

Supplementary data

Table S1. List of top 50 positively and 50 negatively correlated genes with MATR3 in ccRCC.

Positively Correlated Genes			Negatively Correlated Genes		
	Genes	PearsonCC		Genes	PearsonCC
1	SMAD5	0.92	1	C19orf53	-0.6
2	PJA2	0.9	2	SERF2	-0.56
3	PGGT1B	0.9	3	TAF10	-0.56
4	RBM27	0.9	4	POLR2J	-0.55
5	C11orf58	0.9	5	TRAPPC5	-0.55
6	PRKAA1	0.9	6	ZNHIT1	-0.54
7	ACAP2	0.89	7	YDJC	-0.51
8	BCLAF1	0.89	8	GADD45GIP1	-0.51
9	PHAX	0.89	9	COX6B1	-0.5
10	CTDSPL2	0.89	10	NDUFA3	-0.5
11	DEK	0.89	11	BLOC1S1	-0.5
12	GABPA	0.89	12	TIMM16	-0.49
13	CDC73	0.89	13	C17orf90	-0.49
14	TBC1D15	0.88	14	LSM7	-0.49
15	FAM114A2	0.88	15	FKBP2	-0.49
16	DIS3	0.88	16	DNAJC4	-0.49
17	SPOPL	0.88	17	TCEB2	-0.49
18	AGGF1	0.88	18	MRPL23	-0.48
19	SP3	0.88	19	NDUFS8	-0.48
20	UBE3A	0.88	20	ROMO1	-0.48
21	VPS26A	0.88	21	NME3	-0.48
22	NPAT	0.88	22	APRT	-0.47
23	SRFBP1	0.88	23	NCRNA00116	-0.47
24	NEDD1	0.88	24	C9orf142	-0.47
25	SLC25A24	0.87	25	MIF	-0.47
26	MARCH7	0.87	26	POLD4	-0.47
27	HIAT1	0.87	27	PPP1R14B	-0.46
28	CHM	0.87	28	C19orf24	-0.46
29	POLK	0.87	29	ZDHHC24	-0.46
30	PUM2	0.87	30	SSNA1	-0.46
31	WAPAL	0.87	31	KRTCAP2	-0.46
32	TTC33	0.87	32	RNPEPL1	-0.46
33	KHDRBS1	0.87	33	PUSL1	-0.46
34	PRRC1	0.87	34	DRAP1	-0.45
35	ATRX	0.87	35	SHARPIN	-0.45
36	C5orf24	0.87	36	HSPB1	-0.45
37	STAM2	0.87	37	RPS15	-0.45
38	USP1	0.87	38	MRPL41	-0.45
39	FAM98B	0.87	39	MXD3	-0.45
40	CNOT8	0.87	40	PGLS	-0.45
41	FBXL3	0.86	41	MRPS15	-0.45

42	ITCH	0.86	42	PSENEN	-0.45
43	STAG2	0.86	43	C16orf13	-0.45
44	NUS1	0.86	44	ROBLD3	-0.45
45	G3BP1	0.86	45	C7orf47	-0.45
46	API5	0.86	46	SMUG1	-0.45
47	RAB6A	0.86	47	HCFC1R1	-0.45
48	CNOT6	0.86	48	GPX4	-0.44
49	PPP6C	0.86	49	C17orf37	-0.44
50	STX12	0.86	50	NUTF2	-0.44

Table S2. Multivariate analysis of prognostic factors by the Cox proportional hazard model for MRPL23 expression and combination of MRPL23 and MATR3.

Variable	Multivariate analysis: MRPL23				Multivariate analysis: MATR3+MRPL23			
	HR	95% CI		P-value	HR	95.0% CI		P-value
MRPL23	1.94	1.41	2.67	<0.0001	-	-	-	-
MATR3-h/MRPL23-l	-	-	-	-	Ref.			
MATR3-l/MRPL23-h	-	-	-	-	3.15	2.05	4.83	<0.0001
others	-	-	-	-	2.11	1.44	3.11	0.0001
Gender	-	-	-	-	-	-	-	-
Age	-	-	-	-	-	-	-	-
Grade	1.16	0.84	1.61	0.37	1.14	0.83	1.59	0.42
TNM stage	3.10	2.21	4.35	<0.0001	3.22	2.30	4.51	<0.0001

Table S3. Clinical characteristics of 107 patients with ccRCC from our cohort.

Variables	Number (%)
Gender	
Females	32 (29.91)
Males	75 (70.09)
Age	
≤64	59 (55.14)
>64	48 (44.86)
Grade	
G1	26 (24.30)
G2	68 (63.55)
G3	12 (11.21)
G4	1 (0.93)
pT status	
T1	31 (28.97)
T2	30 (28.04)
T3	43 (40.19)
T4	3 (2.80)
pN status	
N0	100 (93.46)
N1	7 (6.54)

Table S4. Clinical characteristics of 475 patients with ccRCC from TCGA cohort.

Variables	Number (%)
Gender	
Females	163 (34.32)
Males	312 (65.68)
Age	
≤60	239 (50.32)
>60	236 (49.68)
Grade	
G1	11 (2.32)
G2	203 (42.74)
G3	189 (39.79)
G4	72 (15.16)
pT status	
T1	237 (49.89)
T2	61 (12.84)
T3	167 (35.16)
T4	10 (2.11)
pN status	
Nx	235 (49.47)
N0	225 (47.37)
N1	15 (3.16)
Stage	
I	234 (49.26)
II	50 (10.53)
III	119 (25.05)
IV	72 (15.16)

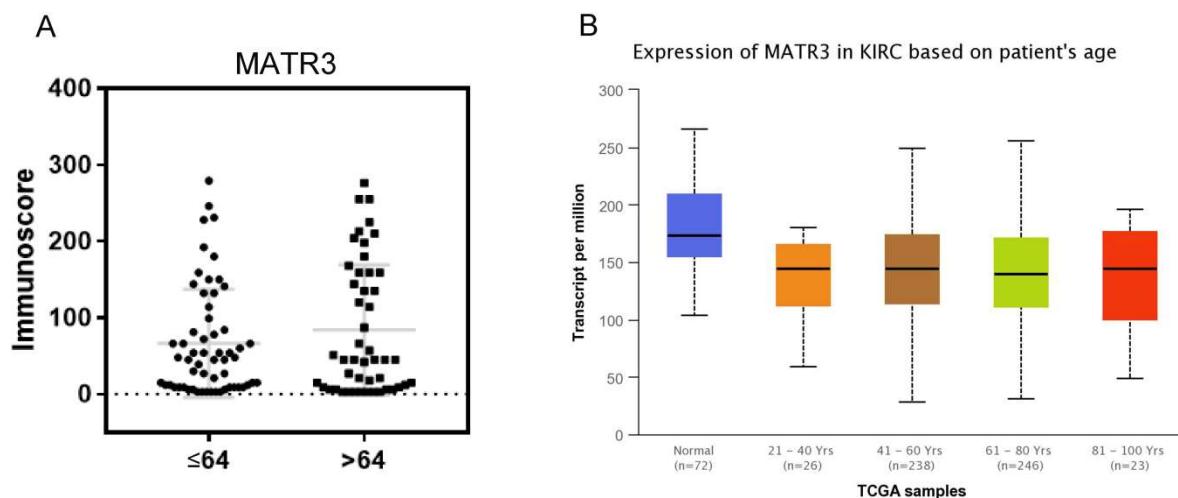


Figure S1. MATR3 expression depending on the age of patients. MATR3 expression depending on the age of patients in our cohort (A); and based on the UALCAN database (B). KIRC - Kidney Renal Clear Cell Carcinoma

DAVID database

A

Annotation Cluster 1	Enrichment Score: 4.52	G		Count	P_Value	Benjamini
☐ UP_KW_MOLECULAR_FUNCTION	Ribosomal protein	RT		5	7.5E-8	1.5E-7
☐ UP_KW_MOLECULAR_FUNCTION	Ribonucleoprotein	RT		5	4.7E-7	4.7E-7
☐ REACTOME_PATHWAY	Translation	RT		5	5.0E-7	2.3E-5
☐ REACTOME_PATHWAY	Mitochondrial translation initiation	RT		4	2.0E-6	2.3E-5
☐ REACTOME_PATHWAY	Mitochondrial translation elongation	RT		4	2.0E-6	2.3E-5
☐ REACTOME_PATHWAY	Mitochondrial translation termination	RT		4	2.0E-6	2.3E-5
☐ REACTOME_PATHWAY	Mitochondrial translation	RT		4	2.4E-6	2.3E-5
☐ GOTERM_CC_DIRECT	ribosome	RT		4	2.9E-6	5.2E-5
☐ GOTERM_MF_DIRECT	structural constituent of ribosome	RT		4	4.5E-6	2.7E-5
☐ GOTERM_BP_DIRECT	translation	RT		4	6.2E-6	8.6E-5
☐ KEGG_PATHWAY	Ribosome	RT		3	3.7E-4	7.5E-4
☐ UP_KW_CELLULAR_COMPONENT	Mitochondrion	RT		4	4.1E-4	8.1E-4
☐ REACTOME_PATHWAY	Metabolism of proteins	RT		5	1.1E-3	8.5E-3
☐ GOTERM_CC_DIRECT	mitochondrion	RT		4	1.3E-3	1.2E-2
☐ GOTERM_MF_DIRECT	RNA binding	RT		4	1.7E-3	5.2E-3
☐ GOTERM_CC_DIRECT	mitochondrial inner membrane	RT		3	2.8E-3	1.7E-2
☐ GOTERM_MF_DIRECT	protein binding	RT		4	5.9E-1	1.0E0

B

Annotation Cluster 2	Enrichment Score: 1.67	G		Count	P_Value	Benjamini
☐ GOTERM_BP_DIRECT	intracellular protein transport	RT		4	4.5E-6	8.6E-5
☐ UP_KW_BIOLOGICAL_PROCESS	Protein transport	RT		3	3.3E-3	1.3E-2
☐ UP_KW_BIOLOGICAL_PROCESS	Transport	RT		3	3.5E-2	7.1E-2
☐ UP_KW_PTM	Acetylation	RT		3	1.5E-1	5.2E-1
☐ UP_KW_PTM	Phosphoprotein	RT		4	2.1E-1	5.2E-1
☐ GOTERM_MF_DIRECT	protein binding	RT		4	3.0E-1	1.0E0
☐ UP_KW_CELLULAR_COMPONENT	Membrane	RT		3	4.5E-1	6.0E-1

Figure S2. The subnetwork functional enrichment analysis of MCODE cluster 1 (A) and cluster 2 (B) using the *DAVID Functional Annotation Clustering Tool*.

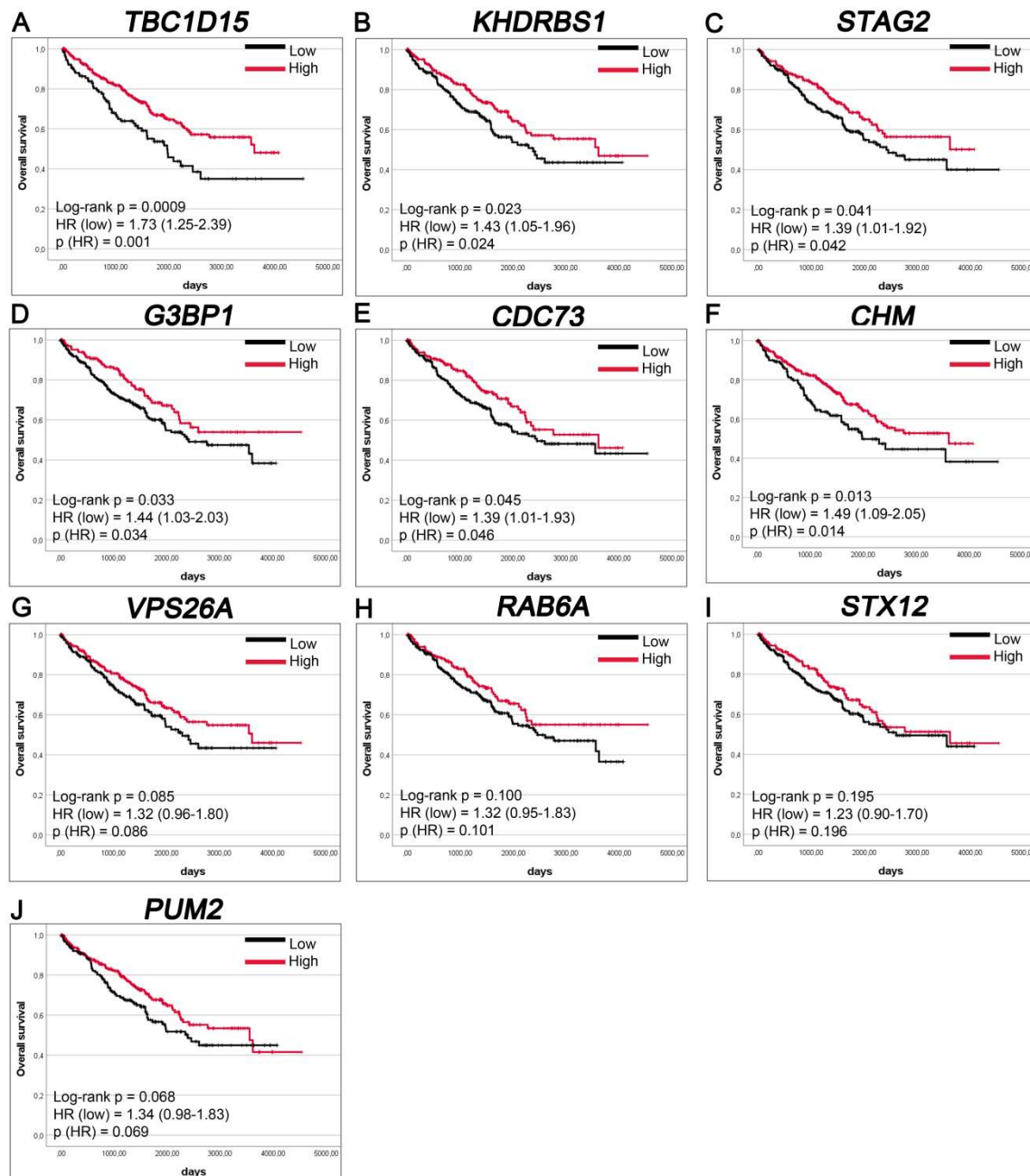


Figure S3. Kaplan–Meier curves for overall survival (OS) of clear cell renal cell carcinoma (ccRCC) patients stratified by *TBC1D15* (A), *KHDRBS1* (B), *STAG2* (C), *G3BP1* (D), *CDC73* (E), *CHM* (F), *VPS26A* (G), *RAB6A* (H), *STX12* (I), *PUM2* (J). The survival curves were plotted based on the TCGA ccRCC dataset sourced from the UCSC Xena database. Cases were divided into expression groups (low and high) according to the optimal cutoff point determined by the Evaluate Cutpoints software. The results are displayed with hazard ratio (HR) from the Cox PH model and Cox p -value or p -value from log-rank test.

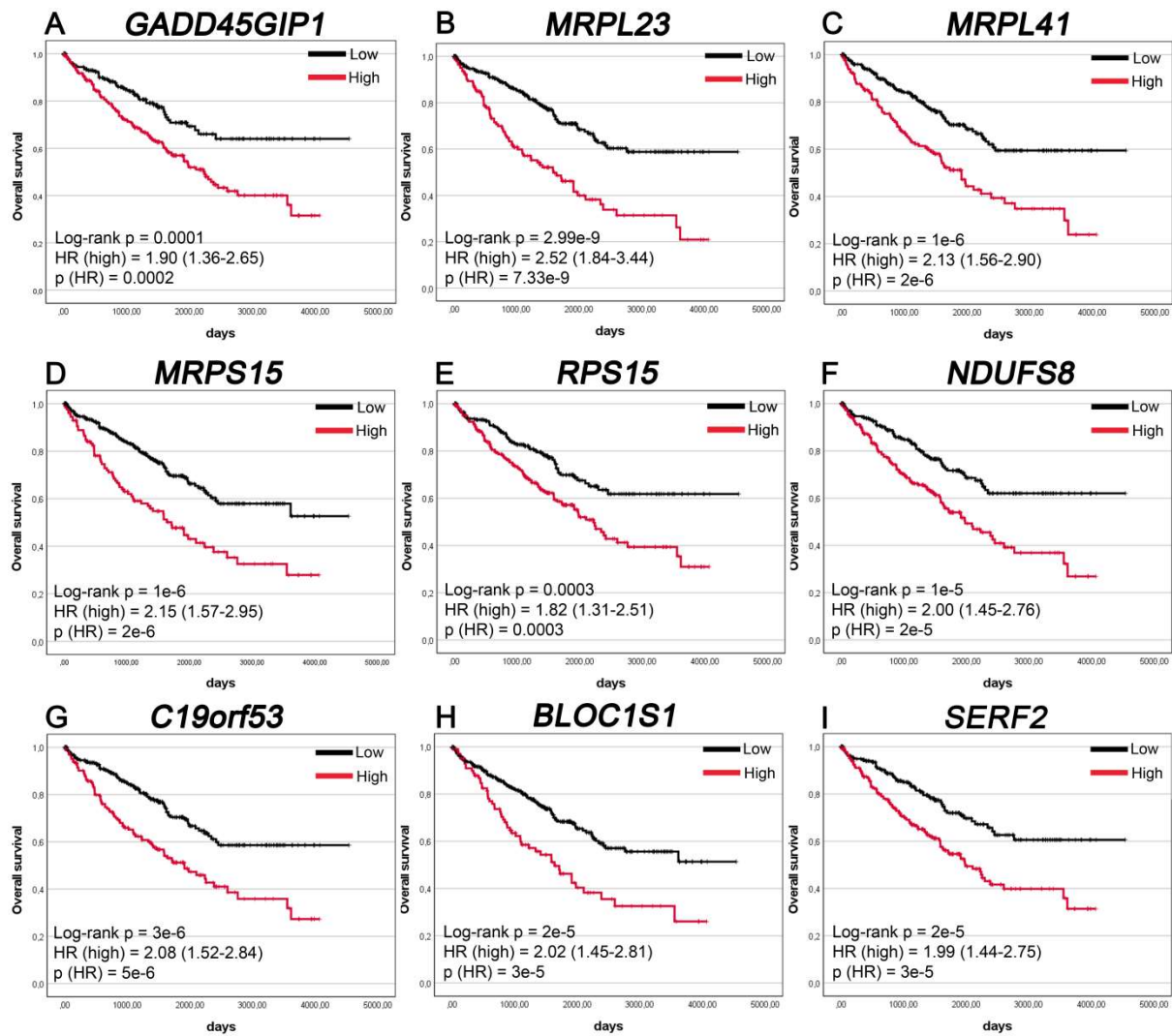


Figure S4. Kaplan–Meier curves for overall survival (OS) of clear cell renal cell carcinoma (ccRCC) patients stratified by *GADD45GIP1* (A), *MRPL23* (B), *MRPL41* (C), *MRPS15* (D), *RPS15* (E), *NDUFS8* (F), *C19orf53* (G), *BLOC1S1* (H), *SERF2* (I). The survival curves were plotted based on the TCGA ccRCC dataset sourced from the UCSC Xena database. Cases were divided into expression groups (low and high) according to the optimal cutoff point determined by the Evaluate Cutpoints software. The results are displayed with hazard ratio (HR) from the Cox PH model and Cox p -value or p -value from log-rank test.

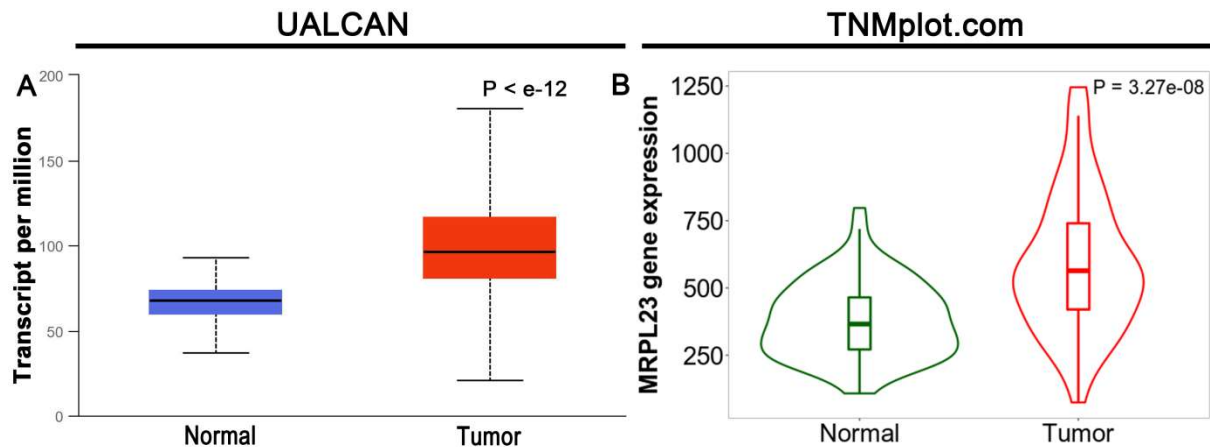


Figure S5. Differential expression of *MRPL23* in clear cell renal cell carcinoma (ccRCC) and normal tissues. Box plot visualized using UALCAN database (A) and violin plot visualized using TNMplot.com web tool (B) of *MRPL23* gene expression in ccRCC when compared to adjacent normal and tumor RNA-seq TCGA data.

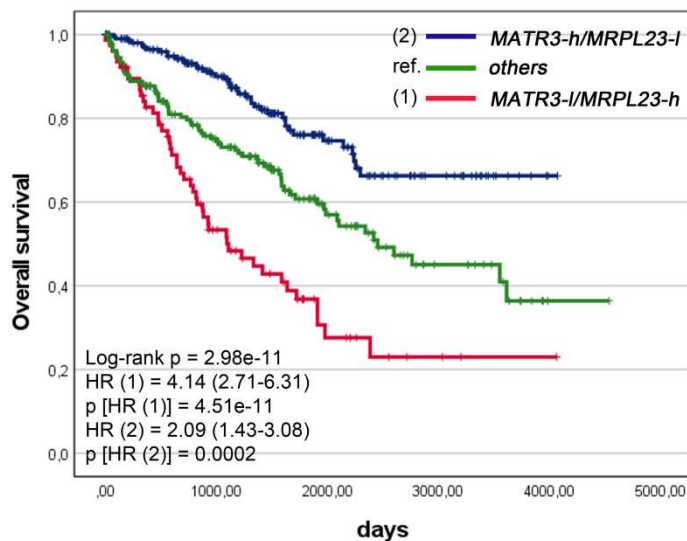


Figure S6. Kaplan–Meier curves for overall survival (OS) of clear cell renal cell carcinoma (ccRCC) patients stratified by combined expression of *MATR3* and *MRPL23*. The survival curves were plotted based on the TCGA ccRCC dataset sourced from the UCSC Xena database. The results are displayed with hazard ratio (HR) from the Cox PH model and Cox *p*-value or *p*-value from log-rank test.