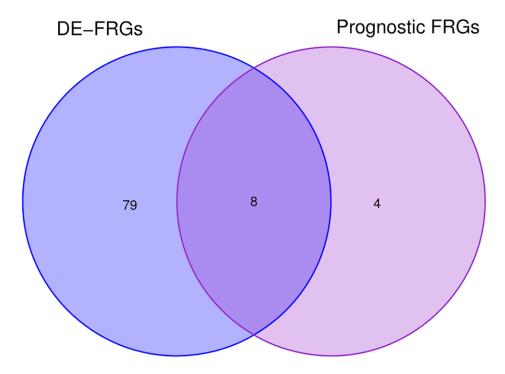
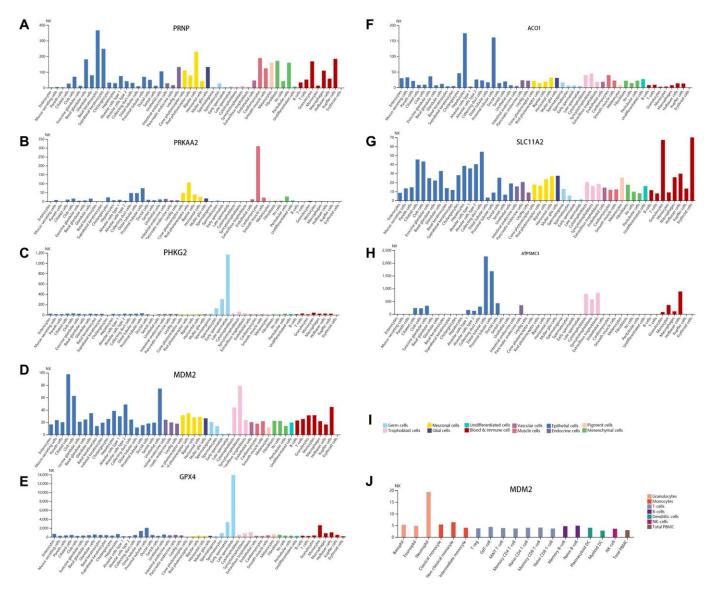
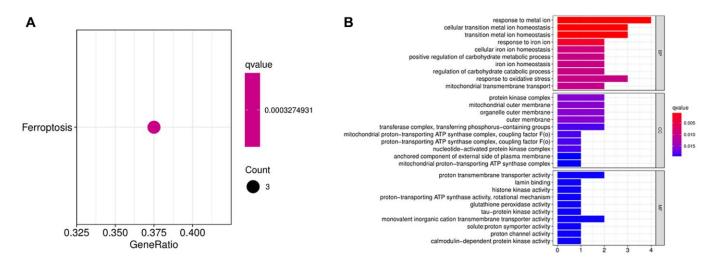
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Venn diagram of 87 differentially expressed ferroptosis-related genes (DE-FRGs) between normal samples and EC patient samples and 12 prognostic FRGs.



Supplementary Figure 2. (A–I) RNA single-cell analysis of 8 FRGs in normal human tissue cells. (J) MDM2 RNA single-cell analysis in blood cells.



Supplementary Figure 3. (A) KEGG analysis of the eight ferroptosis-related genes (FRGs). (B) GO analysis of the eight FRGs.

	pvalue	Hazard ratio	1
MAP1LC3C	0.040	1.287(1.012-1.638)	 -1
ALOX15B	0.006	1.727(1.167-2.556)	! -
MDM2	0.007	0.536(0.340-0.844)	H=H
GPX4	0.017	0.593(0.386-0.909)	 !
PRKAA2	0.006	1.968(1.220-3.176)	;
PRNP	0.013	1.442(1.080-1.925)) -
SAT2	0.003	0.482(0.297-0.784)	⊫ i i
SLC11A2	0.006	0.520(0.325-0.831)	H=H (
ALOX5	0.016	1.380(1.061-1.794)	i = −
ATP5MC3	<0.001	2.685(1.502-4.800)	; —
PHKG2	0.034	0.441(0.207-0.938)	l =−i
ACO1	0.041	1.954(1.029-3.708))
			0 1 2 3 4
			Hazard ratio

Supplementary Figure 4. Results of the univariate Cox analysis of the twelve prognostic ferroptosis-related genes in EC patients.