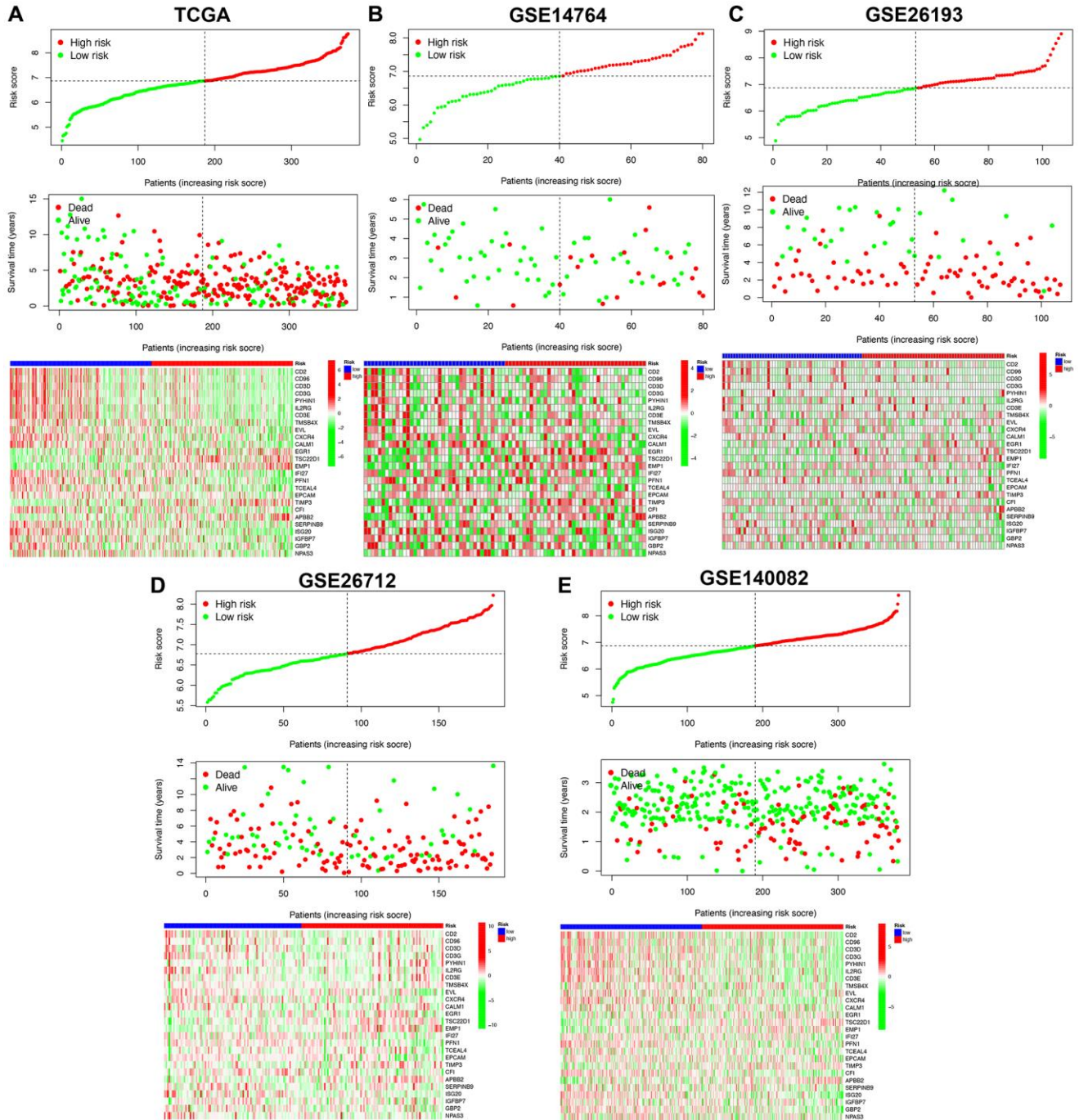
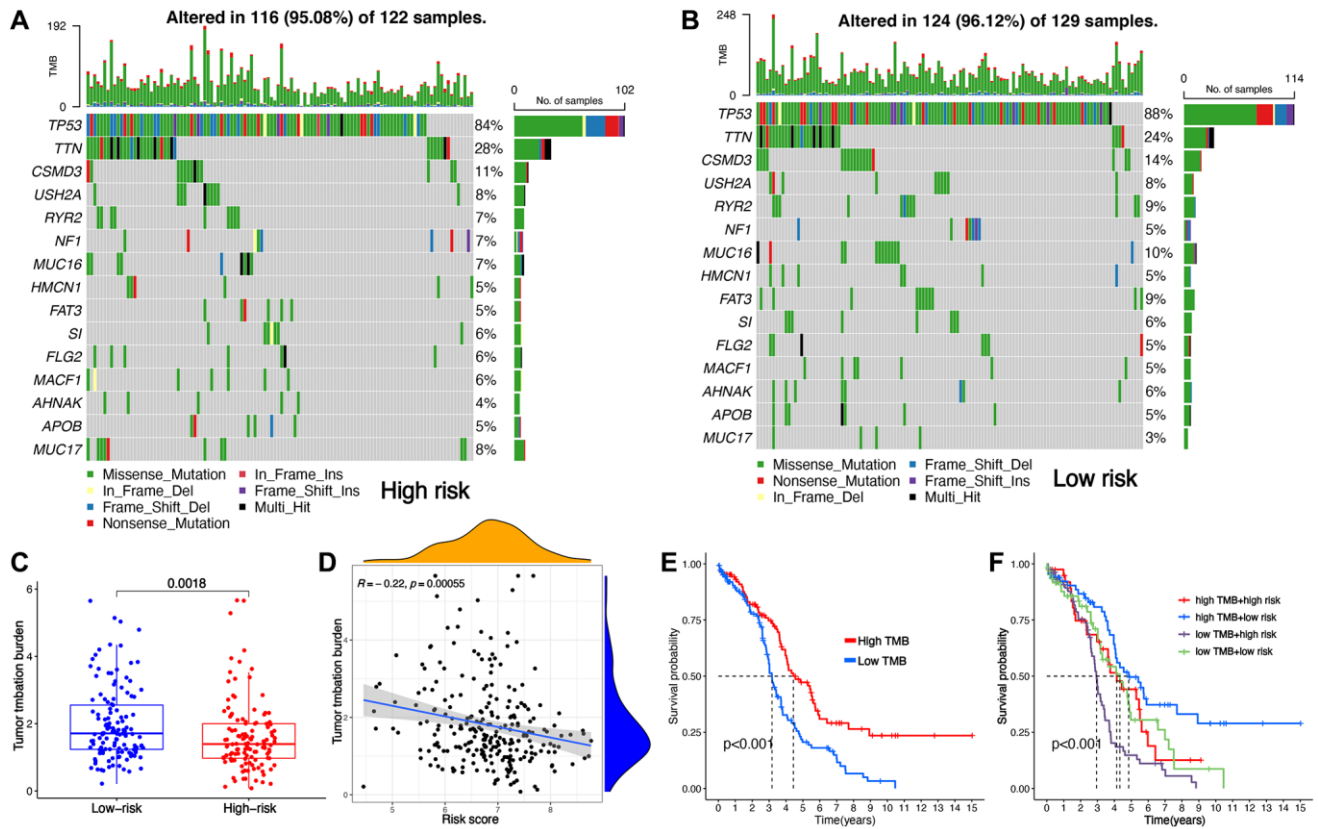


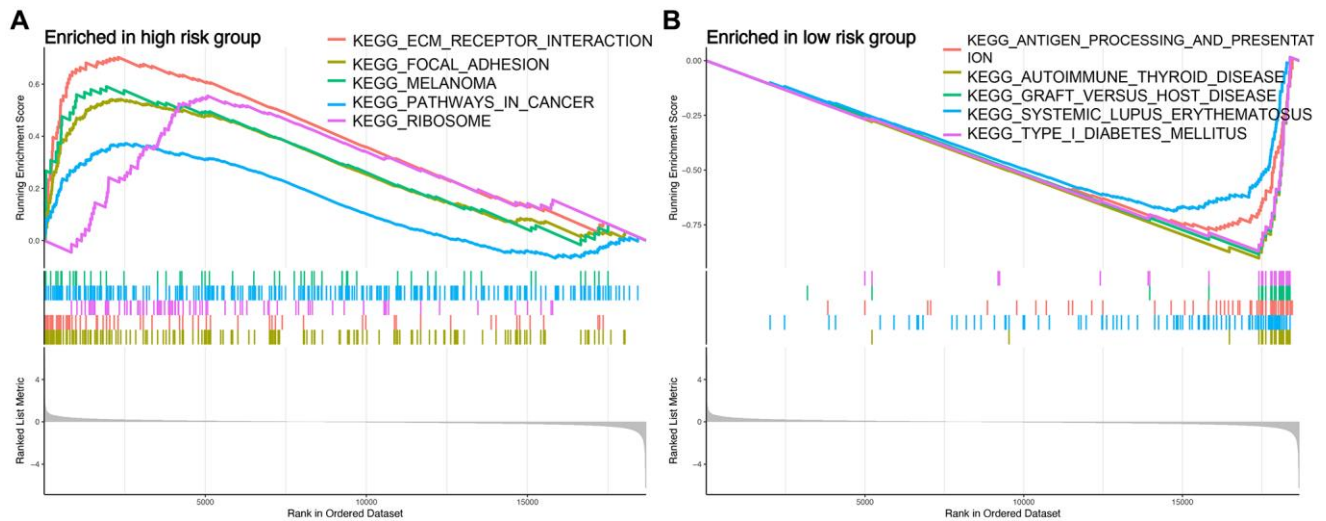
SUPPLEMENTARY FIGURES



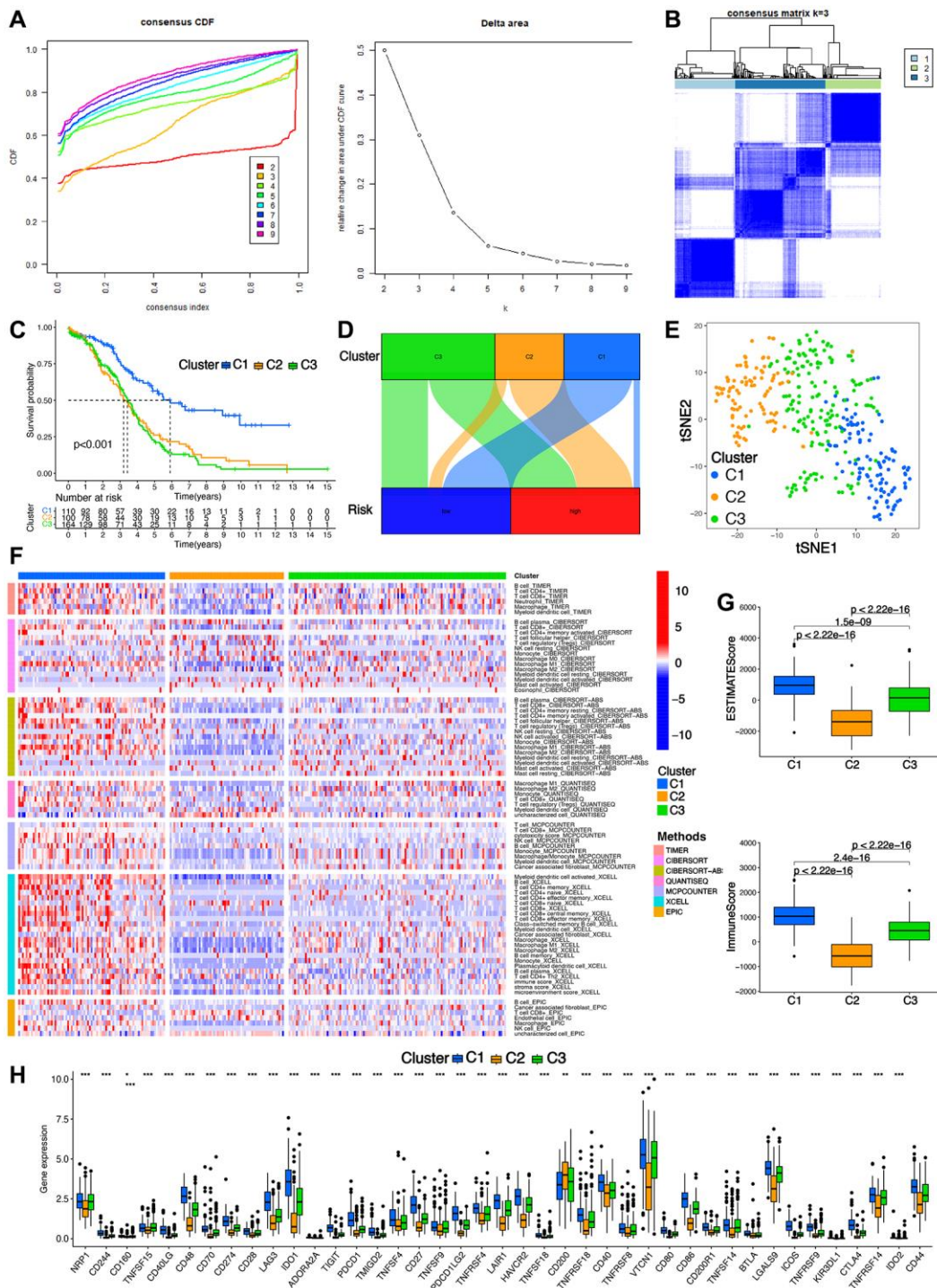
Supplementary Figure 1. Prognostic T cell-related signature (TRS) developed with integrative machine learning analysis. The risk score, survival status, and gene expression of TRS in TCGA (A), GSE14764 (B), GSE26193 (C), GSE26712 (D) and GSE140082 (E) cohort.



Supplementary Figure 2. Dissection of T cell-related signature (TRS)-based genetic mutation. (A, B) Genetic landscape in different risk score group of ovarian cancer. (C, D) The correlation between tumor mutational burden and risk score in ovarian cancer. (E, F) The overall survival curve in ovarian cancer patients with different tumor mutational burden and risk score.



Supplementary Figure 3. T cell-related signature (TRS)-based GSEA analysis. The KEGG pathways associated enriched items in high (A) and low (B) risk score group.



Supplementary Figure 4. Unsupervised clustering in different risk score group of ovarian cancer. (A, B) The consensus CDF, delta area and heatmap in unsupervised clustering analysis. (C) Survival curve of different clusters of ovarian cancer patients. (D) tSNE analysis demonstrated significant differences of gene profile of three clusters. (E) The correlation between risk score and cluster. The level of most of immune cells (F), tumor microenvironment score (G), and immune checkpoints (H) in different clusters of ovarian cancer patients.

