



**Figure S1** Identification of prognostic ICD genes. (A) Scale independence and mean connectivity plots of soft threshold power. (B) Scatter plot of gene significance (GS) and module membership (MM) of blue module.

**Table S1** Comparison of previous studies on machine learning applications in OC prognosis

Methodology	Key findings	Relation to our work
Traditional statistical methods	Identified basic prognostic factors without deep interaction analysis	Our study used advanced ML techniques to investigate the interactions in depth
Basic machine learning models	Applied ML to genomic data with limited algorithmic depth	A range of complex algorithms are used handle high-dimensional data
Single-algorithm machine learning	Focused on one algorithm, missing potential insights from ensemble methods	Our framework integrates multiple algorithms to enhance predictive accuracy
Combination of statistical and basic ML methods	Explored combined approaches but lacked complexity and integration	A comprehensive 101-algorithm combination is used for detailed analysis

ML, machine learning; OC, ovarian cancer; ICD, immunogenic cell death.