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# **The Long Non-coding RNA HNF4A-AS1 Negatively Regulates Cytochrome P450 Enzymes in Huh7 Cells via Histone Modifications**

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**Running Title:** HNF4A-AS1 regulates CYPs via histone modifications

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#### **ABBREVIATIONS:**

AHR, aryl hydrocarbon receptor; CAR, constitutive androstane receptor; ChIP, chromatin immunoprecipitation; CYPs, cytochrome P450s; DMEM, dulbecco's modified Eagle's medium; DMSO, dimethyl sulfoxide; FBS, fetal bovine serum; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; HNF1A, hepatocyte nuclear factor 1 alpha; HNF1A-AS1, HNF1A antisense RNA 1; HNF4A,

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hepatocyte nuclear factor 4 alpha; HNF4A-AS1, HNF4A antisense RNA 1;  
HREs, HNF4A response elements; H3K4me3, histone 3 lysine 4 trimethylation;  
IgG, immunoglobulin G; lncRNA, long non-coding RNA; OE-HNF4A-AS1,  
overexpression of HNF4A-AS1; PXR, pregnane X receptor; qRT-PCR,  
quantitative real-time polymerase chain reaction; RIF, rifampicin; S.D, standard  
deviation; siRNAs, small interfering RNAs.

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## ABSTRACT

The maintenance of homeostasis of cytochrome P450s (CYPs) under both physiological and xenobiotic exposure conditions is ensured by the action of positive and negative regulators. In the current study, the hepatocyte nuclear factor 4 alpha (HNF4A) antisense RNA 1 (HNF4A-AS1), an antisense lncRNA of *HNF4A*, was found to be a negative regulator of the basal and rifampicin (RIF)-induced expression of nuclear receptors and downstream CYPs. In Huh7 cells, knockdown of HNF4A-AS1 resulted in elevated expression of HNF4A, pregnane X receptor (PXR), and CYPs (including CYP3A4) under both basal and RIF-induced conditions. Conversely, overexpression of HNF4A-AS1 led to decreased basal expression of constitutive androstane receptor (CAR), aryl hydrocarbon receptor (AHR), PXR, and all studied CYPs. Of note, significantly-diminished induction levels of PXR, CYP1A2, 2C8, 2C19, and 3A4 by RIF were also observed in HNF4A-AS1 plasmid transfected Huh7 cells. Moreover, the negative feedback of HNF4A on HNF4A-AS1 mediated gene expression was validated using a loss-of-function experiment in this study. Strikingly, our data showed that increased enrichment levels of histone 3 lysine 4 trimethylation (H3K4me3) and HNF4A in the *CYP3A4* promoter contribute to the elevated CYP3A4 expression after HNF4A-AS1 knockdown. Overall, the current study reveals that histone modifications contribute to the negative regulation of nuclear receptors and CYPs by HNF4A-AS1 in basal



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and drug-induced levels.

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### **Significance statement**

Utilizing loss-of-function and gain-of-function experiments, the current study systematically investigated the negative regulation of HNF4A-AS1 on the expression of nuclear receptors (including HNF4A, CAR, AHR, and PXR) and CYPs (including CYP1A2, 2E1, 2B6, 2D6, 2C8, 2C9, 2C19, and 3A4) in both basal and RIF-induced levels in Huh7 cells. Notably, this study is the first to reveal the contribution of histone modification to the HNF4A-AS1 mediated expression of CYP3A4 in Huh7 cells.

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## Introduction

Cytochrome P450 (CYP) enzymes, the predominant phase I enzymes in human liver, are responsible for the metabolism of approximately 75% of the clinically used drugs; additionally, CYPs are also of paramount importance for the detoxification of xenobiotics (Pikuleva, 2006; Fisher et al., 2009). Considerable inter-individual variabilities in the expression and induction of CYPs have been observed, which markedly affect the effectiveness and safety of therapeutic agents (Tang et al., 2005; Zanger and Schwab, 2013). Thus, elucidating the precise mechanism underlying the basal and drug-induced expression of CYPs is essential for precision medicine.

It is well studied that nuclear receptors, such as hepatocyte nuclear factor 4 alpha (HNF4A) and 1 alpha (HNF1A), aryl hydrocarbon receptor (AHR), pregnane X receptor (PXR), and constitutive androstane receptor (CAR) are crucial transcriptional regulators of CYPs (Cheung et al., 2003; Kamiyama et al., 2007; Aleksunes and Klaassen, 2012; Hakkola et al., 2018). Notably, HNF4A is considered to be at the top hierarchy of the transcription factor network (Kuo et al., 1992; Kamiya et al., 2003). HNF4A was reported to be involved in HNF1A-mediated transcriptional activation (Eeckhoutte et al., 2004). Additionally, the indispensable role of HNF4A in the PXR and CAR mediated induction of CYPs has also been reported (Kamiya et al., 2003; Tirona et al., 2003; Li and Chiang, 2006; Takezawa et al., 2012). Whereas, these studies

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are all focused on positive regulatory mechanisms in CYP expression. Far less information is available on the negative regulation of CYPs, thereby limiting our knowledge on the precise mechanism underlying the maintenance of the homeostasis of CYP expression in normal and xenobiotic (including drug) exposure conditions.

Long non-coding RNAs (lncRNAs) are non-coding RNAs with a length of more than 200 nucleotides (Atkinson et al., 2012; Yang et al., 2014; Ning et al., 2019). Recent studies have reported that lncRNAs participate in the regulation of neighboring genes (Halley et al., 2014; Villegas et al., 2014; Villegas and Zaphiropoulos, 2015). Our previous study has unveiled that HNF4A antisense RNA 1 (HNF4A-AS1), a neighboring antisense lncRNA of *HNF4A*, negatively regulated the mRNA expression of nuclear receptors, including HNF4A and PXR, and the downstream CYPs at the basal level (Chen et al., 2018). However, the underlying mechanism and the role of HNF4A-AS1 in the drug-induced expression of CYPs have not been elucidated thus far.

lncRNAs can act as cofactors for transcriptional factors and jointly regulate gene expression (Zhao et al., 2014; Mi et al., 2017). Additionally, lncRNAs can also regulate gene expression by recruiting complexes to the promoters of target genes and causing alterations of histone modifications of genes (Wang et al., 2011). Of note, studies conducted by us and other groups have shown that transcription factors can affect gene transcription by regulating histone

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modifications in gene promoter regions (Xie et al., 2009; Yan et al., 2017).

Therefore, we speculate that HNF4A-AS1 can regulate the expression of CYPs via altering the histone modification status of *CYP* genes, thus affecting the binding of HNF4A.

In the current study, we performed a systematic analysis to investigate the role of HNF4A-AS1 in the expression of transcription factor-mediated CYPs in Huh7 cells. Importantly, the underlying mechanism was elucidated in this study. Our findings reveal that HNF4A-AS1 negatively regulates the basal and rifampicin (RIF)-induced expression of CYPs. Moreover, the elevated expression of CYP3A4 after HNF4A-AS1 knockdown is related to the increased enrichment levels of histone 3 lysine 4 trimethylation (H3K4me3) and of HNF4A in the promoter of *CYP3A4*.

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## Materials and Methods

**Chemicals and Reagents.** Huh7 cells were purchased from the Type Culture Collection of the Chinese Academy of Sciences (Shanghai, China). RIF was obtained from Sigma-Aldrich (St Louis, MO). Small interfering RNAs (siRNAs), including si-HNF4A, si-HNF4A-AS1, and a negative control (si-NC), were provided by GenePharma Co., Ltd. (Shanghai, China). HNF4A-AS1 expression plasmids were obtained from GeneChem Co., Ltd. (Shanghai, China). Lipofectamine 3000, opti-MEM, and SYBR Select Master Mix were purchased from Thermo Fisher Scientific (Carlsbad, CA). Nanofector transfection reagent was obtained from Procell Co., Ltd. (Wuhan, China). The TriPure isolation reagent and protease inhibitor cocktail were purchased from Roche (Basel, Switzerland). Primers were synthesized by SunYa Co. (Zhejiang, China). Antibodies against HNF4A (ab174653), PXR (bs-2334R), CYP3A4 (ab124921), 1A2 (ab151728), 2C9 (ab150364), and 2C19 (ab185213) were obtained from Abcam (Cambridge, MA). Horseradish peroxidase-linked secondary antibodies (SA00001-1 and SA00001-2) and the antibody against glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (60004-1-Ig) were purchased from Proteintech (Wuhan, China). The antibody recognizing H3K4me3 (17-678) and polyvinylidene fluoride (PVDF) membranes were obtained from MD Millipore (Billerica, MA). Dulbecco's modified Eagle's medium (DMEM) and fetal bovine serum (FBS) were purchased from Corning

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Inc. (Armonk, NY). RIPA reagent, penicillin and streptomycin mixture, dimethyl sulfoxide (DMSO), and other chemical reagents were provided by Solarbio Science & Technology Co. (Beijing, China).

**Cell Culture and Transfection.** Huh7 cells were cultured in DMEM medium supplemented with 10% FBS and 1% penicillin and streptomycin mixture at 37°C with 5% CO<sub>2</sub>. Before transfection, Huh7 cells were allowed to grow for up to 24 hours on six-well plates reaching 80%–90% confluence. For gene knockdown experiments, 40 pmol/well of siRNAs targeting HNF4A, HNF4A-AS1, or control siRNAs were transfected into Huh7 cells with the Lipofectamine 3000 reagent according to the manufacturer's instructions. For gene overexpression experiments, Nanofecter transfection reagent was used to transfect 2.5 µg/well of plasmids into Huh7 cells following the manufacturer's protocol. Cells were harvested 48 hours after transfection.

**Drug Treatment.** Twenty-four hours after transfection, cells were incubated with 10 µM RIF or 0.1% DMSO (vehicle) for 24 hours before harvested.

**RNA Isolation and Quantitative Real-Time Polymerase Chain Reaction (qRT-PCR).** Total RNAs were isolated from Huh7 cells using a TriPure isolation reagent according to the manufacturer's instruction. The quality and concentrations of RNAs were measured by a Nanodrop 2000c Spectrophotometer (Thermo Fisher Scientific). One microgram total RNAs were reverse transcribed using a PrimeScript RT reagent kit. qRT-PCR was

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performed using a SYBR Select Master Mix with specific primers (Table 1) in an Applied Biosystems 7500 Fast Real-Time PCR System (Thermo Fisher Scientific). Relative RNA expression levels were determined by normalizing focused gene expression against GAPDH expression using the  $2^{-\Delta\Delta C_t}$  method.

**Protein Isolation and Western Blot Analysis.** Whole protein homogenates of Huh7 cells were prepared using a RIPA reagent supplemented with a protease inhibitor cocktail. Protein concentrations were determined by a bicinchoninic acid method according to the manufacturer's instructions (Beyotime Institute of Biotechnology, Hangzhou, China). Western blot analysis was performed using 80  $\mu$ g total protein samples, as described previously (Yan et al., 2017; Wang et al., 2019a) with minor modifications. The dilutions of primary antibodies against HNF4A, PXR, and CYP3A4 were 1:1,000. The dilutions of primary antibodies against CYP1A2, 2C9, and 2C19 were 1:2,000. The dilutions of the primary antibody against GAPDH was 1:5,000. Horseradish peroxidase-linked secondary antibodies were diluted in 1:10,000. Protein bands were visualized using an enhanced chemiluminescence method with a FluorChem E system (ProteinSample, San Jose, California). The protein expression levels of focused genes were normalized against GAPDH.

**Chromatin Immunoprecipitation (ChIP) Analysis.** ChIP was performed as described previously (Yan et al., 2017; Wang et al., 2019a) with minor



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modifications. Briefly, siRNA-transfected cells were incubated with 1% formaldehyde for 10 minutes; fixation was halted by glycine (125 mM) for 5 minutes at room temperature. Cells were then washed twice with cold phosphate-buffered saline and lysed using an SDS lysis buffer (0.1% SDS, 50 mM Tris-HCl, pH 8.0, 1 mM EDTA, and 1% Triton-X) with a proteinase inhibitor cocktail on ice for 15 minutes. Cell lysates were sonicated with a Bioruptor Pico sonication system (Diagenode, Seraing, Belgium) to obtain DNA fragments ranging between ~200 and 1,000 bp. DNA fragments were immunoprecipitated using antibodies against H3K4me3 and HNF4A. Mouse immunoglobulin G (IgG) was used as a negative control. The purification of DNA was performed with a PCR purification kit (QIAGEN GmbH, Hilden, Germany) followed by qPCR analysis with specific primers (Table 2) using a SYBR green method. Enrichment was calculated as the percentage of chromatin input and normalized against IgG.

**Statistical Analysis.** All studies with Huh7 cells described here were performed as three independent experiments. Data are shown as mean  $\pm$  standard deviation (S.D). Statistical significances between two groups were analyzed by two-tailed unpaired Student's *t* test using SPSS 21.0 software (IBM Corp., Armonk, NY).

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## Results

### **Negative Regulation of HNF4A-AS1 on the Basal Expression of Nuclear Receptors and CYPs in Huh7 Cells.**

To uncover the role of HNF4A-AS1 in the regulation of nuclear receptors and CYPs, loss-of-function and gain-of-function studies were performed in Huh7 cells. The expression of HNF4A-AS1, five nuclear receptors (HNF4A, HNF1A, CAR, AHR, and PXR), and eight CYPs (CYP1A2, 2E1, 2B6, 2D6, 2C8, 2C9, 2C19, and 3A4) was measured.

The knockdown efficiency of HNF4A-AS1 after siRNA transfection into Huh7 cells was confirmed by qRT-PCR. As seen in Fig.1A, the expression of HNF4A-AS1 decreased approximately 57% after si-HNF4A-AS1 transfection. Knockdown of HNF4A-AS1 led to increased expression of HNF4A at both mRNA and protein levels (Fig. 1A and B). For the focused nuclear receptors, 1.7-fold increased expression of PXR was observed by HNF4A-AS1 knockdown, while the basal expression of HNF1A, CAR, and AHR was unchanged at the mRNA level (Fig. 1C). Meanwhile, the basal mRNA expression of CYP1A2, 2C8, 2C9, 2C19, and 3A4 was also significantly higher in the HNF4A-AS1 knockdown group than that in the control group (Fig. 1D). There was no significant difference in the mRNA expression of CYP2E1, 2B6, and 2D6 after HNF4A-AS1 knockdown (Fig. 1D). Importantly, consistent with the increased expression of PXR and CYP3A4 at the mRNA level, the protein

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expression of PXR and CYP3A4 was also significantly elevated after HNF4A-AS1 knockdown (Fig. 1E and F). Moreover, higher protein expression levels of CYP1A2 and 2C9 were also observed in the HNF4A-AS1 group ( $P < 0.05$ ), while the protein expression of CYP2C19 remained unchanged ( $P > 0.05$ ) (supplemental Fig. S1).

The expression of HNF4A-AS1 in the overexpression of HNF4A-AS1 (OE-HNF4A-AS1) group was approximately 673 times that in the control group (Fig. 2A), which confirmed the overexpression efficiency of HNF4A-AS1. Compared with the control group, the mRNA expression of CAR, AHR, and PXR was approximately 50% lower in the HNF4A-AS1 overexpression group (Fig. 2B). However, the mRNA expression of HNF4A and HNF1A was not affected by HNF4A-AS1 overexpression ( $P > 0.05$ ) (Fig. 2A and B). Additionally, as shown in Fig. 2C, HNF4A-AS1 overexpression also resulted in significantly decreased expression of studied CYPs except for CYP2D6 at the mRNA level. These findings indicate that HNF4A-AS1 acts as a negative regulator in the basal expression of CYPs, probably, via the negative regulation of nuclear receptors.

### **HNF4A-AS1 Attenuates the RIF-induced Expression of CYPs in Huh7 Cells.**

To further explore the role of HNF4A-AS1 in the drug-induced expression of CYPs, siRNA or plasmid transfected Huh7 cells were treated with RIF. As seen

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in Fig. 3A, knockdown of HNF4A-AS1 abolished the induction of HNF4A-AS1 expression by RIF, whereas elevated that of HNF4A. Significantly higher induction levels of PXR were also observed in the HNF4A-AS1 knockdown group ( $P < 0.05$ ), whereas the RIF-induced expression of other nuclear receptors (including HNF1A, CAR, and PXR) was unaffected by the HNF4A-AS1 knockdown ( $P > 0.05$ ) (Fig. 3B). Additionally, after HNF4A-AS1 knockdown, the induction of CYP1A2, 2C8, 2C9, 2C19, and 3A4 expression by RIF was significantly increased ( $P < 0.05$ ), while that of CYP2E1, 2B6, and 2D6 was not affected ( $P > 0.05$ ) (Fig. 3C).

Conversely, overexpression of HNF4A-AS1 led to higher induction levels of HNF4A-AS1 and lower that of PXR by RIF (Fig. 3D and E). However, the RIF-induced expression of HNF4A, HNF1A, CAR, and AHR remained unchanged after HNF4A-AS1 overexpression ( $P > 0.05$ ) (Fig. 3D and E). For CYPs, the induction levels of CYP1A2, 2C8, 2C19, and 3A4 decreased after HNF4A-AS1 overexpression (Fig. 3F). Altogether, these results suggest that HNF4A-AS1 attenuates the drug-induced expression of CYPs.

### **Negative feedback of HNF4A on HNF4A-AS1 mediated genes expression.**

To verify the role of HNF4A in the transcriptional regulation of HNF4A-AS1 and the related CYPs, knockdown of HNF4A was performed in Huh7 cells. After effective knockdown of HNF4A, the expression of HNF4A-AS1 decreased (Fig. 4A and B). Lower expression levels of all studied nuclear

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receptors, including HNF1A, CAR, AHR, and PXR, were also observed at the mRNA level after HNF4A knockdown (Fig. 4C). Additionally, the knockdown of HNF4A also led to reduced mRNA expression of CYPs (Fig. 4D). Consistent with the decreased expression at the mRNA level, the protein expression of PXR and CYP3A4 was lower in the HNF4A knockdown group than that in the control group (Fig. 4E and F). Moreover, as seen in Fig. 5, the RIF-induced expression of most focused genes, including HNF1A and CYPs, was significantly diminished after HNF4A knockdown at the RNA level. There was also a trend of lower induced expression levels of CAR, AHR, and PXR by RIF in HNF4A knockdown *versus* control cells ( $P>0.05$ ) (Fig. 5B). These findings demonstrate that HNF4A participates in the transcriptional regulation of HNF4A-AS1, nuclear receptors, and CYPs under both basal and RIF-induced expression-levels conditions.

### **HNF4A-AS1 Knockdown leads to Elevated Enrichment Levels of Histone Modifications and HNF4A in the Promoter of *CYP3A4*.**

To explore the underlying mechanism by which HNF4A-AS1 regulated the expression of CYP3A4, ChIP-qPCR experiments were conducted in si-NC or si-HNF4A-AS1 transfected Huh7 cells. As shown in Fig. 6A, two pairs of primers around the HNF4A response elements (HREs) in the promoter of *CYP3A4* were synthesized. Knockdown of HNF4A-AS1 resulted in elevated enrichment levels of H3K4me3, a gene activate mark, in the HREs of the

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*CYP3A4* promotor, which was consistent with the higher expression of *CYP3A4* in the HNF4A-AS1 knockdown group (Fig. 6B). Moreover, the enrichment level of HNF4A also increased after HNF4A-AS1 knockdown (Fig. 6C). Altogether, these findings indicate that HNF4A-AS1 might regulate the expression of *CYP3A4* by a scaffold mechanism.

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## Discussion

It is well known that the expression of CYPs is transcriptionally regulated by nuclear receptors (Honkakoski and Negishi, 2000; Jover et al., 2009; Nie et al., 2017). As a master regulator, HNF4A plays a curial role in the complex regulatory network of basal and drug-induced CYP expression (Tirona et al., 2003; Kamiyama et al., 2007). Recently, an increasing number of studies have elucidated the epigenetic regulation of CYPs (Klaassen et al., 2011; Tang and Chen, 2015; Li et al., 2019). Notably, as promising epigenetic regulators, lncRNAs were reported to be important for multiple biological or physiological processes (Fatica and Bozzoni, 2014; Schmitt and Chang, 2016; Ghafouri-Fard et al., 2020; Zhou et al., 2020). In the current study, utilizing loss-of-function and gain-of function experiments, we systemically verified that HNF4A-AS1 was involved in the negative regulation of HNF4A-mediated gene expression (including that of CYPs) at the basal level and under drug-induced conditions in Huh7 cells. Importantly, the alteration of histone modification status was proved as the underlying mechanism for the HNF4A-AS1-mediated negative-regulation of CYPs in this study.

Mounting evidence suggests that lncRNAs can be involved in the regulation of their neighboring genes (Villegas and Zaphiropoulos, 2015; Gibbons et al., 2018; Qi et al., 2019). Particularly, lncRNAs are known to interact on their antisense strands with transcription factors (Villegas and Zaphiropoulos, 2015;

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Gil and Ulitsky, 2020). Our previous studies proved that *HNF1A* antisense lncRNA, HNF1A-AS1, played as a positive regulator of HNF1A-mediated gene expression in Huh7 and HepaRG cells (Chen et al., 2018; Wang et al., 2019b). In the present study, using loss-of-function and gain-of-function studies, HNF4A-AS1 was validated to have opposite regulatory effects to HNF1A-AS1, on the basal expression of most studied genes in Huh7 cells (Fig. 1 and 2), which confirmed our previous findings in HNF4A-AS1-knockdown HepaRG cells (Chen et al., 2018).

Though higher mRNA expression of most CYPs (including CYP1A2, 2C9, 2C19, and 3A4) after HNF4A-AS1 knockdown was observed in both Huh7 and HepaRG cells (Fig. 1)(Chen et al., 2018), differential impacts on genes were noticed. For instance, after efficient knockdown of HNF4A-AS1, the basal mRNA expression of HNF4A and PXR was significantly elevated in Huh7 cells (Fig. 1A and C) but remained unchanged in HepaRG cells (Chen et al., 2018). Increased protein expression of HNF4A and PXR by HNF4A-AS1 knockdown was also observed in Huh7 cells (Fig. 1B and E). However, overexpression of HNF4A-AS1 in Huh7 cells did not affect the mRNA expression of HNF4A (Fig. 2A). This may be attributed to the low intrinsic expression of HNF4A in Huh7 cells. Another possible explanation for the above-mentioned findings is that HNF4A-AS1 may serve as a central platform for the binding of effector molecules repressing the expression of HNF4A in Huh7 cells. That is, the



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knockdown of HNF4A-AS1 may lead to dismantling of the lncRNA-effector scaffold, thus increasing the expression of HNF4A, whereas overexpression of HNF4A-AS1 may have no impact on the scaffolding complexes, and consequently on the expression of HNF4A. However, these are aspects that warrant further investigation. Additionally, transfection of siRNA against HNF4A-AS1 into HepaRG cells resulted in the altered mRNA expression of CAR and AHR (Chen et al., 2018); whereas, in Huh7 cells, the expression of CAR and PXR was not affected after HNF4A-AS1 knockdown, although it decreased after overexpression of HNF4A-AS1 (Fig. 1C and 2B). The differential impacts of HNF4A-AS1 on the basal expression of genes in Huh7 and HepaRG cells may be ascribed to differences in the intrinsic expression of HNF4A-AS1, HNF4A-related nuclear receptors, and CYPs. Overall, both studies confirmed the negative regulation of HNF4A-AS1 in the basal and drug-induced expression of HNF4A-mediated genes.

It is well documented that PXR and CAR are xenobiotic receptors that play curial roles in the induction or inhibition of CYPs (Timsit and Negishi, 2007; Hernandez et al., 2009; Chai et al., 2013). Additionally, several studies have reported that HNF4A is indispensable for the PXR- and CAR-mediated induction of CYPs (Tirona et al., 2003; Li and Chiang, 2006; Takezawa et al., 2012). Based on our previous findings, we speculated that HNF4A-AS1 could be involved in the drug-induced expression of CYPs. Importantly, consistent

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with the elevated basal expression of HNF4A, PXR, and CYPs (such as CYP1A2 and 3A4) in HNF4A-AS1 knockdown Huh7 cells, the induction of these genes by RIF was improved after HNF4A-AS1 knockdown (Fig. 3A-C). Conversely, overexpression of HNF4A-AS1 resulted in diminished induction levels of PXR, CYP1A2, 2C8, 2C19, and 3A4 in Huh7 cells (Fig. 3D-F). These results indicate that HNF4A-AS1 is involved in the negative regulation of drug-induced CYP expression. Under both normal physical and xenobiotic exposure conditions, HNF4A-AS1 may act as a “break” to sustain constant intracellular levels of CYPs. Importantly, to better understand the human implications of these findings, studies using primary human hepatocytes, human induced pluripotent stem cell-derived hepatocytes, or HepaRG cells should be conducted in the future.

In a recent study, using dual-luciferase assay, Guo S and Lu H found that the endogenous expression of HNF4A-AS1 in HepG2 and HEK293 cells was transcriptionally regulated by P1-HNF4A, the predominant subtype of HNF4A in adult liver (Guo and Lu, 2019). Thus, in this study, we also assessed the impacts of HNF4A on the expression of HNF4A-AS1, other nuclear receptors, and CYPs under basal and RIF-induced conditions. As shown in Fig. 4, knockdown of HNF4A led to decreased expression of HNF4A-AS1, nuclear receptors (HNF1A, CAR, and PXR), and CYPs (including CYP2E1, 2B6, 2C8, 2C19, and 3A4) in Huh7 cells, which was consistent with our previous findings

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in HepaRG cells. Similarly, the RIF-induced expression of these CYPs was also diminished after HNF4A knockdown in both Huh7 (Fig. 5) and HepaRG cells (Chen et al., 2018). These findings verified the previously published results and further indicated that there was a negative feedback loop in the HNF4A-AS1/HNF4A-CYPs axis. Whereas, the precise mechanisms need to be elucidated in further researches.

The involvement of histone modifications in the regulation of CYPs has been proved by more and more studies (Yan et al., 2017; Wang et al., 2019a; Pande et al., 2020). For instance, H3K27ace was reported to be involved in HNF4A-mediated CYP2C9 expression. Englert N and colleagues found that HNF4A could recruit the co-regulator MED25 to the *CYP2C9* promoter, thus promoting the transcription of CYP2C9 (Englert et al., 2015). However, alterations in histone modification status are usually non-spontaneous, and their activation requires the action of upstream regulatory factors. Therefore, we speculate that HNF4A-AS1, playing as a cofactor, would interact with HNF4A by recruiting histone modification enzymes to the HREs in the *CYP3A4* promoter, thereby regulating the expression of CYPs. Given the highest expression level among the entire CYPs in liver, CYP3A4 was selected as a representative gene to uncover the underlying mechanisms that how HNF4A-AS1 regulated the expression of CYPs in this study. After the efficient knockdown of HNF4A-AS1, the HREs ( -7,836 to -6,093 bp and -362 to +53 bp)

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in the *CYP3A4* promoter were found to have higher enrichment levels of H3K4me3, a gene-active factor. In addition, interference with HNF4A-AS1 resulted in elevated enrichment levels of HNF4A in the promoter of *CYP3A4*. Altogether, these findings validate our hypothesis and indicate that HNF4A-AS1 may regulate the expression of *CYP3A4* by recruiting histone methylation enzymes to the promoter of *CYP3A4*, altering the histone modification status, thereby affecting the binding of HNF4A to *CYP3A4* promoter. However, whether HNF4A-AS1 interacts with HNF4A and histone modification enzymes was not elucidated in this study. This said, these findings provide potential future directions for the investigation of the molecular mechanisms of HNF4A-AS1 in HNF4A-mediated regulatory functions in the human liver.

In summary, this study observed a negative regulation of HNF4A-AS1 on the basal and drug-induced expression of HNF4A, CYPs, and other nuclear receptors. Our study also revealed that elevated enrichment levels of H3K4me3 and HNF4A in the *CYP3A4* promotor was responsible for the induced *CYP3A4* expression after HNF4A-AS1 knockdown. Therefore, the HNF4A-AS1/HNF4A-CYPs axis is an epigenetic-dependent novel negative feedback regulatory loop that should be considered for maintenance of the homeostasis of CYPs in the liver.

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## **Authorship Contributions**

*Participated in research design:* P. Wang, Yan, Zhong, Han, Zhang

*Conducted experiments:* P. Wang, Chen, Y. Wang, X. Wang, Yan, Yang

*Performed data analysis:* P. Wang, Chen, Zhang

*Wrote or contributed to the writing of the manuscript:* P. Wang, Chen, Zhong,

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## Footnotes

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## Figure legends

**Fig. 1.** Impact of HNF4A-AS1 knockdown on the basal expression of genes in Huh7 cells. si-HNF4A-AS1 or negative control siRNA was transfected into Huh7 cells for 24 hours. The RNA and protein expression levels of genes after HNF4A-AS1 knockdown were measured by qRT-PCR and Western Blot, respectively. (A) Expression of HNF4A and HNF4A-AS1 at the RNA level. (B) The protein expression of HNF4A. (C) The relative mRNA expression of selected nuclear receptors. (D) The relative mRNA expression of CYPs. (E) The protein expression of PXR. (F) The protein expression of CYP3A4. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's *t* test. \**P* < 0.05; \*\**P* < 0.01 vs. the si-NC group.

**Fig. 2.** Impact of HNF4A-AS1 overexpression on the basal expression of genes in Huh7 cells. HNF4A-AS1 expression plasmid or negative control plasmid was transfected into Huh7 cells for 24 hours. The RNA expression of genes after HNF4A-AS1 overexpression was measured by qRT-PCR. (A) Expression of HNF4A and HNF4A-AS1 at the RNA level. (B) The relative mRNA expression of selected nuclear receptors. (C) The relative mRNA expression of CYPs. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's *t* test. \**P* < 0.05; \*\**P* < 0.01; \*\*\**P* < 0.001 vs. the OE-NC group. OE-HNF4A-AS1,

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overexpression of HNF4A-AS1.

**Fig. 3.** HNF4A-AS1 repressed the RIF-induced expression of genes in Huh7 cells. si-HNF4A-AS1, si-NC, OE-HNF4A-AS1, or OE-NC transfected Huh7 cells were treated with RIF for 24 hours. The RIF-induced expression of genes after HNF4A-AS1 knockdown or overexpression at the RNA level was detected by qRT-PCR method. (A-C) Knockdown of HNF4A-AS1 elevated the RIF-induced expression of genes. (D-F) Overexpression of HNF4A-AS1 diminished the RIF-induced expression of genes. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's *t* test. \**P* < 0.05; \*\**P* < 0.01; \*\*\**P* < 0.001 vs. the control group.

**Fig. 4.** Impact of HNF4A knockdown on the basal expression of genes in Huh7 cells. si-HNF4A or negative control siRNA was transfected into Huh7 cells for 24 hours. The RNA and protein expression of selected genes after HNF4A knockdown were measured by qRT-PCR and Western Blot method, respectively. (A) Expression of HNF4A and HNF4A-AS1 at the RNA level. (B) The protein expression of HNF4A. (C) The relative mRNA expression of selected nuclear receptors. (D) The relative mRNA expression of CYPs. (E) The protein expression of PXR. (F) The protein expression of CYP3A4. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's *t* test. \**P* < 0.05; \*\**P* < 0.01;



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\*\*\* $P < 0.001$  vs. the si-NC group.

**Fig. 5.** Effect of HNF4A knockdown on the RIF-induced expression of genes in Huh7 cells. si-HNF4A or si-NC transfected Huh7 cells were treated with RIF for 24 hours. The RIF-induced expression of genes after HNF4A knockdown in the RNA level was determined by qRT-PCR method. (A) Expression of HNF4A and HNF4A-AS1 at the RNA level. (B) The relative mRNA expression of selected nuclear receptors. (C) The relative mRNA expression of CYPs. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's *t* test. \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$  vs. the control group.

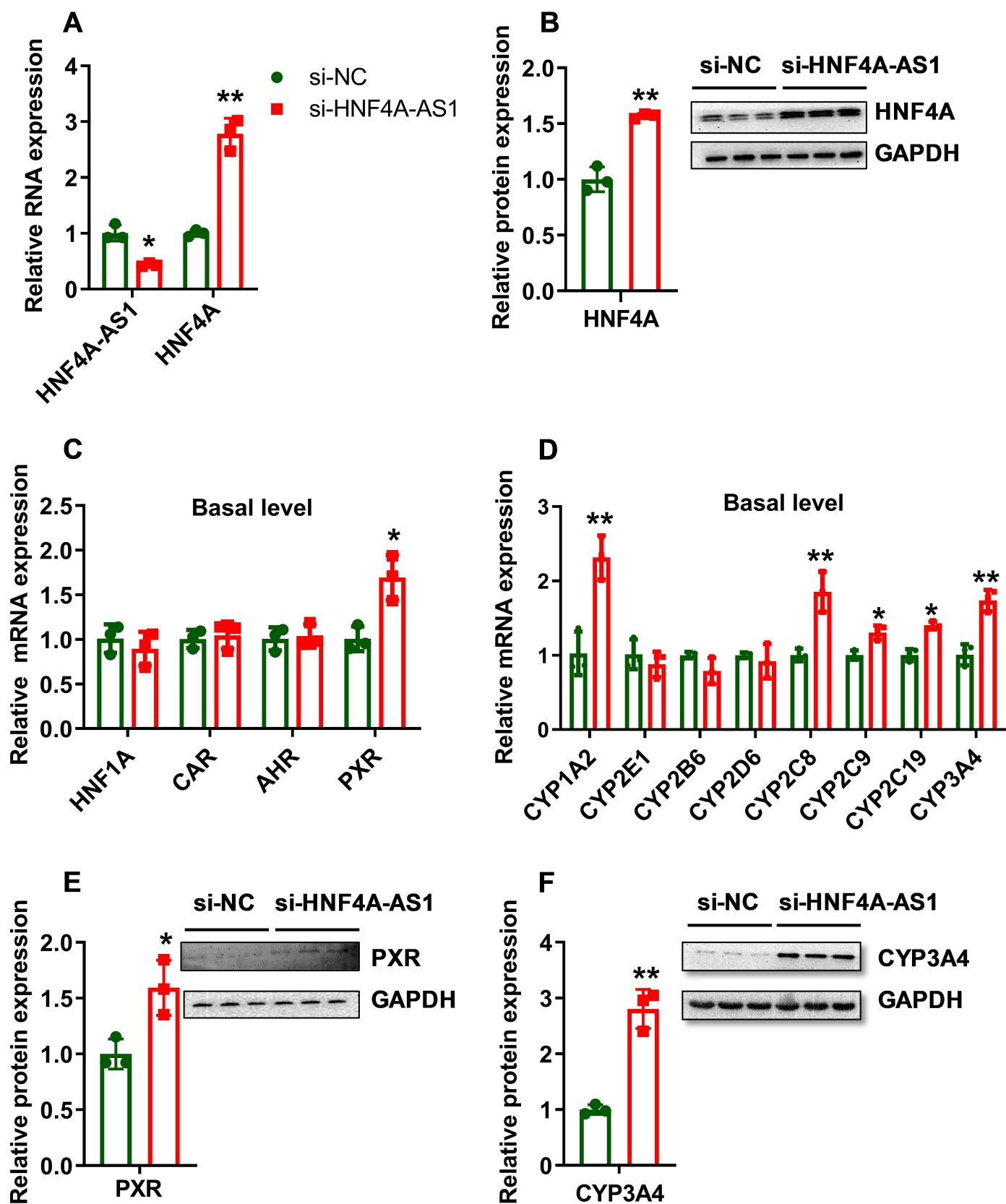
**Fig. 6.** Suppression of HNF4A-AS1 elevated the enrichment levels of histone modifications and HNF4A in the promoter of *CYP3A4* in Huh7 cells. (A) Schematic locations of HNF4A response elements (HREs) and ChIP-qPCR primers in the *CYP3A4* promoter. (B) Enrichment levels of H3K4me3 around the HREs in *CYP3A4* promoter. (C) Enrichment levels of HNF4A around the HREs in *CYP3A4* promoter. ChIP-qPCR analysis was conducted to measure the enrichment levels of H3K4me3 and HNF4A in the promoter of *CYP3A4* and data were presented as fold enrichment over IgG. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's *t* test. \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$  vs. the si-NC group.

**Table 1.** Primer sequences for qRT-PCR analysis

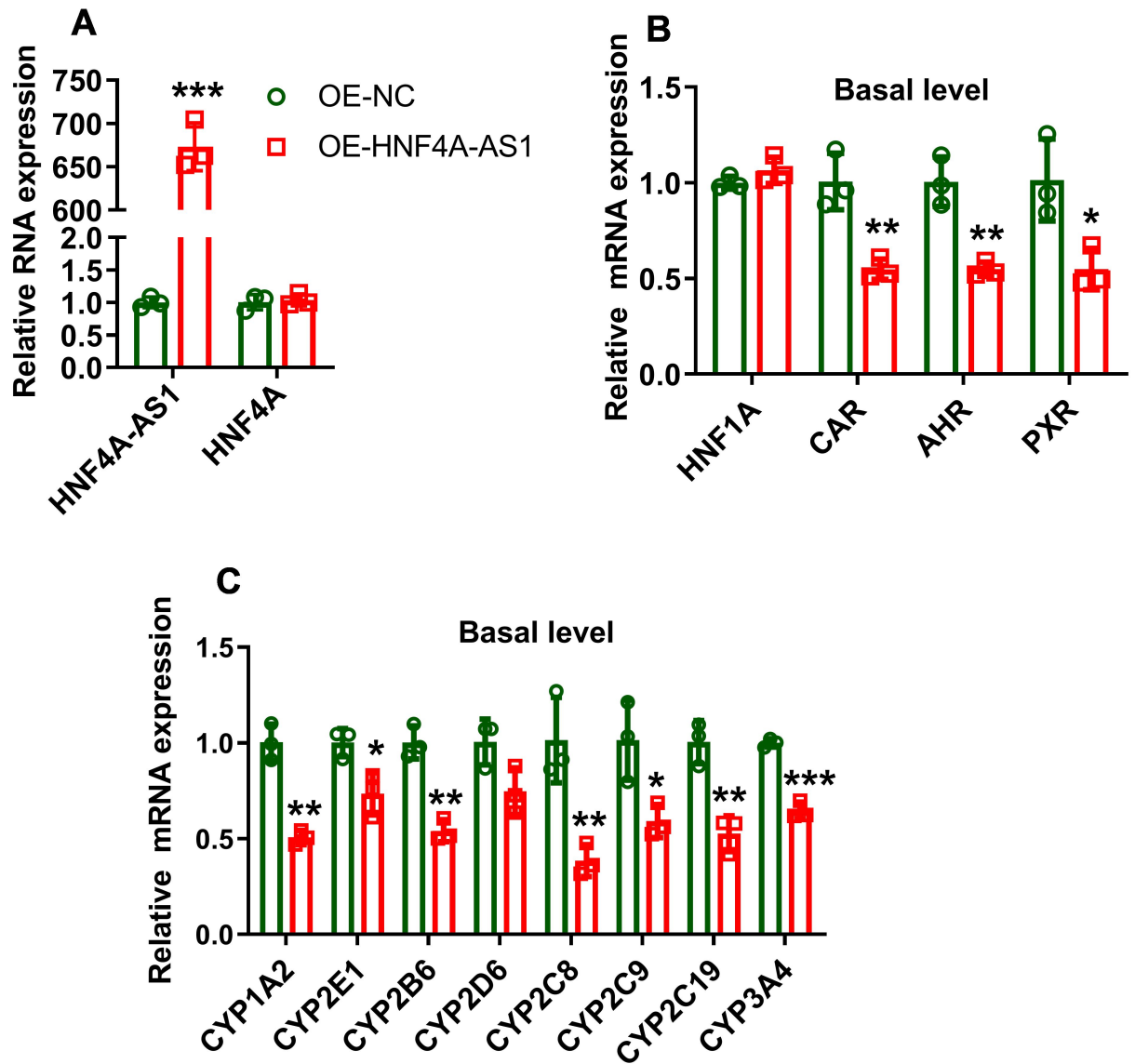
Gene	Sequence (5'-3')	Orientation
<i>GAPDH</i>	GCACCGTCAAGGCTGAGAAC	Sense
	TGGTGAAGACGCCAGTGGA	Antisense
<i>HNF4A-AS1</i>	TGGAGCTGGGATCTGACACT	Sense
	ATGACCGGTGTGCAGTCAAG	Antisense
<i>HNF4A</i>	CGTGCTGCTCCTAGGCAA	Sense
	GTCAAGGATGCGTATGGACAC	Antisense
<i>HNF1A</i>	TGGGTCCTACGTTACCAAC	Sense
	TCTGCACAGGTGGCATGAGC	Antisense
<i>CAR</i>	CAGAAGCGGTGCATACCTCA	Sense
	AGATGGCACTGACTCTGCAA	Antisense
<i>AhR</i>	ACATCACCTACGCCAGTCGC	Sense
	TCTATGCCGCTTGGAAGGAT	Antisense
<i>PXR</i>	CAACCTACATGTTCAAAGGCATC	Sense
	ACACTCCCAGGTTCCAGTCTC	Antisense
<i>CYP1A2</i>	CCAACGTCATTGGTGCCATG	Sense
	GTGATGTCCCGGACACTGTTC	Antisense
<i>CYP2E1</i>	TCCTAGGGCACAGTCGTAGT	Sense
	AGGGAAGGTACTGCCTCTGAT	Antisense
<i>CYP2B6</i>	AGACGCCTTCAATCCTGACC	Sense
	CCTTCACCAAGACAAATCCGC	Antisense
<i>CYP2D6</i>	CCTACGCTTCCAAAAGGCTTT	Sense
	AGAGAACAGGTCAGCCACCACT	Antisense
<i>CYP2C8</i>	GGACTTTATGGATTGCTTCCTG	Sense
	CCATATCTCAGAGTGGTGCTTG	Antisense
<i>CYP2C9</i>	GACATGAACAACCCTCAGGACTTT	Sense
	TGCTTGTCGTCTCTGTCCCA	Antisense
<i>CYP2C19</i>	GAACACCAAGAATCGATGGACA	Sense
	TCAGCAGGAGAAGGAGAGCATA	Antisense
<i>CYP3A4</i>	CCCTTTGGAAGTGGACCCAG	Sense
	ACGGTGCCATCCCTTGACTC	Antisense

**Table 2.** Primer sequences for ChIP-qPCR

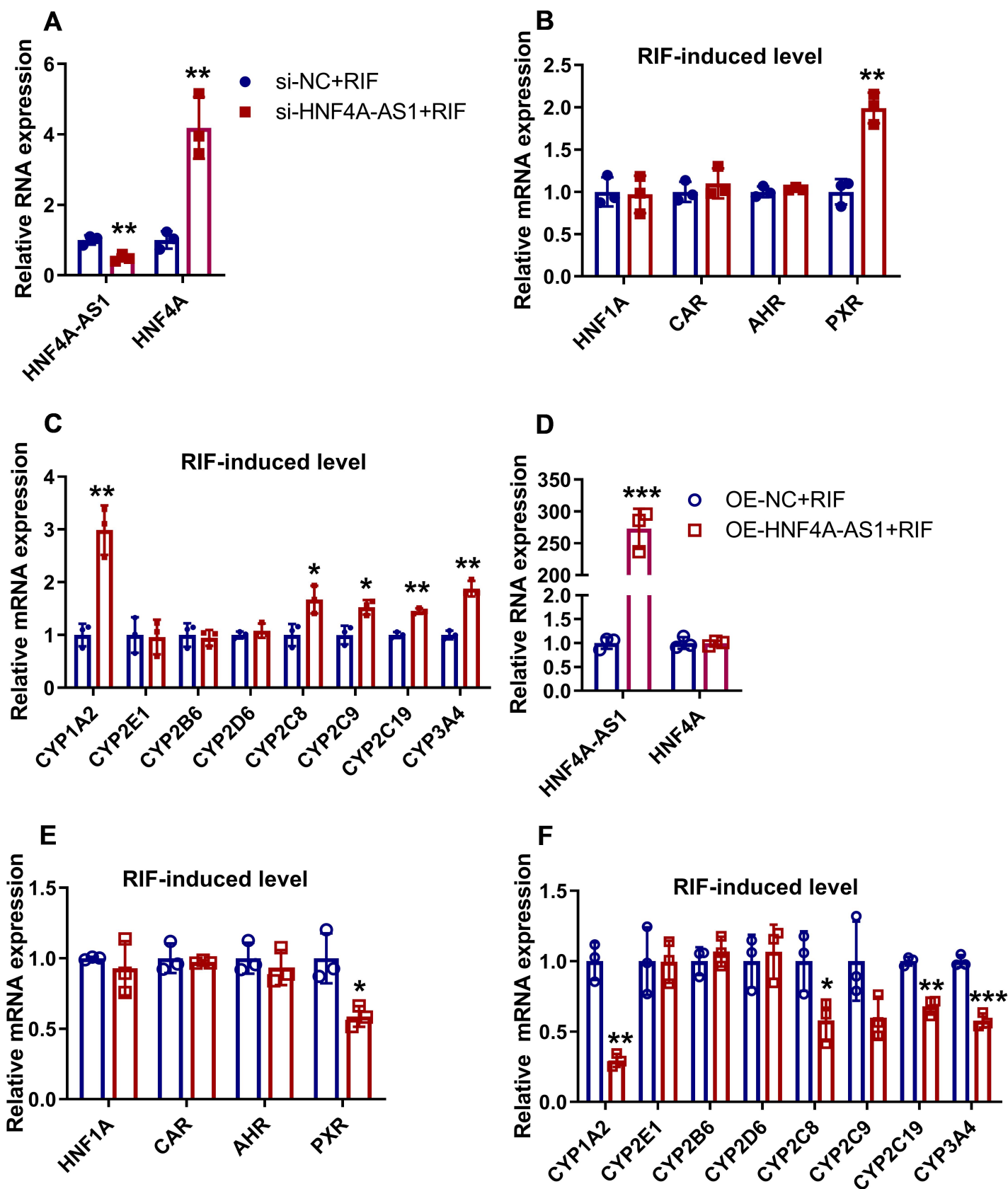
Primer	Position	Sequence (5'-3')	Orientation
Primer 1	-362 ~ +53	GCACCGTCAAGGCTGAGAAC	Sense
		GCCTGAGAACACCAGAGACC	Antisense
Primer 2	-6,093 ~ -6,574	CAGCAGACAGAGAACCCAGA	Sense
		GCCTGAGAACACCAGAGACC	Antisense



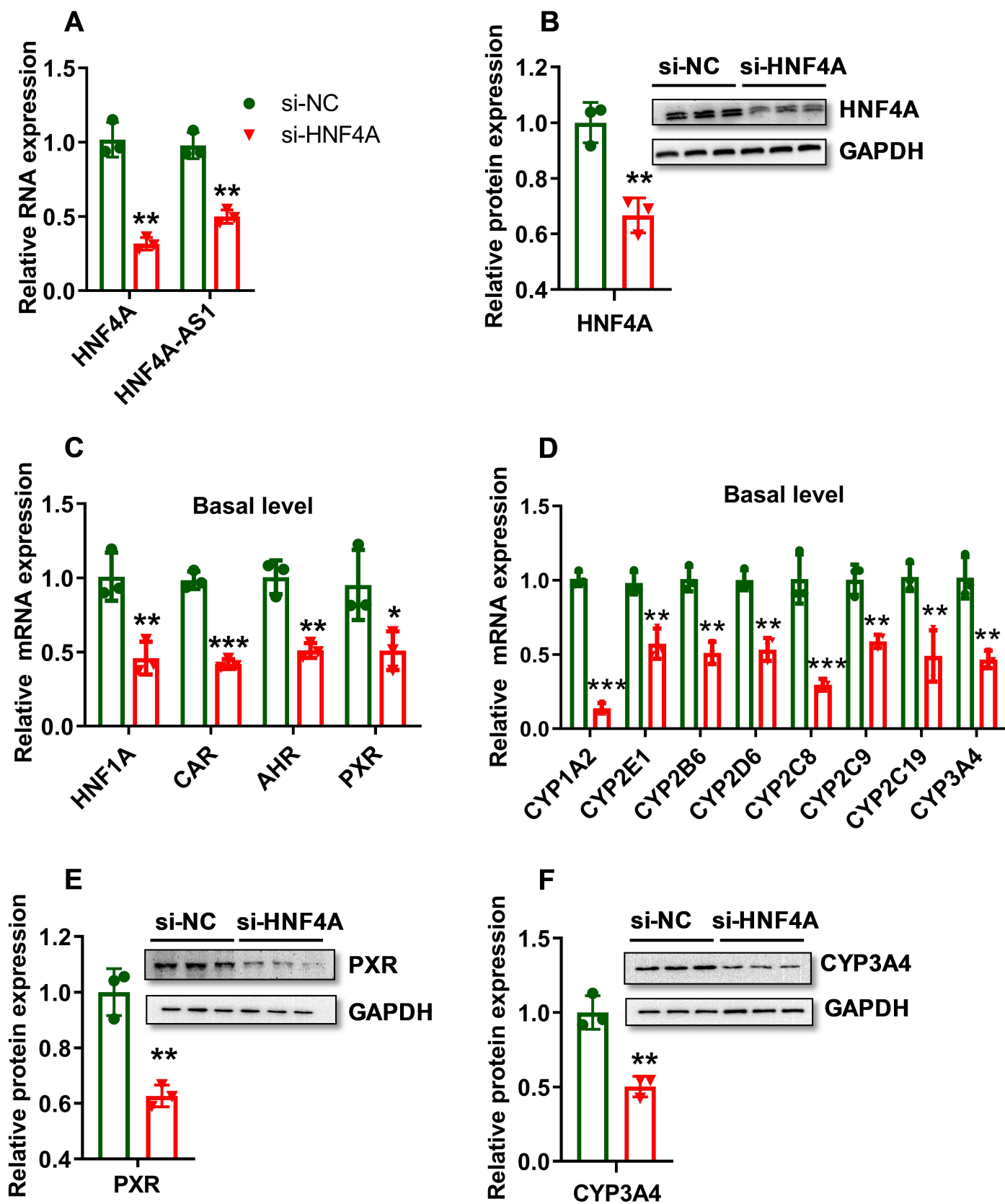
**Fig. 1**



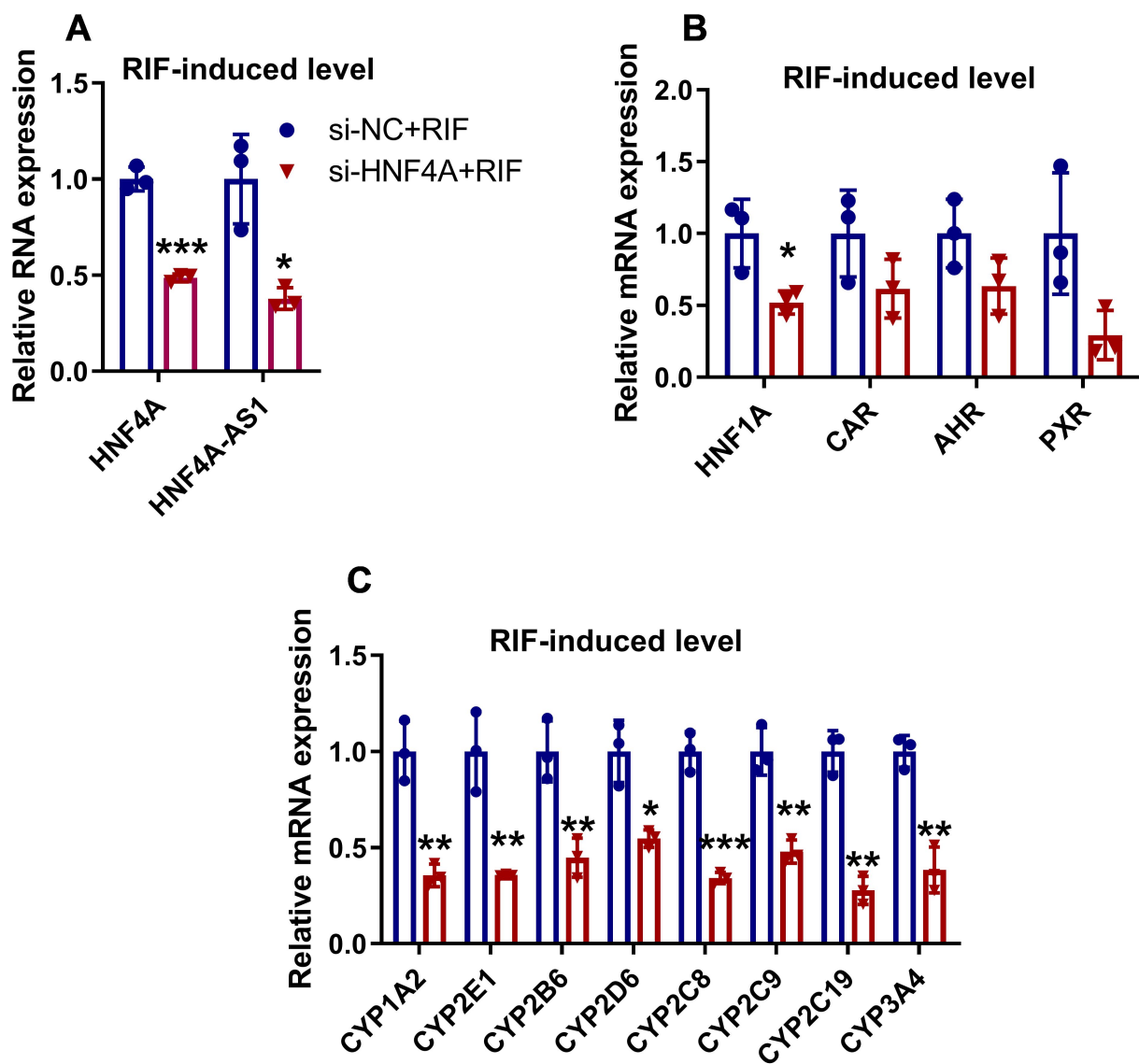
**Fig. 2**



**Fig. 3**

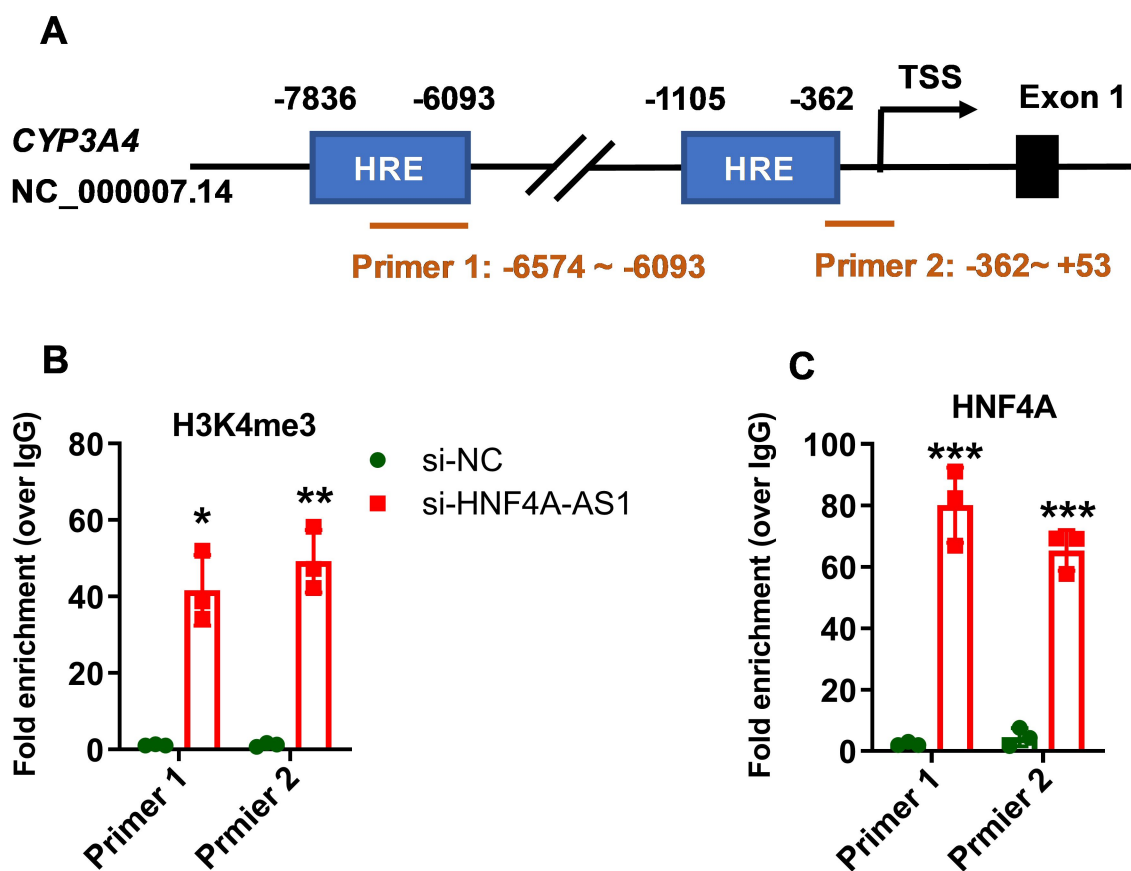


**Fig. 4**

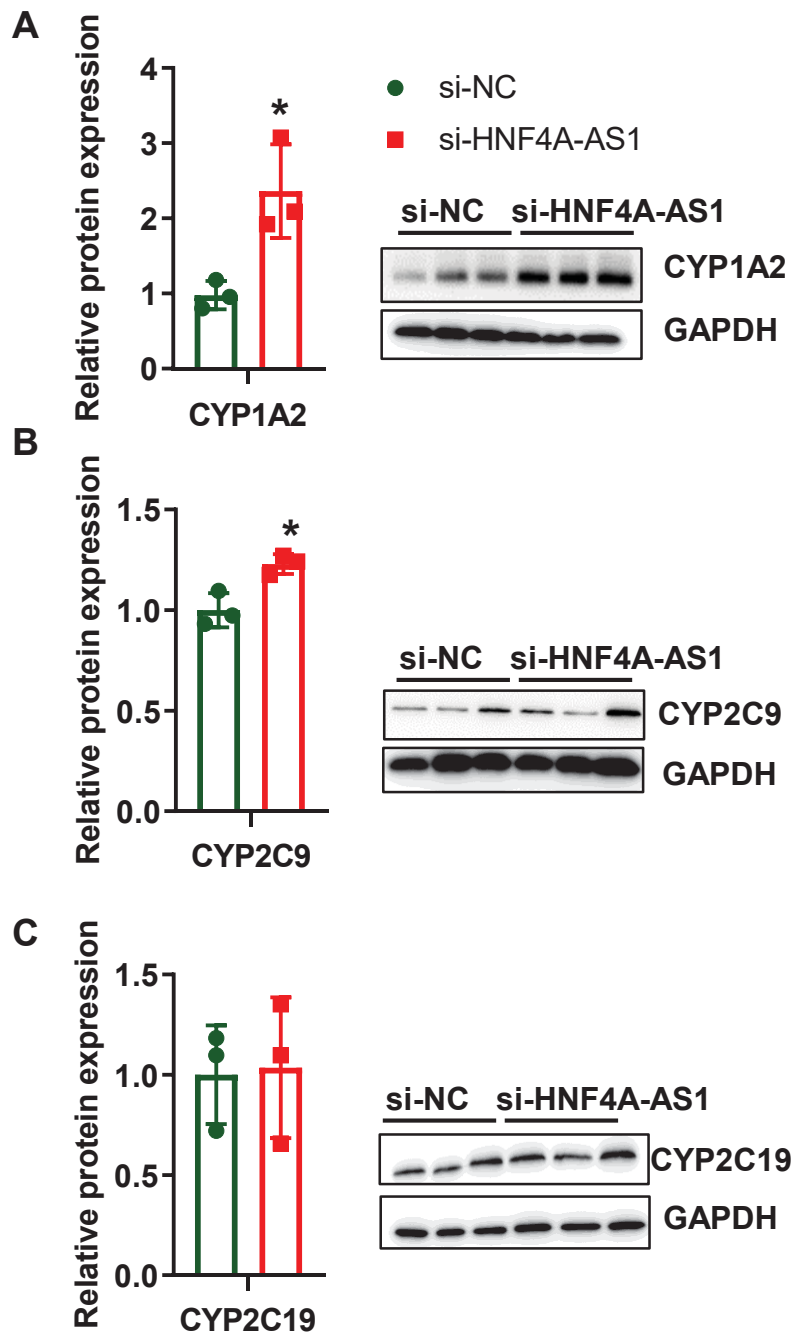


**Fig. 5**





**Fig. 6**

**The Long Non-coding RNA HNF4A-AS1 Negatively Regulates Cytochrome P450 Enzymes in Huh7 Cells via Histone Modifications**

**Supplemental Fig. S1.** Impact of HNF4A-AS1 knockdown on the protein expression of CYPs in Huh7 cells. si-HNF4A-AS1 or negative control siRNA was transfected into Huh7 cells for 24 hours. The protein expression of CYPs after HNF4A-AS1 knockdown were measured by Western Blot. **(A)** The basal expression of CYP1A2 at the protein level. **(B)** The basal expression of CYP2C9 at the protein level. **(C)** The basal expression of CYP2C19 at the protein level. Data are shown as mean  $\pm$  S.D. of three independent experiments. Statistical analysis was performed using unpaired Student's t test. \* $P < 0.05$  vs. the si-NC group.

## **Supporting Materials**

**Title:** Metabolic Retroversion of Piperaquine (PQ) *via* Hepatic CYP-mediated *N*-oxidation and Reduction:  
not an Important Contributor to the Prolonged Elimination of PQ

**Authors:** Yuewu Xie, Yunrui Zhang, Huixiang Liu, Jie Xing\*

**Manuscript Number:** DMD-AR-2020-000306

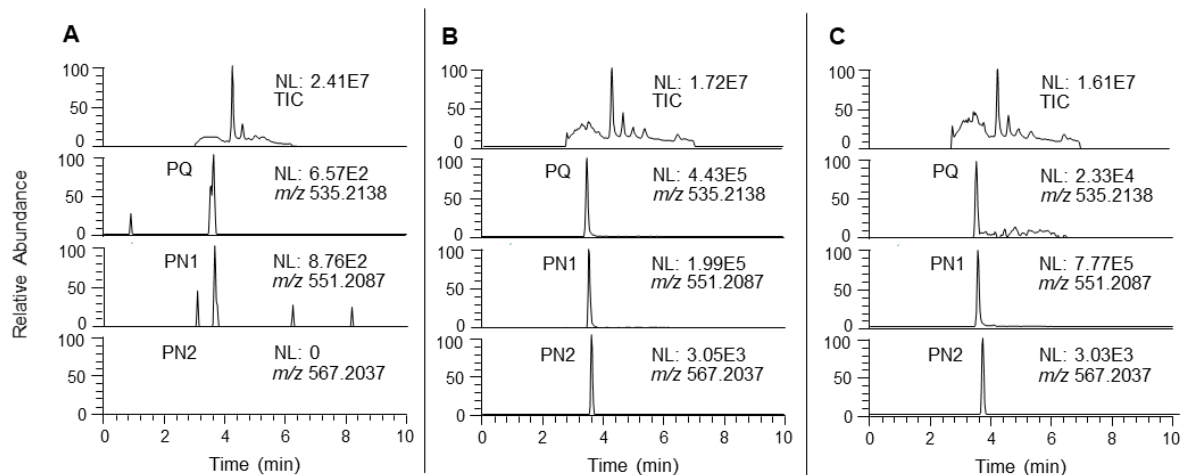
**Journal Title:** Drug Metabolism and Disposition

**TABLE S1**

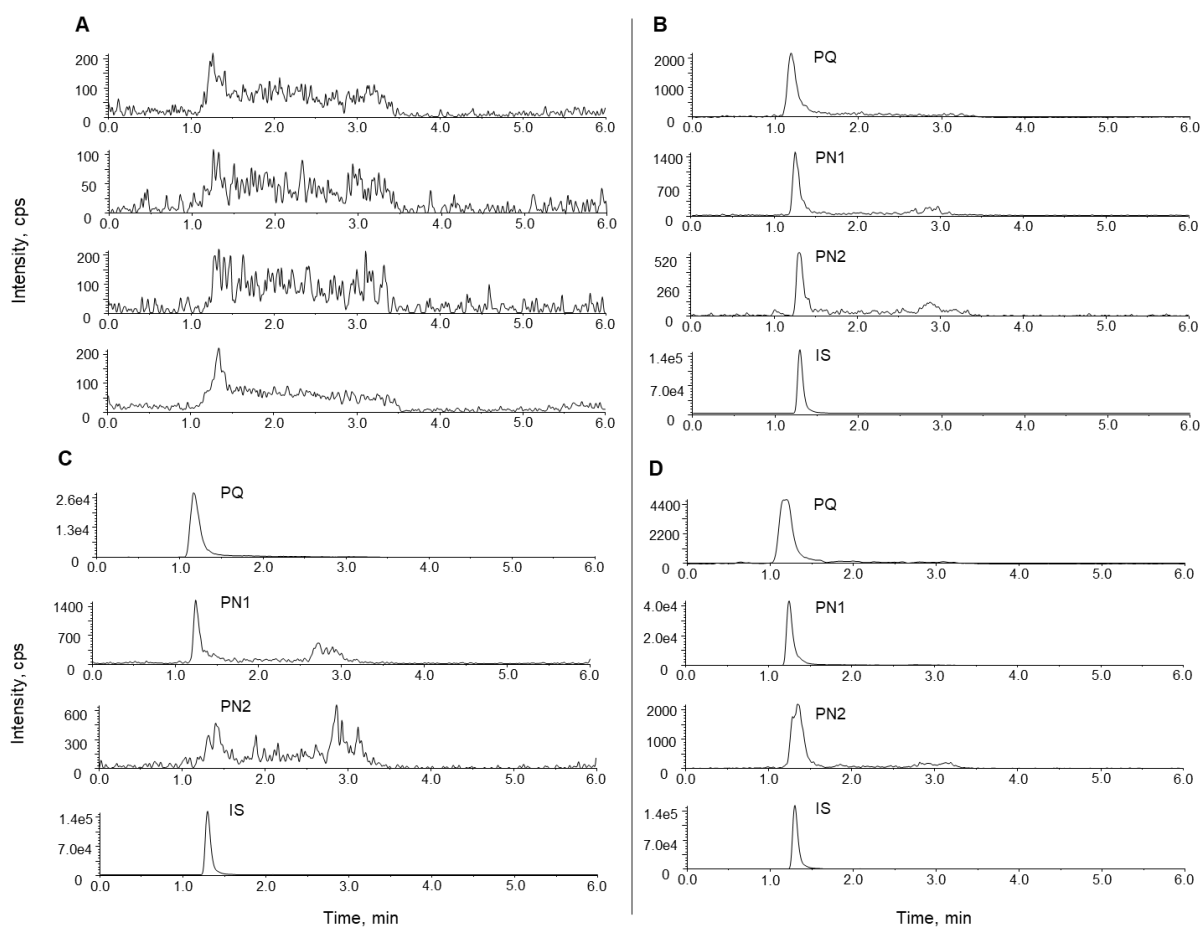
Input data for parameters used in predicting hepatic clearance

Parameters	Mice	Human
$Q_H$ (l/h/kg)	5.4	1.28
$f_{up}$	0.0254 (PQ), 0.0545 (PN1), 0.234 (PN2)	0.0262 (PQ), 0.0324 (PN1), 0.158 (PN2)
$R_{bp}$	4.01	0.55
$f_{uB}$	0.00633 (PQ)	0.0476 (PQ)
Microsomal proteins (mg/g liver)	45	40
Hematocrit	0.45	0.50
$Q_p$ (l/h/kg)	2.97	0.64
Liver weight (g/kg BW)	55.0	21.4
$CL_{int,H}$ (l/h/kg)	4.33 (PQ→PN1), 1.88 (PN1→PN2), PN1→PQ (0.26), PN2→PN1 (0.70)	1.58 (PQ→PN1), 2.91 (PN1→PN2), PN1→PQ (0.088), PN2→PN1 (0.11)
Biliary Excretion (% of dose)	1.47 (PN1), 10.26 (PN2)	N.A.
$AUC_{i.v.}$ (μg/ml·h)	3.06 (PN1), 1.26 (PN2)	N.A.
$CL_{B,in vivo}$ (l/h/kg)	0.024 (PN1), 0.405 (PN2)	N.A.
$CL_{int,sec}$ (l/h/kg)	0.44 (PN1), 1.73 (PN2)	N.A.
$ef_{mi}''$	0.712	0.940
$ef_m''$	0.872	0.973
$CL_H$ in Eq. 3 (l/h/kg)	0.0273	0.0711
$CL_H$ in Eq. 4 (l/h/kg)	0.0238	0.0693

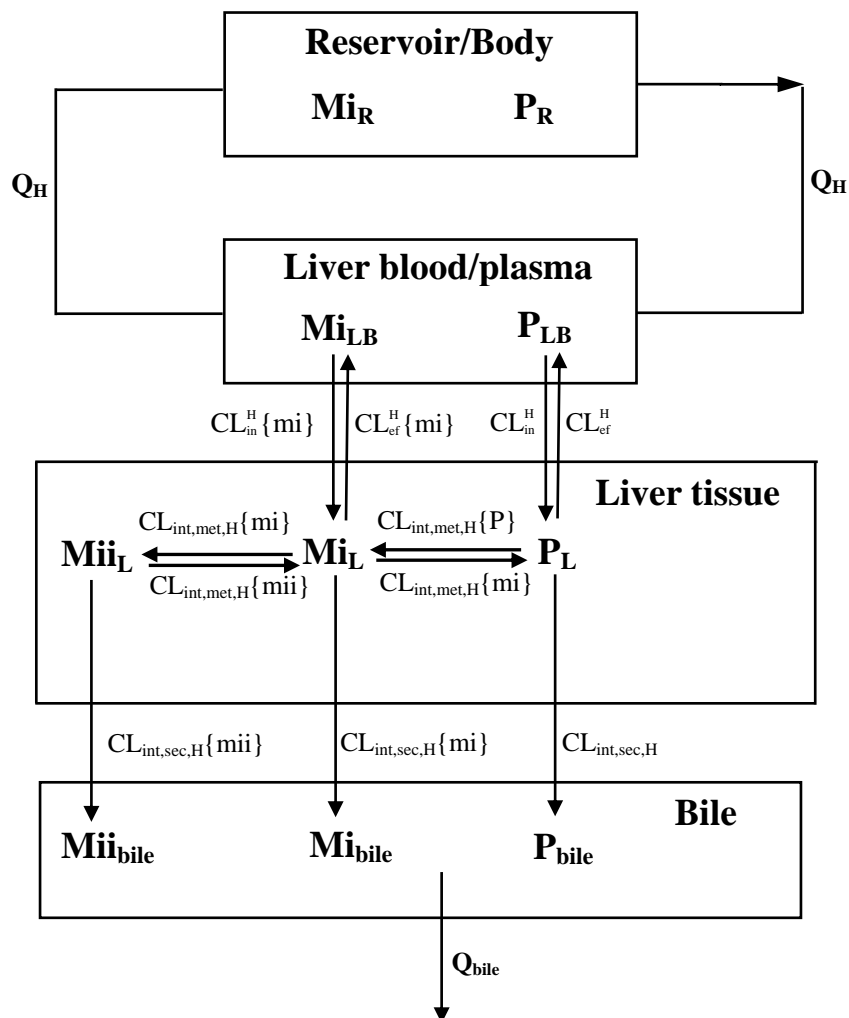
PQ, piperaquine; PN1, piperaquine *N*-oxide; PN2, piperaquine *N,N*-dioxide;  $AUC_{i.v.}$ , area under the plasma concentrations-time curve after an intravenous injection;  $CL_{B,in vivo}$ , biliary clearance;  $R_{bp}$ , blood-to-plasma ratio;  $ef_{mi}''$ , effective coefficient for metabolite formation of PN2;  $ef_m''$ , effective coefficient for metabolite formation of PN1;  $f_{uB}$ , fraction unbound in blood;  $f_{up}$ , fraction unbound in plasma;  $Q_H$ , hepatic blood flow;  $Q_p$ , hepatic plasma flow;  $CL_{int,H}$ , intrinsic hepatic clearance;  $CL_{int,sec}$ , intrinsic biliary clearance. N.A., not acquired due to invasive techniques. The  $CL_{int,sec}$  values of PN1 and PN2 in humans were assumed to be similar to that of mice.



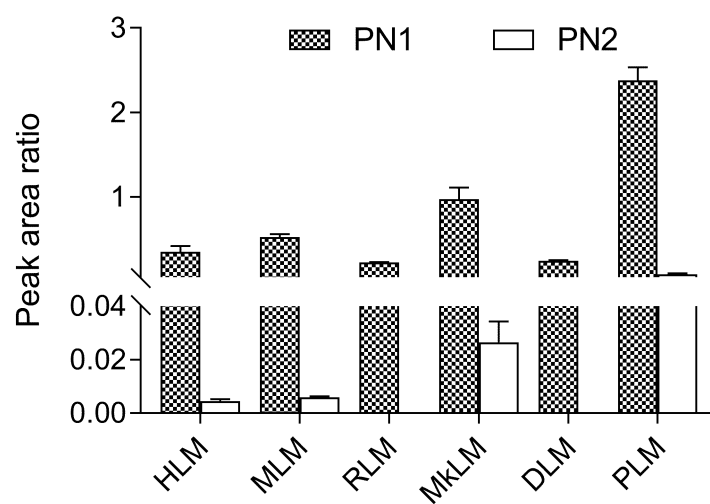
**Fig. S1** Representative high-resolution full-scan chromatograms for determination of piperazine (PQ,  $m/z$  535.2138) and its *N*-oxidation metabolites (PN1, PQ *N*-oxide,  $m/z$  551.2087; PN2, PQ *N,N*-dioxide,  $m/z$  567.2037) in (A) a blank sample, (B) human liver microsomes (0.5 mg/ml) incubated with PQ (1  $\mu$ M) for 30 min, and (C) human liver microsomes (0.5 mg/ml) incubated with PN1 (1  $\mu$ M) for 30 min.



**Fig. S2** Representative multiple reaction monitoring chromatograms for determination of piperazine (PQ) and its *N*-oxidation metabolites (PN1, PQ *N*-oxide; PN2, PQ *N,N*-dioxide) in (A) a blank plasma sample, (B) a blank mouse plasma sample spiked with PQ (2.0 ng/ml), PN1 (2.0 ng/ml), and PN2 (2.0 ng/ml), (C) a mouse plasma sample collected at 2.0 h after a single oral dose of PQ (40 mg/kg), and a mouse plasma sample collected at 2.0 h after a single oral dose of PN1 (40 mg/kg).

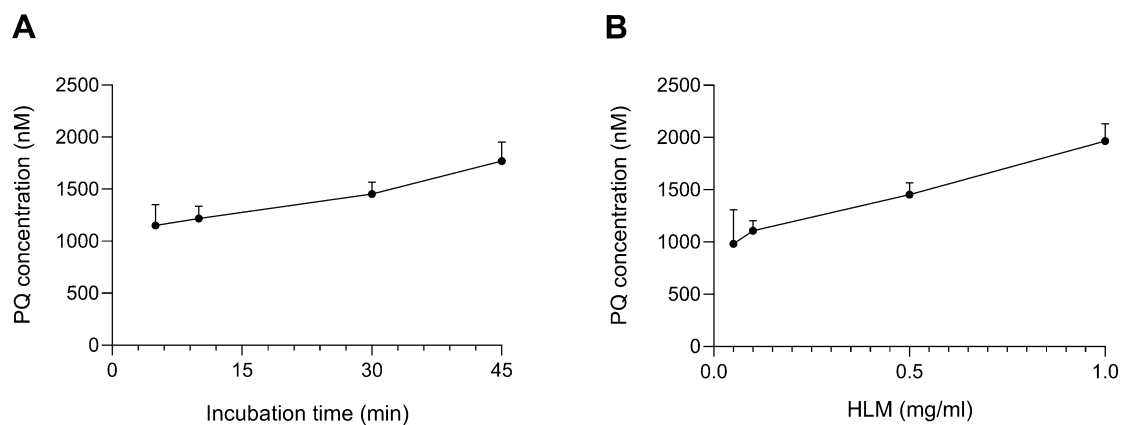


**Fig. S3** Physiologically-based pharmacokinetic model depicting the interconversion metabolism of PQ and its *N*-oxide metabolite (Mi) in the liver as the only tissue for metabolite formation and sequential metabolism. Both PQ and PN1 can undergo *N*-oxidation to their respective sequential metabolites (Mi and Mii), which can reduce back to their parent form. No other metabolites were formed for PQ or PN1, except for a one-step *N*-oxidation and/or reduction. PQ and its metabolites can be excreted into bile.

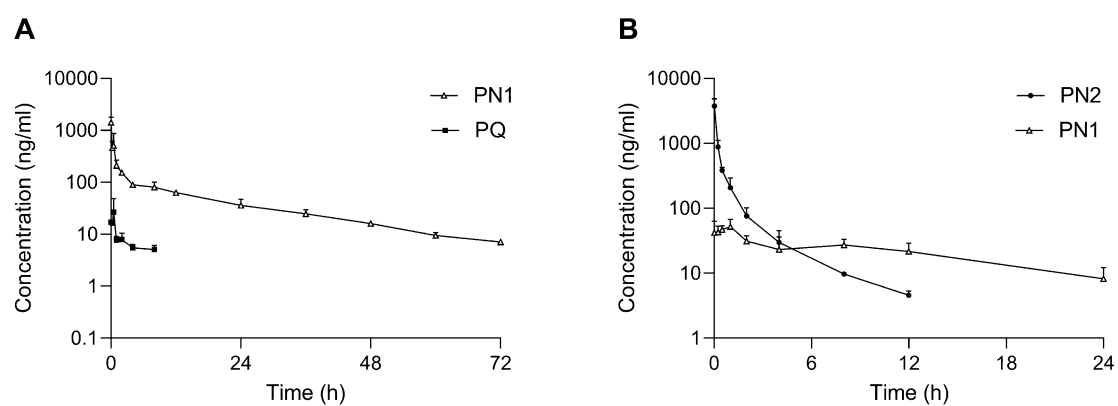


**Fig. S4** The peak area ratio of piperaquine *N*-oxide metabolites to the substrate piperaquine (PQ) in liver microsomes derived from mice (MLM), rat (RLM), dog (DLM), minipig (PLM), monkey (MkLM), and humans (HLM). PN1, PQ *N*-oxide; PN2, PQ *N,N*-dioxide.

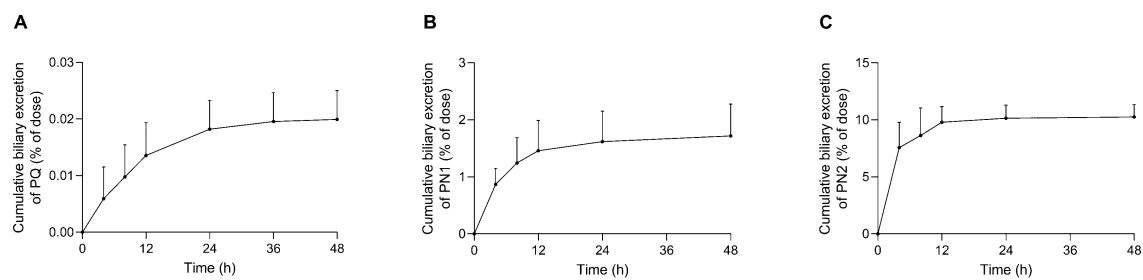




**Fig. S5** Metabolite formation of piperaquine (PQ) from piperaquine *N*-oxide (PN1) when incubated in human liver microsomes (HLM, 0.5 mg/ml) for 5-45 min (A), or incubated in HLM (0.05-1.0 mg/ml) for 30 min (B). The concentration of PN1 was 100  $\mu$ M. The experiment was performed in triplicate.



**Fig. S6** The pharmacokinetic profiles of piperazine *N*-oxide metabolites (PN1 and PN2) in mice (n=6) after an intravenous administration of PN1 (A) or PN2 (B) at the dose of 5 mg/kg. PQ, piperazine; PN1, piperazine *N*-oxide; PN2, piperazine *N,N*-dioxide.



**Fig. S7** Cumulative biliary excretion of piperazine and its *N*-oxide metabolites (PN1 and PN2) in mice (n=6) after an oral dose of PQ (A; 40 mg/kg), intravenous administration of PN1 (B; 5 mg/kg), or intravenous administration of PN2 (C; 5 mg/kg). PQ, piperazine; PN1, piperazine *N*-oxide; PN2, piperazine *N,N*-dioxide.