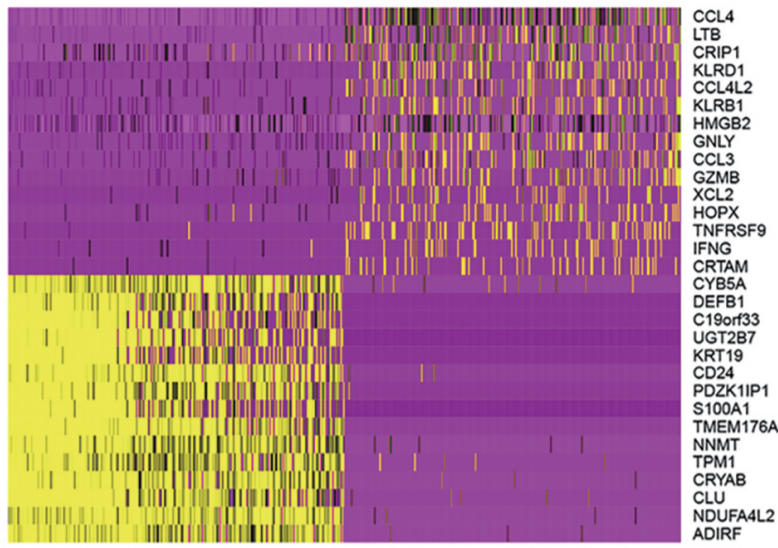
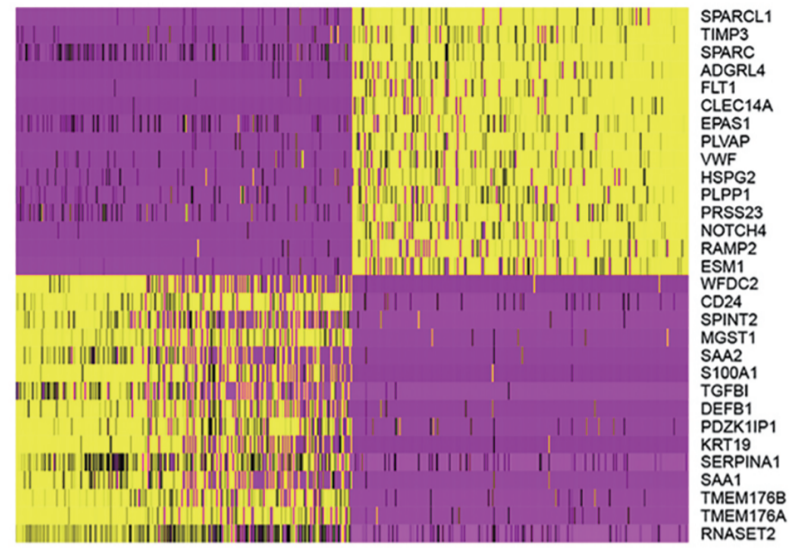
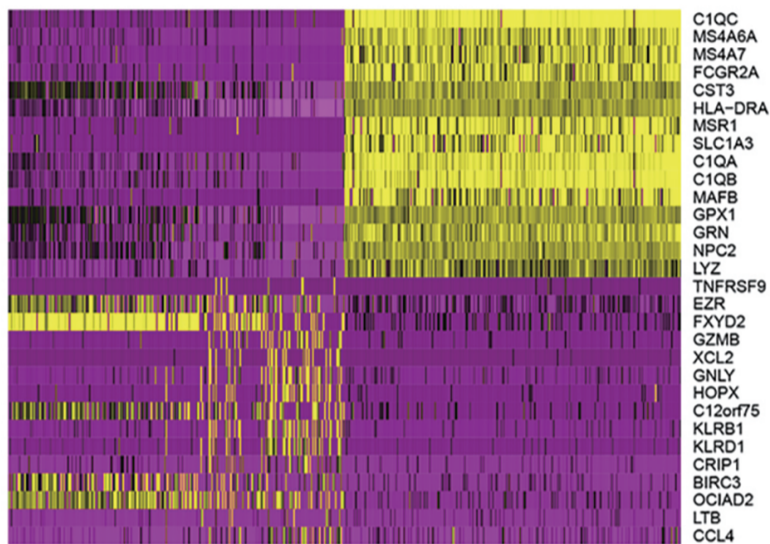


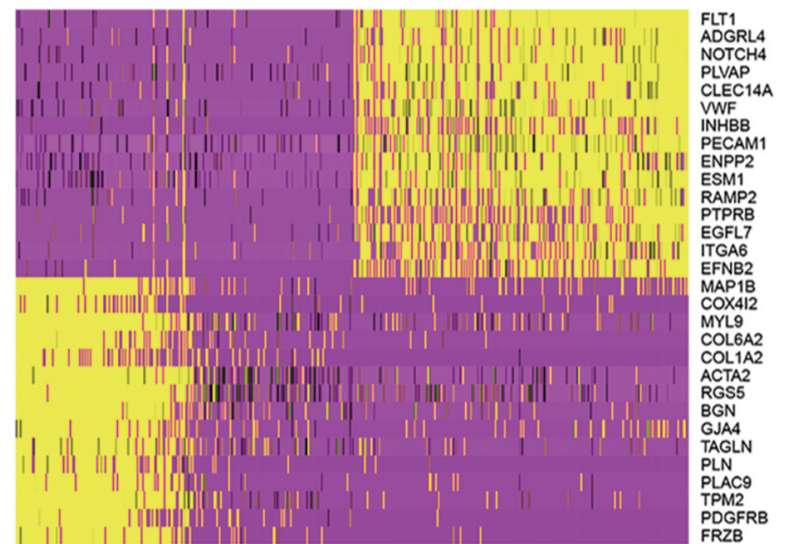
A



PC_3



PC_4



B

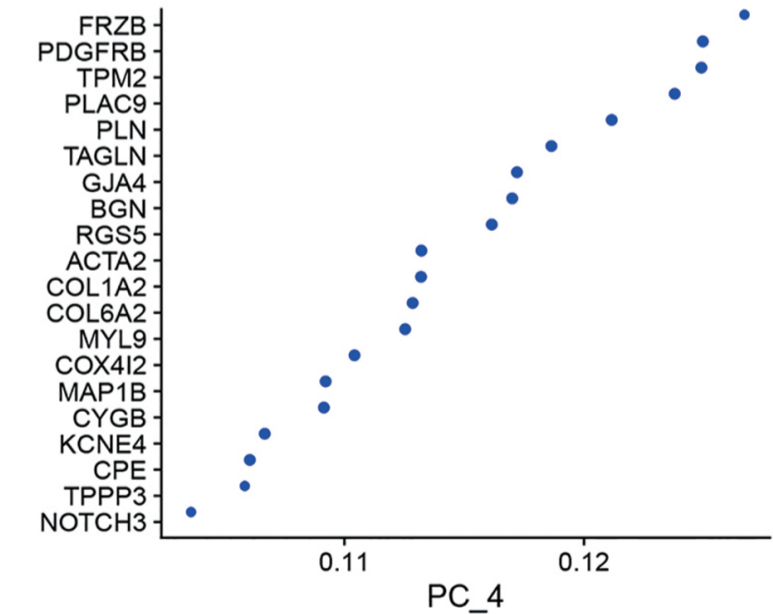
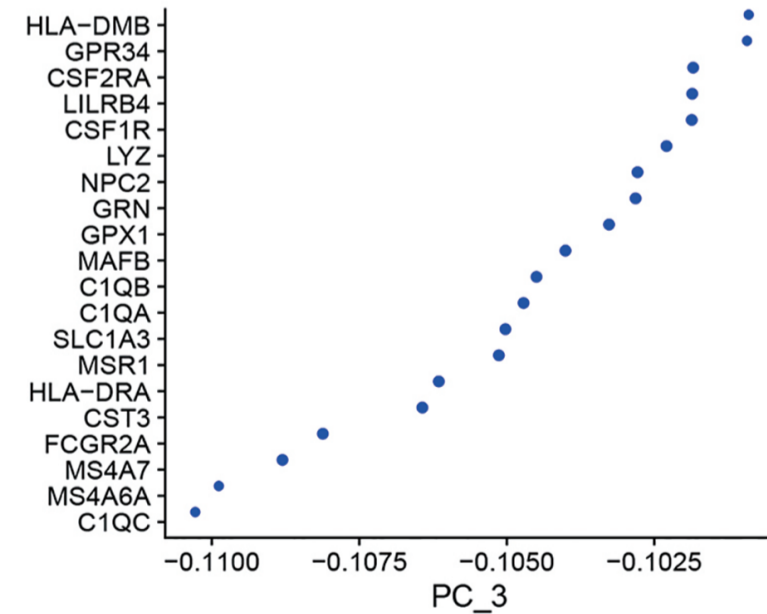
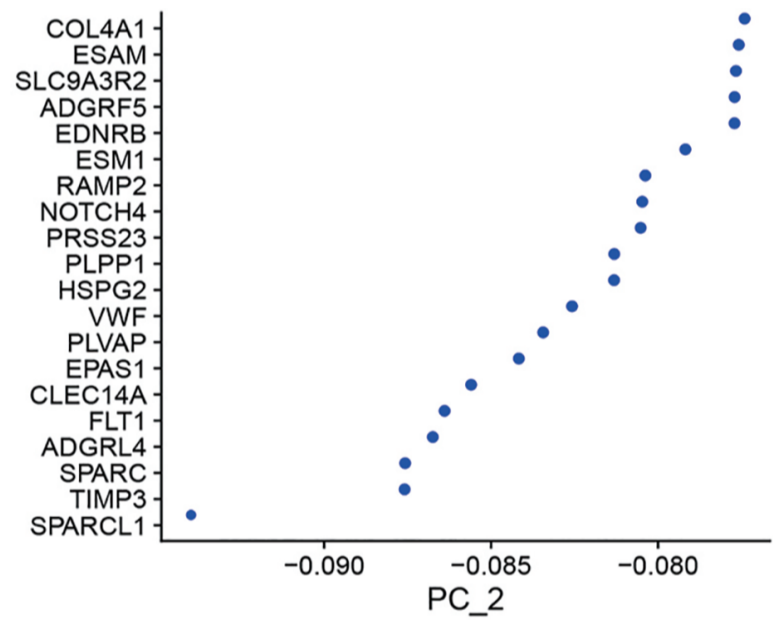
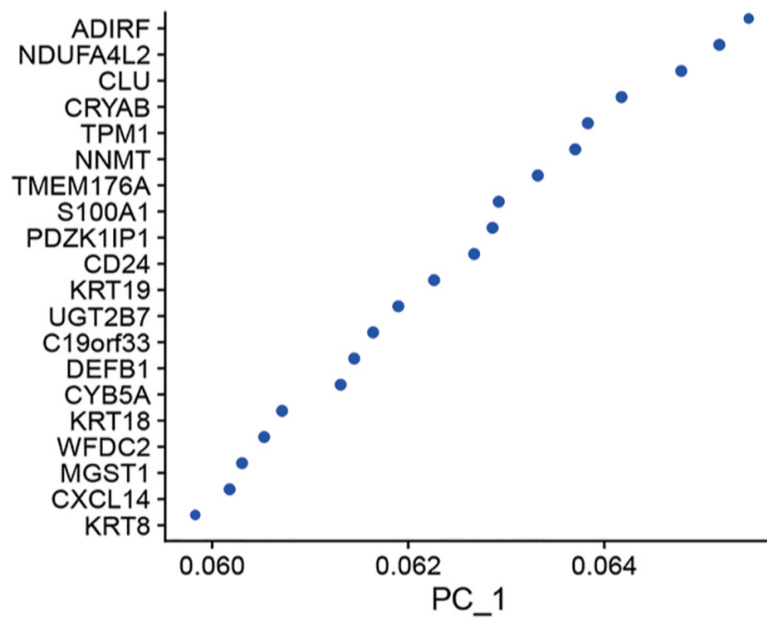


Figure S1 The top 4 components and the correlated genes in each component. (A) The heatmaps showed the expression pattern of the top 30 significantly correlated genes in each component. The color purple indicates low gene expression level, yellow indicates high level. (B) Dot plot showed the top 20 significantly correlated genes in each component.

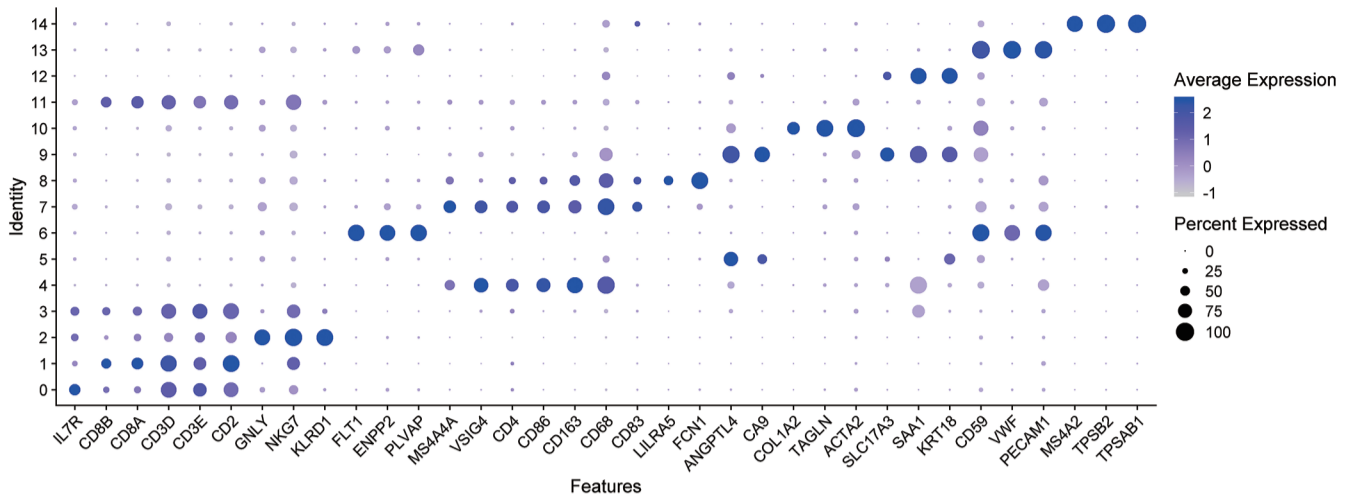


Figure S2 Identification of top marker genes of the 15 cell clusters. Dotplot heatmap showed the expression level and cellular detection rate of selected marker genes.

Table S1 Numbers of primary and metastatic ccRCC patients with PAX8 immunohistochemical staining

IHC	Tumor type		Total
	Primary	Metastatic	
PAX8 (+)	31	4	35
PAX8 (-)	4	2	6
Total	35	6	41

IHC, immunohistochemical staining; ccRCC, clear cell renal cell carcinoma.

Table S2 Genes of each analytical procedure to screen optimal prognosis-related predictors

Analytical procedure	T cell-related genes in ccRCC
Differential analysis of t-SNE clusters	<i>CD8A, CD2, IL7R, CD69, DNAJB1, CENPF, DEK, ZNF331, HSPA1A, H2AFV, HMG2, SMC4, CKS2, DUT, GTSE1, SMC2, PRC1, TK1, HSP90AA1, MKI67, GZMK, PTTG1, HSPA1B, ASPM, HIST1H1D, KIF20B, H2AFZ, KNL1, NUCKS1, LYST, TUBB4B, TOP2A, LTB, CD27, CKS1B, RPS4Y1, HMGB1, TUBA1B, HIST1H4C, UBE2C, BIRC5, RRM2, CRIP1, TTN, CXCR4, ANP32E, KPNA2, STMN1, HSPA6, NR4A2, DUSP4, TPX2, PCNA, TYMS, ATAD2, ZWINT, CENPE, HMGB2, NUSAP1, RAD21, CDK1, ARL6IP1, CCNA2, TNFRSF9, H2AFX, TUBB, PCLAF, TMPO, AURKB, CLSPN</i>
KM survival analysis	<i>UBE2C, AURKB, PTTG1, H2AFX, BIRC5, GTSE1, TPX2, SMC2, CCNA2, RRM2, CENPF, HIST1H1D, ASPM, HSP90AA1, TK1, HIST1H4C, LTB, CENPE, H2AFV, CDK1, NUCKS1, ATAD2, RAD21, NUSAP1, HMGB2, MKI67, TYMS, CKS2, HMG2, PCLAF, ZNF331, HSPA6, PRC1</i>
Lasso regression analysis	<i>CENPF, H2AFV, GTSE1, SMC2, NUCKS1, TYMS, H2AFX, AURKB</i>

ccRCC, clear cell renal cell carcinoma; t-SNE, t-distributed stochastic neighbor embedding; KM, Kaplan-Meier; Lasso, least absolute shrinkage and selection operator.

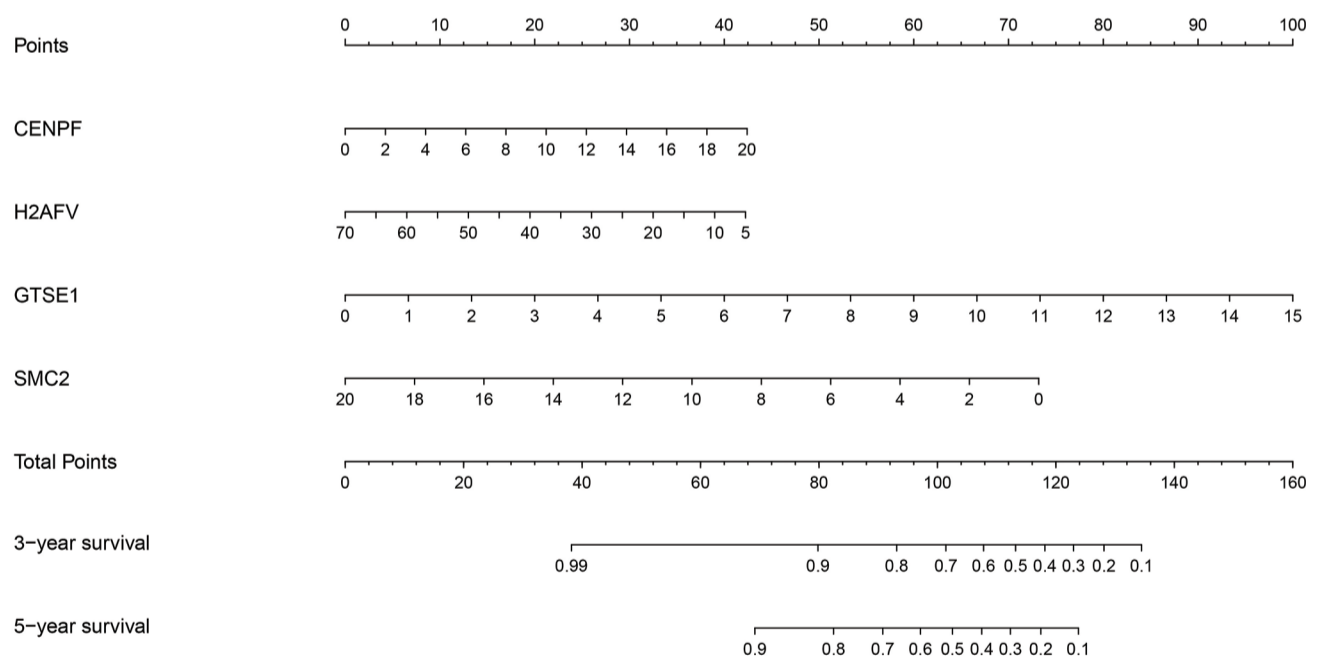


Figure S3 Nomogram base on the four gene expression to predict 3-year and 5-year OS for ccRCC patients. ccRCC, clear cell renal cell carcinoma; OS, overall survival.