



## AKAP12 ameliorates liver injury via targeting PI3K/AKT/PCSK6 pathway

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### ARTICLE INFO

#### Keywords:

AKAP12

PCSK6

Inflammatory factor

Macrophage infiltration

Liver injury

### ABSTRACT

A kinase anchor protein 12 (AKAP12) is a scaffold protein that is critical for cell structure maintenance and signal transduction. However, the role of AKAP12 in liver injury remains unclear. Here, we attempt to explore the potential contribution of AKAP12 in liver injury and elucidate its underlying molecular mechanism. We found that AKAP12 deletion in acute liver injury (ALI) activates the PI3K/AKT phosphorylation signaling pathway, induces the increased expression of PCSK6 and its downstream inflammation-related genes, and prompts macrophages to produce a large number of inflammatory factors. And knockdown of PCSK6 by *in vivo* siRNA assay reversed in liver injury AKAP12<sup>Δhep</sup> mice, demonstrating that PCSK6 has an important role in ALI. Furthermore, we found that signal transducer and activator of transcription 3 (STAT3) and serine/threonine kinase Akt (AKT) were upregulated in AKAP12<sup>Δhep</sup> mice of chronic liver injury. To sum up, our study here demonstrates that AKAP12 has a protective role in ALI and chronic liver fibrosis, at least in part through inhibition of the PI3K/AKT/PCSK6 pathway. Our findings provide a new potential treatment for liver injury with important clinical implications.

### 1. Introduction

A-kinase anchor protein 12 (AKAP12)/Src-suppressed C-kinase substrate (SSECKS) is a member of the AKAP family and a component of the cytoskeleton structure [1]. AKAP12 maintains the stability of cells and tissues, and regulates cell proliferation and metastasis through activation of the phosphoinositide 3-kinase (PI3K)/protein kinase B (AKT) or protein kinase A (PKA)/protein kinase C (PKC) pathways [1–4].

AKAP12 is reportedly decreased, to varying degrees, and closely related to a poor prognosis and high recurrence rate in cancers of the prostate, breast, liver, and lung [5–8]. AKAP12 acts as a regulator of mitosis by anchoring key signaling proteins, such as PKA, PKC, and cyclins, thereby inhibiting the viability of tumor cells and inducing apoptosis via caspase-3 [4,9,10]. Notably, AKAP12 is reportedly downregulated in hepatocellular carcinoma (HCC) via promoter hypermethylation [11–14] and reduced in hepatic cirrhosis and

precancerous lesions via upregulation of microRNA (miR)-183 and miR-186, which both target AKAP12. In addition, miR-1251-5p negatively regulates AKAP12 expression and plays a carcinogenic role in HCC [12]. Collectively, these findings indicate that AKAP12 acts a tumor suppressor in liver tumorigenesis.

Since AKAP12 protects against liver fibrosis and HCC progression [7, 15,16], it is reasonable to speculate that AKAP12 could influence acute liver failure and hepatocyte death [12,17]. Hence, the potential function and mechanism of AKAP12 in hepatocytes during acute liver injury (ALI) and chronic liver fibrosis were explored using hepatocyte-specific AKAP12 knockout (AKAP12<sup>Δhep</sup>) mice. The results showed that disruption of AKAP12 in hepatocytes dramatically aggravated acute and chronic liver injury in a proprotein convertase subtilisin/kexin type 6 (PCSK6)-dependent manner.

PCSK6, also named PACE4, is a member of the encoding subtilisin-like proprotein convertase family [17,18]. The protease encoded by PCSK6 is expressed in many tissues, including the liver, intestine, and brain [18]. The PCSK6 gene is believed to affect the production of

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**Abbreviations**

ALI	Acute liver injury
AKAP12	A kinase anchor protein 12
PCSK6/PACE4	Proprotein convertase subtilisin/kexin type 6
LPS	Lipopolysaccharide
GalN	Galactosamine
CCL4	Carbon tetrachloride
ROS	Reactive oxygen species
siRNA	small interference RNA
HCC	Hepatocellular carcinoma
AKAPS	A kinase anchoring protein
PI3K	phosphatidylinositol 3 kinase
AKT	serine/threonine kinase Akt/protein kinase B
ALT	Alanine aminotransferase
AST	Aspartate aminotransferase

WB	Western Blot
IL-6	Interleukin-6
IL-1 $\beta$	Interleukin 1 $\beta$
TNF- $\alpha$	Tumor necrosis factor- $\alpha$
TIMP	Tissue inhibitor of metalloproteinase
$\alpha$ -SMA	$\alpha$ -smooth muscle actin
Col-1 $\alpha$ 1	Collagen type 1 alpha 1 chain
NAC	N-acetyl cysteine
Bcl-2	B-cell lymphoma-2
Bax	Bcl-2 associated X protein
RASF	Rheumatoid arthritis synovial fibroblast
LSECs	Liver sinusoidal endothelial cells
STAT3	Signal transducers and activators of transcription 3
ERK	Extracellular regulated protein kinases
JNK	C-Jun N-terminal kinase.

inflammatory factors and to play a role in tumor progression [19]. However, no study has yet analyzed the role of PCSK6 in ALI, and the relationship between AKAP12 and PCSK6 remains unclear.

ALI is the initial cause of most liver diseases. Elevated levels of alanine aminotransferase (ALT) and aspartate aminotransferase (AST) are established diagnostic markers of ALI [20,21]. ALI can cause inflammatory storms and even lead to death [22,23]. Although the importance of preventing ALI and liver failure has been recognized for several decades, treatment to relieve symptoms is the most effective approach, as targeted therapies are lacking. At present, there is an urgent need for the identification of potential targets and development of ALI-targeted drugs. Hence, the aim of this study was to explore the potential function and mechanism of AKAP12 in hepatocytes during ALI and chronic liver fibrosis using *AKAP12<sup>Δhep</sup>* mice to develop novel drug target for treatment.

## 2. Material and methods

### 2.1. Animals

The original AKAP12 knockout mouse was obtained from JiCuiYaoKang company in Nanjing, China. (C57BL/6 N genetic background). An alb-Cre tool mouse was provided by the Model Animal Research Center of Nanjing University in Nanjing, China. The breeding environment was standardized. (25 °C, 55% humidity, 12 h daylight and 12 h day/night light cycles). F1 generation mice, (*AKAP12* systemic knockout mice) were crossed with alb-Cre tool mice to obtain F2 generation mic F2 generation mice were then crossed with one another Finally, F3 generation mice (*AKAP12<sup>fl/fl</sup>* and *AKAP12<sup>Δhep</sup>*) were obtained as the target mice. All experimental steps were supported by the Institutional Animal Care and Use Committee of Tenth's People Hospital (Shanghai, China) and the Use Committee of Second Military Medical University (Shanghai, China).

### 2.2. Animal model of liver injury

For the liver acute or chronic injury model, 8- to 10-week-old *AKAP12<sup>fl/fl</sup>* and *AKAP12<sup>Δhep</sup>* male mice were used. Galactosamine (GalN Sigma, USA) was administered intraperitoneally at a dose of 800 mg/kg. Lipopolysaccharide (LPS) was then administered intraperitoneally at 20  $\mu$ g/kg or 5  $\mu$ g/kg (Sigma). The blank control group was given an equal volume of physiological saline via the abdominal cavity. After intraperitoneal administration of GalN/LPS, the survival rate of mice was measured (n = 8–12 per group). For the ALI model, carbon tetrachloride (CCl4) was administered by intraperitoneal injection at a dose of 4 ml/kg. The liver fibrosis model involved treatment with CCl4 mixed

with olive oil (1:9 v/v), three times per week for 10 weeks. Lastly, *siPCSK6* was injected intravenously (40 nmol per mouse).

### 2.3. Cell line construction and RNA interference

The mouse HCC cell line Hepa 1-6 was cultured in a 37 °C, 5% CO<sub>2</sub> environment. The production of lentivirus for stable cell line construction was completed by GenePharma (Shanghai, China). For RNA interference, siRNA was purchased from GenePharma (Shanghai, China). Lipofectamine™ 3000 Transfection Reagent (L3000015 Thermo Fisher, Waltham, MA, USA) was used to transfect (si) RNA.

### 2.4. Immunohistochemical (IHC) analysis

Liver specimens were dewaxed, soaked in H<sub>2</sub>O<sub>2</sub> for 20 min, washed three times with water, and incubated with an acid repair antigen for 5 min at 100 °C. Afterward, the specimens were washed three times, treated with blocking solution containing 1% bovine serum albumin for 30 min, and probed with a primary antibody overnight at 4 °C. The next day, the specimens were washed four times with phosphate-buffered saline (PBS) and probed with a secondary antibody for 30 min at 37 °C. After washing with PBS, the specimens were stained with 3,3'-diaminobenzidine (DAB) followed by hematoxylin for 10 min. Following dehydration, the specimens were coated with 50  $\mu$ L of neutral resin.

### 2.5. Tissue protein extraction

Tissue samples (20 mg) were collected, frozen in liquid nitrogen, ground into powder, and placed in 1.5-mL centrifuge tubes. Following the addition of 1 mL of lysis buffer (P0013J Beyotime Institute of Biotechnology, Haimen, China), the samples were homogenized for 30 s at 1500 $\times$ g, then centrifuged for 30 min. The supernatant was collected for further analysis.

### 2.6. Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assay to assess apoptosis

After full deparaffinization and hydration, the samples were incubated with proteinase K solution for 10–30 min, washed with PBS, and incubated with TUNEL reaction solution for 1 h at 37 °C. Afterward, the samples were immersed in 0.3% H<sub>2</sub>O<sub>2</sub> for 15 min, washed three times with PBS, reacted with 100  $\mu$ L of horseradish peroxidase-conjugated streptavidin (diluted to 1:500 in PBS) for 30 min, then washed three times for 5 min with PBS. Finally, the samples were stained with DAB for 10 min, washed with PBS, and coated with neutral resin.

## 2.7. Isolation of mouse primary hepatocytes

Mouse livers were perfused with egtazic acid solution for 1–2 min at a flow rate of 5 mL/min, followed by pronase solution for 5 min and then infused with collagenase solution for 7 min. Afterward, the liver tissue was minced with 5 mL of pronase/collagenase solution and 1% DNase, then placed in a sterile petri dish. Following centrifugation at 180 rpm for 25 min, the tissue was filtered once through a 7- $\mu$ m cell strainer and then centrifuged at 50 $\times$ g for 10 min at 4 °C. After aspiration of the supernatant, the cells were suspended in 120  $\mu$ L of DNase I, then washed and centrifuged at 50 $\times$ g for 10 min at 4 °C.

## 2.8. mRNA level analysis

Mouse liver tissue was collected, added to Trizol, and stored at -80 °C until total RNA was extracted. The tissue was homogenized with ceramic beads, then RNA was extracted and reverse-transcribed into cDNA. The obtained cDNA was used for quantitative PCR (CFX96/384 TouchTM, Bio-Rad). Prior to use, each set of primers (Table 1) and RT-PCR conditions were extensively optimized to improve the efficiency of the reaction and avoid interference from primer dimers. The cycle parameters were as follows: 1 min at 65 °C, 45 cycles of 30 s at 94 °C, 1 min at 59 °C, and 1 min at 72 °C. Real-time quantitative PCR data were normalized to reference gene  $\beta$ -actin expression using the  $2^{-\Delta\Delta Ct}$  method.

## 2.9. Statistical analysis

Statistical analyses were conducted using GraphPad Prism 7.0 software (GraphPad Software, Inc., San Diego, CA, USA). Values are expressed as the mean  $\pm$  standard error. The two-tailed Student's *t*-test was used to identify significant differences between two groups. Comparisons were made using the two-tailed paired *t*-test. A probability (*p*) value of <0.05 was considered statistically significant.

**Table 1**  
Primer sequence.

Gene		Sequences (5'-3')
m-PCSK6	Forward	CAGGCGGAAGTGA CTCTC
	Reverse	GACCGACAGCGACTGTTCTT
m-Fut8	Forward	GGTTCCTGGCGTTGGATTATG
	Reverse	TCAATGGGGCCTTCTGGTATT
m-Kif21a	Forward	AAGATCGAAGGTTGCCATATCTG
	Reverse	CAGCTCCGGTTTGTCCATAGG
m-Golgb1	Forward	ATCAGGAGATTACACTGACTGGA
	Reverse	GAGCATCCTCTTGCCTGGATT
m-Zfand6	Forward	GCTCAAGAACTAATCACAGCCA
	Reverse	GGTGGGCTTATTCTACCATTCG
m-Sertad2	Forward	AAGGAGGAAAACGGAAGTTTGAT
	Reverse	TGAAGATAGTCTGGCGCTGTA
m-Men1	Forward	ACGGTGCAGATTACAGGGGA
	Reverse	TTGGGGTACTTCAGCGTGTG
m-Trim3	Forward	CCTGGGATTAATCATGGACCAC
	Reverse	TGACAGGACACTTATCAAAGGC
m-Dtx3	Forward	ACCCAATGTCATCACTGGGAAC
	Reverse	CCTCTTGCACCTAGTCAGGT
m-Ap3m2	Forward	CCCAAGAGAGAGCTACCGAG
	Reverse	GAACAGACCCAAAATAGTCTCTG
m- $\beta$ -actin	Forward	GGCTGTATTCCCTCCATCG
	Reverse	CCAGTTGGTAACAAATGCCATGT
m-Bcl 2	Forward	GTGCGTACCCTGCTGACTTC
	Reverse	CAGACATGCACCTACCCAGC
m-cre	Forward	GATGGATGGATGAGATCATAGGAG
	Reverse	GAGGCTCAAGAGGCGAAATG
m-Prkcd	Forward	CTCTTCCAGTCGTAAGCAGC
	Reverse	CCTTGGTAGGTTGAGGAGGTT
m-AKAP12	Forward	TGATGGGTGGAAACACAGG
	Reverse	CTTCTAAAGCAGCACAGGATATG

## 3. Results

### 3.1. Knockdown of AKAP12 in hepatocytes exacerbated galactosamine (D-GalN)/lipopolysaccharide (LPS)-induced ALI

Hepatocyte-specific AKAP12 knockout (*AKAP12<sup>Δhep</sup>*) mice were established by crossing *alb-Cre* mice with *AKAP12<sup>fl/fl</sup>* mice. *AKAP12<sup>Δhep</sup>* mice was validated by real-time quantitative polymerase chain reaction (qPCR) and IHC staining (Supplemental Figs. 1A–C). Subsequently, *AKAP12<sup>fl/fl</sup>* and *AKAP12<sup>Δhep</sup>* mice were subjected to a mouse model of ALI (low concentration group: 800 mg/kg GalN + 5  $\mu$ g/kg LPS). As shown in Fig. 1A, mice were sacrificed at indicated time points and tissues and serum were collected. Another set of mice were used to assess survival after intraperitoneal injection of drugs to induce ALI (Fig. 1B). The results showed that liver congestion was more severe in the *AKAP12<sup>Δhep</sup>* group than the *AKAP12<sup>fl/fl</sup>* group at 4 h and 6 h (Fig. 1C). The livers of the two groups at 4 h were stained with hematoxylin and eosin (H&E). As shown in Fig. 1D, *AKAP12* deletion was associated with more severe liver damage. Glutathione (GSH) is an important regulator of intracellular metabolism. A decrease in serum GSH content is an established marker of oxygen free radical production and subsequent apoptosis [24,25]. Mouse serum was collected for detection of GSH and the liver function indicators ALT and AST. The results showed that serum GSH was significantly decreased, while serum ALT and AST were significantly increased in *AKAP12<sup>Δhep</sup>* group (Fig. 1E and F). The causes of liver congestion and necrosis were further investigated. The IHC results revealed that infiltration of F4/80-positive macrophages around the liver sinusoids was relatively increased in *AKAP12<sup>Δhep</sup>* mice (Fig. 1G). Furthermore, mRNA levels of the inflammatory cytokines interleukin (IL)-1 $\beta$ , IL-2, IL-6, and tumor necrosis factor (TNF)- $\alpha$  were significantly higher in the livers of *AKAP12<sup>Δhep</sup>* mice as compared with *AKAP12<sup>fl/fl</sup>* mice (Fig. 1H). Finally, the expression levels of pro-apoptotic cleaved poly ADP-ribose polymerase (PARP) and cleaved caspase-3 were increased in *AKAP12<sup>Δhep</sup>* mice (Fig. 1I). Collectively, these results confirmed that liver damage was more severe in the *AKAP12<sup>Δhep</sup>* group and that knockout of *AKAP12* promoted liver damage.

Another model of ALI (high concentration group: 800 mg/kg GalN + 20  $\mu$ g/kg LPS) showed that liver damage was also more severe in the *AKAP12<sup>Δhep</sup>* group (Supplemental Figs. 2A–E). Together, these results demonstrate that *AKAP12* plays an important role in maintaining the stability of cellular structures and resisting damage by ROS.

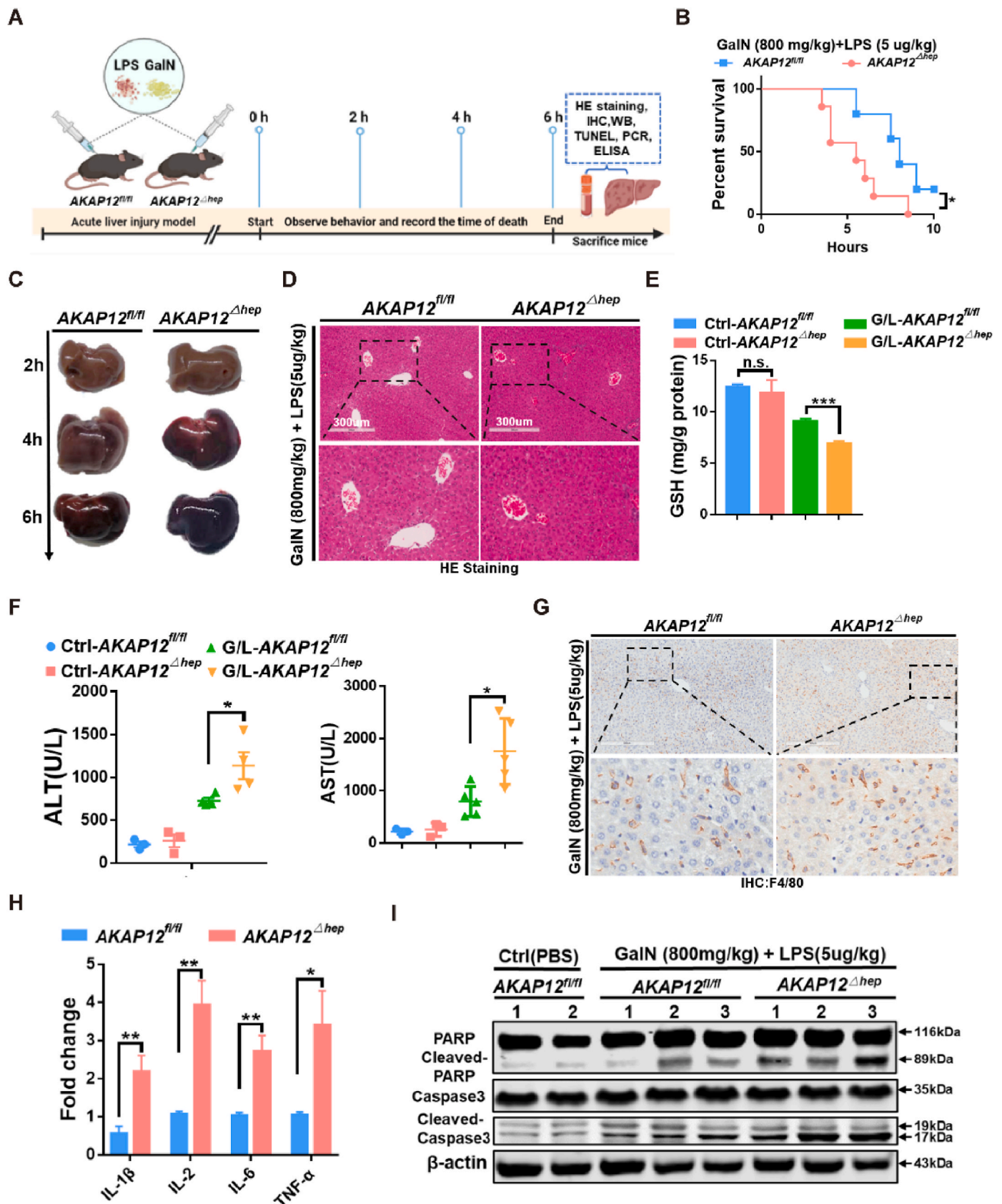
### 3.2. Hepatic AKAP12 deficiency aggravates carbon tetrachloride (CCL<sub>4</sub>)-induced ALI

To further confirm the role of hepatic *AKAP12* in ALI, a mouse model of CCL<sub>4</sub>-induced ALI was constructed (Fig. 2A). Mice were sacrificed at 12 h after intraperitoneal administration of CCL<sub>4</sub> (Fig. 2A). H&E staining of liver tissues demonstrated larger areas of hepatic necrosis in the *AKAP12<sup>Δhep</sup>* group as compared with the control group (Fig. 2B). TUNEL staining showed that the liver tissues of the *AKAP12<sup>Δhep</sup>* mice were enriched with apoptotic hepatocytes (Fig. 2C). In addition, serum GSH levels were significantly decreased in the *AKAP12<sup>Δhep</sup>* group as compared with the control group, indicating early activation of apoptosis (Fig. 2D). Meanwhile, serum levels of ALT and AST were increased in the *AKAP12<sup>Δhep</sup>* group (Fig. 2E). Finally, qPCR analysis showed that the mRNA expression of the inflammatory factors IL-1 $\beta$ , IL-6, and TNF- $\alpha$ , were significantly increased in the liver tissues of *AKAP12<sup>Δhep</sup>* mice (Fig. 2F). Taken together, these results suggest that hepatocyte-specific knockout of *AKAP12* triggers more severe liver injury during ALI.

### 3.3. Loss of AKAP12 results in more severe CCL<sub>4</sub>-induced liver fibrosis

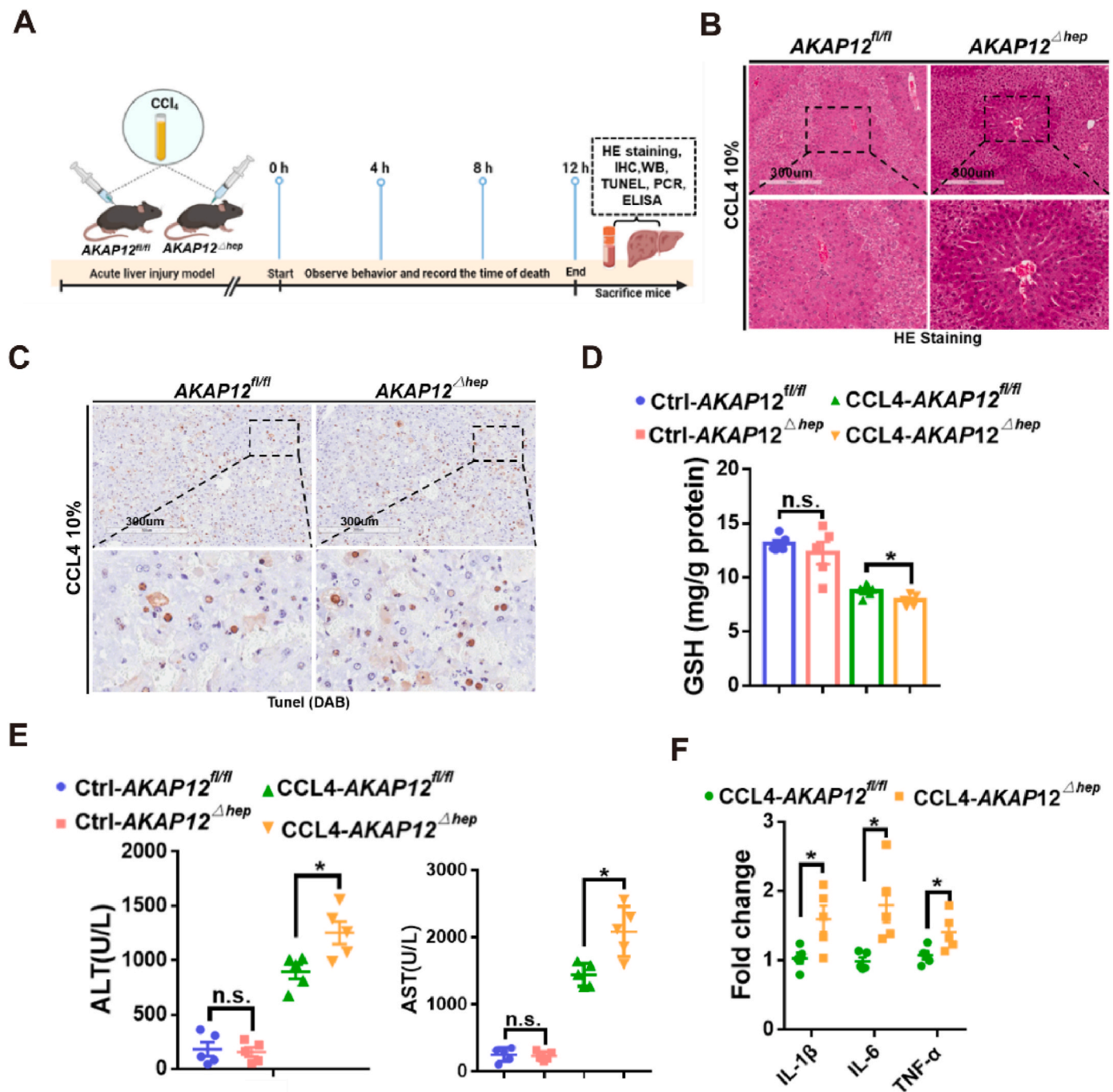
The experimental results confirmed that *AKAP12* knockout induces





**Fig. 1.** AKAP12 knockout exacerbates LPS-GalN ALI. (A) Schematic diagram of the mouse experiments. (B) Statistical analysis of survival time (n = 5–8/group). (C) Mouse livers were collected at 2, 4, and 6 h after intraperitoneal injection of 800 mg/kg GalN + 5 μg/kg LPS. (D) H&E staining. (E) Serum levels of GSH (n = 5/group). (F) AST and ALT levels as markers of liver function (n = 5/group). (G) IHC staining. (H) mRNA expression levels of inflammatory factors in liver tissue (n = 3/group). (I) Western blot (WB) analysis of the apoptotic proteins PARP, cleaved PARP, caspase-3, and cleaved caspase-3 (n = 3/group) (\*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.0001).





**Fig. 2.** AKAP12 knockout aggravates CCl<sub>4</sub>-mediated ALI. (A) CCl<sub>4</sub>-induced acute liver injury model (n = 5–8/group). (B) H&E staining (C) TUNEL staining of apoptotic cells. (D) Serum GSH content (n = 5/group). (E) Serum levels of ALT and AST as indicators of liver function (n = 5/group). (F) Serum levels of inflammatory factors (n = 3/group) (\*p < 0.05, n.s. p > 0.05).

more severe liver injury. To further explore the role of AKAP12 in liver fibrosis, AKAP12<sup>Δhep</sup> and AKAP12<sup>fl/fl</sup> mice were treated with CCl<sub>4</sub> for 10 weeks. The staining results (Masson, Sirius red, and IHC) demonstrated a dramatically increased level of liver fibrosis in the AKAP12<sup>Δhep</sup> group as compared with the AKAP12<sup>fl/fl</sup> group (Fig. 3A–C). Subsequently, markers of early fibrosis and inflammation were detected. The expression levels of  $\alpha$ -smooth muscle actin ( $\alpha$ -SMA) and tissue inhibitor of metalloproteinase 1 were significantly higher in the liver tissues of the AKAP12<sup>Δhep</sup> group than the control group at weeks 2, 4, 6, 8, and 10 (Fig. 3D). The expression levels of inflammatory factors were significantly increased in the liver tissues of AKAP12<sup>Δhep</sup> mice (Fig. 3E). WB analysis of  $\alpha$ -SMA protein levels confirmed that liver fibrosis was more

severe in the AKAP12<sup>Δhep</sup> group than the AKAP12<sup>fl/fl</sup> group at 2, 6, and 10 weeks (Fig. 3F). To further investigate the mechanism by which AKAP12 deficiency exacerbates liver fibrosis, four pathways closely associated with liver fibrosis were examined. The results showed that signal transducer and activator of transcription 3 (STAT3) and serine/threonine kinase Akt (AKT) were phosphorylated (activated) in the liver tissues of the AKAP12<sup>Δhep</sup> group (Fig. 3G). However, there was no significant difference in the expression levels of phosphorylated extracellular regulated protein kinase (ERK) and c-Jun N-terminal kinase (JNK) between the two groups (Fig. 3G). Loss of AKAP12 activates the p-STAT3 and p-AKT pathways and aggravates liver fibrosis.

(A–C) Liver samples were collected from mice treated with CCl<sub>4</sub> at 0,

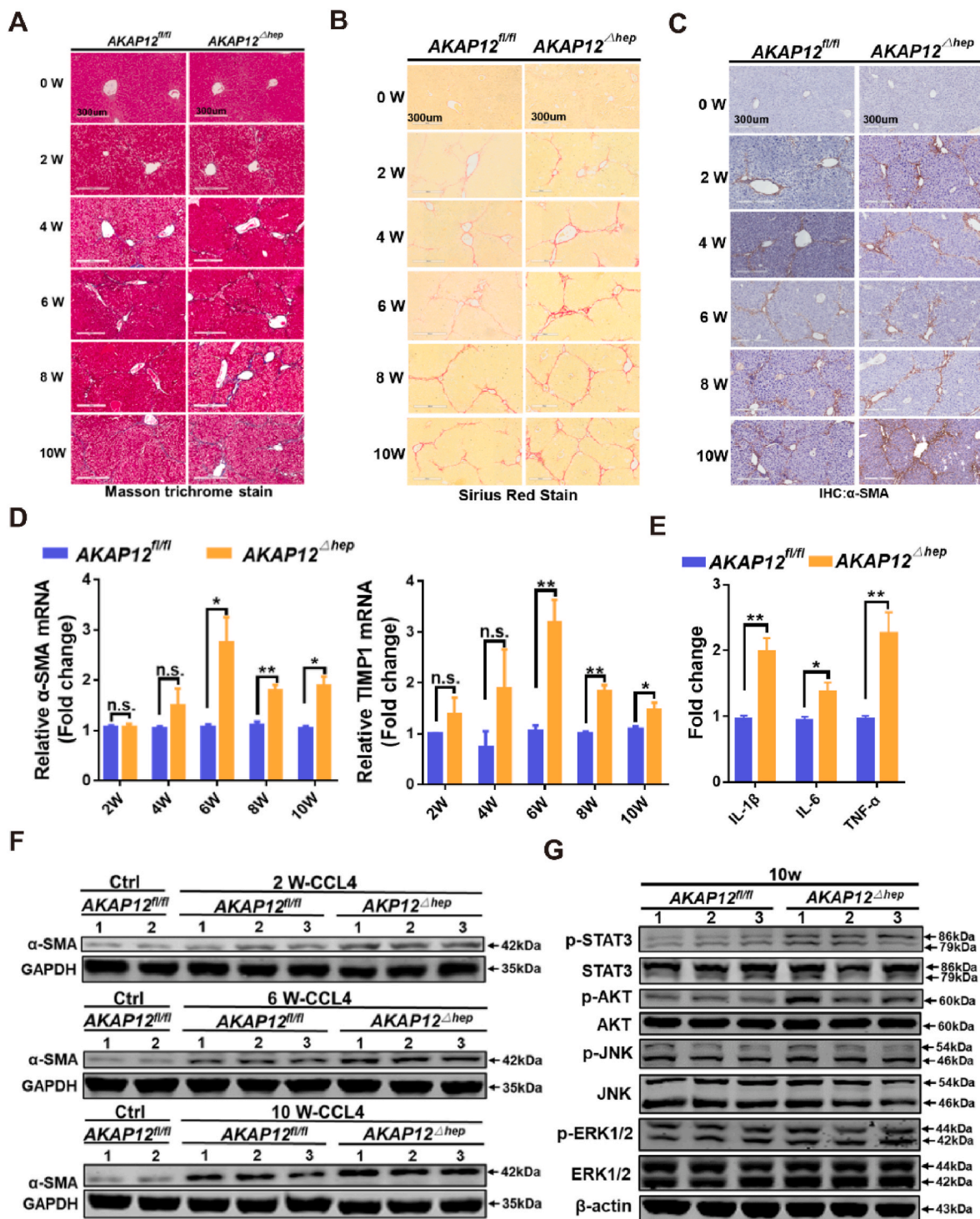


Fig. 3. Knockout of AKAP12 results in more severe CCL4-induced liver fibrosis.

2, 4, 6, 8, and 10 weeks and stained (Masson trichrome, Sirius red, and IHC). (D) Detection of fibrosis-related genes (n = 3/group). (E) Detection of inflammatory factors (n = 3/group). (F) WB analysis of α-SMA protein expression at 2, 6, and 10 weeks (n = 3/group). (G) Phosphorylation pathway detection (n = 3/group) (\*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, n.s. p > 0.05).

### 3.4. Limited role of antioxidants in GalN/LPS-induced ALI of *AKAP12<sup>Δhep</sup>* mice

The use of antioxidants has potential to alleviate acute liver damage. Therefore, we tested if antioxidant N-acetylcysteine (NAC) could reverse exacerbated ALI in *AKAP12<sup>Δhep</sup>* mice. NAC were added to the drinking water of mice 24 h before the experiment, followed by intraperitoneal injection of NAC (150 mg/kg) at 30 min post GalN/LPS dosing. After NAC treatment, H&E staining, liver function and GSH results demonstrated that liver damage was alleviated in both *AKAP12<sup>fl/fl</sup>* and



*AKAP12<sup>Δhep</sup>* mice (Fig. 4A–C). However, the expression levels of liver inflammatory factors remained significantly elevated in the *AKAP12<sup>Δhep</sup>* group as compared with the *AKAP12<sup>fl/fl</sup>* group (Fig. 4D). The IHC staining results demonstrated that the liver tissues of *AKAP12<sup>Δhep</sup>* mice had greater infiltration of macrophages (Fig. 4E). Moreover, the expression levels of apoptotic proteins were significantly elevated in *AKAP12<sup>Δhep</sup>* mice (Fig. 4F).

NAC treatment had no significant effect on high concentration-GalN/LPS and CCL<sub>4</sub> induced ALI. Although liver congestion and necrosis could be relieved, the levels of inflammatory factors in serum were still significantly increased (Supplemental Figs. 3A–D and Supplemental Figs. 4A–E). The results suggested that in addition to oxidative stress, there are other factors that exacerbate liver injury. Taken together, these results revealed that NAC has limited protection against *AKAP12*

knockdown-induced ALI and did not effectively reduce the production and infiltration of inflammatory factors, indicating that factors other than ROS trigger liver injury in *AKAP12<sup>Δhep</sup>* mice.

### 3.5. PCSK6 is a potential target of AKAP12

RNA sequencing was performed to identify targets of AKAP12. Whole transcriptome sequencing of liver tissues from untreated *AKAP12<sup>Δhep</sup>* and *AKAP12<sup>fl/fl</sup>* mice (n = 3/group) identified 1275 genes that were upregulated and 987 that were downregulated. The results are presented in a heat map (Fig. 5A) and volcano plot (Fig. 5B). qPCR was performed to verify the changes of the top 10 upregulated genes (Table 2 and Fig. 5C). PCSK6 was the most significantly elevated gene in the liver of *AKAP12<sup>Δhep</sup>* mice and is strongly associated with inflammation and

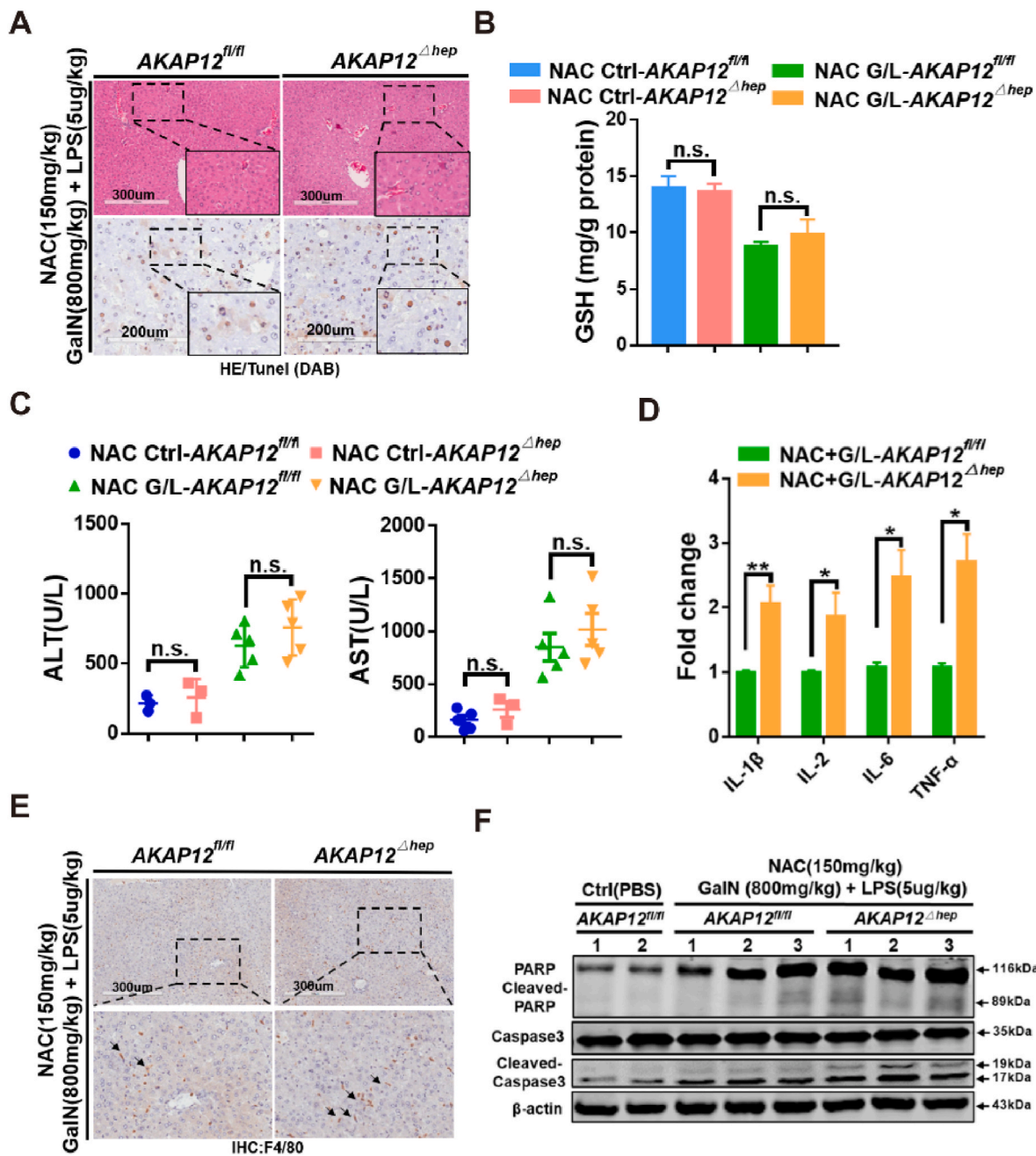
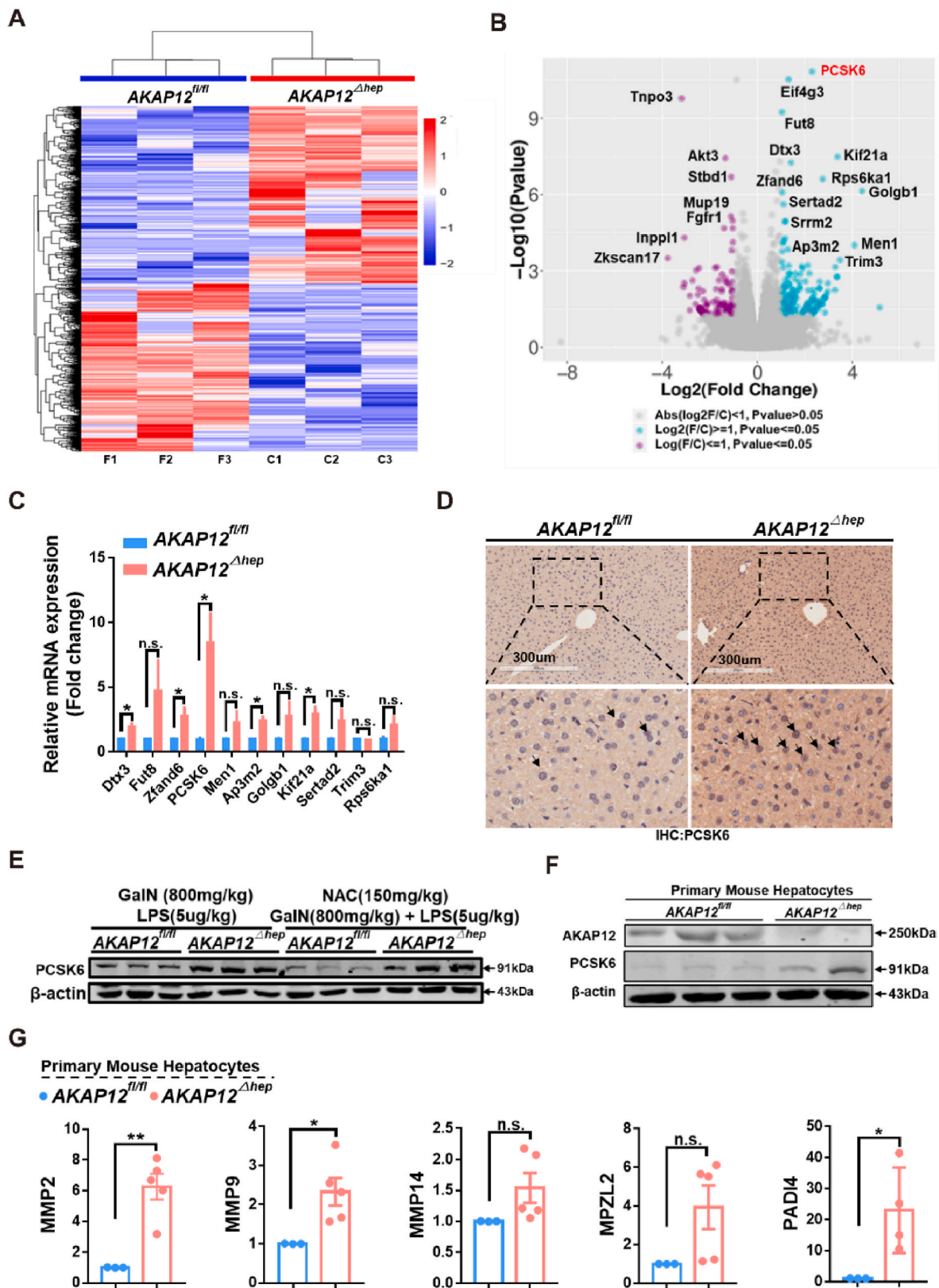


Fig. 4. NAC failed to relieve ALI. (A) Liver tissues were collected from mice with ALI within 4 h of NAC administration (150 mg/kg) for H&E and TUNEL staining (n = 5–12/group). (B) Serum GSH content (n = 5/group). (C) Serum ALT and AST levels (n = 5/group). (D) mRNA expression levels of inflammatory factors in liver tissues (n = 3/group). (E) IHC staining of F4/80. (F) Expression levels of apoptotic proteins in liver tissues (n = 3/group) (\**p* < 0.05, \*\**p* < 0.01, *n.s.* *p* > 0.05).





**Fig. 5.** PCSK6 expression was significantly increased in the liver tissues of *AKAP12<sup>Δhep</sup>* mice. (A) Whole transcriptome sequencing of liver tissues of untreated *AKAP12<sup>Δhep</sup>* and *AKAP12<sup>fl/fl</sup>* mice (n = 3/group). (B) A volcano map. (C) Verification of mRNA levels (n = 3/group). (D) IHC detection of PCSK6 expression. (E) WB detection of PCSK6 protein expression (F) Protein expression of AKAP12 and PCSK6 in primary hepatocytes of *AKAP12<sup>Δhep</sup>* mice (n = 2–3/group). (G) mRNA expression of PCSK6 downstream genes (n = 3/group) (\*p < 0.05, \*\*p < 0.01, n.s. p > 0.05).

**Table 2**  
Differential gene list.

Up genes	F1	F2	F3	C1	C2	C3	FoldChange	C_vs_F_Pvalue
Pcsk6	0	0	0	12.2	11.5	11.6	11.75	4.54E-132
Eif4g3	0	0	0	10.1	10.6	8.3	9.67	2.87E-34
Fut8	0	0	0	8.9	7.81	9.45	8.72	5.73E-36
Kif21a	0	0	0	5.49	7.75	9.33	7.52	2.32E-09
Prkcd	0	0	0	6.58	7.14	7.28	7	4.03E-29
Rps6ka1	0	0	0	7.1	6.03	7.22	6.78	3.92E-22
Golgb1	0	0	0	7.24	6.34	6.54	6.71	6.38E-24
Zfand6	0	3.35	5.1	9.54	9.34	9.24	6.55	6.35E-08
Sertad2	2.4	0	0	7.73	7.88	6.09	6.45	6.21E-13
Srrm2	1	1.02	1.54	11.5	11	0	6.31	0.007822695
Men1	0	3.49	0	6.66	6.89	7.34	5.8	2.38E-05
Trim3	1	1.02	0	6.89	3.24	6.33	4.81	1.60E-06
Dtx3	0	0	0	2.93	5.36	5.76	4.68	1.88E-06
Hook 2	3.4	0	1	6.04	6.16	4.96	4.6	0.001763728
Ap3m2	0	0	0	6.66	6.28	0.83	4.59	0.002569802
AU040320	0	0	3.64	4.59	5.36	7.38	4.57	0.012275122
Tnpo1	1	3.35	5.02	3.12	10.7	9.15	4.53	0.040947987
Khk	6	5.73	6.08	10.6	10.3	10.5	4.52	9.15E-109
Ncmap	0	0	0	5.04	4.24	4.11	4.46	8.70E-09
Exoc3l4	0	0	0	4.46	4.24	4.45	4.38	1.98E-09
Down genes	F1	F2	F3	C1	C2	C3	FoldChange	C_vs_F_Pvalue
Tnpo3	10	10.5	10.8	0	2.06	2.49	-9.06	7.94E-121
Akt 3	8.9	9.09	9.24	1.68	1.63	1.35	-7.51	5.52E-72
Stbd1	6.1	7.38	7.48	0	0	0	-6.99	1.35E-22
Mup19	9.6	7.38	3.4	0	0	0	-6.8	0.043743349
Fgfr1	6.4	7	6.67	0	0	0	-6.7	8.54E-28
Inpp11	8.1	9.44	8.44	2.44	3.53	0	-6.69	2.43E-14
Zkscan17	7.8	8.64	6.22	0	0	2.84	-6.59	1.43E-07
Stat 1	5.7	6.86	6.96	0	0	0	-6.51	7.63E-20
Ppp2r5e	6.5	6.51	6.24	0	0	0	-6.42	2.75E-26
C2cd3	6.5	5.91	6.12	0	0	0	-6.19	4.00E-22
Synpo	3.4	7.13	7.58	0	0	0	-6.03	1.82E-06
Tubd1	6.4	6.18	5.26	0	0	0	-5.93	4.83E-17
Srl	6.6	6.64	6.27	0	0	1.73	-5.92	3.87E-24
Bend 4	5.8	6.42	5.49	0	0	0	-5.91	7.66E-18
Ilvbl	5.8	5.61	6.26	0	0	0	-5.9	1.82E-19
Poli	7.1	6.35	5.18	0	1.04	0	-5.87	9.91E-14
Pus 10	8.4	7.55	8.91	4.46	1.04	2.03	-5.78	8.59E-09
Tipin	7.1	7.78	7.25	4.04	0	0.83	-5.74	4.57E-05
Fign 12	8.4	5.94	7.75	2.44	1.63	0.83	-5.72	1.40E-13
Pds5b	6.5	7.05	6.75	3.3	0	0	-5.68	7.22E-06

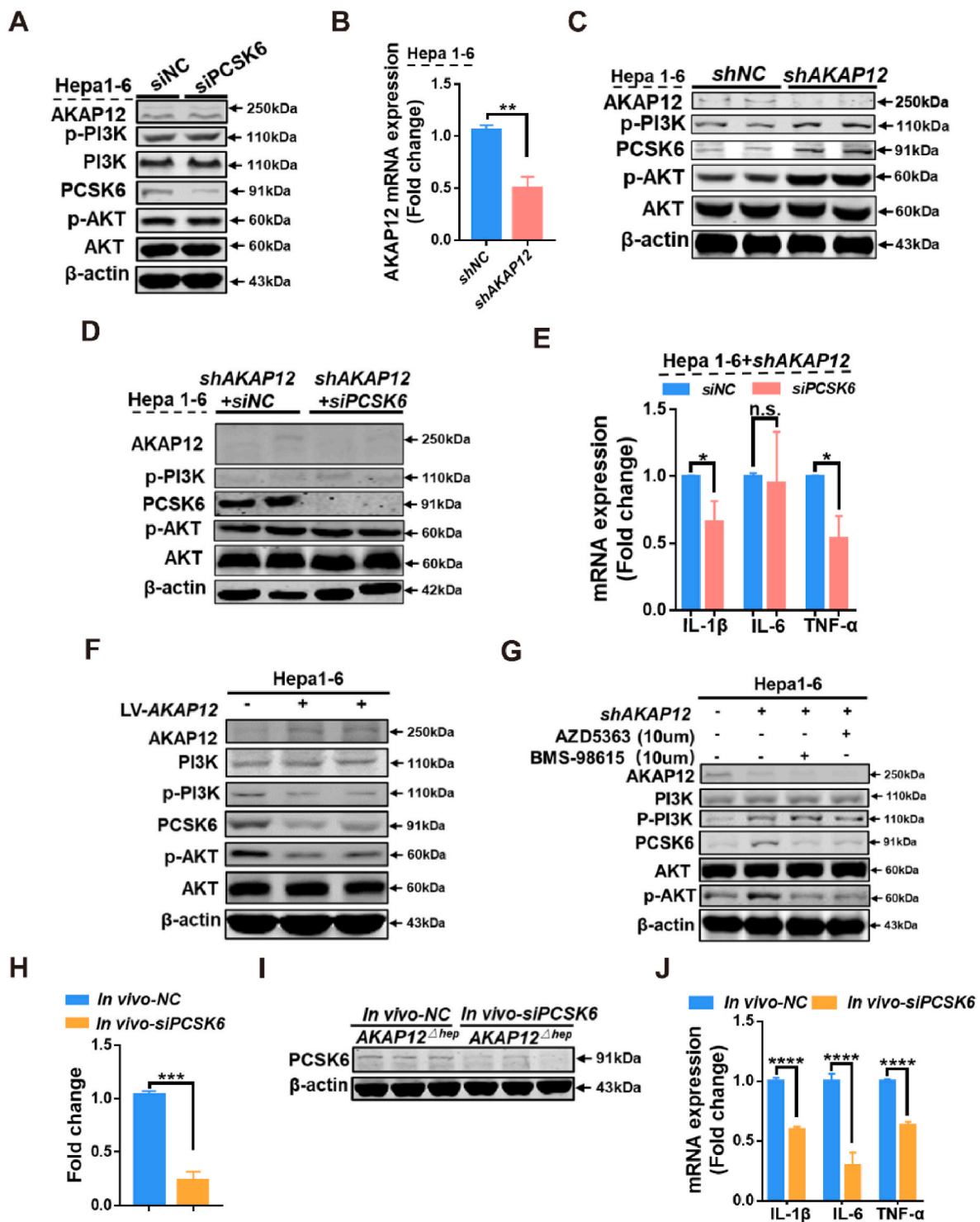
autoimmune disease [26,27] (Fig. 5C). PCSK6, which is expressed in various tissues, including the liver, intestine, and brain [28,29], is reported to affect the production of inflammatory factors and to play a role in tumor progression. Specific knockout of *AKAP12* in hepatocytes triggered increased PCSK6 expression (Fig. 5D and E). Notably, NAC had no effect on PCSK6 expression (Fig. 5E). Moreover, analysis of primary hepatocyte confirmed that knockout of *AKAP12* promoted elevation of PCSK6 protein expression (Fig. 5F). In addition, several studies have reported that increased *PCSK6* induces increased expression of downstream inflammation-related genes [30,31]. In the present study, the downstream target genes of PCSK6, including matrix metalloproteinase 2 (MMP2), MMP4, MMP9, and peptidyl arginine deiminase 4, were significantly increased in the liver tissues of *AKAP12*<sup>Δhep</sup> mice (Fig. 5G). These results suggested that *AKAP12* inhibited expression of PCSK6.

### 3.6. *AKAP12* knockout activated the PI3K/AKT pathway and promoted PCSK6 expression, thereby exacerbating ALI

Various cell lines (*PCSK6* silenced, *AKAP12* silenced, *AKAP12* overexpressed, and *PCSK6/AKAP12* silenced) were constructed to explore the mechanism underlying regulation between *AKAP12* and PCSK6. Silencing of PCSK6 reduced PCSK6 expression, but had no effect on the expression levels of *AKAP12*, PI3K, and AKT (Fig. 6A). To further explore the interaction between PCSK6 and *AKAP12*, a stable knockdown *AKAP12* cell line was constructed using lentiviral transfection. Knockdown of *AKAP12* was verified by qPCR and WB analyses (Fig. 6B and C). Consistent with the *in vivo* data, knockdown of *AKAP12*

increased PCSK6 protein expression, paralleled by increased phosphorylation of PI3K and AKT (Fig. 6C). Subsequently, simultaneous silencing of PCSK6 in *AKAP12*-silenced cell lines had no effect on the expression of phosphorylated PI3K/AKT (Fig. 6D). These results confirm that expression of PCSK6 has no effect on the PI3K/AKT pathway (Fig. 6D). Meanwhile, PCSK6 silencing reduced the expression levels of inflammatory factors (Fig. 6E). Previous studies demonstrated that knockout or silencing of *AKAP12* activates the PI3K/AKT pathway [32,33]. Therefore, cell lines were constructed with *AKAP12* overexpression plasmids, which revealed that *AKAP12* overexpression inhibited the PI3K/AKT pathway (Fig. 6F). To determine whether *AKAP12* regulates PCSK6 expression through the PI3K/AKT pathway, changes in PCSK6 expression in response to an AKT inhibitor were investigated. Pilot experiments have shown that the inhibitor works best at 5 min after Epidermal Growth Factor Receptor stimulation. The results demonstrated that the AKT inhibitor simultaneously inhibited the expression of p-AKT and PCSK6 (Fig. 6G), which strongly imply that activation of the PI3K/AKT pathway promotes the expression of PCSK6 (Fig. 6G). To explore the function of PCSK6 *in vivo*, small interfering RNA targeting PCSK6 were synthesized to verify the knockdown effects at the mRNA and protein levels (Fig. 6H and I). Consistently, the mRNA levels of pro-inflammatory genes in the liver were significantly reduced (Fig. 6G). The PI3K inhibitor LY294002 is reported to block the induction of PCSK6/PACE4 mRNA [15]. These results further confirmed that *AKAP12* influences PCSK6 expression via the PI3K/AKT pathway.

Given the ability of PCSK6 to induce and trigger an inflammatory response, the effect of PCSK6 on ALI was investigated. *AKAP12*<sup>Δhep</sup> mice

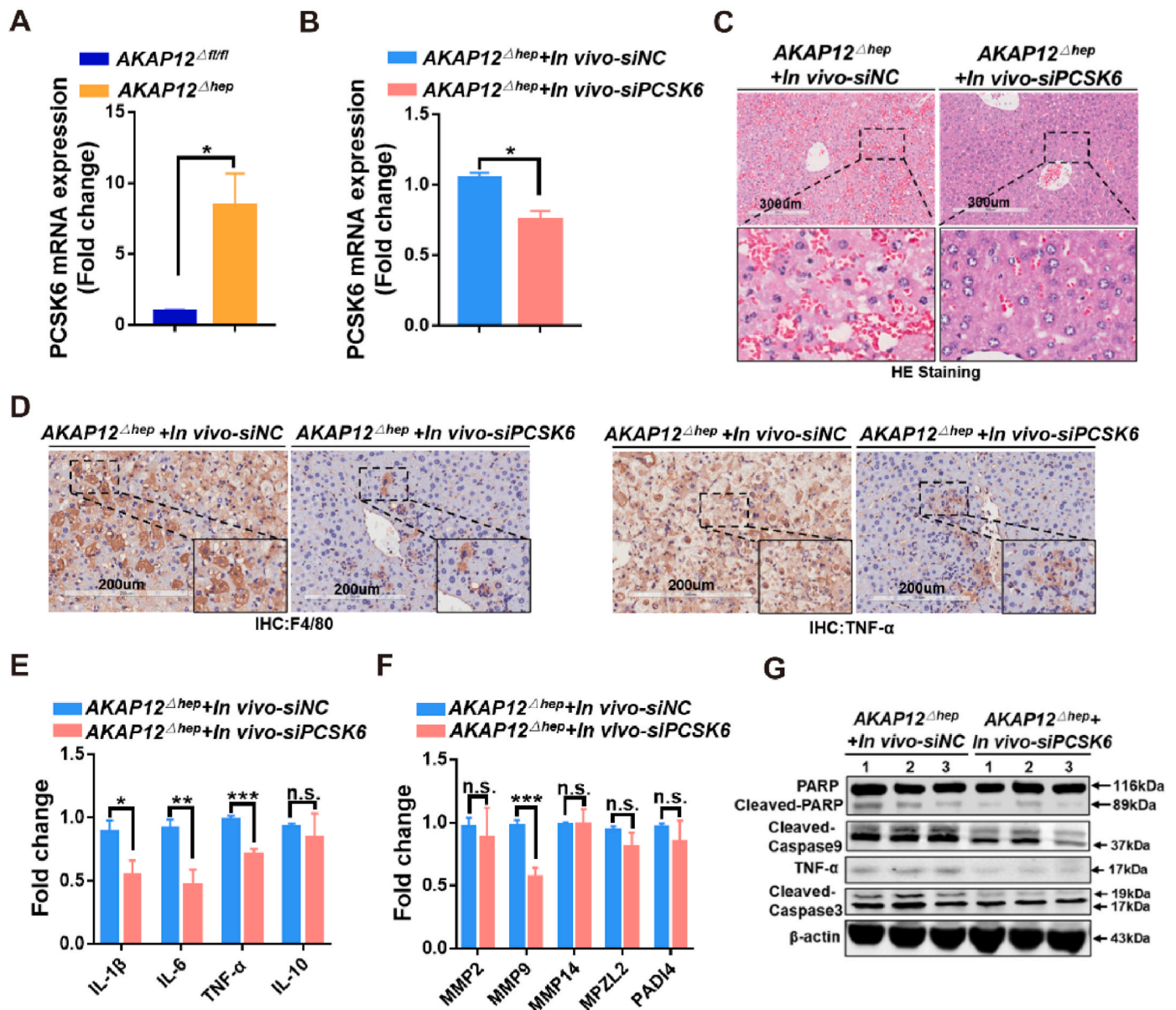


**Fig. 6.** AKAP12 influences PCSK6 expression via the PI3K/AKT pathway. (A) Validation of the effect of PCS6 on the PI3K/AKT pathway and AKAP12. (B) *AKAP12* mRNA expression. (C) Expression of PCSK6, PI3K, and AKT after *AKAP12* silencing. (D) Simultaneous silencing of *PCSK6* in *AKAP12*-silenced cell lines to detect PI3K/AKT expression. (E) Expression of inflammatory factors (n = 3/group). (F) Overexpression of AKAP12 verifies the expression of PI3K/AKT and PCSK6. (G) Detection of protein level expression following the use of AKT phosphorylation inhibitors. (H and I) *In vivo-siPCSK6* treatment and detection of *PCSK6* mRNA and protein expression in liver tissue. (J) Detection of inflammatory factors (\**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001, \*\*\*\**p* < 0.0001, n.s. *p* > 0.05).

were intraperitoneally injected with GalN/LPS (5 μg/kg) to induce ALI and treated with *siPCSK6*. Silencing of *PCSK6* improved liver congestion and swelling in *AKAP12<sup>Δhep</sup>* mice (Supplementary Fig. 5A). The liver-to-body weight ratio and serum ALT and AST levels after *in vivo siPCSK6* treatment were significantly decreased (Supplementary Figs. 5B and C). *PCSK6* mRNA levels were significantly elevated in the livers of

*AKAP12<sup>Δhep</sup>* mice with ALI (Fig. 7A). *siPCSK6* was used to inhibit *PCSK6* expression, which was validated by measuring mRNA levels (Fig. 7B). H&E staining showed that liver congestion and necrosis were significantly relieved in the *siPCSK6* group (Fig. 7C). The expression of inflammatory factors and macrophage infiltration in the liver were significantly reduced following *PCSK6* knockdown, as demonstrated by





**Fig. 7.** *In vivo* PCSK6 effectively relieved ALI. (A) PCSK6 mRNA expression after AKAP12 knockout (n = 3/group). (B) Verification of the efficiency of *siPCSK6* (n = 3/group). (C) H&E staining. (D) IHC staining. (E) Expression of inflammatory factors in liver tissues (n = 3/group). (F) Detection of genes related to PCSK6 (n = 3/group). (G) WB analysis (n = 3/group) (\**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001, n.s. *p* > 0.05).

IHC staining (Fig. 7D). In mice treated with *siPCSK6*, there was a significant decrease in the expression of MMP9, a downstream target of PCSK6, and as well as several pro-inflammatory genes (Fig. 7E and F). Further validation at the protein level found significant reductions in the expression levels of apoptotic proteins (cleaved PARP, cleaved caspase-3, cleaved caspase-9) in addition to TNF $\alpha$  (Fig. 7G). Collectively, these results confirmed that high PCSK6 expression promoted inflammatory factor expression and macrophage infiltration, leading to more severe liver injury in the ALI model.

#### 4. Discussion

The present study confirm that activation of the PI3K/AKT pathway in the livers of *AKAP12<sup>Δhep</sup>* mice triggers increased expression of PCSK6, which promotes macrophage infiltration and inflammatory factor expression, thereby exacerbating liver injury.

Recent studies of endothelial cells, although these cells only account for 5%–18% of liver cells, whereas hepatocytes account for about 80%

[7,15,34]. The role of AKAP12 in hepatocytes remains unclear, thus further studies are warranted. The results of the present study showed that *AKAP12* deficiency promotes acute and chronic liver injury, although the specific mechanism underlying the development of liver fibrosis has yet to be elucidated. Several pathways closely related to liver fibrosis were identified and the phosphorylation levels of STAT3 and AKT were significantly increased in the liver tissues of *AKAP12<sup>Δhep</sup>* mice. Numerous studies have reported that STAT3 acts as an extracellular signaling molecule essential to chronic inflammation and promotes tumorigenesis and tumor-associated inflammation [35–37]. The PI3K/AKT signaling pathway plays an important regulatory role in the progression of liver fibrosis [37]. In addition, activation of the ERK and JNK pathways is significantly positively correlated with activation of hepatic stellate cells, which exacerbates liver fibrosis [37–40]. *AKAP12* knockout in hepatocytes activated PI3K-AKT pathway while had little or no effect on the JNK and ERK pathways. In addition, *AKAP12* knockout promoted the expression of *MMP2/9* and inflammatory factors via activation of the PI3K/AKT/PCSK6 signaling pathway, which

aggravates the progression of liver fibrosis [41,42]. Therefore, enhanced expression of PCSK6 might promote infiltration of inflammatory factors, thereby further aggravating liver fibrosis.

The results of this study showed that AKAP12 has an inhibitory effect on the expression of PCSK6. In *AKAP12<sup>Δhep</sup>* mice, the lack of *AKAP12* during the development of ALI led to activation of the PI3K/AKT pathway and increased expression of PCSK6. Knockout of *AKAP12* compromised the structural stability of hepatocytes and increased sensitivity to ROS [3,43]. Knockout of *AKAP12* accelerated PCSK6-induced inflammation, oxidative stress, and apoptosis, leading to liver damage. Abnormal expression of PCSK6 is reported to promote activation of the vascular endothelium and subsequent vascular regeneration [44,45]. Previous studies have demonstrated that PCSK6 is abnormally expressed in several solid tumors (gastric cancer, breast cancer, melanoma, etc.) [17,46,47]. PCSK6 has also been shown to enhance proliferation, migration, invasion, and inflammation of rheumatoid arthritis fibroblast-like synovial (RASf) cells via activation of the NF- $\kappa$ B, STAT3, and ERK1/2 signaling pathways [17,47–50]. In rheumatoid arthritis, PCSK6 is reportedly significantly increased in RASf cells [51,52]. PCSK6 stimulates secretion of the inflammatory cytokines IL-1 $\alpha$ , IL-1 $\beta$ , and IL-6 in RASf cells, and increases the expression of genes related to angiogenesis, hypoxia, proliferation, and inflammation [51–54].

In addition, PCSK6 is a secreted protein, which is transported from intracellular to extracellular [17,18]. The deletion of *AKAP12* may directly affect the secretion of PCSK6, but no research has been reported and more experiments are still needed. Also, multiple pathways may be involved in the aggravation of ALI caused by *AKAP12* deletion. This paper only explores the PI3K/AKT signaling pathway, which is limited. Increased expression of PCSK6 stimulates macrophages to increase production of inflammatory factors [28,29]. In PCSK6-aggravated liver damage, activated macrophages promote the secretion of various inflammatory cytokines, thereby enhancing the inflammatory response [52]. In the present study, NAC only partially alleviated liver damage, whereas inhibition of PCSK6 expression effectively alleviated ALI. Moreover, hepatocyte-specific knockout of *AKAP12* increased apoptosis both *in vivo* and *in vitro*, which was reversed by PCSK6 knockdown. Taken together, these results demonstrate that aggravation of ALI is due to activation of PI3K/AKT and that *AKAP12* knockout enhanced PCSK6 expression, highlighting *AKAP12* and PCSK6 as potential drug targets for treatment of ALI.

## Ethics statements

Our animal experiments are supported and supervised by the Animal Ethics Committee of Shanghai Tenth People's Hospital (ID Number: SHDSYY-2021-3031).

## Declaration of competing interest

The authors have declared that no competing interest exists.

## Acknowledgments

This study was supported by grant from Special Clinical Research Project of Shanghai Municipal Health Commission (202140147) and Outstanding academic leaders plan of Shanghai (Grant No. 2018BR07). We thank the support of Shanghai Key Laboratory of Hepato-biliary Tumor Biology and Military Key Laboratory on Signal Transduction, and the Key Laboratory of Signaling Regulation and Targeting Therapy of Liver Cancer (SMMU), Ministry of Education.

## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.redox.2022.102328>.

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