Analysis of CCT7 Expression and Its Clinical Significance in Endometrial Cancer

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Primary research

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Abstract

Background: Endometrial cancer (EC) is a common gynecologic malignancy; myometrial invasion (MI) is a typical approach of EC spreads and an important index to assess tumor metastasis and outcome of EC patients. CCT7 is a member of the TCP1 chaperone family, involved in cytoskeletal protein folding and unfolding. In this study, the role of CCT7 in EC development was investigated.

Methods: Clinical data for 87 EC cases and expression of CCT7 were analyzed. *CCT7* was knocked out using siRNA-*CCT7* in Ishikawa and RL95-2 cells, and their function about proliferation, apoptosis and invasion were further tested. Bioinformatics methods were used to predict the potential pathways of *CCT7* in EC development.

Results: The rates of CCT7-positive cells in EC and adjacent normal endometrium tissues had significant difference (67.8% vs. 51.4%, p = 0.035), and the expression rate increased from low to high pathological stage (39.7% in the I/II stage, 71.4% in the III/IV stage, p = 0.029). Similar change was found in protein level. CCT7 expression differed significantly between the deep MI group (>1/2) and the superficial MI group (≤1/2) (P = 0.039). However, there were no differences with respect to age, pathological type and histological grade. *CCT7* suppression induced a function-loss in in both Ishikawa and RL95-2 cells. Bioinformatics analysis demonstrated that EC patients with lower level *CCT7* expression had better Overall survival (p= 0.0081). GO enrichment indicated that “RNA binding”, “Mitochondrion”, “Translation”, and “Spliceosome” were most significantly enriched potential pathways. Five hub genes, *PSMA5, PSMD14, SNRPB, SNRPG* and *TXNL4*A, were all significantly upregulated in EC and had positive correlation with *CCT7.*

Conclusions: *CCT7* may be involved in EC development by excessively activating tumor cell function to promote MI or distant/nodal metastasis, which definitely impaired the prognosis of EC patients.

Background

Endometrial cancer (EC) is the fourth highest malignant tumor in women and the most common gynecologic cancer of the female reproductive system in the United States, with an overall incidence of 4.4% around the world in 2018[1, 2]. When diagnosed at an early stage, EC is highly curable and has excellent overall 5-year survival rates[3]. Although the overall prognosis is better than that of other cancer types, many women (especially young women) have aggressive neoplasms and require a hysterectomy, resulting in a loss of fertility and menstrual function and, accordingly, in physical and mental disability[4].

The International Federation of Gynecology and Obstetrics (FIGO) proposed that EC should be surgically staged, which comprised total hysterectomy, bilateral salpingo-oophorectomy, cytologic washings and pelvic and para-aortic lymphadenectomy[5]. A reliable risk stratification of EC could help to plan therapeutic schedule and predict the clinical outcomes for EC patients. Risk classification of EC is mainly according to tumor histology, tumor grade, and myometrial infiltration (MI) depth[6, 7]. Tumor histology and histological grade may be evaluated preoperatively by endometrial biopsy. MI depth of EC has closely relationship with lymph node involvement and distant metastasis, and is the most important risk factor in apparent early-stage EC, but it is difficult to determine preoperatively[8-10]. Therefore, based on comprehensive MI assessment preoperatively, may assist in better planning surgical procedures and to avoid unnecessary lymph node dissections[11]. Currently, magnetic resonance imaging (MRI) and transvaginal ultrasound (TVS) are the commonest techniques for evaluating preoperatively the depth of MI. However, there are still some controversies and limitations of these techniques in

the evaluation of the depth of MI by the EC[12, 13]. Thus, it is necessary to develop new methods to assist in comprehensively assessing the depth of MI.

The eukaryotic cytoplasmic chaperonin-containing TCP-1 (CCT), also called TRiC (TCP1 ring complex), is a complex composed of two back-to-back stacked hetero-octameric rings, each ring is constituted by eight different types of subunits (CCTα, β, γ, δ, ϵ, ζ, η, θ; CCT1 to CCT8 in yeast)[14, 15]. The eukaryotic chaperonin CCT is involved in the folding of cytoskeletal proteins (actins and tubulins) in an ATP dependent approach[16, 17]. In our previous study, we identified the CCT7 might be closely associated with EC by using isobaric tags for relative and absolute quantitation (iTRAQ)-based proteomic analysis (p= 0.02). In the further experiment, Our results revealed that the mRNA expression of *CCT7* significantly higher in EC tissues than normal pericarcinous tissue (p< 0.001, n=10)[18]. Therefore, in this study, we aimed to detect the CCT7 expression in EC tissues and further explore the developmental mechanism of EC at the cellular level, bioinformatics methods were also used to insight into potential molecular pathways.

Materials And Methods

Tissue sample collection

This retrospective study was approved by the Ethics Committees of Xiangya Hospital, Central South University. Patients were fully informed of the study and provided consent before specimen collection. A total of 87 EC specimens from consecutive patients (cancer and adjacent normal tissues) were confirmed by postoperative pathological diagnosis from March 2015 to November 2015 at Xiangya Hospital Central South University. For all patients, relevant clinical data were collected and checked again for confirmation. The age of patients ranged from 31 to 70 years and mean age was 51.3 ± 12.2 years. A total of 75 cases were endometrioid adenocarcinoma, 5 were adenosquamous carcinoma, 3 were serous papillary adenocarcinoma, 2 were clear cell carcinoma, and 2 were mucinous carcinoma. According to 2009 FIGO guidelines[5] for the surgical staging of EC, 32 were Ia, 36 were Ib, 5 were II, 12 were III, and 2 were IV. Histopathological grading was as follows: 49 cases were G1, 33 cases were G2, and 5 cases were G3.

Immunohistochemistry (IHC)

Specimens were fixed in 10% formalin, embedded in paraffin, and sectioned. Two experienced pathologists made the histological diagnosis, and CCT7 expression was evaluated using SP Immunohistochemistry Kits (Abcam Ltd., Cambridge, UK). Results were evaluated according to the following criteria (where brown staining of the cytoplasm and cell membrane indicated positive results) based on the degree of positive staining: weakly positive (+), 1 point; positive (+), 2 points; strongly positive (+++), 3 points. Additionally, based on the percentage of positive cells, they were scored as follows: <25% positive cells (+), 1 point; 25% to 50% (+), 2 points; ≧50% (+++), 3 points; no positive cells indicated a negative result. Finally, a comprehensive indicator was calculated by summing the two scores, where ≦3 points was defined as negative, 4 to 6 points was interpreted as positive, and >6 points was interpreted as strongly positive.

Western blotting analysis

Proteins were isolated from EC tissues via NP-40 lysis buffer (Abcam Ltd., Cambridge, UK) and then separated in 12% SDS-PAGE gels and blotted on nitrocellulose membranes. The filters were hybridized with polyclonal anti-

CCT7 (Abcam Ltd., Cambridge, UK) at 4°C overnight, followed by incubation with the secondary anti-rabbit (Abcam Ltd., Cambridge, UK) for 1 h at room temperature. Anti-Tubulin (Abcam Ltd., Cambridge, UK) were used as the loading control. Gray-scale values were analyzed by ImageJ software and also was described previously[19]

Cell culture and transfection

Endometrial cancer Ishikawa (Shanghai Zhongqiaoxinzhou Biotech, ZQ0472) and RL95-2 (Shanghai Zhongqiaoxinzhou Biotech, ZQ0362) cell lines were cultured in Dulbecco's Modified Eagle's Medium (Hyclone) supplemented with 5% fetal bovine serum (FBS, Gibco), 300 mmol/L l-glutamine (Hyclone), 5 μg/mL bovine insulin (Hyclone), 10,000 units/mL penicillin (Hyclone), and 10,000 μg/mL streptomycin (Hyclone) at 37 degree under 5% CO_2. The role of *CCT7* in Ishikawa and RL95-2 EC cells was examined using siRNA-mediated *CCT7* knockdown. For this analysis, 50 μM, 100 μM, and 200 μM siRNA targeting *CCT7* (*CCT7*-Homo-914: 5'-CCACACAGUUGAGGAUUAUTT-3', 5'-AUAAUCCUCAACUGUGUGGTT-3';*CCT7*-Homo-986: 5'-CCAUCAUUCUGGAGCCAAATT-3', 5'-UUUGGCUCCAGAAUGAUGGTT-3'; or non-targeting negative control siRNA (5'-UUCUCCGAACGUGUCACGUTT-3', 5'-ACGUGACACGUUCGGAGAATT-3'; Sangon Bio-technology Co. Ltd., Shanghai, China) and Dharma FECT reagent (Thermo Fisher Scientific, Waltham, MA, USA) were transfected into cells according to the manufacturer's instructions. After 48 hours, the expression of *CCT7* was evaluated by qRT-PCR methods described previously[20], and the best *CCT7* siRNA, i.e., the siRNA resulting in the lowest *CCT7* expression level, was selected. Then, Ishikawa and RL95-2 cells were transfected with *CCT7*-targeting siRNA, and cell proliferation, apoptosis, cell cycle, migration and colony formation assay were examined.

Cell proliferation assay

Cell proliferation was determined using an MTT assay. Briefly, cells (5×10^3) were plated on 96-well plates for 24 hours and then cultivated for 24 hours, 48 hours, and 72 hours. By metabolic conversion of MTT dye, viable cell densities were determined. Absorbance was read at 490 nm to evaluate assay results.

Cell apoptosis assay

Cell apoptosis was determined using an Annexin V assay and described previously[21]. After transfection and/or lidocaine treatment, cells were collected, washed, and suspended in Annexin V-binding buffer. FITC-conjugated Annexin V and propidium iodide (PI; Beyotime, Haimen, China) were added to cells successively. After incubation, Annexin V-binding buffer was added, and cells were analyzed using a FAC Scan Flow Cytometer.

Cell cycle analysis

After transfection and/or lidocaine treatment, cells were harvested after trypsinization. Then, cells were rinsed three times with buffer solution, the concentration was adjusted to 1×10^6 cells/mL, and the Cycle TEST PLUS DNA Reagent Kit (Becton Dickinson, Franklin Lakes, NJ, USA) was used according to the manufacturer's instructions. Cell cycle status was analyzed by flow cytometry using PI. The PI fluorescence intensity of 10,000 cells was measured for each sample.

Cell migration assay

Ishikawa and RL95-2 cells were treated with 0.25% trypsin and suspended in serum-free medium. Ten thousand cells were added to each Transwell and serum-free medium was added to reach 100 μL. The lower chamber was

supplemented with 10% fetal bovine serum and 1640 medium, followed by cultivation for 48 hours in an incubator. The broth in each well was discarded, and cells were washed twice with phosphate-buffered saline (PBS). The surfaces of cells were wiped with wet cotton and fixed with acetone: methanol (1:1) at room temperature for 20 minutes. After cells were washed twice with PBS, they were stained for 15 minutes with 0.1% crystal violet and washed with PBS three times or more. Finally, images were obtained under an inverted microscope. Absorbance was read at 550 nm to evaluate assay results.

Cell colony formation assay

As described previously[22], Ishikawa and RL95-2 cells in logarithmic growth phase were treated with 0.25% trypsin and suspended in 10% FBS medium. Then, cells were seeded in 6 well plate with 1ml complete medium (500 cells per well) and cultured at 37 degree under 5% CO_2 for 2-3 weeks until eye-visible cells colony. After washing twice with PBS, fixing cells with 1ml 4% paraformaldehyde, and then staining with 0.5% crystal violet for 30mins. Remove the dye with flow water and dry in air, obtain the image and count the cells colony.

Bioinformation analysis

The *CCT7* expression data of UCEC (Uterine Corpus Endometrial Carcinoma) and normal tissue were carefully downloaded from the TCGA Data Portal website (http://cancergenome.nih.gov). Co-expressed genes of *CCT7* in UCEC were collected from MEM (http://biit.cs.ut.ee/mem), UALCAN (http://ualcan.path.uab.edu), and GEPIA (http://gepia.cancer-pku.cn) for further evaluation. Gathered genes were analyzed using bioinformatics. The enrichment of functions and signaling pathways of the target genes were analyzed in Enrichr (https://amp.pharm.mssm.edu/Enrichr/). The String database (http://www.string-db.org) was applied to construct the protein-protein interaction (PPI) network for the hub gene identification. Moreover, hub genes were selected to obtain their expression and correlation with *CCT7* in UCEC.

Statistical analysis

All results are expressed as means ± standard deviation (SD) from three independent experiments. The Chi-square test was used to compare positive staining rates between subgroups, and the One-way and Two-way ANOVA analysis of variance were used to compare other data implemented in SPSS 18.0. GraphPad Prism was applied to acquire the figure and receiver operating characteristic curves (ROCs). $P < 0.05$ was considered statistically significant.

Results

Overexpression of CCT7 in EC tissues

In our previous study, we found that mRNA expression of *CCT7* significantly higher in EC tissues than in the normal pericarcinous tissue (p□0.001, n=10)[18]. To further re-conformed the association of CCT7 expression between EC and adjacent tissue, we investigated CCT7 protein expression in 87 EC and 72 adjacent normal endometrium tissues by IHC. Overall, the CCT7 positive expression showed a brown staining of the cytoplasm and cell membrane. The criteria of scoring for IHC results was described in M&M, CCT7-positive cell rates had significant difference between EC (Fig. 1b-c) and adjacent normal endometrium tissues (Fig. 1a) (67.8% vs. 51.4%, $p = 0.035$), and for CCT7 strongly positive cell rates, it also had significant difference (50.7% vs. 33.3%, $p = 0.033$). Correlations between CCT7 expression and clinicopathological features in patients with EC were

summarized in Table 1. There was a statistical significance between CCT7 strongly positive expression and FIGO pathological stage (III/IV (71.4%) vs. I/II (39.7%), p = 0.029) of EC. Meanwhile, CCT7 protein level from 13 EC patients with different FIGO stage were evaluated by WB, we observed a pronounced up-regulation of CCT7 protein in patients with a more advanced FIGO (II-IV) stage compared to lower FIGO stage and normal EC (p 0.0001, Fig. 1d-e). Notably, the strongly positive CCT7 expression rates differed significantly between the deep MI group (>1/2) and the superficial MI group (≤1/2) (65.0% vs. 38.8%, p = 0.039), and the AUC of the CCT7 expression of EC for FIGO stage and depth of MI was 0.8502 (p < 0.0001, Fig. 1f) and 0.8694 (p < 0.0001, Fig. 1g), respectively. Collectively, these results suggested that CCT7 was involved in the process of muscle invasive or distant/nodal metastasis of EC. However, there were no differences between the groups in age, menstrual status, histological grade, pathological type (Table 1).

Knockdown of *CCT7* leaded to loss-of-function in EC cellular level

In order to explore the *CCT7* function in cellular levels, we performed an RNA interference approach to knockdown *CCT7* expression in both Ishikawa and RL95-2 cell lines. Two kinds of siRNA targeting *CCT7* (*CCT7*-Homo-914 and *CCT7*-Homo-986) were transfected into cells as described in M&M, the *CCT7* expression levels were unchanged on transient transfection with the negative control siRNA, whereas *CCT7*-specific siRNA significantly reduced mRNA expression levels in the Ishikawa and RL95-2 cell lines (Fig. 2a-b). The best *CCT7* siRNA-986 which resulted in the lowest *CCT7* expression level was selected for subsequent experiment. Upon *CCT7* siRNA-986 transfection, Ishikawa and RL95-2 cells exhibited reduced proliferative activity compared with negative control (p < 0.0001) (Fig. 2c-f).

To further verify whether *CCT7*-downregulation influenced EC cells apoptosis and cell cycle, the flow cytometry was used to detect the proportion of cells in different phases. Cell apoptosis was strikingly promoted by *CCT7* siRNA-986 compared with control in both Ishikawa and RL95-2 cells (Fig. 3a-c). In addition, the knockdown of *CCT7* reduced the proportion of cells in S phase and induced G2/M cell cycle arrest significantly (Fig. 3d-f), suggesting that *CCT7* played a positive role in the development of EC.

We performed the Transwell experiments as an independent method to prove the anti-invasion effect of *CCT7* suppression in EC cells. As described in M&M, *CCT7*-targeting siRNA-986 contributed to an obvious reduction of cell migration capacity of both Ishikawa and RL95-2 cells compared with control siRNA-treated cells (p < 0.0001, Fig. 4a-d), of which indicated *CCT7* was involved in the processes of tumor cell invasion and metastasis. The cell colony formation also revealed that EC cells treated with CCT7-targeting siRNA-986 formed a lower number of colonies than control siRNA-treated cells (Fig. 4e-h). Collectively, these loss-of-function studies demonstrated that the *CCT7*-siRNAs could inhibit tumor cell proliferation and invasion abilities compared with the control.

Potential molecular pathways prediction by bioinformatics

In order to explore the potential molecular pathways about *CCT7* in EC, bioinformatics methods were adopted. As shown in Fig. 5a, a cohort of 546 UCEC and 35 noncancerous adjacent endometrium tissues were obtained from TCGA database. The results demonstrated that the expression of *CCT7* did not significantly differ in UCEC and adjacent endometrium tissues. Notably, the survival analysis showed that the UCEC patients with lower (n= 135) level *CCT7* expression had better Overall survival (OS) than higher (n= 408) group (p= 0.0081, Fig. 5b), which indicated that *CCT7* could be a potential prognostic marker for EC patients. As shown in Venn, 48 genes were obtained from MEM, 105 genes from UALCAN, and 141 co-expression genes from GEPIA, respectively (Fig. 6e).

Twelve genes, *CCT4, NHP2, C1QBP, CYC1, SAE1, PHB, MDH2, XRCC6, NME1, IMMT, RAN, STOML2*, were intersected in various platforms. Then these genes were used to enrich their function and pathways.

The Gene Ontology enrichment analysis comprised three categories: the molecular function (MF), the biological process (BP) and the cellular component (CC). GO enrichment indicated that *CCT7* was enriched in 80 MF, 153 BP, 59 CC. The most valuable 10 pathways of each category were presented in Fig. 6a-c. Among enriched pathways, the most significant pathway was “RNA binding” in MF, “Mitochondrion” in CC and “Translation” in BP. About the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, the 10 most significant pathways were shown in Fig. 6d, of which “Spliceosome” was the most significantly enriched pathway.

The PPI network was displayed (Fig. 6f), ten pairs of hub genes with the highest combined scores were collected from the PPI network (Table 2). Compared with non-cancerous endometrium tissues, the hub genes *PSMA5, PSMD14, SNRPB, SNRPG* and *TXNL4A* were significantly upregulated in UCEC ($p < 0.05$, Fig. 7a-e). Moreover, correlations between hub genes and *CCT7* were analyzed, and all genes were positively correlated with *CCT7* in UCEC ($p < 0.0001$, Fig. 7f-g).

Discussion

EC is one of the most frequent gynecological cancer worldwide[1]. The incidence and mortality of EC are rising throughout the developed world with a tendency for onset at younger age, and this trend is expected to continue mainly due to the increasing prevalence of obesity, hypertension, diabetes, and prolonged life expectancy[23]. For purpose of improving treatment and follow-up of EC patients, the importance of various prognostic factors had been extensively studied over the past few decades, including pathological stage, histological type and grade, age, tumor size, and lymphovascular space involvement[5, 24-26]. In addition, some tumor biomarkers also had been studied for their potential clinical value in patients with EC, including HE4, chaperonin 10, CA125, CA15.3, CA19.9, CA72.4, CEA, OVX1, and M-CSF[23, 27]. However, no good marker was routinely recommended for patients with EC. A study on large sample is probably needed to validate the independent connection of above-mentioned variables and biomarkers with prognosis.

EC typically spreads by invasion of the myometrium into the cervix, or via the fallopian tubes to the ovaries or trans-serosal spread to bladder or bowel[28]. The role of preoperative staging is aiming to establish a recurrence risk group to inform surgical management decisions, mainly based on tumor histology, tumor grade, MI depth and lymph node metastasis[29]. The tumor histology and grade may be evaluated preoperatively by endometrial biopsy, but it is difficult to determine the extent of MI accurately using the techniques in clinical practices. MI by the EC was associated with lymph node involvement, and both prognostic significance for EC patients were well documented[30, 31]. Thus, methods to assess the extent of MI are important. Clinically, TVS is excellent in determining the endometrial thickens, but it is limited in the evaluation of the depth of MI by the EC[32]. MRI is considered the most accurate imaging technique for preoperative assessment of EC due to its excellent soft tissue contrast resolution. However, there are some limitations including the uterine anatomy distorted by leiomyomas, presence of adenomyosis and when the tumor involved a cornu of the uterus[33]. Recent meta-analyses[34] had shown that estimated sensitivity and specificity for diagnosing deep MI were 75% (95% confidence interval [CI]=67%-82%) and 82% (95% CI=75%-93%) for TVS, and 83% (95% CI=76%-89%) and 82% (95% CI=72%-89%) for MRI, respectively. However, all studies included in this systematic review were both high and low risk patients for deep MI, which may affect the clinical applicability of both techniques. Therefore, it is

necessary to develop new methods to assist in evaluating the extent of MI for a precise determination of prognosis and accurate tailoring of adjuvant therapy.

To date, there are no molecular markers could help to assess the depth of MI by the EC. *CCT7,* also known as the *TCP1* ring complex, consists of two identical stacked rings and folds various proteins, which is involved in the folding of cytoskeletal proteins in an ATP dependent approach[16, 35, 36]. Based on our results, *CCT7* may have a critical role in the processes of muscle invasion and distant/nodal metastasis in EC development. Our previous proteomics experiments had shown that the *CCT7* gene was differentially expressed between EC and adjacent normal tissues[18], which was re-verified in the present study ($p = 0.033$). Of note, we found that the rate of CCT7 strongly positive cells differed significantly between the two groups, i.e., patients with and without deep MI ($p = 0.039$). Along with the ROC (AUC = 0.8502, $p < 0.0001$) between CCT7 expression and MI depth, suggesting that CCT7 was related to MI and it could be a valuable biomarker to evaluate the extent of MI by the EC. Better prognosis of EC patients related to lower pathological stages had been suggested[5], additional analyses confirmed that CCT7 expression also had an obvious correlation with pathological stage of patients, for advanced stage (III/IV) EC patients had higher CCT7 strongly positive cells rates and CCT7 protein level compared to lower stage (I/II) ($p = 0.029$ and Fig.1e), same as the ROC (AUC = 0.8694, $p < 0.0001$) between CCT7 expression and FIGO stage, which demonstrated the patients with higher CCT7 expression would be an unfavorable prognosis. Notably, corresponding with the survival analysis based on TCGA data, which showed that the EC patients with lower level *CCT7* expression had better OS ($p= 0.0081$) and *CCT7* had a potential prognostic value for EC patients.

Subsequently work, we attempted to validate the potential function and predict the potential molecular pathways involved of *CCT7* in EC development, the siRNAs method to knockdown *CCT7* expression in Ishikawa and RL95-2 cell lines was performed. We found a diminished proliferation activity, invasion abilities and colony capacity in both Ishikawa and RL95-2 cells after *CCT7* knockdown. At the same time, further studies revealed that loss of *CCT7* significantly stimulated the cell apoptosis and induced G2/M cell cycle arrest in EC cells. Collectively, *CCT7* expression were considerably correlated to EC cells function, which could affect multiple aspects of tumor cell development. For the bioinformatic analysis, based on TCGA, there were no significance about CCT7 expression between UCEC and normal samples, but the imbalance between the tumor and normal data may cause inefficiency for analysis. In addition, GO enrichment indicated that “RNA binding”, “Mitochondrion”, “Translation”, and “Spliceosome” were most significantly enriched potential pathways. In addition, five hub genes were analyzed from PPI network, *PSMA5, PSMD14, SNRPB, SNRPG* and *TXNL4*A, which were all significantly upregulated in UCEC compared to adjacent healthy controls. *PSMA5* and *PSMD14* are the core components of the proteasome complex participates in numerous cellular processes, including cell cycle progression, apoptosis, or DNA damage repair[37, 38]. It was reported that *PSMA5* and *PSMD14* could promote the tumorigenic process and tumor metastasis in various cancers[39, 40]. *SNRPB, SNRPG* and *TXNL4A* are the core components of spliceosome and play a major role in regulating alternative splicing of the pre-mRNA[41, 42]. *SNRPB* was reported that promoted the non-small cell lung cancer tumorigenesis[43]. These five genes were positively correlated with *CCT7* in UCEC, which revealed that *CCT7* may have similar potential tumorigenic function.

In our present work, we first provided a new method based on CCT7 to assess the extent of MI by EC, and CCT7 could also be a potential biomarker to predict the prognosis. However, there are some limitations we have to acknowledge. In this retrospective study, we only investigated the CCT7 expression in EC and adjacent normal

endometrium tissues, but healthy patients were not included, which may affect the clinical utility of this biomarker. And the potential molecular pathway was predicted but further confirmed experiments were needed.

Conclusion

Collectively, our results provided a new view of the molecular changes in EC. CCT7 may be involved in EC development by excessively activating tumor cell function, invasive ability particularly, to promote MI or distant/nodal metastasis, which definitely impaired the prognosis of EC patients.

List Of Abbreviations

EC: Endometrial cancer; MI: Myometrial infiltration; MRI: Magnetic resonance imaging; TVS: Transvaginal ultrasound; FIGO: The International Federation of Gynecology and Obstetrics; UCEC: Uterine Corpus Endometrial Carcinoma.

Declarations

Ethics approval and consent to participate

This study was approved by the Ethics Committee of Xiangya Hospital, Central South University, and all participants provided written informed consent.

Consent for publication

Not applicable.

Availability of data and materials

All data generated or analyzed during this study are included in this published article.

Competing interests

No author has any potential conflict of interest.

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Authors' contributions

NS was responsible for conception, design, quality control of this study, reviewed, and edited the manuscript. LW and WZ performed the experiments, data extraction, statistical analyses, and were major contributors in writing the manuscript. HL and HY participated in experiments and statistical analyses. All authors have read and approved the final version of the manuscript.

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Tables

Characteristic	Cases	CCT7		P-value
		+(%)	-(%)	
Age(years)				
< 60	15	9(60.0)	6(40.0)	0.194
≥ 60	72	30(41.7)	42(58.3)	
Menopause				
Yes	42	23(54.8)	19(45.2)	0.072
No	45	16(35.6)	29(64.4)	
Tissue Type				
Carcinous	87	39(50.7)	38(49.3)	**0.033***
Pericarcinous	72	24(33.3)	48(66.7)	
Pathological Stage				
I-II	73	29(39.7)	44(60.3)	**0.029***
III-IV	14	10(71.4)	4(28.6)	
Histological Grade				
G1	49	19(38.8)	30(61.2)	0.182
G2	33	16(48.5)	17(51.5)	
G3	5	4(80.0)	1(20.0)	
Depth of Invasion				
< 1/2	67	26(38.8)	41(61.2)	**0.039***
≥ 1/2	20	13(65.0)	7(35.0)	
Pathological Type				
Endometrioid adenocarcinoma	75	34(45.3)	41(54.7)	0.813
Other Types§	12	5(41.7)	7(58.3)	
Preoperative Chemotherapy				
Yes	31	16(51.6)	15(48.4)	0.344
No	56	23(41.1)	33(58.9)	

Note: CCT7+: ≥6 points, strongly positive; CCT7-: ≤6 points, negative and positive; §: Other types included(cases/ CCT7+/ CCT7-) : Adenosquamous carcinoma(5/1/4), Serous papillary adenocarcinoma(3/1/2), Clear cell carcinoma(2/1/1) and Mucinous carcinoma(2/2/0); Statistical analyses were performed using Chi-square tests. *P < 0.05 was considered statistically significant.

Table 1

Correlations Between CCT7 and Clinicopathological Features in Patients with Endometrial Cancer.

Node-1	Node-2	Homology	Co-expression	Experimentally determined interaction	Database annotated	Automated text mining	Combined score
SNRPG	*SNRPD3*	0	0.986	0.993	0.9	0.901	0.999
RRP9	*FBL*	0	0.804	0.827	0.9	0.832	0.999
SNRPB	*SNRPG*	0	0.45	0.991	0.9	0.853	0.999
PDCD11	*RRP9*	0	0.864	0.733	0.9	0.757	0.999
TXNL4A	*SNRNP40*	0	0.107	0.989	0.9	0.293	0.999
NOP14	*RRP9*	0	0.879	0.796	0.9	0.755	0.999
SNRPB	*SNRPD3*	0	0.555	0.992	0.9	0.857	0.999
SNRPG	*SNRPC*	0	0.634	0.981	0.9	0.624	0.999
PSMD14	*PSMA5*	0	0.912	0.992	0.9	0.563	0.999
SNRPC	*SNRPD3*	0	0.868	0.96	0.9	0.842	0.999

Table 2
Top 10 pairs of hub genes from the PPI network.

Figures

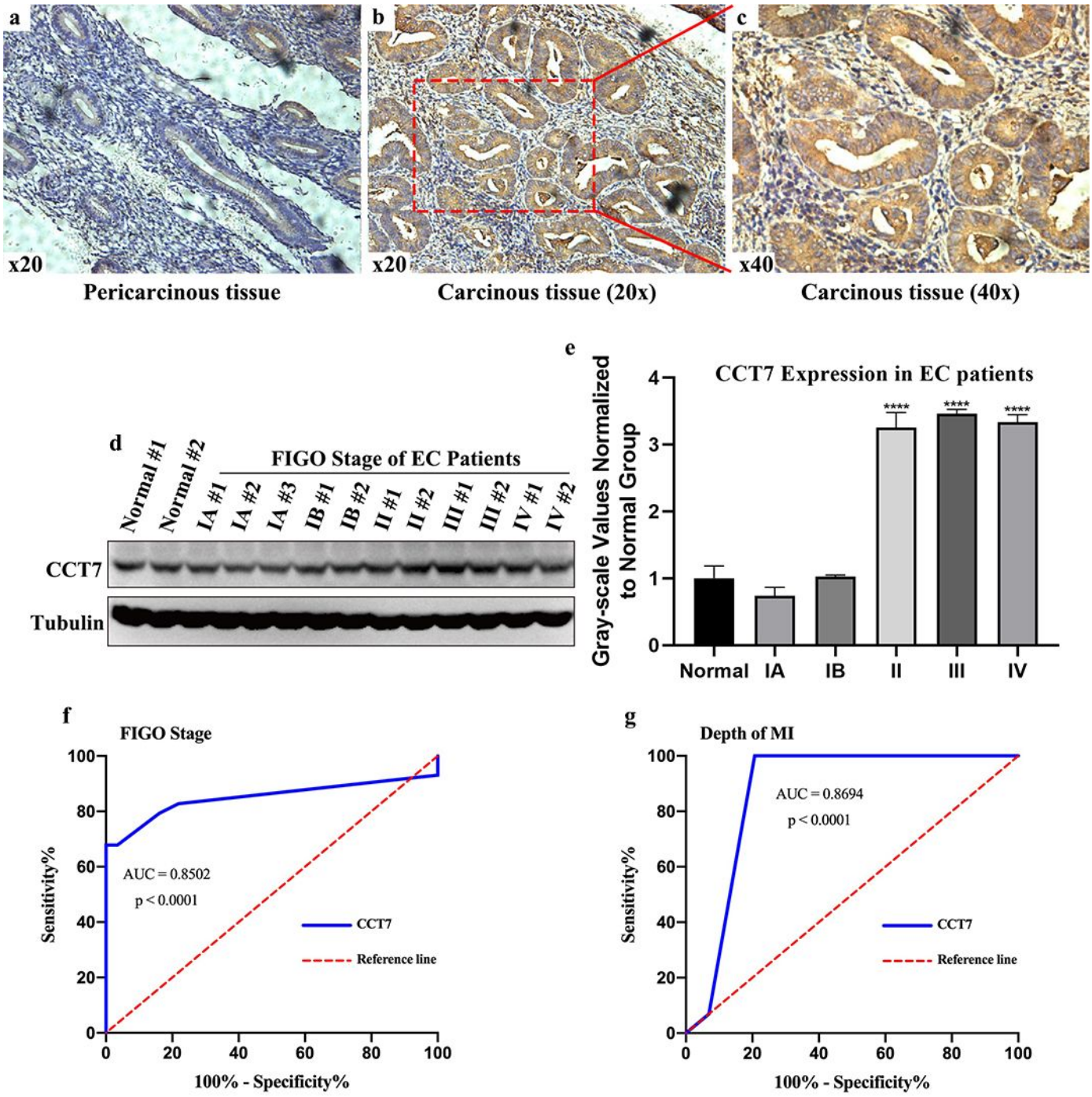

Figure 1

CCT7 Overexpression in Carcinous Tissue. a-c Immunohistochemistry assay for CCT7 in pericarcinous tissue and carcinous tissue (b:20x and c:40x). d-e Western blotting assays were used to evaluate the expression of CCT7 level in the samples from EC patients and quantification also performed. f-g Receiver operating characteristic curves (ROCs) were used to analyzed the association between CCT7 expression and FIGO stage and MI depth. ****p□0.0001, all values represent Mean ± S.D.

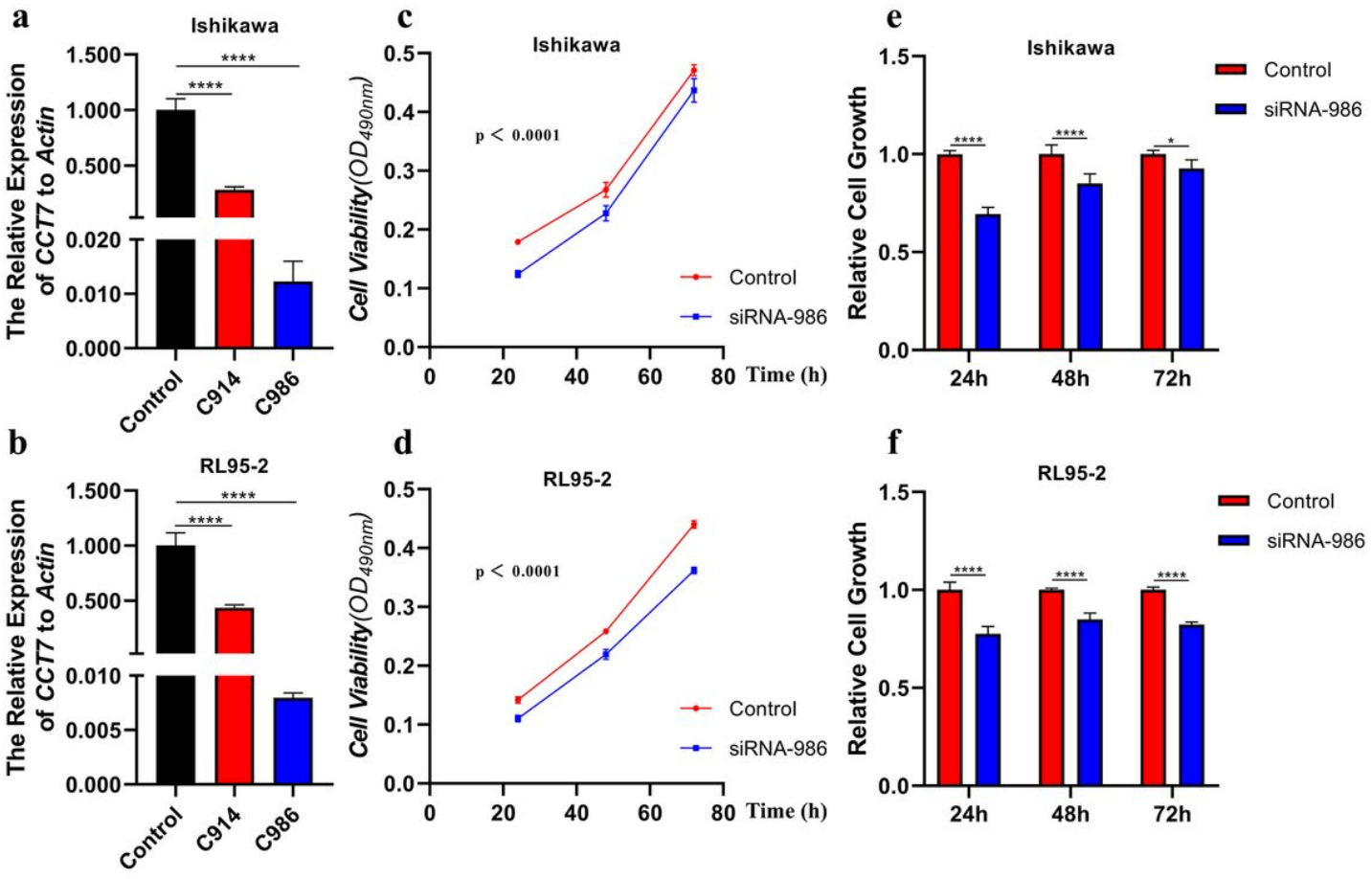

Figure 2

Knockdown of CCT7 Decreased the Tumor Cells Proliferation Abilities. a-b qPCR was performed to test the mRNA level of CCT7 after transferring the CCT7-siRNA into Ishikawa and RL95-2 cells. c-f Proliferative abilities of Ishikawa and RL95-2 cells treated with CCT7 siRNA-986 were determined using an MTT assay after culturing for 24h, 48h, 72h. *p□0.05, ****p□0.0001, all values represent Mean ± S.D.

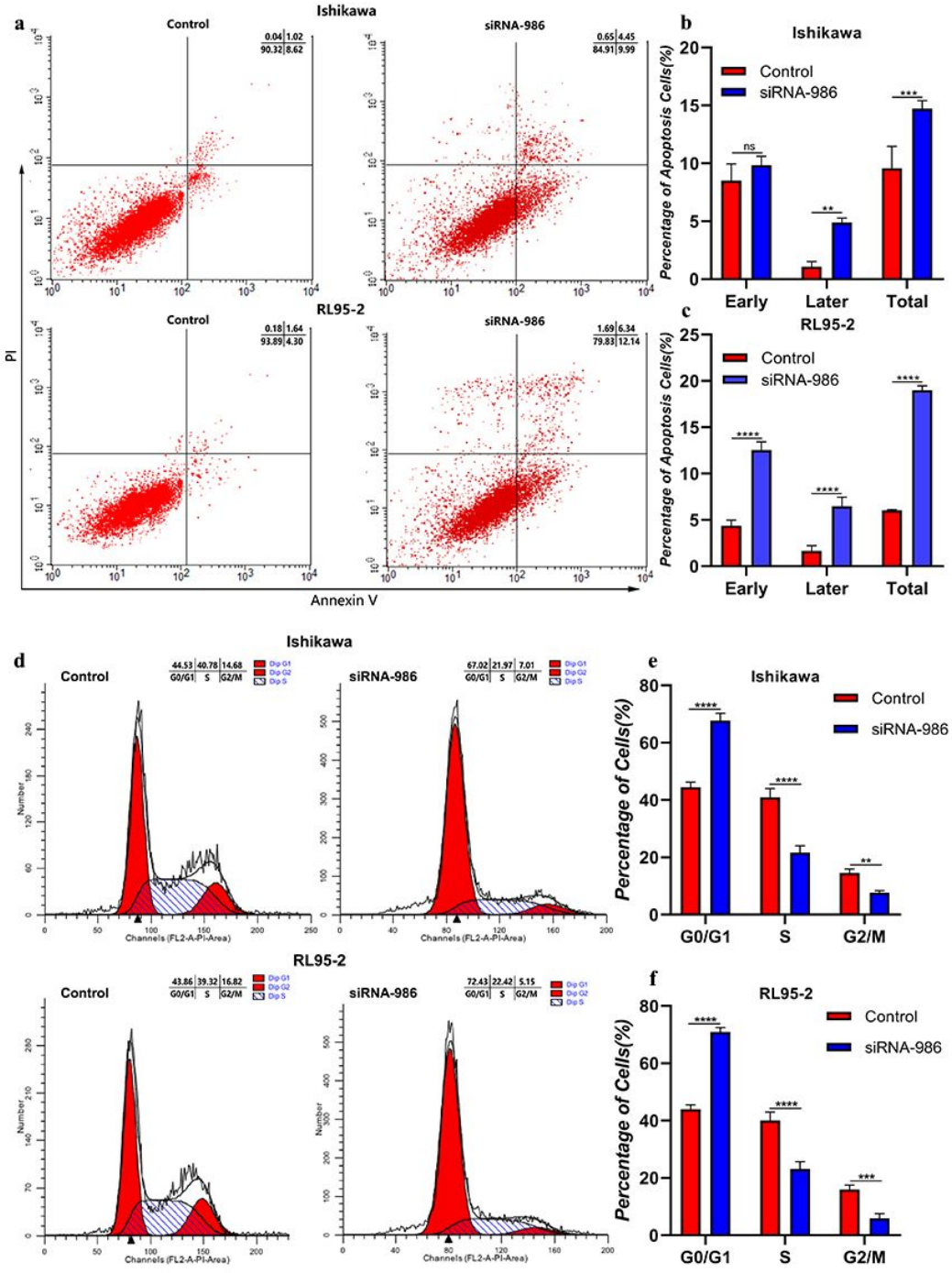

Figure 3

Loss of CCT7 Increased the Tumor Cells Apoptosis and Decreased G2/M Phase of Cells. a-c Cell apoptosis, and d-f cell cycle of Ishikawa and RL95-2 cells treated with CCT7 siRNA-986 were detected by FAC Scan. **p□0.01, ***p□0.001, ****p□0.0001, all values represent Mean ± S.D.

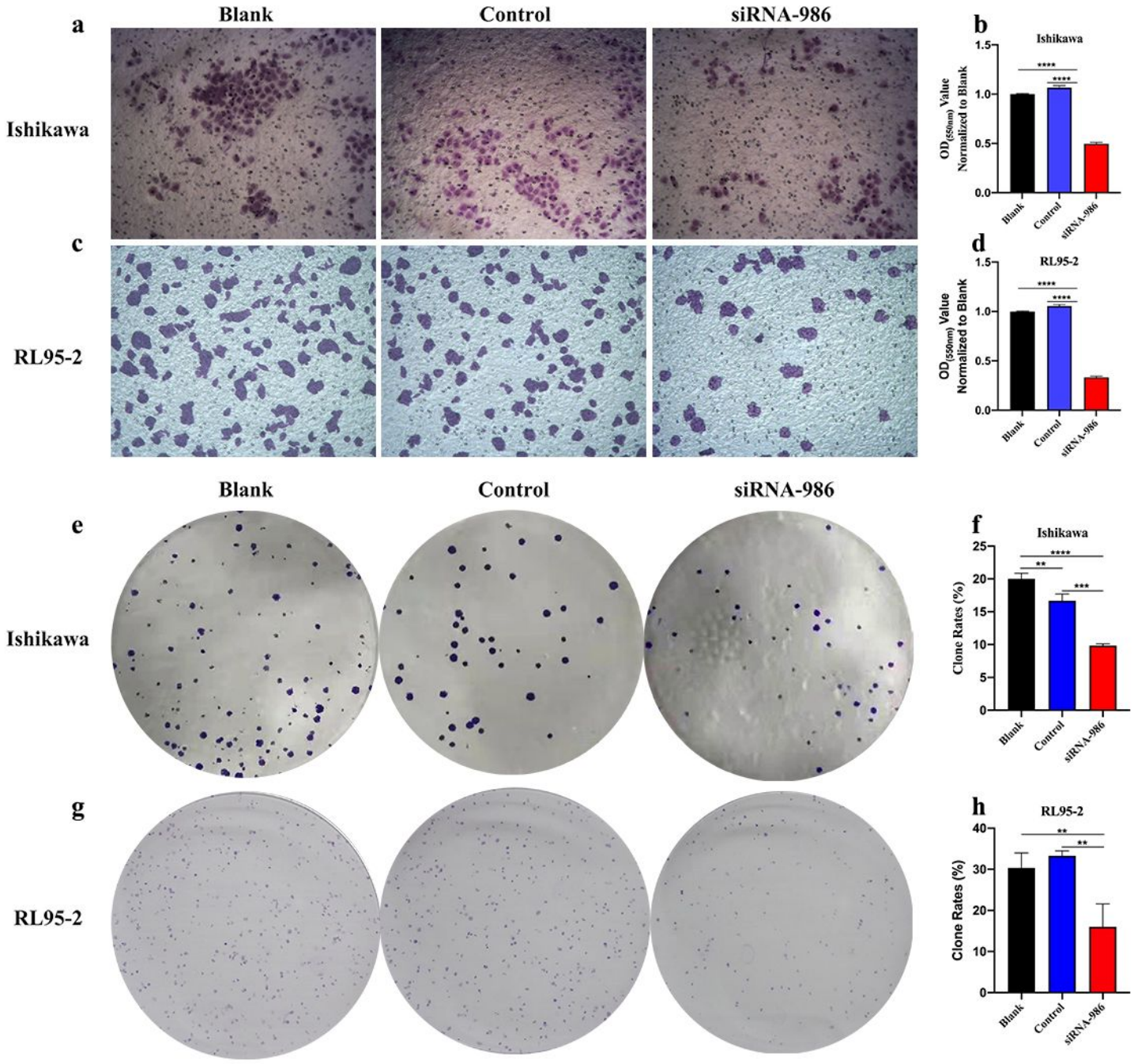

Figure 4

Inhibition of CCT7 Suppressed the Capacity of Tumor Cells Migration and Colony Formation. a-d Cell migration, and e-h colony formation of Ishikawa and RL95-2 cells treated with CCT7 siRNA-986 were examined. **p□0.01, ***p□0.001, ****p□0.0001, all values represent Mean ± S.D.

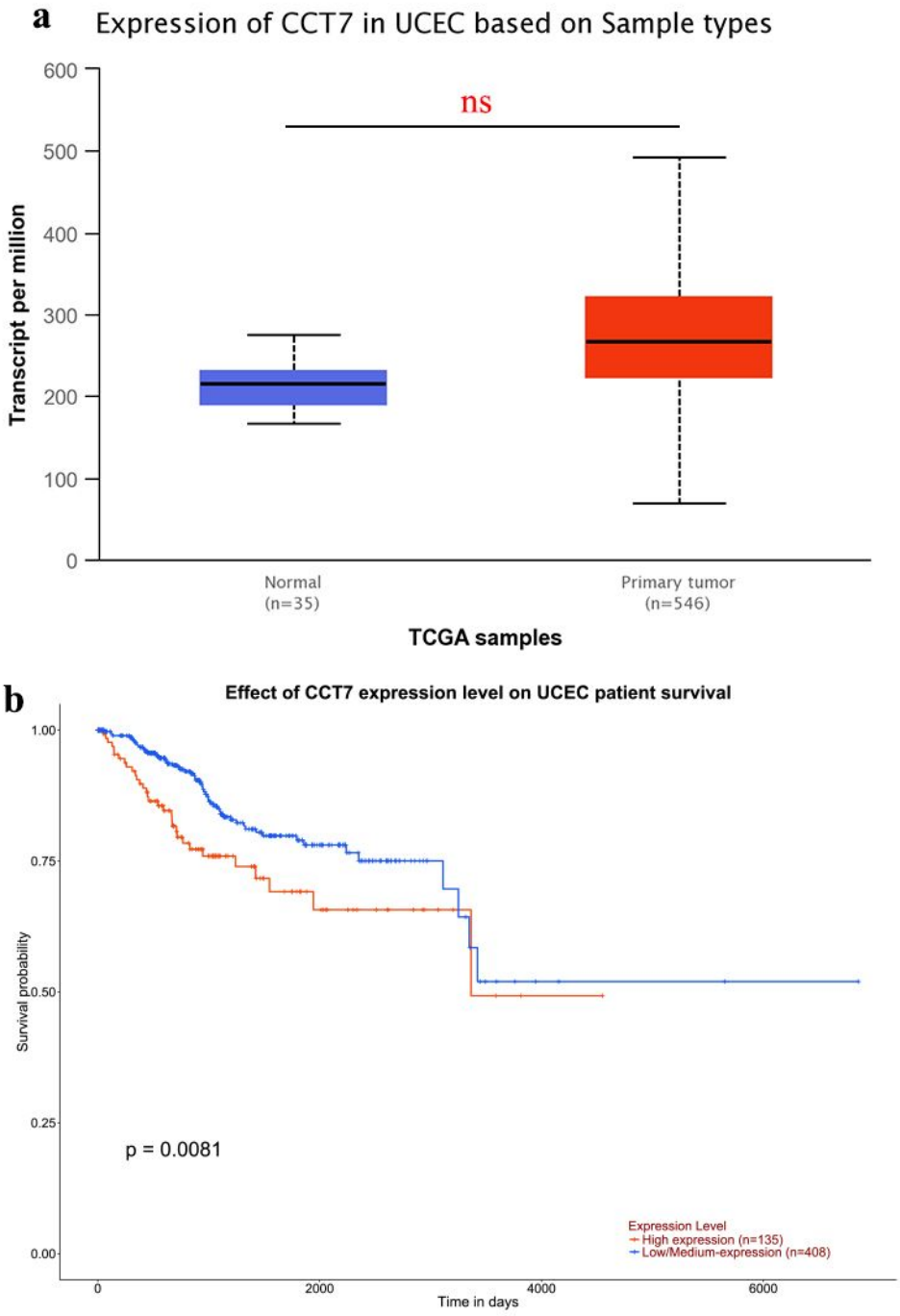

Figure 5

Data Analysis from TCGA. a CCT7 expression in normal samples (n=35) and UCEC (n=546) were analyzed based on TCGA. b Survival analysis was performed to test the effect of CCT7 expression level on UCEC patient survival. UCEC: Uterine Corpus Endometrial Carcinoma.

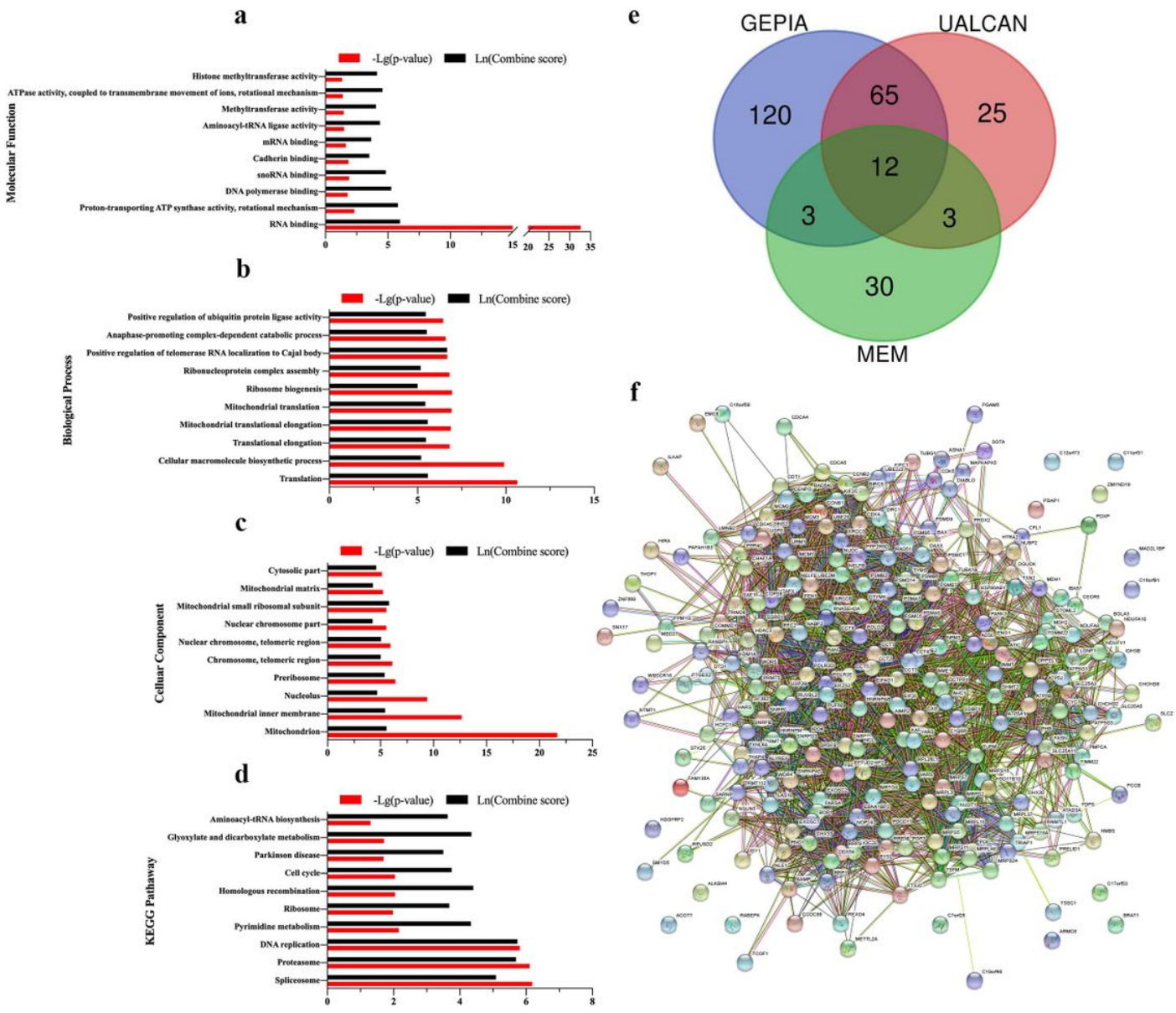

Figure 6

GO Enrichment Analysis of CCT7 in UCEC. a-d Top ten significant enriched pathways of Molecular Function (MF), Biological Process (BP), Cellular Component (CC) and Kyoto Encyclopedia of Genes and Genomes (KEGG) were presented. e 48 co-expression genes of CCT7 obtained from MEM, 105 genes from UALCAN, and 141 genes from GEPIA were summarized in the Venn. f Protein-protein interaction (PPI) network was displayed.

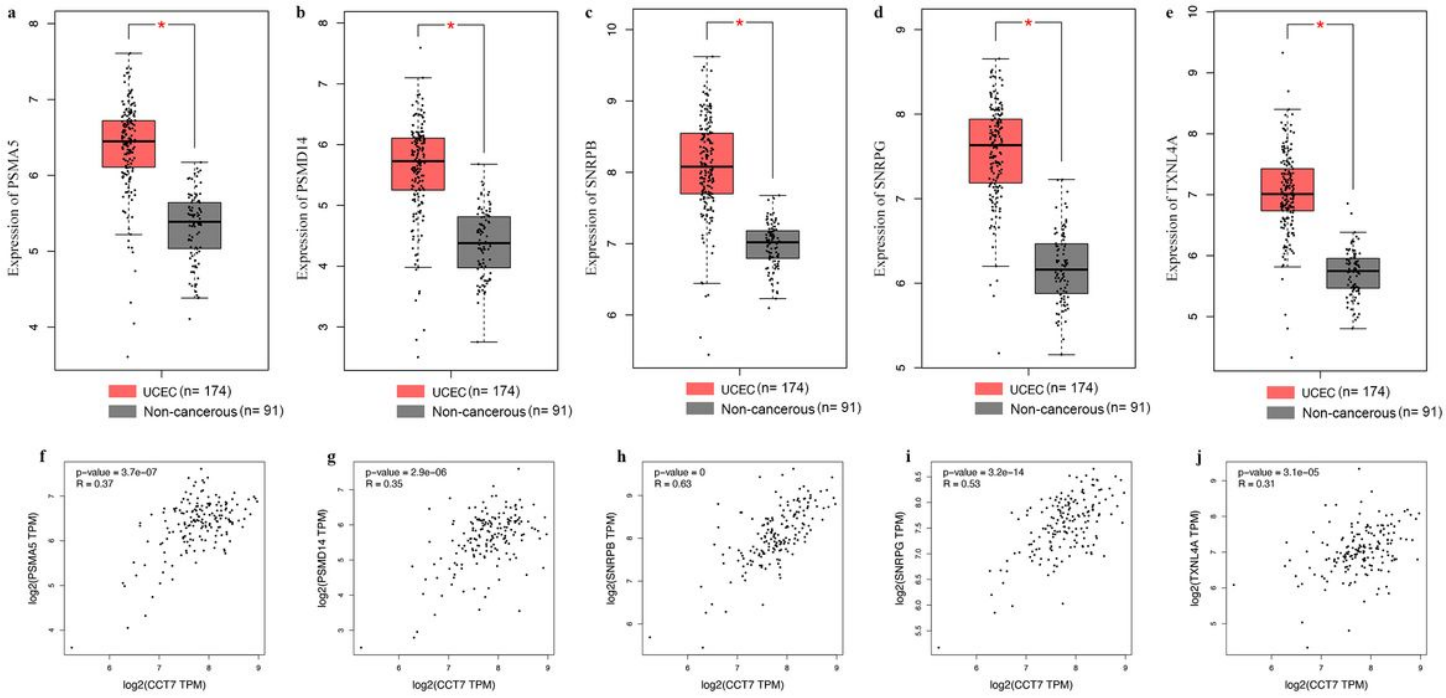

Figure 7

Hub Genes Identification and the Correlation with CCT7 in UCEC. a-e The expression of hub genes in UCEC and non-cancerous were analyzed, and f-g their correlation with CCT7 were also examined. *p□0.05, all values represent Mean ± S.D.