

The Ferroptosis-related Gene MAFG Screened by Machine Learning Is Associated with the Diagnosis and Prognosis of Sepsis

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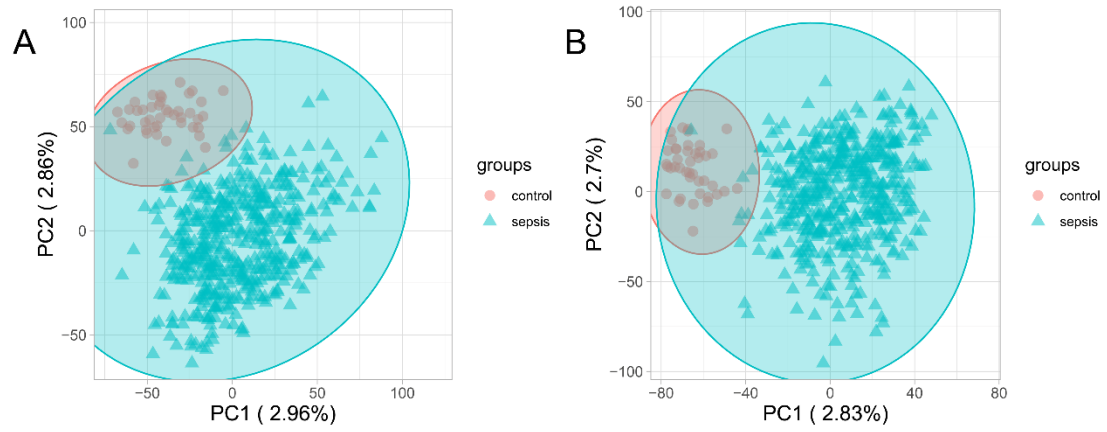
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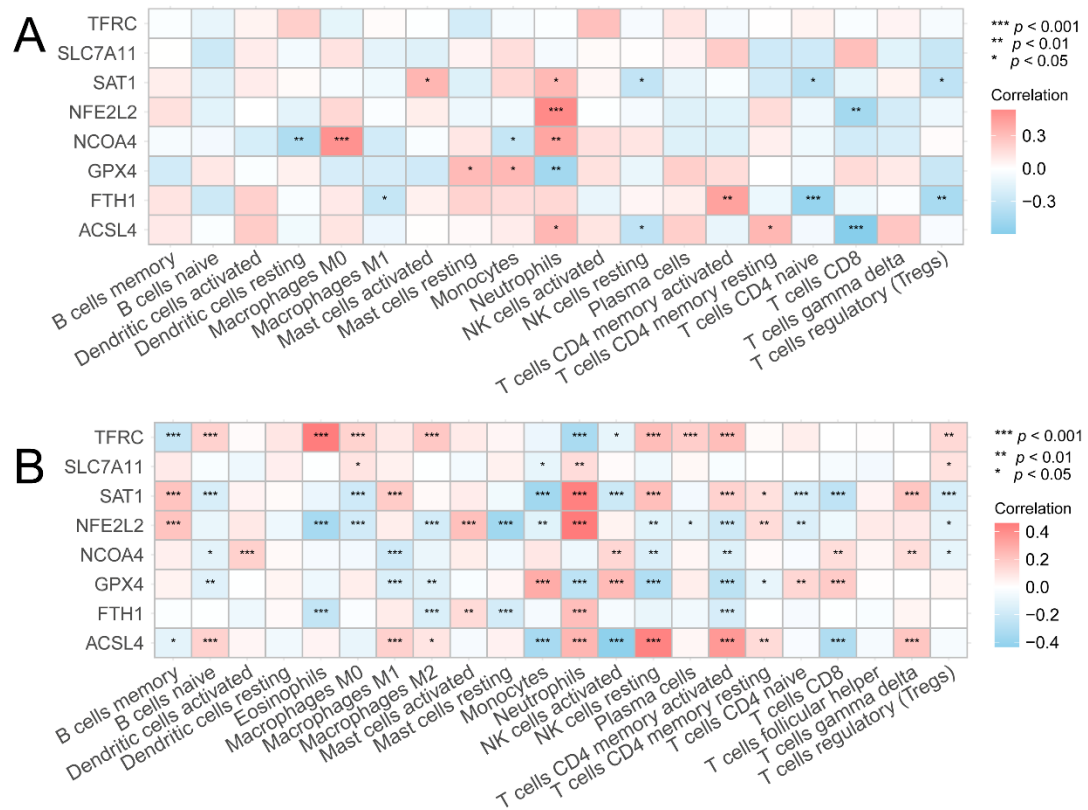
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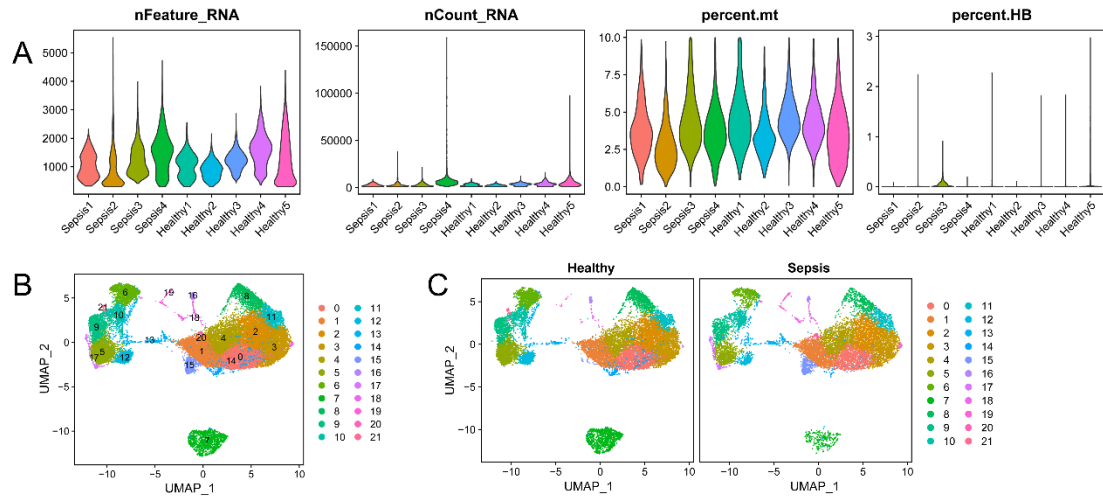
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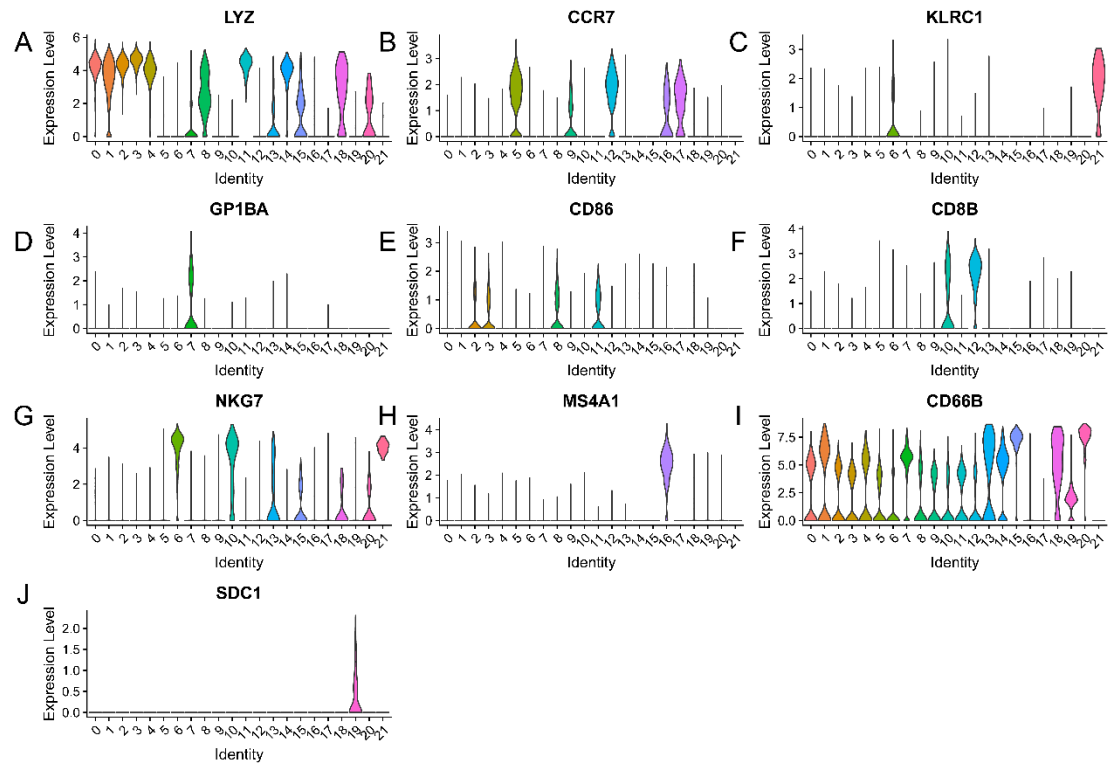
Additional file 5: Figure S1. The PCA demonstrates minimal batch effects pre-correction and post-correction. (A) PCA visualization of pre-correction batch effects. (B) PCA visualization of post-correction batch effects.



Additional file 6: Figure S2. The altered immune cell landscape in sepsis patients is closely correlated with the expression of FRGs. (A) Correlation heatmap of the immune cell landscape with common FRGs in control group. (B) Correlation heatmap of the immune cell landscape with common FRGs in sepsis group.



Additional file 7: Figure S3. The process of quality control and clustering of scRNA-seq data. (A) The low-quality cells were removed with the threshold of $nFeature_RNA > 200$ & $nFeature_RNA < 6000$, $nCount_RNA > 1000$, $percent.mt < 10\%$, and $percent.HB < 3\%$. (B) The featureplot of 22 clusters was obtained after dimensionality reduction and data integration. (C) The featureplot showed that the batch effect between healthy and the sepsis samples has been effectively removed.



Additional file 8: Figure S4. (A-J) The featureplot of specific markers in each cell type during the cellular annotation.