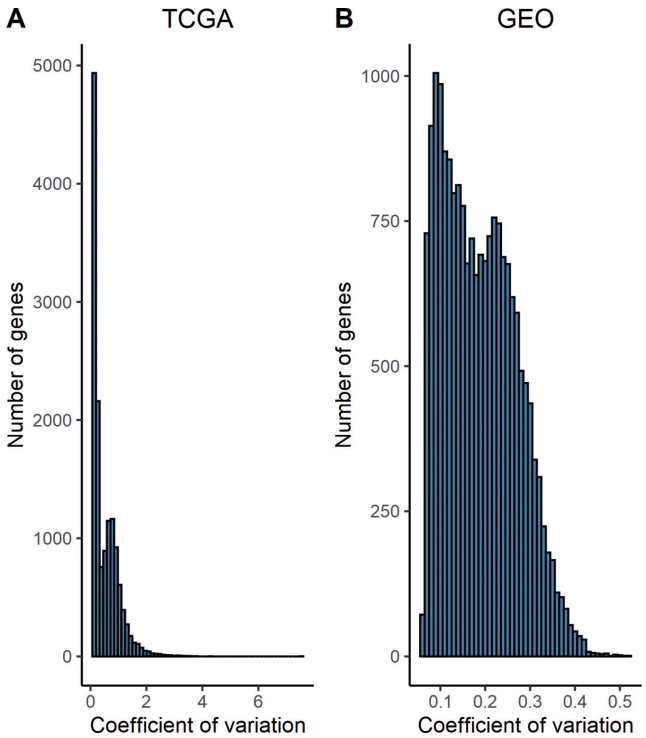

Figure S1 The distribution of coefficient of variation values of *B7-H3* expression in TCGA and GEO cohorts.

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Table S1 Association results of each variable derived from univariate Cox proportional hazards model in TCGA, GEO and UNION cohorts

Variable	TCGA			GEO			UNION		
	HR	95% CI	P	HR	95% CI	P	HR	95% CI	P
Age	1.021	1.003–1.039	0.0225	1.018	1.009–1.028	0.00018	1.006	0.994–1.018	0.3257
Age <65 years	1.462	0.944–2.263	0.0886	1.275	1.001–1.623	0.049	1.439	0.995–2.080	0.0529
Gender	1.124	0.749–1.687	0.5733	1.198	0.9479–1.515	0.130	1.072	0.764–1.505	0.0529
Height	1.001	0.977–1.026	0.9195	–	–	–	0.987	0.966–1.008	0.6864
Weight	0.986	0.971–1.001	0.0746	–	–	–	0.988	0.972–1.004	0.1376
T stage	2.588	1.732–3.867	3.44E–06	–	–	–	1.392	0.900–2.152	0.0125
N stage	2.023	1.592–2.571	8.014E–09	–	–	–	1.327	1.063–1.658	0.3257
M stage	4.753	3.005–7.519	2.70E–11	–	–	–	–	–	–
Clinical stage	2.201	1.728–2.804	1.67e–10	2.274	1.948–2.655	<2E–16	–	–	–
Adenocarcinoma	0.752	0.445–1.272	0.2879	–	–	–	0.927	0.633–1.358	0.6966
Tumor location	0.832	0.529–1.309	0.4263	–	–	–	1.078	0.759–1.532	0.6754
Complete tumor excision	1.229	0.339–4.462	0.7538	–	–	–	1.471	1.046–2.067	0.0265
Carcinoma cell embolus	2.133	1.387–3.281	5.62E–04	–	–	–	1.331	0.929–1.906	0.1189
Tumor size	–	–	–	–	–	–	1.471	1.046–2.067	0.0265
Postoperative therapy	1.16	0.722–1.863	0.5398	–	–	–	0.414	0.283–0.604	4.83E–06
CEA	3.146	1.770–5.591	9.34E–05	–	–	–	0.994	0.708–1.396	0.9744
CA199	–	–	–	–	–	–	1.071	0.761–1.505	0.6949

T, tumor; N, node; M, metastasis; CEA, carcinoembryonic antigen; CA199, carbohydrate antigen 199; HR, hazard ratio; CI, confidence interval; TCGA, The Cancer Genome Atlas; GEO, Gene Expression Omnibus; UNION, Fujian Medical University Union Hospital.

Table S2 Association results of covariates derived from multivariate Cox proportional hazards model in TCGA, GEO and UNION cohorts

Variable	TCGA			GEO			UNION		
	HR	95% CI	P	HR	95% CI	P	HR	95% CI	P
Age	1.033	1.014–1.052	6.38E–04	1.027	1.016–1.039	1.37E–06	1.004	0.992–1.016	0.4969
Gender	0.964	0.631–1.473	0.8663	1.378	1.080–1.757	0.0098	0.987	0.699–1.393	0.9412
T stage	–	–	–	–	–	–	1.214	0.772–1.907	0.4012
N stage	–	–	–	–	–	–	1.286	1.018–1.626	0.0351
Clinical stage	2.386	1.866–3.052	4.34E–12	2.455	2.068–2.916	<2E–16	–	–	–

Clinical stage which composed of T stage, N stage and M stage was included in the model in GEO and TCGA cohort, respectively. T stage and M stage were included in UNION cohort, since all subjects were in M1 stage. Significant variables were screened out by step forward regression model with P value of entry ≤0.05 and P value of remove >0.05 in TCGA, GEO and UNION, respectively. Covariates were defined as significant variables in any one of cohorts, along with two demographic variables (age and gender) common adjusted in COAD prognostic study. T, tumor; N, node; HR, hazard ratio; CI, confidence interval; TCGA, The Cancer Genome Atlas; GEO, Gene Expression Omnibus; UNION, Fujian Medical University Union Hospital.

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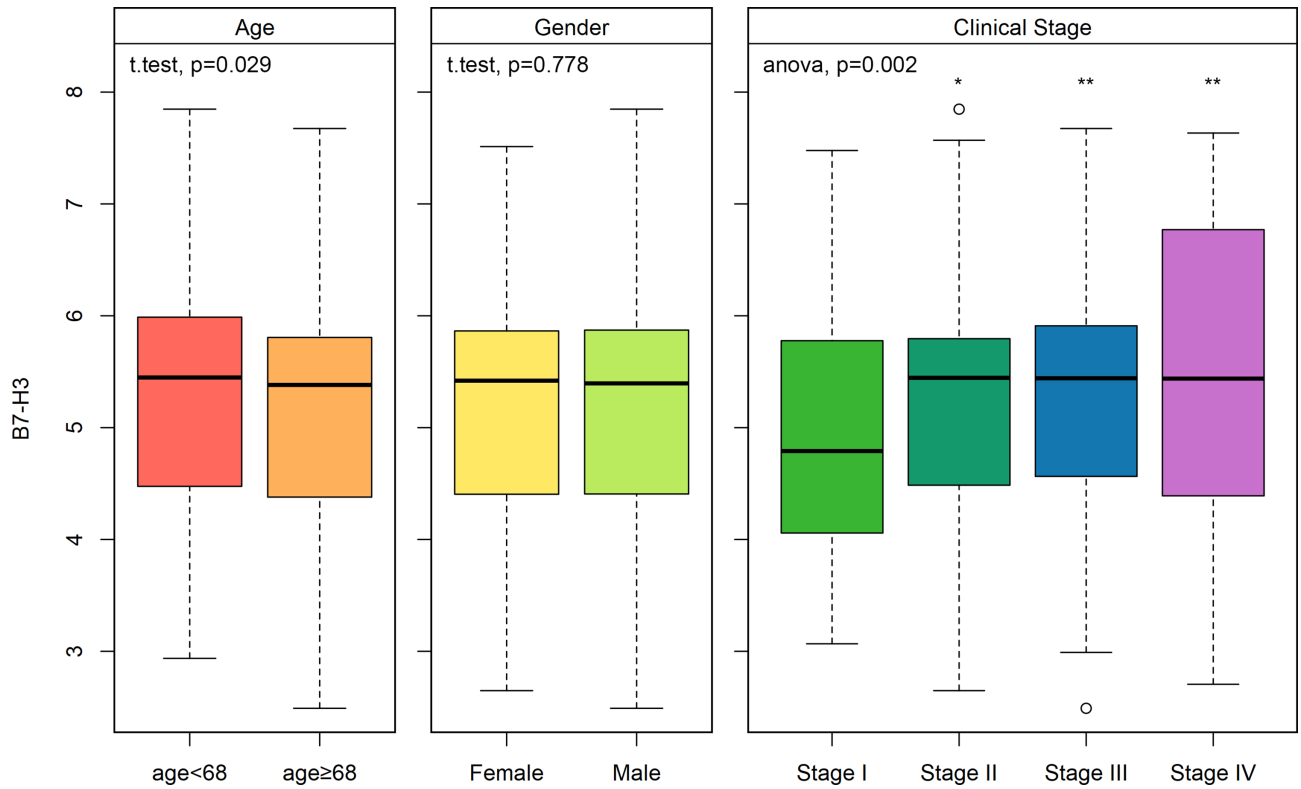

Figure S2 Boxplot of B7-H3 versus clinicopathological factors using all subjects from TCGA and GEO cohorts. The clinical stage for each category was compared with the stage I using a two-sided t test. *, P<0.05; **, P<0.01.

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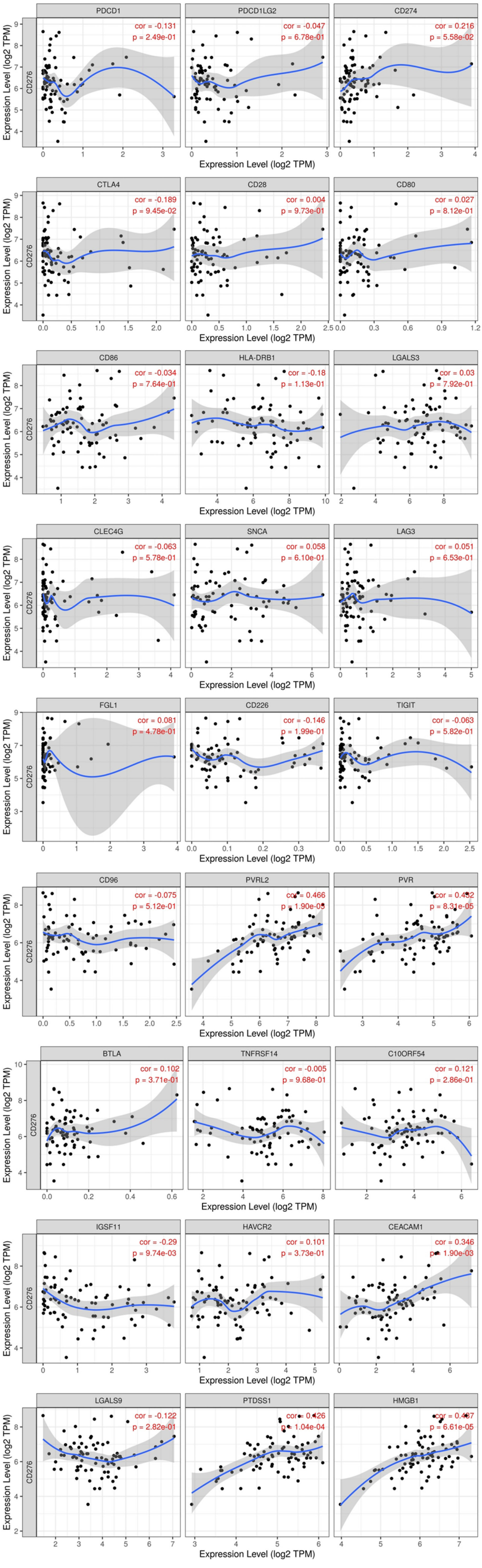

Figure S3 The correlation of between *B7-H3* expression and immune checkpoint genes in colon cancer patients.

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Table S3 The multivariate Cox proportional hazards model using demographic, clinical characteristics and immune checkpoint genes

Variable	TCGA and GEO		
	HR	95% CI	P
Age	1.028	1.018–1.038	3.03E−08
Gender	1.302	1.031–1.642	0.0264
Clinical stage	2.187	1.880–2.543	3.05E−24
Study site	0.874	0.685–1.115	0.2779
B7-H3	1.469	1.067–2.022	0.0184
CTLA4	0.416	0.255–0.681	4.79E−04
LAG3	1.464	1.128–1.900	0.0042
CD80	1.762	1.080–2.875	0.0233
LGALS9	0.725	0.611–0.861	2.53E−04
HMGB1	0.795	0.64–0.988	0.0383
HLA-DOA	1.512	1.110–2.061	0.0088
HLA-DPB1	0.768	0.612–0.964	0.0226

All immune checkpoint genes were screened out by back forward stepwise regression model adjusted for age, gender, clinical stage, study site and B7-H3, with P value of entry ≤0.05 and P value of remove >0.05. HR, hazard ratio; CI, confidence interval; TCGA, The Cancer Genome Atlas; GEO, Gene Expression Omnibus; UNION, Fujian Medical University Union Hospital.

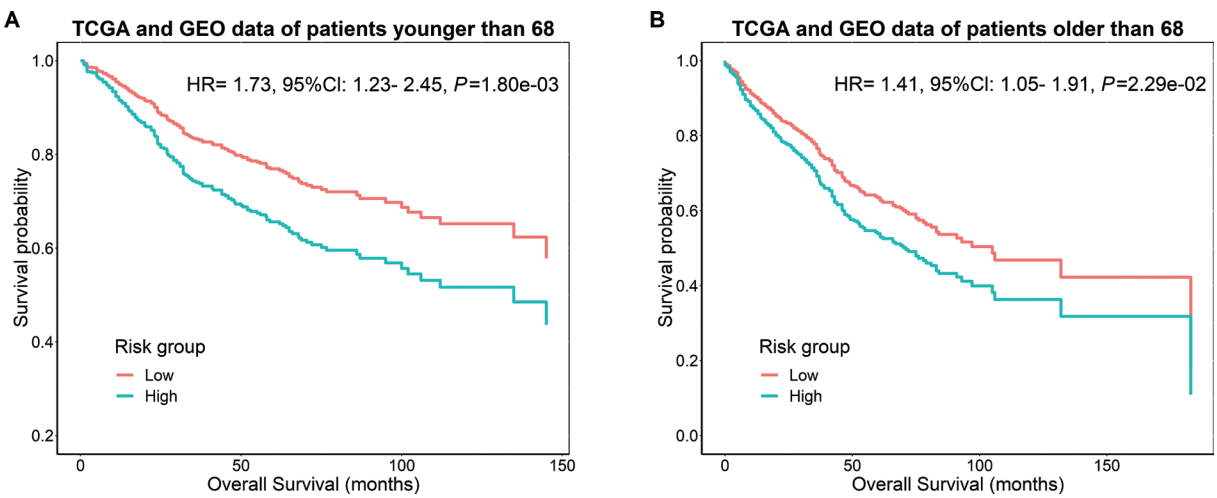

Figure S4 Kaplan-Meier survival curves for patients with high and low level of immune checkpoint prognostic risk score stratified by age using all subjects from TCGA and GEO cohorts.

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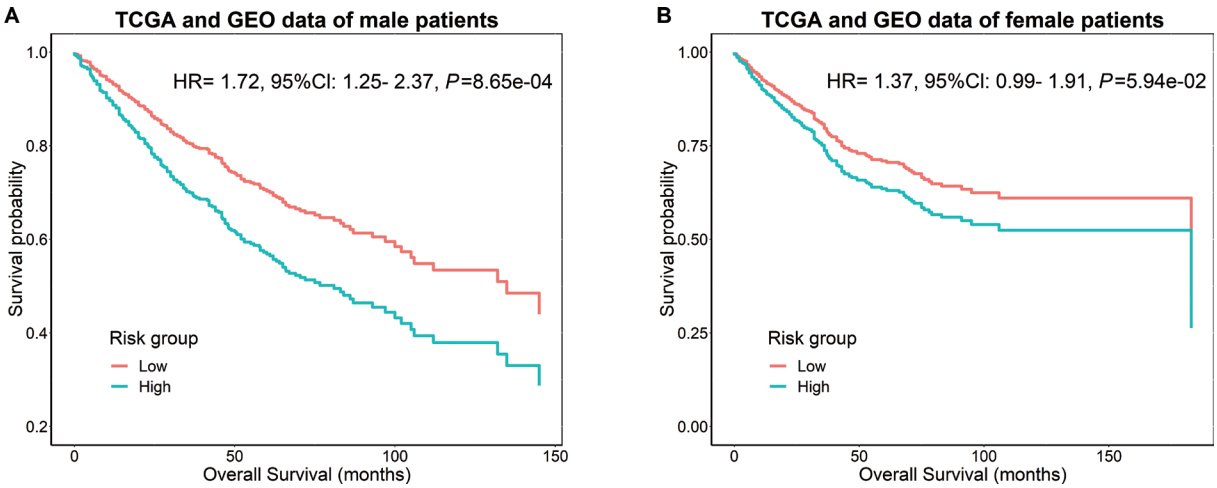

Figure S5 Kaplan-Meier survival curves for patients with high and low level of immune checkpoint prognostic risk score stratified by gender using all subjects from TCGA and GEO cohorts.

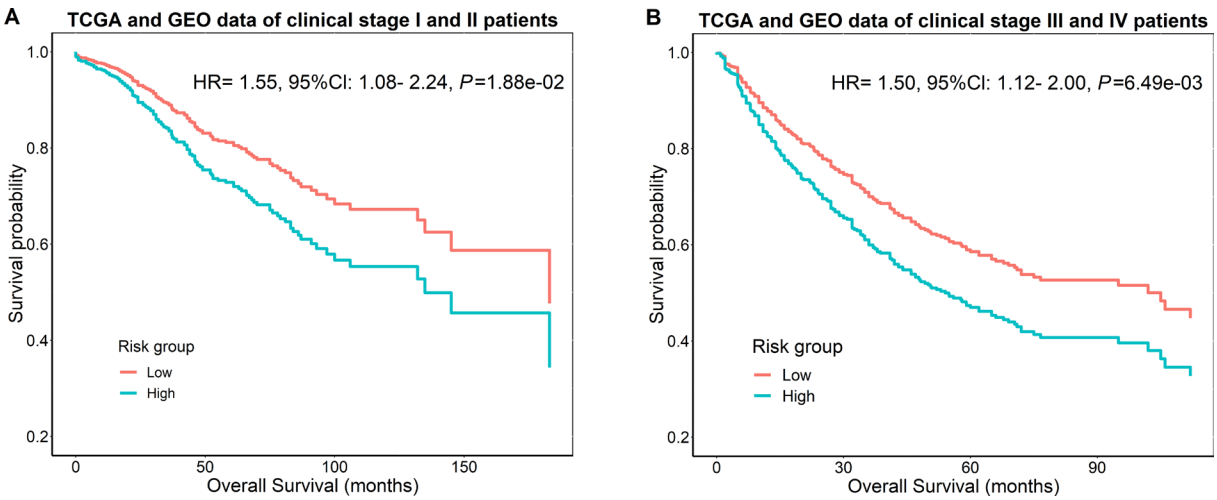

Figure S6 Kaplan-Meier survival curves for patients with high and low level of immune checkpoint prognostic risk score stratified by clinical stage using all subjects from TCGA and GEO cohorts.

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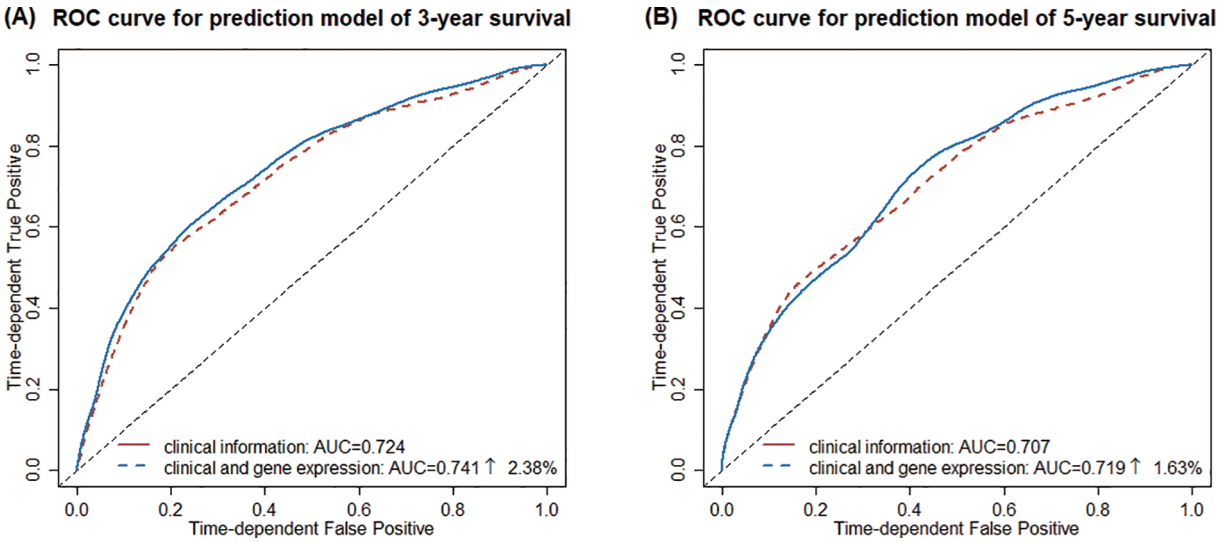

Figure S7 The time-dependent ROC of prognostic prediction model of 3- and 5-year overall survival, respectively.

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