

## Supplementary

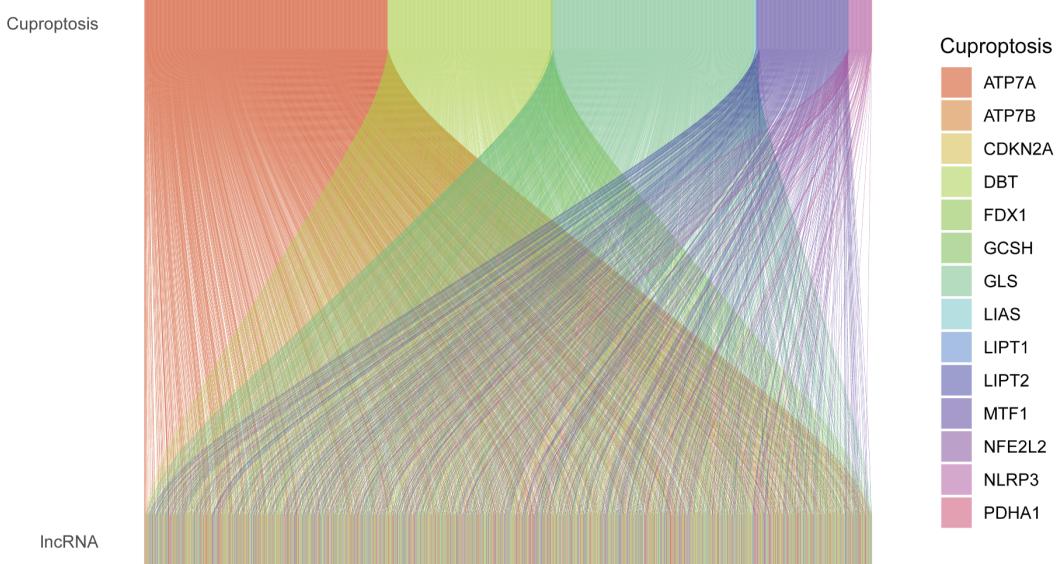
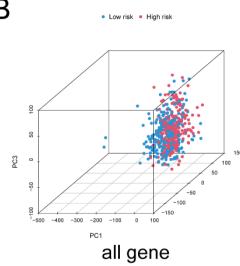
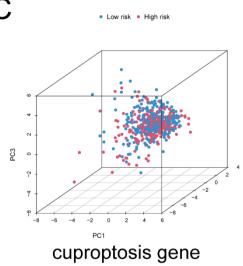
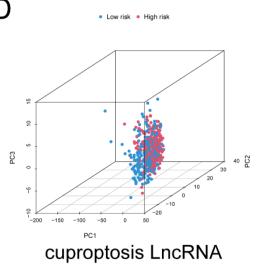
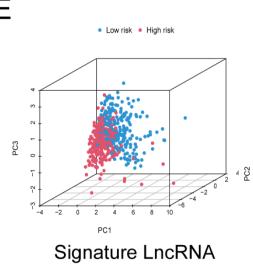
**Table S1** Cuproptosis-related genes

Genes
<i>NFE2L2</i>
<i>NLRP3</i>
<i>ATP7B</i>
<i>ATP7A</i>
<i>SLC31A1</i>
<i>FDX1</i>
<i>LIAS</i>
<i>LIPT1</i>
<i>LIPT2</i>
<i>DLD</i>
<i>DLAT</i>
<i>PDHA1</i>
<i>PDHB</i>
<i>MTF1</i>
<i>GLS</i>
<i>CDKN2A</i>
<i>DBT</i>
<i>GCSH</i>
<i>DLST</i>

**Table S2** Demographic and clinical characteristics between the training and testing cohort

Characteristics	Total	Train	Test	P-value*
Age, years				0.1464
<=65	237 (47.4%)	128 (51.2%)	109 (43.6%)	
>65	253 (50.6%)	119 (47.6%)	134 (53.6%)	
unknow	10 (2%)	3 (1.2%)	7 (2.8%)	
Gender				0.2434
Female	270 (54%)	128 (51.2%)	142 (56.8%)	
Male	230 (46%)	122 (48.8%)	108 (43.2%)	
Stage				0.2969
Stage I	268 (53.6%)	124 (49.6%)	144 (57.6%)	
Stage II	119 (23.8%)	66 (26.4%)	53 (21.2%)	
Stage III	80 (16%)	43 (17.2%)	37 (14.8%)	
Stage IV	25 (5%)	11 (4.4%)	14 (5.6%)	
unknow	8 (1.6%)	6 (2.4%)	2 (0.8%)	

\*Chi-square test.

**A****B****C****D****E**

**Figure S1** Identification of cuproptosis-related lncRNAs and principal component analysis (PCA) in the entire LUAD cohort. (A) Sankey diagram for cuproptosis-related genes and lncRNAs. (B-E) PCA analysis based on (B) all gene, (C) cuproptosis-related gene, (D) cuproptosis-related lncRNAs and (E) signature lncRNAs, respectively.

**Table S3** The cuproptosis-related lncRNAs risk signature

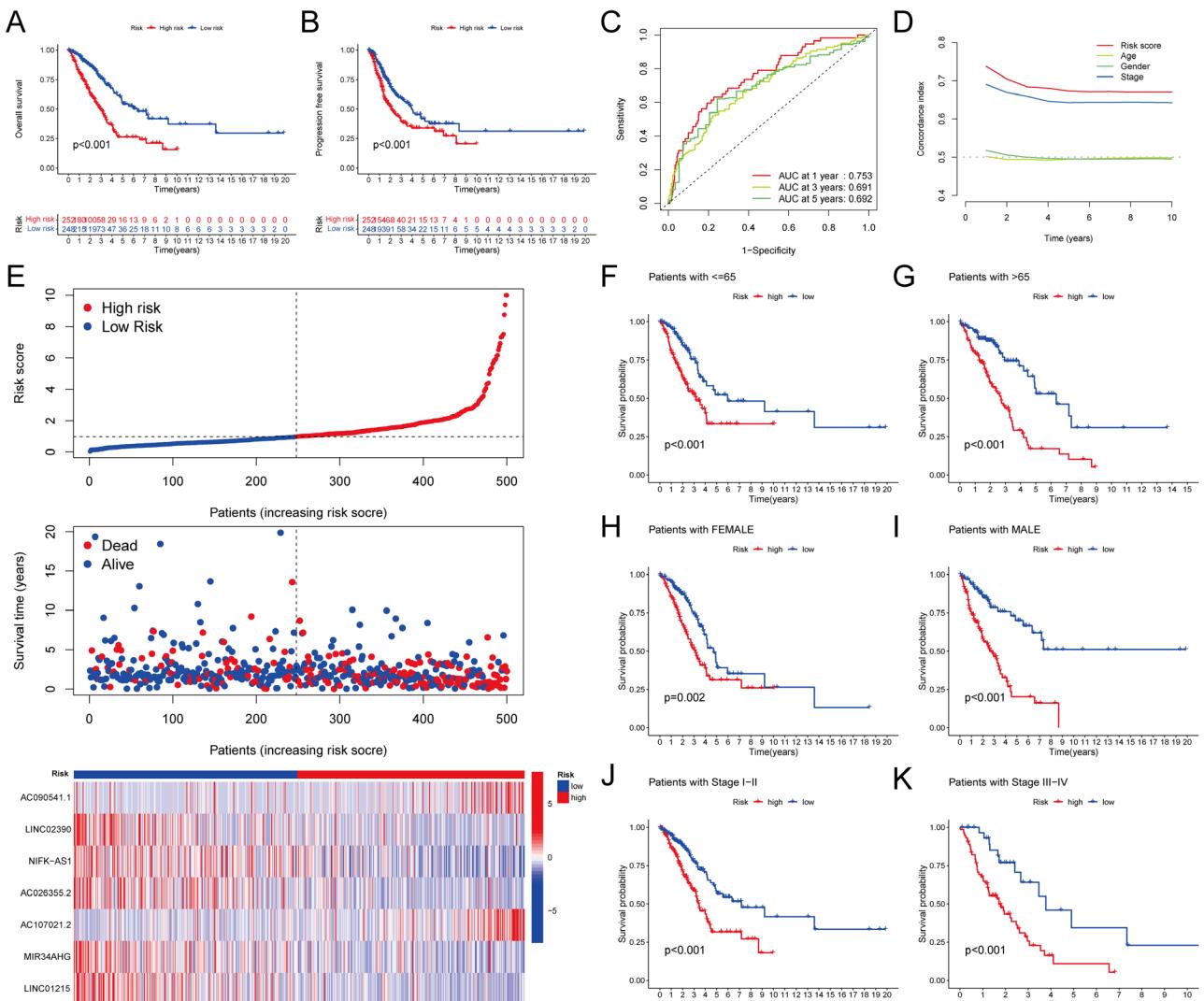
LncRNAs	coefficient
AC090541.1	0.425683724
LINC02390	-1.102861115
NIFK-AS1	-0.766522002
AC026355.2	-0.40311251
AC107021.2	1.174579099
MIR34AHG	-0.944282562
LINC01215	-0.560092802

Table S4 Risk score for patients in the training cohort

Id	AC090541.1	LINC02390	NIFK-AS1	AC026355.2	AC107021.2	MIR34AHG	LINC01215	Risk score	Risk group*
TCGA-MP-A4T6	0.05407954	0.1730156	2.030406	1.02374717	0.12916287	1.65100897	0.56728239	0.12979256	low
TCGA-95-4510	0.53529687	0.17114833	2.05645971	0.48663555	0.2039159	0.10907205	0.20729754	0.2999086	high
TCGA-67-3772	0.11498889	0.04906933	1.83188143	1.5594179	0.25605317	0.2292404	0.57853456	0.63276106	low
TCGA-69-7763	0.97346191	0	1.49093153	0.95376318	0.22287342	0.3536205	0.44025964	1.47463016	high
TCGA-MP-A4TC	0.1230606	0	1.12260186	1.6108648	0.43012655	0.18772754	0.07881453	1.90943537	high
TCGA-95-4AVK	0.93552273	0.31071831	2.22427093	0.10624599	0.08982305	0.67639596	1.16187221	0.3477966	low
TCGA-49-AARO	0	0.67805052	1.30049044	1.25457879	0.35116967	0.36916063	0.94214184	0.37031953	low
TCGA-55-7994	0	0.37533578	1.34517512	2.57861971	0.42155365	0.18201083	1.11584708	0.38053565	low
TCGA-78-T149	0.66626008	0.15632011	2.5959549	1.98104086	0.15337058	0.06691136	0.20987866	0.59771172	low
TCGA-44-7860	0	0	2.32494489	0.24470278	0.37127899	0.26416569	0.63337844	0.85228634	low
TCGA-44-2656	1.19054778	0.74689595	1.51205475	3.45490649	0.57105857	1.11012776	0.82573633	0.15018754	low
TCGA-78-7153	0.13393286	0.21692117	1.29034655	0.25517983	0.23079375	0.3816907	0.12119496	1.47500681	high
TCGA-55-5987	0.04051085	0.19218331	1.33222483	2.20266968	0.5802894	0.16119727	1.60505982	0.52035532	low
TCGA-78-7539	0	0.3211262	1.84495844	0.58443243	0.00958224	0.20804686	0.4273043	0.54420041	low
TCGA-83-5908	0	0.044635384	1.1101615	0.95941826	0.16039329	0.02096602	0.45773947	1.5134234	high
TCGA-95-7567	0	0.03443009	1.51819217	1.50756633	0.05482862	0.34540126	0.10871971	0.73196715	low
TCGA-44-7667	0.09666357	0	1.93891167	0.07742243	0.35394518	0.28184279	0.06170532	1.58218034	high
TCGA-69-8254	0.0670508	0.16232358	1.29749468	0.48274587	0.1863252	0.2600026	0.5364019	1.1660341	high
TCGA-44-447G	0.14679863	0.39245811	1.40247916	1.21463028	0.45426003	0.35357654	1.17227256	0.56346032	low
TCGA-44-2668	1.37103571	0.31680164	1.33544857	1.92934182	2.84672029	1.63825162	2.77767563	1.63857561	high
TCGA-44-6775	1.83067314	0.86223612	1.44579493	2.50184635	1.02708867	1.45097757	0.84149423	0.33174077	low
TCGA-55-5899	0	0.13874567	1.91340526	0.13264825	0.16553457	0.39402993	0.12066856	0.09613065	low
TCGA-J2-A4AD	0	0	2.11547969	2.15024963	0.53690214	0.31838999	0.06056101	0.689187	low
TCGA-69-7974	0	0.06778981	1.27806209	1.07143626	0.15799958	0.12406986	0.44211641	1.16708865	high
TCGA-05-4403	0	0.05170461	1.03842213	0.18807424	0.08868207	0.49433901	0.12520016	0.51816690	high
TCGA-97-7938	0	0.06848124	2.17712836	0.8756000	0.10831055	0.16477389	0.58882596	0.83897535	low
TCGA-62-A46P	0.18386123	0	1.3563664	0.21685948	0.12551152	0.27688921	0.03490403	1.89197267	high
TCGA-92-8399	0.11302346	0.09485599	1.36666856	0.88238599	0.12542361	0.05975047	0.17905505	0.43393126	low
TCGA-64-5775	0	0	0.90479289	0.05104006	0.96979318	0.06622705	0.2334163	8.75318123	high
TCGA-95-4403	0.19118235	0.08281622	1.26853754	0.22559501	0.98490071	0.28756461	0.26812175	4.4023599	high
TCGA-93-A4JO	0	0.17271165	1.85011331	0.40439591	0.24037894	0.14470793	1.13736581	0.64215069	low
TCGA-NJ-A4YP	0.49484126	0.04840569	1.33721441	0.37068679	0.26382431	0.27769044	0.23502398	2.05204986	high
TCGA-97-8171	0	0	1.60156721	0.46550027	0.72020219	0.32763654	0.13764111	1.778579	high
TCGA-44-8147	1.78832632	0.52513295	1.59463026	3.93548085	0.72391442	1.23231452	1.61451997	0.13011433	low
TCGA-55-1592	0.0393526	0.06504908	2.22098243	0.50384929	0.26713388	0.54513364	0.24408307	0.6191049	low
TCGA-99-7760	0	0.06014184	1.20022034	0.25993913	1.14903088	0.39821726	0.03926983	2.5991248	high
TCGA-64-5778	0	0.17051196	2.4191659	0.6766000	0.020976265	0.50216162	1.16789354	0.52532274	low
TCGA-55-8620	0	0	2.62959959	0.13354105	0.3621323	0	0.33749417	0.98971257	high
TCGA-53-7813	0.44775056	0.20381294	1.85244836	0.59153006	0.55231942	0.13015984	0.52864143	1.42945625	high
TCGA-78-7542	0.03878278	0.03241383	1.10851844	0.17639988	0.07095731	0.04022768	0.11563754	0.49586494	high
TCGA-86-8073	0.0389579	0.21333454	1.59686643	1.52528817	0.24932563	0.11768778	0.24121859	1.32265401	high
TCGA-91-6848	0	0	1.43017417	0.32256835	0.29649899	0.21836885	1.61207109	0.8461204	low
TCGA-05-4424	0	0.11483771	1.60737153	1.57340191	0.60252772	0.20746729	0.56000912	0.54338354	low
TCGA-86-A4PT	0	0.26584858	1.63185361	1.64315226	0.30799088	0.32400947	0.68102824	0.49066461	low
TCGA-05-4405	0	0.23290562	1.5046815	0.58633011	0.20927183	0.52210795	0.13873316	0.85945389	low
TCGA-97-7553	0	0.04866405	1.53523405	0.51162096	0.08979486	0.46925635	0.75668067	0.68514377	low
TCGA-49-4761	0	0	0.57870007	0.75232009	0.37302161	0.49784614	0.37640986	1.99856426	high
TCGA-NJ-A4YG	0	0.28260432	1.37027813	0.73169022	0.23084747	0.14758479	0.28101924	1.14735436	high
TCGA-97-8171	0	0	1.60156721	0.46550027	0.72020219	0.32763654	0.13764111	1.778579	high
TCGA-44-8147	1.78832632	0.52513295	1.59463026	3.93548085	0.72391442	1.23231452	1.61451997	0.13011433	low
TCGA-55-1592	0.0393526	0.06504908	2.22098243	0.50384929	0.26713388	0.54513364	0.24408307	0.6191049	low
TCGA-99-7760	0	0.06014184	1.20022034	0.25993913	1.14903088	0.39821726	0.03926983	2.5991248	high
TCGA-64-5778	0	0.17051196	2.4191659	0.6766000	0.020976265	0.50216162	1.16789354	0.52532274	low
TCGA-55-8620	0	0	2.62959959	0.13354105	0.3621323	0	0.33749417	0.98971257	high
TCGA-53-7813	0.44775056	0.20381294</							

Table S5 Risk score for patients in the testing cohort

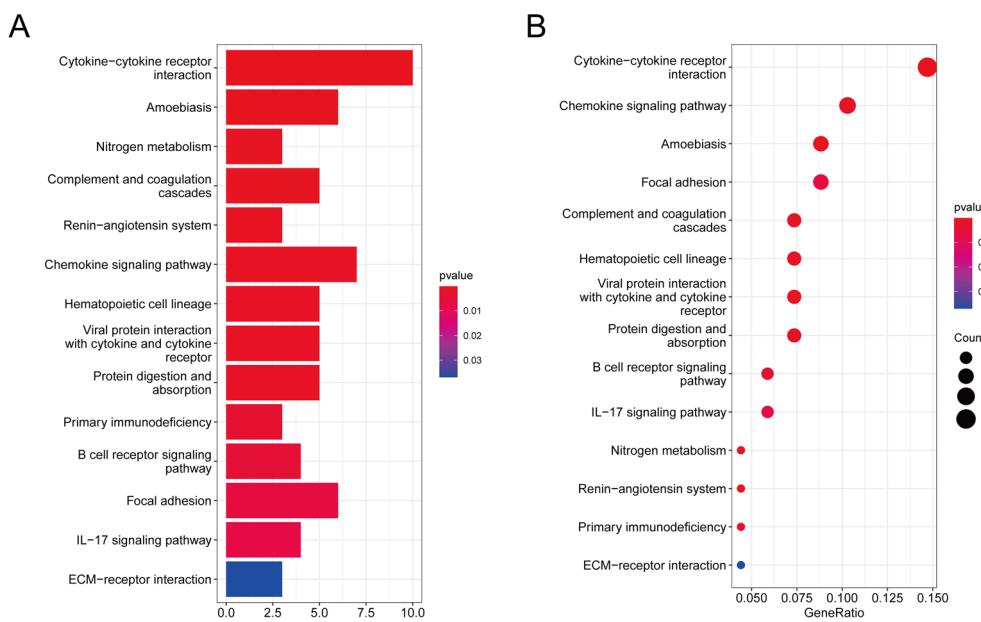
Id	AC005041.1	LINC02390	NIPK-AS1	AC026355.2	AC107021.2	MIR34AHG	LINC01215	Risk score	Risk group*
TCGA-MP-A4T8	0.462189093	0.049617916	0.827135695	1.849496129	0.281101526	0.686717537	0.184056334	1.174838073	high
TCGA-95-T039	0	0.079439228	0.867453818	0.767269747	0.240711939	0.098210119	0.228011479	2.776360244	high
TCGA-82-A46S	0.115275337	0.096757925	1.406284930	0.581425682	0.164173807	0.33224677	0.292549133	1.17802352	high
TCGA-49-A743	0.075822907	0	1.119435863	3.664156263	0.469803371	0.356147304	0.369237309	0.622441881	low
TCGA-53-T626	0.04163676	0.257427551	1.854865688	2.026779879	0.186866005	1.001998011	0.919580353	0.142549274	low
TCGA-44-B119	0.034116639	0.083883141	1.716354871	0.251491163	1.308928731	0.348425748	0.276507147	3.969512342	high
TCGA-95-T574	0	0.258279664	1.509869133	0.645264582	0.120805799	0.492383767	0.082761687	0.254124551	low
TCGA-78-T163	0	0	2.056734817	0.772845466	0.214585076	0.236051443	0.111353277	0.903708009	low
TCGA-91-A48C	0	0.344056392	1.578315141	0.443294529	0.473783899	0.181499261	0.368413791	1.25967579	high
TCGA-89-T980	0	0.036889572	1.99496831	0.603002396	0.329011939	0.330594542	0.423665698	0.855338823	low
TCGA-05-4417	0.246293812	0	1.104930893	0.135841537	0.186907694	0.402701446	0.604616115	0.449741212	high
TCGA-05-5425	0.076928936	0.126112717	1.418458218	0.431451377	0.118310125	0.360686687	0.834691675	0.900527345	low
TCGA-44-B146	2.553693899	0.114651138	1.416562163	2.167833018	1.055850418	0.904188521	0.189959334	3.007591549	high
TCGA-67-3770	0	0.090389553	1.424838802	1.350471405	0.164763499	0.111649415	0.519085323	0.647185823	low
TCGA-MP-A4T4	0	0.318327676	1.260567797	0.594844888	0.36285539	0.441949138	0.448534931	0.20907578	high
TCGA-NJ-A4YF	0	0.06751282	1.359738739	1.37832961	0.971190587	0.237390682	0.100916159	2.739437251	high
TCGA-50-5055	0.112304036	0	1.666322128	0.53687695	0.194545136	0.324273971	2.709824158	0.924849196	low
TCGA-44-B776	0.260497241	0.077255484	1.413222573	1.27317569	0.062276793	0.349165053	0.083271934	0.94760711	low
TCGA-64-1677	0	0	1.595419159	2.744073024	0.542285987	0.471159777	0.435123429	0.570805791	low
TCGA-05-4389	0	0	1.532233662	1.147397882	0.052426662	0.389704247	0.486268703	0.673181002	low
TCGA-05-A425	0	0	1.699276999	0.12571854	0.054178184	0.367474423	1.280159592	1.106357973	high
TCGA-91-A835	0	0.486396563	1.816894848	1.151551375	0.075308675	0.484956032	1.891326192	0.134972855	low
TCGA-55-6982	0	0	1.001427643	1.511789428	0.292567706	0.312125541	0.188752221	1.471379467	high
TCGA-55-A491	0	0.059177313	1.085403665	0.309959802	0.465233445	0.143019066	0.336103808	2.775983044	high
TCGA-55-8094	1.380228518	0.322692636	1.451877862	0.363950795	0.392515374	0.553757129	0.076087697	1.834937301	high
TCGA-82-A46R	0	0.22515613	1.616215212	0.056977006	0.168845281	0.27535146	0.060470566	0.913914945	low
TCGA-49-AAR9	0	0	0.809622046	0	0.29816666	0.188289632	0.034502394	3.867280461	high
TCGA-55-7227	0	0.066558218	1.638057151	0.782994331	0.310120405	0.234202034	0.483192527	1.049901141	high
TCGA-55-A48Z	0.067498429	0.355698693	1.362380795	0.543274011	0.576419695	0.376563206	0.197496056	1.497880545	high
TCGA-MN-A4N4	0.128217753	0.158674748	1.210826474	2.361969933	0.733767695	0.613994963	0.138123487	1.24369245	high
TCGA-49-A744	0	0.222243956	1.501902245	0.811231526	0.638287346	0.390543341	0.736104701	1.067514806	high
TCGA-73-4676	0	0	0.699367607	2.623946189	0.197816377	0.275625174	0.126141474	1.136159018	high
TCGA-38-4630	0	0.104742187	2.293165211	0.507011957	0.386214832	0.459261303	1.264957302	0.466601668	low
TCGA-75-7027	0.5161239	0.099390139	1.694824153	0.513719638	0.378081747	0.188383706	0.08150231	1.916542465	high
TCGA-05-4382	0	0.082491564	1.741347035	2.807858394	0.907358184	0.197184636	0.640983453	0.804608066	low
TCGA-78-B662	0	0	1.781356979	0.386279562	0.014109659	0.094799226	0.175942515	0.82754961	low
TCGA-97-B552	0	0	1.845055141	0.615298391	0.086911959	0.808688098	0.767248798	0.391189379	low
TCGA-91-B847	0	0.198921556	1.863935805	0.040132114	0.316159879	0.198095555	0.009186839	1.398406026	high
TCGA-73-4659	0	0	1.209138902	0.650065188	0.110694404	0.411445879	0.080377706	1.387697208	high
TCGA-55-A4P8	0	0.195900043	1.665393357	0.335320711	0.120977441	0.492865987	0.784674691	0.561124668	low
TCGA-44-A563	0	0	1.730174968	1.623737306	0.0505803842	0.5083395194	0.546936725	0.418217384	low
TCGA-97-A4M7	0	0.265988294	1.472565577	0.504351165	0.545971757	0.505805568	0.825998907	0.900921411	low
TCGA-50-B656	0	0.134599671	1.420474856	0.879401514	0.073516104	0.349146479	0.679983561	0.673062823	low
TCGA-LA-A4E5	0	0	1.294917805	0.840389189	0.111759863	0.459415041	0.176581668	1.091117904	high
TCGA-67-3773	0	0.163817121	1.89893898	2.714517433	0.436766119	0.104095703	0.362635551	0.500016437	low
TCGA-86-8871	0	0	1.40742187	2.293165211	0.507011957	0.386214832	1.264957302	0.466601668	low
TCGA-75-7027	0.5161239	0.099390139	1.694824153	0.513719638	0.378081747	0.188383706	0.08150231	1.916542465	high
TCGA-05-4382	0	0.082491564	1.741347035	2.807858394	0.907358184	0.197184636	0.640983453	0.804608066	low
TCGA-78-B662	0	0	1.781356979	0.386279562	0.014109659	0.094799226	0.175942515	0.82754961	low
TCGA-97-B552	0	0	1.845055141	0.615298391	0.086911959	0.808688098	0.767248798	0.391189379	low
TCGA-91-B847	0	0.198921556	1.863935805	0.040132114	0.316159879	0.198095555	0.009186839	1.398406026	high
TCGA-73-4659	0	0	1.209138902	0.650065188	0.110694404	0.411445879	0.080377706	1.387697208	high
TCGA-55-A4P8	0	0.195900043	1.665393357	0.335320711	0.120977441	0.49286598			



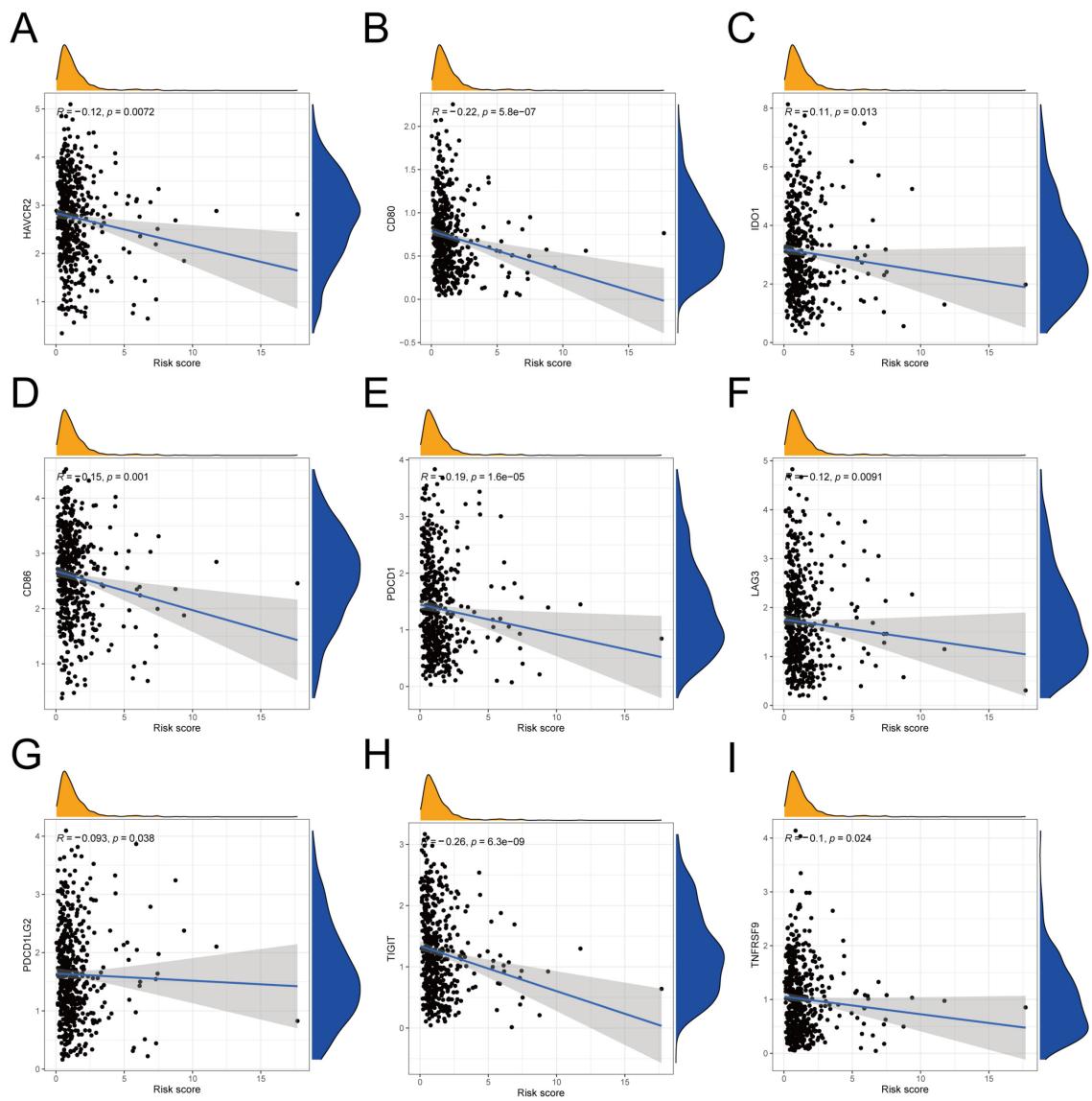
**Figure S2** Survival analysis of the CLPS in the entire LUAD cohort. Kaplan-Meier curves of (A) OS and (B) PFS in the entire cohort. (C) ROC curves for the risk signature at 1, 3, and 5 years in the entire cohort. (D) The C-index of the CLPS risk score and other clinical characteristics in the entire cohort. (E) Survival state (the middle section) of the patients sorted according to the risk scores (the top section) and the differences in the CLPS lncRNAs between the high and low-risk groups (the bottom section) in the entire cohort. (F-K) Kaplan-Meier curves of OS in distinct subgroups with different clinical characteristics: (F) age  $\leq 65$ , (G) age  $> 65$ , (H) female, (I) male, (J) Stage I-II, and (K) Stage III-IV. CLPS, cuproptosis-related lncRNAs prognostic signature; LUAD, lung adenocarcinoma; OS, overall survival; PFS, progression-free survival; ROC, receiver operating characteristic; lncRNAs, long non-coding RNAs; AUC, area under the curve.

**Table S6** Identification of DEGs between low- and high-risk groups

DEGs	lowMean	highMean	logFC	P-Value	FDR*
SNTN	1.575024382	0.751718132	-1.067110455	2.77E-08	2.83E-07
CD40LG	1.509770222	0.718730555	-1.070806072	2.43E-18	1.71E-15
SNORA28	1.558088649	0.702483671	-1.149240723	0.01111661	0.021841023
LYPD3	5.194157605	11.21319845	1.110236156	0.011532043	0.022522053
PI3	8.144978174	48.3185615	2.568594767	1.14E-05	5.25E-05
CFAP157	1.770221411	0.848344995	-1.06120683	4.50E-07	3.17E-06
SCGB3A1	733.0557381	338.0194345	-1.116816701	4.60E-13	2.34E-11
IGFBP1	0.44921233	5.0453141978	3.489425437	7.97E-06	3.85E-05
AC110741.1	1.526780262	0.622075987	-1.295329718	0.018099977	0.033349779
AC083809.1	2.099841734	9.161792285	2.125349259	0.007398223	0.015212433
SLC2A1	25.5801515	52.42149069	1.035133571	5.31E-14	4.08E-12
AKAP12	3.90455062	11.60194342	1.571138067	2.09E-06	1.19E-05
RN7SL8P	2.23517716	0.873030364	-1.356285447	3.02E-07	2.23E-06
SNORA80D	1.784667047	0.416835602	-2.098104536	0.000412247	0.001225148
AC026347.1	2.16201659	1.042840762	-1.051858713	2.53E-06	1.40E-05
SCGB3A2	515.6111989	211.2804455	-1.28712435	2.44E-09	3.53E-08
TF1F1	46.66714472	157.5547506	1.75537415	2.32E-06	1.30E-05
GNG4	1.522552158	3.205815668	1.074199823	0.000116022	0.000401323
LRMP	2.659279438	1.266852448	-1.069786882	8.52E-13	3.92E-11
LINC00926	1.595386228	0.582131075	-1.454489792	1.49E-19	1.81E-16
AC08999.1	2.264697154	1.032042907	-1.133815188	5.06E-06	2.58E-05
SPINK13	2.917467118	0.71690618	-2.024860161	0.000543799	0.001568857
AC084375.1	3.082267239	1.389612427	-1.149309391	2.63E-08	2.70E-07
ACE2	3.840786035	1.899008411	-1.0161553	0.000219378	0.000705046
PTGDS	41.27824486	19.01127682	-1.118526201	1.70E-16	3.60E-14
SLC46A2	3.419820177	1.691114637	-1.015946006	1.65E-06	9.67E-06
AC092071.1	3.547262979	1.398778823	-1.342530843	2.75E-11	7.78E-10
COL11A1	5.666886342	12.7752343	1.172721579	1.13E-06	6.98E-06
ITGB2-AS1	3.636276287	1.500084043	-1.27741849	8.05E-20	1.56E-16
GJB3	3.218857953	7.782395492	1.273665385	9.13E-05	0.000324052
RHOV	13.0209154	27.09117224	1.056991944	0.000270163	0.000847558
IGHD2-2	2.675350688	1.304761001	-1.035942448	0.000578974	0.001656543
CDHR4	1.718337	0.718650319	-1.257651144	2.14E-06	1.22E-05
DEFB1	9.271790551	23.91435186	1.36695681	0.003654087	0.008312119
ADAMTS8	1.655923994	0.735125154	-1.171574664	4.76E-14	3.70E-12
SRGAP3-AS2	2.400857217	1.108268333	-1.115242379	5.54E-06	2.79E-05
SCNN1D	1.638543643	0.781592669	-1.06792526	2.12E-14	2.01E-12
LAMA3	4.745552553	10.72150359	1.175859261	0.001185179	0.03091001
TNFRSF13C	2.30517114	0.908414197	-1.343451705	2.18E-14	2.04E-12
MIR3189	8.501705126	3.599402987	-1.239994587	7.40E-10	1.23E-08
SFTP2D	239.2860937	94.04679918	-1.347285808	6.99E-15	7.89E-13
H19	17.61234305	73.58439571	2.062813011	0.000248292	0.000786853
MALAT1	114.9921504	51.44463754	-1.160442776	3.07E-05	0.000124738
DUSP4	10.61657859	21.25054206	1.001180739	7.19E-06	3.51E-05
CHAD	4.278662922	1.654104787	-1.371109395	2.51E-10	4.82E-09
VPREB3	4.393939383	2.184403142	-1.00827583	1.36E-07	1.13E-06
FCMR	7.8262466	3.83993285	-1.027239487	1.93E-16	3.84E-14
PI15	0.802938259	2.714826473	1.757499024	0.003019998	0.007053844
CR2	4.175032661	1.578793031	-1.402965428	6.02E-10	1.02E-08
SCGB2A1	9.508064165	3.768416304	-1.335193288	1.82E-06	1.06E-05
SFTP2C	468.4184393	215.4065443	-1.120735787	2.93E-08	2.98E-07
PEBP4	24.59743915	11.69430882	-1.072701528	3.92E-11	1.04E-09
SUSD2	55.34045104	20.1330201	-1.458770799	6.92E-13	3.33E-11
WIF1	26.08232092	7.818953171	-1.73802488	7.92E-09	9.66E-08
FGB	37.91906586	162.0721706	2.095641058	0.001710547	0.04263978
SNORA73B	159.2883839	53.57928054	-1.571893948	0.002562681	0.006111184
DMBT1	37.60735922	16.85715732	-1.157653734	0.000114418	0.000396388
CTSG	1.464764951	0.677653365	-1.11204978	1.04E-08	1.22E-07
FCRLA	2.029263727	0.979858284	-1.050311359	4.95E-08	4.69E-07
RNU5F-1	1.554879747	0.707418811	-1.136166521	2.63E-06	1.45E-05
RN7SL381P	2.700689593	1.27015006	-1.088328879	2.74E-05	0.00011318
COL12A1	8.222479607	17.2968233	1.072861669	8.99E-08	7.89E-07
CYCSPL6	0.672224255	1.494910277	1.153044395	0.000301013	0.00092978
SERPINB3	2.754651639	6.391750011	1.214341101	0.003402457	0.007817903
PTCSC3	3.752759741	1.74024457	-1.108661856	5.01E-11	1.27E-09
PCSK1	6.738620651	15.14594665	1.168406535	3.25E-05	0.000131509
CPAMD8	4.374784017	2.041089513	-1.099872339	1.65E-15	2.24E-13
LINC01116	0.736110055	1.854737185	1.333221389	4.91E-06	2.51E-05
FGA	33.24931463	178.7107359	2.426229798	0.015574373	0.029270923
CHRDL1	7.323516877	3.649135384	-1.004981945	6.19E-16	1.01E-13
PITX2	0.910394971	2.088378678	1.197818841	0.001340085	0.003444797
GLB1L3	3.871593464	1.741285494	-1.152774741	1.38E-10	2.97E-09
CCDC78	2.453963096	1.196262767	-1.03657924	2.89E-11	8.10E-10
TUBA4B	1.626312881	0.765576355	-1.086986662	1.15E-06	7.07E-06
CEMIP	6.27631829	14.20589385	1.178499188	2.06E-08	2.19E-07
ATP13A4	9.539770152	4.212704535	-1.179207773	1.50E-13	9.54E-12
RN7SKP80	1.830035034	0.877098137	-1.06106109	2.09E-09	3.09E-08
PAEP	34.40301787	92.74259347	1.430696946	1.31E-06	7.92E-06
WDR38	3.281333836	1.57802485	-1.056162454	4.87E-05	0.000187014
FOSL1	4.691059585	9.903429515	1.078014385	1.28E-06	7.75E-06
CCL17	8.207867489	3.9526097	-1.054201936	1.43E-08	1.59E-07
PRRT2	1.529315452	0.742913185	-1.041620486	1.51E-11	4.58E-10
FAM216B	2.871924723	1.32268777	-1.118545392	2.00E-07	1.58E-06
PTHLH	1.503826356	3.033671345	1.012426808	3.74E-08	3.70E-07
CALB1	4.12937733	0.607574472	-2.764791094	0.010083587	0.020037286
PKP2	1.789732057	4.107741452	1.198601762	1.80E	



**Figure S3** Functional annotation for DEGs between the high-risk and low-risk groups using KEGG pathway analysis. (A) Bar plot and (B) bubble plot showing the significantly enriched KEGG pathways. Bubble color representing the P value, and the bubble size representing the number of genes in the relevant pathway.



**Figure S4** Correlation between the risk score and immune-checkpoint related gene expression: (A) HAVCR2, (B) CD80, (C) IDO1, (D) CD86, (E) PDCD1, (F) LAG3, (G) PDCD1LG2, (H) TIGIT, (I) TNFRSF9.