Figure S1. Layout of the tissue array catalog number HProA150CS01. (A) A schematic diagram of the tissue microarray cat. no. HProA150CS01. (B) The immunohistochemistry staining for E2F7 expression of the tissue microarray cat. no. HProA150CS01 which is turned 90˚ anticlockwise of (A). Scale bar, 5,000 μm. Ca, Cancer tissue; P, matched adjacent non-cancerous tissues.

A

Tissue array	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
A	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P
B	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P
C	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P
D	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P
E	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P
F	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P	Ca	P
G	Ca	P	Ca	P	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca
H	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca
I	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca	Ca
J	Ca	Ca	Ca	Ca	Ca	Ca										

B

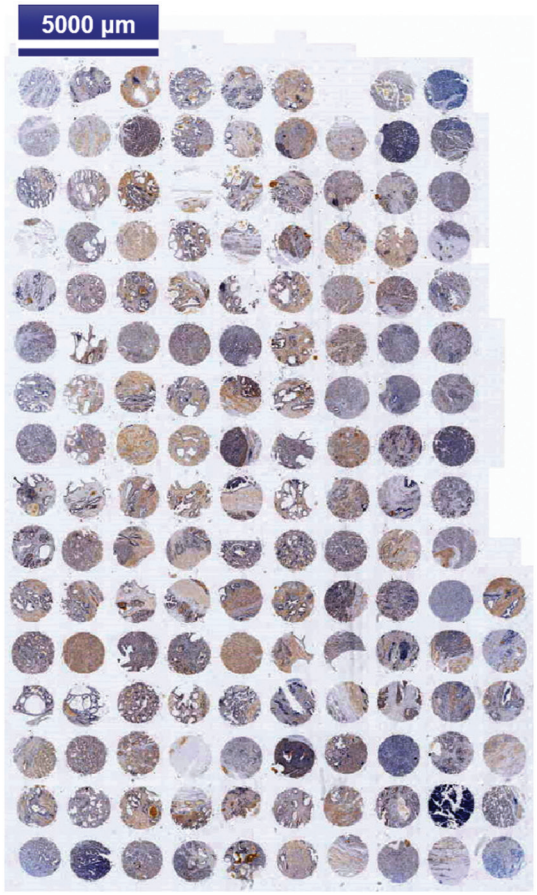

Figure S2. Construction and digestion of the E2F7 3'UTR psiCHECK-2 vector. (A) E2F7 3'UTR PCR amplification product. Lane M represents the 1 kb DNA ladder. Lane E2F7 3'UTR represents the E2F7 3'UTR PCR amplification product (2770 bp). (B) psiCHECK-2 vector digested at the *Xho*I and *Not*I sites. Lane M1 represents the 1 kb DNA marker. Both lanes 1 and 2 represent the recombinant plasmids of E2F7, which were successfully digested into two bands of 2.8 and 6.1 kbp respectively, which were subsequently sequenced; 3'UTR, 3'untranslated region.

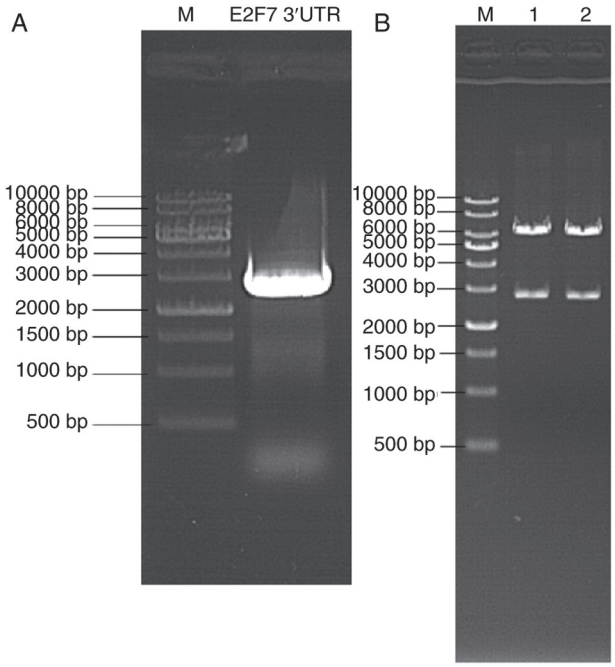

Figure S3. Relative expression levels of E2F7, miR-30c and p21 examined by reverse transcription-quantitative PCR. The relative expression levels of E2F7 in (A) Du145 cells (B) PC3 cells. The relative expression levels of p21 in (C) Du145 cells and (D) PC3 cells. The relative expression levels of miR-30c in (E) Du145 cells and (F) PC3 cells. The values represent the mean ± SD from three experimental repeats. *P<0.05, **P<0.01 and ***P<0.0001. 1, NC; 2, miR-30c; 3, miR-30c i; 4, siE2F7; 5, miR-30c i + siE2F7; miR: microRNA; miR-30c: miR-30c mimics; miR-30c i: miR-30c inhibitor; siE2F7: E2F7 siRNA; NS: not significant.

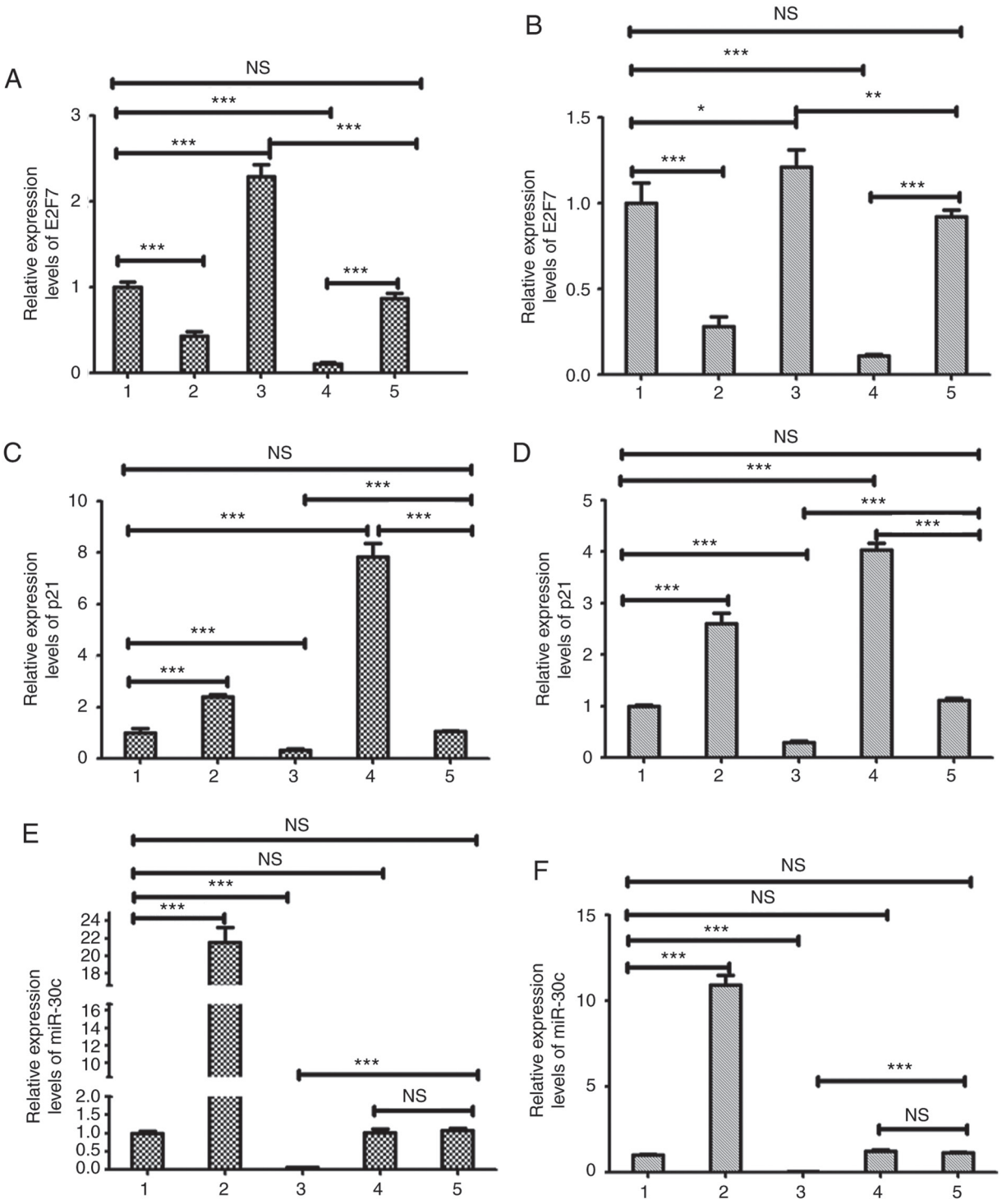

Figure S4. Comparison of E2F7 and p21 expression in tumor microarrays. The relationship between E2F7 and p21 expression were analyzed further by immunohistochemistry. (A) Sample 1, (B) Sample 2 and (C) Sample 3.

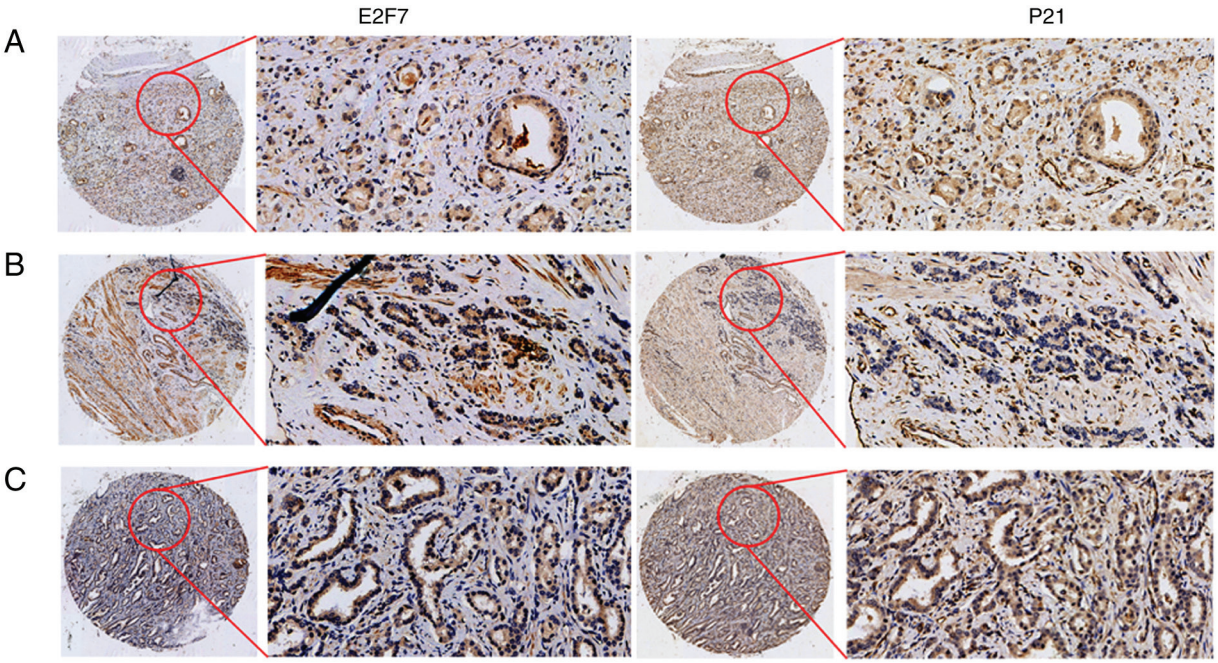

Table SI. Primer sequences used for reverse transcription-quantitative PCR in the present study.

Name	Sequence (5'→3')	Length (bp)
miR-30c-F	ACACTCCAGCTGGGTGTAAACATCCTACACTCT	72
miR-30c-R	CTCAACTGGTGTCGTGGA	
U6-F	CTCGCTTCGGCAGCACA	94
U6-R	AACGCTTCACGAATTTGCGT	
E2F7-F	AATGCAGTGGTTGTTTCTGT	107
E2F7-R	TGCCATTGCTTCTTCACTAC	
P21-F	TGGTGGCAGTAGAGGCTATG	178
P21-R	AGTCCAGGCCAGTATGTTAC	
18srRNA-F	CCTGGATACCGCAGCTAGGA	112
18srRNA-R	GCGGCGCAATACGAATGCCCC	
GAPDH-F	GGGAAACTGTGGCGTGAT	299
GAPDH-R	GAGTGGGTGTCGCTGTTGA	

18srRNA, 18s ribosomal RNA; miR, microRNA; F, forward; R, reverse.