DNA damage repair-related gene signature can influence immune status and predict prognosis in hepatocellular carcinoma

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Abstract

Background: DNA damage repair genes (DDRGs) have an impact on a wide range of malignancies. However, the relevance of these genes in hepatocellular carcinoma (HCC) prognosis has received little attention. In this study, we want to develop a prognostic signature that will open up novel therapy options for HCC. Methods: We acquired mRNA expression profiles and clinical data of HCC patients from the TCGA database. A polygenic prognostic model for HCC was constructed using LASSO Cox regression and was validated using the ICGC database. Correlations between risk signature and immune status, clinical characteristics and drug sensitivity were investigated. Protein expression levels of prognostic genes were verified using immunohistochemistry. Results: A DDRGs signature model was developed using LASSO Cox regression analysis. Patients in the high-risk group had worse overall survival compared to the low-risk group. Multivariate Cox analysis showed that the risk score is an independent predictor of OS. Functional analysis revealed a strong association with cell cycle and antigen binding pathways, and the risk score was highly correlated with tumor grade, tumor stage, and types of immune infiltrate. High expression levels of prognostic genes were significantly correlated with increased sensitivity of cancer cells to anti-tumor drugs. Immunohistochemistry staining indicated that, except for NEIL3, the other 9 genes were highly expressed in HCC. Conclusion: Ten DDRGs were utilized to create a new signature that might influence the immunological state in HCC and be used for prognostic prediction. In addition, blocking these genes could be an alternate treatment.

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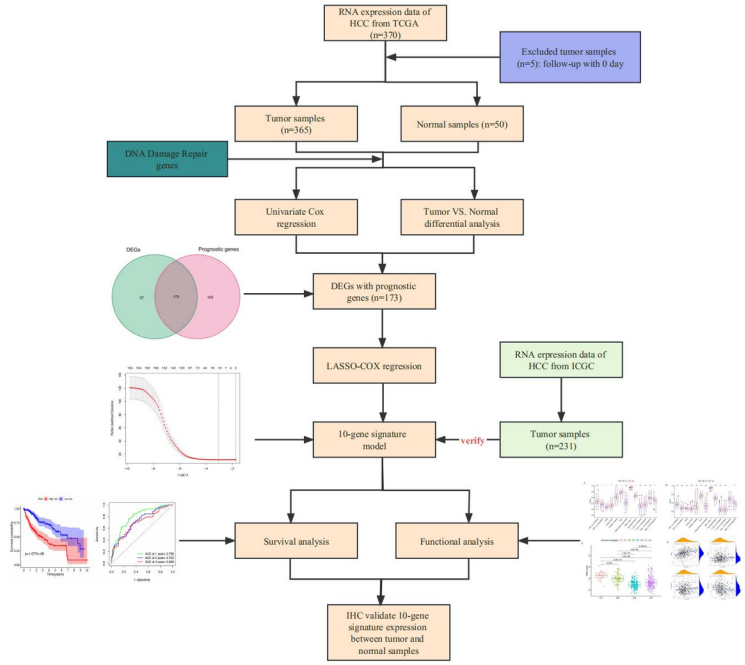

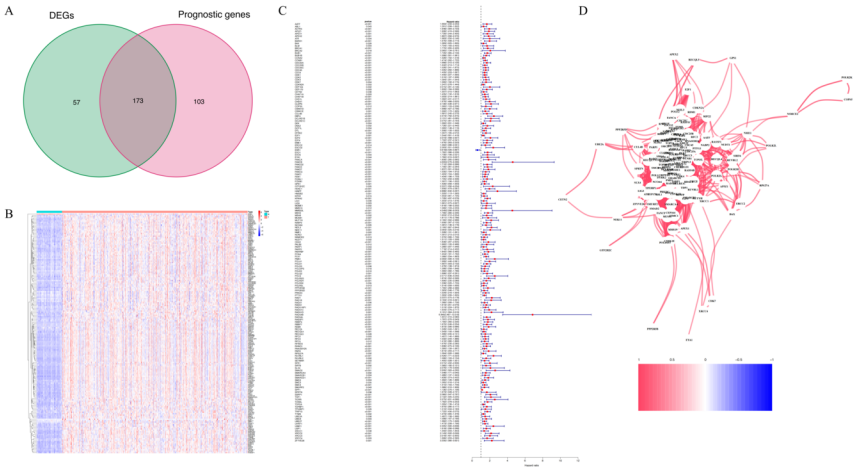

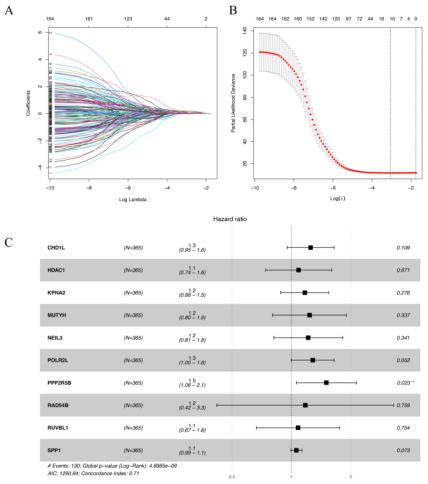

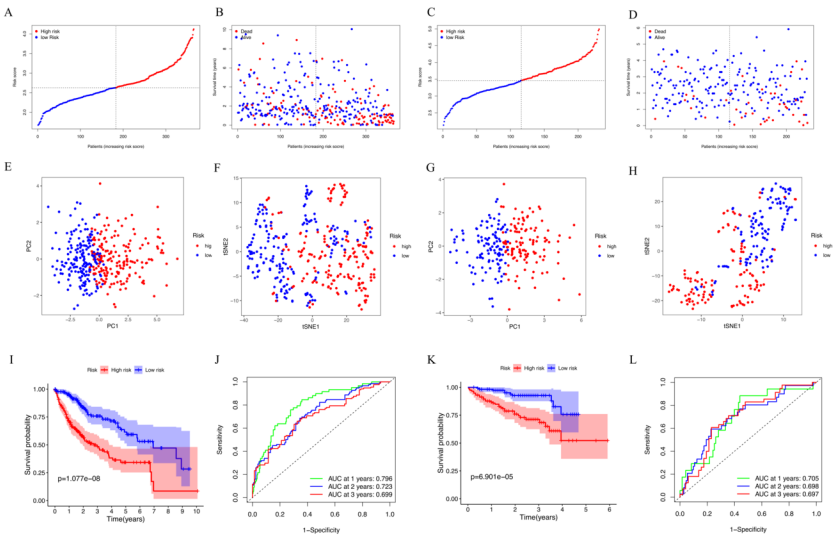

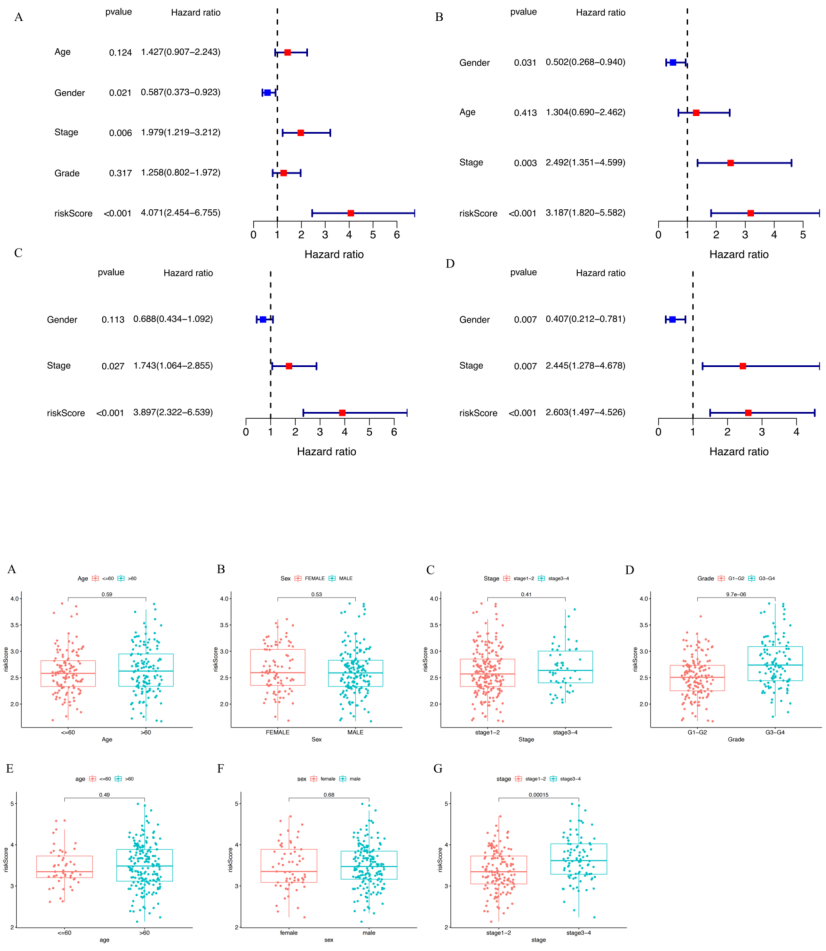

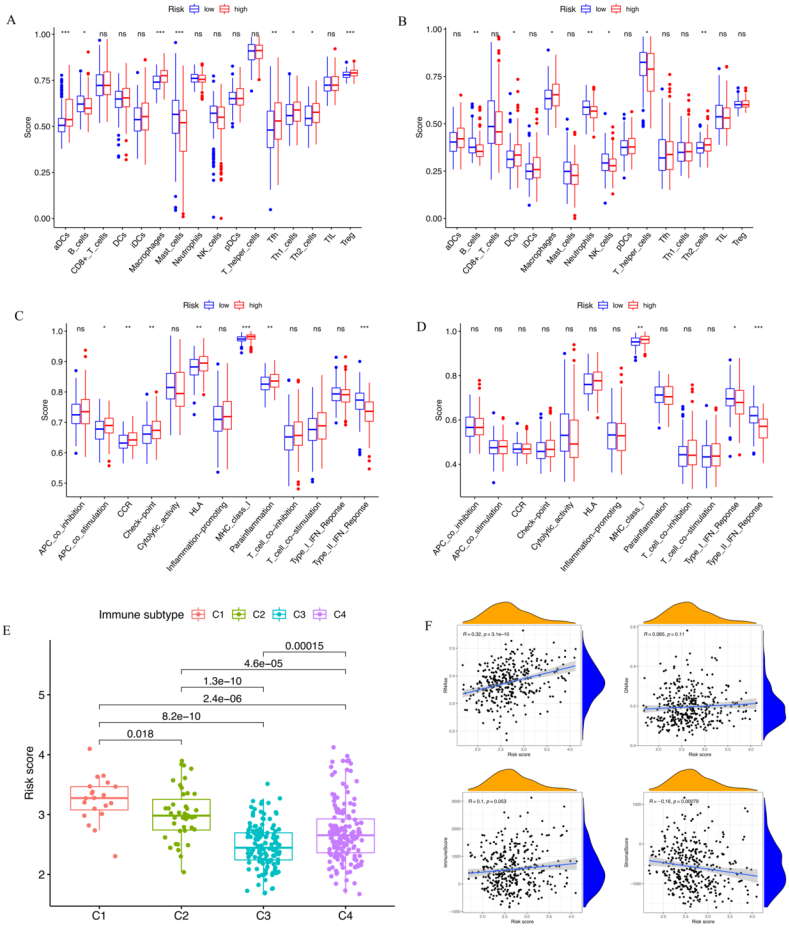

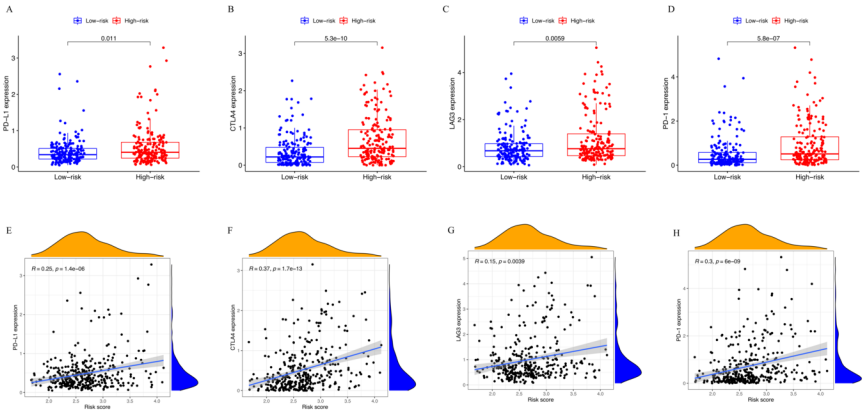

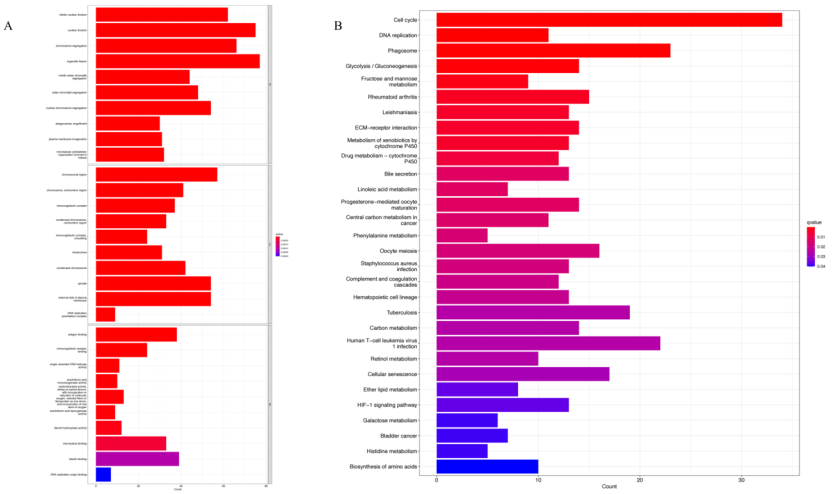

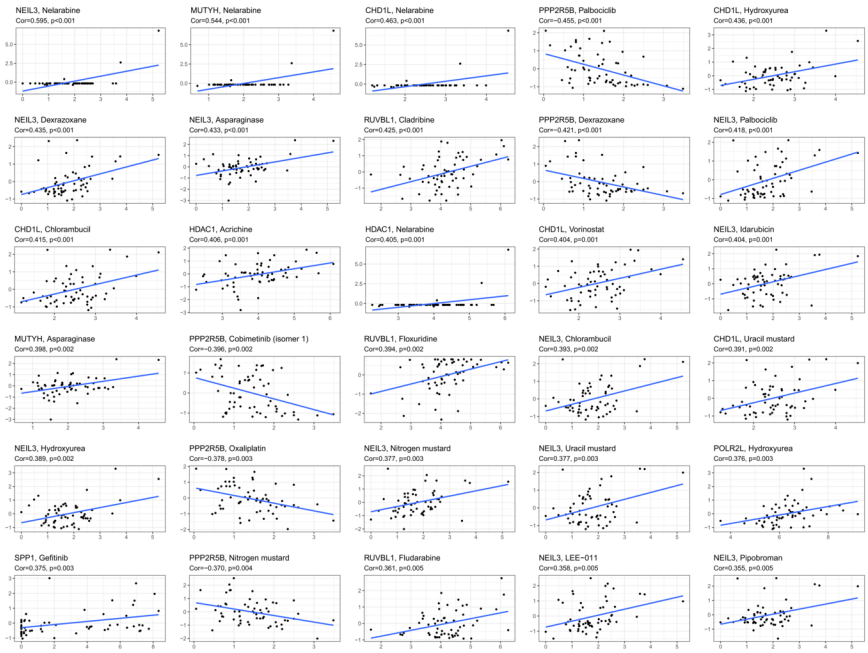

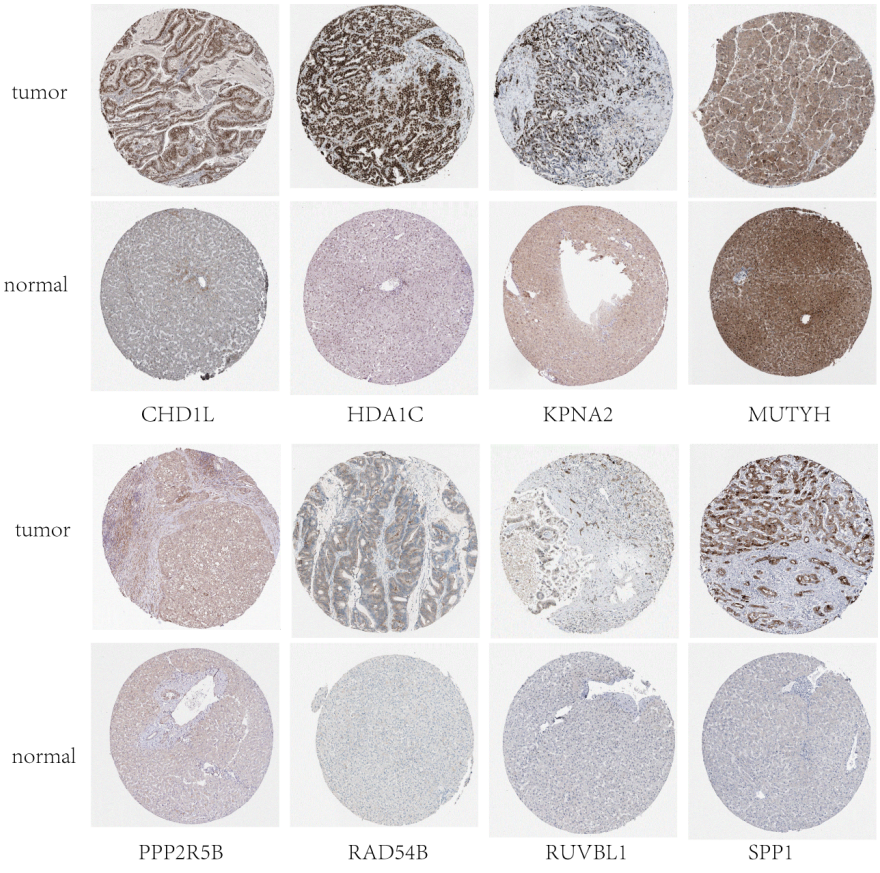

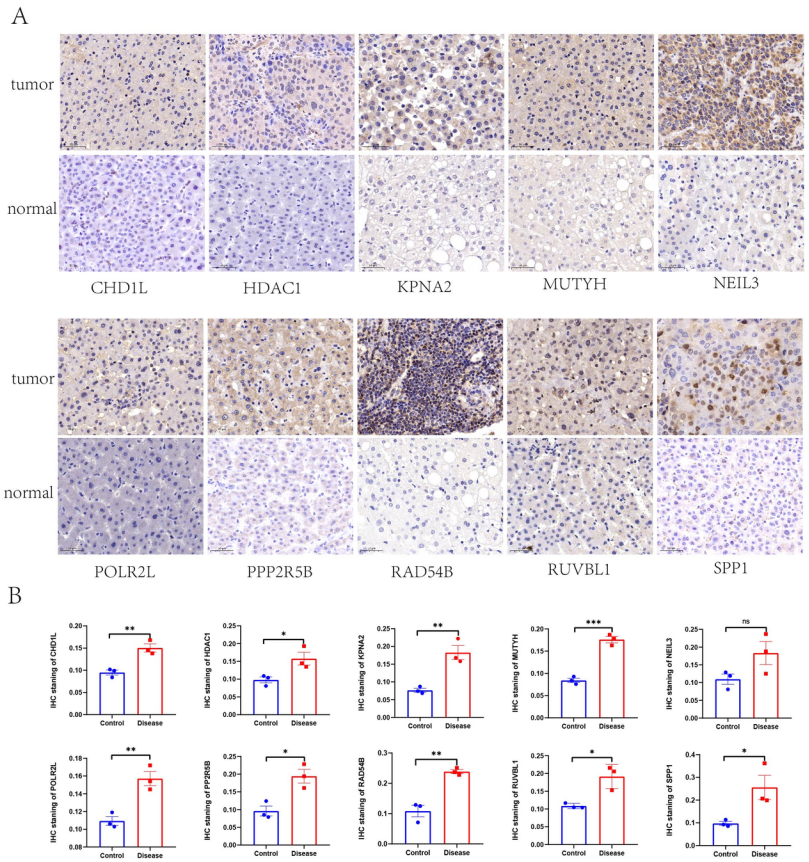

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