

Supplemental Table S1

Author, year	PMID	Tissue	Tumor type	Sample size (total)	Sample size (survival)	Biomarker studied	Study design	Method	Outcome measure	LOE
Arai, 2006	16453286	PT	ccRCC	60	46	hMLH1, VHL, THBS-1, MINT1, MINT2, MINT12, MINT25, MINT31	retrospective	MSP, COBRA	RFS, OS	IV/V
Atschekzei, 2012	22419128	PT	mixedRCC	42	42	SFRP1	retrospective	Pyrosequencing	RFS	IV/V
Awakura, 2008	18813805	PT	ccRCC	53	53	TU3A	retrospective	COBRA	RFS	IV/V
Breault, 2005	15701841	PT	mixedRCC	54	54	Y-catenin	retrospective	MSP	PFS, OS	IV/V
Cancer Genome Atlas Research Network, 2013	23792563	PT	ccRCC	252	252	miR-21	retrospective	Illumina 450K	OS	IV/V
				445	445	GBR10	retrospective	Illumina 450K	OS	IV/V
				445	445	25gene panel*	retrospective	Illumina 450K	OS	IV/V
				445	445	3gene panel**	retrospective	Illumina 450K	OS	IV/V
Cancer Genome Atlas Research Network, 2016	26536169	TCGA	PRCC	161	159	CIMP	retrospective	Illumina 450K	OS	IV/V
Chen E, 2017	28128743	PT	ccRCC	42	42	TMEFF2	retrospective	MSP	PFS	IV/V
Chen G, 2017	28029655	TCGA	ccRCC	316	158	RAC2, PARVG, PLCB2, VAV1 4-gene panel	retrospective	Illumina 450K	OS	IV/V

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Christoph, 2006	16951219	PT	ccRCC	90	71	APAF1, DAPK1	retrospective	MSP	RFS, OS, CSS	IV/V
de Martino, 2012	21713763	cfDNA	mixedRCC	157	157	VHL, RASSF1A, p16, PTGS2	prospective	qPCR	RFS	III
Deckers, 2015	25904753	PT	ccRCC	356	307	CDO1	retrospective	MSP	CSS	III
		TCGA	ccRCC	280	280	CDO1	retrospective	Illumina 450K	CSS	III
Dubrowinskaja, 2014	24464810	PT	mixedRCC	114	50	NEFH1	retrospective	MSP	PFS	IV/V
Eggers, 2012	22327210	PT	mixedRCC	98	57	HIC1	retrospective	Pyrosequencing	RFS	IV/V
Ellinger, 2011	20553257	PT	PRCC	32	26	RASSF1A, CDH1	retrospective	MSP	PFS	IV/V
Evelönn EA, 2019	30642274	PT	ccRCC	115	115	Cluster A /B	retrospective	Illumina 450K	CSS, PFS	IV/V
Fabrizio FP, 2017	28061437	PT	chrRCC	89	13	KEAP1	retrospective	MSP	RFS, PFS, OS	IV/V
			PRCC Type I	89	15					
			PRCC Type II	89	10					
			Oncocytoma	89	14					
		TCGA	ccRCC	481	481	cg06911149, cg02428100, cg03890664, cg15204119, cg15676203, cg26500801, cg26988016	retrospective	Illumina 450K	OS	IV/V
Fisel, 2015	26384346	PT	ccRCC	362	59	SLC16A3	retrospective	MALDI_TOF MS	CSS	IV/V
		TCGA	ccRCC	303	303	SLC16A3	retrospective	Illumina 450K		

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Fisel, 2013	23881922	PT	ccRCC	347	64	SLC16A3	retrospective	MALDI_TOF MS	OS	IV/V
		TCGA	ccRCC	347	283	SLC16A3	retrospective	Illumina 450K		
Gebauer, 2013	23321515	PT	ccRCC	111	37	miR-124-3	retrospective	MSP	RFS	IV/V
Girgis, 2012	22926558	TCGA	ccRCC	NA	NA	CA9	retrospective	Illumina 450K	OS	IV/V
Golovastova, 2016	26813565	PT	mixedRCC	22	22	RCVRN	retrospective	Bisulfite Seq	OS	IV/V
Gu Y, 2017	29079774	TCGA	ccRCC	265	265	CA9, RAB25	retrospective	Illumina 450K	CSS, OS	IV/V
Hildebrandt, 2010	20676129	PT	ccRCC	74	59	miR-9-1	prospective	RT-PCR	RFS	III
Kagara, 2008	18499164	PT	mixedRCC	131	126	UCHL1	retrospective	MSP	OS	IV/V
Kawai, 2010	20038516	PT	ccRCC	179	179	RASSF1A	retrospective	COBRA	CSS	IV/V
Klacz, 2016	26648328	PT	ccRCC	86	58	RASSF1A	retrospective	MSP	CSS	IV/V
Li, 2013	23722653	PT	ccRCC	149	149	KLF4	retrospective	MALDI_TOF MS	RFS, OS	IV/V
Lin, 2015	26404644	PT	ccRCC	191	191	PCDH17	retrospective	MSP	PFS, OS	IV/V
Lin, 2014	25416427	PT	ccRCC	153	153	PCDH8	retrospective	MSP	PFS	IV/V
Lin, 2017	28688232	preoperative serum	ccRCC	142	142	PCDH17	prospective	MSP	PFS, OS	III
Mendoza-Perez J, 2017	28543182	PT	mixedRCC	177	177	LEPR, LEP, NPY	retrospective	Pyrosequencing	RFS	IV/V
Mitsui, 2015	25797254	PT	mixedRCC	96	96	BMP2	retrospective	MSP, Bisulfite Seq	OS	IV/V

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Morris, 2011	21132003	PT	mixedRCC	69	69	ATP5G2, CCD8, CORO6, FBN2, KLH35L, PCDH8, QPCT, ZSCAN, SCUBE3,	retrospective	COBRA	CSS, OS	IV/V
Morris, 2010	20154727	PT	mixedRCC	61	61	CST6, COL15A1, GREM1, RPRM, PDLIM4, BNC1, COL14A1, SFRP1,	retrospective	MSP	CSS, OS	IV/V
Peters, 2014	24633192	PT	mixedRCC	18	18	CST6, LAD1, miR-9-1, miR-124-3	retrospective	MSP	PFS, OS	IV/V
Peters, 2014	24549248	PT	mixedRCC	119	119	GATA3	retrospective	MSP	PFS	IV/V
				109	109	GATA5				
				ccRCC	78	78				
Peters, 2012	22289415	PT	mixedRCC	64	64	GATA5	retrospective	COBRA	PFS	IV/V
				ccRCC	47	47				
Peters, 2018	30272321	PT	ccRCC	98	24	NELL1	retrospective	Pyrosequencing	RFS	IV/V
Pires-Luis AS, 2017	28662726	PT	mixedRCC	120	30	OXR1, HOXA9	retrospective	MSP	OS	IV/V
Pompas- Veganzones, 2016	27592258	PT	mixedRCC	88	88	Myopodin	retrospective	MSP	CSS, OS	IV/V
Ricketts, 2014	24454902	TCGA	ccRCC	326	181	SFRP1	retrospective	Illumina 27K	OS	IV/V
				326	145	SFRP1, GREM1, GATA5	retrospective	Illumina 450K	OS	IV/V

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Ricketts, 2013	24034811	TCGA	ccRCC	237	193	GCM2, NEFM, RGS7, AEBP1, TMEM74	retrospective	Illumina 450K	OS	IV/V
						Meth_signature (GCM2,NEFM,RGS7)	retrospective	Illumina 450K	OS	IV/V
Smits, 2008	18245539	PT	ccRCC	185	147	VHL	retrospective	MSP	CSS	III
Su X, 2017	28754676	PT	ccRCC	222	222	NSD1	retrospective	Pyrosequencing	RFS	IV/V
		TCGA	ccRCC	271	271	NSD1	retrospective	Illumina 450K	OS	IV/V
Tian, 2014	25332168	PT	ccRCC	100	100	CIMP	retrospective	MALDI_TOF MS	PFS, OS, CSS	IV/V
Urakami, 2006	17145819	PT	mixedRCC	62	62	M-Score (SFRP1, SFRP2, SFRP4, SFRP5,DKK3,WIF1)	retrospective	MSP	OS	IV/V
van Vlodrop, 2017	27756787	PT	ccRCC	335	150	GREM1, NEURL, LAD1, NEFH	prospective	MSP	CSS, OS	III
				335	150	Meth_signature (GREM1, LAD1, NEURL, NEFH)	prospective	MSP	CSS, OS	III
				335	185	GREM1, NEURL, LAD1, NEFH	prospective	MSP	CSS, OS	III
				335	185	Meth_signature (GREM1, LAD1, NEURL, NEFH)	prospective	MSP	CSS, OS	III
		TCGA	ccRCC	264	264	Meth_signature (GREM1, LAD1, NEURL, NEFH)	retrospective	Illumina 450K	OS	III

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van Vlodrop, 2010	20042676	PT	ccRCC	335	150	GREM1_reg1 – reg3	retrospective	MSP	OS	IV/V
Vidaurreta, 2008	18452812	PT	mixed RCC	48	48	p16	retrospective	MSP	RFS	III
Wang, 2016	27129174	TCGA	ccRCC	781	318	DAB2IP	retrospective	Illumina 450K	OS	IV/V
		PT	ccRCC	781	224	DAB2IP	retrospective	Pyrosequencing	OS	IV/V
Wei, 2015	26515236	TCGA	ccRCC	993	298	Meth_signature (PITX1, FOXE3, TWF2, EHBP1L1, RIN1)	retrospective	Illumina 450K	OS	IV/V
		PT_SYSU	ccRCC	993	168	Meth_signature (PITX1, FOXE3, TWF2, EHBP1L1, RIN1)	retrospective	Pyrosequencing	OS	IV/V
		PT_MCHC	ccRCC	993	284	Meth_signature (PITX1, FOXE3, TWF2, EHBP1L1, RIN1)	retrospective	Pyrosequencing	OS	IV/V
		PT_UTSW	ccRCC	993	243	Meth_signature (PITX1, FOXE3, TWF2, EHBP1L1, RIN1)	retrospective	Pyrosequencing	OS	IV/V
Xu, 2015	25569086	PT	ccRCC	101	91	ADAMTS18	retrospective	MSP	PFS	IV/V
Yamada, 2006	16152585	PT	ccRCC	55	53	DAL-1/4.1B	retrospective	Bisulfite seq	RFS	IV/V
Yoo, 2013	23255890	PT	ccRCC	46	46	IL-8	retrospective	Bisulfite seq	OS	IV/V
				62	62	HOXA5, MSH2	retrospective	Bisulfite seq	OS	IV/V
Young, 2009	19996202	PT	ccRCC	177	163	VHL	retrospective	MSP	CSS	IV/V

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Zhao, 2016	26814892	PT	ccRCC	208	208	AR	retrospective	Illumina 450K	OS	IV/V
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*25gene panel: BEX2 C11orf2, CCnD1, CLEC3B, CPEB4, CUBN, CYR1, EPB49, FAM176A, GPR56, HNMT, KCNJ15, MALL, MGAM, MMRN2, MUPCDH, PIK3C2A, PREPL, RORC, SLC22A2, SLC28A1, SLC39A5, SORBS2, TM4SF18, USP10

**3gene panel: SAA1, SERPINA3, SERPINF1

Abbreviations: ccRCC, clear cell renal cell carcinoma; COBRA, combined bisulfite restriction analysis; CIMP, CpG island methylator phenotyp; MSP, methylation specific PCR; PT, primary tumor; PRCC, papillary RCC; KM, kaplan meier; cox_uni, univariate cox regression analysis; cox_multi, multivariate cox regression analysis; OS, overall survival; RFS, recurrence free survival; PFS, progression free survival; CSS, cancer-specific survival; TCGA, The Cancer Genome Atlas; 95%CI, 95% confidence interval

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Author, year (Reference)	N (survival analyses)	Tumor type	Statistical method	Biomarker studied	Outcome associations with methylation	HR (95% CI)	p-value	Outcome parameter
Arai, 2006 [42]	46	ccRCC	KM	hMLH1, VHL, THBS-1, MINT1, MINT2, MINT12, MINT25, MINT31	hypermethylation associates with shortened RFS and OS	-	0.0002 0.0787	RFS OS
Atschekzei, 2012 [12]	42	mixedRCC	Cox_bivariate	SFRP1	>3.9% meth associates with better RFS	0.06-0.15 (0.01- 0.63)	0.003 – 0.01	RFS
Awakura, 2008 [43]	53	ccRCC	KM	TU3A	>20% meth associates with worse RFS	-	0.0038	RFS
Breault, 2005 [44]	54	mixedRCC	KM Cox_multi	Y-catenin	meth associates with worse PFS and OS meth associates with worse PFS and OS	- NR	<0.01 0.012 0.039	PFS / OS PFS OS
Cancer Genome Atlas Research Network, 2013 [5]	252 445 445	ccRCC	KM KM Cox_uni	miR-21 GBR10 25gene panel*	Associates with better OS Associates with worse OS Associates with worse outcome	- - -	0.013 <0.001 <0.05	OS OS OS

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Deckers, 2015	307	ccRCC	KM	CDO1	Associates with	-	0.006	RFS
[48]			Cox_uni		worsened RFS	1.66 (1.13-2.44)	-	RFS
			Cox_multi			1.89 (1.25-2.85)	-	RFS
	280	ccRCC (TCGA)	KM	CDO1	Meth. associates with	-	<0.001	RFS
					poorer RFS			
Dubrowskaja, 2014	50	mixedRCC	Cox_uni	NEFH1	Associates with	8.61 (3.03-24.5)	<0.001	PFS
[14]			Cox_bivariate		shortened PFS	5.1 – 17.1	<0.001 – 1.26	PFS
Eggers, 2012	57	mixedRCC	Cox_uni	HIC1	Associates with	4.0 (1.45-11.03)	0.0074	RFS
[49]			Cox_bivariate		shortened RFS	3.1 - 5.4	0.001-0.028	
Ellinger, 2011	26	PRCC	KM	RASSF1A, CDH1	Associates with	-	0.046	PFS
[40]					shortened PFS	-	0.057	
Evelönn EA, 2019	115	ccRCC	Cox_uni	Cluster A /B	High PCM classifier ^o	-	<0.001	CSS
[50]			Cox_multi		associates with worse CSS	-	n.s.	CSS/PFS
Fabrizio FP, 2017	13	chrRCC	RFS, PFS, OS	KEAP1	No association with	-	n.s.	RFS/PFS/OS
[51]					survival			
	15	PRCC I				-		
	10	PRCC II				-		
	14	Oncocyt.				-		
	481	ccRCC	Cox_uni	cg06911149,		-	0.01	OS
				cg02428100,		-	0.426	
				cg03890664,		-	0.139	
				cg15204119,		-	0.002	
				cg15676203,		-	0.009	

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				cg26500801, cg26988016		- -	0.013 <0.001	
Fisel, 2015	59	ccRCC	Cox_uni	SLC16A3	Associates with better CSS	0.0068 (0.0002- 0.3022)	0.0076	CSS
[52]			Cox_multi			0.004 (0.00-0.76)	-	
	303	ccRCC (TCGA)	Cox_uni	SLC16A3	Associates with better CSS	0.018 (0.003- 0.119)	<0.0001	CSS
			Cox_multi			0.03 (0.004-0.22)	-	
Fisel, 2013	64	ccRCC	KM	SLC16A3	Associates with better OS	0.05 (0.01-0.40)	0.0007	OS
[53]	283	ccRCC (TCGA)	KM	SLC16A3		0.39 (0.24-0.64)	0.0012	OS
Gebauer, 2013	37	ccRCC	Cox_uni	miR-124-3	Associates with worse RFS	9.37 (2.68-32.8)	0.0005	RFS
[54]								
Girgis, 2012	NA	ccRCC	KM	CA9	Non-hypometh associates with worse OS	-	0.0004	OS
[55]								
Golovastova, 2016	22	mixedRCC	KM	RCVRN	Meth at position 80 from TSS associates with better OS	-	0.0363	OS
[56]								
Gu Y, 2017	265	ccRCC (TCGA)	Cox_uni	CA9	High Meth associates with shortened OS and CSS	1.70 (1.09-2.67)	0.02	OS
[57]			Cox_multi			0.59 (0.39-0.92)	0.018	CSS
			KM	RAB25		1.32 (0.83-2.10)	0.238	OS
						-	0.192	CSS

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Hildebrandt, 2010	59	ccRCC	KM	miR-9-1	High meth associates with shorter RFS	-	0.034	RFS
[58]			Cox_multi			2.74 (0.78-9.60)	-	RFS
Kagara, 2008	126	mixedRCC	KM	UCHL1	PIM ⁹⁰ associates with worse OS	-	0.048	OS
[59]								
Kawai, 2010	179	ccRCC	KM	RASSF1A	Hypermethylation associates with shortened CSS	-	0.040	CSS
[41]			Cox_uni			1.49 (1.02-2.26)	0.037	CSS
			Cox_multi			1.78 (1.18-2.78)	0.0053	CSS
Klacz, 2016	58	ccRCC	KM	RASSF1A	>50% Meth associates with worse OS	-	0.038	OS
[60]			Cox_uni		>25% associates with poor OS, but not with PFS	3.00 (1.18-7.65)	0.02	OS
						1.56 (0.69-3.55)	0.28	PFS
			Cox_multi			1.88 (0.68-3.55)	0.22	OS
Li, 2013	149	ccRCC	KM	KLF4	>50% associates with worse RFS and OS	-	0.0392	RFS
[61]							0.0109	OS
Lin, 2015	191	ccRCC	KM	PCDH17	Meth associates with shortened PFS and 5-y OS	-	0.0002	PFS
[62]							<0.0001	OS
			Cox_uni		Meth associates with shortened PFS and 5-y OS	3.973 (1.795-8.792)	0.0007	PFS
						3.673 (1.615-7.435)	0.0003	OS
			Cox_multi			3.014 (1.235-7.463)	0.0028	PFS
						2.876 (1.347-	0.0097	OS

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						8.065)		
Lin, 2014	153	ccRCC	KM	PCDH8	Meth associates with shorter PFS	-	0.0022	PFS
[63]			Cox_uni			3.061 (1.439-6.513)	0.0037	OS
			Cox_multi			2.35 (1.54-6.03)	0.0316	OS
Lin, 2017	142	ccRCC	KM	PCDH17	Meth associates with shortened PFS and OS	-	<0.001	PFS
[64]			Cox_multi	PCDH17		4.01 (1.14-8.04)	<0.001	PFS
						3.93 (1.35-9.14)	0.046	OS
Mendoza-Perez J, 2017	177	mixedRCC	KM	LEPR, LEP, NPY	High meth associates with shorter RFS	-	<0.001	RFS
[65]						-	0.09	
						-	0.07	
Mitsui, 2015	96	mixedRCC	KM	BMP2	Meth associates with poorer OS	-	0.0224	OS
[66]			Cox_uni		Non-meth was associated with better OS	0.363 (0.146-0.901)	0.0289	OS
			Cox_multi			0.631 (0.245-1.624)	0.3393	OS
Morris, 2011	69	mixedRCC	CSS, OS	ATP5G2, CCD8, CORO6, FBN2, KLH35L, PCDH8, QPCT, ZSCAN, SCUBE3	No association with survival	-	>0.05	OS
[67]					SCUBE3 meth associates with worse CSS and OS	-	0.009	OS
							0.0046	CSS
Morris, 2010	61	mixedRCC	KM	CST6, COL15A1,	No association with	-	n.s.	CSS/OS

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[10]				GREM1, RPRM, PDLIM4	survival			
			Cox_uni	BNC1,	Meth associates with poorer CSS and OS	3.69 (1.27-10.93)	0.017	OS
				COL14A1,		3.07 (1.22-8.16)	0.018	CSS
				SFRP1		4.07 (1.73-20.3)	0.005	OS
						3.49 (1.55-16.1)	0.007	CSS
						4.88 (2.76-87.95)	0.002	OS
						4.44 (2.75-86.2)	0.003	CSS
			Cox_multi	BNC1, COL14A1, SFRP1	independent prognosticator for OS	4.87 (1.14-20.88)	0.033	
						6.56 (1.69-25.38)	0.0067	
						NR	0.4	
Peters, 2014	18	mixedRCC	KM	CST6, LAD1,	Meth associates with worse outcome	-	0.009/0.011	PFS/OS
[68]				miR-9-1, miR-124-3			0.004/0.043	PFS/OS
			Cox_uni	CST6, LAD1, miR-9-1, miR-124-3	Meth associates with worse outcome	4.1 (1.3-12.6)	0.319/0.624	PFS/OS
						6.4 (1.6-26.0)	0.339/0.786	PFS/OS
						1.7 (0.6-4.7)		PFS
						1.8 (0.5-6.6)		
Peters, 2014	119	mixedRCC	KM	GATA3	No association with survival	NR	NR	RFS
[22]								
	109	mixedRCC	Cox_uni	GATA5	High meth associates with shortened RFS	17.8 (4.89-65.1)	<0.001	RFS
	78	ccRCC	Cox_uni	GATA5		13.0 (3.57-47.4)	<0.001	RFS
Peters, 2012	64	mixedRCC	Cox_uni	GATA5	High meth associates with decreased PFS	3.48 (1.38-8.83)	0.008	PFS
[69]								
	47	ccRCC	Cox_uni	GATA5		4.59 (1.57-13.4)	0.005	PFS

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Peters, 2018	24	ccRCC	RFS	NELL1	High meth associates with worse RFS	4.15 (1.10-15.6)	0.035	RFS
[70]								
Pires-Luis AS, 2017	30	mixedRCC	KM	OXR1, HOXA9	No association with OS	-	n.s.	OS
[71]								
Pompas-Veganzones, 2016	88	mixedRCC	Cox_uni	Myopodin	Meth associates with better CSS and OS	0.30 (0.15-0.58)	<0.0005	CSS
[21]			Cox_multi			0.34 (0.19-0.60)	<0.0005	OS
						0.30 (0.14-0.62)	0.001	CSS
						0.34 (0.17-0.65)	0.001	OS
Ricketts, 2014	181	ccRCC (Infinium 27K)	Cox_uni Cox_multi	SFRP1	Meth associates with poorer OS	3.22 (1.23-8.20)	0.0003	OS
[72]						2.40 (1.25-4.64)	0.009	
	145	ccRCC (Infinium 450K)	Cox_uni Cox_multi Cox_uni Cox_multi Cox_uni	SFRP1, GREM1, GATA5		2.51 (1.14-5.53)	0.001	OS
						1.92 (1.05-3.50)	0.036	
						3.01 (0.85-10.67)	0.011	OS
						3.05 (1.36-6.86)	0.007	
						2.82 (1.02-7.82)	0.003	OS
Ricketts, 2013	193	ccRCC	Cox_uni	GCM2, NEFM, RGS7, AEBP1, TMEM74	Meth associates with poorer OS	1.93 (0.90-4.14)	0.032	OS
[73]						2.15 (1.22-3.79)	0.0024	
						1.99 (1.17-3.38)	0.0067	
						1.64 (0.73-3.69)	0.15	
						1.24 (0.60-2.59)	0.53	
				Meth_signature (GCM2,NEFM,RGS7)		3.58 (1.22-10.47)	<0.0001	OS
Smits, 2008	147	ccRCC	KM	VHL	No association with CSS	-	0.439	CSS
[74]			Cox_uni				1.28 (0.64-2.59)	-

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			Cox_multi			1.04 (0.48-2.22)	-	
Su X, 2017	222	ccRCC	KM	NSD1	No association in RFS	-	0.57	RFS
[26]	271	ccRCC (TCGA)	KM	NSD1	High meth associates with worse OS	-	<0.001	OS
Tian, 2014	100	ccRCC	KM	23 CpG units (7gene panel***)	Meth >16CpG sites associates with shorter CSS and OS	-	0.0001 <0.0001	CSS OS
[75]			Cox_uni			10.6 (2.81-40.2) 75.8 (7.81-735)	0.005 0.0019	RFS CSS
Urakami, 2006	62	mixedRCC	KM	M-Score (SFRP1, SFRP2,SFRP4,SFRP5, DNK3,WIF1)	High score associates with poor OS		<0.05	OS
[24]			Cox_multi			1.04 (0.48-2.22)	n.s.	
van Vlodrop, 2017	150	ccRCC	KM	GREM1 NEURL LAD1 NEFH 4gene panel	Meth associates with worse OS not associated		0.002 <0.001 0.013 0.173 0.0055	OS
[76]			Cox_multi	GREM1 NEURL LAD1 NEFH 4gene panel		0.9 (0.5-1.7) 1.4 (0.7-2.7) 0.8 (0.4-1.6) 0.6 (0.3-1.2) 0.3 (0.1-1.9)	0.72 0.414 0.483 0.117 0.211	OS
	185	ccRCC	KM	GREM1 NEURL LAD1 NEFH 4gene panel	not independent Meth associates with worse OS		<0.002 0.002 <0.001 <0.0001 <0.001	OS
			Cox_multi	GREM1		2.3 (1.5-3.6)	<0.0001	OS

Supplemental Table S2

*25gene panel: BEX2, C11orf2, CCND1, CLEC3B, CPEB4, CUBN, CYR1, EPB49, FAM176A, GPR56, HNMT, KCNJ15, MALL, MGAM, MMRN2, MUPCDH, PIK3C2A, PREPL, RORC, SLC22A2, SLC28A1, SLC39A5, SORBS2, TM4SF18, USP10

**3gene panel: SAA1, SERPINA3, SERPINF1

°PCM classifier: promoter methylation classifier – a panel consisting of 172 differently methylated CpGs

°°PIM: positive index methylation

Abbreviations: ccRCC, clear cell renal cell carcinoma; PRCC, papillary RCC; KM, kaplan meier; cox_uni, univariate cox regression analysis; cox_multi, multivariate cox regression analysis; OS, overall survival; RFS, recurrence free survival; PFS, progression free survival; CSS, cancer-specific survival; TCGA, The Cancer Genome Atlas; 95%CI, 95% confidence interval