Supplementary Figure 1. PAS and MTS staining at 16 weeks after the induction of diabetes in male CD-1 mice. A single injection of STZ was performed in 8-week-old male CD-1 mice, which were sacrificed 16 weeks after the induction of diabetes. A: PAS staining and B: MTS staining are shown. The original magnifications were 300x in (A) and 100x in (B). Scale bar: 50 μm in each panel.

Supplementary Figure 2. TGF-β2-induced apoptosis in endothelial cells was suppressed with DPP-4 inhibitors. HMVECs were incubated with TGF-β2 (2.5 ng/ml) in the presence or absence of either linagliptin (A-D) or KR-62436 (E-H). Apoptosis was analyzed by AnnexinV labeling. The original magnification was 200x. Scale bar: 50 μm. D, H: Quantification of apoptotic cells per field. In each group, 6 fields were analyzed. The experiment was repeated twice and yielded the same data both times. Data are expressed as the means ± s.e.m. in the graph.
Supplementary Figure 3. mRNA microarray analysis. A. Heat map of the entire analyzed gene expression. Total RNA was isolated and used for synthesizing cDNA. cDNA was hybridized with Affymetrix Mouse Gene 1.0 ST Array. B. Ingenuity Pathway Analysis was utilized to select a cluster of genes that were involved in profibrotic programs. C. The profibrotic genes restored by linagliptin treatments are listed. Red and blue bars indicate the genes that were reduced and induced, respectively, in the diabetic kidneys. The x-axis indicates the ratio of restoration, and 1.0 (or -1.0) means the complete restoration of genes that were reduced (or induced) in diabetic mice by linagliptin. n=2 and representative data are shown for each group.
Supplementary Figure 4. qPCR analysis for microRNA 29 family. microRNAs are isolated from HMVEC cells in the presence or absence of TGF-\(\beta\)2 (5ng/ml) with or without linagliptin. Cells are harvested after 48 hours stimulation. N=5 or 6 in each group.

Supplementary Figure 5. inhibition of microRNA 29 family induced EndMT. A. Cells were transfected with antagomir or inhibitor for microRNA 29s (75 nM in final concentration) and 48 hours after transfection, cells were harvested and isolated protein were analyzed by western blot analysis. B. Boyden chamber cell migration assays were performed as described in the methods section. C. Migrated cells in the bottom layer of the Boyden chamber were counted in 5 different areas, and quantification was performed. Experiment was performed twice showing similar results.