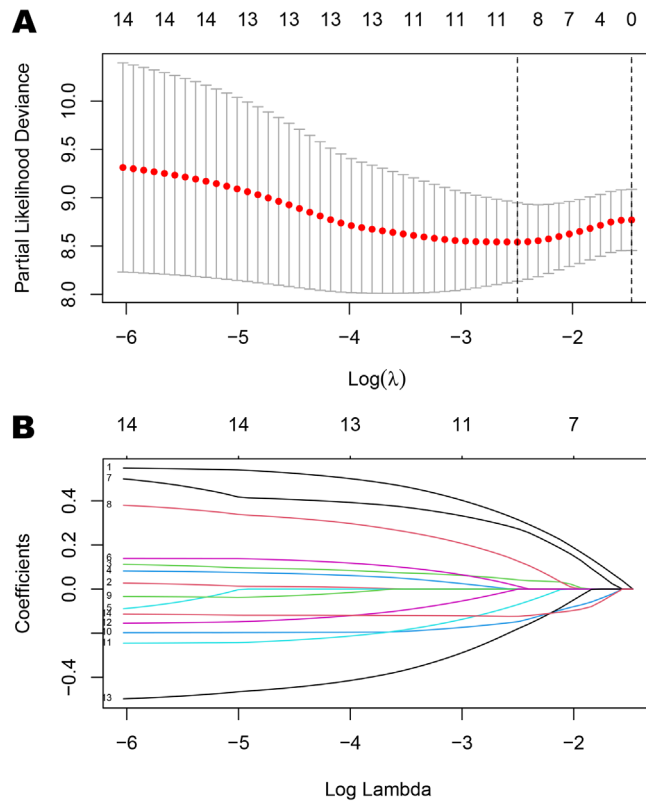




**Table S1** Genes with significant effects on prognosis of EAC identified after univariate Cox proportional hazards regression analysis

Gene	HR	HR.95L	HR.95H	p value
<i>EPB41L4A</i>	0.6157530047	0.4410112281	0.8597326749	0.0044072838
<i>CLDN3</i>	1.6627728118	1.1509193760	2.4022650773	0.0067538764
<i>ALAD</i>	0.6027127531	0.4141172342	0.8771976453	0.0081876380
<i>RGS16</i>	1.5909430862	1.1129415615	2.2742433126	0.0108680392
<i>ESM1</i>	1.4246396425	1.0697435866	1.8972753251	0.0154701518
<i>SERPINH1</i>	1.3998831566	1.0402640785	1.8838224762	0.0263821135
<i>PINK1</i>	0.7192522011	0.5366197615	0.9640415167	0.0274542939
<i>PLAU</i>	1.4582772199	1.0400323117	2.0447176747	0.0287008654
<i>PAQR5</i>	0.6918505279	0.4962175613	0.9646114735	0.0298225598
<i>MT1X</i>	0.7008389268	0.5068875992	0.9690022051	0.0315194474
<i>ANGPT2</i>	1.3320308066	1.0207404864	1.7382538397	0.0347617953
<i>CDC25B</i>	1.5273743103	1.0285739030	2.2680648195	0.0357618666
<i>CRTAC1</i>	0.6821840045	0.4683125435	0.9937274210	0.0462888743
<i>IL1B</i>	1.4107458375	1.0035642387	1.9831354497	0.0476540975

EAC, esophageal adenocarcinoma; HR, hazard ratio; HR.95L, hazard ratio 95% lower; HR.95H, hazard ratio 95% higher.

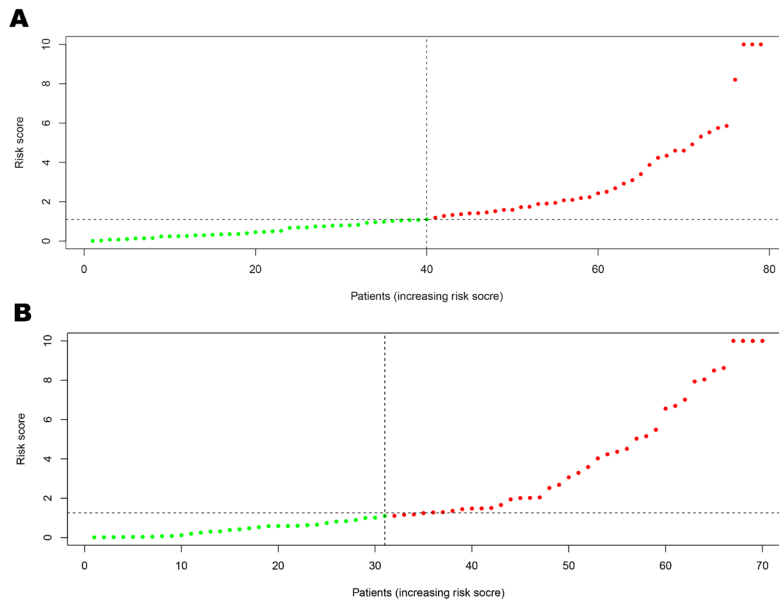


**Figure S3** Lasso regression analysis of selected genes. (A) Results of lasso regression.  $\lambda$  was determined when the partial likelihood deviance was smallest. (B) Coefficient curve. The different colored lines represent coefficient sizes of individual genes in different cases. The abscissa represents  $\log(\lambda)$  and the number of coefficients (top) that are not 0 under this penalty factor.

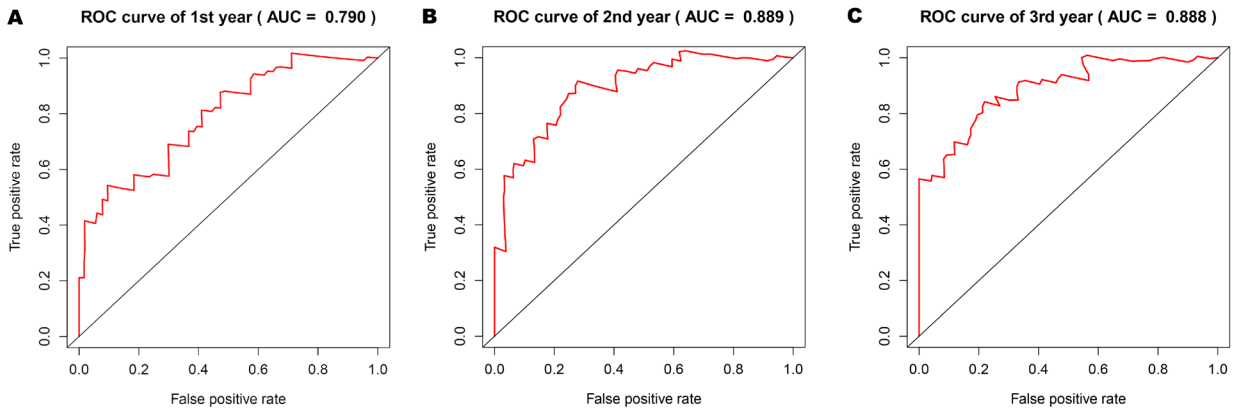
**Table S2** Six genes obtained to establish a prognostic risk score model through multivariate Cox proportional hazards regression analysis

Gene	cOef	HR	HR.95L	HR.95H	p value
<i>CLDN3</i>	0.5864	1.7975	1.2061	2.6789	0.003965
<i>ESM1</i>	0.5773	1.7813	1.2395	2.5598	0.001802
<i>PLAU</i>	0.3891	1.4757	1.0283	2.1175	0.034699
<i>EPB41L4A</i>	-0.3769	0.6859	0.4818	0.9764	0.036411
<i>PAQR5</i>	-0.2727	0.7612	0.5504	1.0529	0.099345
<i>MT1X</i>	-0.4981	0.6076	0.4281	0.8625	0.005315

COEF, coefficients; HR, hazard ratio; HR.95L, hazard ratio 95% lower; HR.95H, hazard ratio 95% higher.



**Figure S4** Risk score distribution in the training data (A) and test data (B). The x-axis represents the number of patients, and the y-axis represents the risk score. The red and green dots in the plot represent patients with high and low risk, respectively.



**Figure S5** ROC curves for the prognostic model representing 1-, 2- and 3-year predictions in the training data, respectively. The values of the AUC are 0.790, 0.889, and 0.888, respectively. ROC, receiver operator characteristic; AUC, area under the curve.