



Figure S1 GSEA enrichment analysis results. *TLK2* was most significantly associated with oocyte-meiosis, cell cycle, and ubiquitin-mediated proteolysis pathways in hepatocellular carcinoma. Fatty acid metabolism, retinol metabolism, and primary bile acid biosynthesis activities were significantly inhibited. KEGG, Kyoto Encyclopedia of Genes and Genomes; GSEA, gene set enrichment analysis.