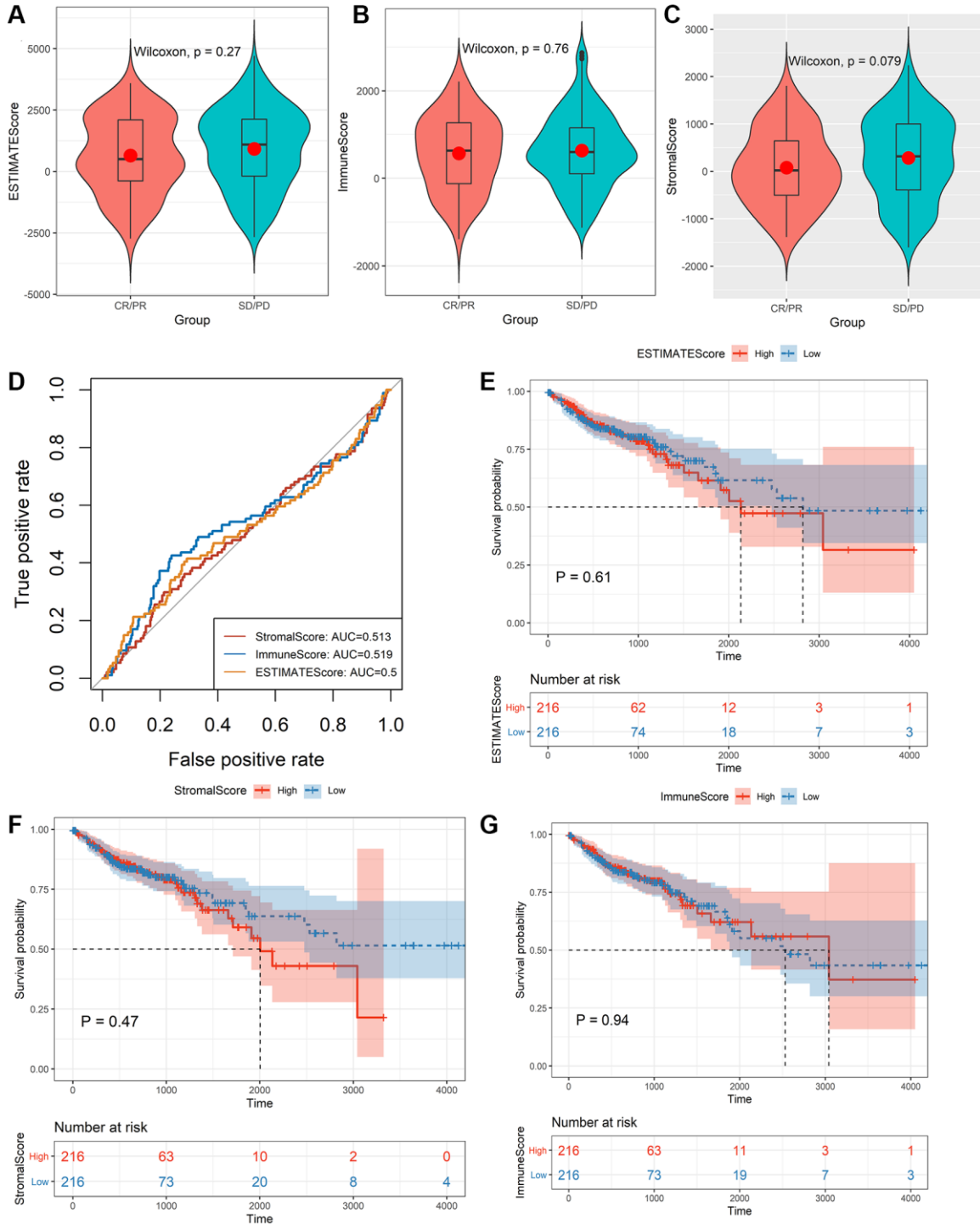
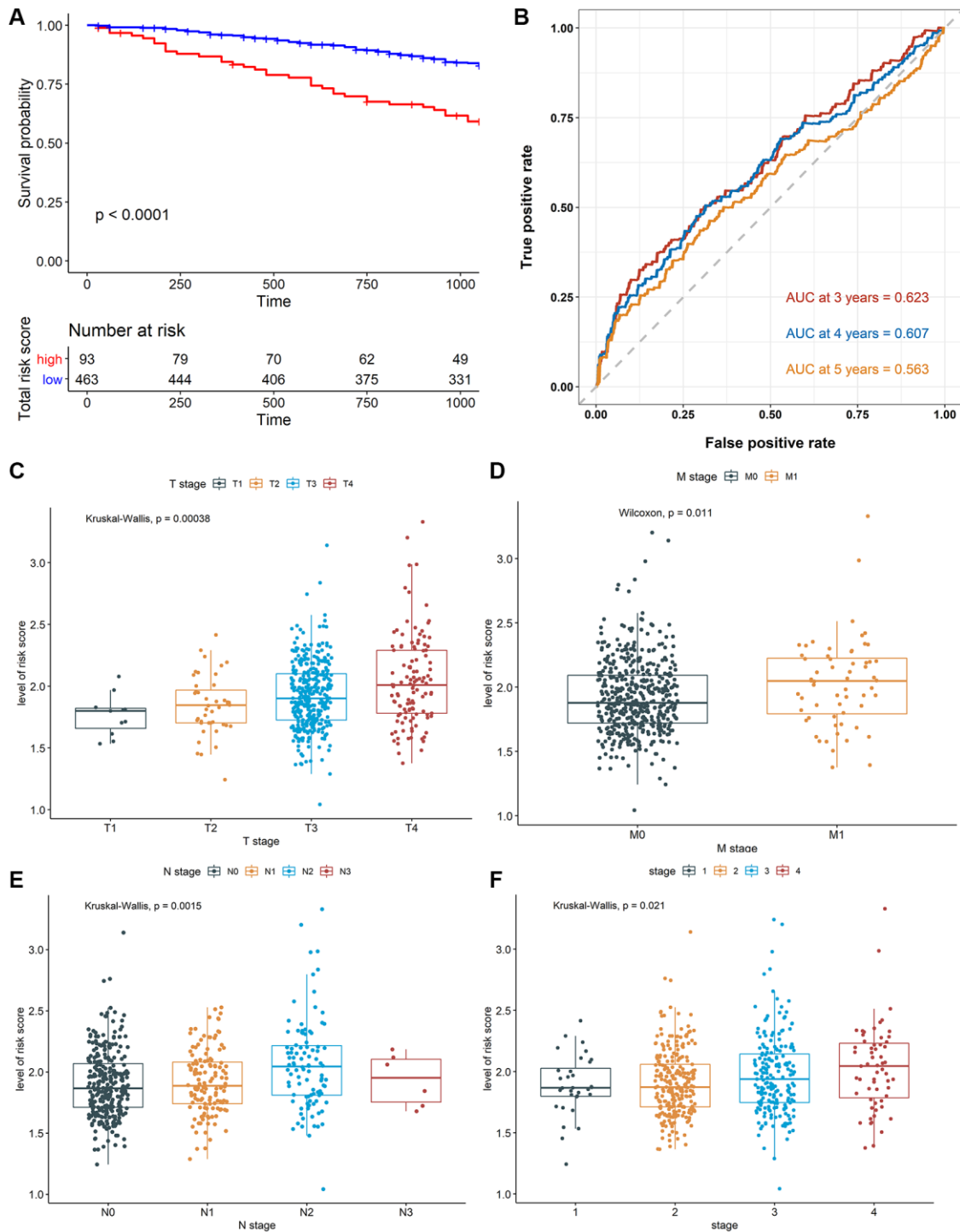


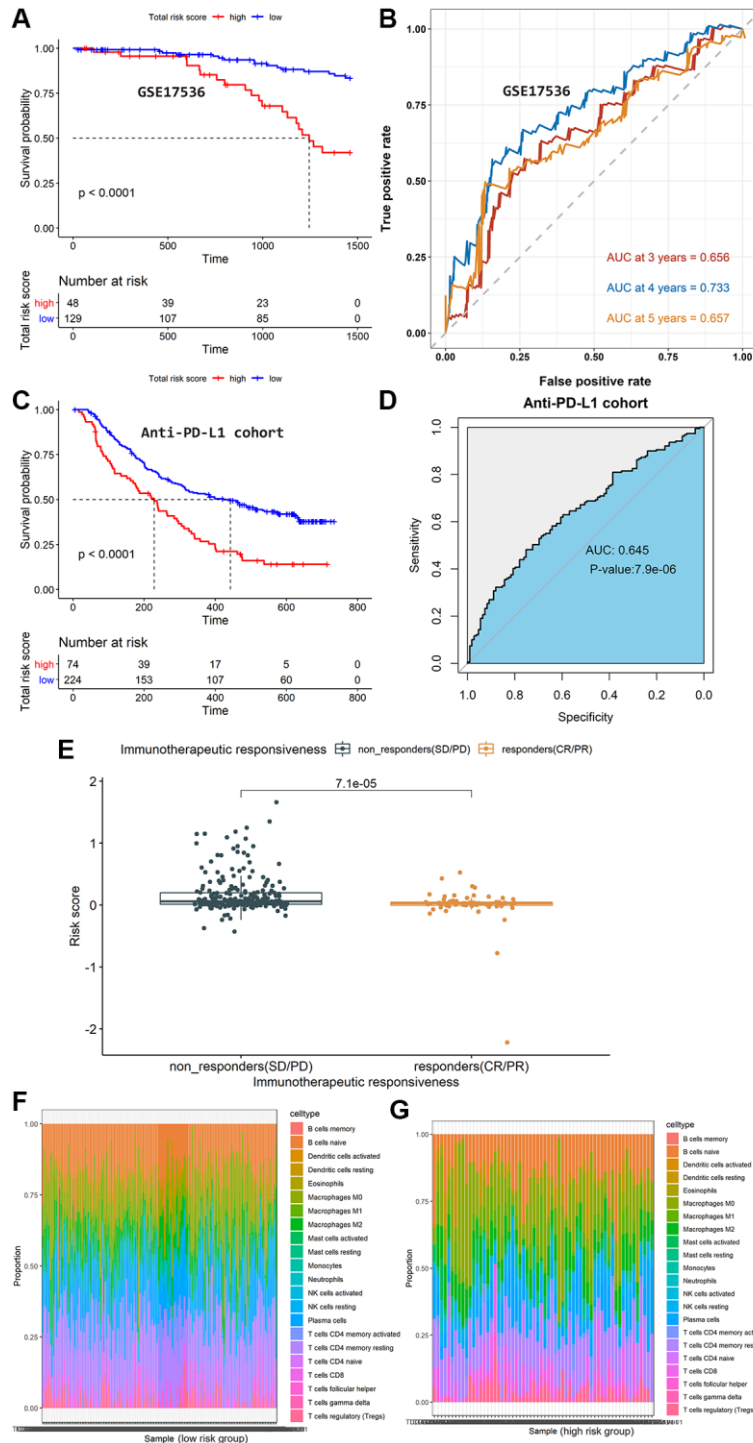
SUPPLEMENTARY FIGURES



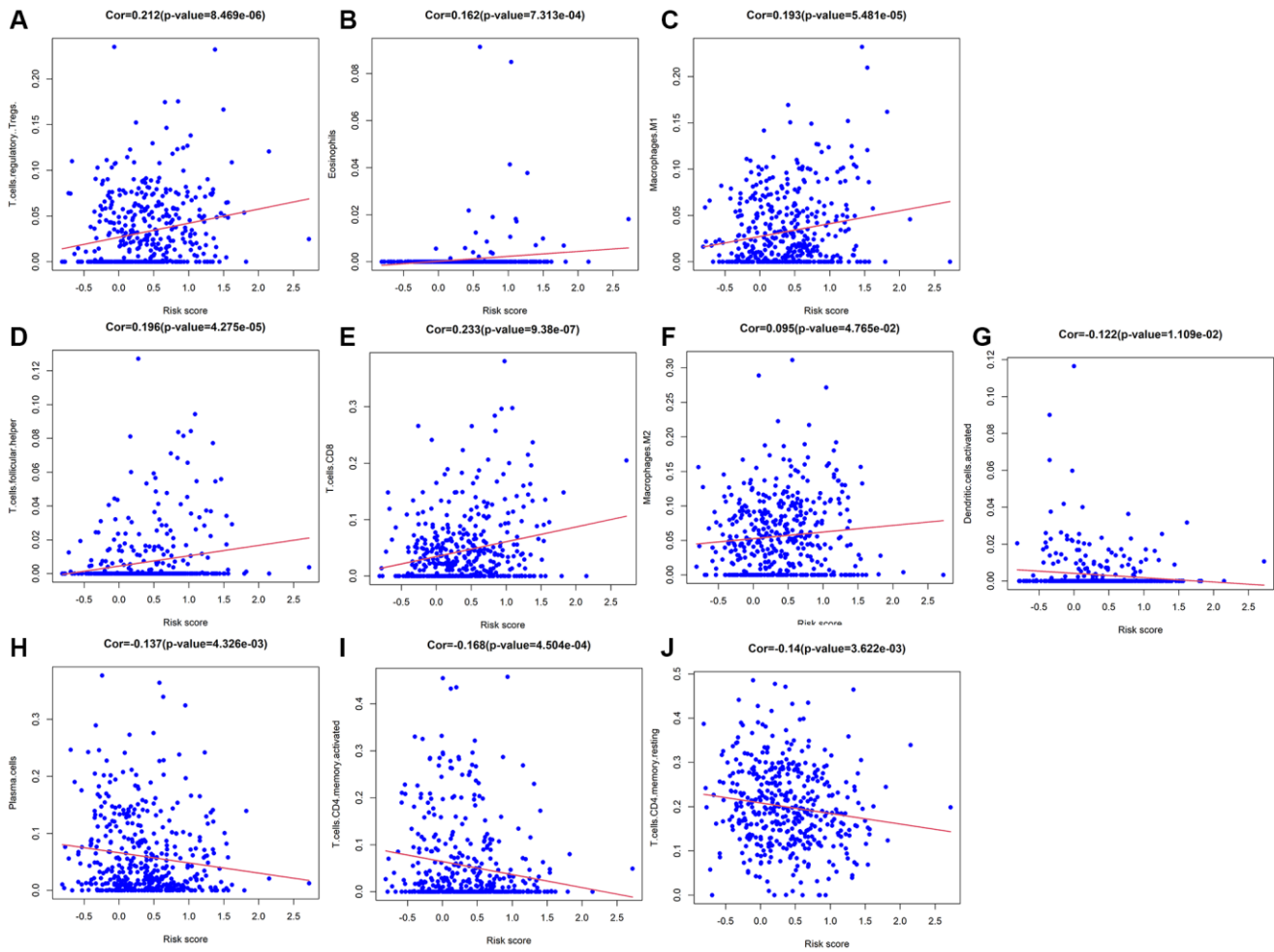
Supplementary Figure 1. Construction and assessment of estimate-stromal-immune scores model. (A–C) Comparison of the differences of the estimate-stromal-immune scores between responders and non-responders using Wilcoxon test. **(D)** The AUCs of the estimate-stromal-immune scores model. **(E–G)** Kaplan-Meier curves analyses of the association between the scores (estimate, stromal, or immune) and patients’ OS.



Supplementary Figure 2. Validation of the identified immune-related prognostic signatures using GSE39582. (A) Kaplan-Meier curve analysis. (B) Time-dependent ROC curve analysis. (C–F) Comparison of the association between the IRIRScore of the colon cancer patients and the clinical-pathological characteristics, including (C) T stages, (D) M stages, (E) N stages and (F) advanced pathological stages.



Supplementary Figure 3. Validation of the identified immune-related prognostic signatures using GSE17536 and anti-PD-L1 cohort. (A) Kaplan-Meier curve analysis using GSE17536. (B) Time-dependent ROC curve analysis using 17536. (C) Kaplan-Meier curve analysis using anti-PD-L1 cohort. (D) Time-dependent ROC curve analysis using anti-PD-L1 cohort. (E) Comparing the difference in the risk score between responders and non-responders in anti-PD-L1 cohort. (F–G) The profiles of relative proportions of immune infiltration. (F) Patients in low-risk group, (G) patients in high-risk group.



Supplementary Figure 4. The correlation between IRIScore and the proportions of immune cells infiltrating, including (A) T cells regulatory (Tregs), (B) Eosinophils, (C) Macrophages M1, (D) T cells follicular helper, (E) T cells CD8, (F) Macrophages M2, (G) Dendritic cells activated, (H) Plasma cells, (I) T cells CD4 memory activated, (J) T cells CD4 memory resting.