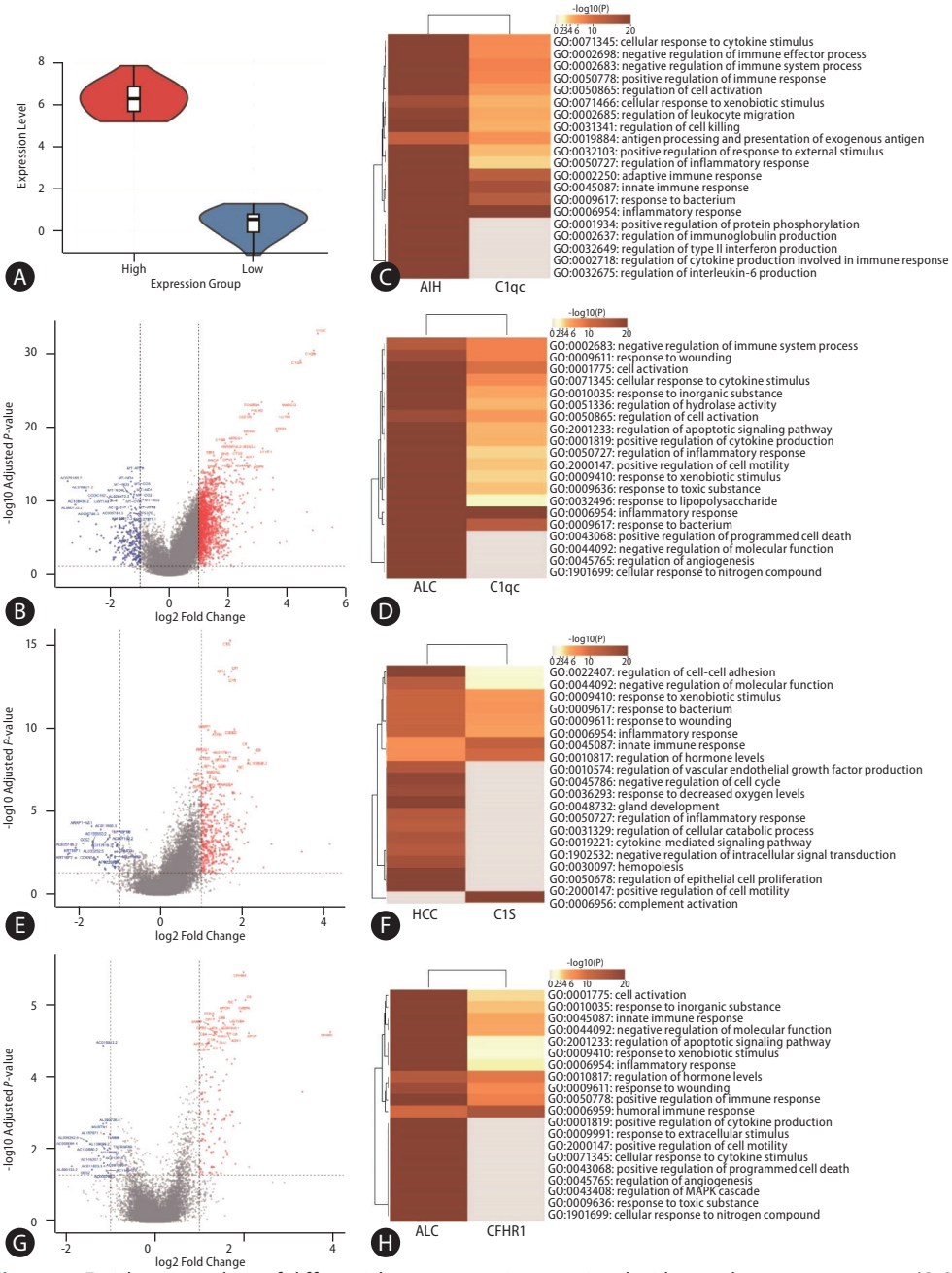

Supplementary Figure 1. Enrichment analysis of differential gene expression associated with complement components (C1QC, C1S, and CFHR1) in the context of liver diseases.(A) Distribution of C1QC expression levels (log10(TPM)) in 226 human liver tissues from the GTEx database. The expression levels are categorized into two groups for comparative analysis: the top 25% (high expression, shown in red) and the bottom 25% (low expression, shown in blue). (B, E, G) Volcano plots for differential gene expression in liver tissues associated with varying expression levels of C1QC (B), C1S (E), and CFHR1 (G). 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 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. (C, D, F, H) 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 C1QC (C, D), C1S (F), and CFHR1 (H). Heatmap C details enrichment for AIH in relation to C1QC, D for ALC in relation to C1QC, F for HCC in relation to C1S, and H for ALC in relation to CFHR1. 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; ALC, alcohol-related cirrhosis; HCC, hepatocellular carcinoma; C1QC, complement C1q subcomponent subunit C; C1S, complement C1s subcomponent; CFHR1, complement factor H-related protein 1.