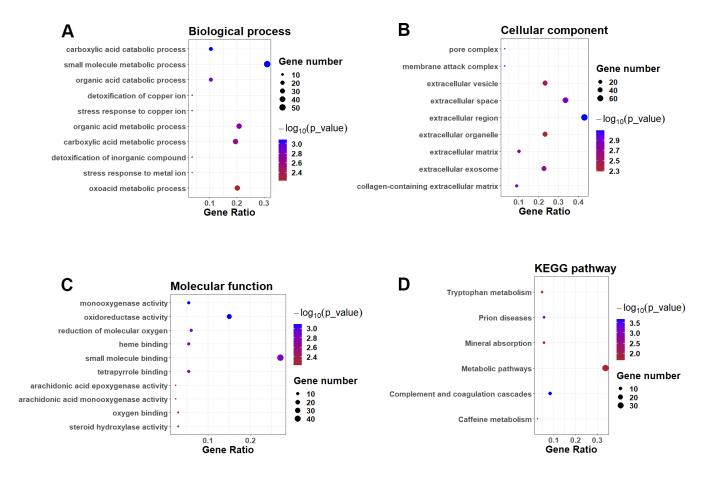
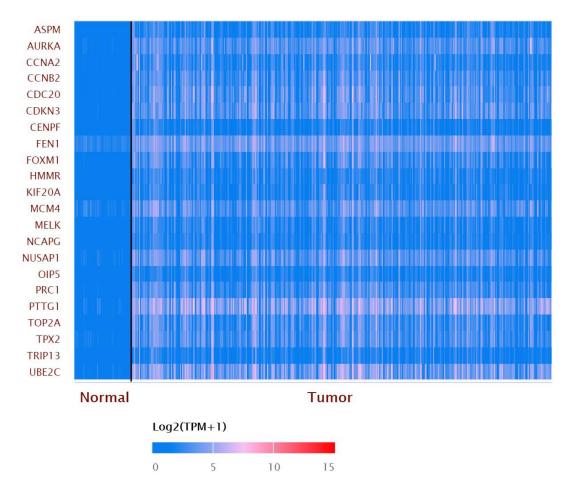
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Functional enrichment analysis of common DEGs. GO enrichment of common DEGs in (A) biological process, (B) cellular component and (C) molecular function. (D) KEGG pathway enrichment analysis of common DEGs.

Expression pattern of input genes in Liver hepatocellular carcinoma (LIHC)



Supplementary Figure 2. Heatmap illustrates the expression pattern of hub genes in normal liver tissues and HCC tissues. TPM = transcripts per million.