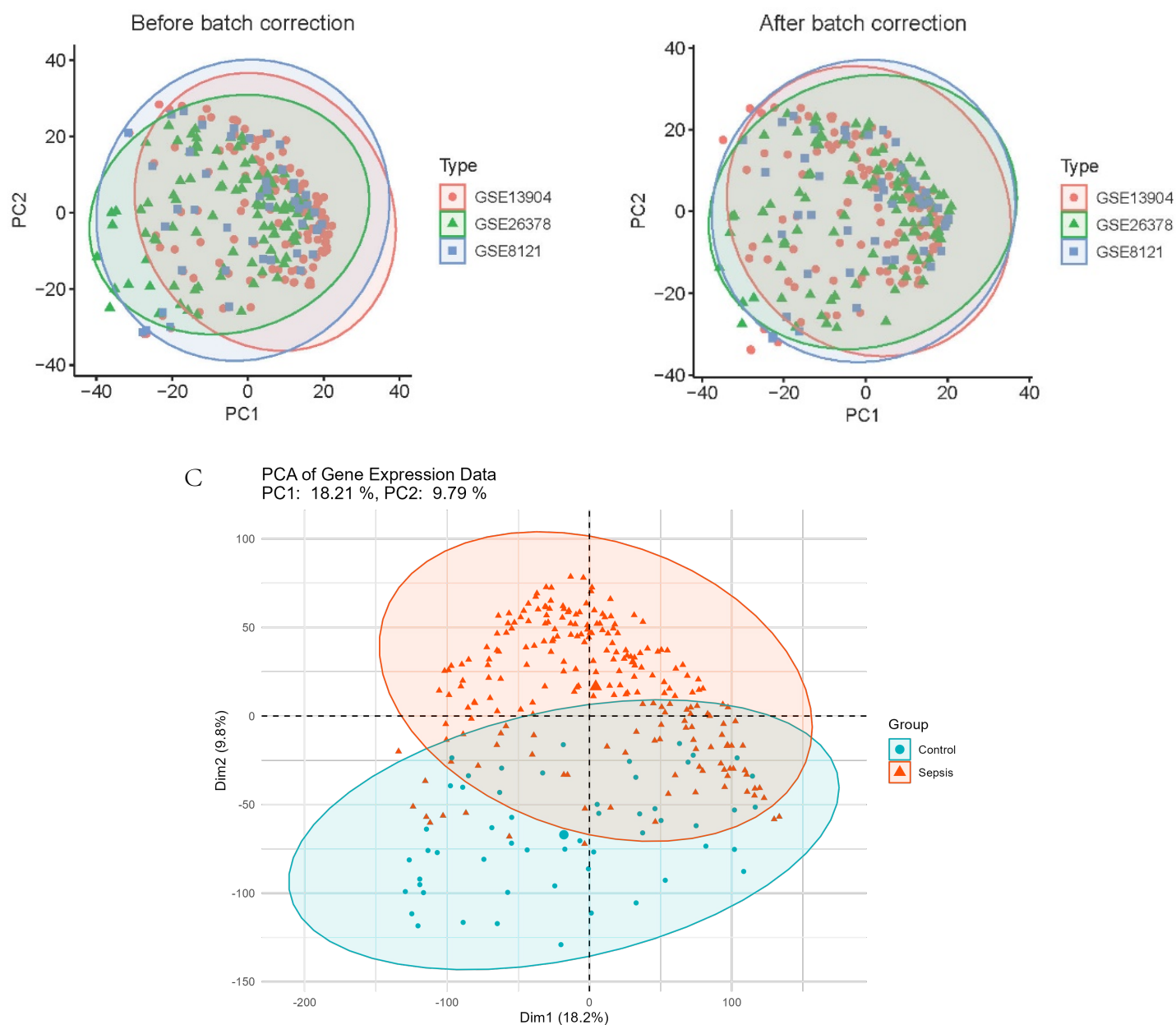


A

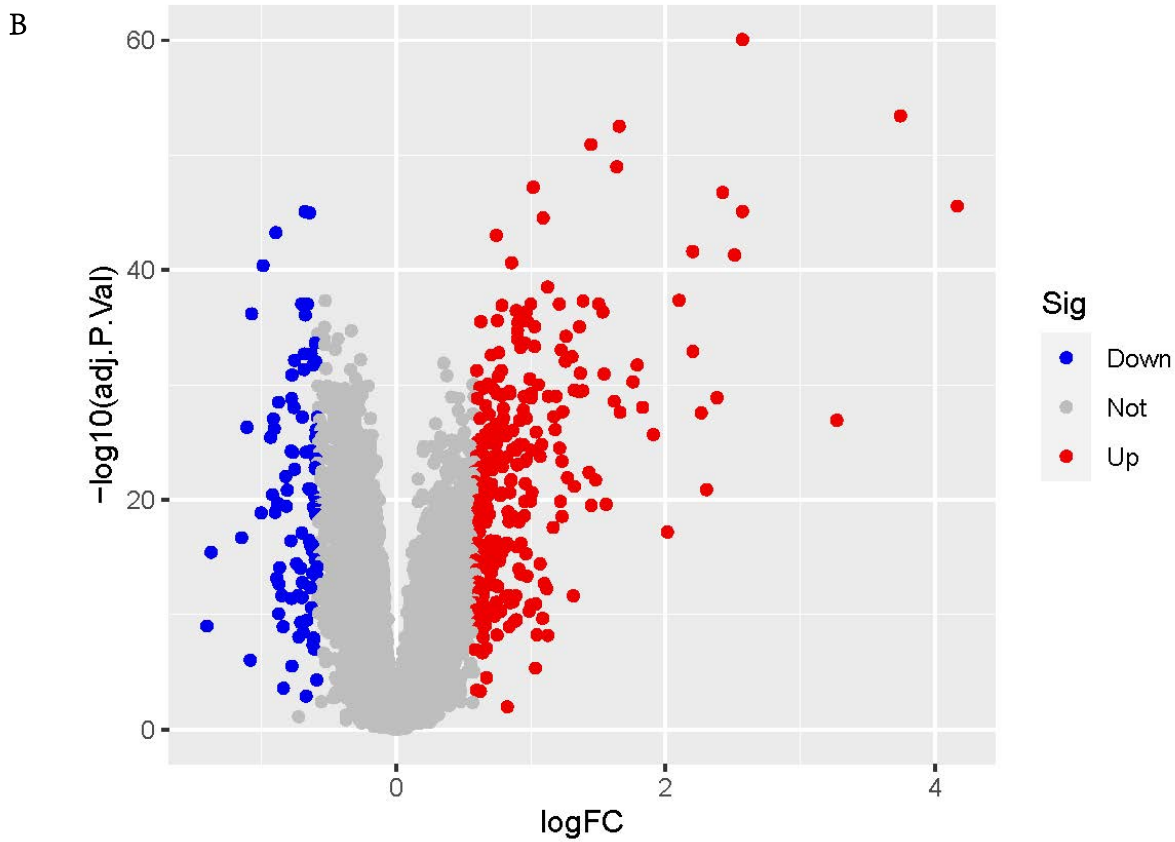
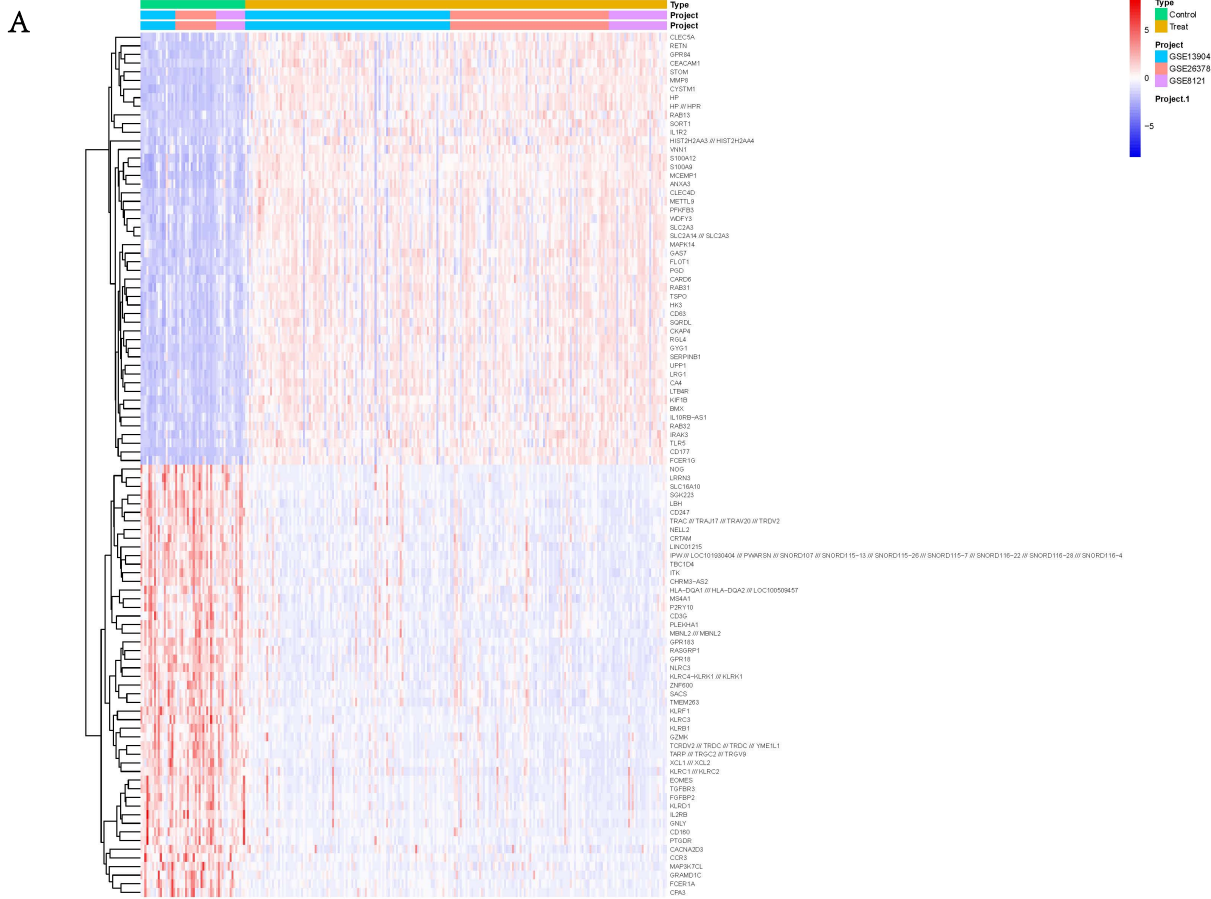
B

Supplementary Figure S1: The Principal Component Analysis and Batch Correction.



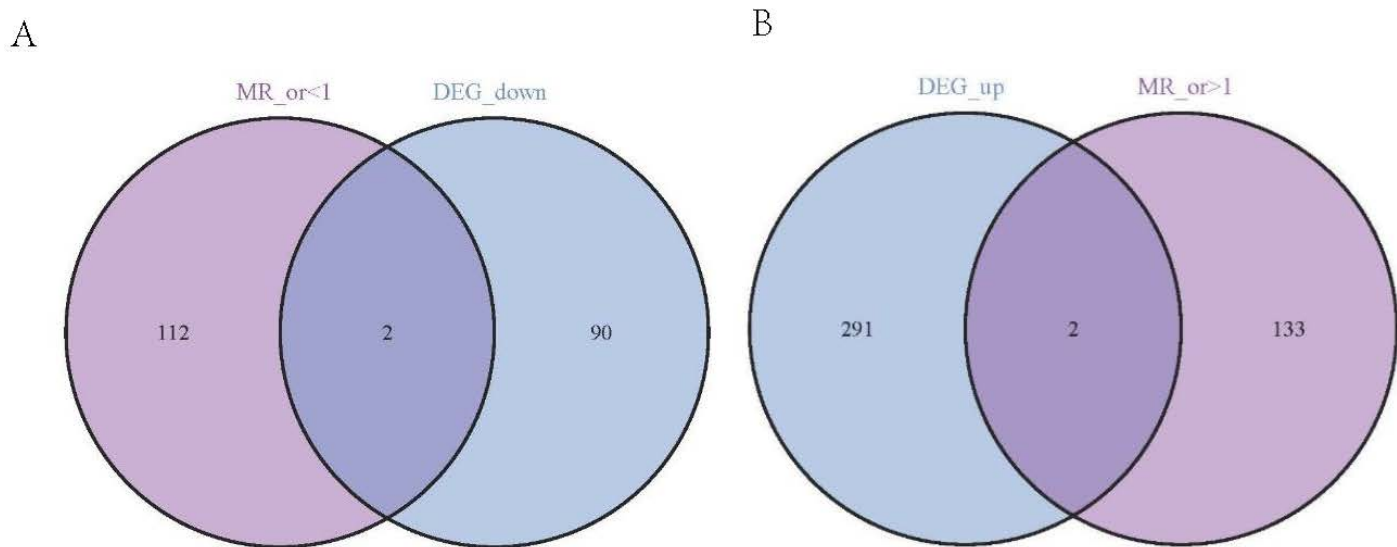
Supplementary Figure S1. The Principal Component Analysis and Batch Correction. **(A,B,C)** A total of 272 samples from the three data sets were included in the study, including 218 sepsis cases and 54 control cases. **(A)** before batch correction. **(B)** after batch correction. **(C)** Principal Component Analysis (PCA) of total samples between pediatric sepsis and control groups after batch correction.

Supplementary Figure S2: Differential Expression Analysis.



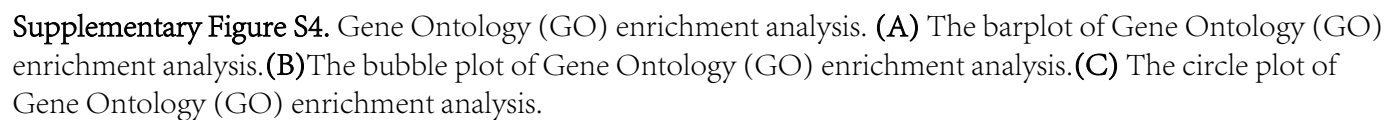
Supplementary Figure S2. Differential Expression Analysis. **(A)**The heatmap of Differential Expression Analysis . **(B)**The The volcano plot of Differential Expression Analysis

Supplementary Figure S3: The Venn diagrams of intersection genes.

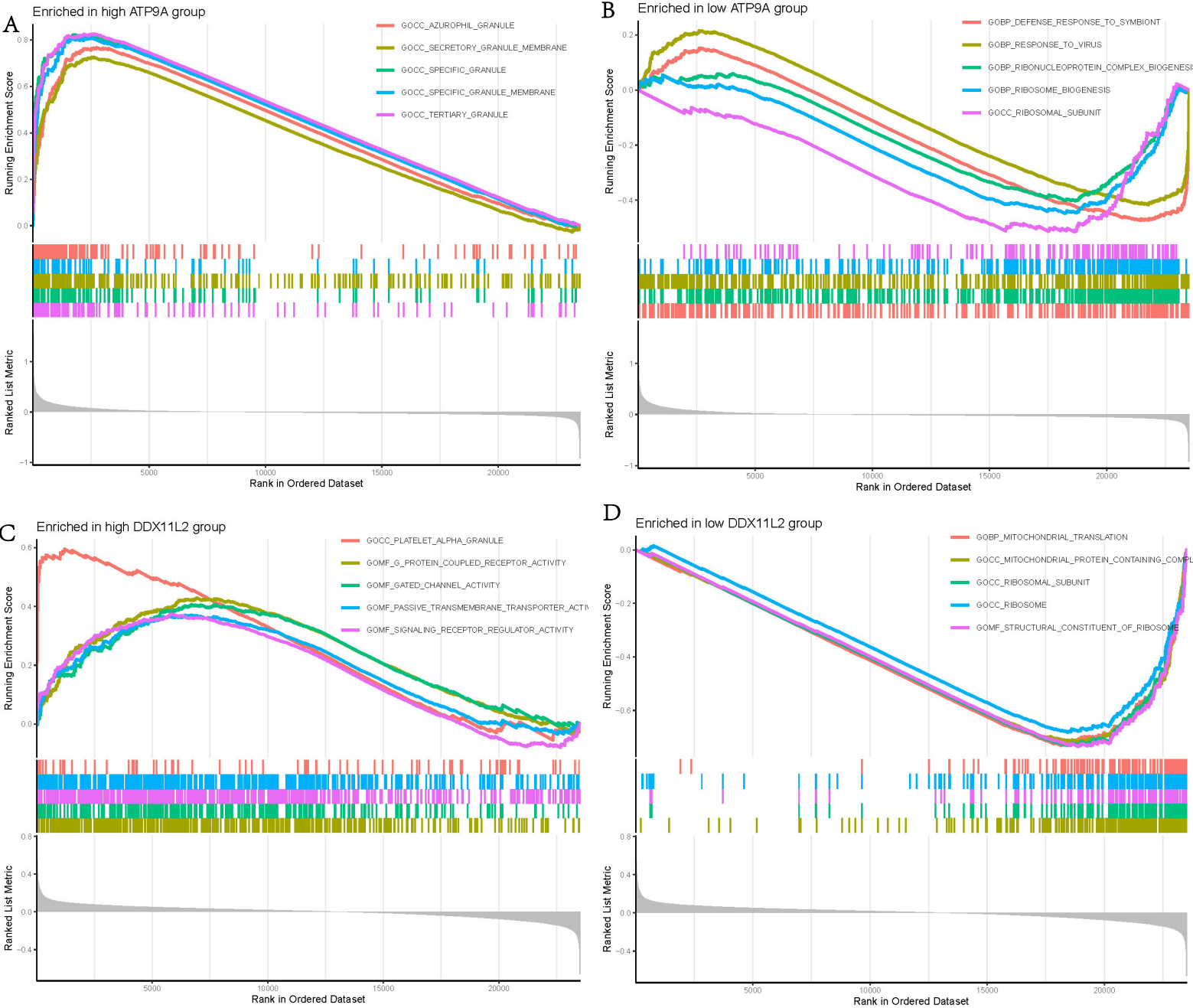


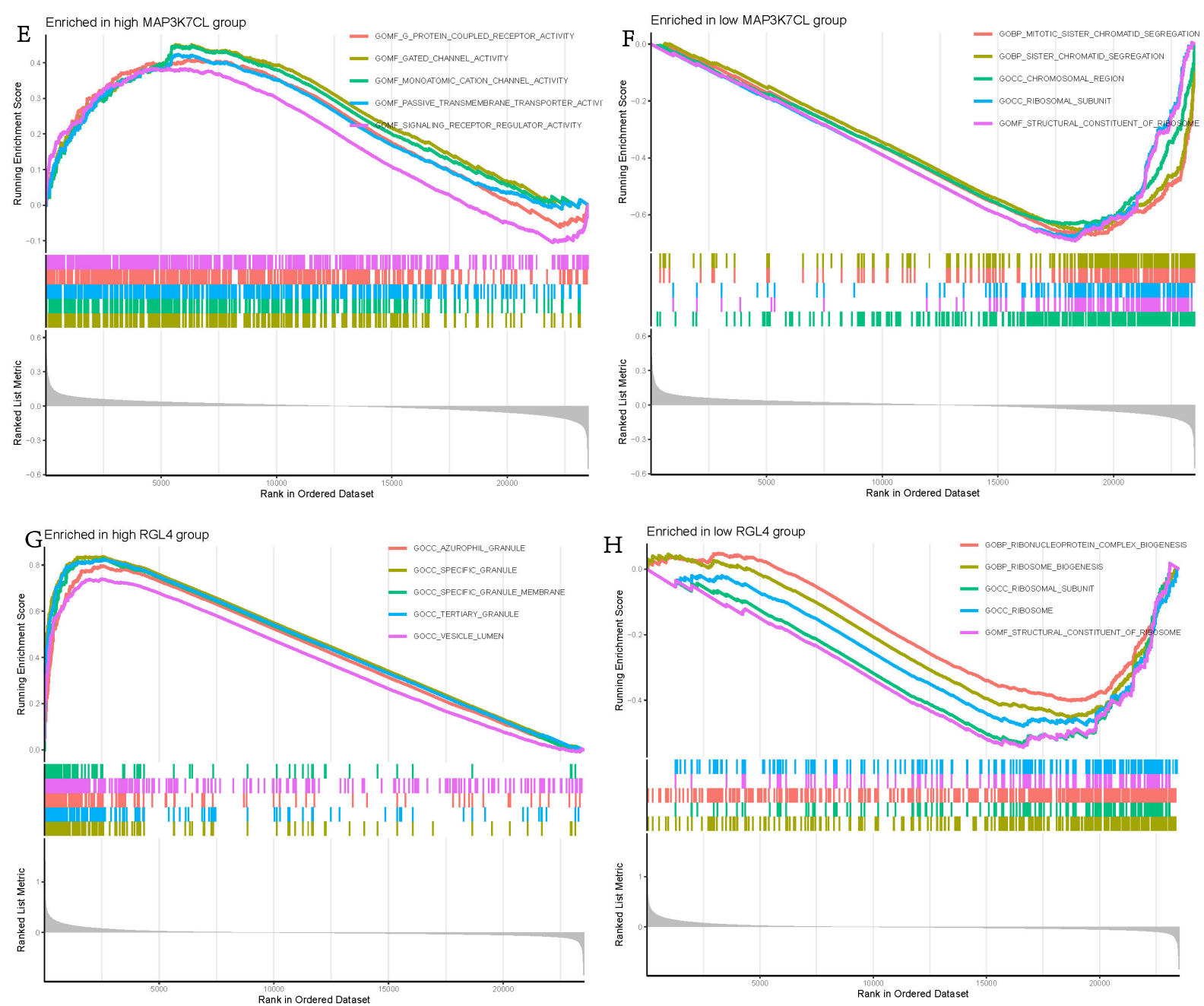
Supplementary Figure S3. The Venn diagrams of intersection genes. (A) depicts an overlap between PBMCs-expressed genes suppressed in sepsis and that associated with low-risk for pediatric sepsis. (B) depicts an intersection between PBMCs-expressed genes upregulated in sepsis and that associated with high-risk for pediatric sepsis

A



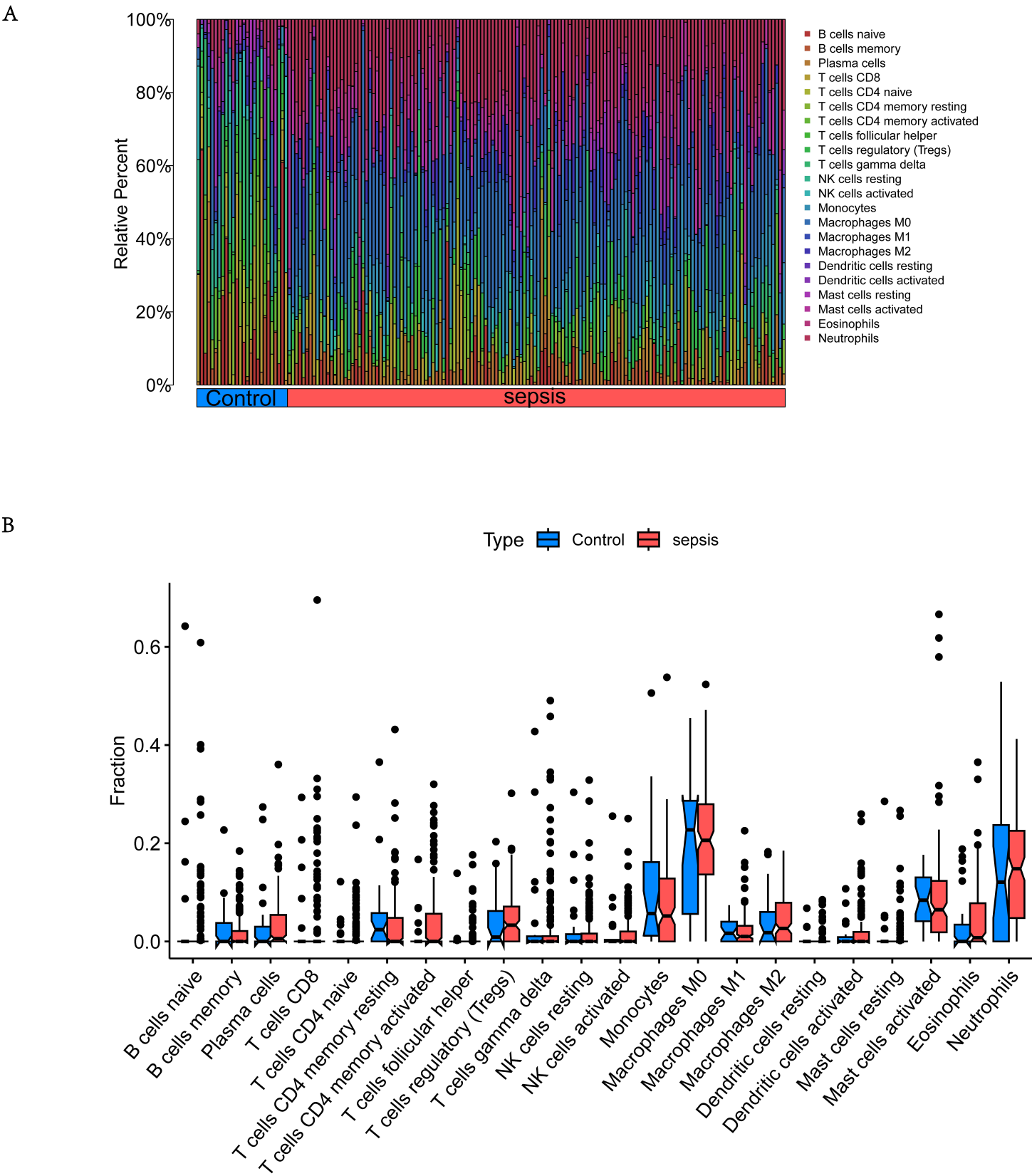
Supplementary Figure S5. Gene Set Enrichment Analysis (GSEA)



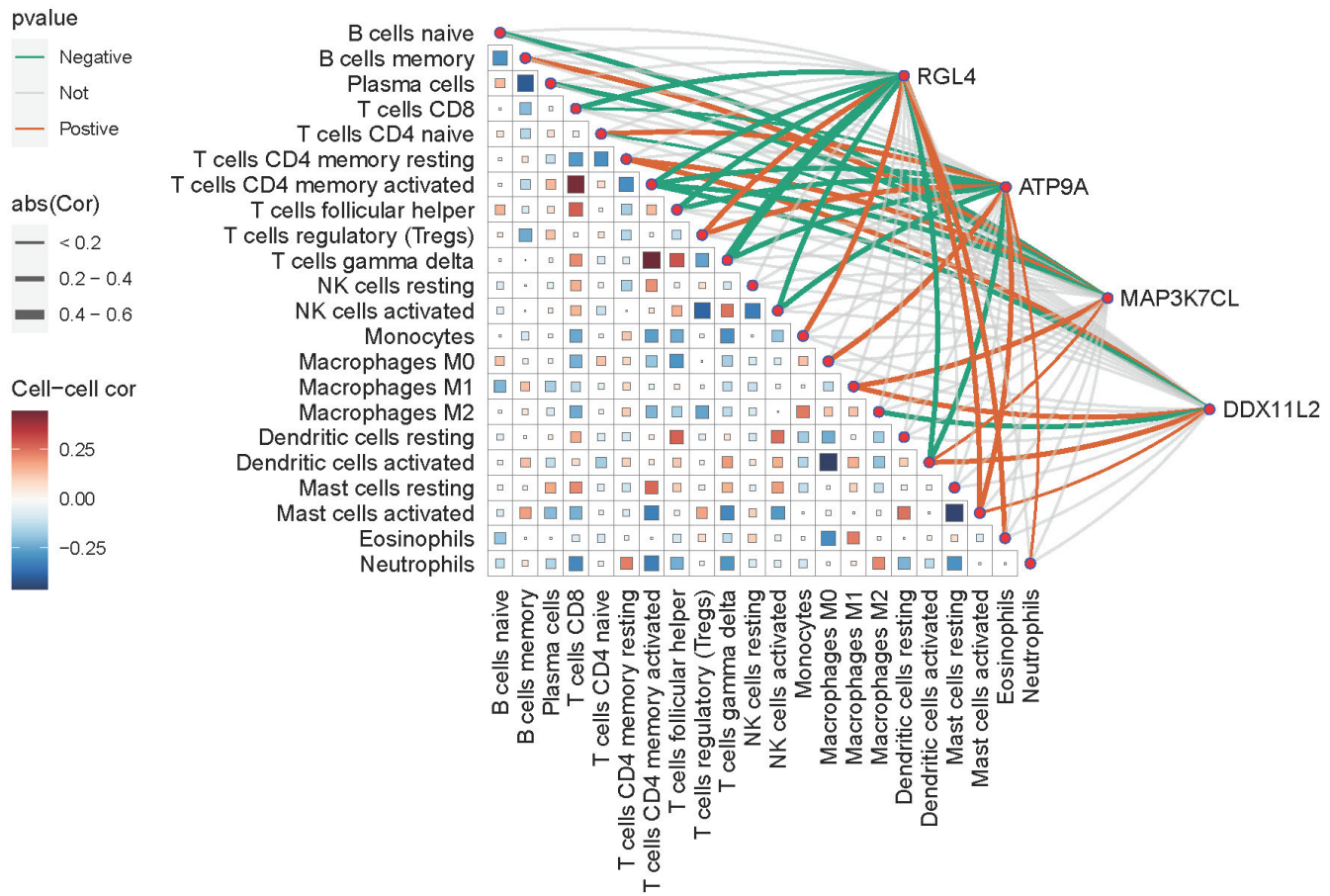


Supplementary Figure S5. Gene Set Enrichment Analysis (GSEA). (A) GO pathways showed that “tertiary granule”, “specific granule” and “specific granule membrane” were significantly enriched in the high *ATP9A* group. (B) GO pathways showed that “ribosomal subunit”, “ribosome biogenesis” and “defense response to symbiont” were significantly enriched in the low *ATP9A* group. (C) GO pathways showed that “platelet alpha granule”, “g protein coupled receptor activity” and “gated channel activity” were significantly enriched in the high *DDX11L2* group. (D) GO pathways showed that “structural constituent of ribosome”, “ribosomal subunit”, “mitochondrial translation” and “mitochondrial protein containing complex” were significantly enriched in the low *DDX11L2* group. (E) GO pathways showed that “gated channel activity”, “monoatomic cation channel activity” and “passive transmembrane transporter activity” were significantly enriched in the high *MAP3K7CL* group. (F) GO pathways showed that “structural constituent of ribosome”, “ribosomal subunit” and “mitotic sister chromatid segregation” were significantly enriched in the low *MAP3K7CL* group. (G) GO pathways showed that “specific granule”, “tertiary granule” and “specific granule membrane” were significantly enriched in the high *RGL4* group. (H) GO pathways showed that “structural constituent of ribosome”, “ribosomal subunit” and “ribosome” were significantly enriched in the low *RGL4* group.

Supplementary Figure S6. Immune Cell Infiltration Analysis .

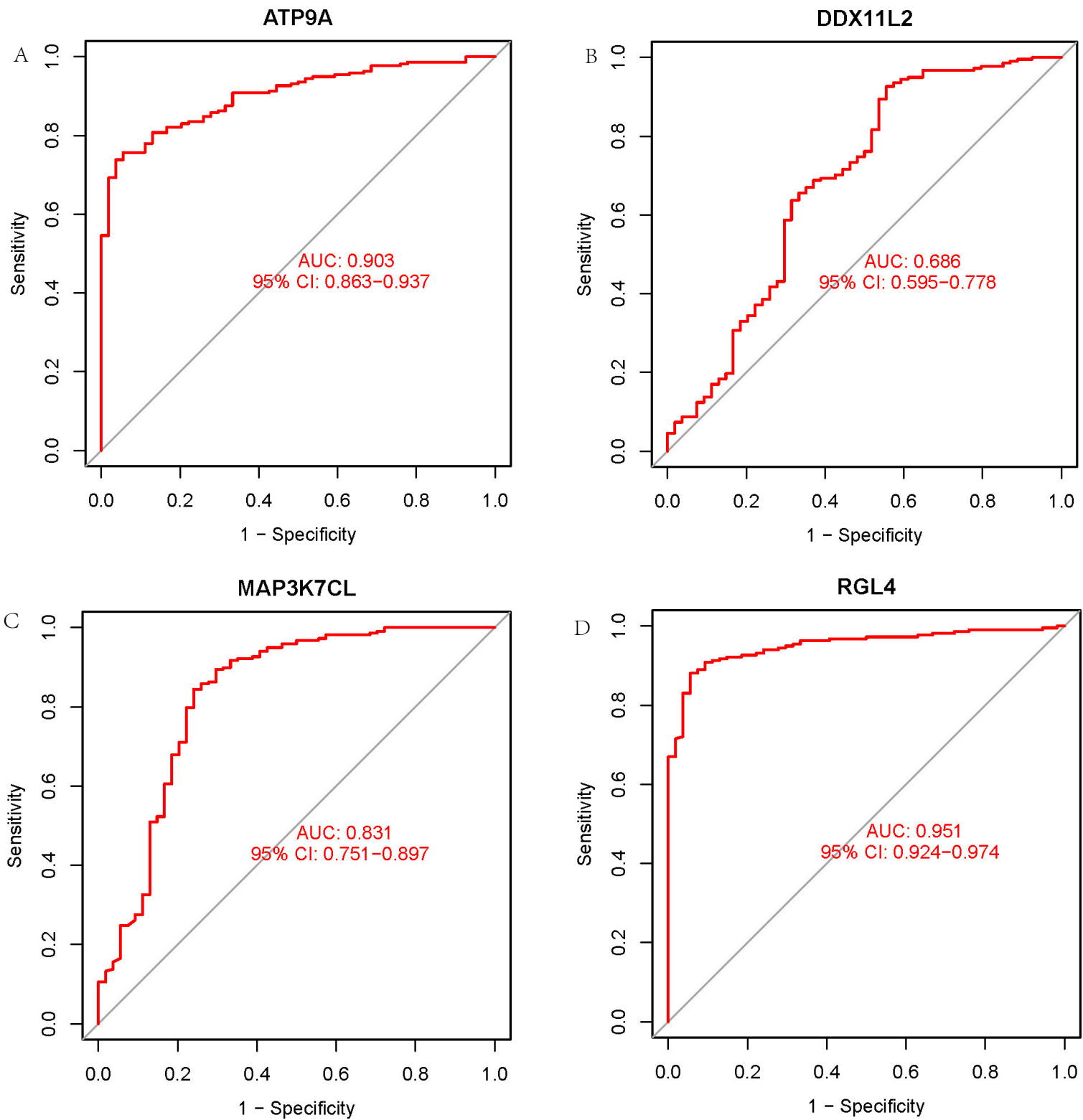


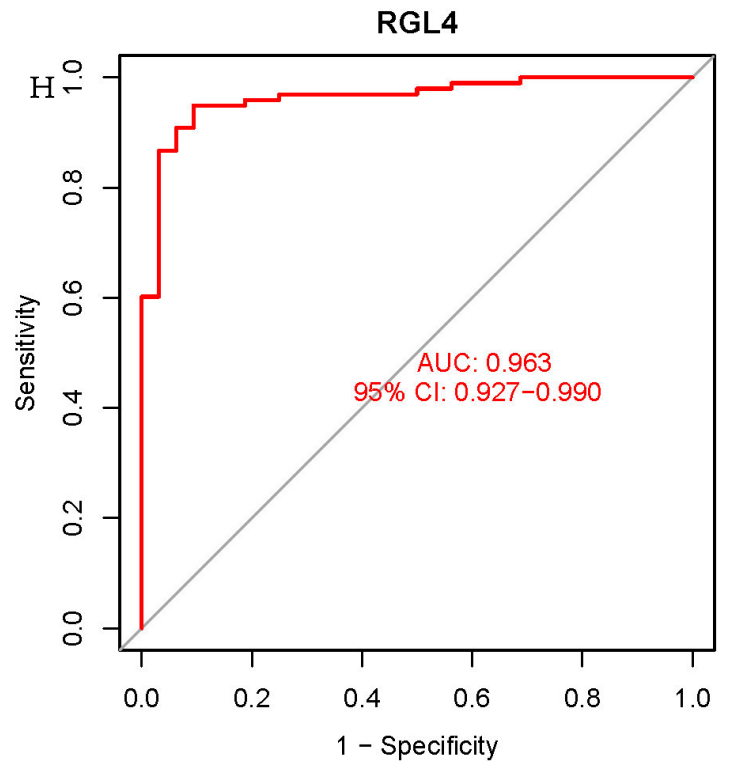
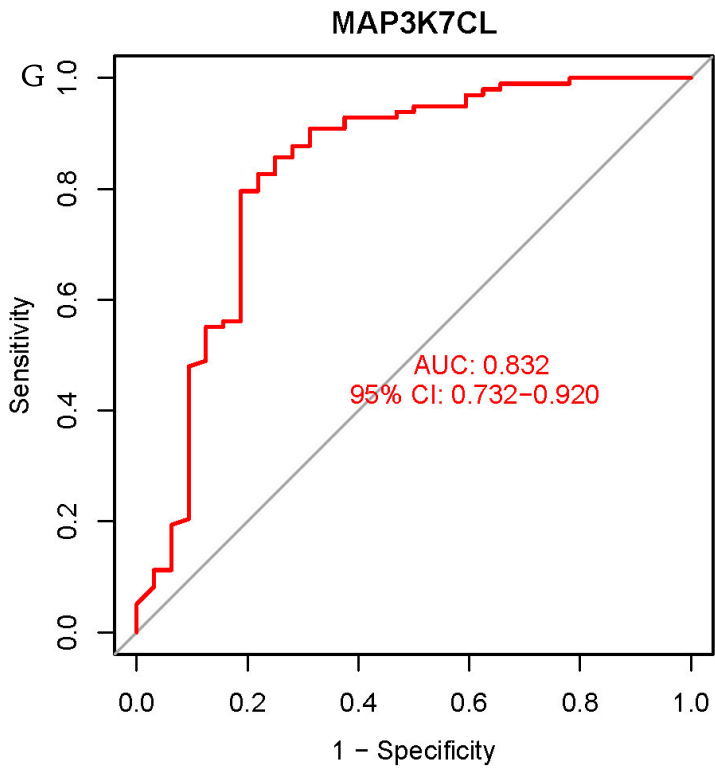
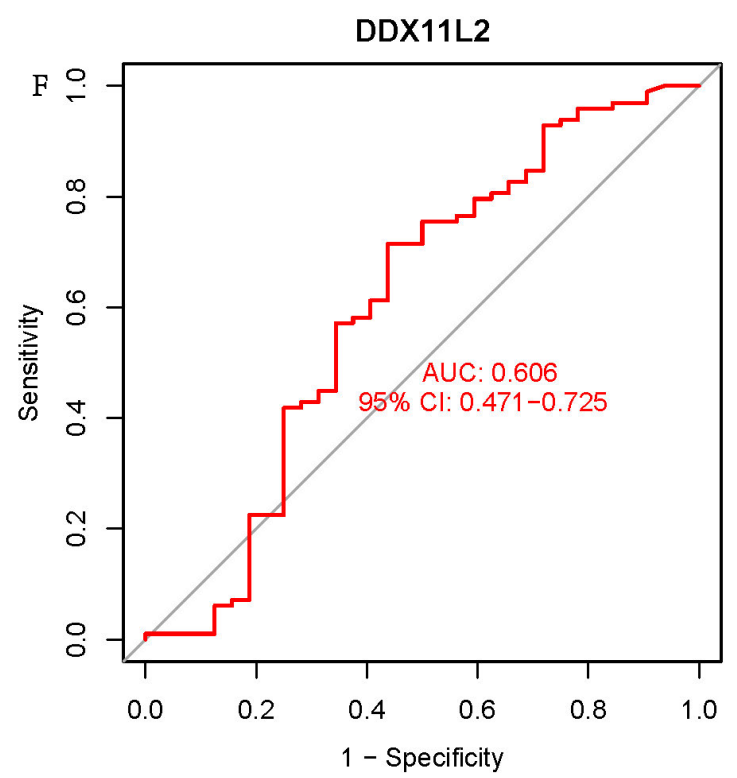
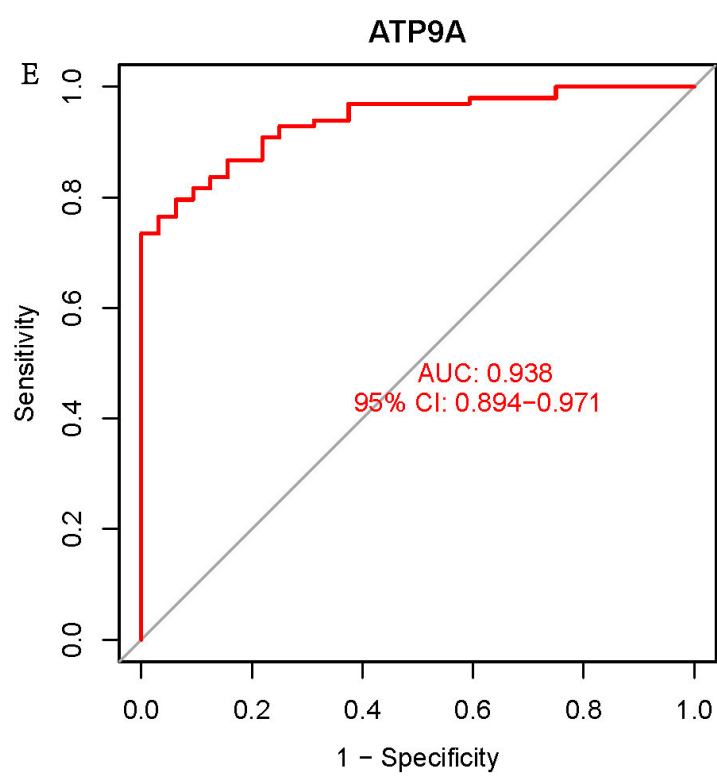
C



Supplementary Figure S6. Immune Cell Infiltration Analysis . Immune Cell Infiltration Analysis . **(A)** The bar plot of the distribution of 22 immune cells in each sample of the GEO cohort. **(B)** The bar plot of the differential expression of 22 immune cells in each sample of the GEO cohort. **(C)** Analysis of correlation between genes and immune cells

Supplementary Figure S7. ROC curves for intersection genes and the verifying ROC curves

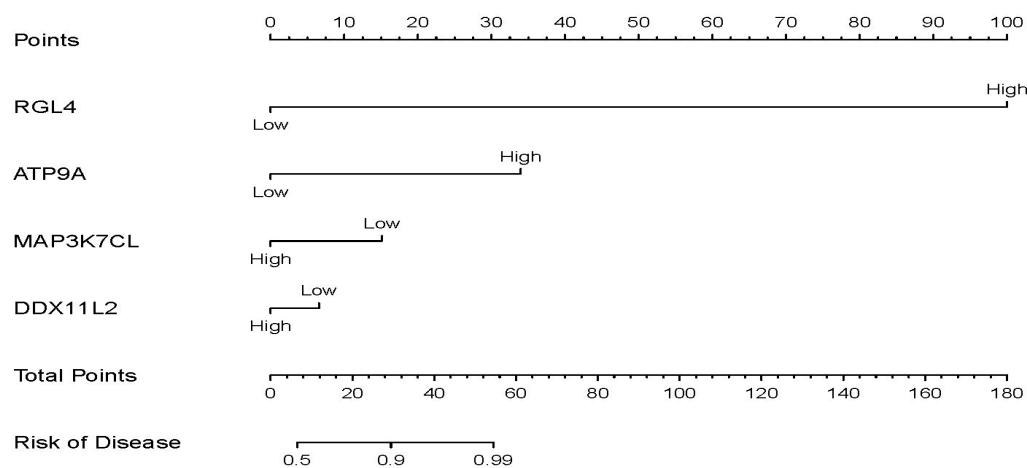




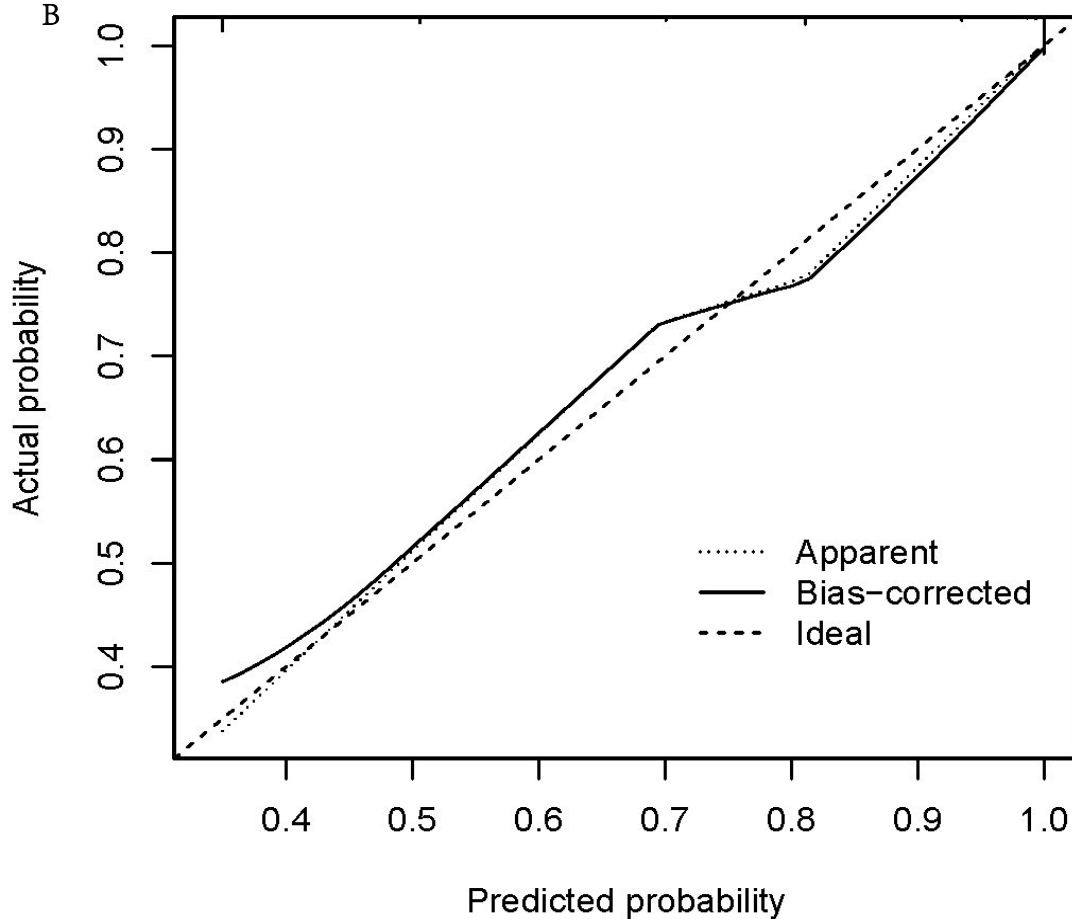
Supplementary Figure S7. ROC curves for intersection genes and the verifying ROC curves . **(A)** ROC curve for gene *ATP9A* prediction. **(B)** ROC curve for gene *DDX11L2* prediction. **(C)** ROC curve for gene *MAP3K7CL* prediction. **(D)** ROC curve for gene *RGL4* prediction. **(E)** verifying ROC curve for gene *ATP9A* prediction. **(F)** verifying ROC curve for gene *DDX11L2* prediction. **(G)** verifying ROC curve for gene *MAP3K7CL* prediction. **(H)** verifying ROC curve for gene *RGL4* prediction.

Supplementary Figure S8. Nomogram and Calibration analysis.

A

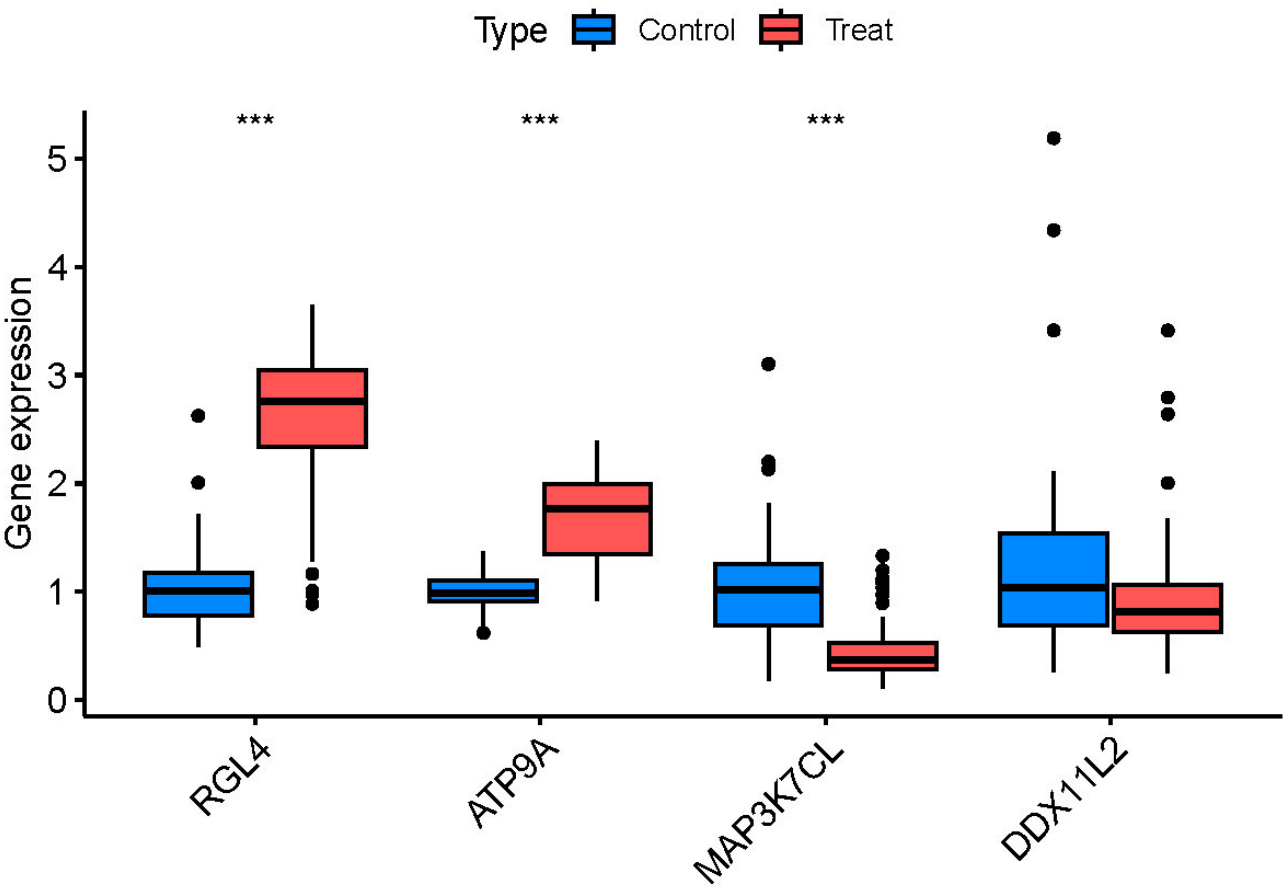


B



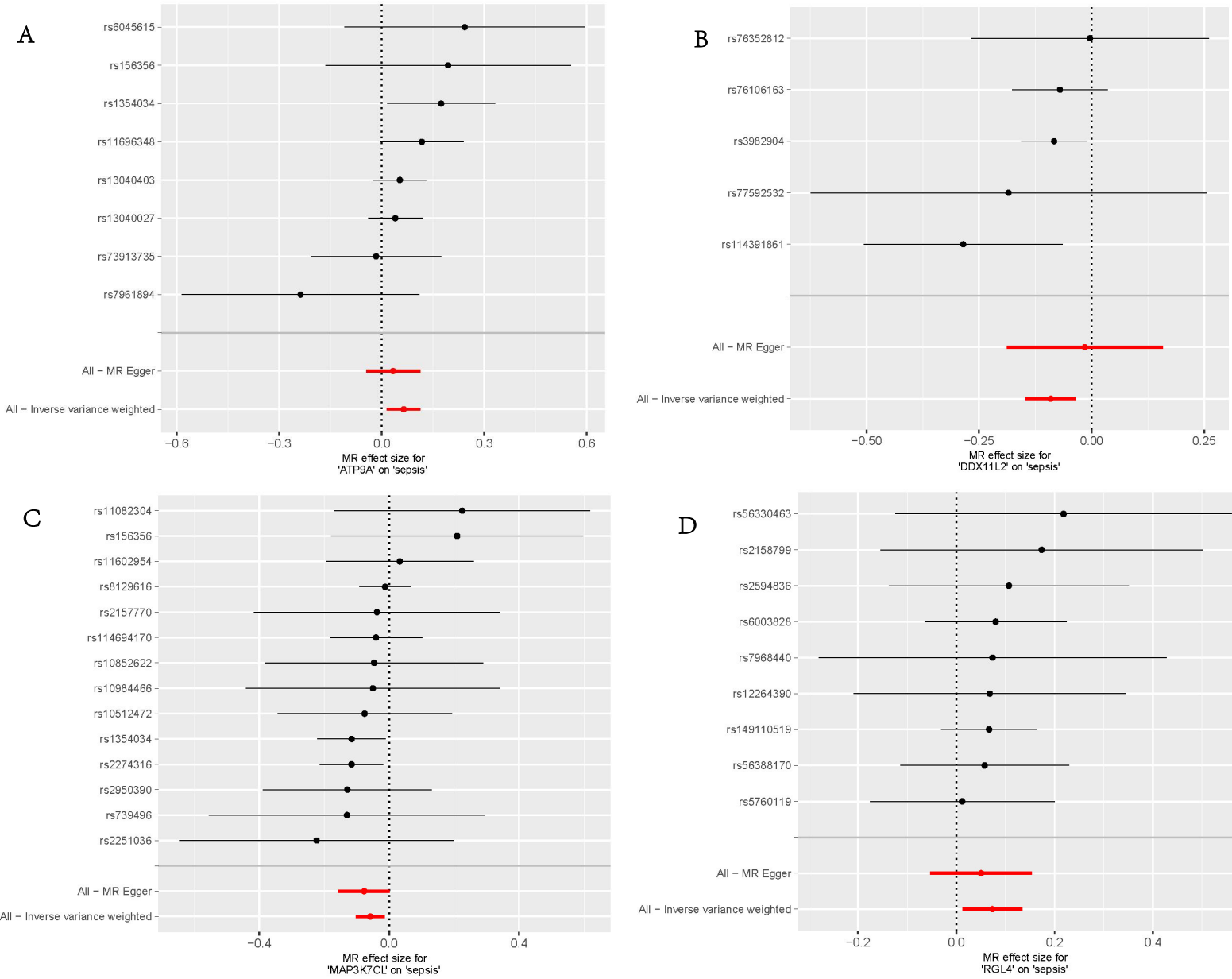
Supplementary Figure S8. Nomogram and Calibration analysis. (A) The nomogram for predicting the pediatric sepsis patients. (B) The calibration curve of the nomogram prediction accuracy

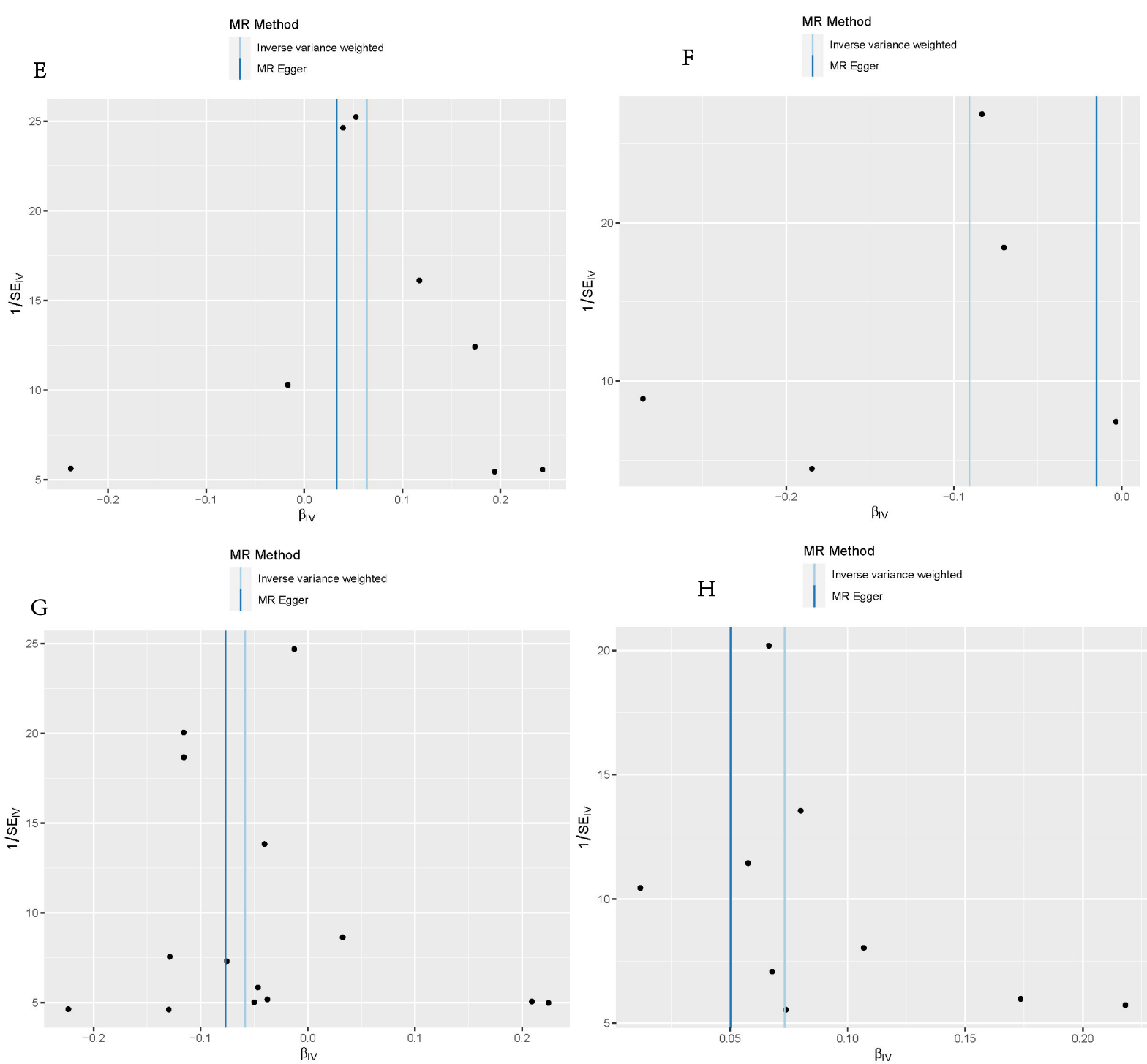
Supplementary Figure S9. Validation of the intersection genes



Supplementary Figure S9. Validation of the intersection genes

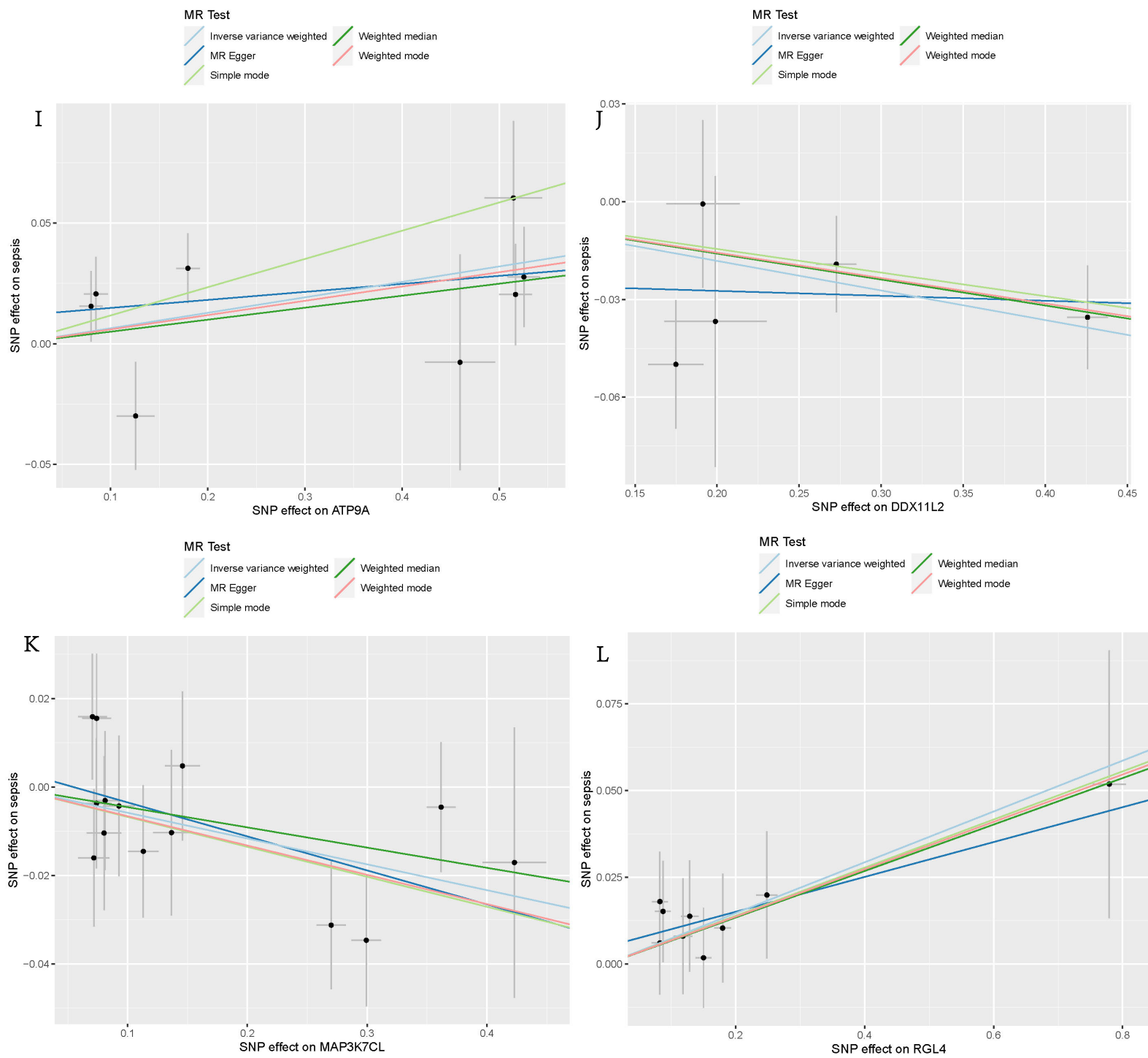
Supplementary Figure S10. forest and funnel plots for the causal association between intersection genes and sepsis.

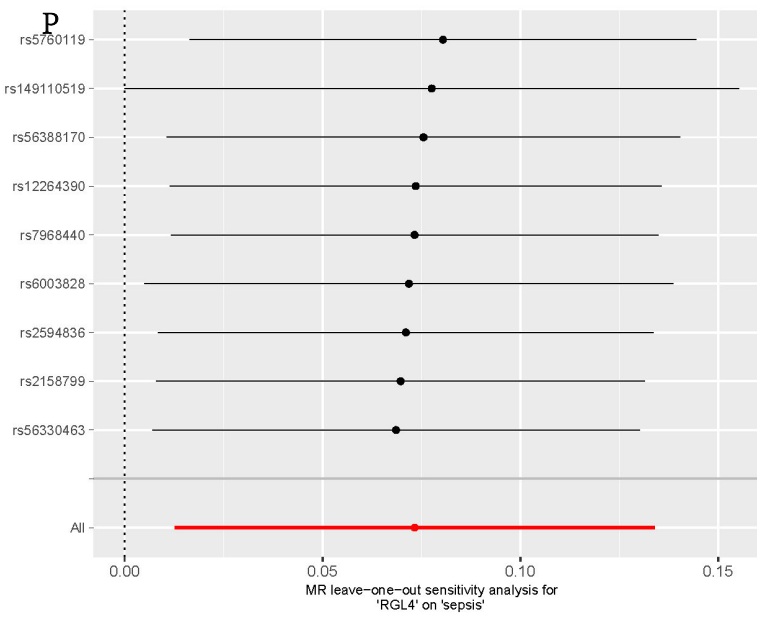
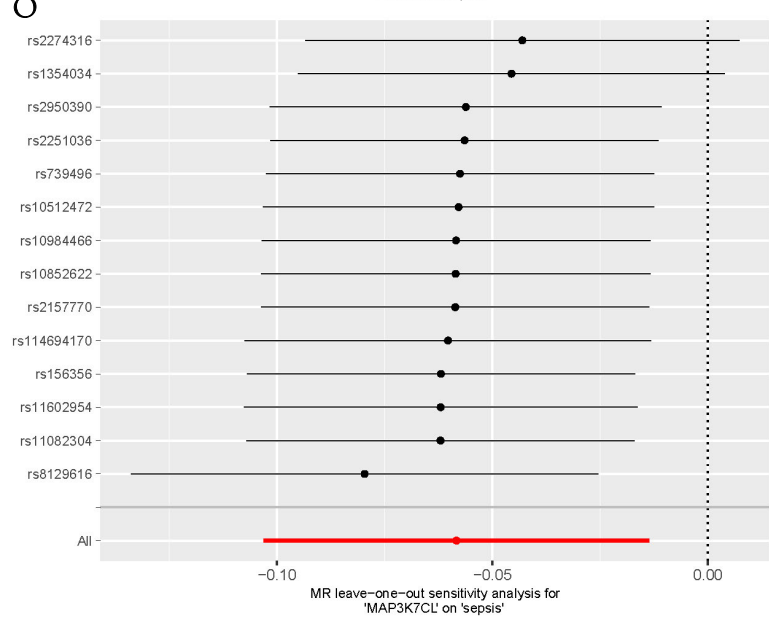
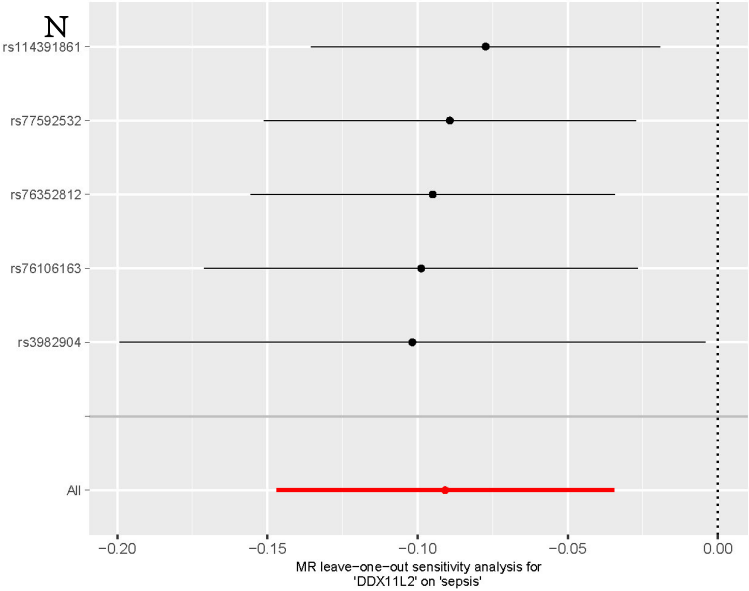
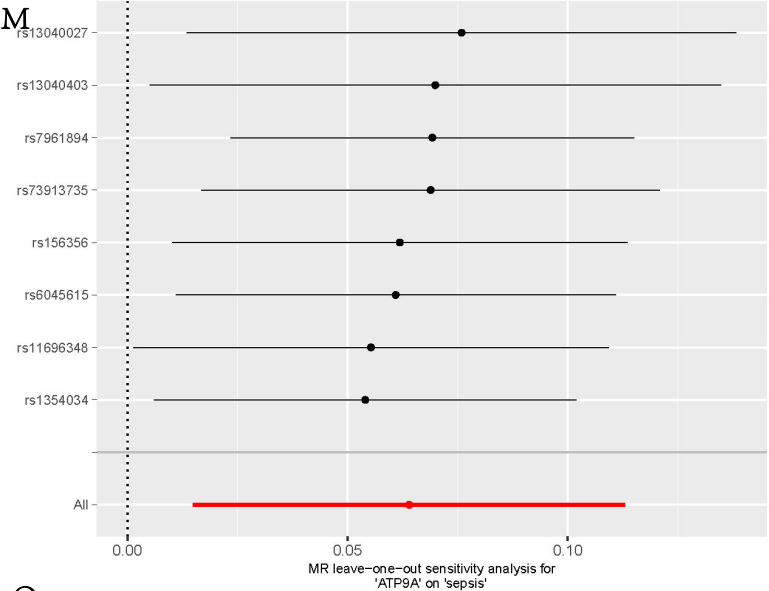




Supplementary Figure S10. forest and funnel plots for the causal association between intersection genes and sepsis. (A-D) The forest plots for the causal association between intersection genes and sepsis. (E-H) The funnel plots for the causal association between intersection genes and sepsis.

Supplementary Figure S11. Scatter and Leave-one-out plots for the causal association between intersection genes and sepsis





Supplementary Figure S11. Scatter and Leave-one-out plots for the causal association between intersection genes and sepsis. **(I-L)** The Scatter plots for the causal association between intersection genes and sepsis. **(M-P)** The Leave-one-out plots