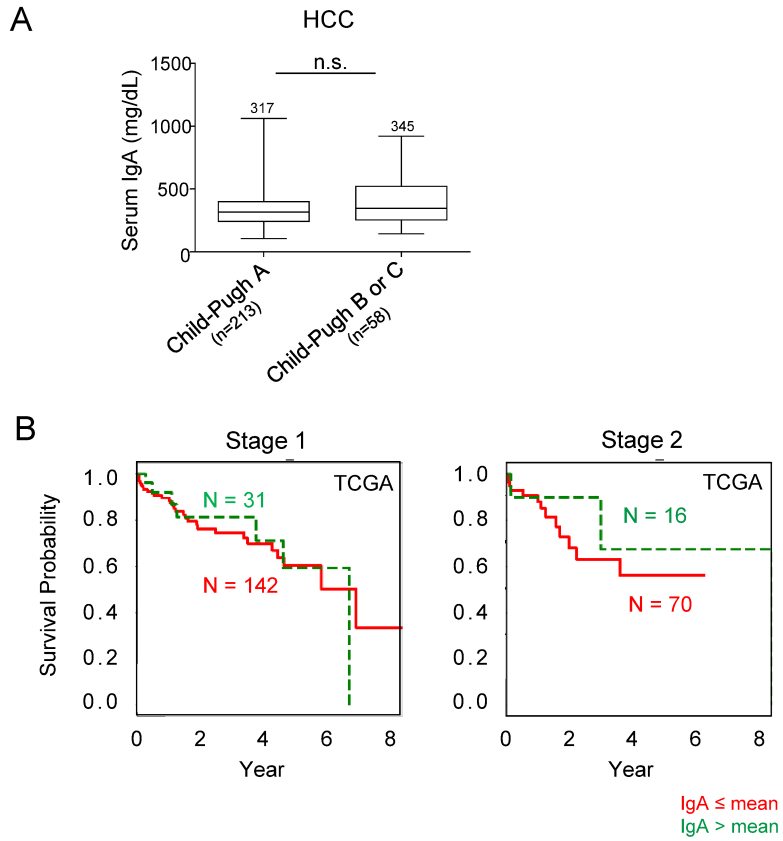
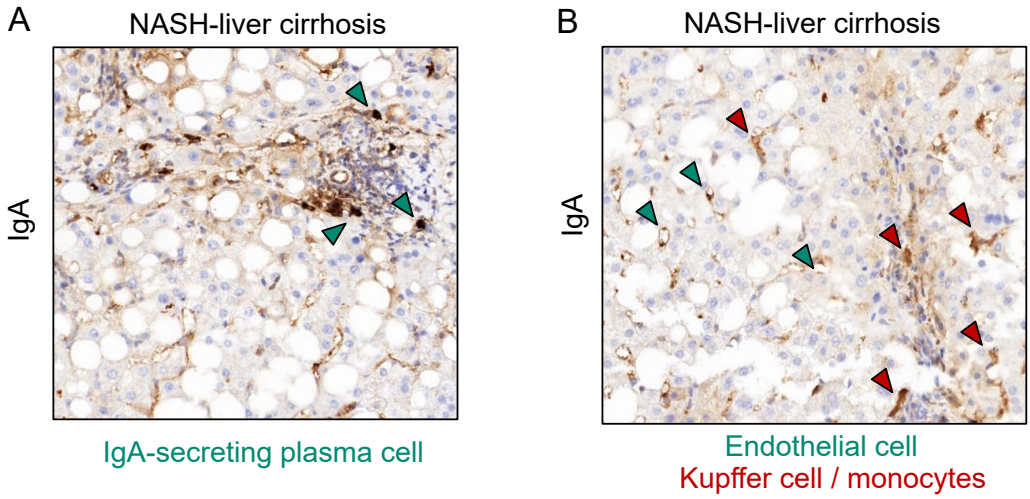
Supplementary Figure 1



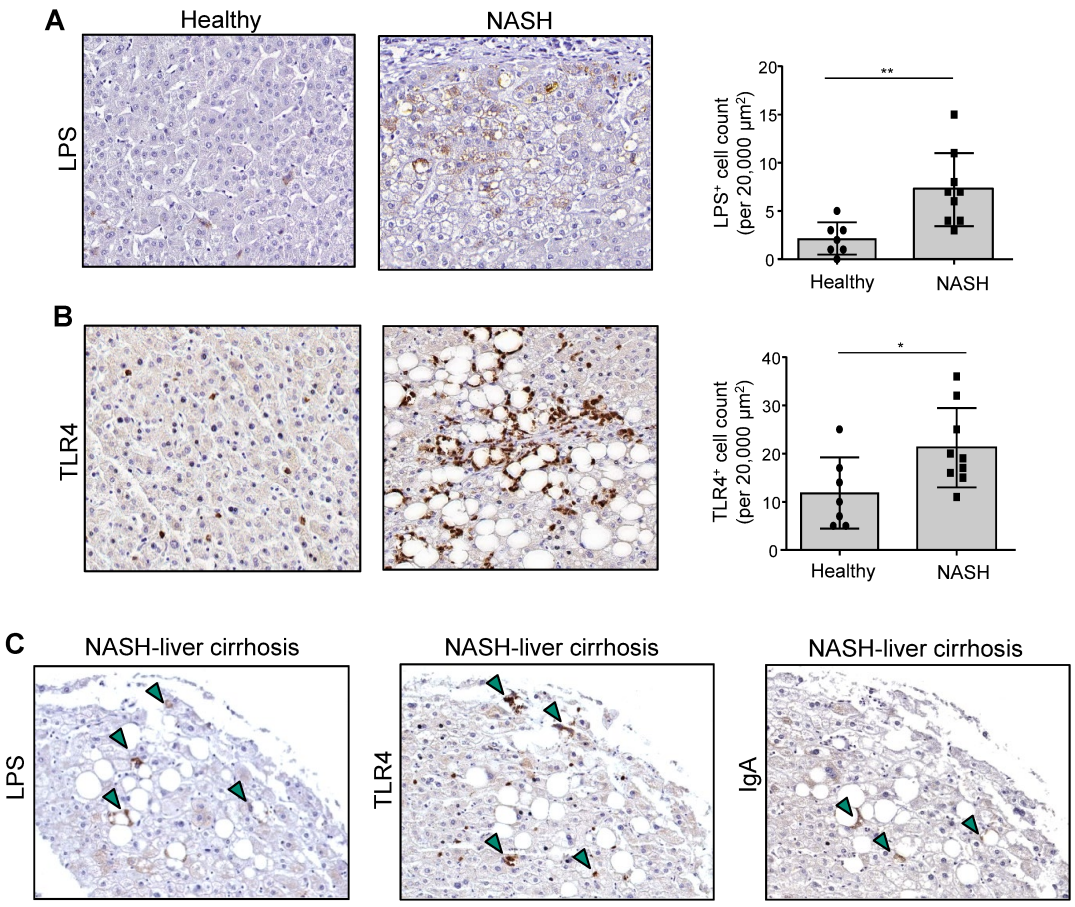
(A) Serum IgA level in HCC patients according to the Child-Pugh class.
(B) Survival analysis according to intrahepatic IgA transcript level in patients with HCC stage 1 and 2 (from TCGA dataset).

Supplementary Figure 2



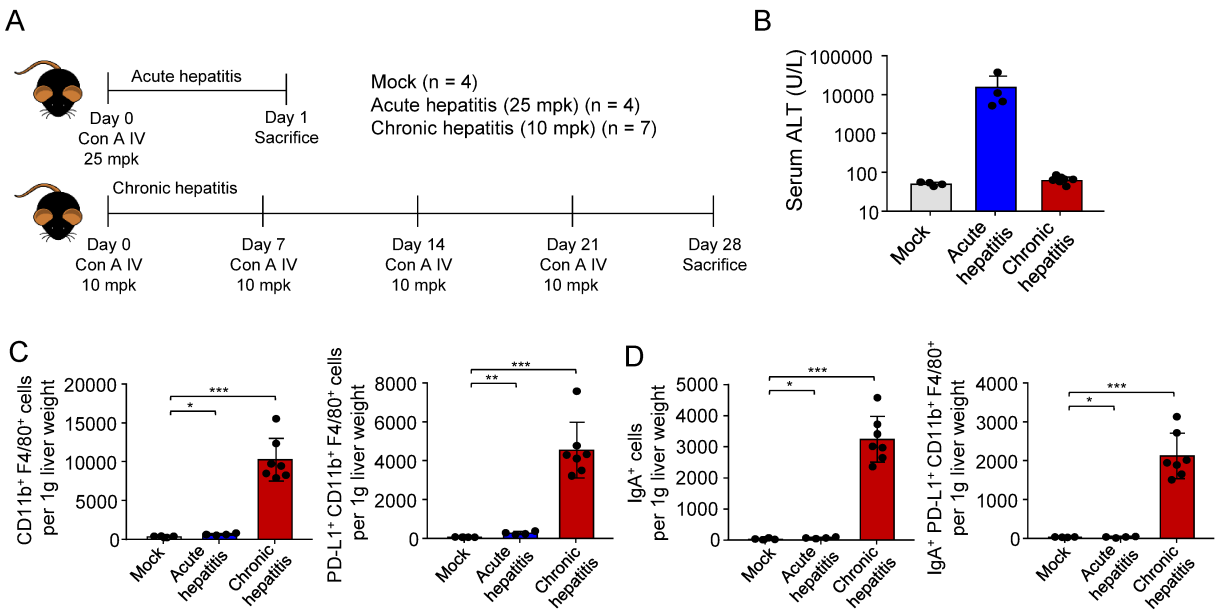
(A) Strong IgA staining in IgA-secreting plasma cells in NASH-cirrhotic liver
(B) IgA staining in endothelial cells and monocytes/Kupffer cells in NASH-cirrhotic liver

Supplementary Figure 3



(A) LPS staining in healthy and NASH livers. **p<0.01. (B) TLR4 staining in healthy and NASH livers. *p<0.05. (C) LPS, TLR4, and IgA staining in NASH-induced cirrhotic liver.

Supplementary Figure 4



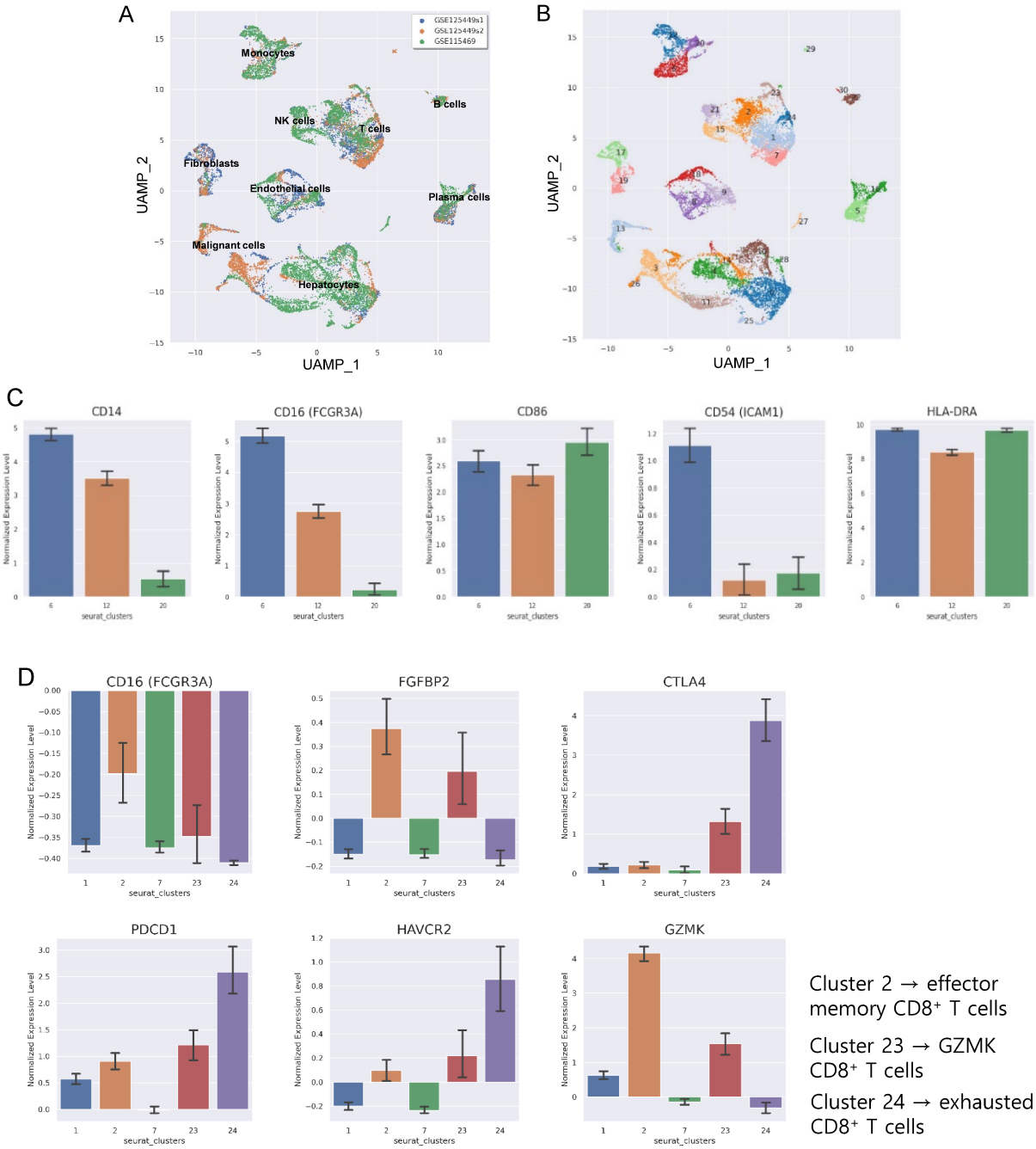
(A) Experiment scheme to establish acute and chronic hepatitis mouse model using injection of Con A with different doses and schedules.

(B) Alanine aminotransferase levels acute and chronic hepatitis model. ***p<0.001.

(C) The number of intrahepatic CD11b+F4/80+ macrophages and PD-L1+CD11bF4/80+ macrophages per 1g liver weight in acute and chronic hepatitis models. *p<0.05, **p<0.01.

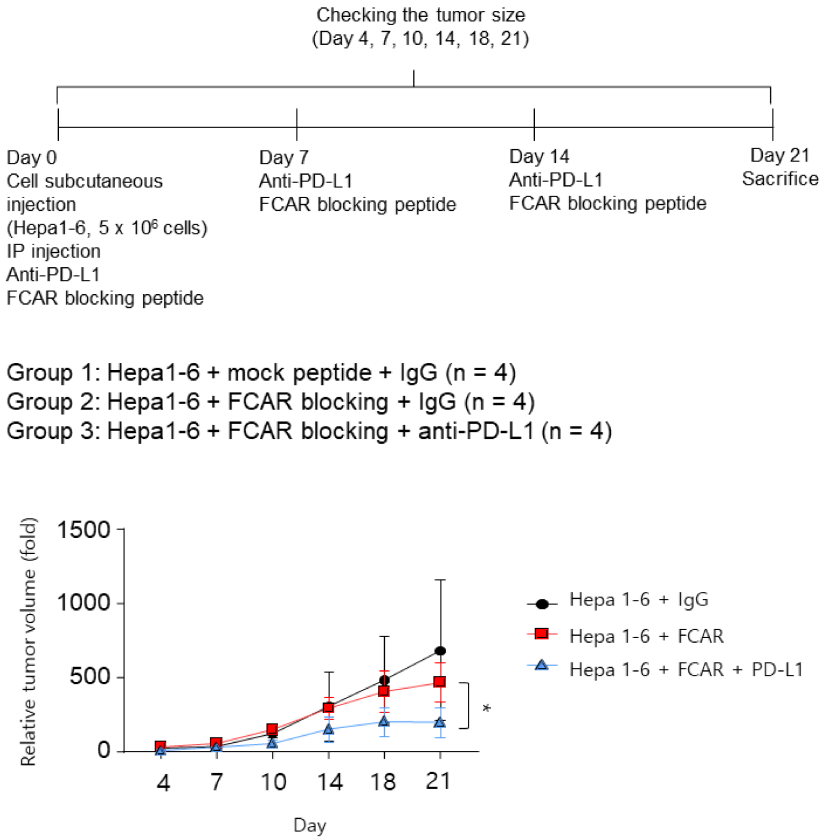
(D) The number of intrahepatic IgA+ cells and IgA+PD-L1+CD11bF4/80+ macrophages per 1g liver weight increased in acute and chronic hepatitis models. *p<0.05, **p<0.01.

Supplementary Figure 5



(A–B) UMAP plot of total of the 18,385 cells in 5 normal livers and 19 HCC tissues (GSE125449_Set1, GSE125449_Set2, and GSE115469). Clusters were defined by SNN clustering as previously described (36) (B). (C) The expression of CD14, CD16, CD86, CD54, and HLA-DRA in cluster 6, 12, and 20 is presented. (D) The expression of CD16, FGFBP2, CTLA4, PDCD1, HAVCR2, and GZMK in cluster 1,2,7,23,and 24 is presented.

Supplementary Figure 6



Syngeneic HCC mouse model (5×10^6 cells) using FACR-blocking peptide and/or anti-PD-L1 antibody. Drugs are started concomitantly with the injection of the tumor cells. Serial changes in the sizes of tumors generated from Hepa1-6 cells (5×10^6 cells) after FACR-blocking peptide and/or anti-PD-L1 antibody administration. *$p<0.05$