SUPPLEMENTARY FIGURES



Supplementary Figure 1. CBX8 positively correlates with the cell cycle signaling pathway. (A) Cell cycle-related gene mRNA levels in CBX8-knockdown Huh7 cells, as detected by q-RT-PCR.



Supplementary Figure 2. CBX8 interact with YBX1. (A–C) Correlation between CBX8 mRNA and ILF3, TFCP2 and UBE2S mRNA in TCGA cohort. (D) Huh7 Cells were transfected with Flag-CBX8 overexpression vector for 48 h. An IP assay, using anti-Flag antibody, was used to detect the binding of CBX8 and ILF3, TFCP2, UBE2S.







Supplementary Figure 3. CBX8 increase levels of CyclinD1 through YBX1. (A–B) Both protein and mRNA levels of CyclinD1 in CBX8overexpressing or YBX1-knock-down SK-Hep1 cells, as detected by western blotting and q-RT-PCR. (C) Protein levels of CyclinD1 in CBX8knock-down or YBX1-overexpressing Huh7 cells as detected by western blotting.



Supplementary Figure 4. CBX8 overexpression promotes cell proliferation. (A) Cell proliferation was evaluated by the CCK-8 assay. (B–C) Effect of CBX8 on cell proliferation, as measured by EDU assays *P < 0.05; **P < 0.01; ***P < 0.001.







D

Ε



Supplementary Figure 5. Knockdown of CBX8 dramatically decreases cell proliferation in vitro. (A–C) Cell proliferation was evaluated by the CCK-8 assay. (**D–E**) Effect of CBX8 on cell proliferation, as measured by EdU assays **P* < 0.05; ***P* < 0.01; ****P* < 0.001.



Supplementary Figure 6. Knockdown of CBX8 dramatically decreases cell proliferation in vivo (**A**) Representative images of tumors formed in nude mice injected subcutaneously with CBX8–silenced SK-Hep-1 cells. (**B**) Tumor weights (***P <0.001). (**C**) Tumors induced by CBX8 silencing in SK-Hep-1 cells (***P <0.001) showed markedly lower growth rates than control cells.



Supplementary Figure 7. CBX8 promotes HCC cell proliferation through YBX1. (A–D) Cell proliferation, as detected by EdU assays ***P*< 0.01; ****P* < 0.001.



Supplementary Figure 8. CBX8 expression in human cancers (**A**) Relative CBX8 mRNA expression determined by RNA sequencing in human cancers from TCGA data (<u>http://cancergenome.nih.gov/</u>) using the GCBI website (<u>https://www.gcbi.com.cn</u>).



Supplementary Figure 9. The prognostic value of CBX8 in HCC. (A–I) Stratified analysis showed the correlation of CBX8 expression and overall survival in indicated groups in HCC from TCGA data using the Kaplan Meier-plotter website (<u>http://kmplot.com/analysis/</u>).



Supplementary Figure 10. YBX1 expression is up-regulated in HCC and is correlated with prognosis. (A–B) Expression of YBX1 in the GSE14520 cohort1 (P < 0.001) and GSE14520 cohort2 (P < 0.05). (C, D) Kaplan-Meier analysis of the overall and disease-free survival in the TCGA cohort based on YBX1 expression.



Supplementary Figure 11. The prognostic value of YBX1 in HCC. (A–I) Stratified analysis showed the correlation of YBX1 expression and overall survival in indicated groups in HCC from TCGA data using the Kaplan Meier-plotter website (<u>http://kmplot.com/analysis/</u>).