

Supplementary Materials

Table S1. 201 human genes related to ferroptosis download from the FerrDb database.

Gene symbol	Biotype
RPL8	protein_coding
IREB2	protein_coding
ATP5MC3	protein_coding
CS	protein_coding
EMC2	protein_coding
ACSF2	protein_coding
NOX1	protein_coding
CYBB	protein_coding
NOX3	protein_coding
NOX4	protein_coding
NOX5	protein_coding
DUOX1	protein_coding
DUOX2	protein_coding
G6PD	protein_coding
PGD	protein_coding
VDAC2	protein_coding
TP53	protein_coding
ACSL4	protein_coding
LPCAT3	protein_coding
NRAS	protein_coding
KRAS	protein_coding
HRAS	protein_coding
CARS1	protein_coding
KEAP1	protein_coding
HMOX1	protein_coding
ATG5	protein_coding
ATG7	protein_coding
NCOA4	protein_coding
TF	protein_coding
ALOX5	protein_coding
ALOX12	protein_coding
ALOX12B	protein_coding
ALOX15	protein_coding
ALOX15B	protein_coding
ALOXE3	protein_coding
PHKG2	protein_coding
SAT1	protein_coding
EGFR	protein_coding
MAPK3	protein_coding

MAPK1	protein_coding
ZEB1	protein_coding
DPP4	protein_coding
CDKN2A	protein_coding
PEBP1	protein_coding
SOCS1	protein_coding
CDO1	protein_coding
MYB	protein_coding
SLC1A5	protein_coding
CHAC1	protein_coding
GOT1	protein_coding
BECN1	protein_coding
PRKAA2	protein_coding
PRKAA1	protein_coding
ELAVL1	protein_coding
BAP1	protein_coding
ABCC1	protein_coding
ACVR1B	protein_coding
TGFBR1	protein_coding
IFNG	protein_coding
ANO6	protein_coding
HMGB1	protein_coding
TNFAIP3	protein_coding
ATF3	protein_coding
ATM	protein_coding
YY1AP1	protein_coding
EGLN2	protein_coding
MIOX	protein_coding
TAZ	protein_coding
MTDH	protein_coding
IDH1	protein_coding
FBXW7	protein_coding
PANX1	protein_coding
DNAJB6	protein_coding
LONP1	protein_coding
SLC7A11	protein_coding
GPX4	protein_coding
AKR1C1	protein_coding
AKR1C2	protein_coding
AKR1C3	protein_coding
RB1	protein_coding
HSPB1	protein_coding
HSF1	protein_coding
NFE2L2	protein_coding

SQSTM1	protein_coding
NQO1	protein_coding
FTH1	protein_coding
MUC1	protein_coding
MT1G	protein_coding
SLC40A1	protein_coding
CISD1	protein_coding
HSPA5	protein_coding
ATF4	protein_coding
HELLS	protein_coding
SCD	protein_coding
FADS2	protein_coding
SRC	protein_coding
STAT3	protein_coding
PML	protein_coding
NFS1	protein_coding
TP63	protein_coding
CDKN1A	protein_coding
FH	protein_coding
CISD2	protein_coding
CBS	protein_coding
ISCU	protein_coding
ACSL3	protein_coding
OTUB1	protein_coding
CD44	protein_coding
BRD4	protein_coding
PRDX6	protein_coding
SESN2	protein_coding
NF2	protein_coding
ARNTL	protein_coding
HIF1A	protein_coding
JUN	protein_coding
CA9	protein_coding
TMBIM4	protein_coding
PLIN2	protein_coding
AIFM2	protein_coding
LAMP2	protein_coding
ZFP36	protein_coding
PROM2	protein_coding
CHMP5	protein_coding
CHMP6	protein_coding
CAV1	protein_coding
GCH1	protein_coding
PTGS2	protein_coding

DUSP1	protein_coding
NOS2	protein_coding
NCF2	protein_coding
MT3	protein_coding
UBC	protein_coding
ALB	protein_coding
TXNRD1	protein_coding
SRXN1	protein_coding
GPX2	protein_coding
BNIP3	protein_coding
OXSRI	protein_coding
SELENOS	protein_coding
ANGPTL7	protein_coding
DDIT4	protein_coding
ASNS	protein_coding
TSC22D3	protein_coding
DDIT3	protein_coding
JDP2	protein_coding
SLC1A4	protein_coding
PCK2	protein_coding
TXNIP	protein_coding
VLDLR	protein_coding
GPT2	protein_coding
PSAT1	protein_coding
LURAP1L	protein_coding
SLC7A5	protein_coding
HERPUD1	protein_coding
XBP1	protein_coding
SLC3A2	protein_coding
ZNF419	protein_coding
KLHL24	protein_coding
TRIB3	protein_coding
ZFP69B	protein_coding
ATP6V1G2	protein_coding
VEGFA	protein_coding
GDF15	protein_coding
TUBE1	protein_coding
ARRDC3	protein_coding
CEBPG	protein_coding
RGS4	protein_coding
BLOC1S5-TXNDC5	protein_coding
EIF2S1	protein_coding
HSD17B11	protein_coding
AGPAT3	protein_coding

SETD1B	protein_coding
FTL	protein_coding
TFRC	protein_coding
MAFG	protein_coding
DRD5	protein_coding
DRD4	protein_coding
MAP3K5	protein_coding
MAPK14	protein_coding
SLC2A1	protein_coding
SLC2A3	protein_coding
SLC2A6	protein_coding
SLC2A8	protein_coding
SLC2A12	protein_coding
SLC2A14	protein_coding
EIF2AK4	protein_coding
HBA1	protein_coding
NNMT	protein_coding
PLIN4	protein_coding
HIC1	protein_coding
STMN1	protein_coding
RRM2	protein_coding
CAPG	protein_coding
HNF4A	protein_coding
NGB	protein_coding
YWHAE	protein_coding
GABPB1	protein_coding
AURKA	protein_coding
RIPK1	protein_coding
PRDX1	protein_coding
NR1D2	protein_coding

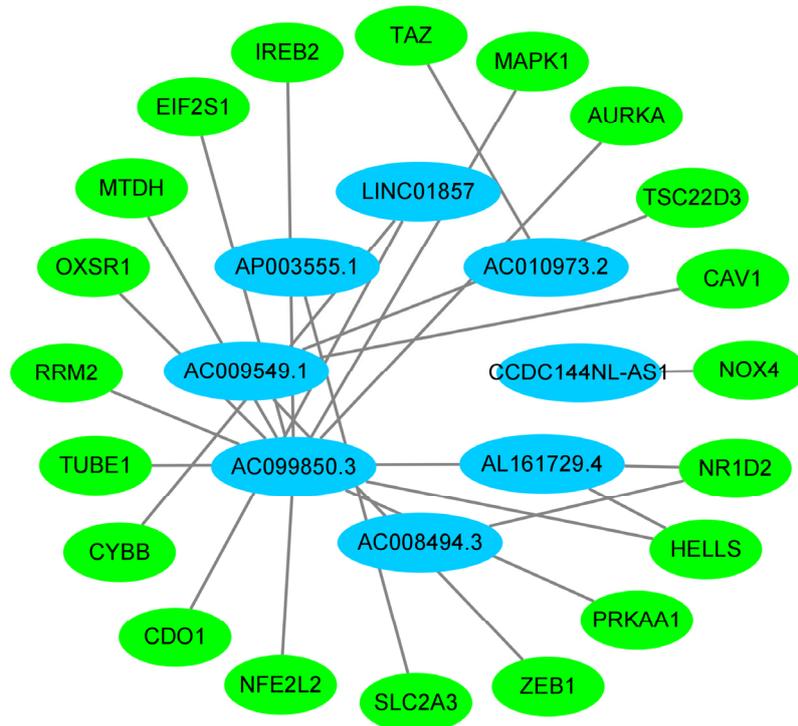
Table S2. The clinical characteristics of colorectal cancer patients between the training and test sets.

Characteristics	Training set (<i>n</i> =354)		Test set (<i>n</i> =151)		Entire set (<i>n</i> =505)		<i>p</i> -value
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	
Age(year)							0.767
<65	144	40.68%	64	42.38%	208	41.19%	
≥65	210	59.32%	87	57.62%	297	58.81%	
Sex							0.285
Female	155	43.79%	74	49.00%	228	45.35%	
Male	199	56.21%	77	51.00%	277	54.65%	
TNM stage							0.861
I	60	16.95%	30	19.87%	90	17.82%	
II	134	37.85%	54	35.76%	188	37.23%	
III	96	27.12%	44	29.14%	140	27.72%	
IV	54	15.26%	19	12.58%	73	14.46%	
Unknown	10	2.82%	4	2.65%	14	2.77%	
T stage							0.496
Tis	1	0.28%	0	0.00%	1	0.20%	
T1	12	3.39%	2	1.33%	14	2.77%	
T2	59	16.67%	32	21.19%	91	18.02%	
T3	244	68.93%	99	65.56%	343	67.92%	
T4	38	10.73%	18	11.92%	56	11.09%	
N stage							0.556
N0	206	58.19%	89	58.94%	295	58.41%	
N1	86	24.29%	37	24.50%	123	24.36%	
N2	62	17.52%	24	15.90%	86	17.03%	
Unknown	0	0.00%	1	0.66%	1	0.20%	
M stage							0.698
M0	261	73.73%	117	77.48%	378	74.85%	
M1	53	14.97%	19	12.58%	72	14.26%	
Unknown	40	11.30%	15	9.94%	55	10.89%	
Recurrence status							0.719
Non-recurrence	279	78.81%	122	80.79%	401	79.41%	
Recurrence	75	21.19%	29	19.21%	104	20.59%	
Survival status							0.146
Alive	277	78.25%	127	84.11%	404	80.00%	
Dead	77	21.75%	24	15.89%	101	20.00%	

Table S4. The clinical characteristics of patients between the high- and low-risk groups of the entire set.

Characteristics	High-risk group (n=184)		Low-risk group (n=321)		Entire set (n=505)		p-value
	n	%	n	%	n	%	
Age(year)							0.398
<65	71	38.59%	137	42.68%	208	41.19%	
≥65	113	61.41%	184	57.32%	297	58.81%	
Gender							0.405
Female	88	47.83%	141	43.93%	229	45.35%	
Male	96	52.17%	180	56.07%	276	54.65%	
TNM stage							0.026
I	24	13.04%	66	20.56%	90	17.82%	
II	62	33.70%	126	39.25%	188	37.23%	
III	57	30.98%	83	25.86%	140	27.72%	
IV	36	19.56%	37	11.53%	73	14.46%	
unknow	5	2.72%	9	2.80%	14	2.77%	
T Stage							0.001
Tis	1	0.54%	0	0.00%	1	0.20%	
T1	2	1.09%	12	3.74%	14	2.77%	
T2	23	12.50%	68	21.18%	91	18.02%	
T3	127	69.02%	216	67.29%	343	67.92%	
T4	31	16.85%	25	7.79%	56	11.09%	
N Stage							0.001
N0	90	48.91%	205	63.86%	295	58.41%	
N1	48	26.09%	75	23.37%	123	24.36%	
N2	46	25.00%	40	12.46%	86	17.03%	
unknow	0	0.00%	1	0.31%	1	0.20%	
M Stage							0.036
M0	128	69.56%	250	77.88%	378	74.85%	
M1	36	19.57%	36	11.22%	72	14.26%	
unknow	20	10.87%	35	10.90%	55	10.89%	
Recurrence status							0.004
Non-recurrence	133	72.28%	268	83.49%	401	79.41%	
Recurrence	51	27.72%	53	16.51%	104	20.59%	
Survival status							<0.001
Alive	116	63.04%	288	89.72%	404	80%	
Dead	68	36.96%	33	10.28%	101	20.00%	

A



B

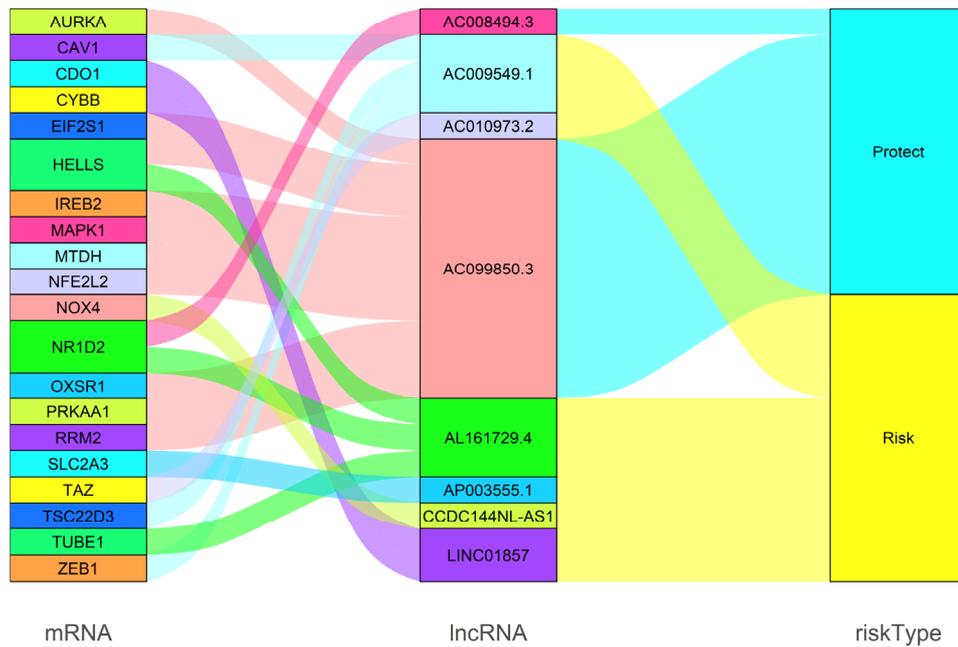


Figure S1. Co-expression network and Sankey relationship diagram between eight lncRNAs in the prognostic signature and their related mRNAs associated with ferroptosis. (A) A co-expression network comprised of 20 ferroptosis-related mRNAs and 8 lncRNAs. **(B)** The Sankey relationship diagram shows the relationship between 20 ferroptosis-related mRNAs and eight lncRNAs.

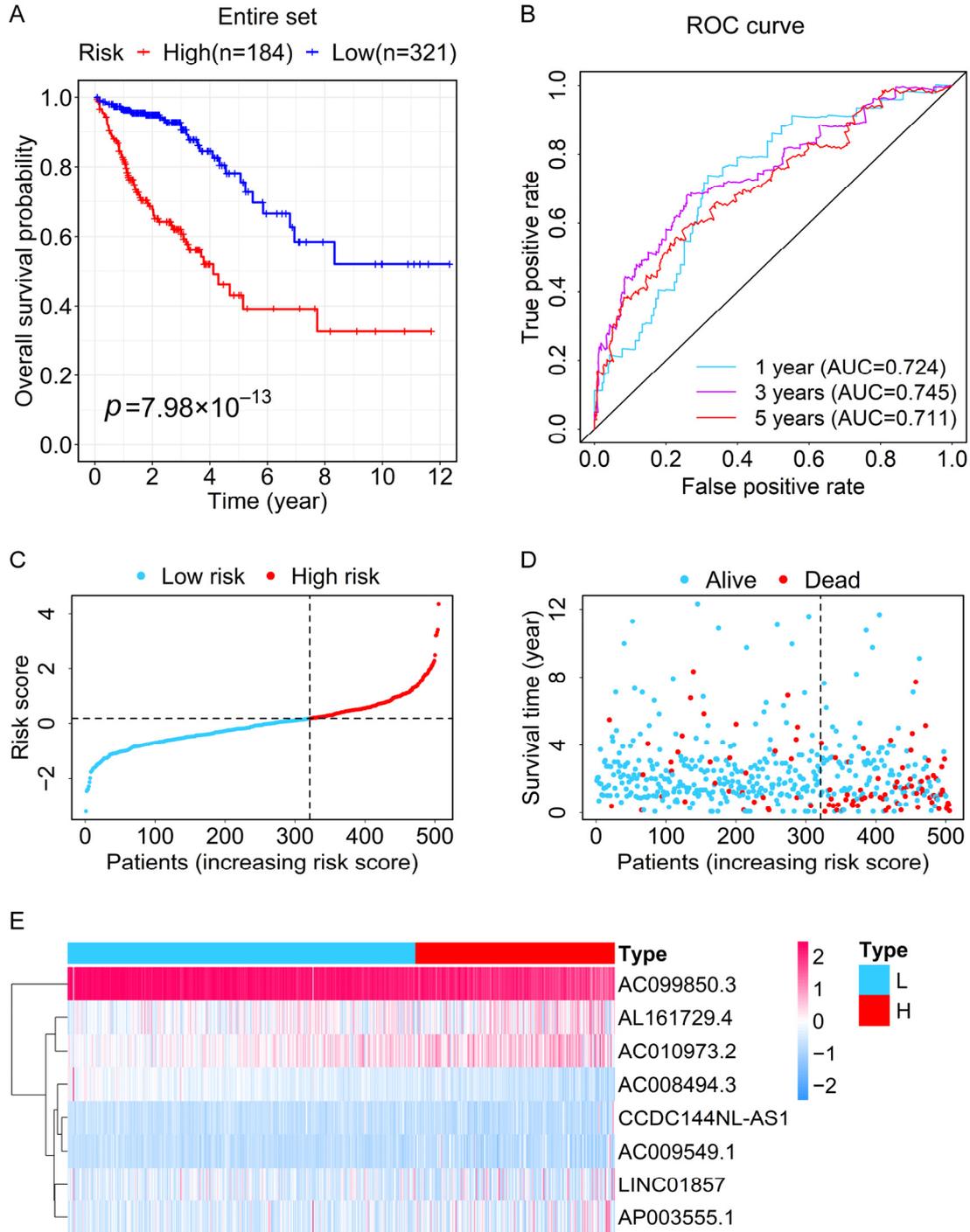


Figure S2. Verification for the prognostic value of the prognostic signature in the entire set. (A) Kaplan-Meier survival curve for OS of CRC patients in the high- and low-risk groups. (B) The time-dependent ROC curves of OS based on the risk score indicate the prognostic accuracy of the 8-lncRNAs signature. (C) The distribution of risk scores of CRC patients. (D) The scatter plot shows the overall survival time and survival status of CRC patients in the high-and low-risk groups. (E) Heatmap of clustering analysis for the expression of eight ferroptosis-related lncRNAs. L, low risk; H, high risk.

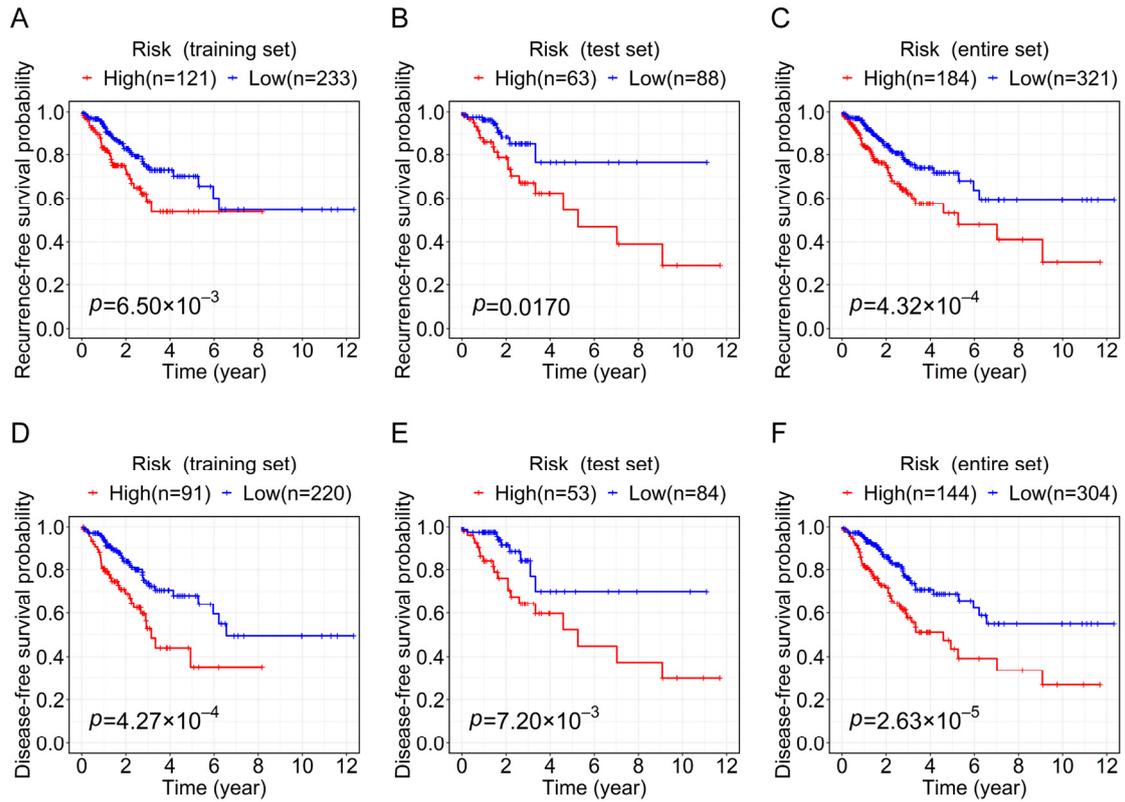


Figure S3. Evaluation and verification of the ferroptosis-related lncRNA prognostic signature for predicting RFS and DFS of CRC patients. The RFS curves for CRC patients in the high- and low-risk groups of the training set (A), test set (B), and entire set (C). The DFS curves for CRC patients in the high- and low-risk groups of the training set (D), test set (E), and entire set (F).

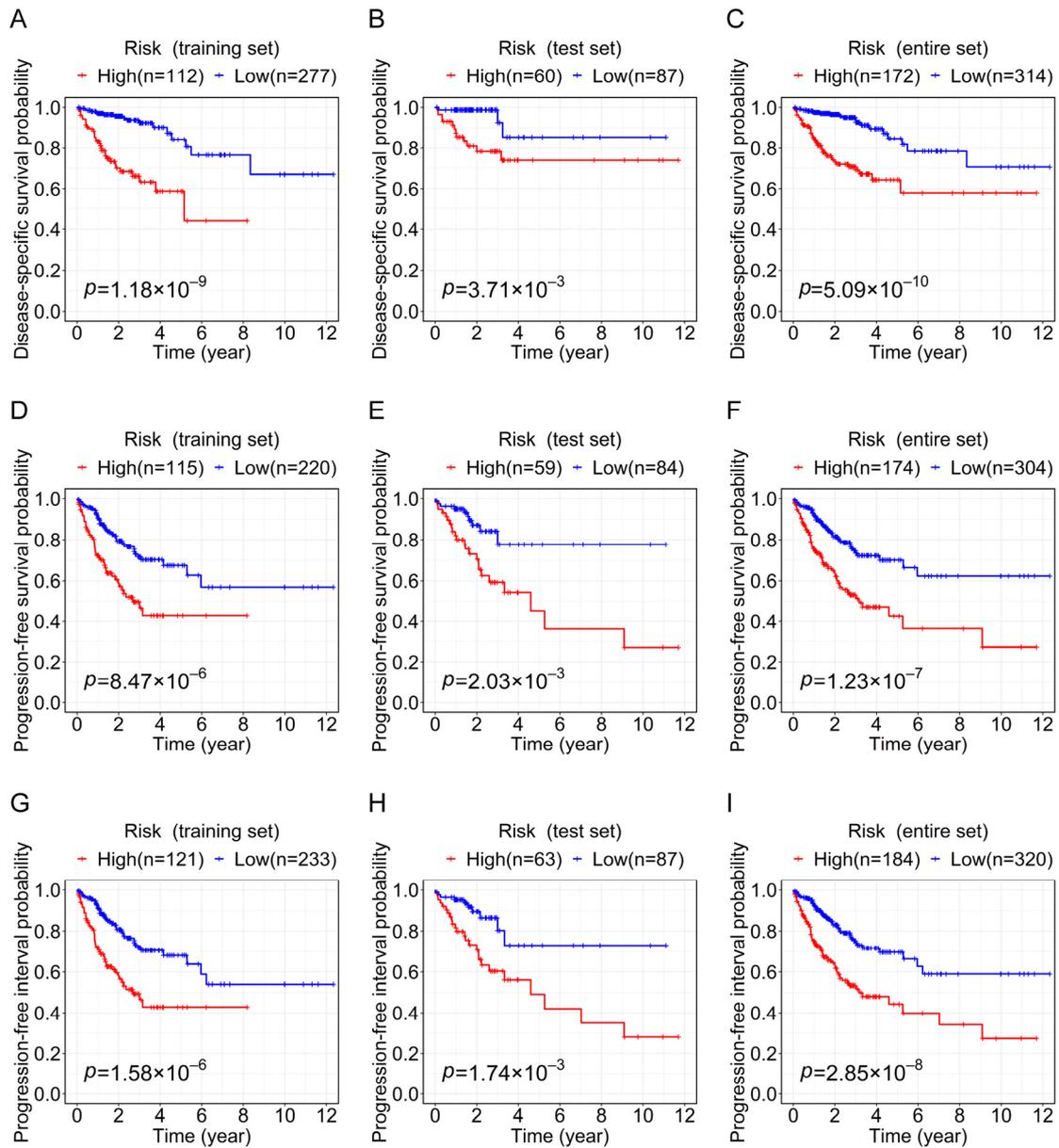


Figure S4. Evaluation and verification of the ferroptosis-related lncRNA prognostic signature for predicting DSS, PFS, and PFI of CRC patients. The DSS curves for CRC patients in the high- and low-risk groups of the training set (**A**), test set (**B**), and entire set (**C**). The PFS curves for CRC patients in the high- and low-risk groups of the training set (**D**), test set (**E**), and entire set (**F**). The PFI curves for CRC patients in the high- and low-risk groups of the training set (**G**), test set (**H**), and entire set (**I**).

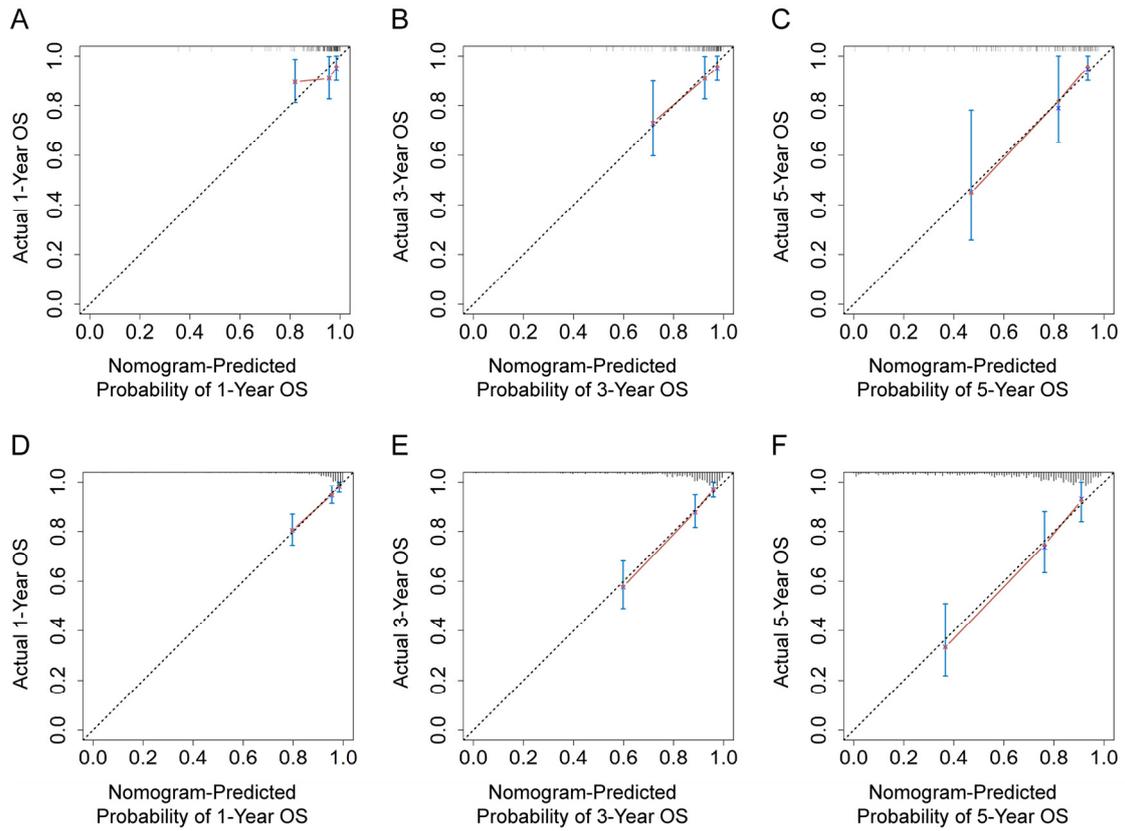


Figure S5. The calibration curves for the nomogram derived from the training set. The calibration curves at 1-year (A), 3-year (B), and 5-year (C) OS of the nomogram in the test set show the predicted result of the nomogram is close to the actual OS rate. The calibration curves at 1-year (D), 3-year (E), and 5-year (F) OS of the nomogram in the entire set show the predicted result of the nomogram is close to the actual OS rate.

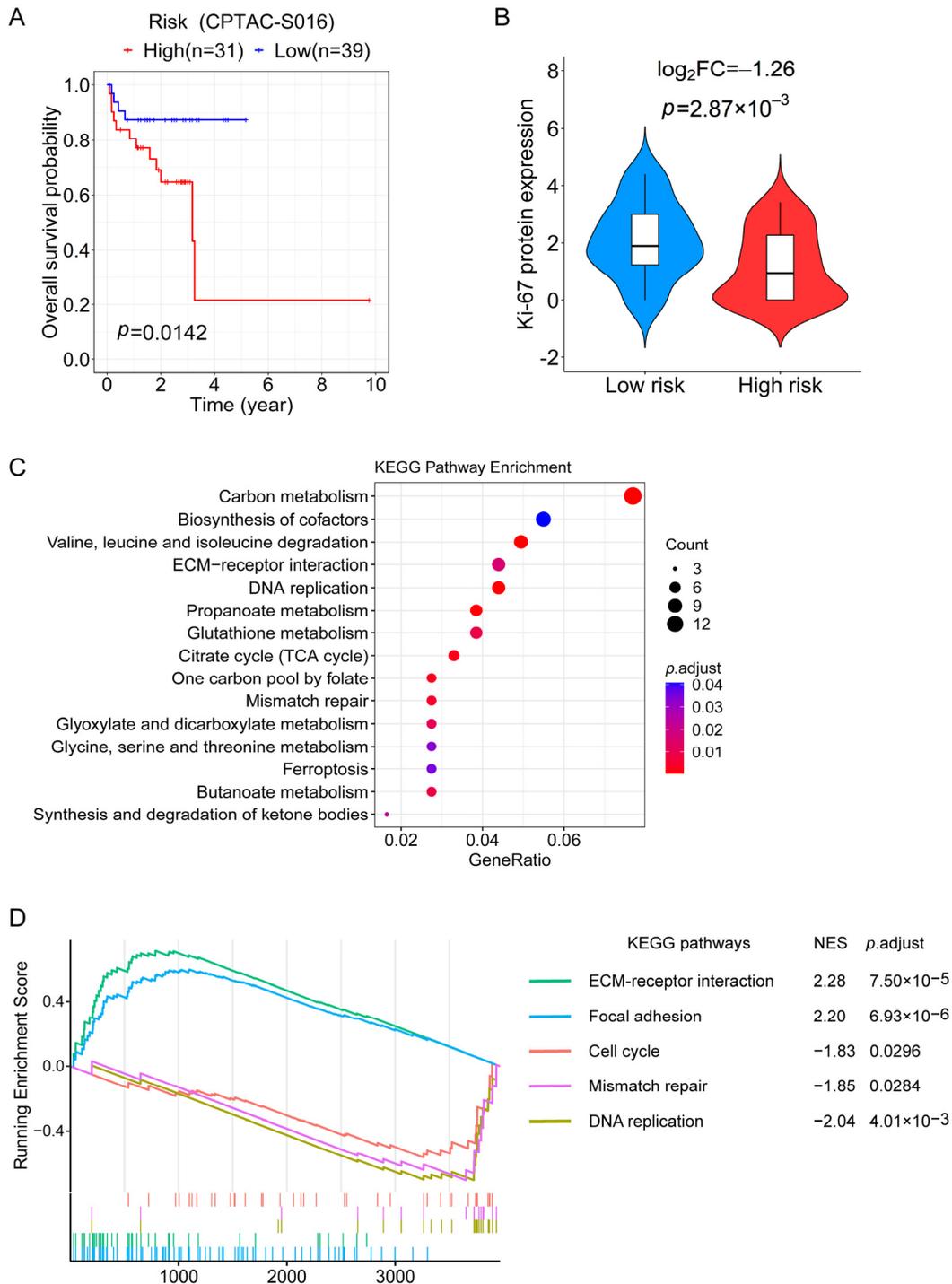


Figure S6. The functional enrichment analysis between the high- and low-risk groups in the proteomics dataset. (A) Kaplan-Meier survival curve analysis for OS shows the differences between the high- and low-risk groups in the proteomics dataset. **(B)** The violin plot shows the differential expression levels of Ki-67 protein analyzed by DESeq2 between the high- and low-risk groups in the proteomics dataset. **(C)** The significantly enriched KEGG pathways of the differentially expressed proteins between the high- and low-risk groups in the proteomics dataset. **(D)** The significantly enriched KEGG pathways between the high- and low-risk groups in the proteomics dataset through the GSEA analysis. \log_2FC : \log_2 (fold change).