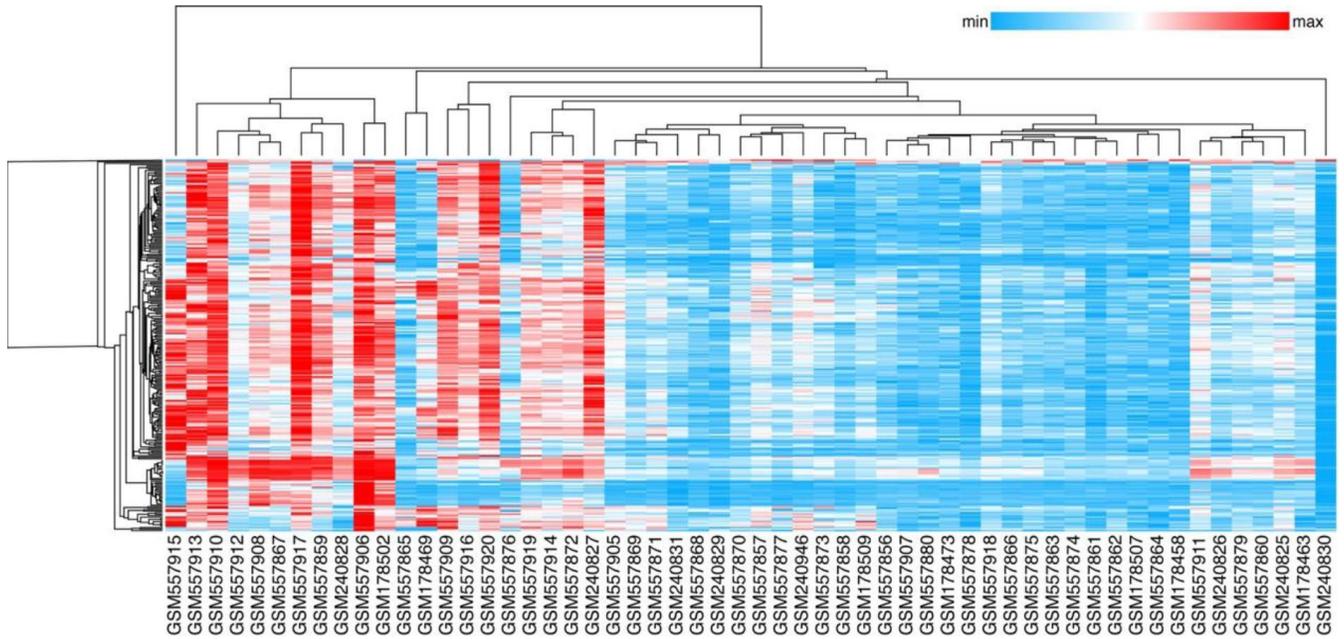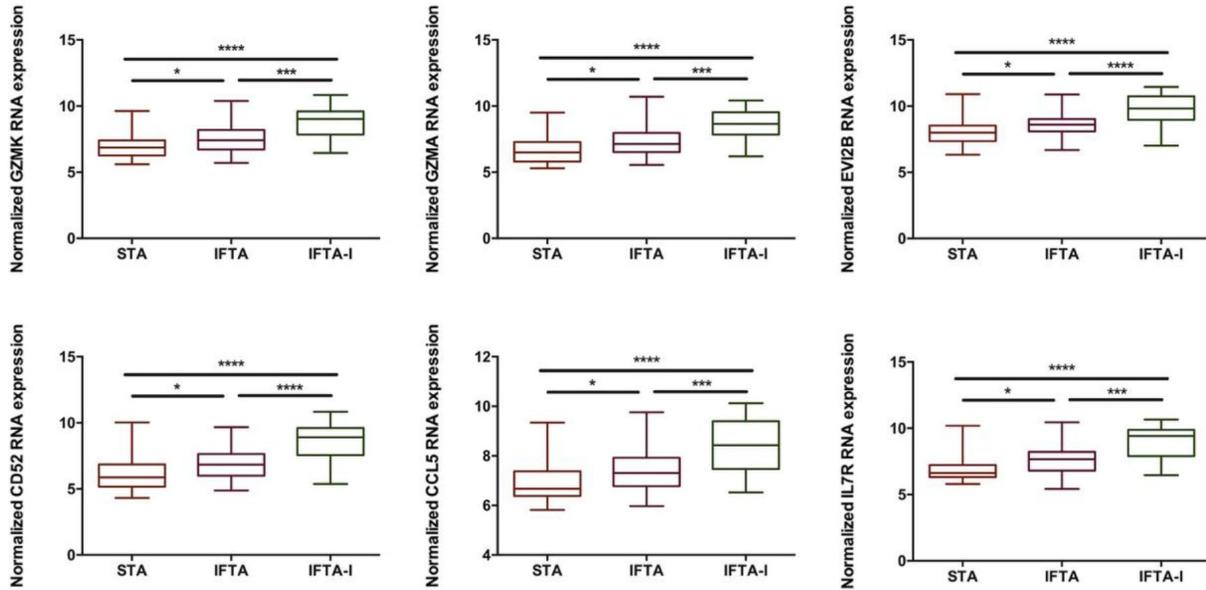# SUPPLEMENTARY MATERIALS

Supplementary Figures

Supplementary Figure 1. Identification and analysis of DEGs. After the inclusion and exclusion, a total of 249 genes with log2 fold change (log2 |FC|) >1, FDR adjusted *P* < 0.001) were identified finally. All those genes were up-regulated.

Supplementary Figure 2. RNA expressions of the key genes. The gene expressions of GZMK, GZMA, EVI2B, CD52, CCL5, and IL7R had significant differences among the STA, IFTA, and IFTA-I groups. *P* < 0.05, ***P* < 0.001, ****P* < 0.0001.
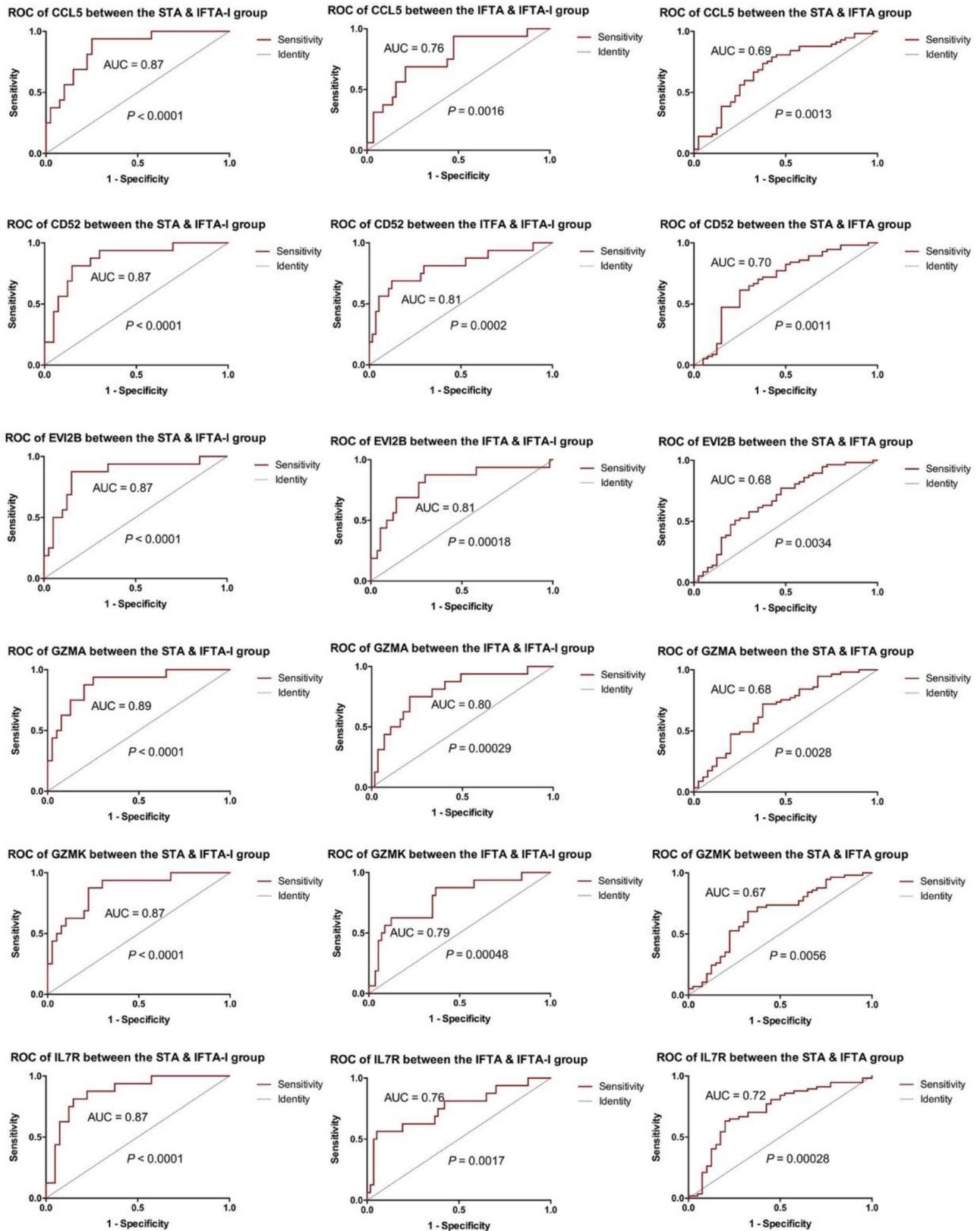
Supplementary Figure 3. ROC curve of the key genes. ROC curves showed that CCL5, CD52, EVI2B, GZMA, GZMK, and IL7R could be also used for differentiate IFTA-I from IFTA and STA respectively.
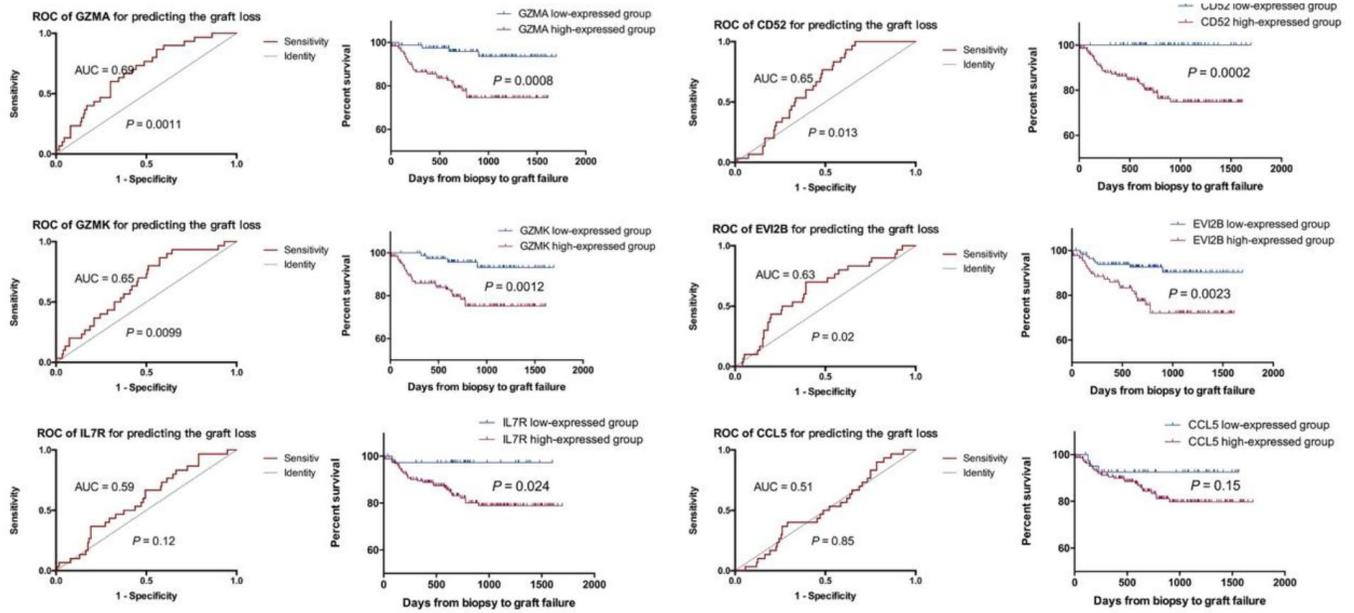
Supplementary Figure 4. ROC and graft loss prediction analysis. ROC and survival analysis of GZMA, CD52, GZMK, EVI2B, IL7R, and CCL5.