

Table S1 siRNA sequences used in this study

| siRNA name | Sequence |
|----------------|--|
| GLYAT-siRNA #1 | Sense: CCAGCAUCCUUAAGGUUUTT Antisense: AAACCUUUUAAGGAUGCUGGTT |
| GLYAT-siRNA #2 | Sense: GGAUCACCAGAACUCAUCATT Antisense: UGAUGAGUUCUGGUGAUCCTT |
| GLYAT-siRNA #3 | Sense: CCAAGGAACUGACUCCUUUTT Antisense: AAAGGAGUCAGUCCUUGGTT |
| siRNA control | Sense: UUCUCCGAACGUGUCACGUTT Antisense: ACGUGACACGUUCGGAGAATT |

siRNA, short interfering RNA; GLYAT, glycine-N-acyltransferase.

Table S2 Prognostic value of candidate genes for OS in liver cancer patients based on GEPIA

| Gene | Function | P value |
|----------------|-------------------|---------|
| <i>ACAT1</i> | Protective factor | <0.001 |
| <i>ADI1</i> | Protective factor | 0.0045 |
| <i>ALDH8A1</i> | Protective factor | 0.0075 |
| <i>BHMT</i> | Protective factor | 0.0095 |
| <i>CARS2</i> | Risk factor | <0.001 |
| <i>DARS2</i> | Risk factor | 0.003 |
| <i>DPYS</i> | Protective factor | 0.0044 |
| <i>FARSB</i> | Risk factor | <0.001 |
| <i>FTCD</i> | Protective factor | <0.001 |
| <i>GCDH</i> | Protective factor | 0.0083 |
| <i>GLYAT</i> | Protective factor | 0.01 |
| <i>GMPS</i> | Risk factor | <0.001 |
| <i>GNMT</i> | Protective factor | 0.0088 |
| <i>GPT</i> | Protective factor | 0.0024 |
| <i>HAAO</i> | Protective factor | 0.029 |
| <i>HARS2</i> | Risk factor | 0.0072 |
| <i>MAT1A</i> | Protective factor | 0.0067 |
| <i>MSRA</i> | Protective factor | 0.0081 |
| <i>MTHFD1</i> | Protective factor | 0.0088 |
| <i>NARS1</i> | Risk factor | 0.0026 |
| <i>QDPR</i> | Protective factor | 0.022 |
| <i>UROC1</i> | Protective factor | 0.0049 |

OS, overall survival.

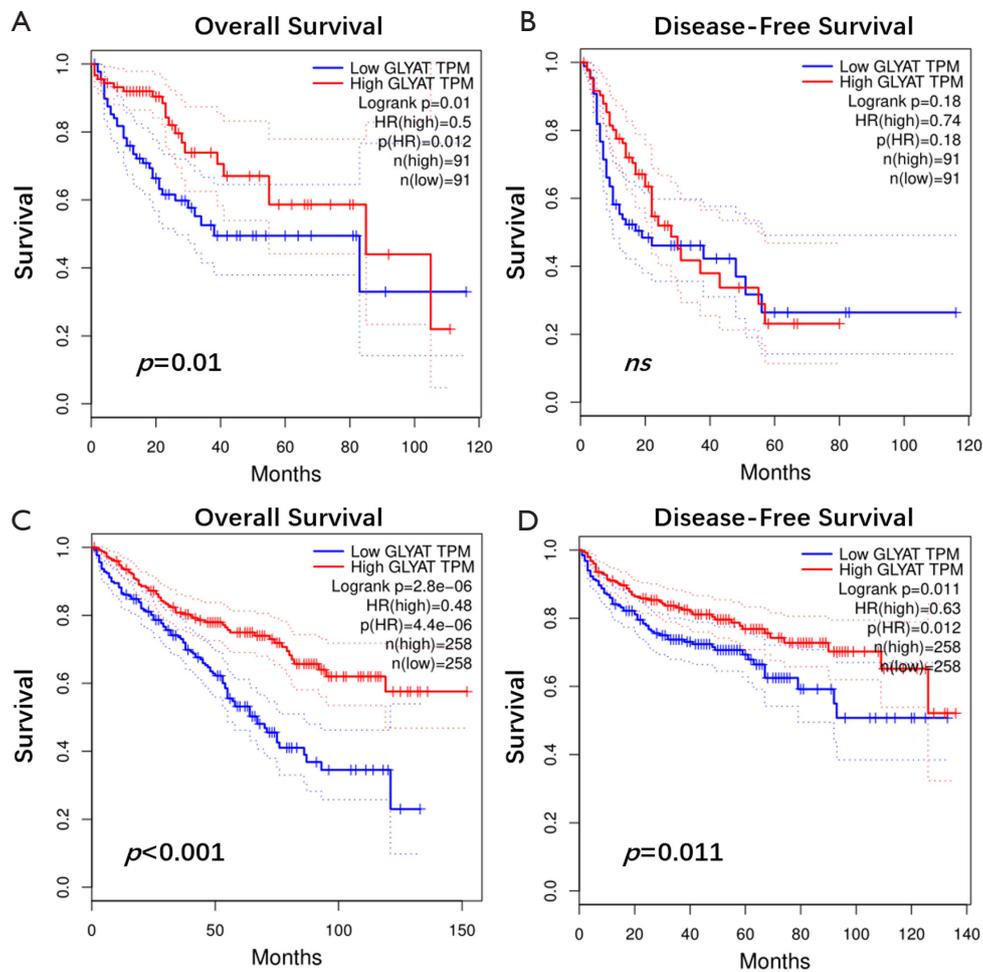


Figure S1 Kaplan-Meier analysis of GLYAT in liver cancer and ccRCC based on the GEPIA database. (A,B) Liver cancer patients with low GLYAT mRNA expression had short OS but not TTR. (C,D) ccRCC patients with low GLYAT mRNA expression had short OS and TTR. GLYAT, glycine-N-acyltransferase; TPM, transcripts per million; HR, hazard ratio; ccRCC, clear cell renal cell carcinoma; mRNA, messenger RNA; OS, overall survival; TTR, time to recurrence.

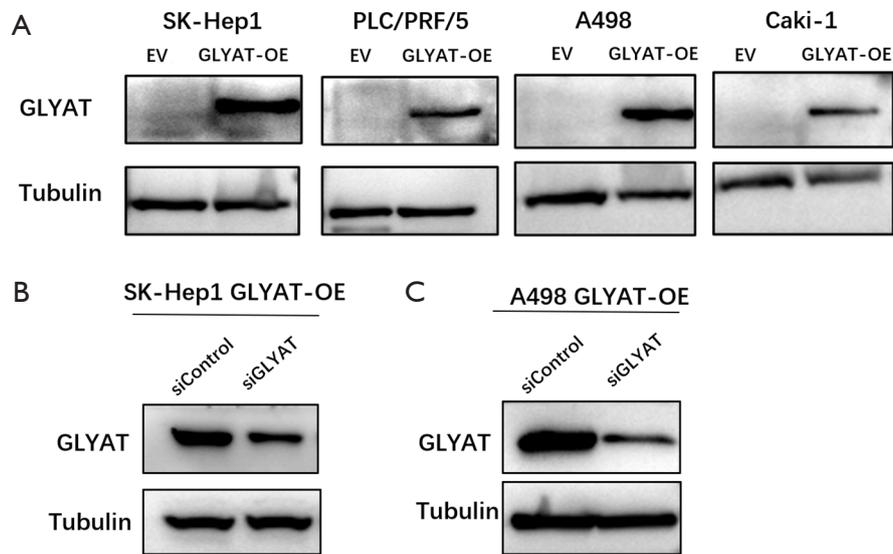


Figure S2 Western blot for detecting GLYAT protein expression. (A) GLYAT was overexpressed in the SK-Hep1, PLC/PRF/5, A498, and Caki-1 cells. (B,C) GLYAT was disturbed in the SK-Hep1 GLYAT-OE cells, and the A498 GLYAT-OE cells by siRNA. EV, empty vector; GLYAT-OE, GLYAT overexpression; GLYAT, glycine-N-acyltransferase; si, short interfering RNA; siRNA, short interfering RNA.

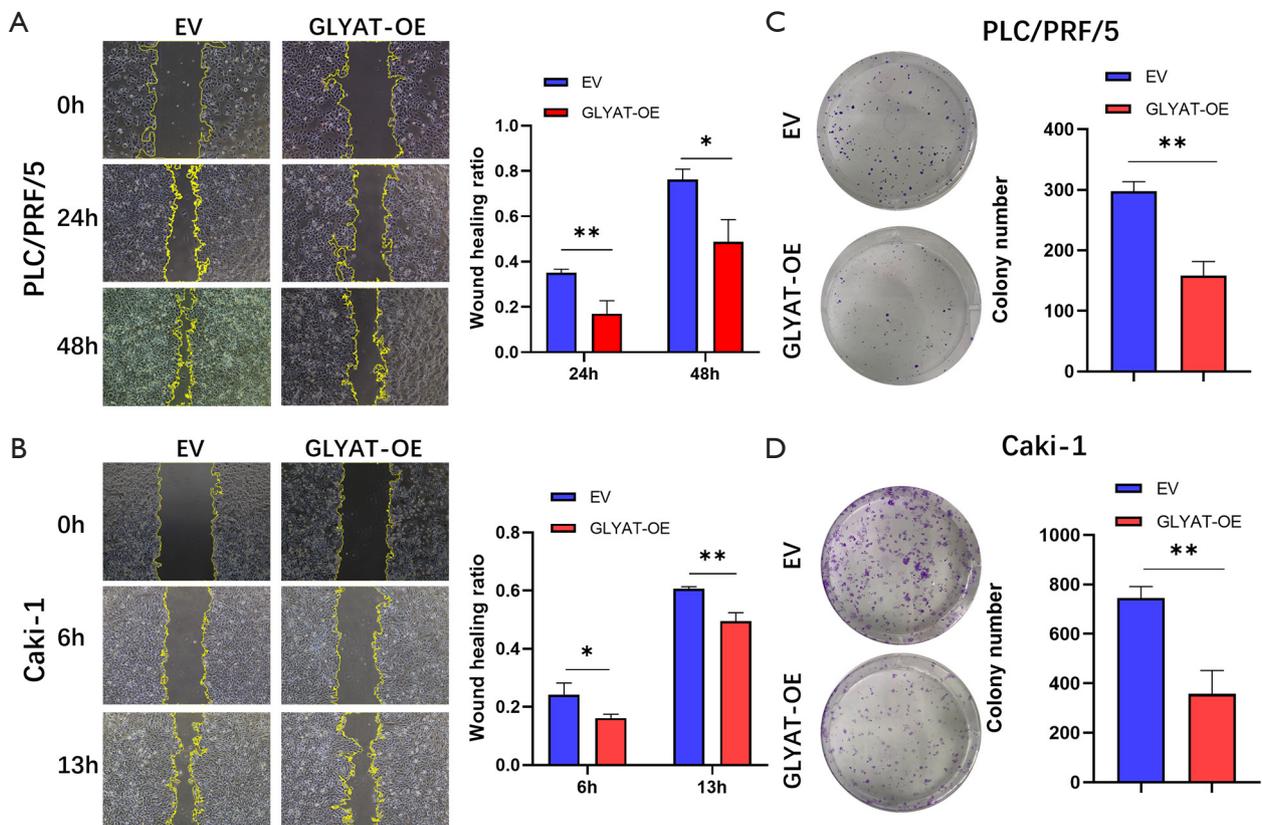


Figure S3 The overexpression of GLYAT suppressed the migration and proliferation abilities of the cells. (A,B) Wound healing assay showed that overexpressed GLYAT inhibited the migration ability of the PLC/PRF/5 and Caki-1 cells (40 \times). (C,D) The overexpression of GLYAT inhibited the proliferation ability of the PLC/PRF/5 and Caki-1 cells. Cells were stained by crystal violet. *, $P < 0.05$; **, $P < 0.01$. Error bars denote mean \pm SD. EV, empty vector; GLYAT-OE, GLYAT overexpression; GLYAT, glycine-N-acyltransferase; SD, standard deviation.

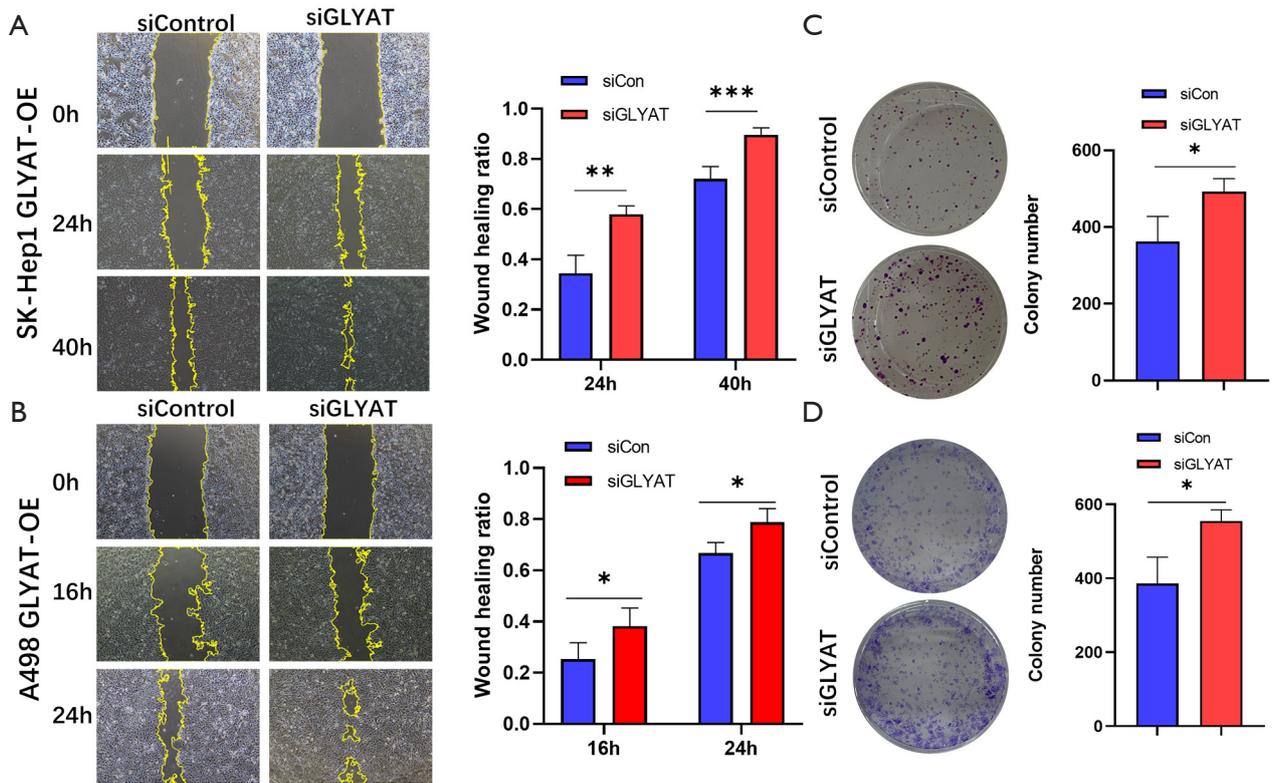


Figure S4 Disturbing GLYAT rescued the migration and proliferation abilities of the cells. (A,B) Wound healing assay showed that disturbing GLYAT rescued the migration ability of the SK-Hep1 GLYAT-OE cells and A498 GLYAT-OE cells (40x). (C,D) Disturbing GLYAT rescued the proliferation ability of the SK-Hep1 GLYAT-OE cells and A498 GLYAT-OE cells. Cells were stained by crystal violet. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. Error bars denote mean \pm SD. si, short interfering RNA; GLYAT, glycine-N-acyltransferase; GLYAT-OE, GLYAT overexpression; Con, control group; SD, standard deviation.

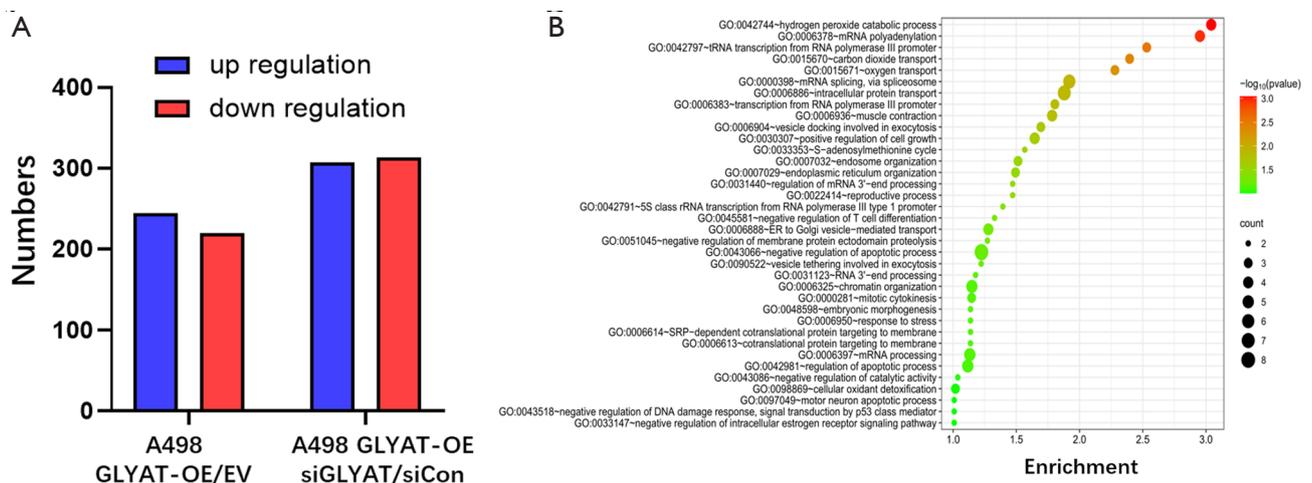


Figure S5 Screening for downstream proteins of GLYAT. (A) Differential expression protein profiles were analyzed by proteomics in the indicated cell lines. (B) Biological processes of the differentially expressed proteins by GO analysis. GLYAT-OE, GLYAT overexpression; GLYAT, glycine-N-acyltransferase; EV, empty vector; si, short interfering RNA; Con, control group; GO, Gene Ontology.