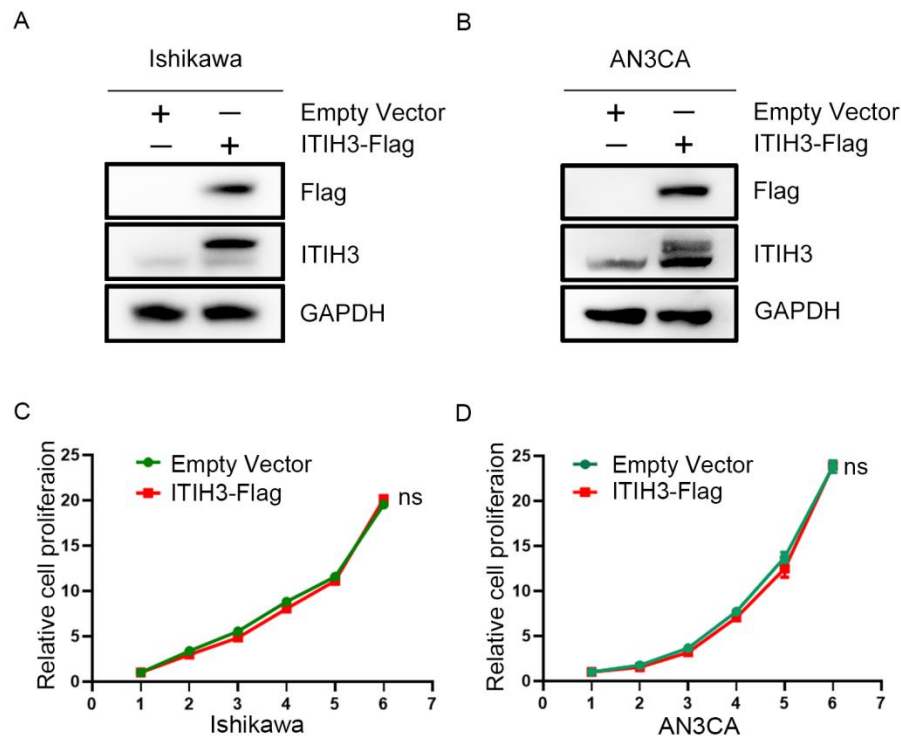


**Supplementary Figure S1.** The expression and survival analyses of five signature genes in EC and normal tissues. A. Genetic alterations of *CDC25B*, *PRXL2A*, *GNG3*, *ITIH3* and *SDHB*. B. Differential mRNA levels between EC and normal tissues. C-G. The mRNA levels of *CDC25B* (C), *GNG3* (D), *ITIH3* (E), *PRXL2A* (F) and *SDHB* (G) in paired EC and normal tissues. H-L. KM survival curves of patients stratified by *CDC25B* (H), *GNG3* (I), *ITIH3* (J), *PRXL2A* (K) and *SDHB* (L) mRNA levels. \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ .



**Supplementary Figure S2.** The cell growth curve was measured after overexpression of ITIH3. A-B. Western blot analysis of ITIH3 expression in Ishikawa (A) and AN3CA (B) cells transfected with pLVX-ITIH3-Flag-IRES-Neo or an empty vector. C-D. Cell proliferation was detected by the CCK-8 assay in Ishikawa (C) and AN3CA (D) cells. ns, no significance.

**Table S1: Names of the estrogen/progesterone-related genes sets**

GO_ESTROGEN_2_HYDROXYLASE_ACTIVITY
GO_ESTROGEN_16_ALPHA_HYDROXYLASE_ACTIVITY
GO_ESTROGEN_RECEPTOR_ACTIVITY
GO_ESTROGEN_RECEPTOR_BINDING
GO_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY
GO_PROGESTERONE_RECEPTOR_SIGNALING_PATHWAY
GO_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY
GO_RESPONSE_TO_PROGESTERONE
GSE22025_PROGESTERONE_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_DN
GSE22025_PROGESTERONE_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_UP
GSE22025_TGFB1_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_DN
GSE22025_TGFB1_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_UP
GSE22025_UNTREATED_VS_PROGESTERONE_TREATED_CD4_TCELL_DN
GSE22025_UNTREATED_VS_PROGESTERONE_TREATED_CD4_TCELL_UP
GSE22025_UNTREATED_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_DN
GSE22025_UNTREATED_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_UP
HP_ABNORMAL_CIRCULATING_ESTROGEN_LEVEL
HP_DECREASED_CIRCULATING_PROGESTERONE
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION
MALIK_REPRESSED_BY_ESTROGEN
REACTOME_ESTROGEN_BIOSYNTHESIS
REACTOME_EXTRA_NUCLEAR_ESTROGEN_SIGNALING
REACTOME_RUNX1_REGULATES_ESTROGEN_RECEPTOR_MEDIATED_TRANSCRIPTION
STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA
WILCOX_RESPONSE_TO_PROGESTERONE_DN
WILCOX_RESPONSE_TO_PROGESTERONE_UP
WP_ESTROGEN_METABOLISM
WP_ESTROGEN_RECEPTOR_PATHWAY
WP_ESTROGEN_SIGNALING_PATHWAY
YAO_HOXA10_TARGETS_VIA_PROGESTERONE_DN
YAO_HOXA10_TARGETS_VIA_PROGESTERONE_UP
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_2
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_3
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_4
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_5
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_6
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_7

YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_8
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_11
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_15
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17

**Table S2: Primers for qRT-PCR analysis.**

Gene	Primer	Sequence (5' to 3')
GAPDH	Forward	CAGCCTCAAGATCATCAGCA
	Reverse	TGTGGTCATGAGTCCTTCCA
PRXL2A	Forward	GGAAACCTGGAAGGAGAAGG
	Reverse	CTGATCCCACCACGAAACT
GNG3	Forward	CCGGTGAACAGCACTATGAG
	Reverse	TGCCTTGGACACCTTTATCC
ITIH3	Forward	AAGGAAGTTGCCAAGAAGCA
	Reverse	GTGATGAAAGAGGCCTCAGC

**Table S3: Human specific siRNA.**

Gene	Sequence of siRNA (5' to 3')
siGNG3-1	GTGTCGGATAAAGGTGTCCAA
siGNG3-2	GCTTAAGATTGAAGCCAGCTT
siPRXL2A-1	GAGACAAAGTAAACCTACTTT
siPRXL2A-2	CTTTCAAAGCAAAGGAGCTAT