Figure S1. CDK16 knockdown cells were reconstituted with siRNA-resistant CDK16 plasmid (Myc-CDK16-R#1 and Myc-CDK16-R#2) as indicated. The ratio shows relative p53 protein expression normalized for GAPDH (scramble, set at 1)

Figure S2. CDK16 knockdown did not affect the protein level of MDM2. A549 cells were transfected with the indicated siRNAs. 48h later, cells were harvested and analyzed by immunoblotting. The ratio shows relative MDM2 protein expression normalized for GAPDH (scramble, set at 1)

Figure S3. A549 and H292 cells were either untreated or irradiated (8 Gy). After 24 h, cells were collected analyzed by immunoblotting. The ratio shows relative CDK16 protein expression normalized for GAPDH (control, set at 1)

Figure S1.

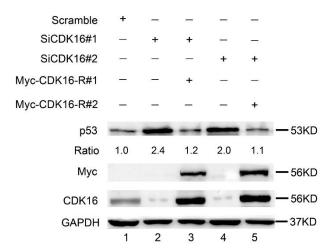


Figure S2.

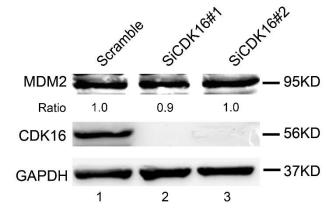


Figure S3.

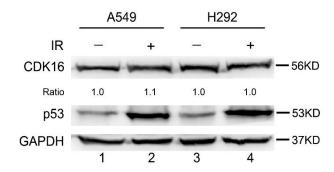


Table S1. Sequences of primers used for Real-time quantitative PCR

Genes	Sequences (5'3')	Size (bp)	
D52	F ^a : GCTTTCCACGACGGTGAC	07	
P53	R: GCTCGACGCTAGGATCTGAC	97	
P21	F: TACCCTTGTGCCTCGCTCAG	120	
F21	R: GAGAAGATCAGCCGGCGTTT	129	
NOXA	F: CGGGCTCTGTAGCTGAGTG	160	
NOXA	R:TTCTGCCGGAAGTTCAGTTT	160	
PUMA	F: ACGACCTCAACGCACAGTACG	108	
FUMA	R: GTAAGGGCAGGAGTCCCATGATG	108	
MDM2	F: GAATCTACAGGGACGCCATC	77	
IVIDIVIZ	R: TCCTGATCCAACCAATCACC	77	
CDK16	F: TATCCACACGGAGAAGTCCC	116	
CDK10	R: ACAGGAACAGTTTCACGTTG	110	
GAPDH	F: GAGTCAACGGATTTGGTCGT	185	
	R: GACAAGCTTCCCGTTCTCAG		

^a F, forward primer; R, reverse primer.

Table S2. Correlation between the clinicopathologic variables and expression of CDK16 in human lung cancer tissues

Factories	CDK16 expression		P-value
Features	low high		
Sex			
Male	13	35	0.473
Female	12	28	
Age(years)			
≤60	15	25	0.068
> 60	10	38	
Tumor size			
T1 (≤3cm)	6	26	0.137
T2 (> 3 cm, ≤ 7 cm)	16	35	
T3 (> 7cm)	3	2	
Stage			
I - II	15	32	0.294
III-IV	10	31	
T			
1	3	14	0.626
2	14	35	
3	6	10	
4	2	4	
N			
0	18	28	0.026
1	5	14	
2	2	15	
3	0	6	
M			
0	25	62	0.716
1	0	1	