

1 **SUPPLEMENTARY FIGURE 1.** Kaplan–Meier curves of the ccRCC patient  
2 subgroups stratified by the PRMTs expressions.

3 (A-H) Survival analyses of ccRCC patients subgroups stratified by the expressions of  
4 PRMT1, PRMT2, PRMT3, CARM1, PRMT5, PRMT6, PRMT7, and PRMT8.

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6 **SUPPLEMENTARY FIGURE 2.** Identification of arginine methylation modification  
7 patterns based on the expression levels of the 8 PRMTs .

8 (A-H) Consensus matrices of ccRCC patients from  $k = 2$  to  $k = 9$ .

9 (I-K) The cumulative distribution function (CDF) curves plot, delta plot, and tracking  
10 plot corresponding to the consensus matrices from  $k = 2$  to  $k = 9$ .

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12 **SUPPLEMENTARY FIGURE 3.** Generation of genetic clusters based on the DEGs  
13 and differential biological pathways among GeneClusters.

14 (A-H) Consensus matrices of ccRCC from  $k = 2$  to  $k = 9$ .

15 (I-K) The CDF curves plot, delta plot, and tracking plot corresponding to the consensus  
16 matrices from  $k = 2$  to  $k = 9$ .

17 (L-M) GSVA enrichment analysis showing the activation states of biological pathways  
18 among three GeneClusters.

19 (N) Abundance of immune cell types in different GeneClusters.

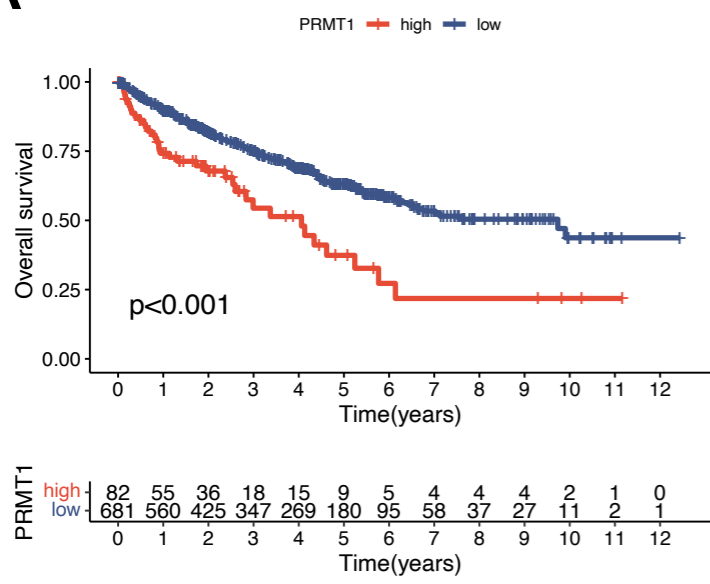
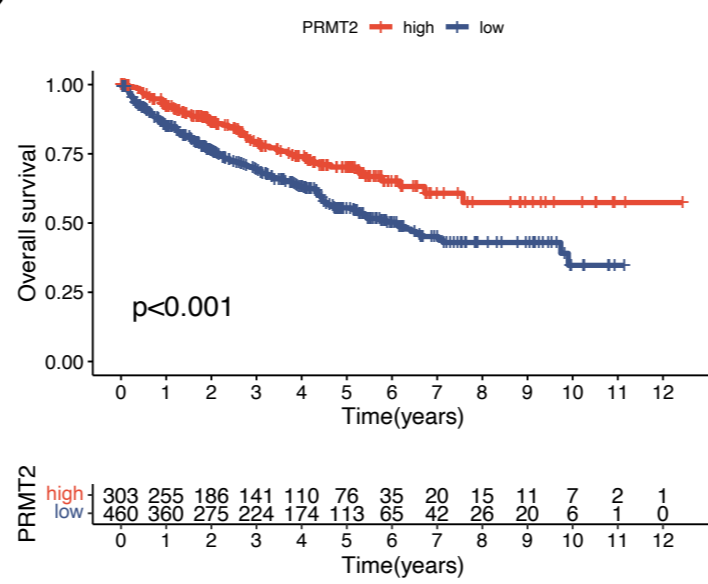
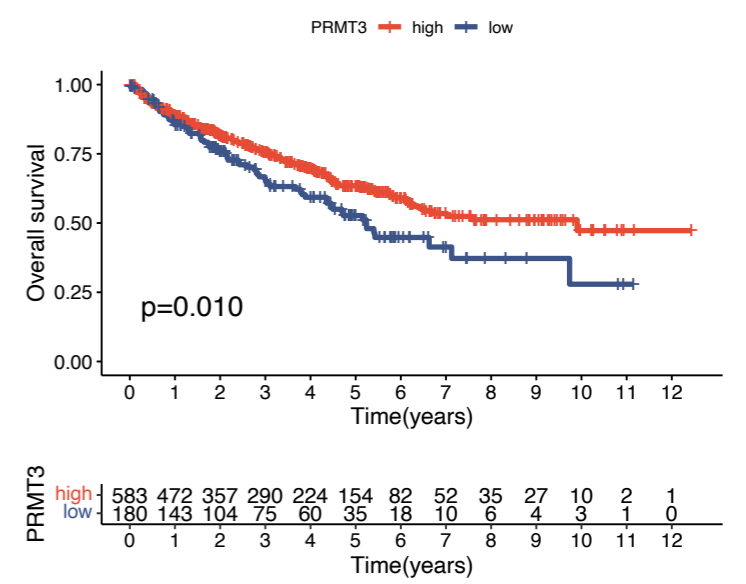
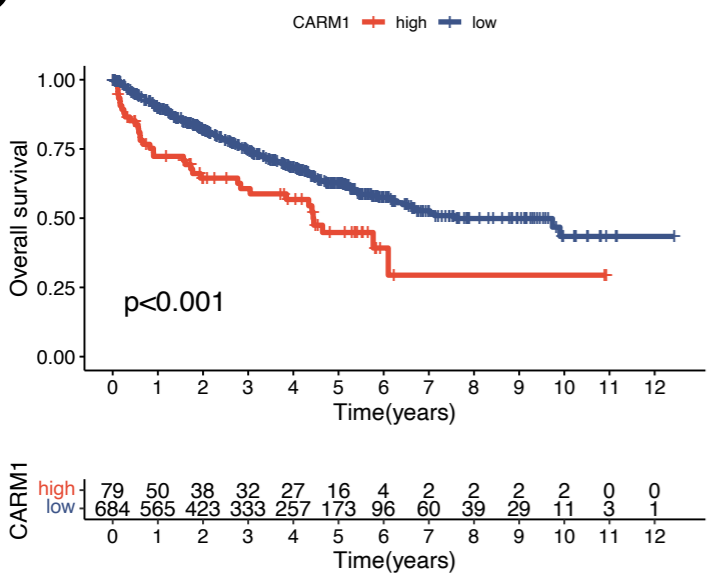
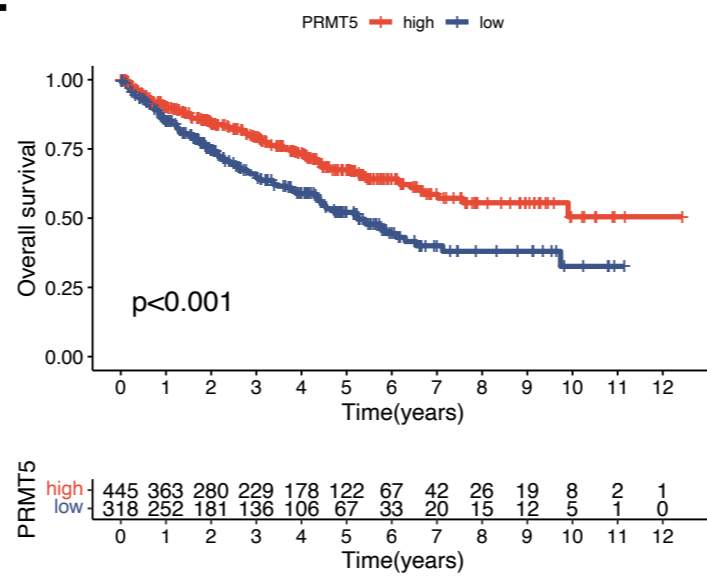
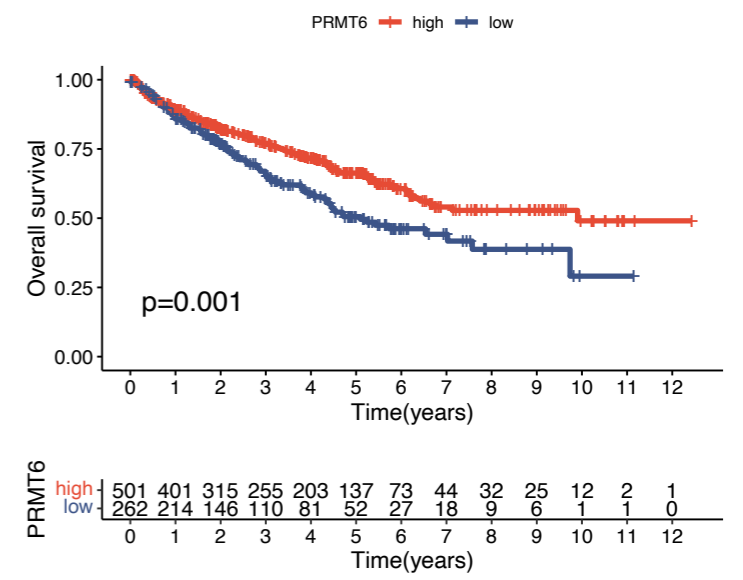
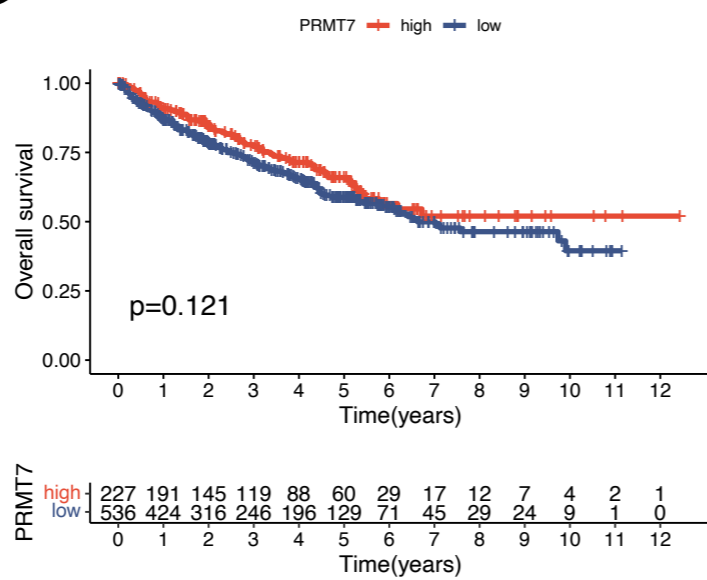
20 (O) Expressions of immune checkpoints (ICPs) in different GeneClusters.

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22 **SUPPLEMENTARY FIGURE 4.** Correlation between clinical characteristics and the  
23 predictive signature.

24 (A-F) The proportions of clinical features (T stage, age, and gender) of ccRCC patients  
25 in different PRMTGroups.

26 (G-L) Kaplan–Meier analyses for patients in different PRMTGroups stratified by  
27 clinical features (T stage, age, and gender).

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**A****B****C****D****E****F****G****H**