

Supplementary Data for

**Polynucleotide phosphorylase protects against renal tubular injury via blocking mt-dsRNA-
PKR-eIF2 α axis**

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26 **Supplementary Table 1. Oligonucleotide primers used in the study.**

Primer (qRT-PCR)	Gene	Sequence (5'-3')
<i>mt-ND6</i> forward	<i>mt-ND6</i>	CCAATAGGATCCTCCCGAAT
<i>mt-ND6</i> reverse	<i>mt-ND6</i>	AGGTAGGATTGGTGCTGTGG
<i>mt-CO1</i> forward	<i>mt-CO1</i>	ACGTTGTAGCCCACTTCCAC
<i>mt-CO1</i> reverse	<i>mt-CO1</i>	TGGCGTAGGTTTGGTCTAGG
<i>mt-ND5</i> forward	<i>mt-ND5</i>	TCGAAACCGCAAACATATCA
<i>mt-ND5</i> reverse	<i>mt-ND5</i>	CAGGCGTTTAATGGGGTTTA
<i>mt-ND4</i> forward	<i>mt-ND4</i>	AACGGATCCACAGCCGTA
<i>mt-ND4</i> reverse	<i>mt-ND4</i>	AGTCCTCGGGCCATGATT
<i>mt-CYB</i> forward	<i>mt-CYB</i>	AGACAGTCCCACCCCTCACAC
<i>mt-CYB</i> reverse	<i>mt-CYB</i>	GGTGATTCTAGGGGGTTGT
β -actin mRNA forward	β -actin	CTGTGGCATCCACGAAACTA
β -actin mRNA reverse	β -actin	AGTACTTGCGCTCAGGAGGA

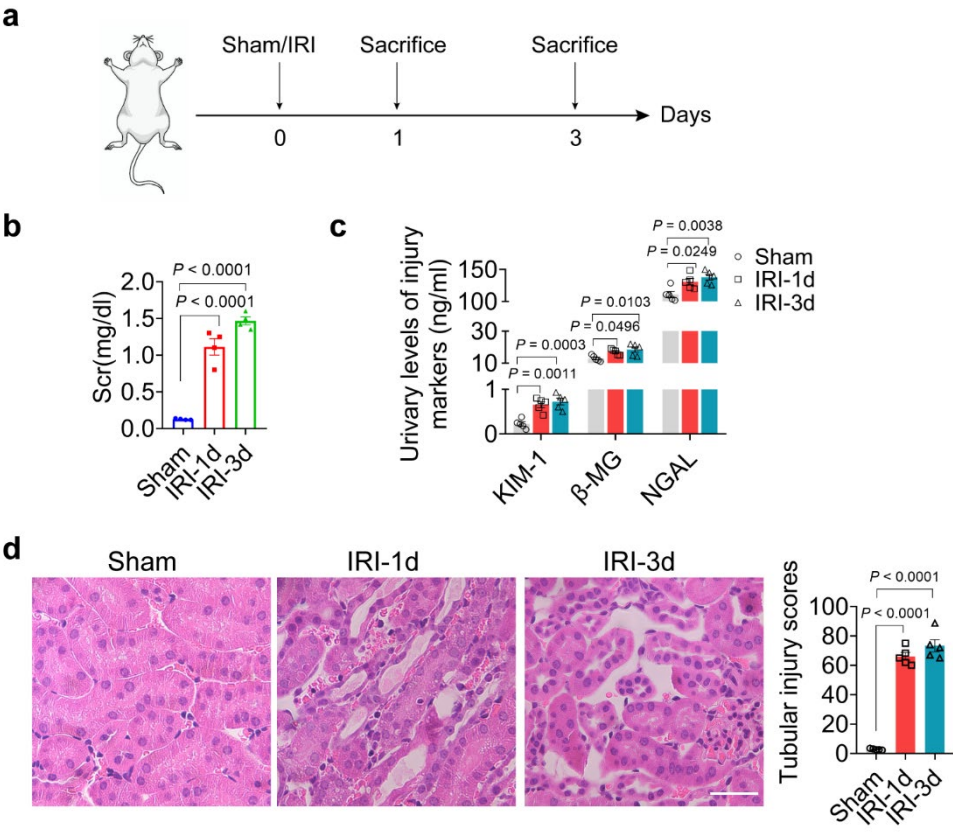
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28 **Primer sequences for strand-specific reverse transcription**

Primer	Sequences (5'-3')
<i>COI</i> Heavy	CGCAAATGGGCGGTAGGCGTGGTTGTGATAAGGGTGGAGAGG
<i>COI</i> Light	CGCAAATGGGCGGTAGGCGTGTCAAACCTCAAACCTACGCCCTG
<i>ND4</i> Heavy	CGCAAATGGGCGGTAGGCGTGTGTTTGTCTAGGCAGATGG
<i>ND4</i> Light	CGCAAATGGGCGGTAGGCGTGCCTCACACTCATTCTCAACCC
<i>ND5</i> Heavy	CGCAAATGGGCGGTAGGCGTGTGTTGGGTTGAGGTGATGATG
<i>ND5</i> Light	CGCAAATGGGCGGTAGGCGTGCAATTGTCGCATCCACCTTTA
<i>ND6</i> Heavy	CGCAAATGGGCGGTAGGCGTGGGTTGAGGTCTTGGTGAGTG
<i>ND6</i> Light	CGCAAATGGGCGGTAGGCGTGCCCATATCATACAAAGCCCC
<i>CYB</i> Heavy	CGCAAATGGGCGGTAGGCGTGGGATAGTAATAGGGCAAGGACG
<i>CYB</i> Light	CGCAAATGGGCGGTAGGCGTGCAATTATACCCTAGCCAACCCC
β -actin	CGCAAATGGGCGGTAGGCGTGACA CAG AGTACTTGCGCTCAG

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30 **Primer sequences for strand-specific qPCR**

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
<i>COI</i> Heavy	TCAAACCTCAAACCTACGCCCTG	CGCAAATGGGCGGTAGGCGTG
<i>COI</i> Light	GTTGTGATAAGGGTGGAGAGG	CGCAAATGGGCGGTAGGCGTG
<i>ND4</i> Heavy	CTCACACTCATTCTCAACCCC	CGCAAATGGGCGGTAGGCGTG
<i>ND4</i> Light	TGTTTGTCTAGGCAGATGG	CGCAAATGGGCGGTAGGCGTG
<i>ND5</i> Heavy	CTAGGCCTTCTTACGAGCC	CGCAAATGGGCGGTAGGCGTG
<i>ND5</i> Light	TAGGGAGAGCTGGGTTGTTT	CGCAAATGGGCGGTAGGCGTG
<i>ND6</i> Heavy	TCATACTCTTTCACCCACAGC	CGCAAATGGGCGGTAGGCGTG
<i>ND6</i> Light	TGCTGTGGGTGAAAGAGTATG	CGCAAATGGGCGGTAGGCGTG
<i>CYB</i> Heavy	CAATTATACCCTAGCCAACCCC	CGCAAATGGGCGGTAGGCGTG
<i>CYB</i> Light	GGATAGTAATAGGGCAAGGACG	CGCAAATGGGCGGTAGGCGTG
β -actin	ACACAGTGCTGTCTCGTGGA	CGCAAATGGGCGGTAGGCGTG

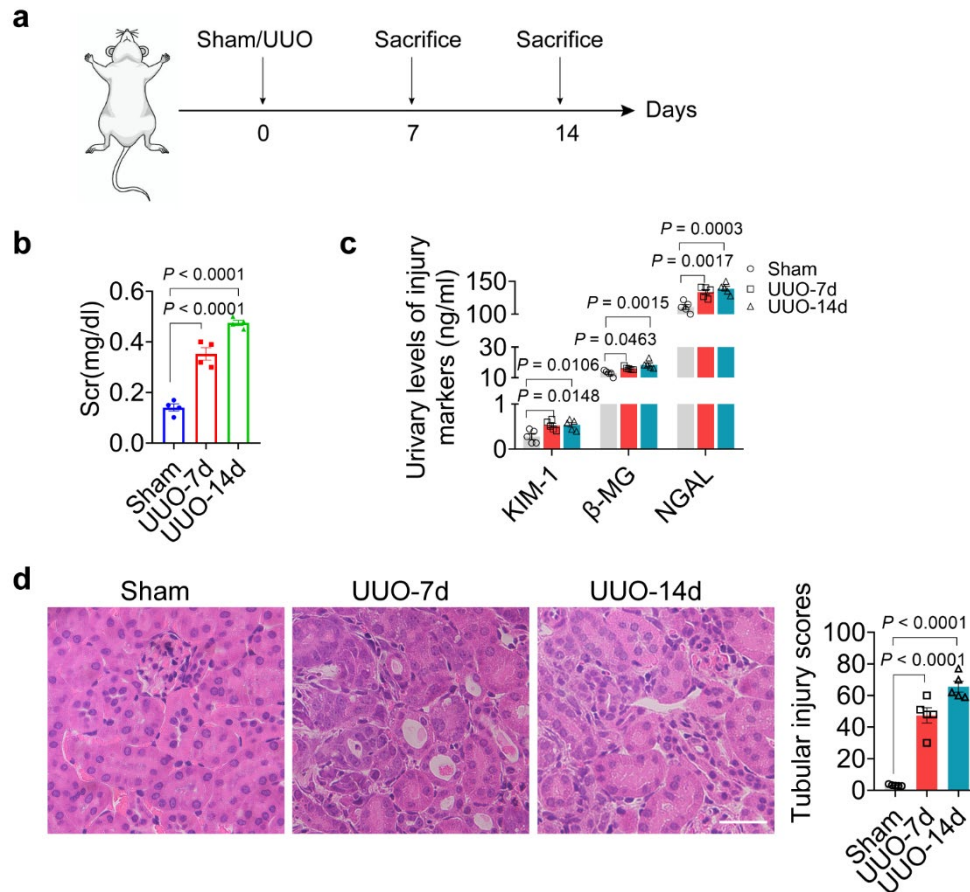
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34 **Supplementary figure 1. Establishment of IRI mouse model.** **a**, Schematic of IRI mouse model
35 experimental approach. **b**, Scr in WT and IRI mice. **c**, Urinary levels of renal tubular injury markers in WT
36 and IRI mice. **d**, Left: H&E staining of kidney tissue sections from WT and IRI mice. Right: quantification of
37 tubular injury score. $n = 5$ mice/group, 8w. Scale bar, $50\mu\text{m}$. The above experiments were successfully repeated
38 three times. One-way ANOVA with Dunnett's multiple comparisons test was performed in (b, d). One-way
39 ANOVA with Sidak's multiple comparisons test was performed in (c), and the results were presented as mean
40 \pm SEM. Image of mouse in (a) was created with BioRender.com. Source data are provided in Source Data file.

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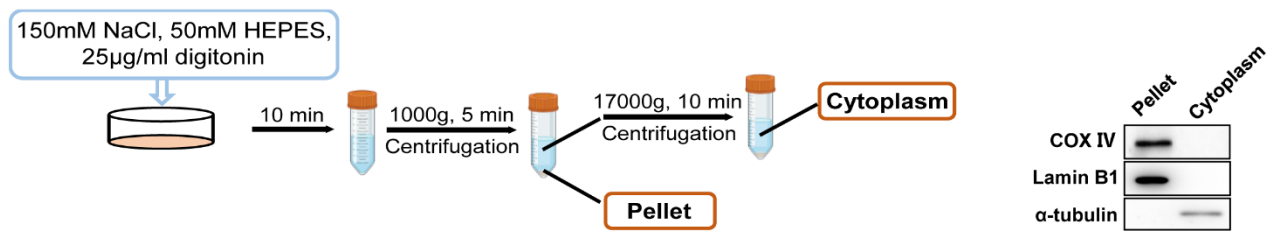


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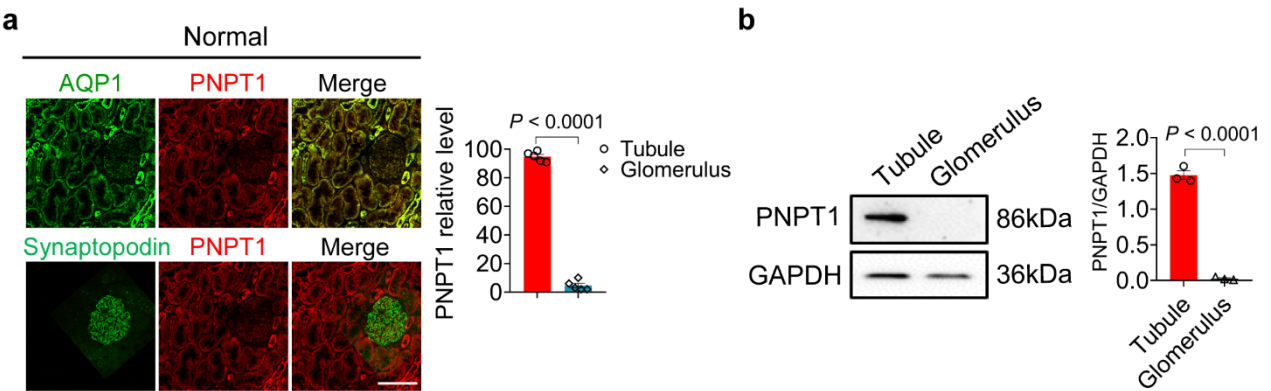
43 **Supplementary figure 2. Establishment of UUO mouse model.** a, Schematic of UUO mouse model
 44 experimental approach. b, Scr in WT and UUO mice. c, Urinary levels of renal tubular injury markers in WT
 45 and UUO mice. d, Left: H&E staining of kidney tissue sections from WT and UUO mice. Right: quantification
 46 of tubular injury score. n = 5 mice/group, 8w. Scale bar, 50µm. The above experiments were successfully
 47 repeated three times. One-way ANOVA with Dunnett's multiple comparisons test was performed in (b, d).
 48 One-way ANOVA with Sidak's multiple comparisons test was performed in (c), and the results were presented
 49 as mean ± SEM. Image of mouse in (a) was created with BioRender.com. Source data are provided in Source
 50 Data file.

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Supplementary figure 3. Isolation and validation of mitochondria-free cytosolic fraction. Left, schematic of experimental approach to isolate mitochondria-free cytosolic fraction from renal tubules or cells. Right, WB validation of isolated cytosolic fraction. Data were from 3 independent experiments. Images of test tubes were created with BioRender.com.

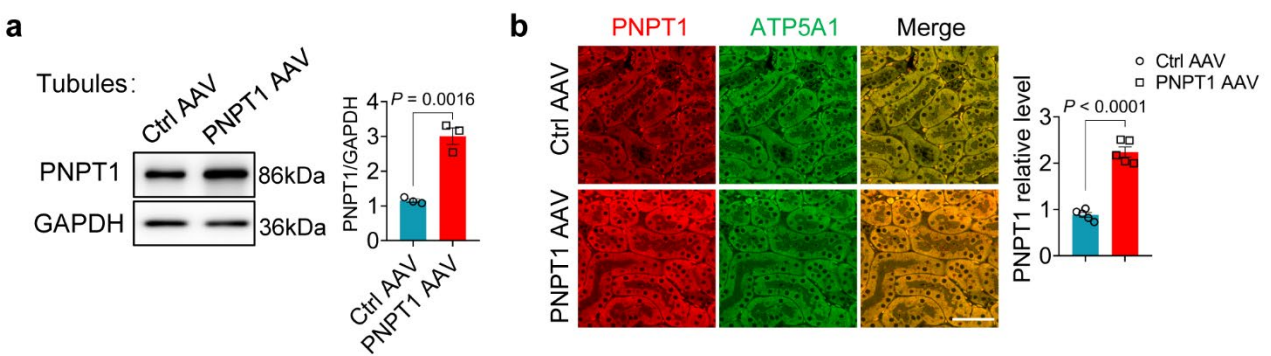


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61 **Supplementary figure 4. Expression and distribution of PNPT1 in normal human kidney. a, Left:**
62 **immunofluorescence labeling of PNPT1 in human renal tubule and glomerulus. Scale bar, 50μm. Right:**
63 **quantification of PNPT1 level (n = 5); b, WB analysis of PNPT1 in human renal tubule and glomerulus (n =**
64 **3). The above experiments were successfully repeated three times. Two-tailed unpaired t test was performed**
65 **for the statistical analyses in (a-b), and the results were presented as the mean ± SEM. Source data are provided**
66 **in Source Data file.**

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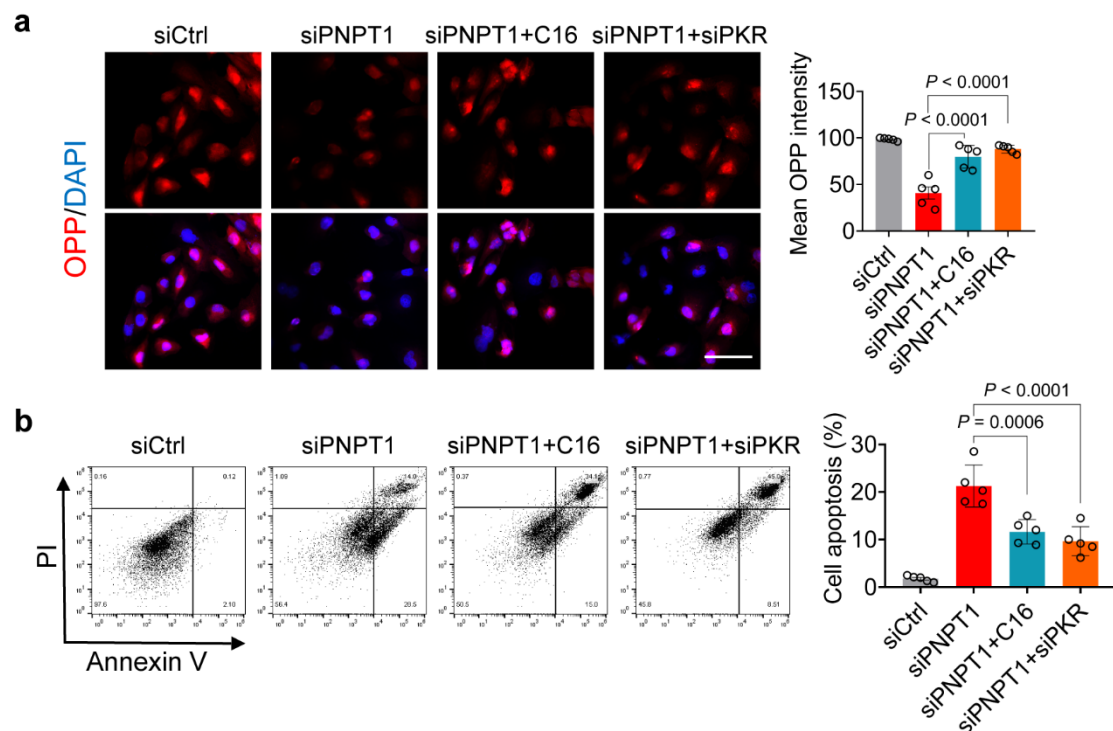
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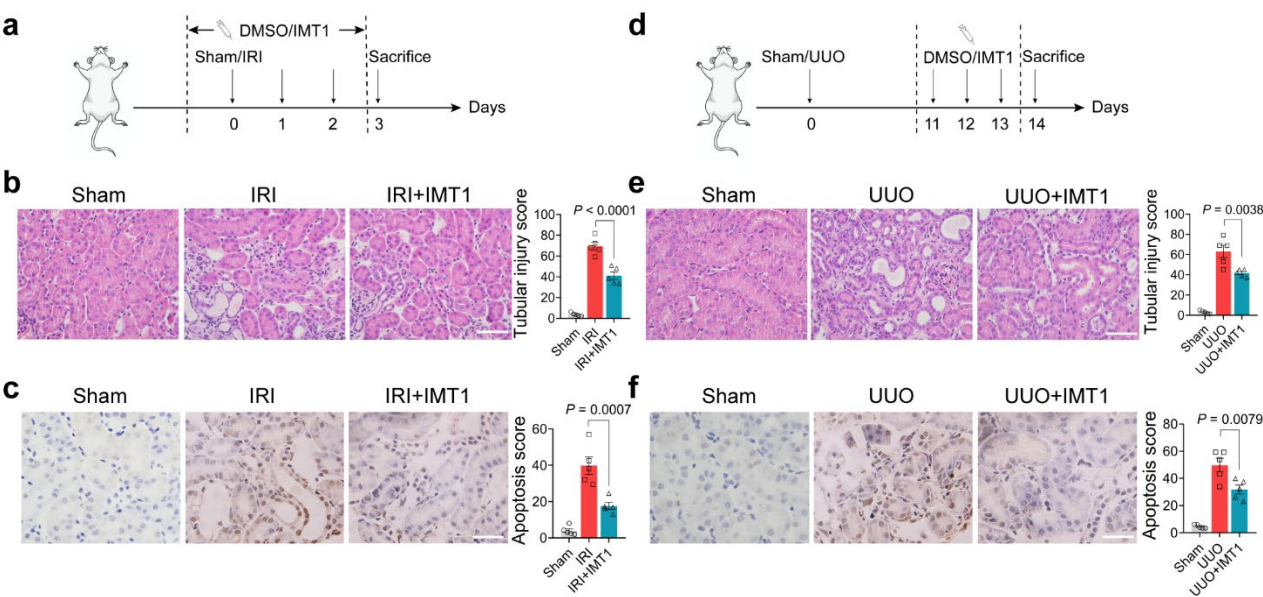
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71 **Supplementary figure 5. PNPT1 AAV increased PNPT1 expression in mouse renal tubules. a**, WB
72 analysis of PNPT1 in mouse renal tubules after Ctrl AAV or PNPT1 AAV infections (3 mice/group, 8w); **b**,
73 Left: Co-localization of PNPT1 (red) and mitochondria (ATP5A1, green) in mouse renal tubules. Right:
74 quantification of PNPT1 relative level (n=5 mice/group, 8w). Scale bar, 50μm. The above experiments were
75 successfully repeated three times. Two-tailed unpaired t test was performed for the statistical analyses in (a-b),
76 and the results were presented as the mean ± SEM. Source data are provided in Source Data file.

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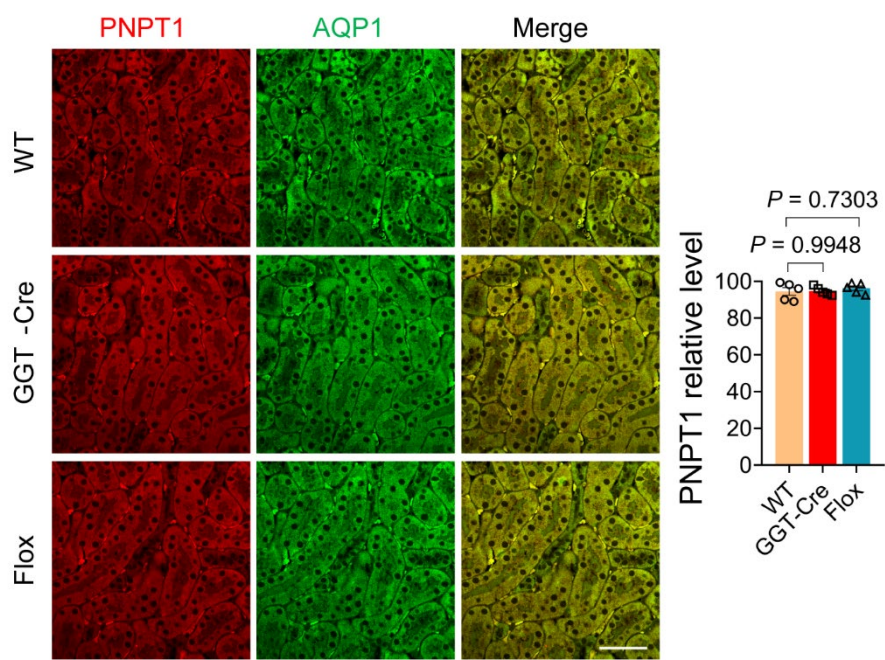


80 **Supplementary figure 6. Knockdown of PKR resulted in a similar phenotype as that of C16 in PNPT1-**
81 **deficient HK2 cells. a**, Left, measurement of total protein synthesis in PNPT1-deficient HK2 cells transfected
82 with siPKR plasmid or treated with C16 using Click-iT® Plus OPP Protein Synthesis Assay Kit. Right:
83 quantification of OPP protein synthesis (n = 5). **b**, Apoptosis of siPNPT1-transfected HK2 cells treated with
84 siPKR plasmid or C16 (n = 5). Scale bar, 50µm. The above experiments were successfully repeated three times.
85 One-way ANOVA with Tukey's multiple comparisons test was performed in (a-b) and the results were
86 presented as mean ± SEM. Source data are provided in Source Data file.



Supplementary figure 7. IMT1 treatment markedly attenuated renal tubular damage induced by IRI or UUO procedure. **a**, Schematic of experimental approach in IRI mouse model. **b**, Left: H&E staining of kidney tissue sections from IRI mice treated with or without IMT1. Right: quantification of tubular injury score. **c**, Left: TUNEL assay of kidney tissue sections from IRI mice treated with or without IMT1. Right: quantification of apoptosis in kidney tissues. **d**, Schematic of experimental approach in UUO mice. **e**, Left: H&E staining of kidney tissue sections from UUO mice treated with or without IMT1. Right: quantification of tubular injury score. **f**, Left: TUNEL assay of kidney tissue sections from UUO mice treated with or without IMT1. Right: quantification of apoptosis in kidney tissues. $n=5$ mice/group, 8w. Scale bars, 50 μ m. The above experiments were successfully repeated three times. One-way ANOVA with Tukey's multiple comparisons test was performed in (b-c, e-f) and the results were presented as mean \pm SEM. Images of mouse in (a, d) were created with BioRender.com. Source data are provided in Source Data file.

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Supplementary figure 8. Immunofluorescence analysis of PNPT1 level and distribution in mouse tubules with GGT-Cre only or floxed only genetic modification. n=5 mice/group, 8w. Scale bar, 50 μm . The above experiments were successfully repeated three times. One-way ANOVA with Tukey's multiple comparisons test was performed, and the results were presented as mean \pm SEM. Source data are provided in Source Data file.