

Supplementary materials

The mRNA Expression Signature and Prognostic Analysis of Multiple Fatty Acid Metabolic Enzymes in Clear Cell Renal Cell Carcinoma

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Running title: The expression and prognosis of FA metabolic enzymes in ccRCC

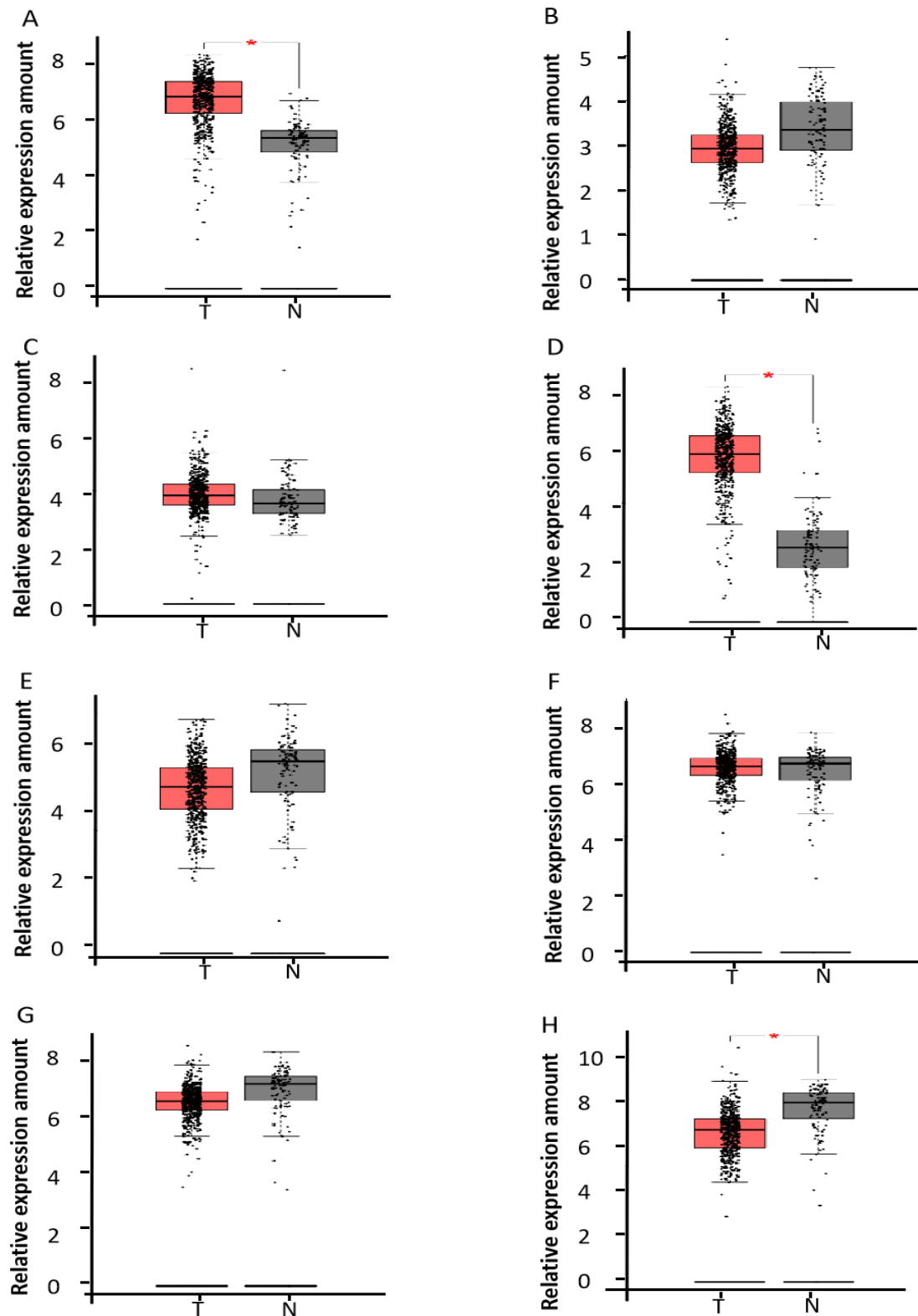


Figure S1. The box plots validated the mRNA expression profiles of FA metabolic enzymes in ccRCC and normal kidney tissues using GEPIA database. The box plot showed the relative mRNA expression of ACLY (A), ACC (B), FASN (C), SCD (D), CPT1A(E), HADHA (F), HADHB (G), and ACAT1 (H), in ccRCC (T, left, n=523) and normal tissues (N, right, n=100), respectively. * P<0.05.

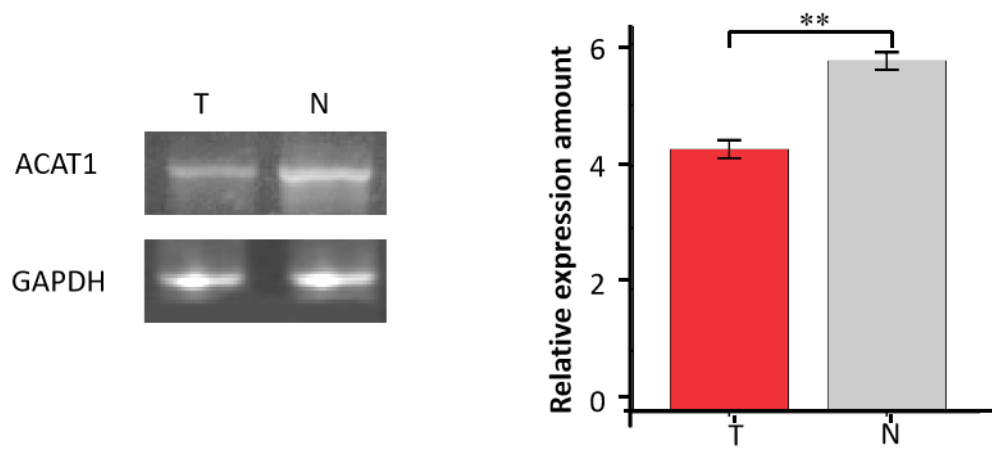


Figure S2. RT-PCR confirmed the lower mRNA expression of ACAT1 in ccRCC than normal kidney tissues. Representative ACAT1 expression by RT-PCR (left) and relative ACAT1 mRNA expression (right). T: ccRCC, N: normal tissues, n=3. * P<0.05, ** P<0.01.

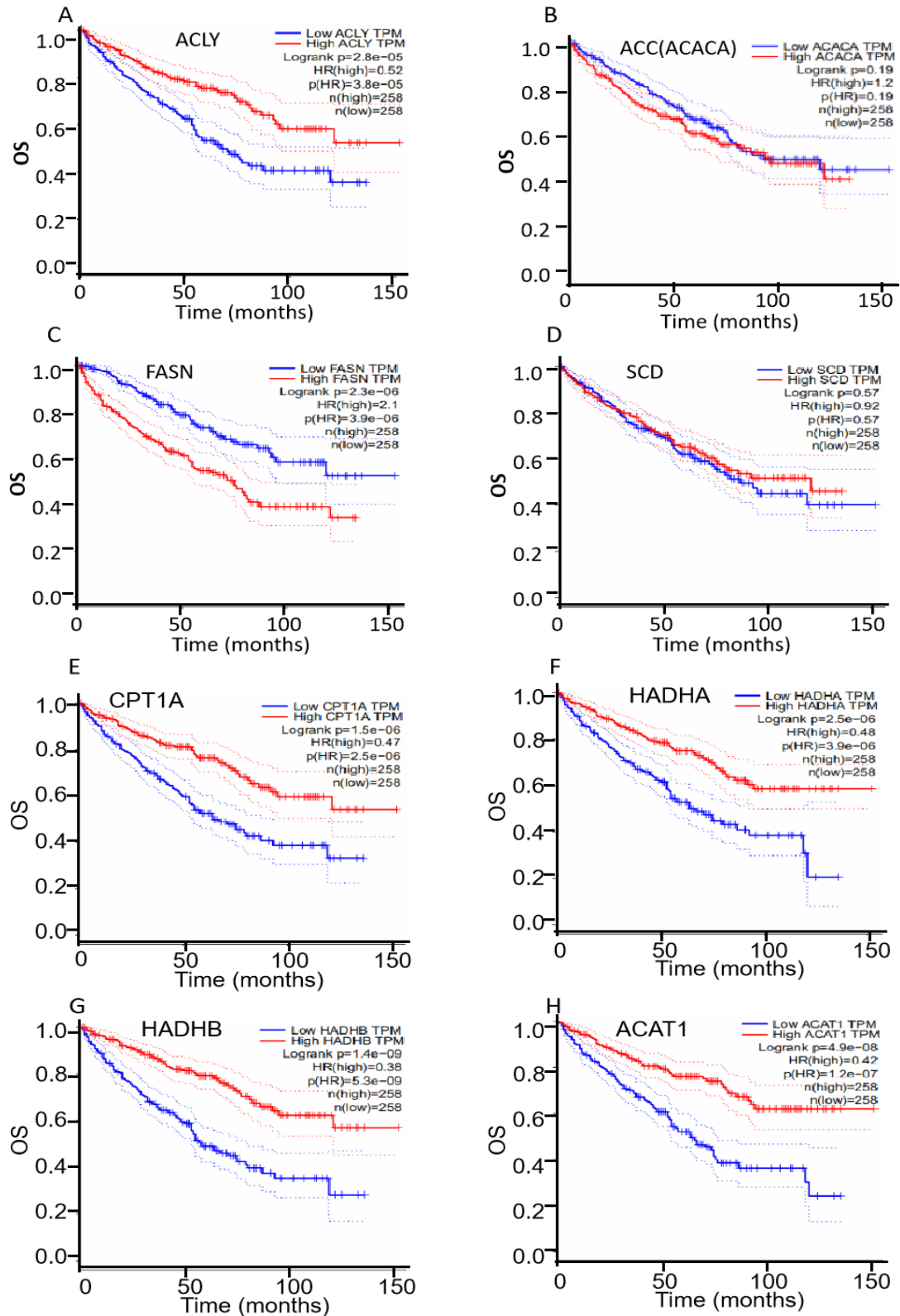


Figure S3. Overall survival (OS) curves of ACLY (A), ACC (B), FASN (C), SCD (D), CPT1A(E), HADHA (F), HADHB (G), and ACAT1 (H), were plotted by GEPIA analysis.