Figure S1. SOAT1 expression evaluation in public cancer databases. The UALCAN platform was used to validate SOAT1 expression at both (A) mRNA and (B) protein levels in uterine corpus endometrial carcinoma (UCEC) and matched normal tissues. Information was obtained from the public database available at http://ualcan.path.uab.edu/. SOAT1, sterol-o-acyl transferase 1; UCEC, uterine corpus endometrial carcinoma; CPTAC, Clinical Proteomic Tumor Analysis Consortium.

A mRNA expression of SOAT1 in UCEC
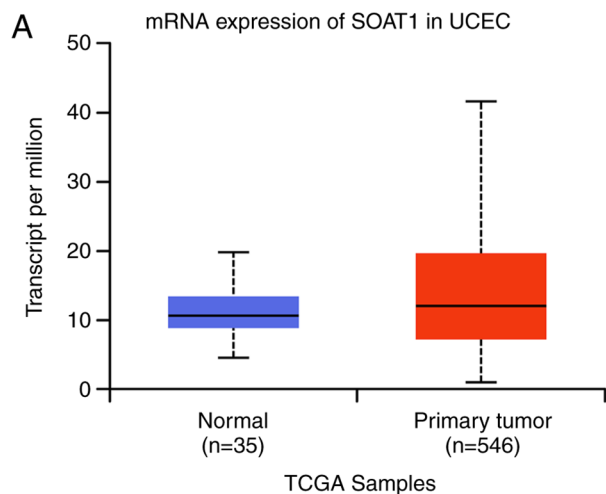
Comparison	Statistical significance
Normal vs. Primary	$2.24540000000051 \times 10^{-5}$

B Protein expression of SOAT1 in UCEC
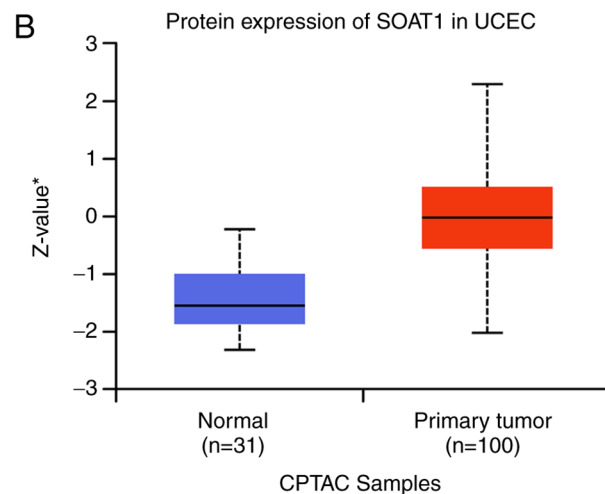
Comparison	Statistical significance
Normal vs. Primary	$3.28640412725626 \times 10^{-17}$

*Z-values represent standard deviations from the median across samples for the given cancer type. Log_2 spectral count ratio values from CPTAC were first normalized within each sample profile, then normalized across samples.

Figure S2. Spearman correlations of SOAT1 protein levels between tissue, peritoneal fluid and plasma. (A) Correlation between peritoneal fluid and tissue, (B) correlation plasma and tissue and (C) correlation between peritoneal fluid and plasma. Peritoneal fluid, n=37; plasma, n=40; and tissue, n=28. SOAT1, sterol-o-acyl transferase 1.
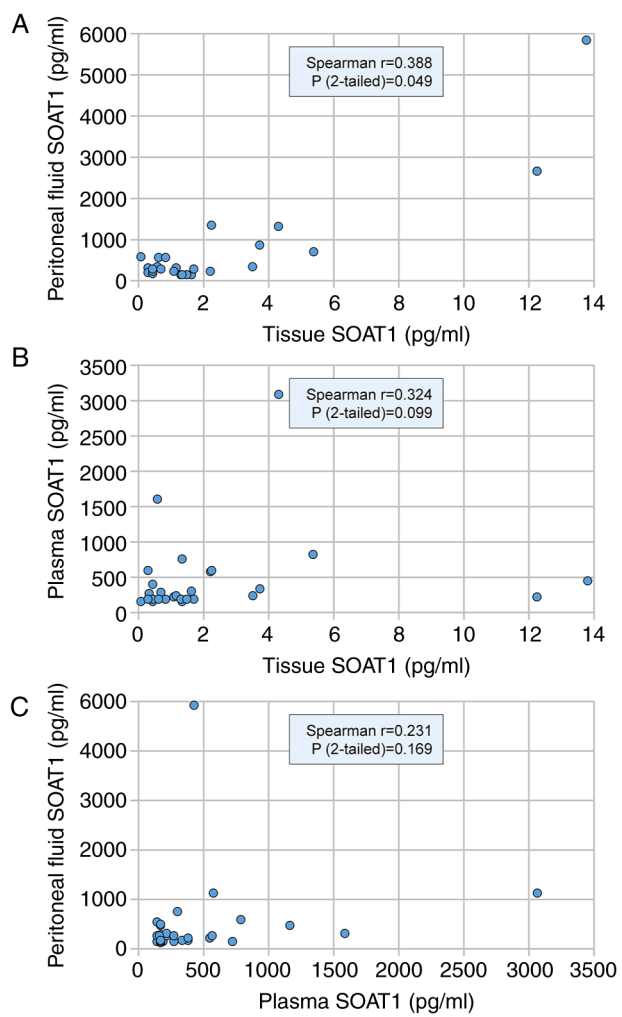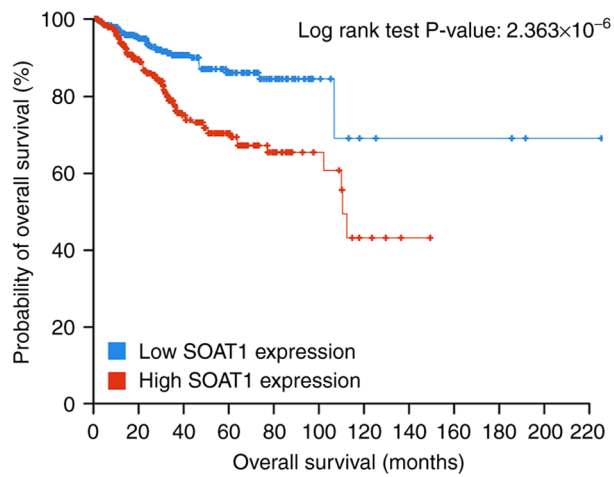
Figure S3. cBioPortal database analysis. Overall survival curves for endometrial cancer patients divided into two groups based on their median SOAT1 gene expression. Information was obtained from the public database available at https://www.cbioportal.org. SOAT1, sterol-o-acyl transferase 1; CI, confidence interval.

	Number of cases	Number of events	Median months overall (95% CI)
Low expression (−0.65–0.02)	450	40	NA
High expression (0.02–2.04)	448	88	110.55 (110.02 - NA)