

Table SI. Sequences of shRNA for lentivirus infection.

Group	Sequences of shRNA (5'-3')
ELF5 shRNA	GCCCTGAGATACTACTATAAATCAAGAGTTTATAGTAGTATCTCAGGGC
Control shRNA	GCTTCGCGCCGTAGTCTTATCAAGAGTAAGACTACGGCGCGAAGC

Table SII. Sequences of forward and reverse primers used in quantitative PCR.

Gene symbol	Forward primer (5'-3')	Reverse primer (5'-3')
Gapdh	AATGGATTTGGACGCATTGGT	TTTGCACTGGTACGTGTTGAT
Apc2	GCCTGGAATACTGTGAGCACC	ATTGCCTTGAAGGTCGTTCTG
Tdrd6	TTCGCTGCTCAAACGCTAC	GGGATGGCATACTTGGGTACT
Tal2	AGAGTGTCACAATGCCTTTGC	GAAGCGTCTCGTTCTTGCTC
Dsg3	GAAGGTACAAACGTGAATGGGT	ACTCCAGAAATGCGGTAGGTA
Marco	CCTCCAGGGACTTACGGGT	CCAGTGAGACCTATGTCACCT
Il10	TTGTCGCGTTTGCTCCCAT	GAAGGGCTTGGCAGTTCTG

Table SIII. Association of ELF5 with the pathological characteristics of patients with lung adenocarcinoma.

Characteristics	ELF5-positive cases (n)	ELF5-negative cases (n)	P-value
Sex	39	33	0.953
Males	21 (53.8%)	18 (54.5%)	
Females	18 (46.2%)	15 (45.5%)	
Age, years	39	33	0.966
≤55	12 (30.8%)	10 (30.3%)	
>55	27 (69.2%)	23 (69.7%)	
Localization	39	33	0.984
Right lung	20 (51.3%)	17 (51.5%)	
Left lung	19 (48.7%)	16 (48.5%)	
T classification	39	33	0.207
T1-T2	11 (28.2%)	14 (42.4%)	
T3-T4	28 (71.8%)	19 (57.6%)	
N classification	39	33	0.217
N1-N2	9 (23.1%)	12 (36.4%)	
N3-N4	30 (76.9%)	21 (63.6%)	
M classification	39	33	0.657
M0	37 (94.9%)	32 (97.0%)	
M1	2 (5.1%)	1 (3.0%)	
Lymph nodes involved	39	33	0.013 ^a
≤5	3 (7.7%)	10 (30.3%)	
>5	36 (92.3%)	23 (69.7%)	
Stage classification	39	33	0.030 ^a
<III stage	16 (41.0%)	22 (66.6%)	
≥III stage	23 (59.0%)	11 (33.3%)	

^aP<0.05.