Table S1 Basic information of the included Gene Expression Omnibus (GEO) datasets

Study	GEO accession	Publication year	Tumor sample	Normal sample
Whole-Tissue Gene Expression Study of Pancreatic Ductal Adenocarcinoma	GSE15741	2009	39	39
Microarray gene-expression profiles of 69 pancreatic tumors and 61 adjacent non-tumor tissue from patients with pancreatic ductal adenocarcinoma	GSE62452	2016	69	69
Pancreatic Tumor vs Various Tissue Normals	GSE11838	2008	28	4
Integrative Survival-Based Molecular Profiling of Human Pancreatic Cancer [mRNA]	GSE32676	2011	42	7
Combinatorial analysis of miRNA and mRNA expression in pancreatic ductal adenocarcinoma (PDAC)_Mrna	GSE41368	2013	6	6
Gene expression of pancreatic tumors	GSE43795	2013	26	5
Molecular analysis of precursor lesions in familial pancreatic cancer	GSE43288	2013	34	6

Table S2 Activity levels of 29 immune-related pathways in pancreatic cancer

id	Mean level
aDCs	0.423455
APC_co_inhibition	0.526804
APC_co_stimulation	0.398148
B_cells	0.351248
CCR	0.456014
CD8+_T_cells	0.461524
Check-point	0.407763
Cytolytic_activity	0.547714
DCs	0.450642
HLA	0.861894
iDCs	0.301289
Inflammation-promoting	0.46859
Macrophages	0.614004
Mast_cells	0.401765
MHC_class_I	0.967318
Neutrophils	0.532509
NK_cells	0.182109
Parainflammation	0.728432
pDCs	0.406689
T_cell_co-inhibition	0.325036
T_cell_co-stimulation	0.33536
T_helper_cells	0.777595
Tfh	0.302339
Th1_cells	0.238486
Th2_cells	0.273066
TIL	0.488722
Treg	0.608353
Type_I_IFN_Reponse	0.638098
Type_II_IFN_Reponse	0.567161

Table S3 Changes in the expression levels of ferroptosis regulators in gemcitabine-resistant pancreatic cancer cells

Gene_Name	P_VAL	logF2
ACSL4	0.5887	0.165
ATP5G3	0.235	0.377
CARS	0.19	0.47
CBS	0.12	1.8
CHAC1	0.019	1.83
CISD1	0.079	0.64
CS	0.046	0.82
DPP4	0.37	–0.61
FANCD2	0.06	1
GCLC	0.11	0.6
GCLM	0.027	2.02
GLS2	0.32	–0.95
GPX4	0.92	0.03
GSS	0.68	0.15
HMGCR	0.31	0.6
HSPB1	0.1	–0.68
HSPB5	\	
LPCAT3	0.47	–0.32
MT1G	\	
NCOA4	0.8	0.09
NFE2L2	0.52	0.26
PTGS2	0.11	–1.14
RPL8	\	
SAT1	0.02	–1.6
SLC7A11	0.017	3.27
SQS	\	
TP53	0.95	–0.02
TFRC	0.09	1.15
EMC2	\	
AIFM2	0.08	1.26
OSGIN1	1.99	0.45
SLC3A2	0.019	1.61
NQO1	0.47	0.36
PIR	0.06	1.05
FXYD3	0.02	–1.64
TMEM87A	0.31	–1.34
ST6GALNAC2	0.21	–0.79
ALDH3A2	0.31	0.33
PERP	0.06	–1.08
HES1	0.037	–1.21
DBN1	0.09	0.68
PKIA	0.17	1.008
WASF1	0.46	–0.22
GLS1	\	

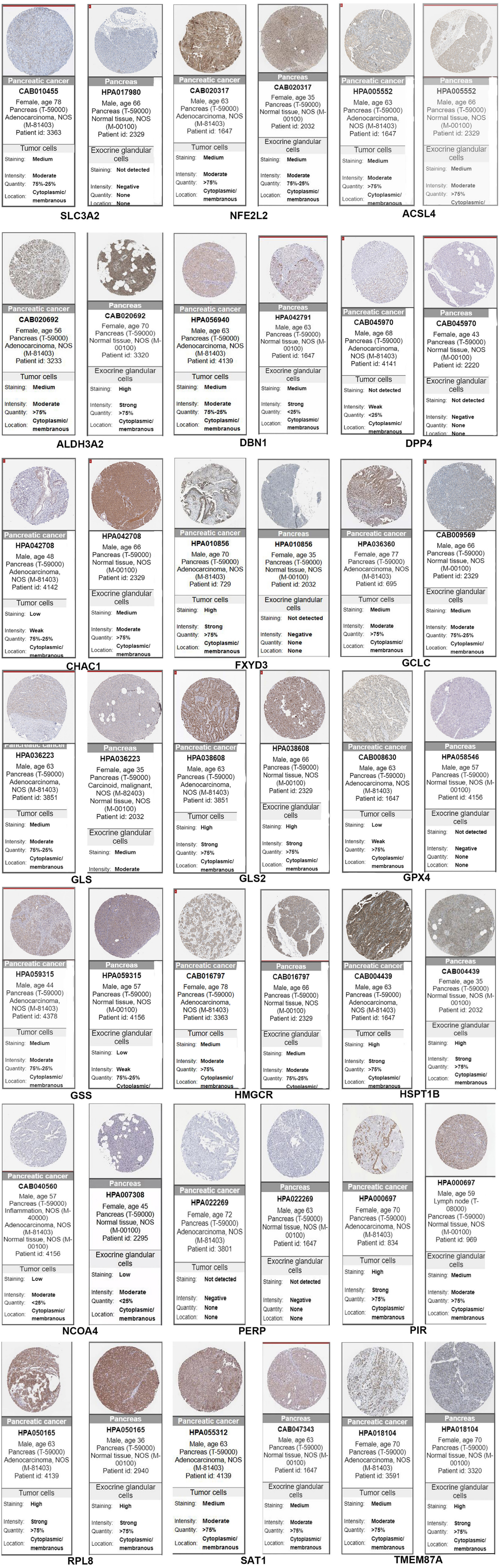

Figure S1 Immunohistochemical presentation of the 43 ferroptosis regulators in pancreatic cancer.

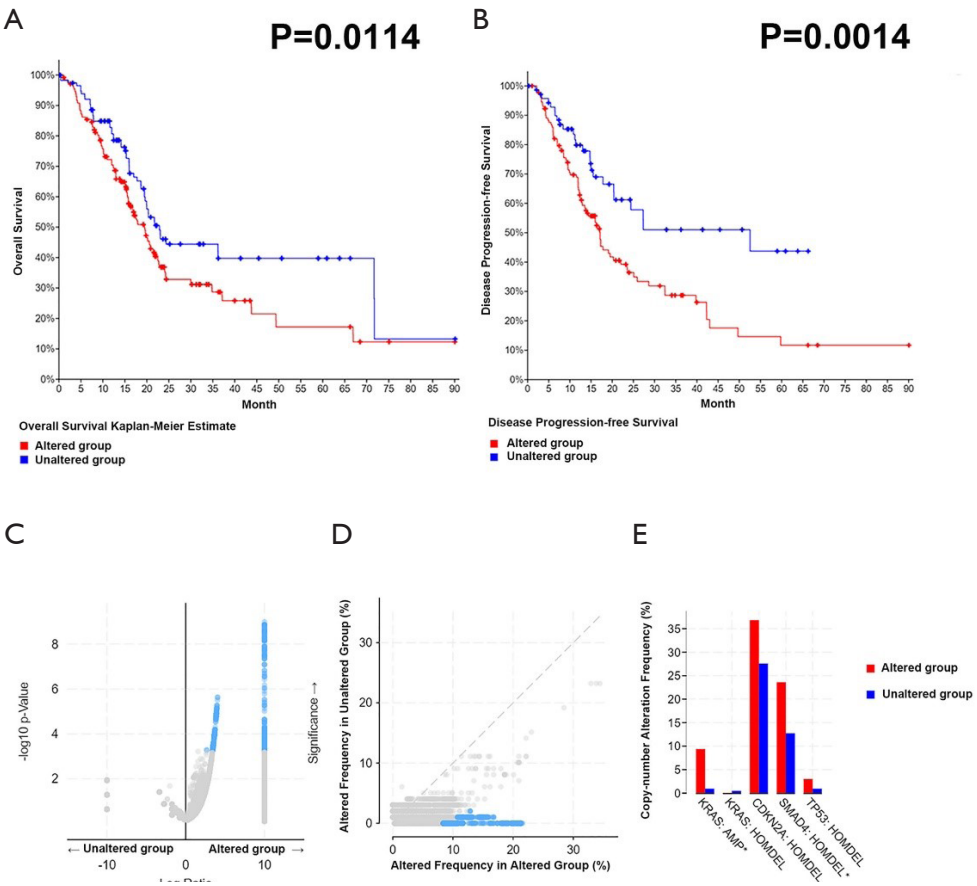

Figure S2 Analysis of the role of copy number alterations in ferroptosis regulators in pancreatic cancer. (A) Patients without copy number alterations in ferroptosis regulators had longer overall survival times; (B) patients without copy number alterations in ferroptosis regulators had longer disease-free survival times; (C,D) the frequency of copy number alterations in ferroptosis regulators dictated copy number alterations in other genes; (E) the four driver genes of pancreatic cancer were altered more frequently in samples harboring mutations in ferroptosis regulators.

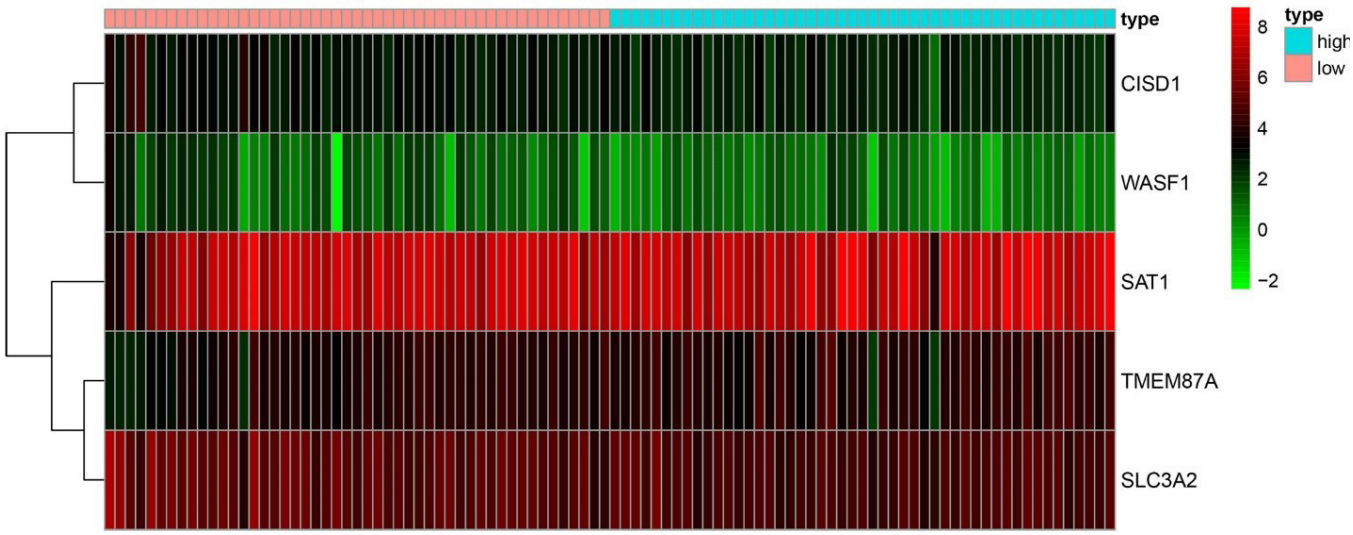

Figure S3 Five ferroptosis regulators were included in the construction of the prognostic model.

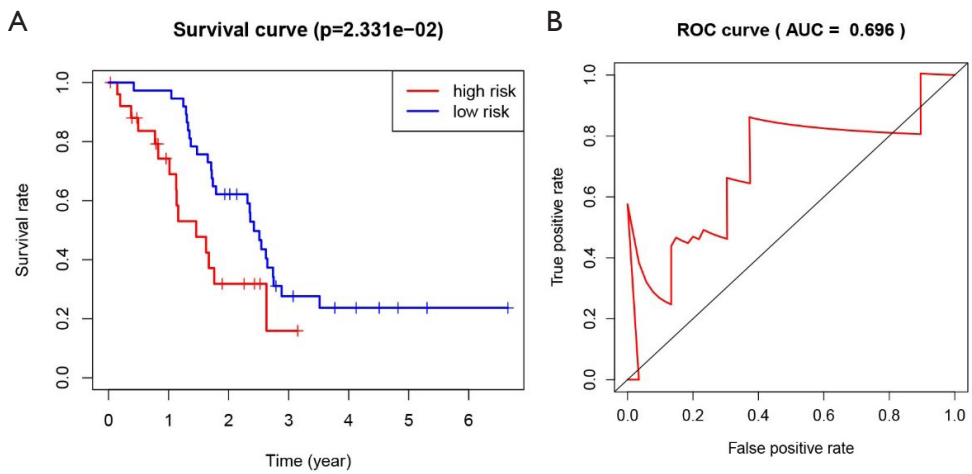

Figure S4 Validation for the accuracy of the predictive model with a Gene Expression Omnibus (GEO) dataset. (A) The survival curve shows a significant difference between the high- and low-risk groups in the GEO validation cohort stratified using our prognostic model in terms of the survival outcome; (B) the receiver operating characteristic (ROC) curve shows the good accuracy of our model for predicting pancreatic cancer survival in the GEO validation cohort.

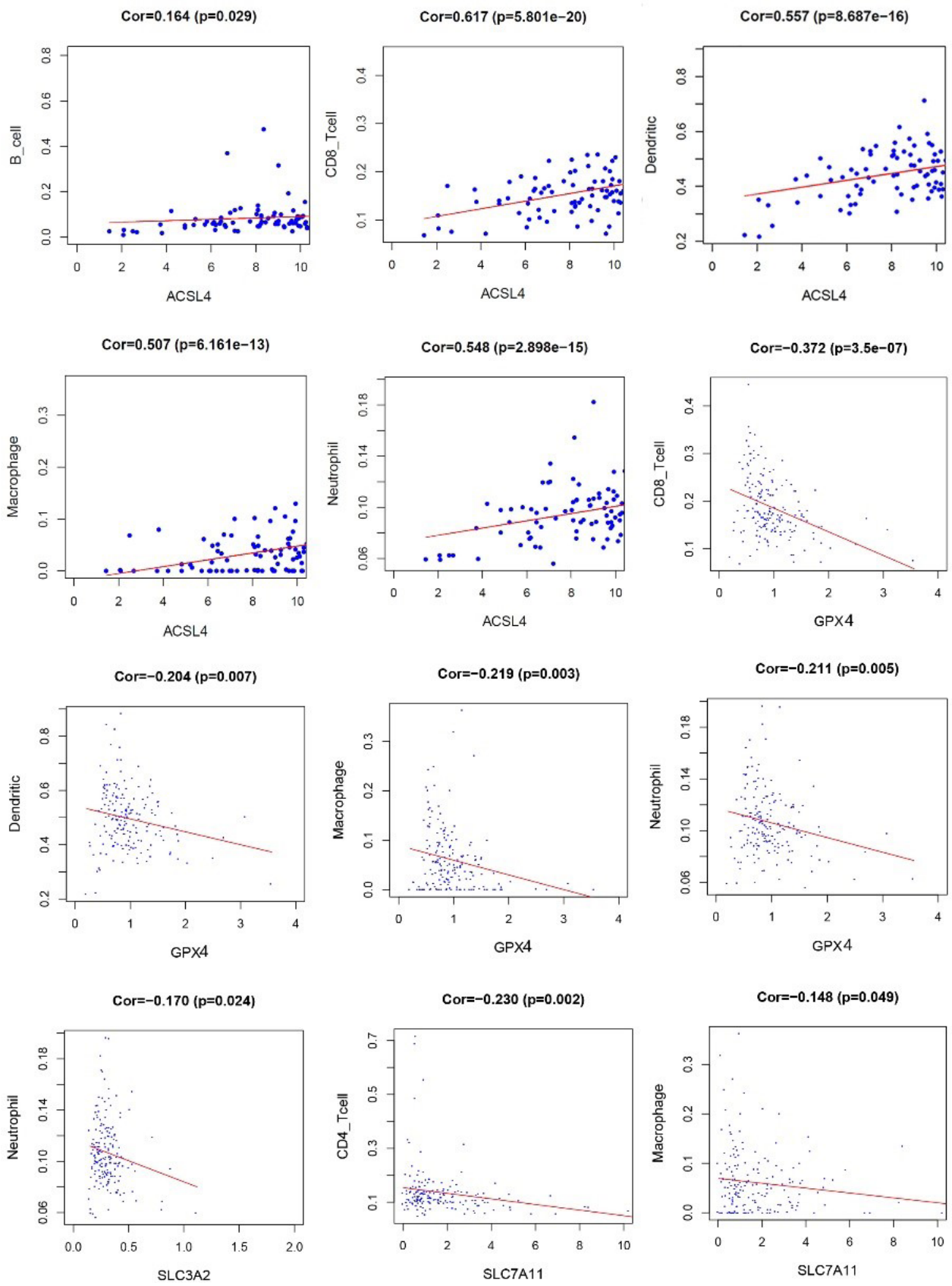

Figure S5 Correlations between key ferroptosis regulators and infiltrating immune cells.

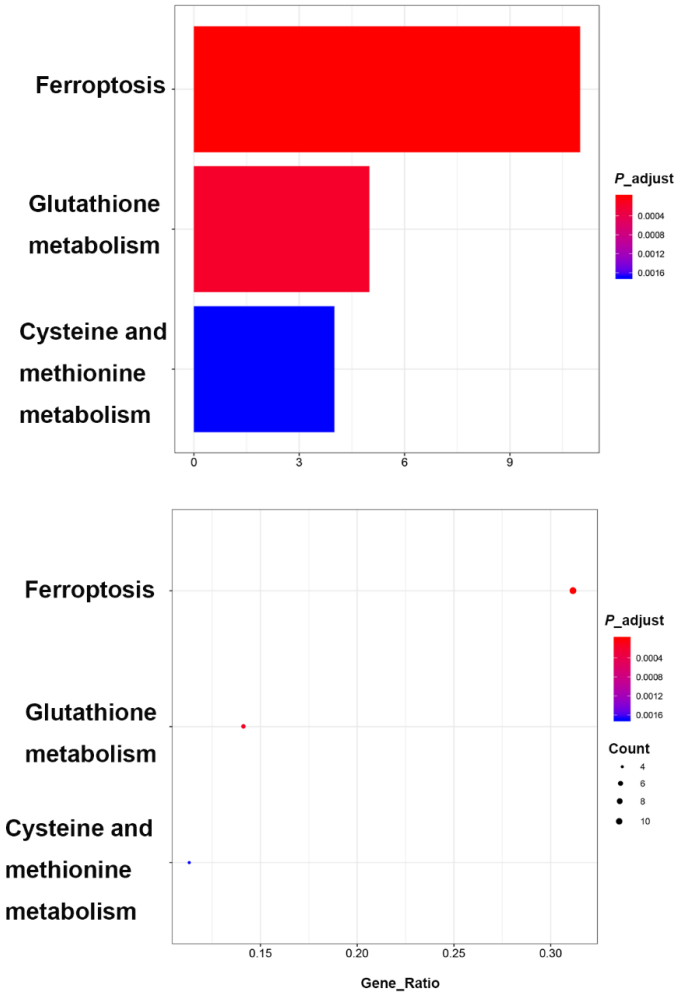

Figure S6 KEGG analyses of the 43 ferroptosis regulators.