

Original Article

Decoding the DSCC1 gene as a pan-cancer biomarker in human cancers via comprehensive multi-omics analyses

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Abstract: Objectives: While dysregulation of DSCC1 (DNA Replication And Sister Chromatid Cohesion 1) has been established in breast cancer and colorectal cancer, its associations with other tumors remain unclear. Therefore, this study was launched to explore the role of DSCC1 in pan-cancer. Methodology: In this study, we investigate the biological functions of DSCC1 across 33 solid tumors, elucidating its role in promoting oncogenesis and progression in various cancers through comprehensive analysis of multi-omics data. Results: We conducted a comprehensive analysis of DSCC1 expression using RNA-seq data from TCGA and GTEx databases across 30 cancer types. Striking variations were observed, with significant overexpression of DSCC1 identified in numerous cancers. Elevated DSCC1 level was strongly associated with poorer prognosis, shorter survival, and advanced tumor stages in kidney renal papillary cell carcinoma (KIRP), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), as indicated by Kaplan-Meier curves and GEPIA2 analysis. Further investigation into the molecular mechanisms revealed reduced DNA methylation in the DSCC1 promoter region in KIRP, LIHC, and LUAD, supporting enhanced RNA transcription. Protein expression analysis via the Human Protein Atlas (HPA) corroborated mRNA expression findings, showcasing elevated DSCC1 protein in KIRP, LIHC, and LUAD tissues. Mutational analysis using cBioPortal revealed alterations in 0.4% of KIRP, 17% of LIHC, and 5% of LUAD samples, predominantly characterized by amplification. Immune cell infiltration analysis demonstrated robust positive correlations between DSCC1 expression and CD8+ T cells, CD4+ T cells, and B cells, influencing the tumor microenvironment. STRING and gene enrichment analyses unveiled DSCC1's involvement in critical pathways, emphasizing its multifaceted impact. Notably, drug sensitivity analysis highlighted a significant correlation between DSCC1 mRNA expression and responses to 78 anticancer treatments, suggesting its potential as a predictive biomarker and therapeutic target for KIRP, LIHC, and LUAD. Finally, immunohistochemistry staining of clinical samples validated computational results, confirming elevated DSCC1 protein

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expression. Conclusion: Overall, this study provides comprehensive insights into the pivotal role of DSCC1 in KIRP, LIHC, and LUAD initiation, progression, and therapeutic responsiveness, laying the foundation for further investigations and personalized treatment strategies.

Keywords: DSCC1, cancer, prognosis, treatment

Introduction

Cancer stands as a predominant contributor to global mortality, exerting a substantial impact on human life expectancy [1-5]. Characterized by intricate genomic aberrations, cancers encompass a spectrum of molecular anomalies, ranging from somatic mutations and copy number alterations to alterations in transcriptional expression and epigenetic modifications [6]. In this regard, The Cancer Genome Atlas (TCGA) platform was established to delineate the molecular events within cancers. This extensive database compiles genome sequencing data from over 11,000 samples across 33 diverse cancer types. It serves as a valuable resource, empowering users to conduct in-depth investigations into the molecular aberrations associated with human cancers through the application of genomic technologies [7]. Genetic pan-cancer analysis offers a comprehensive and multifaceted perspective, shedding light on the overarching mechanisms driving genomic alterations in various cancers.

DSCC1 (DNA Replication And Sister Chromatid Cohesion 1), alternatively referred to as DCC1, serves as a constituent of the selective replication factor C complex (RFC). This complex is actively involved in the S phase of the cell cycle. In eukaryotes, RFC forms a complex comprising 1-5 subunits, including a substantial subunit, Rfc1, along with four smaller subunits, namely Rfc2 to Rfc5. Previous investigations have indicated that RFC plays a crucial role in loading proliferating cell nuclear antigen (PCNA) onto fully formed duplex DNA and subsequently unloading PCNA from DNA structures [8-10]. The alignment marker for the chromosome transmission fidelity protein 18 (Ctf18) is RFC1 [11, 12]. Sister chromatid cohesion necessitates the use of the RFC complex, wherein the RFC1 subunit is replaced to form the isoheptamer Ctf18-RFC complex [13]. This loader complex, Ctf18-RFC, encompasses Ctf18-DSCC1-Ctf8 modules, featuring unique DSCC1 and CTF8 binding in the absence of RFC subunits [14]. The Ctf18-RFC complex, directed

toward proliferating cell nuclear antigen (PCNA), plays a pivotal role in activating sister chromatid cohesion and contributing to replication stress checkpoints. A previous investigation demonstrated that Ctf18-RFC and double-stranded DNA both interact with the same winglike helix domain on DSCC1 [15]. Furthermore, studies indicated that DSCC1 harbors mitotic genes, implying a direct involvement in the cell cycle [16]. These findings strongly suggest a crucial role for DSCC1 in DNA replication, prompting consideration of its potential impact on tumor proliferation. Notably, DSCC1 exhibited high expression in tumor tissues and promoted cell proliferation in breast cancer, colorectal cancer, and hepatocellular carcinoma [11, 17, 18]. However, the precise role of DSCC1 in other cancers remains unclear.

In this investigation, we sought pertinent data from online databases and conducted molecular experiments to assess the diagnostic and prognostic significance of aberrant DSCC1 expression in a pan-cancer analysis.

Methodology

DSCC1 expression in pan-cancer view

The UALCAN database, an open standards-based platform, encompasses RNA-seq and clinical information from patients across 31 cancer types, allowing for a comprehensive analysis of gene expression differences between tumor and paired normal tissues [19]. In this study, we acquired pan-cancer observations of DSCC1 expression in tumor versus normal tissues using the "TCGA" module.

We acquired DSCC1 gene expression profiles from pan-cancer tissues and normal tissues, encompassing a total of 15,776 samples sourced from the UCSC XENA database. The normalized RNA sequencing data, provided in transcripts per million (TPM) format, underwent processing using the Toil algorithm [15]. Subsequently, the TPM format was log₂-transformed for expression analysis ($\log_2^{\text{TPM}+1}$).

GEPIA2 analysis

In this study, we employed the “Survival Plot” module within GEPIA2 to assess the association between DSCC1 expression and the prognosis (Overall survival, OS) of different cancers [20]. Samples were categorized into high and low expression groups based on the median of expression values. Additionally, the “Stage Plot” module was utilized to examine the variation in DSCC1 expression across different stages. Expression data from the violin plot were transformed using $(\log_2^{\text{TPM}+1})$ [21].

The Human Protein Atlas database analysis

The Human Protein Atlas (HPA) database [22, 23] was utilized to investigate the protein expression levels of DSCC1 in both cancerous and normal control human tissues.

OncoDB database analysis

OncoDB is a pivotal database for investigating promoter methylation patterns in cancer [24]. It offers insights into the epigenetic modifications occurring in cancer genomes, particularly focusing on methylation alterations in the promoter regions of genes. By providing data on the methylation status of specific genes across diverse cancer types, OncoDB aids researchers in unraveling the regulatory mechanisms influenced by DNA methylation, ultimately contributing to the identification of potential biomarkers and therapeutic targets for cancer treatment. In our study, this database was used to analyze the promoter methylation level of DSCC1 across different cancers.

Mutational analysis of DSCC1

cBioPortal stands out as a robust and user-friendly platform extensively employed for investigating genetic alterations in diverse cancers [25]. Within our study, we leveraged the capabilities of cBioPortal to perform a comprehensive mutational analysis of the DSCC1 gene across designated cancer types.

STRING and gene enrichment analyses

STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) is a comprehensive database that facilitates the exploration of protein-protein interactions [26, 27]. It integrates diverse interaction sources, including

experimental data and computational predictions, offering a holistic view of the interactome landscape. In the present study, STRING database was used to construct the protein-protein (PPI) interaction network of the DSCC1-interacting proteins.

DAVID (Database for Annotation, Visualization, and Integrated Discovery) is a bioinformatics resource that aids researchers in comprehending the functional significance of gene lists [28, 29]. By offering tools for functional annotation, gene set enrichment analysis, and visualization, DAVID streamlines the interpretation of large-scale genomic data, enhancing insights into biological pathways and processes. In our study, the DAVID tool was used to conduct gene enrichment analysis of DSCC1 interacting proteins.

TIMER2 database analysis

TIMER2 (Tumor Immune Estimation Resource) is an online tool that facilitates the exploration of immune cell infiltration across diverse cancer types [19]. Utilizing transcriptomic data from TCGA, TIMER2 enables researchers to evaluate the abundance of immune cells within tumor tissues, contributing valuable insights into the tumor microenvironment and its impact on cancer progression. In our study, TIMER2 database was employed to explore correlations between DSCC1 expression and infiltration level of different immune cells.

Drug sensitivity analysis

The GSCA database is pivotal for drug sensitivity analysis, offering a curated collection of synthetic control arms for clinical trials. Researchers leverage its wealth of data to assess and compare drug responses across diverse populations. In the present study, the GSCA database was used to conduct drug sensitivity analysis of the DSCC1 gene.

Immunohistochemistry staining

Following ethical approval from the relevant department, we acquired a total of 2 KIRP tissue samples, 2 LIHC tissue samples, and 2 LUAD tissue samples, each matched with their respective normal control tissue samples from Nishter Hospital in Multan, Pakistan. Protein extraction was performed utilizing the urea

method, as referenced [30]. The freshly resected tumor and adjacent noncancerous tissue samples were promptly fixed in 10% formalin, embedded in paraffin, and sectioned into 3-4- μ m slices. These sections were placed on glass slides, baked at 60°C for 2 hours, dewaxed with xylene, and subjected to an alcohol gradient for hydration. Blocking of endogenous peroxidase activity was carried out with 0.3% H₂O₂ for 20 minutes. Following antigen retrieval, the slides were incubated overnight with primary rabbit antihuman DSCC1 antibody (1:500, ab254752, Abcam) at 4°C, and then with secondary anti-horseradish peroxidase antibody at 37°C for 30 minutes. Tissue sections were stained with hematoxylin, visualized with 3,3'-diaminobenzidine (DAB), and, after dehydration and sealing, images were captured using light microscopy.

Statistics

R software (version 3.6.3) was employed for all additional analyses. Statistical significance was established with a *p*-value below 0.05. The Spearman test was utilized for correlation analysis between two variables.

Results

DSCC1 expression in pan-cancer

The analysis of DSCC1 expression in pan-cancers was carried out using RNA-seq data sourced from TCGA and GTEx databases. With the exception of cancers lacking normal tissue data, noticeable variations in DSCC1 expression were observed in 30 cancer types.

Notably, DSCC1 exhibited significant overexpression in cancers, including Adenoid cystic carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast cancer (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), cholangiocarcinoma (CHOL), colon adenocarcinoma (COAD), diffuse large B cell lymphoma (DLBC), esophageal carcinoma (ESCA), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), pediatric low-grade gliomas (LGG), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), ovarian serous cystadenocarcinoma (OV), pancreatic

adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), sarcoma (SARC), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thymoma (THYM), Uterine corpus endometrial carcinoma (UCEC), and uterine carcinosarcoma (UCS) (**Figure 1A, 1B**). Conversely, lower DSCC1 expressions were noted in tumor tissues relative to control counterparts in cancers, including kidney chromophobe (KICH), acute myeloid leukemia (LAML), pheochromocytoma and paraganglioma (PCPG), and thyroid cancer (THCA) (**Figure 1A, 1B**).

Higher DSCC1 expression correlates with the prognosis of cancer patients

To further investigate the impact of elevated DSCC1 levels on the prognosis of cancer patients, we employed the KM plotter tool to generate Kaplan-Meier curves, exploring the correlation between DSCC1 expression and overall survival (OS) across 33 cancer types. As depicted in **Figure 2A, 2B**, increased DSCC1 expression exhibited a significant association with poorer prognosis in patients with KIRP, LIHC, and LUAD. This emphasizes the substantial correlation between DSCC1 overexpression and the onset and metastasis of KIRP, LIHC, and LUAD.

DSCC1 expression across KIRP, LIHC, and LUAD patients of different tumor stages

The GEPIA2 database was utilized to examine the correlation between DSCC1 mRNA expression levels and distinct tumor stages in KIRP, LIHC, and LUAD. The findings revealed a significant up-regulation of DSCC1 in advanced stages (stage 1, stage 2, and stage 3) of KIRP, LIHC, and LUAD when compared to the early stage (stage 1), as illustrated in **Figure 3A**.

DNA methylation analysis

Elevated RNA transcription can be attributed to reduced levels of DNA methylation. Hence, we examined the methylation status of the DSCC1 promoter in KIRP, LIHC, LUAD, and normal tissues using the OncoDB database. The analysis results demonstrated that the DSCC1 promoter methylation in KIRP, LIHC, and LUAD was significantly lower compared to the corresponding normal tissues (Wilcoxon test, *P* < 0.05), as depicted in **Figure 3B**.

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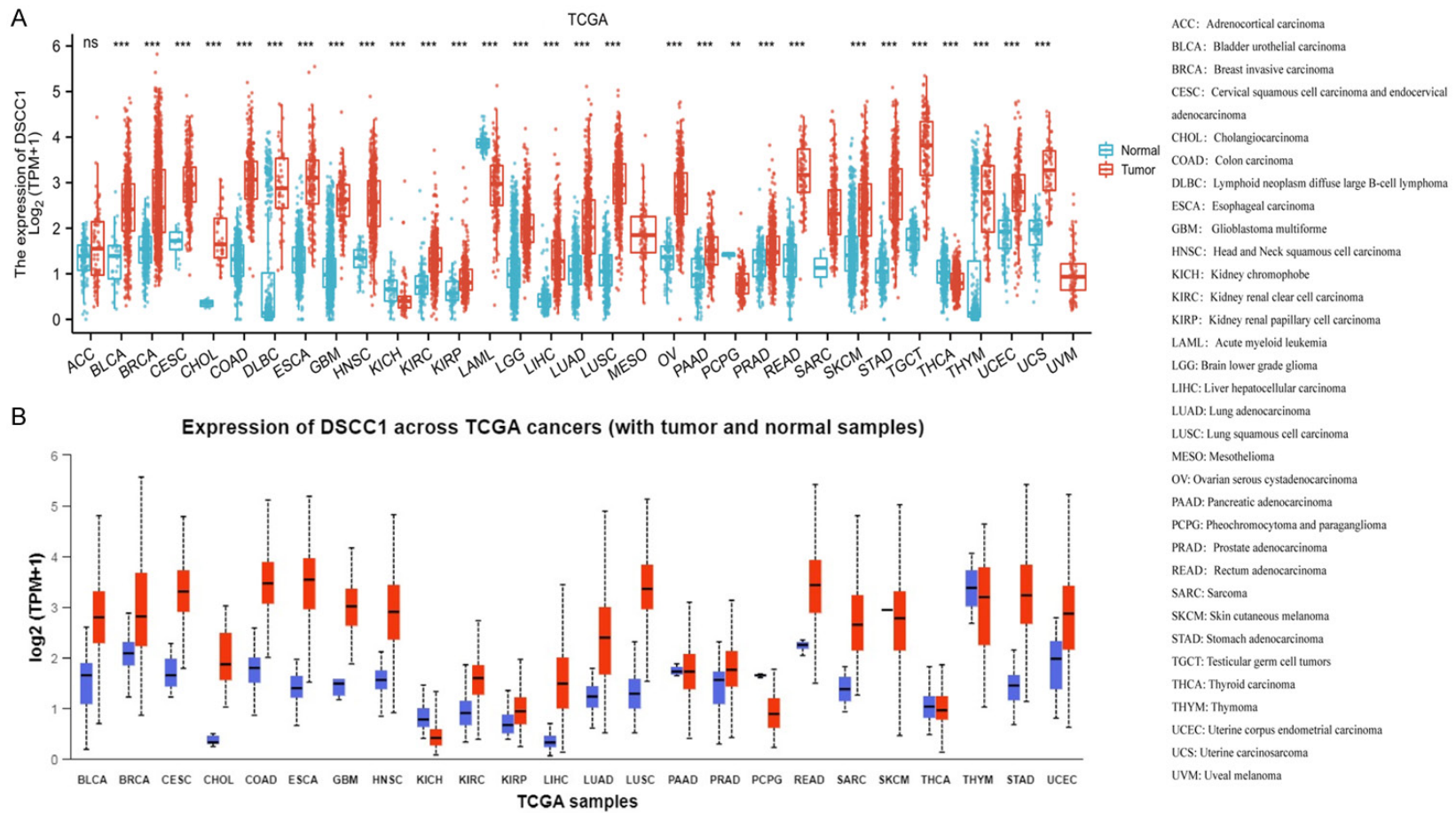


Figure 1. DSCC1 expression across different tumor samples and normal control tissues. A. DSCC1 expression across different tumor samples and normal control tissues sourced from The Cancer Genome Atlas database. B. DSCC1 expression across different tumor samples and normal control tissues sourced from the UALCAN database. *P*-value < 0.05. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1.

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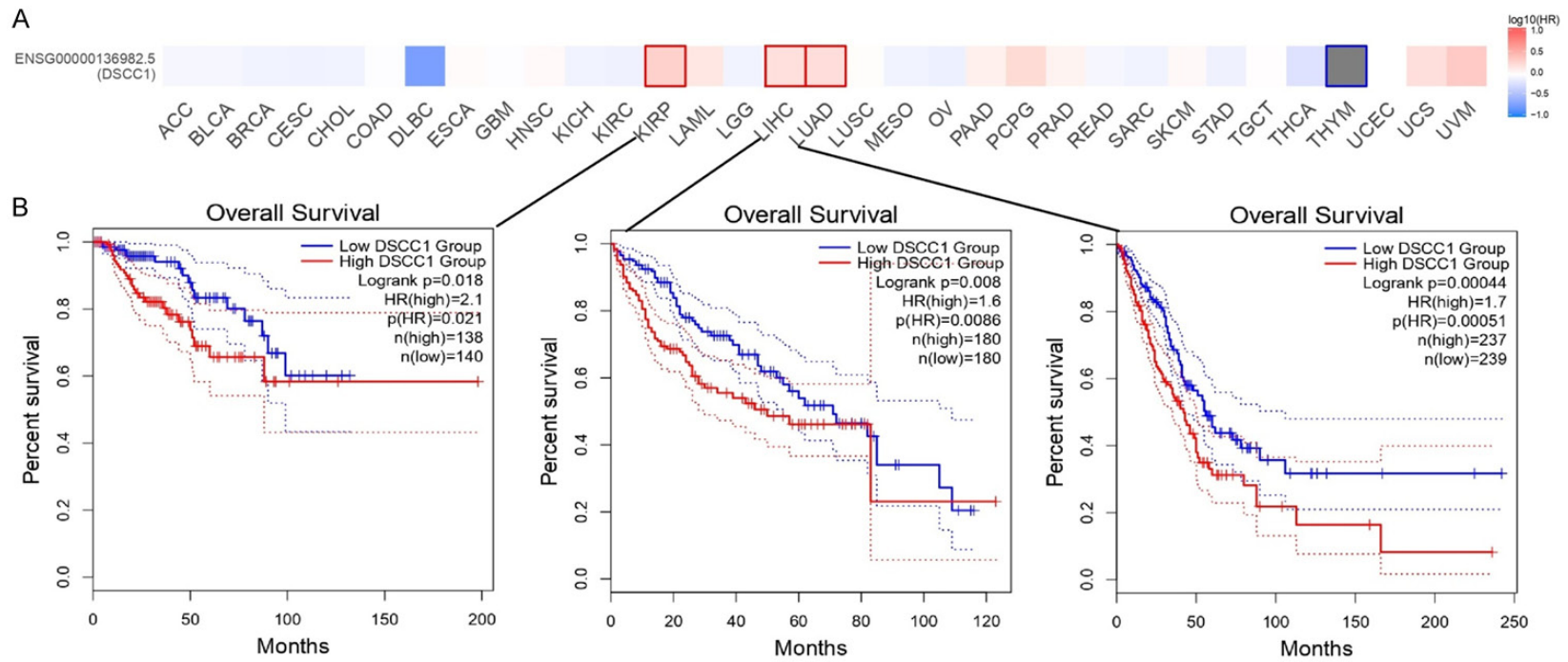


Figure 2. Prognostic value of DSCC1 in the pan-cancer. A. Survival map of DSCC1 across different cancer. B. KM curves of DSCC1 in KIRP, LIHC, and LUAD samples. P -value < 0.05. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1, KIRP = Kidney renal papillary cell carcinoma, LIHC = Liver hepatocellular carcinoma, LUAD = Lung adenocarcinoma.

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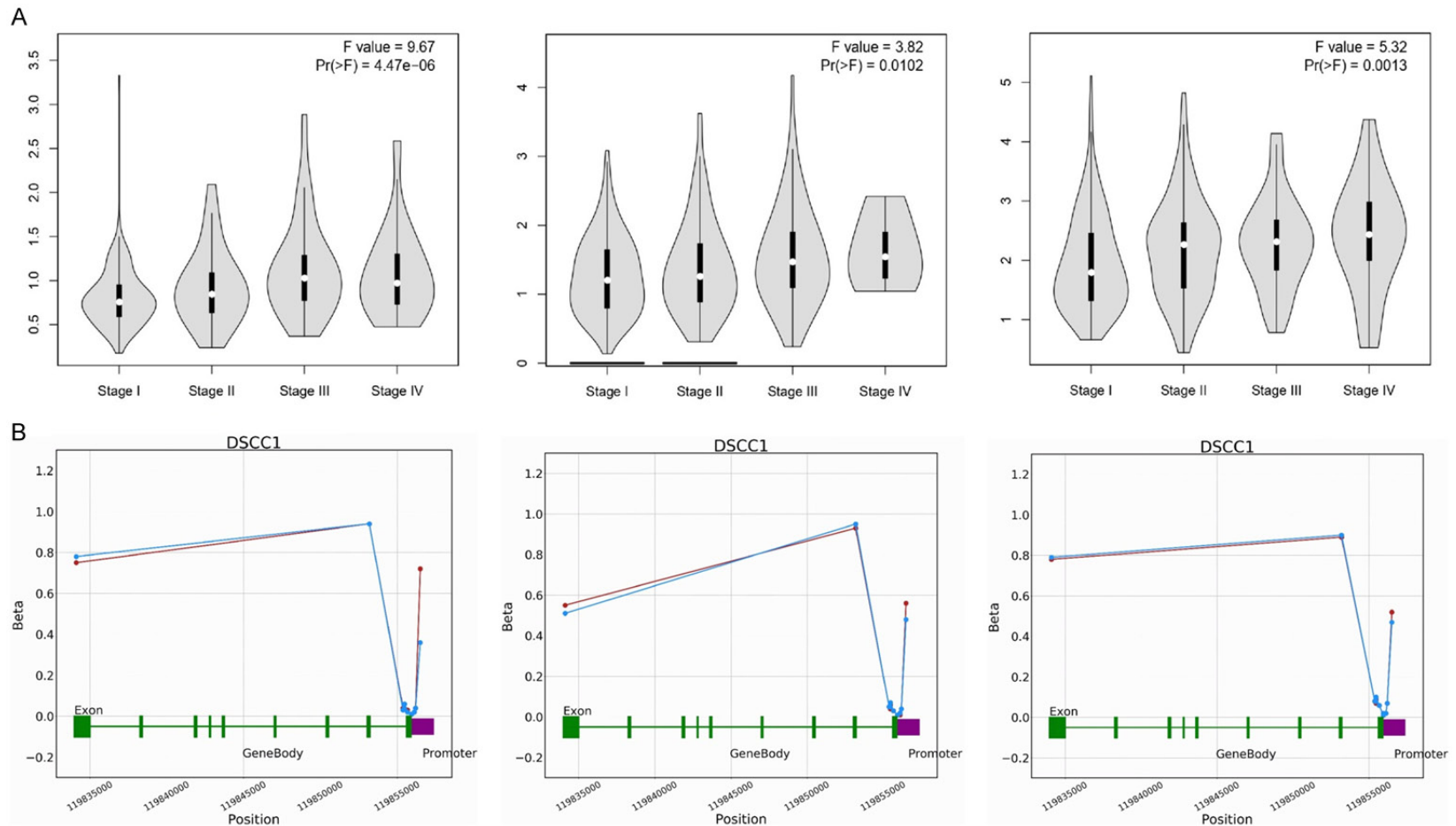


Figure 3. DSCC1 expression across different cancer stages and DNA methylation analysis. A. GEPIA-based DSCC1 expression across different stages of KIRP, LIHC, and LUAD. B. Promoter methylation analysis of DSCC1 across KIRP, LIHC, and LUAD via the OncoDB. P -value < 0.05. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1, KIRP = Kidney renal papillary cell carcinoma, LIHC = Liver hepatocellular carcinoma, LUAD = Lung adenocarcinoma.

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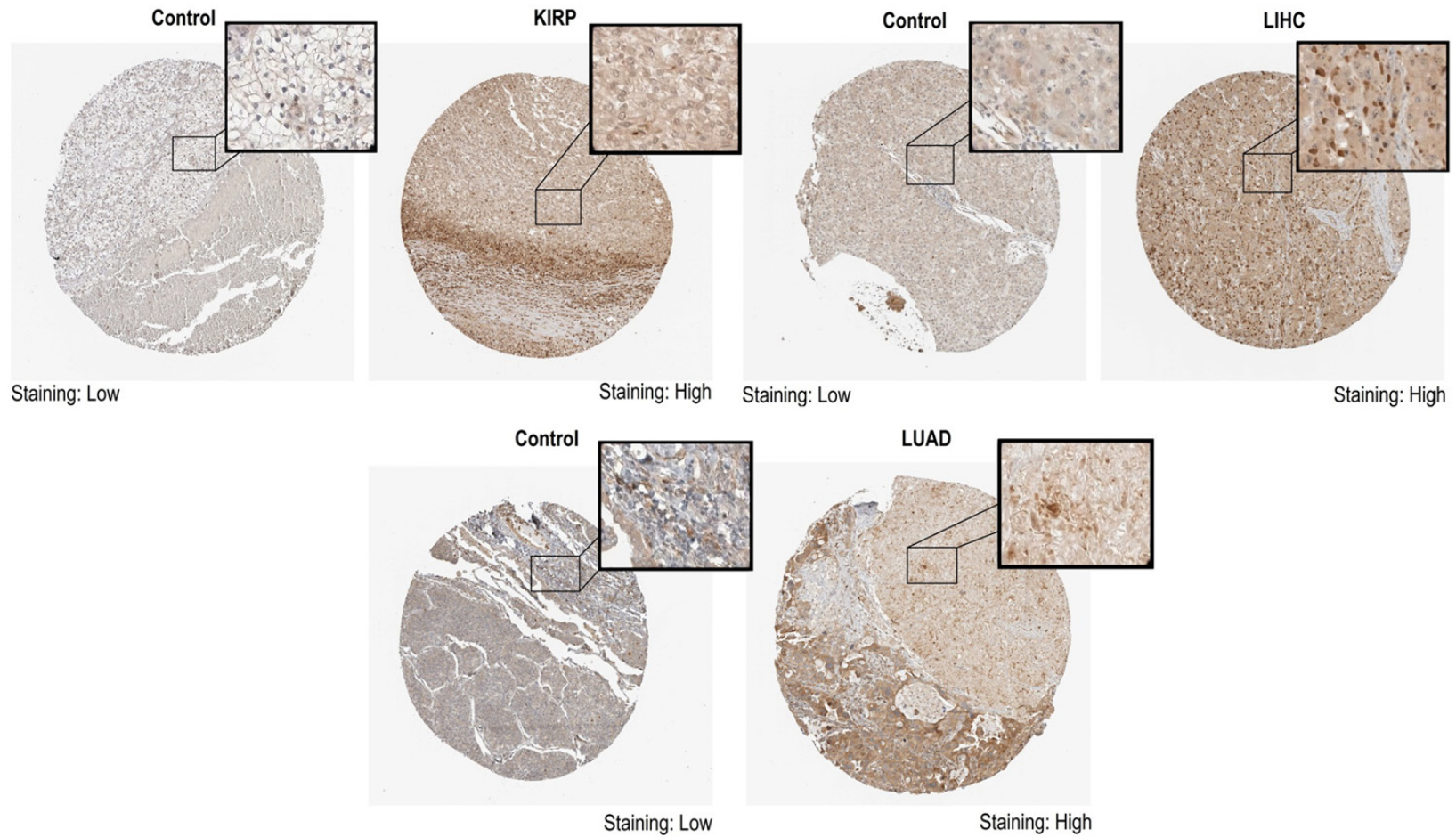


Figure 4. Human Protein Atlas-based immunohistochemical images of the DSCC1 across KIRP, LIHC, and LUAD tissue samples paired with normal control tissues samples. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1, KIRP = Kidney renal papillary cell carcinoma, LIHC = Liver hepatocellular carcinoma, LUAD = Lung adenocarcinoma.

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DSCC1 protein expression in KIRP, LIHC, and LUAD tissues via the Human Protein Atlas (HPA)

To investigate the protein expression levels of DSCC1 in KIRP, LIHC, LUAD, and their respective normal tissues, we assessed DSCC1 protein expression through the Human Protein Atlas (HPA) database. As illustrated in **Figure 4**, the tissue samples from KIRP, LIHC, and LUAD patients exhibited elevated expression (staining: high) compared to the normal control tissues, which displayed lower expression (staining: low).

Mutational analysis

Cancer onset and progression are intricately linked to genetic changes. To ascertain the mutational characteristics of DSCC1 in KIRP, LIHC, and LUAD, a comparative analysis of DSCC1 was conducted using cBioPortal. The findings revealed that DSCC1 underwent alterations in 0.4% of KIRP samples, 17% of LIHC samples, and 5% of LUAD samples, with amplification being the predominant type of change, as depicted in **Figure 5**.

Immune cell infiltration analysis

Subsequently, we investigated the associations between DSCC1 expression and the degree of immune cell infiltration, encompassing CD8+ T cells, CD4+ T cells, and B cells, utilizing the TIMER2 database. Our findings revealed robust positive correlations between DSCC1 expression and the presence of these immune cell types (CD8+ T cells, CD4+ T cells, and B cells) (**Figure 6**).

STRING and gene enrichment analyses

Utilizing the String database with a protein-protein interaction (PPI) enrichment significance of $P < 1.0E-16$, we established a network comprising 10 proteins that exhibited significant interactions with DSCC1. The graphical representation of the network indicated that ESCO1, RFC5, RFC3, RFC2, POLE, ESCO2, CHTF18, CHTF8, RFC4, and SMC3 were interconnected with DSCC1, as illustrated in **Figure 7A**. Furthermore, results of the gene enrichment analysis showed that DSCC1 interacting genes were strongly associated with “DNA replication factor c complex, Ctf18 RFC-like complex, Elg1 RFC-like

complex, and Nuclear cohesion complex” etc. CC terms (**Figure 7B**), “DNA clamp loader activity, Single-stranded DNA helicase activity, Mediator complex binding, and ATP-dependent activity, acting on DNA” etc. MF terms (**Figure 7C**), “Reg. of DNA-directed DNA polymerase activity, Error-prone translesion synthesis, and Nucleotide-excision repair, DNA gap filling” etc. BP terms (**Figure 7D**), and “Mismatch repair, DNA replication, Nucleotide excision repair, Cell cycle, and Oocyte meiosis signaling pathways (**Figure 7E**)”.

Drug sensitivity analysis

Exploration through the GSCA database unveiled a significant correlation between DSCC1 mRNA expression and the predicted response to 78 anticancer treatments. DSCC1 expression exhibited a positive association with drug sensitivity, including 17-AAG, Bleomycin, FTI-277, RDEA119, Trametinib, and Selumetinib (**Figure 8**). Conversely, an inverse relationship was observed between DSCC1 expression and sensitivity to 23 other drugs, including, AR-42, AT-7519, BMS345541, BX-912, CP466722, FK866, GSK1070916, GSK690693, I-BET-762, KIN001-102, Methotrexate, NPK76-II-72-1, Navitoclax, PHA-793887, PI-103, PIK-93, Phosphoinositide-dependent kinase-1, TG101348, THZ-2-102-1, TL-2-105, TPCA-1, Vorinostat, and WZ3105 (**Figure 8**). Based on these findings, DSCC1 emerges as a potential therapeutic target for treating KIRP, LIHC, and LUAD.

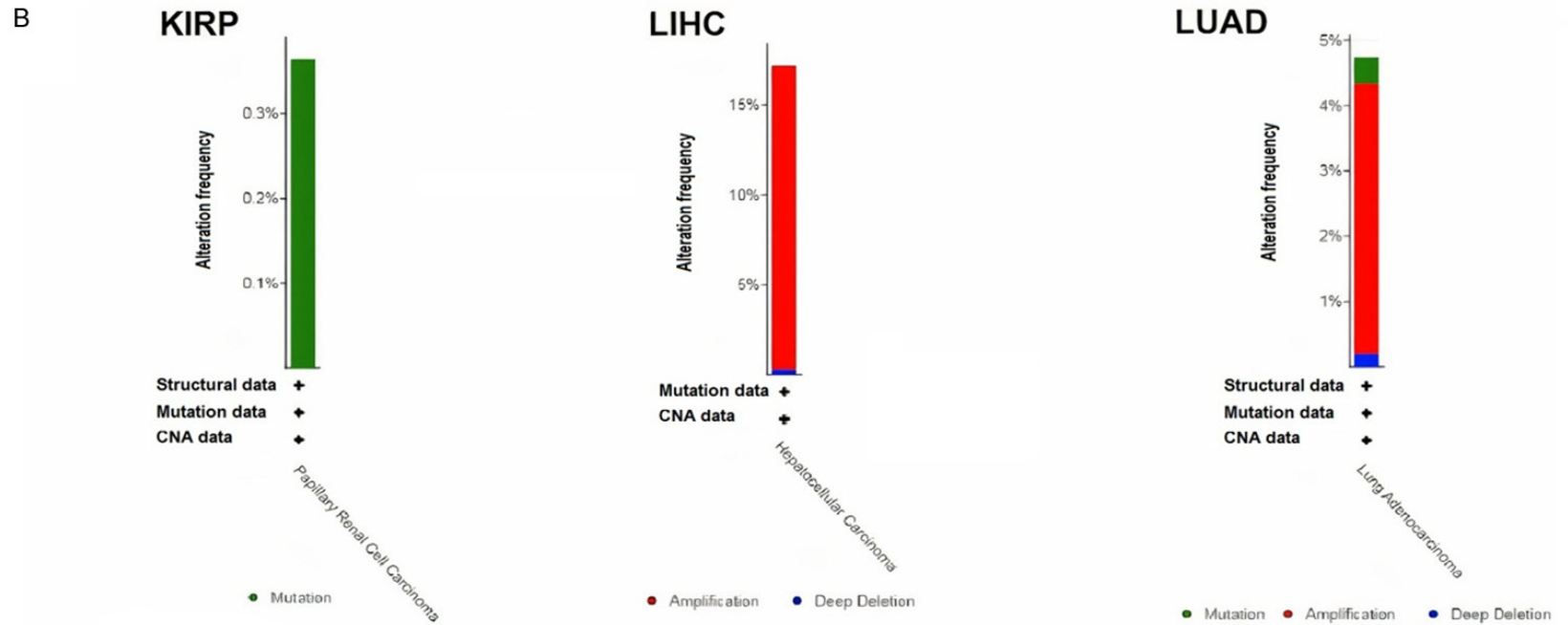
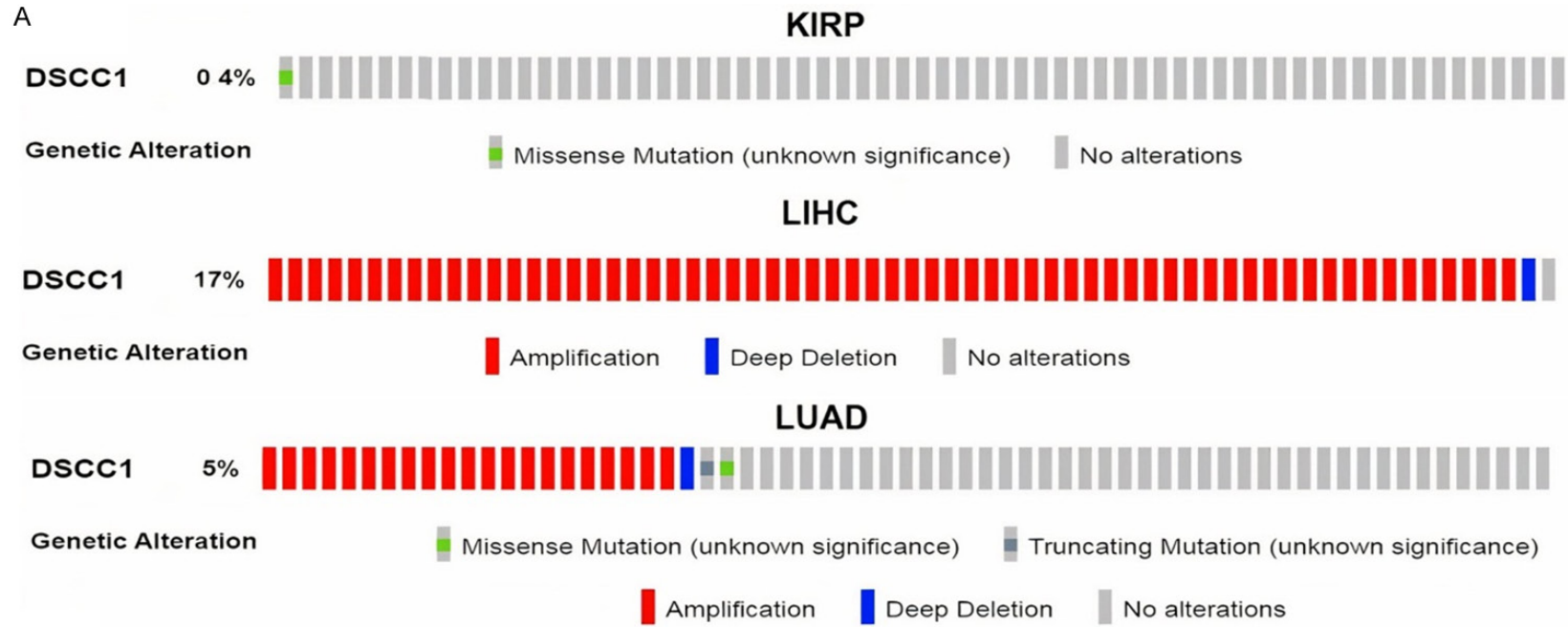
Immunohistochemistry staining

In this phase of our investigation, the computational expression results of DSCC1 were corroborated through immunohistochemistry (IHC) conducted on clinical tissue samples. Specifically, we analyzed 2 KIRP samples, 2 LIHC samples, and 2 LUAD samples, each paired with their corresponding normal control samples. The results depicted in **Figure 9** demonstrate elevated DSCC1 protein expression (Staining: high) in KIRP, LIHC, and LUAD samples compared to the corresponding normal tissues (Staining: low) (**Figure 9**).

Discussion

The role of DSCC1 in tumorigenesis and development has attracted increasing attention in recent years. The elevated expression of

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Figure 5. Genetic alteration analysis of DSCC1 across KIRP, LIHC, and LUAD samples via the cBioPortal database. A. Percentage of the KIRP, LIHC, and LUAD samples having mutations in DSCC1 gene. B. Summary of the genetic mutations observed in DSCC1 gene across KIRP, LIHC, and LUAD samples. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1, KIRP = Kidney renal papillary cell carcinoma, LIHC = Liver hepatocellular carcinoma, LUAD = Lung adenocarcinoma.

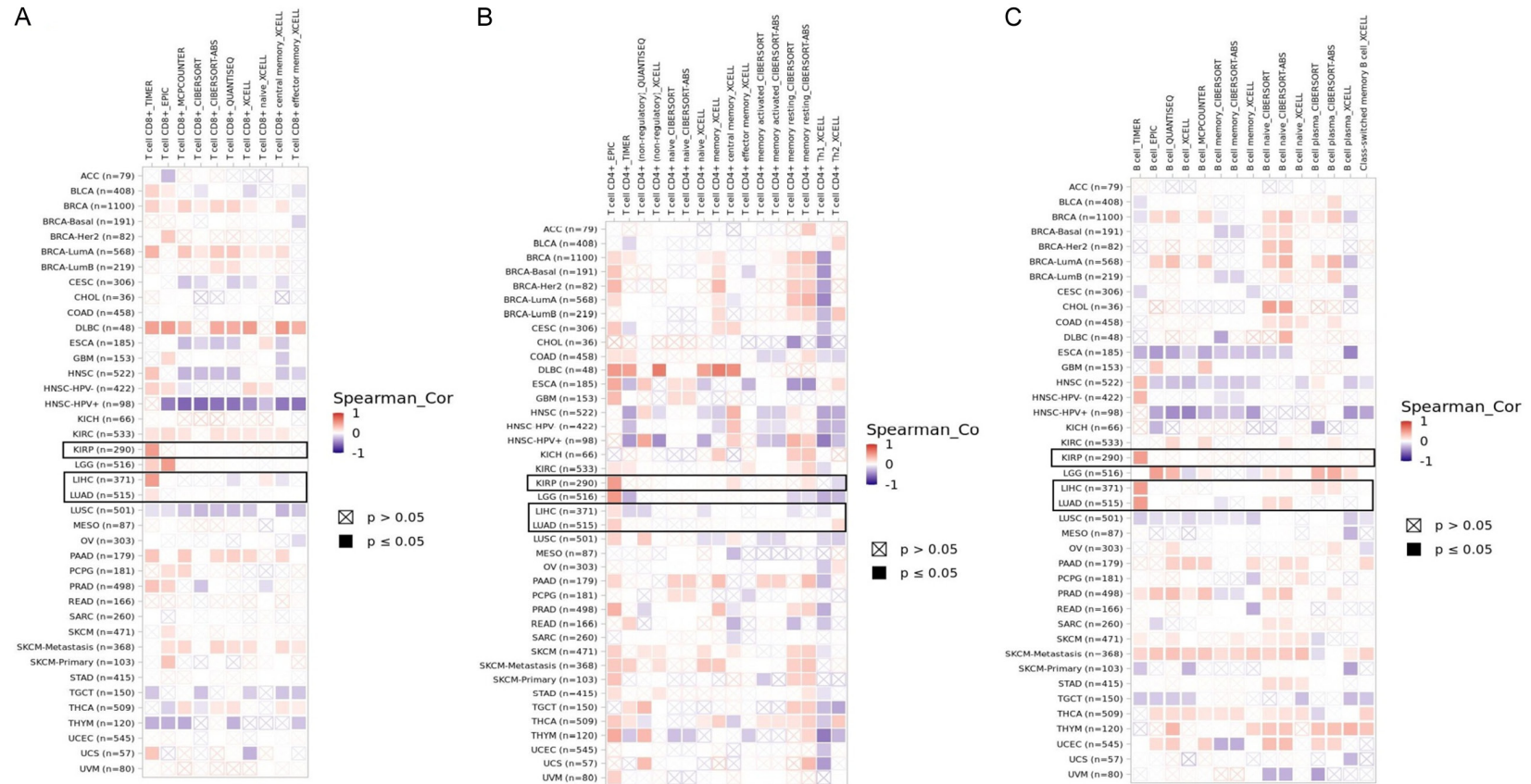


Figure 6. Correlation analysis of DSCC1 expression with infiltration levels of CD8+ T, CD4+ T, and B cells across KIRP, LIHC, and LUAD samples. A. Correlation analysis of DSCC1 expression with infiltration level of CD8+ T across KIRP, LIHC, and LUAD samples. B. Correlation analysis of DSCC1 expression with infiltration level of CD4+ T across KIRP, LIHC, and LUAD samples. C. Correlation analysis of DSCC1 expression with infiltration level of B cells across KIRP, LIHC, and LUAD samples. *P*-value < 0.05. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1, KIRP = Kidney renal papillary cell carcinoma, LIHC = Liver hepatocellular carcinoma, LUAD = Lung adenocarcinoma.

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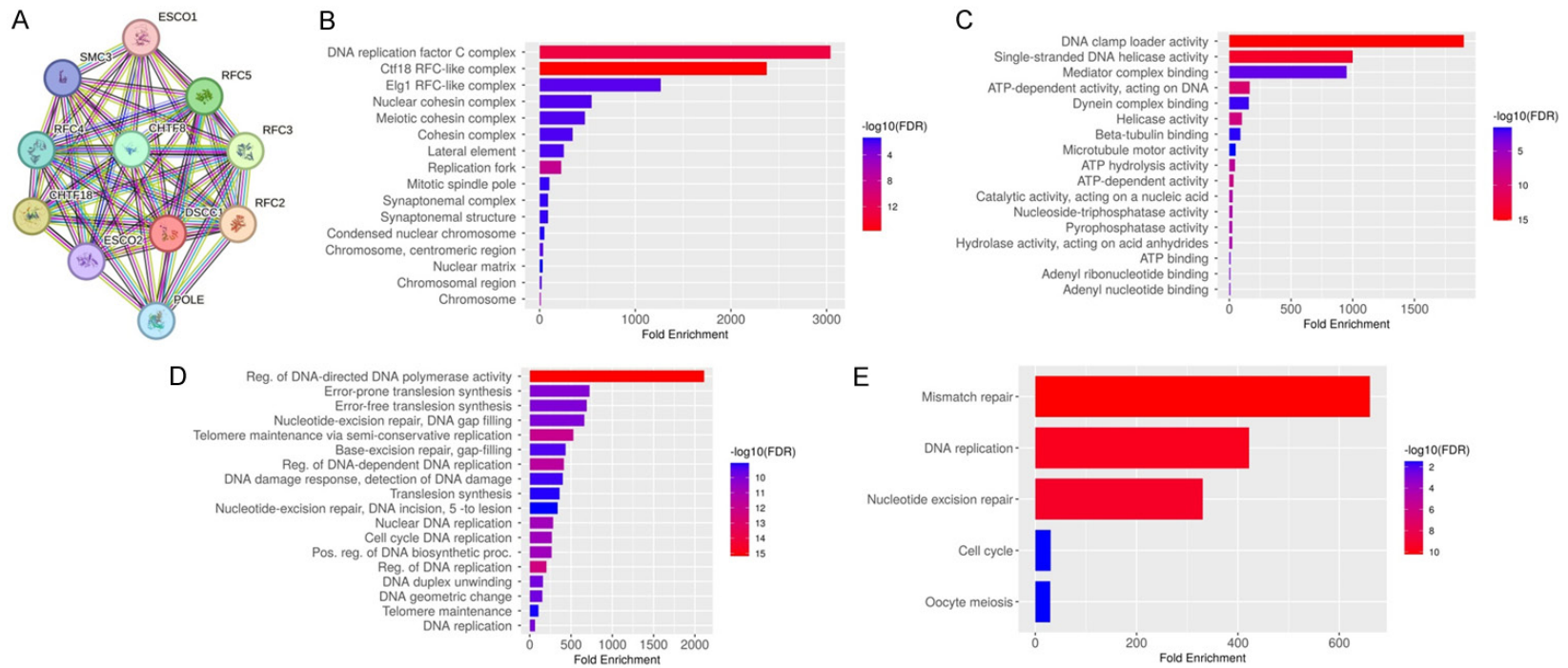


Figure 7. This figure showcases the protein-protein interaction network and gene enrichment analysis of DSCC1. (A) presents the protein-protein interaction network involving DSCC1 and its binding partners. (B-D) detail the cellular component (CC), molecular function (MF), and biological process (BP) terms, respectively, of DSCC1 and its binding partners. Additionally, (E) outlines the Kyoto Encyclopedia of Genes and Genomes (KEGG) terms associated with DSCC1 and its interacting proteins. Significance was determined at a p -value < 0.05 . DSCC1 = DNA Replication And Sister Chromatid Cohesion 1.

Pan-cancer analysis of DSCC1

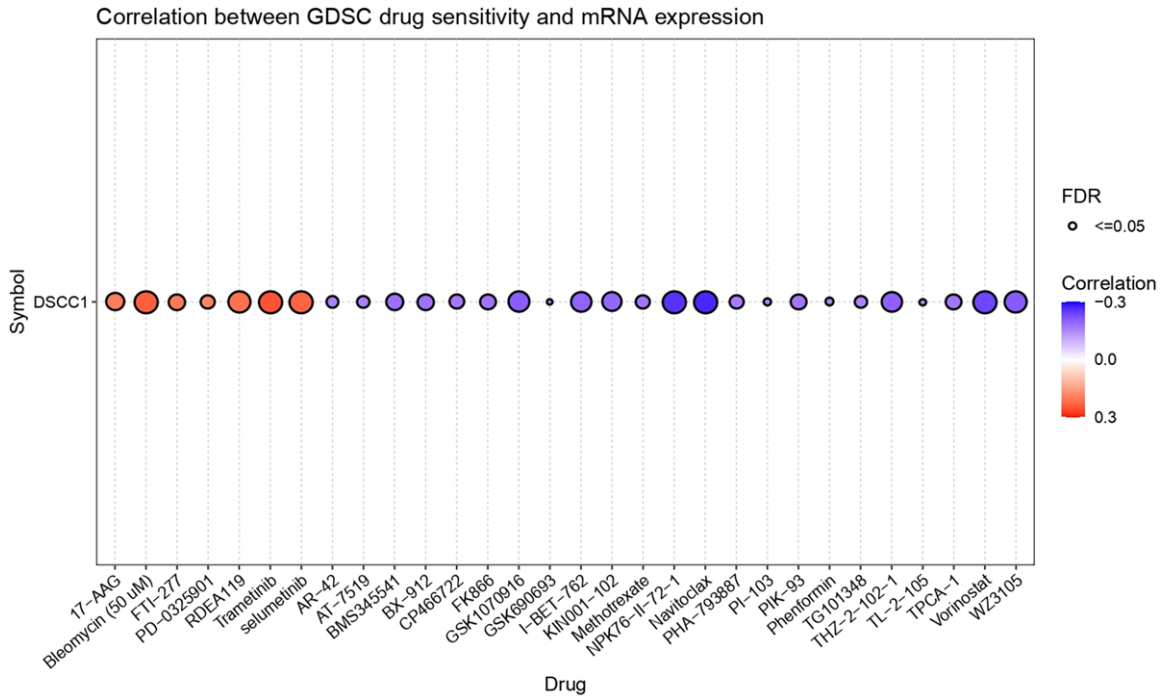


Figure 8. Drug sensitivity analysis outcomes of DSCC1 via GSCA database. P -value < 0.05. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1.

DSCC1 has been documented in colorectal cancer cells and hepatocellular carcinoma cells, as reported in previous studies [31, 32]. Additionally, DSCC1 exhibited heightened expression in breast cancer compared to non-tumor tissues, with experiments demonstrating its role in cell invasiveness [17]. In this pan-cancer study, the results showed that the expression of DSCC1 was higher in 26 types of tumor tissues than the paracancerous tissues. The high expression of DSCC1 was related to poor prognosis, pathological stage, and shorter survival time in KIRP, LIHC, and LUAD, thus supporting the theory that the higher expression of DSCC1 is closely related to the development of these three types of cancers.

The up regulation of DSCC1 in advanced stages of KIRP, LIHC, and LUAD, aligning with its reported association with adverse outcomes in breast cancer [17, 33]. Additionally, our DNA methylation analysis, in agreement with earlier studies, revealed significantly reduced DSCC1 promoter methylation in KIRP, LIHC, and LUAD compared to normal tissues, suggesting a mechanism for enhanced RNA transcription. Confirming these expression trends, the HPA database and immunohistochemistry analysis using clinical samples demonstrated elevated DSCC1

protein expression in KIRP, LIHC, and LUAD tissues, correlating with its reported role in breast and other cancers [31, 33, 34].

In tandem with genetic alterations being pivotal in cancer, our mutational analysis of DSCC1 in KIRP, LIHC, and LUAD, aligns with prior research on the gene's mutational landscape. Utilizing cBioPortal, we observed alterations in 0.4% of KIRP, 17% of LIHC, and 5% of LUAD samples, predominantly characterized by amplification. This resonates with earlier studies, emphasizing the role of genetic changes in the dysregulation of DSCC1, particularly in LIHC where alterations were prominently observed [35]. Our study contributes by delineating the mutation landscape in KIRP and LUAD.

Expanding our investigation to immune cell infiltration, we uncovered significant positive correlations between DSCC1 expression and the presence of immune cell types (CD8+ T cells, CD4+ T cells, and B cells) using the TIMER2 database. This aligns with prior findings linking increased DSCC1 expression to immune cell modulation, potentially influencing the tumor microenvironment and contributing to cancer progression [36-38]. Our results thus complement earlier studies, collectively emphasizing

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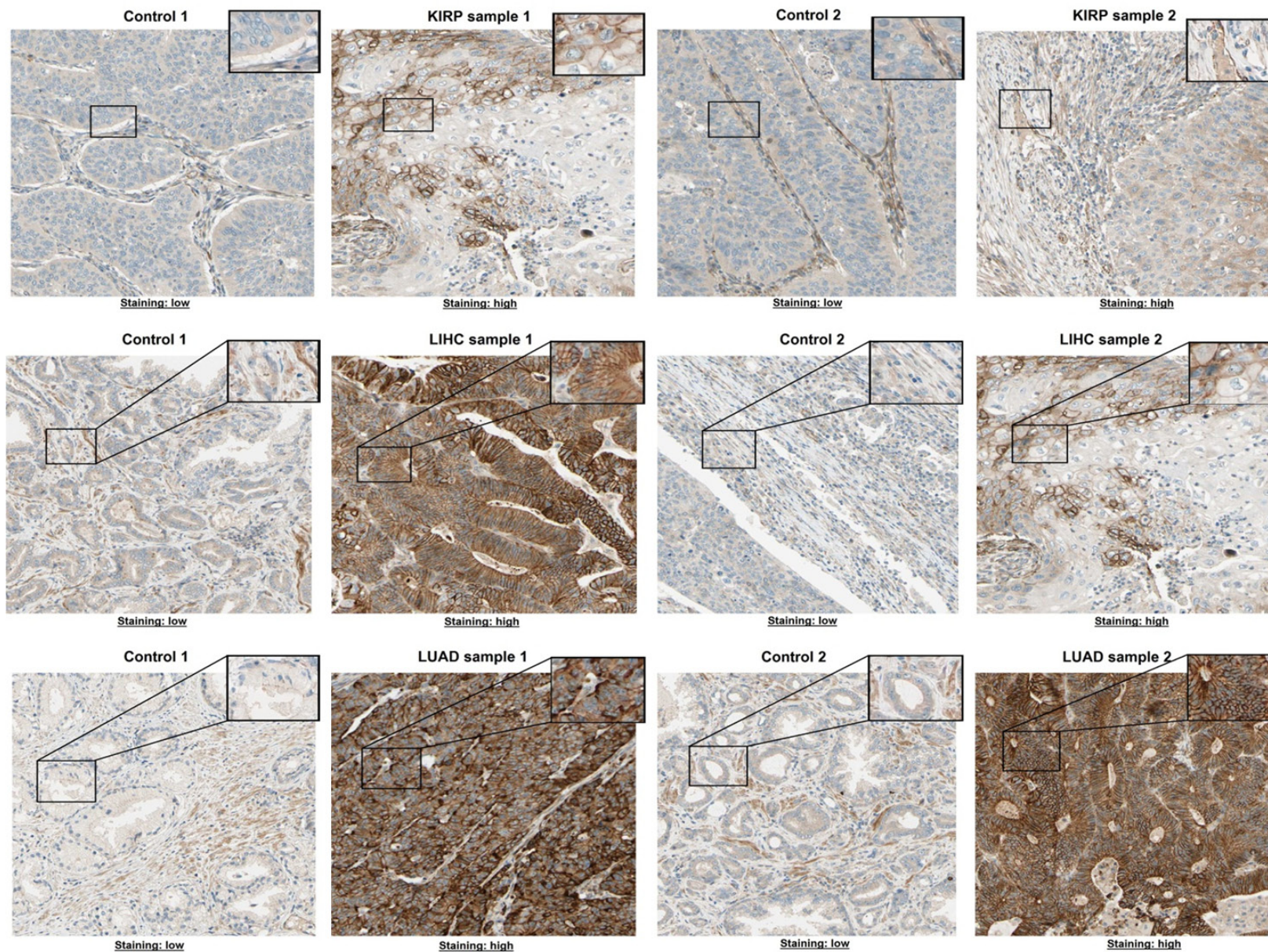


Figure 9. This figure displays immunohistochemical staining images depicting DSCC1 expression in KIRP, LIHC, LUAD (left) and normal (right) tissues. The protein levels of DSCC1 were significantly elevated in KIRP, LIHC, and LUAD tissues compared to the control tissues. DSCC1 = DNA Replication And Sister Chromatid Cohesion 1, KIRP = Kidney renal papillary cell carcinoma, LIHC = Liver hepatocellular carcinoma, LUAD = Lung adenocarcinoma.

the multifaceted impact of DSCC1 in shaping the tumor microenvironment.

This study further revealed that DSCC1 was involved in the dysregulation of various important pathways, including “Mismatch repair, DNA replication, Nucleotide excision repair, Cell cycle, and Oocyte meiosis signaling pathways (Figure 7E)”. The dysregulation of these pathways is already well studied across different cancers [39-41].

Lastly, the comprehensive analysis conducted via the GSCA database revealed a compelling correlation between DSCC1 mRNA expression and the predicted response to a diverse panel of 78 anticancer treatments. Notably, DSCC1 expression exhibited a positive association with drug sensitivity, indicating its potential as a predictive biomarker for favorable responses to specific agents such as 17-AAG, Bleomycin, FTI-277, RDEA119, Trametinib, and Selumetinib. Conversely, an inverse relationship was noted with sensitivity to 23 other drugs, including AR-42, AT-7519, BMS345541, and others. These findings are particularly significant in the context of therapeutic interventions for KIRP, LIHC, and LUAD. DSCC1's positive association with drug sensitivity suggests its potential as a target for treatments in these cancer types. The identified drugs exhibiting sensitivity or resistance based on DSCC1 expression profiles could guide personalized therapeutic strategies, emphasizing the importance of considering DSCC1 as a potential therapeutic target.

Conclusion

In summary, our first pan-cancer analysis of DSCC1 emphasizes its prevalent overexpression across diverse tumor tissues compared to normal counterparts. The study discloses a notable association between heightened DSCC1 expression and unfavorable prognoses in KIRP, LIHC, and LUAD. These findings hint at DSCC1 potentially serving as an independent prognostic indicator in multiple cancers, although a more in-depth exploration of its specific role in each tumor context remains imperative for comprehensive understanding.

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Disclosure of conflict of interest

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