

# The RNA-seq data and clinical data of ccRCC patients

TCGA ICGC GEO

Tumor samples (n=526) Normal samples (n=72)

239 Ferroptosis-associated genes

3012 Ferroptosis-related LncRNAs

60 differentially expressed Ferroptosis-related LncRNAs

Training cohorts (n=264)

Testing cohorts (n=262)

Overall cohorts

Unicox and LASSO Survival analysis

10 prognostic LncRNAs

Multicox analysis

Seven Ferroptosis-related LncRNAs signature

Validation of risk signature

Kaplan-Meier survival analysis  
AUC analysis  
Risk score and survival status

PCA analysis  
Stratified survival analysis  
Correlation with clinical factors

Construction a nomogram and in comparison with other factors

lncRNA-mRNA coexpression network  
GEPIA, K-M Plotter, and qRT-PCR validation for major FRlncRNAs

Relationship with immune infiltration, checkpoints expression; Treatment responsiveness.

