Supplementary

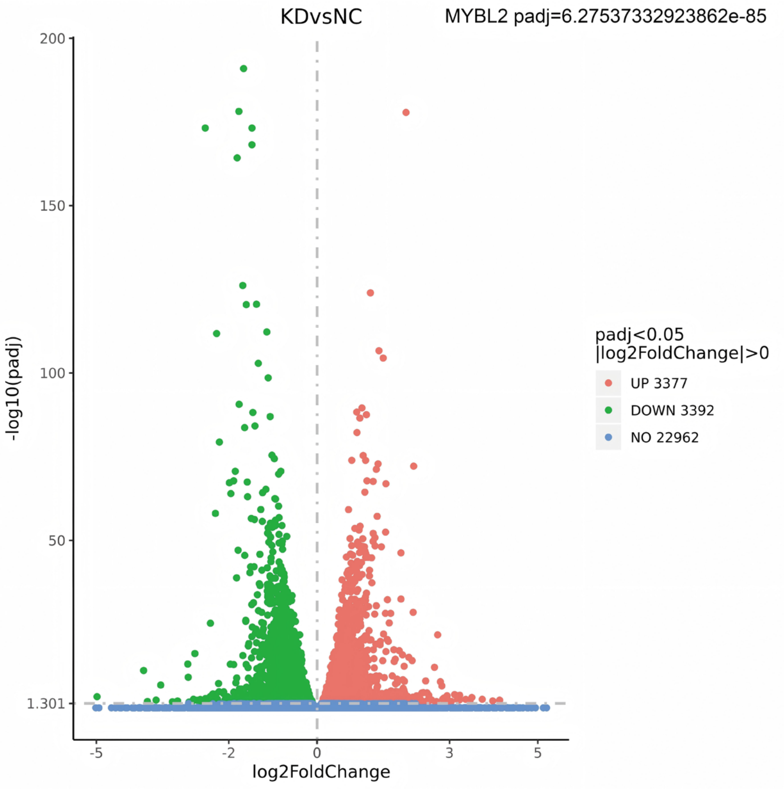

Figure S1 Volcano plot for SNX10 difference analysis.

https://dx.doi.org/10.21037/tau-2025-169

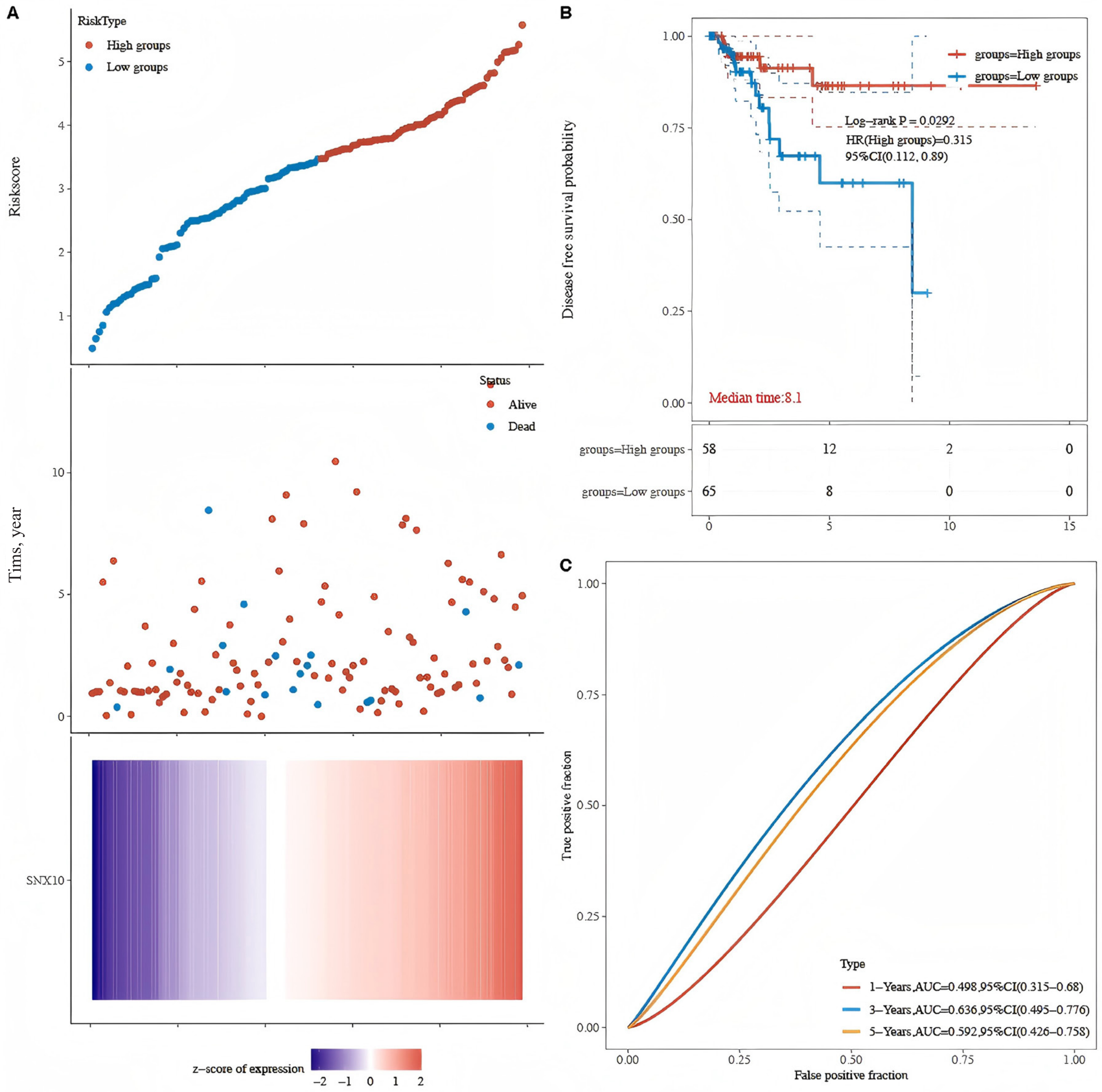

Figure S2 SNX10 expression strongly correlates with poor prognostic risk scores, stratifies patients into distinct disease-free survival groups, and outperforms clinical staging in predicting survival. (A) Association between SNX10 expression z-score and prognostic risk score in bladder cancer. (B) SNX10 expression stratifies DFS in bladder cancer. (C) Diagnostic performance of the SNX10-based risk model.

https://dx.doi.org/10.21037/tau-2025-169

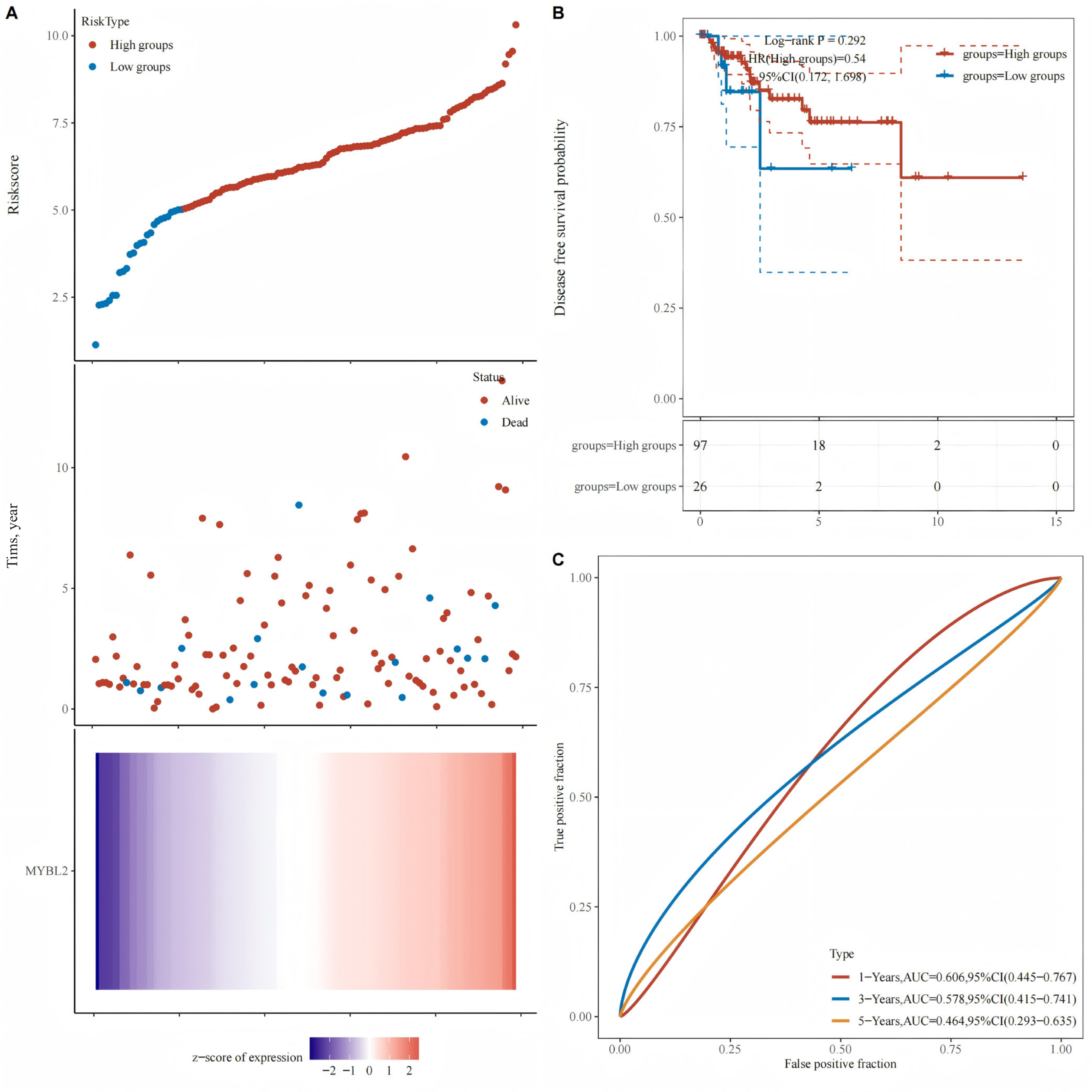

Figure S3 MYBL2-driven risk stratification quantitatively captures tumor aggressiveness, defines DFS divergence, and achieves temporal prediction superiority over conventional staging systems. (A) MYBL2 expression quantitatively associates with aggressive risk stratification. (B) MYBL2 expression dichotomy reveals divergent DFS outcomes. (C) Temporal superiority of the MYBL2-centric prognostic model.

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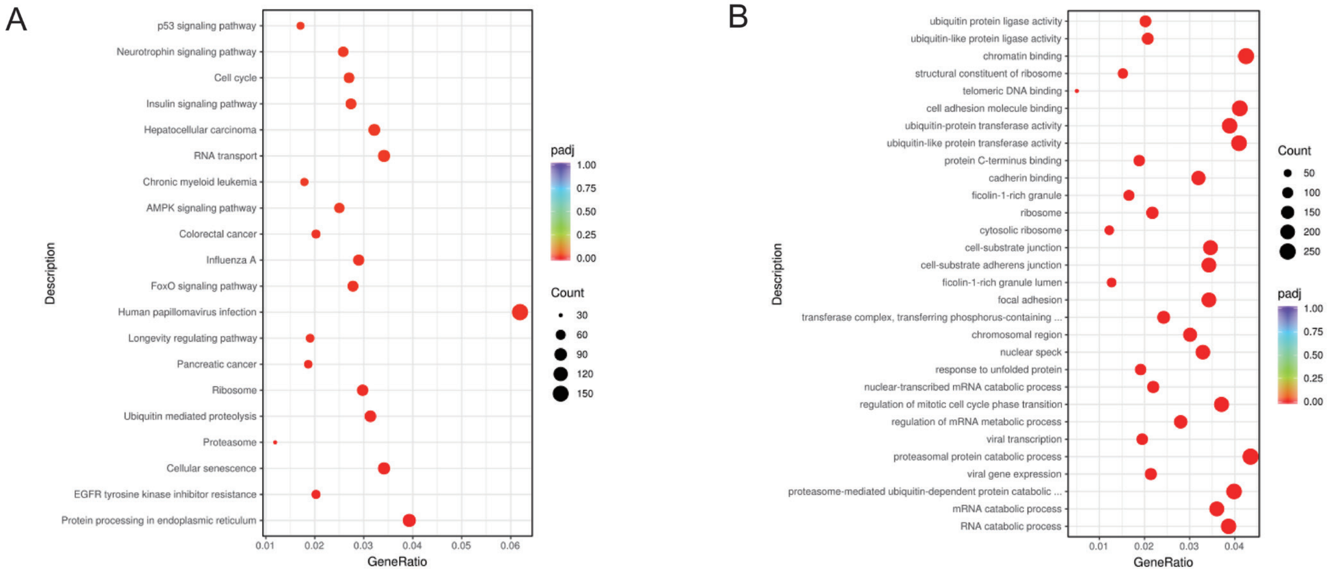

Figure S4 Functional annotation of SNX10 and associated genes. (A) KEGG pathway enrichment analysis and (B) GO term analysis of SNX10-related genes.

https://dx.doi.org/10.21037/tau-2025-169