Identification and validation of blood miRNAs as diagnostic markers of gastric cancer

Zhouhan Xu
Shandong University
Xuesi Yang
Shandong University
Ruiqi Zhao
Shandong University
Xueling Li
Shandong University
Shujie Li
Shandong University
Qingyu Wang
Shandong University
Xize Li
Shandong University
Fen Liu
Shandong University
Jiping Zeng (zengjp@sdu.edu.cn)
Shandong University

Research Article

Keywords: Gastric cancer, Blood-based miRNAs, Differentially expressed genes, Biomarkers, Bioinformatics

Posted Date: June 22nd, 2022

DOI: https://doi.org/10.21203/rs.3.rs-1750380/v1

Abstract

Objective: Gastric cancer (GC) is one of the leading causes of cancer-related deaths. MicroRNAs (miRNAs) have been identified to play an important role in gastric carcinoma. It can provide a new direction for the diagnosis and treatment of gastric cancer to evaluate the blood-based miRNAs that are differentially expressed in gastric carcinoma.

Methods: The gastric cancer patients' blood-based miRNAs datasets GSE113486 GSE112264 and GSE113740 were obtained from the Gene Expression Omnibus (GEO) database. The miRNAs which were differentially expressed in gastric cancer patients' blood compared with the corresponding normal ones were analyzed by the SangerBox. The target genes of the differentially expressed miRNAs were predicted through three miRNA - target genes prediction websites which are Targetscan, Mirtarbase and miRDB, respectively. Subsequently Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG functional enrichment analyses were performed using DAVID 6.8 to acquire key biological pathways associated with the differentially expressed miRNAs - target genes. The STRING database and Cytoscape were selected to analyze and visualize the interaction network between the encoded proteins of the target genes. QRT-PCR was used to detect the expression of the selected out possible key miRNAs in human blood species. The correlation of the key miRNAs expression with prognosis of gastric cancer patients and the corresponding diagnostic value were also analyzed by survival prognosis and receivers operating characteristic (ROC) curve.

Results: This study identified potential novel blood miRNA biomarkers of gastric cancer. There are a total of 5654 data of the statistically significant abnormal blood miRNAs of gastric cancer patients obtained from GEO database. Combined the data of the three datasets with the RRA method, 20 miRNAs which have the maximum changes were chosen as the differentially expressed miRNAs, 10 up-regulated and 10 down-regulated, respectively. On this basis, 691 up-regulated differentially expressed target genes and 1074 down-regulated ones were selectively predicted. The main biological processes involved in up-regulated genes included autophagosomes maturation, cytosol and protein binding. While for 1074 down-regulated ones, the main biological functions were negative regulation of transcription from RNA polymerase II promoter, nucleoplasm and protein binding. With the help of the protein network analysis, five key blood-based miRNAs were determined, including hsa-miR-125a-3p, hsa-miR-124-3p, hsa-miR-29b-3p, hsa-miR-4276 and hsa-miR-575. The check in human blood species and analysis of patient prognosis and diagnostic value confirmed the prediction could be useful for the early diagnosis and efficacy monitoring.

Conclusion: The key blood-based miRNAs in gastric carcinoma determined by bioinformatics and human blood species detection may give a new possibility of the important biomarkers for the diagnosis and prognosis of gastric cancer.

Introduction

Gastric cancer is a kind of malignant tumors which organizes from the gastric mucosal epithelium whose number of patients is the second largest in the world. There are about 1,000,000 new patients suffering from gastric cancer every year. At the same time, about 770,000 people lose their lives every year due to it [1, 2]. Gastric cancer has been bringing enormous mental and financial burden to individuals and the whole society. There is progress on the early diagnosis and treatment of gastric cancer, however it is needed of breakthrough on the new molecular mechanism of gastric carcinoma to achieve efficient, reliable and measurable biomarkers.

MiRNA is a class of non-coding single-stranded RNA molecules of approximately 22 nucleotides in length encoded by endogenous gene [3]. It plays an important role in the regulation of the post-transcriptional gene expression in plants and animals [4]. MiRNA acts through base pairing with complementary sequences within the mRNA molecule, resulting in silencing of these mRNA molecules. This disorder of negative expression regulation is closely related to the most of tumorigenesis. In the past few years, manipulation of miRNA clusters expression is attempted for diagnosis, treatment and prognosis in cancers [5].

As a common test material, blood is easy to obtain, easy to detect and minimally invasive. At the same time, since the tumor microenvironment has a great influence on the carcinogenesis, invasion and metastasis, the components in the blood might also affect the tumorigenesis. Therefore, the study of miRNAs in blood may have great effect on the prediction and diagnose of tumors [6]. After searching for the most cutting-edge data, we found that the research on differentially expressed miRNAs in the blood of patients with gastric cancer is not perfect. Therefore, the study on differentially expressed miRNAs in the gastric cancer patients' blood is promising to promote the discovery of new tumor markers and determine new research directions.

In recent years, with the establishment of tumors databases, sequencing technology and bioinformatics analysis have been widely used in the research of cancer at the molecular level [7]. Drug designed based on bioinformatics analysis is also emerging [8]. This provides new ideas and tools for us to find out differentially expressed miRNAs from patients' blood samples and explore their functional pathways that might affect gastric carcinoma. Therefore, this study searched for the corresponding dataset through the GEO database [9]. Next the bioinformatics tools were used to analyze the obtained data for screening out key miRNAs which were predicted biological mechanism through functional enrichment and protein network construction. The results were detected in human blood species with analysis of patient prognosis and diagnostic value. These determined crucial blood miRNAs and the corresponding target genes might become biomarkers for early screening and diagnosis of gastric cancer. The flow chart of the methods used in this study is shown in Fig. 1.

Materials And Methods

1. Data selection

GEO (https://www.ncbi.nlm.nih.gov/geo/)is built by the National Center for Biotechnology Information (NCBI) which contains high-throughput gene expression data submitted by the scientific researchers around the world. The database was scanned with the keywords "gastric cancer", "blood", "human" and "miRNA". GSE113486, GSE112264 and GSE113740 were confirmed as the most suitable datasets. The datasets contain 115 cases of gastric cancer samples and 151 cases of normal samples.

2. Preliminary screening of differentially expressed miRNAs and predicted target genes

SangerBox is one of the biometric analysis platforms based on R language (http://sangerbox.com). Using the GEO convenience converter in SangerBox, the sample files were carried on differential analysis by DECenter. Then its network tool library was used to execute RRA analysis. Thus 20 miRNAs which showed the most significant changes in the gastric cancer group compared with the normal were screened out as the research targets (10 up-regulated and 10 down-regulated, respectively). Targetscan (http://www.targetscan.org/), miRDB (http://mirdb.org/) and mirtarbase (http://mirtarbase.mbc.nctu.edu.tw) are the three websites for online prediction of the miRNA's possible target genes.

3. Functional enrichment of differentially expressed genes

DAVID6.8(https://david.ncifcrf.gov/)is one of widely used bioinformatics databases that can provide systematic and comprehensive information for large-scale genes or proteins lists. In this research, it was used to proceed GO and KEGG enrichment analysis on differentially expressed genes and relative signal pathways that might play key roles in gastric carcinoma, which provided a rough understanding of the relevant molecular mechanisms. The $P < 0.05$ and gene counts ≥ 2 were rated to be statistically significant.

4. Protein-protein interaction network (PPI network)

PPI network is composed of individual proteins through their interactions. The study of PPI network can help to understand the functional links among proteins and to obtain the core regulators. String (https://string-db.org) is one of the proteins interaction databases with the most exhaustive species and the most comprehensive interaction information. After obtaining the PPI network of genes targeted by 20 most differentially expressed miRNAs, the important sub-network and the corresponding genes were analyzed with the MCODE plug-in clustering function module of Cytoscape (version 3.6.1). The minimum score required for interaction is medium confidence (0.400). And then, miRNAs targeting these important sub-networks and the corresponding genes were selected, and the 5 miRNAs with the highest frequency of occurrence were regarded as key blood miRNAs for subsequent analysis.

5. Selection and survival curve analysis of the key miRNAs and relative target genes

It was to cluster the sub-network nodes of the PPI network, and sort the most important genes which were negatively regulated by the corresponding key miRNAs. The occurrence number of a miRNA was used to decide whether it should be regarded as the key one in the research. ONCOLNC and GEPIA are the two

tools that can interactively explore survival dependencies. In this study, the correlation between the key nodal genes and the survival rate of gastric cancer patients was analyzed with ONCOLNC and GEPIA. The survival curves of the key miRNAs and the target genes were examined by the Kapler-Meier Plotter online tools (https://kmplot.com/analysis/) to determine the influence of their expression level on the prognosis of gastric cancer patients. The significance was defined as a P value of 0.05.

6. The human blood species and qRT-PCR determination

The human blood species were collected from Xiajin County People's Hospital, Dezhou, Shandong Province. They were divided into two groups: one control group (n = 10)which came from randomly selected normal volunteers, and the other experimental group n = 22 which came from patients who were newly diagnosed with gastric cancer without any treatment. This research has been approved by the Ethics Committee of Shandong University School of Basic Medical Sciences.

Total RNA was extracted using Invitrogen TRIzol (Thermo Fisher SCIENTIFIC, Code: 15596018). For miRNA quantification, the synthesis of cDNA was performed using Evo M-MLV RT Kit for qPCR (Accurate Biology, Code: AG11707). The qPCR primers of miR-575, miR-125a-3p, miR-124-3p, miR-4276 and miR-29b-3p were designed and synthesized with the Bulge-Loop miRNA qRT-PCR Primer sets (RIBOBIO, Code: MQPSCM001). Real-time PCR was carried on with SYBR Green Premix Pro Taq HS qPCR Kit (Accurate Biology, Code: AG11701) on a Bio-Rad CFX-96 real-time system. U6 was detected as the internal control. All qRT-PCR reactions were conducted in triplicates, and relative quantification was calculated by the $2^{-\Delta\Delta Ct}$ method (95% confidence interval) with calibration to the corresponding control. The expression data were analyzed with a Student's t-test. The $P < 0.05$ was considered significant difference in statistics.

7. ROC analysis

The expression data of key miRNAs were used to construct the ROC curves by software SPSS 26.0 with area under the curve (AUC) values as the diagnosis value indicator. The $P < 0.05$ was considered to be statistically significant.

Results

1. The differentially expressed blood miRNAs in gastric carcinoma.

The SangerBox was used to analyze the GSE113486, GSE112264 and GSE113740 data to screen and obtain the abnormally expressed miRNAs in the blood of gastric cancer patients. The results detected that in the chip GSE113486, compared with the normal controls, there were 2086 miRNAs with statistically significant difference in the group of gastric cancer. Therein to raised miRNAs were 1784 and decreased miRNAs were 302 (Fig. 2A). The most remarkably up-regulated 50 miRNAs and down-regulated 50 miRNAs were shown in the Fig. 2B. In the chip GSE112264, there were a total of 2086 abnormal miRNAs in the blood of patients with gastric cancer that are statistically significant, with an increase of 1831 and a decrease of 255 (Fig. 2C). The 50 miRNAs with the most significant up-regulation and down-

regulation were shown in the Fig. 2D. In the chip GSE113740, compared with the normal blood of the control, there were 1482 abnormal miRNAs in the blood of gastric cancer patients, which were statistically significant, with an increase of 1340 and a decrease of 142 (Fig. 2E), of which the most significant up-regulation and down-regulation and the 50 miRNAs were shown in the Fig. 2F.

2. The prediction of target genes directly silenced by the most differentially expressed miRNAs and the enrichment results of GO and KEGG

The RRA algorithm was used to find the top 10 up-regulated miRNAs and the top 10 down-regulated miRNAs from the three chip datasets (Fig. 3A). With the combination and comparison of the predictions from Targetscan, Mirtarbase and miRDB, 691 over-expressed genes and 1074 down-regulated ones were obtained as the possible targets of the selected 20 miRNAs. GO and KEGG enrichment analysis on differentially expressed genes by DAVID received the molecular functions, cellular components, corresponding biological processes and signaling pathways of the target genes. Up-regulated genes (targets of down-regulated miRNAs) GO enrichment results suggested that the main biological processes involve included autophagosomes maturation, regulation of mitochondrial membrane potential and folic acid metabolic process. The corresponding main molecular functions included protein binding, metal ion binding and RNA polymerase II core promoter proximal region sequence-specific DNA binding. The cellular components included cytosol, cytoplasm and nucleus (Fig. 3B). KEGG enrichment results showed that Endocytosis, Proteoglycans in cancer and Glycosylphosphatidylinositol (GPI)-anchor biosynthesis were the main signaling pathways involved in overexpressed target genes-related mechanism (Fig. 3C). On the contrary, for the down-regulated genes (targets of up-regulated miRNAs), the main involved biological processes included regulation of transcription from RNA polymerase II promoter, platelet-derived growth factor receptor signaling pathway and DNA-templated positive regulation of transcription. The main molecular functions included protein binding, chromatin binding, transcriptional activator activity, and RNA polymerase II core promoter proximal region sequence-specific binding. The cellular components included nucleoplasm, nucleus and focal adhesion (Fig. 3D). And the signaling pathways involved in down-expressed genes regulation were Focal adhesion, Prolactin signaling pathway, PI3K-Akt signaling pathway, and Focal adhesion (Fig. 3E).

3. The analysis of the proteins interaction network and selection of the key blood miRNAs with the correlant target genes

Genes targeted by the 20 most differently expressed blood miRNAs were analyzed in the STRING database (Fig. 4A-C). The results of the PPI network were imported into Cytoscape software for analysis. Then a total of 38 nodes were obtained which indicated that genes targeted by the 20 most differently expressed blood miRNAs were closely related to each other. And they were involved in multiple signaling pathways which might play important roles in the tumorigenesis. At the same time, the number of nodes in the up-regulated genes-encoded proteins network was 650. The number of edges was 1571. The average node degree was 4.83. The average local clustering coefficient was 0.337. And the enrichment P value was less than 0.0123. The number of nodes in the down-regulated genes-encoded proteins network

was 1007. The number of edges was 5171. The average node degree was 10.3. The average local clustering coefficient was 0.308. And the enrichment P value is less than 1.0e-16. The results showed the data was reliable and can be used for further analysis. With the help of MCODE analysis, the miRNAs targeting the key nodes was obtained(Table S1). And then, the most frequent miRNAs were selected as the key blood miRNA. The results suggested the key blood miRNAs involved in the up-regulated ones were hsa-miR-124-3p and hsa-miR-29b-3p, whereas in down-regulated ones were hsa-miR-4276, hsa-miR-575 and hsa-miR-125a-3p. They could be the possible miRNAs for the early diagnosis and treatment of gastric carcinoma. Survival analysis was performed on sub-network genes obtained in PPI networks that may be targets of key miRNAs. The results showed there were 31 blood miRNAs-targeted genes which were associated with gastric cancer (Table S2).

4. The key blood miRNAs with the correlant target genes were detected by the examination of the expression levels in human blood species and the survival curve analysis.

The basic information of the patients and volunteers who provided the blood samples was shown in Table S3. The results of qRT-PCR which determined the expression of selected miRNAs was shown in Fig. 5A-E. The survival curves which suggested the correlation of selected miRNAs expression with the patient prognosis were shown in Fig. 6A-D. The survival curves of the corresponding target genes with the patient prognosis were shown in Figure S1. From the results, it was preliminarily found that the significant down-regulation of hsa-miR-124-3p ($P < 0.05$ *vs.* normal volunteers) and hsa-miR-125a-3p ($P < 0.01$ *vs.* normal volunteers) was closely related to the prognosis of gastric cancer patients ($P < 0.05$) in human blood species, whose expression had nothing to do with the patients' age and gender ($P > 0.05$). Whereas of hsa-miR-4276, hsa-miR-575 and hsa-miR-29b-3p, the expression in human blood species was inconsistent with bioinformatics prediction results ($P > 0.05$ *vs.* normal volunteers). At the same time, hsa-miR-29b-3p was positive correlation with prognosis of gastric cancer patients ($P < 0.05$). Although the prognosis analysis suggested the expression of hsa-miR-4276 and hsa-miR-575 had nothing to do with the patient survival rate ($P > 0.05$). However, the lower expression of these two miRNAs has a tendency to reduce the survival rate of patients. The prognosis analysis also identified that the expression of most target genes was associated with the patient survival possibility. All these results determined that the prediction of bioinformatics could be useful for diagnosis, which might not be completely consistent with the patient condition. It will be necessary to use more patient blood samples for testing and verification.

5. The diagnostic value of key blood miRNAs in patients with GC.

In order to further clarify the value of key blood miRNAs in the diagnosis of gastric carcinoma, ROC analysis was conducted in an expression-dependent manner. The results showed that miR-124-3p could have the potential application in diagnosis, with high AUC value of 0.952 (Fig. 7A). MiR-125-3p showed AUC values 0.812 with possibility in diagnosis (Fig. 7B). MiR-29b-3p also showed its possibility with AUC value 0.824 (Fig. 7C). The combination of miR-124-3p and miR-125-3p can increase the potential application in diagnosis with AUC values of 0.969 (Fig. 7D). While the three potential miRNAs together in gastric carcinoma diagnosis can get the AUC values to 0.975 (Fig. 7E), which suggested the value of the

key blood miRNAs in clinical prevention, diagnosis and prognosis. Hsa-miR-575 and hsa-miR-4276 showed less diagnostic application with AUC values of 0.41 and 0.556, respectively (Fig. 7F and G).

Discussion

In the research, GSE113486, GSE112264 and GSE113740 selected from the GEO database were analyzed with the bioinformatics tools to get the key blood miRNAs in gastric carcinoma. RRA analysis were performed to get the ranking of the corresponding miRNAs. Then the 20 most differentially expressed blood miRNAs (10 up-regulated and the other 10 down-regulated) became the aims to predict the target genes and the relative biological activities. There were 691 up-regulated differentially expressed genes and 1074 down-regulated genes which might be directly silenced by the 20 blood miRNAs. GO and KEGG enrichment analysis were proceeded on the differentially expressed genes by DAVID. The results suggested the biological processes and the signaling pathways in which the differentially expressed genes were mainly involved in this system. On this basis, analysis of the target genes – encoded proteins with PPI network suggested five crucial blood miRNAs which were hsa-miR-4276, hsa-miR-575, hsa-miR-125a-3p, hsa-miR-124-3p and hsa-miR-29b-3p. The results in human blood detection and survival curve analysis confirmed the important roles of the key blood miRNAs in gastric carcinoma. ROC analysis suggested hsa-miR-124-3p, hsa-miR-125a-3p and hsa-miR-29b-3p could be useful in gastric cancer diagnosis, especially in combination.

MiRNAs have been identified as a key regulator in complex biological processes, including the pathogenesis of cancer [10]. Human cancers express the characteristics such as sustained proliferation signals, activation of invasion and metastasis, angiogenesis, escape from immune destruction and so on [11]. MiRNAs can be involved in the every feature and affect multiple signal pathways [12]. Blood miRNAs are becoming one of the most useful biomarkers in the diagnosis and treatment of tumors. MiRNAs have the specific expression profile in different cancer cells and tissues which can enter the circulation [13]. Circulating free miRNA can be detected in blood, plasma and other body fluids [14]. Mature miRNAs are very stable in body fluids [15] and have high specificity in different cancer states [16], which determines miRNAs a potential non-invasive tumor marker. There have been some research on the blood miRNAs in gastric carcinoma, such as miR-210, miR-1, miR-20a, miR-34a, miR-423-5p, and so on [17, 18]. In this research, with the bioinformatics tools, five new blood miRNAs, which were hsa-miR-125a-3p, hsa-miR-124-3p, hsa-miR-29b-3p, hsa-miR-4276 and hsa-miR-575, especially hsa-miR-124-3p and hsa-miR-125a-3p, might be the potential targets in gastric carcinoma diagnosis and treatment. The predicted key miRNAs and the relative target genes were also involved in the biological activities which are closely correlant to tumorigenesis. For example, platelet-derived growth factor receptor signaling pathway and transcription RNA polymerase II both play important roles in gastric carcinoma and development [19, 20]. Focal adhesion and PI3K-Akt signaling pathway are closely related to the carcinogenesis [21, 22]. These results detected the importance of the selected blood miRNAs in gastric carcinoma.

It has been explored that hsa-miR-125a-3p could influence breast cancer stem cells by targeting leukemia inhibitory factor receptor and regulating the Hippo signal pathway [23]. In addition, hsa-miR-125a-3p is

related to the tumorigenesis of prostate cancer, colon cancer, and so on [24]. However, the research of hsa-miR-125a-3p on gastric carcinoma is still few. In this research, the abnormal expression of hsa-miR-125a-3p was identified in the blood of gastric cancer patients, and the correlation between its expression and disease might be related to age and gender. At the same time, the downstream target of hsa-miR-125a-3p was predicted as PR domain zinc finger protein 1 (PRDM1) gene. PRDM1 is the protein involved in regulating the differentiation of B cells and T cells, which plays an important role in immunosuppression [25]. Previous reports have shown that PRDM1 is associated with many kinds of cancers, such as adrenocortical cancer, colon cancer, acute myeloid leukemia, brain cancer and lung cancer [26]. The expression of PRDM1in non-germinal center B cell-like (non-GCB) patients was also associated with a worse prognosis [27]. In this research, PRDM1also showed its correlation with the survival possibility of gastric cancer patients. Therefore, it may have high probability that hsa-miR-125a-3p is participating in the gastric carcinogenesis by inhibiting the expression of PRDM1, which need in-depth research later.

By tracing the upstream miRNAs of the target genes, the results of Cytoscape which screened out key node genes from the PPI network showed the appearance frequency of hsa-miR-124-3p was the highest in the key miRNAs. However, there was no clear conclusion about the relationship between hsa-miR-124-3p and tumorigenesis in the miRbase database. Both the examination in human blood species and the analysis of the survival curve suggested the correlation between hsa-miR-124-3p and the gastric carcinogenesis. The further ROC analysis also suggested the importance of hsa-miR-124-3p in gastric cancer diagnosis. In the predicted target genes of hsa-miR-124-3p, a number of genes had a higher correlation with the prognosis of gastric cancer, such as ANXA5 and CAV1. ANXA5 is a member of the Annexin family and is involved in the tumorigenesis and development of a variety of cancers [28]. It plays the role on gastric cancer by regulating the ERK signal pathway [29]. Then low expression of CAV1 means decreased expression of E-cadherin, cell morphology changes and an increase in the migration ability of gastric cancer cells [30]. Other miRNAs, such as miR-6792-3p, can also be involved in gastric carcinogenesis by their inhibitory effect on the target CAV1 [31]. So, it can be speculated that hsa-miR-124-3p may facilitate gastric carcinoma by negatively regulating multiple downstream target genes in one network.

Hsa-miR-29b-3p plays a key role in the tumorigenesis of glioblastoma [32] and metastatic colorectal cancer [33]. Hsa-miR29b-3p can also regulate the expression of VEGFA in pancreatic ductal adenocarcinoma [34]. In addition, as one of the important target genes of hsa-miR-29b-3p, activation of PER1 can inhibit the progression of pancreatic cancer [35]. Although the blood check results didn't display the correlation between hsa-miR-29b-3p and gastric cancer, the analysis of the patient prognosis and diagnostic value analysis detected the importance of hsa-miR-29b-3p in gastric cancer diagnosis. Blood miR-125-3p, hsa-miR-124-3p and hsa-miR-29b-3p together showed the highest AUC value in ROC curve, and the second one is for the combination of miR-125-3p and hsa-miR-124-3p, while the third is among the single miRNAs. The joint detection of the key blood miRNAs could be the biomarkers for the diagnosis and treatment monitor in gastric cancer. The role of the miRNAs on the negatively regulation of target genes can also be studied deeply.

MSRB3 has been identified to be the key protein that can regulate the proliferation and migration of gastric cancer cells which might be an effective marker to predict gastric cancer peritoneal metastasis and poor prognosis [36, 37]. MSRB3 was predicted the target gene of hsa-miR-575 in this research. It was also detected in blood check that hsa-miR-575 was differentially expressed in gastric cancer, and the correlation between its expression and disease might be related to age and gender. Hsa-miR-575 might has the trend correlated with the prognosis of gastric cancer patients, but without significant difference. More research will be needed to determine the role of hsa-miR-575 which can negatively regulateMSRB3 in gastric carcinogenesis.

Hsa-miR-4276 is involved in the apoptosis process of pulmonary endothelial cells during acute lung injury [38]. There is few relevant research to prove that hsa-miR-4276 is related to tumorigenesis, also with its target genes RNF217 and IP6K1. On the other hand, among the key nodes obtained by Cytoscape, the number of downstream genes of hsa-miR-4276 was 24 times. This suggested that hsa-miR-4276 and its target genes may have a strong correlation with gastric cancer. Unfortunately, none of the results from patient blood check, prognosis analysis, and ROC analysis suggested this possibility. However, it might need more in-depth exploration.

In summary, all the research implied the accuracy and feasibility with the abnormal expression level of the key miRNAs in blood for gastric cancer prevention, diagnosis and treatment result testing. Through bioinformatics analysis and check in human blood species, five key blood miRNAs could be involved in gastric carcinoma which were hsa-miR-125a-3p, hsa-miR-124-3p, hsa-miR-29b-3p, hsa-miR-575 and hsa-miR-4276, especially the combination of hsa-miR-125a-3p, hsa-miR-124-3p and hsa-miR-29b-3p. More research is needed in the future to further confirm the mechanism and biological activities of the miRNAs in gastric carcinoma. The blood miRNAs may become new biomarkers for the early diagnosis of gastric cancer.

Declarations

Ethics approval and consent to participate The work has been approved by the Ethics Committee of Shandong University School of Basic Medical Sciences (No. ECSBMSSDU2021-1-097).

Consent for publication: Not applicable.

Availability of data and materials: The data that were used for Bioinformatics analysis in this study are openly available in GEO at https://www.ncbi.nlm.nih.gov/geo/. The authors confirm that the data supporting the findings of this study are available within the manuscript and its supplementary materials. The specific data are available from the corresponding author upon reasonable request.

Competing interests: The authors declare that they have no competing interests.

Funding: The work has been granted by Shandong University Student Innovation and Entrepreneurship Training Program (No.: 2019325, S202110422208) and National Natural Science Foundation of China

(No.: 81871627).

Authors' contributions: ZX, XY, RZ and JZ designed the manuscript, reviewed the literature, compiled the data and wrote the manuscript. XLL collected the human blood samples and helped in organizing information. SL, QW, XZL and FL analyzed the data and revised the manuscript. JZ supervised the study. All authors read and approved the final manuscript for publication.

Acknowledgements: Thanks to Prof. Lixiang Wang and Dr. Kaiyue Sun of Shandong University for additional revision of the manuscript.

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Figures

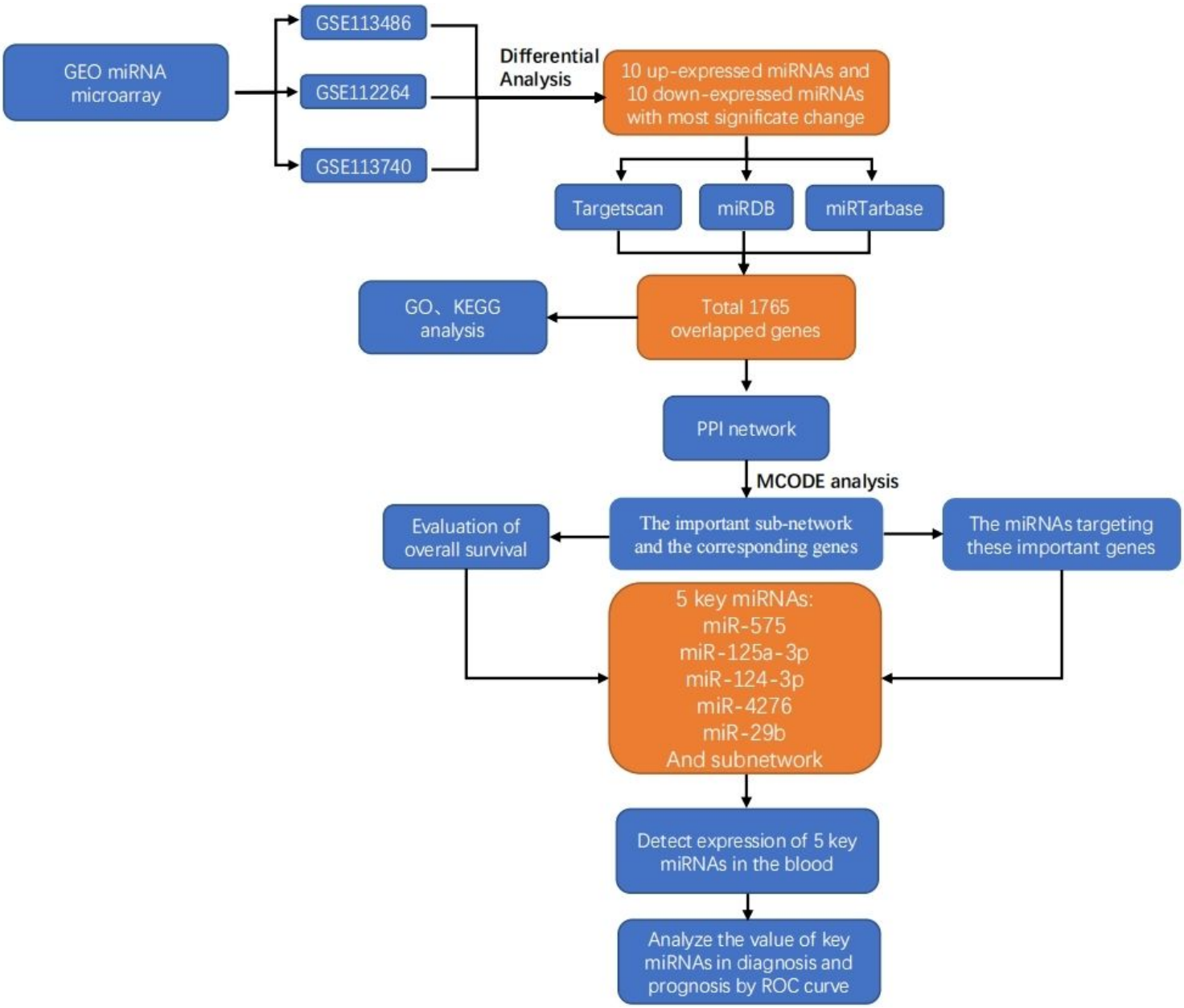

Figure 1

Flow chart of the methods utilized in the study.

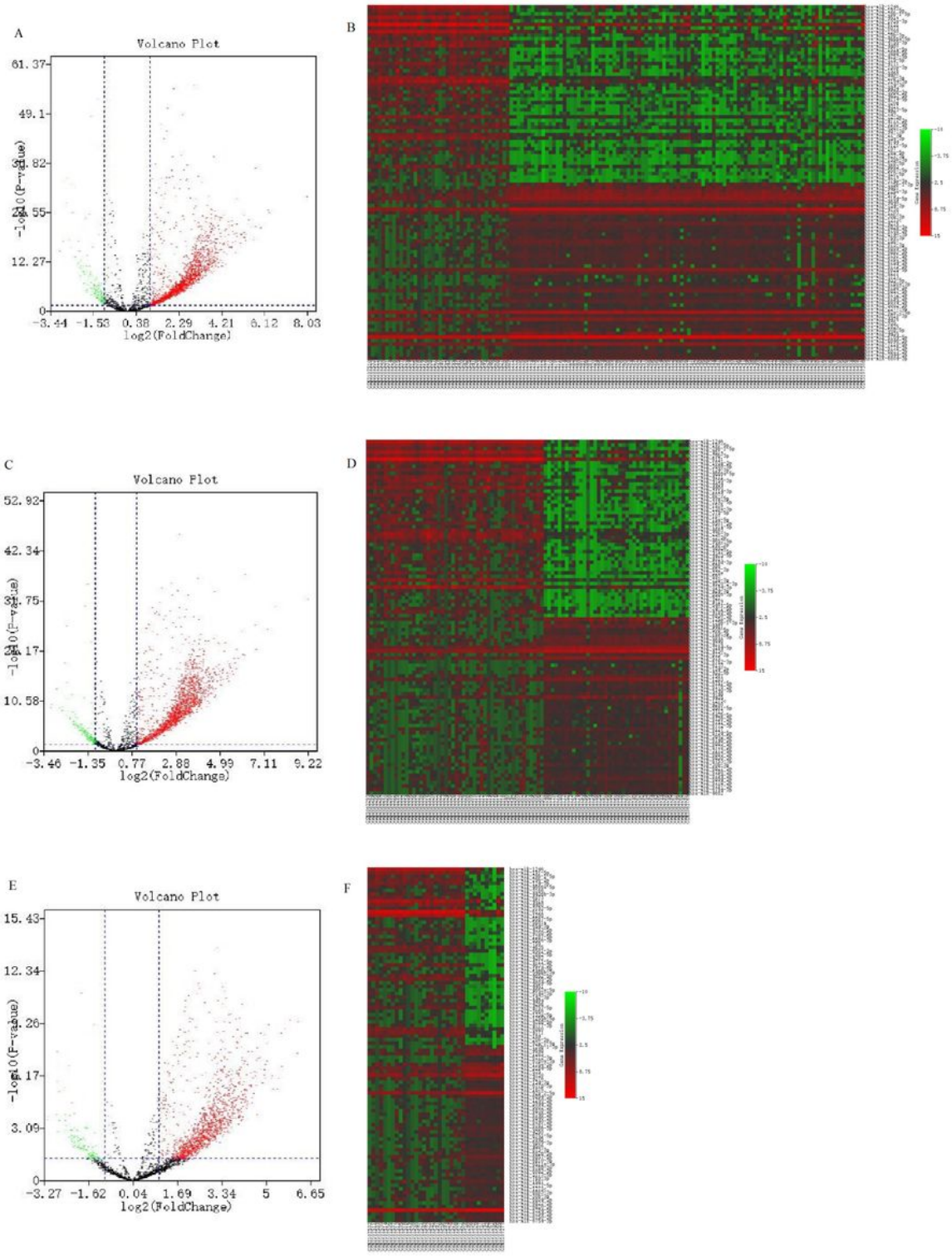

Figure 2

The differentially expressed blood miRNAs in gastric carcinoma. (A) The differently expressed miRNAs in the bloods of gastric cancer patients compared with the normal controls from the dataset GSE113486. (B) The most significantly up-regulated 50 miRNAs and down-regulated 50 miRNAs in GSE113486. (C) The differently expressed miRNAs in the bloods of gastric cancer patients compared with the normal controls from the dataset GSE112264. (D) The most significantly up-regulated 50 miRNAs and down-

regulated 50 miRNAs in GSE112264. (E) The differently expressed miRNAs in the bloods of gastric cancer patients compared with the normal controls from the dataset GSE113740. (F) The most significantly up-regulated 50 miRNAs and down-regulated 50 miRNAs in GSE113740.

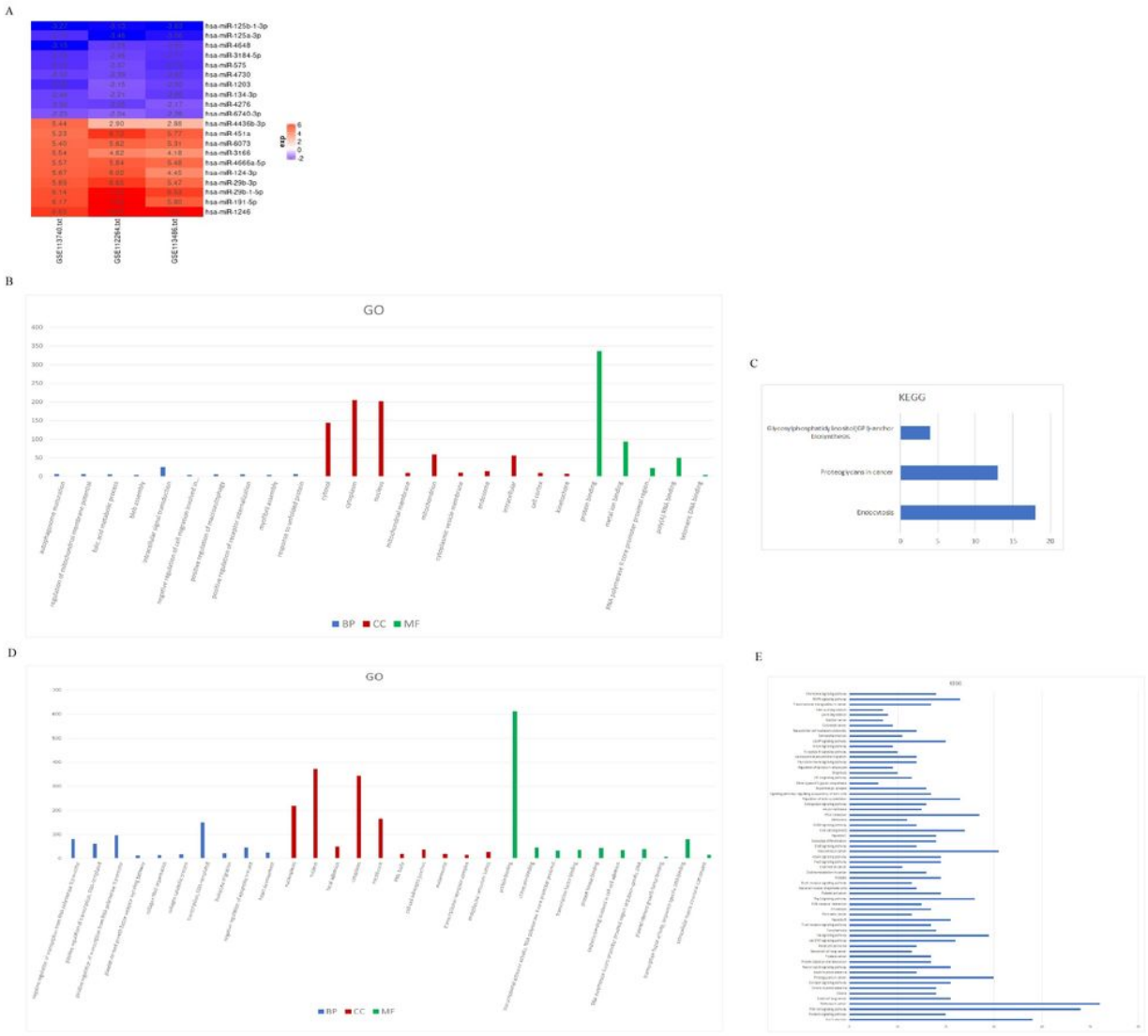

Figure 3

The GO and KEGG enrichment results of target genes that were directly regulated by the key blood miRNAs. (A) The highest-scoring up-regulated and down-regulated miRNAs obtained by the RRA algorithm. (B) The main biological processes, molecular functions and cellular components of down-regulated miRNAs and the corresponding up-regulated target genes. (C) KEGG- signaling pathway enrichment results of down-regulated miRNAs and the corresponding up-regulated target genes. (D) The main biological processes, molecular functions and cellular components of up-regulated miRNAs and the corresponding down-regulated target genes. (E) KEGG- signaling pathway enrichment results of up-regulated miRNAs and the corresponding down-regulated target genes.

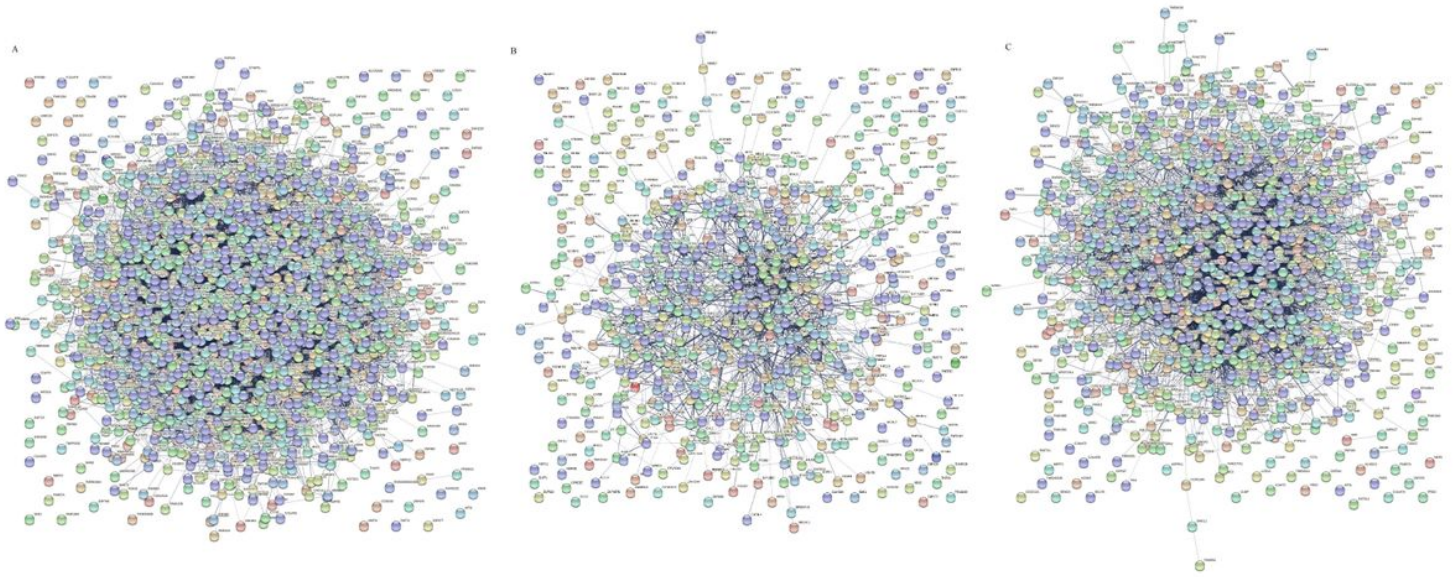

Figure 4

The analysis of the proteins interaction network by STRING database. (A) The network of all the 20 most differently expressed blood miRNAs and the corresponding target genes-coded proteins. (B) The PPI of the up-regulated genes-encoded proteins. (C) The PPI of the down-regulated genes-encoded proteins.

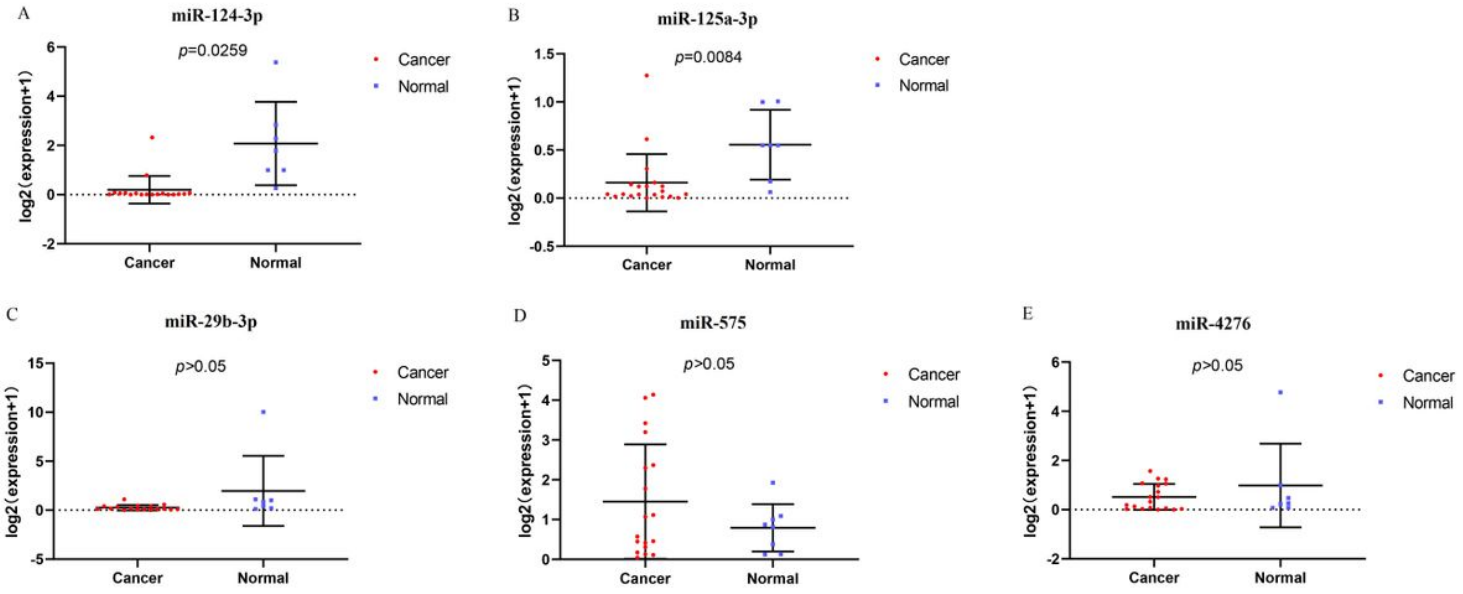

Figure 5

The expression of key miRNAs in human blood species by qRT-PCR detection. (A) The expression of hsa-miR-124-3p showed significant difference in the blood samples of gastric cancer patients ($P < 0.05$ *vs.* normal volunteer). (B) The expression of hsa-miR-125a-3p increased remarkably in the blood samples of gastric cancer patients ($P < 0.01$ *vs.* normal volunteer). (C) The expression of hsa-miR-29b-3p showed no significant difference in the blood samples of gastric cancer patients compared with the normal volunteer ($P > 0.05$). (D) The expression of hsa-miR-575 showed no significant difference in the blood samples ($P >$

0.05, gastric cancer patients *vs.* normal volunteer) (E) The expression of hsa-miR-4276 showed no significant difference in the blood samples ($P > 0.05$, gastric cancer patients *vs.* normal volunteer).

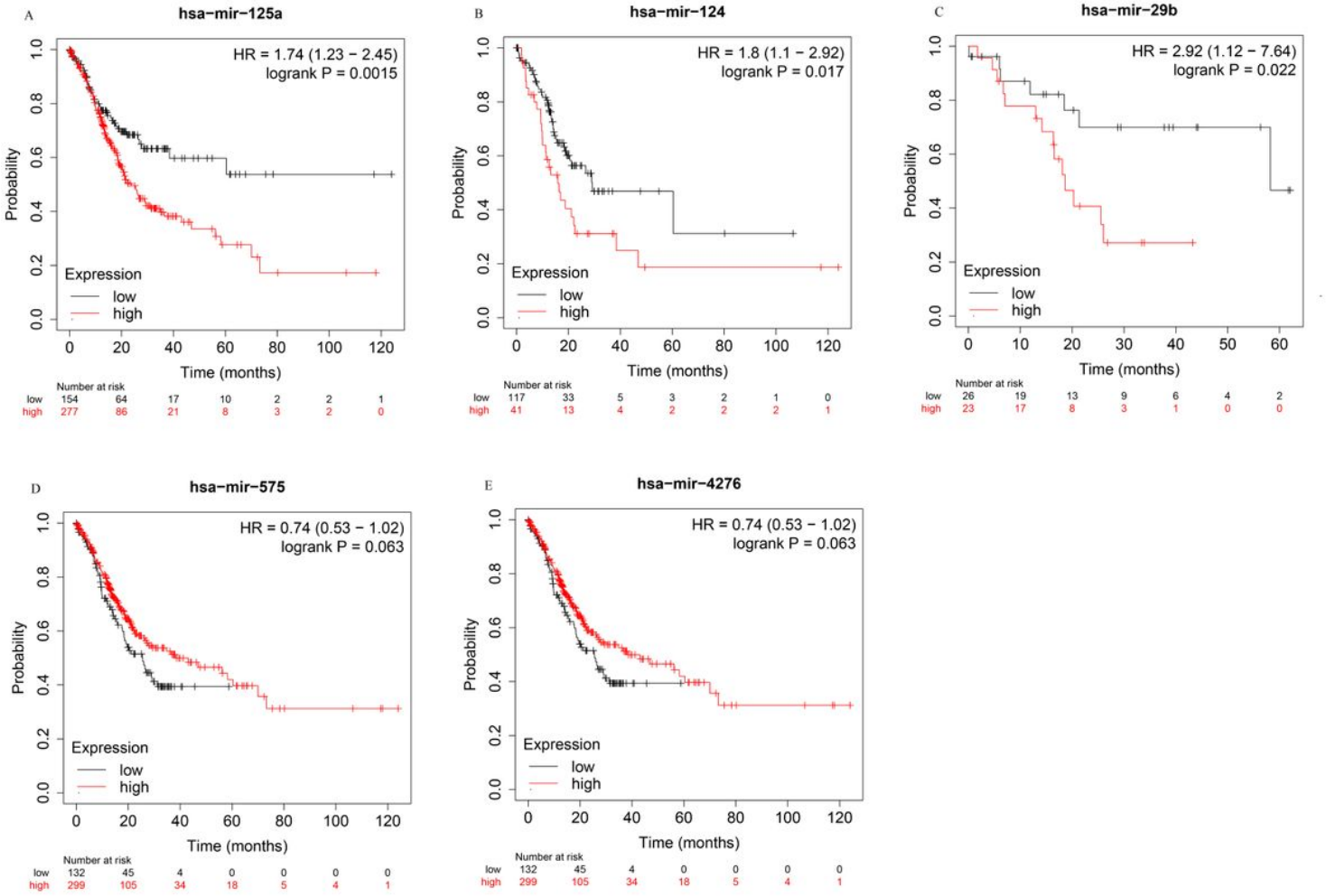

Figure 6

Survival analysis results of the key miRNAs. (A) Kapler-Meier Plotter analysis showed that the high expression of hsa-miR-125-3p, which was predicted as an oncogene, significantly reduced the survival rate of patients ($P < 0.01$). (B) High expression of hsa-miR-29b-3p with tumor suppressive effect could improve the survival rate of patients ($P < 0.05$). (C) The high expression of hsa-miR-29b-3p, which was predicted as an oncogene, significantly reduced the survival rate of patients ($P < 0.05$). (D) High expression of hsa-miR-575 with tumor suppressive effect could improve the survival rate of patients to a certain extent, but there was no significant difference (P=0.063). (D) High expression of hsa-miR-4276 with tumor suppressive effect could improve the survival rate of patients to a certain extent, but there was no significant difference (P=0.063).

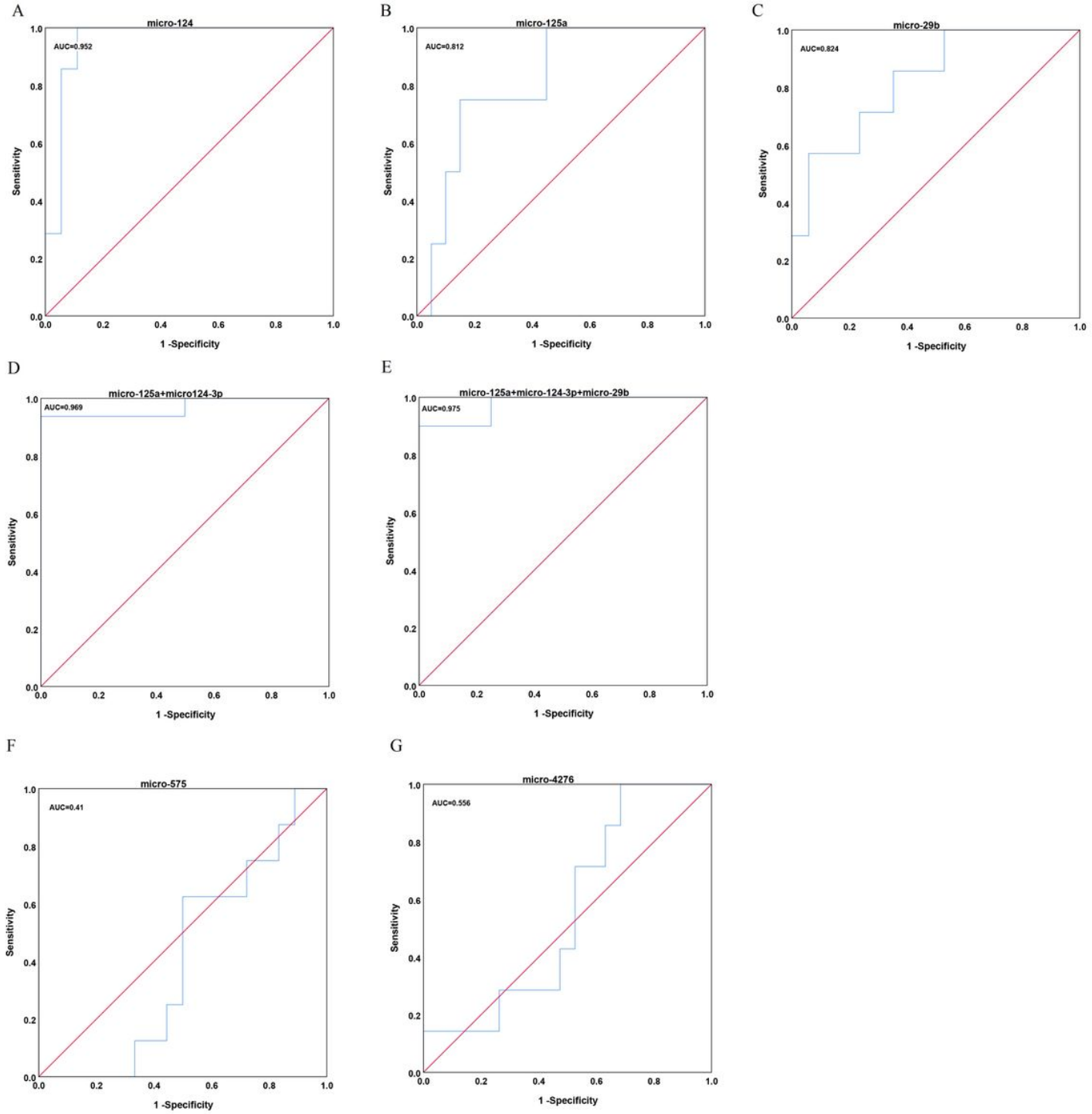

Figure 7

Hsa-miR-124-3p, Hsa-miR-125-3p and hsa-miR-29b-3p could have diagnostic value in gastric cancer determined by ROC analysis. (A) The value of hsa-miR-124-3p area under the ROC curve (AUC) was 0.952, $P < 0.001$. (B) The value of hsa-miR-125a-3p AUC was 0.812, $P < 0.01$. (C) The value of miR-29b-3p AUC was 0.824, $P < 0.01$. (D) The combination of miR-124-3p and miR-125-3p AUC was 0.969, $P < 0.001$. (E) The combination of miR-124-3p, miR-125-3p and miR-29b-3p AUC was 0.975, $P < 0.001$. (F) The value of hsa-miR-575 AUC was 0.41, $P > 0.05$. (G) The value of hsa-miR-4276 AUC was 0.556, $P > 0.05$.

Supplementary Files

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