Supplementary Tables

Table S1: PCR primer sequences

| Gene	Forward Primer	Reverse Primer
PPIA	ATGCTGGACCCAACACAAAT	TCTTTCACTTTGCCAAACACC
ACTB	CCAACCGCGAGAAGATGA	CCAGAGGCGTACAGGGATAG
ATP5A1	TGCTATTGGTCAAAAGAGATCCA	GTAGCCGACACCACAATGG
ATP5B	CAGCAGATTTTGGCAGGTGAA	ACCCCTCACGATGAATGCTC
ATPAF1	GGCTCAGTCCTGTCCAACAT	AGTTCAGTACCTGTCCATTGTCC
ATP5C1	AGCCGCAATGGATTCAAGTT	TCTCTCTCAGCTCGGGCATA
ATP5D	GTCGTGGTGCATGCAGAG	GAAGAGTCGGCGTTCACTG
ATP5O	GGTACCTTGCACAGTGACCT	CGGATCAGTCTTAGCCTCCAA
ATPG5F1	CCTTCCTAGGTCCAGGGGTA	CCTCAGGGATCAGTCCATAACG
ATP5G1	GGGTAGTAGGAGTGCAGACTGA	GGGCTATTCAAGAAGGAGGCA
ATP5G2	CTGAGCTGATCCTCTCTCCTGC	TTCAGCACCACTGCAGATAGC
ATP5G3	TCAGACCAGTGCAATCAGCA	GCGAAGGGTTTCTGGCATAAC

Supplementary Figures

Figure S1: Validation of gene expression using PCR in a of cohort of 18 ccRCC and 10

normal renal tissue samples.
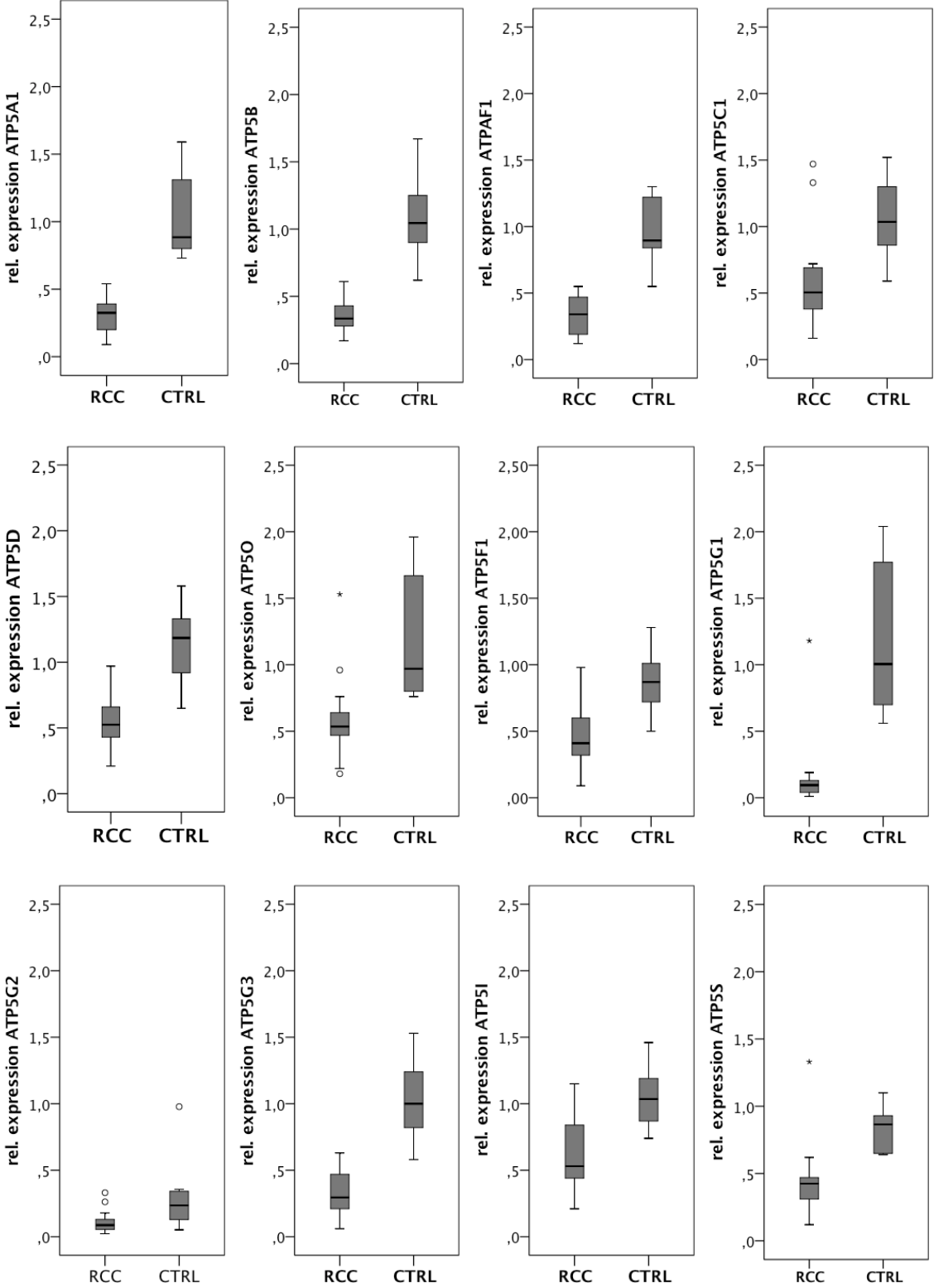
Figure S2: Validation of gene expression using PCR in a of cohort of 74 ccRCC and 36
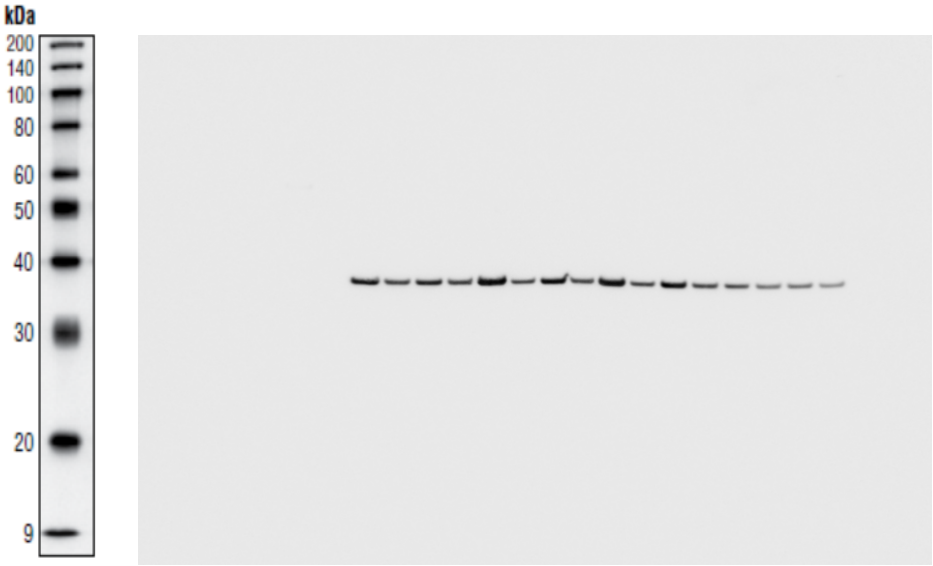
normal renal tissues.
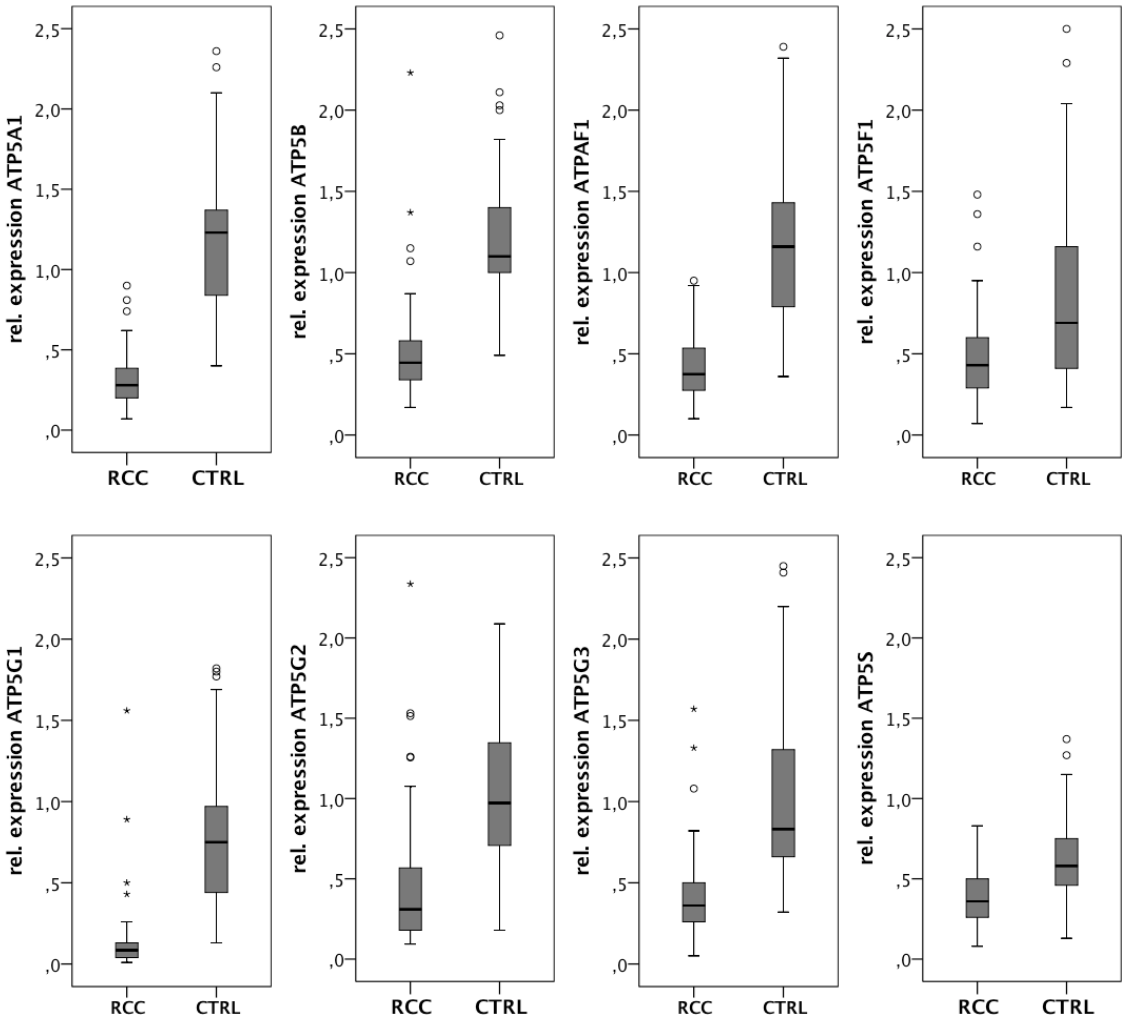
Figure S3: Kaplan Meier estimate for the expression of ATP5G2 mRNA expression
(dichotomized according the median expression level) as predictor of overall survival
in patients with clear cell renal cell carcinoma.
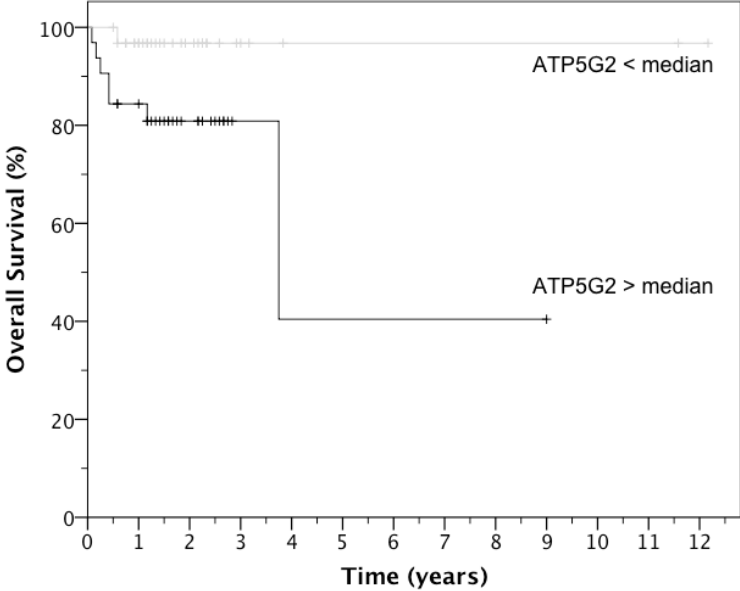
Figure S4: Western blot experiments were performed to determine the protein expression in 8 corresponding normal (N) and clear cell renal cell carcinoma (T) tissue. All proteins were decreased in higher grades of the tumor tissue, ATP5G1/G2/G3 showed band of different sizes in some tumor and normal samples.
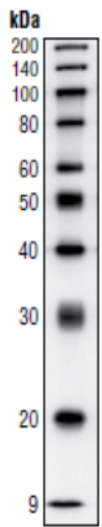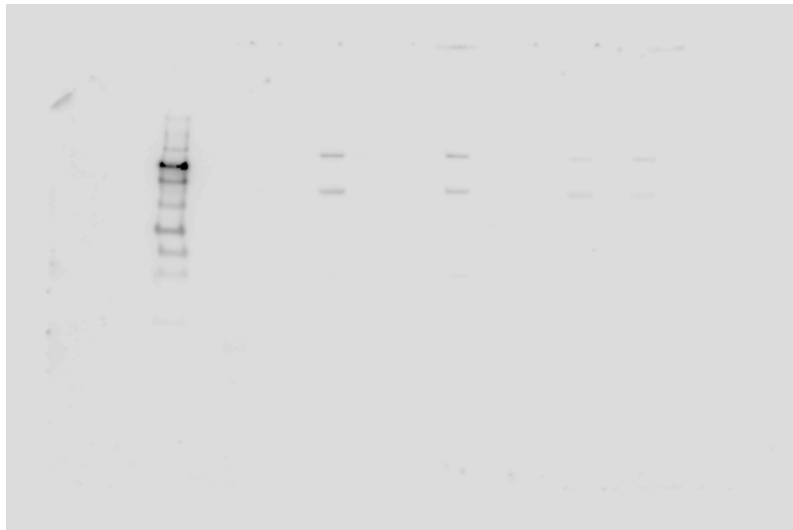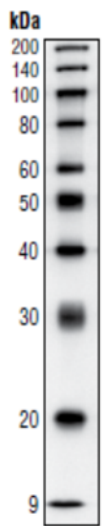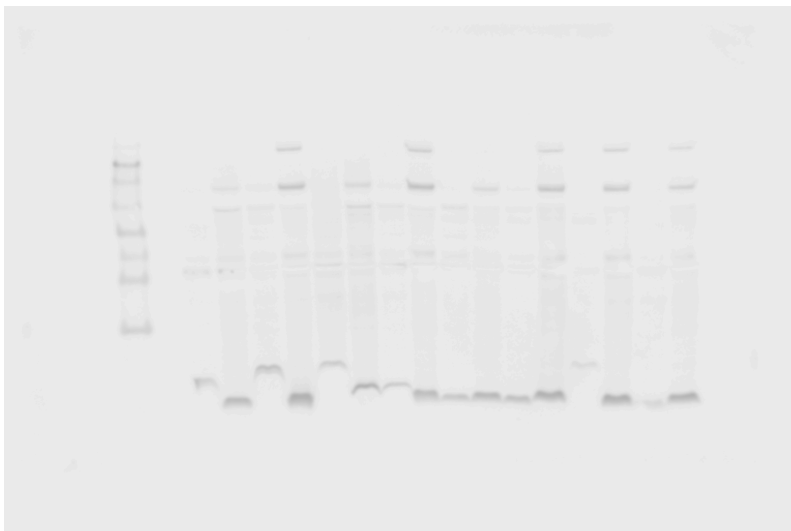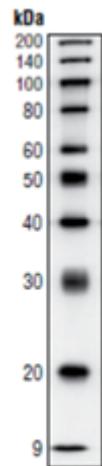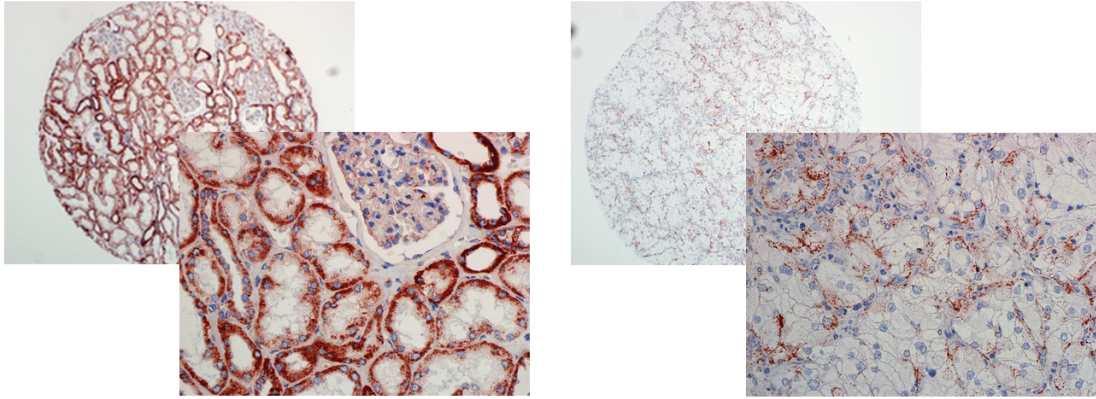
GAPDH:

Actin:

ATP5A1
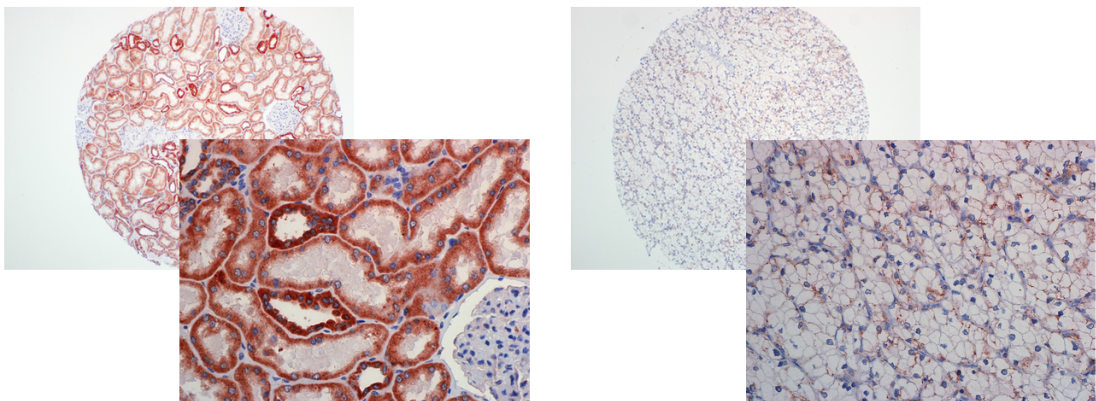

ATPAF1

ATP5G1/G2/G3:

Figure S5: Immunohistochemical staining of ATP5A1, ATP5G1/G2/G3 and ATPAF1 in normal renal tissue (left) and clear cell renal cell carcinoma (right).

ATP5A1

ATP5G1/G2/G3

ATPAF1