Supplementary Information

Anti-inflammatory role of miR-146a in the pathogenesis of Diabetic Nephropathy

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Supplementary Figure Legends

Supplementary Figure 1: Characterization of renal function and gene expression in the non-diabetic miR-146a$^{-/-}$ mice. Non-diabetic 24 week old mice were used for phenotypic characterization (n=6) **(a)** Glomerular area and mesangial matrix expansion in WT and miR-146a$^{-/-}$ mice kidneys **(b)** Urinary albumin levels **(c)** Inflammatory and fibrotic gene expression in WT and miR-146a$^{-/-}$ mice kidneys. In all figures, data is presented as mean ± SEM. * represents statistically significant difference as compared to WT group; p values < 0.05.

Supplementary Figure 2: Baseline Macrophage gene expression in the non-diabetic miR-146a$^{-/-}$ mice. Inflammatory and M1/M2 gene expression in WT and miR-146a$^{-/-}$ mice (non-diabetic) peritoneal macrophages (n=6). Data is presented as mean ± SEM. data is presented as mean ± SEM. * represents statistically significant difference as compared to WT group; p values < 0.05.
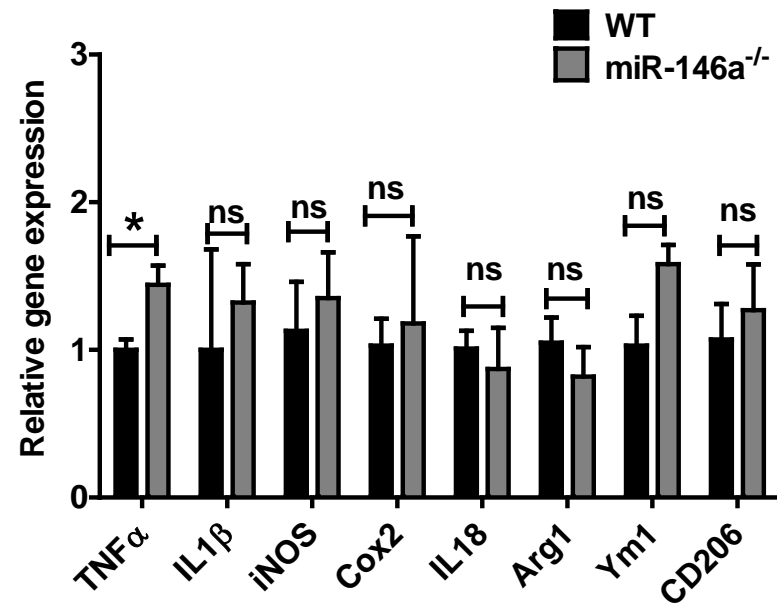

Supplementary Figure 3: Effect of miR-146a overexpression in macrophages. miR-146a mimic and scrambled control oligonucleotides were transfected (40 pmol) in peritoneal macrophages isolated from WT mice followed by TNFα (10ng/ml) treatment for 3 hours (n=5). Gene expression analysis was carried out for miR-146a target genes and other inflammatory markers. Data is presented as mean ± SEM. * represents statistically significant difference as compared to Scrambled-control group, # represents statistically different as compared to

Scrambled-TNFα group and $ indicates statistically significant as compared to miR-146a-mimic-control group; p values < 0.05.

Supplementary Figure 1
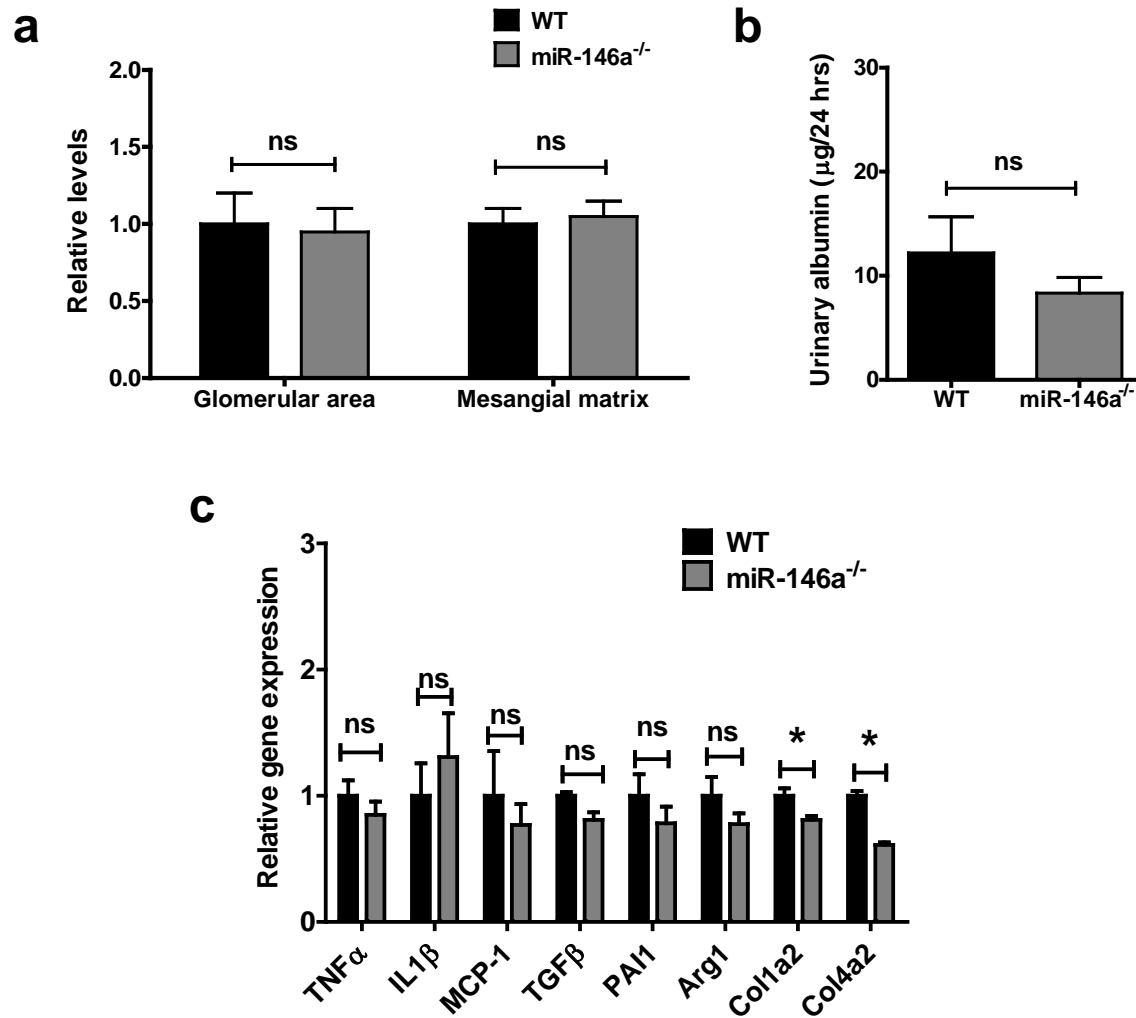
Supplementary Figure 2

Supplementary Figure 3