Foxo3a suppression of urothelial cancer invasiveness through twist1, Y-box-binding protein 1, and E-cadherin regulation

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http://hdl.handle.net/2324/26053

出版情報: Clinical Cancer Research. 16 (23), pp.5654-5663, 2010-12-01. American Association for Cancer Research
バージョン: accepted
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Foxo3a suppression of urothelial cancer invasiveness through Twist1, Y-box-binding protein 1 and E-cadherin regulation

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Running title: Foxo3a regulates cancer cell invasion

Keywords: E-cadherin; Foxo3a; invasion; Twist1; YB-1

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Translational Relevance

The role of Foxo3a in urothelial cancer development has not been investigated and its prognostic relevance is still poorly understood. This study revealed that Foxo3a expression was inversely correlated with tumor stage, and that low Foxo3a expression level was an independent prognostic factor for poor disease-free survival, cancer-cause specific survival, and overall survival. Moreover, Foxo3a expression was also found to regulate the motility of urothelial cancer cells through the regulation of several epithelial-mesenchymal transition-associated proteins. Thus, although Foxo3a is already known to be implicated in cancer cell growth, this study showed that it also regulates cancer cell motility. Taken together, these results suggest that Foxo3a could act as a novel prognostic factor and therapeutic target in urothelial cancer.
Abstract

Purpose: Invasion and metastasis are key steps in the progression of urothelial cancer (UC) into a critical disease. Foxo3a is a member of the Foxo transcription factor family, which modulates the expression of various genes. We aimed to elucidate the role of Foxo3a in UC invasion.

Experimental Design: Foxo3a mRNA and protein expressions in UC samples were investigated by gene expression assays and immunohistochemistry, respectively. Foxo3a expression was compared with clinicopathologic characteristics and patient prognoses based on UC samples. Quantitative real-time polymerase chain reaction, western blotting, and migration assays were also conducted in UC cells.

Results: Foxo3a expression decreased in invasive UC; patients with low Foxo3a expression had poor disease-free survival, cancer-specific survival, and overall survival; Foxo3a knockdown in UC cells increased cellular motility. Foxo3a negatively regulated Twist1 and Y-box-binding protein 1 (YB-1), and positively regulated E-cadherin in KK47 and TCCsup cells that expressed Twist1, but not in T24 cells that did not express Twist1. Foxo3a-associated acetyltransferase p300 and Foxo3a acetylation status also affected UC motility.

Conclusion: The results of this study indicate that Foxo3a regulates motility of UC.
through negative regulation of Twist1 and YB-1, and through positive regulation of E-cadherin. This suggests that Foxo3a could act as an independent prognostic factor in UC and could represent a promising molecular target for cancer therapeutics.
**Introduction**

Bladder cancer is the second most common malignancy of the genitourinary tract and the fourth major cause of cancer death among men (1). Urothelial carcinoma of the bladder accounts for more than 90% of bladder cancers (2). Most urothelial carcinomas (about 80%) present as superficially invasive tumors, which include Ta (non-invasive) or T1 (lamina propria-invasive) tumors. Muscle-invasive cancer (T2–4) has a much less favorable prognosis than superficial cancer, despite aggressive multimodal therapy (3). Due to the unfavorable prognosis of muscle-invasive cancer, there is a need to develop markers that can identify superficial cancers with a high risk of progression. The characterization of such markers will help to detect more invasive urothelial cancer (UC), and thus improve the prognosis of this disease.

Foxo3a is a member of the Foxo transcription factor family. Foxo transcription factors, which belong to the ‘other’ class of the Fox superfamily, are involved in multiple signaling pathways and play critical roles in a number of physiologic and pathologic processes (4). It has been recently reported that the Forkhead transcription factor, Foxo3a, regulates DNA damage response and stimulates DNA repair pathways (5,6). Foxo transcription factors also regulate oxidative detoxification and cell cycle-related genes (7), apoptosis-related genes, such as Bim (8), tumor necrosis factor
receptor ligand (TRAIL) (9) and Fas ligand (10). Foxo transcription factors are known to be reversibly acetylated and deacetylated by calcium-responsive element binding-binding protein (CBP)/p300 and Sirt1, respectively (11–16). These modifications modulate the transcriptional abilities and gene target selections of Foxo transcription factors, thus affecting biological behavior.

Epithelial–mesenchymal transition (EMT) is a characteristic of cancer cell intravasation and metastasis. E-cadherin is a cell-to-cell adhesion molecule, and loss of its expression is a hallmark of EMT. Reduction of E-cadherin increases cell motility and promotes cancer cell invasion (17,18). Foxe3 (also called HNF3 and forkhead box E3) and p300 have been shown to play important roles in promoting E-cadherin expression (19). E-cadherin expression, in turn, is regulated by other factors, including Twist1 (20). An inverse correlation between Twist1 and E-cadherin expression was observed in invasive lobular breast carcinoma, suggesting that Twist1 affects cancer cell intravasation and entry into the circulation to seed metastases (21). Y-box-binding protein 1 (YB-1) has recently been shown to regulate cancer cell invasion through translational control of Twist1 (22,23); Twist1 transcriptionally regulates YB-1 expression, while p53 and programmed cell death protein 4 (PDCD4) affect YB-1 expression through interactions with Twist1 (24–26).
In this study, we investigated the correlation between Foxo3a expression and clinicopathologic parameters in patients with UC. We also examined the molecular mechanism of cancer cell motility control by Foxo3a and its associated acetyltransferase, p300.

**Materials and methods**

**Cell culture.** Human bladder cancer TCCsup (RPMI1640) cells (kindly provided by Dr. Osamu Ogawa, Kyoto University, Kyoto, Japan), KK47 (MEM) and T24 (MEM) cells were cultured in the media indicated (Invitrogen, San Diego, CA), containing 10% fetal bovine serum. The stable transfectants KK47-Ac green fluorescent protein (GFP) (#1 and #2), KK47-Foxo3a-GFP (#1 and #2) and KK47-Foxo3a-GFP KR (#1 and #2) cells were derived from KK47 cells and stably expressed the corresponding proteins. These transfectants were established as previously described (27). Cell lines were maintained in a 5% CO2 atmosphere at 37°C.

**Antibodies and plasmids.** Anti-Foxo3a (EP1949Y) and anti-YB-1 (EP2708Y) antibodies were purchased from Epitomics (Burlingame, CA). Antibodies against p300 (sc-585) and Twist1 (sc-81417) were purchased from Santa Cruz Biotechnology (Santa Cruz, CA). Anti-E-cadherin and Anti-β-actin (AC-15) antibodies were purchased from BD Biosciences (San Jose, CA) and Sigma (St. Louis, MO), respectively. Foxo3a-GFP
plasmid expressing C-terminal-GFP-tagged Foxo3a protein and mutated Foxo3a-GFP expression plasmid (Foxo3a-GFP KR) were created as described previously (27).

**Gene expression assay.** Tissues for gene expression assays were collected from 71 patients who underwent transurethral resection or radical cystectomy, without preoperative chemotherapy, at the Kyushu University Hospital, Japan, between 1992 and 2004, and who provided enough suitable UC tissue for evaluation. Tissues that were suspected to be necrotic by endoscopic and macroscopic examination were avoided. The samples were collected under careful endoscopic and macroscopic observation, to avoid contamination by normal urothelial tissues. If multiple tumors were present, then samples were collected from the major tumors, in order to select the predominant representative tumor. Written informed consent was obtained from all subjects. RNA isolation, reverse transcription and quantitative real-time polymerase chain reaction (PCR) were performed as described below. The median transcript level corresponded to 1.

**Patients and samples for immunohistochemistry.** Tissues for immunohistochemistry were collected from 53 patients who underwent radical cystectomies, without preoperative chemotherapy, at the Kyushu University Hospital, Japan, between April 1993 and March 2008, and who provided sufficient UC tissue for
immunohistochemical evaluation. Bladder blocks containing the largest and most representative area of the tumor were prepared. All surgical specimens were completely reviewed to establish histologic grading and disease staging of the respective UCs, based on the criteria of the 2004 WHO classification and 2002 TNM system. Clinical follow-up data were available for all patients. There were 21 deaths, 24 recurrences and 15 disease-specific deaths during the follow-up period. The median follow-up period was 25.0 months (mean: 46.5 months).

**Immunohistochemistry.** Immunohistochemistry was performed as previously described (28) using anti-Foxo3a antibody (dilution 1:50).

**Immunohistochemical analysis.** Foxo3a expression was assessed by evaluating the proportion and intensity of positively stained carcinoma cells. A score was assigned to represent the estimated percentage of positively stained carcinoma cells as follows: 0 = none; 1 = ≤ 1%; 2 = 1–10%; 3 = 10–33%; 4 = 33–67%; 5 = ≥ 67%. An intensity score was assigned to represent the average estimated intensity of staining in positive carcinoma cells as follows: 0 = none, 1 = weak, 2 = intermediate, 3 = strong. The proportion score and intensity score were added to obtain a total score ranging from 0–8 (29). The immunohistochemistry results were classified based on the total scores, with 0–4 classified as low expression, and 5–8 as high expression. The immunohistochemistry
results were independently judged by two trained uropathologists (YS and KKi). Differences in evaluations were discussed using a double-headed microscope until consensus was reached.

**Knockdown analysis using small interfering (si)RNAs.** Knockdown analysis using siRNAs was performed as previously described (27,30). Briefly, the double-stranded RNA 25-base-pair oligonucleotides presented in Supplementary Table 1 were commercially generated (Invitrogen). KK47, TCCsup and T24 cells were transfected with siRNA using Lipofectamine 2000 (Invitrogen), according to the manufacturer’s instructions.

**Scratch-wound assay.** Scratch-wound assays were performed, as previously described (30). Briefly, KK47, TCCsup and T24 cells (1×10^5) transfected with 40 nmol/L of the indicated siRNAs, or KK47 stable transfectants (1×10^5), were seeded into 12-well plates and incubated for 72 h until they reached confluency. The invasive abilities of the KK47, TCCsup and T24 cells were represented by the ratios of the decreased scratch width after 48, 24, and 12 h, respectively, relative to the initial scratch width in the same field.

**Boyden-chamber assay.** Boyden-chamber assays were performed, as previously described (30). Briefly, KK47, TCCsup and T24 cells (5×10^4) transfected with 40 nmol/L
of the indicated siRNAs for 72 h, or KK47 stable transfectants (5×10^4), were placed in the top compartment of a standard 3-μm pore Boyden chamber (BD Biosciences, San Jose, CA). The numbers of migrated cells were determined from three random fields.

**RNA isolation, reverse transcription and quantitative real-time PCR.** These procedures were performed as previously described (27,30). Quantitative real-time PCR was performed using the following TaqMan Gene Expression Assays for Foxo3a (Hs00921424_m1), Twist1 (Hs00361186_m1), YB-1 (Hs00698625_g1) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH, Hs02758991_g1) (Applied Biosystems, Foster City, CA) and TaqMan Gene Expression Master Mix (Applied Biosystems), or the following primer pairs: 5′-ATGCTTGCCAGTGTCGGAAT-3′ (Fw) and 5′-CAACCCGCTTCATCTTCTGG-3′ (Rv) for p300, 5′-

GCTCAGACGGCTTCACAC-3′ (Fw) and 5′-TGCTCTGTGTCCAGCTACT-3′ (Rv) for E-cadherin and 5′-GGAACGGTGAAGGTGACAGC-3′ (Fw) and 5′-

AATCAAAGGTGTCGCCA-3′ (Rv) for β-actin and SYBR Premix Ex Taq II (Takara Bio, Shiga, Japan), on a 7900HT PCR system (Applied Biosystems). The transcript levels of Foxo3a, Twist1, YB-1 and E-cadherin were corrected according to the corresponding GAPDH and β-actin transcript levels. All values represent the results of at least three independent experiments.
Western blot analysis. The preparation of whole-cell lysates and western blotting were performed as previously described (27,30).

Statistical analysis. The Mann-Whitney U-test was used to analyze correlations between gene expression and clinicopathologic parameters and the in vitro experiments. Fisher’s exact test and the χ2 test were used to analyze correlations between Foxo3a expressions and clinicopathologic parameters. The Kaplan-Meier method was used to show that patients could be stratified into significantly different risk groups for disease recurrence, bladder cancer-specific survival, and overall survival. The Cox proportional hazards model was used for multivariate survival analysis. Values of P < 0.05 were considered to be statistically significant.

Results

Foxo3a mRNA levels decrease in invasive UC. The Foxo3a transcription factor is implicated in cancer cell growth and clinicopathologic parameters in various cancers (31–35). We therefore investigated Foxo3a mRNA expression levels in 71 UC samples (Supplementary Table 2). Foxo3a was expressed, at various levels, in all 71 samples. The mean level of Foxo3a mRNA expression was lower in high-grade than in low-grade tumors, although the difference was not significant (Fig. 1A). This was in accordance with previous results indicating that Foxo3a regulates cell proliferation (27). Foxo3a
expression levels were compared in non-invasive (Ta, T1, Tis) and invasive cancers (T2, T3, T4): surprisingly, Foxo3a mRNA expression levels were clearly lower in invasive than in non-invasive cancers (Fig. 1B: \( P = 0.049 \)). Moreover, five metastatic urothelial tumors had decreased Foxo3a mRNA expression levels compared with non-metastatic cancers, although the difference was not significant (Fig. 1C).

**Foxo3a immunohistochemical expression is downregulated in UC cases with high tumor stage and poor prognosis.** To strengthen the finding of gene expression assay, we conducted immunohistochemistry against Foxo3a. Foxo3a staining was detected in the nucleus and cytoplasm of normal urothelial epithelium and carcinoma cells. Stromal cell nuclei from normal bladder parenchyma displayed discontinuous equivocal-to-moderate expression. Foxo3a expression was high in non-invasive UC and low in invasive UC (Fig. 2A). The relationships between Foxo3a expression and clinicopathologic parameters are summarized in Table 1. Foxo3a expression was significantly lower in high \( pT \) stage cancer than in low \( pT \) stage cancer (\( P = 0.009 \)), supporting the finding of gene expression assay. Patients with low Foxo3a expression had lower cancer-specific survival rates (Fig. 2B), disease-free survival rates (Fig. 2C), and overall survival rates (Fig. 2D), than the high expression group (log-rank test: \( P = \))
0.002; P = 0.020; P = 0.002, respectively). The effects of Foxo3a expression on patient prognosis was recognized in multivariate survival analysis, even when stage and lymph node status were included, demonstrating the independent prognostic significance of Foxo3a expression (Table 2; P = 0.037; hazard ratio = 2.974).

**Foxo3a regulates cancer cell motility in KK47 and TCCsup cells, but not in T24 cells.** Because Foxo3a expression was inversely correlated with tumor stage, the effect of Foxo3a on UC motility was investigated using the scratch-wound assay. Foxo3a-specific siRNA was used to suppress Foxo3a expression, as previously described (27). Silencing Foxo3a led to increased motility of KK47 and TCCsup cells, but had no significant effect on the motility of T24 cells (Fig. 3A). Cell motility in the Foxo3a-knockdown cells was also assayed using a Boyden chamber. As in the scratch-wound assay, Foxo3a silencing increased the motility of KK47 and TCCsup cells, but not of T24 cells (Fig. 3B).

**Foxo3a regulates YB-1 and E-cadherin expression through negative Twist1 regulation.** Twist1 and E-cadherin are known to be master regulators, regulating cell migration and metastasis (21); YB-1 is also involved in cancer-cell migration (22,23). As
Foxo3a expression levels were inversely correlated with invasive UC phenotypes, we speculated that Foxo3a might be inversely correlated with Twist1 and YB-1, and positively correlated with E-cadherin expression. Twist1, YB-1, and E-cadherin expression levels were examined in KK47, TCCsup, and T24 cells transfected with Foxo3a-specific siRNAs. Twist1 and YB-1 expression were elevated in Foxo3a-knockdown KK47 and TCCsup cells, while E-cadherin expression was decreased. However, Twist1 expression was barely detectable or affected by Foxo3a suppression in knockdown T24 cells, and consequently had no effect on YB-1 and E-cadherin expression levels. Twist1 and YB-1 protein levels analyzed by western blotting showed similar changes to those detected at the mRNA level, although E-cadherin expression in KK47 and TCCsup cells was not detected as previously reported (31) (Fig. 3C). The motilities of Foxo3a- and/or Twist1-knockdown KK47 cells were examined to determine the effect Foxo3a on cell motility mediated via Twist1. As shown in Fig. 3D, Twist1 knockdown abolished KK47 motility which was increased by Foxo3a knockdown, suggesting that Foxo3a regulated KK47 motility through Twist1.

**Foxo3a acetylation level is implicated in KK47 cell motility.** Foxo3a is known to interact with, and be acetylated by p300, which modulates transcriptional ability.
Modulation of Foxo3a, Twist1, YB-1 and E-cadherin expression was therefore investigated in p300-knockdown cells, using p300-specific siRNA, as previously described (27). As in Foxo3a-knockdown cells, p300 downregulation increased Twist1 expression and decreased E-cadherin expression in KK47 cells. However, YB-1 expression was not affected; this may be due to the effects of p300 on YB-1 transcription by Twist1. Also as in Foxo3a-knockdown cells, Twist1, YB-1 and E-cadherin expression were unaffected by p300 knockdown in T24 cells. These findings were confirmed by western blotting (Fig. 4A). As the transcription co-activator p300 regulated Twist1, YB-1 and E-cadherin expression in KK47 cells, the effects of p300 silencing on KK47 cell motility were then investigated. Knockdown of p300 expression in KK47 cells led to increased cell motility (Fig. 4B).

Because the expression and acetylation levels of Foxo3a are implicated in cellular motility, the effects of wild-type and non-acetylation-mimicking Foxo3a overexpression on cell motility were investigated, using stable transfectants of KK47 cells expressing GFP, Foxo3a-GFP or Foxo3a-GFP KR protein. These stable transfectants expressed almost equal amounts of exogenous GFP-tagged proteins and the mutated Foxo3a protein (Foxo3a-GFP KR) was not acetylated, as shown previously (27). The results of quantitative real-time PCR showed that Foxo3a-GFP overexpression in KK47 cells
reduced Twist1 and YB-1 expression, whereas E-cadherin expression was increased by Foxo3a overexpression. However, Foxo3a-GFP KR overexpression in KK47 cells affected the expression of these genes to a lesser extent, compared with wild-type Foxo3a overexpression. These findings were confirmed at the protein level by western blotting (Fig. 4C). The motility of KK47-Foxo3a-GFP (#1 and #2) cells determined by scratch-wound assay was lower than that of KK47-AcGFP (#1 and #2) cells. However, KK47-Foxo3a-GFP KR (#1 and #2) cells were more motile than KK47-Foxo3a-GFP (#1 and #2) cells, but less motile than KK47-AcGFP (#1 and #2) cells. Similarly, using Boyden-chamber assays, the motility of KK47-Foxo3a-GFP (#1 and #2) cells was clearly lower than that of KK47-AcGFP (#1 and #2) cells. KK47-Foxo3a-GFP KR (#1 and #2) cells were more motile than KK47-Foxo3a-GFP (#1 and #2) cells, but less motile than KK47-AcGFP (#1 and #2) cells (Fig. 4D).

**Discussion**

The results of this study demonstrated that Foxo3a expression levels were inversely correlated with UC invasiveness, as represented by tumor stage. Although the samples used for gene expression assay contained some amount of stroma, the bias by stroma contamination doesn’t seem so variable among these samples. In addition, immunohistochemistry clearly revealed the association between Foxo3a expression and
UC invasiveness although hereafter the method such as micro-dissection might be more suitable to avoid a potential bias. Human prostate cancer cells, xenografts, and clinical samples have been shown to harbor heterozygosity losses on chromosome 13q14, which is the known gene locus for Foxo1 (32). Loss of Foxo1 gene expression is therefore directly related to increased cell proliferation in cancer cells, suggesting that Foxo1 protects against prostate carcinogenesis. Furthermore, chromosomal breakpoints in human acute myeloid leukemia were found to involve Foxo3a and Foxo4. For example, the mixed-lineage leukemia gene can fuse with Foxo3a and Foxo4, thereby potentially disturbing their tumor suppressive functions (33,34).

Immunohistochemical analyses have also shown a direct relationship between low levels of Foxo3a and rapid proliferation and a positive correlation between Foxo3a and the cell cycle inhibitor p27kip1 in non-Hodgkin’s lymphoma cells (35). Expression of phosphorylated Foxo1, an inactivated form, was higher in early pTNM stages of gastric cancer, and was inversely correlated with lymphatic invasion and lymph node metastasis, and positively correlated with longer patient survival (36). On the other hand, an association between expression of phosphorylated Foxo1 and unfavorable outcomes in acute myeloid leukemia or advanced-stage colon cancer was reported (37,38). The biological significance of Foxo expression thus appears to differ among
cancer types.

Twist1 is known to regulate the invasive and metastatic characteristics of cancer cells (21). YB-1 has also recently been shown to regulate cancer cell invasiveness (22,23). In the current study, Foxo3a expression levels in UC were shown to be inversely correlated with tumor stage, and cancer cell motility was augmented in Foxo3a-knockdown cells, an effect that was abolished by Twist1 knockdown. These findings may reflect Foxo3a's negative regulation of Twist1 and YB-1, which are known promoters of tumor invasion. No direct link between Foxo transcription factors and Twist1/YB-1 signaling has been previously reported, but this negative regulation of Twist1 and YB-1 by Foxo3a might be a crucial factor affecting various aspects of cancer biology.

Several researchers have reported that the acetylation status of Foxo transcription factors influences their transcriptional activity (11). Foxo transcription factors were found to interact with Sirt1 and p300, which deacetylate and acetylate, respectively (11–15). Sirt1 represses Foxo3a's ability to transcribe the pro-apoptotic factor Bim (39). The transcription of Fas ligand is also reportedly decreased by Sirt1 (16), while the DNA-repair-related gene GADD45α, and the antioxidant protein MnSOD are induced by Sirt1 overexpression (16,40).
The results of this study showed that Foxo3a regulates Twist1, YB-1 and E-cadherin expression. Twist1 and YB-1 are well-known proto-oncogenes, involved in cancer cell aggressiveness and invasiveness. In addition, Foxo3a silencing increases cell motility, and aggressive UCs express less Foxo3a. Foxo3a may therefore repress cancer cell aggressiveness through negative regulation of Twist/YB-1 signaling, in addition to its positive effects on E-cadherin.
Acknowledgments


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We are grateful to Dr. Osamu Ogawa (Kyoto University, Kyoto, Japan) for kindly providing the TCCsup cells. We would like to thank Dr. Dongchon Kang (Kyushu University, Fukuoka, Japan) for helping with quantitative real-time PCR, Edanz Group Japan for editorial assistance, and Ms. Noriko Hakoda and Ms. Seiko Kamori for their technical assistances. The authors would like to acknowledge the technical expertise of the Support Center for Education and Research, Kyushu University.
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**Figure legends**

**Fig. 1** Foxo3a mRNA level is decreased in invasive urothelial cancer. (A)–(C) Twist1 and YB-1 transcript levels are indicated according to tumor grade (A), tumor stage (B) and metastasis status (C). Middle lines, median; upper lines, upper quartile; lower lines, lower quartile; 75%; bars: ± s.d.

**Fig. 2** Foxo3a immunohistochemical expression is downregulated in urothelial cancers (UCs) with high tumor stage and poor prognosis. (A) Foxo3a expression was high in non-invasive UC, and low in invasive UC. Hematoxylin-eosin (H&E) staining of the same samples is also shown. (B)–(D) Disease-free survival curves (B), cancer-specific survival curves (C), and overall survival curves (D) of patients in Foxo3a low-expression and high-expression groups.

**Fig. 3** Foxo3a regulates YB-1 and E-cadherin expression through negative Twist1 regulation, and regulates cancer-cell motility in KK47 and TCCsup cells, but not in T24 cells. (A) KK47, TCCsup and T24 cells were transfected with 40 nmol/L of the indicated siRNA. The cells were scratched 72 h after transfection. The scratch widths were measured after 48 h (KK47 cells), 24 h (TCCsup cells) or 12 h (T24 cells) of incubation.
The motility of cells transfected with control siRNA corresponded to 1. Boxes, mean; bars, ±s.d. *P < 0.05 (compared with cells transfected with control siRNA). (B) KK47, TCCsup and T24 cells were transfected with 40 nmol/L of the indicated siRNA. The cells were applied to a Boyden chamber 72 h after transfection. The mobilized cell count when transfected with control siRNA corresponded to 1. Boxes, mean; bars, ± s.d. *P < 0.05 (compared with cells transfected with control siRNA). (C) KK47, TCCsup and T24 cells were transfected with 40 nmol/L of the indicated siRNA. Quantitative real-time PCR analysis of Foxo3a, Twist1, YB-1, E-cadherin, glyceraldehyde 3-phosphate dehydrogenase (GAPDH) and β-actin was performed. The levels of Foxo3a, Twist1, YB-1 and E-cadherin transcripts in cells transfected with control siRNA corresponded to 1. Boxes: mean; bars: ± s.d. *P < 0.05 (compared with cells transfected with control siRNA). Whole-cell extracts were subjected to SDS-PAGE, and western blotting was performed using the indicated antibodies. (D) KK47 cells were transfected with 20 nmol/L of control siRNA or Foxo3a siRNA #1, and 20 nmol/L of control siRNA or Twist1 siRNA. (Left panel) Whole-cell extracts were subjected to SDS-PAGE, and western blotting was performed using the indicated antibodies. (Right panel) The cells were scratched 72 h after transfection and the scratch widths were measured after 48 h of incubation. The motility when transfected with control siRNA corresponded to 1. Lane
1, control siRNA; lane 2, Foxo3a siRNA #1; lane 3, Twist1 siRNA; lane 4, Foxo3a siRNA #1 and Twist1 siRNA. Boxes, mean; bars, ±s.d. *P < 0.05 (compared with lane 1).

**P < 0.05 (compared with lane 2).

**Fig. 4** Foxo3a acetylation level is implicated in KK47 cell motility. (A) KK47 and T24 cells were transfected with 40 nmol/L of the indicated siRNA. Quantitative real-time PCR analysis of p300, Foxo3a, Twist1, YB-1, E-cadherin, glyceraldehyde 3-phosphate dehydrogenase (GAPDH) and β-actin was performed. The levels of p300, Foxo3a, Twist1, YB-1 and E-cadherin transcripts from cells transfected with control siRNA corresponded to 1. Boxes: mean; bars: ± s.d. *P < 0.05 (compared with cells transfected with control siRNA). Whole-cell extracts were subjected to SDS-PAGE, and western blotting was performed using the indicated antibodies. (B) KK47 cells were transfected with 40 nmol/L of the indicated siRNA. (Upper panel) The cells were scratched 72 h after transfection and the scratch widths were measured after 48 h of incubation. The motility when transfected with control siRNA corresponded to 1. Boxes: mean; bars: ± s.d. *P < 0.05 (compared with cells transfected with control siRNA). (Lower panel) The cells were applied to a Boyden chamber 72 h after transfection. Mobilized cells were then counted. The cell count when transfected with control siRNA corresponded to 1.
Boxes: mean; bars: ± s.d. *P < 0.05 (compared with cells transfected with control siRNA). (C) Quantitative real-time PCR analysis of Foxo3a, Twist1, YB-1, E-cadherin, GAPDH and β-actin was performed after extraction of total RNA from the indicated KK47 stable transfectants and synthesis of cDNA. The levels of Foxo3a, Twist1, YB-1 and E-cadherin transcripts from KK47-AcGFP #1 cells corresponded to 1. Boxes: mean; bars: ± s.d. *P < 0.05 (compared with KK47-AcGFP #1 cells). **P < 0.05 (compared with KK47-Foxo3a-GFP #1 cells). Whole-cell extracts were subjected to SDS-PAGE, and western blotting was performed using the indicated antibodies. (D) The indicated KK47 stable transfectants were seeded. Scratch-wound and Boyden chamber assays were performed the following day, as described in (B). *P < 0.05 (compared with KK47-AcGFP #1 cells). **P < 0.05 (compared with KK47-Foxo3a-GFP #1 cells).
A

Invasive Non-invasive
Foxo3a

B

Low grade High grade
Foxo3a

C

Meta- Meta+
Foxo3a

p = 0.049

p = 0.16

p = 0.83
High Foxo3a expression

Low Foxo3a expression

P = 0.002

(n = 28)

(n = 25)

High Foxo3a expression

Low Foxo3a expression

P = 0.020

(n = 25)

(n = 28)

High Foxo3a expression

Low Foxo3a expression

P = 0.002

(n = 25)

(n = 28)
Shiota et al. Figure 3

A

Relative decreased width

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B

Relative mobilized cell count

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C

Relative mRNA expression

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D

Relative decreased width

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<tr>
<th></th>
<th>Control siRNA</th>
<th>Foxo3a siRNA #1</th>
<th>Foxo3a siRNA #2</th>
</tr>
</thead>
<tbody>
<tr>
<td>KK47</td>
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</tr>
</tbody>
</table>
**Shiota et al. Figure 4**

(A) Graphs showing relative mRNA expression of various genes across different conditions. **KK47** and **T24** cell lines are compared.

(B) Graphs showing relative decrease in width and relative mobilized cell count.

(C) Graphs showing relative mRNA expression across different conditions.

(D) Graphs showing relative decrease in width and relative mobilized cell count.
Table 1 Relationships between Foxo3a expression and clinicopathologic parameters

<table>
<thead>
<tr>
<th>Variable</th>
<th>n = 53</th>
<th>Foxo3a expression</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;70</td>
<td>31</td>
<td>13</td>
<td>18</td>
</tr>
<tr>
<td>&gt;=70</td>
<td>22</td>
<td>15</td>
<td>7</td>
</tr>
<tr>
<td>Sex</td>
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<td></td>
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<td>21</td>
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</tr>
<tr>
<td>pT1a, pT1, pTis</td>
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<td>15</td>
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<td>pT2, pT3, pT4</td>
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<td>21</td>
<td>10</td>
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<tr>
<td>Lymph node status</td>
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</tr>
<tr>
<td>N0</td>
<td>40</td>
<td>18</td>
<td>22</td>
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<tr>
<td>N1, N2</td>
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<td>9</td>
<td>3</td>
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* Statistically significant ($\chi^2$ test)
<table>
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<tr>
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<th>Univariate analysis</th>
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<th>Multivariate analysis</th>
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<tbody>
<tr>
<td></td>
<td>HR</td>
<td>95%CI</td>
<td>P value</td>
<td>HR</td>
<td>95%CI</td>
<td>P value</td>
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<td>Foxo3a</td>
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<td>High expression</td>
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<td>Low expression</td>
<td>4.421</td>
<td>1.709–13.653</td>
<td>0.002*</td>
<td>2.974</td>
<td>1.063–9.964</td>
<td>0.037*</td>
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<td></td>
<td></td>
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<td>0.118</td>
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<td>Stage</td>
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<tr>
<td>pTa, pT1, pTis</td>
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<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>pT2, pT3, pT4</td>
<td>8.819</td>
<td>2.932–38.015</td>
<td>&lt;0.001*</td>
<td>4.623</td>
<td>1.244–21.994</td>
<td>0.022*</td>
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<tr>
<td>Lymph node status</td>
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<tr>
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<td>N1, N2</td>
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<td>&lt;0.001*</td>
<td>4.407</td>
<td>1.536–14.041</td>
<td>0.006*</td>
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</table>

HR = hazard ratio.; CI = confidence interval. *Statistically significant (Cox proportional hazards model)
Supplementary Table 1 Sequence of siRNAs used

<table>
<thead>
<tr>
<th>siRNA</th>
<th>Sense sequence</th>
<th>Antisense sequence</th>
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<tr>
<td>Foxo3a siRNA #1</td>
<td>5′-UAGAAUUUGUGCGUGAAGCAGGAAGUC-3′</td>
<td>5′-GACUUCCGUUCACGCAACUAUAUUCA-3′</td>
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<tr>
<td>Foxo3a siRNA #2</td>
<td>5′-UAUACGGGAAGCUAGACUCUGCUAG-3′</td>
<td>5′-CAGCGGAGCUAGCUUCCGUUAU-3′</td>
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<td>Twist1 siRNA</td>
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<td>5′-GACCGCGCUAGCUUCCGUUAU-3′</td>
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<td>p300 siRNA #1</td>
<td>5′-AUUAUAGGCUAGGCAGCUUCCUA-3′</td>
<td>5′-CCUGCCAGGUGACUCUCUAUAUU-3′</td>
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<tr>
<td>p300 siRNA #2</td>
<td>5′-UUAAACAGCCACAGACAGAAUCC-3′</td>
<td>5′-GGAUUCUGUGAUGCGUUUAA-3′</td>
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</table>
Supplementary Table 2 Clinicopathologic characteristics of patients subjected to gene expression assay

<table>
<thead>
<tr>
<th>Variable</th>
<th>n = 71</th>
<th>Percent (%)</th>
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<td>Age at operation, years</td>
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