

# KDM5B expression in cisplatin resistant neuroblastoma cell lines

MARIE BELHAJOVA, NATALIA PODHORSKA, ALES VICHA and TOMAS ECKSCHLAGER

Department of Pediatric Hematology and Oncology, 2nd Faculty of Medicine,  
Charles University and Motol University Hospital, 15006 Prague, Czech Republic

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**Abstract.** Chemoresistance is a major problem in successful cancer therapy. Lysine-specific demethylase 5B (KDM5B), is a member of the KDM5 family of histone demethylases, whose dysregulation has been observed in numerous types of cancer and plays a role in drug tolerance. The present study examined KDM5B expression in high risk neuroblastoma cell lines. Its level was markedly reduced in cisplatin-resistant cells, UKF-NB-4<sup>CDDP</sup>, compared with parental sensitive cells UKF-NB-4. Moreover, *KDM5B*-silencing did not affect either viability nor the response to CDDP in resistant cells, and led to increase of proliferation and migration in CDDP resistant cells but not in sensitive ones. Compliant with these results, short interfering *KDM5B* transfection resulted in increased S phase in resistant cells. Overall, these findings suggested that *KDM5B* may be involved in the survival mechanisms of neuroblastoma cells, which makes *KDM5B* a promising factor for the prediction of sensitivity to CDDP that should therefore be considered for future research.

## Introduction

Epigenetic mechanisms are essential for the normal development and maintenance of cell and tissue-specific gene expression patterns in mammals (1). DNA methylation, histone modification, nucleosome remodeling, and RNA-mediated targeting regulate numerous biological processes that are fundamental to the genesis of cancer. Disruption of epigenetic processes can lead to altered gene function that can induce malignant cell transformation (2). Histone methylation plays an important role in the regulation of genes expression, its dysregulation has been observed in various cancers (3-7). Regulation of methylation is mediated by two types of enzymes-histone methyltransferases, which add methyl groups to arginine

and lysine residues, and histone demethylases (lysine demethylase-KDM), which remove methyl groups (3). The KDM5 family of lysine demethylases known also as Jumonji C (JmjC) or JARID1 that have four members (KDM5A-D), demethylate di- and tri-methylated H3K4 (8). These enzymes are 2-oxoglutarate-dependent dioxygenases that require for their function Fe<sup>2+</sup> and oxygen in order to undergo the hydroxylation necessary to remove the methyl groups (8). *KDM5B*, also known as JARID1B, has been found to associate with transcription factors PAX9, FOXC2 and FOXG1. It can also repress or promote activation of target genes by interacting with nuclear hormonal receptors (9). The levels of enzyme modifying histones *KDM5B* determine the hyperactivation of PI3K/AKT signaling in prostate cancer (10). Dysregulation of *KDM5B* has been identified in numerous cancers e.g. laryngeal squamous cell carcinoma, bladder, breast cancer, and is closely correlated with tumorigenesis, metastasis, and worse survival in humans (5-7). Therefore, this enzyme might be a potential promising target for novel cancer diagnostic and/ or treatment.

*KDM5B* has been described as important for the formation and maintenance of cancer stem cells in neuroblastoma cell lines (NBL) (11). In addition, its overexpression was a marker of shorter relapse-free survival in patients with NBL (11). NBL is a malignant embryonal tumor in children, emerging from the peripheral nervous system. The biology of NBL is heterogeneous; small groups of NBL regress spontaneously, while numerous cases have aggressive behavior. For high-risk neuroblastoma (HR-NBL) is characteristic development of chemoresistance (12). Patients suffering from HR-NBL have a 5-year overall survival rate of ~40% despite all intensive multimodal therapies. To date, there are no salvage treatment regimens known to be curative (12,13). Knowledge of MYCN properties is limited because its expression is in physiological conditions limited to the early stages of embryonic development (14). N-myc protein interacts with Max and its high levels, which occurs in MYCN amplified NBL, lead to a large number of transcription-activating complexes (15). MYCN overexpression induces proliferation and suppresses apoptosis and differentiation in NBL cells (16). Several studies proved that MYCN silencing in MYCN amplified NBL cells suppressed growth and induced apoptosis and differentiation e.g. (14,16,17). Its expression was higher in MYCN amplified NBL cell lines than in MYCN-non-amplified NBL cells (11).

MYCN amplification correlates with poor outcome of NBL patients. Examination of MYCN amplification is part of diagnostic scheme in NBL. MYCN is MYC family of transcription

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*Correspondence to:* Professor Tomas Eckschlagel, Department of Pediatric Hematology and Oncology, 2nd Faculty of Medicine, Charles University and Motol University Hospital, V Úvalu 84, 15006 Prague 5, Czech Republic  
E-mail: tomas.Eckschlagel@lfmotol.cuni.cz

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factors member. Those transcription factors are regulators of cellular proliferation, differentiation and survival (12,13).

The aim of this study is to investigate the importance of KDM5 expression for the growth of NBL cells and their chemoresistance to cisplatin [CDDP abbreviation of cis-diaminedichloroplatinum (II)].

## Materials and methods

**Cell culture and chemicals.** Human HR-NBL cell lines UKF-NB-4, UKF-NB-4<sup>CDDP</sup>, SK-N-AS, SK-N-AS<sup>CDDP</sup>, UKF-NB-3 and UKF-NB-3<sup>CDDP</sup> were donated by prof. J. Cinatl, Dr. Sc. From Goethe University in Frankfurt am Main. Cells were grown in Iscove's Modified Dulbecco's medium (IMDM) supplemented with 10% (v/v) fetal bovine serum (both Thermo Fisher Scientific) and incubated at 37°C in 5% CO<sub>2</sub>. For experiments, 8x10<sup>5</sup> cells were seeded in 22,1 cm<sup>2</sup> dishes and after 24 h treated with cisplatin (Ebewe) in final concentration 20 µM for 48 h. Both cell lines amplified MYCN gene as we proved by FISH (data not shown).

**Assessment of cisplatin cytotoxicity.** To evaluate CDDP cytotoxicity, MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay was performed. 10<sup>4</sup> cells/well were seeded in 96-well cell culture plate and cells were treated with CDDP at final concentration 0.6-300 µM for 48 h. Subsequently, MTT solution (2 mg/ml in PBS) (Fluka) was added and the plate was placed in an incubator for 2 h. Cells were then lysed in solution of 20% of SDS (Invitrogen) containing 50% *N,N*-dimethylformamide (Sigma-Aldrich), pH 4.5, and the absorbance at 570 nm was measured by multiwell ELISA reader Versamax (Molecular Devices). The optical density of the medium was read as background and the optical density value of the live control cells was taken as 100%. The values of IC<sub>50</sub> were determined using at least 3 independent measurements by SOFTmaxPro software.

**Transfection.** NB cells were transfected with a smart pool siRNA to KDM5B ON-TARGETplus Human KDM5B siRNA, cat. No. L-009899-00-0020 (<https://horizondiscovery.com/en/search?searchterm=L-009899-00-0020>) and Lincode non-targeting siRNA Lincode Non-targeting siRNA #1, cat. No. D-001320-01-20 (<https://horizondiscovery.com/en/search?searchterm=D-001320-01-20>) using Dharmafect transfection reagent (all purchased from Dharmacon) according to the manufacturer's instructions. The siRNA concentration was 25 nM.

**RNA isolation and quantitative RT-PCR.** RNA was isolated using PureLink RNA Mini Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. Quantity and quality were verified using the NanoDrop One spectrophotometer (Thermo Fisher Scientific). Reverse transcription was performed using gb Reverse Transcription Kit (Generi Biotech) and 1,000 ng of RNA was used for complementary DNA synthesis. Primers and probes hKDM5B\_Q1 and POLR2A that was used as an endogenous control (18), were designed and produced by Generi Biotech. Custom oligo synthesis, cat. No. 1000-020 for gene: KDM5B; Gene ID: 10765 POLR2A; Gene ID: 5430 (<https://www.generi-biotech.com/products/custom-oligo-synthesis/>). We used POLR2A

as an internal standard because it is homogeneously and uniformly expressed in NBL cells (18). It is also used by other groups studying NBL (19,20). The quantification of gene expression was performed using QuantStudio 3 Real-Time PCR System (Thermo Fisher Scientific) in triplicate. The temperature profile was: 95°C for 3 min, 50 cycles of 95°C for 10 sec, 60°C 20 sec. Fold change values were determined using REST 2009 software.

**Western blot analysis.** Proteins were extracted in RIPA Buffer supplemented with Complete protease inhibitor cocktail (Roche) and their concentration was measured by DC protein assay (Bio-Rad Laboratories). Samples (40 µg) were resolved on SDS polyacrylamide gels and blotted on nitrocellulose membranes (Bio-Rad). Primary antibody JARID1B Rabbit mAb (Cell Signaling Technology) was diluted 1:1,000, β-actin Mouse mAb (Sigma-Aldrich) diluted 1:3,000 was used as a loading control. Secondary antibodies Europium conjugated anti-IgG (Molecular Devices) were diluted 1:5,000. Membranes were visualized by SpectraMax i3x Multi-Mode Microplate Reader (Molecular Devices). ImageJ 1.52a software was employed for the analysis.

**Cell viability assay.** Cells were seeded in 24-well cell culture plate at a density of 4x10<sup>4</sup> cells/well and incubated with PrestoBlue Cell Viability Reagent (Thermo Fisher Scientific) for 30 min at 37°C. The fluorescence was measured using an excitation wavelength of 560 nm and emission of 590 nm by SpectraMax i3x Multi-Mode Microplate Reader (Molecular Devices). Each sample was analyzed in triplicate.

**Cell proliferation.** Cells after transfection were seeded into 16-well E-plates for impedance-based detection (ACEA Bioscience Inc) at density of 10<sup>4</sup> cells per well. The xCELLigence RTCA DP Instrument (ACEA Bioscience Inc) placed in a humidified incubator at 37°C and 5% CO<sub>2</sub> was used for real-time monitoring of cell proliferation. The cell index was monitored every 30 min for 85 h and data were recorded by the supplied RTCA software. Each sample was analyzed in triplicate.

**Determination of histone H3K4 methylation status and KDM5B level.** Flow cytometry was used for the detection of H3K4 trimethylation and expression of KDM5B on protein level. Cells after treatment and/or transfection were washed with cold PBS (Thermo Fisher Scientific), trypsinized (trypsin-Thermo Fisher Scientific) and collected by centrifugation. Pellets of cells were washed with PBS and fixed in 3.6% paraformaldehyde for 15 min at room temperature. Cell pellets were then washed with PBS and permeabilized by 90% methanol for 1 h at -20°C. Pellets were subsequently washed 3 times with 0.5% bovine serum albumin (BSA-Roth) in PBS and were resuspended in primary antibody JARID1B Rabbit mAb diluted 1:1,000 (Cell Signaling Technology) or Anti-trimethyl-Histone H3 (Lys4) Rabbit (EMD Millipore Corp.) at dilution 1:400 and incubated for 1 h at laboratory temperature. Cells were then washed with 0.5% BSA, resuspended in fluorochrome-conjugated secondary antibody Anti-Rabbit IgG (H+L) Alexa Fluor® 647 Conjugate (Thermo Fisher Scientific) diluted 1:500 and incubated for 30 min at room temperature in dark. Washed and re-suspended cells were

measured using a BD FACSCelesta (BD Bioscience), and data were analyzed by Flowlogic software (Inivai Technologies).

**Cell cycle analysis.** Cells after treatment and/or transfection were washed with cold PBS, trypsinized and collected by centrifugation. Pellets of cells were washed with PBS and fixed in 3.6% paraformaldehyde for 10 min at room temperature. Cell pellets were then washed with PBS and permeabilized by 90% methanol for 1 h at  $-20^{\circ}\text{C}$ . Pellets were washed with PBS, resuspended in 500  $\mu\text{l}$  PBS and one drop of FxCycle™ Violet Ready Flow™ Reagent (Thermo Fisher Scientific) was added and after 30 min incubation were cells measured using a BD FACSCelesta (BD Bioscience), and data were analyzed by Flowlogic software (Inivai Technologies).

**Wound healing assay.** Neuroblastoma cells were seeded in 9.2  $\text{cm}^2$  dish in number  $1.6 \times 10^5$  cells/ml of sensitive cells and  $2.2 \times 10^5$  cells/ml of resistant cells, that allowed to reach 70% confluence for 24 h at  $37^{\circ}\text{C}$  in 5%  $\text{CO}_2$  and then transfected with siRNA to KDM5B and Lincode non-targeting siRNA. 48 h after transfection was drawn the line across the dish's surface using a 1,000  $\mu\text{l}$  sterile plastic tip, at that time the confluence was more than 80%. After wounding, cells were grown in Iscove's Modified Dulbecco's medium (IMDM) with 5% (v/v) FBS (both Thermo Fisher Scientific) and incubated at  $37^{\circ}\text{C}$  in 5%  $\text{CO}_2$ . For scratch assay, 80-90% confluence is recommended so that the cells do not overgrow (21,22). Pictures were captured at the same field immediately, 24 and 48 h after the wounding by microscope Olympus IX71 (Olympus) and ImageJ 1.52a software was employed for the analysis.

**Statistical analysis.** All experiments were independently repeated at least three times and data are shown as averages  $\pm$  standard error. One-way Anova with post-hoc Tukey HSD and two-way ANOVA followed by Bonferroni test ([https://astatsa.com/OneWay\\_Anova\\_with\\_TukeyHSD/](https://astatsa.com/OneWay_Anova_with_TukeyHSD/)) were utilized when comparing the situations. Results from RT-qPCR were statistically compared using REST 2009 software (23). Significances ( $P < 0.05$  was considered as significant) of the statistical analyses are shown in individual Figures and described in their legends.

## Results

**KDM5B is downregulated in resistant neuroblastoma cell line.** UKF-NB-4<sup>CDDP</sup> resulting from long-term cultivation with an increasing dose of CDDP was used as a model of drug resistance (24,25). We used this wide concentration range only to determine  $\text{IC}_{50}$  using MTT test to demonstrate lower sensitivity in the cell line with experimentally induced chemoresistance (UKF-NB-4<sup>CDDP</sup>) compared to sensitive cells (UKF-NB-4). We used only one concentration (20  $\mu\text{M}$ ) in further experiments. This cell line has  $\sim 4$  times higher  $\text{IC}_{50}$  compared to the parental line UKF-NB-4 (Fig. 1A). We examined the level of KDM5B mRNA and protein in both cell lines and the expression of this gene in UKF-NB-4<sup>CDDP</sup> and in both lines after incubation with cisplatin was related to the expression in UKF-NB-4 control. QRT-PCR results showed that KDM5B expression was noticeably lower in resistant cell line ( $P < 0.01$ ). The same result was observed after incubation of these cells

with CDDP; however, this compound did not further alter expression in resistant cell line (Fig. 1B). A decrease in the level of KDM5B expression was also observed in UKF-NB-4<sup>CDDP</sup> at the protein level (Fig. 1C, D). Furthermore, we observed the same results in another NBL cell line UKF-NB-3, where UKF-NB-3<sup>CDDP</sup> had lower levels of KDM5B mRNA ( $P < 0.05$ ) and protein. CDDP did not modulate KDM5B expression (Fig. S1). In SK-N-AS KDM5B level was decreased by 48 h incubation with CDDP. In SK-N-AS<sup>CDDP</sup>, KDM5B was not modulated by cisplatin and there was no significant difference between sensitive SK-N-AS and resistant SK-N-AS<sup>CDDP</sup> (Fig. S2). UKF-NB-4 and UKF-NB-3 cell lines have MYCN amplification, while SK-N-AS has no MYCN amplification. For further experiments, we selected UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cell lines.

**KDM5B knockdown reduced KDM5B expression and upregulated histone H3K4 trimethylation in neuroblastoma cells.** UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cells were transfected with KDM5B siRNA for 48 h and transfection resulted in a significant suppression of KDM5B level compared to cells transfected with non-coding siRNA transfected cells ( $P < 0.001$ ) (Fig. 2A). Flow cytometry was performed to determine the level of KDM5B protein, which decreased in both siRNA transfected cell lines ( $P < 0.01$ ), while the trimethylation of histone H3K4me3 was significantly increased compared to the control group in UKF-NB-4 ( $P < 0.01$ ) and UKF-NB-4<sup>CDDP</sup> ( $P < 0.05$ ) (Fig. 2B, C). The results demonstrated that KDM5B siRNA reduced KDM5B mRNA and protein expression and elevated protein H3K4me3 increased the trimethylation of histone H3K4 in UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cell lines.

**KDM5B knockdown promoted cell proliferation and migration in resistant cell line.** Proliferation of neuroblastoma cells after KDM5B siRNA transfection was evaluated by xCELLigence system. We found that KDM5B knockdown inhibited cell proliferation in sensitive cell line; however, silencing of KDM5B in resistant cells led to increased proliferation (Fig. 3A). The wound healing assay showed that down-regulation of KDM5B promoted the migration of UKF-NB-4<sup>CDDP</sup> cells compared to UKF-NB-4 (Fig. 3B). We also performed a cell viability assay, to see the impact of transfection on neuroblastoma cell lines. Results show, that KDM5B siRNA reduced the number of viable cells compared with non-coding siRNA transfected cells in sensitive cell line more significantly ( $P < 0.01$ ), than in resistant cell line ( $P < 0.05$ ). Increased sensitivity to CDDP (48 h treatment of these cells with CDDP) after silencing of KDM5B in sensitive cell line was observed ( $P < 0.05$ ). Interestingly, KDM5B knockdown affected neither viability nor response to CDDP in resistant cells (Fig. 3C).

**KDM5B knockdown increases cell cycle S phase in resistant cell line.** As shown above, KDM5B downregulation promotes cell proliferation and migration in resistant NBL cells (Fig. 3). Thus, we explored the role of KDM5B in cell cycle, using flow cytometry. Consistent with proliferation and migration data, we found that KDM5B knockdown resulted in a significant increase in the S phase in UKF-NB-4<sup>CDDP</sup> resistant cell line ( $P < 0.05$ ). In the sensitive cell line UKF-NB-4, silencing did not lead to any significant change in cell cycle (Fig. 4).

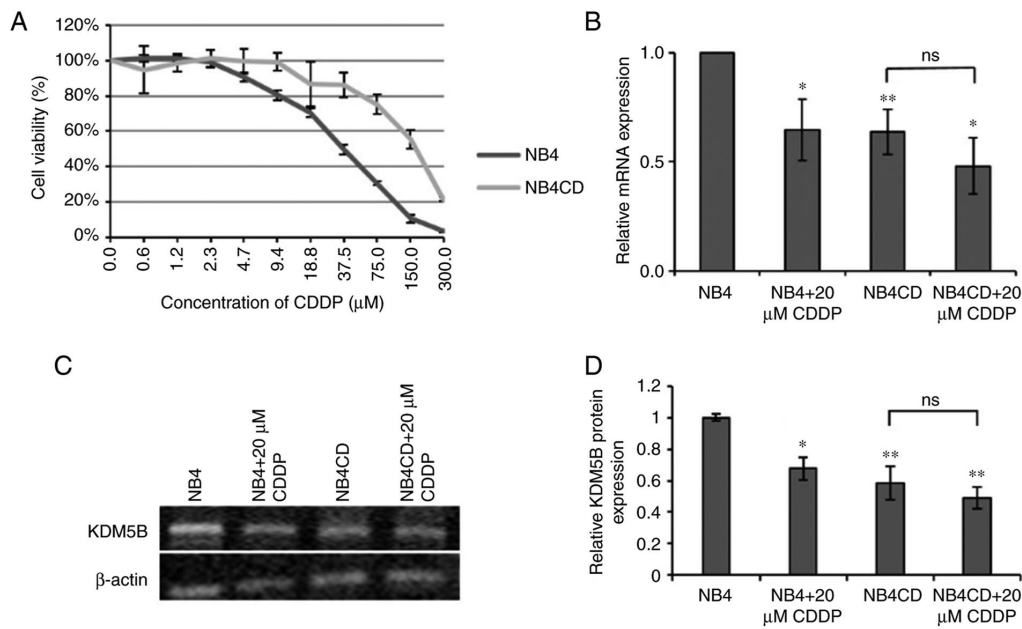


Figure 1. KDM5B is downregulated in resistant neuroblastoma cell line. (A) MTT assay results indicated cytotoxicity of CDDP after 48 h. UKF-NB-4 has a  $IC_{50}$   $37.5 \pm 1.9$  and CDDP resistant UKF-NB-4<sup>CDDP</sup> has  $IC_{50}$   $150 \pm 12.5$ . Expression levels of KDM5B mRNA and protein were detected using (B) reverse transcription-quantitative PCR and (C) western blotting in UKF-NB-4 (NB4) and CDDP resistant UKF-NB-4<sup>CDDP</sup> (NB4CD) cell lines. (D) Quantification of western blotting. Average and standard error from three independent experiments are shown. \* $P < 0.05$ , \*\* $P < 0.01$  compared with UKF-NB-4 cultured in the absence of CDDP (NB4). KDM5B, lysine-specific demethylase 5B; CDDP, cisplatin.

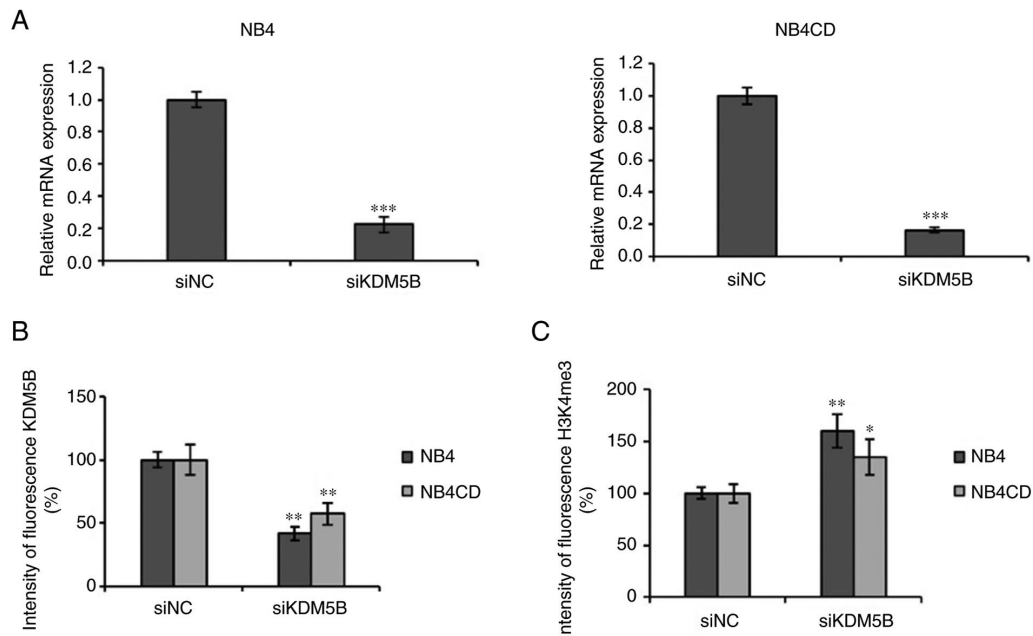


Figure 2. KDM5B-knockdown reduces KDM5B expression and upregulates histone H3K4 trimethylation in neuroblastoma cells. (A) Reverse transcription-quantitative PCR showed decrease in expression of *KDM5B* in UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cells transfected with siKDM5B compared with siNC. (B) Lower expression of KDM5B protein after siKDM5B transfection was detected using flow cytometry. (C) Flow cytometry also showed an increase of H3K4me3 after siKDM5B transfection. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\* $P < 0.001$ , NB4 and NB4CD cell lines were compared with their siNC control. KDM5B, lysine-specific demethylase 5B; CDDP, cisplatin; H3K4me3, tri-methylation of histone H3 at lysine 4; H3K4, lysine 3 of histone H3; si, short-interfering RNA; NC, negative control.

## Discussion

Aberrant epigenetic modifications, such as histone methylation, are widely described as essential players in cancer development and progression (3,26). KDM5B, is a histone lysine demethylase, whose dysregulation has been

observed in numerous types of cancers and also has a role in the appearance of a drug-tolerant population (11,27,28). Growing evidence indicates that KDM5B act as an oncogene in numerous types of cancer, such as bladder, breast, lung, prostate, and ovarian cancer, and also in NBL (29-35). Since the development of chemoresistance in high-risk NBL is a



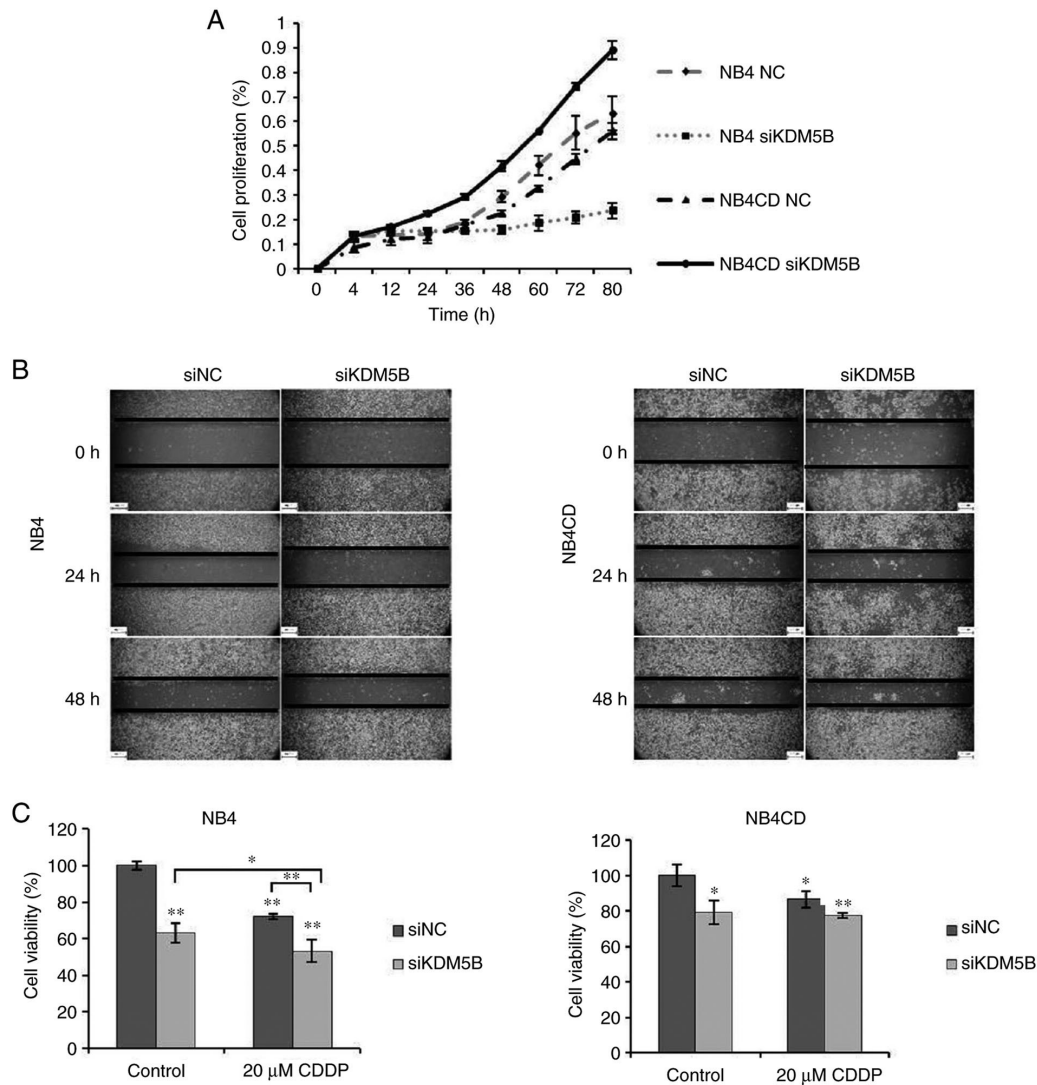


Figure 3. KDM5B-knockdown promotes cell proliferation and migration in resistant cell lines. (A) Proliferation was assayed using xCELLigence system after *KDM5B* downregulation in UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cells. (B) Result of wound healing assay in UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cells after *KDM5B*-knockdown demonstrated increased cell migration in resistant cell line after *KDM5B*-knockdown. Representative images taken immediately, 24 and 48 h after the wounding. (C) Viability of UKF-NB-4 and UKF-NB-4<sup>CDDP</sup> cells after *KDM5B*-knockdown and 48 h cisplatin treatment was measured using PrestoBlue. \* $P < 0.05$  and \*\* $P < 0.01$  compared with the control si-NC group or where indicated using umbrella lines. KDM5B, lysine-specific demethylase 5; CDDP, cisplatin; NC, negative control; si, short-interfering RNA.

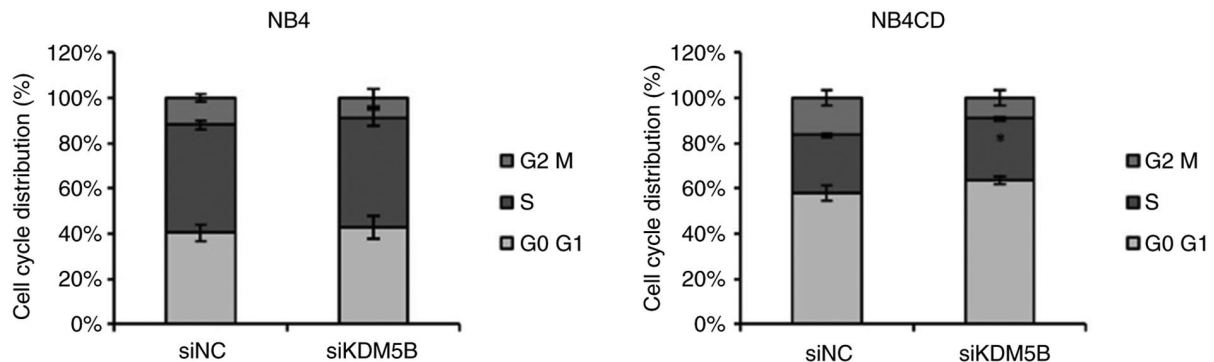


Figure 4. KDM5B-knockdown increases cell cycle S phase in resistant cell line. Flow cytometry results, showing cell cycle distribution in UKF-NB-4 (NB4) and UKF-NB-4<sup>CDDP</sup> (NB4CD) cells after *KDM5B*-knockdown. \* $P < 0.05$  compared with S phase in the siNC group. KDM5B, lysine-specific demethylase 5B.

negative prognostic marker, we decided to investigate the importance of *KDM5B* expression for NBL cell growth and

its chemoresistance to CDDP that is used in high-risk NBL therapy.

In this study, we demonstrated that *KDM5B* expression is markedly reduced in NBL cisplatin chemoresistant cells, compared to parental sensitive cells (Fig. 1) which is associated with enhanced cell migration and invasion, as well as it may be possibly involved in drug resistance (Fig. 3). However, *KDM5B* silencing did not change the sensitivity of resistant cells to CDDP. Several different mechanisms in chemoresistance that were described in several studies may be involved and *KDM5B* expression is only one of those mechanisms. For example in (25) we described several different mechanisms of chemoresistance in one cell line with experimentally induced chemoresistance to ellipticine. These findings are consistent with the reported data, showing that *KDM5B* can play a dual role in cancer (36). Roesch *et al* found that *KDM5B* expression in malignant melanoma, especially in advanced and metastatic melanoma tissues, was significantly downregulated and this lysine demethylase has been shown to have immediate antiproliferative effects, but later has a role in continuous tumor growth and maintenance (37). Furthermore, the elimination of *KDM5B* leads to an initial acceleration of melanoma growth (28). The *MYCN* plays a crucial role in the malignant behavior of NBL and is associated with a poor prognosis (13,38). We detected a decrease in the level of *KDM5B* in UKF-NB-4<sup>CDDP</sup> and UKF-NB-3<sup>CDDP</sup> cisplatin resistant cell lines that are *MYCN* amplified while in SK-N-AS<sup>CDDP</sup> cell line without *MYCN* amplification *KDM5B* level has not been changed compared to sensitive SK-N-AS cells. We suppose that this may be caused by increased expression of *MYCN* in lines with amplification of this gene (39). Zhang *et al* suggested that n-Myc represses *KDM5B* gene transcription by direct binding to the Sp1-binding site-enriched region of the *KDM5B* gene promoter, most likely through the recruitment of histone deacetylases (40). This work showed that the suppression of *KDM5B* expression reduces NBL cell proliferation. However, n-Myc induces the proliferation of NBL cells and represses *KDM5B* expression, suggesting that n-Myc-mediated transcriptional repression of *KDM5B* counterintuitively reduces tumor cell proliferation (30).

In conclusion, the results of this study show that *KDM5B* knockdown leads to increased levels of H3K4me in both cisplatin sensitive and resistant cell lines (Fig. 2). Based on this finding, it can be concluded that the function of lysine demethylase *KDM5B* i.e. demethylation of di- and tri-methylated histone H3K4 cannot be fully replaced by the other *KDM5* family members in NBL cells. We proved increased H3K4 me 3 also after silencing of *KDM5D* (Podhorska N. unpublished results) and *KDM5A* and *C* we did not tested. We supposed that all *KDM5* isoforms are necessary to ensure the adequate level of H3K4 me3. It can be concluded that the function of this histone lysine demethylase cannot be fully replaced by the others *KDM5*. Also, *KDM5B* silencing led to an increase of proliferation, and wound healing assay showed an increase in migration in resistant cell line. Moreover, in chemoresistant cells, it only minimally decreased viability after cisplatin treatment compared to sensitive cells (Fig. 3). Compliant with these results in resistant cells, si*KDM5B* transfection resulted in an increase in cell cycle S phase (Fig. 4). The effect of *KDM5B* on cell proliferation and the cell cycle of tumor cells varies in different tumors. The

mechanism of the relationship between *KDM5B* and the cell cycle is not yet known, PI3K-AKT pathway activation (41), BRCA1 (42) and transcription factors E2F1 and E2F2 (43) are expected to be affected, but other mechanisms are also possible. In a series of tumors, its silence inhibits and reduces the percentage of cells in S phase, for example in prostate cancer (44), hepatocellular carcinoma (43), bladder cancer and small cell lung carcinoma (33) or acute lymphoblastic leukemia (42). On the other hand, in melanoma it has the opposite effect, i.e. the silencing of *KDM5B* accelerates growth and increases the proportion of cells in the S phase (37). *KDM5B* transfection induced cell differentiation in hypopharyngeal squamous cell carcinoma and, on the contrary, its silencing accelerated growth of cells (41). The explanation of different response of sensitive and resistant NBL cells to *KDM5B* silencing is not clear and will be subject of further studies. However, we hypothesized that it is related to the different expression of this gene in sensitive and resistant NBL cell lines.

There is emerging evidence for the deregulation of *KDM5B* and the important phenotypic consequences in various types of cancer, making this enzyme a promising factor for the prediction of sensitivity to CDDP. It will be necessary to study the relationship between cisplatin sensitivity and histone methylation to understand resistance to this drug.

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## Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

## Authors' contributions

TE designed and led this study. MB performed RT-qPCR, western blotting, flow cytometry and cell proliferation assays. NP performed siRNA transfection, RT-qPCR, western blotting and flow cytometry. MB and NP analyzed the data and performed the statistical analysis. MB and NP wrote the manuscript. AV designed experiments. MB, NP, AV and TE confirm the authenticity of all the raw data. All authors have reviewed the manuscript and read and approved the final manuscript.

## Ethics approval and consent to participate

Not applicable.

## Patient consent for publication

Not applicable.

## Competing interests

The authors declare that they have no competing interests.

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