

Table S1. Performance of models and protein biomarkers

	Train		Valid	
	Specificity	Sensitivity	Specificity	Sensitivity
CA125	0.980 (0.897–0.997)	0.750 (0.598–0.858)	1.000 (0.867–1.000)	0.714 (0.500–0.862)
	0.961 (0.868–0.989)	0.775 (0.625–0.877)	0.960 (0.805–0.993)	0.714 (0.500–0.862)
	0.941 (0.841–0.980)	0.825 (0.681–0.913)	0.960 (0.805–0.993)	0.762 (0.549–0.894)
HE4	0.999 (0.930–1.000)	0.750 (0.598–0.858)	0.960 (0.805–0.993)	0.714 (0.500–0.862)
	0.961 (0.868–0.989)	0.775 (0.625–0.877)	0.920 (0.750–0.978)	0.857 (0.654–0.950)
	0.941 (0.841–0.980)	0.875 (0.739–0.945)	0.920 (0.750–0.978)	0.905 (0.711–0.973)
Stacked	0.980 (0.897–0.997)	0.450 (0.307–0.602)	1.000 (0.867–1.000)	0.571 (0.365–0.755)
	0.961 (0.868–0.989)	0.675 (0.520–0.799)	0.920 (0.750–0.978)	0.807 (0.654–0.950)
	0.941 (0.841–0.980)	0.775 (0.625–0.877)	0.920 (0.750–0.978)	0.855 (0.711–0.973)
Combined	0.999 (0.930–1.000)	0.800 (0.652–0.895)	0.960 (0.805–0.993)	0.805 (0.711–0.973)
	0.961 (0.868–0.989)	0.850 (0.709–0.929)	0.960 (0.805–0.993)	0.857 (0.711–0.973)
	0.941 (0.841–0.980)	0.955 (0.835–0.986)	0.880 (0.700–0.958)	0.950 (0.845–1.000)

Table S2. Performance of the model in different subgroups

Subgroups	AUC(95%CI)	Sensitivity(95%CI)
Stage,n		
Early	0.938(0.864, 0.988)	72.2%(46.5%-90.3%)
Advanced	0.991(0.974, 1.000)	97.7%(87.7%-99.9%)
Subtypes,n		
Serous	0.991(0.987, 1.000)	97.1%(85.3%-99.9%)
Mucinous	0.944(0.854, 1.000)	75.0%(68.0%-93.2%)
Endometrioid	0.984(0.955, 1.000)	88.9%(55.5%-99.7%)
Clear cell	0.925(0.801, 0.996)	80.0%(44.4%-97.5%)
Grade,n		
High	0.977(0.939, 1.000)	85.7%(42.1%-99.6%)
Intermediate	0.976(0.932, 1.000)	80.0%(71.3%-90.5%)
Low	0.977(0.942, 0.999)	93.5%(82.1%-98.6%)

Note: Sensitivity values were calculated when specificity was 96%.

Table S3. Standardized mean differences before and after matching

Variables		Before matching			After matching		
		Control	OC	SMD	Control	OC	SMD
Total,n		76	61		39	39	
Age	Mean	40.21	53.89	1.197	49.82	50.74	0.081
	SD	14.35	11.42		11.32	11.03	
BMI	Mean	22.81	21.47	-0.386	22.45	22.18	-0.086
	SD	2.82	3.2		2.54	2.8	

Figure S1. LASSO Coefficient Path Plot and MSE Plot

(A) LASSO coefficient path plot: Features with smaller contributions to the model are gradually eliminated as the penalty increases. Seven variables remain when $\log(\lambda) = -2$.
(B) Mean squared error (MSE) plot: The optimal value of λ is selected based on the minimum MSE, corresponding to a model with seven retained variables.

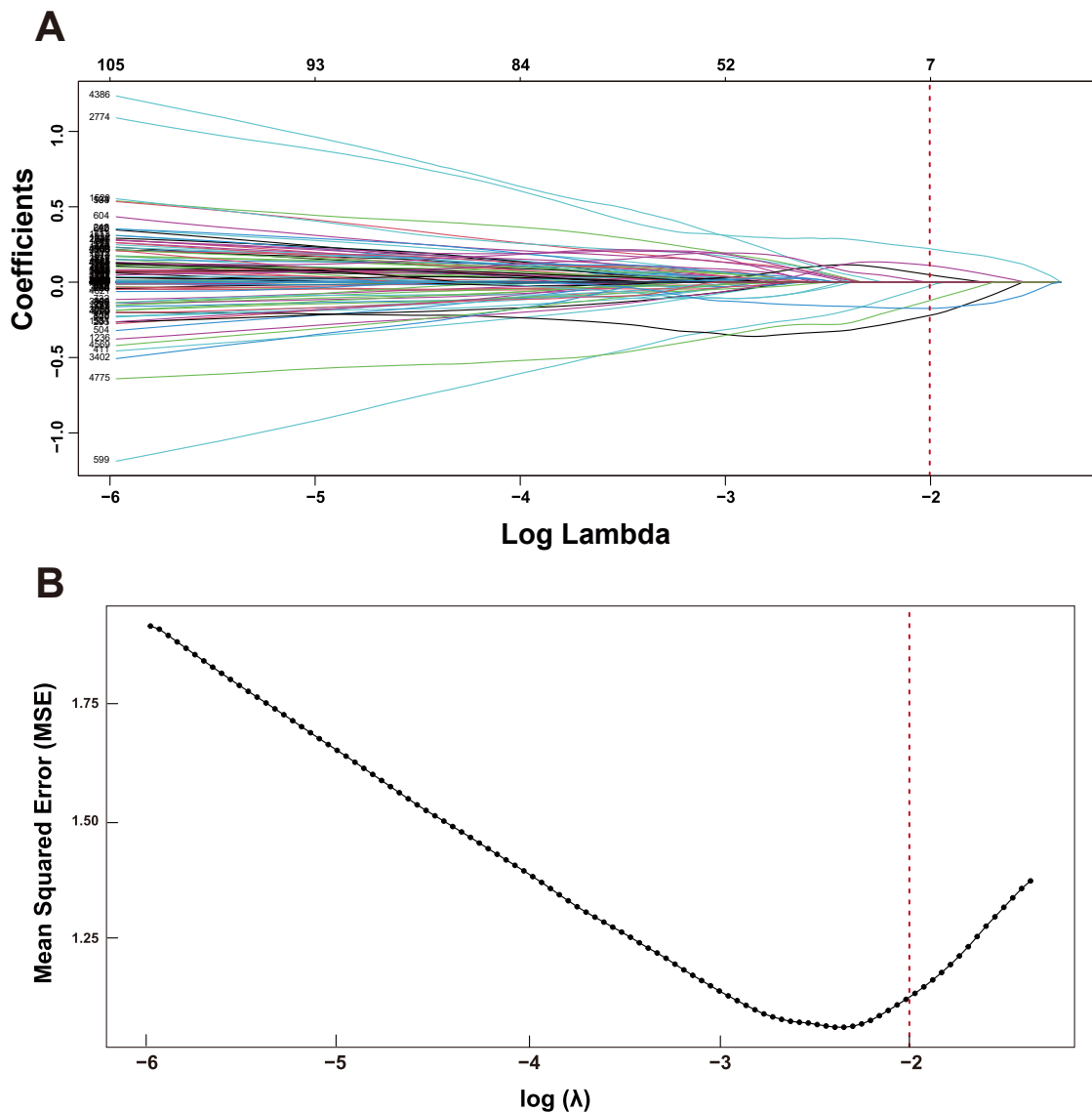


Figure S2. Permutation test

(A)Permuted AUC distribution in the training cohort. **(B)** Permuted AUC distribution in the independent validation cohort.
The dashed vertical line indicates the mean AUC under label permutation (chance level).

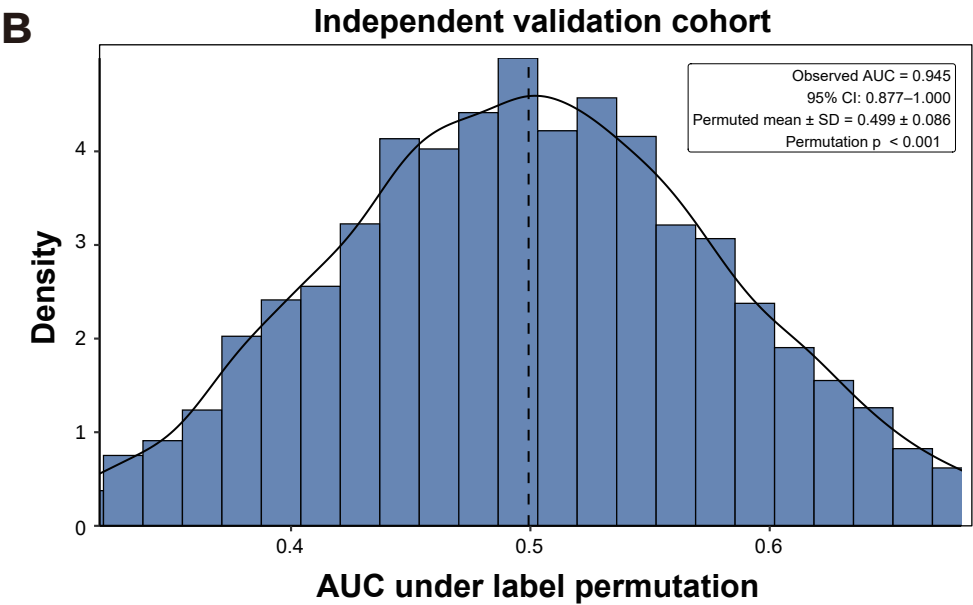
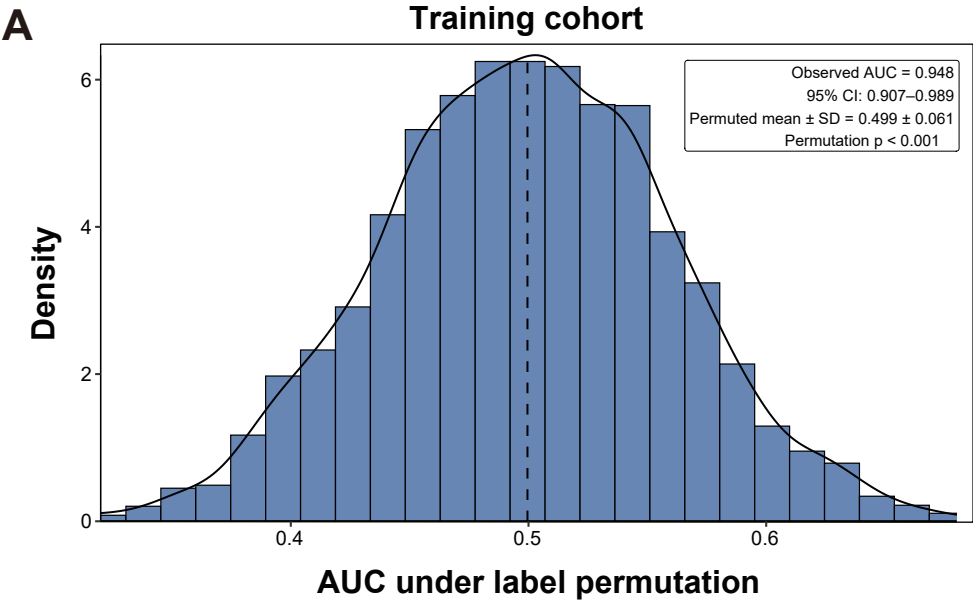


Figure S3. Performance assessment in the Early-Stage Ovarian Cancer Subgroup
(A) Calibration curve of the predictive model in the early-stage ovarian cancer subgroup from the validation dataset. Dotted line: apparent performance; solid line: bias-corrected performance after bootstrapping; dashed line: ideal calibration. **(B)** Decision curve analysis for the model in the early-stage ovarian cancer subgroup. The blue curve represents the model, the gray curve represents the treat-all strategy, and the black curve represents the treat-none strategy.

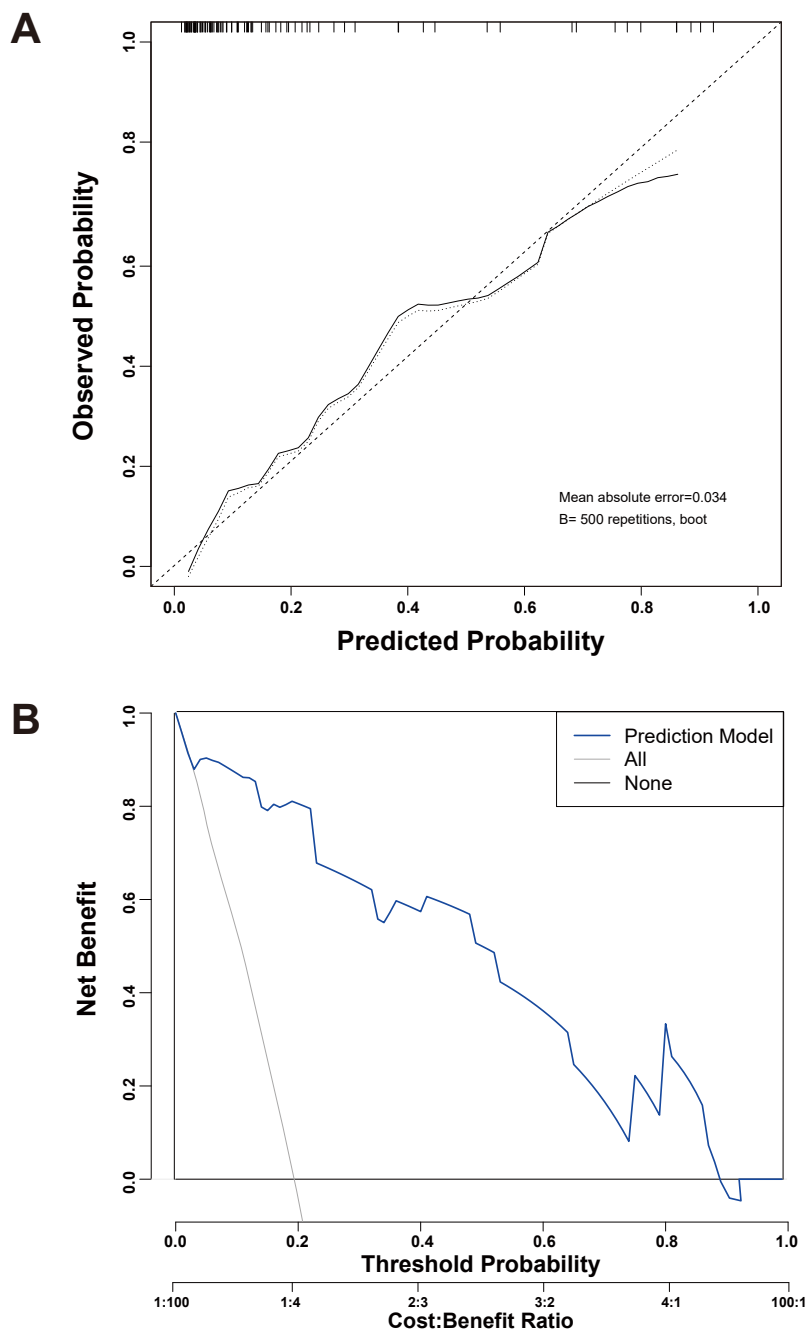


Figure S4. Comparison of Model Performance Before and After Propensity Score Matching

(A) ROC Curves and AUC Values before and after matching. **(B)** Diagnostic Metrics before and after PSM.

