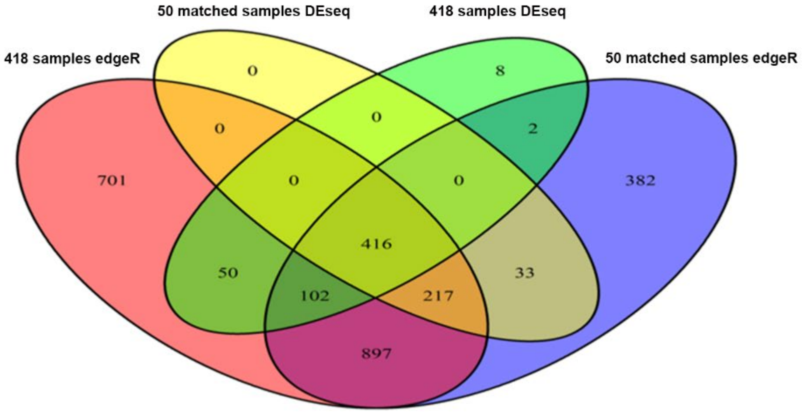
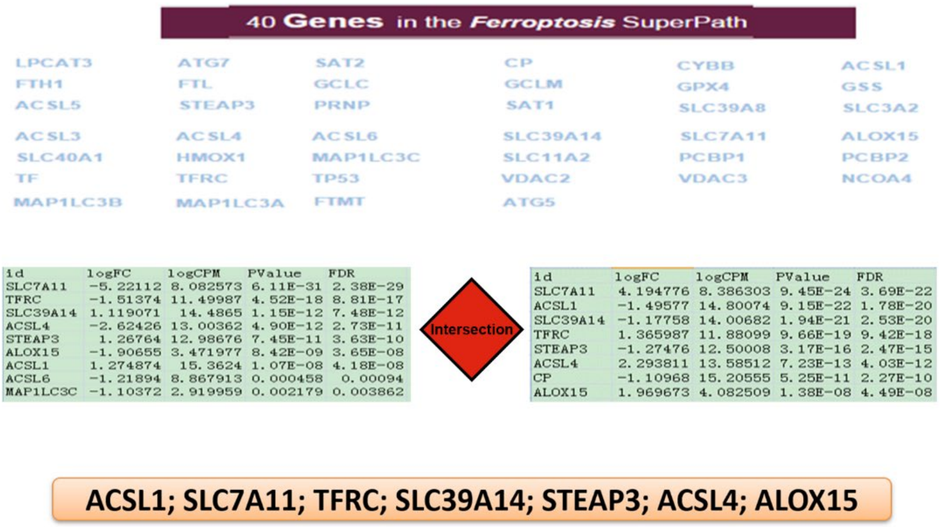


Figure S1. DEseq and edgeR differential expression analysis on 368 samples and 50 paired samples to filter lncRNAs.



id	logFC	logCPM	PValue	FDR
SLC7A11	-5.22112	8.082573	6.11E-31	2.38E-29
TFRC	-1.51374	11.49987	4.52E-18	8.81E-17
SLC39A14	1.119071	14.4865	1.15E-12	7.48E-12
ACSL4	-2.62426	13.00362	4.90E-12	2.73E-11
STEAP3	1.26764	12.98676	7.45E-11	3.63E-10
ALOX15	-1.90655	3.471977	8.42E-09	3.65E-08
ACSL1	1.274874	15.3624	1.07E-08	4.18E-08
ACSL6	-1.21894	8.867913	0.000458	0.00094
MAP1LC3C	-1.10372	2.919959	0.002179	0.003862

id	logFC	logCPM	PValue	FDR
SLC7A11	4.194776	8.386303	9.45E-24	3.69E-22
ACSL1	-1.49577	14.80074	9.15E-22	1.78E-20
SLC39A14	-1.17758	14.00682	1.94E-21	2.53E-20
TFRC	1.365987	11.88099	9.66E-19	9.42E-18
STEAP3	-1.27476	12.50008	3.17E-16	2.47E-15
ACSL4	2.293811	13.58512	7.23E-13	4.03E-12
CP	-1.10968	15.20555	5.25E-11	2.27E-10
ALOX15	1.969673	4.082509	1.38E-08	4.49E-08

Figure S2. edgeR differential expression analysis on 368 samples and 50 paired samples to filter ferroptosis-related genes.

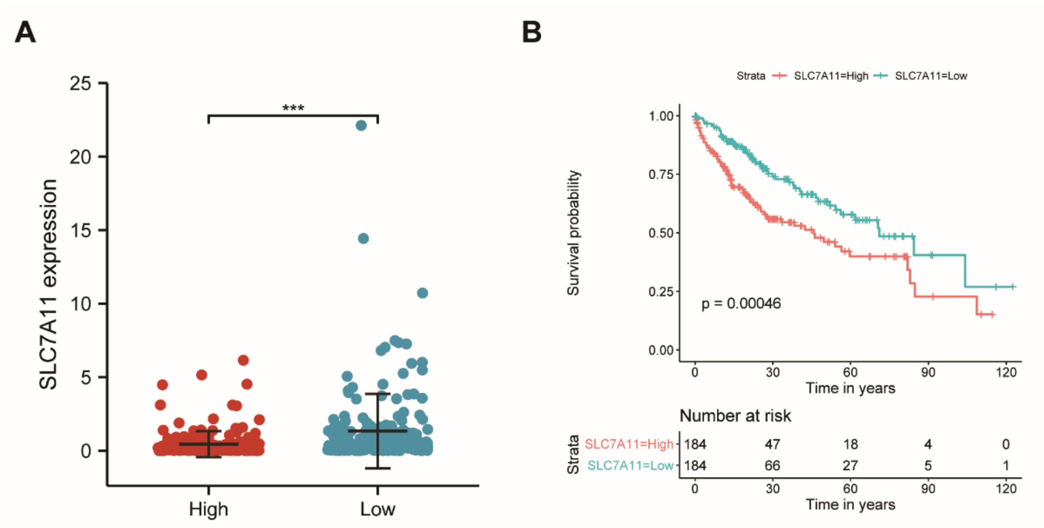


Figure S3. SLC7A11 is associated with LncRNA HEPFAL and affects the prognosis of patients. **A)** Expression of SLC7A11 in high and low expression LncRNA tissues. **B)** SLC7A11 affects OS in HCC patients.

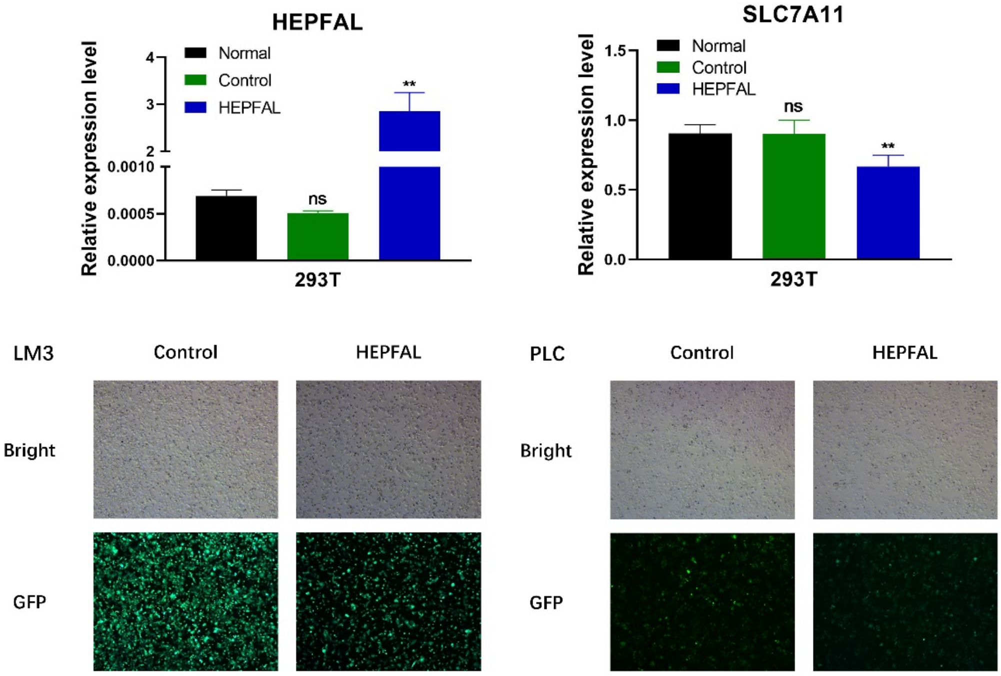
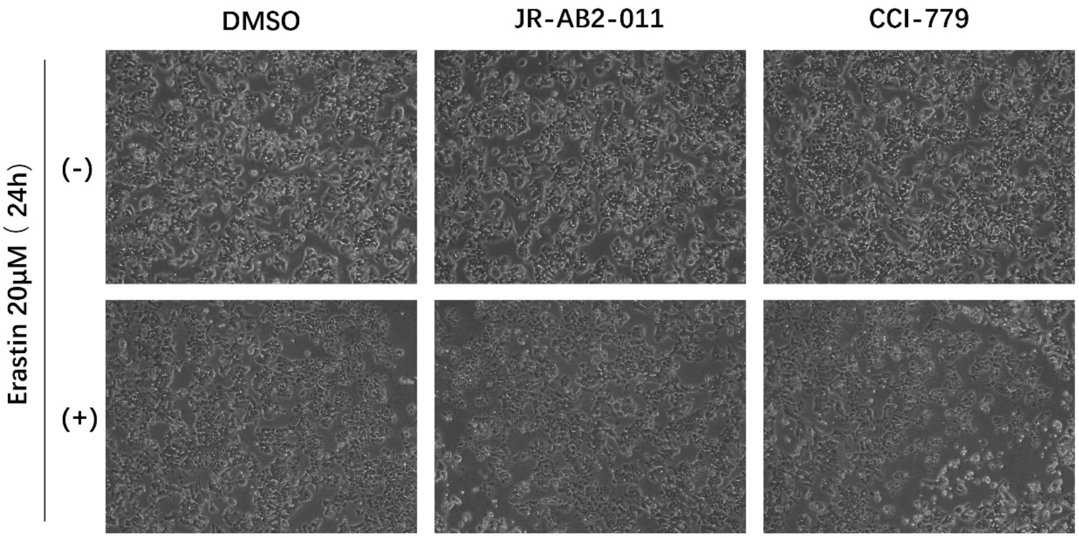
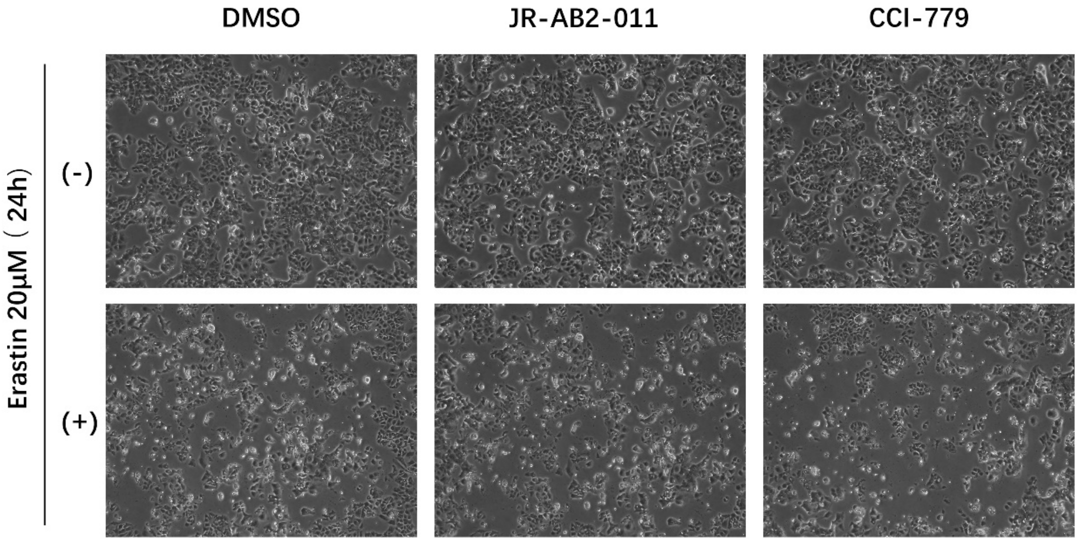


Figure S4. Relative expression of lncRNA HEPFAL and SLC7A11 in 293T cells transfected with lncRNA HEPFAL expression vector and control vector was detected by qRT-PCR. And GFP fluorescence in cells after overexpression lncRNA HEPFAL.



LM3



PLC

Figure S5. HCCLM3 and PLC cells were treated with 20μM erastin or untreated and treated with DMSO, JR-AB2-001 and CCI-779, respectively.

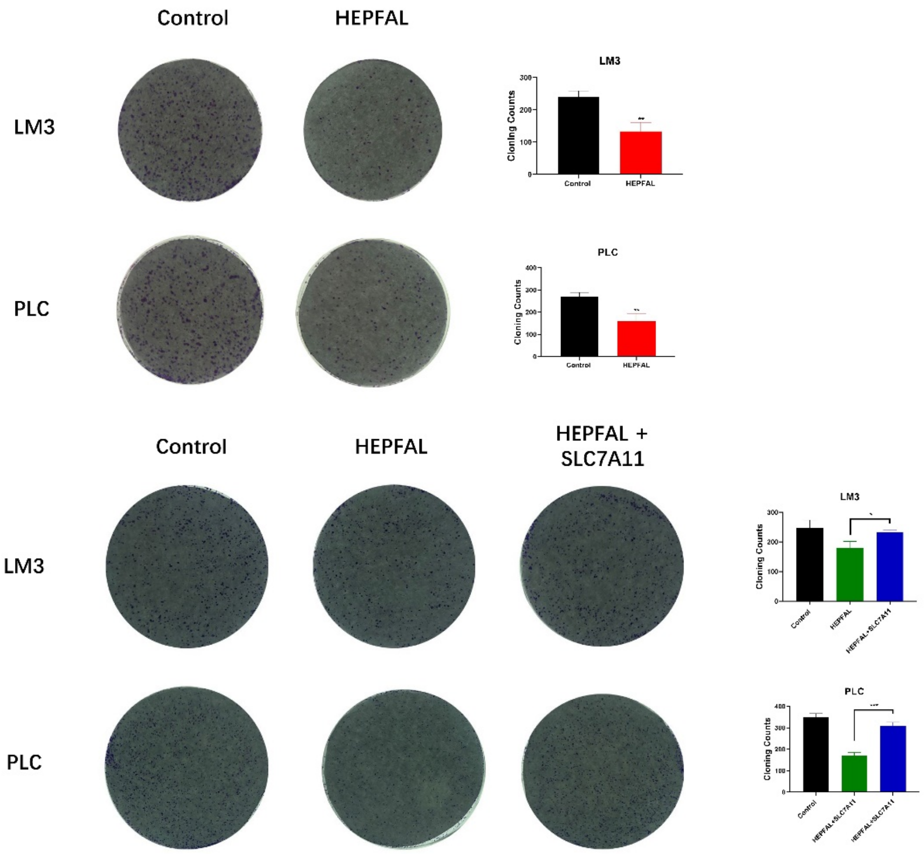
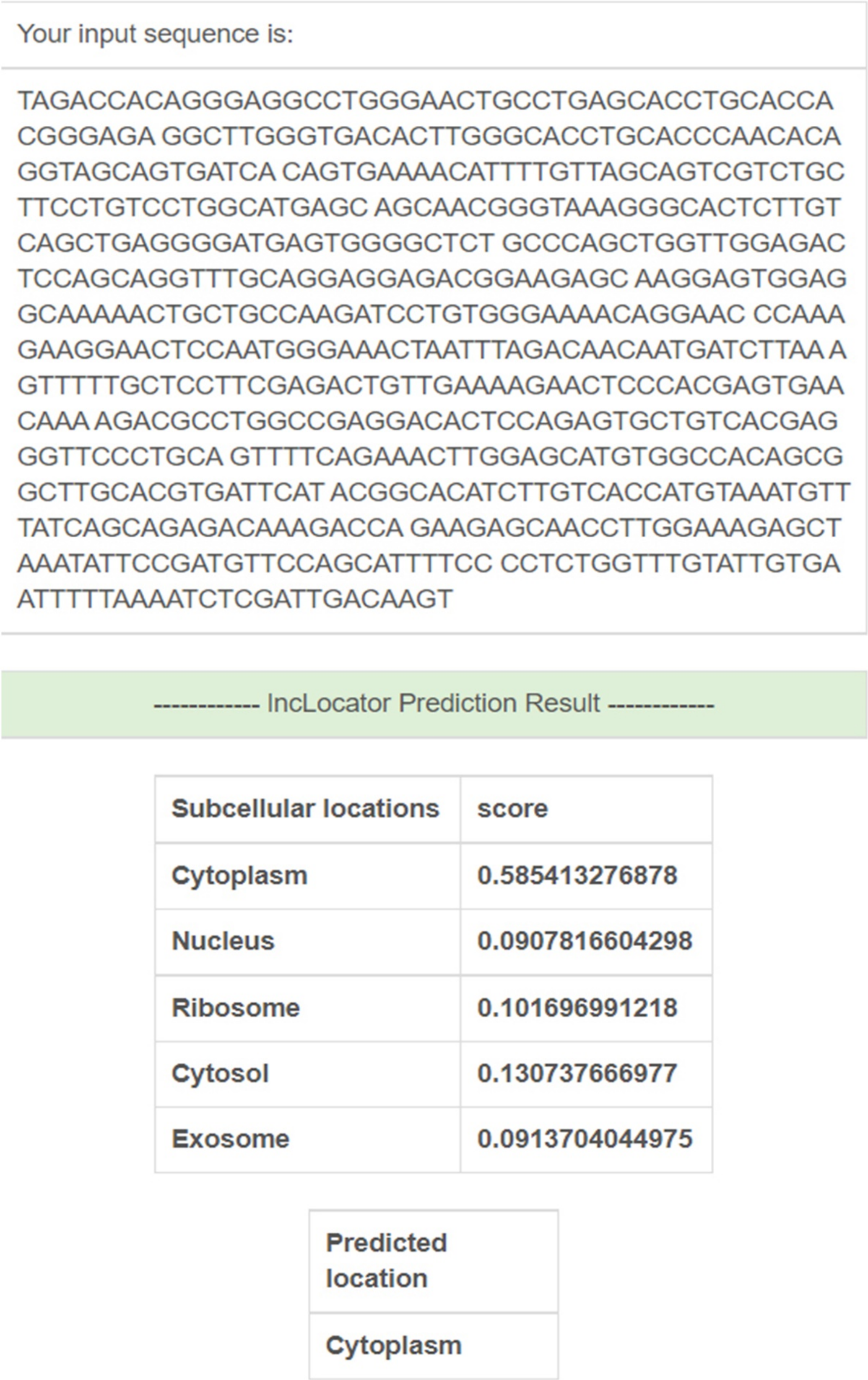


Figure S6. the number of colonies of LM3 and PLC cells after transfected as indicated.



Your input sequence is:

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AAATATTCCGATGTTCCAGCATTTTCC CCTCTGGTTTGTATTGTGA
ATTTTTAAAATCTCGATTGACAAGT
```

------------ lncLocator Prediction Result ------------

Subcellular locations	**score**
Cytoplasm	**0.585413276878**
Nucleus	**0.0907816604298**
Ribosome	**0.101696991218**
Cytosol	**0.130737666977**
Exosome	**0.0913704044975**

Predicted location
Cytoplasm

Figure S7. The predicted location of lncRNA HEPFAL.

Table S1. Sequences of the primers used for quantitative real-time PCR.

Gene	Forward primer(5’-3’)	Reverse primer(5’-3’)
SLC7A11	CCATGAACGGTGGTGTGTT	GACCCTCTCGAGACGCAAC
lncRNA HEPFAL	CGGGTAAAGGGCACTCTTGTCAG	TCCACTCCTTGCTCTTCCGTCTC
GAPDH	CAAGGTCATCCATGACAACTTTG	GTCCACCACCCTGTTGCTGTAG