Knockdown of KCNQ1OT1 Suppresses Cell Invasion and Sensitizes Osteosarcoma Cells to CDDP by Upregulating DNMT1-Mediated Kcnq1 Expression

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Osteosarcoma is a malignant bone tumor, with a high incidence worldwide. The involvement of long non-coding RNAs (lncRNAs) in cancers and their molecular association with the progression of osteosarcoma have been previously discussed. We conducted the present study to examine the effect of lncRNA KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1) on osteosarcoma cell invasion and chemosensitivity to cisplatin (CDDP). After determination of the expression of Kcnq1 in osteosarcoma tissues and cells, the plasmids with overexpression or knockdown KCNQ1OT1 were introduced into the cells to aid the identification of cell proliferation, migration, invasion, chemosensitivity to CDDP, and apoptosis. Then, the interaction between KCNQ1OT1 and the Kcnq1/ DNA methyltransferase 1 (DNMT1) axis was evaluated by measuring the level of Kcnq1 promoter region methylation and DNMT1 enrichment of the Kcnq1 promoter region. Low Kcnq1 expression and high KCNQ1OT1 expression were shown in osteosarcoma tissues and cells. Kcnq1 was negatively mediated by KCNQ1OT1 via DNMT1. The overexpression of Kcnq1 or knockdown of KCNQ1OT1 inhibited the proliferation, migration, and invasion, and it promoted the chemosensitivity to CDDP and apoptosis of MG-63 cells and its CDDP-resistant cell lines. Moreover, the same trend was observed in the cells following methylation inhibitor treatment. Collectively, knockdown of KCNQ1OT1 can inhibit the osteosarcoma progression through the Kcnq1/DNMT1 axis.

INTRODUCTION

Osteosarcoma is characterized as a skeletal system-associated tumor that has a very high malignancy and is common among the younger population worldwide.[1] The incidence of osteosarcoma is higher in adolescence, with the highest incidence reported to be 8–11 million/year in young patients within the age range of 15–19 years, and it can result in local and metastatic progression if left untreated.[2] The currently used treatment options include neoadjuvant and adjuvant chemotherapy along with local control (usually limb-sparing surgery), both of which have been found with high efficacy.[3] However, patients with a chemotherapy-resistant form have an unsatisfactory 5-year overall survival rate.[4] Therefore, there is an urgent need in understanding the mechanism of migration and cisplatin

(CDDP) resistance of osteosarcoma cells in order to develop a novel therapeutic method.

Aberrant levels of long non-coding RNAs (lncRNAs) are correlated with cancers.[5] lncRNAs can also mediate the initiation and progression of osteosarcoma; lncRNA differentiation antagonizing non-protein-coding RNA overexpression has been previously elucidated to induce osteosarcoma cell proliferation, migration, and invasion and to advance xenograft tumor growth and lung migration *in vivo*.[6] In a recent study, it was demonstrated that resveratrol can lead to reduced osteolysis by promoting osteogenic differentiation with elevated KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1) via Wnt and β-catenin activation.[7] However, there is very little known research regarding the underlying mechanism and functional role of lncRNA KCNQ1OT1 in cancer development.[8] CDDP is a well-established chemotherapeutic drug widely used for various cancers; however, its efficacy is limited by tumor cell resistance and severe side effects.[9] In addition, lncRNA KCNQ1OT1 can promote cell proliferation and tongue squamous cell carcinoma (TSCC) resistance to CDDP-induced apoptosis, highlighting the role of KCNQ1OT1 in CDDP resistance.[10]

DNA methyltransferase 1 (DNMT1) plays a key role in maintaining genomic methylation patterns by DNA replication cycles.[11] It has previously been demonstrated that DNMT1 activity plays a positive role in the malignancy progression of hepatocellular carcinoma cells.[12] Moreover, DNMT1 expression in cells can be elevated by exogenous exosome, followed by the enrichment of DNMT1 transcripts, contributing to CDDP resistance in human ovarian cancer.[13] DNMT1 is also involved in cell development, an example of such being the correlation between DNMT1 to suppressed cell invasion and migration by miR-148a in gastric cancer.[14] Moreover, downregulated DNMT1 can result in the inhibition of proliferation,
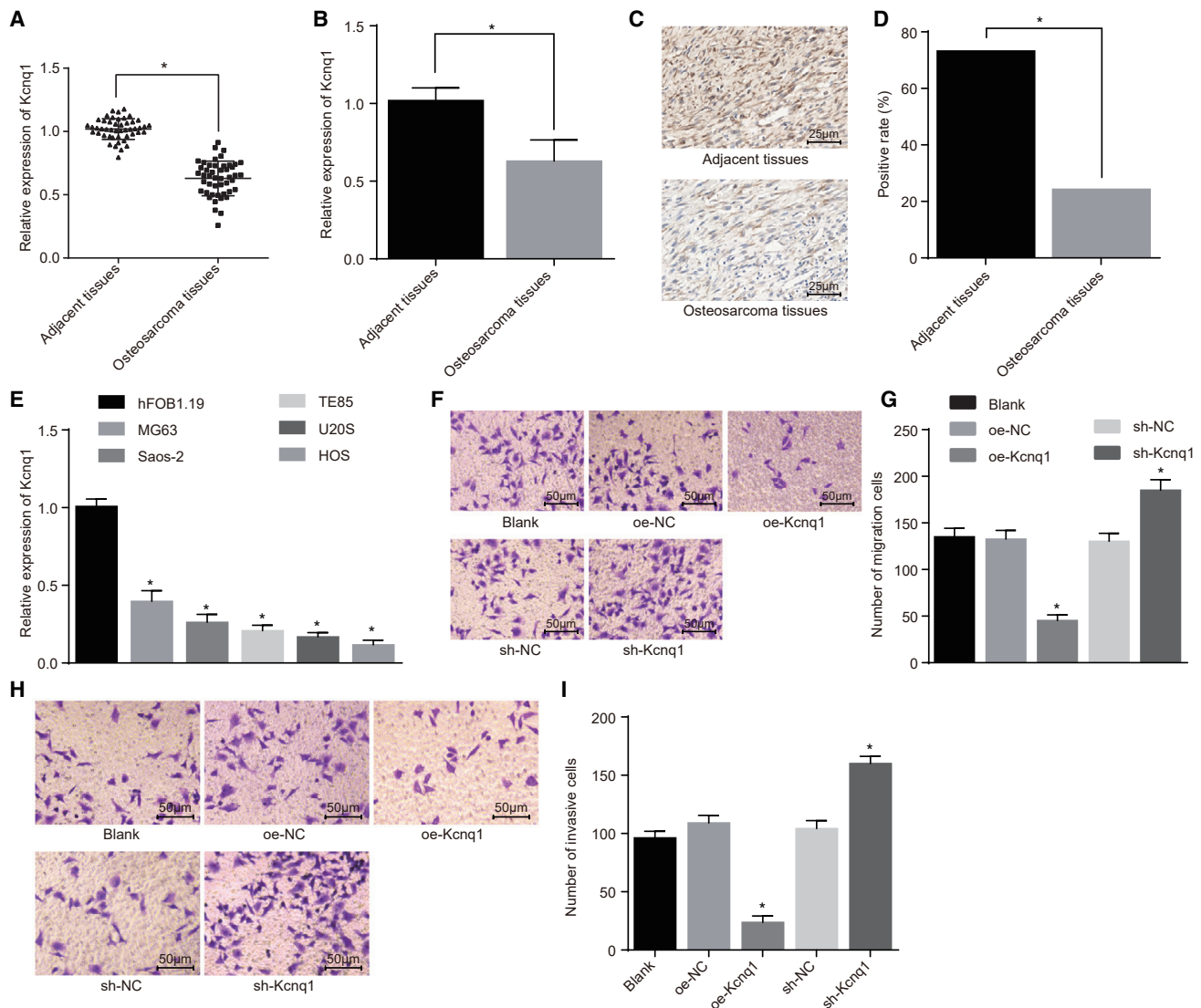
Figure 1. Kcnq1 Expression and Its Impacts on Osteosarcoma Cell Migration and Invasion (n = 47)

(A and B) Kcnq1 expression in osteosarcoma and normal tissues. (C and D) Kcnq1-positive expression in osteosarcoma and normal tissues (400×). (E) The expression of Kcnq1 in osteosarcoma cell lines. MG-63 cells were treated with oe-Kcnq1 or sh-Kcnq1, with oe-NC and sh-NC as the controls. (F and G) The migration situation of MG-63 cells in each group (200×). (H and I) The invasion situation of MG-63 cells in each group (200×). *p < 0.05 versus adjacent tissues or hFOB1.19 cells or the blank group. The measurement data were expressed as mean ± SD, and the enumeration data were presented by number of cases or percentage. Comparison between the osteosarcoma and normal tissues was analyzed by paired t test, and comparison between the other two groups was processed with independent t test. Comparisons among multiple groups were analyzed by one-way ANOVA. The analysis of comparison of enumeration data was performed with chi-square analysis. The experiment was repeated 3 times. NC, negative control.

migration, and invasion of esophageal squamous cell carcinoma cell, through the suppression of methylation of promoter of tumor suppressor genes, RASSF1A, and death-associated protein kinase.[15] Based on the aforementioned findings, we propose a hypothesis that KCNQ1OT1 might be involved in the progression of osteosarcoma by regulating Kcnq1 and DNMT1, and we conducted the present study to investigate the effects of KCNQ1OT1, Kcnq1, and DNMT1 in osteosarcoma.

RESULTS

Low Expression of Kcnq1 in Osteosarcoma

The expression of Kcnq1 was determined in 47 cases of osteosarcoma and normal bone tissues. The results from qRT-PCR revealed that the expression of Kcnq1 in cancer tissues of patients with osteosarcoma was significantly lower than that in adjacent tissues (p < 0.05; Figures 1A and 1B). Subsequently, the positive expression rate of Kcnq1 in the osteosarcoma and normal tissues was assessed. It was found that there
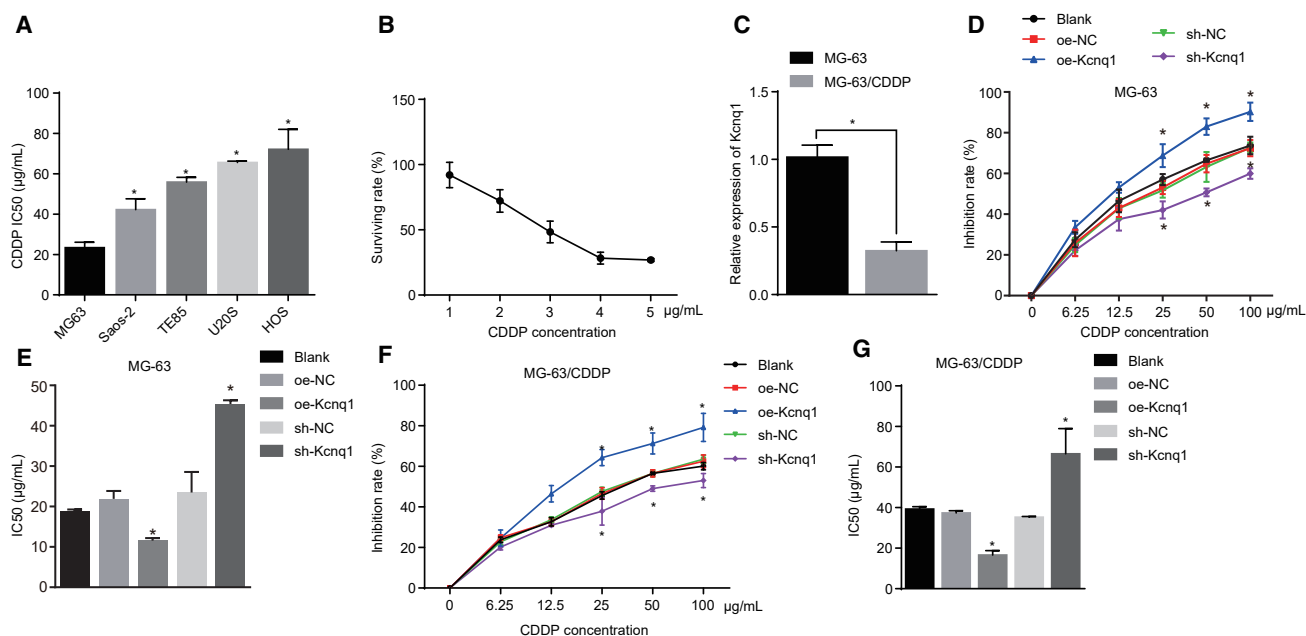
Figure 2. Kcnq1 Exerts Functions on Osteosarcoma Cell Chemosensitivity to CDDP

MG-63 cells and MG-63/CDDP cells were treated with oe-Kcnq1 or sh-Kcnq1, with oe-NC and sh-NC as the controls. (A) IC_{50} values in osteosarcoma cell lines. (B) The surviving rates under different concentrations of CDDP. (C) The expression of Kcnq1 in the MG-63 cell line and the corresponding CDDP-resistant cell lines. (D and E) The inhibitory rate (D) and IC_{50} values (E) of MG-63 cells in each group. (F and G) The inhibitory rate (F) and IC_{50} values (G) of MG-63/CDDP cells in each group. *$p < 0.05$ versus the blank group. The measurement data were expressed as mean ± SD. Comparisons among multiple groups were analyzed by one-way ANOVA. The analysis of comparison between groups at different time points was performed with repeated-measures ANOVA. The experiment was repeated 3 times. WST-1, water-soluble tetrazolium salt; CDDP, cisplatin; IC_{50}, inhibitory concentration 50%; NC, negative control.

was a positive expression of Kcnq1 in the cytoplasm and membrane, presenting with a brownish yellow appearance. Meanwhile, the positive expression rate of Kcnq1 in the osteosarcoma tissues was significantly lower than that in the adjacent tissues ($p < 0.05$; Figures 1C and 1D). Furthermore, qRT-PCR results indicated that, compared with human normal osteoblast cell line hFOB1.19, human osteosarcoma cell lines MG-63, Saos-2, TE85, U20S, and HOS had poorly expressed Kcnq1, among which the MG-63 cell line showed the highest Kcnq1 expression ($p < 0.05$). Therefore, the MG-63 cell line was selected for subsequent experiments (Figure 1E).

Following interference on Kcnq1, the expression of Kcnq1 was determined in each group with the use of qRT-PCR. No significant difference was observed in the overexpressed-negative control (oe-NC) group and the short hairpin (sh)-NC group when compared with the blank group ($p > 0.05$), and the mRNA expression of Kcnq1 increased significantly in the oe-Kcnq1 group and decreased in the sh-Kcnq1 group (Figure S1). Next, migration and invasion of the MG-63 cell line were detected. No difference was observed in the oe-NC group and the sh-NC group compared to the blank group ($p > 0.05$), while the migration ability (Figures 1F and 1G) and invasion ability (Figures 1H and 1I) were significantly reduced in the oe-Kcnq1 group, and they were elevated in the sh-Kcnq1 group. Therefore, Kcnq1 was poorly expressed in osteosarcoma tissues and cells, and the low expression of Kcnq1 was considered to promote

the migration and invasion of osteosarcoma cells. These findings suggest that Kcnq1 overexpression could lead to the inhibition of migration and invasion of osteosarcoma cells.

Kcnq1 Overexpression Promotes the Chemosensitivity to CDDP in Osteosarcoma Cells

Based on the previous studies on the characteristics of osteosarcoma cells, 5 human osteosarcoma cell lines (MG-63, Saos-2, TE85, U20S, and HOS) were selected, and the water-soluble tetrazolium salt (WST-1) experiment was used for the test of chemosensitivity to CDDP. Compared with the remaining osteosarcoma cell lines (Saos-2, TE85, U20S, and HOS), the MG-63 cell line was the most sensitive to CDDP ($p < 0.05$; Figure 2A). The corresponding CDDP-resistant cell lines were screened by increasing concentrations of CDDP through intermittent administration. We found that 5 µg/mL CDDP stabilized drug resistance in MG-63 cells, which we named MG-63/CDDP (Figure 2B).

To confirm the association between Kcnq1 and the drug resistance of osteosarcoma cells, we determined the expression of Kcnq1 in the MG-63 cell line and its corresponding CDDP-resistant cell lines. The findings demonstrated that, compared with the MG-63 cell line, there was a decrease in Kcnq1 expression in the MG-63/CDDP cell line ($p < 0.05$; Figure 2C). MG-63 and MG-63/CDDP cells were transfected with blank, oe-NC, oe-Kcnq1, sh-NC, and sh-Kcnq1
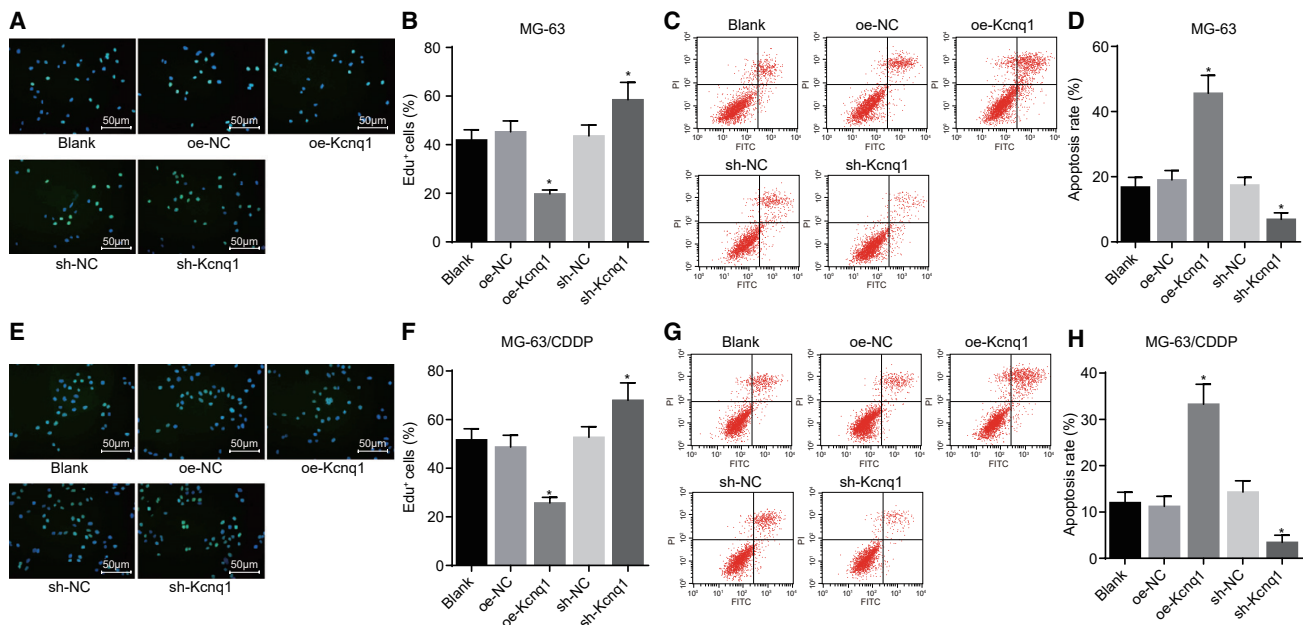
Figure 3. Kcnq1 Is Associated with the Proliferation and Apoptosis of Osteosarcoma Cells Treated with CDDP

MG-63 cells and MG-63/CDDP cells were treated with oe-Kcnq1 or sh-Kcnq1, with oe-NC and sh-NC as the controls. (A and B) The proliferation of MG-63 cells (200×) in each group. (C and D) The apoptosis of MG-63 cells in each group. (E and F) The proliferation of MG-63/CDDP cells (200×) in each group. (G and H) The apoptosis of MG-63/CDDP cells in each group. *p < 0.05 versus the blank group. The measurement data were expressed as mean ± SD. Comparisons among multiple groups were analyzed by one-way ANOVA. This experiment was repeated 3 times. CDDP, cisplatin; NC, negative control.

vectors to investigate cell viability and inhibitory concentration 50% (IC$_{50}$) value. The knockdown of Kcnq1 promoted the MG-63 cell survival while decreasing inhibitory rate (Figure 2D) and increasing the IC$_{50}$ value, indicating that the knockdown of Kcnq1 could result in the inhibition of chemosensitivity to CDDP in MG-63 cells and further promote drug resistance (Figure 2E). On the contrary, overexpression of Kcnq1 was considered to block MG-63/CDDP cell survival, elevate inhibitory rate (Figure 2F), and downregulate the IC$_{50}$ value, which indicated that overexpressed Kcnq1 could promote the chemosensitivity to CDDP in MG-63/CDDP cells and inhibit the drug resistance (Figure 2G; p < 0.05). Tumor cells with a high expression in Kcnq1 might be more susceptible to apoptosis as a result of CDDP, while cells with a low expression of Kcnq1 might be resistant to CDDP at a certain level.

Kcnq1 Overexpression Inhibits Proliferation and Promotes Apoptosis of Osteosarcoma Cells Treated with CDDP

Following transfection of MG-63 cells with blank, oe-NC, oe-Kcnq1, sh-NC, and sh-Kcnq1 vectors, we measured cell proliferation. We found that the overexpression of Kcnq1 could inhibit the proliferation of MG-63 cells, while knockdown of Kcnq1 could promote the proliferation of MG-63 cells (p < 0.05; Figures 3A and 3B). Flow cytometry was used to detect the apoptosis, and the results revealed that overexpression of Kcnq1 could promote the apoptosis of MG-63 cells while knockdown of Kcnq1 could inhibit MG-63 cell apoptosis (p < 0.05; Figures 3C and 3D). 5-Ethynyl-2′-deoxyuridine (EdU) assay showed that the overexpression of Kcnq1 could inhibit the proliferation of

MG-63/CDDP cells while the knockdown of Kcnq1 could promote the proliferation of MG-63/CDDP cells (p < 0.05; Figures 3E and 3F). The detection of apoptosis using flow cytometry showed that the overexpression of Kcnq1 could promote the apoptosis of MG-63/CDDP cells while the knockdown of Kcnq1 could block MG-63/CDDP cell apoptosis (p < 0.05; Figures 3G and 3H). The overexpression of Kcnq1 dampened proliferation and advanced apoptosis of osteosarcoma cells treated with CDDP.

Demethylation of Kcnq1 Suppresses Cell Proliferation, Invasion, and Migration yet Enhances Apoptosis and Chemosensitivity to CDDP in Osteosarcoma Cells Treated with CDDP

Next, we conducted an analysis of the CpG island in the promoter region using the MethPrimer software, by inputting the nucleotide sequence at the 2,000 bp of the Kcnq1 gene promoter upstream. The findings showed a CpG island in the promoter region of the Kcnq1 gene (Figure 4A), suggesting that the expression of the Kcnq1 gene was affected by promoter methylation. Furthermore, the expression of the Kcnq1 gene was affected by promoter methylation, based on the findings from 47 cases of osteosarcoma and normal tissues.

Bisulfite sequencing PCR (BSP) and methylation-specific PCR (MSP), detecting the CpG island methylation level in the Kcnq1 gene promoter region, displayed that the methylation level of the Kcnq1 gene promoter region in osteosarcoma tissues was higher, with the methylation rate of 53.19% (25/47) (p < 0.05), while the level of
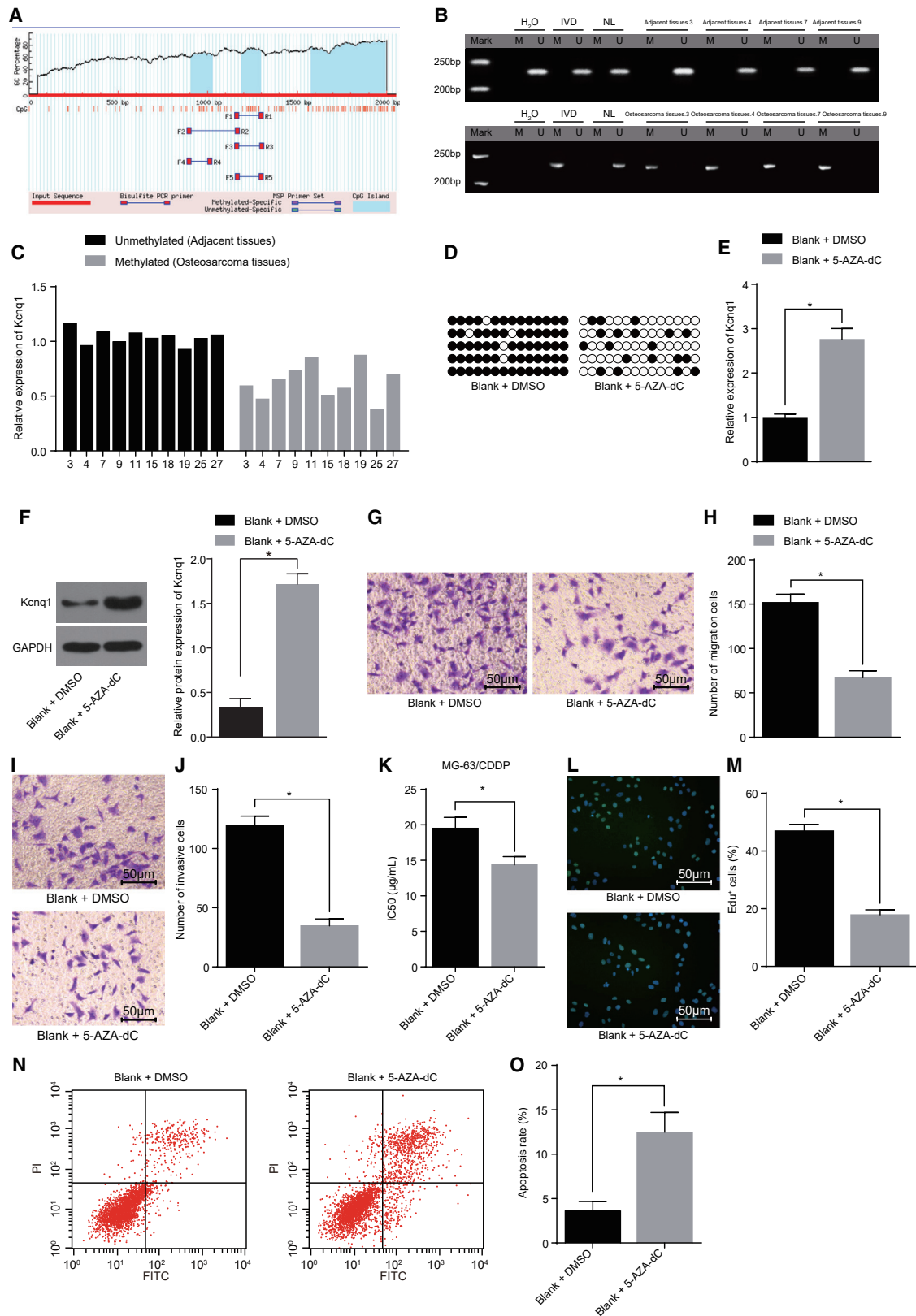
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methylation in the promoter region of the Kcnq1 gene was lower in normal tissues, with the methylation rate of 27.66% (13/47) (p < 0.05; Figure 4B). Kcnq1 expression and promoter methylation status (Figure 4C) were determined, and the results revealed that, in osteosarcoma tissues, the Kcnq1 promoter of the tumor tissue specimens presented methylation and Kcnq1 was poorly expressed while the corresponding adjacent tissues presented unmethylation and overexpression of Kcnq1, indicating that there existed a negative correlation between the expression of Kcnq1 and Kcnq1 methylation level. Therefore, the methylation level in the Kcnq1 promoter region of osteosarcoma was higher, and the Kcnq1 expression was lower.

To investigate the effects of the Kcnq1 gene on osteosarcoma cells after demethylation, DNA methylation transferase inhibitor 5-Aza-CdR was used for demethylation of the Kcnq1 gene promoter region in the CDDP-resistant cell line MG-63/CDDP. In contrast to the MG-63/CDDP cells treated with DMSO, in cells treated with 5-Aza-CdR, the Kcnq1 methylation level decreased (Figure 4D) and Kcnq1 expression increased (Figures 4E and 4F); the cell numbers of migration (Figures 4G and 4H), invasion (Figures 4I and 4J), and proliferation (Figures 4L and 4M) and the IC_{50} value (Figure 4K) were diminished; and the apoptosis rate was enhanced (Figures 4N and 4O; all p < 0.05). Thus, following the demethylation of the Kcnq1 gene promoter region, an increase in Kcnq1 expression was detected, and the highly expressed Kcnq1 could further inhibit the proliferation, migration, and invasion of CDDP-resistant cell lines, and it could promote chemosensitivity to CDDP and the apoptosis of CDDP-resistant cell lines.

KCNQ1OT1 Negatively Regulates Kcnq1 Expression in Osteosarcoma Cells by Recruiting DNMT1

The reverse transcription of lncRNA KCNQ1OT1 was known to exist in the Kcnq1-coding region, and KCNQ1OT1 could regulate the expression of genes on both sides of its transcript. We conducted a series of experiments to investigate whether the expression and role of Kcnq1 in osteosarcoma were regulated by KCNQ1OT1. The results showed that the expression of KCNQ1OT1 in osteosarcoma was higher than that in controls (p < 0.05; Figures 5A and 5B). qRT-PCR that was conducted to determine KCNQ1OT1 expression revealed that each osteosarcoma cell line presented with a high expression in KCNQ1OT1 in human osteosarcoma cell lines MG-63, Saos-2, TE85, U20S, and HOS, when compared with the hFOB1.19 cells, with the MG-63 cell line presenting with the lowest expression of KCNQ1OT1 (p < 0.05; Figure 5C). The expression of KCNQ1OT1 was determined by

qRT-PCR in the MG-63 cell lines and the corresponding CDDP-resistant cell lines. The results showed that the expression of KCNQ1OT1 in the MG-63 CDDP-resistant cell line was significantly higher than that in the MG-63 cell line (p < 0.05; Figure 5D). Moreover, the lncATLAS website was utilized to predict subcellular localization of KCNQ1OT1, and KCNQ1OT1 was mainly found to be located in the nucleus of multiple cell lines (Figure 5E). A subsequent investigation using fluorescence *in situ* hybridization (FISH) further verified that KCNQ1OT1 was mainly expressed in the nucleus (Figure 5F).

The BLAST comparison website was used for comparison of the similarities between KCNQ1OT1 and Kcnq1 promoter regions in order to figure out the correlation of methylation level in the promoter region of the Kcnq1 gene and KCNQ1OT1. The results revealed that there were binding sites for complementary base pairing in KCNQ1OT1 and the Kcnq1 gene promoter region (Figure 5G). According to a dual luciferase reporter gene assay, KCNQ1OT1 or DNMT1 was found to negatively regulate the transcriptional activity of the Kcnq1 promoter region (p < 0.05; Figure 5H).

Next, the enrichment of the DNA methyltransferase DNMT1 in the Kcnq1 gene promoter region was detected using chromatin immunoprecipitation (ChIP), and the results revealed the significant enrichment of the Kcnq1 promoter region and DNMT1 in cell lines with a high expression in KCNQ1OT1 in comparison to cells in the blank group (p < 0.05; Figure 5I). The effect of KCNQ1OT1 expression on the enrichment of DNMT1 was detected by RNA immunoprecipitation (RIP). The results showed that the enrichment of DNMT1 was significantly higher in cell lines with highly expressed KCNQ1OT1 (p < 0.05; Figure 5J). Subsequently, RNA pull-down was used to detect the effect of KCNQ1OT1 on pulling down DNMT1 protein, and the results exhibited that, compared with the Bio-probe NC group, the groups with overexpressed KCNQ1OT1 could pull down more DNMT1 proteins, indicating that KCNQ1OT1 promoted DNMT1 protein enrichment (p < 0.05; Figures 5K and 5L), which was consistent with the RIP detection results.

Osteosarcoma cells were transfected with KCNQ1OT1-NC, oe-KCNQ1OT1, GapmeR-NC, and GapmeR-KCNQ1OT1 vectors to detect the methylation level of the Kcnq1 promoter region. In contrast to the blank group, there was no statistical significance between the KCNQ1OT1-NC and GapmeR-NC groups (p > 0.05). Overexpressed KCNQ1OT1 could promote methylation of the Kcnq1 promoter region in MG-63 cells and MG-63/CDDP cells. The knockdown of

Figure 4. Kcnq1 Influences Osteosarcoma Cell Proliferation, Migration, and Invasion through Its Demethylation
(A) Distribution status of CpG island in the promoter region of the Kcnq1 gene. (B) The electrophoresis of methylation level in the Kcnq1 promoter region of osteosarcoma tissues and their normal tissues (H_2O, double negative control; IVD, methylation positive control; NL, unmethylation positive control; U, unmethylation; and M, methylation). (C) The expression of Kcnq1 and methylated level of the promoter region. MG-63/CDDP cells were treated with 5-Aza-dC, with DMSO as the control. (D) The level of Kcnq1 methylation in each group. (E) mRNA expression of Kcnq1 in each group. (F) The protein expression of Kcnq1 in each group. (G and H) The cell migration situation (200×) in each group. (I and J) The cell invasion situation (200×) in each group. (K) The IC_{50} values of the cells. (L and M) The proliferation of cells (200×). (N and O) The cell apoptosis rate in each group. *p < 0.05 versus the blank + DMSO group. The data were measurement data expressed as mean ± SD. Comparison between two groups was processed with independent t test. This experiment was repeated 3 times. WST-1, water-soluble tetrazolium salt; EdU, 5-Ethynyl-2′-deoxyuridine; BSP, bisulfite sequencing PCR; 5-Aza-dC, 5-Aza-2 deoxycytidine; NC, negative control; IC_{50}, inhibitory concentration 50%; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.
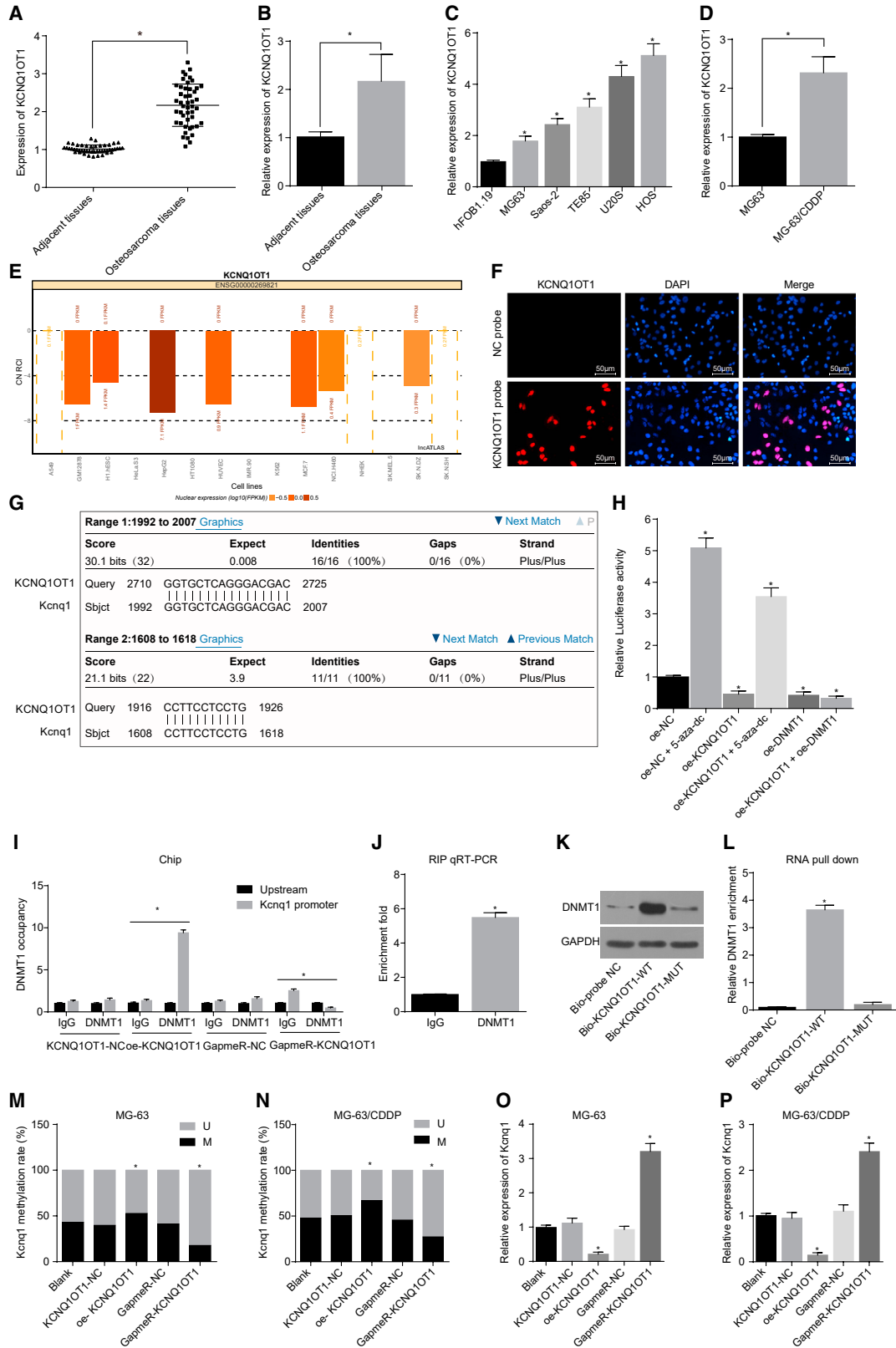
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KCNQ1OT1 could result in the inhibition of methylation of the Kcnq1 promoter region in MG-63 cells and MG-63/CDDP cells (p < 0.05; Figures 5M and 5N). The expression of Kcnq1 in each group was determined by qRT-PCR. The results showed that overexpression of KCNQ1OT1 inhibited Kcnq1 expression in MG-63 cells and MG-63/CDDP cells while KCNQ1OT1 knockdown promoted the expression of Kcnq1 in MG-63 cells and MG-63/CDDP cells (all p < 0.05; Figures 5O and 5P). The aforementioned findings indicated that KCNQ1OT1 was located in the nucleus, with high expression in the tissues and cells of osteosarcoma, and the methylation level of the promoter region of Kcnq1 gene was negatively regulated by KCNQ1OT1, which inhibited Kcnq1 expression by recruiting DNMT1.

Knockdown of KCNQ1OT1 Restrains Cell Proliferation, Migration, and Invasion while Inducing the Apoptosis and Chemosensitivity of Osteosarcoma CDDP-Resistant Cells to CDDP

Following transfection of MG-63/CDDP cells with KCNQ1OT1-NC, oe-KCNQ1OT1, GapmeR-NC, GapmeR-KCNQ1OT1, oe-Kcnq1 + oe-KCNQ1OT1-NC, and oe-Kcnq1 + oe-KCNQ1OT1 vectors, Kcnq1 protein expression was determined. Compared with the KCNQ1OT1-NC group, overexpressed KCNQ1OT1 could block Kcnq1 protein expression; compared with the GapmeR-NC group, knockdown of KCNQ1OT1 could promote Kcnq1 protein expression (p < 0.05; Figures 6A and 6B). EdU assay was used to detect cell proliferation, and, based on the results, the overexpression of KCNQ1OT1 promoted cell proliferation, while the knockdown of KCNQ1OT1 inhibited cell proliferation (p < 0.05; Figures 6C and 6D).

Next, we detected migration and invasion of MG-63/CDDP cells by Transwell assay. Overexpression of KCNQ1OT1 was found to promote cell migration and invasion, while knockdown of KCNQ1OT1 suppressed cell migration (Figures 6E and 6F) and invasion (Figures 6G and 6H; p < 0.05). Subsequently, flow cytometry was used to detect apoptosis, the results of which indicated that overexpression of KCNQ1OT1 inhibited apoptosis and knockdown of KCNQ1OT1 resulted in the opposite trend (p < 0.05; Figures 6I and 6J).

Finally, WST-1 was used to measure IC_{50} values in each group. The results showed that the overexpression of KCNQ1OT1 could promote drug resistance and increase the IC_{50} values of MG-63/CDDP cells and that knockdown of KCNQ1OT1 could suppress drug resis-

tance and decrease the IC_{50} values of MG-63/CDDP cells (all p < 0.05; Figure 6K). These results suggest that KCNQ1OT1 knockdown suppresses MG-63/CDDP cell proliferation, migration, and invasion while promoting apoptosis and chemosensitivity.

The MG-63/CDDP cells were transfected with both oe-Kcnq1 and oe-KCNQ1OT1, with co-treatment of oe-Kcnq1 and oe-KCNQ1OT1-NC as the control to observe its functions over the biological properties of MG-63/CDDP cells. A series of experiments were carried out, and the results revealed that, compared with the oe-Kcnq1 + oe-KCNQ1OT1-NC group, there was a significant decrease in Kcnq1 protein expression in the oe-Kcnq1 + oe-KCNQ1OT1 group (p < 0.05; Figures 6A and 6B), the numbers of EdU-positive (Figures 6C and 6D), migrating (Figures 6E and 6F), and invasive (Figures 6G and 6H) cells were elevated (all p < 0.05); the cell apoptosis rate was evidently decreased (p < 0.05; Figures 6I and 6J); while the IC_{50} value of cells and the cell drug resistance were elevated (p < 0.05; Figure 6K). Overexpression of KCNQ1OT1 reduced Kcnq1 expression, thus promoting proliferation, migration, and invasion and suppressing CDDP-induced apoptosis and CDDP resistance of MG-63/CDDP cells.

Kcnq1 Overexpression Facilitates *In Vivo* Chemosensitivity of Osteosarcoma Cells to CDDP

The potential effects of KCNQ1OT1 in inhibiting *in vivo* chemosensitivity of osteosarcoma cells to CDDP were further investigated through the transfection of MG-63/CDDP with blank, oe-NC, oe-Kcnq1, sh-NC, and sh-Kcnq1 vectors, which were inoculated into nude mice. Following tumor formation, the mice were treated with CDDP. According to the analysis on tumor growth curve and body weight of nude mice, MG-63/CDDP cells with overexpressed Kcnq1 had hindered tumor growth in nude mice versus that of blank and oe-NC groups, and sh-Kcnq1-transfected MG-63/CDDP cells contributed to accelerated tumor growth in comparison to the blank and sh-NC groups. After 4 weeks of CDDP injection in nude mice, the tumor volume (Figure 7B), tumor size (Figure 7A), and tumor mass (Figure 7C) were significantly increased in the sh-Kcnq1 group, while an opposite tendency was found in the oe-Kcnq1 group. In conclusion, Kcnq1 promoted *in vivo* chemosensitivity of nude mice osteosarcoma cells to CDDP.

DISCUSSION

Osteosarcoma is a common primary malignant bone tumor that occurs among children and young adults, accounting for 20% of all

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Figure 5. The Correlation between Kcnq1 Expression and KCNQ1OT1 in Osteosarcoma Cells

(A and B) KCNQ1OT1 expression in osteosarcoma cells and normal cells. (C) KCNQ1OT1 expression in each osteosarcoma cell line. (D) KCNQ1OT1 expression in the MG-63 cell line and MG-63/CDDP cell line. (E) The subcellular localization of KCNQ1OT1 predicted on the lncATLAS website. (F) The subcellular localization of KCNQ1OT1 (200×). (G) Similarities between KCNQ1OT1 and Kcnq1 gene promoter, compared using BLAST. (H) Luciferase activity in each group. (I) The enrichment of DNA methyltransferase DNMT1 in the Kcnq1 promoter region. (J) The effect of KCNQ1OT1 on the enrichment of DNA methyltransferase DNMT1. (K and L) The effect of KCNQ1OT1 on pulling down DNMT1 protein. MG-63 and MG-63/CDDP cells were treated with oe-KCNQ1OT1 or GapmeR-KCNQ1OT1, with KCNQ1OT1-NC and GapmeR-NC as the controls. (M and N) The level of Kcnq1 methylation in each group. (O and P) The mRNA expression of Kcnq1 in each group, determined by qRT-PCR. *p < 0.05 versus the normal group, the hFOB1.19 cell line, the MG-63 cell line, the NC group, the blank group, the IgG group, or the Bio-probe NC group. The measurement data were expressed as mean ± SD. Comparison between two groups was analyzed by independent t test, and comparisons among multiple groups were processed with one-way ANOVA. The experiment was repeated 3 times. ChIP, chromatin immunoprecipitation; FISH, fluorescence *in situ* hybridization; BSP, bisulfite sequencing PCR; RIP, RNA immunoprecipitation; 5-Aza-dC, 5-Aza-2 deoxycytidine; NC, negative control; IC_{50}, inhibitory concentration 50%; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; WT, wild-type; KCNQ1OT1, KCNQ1 opposite strand/antisense transcript 1; DNMT1, DNA methyltransferase 1.
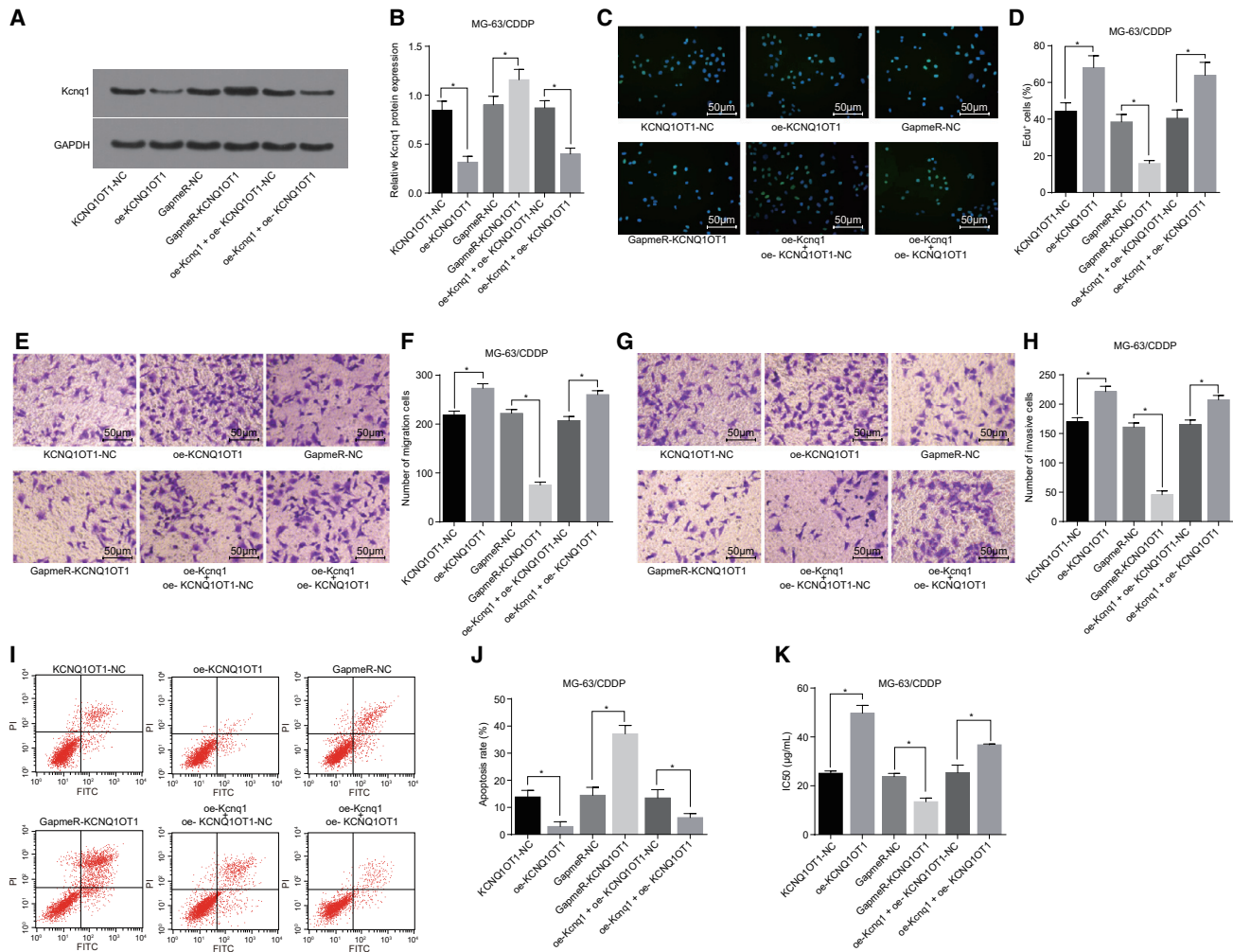
Figure 6. KCNQ1OT1 Influences Osteosarcoma CDDP-Resistant Cell Proliferation, Migration, and Invasion

MG-63/CDDP cells were treated with oe-KCNQ1OT1, GapmeR-KCNQ1OT1, or oe-Kcnq1 + oe-KCNQ1OT1, with KCNQ1OT1-NC, GapmeR-NC, and oe-Kcnq1 + oe-KCNQ1OT1-NC as the controls. (A and B) The protein expression of Kcnq1 in MG-63/CDDP cells. (C and D) The proliferation situation of MG-63/CDDP cells (200×). (E and F) The migration situation of MG-63/CDDP cells (200×). (G and H) The invasion situation of MG-63/CDDP cells (200×). (I and J) The apoptosis situation of MG-63/CDDP cells. (K) IC_{50} value of MG-63/CDDP cells. *$p < 0.05$ versus the KCNQ1OT1-NC group, the GapmeR-NC group, or the oe-Kcnq1 + oe-KCNQ1OT1-NC group. The measurement data were expressed as mean ± SD. Comparisons among multiple groups were analyzed by one-way ANOVA. The experiment was repeated 3 times. 5-Aza-dC, 5-Aza-2 deoxycytidine; NC, negative control; WST-1, water-soluble tetrazolium salt; CDDP, cisplatin; EdU, 5-Ethynyl-2′-deoxyuridine; IC_{50}, inhibitory concentration 50%; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; WT, wild-type; KCNQ1OT1, KCNQ1 opposite strand/antisense transcript 1.

primary bone cancers.[16,17] The present study focused on the role of KCNQ1OT1 in osteosarcoma. The knockdown of KCNQ1OT1 could potentially promote Kcnq1 expression by regulating DNMT1, thus contributing to the suppression of proliferation, migration, and invasion and promotion of CDDP-induced apoptosis and chemosensitivity to CDDP in CDDP-resistant osteosarcoma cells.

One of the significant findings from our study revealed a poor expression level of Kcnq1 and a high expression level of KCNQ1OT1 in osteosarcoma tissues and cells. KCNQ1OT1 was upregulated in chemo-insensitive TSCC; knockdown of KCNQ1OT1 combined with miR-211-5p suppression exerted an inhibitory effect on TSCC

cell proliferation, and KCNQ1OT1 induced chemoresistance to CDDP.[10] Moreover, the downregulation of KCNQ1OT1 has also been found to restrain chemoresistance to paclitaxel in lung adenocarcinoma.[18] Moreover, glioma malignancy was reported to be suppressed following the downregulation of KCNQ1OT1.[19] KCNQ1OT1 was upregulated, which was considered to promote cell proliferation and migration in melanoma tissues and cells.[20] Kcnq1 mutations play a role in the development of metaplasia, dysplasia, and pre-malignant adenomatous hyperplasia as well as gastric cancer.[21] A low expression of Kcnq1 has also been linked with a poor overall survival rate for patients with several kinds of cancers, including gastrointestinal cancer[22] and gastric cancer.[23]
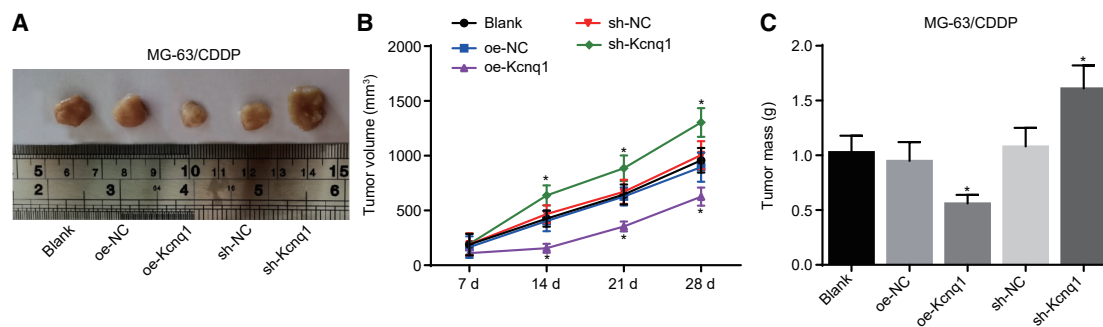
Figure 7. The Functions of Kcnq1 on Osteosarcoma Tumor Growth and Enhancing Chemosensitivity to CDDP *In Vivo*

Nude mice were injected with MG-63/CDDP cells treated with oe-Kcnq1 or sh-Kcnq1. (A) Xenograft tumor size of nude mice. (B) Xenograft tumor volume growth of nude mice. (C) Xenograft tumor mass of nude mice. *p < 0.05 versus the blank group. n = 5. The measurement data were expressed as mean ± SD. Comparisons among multiple groups were analyzed by one-way ANOVA, and comparisons between groups at different time points were processed with repeated-measures ANOVA. The experiment was repeated 3 times. CDDP, cisplatin; NC, negative control.

Subsequently, we also identified Kcnq1 as a target gene of KCNQ1OT1. Kcnq1 is well recognized in regulating the repolarization of the cardiac action potential along with water and salt transport in epithelial tissues.[24] A previous study has shown that the absence of Kcnq1 in stage II and III colon cancer might provide a prognostic biomarker for the disease recurrence.[21] In addition, Kcnq1 played a role as a tumor suppressor gene in colorectal cancer (CRC)[25] and human gastrointestinal cancers.[22] Another previous study highlighted that deficiency of KCNQ1OT1 could result in an increase in the expression of Kcnq1 in later cardiac development stages, which was featured by the increased flexibility of chromatin permitting the establishment of ectopic regulatory contacts for the Kcnq1.[26] Upregulation of Kcnq1 attenuated osteosarcoma cell proliferation, migration, and invasion, yet it promoted cell apoptosis and chemosensitivity to CDDP, which were identified with the results caused by KCNQ1OT1 knockdown.

Moreover, proliferation, migration, and invasion were restrained while cell apoptosis and chemosensitivity to CDDP were facilitated in osteosarcoma cells following the downregulation of KCNQ1OT1. The methylation level of the Kcnq1 promoter region was high, which had a negative correlation with the Kcnq1 gene levels in osteosarcoma. KCNQ1OT1 could also negatively regulate Kcnq1 expression by promoting DNMT1 expression. KCNQ1OT1 might mediate the ubiquitously imprinted gene downregulation through allele-specific methylation maintenance by interacting with the DNMT1 enrichment.[27]

The involvement of dysregulated DNMT1 is known to be involved in cancer pathogenesis.[28] In a previous xenograft tumor analysis, overexpression of miR-139-5p was suggested to reduce tumor growth in osteosarcoma *in vivo* by inhibiting DNMT1.[29] The downregulation of CXCL12 in osteosarcoma was previously illustrated to be mediated by DNMT1, and diminished levels of DNMT1 by short hairpin RNA (shRNA) or the inhibitor decitabine could induce CXCL12 restoration, which provided further protection from the migration of osteosarcoma to the lungs.[30] Radio-sensitivity of cell was also stated to be

enhanced by DNMT inhibitor by promoting apoptosis.[31] Osteosarcoma cells that had received treatment with 5-Aza-2 deoxycytidine (5-Aza-dC, a DNA methyltransferase inhibitor) presented with restored APCDD1 expression, which contributed to the inhibition of cell invasion and migration.[32] Methylation of Kcnq1 was revealed in osteosarcoma cells, which potentially occurred as a result of KCNQ1OT1-mediated DNMT1 promotion. After the demethylation of Kcnq1 following the treatment of the osteosarcoma cell with 5-Aza-dC, the elevated expression of Kcnq1 was conducive to the inhibited proliferation, migration, and invasion and the promoted chemosensitivity to CDDP and apoptosis in CDDP-resistant cell lines, while KCNQ1OT1 knockdown could exert similar effects.

In conclusion, the knockdown of lncRNA KCNQ1OT1 might inhibit the proliferation, migration, and invasion of osteosarcoma cells and promote cell apoptosis and the chemosensitivity to CDDP through the upregulation of Kcnq1 via DNMT1 (Figure S2). Therefore, lncRNA KCNQ1OT1 is a promising novel therapeutic direction for the treatment of osteosarcoma. However, further studies are required to provide a detailed understanding of the clinical translation of the KCNQ1OT1/Kcnq1/DNMT1 axis in osteosarcoma treatment. We hope this study will pave the way for developing a target-based treatment option for osteosarcoma.

MATERIALS AND METHODS
Ethical Statement
Signed informed consents were acquired from patients. This study was carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the NIH. This protocol was carried out with the approval of the ethics committee of the First Affiliated Hospital of Harbin Medical University.

Study Subjects
A total of 47 operative specimens and the corresponding normal bone tissues were obtained from patients diagnosed with osteosarcoma (mean age: 19.7 years, ranging from 7 to 42 years, including 35 males and 12 females) from June 2015 to February 2017 in the First

Affiliated Hospital of Harbin Medical University. None of the patients had received any radiotherapy, chemotherapy, or hormone drugs prior to the operation, and all patients had been diagnosed pathologically after operation. The normal bone tissues ≥5 cm from the tumor lesions were taken as the control specimens (no sarcomatous skip lesions after X-ray and MRI examinations). After the operation, a part of the above specimens was immediately preserved in liquid nitrogen at −80°C for cryopreservation, with the remainder soaked in 4% formalin, embedded with paraffin, fixed, and sliced. All the cases were morphologically observed, and the diagnosis had been carried out according to World Health Organization classification standard[33] by two or more pathology associate chief physicians. The individuals diagnosed with high, moderate, and low differentiations were 12, 16, and 19 cases, respectively. All the cases were staged according to tumor-node-migration (TNM) standard,[34] based on which there were 38 cases at stage I + II and 9 cases at stage III + IV.

Immunohistochemistry

The paraffin-embedded sections of clinical tissue specimens were dewaxed, dehydrated with gradient alcohol, and treated with methanol and 3% H_2O_2 for 20 min. Following antigen retrieval in a water bath, the sections were blocked with normal goat serum blocking reagent (C-0005, Shanghai Haoran Biological Technology, Shanghai, China) at room temperature for 20 min. With the primary antibody rabbit anti-human antibody to Kcnq1 (1:50, ab135737; Abcam, Cambridge, MA, USA) added, the sections were cultured overnight at 4°C. Subsequently, the sections were probed with the goat anti-rabbit immunoglobulin G (IgG) secondary antibody (1:1,000, ab6785; Abcam, Cambridge, MA, USA) at 37°C for 20 min.

Following an incubation with horseradish peroxidase (HRP)-labeled streptavidin protein working solution (0343-10000U, Imunbio Biotechnology, Beijing, China) at 37°C for 20 min, the sections were developed with diaminobenzidine (DAB; ST033, Whiga Biosmart, Guangzhou, Guangdong, China), followed by counter-staining with hematoxylin (PT001, Bogoo Biotechnology, Shanghai, China) for 1 min, until there was a change in color to blue using 1% ammonia. Subsequently, sections were dehydrated with gradient alcohol, cleared by xylene, and sealed with neutral resin. Finally, 5 high-power fields were randomly selected from each section with a total of 100 cells counted per field, and the images were obtained under the microscope.

Cell Culture

The normal osteoblast cell line hFOB1.19 and 5 osteosarcoma cell lines (U20S, Saos-2, HOS, TE85, and MG-63) were purchased from American Type Culture Collection cell bank (https://www.atcc.org/; ATCC, Manassas, VA, USA). The cells were exposed to 1640 culture medium containing 10% calf serum and mixed penicillin-streptomycin solution at a ratio of 1:1 with a final concentration of 100 U/mL and incubated in 5% CO_2 at 37°C. The cells were detached with 0.25% trypsin, passaged at a ratio of 1:3, and then seeded in 6-well plates at a density of 3×10^5 cells/well. When cell confluence reached 70%–80%, the cell line with the highest expression of Kcnq1 was screened out by means

of qRT-PCR. Finally, the cell line at the logarithmic growth phase with the highest expression of Kcnq1 was used for subsequent experiments.

CDDP-Resistant Cell Line Screening

Following routine resuscitation, the human osteosarcoma cell lines were cultured in RPMI 1640 complete medium containing 10% fetal bovine serum (FBS), 100 kU/L penicillin, and 100 mg/L streptomycin in a 5% CO_2 incubator at 37°C. The human osteosarcoma CDDP-resistant cell line (MG-63/CDDP) was established by continuous exposure to CDDP with a gradually increasing concentration of 1, 2, 3, 4, and 5 mg/L through intermittent administration. From the first addition of CDDP at a concentration of 1 mg/L, CDDP-free culture medium was renewed every 24 h, and the cells in a stable growth manner were passaged. After 5 cycles of the previous steps, the cells were cultured in another medium containing CDDP at different concentrations. The above processes were repeated until cells were cultured in 5 mg/L CDDP. After a total of 190 days' induction, MG-63 cells were able to grow steadily and passaged normally in the 5 mg/L CDDP culture medium, indicating that the cell line could resist 5 mg/L CDDP, which was indicative of the successful screening of the CDDP-resistant cell line.

Cell Grouping and Transfection

The osteosarcoma cells in logarithmic growth phase and their corresponding CDDP-resistant cells were seeded into 24-well plates. After the cell confluence reached 50% and a good growth manner was obtained, a total of 1 mL virus suspension of lncRNA KCNQ1OT1 and Kcnq1 or KCNQ1OT1-NC vector and Kcnq1 were added into the plate. Following a 24-h culture, the cells were exposed to fresh medium and incubated for another 48 h in a 5% CO_2 incubator at 37°C. The infection efficiency was observed under a fluorescence microscope. After lentivirus infection, the MG-63 and MG-63/CDDP cells with stable overexpression of lncRNA KCNQ1OT1 and Kcnq1 were screened with neomycin and used for the subsequent experiments. In addition, Kcnq1-silenced MG-63 and MG-63/CDDP cells were constructed with the use of shRNA lentiviral vector against Kcnq1. The construction, sequencing, virus packaging, and titer detection of each lentiviral vector were commissioned by Genechem (Shanghai Genechem, Shanghai, China). Locked nucleic acid antisense oligonucleotides (LNA-GapmeR) technology was used for the knockdown of the expression of lncRNA KCNQ1OT1.

MG-63 cells were then assigned into 11 groups: blank (without any transfection), oe-NC (transfected with overexpressed NC vector), oe-Kcnq1 (transfected with overexpressed Kcnq1 vector), sh-NC (transfected with silenced NC vector), sh-Kcnq1 (transfected with silenced Kcnq1 vector), KCNQ1OT1-NC (transfected with KCNQ1OT1-NC vector), oe-KCNQ1OT1 (transfected with overexpressed KCNQ1OT1 vector), GapmeR-NC (transfected with KCNQ1OT1-silenced GapmeR-NC), GapmeR-KCNQ1OT1 (transfected with GapmeR-KCNQ1OT1 against KCNQ1OT1), oe-Kcnq1 + oe-KCNQ1OT1-NC (co-transfected with oe-Kcnq1 and oe-KCNQ1OT1-NC vectors), and oe-Kcnq1 + oe-KCNQ1OT1 (co-transfected with oe-Kcnq1 and oe-KCNQ1OT1 vectors). The MG-63/CDDP cells were also grouped in

Table 1. Primer Sequences for qRT-PCR

Gene	Forward Sequence	Reverse Sequence
BSP-Kcnq1	5′-TTTTATTGGGAGGTATTTGATAGTG-3′	5′-TCCTAAATAAAAATATACTAACCCC-3′
MSP-Kcnq1-M	5′-ATTAGGTTTAGATTTCGGTTGTGTC-3′	5′-AATAAAAATATACTAACCCCGCGAT-3′
MSP-Kcnq1-U	5′-AAATTAGGTTTAGATTTTGGTTGTGTT-3′	5′-AATAAAAATATACTAACCCCACAAT-3′
KCNQ1OT1	5′-CCTCCCTCACTGAGCTTTGG-3′	5′-GTGCGGACCCTATACGGAAG-3′
Kcnq1	5′-GGCAGGCCCTCCTCGTTATG-3′	5′-CGCGTGCTGTAGATGGAGAC-3′
GAPDH	5′-GCTGCTGAGTATGTCGTGGAGT-3′	5′-AGTCTTCTGGGTGGCAGTGAT-3′

BSP, bisulfite sequencing PCR; MSP, methylation-specific PCR; KCNQ1OT1, KCNQ1 opposite strand/antisense transcript 1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; M, methylation; U, unmethylation.

the same way mentioned above. In addition, DNA methylation transferase inhibitor 5-Aza-dC was added to MG-63/CDDP cells at a concentration of 2.5 μM, according to a previous study;[35] thus, the blank + 5-Aza-dC (MG-63/CDDP cells added with 5-Aza-dC) group was set with the blank + DMSO group as the control. The experiment was conducted in triplicates.

RNA Isolation and Quantitation

The total RNA was extracted according to the instructions provided on the TRIZOL kit (15596-018, Beijing Solarbio Science & Technology, Beijing, China), and the RNA concentration was determined. The primers (Table 1) used in this study were synthesized by Takara Biotechnology (Dalian, Liaoning, China). According to the instructions of the cDNA RT kit (K1622, Beijing Reanta Biotechnology, Beijing, China), the reversely transcribed cDNA was diluted to 50 ng/μL for the following qPCR. The detection was then carried out on the qRT-PCR instrument (ViiA 7, Daan Gene, Sun Yat-sen University, Guangzhou, Guangdong, China); 2 μg total cDNA was used as the template. Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was used as the internal reference. The relative transcription level of the target gene was calculated by the $2^{-\Delta\Delta Ct}$ method,[36] with ΔΔC obtained using the following formula: $\Delta\Delta Ct = \Delta Ct_{experimental\ group} - \Delta Ct_{blank\ group}$, $\Delta Ct = Ct_{target\ gene} - Ct_{internal\ reference}$.

Western Blot Analysis

The total protein of tissues or cells was extracted with high efficiency radioimmunoprecipitation assay (RIPA) lysis buffer (R0010, Beijing Solarbio Science & Technology, Beijing, China), in strict accordance with the instructions. The bicinchoninic acid (BCA) kit (20201ES76, Yeasen Biotechnology, Shanghai, China) was used to determine the protein concentration of each specimen. The quantification was carried out according to the different concentrations. Following separation by PAGE, the proteins were transferred onto the polyvinylidene fluoride (PVDF) membrane by the wet transfer method and blocked in 5% BSA for 1 h at room temperature.

Next, the membrane was incubated with diluted primary antibodies to Kcnq1 (ab135737, 1:300) and rabbit anti-human antibody to DNMT1 (ab19905, 1:1,000) in a shaking table at 4°C overnight. The following day, the membrane was probed with diluted HRP-

labeled goat anti-rabbit antibody to IgG (ab205718, 1:20,000) for 1 h. All antibodies were purchased from Abcam (Cambridge, MA, USA). Next, the membrane was washed 3 times using Tris-buffered saline with Tween (each for 5 min), and the images were developed using developing liquid. The ImageJ 1.48u software (NIH, Bethesda, MA, USA) was used for protein quantification analysis based on the ratio of the gray value of target protein band to the GAPDH band.

WST-1 Experiment

The cells (2×10^5 cell/mL) in logarithmic growth phase were seeded in 96-well plates (0.1 mL each well) and cultured for 6 h. The cells in the experimental groups were added with CDDP culture medium at different concentrations (0, 6.25, 12.5, 25, 50, and 100 μg/mL), while the cells in the blank group were cultured with equal volume of culture medium. Cells in all groups were cultured in an incubator with saturated humidity containing 5% CO_2 at 37°C, with more than 3 parallel wells set.

After administration, cell proliferation was detected in accordance with the WST-1 kit (Roche, Penzberg, Upper Bavaria, Germany). Following the removal of the original medium in each well, the cells were added with 100 μL DMEM and 10 μL WST-1, and incubation was carried out in an incubator at 37°C. After 1 h of reaction, the absorbance value (A) at a wavelength of 450 nm was read using the microplate reader. The growth inhibition rate was equal to the following: $[(1 - A450_{the\ experimental\ groups})/A450_{the\ blank\ group}] \times 100\%$. IC_{50}, which refers to the drug concentration when 50% of cells survived, was calculated by EXCE software FORECAST function according to the least square method.

EdU Assay

After transfection for 48 h, cells were cultured with EdU medium (100 μL/well) for 2 h. Subsequently, the cells in each well were fixed with 100 μL cell fixative for 30 min, reacted with 2 mg/mL glycine for 5 min, and cultured with 100 μL PBS containing 0.5% Triton X-100 for 10 min. Next, the cells were reacted with 1× Apollo staining reaction solution under dark conditions for 30 min and added with a penetrating agent and with 100 μL 1× Hoechst 33342 reaction solution under dark conditions for 30 min on the shaking table to facilitate de-coloration. A total of 6–10 visual fields were randomly selected

from each well, observed, and photographed under the fluorescence microscope. The number of EdU-labeled cells was recorded, among which a red-stained nucleus indicated positively labeled cells. EdU-labeled rate was calculated as follows: EdU-labeled rate (%) = the number of positive cells/(the number of positive cells + the number of negative cells) × 100%.

Flow Cytometry

Following transfection for 48 h, the Annexin V-fluorescein isothiocyanate (FITC) and propidium iodide (PI) double staining kit (556547, Shanghai Shuojia Biotechnology, Shanghai, China) was used for the detection of apoptosis of osteosarcoma cells. The 10× binding buffer was diluted into 1× binding buffer with deionized water. Following centrifugation at 716 × g for 5 min at room temperature, the cells were resuspended with pre-chilled 1× PBS and centrifuged again at 716 × g for 5–10 min. Subsequently, cells were resuspended with 300 μL 1× binding buffer and incubated with 5 μL Annexin V-FITC at room temperature for 15 min under dark conditions. Prior to cell apoptosis detection on the flow cytometer (Cube6, Partec, Munster, Germany), the cells were added with 5 μL PI for a 5-min ice bath under dark conditions, and the FITC was detected at 530 nm and PI was detected at >575 nm with an excitation wavelength of 480 nm.

Transwell Assay

The precooled Matrigel (40111ES08, Shanghai Yeasen Biotechnology, Shanghai, China) diluted with serum-free DMEM at a ratio of 1:2 was spread in the apical chamber (3413, Beijing Unique Biotechnology, Beijing, China) and placed in a 37°C incubator. Following a 4- to 5-h culture until the Matrigel was solidified, the transfected cells were dispersed into the cell suspension (1 × 10^6 cells/mL) with 100 μL serum-free medium. The cell suspension was then seeded, and the basolateral chamber was added with 500 μL DMEM containing 20% FBS. Three parallel wells were set in each group. After a 24-h culture at 37°C with 5% CO$_2$, the Transwell chambers were fixed with 4% paraformaldehyde and stained with 0.1% crystal violet for 5 min. Then, the cells on the surface were wiped out with cotton ball. Finally, the invasive cells were observed under the fluorescence microscope (TE2000, Nikon, Shanghai, China), and 5 fields were randomly selected and the images were obtained. The number of cells passing through the Transwell chamber was counted in each group to obtain the mean value.

FISH

KCNQ1OT1 subcellular localization information was obtained using a bioinformatics tool (http://lncatlas.crg.eu/). The subcellular localization of KCNQ1OT1 in osteosarcoma cells was identified by the FISH method. The following specific method was processed according to the instructions of Ribo lncRNA FISH probe Mix (Red) (BiboBio, Guangzhou, Guangdong, China). The cover slides were placed in the 6-well culture plate, and the osteosarcoma cells were seeded into the 24-well culture plate for 1-day culture until the cell confluence reached about 80%. Next, the cover slides were fixed in 1 mL 4% paraformaldehyde. Following treatment with 2 μg/mL

protease K, glycine, and acetylation reagents, the cover slides were added with 250 μL prehybridization solution for incubation at 42°C for 1 h. Subsequently, 250 μL hybridization solution-containing probe (300 ng/mL) was added to the cover slides for hybridization at 42°C overnight. After the cover slides were rinsed 3 times with PBS with Tween 20 (PBST), the PBST-diluted DAPI (1:800) staining solution was added to stain the nucleus in the 24-well plate for 5 min. Finally, the cover slides were sealed with anti-fluorescence quenching agent, and 5 different visual fields were selected, observed, and photographed under the fluorescence microscope (Olympus, Tokyo, Japan).

MSP

The genomic DNA in osteosarcoma tissues and cells was extracted and subjected to bisulfite modification. Next, methylation of the modified DNA was detected by the MSP method. A part of modified total DNA was added with Kcnq1 gene methylation and unmethylation primers (for the rich CpG island) to carry out PCR amplification (Table 1) (GenBank: ABl62145). The reaction products were subjected to agarose gel electrophoresis and gel electrophoresis imaging, and the captured images were analyzed by the image analysis system.

BSP

The DNA of osteosarcoma tissues and cells was extracted in line with the instructions of the Dneasy Blood & Tissue Kit, and the DNA purity and content were detected with the UV spectrophotometer. A total of 2 μg DNA was extracted and processed with hydrosulfite modification according to the EpiTect Bisulfite Handbook. The hydrosulfite-modified DNA was used as a template and PCR amplification was conducted. A total of 5 μL PCR amplification products was detected by 2.5% agarose gel electrophoresis, the results of which were observed under the Gel Imager. An additional 20 μL PCR products was sequenced by Langkang (Shanghai Langkang, Shanghai, China) after being purified with QIAquick purification kit, and the CpG viewer software was used for result analysis (Table 1).

ChIP

A ChIP kit (Millipore, Billerica, MA, USA) was applied for the analysis of the enrichment status of DNMT1 in the Kcnq1 gene promoter region. Until the cell confluence reached 70%–80%, osteosarcoma cells were fixed with 1% formaldehyde for 10 min for the crosslinking of DNA and protein in the cells. Next, the ultrasonic breaker was set to 10 s/ultrasonic cycle with 10-s intervals, with 15 cycles to break the chromatin, followed by centrifugation at 30,237 × g at 4°C (part of the DNA fragments was taken as input). The supernatant was collected into 3 tubes, and incubation was carried out with NC antibody, normal mouse antibody to IgG and target protein-specific antibody, and rabbit antibody to DNMT1 (ab13537, Abcam, Cambridge, MA, USA) at 4°C overnight, respectively. The endogenous DNA-protein complex was precipitated using Protein Agarose or Sepharose, and centrifugation was carried out. The non-specific complex was washed off. The DNA was de-crosslinked at 65°C overnight and purified by phenol or chloroform to retrieve the DNA fragment. The input was used as an internal reference, and the specific primers of

the Kcnq1 gene promoter region are shown in Table 1. The binding ability of DNMT1 to the Kcnq1 promoter region was examined.

RIP

The experiment was processed based on the Magna RIP RNA-Binding Protein Immunoprecipitation kit (Millipore, Billerica, MA, USA) instructions. Osteosarcoma cells were lysed with 100 μL lysis buffer containing protease inhibitor and ribonuclease inhibitor for 30 min on ice, after which centrifugation was carried out at $257,643 \times g$ for 5 min at 4°C. Afterward, the supernatant was used as an input positive control. A total of 1 μg normal human antibody to IgG and protein-specific antibody, rabbit antibody to DNMT1 (ab13537, Abcam, Cambridge, MA, USA), and 50 μL protein A/G-beads were added to the remaining supernatant. The sample was rotated at 4°C for incubation overnight. Next, the sample was centrifuged at $1,610 \times g$ for 5 min at 4°C. Protein A/G-bead precipitate was washed 3–4 times with 1 mL lysis buffer, followed by a centrifugation at $179 \times g$ for 1 min at 4°C between each wash. Subsequently, the sample was added with 15 μL $2\times$ SDS loading buffer and heated for 10 min. The relevant RNA was obtained from the precipitation after isolation and purification by conventional TRIZOL method, and the interaction between DNMT1 and KCNQ1OT1 was verified by qRT-PCR with KCNQ1OT1-specific primers (Table 1).

RNA Pull-Down

Osteosarcoma cells were transfected with wild-type (WT)-biotinylated KCNQ1OT1 (50 nM) and mutant (mut)-biotinylated KCNQ1OT1 (50 nM). Following a 48-h transfection, the cells were incubated in specific cell lysis buffer (Ambion, Austin, TX, USA) for 10 min. Subsequently, 50 mL sample cell lysate was sub-packaged. The remaining lysate was incubated with M-280 streptavidin magnetic beads (Sigma, St. Louis, MO, USA), which was pre-coated with RNase-free and yeast tRNA (Sigma, St. Louis, MO, USA). After incubation for 3 h at 4°C, the specimen was washed twice with cold lysis buffer, 3 times with low-salt buffer, and one time with high-salt buffer. The total protein was extracted with high-efficiency RIPA lysis buffer. Finally, the DNMT1 expression was determined by means of western blot analysis.

Dual Luciferase Reporter Gene Assay

Dual luciferase reporter gene assay was used for the verification of the target relationship between Kcnq1 and lncRNA KCNQ1OT1. The Kcnq1 gene promoter region was cloned onto the luciferase reporter gene carrier pGL3-basic (Promega, Madison, WI, USA), named KCNQ1 prom WT, based on the binding sequence of the Kcnq1 mRNA promoter region to lncRNA KCNQ1OT1. KCNQ1 prom WT plasmid was co-transfected to MG-63 cells with oe-KCNQ1OT1/oe-DNMT1, respectively, or MG-63 cells were simultaneously treated with 5 μmol/L 5-Aza-dC (DNMT1 methylation enzyme inhibitor). The cells were assigned into the oe-NC + KCNQ1 prom WT, oe-NC + 5-Aza-dC + KCNQ1 prom WT, oe-KCNQ1OT1 + KCNQ1 prom WT, oe-KCNQ1OT1 + 5-Aza-dC + KCNQ1 prom WT, oe-DNMT1 + KCNQ1 prom WT, and oe-KCNQ1OT1 + oe-DNMT1 + KCNQ1 prom WT groups. All the above groups were treated with renilla luciferase vector as an internal reference.

After transfection for 48 h, the cells were lysed and centrifuged at $25,764 \times g$ for 1 min, after which the supernatant was collected. Next, the luciferase intensity was detected by a Dual-Luciferase Reporter Assay System (E1910, Promega, Madison, WI, USA). A total of 100 μL firefly luciferase working solution and 100 μL renilla luciferase working solution were added to each cell sample to detect the activity of firefly luciferase and renilla luciferase, respectively. The ratio of the activity of firefly luciferase to that of renilla luciferase was used as the relative luciferase activity.

Xenograft Tumor in Nude Mice

BALB/c nude mice (no sex limitation; 5–6 weeks) were raised in an environment with constant temperature (25°C–27°C) and constant humidity (45%–50%). The mice were randomly assigned into 5 groups with 5 mice in each group. MG-63/CDDP cells transfected with sh-Kcnq1, oe-Kcnq1, or their controls (sh-NC and oe-NC) were cultured. Following the stable transfection of the cell lines, the cells were resuspended to adjust the cell concentration into 1×10^7 cells/mL. Then 20 μL cell suspension was subcutaneously inoculated into the thighs of nude mice. When the volume of the xenograft tumor reached 50 mm^3, nude mice with the same tumor size in each group were selected to treat with intravenous injection of 5.0 mg/kg CDDP every day. After 6 weeks, the nude mice were euthanized by CO_2. The tumor was removed, the weight and size of which were measured. The tumor volume was recorded to plot a growth curve according to the following formula: V (mm^3) = (a × b^2)/2 (a indicates the maximum diameter and b indicates the minimum diameter).[37]

Statistical Analysis

All data were processed using SPSS 21.0 statistical software (IBM, Armonk, NY, USA). Measurement data were expressed as mean ± SD, and enumeration data were presented by the number of cases or percentage. The comparison between cancer tissues and adjacent tissues was performed by paired t test. The comparison between two groups was performed by independent sample t test, and the comparison among multiple groups was analyzed by the one-way ANOVA. Comparisons among multiple groups at different time points were analyzed by repeated-measures ANOVA. A p value less than 0.05 was statistically significant.

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at https://doi.org/10.1016/j.omtn.2019.06.010.

AUTHOR CONTRIBUTIONS

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Supplemental Information

Knockdown of KCNQ1OT1 Suppresses Cell Invasion
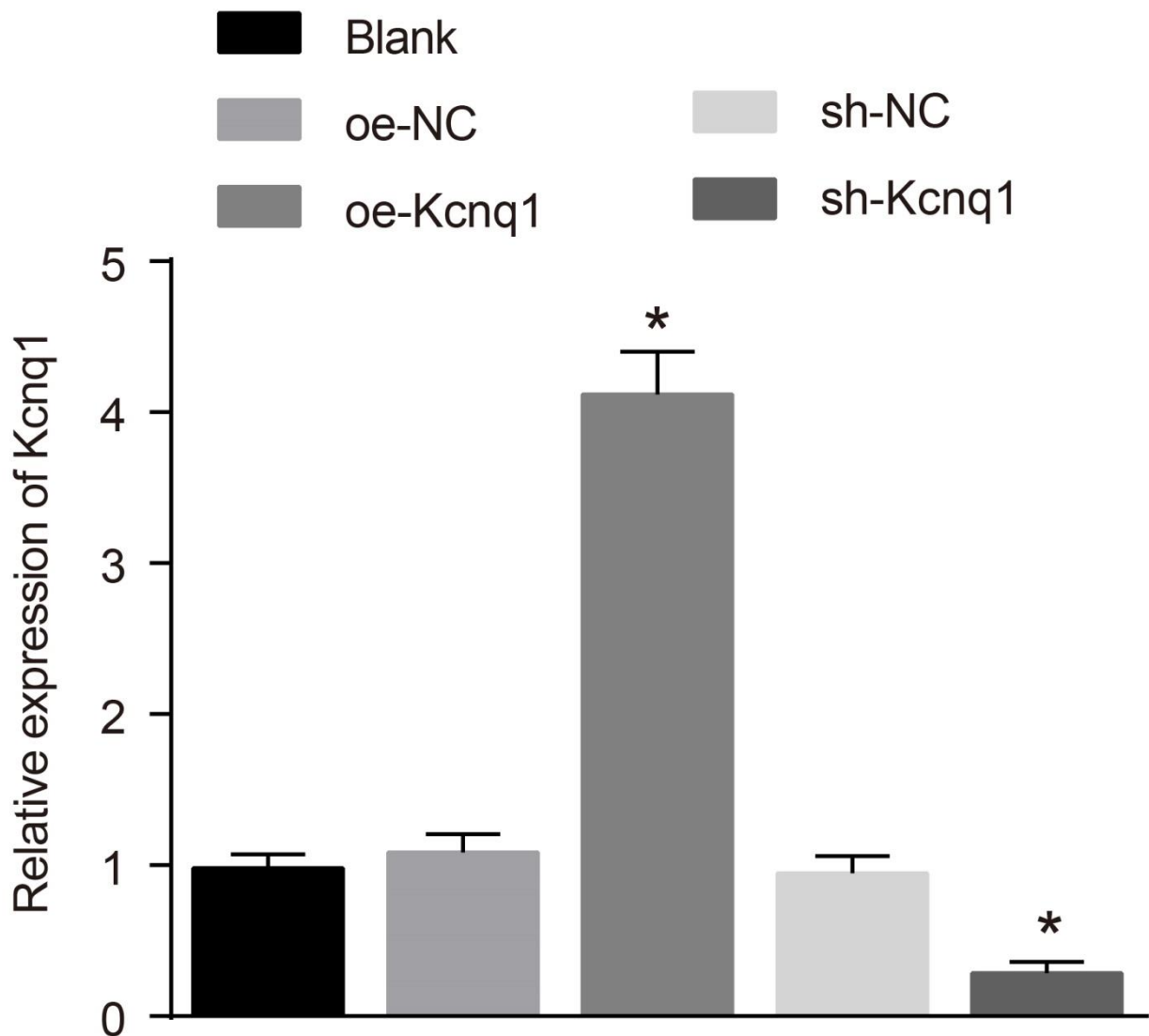
and Sensitizes Osteosarcoma Cells to CDDP

by Upregulating DNMT1-Mediated Kcnq1 Expression

Xu Qi, Xiao-Jun Yu, Xu-Ming Wang, Tie-Nan Song, Jie Zhang, Xin-Zhen Guo, Guo-Jun Li, and Ming Shao
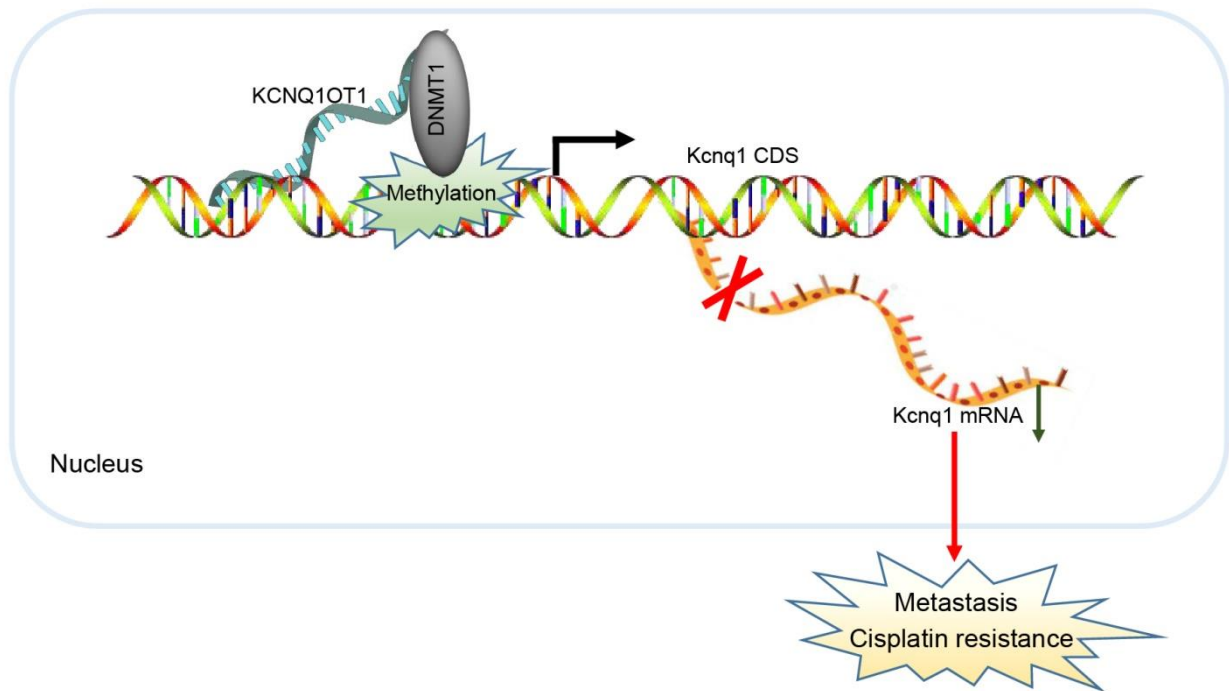
SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. The mRNA expression of Kcnq1 following oe-Kcnq1 and sh-Kcnq1 treatments. *, $p < 0.05$ *vs.* the oe-NC group or the sh-NC group. The measurement data were expressed by mean ± standard deviation. Comparisons among multiple groups were analyzed by one-way analysis of variance. The experiment was repeated 3 times.

Supplemental Figure 2. Molecular mechanism of LncRNA mediated DNMT1 regulation of Kcnq1 expression on osteosarcoma cell invasion and CDDP chemosensitivity. In osteosarcoma, KCNQ1OT1 shows abundant expression while Kcnq1 presents poor expression. Down-regulation of KCNQ1OT1 is considered to suppress Kcnq1 methylation and promote the level of Kcnq1 gene, thus inhibiting osteosarcoma cell proliferation, migration, invasion, and promoting CDDP chemosensitivity and apoptosis. CDDP, cisplatin; KCNQ1OT1, KCNQ1 opposite strand/antisense transcript 1; DNMT1, DNA methyltransferase 1.

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