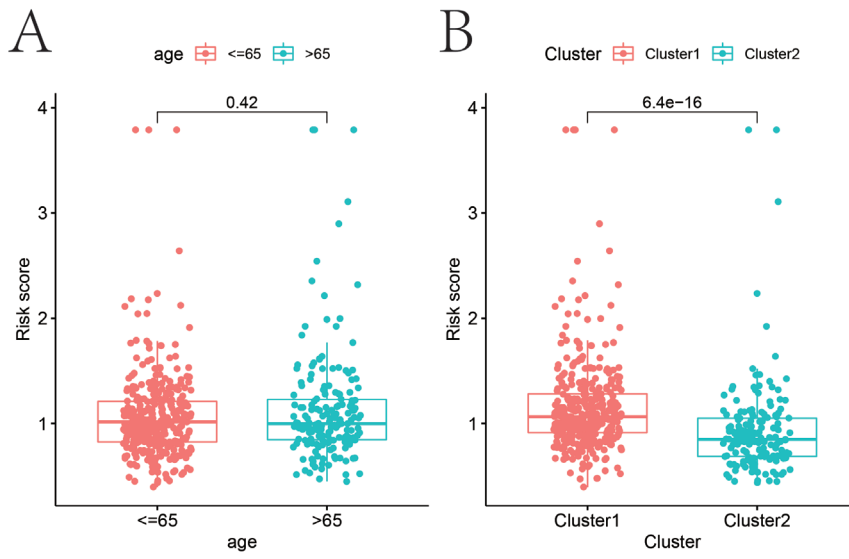
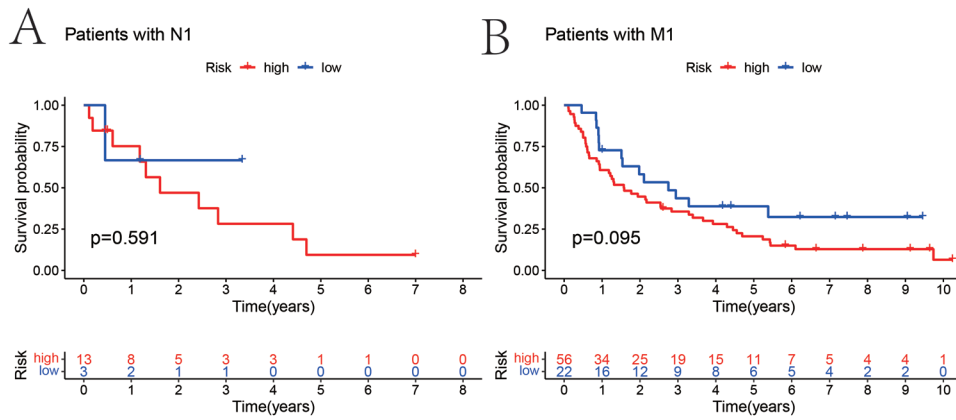


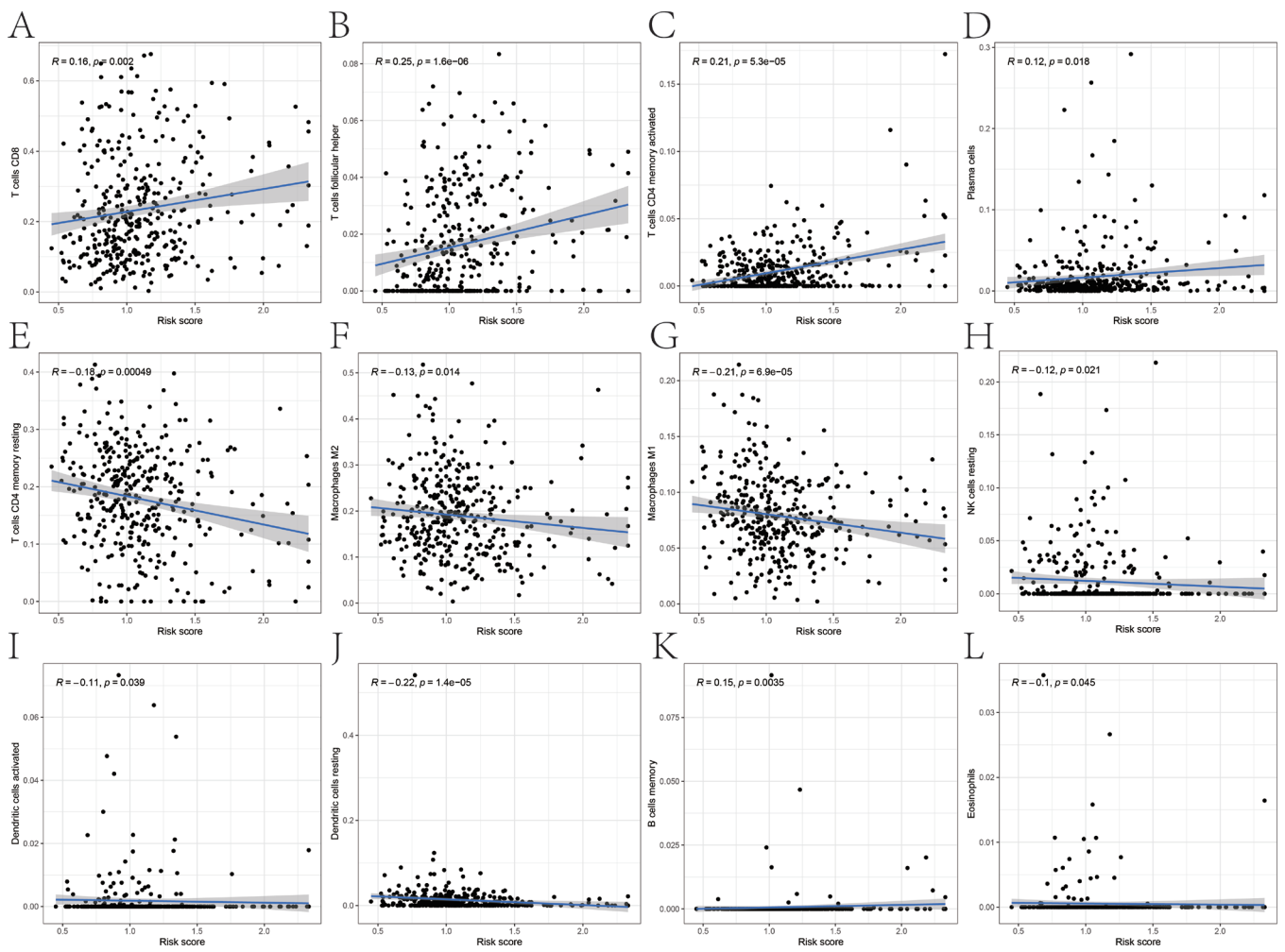
**Figure S1** Evaluation of the CRL signature in total TCGA cohort. (A) Overall survival rate of different risk score groups in the total TCGA cohort; (B) ROC curve of the total TCGA cohort; (C) the total TCGA cohort risk score and survival scatterplot; (D) the t-SNE distribution in the total TCGA cohort; (E) univariate Cox forest map for the total TCGA cohort; (F) multivariate Cox forest map for the total TCGA cohort. AUC, area under the curve; t-SNE, t-distributed stochastic neighbor embedding; CRL, cuproptosis-related long noncoding RNA; TCGA, The Cancer Genome Atlas.



**Figure S2** Differences in risk scores by age (A) and cluster (B).



**Figure S3** The differences in OS between the high- and low-risk groups according to N1 stage (A) and M1 stage (B). OS, overall survival.



**Figure S4** Correlation analysis between the risk score and immune cell infiltration. NK, natural killer.

**Table S1** The cuproptosis-related prognosis DElncRNAs

Gene	HR (95% CI)	P value
<i>LINC02595</i>	1.565 (1.209–2.025)	0.000679925
<i>PINK1-AS</i>	0.864 (0.798–0.935)	0.000277118
<i>AC021483.2</i>	0.492 (0.382–0.633)	3.43E–08
<i>AC015912.3</i>	1.183 (1.129–1.24)	2.30E–12
<i>AC016831.1</i>	1.069 (1.045–1.094)	9.95E–09
<i>AC016877.3</i>	1.29 (1.122–1.483)	0.000348672
<i>LINC02027</i>	0.885 (0.843–0.929)	7.00E–07
<i>LINC02569</i>	0.501 (0.353–0.713)	0.000120216
<i>LINC01963</i>	0.948 (0.918–0.978)	0.000921454
<i>CTBP1-DT</i>	0.909 (0.861–0.959)	0.000539569
<i>TNFRSF10A-AS1</i>	0.928 (0.891–0.966)	0.000311317
<i>EPB41L4A-DT</i>	0.832 (0.791–0.876)	1.69E–12
<i>LINC01711</i>	1.064 (1.049–1.08)	7.96E–17
<i>LINC00886</i>	0.824 (0.748–0.907)	8.29E–05
<i>AC018809.2</i>	0.65 (0.529–0.799)	4.26E–05
<i>AC112493.1</i>	2.023 (1.426–2.869)	7.80E–05
<i>AC112721.2</i>	1.079 (1.049–1.109)	8.93E–08
<i>AL078581.2</i>	0.827 (0.763–0.897)	3.91E–06
<i>AL133355.1</i>	0.857 (0.808–0.909)	3.21E–07
<i>LINC02195</i>	1.197 (1.12–1.28)	1.26E–07
<i>OTUD6B-AS1</i>	0.939 (0.912–0.966)	1.28E–05
<i>AC107308.1</i>	1.063 (1.038–1.09)	8.03E–07
<i>MKLN1-AS</i>	0.845 (0.767–0.932)	0.000728425
<i>AL451164.2</i>	0.314 (0.187–0.527)	1.16E–05
<i>AC108673.3</i>	1.059 (1.037–1.082)	8.01E–08
<i>AC092295.2</i>	0.769 (0.659–0.898)	0.000865784
<i>AC017076.1</i>	1.058 (1.027–1.09)	0.000207033
<i>AC098484.1</i>	0.848 (0.798–0.9)	6.91E–08
<i>SNHG8</i>	0.995 (0.992–0.997)	6.48E–05
<i>AC104211.2</i>	0.875 (0.819–0.934)	6.74E–05
<i>AC064807.1</i>	0.814 (0.738–0.898)	4.01E–05
<i>AL135818.2</i>	1.673 (1.375–2.035)	2.73E–07
<i>EIF3J-DT</i>	0.918 (0.883–0.954)	1.61E–05
<i>AL162377.1</i>	0.558 (0.451–0.691)	7.71E–08
<i>AC005332.6</i>	0.977 (0.966–0.988)	4.98E–05

**Table S1** (continued)**Table S1** (continued)

Gene	HR (95% CI)	P value
<i>AL078644.2</i>	0.71 (0.59–0.853)	0.00026011
<i>EDRF1-DT</i>	0.309 (0.19–0.5)	1.81E–06
<i>AL133215.2</i>	2.043 (1.702–2.452)	1.80E–14
<i>LINC00941</i>	1.114 (1.081–1.148)	2.23E–12
<i>UGDH-AS1</i>	0.776 (0.692–0.87)	1.46E–05
<i>AP001625.2</i>	0.863 (0.796–0.936)	0.000386563
<i>AC034236.3</i>	1.849 (1.483–2.305)	4.64E–08
<i>MANCR</i>	1.06 (1.039–1.082)	1.62E–08
<i>AC116021.1</i>	1.948 (1.658–2.288)	4.84E–16
<i>SNHG4</i>	1.264 (1.166–1.37)	1.29E–08
<i>AL132800.1</i>	0.697 (0.589–0.825)	2.70E–05
<i>AC112721.1</i>	1.106 (1.063–1.151)	8.34E–07
<i>DHRS4-AS1</i>	0.969 (0.952–0.985)	0.000247212
<i>MYOSLID</i>	1.032 (1.02–1.043)	5.56E–08
<i>AC018647.2</i>	0.929 (0.89–0.969)	0.000681983
<i>AC026992.2</i>	0.737 (0.639–0.851)	3.24E–05
<i>PPP1R12A-AS1</i>	0.658 (0.52–0.833)	0.000495515
<i>NNT-AS1</i>	0.908 (0.871–0.946)	5.46E–06
<i>AC073896.4</i>	1.011 (1.005–1.017)	0.000178064
<i>AP001160.3</i>	0.836 (0.777–0.9)	1.69E–06
<i>AL731577.2</i>	0.593 (0.489–0.72)	1.29E–07
<i>AC097639.1</i>	0.68 (0.568–0.814)	2.57E–05
<i>AC103746.1</i>	0.737 (0.619–0.878)	0.00063198
<i>AC007743.1</i>	0.832 (0.767–0.903)	9.85E–06
<i>AC099850.4</i>	1.032 (1.021–1.044)	2.69E–08
<i>AC112220.2</i>	0.774 (0.695–0.862)	3.28E–06
<i>SNHG3</i>	1.042 (1.031–1.053)	5.53E–14
<i>AC121338.2</i>	0.695 (0.618–0.78)	8.92E–10
<i>AC016394.3</i>	1.176 (1.109–1.248)	7.71E–08
<i>AC080038.2</i>	1.166 (1.113–1.221)	6.25E–11
<i>FAM160A1-DT</i>	0.787 (0.687–0.901)	0.000506828
<i>SNHG29</i>	0.998 (0.997–0.999)	0.000985994
<i>AC013451.2</i>	1.31 (1.19–1.442)	3.47E–08
<i>LINC01812</i>	1.206 (1.117–1.303)	1.88E–06

**Table S1** (continued)

Table S1 (continued)

Gene	HR (95% CI)	P value
AC018752.1	0.863 (0.816–0.913)	3.29E-07
DNMBP-AS1	0.497 (0.351–0.704)	8.21E-05
AC007365.1	0.7 (0.57–0.86)	0.000671567
LYPLAL1-DT	0.501 (0.353–0.713)	0.000117909
LIFR-AS1	0.814 (0.73–0.908)	0.000217501
AC005034.6	0.887 (0.83–0.947)	0.000353458
FAM225B	4.192 (2.636–6.666)	1.42E-09
AC026401.3	1.069 (1.052–1.087)	3.11E-15
USP27X-AS1	0.762 (0.681–0.852)	1.75E-06
NAPA-AS1	0.85 (0.78–0.926)	0.000212555
UBL7-AS1	0.75 (0.64–0.878)	0.000357837
AC007637.1	0.851 (0.781–0.927)	0.000207958
TRAM2-AS1	0.931 (0.903–0.96)	4.99E-06
AC015922.2	0.976 (0.964–0.989)	0.000225266
AC124242.1	0.554 (0.415–0.739)	5.94E-05
AL161782.1	0.612 (0.521–0.719)	2.33E-09
AC007376.2	0.598 (0.446–0.803)	0.000626628
LINC02446	1.047 (1.029–1.065)	1.20E-07
LINC01132	0.644 (0.54–0.768)	9.79E-07
GNG12-AS1	0.458 (0.337–0.621)	5.44E-07
APCDD1L-DT	1.031 (1.022–1.041)	1.17E-10
AC095055.1	0.634 (0.536–0.75)	1.02E-07
AP001922.5	0.735 (0.626–0.862)	0.000150883
LINC01624	0.094 (0.027–0.326)	0.000200994
AC103706.1	1.23 (1.175–1.288)	8.69E-19
AC008555.1	0.839 (0.78–0.904)	3.20E-06
AC005291.1	1.057 (1.033–1.082)	2.57E-06
AL606489.1	0.897 (0.843–0.955)	0.000634993
AC009486.1	0.692 (0.561–0.854)	0.000612335
CNIH3-AS2	1.163 (1.11–1.218)	1.66E-10
AC073254.1	0.584 (0.442–0.77)	0.000141176
AC006213.1	0.264 (0.139–0.499)	4.31E-05
PLBD1-AS1	0.896 (0.846–0.949)	0.000180431
AC005670.3	0.875 (0.819–0.934)	6.79E-05

Table S1 (continued)

Table S1 (continued)

Gene	HR (95% CI)	P value
LINC00571	0.764 (0.652–0.895)	0.000863463
AC104109.2	0.64 (0.511–0.802)	0.000100522
RGMB-AS1	1.597 (1.391–1.832)	2.67E-11
SEPTIN7-DT	0.701 (0.589–0.833)	5.81E-05
AL449423.1	3.16 (2.063–4.84)	1.23E-07
AC120114.1	0.767 (0.667–0.882)	0.000191843
U91328.1	0.846 (0.789–0.907)	2.62E-06
AP001372.2	0.885 (0.847–0.926)	8.28E-08
LINC02725	1.178 (1.105–1.255)	4.51E-07
AC017100.1	0.792 (0.697–0.9)	0.000353668
EMX2OS	0.971 (0.962–0.98)	3.92E-10
AP003068.2	0.887 (0.838–0.938)	2.84E-05
AC008543.1	0.479 (0.327–0.703)	0.000168705
BDNF-AS	0.668 (0.564–0.791)	2.85E-06
LINC02454	1.234 (1.162–1.31)	5.41E-12
LINC01852	0.808 (0.715–0.913)	0.0006294
AC005291.2	1.039 (1.024–1.054)	1.93E-07
MIR100HG	1.05 (1.03–1.07)	6.35E-07
AC115522.1	0.633 (0.49–0.817)	0.000438064
SNHG1	1.012 (1.006–1.018)	0.000162164
AC079922.2	1.258 (1.177–1.346)	1.90E-11
AC124067.2	1.082 (1.048–1.116)	8.01E-07
AC093278.2	0.956 (0.94–0.972)	9.14E-08
PARAL1	2.324 (1.647–3.278)	1.56E-06
STX17-AS1	0.836 (0.757–0.922)	0.000364766
ATP1A1-AS1	0.76 (0.688–0.839)	5.83E-08
AL355312.4	1.079 (1.045–1.114)	2.53E-06
AC242426.2	0.701 (0.571–0.861)	0.000725064
AC079848.1	0.606 (0.481–0.764)	2.24E-05
LINC00665	0.935 (0.9–0.971)	0.000575704
AC068870.2	0.958 (0.937–0.979)	0.000124853
RAP2C-AS1	0.668 (0.544–0.82)	0.000110803
FAM225A	2.74 (2.077–3.615)	1.01E-12
LINC00460	1.035 (1.026–1.044)	1.34E-14

Table S1 (continued)

**Table S1** (continued)

Gene	HR (95% CI)	P value
<i>PICRAR</i>	1.068 (1.04–1.097)	1.01E–06
<i>CDK6-AS1</i>	1.125 (1.086–1.166)	5.52E–11
<i>ITGA9-AS1</i>	0.566 (0.417–0.767)	0.000241135
<i>SUCLG2-AS1</i>	0.619 (0.474–0.808)	0.000412821
<i>SGMS1-AS1</i>	0.649 (0.546–0.771)	8.66E–07
<i>WDFY3-AS2</i>	0.903 (0.865–0.942)	2.74E–06
<i>AC073130.1</i>	2.964 (1.893–4.64)	2.01E–06
<i>LINC01671</i>	0.986 (0.981–0.991)	2.12E–07
<i>AC006058.3</i>	1.271 (1.156–1.398)	6.83E–07
<i>KIAA1671-AS1</i>	0.742 (0.652–0.845)	6.88E–06
<i>LINC02657</i>	1.044 (1.027–1.06)	8.01E–08
<i>AC008669.1</i>	0.881 (0.832–0.932)	1.07E–05
<i>AC005224.3</i>	1.364 (1.212–1.536)	2.79E–07
<i>AL162171.1</i>	0.786 (0.701–0.882)	3.97E–05
<i>AC134312.5</i>	1.162 (1.078–1.254)	9.59E–05
<i>LINC01801</i>	0.783 (0.7–0.875)	1.70E–05

DElncRNAs, differentially expressed lncRNAs; HR, hazard ratio; CI, confidence interval.

**Table S2** The Ensembl ID, coefficients, HRs and P values of 5 cuproptosis-related lncRNAs

LncRNA	Ensembl ID	Coef	Unicox	
			HR (95% CI)	P value
<i>AC015912.3</i>	ENSG00000274213	0.011	1.183 (1.129–1.240)	2.300E–12
<i>AC026401.3</i>	ENSG00000280206	0.015	1.070 (1.052–1.087)	3.109E–15
<i>AC103706.1</i>	ENSG00000261220	0.068	1.230 (1.175–1.288)	8.686E–19
<i>AC134312.5</i>	ENSG00000261327	0.102	1.162 (1.078–1.254)	9.591E–05
<i>EMX2OS</i>	ENSG00000229847	–0.011	0.971 (0.962–0.980)	3.922E–10

LncRNAs, long noncoding RNAs; Coef, coefficient; HR, hazard ratio; CI, confidence interval; Unicox, univariate Cox analysis.

**Table S3** Univariate and multivariate Cox regression analysis of the association between clinicopathological factors (including risk score) and OS of ccRCC patients in the training, testing and overall cohorts

Variables	Training cohorts				Testing cohorts				Overall cohorts			
	Univariate		Multivariate		Univariate		Multivariate		Univariate		Multivariate	
	HR (95% CI)	P value	HR (95% CI)	P value	HR (95% CI)	P value	HR (95% CI)	P value	HR (95% CI)	P value	HR (95% CI)	P value
Age	1.027 (1.008–1.046)	0.004	1.030 (1.009–1.050)	0.004	1.036 (1.017–1.057)	<0.001	1.035 (1.013–1.058)	0.002	1.032 (1.018–1.045)	<0.001	1.032 (1.017–1.047)	<0.001
Gender	1.222 (0.761–1.960)	0.407	1.158 (0.711–1.866)	0.556	0.767 (0.505–1.166)	0.215	0.822 (0.536–1.261)	0.37	0.950 (0.695–1.298)	0.748	0.944 (0.686–1.299)	0.724
Grade	2.577 (1.881–3.530)	<0.001	1.225 (0.834–1.799)	0.3	2.054 (1.574–2.680)	<0.001	1.331 (0.988–1.795)	0.06	2.279 (1.859–2.795)	<0.001	1.465 (1.164–1.843)	0.001
Stage	1.943 (1.596–2.365)	<0.001	1.631 (1.291–2.061)	<0.001	1.816 (1.518–2.172)	<0.001	1.627 (1.324–2.000)	<0.001	1.863 (1.633–2.126)	<0.001	1.622 (1.394–1.889)	<0.001
Risk score	3.703 (2.719–5.043)	<0.001	2.578 (1.751–3.798)	<0.001	1.229 (1.142–1.323)	<0.001	1.150 (1.060–1.248)	0.001	1.288 (1.212–1.370)	<0.001	1.192 (1.111–1.279)	<0.001

OS, overall survival; ccRCC, clear cell renal cell carcinoma; HR, hazard ratio; CI, confidence interval.