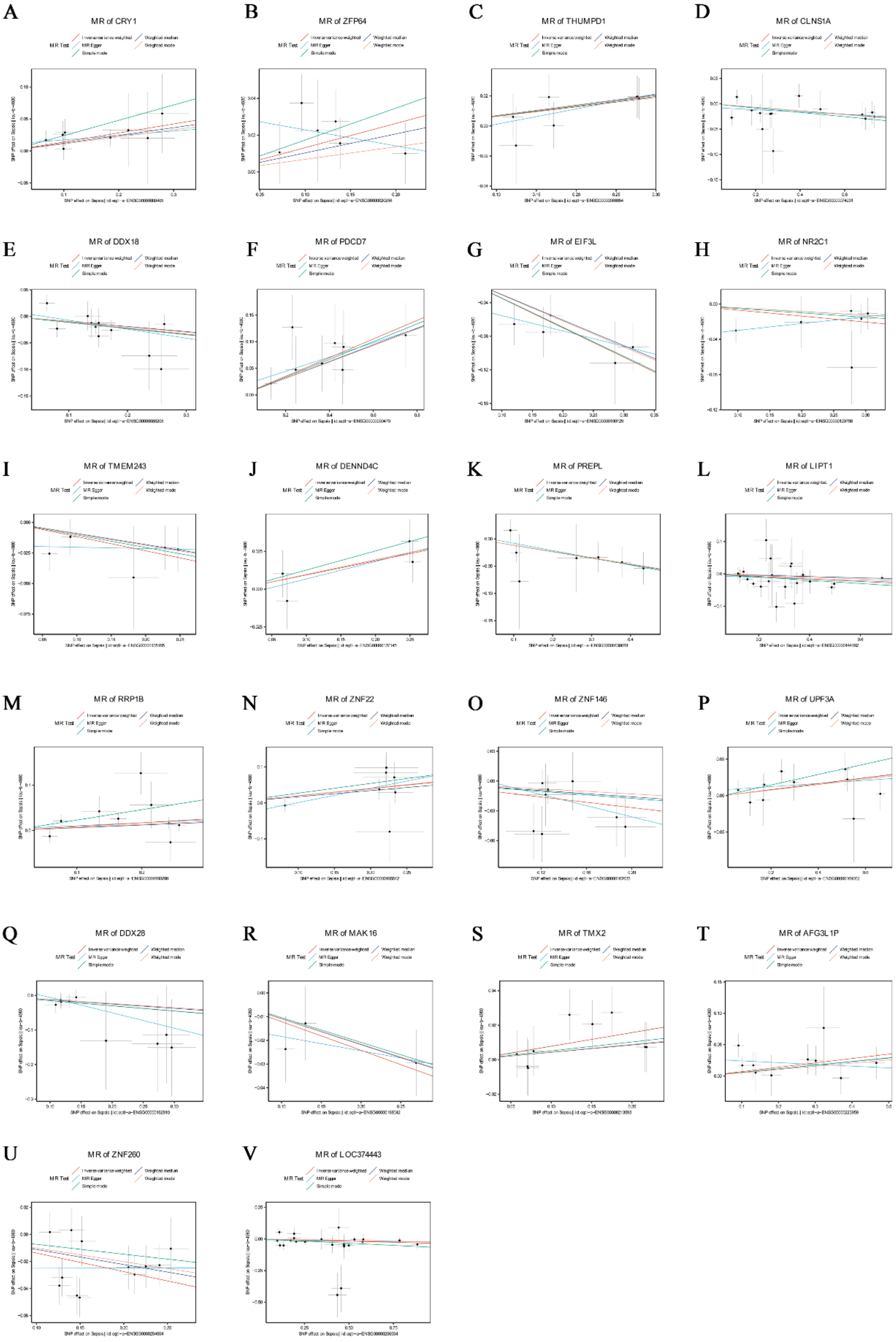
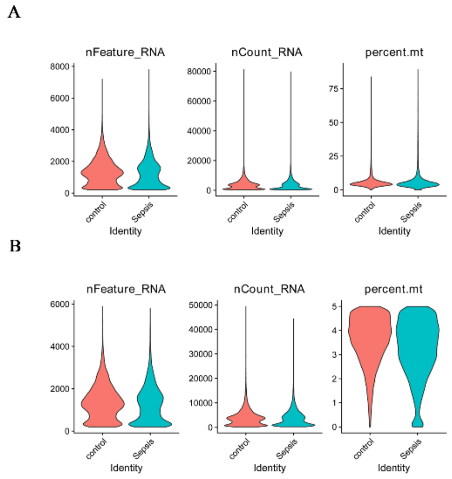
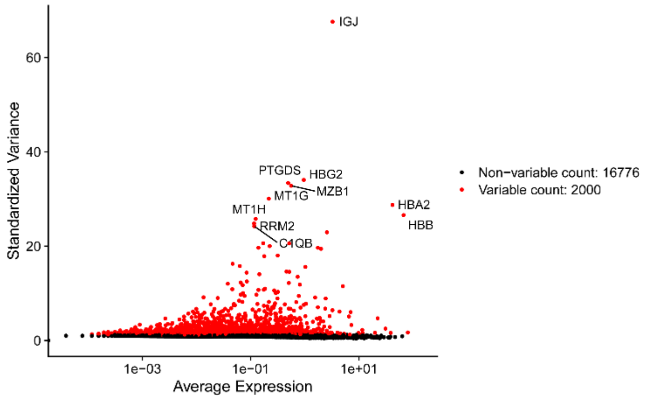

A
MR of CRY1
B
MR of ZFP64
C
MR of THUMPD1
D
MR of CLNS1A
E
MR of DDX18
F
MR of PDCD7
G
MR of EIF3L
H
MR of NR2C1
I
MR of TMEM243
J
MR of DENND4C
K
MR of PREPL
L
MR of LIPT1
M
MR of RRP1B
N
MR of ZNF22
O
MR of ZNF146
P
MR of UPF3A
Q
MR of DDX28
R
MR of MAK16
S
MR of TMX2
T
MR of AFG3L1P
U
MR of ZNF260
V
MR of LOC374443
MR Test
Inverse variance weighted
Weighted median
MR Egger
Weighted mode
Simple mode
SNP effect on Sepsis

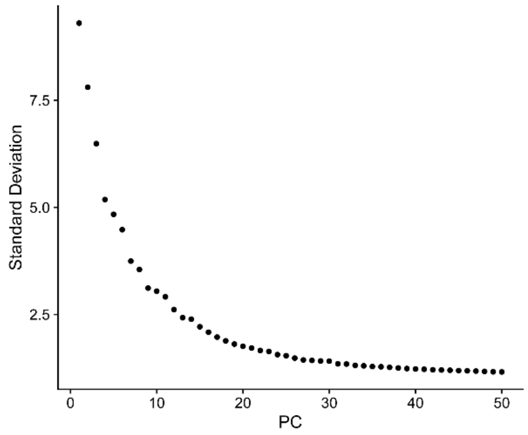
Supplementary Figure 1 Scatter plots of Mendelian randomization analyses. Scatter plots are presented to depict the Mendelian randomization analyses of 22 candidate genes and their potential causal associations with sepsis. Each panel (A–V) corresponds to a specific gene, with various Mendelian randomization methods applied, including inverse variance weighted (IVW), MR Egger, weighted median, and weighted mode. The x-axis denotes the single nucleotide polymorphism (SNP) effect on gene expression, while the y-axis represents the SNP effect on sepsis risk. Colored lines illustrate the estimated causal effect derived from each method, and error bars reflect the standard errors associated with individual SNPs.



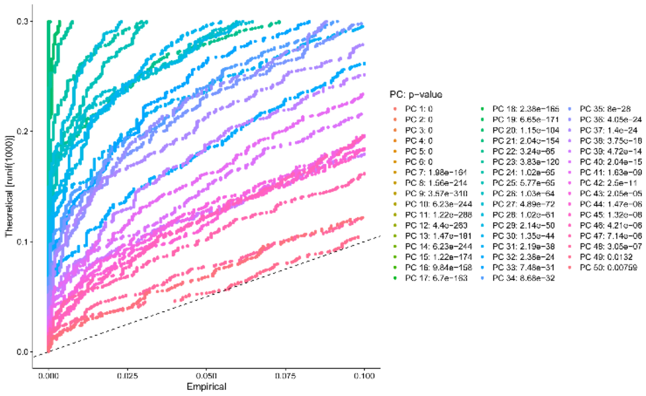
Supplementary Figure 2 Quality control of single-cell data. (**A**) Number of genes, number of cells, and percentage of mitochondria sequenced for dataset GSE175453. (**B**) Number of genes, number of cells, and percentage of mitochondria sequenced for single-cell self-test data.



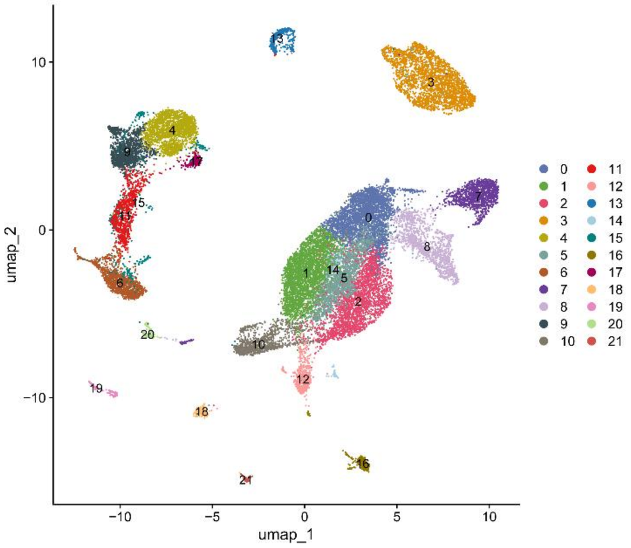
Supplementary Figure 3 2000 highly variable genes in self-assay data.



Supplementary Figure 4 Elbow plot of the PCA analysis.



Supplementary Figure 5 Empirical score and P value of each PCA component.



Supplementary Figure 6 UMAP plot colored by 22 cell clusters.