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ORIGINAL RESEARCH ARTICLE

Integrated transcriptomic analysis and RT-qPCR validation using FFPE patient tissues reveal the role of *FOXQ1* and *MCM10* in ovarian cancer

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Abstract

Introduction: Ovarian cancer has a high mortality rate due to late diagnosis and limited availability of reliable molecular biomarkers. Integrated transcriptomic analysis may facilitate the identification of key regulatory genes involved in tumor progression.

Objective: To identify and validate key regulatory genes associated with ovarian cancer progression through integrated transcriptomic analysis and experimental validation.

Methods: Differential gene expression analysis was conducted using the GSE18520 microarray dataset to compare ovarian cancer tissues with normal ovarian epithelium. Genes with $\log_2$ fold change ≥ 1, and adjusted *p*-value < 0.05 were considered significant. Functional enrichment and protein–protein interaction (PPI) network analyses were performed to prioritize hub genes. *FOXQ1* and *MCM10* were selected for experimental validation using quantitative real-time polymerase chain reaction (RT-qPCR) in formalin-fixed paraffin-embedded (FFPE) ovarian cancer tissues. Relative expression levels were calculated using the $2^{-\Delta\Delta Ct}$ method and normalized to *GAPDH*.

Results: Transcriptomic analysis identified multiple differentially expressed genes associated with cell cycle regulation, DNA replication, and transcriptional control. *FOXQ1* ($\log_2$ fold change = +5.00) and *MCM10* ($\log_2$ fold change = +2.74) were significantly upregulated and occupied central hub positions in the PPI network. RT-qPCR validation confirmed marked overexpression of *FOXQ1* (45.3×) and *MCM10* (11.3×) in FFPE ovarian cancer tissues.

Conclusion: This integrated transcriptomic and experimental validation study identifies *FOXQ1* and *MCM10* as key regulators in ovarian cancer, highlighting their potential as biomarkers for disease progression.

Keywords: Ovarian cancer; GSE18520; Differential gene expression; *FOXQ1*; *MCM10*; Quantitative reverse transcription polymerase chain reaction

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1. Introduction

Ovarian cancer remains the deadliest of all gynecological malignancies, with an estimated 313,000 new cases and 207,000 deaths globally in 2020 alone.[1] High-grade serous ovarian carcinoma, the most prevalent subtype, is frequently diagnosed at advanced stages due to its asymptomatic progression and lack of effective early diagnostic markers. Despite advances in surgery and platinum-based chemotherapy, the five-year survival rate remains below 45%, largely due to late detection, resistance to treatment, and disease recurrence.[2,3] Thus, identifying molecular targets that regulate tumor proliferation and contribute to disease progression is essential for improving prognostic stratification and therapeutic strategies.

Transcriptomic profiling, particularly through publicly available microarray datasets such as GSE18520, has significantly expanded our understanding of ovarian cancer biology. Analysis of GSE18520 has revealed several differentially expressed genes (DEGs) involved in cell cycle regulation, DNA replication, and epithelial–mesenchymal transition (EMT), suggesting their potential as oncogenic drivers. Among these, two genes of interest, forkhead box Q1 (*FOXQ1*) and minichromosome maintenance 10 (*MCM10*), have emerged as promising candidates for further functional validation due to their consistent upregulation in ovarian tumor tissues and reported oncogenic functions in other cancers.[4,5]

Forkhead box Q1 is a transcription factor in the forkhead box (FOX) family that plays pivotal roles in cell differentiation, proliferation, and EMT. Several studies have demonstrated that *FOXQ1* is overexpressed in a range of malignancies, including gastric, colorectal, and ovarian cancers, and contributes to tumor aggressiveness by activating TGF-β and Wnt/β-catenin signaling pathways.[3,6] In ovarian cancer, *FOXQ1* has been shown to enhance EMT and metastasis, although its precise mechanistic contributions to cellular proliferation remain insufficiently explored.

Similarly, *MCM10* is a crucial DNA replication licensing factor involved in the initiation and elongation phases of DNA synthesis. It forms part of the *MCM2-7* helicase complex and ensures genomic stability during cell division. Aberrant expression of *MCM10* has been linked to uncontrolled proliferation and poor prognosis in various cancers, including breast and ovarian cancer.[7,8] Recent studies suggest that *MCM10* may function as a proliferation marker and therapeutic target, particularly in rapidly dividing tumor cells.[5] However, functional studies in ovarian cancer models, such as formalin-fixed paraffin-embedded (FFPE) ovarian tissue samples, remain limited, and the gene's regulatory role in tumor growth requires further elucidation.

Given the established oncogenic potential of *FOXQ1* and *MCM10*, the current study aims to functionally validate their roles in ovarian cancer cell proliferation using the FFPE ovarian tissue samples. We selected these genes from GSE18520 transcriptomic analysis based on their significant differential expression, network centrality in protein–protein interaction (PPI) analyses, and associations with survival outcomes. Through integrated transcriptomic analysis and quantitative real-time polymerase chain reaction (RT-qPCR) validation in patient-derived ovarian cancer tissues, this study aimed to assess the differential expression and potential biological significance of *FOXQ1* and *MCM10* as candidate biomarkers for epithelial ovarian cancer.

This work provides an important translational link between transcriptomic data mining and functional genomics in ovarian cancer research. Furthermore, elucidating the mechanistic roles of *FOXQ1* and *MCM10* may open avenues for novel diagnostic and therapeutic strategies, particularly in personalizing treatment approaches for patients with chemoresistant or recurrent ovarian cancer.

2. Materials and methods

2.1. Bioinformatic analysis

This study applied a systematic bioinformatics strategy to identify genes associated with cell proliferation in ovarian cancer, using the publicly available dataset GSE18520.[9] This dataset includes transcriptomic data from both malignant ovarian tissue and healthy ovarian epithelium. Raw data files were obtained from the National Center for Biotechnology Information (NCBI) GEO database and analyzed in the R environment (version 4.3.0) using Bioconductor packages.[10] Preprocessing steps, including background correction, $\log_2$ transformation, and quantile normalization, were performed using the affy and limma packages to ensure consistent quality across samples. DEGs were selected using the criteria of $\log_2$ fold change ≥ 1 and an adjusted p-value <0.05.

To identify genes showing significant differences in expression between cancerous and normal tissues, differential expression analysis was performed using the limma package. The criteria used to define significantly altered genes were a $\log_2$ fold change of at least 2 and an adjusted p-value (Benjamini–Hochberg method) of less than 0.05. This allowed for the selection of both upregulated and downregulated genes with high statistical confidence.

Following this, functional annotation and pathway enrichment analysis were conducted to better understand

the biological relevance of the identified DEGs. The DAVID database and the Enrichr platform were used to perform Gene Ontology analysis covering biological processes, molecular functions, and cellular components, as well as Kyoto Encyclopedia of Genes and Genomes pathway mapping.[11,12] Only the most statistically significant terms, based on corrected *p*-values and the number of genes involved, were highlighted in the results.

To further examine how these DEGs may interact at the protein level, a PPI network was generated using the Search Tool for the Retrieval of Interacting Genes/Proteins (STRING) database (version 12.0),[13] applying a minimum interaction confidence score of 0.7 to focus on high-confidence connections. The resulting network was imported into Cytoscape (version 3.9.1) for visualization and network analysis.[14] Key hub genes, in particular those occupying central positions within the interaction network, were identified using the CytoHubba plugin, which evaluates node importance based on several topological metrics, including degree, maximal clique centrality (MCC), and betweenness centrality.

2.2. Ethical approval and experimental validation

All experimental validation procedures involving human ovarian tissue were conducted in accordance with ethical principles for biomedical research and received formal approval from the Ethics Committee of the Faculty of Medicine, Universitas Indonesia (ethical approval number: KET-521/UN2.F1/ETIK/PPM.00.02/2025). The study strictly adhered to the Declaration of Helsinki and relevant institutional regulations governing the use of human biological materials.

Experimental validation was performed using archived FFPE ovarian tissue samples obtained from the institutional biobank. A total of 22 samples were included, comprising 12 ovarian tumour tissues and 10 normal ovarian tissues from benign, non-cancer cases. The use of archival specimens ensured that no additional procedures or risks were imposed on patients.

All samples were fully anonymized and de-identified prior to analysis, and no personally identifiable information was accessible to the investigators. Due to the retrospective nature of the study and the exclusive use of biobanked archival tissues, the Ethics Committee waived the requirement for informed consent. Molecular validation, including quantitative polymerase chain reaction (PCR) and genotyping analyses, was performed in accordance with standardized laboratory protocols to ensure reproducibility, data integrity, and ethical compliance throughout the validation process.

2.3. RNA isolation and cDNA synthesis

Total RNA was extracted from cultured FFPE ovarian tissue samples using a triazole reagent (Invitrogen, United States of America [USA]), following the manufacturer's standard protocol. The concentration and purity of the isolated RNA were assessed using a NanoDrop spectrophotometer (Thermo Scientific 2000, Thermo Fisher Scientific, USA), ensuring that only high-quality RNA samples were used for downstream applications. Subsequently, 1 µg of total RNA was reverse transcribed into cDNA using the Revert Aid First Strand cDNA Synthesis Kit (Thermo Fisher Scientific, USA), in accordance with the manufacturer's instructions.

2.4. Primer design

Gene-specific primers for *MCM10*, *FOXQ1*, and the housekeeping gene *GAPDH* were designed using NCBI's Primer-BLAST tool or adopted from previously validated sources. Primer specificity was confirmed by melting curve analysis to ensure amplification of a single, specific product for each gene target, with no evidence of primer dimers or nonspecific amplification.

2.5. Quantitative real-time polymerase chain reaction (qRT-PCR)

Gene expression quantification was performed using SYBR Green-based qRT-PCR. Reactions were set up with SYBR Green PCR Master Mix (Applied Biosystems, USA) and were carried out on a compatible real-time PCR instrument (StepOnePlus™; Applied Biosystems, USA). Each 20 µL reaction mixture consisted of 2 µL of cDNA template, 10 µL of master mix, 0.5 µM of each primer (forward and reverse), and nuclease-free water to bring the total volume to 20 µL. The thermal cycling conditions included an initial denaturation at 95 °C for 10 minutes, followed by 40 amplification cycles comprising denaturation at 95 °C for 15 seconds, annealing at 60 °C for 30 seconds, and extension at 72 °C for 30 seconds. The primers used in this study are shown in Table 1.

2.6. Data analysis

Gene expression data were normalized to *GAPDH* using the $2^{-\Delta\Delta Ct}$ approach. Each assay was conducted in triplicate, with results expressed as the mean ± standard error of the mean. Statistical comparisons between groups were performed using a Student's *t*-test, with significance defined at $p < 0.05$. Data visualization was carried out using GraphPad Prism version 9 (GraphPad Software, USA).[15]

Table 1. Primers for *MCM10* and *FOXQ1* gene detection, and the housekeeping gene *GAPDH*

Gene	Primer type	Sequence (5' → 3')	Tm (°C)	Amplicon size (bp)
MCM10	Forward	AGGAGAGGAAGTTTGGCGAC	~60	118
	Reverse	GCTTTCTTCAGGGTCCATGT	~60	
FOXQ1	Forward	TGGCAATCAGCGACGATCTT	~60	103
	Reverse	CAGAGGCTGTTGACAGGTTG	~60	
GAPDH (housekeeping)	Forward	GAAGGTGAAGGTCGGAGT	~60	~140
	Reverse	GAAGATGGTGATGGGATTTC	~60	

3. Results

3.1. Differential gene expression analysis of GSE18520

Differential gene expression analysis was performed on the GEO dataset GSE18520, which includes ovarian cancer tissue samples and normal ovarian controls. After data normalization and statistical analysis using the limma method, DEGs were identified with an adjusted *p*-value <0.05 and a $\log_2$ fold change ≥ 1.

The volcano plot in Figure 1 illustrates the global distribution of DEGs. Significantly upregulated genes ($\log_2$ fold change > 1, adjusted p <0.05) were shown in red, whereas significantly downregulated genes ($\log_2$ fold change <−1, adjusted p <0.05) were shown in blue. Genes without significant differential expression were displayed in gray. The majority of genes fall into the non-significant category, while a distinct subset demonstrated marked expression changes between ovarian cancer and normal tissues.

3.2. Identification of key differentially expressed genes

Table 2 summarizes the top upregulated and downregulated genes in ovarian cancer tissues compared with normal ovarian epithelium, as determined by microarray analysis (platform GPL570). Differential expression was determined using the limma package, with genes ranked according to the magnitude of $\log_2$ fold change. Upregulated genes include *FOXQ1*, *MCM10*, *RBL1*, and *SPIN3*, while significantly downregulated genes include *CALB2*, *VGLL3*, and *RNF128*. Only genes meeting the significance criteria of $\log_2$ fold change ≥ 2 and an adjusted *p*-value (false discovery rate, FDR) <0.05 are shown.

Table 2 presents the top significantly DEGs in ovarian cancer, classified as upregulated or downregulated based on their $\log_2$ fold changes. The expression profile depicted in Figure 1 highlights a shift toward oncogenic and proliferative signaling accompanied by loss of tumor-suppressive and regulatory functions, supporting the biological relevance of *FOXQ1* and *MCM10* as potential biomarkers of ovarian cancer progression.

3.3. Pathway enrichment analysis

According to the functional enrichment analysis of the DEGs listed in Table 2, upregulated genes were primarily enriched in pathways related to cell cycle progression and DNA replication, whereas downregulated genes were associated with cell differentiation, adhesion, and signaling processes.

Figure 2 summarizes the significantly enriched biological pathways among DEGs in ovarian cancer compared with those in normal ovarian tissue. Upregulated pathways (red) were predominantly associated with cell cycle regulation, p53 signaling, oocyte maturation, and DNA conformation changes, whereas downregulated pathways (blue) included blood coagulation, transcription regulation, axonogenesis, and extracellular matrix organization. Bar length represents $-\log_{10}$ (*p*-value; FDR), indicating the statistical significance of pathway enrichment.

3.4. Protein–protein interaction network and gene prioritization

Protein–protein interaction network analysis of selected DEGs identified coordinated regulation of pathways associated with ovarian cancer progression (Figure 3). *MCM10* and *FOXQ1* emerged as hub genes within the network, while *INHBB* and *CTCFL* functioned as connector nodes. Downregulated genes such as *VGLL3, RNF128, CALB2,* and *MUM1L1* were positioned as peripheral nodes (Figure 3).

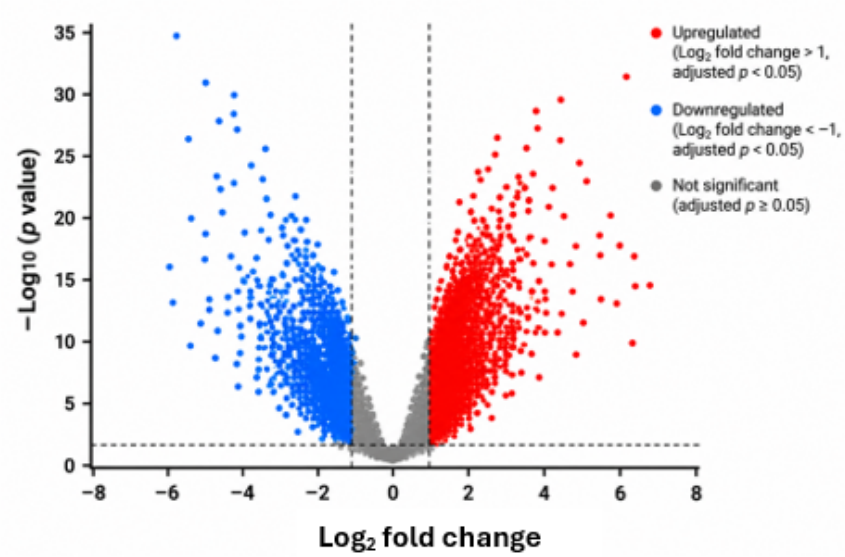


Figure 1. Volcano plot of differentially expressed genes in the GSE18520 dataset

Table 2. Differential gene expression analysis from dataset GSE18520

Regulation	Rank	Probe ID (GPL570)	Gene symbol	Log_2 fold change	Adjusted *p*-value (false discovery rate)
Upregulated	1	218898_at	*FOXQ1*	+5.00	<0.001
	2	218039_at	*MCM10*	+2.74	<0.001
	3	203687_s_at	*RBL1*	+3.12	<0.001
	4	219490_at	*SPIN3*	+3.01	<0.001
	5	203206_s_at	*BNC1*	+2.95	<0.001
	6	218675_at	*SHISA3*	+2.90	<0.001
	7	206881_at	*ITLN1*	+2.85	<0.001
	8	205635_at	*ADH1B*	+2.79	<0.001
	9	204087_s_at	*OGN*	+2.68	<0.001
	10	204241_at	*BCHE*	+2.62	<0.001
Downregulated	1	205808_at	*CALB2*	−4.21	<0.001
	2	219683_at	*VGLL3*	−3.98	<0.001
	3	219613_at	*RNF128*	−3.76	<0.001
	4	219482_at	*ANKRD29*	−3.65	<0.001
	5	219746_at	*SYT4*	−3.52	<0.001
	6	203865_at	*GPM6A*	−3.40	<0.001
	7	204890_s_at	*PLP1*	−3.28	<0.001
	8	207897_at	*CLDN10*	−3.14	<0.001
	9	219261_at	*CNTNAP2*	−2.36	<0.001
	10	206432_at	*GRIA2*	−2.31	<0.001

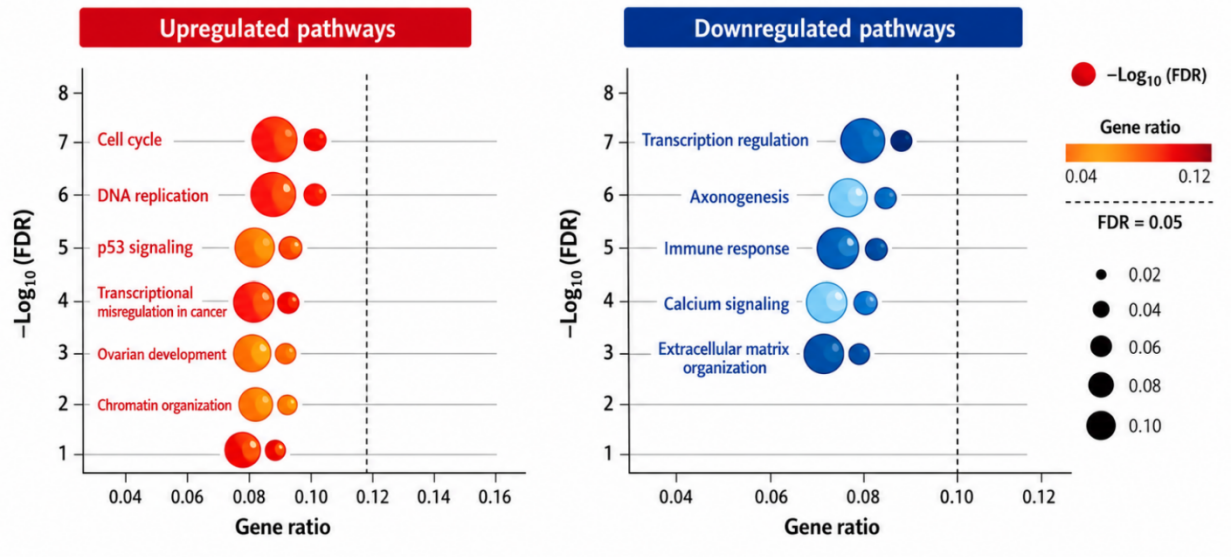


Figure 2. Enrichment analysis of differentially expressed genes in ovarian cancer from GSE18520
Abbreviation: FDR: False discovery rate.

Table 3. Enrichment analysis of differentially expressed genes from GSE18520

Functional category	Regulation	Representative genes
Cell cycle regulation	Upregulated	*FOXQ1*, *MCM10*, *RBL1*
DNA replication	Upregulated	*MCM10*
Transcriptional control	Upregulated	*FOXQ1*, *SPIN3*
p53 signaling pathway	Upregulated	*MCM10*, *RBL1*
Cell differentiation	Downregulated	*CALB2*, *CLDN10*
Cell adhesion and signaling	Downregulated	*VGLL3*, *RNF128*
Axon/neuronal-related processes	Downregulated	*SYT4*, *GPM6A*

Protein–protein interaction analysis was performed to prioritize key genes involved in ovarian cancer using the GSE18520 dataset. DEGs were imported into the STRING database to construct a PPI network, which was subsequently analyzed using Cytoscape. Candidate hub genes were identified based on network topology parameters, including degree, MCC, and molecular complex detection (MCODE) clustering, as shown in Figure 3. Genes exhibiting high degrees and MCC values, as well as those located within significant MCODE modules, were considered critical regulators within the PPI network.

Within the network, *FOXQ1* and *MCM10* emerged as key upregulated hub genes, showing high connectivity and central positions, indicating major regulatory roles. Additional upregulated hub genes included *RBL1* and *BCHE*, while *BNC1*, *ITLN1*, and *MMP11* were classified as peripheral nodes. Among the downregulated genes, *CALB2* remained a central hub, whereas *RNF128*, *NPY1R*, and *GAD1* played peripheral roles in the network.

3.5. Rationale for selecting *MCM10* and *FOXQ1*

Based on the enrichment analysis summarized in Table 3, the selection of *FOXQ1* and *MCM10* was based on the convergence of (i) significant upregulation, (ii) central positions within the PPI network, and (iii) functional involvement in proliferation- and replication-related pathways. *FOXQ1* was prioritized due to its role in transcriptional reprogramming and cancer-associated gene regulation, while *MCM10* was selected for its essential function in DNA replication initiation and S-phase progression. *FOXQ1* and *MCM10* were selected as key hub genes for experimental validation, as summarized in Table 4.

3.6. Validation of candidate genes by quantitative real-time polymerase chain reaction

Quantitative real-time polymerase chain reaction analysis was performed to validate the expression of *MCM10* and *FOXQ1* in FFPE ovarian tissue samples, using *GAPDH* as a reference gene. Both genes showed significant upregulation (Table 5 and Figure 4). *FOXQ1* demonstrated the highest relative expression with an approximate 45.3-fold increase,

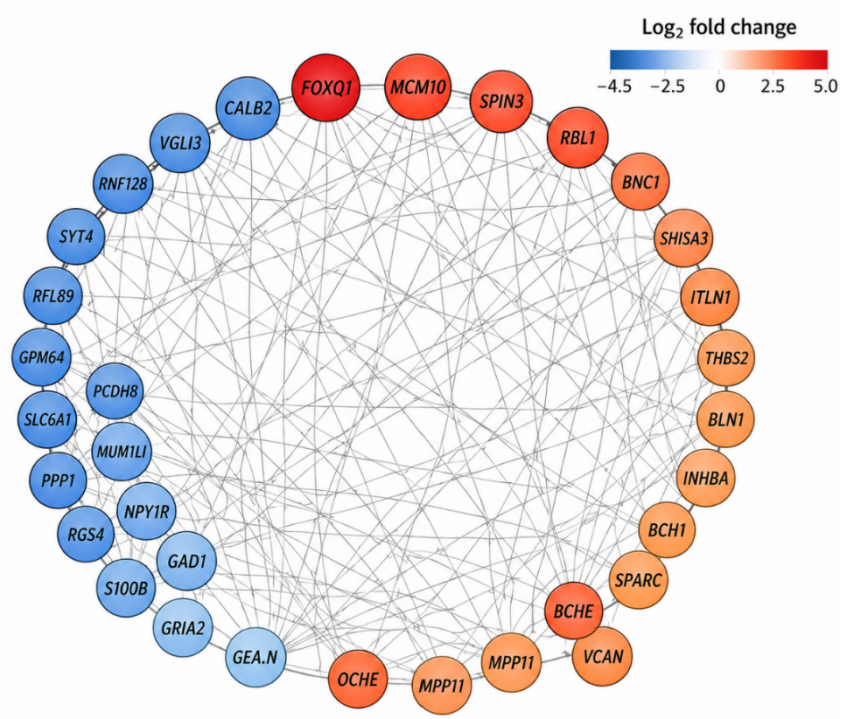


Figure 3. Network interaction map among upregulated and downregulated genes from GSE18520

Table 4. Candidate gene prioritization from the GSE18520 dataset based on protein–protein interaction network analysis

Gene symbol	Regulation	Log_2 fold change	Adjusted *p*-value	Key biological pathways	Protein–protein interaction network role
FOXQ1	Upregulated	+5.00	<0.001	Transcriptional regulation, epithelial–mesenchymal transition, Wnt/β-catenin signaling	Hub gene
MCM10	Upregulated	+2.74	<0.001	DNA replication, cell cycle progression	Hub gene
RBL1	Upregulated	+3.12	<0.001	Cell cycle control, E2F transcription factor signaling	Co-hub gene
BCHE	Upregulated	+2.62	<0.001	Metabolic regulation, cellular signaling	Co-hub gene
BNC1	Upregulated	+2.95	<0.001	Transcriptional regulation	Peripheral gene
ITLN1	Upregulated	+2.85	<0.001	Metabolic pathways, tumor microenvironment	Peripheral gene
CALB2	Downregulated	−4.21	<0.001	Calcium signaling pathway	Hub gene
RNF128	Downregulated	−3.76	<0.001	Immune regulation, ubiquitination	Peripheral gene
NPY1R	Downregulated	−2.66	<0.001	Neuroactive ligand–receptor interaction	Peripheral gene
GAD1	Downregulated	−2.60	<0.001	Neurotransmitter metabolism	Peripheral gene

while *MCM10* showed an 11.3-fold increase compared to controls. *GAPDH* expression remained stable.

Table 5. Quantitative real-time polymerase chain reaction expression levels of *MCM10*, *FOXQ1*, and *GAPDH*

Gene	Expression trend	Predicted ΔΔCt	Predicted fold change ($2^{-\Delta\Delta Ct}$)	Mean ± SEM (fold change)
MCM10	Upregulated	−3.5	~11.3×	11.3 ± 1.2
FOXQ1	Strongly upregulated	−5.5	~45.3×	45.3 ± 3.8
GAPDH	Stable (Reference)	0	1×	1.0 ± 0.05

Abbreviation: SEM: Standard error of the mean.

Table 5 summarizes qRT-PCR results showing the relative expression levels of *MCM10* and *FOXQ1* in ovarian cancer samples, calculated using the ΔΔCt method with *GAPDH* as the reference gene. Both target genes exhibited significant upregulation, with *FOXQ1* showing the highest fold change (~45.3×) and *MCM10* demonstrating marked overexpression (~11.3×). In contrast, GAPDH expression remained stable, confirming its suitability as an internal control (Figure 4).

4. Discussion

This study integrates transcriptomic profiling, pathway enrichment, PPI analysis, and RT-qPCR validation using FFPE patient tissues to identify key molecular drivers of ovarian cancer. Through stepwise refinement from genome-wide differential expression to experimentally validated targets, *FOXQ1* and *MCM10* emerged as central genes linking dysregulated cell cycle control, tumor aggressiveness, and clinical relevance.

At the molecular level, the overexpression of *FOXQ1* and *MCM10* reflects two complementary oncogenic processes: transcriptional reprogramming and aberrant DNA replication. *FOXQ1*, a member of the forkhead box transcription factor family, has been widely implicated in EMT, a process essential for tumor invasion, metastasis, and therapeutic resistance.[16] Elevated *FOXQ1* expression has been reported in aggressive ovarian cancer subtypes and is associated with enhanced migratory capacity and poor clinical outcome.[17]

In contrast, *MCM10* plays a critical role in DNA replication initiation and replication fork stability. Overexpression of *MCM10* promotes uncontrolled cell proliferation and tolerance to replication stress, a hallmark of rapidly dividing cancer cells.[18] Recent studies have shown that increased *MCM10* expression correlates with high proliferative index and unfavorable prognosis in ovarian and other gynecological malignancies.[5,6]

Importantly, the oncogenic functions of *FOXQ1* and *MCM10* are mechanistically consistent with the reported involvement of mitotic kinesin (KIF) family proteins in ovarian cancer (Figure 5). Mitotic kinesins such as *KIF11, KIF14, KIF17,* and *KIF18A* regulate spindle assembly, chromosome segregation, and mitotic checkpoint fidelity, and their dysregulation has been linked to chromosomal instability and poor survival in ovarian cancer.[19,20] Enhanced replication stress driven by *MCM10* overexpression may increase cellular dependency on accurate mitotic machinery, including kinesins, to ensure successful chromosome segregation. Concurrently, *FOXQ1*-driven EMT has been associated with increased cell cycle plasticity and resistance to mitotic checkpoint-mediated apoptosis, a phenotype frequently observed in cancers with aberrant kinesin activity.[19]

Pathway enrichment and network analyses further support this integrative model (Figure 3). Upregulated pathways were predominantly associated with cell cycle regulation, DNA replication, and p53 signaling, whereas downregulated pathways were associated with immune regulation, differentiation, and extracellular matrix organization. Within the PPI network, *FOXQ1* and *MCM10* functioned as hub genes, while *CTCFL* (*BORIS*) emerged as a connector node. Previous studies have implicated *CTCFL* in oncogenic transcriptional regulation and epigenetic reprogramming, processes that contribute to tumor progression and cellular plasticity.[21,22]

Figure 5 indicates that *FOXQ1*, a transcription factor, contributes to transcriptional reprogramming by promoting EMT, thereby enhancing tumor invasiveness, metastatic potential, and resistance to apoptosis. *MCM10*, a critical regulator of DNA replication initiation and fork stability, drives replication stress and accelerates cell cycle progression, particularly during the S phase. The combined dysregulation of *FOXQ1* and *MCM10* disrupts cell cycle control and p53-mediated pathways, leading to aberrant mitosis and genomic instability. This state is further supported by the coordinated activation of mitotic kinesins (*KIF11, KIF14, KIF17*, and *KIF18A*), which facilitate spindle assembly and chromosome segregation but, when overexpressed, contribute to mitotic errors. Additionally, altered expression of genes involved in tumor suppression and immune regulation (*CALB2, VGLL3, RNF128*, and *SYT4*) is associated with reduced

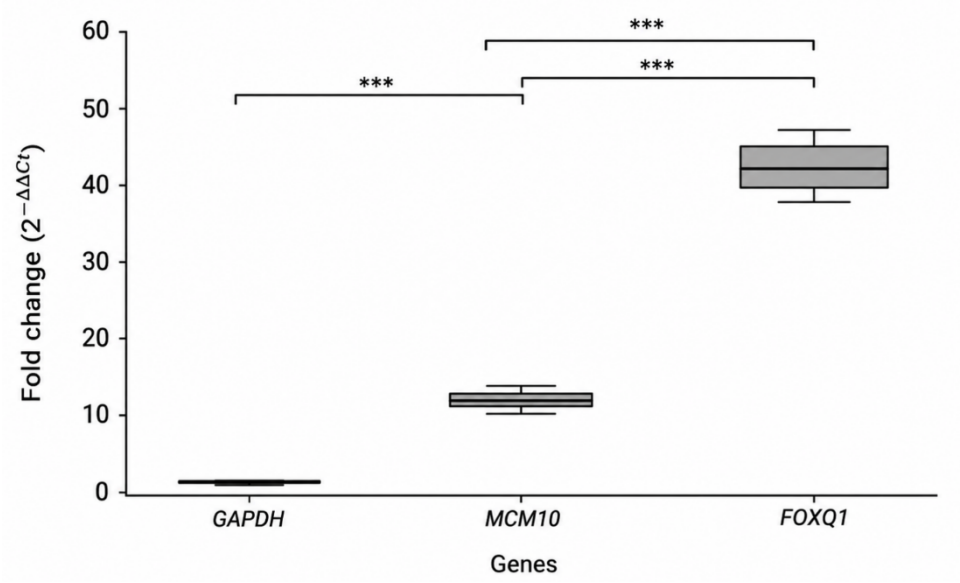


Figure 4. Relative expression levels of *MCM10* and *FOXQ1* determined by quantitative real-time polymerase chain reaction analysis using the $2^{-\Delta\Delta Ct}$ method. Expression levels are presented as fold changes relative to the reference gene *GAPDH*. ***$p < 0.001$.

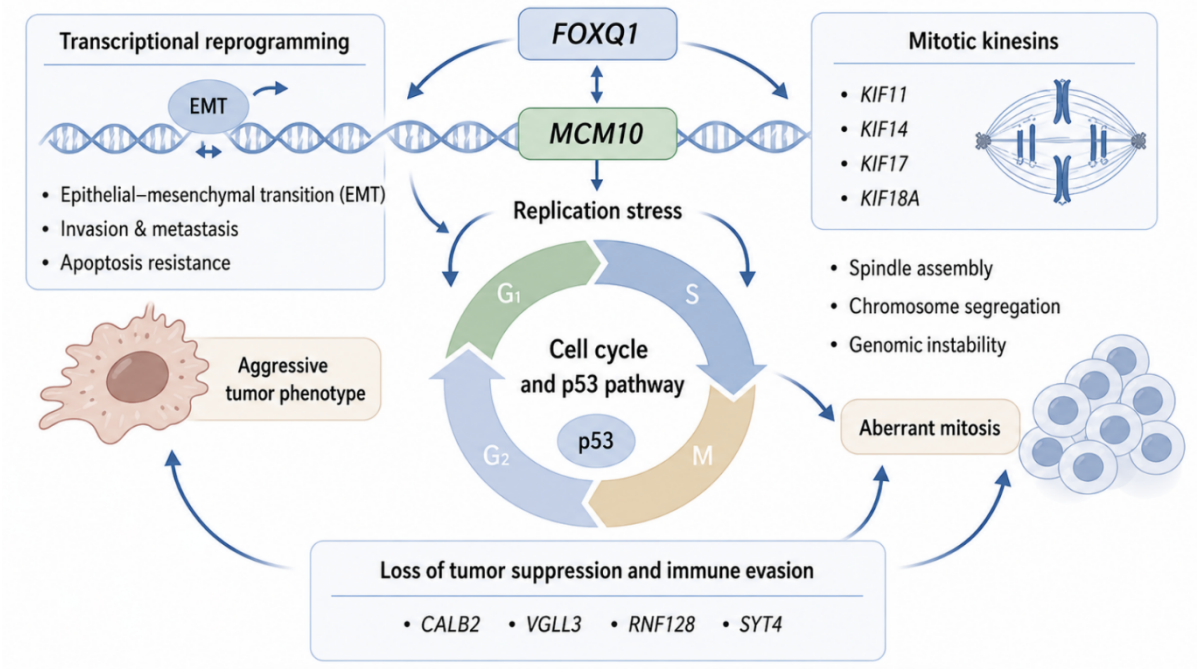


Figure 5. Proposed mechanism of *FOXQ1* and *MCM10* in ovarian cancer progression. Overexpression of *FOXQ1* may promote transcriptional reprogramming, epithelial–mesenchymal transition, invasion and metastasis, and resistance to apoptosis. Increased *MCM10* expression may induce replication stress, cell cycle dysregulation, and aberrant mitosis. Dysregulation of mitotic kinesin genes (*KIF11*, *KIF14*, *KIF17*, and *KIF18A*) and reduced expression of tumor suppressor- and immune-related genes (*CALB2*, *VGLL3*, *RNF128*, and *SYT4*) may further contribute to ovarian cancer progression.

cellular differentiation and immune evasion. Collectively, these molecular events converge to promote an aggressive ovarian cancer phenotype, underscoring the clinical relevance of *FOXQ1* and *MCM10* as key regulatory genes and potential biomarkers.

Clinically, RT-qPCR validation of *FOXQ1* and *MCM10* expression in FFPE tissues enhances the translational relevance of these findings. *FOXQ1* may serve as a biomarker

of invasive or chemoresistant disease, whereas *MCM10* reflects proliferative capacity and genomic instability. When considered alongside dysregulation of mitotic kinesins, these genes define a convergent oncogenic axis integrating transcriptional reprogramming, replication stress, and mitotic control. This integrated framework may inform patient stratification and support the rationale for therapeutic strategies targeting replication stress or mitotic machinery in selected ovarian cancer subgroups.

5. Conclusion

In this study, a combined transcriptomic and quantitative PCR analysis was employed to identify genes implicated in chemoresistance in ovarian cancer. Through this integrative approach, *MCM10* and *FOXQ1* were consistently overexpressed, highlighting their involvement in cell proliferation and EMT. The alignment between bioinformatics predictions and experimental results underscores their promise as molecular biomarkers and potential targets for therapy. These findings enhance our understanding of the genetic basis of drug resistance in ovarian carcinoma and may support the development of more precise, individualized treatment strategies to improve clinical outcomes.

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Conflict of interest

There is no conflict of interest in this research.

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Ethics approval and consent to participate

All procedures involving human FFPE tissue samples were reviewed and approved by the Ethics Committee of the Faculty of Medicine, Universitas Indonesia, which authorized the use of archival human tissue specimens for research purposes in accordance with institutional ethical and biobank regulations (Ethical approval number: KET-521/UN2.F1/ETIK/PPM.00.02/2025). All FFPE tissue samples used in this study were retrospective archival specimens that had been fully anonymized and de-identified prior to analysis. Due to the retrospective nature of the study and the use of anonymized samples, the Ethics Committee of the Faculty of Medicine, Universitas Indonesia, waived the requirement for written informed consent.

Consent for publication

Due to the retrospective nature of the study and the use of anonymized archival samples, the requirement for written informed consent and consent for publication was waived by the Ethics Committee of the Faculty of Medicine, Universitas Indonesia.

Availability of data

All data generated or analyzed during this study are included in this published article. Additional supporting data are available from the corresponding author upon reasonable request.

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