Supporting information

Table S1. siRNAs, shRNAs, primers and antibodies used in this study.

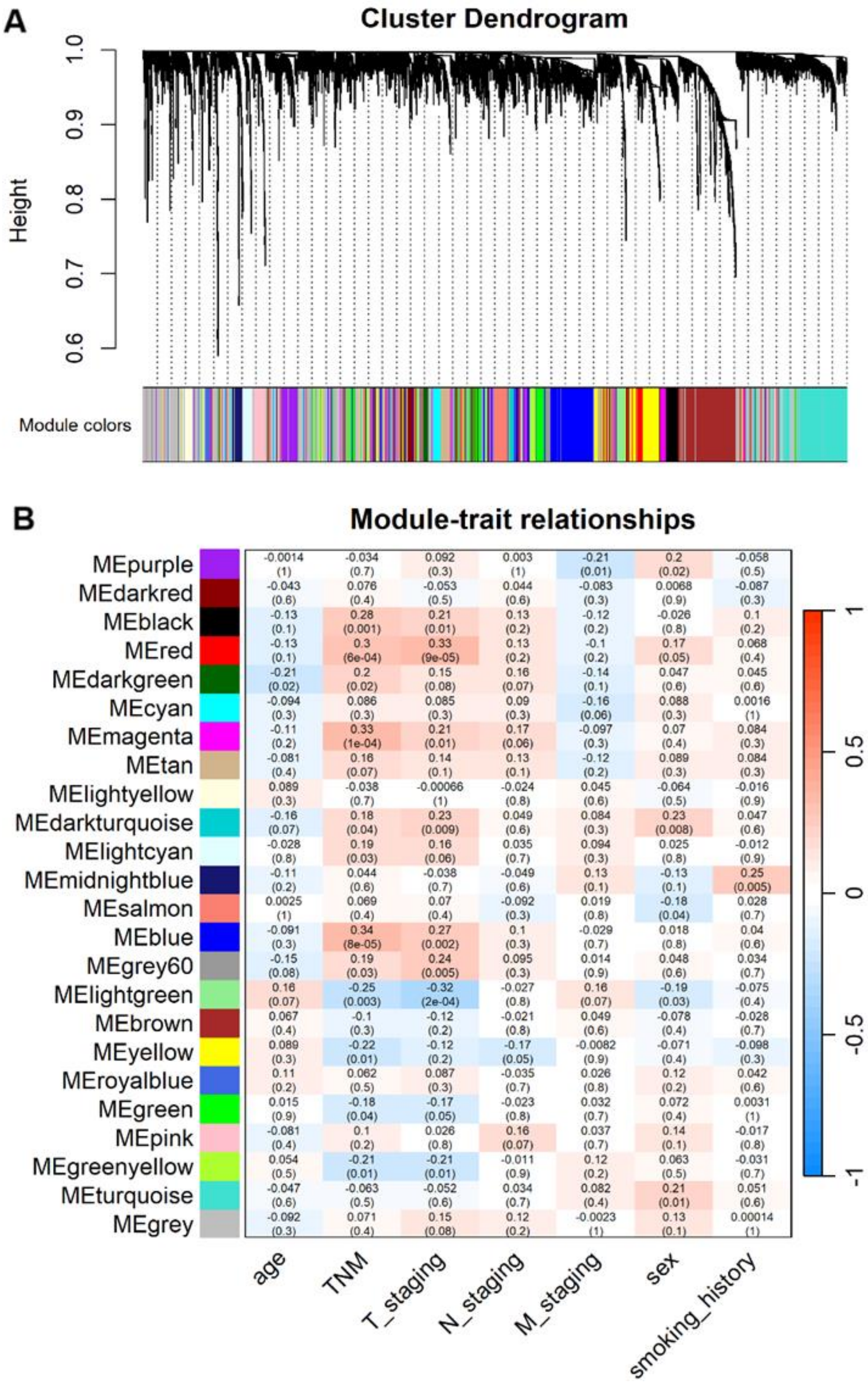
siRNA	**Sense (5' →3')**
human si*CHAF1B*-1	GCUGCGAGUAUACAGUAUATT
human si*CHAF1B*-2	GGGUCAAUAUGUUGCUACUTT
human sh*CHAF1B*	GCAACTGATGGGGAATTTAATG
human si*SETD7*-1	GGGCAGUAUAAAGAUAACATT
human si*SETD7*-2	GAACUUUGUUCACGGAGAATT
human si*SETD7*-3	CAGUGUACCACUUUGAUAATT
human si*SETD7*-4	GCAUCUACGAUAUGUUUGUTT
qRT-PCR primers	**Sequence (5' →3')**
Human *GAPDH* forward	GCACCACCAACTGCTTAGCA
Human *GAPDH* reverse	GTCTTCTGGGTGGCAGTGATG
Human *CHAF1B* forward	GCGTGGACACCAATGTCAG
Human *CHAF1B* reverse	GCTCCGGCTCCTTGTTATCAT
Human *SETD7* forward	ATGGATAGCGACGACGAGATG
Human *SETD7* reverse	GCAGAACCCGTGCGGTAAT
Human *HABP4* forward	AAGAGCTGAGCGGAGATCCTAC
Human *HABP4* reverse	TCCTCTCAACGGTCTCTCTCGA
Human *DHRS2* forward	TCTGTGTCTACCTCTCTCAGC
Human *DHRS2* reverse	CAATCCCTCTCGTGGAACCAG
Human *TPM4* forward	ACGGTTGCAAAACTGGAAAA
Human *TPM4* reverse	TTGGCTCTGGATGGAAAATC
Human CASP7 forward	CGGTCCTCGTTTGTACCGTC
Human *CASP7* reverse	CGCCCATACCTGTCACTTTATCA
Human *NPTN* forward	GAGGTCATTATTCGAGACAGCC
Human *NPTN* reverse	TTGATCCTGTACTCCATGTTGC
Human *HMOX1* forward	AAGACTGCGTTCCTGCTCAAC
Human *HMOX1* reverse	AAAGCCCTACAGCAACTGTCG
Human *RSC1A1* forward	ATGGACCCAAAATGAGCATCTT
Human *RSC1A1* reverse	CCATCACCTAGACTCCTGAAGT
(Promoter)-*SETD7*-3-F	CACCTTCTCTGTTTAGCCTTG
(Promoter)-*SETD7*-3-R	CTCTCTGAAGTCTCTTGGCTT
(Promoter)-*SETD7*-4-F	AGACTAAGCTAGAGGGTGTCT
(Promoter)-*SETD7*-4-R	ATTGACATAAGGTCCTTGGGG
(Promoter)-*SETD7*-5-F	CCCCAAGGACCTTATGTCAAT
(Promoter)-*SETD7*-5-R	CTGGACCAGAAGTTAGGAGAC
(Promoter)-*SETD7*-8-F	GGCGCTGGAAGTATTTTGAAA
(Promoter)-*SETD7*-8-R	CAAGAACAGCTACTGCATGGA
(Promoter)-*SETD7*-16-F	CAGAAACGCTTCCTTAGCTTC
(Promoter)-*SETD7*-16-R	GGAGCAACTTGAAAGTCCGTC

(Promoter)-*SETD7*-17-F	GACGGACTTTCAAGTTGCTCC
(Promoter)-*SETD7*-17-R	GCGTTTCTCTTTTGCTTAGGT
Antibody	**Source**
Mouse anti-Beta Actin	Proteintech (66009-1-Ig)
Mouse anti-GAPDH	Proteintech (60004-1-Ig)
Rabbit anti-CHAF1B	Abcam (ab109442)
Rabbit anti-SETD7	Abcam (ab124708)
Rabbit anti-Ki67	Abcam (ab15580)
Normal Rabbit IgG	Cell SignalingTechnology (2729S)

Table S2. Top 27 genes in network string interactions ranked by Neighborhood Component Centrality method[1].

GENE	Log_2 (Fold Change)	adj. p	Score
KIF20B	1.207	6.29E-125	25
NEIL3	1.539	5.29E-140	31
CENPE	1.553	5.57E-144	37
MSH2	1.576	2.11E-125	23
CHAF1B	1.613	9.75E-151	27
GMNN	1.674	1.34E-151	30
KIF14	1.731	8.71E-169	35
PCNA	1.981	2.26E-167	36
ORC1	2.019	4.92E-187	36
RECQL4	2.297	1.75E-143	26
KIF23	2.539	1.28E-192	42
PRC1	2.542	7.13E-176	39
BUB1B	2.667	8.89E-188	47
EXO1	2.744	1.05E-235	49
RAD51AP1	2.744	1.07E-206	43
DTL	2.762	1.57E-160	43
KIFC1	3.029	9.14E-221	33
TTK	3.043	7.74E-241	45
ASF1B	3.14	1.48E-220	38
MELK	3.239	3.68E-229	42
MAD2L1	3.328	6.22E-251	43
CDC45	3.405	3.31E-227	49
ZWINT	3.418	3.83E-234	36
CEP55	3.512	3.90E-264	34
TRIP13	3.52	1.40E-234	39
CCNB2	3.886	2.89E-278	41
UBE2C	4.555	6.08E-279	40

1. Chin CH, Chen SH, Wu HH, Ho CW, Ko MT, Lin CY. cytoHubba: identifying hub objects and sub-networks from complex interactome. *BMC Syst Biol.* 2014;8 Suppl 4(Suppl 4):S11.



	age	TNM	T_staging	N_staging	M_staging	sex	smoking_history
MEpurple	-0.0014 (1)	-0.034 (0.7)	0.092 (0.3)	0.003 (1)	-0.21 (0.01)	0.2 (0.02)	-0.058 (0.5)
MEdarkred	-0.043 (0.6)	0.076 (0.4)	-0.053 (0.5)	0.044 (0.6)	-0.083 (0.3)	0.0068 (0.9)	-0.087 (0.3)
MEblack	-0.13 (0.1)	0.28 (0.001)	0.21 (0.01)	0.13 (0.2)	-0.12 (0.2)	-0.026 (0.8)	0.1 (0.2)
MEred	-0.13 (0.1)	0.3 (6e-04)	0.33 (9e-05)	0.13 (0.2)	-0.1 (0.2)	0.17 (0.05)	0.068 (0.4)
MEdarkgreen	-0.21 (0.02)	0.2 (0.02)	0.15 (0.08)	0.16 (0.07)	-0.14 (0.1)	0.047 (0.6)	0.045 (0.6)
MEcyan	-0.094 (0.3)	0.086 (0.3)	0.085 (0.3)	0.09 (0.3)	-0.16 (0.06)	0.088 (0.3)	0.0016 (1)
MEmagenta	-0.11 (0.2)	0.33 (1e-04)	0.21 (0.01)	0.17 (0.06)	-0.097 (0.3)	0.07 (0.4)	0.084 (0.3)
MEtan	-0.081 (0.4)	0.16 (0.07)	0.14 (0.1)	0.13 (0.1)	-0.12 (0.2)	0.089 (0.3)	0.084 (0.3)
MElightyellow	0.089 (0.3)	-0.038 (0.7)	-0.00066 (1)	-0.024 (0.8)	0.045 (0.6)	-0.064 (0.5)	-0.016 (0.9)
MEdarkturquoise	-0.16 (0.07)	0.18 (0.04)	0.23 (0.009)	0.049 (0.6)	0.084 (0.3)	0.23 (0.008)	0.047 (0.6)
MElightcyan	-0.028 (0.8)	0.19 (0.03)	0.16 (0.06)	0.035 (0.7)	0.094 (0.3)	0.025 (0.8)	-0.012 (0.9)
MEmidnightblue	-0.11 (0.2)	0.044 (0.6)	-0.038 (0.7)	-0.049 (0.6)	0.13 (0.1)	-0.13 (0.1)	0.25 (0.005)
MEsalmon	0.0025 (1)	0.069 (0.4)	0.07 (0.4)	-0.092 (0.3)	0.019 (0.8)	-0.18 (0.04)	0.028 (0.7)
MEblue	-0.091 (0.3)	0.34 (8e-05)	0.27 (0.002)	0.1 (0.3)	-0.029 (0.7)	0.018 (0.8)	0.04 (0.6)
MEgrey60	-0.15 (0.08)	0.19 (0.03)	0.24 (0.005)	0.095 (0.3)	0.014 (0.9)	0.048 (0.6)	0.034 (0.7)
MElightgreen	0.16 (0.07)	-0.25 (0.003)	-0.32 (2e-04)	-0.027 (0.8)	0.16 (0.07)	-0.19 (0.03)	-0.075 (0.4)
MEbrown	0.067 (0.4)	-0.1 (0.3)	-0.12 (0.2)	-0.021 (0.8)	0.049 (0.6)	-0.078 (0.4)	-0.028 (0.7)
MEyellow	0.089 (0.3)	-0.22 (0.01)	-0.12 (0.2)	-0.17 (0.05)	-0.0082 (0.9)	-0.071 (0.4)	-0.098 (0.3)
MEroyalblue	0.11 (0.2)	0.062 (0.5)	0.087 (0.3)	-0.035 (0.7)	0.026 (0.8)	0.12 (0.2)	0.042 (0.6)
MEgreen	0.015 (0.9)	-0.18 (0.04)	-0.17 (0.05)	-0.023 (0.8)	0.032 (0.7)	0.072 (0.4)	0.0031 (1)
MEpink	-0.081 (0.4)	0.1 (0.2)	0.026 (0.8)	0.16 (0.07)	0.037 (0.7)	0.14 (0.1)	-0.017 (0.8)
MEgreenyellow	0.054 (0.5)	-0.21 (0.01)	-0.21 (0.01)	-0.011 (0.9)	0.12 (0.2)	0.063 (0.5)	-0.031 (0.7)
MEturquoise	-0.047 (0.6)	-0.063 (0.5)	-0.052 (0.6)	0.034 (0.7)	0.082 (0.4)	0.21 (0.01)	0.051 (0.6)
MEgrey	-0.092 (0.3)	0.071 (0.4)	0.15 (0.08)	0.12 (0.2)	-0.0023 (1)	0.13 (0.1)	0.00014 (1)

Figure S1. Genes altered in Gene Expression Omnibus (GEO) dataset GSE68793 containing 134 LUSCs. (A) Cluster dendrogram. (B) Module-trait relationships. The gradient-filled strip indicates the association between gene modules and sample traits, with red denoting positive correlation and blue indicating negative correlation.

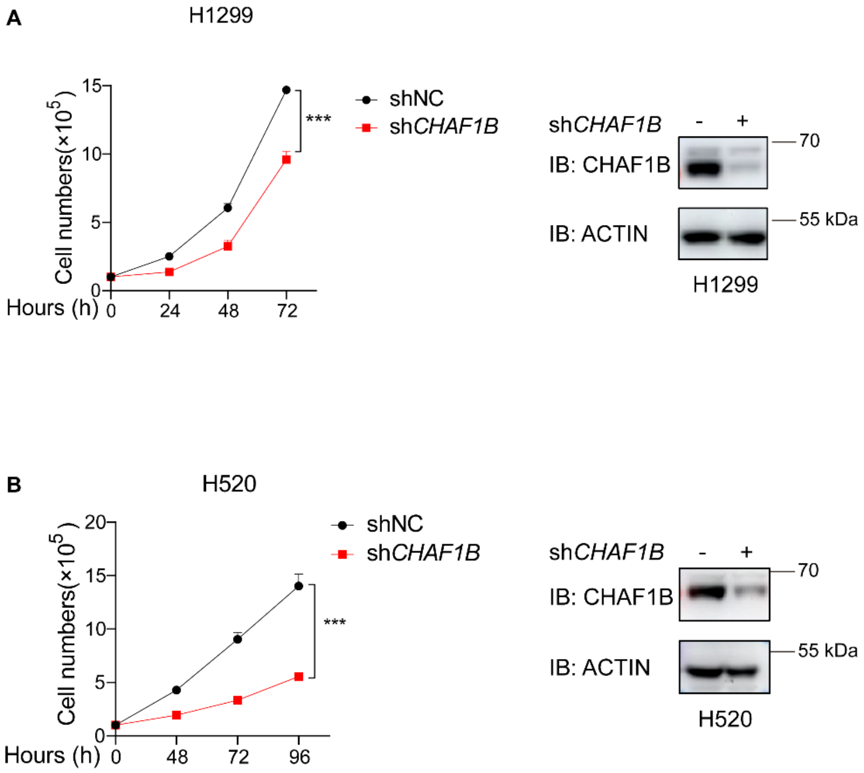


Figure S2. Knockdown of *CHAF1B* inhibits proliferation of H1299 and H520 cells. Proliferation curves and western blot analysis of H1299 cells (A) and H520 cells (B) after stably knockdown of *CHAF1B*.

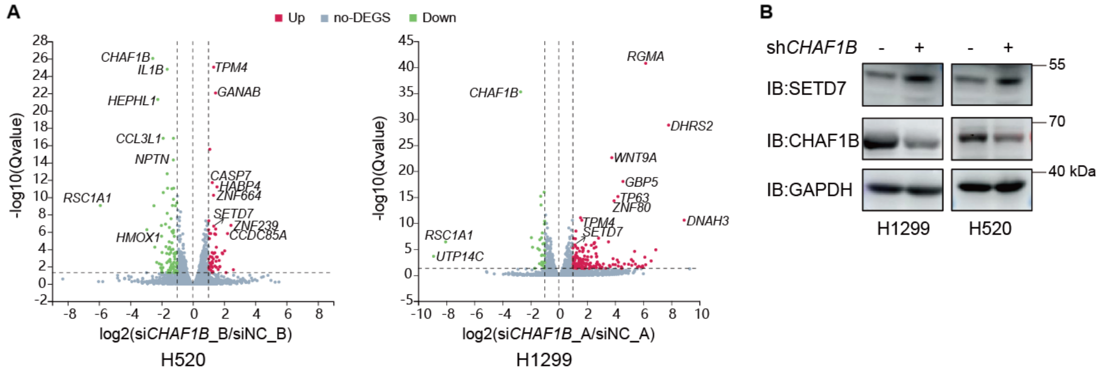


Figure S3. Differentially expressed genes in siNC- and si*CHAF1B*-transfected cells. (A) Volcano plots of up-regulated and down-regulated genes in the si*CHAF1B*-transfected H520 and H1299 cells. (B) Changes in the protein level of SETD7 after stably knockdown of *CHAF1B*.