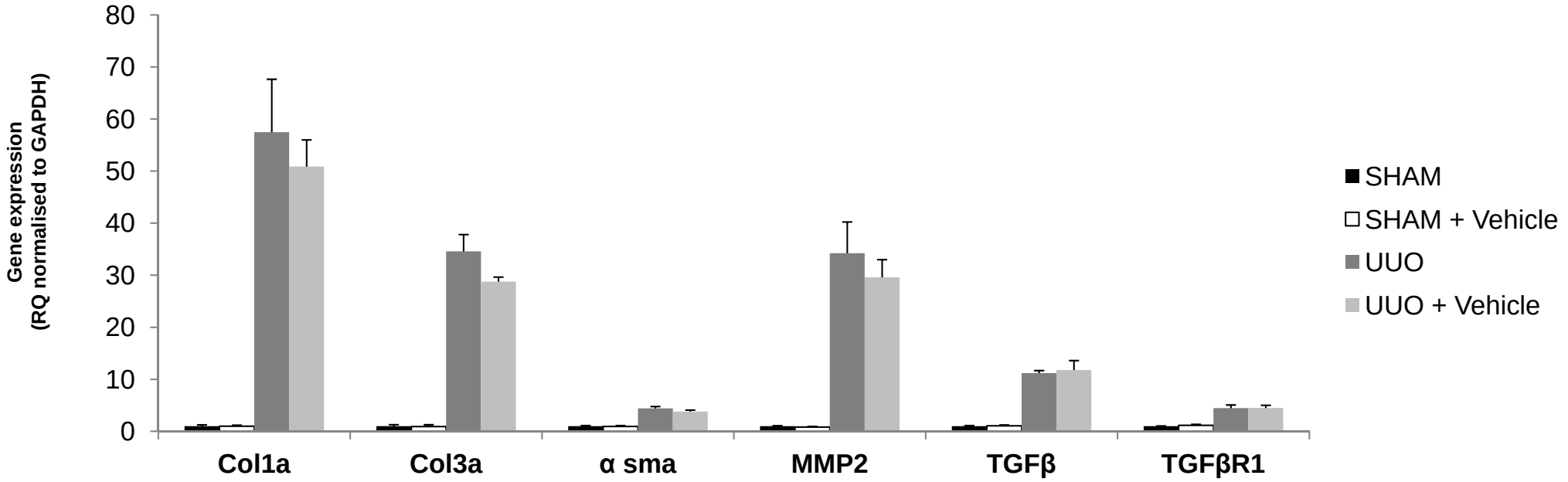
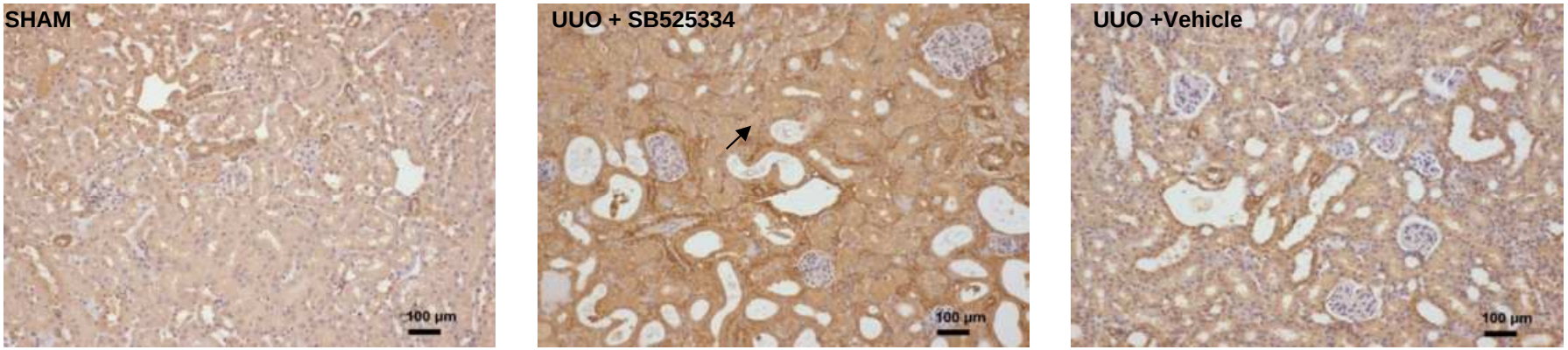
a

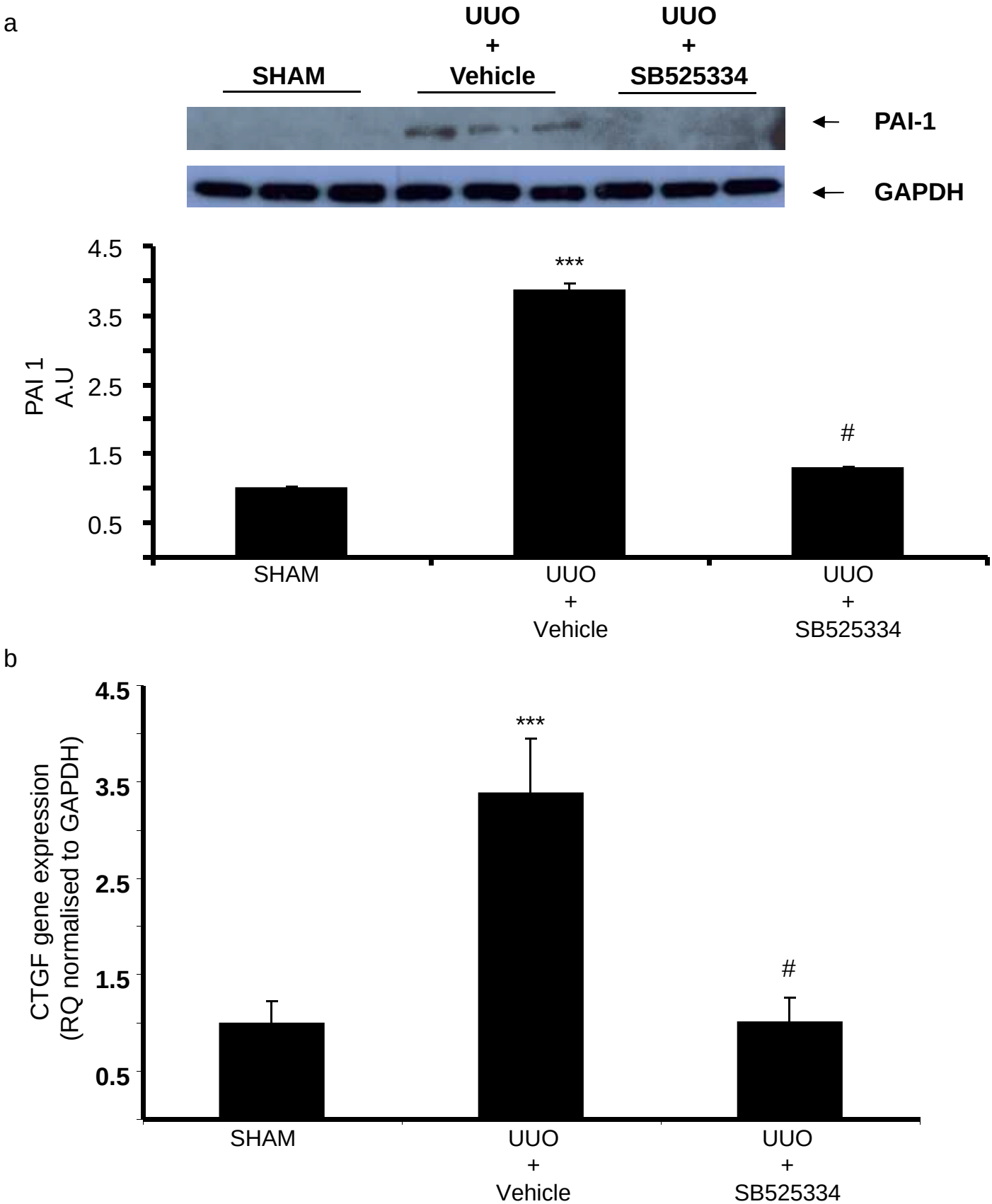


b



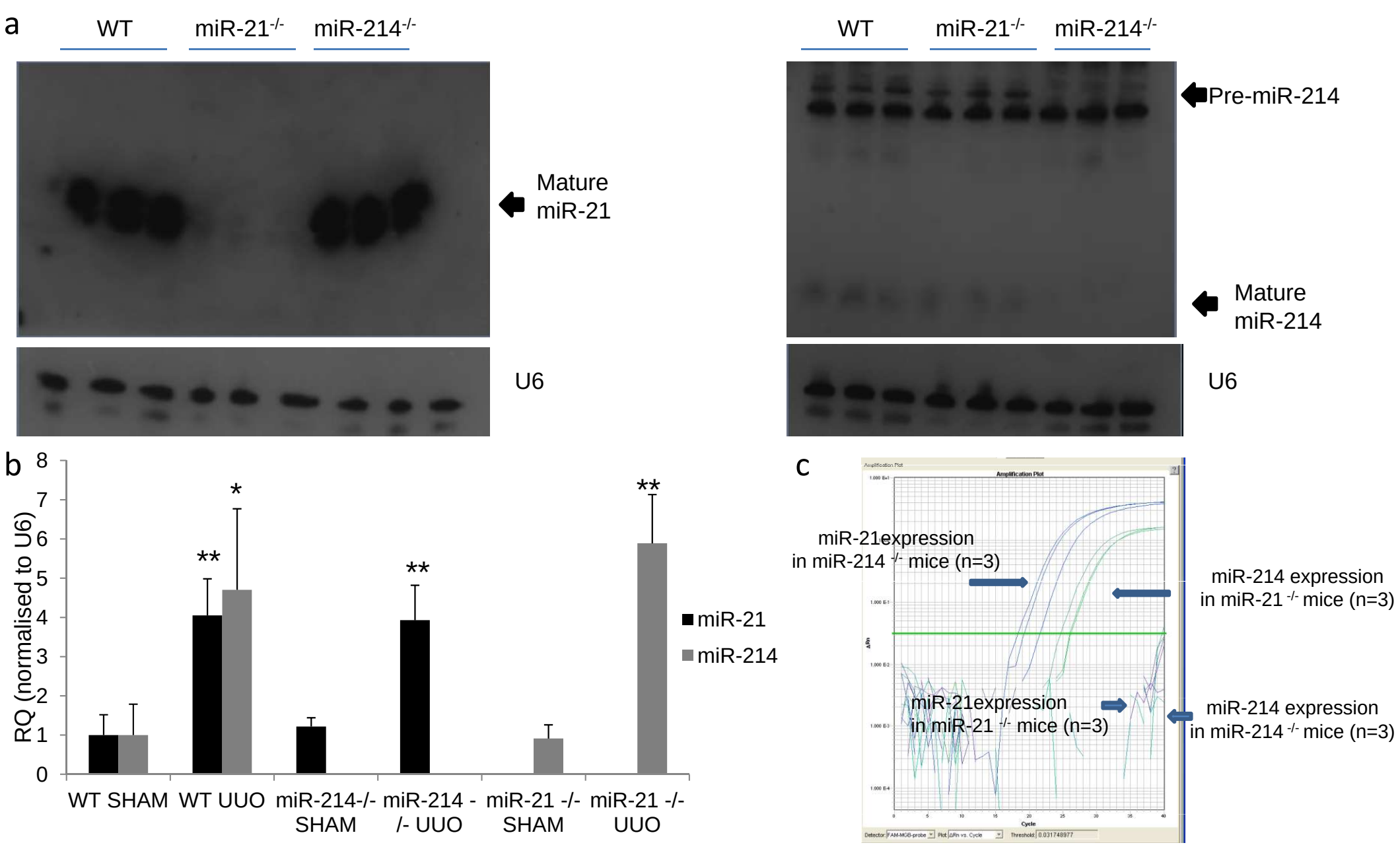
Supplementary Figure 1: Effect of inhibition of TGFβ signalling on pro-fibrotic gene expression.

C57bl/6 mice were treated daily with SB525334 or vehicle (0.1% DMSO) for -1d – + 7d at a dose of 10mg/kg by oral gavage. UUO or SHAM surgery was performed at day 0 and animals sacrificed at +7days. Total kidney RNA was extracted (n=6/gp) using miRNasy kit (Qiagen). a) Gene expression was assessed using specific probes (ABI) and normalised to mouse GAPDH. No significant differences were observed with vehicle administration on sham or UUO gene expression. b) αSMA expression in FFPE 3µM sections. Arrows indicates positive interstitial staining.

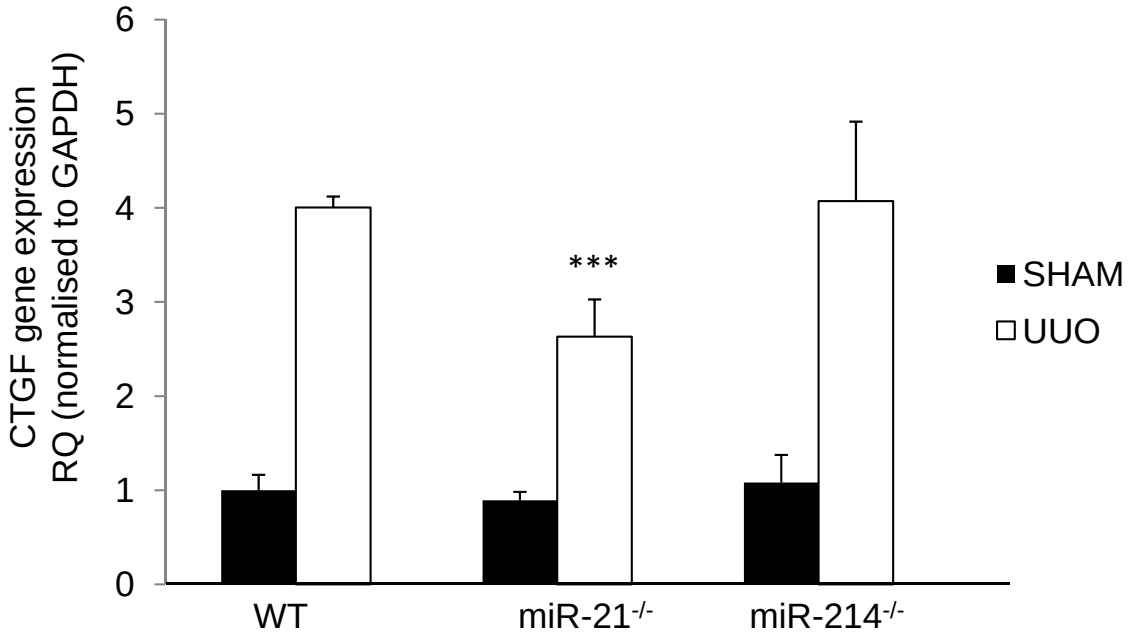


Supplementary Figure 2: Effect of SB525334 treatment on TGFβ downstream signalling.

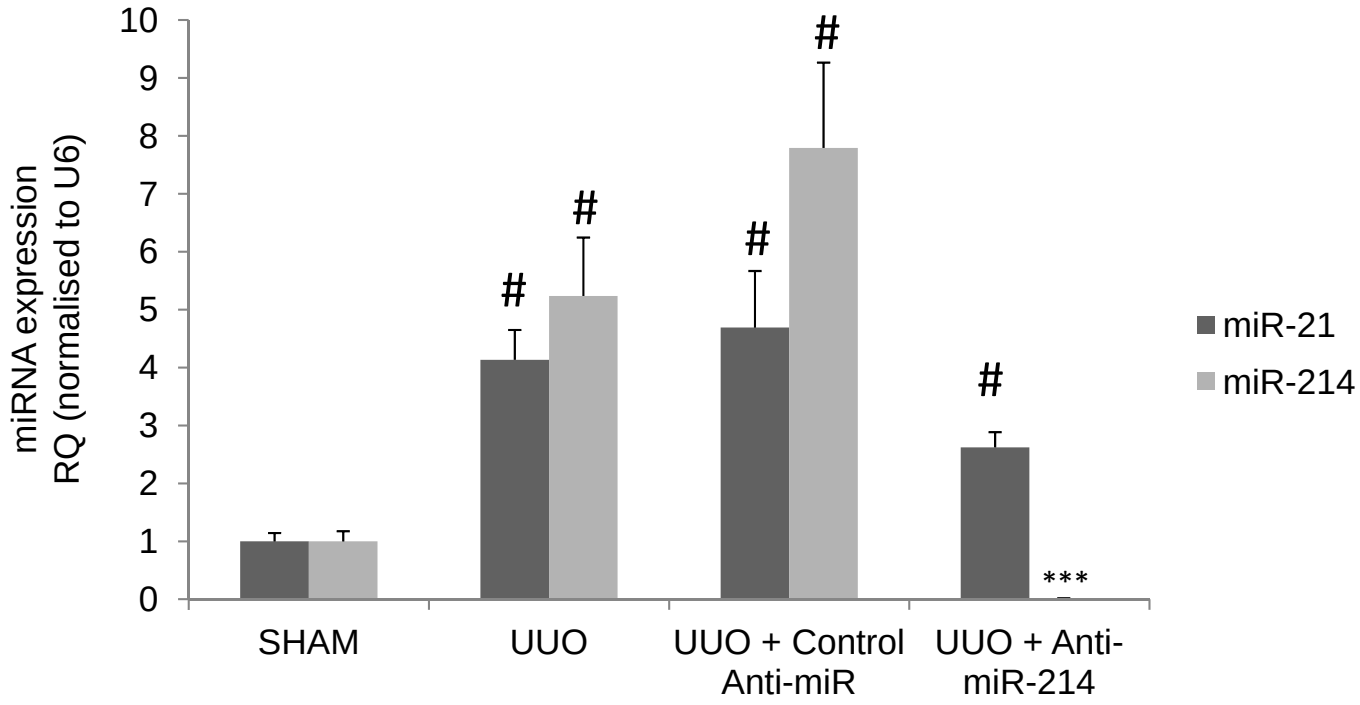
C57bl/6 mice were treated daily with SB525334 or vehicle (0.1% DMSO) for -1d –+ 7d at a dose of 10mg/kg by oral gavage. UUO or SHAM surgery was performed at day 0 and animals sacrificed at +7days. A. Protein lysates were prepared and quantified and 50µg fractionated on SDS polyacrylamide gels. Proteins were transferred onto nitrocellulose membranes and probed for PAI-1 (1:1000, rabbit-anti PAI-1, ABCAM) . Densitometry was performed using Quantity One software. B. Total kidney RNA was extracted (n=6/gp) using miRNeasy kit (Qiagen) and gene expression was assessed using specific probes (ABI) and normalised to mouse GAPDH. One-way ANOVA was used to assess data $p< 0.001$*** vs SHAM; # $p<0.05$ vs UUO + Vehicle.



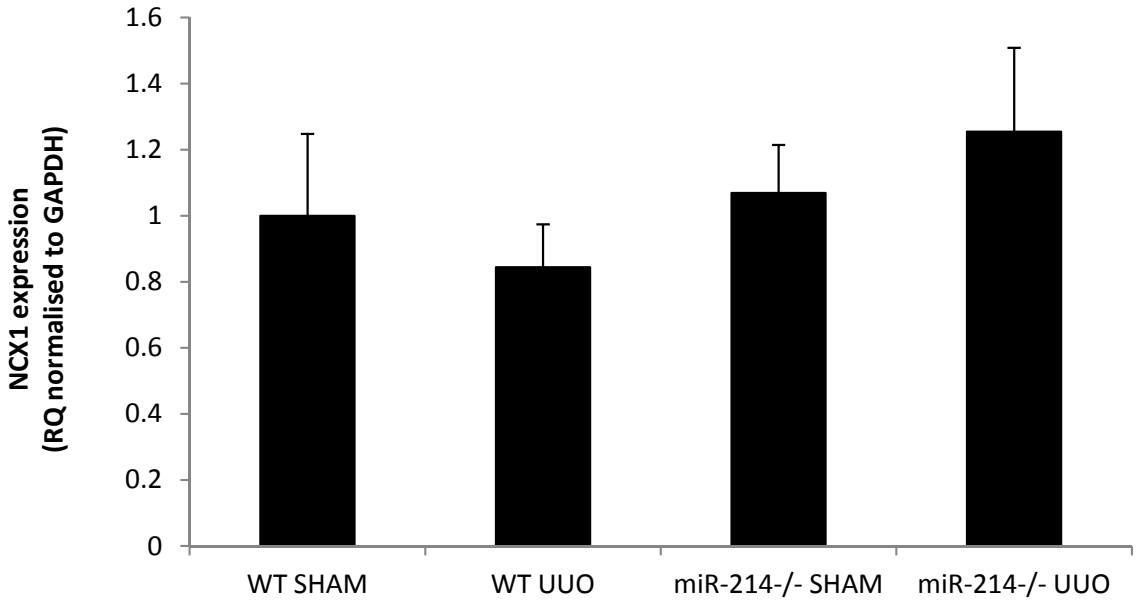
Supplementary Figure 3: Confirmation of global miR deletion. Total RNA was extracted from mouse kidney tissues (n=3/gp) using miRNeasy Mini kit (Qiagen). a) Three to ten micrograms of total RNA was resolved in a 15% TBE-Urea denaturing gel (Invitrogen), transferred onto Hyband-NX membrane (GE Healthcare). Following EDC cross-linking, membranes were hybridised with 5'-DIG-labeled LNA Mercury probes (Exiqon) at 40℃ (mi R-21 probe) or 60℃ (miR-214 probe) and 55℃ (U6) o vernight. b) miRNA expression was determined by qRT-PCR using specific Taqman probes (ABI) and normalised to U6. *p<0.05 vs SHAM; ** p<0.01 vs SHAM. c) Amplification plot show raw data from n=3 miR 21$^{-/-}$ UUO mice vs miR-214 $^{-/-}$ UUO mice detecting miR-21 and miR-214 expression in the same mouse.



Supplementary Figure 4: Expression of downstream TGFβ signalling mediators.
Total kidney RNA was extracted (n=5-6/gp) using miRNeasy kit (Qiagen) following SHAM or UUO surgery. Gene expression was assessed using specific probes (ABI) and normalised to mouse GAPDH. One-way ANOVA with Tukey's post-hoc test was used to analyse data. ***p<0.001 vs WT UUO.



Supplementary Figure 5: Expression of mature miRNA in kidney following anti-miR treatment. C57bl/6 mice were *sc* injected with PBS, Control anti-miR or anti-miR-214 (n=10/gp) as outlined in methods and had either UUO or sham surgery performed. Total kidney RNA was extracted using miRNeasy kit (Qiagen) 7 days post SHAM or UUO surgery. MiRNA expression was assessed using specific probes (ABI) and normalised to mouse GAPDH. One-way ANOVA with Tukey's post-hoc test was used to analyse data ***p<0.001 vs WT UUO, # p<0.001 vs SHAM.



Supplementary Figure 6: Expression of NCX1 following UUO.

Total kidney RNA was extracted (n=4-6/gp) using miRNeasy kit (Qiagen) following SHAM or UUO surgery. Gene expression was assessed using specific probes (ABI) and normalised to mouse GAPDH. One-way ANOVA with Tukey's post-hoc test was used to analyse data.