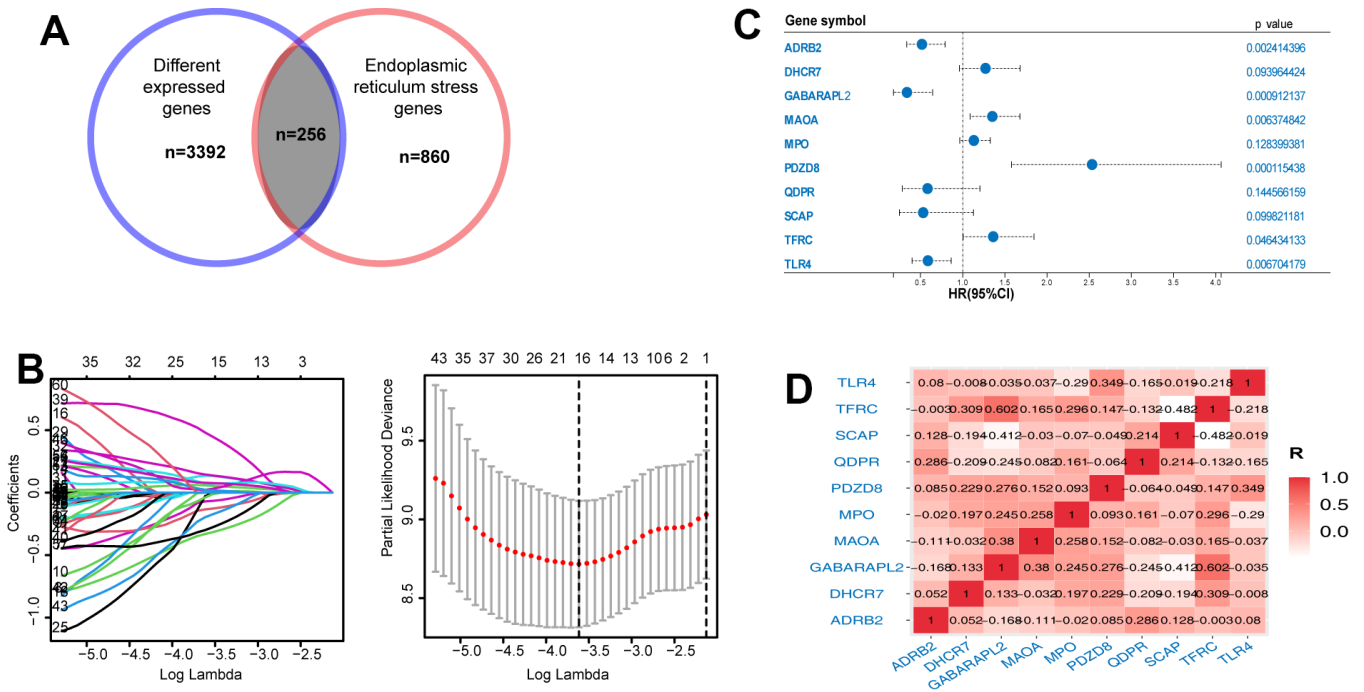
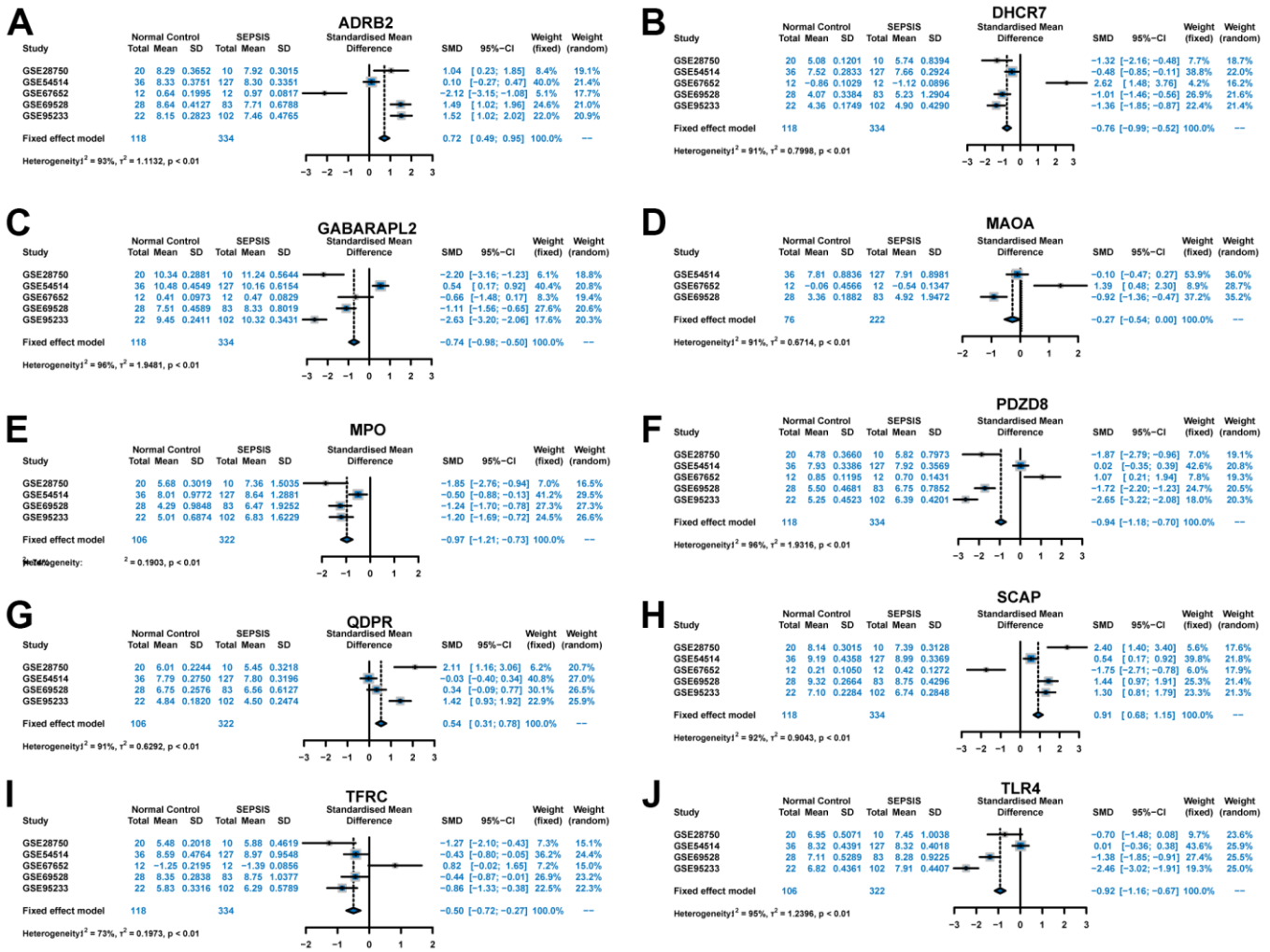


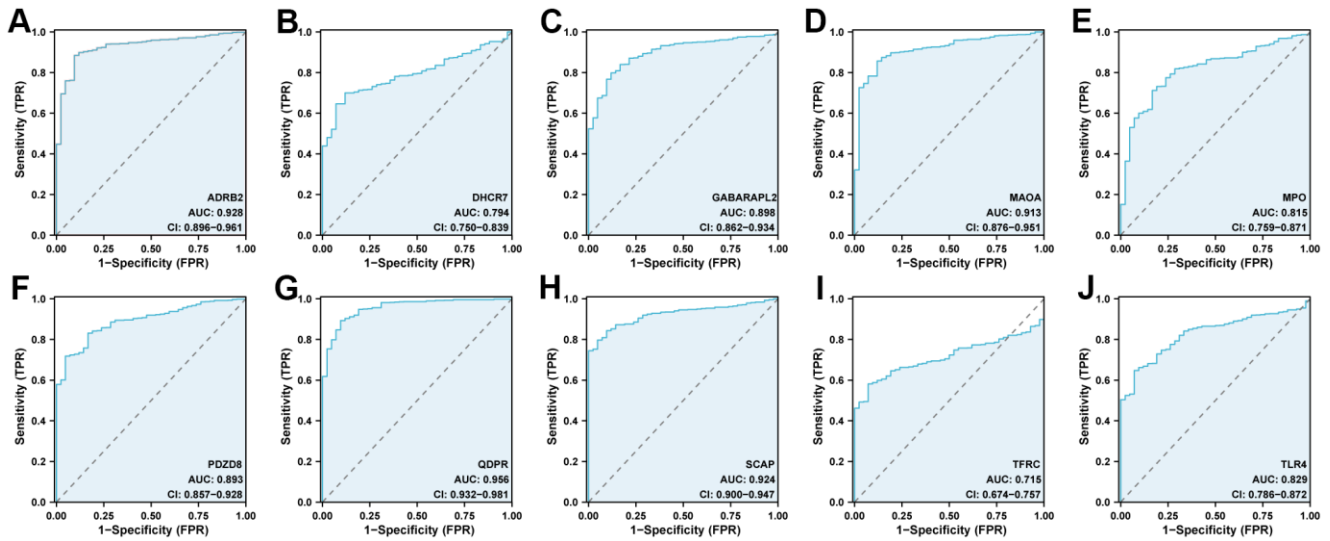
SUPPLEMENTARY FIGURES



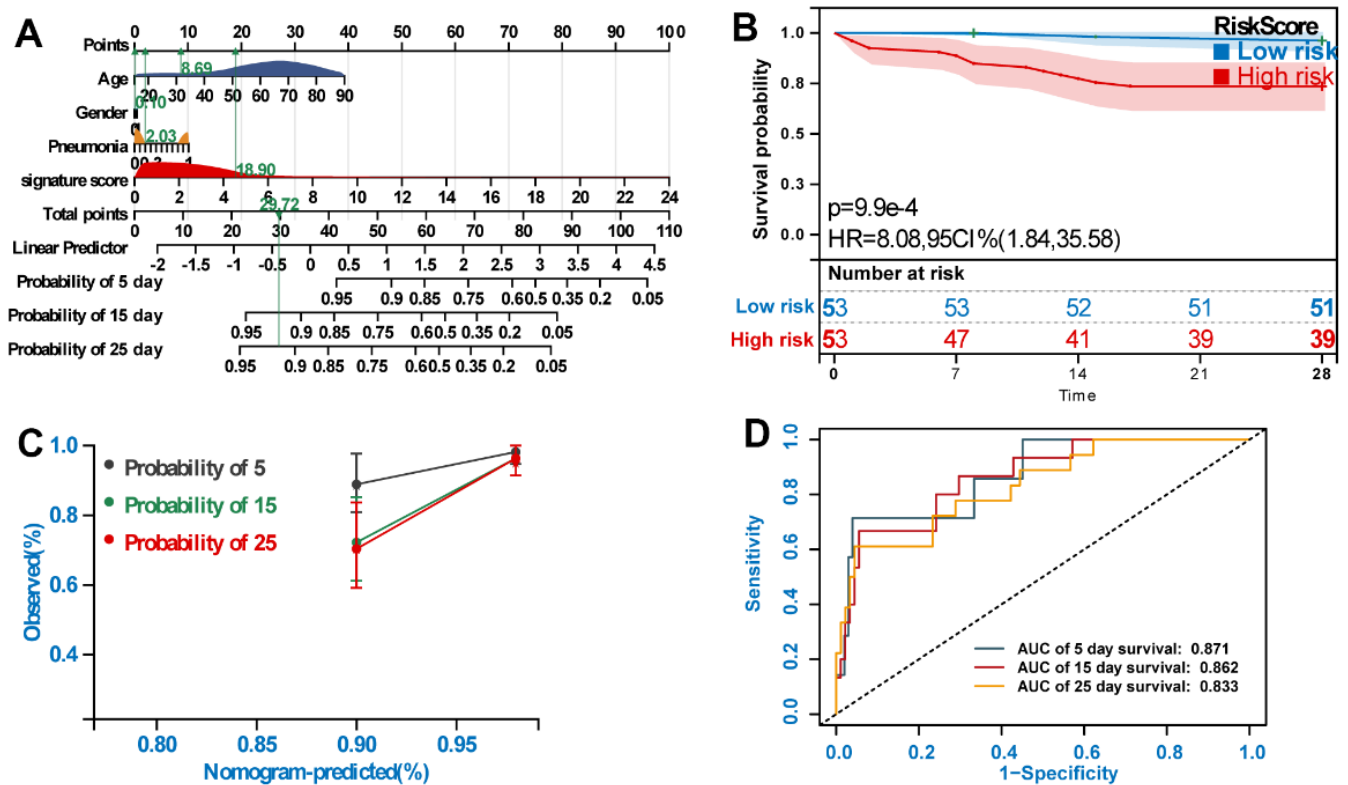
Supplementary Figure 1. Construction of signature model for risk of endoplasmic reticulum stress. (A) Identification of differentially expressed ERGs. **(B)** LASSO coefficient of the 64 survival ERGs, and the 100-fold cross-validation for variable screening and complexity adjustment in the Lasso Cox regression model. **(C)** Construction of the ER risk signature based on the multivariate Cox regression analysis. **(D)** Heatmap represents the correlation between the identified ERGs.



Supplementary Figure 2. Meta-analysis of the expression level (pooled results) of identified ERGs based on BIOS database: (A) ADRB2, (B) DHCR7, (C) GABARAPL2, (D) MAOA, (E) MPO, (F) PDZD8, (G) QDPR, (H) SCAP, (I) TFRC, and (J) TLR4.



Supplementary Figure 3. Diagnostic value of identified ERGs in sepsis. ROC analyses of (A) ADRB2, (B) DHCR7, (C) GABARAPL2, (D) MAOA, (E) MPO, (F) PDZD8, (G) QDPR, (H) SCAP, (I) TFRC, and (J) TLR4.



Supplementary Figure 4. Establishment of a nomogram for predicting the survival probability of patients with sepsis. (A) Nomogram for predicting OS developed in training dataset. (B) Kaplan–Meier (KM) survival curves for the survival of the nomogram. (C) Calibration curves of the nomogram for 5, 15, and 25 days. (D) Time-dependent ROC analysis of the survival-related nomogram.