Figure S1. Differentially expressed immune-related genes. (A) Heatmap and (B) volcano plot of differentially expressed immune-related genes. FDR, false-discovery rate; FC, fold change.

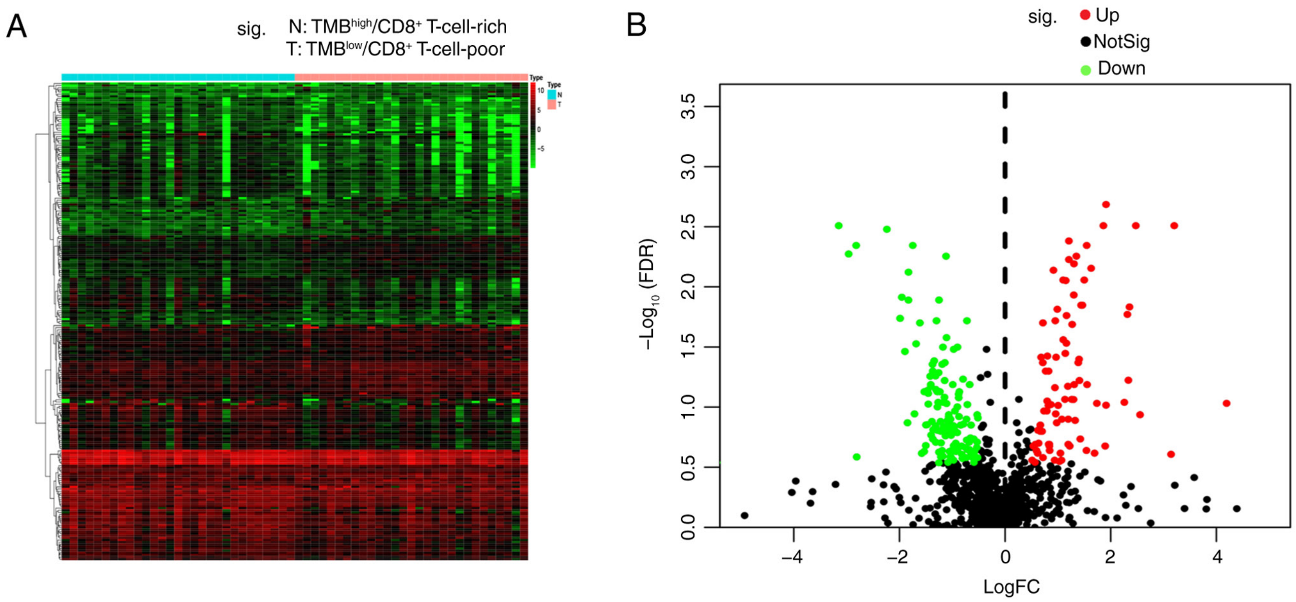

Figure S2. TCGA prognostic model and validation model for outcome prediction. (A) In TCGA prognostic model, the high-risk score group had worse OS compared with the low-risk score group. (B) In the validation model, high risk score group had worse OS compared with the low-risk score group. TCGA, The Cancer Genome Atlas; OS, overall survival; FDR, false-discovery rate; FC, fold-change.

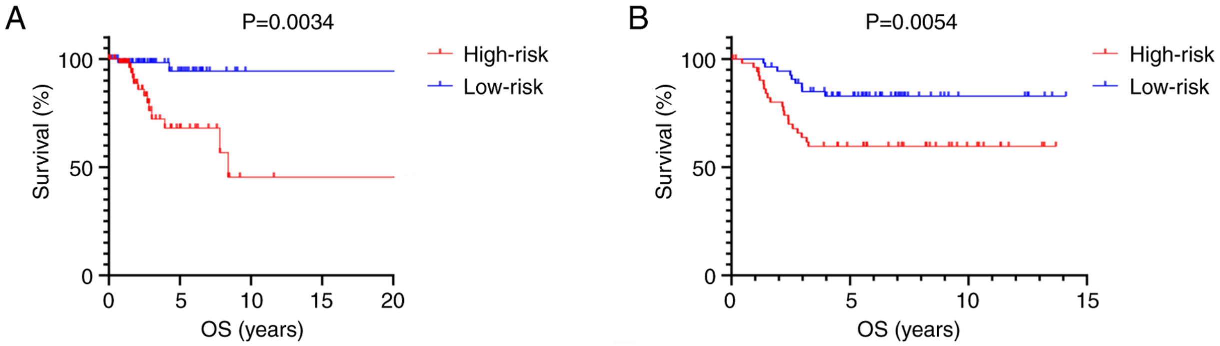

Figure S3. Development of the IRGPI and validation model. (A) Heatmap of expression profiles of included genes in IRGPI. (B) Heatmap of expression profiles of included genes in validation model. (C) Survival status of patients in different groups in IRGPI. (D) Survival status of patients in different groups in validation model. (E) Rank of prognostic index and distribution of groups in IRGPI. (F) Rank of prognostic index and distribution of groups in validation model. IRGPI, immune-related gene prognostic index; CXCL13, C-X-C motif chemokine ligand 13; TAPBPL, transporter associated with antigen processing binding protein like; PGF, placental growth factor; LTBP2, latent TGF-β binding protein 2.

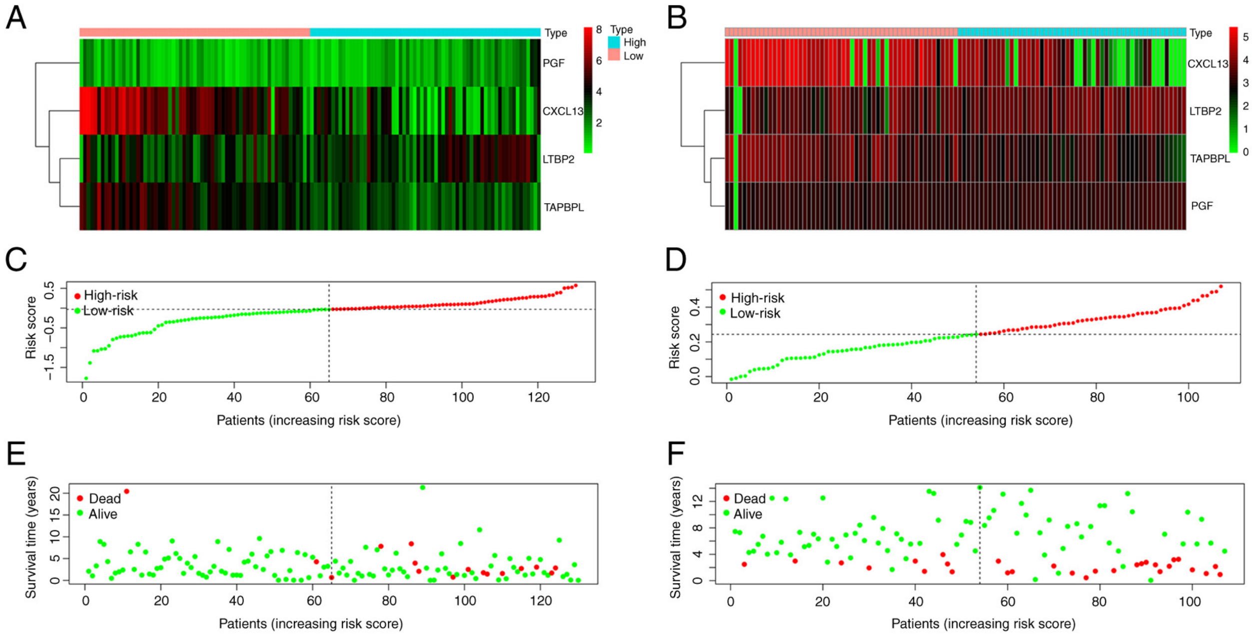

Figure S4. Risk score and clinical characteristics association analysis by t-test. (A) Age, (B) AJCC stage and (C) N stage had no association with risk score, while (D) lower T stage was associated with a lower risk score. AJCC, American Joint Committee on Cancer; N, lymph node.

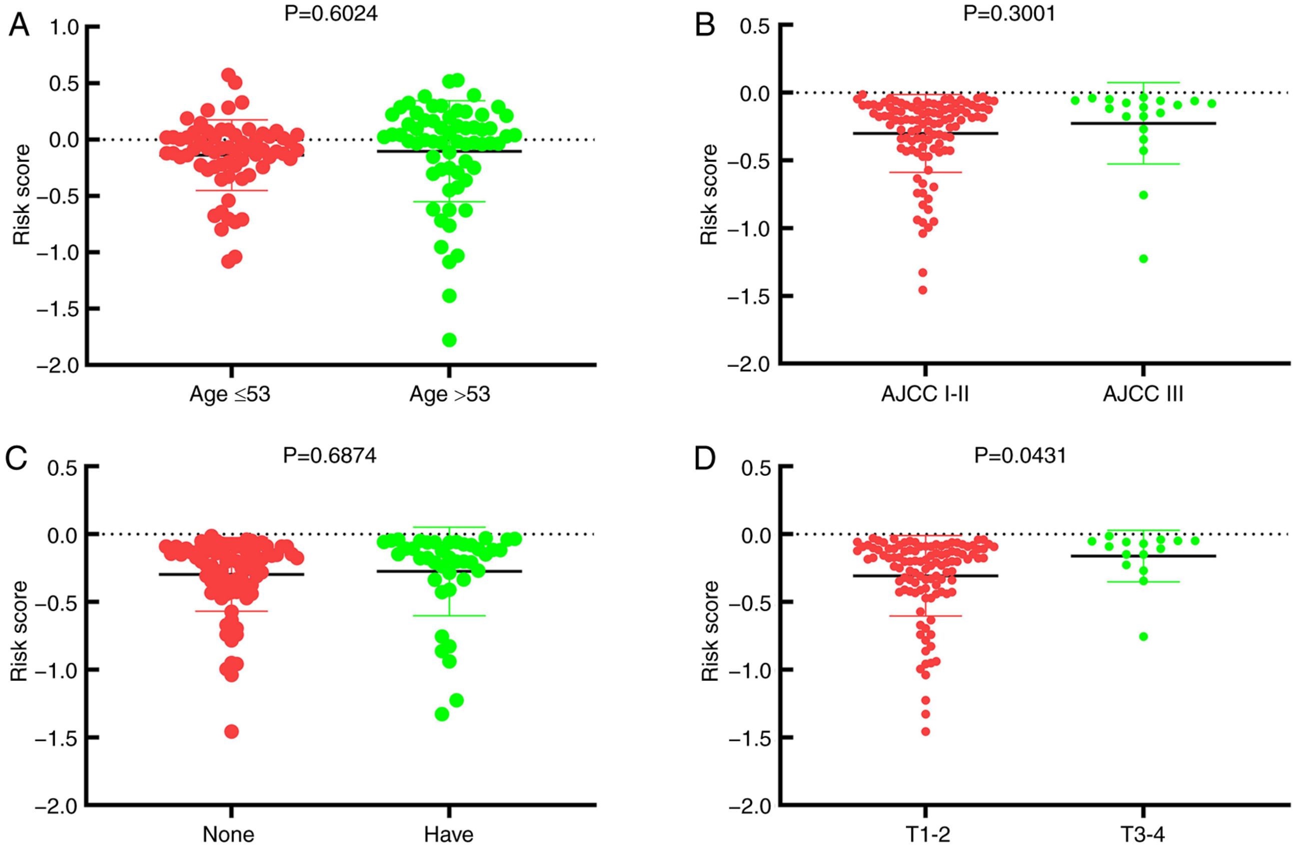

Figure S5. Validation of the accuracy of the prognostic model. (A) Receiver operating characteristic curve of the prognostic model compared among age, AJCC stage, T stage, N stage and risk score. (B) A nomogram based on age, AJCC, T and N stages and risk score. AJCC, American Joint Committee on Cancer; AUC, area under the curve; T, tumour; N, lymph node.

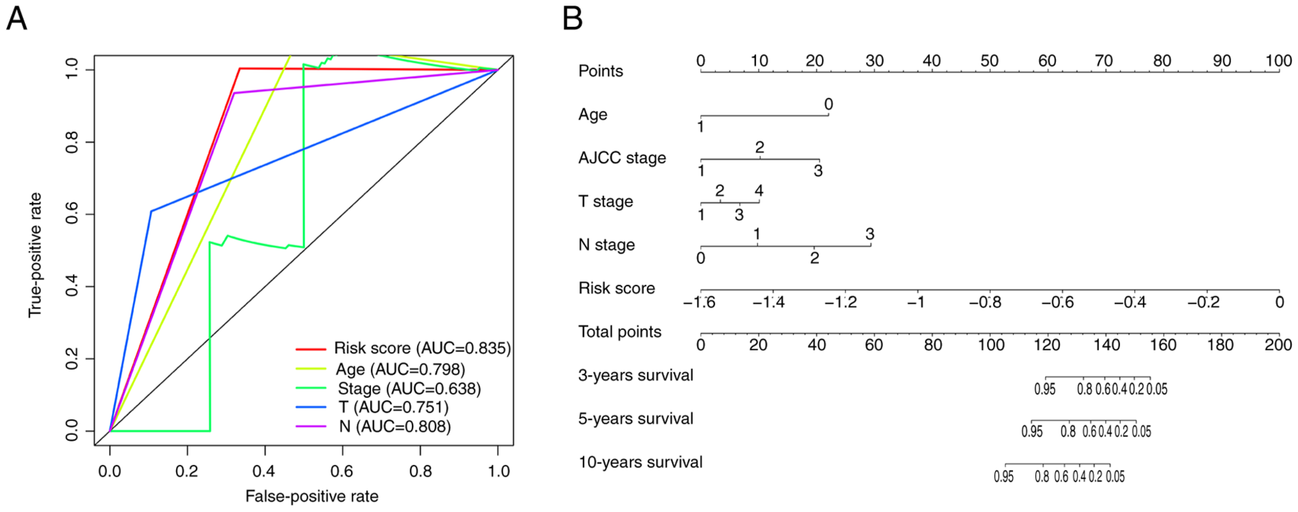

Figure S6. Validation of survival-associated IRGs expression in TNBC tissues by immunohistochemistry. In TNBC tissues with high expression levels of (A) $CD8^+$, high expression levels of (B) CXCL13 and (C) TAPBPL, while low expression level of (D) LTBP2 and (E) PGF expression were also seen. In TNBC tissues with low expression levels of (F) $CD8^+$, low expression levels of (G) CXCL13 and (H) TAPBPL, while high expression level of (I) LTBP2 and (J) PGF expression were observed (scale bar, 50 $\mu$m). CXCL13, C-X-C chemokine motif ligand 13; TAPBPL, transporter associated with antigen processing binding protein-like; TNBC, triple-negative breast cancer; LTBP2, latent TGF-β binding protein 2; PGF, placental growth factor.