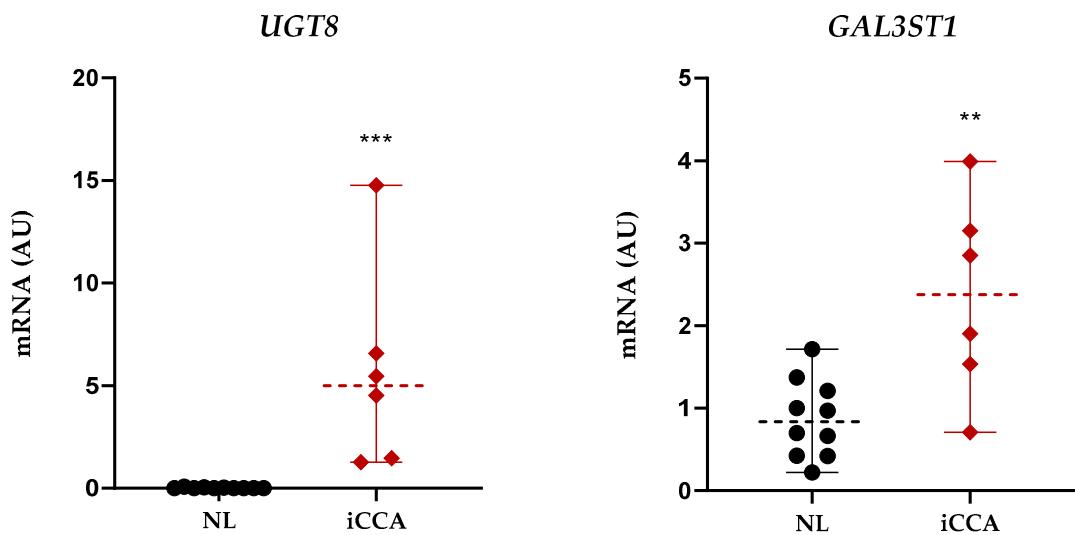


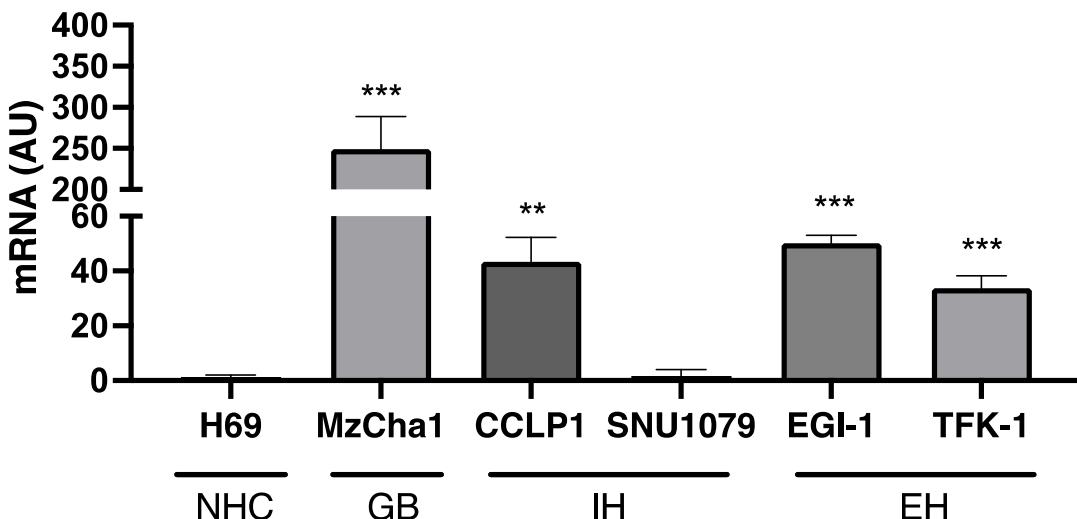
**Table S1. List of primers used for qRT-PCR**

Gene	Forward primers (5'-3')	Reverse primers (5'-3')
<i>36B4</i>	CCTCGTGGAAAGTGACATCGT	ATCTGCTTGGAGCCCACATT
<i>GAL3ST1</i>	AACCACATGCGCTTCCACTA	GTCTTCAGGAACTCGGTCA
<i>HK2</i>	AGACGAGAGTTCTGGTCTC	GATGCCCTCCGGATCAGAG
<i>PGK1</i>	AGCGGGTCGTTATGAGAGTC	TGGGACAGCAGCCTTAATCC
<i>HIF1A</i>	TCACCTGAGCCTAACATAGTC	AAATGGGTTCTTGCTTCTG
<i>ZO-1</i>	AGGGGCAGTGGTGGTTCTGTTCTTC	GCAGAGGTCAAAGTTCAAGGCTCAAGAGG
<i>OCLN</i>	TCAGGGAATATCCACCTATCACTTCAG	CATCAGCAGCAGCCATGTA CTTCAC
<i>E-cadherin</i>	CACCTGGAGAGAGGCCCGGT	AACGGAGGCCTGATGGGGCG
<i>CLDN-1</i>	GGGCTGCAGCTGTGGGCTT	GGG TTG CTT GCA ATG TGC TGC T
<i>Fibronectin</i>	CAGTGGGAGACCTCGAGAAG	GTCCCTCGAACATCAGAAA
<i>Vimentin</i>	GAGAACTTGCCGTGAAGC	TCCAGCAGCTCCTGTAGGT

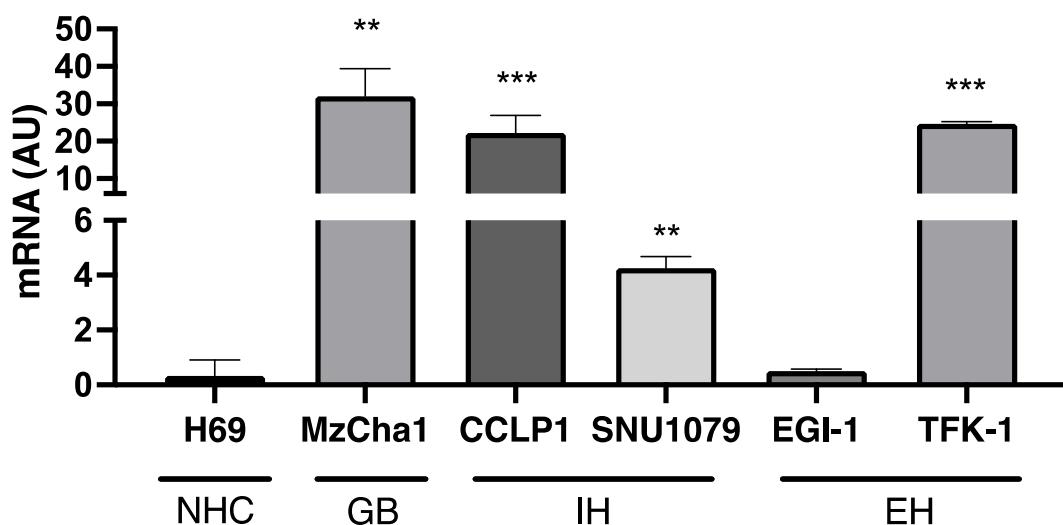


**Figure S1A. *UGT8* and *GAL3ST1* expression in human iCCA tumor specimens.** Relative mRNA levels of *UGT8* and *GAL3ST1* in intrahepatic CCA (iCCA) tissue ( $n = 6$ ) compared to non-malignant liver (NL) tissue ( $n = 10$ ). Data are shown as median with range \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .

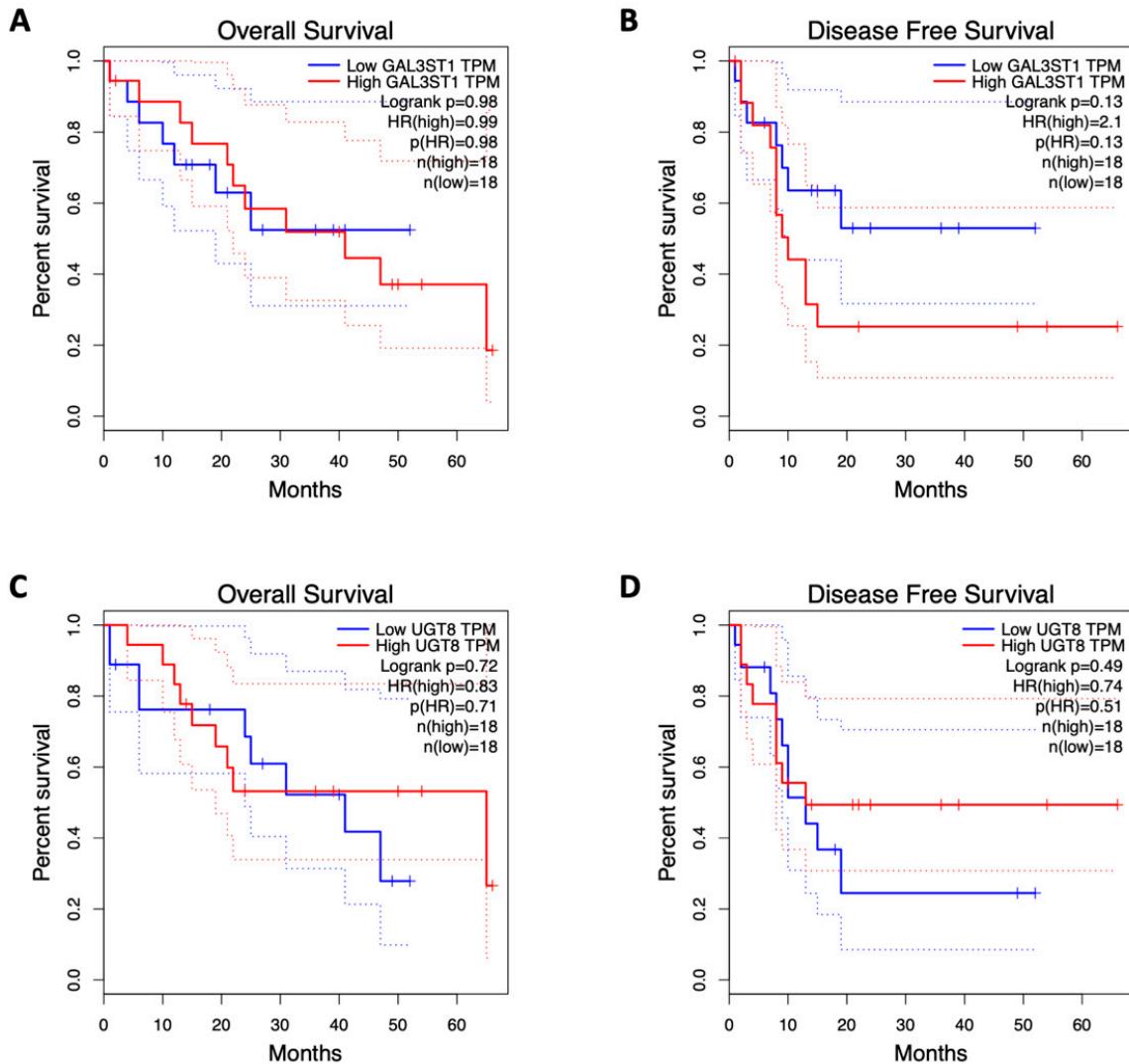
### *UGT8*



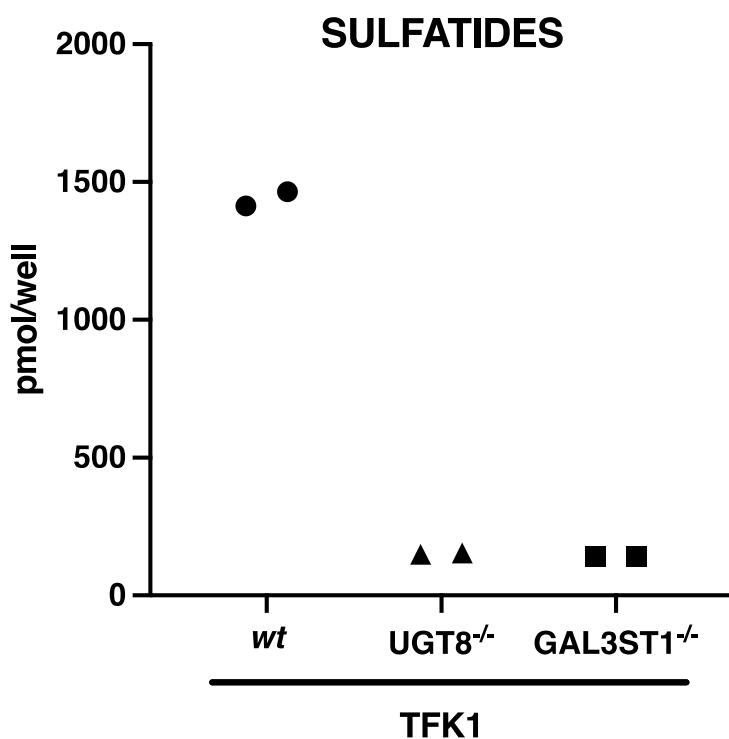
### *GAL3ST1*



**Figure S1B. *UGT8* and *GAL3ST1* expression in human CCA cell lines.** Relative mRNA levels of *UGT8* and *GAL3ST1* in human CCA cell lines, including extrahepatic (EH) CCA (TFK1, EGI-1), intrahepatic (IH) CCA (CCLP1, SNU1079), and gallbladder (GB) carcinoma (Mz-Cha-1) cell lines compared to normal human cholangiocyte (NHC) cell line (H69). Data are shown as mean  $\pm$  SD. \*\* $p$  < 0.01, \*\*\* $p$  < 0.001 vs. H69.



**Figure S1C. Overall survival (OS) analysis and disease free survival (RFS) analysis of *GAL3ST1* (A and B) and *UGT8* (C and D) with GEPIA database.** Patients were divided into high and low expression groups based on the median expression level of each gene; Each group contains 18 patients ( $n = 18$ ).



**Figure S2. Sulfatide levels in TFK1 *wt*, *UGT8<sup>-/-</sup>* and *GAL3ST1<sup>-/-</sup>* cells.** Total sulfatide levels were determined by LC-MS analysis of cell lysates of TFK1 *wt*, *UGT8<sup>-/-</sup>* and *GAL3ST1<sup>-/-</sup>* cells; *n* = 2.