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Original Article

Bioinformatics analysis identifies IL-23A and JAK2 as regulatory factors in sepsis immune response via the JAK/STAT3 pathway

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Abstract

Introduction: Sepsis is a life-threatening organ dysfunction caused by dysregulated host responses to infection. Identifying key genes associated with sepsis and exploring their interactions with immune cells are crucial for advancing diagnostic and therapeutic strategies. Methodology: In order to explore the genetic underpinnings, five datasets—GSE28750, GSE57065, GSE64457, GSE65682, and GSE95233—were analyzed using the "Limma" package in R to identify differentially expressed genes (DEGs). Functional enrichment analysis was conducted using Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG). Protein-protein interaction (PPI) networks and key modules were analyzed using STRING and Cytoscape. The core genes were selected using the least absolute shrinkage and selection operator (LASSO) regression, and their diagnostic value was validated through receiver operating characteristic (ROC) curve analysis. Immune cell infiltration was assessed using the CIBERSORT algorithm.

Results: A total of 230 DEGs were identified, including 183 upregulated and 47 downregulated genes. GO and KEGG analysis revealed significant enrichment in immune-related pathways. Two core genes, *IL-23A* and *JAK2*, emerged as key players. ROC curve analysis demonstrated high diagnostic value with area under the curve (AUC) values of 0.82 and 0.90 for *IL-23A* and *JAK2*, respectively. *IL-23A* showed a strong positive correlation with CD8+ T cells and activated natural killer (NK) cells, while also activating the *JAK/STAT3* signaling pathway and mitigating *JAK2*-mediated immune cell infiltration.

Conclusions: This study highlights the potential role of *IL-23A* and *JAK2* in the immune regulation of sepsis and provides new insights into immune therapeutic strategies via the *JAK/STAT3* signaling pathway.

Key words: sepsis; *IL-23A*; *JAK*; immune; therapeutic.

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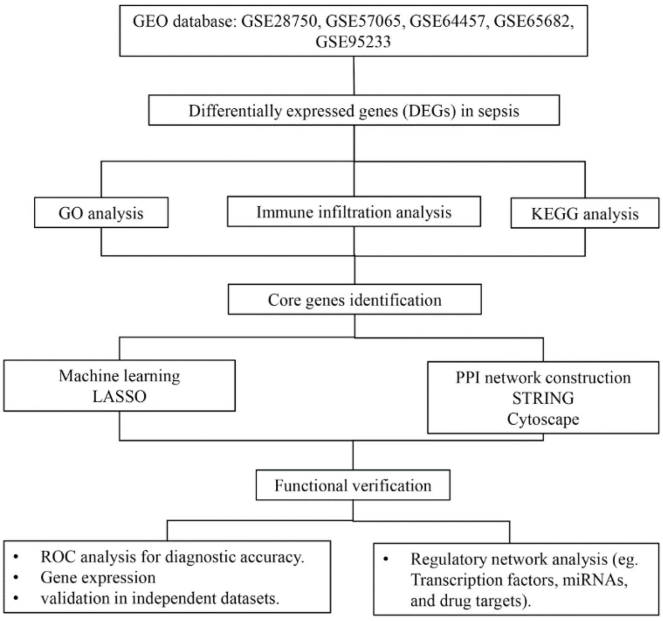
Introduction

Sepsis is a life-threatening organ dysfunction caused by the dysregulation of host response to infection. It is responsible for an estimated 6 million deaths annually, and is the leading cause of mortality in intensive care units (ICUs) worldwide [1–3]. Despite substantial progress in research [4], its pathogenesis remains highly complex. The increasing incidence and mortality rates of sepsis highlight the urgent need for improved diagnostic and therapeutic strategies [5,6]. Reasonable distinction between patients with early sepsis and non-infectious critically ill patients is essential to improve the clinical outcomes of patients with sepsis. While blood culture remains the gold standard for diagnosis, its lengthy processing time and limited sensitivity hinder timely clinical decision-making, underscoring the need for novel biomarkers to support early diagnosis and effective management [7]. At present, non-specific acute phase reactive proteins such as procalcitonin (PCT), C-reactive protein (CRP), and inflammatory cytokine interleukin-6 (IL-6) play a certain role in the early diagnosis of sepsis [8]. However, there is currently insufficient evidence to support PCT, CRP, and IL-6 as biomarkers for initiating antimicrobial therapy in sepsis [9]. Non-invasive, blood-based biomarkers with strong diagnostic potential are essential for enabling personalized treatment strategies, enabling clinicians to design therapies based on individual molecular profiles. Recent advancements in high-throughput sequencing technologies and bioinformatics have provided valuable tools to investigate the genomic alterations associated with sepsis, shedding light on its complex molecular mechanisms [10–12]. Publicly accessible databases, such as the Gene Expression Omnibus (GEO), provide extensive resources for transcriptomic data, facilitating the identification of comprehensive genomic changes and potential therapeutic targets [13,14]. Bioinformatics tools are instrumental in systematically analyzing these datasets, revealing key

molecular pathways, and supporting the development of immunotherapies and precision medicine approaches [15].

Recent studies have identified specific genes involved in the pathogenesis and progression of sepsis [16,17], yet their diagnostic utility remains largely underexplored. Furthermore, the interactions between these genes and immune cells in sepsis patients are not well understood. To address these gaps, data from 5 GEO datasets: GSE28750, GSE57065, GSE64457, GSE65682, and GSE95233, were integrated and analyzed. Bioinformatics methods were used to identify differentially expressed genes (DEGs), construct protein-protein interaction (PPI) networks, and conduct functional enrichment analyses. Machine learning approaches were applied, including least absolute shrinkage and selection operator (LASSO) regression and support vector machine-recursive feature elimination (SVM-RFE) to pinpoint key genes. The diagnostic potential of these core genes was validated using receiver operating characteristic (ROC) curve analysis. Therefore, this study provides new insights into diagnostic approaches and potential immune modulation therapies for sepsis in critically ill patients.

Figure 1. Flow chart.



GEO datasets were used to identify DEGs ($p < 0.05$, $|\log_2 FC| > 1$). Functional analyses included GO, KEGG, and immune infiltration analysis. Core genes were identified via machine learning and PPI network construction, followed by ROC validation and regulatory network analysis. GEO: gene expression omnibus; GO: gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes; PPI: protein-protein interaction; LASSO: least absolute shrinkage and selection operator; ROC: receiver operating characteristic.

Methodology

Data sources and selection criteria

Gene expression data was obtained from the GEO database, a publicly available repository for high-throughput gene expression datasets. Five datasets were selected for their relevance to sepsis and their inclusion of both sepsis patient samples and healthy controls: GSE28750, GSE57065, GSE64457, GSE65682, and GSE95233. These datasets included 875 sepsis patients and 117 healthy individuals, and provided a comprehensive resource for identifying DEGs associated with sepsis.

Raw data from these microarray datasets were processed to ensure consistency and compatibility. Probe IDs were mapped to gene symbols using the annotation files associated with each platform. Data preprocessing included normalization using logarithmic transformation and imputation of missing values. These steps were performed using the "limma" and "impute" packages in R software.

Identification of DEGs

DEGs between sepsis patients and healthy controls were identified using the "limma" package in R. Stringent filtering were applied to ensure the robustness of the results: genes were considered differentially expressed if they had a p value < 0.05 and a fold change (FC) > 2. This dual-threshold approach ensured that the identified DEGs exhibited both statistical and biological significance. The results were visualized using volcano plots and heatmaps to highlight upregulated and downregulated genes.

Functional enrichment analysis

Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses were performed to investigate the biological functions and pathways associated with the DEGs. The GO terms were categorized into three categories: biological processes (BP), cellular components (CC), and molecular functions (MF). The KEGG pathway analysis was used to identify metabolic and signaling pathways enriched among the DEGs. These functional enrichment analyses were conducted using the "clusterProfiler" package in R, and adjusted *p values* < 0.05 were considered statistically significant. The results were visualized through bar plots and bubble plots to effectively convey the enriched functions and pathways.

PPI network construction

A PPI network was constructed to investigate

potential interactions among the DEGs at the protein level. The STRING database was used to predict and visualize protein interactions [18], by applying a confidence score threshold of > 0.15 to ensure reliable connections. The Cytoscape software (version 3.8.0) was employed for network visualization and analysis. Functional modules within the network were identified using the molecular complex detection (MCODE) plug-in which prioritizes clusters of highly interconnected nodes.

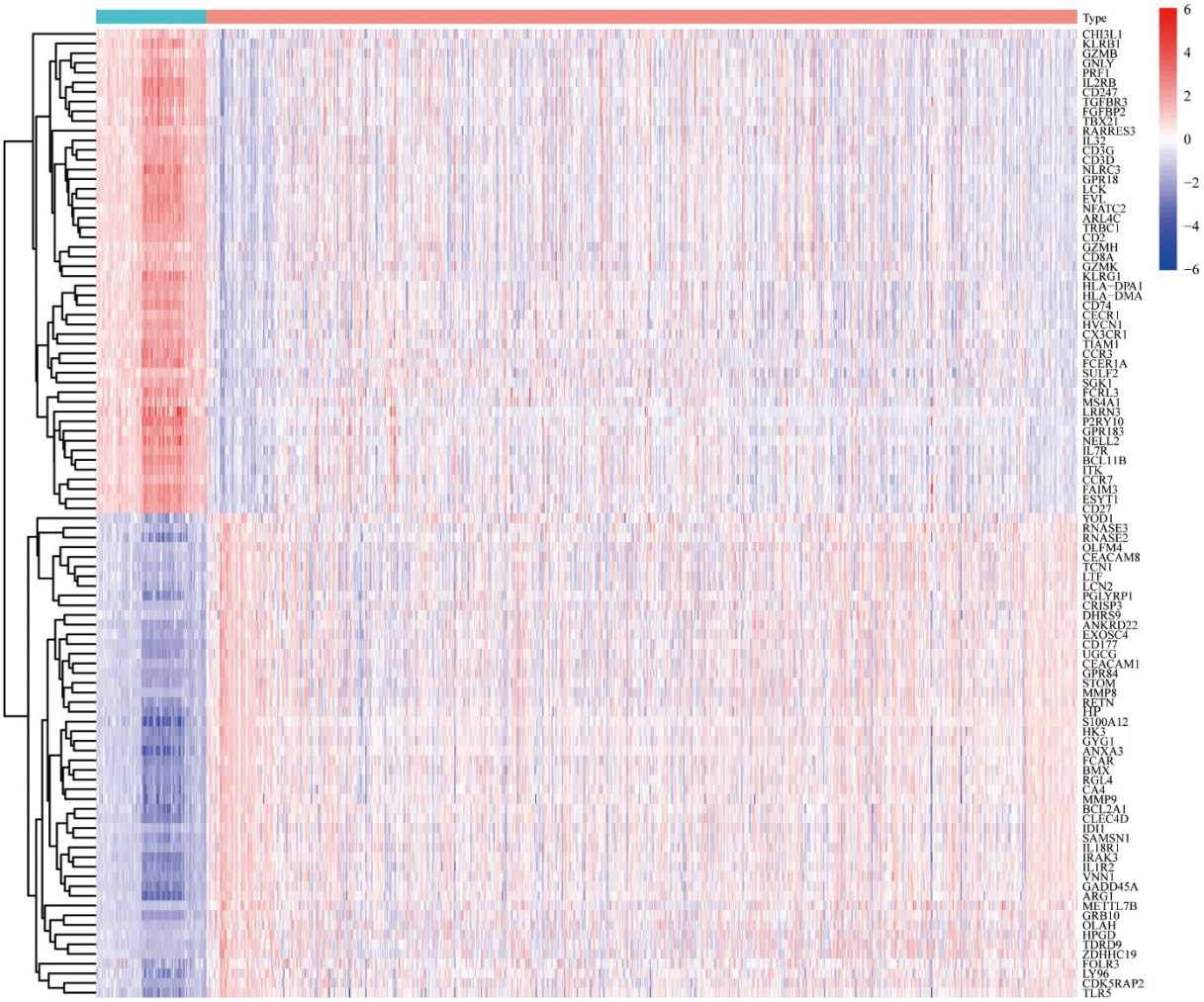
Screening of core genes

Two machine learning algorithms were employed to identify key prognostic variables and sepsis characteristic genes. First, a LASSO Cox regression model was constructed using the "glmnet" package in R to prevent over-fitting and increase the plasticity of selecting core genes [19–21]. The genes that were significantly related to the difference between normal and sepsis specimens were further screened out. Support vector machine (SVM) is a supervised machine learning technology for disease classification that creates a decision boundary between two categories so that labels can be predicted from one or more feature vectors [22]. SVM recursive feature elimination (SVM-RFE) could select the most important genes according to the weight of the classifier [23]. While SVM-RFE has been widely used in the screening tumor-related core genes (such as skin cancer [24], colon cancer [25], and gastric cancer [26]), little research has been done in sepsis [27]. Finally, the intersection of genes identified by both methods was considered the core gene signature.

Diagnostic evaluation of core genes

The diagnostic potential of the core genes was evaluated using ROC curve analysis. ROC curves were generated using gene expression data from sepsis patients and healthy controls, and the area under the curve (AUC) was calculated to assess diagnostic

Figure 2. Heatmap of the top 20 upregulated and downregulated differentially expressed genes (DEGs) in sepsis patients and controls.



accuracy. AUC values closer to 1 indicated stronger diagnostic performance. The analysis was performed using the "pROC" package in R.

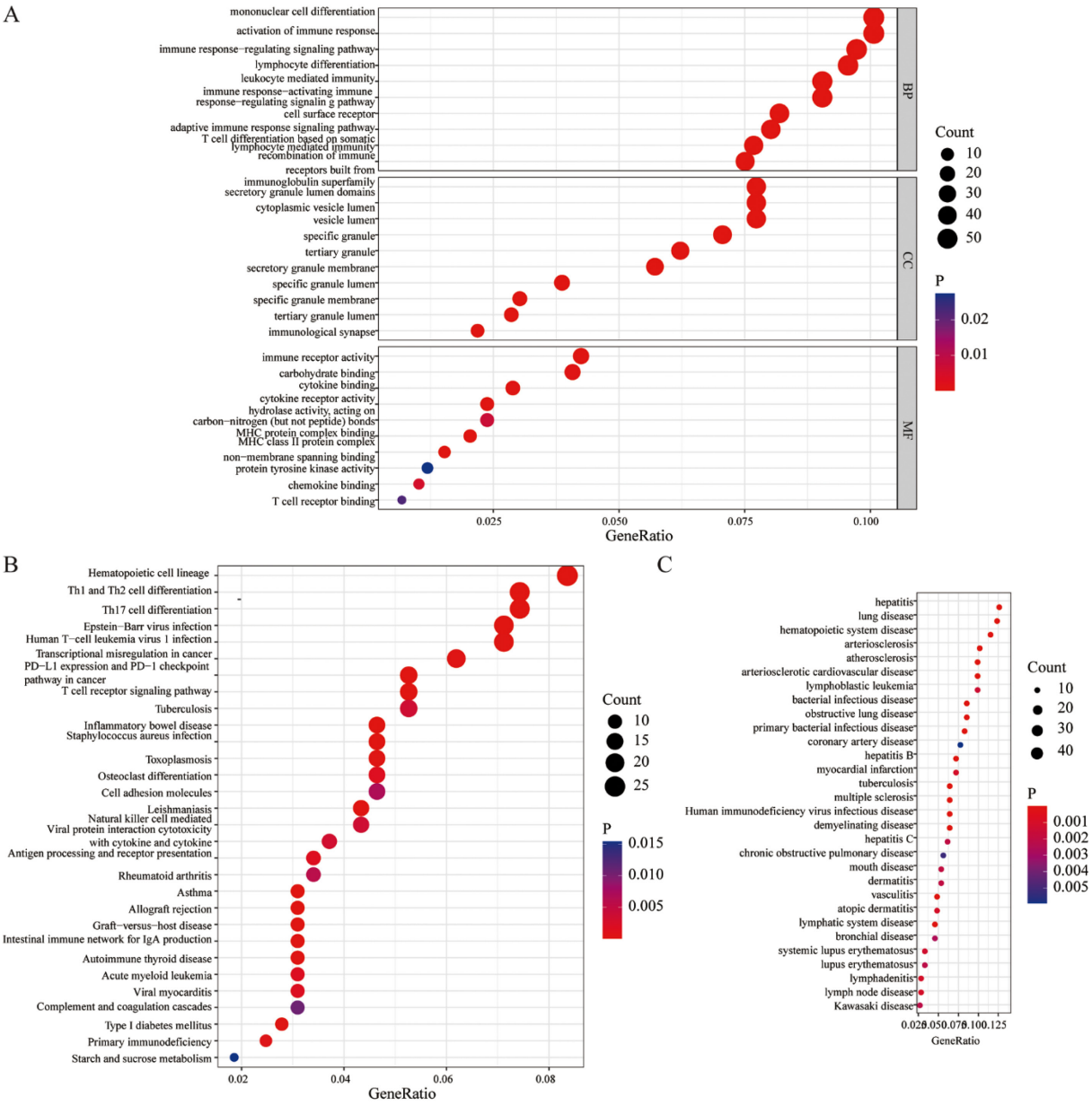
Immune infiltration analysis

Immune cell infiltration analysis was performed using the CIBERSORT algorithm to explore the immune landscape in sepsis. This computational method estimates the relative abundance of 22 immune cell types in sepsis and control samples based on gene expression data. The results were visualized using bar plots and box plots, and correlation analysis was conducted to assess the relationship between core genes and specific immune cell populations, offering insights into the immune-modulatory roles of these genes.

Statistical analysis

The Student's *t*-test was used to compare differences in gene expression between sepsis and normal samples. All statistical analyses were performed using R software (version 4.2.2). with an adjusted p value < 0.05 considered statistically significant. Data visualization was performed using the "ggplot2" and "ComplexHeatmap" packages, ensuring clear and informative graphical representation of the results.

Figure 3A. Gene ontology (GO) analysis of differentially expressed genes (DEGs). **B.** Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis highlighting immune-related pathways.



Results

Dataset combination and identification of DEGs

The overall workflow of this study is illustrated in Figure 1. This study analyzed 5 microarray datasets retrospectively—GSE28750, GSE57065, GSE64457, GSE65682, and GSE95233. DEGs were identified from the combined dataset using the LIMMA package, after correcting for batch effects. A total of 230 DEGs were identified, comprising 183 upregulated and 47 downregulated genes in sepsis patients compared to healthy controls (Supplementary Figure 1). These DEGs were selected using stringent filtering criteria: $p < 0.05$ and FC > 2. A heatmap was used to visualize the top 20 upregulated and downregulated genes (Figure 2).

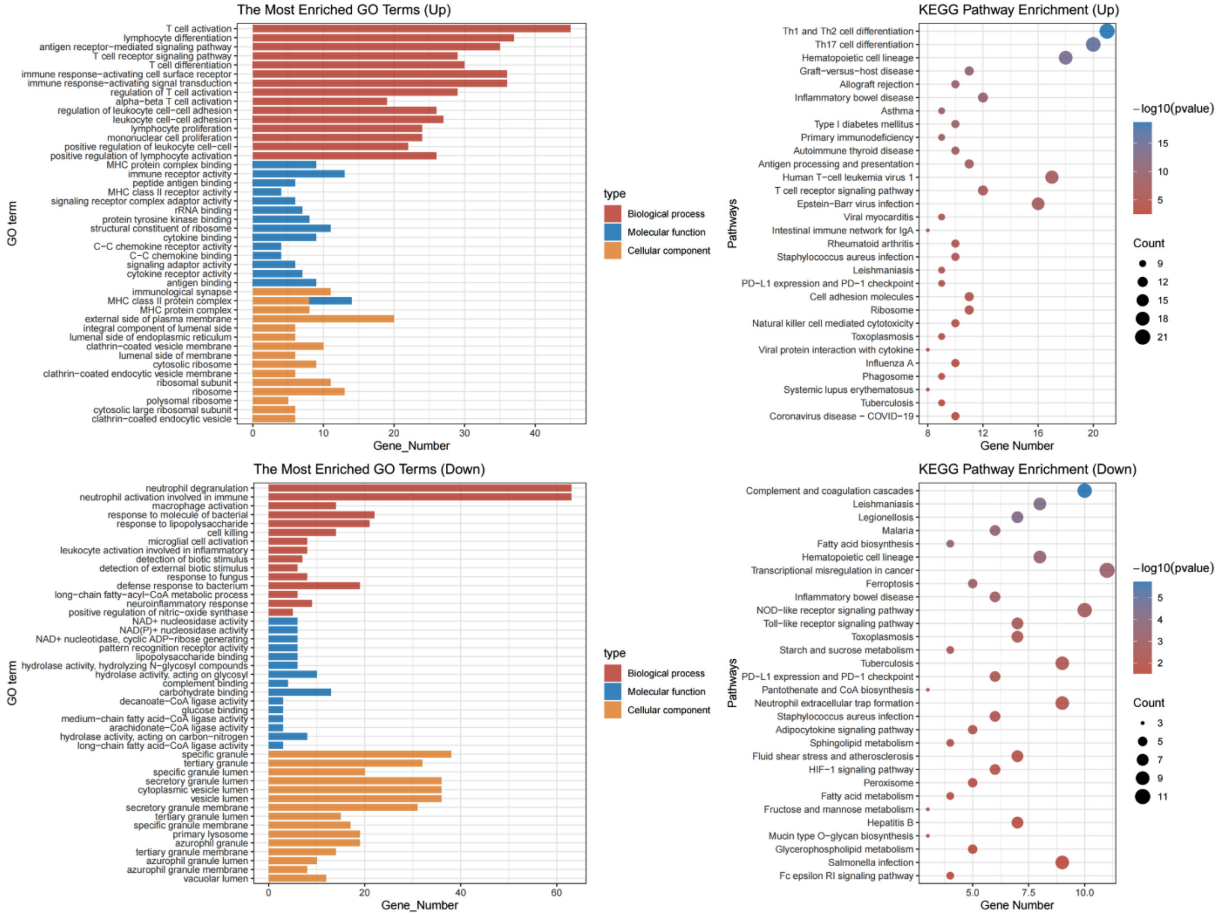
Functional enrichment analysis DEGs in sepsis

GO and KEGG enrichment analysis of the 230 DEGs was performed using the ClusterProfiler R package. GO enrichment analysis revealed that the DEGs were primarily enriched in processes such as neutrophil activation, neutrophil degranulation, immune response-related neutrophil activation, neutrophil-mediated immunity, T cell activation, T cell differentiation, and lymphocyte differentiation (Figure 3A). The KEGG pathway analysis identified significantly enriched pathways, including Th1 and Th2 cell differentiation, Th17 cell differentiation, hematopoietic cell lineage, inflammatory bowel disease, PD-L1 expression and PD-1 checkpoint pathways in cancer, *Staphylococcus aureus* infection, and T cell receptor signaling pathways (Figure 3B).

Disease ontology (DO) analysis revealed associations between the DEGs and various diseases, including hepatitis, tuberculosis, primary bacterial infections, arteriosclerosis, atherosclerosis, cardiovascular diseases related to atherosclerosis, multiple sclerosis, hematologic diseases, demyelinating diseases, and bacterial infections (Figure 3C).

Based on the functional enrichment analysis of all

Figure 4. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of up- and down-regulated genes in sepsis. Bar plots (left) show the top enriched GO terms for BP, MF, and CC. Bubble plots (right) highlight key KEGG pathways, with bubble size representing gene count and color indicating p value. Up-regulated genes are linked to adaptive immunity, while down-regulated genes are associated with innate immunity and metabolic dysregulation.



DEGs, the specific roles of the upregulated and downregulated genes were further investigated by analyzing their different enrichment patterns (Figure 4). This detailed analysis provided a deeper understanding of how adaptive and innate immune responses, as well as metabolic processes, are differentially regulated in sepsis.

GO enrichment analysis indicated that upregulated genes were significantly enriched in biological processes such as T cell activation, lymphocyte differentiation, and immune response regulation via cell surface receptor signaling pathways, highlighting their critical role in adaptive immune regulation. In terms of molecular functions, upregulated genes were involved in major histocompatibility complex (MHC) protein complex binding and cytokine receptor activity, emphasizing their contribution to antigen presentation and immune signal transduction. At the cellular component level, these genes were associated with the outer side of the plasma membrane and membrane components, suggesting their involvement in immune signal perception on the cell surface. In contrast, downregulated genes were enriched in processes related to neutrophil degranulation and bacterial defense responses, indicating inhibition of the innate immune response. Their related molecular functions included hydrolase activity and enzymes involved in fatty acid metabolism, reflecting potential metabolic dysregulation. KEGG pathway analysis showed that upregulated genes were primarily enriched in immune-related pathways such as Th1 and Th2 cell differentiation, Th17 cell differentiation, PD-L1 expression, and PD-1 checkpoint pathways. In addition, pathways such as NK cell-mediated cytotoxicity were highlighted, further supporting their significance in immune activation during sepsis. Conversely, downregulated genes were enriched in pathways related to complement and coagulation cascades, NOD-like receptor signaling, as well as metabolic processes such as fatty acid metabolism and iron homeostasis, indicating suppression of innate immune activity and disruption of metabolic functions.

PPI network analysis

A PPI network consisting 180 nodes and 351 edges was constructed using the STRING database (Supplementary Figure 2). Functional modules within the network were identified using the MCODE plug-in in Cytoscape. The largest module included 20 nodes and 63 edges, while the remaining 3 modules showed smaller but tightly interconnected clusters. These modules revealed critical interaction patterns among the DEGs, providing insights into their potential roles in sepsis pathophysiology.

Screening and validation of core genes

Screening core genes

Two machine learning algorithms were employed—LASSO regression and SVM-RFE—to refine the core genes associated with sepsis. These analyses identified *IL-23A* and *JAK2* as core genes with significant biological relevance and strong connectivity within the PPI network. LASSO regression highlighted 68 potential core genes, among which *SOCS3*, *JAK2*, *SH2B3*, and *IL-23A* stood out due to their prominent interconnections in the PPI network (Supplementary Figure 3). *JAK2* and *IL-23A* were prioritized for further analysis based on their established roles in sepsis (Figure 5A).

Figure 5A. Least absolute shrinkage and selection operator (LASSO) regression. **B–C.** Receiver operating characteristic (ROC) curves for IL-23A and JAK2 diagnostic accuracy.

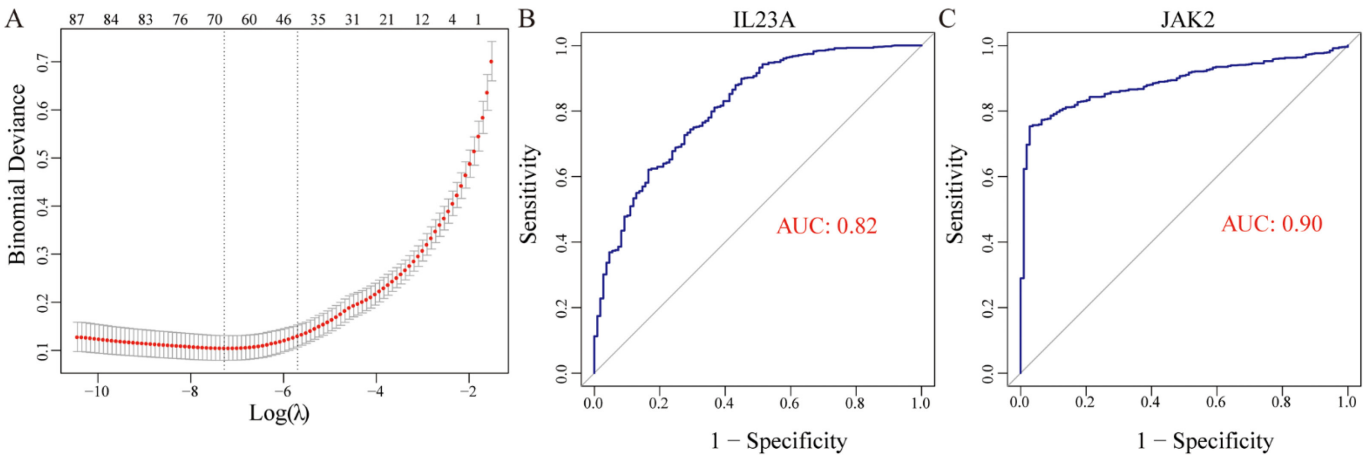


Figure 6. Correlation and pathway analysis of IL-23A and JAK2 via the JAK/STAT3 pathway.

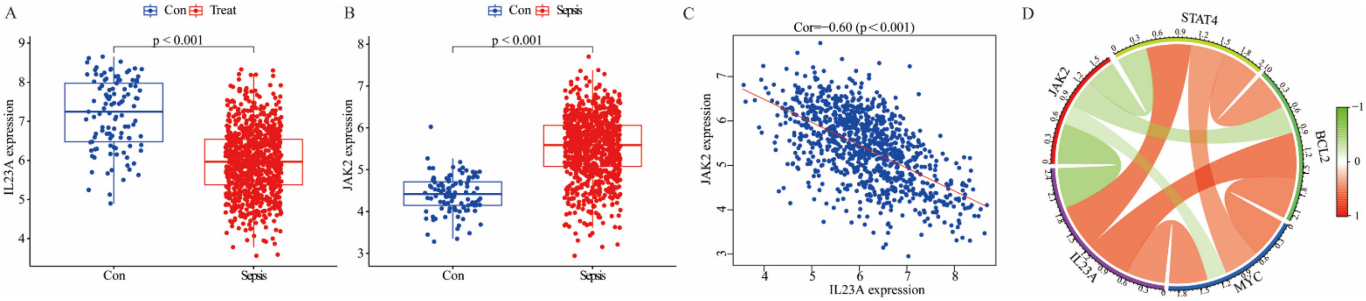
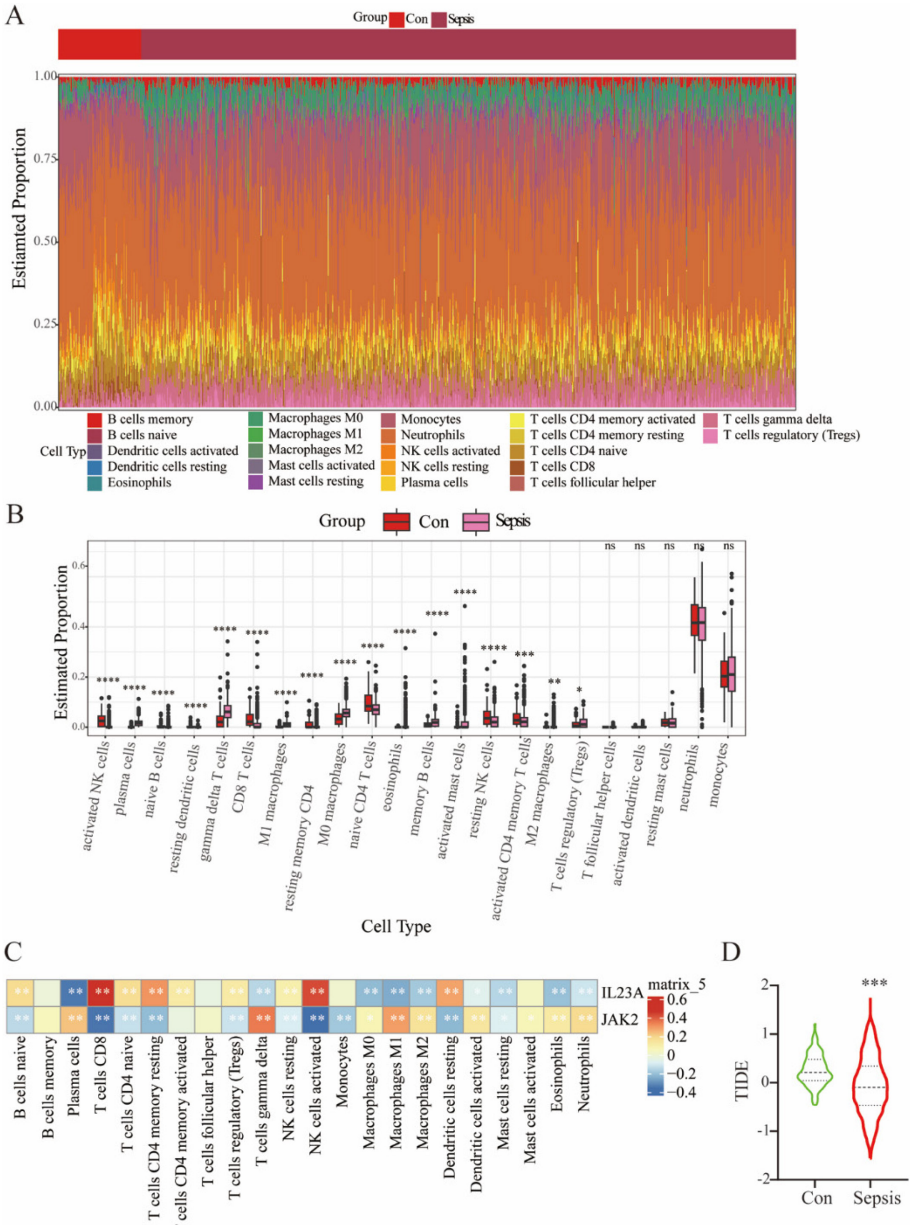


Figure 7. Immune infiltration analysis in sepsis. **A.** proportions of immune cell types in sepsis and controls; **B.** box plots of macrophages, plasma cells; **C.** correlation of IL-23A and JAK2 with immune cell infiltration; **D.** tumor immune dysfunction and exclusion (TIDE) scores showing higher immune dysfunction in sepsis samples.



Validation of core genes

The mRNA expression levels of *IL-23A* and *JAK2* in sepsis and normal blood samples were analyzed from the GEO database to confirm the roles of the core genes in sepsis. ROC curve analysis demonstrated the diagnostic potential of these genes, with AUC values 0.82 for *IL-23A* and 0.9 for *JAK2* (Figure 5B–C). Validation with an independent dataset (GSE9600) yielded consistent results (Supplementary Figure 4A–B).

The expression of *IL-23A* and *JAK2* in sepsis were analyzed (Figure 6A–B and Supplementary Figure 5A–B). Further integrative analysis revealed a negative correlation between the expression of *IL-23A* and *JAK2* in sepsis, with a correlation coefficient of – 0.60 (Figure 6C). Mechanistic analysis indicated that *IL-23A* is closely associated with targets in the *JAK/STAT3* signaling pathway, suggesting its potential role in modulating immune responses during sepsis (Figure 6D).

Immune infiltration analysis

Immune infiltration was assessed using the CIBERSORT algorithm, revealing significant differences in immune cell population proportions between sepsis patients and healthy controls. Sepsis samples showed elevated levels of macrophages, plasma cells, and γδT cells (Figure 7A–B and Supplementary Figure 6A–B), indicative of a hyperactivated immune response. Correlation analysis demonstrated that *IL-23A* was negatively associated with macrophages, plasma cells, and γδT cells; while *JAK2* exhibited a positive correlation with these immune cell types (Figure 6C and Supplementary Figure 6C). The tumor immune dysfunction and exclusion (TIDE) score was significantly higher in sepsis samples compared to normal controls (Figure 7D), highlighting the immune dysfunction characteristic of sepsis and supporting the robustness and reliability of the immune classification.

Discussion

Despite advancements in intensive care and antimicrobial therapies, sepsis remains a leading cause of mortality and morbidity globally, with an estimated 31.5 million cases and 5.3 million deaths annually [28]. The complexity of sepsis pathogenesis, involving dysregulated immune responses, coagulation abnormalities, bacterial and endotoxin translocation, and genetic polymorphisms; underscores the urgent need for novel diagnostic and therapeutic strategies [29]. Accumulating evidence indicates that systemic immune responses play a critical role in the pathogenesis and progression of sepsis [30–32]. The immune system typically exhibits a robust pro-inflammatory response aimed at eliminating pathogens in the early stages of the disease [33]. However, as the condition advances, immune dysfunction emerges as a hallmark of progressive sepsis [34]. Recent studies have identified specific genes involved in the pathophysiology and progression of sepsis [16,17]; nonetheless, the interactions between these genes and immune cells remain poorly understood. To tackle this issue, a comprehensive bioinformatics analysis of gene expression data from 5 datasets, including 875 sepsis patients and 117 healthy controls was utilized. A total of 230 DEGs, with 183 upregulated and 47 downregulated genes were identified. GO analysis revealed enrichment in immune-related processes, such as neutrophil and T cell activation and differentiation. Further analysis highlighted *IL-23A* and *JAK2* as core genes with significant biological relevance and high diagnostic accuracy (AUC values of 0.82 and 0.90, respectively). These genes were validated in an independent external dataset (GSE9600). Immune infiltration analysis showed differences in immune cell populations, with *IL-23A* and *JAK2* closely associated with key immune responses. These findings highlight the potential of *IL-23A* and *JAK2* as indicators of immune responses and therapeutic targets in sepsis.

Compared to healthy individuals, immune-related pathways are significantly enriched in septic patients. This finding is consistent with several previous bioinformatics studies and further supports the view that the pathogenesis of sepsis is primarily driven by the body's abnormal or dysregulated immune response to infection [35–38]. This is also in line with the current definition of sepsis. The core genes identified in different bioinformatics studies may not be consistent due to differences in dataset selection and core gene screening methods. To the best of our knowledge, this study has the largest number of septic cases included in bioinformatics research using GEO data. We are able to provide a more comprehensive understanding of the complexity of immune responses in septic patients and the potential roles of related genes through the analysis of this large-scale dataset; thus, offering important insights for future precision medicine and therapeutic strategies.

Role of IL-23A in sepsis

IL-23 is a member of the IL-12 cytokine family. It is composed of two subunits: IL-23A (p19) and IL-12/23B (p40), the latter being shared with IL-12 [39].

The IL-23/IL-17 axis plays a protective role against bacterial and fungal infections. Dysregulated IL-23 can lead to chronic inflammation and autoimmunity, contributing to the pathogenesis of diseases such as psoriasis, psoriatic arthritis, inflammatory bowel disease, rheumatoid arthritis, and multiple sclerosis [40]. The triggering receptor expressed on myeloid cells 2 (TREM-2) is a novel immune regulatory factor with multiple activities. Animal experiments have shown that the IL-23 levels in TREM-2 overexpressing macrophages are significantly lower compared to GFP-expressing macrophages [41]. Blocking IL-23 after the administration of GFP-expressing macrophages also protects elderly mice from sepsis [41]. These findings suggest that targeting the IL-23/IL-17A immune pathway could be a potential strategy for treating aging-related sepsis.

Several studies, including this one, have demonstrated the critical role of *IL-23A* in mitigating excessive immune activation and immune dysfunction in sepsis through the *JAK/STAT3* signaling pathway. Previous research has indicated that *IL-23* plays a crucial role in NK cell activation and IFN-γ secretion, influencing the adaptive immune response, especially during early infection [42]. The synergy between IL-23 and IL-18 suggests its importance in initiating adaptive immunity responses. This highlights the potential of *IL-23A* as a therapeutic target for managing immune dysregulation in sepsis.

A study involving 74 adult sepsis patients, 45 ICU controls, and 50 healthy individuals participating in routine physical examinations emphasized that IL-1 β and IL-23 are potential biomarkers for the diagnosis and prognosis of sepsis [43]. Sepsis patients, especially non-survivors, have significantly elevated levels of both. IL-1 β and IL-23 are independent risk factors for 28-day mortality and are associated with the severity of sepsis [43]. ROC analysis shows that IL-23 has better predictive value for mortality [43]. Additionally, the robust ROC analysis presented in this study underscores the diagnostic potential of *IL-23A*, providing new insights into its clinical application.

Role of JAK/STAT3 signaling pathway in sepsis

Activation of the *JAK/STAT3* pathway drives inflammation and immune activation [44]. This study demonstrates that *JAK2* expression is significantly upregulated in sepsis patients compared to healthy controls, aligning with previous findings that link increased *JAK2* activity to sepsis-associated inflammation [45,46]. Furthermore, the findings support *IL-23A* and *JAK2* as key immune regulators in sepsis, consistent with Clere-Jehl *et al.* [47], who emphasized the dual role of *JAK/STAT3* in hyperinflammation and immunosuppression. Additionally, a unique negative correlation between IL-23A and JAK2 was revealed, offering novel insights into sepsis pathogenesis.

However, unlike previous studies that emphasized the pro-inflammatory role of *IL-23A* [48], this study revealed a negative correlation between the expression of *IL-23A* and *JAK2* in sepsis patients. Earlier research also demonstrated that IL-23-dependent activation of the *JAK/STAT* pathway can be inhibited in *IL-23R*-expressing cells, suggesting that *IL-23* is involved in specific regulatory mechanisms of the *JAK/STAT* pathway [49]. Further research is required to elucidate the mechanisms through which *IL-23A* regulates *JAK2* expression and the downstream effects of this interaction in sepsis.

Limitations and future directions

Although the results of this study are promising, some limitations should be acknowledged. First, the analysis is based on gene expression data from public databases and confirmed on external independent datasets. These data may not fully represent the complexity and heterogeneity of sepsis in clinical practice. Therefore, the results should be interpreted with caution. Further experimental studies and validation in a larger prospective patient cohort are essential to confirm the diagnostic and therapeutic potential of *IL-23A* and *JAK2* in sepsis. Second, 875 septic patients and 117 healthy individuals were included in this study. Considering the potential limitations of the control group size, the small sample size of the control group may affect the statistical power and generalizability of the survey results. Future research should focus on clarifying the precise molecular mechanism of *IL-23A* regulating *JAK2* and *JAK/STAT3* pathways in sepsis. Further in vivo studies and large-scale longitudinal clinical trials are needed to validate the diagnostic and prognostic value of *IL-23A* and *JAK2*. In addition, exploring the therapeutic potential of targeting the *IL-23A/JAK2* axis through pharmacological inhibitors or combination therapies in animal models will provide valuable insights.

Conclusions

This study identifies *IL-23A* and *JAK2* as key genes associated with sepsis, highlighting their potential as assistant diagnostic indicators and therapeutic targets. The involvement of the *JAK/STAT3* signaling pathway and the observed immune dysregulation underscore the

complex interplay of immune responses in sepsis. These findings provide a foundation for future research aimed at developing targeted therapies to modulate immune responses and improve outcomes in sepsis patients.

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Availability of data and materials
The datasets generated for this study can be found at https://www.ncbi.nlm.nih.gov/.

Authors' contributions
ZYL, CLY, conception and design of the work, manuscript draft, critical revision for important intellectual content; ZYL, WF, acquisition, analysis, and interpretation of data; All authors approved the final version of this manuscript.

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Conflict of interest
No conflict of interest is declared.

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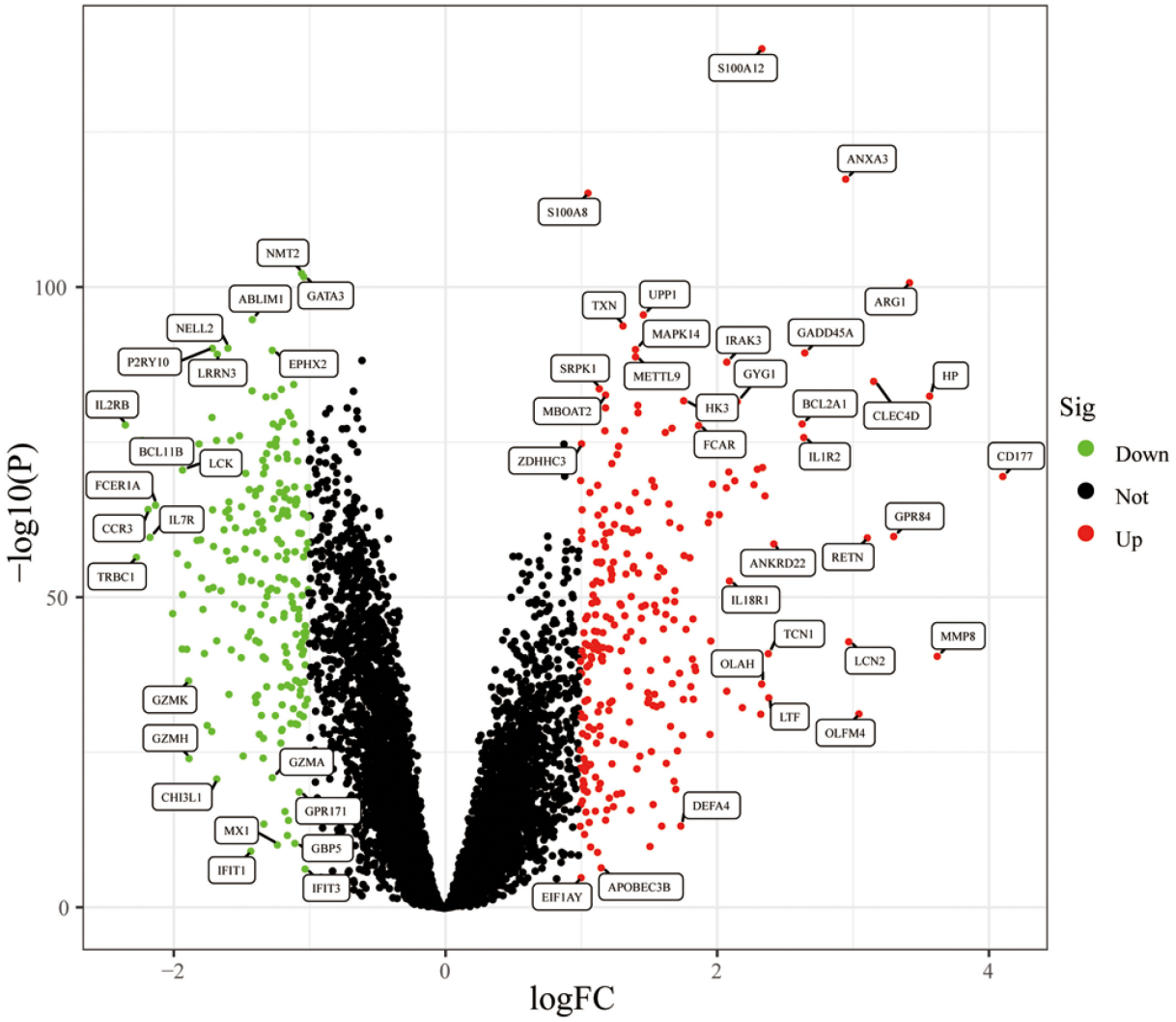
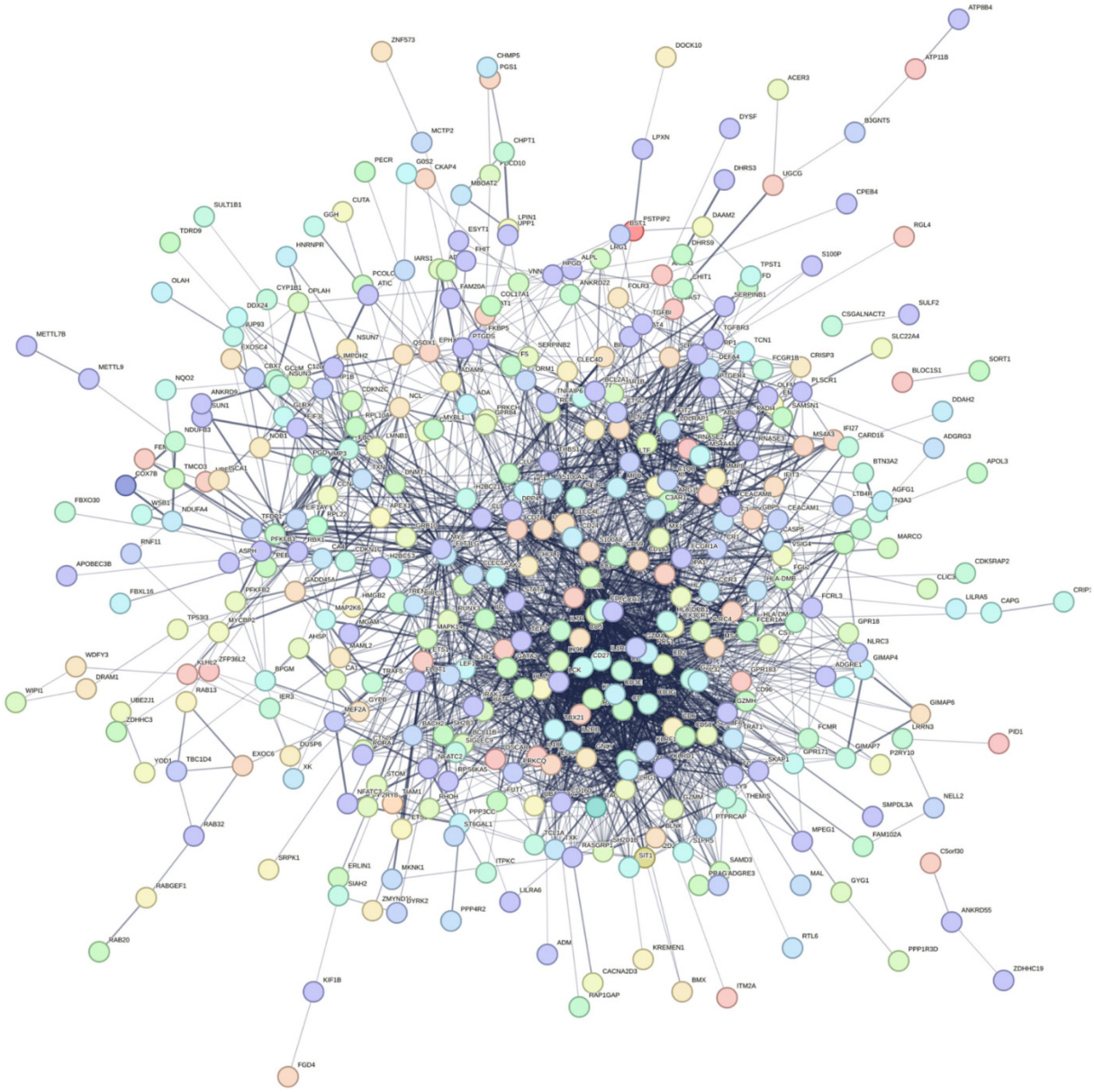
Annex – Supplementary Items

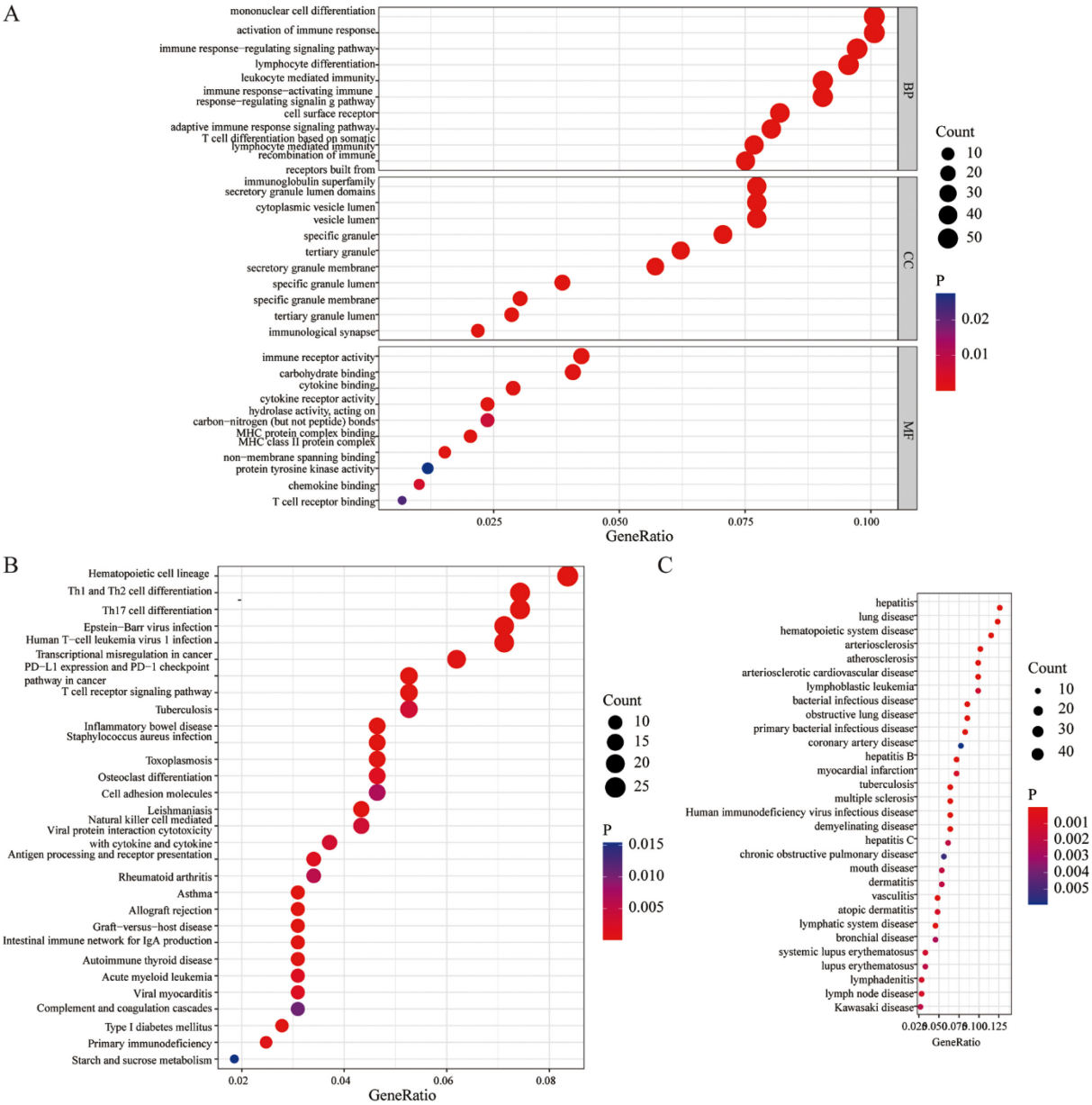
Supplementary Figure 1. Thermograms of the top 20 genes that were up-regulated and down-regulated.



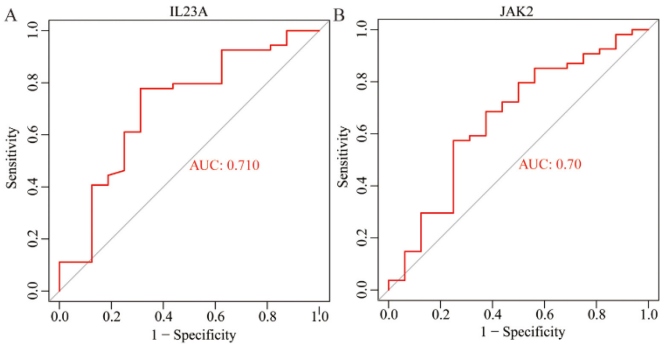
Supplementary Figure 2. The protein-protein interaction (PPI) network constructed by differentially expressed genes (DEG).



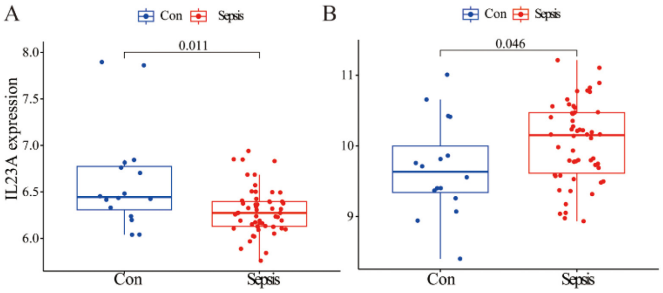
Supplementary Figure 3. Protein-protein interaction (PPI) network of key genes obtained by the least absolute shrinkage and selection operator (LASSO) regression analysis.



Supplementary Figure 4. Receiver operating characteristic (ROC) curve analysis of GSE9600 database. A: IL23A; B: JAK2.



Supplementary Figure 5. Analysis of IL23A gene expression. A. GSE9600 database; B. GSE9600 database.



Supplementary Figure 6. Immune correlation analysis in the GSE9600 dataset. **A.** the proportion of immune cells in each sepsis sample; **B.** level of immune cell population; **C.** correlation between C:IL-23A and JAK2 in each immune cell population.