Supplementary information

Table S1. Characteristics of patients with early-stage NSCLC (stage I-II)

	Pro-SFTPB expression		*P*
	Normal（n=72）	Low（n=57）	
Sex			0.6205
Male	36	31	
Female	36	26	
Age			0.5937
60≤	37	27	
＜60	35	30	
Smoking			0.3387
Never	50	35	
Current/former	22	22	
Stage			0.1840
I	67	49	
II	5	8	

Table S2. Target sequences of shRNAs and siRNAs

Gene	Sequences
pro-SFTPB Scramble	5'-GCTTCGCGCCGTAGTCTTA-3'
	5'-TAAGACTACGGCGCGAAGC-3'
pro-SFTPB shRNA#1	5'-GATCAAGCGGATCCAAGCCAT-3'
	5'-ATGGCTTGGATCCGCTTGATC-3'
pro-SFTPB shRNA#2	5'-GACTCAAACGGCATCTGTATG-3'
	5'-CATACAGATGCCGTTTGAGTC-3'
pro-SFTPB shRNA#3	5'-GAGGACATCGTCCACATCCTT-3'
	5'-AAGGATGTGGACGATGTCCTC-3'
eIF4A1 siRNA#1	5'-ACCAAGUGCUUGACGACUA-3'
	5'-UAGUCGUCAAGCACUUGGU-3'
eIF4A1 siRNA#2	5'-GACUCAAACGGCAUCUGUA-3'
	5'-UACAGAUGCCGUUUGAGUC-3'

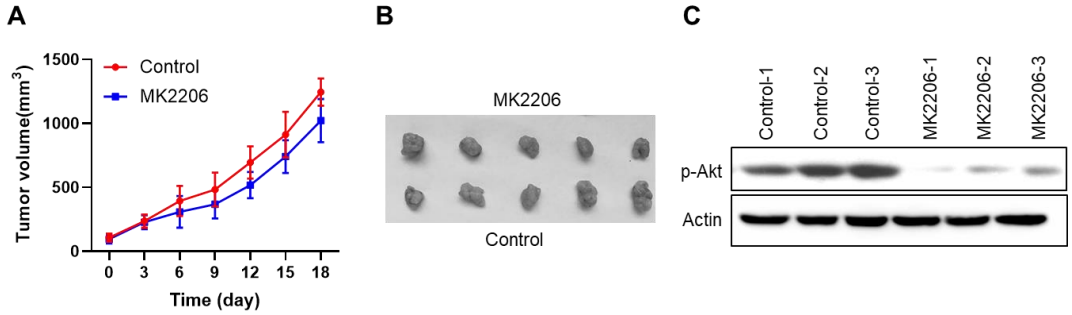


Figure S1. Akt inhibitor treatment did not significantly inhibited tumor growth in C57BL/6J xenograft models constructed using pro-SFTPB silenced Lewis lung cancer cells. **(A)** Tumor growth curve. **(B)** Tumor images. **(C)** p-Akt expression levels in xenograft tumors that from control group and MK2206 treatment group. Xenograft models were constructed using pro-SFTPB silenced Lewis lung cancer cells. When, tumor volumes were reached about 100mm^3, mice were orally administered PBS or MK2206 (50mg/Kg body weight) every three days.

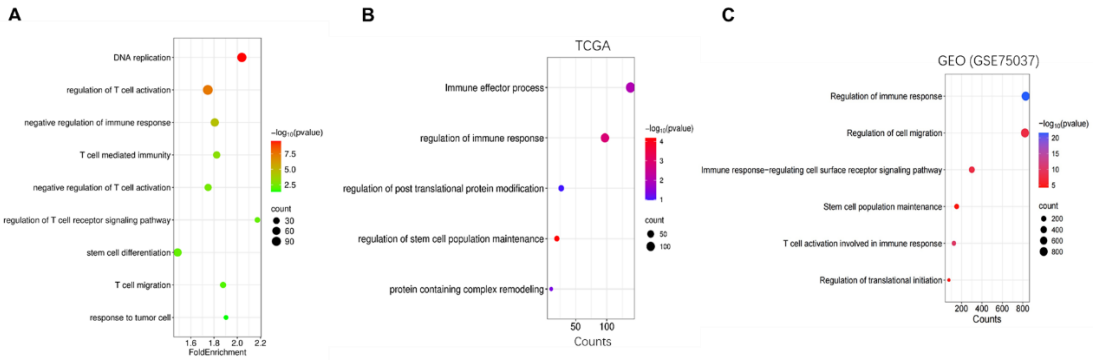


Figure S2. Gene ontology (GO) analysis using early-stage non-small cell lung cancer data. (A-C) GO analysis was performed using sequencing data from our clinical samples, TCGA database, and GEO database.

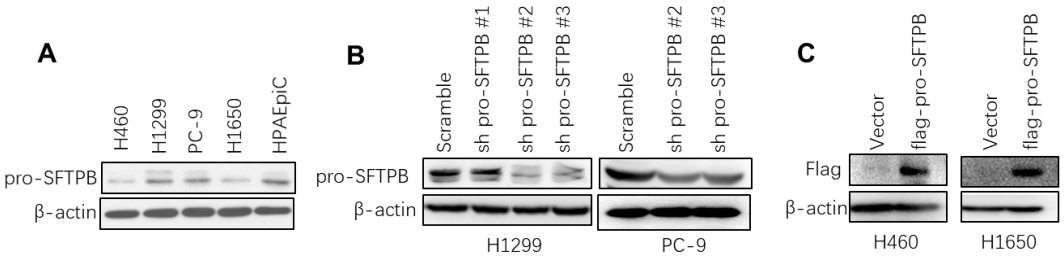


Figure S3. Western blot (WB) analysis of pro-SFTPB in NSCLC cells. (**A)** Detection of pro-SFTPB expression levels by WB in indicated cell lines. (**B)** Indicated cells were transfected with pro-SFTPB shRNA expressing plasmids for 72 hours, then the expression of pro-SFTPB was measured by WB. (**C)** Indicated cells were transfected with pro-SFTPB expressing plasmids for 72 hours, then measured the expression of pro-SFTPB by WB.

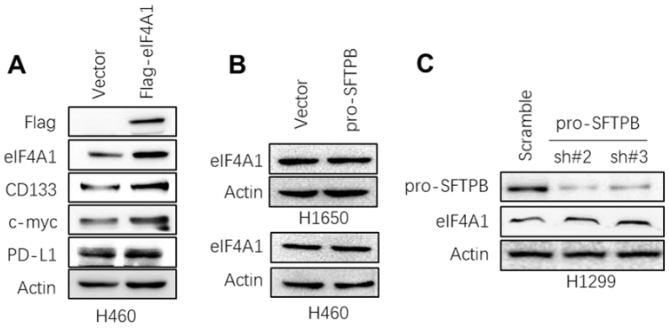
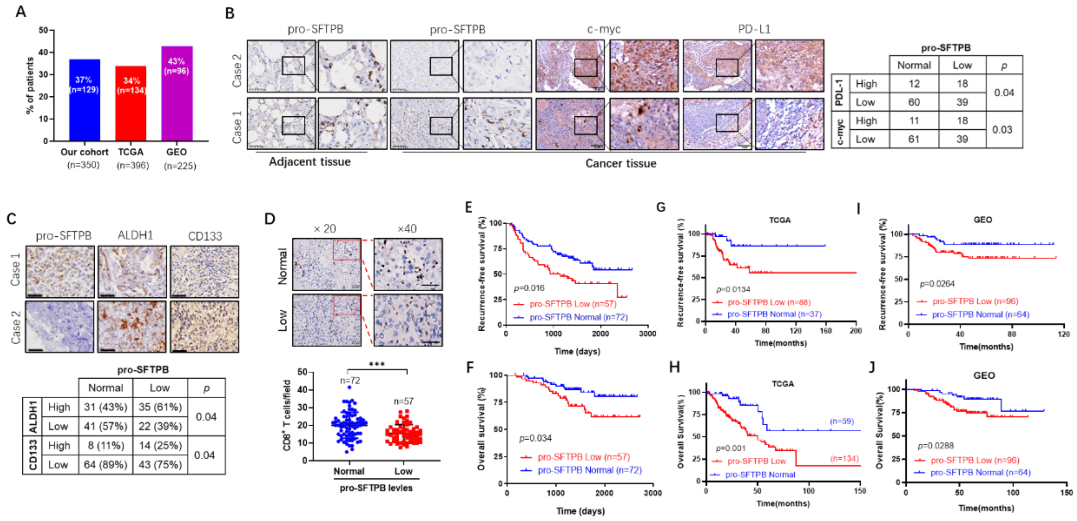


Figure S4. Effect of eIF4A1 on the expression of c-myc and PD-L1, and the effects of pro-SFTPB on the expression of eIF4A1 in NSCLC cells. (A) Western blot (WB) analysis showed eIF4A1 overexpression upregulated c-myc, PD-L1 and CD133 expression in H460 cells. (**B)** WB analysis showed overexpression of pro-SFTPB in H1650 and H460 cells did not change the expression of eIF4A1. (**C)** WB analysis showed knockdown of pro-SFTPB in H1299 cells did not change the expression of eIF4A1. Indicated NSCLC cells were transfected with indicated plasmids for 72 hours, then subjected to WB analysis.



		Normal	Low	p
PDL-1	High	12	18	0.04
	Low	60	39	
c-myc	High	11	18	0.03
	Low	61	39	

		Normal	Low	p
ALDH1	High	31 (43%)	35 (61%)	0.04
	Low	41 (57%)	22 (39%)	
CD133	High	8 (11%)	14 (25%)	0.04
	Low	64 (89%)	43 (75%)	

Figure S5. Low expression of pro-SFTPB in tumor tissues compared to in adjacent tissues related to increased cancer stemness, immune evasion, and poor prognosis in NSCLC patients with stage I and II. **(A)** The proportion of early-stage NSCLC patients with low expression of pro-SFTPB in tumors compared to adjacent tissues. **(B)** Immunohistochemistry (IHC) images of pro-SFTPB, c-myc and PD-L1 in early-stage NSCLC tissues. The significance was calculated by Chi-square test. **(C)** IHC images of pro-SFTPB, ALDH1 and CD133 in early-stage NSCLC tissues. The significance was examined using Chi-square test. **(D)** $CD8^+$ T cells in early-stage NSCLC tissues with low or normal expression of pro-SFTPB was detected by IHC. The significance was calculated by T test. **(E-F)** Low expression of pro-SFTPB on NSCLC tissues compared to adjacent tissues correlated with lower recurrence-free survival rate, and lower overall survival rate in early-stage NSCLC patients. **(G-H)** TCGA dataset analysis showed low expression of pro-SFTPB mRNA in NSCLC tissues compared to adjacent tissues correlated with lower recurrence-free survival rate, and lower overall survival rate in early-stage NSCLC patients. **(I-J)** GEO dataset (GSE31210) analysis showed low expression of pro-SFTPB mRNA in NSCLC tissues compared to adjacent tissues correlated with lower recurrence-free survival rate and lower overall survival rate in early-stage NSCLC patients. *S*cale bar=50 μm, ***, p <0.001.