

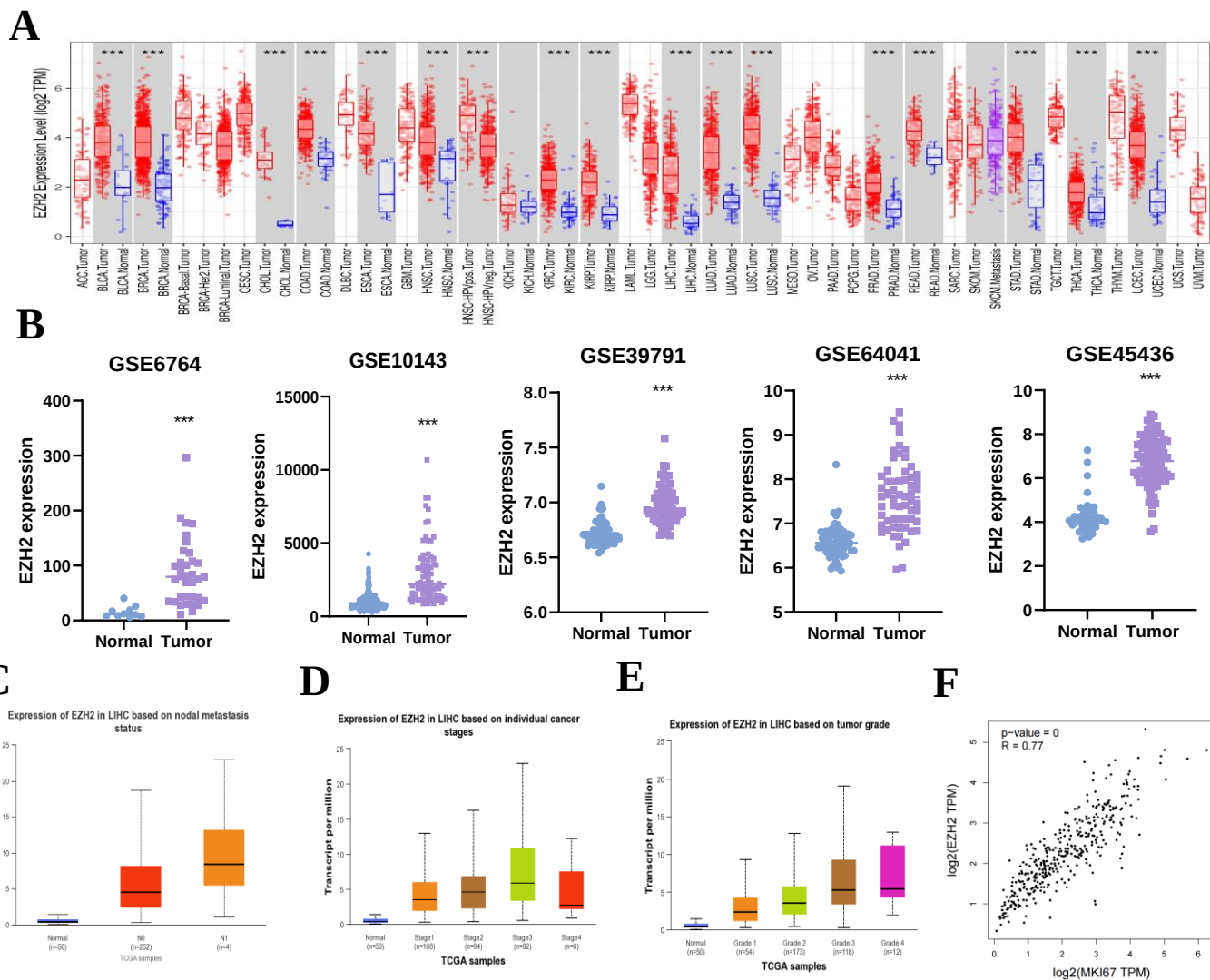


Fig S1. EZH2 expression is upregulated in HCC and predicts an unfavorable prognosis. (A) TIMMER2 database analysis of EZH2 expression in various tumors. (B) Expression of EZH2 in 5 HCC-related GEO datasets. (C) Expression of EZH2 in LIHC based on nodal metastasis status. (D) Expression of EZH2 in LIHC based on individual cancer stages. (E) Expression of EZH2 in LIHC based on tumor grade. (F) Spearman's correlation coefficient test showed the correlation between the expression of EZH2 and Ki-67 in hepatocellular carcinoma samples by the GEPIA database. ** $P < 0.01$; *** $P < 0.001$.

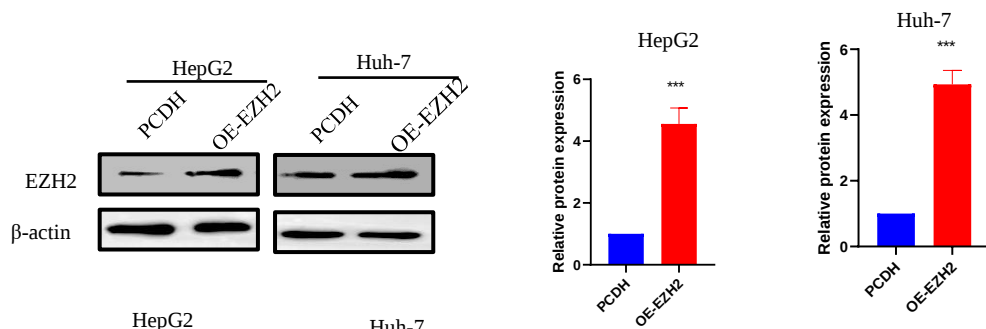
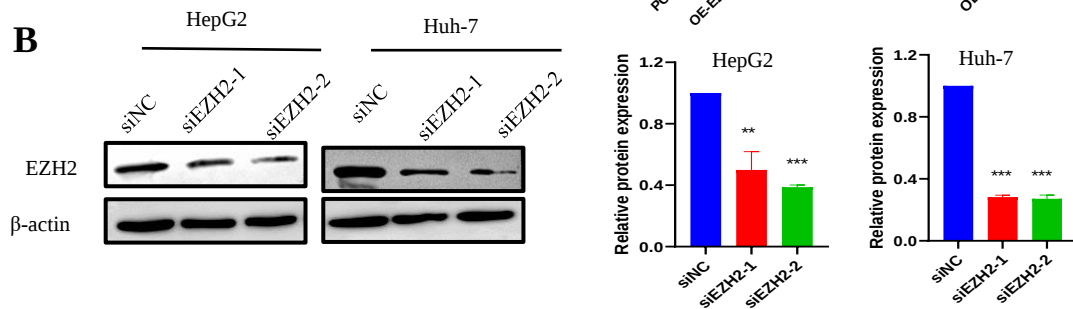
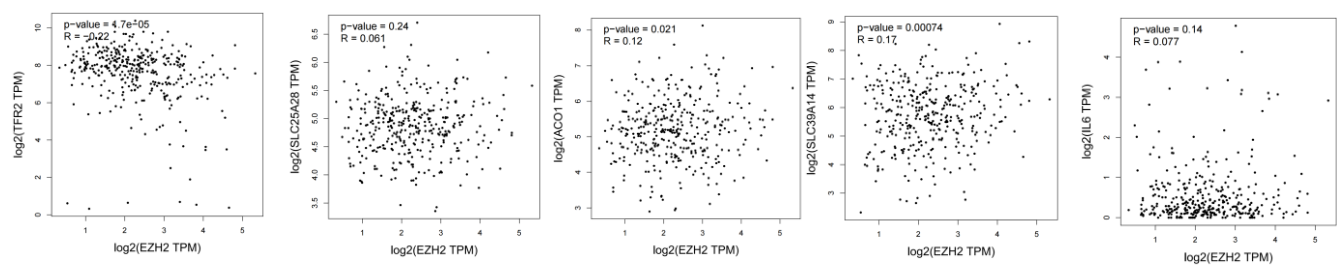
A**B**

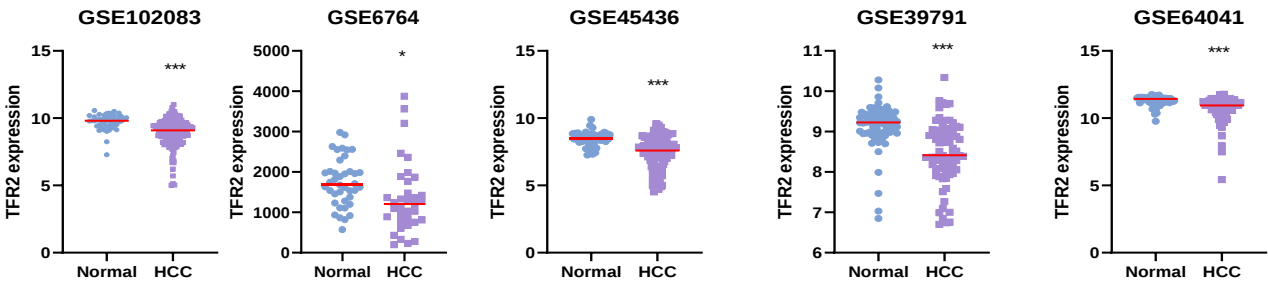
Fig.S2 Overexpression and knockdown efficiency of EZH2 in HepG2 and Huh-7 cell lines

(A). Transfection of EZH2 expression plasmid in HepG2 and Huh-7 cells, Western blot detection of EZH2 overexpression efficiency (B). Transfection of two types of EZH2 siRNAs in HepG2 and Huh-7 cells, Western blot detection of EZH2 overexpression efficiency. ** P < 0.01; *** P < 0.001.

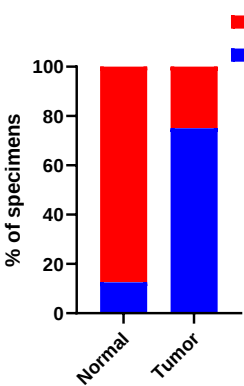
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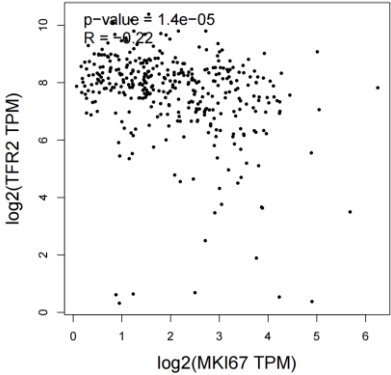
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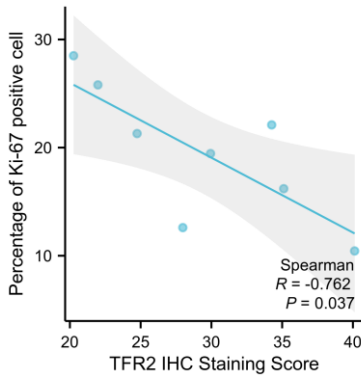
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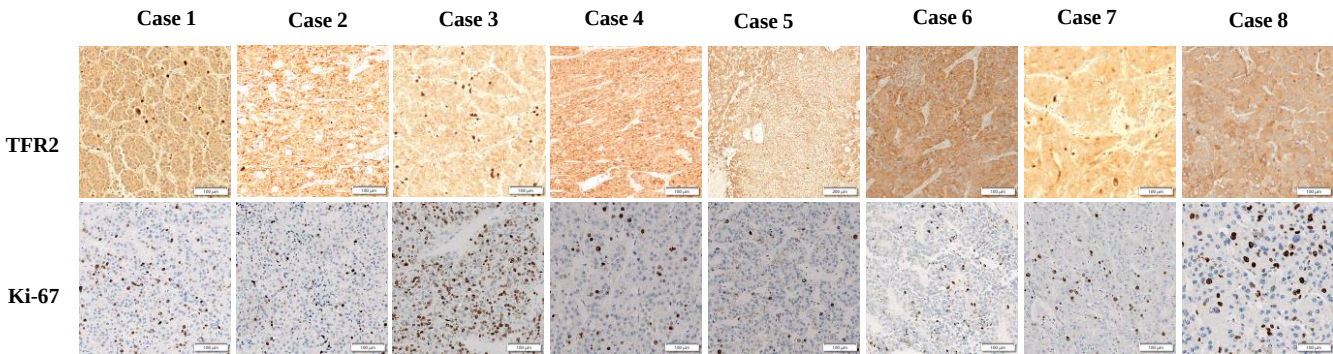
D



F



E



FigS3. Screening of EZH2 related genes and expression of TFR2 in HCC. (A) Correlation expression between EZH2 and TFR2, SLC25A28, ACO1, SLC39A14, and IL-6. (B) Expression of TFR2 in HCC-related GEO datasets. (C) Percentage of high expression of TFR2 in 8 pairs of HCC patients. (D) Spearman's correlation coefficient test showed the correlation between the expression of NRF2 and Ki-67 in hepatocellular carcinoma samples by the GEPIA database. (E). IHC detection of TFR2 and Ki-76 expression in 8 pairs of HCC patients. (F). The correlation between Ki-67 and EZH2 expression. * P<0.05; *** P<0.001.

