Supplementary Figure 1. Kaplan-Meier survival curves for low- and high-risk populations by different clinical variables. (A, B) Age; (C, D) N0 and N1–3; (E, F) Stage I–II and Stage III–IV.
Supplementary Figure 2. Kaplan-Meier survival curves for low- and high-risk populations by different clinical variables. (A, B) Sex; (C, D) T1–2 and T3–4.
Supplementary Figure 3. PCA analysis of the prognostic signature. (A) PCA of all genes; (B) PCA of apoptosis genes; (C) PCA of CuRLs; (D) PCA of risk LncRNAs.
Supplementary Figure 4. Independent prognostic analysis of the prognostic signature. (A) Univariate and (B) Multivariate Cox regression analysis to examine the value of clinical characteristics and risk score as independent prognostic predictors. Nomograms for predicting 1-, 2-, 3-year overall survival (OS) for a randomly selected patient in test cohort (C).
Supplementary Figure 5. Risk model external validation in the GSE53625 group. (A) Overall survival Kaplan-Meier survival curves. (B) 1-, 3-, and 5-years overall survival area under the ROC curve of the signature. (C) Univariate and (D) Multivariate Cox regression analysis to examine the value of clinical characteristics and risk score as independent prognostic predictors in GSE53625. (E) Nomograms for predicting 1-, 3-, 5-year overall survival (OS) for a randomly selected patient in test cohort. (F) Calibration curves for 1, 2, and 3 years of nomogram.

Supplementary Figure 6. Relative mRNA expression of cuproptosis-related long non-coding RNAs in four cell lines (HEEC, TE-1, KYSE-30, KYSE-410 and KYSE-520). (A) AC021321.1, (B) AC138696.2, (C) EWSAT1, (D) LINC00601 and (E) LINC01775.
Supplementary Figure 7. Relative mRNA expression of cuproptosis-related long non-coding RNAs in cancer tissue and paracancerous tissue. (A) AC021321.1, (B) AC138696.2, (C) EWSAT1, (D) LINC00601 and (E) LINC01775.