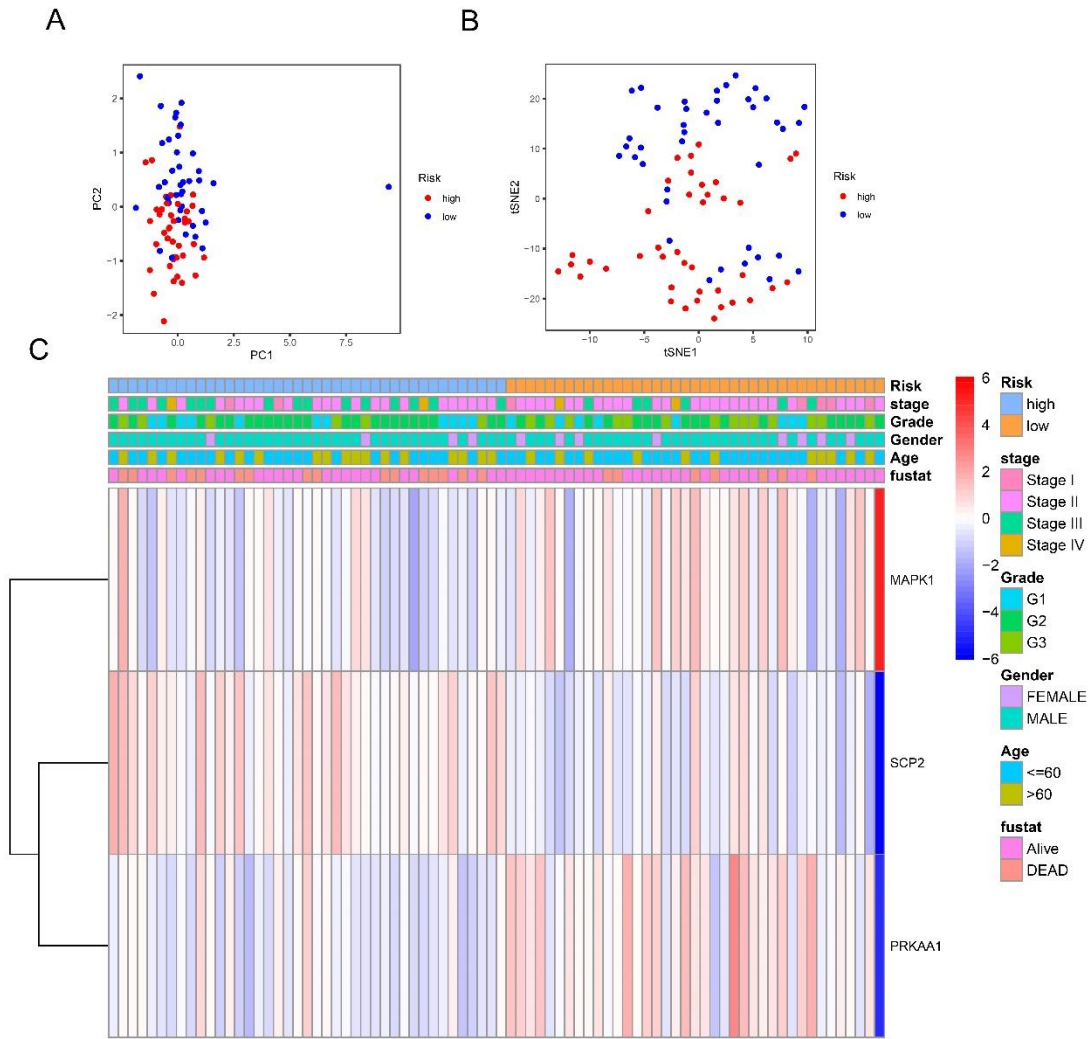


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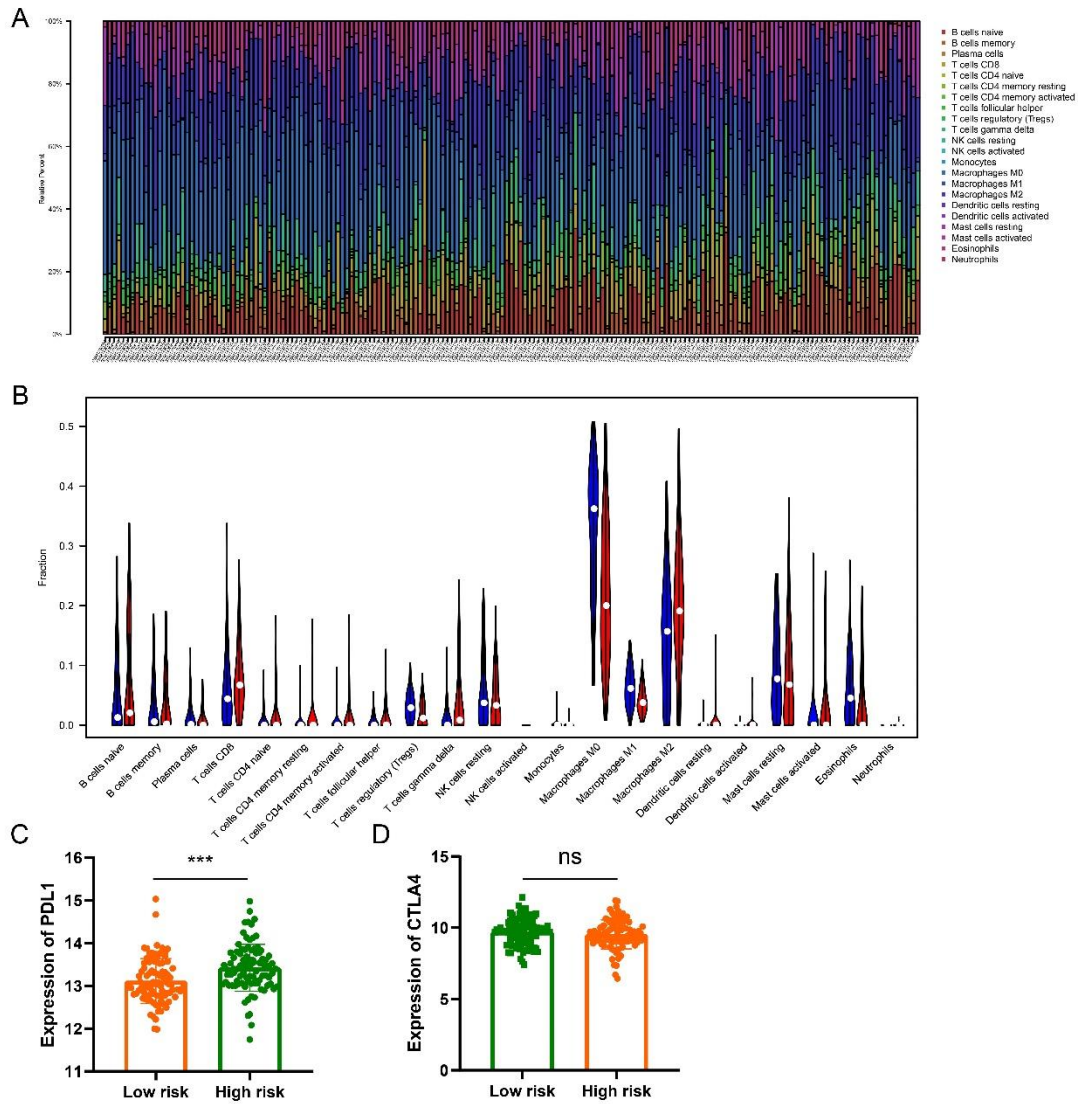
Supplemental information

**Systematic profiling of ferroptosis gene
signatures predicts prognostic factors
in esophageal squamous cell carcinoma**

**Tong Lu, Ran Xu, Qi Li, Jia-ying Zhao, Bo Peng, Han Zhang, Ji-da Guo, Sheng-qiang
Zhang, Hua-wei Li, Jun Wang, and Lin-you Zhang**



Supplementary Figure 1. Distribution of the high- and low-risk group according to the prognostic model. The PCA and t-SNE plot showing the patients in different risk groups were distributed in two directions. (A-B) The clinical heatmap showing the distribution of 3 ferroptosis genes according to the model. (C)



Supplementary Figure 2. Immune cell landscapes in different ferroptosis risk score groups in GSE53625 dataset. The bar plot showing the proportion of infiltrated immune cells calculated by the CIBERSORT algorithm in GSE53625. (A) The violin plot showing the difference between 22 infiltrated immune cells in the tumor microenvironment in GSE53625. (B) Graph showing different expression of PD-1 and CTLA4 in GSE53625. (C-D)