



Supplementary Figure 2. Enrichment analysis of differential gene expression associated with complement components (CFHR2, CFHR5, C7, and C8G) in the context of liver diseases. (A, D, F, H) Volcano plots for differential gene expression in liver tissues associated with varying expression levels of CFHR2 (A), CFHR5 (D), C7 (F), and C8G (H). Each plot represents genes as points, plotted based on their log fold change (log FC) on the x-axis and the negative log10 of the false discovery rate (FDR) on the y-axis. Genes meeting the criteria of $FDR < 0.05$ and $|\log FC| > 1$ are highlighted: upregulated genes in red and downregulated genes in blue. The top 25 significantly upregulated and downregulated genes are labeled for identification. (B, C, E, G, I, J) Heatmaps analyzing GO biological process enrichment in gene sets associated with liver diseases, correlated with differential gene expression in the liver relative to the levels of CFHR2 (B, C), CFHR5 (E), C7 (G), and C8G (I, J). Heatmap B details enrichment for ALC in relation to CFHR2. C for HCC in relation to CFHR2, E for PSC in relation to CFHR5, G for HCC in relation to C7, I for MASLD in relation to C8G, and J for PSC in relation to C8G. Each heatmap employs a color gradient to represent the significance of enrichment, elucidating the biological processes significantly affected by these liver diseases in the context of complement component levels. GO, gene ontology; AIH, autoimmune hepatitis; PSC, primary sclerosing cholangitis; MASLD, metabolic dysfunction-associated steatotic liver disease; ALC, alcohol-related cirrhosis; HCC, hepatocellular carcinoma; CFHR2, complement factor H-related protein 2, CFHR5, complement factor H-related protein 5; C7, complement component 7; C8G, complement component C8 gamma chain.