SUPPLEMENTARY METHODS

Immunohistochemistry (IHC) analysis

Liver and gallbladder specimens were embedded in paraffin and sectioned after formalin fixation. Microwave heating was conducted for antigen repair before the staining. Gradient concentrations of antibodies were used in the pre-experiment to determine the optimal concentration. Staining results were evaluated by two pathologists independently. Antibodies are detailed in Supplementary Table 2.

Quantitative real-time polymerase chain reaction (qRT-PCR)

RNAs of cells and tissues were extracted using TRI reagent and were reverse transcribed into complementary DNAs (cDNAs) using 5×PrimeScript Buffer. Specific primers were used for cDNA amplification. Sequences of the primers are described in Supplementary Table 3. Target gene expressions were analyzed using TB Green Premix Ex Taq on the QuantStudio 6 Flex Real-Time PCR Platform.

Western blotting (WB)

Cells and tissues were lysed using RIPA Lysis Buffer. The centrifugation was carried out to extract the total protein, the concentration of which was determined using the BCA Protein Assay Kit. Nuclear and cytosolic proteins were separated using the Nuclear Protein Extraction Kit. After denaturing, proteins were separated by 8–15% Bis-Tris gels and transferred to nitrocellulose membranes. The membranes were blocked in 5% non-fat milk and sequentially incubated with primary and secondary antibodies. The target protein signal detection was carried out using Amersham Imager600. Antibodies are detailed in Supplementary Table 2.

Immunofluorescence (IF)

Cells seeded on coverslips were fixed with 4% paraformaldehyde, permeabilized, and incubated sequentially with primary antibodies and Alexa 488- or 594-conjugated secondary antibodies. The nucleus was counterstained with DAPI. Cellular fluorescence images were captured by the DMI 6000 CS confocal microscope (Leica, Mannheim, Germany). Antibodies are detailed in Supplementary Table 2.

Tissue-specific enrichment

GTEx data was downloaded from UCSC Xena (https://xenabrowser.net/). High-throughput RNA-sequencing data from 110 normal liver samples were extracted from the dataset. The samples were classified into low (bottom 25%) and high (top 25%) groups based on the expression of GOLM1. The differentially expressed genes were defined by comparing the two group samples with a log fold change >3 and adjusted *P*-value <0.05 using the Wilcoxon signed-rank test.

Chromatin immunoprecipitation (ChIP) assay

ChIP assay was carried out according to the instructions with the antibody against GOLM1. Histone H3 and IgG antibodies were used as positive and negative controls during the acquisition of DNA fragments. The ChIP assay product was quantified by qRT-PCR utilizing SimpleChIP® Universal qPCR Master Mix. The percent input was calculated as $2\%\times2^{(Ct\ 2\%Input\ Sample-Ct\ IP\ Sample)}$. The forward primer sequence was 5'-TCT TCC TGG ATG CTG AAT GC-3', and the reverse primer sequence was 5'-CCA AGC CCT CCC AGA ATT TAA-3'.

Construction of expression vectors

Five designed fragments of OPN promoter (–500/+20, –267/+20, –127/+20, –70/+20 and –20/+20) were generated by PCR. After digested with Kpn I and Xho I, the resulting PCR-amplified fragments were cloned into the promoterless luciferase reporter plasmid pGL3-Basic to create OPN promoter-luciferase fusion reporter vectors.

Transfection and dual luciferase reporter assay

HepG2 cells were seeded in 12-well plates and transfected with OPN promoter luciferase fusion reporter vectors using Lipo2000 reagent according to the instruction manual. The pRL-TK plasmid expressing Renilla luciferase was co-transfected for internal normalization. After 6 hours, the

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transfected medium was replaced by DMEM medium supplemented with 10% FBS. Cell lysis and luciferase activity measurements were performed using the Dual-Luciferase Reporter Gene Assay Kit. The ratio of Firefly luciferase activity to Renilla luciferase activity was employed to determine the relative luciferase activity, which was represented as fold change for each reporter luciferase normalized to the control.