Fig. S1 PCA (A) plot between GTEx and TCGA datasets. Forest plot (B) to show the results of the univariate cox regression analysis between ferroptosis-related gene expression and prognosis. Figure (C) to show the Log Lambda value corresponding to the minimum cross-validation error point. Figure (D) to show the prognostic ferroptosis-related genes with non-zero coefficient corresponding to the same Log Lambda value were selected for subsequent signature construction.
Fig. S2 The OS status plots, OS and risk score plots, heatmaps, Kaplan–Meier survival plots and ROC plots of these 10 genes between left-hemi (A-E) and right-hemi (F-L) CRC patients in the GSE14333 dataset.
Fig. S3 The maf-summary plots and oncoplots of the somatic mutation and the violin plot (E) for the TMB scores between the high-risk (A-B) and low-risk (C-D) groups in the ICGC dataset.
Fig. S4 The violin plots for the relationships between the risk scores and the expressions levels of the PD-1 (A) and PD-L1 (B) in the TCGA dataset.