Figure S1. GO and KEGG pathway analyses on the pre-mRNAs reported to bind with MALAT1. (A) Biological processes associated with the pre-mRNAs that interacted with MALAT1. The top 20 biological processes are shown. (B) KEGG pathway analysis of the pre-mRNAs interacting with MALAT1. Pathways with P<0.05 are shown. GO and KEGG pathway enrichment analysis were conducted by clusterProfiler R/bioconductor package (v3.12.0) (30) in R. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; MALAT1, metastasis-associated lung adenocarcinoma transcript 1.

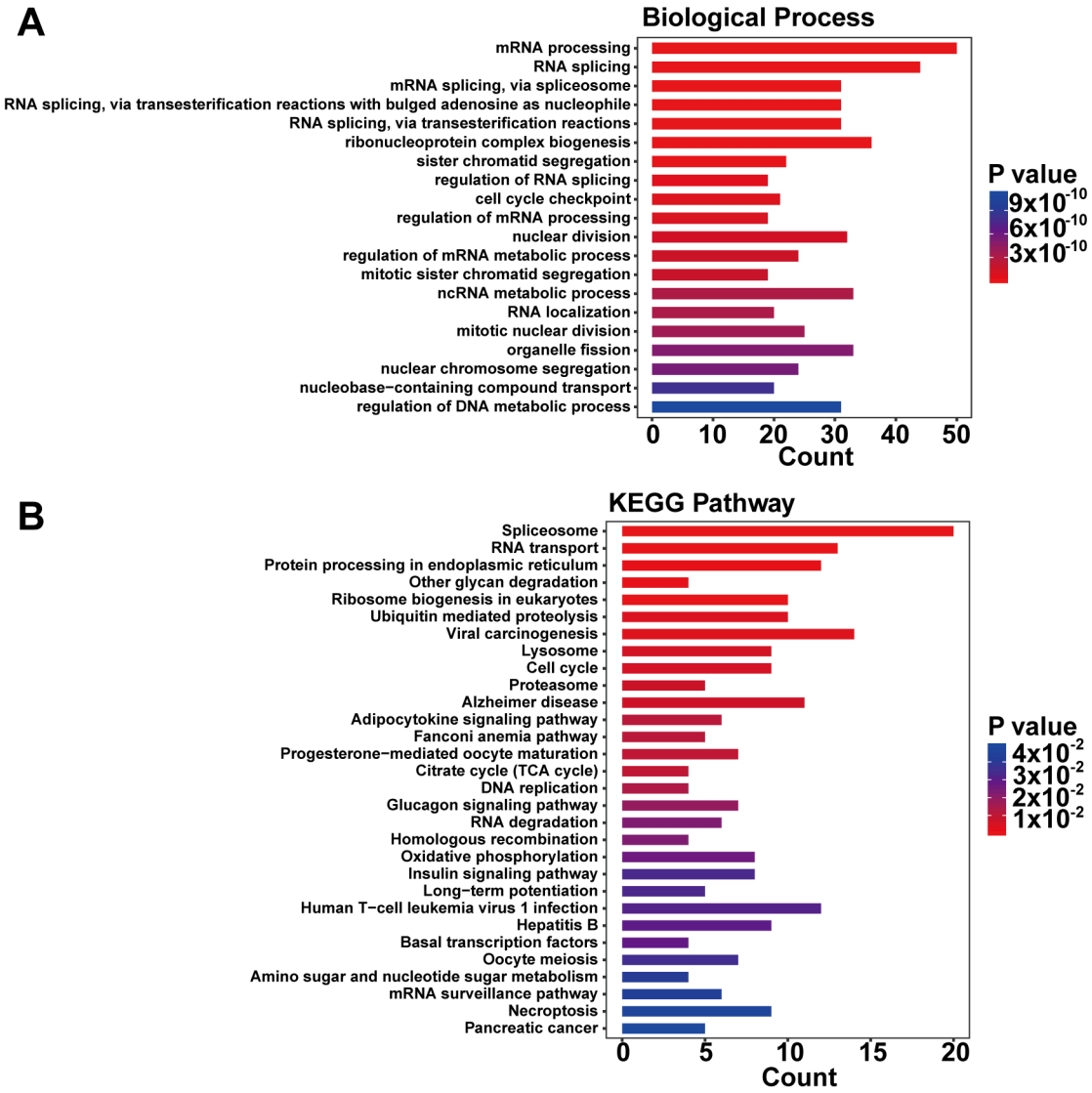

Figure S2. RT-qPCR and western blotting analyses of CFL1 in ACHN (A) and 786-O (B) cells transfected with CFL1 overexpression plasmids and the corresponding control cells transfected with the empty vector. The data are shown as mean ± SD (n=3) and unpaired Student's t-test was used for statistical analysis. CFL1, cofilin-1; OE, overexpression.

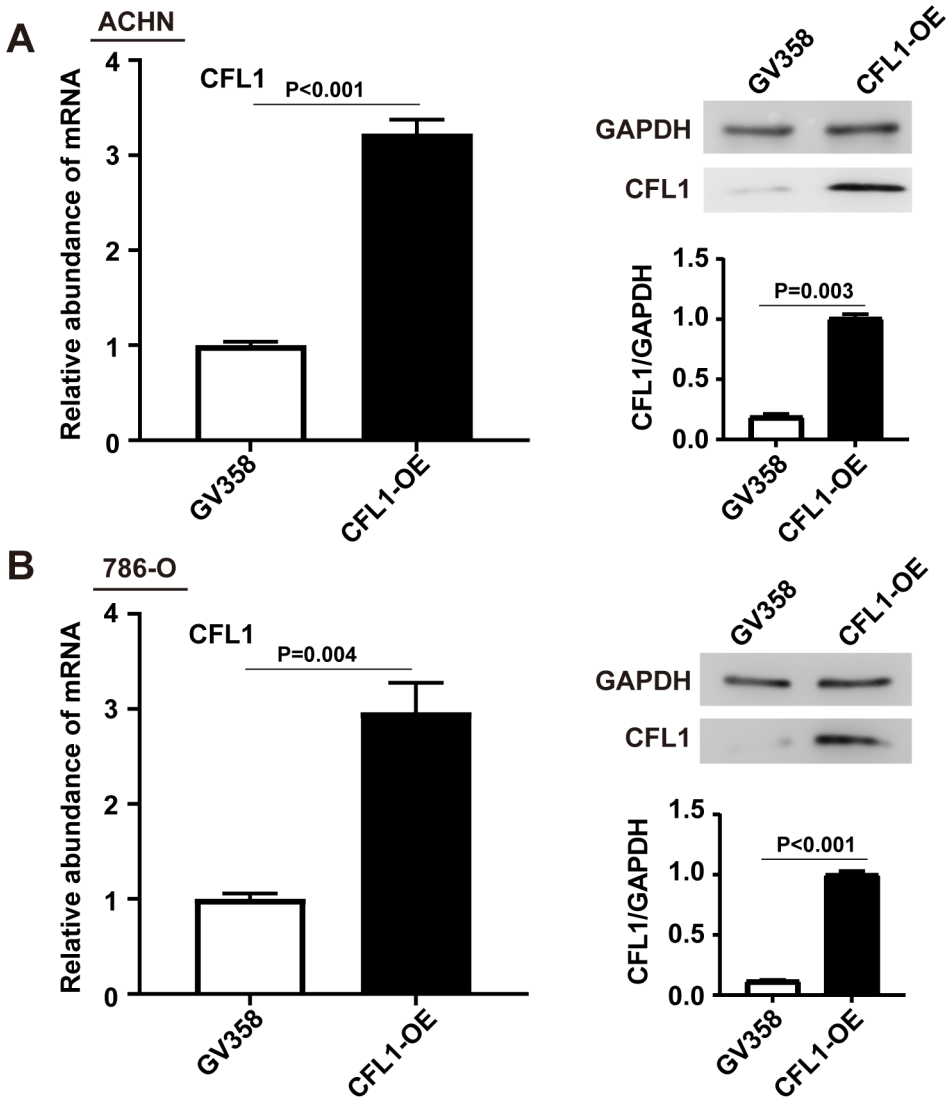

Table SI. Sequences of the siRNAs targeting MALAT1.

siRNA	Sequence
si-MALAT1-1	
Forward	5'-CACAGGGAAAGCGAGTGGTTGGTAA-3’
Reverse	3'-GTGTCCCTTTCGCTCACCAACCATT-5’
si-MALAT1-2	
Forward	5'-GAGGTGTAAAGGGATTTAT-3'
Reverse	3' CTCCACATTTCCCTAAATA 5'

MALAT1, metastasis-associated lung adenocarcinoma transcript 1; si, small interfering.

Table SII. Primer sequences for reverse transcription-quantitative PCR.

Gene	Forward primer	Reverse primer
GAPDH	5'-TGCACCACCAACTGCTTAGC-3'	5'-GGCATGGACTGTGGTCATGAG-3'
MALAT1	5'-CTCCCCACAAGCAACTTCTC3'	5'-TTCAACCCACCAAAGACCTC-3'
CFL1	5'-AGATAAGGACTGCCGCTATGC3'	5'-GCAATTCATGCTTGATCCCTGT-3'
pre-CFL1	5'-GCAACCTATGAGACCAAGGAGA-3'	5'-ACAGGAAGAAGTGCCAGAATGA-3'

MALAT1, metastasis-associated lung adenocarcinoma transcript 1; CFL1, cofilin-1.

Table SIII. Clinicopathological characteristics of patients with renal cell carcinoma.

Characteristic	Cases, n
Age, years	
≤60	7
>60	13
Sex	
Male	15
Female	5
Pathological grade	
I/II	12
III/IV	8
ISUP stage	
I/II	10
III/IV	6
NA	4

ISUP, The International Society of Urological Pathology; NA, not applicable.