Oncogenes and Tumor Suppressors

DDB2 Suppresses Tumorigenicity by Limiting the Cancer Stem Cell Population in Ovarian Cancer

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Abstract

Ovarian cancer is an extremely aggressive disease associated with a high percentage of tumor recurrence and chemotherapy resistance. Understanding the underlying mechanism of tumor relapse is crucial for effective therapy of ovarian cancer. DNA damage-binding protein 2 (DDB2) is a DNA repair factor mainly involved in nucleotide excision repair. Here, a novel role was identified for DDB2 in the tumorigenesis of ovarian cancer cells and the prognosis of patients with ovarian cancer. Overexpressing DDB2 in human ovarian cancer cells suppressed its capability to recapitulate tumors in athymic nude mice. Mechanistic investigation demonstrated that DDB2 is able to reduce the cancer stem cell (CSC) population characterized with high aldehyde dehydrogenase activity in ovarian cancer cells, probably through disrupting the self-renewal capacity of CSCs. Low DDB2 expression correlates with poor outcomes among patients with ovarian cancer, as revealed from the analysis of publicly available gene expression array datasets. Given the finding that DDB2 protein expression is low in ovarian tumor cells, enhancement of DDB2 expression is a promising strategy to eradicate CSCs and would help to halt ovarian cancer relapse.

Implications: DDB2 status has prognostic potential, and elevating its expression eradicates CSCs and could reduce ovarian cancer relapse. Mol Cancer Res; 1–11. ©2014 AACR.

Introduction

Epithelial ovarian cancer is the fifth leading cause of cancer-related deaths in women in the United States and the leading cause of gynecologic cancer deaths. Most of the tumors are initially responsive to platinum-based chemotherapy and the patients enter into clinical remission after initial treatment. However, recurrence occurs in more than 70% of patients despite treatment (1). The high relapse rate in ovarian cancer results in greater mortality and is estimated to account for 5% of all deaths by cancer in women for 2013 (2). Therefore, reducing ovarian cancer relapse is especially important to prolonging progression-free survival and decreasing the mortality in patients with ovarian cancer.

Over the past several years, it has been increasingly evident that a small population of cancer cells, referred to as “cancer stem cells (CSC),” is the most important trigger of tumor progression (3, 4). The CSC theory suggests that tumor cells are organized hierarchically with a small self-renewing population of stem cells generating a large population of proliferative cells to maintain the tumors. These CSCs have been identified in a variety of solid tumors including ovarian cancers (5–8). Each type of CSC has a distinctive pattern of surface markers (i.e., CD44, CD133, and CD117) and nonsurface markers [i.e., aldehyde dehydrogenase (ALDH) activity] that can be targeted for CSC isolation (9). In addition, CSCs can also be isolated by detection of side-population (SP) phenotypes with Hoechst 33342 dye efflux technique (10) and their ability to grow as floating spheres in serum-free medium (11). Ovarian CSCs have been successfully isolated based on the expression of distinctive cell surface markers CD44, CD117, MyD88, and CD133 (5, 12, 13), as well as the activity of ALDH (13). All isolated ovarian CSCs fulfill all currently accepted criteria of the existence of a subpopulation of tumor-initiating cells.

CSCs possess several key properties, including (i) self-renewal, (ii) multipotent differentiation into nontumorigenic cells, (iii) resistance to toxic xenobiotics, and (iv) the ability to induce tumors when transplanted into immunodeficient mice (14). A number of reports support the presence of rare CSCs that are resistant to chemotherapy and radiotherapy. These resistant CSCs are believed to be the main source of tumor relapse (15). Thus, there is an urgent need for detailed characterization of these CSCs to devise new treatment modalities.

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DDB2 is a 48-kDa protein originally identified as a component of the damage-specific DNA-binding heterodimeric complex DDB (16). DNA damage-binding protein 2 (DDB2) is able to bind UV-damaged DNA and serves as the initial damage recognition factor during nucleotide excision repair (NER; ref. 17). The low expression of DDB2 in cisplatin-resistant ovarian cancer cell lines (18) and high-grade colon cancer (19) and skin cancer (20) indicates a link between DDB2 expression and tumor progression. Recently, new functions of DDB2 beyond its role in DNA repair have been identified, e.g., inhibiting cellular apoptosis through downregulation of Bcl-2 (18, 21) and p21 (22), suppressing colon tumor metastasis through blocking epithelial–mesenchymal transition (EMT; ref. 19), and limiting the motility and invasiveness of invasive human breast tumor cells by regulating NF-κB activity (23), as well as mediating premature senescence (24). In this study, we reveal a novel role of DDB2 in the inhibition of tumorigenesis. DDB2 overexpression resulted in a reduction of the CSC population associated with repression of the tumorigenicity of ovarian cancer cells, whereas DDB2 knockdown resulted in an expansion of the CSC population.

Material and Methods

Cell culture

Human ovarian cancer cell line A2780 and its derived cisplatin-resistant cell line CP70 (25) were kindly provided by Dr. Paul Modrich (Duke University, Durham, NC). Ovarian cancer cell line 2008 and its resistant cell line 2008C13 (26) were kindly provided by Dr. Francois X. Claret (University of Texas M.D. Anderson Cancer Center, Houston, TX). The A2780 derivative and 2008 derivative cisplatin-resistant cell lines were produced by intermittent, incremental exposure of the sensitive parental cell line to various concentrations of cisplatin. SKOV3 ovarian cancer cell line was kindly provided by Dr. Thomas C. Hamilton (Fox Chase Cancer Center, Philadelphia, PA). CP70 cells with overexpression of DDB2 (CP70-DDB2) were established in our laboratory (18). All cell lines were cultured by DNA (STR) profiling, and maintained in RPMI 1640 supplemented with 10% FBS, 100 μg/mL streptomycin, and 100 units/mL penicillin. Cells were grown at 37°C in humidified atmosphere of 5% CO₂ in air.

Tissue microarray and immunohistochemistry

Confirmed, formalin-fixed, paraffin-embedded human ovarian normal tissue and epithelial tumors were obtained from the Department of Pathology, The Ohio State University (Columbus, OH). Cores were obtained from the most viable/nonnecrosis areas of the tissue. Each sample had 2 independent cores. A tissue microarray (TMA) was constructed from 16 normal tissues and 43 patients with ovarian cancer (grade 1, 4; grade 2, 14; grade 3, 25). TMA sections were subjected to deparaffinization and rehydration. The endogenous peroxidase was quenched by 3% (v/v) hydrogen peroxide. The epitope retrieval was performed using Dako TRS solution (Dako) for 25 minutes at 96°C in a vegetable steamer. Primary mouse antibody against DDB2 (ab51017; 1:10; Abcam) was incubated for 1 hour at room temperature, and detected using a Mach 3 Mouse HRP-Polymer kit (Biocare Medical) and diaminobenzidine tetrahydrochloride (Dako). Tissues were counterstained with Richard Allen hematoxylin. Intensity of staining was blind scored from 1 (no staining) to 4 (highest intensity of staining).

Plasmids and gene transfection

pReceiver-Lv105-DDB2 (GeneCopoeia) and pcDNA3.1-His-DDB2 plasmids were introduced into cells by using either lentivirus infection or electroporation with NEPA-21 Electroporator (Nepa Gene Co., Ltd). DDB2 expression lentiviruses were generated as described before (21). To establish shDDB2 stably transfected cell lines, MISSION shDDB2 (TRCN0000083993) plasmids (Sigma) were transfected into 2008 cells using electroporation. The transfected cells were selected in the medium containing 2 μg/mL Puromycin, and the transfectant lines with stable DDB2 downregulation were confirmed by Western blotting.

Immunoblotting

Whole cell lysates were prepared by boiling cell pellets for 10 minutes in SDS lysis buffer [2% SDS, 10% Glycerol, 62 mmol/L Tris-HCl, pH 6.8 and a complete mini-protease inhibitor cocktail (Roche Applied Science)]. After protein quantification with Bio-Rad Dc Protein Assay (Bio-Rad Laboratories), equal amounts of proteins were loaded, separated on a polyacrylamide gel, and transferred to a nitrocellulose membrane. Protein bands were immunodetected with appropriate antibodies, e.g., goat anti-DDB2 (R&D Systems), rabbit anti-Nanog (Cell Signaling Technology), mouse anti-Tubulin (Millipore), and mouse anti-InBα (Cell Signaling Technology).

Semisolid colony-forming assay

Cells were trypsinized and counted. A total of 1,000 cells were mixed with semisolid media (MethoCult H4100; STEMCELL Technologies Inc.) containing serum-free DMEM/F12 (Life Technologies) supplemented with 20% KnockOut Serum Replacement (Life Technologies), 20 ng/mL EGF (Life Technologies), 10 ng/mL basic fibroblast growth factor (bFGF; Life Technologies), 100 μg/mL streptomycin, and 100 units/mL penicillin (Life Technologies), and seeded in 6-well Ultra-Low Attachment plates (Corning). The number of larger (more than 50 cells), symmetric, and prototypical colonies was counted after 6 days.

Flow cytometry analysis and cell sorting

Anti–CD117-PE and anti–CD44-FITC (BD Pharmingen) were used for flow cytometric analysis and cell sorting. Detection of ALDH activity was conducted using the ALDEFLUOR assay (STEMCELL Technologies) according to the manufacturer’s instruction. For each sample, one half of cells was treated with 50 mmol/L diethylaminobenzaldehyde to define negative gates. Flow
cytometric analysis and sorting were performed on a BD FACSC Aria III at The Ohio State University Analytical Cytometry Shared Resource. CP70-ALDH^+, 2008-CD44^+CD117^+, and 2008C13-CD44^+CD117^+ cells were maintained in Ultra-Low Attachment plates in KnockOut DMEM/F12 medium supplemented with 20% KnockOut Serum Replacement, 20 ng/mL EGF, and bFGF. A total of 10 μL of fresh medium was added every 2 days. After 1 month, wells that contain just a single colony were marked. These SKOV3 spheroids were then subcultured from the wells into larger vessels for further growing and defined as putative CSCs.

**Sphere-forming assay**

A total of 1,000 of CSCs were plated in triplicate in Ultra-Low Attachment plates in serum-free DMEM/F12 medium supplemented with serum replacement, EGF, and bFGF. Sphere formation was assessed 2 weeks after cell seeding. Spheres are de
defined as floating nonadherent multicellular cell aggregates.

**Quantitative real-time PCR**

Total RNA was extracted using Trizol reagent (Invitrogen), and the first strand cDNA was generated by the Reverse Transcription System (Promega) in a 20-μL reaction containing 1 μg of total RNA. A 0.5 μL aliquot of cDNA was amplified by Fast SYBR Green PCR Master Mix (Life Technologies) in each 20 μL reaction with the following primers: **DDB2**, forward, 5'-CTCCTCAATGAGGGAAGGAA-CAA-3', reverse, 5'-GTGACCCACCATTTCCGACT-3'; **Nanog**, forward, 5'-GTCCCAAGGGCAAACAACCC-3', reverse, 5'-TTGACCGGACCTGTCTTC-3'; **GAPDH**, forward, 5'-GAAGGTGAAGGTCGGAGT-3', reverse, 5'-GAAGATGCTGATGGATTC-3'. PCR reactions were run on the ABI 7900 Fast Real-Time PCR system in the OSUCCC Nucleic Acid Core Facility.

**Xenograft tumor growth**

Athymic NCr-nu/nu mice and nonobese diabetic/severe combined immunodeficient (NOD/SCID) mice (6–8 weeks, female, 20 to 25 g body weight) were obtained from National Cancer Institute. Animals were maintained in accordance with institutional policies, and all studies were performed with approval of the Institutional Animal Care and Use Committee of The Ohio State University. To assess the tumorigenicity of DDB2-overexpressing CP70 cells, 5 × 10^6 cells were resuspended (1:1) in PBS:Matrigel (BD Biosciences) and injected subcutaneously into the flank of nude mice. To evaluate the effect of DDB2 on the tumorigenicity of SKOV3 spheroids, pcDNA3.1-His-DDB2 plasmids or empty vectors were cotransfected with pcDNA3.1-GFP plasmids into SKOV3 spheroids by electroporation. Cells were cultured for 2 days, and viable cells with GFP expression were sorted by fluorescence-activated cell sorting (FACS). A total of 1 × 10^4 of these cells were mixed (1:1) with Matrigel and injected subcutaneously into the axillae of NOD/SCID mice. Tumor growth was measured using calipers, and volumes were calculated based on the formula V = (a × b^2)/2, in which a is the longest and b is the shortest diameter of the tumor. Tumor growth curves were compared using a Student t test.

**Statistical analysis**

Student t test and nonparametrics Mann–Whitney test were performed for data analysis by using the Minitab software. Log-rank analysis was used to determine statistical significance of the Kaplan–Meier survival curve. For all statistical methods, P < 0.05 was considered statistically significant.

**Results**

**DDB2 is downregulated in ovarian cancers**

It has been reported that DDB2 protein expression is downregulated in human colon cancer and skin cancer demonstrated by immunohistochemical (IHC) staining (19, 20). To determine the DDB2 protein expression level in primary ovarian carcinoma, we constructed TMA and analyzed DDB2 expression using IHC with an antibody specific for DDB2. IHC staining of the samples showed that normal ovary epithelial cells exhibit strong DDB2 staining, whereas ovarian carcinoma cells in most of tumor tissue samples display low DDB2 expression (Fig. 1A). Statistical analysis revealed a significant decrease of DDB2 expression in ovarian carcinomas regardless the grade (Fig. 1B), indicating a strong correlation between the loss of DDB2 expression and the ovarian carcinoma.

**DDB2 represses tumorigenicity of ovarian cancer cells in vitro and in vivo**

To further investigate the role of DDB2 in the tumorigenicity of ovarian cancer cells, we overexpressed DDB2 in cisplatin-resistant ovarian cancer cell line CP70, which expresses low level of endogenous DDB2 (18), and established two stable cell lines with DDB2 overexpression (Fig. 2A, left). We also transfected DDB2 short hairpin RNA (shRNA) into another ovarian cancer cell line 2008 and selected two stable DDB2-knockdown cell lines (Fig. 2A, right). We then assessed the anchorage-independent growth of these cells in vitro by culturing them in semisolid serum-free medium. As shown in Fig. 2B–E, DDB2 overexpression significantly inhibited anchorage-independent growth of CP70 cells, whereas DDB2 knockdown promoted anchorage-independent growth of 2008 cells.
We next sought to determine the effects of DDB2 overexpression on the tumorigenicity of CP70 cells in vivo in immunocompromised mice. CP70-vector cells and two clones of CP70-DDB2 cells were injected separately into nude mice subcutaneously. Tumors were formed in all mice injected with CP70-vector cells within 1 month, whereas tumors could only be found in 3 of 9 mice injected with two different CP70 cell lines stably overexpressing DDB2 up to 3 months. The tumor growth curves and the final tumor sizes also indicate that DDB2 overexpression suppresses the growth of implanted human ovarian cancer cells (Fig. 2F and G). Taken together, these in vitro and in vivo data indicate that DDB2 is able to suppress tumorigenicity of ovarian cancer cells.

DDB2 overexpression reduces the CSC subpopulation in ovarian cancer cells

It has recently been reported that DDB2 suppresses the tumorigenicity and invasiveness of colon cancer cells through suppressing EMT (19). We then analyzed the EMT markers in CP70 cells with or without overexpression of DDB2. We were unable to find any effect of DDB2 overexpression on the cellular levels of epithelial marker E-cadherin and mesenchymal marker vimentin (Supplementary Fig. S1A). In addition, we failed to see any change in morphology of the cells with DDB2 overexpression (Supplementary Fig. S1B). Similarly, we did not find any change of EMT in various clones of ovarian cancer cell line 2008 with stable DDB2 knockdown (Supplementary Fig. S1C). These results indicate that DDB2 may not suppress EMT of ovarian cancer cells.

CSCs are thought to contribute to the initiation of the tumor (15). We thus hypothesized that DDB2 may regulate the amount of CSC subpopulation in cancer cells. ALDH has been proposed to be a marker of both normal and cancer stem cells (29) and has been used to identify CSCs from ovarian cancers (13). We thus analyzed the abundance of putative CSC subpopulations characterized with ALDH in CP70 and DDB2-overexpressing CP70 cells using FACS. It is clear that two DDB2-overexpressing CP70 cell lines exhibit reduced ALDH subset, in comparison with CP70-vector cells (Fig. 3A and B, Supplementary Fig. S2A and S2B). Our immunoblotting analysis also revealed diminished ALDH1A1 expression in both DDB2-overexpressing CP70 cell lines (Supplementary Fig. S3). In contrast, downregulation of DDB2 expression in A2780 cells increased the percentage of ALDH+ cells (Fig. 3C–E), further supporting that DDB2 is able to decrease the abundance of ALDH+ cells in ovarian cancer cells. In addition, we also analyzed ALDH+ cells in DDB2-knockdown 2008 cells and demonstrated the similar result (Supplementary Fig. S4A and S4B). Besides ALDH activity, CD44+CD117+ was also used as a phenotypic marker of ovarian CSCs (5). We then sought to determine whether DDB2 expression also affects the percentage of CD44+CD117+ fraction. Indeed, we found a decrease in CD44+CD117+ population in CP70 cells with DDB2 overexpression, and an increase in CD44+CD117+ population in 2008 cells with DDB2 knockdown (Supplementary Fig. S5A–S5D). SP cells, identified based on their ability to efflux the Hoechst 33342 fluorescent dye, have been shown to possess CSC properties (10). We then attempted to determine the effect of DDB2 on the percentage of SP cells. Different from above-detected ALDH+ and CD44+CD117+ populations, SP cells only account for a very small fraction of the total cancer cell population (less than 0.1%). Nevertheless, the overexpression of DDB2 reduced the SP fraction in one cell line (Supplementary Fig. S6A and S6B). Collectively, these results indicate that DDB2 is able to reduce the CSCs pool existing in ovarian cancer cells.
Figure 2. DDB2 represses tumorigenicity of ovarian cancer cells in vitro and in vivo. A, two clones of DDB2 stably overexpressing CP70 cells and two clones of DDB2 stably knockdown 2008 cells were selected, and DDB2 expression was determined. Exo-DDB2, Exogenous His-Xpress-tagged DDB2; End-DDB2, Endogenous DDB2. B to E, the DDB2-manipulated CP70 cells (B and D) and 2008 cells (C and E) were seeded in semisolid media containing serum-free DMEM/F12 supplemented with EGF and bFGF in Ultra-Low Attachment plate and allowed to grow for 6 days. Representative images of colonies were shown (B and C). The number of colonies were counted and plotted (D and E). Bar, SD, n = 6; *, P < 0.01 compared with control cells. F and G, CP70-vector and two DDB2-overexpressing CP70 cell lines were injected subcutaneously into nude mice and the tumors formed were counted after 4 weeks. Tumor sizes were measured (F), and tumors were removed from mice after 4 weeks (G). Bar, SD; *, P < 0.01 compared with CP70-vector.
Ovarian CSCs exhibit low DDB2 expression level

To elucidate the mechanism of the DDB2-mediated regulation of the CSC population, we isolated the putative CSCs from various ovarian cancer cell lines, e.g., CP70, SKOV3, 2008, and 2008C13 based on the activity of ALDH, expression of specific surface markers CD44 and CD117, as well as the ability to form spheres and grow in nonadherent serum-free culture condition, respectively (9). The characteristics of isolated CSCs, including the ability to form tumor spheres in ultra-low attachment plates and the ability to form xenografts in immunodeficient mice at lower cell numbers, have been authenticated (Supplementary Figs. S7A–S7C; S8A–S8D; S9A–S9G). Both immunoblotting (Fig. 4A–D) and real-time (RT) PCR (Fig. 4E–F) analyses showed enhanced expression of Nanog, one of the self-renewal markers of stem cells and upregulated in various ovarian CSCs (5, 30), in these CSC populations in comparison with their parent bulk cancer cells, further supporting the stemness of these CSC populations. Interestingly, DDB2 protein level was found to decrease, while its mRNA level did not change in all CSC populations compared with their parent bulk cells (Fig. 4A–H). These data indicate that low DDB2 protein expression might be required for the maintenance of CSCs, whereas cellular DDB2 expression in CSCs is most likely regulated at posttranscription level.

DDB2 inhibits the self-renewal property and tumorigenicity of ovarian CSCs through suppressing the NF-κB pathway

To further investigate whether low DDB2 expression is required to maintain the stem cell properties of ovarian CSCs, we transfected DDB2-expressing plasmids into three ovarian CSCs (5, 30), in these CSC populations in comparison with their parent bulk cancer cells, further supporting the stemness of these CSC populations. Interestingly, DDB2 protein level was found to decrease, while its mRNA level did not change in all CSC populations compared with their parent bulk cells (Fig. 4A–H). These data indicate that low DDB2 protein expression might be required for the maintenance of CSCs, whereas cellular DDB2 expression in CSCs is most likely regulated at posttranscription level.
found that cbioportal.org; Supplementary Materials and Methods), we Through the analysis of publicly available datasets (www.

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It has been recently reported that DDB2 is able to

value of the microarray-quantified DDB2 expression level in patients with ovarian cancer included in 10 datasets (35). Kaplan–Meier survival curves showed that low DDB2 mRNA expression correlates with poor overall and progression-free survival among patients with ovarian cancer (Fig. 6A and B). We then used another online tool cBioPortal (http://cbioportal.org) to analyze the effect of extremely low DDB2 expression or high DDB2 expression on the overall survival of patients with ovarian cancer from The Cancer Genome Atlas (TCGA) data portal (36–38). Similarly, the Kaplan–Meier survival analyses demonstrated that patients with ovarian cancer with DDB2 mRNA expression Z-score less than −2 exhibited poor prognosis compared with those patients with DDB2 expression Z-score greater than −2 (median survival months, 26.94 vs. 44.29), while the patients with DDB2 expression Z-score higher than 0.5 exhibited better prognosis than those with DDB2 expression Z-score less than 0.5 (median survival months, 55.88 vs. 41.53; Fig. 6C and D). However, although the TCGA dataset demonstrates that overall survival is different, there is no difference in progression-free survival. These analyses suggest that DDB2 low expression is associated with poor outcome in patients with ovarian cancer.

Discussion

Despite significant advances in diagnosing and treating ovarian cancer, one of the major clinical and scientific problems that remain unresolved is the prediction and
inhibition of ovarian tumor recurrence after clinical remission. In the present study, we provide evidence showing that low DDB2 expression is correlated with poor outcome of patients with ovarian cancer, overexpression of DDB2 in ovarian cancer cells reduces their tumorigenicity through limiting the CSC population, thus defining a novel function for DDB2 in the control of tumor relapse. DDB2 has been considered a tumor suppressor based on the findings that DDB2−/− mice were not only susceptible to UV-induced carcinogenesis, but also developed spontaneous malignant tumors at a high rate (39, 40). The analysis of publicly available datasets in this study indicates that low DDB2 mRNA expression correlates with poor outcome of patients with ovarian cancer. Indeed, this kind of correlation can also be found in patients with breast (23) and lung cancer (http://www.kmplot.com). Therefore, in combination with our findings in this study and others (19), we believe that DDB2 plays an important role in impeding tumor progression and tumor relapse.

DDB2 has been reported to inhibit metastasis of colon cancer (19) and limit the invasiveness of breast cancer (23). Mechanistically, DDB2 constitutively represses genes that are the key activators of EMT through its transcriptional regulation function in various colon cancer cell lines (19). In addition, DDB2 attenuates the activity of NF-kB by upregulating expression of IkB in breast cancer cells. EMT is believed to be a crucial mechanism for tumor metastatic progression (41), whereas NF-kB plays a causal role in migration and invasion of tumor cells and is required for maintenance of the malignant phenotype (42). Thus, the DDB2-dependent decrease of EMT and NF-kB activity could explain in part the correlation between high DDB2 expression and an improvement of the outcome in patients with cancer. Besides these known mechanisms, we demonstrated for the first time in this study that DDB2 is able to reduce the abundance of CSCs in the bulk ovarian cancer cells, which provide a novel mechanism to explain the DDB2-mediated suppression of tumorigenicity. Our data demonstrated that the low expression of DDB2 is required for the maintenance of CSCs. Given that CSCs are believed to be the source of tumor recurrence and metastasis, enhancement of DDB2 expression in ovarian tumors bears great potential in the improvement of the prognosis of patients with tumor.

Mechanistic investigations demonstrated that overexpression of DDB2 reduces the expression of several CSCs self-renewal markers and their capability to form spheres in nonadherent condition. The maintenance and survival of CSCs are controlled by many pathways, such as Wnt, Notch, and Hedgehog (43). It has been reported that the Notch pathway in glioblastoma CSCs involves the constitutive activation of NF-kB signaling, which upregulates Notch

Figure 6. Prognostic significance of DDB2 in ovarian cancer. A and B, the effect of DDB2 mRNA expression level on the overall survival (A) and progression-free survival (B) in 1,464 patients with ovarian cancer was analyzed and the Kaplan–Meier plots were generated by the Kaplan–Meier Plotter (http://www.kmplot.com). C and D, TCGA data were also analyzed to reveal the effect of extremely low DDB2 mRNA level (C) and high DDB2 mRNA level (D) on the overall survival of patients with ovarian serous cystadenocarcinoma by using cBioPortal (http://cbioportal.org).
constitutively repressing genes that are the key activators of EMT could suppress the survival of CSCs through downregulating the NF-κB pathway, leading to a reduction of CSC subpopulation, and finally results in an impediment of tumor progression.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors’ Contributions
Conception and design: C. Han, Q.-E. Wang
Development of methodology: L. Gong, W. Zhao, Q.-E. Wang
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): R. Zhao, A. Srivastava, M. Qu, W. Zhao, Q.-E. Wang
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Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): H. Mao
Study supervision: Q.-E. Wang

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References
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