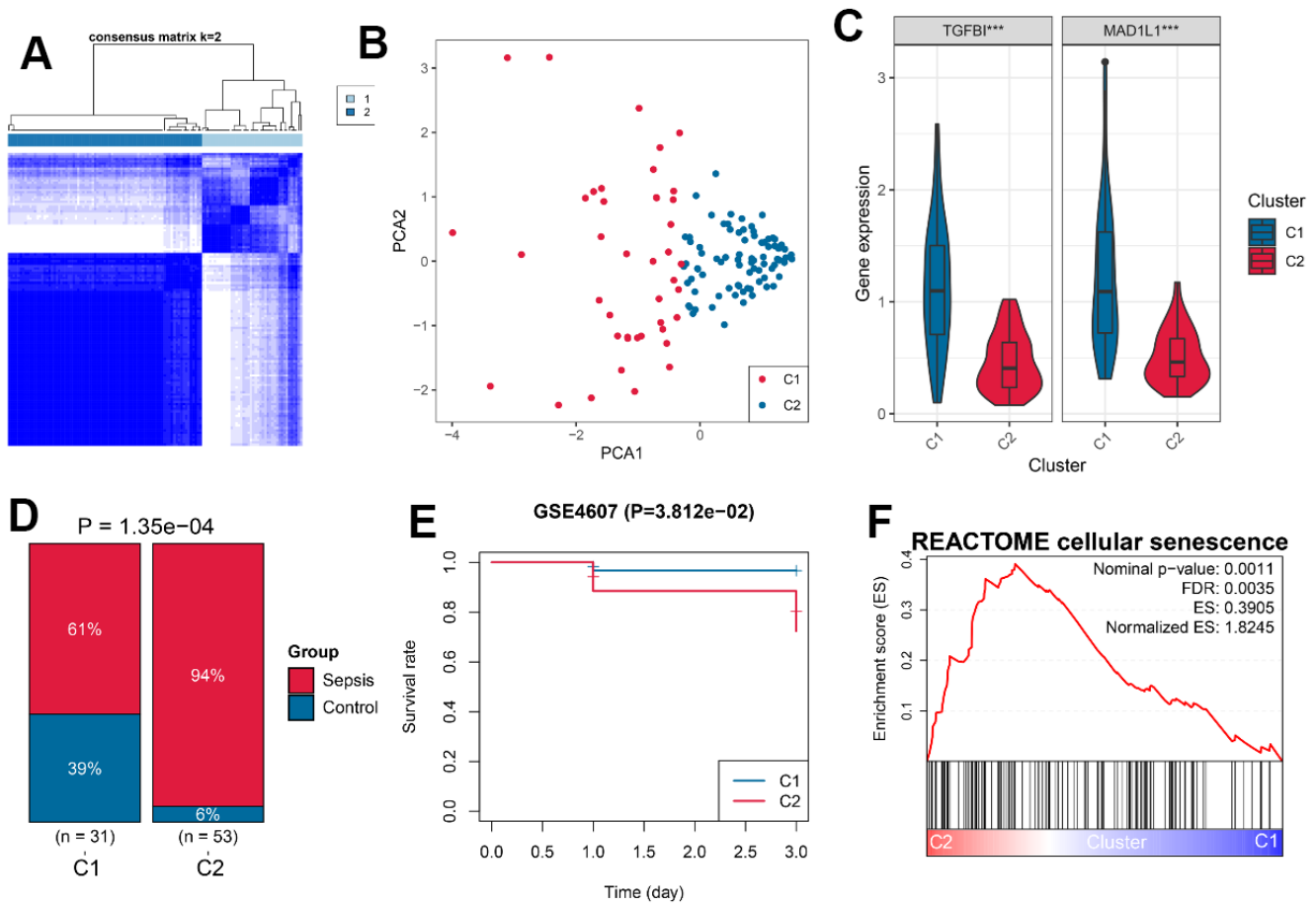
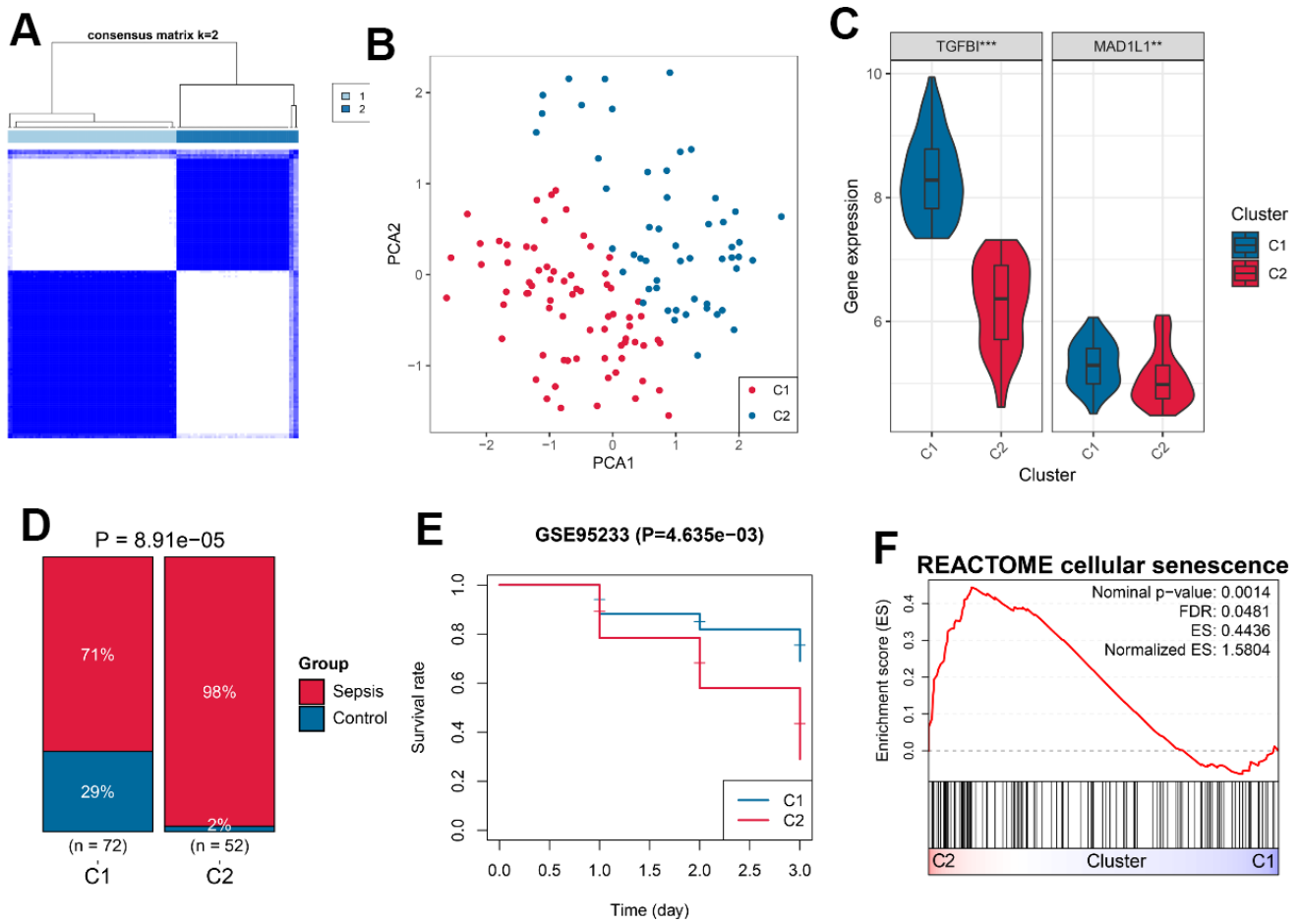


SUPPLEMENTARY FIGURES



**Supplementary Figure 1. Unsupervised clustering analysis of TGFBI and MAD1L1 gene expressions in the GSE4607 cohort.** (A) Consensus clustering was conducted to classify subjects into C1 and C2 subgroups. (B) PCA was performed to validate the clustering results. (C) The expression levels of TGFBI and MAD1L1 were significantly downregulated in the C2 subgroup. (D) The clustering analysis was associated with sepsis characteristics. (E) Sepsis patients in the C2 subgroup had unfavorable clinical outcomes. (F) The C2 subgroup exhibited higher levels of cellular senescence. Abbreviations: C1, cluster 1; C2, cluster 2; PCA, principal component analysis; \*\*\*P < 0.001.



**Supplementary Figure 2. Unsupervised clustering analysis of TGFBI and MAD1L1 gene expressions in the GSE95233 cohort.** (A) Consensus clustering was conducted to classify subjects into C1 and C2 subgroups. (B) PCA was performed to validate the clustering results. (C) The expression levels of TGFBI and MAD1L1 were significantly downregulated in the C2 subgroup. (D) The clustering analysis was associated with sepsis characteristics. (E) Sepsis patients in the C2 subgroup had unfavorable clinical outcomes. (F) The C2 subgroup exhibited higher levels of cellular senescence. \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ .