Bile acid composition regulates the manganese transporter Slc30a10 in intestine

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Tables S1 to S3
Supp. Fig. 1

Table S1. Composition of BA pools with and without LCA

BA group	BA species	% in H10	% in H90	% in H10 –LCA	% in H90 –LCA
12HBA	G-CA	7	63	7	63
12HBA	G-DCA	3	27	3	27
Non-12HBA	G-CDCA	86.85	9.65	87.7	9.75
Non-12HBA	G-UDCA	2.25	0.25	2.3	0.25
Non-12HBA	LCA	0.90	0.10	0	0

G- = Glycine-conjugated

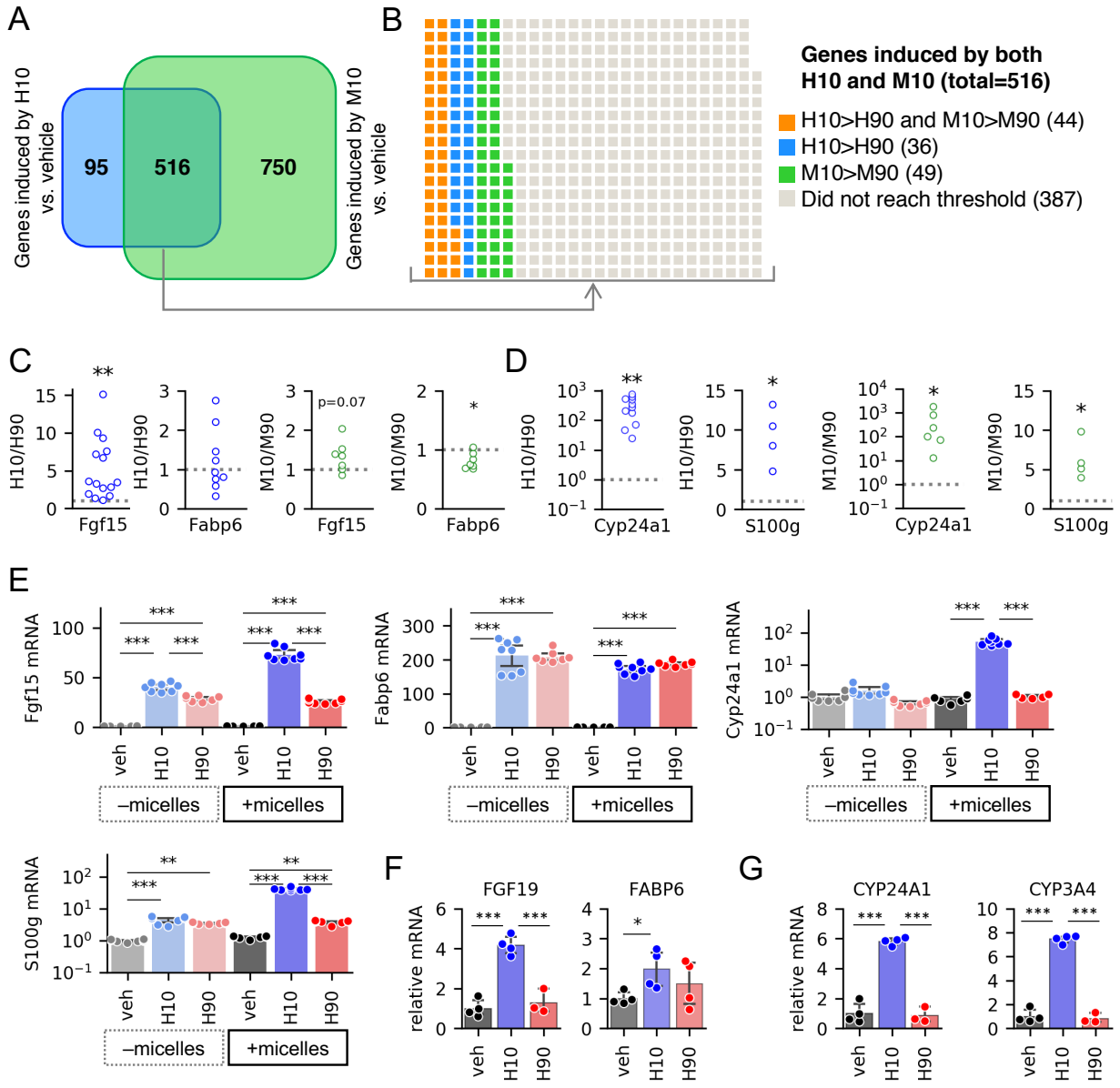
Table S2. Composition of BA pools with and without CDCA

BA group	BA species	% in M10	% in M90	% in M10 –CDCA	% in M90 –CDCA
12HBA	T-CA	9.0	81.0	9.0	81.0
12HBA	T-DCA	1.0	9.0	1.0	9.0
Non-12HBA	T-CDCA	13.5	1.5	0	0
Non-12HBA	T-UDCA	8.1	0.9	8.1	0.9
Non-12HBA	LCA	0.9	0.1	0.9	0.1
Non-12HBA	T-α-MCA	22.5	2.5	27.0	3.0
Non-12HBA	T-β-MCA	45.0	5.0	54.0	6.0

T- = Taurine-conjugated

Table S3. Primer sequences

Gene	Primer 1	Primer 2
Mouse primers		
36b4	AGATGCAGCAGATCCGCAT	GTTCTTGCCCATCAGCACC
Cyp24a1	CCAAGGTCCGTGACATCCAA	GATGCACCGAGTCGAAGGAG
Fabp6	GACGTGATTGAAAGGGGACG	CTCATCTTCACGGTAGCCT
Fgf15	ACGGGCTGATTCGCTACTC	TGTAGCCTAAACAGTCCATTTCCT
S100g	GCTGTTCCTGTCTGACTCCT	GCTGGGGAACTCTGACTGAA
Slc11a2	CAGGAAGTCATTGGCTCAGC	TATCCAAACGTGAGGGCCAT
Slc30a10	GAGATGGGCCGTTACTCAGG	GCCTCCACGAAGATGGTGAA
Slc39a14	ATCCAGAATCTTGGCCTCCT	AAGAGCTGCCTTTTCCATGA
Slc39a8	CTGTCACTGAGCCTAACGGA	GCCGTCGATGAAATTGTGGA
Slc51b	GAAGATGCGGCTCCTTGGA	GCTCTCTGTTTCCTGTGGGT
Human primers		
RPLP0	QIAGEN PPH21138F-200	
CYP3A4	GCAGGAGGAAATTGATGCAGTT	GTCAAGATACTCCATCTGTAGCACAGT
CYP24A1	GGGTCTCAAGAAACAGCACG	GCCTTCCACGGTTTGATCTC
FABP6	ACTTGGTCCCAGCACTACTC	TAGGCCAGTCTCTTGCTCAC
FGF19	CTGACATGTTCTCTTCGCCC	CGTGGACTCAGGACTGTTCT
SLC11A2	TGCATCTTGCTGAAGTATGTCACC	CTCCACCATCAGCCACAGGAT
SLC30A10	TTCAACATGCTCTCCGACCT	GAAGATGGTGAAGCAGAGCG
SLC39A14	TTCACCCCTGGCATTAGCAG	CACCCGTGGGATTCTCAACA
SLC39A8	TGCCTGGATGATAACGCTCT	AGCCCAACATAGCAGGAACA



Supporting Figure 1. Validation of differential expression of FXR and VDR target genes. (A) Venn diagram of differentially expressed genes induced by H10 and/or M10 compared to vehicle. (B) Genes preferentially induced by low 12HBA pools. Grouped based on $\log_2$(expression in H10/expression in H90)>1 or log2(expression in M10/expression in M90)>1 and p_{adj}<0.05. (C, D) Ratio of gene expression induced by low 12HBA to high 12HBA. Each point represents the data derived from a different mouse (n=7-15). The data point plotted is the ratio of (average mRNA levels in low 12HBA-treated organoids [n=3-8 wells])/(average mRNA levels in high 12HBA-treated organoids [n=3-8 wells]). Ratios >1 signify higher expression in low 12HBA-treated group, ratios <1 signify higher expression in high 12HBA-treated group, ratios = 1 signify no difference between low- versus high- 12HBA-treated groups. The gray dotted line marks ratio = 1. *p<0.05, **p<0.01 one-sample t-test vs. μ=1. (C) FXR targets, (D) VDR targets. (E) Gene expression in gut organoids treated with BA pools in the absence or presence of micelles. N=8 wells of organoids per group. (F, G) Gene expression of FXR and VDR targets in Caco-2 cells. N=3-4 wells of cells per group. **p<0.01 and ***p<0.001.