

## Supplementary

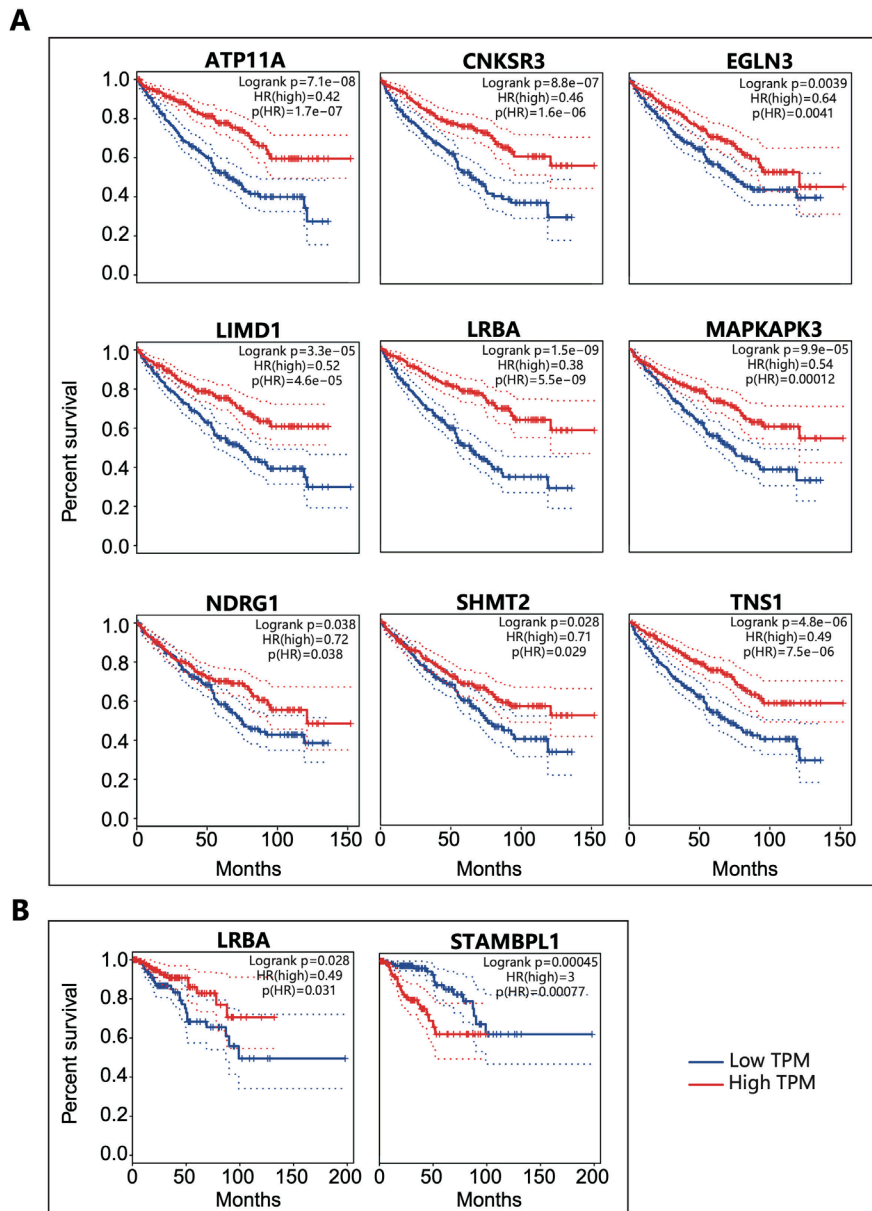
**Table S1** Difference in the DNA methylation between KIRC and KIRP normal

Sites	KIRP(N)_mean	KIRC(N)_mean	KIRP(N)_median	KIRC(N)_median	diff_mean	diff_median	P-value	FDR
cg22274117	0.43	0.43	0.43	0.43	0.00	0.00	0.82	0.82
cg20740711	0.88	0.87	0.88	0.88	-0.01	0.00	0.30	0.34

diff\_mean: KIRC(N)\_mean minus KIRP(N)\_mean; diff\_median: KIRC(N)\_median minus KIRP(N)\_median

**Table S2** Characteristics of 15 methylation markers and their corresponding genes in RCC diagnosis and prognosis

Sample	Marker	Ref Gene	Diagnosis	Prognosis
Normal	cg20740711	Intergenic	√	
	cg22274117	ATXN1	√	
KIRC	cg09643398	BCL6	√	
	cg23264429	STAMBPL1	√	√
	cg03290131	DUSP5	√	
	cg16284684	C7orf50	√	
	cg24170040	EGLN3	√	√
	cg08163918	SHMT2	√	√
KIRP	cg06215107	LRBA	√	√
	cg22571393	ATP11A	√	√
	cg08223003	NDRG1	√	√
	cg12496156	TNS1	√	√
	cg16283183	LIMD1	√	√
	cg05548488	MAPKAPK3	√	√
	cg23528791	CNKSR3	√	√



**Figure S1** The genes DNA methylation markers located could predict the prognosis of KIRC and KIRP. Ten genes were associated with the prognosis of KIRC and KIRP; 9 of 10 genes improved the predictive ability of KIRC (A),  $n(\text{high})=258$ ,  $n(\text{low})=258$ , and 2 of 10 genes had value for predicting the prognosis of KIRP (B),  $n(\text{high})=141$ ,  $n(\text{low})=141$ . LRBA could be used as a shared predictive factor for the prognosis of KIRP and KIRC.