

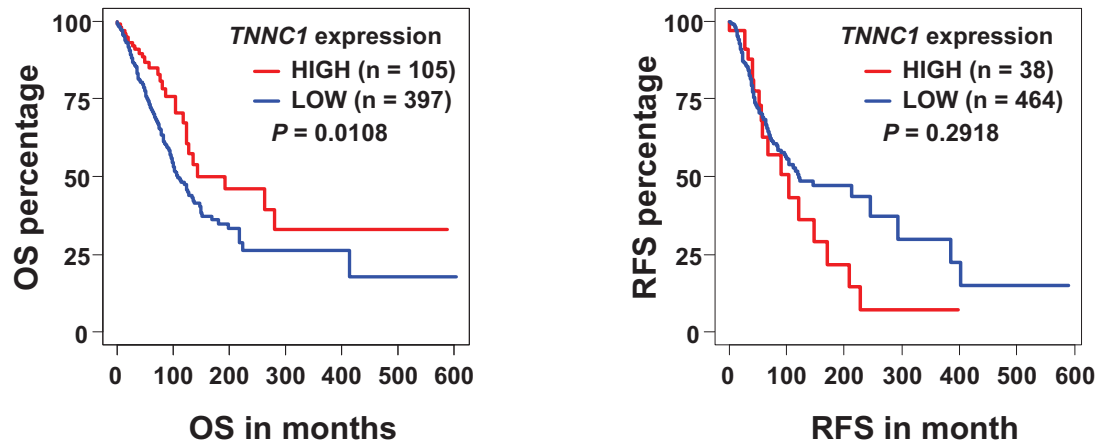


Supplementary Table S1. Sequences of KRAS siRNAs used in RNA interference

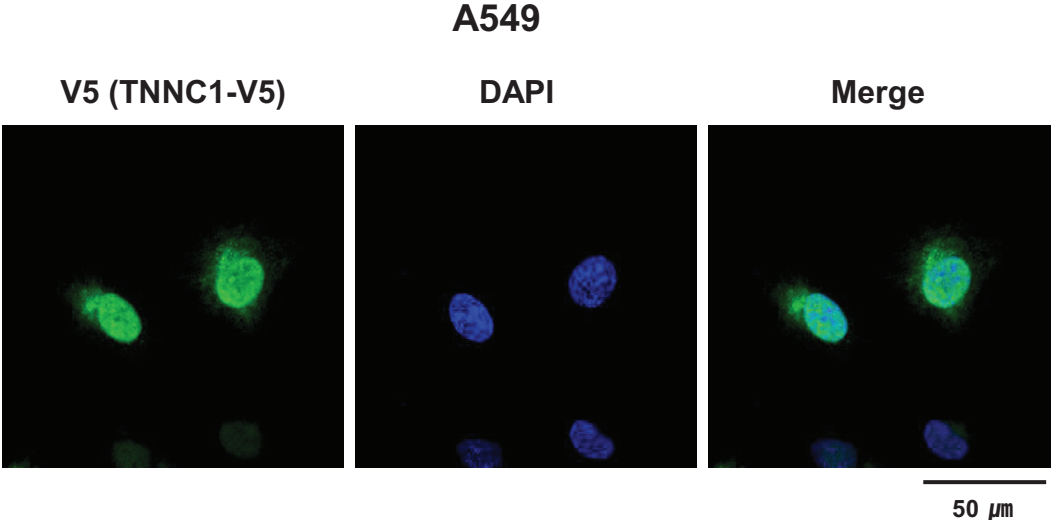
Name	Target sequence (sense strand, 5'- to 3'-)
siKRAS #1	GTGGACGAATATGATCCAACA
siKRAS #2	AAGGAGAATTTAATAAAGATA
siTNNC#1	UCAUGAAGGGUGUGGAGUA
siTNNC#2	CGGUAGAGCAGCUGACAGA
siTNNC#3	AAGAUAAUGCUGCAGGCUA

Supplementary Table S2. Sequences of oligonucleotide primer used in RT-PCR analyses

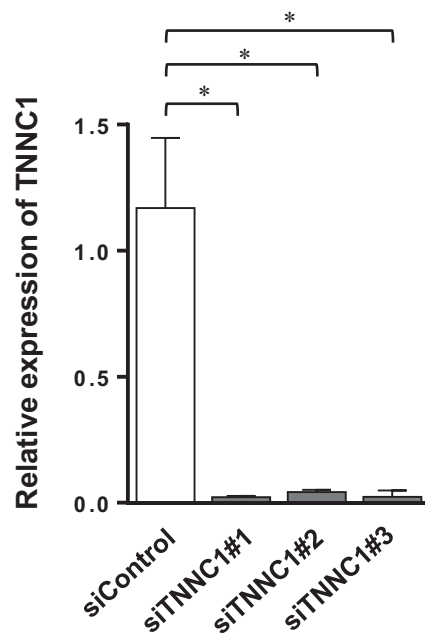
Gene	Forward primer (5'- to 3'-)	Reverse primer (5'- to 3'-)
<i>CLDN5</i>	ACCTCAGCTTCCCCGTGA	CGCCCTCAGACGTAGTTCTT
<i>CLEC3B</i>	GAGGTGGCCCTGCTGAAG	CTCGTGGAAGGTCTTCGTCT
<i>FGFR4</i>	CTGGAGGCCTCTGAGGAAGT	AGGGCTACTGTCAGCTCCTG
<i>GPIHBP1</i>	CTGTCCTGCTTGCCCTCTT	GTGGTCCTCGTCCTCTTCCT
<i>IGSF10</i>	ACAGTGGCCACAGGACTAGG	TAGGGTGTTCTGGGCATAGC
<i>KCNK3</i>	GGAGCAGAGCCACTCGTC	CGTGGACACCGAGCTGAT
<i>LGI3</i>	CACCATCCTGAAGTGGGACT	TACAGCTGGCTGTCCACCAC
<i>NCKAP5</i>	GAAGACGATGCAGTTGCAGA	CTGGCATAGGTAGCGTCCTG
<i>PRX</i>	GAATCTTCGTTCCGGGAGCTG	AAGAACACTCGGGCACTCAG
<i>RTKN2</i>	CAGACTGGAAGATGTGATGTGA	GCTGAAGTGATCAGAGTCTTTCC
<i>SLC6A4</i>	CCATCAGCCCTCTGTTTCTC	GGTTCCTATGCAGTAACCCAAG
<i>STXBP6</i>	GCTTCGCCAGGTTAATGGTA	GGATCTGGAAGAAGGTGCAT
<i>TCF21</i>	AGCTACATCGCCCACTTGAG	TCAGGTCACTCTCGGGTTTC
<i>TNNC1</i>	GTCTGACCTCTTCCGCATGT	ATGAGCTCCTCGATGTCGTC
<i>UPK3B</i>	TTCTTGCCAGCCTCTACCAT	GATGTGGTGGGTCATGTAGC
<i>KRAS</i>	TGCAATGAGGGACCAGTACA	AGGACCATAGGTACATCTTCAGAGTC
<i>ACTB</i>	ACAGAGCCTCGCCTTTGC	GAAGCCGGCCTTGACAT
<i>HPRT1</i>	ACACTGGCAAACAATGCAG	GTGGGGTCCTTTTCACCAG



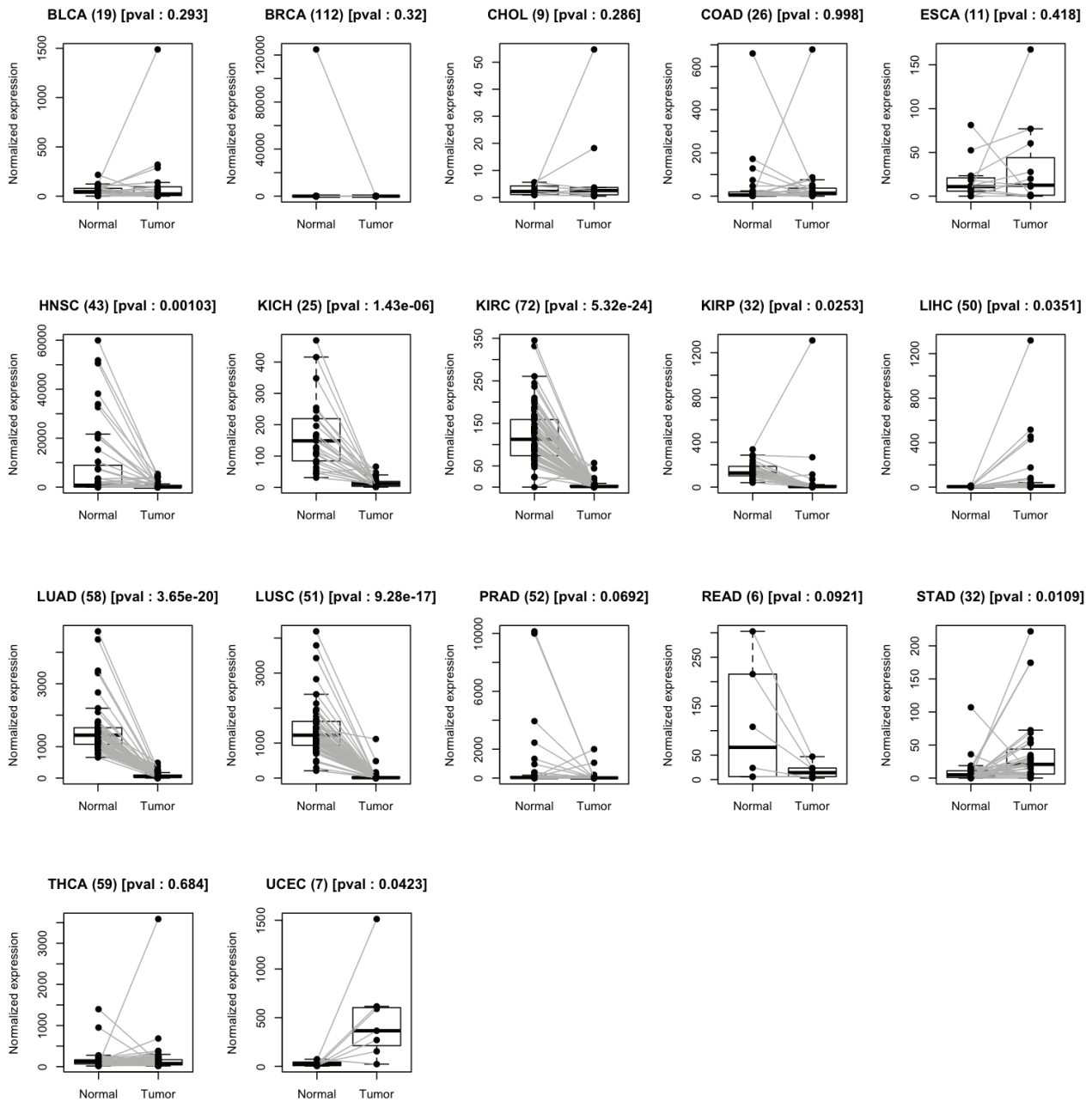
Supplementary Fig. S1. Kaplan-Meier survival curves. TCGA -LUAD patients (n = 502) from were divided into two groups based on the *TNNC1* expression level, and the survival data from high and low groups were used for Kaplan-Meier analyses. Long-term overall survival was significantly correlated with the higher expression of *TNNC1*, but recurrence-free survival showed limited statistical significance.



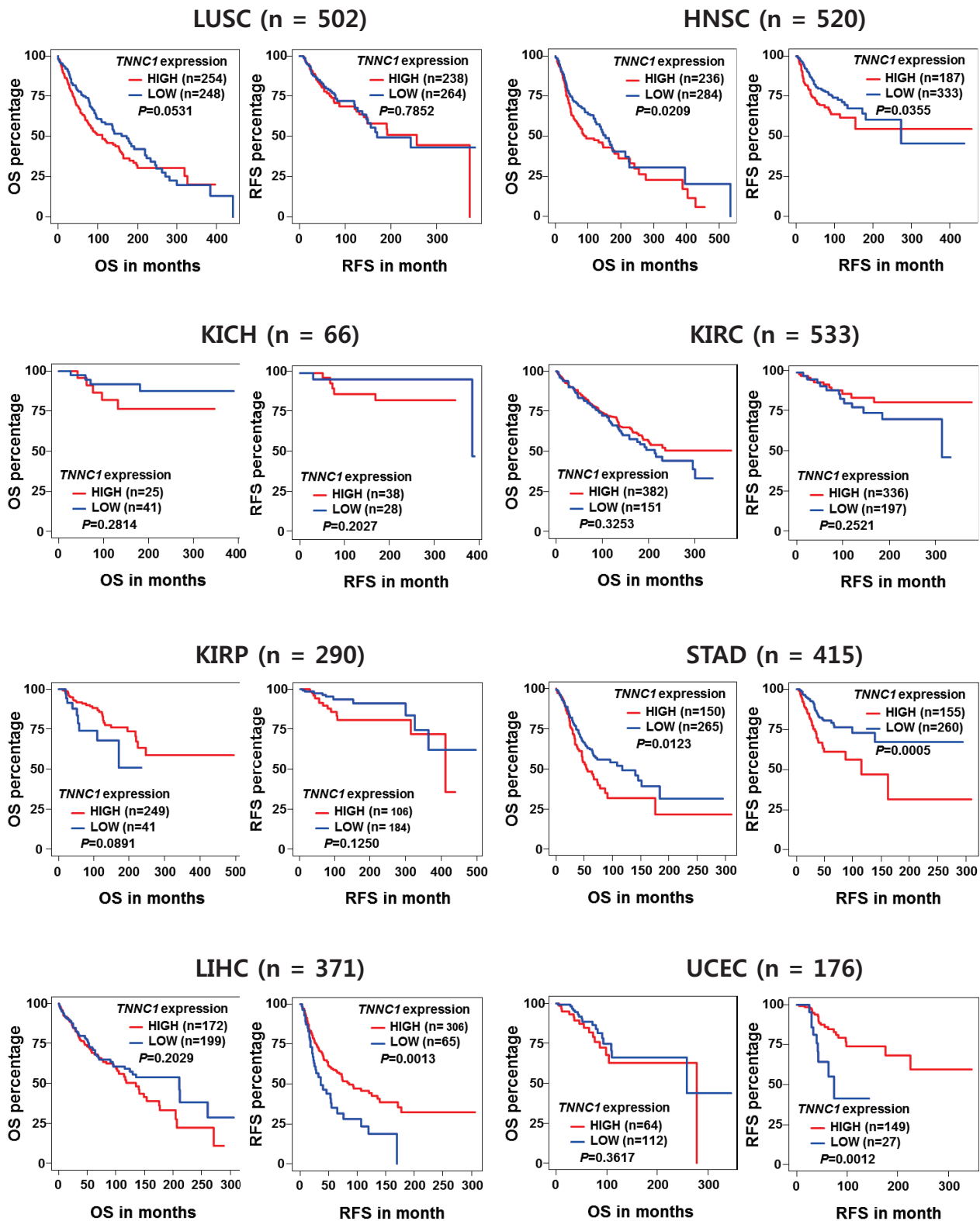
Supplementary Fig. S2. Ectopically expressed *TNNC1* is localized in nucleus of A549 cells. Anti-V5 epitope antibody were used.



Supplementary Fig. S3. RNA interference-mediated knockdown of *TNNC1* RNA expression examined by real-time RT-PCR. A549 cells were transfected with either siControl or one of the three independent siRNAs specifically targeting *TNNC1*. Data are mean \pm SEM of three independent experiments.



Supplementary Fig. S4. Expression analysis of *TNNC1* using normal-tumor matched patient data from TCGA RNA-seq data. From 33 Pan-Cancer data, expression levels of *TNNC1* from 17 types of cancer with at least 5 matched normal-tumor patient data were used to show the changes. BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PRAD, prostate adenocarcinoma; READ, rectum adenocarcinoma; STAD, stomach adenocarcinoma; THCA, thyroid carcinoma; UCEC, uterine corpus endometrial carcinoma.



Supplementary Fig. S5. Kaplan-Meier survival curves of TCGA data. Cancers with significantly up- or down-regulated ($P < 0.05$) levels of *TNNC1* in tumor tissues were analyzed (Down-regulation in LUSC, HNSC, KICH, KIRC and KIRP; Up-regulation in STAD, LIHC, and UCEC). Patients were divided into two groups based on *TNNC1* expression using the optimal youden index cut-off, and overall survival (OS) and recurrence-free survival (RFS) of the two groups were analyzed. OS and RFS were significantly correlated with the lower expression of *TNNC1* in STAD.