

Long noncoding RNA MIAT acts as an oncogene in Wilms' tumor through regulation of DGCR8

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Abstract. – **OBJECTIVE:** Recent researches have proved that long noncoding RNAs (lncRNAs) cover an important role in malignant tumors. Our study showed how lncRNA myocardial infarction-associated transcript (MIAT) functions in the development of Wilms' tumor.

PATIENTS AND METHODS: Real Time-quantitative Polymerase Chain Reaction (RT-qPCR) was utilized to detect the MIAT expression in Wilms' tumor patients. The MIAT expression level and the patients' overall survival time were analyzed. Then, we conducted functional experiments to identify the changes in the biological behaviors of Wilms' tumor cells due to the loss of MIAT. Moreover, further experiments were performed to explore the potential mechanism.

RESULTS: By comparing with MIAT expression in adjacent tissues, the MIAT expression level was significantly higher in Wilms' tumor samples. Moreover, the cell proliferation of Wilms' tumor cells was inhibited due to the loss of MIAT. The migration and invasion ability of the Wilms' tumor cells was inhibited due to the loss of MIAT. Furthermore, the expression of DGCR8 was downregulated due to the loss of MIAT. In addition, it was found that the DGCR8 expression was positively correlated with MIAT expression in Wilms' tumor tissues.

CONCLUSIONS: These results suggested that MIAT could promote cell proliferation and the metastasis of Wilms' tumor by upregulating DGCR8, which indicated that MIAT might be a potential target for the diagnosis and therapy of Wilms' tumor.

Key Words: Long noncoding RNA, MIAT, Wilms' tumor, DGCR8.

Introduction

Wilms' tumor accounts for the most common pediatric renal cancer. 10,000 children are diagnosed with Wilms' tumor annually, with an

overall survival rate of more than 90%¹. Wilms' tumor happens with the embryonic nephrogenic cells fail to undergo terminal differentiation. Although the combination therapy was available for Wilms' tumor, almost 40% of patients with Wilms' tumors presents distant metastasis and recurrence^{2,3}. Thus, it is crucial to realize the underlying molecular mechanism and find a new treatment strategy for Wilms' tumors.

Long noncoding RNAs (lncRNAs) are one of the newly discovered subgroups of noncoding RNAs (ncRNAs) which are longer than 200 nucleotides. Numerous studies showed that lncRNAs are a new frontier in the research of the biological processes in the malignant cancers. For instance, lncRNA FAL1 is found to be a potential oncogene for colon cancer by promoting proliferation and inhibiting apoptosis of colon cancer cells⁴. lncRNA LINC01133 promotes colorectal cancer metastasis by inducing the epithelial-mesenchymal transition⁵. lncRNA ZNF1 is significantly increased in the hepatocellular carcinoma and gastric cancer, which contributes to the development and progression of cancer⁶. Recent researches have revealed that lncRNA myocardial infarction-associated transcript (MIAT) functions as a novel oncogene in tumorigenesis. However, the function of lncRNA MIAT in Wilms' tumor and the potential molecular mechanism remain unknown so far. In this study, we discovered that the expression of MIAT was remarkably higher in the Wilms' tumor tissues. Moreover, the proliferation and metastasis of Wilms' tumor cells were inhibited due to the loss of MIAT. Previous studies have identified that DGCR8 is a fundamental regulator in tumor development. Our further experiment also found that MIAT functioned in the Wilms' tumor development by regulating DGCR8.

Patients and Methods

Tissue Samples

A total of 50 Wilms' tumor patients were gathered from Wilms' tumor patients at The First Hospital of Jilin University from March 2016 to December 2018. The written informed consent was taken before the operation. No radiotherapy or chemotherapy was performed before the surgery. All the fresh tissues obtained from the surgery were preserved immediately at -80°C . This study was approved by the Ethics Committee of The First Hospital of Jilin University. The signed written informed consents were obtained from all participants before the study.

Cell Culture

The human Wilms' tumor cells were collected and digested from the fresh Wilms' tumor tissues. The culture medium consisted of 10% fetal bovine serum (FBS; Life Technologies, Gaithersburg, MD, USA), Dulbecco's Modified Eagle's Medium (DMEM; Gibco, Rockville, MD, USA), as well as penicillin. The cells were cultured in an incubator containing 5% CO_2 at 37°C .

Cell Transfection

The cDNA oligonucleotides specifically targeting MIAT (sh-MIAT) and the negative control (NC) were synthesized by GenePharma (Shanghai, China) and were cloned into pLVH1/GFP+Puro vector (GenePharma, Shanghai, China). Then, sh-MIAT or NC was used for transfection in Wilms' tumor cells, and the cells which the relative cells were selected for further experiment.

RNA Extraction and Real Time Quantitative Polymerase Chain Reaction (RT-qPCR)

The total RNA was separated by using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). Through reverse transcription Kit (TaKaRa Biotechnology Co., Ltd., Dalian, China), the total RNA was reverse transcribed to complementary deoxyribose nucleic acids (cDNAs). The primers using for RT-qPCR were as follows: MIAT primers forward: 5'-ACGTTTCCACACTG-3', reverse: 5'-CACTTTCATTCTAGG-3'; glyceraldehyde 3-phosphate dehydrogenase (GAPDH) primers forward: 5'-CCAAATCAGATGGGGTATGCT-3' and reverse 5'-TGATGGCATCTGTGGTCATTCA-3'. The thermal cycle was as follows: 30 sec at 95°C , 5 sec for 40 cycles at 95°C , 35 sec at 60°C .

MTT (3-[4,5-Dimethylthiazol-2-yl]-2,5-Diphenyl Tetrazolium Bromide)

2×10^3 transfected cells were seeded in 96-well plates. Following the manufacturer's protocol, the cell proliferation was assessed by the Cell Proliferation Reagent Kit I (MTT; Roche, Basel, Switzerland) every 24 h. The absorbance at 490 nm was assessed using a ELISA reader (Multiskan Ascent, ThermoFisher, Helsinki, Finland).

Colony Formation Assay

The transfected cells were seeded in a 6-well plate for 2 weeks. The colonies were treated with methanol for 24 h. Then, 0.5% crystal violet was used for staining for 5 min. The colonies containing more than 50 cells were counted, and the mean colony numbers were calculated. The analysis was conducted with Image-Pro Plus 6.0 (Silicon Graphics, MD, USA).

EdU (5-Ethynyl Deoxyuridine (EdU)) Incorporation Assay

Following the manufacturer's manual, an EdU Kit (Roche, Mannheim, Germany) was utilized to monitor the cell proliferation of transfected cells. A Zeiss Axiophot Photomicroscope (Carl Zeiss, Oberkochen, Germany) was performed to take the representative images.

Transwell Assay

For detecting the invading ability of these treated cells, 5×10^4 cells in serum-free DMEM were replanted in the top chamber (Corning, Inc., Corning, NY, USA) of 24-well plates pre-coated with or without Matrigel Matrix dilution (BD Biosciences, San Jose, CA, USA). In addition, in the bottom chamber DMEM and FBS were added. The top surface of the chambers was wiped by cotton swab 48 h later and immersed for 10 min with precooling methanol. Then, they were stained in crystal violet for 30 min. Three fields were randomly chosen to count the data for the invasion membrane under a Leica DMI4000B microscope (Leica Microsystems, Heidelberg, Germany).

Western Blot Analysis

The protein was extracted from cells by Reagent radioimmunoprecipitation assay (RIPA; Beyotime, Shanghai, China). The bicinchoninic acid (BCA) protein assay kit was used for quantifying the protein concentrations (TaKaRa Ltd., Dalian, China). The sodium dodecyl sulphate-polyacrylamide gel

electrophoresis (SDS-PAGE) was utilized to separate the target proteins. Then the gels were transferred to the polyvinylidene difluoride (PVDF) membranes (Millipore, Billerica, MA, USA) and further incubated with antibodies. The rabbit anti-GAPDH and rabbit anti-DGCR8 were provided by Cell Signaling Technology (CST, Danvers, MA, USA), as well as the goat anti-rabbit secondary antibody. The Image J software was applied for the assessment of the protein expression.

Statistical Analysis

The GraphPad Prism 5.0 (La Jolla, CA, USA) was adopted to conduct the statistical analysis. The data were expressed as mean \pm SD (standard deviation). The Student's *t*-test and the Kaplan-Meier method were utilized. A *p*-value of less than 0.05 was considered statistically significant.

Results

MIAT Expression Level in Wilms' Tumor Tissues and Cells

Firstly, the MIAT expression was detected by RT-qPCR in 50 Wilms' tumor patients' tissues. The results showed that MIAT was significantly upregulated in tumor tissue samples (Figure 1A). We divided 50 patients into two groups, according to the median expression of MIAT. Patients with high MIAT expression level had poor overall survival than those with low MIAT expression level (Figure 1B).

Cell Proliferation of Wilms' Tumor Cells Was Inhibited Due to Loss of MIAT

Wilms' tumor cells were transfected with MIAT shRNA or NC, and the transfection efficiency was detected by RT-qPCR (Figure 2A). The results of the MTT assay showed that the cell growth ability of Wilms' tumor cells was inhibited due to the loss of MIAT (Figure 2B). Colony formation assay also showed that the number of colonies was remarkably decreased due to the loss of MIAT in Wilms' tumor cells (Figure 2C). Moreover, the results of EdU incorporation assay also revealed that the percentage of the EdU positive cells reduced due to the loss of MIAT in Wilms' tumor cells (Figure 2D).

Cell Invasion of Wilms' Tumor Cells Was Inhibited Due to Loss of MIAT

To detect the function of MIAT in Wilms' tumor metastasis, the transwell assay was performed. The results showed that the cell migration ability of Wilms' tumor cells was inhibited due to the loss of MIAT (Figure 3A). The outcome of the transwell assay also revealed that the cell invasion ability of Wilms' tumor cells was remarkably decreased due to the loss of MIAT (Figure 3B).

The Interaction Between DGCR8 and MIAT in Wilms' Tumor

DGCR8 was predicted as the target proteins of MIAT through StarBase v2.0 (<http://starbase.sysu.edu.cn/starbase2/rbpLncRNA.php>). RT-qPCR results showed that the expression level of DGCR8 in Wilms' tumor cells was remarkably lower in the

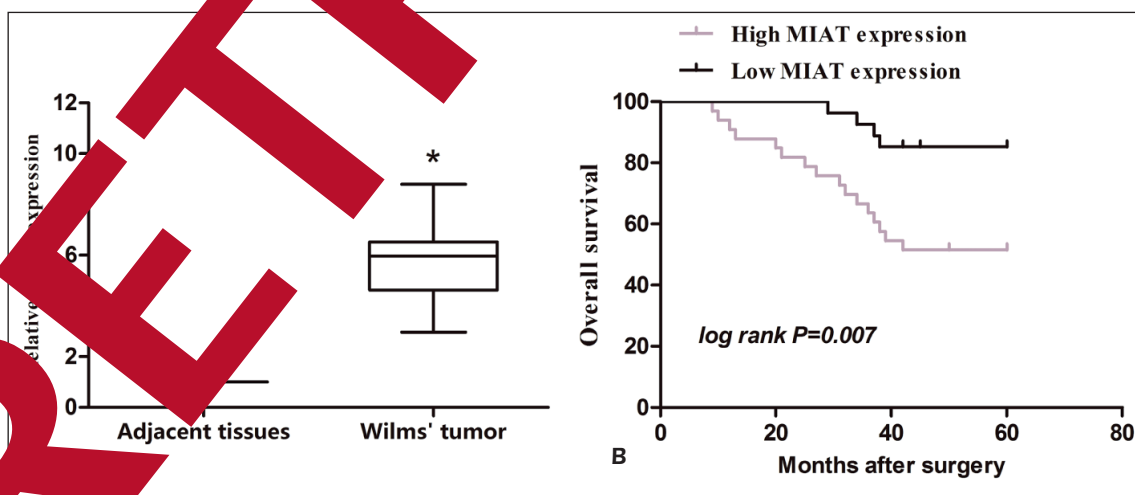


Figure 1. The expression levels of MIAT were increased in Wilms' tumor tissues. **A**, The MIAT expression was significantly increased in the Wilms' tumor tissues compared with adjacent tissues. **B**, The expression levels of MIAT was negatively associated with patients' overall survival time. The data are presented as the mean \pm standard error of the mean. **p*<0.05.

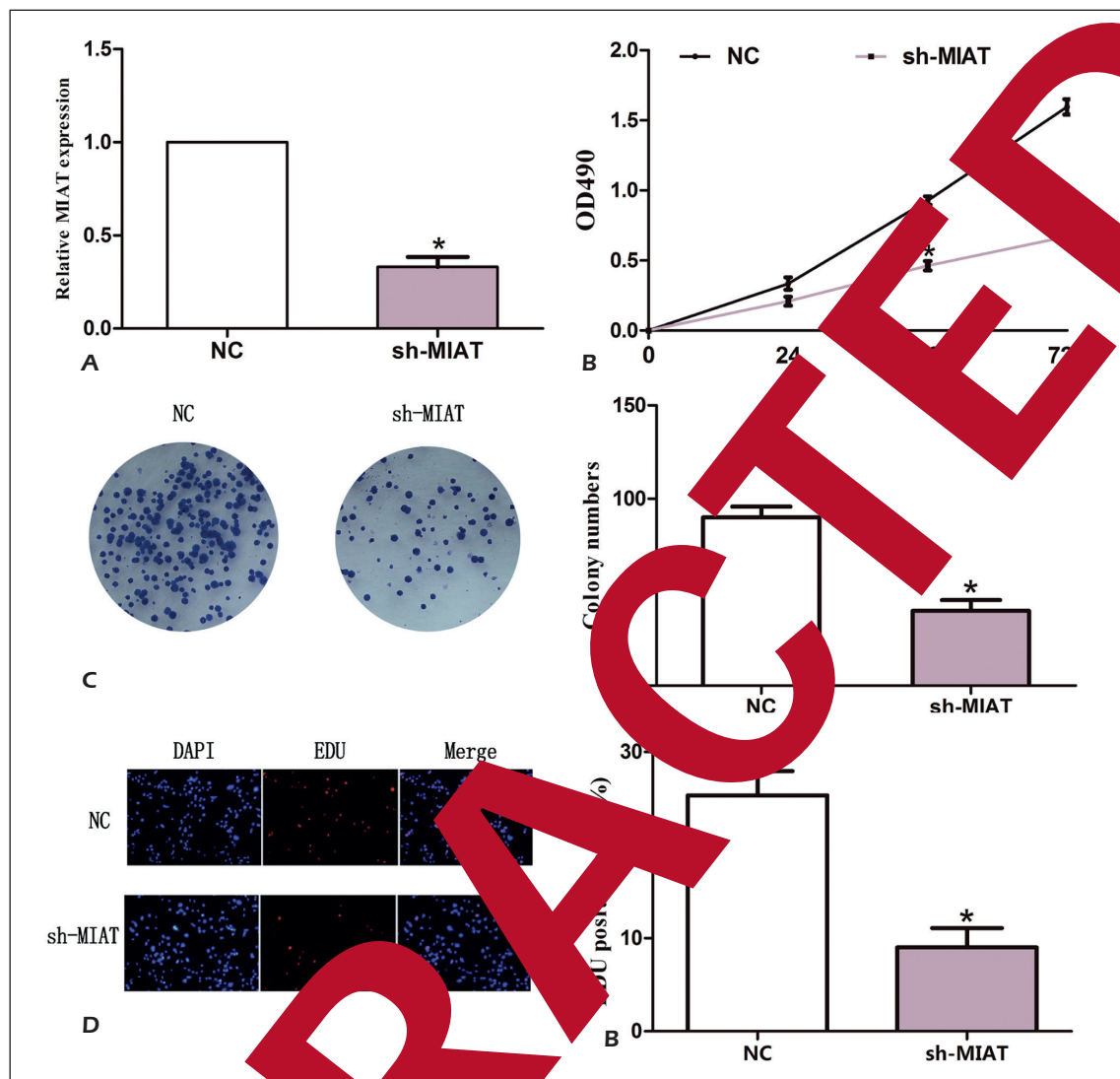


Figure 2. Wilms' tumor cell proliferation is inhibited due to the loss of MIAT. **A**, The MIAT expression in Wilms' tumor cells transfected with sh-MIAT and NC was detected by RT-qPCR. GAPDH was used as an internal control. **B**, The MTT assay showed that the knockdown of MIAT significantly depressed cell proliferation in Wilms' tumor cells. **C**, The colony formation assay showed that the number of colonies was significantly decreased via knockdown of MIAT in Wilms' tumor cells (magnification: 10 \times). **D**, The EdU incorporation assay showed that the number of EdU positive cells was significantly decreased via knockdown of MIAT in Wilms' tumor cells. The results represent the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$ compared with the control cells.

sh-MIAT group compared with that in the NC group (Figure 4A). The Western blot assay results showed that the expression level of DGCR8 in Wilms' tumor cells was significantly lower in the sh-MIAT group compared with that in the NC group (Figure 4B). Besides, the DGCR8 expression in Wilms' tumor cells was remarkably higher when compared with that in the adjacent tissues (Figure 4C). The correlation analysis demonstrated that the DGCR8 expression level positively correlated to MIAT expression in cancer tissues (Figure 4D).

Discussion

Numerous studies have proved that lncRNAs are important regulators in the initiation and progression of the Wilms' tumor. For example, lncRNA LINP1 promotes tumorigenesis of Wilms' tumor via Wnt/ β -catenin signaling pathway⁷. LINC00473 suppresses miR-195 and further participates in regulating the Wilms' tumor via IKK α ⁸.

Located on chromosome 22q12, lncRNA MIAT has been found to be involved in numerous

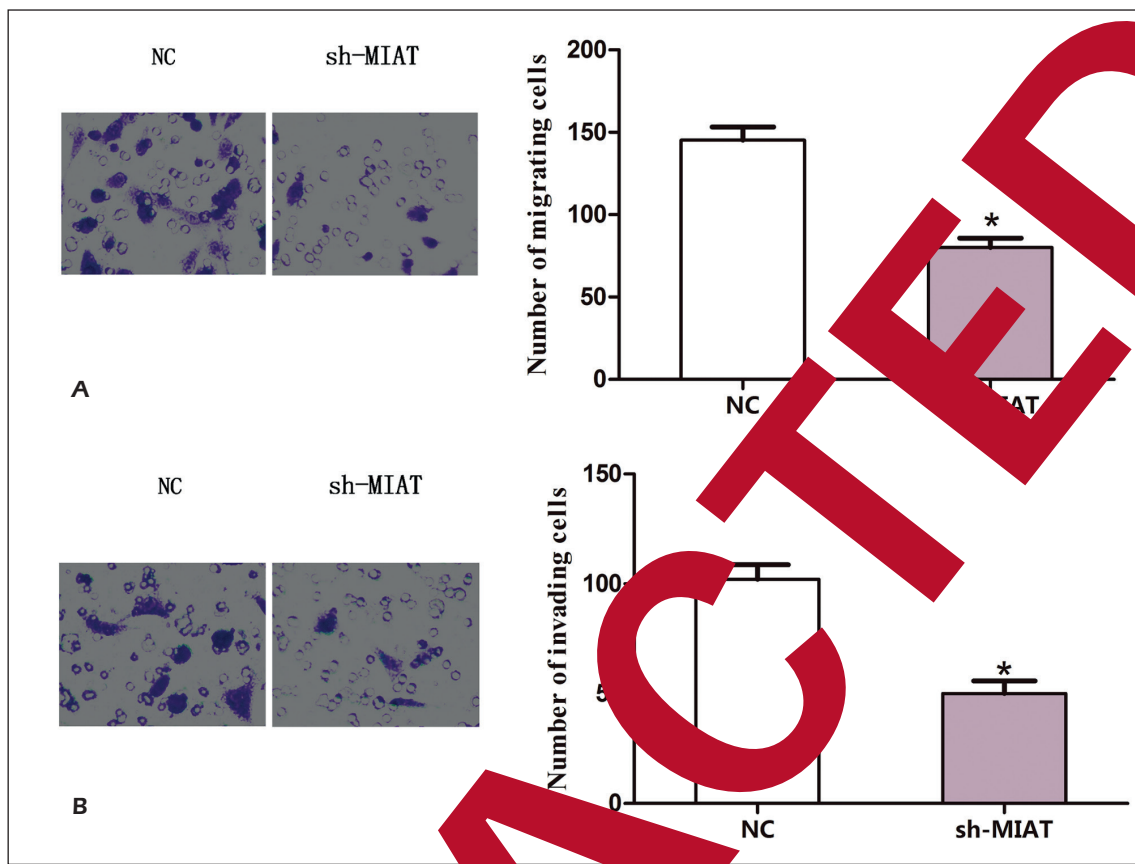


Figure 3. The transwell assay showed that the knockdown of MIAT inhibited Wilms' tumor cell migration and invasion. **A,** The transwell assay showed that number of migrated cells was significantly decreased due to the knockdown of MIAT in Wilms' tumor cells (magnification: 40×). **B,** The transwell assay showed that number of invaded cells was significantly decreased due to the knockdown of MIAT in Wilms' tumor cells (magnification: 40×). The results represent the average of three independent experiments (mean ± standard deviation). *P < 0.05, as compared with the control cells.

diseases, including the development of cancers. MIAT enhances cervical cancer growth and tumor metastasis by regulating miR-141/Derlin-1 pathway⁹. MIAT enhances the progression of breast cancer by serving as a ceRNA for miR-155-5p¹⁰. By modulating miR-141/DDX5 signaling pathway, MIAT facilitates tumor growth and metastasis in gastric cancer¹¹. In this study, we found that MIAT was highly expressed in Wilms' tumor samples. Besides, the cell proliferation and metastasis of Wilms' tumor cells were inhibited due to the loss of MIAT. The above results indicated that MIAT promotes the tumorigenesis of Wilms' tumor and might act as a oncogene.

To further identify the underlying mechanism by which MIAT affects Wilms' tumor, we used miRBase 22.1 to predict the target proteins of MIAT and picked DGCR8 as the potential target of MIAT. DGCR8 gene has been reported to participate in the progression of cancers. For exam-

ple, cell proliferation and invasion were inhibited due to the knockdown of DGCR8 in ovarian cancer¹². DGCR8 inhibits tumor progression of prostate cancer¹³. Some researches^{14,15} revealed that DGCR8 has a role in the development and metastasis of Wilms' tumor. In the present study, we first discovered the interaction between DGCR8 and MIAT. DGCR8 could be downregulated after the knockdown of MIAT in Wilms' tumor tissues. Besides, the DGCR8 expression was also higher in Wilms' tumor tissues and was positively related to MIAT expression.

Conclusions

In summary, MIAT could facilitate cell proliferation and metastasis in Wilms' tumor by upregulating DGCR8, which might serve as a candidate target for Wilms' tumor diagnosis and therapy.

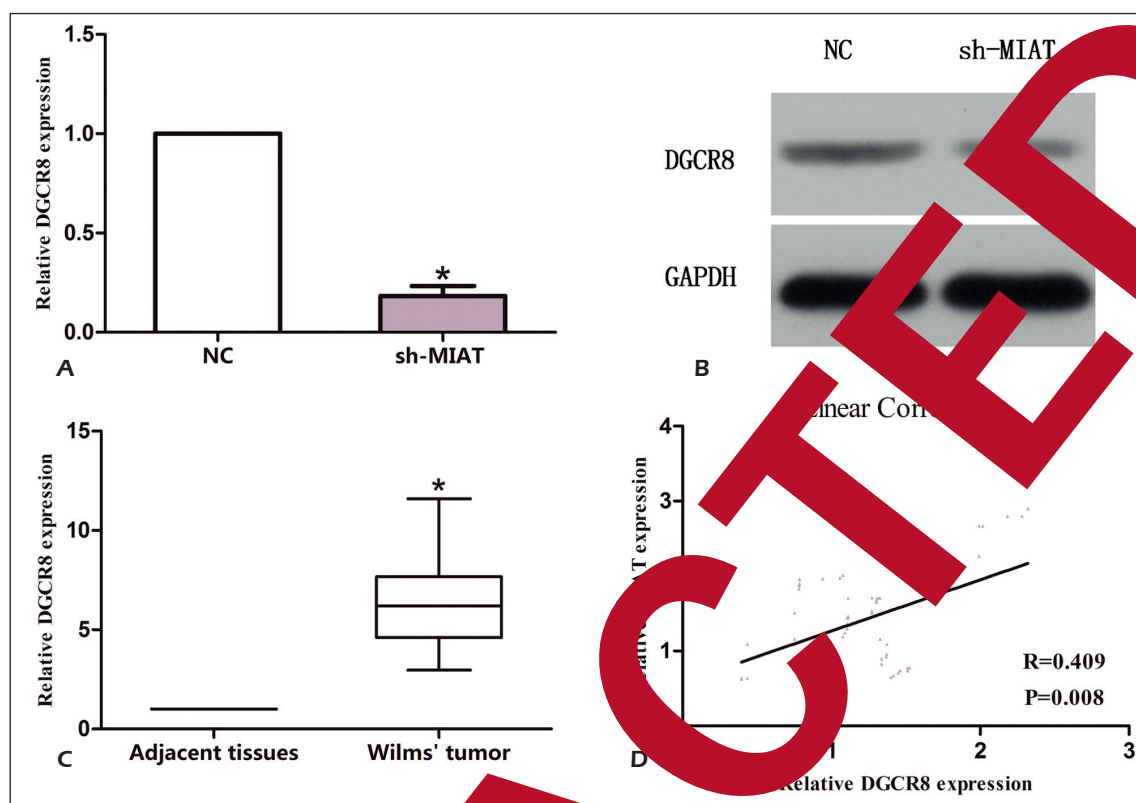


Figure 4. The interaction between MIAT and DGCR8. **A**, The bar graph results showed that DGCR8 expression was decreased in sh-MIAT compared with the NC group. **B**, The Western blot results showed that DGCR8 expression was decreased in sh-MIAT compared with the NC group. **C**, DGCR8 was significantly upregulated in Wilms' tumor tissues compared with adjacent tissues. **D**, The linear correlation analysis of the expression level of DGCR8 and MIAT in Wilms' tumor tissues. The results represent the average of three independent experiments. The data are presented as the mean \pm standard error of the mean. * $p < 0.05$.

Conflict of Interests

The Authors declare that they have no conflict of interests.

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