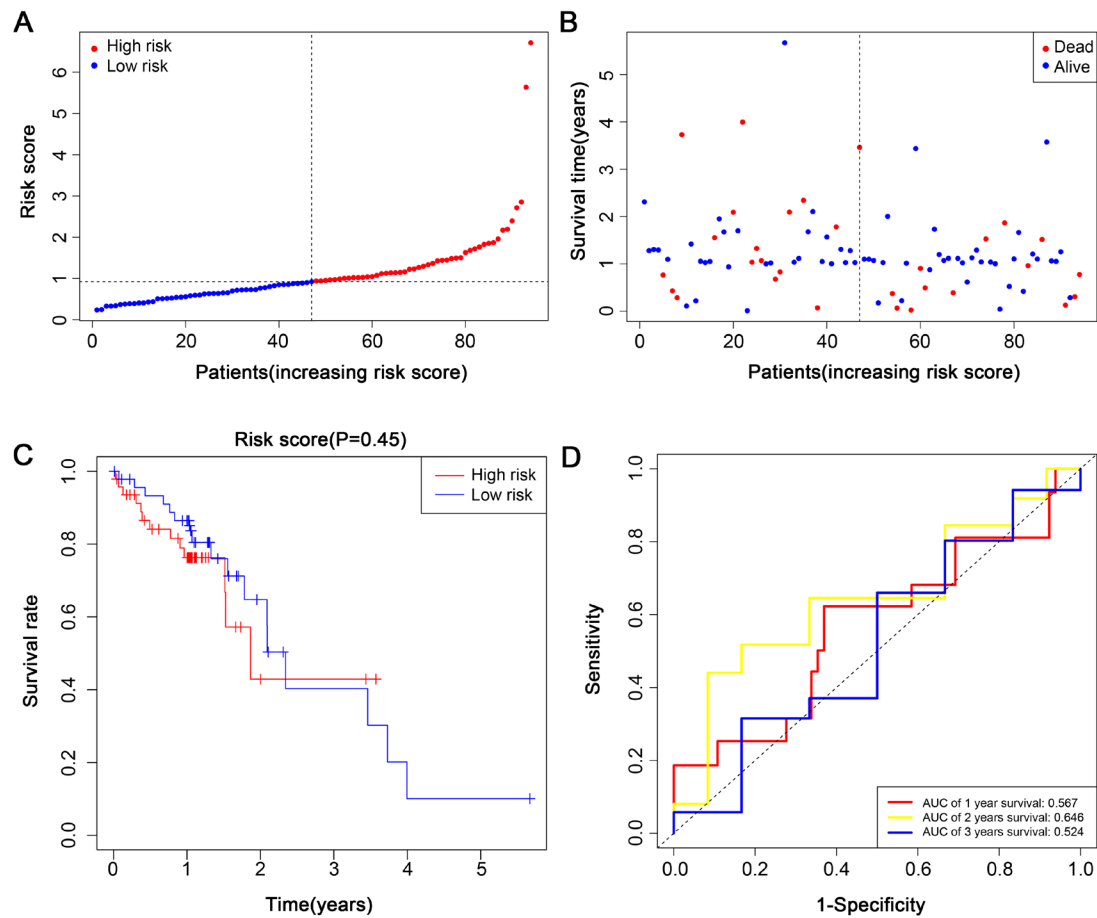
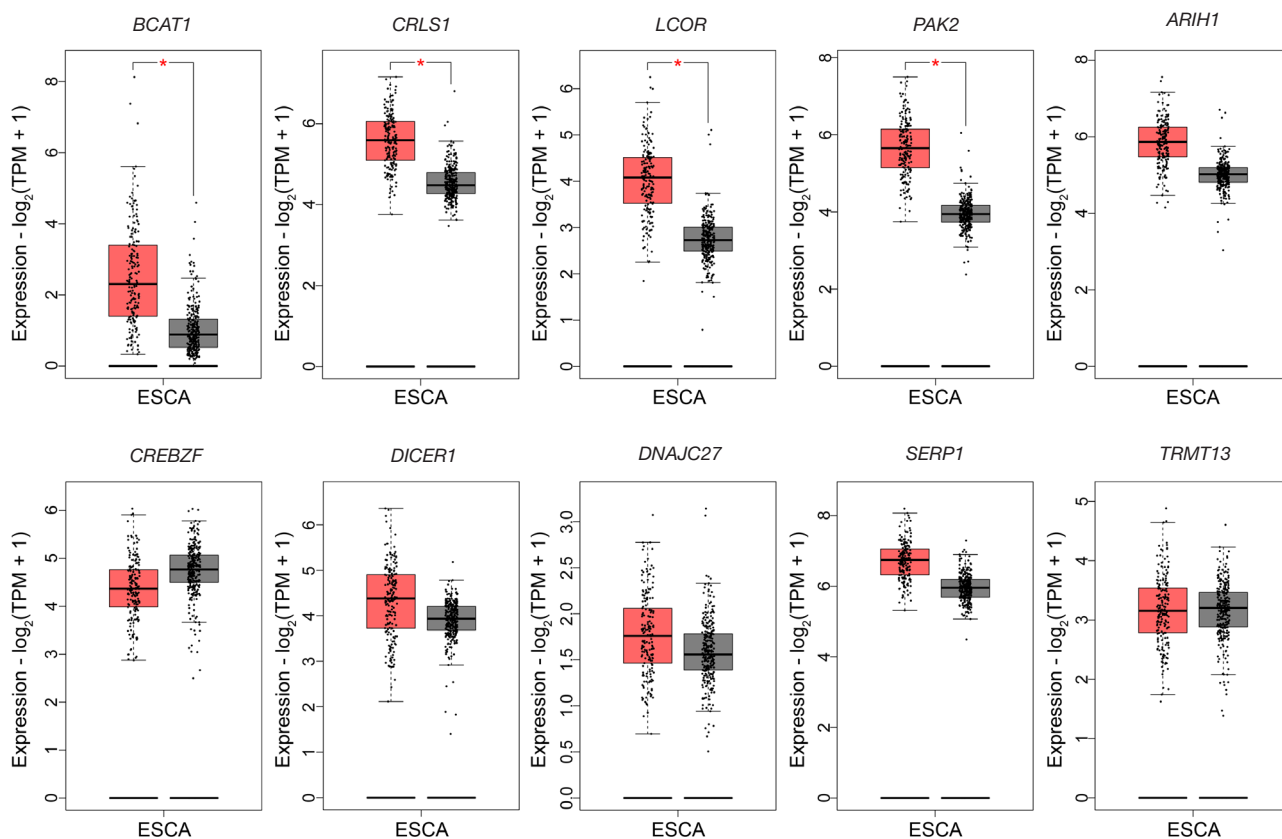


**Figure S1** Validation of the risk model in esophageal adenocarcinoma patients. (A,B) Distribution of risk scores (A) and survival status (B) in esophageal adenocarcinoma patients. (C) Kaplan-Meier survival curve analysis showing the OS of esophageal adenocarcinoma patients in the high- and low-risk groups. (D) The AUC of time-dependent ROC curves to evaluate the prognostic performance of the risk model in esophageal adenocarcinoma patients. AUC, area under the curve; ROC, receiver operating characteristic; OS, overall survival.



**Figure S2** Validation of the risk model in esophageal squamous cell carcinoma patients. (A,B) Distribution of risk scores (A) and survival status (B) in esophageal squamous cell carcinoma patients. (C) Kaplan-Meier survival curve analysis showing the OS of esophageal squamous cell carcinoma patients in the high- and low-risk groups. (D) The AUC of time-dependent ROC curves to evaluate the prognostic performance of the risk model in esophageal squamous cell carcinoma patients. AUC, area under the curve; ROC, receiver operating characteristic; OS, overall survival.



**Figure S3** The expression level of ten target genes of miR-425-5p in tumor and normal tissue [the red represents tumor (n=182), the black represents normal (n=286)]. \*,  $P < 0.05$ . ESCA, esophageal cancer; TPM, transcripts per kilobase million; *BCAT1*, branched chain amino acid transaminase 1; *CRLS1*, cardiolipin synthase 1; *LCOR*, ligand dependent nuclear receptor corepressor; *PAK2*, P21 (RAC1) activated kinase 2; *ARIH1*, E3 ubiquitin-protein ligase ARIH1; *CREBZF*, CREB/ATF bZIP transcription factor; *DICER1*, endoribonuclease dicer; *DNAJC27*, DNAJ homolog subfamily C member 27; *SERP1*, stress-associated endoplasmic reticulum protein 1; *TRMT13*, tRNA: m(4)X modification enzyme TRM13 homolog.