Supplementary

Table S1 The interrelationship between infringement and other clinical indices of ccRCC

	Infringement		Phi coefficient	Fisher's P-value
	No (n=47)	Yes (n=58)		
Clinical stage			0.923	<0.001
I/II	45/47 (95.7%)	2/58 (3.4%)		
III/IV	2/47 (4.3%)	56/58 (96.6%)		
pT			0.943	<0.001
T1/T2	46/47 (97.9%)	2/58 (3.4%)		
T3/T4	1/47 (2.1%)	56/58 (96.6%)		

ccRCC, clear cell renal cell carcinoma; pT, pathological T stage.

Table S2 The interrelationship between Fuhrman grade and other clinical indices of ccRCC

	Fuhrman grade				Phi coefficient	Fisher's P-value
	1 (n=5)	2 (n=62)	3 (n=25)	4 (n=13)		
Infringement					0.342	0.004
No	4/5 (80.0%)	33/62 (53.2%)	9/25 (36.0%)	1/13 (7.7%)		
Yes	1/5 (20.0%)	29/62 (46.8%)	16/25 (64.0%)	12/13 (92.3)		
Metastasis					0.336	0.007
No	5/5 (100%)	46/62 (74.2%)	16/25 (64.0%)	4/13 (30.8%)		
Yes	0/5 (0%)	16/62 (25.8%)	9/25 (36.0%)	9/13 (69.2%)		
Tumor thrombus					0.288	0.035
No	5/5 (100%)	50/62 (80.6%)	19/25 (76.0%)	6/13 (46.2%)		
Yes	0/5 (0%)	12/62 (19.4%)	6/25 (24.0%)	7/13 (53.8%)		
Necrosis					0.477	<0.001
No	4/5 (80.0%)	54/62 (87.1%)	18/25 (72.0%)	3/13 (23.1%)		
Yes	1/5 (20.0%)	8/62 (12.9%)	7/25 (28.0%)	10/13 (76.9%)		
Sarcomatoid					0.575	<0.001
No	5/5 (100%)	61/62 (98.4%)	23/25 (92.0%)	6/13 (46.2%)		
Yes	0/5 (0%)	1/62 (1.6%)	2/25 (8.0%)	7/13 (53.8%)		
Clinical stage					0.326	0.006
I/II	4/5 (80.0%)	32/62 (51.6%)	10/25 (40.0%)	1/13 (7.7%)		
III/IV	1/5 (20.0%)	30/62 (48.4%)	15/25 (60.0%)	12/13 (92.3%)		
pT					0.334	0.005
T1/T2	4/5 (80.0%)	33/62 (53.2%)	10/25 (40.0%)	1/13 (7.7%)		
T3/T4	1/5 (20.0%)	29/62 (46.8%)	15/25 (60.0%)	12/13 (92.3%)		

ccRCC, clear cell renal cell carcinoma; pT, pathological T stage.

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Table S3 The interrelationship between metastatic disease at diagnosis and other clinical indices of ccRCC

	Metastatic disease at diagnosis		Phi coefficient	Fisher's P-value
	No (n=71)	Yes (n=34)		
Infringement			0.459	<0.001
No	43/71 (60.6%)	4/34 (11.8%)		
Yes	28/71 (39.4%)	30/34 (88.2%)		
Clinical stage			0.541	<0.001
I/II	45/71 (63.4%)	2/34 (5.9%)		
III/IV	26/71 (36.6%)	32/34 (94.1%)		
pT			0.512	<0.001
T1/T2	45/71 (63.4%)	3/34 (8.8%)		
T3/T4	26/71 (36.6%)	31/34 (91.2%)		

ccRCC, clear cell renal cell carcinoma; pT, pathological T stage.

Table S4 The interrelationship between tumor thrombus and other clinical indices of ccRCC

	Tumor thrombus		Phi coefficient	Fisher's P-value
	No (n=80)	Yes (n=25)		
Infringement			0.458	<0.001
No	46/80 (57.5%)	1/25 (4.0%)		
Yes	34/80 (42.5%)	24/25 (96.0%)		
Metastasis			0.569	<0.001
No	66/80 (82.5%)	5/25 (20.0%)		
Yes	14/80 (17.5%)	20/25 (80.0%)		
Necrosis			0.249	0.016
No	65/80 (81.3%)	14/25 (56.0%)		
Yes	15/80 (18.8%)	11/25 (44.0%)		
Clinical stage			0.458	<0.001
I/II	46/80 (57.5%)	1/25 (4.0%)		
III/IV	34/80 (42.5%)	24/25 (96.0%)		
pT			0.468	<0.001
T1/T2	47/80 (58.8%)	1/25 (4.0%)		
T3/T4	33/80 (41.3%)	24/25 (96.0%)		

ccRCC, clear cell renal cell carcinoma; pT, pathological T stage.

Table S5 The interrelationship between necrosis and other clinical indices of ccRCC

	Necrosis		Phi coefficient	Fisher's P-value
	No (n=79)	Yes (n=26)		
Infringement			0.295	0.003
No	42/79 (53.2%)	5/26 (19.2%)		
Yes	37/79 (46.8%)	21/26 (80.8%)		
Metastasis			0.357	<0.001
No	61/79 (77.2%)	10/26 (38.5%)		
Yes	18/79 (22.8%)	16/26 (61.5%)		
Clinical stage			0.339	0.001
I/II	43/79 (54.4%)	4/26 (15.4%)		
III/IV	36/79 (45.6%)	22/26 (84.6%)		
pT			0.349	<0.001
T1/T2	44/79 (55.7%)	4/26 (15.4%)		
T3/T4	35/79 (44.3%)	22/26 (84.6%)		

ccRCC, clear cell renal cell carcinoma; pT, pathological T stage.

Table S6 The interrelationship between sarcomatoid and other clinical indices of ccRCC

	Sarcomatoid		Phi coefficient	Fisher's P-value
	No (n=95)	Yes (n=10)		
Infringement			0.292	0.002
No	47/95 (49.5%)	0/10 (0%)		
Yes	48/95 (50.5%)	10/10 (100.0%)		
Metastasis			0.330	0.002
No	69/95 (72.6%)	2/10 (20.0%)		
Yes	26/95 (27.4%)	8/10 (80.0%)		
Necrosis			0.415	<0.001
No	77/95 (81.1%)	2/10 (20.0%)		
Yes	18/95 (18.9%)	8/10 (80.0%)		
Clinical stage			0.292	0.002
I/II	47/95 (49.5%)	0/10 (0%)		
III/IV	48/95 (50.5%)	10/10 (100.0%)		
pT			0.298	0.002
T1/T2	48/95 (50.5%)	0/10 (0%)		
T3/T4	47/95 (49.5%)	10/10 (100.0%)		

ccRCC, clear cell renal cell carcinoma; pT, pathological T stage.

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Table S7 The interrelationship between gender and age of ccRCC

	Gender		Phi coefficient	Fisher's P-value
	Male (n=82)	Female (n=23)		
Age			0.245	0.017
<58	42/82 (51.2%)	5/23 (21.7%)		
≥58	40/82 (48.8%)	18/23 (78.3%)		

ccRCC, clear cell renal cell carcinoma.

Table S8 The relationship between individual genes and gender

	Gender		Phi coefficient	Fisher's P-value
	Male (n=82)	Female (n=23)		
BAP1			0.220	0.039
WT	77/82 (93.9%)	18/23 (78.3%)		
Mut	5/82 (6.1%)	5/23 (21.7%)		
PIK3CB			0.331	0.003
WT	79/82 (96.3%)	17/23 (73.9%)		
Mut	3/82 (3.7%)	6/23 (26.1%)		
WWTR1			0.266	0.02
WT	80/82 (97.6%)	19/23 (82.6%)		
Mut	2/82 (2.4%)	4/23 (17.4%)		
MTOR			0.255	0.032
WT	81/82 (98.8%)	20/23 (87.0%)		
Mut	1/82 (1.2%)	3/23 (13.0%)		

WT, wild type; Mut, mutant.

Table S9 The relationship between individual genes and Fuhrman grade

	Fuhrman grade				Phi coefficient	Fisher's P-value
	1 (n=5)	2 (n=62)	3 (n=25)	4 (n=13)		
TP53					0.296	0.067
WT	5/5 (100%)	61/62 (98.4%)	21/25 (84.0%)	13/13 (100%)		
Mut	0/5 (0%)	1/62 (1.6%)	4/25 (16.0%)	0/13 (0%)		
BAP1					0.374	0.01
WT	5/5 (100%)	58/62 (93.5%)	24/25 (96.0%)	8/13 (61.5%)		
Mut	0/5 (0%)	4/62 (6.5%)	1/25 (4.0%)	5/13 (38.5%)		
PTEN					0.388	0.004
WT	5/5 (100%)	62/62 (100%)	24/25 (96.0%)	10/13 (76.9%)		
Mut	0/5 (0%)	0/62 (0%)	1/25 (4.0%)	3/13 (23.1%)		

WT, wild type; Mut, mutant.

Table S10 The relationship between individual genes and infringement

	Infringement		Phi coefficient	Fisher's P-value
	No (n=47)	Yes (n=58)		
BAP1			0.227	0.022
WT	46/47 (97.9%)	49/58 (84.5%)		
Mut	1/47 (2.1%)	9/58 (15.5%)		
ERBB2			0.203	0.061
WT	45/47 (95.7%)	48/58 (82.8%)		
Mut	2/47 (4.3%)	10/58 (17.2%)		
PARP1			0.201	0.063
WT	47/47 (100%)	53/58 (91.4%)		
Mut	0/47 (0%)	5/58 (8.6%)		

WT, wild type; Mut, mutant.

Table S11 The relationship between individual genes and metastasis at diagnosis

	Metastasis at diagnosis		Phi coefficient	Fisher's P-value
	No (n=71)	Yes (n=34)		
PTEN			0.181	0.099
WT	70/71 (98.6%)	31/34 (91.2%)		
Mut	1/71 (1.4%)	3/34 (8.8%)		
BTG1			-0.170	0.099
WT	61/71 (85.9%)	33/34 (97.1%)		
Mut	10/71 (14.1%)	1/34 (2.9%)		
BLM			-0.185	0.093
WT	64/71 (90.1%)	34/34 (100%)		
Mut	7/71 (9.9%)	0/34 (0%)		
BAP1				0.074
WT	67/71 (94.4%)	28/34 (82.4%)		
Mut	4/71 (5.6%)	6/34 (17.6%)		
ERBB2			0.199	0.053
WT	66/71 (93.0%)	27/34 (79.4%)		
Mut	5/71 (7.0%)	7/34 (20.6%)		

WT, wild type; Mut, mutant.

Table S12 The relationship between individual genes and pT stage

	pT stage		Phi coefficient	Fisher's P-value
	T1/T2 (n=48)	T3/T4 (n=57)		
BAP1			0.233	0.02
WT	47/48 (97.9%)	48/57 (84.2%)		
Mut	1/48 (2.1%)	9/57 (15.8%)		
PARP1			0.205	0.061
WT	48/48 (100%)	52/57 (91.2%)		
Mut	0/48 (0%)	5/57 (8.8%)		

WT, wild type; Mut, mutant.

Table S13 The relationship between individual genes and sarcomatoid

	Sarcomatoid		Phi coefficient	Fisher's P-value
	No (n=95)	Yes (n=10)		
BAP1			0.226	0.053
WT	88/95 (92.6%)	7/10 (70.0%)		
Mut	7/95 (7.4%)	3/10 (30.0%)		
MET			0.207	0.069
WT	87/95 (91.6%)	7/10 (70.0%)		
Mut	8/95 (8.4%)	3/10 (30.0%)		

WT, wild type; Mut, mutant.

Table S14 The relationship between individual genes and clinical stage

	Clinical stage		Phi coefficient	Fisher's P-value
	I/II (n=47)	III/IV (n=58)		
BAP1			0.227	0.022
WT	46/47 (97.9%)	49/58 (84.5%)		
Mut	1/47 (2.1%)	9/58 (15.5%)		

WT, wild type; Mut, mutant.

Table S15 The relationship between individual genes and ages

	Age		Phi coefficient	Fisher's P-value
	≥58 (n=58)	<58 (n=47)		
CCND1			0.247	0.021
WT	57/58 (98.3%)	40/47 (85.1%)		
Mut	1/58 (1.7%)	7/47 (14.9%)		

WT, wild type; Mut, mutant.

Table S16 The relationship between individual genes and tumor thrombus

	Tumor thrombus		Phi coefficient	Fisher's P-value
	No (n=80)	Yes (n=25)		
PTEN			0.239	0.041
WT	79/80 (98.8%)	22/25 (88.0%)		
Mut	1/80 (1.2%)	3/25 (12.0%)		

WT, wild type; Mut, mutant.

Table S17 The relationship between individual genes and necrosis

	Necrosis		Phi coefficient	Fisher's P value
	No (n=79)	Yes (n=26)		
BTG1			-0.196	0.062
WT	68/79 (86.1%)	26/26 (100%)		
Mut	11/79 (13.9%)	0/26 (0%)		

WT, wild type; Mut, mutant.

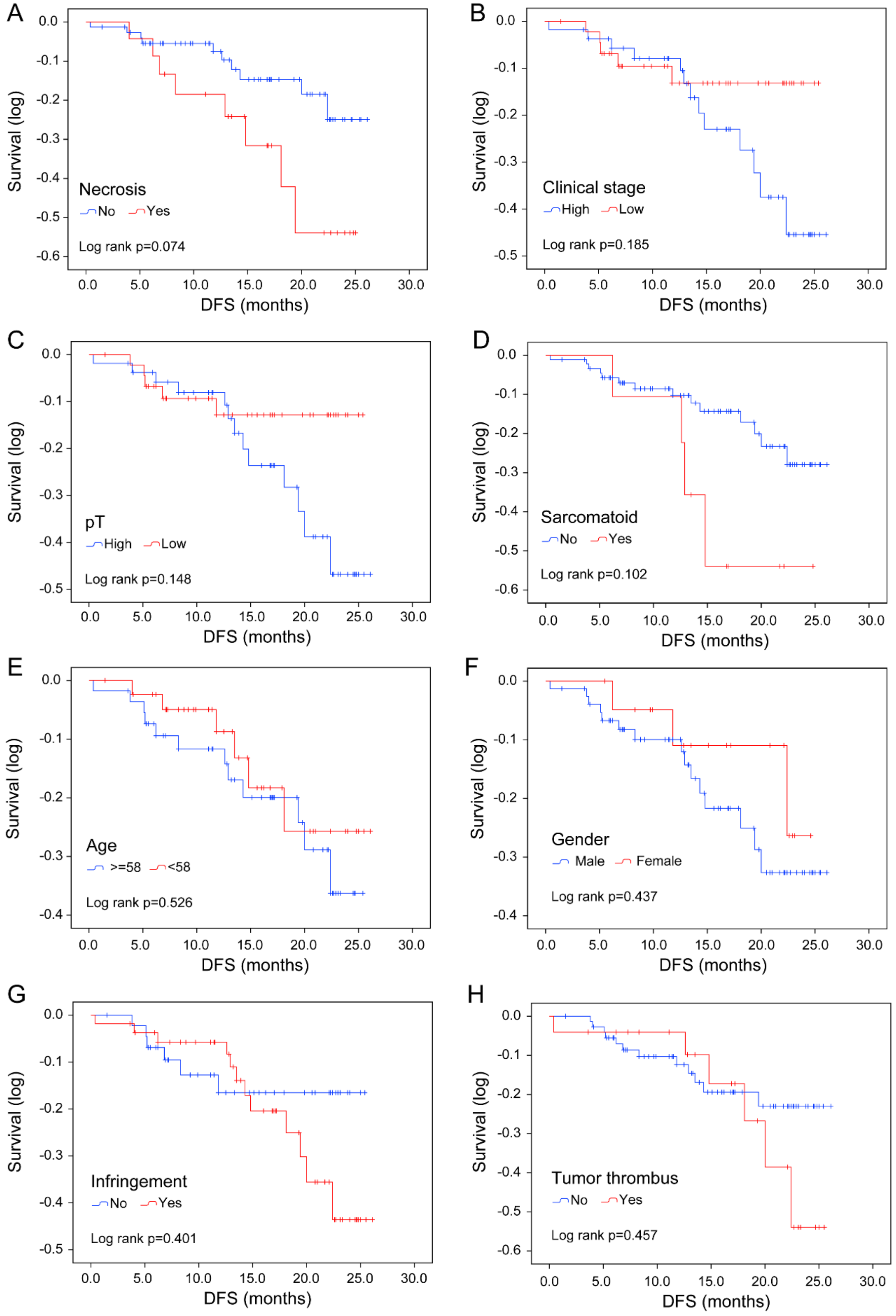

Figure S1 Kaplan-Meier curves for DFS of Chinese ccRCC patients with different clinical features. DFS, disease-free survival; ccRCC, clear cell renal cell carcinoma.

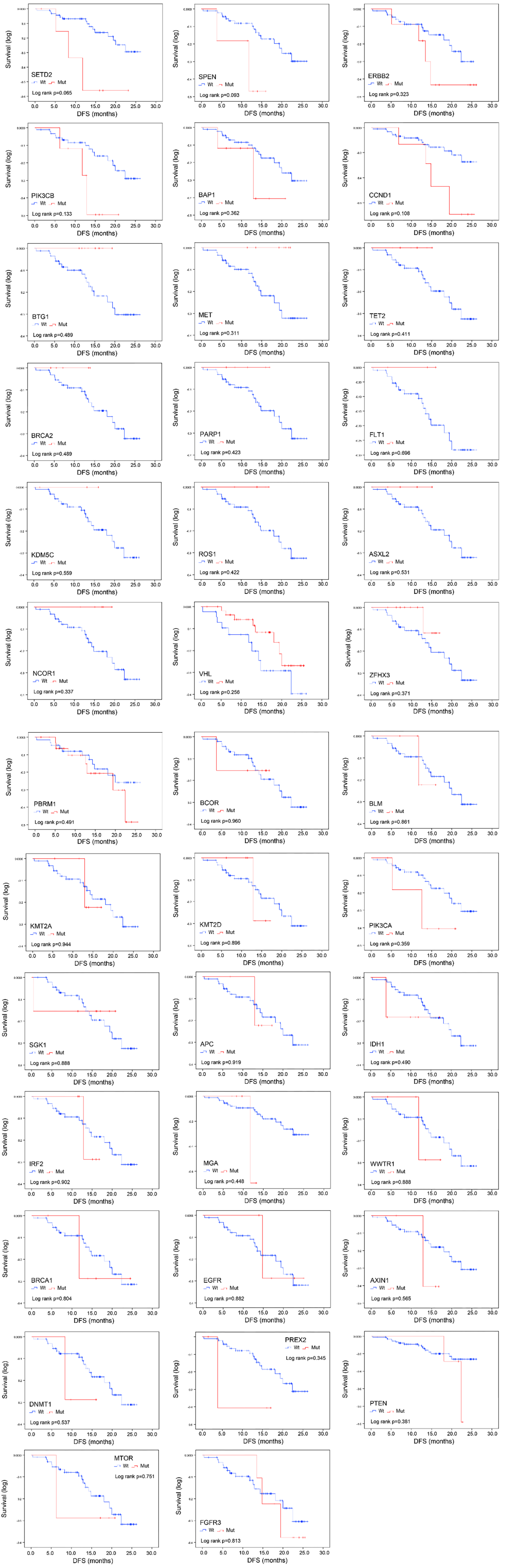

Figure S2 Kaplan-Meier curves for DFS of Chinese ccRCC patients with each mutated gene. DFS, disease-free survival; ccRCC, clear cell renal cell carcinoma.

Table S18 The mutations of genes associated with prognosis of Chinese ccRCC

Genes	Mutations
BAP1	p.S460fs, p.R179W, p.C320fs, p.S460*, p.Q684*, p.L361fs, p.S705fs, p.G194R, p.K205_A206deli nsS, p.A92V
PTEN	p.Y76Mfs*23, p.P246L, p.A151*fs*1, p.L112P, p.L182*
ERBB2	p.A241V, p.V1085L, CNV amplification
TP53	p.R175H, p.R273H, p.G325Ifs*10, p.H168Lfs*5
CDK8	p.Q377del
TSC1	p.R500*, p.Q527*, p.W1063G, p.R509Q
SETD2	p.Q2484*, p.G704R, p.K568fs, p.W2395*, p.Y480*, p.K568*, p.N1289fs, p.Thr305fs, p.N801Tfs*17
SPEN	p.D3010Y, p.H1165L, p.P2465L, p.E1412K
BTG1	p.G64R

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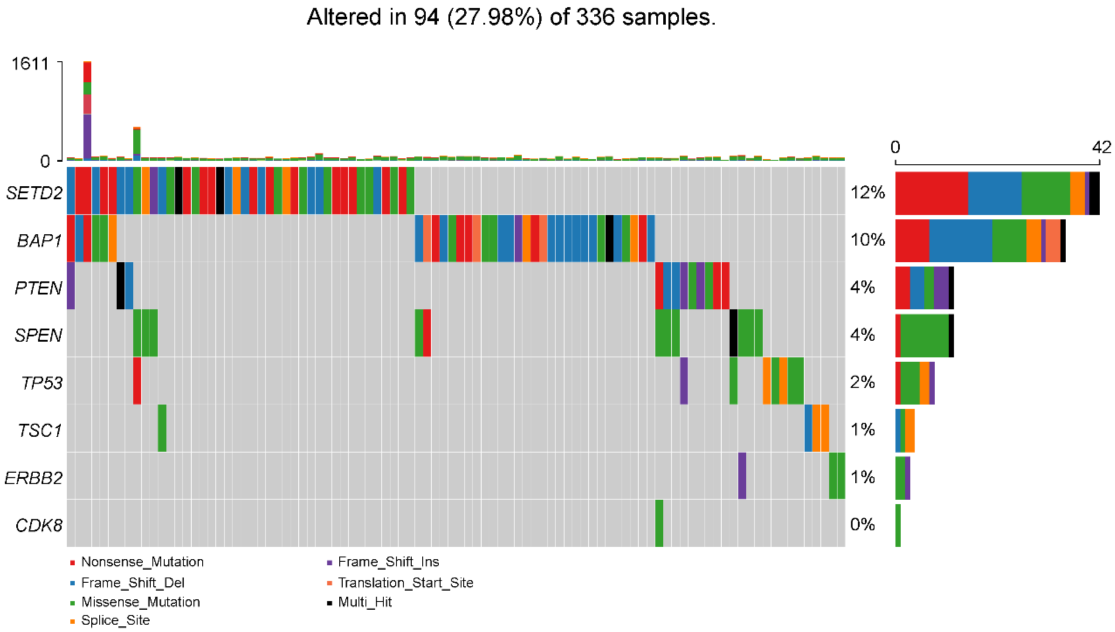

Figure S3 The mutation frequencies of the eight genes associated with poor prognosis in TCGA cohort. TCGA, The Cancer Genome Atlas.

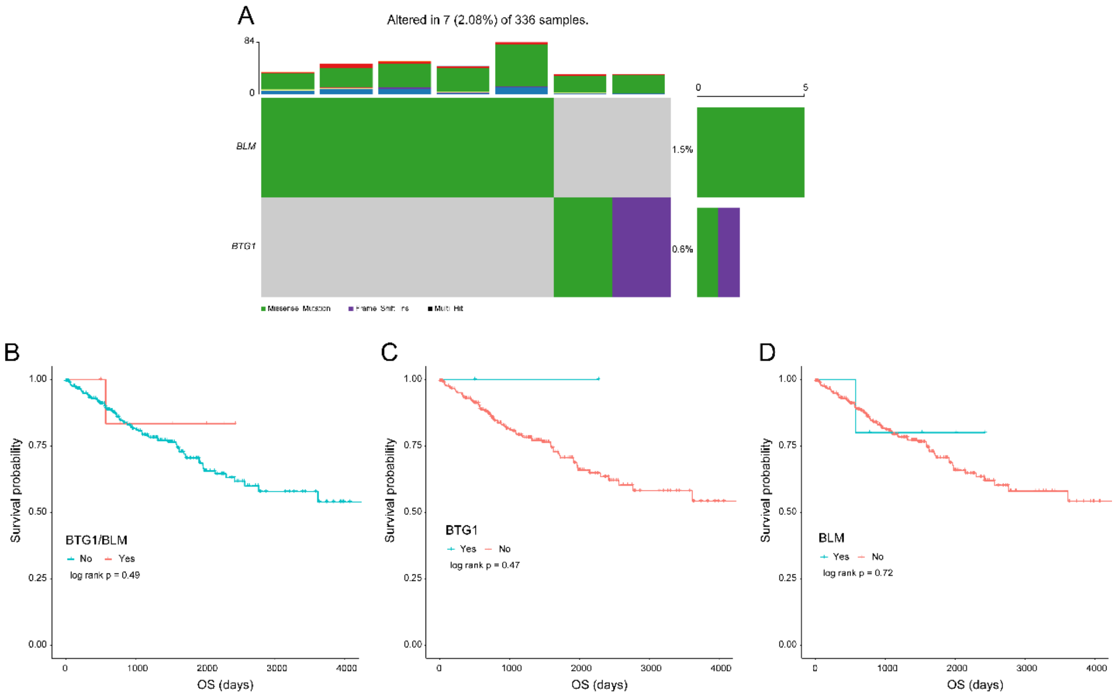

Figure S4 Validation of two genes (*BTG1*, *BLM*) associated with good prognosis using TCGA cohort. (A) The mutation frequencies of *BTG1* and *BLM* in TCGA cohort. (B) Kaplan-Meier curves for OS of ccRCC patients in TCGA cohort with mutated *BTG1/BLM*, (C) mutated *BTG1*, (D) mutated *BLM*. TCGA, The Cancer Genome Atlas; OS, overall survival; ccRCC, clear cell renal cell carcinoma

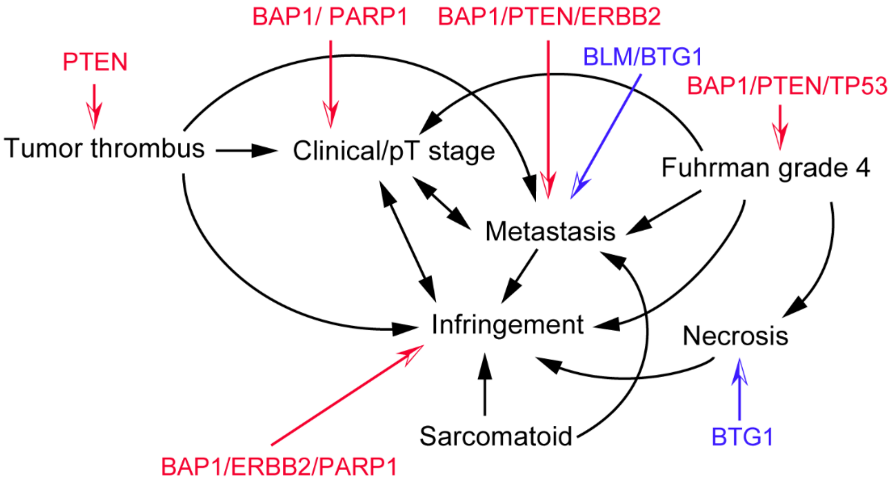

Figure S5 The interactions of different clinical indices. Genes associated with each clinical index were shown. Red, positively correlated; blue, negatively correlated.

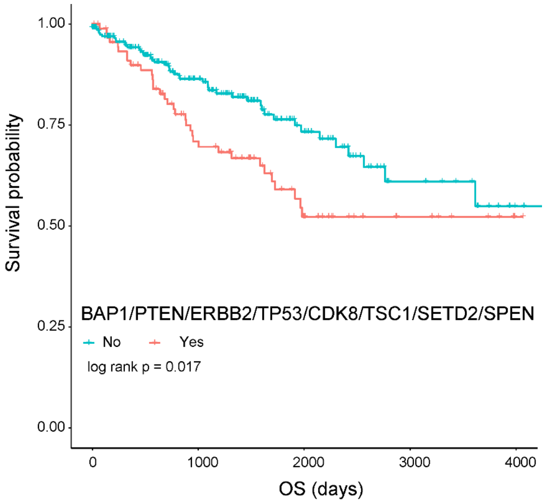

Figure S6 Kaplan-Meier curve for OS of ccRCC patients in TCGA cohort with 8 mutated genes associated with poor prognosis. TCGA, The Cancer Genome Atlas; OS, overall survival; ccRCC, clear cell renal cell carcinoma.

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