**Supplementary Fig. 1** Schematic diagram of work flow. The orders of analyses to generate the risk mode and validate prognostic value of lncRNA signature in GC.

**Supplementary Fig. 2** Heatmap of the lncRNA expression profiles in GSE79973 series (N=20). Rows represent lncRNAs, and columns represent patients.

**Supplementary Fig. 3** Cross-validation for tuning parameter selection in the LASSO model. The red dotted line represents the cross-validation curve. The solid vertical lines are partial likelihood deviance standard error (SE). The dotted vertical lines are drawn at the optimal values by minimum criteria and 1-SE criteria. We plotted the partial likelihood deviance versus log (lambda), where is the tuning parameter.
Affy HG-U133 Plus 2.0 probe sets anotation

Non-coding RNA(ncRNA) expression profile

339 differentially expressed IncRNAs in data set GSE79973

Lasso regression model

12 IncRNAs significantly associated with survival in data set GSE62254

Comparison between low and high risk groups

Validation in test data set GSE15459

Multivariable Cox regression analysis in GSE62254

Stratification analysis in GSE62254

ROC analysis in GSE62254

ssGSEA analysis in GSE62254

Construction and assessment of nomogram
Supplementary Fig. 3

[Graph showing Partial Likelihood Deviance against log(Lambda)]

- Log(Lambda) scale ranges from -6 to -3.
- Deviance scale ranges from 250 to 0.

The graph illustrates the relationship between log(Lambda) and Partial Likelihood Deviance, with data points plotted along the curve.