**Supplementary information**

**Additional file 1: Table S1. The list of ferroptosis-related genes.**

|  |  |
| --- | --- |
| **Ferroptosis-related genes** | **Name** |
| ABCC1 | ATP binding cassette subfamily C member 1 |
| ACACA | Acetyl-CoA carboxylase alpha |
| ACO1 | aconitase 1 |
| ACSF2 | acyl-CoA synthetase family member 2 |
| ACSL3 | acyl-CoA synthetase long-chain family member 3 |
| ACSL4 | acyl-CoA synthetase long-chain family member 4 |
| AIFM2 | apoptosis inducing factor mitochondria associated 2 |
| AKR1C1 | aldo-keto reductase family 1 member C1 |
| AKR1C2 | aldo-keto reductase family 1 member C2 |
| AKR1C3 | aldo-keto reductase family 1 member C3 |
| ALOX12 | [arachidonate 12-lipoxygenase](https://www.ncbi.nlm.nih.gov/gene/240) |
| ALOX15 | [arachidonate 15-lipoxygenase](https://www.ncbi.nlm.nih.gov/gene/246) |
| ALOX15B | arachidonate 15-lipoxygenase second type |
| ALOX5 | [arachidonate 5-lipoxygenase](https://www.ncbi.nlm.nih.gov/gene/240) |
| ATP5MC3 | ATP synthase membrane subunit c locus 3 |
| CARS | cysteinyl tRNA synthetase |
| CBS | cystathion ine beta synthase |
| CD44 | CD44 molecule |
| CHAC1 | ChaC glutathione- specific gamma-glutamyl cyclotransferase 1 |
| CISD1 | CDGSH iron sulfur domain 1 |
| CRYAB | heat shock protein beta 5 |
| CS | citrate synthase |
| DPP4 | dipeptidyl-dippeptidase-4 |
| EMC2 | ER membrane protein complex subunit 2 |
| FADS2 | fatty acid desaturase 2/acyl-CoA 6-desaturase |
| FANCD2 | Fanconi anemia comple mentation group D2 |
| FDFT1 | farnesyl-diphosphate farnesyltransferase 1 |
| FTH1 | ferritin heavy chain 1 |
| G6PD | glucose-6-phosphate dehydrogenas e |
| GCLC | glutamate-cysteine ligase catalytic subunit |
| GCLM | glutamate-cysteine ligase modifier subunit |
| GLS2 | glutaminase 2 |
| GOT1 | glutamic-oxa loacetic transaminase 1 |
| GPX4 | glutathio ne peroxidase 4 |
| GSS | glutathione synthetase |
| HMGCR | 3-hydroxy-3- methylglutaryl-CoA reductase |
| HMOX1 | heme oxygenase 1 |
| HSBP1 | heat-shock 27-k Da protein 1 |
| HSPB1 | heat shock protein beta 1 |
| IREB2 | iron response element-binding protein 2 |
| KEAP1 | kelch-like ECH- associated protein 1 |
| LPCAT3 | lysophosp hatidylcholine acyltransferase 3 |
| MT1G | metallothionein-1G |
| NCOA4 | nuclear receptor coactiva tor 4 |
| NFE2L2 | nuclear factor, erythroid 2 like 2 |
| NFS1 | cysteine desulfurase |
| NOX1 | NADPH oxidase 1 |
| NQO1 | quinone oxidoreductas e-1 |
| PEBP1 | phosphatidy lethanolamine-binding protein 1 |
| PGD | phosphoglycerate dehydrogenas e |
| PHKG2 | phospho rylase kinase ,g2 |
| PTGS2 | prostagla ndin-endoperoxide synthase 2 |
| RPL8 | ribosomal protein L8 |
| SAT1 | spermidine/spermine N1-acetyltra nsferase 1 |
| SLC1A5 | solute carrier family 1 member 5 |
| SLC7A11 | solute carrier family 7 member 11 |
| SQLE | squalene monooxygenase |
| STEAP3 | six-transm embrane epithelial antigen of prostate 3 |
| TFRC | transferrin receptor |
| TP53 | tumor protein 53 |
| ZEB1 | zinc finger E-box-binding homeobox 1 |



**Additional file 2: Figure S1. Pathway analysis of differentially expressed** **ferroptosis-related genes (FRGs).** (A)The pie chart of the correlation between differentially expressed FRGs and classical cancer pathways. Red color represents activates pathways and green color represents inhibits pathways. (B) Network diagram of the correlation between differentially expressed FRGs and classical cancer pathways. Red color represents activates pathways and blue color represents inhibits pathways.



**Additional file 3: Figure S2. Survival analyses of each gene from the constructed prognostic risk signature based on the optimal cut-off expression value in the TCGA cohort.** (A) CBS, (B) HMOX1, (C) CD44, (D) AKR1C2, (E) CHAC1, (F) HMGCR, and (G) SLC7A11



**Additional file 4: Figure S3. Validation of the prognostic risk signature in the ICGC databased of KIRP patients.** (A) Kaplan-Meier curve analysis of overall survival of KIRC patients in high- and low-risk groups. (B) ROC curve analysis. (C) Risk score distribution, survival status, and lncRNA expression patterns for KIRC patients in high- and low-risk groups by the prognostic signature.



**Additional file 5: Figure S4. The single nucleotide variations (SNVs) and copy number variations (CNVs) of the seven candidate ferroptosis-related genes (FRGs) in the TCGA-KIRC dataset.** (A) The type of genetic alterations of KIRC patients.(B) The variant classification of KIRC patients.(C) The SNV class of KIRC patients.(D) The characteristic of the frequently mutated genes. (E)The CNV alteration frequency of FRG in KIRC patients.



**Additional file 6: Figure S5. Association of the seven candidate ferroptosis-related genes (FRGs) expression with drug sensitivity.** (A) The heatmap shows the difference of the seven candidate FRGs expression among seven human kidney cancer cell lines. (B) The sensitivity of seven candidate FRGs in various drugs. The red dots represent sensitivity to the drug, while blue dots represent the opposite.