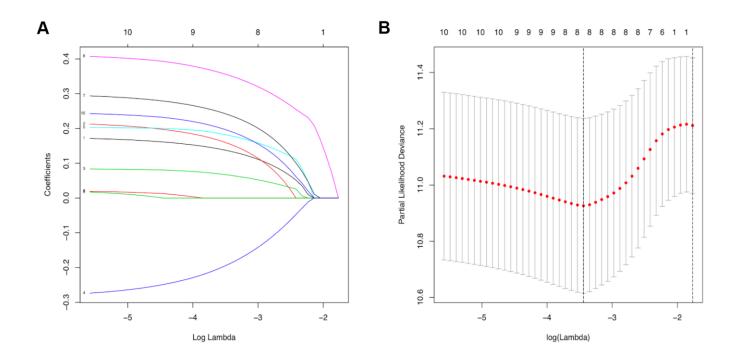
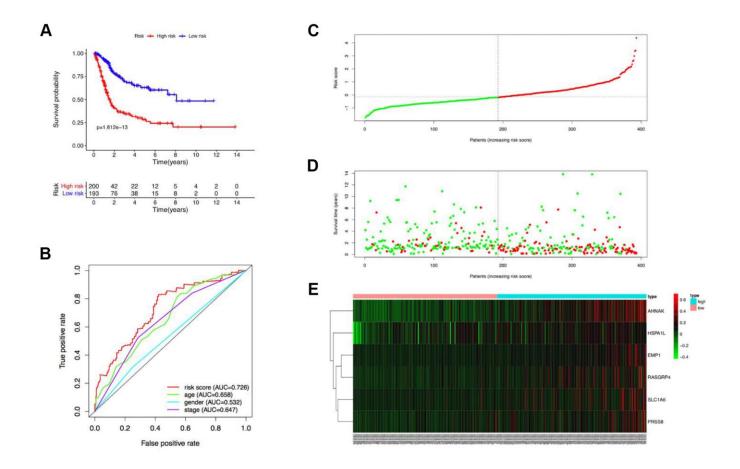
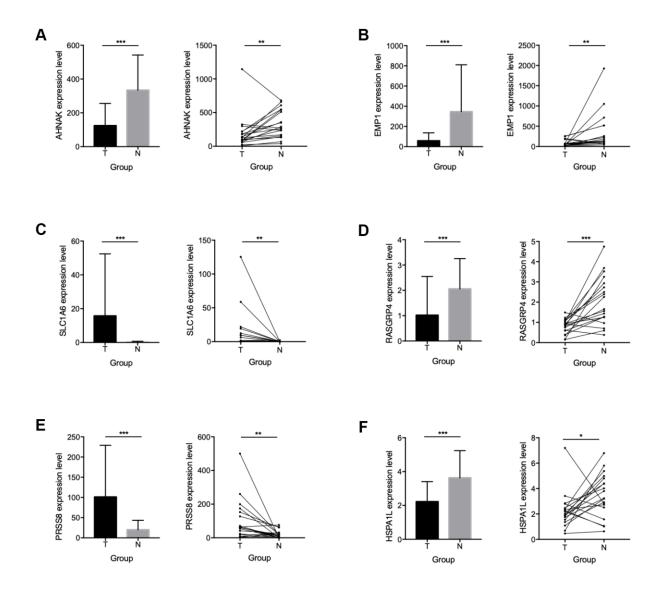
SUPPLEMENTARY FIGURES



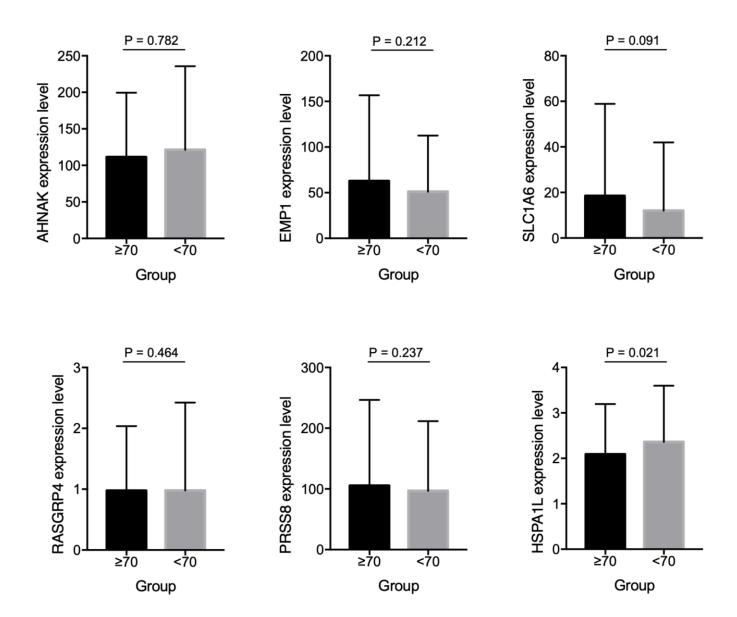
Supplementary Figure 1. Lasso regression analysis screened out 8 genes without redundancy. Lasso coefficient profiles of the T cell and neutrophil-associated genes (A). A coefficient profile plot against the log (lambda) sequence was generated to select the optimal parameter (lambda) in the Lasso model (B).



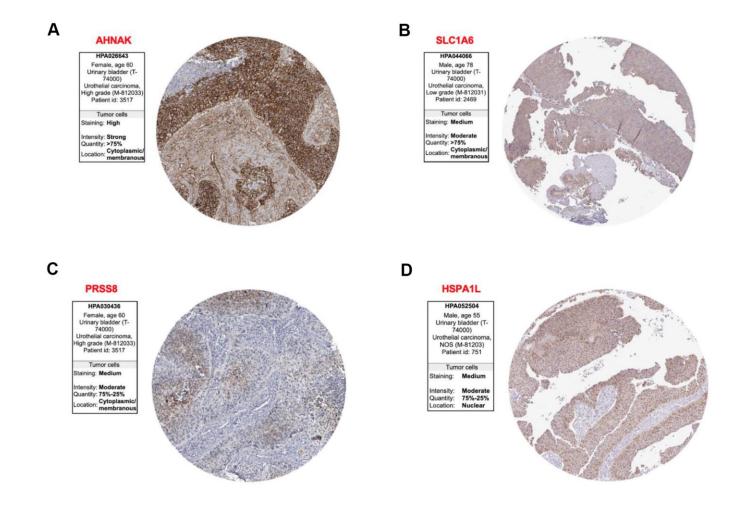
Supplementary Figure 2. The prognostic performance of the identified model in the whole TCGA-BLCA dataset. (A) Comparison of the overall survival between the estimated high-risk and low-risk patients. (B) The survival receiver operating characteristic (ROC) curves comparing prognostic value of the model and other clinical factors. (C–E) The change of patients' survival status (red dot represents dead case) and gene expression levels when risk score increased.



Supplementary Figure 3. Expression levels of the 6 key genes in BUC tumor tissues and adjacent normal tissues in the TCGA-BLCA dataset. (A) AHNAK; (B) EMP1; (C) SLC1A6; (D) RASGRP4; (E) PRSS8; (F) HSPA1L. Unpaired (left) and paired (right) nonparametric tests were performed for comparison. *** P < 0.001, ** P < 0.01, * P < 0.05.



Supplementary Figure 4. Expression levels of the 6 key genes in different age groups. Mann-Whitney test was performed.



Supplementary Figure 5. Typical immunostaining graphs of the identified key genes in BUC tumor tissues provided in the human protein atlas database. (A) AHNAK; (B) SLC1A6; (C) PRSS8; (D) HSPA1L.