Supplementary Figure S1: Vector information. (A) psi-check2 vector. (B) vector for circRNA_010383. (C) vector for linear-010383.

Supplementary Figure S2. Bioinformatics analysis of the differentially expressed circRNAs in a mouse model of DN. (A) A scatter plot was used to assess the variation in circRNA expression between db/db mice (Y-axis) and control mice (db/m, X-axis; n=5, per group). The values of the x and y-axes in the scatter plot are the normalized signal values of the samples (log2 scaled). The green lines are fold-change lines. The top green line indicates a 2.0-fold increase in circRNA expression between the two compared groups, whereas the bottom green line indicates a 2.0-fold decrease in the expression. The distributions of the log2 ratios among samples were nearly the same after normalization. Black arrows indicate the location of the circRNA_010383. (B) The Volcano plot was constructed using the db/db mouse circRNA expression fold-change values and P-values. Red squares indicate differentially expressed circRNAs in db/db mice versus db/m mice (p<0.05). The vertical lines mark the fold-change values. The left vertical line corresponds to a 2-fold decrease, the right vertical line indicates a 2-fold increase, and the horizontal line marks a p-value of 0.05. Black arrows indicate the location of the circRNA_010383. (C) The circRNA category is shown in the bar diagram. Most of the differentially expressed circRNAs originate from the exons, some are from introns, and some are from other sources. (D) The distribution of differentially expressed circRNAs on mouse chromosomes.

Supplementary Figure S3: Schematic model of mutant miRNA-135a binding sequence in circRNA_010383. (A) Schematic model of mutation. (B-D) Sequencing

of mutation.

Supplementary Figure S4. Linear_010383 had no effects on synthesis of ECM proteins in mMCs and mTECs. (A-F) Representative western blot (A) and quantitative analysis of western blots of fibronectin, collagen Ⅰ (Col Ⅰ), α-SMA, TRPC1 and PCNA(B-F) of mMCs with linear-010383. (G-K) Representative western blot (G) and quantitative analysis of western blots of fibronectin, collagen Ⅰ (Col Ⅰ), α-SMA, and TRPC1 (H-K) of mTECs with linear-010383. Data are presented as the mean ± SD (n=3). **$p < 0.01$, *$p < 0.05$ versus normal glucose+vector.

Supplementary Figure S5: The circRNA_010383-induced inhibition of the synthesis of ECM proteins is reversed by the re-introduction of miR-135a. mMCs cultured in high-glucose medium were cotransfected with a circRNA_010383 vector or empty vector and miR-135a or NC. (A-F) Representative western blots (A) and quantitative analysis (B-F) of fibronectin, collagen Ⅰ (Col Ⅰ), α-SMA, TRPC1 and PCNA. Each bar represents the mean ± SD (n=3); *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$ versus NC + vector; #$p < 0.05$, ##$p < 0.01$ versus NC + circRNA_010383; \$\$\$$p < 0.001$, \$\$$p < 0.01$, \$$p < 0.05$ versus miRA-135a + vector.

Supplementary Figure S6: In vivo delivery of circRNA_010383 reduces proteinuria. Weight (A), and blood glucose (B) in circRNA_010383-treated db/db mice(triangles), db/db mice (squares), and db/m littermates (circles) were measured at the indicated weeks of age. Data are shown as mean ± SD. **$p < 0.01$ versus db/m mice at the same time point, &$p < 0.05$, &&$p < 0.01$ versus db/db mice at the same time point.