**MED12 overexpression is a frequent event in castration-resistant prostate cancer**

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**Abstract**

In a recent effort to unravel the molecular basis of prostate cancer (PCa), Barbieri and colleagues using whole-exome sequencing identified a novel recurrently mutated gene, **MED12**, in 5.4% of primary PCa. **MED12**, encoding a subunit of the Mediator complex, is a transducer of Wnt/b-catenin signaling, linked to modulation of hedgehog signaling and to the regulation of transforming growth factor beta (TGFβ)-receptor signaling. Therefore, these studies prompted us to investigate the relevance of **MED12** in PCa. Expression of **MED12**, SMAD3 phosphorylation, and proliferation markers was assessed by immunohistochemistry on tissue microarrays from 633 patients. siRNA-mediated knockdown of **MED12** was carried out on PCa cell lines followed by cellular proliferation assays, cell cycle analysis, apoptosis assays, and treatments with recombinant TGFβ3. We found nuclear overexpression of **MED12** in 40% (28/70) of distant metastatic castration-resistant prostate cancer (CRPCMET) and 21% (19/90) of local-recurrent CRPC (CRPCLOC) in comparison with frequencies of less than 11% in androgen-sensitive PCa, and no overexpression in benign prostatic tissues. **MED12** expression was significantly correlated with high proliferative activity in PCa tissues, whereas knockdown of **MED12** decreased proliferation, reduced G1- to S-phase transition, and increased the expression of the cell cycle inhibitor p27. TGFβ signaling activation associates with **MED12** nuclear overexpression in tissues and results in a strong increase in **MED12** nuclear expression in cell lines. Furthermore, **MED12** knockdown

**Key Words**
- MED12
- overexpression
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- castration-resistant

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reduced the expression of the TGFβ target gene vimentin. Our findings show that MED12 nuclear overexpression is a frequent event in CRPC in comparison with androgen-sensitive PCa and is directly implicated in TGFβ signaling.

Introduction

Prostate cancer (PCa) is a clinically heterogeneous disease and a leading cause of cancer death worldwide, thus unraveling the molecular basis of this disease is of great importance.

Therefore, a notable effort has been made recently by Barbieri et al. (2012) in which new recurrently mutated genes were identified in primary PCa through whole-exome sequencing.

Among the recurrently mutated genes identified, MED12, encoding a subunit of the Mediator complex, is mutated in 5.4% of primary PCa (Barbieri et al. 2012). Interestingly, in an earlier study, MED12 has been reported to be mutated at a high frequency in uterine leiomyomas (Makinen et al. 2011). MED12 is part of the multi-protein complex Mediator, which is essential for the transcription of protein-coding genes, and serves as hub for diverse signaling pathways (Malik & Roeder 2010). The division of the Mediator complex into four distinct modules, namely head, middle, tail, and kinase, reflects different functions of distinct Mediator subunits (Cai et al. 2009). MED12 is a subunit of the kinase module and has been shown to function as a transducer of Wnt/β-catenin signaling (Kim et al. 2006), linked to the modulation of hedgehog signaling (Zhou et al. 2006) and to the regulation of transforming growth factor beta (TGFβ) receptor signaling (Huang et al. 2012).

TGFβ signaling regulates prostate growth by inhibiting proliferation and inducing apoptosis, and thus serves as a tumor-suppressor in normal prostatic tissue and early stages of PCa (Tang et al. 1999). Loss or mutations of components of TGFβ pathway (Tang et al. 1999), as well as altered TGFβ signaling, promote cell invasion, metastasis, angiogenesis, and epithelial–mesenchymal transition, indicative of an oncogenic role of TGFβ signaling during prostate tumorigenesis and progression. In addition, activation of TGFβ signaling has been shown to increase the invasive and migratory behavior of PCa cells (Walker et al. 2013), and inhibition of TGFβ signaling reduced tumor growth and/or invasiveness in vivo (Gaspar et al. 2007, Moore et al. 2008). Furthermore, a study in 2007 has shown that SMAD-dependent TGFβ signaling is critical for PCa growth and progression in nude mice (Lu et al. 2007). The response of metastatic PCa cell lines to TGFβ depends on the cellular microenvironment. In a recent study, we observed increased proliferation of the PCa cell line PC3 in response to exogenous TGFβ3 when cells were grown in the presence of all growth factors (Shaikhibrahim et al. 2013). Other studies showed that TGFβ treatment had no effect upon proliferation in PC3 cells when cells were plated in serum-free medium (Vo et al. 2012).

Prompted by the reports about mutations in MED12 in PCa tissues, and the critical role of MED12 in signaling pathways that have been reported to be involved in PCa (Yardy & Brewster 2005, Chen et al. 2011), in this study, we investigated the relevance of MED12 in PCa and its relationship with TGFβ signaling.

Materials and methods

The study was approved by the Internal Review Board of the University Hospital of Bonn and performed in accordance with the Declaration of Helsinki.

Cohorts

The study cohort comprised 656 tissue samples, consisting of 40 benign tissue samples, 405 non-metastasized primary PCa samples, 91 lymph node metastasized primary PCa samples or lymph node metastases, and 160 castration-resistant prostate cancer (CRPC) samples (90 local recurrent CRPC and 70 distant metastatic CRPC). These samples were obtained from patients at the University Hospital of Bonn, Basel and Örebro. We collected both primary tumor and corresponding lymph node metastases from 32 patients. We assessed the expression of pSMAD3 in 110 primary PCa, 78 lymph node metastases, and 40 CRPC samples.

Tissue microarrays

The tissue microarrays were constructed as described previously (Braun et al. 2011).
Immunohistochemistry

The following primary antibodies were used (dilutions, clones, and manufacture): anti-MED12 rabbit polyclonal (1:50, A300-774A, Bethyl Laboratories, Montgomery, TX, USA), anti-PHH3 rabbit polyclonal (1:100, CMC36911010; Cell Marque, Rocklin, CA, USA), ready-to-use anti-Ki-67 rabbit monoclonal (1:100, 30-9, Ventana, Tucson, AZ, USA), anti-pSMAD3 rabbit monoclonal (1:50, D12E11, Cell Signaling, Danvers, MA, USA), anti-p27 Kip1 rabbit polyclonal (1:100, 30-9, Ventana, Tucson, AZ, USA), anti-pha3 rabbit polyclonal (1:100, DCS60.2, Emergo Europe, Hamburg, Germany), and anti-Vimentin rabbit monoclonal (1:100, D69C12 XP, Cell Signaling), anti-p21 rabbit monoclonal (1:100, D69C12 XP, Cell Signaling), anti-p21 mouse monoclonal (1:100, DC560.2, Emergo Europe, Hamburg, Germany), and anti-Vimentin rabbit monoclonal (1:100, D21H3, 3932, Cell Signaling) antibody. Negative controls for antibodies were performed using the same immunohistochemistry (IHC) protocol without primary antibody. Protein expression was quantified based on the immunoreactivity score (IRS; Remmele & Stegner 1987). IRS takes into account both the amount of immunoreactive cells and the intensity of the staining and is calculated as the percentage of immunoreactive tumor cells (0, 0%; 1, <10%; 2, 10–50%; 3, 51–80%; and 4 ≥80%) × staining intensity (from 0, no expression to 3, strong expression). An IRS with a value of 0 was considered as none or as a very weak expression, whereas an IRS of 1–2 was considered as weak to medium expression. Furthermore, an IRS of 3 and above was considered as high expression (overexpression, IRS ≥3). These categories were decided upon before the analyses to avoid the risk of ‘data overfitting’. We chose a score of 3 or higher, as it reflects cases which were either visibly expressing MED12 in virtually all cancer cells or harbor at least a marked or strong expression in 11–50% (or more) of cancer cells. Notably, the statistical correlations were performed with the full-range MED12 IRS and not with the dichotomized categories (i.e. overexpression vs weak-to-medium expression), thus the distinction between overexpressing and nonoverexpressing cases had no effect on these analyses. The association between MED12 and TGFβ signaling activation was examined dichotomizing the full-range of MED12 IRS in overexpressing and nonoverexpressing cases. For each tissue sample, we analyzed 3 scores and calculated the mean IRS, considering all 3 scores or at least 2 scores excluding outliers.

Cell lines

All cell lines were purchased from the American Type Culture Collection (ATCC, Manassas, VA, USA) and were grown in a 5% CO2 incubator at 37 °C and 85% humidity. Monolayer cultures of PC3 and BPH1 cells were maintained in RPMI-1640 medium (Biochrom, Berlin, Germany) containing 10% heat-inactivated FCS (Sigma), 1% streptomycin–penicillin antibiotics (Gibco), and 1% glutamine. Furthermore, for the cell lines LNCaP and DU145, the medium mentioned earlier was supplemented with 25 mM HEPES buffer (PAA Laboratories GmbH, Pasching, Austria) and 1% NEAA (Gibco). The cell lines were authenticated using Multiplex Cell Authentication by Multiplexion (Heidelberg, Germany), as described previously (Castro et al. 2013).

Immunofluorescence

Immunofluorescence (IF) was carried out using anti-MED12 rabbit polyclonal antibody (1:50, A300-774A, Bethyl Laboratories) on BPH1, DU145, PC3, and LNCaP cells as described by Cell Signaling Technology, Inc.

siRNA-mediated MED12 knockdown

For MED12 knockdown, we used SMARTpool–ON-TARGETplus MED12 siRNA (Thermo Scientific, Darmstadt, Germany) and as control, we used ON-TARGETplus nontargeting pool (Thermo Scientific). DU145 and LNCaP were transfected with 100 nmol/l siRNA using Screenfect A (Genaxxon Bioscience GmbH, Ulm, Germany). The MTT proliferation assay was carried out using siRNA-transfected cells in 96-well plates. For immunocytochemistry (ICC), western blotting analysis, cell cycle analysis, and apoptosis assay, siRNA transfection was carried out in six-well plates; after 72 h, the cells were plated on glass slides for ICC or harvested for protein extraction or functional assays. Quantitative analysis of p27, p21, and Vimentin expression was carried out using Tissue Studio (Definiens Developer XD 2.0, Definiens AG, Munich, Germany).

QRT-PCR

RNA was isolated using the RNeasy Mini Kit (Qiagen) and reverse transcribed using an iScript cDNA synthesis kit, according to manufacturer’s instructions (Bio-Rad).

PCRs were carried out using a Power SYBR Green Kit (Thermo Fisher Scientific) according to the manufacturer’s instructions using Light-Cycler 480 II (Roche). For each sample in a given experiment, technical duplicate reactions were carried out using β-actin as an housekeeping gene. Fold changes were calculated using the formula 2−ΔΔCT. Primer pairs used for MED12 (Applied Biosystems): MED12: F, 5’-attaacgagcttgagaccctg-3’ and MED12: R, 5’-ctggacgaagctgctgct-3’.
Western blotting

For the preparation of whole-protein cell lysates, cell pellets were washed with ice-cold PBS and re-suspended in an extraction buffer containing 1% dithiothreitol, phosphatase inhibitor, protease inhibitor, and the phenylmethanesulfonylfluoride for 60 min. The lysates were then centrifuged for 30 min at 13,000 g at 4 °C. The supernatant with whole-protein lysate was harvested, and the protein concentration was measured using the bicinchoninic acid–Protein Assay Kit (Thermo Scientific). Thereafter, whole-cell extracts were fractionated by SDS–PAGE and transferred to a PVDF membrane using a transfer apparatus according to the manufacturer’s protocols (Bio-Rad). After incubation with 5% nonfat milk in TBST (10 mM Tris, pH 8.0, 150 mM NaCl, and 0.5% Tween 20) for 30 min, the membrane was incubated with anti-MED12 rabbit polyclonal (1:50, A300-774A, Bethyl Laboratories), anti-phospho (S423+S425)-SMAD3 rabbit MAB (1:1000, EP823Y, Abcam, Cambridge, UK), anti-β-actin MAB (1:5000, A1978, Sigma Aldrich, St Louis, MO, USA), and anti-Vimentin rabbit monoclonal (1:1000, 3932, Cell Signaling) primary antibodies at 4 °C overnight. The membranes were washed three times with TBST for 10 min and incubated with a 1:5000 dilution of HRP-conjugated anti-mouse or anti-rabbit antibodies for 1 h. The blots were washed with TBST three times and developed with the ECL System (GE Healthcare Life Science, Freiburg, Germany) according to the manufacturer’s protocol.

TGFβ treatment

PC3 cells were serum starved in a medium without FCS for 48 h, and then treated with recombinant TGFβ3 (Immuntools, Friesoythe, Germany) at a concentration of 10 ng/ml for 1 h, followed by preparation of whole-protein lysate.

For ICC, PC3 cells were seeded on slides in a medium containing 10% FCS. When cells were attached, they were grown in serum-free medium for 48 h, and then treated with serum-starved medium with or without 10 ng/ml TGFβ3 for 1 or 24 h. The slides were then washed with PBS and cells were fixed in paraformaldehyde (PFA) overnight. For detection of pSMAD3 after 1 h of TGFβ3 treatment, ICC was carried out using a primary antibody against pSMAD3. ICC using a primary antibody against MED12 was carried out on 24 h-treated cells. pSMAD3 and MED12 cytoplasmic and nuclear expression were analyzed by two independent pathologists.

For vimentin analysis, PC3 cells treated with scrambled or MED12 siRNA were plated on slides 72 h after siRNA transfection and grown in a medium containing 10% FCS and 20 ng/ml recombinant TGFβ3 for 48 h. The slides were then washed with PBS and cells were fixed in 4% PFA overnight. For detection of vimentin, ICC was carried out using a primary antibody against vimentin.

MTT cell proliferation assay

The cells were analyzed for proliferation using the MTT assays according to the manufacturer’s protocol (Roche) after siRNA transfection. DU145 and LNCaP cells were grown in a medium containing 10% FCS with physiological levels of androgens (1–10 nM dihydrotestosterone). Cellular proliferation was measured 3, 4, and 5 days after siRNA transfection. Each experiment was independently repeated twice in triplicates.

Cell cycle analysis

For cell cycle analysis, we performed propidium iodide (PI) DNA staining followed by FACS according to standard protocols (Sigma–Aldrich) as well as ICC for cell cycle markers p21 and p27. In more detail, 72 h (LNCaP cells) or 144 h (DU145 cells) after siRNA transfection, the cells were harvested and then plated on slides for ICC or used for FACS analysis. For FACS, the cells were washed with ice-cold PBS followed by resuspension in 200 μl staining buffer (Tris-buffered saline, Nonidet p-40, 1:1000) containing 7.5 mg/ml PI (Sigma–Aldrich) and ribonuclease A (Sigma–Aldrich) at a concentration of 1:1000. After 30 min incubation at room temperature, PI staining of cells was analyzed using FACSCanto II Cell Analyzer. FlowJo Software Package (Treestar, OR, USA) was used for analyzing flow cytometry data. For ICC, the cells were grown overnight on slides, washed with PBS, and fixed with PFA. ICC staining was carried out using antibodies against p21 and p27 and analyzed by two independent pathologists.

Annexin V/PI apoptosis assay

For apoptosis assay, the cells were stained with Annexin V and PI, and evaluated for apoptosis by flow cytometry according to the manufacturer’s protocol (eBioscience, San Diego, CA, USA). Briefly, cells were washed twice with PBS and binding buffer, stained with 5 μl of Annexin V–FITC and 2.5 μl of PI in 1× binding buffer for 15 min
at room temperature protected from light. Apoptotic cells were determined using FACSCanto II Cell Analyzer. Analysis of apoptotic cells included both, early apoptotic (Annexin V-positive and PI-negative) and late apoptotic (Annexin V-positive and PI-positive) cells.

Statistical analyses

Statistical analyses were performed using Microsoft Excel 2010 and SPSS 20 (SPSS).

Results

Nuclear expression and overexpression of MED12 in PCa tissues

IHC showed that nuclear expression of MED12 was significantly higher in 70 distant metastatic CRPC samples (CRPC^{MET}) and 90 local recurrent CRPC samples (CRPC^{LOC}) in comparison with androgen-sensitive PCa and benign prostatic tissues (Fig. 1a and b). Androgen-sensitive PCa consisted of 110 analyzed non-metastasized primary PCa (PCaN^{0}) as well as 91 lymph-node-metastasized primary PCa or lymph node metastases (PCaN^{1}). An independent PCa validation cohort (PCa^{VAL}), comprising 295 primary PCa tissue samples, was analyzed and included in our results. Nuclear overexpression of MED12 is defined as expression IRS ≥3, and thus MED12 is overexpressed more frequently in CRPC in comparison to androgen-sensitive PCa (Fig. 1c).

Nuclear expression of MED12 in prostate cell lines

ICC and IF indicated a medium to strong MED12 nuclear expression in metastatic CRPC cells (PC3 and DU145) and metastatic androgen-sensitive LNCaP cells, compared with medium expression of MED12 in benign prostatic BPH1 cells (Fig. 2a and b).

MED12 effects proliferative activity of PCa cells

IHC results for the proliferation markers Ki67 and pHH3 were assessed for 110 primary PCa, 91 lymph-node-metastasized primary PCa with corresponding lymph node metastases, and 40 CRPC samples. MED12 expression was found to correlate significantly with the expression of nuclear overexpression (defined as expression IRS ≥3) (c). Bars and error bars indicate mean IRS ± t.o. Independent t-test, ***P < 0.005. A full colour version of this figure is available at http://dx.doi.org/10.1530/ERC-14-0171.
the tumor proliferation markers Ki67 and pHH3 (Pearson correlation, \( P < 0.01 \)).

To assess the effect of MED12 on proliferative activity in PCa cell lines, we carried out siRNA-mediated MED12 knockdown followed by MTT cell proliferation assay. siRNA treatment led to decreased MED12 expression at the mRNA level and protein level in DU145 and LNCaP cells, as illustrated by qRT-PCR and western blotting respectively (Fig. 3a and b). The MTT proliferation assay indicates significantly reduced cell proliferation 5 days after MED12-siRNA transfection in both androgen-independent DU145 and androgen-dependent LNCaP cells (Fig. 3c).

Knockdown of MED12 inhibits cell cycle progression in PCa cells

To assess the effect of MED12 upon cell cycle distribution, we carried out FACS analysis using PI DNA staining in DU145 and LNCaP cells. Cell cycle distribution revealed that DU145 cells with MED12 knockdown accumulated in G0/G1 phase (46%) in comparison with control cells (11%), and that the percentage of cells in G2/M phase was reduced upon MED12 knockdown (17 vs 48% in control cells) 6 days after siRNA transfection (Fig. 3d). The proportion of LNCaP cells in S phase of the cell cycle decreased upon MED12 knockdown (9 vs 28% of control cells), whereas the percentage of cells in G2/M phase increased to 29% upon MED12 knockdown compared with control cells (11%) 72 h after siRNA transfection (Fig. 3e).

We next carried out expression analysis for the cyclin-dependent kinase inhibitors (CDKi) p21 and p27 in control and MED12-knockdown cells. Immunocytochemical staining revealed increased p27 protein expression and nuclear localization of p27 upon MED12 knockdown in DU145 (Fig. 4a) and LNCaP (Fig. 4b) cells. To quantify the expression of p27 in control and MED12 knockdown cells, we analyzed the immunocytochemical staining intensity (Fig. 4c and d). In DU145 and LNCaP cells with MED12 knockdown, p27 protein expression was increased 2.9- and 1.3-fold compared with control cells respectively (Fig. 4c and d). In contrast, DU145 control and MED12 knockdown cells exhibit no difference in p21 protein expression profile (Supplementary Fig. 1a, see section on supplementary data given at the end of this article), whereas p21 is slightly more expressed in LNCaP cells upon MED12 knockdown when compared with control cells (Supplementary Fig. 1b).

MED12 knockdown has no effect upon apoptosis rate in PCa cells

To examine whether reduced cell proliferation upon MED12 knockdown is a result of increased apoptosis, we carried out Annexin V–PI staining assay. We observed no significant difference in the apoptosis rate between DU145 control (4.2%) and MED12 knockdown cells (5.9%) (Supplementary Fig. 2a, see section on supplementary data given at the end of this article). The percentage of apoptotic cells was slightly increased upon MED12 knockdown in LNCaP cells, indicated by 5.7% Annexin V-positive MED12 knockdown cells compared with 1.8% Annexin V-positive control cells (Supplementary Fig. 2b).
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**Figure 3**
Effect of MED12 upon proliferation and cell cycle distribution in prostate cancer cells. siRNA-mediated MED12 knockdown in DU145 and LNCaP cell lines shows reduced MED12 expression by qRT-PCR (a) and western blotting (b) 72 h after siRNA transfection. MED12 mRNA expression in cells treated with scrambled siRNA was normalized to one. Reduced proliferation of MED12-knockdown cells compared with cells treated with scrambled siRNA in DU145 and LNCaP cells 5 days after siRNA transfection by MTT proliferation assay (c). Bars and error bars indicate the mean of the absorbance at 595 nm ± s.d. The percentages of cells in different phases of the cell cycle are shown for DU145 (d) and LNCaP (e) cells 6 days (DU145) or 72 h (LNCaP) after transfection with scrambled or MED12-specific siRNA. Bars and error bars indicate mean percentages of cells in each phase ± s.d. Independent t-test, *P<0.05 and **P<0.01. A full colour version of this figure is available at http://dx.doi.org/10.1530/ERC-14-0171.

**MED12 is implicated in TGFβ signaling in PCa cells**

In order to examine whether TGFβ signaling activation is associated with MED12 nuclear overexpression in PCa tissues, we carried out IHC for pSMAD3 on 110 primary PCa, 78 lymph node metastases, and 40 CRPC samples. In contrast to low/absent MED12 expression, MED12 nuclear overexpression was significantly associated with pSMAD3 expression in PCa tissues (Fig. 5a and Supplementary Table 1, see section on supplementary data given at the end of this article).

To investigate whether TGFβ signaling activation effects expression and cellular localization of MED12, PC3 cells were treated with recombinant TGFβ3 followed by ICC or MED12. Treatment of PC3 cells with recombinant TGFβ3 leads to the activation of TGFβ signaling as indicated by the increased expression and nuclear localization of pSMAD3 (Fig. 5b and c). TGFβ signaling activation results in a strong increase in MED12 nuclear expression, and a decrease in the cytoplasmic expression (Fig. 5d). Next, we investigated the effect of MED12 on the expression of TGFβ target genes. ICC (Fig. 5e) as well as western blotting analysis (Fig. 5g) showed reduced Vimentin expression in response to exogenous TGFβ3 in MED12-knockdown PC3 cells compared with control cells.
Analysis of the immunocytochemical staining intensity revealed that control cells expressed twofold higher Vimentin levels compared with MED12 knockdown cells (Fig. 5f).

**Discussion**

In our study, we found MED12 nuclear expression to be significantly higher in distant metastatic CRPC (CRPC\textsuperscript{MET}) and local recurrent CRPC (CRPC\textsuperscript{LOC}) as compared with androgen-sensitive PCa and benign prostatic tissues (Fig. 1a and b). MED12 was overexpressed in 40% of CRPC\textsuperscript{MET} and 21% CRPC\textsuperscript{LOC} (Fig. 1c).

In the majority of cases, we observed a heterogeneous expression pattern for MED12 within the samples from single patients of primary PCa and lymph node metastases. The focal heterogeneity in staining profiles concerned both, the amount of immunoreactive cells as well as the staining intensity.
as the intensity of the staining. This result may be due to the known heterogeneous and multifocal nature of PCa (Karavitakis et al. 2011). Interestingly, MED12 expression was more homogeneous in CRPC tissues compared with primary PCa and lymph node metastasis. The reduced heterogeneity of MED12 expression in advanced stages may be indicative of an important role of MED12 in the progression of PCa to castration resistance.

In light of our findings from tissue samples, we examined the expression of MED12 in benign prostatic BPH1 as well as metastatic androgen-sensitive LNCaP cells and PCa cells with dispensed androgen signaling (PC3 and DU145). In support of our findings from tissue samples, we found that MED12 exhibits medium to strong nuclear expression in PCa cells, compared with medium expression in benign prostatic cells (Fig. 2a and b). As MED12 is part of the Mediator complex, a co-activator of the general transcription machinery (Malik & Roeder 2010), it is expressed in nonmalignant cells. Consistent with that, we observed a weak staining for MED12 in benign prostate tissues (Fig. 1a and b).

Our observation that MED12 nuclear overexpression is a frequent event in CRPC in comparison with androgen-sensitive PCa, prompted us to examine whether MED12 expression was correlated with high proliferative activity in PCa. MED12 expression correlated significantly with the proliferation markers Ki67 and pHH3 in PCa tissues. Based upon these results, we found that knockdown of MED12 decreased proliferation in both androgen-independent CRPC DU145 cells and androgen-dependent LNCaP cells (Fig. 3b and c). In order to examine whether the reduced proliferation of MED12-knockdown cells may be affected by cell cycle arrest and/or increased apoptosis, we carried out cell cycle assays as well as apoptosis assays in DU145 and

Figure 5
MED12 is implicated in TGFβ signaling. Expression of pSMAD3 is associated significantly with MED12 nuclear overexpression in PCa tissues (a). **P < 0.01. Phosphorylation of SMAD3 in PC3 cells following treatment with 10 ng/ml recombinant TGFβ3 shown by western blotting (b). Immunocytochemical staining showed increased pSMAD3 after 1 h (c) and increased expression and nuclear localization of MED12 (d) in PC3 cells treated with TGFβ for 24 h compared with untreated cells. Immunocytochemical staining (e) showed reduced vimentin expression in PC3 cells with MED12 knockdown compared with control cells grown in a medium with or without 20 ng/ml recombinant TGFβ3 for 48 h. Bar graph shows reduced vimentin staining intensity in MED12-knockdown cells compared with control cells grown in medium with or without 20 ng/ml recombinant TGFβ3 for 48 h (g). A full colour version of this figure is available at http://dx.doi.org/10.1530/ERC-14-0171.
LNCaP cells. While we found no effect of MED12 knockdown upon the percentage of apoptotic cells (Supplementary Fig. 2), we observed significant differences in the cell cycle distribution between control and MED12-knockdown DU145 and LNCaP cells (Fig. 3d and e). In DU145 cells, we found that MED12-knockdown cells being significantly arrested in G0/G1 phase (Fig. 3d), and in LNCaP cells we observed that the percentage of cells in S phase was reduced upon MED12 knockdown (Fig. 3e). These results are indicative of a role of MED12 in the G1- to S-phase transition. To get further support for MED12-knockdown-induced cell cycle arrest at G0/G1 phase, we analyzed the expression levels of G1- to S-phase negative regulators p21 and p27. These proteins are able to block the kinase activity of CDKs at the G1- to S-phase checkpoint during cell cycle, and their upregulation has been shown to cause growth inhibition (Sherr & Roberts 1999). At the same time, reduced p27 expression has been associated with a more aggressive phenotype and poor survival (Doganavargil et al. 2006). Increased p27 expression in MED12-knockdown DU145 and LNCaP cells (Fig. 4a and b) may provide evidence that MED12 is a negative regulator of p27 expression, which is consistent with the observation that MED12-knockdown cells showed reduced proliferation in MTT assays and decreased G1- to S-phase transition in cell cycle analysis. Differences in p21 expression upon MED12 knockdown were only slightly detectable in LNCaP cells (Supplementary Fig. 1b), and could not be observed in DU145 cells (Supplementary Fig. 1a). However, studies uncovered important differences between several cell types with regard to the regulation of CDK inhibitors such as p21 and p27 (Sherr & Roberts 1999) which could explain our different results in DU145 and LNCaP cells for p21 and p27 expression. Furthermore, several reports indicate that p21 and p27 have different functions (Martin-Caballero et al. 2004, Munoz-Alonso et al. 2005), and can be differentially expressed in cancer cells (Sherr & Roberts 1999). Interestingly, MED12 knockdown may affect signaling pathways, including β-catenin signaling, whose inhibition has been shown to cause G1 arrest in colorectal cancer cells (van de Wetering et al. 2002). In addition to reduced G1- to S-phase transition in MED12-knockdown cells, in LNCaP cells we observed that the percentage of cells in G2/M phase was increased upon MED12 knockdown (Fig. 3e). Notably, we found MED12 expression in PCa tissues was correlated with the expression of the M-phase marker pHH3, which is upregulated during G2- to M-phase transition (Hesse et al. 2012). Together with our results indicating that LNCaP cells with MED12 knockdown exhibited reduced cell viability by MTT assay, we propose that MED12 may be involved in the checkpoint regulation during G2- to M-phase transition. Interestingly, in malignant melanoma cells, the loss of CDK8 activity, which requires MED12 (Knuesel et al. 2009), reduced proliferation mediated by G2/M-phase arrest (Kapoor et al. 2010). Previous studies revealed fundamental differences in cell cycle regulator patterns between LNCaP and DU145 cells, and specific cell-cycle-regulating pathways in the two cell lines (Mad’arova et al. 2002, Cifuentes et al. 2003, Benavides et al. 2010). Results from studies indicated that the androgen receptor and p53 status might determine different responses to CDK inhibitors and cell-cycle-modulating agents between LNCaP and DU145 cells (Mad’arova et al. 2002, Benavides et al. 2010). Our results show different effects of MED12 knockdown upon cell cycle regulation in LNCaP and DU145 cells, and may support previous observations described earlier. Further experiments are needed to unravel the molecular basis of MED12-mediated cell cycle regulation.

Recent studies have reported that SMAD3 is over-expressed in PCa tissues and is necessary for progressive growth of PCa cells in nude mice (Lu et al. 2007). On the basis of these results and results from other studies showing that MED12 is implicated in TGF-β-receptor regulation (Huang et al. 2012) and our findings that MED12 has increased expressed in castration-resistant PCa tissues, we aimed to investigate whether MED12 is implicated in TGF-β signaling in PCa. We found that the activation of TGF-β signaling was associated with MED12 nuclear overexpression in PCa tissue (Fig. 5a and Supplementary Table 1). Results of recent studies have indicated that the TGF-β isoform 3 is highly expressed in PCa and androgen-independent PCa cells (Karan et al. 2002). Furthermore, TGF-β3 is more potent in increasing motility and invasive behavior in PCa cells (Walker et al. 2013), as well as in endometrial cancer cells compared with other isoforms (Van Themsche et al. 2007). Therefore, we used TGF-β3 to activate TGF-β signaling in PC3 cells and found a strong increase in MED12 nuclear expression and a decrease in the cytoplasmic expression (Fig. 5d). Our observations indicate that the nuclear MED12 overexpression is a response to the activation of TGF-β signaling in PCa.

Based on these observations, we aimed to investigate the role of MED12 in TGF-β-regulated gene expression. TGF-β signaling activation leads to increased expression of vimentin, a crucial event during PCa progression and metastasis (Zavadil & Bottinger 2005). We observed reduced Vimentin expression in PC3 cells with MED12 knockdown grown under TGF-β3 stimulation, when compared with control cells (Fig. 5e and f). We suggest that MED12, as part of the Mediator complex, is required...
for TGFβ-regulated gene expression, and that MED12 is therefore shuttled into the nucleus in response to TGFβ signaling activation. Recently, a study by Huang and colleagues revealed that MED12 has an additional function in the cytoplasm distinct from its role within the Mediator complex, and there it negatively regulates TGFβ receptor signaling. In contrast, the aim of our study was to investigate the role of MED12 as part of the Mediator complex, and there it negatively regulates TGFβ signaling activation. In addition, Huang and colleagues revealed that MED12 has an additional function in the nucleus as a co-activator for the transcription machinery. In addition, Huang et al. (2012) performed whole-exome sequencing of primary PCa tissues and found MED12 to be mutated in six out of 111 samples, Stoeht et al. (2013) reported a lack of evidence for MED12 mutations using Sanger sequencing of PCa samples from a small subgroup of patients. Taken together, our findings indicate that MED12 expression clearly plays a role in PCa and is directly implicated in TGFβ signaling in PCa.

Supplementary data
This is linked to the online version of the paper at http://dx.doi.org/10.1530/ERC-14-0171.

Declaration of interest
The University of Bonn has filed a patent which includes and is not limited to the use of MED12 in prostate cancer, on which S Perner, Z Shaikhibrahim, R Menon, and M Braun are co-inventors.

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Author contribution statement
S Perner and Z Shaikhibrahim study concept and approach. S Perner, Z Shaikhibrahim, A Offermann, and M Braun designed experiments. S Perner and Z Shaikhibrahim carried out the experiments. L Bubendorf, C A Rentsch, O Andren, and M Svensson provided tissues. S Perner, Z Shaikhibrahim, and Z Shaikhibrahim carried out the experiments. L Bubendorf, C A Rentsch, O Andren, and M Svensson provided tissues. S Perner, Z Shaikhibrahim, A Offermann, and M Braun analyzed and interpreted data. S Perner, Z Shaikhibrahim, and A Offermann wrote manuscript. S Duensing, L Bubendorf, S Biskup, J Kirfel, C Ruiz, O Andren, and M Svensson revised manuscript.

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