SUPPLEMENTARY FIGURE

Gene expression data from TCGA database

GSEA analysis between cancer and normal samples

The Hallmark, BioCarta, KEGG, GO and Reactome gene sets were analyzed

The Hallmark, GO and Reactome gene sets were enriched

Differently expressed genes in these gene sets were extracted

CLDN9, GFPT1, HMMR, RARS and STMN1 were related to survival of EAC patients

Clinical data were matched and Cox analysis was performed

Five genes based risk model was established

All patients were separated into low and high risk groups

Overall survival analysis in groups stratified by risk score, age, gender, grade, stage, et al

Nomogram model incorporating risk score with age, gender, grade, stage

Nomogram plot Survival curve Calibration plots

Further overall survival analysis in low and high risk groups were performed in subgroups stratified by age, gender, grade, stage, et al

Supplementary Figure 1. Flow chart of the analysis procedure in this study.