

A 5-mRNA-Based Prognostic Signature of Survival in Lung Adenocarcinoma

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Research

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Abstract

Background: Lung adenocarcinoma (LUAD) is the most common non-small cell lung cancer, with an increasing incidence and poor prognosis. To evaluate the prognosis of LUAD patients and optimize treatment, effective clinical research prediction models are urgently needed.

Methods : In this study, we thoroughly mined LUAD genomic data from GEO (GSE43458, GSE32863, and GSE27262) and TCGA datasets, including 698 LUAD and 172 healthy (or adjacent normal) lung tissue samples. Single-factor Cox and LASSO regression analyses were used to screen DEGs related to patient prognosis, and multivariate Cox regression analysis was applied to establish the risk score equation and construct the survival prognosis model. Receiver operating characteristic (ROC) curve and Kaplan-Meier (KM) survival analyses with clinically independent prognostic parameters were performed to verify the predictive power of the model and further establish a prognostic nomogram.

Results: A total of 380 DEGs were identified in LUAD tissues through GEO and TCGA datasets, and 5 DEGs (TCN1, CENPF, MAOB, CRTAC1 and PLEK2) were screened out by multivariate Cox regression analysis, indicating that the prognostic risk model could be used as an independent prognostic factor (HR = 1.520, P < 0.001). Internal and external validation of the model confirmed that the prediction model had good sensitivity and specificity (AUC = 0.754, 0.737). Combining genetic models and clinical prognostic factors, nomograms can also predict overall survival more effectively.

Conclusion: A 5-mRNA-based model was constructed to predict the prognosis of lung adenocarcinoma, which may provide clinicians with reliable prognostic assessment tools and help clinical treatment decisions.

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