

Appendix 1

1. The following primer sequences were used in this study:

| | |
|-------------------|---------------------------|
| TFR1-F | GCTCGGCAAGTAGATGGCGATAAC |
| TFR1-R | ATTGTCAATGTCCCAAACGTCACC |
| SLC7A11-F | AGCCTGTTGTCCACCATCTCC |
| SLC7A11-R | GTCAGAGTGATGACGAAGCCAATC |
| PRKAA2-F | GTGAAGATCGGACACTACGTG |
| PRKAA2-R | CTGCCACTTATGGCCTGTTA |
| 18S-F | CAGCCACCCGAGATTGAGCA |
| 18S-R | TAGTAGCGACGGCGGTGTG |
| DMT1-F | TGGCTTATCTGGGCTTGTG |
| DMT1-R | CACACTGGCTCTGATGGCTA |
| FPN-F | ACAATACGAAGGATTGACCAAGT |
| FPN-R | ATACCAAGTTCCATCCGAAAT |
| FTH1-F | GCCGAGAAACTGATGAAGCTGC |
| FTH1-R | GCACACTCCATTGCATTAGCC |
| HIF-1 α -F | CCATTAGAAAGCAGTCCGCAAGC |
| HIF-1 α -R | GTGGTAGTGGTGGCATTAGCAGTAG |
| HIF-2 α -F | CCAGGGAAAAAGGAACCTGGGT |
| HIF-2 α -R | GACCCGAAAAGAGGGACGGAGA |
| IRP1-F | AACTGACCACATCTCCCCAG |
| IRP1-R | ATAGTCTGTGGTGCCTGCTT |
| IRP2-F | TACGGGTCTTGTGGAAGCT |
| IRP2-R | ATCTGTCGGACAAGCAGGAT |

2. Target sequences for siRNAs and shRNAs were as follows:

siPRKAA2-1: GUCAUCCUCAUUAUUAUCAAAC

siPRKAA2-2: CAACUUUACCUUGGUUGAUAC

ShPRKAA2:CCGGGTCATCCTCATATTATCAAACCTCGAGGTTGATAATATGAGGATGACTTTTG

3. The following information was provided regarding the primary antibodies used in western blotting assays:

Anti-PRKAA2 antibodies (1/1000; Proteintech, 18167-1-AP, RRID:AB_10695046);

Anti-TFR1 antibodies (1/1000; Abcam, ab214039, RRID:AB_2904534);

Anti-IRP1 antibodies (1/1000; Abcam, ab183721);

Anti-IRP2 antibodies (1/1000; ABclonal, A6382, RRID:AB_2766984);

Anti-HIF-1 α antibodies (1/1000; Abcam, ab179483, RRID:AB_2732807);

Anti-HIF-2 α antibodies (1/1000; Abclonal, A7553, RRID:AB_2768078);

Anti-GAPDH antibodies (1/10000; Abcam, ab181602, RRID:AB_2630358)

1. Detail about the five patients with low AFP level and low PRKAA2 expression

| Number | AFP at Diagnosis | Age at diagnosis | PRETEXT | Histology | Tumor Size | Metastasis | Extrahepatic spread | Multifocality | Tumor rupture | Vascular involvement | Caudate involvement |
|--------|------------------|------------------|---------|------------|---------------------|------------|---------------------|---------------|---------------|----------------------|---------------------|
| 1 | 696.4 ng/ml | 11 months | I | MIX | 590 cm ³ | NO | NO | NO | NO | NO | NO |
| 2 | 943.5 ng/ml | 10 months | I | MIX | 448 cm ³ | NO | NO | NO | NO | NO | NO |
| 3 | 856.9 ng/ml | 31 months | II | Epithelial | 643 cm ³ | NO | NO | NO | NO | NO | NO |
| 4 | 1010.2 ng/ml | 45 months | II | Epithelial | 540 cm ³ | NO | NO | NO | YES | YES | NO |
| 5 | 690.1 ng/ml | 22 months | II-III | NA | 252 cm ³ | NO | NO | NO | NO | NO | NO |

2. Specific data of $\Delta\Delta Ct$

| Pair Number | $\Delta\Delta Ct = \Delta Ct(\text{normalized-noncancerous}) - \Delta Ct(\text{normalized-Tumor})$ | Average $\Delta\Delta Ct$ |
|-------------|--|---------------------------|
| 1 | 0.187351015 | 0.750443124 |
| 1 | 0.800498056 | |
| 1 | 1.2634803 | |
| 2 | 1.555538501 | 1.217900169 |
| 2 | 0.869679343 | |
| 2 | 1.228482663 | |
| 3 | 9.25643847 | 8.321005907 |
| 3 | 8.459185325 | |
| 3 | 7.247393924 | |
| 4 | 1.157398133 | 1.356692126 |
| 4 | 1.55598612 | |
| 4 | 1.356692126 | |
| 5 | 0.53221911 | 0.561389829 |
| 5 | 0.590560547 | |
| 5 | 0.561389829 | |
| 6 | -1.638684877 | -1.316081323 |
| 6 | -1.292519957 | |
| 6 | -1.017039135 | |
| 7 | 4.111432552 | 3.461021244 |
| 7 | 4.708573759 | |
| 7 | 1.56305742 | |
| 8 | 0.471147838 | -0.081526378 |
| 8 | -0.497106906 | |
| 8 | -0.218620067 | |
| 9 | 10.95563585 | 8.931872441 |
| 9 | 7.157972881 | |
| 9 | 8.682008593 | |
| 10 | 1.774275047 | 2.507484573 |
| 10 | 1.763643632 | |
| 10 | 3.984535039 | |
| 11 | -1.193641773 | -0.835490099 |
| 11 | 0.025653702 | |
| 11 | -1.338482226 | |
| 12 | 0.727220454 | 0.424500389 |
| 12 | 0.658794265 | |
| 12 | -0.112513553 | |
| 13 | -0.008552379 | -0.197565551 |
| 13 | 0.141298434 | |
| 13 | -0.725442709 | |
| 14 | -2.46922674 | -0.474150913 |
| 14 | 0.166230644 | |
| 14 | 0.880543357 | |
| 15 | 0.369754301 | -0.096661473 |
| 15 | 0.141497274 | |
| 15 | -0.801235992 | |
| 16 | 8.014684308 | 8.811174364 |
| 16 | 9.666180917 | |
| 16 | 8.752657867 | |
| 17 | 6.701586931 | 6.327822258 |
| 17 | 5.279048674 | |
| 17 | 7.002831169 | |
| 18 | 2.135016937 | 2.196510297 |
| 18 | 2.207521069 | |
| 18 | 2.246992885 | |
| 19 | 3.477338478 | 3.297944832 |
| 19 | 3.20062303 | |
| 19 | 3.215872987 | |
| 20 | 2.612746572 | 2.723212248 |
| 20 | 2.903221421 | |
| 20 | 2.653668751 | |
| 21 | 5.325581803 | 4.951347183 |
| 21 | 4.565270361 | |
| 21 | 4.963189385 | |
| 22 | 1.741058643 | 1.802038974 |
| 22 | 2.084580179 | |
| 22 | 1.580478101 | |
| 23 | 2.551942839 | 3.100305693 |
| 23 | 3.648668547 | |
| 23 | 3.100305693 | |
| 24 | 4.911576917 | 5.06152224 |
| 24 | 5.211467563 | |
| 24 | 5.06152224 | |
| 25 | 6.16158126 | 5.820394884 |
| 25 | 5.479208508 | |
| 25 | 5.820394884 | |
| 26 | 4.064519051 | 3.844358365 |
| 26 | 3.62419768 | |
| 26 | 3.844358365 | |
| 27 | 8.120304956 | 8.312927469 |
| 27 | 7.891600494 | |
| 27 | 8.926876957 | |
| 28 | 4.077108354 | 5.483701346 |
| 28 | 6.631571714 | |
| 28 | 5.742423971 | |
| 29 | 2.744173446 | 2.183797763 |
| 29 | 1.551523796 | |
| 29 | 2.255696047 | |
| 30 | 8.161786668 | 7.690549381 |
| 30 | 7.725493653 | |
| 30 | 7.184367824 | |

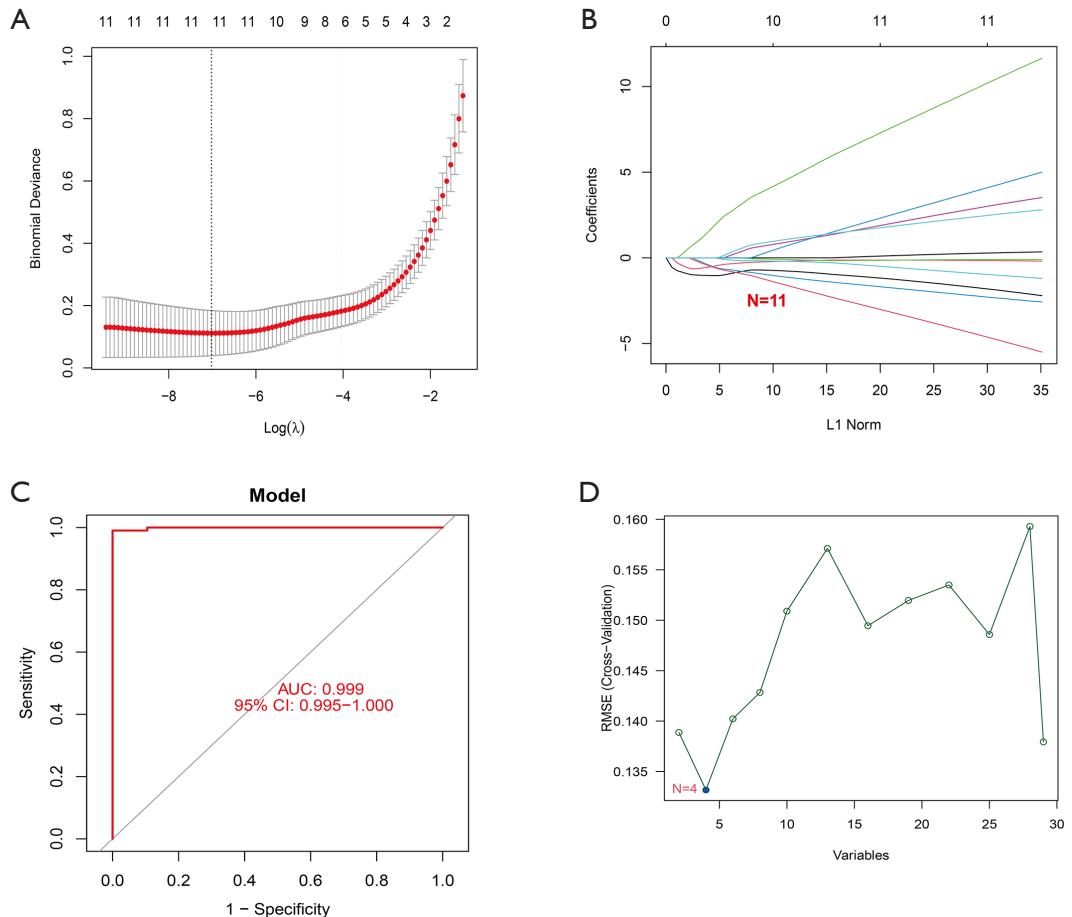


Figure S1 Selection of diagnosis marker candidates for HB by two algorithms. (A) and (B) Eleven gene expression signatures based on ferroptosis-related clusters were selected using the LASSO Cox model. (C) and (D) A visual representation of the SVM-RFE biological marker screening process. HB, hepatoblastoma; LASSO, least absolute shrinkage and selection operator; SVM-RFE, support vector machine recursive feature elimination.

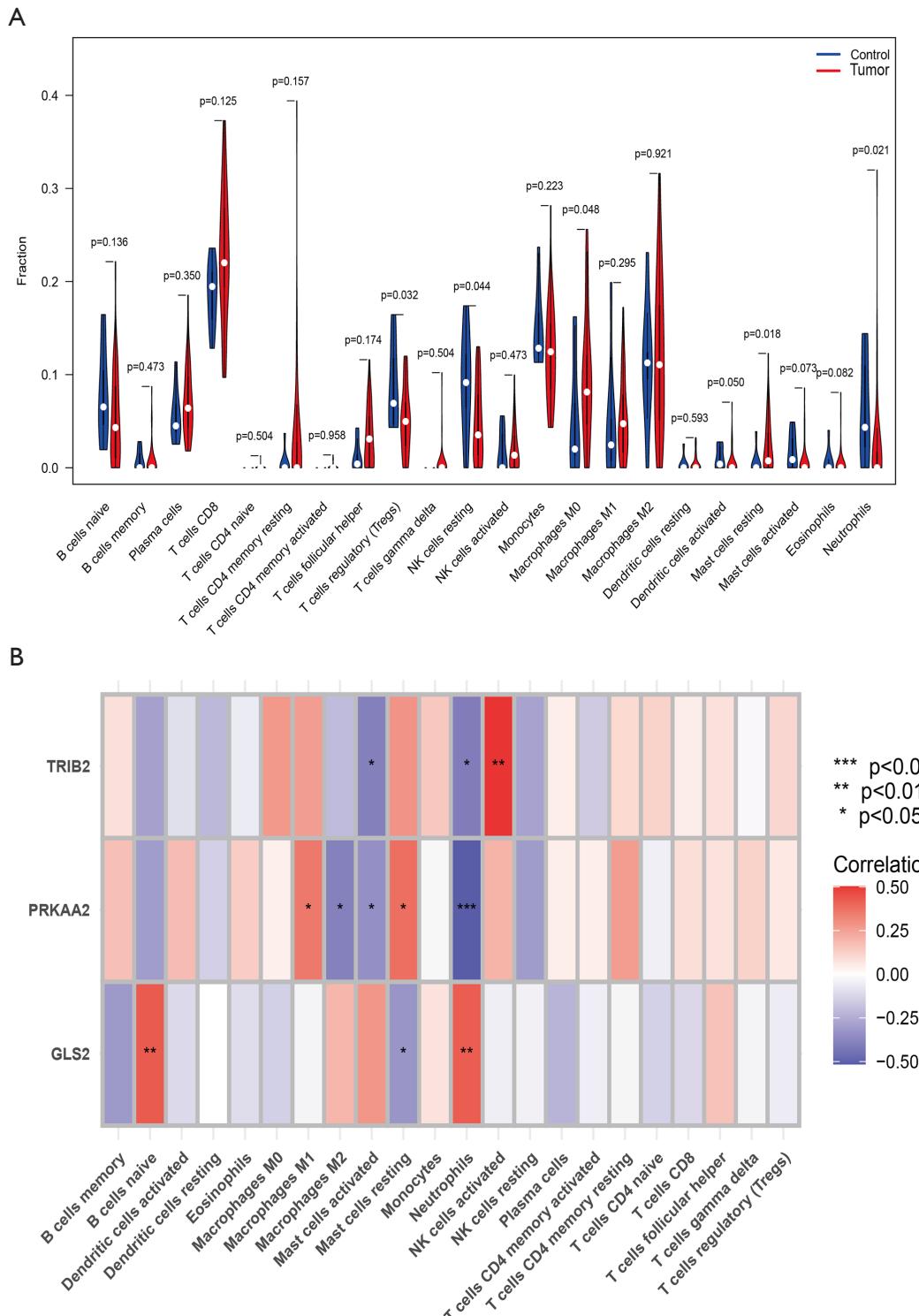


Figure S2 Analysis of immune infiltration level. (A) The differences in immunocytes' structural makeup between HB and noncancerous liver samples. Names of 22 types of infiltrating immune cells are shown in the bottom of the graph. (B) Correlation between 22 immune infiltration cells and three key genes. Gene names are on the left of the graph. *, P<0.05, **, P<0.01, and ***, P<0.001. The gradual colour change from red to blue indicates the changing process from positive correlation to negative correlation. HB, hepatoblastoma; PRKAA2, protein kinase AMP-activated catalytic subunit alpha 2; TRIB2, tribbles homolog 2; GLS2, liver-type glutaminase.

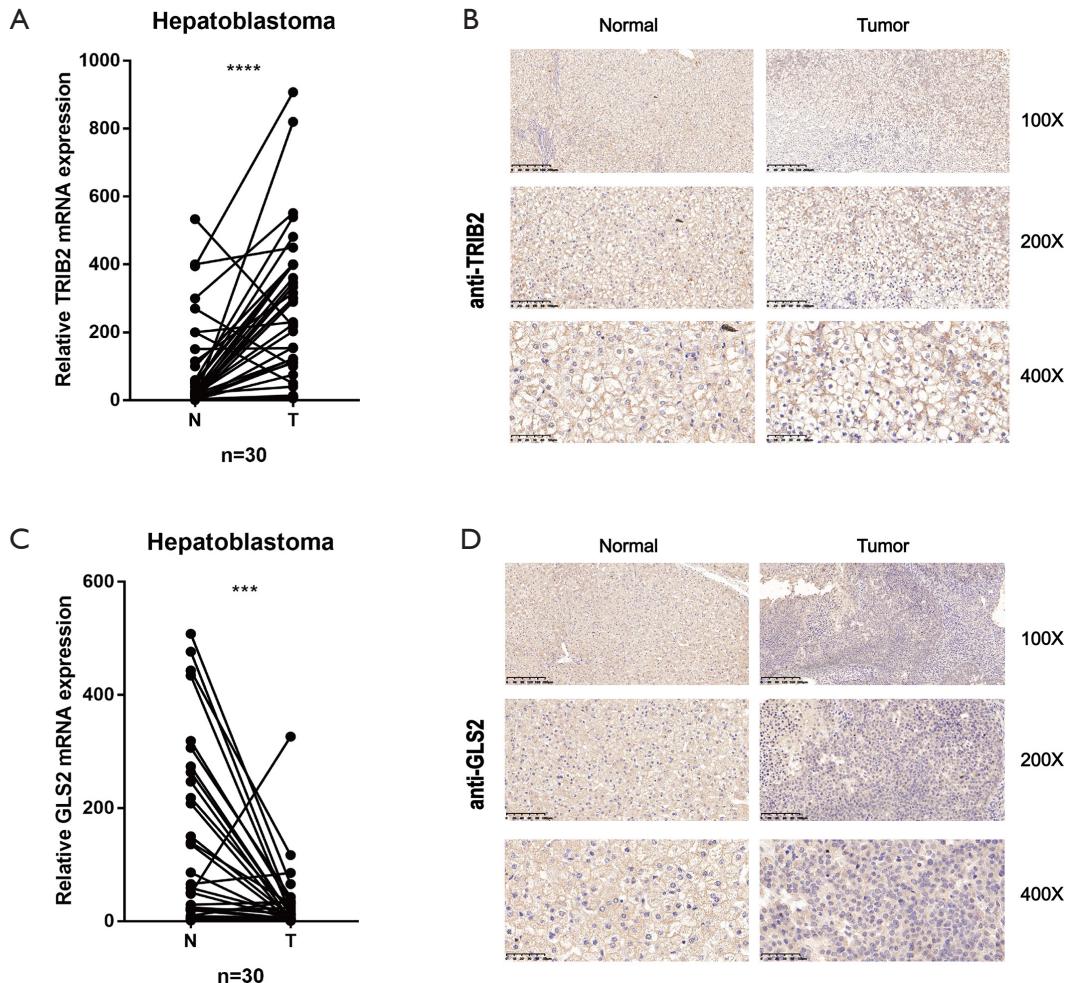


Figure S3 Expression of TRIB2 and GLS2 in paired samples. (A) Expression of TRIB2 mRNA in paired samples (****, $P<0.0001$ by paired t-test). (B) Analysis of TRIB2 expression in paired samples using immunohistochemistry. Scale bar represents $\times 100$, $\times 200$ and $\times 400$. (C) Expression of GLS2 mRNA in paired samples (***, $P=0.0004$ by paired t-test). (D) Analysis of GLS2 expression in paired samples using immunohistochemistry. Scale bar represents $\times 100$, $\times 200$ and $\times 400$. TRIB2, tribbles homolog 2; GLS2, liver-type glutaminase.

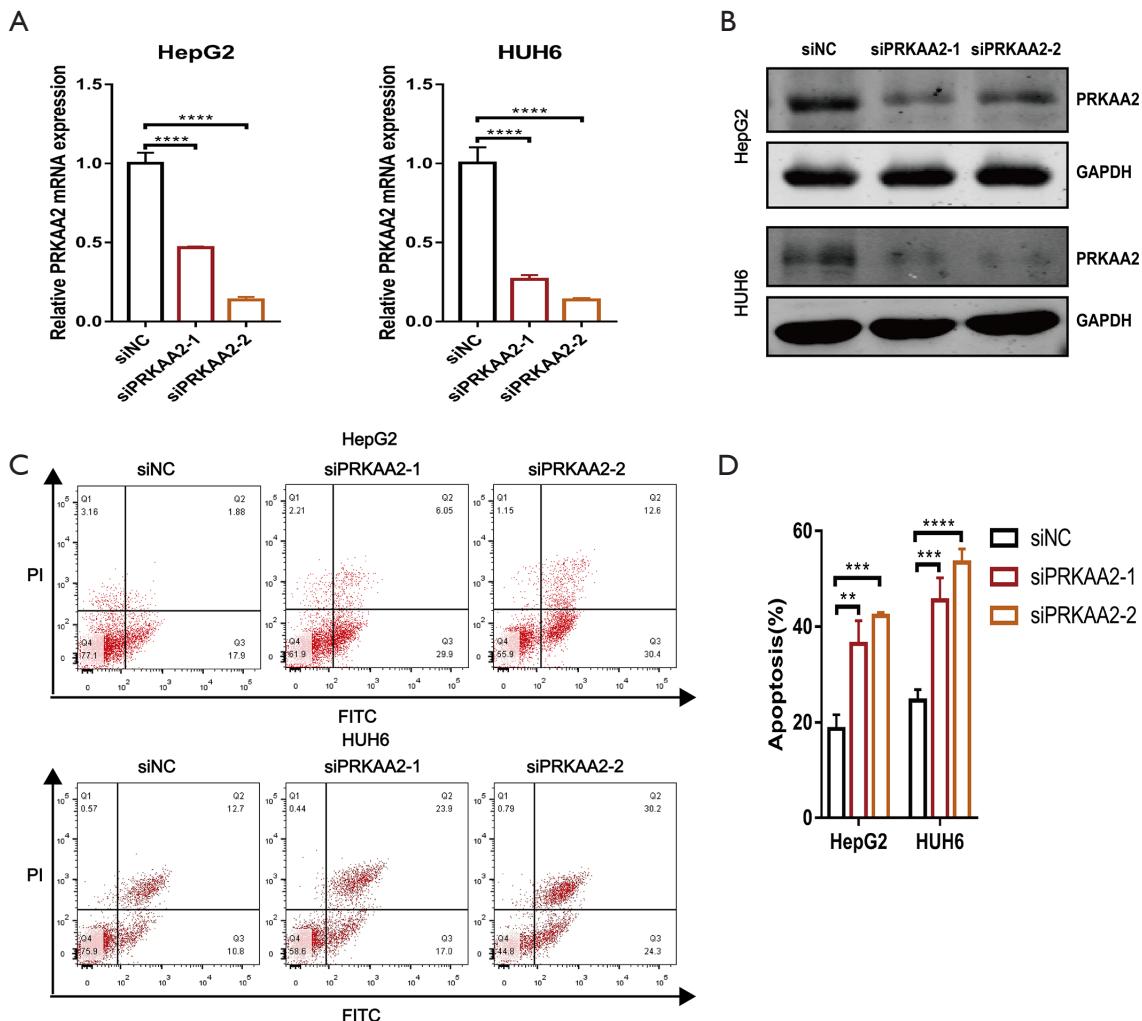


Figure S4 PRKAA2 plays a carcinogenic role in HB. (A) PRKAA2 mRNA expression in siPRKAA2 HB cells compared with the controls was measured. (****, $P<0.0001$ by *t*-test). (B) The protein level of PRKAA2 in siPRKAA2 HB cells compared with the controls was measured. (C) and (D) FACS assays were used to measure the apoptosis in HB cells with PRKAA2 knockdown compared with controls. **, $P<0.01$, ***, $P<0.001$, and ****, $P<0.0001$. HB, hepatoblastoma; PRKAA2, protein kinase AMP-activated catalytic subunit alpha 2.

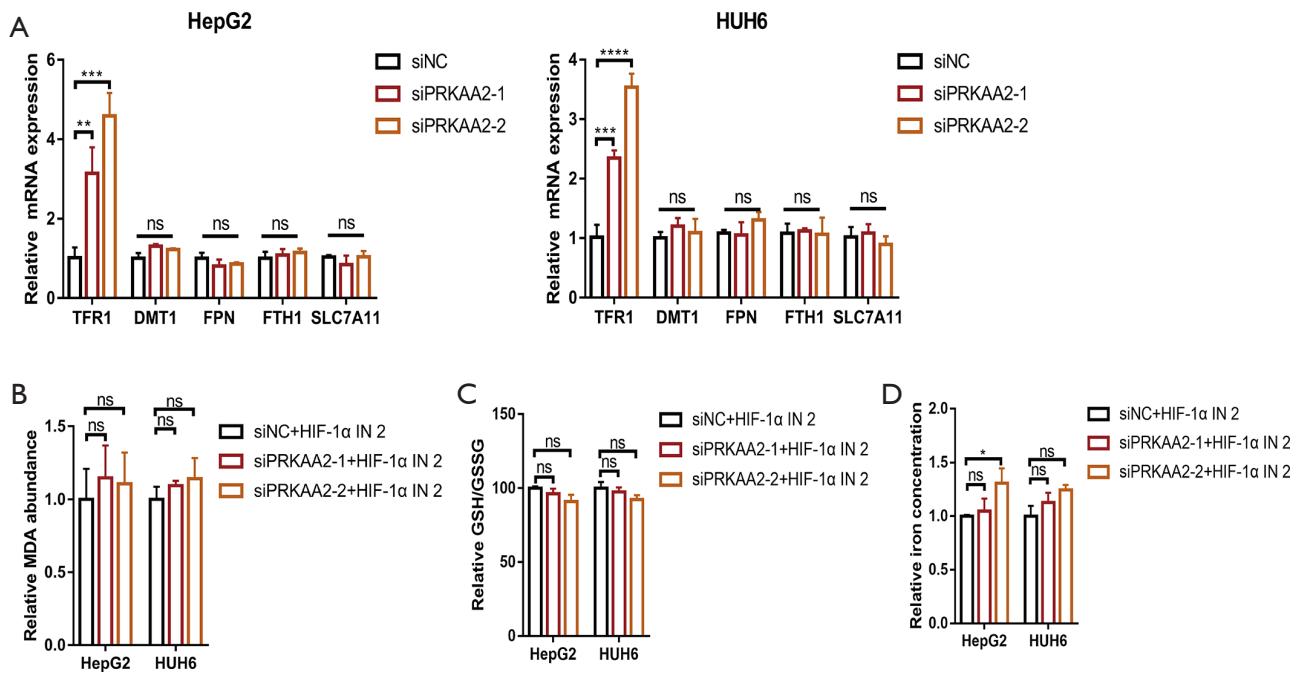


Figure S5 PRKAA2 regulates TFR1 through HIF-1 α . (A) Relative mRNA expression of several genes regulating ferroptosis in siPRKAA2 HB cells compared with the controls were measured. (B-D) The relative MDA concentration (B), GSH/GSSG ratio (C) and iron concentration (D) in HB cells, which were transfected with PRKAA2 siRNA, were detected using lipid peroxidation assay kits, GSH and GSSG assay kits and iron assay kits respectively after treatment with HIF-1 α -IN-2 (1 μ M) for 48 h. * $P<0.05$, **, $P<0.01$, ***, $P<0.001$, and ****, $P<0.0001$. ns, no significant difference. PRKAA2, protein kinase AMP-activated catalytic subunit alpha 2; TFR1, transferrin receptor 1; HIF-1 α , hypoxia-inducible factor 1 α ; MDA, malondialdehyde; GSH, glutathione; GSSG, glutathione oxidized.