

Figure S1 The flow-process diagram of the study. TCGA, The Cancer Genome Atlas; ROC, receiver operating characteristic; CC, cervical cancer; qRT-PCR, quantitative real-time polymerase chain reaction.

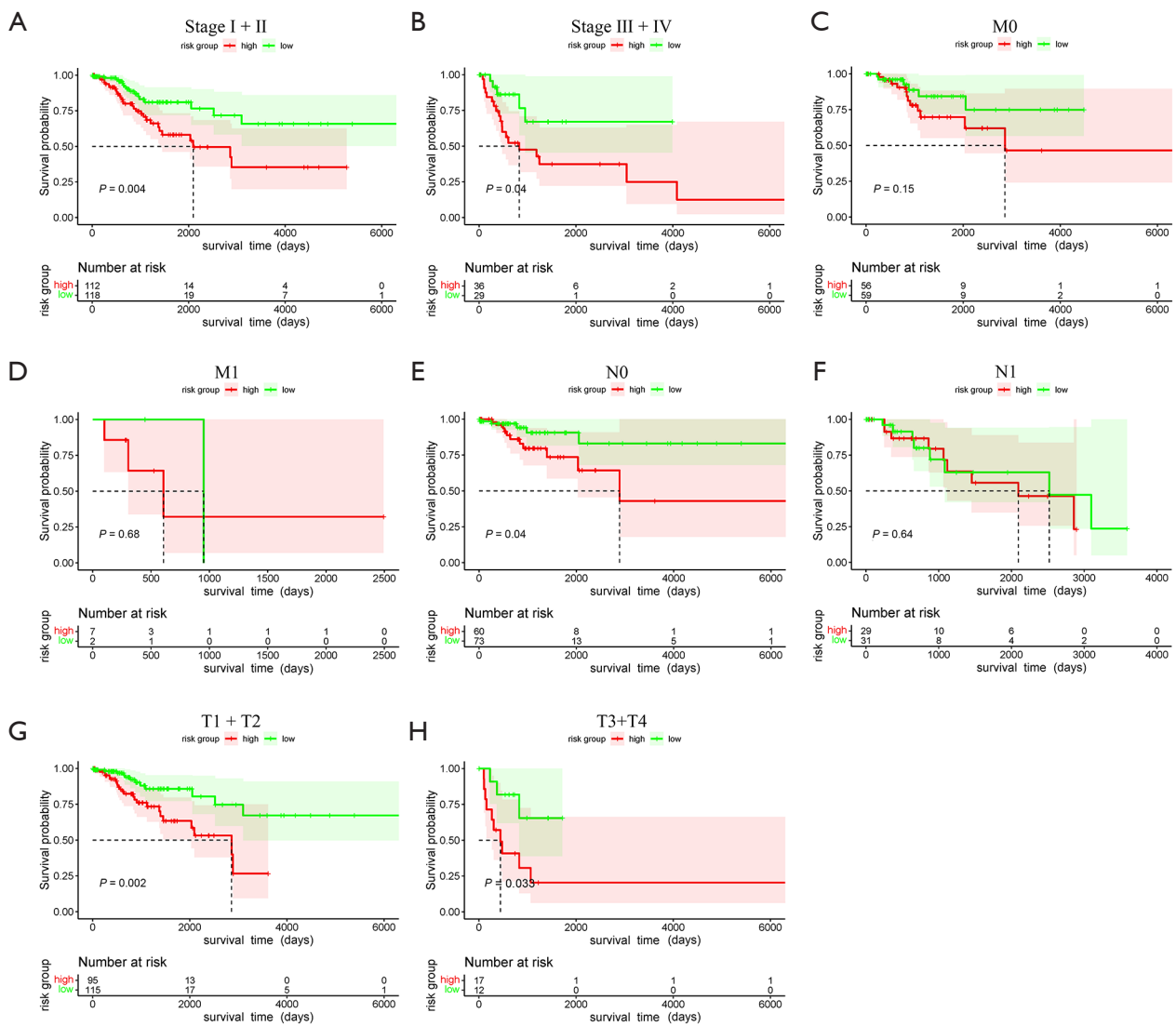


Figure S2 Stratified analysis for overall survival according to the risk score. (A) Stage I + II. (B) Stage III + IV. (C) M0. (D) M1. (E) N0. (F) N1. (G) T1 + T2. (H) T3 + T4.

Table S1 The baseline clinical characteristics of the cervical cancer patients in the TCGA database and the validated clinical cohort

Clinical characteristics	TCGA (n=303)	Validated clinical cohort (n=10)
Age (years), n (%)		
≤55	221 (72.94)	6 (60.00)
>55	81 (26.73)	4 (40.00)
Unknown	1 (0.33)	0 (0.00)
Stage, n (%)		
I	161 (53.14)	3 (30.00)
II	69 (22.77)	7 (70.00)
III	45 (14.85)	0 (0.00)
IV	20 (6.60)	0 (0.00)
Unknown	8 (2.64)	0 (0.00)
Survival state, n (%)		
Survival	231 (76.24)	10 (100.00)
Dead	71 (23.43)	0 (0.00)
Unknown	1 (0.33)	0 (0.00)

TCGA, The Cancer Genome Atlas.

Table S2 Primer sequences for qRT-PCR

Primes	Sequence (5'-3')
SLC2A1-F	ACAGGCTTCGTGCCCATGTA
SLC2A1-R	GATGGAGTCCAGGCCGAACA
CA9-F	GGTCTCTGACTACACCGCCC
CA9-R	CATTCAAAGGCTGCGTCGCT
DUOX1-F	CGGAGACAAGTTCAGTCCC
DUOX1-R	CTGCTTGGGGATCAGGAGAC
GAPDH-F	GGTCGTACCACCGGTATCGT
GAPDH-R	ATGTCACGGACGATTCACG

qRT-PCR, quantitative real-time polymerase chain reaction.

Table S3 The significantly different ferroptosis-related genes identified from TCGA database

Gene	log2FC	P value	FDR
Upregulation			
CDKN2A	7.31	<0.001	<0.001
RRM2	6.9	<0.001	<0.001
TFAP2A	6.31	<0.001	<0.001
CDH1	5.93	<0.001	<0.001
CA9	5.88	<0.001	0.001
TP63	5.84	0.007	0.03
TFR2	5.35	<0.001	<0.001
MT1G	4.81	<0.001	<0.001
CDCA3	4.59	<0.001	<0.001
AURKA	4.55	<0.001	<0.001
PROM2	4.52	<0.001	<0.001
DUOX2	4.49	0.006	0.02
PSAT1	4.49	<0.001	<0.001
AQP3	4.27	0.001	0.007
HELLS	4.25	<0.001	<0.001
DUOX1	4.16	<0.001	<0.001
SLC7A5	4.12	<0.001	<0.001
ALOX12B	4.06	0.01	0.046
MYB	3.71	<0.001	<0.001
SCD	3.66	<0.001	<0.001
SLC2A1	3.62	<0.001	<0.001
FANCD2	3.44	<0.001	<0.001
SLC7A11	3.37	0.004	0.02
VDR	3.21	<0.001	<0.001
PPP1R13L	3.03	<0.001	<0.001
AMN	3.01	0.004	0.02
TFAP2C	2.82	<0.001	<0.001
PGD	2.41	<0.001	<0.001
CD82	2.31	<0.001	0.003
GPT2	2.24	<0.001	<0.001
IDH2	2.21	<0.001	<0.001
STEAP3	2.14	<0.001	<0.001
SQLE	2.03	0.002	0.009
Downregulation			
CDO1	-5.87	<0.001	<0.001
PLIN4	-5.3	<0.001	<0.001
ENPP2	-4.57	<0.001	<0.001
ZEB1	-4.11	<0.001	<0.001
IL33	-4.03	0.004	0.02
AR	-3.99	<0.001	0.004
ANGPTL7	-3.99	<0.001	<0.001
SNCA	-3.87	<0.001	0.005
FNDC5	-3.58	<0.001	<0.001
HIC1	-3.57	<0.001	<0.001
NR5A2	-3.42	<0.001	<0.001
CAV1	-3.33	<0.001	0.003
DPP4	-3.19	0.01	0.04
ATP6V1G2	-3.08	<0.001	<0.001
NR4A1	-3.01	0.003	0.01
HSD17B11	-2.71	<0.001	<0.001
AQP8	-2.71	<0.001	<0.001
GRIA3	-2.67	<0.001	0.003
FZD7	-2.66	0.002	0.01
SLC40A1	-2.6	0.01	0.04
TXNIP	-2.55	<0.001	0.003
PRKCA	-2.49	<0.01	0.003
TLR4	-2.48	0.001	0.006
NOX4	-2.36	0.003	0.01
DUSP1	-2.28	0.01	0.04
TSC22D3	-2.16	0.001	0.007
ZFP36	-2.13	0.004	0.02
MAP1LC3A	-2	0.01	0.046

TCGA, The Cancer Genome Atlas; FC, fold change; FDR, false discovery rate.