

Fig.S1 Volcano plots of DEGs in TCGA cohort. (X-axis: $\log_2(\text{FC})$; Y-axis: $-\log_{10}(\text{FDR})$ for each gene. Genes with $\text{FDR} < 0.01$ and $\text{FC} > 1.5$ or < -1.5 were considered as DEGs. Blue: down-regulated genes; Grey: non-differential genes; Red: up-regulated genes.

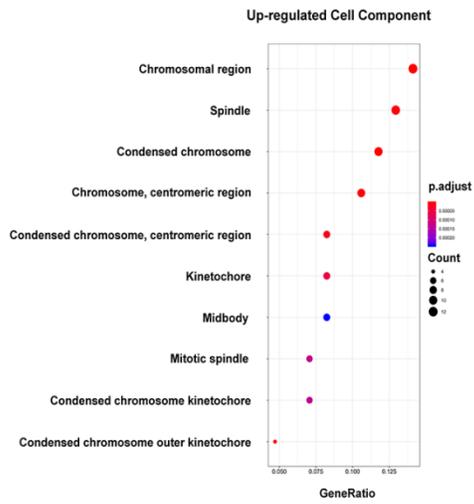
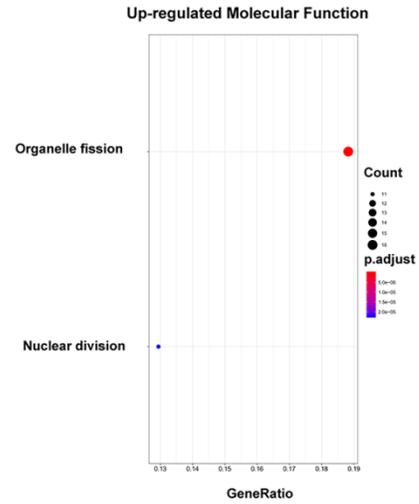
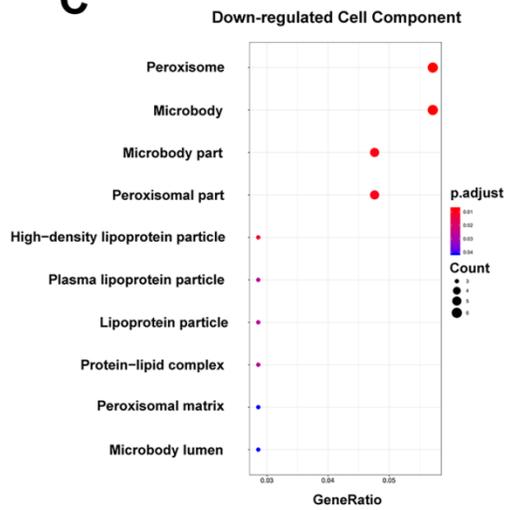
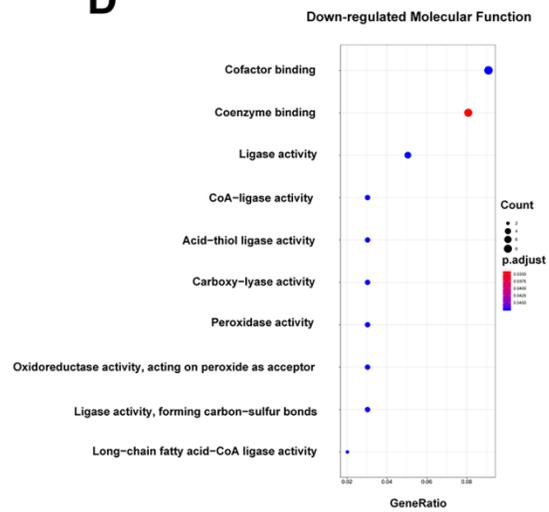
A**B****C****D**

Fig.S2 GO cell component (CC) enrichment analysis of upregulated DEGs (A) and downregulated DEGs (C). GO molecular function (MF) analysis of upregulated DEGs (B) and downregulated DEGs (D).

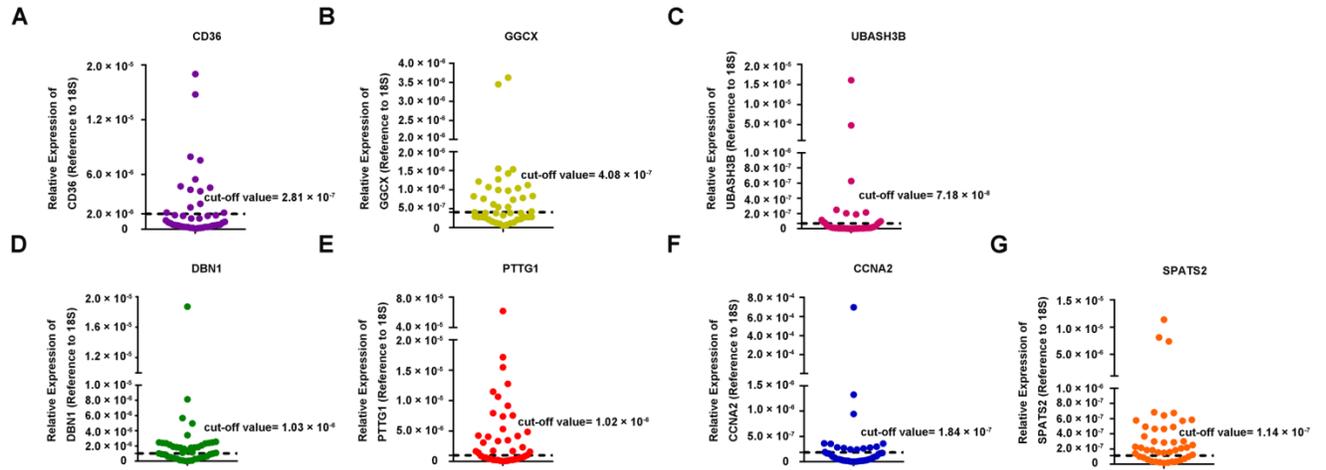


Fig.S4 mRNA expression levels of 7 genes in 44 CCA samples from Renji hospital and each cut-off value were shown in figure. (A-G)

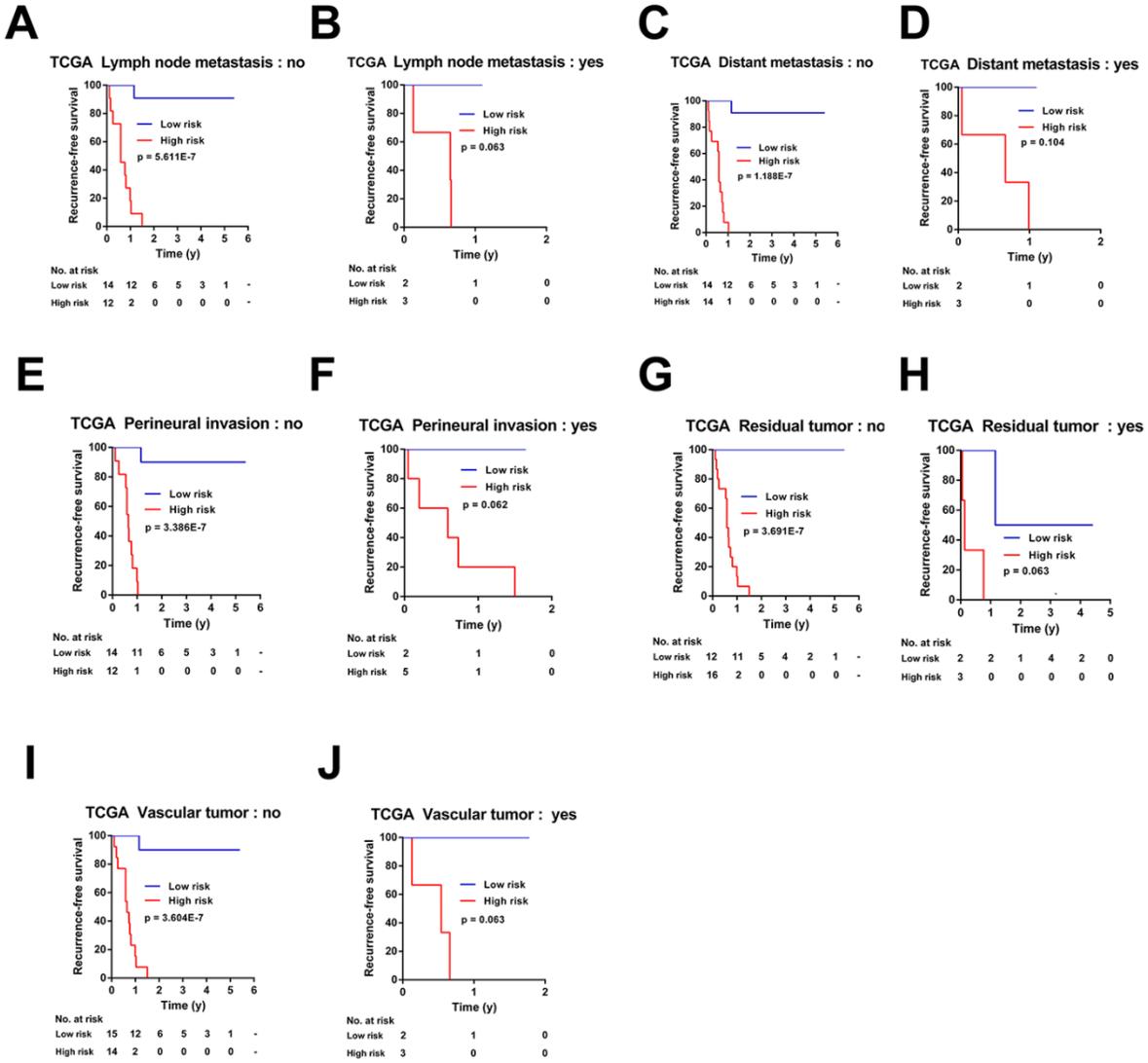


Fig.S5 Kaplan-Meier survival analyses of the TCGA cohort, according to the 7-mRNA-based classifier stratified by clinicopathological risk factors. (A, B) Lymph node metastasis, (C, D) Distant metastasis, (E, F) perineural invasion, (G, H) Residual tumor, and (I, J) Vascular tumor.

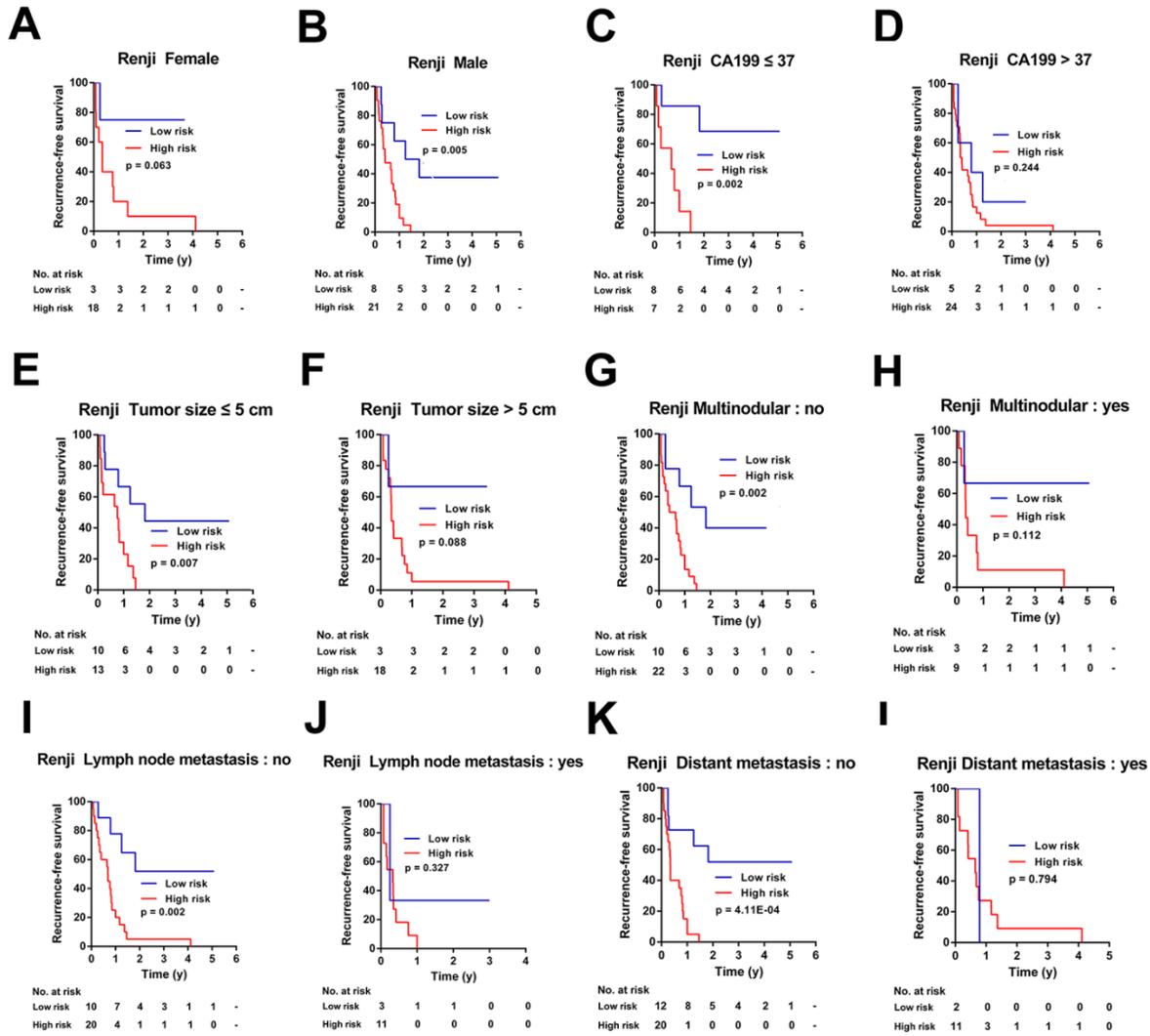


Fig-S6 Kaplan-Meier survival analyses of the Ren Ji cohort, according to the 7-mRNA-based classifier stratified by clinicopathological risk factors. (A, B) Gender, (C, D) Age, (E, F) Tumor size, (G, H) Multinodular, (I, J) Lymph node metastasis, and (K, L) Distant metastasis.