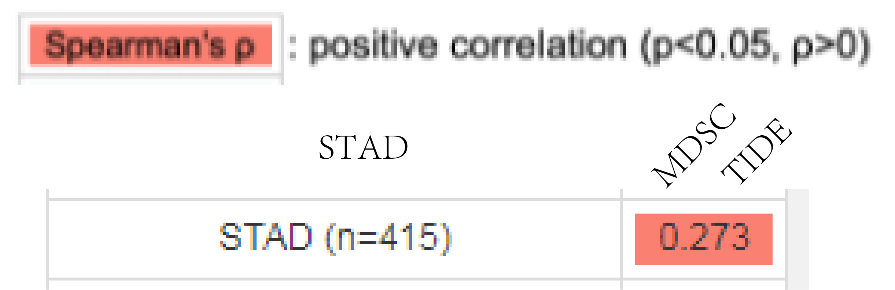
**Supplementary Figure**



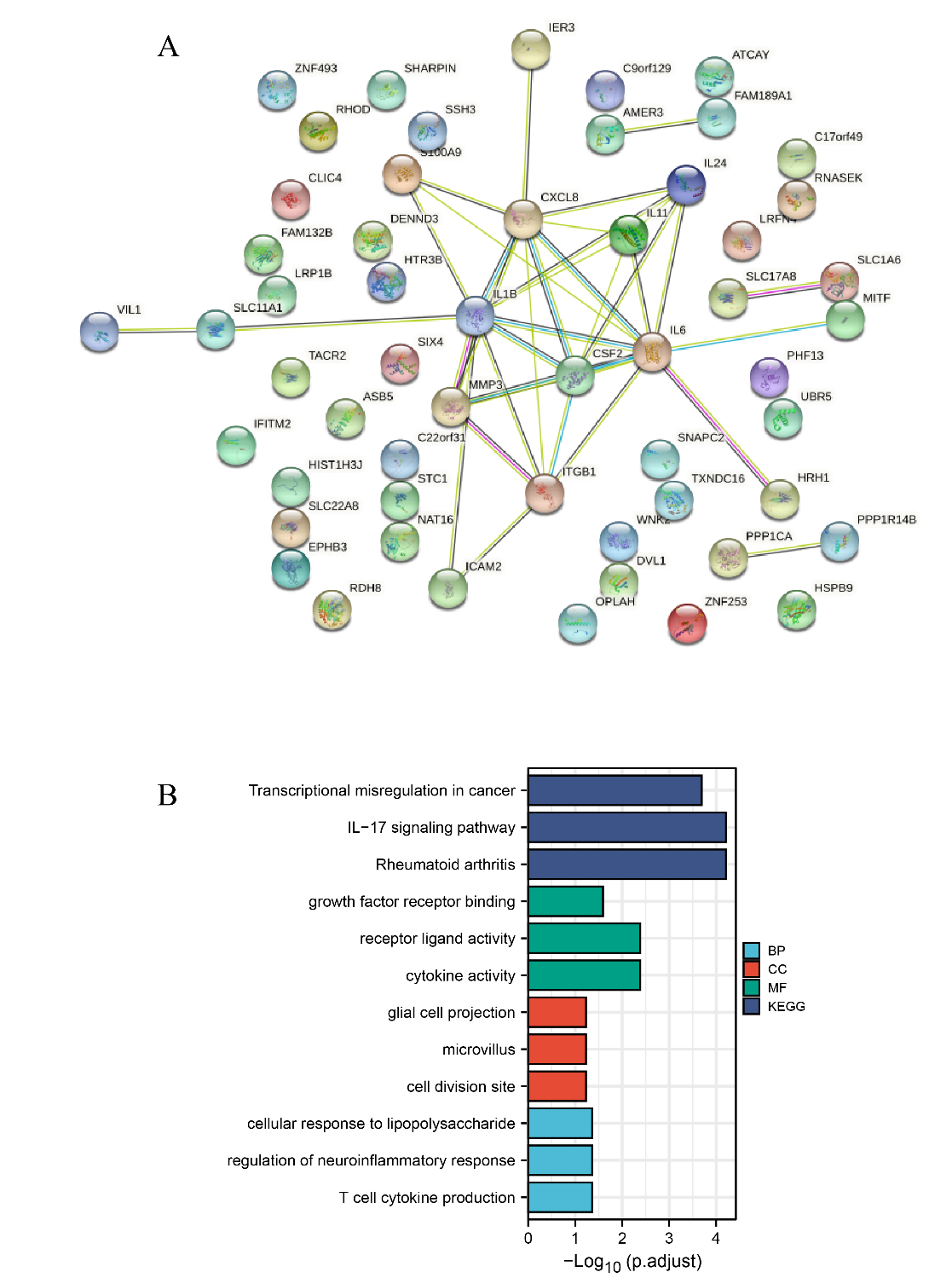
**Supplementary Figure 1.**. The correlation between ferroptosis-related genes and tumour stage in LIHC patients (GEPIA). The mRNA expression levels of these genes were not correlated with patients’ individual tumour stage.

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**Supplementary Figure 2.** The correlation of AIFM2 expression with tumour-infiltrating lymphocytes in LIHC and STAD. A, B. The relationship of AIFM2 to immune infiltration levels in LIHC and STAD.



**Supplementary Figure 3.** The correlation of AIFM2 with STAD analysed by using TIMER.



**Supplementary Figure 4.** GO and KEGG enrichment analyses of ferroptosis-related genes and their coexpressed genes in STAD. (STRING and DAVID). (A) PPI network. The nodes indicate proteins; the edges indicate the interaction of proteins. (B) BP, CC, MF and KEGG. Systematic Analysis of Expression Profiles and Prognostic Significance for Ferroptosis-related Genes in STAD.

**Supplementary Figure 5.**



A, B, the relative expression of GPX4 was shown in the graph.