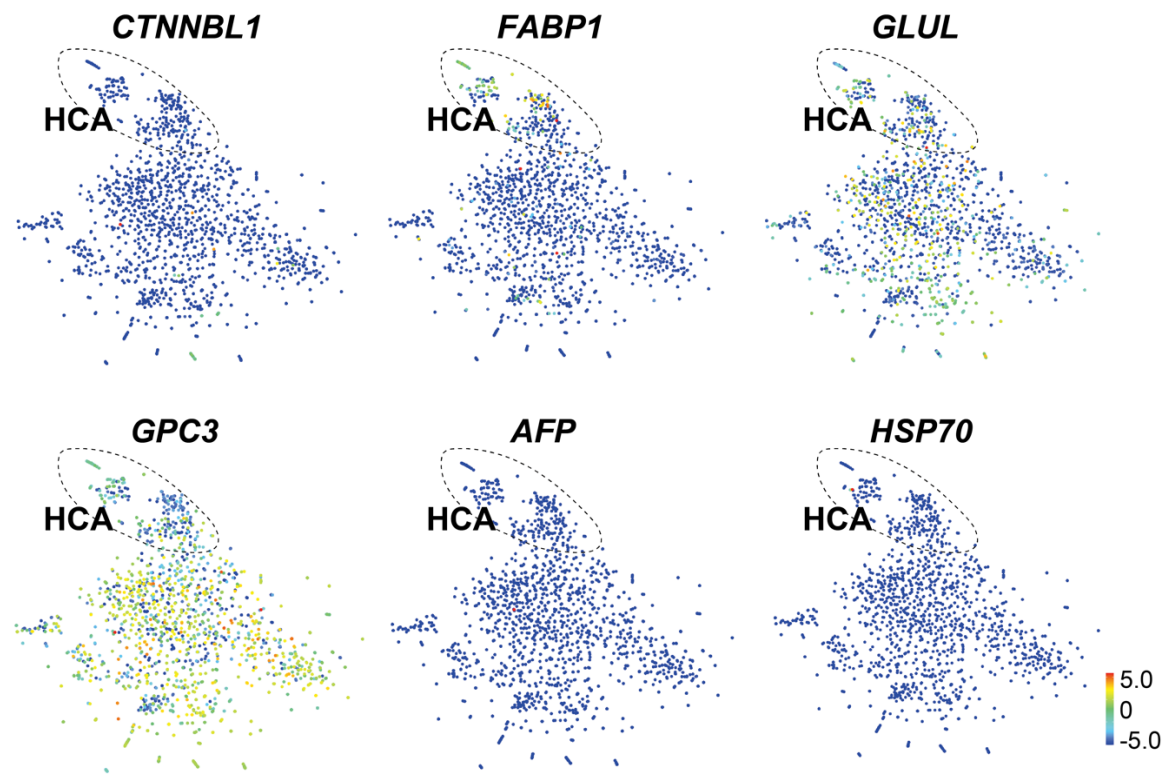
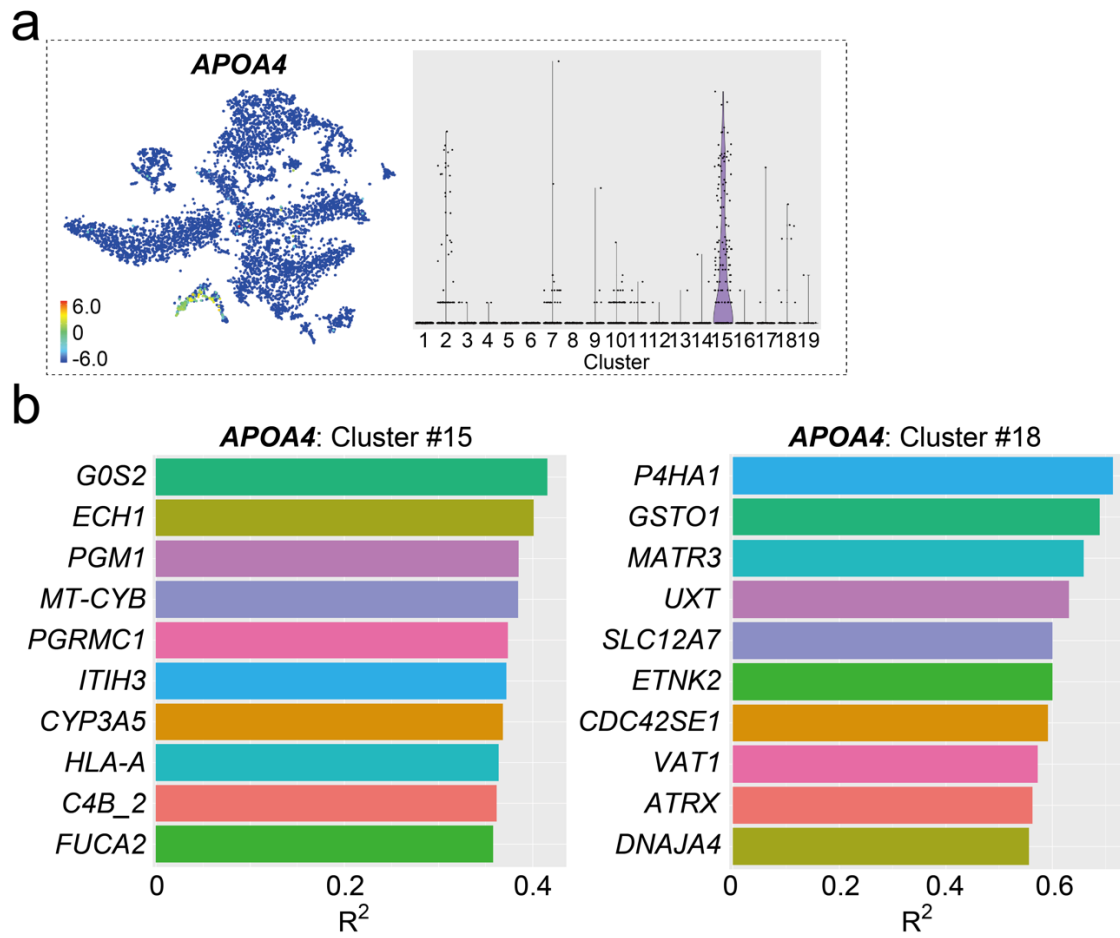


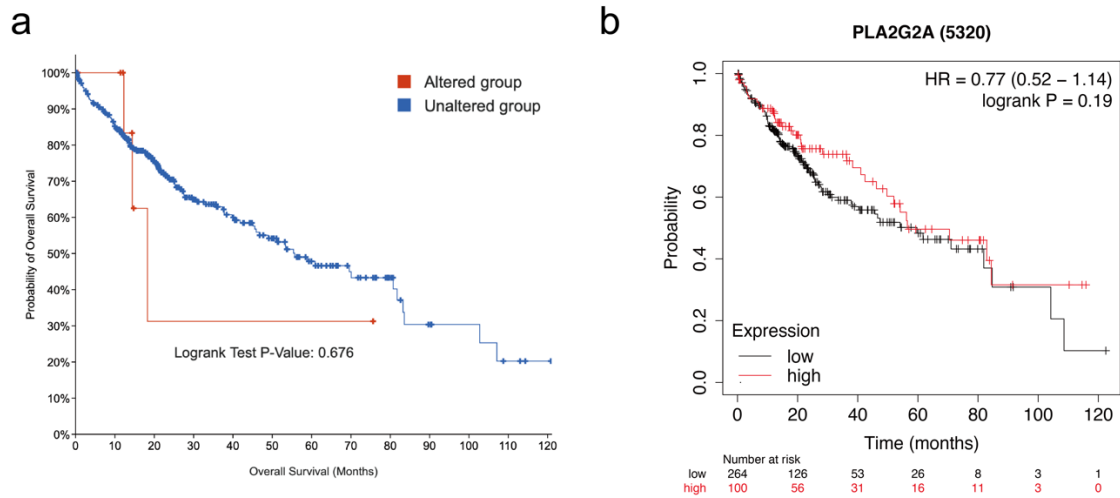
Supplementary Figures



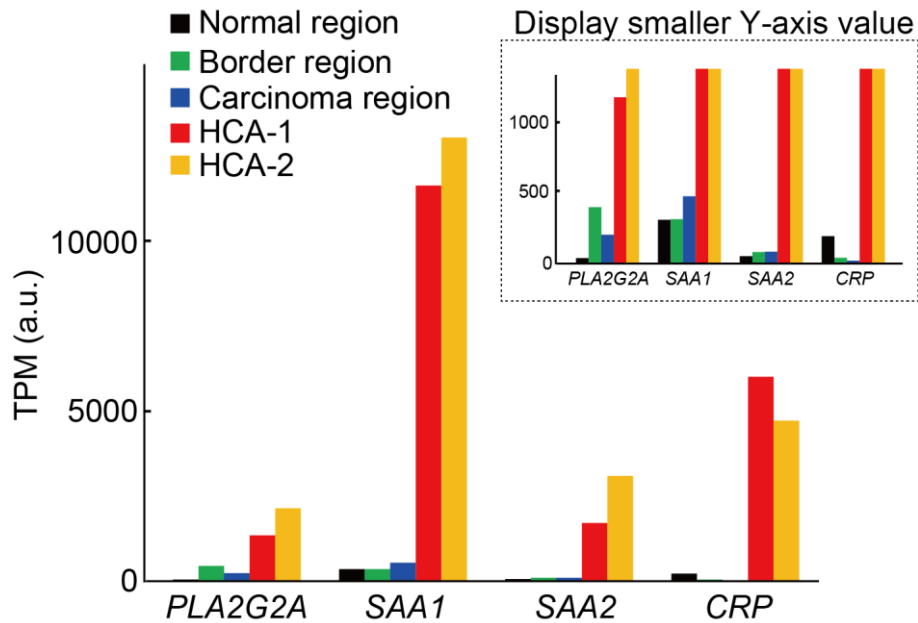
Supplementary Figure S1. Feature plots of other representative genes of HCA markers in scRNA-seq data. Feature plots of six genes, *CTNNBL1*, *FABP1*, *GLUL*, *GPC3*, *AFP* and *HSP70*. The color bar red to blue through yellow reveals the gradual expression intensity differences from high to low through middle.



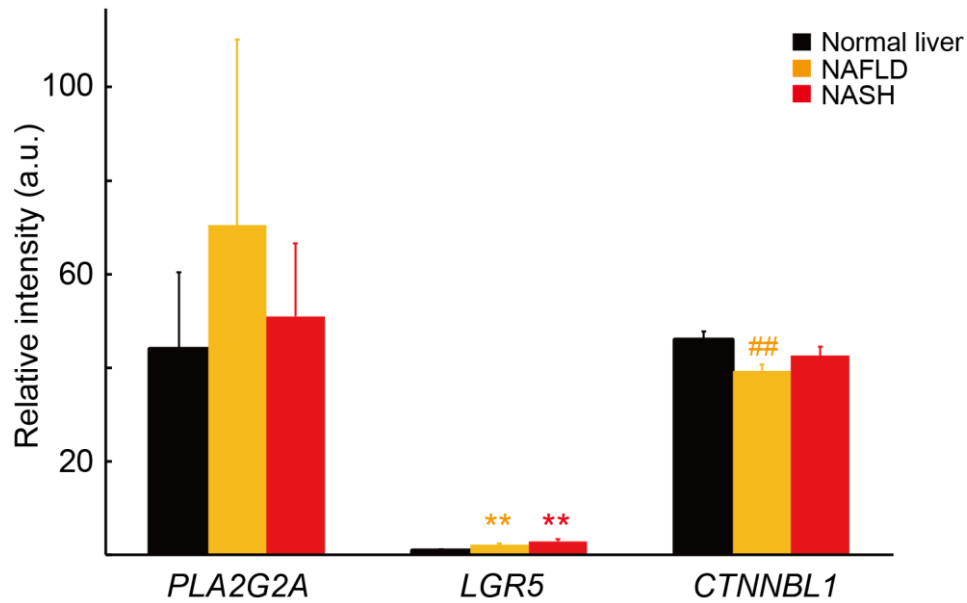
Supplementary Figure S2. The detailed expression of *APOA4* in I-HCA cell clusters. (a) The *APOA4* feature plot and violin plot. (b) Gene-gene correlation plots associated with *APOA4* in cluster#15 and cluster#18. X-axis indicates coefficient of determination (R^2).



Supplementary Figure S4. KM Plotter related to the high expression of *PLA2G2A* mRNA on overall survival (OS) of liver cancer. (a) KM plotter obtained from liver Hepatocellular Carcinoma (TCGA, PanCancer Atlas) in cBio-portal for Cancer genomics. Samples with *PLA2G2A* mRNA data (RNA Seq V2, 366 patients, z-scores $\geq \pm 2.0$) is shown. Red line: OS of *PLA2G2A* mRNA high expression cases. Blue line: OS of control groups. (b) KM plotter obtained from Liver cancer RNA-seq. The analysis was performed of 364 patients. The red line indicates OS of *PLA2G2A* mRNA high expression cases. Black line: OS of control groups.



Supplementary Figure S5. RNA-seq analysis of one HCC and two HCAs. The HCC tissue had normal, borderline, and cancerous regions. Total RNA was obtained from each region, and RNA-seq analysis was performed. Y axis: TPM value. Bars indicate raw TPM value. Black bars: normal region, green bars: borderline, blue bars: HCC region, red bars: HCA tissue from patient#1, yellow bars: HCA tissue from patient#2. The raw TPM expression values for PLA2G2A, SAA1, SAA2 and CRP are shown. The right-top panel displays smaller Y-axis TPM value. PLA2G2A expression was relatively higher in border region (green bar in PLA2G2A) than in normal (black) or HCC (blue) region.



Supplementary Figure S6. The expression of *PLA2G2A*, *LGR5* and *CTNNB1* mRNA in healthy, NAFLD and NASH patients. Original data was obtained from GSE126848 [30]. The raw count number of genes were normalized by total count. Y axis: Relative intensity (arbitrary unit; a.u.). Bars indicate mean \pm S.E. Black bars: normal liver (n=14), yellow bars: NAFLD (n=15), red bars: NASH (n=11). There is no significant difference for *PLA2G2A* expression among three different conditions. In contrast, *LGR5* expression increases significantly (** $p < 0.01$) with the progress of liver disease. Inflammatory NAFLD stage, *CTNNB1* mRNA expression is reduced (## $p < 0.01$).