SUPPLEMENTARY MATERIALS

Supplementary S1:

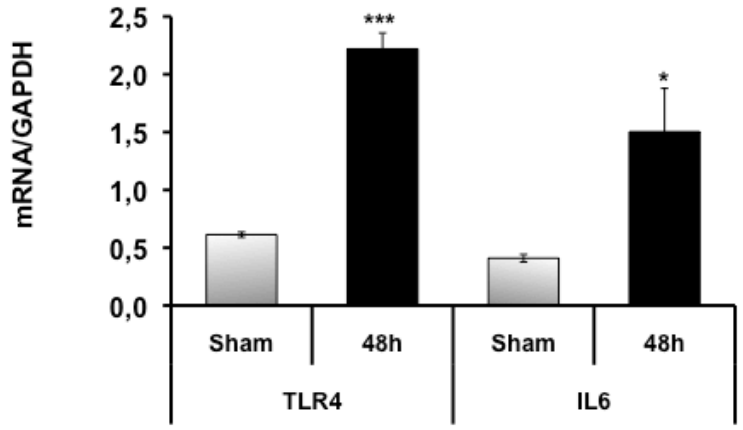

Figure S1: TLR4 and IL6 mRNA expressions in the kidney
The kidneys of Sham and 48-hour-infected WT mice were harvested, and the mRNA levels of both TLR4 and IL-6 were quantified by RT-qPCR. Data were normalized by GAPDH-mRNA levels. The results are the mean ± s.e.m. of at least six individual mice in each group. *P <0.05, ***P <0.0001.

Supplementary S2:

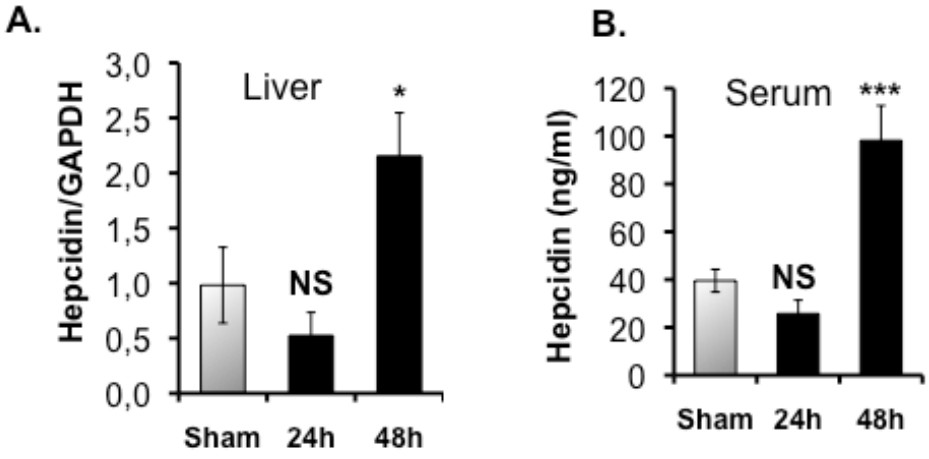

Figure S2:
CBA/J WT mice were infected with 10^9 CFUs of CFT073, and bacterial counts were performed on bladder and kidneys at 24 and 48 h postinfection. (A) Hepcidin mRNA quantification in WT liver at 24 and 48 hours postinfection. (B) WT serum hepcidin measured by LC-MS/MS at 24 and 48 hours post-infection. (Sham) means unifected mice. The results are the mean ± s.e.m. of at least six individual mice in each group. *P < 0.05, ***P <0.0001. NS indicates non-significant.

Supplementary S3:

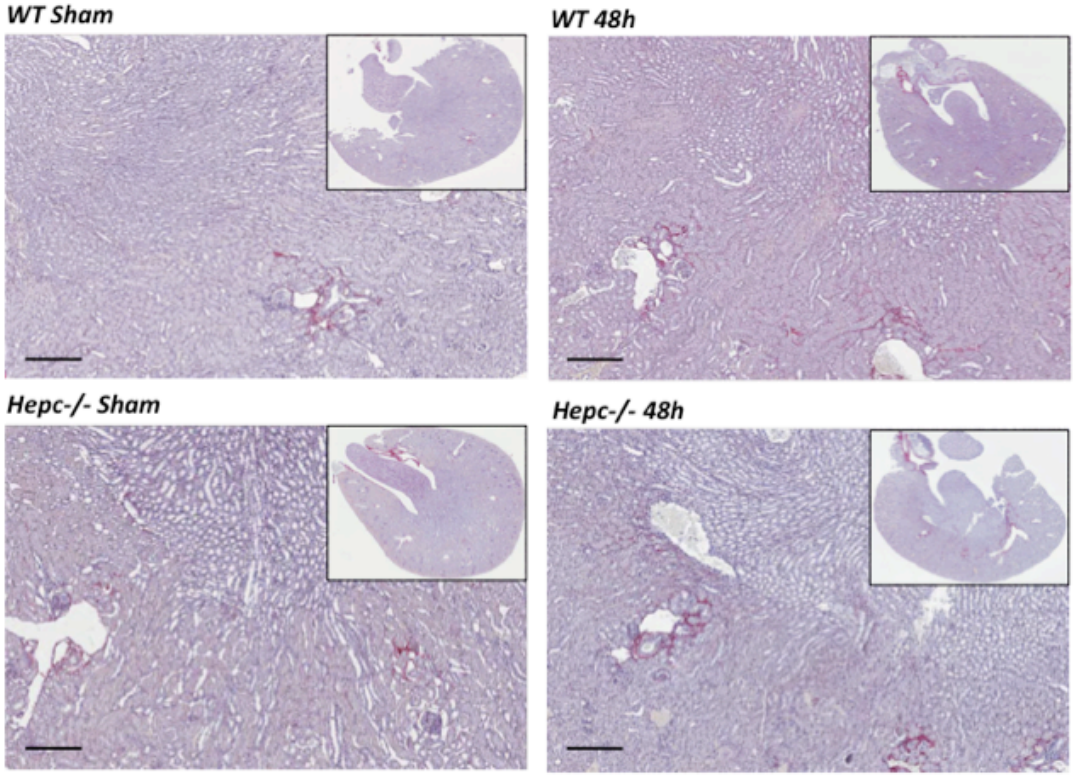

Figure S3:
Histologic examination
The kidneys were fixed in 4% formaldehyde, embedded in paraffin and sections of 4-µm were then stained with picro-sirius red (PSR). Images were acquired using a ScanScope digital scanner (Aperio, TRIBVN, France). Morphologic assessments were conducted by two independent renal pathologists who were uninformed about the treatments and mice phenotypes.

Supplementary S4:

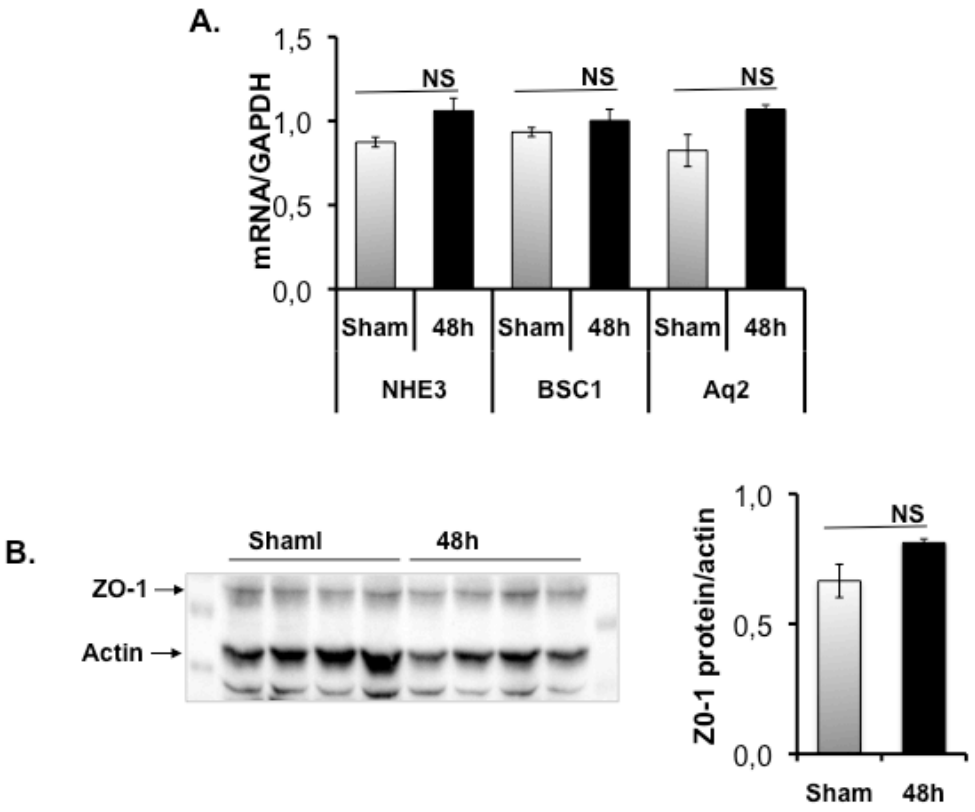

Figure S4: Renal cell damage evaluation
The kidneys of Sham and 48-hour-infected WT mice were harvested for the following studies. (A) The mRNA levels of Na+/H+ exchanger 3 (NHE3), bumetanide-sensitive Na+/K+/2Cl- cotransporter 1 (BSC1) and the water channel aquaporin-2 (AQ2) were quantified by RT-qPCR. Data were normalized by GAPDH-mRNA levels. (B) Protein levels of tight junction ZO-1 were quantified by Western blot. The left panel shows a representative western blot, and the right panel shows the quantification. Data were normalized by β-actin protein level. The results are the mean ± s.e.m. of at least six individual mice in each group. NS indicates non-significant

Supplementary S5:

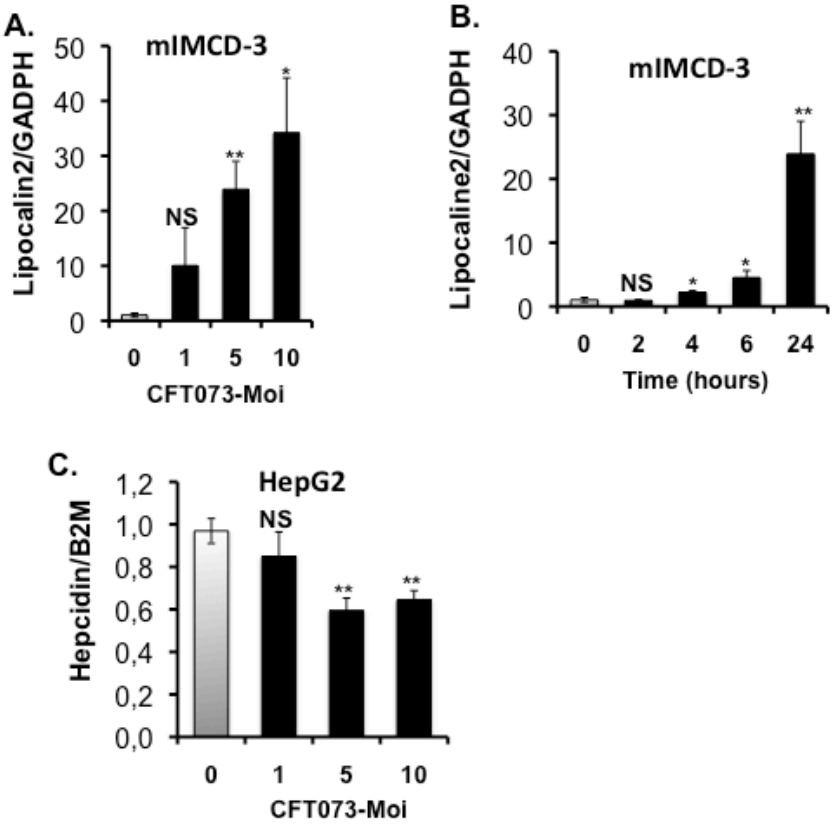

Figure S5: Effect of CFT073 on lipocalin-2 and hepcidin expressions in cultured renal mIMCD-3 and hepatic HepG2 cells respectively.
mIMCD-3 and HepG2 cell lines were infected with PFA-fixed CFT073, and the mRNA level of lipocalin-2 was explored at different MOIs (MOI, multiplicity of infection, number of bacteria per number of monolayer cells) and different incubation times. (A) shows the effect of different MOIs on lipocalin-2 mRNA abundance in mIMCD-3 cells. (B) shows the time-course effect using an MOI of 5:1. (C) Hepcidin-mRNA repression in HepG2 cells in response to different MOIs of CFT073. All mRNA quantifications were determined by RT-qPCR. Data were normalized by GAPDH-mRNA levels. The results are the mean ± s.e.m. of at least three independent cultures. *$P < 0.05$, **$P < 0.03$. NS indicates non-significant.

Table S1

	WT	Hepc-/-	Genotype (Sham)
(ng/ml)	**Sham**	**Sham**	*P* value
IL-6	15.9 ± 0.7	7.5 ± 4.4	**NS**
IFN-γ	51 ± 3.1	65.5 ± 5.6	**NS**
TNF-α	2.3 ± 0.3	5.3 ± 1.1	**0.05**
IL-1α	272 ± 12.3	417± 19.3	**0.002**
CXCL2	12.6 ± 1.6	27.4 ± 4.2	**NS**
CCL5	58.1 ± 9.6	141.3 ± 18.8	**NS**

Table S1
Expression profile of inflammatory cytokines in WT and Hepc-/- kidneys prior CFT073 infection (Sham). The results are the mean ± s.e.m. NS indicates non-significant.