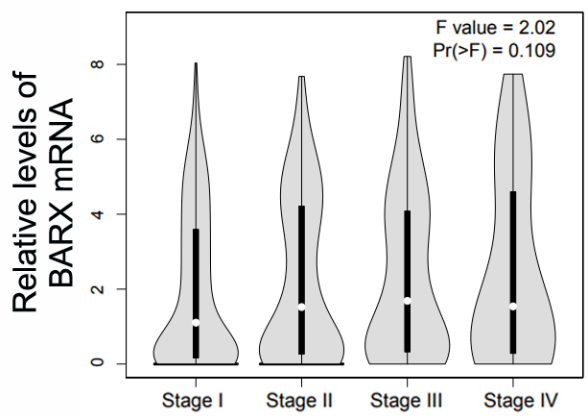

Figure S1. Analysis of BARX1 expression in LUAD and LUSC samples.

Comparison of BARX1 mRNA level in different stages of the LUAD and LUSC tissues. F statistic value and p value associated with the F statistic were shown upright.

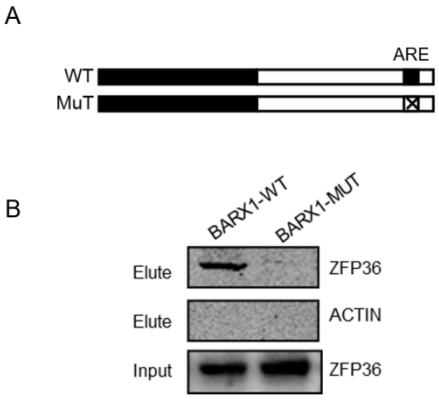

Figure S2. Specific interaction of ZFP36 with the 3'-UTR sequence of BARX1.

(A) Construction of wild-type and mutant probe. (B)The effect of mutation on the ability of 3'-UTR sequence of BARX1 to bind ZFP36 was evaluated by the RNA-Protein pull down assay. Wild-type and mutant 3'-UTR sequence of BARX1 were labeled with biotin and used for the pull-down assay. Samples were normalized by volume, and ACTIN was used as a negative control.

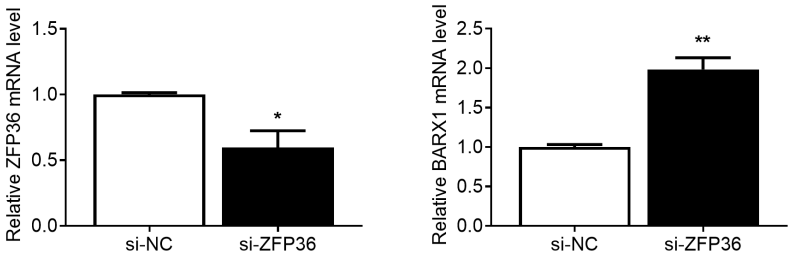

Figure S3. Silencing of ZFP36 negatively regulates BARX1 expression.

Upregulation of BARX1 expression (right panel) induced by ZFP36 knockdown (left panel) in A549 cells was verified by RT-qPCR, (n=3, *p<0.05, **p<0.01).

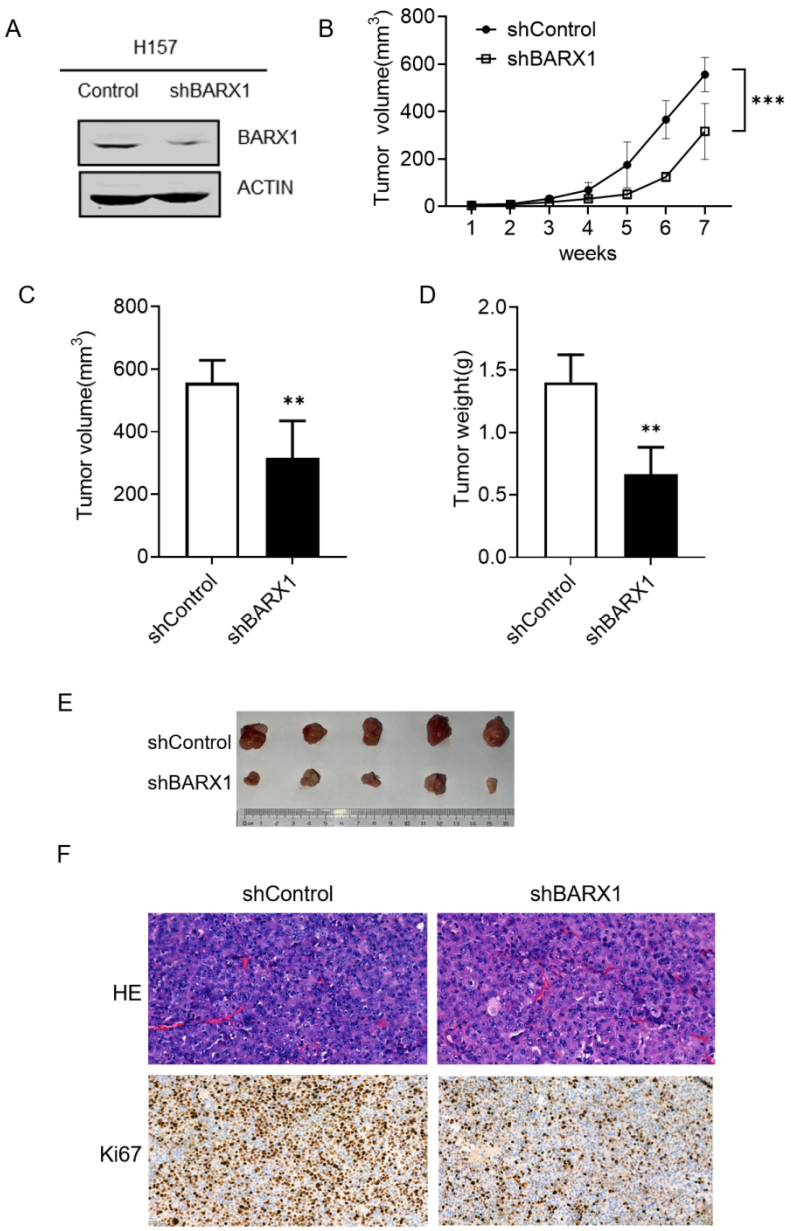

Figure S4. Silencing BARX1 inhibits tumor progression in H157 cells in vivo.

(A) Knockdown of BARX1 in H157 cells was verified by Western blot. (B) The change in tumor volume was determined every week during the tumor growth after tumor cells implanted. (C) Tumor volume and (D) weight of the mice were significantly decreased in shBARX1 group compared with that of shControl (n=5, p**<0.01, p***<0.001). (E) Morphology of tumor was photographed seven weeks after inoculation. (F) HE and immunohistochemical staining of the shControl and shBARX1 group tumor tissues, the expression of Ki67 of tumor sections were determined by IHC.

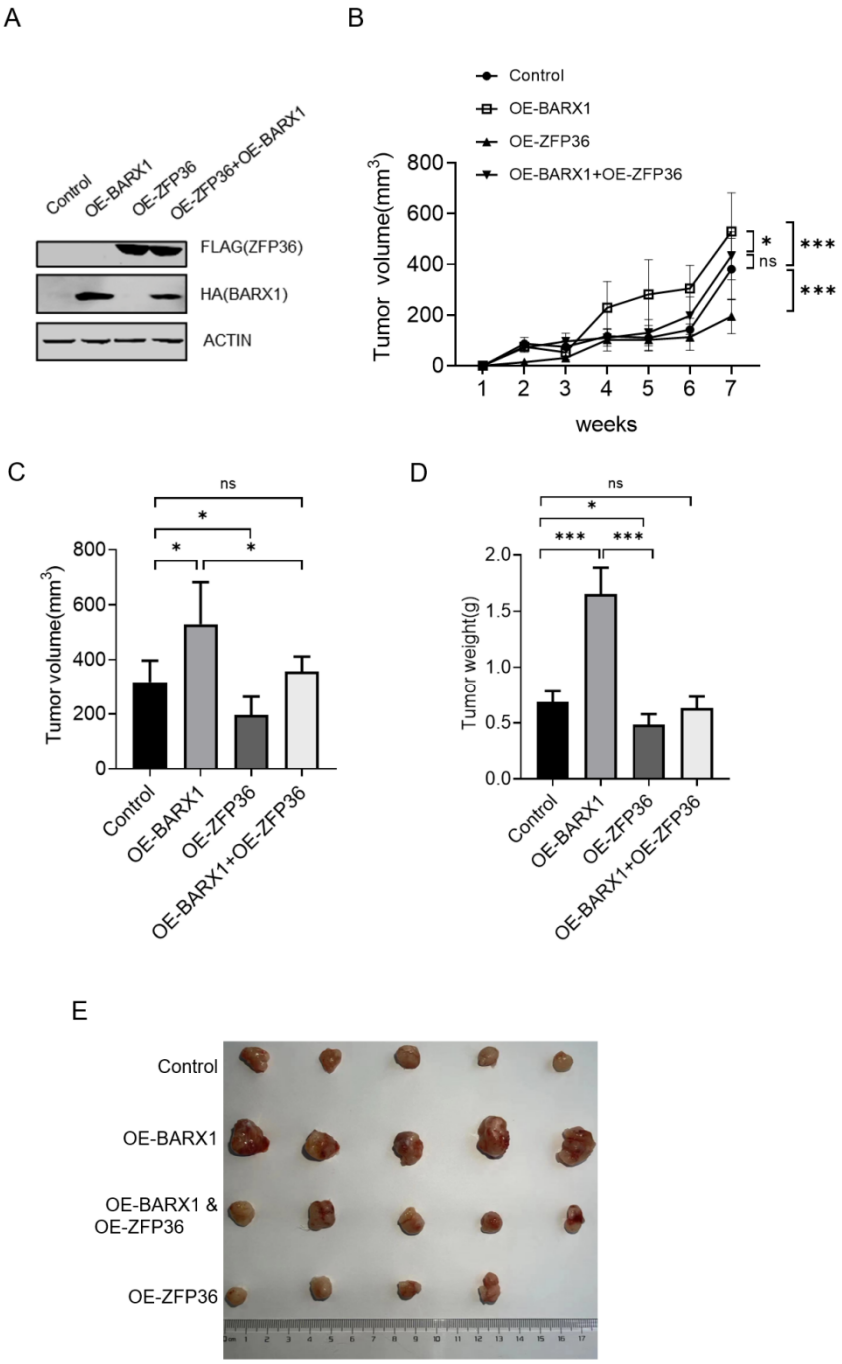

Figure S5. ZFP36 attenuates BARX1-medaited tumor progression in vivo.

(A) Western blot was performed to verify the overexpression of BARX1 and/or ZFP36 in A549 cells. BARX1 was fused with HA tag, and ZFP36 was fused with FLAG tag. OE-BARX1: BARX1 overexpression; OE-ZFP36: ZFP36 overexpression; OE-BARX1+ OE-ZFP36: BARX1 and ZFP36 co-overexpression. (B) The change in tumor volume was determined every week during the tumor growth after tumor cells implanted ($n \geq 4$, $p^{*} < 0.05$, $p^{***} < 0.001$). (C) Tumor volume and (D) weight of the mice were significantly attenuated in OE-BARX1+ OE-ZFP36 group compared with that of OE-BARX1. (E) Morphology of tumor was photographed seven weeks after inoculation.

Supplementary Table 1. The clinical information of patients.

Characteristics	Number
age	
>60	16
<60	7
Pathological_stage	
IA	9
IB	6
IIA	1
IIB	2
IIIA	4
IVA	1
Sex	
male	13
female	10
T	
T1a	3
T1b	4
T1c	3
T2a	8
T2b	1
T3a	2
T4	2
Postperative diagnosis	
LUAD	19
LUSC	4

Supplementary Table 2. Primers used in this study.

Name	Sequences	Application
CDC45-F	CAACAGTGTTTGCGTTCG	ChIP-qPCR
CDC45-R	GCTTCTTAGTTCCCAGCC	ChIP-qPCR
TRIM37-F	AGCATCTTGCCAACTAAAT	ChIP-qPCR
TRIM37-R	AGTTAAGATTCTTGTATG	ChIP-qPCR
MMP-9-F	AGGATATCTGACCTGGGA	ChIP-qPCR
MMP-9-R	CTTGTGGGAACTGTATGA	ChIP-qPCR
CDC20-F	ACCTCTAACCTAAGCATAT	ChIP-qPCR
CDC20-R	GTCATTAGCTTAAAGTCCACT	ChIP-qPCR
shBARX1-1	GCCGGACAGAATAGATCTTGC	shRNA
shBARX1-2	CCTGACAGAATAGATCTAGCT	shRNA
shZFP36-1	GATCCGACCCTGATGAATATG	shRNA
shZFP36-2	GCGCTACAAGACTGAGCTATG	shRNA
GAPDH-F	TGTCAGTGGTGGACCTGACCT	qPCR
GAPDH-R	AGGGGAGATTCAGTGTGGTG	qPCR
BARX1-F	TTCCACGCCGGACAGAATAG	qPCR
BARX1-R	CTGCTCGCTCGTTGGAATTG	qPCR
ZFP36-F	CGCTACAAGACTGAGCTATG	qPCR
ZFP36-R	CCTGGAGGTAGAACTTGTG	qPCR
MMP-9-F	GTGCTGGGCTGCTTTGCTG	qPCR
MMP-9-R	GTCGCCCTCAAAGGTTTGGAAT	qPCR
CDC20-F	GCACAGTTCGCGTTCGAGA	qPCR
CDC20-R	CTGGATTTGCCAGGAGTTCGG	qPCR
CDC45-F	TTCGTGTCCGATTTCCGCAAA	qPCR
CDC45-R	TGGAACCAGCGTATATTGCAC	qPCR
TRIM37-F	TATGGAGAAATTGCGGGATGC	qPCR
TRIM37-R	GTCAGCCAGCGCCTAATACAG	qPCR
BARX1-WT-F	GCTAGCGGGCGGTATACGGTG	Cloning
BARX1-WT-R	TCTAGATTGTGTCATAAAATA	Cloning
BARX1-MT-F	GCTAGCGGGCGGTATACGGTGC	Cloning
BARX1-MT-R	TCTAGATTGTGTCATAAGGAG	Cloning