



**Original Article**

## Hsa-miR-5581-3p and Hsa-miR-542-3p Target the *F8* Gene in Hemophilia A without *F8* Mutations

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**Competing interests:** The authors declare no conflict of Interest.

**Abstract. Objective:** This study aims at uncovering the effects of microRNAs (miRNAs) on the *F8* gene and FVIII protein in hemophilia A (HA).

**Methods:** *F8*-targeting miRNAs were predicted by TargetScan, miRDB, and starBase. MiRNAs, predicted by at least two of the three databases, were selected for further study, and their expressions in the blood of HA patients without *F8* mutations and healthy controls were detected. A dual-luciferase reporter assay was performed to verify the binding between hsa-miR-5581-3p/hsa-miR-542-3p and *F8*. In addition, the regulation of *F8* by hsa-miR-5581-3p/hsa-miR-542-3p was investigated in human umbilical vein endothelial cells (HUVECs) and lymphoblastoid cell line (LCL) that displayed endogenous expression of FVIII. qRT-PCR was used to detect the expressions of miRNAs and *F8* gene, and Western blotting was conducted to measure the expression of FVIII protein.

**Results:** A total of 42 *F8*-targeting miRNAs were predicted by at least two of the three databases. Among these miRNAs, hsa-miR-5581-3p and hsa-miR-542-3p were highly expressed in the blood of HA patients and have not been reported in previous studies of HA. Both hsa-miR-5581-3p and hsa-miR-542-3p could bind the 3'UTR of *F8* mRNA. Upregulation of hsa-miR-5581-3p or hsa-miR-542-3p suppressed the expressions of *F8* mRNA and FVIII protein in HUVECs and LCL cells.

**Conclusion:** Hsa-miR-5581-3p and hsa-miR-542-3p target the *F8* gene and suppress the expression of FVIII protein, which may contribute to the development of HA without *F8* mutations.

**Keywords:** Hsa-miR-5581-3p; Hsa-miR-542-3p; *F8* gene; FVIII; Hemophilia A.

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**Introduction.** Hemophilia is a hereditary bleeding disorder resulting from deficiency or dysfunction of coagulation protein factor VIII (FVIII) and IX (FIX), leading to hemophilia A (HA) and hemophilia B (HB), respectively. The prevalence of HA is about fourfold higher than that of HB, and the prevalence of severe

hemophilia is about 37% of all cases.<sup>1</sup> Severe hemophilia is manifested by spontaneous muscle or intraarticular hemorrhage, and recurrent joint hemorrhages can result in progressive tissue damage and joint.<sup>2</sup> Prophylactic factor replacement is currently the standard treatment option for hemophilia, which is dependent on frequent

intravenous injections.<sup>3</sup> However, among a list of novel treatment strategies for hemophilia, gene therapy shows a great appeal due to its potential for endogenous production of FVIII or FIX by transferring a functional gene to replace the deficient gene.<sup>4</sup>

In HA, the deficiency of FVIII is mainly caused by mutations in the *F8* gene. Intron 22 and intron 1 inversions are the most frequent *F8* variants in HA patients, followed by recurrent mutation at nucleotide 6046 (c.6046C>T) in the *F8* gene.<sup>5</sup> Missense mutations in this region (c.6046C>T/p.R2016W) damage secretion and activity of FVIII and also impede the correct pre-mRNA splicing, which further impairs FVIII activity.<sup>6</sup> Despite clinically reportable DNA variants in 98.1% of HA patients,<sup>7</sup> a small portion of HA patients is not affected by *F8* variants, which encourages us to find the mechanism for mutation-independent FVIII deficiency.

MicroRNAs (miRNAs) are the most-investigated class of small non-coding RNAs (ncRNAs) for their ubiquitous regulation in the human genome. MiRNAs mainly regulate gene expression in cell cytoplasm in a sequence-specific manner by recruiting an RNA-induced silencing complex to their target RNAs.<sup>8</sup> This miRNA-target interaction results in mRNA degradation or translational repression according to the degree of complementarity.<sup>9</sup> Numerous functional studies have proved a causal link between miRNA dysregulation and human diseases, particularly cancers.

Rosset et al. firstly found a single nucleotide polymorphism in the 3'UTR of *F8* (c.8728A>G, rs1050705) contributed to the complementarity between *F8* 3'UTR and the seed sequences of miR-26a-5p and miR-26b-5p, which further modified the FVIII residual clotting activity in HA patients.<sup>10</sup> A previous study reported that miR-1246 was upregulated in the whole blood of HA patients, and this ncRNA could suppress *F8* expression by binding to the non-coding region of *F8* mRNA.<sup>11</sup> Jankowska et al. identified miR-30c-5p and miR-374b-5p as direct mediators of *F8* gene and FVIII in HA patients with normal *F8* genotypes.<sup>12</sup> They also found that murine miRNAs, including miR-208a, miR-351 and miR-125a, could target the 3'UTR of *F8* mRNA in mouse models and mammalian cells.<sup>13</sup> The above evidence strongly supports the involvement of miRNAs in the pathogenesis of HA.

The author applied three online databases to predict the *F8*-binding miRNAs and detected their expressions in the blood of HA patients without *F8* gene mutations. Among the upregulated *F8*-binding miRNAs, hsa-miR-5581-3p and hsa-miR-542-3p were selected for further investigations since they were not reported in previous studies of HA. The function of these two miRNAs was experimentally verified.

## Materials and methods.

*Prediction of F8-targeting miRNAs.* *F8*-targeting

miRNAs were predicted by TargetScan ([http://www.targetscan.org/vert\\_72/](http://www.targetscan.org/vert_72/)), miRDB (<http://www.mirdb.org/>) and starBase (<http://starbase.sysu.edu.cn/index.php>). MiRNAs predicted by at least two of the three databases were selected for further investigations.

*Blood samples.* Blood samples were taken from two HA patients (one mild and one moderate) without mutations in the *F8* gene and three healthy controls. The participants were enrolled at the Hematology Department of Henan Provincial People's Hospital. Tubes containing sodium citrate anticoagulant were used for the blood collection. The blood samples were mixed with RNAlater Solution (Qiagen, Valencia, CA, USA) and stored at -20°C until RNA isolation. Mutations in intron 1/22 and all exons of the *F8* gene were analyzed by next-generation sequencing and determined by comparison with the reference (NG\_011403.1). Both the two HA patients had low FVIII activity (4.7 IU/dL and 19 IU/dL), but the RNA sequencing showed no mutations in the exon and intron of the *F8* gene in these two patients. Moreover, the level of vWF:Ag and the activity of other coagulation factors, including FII, FV, FVII, FIX, and FX, remained unchanged in these two HA patients. Mutations of the vWF, LMAN1, and MCFD2 genes were excluded. The collection and use of the blood samples obtained informed consent from all the participants and approval of the ethics committee of Henan Provincial People's Hospital.

*qRT-PCR.* A GenElute™ Plasma/Serum RNA Purification Mini Kit (Sigma-Aldrich, St. Louis, MO, USA) and TRIzol reagent (Invitrogen, Carlsbad, CA, USA) were used for total RNA extraction from blood samples and cells, respectively. Extracted RNA was reverse-transcribed using a reverse transcription kit (TaKaRa, Tokyo, Japan) based on the user's manual. Gene expression was detected by LightCycler 480 (Roche Diagnostics, Indianapolis, IN, USA) under the conditions provided by the SYBR Green Mix (Roche Diagnostics). The thermal cycling consisted of 10 s at 95°C, 45 cycles of 5 s at 95°C, 10 s at 60°C and 10 s at 72°C, and a final extension for 5 min at 72°C. PCR test of each sample was duplicated three times. U6 and GAPDH were used as the internal references of miRNA and mRNA, respectively. Data were analyzed using the  $2^{-\Delta\Delta Ct}$  method.  $\Delta\Delta Ct = (Ct_{\text{target gene}} - Ct_{\text{reference gene}})_{\text{experimental group}} - (Ct_{\text{target gene}} - Ct_{\text{reference gene}})_{\text{control group}}$ . Primers used for PCR amplification and their sequences are presented in **Table 1**.

*Dual-luciferase reporter assay.* Wild and mutant sequences of the binding sites of *F8* (wt-*F8* and mut-*F8*) were designed and synthesized according to the online prediction. The sequence contained the 3'UTR fragment

**Table 1.** Primer sequences.

Name of primer	Sequences
miR-5581-3p-F	CCTGAAGATCCTCCG
miR-5581-3p-R	TGGTGTCTGGAGTCG
miR-542-3p-F	AAAGTCAATAGTTAGA
miR-542-3p-R	TGGTGTCTGGAGTCG
U6-F	CTCGCTTCGGCAGCACA
U6-R	AACGCTCACGAATTTGCGT
F8-F	TGTGTGGTTTTGGTGCCGT
F8-R	GTTGCCACATAGGAGGCAT
GAPDH-F	GTGGCTGGCTCAGAAAAGG
GAPDH-R	GGGAGATTCAGTGTGGTGG

Note: F, forward; R, reverse.

complementary to the target miRNA. Wt-*F8* or mut-*F8* was inserted into pGL3-Promoter vector and cotransfected with 50 nM hsa-miR-5581-3p mimic, hsa-miR-542-3p mimic or mimic NC together with Renilla luciferase reporter vector pRL-TK into HEK293T cells. The cells were added with 100 µl of lysis buffer and placed on a shaker for 20 min at room temperature. Suspension of the cell lysates (50 µl) was added with luciferase reaction solution (50 µl, Promega, Madison, WI, USA) before Firefly luciferase activity was measured. The suspension was then mixed with 50 µl of Stop&Glo reagent (Promega) to measure Renilla luciferase activity (internal reference). The ratio of firefly luciferase activity to Renilla luciferase activity was the relative luciferase activity.

**Cell culture.** Human umbilical vein endothelial cells (HUVECs) and lymphoblastoid cell line (LCL) that displayed endogenous expression of FVIII, and human embryonic kidney cells (HEK293T) were acquired from the American Type Culture Collection (ATCC, Manassas, Virginia, USA). HUVECs were cultured in an endothelial basal medium (EBM-2, PromoCell, Heidelberg, Germany) containing the Supplement Mix (PromoCell). HEK293T cells were cultured in DMEM (Gibco, Grand Island, NY, USA) and LCL cells were in RPMI medium (Gibco). The media for HEK293T and LCL cells were supplemented with 10% fetal bovine serum, 100 U/ml penicillin and 100 mg/ml streptomycin. The cells were cultured at 37°C with 5% CO<sub>2</sub>.

**Cell transfection.** HUVECs and LCL cells were transfected with hsa-miR-5581-3p mimic, hsa-miR-542-3p mimic, hsa-miR-5581-3p inhibitor, hsa-miR-542-3p inhibitor or relevant negative controls (NC) (50 nM, GenePharma, Shanghai, China) using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA, USA). The cells were transfected in a 6-well plate containing serum-free medium, and each well was seeded with  $2 \times 10^5$  cells. Cells with over 70% transfection efficiency were

selected 24 h after the transfection for the following experiments.

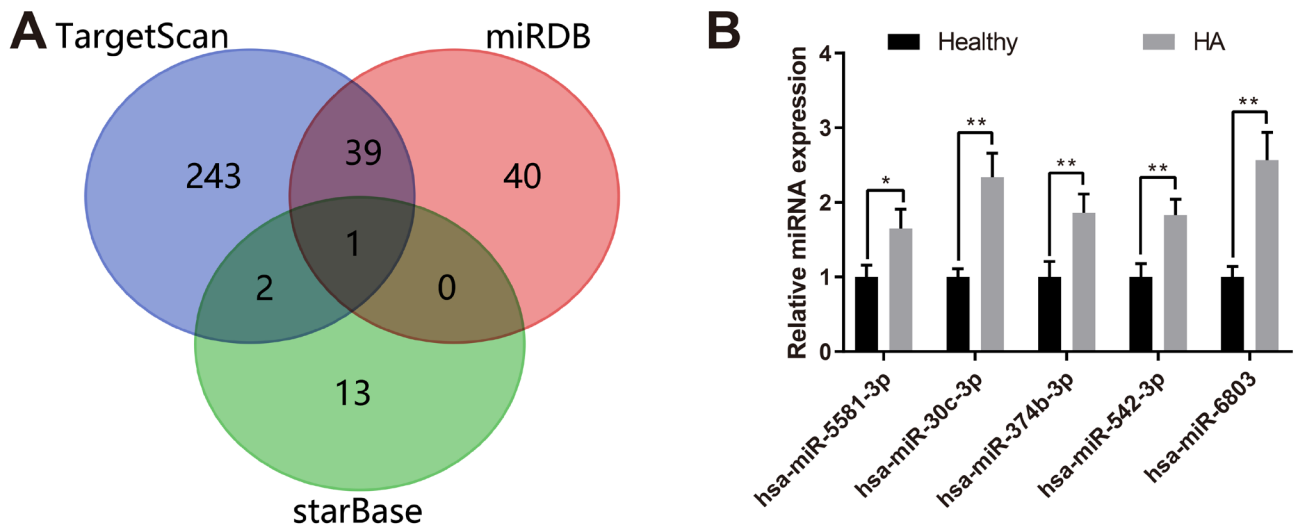
**Western blotting.** Cells were treated with RIPA lysis buffer (Beyotime, Shanghai, China) for protein extraction. Protein concentration was measured using a BCA kit (Beyotime). Protein samples were added into reducing SDS-PAGE loading buffer and boiled for 3 min. The proteins were electrophoresed at 80 V for 30 min. After bromophenol blue entered the separation gel, the electrophoresis was shifted to 120 V and maintained for 1 ~ 2 h. The proteins were transferred to a membrane in an ice bath. The protein transfer was carried out for 60 min with a current of 300 mA. The membrane was immersed in blocking buffer at room temperature for 60 min or at 4°C overnight. Primary antibodies against GAPDH (ab8245, 1:5000, Abcam, Cambridge, MA, USA) and FVIII (ab171825, 1:1000, Abcam) were incubated with the membrane on a shaker for 1 h at room temperature, followed by incubation of secondary antibody for 1 h at room temperature. The membrane was added with a color-developing solution and subjected to protein expression analysis. Recombinant FVIII protein antibody (ab158403, Abcam) was used as a positive control to detect FVIII protein. The bands were quantified by Image J software (version 1.46, National Institutes of Health).

**Statistical analysis.** GraphPad Prism 7 was used for statistical analysis. All data were expressed as mean ± standard deviation. *T*-test and One-way analysis of variance were used for two-group and multigroup comparisons, respectively. Tukey's test was conducted for post hoc multiple comparisons. Each experiment was repeated three times. *P* < 0.05 was considered statistically significant.

## Results.

***F8*-targeting miRNAs.** TargetScan, miRDB, and starBase predicted miRNAs that targeted the *F8* gene. Among these *F8*-targeting miRNAs, hsa-miR-5581-3p was predicted by all the three databases, and 41 miRNAs were predicted by two of the three databases (**Figure 1A**). qRT-PCR was used to detect the expressions of these 42 miRNAs (**Supplementary Table 1**) in the blood of two HA patients without *F8* mutations and three healthy controls. The experiment results showed higher expressions of hsa-miR-5581-3p, hsa-miR-30c-3p, hsa-miR-374b-3p, hsa-miR-542-3p and hsa-miR-6803-3p in HA patients than in healthy controls (**Figure 1B**, *P* < 0.05). Since hsa-miR-5581-3p and hsa-miR-542-3p have not been reported in previous studies of hemophilia without *F8* mutations, these two miRNAs were selected for further investigations in our study.

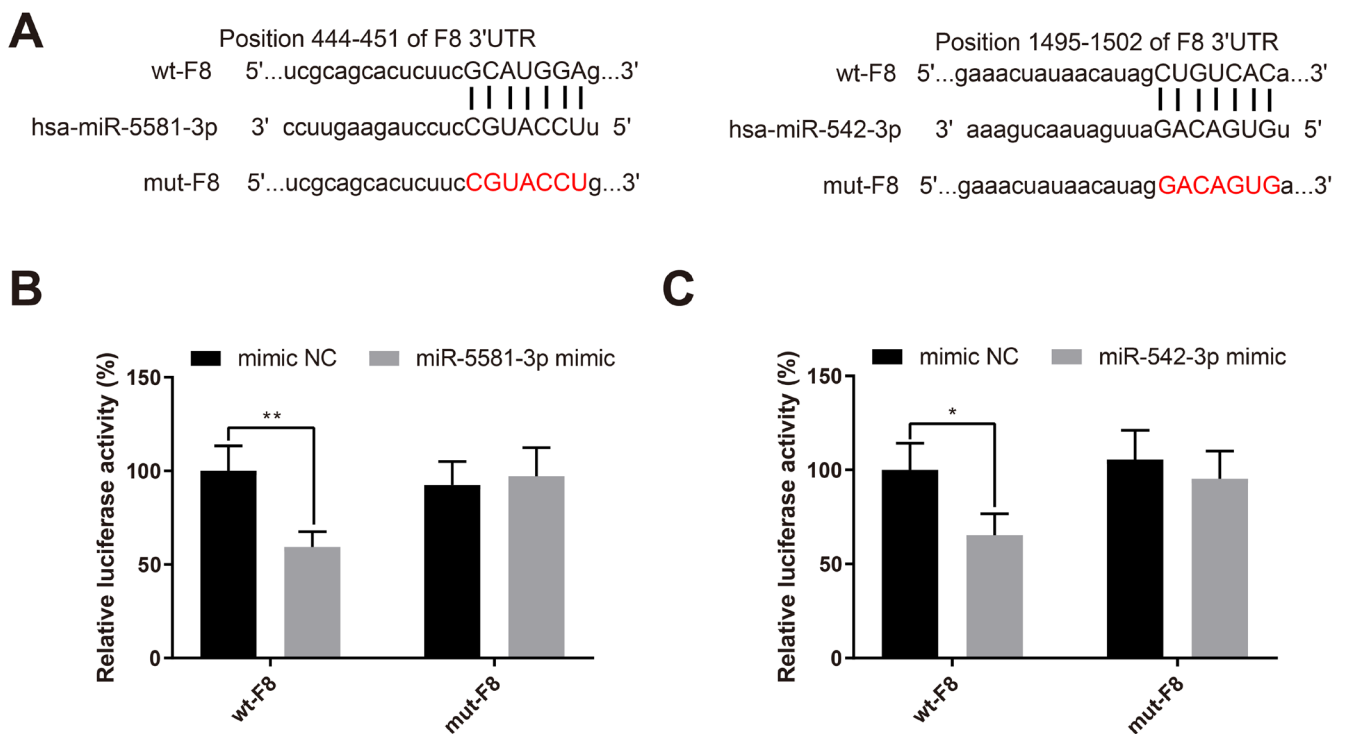
*F8* is a target gene of hsa-miR-5581-3p and hsa-miR-



**Figure 1.** *F8*-targeting miRNAs. Note: (A) TargetScan, miRDB and starBase predicted miRNAs that targeted the *F8* gene; (B) qRT-PCR was used to detect the expressions of *F8*-targeting miRNAs in HA patients and healthy controls. The data are presented as mean  $\pm$  standard deviation. Each experiment was repeated three times. \*  $P < 0.05$ , \*\*  $P < 0.01$ ; HA, hemophilia A.

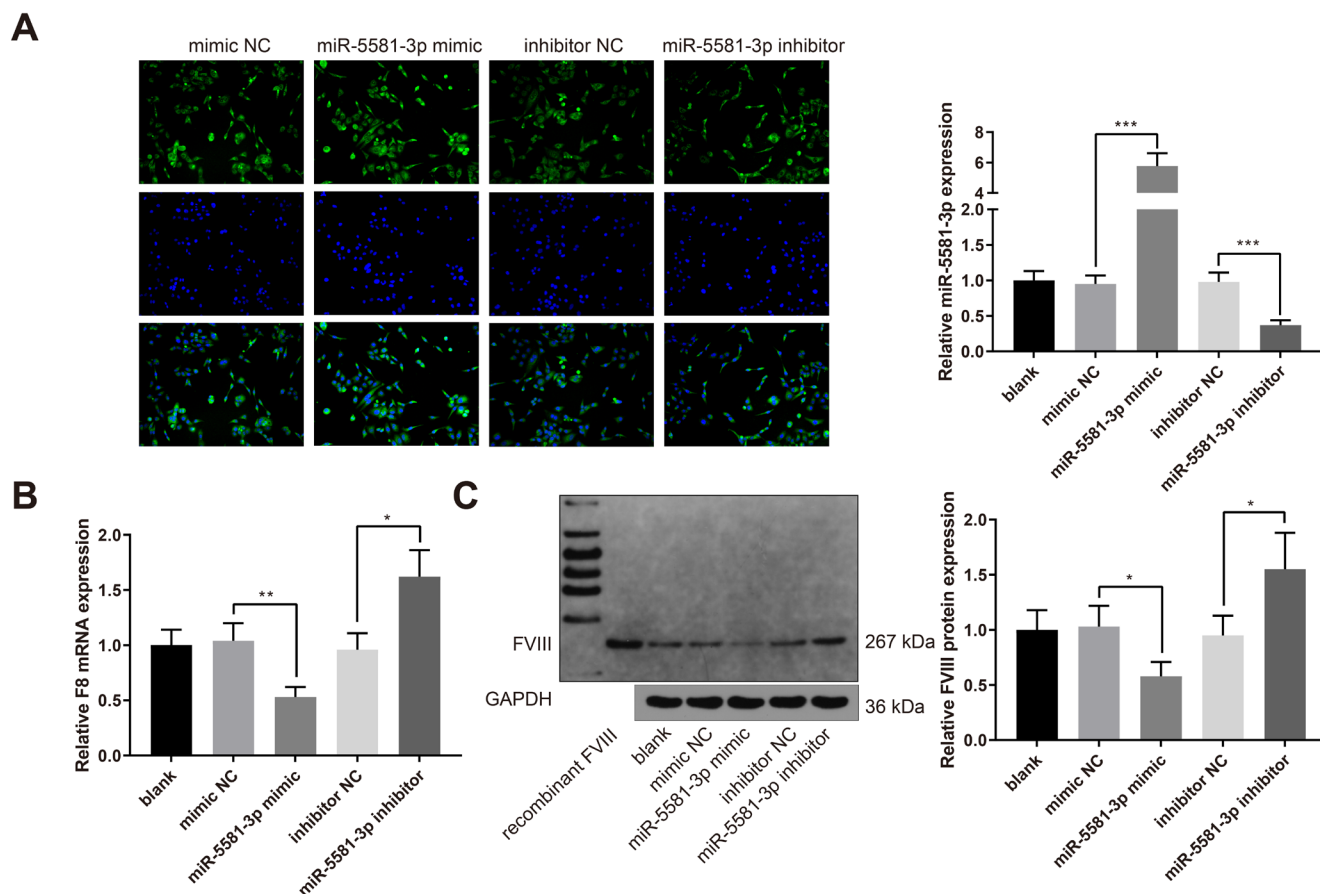
*542-3p*. The binding sites between *F8* and hsa-miR-5581-3p/hsa-miR-542-3p and the designed mutations are presented in **Figure 2A**. A dual-luciferase reporter assay was performed to verify the binding between *F8* and hsa-miR-5581-3p/hsa-miR-542-3p. HEK293T cells were transfected with hsa-miR-5581-3p mimic, hsa-miR-542-3p mimic or mimic NC together with luciferase reporter plasmids inserted with wt-*F8* or mut-*F8*. Transfection of

wt-*F8* + hsa-miR-5581-3p mimic or hsa-miR-542-3p mimic reduced the luciferase activity in the HEK293T cells (**Figure 2B-C**,  $P < 0.05$ ), while the luciferase activity in HEK293T cells transfected with mut-*F8* + hsa-miR-5581-3p/hsa-miR-542-3p mimic remained unchanged. These results validated the prediction that *F8* was targeted by hsa-miR-5581-3p and hsa-miR-542-3p.



**Figure 2.** *F8* is a target gene of hsa-miR-5581-3p and hsa-miR-542-3p. Note: (A) The binding sites between *F8* and hsa-miR-5581-3p/hsa-miR-542-3p and the designed mutations; dual-luciferase reporter assay was performed to verify the binding between *F8* and hsa-miR-5581-3p (B) or hsa-miR-542-3p (C) in HEK293T cells. The data are presented as mean  $\pm$  standard deviation. Each experiment was repeated three times. \*  $P < 0.05$ , \*\*  $P < 0.01$ .





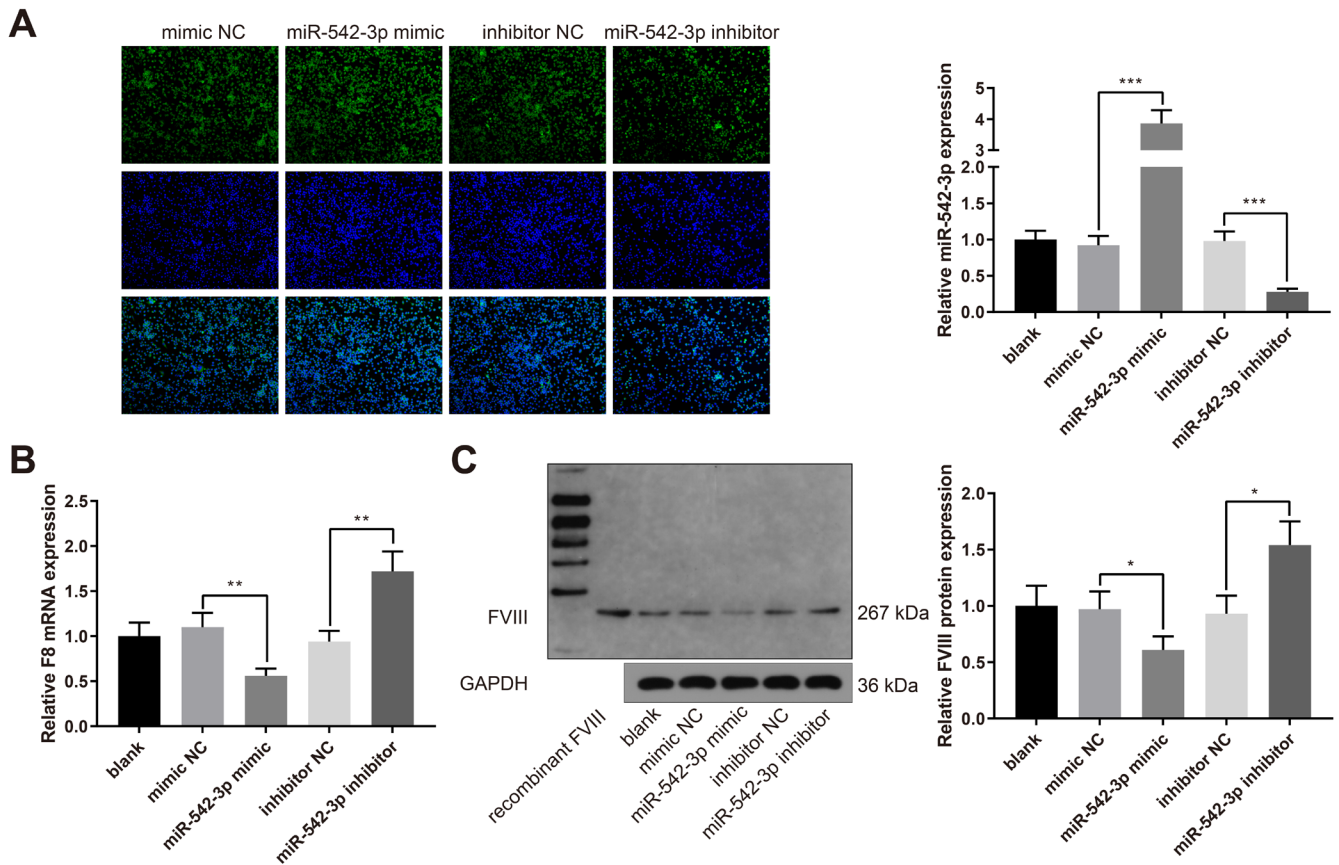
**Figure 3.** Hsa-miR-5581-3p suppresses the expressions of *F8* gene and FVIII protein in HUVECs. Note: HUVECs were transfected with mimic NC, hsa-miR-5581-3p mimic, inhibitor NC or hsa-miR-5581-3p inhibitor. qRT-PCR was used to detect the expressions of miR-5581-3p (A) and *F8* mRNA (B); (C) Western blotting was conducted to measure the expression of FVIII protein. The data are presented as mean  $\pm$  standard deviation. Each experiment was repeated three times. \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ ; HUVEC, human umbilical vein endothelial cells.

*Hsa-miR-5581-3p* suppresses the expressions of *F8* gene and FVIII protein. HUVECs exhibiting endogenous expression of FVIII were transfected with mimic NC, hsa-miR-5581-3p mimic, inhibitor NC or hsa-miR-5581-3p inhibitor. The results of qRT-PCR experiments showed that hsa-miR-5581-3p was upregulated in the miR-5581-3p mimic group while downregulated in the miR-5581-3p inhibitor group (Figure 3A,  $P < 0.001$ , vs. the mimic NC or inhibitor NC group). The expression of *F8* mRNA was decreased in the miR-5581-3p mimic group while increased in the miR-5581-3p inhibitor group (Figure 3B,  $P < 0.05$ , vs. the mimic NC or inhibitor NC group). Western blot analysis showed that the expression of FVIII protein was also decreased in the miR-5581-3p mimic group while increased in the miR-5581-3p inhibitor group (Figure 3C,  $P < 0.05$ , vs. the mimic NC or inhibitor NC group). Taken together, hsa-miR-5581-3p suppresses the expressions of *F8* gene and FVIII protein in HUVECs.

*Hsa-miR-542-3p* inhibits the expressions of *F8* gene and FVIII protein. LCL cells were transfected with mimic NC, hsa-miR-542-3p mimic, inhibitor NC, or hsa-miR-

542-3p inhibitor. The qRT-PCR experiments indicated that hsa-miR-542-3p was upregulated in the miR-542-3p mimic group while downregulated in the miR-542-3p inhibitor group (Figure 4A,  $P < 0.001$ , vs. the mimic NC or inhibitor NC group). The expression of *F8* mRNA was decreased in the miR-542-3p mimic group while increased in the miR-542-3p inhibitor group (Figure 4B,  $P < 0.01$ , vs. the mimic NC or inhibitor NC group). Western blot analysis showed that the expression of FVIII protein was also decreased in the miR-542-3p mimic group while increased in the miR-542-3p inhibitor group (Figure 4C,  $P < 0.05$ , vs. the mimic NC or inhibitor NC group). Taken together, hsa-miR-542-3p suppresses the expressions of *F8* gene and FVIII protein in LCL cells.

**Discussion.** Numerous causative DNA variants of the *F8* and *F9* genes are reported to impact bleeding severity and inhibitor development in hemophilia patients.<sup>14</sup> However, no causal mutations in the *F8* gene are detected in a small group of HA patients. Mutations in the 3'UTR of *F8* affect the splicing and expression of mRNA, which leads to reduced FVIII level and a mild



**Figure 4.** Hsa-miR-542-3p inhibits the expressions of *F8* gene and FVIII protein in LCL cells. Note: LCL cells were transfected with mimic NC, hsa-miR-542-3p mimic, inhibitor NC or hsa-miR-542-3p inhibitor. qRT-PCR was used to detect the expressions of miR-542-3p (A) and *F8* mRNA (B); (C) Western blotting was conducted to measure the expression of FVIII protein. The data are presented as mean  $\pm$  standard deviation. Each experiment was repeated three times. \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ ; LCL, lymphoblastoid cell line.

HA.<sup>15</sup> MiRNAs inhibit their targets through base-pairing interactions with the 3'UTR of target mRNAs, resulting in translation inhibition or mRNA degradation.<sup>16</sup> In this study, hsa-miR-5581-3p and hsa-miR-542-3p were found to interact with the *F8* gene and regulate the expression of FVIII.

A total of three databases, including TargetScan, miRDB, and starBase, were utilized to predict miRNAs that target the 3'UTR of *F8*. At least two databases predicted 42 miRNAs. Subsequently, their expressions in the blood of HA patients with normal *F8* genotypes were quantified. Hsa-miR-5581-3p, hsa-miR-30c-3p, hsa-miR-374b-3p, hsa-miR-542-3p, and hsa-miR-6803-3p were highly expressed in HA patients. Hsa-miR-5581-3p and hsa-miR-542-3p were selected for further investigations since they were not reported in previous studies of HA. In addition, luciferase reporter plasmids were used to validate the binding sites between hsa-miR-5581-3p/hsa-miR-542-3p and *F8*. The experiment results suggest that *F8* is a target of hsa-miR-5581-3p and hsa-miR-542-3p. Furthermore, the function of these two miRNAs was investigated in HUVECs and LCL that displayed endogenous expression of FVIII.

Hsa-miR-542-3p suppressed the expressions of *F8* mRNA and FVIII in LCL cells. MiR-542-3p is a versatile ncRNA that has been largely investigated. MiR-542-3p

acted as a tumor suppressor in many cancers such as colorectal cancer,<sup>17</sup> epithelial ovarian cancer,<sup>18</sup> hepatocellular carcinoma,<sup>19</sup> and breast cancer.<sup>20</sup> MiR-542-3p could also reduce chemoresistance in tumor cells and improve the antitumor efficacy of chemotherapy.<sup>21</sup> MiR-542-3p was upregulated in activated hepatic stellate cells and promoted fibrosis via inhibiting BMP-7.<sup>22</sup> In kidney, it contributed to fibrosis by targeting AGO1.<sup>23</sup> Through inhibition of BMP-7, miR-542-3p also suppressed the osteogenic differentiation of vascular smooth muscle cells in aging rats.<sup>24</sup> A study by Zhang et al. demonstrated that miR-542-3p facilitated bone formation by promoting SFRP1-mediated osteogenic differentiation in mesenchymal stem cells.<sup>25</sup> This study firstly proved the involvement of hsa-miR-542-3p in HA without *F8* mutations.

Overexpression of the-miR-5581-3p decreased the expressions of *F8* mRNA and FVIII in HUVECs, whereas its inhibition increased their expressions. MiR-5581-3p was the only one *F8*-targeting miRNA predicted by all the three databases; however, it has been seldom reported for its function. Available data showed that overexpression of miR-5581-3p promoted cellular activities in hepatocellular carcinoma by inhibiting cardiolipin synthase 1.<sup>26</sup> This study supplemented the knowledge regarding the physiological function of hsa-

miR-5581-3p.

**Conclusions.** Hsa-miR-542-3p and hsa-miR-5581-3p promote HA by targeting *F8* mRNA and inhibiting the expression of FVIII. Not all HA cases are caused by mutations in the *F8* gene, and the pathogenic mechanisms for atypical HA are worthy of investigation.

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<https://doi.org/10.1002/jcp.28383>

PMid:30825207



## Supplementary Files:

**Supplementary table 1.** The 42 *F8*-targeting miRNAs predicted by at least two of the bioinformatics tools.

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miR-1183  
miR-1244  
miR-1270  
miR-1286  
miR-1305  
miR-30a-3p  
miR-30c-3p  
miR-30e-3p  
miR-3151-3p  
miR-3188  
miR-3202  
miR-33a-5p  
miR-33b-5p  
miR-3682-3p  
miR-374b-3p  
miR-4264  
miR-4288  
miR-432-3p  
miR-4510  
miR-4522  
miR-4533  
miR-4749-3p  
miR-4768  
miR-4772-5p  
miR-4774-3p  
miR-4803  
miR-511-3p  
miR-532-5p  
miR-542-3p  
miR-5571-5p  
miR-5581-3p  
miR-5680  
miR-5695  
miR-585-5p  
miR-6127  
miR-6129  
miR-6130  
miR-6133  
miR-620  
miR-660-3p  
miR-6801-5p  
miR-6803

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