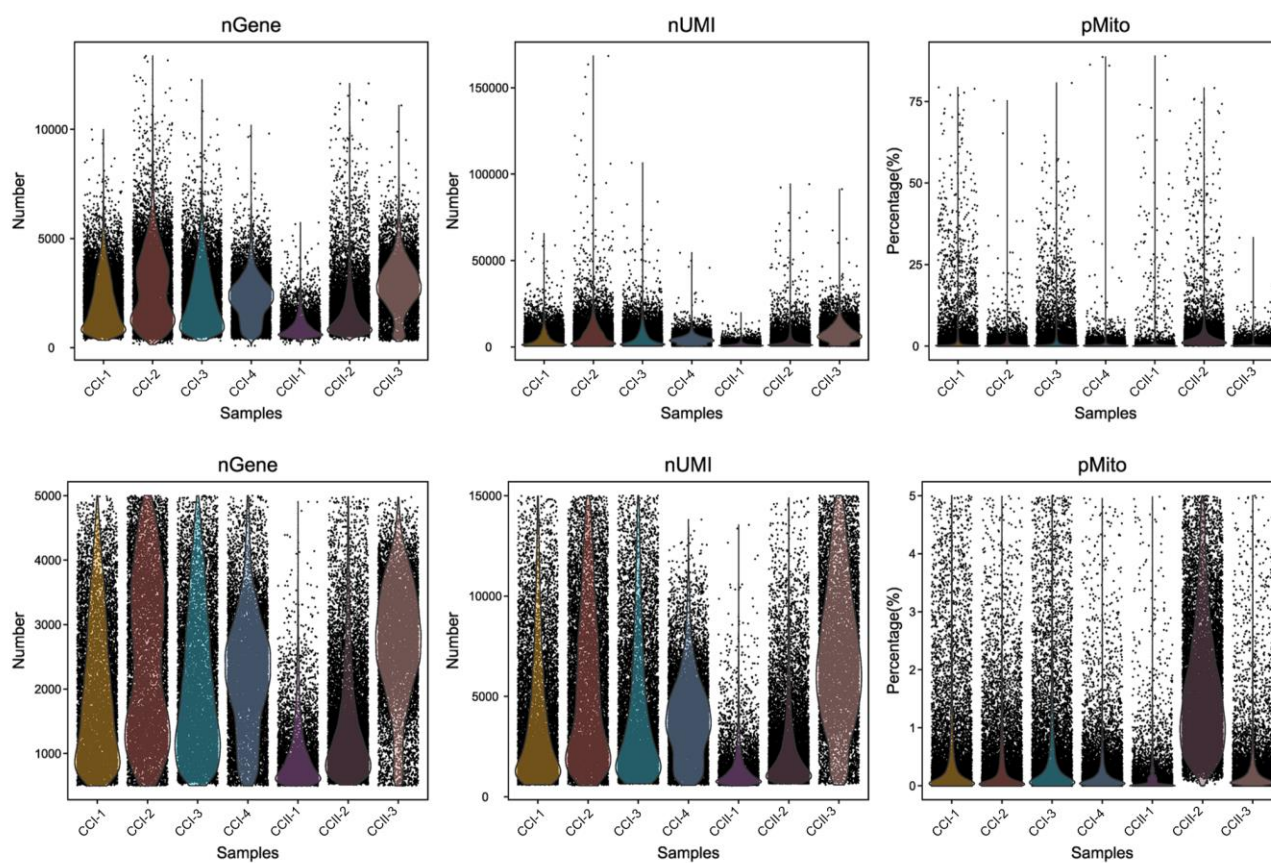


Figure S1 Quality metrics including the number of unique molecular identifiers (UMI), genes detected per cell, and reads aligned to the human genome.

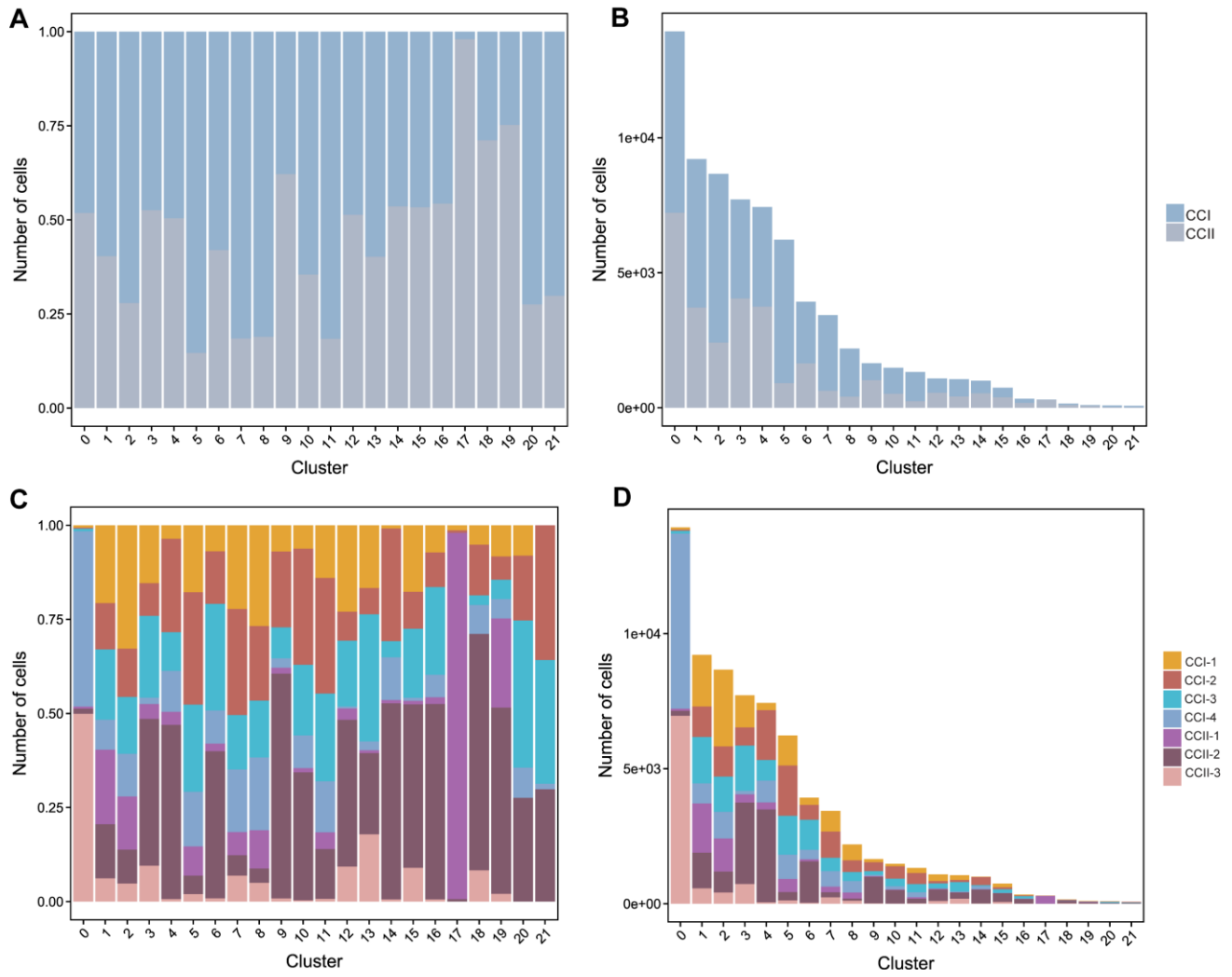


Figure S2 The populations of different cell types detected in the CCI and CCII groups in percentage (A) and the number of cells (B). The individual patient's contribution to each cell type in percentage (C) and the number of cells (D).

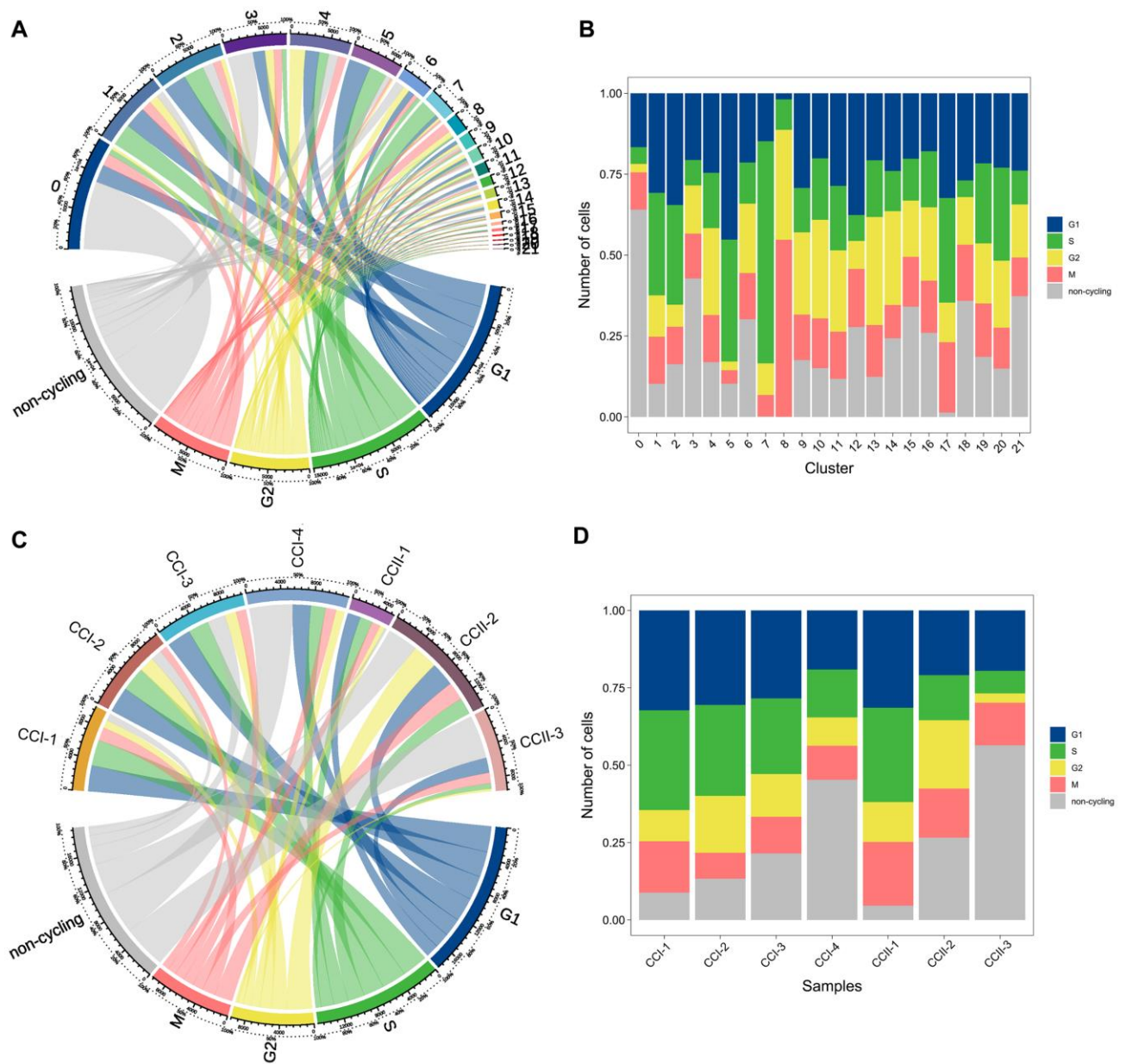


Figure S3 Cell cycle analysis of different cell types and individual patients. **(A)** The correlation between 21 cell types and cell cycles; **(B)** The number of cells (in percentage) with different cell cycles in each cell type; **(C)** The correlation between the patients and cell cycles; **(D)** The number of cells (in percentage) with different cell cycles in each patient.

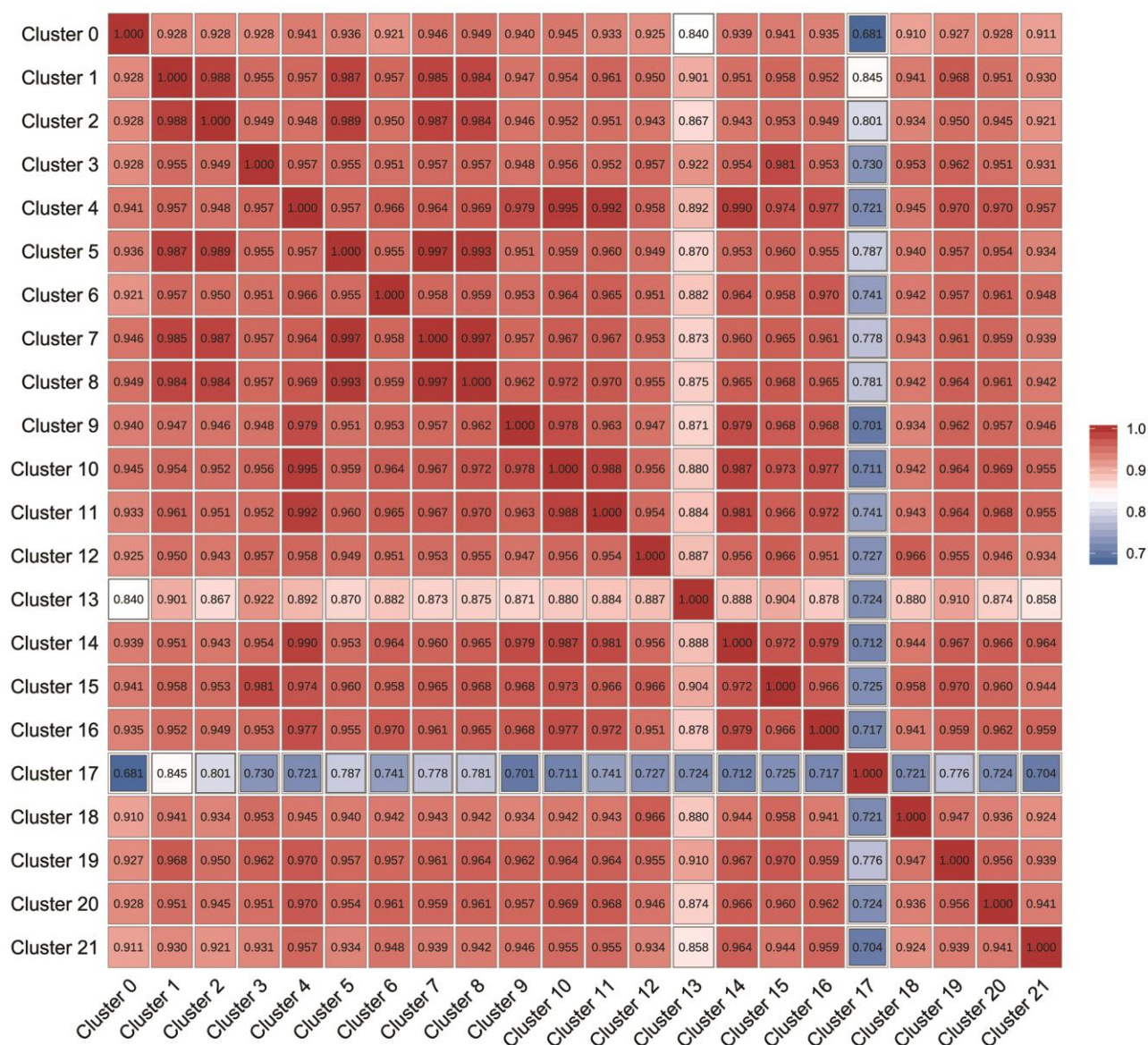


Figure S4 The correlation between different cell types predicted based on gene expression.

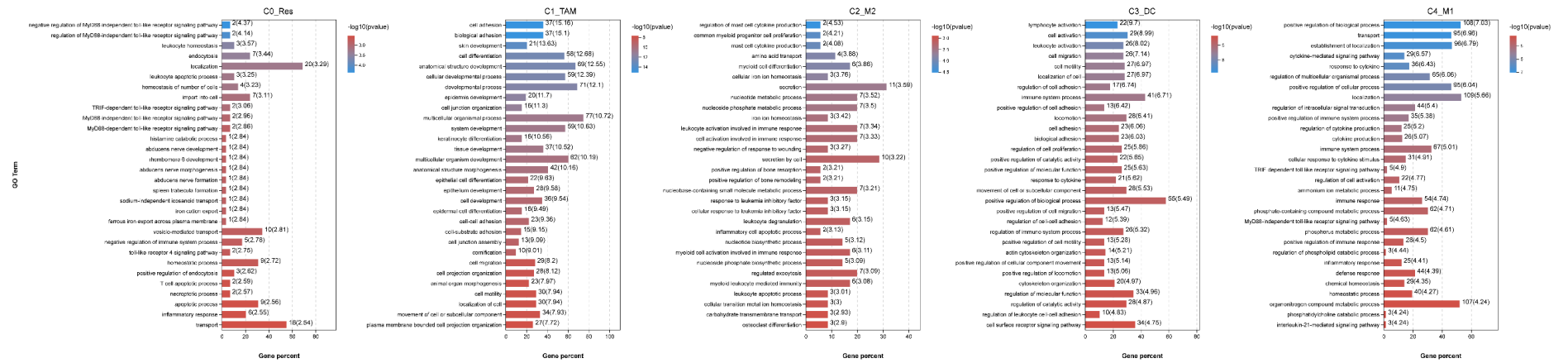


Figure S5 Enrichment analysis of biological processes in subtypes of macrophages.

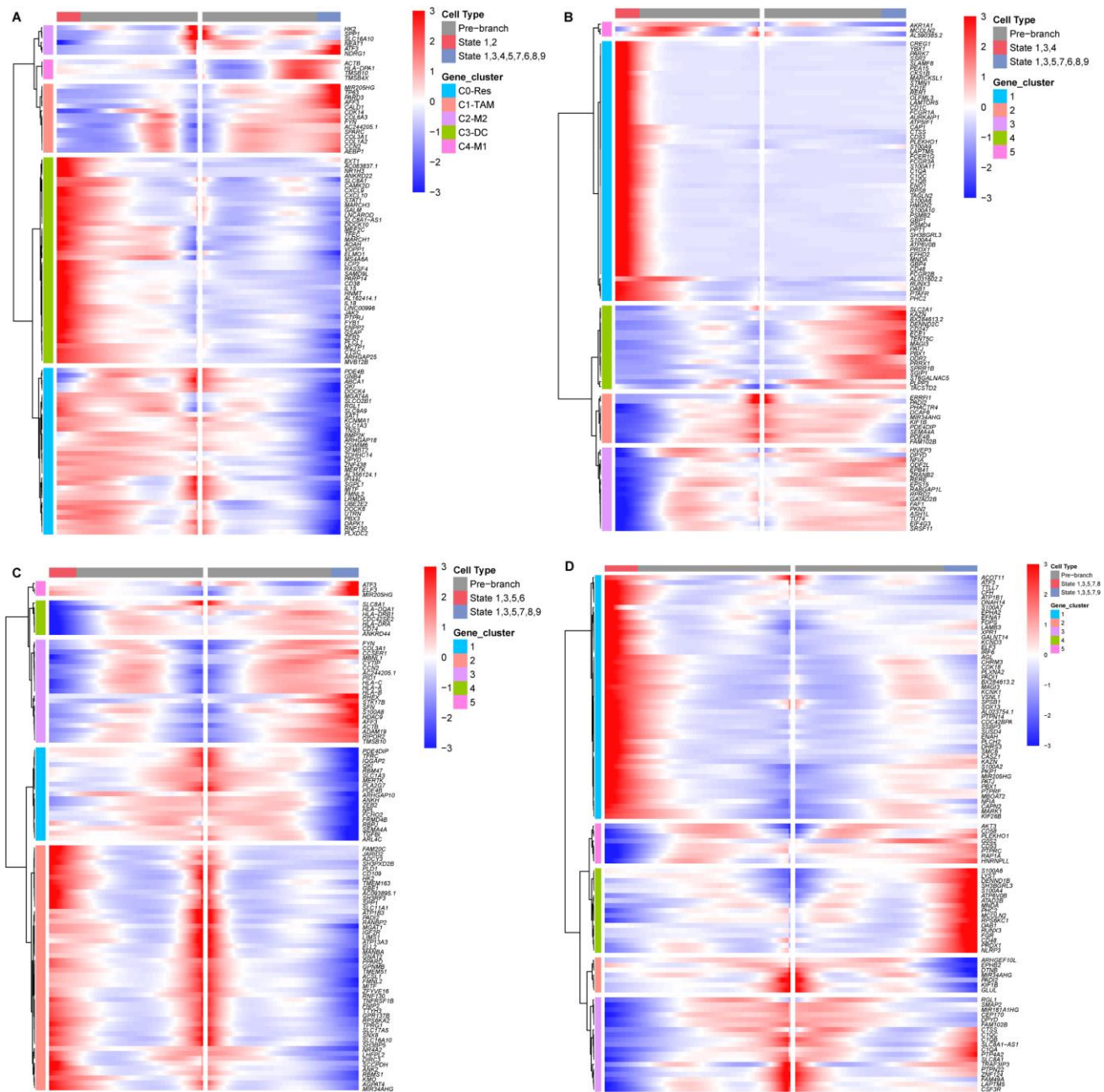


Figure S7 Hierarchy clustering of the gene set with similar expression trend in different branches of the trajectory of MΦ cells. The horizontal axis is the pseudo-time point (the pseudo-time point gradually increases from left to right), the vertical axis is the gene expression level, and different colours indicate the level of gene expression level.

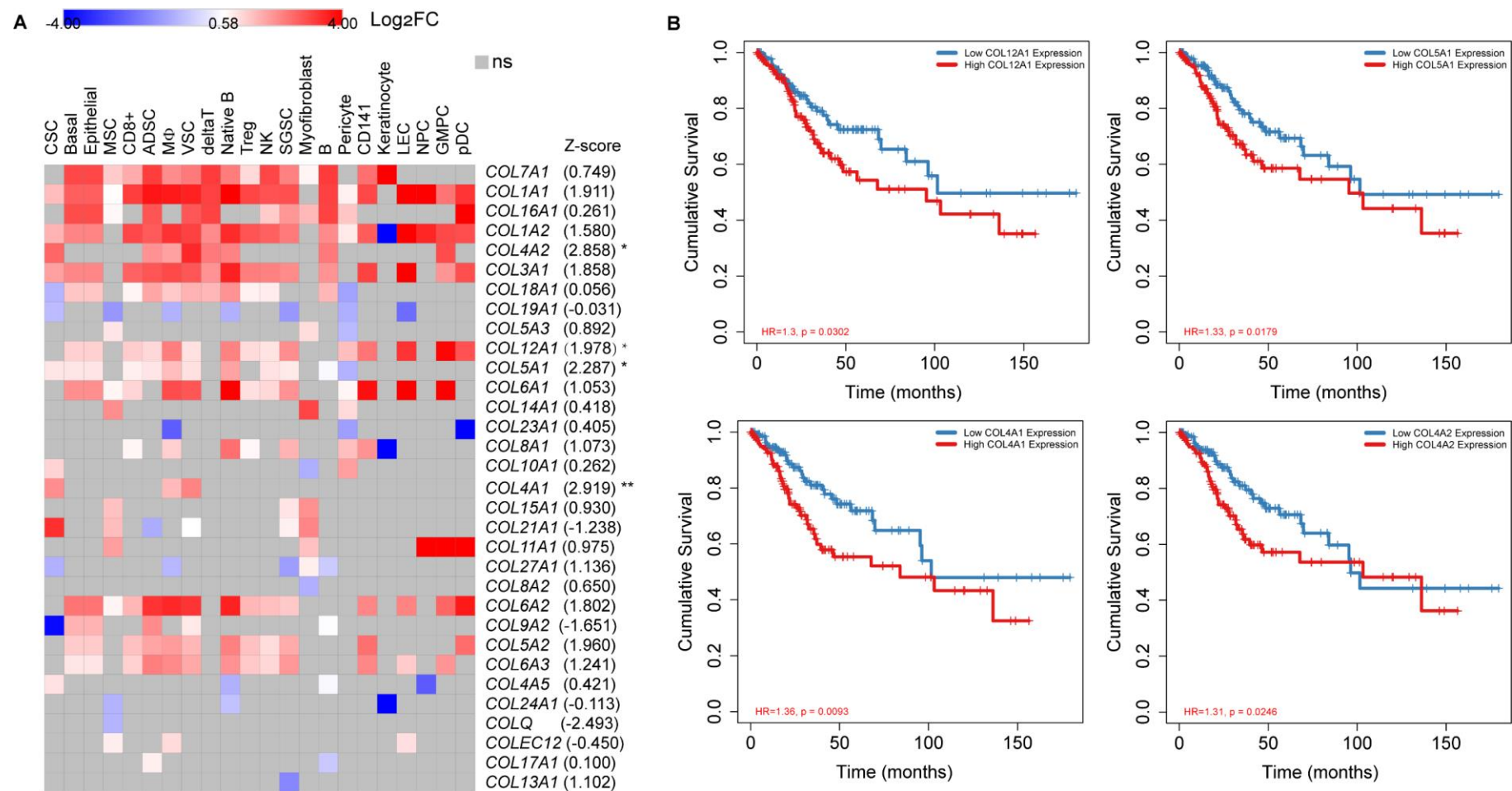


Figure S8 The high relevance of collagens to CC patients and their survival outcomes. **(A)** The heatmap shows the expression (in Log₂FC value) of collagens significantly regulated in the CCII with respect to the CCI group. Z-score shows the correlation between the expression and the risk of CC derived from TCGA. *, *P*-value < 0.05; **, *P*-value < 0.01. **(B)** Association of COL12A, COL5A1, COL4A1 and COL4A2. with survival outcomes in CC patients.

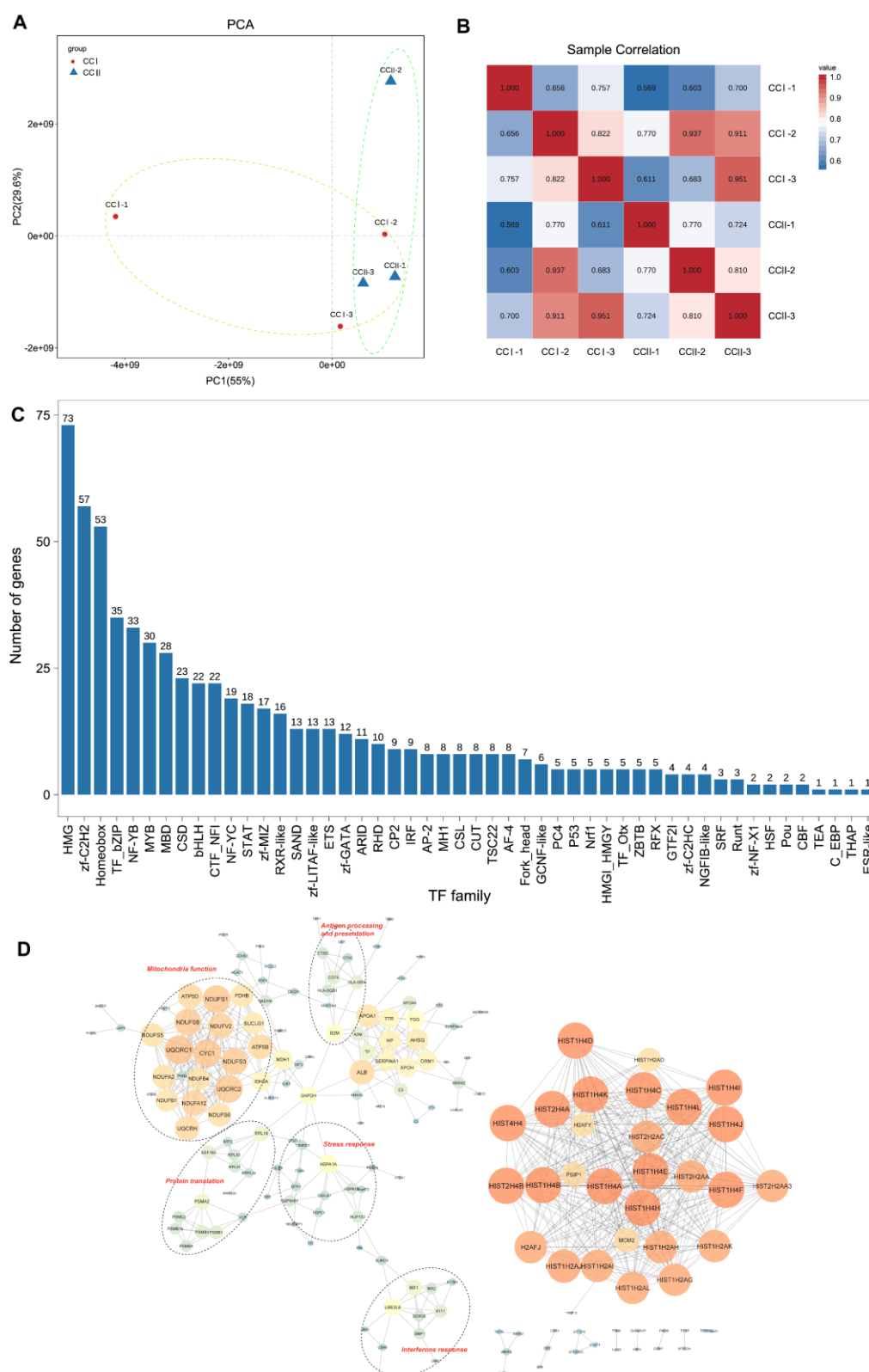


Figure S9 (A) PCA analysis of the samples for proteomic analysis; (B) Correlation between the protein profiles of CCI and CCII samples; (C) Enrichment analysis of transcription factors (TFs); (D) protein-protein interactions between proteins significantly upregulated in the CCI group.

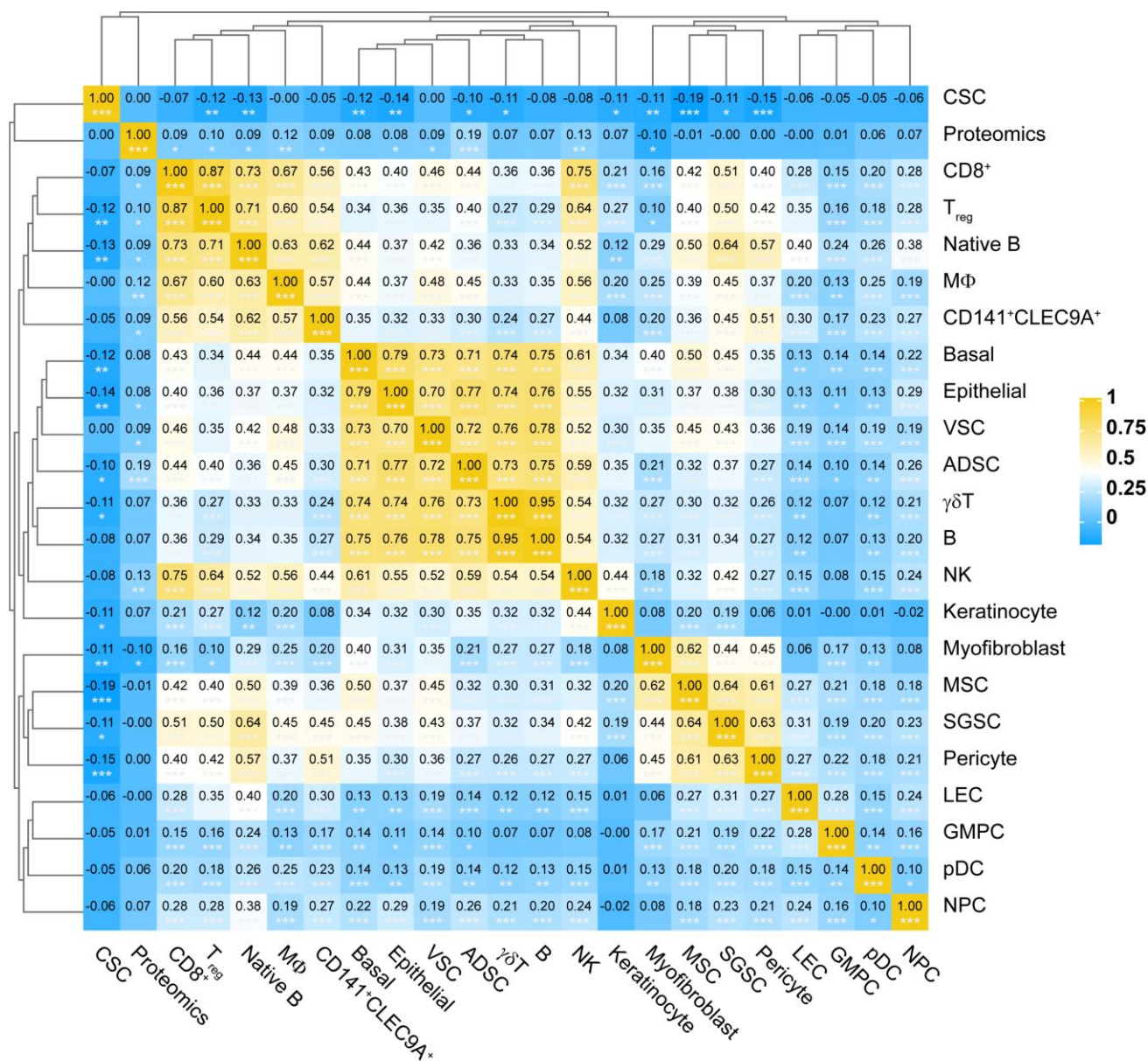


Figure S10 Correlation analysis between all cell types and overall protein profile.

Supplementary tables

Table S1 Patient information and the populations of different cell types

Table S2 The normalised expression of top 5 marker genes of each cell cluster; all significantly upregulated genes of each cell cluster; the gene expression of the marker genes in all clusters. The annotations of these genes are shown.

Table S3 Comparative analysis of MΦs in CCI and CCII groups.

Table S4 Comparative analysis of MΦ subtypes and states in CCI and CCII groups.

Table S5 Comparative analysis of NK cells in CCI and CCII groups.

Table S6 Quantitative proteomic analysis results, including all identified proteins and supporting peptides.

Table S7 Comparative analysis of GO terms, KEGG pathways and TFs enriched by the DEGs between CCI and CCII groups.