

## Methods

### RNA sequencing

Total RNA was extracted from 10 pairs of NSCLC and adjacent non-tumorous tissues using the TRIzol reagent (Invitrogen, Carlsbad, CA, USA). RNA sequencing was performed using Illumina Genome Analyzer using the standard protocol. Sequencing data were deposited in NCBI's Sequence Read Archive database (<http://www.ncbi.nlm.nih.gov/sra>, AC: SRP075725).

### Bioinformatics analysis

Gene set enrichment analysis (GSEA) was performed with our RNA-seq data by using GSEA version 2.0 from the Broad Institute at MIT as previously described [1]. Gene set permutations were performed 1000 times, and the pathway set list is sorted by the Normalized Enrichment Score (NES).

**Table S1. Primers sequences for real-time PCR**

Primer	Primer sequence	Size (bp)
FKBP3	F: 5'- AAGGTCGGAGTAGGCAAAG -3'	103
	R: 5'- CGTAAGCCCATTCTGGTTC -3'	
p53	F: 5'-CCACCATCCACTACA ACTAC -3'	135
	R: 5'-AAACACGCACCTCAAAGC -3'	

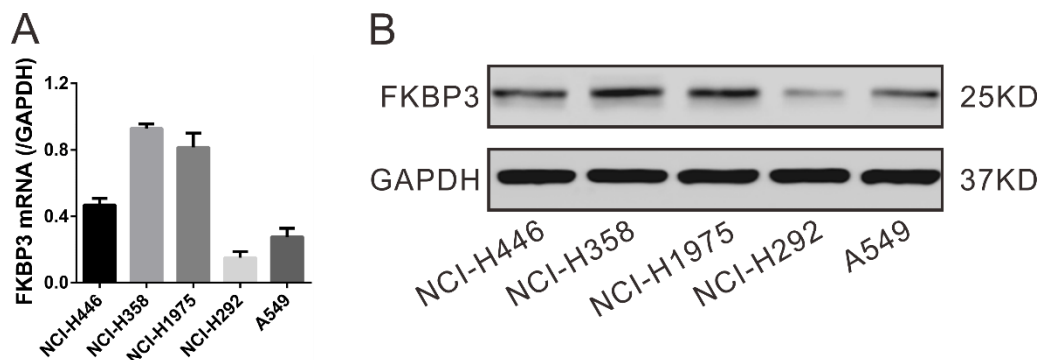
CCND1	F: 5'-TTCGTGGCCTCTAAGATG -3' R: 5'-GTGTTTGCGGATGATCTG -3'	222
CDC25A	F: 5'-GCCTCTTCTGTCCCTGTTAG -3' R: 5'-GCCAGCAGCATTCTGTG-3'	190
p16	F: 5'-GGTGCCACATTCGCTAAG -3' R: 5'-ACCCTGTCCCTCAAATCC -3'	116
p21	F: 5'-TAGCAGCGGAACAAGGAG -3' R: 5'-AAACGGGAACCAGGACAC -3'	249
p27	F: 5'-GATGGACGCCAGACAAACC -3' R: 5'-ACCTCCTGCCACTCGTATC-3'	192
MYC	F: 5'-GGCTCCTGGCAAAAGGTCA -3' R: 5'-CTGCGTAGTTGTGCTGATGT -3'	119
HDAC1	F: 5'-GCTCCACATCAGTCCTTCC -3' R: 5'-GGTCGTCTTCGTCCTCATC -3'	176
HDAC2	F: 5'-GCTGGGATTACAGGTGTGAG -3' R: 5'-AGGCTGAGGTGGGAGAATAC -3'	153
HDAC3	F: 5'-CCTGGCATTGACCCATAGCC -3' R: 5'-CTCTTGGTGAAGCCTTGCATA -3'	168
HDAC4	F: 5'-CCTGGGAATGTACGACGCC -3' R: 5'-CCCGTCTTTCCTGCGTAAC -3'	136
HDAC5	F: 5'-TCTTGTCGAAGTCAAAGGAGC -3' R: 5'-GAGGGGA ACTCTGGTCCAAAG -3'	108

HDAC6	F: 5'-AAGAAGACCTAATCGTGGGACT -3' R: 5'-GCTGTGAACCAACATCAGCTC -3'	248
HDAC7	F: 5'-GGCGGCCCTAGAAAGAACAG -3' R: 5'-CTTGGGCTTATAGCGCAGCTT -3'	205
HDAC8	F: 5'-TCGCTGGTCCCGGTTTATATC -3' R: 5'-TACTGGCCCGTTTGGGGAT -3'	82
HDAC9	F: 5'-AGTAGAGAGGCATCGCAGAGA -3' R: 5'-GGAGTGTCTTTCGTTGCTGAT -3'	141
Sp1	F: 5'-TGGCAGCAGTACCAATGGC -3' R: 5'-CCAGGTAGTCCTGTCAGAACTT-3	126
GADPH	F: 5'-CACCCACTCCTCCACCTTTG -3' R: 5'-CCACCACCCTGTTGCTGTAG -3'	110

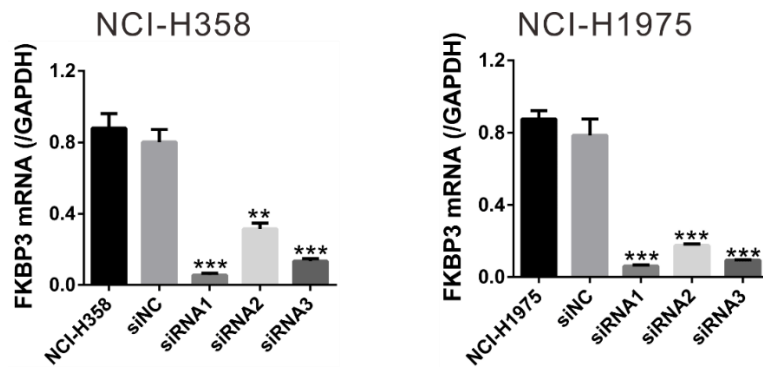
**Table S2.** Primers for real time PCR in ChIP DNA

Gene		Range	Sequences 5'-3'
p27	Primer 1	-1523~-1294	CTGTCACATTCTGGAGCGTA AGTGGATCTTCAACTGCCTC
	Primer 2	-1273~-1020	CCTGCTCATCGTCCTACTTT CCAGATTTCACTGCTCCAAC
	Primer 3	-997~-7047	GAAGGAGCTGCTGTATTTGG ACTCAAGCTCTCCCTCAATG
	Primer 4	-592~-262	CTGAGCGAACCATTGCCCA

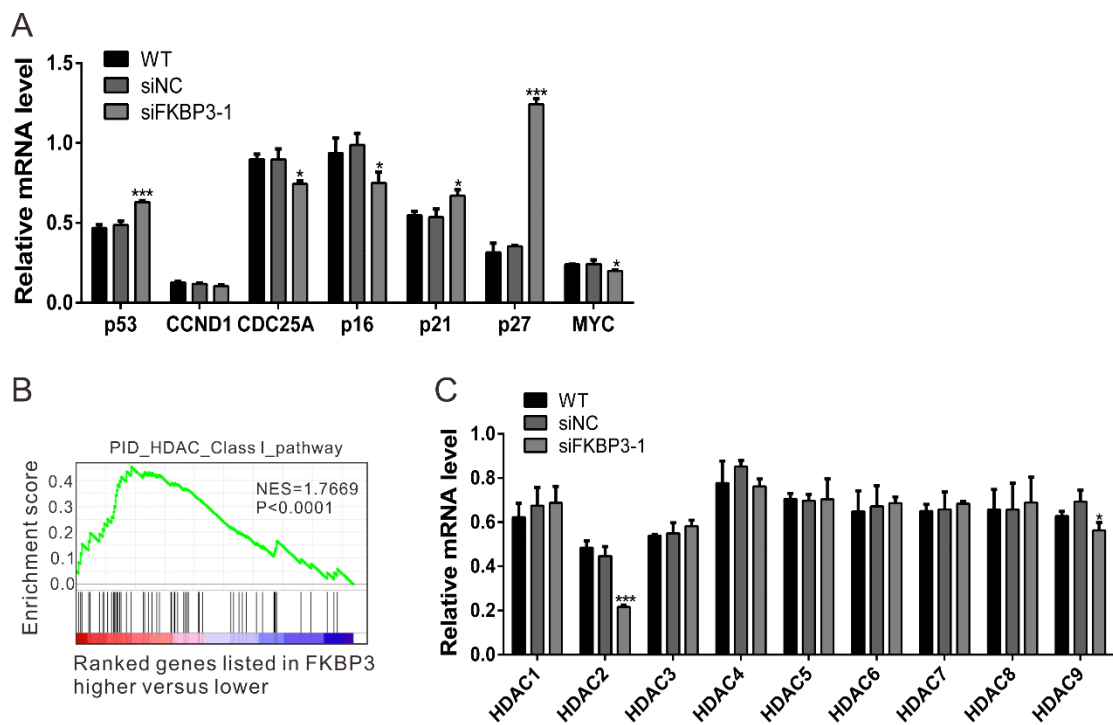
	Primer 5	-74~+145	AACAAACTAGCCAAACGGCC GCTCCCGCCGCCGCAACCAAT CGAACCCAGCCGCTCTCCAACC
HDAC2	Primer 1	-490~-350	ACTGGGGCGATGGGCCACAG TCGTAGCCTTGGCGGTCTGG
	Primer 2	-350~-250	GTCCAGACCGCCAAGGCTACG TAGATCCAGGGAGCGTGCAGC
	Primer 3	-140~-10	CTAACCTCGAGCCCGAAACG AAGCTCGGAATCGGAGGTGG



**Figure S1.** FKBP3 protein and mRNA expression in 5 NSCLC cell lines was analyzed by real-time PCR (A) and Western blot (B), respectively. Data were based on at least 3 independent experiments.

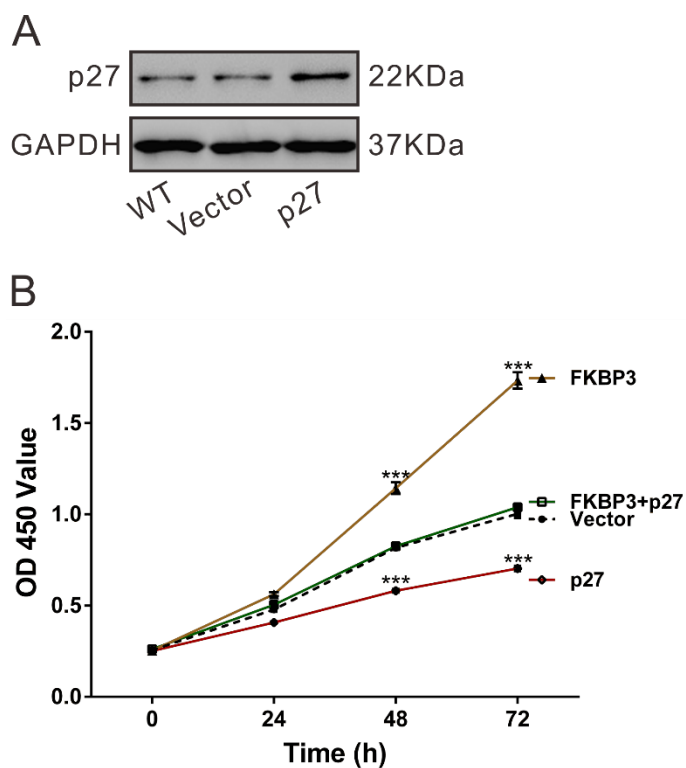


**Figure S2.** FKBP3 expression was suppressed by siRNA transfection in NSCLC cells. Real-time PCR analysis showed the efficiency of FKBP3 knockdown in NCI-H358 (left panel) and NCI-H1975 cells (right panel). \*\* $P < 0.01$ , \*\*\* $P < 0.001$  versus siNC.

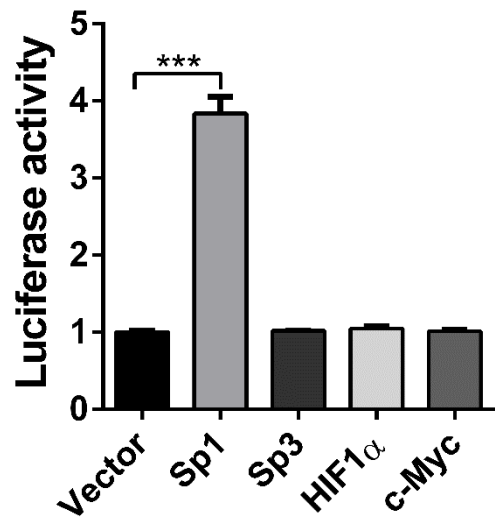


**Figure S3.** Effects of FKBP3 knockdown on the mRNA levels of proliferation-related genes and HDACs. (A) Real-time PCR analysis of the effects of FKBP3 knockdown on the mRNA levels of p53, CCND1, CDC25A, p16, p21, p27 and MYC. (B) Association between FKBP3 and HDAC Class I pathway. GSEA analysis in NSCLC patients with higher FKBP3 expression versus lower FKBP3 expression. NES,

normalized enrichment score. (C) Real-time PCR analysis of the effects of FKBP3 knockdown on the mRNA levels of HDAC proteins. \* $P < 0.05$ , \*\*\* $P < 0.001$  versus siNC.

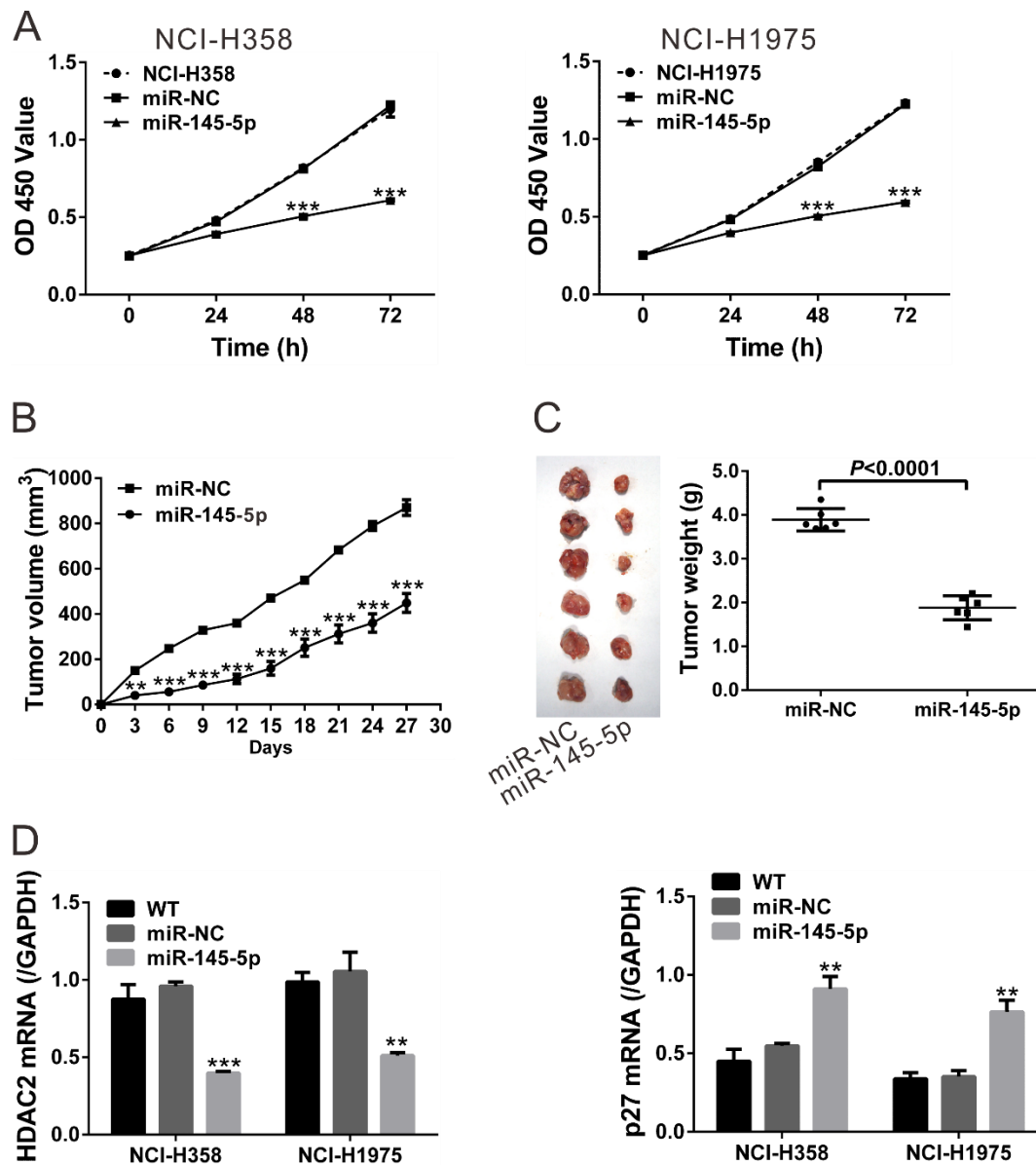


**Figure S4.** Effects of p27 overexpression on cell proliferation of NCI-H358 cells with FKBP3 overexpression. (A) The full-length human p27 were cloned into pLVX-puro. P27 expressing (p27) and control (Vector) lentivirus were generated. Protein levels of p27 in NCI-H358 cells were detected at 48 h after viral infection. (B) NCI-H358 cells were infected with Vector, p27, FKBP3 or FKBP3+p27, and CCK-8 assays were performed. P27 overexpression resulted in a decreased cell growth rate at 48 h and 72 h. \*\*\* $P < 0.001$  versus Vector and FKBP3+p27.



**Figure S5.** Luciferase Reporter assay was performed to evaluate the activities of HDAC2 promoter in NCI-H358 cells with Sp1, Sp3, HIF1 $\alpha$  or c-Myc overexpression.

\*\*\* $P < 0.001$ .



**Figure S6.** miR-145-5p inhibits NSCLC cell proliferation. (A) Cell proliferation was detected at 0, 24, 48 and 72 h after miR-145-5p mimic transfection in NCI-H358 and NCI-H1975. (B) Growth of miR-145-5p or miR-NC stable transfected NCI-H358 tumors in nude mice (n=6). (C) At day 27, tumors were excised from mice. (D) mRNA levels of HDAC2 and p27 in NCI-H358 and NCI-H1975 cells with miR-145-5p overexpression were analyzed by real-time PCR. \*\**P* < 0.05, \*\*\**P* < 0.001.

## References



1. Qiao W, Han Y, Jin W, Tian M, Chen P, Min J, Hu H, Xu B, Zhu W, Xiong L. Overexpression and biological function of TMEM48 in non-small cell lung carcinoma. *Tumor Biology*. 2015:1-12.