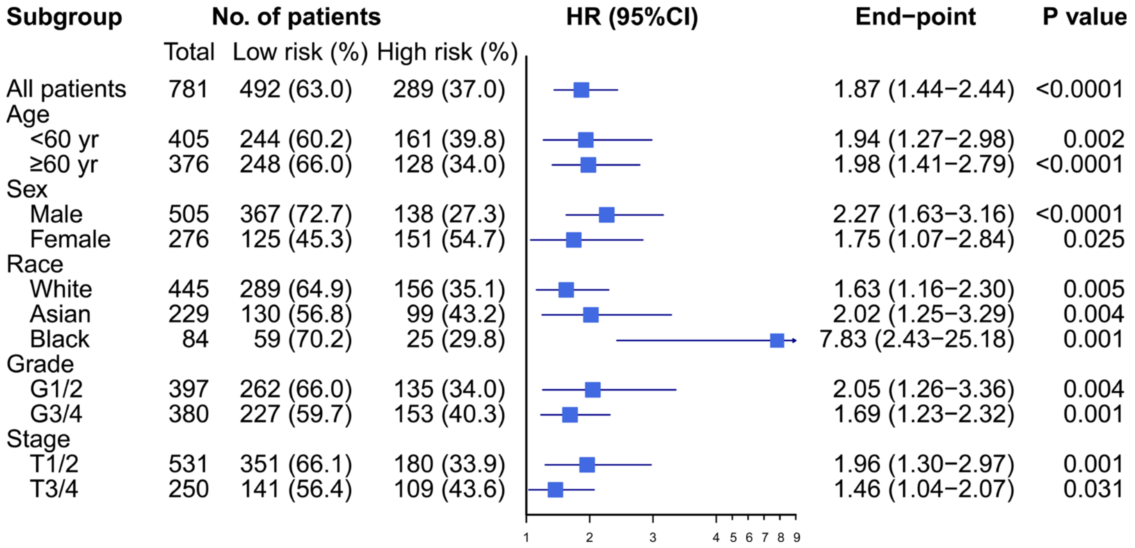
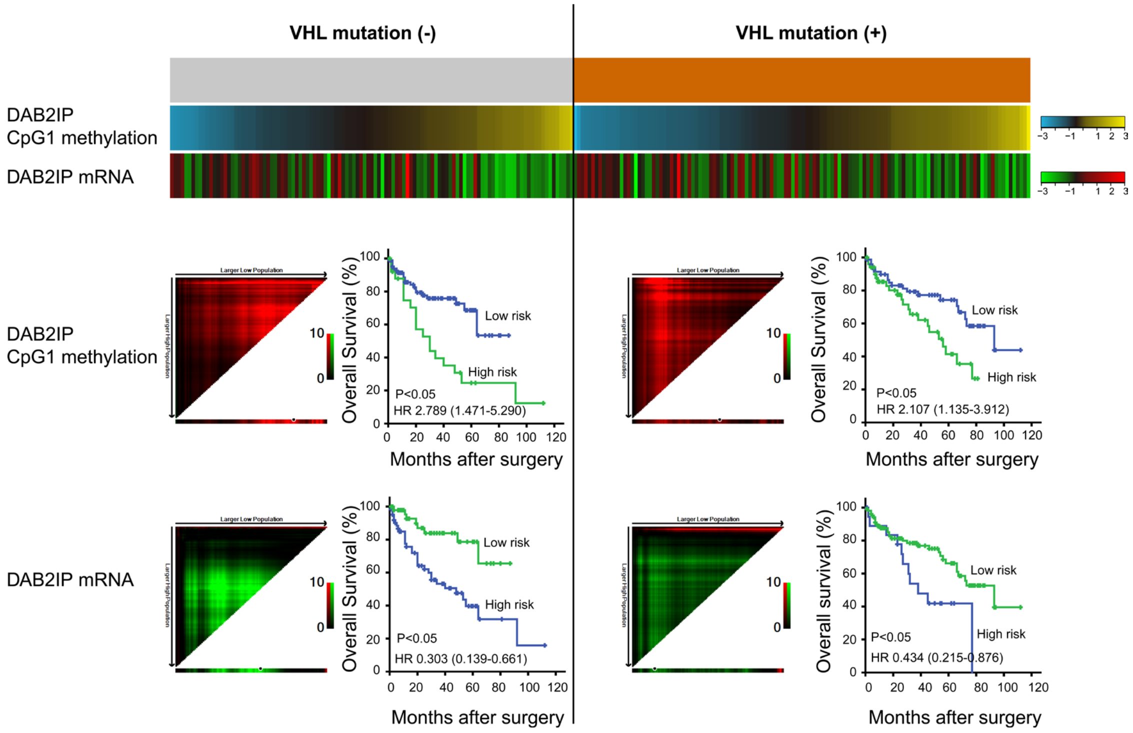
Validation of DAB2IP methylation and its relative significance in predicting outcome in renal cell carcinoma

SUPPLEMENTARY FIGURES AND TABLE



Subgroup	No. of patients Total	Low risk (%)	High risk (%)	End−point HR (95%CI)	P value
All patients	781	492 (63.0)	289 (37.0)	1.87 (1.44−2.44)	<0.0001
Age					
<60 yr	405	244 (60.2)	161 (39.8)	1.94 (1.27−2.98)	0.002
≥60 yr	376	248 (66.0)	128 (34.0)	1.98 (1.41−2.79)	<0.0001
Sex					
Male	505	367 (72.7)	138 (27.3)	2.27 (1.63−3.16)	<0.0001
Female	276	125 (45.3)	151 (54.7)	1.75 (1.07−2.84)	0.025
Race					
White	445	289 (64.9)	156 (35.1)	1.63 (1.16−2.30)	0.005
Asian	229	130 (56.8)	99 (43.2)	2.02 (1.25−3.29)	0.004
Black	84	59 (70.2)	25 (29.8)	7.83 (2.43−25.18)	0.001
Grade					
G1/2	397	262 (66.0)	135 (34.0)	2.05 (1.26−3.36)	0.004
G3/4	380	227 (59.7)	153 (40.3)	1.69 (1.23−2.32)	0.001
Stage					
T1/2	531	351 (66.1)	180 (33.9)	1.96 (1.30−2.97)	0.001
T3/4	250	141 (56.4)	109 (43.6)	1.46 (1.04−2.07)	0.031

Supplementary Figure S1: Hazard ratio of overall mortality for all 781 patients with ccRCC according to the methylation of the DAB2IP CpG1 in different subgroups stratified by clinical parameters.



Supplementary Figure S2: DAB2IP CpG1 methylation and DAB2IP mRNA in subsets of different VHL mutation status. Based on the TCGA dataset analysis, DAB2IP CpG1 methylation and DAB2IP mRNA successfully predicted the prognosis of ccRCC in both VHL mutation (+) subtype and VHL mutation (-) subtype (all $p<0.05$). Patients in each subset were separated into high-risk and low-risk groups using X-tile plots to generate the optimum cut-off.

Supplementary Table S1: 3 Probes located in UTSS of DAB2IP by the annotations provided by Illumina for the HumanMethylation450 platform

ID	CHR	MAPINFO	UCSC_RefGene_Name	UCSC_RefGene_Group
cg01305539	9	124328327	DAB2IP	TSS1500
cg14122599	9	124503625	DAB2IP	TSS1500
cg14383549	9	124503795	DAB2IP	TSS1500