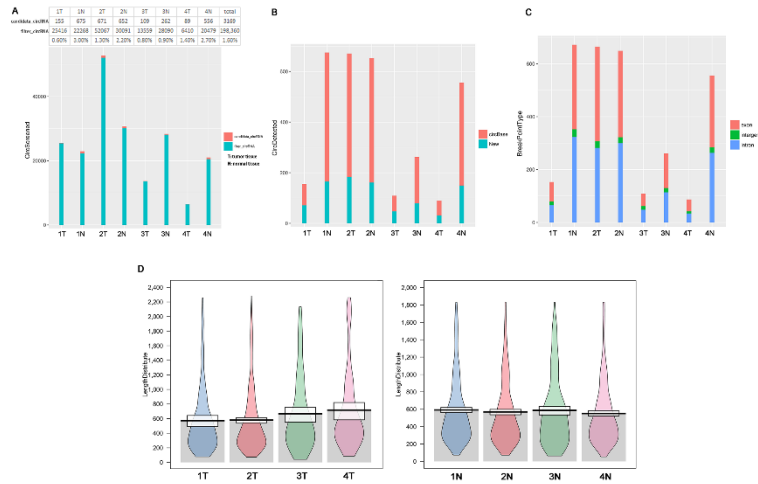
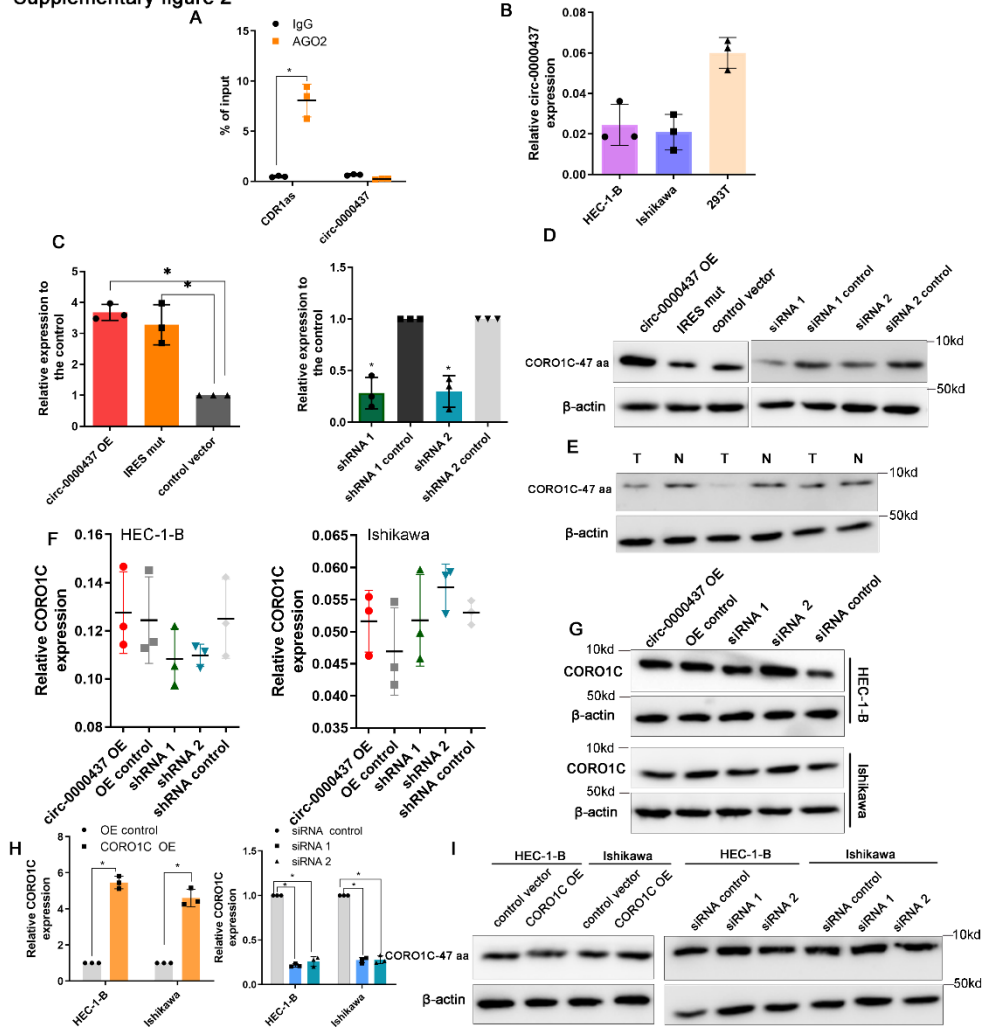


Supplementary figure 1



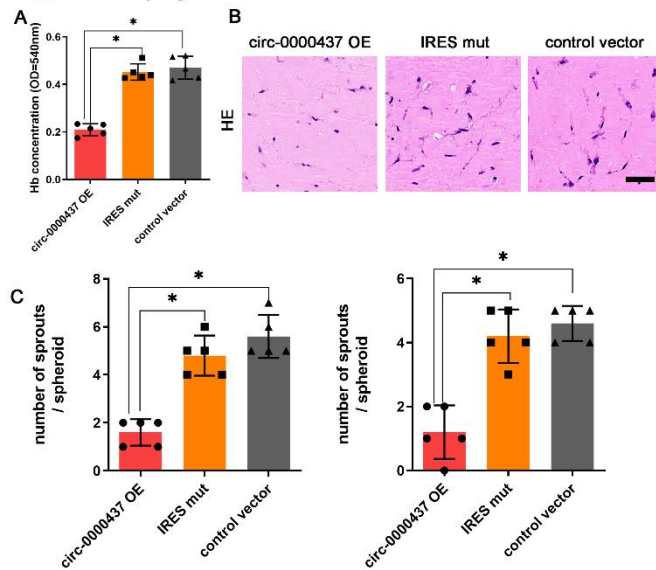
Supplementary figure 2



Supplementary figure 3



Supplementary figure 4



Supplementary Figure 1- Profiling of circular RNA in human EC and adjacent normal tissues.

- (A) The proportion of the candidate circRNAs in the filter circRNAs. The filter circRNAs is the identified total circRNAs; the candidate circRNAs is the selected circRNAs according our screening rules (T: tumor tissues; N: normal tissues).
- (B) The proportion of the known circRNAs in sequencing results compared with circBase.
- (C) The distribution of the number of identified circRNAs derived from different genomic regions.
- (D) Length distribution of the identified circRNAs in human EC (left) and adjacent normal tissues (right). y-axis: the length of circRNAs detected in this study.

Supplementary Figure 2- Expression of *circ-0000437* and *CORO1C-47aa* in cell lines and clinical samples.

- (A) RIP analysis of *circ-0000437* and *CDR1as* using antibodies against AGO2. The RIP enrichment of the AGO2-associated circular RNAs was measured by RT-qPCR, and each value was normalized to the level of input RNA used in RIP analysis.
- (B) The background expression of *circ-0000437* in EC cell lines and 293T cell. The expression level of circRNAs was analyzed by qRT-PCR and normalized to GAPDH. Data are represented as mean \pm SD from three independent experiments.
- (C) Relative expression levels of *circ-0000437* as determined by qPCR in Ishikawa cells transfected with *circ-0000437* or *circ-0000437*-targeting siRNAs. Results are shown as means \pm SD relative to vector control.

- (D) The protein level of CORO1C-47aa were detected by western blot in Ishikawa cells transfected with *circ-0000437* or *circ-0000437*-targeting siRNAs.
- (E) The protein level of CORO1C-47aa were detected by western blot in EC tumor tissues and matched normal tissues (T: tumor, N: normal).
- (F) Relative expression levels of *CORO1C* as determined by qPCR in EC cells transfected with *circ-0000437* or *circ-0000437*-targeting siRNAs. Results are shown as means \pm SD relative to vector control.
- (G) The protein level of CORO1C were detected by western blot in EC cells transfected with *circ-0000437* or *circ-0000437*-targeting siRNAs.
- (H) Relative expression levels of *CORO1C* as determined by qPCR in EC cells transfected with *CORO1C* or *CORO1C*-targeting siRNAs. Results are shown as means \pm SD relative to vector control.
- (I) The protein level of CORO1C were detected by western blot in EC cells transfected with *CORO1C* or *CORO1C*-targeting siRNAs.

Supplementary Figure 3- Sequence of CORO1C-47aa and IRES structure of CORO1C-47aa

- (A) The genomic sequence of *circ-0000437* and conservation analysis of *circ-0000437* exons in different species.
- (B) Schematic diagram of CORO1C-47aa (upper) and the CORO1C-47aa peptides sequence corresponding to the *circ-0000437* nucleotide sequence.
- (C) Putative IRES sequences in *circ-0000437* and Mutated IRES sequences in *circ-0000437* IRES mutation plasmids.

Supplementary Figure 4- Effect of CORO1C-47aa in angiogenesis

- (A) Matrigel plugs were harvested. Angiogenesis was quantified by measuring haemoglobin concentration in the recovered Matrigel plugs (mean±SD, *p<0.05).
- (B) Representative photographs of HE-staining in the indicated experimental conditions (Scale bars: 100µm).
- (C) HUVEC spheroids embedded in fibrin gel were incubated with indicated medium. Then, radially growing cell sprouts were counted (mean±SD, *p<0.05).

Supplemental table 1. Clinicopathological characteristics of endometrial cancer patients in Chinese population.

Characteristics	Beijing population		Suzhou population		Overall	
	N ^a	(%)	N ^a	(%)	N ^a	(%)
Age (years)						
≤65	41	(43.6)	53	(51.0)	94	(47.5)
>65	53	(56.4)	51	(49.0)	104	(52.5)
Age at menarche (years)						
≤11	4	(4.3)	7	(6.7)	11	(5.6)
11-16	71	(75.5)	67	(64.4)	138	(69.7)
≥16	19	(20.2)	30	(28.8)	49	(24.7)
Menopausal status						
Premenopausal	22	(23.4)	32	(30.8)	54	(27.3)
Postmenopausal	72	(76.6)	72	(69.2)	144	(71.7)
Family history of cancer						
Positive	15	(16.0)	8	(7.7)	23	(11.6)
Negative	79	(84.0)	96	(92.3)	175	(88.4)
BMI^b						
≤25	39	(41.5)	41	(39.4)	80	(40.4)
>25	55	(58.5)	63	(60.6)	118	(59.6)
FIGO^c stage						
I	67	(71.3)	79	(76.0)	146	(73.7)
II	14	(14.9)	7	(6.7)	21	(10.6)
III	13	(13.8)	18	(17.3)	31	(15.7)
Histologic type						
Endometrioid	74	(78.7)	91	(87.5)	165	(83.3)
Non-endometrioid	20	(21.3)	13	(12.5)	33	(16.7)
Grade						
G1	25	(26.6)	44	(42.3)	69	(34.8)
G2	57	(60.6)	53	(51.0)	110	(55.6)
G3	12	(12.8)	7	(6.7)	19	(9.6)

^aN, Number of patients

^bBMI, Body mass index.

^cFIGO, The International Federation of Gynecology and Obstetrics.

Supplementary Table 2. Oligonucleotides used in PCRs

PCR

<i>Hsa-circ-0000437</i>	Forward	5'-GGTGACAGCAGTATTCGCTATTT-3'
	Reverse	5'-TGGTTCCTGCATATTTTTCTGG-3'
<i>CORO1C</i>	Forward	5'-AAGAGGGTAGAGCAGGAGCTTT-3'
	Reverse	5'-CAGCAGCTCGAATTTCTTCC-3'
Linear <i>CORO1C</i>	Forward	5'-CAGGAACCAATTGCTCTTCAT-3'
	Reverse	5'-TTAACATCAAGTCCCCTCTTGG-3'
ARNT	Forward	5'-GCTACCCAGGCTACTGCTAAGA-3'
	Reverse	5'-CGATTGGTGAGACTAGGGTAGG-3'
TACC3	Forward	5'-CACAGACGCACAGGATTCTAAG-3'
	Reverse	5'-TAGTTTTGGCATCCACTTCCTT-3'
VEGFA	Forward	5'-ATGAGCTTCCTACAGCACAACA-3'
	Reverse	5'-ACGTACACGCTCCAGGACTTAT-3'
CD31	Forward	5'-GACCAAGGTGAAAGACTGAACC-3'
	Reverse	5'-TGCAGATATACGTCCCCTGTC-3'
circHIPK3	Forward	5'-TCGGCCAGTCATGTATCAAA-3'
	Reverse	5'-ACCAAGACTTGTGAGGCCAT-3'
<i>GAPDH</i> cDNA	Forward	5'-GAAGGTGAAGTTCGGAGTC-3'
	Reverse	5'-GAAGATGGTGATGGGATTTCC-3'

siRNA

<i>Hsa-circ-0000437</i> siRNA1	5'-ATGTGAGATTGCCAGAAAA-3'
<i>Hsa-circ-0000437</i> siRNA2	5'-CCAGAAAAATATGCAGGAA-3'
<i>Hsa-circ-0000437</i> siRNA3	5'-GAGATTGCCAGAAAAATAT-3'
ARNT siRNA 1	5'-GAGAAGTCAGATGGTTTATTTCTC-3'
ARNT siRNA 2	5'-GAGAAATAAACCATCTGACTTCTC-3'

Northernblot

<i>Hsa-circ-0000437</i>	Forward	5'-GGTGACAGCAGTATTCGCTATTT-3'
	Reverse	5'-TGGTTCCTGCATATTTTTCTGG-3'

CHIP

C1-VEGFA	Forward	5'-GAGCGTTTTGGTTAAATTGAGG-3'
	Reverse	5'-GAAGAGTGGGACCAGTCAGTCT-3'
C2-VEGFA	Forward	5'-GGTAGGTTTGAATCATCACG-3'
	Reverse	5'-CACGTATGCACTGTGGAGTCTG-3'
C3-VEGFA	Forward	5'-GCCAGACTCCACAGTGCATAC-3'
	Reverse	5'-GTCCTTTGGGAAGTGTCCAG-3'
C4-VEGFA	Forward	5'-ATTCCTAGCAAAGAGGGAACG-3'
	Reverse	5'-GTTACAGCCTGAAAATTACCC-3'
