1 Supplemental Figure Legend

Fig. S1. The elevated METTL14-mediated RNA m6A modification in isolated 2 glomeruli from ADR-treated mice and diabetic db/db mice. (A) The m6A levels of 3 total RNAs in isolated glomeruli from kidneys of ADR-treated mice and their 4 corresponding controls quantified by colorimetric ELISA assay. (n=4). (B) The m6A 5 contents of total RNAs in isolated glomeruli from kidneys of diabetic db/db mice and 6 control db/m mice. (n=4). (C) Quantitative RT-PCR analysis of major methyltransferases 7 and demethyltransferases in isolated glomeruli from mice with ADR treatment or normal 8 9 controls. (n=4.) (D) Quantitative RT-PCR analysis of major m6A modifying enzymes in isolated glomeruli from db/db mice compared with control db/m mice. (n=4). (E) 10 Representative western blots and statistical analysis of METTL14 in isolated glomeruli 11 12 from kidneys of saline- or ADR-treated mice. (n=4). (F) Representative western blots and statistical analysis of METTL14 in isolated glomeruli from kidneys of db/db mice and 13 control db/m mice. (n=4). Data are presented as mean \pm SEM. *P < 0.05, **P < 0.01 vs. 14 15 control group.

Fig. S2. The up-regulated RNA m6A levels in human cultured podocytes under ADR or AGE condition. (A) The m6A levels of total RNAs in human cultured podocytes with 0.4 µg/ml ADR treatment and their normal controls quantified by colorimetric ELISA assay. (n=6). (B) The m6A contents of total RNAs in human cultured podocytes treated with 50 µg/ml AGE or BSA. (n=6).

Fig. S3. The decreased m6A modification of Sirt1 mRNA in isolated glomeruli of
 mice with podocyte-specific METTL14 deletion. Relative methylated Sirt1 mRNA
 levels in isolated glomeruli from METTL14^{flox/flox}/Cre⁺ mice compared with those from
 wild-type mice. (n=4).