Figure S1. Expression of SMYD2 in OCCC cell lines. SMYD2 mRNA levels in four OCCC cell lines were quantified using reverse transcription-quantitative PCR. Data are presented as the mean ± SD. $^*P<0.05$. SMYD2, SET and MYND domain containing 2; OCCC, ovarian clear cell carcinoma.

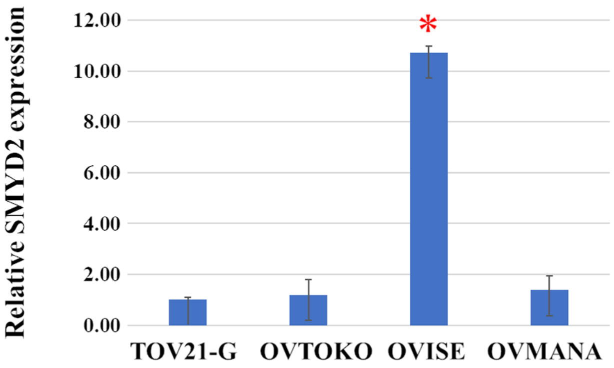

Figure S2. Cell cycle analysis. Representative flow cytometry dot plots of OVISE and OVTOKO cells following SMYD2 knockdown. The cell population was gated according to FSC and SSC (R1). Dead cells and doublets were gated out, and the target population was detected in the fluorescence 2 channel (R2). SMYD2, SET and MYND domain containing 2; SSC, side scatter; FSC, forward scatter; H, height; W, width; si, small interfering; NC, negative control.

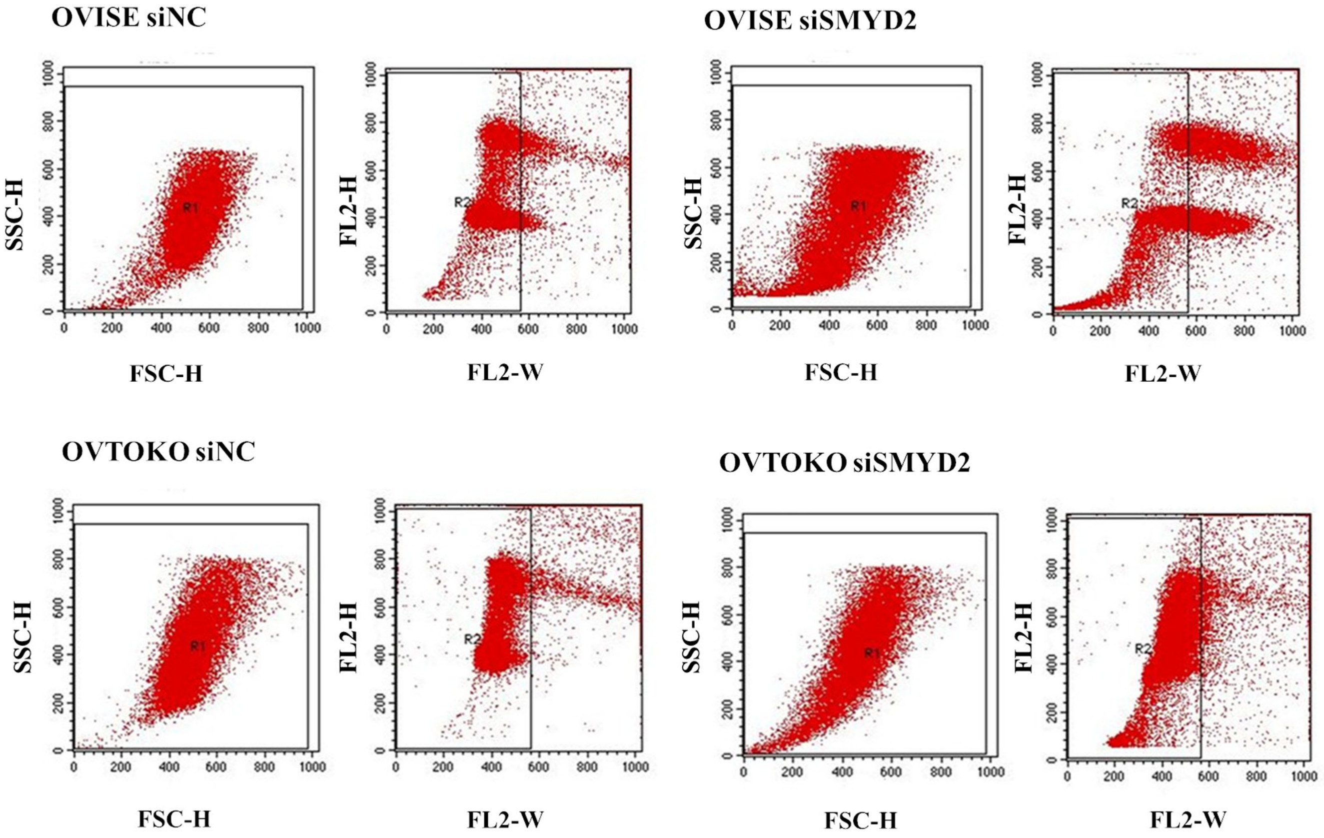

Table SI. Clinicopathological background of the study participants.

Patient no.	Age range, years	Histological diagnosis	TNM stage
1	60-69	OCCC	pT1c1N0M0
2	50-59	OCCC	pT3cN0M0
3	50-59	OCCC	pT1c3N0M0
4	70-79	OCCC	pT1c2N0M0
5	40-49	OCCC	pT3cN0M0
6	40-49	OCCC	pT3bN1M0
7	50-59	OCCC	pT1c3N0M0
8	40-49	OCCC	pT1c1N0M0
9	40-49	OCCC	pT1c1N0M0
10	50-59	OCCC	pT1aN0M0
11	40-49	OCCC	pT3bN1M0
12	70-79	OCCC	pT1c2N0M0
13	50-59	OCCC	pT3bN1M1
14	50-59	OCCC	pT1c3N0M1
15	60-69	OCCC	pT1c1N0M0
16	50-59	OCCC	pT1bN0M0
17	60-69	OCCC	pT1c3N0M0
18	50-59	OCCC	pT1c3N0M0
18	50-59	OCCC	pT2aN0M0
20	50-59	OCCC	pT1aN0M0
21	30-39	OCCC	pT1c3NXM0
22	60-69	OCCC	pT1c2NXM0
23	70-79	OCCC	pT3cN0M0
N1	30-39	Normal	NA
N2	60-69	Normal	NA
N3	50-59	Normal	NA

OCCC, ovarian clear cell carcinoma; NA, not applicable; NX, N stage was not determined.

Table SII. Primer sequences.

Gene name	Primer sequence (5'-3')
GAPDH	Forward: GAAGGTGAAGGTCGGAGTC Reverse: GAAGATGGTGATGGGATTTC
EZH2	Forward: CGCTTTTCTGTAGGCGATGT Reverse: TGGGTGTTGCATGAAAAGAA
SMYD2	Forward: ATCTCCTGTACCCAACGGAAG Reverse: CACCTTGGCCTTATCCTTGTCC
SMYD3	Forward: TTCCCGATATCAACATCTACCAG Reverse: AGTGTGTGACCTCAATAAGGCAT
SETD8	Forward: TCTTGTGATTCCACCAATGCAG Reverse: CCTTCGGACAGGGTAGAAATCC
SETD1A	Forward: AAGGTGTACCGCTATGAT Reverse: CCAATATAGAACTCGTCCAG
SUV39H2	Forward: TGGGGTGTAAAGACCCTTGTG Reverse: ATTCCCTTGTTGTCATAGAAC
EHMT2	Forward: GGAGGAAGCTGAACTCAGGAGG Reverse: GACTGAAGTCATCACCCACCAC
SETD7	Forward: GACACAAGGCAAATCACTCC Reverse: TGGTCATAGCCATAGGCAAC

EZH2, enhancer of zeste 2 polycomb repressive complex 2 subunit; SMYD, SET and MYND domain containing; SETD, SET domain containing lysine methyltransferase; SUV39H2, suppressor of variegation 3-9 homolog 2; EHMT2, euchromatic histone lysine methyltransferase 2.

Table SIII. siRNA sequences.

siRNA name	siRNA sequence (5'-3')
siSMYD2#1	Sense: GAAUGACCGGUUAAGAGA Antisense: UCUCUUAACCGGUCAUUUC
siSMYD2#2	Sense: GGUUAAGAGAUUCUUAUUU Antisense: AAAUAAGAAUCUCUUaAACC

si, small interfering; SMYD2, SET and MYND domain containing 2.

Table SIV. SMYD2 expression according to age and TNM stage.

Clinipathological characteristic	Relative SMYD2 expression levels		
	High	Low	P-value
Mean age ± SD, years	53±10.431	53±8.055	0.612
TNM stage, n			
I	9	7	0.6640
II	1	0	
III	2	4	
IV	0	0	

Patients were divided into two groups according to SMYD2 expression: 'High' expression (≥ median SMYD2 expression) and 'low' expression (<median). SMYD2, SET and MYND domain containing 2.