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| 1 | A gut-restricted lithocholic acid analog as an |
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| 2 | inhibitor of gut bacterial bile salt hydrolases |
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14 Abstract

Bile acids play crucial roles in host physiology by acting as both detergents that aid in digestion 15 16 and as signaling molecules that bind to host receptors. Gut bacterial bile salt hydrolase (BSH) 17 enzymes perform the gateway reaction leading to the conversion of host-produced primary bile 18 acids into bacterially modified secondary bile acids. Small molecule probes that target BSHs will 19 help elucidate the causal roles of these metabolites in host physiology. We previously reported the 20 development of a covalent BSH inhibitor with low gut permeability. Here, we build on our 21 previous findings and describe the development of a second-generation gut-restricted BSH 22 inhibitor with enhanced potency, reduced off-target effects, and durable in vivo efficacy. SAR 23 studies focused on the bile acid core identified a compound, AAA-10, containing a C3-sulfonated 24 lithocholic acid scaffold and an alpha-fluoromethyl ketone warhead as a potent pan-BSH inhibitor. 25 This compound inhibits BSH activity in conventional mouse fecal slurries, bacterial cultures, and 26 purified BSH proteins and displays reduced toxicity against mammalian cells compared to first 27 generation compounds. Oral administration of AAA-10 to wild-type mice for 5 days resulted in a 28 decrease in the abundance of the secondary bile acids deoxycholic acid (DCA) and lithocholic acid 29 (LCA) in the mouse GI tract with low systemic exposure of AAA-10, demonstrating that AAA-10 30 is an effective tool for inhibiting BSH activity and modulating bile acid pool composition in vivo.

31

32 Metabolites derived from the human gut microbiota have been implicated as causal agents in the maintenance of host health and the progression of disease.¹ Advances in metabolomics, sequencing 33 34 technologies, and the development of genetic tools have facilitated the identification of bacterial 35 metabolites and the biosynthetic pathways responsible for their production. However, the lack of 36 specific tools to control the levels of these metabolites in complex microbial communities has 37 hindered our ability to interrogate the roles of these metabolites in host physiology. Encouragingly, 38 the recent development of small molecule modulators of bacterial metabolites has revealed the 39 potential of microbiota-targeted therapies to treat disease, including colon cancer, cardiovascular disease, and Parkinson's disease.²⁻⁴ 40

41 Bile acids are one large class of molecules that undergo substantial metabolism by gut 42 bacteria.⁵ While bile acids have long been studied for their detergent properties,^{6,7} recent findings 43 have illustrated the key role that these metabolites play as signaling molecules. Specific bile acids 44 act as ligands for host nuclear hormone receptors (NhRs) and G-protein-coupled receptors (GPCRs), thereby affecting host metabolic and immunomodulatory processes.⁸⁻¹¹ Disruption of 45 46 bile acid homeostasis has been implicated in the initiation and progression of disease, including cancer, obesity, and hypercholesterolemia,^{8,12-15} underscoring the need for tools that control the 47 48 levels of these metabolites in vivo.

Host-produced primary bile acids are conjugated to taurine or glycine in the mammalian liver, stored in the gallbladder, and secreted into the small intestine post-prandially where they act as detergents that facilitate digestion. In the lower GI tract, resident bacteria chemically modify these metabolites, producing a large class of molecules called secondary bile acids. Before these modifications can occur, the C24 amide of conjugated bile acids must be hydrolyzed, a gateway reaction that is carried out exclusively by gut bacterial bile salt hydrolases (BSHs) (EC 3.5.1.24) 55 (Figure 1A).¹⁶ BSHs are widespread in human gut bacteria and have been identified in members 56 of 12 different phyla, including Bacteroidetes and Firmicutes, the two dominant phyla in the 57 human gut.¹⁷ Recent studies have found that BSH abundance or activity are correlated with human diseases, including inflammatory bowel diseases, type 2 diabetes, and cardiovascular disease.¹⁷⁻¹⁹ 58 59 The causal role of BSH activity in host physiology, however, remains unclear. For example, 60 studies involving antibiotic-treated and germ-free mice colonized with BSH-containing or BSHdeficient bacteria^{20,21} or conventional mice treated with non-selective small molecules^{22,23} have 61 62 reported conflicting results about the effects of BSH activity on host metabolism. An inhibitor that 63 targets a wide array of BSHs but exhibits limited off-target effects against bacterial and host cells 64 would allow for the selective in vivo modulation of bile acid composition, shifting the bile acid 65 pool toward conjugated bile acids and decreasing the abundance of deconjugated and secondary 66 bile acids. Such a tool could be utilized in fully colonized animals and would provide valuable 67 information about how bile acids affect host physiology.

68 In prior work, we took advantage of the nucleophilicity of the highly conserved active site 69 N-terminal cysteine residue (Cys2) in BSHs to develop first-in-class covalent pan-BSH inhibitors 70 (Figure 1B).²⁴ In this study, we screened electrophilic warheads appended to the core of 71 chenodeoxycholic acid (CDCA), an abundant human bile acid that is recognized by a broad 72 spectrum of BSHs.^{20,25,26} This work established an alpha-fluoromethylketone (FMK)-containing 73 molecule, compound 7 (referred to here as AAA-1, 1), as a potent and selective pan-BSH inhibitor. 74 Treatment of conventional mice with a single dose of AAA-1 allowed us to inhibit BSH activity 75 and shift the in vivo bile acid pool toward host-produced bile acids for one day. We also showed 76 that appending a sulfonate²⁷ to the C3 hydroxyl group resulted in gut-restriction of the inhibitor, a 77 change that limited the systemic exposure of this compound (GR-7, referred to here as AAA-2, 2).

78 These studies demonstrated the potential of alpha-fluoromethyl ketone-containing inhibitors to

79 target BSHs in vivo.

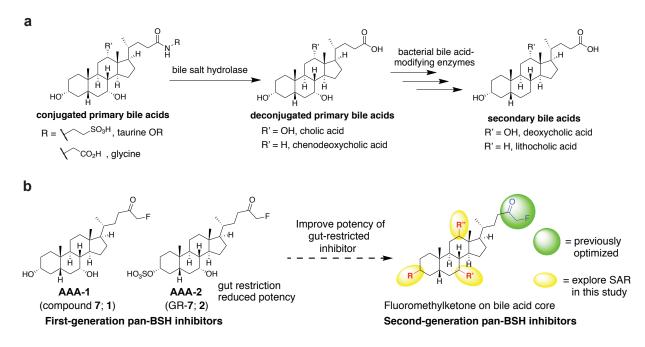


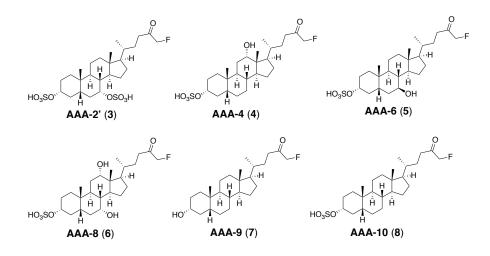


Figure 1. Targeting gut bacterial BSHs. a, Bacterial bile salt hydrolases (BSHs) perform the
gateway reaction leading from host-produced conjugated primary bile acids to bacterially
modified secondary bile acids. b, Development of second-generation BSH inhibitors starting
from previously reported covalent pan-BSH inhibitors. Sulfonation of AAA-1 at the C3-OH
position previously resulted in an inhibitor with low systemic exposure but decreased potency
(AAA-2). Here, SAR studies focusing on the bile acid core were performed with the goal of
yielding a second-generation pan-BSH inhibitor with improved potency.

~

90 To increase the utility of BSH inhibitors for use in vivo as well as to overcome several 91 limitations in our prior study, we sought to develop second-generation inhibitors. The gut-92 restricted inhibitor AAA-2 exhibited lower potency than AAA-1, motivating the synthesis of new 93 lead compounds. Moreover, while we previously demonstrated proof-of-principle that a gut-94 restricted inhibitor could affect BSH activity in vivo, we did not demonstrate a shift in the in vivo 95 bile acid pool in our prior work. Finally, to demonstrate the potential utility of these compounds 96 in animal models, we sought to show that a gut-restricted inhibitor could shift the bile acid pool 97 over a multi-day period. Here, we have built on our previous findings and report the development

of a second-generation gut-restricted BSH inhibitor with enhanced potency, reduced off-target 98 effects, and multi-day in vivo efficacy. Our structure-activity relationship (SAR) studies focused 99 100 on the bile acid core, and we identified a lithocholic acid core-based inhibitor, AAA-10 (8) (Figure 2), as a potent pan-BSH inhibitor through screening against conventional mouse fecal slurries, 101 102 bacterial cultures, and recombinant proteins. This compound is not antibacterial, displays reduced toxicity against mammalian cells compared to AAA-1 and AAA-2, and does not affect signaling 103 104 through the farnesoid X receptor (FXR) or Takeda G-protein receptor 5 (TGR5), key bile acid-105 mediated receptors. Finally, we demonstrate that AAA-10 (8) can modulate the in vivo bile acid 106 pool for 5 days, resulting in the decreased abundance of the secondary bile acids deoxycholic acid 107 (DCA) and lithocholic acid (LCA).





109 Figure 2. Library of sulfonated inhibitors. A small library of inhibitors was generated with 110 SAR focused on incorporating the cores of naturally occurring bile acids found in both mouse 111 and humans while maintaining an α -fluoromethyl ketone electrophile.

112

113 RESULTS AND DISCUSSION

114 Synthesis of BSH inhibitor candidates

115 In prior work, sulfonation of AAA-1 (1) at C3, a position that is exposed to solvent in the 116 co-crystal structure of this compound with the BSH from the gut bacterium Bacteroides 117 thetaiotaomicron (B. theta), increased the solubility of this compound and limited its systemic exposure.^{24,28} The resultant compound AAA-2, (2), however, was less potent than AAA-1.²⁴ With 118 119 the goal of improving potency while still maintaining gut restriction, we decided to append the 120 optimized FMK warhead on naturally occurring bile acid cores found in both the murine and 121 human gut (CDCA, DCA, ursodeoxycholic acid (UDCA), cholic acid (CA), and LCA). These 122 compounds could then be sulfonated at the C3 position to produce second-generation inhibitor 123 candidates (Figure 1B).

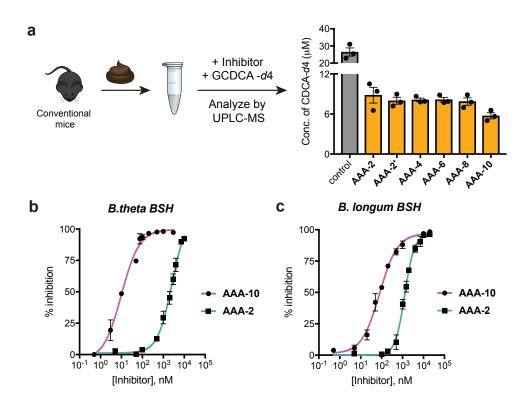
124 In order to expedite the synthesis of the library, an optimized protecting group-free 125 synthesis was developed (Scheme S1).²⁹ Following activation of the unprotected bile acid with 126 CDI, addition of magnesium benzyl fluoromalonate provided the fluoro beta-ketoester. Removal 127 of the benzyl group followed by decarboxylation under hydrogenation conditions provided the 128 FMK compounds. Finally, the sulfonate group was installed using SO₃.pyridine. Because the C3-129 α -OH group on the bile acid core is more sterically accessible than the C7 and C12 α -alcohols, 130 the sulfonation reactions proceeded selectively to provide the candidate C3-sulfonated inhibitors 131 (Figure 2, **3-6**, **8**).

132

133 Library screen in conventional mouse feces

We previously reported the use of a wild-type conventional mouse fecal slurry assay²³ to identify pan-inhibitors of BSHs.²⁴ Because fecal slurry should contain BSHs from nearly all bacteria in the distal region of the murine GI tract, demonstrating inhibition of BSH activity in this assay represents an important benchmark that all inhibitor candidates should meet. We therefore

utilized this assay as the first screen in the process of developing second-generation BSH 138 inhibitors. Inhibitor candidates were added to fresh feces obtained from conventional wild-type 139 140 mice (C57Bl/6J) and suspended in buffer under reducing conditions (Figure 3A). To facilitate identification of an inhibitor with enhanced potency compared to AAA-2, the first-generation gut-141 142 restricted inhibitor, compounds were intentionally tested at 10 μ M, a concentration at which neither AAA-1 nor AAA-2 completely inhibits enzyme activity.²⁴ After 30 min, glycine-143 144 conjugated deuterated chenodeoxycholic acid (GCDCA-d4) was added and its conversion to the 145 deconjugated product CDCA-d4 was quantified using ultra-high performance liquid 146 chromatography-mass spectrometry (UPLC-MS).



147

Figure 3. Identification of AAA-10 as a second-generation pan-BSH inhibitor. a, Assay design for screening the inhibitor library. Screening in fresh mouse feces identified **AAA-10** as a potent second-generation pan-inhibitor of BSHs. Inhibitors were tested at a concentration of 10 μ M. Assays were performed three times independently in biological triplicate with similar results. **b** and **c, AAA-10** is more potent than **AAA-2** against recombinant BSHs. Comparison of **AAA-10** and **AAA-2** dose-response curves against *Bacteroides thetaiotaomicron (B. theta)* and

154 *Bacteroides adolescentis (B. adolescentis)* BSHs using tauro-ursodeoxycholic acid (TUDCA)

- and tauro-deoxycholic acid (TDCA) as the respective substrates. See Table S1 for comparison of
- 156 IC₅₀ values of AAA-1, AAA-2 and AAA-10. For **b** and **c**, Graphpad was used to fit IC₅₀ curves.
- 157 All assays were performed in biological triplicate, and data are presented as mean \pm s.e.m.
- Mono-sulfonated inhibitor candidates containing DCA, UDCA, and CA cores (AAA-4 (4), AAA-6 (5), and AAA-8 (6), respectively) inhibited BSH activity but were not more potent than AAA-2 in this assay (Figure 3A). The C3, C7-disulfonated derivative AAA-2' (3) was also equipotent to AAA-2. Notably, the LCA core-based analog AAA-10 was more potent than both AAA-2 and the inhibitor candidates AAA-2', AAA-4, AAA-6, and AAA-8. AAA-10 was equipotent to its unsulfonated analog AAA-9 (7), indicating that C3-sulfonation did not hinder BSH inhibitory activity (Figure S1A).
- Mice fed a high-fat diet (HFD) possess higher levels of bile acids, including conjugated bile acids, than mice fed a chow diet.³⁰ Because increased substrate concentration may increase in vivo BSH activity, we also evaluated the ability of **AAA-10** to inhibit the enzyme activity in feces obtained from HFD-fed mice. We found that **AAA-10** inhibited BSH activity in this assay as effectively as **AAA-1**, our most potent first-generation BSH inhibitor (Figure S1B). Together, our data suggest that **AAA-10** is a potent inhibitor of BSHs found in the murine gut.

171

172 AAA-10 inhibits recombinant BSHs and is more potent than AAA-2

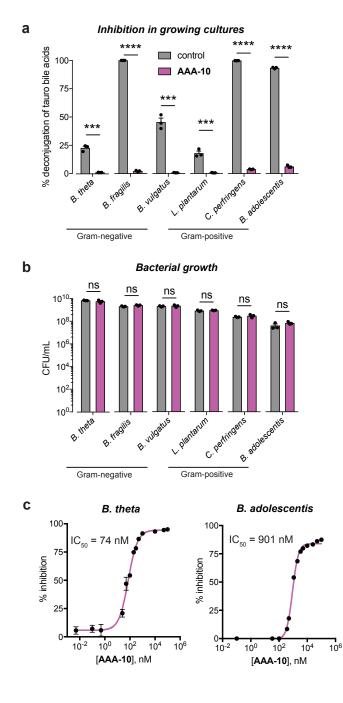
To further characterize the potency of AAA-10 compared to AAA-1 and AAA-2, we determined the IC₅₀ values of both AAA-10 and AAA-2 against purified recombinant *B. theta* (Gram-negative) and *B. longum* (Gram-positive) BSHs and compared these values to the IC₅₀ values for AAA-1 which had been determined in our previous work²⁴ (Figure 3B-C). The IC₅₀ values were evaluated using a conjugated bile acid substrate for which the enzymes demonstrated the best hydrolytic efficiency (TUDCA and TDCA, respectively).²⁴ AAA-10 exhibited an IC₅₀ 179 value of 10 nM against B. theta rBSH and 80 nM against B. longum rBSH, demonstrating that 180 AAA-10 was ~250 fold more potent than AAA-2 against B. theta rBSH and ~15 fold more potent 181 against B. longum rBSH (Table S1). Compared to AAA-1, AAA-10 was ~40 fold more potent 182 against B. theta rBSH and equally potent against B. longum rBSH (Table S1). The increased 183 potency of **AAA-10** against *B*. theta rBSH, a selective BSH, compared to both first-generation 184 inhibitors highlights the potential of this compound to target BSHs which might otherwise be 185 difficult to inhibit. These data demonstrate that we have developed a second-generation sulfonated 186 inhibitor with increased potency compared to first-generation compounds.

187

188 AAA-10 inhibits BSH activity in bacterial cultures

189 Next, we evaluated the ability of AAA-10 to inhibit enzyme activity in growing cultures 190 of BSH-containing bacteria using three Gram-negative and three Gram-positive strains found in 191 the human gut (Figure 4A). Each bacterial culture was diluted to pre-log phase and co-incubated 192 with 100 μ M of AAA-10 and 100 μ M of an equimolar mixture of taurine-conjugated bile acids 193 that are abundant in the murine gallbladder and small intestine (tauro-betamuricholic acid (TβMCA), taurocholic acid (TCA), TUDCA, and TDCA).³¹ Bacteria were then allowed to grow 194 195 into stationary phase over 24 h. Because bacteria vary in their ability to metabolize different 196 conjugated bile acids, this approach provides an unbiased way of testing the inhibitory activity of 197 AAA-10. After 24 h, percent deconjugation was determined by quantifying bile acid 198 concentrations in bacterial cultures by UPLC-MS. AAA-10 exhibited near-complete inhibition of 199 enzyme activity in all six bacterial cultures (<7% deconjugation) (Figure 4A, Figure S2). AAA-10 200 displayed equivalent inhibitory activity to AAA-1, except in the case of C. perfringens, where AAA-10 inhibited deconjugation to a greater extent than AAA-1 (4% vs 22% deconjugation,

202 respectively).²⁴



203

204 Figure 4. AAA-10 inhibits BSH activity in bacterial cultures without exhibiting

antibacterial effects. a, AAA-10 inhibits bacterial BSH activity. The BSH inhibitory activity of
 AAA-10 against three Gram-negative (*B. theta* VPI-5482, *Bacteroides fragilis* ATCC 25285, and

207 Bacteroides vulgatus ATCC 8482) and three Gram-positive (Lactobacillus plantarum WCFS1,

208 *Clostridium perfringens* ATCC 13124, and *Bifidobacterium adolescentis* L2–32) human gut 209 bacteria was evaluated. BSH activity was quantified as percent deconjugation of tauroconjugated bile acids at 24 h as determined by UPLC-MS (for absolute concentrations of 210 211 substrates and products recovered, see Figure S2). b, AAA-10 did not affect bacterial cell 212 viability. At the end of the assay in (a), the bacteria were plated to determine cell viability. c, AAA-10 is a nanomolar inhibitor of bacterial BSHs. Dose-response curves of AAA-10 against B. 213 214 theta and B. adolescentis cultures were generated using tauro-ursodeoxycholic acid (TUDCA) 215 and tauro-deoxycholic acid (TDCA) as substrates, respectively. For a, and b, two-tailed 216 Student's t-test were performed. For **c**, Graphpad was used to fit IC₅₀ curves. *p<0.05, **p<0.01, 217 ***p<0.001, ****p<0.0001, ns = not significant. All assays were performed in biological triplicate, and data are presented as mean \pm s.e.m. 218 219

To demonstrate that the BSH inhibitory activity of **AAA-10** in bacterial cultures was not due to growth inhibition, we evaluated the colony forming units in aforementioned bacterial cultures treated with **AAA-10**. We found that this compound did not significantly affect the growth of any of the tested bacterial strains at a concentration of $100 \ \mu$ M (Figure 4B).

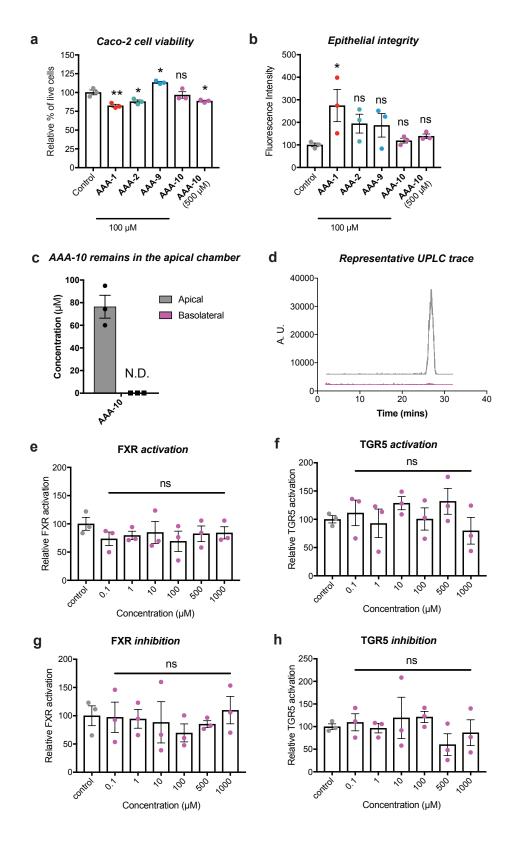
224 We also determined the IC₅₀ values of **AAA-10** against *B*. *theta* (Gram-negative) and *B*. adolescentis (Gram-positive) whole cell cultures. For this purpose, we used a single conjugated 225 226 bile acid against which the enzyme demonstrated the highest deconjugation efficiency (TUDCA 227 and TDCA, respectively). While the IC₅₀ value for AAA-10 against *B. adolescentis* was higher than the previously reported value for AAA-1 (901 nM versus 108 nM, respectively), AAA-10 228 displayed a lower IC₅₀ value against *B*. theta than AAA-1 (74 nM versus 427 nM, respectively)²⁴ 229 (Figure 4c). These data are consistent with our results using purified protein and show that AAA-230 231 10 is the most potent inhibitor of the *B*. theta BSH yet developed. Together, these results 232 demonstrate that AAA-10 is a nanomolar inhibitor of gut bacterial BSHs that does not display anti-233 bacterial properties.

234

235 AAA-10 displays limited off-target effects on mammalian cells

| 236 | At high in vivo concentrations, bile acids have been shown to disrupt cell membranes and |
|-----|---|
| 237 | can induce apoptosis in mammalian cells ^{15,32,33} . Because AAA-10 is based on a bile acid scaffold, |
| 238 | we evaluated the toxicity of AAA-10 on intestinal cells as well as its off-target effects on host bile |
| 239 | acid receptors. Human intestinal Caco-2 cells were differentiated in transwell inserts to form a |
| 240 | polarized monolayer with tight junctions ³⁴ (Figure S3A). Incubation of these cells with AAA-1, |
| 241 | AAA-2 or AAA-10 showed that while AAA-1 and AAA-2 (100 μ M) negatively affected the cell |
| 242 | viability, AAA-10 did not have an effect on the cell viability at this concentration (Figure 5A). |
| 243 | AAA-10 also had no effect on the viability of human liver cells (Hep-G2) at 100 μ M or 500 μ M |
| 244 | concentrations (Figure S3B). We next determined whether BSH inhibitors affected intercellular |
| 245 | tight junctions by measuring the passive diffusion of FITC-dextran (4 kDa) from the apical to the |
| 246 | basolateral chamber of the transwells containing differentiated Caco-2 cells treated apically with |
| 247 | our compounds. AAA-10 did not appear to damage epithelial integrity at 100 μ M or 500 μ M |
| 248 | concentrations, while AAA-1, AAA-2, and AAA-9 increased FITC-d permeability by over 85% |
| 249 | (~1.5-3 fold) at a concentration of 100 μ M (Figure 5B). In order to test the gut-restricted properties |
| 250 | of AAA-10, we also quantified the amount of inhibitor in the apical and basolateral chambers in |
| 251 | these transwell assays. We have previously shown that bile acids, including LCA, pass through |
| 252 | Caco-2 monolayers. ³⁵ In contrast, while we were able to detect AAA-10 in the apical chamber, no |
| 253 | inhibitor was detected in the basolateral chamber 16 h after apical application, indicating that |
| 254 | AAA-10 does not pass through an epithelial monolayer (Figure 5C-D). |

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255

256 Figure 5. AAA-10 is not toxic to mammalian cells and not a ligand for FXR or TGR5. a,

257 Incubation of differentiated Caco-2 cells with AAA-10 (100 µM) did not result in toxicity, while

258 incubation with an equivalent concentration of AAA-1 and AAA-2 resulted in decreased cell 259 viability. **b**, **AAA-10** did not damage epithelial tight junctions at 100 µM or 500 µM, while treatment with AAA-1 resulted in loss of epithelial integrity. Epithelial junction integrity was 260 261 determined by measuring the transport of 4 kDa FITC-dextran from the apical to the basolateral 262 chamber. c, AAA-10 did not pass through an epithelial monolayer in an in vitro transwell assay 263 (for assay setup see Figure S3A). Passage of the molecule from apical chamber to basolateral 264 chamber was quantified by UPLC-MS. d, Representative UPLC-MS extracted ion chromatogram 265 (EIC) traces of apical and basolateral chamber showing that no AAA-10 was detected in the 266 basolateral chamber. e and f, FXR and TGR5 agonist activity was measured by incubating Caco-267 2 cells with varying concentrations of **AAA-10** overnight. g and h, FXR and TGR5 antagonist activity was measured by incubating Caco-2 cells with varying concentrations of AAA-10 268 overnight in the presence of 10 µM of the FXR agonist chenodeoxycholic acid (CDCA) or 10 269 270 µM of the TGR5 agonist lithocholic acid (LCA), respectively. For **a-b** and **e-h**, one-way ANOVA followed by Dunnett's multiple comparisons test. *p<0.05, **p<0.01, ***p<0.001, 271 ****p<0.0001, ns = not significant. All assays were performed in biological triplicate, and data 272

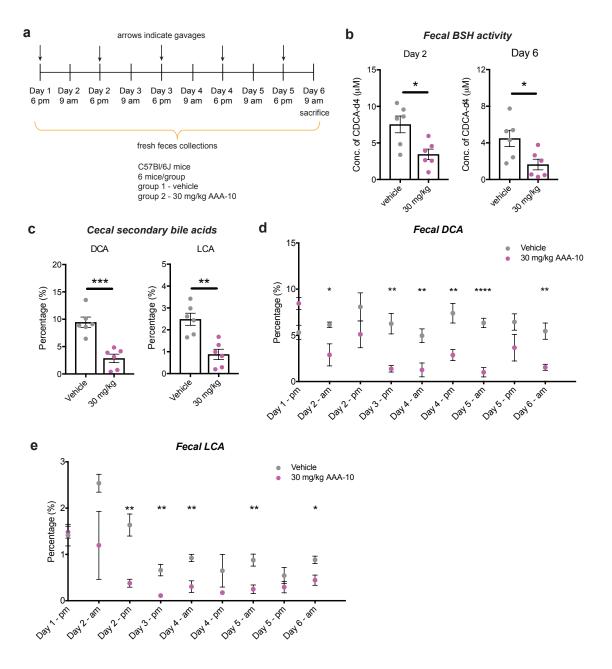
- are presented as mean \pm s.e.m.
- 274

| 275 | Bile acids can signal through the host receptors FXR and TGR5, thereby affecting host |
|-----|--|
| 276 | metabolism and immune function. ³⁶ Incubation of Caco-2 cells with increasing concentrations of |
| 277 | AAA-10 revealed that this compound did not act as an agonist of FXR or TGR5 (Figures 5E-F). |
| 278 | Incubation of Caco-2 cells with either GW4062 (FXR agonist) or LCA (TGR5 agonist) followed |
| 279 | by treatment with increasing concentrations of AAA-10 revealed that this compound did not |
| 280 | antagonize FXR or TGR5 (Figures 5G-H). Collectively, these data suggest that AAA-10 is a potent |
| 281 | pan-BSH inhibitor with low epithelial permeability that exhibits reduced off-target effects on host |
| 282 | cells compared to the first-generation inhibitors AAA-1 and AAA-2. |
| 283 | |
| | |

284 AAA-10 reduces secondary bile acid abundance in vivo

- 285 We next evaluated the ability of AAA-10 to inhibit BSH activity and modulate bile acid
- levels in vivo. Wild-type C57Bl/6J mice were gavaged once daily with AAA-10 at a dose of 30
- 287 mg/kg for 5 days (Figure 6A). The inhibitor was administered at 6 pm to coincide with the start
- 288 of the dark photoperiod when mice exhibit increased food consumption.³⁷ Fecal BSH activity

| 289 | was significantly decreased on days 2 and 6 in AAA-10-treated mice compared to vehicle-treated |
|--|---|
| 290 | mice (Figure 6B and Figure S4A), indicating that we were able to achieve durable BSH |
| 291 | inhibition in vivo using AAA-10. Analysis of the cecal bile acid pool after sacrifice revealed that |
| 292 | the abundances of DCA and LCA were significantly lowered in the AAA-10-treated group |
| 293 | (Figures 6C). DCA and LCA are secondary bile acids that are produced exclusively by gut |
| 294 | bacteria. ⁵ Cecal AAA-10 concentration was also negatively correlated with cecal concentrations |
| 295 | of both DCA and LCA (Figures S4B-C). In addition, the abundances of DCA and LCA were |
| 296 | decreased in feces each day starting on day 2 and overall in feces throughout the course of the |
| 297 | study in AAA-10-treated mice compared to vehicle-treated mice (Figures 6D-E and Figure S4D). |
| 298 | Together, these findings indicate that AAA-10 treatment resulted in a sustained reduction in |
| | |
| 299 | secondary bile acids in vivo over the period of study. |
| 299 300 | secondary bile acids in vivo over the period of study. Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this |
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| 300 | Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this |
| 300 301 | Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this compound in cecal contents and plasma at sacrifice and in feces over the course of the |
| 300 301 302 | Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this compound in cecal contents and plasma at sacrifice and in feces over the course of the experiment (Figures S4E-G). We observed a mean value of 276 picomol/mg wet mass (~276 |
| 300 301 302 303 | Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this compound in cecal contents and plasma at sacrifice and in feces over the course of the experiment (Figures S4E-G). We observed a mean value of 276 picomol/mg wet mass (~276 μ M) of AAA-10 in cecal contents and a range of 66-2087 picomol/mg (~66-2087 μ M) in feces. |
| 300 301 302 303 304 | Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this compound in cecal contents and plasma at sacrifice and in feces over the course of the experiment (Figures S4E-G). We observed a mean value of 276 picomol/mg wet mass (~276 μ M) of AAA-10 in cecal contents and a range of 66-2087 picomol/mg (~66-2087 μ M) in feces. In contrast, five of the six mice exhibited undetectable levels of AAA-10 in plasma (Figure |
| 300 301 302 303 304 305 | Finally, to evaluate the gut permeability of AAA-10 , we quantified the levels of this compound in cecal contents and plasma at sacrifice and in feces over the course of the experiment (Figures S4E-G). We observed a mean value of 276 picomol/mg wet mass (~276 μ M) of AAA-10 in cecal contents and a range of 66-2087 picomol/mg (~66-2087 μ M) in feces. In contrast, five of the six mice exhibited undetectable levels of AAA-10 in plasma (Figure S4G). In a separate experiment in which mice were sacrificed 4 hours after the final gavage, we |



309

Figure 6. AAA-10 inhibits BSH activity in vivo and reduces secondary bile acid abundance.

a, In vivo study design. C57Bl/6J mice were orally gavaged with **AAA-10** (30 mg/kg) once

- daily for 5 days. Feces were collected daily and utilized to evaluate bile acid changes and BSH
- activity. Mice were sacrificed on day 6 and tissues and blood were collected. **b**, **AAA-10**-treated
- mice exhibited decreased BSH activity compared to vehicle-treated mice in fresh feces collected
- on days 2 and 6. **c**, Percentages of the secondary bile acids deoxycholic acid (DCA) and
- 316 lithocholic acid (LCA) were reduced in cecal contents of mice treated with AAA-10. d and e,
- Analysis of fecal bile acid contents over the period of the study showed that abundances of the
- two secondary bile acids DCA and LCA were consistently decreased throughout the experiment.
- For **b-e**, n=6 mice/group, two-tailed Welch's t test was performed. *p<0.05, **p<0.01,
- 320 ***p < 0.001, ****p < 0.0001, ns = not significant. All data are presented as mean \pm s.e.m.

321 CONCLUSION

The studies reported herein were initiated with the goal of improving the potency of the 322 323 first-generation gut-restricted inhibitor AAA-2. Structure-activity relationship studies that focused 324 on incorporating the carbon scaffolds of different abundant bile acids into our inhibitor design led 325 to the identification of a second-generation inhibitor, AAA-10. This compound exhibited increased potency in an array of in vitro assays compared to AAA-2. The structure of AAA-10 is based on 326 327 the core of LCA, a bile acid that contains a single hydroxyl group at C3. In previous work, we 328 characterized the BSH activity of 20 abundant human gut Bacteroidetes species against glyco- and 329 tauro-conjugated bile acids.²⁰ Glyco-lithocholic acid (GLCA) and tauro-lithocholic acid (TLCA) 330 were effectively deconjugated (>90% conversion) by all BSH-containing Bacteroidetes species 331 tested. In contrast, all other bile acids were incompletely deconjugated (<70%) by two or more of 332 the species tested. Taken together, these results suggest that the LCA core may be effective as a 333 scaffold for BSH inhibitors because it is recognized as a substrate by a range of gut bacteria. Future 334 studies testing the deconjugating ability of a variety of Gram-positive and Gram-negative strains 335 against a panel of conjugated bile acid substrates may further elucidate the substrate scope of gut 336 bacterial BSHs and thus aid in next-generation inhibitor design.

AAA-10 also exhibited an improved off-target effects profile compared to AAA-1 and
AAA-2. This compound inhibited BSH activity without inhibiting the growth of the Gramnegative and Gram-positive bacteria tested, did not activate or inhibit the host bile acid receptors
FXR or TGR5 at concentrations expected to be effective in vivo, and was found to be non-toxic to
intestinal and liver cells at higher concentrations than AAA-1 and AAA-2.

Finally, we demonstrated that AAA-10 inhibits BSH activity in vivo. Once-daily
administration of AAA-10 by gavage at a dose of 30 mg/kg resulted in significant BSH inhibition

344 in feces and a decrease in the abundance of the secondary bile acids DCA and LCA in feces and cecal contents. DCA and LCA are known to play crucial roles in host physiology. On the one hand, 345 346 DCA and LCA are strongly associated with colon cancer development in patients, and evidence 347 indicates that these compounds promote carcinogenesis in the colon and liver.^{13,14,38-40} On the other hand, DCA has been shown to limit growth of the pathogen *Clostridium difficile*,⁴¹ and recent work 348 has shown that LCA induces the production of the anti-diabetic metabolite cholic acid-7-sulfate.³⁵ 349 350 The ability to modulate the abundance of these compounds in vivo in fully colonized animals will 351 facilitate investigations of the roles of these molecules in host physiology.

352 Looking ahead, it will be valuable to consider whether long-term use of BSH inhibitors in 353 vivo affects microbial community composition. In addition, once-daily dosing via oral gavage may 354 not be optimal in the case of ad libitum feeding, and further optimization of a strategy for inhibitor 355 administration may be required. Nonetheless, our data indicate that we have developed a potent, 356 non-toxic BSH inhibitor that modulates the in vivo bile acid pool, shifting the bile acid pool away 357 from DCA and LCA. Importantly, we have shown that AAA-10 exhibits in vivo efficacy using a 358 daily dosing strategy in a 5 day experiment, a finding that paves the way for the use of **AAA-10** in 359 longer-term animal models to elucidate how bile acids affect host health and either drive or 360 ameliorate disease phenotypes. Because bile acids are absorbed and recirculated to the liver via the portal vein,^{5,42} BSH inhibitors will facilitate investigations of how bile acids are causally 361 362 involved in the initiation and progression of both liver and GI tract disorders, including 363 inflammatory bowel diseases, non-alcoholic fatty liver disease (NAFLD), non-alcoholic 364 steatohepatitis (NASH), liver cirrhosis, and liver and colon cancer.^{17,19} Demonstration of prevention or amelioration of disease phenotypes in animals would suggest that BSHs could be 365 366 targeted in a therapeutic context to treat human disease.

367

368 METHODS

Full details for all materials and methods are provided in the Supporting Information.

370

371 ASSOCIATED CONTENT

372 Supporting Information

- 373 Materials and methods (including detailed synthetic protocols and characterization data), Figures
- 374 S1-4, Table S1, Scheme S1.

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378 Author Contributions

379 A.A.A. and A.S.D. conceived the project and designed the experiments. A.A.A. performed the

- 380 synthesis and most of the experiments. D. R. and A.S.B. performed the in vivo BSH inhibition and
- bile acid pool modulation study. S.N.C. performed the cell culture assays. C.E.P. performed the
- 382 experiments with Gram-negative bacteria. M.D.M. heterologously expressed and purified B.
- 383 longum recombinant BSH. A.A.A. and A.S.D. wrote the manuscript. All authors edited and
- 384 contributed to the review of the manuscript.

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398

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409 **REFERENCES**

Donia, M. S. & Fischbach, M. A. Small molecules from the human microbiota. *Science* 349, 1254766 (2015).

412 2. Wallace, B. D. *et al.* Alleviating cancer drug toxicity by inhibiting a bacterial enzyme.
413 *Science* 330, 831–835 (2010).

A. B. *et al.* Development of a gut microbe-targeted nonlethal therapeutic to inhibit thrombosis potential. *Nat. Med.* 24, 1407–1417 (2018).

- 4. Maini Rekdal, V., Bess, E. N., Bisanz, J. E., Turnbaugh, P. J. & Balskus, E. P. Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. *Science*418 364, eaau6323 (2019).
- 419 5. Ridlon, J. M., Kang, D.-J. & Hylemon, P. B. Bile salt biotransformations by human intestinal bacteria. *J. Lipid Res.* 47, 241–259 (2006).
- 421 6. Hofmann, A. F. The function of bile salts in fat absorption. The solvent properties of dilute micellar solutions of conjugated bile acids. *Biochem. J.* 89, 57–68 (1963).
- Roda, A., Hofmann, A. F. & Mysels, K. J. The influence of bile salt structure on self-association in aqueous solutions. J. Biol. Chem. 258, 6362–6370 (1983).
- 425 8. Fiorucci, S. & Distrutti, E. Bile Acid-Activated Receptors, Intestinal Microbiota, and the
 426 Treatment of Metabolic Disorders. *Trends Mol Med* 21, 702–714 (2015).
- 427 9. Schaap, F. G., Trauner, M. & Jansen, P. L. M. Bile acid receptors as targets for drug development. *Nat Rev Gastroenterol Hepatol* 11, 55–67 (2014).
- Pols, T. W. H. *et al.* Lithocholic acid controls adaptive immune responses by inhibition of
 Th1 activation through the Vitamin D receptor. *PLOS ONE* 12, e0176715 (2017).
- Hang, S. *et al.* Bile acid metabolites control TH17 and Treg cell differentiation. *Nature*576, 143–148 (2019).
- 433 12. Begley, M., Hill, C. & Gahan, C. G. M. Bile salt hydrolase activity in probiotics. *Appl.*434 *Environ. Microbiol.* 72, 1729–1738 (2006).
- Ridlon, J. M., Wolf, P. G. & Gaskins, H. R. Taurocholic acid metabolism by gut microbes
 and colon cancer. *Gut Microbes* 7, 201–215 (2016).
- 437 14. Ma, C. *et al.* Gut microbiome-mediated bile acid metabolism regulates liver cancer via
 438 NKT cells. *Science* 360, eaan5931 (2018).
- 439 15. Ajouz, H., Mukherji, D. & Shamseddine, A. Secondary bile acids: an underrecognized cause of colon cancer. *World J Surg Oncol* 12, 164–5 (2014).
- Ridlon, J. M., Harris, S. C., Bhowmik, S., Kang, D.-J. & Hylemon, P. B. Consequences of bile salt biotransformations by intestinal bacteria. *Gut Microbes* 7, 22–39 (2016).
- 443 17. Song, Z. *et al.* Taxonomic profiling and populational patterns of bacterial bile salt
 444 hydrolase (BSH) genes based on worldwide human gut microbiome. *Microbiome* 7, 9
 445 (2019).
- Parasar, B. *et al.* Chemoproteomic Profiling of Gut Microbiota-Associated Bile Salt
 Hydrolase Activity. *ACS Cent Sci* 5, 867–873 (2019).
- Jia, B., Park, D., Hahn, Y. & Jeon, C. O. Metagenomic analysis of the human microbiome reveals the association between the abundance of gut bile salt hydrolases and host health. *Gut Microbes* 11, 1300–1313 (2020).
- 451 20. Yao, L. *et al.* A selective gut bacterial bile salt hydrolase alters host metabolism. *eLife* 7,
 452 675 (2018).
- 453 21. Joyce, S. A. *et al.* Regulation of host weight gain and lipid metabolism by bacterial bile
 454 acid modification in the gut. *Proc. Natl. Acad. Sci. U.S.A.* 111, 7421–7426 (2014).
- Li, F. *et al.* Microbiome remodelling leads to inhibition of intestinal farnesoid X receptor signalling and decreased obesity. *Nat Commun* 4, 2384 (2013).
- 457 23. Xie, C. *et al.* An Intestinal Farnesoid X Receptor-Ceramide Signaling Axis Modulates
 458 Hepatic Gluconeogenesis in Mice. *Diabetes* 66, 613–626 (2017).
- 459 24. Adhikari, A. A. *et al.* Development of a covalent inhibitor of gut bacterial bile salt
 460 hydrolases. *Nature Chemical Biology* 16, 318–326 (2020).

| 461 | 25. | Tanaka, H., Hashiba, H., Kok, J. & Mierau, I. Bile salt hydrolase of Bifidobacterium |
|------------|-----|---|
| 462 | | longum-biochemical and genetic characterization. Appl. Environ. Microbiol. 66, 2502- |
| 463 | | 2512 (2000). |
| 464 | 26. | Wang, Z. et al. Identification and Characterization of a Bile Salt Hydrolase from |
| 465 466 | | Lactobacillus salivarius for Development of Novel Alternatives to Antibiotic Growth Promoters. <i>Appl. Environ. Microbiol.</i> 78 , 8795–8802 (2012). |
| | 27. | Strott, C. A. Sulfonation and molecular action. <i>Endocr Rev</i> 23, 703–732 (2002). |
| 467 | | |
| 468 469 | 28. | Alnouti, Y. Bile Acid sulfation: a pathway of bile acid elimination and detoxification. <i>Toxicol. Sci.</i> 108 , 225–246 (2009). |
| 470 | 29. | Palmer, J. T. & Inc, P. Process for forming a fluoromethyl ketone. (1994). |
| 471 | 30. | Zheng, X. et al. Bile acid is a significant host factor shaping the gut microbiome of diet- |
| 472 | | induced obese mice. BMC Biol 15, 120–15 (2017). |
| 473 | 31. | Sayin, S. I. et al. Gut microbiota regulates bile acid metabolism by reducing the levels of |
| 474 | | tauro-beta-muricholic acid, a naturally occurring FXR antagonist. Cell Metab. 17, 225- |
| 475 | | 235 (2013). |
| 476 | 32. | Perez, MJ. & Briz, O. Bile-acid-induced cell injury and protection. World J. |
| 477 | | Gastroenterol. 15, 1677–1689 (2009). |
| 478 | 33. | Glinghammar, B., Inoue, H. & Rafter, J. J. Deoxycholic acid causes DNA damage in |
| 479 | | colonic cells with subsequent induction of caspases, COX-2 promoter activity and the |
| 480 | | transcription factors NF-kB and AP-1. Carcinogenesis 23, 839–845 (2002). |
| 481 | 34. | Ferruzza, S., Rossi, C., Scarino, M. L. & Sambuy, Y. A protocol for differentiation of |
| 482 | | human intestinal Caco-2 cells in asymmetric serum-containing medium. Toxicol In Vitro |
| 483 | | 26, 1252–1255 (2012). |
| 484 | 35. | Chaudhari, S. N. et al. A microbial metabolite remodels the gut-liver axis following |
| 485 | | bariatric surgery. Cell Host & Microbe 317, 571 (2020). |
| 486 | 36. | Wahlström, A., Sayin, S. I., Marschall, HU. & Bäckhed, F. Intestinal Crosstalk between |
| 487 | | Bile Acids and Microbiota and Its Impact on Host Metabolism. Cell Metab. 24, 41-50 |
| 488 | | (2016). |
| 489 | 37. | Ellacott, K. L. J., Morton, G. J., Woods, S. C., Tso, P. & Schwartz, M. W. Assessment of |
| 490 | | feeding behavior in laboratory mice. Cell Metab. 12, 10–17 (2010). |
| 491 | 38. | Reddy, B. S., Narasawa, T., Weisburger, J. H. & Wynder, E. L. Promoting effect of |
| 492 | | sodium deoxycholate on colon adenocarcinomas in germfree rats. J. Natl. Cancer Inst. 56, |
| 493 | | 441–442 (1976). |
| 494 | 39. | Narisawa, T., Magadia, N. E., Weisburger, J. H. & Wynder, E. L. Promoting effect of bile |
| 495 | | acids on colon carcinogenesis after intrarectal instillation of N-methyl-N'-nitro-N- |
| 496 | | nitrosoguanidine in rats. J. Natl. Cancer Inst. 53, 1093–1097 (1974). |
| 497 | 40. | Yoshimoto, S. et al. Obesity-induced gut microbial metabolite promotes liver cancer |
| 498 | | through senescence secretome. Nature 499, 97–101 (2013). |
| 499 | 41. | Buffie, C. G. et al. Precision microbiome reconstitution restores bile acid mediated |
| 500 | | resistance to Clostridium difficile. <i>Nature</i> 517 , 205–208 (2015). |
| 501 | 42. | van de Peppel, I. P., Verkade, H. J. & Jonker, J. W. Metabolic consequences of ileal |
| 502 | | interruption of the enterohepatic circulation of bile acids. Am. J. Physiol. Gastrointest. |
| 503 | | Liver Physiol. 319 , G619–G625 (2020). |
| 504 | | |

- Donia, M. S. & Fischbach, M. A. Small molecules from the human microbiota. *Science* 349, 1254766 (2015).
- Wallace, B. D. *et al.* Alleviating cancer drug toxicity by inhibiting a bacterial enzyme.
 Science 330, 831–835 (2010).
- 510 3. Roberts, A. B. *et al.* Development of a gut microbe-targeted nonlethal therapeutic to inhibit thrombosis potential. *Nat. Med.* **24**, 1407–1417 (2018).
- Maini Rekdal, V., Bess, E. N., Bisanz, J. E., Turnbaugh, P. J. & Balskus, E. P. Discovery
 and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. *Science*364, eaau6323 (2019).
- 5. Ridlon, J. M., Kang, D.-J. & Hylemon, P. B. Bile salt biotransformations by human
 intestinal bacteria. J. Lipid Res. 47, 241–259 (2006).
- 517 6. Hofmann, A. F. The function of bile salts in fat absorption. The solvent properties of
 518 dilute micellar solutions of conjugated bile acids. *Biochem. J.* 89, 57–68 (1963).
- 7. Roda, A., Hofmann, A. F. & Mysels, K. J. The influence of bile salt structure on self-association in aqueous solutions. *J. Biol. Chem.* 258, 6362–6370 (1983).
- Fiorucci, S. & Distrutti, E. Bile Acid-Activated Receptors, Intestinal Microbiota, and the
 Treatment of Metabolic Disorders. *Trends Mol Med* 21, 702–714 (2015).
- 523 9. Schaap, F. G., Trauner, M. & Jansen, P. L. M. Bile acid receptors as targets for drug development. *Nat Rev Gastroenterol Hepatol* 11, 55–67 (2014).
- Pols, T. W. H. *et al.* Lithocholic acid controls adaptive immune responses by inhibition of
 Th1 activation through the Vitamin D receptor. *PLOS ONE* 12, e0176715 (2017).
- 527 11. Hang, S. *et al.* Bile acid metabolites control TH17 and Treg cell differentiation. *Nature*528 576, 143–148 (2019).
- Begley, M., Hill, C. & Gahan, C. G. M. Bile salt hydrolase activity in probiotics. *Appl. Environ. Microbiol.* 72, 1729–1738 (2006).
- 13. Ridlon, J. M., Wolf, P. G. & Gaskins, H. R. Taurocholic acid metabolism by gut microbes and colon cancer. *Gut Microbes* 7, 201–215 (2016).
- 533 14. Ma, C. *et al.* Gut microbiome-mediated bile acid metabolism regulates liver cancer via
 534 NKT cells. *Science* 360, eaan5931 (2018).
- Ajouz, H., Mukherji, D. & Shamseddine, A. Secondary bile acids: an underrecognized cause of colon cancer. *World J Surg Oncol* 12, 164–5 (2014).
- Ridlon, J. M., Harris, S. C., Bhowmik, S., Kang, D.-J. & Hylemon, P. B. Consequences of
 bile salt biotransformations by intestinal bacteria. *Gut Microbes* 7, 22–39 (2016).
- 539 17. Song, Z. *et al.* Taxonomic profiling and populational patterns of bacterial bile salt
 540 hydrolase (BSH) genes based on worldwide human gut microbiome. *Microbiome* 7, 9
 541 (2019).
- 18. Parasar, B. *et al.* Chemoproteomic Profiling of Gut Microbiota-Associated Bile Salt
 Hydrolase Activity. *ACS Cent Sci* 5, 867–873 (2019).
- Jia, B., Park, D., Hahn, Y. & Jeon, C. O. Metagenomic analysis of the human microbiome reveals the association between the abundance of gut bile salt hydrolases and host health. *Gut Microbes* 11, 1300–1313 (2020).
- 547 20. Yao, L. *et al.* A selective gut bacterial bile salt hydrolase alters host metabolism. *eLife* 7, 675 (2018).
- Joyce, S. A. *et al.* Regulation of host weight gain and lipid metabolism by bacterial bile
 acid modification in the gut. *Proc. Natl. Acad. Sci. U.S.A.* 111, 7421–7426 (2014).

| 551 | 22. | Li, F. et al. Microbiome remodelling leads to inhibition of intestinal farnesoid X receptor |
|-----|-----|--|
| 552 | | signalling and decreased obesity. Nat Commun 4, 2384 (2013). |
| 553 | 23. | Xie, C. et al. An Intestinal Farnesoid X Receptor-Ceramide Signaling Axis Modulates |
| 554 | | Hepatic Gluconeogenesis in Mice. Diabetes 66, 613–626 (2017). |
| 555 | 24. | Adhikari, A. A. et al. Development of a covalent inhibitor of gut bacterial bile salt |
| 556 | | hydrolases. Nature Chemical Biology 16, 318–326 (2020). |
| 557 | 25. | Tanaka, H., Hashiba, H., Kok, J. & Mierau, I. Bile salt hydrolase of Bifidobacterium |
| 558 | | longum-biochemical and genetic characterization. Appl. Environ. Microbiol. 66, 2502- |
| 559 | | 2512 (2000). |
| 560 | 26. | Wang, Z. et al. Identification and Characterization of a Bile Salt Hydrolase from |
| 561 | | Lactobacillus salivarius for Development of Novel Alternatives to Antibiotic Growth |
| 562 | | Promoters. Appl. Environ. Microbiol. 78, 8795–8802 (2012). |
| 563 | 27. | Strott, C. A. Sulfonation and molecular action. <i>Endocr Rev</i> 23, 703–732 (2002). |
| 564 | 28. | Alnouti, Y. Bile Acid sulfation: a pathway of bile acid elimination and detoxification. |
| 565 | | <i>Toxicol. Sci.</i> 108 , 225–246 (2009). |
| 566 | 29. | Palmer, J. T. & Inc, P. Process for forming a fluoromethyl ketone. (1994). |
| 567 | 30. | Zheng, X. <i>et al.</i> Bile acid is a significant host factor shaping the gut microbiome of diet- |
| 568 | 200 | induced obese mice. <i>BMC Biol</i> 15 , 120–15 (2017). |
| 569 | 31. | Sayin, S. I. <i>et al.</i> Gut microbiota regulates bile acid metabolism by reducing the levels of |
| 570 | | tauro-beta-muricholic acid, a naturally occurring FXR antagonist. Cell Metab. 17, 225- |
| 571 | | 235 (2013). |
| 572 | 32. | Perez, MJ. & Briz, O. Bile-acid-induced cell injury and protection. <i>World J</i> . |
| 573 | | <i>Gastroenterol.</i> 15 , 1677–1689 (2009). |
| 574 | 33. | Glinghammar, B., Inoue, H. & Rafter, J. J. Deoxycholic acid causes DNA damage in |
| 575 | | colonic cells with subsequent induction of caspases, COX-2 promoter activity and the |
| 576 | | transcription factors NF-kB and AP-1. Carcinogenesis 23, 839–845 (2002). |
| 577 | 34. | Ferruzza, S., Rossi, C., Scarino, M. L. & Sambuy, Y. A protocol for differentiation of |
| 578 | | human intestinal Caco-2 cells in asymmetric serum-containing medium. Toxicol In Vitro |
| 579 | | 26, 1252–1255 (2012). |
| 580 | 35. | Chaudhari, S. N. et al. A microbial metabolite remodels the gut-liver axis following |
| 581 | | bariatric surgery. Cell Host & Microbe 317, 571 (2020). |
| 582 | 36. | Wahlström, A., Sayin, S. I., Marschall, HU. & Bäckhed, F. Intestinal Crosstalk between |
| 583 | | Bile Acids and Microbiota and Its Impact on Host Metabolism. Cell Metab. 24, 41-50 |
| 584 | | (2016). |
| 585 | 37. | Ellacott, K. L. J., Morton, G. J., Woods, S. C., Tso, P. & Schwartz, M. W. Assessment of |
| 586 | | feeding behavior in laboratory mice. Cell Metab. 12, 10–17 (2010). |
| 587 | 38. | Reddy, B. S., Narasawa, T., Weisburger, J. H. & Wynder, E. L. Promoting effect of |
| 588 | | sodium deoxycholate on colon adenocarcinomas in germfree rats. J. Natl. Cancer Inst. 56, |
| 589 | | 441–442 (1976). |
| 590 | 39. | Narisawa, T., Magadia, N. E., Weisburger, J. H. & Wynder, E. L. Promoting effect of bile |
| 591 | | acids on colon carcinogenesis after intrarectal instillation of N-methyl-N'-nitro-N- |
| 592 | | nitrosoguanidine in rats. J. Natl. Cancer Inst. 53, 1093–1097 (1974). |
| 593 | 40. | Yoshimoto, S. et al. Obesity-induced gut microbial metabolite promotes liver cancer |
| 594 | | through senescence secretome. <i>Nature</i> 499 , 97–101 (2013). |
| 595 | 41. | Buffie, C. G. et al. Precision microbiome reconstitution restores bile acid mediated |
| 596 | | resistance to Clostridium difficile. Nature 517, 205–208 (2015). |
| | | |

- 597 42. van de Peppel, I. P., Verkade, H. J. & Jonker, J. W. Metabolic consequences of ileal
- interruption of the enterohepatic circulation of bile acids. Am. J. Physiol. Gastrointest.
 Liver Physiol. 319, G619–G625 (2020).

600