Supplementary Materials for

Targeting carnitine palmitoyl transferase 1A (CPT1A) induces ferroptosis

and synergizes with immunotherapy in lung cancer

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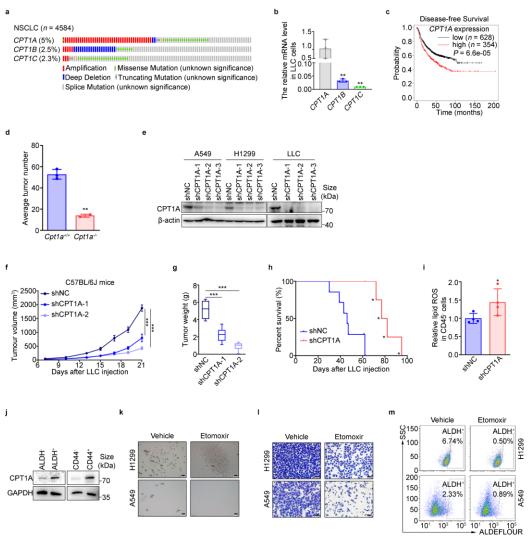


Figure. S1.

CPT1A is essential for LCSCs maintenance and NCSLC progression.

a, Mutation frequency of *CPT1A*, *CPT1B* and *CPT1C* genes in NSCLC patients analyzed with cibioportal website. **b**, Quantification of mRNA for *Cpt1a*, *Cpt1b* and *Cpt1c* in LLC cells. **c**, Disease-free survival of NSCLC patients stratified according to tumor CPT1A expression analyzed with Kaplan-Meier Plotter websites. **d**, Qualification of lung tumor number from SKC (*Sftpc*-CreER^{T2}; *Kras*^{G12D}; *Cpt1a*^{flox/flox}) or control mice. **e**, Representative western blot for CPT1A in A549, H1299 and LLC cells. **f-i**, Effects of CPT1A on tumor progression in C57BL/6J mice subcutaneously transplanted with LLC-shNC/shCPT1A cells. Data represent the mean \pm s.d., n = 5 samples. Tumor growth curve (**f**). tumor weights (**g**). Overall survival of tumor-bearing mice (**h**). Lipid ROS levels in CD45⁻ cells of H1299 cells. **k-m**, Effects of etomoxir on stemness phenotypes of H1299 and A549 cells. Sphere-forming assay Scale bars, 200 µm (insets) (**k**). Transwell assay Scale bars, 50 µm (insets) (**l**). Percentage of ALDH⁺ cells (**m**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001; significance was determined

by unpaired two-tailed Student's t test, or one way ANOVA test followed by Tukey's correction.

Supplementary Figure 2

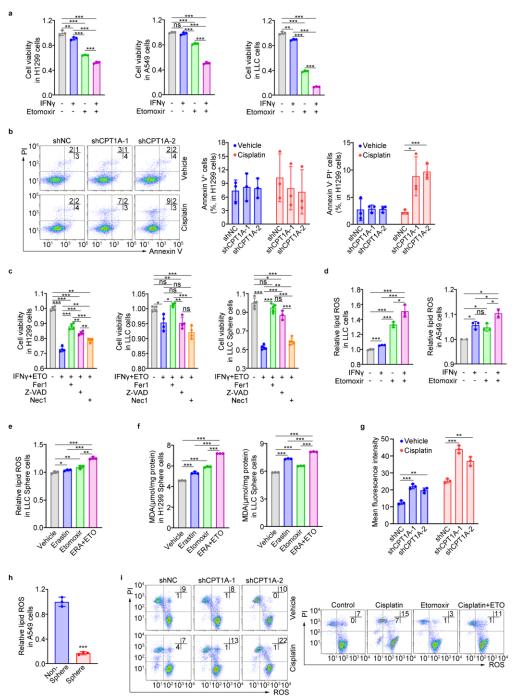


Figure. S2.

CPT1A is an essential driver for the ferroptosis resistance in LCSCs.

a, Cell viability of H1299 (left), A549 (middle) and LLC (right) cells treated with IFN γ (100 μ M) or etomoxir (100 μ M) for 2 days. **b**, Percentages of AnnexinV⁺ or AnnexinV⁻ PI⁺ cells in H1299-shNC/shCPT1A cells treated with DMSO or cisplain for 2 days. **c**, Cell viability of H1299 cells (left), LLC cells (middle) or LLC sphere cells (right) treated with IFN γ (100 μ M) or etomoxir (100 μ M) in the presence of ferrostatin-1 (Fer1, 2 mM), necostatin-1 (Nec1, 1 mM), or z-VAD-FMK (z-VAD, 10 mM) for 2 days (*n* = 3). **d**, Lipid ROS levels in LLC (left) and A549 (right) cells treated with IFN γ (100 μ M)

or etomoxir (100 µM) for 2 days determined by flow cytometry. **e**, Lipid ROS levels in LLC sphere cells treated with etomoxir (100 µM) for 2 days and then erastin (2 µM) for 6 h determined by flow cytometry. Data represent the mean \pm s.d.; n = 3 samples. **f**, The MDA levels in H1299 (left) or LLC (right) sphere cells treated with etomoxir (100 µM) for 2 days and then erastin (2 µM) for 6 h determined by flow cytometry. Data represent the mean \pm s.d.; n = 3 samples. **g**, Quantification of ROS levels in H1299-shNC/shCPT1A cells treated with DMSO or cisplain for 2 days determined by flow cytometry. Data represent the mean \pm s.d.; n = 3 samples. **h**, Lipid ROS levels in spheres or non-spheres of A549 cells determined by flow cytometry. **i**, Representative flow cytometry for ROS⁺PI⁺ or ROS⁻PI⁻ cells in H1299-shNC/shCPT1A cells treated with DMSO or cisplain for 2 days (right). Data represent the mean \pm s.d., n = 3-5 samples. *P < 0.05, **P < 0.01, ***P < 0.001; significance was determined by unpaired two-tailed Student's t test, or one way ANOVA test followed by Tukey's correction.



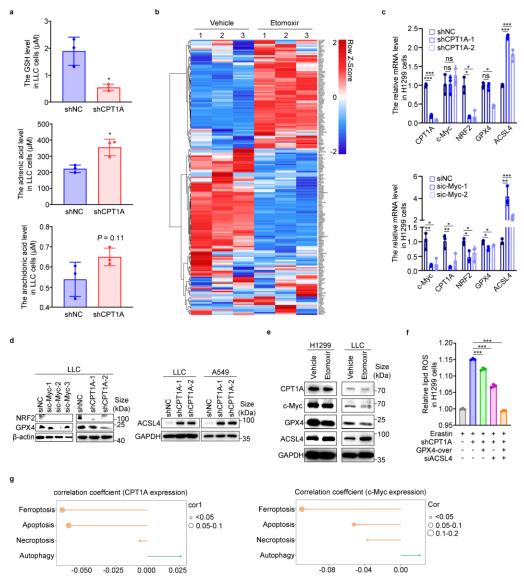


Figure. S3.

CPT1A regulates ferroptosis of LCSCs via GPX4 and ACSL4.

a, Levels of GSH (up), adrenic acid (middle) and arachidomic acid (down) in LLC-shNC/shCPT1A cells calculated by LC-MS. Data represent the mean \pm s.d.; n=3 samples. **b**, A heatmap of RNA-seq data depicting the differential genes regulating ferroptosis upon H1299 cells treated with etomoxir (100 μ M) or not for 2 days (Q < 0.05). **c**, Quantification of mRNA for *CPT1A*, *c-Myc*, *NRF2*, *GPX4* and *ACSL4* in H1299-shNC/shCPT1A cells (up) or H1299 cells transfected with sic-Myc or control siRNA (down). **d**, Representative western blot for NRF2 and GPX4 in LLC-shNC/shCPT1A cells or in LLC cells transfected with sic-Myc or control siRNA (left). Representative western blot for ACSL4 in LLC-shNC/shCPT1A cells (right). **e**, Representative western blot for CPT1A, c-Myc, GPX4 and ACSL4 in H1299/LLC cells treated with etomoxir (100 μ M) or not for 2 days. **f**, Lipid ROS levels in H1299-shNC/shCPT1A cells transfected with GPX4 plasmid or

ACSL4 siRNA determined by flow cytometry. Data represent the mean \pm s.d., n = 3 samples. **g**, Correlation analysis of *CPT1A/c-Myc* transcripts with distinct types of cellular death in NSCLC patients by informatic analysis. *P < 0.05, **P < 0.01, ***P < 0.001; ns: not significant. The statistical analysis was performed using a two-tailed Student's t-test.

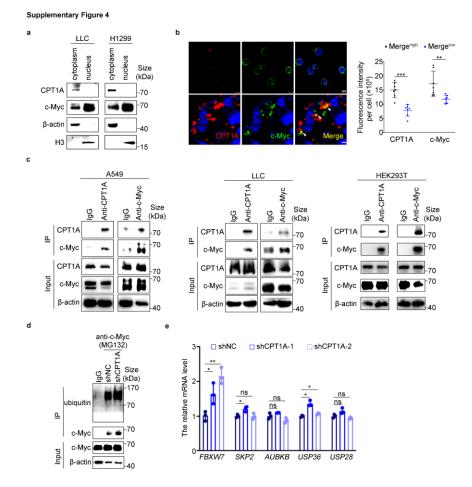


Figure. S4.

CPT1A inhibits ubiquitination degradation of c-Myc.

a, Representative western blot for CPT1A, c-Myc, β -actin and Histone H3 in cytoplasm or nucleus of H1299/LLC cells. **b**, Representative immunofluorescence staining for CPT1A and c-Myc in H1299 cells. Scale bar: 10 µm (up); 0.5 µm (down). Quantifications of immunofluorescence are shown on the right. Data represent the mean \pm s.d., n = 7 samples. **c**, Co-immunoprecipitation with CPT1A or c-Myc antibody and representative western blot for CPT1A and c-Myc in A549 (left), LLC (middle) and HEK293T (right) cells. **d**, Co-Immunoprecipitation with c-Myc antibody and representative western blot for ubiquitin and c-Myc in H1299-shNC/shCPT1A cells treated with MG132 (10 µM) for 12 h. **e**, Quantification of mRNA for *FBXW7*, *SKP2*, *AUBKB*, *USP36*, and *USP28* in H1299-shNC/shCPT1A cells. *P < 0.05, **P < 0.01; significance was determined by unpaired two-tailed Student's t test, or one way ANOVA test followed by Tukey's correction.

Supplementary Figure 5

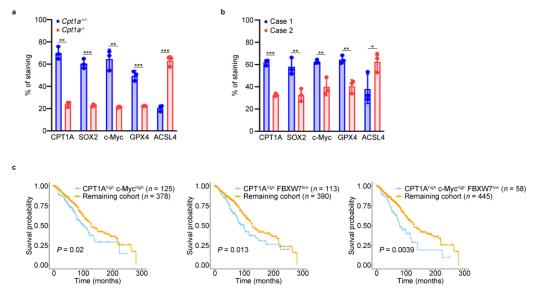


Figure. S5.

The clinical significance of CPT1A, c-Myc and FBXW7 in NSCLC patients.

a, Qualification of IHC staining for CPT1A, SOX2, c-Myc, GPX4 and ACSL4 in the tumor of $Cpt1a^{+/+}$ or $Cpt1a^{-/-}$ transgenic mice **b**, Qualification of IHC staining for CPT1A, SOX2, c-Myc, GPX4 and ACSL4 in the tumor of NSCLC patients. **c**, Overal survival (OS) of NSCLC patients stratified according to the expression of *CPT1A*, *c*-*Myc* and *FBXW7*. **P* < 0.05, ***P* < 0.01, ****P* < 0.001; ns: not significant. The statistical analysis was performed using a two-tailed Student's t-test, Pearson's correlation test or log-rank (Mantel–Cox) test.

Supplementary Figure 6

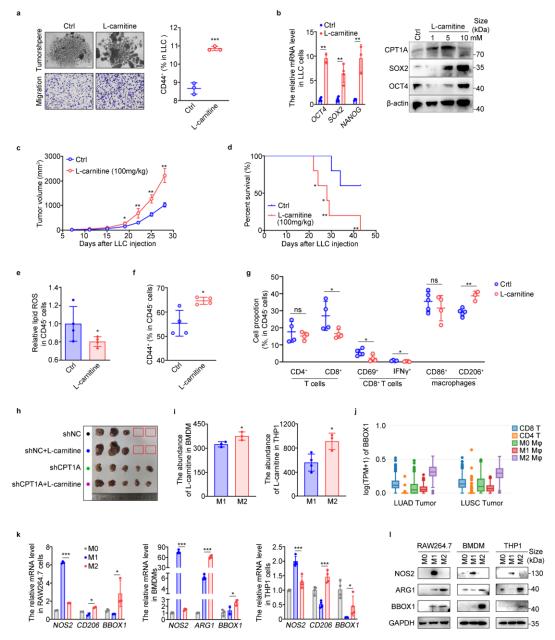


Figure. S6.

L-carnitine promotes cancer stemness and ferroptosis resistance in lung cancer.

a, Effects of L-carnitine on stemness phenotypes of LLC cells. Sphere-forming assay (up). Scale bar: 100 µm. Transwell assay (down). Scale bar: 100 µm. Percentage of CD44⁺ cells (right). **b**, Quantification of mRNA for *OCT4*, *SOX2* and *NANOG* (left) and representative western blot for CPT1A, SOX2 and OCT4 in LLC cells treated with L-carnitine or not. **c-g**, Effects of L-carnitine on tumor progression in tumor-bearing mice inoculated with LLC-shNC/shCPT1A cells (n = 5). C57BL/6J mice subcutaneously transplanted with LLC-shNC/shCPT1A cells (1×10^6 cells/100 µL), intragastric administration of L-carnitine for 22 days, and sacrificed at day 28. Tumor growth curve (data represent the mean \pm s.e.m.) (**c**). Overall survival of tumor-bearing mice (**d**). Lipid ROS levels of CD45⁻ cells in mouse tumor (**e**). Percentage of CD44⁺

tumor cells in the mouse tumor (**f**). Percentage of distinct immune cells in the mouse tumor (**g**). **h**, Tumor photograph of the mice inoculated with LLC-shNC/shCPT1A cells and treated with L-carnitine (IG, 100 mg/kg). **i**, L-carnitine levels in BMDM or THP1 cells calculated by LC-MS. Data represent the mean \pm s.d., n = 3 samples. **j**, Expression levels of *BBOX1* in CD8⁺ T cells, CD4⁺ T cells or macrophages-M0/M1/M2 in the tumor of NSCLC patients, respectively analyzed with TIMER2 website. **k**, Quantification of mRNA for *NOS2*, *CD206*, *ARG1* and *BBOX1* in RAW264.7, BMDM and THP-1 cells. Data represent the mean \pm s.d., n = 3 samples. **l**, Representative western blot for NOS2, ARG1 and BBOX1 in RAW264.7, BMDM and THP-1 cells. *P < 0.05, **P < 0.01, ***P < 0.001; significance was determined by unpaired two-tailed Student's t test or one way ANOVA test.

Supplementary Figure 7

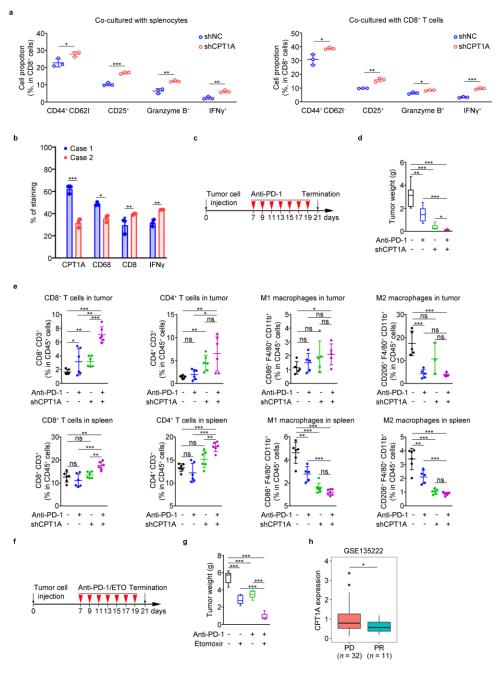
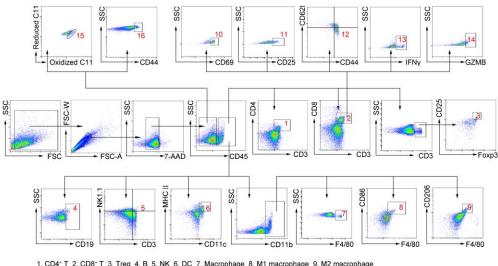


Figure. S7.

Targeting CPT1A promotes the anti-tumoral immunity in lung cancer.

a, Phenotype of CD8⁺ T cells (isolated from the spleen of tumor-bearing mice) cocultured with LLC-shNC/shCPT1A cells determined by flow cytometry. **b**, Qualification of IHC staining for CPT1A, CD68, CD8 and IFN γ in the tumor of NSCLC patients. **c-d**, Effects of PD-1 antibody on tumor progression in tumor-bearing mice inoculated with LLC-shNC/shCPT1A cells (n = 7). Experimental scheme. C57BL/6J mice were subcutaneously transplanted with LLC-shNC/shCPT1A cells (1×10^6 cells/100 µL), intraperitoneal injection of PD-1 antibody for seven times and were sacrificed at day 21 (**c**). Tumor weight (**d**). **e**, Quantification of CD4⁺ T cells, CD8⁺ T cells, CD86⁺ macrophages, and CD206⁺ macrophages gated on CD45⁺ cells in the tumor or spleen from tumor-bearing mice determined by flow cytometry. **f-g**, Effects of PD-1 antibody and etomoxir on tumor progression in tumor-bearing mice inoculated with LLC-shNC/shCPT1A cells (n = 6). Experimental scheme. C57BL/6J mice were subcutaneously transplanted with LLC-shNC/shCPT1A cells (1×10^6 cells/100 µL), intraperitoneal injection of PD-1 antibody or etomoxir for seven times and were sacrificed at day 21 (**f**). Tumor weight (**g**). **h**, *CPT1A* expression in NSCLC patients with PD-1-blocked immunotherapy by bioinformatic analysis. (PD: progressive disease. PR: partial response). *P < 0.05, **P < 0.01, ***P < 0.001; ns: not significant. The statistical analysis was performed using a two-tailed Student's t-test.

Supplementary Figure 8



1. CD4* T 2. CD8* T 3. Treg 4. B 5. NK 6. DC 7. Macrophage 8. M1 macrophage 9. M2 macrophage 10. CD69* CD8* T 11. CD25* CD8* T 12. CD44* CD62I T 13. IFNγ* CD8* T 14. GZMB* CD8* T 15. CD45* cells of lipid peroxidation 16. CD44* CD45* cells

Figure. S8.

Gating strategy for flow cytometry.

Gating strategy for flow cytometry to identify distinct cell populations in mouse tumor or spleen. CD4⁺ T cells (CD3⁺, CD8⁺), CD8⁺ T cells (CD3⁺, CD8⁺), Treg cells (CD3⁺, CD25⁺, Foxp3⁺), B cells (CD19⁺), NK cells (CD3⁺, NK1.1⁺), DC cells (CD11c⁺, MHC II⁺), Macrophages (CD11b⁺, F4/80⁺), M1 macrophages (CD11b⁺, F4/80⁺, CD86⁺), M2 macrophages (CD11b⁺, F4/80⁺, CD206⁺), CD69⁺ CD8⁺ T cells (CD3⁺, CD8⁺, CD69⁺), CD25⁺ CD8⁺ T cells (CD3⁺, CD8⁺, CD25⁺), CD44⁺ CD62L⁻ CD8⁺ T cells (CD3⁺, CD8⁺, CD44⁺, CD62L⁻), IFNγ⁺ CD8⁺ T cells (CD3⁺, CD8⁺, IFNγ⁺), GZMB⁺ CD8⁺ T cells (CD3⁺, CD8⁺, GZMB⁺) gated on CD45⁺ cells, lipid ROS level (oxidized C11, reduced C11) and CD44⁺ cells gated on CD45⁻ cells.

Table S1.

Erastin

Ferrostatin-1

Necrostatin-1

Van resources tables		
Key resources tables. REAGENT or RESOURCE	SOURCE	IDENTIFIER
CPT1A Polyclonal antibody	Proteintech	Cat No: 15184-1-AP
CPT1A Monoclonal antibody	Proteintech	Cat No: 66039-1-Ig
c-MYC Polyclonal antibody	Proteintech	Cat No: 10828-1-AP
	Proteintech	
c-MYC Monoclonal antibody SOX2	Abcam	Cat No: 67447-1-Ig ab59776
OCT4	Abcam	ab19857
NANOG	Cell Signaling	#4903
le actin Decembinant antihady	Technology Proteintech	Cot No. 91115 1 DD
β -actin Recombinant antibody		Cat No: 81115-1-RR
Anti-FACL4 antibody	Abcam	Cat# ab155282
GPX4	Abcam	ab125066
BBOX1	Abcam	ab189827
OCTN2	Abcam	ab180757
NOX2	Abcam	ab129068
ARG1	Cell Signaling	#93668
	Technology	
GAPDH	Cell Signaling	#5174
	Technology	
Ubiqutin	Proteintech	Cat No: 10201-2-AP
FBXW7	Proteintech	Cat No: 28424-1-AP
NRF2	Proteintech	Cat No: 16396-1-AP
Histone H3	Abcam	ab1791
Normal Rabbit IgG antibody	Cell Signaling	# 2729
	Technology	
Mouse IgG	Proteintech	Cat No: B900620
Anti-Rabbit IgG, Light Chain	Proteintech	Cat No: SA00001-7L
Specific		
Chemicals, peptides, and		
inhibitors		
L-carnitine	Sigma-Aldrich	C0283
Cytidine	Sigma-Aldrich	C4654
Phenyllactic acid	Sigma-Aldrich	P7251
Hippuric acid	Sigma-Aldrich	112003
Niacinamide	Sigma-Aldrich	N5535
Indole	Sigma-Aldrich	I3408
Sodium palmitate	Sigma-Aldrich	90951
Etomoxir	Sigma-Aldrich	236020

Sigma-Aldrich MedChemExpress HY-15763 MedChemExpress HY-100579

MedChemExpress

HY-15760

Z-VAD-FMK Cisplatin BODIPY TM 581/591 C11 7-AAD (7-Aminoactinomycin D) PI (Propidium Iodide)	MedChemExpress MedChemExpress Thermo Fisher Thermo Fisher Thermo Fisher	HY-16658B HY-17394 Cat# D3861 Cat# A1310 Cat# P1304MP
Critical commercial assays L-Carnitine Assay kit FFA Assay kit NADP/NADPH Assay kit SimpleChIP® Enzymatic Chromatin IP Kit (Magnetic Beads) Lillie's Ferrous Iron Stain Kit	Abcam Abcam Abcam Cell Signaling Technology Solarbio	ab83392 ab65341 ab65349 Cat# 9003 G3320
Nuclear and Cytoplasmic Protein Extraction Kit Lipid Peroxidation MDA Assay Kit Experimental models: Cell lines Mouse cell line: LLC	Beyotime Biotechnology Beyotime Biotechnology ATCC	P0027 S0131S
Mouse cell line: RAW264.7 Human cell line: THP1 Human cell line: H1299 Human cell line: A549	ATCC ATCC ATCC ATCC ATCC	Cat# CRL-1642 Cat# TIB-71 Cat# TIB-202 Cat# CRL-5803 Cat# CRM-CCL-185
Experimental models: Organisms/strains Mouse: C57BL/6J Mouse: NOD.SCID Mouse: transgenic mice	Vital River Laboratory Vital River Laboratory Shanghai Model Organisms Center, Inc.	NA NA NA
Oligonucleotides ChIP-qPCR primers Mouse-qPCR primers Human -qPCR primers	This paper This paper This paper	listed in Table S1 listed in Table S1 listed in Table S1
Recombinant DNA pcDNA3.1-CPT1A -His-C	Yixiang Biotechnology	NA

	(Tianjin) Co., Ltd.	NT A
pcDNA3.1-3FLAG-MYC	Tsingke	NA
	Biotechnology Co.,	
	Ltd.	
pLV2N-U6-Puro vector	GenePharma Co., Lt	d. listed in Table S1
Software and algorithms		
Graphpad Prism 8.0 software	GraphPad	https://www.graphpad.c
	Software, Inc	<u>om/</u>
ImageJ	ImageJ: Image	https://imagej.nih.gov/ij/
	Processing and	
	Analysis in Java	https://www.flowjo.com/
FlowJo	Tree Star	http://timer.cistrome.org/
Timer 2.0	(Li et al., 2020)	https://doi.org/10.1093/n
GEPIA	(Li et al., 2021)	<u>ar-/gkab418</u>
Deposited Data		
Gene expression profile of patient	(Jung et al., 2019)	GSE135222
samples after immunotherapy	(Cho et al., 2020)	GSE126044
Transcriptome data	This paper	HRA006509

Table S2.

List of primers u	used in t	this	study.
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rimers for real-time PCR (human)	PCR Primer sequence (5'-3')	
	F: ATCAATCGGACTCTGGAAACGG	
CPT1A	R: TCAGGGAGTAGCGCATGGT	
gov2	F: AAAACAGCCCGGACCGCGTC	
SOX2	R: CTCGTCGATGAACGGCCGCT	
	F: AAGCGATCAAGCAGCC	
OCT4	R: GGAAAGGGACCGAGGAGTA	
NANOC	F: ACCTCAGCCTCCAGCAGATGCA	
NANOG	R: GGTGCTGAGGCCTTCTGCGT	
	F: GGCTCCTGGCAAAAGGTCA	
c-Myc	R: CTGCGTAGTTGTGCTGATGT	
	F: CATCCCTGGAGCAGATACTCT	
ACSL4	R: TCACTTAGGATTTCCCTGGTCC	
<u>ρρανι</u>	F: CATGGCCCGATGAGCATTACA	
BBOX1	R: TGAGCCCCAGTATTGGCATTC	
SLC16A9	F: CAGGATCACGTTAGCCAATGG	
	R: AAAGAGCCACAGTTTCACCAC	
ARG1	F: TGGACAGACTAGGAATTGGCA	
	R: CCAGTCCGTCAACATCAAAACT	
MRC1	F: GGGTTGCTATCACTCTCTATGC	
	R: TTTCTTGTCTGTTGCCGTAGTT	
CDVA	F: GAGGCAAGACCGAAGTAAACTAC	
GPX4	R: CCGAACTGGTTACACGGGAA	
CL C7 411	F: TCTCCAAAGGAGGTTACCTGC	
SLC7A11	R: AGACTCCCCTCAGTAAAGTGAC	
	F: GCCGAGTGGATGATAGCTGC	
ACSL3	R: ATGGCTGGACCTCCTAGAGTG	
IDCAT2	F: GGCTGGATACTATTACACTGCC	
LPCAT3	R: GATCTTTCCCTCCGTCAAAGTAG	
NDEO	F: TCAGCGACGGAAAGAGTATGA	
NRF2	R: CCACTGGTTTCTGACTGGATGT	
FBXW7	F: CGACGCCGAATTACATCTGTC	
ΓDΛΨ	R: CGTTGAAACTGGGGTTCTATCA	
LICD22	F: CACCACCTCTAGCCAACTACC	
USP36	R: GGCGATCTTTTTCAGGTCTCG	
LICD 10	F: CACTGTTGCTACAGAACCATCT	
USP28	R: TGGGAGACTCCAGTAGACTCA	
CVD1	F: ATGCCCCAATCTTGTCCATCT	
SKP2	R: CACCGACTGAGTGATAGGTGT	
	F: CGCAGAGAGATCGAAATCCAG	
AURKB		

ALOX15	F: GACCCTGCTATACCAGAGCC R: ACCAGTCCCACTTGTCATCAG
β-actin	F: TCATGAAGTGTGACGTGGACATC R: CAGGAGGAGCAATGATCTTGATCT
GAPDH	F: GGAGCGAGATCCCTCCAAAAT R: GGCTGTTGTCATACTTCTCATGG
Primers for real-time PCR	
(mouse)	
CPT1A	F: TGGTGGTGGGTGTGATAT
	R: GGTGTCTAGGGTCCGATT
CPT1B	F: GAGACGGACACAGATAGCCC
	R: TCTTCACTGAGTTCCGATGGG
CPT1C	F: TTCATCTGCGATCCTGACGAC
	R: CACTGAGGGGTCAATGCACTC
c-Myc	F: GATCCGAACACGGAATATCAGG
2	R: GTCCCCATGCAAGTTAGGAGT
SLC22A5	F: GATCCGAACACGGAATATCAGG
	R: GTCCCCATGCAAGTTAGGAGT
SOX2	F: GCGGCAACCAGAAAAACAG
	R: CTCCGTCTCCGACAAAGT
OCT4	F: GGGCTCTCCCATGCATTCAAAC
	R: CACCTTCCCTCCAACCAGTTGC
NANOG	F: CACCTTCCCTCCAACCAGTTGC
	R: GGTGCTGAGGCCTTCTGCGT F: CGGAGCCTTTAGACCTCAACA
INOS	R: CCCTCGAAGGTGAGCTGAAC
	F: TGTCCCTAATGACAGCTCCTT
ARG1	R: GCATCCACCCAAATGACACAT
	F: CTGACAAACGTGGTGAGATCA
BBOX1	R: CCACATTGTTGGCATCAATCTTG
	F: GCCTGGATAAGTACAGGGGTT
GPX4	R: CATGCAGATCGACTAGCTGAG
	F: TGAACGTATCCCTGGACTAGG
ACSL4	R: TCAGACAGTGTAAGGGGTGAA
	F: CTACCCGTTGGCTCTGTTTTAC
LPCAT3	R: TGAAGCACGACACATAGCAAG
	F: CTGAACTCCTGGACGGGACTA
NRF2	R: CGGTGGGTCTCCGTAAATGG
	F: TACAAACTGGAGACGAGGAGAA
FBXW7	R: CCACAAAACTGTAGGCATGTGAT
	F: CTACCCGTTGGCTCTGTTTTAC
SKP2	R: TGAAGCACGACACATAGCAAG
0	F: TCATGAAGTGTGACGTGGACATC
β -actin	R: CAGGAGGAGCAATGATCTTGATCT

Primers for ChIP assay

ChIP-hCPT1A-BS1	F: CAGCTTCCGTAGTGCAAACC
Chip-hCP11A-BS1	R: AGATTTCACCGCCCCAAGAG
ChIP-hCPT1A-BS2	F: TGGCCTGTGTCACCAAAATG
Chir-hCr11A-B52	R: TCCTGGAGCTCCTGATTATCC
shRNA sequences (human)	
shNC	TTCTCCGAACGTGTCACGT
shCPT1A-619	GGATGGGTATGGTCAAGATCT
shCPT1A-941	GGATCTGCTGTATATCCTTCC
shRNA sequences (mouse)	
ShNC	TTCTCCGAACGTGTCACGT
shCPT1A-2063	GCCTCTATGTGGTGTCCAAGT
shCPT1A-332	GCATGATTGCAAAGATCAATC

Histologic type	Characteristics	Patients (n=155)
	1	21
	2	44
Pathology staging	3	35
	4	11
	T1	36
Tumor size	T2	103
	Т3	10
	Τ4	6
Lymph node metastasis	N0	100
	N1	38
	N2	17
Metastasis	M0	146
	M1	9
Gender	Male	71
	Female	84

 Table S3.

 Clinicopathological characteristics of patients from NSCLC tumor tissue array.

Table S4.

Туре	Case1	Case2
Histologic type	Invasive adenocarcinoma	Invasive adenocarcinoma
Gender	Female	Male
Age	47	65
Clinical staging	Ia2	IIa
Tumor size	T1b	T2b
Lymph node metastasis	NO	N0
Metastasis	M0	M0

Clinicopathological characteristics of patients from NSCLC tumor tissue immunohistochemistry.