

Table S1 Common miRNAs containing CHEK1-binding sequences predicted by miRDB, TargetScan, and mirWalk databases in HCC

Predicted targeted miRNA	Normal vs. tumor (P value)
hsa-miR-1273h-5p	N/A
hsa-miR-195	1.11E-16
hsa-miR-1286	N/A
hsa-miR-1251-5p	N/A
hsa-miR-3678-3p	4.96E-01
hsa-miR-4700-3p	4.20E-04
hsa-miR-4714-3p	N/A
hsa-miR-4755-3p	7.22E-01
hsa-miR-5093	N/A
hsa-miR-6734-3p	N/A
hsa-miR-6740-5p	N/A
hsa-miR-7151-3p	N/A
hsa-miR-1273h-3p	N/A
hsa-miR-4534	N/A
hsa-miR-15b-5p	1.37E-06
hsa-miR-6885-3p	N/A
hsa-miR-2467-3p	N/A
hsa-miR-16-5p	1.36E-03
hsa-miR-3156-3p	N/A

miRNA, microRNA; CHEK1, checkpoint kinase 1; HCC, hepatocellular carcinoma; N/A, not applicable.

Table S2 Detailed information on the top 5 TFs of CHEK1 DEGs

TF	Total	Expected	Hits	P value	FDR
V\$E2F_Q6	232	2.12	31	1.08E-27	3.95E-25
V\$E2F1_Q6	232	2.12	31	1.08E-27	3.95E-25
V\$E2F_Q4	234	2.14	31	1.42E-27	3.95E-25
V\$E2F4DP1_01	239	2.19	30	5.70E-26	1.19E-23
V\$E2F_02	235	2.15	29	6.85E-25	7.16E-23

TFs, transcriptional factors; CHEK1, checkpoint kinase 1; DEG, differentially expressed gene; FDR, false discovery rate.

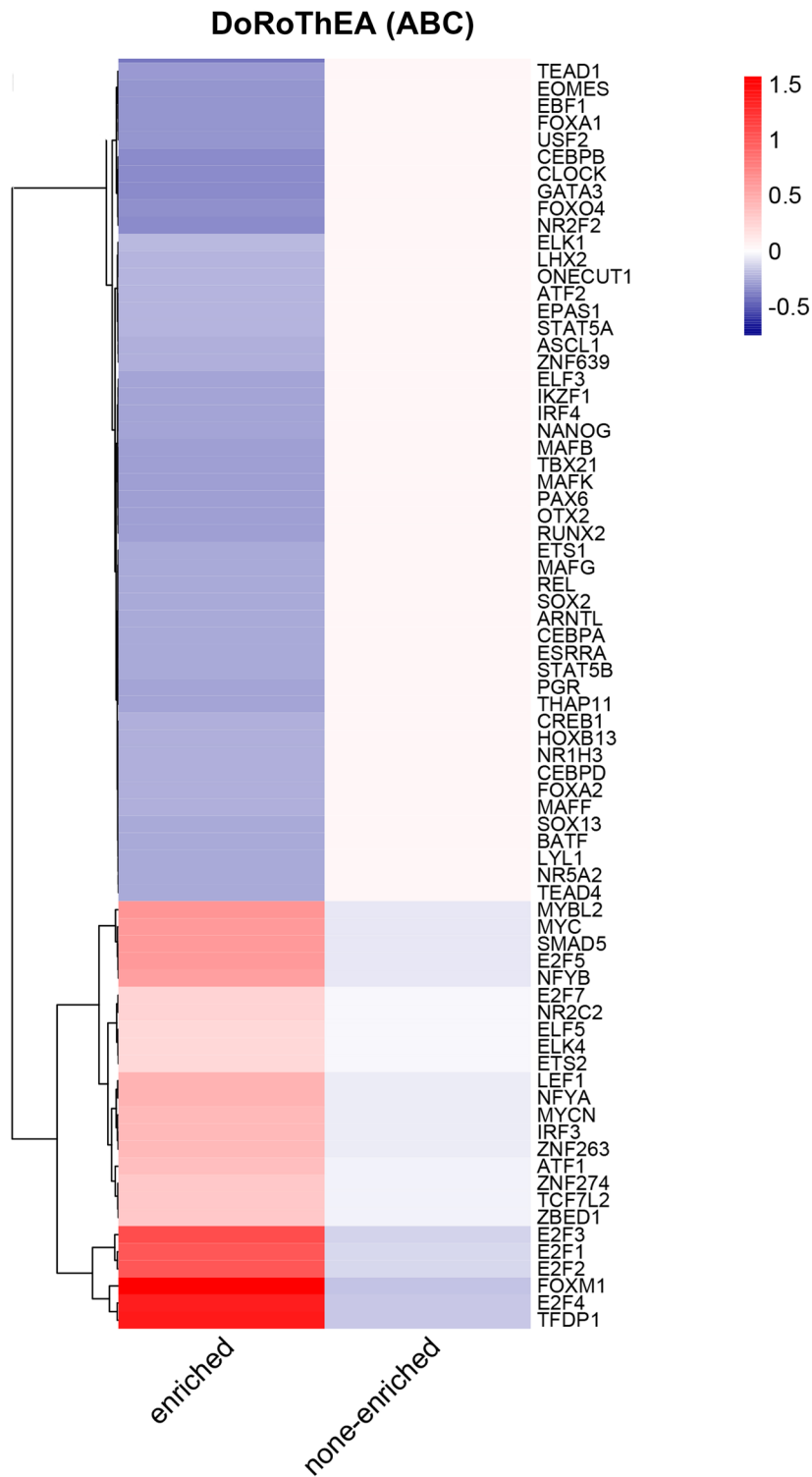


Figure S1 TF activity analysis on a representative single-cell RNA-sequence dataset. Heatmap of selected TF activities inferred from DoRoThEA on single-cell RNA-sequence data in GSE151530. DoRoThEA, Discriminant Regulon Expression Analysis; TF, transcriptional factor.

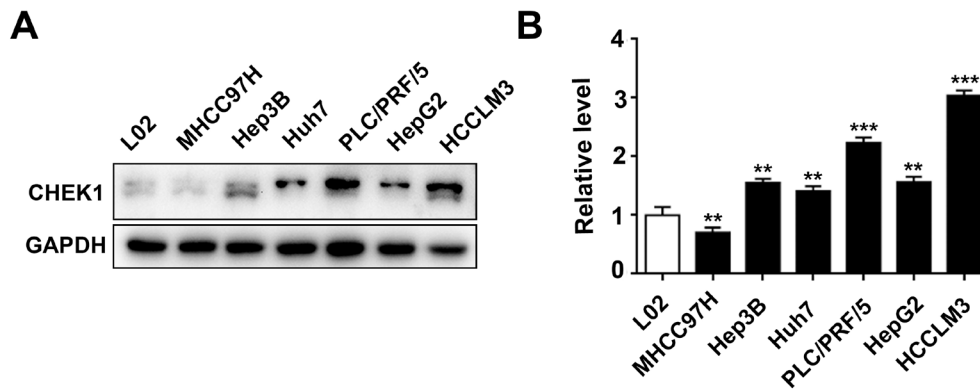


Figure S2 Protein levels of CHEK1 in a normal liver cell and 6 HCC cell lines. (A) Representative Western blotting pattern of CHEK1 in a normal liver cell and 6 HCC cell lines. (B) The relative intensity of CHEK1 normalized to GAPDH was calculated. **, $P < 0.01$; ***, $P < 0.001$. HCC, hepatocellular carcinoma; CHEK1, checkpoint kinase 1; GAPDH, glyceraldehyde 3-phosphate dehydrogenase.

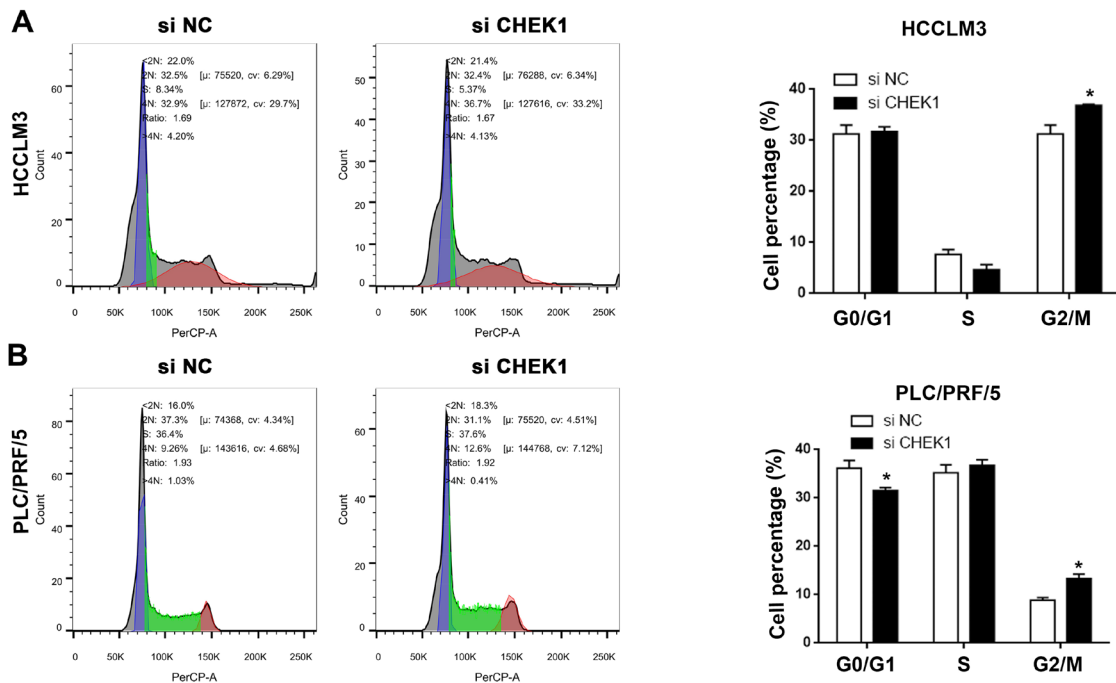


Figure S3 Flow cytometry. Cell cycle distribution of HCCLM3 (A) and PLC/PRF/5 (B) cells. *, $P < 0.05$. NC, negative control; CHEK1, checkpoint kinase 1.