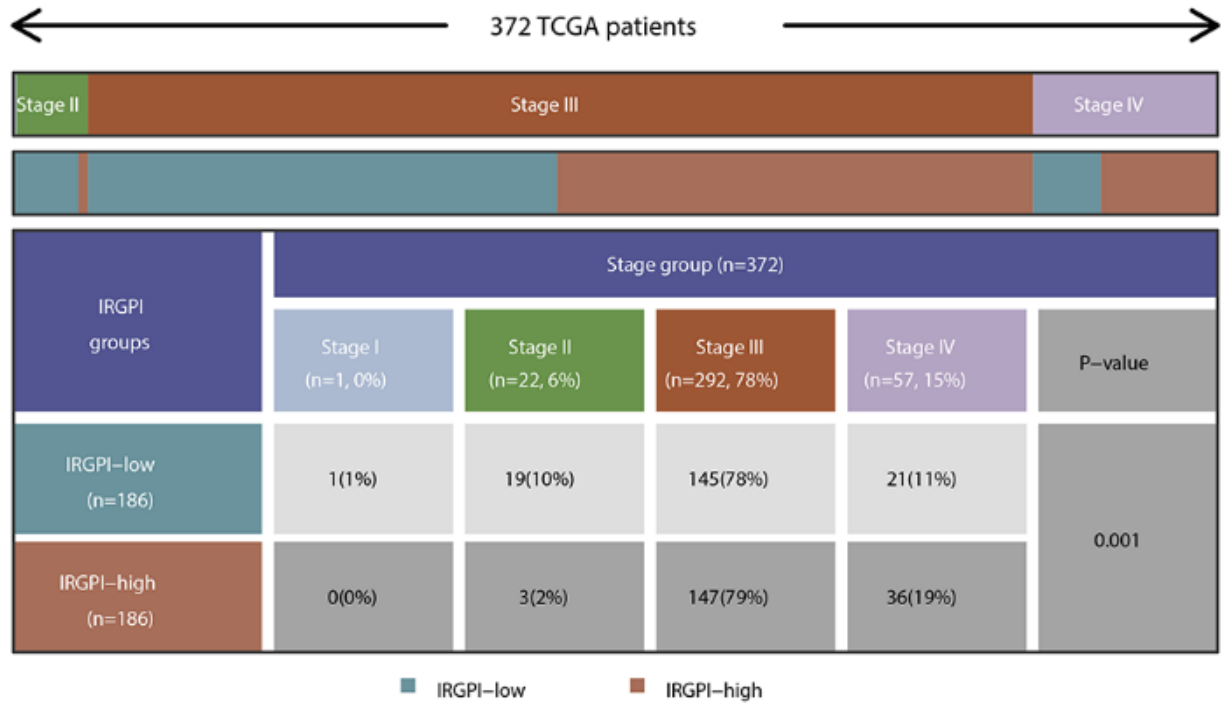
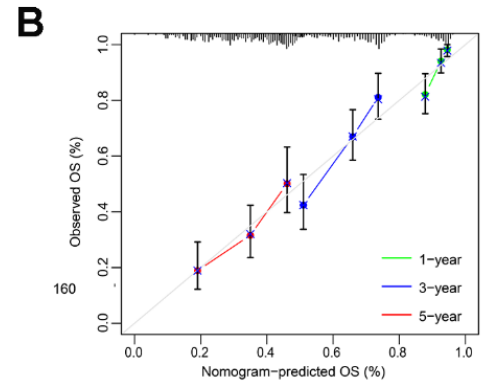
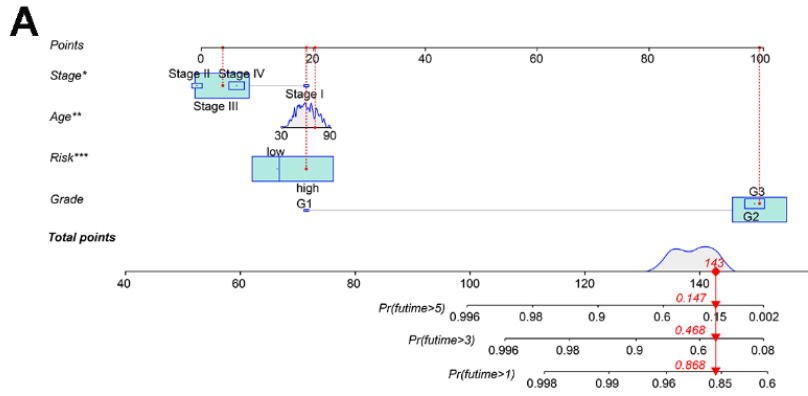


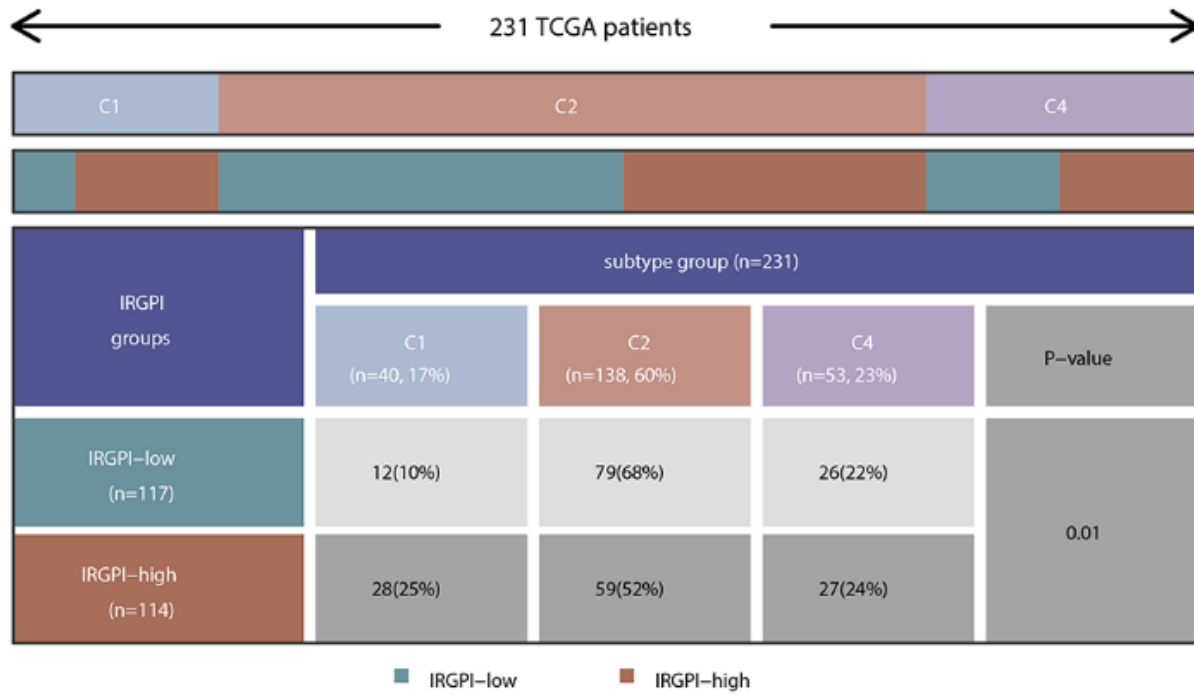
Supplementary Figure S1. Analysis of IRLRPI with patient staging. Heat map and table showing the relationship between clinical stage and IRLRPI distribution of ovarian cancer patients



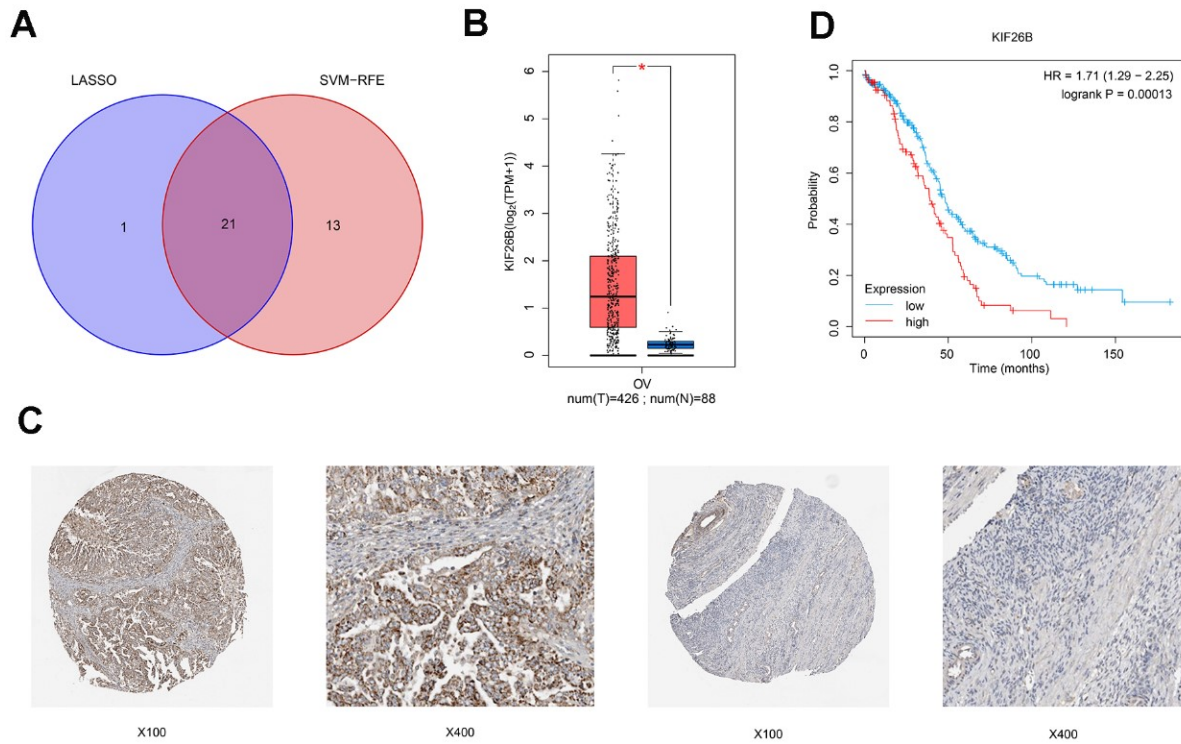
Supplementary Figure S2. Multiple factors were combined to create nomogram to assess patient prognosis. The developed nomogram (A) and calibration curves (B) of the nomogram



Supplementary Figure S3. Analysis of IRLRPI with patient immune status. Heat map and table showing the relationship between the distribution of immune subtypes (C1: wound healing; C2: IFN- γ dominant; C4: lymphocyte depleted) and IRLPI in ovarian cancer patients

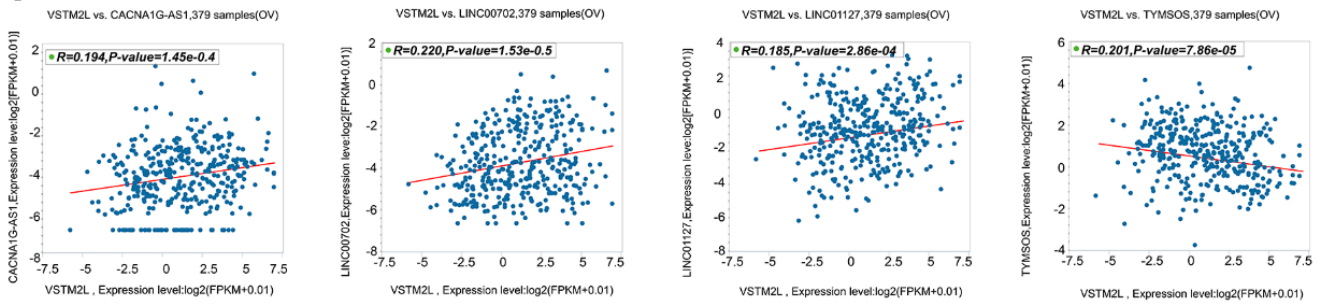


Supplementary Figure S4. IRLRPI typing-related marker KIF26B in ovarian cancer **(A)** Venn diagram of the intersection of the genes selected by both LASSO and SVM-RFE methods. **B** – Box plot of the difference in KIF26B expression between normal and tumor tissues (\log_2 fold change > 1 ; $p < 0.05$). **C** – Pathological section of KIF26B with TCGA ovarian cancer and GTEx normal ovaries in the HPA database. **D** – K-M curves of survival differences between high and low KIF26B expression in ovarian cancer patients



Supplementary Figure S5. Scatter plots depicting expression correlations between IRLRPI feature genes and the lncRNAs incorporated in IRLRPI construction. **A** – Scatter plot of expression correlation between VSTM2L and the lncRNA used in IRLRPI construction. Red line represents fitted regression curve. Correlation coefficient (r) indicates: $r > 0$ denotes a positive correlation between variables, while $r < 0$ signifies a negative correlation. **B** – Scatter plot of expression correlation between KIF26B and the lncRNA used in IRLRPI construction. The correlation coefficient (r) is shown

A



B

