

Table SII. Comparisons between previous research and the present study.

First author/s, year	Topic	Cancer	Screening gene method	Modeling method	Set	Training	Test	ROC (1, 3 and 5 years)		TME	TMB	IC ₅₀	Experimental validation	(Refs.)
								Training	Test					
Zhao <i>et al</i> , 2024	Hypoxia and mitochondrial-related genes	LUAD	WGCNA	LASSO	TCGA 094	GSE31210; GSE72	0.721, 0.711 and 0.671	GSE31210: 0.756, 0.641 and 0.669; GSE72094: 0.672, 0.670 and 0.673	ssGSEA (checkpoint expression, 13 immune-related pathways)	Waterfall plot; TMB-related KM	Yes	None	(21)	
Jiang <i>et al</i> , 2023	Cuproptosis-anoikis-related genes	LUAD	Pearson correlation (>0.3)	LASSO	TCGA	GSE26939	0.732, 0.743 and 0.712	0.663, 0.614 and 0.599	CIBERSORT (proportion of 22 types of infiltrating immune cell)); Estimate score	Waterfall plot; Correlations between risk score and TMB	Yes	Immunohistochemistry (HPA online database)	(26)	
Present study	Cuproptosis-related mitochondrial genes	LUAD	Pearson correlation (>0.3)	117 machine learning	TCGA	GSE26939; GSE31210; GSE72094	0.743, 0.741 and 0.693	GSE26939: 0.811 and 0.714, 0.708; GSE31210: 0.824, 0.657 and 0.732; GSE72094: 0.714, 0.671 and 0.769	ssGSEA (checkpoint expression, immune-related pathways); Estimate score; CIBERSORT (Fig. S1); TIDE score	Waterfall plot; TMB in high and low risk groups; TMB-related KM	Yes	RT-qPCR; CCK-8 assay; colony formation assay; Transwell assay; Mitochondrial immunofluorescence assay	-	

ROC, receiver operating characteristic; TME, tumor microenvironment; TMB, tumor mutational burden; LUAD, lung adenocarcinoma; WGCNA, weighted gene co-expression network analysis; LASSO, least absolute shrinkage and selection operator; TCGA, The Cancer Genome Atlas; ssGSEA, single-sample gene set enrichment analysis; KM, Kaplan-Meier; TIDE, Tumor Immune Dysfunction and Exclusion; HPA, Human Protein Atlas; RT-qPCR, reverse transcription-quantitative PCR; CCK-8, Cell Counting Kit-8.