

Figure S1 The overall design of this study. FRGs, ferroptosis-related genes; PCA, principal component analysis; KM, Kaplan-Meier; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; WGCNA, weighted correlation network analysis; ROC, receiver operating characteristic; TIDE, Tumor Immune Dysfunction and Exclusion; ssGSEA, single-sample gene set enrichment analysis; SVM, support vector machine; LDA, linear discriminant analysis; KNN, K-nearest neighbor.

Table S1 232 ferroptosis-related genes calculated by the univariate Cox analysis

| Characteristics | Hazard ratio | 95% CI | P value |
|-----------------|--------------|------------------------------------|---------|
| MIR539 | 3.63515E+14 | 44.46-2972121065941969354729979904 | 0.027 |
| MIR17 | 5.06653E+13 | 661.82-3878670926851328394133504 | 0.014 |
| MIR9_3 | 8097398.76 | 4.2-15628781547150.1 | 0.031 |
| MIR130B | 6734.16 | 781.35-58038.94 | <0.001 |
| USP7 | 30.55 | 14.47-64.48 | <0.001 |
| ELAVL1 | 15.32 | 8.95-26.22 | <0.001 |
| METTL14 | 10.76 | 6.5-17.8 | <0.001 |
| DAZAP1 | 9.53 | 6.09-14.9 | <0.001 |
| KEAP1 | 9.35 | 6.04-14.49 | <0.001 |
| CISD2 | 7.78 | 5.04-12.01 | <0.001 |
| BRD7 | 7.04 | 3.63-13.65 | <0.001 |
| LONP1 | 7.01 | 4.85-10.12 | <0.001 |
| PRDX6 | 6.81 | 4.72-9.84 | <0.001 |
| TFAM | 6.58 | 4.26-10.16 | <0.001 |
| DHODH | 5.61 | 3.79-8.3 | <0.001 |
| HDCC3 | 5.48 | 3.47-8.65 | <0.001 |
| SNX5 | 5.25 | 3.23-8.54 | <0.001 |
| ABCC1 | 4.82 | 3.36-6.92 | <0.001 |
| IDH2 | 4.48 | 3.26-6.14 | <0.001 |
| SUV39H1 | 4.48 | 3.18-6.3 | <0.001 |
| VDAC2 | 4.26 | 2.82-6.41 | <0.001 |
| FADS1 | 4.05 | 2.95-5.58 | <0.001 |
| ARF6 | 4.02 | 2.6-6.23 | <0.001 |
| HELLS | 4.02 | 3.1-5.21 | <0.001 |
| SRSF9 | 4.02 | 2.85-5.67 | <0.001 |
| FH | 3.95 | 2.72-5.73 | <0.001 |
| SLC3A2 | 3.94 | 2.85-5.45 | <0.001 |
| SIRT6 | 3.89 | 2.39-6.33 | <0.001 |
| HMGB1 | 3.82 | 2.5-5.82 | <0.001 |
| ALOX12B | 3.74 | 2.82-4.96 | <0.001 |
| GSTZ1 | 3.74 | 2.69-5.2 | <0.001 |
| G6PD | 3.73 | 2.6-5.35 | <0.001 |
| PAQR3 | 3.66 | 2.77-4.84 | <0.001 |
| CFL1 | 3.64 | 2.54-5.23 | <0.001 |
| HILPDA | 3.57 | 2.81-4.55 | <0.001 |
| SLC16A1 | 3.47 | 2.81-4.28 | <0.001 |
| SIAH2 | 3.44 | 2.38-4.98 | <0.001 |
| OTUB1 | 3.43 | 2.32-5.07 | <0.001 |
| TXN | 3.41 | 2.58-4.51 | <0.001 |
| GLRX5 | 3.37 | 2.31-4.92 | <0.001 |
| SMG9 | 3.34 | 1.95-5.72 | <0.001 |
| ALOXE3 | 3.3 | 2.04-5.34 | <0.001 |
| HSF1 | 3.27 | 1.84-5.81 | <0.001 |
| SRC | 3.22 | 1.93-5.38 | <0.001 |
| CS | 3.17 | 1.78-5.64 | <0.001 |
| FXN | 3.13 | 2-4.9 | <0.001 |
| ATG3 | 3.07 | 1.73-5.46 | <0.001 |
| PGRMC1 | 3 | 2.19-4.11 | <0.001 |
| BEX1 | 2.94 | 2.22-3.89 | <0.001 |
| TP53 | 2.91 | 2.33-3.63 | <0.001 |
| SENP1 | 2.88 | 1.65-5.05 | <0.001 |
| KIF20A | 2.85 | 2.29-3.56 | <0.001 |
| STK11 | 2.81 | 1.62-4.87 | <0.001 |
| ATF4 | 2.77 | 1.76-4.36 | <0.001 |
| HIF1A | 2.76 | 1.95-3.88 | <0.001 |
| KDM5A | 2.75 | 1.81-4.17 | <0.001 |
| OIP5_AS1 | 2.74 | 2.01-3.73 | <0.001 |
| SLC1A5 | 2.74 | 2.31-3.25 | <0.001 |
| RELA | 2.73 | 1.63-4.55 | <0.001 |
| RPL8 | 2.7 | 2.11-3.45 | <0.001 |
| FADS2 | 2.69 | 1.94-3.72 | <0.001 |
| KDM5C | 2.68 | 1.61-4.45 | <0.001 |
| BAP1 | 2.63 | 1.45-4.78 | 0.001 |
| TFRC | 2.59 | 2.08-3.23 | <0.001 |
| ACOT1 | 2.56 | 1.94-3.36 | <0.001 |
| CDC25A | 2.56 | 2.06-3.19 | <0.001 |
| HSPA5 | 2.54 | 1.73-3.74 | <0.001 |
| BID | 2.44 | 1.58-3.75 | <0.001 |
| FANCD2 | 2.44 | 1.91-3.12 | <0.001 |
| PROK2 | 2.38 | 1.76-3.21 | <0.001 |
| CISD1 | 2.28 | 1.52-3.44 | <0.001 |
| MPC1 | 2.27 | 1.54-3.33 | <0.001 |
| SCD | 2.26 | 1.88-2.72 | <0.001 |
| FAR1 | 2.19 | 1.34-3.6 | 0.002 |
| MYB | 2.19 | 1.76-2.73 | <0.001 |
| EMC2 | 2.18 | 1.28-3.71 | 0.004 |
| MIR214 | 2.16 | 1.11-4.19 | 0.023 |
| PIR | 2.12 | 1.69-2.65 | <0.001 |
| CBS | 2.1 | 1.7-2.6 | <0.001 |
| DDR2 | 2.07 | 1.76-2.43 | <0.001 |
| GPX4 | 2.03 | 1.47-2.81 | <0.001 |
| SIRT1 | 2.02 | 1.07-3.82 | 0.03 |
| GCLC | 2 | 1.3-3.09 | 0.002 |
| PHKG2 | 1.97 | 1.1-3.53 | 0.023 |
| CAMKK2 | 1.96 | 1.34-2.86 | <0.001 |
| FTH1 | 1.94 | 1.4-2.7 | <0.001 |
| RRM2 | 1.93 | 1.66-2.24 | <0.001 |
| MDM2 | 1.92 | 1.58-2.34 | <0.001 |
| PEX12 | 1.92 | 1.22-3.01 | 0.005 |
| CHMP5 | 1.91 | 1.21-3.01 | 0.005 |
| QSOX1 | 1.89 | 1.18-3.05 | 0.009 |
| CA9 | 1.86 | 1.38-2.5 | <0.001 |
| PIK3CA | 1.74 | 1.13-2.67 | 0.011 |
| ETV4 | 1.73 | 1.54-1.94 | <0.001 |
| SLC38A1 | 1.73 | 1.09-2.75 | 0.021 |
| EZH2 | 1.7 | 1.25-2.3 | <0.001 |
| CHAC1 | 1.68 | 1.34-2.1 | <0.001 |
| COPZ1 | 1.68 | 1.05-2.71 | 0.032 |
| ATG5 | 1.66 | 1.13-2.44 | 0.01 |
| BACH1 | 1.61 | 1.07-2.44 | 0.023 |
| TERT | 1.6 | 1.47-1.74 | <0.001 |
| GALNT14 | 1.53 | 1.34-1.75 | <0.001 |
| MYCN | 1.53 | 1.41-1.67 | <0.001 |
| PVT1 | 1.52 | 1.21-1.91 | <0.001 |
| NOS2 | 1.5 | 1.13-1.97 | 0.004 |
| CDKN2A | 1.49 | 1.25-1.77 | <0.001 |
| FTL | 1.45 | 1.1-1.9 | 0.008 |
| PPARA | 1.32 | 1.03-1.69 | 0.026 |
| CPEB1 | 1.31 | 1.14-1.5 | <0.001 |
| HCAR1 | 1.3 | 1.09-1.54 | 0.003 |
| H19 | 1.16 | 1.04-1.3 | 0.008 |
| MEG3 | 0.88 | 0.81-0.95 | 0.001 |
| EGR1 | 0.84 | 0.75-0.95 | 0.007 |
| CAV1 | 0.81 | 0.66-0.98 | 0.035 |
| GSTM1 | 0.78 | 0.62-0.98 | 0.032 |
| IL1B | 0.78 | 0.62-0.98 | 0.035 |
| PTGS2 | 0.78 | 0.65-0.94 | 0.009 |
| IDO1 | 0.76 | 0.63-0.92 | 0.005 |
| PRKCA | 0.76 | 0.64-0.91 | 0.002 |
| RARRES2 | 0.76 | 0.64-0.89 | <0.001 |
| PKD4 | 0.74 | 0.64-0.86 | <0.001 |
| PTPN6 | 0.73 | 0.6-0.89 | 0.002 |
| ZFP36 | 0.72 | 0.64-0.81 | <0.001 |
| WWTR1 | 0.71 | 0.59-0.86 | <0.001 |
| ATF3 | 0.7 | 0.58-0.84 | <0.001 |
| SNCA | 0.7 | 0.59-0.83 | <0.001 |
| KLF2 | 0.68 | 0.58-0.79 | <0.001 |
| VDR | 0.68 | 0.54-0.86 | 0.001 |
| CTSB | 0.67 | 0.48-0.92 | 0.013 |
| GCH1 | 0.67 | 0.58-0.77 | <0.001 |
| PIEZO1 | 0.66 | 0.55-0.78 | <0.001 |
| SOCS1 | 0.66 | 0.49-0.9 | 0.008 |
| CD44 | 0.65 | 0.6-0.72 | <0.001 |
| HSPB1 | 0.65 | 0.53-0.81 | <0.001 |
| SAT1 | 0.65 | 0.5-0.83 | <0.001 |
| SLC40A1 | 0.65 | 0.55-0.77 | <0.001 |
| EGFR | 0.64 | 0.5-0.82 | <0.001 |
| TLR4 | 0.64 | 0.51-0.79 | <0.001 |
| ALOX5 | 0.63 | 0.5-0.79 | <0.001 |
| CD82 | 0.63 | 0.51-0.79 | <0.001 |
| EPAS1 | 0.63 | 0.54-0.75 | <0.001 |
| PRKAA2 | 0.63 | 0.51-0.77 | <0.001 |
| SCP2 | 0.63 | 0.43-0.93 | 0.02 |
| NFE2L2 | 0.62 | 0.43-0.91 | 0.015 |
| YAP1 | 0.62 | 0.52-0.74 | <0.001 |
| NEDD4L | 0.61 | 0.47-0.78 | <0.001 |
| CDO1 | 0.6 | 0.48-0.74 | <0.001 |
| TNFAIP3 | 0.59 | 0.52-0.66 | <0.001 |
| CYGB | 0.57 | 0.45-0.73 | <0.001 |
| MEF2C | 0.57 | 0.47-0.7 | <0.001 |
| CDH1 | 0.56 | 0.44-0.73 | <0.001 |
| SMPD1 | 0.56 | 0.38-0.82 | 0.003 |
| NEAT1 | 0.55 | 0.48-0.62 | <0.001 |
| NF2 | 0.55 | 0.31-0.96 | 0.035 |
| SREBF1 | 0.55 | 0.42-0.73 | <0.001 |
| TRIB2 | 0.54 | 0.41-0.7 | <0.001 |
| AIFM2 | 0.53 | 0.39-0.73 | <0.001 |
| AKR1C2 | 0.53 | 0.46-0.61 | <0.001 |
| ALOX15B | 0.53 | 0.39-0.72 | <0.001 |
| RBMS1 | 0.53 | 0.41-0.7 | <0.001 |
| SLC25A28 | 0.53 | 0.29-0.95 | 0.034 |
| AKR1C3 | 0.51 | 0.38-0.68 | <0.001 |
| SLC11A2 | 0.51 | 0.27-0.96 | 0.038 |
| ABHD12 | 0.5 | 0.28-0.89 | 0.018 |
| ACSF2 | 0.49 | 0.36-0.67 | <0.001 |
| AKR1C1 | 0.49 | 0.42-0.56 | <0.001 |
| TFAP2A | 0.49 | 0.38-0.63 | <0.001 |
| TFR2 | 0.49 | 0.38-0.65 | <0.001 |
| ARNTL | 0.48 | 0.35-0.64 | <0.001 |
| ISCU | 0.48 | 0.31-0.76 | 0.002 |
| LIFR | 0.48 | 0.4-0.57 | <0.001 |
| TRIM46 | 0.48 | 0.33-0.7 | <0.001 |
| NEDD4 | 0.47 | 0.36-0.61 | <0.001 |
| NFS1 | 0.47 | 0.28-0.79 | 0.004 |
| ZEB1 | 0.47 | 0.36-0.62 | <0.001 |
| ARHGGEF26_AS1 | 0.45 | 0.2-0.98 | 0.044 |
| FLT3 | 0.45 | 0.32-0.64 | <0.001 |
| SLC39A7 | 0.45 | 0.23-0.88 | 0.019 |
| ABCC5 | 0.44 | 0.31-0.61 | <0.001 |
| CCDC6 | 0.44 | 0.24-0.81 | 0.008 |
| DPP4 | 0.44 | 0.34-0.57 | <0.001 |
| PANX2 | 0.44 | 0.36-0.53 | <0.001 |
| PDSS2 | 0.44 | 0.25-0.8 | 0.007 |
| YML | 0.44 | 0.27-0.74 | 0.002 |
| PTHDC2 | 0.44 | 0.28-0.7 | <0.001 |
| ANO6 | 0.43 | 0.35-0.52 | <0.001 |
| SQSTM1 | 0.43 | 0.31-0.61 | <0.001 |
| DPEP1 | 0.42 | 0.28-0.61 | <0.001 |
| MICU1 | 0.42 | 0.25-0.72 | 0.001 |
| LPIN1 | 0.41 | 0.28-0.59 | <0.001 |
| MAPK3 | 0.41 | 0.26-0.64 | <0.001 |
| CISD3 | 0.4 | 0.26-0.64 | <0.001 |
| PEX10 | 0.4 | 0.26-0.63 | <0.001 |
| PTPN18 | 0.4 | 0.25-0.65 | <0.001 |
| AR | 0.39 | 0.25-0.59 | <0.001 |
| PROM2 | 0.39 | 0.31-0.49 | <0.001 |
| KDM6B | 0.38 | 0.29-0.5 | <0.001 |
| ASMTL_AS1 | 0.37 | 0.28-0.47 | <0.001 |
| MTF1 | 0.37 | 0.27-0.52 | <0.001 |
| MAPK9 | 0.36 | 0.22-0.58 | <0.001 |
| MTOR | 0.36 | 0.26-0.49 | <0.001 |
| PPARD | 0.36 | 0.28-0.48 | <0.001 |
| PRKAA1 | 0.35 | 0.25-0.49 | <0.001 |
| TSC1 | 0.35 | 0.24-0.52 | <0.001 |
| PLA2G6 | 0.34 | 0.25-0.46 | <0.001 |
| CIRBP | 0.33 | 0.21-0.51 | <0.001 |
| STAT3 | 0.32 | 0.26-0.4 | <0.001 |
| ACVR1B | 0.3 | 0.22-0.41 | <0.001 |
| ALOX12 | 0.3 | 0.19-0.49 | <0.001 |
| ATF2 | 0.29 | 0.2-0.43 | <0.001 |
| LINC00472 | 0.28 | 0.11-0.77 | 0.013 |
| ULK1 | 0.28 | 0.2-0.39 | <0.001 |
| TMBIM4 | 0.27 | 0.18-0.39 | <0.001 |
| TP63 | 0.27 | 0.19-0.4 | <0.001 |
| MIB2 | 0.26 | 0.2-0.34 | <0.001 |
| KDM4A | 0.25 | 0.16-0.37 | <0.001 |
| ALDH3A2 | 0.24 | 0.18-0.32 | <0.001 |
| TF | 0.23 | 0.16-0.32 | <0.001 |
| ATG7 | 0.22 | 0.15-0.33 | <0.001 |
| CYB5R1 | 0.22 | 0.14-0.34 | <0.001 |
| MYN2 | 0.22 | 0.16-0.3 | <0.001 |
| SIRT2 | 0.21 | 0.12-0.36 | <0.001 |
| ULK2 | 0.21 | 0.16-0.29 | <0.001 |
| MAPK1 | 0.2 | 0.13-0.3 | <0.001 |
| USP35 | 0.2 | 0.14-0.28 | <0.001 |
| TRIM26 | 0.17 | 0.1-0.3 | <0.001 |
| MIR27A | 0.06 | 0.01-0.56 | 0.013 |
| MIR324 | 0.03 | 0.01-0.07 | <0.001 |
| MIR137 | | | |

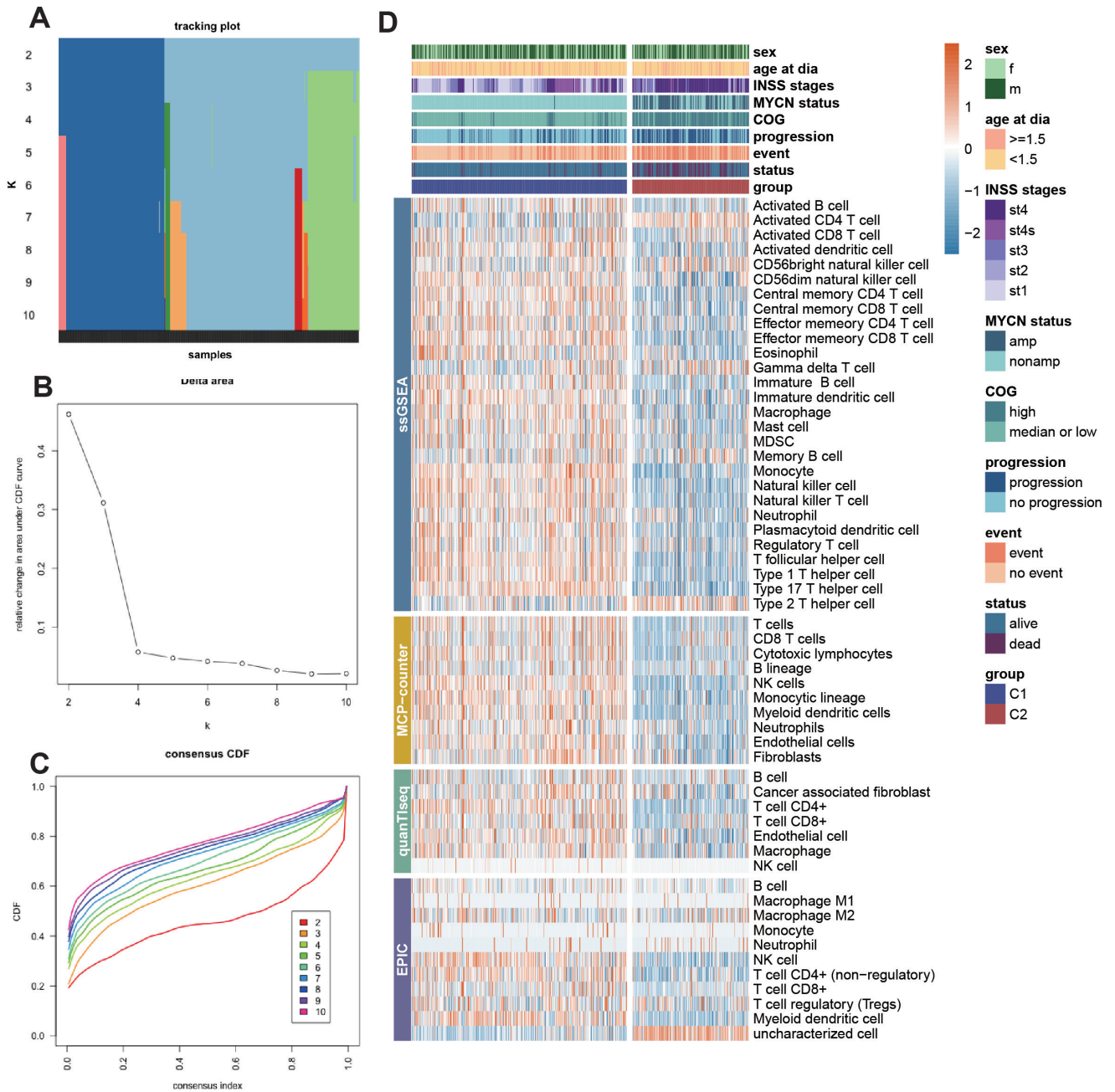


Figure S2 Selection of K-value and validation of immune cell infiltration results. (A) The tracking plot of the consensus score matrix. (B) The cumulative distribution function curves of the consensus score matrix. (C) The index curves of the consensus score matrix. (D) The heatmap of the results of ssGSEA, quanTIseq, MCP-counter, and EPIC. CDF, cumulative distribution function; dia, diagnosis; amp, amplification.

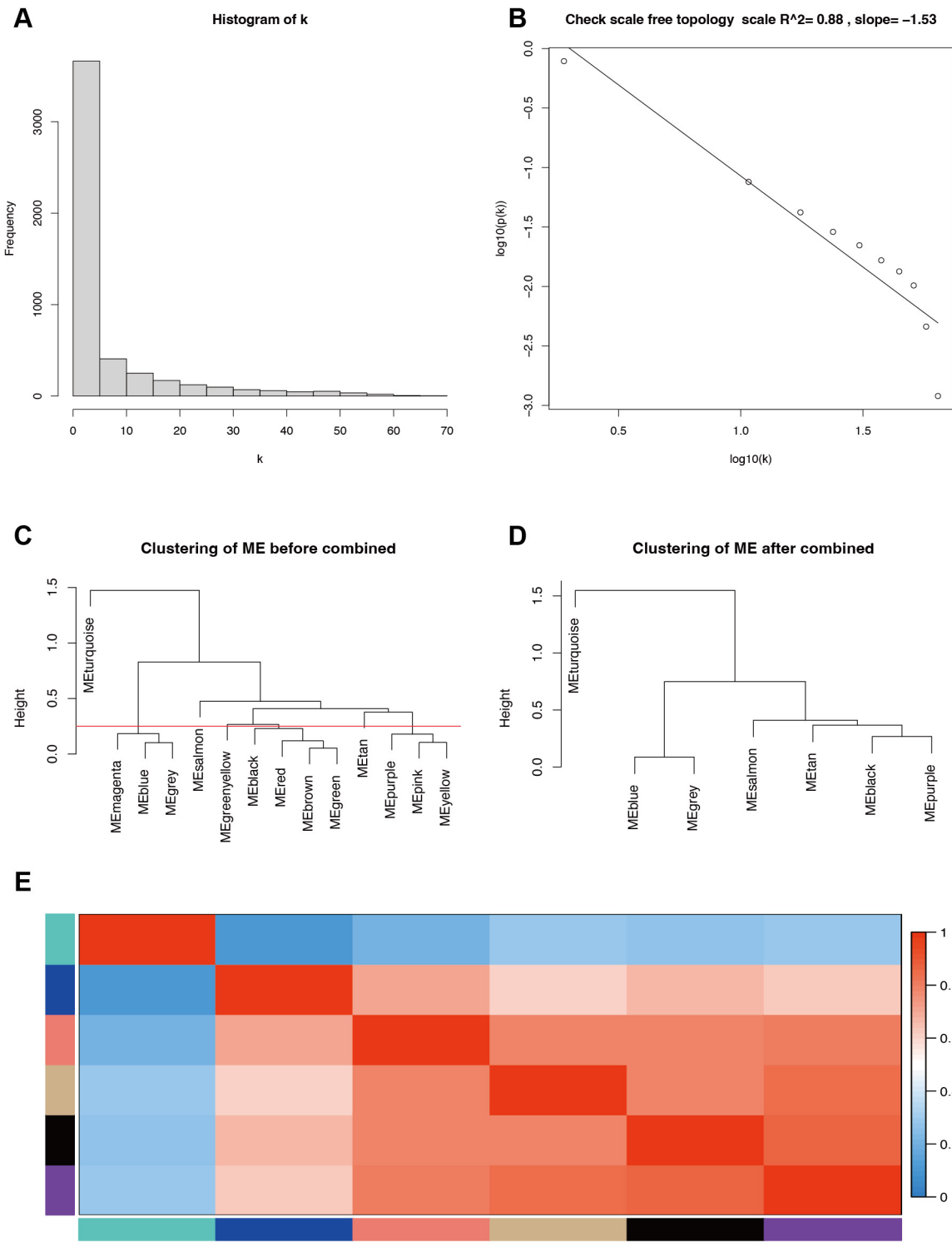


Figure S3 Selection of soft thresholding and merging of modules. (A) The Histogram of K in the process of selecting the soft threshold. (B) The check scale free topology in the process of selecting the soft threshold. (C-D) The tree of modules before and after merging. (E) The heatmap that revealed the eigengene adjacency of modules. ME, module eigengene.

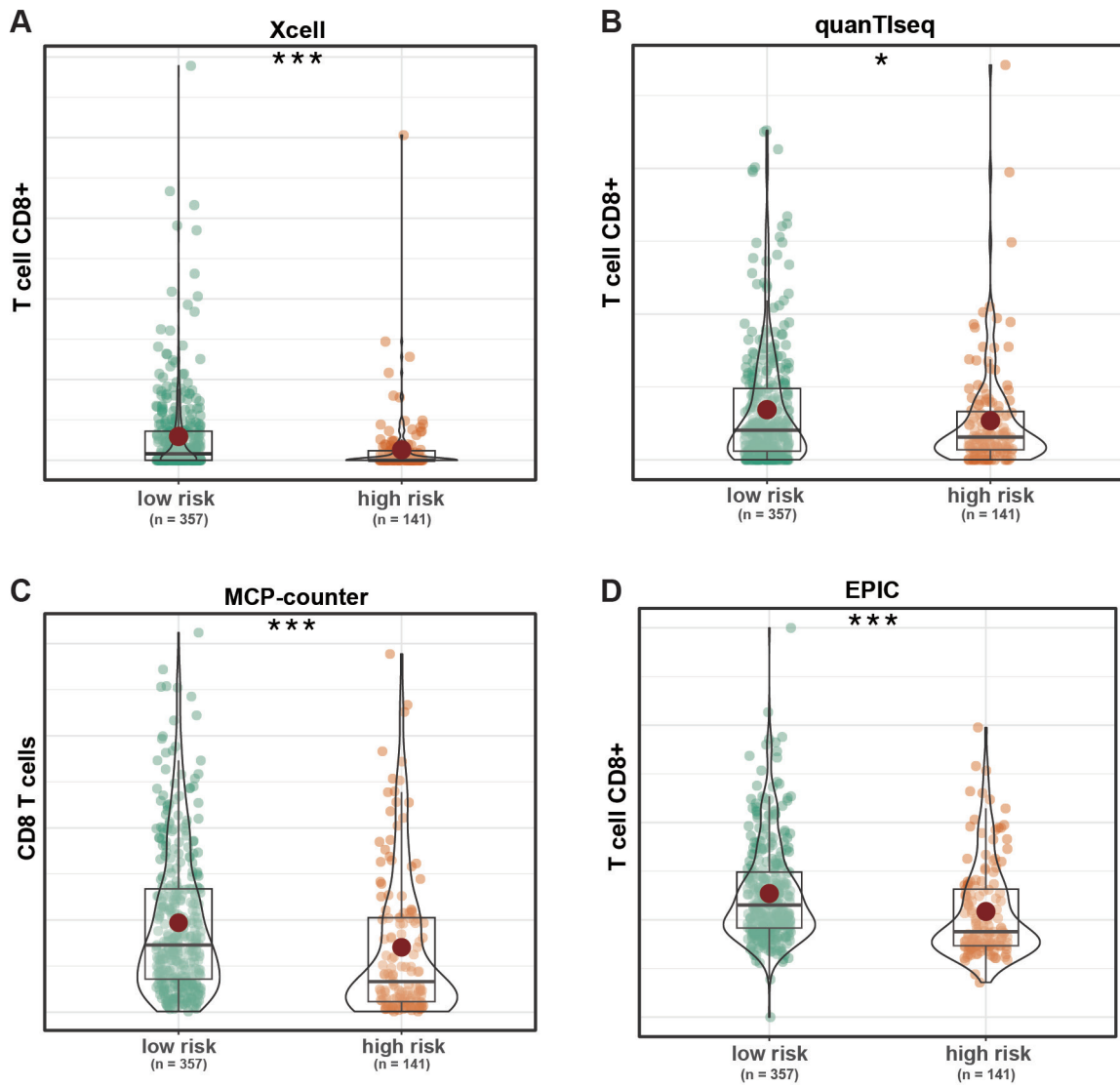


Figure S4 Validation of CD8+ T cell infiltration differences between the high- and low-risk groups. (A) Calculation of CD8+ T cell infiltration between groups by Xcell algorithm. (B) Calculation of CD8+ T cell infiltration between groups by quanTiseq algorithm. (C) Calculation of CD8+ T cell infiltration between groups by MCP-counter algorithm. (D) Calculation of CD8+ T cell infiltration between groups by EPIC algorithm. *, $P < 0.05$, ***, $P < 0.001$.