

Fig.S1 Volcano plots of DEGs in TCGA cohort. (X-axis: log[2](FC); Y-axis: -log[10](FDR) for each gene. Genes with FDR < 0.01 and FC>1.5 or <-1.5 were considered as DEGs. Blue: down-regulated genes; Grey: non-differential genes; Red: up-regulated genes.



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).



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Fig.S3 Complete LASSO coefficient profiles of the 127 mRNAs. Each curve represents a variable. The above axis: the number of nonzero coefficients at as  $\lambda$  varies. X-axis: L1 Norm, the summation of absolute nonzero coefficients at as  $\lambda$  varies. Y-axis: the values of nonzero coefficients at as  $\lambda$  varies.



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.