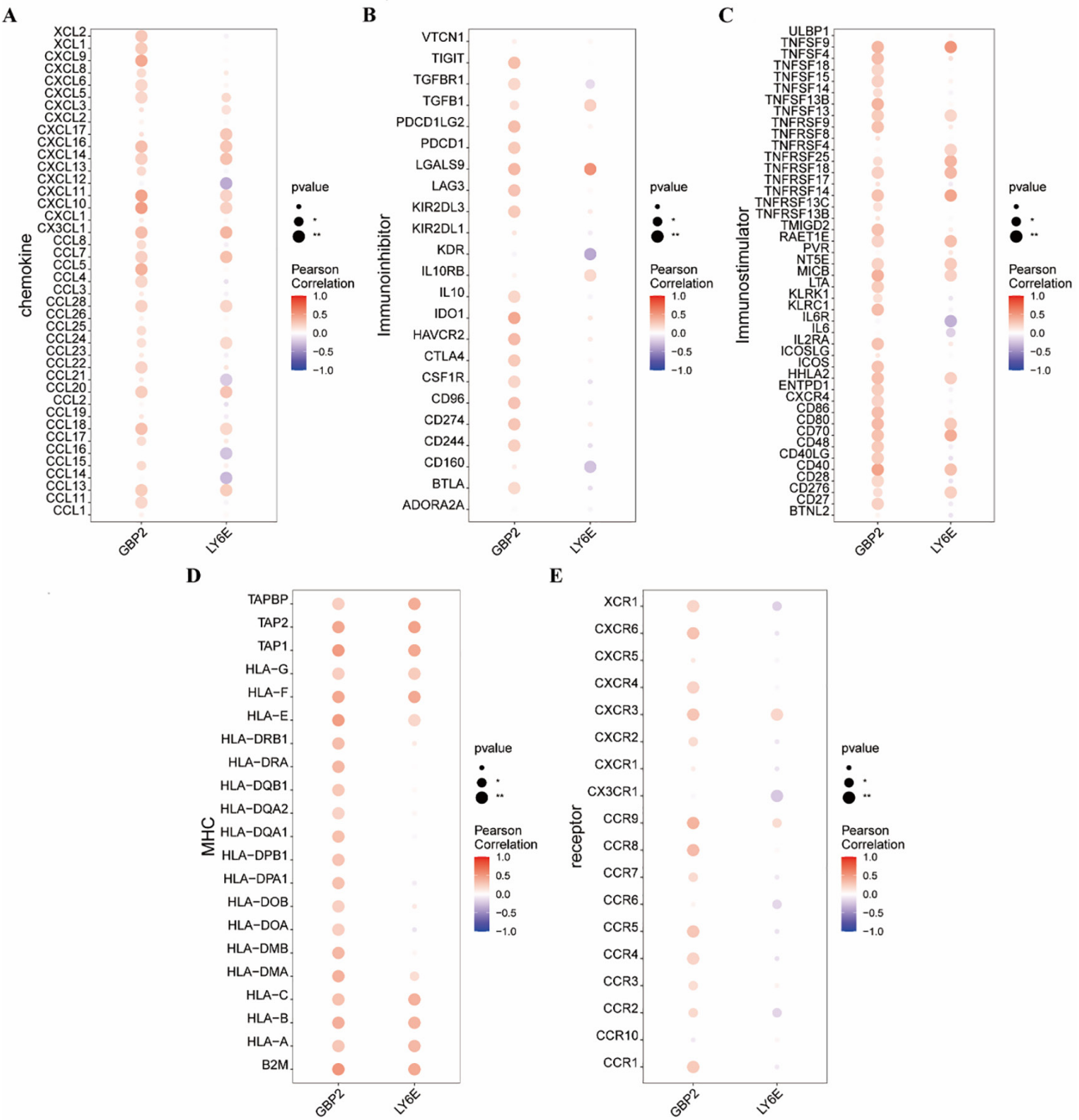

Figure S1 Correlation analysis of key genes with various immune factors obtained from TISIDB database. (A) Heatmap showing the correlation between GBP2 and LY6E with chemokines, including CCL and CXCL families. (B) Heatmap showing the correlation between GBP2 and LY6E with immunoinhibitors, such as ADORA2A, BTLA, and CTLA4. (C) Heatmap showing the correlation between GBP2 and LY6E with immunostimulators, including CD27, CD28, and ICOS. (D) Heatmap showing the correlation between GBP2 and LY6E with MHC molecules, such as HLA-A, HLA-B, and TAP1. (E) Heatmap showing the correlation between GBP2 and LY6E with receptors, including CCR, CXCR, and XCR families. The color scale represents the Pearson correlation coefficients, with significant correlations indicated by asterisks (*P<0.05, **P<0.01). These analyses indicate that the key genes are closely related to immune cell infiltration levels and play important roles in the immune microenvironment.

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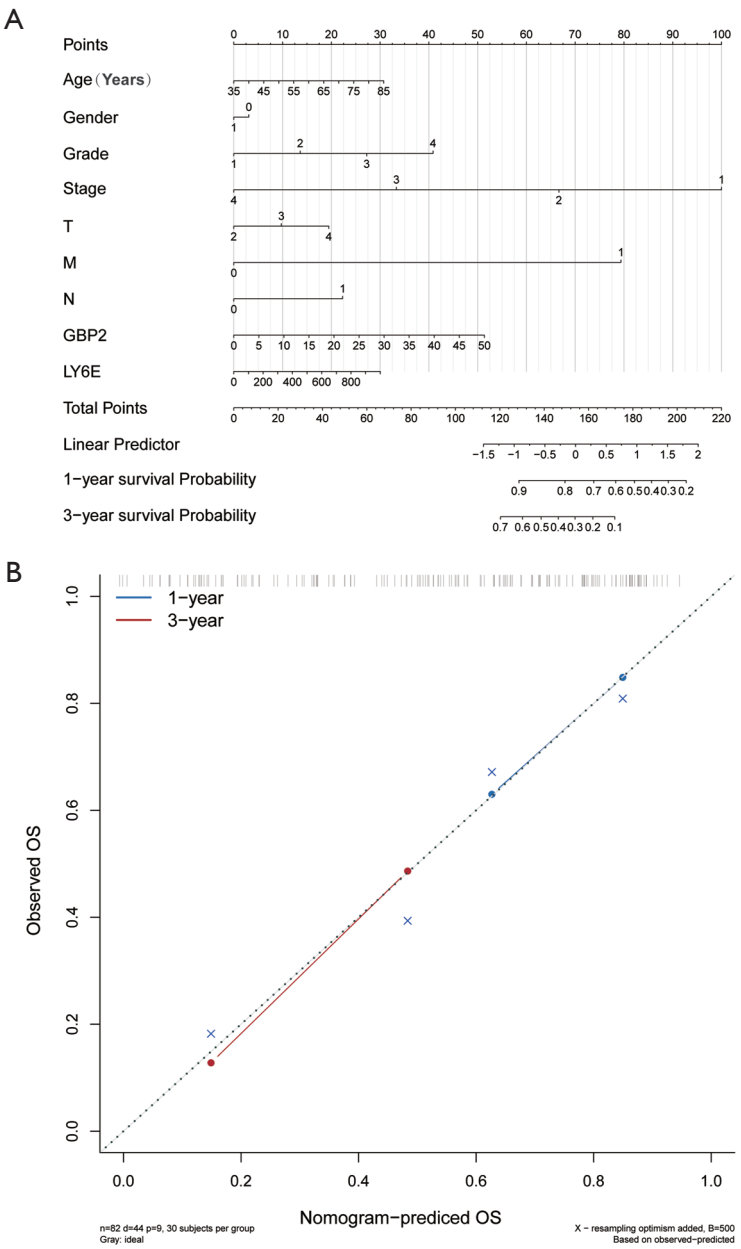

Figure S2 Development and validation of a nomogram for predicting OS in pancreatic cancer patients based on clinical indicators and key gene expression levels. (A) Nomogram illustrating the points assigned to various clinical factors and gene expressions (GBP2 and LY6E). Each factor is assigned a specific number of points based on the regression analysis results. The total points are then used to estimate the 1- and 3-year survival probabilities using the nomogram-predicted OS scale. The categorical variables were coded as follows: Gender (0= female, 1= male); Grade (1= G1, 2= G2, 3= G3, 4= G4); Stage (1= Stage I, 2= Stage II, 3= Stage III, 4= Stage IV); T stage (2= T2, 3= T3, 4= T4); N stage (0= N0, 1= N1); M stage (0= M0, 1= M1). (B) Calibration plot comparing the observed OS rates with the nomogram-predicted OS rates at 1- and 3-year intervals. The gray line represents the ideal scenario where the predicted probabilities perfectly match the observed probabilities. The black line shows the observed versus predicted OS rates based on the nomogram model. The close alignment between the two lines indicates that the nomogram model has good predictive accuracy. OS, overall survival.

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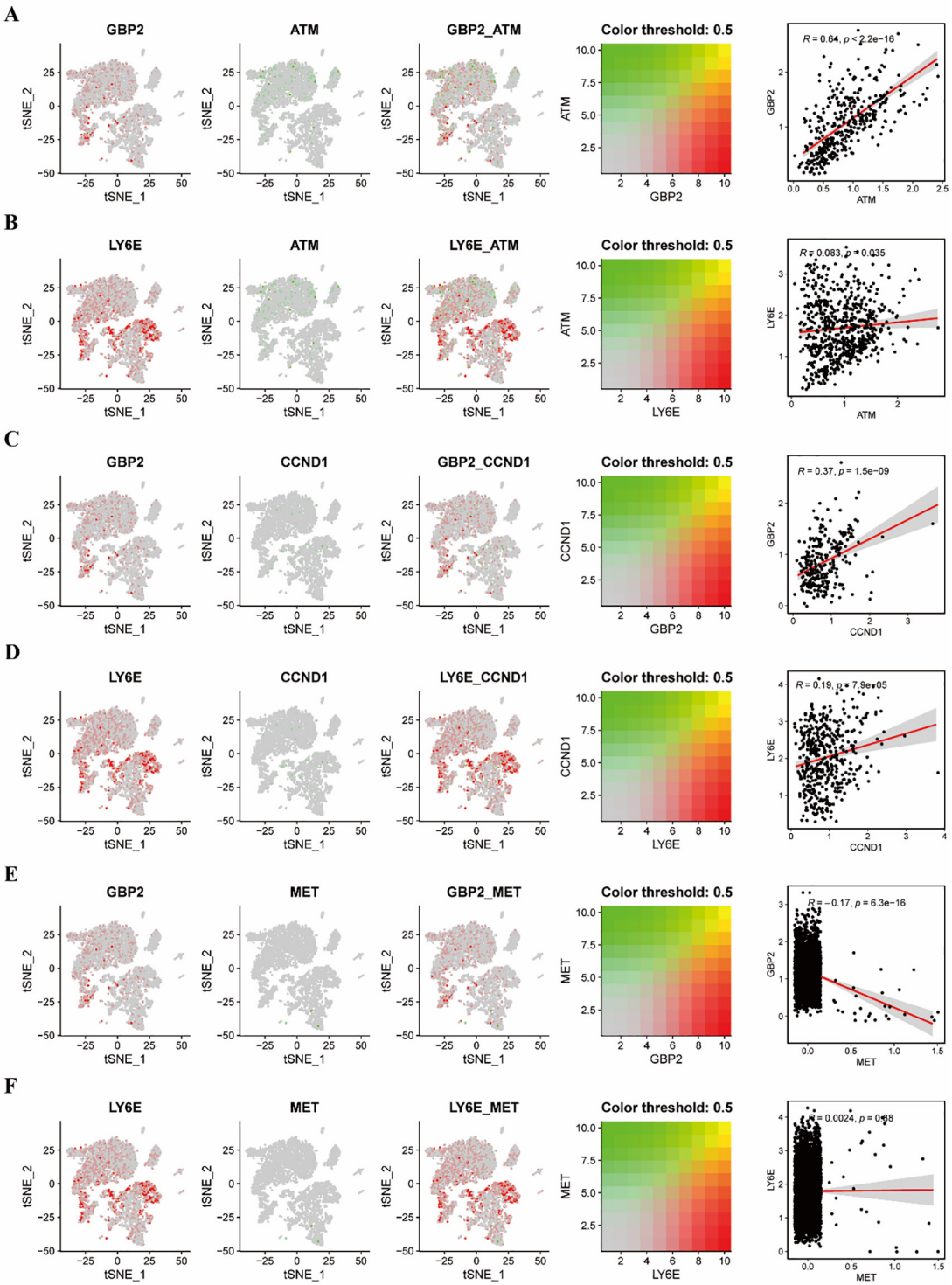

Figure S3 Interactions between key genes in the GeneCards database and genes associated with pancreatic cancer progression. (A) Co-expression analysis of ATM and GBP2 key genes in different cell types. (B) Co-expression analysis of ATM and LY6E key genes in different cell types. (C) Co-expression analysis of CCND1 and GBP2 key genes in different cell types. (D) Co-expression analysis of CCND1 and LY6E key genes in different cell types. (E) Co-expression analysis of MET and GBP2 key genes in different cell types. (F) Co-expression analysis of MET and LY6E key genes in different cell types.

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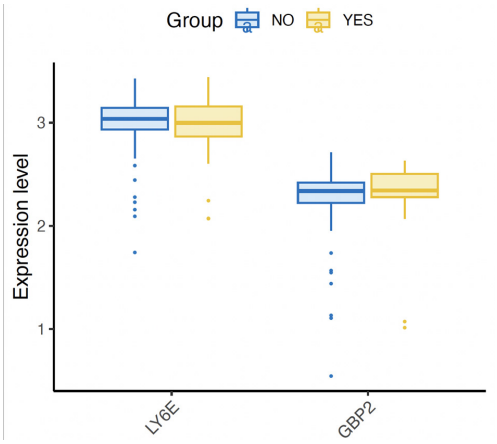

Figure S4 Box plots showing expression levels of key genes *LY6E* and *GBP2*. Non-diabetic patients (NO, blue) versus diabetic patients (YES, n=34, yellow).

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