Figure S1. Generation of ELOVL2 knockout ACHN cells using CRISPR/Cas9 systems. (A) Schematic illustration of two sgRNA target sites and sequences for ELOVL2 knockout. (B) Sequence analysis confirmed the mutations with one nucleotide deletion or insertion in the selected ELOVL2 knockout cell lines (sgELOVL2-1 and sgELOVL2-2) compared to the wild-type human ELOVL2 sequence. (C) Analysis of cellular proliferation by MTT assay in ACHN/sgControl cells or ACHN/sgELOVL2 cells after 72 h., ***P<0.001, vs. control; determined by using ANOVA with post hoc comparisons using Dunnett's test. ELOVL, elongation of very-long-chain fatty acids; sgRNA, single-guide RNA.
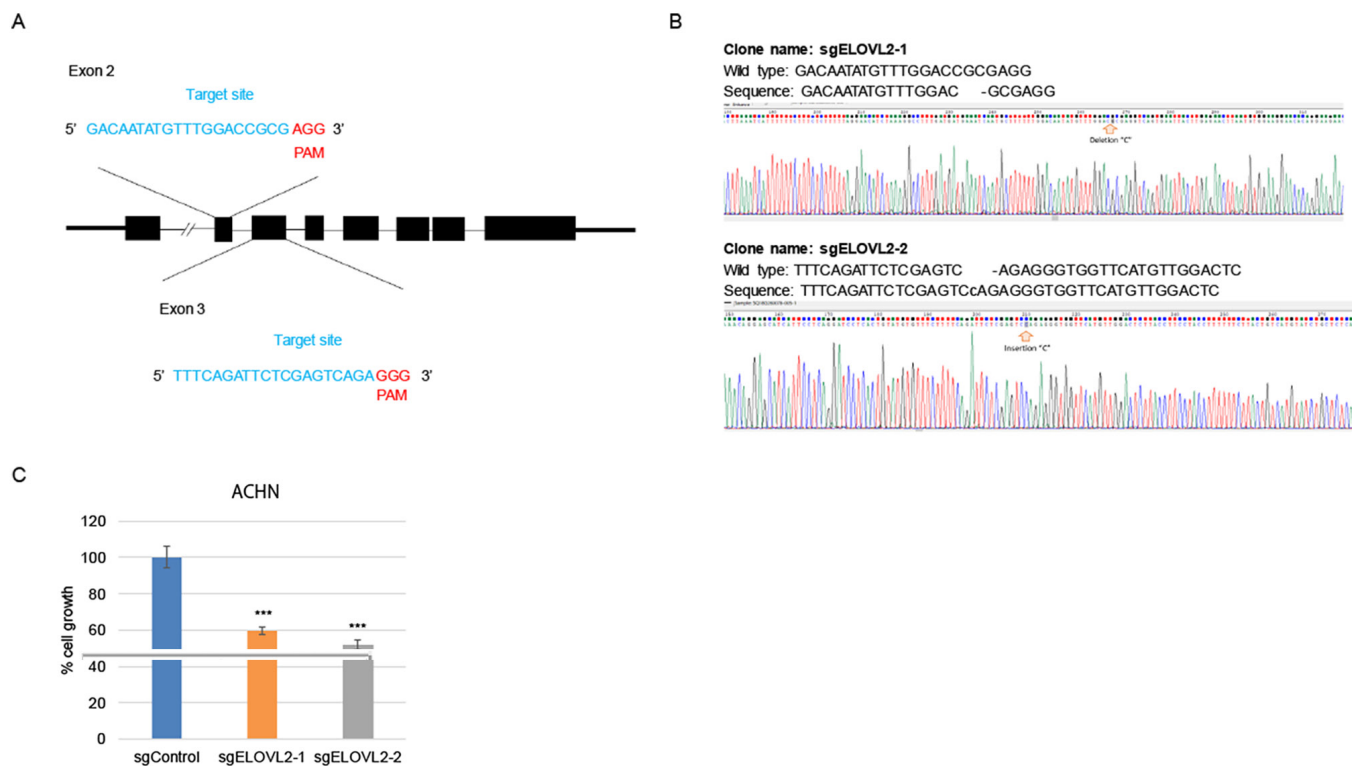
Figure S2. GC-MS analysis for ACHN/sgControl and ACHN/sgELOVL2 cells. (A) The sample weights of ACHN/sgControl and ACHN/sgELOVL2 cells. (B) Representative graphs of SI-MS and average peak area of FAMEs in ACHN/sgControl cells. (C) Representative graphs of SI-MS and average peak area of FAMEs in ACHN/sgELOVL2-1 cells. (D) Representative graphs of SI-MS and average peak area of FAMEs in ACHN/sgELOVL2-2 cells. GC-MS, gas chromatography-mass spectrometry; sg, single-guide; ELOVL, elongation of very-long-chain fatty acids; SI-MS, secondary ion mass spectrometry; FAMES, fatty acid methyl esters.
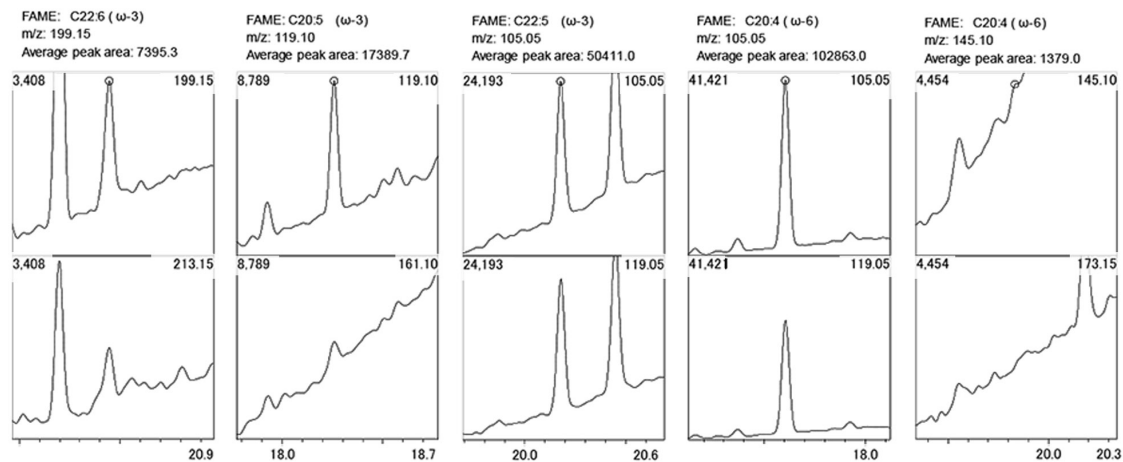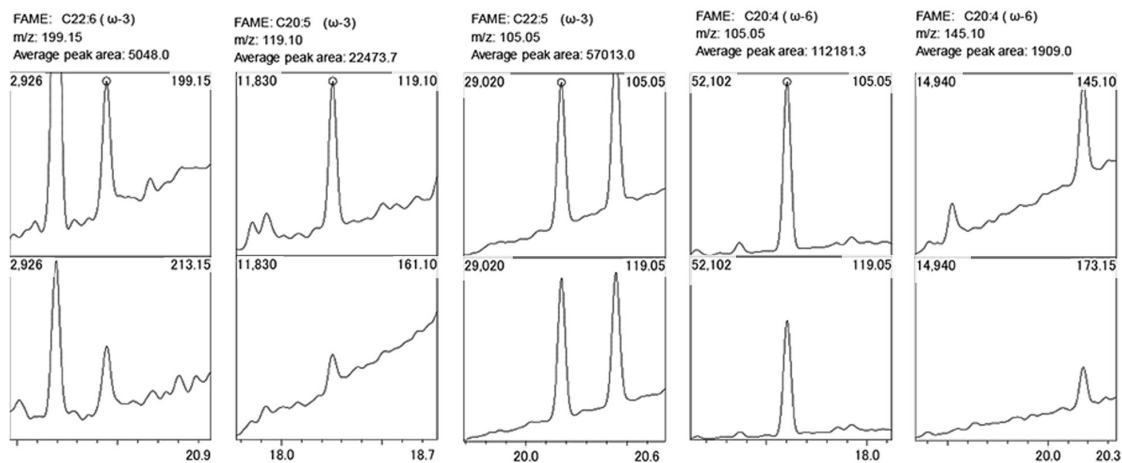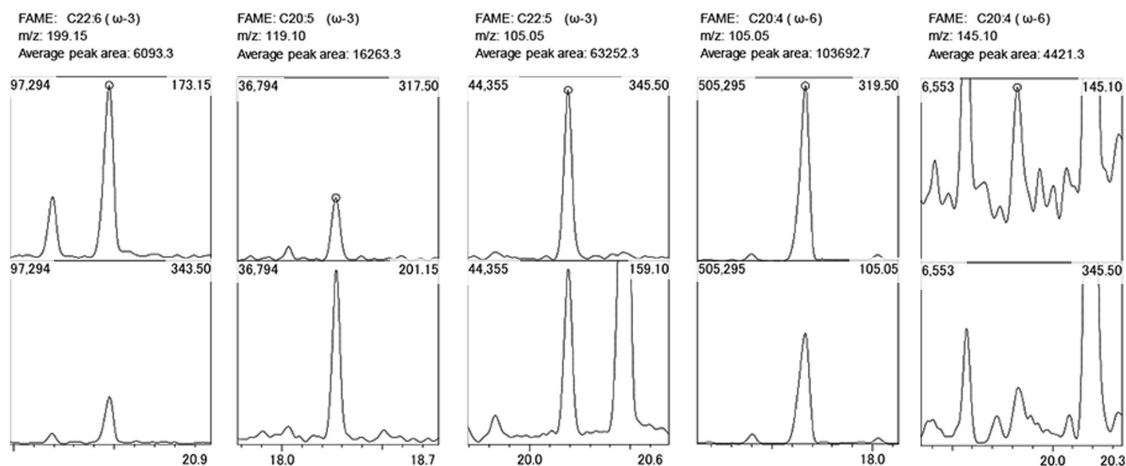
Table SI. Characteristics of the 46 patients with ccRCC and list of samples in the present study.

Patient no.	Age at diagnosis (years)	Sex	Stage	Fuhrman grade	Duration of observation (months)	Alive/deceased
1	71	M	1	2	89.7	Alive
2	69	M	1	2	50.0	Alive
3	60	M	2	2	7.2	Alive
4	79	M	1	2	5.9	Alive
5	41	F	1	3	51.3	Alive
6	66	M	1	2	54.1	Alive
7	62	F	4	4	6.7	Deceased
8	64	M	3	4	5.9	Alive
9	52	M	4	3	9.4	Alive
10	64	M	1	2	4.0	Alive
11	81	M	3	4	45.4	Alive
12	79	M	3	4	2.0	Alive
13	68	M	4	4	1.4	Alive
14	40	M	1	2	2.8	Alive
15	85	M	1	2	35.2	Deceased
16	76	F	1	2	36.8	Alive
17	40	M	1	2	31.9	Alive
18	55	M	4	4	7.9	Deceased
19	58	M	1	2	24.9	Alive
20	62	M	1	2	9.5	Alive
21	78	F	1	2	32.3	Alive
22	57	M	3	4	32.5	Alive
23	59	M	1	3	33.7	Alive
24	57	F	1	1	32.3	Alive
25	58	M	3	2	31.1	Alive
26	68	M	1	2	38.4	Alive
27	63	M	1	2	25.4	Alive
28	75	F	1	2	22.8	Alive
29	51	F	1	2	4.8	Alive
30	81	M	3	2	25.2	Alive
31	73	F	3	2	24.7	Alive
32	59	F	4	4	26.3	Alive
33	54	M	4	3	7.4	Deceased
34	65	F	1	1	22.1	Alive
35	75	M	1	2	22.3	Alive
36	66	M	3	3	18.2	Alive
37	68	M	3	2	3.8	Alive
38	52	M	1	3	15.5	Alive
39	71	F	3	2	19.8	Alive
40	59	M	3	3	7.1	Alive
41	82	F	3	3	16.9	Alive
42	64	M	1	2	4.6	Alive
43	78	F	3	2	2.5	Alive
44	66	M	1	2	15.6	Alive
45	46	M	1	1	62.3	Alive
46	71	M	3	3	35.5	Deceased

ccRCC, clear cell renal cell carcinoma; F, female; M, male.

Table SII. List of primer sequences used for RT-qPCR.

Gene	Primer sequence
Human ELOVL1	
Sense	5'-CTCCGTGGCTTCATGATTGT-3'
Antisense	5'-CGCCAGGTATAGGTGCTCAG-3'
Human ELOVL2	
Sense	5'-CCACTTGGGAAGGAGGCTAC-3'
Antisense	5'-CACCAAAGCACCTTGGCTAC-3'
Human ELOVL3	
Sense	5'-ACTCGGAGACACAGCCTTCA-3'
Antisense	5'-TCCTGCAGGCACTTTGTTCT-3'
Human ELOVL4	
Sense	5'-TGGAAAATTGGCCTCTGATG-3'
Antisense	5'-CGCATCTGAAAAGGTTCTCG-3'
Human ELOVL5	
Sense	5'-CACCTGAAGGACCACCAGAA-3'
Antisense	5'-GCTTCCTTGGCTTCACATTG-3'
Human ELOVL6	
Sense	5'-CTGGTCTCTGACCCTTGCAG-3'
Antisense	5'-CTGACTGCTTCAGGCCTTTG-3'
Human ELOVL7	
Sense	5'-CTCTGCCACAAACCATCCTC-3'
Antisense	5'-AGTTCAAAGGGCTTGCGATT-3'
Human BAX	
Sense	5'-GGTTGTCGCCCTTTTCTA-3'
Antisense	5'-CGGAGGAAGTCCAATGTC-3'
Human BAK1	
Sense	5'-TCGACTTCATGCTGCATCAC-3'
Antisense	5'-ACAAACTGGCCCAACAGAAC-3'
Human PMAIP1	
Sense	5'-AGAGCTGGAAGTCGAGTGTG-3'
Antisense	5'-GAAGTTTCTGCCGGAAGTTCAG-3'
Human BBC3	
Sense	5'-ACGACCTCAACGCACAGTAC-3'
Antisense	5'-AGATTGTACAGGACCCTCCAG-3'
Human BCL2	
Sense	5'-TGTGGCCTTCTTTGAGTTCG-3'
Antisense	5'-TCATCCACAGGGCGATGTTG-3'
Human MCL1	
Sense	5'-GGCAGTCGCTGGAGATTATC-3'
Antisense	5'-ATTGGCTTTGTGTCCTTGGC-3'
Human HPRT1	
Sense	5'-GACTTTGCTTTCCTTGGTC-3'
Antisense	5'-AGTCAAGGGCATATCCTAC-3'

Table SIII. List of the oligonucleotide sequences used in the construction of the shRNA vector.

shRNAs	Oligonucleotide sequence
shELOVL2 #1	CCGG*TATGTTTGGACCGCGAGATTC*CTCGAG**GAATCTCGCGGTCCAAACATA**TTTTTG
shELOVL2 #2	CCGG*GGTGCTTTGGTGGTACTATTT*CTCGAG**AAATAGTACCACCAAAGCACC**TTTTTG
Control scramble	CCGG*GCACGACTTCTTCAAGTCCGC*CTCGAG**GCGGACTTGAAGAAGTCGTGC**TTTTTG

Sense strands are indicated in italics; antisense strands are indicated in bold font.