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Supplemental information

Dissecting the single-cell transcriptome underlying chronic liver injury

Junjun Wang, Wei Hu, Zhenyang Shen, Teng Liu, Weiming Dai, Bo Shen, Xiaoman Li, Jingni Wu, Lungen Lu, Shengli Li, and Xiaobo Cai

Supplemental Tables

Supplemental Table S1. Top 300 expressed genes in each cluster.

Supplemental Table S2. Top 30 biological functions enriched by top expressed genes in each cell cluster.

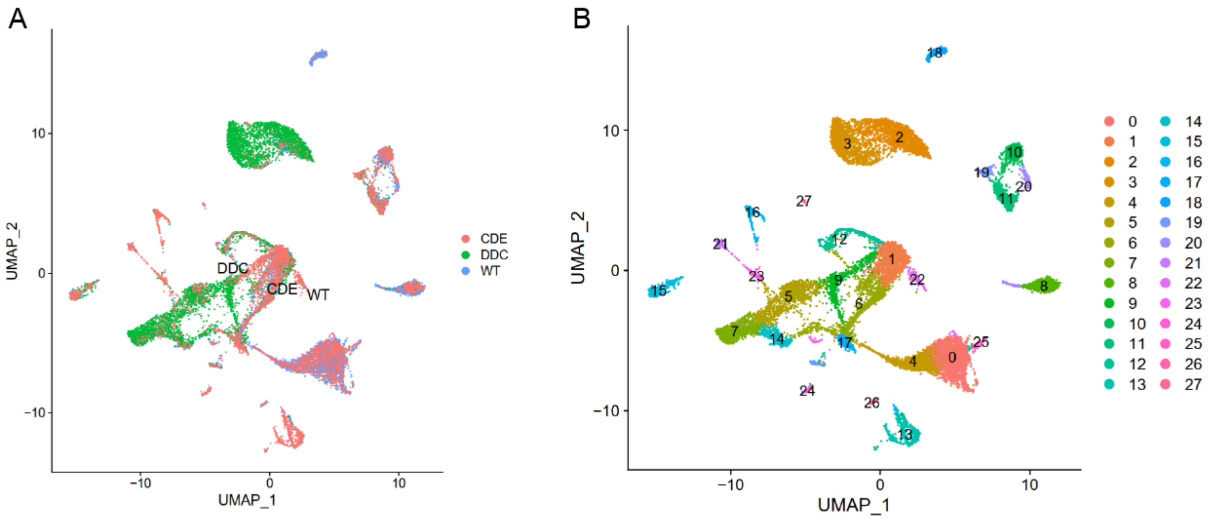
Supplemental Table S3. Gene markers used to annotate different cell types in this study.

Supplemental Table S4. Differential expressed genes of macrophages between CDE and normal samples.

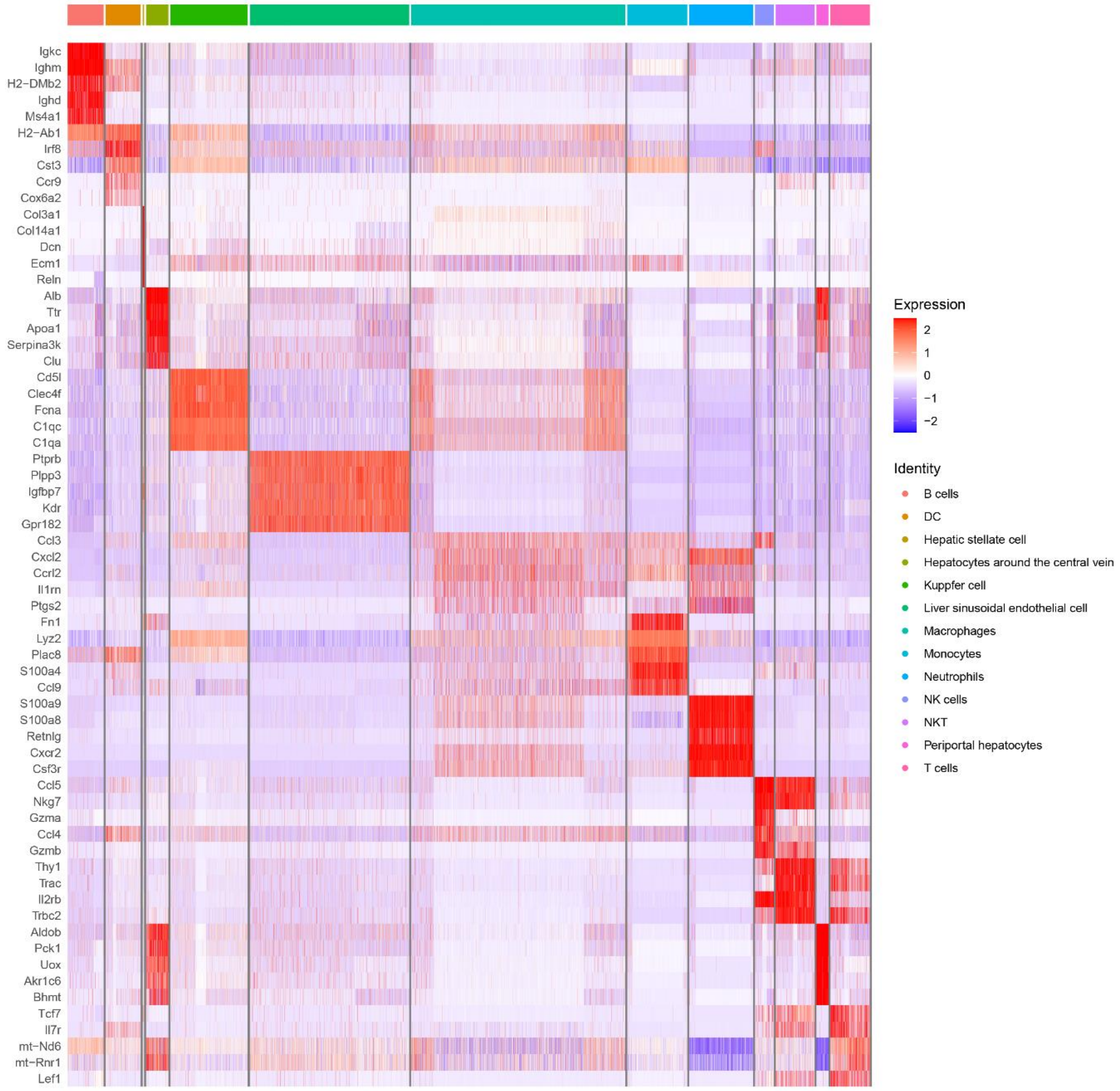
Supplemental Table S5. Differential expressed genes of macrophages between DDC and normal samples.

Supplemental Table S6. Differential expressed genes of macrophages between different pseudo-time states.

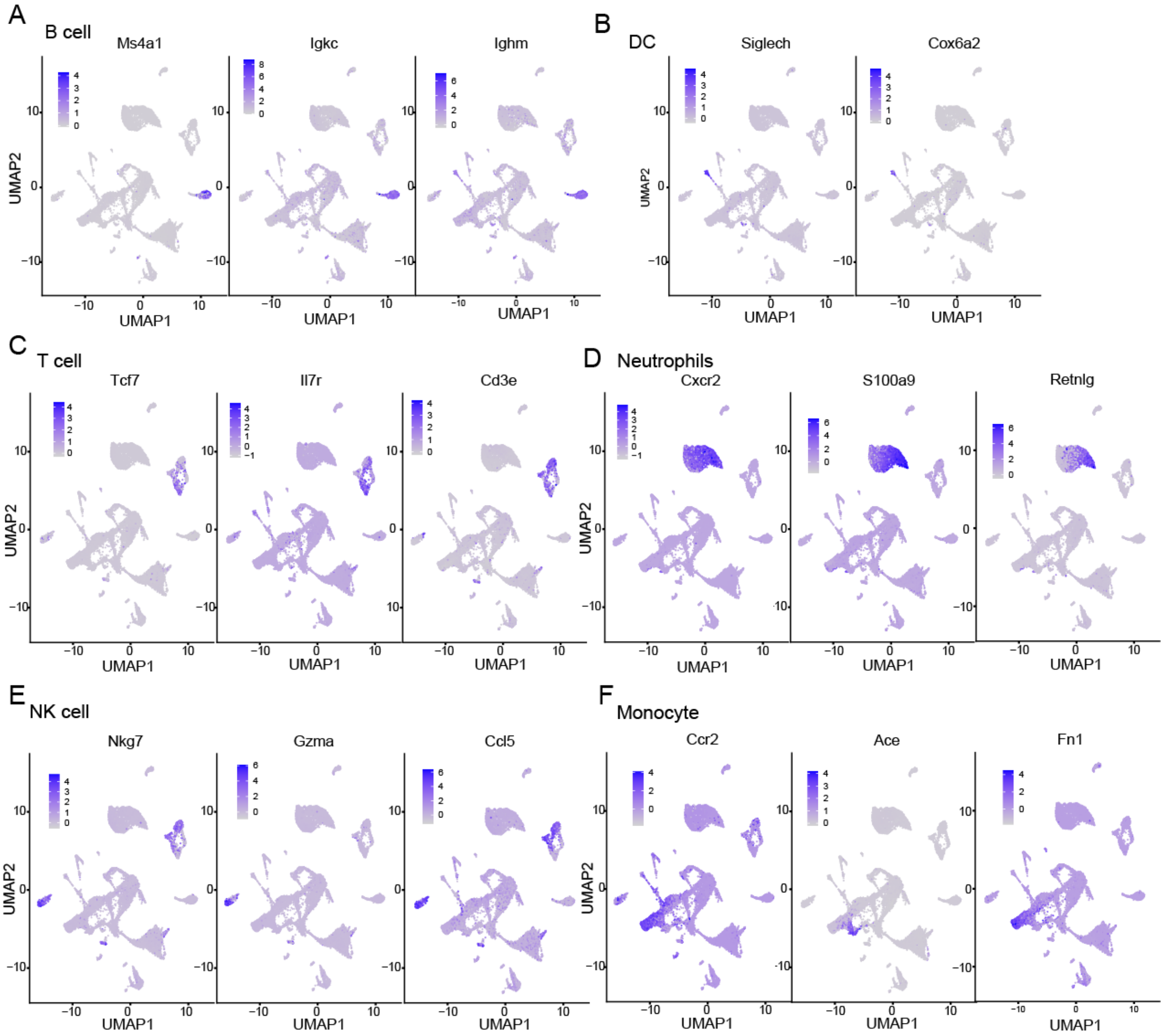
Supplemental Figures



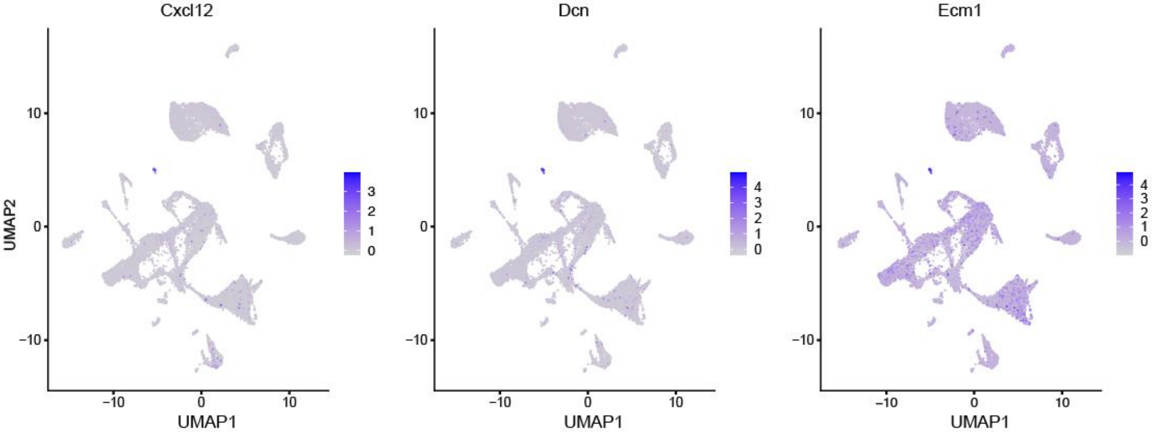
Supplemental Figure S1. The UMAP dimensionality reduction and clustering of all cells. (**A**) UMAP visualization of all cells in WT, CDE, and DDC samples. (**B**) Clustering results of all cells.



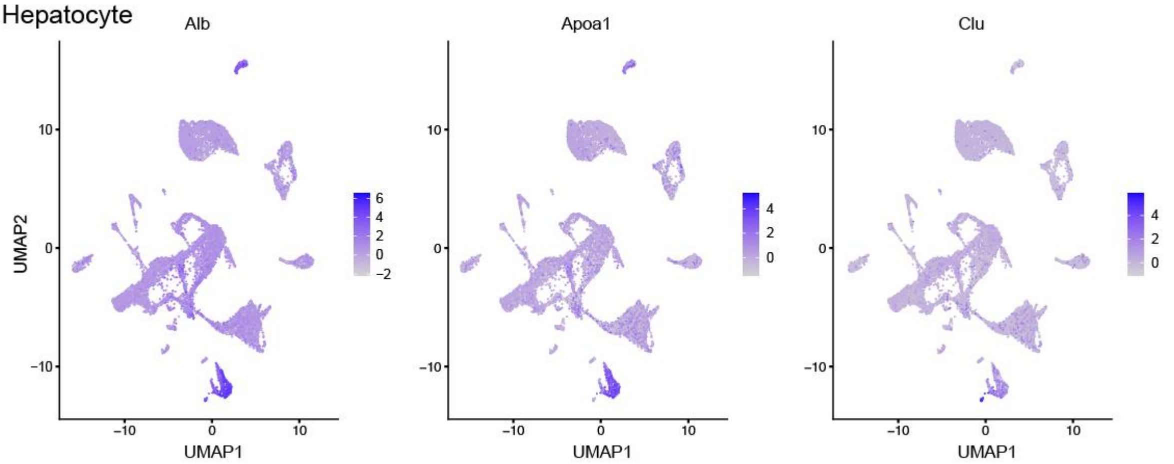
Supplemental Figure S2. Heatmap shows the top differentially expressed genes in each cluster.



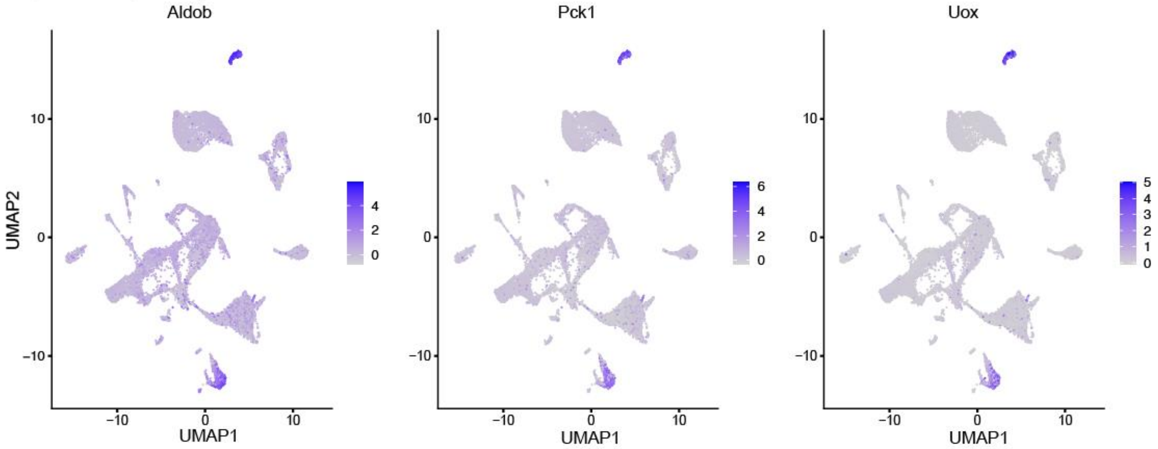
Supplemental Figure S3. UMAP visualization highlights gene markers in specific immune cell types. (**A**) Expression highlights of Ms4a1, Igkc, and Ighm in B cells. (**B**) Expression highlights of Siglech and Cox6a2 in DC. (**C**) Expression highlights of Tcf7, Il7r, and Cd3e in T cells. (**D**) Expression highlights of Cxcr2, S100a9, and Retnlg in neutrophils. (**E**) Expression highlights of Nkg7, Gzma, and Ccl5 in NK cells. (**F**) Expression highlights of Ccr2, Ace, and Fn1 in monocytes.



A Hepatic stellate cell

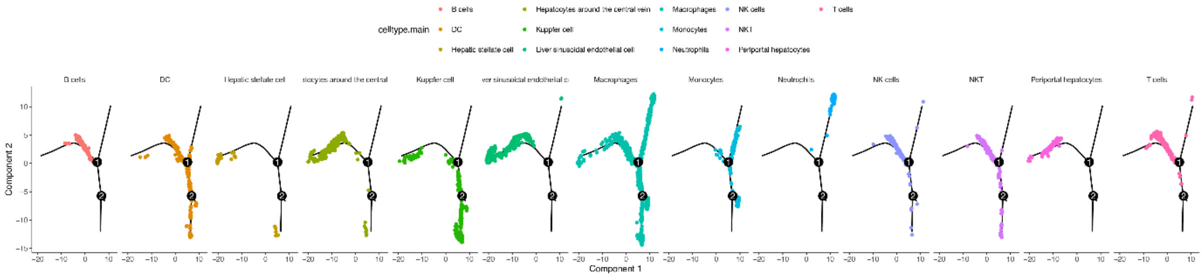


B Hepatocyte



C Periportal hepatocyte

Supplemental Figure S4. UMAP visualization highlights gene markers in specific hepatic cell types. (**A**) Expression highlights of Cxcl12, Dcn, and Ecm1 in hepatic stellate cells. (**B**) Expression highlights of Alb, Apoa1, and Clu in hepatocytes. (**C**) Expression highlights of Aldob, Pck1, and Uox in periportal hepatocytes.



Supplemental Figure S5. Pseudo-time trajectories in separated cell types.