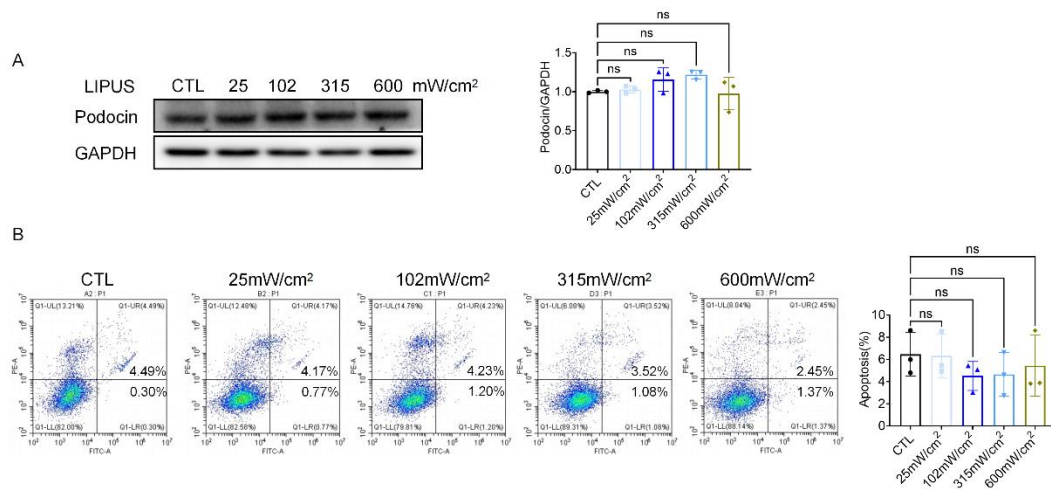


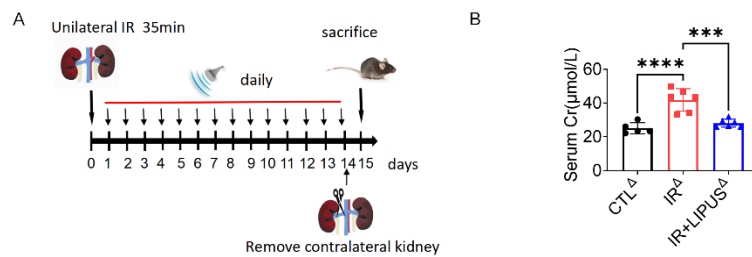


Supplemental Figure 1 The impact of LIPUS on podocytes.

(A) Protein level of podocin in podocytes, and the quantitative analysis ($n=3$).

(B) Apoptosis of podocytes and quantification of apoptotic cells (Q2 + Q3)

($n=3$). Data information: Data are presented as mean $\pm$ SD. Data were analyzed by one-way ANOVA with Tukey's post-hoc test. ns, no significant difference.



Supplemental Figure 3 Protective role of LIPUS in an IR-induced CKD model with contralateral nephrectomy.

(A) Study protocol. **(B)** Serum Cr levels in IR-induced mice with LIPUS after contralateral nephrectomy. Data information: Data are presented as mean±SD. One-way ANOVA with Tukey's post-hoc test was used for statistics. *** $P < 0.001$, **** $P < 0.0001$. $n=5$ in control^Δ group with contralateral nephrectomy, $n=6$ in IR^Δ group and IR treated with LIPUS group (IR+LIPUS^Δ) with contralateral nephrectomy.

Figure 2: PT cell heterogeneity and gene expression analysis.

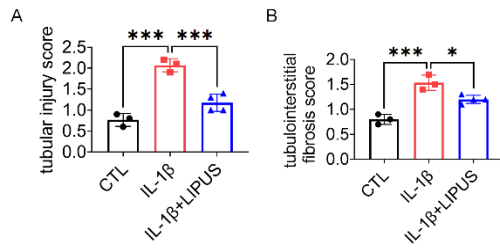
Top-left: t-SNE plot of 130,503 PT cells. The plot shows various cell types labeled with gene names: PT-H, FR-PTC, PT-R, PTA, Mafk, Maf, Bcl2, Pdx, DTL, TAL, DCT, Pdx, PC, CMT, ICA, ICB.

Top-right: Heatmaps of gene expression for 11b and 11r1. The heatmaps show mean expression levels (0.00 to 1.00) for 11b and 11r1 across different conditions: Health, RI, Day, UUO, Day. The color scale indicates mean expression.

Bottom-left: t-SNE plot of 130,503 PT cells. The plot shows different injury types: Type1, Type2, Healthy, Acute, Failed Repair, Repairing.

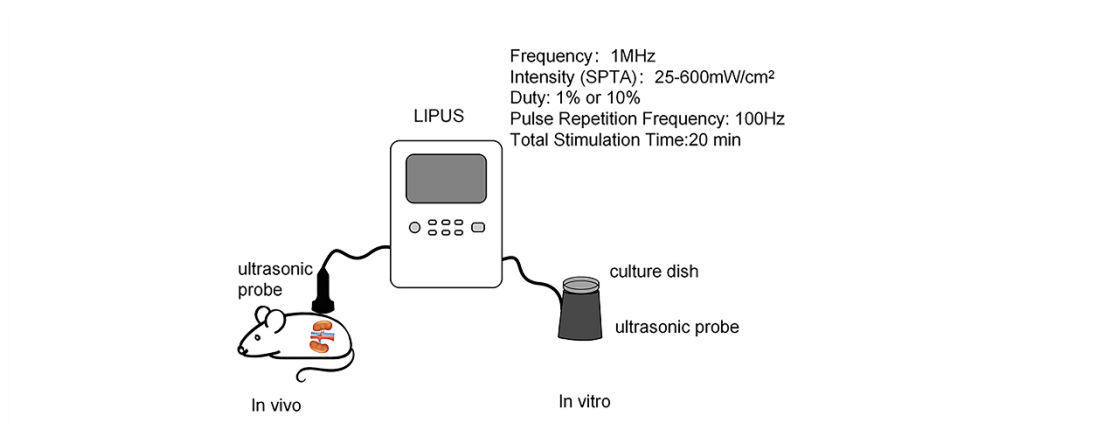
Bottom-right: Heatmaps of gene expression for 11r1. The heatmaps show mean expression levels (0 to 1) for 11r1 across different conditions: Acute Injury, Failed Repair, Healthy S1, Healthy S2, Healthy S3, Repairing, Type1, Type2, Injured S1, Injured S2, Injured S3. The color scale indicates mean expression.

(A) Integrated single-cell transcriptome map of mouse kidneys with blank control, unilateral IR injury, and unilateral ureteral obstruction. Dot plot of single-cell RNA sequencing analyses showing the expression levels of *Il1b* and *Il1r1* at various time points in mouse kidneys, and *Il1b* in multiple cell lineages. **(B)** UMAP plots of all proximal tubule cells in sub-clustering analysis. Connected bar plots displaying the proportional abundance of each cell cluster in each disease condition. Dot plot of single-cell RNA sequencing analyses showing the up-regulation of *Il1r1* in injured proximal tubules at 6 h, 14 d, and 28 d after unilateral IR injury, and 14 d after unilateral ureteral obstruction.



Supplemental Figure 5 Batch 2 replication: LIPUS-mediated protection against tubular injury and interstitial fibrosis in IL-1 β -induced renal damage

(A) Tubular injury scores. (n=3-4) **(B)** Tubulointerstitial fibrosis scores. (n=3-4) Data information: Data are presented as mean $\pm$ SD, with significance determined by one-way ANOVA with Tukey's post hoc test. * $P < 0.05$, *** $P < 0.001$.



Supplemental Figure 6 Schematic of Low-Intensity Pulsed Ultrasound (LIPUS) stimulation. Simplified unilateral depiction of LIPUS application. In actual experiments, bilateral kidneys were treated using two transducers (one per kidney), each delivering 20 min of continuous exposure.

Supplemental Table 1 Sequences of primers used in RT-qPCR

gene name	primer sequences
<i>Gapdh</i>	F:CATCACTGCCACCCAGAAGACTG
	R:ATGCCAGTGAGCTTCCCGTTCAG
<i>Fnl</i>	F:CCGTGGGATGTTTGAGACTT
	R:GGCAAAGAAAGCAGAGGTG
<i>Acta2</i>	F:CGGGAGAAAATGACCCAGATT
	R:AGGGACAGCACAGCCTGAATAG
<i>Tgfb1</i>	F:TGAGTGGCTGTCTTTTGACG
	R:TCTCTGTGGAGCTGAAGCAA
<i>Serpine1</i>	F:AGTCTTTCCGACCAAGAGCA
	R:ATCACTTGCCCCATGAAGAG
<i>Lcn2</i>	F:ATGTCACCTCCATCCTGGTCAG
	R:GCCACTTGCACATTGTAGCTCTG
<i>Havcr1</i>	F:ACATATCGTGGAATCACAACGAC
	R:ACTGCTCTTCTGATAGGTGACA
<i>Il1r1</i>	F:GTGCTACTGGGGCTCATTGT
	R:GGAGTAAGAGGACACTTGCGAAT
<i>Tnf</i>	F:CAGGCGGTGCCTATGTCTC
	R:CGATCACCCCGAAGTTCAGTAG
<i>Il6</i>	F:TACCACTTCACAAGTCGGAGGC
	R:CTGCAAGTGCATCATCGTTGTTC
<i>Ccl2</i>	F:GCTACAAGAGGATCACCAGCAG
	R:GTCTGGACCCATTCCTTCTTGG