



Supplementary Fig. 2. Enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways of differentially expressed genes (DEGs) of non-alcoholic fatty liver disease (NAFLD) patients and hepatocellular carcinoma (HCC) patients. (A) Significantly enriched KEGG pathways of DEGs both upregulated in NAFLD and HCC patients. (B) DEGs both downregulated in NAFLD and HCC patients. (C) DEGs upregulated in NAFLD patients but downregulated in HCC patients. (D) DEGs downregulated in NAFLD patients but upregulated in HCC patients. The significance of following functional profiling is determined via false discovery rate. TNF, tumor necrosis factor; AGE-RAGE, advanced glycation endproducts-receptor for advanced glycation end products; MAPK, mitogen-activated protein kinase; IL, interleukin; JAK-STAT, Janus kinase/signal transducers and activators of transcription; NF, nuclear factor.