**a**

|	
Human HSP70	ALESYAFNMKSAVED-EGLKGKISEADKKKVLDKCQEVISML
Human HSC70	SLESYAFNMKATVED-EKLQGKINDEDKQKILDKCNEIINML
Human BIP	ELESYAYSLKNQIGDKEKLGGKLSSEDKETMEKAVEEKIEML
Mus musculus	ALESYAFNMKSAVEDEGLKGKLSEADKKKVLDKCQEV
Drosophila auraria	ALESYVFNVKQAVEQAG--AGKLDEADKNSVLEKCNET
S. Cerevisiae Ssa1	QLESIAYSLKNTIS---EAGDKLEQADKDTVTKKAEETISML
S. Pombe SPAC13G7.02c	HLESYAYSLRNSLDD--PNLKDKVDASDKEAIDKAVKETIEML
E.Coli DnaK	QGDHLLHSTRKQVEE---AGDKLPADDKTAIESALTALETAL

b
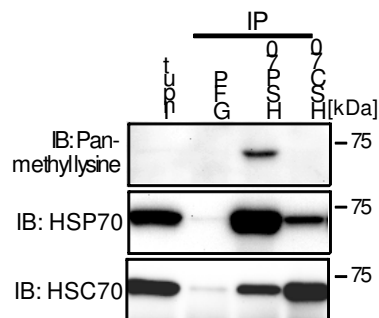
Supplementary Figure S1 | Amino acid sequence alignment of HSP70.
a, Lys 561 is conserved across various species, including *Homo sapiens*, *Mus musculus* and *Drosophila auraria*. **b,** MCF7 cells were lysed with RIPA buffer and whole cell extracts were immunoprcipitated with anti-GFP, anti-HSP70 (clone# C92F3A-5, MBL) and anti-HSC70 (clone# 1B5, MBL) antibodies. After denatured immunoprecipitants with sample buffer, samples were fractionated by SDS-PAGE and immunoblotted with anti-pan-methyllysine, anti-HSP70 and anti-HSC70 antibodies.

a

b

c
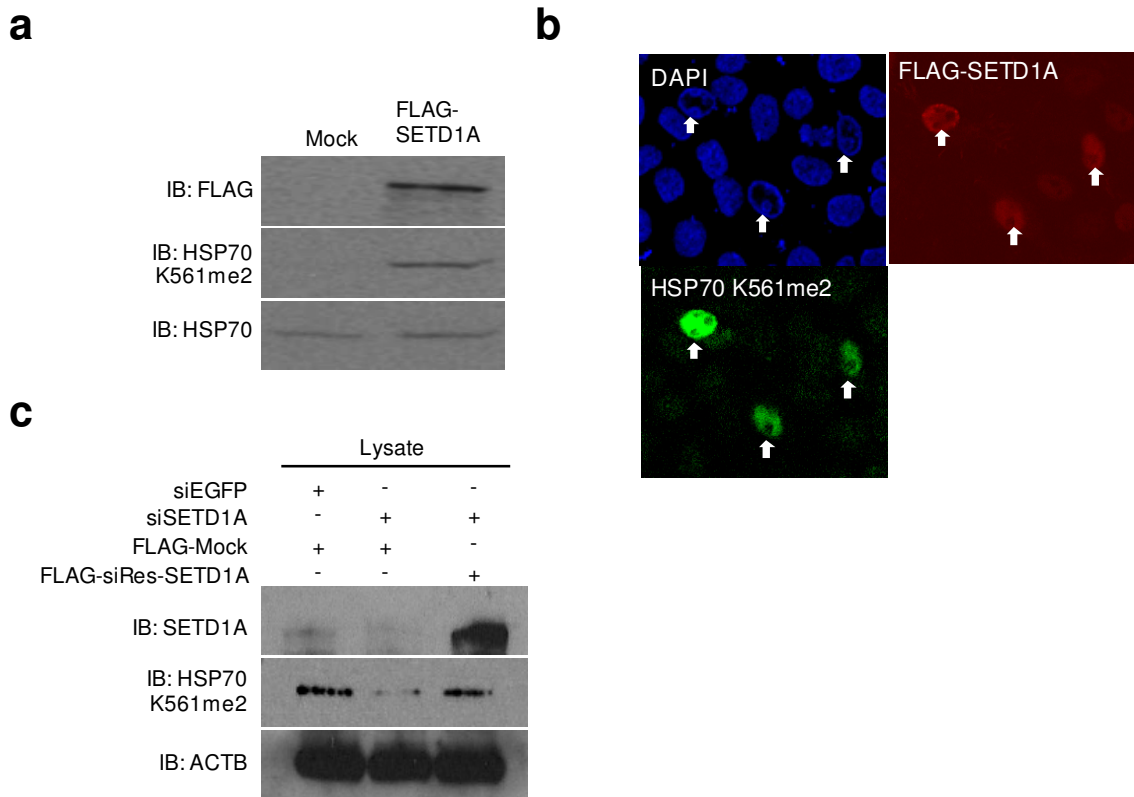
Supplementary Figure S2 | Methylation of HSP70 by SETD1A.
a, COS7 cells were transfected with FLAG-tagged SETD1A (FLAG-SETD1A) and mock (negative control) vectors. Immunoblot analysis was conducted with anti-FLAG, anti-HSP70K561me2 and anti-HSP70 antibodies, respectively. **b,** Immunocytochemical analysis of K561 di-methylation of HSP70. After transfection of COS7 cells with FLAG-SETD1A, immunocytochemical analysis was performed. The cells were stained with an anti-HSP70K561me2 antibody (Alexa 488, green), an anti-FLAG antibody (Alexa 594, red) and DAPI (blue). Scale bar; 20 µm. **c,** Either a FLAG-Mock or a FLAG-siRes-SETD1A expression vector was transfected into HeLa cells treated with siEGFP or siSETD1A for 24 h. The cells were collected 24 h after transfection, and cell lysates were immunobloted with anti-HSP70K561me2, anti-SETD1A and anti-ACTB antibodies.
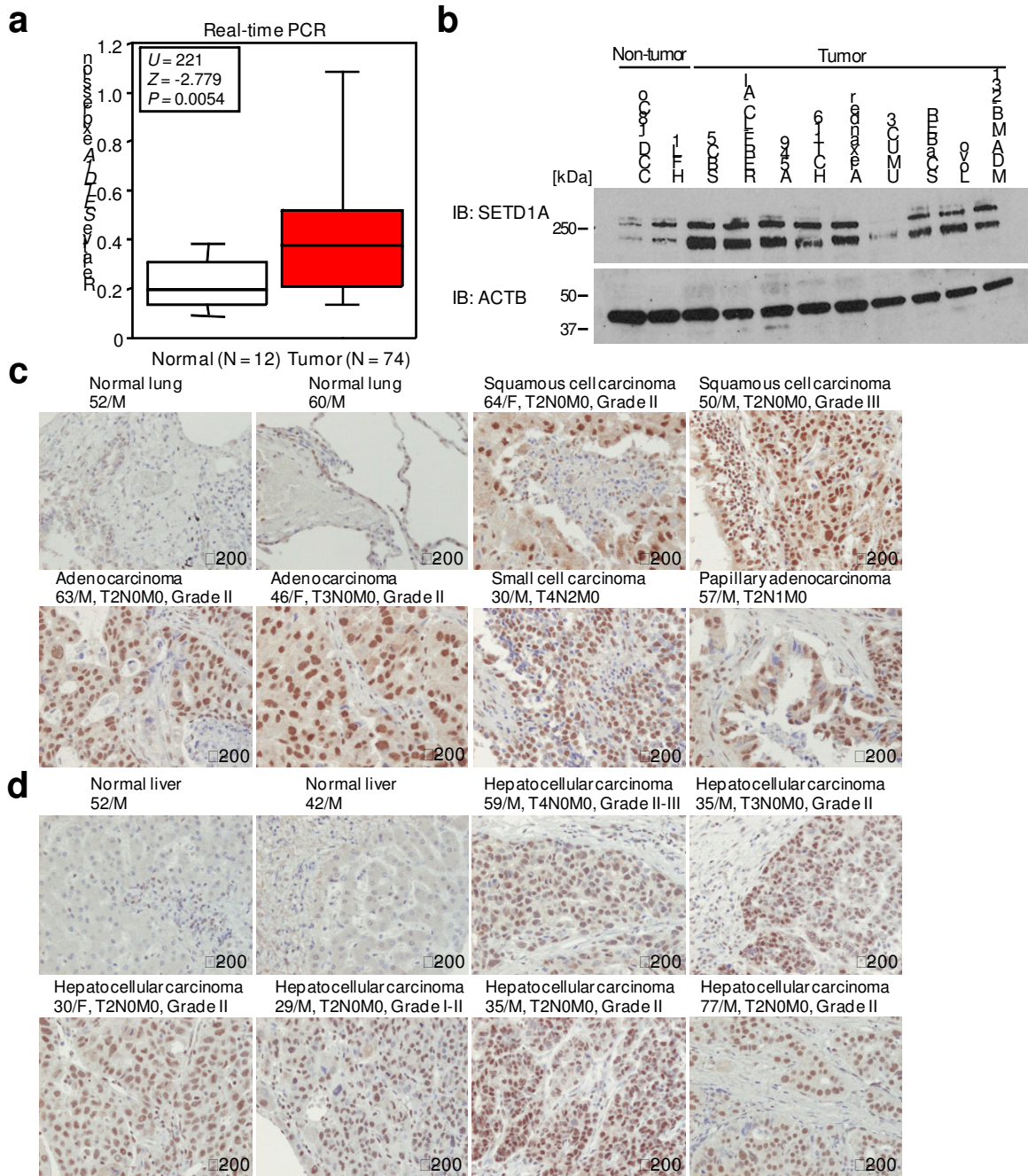
Supplementary Figure S3 | SETD1A is overexpressed in human cancer cells.
a, Expression analysis of *SETD1A* at mRNA levels in 74 bladder cancer cases and 12 normal bladder cases by qRT-PCR, and results are shown by box-whisker plot. *GAPDH* and *SDH* were used as housekeeping genes. The Mann-Whitney *U*-test was used for statistical analysis ($P = 0.0054$). **b**, Expression levels of SETD1A in two non-tumor cell lines (CCD-18Co and HFL1) and nine tumor cell lines (SBC5, RERF-LC-AI, A549, HCT116, Alexander, UMUC3, SCaBER, LoVo and MDA-MB-231). Cell lysates were immunoblotted with an anti-SETD1A antibody (NB100-558, Novus Biologicals). ACTB expression served as an internal control of each sample. **c, d,** Immunohistochemical staining of SETD1A in lung (**c**) and liver (**d**) tissues. Clinical information for each section is represented above histological pictures. Tissue samples were purchased from BioChain. Original magnification, x200.
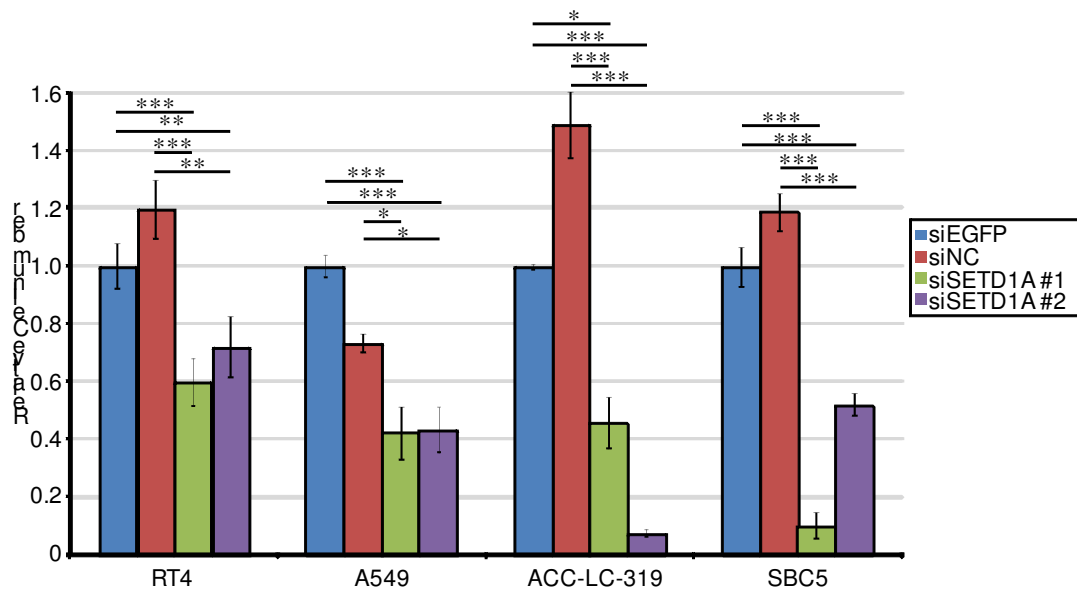
Supplementary Figure S4 | SETD1A is important for the growth regulation of cancer cells.
Effects of *SETD1A* siRNA knockdown on the viability of bladder (RT4) and lung (A549, ACC-LC-319 and SBC5) cancer cell lines. Relative cell numbers were normalized to the number of siEGFP-treated cells (siEGFP = 1): results are the mean ±SD of three independent experiments. *P* values were calculated using Student's *t*-test (*, *P* < 0.05; **, *P* < 0.01; ***, *P* < 0.001).
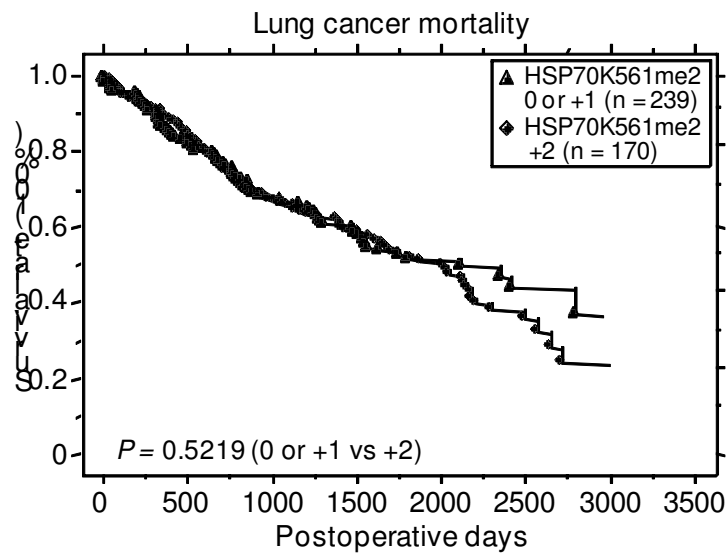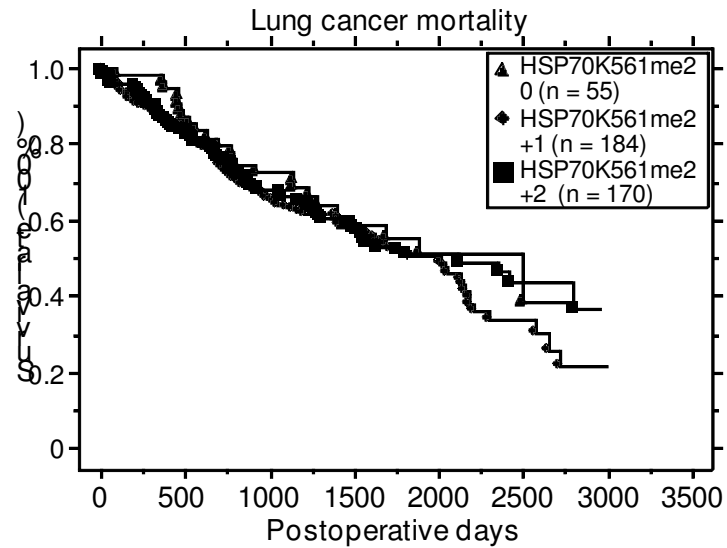
Supplementary Figure S5 | No correlation between HSP70 methylation status and the prognosis of lung cancer.
Kaplan-Meier estimates of overall survival time of patients with non-small cell lung cancer (NSCLC).
P-value was calculated using log-rank test.
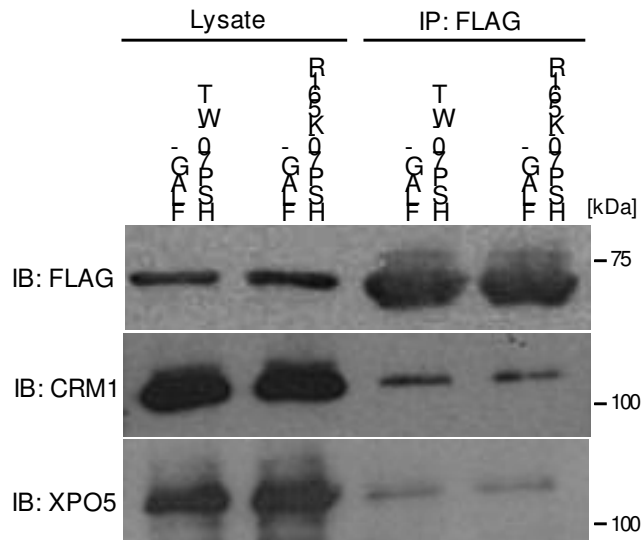
Supplementary Figure S6 | Lys 561 di-methylation of HSP70 does not affect its interactions with CRM1 and XPO5 proteins.
293T cells were transfected with HSP70-WT and HSP70-K561R, respectively. After immunoprecipitation using anti-FLAG M2 agarose, immunoblot analysis was performed with anti-FLAG, anti-CRM1 and anti-XPO5 antibodies.
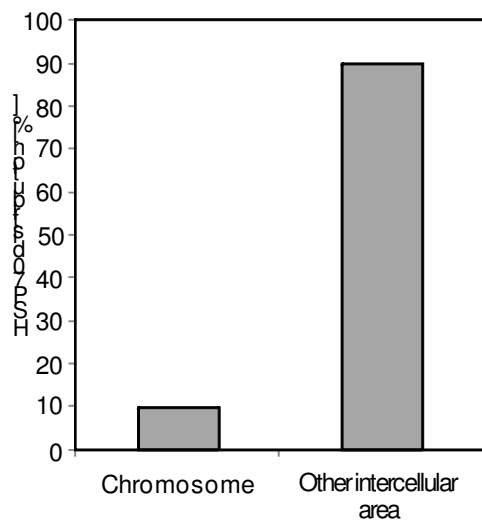
Supplementary Figure S7 | Distribution of HSP70 protein in HeLa cells at the metaphase plate.
Fluorescence signal intensity of HSP70 in each subcellular localization was quantitatively analyzed (Leica Microsystems). The value shows percentage ratio of HSP70 fluorescence signal intensity in chromosome or other intercellular area in comparison to that in the whole cell.
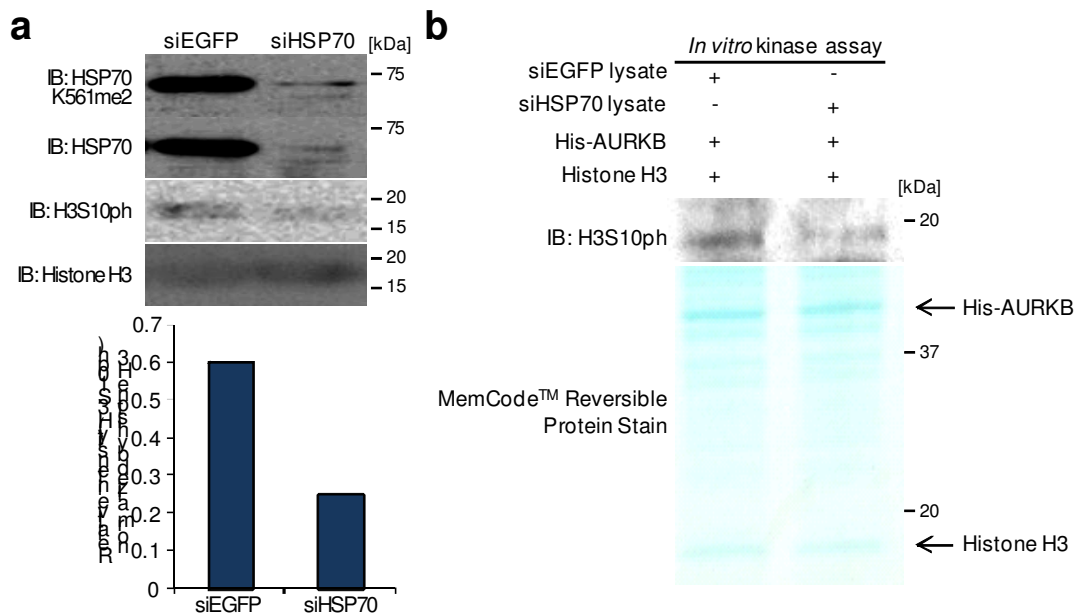
Supplementary Figure S8 | Effect of HSP70 on AURKB kinase activity.
a, Effect of HSP70 knockdown on phosphorylation of histone H3 at Ser 10. HeLa cells were synchronized using 7.5 µg of aphidicolin for 24 h following treatment with HSP70 siRNA for 24 h. Cells were collected 12 h after release from cell cycle arrest, and immunoblot was performed with anti-HSP70 K561me2, anti-HSP70, anti-phospho-histone H3 (Ser 10) and anti-histone H3 antibodies. Signal intensity of phospho-histone H3 (Ser 10) and histone H3 was quantitatively analyzed using GS-800 calibration densitometer (BIO-RAD). Relative intensity of phospho-histone H3 (Ser 10) shows the value normalized the intensity of histone H3.**b,** HeLa cells were lysed with CelLytic[TM]M Cell Lysis Reagent (Sigma-Aldrich) 48 h after treatment with siEGFP (control) or siHSP70. Cell lysates were mixed with His-AURKB enzyme and histone H3 substrate, in the reaction buffer (40 mM MOPS [pH7.0], 1 mM EDTA) and incubated for 10 min at 30°C, then the mixture was immunobloted with an anti-phospho-histone H3 (Ser 10) antibody. His-AURKB and histone H3 proteins used in the reaction were visualized by MemCode[TM] Reversible Protein Stain (Thermo Scientific).
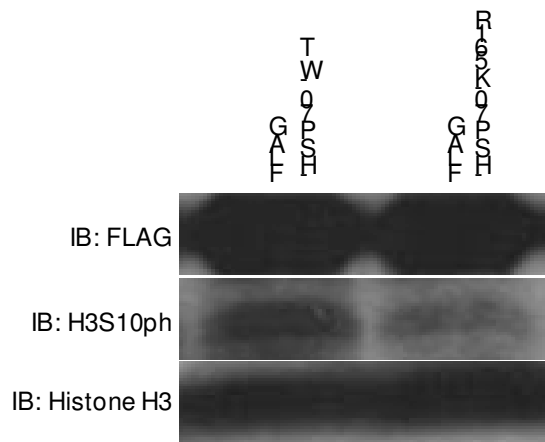
Supplementary Figure S9 | Construction of HeLa stable cell lines overexpressing HSP70-WT and HSP70-K561R.
Immunoblot analysis was performed with anti-FLAG, anti-phospho-H3 Ser 10 and anti-histone H3 antibodies.
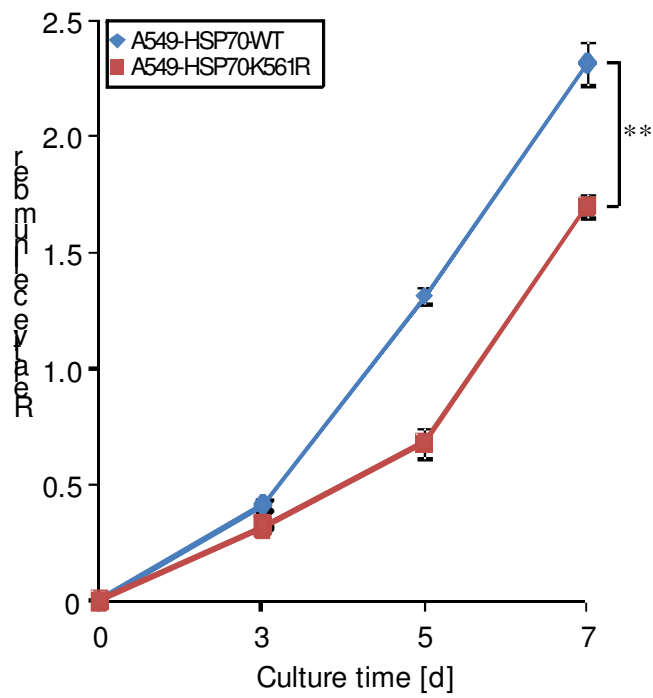
Supplementary Figure S10 | Cell growth assay of A549 stable cell lines.
Cell growth was measured by Cell Counting Kit-8 (Dojindo). Results are the mean ± SD in three independent experiments. *P*-values were calculated using Student's *t*-test (**, *P* < 0.01).

siHSP70 treatment $\xrightarrow{\text{24 h}}$ pCAGGS-n3FC-HSP70 (siRNA resistant)
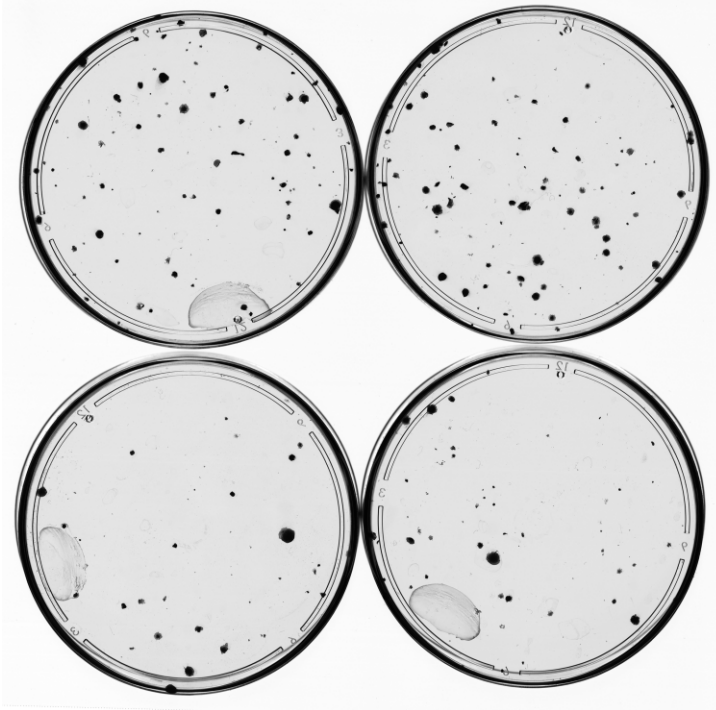
siHSP70 treatment $\xrightarrow{\text{24 h}}$ pCAGGS-n3FC-HSP70 K561R
(siRNA resistant)
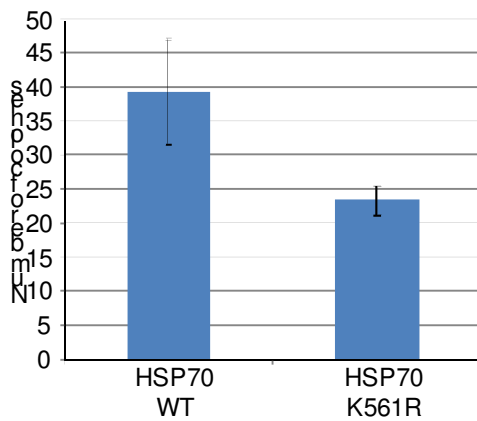
Supplementary Figure S11 | Methylation of K561 on HSP70 promotes oncogenic activity.
HEK293 cells were transfected with a FLAG-siRes-WT-HSP70 vector and a FLAG-siRes-K561R-HSP70 vector after treatment with siHSP70 for 24 h. The cells were cultured in a selection medium (D-MEM containing 10% FBS and 0.9 mg/ml Geneticin/G-418) for 2 weeks. Colonies were stained with Giemsa (MERCK, Whitehouse station, NJ, USA) and counted by Colony Counter software. Results are the mean ± SD in three independent experiments.
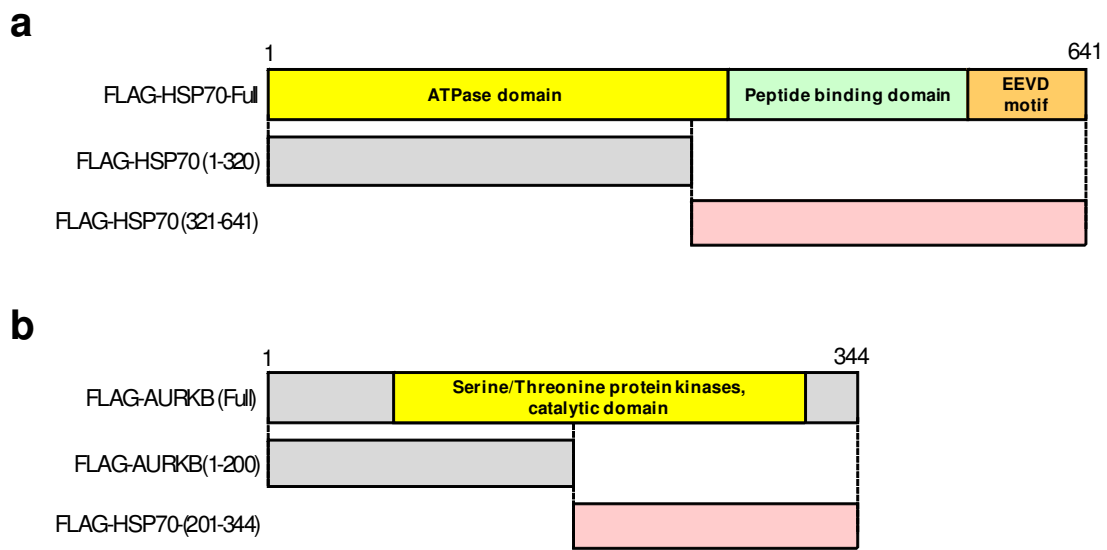
Supplementary Figure S12 | Structure of HSP70 and AURKB constructs.
a, For HSP70 functional analysis, an N-term HSP70 expression vector (1-320) and a C-term HSP70 expression vector (321-641) were constructed besides a full-length HSP70 expression vector. **b,** An N-term AURKB expression vector (1-200) and a C-term AURKB expression vector (201-344) were constructed besides a full-length AURKB expression vector to identify the binding region with HSP70.

Supplementary Table S1 | Methylated peptides

Position	Start - End	Sequence	Methylation status	Ion score
K71	57 - 71	NQVALNPQNTVFDA<u>K</u>	2	39
K77	73 - 88	LIGR<u>K</u>FGDPVVQSDMK	3	42
K88	78 - 88	FGDPVVQSDM<u>K</u>	2	40
K112	103 - 112	VQVSYKGET<u>K</u>	2	41
K126	113 - 126	AFYPEEISSMVLT<u>K</u>	2	41
	551 - 561	SAVEDEGLKG<u>K</u>	1	49
	551 - 567	SAVEDEGLKG<u>K</u>ISEADK	1	57
	551 - 567	SAVEDEGLKG<u>K</u>ISEADKK	2	60
K561	551 - 568	SAVEDEGLKG<u>K</u>ISEADKK	1	46
	560 - 568	G<u>K</u>ISEADKK	1	49
	560 - 568	G<u>K</u>ISEADKK	2	28
	560 - 569	G<u>K</u>ISEADKKK	2	28
K559/561	551 - 567	SAVEDEGL<u>K</u>G<u>K</u>ISEADK	2, 1	35

Supplementary Table S2 | Clinicopathologic characteristics of lung tissues on the tissue microarray*

Case number	Age	Gender	Pathology	Grade	Stage (TNM)	Nature	Reactivity (Nu, density)
1	52	M	Normal			Normal	Weak: 1
2	47	M	Normal			Normal	Moderate: 2
3	59	M	Normal			Normal	Weak: 1
4	60	M	Normal			Normal	Moderate: 1
5	51	M	Squamous cell carcinoma	I	T2N1M0	Malignant	Strong: 3
6	77	M	Squamous cell carcinoma	I-II	T2N0M0	Malignant	Moderate: 2
7	51	M	Squamous cell carcinoma	II	T2N0M0	Malignant	Strong: 3
8	72	M	Squamous cell carcinoma	II	T1N0M0	Malignant	Moderate: 2
9	64	F	Squamous cell carcinoma	II	T2N0M0	Malignant	Moderate: 2
10	76	M	Squamous cell carcinoma	II	T2N1M0	Malignant	Moderate: 2
11	50	M	Squamous cell carcinoma	III	T2N0M0	Malignant	Strong: 3
12	53	F	Squamous cell carcinoma	III	T2N1M0	Malignant	Strong: 3
13	74	M	Squamous cell carcinoma	III	T2N0M0	Malignant	Moderate: 2
14	53	F	Squamous cell carcinoma	III	T2N1M0	Malignant	Moderate: 2
15	72	M	Squamous cell carcinoma	III	T2N1M0	Malignant	Moderate: 2
16	65	M	Squamous cell carcinoma	III	T2N1M0	Malignant	Strong: 2
17	50	M	Adenocarcinoma	I	T2N1M0	Malignant	Moderate: 2
18	49	F	Adenocarcinoma	I-II	T2N1M0	Malignant	Moderate: 2
19	65	F	Adenocarcinoma	I	T2N0M0	Malignant	Moderate: 2
20	55	F	Adenocarcinoma	II	T2N0M0	Malignant	Strong: 3
21	63	M	Adenocarcinoma	II	T2N2M0	Malignant	Strong: 3
22	46	F	Adenocarcinoma	II	T3N0M0	Malignant	Strong: 3
23	41	F	Adenocarcinoma	II	T2N0M0	Malignant	Strong: 3
24	61	F	Metastatic adenocarcinoma			Metastasis	Moderate: 2
25	55	F	Adenocarcinoma	III	T2N0M0	Malignant	Moderate: 2
26	51	M	Adenocarcinoma	III	T2N0M0	Malignant	Moderate: 2
27	59	M	Adenocarcinoma	III	T2N0M0	Malignant	Strong: 3
28	52	M	Adenocarcinoma	III	T2N0M0	Malignant	Moderate: 2
29	38	M	Adenosquamous carcinoma		T2N1M0	Malignant	Weak: 1
30	76	M	Adenosquamous carcinoma		T2N0M0	Malignant	Moderate: 2
31	38	M	Adenosquamous carcinoma		T2N0M0	Malignant	Strong: 3
32	30	M	Small cell carcinoma		T4N2M0	Malignant	Strong: 3
33	1.5	M	Small cell carcinoma		T2N0M0	Malignant	Strong: 3
34	52	M	Small cell carcinoma		T2N1M0	Malignant	Strong: 3
35	56	M	Bronchioloalveolar carcinoma		T2N0M0	Malignant	Strong: 3
36	56	M	Undifferentiated carcinoma, large cell		T2N0M0	Malignant	Moderate: 2
37	49	M	Papillary adenocarcinoma		T2N0M0	Malignant	Strong: 3
38	57	M	Papillary adenocarcinoma		T2N1M0	Malignant	Strong: 3
39	40	F	Papillary adenocarcinoma		T2N0M0	Malignant	Strong: 3
40	61	M	Papillary adenocarcinoma		T4N1M0	Malignant	Strong: 3

*All tissue samples were purchased from BioChain

Negative: 0
Weak: 1
Moderate: 2
Strong: 3

Supplementary Table S3 | Clinicopathologic characteristics of liver tissues on the tissue microarray*

Case number	Age	Gender	Histology	Grade	Stage (TNM)	Anatomic site	Reactivity (Nu, density)
1	52	M	Normal			Liver	Weak: 1
2	42	M	Normal			Liver	Weak: 1
3	35	F	Hepatocellular carcinoma	III	T3N0M0	Liver	Weak: 1
4	57	M	Hepatocellular carcinoma	III	T3N0M0	Liver	Moderate: 2
5	47	M	Hepatocellular carcinoma	III	T3N0M0	Liver	Negative: 0
6	31	F	Hepatocellular carcinoma	II~III	T3N0M0	Liver	Moderate: 2
7	49	M	Hepatocellular carcinoma	II~III	T3N0M0	Liver	Strong: 3
8	54	M	Hepatocellular carcinoma	III	T4N1M0	Liver	Moderate: 2
9	33	M	Hepatocellular carcinoma	II~III	T3N0M0	Liver	Moderate: 2
10	40	M	Hepatocellular carcinoma	I~II	T3N0M0	Liver	Weak: 1
11	55	F	Hepatocellular carcinoma	II	T3N0M0	Liver	Weak: 1
12	50	M	Hepatocellular carcinoma	II-III	T3N0M0	Liver	Weak: 1
13	47	M	Hepatocellular carcinoma	II-III	T3N0M0	Liver	Weak: 1
14	79	M	Hepatocellular carcinoma	II-III	T3N0M0	Liver	Weak: 1
15	44	M	Hepatocellular carcinoma	II-III	T3N0M0	Liver	Weak: 1
16	45	M	Hepatocellular carcinoma	III	T3N0M0	Liver	Weak: 1
17	48	M	Clear cell carcinoma	III	T3N0M0	Liver	Moderate: 2
18	59	M	Hepatocellular carcinoma	II-III	T4N0M0	Liver	Weak: 1
19	35	F	Hepatocellular carcinoma	II	T3N0M0	Liver	Moderate: 2
20	42	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Negative
21	57	F	Hepatocellular carcinoma	II-III	T4N1M1	Liver	Weak: 1
22	61	M	Hepatocellular carcinoma	II-III	T4N0M0	Liver	Weak: 1
23	44	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Moderate: 2
24	37	F	Hepatocellular carcinoma	II	T4N0M0	Liver	Moderate: 2
25	35	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Weak: 1
26	35	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Moderate: 2
27	43	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
28	0.38	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
29	30	F	Hepatocellular carcinoma	II	T2N0M0	Liver	Moderate: 2
30	36	M	Hepatocellular carcinoma	I-II	T3N0M0	Liver	Moderate: 2
31	39	M	Hepatocellular carcinoma	I	T2N0M0	Liver	Weak: 1
32	77	M	Hepatocellular carcinoma	I-II	T2N0M0	Liver	Moderate: 2
33	29	M	Hepatocellular carcinoma	I-II	T2N0M0	Liver	Moderate: 2
34	77	F	Hepatocellular carcinoma	II-III	T2N0M0	Liver	Weak: 1
35	60	F	Leiomyosarcoma?			Liver	Moderate: 2
36	41	M	Hepatocellular carcinoma	II-III	T2N0M0	Liver	Moderate: 2
37	39	F	Clear cell carcinoma	II	T2N0M0	Liver	Moderate: 2
38	38	F	Hepatocellular carcinoma	II-III	T2N0M0	Liver	Moderate: 2
39	69	F	Hepatocellular carcinoma	II	T3N0M0	Liver	Moderate: 2

*All tissue samples were purchased from BioChain

Negative: 0

Weak: 1

Moderate: 2

Supplementary Table S3 | (Continued) Clinicopathologic characteristics of liver tissues on the tissue microarray*

Case number	Age	Gender	Histology	Grade	Stage (TNM)	Anatomic site	Reactivity (Nu, density)
40	38	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Weak: 1
41	76	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Negative: 0
42	38	M	Hepatocellular carcinoma	I-II	T3N0M0	Liver	Weak: 1
43	30	M	Bile duct carcinoma	II	T2N0M0	Liver	Moderate: 2
44	1.5	M	Hepatoblastoma			Liver	Weak: 1
45	52	M	Hepatocellular carcinoma	I-II	T3N0M0	Liver	Weak: 1
46	56	M	Hepatocellular carcinoma	II	T4N0M0	Liver	Weak: 1
47	56	M	Hepatocellular carcinoma	II	T4N1M0	Liver	Weak: 1
48	49	M	Hepatocellular carcinoma	II	T4N0M0	Liver	Moderate: 2
49	57	M	Hepatocellular carcinoma	II-III	T4N1M0	Liver	Moderate: 2
50	40	F	Leiomyosarcoma?	II	T2N0M0	Liver	Weak: 1
51	61	M	Hepatocellular carcinoma	II-III	T4N1M1	Liver	Moderate: 2
52	73	F	Clear cell carcinoma	II	T3N0M0	Liver	Negative: 0
53	41	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
54	58	F	Hepatocellular carcinoma	III	T2N0M0	Liver	Moderate: 2
55	43	F	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
56	67	F	Hepatocellular carcinoma	II	T2N0M0	Liver	Negative: 0
57	50	M	Hepatocellular carcinoma	I	T2N0M0	Liver	Weak: 1
58	52	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
59	54	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
60	40	F	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
61	81	M	Hepatocellular carcinoma	II	T3N0M0	Liver	Weak: 1
62	64	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
63	82	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Weak: 1
64	43	F	Hepatocellular carcinoma	II	T2N0M0	Liver	Moderate: 2
65	79	F	Hepatocellular carcinoma	I	T2N0M0	Liver	Moderate: 2
66	73	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Moderate: 2
67	62	M	Hepatocellular carcinoma	II	T2N0M0	Liver	Moderate: 2
68	69	F	Fibrosarcoma?			Liver	Moderate: 2
69	56	F	Hepatocellular carcinoma	II	T3N0M0	Liver	Moderate: 2

Negative: 0
Weak: 1
Moderate: 2
Strong: 3

Supplementary Table S4 | Association between dimethylated HSP70-status in NSCLC and patients' characteristics (n = 409)

		Total (n = 409)	HSP70me2 +2 (n = 170)	HSP70me2 +1 (n = 184)	HSP70me2 0 (n = 55)	*P* value (+2 vs 0 or +1)
Gender						
	Male	286	128	122	36	0.0215*
	Female	123	42	62	19	
Age (years)						
	65	201	88	89	24	NS (0.5481)
	65	208	82	95	31	
Histological type						
	ADC	259	95	123	41	
	SCC	103	57	40	6	0.0093*·**
	Others	47	18	21	8	
pT factor						
	pT1	136	49	63	24	
	pT2	146	65	68	13	NS (0.1374***)
	pT3	43	20	16	7	
	pT4	84	36	37	11	
pN factor						
	N0	253	98	121	34	
	N1	49	18	21	10	NS (0.3021****)
	N2	107	54	42	11	

Others, large-cell carcinoma (LCC) plus adenosquamous-cell carcinoma (ASC).

*P 0.05 (Fisher's exact test).

**ADC versus non-ADC.

***T1 versus T2/T3/T4.

****N0 versus N1/N2.

Abbreviation: ADC, adenocarcinama; SCC, squamous-cell carcinoma; NS, not significant.

Supplementary Table S5 | List of proteins we have been examined to indetify K561 methylation-dependent binding partners of HSP70

Gene Symbol	Gene Description
AURKA	Aurora A kinase
AURKB	Aurora B kinase
DNMT1	DNA (cytosine-5)-methyltransferase 1
POLD1	Polymerase (DNA directed), delta 1, catalytic subunit 125kDa
UHRF1	Ubiquitin-like with PHD and ring finger domains 1
HDAC1	Histone deacetylase 1
HDAC2	Histone deacetylase 2
RCOR1	REST corepressor 1
NCOR1	Nuclear receptor corepressor 1
BIRC5	Baculoviral IAP repeat containing 5
SIN3A	SIN3 transcription regulator homolog A (yeast)
CBX1	Chromobox homolog 1
NCL	Nucleolin
NPM1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)
MCM7	Minichromosome maintenance complex component 7
MCM2	Minichromosome maintenance complex component 2
MCM10	Minichromosome maintenance complex component 10
PCNA	Proliferating cell nuclear antigen
Rad51	RAD51 homolog

Supplementary Table S6 | Characteristics of bladder tissue samples*

Patient ID	Age/Gender	Histology	Grade	Stage (TNM)
Case 1	49/F	TCC	I	T1N0M0
Case 2	64/M	TCC	III	T3N2M1
Case 3	51/M	TCC	I	T1N0M0
Case 4	50/M	ADC	III	T2N0M0
Case 5	52/M	TCC	II	T1N0M0
	71/M	Normal		

*All tissue samples were purchased from BioChain.
Abbreviation: TCC, transitional cell carcinoma; ADC, adenocarcinoma

Supplementary Table S7 | Characteristics of lung tissue samples*

Patient ID	Age/Gender	Histology	Tumor size (cm)	Differentiation	Stage (TNM)
Case 1	65/F	SCC	2.5 (diameter)	Poorly	T1N0M0
Case 2	68/F	SCC	3 x 5	Moderately	T2N0M0
Case 3	58/M	SCC	3 x 2	Moderately	T2N1M0
Case 4	N/A	ADC			T0NxMx
Case 5	52/M	ADC	6.5 x 6 x 1	Moderately	T3N0M0
	N/A	Normal			

*All tissue samples were purchased from BioChain.

Abbreviation: SCC, squamous cell carcinoma; ADC, adenocarcinoma; N/A, no applicable

Supplementary Table S8 | Characteristics of kidney tissue samples*

Patient ID	Age/Gender	Histology	Stage (TNM)
Case 1	58/M	Clear cell carcinoma	T1N0M0
Case 2	50/M	Clear cell carcinoma	T2N0M0
Case 3	71/M	Transitional cell carcinoma	T2N0M0

*All tissue samples were purchased from BioChain.

Supplementary Table S9 | siRNA sequences

siRNA name		Sequence
siEGFP (control)		Sense: 5' GCAGCACGACUUCUUCAAG 3'
		Antisense: 5' CUUGAAGAAGUCGUGCUGC 3'
siFFLuc (control)		Sense: 5' GUGCGCUGCUGGUGCCAAC 3'
		Antisense: 5' GUUGGCACCAGCAGCGCAC 3'
siNegative control (cocktail)	Target #1	Sense: 5' AUCCGCGCGAUAGUACGUA3'
		Antisense: 5' UACGUACUAUCGCGCGGAU 3'
	Target #2	Sense: 5' UUACGCGUAGCGUAAUACG 3'
		Antisense: 5' CGUAUUACGCUACGCGUAA 3'
	Target #3	Sense: 5' UAUUCGCGCGUAUAGCGGU 3'
		Antisense: 5' ACCGCUAUACGCGCGAAUA 3'
siHSP70		Sense: 5' CCGAGAAGGACGAGUUUGA 3'
		Antisense: 5' UCAAACUCGUCCUUCUCGG 3'
siSETD1A #1		Sense: 5' CUCAGAAGGUGUACCGCUA 3'
		Antisense: 5' UAGCGGUACACCUUCUGAG 3'
siSETD1A #2		Sense: 5' GGAAGAAGAAGCUCCGAUU 3'
		Antisense: 5' AAUCGGAGCUUCUUCUUCC 3'