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Construction and Validation of a CNV-Driven Ferroptosis Related Gene Signature for Predicting the Prognosis of Lung Adenocarcinoma

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Introduction

Lung cancer is a disease and has the highest morbidity and mortality in China. The 5-year serial of most LUAD patients is less than 15% because of the lack of early diagnosis and post-diagnosis biomarkers.Therefore, new sensitive biomarkers are starved for evaluatethe prognosis of patients with LUAD, which is especially critical for the prognosis and treatment of patients. Previous studies have shown that ferroptosis plays an integral role in the development of cancer and copy number variations (CNVs) have been reported to associated with the ferroptosis.However, the role of CNVs-driven ferroptosis-relatedgenes (FRGs) in LUAD continues to be poorly understood.

Methods

- The transcriptome data and clinical features of LUAD patients were downloaded from the Gene Expression Omnibus (GEO) database and The Cancer Genome.
- Differential analysis was carried out to recognize differentially expressed CNV-driven FRGs.
- Univariate Cox and least absolute shrinkage and selection operator (LASSO) regression analyses were utilized to identify prognosis-associated genes.
- Kaplan-Meier (K-M) analysis was a builder to estimate the worth of model.
- Thenomogram was created to estimate survival probability of each patient.
- the immune microenvironment landscape between high and low risk groups was evaluated.

Graphics / Images

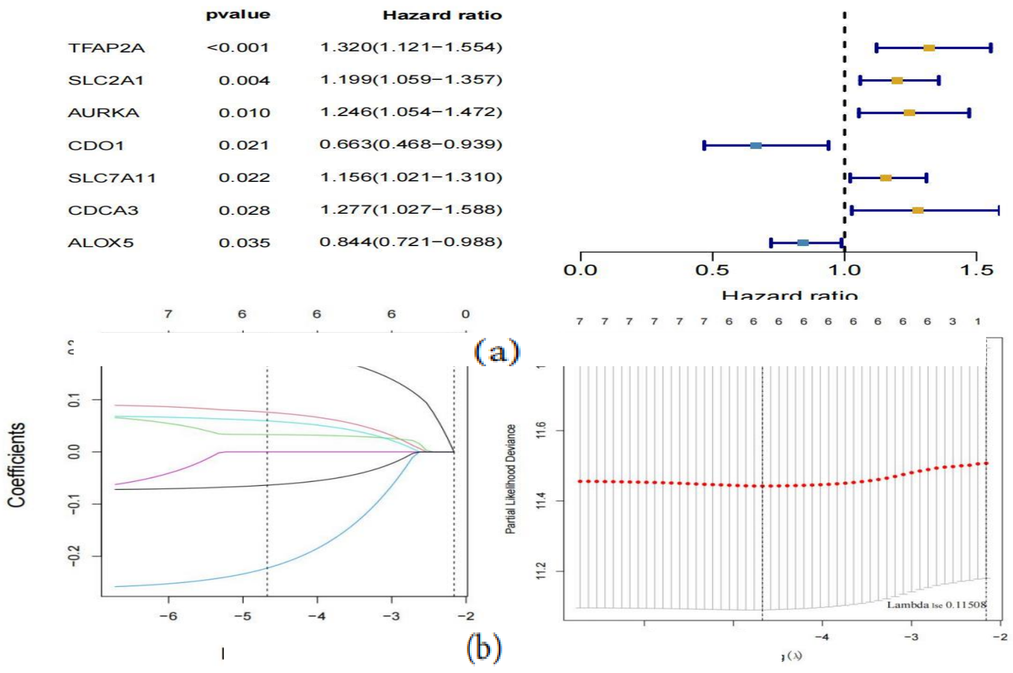

Figure 3: CNV-driven ferroptosis-related genes are associated with LUAD prognosis. (a) Forest map of CNV-driven ferroptosis-related genes by univariate Cox regression. Yellow: risk factors; blue: protective factors. (b) The LASSO Cox analysis identified regression coefficient and 6 genes most correlated with prognostics.

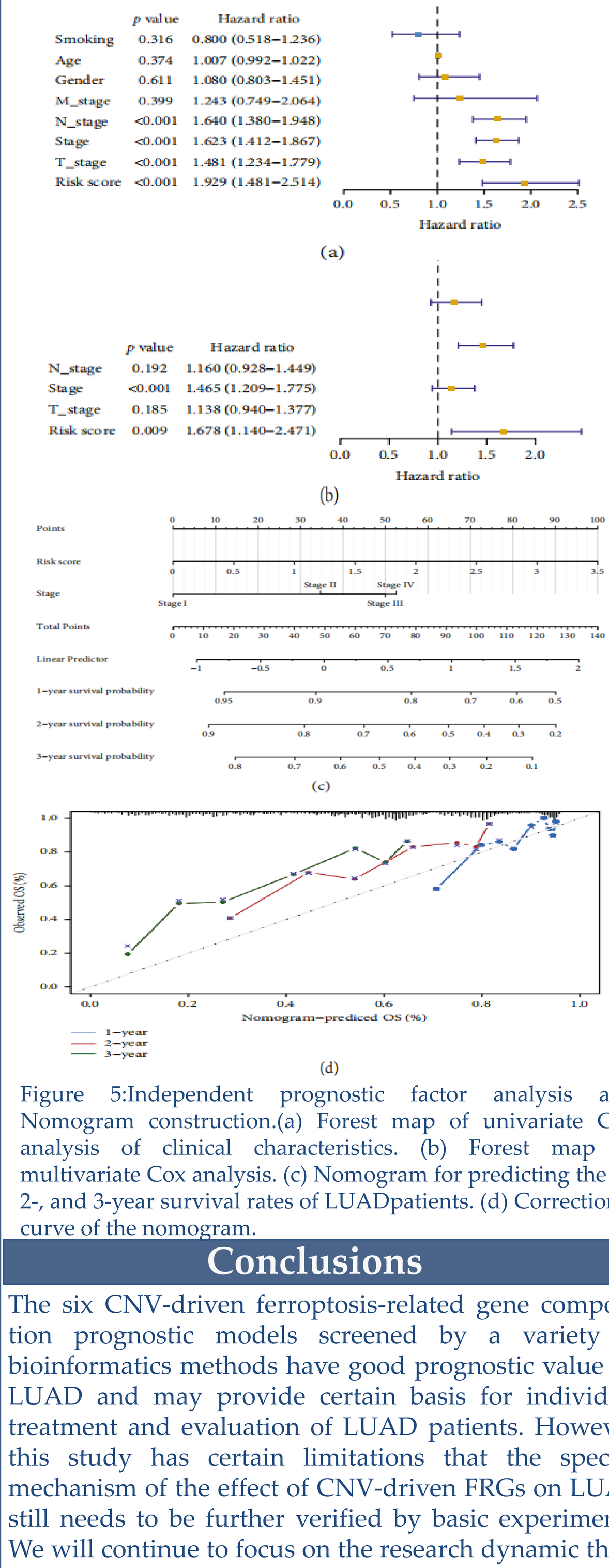

Figure 5:Independent prognostic factor analysis and Nomogram construction.(a) Forest map of univariate Cox analysis of clinical characteristics. (b) Forest map of multivariate Cox analysis. (c) Nomogram for predicting the 1-, 2-, and 3-year survival rates of LUADpatients. (d) Correctional curve of the nomogram.

Conclusions

The six CNV-driven ferroptosis-related gene composition prognostic models screened by a variety of bioinformatics methods have good prognostic value for LUAD and may provide certain basis for individual treatment and evaluation of LUAD patients. However, this study has certain limitations that the specific mechanism of the effect of CNV-driven FRGs on LUAD still needs to be further verified by basic experiments. We will continue to focus on the research dynamic these genes.