Dynamin Related Protein 1 Deficiency Promotes Recovery from Acute Kidney Injury

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Supplemental material

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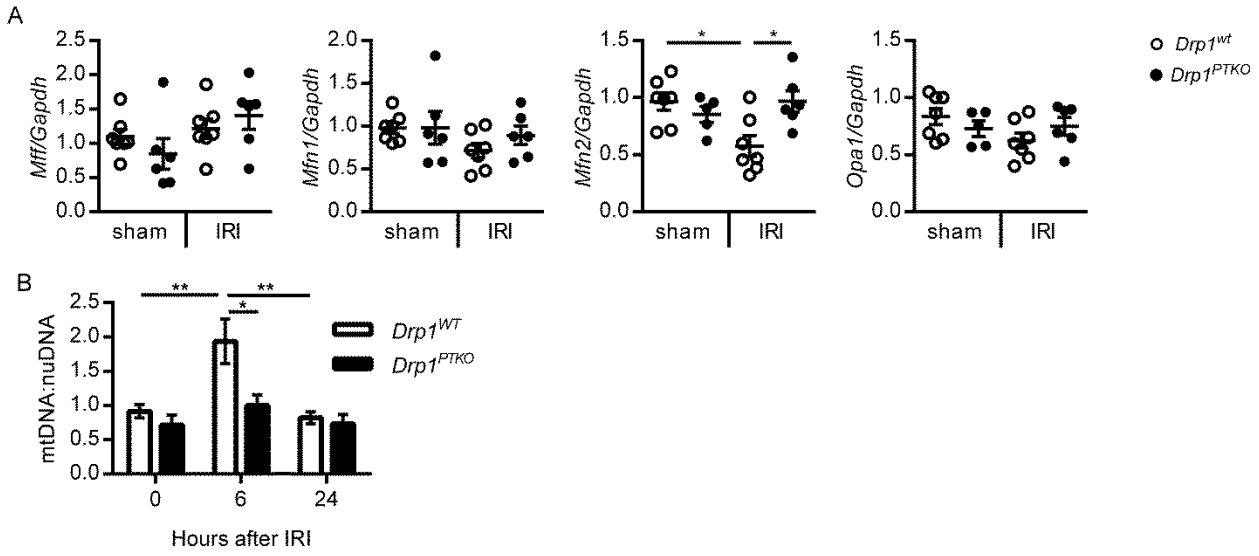
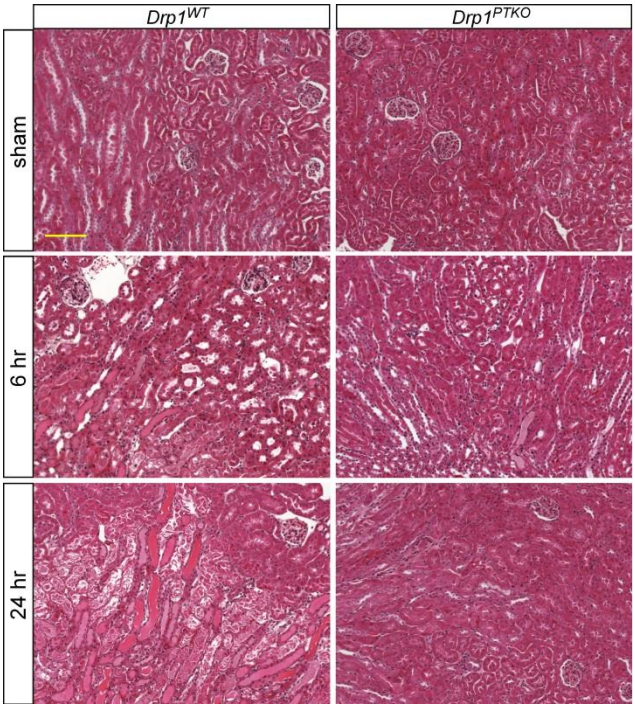
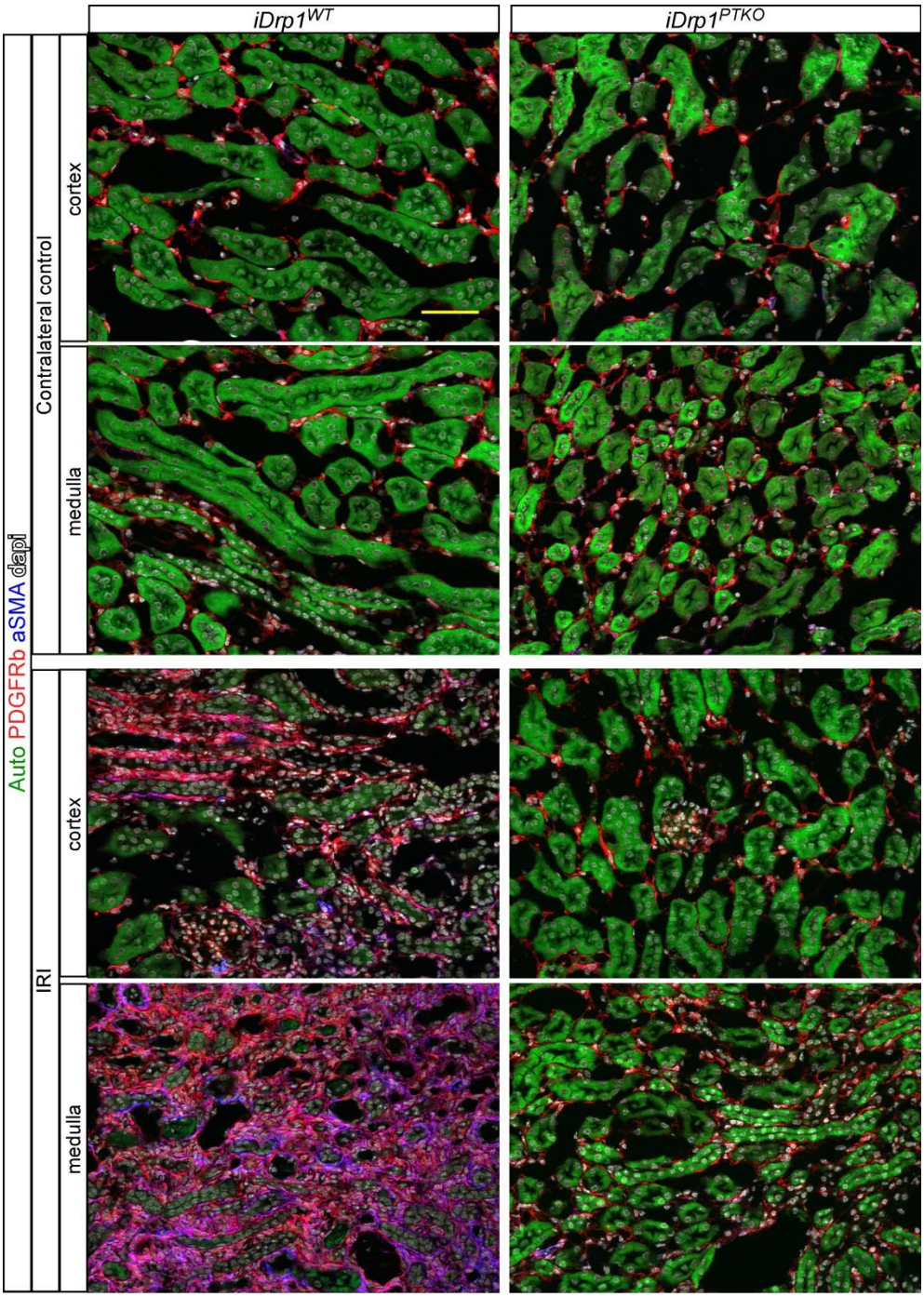


Supplemental Figure I. Fission and fusion gene expression and mitochondrial mass in *Drp1*^{PTKO} mice. *PepCKCre- Drp1*$^{fl/fl}$ (*Drp1*^{WT}, open circles) mice and littermate *PepCKCre+ Drp1*$^{fl/fl}$ (*Drp1*^{PTKO}, closed circles) mice underwent bilateral ischemia-reperfusion injury (IRI) or sham operation and were euthanized after (A) 24 or (B) 6 and 24 hours of reperfusion. (A) Kidney *Mff* (mitochondrial fission factor), *Mfn1* (mitofusin 1), *Mfn2* (mitofusin 2), *Opa1* (OPA1, mitochondrial dynamin like GTPase) relative to *Gapdh* transcript levels. (B) Mitochondrial mass assessed by mitochondrial (mt) to nuclear (nc) DNA ratio. *p<0.05, **p<0.01.



Supplemental Figure II. Representative renal histology (H&E) from experiments in Figure 2 of the outer medulla in *PepCKCre- Drp1*$^{fl/fl}$ (*Drp1*^{WT}) mice and littermate *PepCKCre+ Drp1*$^{fl/fl}$ (*Drp1*^{PTKO}) mice that underwent bilateral IRI or sham operation and were euthanized after 6 or 24 hours of reperfusion. Scale bar, 100 µm.



Supplemental Figure III. Full size images of Figure 7D. Detection of myofibroblasts (pink) by colocalization of αSMA (blue) and PDGFRβ pericytes/fibroblasts (red), CD31+ endothelial cells and F4/80+ macrophages in kidneys from *iDrp1*^{WT} and *iDrp1*^{PTKO} mice by immunofluorescence microscopy; scale bar 50 µm. *Acta2*/αSMA, actin, alpha 2, smooth muscle, aorta; Con: contralateral control kidney; IRI, kidney exposed to unilateral ischemia–reperfusion.

Table. Primer sequences for real-time quantitative PCR

Transcript	Seq ID	Forward 5' to 3'	Reverse 5' to 3'
Acta2 (αSMA)	NM_007392.3	ATTGTGCTGGACTCTGGAGATGGT	TGATGTCACGGACAATCTCACGCT
Aqp1	NM_007472.2	CCGAGACTTAGGTGGCTCAG	TGATACCGCAGCCAGTGTAG
Ccl2	NM_011333.3	TCA CCT GCT GCT ACT CAT TCA CCA	TAC AGC TTC TTT GGG ACA CCT GCT
Col1a1	NM_007742.3	GAG CGG AGA GTA CTG GAT CG	TAC TCG AAC GGG AAT CCA TC
Col3a1	NM_009930.2	TCC TAA CCA AGG CTG CAA GAT GGA	ACC AGA ATC TGT CCA CCA GTG CTT
Dnm1l (*Drp1*)	NM_001025947.2	TAGTGGGCAGGGACCTTCTT	TGCTTCAACTCCATTTTCTTCTCC
Fn1	NM_010233.2	ACC AAC CTT AAT CCG GGC AC	TCA GAA ACT GTG GCT TGC TGG
Gapdh	NM_001289726.1	ACG GCA AAT TCA ACG GCA CAG TCA	TGG GGG CAT CGG CAG AAG G
Havcr1 (Kim1)	NM_001166632.1	ACA TAT CGT GGA ATC ACA ACG AC	ACT GCT CTT CTG ATA GGT GAC A
Ho1	NM_010442.2	TAGCCCACTCCCTGTGTTTCCTTT	TGCTGGTTTCAAAGTTCAGGCCAC
Il6	NM_031168.1	TGG CTA AGG ACC AAG ACC ATC CAA	AAC GCA CTA GGT TTG CCG AGT AGA
Lcn2 (Ngal)	NM_008491.1	TGG CCC TGA GTG TCA TGT G	CTC TTG TAG CTC ATA GAT GGT GC
Mff	NM_001310695.1	AAGTGGCTCTCACCCTAGCA	TGCCCCACTCACCAAATGT
Mfn1	NM_024200.4	TTGGCAGGACAAGTAGTGGC	AGCAGTTGGTTGTGTGACCA
Mfn2	NM_001285920.1	CAGCAAGTTGACATCACCCG	ACCAGCCAGCTTTATTCCTGA
Nampt	NM_021524.2	TACTGTGGCGGGAATTGCTC	GCCGTTATGGTACTGTGCTCT
Nfe2l2 (Nrf2)	NM_010902.4	AGATGACCATGAGTCGCTTGC	CCTGATGAGGGGCAGTGAAG
Opa1	NM_133752.3	TTGCCAGTTTAGCTCCCGAC	CCAGGTGAACCTGCAGTGAA
Pgc1a	NM_008904.2	GCT CTT CCT TTA ACT CTC CGT GTC	CTT GAC CTG GAA TAT GGT GAT CGG
Sirt3	NM_022433.2	AGGGGAAGACATATGGGCTGA	GGAGTAGGAACCTTGCAGGC
Slc12a1	NM_001079690.1	GGCTTGATCTTTGCTTTTGC	CCATCATTGAATCGCTCTCC
Vim	NM_011701.4	AGA TGG CTC GTC ACC TTC GTG AAT	TTG ACT GGG TGT CAA CCA GAG GAA