Development and validation of a disulfidptosis-related genes signature for predicting outcomes and immunotherapy in acute myeloid leukemia

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Introduction

Acute myeloid leukemia (AML) is a hematopoietic malignancy with poor outcomes and high recurrence. Disulfidptosis, a novel form of programmed cell death driven by aberrant disulfide bonds and F-actin collapse, provides insights into cancer progression and treatment.

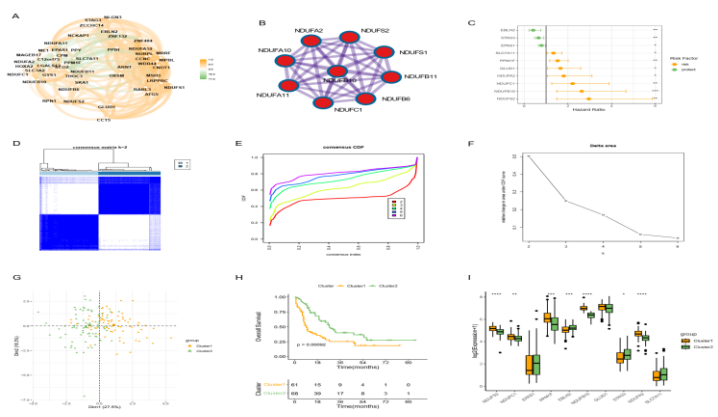


Figure 1. Molecular subtypes of AML patients based on 10 DRGs with prognostic values.

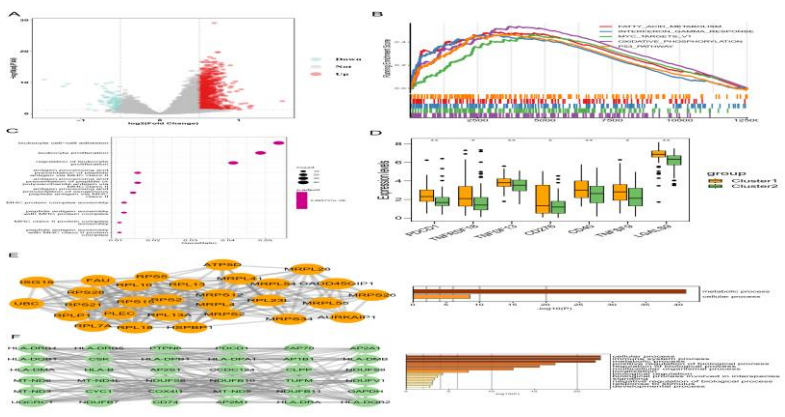


Figure 2. Molecular subtypes of AML patients based on 10 DRGs with prognostic values.

Figure 3. Generation and validation of a disulfidptosis-related 6-gene signature in AML.

Methods

We investigated the correlation network and prognostic values of disulfidptosis-related genes (DRGs) in AML.. We implemented the differential analysis and enrichment analysis to explore the difference of the distinct subtypes in biological processes. Least absolute shrinkage and selection operator (LASSO) Cox model was used to generate a disulfidptosis-related signature. We employed the ESTIMATE, CIBERSORT, and scRNA analyses to assess the tumor microenvironment of AML. Moreover, experiments validated the functions of PTPN6 and CSK in OCI-AML2 cells.

Results

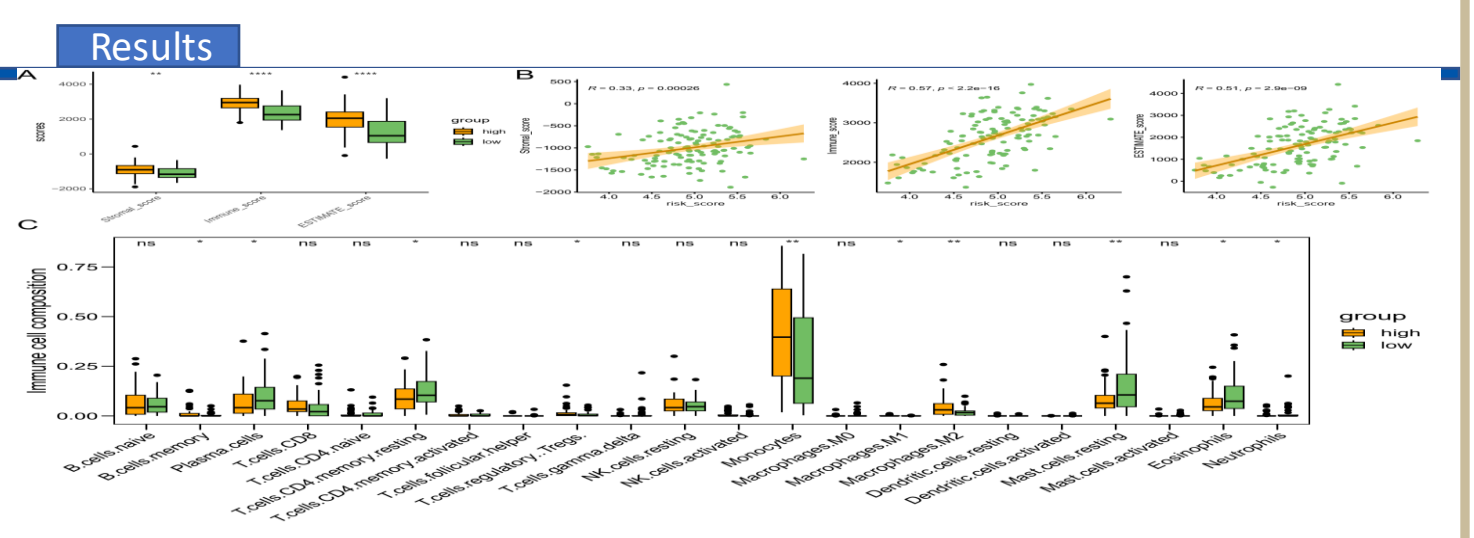


Figure 4. Differences in tumor microenvironments between risk subgroups of AML patients.

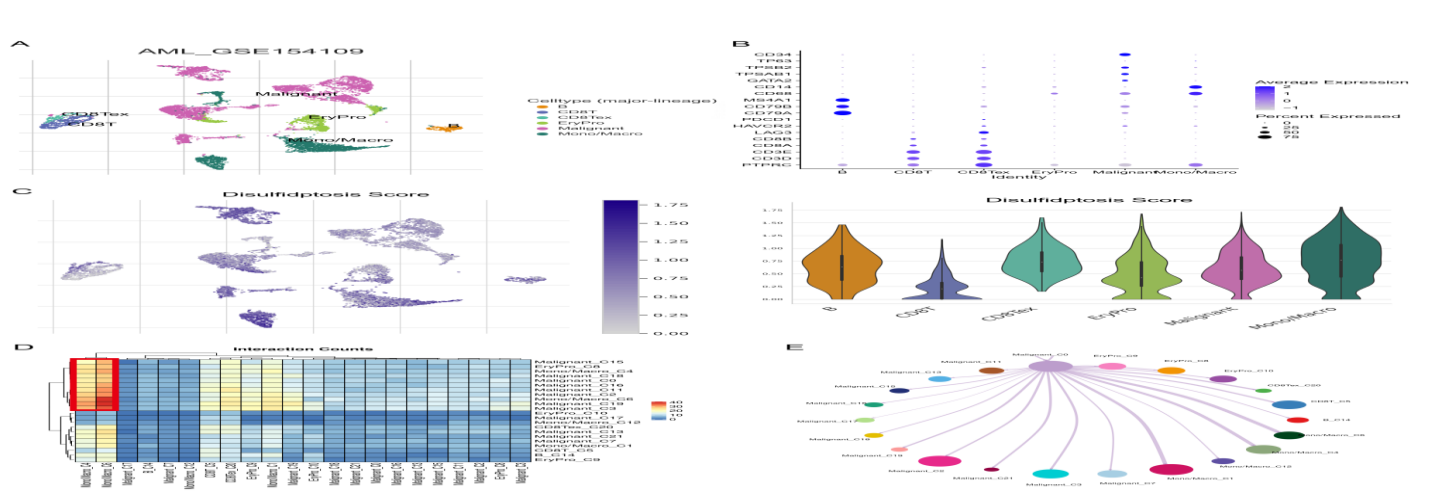


Figure 5. The relationship between risk score and TME in scRNA-seq dataset GSE154109.

Figure 6. Somatic mutation profile in the two risk subgroups.

Conclusion

Our study provides insights into DRG prognoses and immunomodulation, establishing a robust 6-gene risk model for predicting AML outcomes that may enhance precision medicine and treatment strategies.