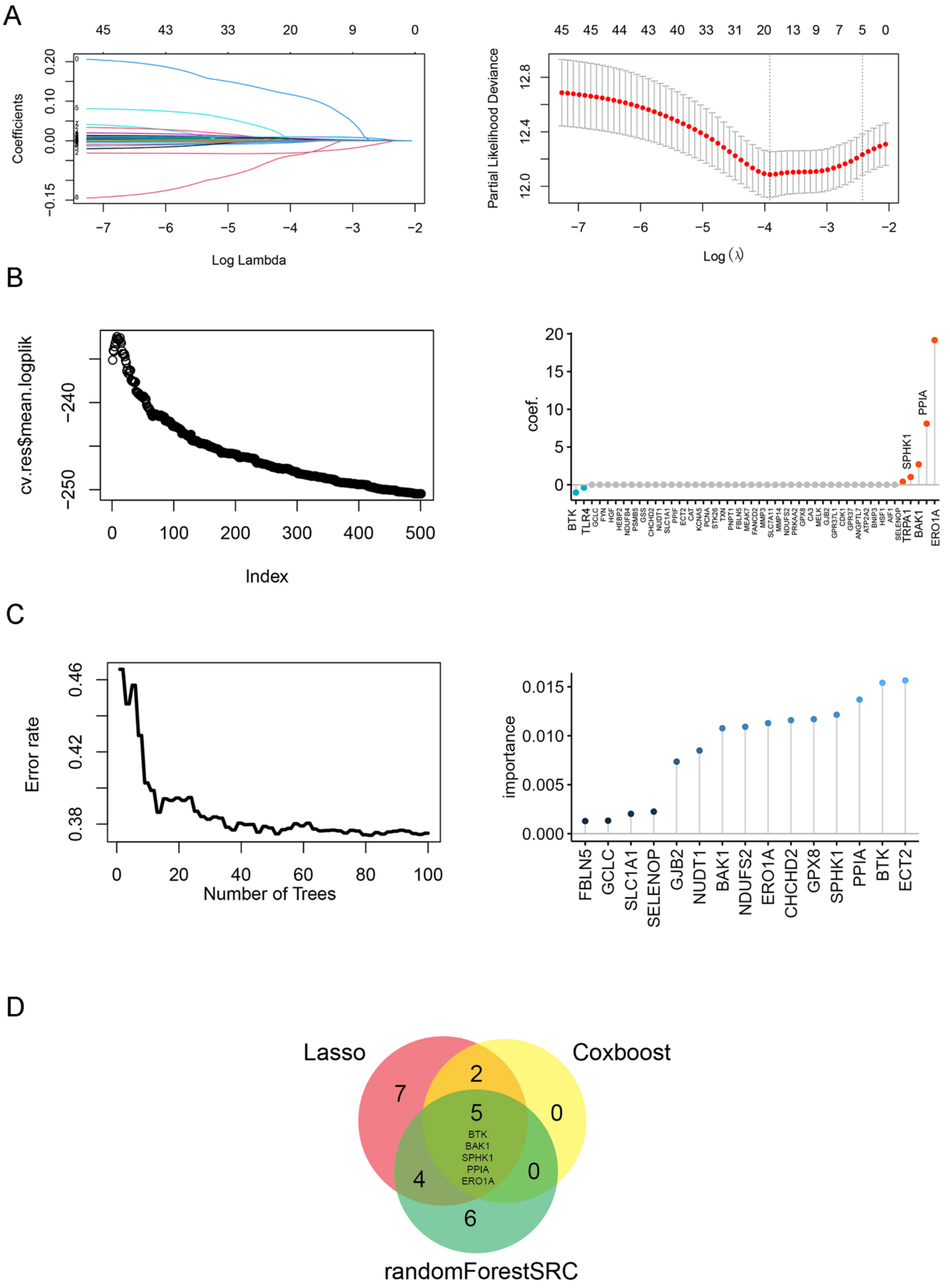

Figure S1 Identification of key genes in the Riskscore model. (A) LASSO Cox regression analysis screened 18 genes (“*BTK*”, “*FYN*”, “*HGF*”, “*BAK1*”, “*TRPA1*”, “*SLC1A1*”, “*ECT2*”, “*TXN*”, “*TLR4*”, “*PNPT1*”, “*MEAK7*”, “*NDUFS2*”, “*GPX8*”, “*GPR37*”, “*ANGPTL7*”, “*SPHK1*”, “*PPIA*”, and “*ERO1A*”). LASSO coefficient profiles for the expression of 18 candidate genes (left) and selection of the penalty parameter (λ) in the LASSO via 10-fold cross-validation (right). (B) CoxBoost analysis screened 7 genes (“*BTK*”, “*BAK1*”, “*TRPA1*”, “*TLR4*”, “*SPHK1*”, “*PPIA*”, and “*ERO1A*”). The goodness-of-fit of CoxBoost was analyzed using the log-likelihood (left) and coefficient of each gene (right). (C) randomForestSRC analysis screened 15 genes (“*BAK1*”, “*ERO1A*”, “*GPX8*”, “*SPHK1*”, “*ECT2*”, “*SELENOP*”, “*PPIA*”, “*GJB2*”, “*BTK*”, “*FBLN5*”, “*NDUFS2*”, “*SLC1A1*”, “*CHCHD2*”, “*GCLC*”, and “*NUDT1*”). Relationship between decision tree and error rate (light), and importance ranking of the 15 screened genes (right). (D) Venn diagram of the number of genes found in LASSO Cox regression, CoxBoost, and randomForestSRC analyses. LASSO, least absolute shrinkage and selection operator.

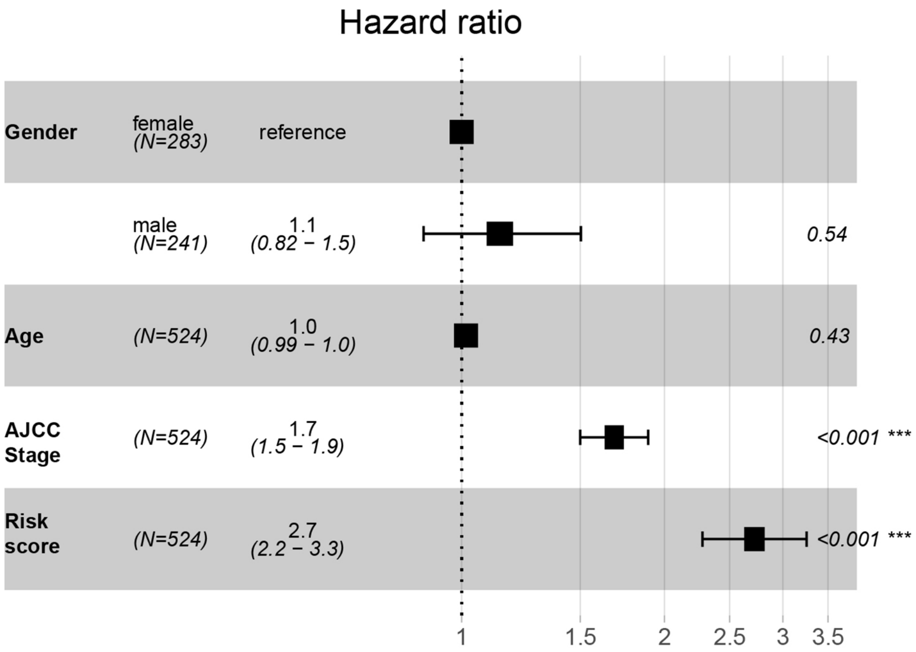

Figure S2 Independent prognostic univariate Cox analysis for Riskscore and clinical factors. ***, P<0.001.

https://dx.doi.org/10.21037/jtd-2025-854

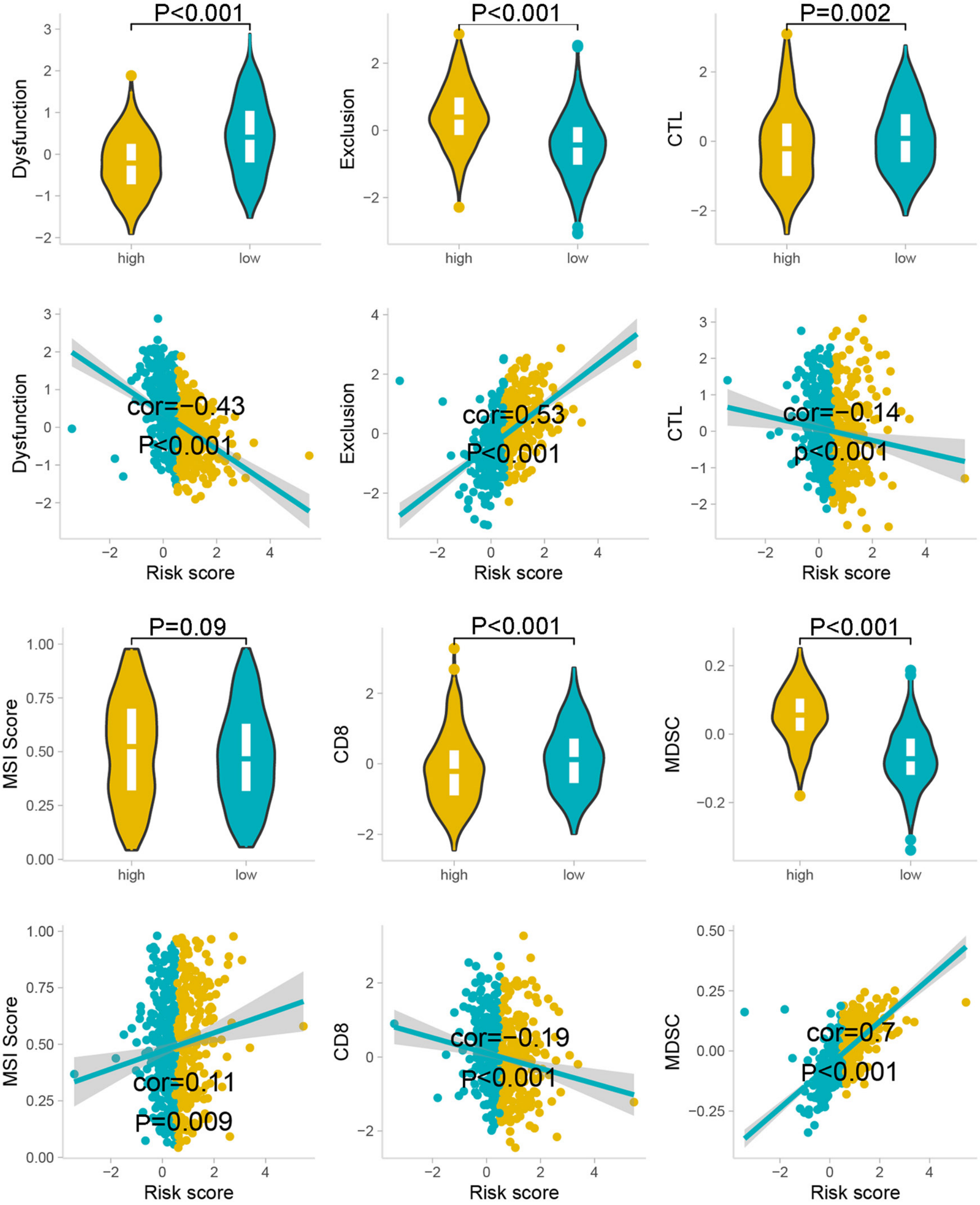

Figure S3 Comparisons of TIDE score between high- and low-Riskscore groups. TIDE, tumor immune dysfunction and exclusion. TIDE, Tumor Immune Dysfunction and Exclusion.