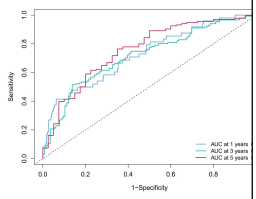
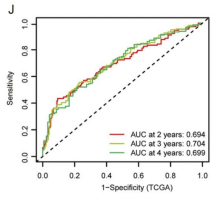
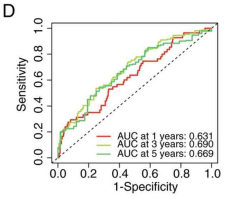
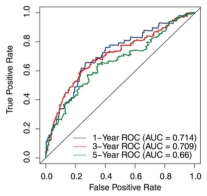
Integrating Functional Genomic Screens and Multi-Omics Data to Construct a Prognostic Model for Lung Adenocarcinoma and Validating SPC25	Multi-omics data-based modeling reveals tumorigenesis- and prognosis-associated genes with clinical potential in lung adenocarcinoma(PMC12604227)	A 4-cuproptosis-related lncRNA theragnostic signature predicts survival and immunotherapy response in patients with lung adenocarcinoma(PMC12598532)	Identification and validation of prognostic genes for lung adenocarcinoma prognosis based on PANoptosis-related genes(PMC12540239)
			
Our model achieved AUC values of 0.714, 0.709, and 0.66 for predicting 1-year, 3-year, and 5-year OS in TCGA LUAD patients, respectively.	The model achieved AUC values of 0.694, 0.704, and 0.699 for predicting 2-year, 3-year, and 4-year OS in TCGA LUAD patients, respectively.	The model achieved AUC values of 0.631, 0.690, and 0.699 for predicting 1-year, 3-year, and 5-year OS in TCGA LUAD patients, respectively.	The model achieved AUC values of 0.714, 0.709, and 0.66 for predicting 1-year, 3-year, and 5-year OS in TCGA LUAD patients, respectively.

In comparison with the other models, our model demonstrates significant advantages:

（1）Superior Short-Term Prediction: For the critical 1-year overall survival (OS) prediction, our model's AUC (0.714) is substantially higher than that of Model 3 (0.631), highlighting its exceptional capability for early risk stratification.

（2）Stable Mid-Term Prediction: For 3-year OS prediction, our model (AUC=0.709) also consistently outperforms both Model 2 and Model 3.

（3）0Comprehensive Time-Point Coverage: Unlike Model 2, our model provides predictions across the complete range from 1 to 5 years, making it more practical for a comprehensive assessment.

In conclusion, our model achieves the best overall performance in short- and mid-term predictions, establishing itself as a more reliable and comprehensive prognostic tool.