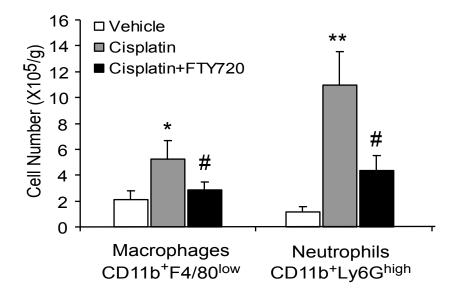
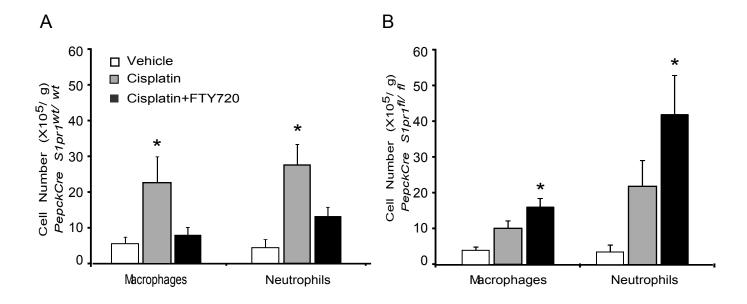
Supplemental Figure 1

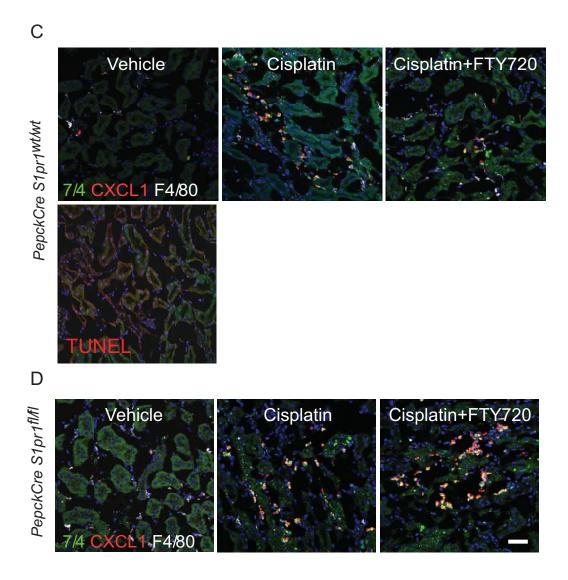


FTY720 treatment attenuates leukocyte infiltration into kidneys following cisplatin. WT mice were treated with FTY720 (240 μ g/kg) 1 hr prior to a single dose of cisplatin (27 mg/kg) and once each day on the next 2 days. FACS analysis of subsets of total live (7AAD-) leukocytes (CD45⁺) as determined by cell count of CD45⁺ cells per gram of kidney weight. Values are mean \pm SE; n=4-11, **p<0.01 and *p<0.05 compared to vehicle; # p<0.05 compared to cisplatin.

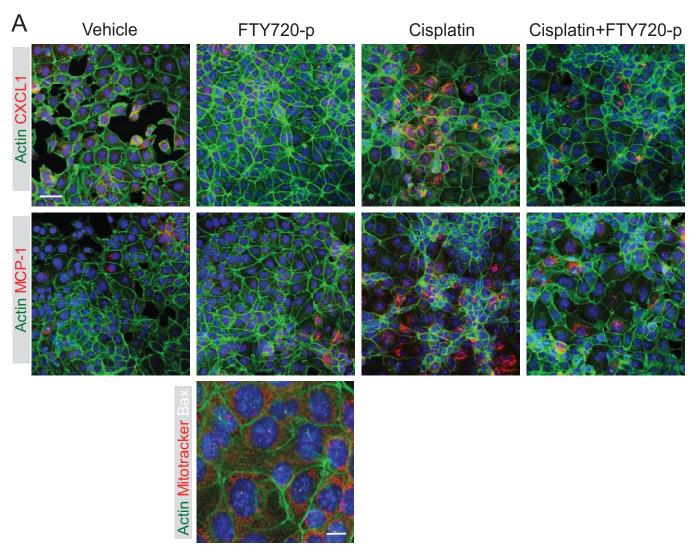
Supplemental Figure 2 - page 1



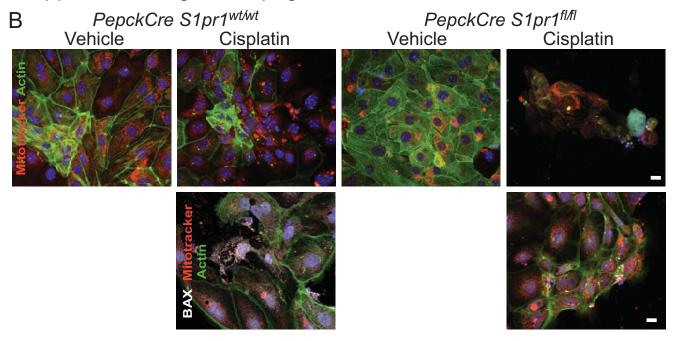
Supplemental Figure 2 - page 2



Supplemental Figure 3 - pg 1

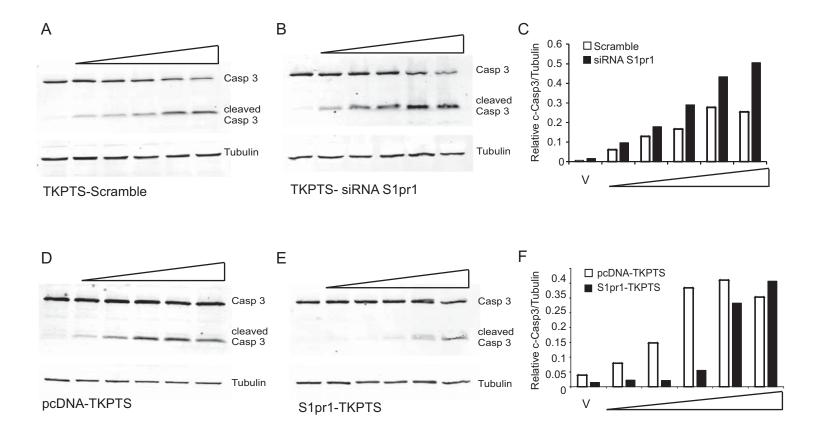


Supplemental Figure 3 - page 2



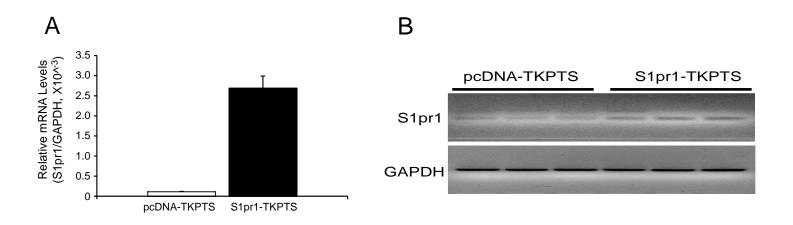
Phosphorylated FTY-720 (FTY720-p)-mediated protection of cisplatin-induced injury in TKPTS cells and primary cultures of tubule epithelial cells is attenuated in cultures from $PepckCreS1pr1^{fl/f}$ mice. (A) Immunofluorescent labeling of actin cytoskeleton (FITC-phalloidin; Actin), cytokine (MCP-1), chemokine (CXCL1), apoptotic marker (Bcl-2-associated X protein; BAX, white), and mitochondria (MitoTracker, Red) in mouse kidney proximal tubule (TKPTS) cells treated with vehicle or cisplatin (20 μ M for 24 hr). Blue, nuclei stained with DAPI, White and blue overlap is shown as pink. Scale bar = 50 μ m. (B) Immunofluorescence labeling of mitochondria (MitoTracker, Red), actin cytoskeleton (FITC-phalloidin; Actin), BAX and nuclei (DAPI) in primary cell cultures of proximal tubule epithelial cells isolated from $PepckCreS1pr1^{ml/m}$ and $PepckCreS1pr1^{nl/m}$ mice and treated with vehicle or cisplatin (20 μ m for 24 hr). Scale bar = 50 μ m. Images are from a representative experiment that was performed at least three times with n = 2-3 replicates of each treatment.

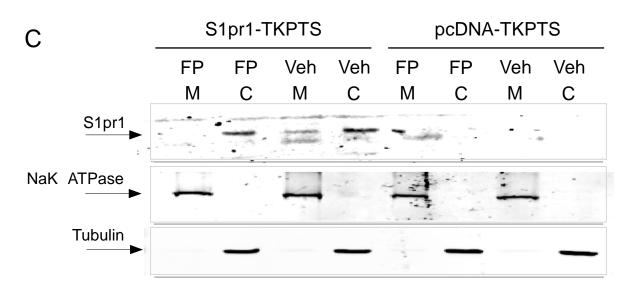
Supplemental Figure 4

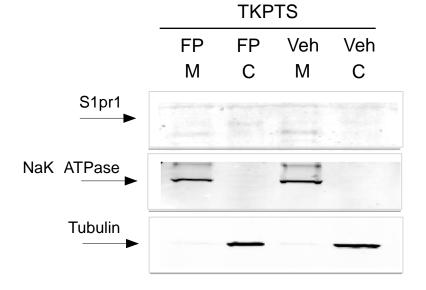


Knockdown or over-expression of S1P1 alters the sensitivity of TKPTS cells to the apoptotic effects of cisplatin in a concentration-dependant manner. Changes in cleaved caspase 3 in response to incubations for 24 hr with vehicle (saline; V) or increasing concentrations of cisplatin in control TKPTS cells (siRNA scramble sequence (A), pcDNA-TKPTS (D)), after receptor knockdown in TKPTS cells with S1pr1 siRNA (B), and in S1P1 over-expressing TKPTS cells (E). Corresponding densitometric analyses of cleaved caspase 3 (c-Casp3)/tubulin) are shown in C and F. Concentrations of cisplatin (indicated on blot and bar graph by widening triangle): 20, 30, 40, 60, or 80 μM . n = 2 samples per treatment in each of 3 replicate experiments.

Supplemental Figure 5 - pg 1





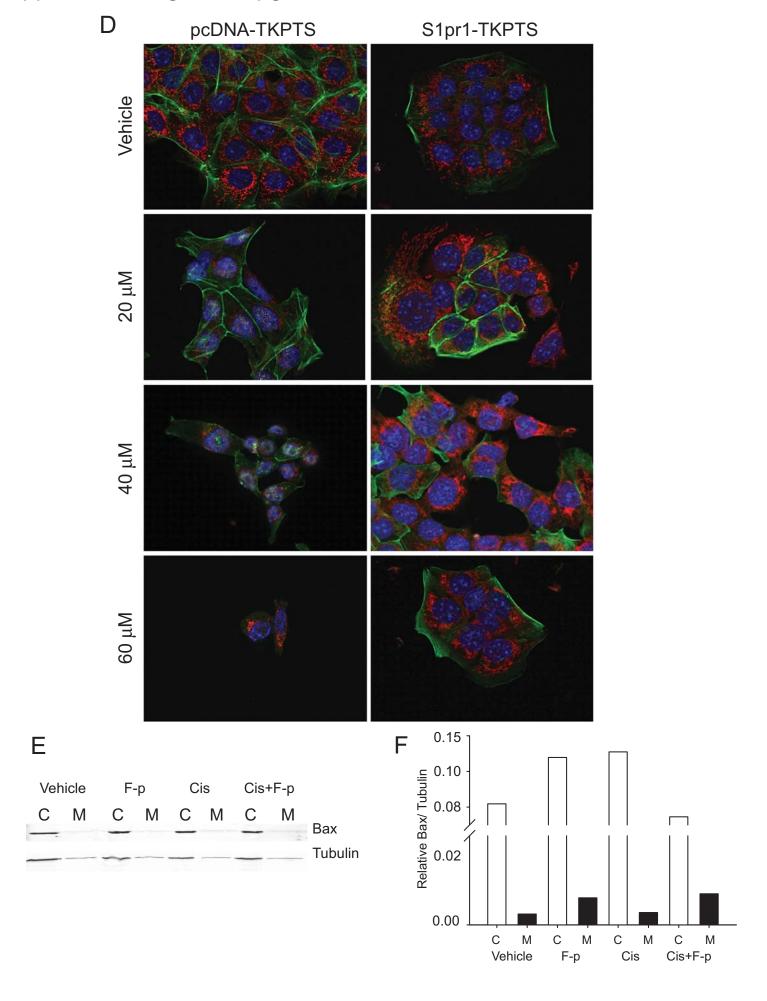


FP: FTY720-p

Veh: Vehicle

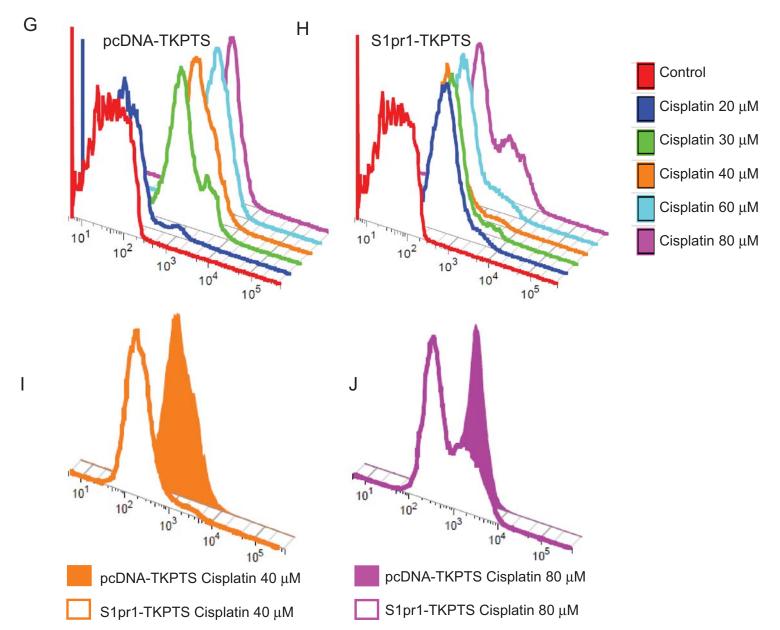
M: Membrane fraction C: Cytoplasmic fraction

Supplemental Figure 5 - pg 2



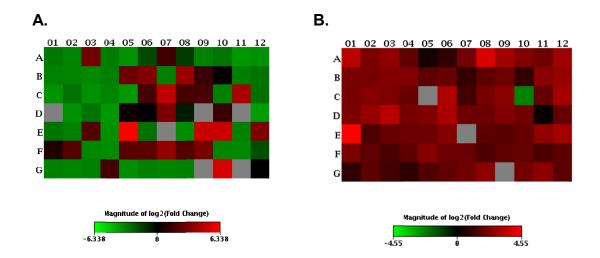
Supplemental Figure 5: Over-expression of S1P1 in TKPTS cells. TKPTS cells were stably transfected (and maintained under G418 selection) with empty pcDNA3.1/V5-His vector (pcDNA-TKPTS) or vector containing the sequence for S1p1r (S1pr1-TKPTS). A, B. Stable over-expression of S1p1r was confirmed by RT-PCR in 3 separate cultures. Relative mRNA levels (A; n = 3; mean \pm SE) and representative agarose gel of PCR products from one experiment (B). C. Cells were treated with vehicle or 10 nM FTY-720-p for 24 hr, cytoplasmic (C) and membrane (M) cell fractions were isolated, and western blotting for S1P1 was performed with NaK-ATPase or tubulin as controls for equal loading. S1P1 is evident in cytoplasmic and membrane fractions of vehicle-treated S1pr1-TKPTS cells but not in the membrane fraction after FTY720-p treatment. S1P1 is undetectable in untransfected TKPTS cells or pcDNA-TKPTS. D. Cells were incubated with vehicle (saline) or cisplatin (20 µM) for 24 hr and then were labeled with FITC-phalloidin to label actin (green) or Mitotracker to label mitochondrai (red). E-F. S1pr1-TKPTS were incubated with vehicle (saline) or 20 µM cisplatin (Cis) for 24 hr or with 10 nM phosphorylated FTY720 (F-p) for 1 hr prior to vehicle or cisplatin. Cytoplasmic (C) and mitochondrial (M) cell fractions were isolated and western blotting was performed for BAX with tubulin as a control for equal loading.

Supplemental Figure 5 - pg 3



Susceptibility of control and S1P1 over-expressing TKPTS cells to increasing concentrations of cisplatin. Cells were incubated with vehicle (saline) or cisplatin (20-60 μ M) for 24 hr and then with FITC-phalloidin to label actin (green) or Mitotracker to label mitochondria (red). S1P1 over-expressing cells were less susceptible than control cells to the apoptotic effects of increasing concentrations of cisplatin. (G-J) Stable over-expression of S1P1 protects TKPTS cells from cisplatin-induced increases in mitochondrial superoxide. Cells were incubated with vehicle (saline) or cisplatin (20-80 μ M) for 24 hr then were labeled with Mitosox (5 μ M for 10 min) and analyzed by flow cytometry (BBRC 358:203-208, 2007). (G) Histograms for cells incubated with saline (control) or 20-80 μ M cisplatin are shown for pcDNA- (H) and S1pr1-TKPTS cells (I). Mitosox fluorescence intensity increased in a concentration-dependent manner with increasing concentrations of cisplatin in control but not over-expressing cells (mean values of replicate experiments shown in Figure 4). To more clearly illustrate the increase in Mitosox fluorescence in control but not in over-expressing cells after cisplatin, examples are illustrated for two concentrations of cisplatin: 40 μ M (J) and 80 μ M (J).

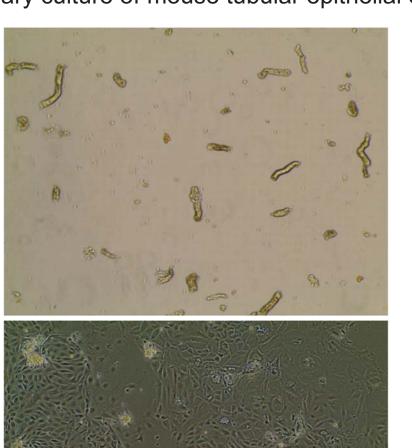
SUPPLEMENTAL FIGURE 6



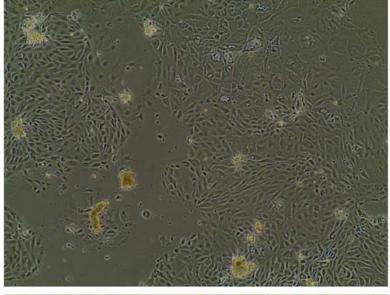
- A. Changes in gene expression in PepckCreS1pr1fl/fl mice compared to PepckCreS1pr1wt/wt
- B. Changes in gene expression in S1pr1-TKPTS cells compared to pcDNA-TKPTS

Expression analysis by PCR array demonstrates mitochondrial genes that are regulated in mouse proximal tubule cells deficient in or over-expressing S1P1. Heat map comparisons generated from PCR array and reflecting relative gene expression values in (A) primary tubule cell cultures from $PepckCreS1pr1^{fl/fl}$ mice compared to $PepckCreS1pr1^{wt/wt}$ mice and (B) S1P1 over-expressing compared to control (V5-transfected) TKPTS cells. Details of specific genes are shown in Table 4.

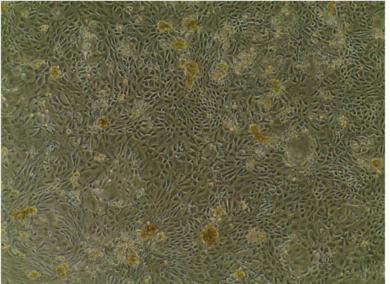
A. Primary culture of mouse tubular epithelial cells



Day 0 - just after plating

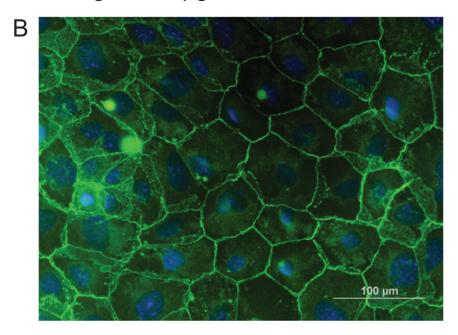


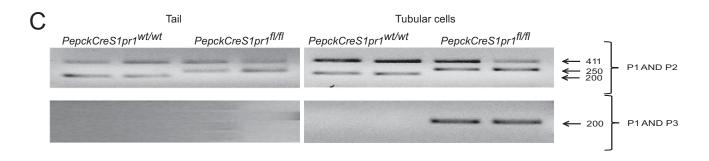
Day 5



Day 7-10

Supplemental Figure 7 - pg 2





Isolation and primary culture of renal tubular epithelial cells (TECs) from PEPCK-Cre-S1P1^{wt/wt} and PEPCK-Cre-S1P1^{fl/fl} mice. (A) Phase contrast photomicrographs of live primary cell cultures on day 0, 5 and 7-10 after plating. For experiments, cells were used between day 7 and 10 of culture when a confluent monolayer is evident. (B) Immunofluorescent labeling of E-cadherin (green) in 7 day cultures (20 μg/ml Alexa 488-labeled ms x E-cadherin, clone DECMA-1, eBioscience, San Diego, CA). Blue, nuclei stained with DAPI. (C) Agarose gel of PCR products resulting from genotyping of samples of tail and isolated tubular epithelial cells from *PepckCreS1pr1^{wt/wt}* and *PepckCreS1pr1^{fl/ft}* mice using primers (P1-3) specific for wt and floxed alleles demonstrates selective deletion of *S1pr1* from kidney tubules. Molecular weight of bands indicated at right.

Supplemental Table 1. Morphometric analysis of mitochondria in TKPTS cells: contour measurements^d

	Feret Maximum ^a	Compactness ^b	Shape Factor ^b	n (mitochondria)	n (cells)
Vehicle	0.50 ± 0.01	0.61 ± 0.01	4.06 ± 0.02	385	22
Scramble	0.52 ± 0.01	0.62 ± 0.01	3.98 ± 0.02	326	22
siRNA #1	0.52 ± 0.01	0.62 ± 0.01	4.00 ± 0.02	374	20
siRNA #4	0.55 ± 0.01	0.58 ± 0.01	4.16 ± 0.03	421	24
FTY720	0.55 ± 0.01	0.61 ± 0.01	4.03 ± 0.02	394	20

^a the longest projection of the minimal bounding box, i.e. parallel tangents apposing opposite sides of the profile; μm

^bvalues are 0-1; a circle has a value of 1

^cdefines a relationship of perimeter to area; a circle has a value of 3.54

^dTKPTS cells were 1) transiently transfected with one of two *S1pr1* siRNAs or a scrambled sequence and harvested after 48 hr or 2) were incubated with 10 nM FTY720 on day 0, 3 and 6 and harvested 24 hr after the last treatment. Cells were prepared for electron microscopy. 20-25 cells were photographed at 6000X from each treatment, and mitochondrial morphometrics were analyzed by using MBF Bioscience StereoInvestigator software (Williston, VT).