

Fig. S1 Comprehensive analyses involved in the article. (a, b) PCA plot and *t*-SNE analysis for OvCa in TCGA cohort, respectively. (c, d) PCA plot and *t*-SNE analysis for OvCa in ICGC cohort, respectively. (e, f) PCA plot and *t*-SNE analysis for OvCa in GEO cohort, respectively. (g) Univariate (upper) and multivariate (lower) analysis for ICGC cohort. (h) Univariate (upper) and multivariate (lower) analysis for GEO cohort. (i, j) Nomograms for predicting the OS of ICGC and GEO cohorts, respectively. (k, l) Calibration curves for internal verification nomogram in ICGC and GEO cohorts, respectively. PCA: principal component analysis; *t*-SNE: *t*-stochastic neighbor embedding; OvCa: ovarian cancer; TCGA: The Cancer Genome Atlas; ICGC: International Cancer Genome Consortium; GEO: Gene Expression Omnibus.

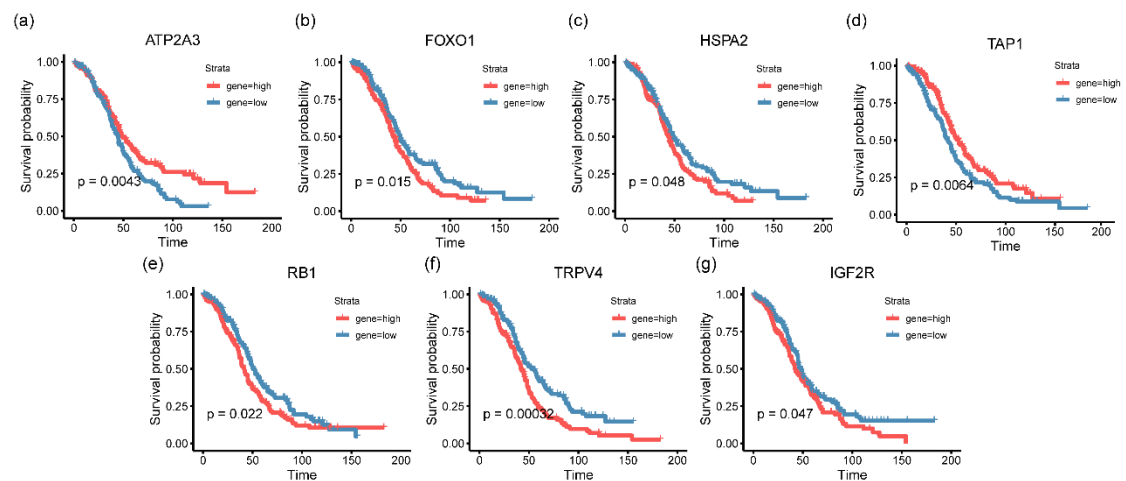


Fig. S2 K-M curves of seven prognostic genes related to ER stress. $P < 0.05$ were considered statistically significant. K-M: Kaplan-Meier curve.

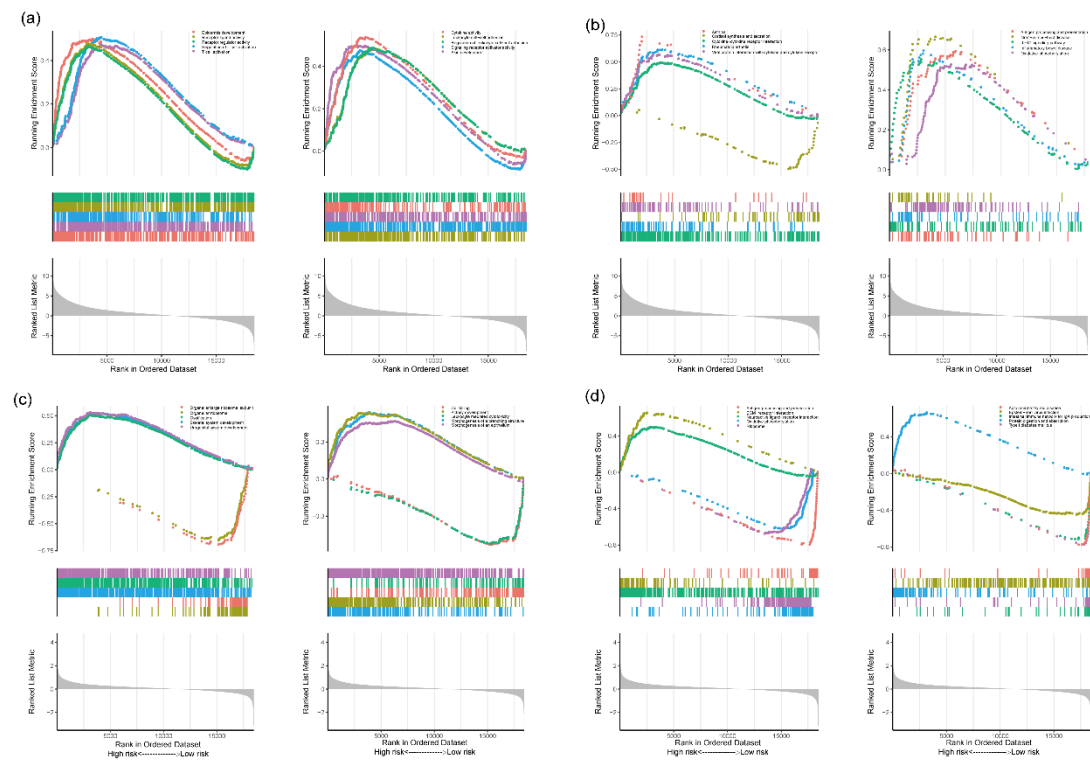


Fig. S3 Functional annotation enrichment via GSEA (top 10 in each group). (a) GSEA approach for GO enrichment. (b) GSEA approach for KEGG pathways. (c, d) GO enrichment and KEGG pathways based on the risk distinction, respectively. GSEA: gene set enrichment analysis; GO: Gene Ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes.