

SUPPLEMENTARY TABLES

Supplementary Table 1. Association between Cluster A, Cluster B, clinicopathological parameters and common renal carcinoma genomic mutation characteristics in TCGA-KIRC (n=496).

	Cluster A (n=206)	Cluster B (n=290)	Total (n=496)	P value
Age				
Mean±SD	61.4 (11.7)	59.8 (12.3)	60.5 (12.1)	0.175
Gender				
Female	67 (32.5%)	106 (36.6%)	173 (34.9%)	0.406
Male	139 (67.5%)	184 (63.4%)	323 (65.1%)	
Stage				
I	84 (40.8%)	166 (57.2%)	250 (50.4%)	0.002*
II	22 (10.7%)	30 (10.3%)	52 (10.5%)	
III	60 (29.1%)	58 (20.0%)	118 (23.8%)	
IV	40 (19.4%)	36 (12.4%)	76 (15.3%)	
Grade				
I-II	72 (35.0%)	149 (51.4%)	221 (44.6%)	3e-04*
III-IV	131 (63.6%)	136 (46.9%)	267 (53.8%)	
VHL status				
Wild-type	62 (35.0%)	95 (51.4%)	157 (44.6%)	0.652
Mutant	56 (63.6%)	98 (46.9%)	154 (53.8%)	
PBRM1 status				
Wild-type	69 (33.5%)	108 (37.2%)	177 (35.7%)	0.751
Mutant	49 (23.8%)	85 (29.3%)	134 (27.0%)	
TP53 status				
Wild-type	113 (54.9%)	191 (65.9%)	304 (61.3%)	0.146
Mutant	5 (2.4%)	2 (0.7%)	7 (1.4%)	
MTOR status				
Wild-type	107 (51.9%)	184 (63.4%)	291 (58.7%)	0.165
Mutant	11 (5.3%)	9 (3.1%)	20 (4.0%)	

Supplementary Table 2. Referenced model accuracy corresponding to the number of variables included in features selection.

Variables	Accuracy	Kappa	AccuracySD	KappaSD
2	0.885	0.76685814	0.15621254	0.31530365
3	0.90183333	0.79766067	0.14147878	0.28676197
4	0.91633333	0.8291625	0.11966986	0.23714195
5	0.91233333	0.81825341	0.12669989	0.26149403
6	0.927	0.85192641	0.11011625	0.22121793
7	0.95016667	0.89943057	0.09585972	0.19280668
8	0.956	0.91039794	0.09246348	0.1873606
9	0.94566667	0.88912754	0.09456677	0.19169125
10	0.95366667	0.9039627	0.08562768	0.17805629
11	0.9695	0.93625874	0.07313161	0.15326379
12	0.9695	0.93695804	0.07313161	0.15161329
13	0.9655	0.92932401	0.08186432	0.16845566
14	0.967	0.93201632	0.08140806	0.16819983
15	0.969	0.93516317	0.07970273	0.16676898
16	0.9695	0.93631702	0.07846218	0.16410564
17	0.9715	0.94086247	0.07662548	0.15939759
18	0.9735	0.94465035	0.06906848	0.14463067
19	0.9675	0.93317016	0.08020649	0.16558167
20	0.9735	0.94395105	0.06906848	0.14639705
21	0.9715	0.93946387	0.07662548	0.1625547
22	0.9695	0.93631702	0.07846218	0.16410564
23	0.9695	0.93631702	0.07846218	0.16410564
24	0.9695	0.93631702	0.07846218	0.16410564
25	0.96833333	0.93337995	0.07299509	0.15425558
26	0.9735	0.94395105	0.06906848	0.14639705
27	0.9735	0.94395105	0.06906848	0.14639705
28	0.978	0.9527972	0.06289321	0.1354076
29	0.9775	0.95164336	0.0645008	0.13876189
30	0.9755	0.9477972	0.0668539	0.14268294
31	0.978	0.9527972	0.06289321	0.1354076

32	0.9755	0.9477972	0.0668539	0.14268294
33	0.9735	0.94400932	0.07468959	0.15770879
34	0.974	0.94370629	0.06759953	0.14682918
35	0.978	0.9527972	0.06289321	0.1354076
36	0.96783333	0.93228438	0.07957008	0.16766191
37	0.9715	0.93940559	0.07115746	0.15160319
38	0.97183333	0.94061772	0.07042022	0.14888174
39	0.9755	0.9477972	0.0668539	0.14268294
40	0.974	0.94446387	0.07333333	0.15647684
41	0.978	0.9527972	0.06289321	0.1354076
42	0.9755	0.94785548	0.07264658	0.1542658
43	0.974	0.94440559	0.06759953	0.14506925
44	0.9755	0.9477972	0.0668539	0.14268294
45	0.976	0.94895105	0.06531973	0.13945516
46	0.978	0.9534965	0.06289321	0.13344907
47	0.976	0.94895105	0.06531973	0.13945516
48	0.974	0.94370629	0.06759953	0.14682918
49	0.976	0.94900932	0.07123726	0.1512849
50	0.976	0.94825175	0.06531973	0.14130776
51	0.972	0.93991841	0.07531751	0.16137269
52	0.9715	0.93870629	0.07115746	0.15326508
53	0.9735	0.94325175	0.06906848	0.14813903
54	0.9715	0.93940559	0.07115746	0.15160319
55	0.9675	0.93037296	0.08020649	0.1714723
56	0.9735	0.94325175	0.06906848	0.14813903
57	0.976	0.94825175	0.06531973	0.14130776
58	0.972	0.93916084	0.06974702	0.15201314
59	0.978	0.9527972	0.06289321	0.1354076
60	0.9715	0.93800699	0.07115746	0.15490595
61	0.9695	0.93416084	0.07313161	0.15809319
62	0.9735	0.94400932	0.07468959	0.15770879
63	0.976	0.94900932	0.07123726	0.1512849
64	0.978	0.9527972	0.06289321	0.1354076
65	0.9775	0.95234266	0.0645008	0.13685734
66	0.974	0.94370629	0.06759953	0.14682918
67	0.976	0.94895105	0.06531973	0.13945516
68	0.976	0.94825175	0.06531973	0.14130776
69	0.9675	0.92961538	0.075	0.16264989
70	0.976	0.94755245	0.06531973	0.14313293
71	0.98	0.95664336	0.06030227	0.13112135
72	0.9715	0.93870629	0.07115746	0.15326508
73	0.976	0.94825175	0.06531973	0.14130776
74	0.978	0.95285548	0.0690191	0.14756065
75	0.98	0.95664336	0.06030227	0.13112135
76	0.976	0.94755245	0.06531973	0.14313293
77	0.974	0.94376457	0.07333333	0.1581101
78	0.976	0.94825175	0.06531973	0.14130776
79	0.974	0.94446387	0.07333333	0.15647684
80	0.9715	0.93870629	0.07115746	0.15326508
81	0.98	0.95734266	0.06030227	0.12907677
82	0.978	0.9520979	0.06289321	0.1373346
83	0.98	0.95664336	0.06030227	0.13112135
84	0.9755	0.9470979	0.0668539	0.14448852
85	0.9755	0.9477972	0.0668539	0.14268294
86	0.9675	0.93037296	0.08020649	0.1714723
87	0.976	0.94825175	0.06531973	0.14130776

Supplementary Table 3. Order of the 38 variables to be included according to the highest accuracy of the model.

Variable order	Selected genes
1	CNOT1
2	SIN3A
3	BPTF
4	CHD8
5	CHD9
6	DEK
7	SIRT6
8	SAP30L
9	C6orf89
10	SUPT16H
11	SMARCA5
12	CHD6
13	RBBP5
14	SMARCA2
15	CNOT6L
16	CNOT8
17	CNOT6
18	BAZ1B
19	CHD4
20	BRMS1
21	ACTR8
22	INO80B
23	BRD3
24	CNOT7
25	PHF8
26	CBX5
27	RUVBL2
28	TOP1
29	ACTR6
30	MORF4L1
31	CHD1
32	ANP32E
33	INO80E
34	ACTB
35	BRD7
36	PABPC1L
37	SMARCD3
38	UTY
39	PIH1D1
40	DPF2
41	BRD1
42	CAMK2D
43	MIER2

44	ACTR5
45	PHF1
46	SS18
47	CNOT3
48	DAXX
49	BRD8
50	SAP30BP
51	CHD3
52	WDR77
53	SUPT20H
54	BAZ1A
55	WDR61
56	NUDT5
57	RBBP7
58	SAP18
59	LRRK2
60	INO80C
61	ACTN4
62	ANP32B
63	SIRT2
64	CNOT9
65	SMARCB1
66	HIST1H1C
67	PHF21A
68	RBBP8
69	SMYD2
70	SS18L1
71	SUPT5H

Supplementary Table 4. TCGA pan-cancer survival analysis of BPTF, CNOT1 and SIN3A.

		BLCA	BRCA	CESC	CHOL	COAD	ESCA	GBM
BPTF	HR (high)	0.86	1.1	1.2	0.38	0.96	1.2	0.78
	Logrank p	0.32	0.51	0.42	0.049	0.86	0.54	0.17
SIN3A	HR (high)	1	1	0.85	0.58	1.2	0.86	0.99
	Logrank p	0.9	0.98	0.48	0.27	0.55	0.51	0.95
CNOT1	HR (high)	1	1.1	0.86	0.8	0.67	1.7	0.92
	Logrank p	0.86	0.42	0.53	0.64	0.11	0.03*	0.65
		HNSC	KIHC	KIRP	LAML	LIHC	LUAD	LUSC
BPTF	HR (high)	0.93	3.8	0.92	1.1	1.4	1.4	1.1
	Logrank p	0.62	0.075	0.78	0.84	0.065	0.025*	0.36
SIN3A	HR (high)	1	3.6	1.4	1.2	1.1	1.1	1.1
	Logrank p	0.93	0.087	0.32	0.5	0.6	0.67	0.71
CNOT1	HR (high)	1.1	0.45	0.85	1.4	1.3	1.3	1.1
	Logrank p	0.7	0.24	0.6	0.19	0.17	0.12	0.47
		OV	PAAD	PRAD	READ	STAD	THCA	UCEC
BPTF	HR (high)	1.1	0.76	1.3	0.51	1.1	2.3	1.1
	Logrank p	0.59	0.19	0.72	0.17	0.7	0.12	0.84
SIN3A	HR (high)	0.94	1.3	0.79	0.6	1.2	1.7	1.2
	Logrank p	0.59	0.26	0.72	0.28	0.33	0.3	0.59
CNOT1	HR (high)	0.95	1.1	1.8	0.53	1.3	1.8	0.98
	Logrank p	0.67	0.53	0.35	0.19	0.083	0.26	0.96