



Contents lists available at ScienceDirect

Biochimica et Biophysica Acta

journal homepage: [www.elsevier.com/locate/bbadis](http://www.elsevier.com/locate/bbadis)

## Untranslated regions of thyroid hormone receptor beta 1 mRNA are impaired in human clear cell renal cell carcinoma

Adam Master<sup>a</sup>, Anna Wójcicka<sup>a</sup>, Agnieszka Piekiełko-Witkowska<sup>a</sup>, Joanna Bogusławska<sup>a</sup>, Piotr Popławski<sup>a</sup>, Zbigniew Tański<sup>b</sup>, Veerle M. Darras<sup>c</sup>, Graham R. Williams<sup>d,\*</sup>, Alicja Nauman<sup>a,\*</sup>

<sup>a</sup> The Medical Centre of Postgraduate Education, Department of Biochemistry and Molecular Biology, ul. Marymoncka 99/103, 01-813 Warsaw, Poland

<sup>b</sup> Regional Hospital Ostrołęka, Ostrołęka, Poland

<sup>c</sup> Laboratory of Comparative Endocrinology, Division of Animal Physiology and Neurobiology, Katholieke Universiteit Leuven, Leuven, Belgium

<sup>d</sup> Molecular Endocrinology Group, Department of Medicine, Imperial College London, Hammersmith Campus, London W12 0NN, UK

### ARTICLE INFO

#### Article history:

Received 8 April 2010

Received in revised form 26 July 2010

Accepted 29 July 2010

Available online xxx

#### Keywords:

Translational control in cancer

Untranslated region

miRNA

Thyroid hormone receptor beta 1

Thyroid hormone

Renal cancer

ccRCC

### ABSTRACT

Thyroid hormone receptor  $\beta 1$  (TR $\beta 1$ ) is a hormone-dependent transcription factor activated by 3,5,3'-L-triiodothyronine (T3). TR $\beta 1$  functions as a tumor suppressor and disturbances of the *THRB* gene are frequent findings in cancer. Translational control mediated by untranslated regions (UTRs) regulates cell proliferation, metabolism and responses to cellular stress, processes that are involved in carcinogenesis. We hypothesized that reduced TR $\beta 1$  expression in clear cell renal cell cancer (ccRCC) results from regulatory effects of TR $\beta 1$  5' and 3'UTRs on protein translation. We determined TR $\beta 1$  expression and alternative splicing of TR $\beta 1$  5' and 3' UTRs in ccRCC and control tissue together with expression of the type 1 deiodinase enzyme (coded by *DIO1*, a TR $\beta 1$  target gene). Tissue concentrations of T3 (which are generated in part by D1) and expression of miRNA-204 (an mRNA inhibitor for which a putative interaction site was identified in the TR $\beta 1$  3'UTR) were also determined. TR $\beta 1$  mRNA and protein levels were reduced by 70% and 91% in ccRCC and accompanied by absent D1 protein, a 58% reduction in tissue T3 concentration and 2-fold increase in miRNA-204. Structural analysis of TR $\beta 1$  UTR variants indicated that reduced TR $\beta 1$  expression may be maintained in ccRCC by posttranscriptional mechanisms involving 5'UTRs and miRNA-204. The tumor suppressor activity of TR $\beta 1$  indicates that reduced TR $\beta 1$  expression and tissue hypothyroidism in ccRCC tumors is likely to be involved in the process of carcinogenesis or in maintaining a proliferative advantage to malignant cells.

© 2010 Elsevier B.V. All rights reserved.

### 1. Introduction

The thyroid hormones, T3 (3,5,3'-L-triiodothyronine) and T4 (thyroxine), regulate key cellular processes including differentiation, proliferation, apoptosis and metabolism. Thyroid hormone action is mediated via the thyroid hormone receptors TR $\alpha 1$  and  $\beta 1$ , which are expressed widely and act as T3-inducible transcription factors [1]. TRs bind specific thyroid hormone response elements (TREs) in T3 responsive genes and regulate expression of target genes including oncogenes [2] and tumor suppressors [3]. Human *THRB* gene contains 10 exons (Fig. 1A) with an open reading frame extending from exon 3 to exon 10. Previous studies indicate that TR $\beta 1$  expression is perturbed in tumors, including clear cell renal cell cancer (ccRCC) [4]. Several mechanisms have been proposed to contribute to reduced TR $\beta 1$  expression in cancer cells. Examples include hypermethylation of the TR $\beta 1$  promoter and loss of heterozygosity (LOH) at the *THRB*

locus [5] and mutations found in TR $\beta 1$  transcripts [6]. Although all these mechanisms may lead to reduced transcript expression, aberrant TR $\beta 1$  mRNA expression correlates poorly with protein expression in ccRCC [4], suggesting that TR $\beta 1$  translation in human renal carcinomas may involve post-transcriptional regulation.

The final concentration of expressed protein depends on its translation efficiency and stability. Since initiation of translation is a rate-limiting step [7], factors influencing this process limit the efficiency of protein synthesis. Translation initiation events are controlled by secondary structures of UnTranslated Regions (UTRs) within mRNAs. The UTRs contain cis-acting sequences recognized by trans-acting factors including translation initiation and elongation factors and microRNAs [8]. Alternative splicing of the TR $\beta 1$  mRNA 5' UTR results in expression of multiple 5'UTR variants [9,10]. Expression of these variants is tissue-specific, and previous studies indicated they differentially regulate the efficiency of protein translation [10]. Similarly, cis-acting elements in the 3'UTR of TR $\beta 1$  may influence the efficiency of protein translation [11].

It is well known that UTRs can be involved in carcinogenesis. For instance, mammary gland BRCA1 suppressor is characterized by a short, efficiently translated 5'UTR variant. In some breast cancers the

\* Corresponding authors.

E-mail addresses: [graham.williams@imperial.ac.uk](mailto:graham.williams@imperial.ac.uk) (G.R. Williams), [anauman@cmkp.edu.pl](mailto:anauman@cmkp.edu.pl) (A. Nauman).

BRCA1 transcripts possess a longer structured UTR containing upstream open reading frames (uORFs) resulting in reduced BRCA1 protein synthesis [12]. Moreover, tumor cells expressing a shorter, readily translated variant of the retinoic acid receptor RAR $\beta$ 2 5'UTR exhibited greater sensitivity to retinoic acid in comparison to cells expressing a longer 5'UTR variant less efficiently translated [13,14].

Although the protein coding region of TR $\beta$ 1 has been extensively investigated in various tumor cell types, there is little information regarding UTR-dependent control of the efficiency of TR $\beta$ 1 translation. In these studies we hypothesized that aberrant TR $\beta$ 1 protein expression in ccRCC results from reduced levels of TR $\beta$ 1 mRNA, alternative splicing of 5' and 3'UTR TR $\beta$ 1 mRNA and altered expression of miRNAs that regulate TR $\beta$ 1 translation. To address these possibilities we characterized TR $\beta$ 1 mRNA and protein expression and alternative splicing of TR $\beta$ 1 UTRs in ccRCC and control tissue as well as the levels of the type 1 deiodinase enzyme (D1, a TR $\beta$ 1 target gene) and the tissue concentrations of T3 and T4, which are regulated by activity of the D1 enzyme. Finally, we investigated the possible role of mRNA UTRs in the control of TR $\beta$ 1 protein translation.

## 2. Materials and methods

### 2.1. Tissue samples

Tissue samples were obtained from nephrectomies performed on patients with clear cell renal cell cancer ( $n=39$ ) or non-neoplastic abnormalities (nephrolithiasis, hydronephrosis, injury,  $n=10$ ) under permission of the Ethical Committee of Human Studies (The Medical Centre of Postgraduate Education). Samples were divided into three groups: cancer tissue ( $n=39$ , T) and two control tissues: paired normal tissue from the opposite pole of the malignant kidney with no histological evidence of tumor ( $n=39$ , C) and tissue from kidney removed for non-neoplastic disease ( $n=10$ , N). The aim of using controls "N" was to clearly separate cancer-specific molecular changes from those resulting from non-cancerous pathologies. Clear cell renal cell cancer was diagnosed according to WHO criteria [15].

### 2.2. Plasmids and transient transfection assays

TR $\beta$ 1 5'UTR variants A-G pGL3 constructs were described previously [10] pGL3-F1 was constructed using *HindIII/NcoI* cloning of PCR amplified F1 variant (primers p1d1F and pex3R-Pscl, Supplementary Data Table 3).

Caki-2 cells (clear cell renal cell cancer, American Type Culture Collection, Manassas, VA) were seeded at  $5 \times 10^5$  cells per well and after 24 h were transfected with 100 ng pRL-TK and 1  $\mu$ g of pGL-5'UTR vectors, using 1  $\mu$ g/ $\mu$ l PEI (Linear Polyethylenimine, Cat. No. 23966-2, Polysciences Inc., Warrington, PA) and 150 mM NaCl in FBS-free McCoy's medium (Gibco/Invitrogen, Carlsbad, Ca). Five hours after transfection, the medium was replaced with medium plus 10% FBS (Sigma-Aldrich, Saint Louis, MO) and penicillin-streptomycin solution (Sigma-Aldrich, Saint Louis, MO). Cells were grown for 24 hrs at 37 °C in 5% CO $_2$  and harvested for dual-luciferase assay (Promega, Madison, WI) using a Synergy2 luminometer (BioTek, Winooski, VT). All transfections and luciferase assays were performed in triplicate.

For transfection with miRNA precursors, Caki-2 cells were plated at  $5 \times 10^5$  cells per 12-well dish and transfected 24 h later using

Lipofectamine 2000 reagent (Invitrogen, Carlsbad, Ca) following manufacturer's protocol. Each transfection reaction contained 37.5 nM of precursor miRNA-204 (PremiR™ miRNA Precursor Molecule, Ambion, Foster City, CA). As control, transfection with scrambled microRNA (Negative microRNA Control, Ambion, Foster City, CA) was performed. Cells were harvested 48 h after transfection for total RNA isolation for real-time RT-PCR and 72 h after transfection for protein isolation.

Coupled *in vitro* transcription and translation assay: *In vitro* protein synthesis was performed from pKS derived plasmids: UTR\_A + Luc, TR $\beta$ 1 ORF + Luc, UTR\_A + TR $\beta$ 1 ORF + Luc and Control plasmid. Control plasmid was constructed by cloning LUC gene downstream of the T7 promoter in pKS vector [10] and served as a basis for construction of other plasmids used in the study: (1) UTR\_A + Luc (THRB UTR-A cloned upstream of luciferase in pKS vector), TR $\beta$ 1 ORF + Luc (TR $\beta$ 1 ORF cloned upstream of luciferase in pKS vector), UTR\_A + TR $\beta$ 1 ORF + Luc (5'UTR A inserted upstream of TR $\beta$ 1ORF and luciferase reporter gene). Reaction was conducted in RTS 100 Wheat Germ CRCF system (Roche Diagnostics, Mannheim, Germany) in conditions recommended by the manufacturer, using 2  $\mu$ g of each plasmid.

### 2.3. RNA and miRNA isolation and reverse transcription

RNAs were isolated from ~100 mg of frozen tissue using GeneMATRIX Universal RNA Purification Kit (EURx, Gdansk, Poland) or mirPremier microRNA Isolation Kit (Sigma-Aldrich, St. Louis, MO). Reverse transcription was performed using RevertAid™ H Minus First Strand cDNA Synthesis Kit (Fermentas, Vilnius, Lithuania) and 200 ng total RNA with Random Hexamer primers, or 30 ng miRNA and specific stem-loop primers with 5'-overhangs (Supplementary Data, Table 1).

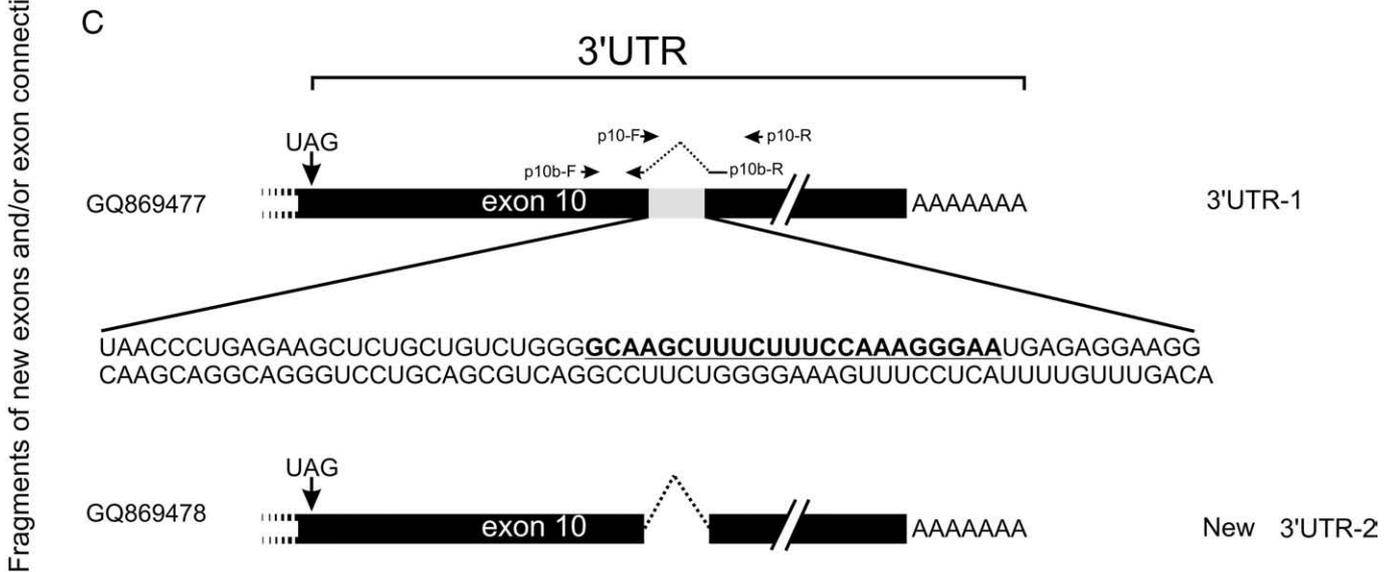
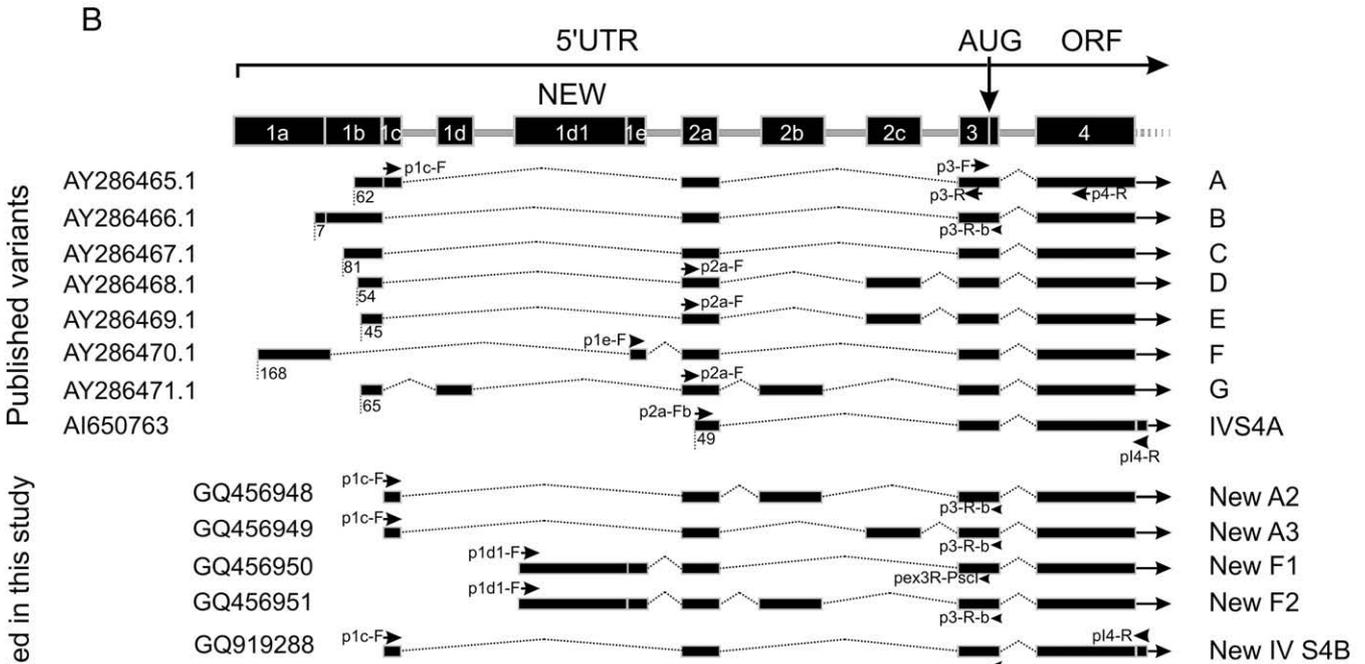
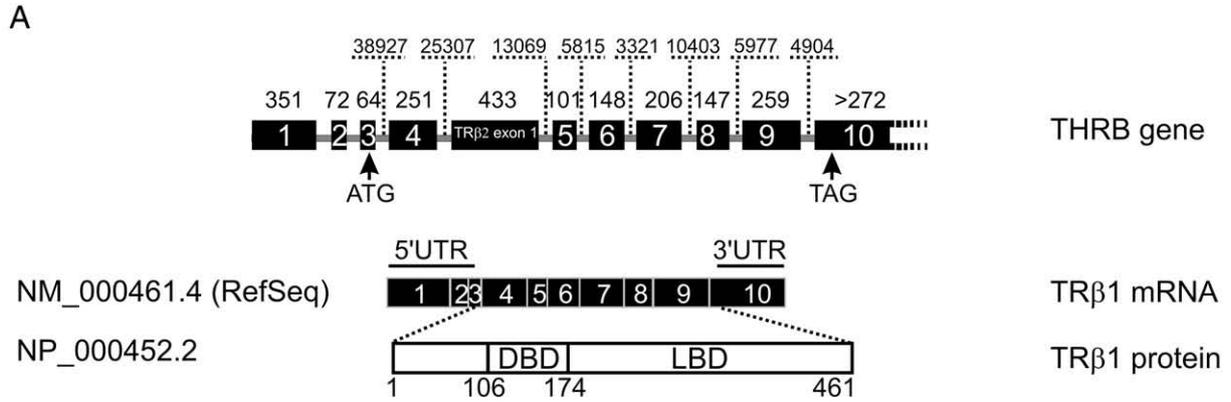
### 2.4. Real-time PCR

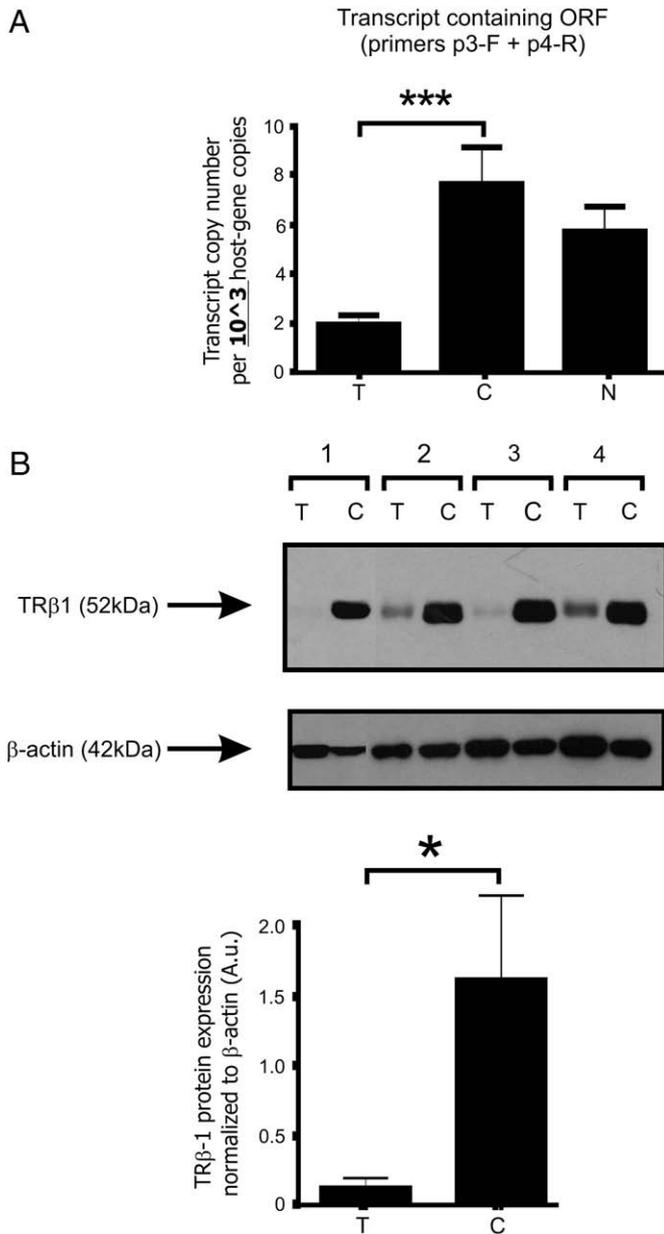
Quantitative real-time PCR of UTRs was performed using QuantiFast SYBR Green PCR Kit (Qiagen, Hilden, Germany) under conditions: 95 °C, 5 min; 50 cycles: 95 °C, 10 s, 60 °C, 30 s; melting curve analysis: 135 cycles: 50 °C; 0.3 °C increase in each cycle. Ct data were acquired after reaching the threshold in real-time module, usually between 18 and 36 cycle; cycle efficiency was corrected using iQ5 thermocycler software (Bio-Rad, Hercules, CA). Quantitation of transcripts was determined using serial dilutions of a known number of DNA amplicons and normalized to expression of endogenous *ACTB1*.

Semi-quantitative real-time PCR of *DIO1* was performed using SYBR Green I Master (Roche Diagnostics, Mannheim, Germany) under conditions: 95 °C for 10 min; 3 cycles: 95 °C, 30 s; 61 °C, 30 s; 72 °C, 30 s; 50 cycles: 95 °C, 20 s; 57 °C, 30 s; 72 °C, 30 s, 68 °C, 15 s (acquisition); melting curve analysis 120 cycles: 58 °C; 0.3 °C increase in each cycle. Results were normalized to expression of *ACTB1*.

Real-time PCR quantitation of miRNAs was performed using QuantiFast SYBR Green PCR Kit (Qiagen, Hilden, Germany) and universal primer UniAmp*HindIII* with sequence homology to overhangs of primers used in reverse transcription and miRNA-specific primers. The conditions used were: initial denaturation: 95 °C, 5 min., 32 cycles: denaturation 95 °C, 11 s, annealing 52 °C, 11 s, and extension 65 °C, 30 s; followed by melting curve analysis: 81 cycles: 55 °C with 0.5 °C temperature increase in each cycle. For normalization of miRNA expression, U6 snRNA [16] was used as an internal

**Fig. 1.** Human *THRB* gene. A. *THRB* gene (Ref.seq.:NC\_000003.11: 378609 bp region of chromosome 3 from base 24133709 to 24512317), TR $\beta$ 1 mRNA (NM\_000461.4) and protein (NP\_000452.2). Exons are numbered 1–10 and sized above. Amino acid positions below the protein demonstrate boundaries of the DNA and ligand binding domains (DBD and LBD) in TR $\beta$ 1 protein. B. Previously published (A-IVS4A) [10] and newly identified (A2-IVS4B) splice variants of TR $\beta$ 1 mRNA 5'UTR. Exons are labeled 1a–1e, 2a–2c and 3. C. Previously published (3'UTR-1) and newly identified (3'UTR-2) splice variant of TR $\beta$ 1 3'UTR that lacks the 61 bp region shown, which contains a potential binding site for miRNA-204 (bold underlined). Primers are indicated by arrows.





**Fig. 2.** Expression of TRβ1 mRNA and protein in ccRCC. **A.** Expression of TRβ1 mRNA containing the TRβ1 protein ORF. T: ccRCC tissue, C: paired normal control tissue from ccRCC kidneys, N: non-neoplastic kidney. The data are means ± S.E. ( $n = 10$  for N,  $n = 39$  for C,  $n = 39$  for T). **B.** Expression of TRβ1 protein. Upper panel: Western blot showing expression of TRβ1 (52 kDa protein) and β-actin (42 kDa protein) in four representative C and T paired samples. Lower panel: mean TRβ1 expression in paired samples C and T normalized to β-actin ( $n = 11$  for C,  $n = 11$  for T). The data are means ± S.E. Statistical analysis was performed using paired *t*-test to compare C and T. \* $p < 0.05$ .

control. Relative miRNA expression was calculated using the  $2^{-\Delta Ct}$  method [53].

Primer sequences (Biote21, Krakow, Poland) for all real-time PCR reactions are shown in [Supplementary Data, Tables 1–2](#).

### 2.5. Identification of THRB UTR splice variants

5'UTR variants were amplified using Perpetual OptiTaQ Polymerase (EURx, Gdansk, Poland), 8 μM of primers ([Supplementary Data, Table 3](#)) and conditions: 95 °C for 10 min, 5 cycles (95 °C, 30 s; 62 °C, 45 s; 72 °C, 45 s), 50 cycles (95 °C, 30 s; 58 °C, 30 s; 72 °C, 90 s); final extension 30 min, 61 °C. Sequencing was performed with BigDye Terminator v3.1 (Applied Biosystems, Foster City, CA).

Newly described exons were identified using PCR primers designed basing on the THRB genomic sequence (ref.seq.: NC\_000003.10) and the most probable donor and acceptor splice sites, predicted using NNSPLICE0.9 [20].

### 2.6. Protein isolation

TRβ1: tissue samples were homogenized (buffer: 150 mM NaCl, 1% Triton X-100, 50 mM Tris-HCl pH 8.0, protease inhibitor cocktail (Sigma-Aldrich, Saint Louis, MO), and 0.5 mM PMSF), incubated for 2 h at 4 °C with shaking and centrifuged at 12,000 rpm for 20 min at 4 °C. Caki-2 cells were harvested 72 h after transfection with precursor miRNA-204 (pre-miR-204) or scrambled microRNA, washed once in PBS, and lysed in RIPA buffer (150 mM NaCl, 1% NP40, 0.5% sodium deoxycholate, 0.1% SDS, 50 mM Tris-HCl at pH 8, 2 mM EDTA) containing protease inhibitor cocktail (Sigma-Aldrich, St. Louis, MO) and 1 mM PMSF.

D1: samples were homogenized (buffer: 0.1 phosphate buffer pH 7.0, 1 mM EDTA, 10 mM DTT, 250 mM sucrose, protease inhibitor cocktail (Sigma-Aldrich, St. Louis, MO), and 1 mM PMSF), and centrifuged at 15,000 g for 30 min, at 4 °C. The supernatant was centrifuged at 75,000g for 1.5 h at 4 °C. The microsome fraction pellet resuspended in homogenization buffer.

Protein extracts were stored at –70 °C.

### 2.7. Western blotting

40 μg of protein was resolved by 10% SDS-PAGE and transferred to nitrocellulose membrane. Membranes were blocked overnight (8 °C, 5% non-fat milk in TBS-T buffer: 10 mM Tris-HCl, 150 mM NaCl, 0.1% Tween-20; pH 7.6), washed three times in TBS-T for 10 min, and incubated overnight at 8 °C with primary antibody diluted 1:1000 in TBS-T buffer with 5% non-fat milk (anti-TRβ1 antibody: cat. no. ab2744, Abcam plc, Cambridge, UK; anti-D1 serum [54], a kind gift of T.J. Visser). After washing 3 times for 10 min, membranes were incubated for 1 h at RT with horseradish peroxidase-conjugated goat anti-mouse secondary antibody (1:10000, DakoCytomation, Glostrup, Denmark) (TRβ1) or goat anti-rabbit secondary antibody (1:10000, DakoCytomation, Glostrup, Denmark) (D1), and washed 3 times for 10 min. Proteins were detected using Supersignal West Pico Chemiluminescent Substrate (Pierce Biotechnology, Rockford, IL). Subsequently, membranes were stripped and incubated with anti-β-actin antibody diluted 1:10000 (cat. no. ab6276, Abcam plc, Cambridge, UK) in TBS-T buffer for 1 h, washed three times and used for detection. Levels of TRβ1 and Dio proteins were normalized to β-actin expression.

### 2.8. Thyroid hormone levels in tissue samples

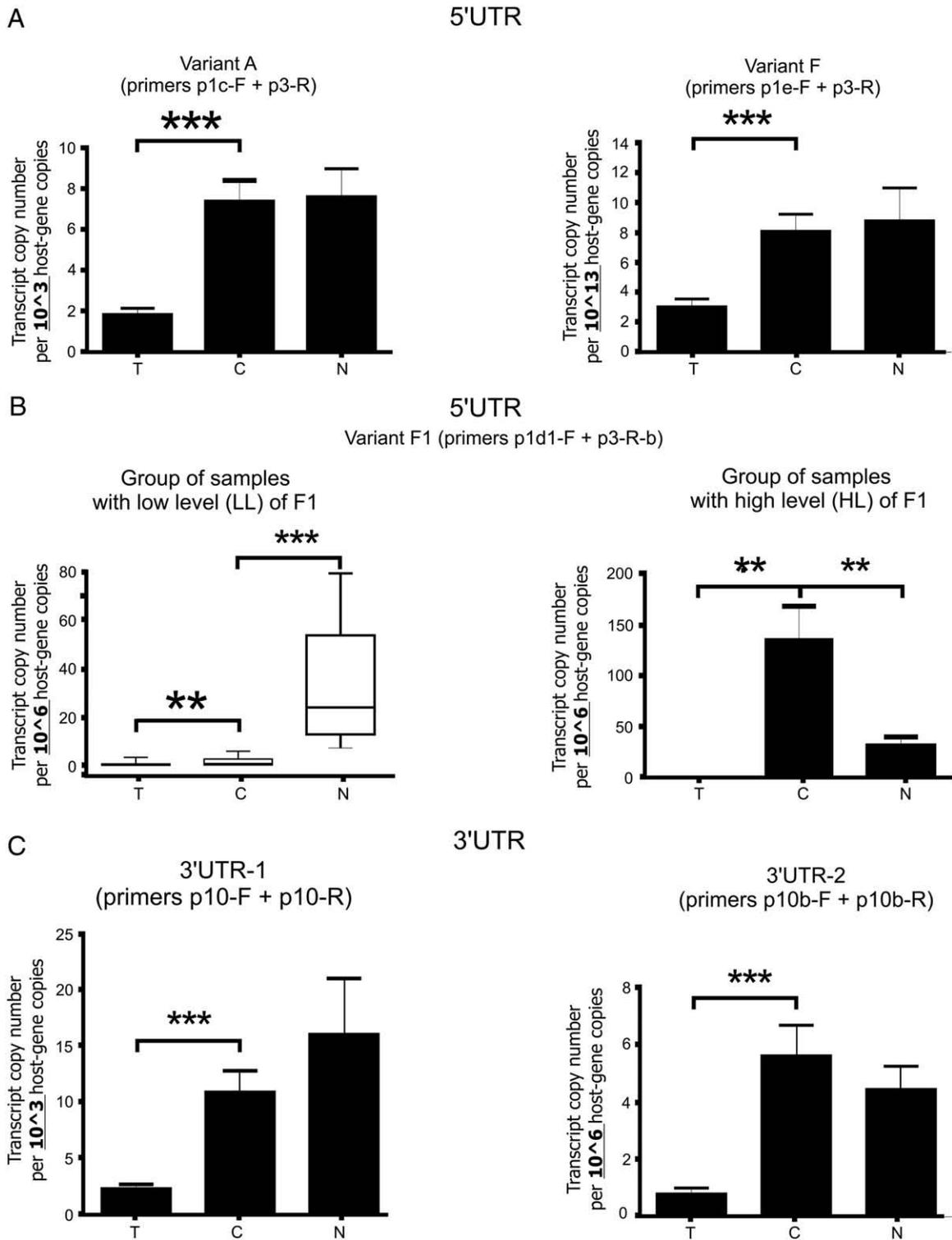
Intracellular T4 and T3 concentrations were measured by radioimmunoassay following tissue extraction as described [17].

### 2.9. Bioinformatic analysis

5'UTR secondary structures were predicted using RNAstructure 5.0 [18]. Splice site predictions were determined using NetGene2 Server [19], and NNSPLICE 0.9 [20].

Identification of miRNA target sites in the 3'UTR-1 was performed using: RNAhybrid [21], PicTar [22], TargetScan 5.1 [23] and miRanda [24].

Detailed descriptions of bioinformatic analyses are provided in [Supplementary Data](#).



**Fig. 3.** Expression of TR $\beta$ 1 5' and 3'UTR variants. Expression of 5'UTR variants A and F (Panel A), F1 (Panel B) and 3'UTR variants (Panel C) in paired tumor (T) and control tissue (C) and in non-neoplastic kidney (N). Analysis of F1 expression revealed two groups of samples: one with low levels (LL) of F1 (74% of samples) and one with high levels (HL) of F1 in control tissues C and N. The data are means  $\pm$  S.E. in HL samples and as median values with 95%CI in LL samples as data were not normally distributed in this group. Statistical analysis was performed using paired *t*-test for variants A, F, F1 in HL samples, 3'UTR-1, and 3'UTR-2 or Wilcoxon paired test for F1 in LL samples. Variant A:  $n = 10$  for N,  $n = 37$  for C,  $n = 37$  for T; variant F:  $n = 10$  for N,  $n = 35$  for C,  $n = 35$  for T; F1 LL samples:  $n = 30$  for C,  $n = 30$  for T; F1 HL samples:  $n = 10$  for N,  $n = 8$  for C,  $n = 8$  for T; variant 3'UTR-1:  $n = 10$  for N,  $n = 32$  for C,  $n = 32$  for T, variant 3'UTR-2:  $n = 30$  for C,  $n = 30$  for T. \*\*\* $p < 0.001$ . \*\* $p < 0.01$ .

### 2.10. Statistical analysis

The Shapiro–Wilk test was used to determine normality of data distribution. Normally distributed data were analyzed by paired *t*-test

and non-parametric data by Wilcoxon matched pairs test. Data from luciferase assays were analyzed by ANOVA followed by Dunnett's multiple comparison test.  $p < 0.05$  was considered statistically significant.

### 3. Results

#### 3.1. Identification of new UTR splice variants

The previously described TR $\beta$ 1 5'UTR variants A-G and variant IVS4A encoding truncated protein [10] were expressed in benign and malignant kidney tissue. Moreover, four new TR $\beta$ 1 5'UTR variants (A2, A3, F1, F2) were identified (Fig. 1B). Two variants, F1 and F2, contained a previously unknown exon located between exons 1d and 1e, designated here as exon 1d1 (Fig. 1B). The new variants A2 and A3 were similar in structure to the previously described variant A but contained an additional exon between exons 2a and 3. Variant A2 additionally contained exon 2b and variant A3 additionally contained exon 2c. Finally, a new variant of IVS4A containing a fragment of intron 4 was also identified and named IVS4B. Variant IVS4B, in contrast to IVS4A, contained exon 1c and open reading frame (ORF) that predicts expression of a 28 amino acid protein with a stop codon located in intron 4.

The structure of TR $\beta$ 1 3'UTR was less complex (Fig. 1C). The previously described TR $\beta$ 1 mRNA contains a 3'UTR sequence designated here as 3'UTR-1. Sequencing revealed that 3'UTR-2 lacks a 123 nucleotide region of exon 10 that is located between nucleotides 2272–2394. This region contains a putative binding site for miRNA-204, located between nucleotides 2313–2319. The sequences of the new UTR variants with splice consensus sites are shown in Supplementary Data.

#### 3.2. Reduced expression of TR $\beta$ 1 mRNA and protein in ccRCC

Levels of TR $\beta$ 1 mRNA were determined in ccRCC and control tissues by real-time PCR using primers which amplified the 5'-end of the TR $\beta$ 1 coding sequence. TR $\beta$ 1 mRNA expression was reduced by 70% in ccRCC tumor tissue (T) compared with paired control tissue (C). There was no significant difference in TR $\beta$ 1 mRNA expression between control samples (C) and (N) (Fig. 2A). Accordingly, TR $\beta$ 1 protein expression was reduced by 91% or was undetectable in ccRCC tissue compared with paired control samples (Fig. 2B). This 20% difference in reduction of TR $\beta$ 1 protein compared to mRNA in tumors versus paired controls may result from aberrant post-transcriptional regulation of TR $\beta$ 1 protein expression in ccRCC. Thus, we analyzed expression of the TR $\beta$ 1 5'UTR variants and investigated expression of miRNAs predicted to interact with the TR $\beta$ 1 3'UTR.

#### 3.3. Expression of TR $\beta$ 1 UTRs in ccRCC

Expression of 5'UTR variants A, F, F1, as well as 3'UTR-1, 3'UTR-2 and the coding sequence of TR $\beta$ 1 were analyzed by real-time PCR. Variants, B-E, F2, G, A2 and A3 were either expressed at very low levels or were undetectable in most samples and accurate quantification of their expression was not possible (data not shown). Expression of 5'UTR variants A and F were reduced in tumors by 75% and 62%, respectively, compared to (C) control samples (Fig. 3A). 5'UTR variant A was expressed at the highest level in ccRCCs and their controls (1.8–7.4 transcripts per  $10^3$  copies of *ACTB1*), whereas variant F was expressed in all samples at very low levels (3–8 transcripts per  $10^{13}$  copies of *ACTB1*). Expression of newly identified variant F1 (0.05–172 transcripts per  $10^6$  copies of *ACTB*) was higher than expression of variant F but lower than variant A. The expression profile of variant F1 was complex, however, and two distinct groups of paired samples

were defined. In one group ( $n=8$ ) there was a very high level of F1 expressed in controls compared to ccRCCs (HL, in Fig. 3B), whereas in a second group, containing most of the tested pairs ( $n=30$ ) F1 expression was much lower (LL, in Fig. 3B) and decreased by 90% in paired tumor tissue. In the HL group, expression of F1 in ccRCC tissue was almost undetectable. There was a significantly ( $p<0.0001$ ) higher level of expression of F1 in N noncancerous samples from the LL group compared to C normal control tissue (Fig. 3B). Expression of the variants IVS4A and IVS4B was reduced by 99% in tumor (T) compared to paired control (C) tissue although levels were much higher in samples from non-malignant diseased kidneys (N) (Supplementary Data, Fig. 1S).

Expression of the 3'UTR-1 and 3'UTR-2 variants was decreased by 79% and 86%, respectively, in tumors, compared to control samples (Fig. 3C). 3'UTR-1 (2.3–11 transcripts per  $10^3$  copies of *ACTB1*) was expressed at a similar level to 5'UTR variant A, whereas 3'UTR-2 expression was 1000-fold lower (0.8–5.7 transcripts per  $10^6$  copies of *ACTB1*).

The levels of expression of the TR $\beta$ 1 transcript containing the coding sequence (ORF) of TR $\beta$ 1 protein (2.0–7.7 transcripts per  $10^3$  copies of *ACTB1*) were similar to levels of the 5'UTR A and 3'UTR-1 variants (Figs. 2 and 3). Abundances of particular UTR variants relative to the most highly expressed variant A are shown in Fig. 2S.

#### 3.4. The expression of miRNA-204 regulating TR $\beta$ 1 expression in ccRCC

Bioinformatic analysis of the TR $\beta$ 1 mRNA 3'UTR identified multiple potential miRNA binding sites, 14 of which were selected for further analysis (Supplementary Data, Table 4) based on their identification by at least two of four independent bioinformatic approaches. In preliminary studies we determined the relative expression of 14 candidate miRNAs in paired control and ccRCC tissue from two kidneys. These studies revealed differential expression of seven miRNAs: miRNA-1, miRNA-211, miRNA-204, miRNA-206, miRNA-154, miRNA-335 and miRNA-512-3p. Subsequent analysis in 39 paired samples revealed that expression of miRNA-204 was increased by 1.2- to 2.0-fold in ccRCC compared to paired control tissue (Fig. 4), whereas expression of the six other candidate miRNAs did not differ significantly between ccRCC and control tissue (data not shown). The predicted miRNA binding site for miRNA-204 was located in the 61 bp region of exon 10 that was present in 3'UTR-1 but absent from 3'UTR-2 (Figs. 1C and 4A).

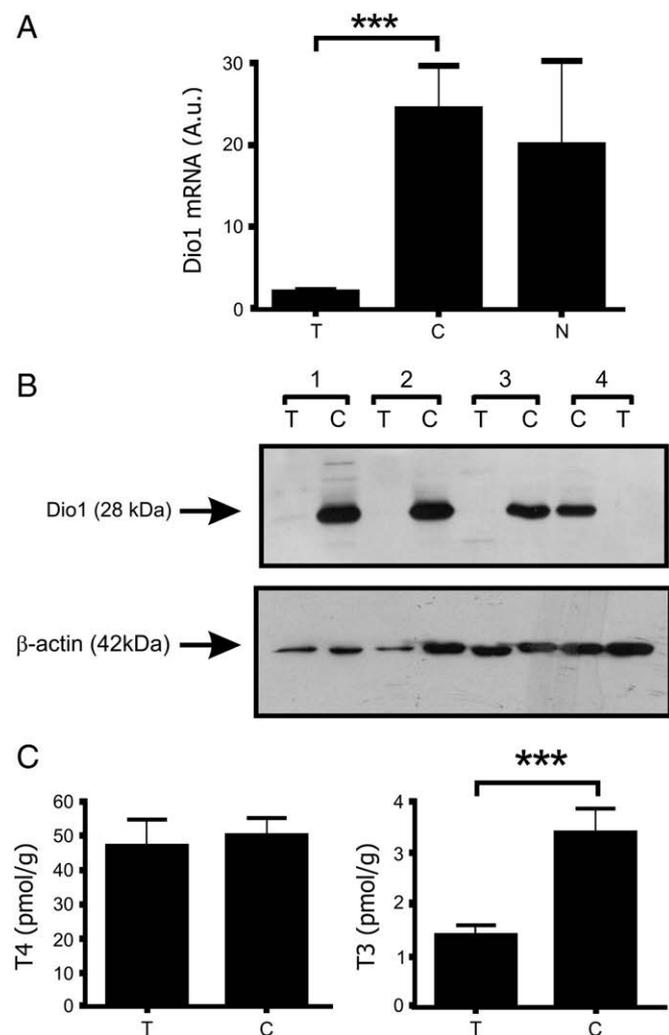
In order to test whether miR-204 is a true TR $\beta$ 1 regulator, Caki-2 cells were transfected with miR-204 precursor and scrambled control. Subsequent real-time PCR and Western blot analysis of TR $\beta$ 1, as well as real-time PCR of TR $\beta$ 1 dependent gene, *DIO1* were performed. Transfection with miR-204 precursor resulted in a large (three magnitudes of order) induction of miR-204 expression (Fig. 3S. in Supplementary Data) which was followed by ~42% decrease of TR $\beta$ 1 mRNA expression and ~35% decrease of *DIO1* mRNA expression when compared with scrambled control. Moreover, the protein expression of TR $\beta$ 1 is also almost twice lower in pre-miR-204 transfected cells in comparison with scrambled control (Fig. 4).

#### 3.5. TR $\beta$ 1 5'UTR variants influence protein translation efficiency in ccRCC cells

To analyze the effect of the TR $\beta$ 1 5'UTR variants A-G and new variant F1 on translation efficiency, ccRCC derived Caki-2 cells were

**Fig. 4.** Levels of miRNA-204 in tissues and its regulatory effect on TR $\beta$ 1 expression. A. Positions of potential miRNA binding sites in TR $\beta$ 1 3'UTR identified by TargetScan and RNAHybrid. miRNAs binding to 3'UTRs requires only partial complementarity to the target. Nucleotides of perfect complementarity are shown as seed match. B. Increased miRNA204 expression in ccRCC tumor tissue (T). Data are means  $\pm$  S.E. ( $n=35$  for T,  $n=35$  for C,  $n=10$  for N). Statistical analysis was performed using paired *t*-test to compare C and T samples. \* $p<0.05$ . C. miR-204 mediated downregulation of TR $\beta$ 1 and its target gene D1 transcript in Caki-2 cell line. Semi-quantitative real-time PCR assay for TR $\beta$ 1 and D1 in the Caki-2 cell line transfected with pre-miR-204 or scrambled microRNA (negative control). Data are expressed as mean values  $\pm$  SEM. Statistical analysis was performed using paired *t*-test to compare cells transfected with pre-miR-204 and with scrambled microRNA. \*\*\* $p<0.0001$ . Western blotting for TR $\beta$ 1 and  $\beta$ -actin (loading control) in the Caki-2 cell line transfected with pre-miR-204 or scrambled pre-miR-204 (negative control). Cells were harvested 72 h after transfection; the relative density of bands was quantified by densitometry.





**Fig. 5.** Expression of *DIO1* and tissue concentrations of thyroid hormones in ccRCC. A. Expression of *DIO1* mRNA in tissue samples.  $n = 33$  for T,  $n = 33$  for C,  $n = 10$  for N. Data are means  $\pm$  S.E., \*\*\* $p < 0.001$ . Statistical analysis was performed using a paired *t*-test. B. Western blot showing expression of D1 (28 kDa protein) and  $\beta$ -actin (42 kDa protein) in four representative C and T paired samples. C. Tissue concentrations of T4 and T3, in paired control (C) and ccRCC (T) samples. Data are shown as mean  $\pm$  S.E. ( $n = 12$  for T,  $n = 12$  for C). Statistical analysis was performed using paired *t*-test. \*\*\* $p < 0.001$ .

transfected with 5'UTR-pGL3 constructs and luciferase activity was determined. In ccRCC Caki-2 cells, inclusion of 5'UTR variant A (folding free energy  $\Delta G = -69.0$  kcal/mol), resulted in the highest degree of luciferase activity when compared to other 5'UTR variants (Supplementary Data, Fig. 4S.A). By contrast, variant F1 ( $\Delta G = -124.4$  kcal/mol) exerted the strongest inhibitory effect on luciferase expression, decreasing activity by more than 98% comparing to activity of the control vector lacking a TR $\beta$ 1 5'UTR.

To check whether the presence of TR $\beta$ 1 ORF influences the regulatory effect of UTR on translational efficiency, we performed an *in vitro* experiment using pKS-derived plasmids (Fig. 4S.B). To do this, luciferase transcription and translation rates from construct UTR-A + TR $\beta$ 1ORF + Luc were tested in *in vitro* transcription/translation assay together with the following constructs: UTR-A + Luc; TR $\beta$ 1ORF + Luc; Control. These assays revealed that: (1) there were no differences between transcriptional efficiency of control and none of the constructs; (2) translational efficiency of TR $\beta$ 1ORF + Luc did not statistically significantly differ when compared with control; (3) translational efficiency of UTR-A + Luc was 22% lower when compared to control ( $p < 0.01$ ); (4) translational efficiency of UTR-A + TR $\beta$ 1ORF +

Luc was 28% lower when compared to control ( $p < 0.01$ ); (5) there was no statistically significant difference between translational efficiency of UTR-A + Luc and UTR-A + TR $\beta$ 1ORF + Luc. Thus, we concluded that TR $\beta$ 1ORF did not influence the regulatory effect of 5'UTR A on translational efficiency.

The prediction of secondary structures formed by the 5'UTRs revealed that the variants A2, A3, F1, and F2 fold into structures of different free energies. Variant F2 formed the most stable secondary structure ( $\Delta G = -171.0$  kcal/mol) and variant A3 was the least stable ( $\Delta G = -86.6$  kcal/mol) (Supplementary Data, Table 5 and Fig. 5S–9S).

### 3.6. Reduced expression of the TR $\beta$ 1 target gene, *DIO1*, in ccRCC

The promoter of type 1 iodothyronine deiodinase (*DIO1*) was shown to be bound *in vitro* by both thyroid hormone receptors: TR $\alpha$  and TR $\beta$  [25]. It was also suggested, however, that in the kidney *DIO1* expression is solely activated by TR $\beta$ 1 [26]. In addition, our unpublished results of experiments performed on the material used in this study show lack of changes between the expression of TR $\alpha$ 1 in ccRCC tissues in comparison with control samples. Therefore we assumed that *DIO1* expression would be a good marker of changes of TR $\beta$ 1 level in kidney samples. To determine whether decreased expression of TR $\beta$ 1 mRNA and protein observed in ccRCC was accompanied by changes in T3-target gene expression, we analyzed expression of *DIO1* in eleven paired samples of ccRCC and normal kidney tissue. In accordance with the reduced TR $\beta$ 1 expression in ccRCC, *DIO1* mRNA was decreased by 92% in tumor tissue compared to normal (Fig. 5A) and D1 protein was undetectable in tumors but detectable in samples of paired normal tissue (Fig. 5B).

### 3.7. Tissue T3 concentrations are reduced in ccRCC compared with normal kidney

TR $\beta$ 1 regulates target gene expression in response to T3, whereas T4 does not bind and activate the receptor at physiological concentrations. T4 is a pro-hormone that is converted to T3 by the type 1 and 2 deiodinase enzymes, of which *DIO1* gene is regulated directly by T3 whereas *DIO2* is not [27]. Thus, the level of deiodinase activity determines the intracellular level of T3 available to bind and activate TRs. In order to determine whether reduced expression of *DIO1* correlated with reduced tissue T3 concentration, the levels of T4 and T3 were determined in 11 paired ccRCC and normal kidney tissue samples. The level of T4 did not differ between normal and ccRCC tissue, whereas the concentration of T3 was reduced by 58% in ccRCC tissue (Fig. 5C).

## 4. Discussion

These studies demonstrate reduced TR $\beta$ 1 mRNA and protein expression in human ccRCC (Fig. 2). We found discordance in the magnitude of the change in TR $\beta$ 1 mRNA level (70% reduction in ccRCC) compared to protein (91% reduction). These results confirm our previous findings achieved by different mRNA analysis method (Northern blot) and different antibodies as well as Western blot protocol and in different tissue samples [28]. These repeatedly obtained, coherent results suggest that TR $\beta$ 1 expression is subject to posttranscriptional regulation in ccRCC. Reduced TR $\beta$ 1 expression in ccRCC was accompanied by absent D1 protein and a 58% reduction in tissue T3 concentration (Fig. 5). The current findings are consistent with previous findings of abnormal TR $\beta$ 1 expression [4] and reduced D1 activity [29] in renal cancer. Taken together, the data provide powerful evidence of tissue hypothyroidism and impaired T3 action in ccRCC that is maintained by reduced expression of TR $\beta$ 1 and D1 (Fig. 6).

Previous studies have shown that TR $\beta$ 1 mRNA 5'UTR undergoes complex alternative splicing, and eight 5'UTR variants that regulate efficiency of TR $\beta$ 1 protein translation in a tissue-specific manner were



translation from pools of mRNAs containing 5'UTRs with complex secondary structure [35]. Although the functional significance of alternative splicing of the TR $\beta$ 1 5'UTR in ccRCC is currently unknown, aberrant expression of alternative 5'UTRs has been shown to contribute to carcinogenesis mediated by tumor suppressors [12,36], and oncogenes [37]. In the light of the complex secondary structures of low copy number TR $\beta$ 1 5'UTRs and evidence for selective translation of structured mRNAs in aggressive metastatic cancer or oxygen deprived tumors [35] it is likely that the 5'UTR of TR $\beta$ 1 plays an important role in controlling levels of receptor protein in ccRCC and this may influence tumor progression.

In addition to the role of the 5'UTR, alternative splicing of the 3' UTR is likely to be important. Analysis of the main TR $\beta$ 1 3'UTR variant (3'UTR-1) identified miRNA-204 as a candidate regulator of TR $\beta$ 1 expression. A binding site for miRNA-204 was identified in TR $\beta$ 1 3' UTR-1 but not in the minor 3'UTR-2 splice variant and miRNA-204 expression was found to be increased 2-fold in ccRCC (Fig. 4). Moreover, as we showed, overexpression of miR-204 in Caki-2 cells leads to downregulation of TR $\beta$ 1 mRNA and protein. These findings are consistent with studies indicating that miRNA-204 acts as an inhibitor of mRNA expression [38].

Apart from TR $\beta$ 1, another TR isoform is present in the kidney, TR $\alpha$ 1, which has been also shown to bind the promoter of *DIO1* gene *in vitro* [25]. It was suggested, however, that *DIO1* expression in the kidney is solely activated by TR $\beta$ 1 [26]. In addition, our unpublished results of experiments performed on the material used in this study show that expression of TR $\alpha$ 1 does not change in ccRCC when compared control samples. Finally, miR-204-mediated downregulation of TR $\beta$ 1 in Caki-2 cells is accompanied by decrease of *DIO1* mRNA expression, what additionally confirms the linkage between changes in TR $\beta$ 1 and *DIO1* expression in the kidney.

The biological significance of our findings comes from emerging evidence demonstrating that TR $\beta$ 1 functions as a tumor suppressor [39–41]. Its role is complex, however, as the T3-dependent activity of TR $\beta$ 1 may have a biphasic effect on cell growth and proliferation. Knockout mice lacking TR $\beta$ 1 show delayed hepatocyte proliferation and enhanced apoptosis in response to partial hepatectomy [42] and tumor cell growth is retarded in hypothyroid mice [39]. On the other hand, the phenotype of tumors induced in hypothyroid hosts is more mesenchymal, and their invasiveness and metastatic behaviour are enhanced [39]. These findings are in line with previous reports documenting reduced tissue T3 in human gliomas [43] and demonstrating an association between the low T3 syndrome and renal cancer [44], although decreased concentrations of T3 have also been shown to reduce proliferation of Caki-2 cells *in vitro* [45]. Interestingly, variations in T3 and TRs level may directly initiate changes in activity of other target genes with direct effect on proliferation including those engaged in the regulation of cell cycle progression. An example of such a gene is E2F1, a transcription factor controlling G1 to S phase transition whose expression is negatively regulated by TRs [46]. As we showed, the expression of E2F1 is increased in renal cancer tissues, and this is in agreement with disturbed function of TRs [47]. E2F1 is known to regulate cellular proliferation [48] therefore its disturbed expression may contribute to ccRCC carcinogenesis. Moreover, Liu et al. [49] showed that CD74 induced tumorigenesis of ccRCC is mediated by PI3K/AKT pathway and it is known that this pathway is regulated by TR $\beta$ 1/T3 [50]. Thus, it is highly probable that disturbances of TR $\beta$ 1 and T3 observed in this study may initiate wide net of changes in multiple target genes, causing direct effect on proliferation.

In summary, we demonstrate that reduced expression of TR $\beta$ 1 in ccRCC is likely to be maintained by posttranscriptional mechanisms mediated by alternative splicing of the TR $\beta$ 1 mRNA 5' and 3'UTRs along with increased expression of miRNA-204. Reduced expression of TR $\beta$ 1 results in tissue T3 deficiency mediated by inhibition of *DIO1* expression. The recently identified tumor suppressor activity of TR $\beta$ 1 [39–41] indicates that reduced TR $\beta$ 1 expression and tissue hypothyroidism in

ccRCC tumors may be involved in the process of carcinogenesis itself or in maintaining a proliferative advantage to the malignant cells.

#### Conflict of interest statement

None declared.

#### Acknowledgments

We thank Prof. Theo J. Visser for anti-D1 serum.

This work was supported by the Polish State Committee for Scientific Research Grants NN401073636, N40101732/0286 and the Medical Centre of Postgraduate Education Grant 501-2-1-22-15/06 (to A.N.).

#### Appendix A. Supplementary data

Supplementary materials related to this article can be found online at doi:10.1016/j.bbadis.2010.07.025.

#### References

- [1] J.H. Bassett, C.B. Harvey, G.R. Williams, Mechanisms of thyroid hormone receptor-specific nuclear and extra nuclear actions, *Mol. Cell. Endocrinol.* 213 (2003) 1–11.
- [2] J.S. Qi, Y. Yuan, V. Desai-Yajnik, H.H. Samuels, Regulation of the mdm2 oncogene by thyroid hormone receptor, *Mol. Cell. Biol.* 19 (1999) 864–872.
- [3] S. Dinda, A. Sanchez, V. Moudgil, Estrogen-like effects of thyroid hormone on the regulation of tumor suppressor proteins, p53 and retinoblastoma, in breast cancer cells, *Oncogene* 21 (2002) 761–768.
- [4] M. Puzianowska-Kuznicka, A. Nauman, A. Madej, Z. Tanski, S. Cheng, J. Nauman, Expression of thyroid hormone receptors is disturbed in human renal clear cell carcinoma, *Cancer Lett.* 155 (2000) 145–152.
- [5] Z. Li, Z.H. Meng, R. Chandrasekaran, W.L. Kuo, C.C. Collins, J.W. Gray, S.H. Dairkee, Biallelic inactivation of the thyroid hormone receptor beta1 gene in early stage breast cancer, *Cancer Res.* 62 (2002) 1939–1943.
- [6] Y. Kamiya, M. Puzianowska Test, Expression of mutant thyroid hormone nuclear receptors is associated with human renal cell carcinoma, *Carcinogenesis* 23 (2002) 25–33.
- [7] A.G. Myasnikov, A. Simonetti, S. Marzi, B.P. Klaholz, Structure-function insights into prokaryotic and eukaryotic translation initiation, *Curr. Opin. Struct. Biol.* 19 (2009) 300–309.
- [8] S. Chatterjee, J.K. Pal, Role of 5'- and 3'-untranslated regions of mRNAs in human diseases, *Biol. Cell.* 101 (2009) 251–262.
- [9] D. Mannavola, L.C. Moeller, P. Beck-Peccoz, L. Persani, R.E. Weiss, S. Refetoff, A novel splice variant involving the 5' untranslated region of thyroid hormone receptor beta1 (TRbeta1), *J. Endocrinol. Invest.* 27 (2004) 318–322.
- [10] S. Frankton, C.B. Harvey, L.M. Gleason, A. Fadel, G.R. Williams, Multiple messenger ribonucleic acid variants regulate cell-specific expression of human thyroid hormone receptor beta1, *Mol. Endocrinol.* 18 (2004) 1631–1642.
- [11] F. Mignone, C. Gissi, S. Liuni, G. Pesole, Untranslated regions of mRNAs, *Genome Biol.* 3 (3) (2002) (REVIEWS0004).
- [12] K. Sobczak, W.J. Krzyzosiak, Structural determinants of BRCA1 translation regulation, *J. Biol. Chem.* 277 (2002) 17349–17358.
- [13] L.I. Chen, K.M. Sommer, K. Swisshelm, Downstream codons in the retinoic acid receptor beta-2 and beta-4 mRNAs initiate translation of a protein isoform that disrupts retinoid-activated transcription, *J. Biol. Chem.* 277 (2002) 35411–35421.
- [14] X. Peng, R.G. Mehta, D.A. Tonetti, K. Christov, Identification of novel RARbeta2 transcript variants with short 5'-UTRs in normal and cancerous breast epithelial cells, *Oncogene* 24 (2005) 1296–1301.
- [15] D.J. Grignon, M. Che, Clear cell renal cell carcinoma, *Clin. Lab. Med.* 25 (2005) 305–316.
- [16] H.J. Peltier, G.J. Latham, Normalization of microRNA expression levels in quantitative RT-PCR assays: identification of suitable reference RNA targets in normal and cancerous human solid tissues, *RNA* 14 (2008) 844–852.
- [17] G.E. Reynolds, K. Venken, G. Morreale de Escobar, E.R. Kühn, V.M. Darras, Dynamics and regulation of intracellular thyroid hormone concentrations in embryonic chicken liver, kidney, brain, and blood, *Gen. Comp. Endocrinol.* 134 (2003) 80–87.
- [18] D.H. Mathews, M.D. Disney, J.L. Childs, S.J. Schroeder, M. Zuker, D.H. Turner, Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure, *Proc. Natl. Acad. Sci. U. S. A.* 101 (2004) 7287–7292.
- [19] S. Brunak, J. Engelbrecht, S. Knudsen, Prediction of Human mRNA Donor and Acceptor Sites from the DNA Sequence, *J. Mol. Biol.* 220 (1991) 49–65.
- [20] M.G. Reese, F.H. Eeckman, D. Kulp, D. Haussler, Improved splice site detection in gene, *J. Comput. Biol.* 4 (1997) 311–323.
- [21] M. Rehmsmeier, P. Steffen, M. Hochsmann, R. Giegerich, Fast and effective prediction of microRNA/target duplexes, *RNA* 10 (2004) 1507–1517.
- [22] A. Krek, D. Grun, M.N. Poy, R. Wolf, L. Rosenberger, E.J. Epstein, P. MacMenamin, I. de Piedad, K.C. Gunschul, M. Stoffel, N. Rajewski, Combinatorial microRNA target predictions, *Nat. Genet.* 37 (2005) 495–500.

- [23] B.P. Lewis, C.B. Burge, D.P. Bartel, Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets, *Cell* 120 (2005) 15–20.
- [24] D. Betel, M. Wilson, A. Gabow, D.S. Marks, C. Sander, The microRNA.org resource: targets and expression, *Nucleic Acids Res.* 36 (2008) D149–D153.
- [25] N. Toyoda, A.M. Zavacki, A.L. Maia, J.W. Harney, P.R. Larsen, A novel retinoid X receptor-independent thyroid hormone response element is present in the human type 1 deiodinase gene, *Mol. Cell. Biol.* 15 (1995) 5100–5112.
- [26] L.L. Amma, A. Campos-Barros, Z. Wang, B. Vennström, D. Forrest, Distinct tissue-specific roles for thyroid hormone receptors beta and alpha1 in regulation of type 1 deiodinase expression, *Mol. Endocrinol.* 15 (2001) 467–475.
- [27] A.C. Bianco, D. Salvatore, B. Gereben, M.J. Berry, P.R. Larsen, Biochemistry, cellular and molecular biology, and physiological roles of the iodothyronine selenodeiodinases, *Endocr. Rev.* 23 (2002) 38–89.
- [28] M. Puzianowska-Kuznicka, A. Nauman, A. Madej, Z. Tanski, S. Cheng, J. Nauman, Expression of thyroid hormone receptors is disturbed in human renal clear cell carcinoma, *Cancer Lett.* 155 (2000) 145–152.
- [29] J. Pachucki, M. Ambroziak, Z. Tanski, J. Luczak, J. Nauman, A. Nauman, Type I 5'-iodothyronine deiodinase activity and mRNA are remarkably reduced in renal clear cell carcinoma, *J. Endocrinol. Invest.* 24 (2001) 253–261.
- [30] A. Piekuelko-Witkowska, A. Master, A. Wojcicka, J. Boguslawska, I. Brozda, Z. Tanski, A. Nauman, Disturbed expression of type 1 iodothyronine deiodinase splice variants in human renal cancer, *Thyroid* 19 (2009) 1105–1113.
- [31] D.O. Bates, T.G. Cui, J.M. Doughty, M. Winkler, M. Sugiono, J.D. Shields, D. Peat, D. Gillatt, S.J. Harper, VEGF165b, an inhibitory splice variant of vascular endothelial growth factor, is down-regulated in renal cell carcinoma, *Cancer Res.* 62 (2002) 4123–4131.
- [32] E. Tsuji, Y. Tsuji, T. Fujiwara, S. Ogata, K. Tsukamoto, K. Saku, Splicing variant of Cdc42 interacting protein-4 disrupts beta-catenin-mediated cell-cell adhesion: expression and function in renal cell carcinoma, *Biochem. Biophys. Res. Commun.* 339 (2006) 1083–1088.
- [33] C. Mahotka, T. Krieg, A. Krieg, M. Wenzel, C.V. Suschek, M. Heydthausen, H.E. Gabbert, C.D. Gerharz, Distinct in vivo expression patterns of survivin splice variants in renal cell carcinomas, *Int. J. Cancer.* 100 (2002) 30–36.
- [34] A.E. Willis, Translational control of growth factor and proto-oncogen expression, *Int. J. Biochem. Cell. Biol.* 31 (1999) 73–86.
- [35] A. De Benedetti, J.R. Graff, eIF-4E expression and its role in malignancies and metastases, *Oncogene* 23 (2004) 3189–3199.
- [36] G.I. Frost, G. Mohapatra, T.M. Wong, A.B. Csóka, J.W. Gray, R. Stern, HYAL1/UC1, a candidate tumor suppressor gene on chromosome 3p21.3, is inactivated in head and neck squamous cell carcinomas by aberrant splicing of pre-mRNA, *Oncogene* 19 (2000) 870–877.
- [37] X.-Q. Wang, J.A. Rothnagel, Post-transcriptional regulation of the GLI1 oncogene by the expression of alternative 5' untranslated regions, *J. Biol. Chem.* 276 (2001) 1311–1316.
- [38] V.J. Findlay, D.P. Turner, O. Moussa, D.K. Watson, MicroRNA-mediated inhibition of prostate-derived Ets factor messenger RNA translation affects prostate-derived Ets factor regulatory networks in human breast cancer, *Cancer Res.* 68 (2008) 8499–8506.
- [39] O. Martínez-Iglesias, S. García-Silva, J. Regadera, A. Aranda, Hypothyroidism Enhances Tumor Invasiveness and Metastasis Development, *PLoS ONE* 4 (2009) e6428.
- [40] O. Martínez-Iglesias, S. García-Silva, S.P. Tenbaum, J. Regadera, F. Larcher, J.M. Paramio, B. Vennström, A. Aranda, Thyroid hormone receptor beta1 acts as a potent suppressor of tumor invasiveness and metastasis, *Cancer Res.* 69 (2009) 501–509.
- [41] X.G. Zhu, L. Zhao, M.C. Willingham, S.Y. Cheng, Thyroid hormone receptors are tumor suppressors in a mouse model of metastatic follicular thyroid carcinoma, *Oncogene* 29 (2010) 1909–1910.
- [42] R. López-Fontal, M. Zeini, P.G. Través, M. Gómez-Ferrera, A. Aranda, G.T. Sáez, C. Cerdá, P. Martín-Sanz, S. Hortelano, L. Boscá, Mice lacking thyroid hormone receptor Beta show enhanced apoptosis and delayed liver commitment for proliferation after partial hepatectomy, *PLoS One* 5 (2010) e8710.
- [43] P. Nauman, W. Bonicki, R. Michalik, A. Warzecha, Z. Czernicki, The concentration of thyroid hormones and activities of iodothyronine deiodinases are altered in human brain gliomas, *Folia Neuropathol.* 42 (2004) 67–73.
- [44] A. Nauman, J. Nauman, A. Pietrzykowski, D. Lazecki, S. Dutkiewicz, Z. Tanski, A. Witeska, M. Kauczak, The Low T3 Syndrome in patients with kidney cancer—the effect of cancer differentiation, *Polish J. Endocrinol.* 47 (1996) 365–374.
- [45] P. Poplawski, A. Nauman, Thyroid hormone–triiodothyronine–has contrary effect on proliferation of human proximal tubules cell line (HK2) and renal cancer cell lines (Caki-2, Caki-1)—role of E2F4, E2F5 and p107, p130, *Thyroid Res.* 13 (2008) 1:5.
- [46] M. Nygård, G.M. Wahlström, M.V. Gustafsson, Y.M. Tokumoto, M. Bondesson, Hormone-dependent repression of the E2F-1 gene by thyroid hormone receptors, *Mol. Endocrinol.* 17 (2003) 79–92.
- [47] O. Turowska, A. Nauman, M. Pietrzak, P. Poplawski, A. Master, M. Nygard, M. Bondesson, Z. Tanski, M. Puzianowska-Kuznicka, Overexpression of E2F1 in clear cell renal cell carcinoma: a potential impact of erroneous regulation by thyroid hormone nuclear receptors, *Thyroid* 17 (2007) 1039–1048.
- [48] D.G. Johnson, J. Degregori, Putting the Oncogenic and Tumor Suppressive Activities of E2F into Context, *Curr. Mol. Med.* 6 (2006) 731–738.
- [49] Y.H. Liu, C.Y. Lin, W.C. Lin, S.W. Tang, M.K. Lai, J.Y. Lin, Up-regulation of vascular endothelial growth factor-D expression in clear cell renal cell carcinoma by CD74: a critical role in cancer cell tumorigenesis, *J. Immunol.* 181 (2008) 6584–6594.
- [50] F. Furuya, C. Lu, C.J. Guigon, S.Y. Cheng, Nongenomic activation of phosphatidylinositol 3-kinase signaling by thyroid hormone receptors, *Steroids* 74 (2009) 628–634.
- [51] M. Chen, Y. Ye, H. Yang, P. Tamboli, S. Matin, N.M. Tannir, C.G. Wood, J. Gu, X. Wu, Genome-wide profiling of chromosomal alterations in renal cell carcinoma using high-density single nucleotide polymorphism arrays, *Int. J. Cancer.* 125 (2009) 2342–2348.
- [52] M.D. Rosen, M.L. Privalsky Thyroid, hormone receptor mutations found in renal clear cell carcinomas alter corepressor release and reveal helix 12 as key determinant of corepressor specificity, *Mol. Endocrinol.* 23 (2009) 1183–1192.
- [53] K.J. Livak, T.D. Schmittgen, Analysis of relative gene expression data using real-time quantitative PCR and the 2<sup>(-Delta Delta C(T))</sup>, *Method. Methods* 25 (2001) 402–408.
- [54] G.G. Kuiper, F. Wassen, W. Klootwijk, H. Van Toor, E. Kaptein, T.J. Visser, Molecular basis for the substrate selectivity of cat type I iodothyronine deiodinase, *Endocrinology* 144 (2003) 5411–5421.