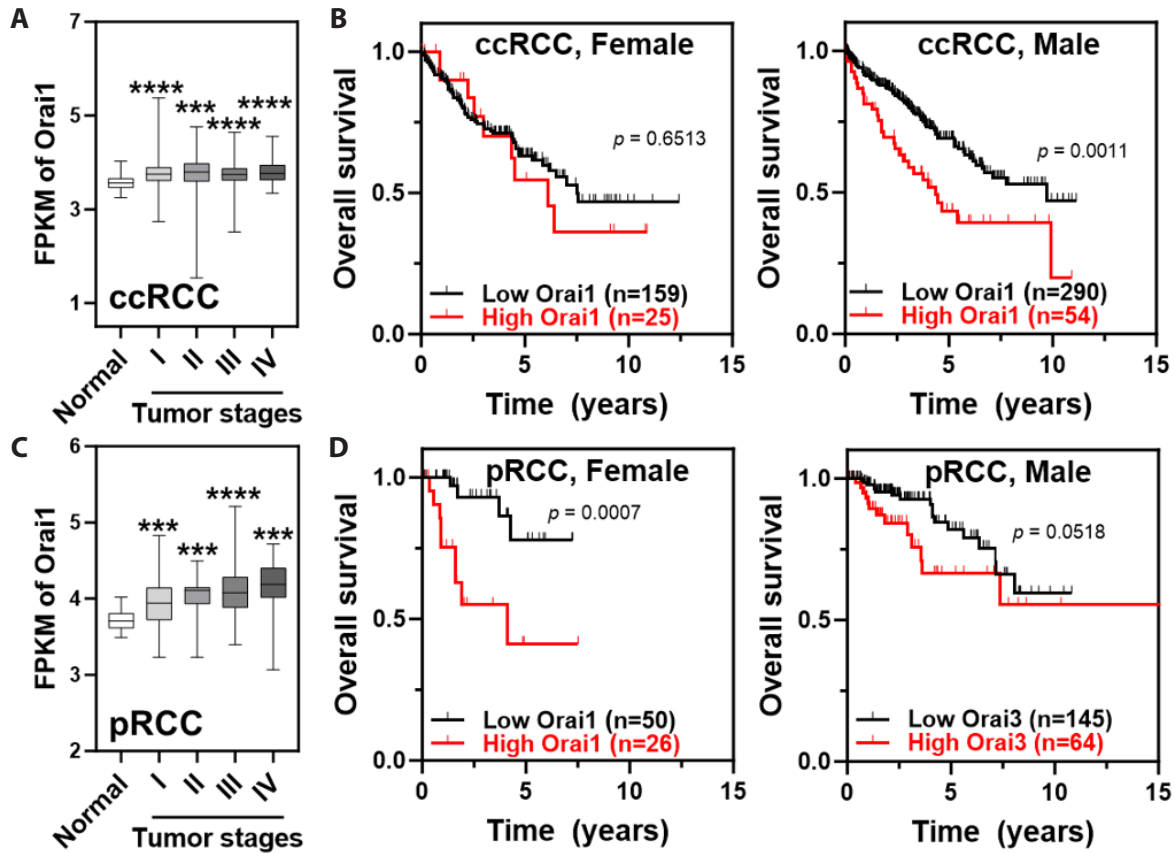
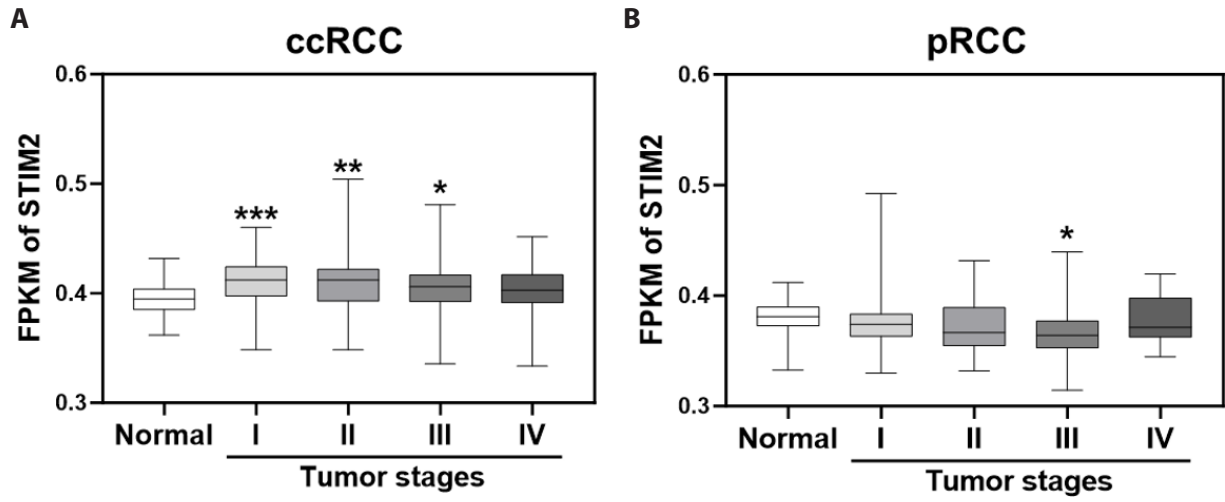


**Supplementary Table 1. List of human primer sequences used for PCR**

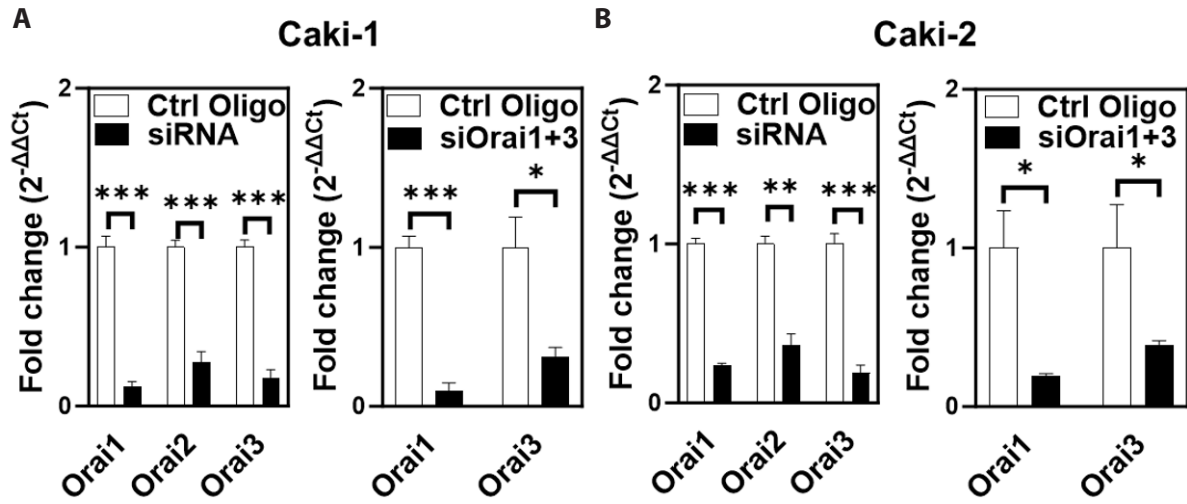
Gene (Accession no.)		Primer sequence (5' to 3')	Size (bp)
18s (NR_145820.1)	Forward	AACCCGTTGAACCCATT	149
	Reverse	CCATCCAATCGGTAGTAGCG	
Orai1 (NM_032790.4)	Forward	TTGAGCCGCGCCAAGCTTAAA	72
	Reverse	CATTGCCACCATGGCGAAGC	
Orai2 (NM_001126340.3)	Forward	AAGTGCTTGGATGCGGTGCTG	96
	Reverse	GGAGCCAGGCAGGTCATTTATACG	
Orai3 (NM_152288.3)	Forward	TCAGCCGGGCCAAGCTCAAA	71
	Reverse	CATGGCCACCATGGCGAAGC	
STIM1 (NM_001277961.3)	Forward	GTACACGCCCCAACCCCTGCT	97
	Reverse	AGGCTAGGGGACTGCATGGACA	
STIM2 (NM_001169118.2)	Forward	TGGACCTCTAACACGCCACCT	100
	Reverse	CTGCGTATAAGCAAACCAGCAGCC	



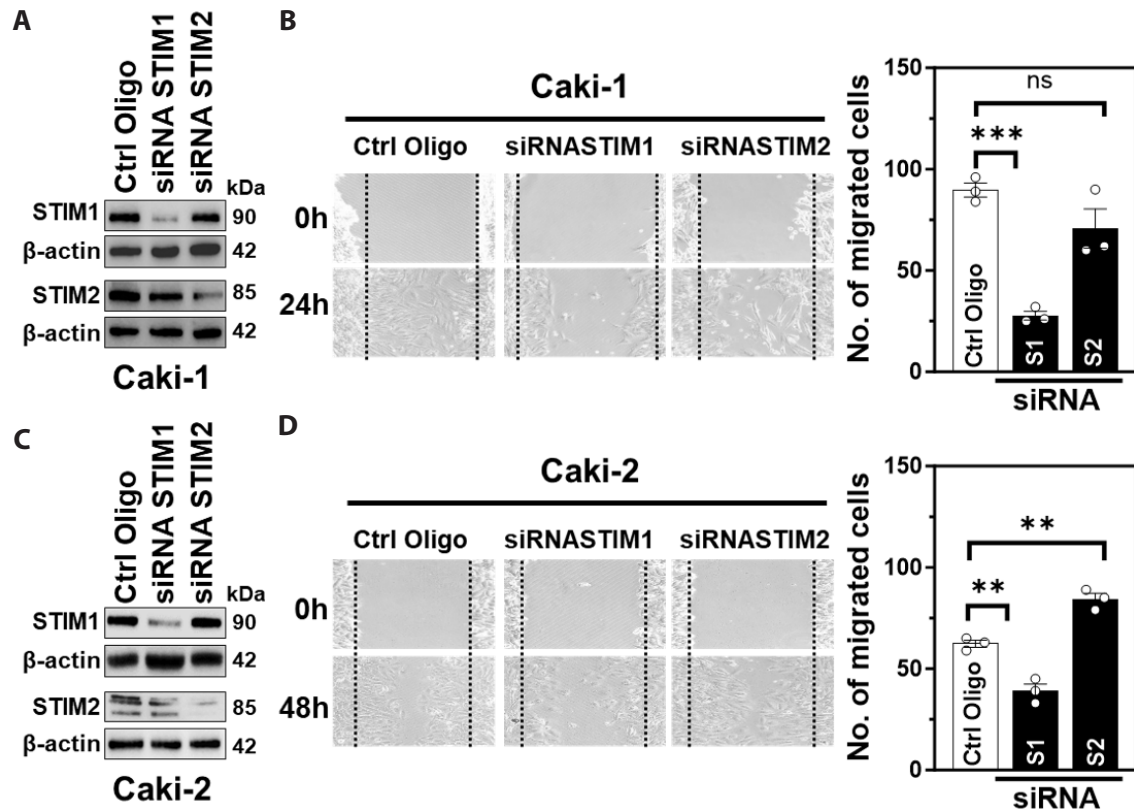
**Supplementary Fig. 1. Prognostic impact of Orai1 expression in renal cell carcinoma (RCC) subtypes.** (A, C) FPKM for Orai1 according to normal and RCC grades (Stage I, II, III, and IV) in clear cell RCC (ccRCC) and papillary RCC (pRCC), respectively. Box whisker plots express the minimum, median, and maximum values of FPKM (expressed as  $\log(\text{expr} + 1)$ ), where FPKM was adjusted using a scaling factor instead of total mapped reads to remove a million units. \*\*\* $p \leq 0.001$ , \*\*\*\* $p \leq 0.0001$  of one-way ANOVA (normal vs. tumor stages). (B, D) Kaplan-Meier survival analysis comparing females (left) and males (right) in the low and high mRNA levels of Orai1 in ccRCC and pRCC, respectively. The cut-off value for Orai1 in ccRCC is 11.4, and in pRCC is 12.16.



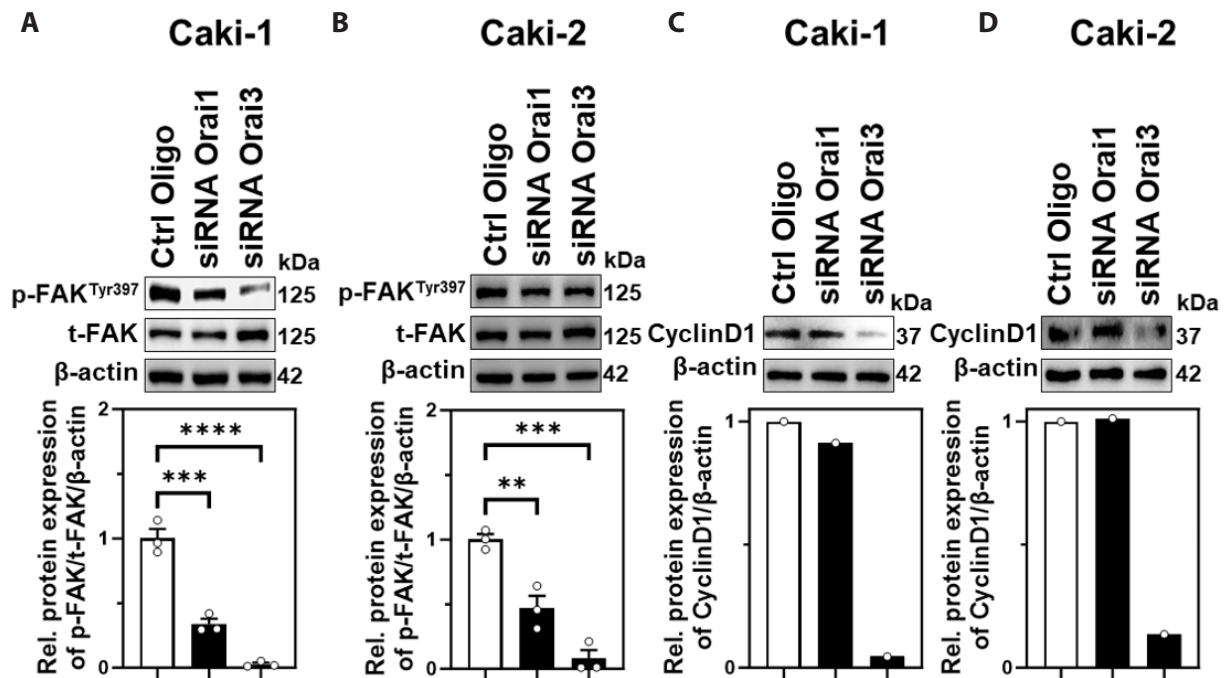
**Supplementary Fig. 2. RNAseq-based gene expression values (FPKM) for STIM2 according to normal and renal cell carcinoma (RCC) grades (Stage I, II, III, and IV) in (A) clear cell RCC (ccRCC) and (B) papillary RCC (pRCC).** Box whisker plots are expressed in minimum, median, and maximum. \* $p \leq 0.05$ , \*\* $p \leq 0.01$ , and \*\*\* $p \leq 0.001$  of one-way ANOVA (normal vs. tumor stages).



**Supplementary Fig. 3.** Real-time PCR was carried out to assess the knockdown efficiency of siRNA targeting Orai1-3 each (left) and Orai1+3 (right) in (A) Caki-1 and (B) Caki-2, respectively. Bar graphs expressed as mean  $\pm$  S.E.M. analyzed with Student's t-test. \* $p \leq 0.05$ , \*\* $p \leq 0.01$ , \*\*\* $p \leq 0.001$ .



**Supplementary Fig. 4. Regulation of migration by STIM1 and STIM2 in Caki-1 and -2.** (A, C) Western blotting was carried out to assess the knock-down efficiency of siRNA targeting STIM1 and STIM2 in Caki-1 and -2, respectively.  $\beta$ -actin was used as a loading control. (B, D) Representative images (left) and the number of migrated cells (right) demonstrate the impact of STIM1 (S1) and STIM2 (S2) silencing on cell migration in Caki-1 and -2, respectively. Data are expressed as mean  $\pm$  S.E.M. and analyzed with one-way ANOVA (B, D). ns., not significant. \*\* $p \leq 0.01$ , \*\*\* $p \leq 0.001$ . All experiments were performed three times with similar results.



**Supplementary Fig. 5. Orai1 and Orai3 are involved in renal cell carcinoma (RCC)'s focal adhesion and cell proliferation.** (A, B) Western blot analysis of phosphorylated FAK (p-FAK<sup>Tyr397</sup>) and total FAK (t-FAK), and (C, D) Cyclin D1 in Caki-1 and -2 cells following siRNA knockdown of Orai1 or Orai3. β-actin was used as a loading control. Bar graphs represent the mean ± S.E.M. of relative protein expression normalized to the control oligo (Ctrl Oligo). Experiments in (A) and (B) were performed three times with similar results and analyzed using one-way ANOVA; \*\*p ≤ 0.01, \*\*\*p ≤ 0.001, \*\*\*\*p ≤ 0.0001 (Ctrl Oligo vs. siRNA Orai1 or Orai3).