



Supplementary Fig. S2 KEGG pathway enrichment analysis of differentially expressed genes. (a) Significantly enriched KEGG pathways from the DEGs between the Model and Control groups. (b) Significantly enriched KEGG pathways from the DEGs between the Combo and Model groups. The treatment specifically modulated pathways related to canonical pathways of HSC activation, such as the ECM-receptor interaction and Wnt signaling pathway. The line plot corresponds to the candidate gene count, and the bar height represents the $-\log_{10}(\text{Q value})$, indicating the statistical significance of the enrichment.