Bioinformatics Analysis and Experimental Verification of Prognostic and Biological Significance of Autophagy-Related Long Non-Coding RNAs in Gastric Carcinoma
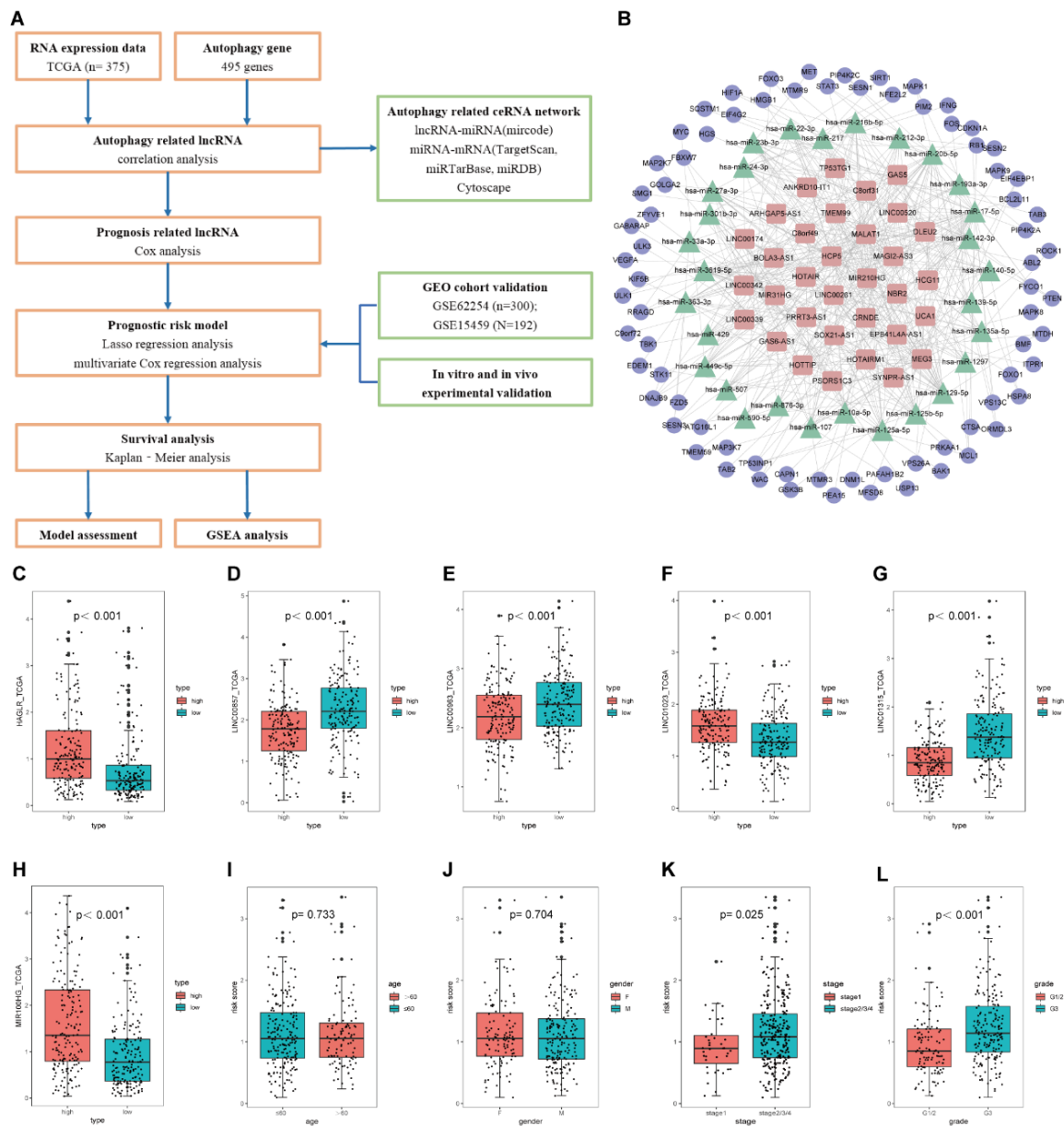
Supplementary Figures

Figure S1. (A) Workflow of prognostic signature identification in gastric cancer based on six autophagy-related long non-coding (lnc)RNAs. (B) Autophagy-related competing endogenous RNA network including 33 lncRNAs, 29 microRNAs, and 75 messenger RNAs. (C–H) Boxplot showing the expression of LINC01023, LINC00963, HAGLR, MIR100HG, LINC01315, and LINC00857 in the high- and low-risk groups in The Cancer Genome Atlas dataset. (I–L) Correlation analysis between the prognostic signature risk score and clinicopathological features in GC patients: (I) age; (J) gender; (K) TNM stage; (L) pathological grade.
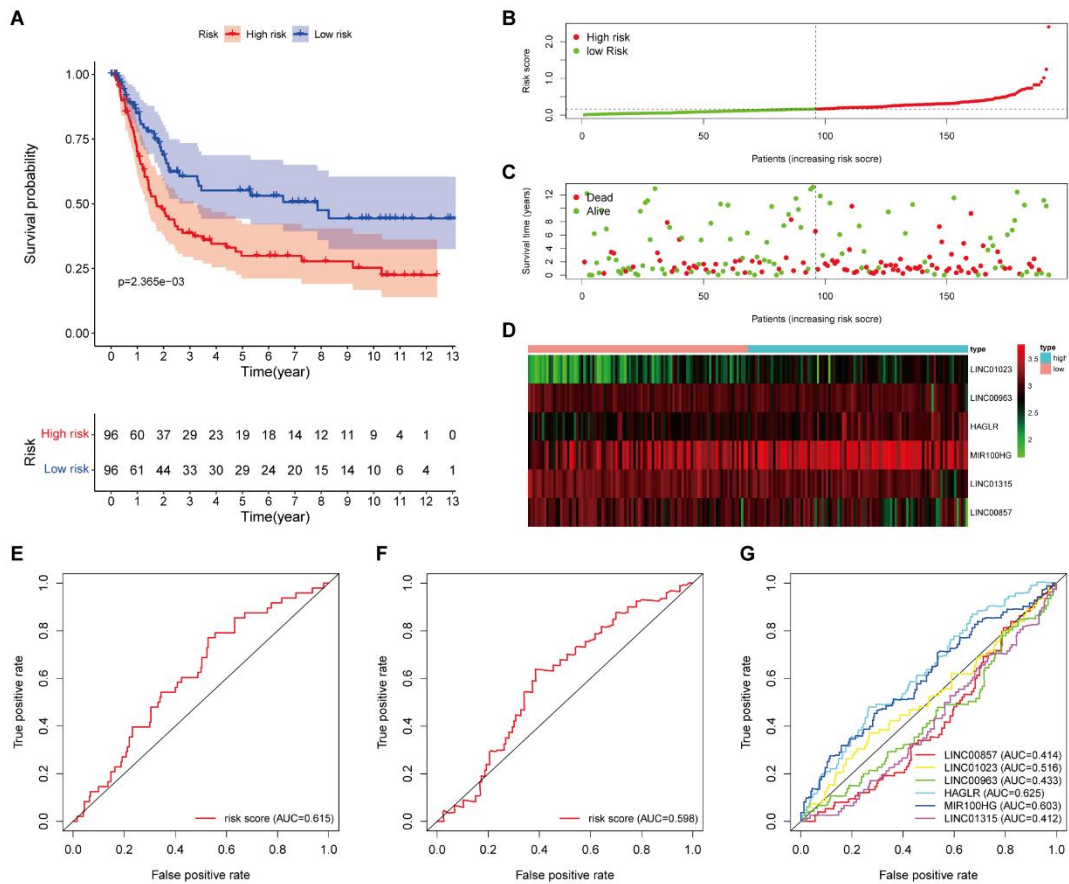
Figure S2. (A) Kaplan-Meier survival analysis of high- and low-risk groups based on the risk model for gastric cancer (GC) patients in the GEO dataset (GSE15459). (B) Distribution of risk scores for each patient. (C) Survival status of GC patients. (D) Expression heatmap of six autophagy-related lncRNAs. (E–F) Receiver operating characteristic (ROC) curve showing the predictive accuracy of the prognostic signature in the Gene Expression Omnibus datasets (E) GSE62254 and (F) GSEGSE15459. (G) Multivariate ROC curve showing the predictive accuracy of the six lncRNAs.