

Supplementary materials

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1. Supplementary Tables

Table S1. Primers for qRT-PCR

Gene names	Primer sequences (5' to 3')
human CTNNB1	5'-AGCTTCCAGACACGCTATCAT-3' (F)
	5'-CGGTACAACGAGCTGTTTCTAC-3' (R)
human CCL4	5'- CTGTGCTGATCCCAGTGAATC-3' (F)
	5'- TCAGTTCAGTTCCAGGTCATACA-3' (R)
human CCL5	5'- CCAGCAGTCGTCTTTGTCAC -3'(F)
	5'- CTCTGGGTTGGCACACACTT -3' (R)
human CXCL12	5'- ATTCTCAACACTCCAAACTGTGC -3' (F)
	5'- ACTTTAGCTTCGGGTCAATGC-3' (R)
human β -actin	5'-CACCATTGGCAATGAGCGGTTC-3' (F)
	5'-AGGTCTTTGCGGATGTCCACGT-3' (R)
mouse Ctnnb1	5'-ATGGAGCCGGACAGAAAAGC-3' (F)
	5'-CTTGCCACTCAGGGAAGGA-3' (R)
mouse Cxcr4	5'-GAAGTGGGGTCTGGAGACTAT-3' (F)
	5'-TTGCCGACTATGCCAGTCAAG-3' (R)
mouse β -actin	5'-GGCTGTATTCCCCTCCATCG-3' (F)
	5'-CCAGTTGGTAACAATGCCATGT-3' (R)

Table S2. Primers for promoter regions of CXCL12

Location from TSS	Primer sequences (5' to 3')
-1200bp to -800bp	GGAGCCTGAGAAGGTCAAAG
	GGCGCTTTAGAGGGGAGA
-800bp to -400bp	ACTGCAAAGACGGGTCTCAT
	GATGGCGGGAAGTGAATG
-400bp to 0bp	TCCGTGGGAAGAGTTTTCTG
	GGACGGGAGATTCAATGAGA

Table S3. Target sequences of siRNAs against CTNNB1

Gene names	Target sequences (5' to 3')
Human CTNNB1	Sense: 5'-GUAAUAAGCCGGCUAUUGU-3'
	Antisense: 5'-ACAAUAGCCGGCUUAUUAC-3'
Mouse Ctnnb1	Sense: 5'-GCAGAAUACAAAUGAUGUA-3'
	Antisense: 5'-UACAUCAUUUGUAUUCUGC-3'

2. Supplementary Figures

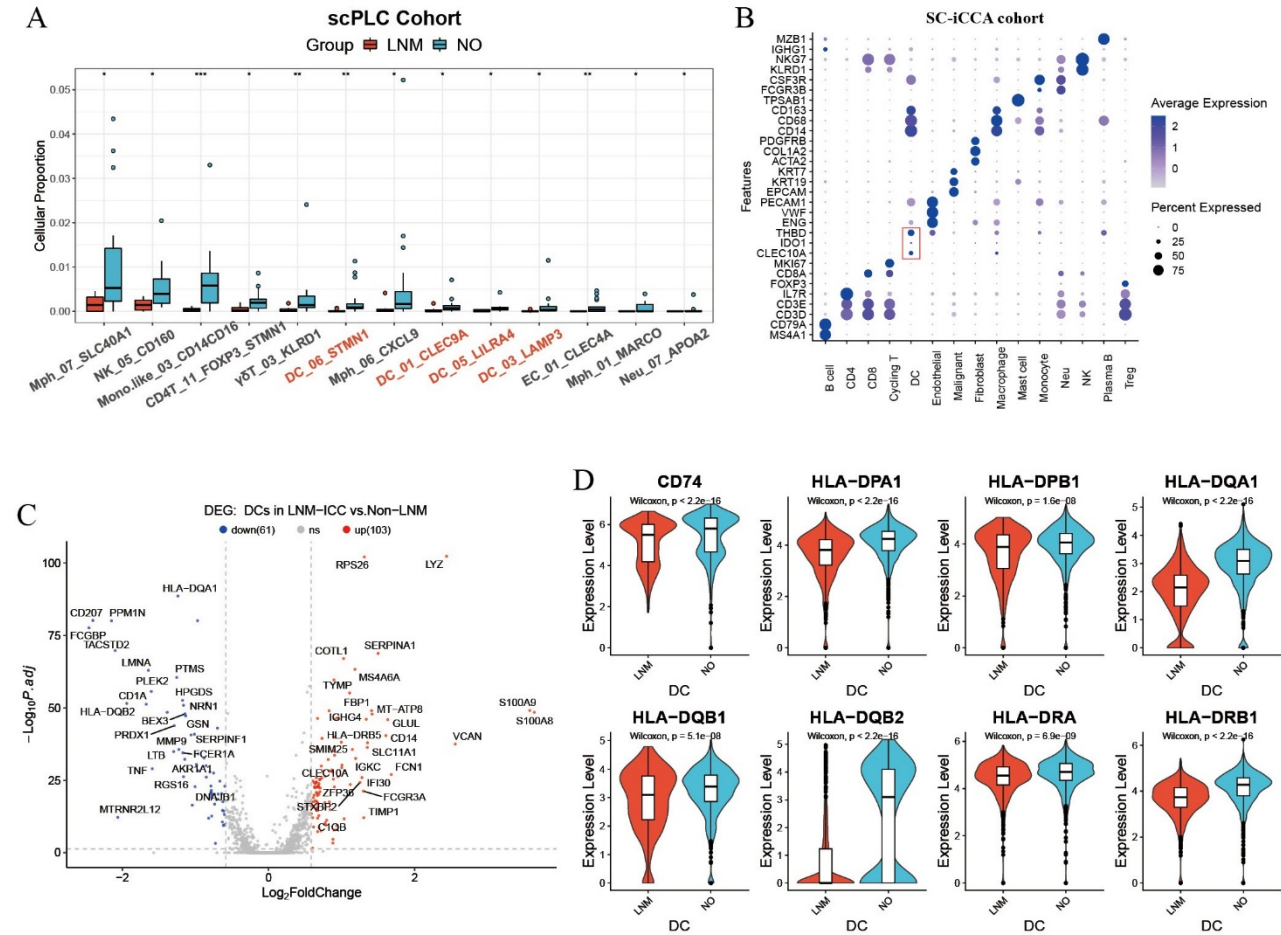
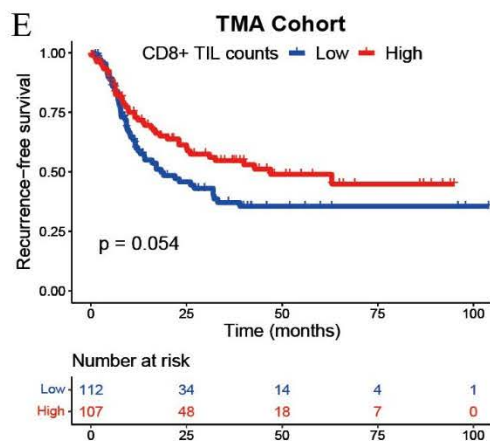
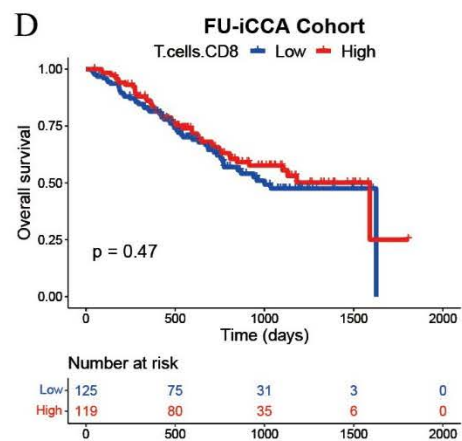
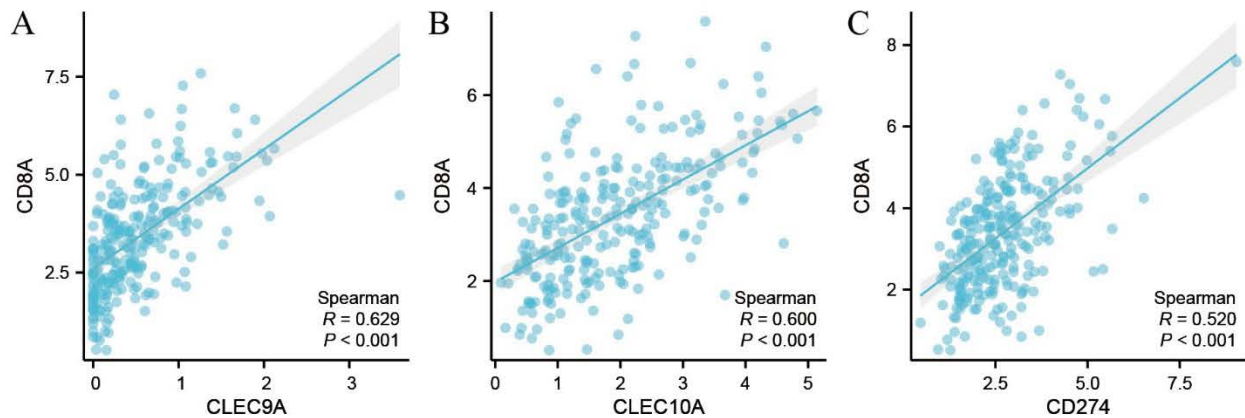


Figure S1. scRNA-seq analysis of cell type fractions between ICC samples with or without LNM. (A) Boxplots showing the fractions of differentially distributed cell subclusters identified in scPLC cohort. (B) Dot plot showing the expression pattern of marker genes of indicated cell types in SC-iCCA cohort. (C) Volcano plot showing differentially expressed genes of DCs between ICC samples with or without LNM. (D) Violin plots showing the expression of MHC-II related molecules (CD74, HLA-DP, HLA-DQ, and HLA-DR) in DCs between ICC samples with or without LNM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



F **LMVD (LYVE-1)**

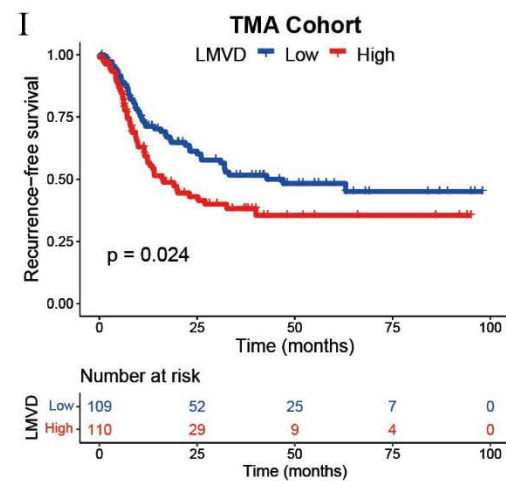
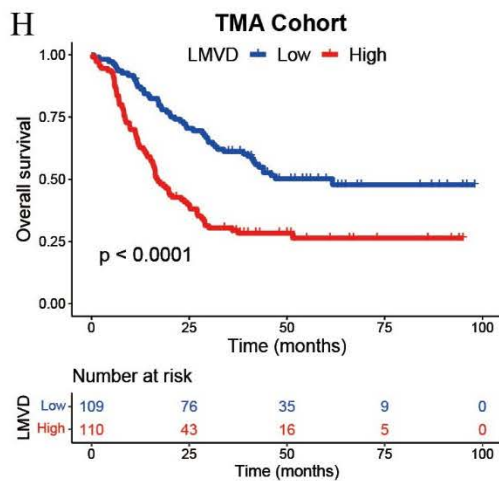
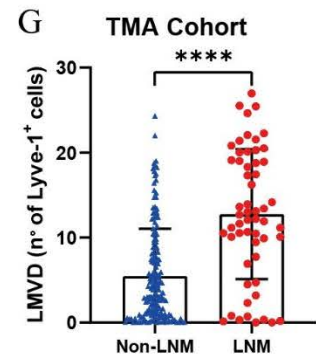
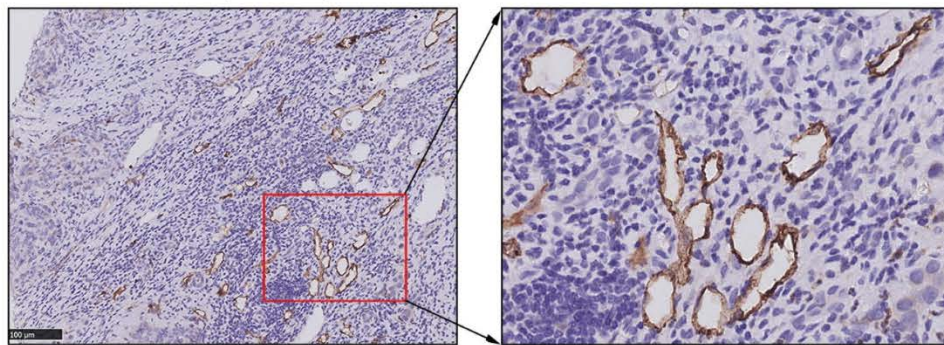


Figure S2. Correlation of CD8A transcripts with DC marker genes and survival analysis of CD8⁺ T cells. Spearman correlation analysis of CD8A transcripts with conventional DC marker genes CLEC9A (A), CLEC10A (B) as well as PD-L1 (C) in FU-iCCA cohort. Survival analysis of ICC patients grouped by infiltration levels of tumor-infiltrating CD8⁺ T cells in FU-iCCA cohort (D) and TMA cohort (E). Representative IHC staining images of anti-LYVE-1 (F) and quantification of LMVD (G). Kaplan-Meier survival curves for OS (H) and RFS (I) of ICC patients grouped by LMVD in TMA cohort. LMVD, lymphatic micro-vessel density. ****p < 0.0001.

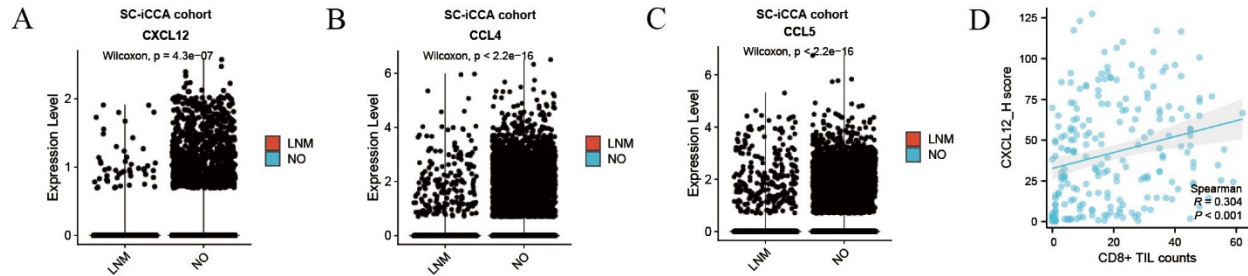


Figure S3. Defective production of chemokines in ICC malignant cells with LNM. Expression levels of chemokines CXCL12 (A), CCL4 (B), and CCL5 (C) in ICC single malignant cells with or without LNM in SC-iCCA cohort. (D) Spearman correlation of CXCL12 H-score with cell counts of CD8⁺ TILs in TMA cohort.

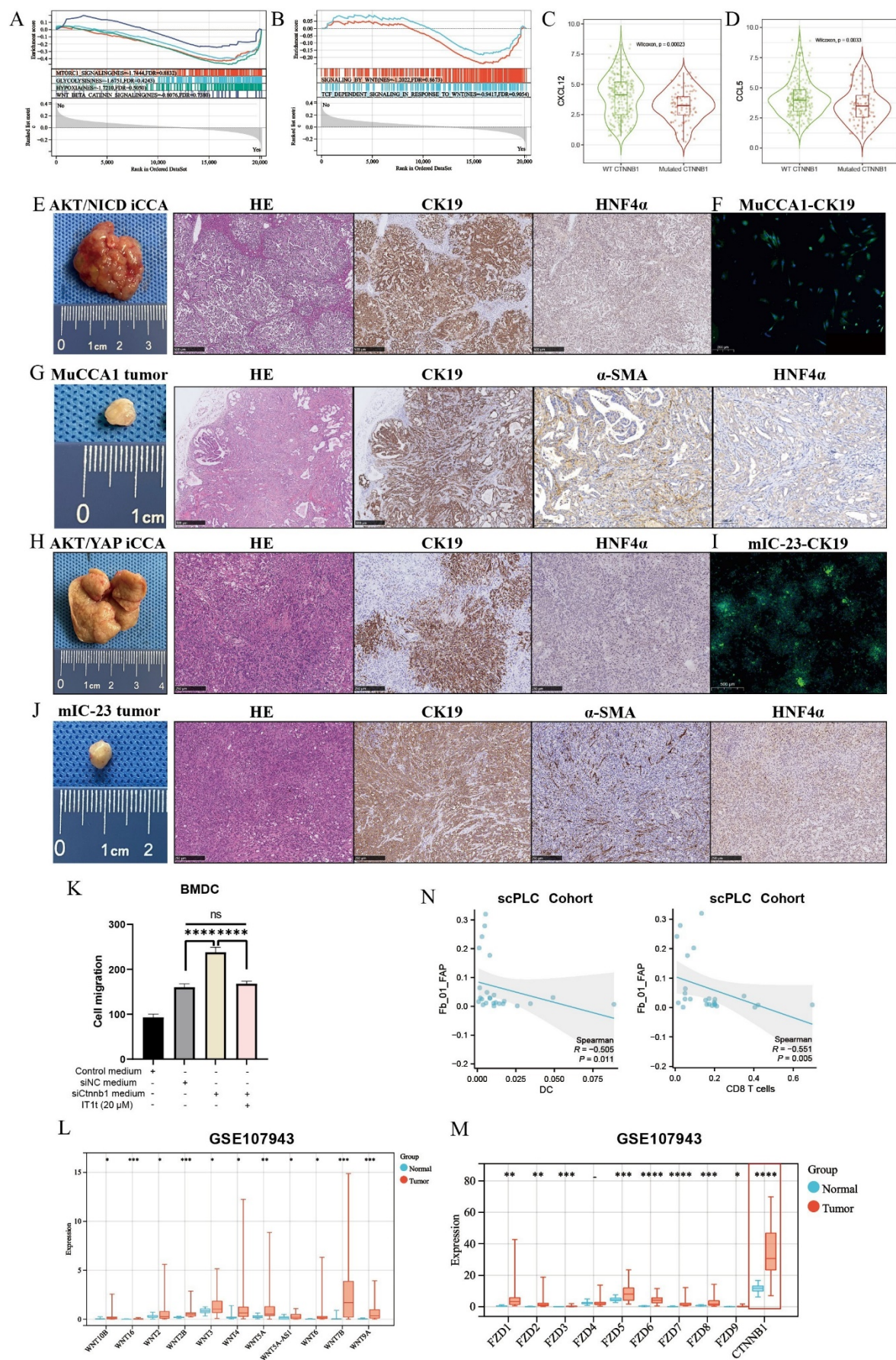


Figure S4. β -catenin activation impairs DC recruitment by suppressing CXCL12 expression.

Gene set enrichment analysis (GSEA) of differential Hallmark (A) and REACTOME (B) gene sets based on RNA-seq data between LNM and non-LNM ICC samples in FU-iCCA cohort. Expression of CXCL12 (C) and CCL5 (D) in human CTNNB1-wild type or mutant HCC samples from TCGA-LIHC cohort. (E) Gross liver images, H&E staining and IHC staining for CK19 and HNF4 α of liver sections from AKT/NICD-driven murine ICCs (scale bar: 500 μ m). (F) IF staining of CK19 in MuCCA1 cells (scale bar: 200 μ m). (G) Gross images, H&E staining and IHC staining for CK19, α -SMA and HNF4 α of subcutaneous tumor tissues derived from MuCCA1 cells. (H) Gross liver images, H&E staining and IHC staining for CK19 and HNF4 α of liver sections from AKT/YAP-driven murine ICCs (scale bar: 250 μ m). (I) IF staining of CK19 in mIC-23 cells (scale bar: 500 μ m). (J) Gross images, H&E staining and IHC staining for CK19, α -SMA and HNF4 α of subcutaneous tumor tissues derived from mIC-23 cells (scale bar: 250 μ m). (K) Trans-well migration assay of BMDCs attracted by condition medium and siRNA-treated mIC-23 cell supernatants, with or without IT1t dihydrochloride (20 μ M) for 24h. (L-M) Expression levels of indicated WNT ligands and FZD receptors, as well as CTNNB1 in human ICC samples compared with nontumorous surrounding liver tissues based on the RNA-seq dataset GSE107943. (N) Spearman correlation analysis between Fb_01_FAP and the infiltration of DC and CD8 T cells in scPLC Cohort.

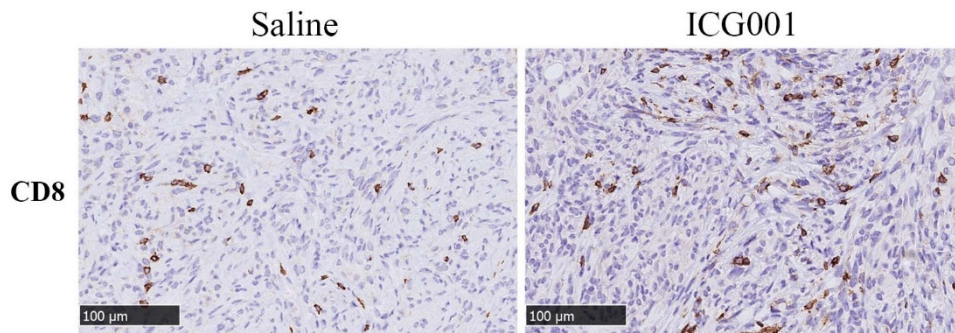


Figure S5. β -catenin inhibitor ICG-001 promoted intra-tumoral CD8⁺ T cell infiltration. Representative IHC staining images of CD8⁺ T cells in mIC-23 footpad tumors from indicated groups.

3. Original western blots

Figure 4F

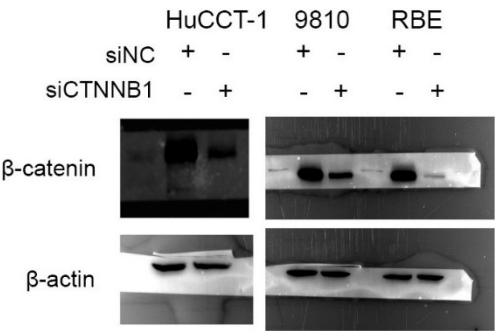


Figure 4L

