

1 Supplemental Table 1 PCR and quantitative PCR primers used in this study

Primer	Forward primer (5'-3')	Reverse primer (5'-3')	Reference
PCR			
411-BSH	CATGCCATGGGAATGTGTACTGGTTAAGATTC	CGGCTCGAGCTAGTAAGTCACAAGACTGGTTG	This study
338F/806R	ACTCCTACGGGA-GGCAGCAG	GGACTACHVGGGTWTCTAAT	
qPCR			
CYP7A1	ACAGAAGCATAGACCCAA	TGCCAAACAGCGTTAGAT	13
CYP8B1	AAGGCTGGCTTCTGAGCTT	AACAGCTCATCGGCCTCATC	
CYP27A1	TGCCTGGGTCGGAGGAT	GAGCCAGGGCAATCTCATACTT	18
CYP7B1	TAGCCCTCTTCTCCACTCATA	GAACCGATCGAACCTAAATTCCT	
FXR	ACATCCCCATCTCTCTGCAC	TGTGAGGGCTGCAAAGGTTT	
SHP	CCTGGAGTCTTCTGGAGCCTTGA	TGTTGCAGGTGTGCGATGTGG	
FGFR4	GCATCTTTCAGGGGACACCA	TTGTACCAGTGACGACCACG	19
KLB	TCAGGCCTGCATAGGAAATG	CTGGATCGGGAGACTTAGGA	20
LRH-1	TTGAGTGGGCCAGGAGTAGT	ACGCGACTTCTGTGTGTGAG	
FGF15	ACGTCCTTGATGGCAATCG	GAGGACCAAACGAACGAAATT	
IBABP	CAGGAGACGTGATTGAAAGGG	GCCCCAGAGTAAGACTGGG	
ABCG5	GCAGGGACCGAATTGTGATTG	AGGGATTGGAATGTTTCAGGACAG	
ABCG8	GGCTCAGGATCGGCTTTCAC	CCTTGACACAGGCATGAAGCA	21
HMGCR	GGACCAACCTTCTACCTC	CCATCACAGTGCCACATAC	
LDL-R	CAGTCCCAGGCAGCGTAT	TTGATCTTGGCGGGTGT	
rpL32	TCTGGTCCACAACGTCAAGG	GGATTGGTGACTCTGATGGC	

3 Supplemental Table 2 Primer sequence for *bsh* qPCR

Group Expected ²³	Primer sequence (5'-3')	F/R	Reference <i>bsh</i> (Accession number)*	Product size (bp)
2	TGTGTGAGCAACGAGATGGC	F	AAR39435, BAF39637, AAF67801, AAN24611, CDB23390, BAQ98062, BAP83517, AAX86039	105
	ACACGAACGAAACGCGACGG	R		
3A	AYTTTGGHMGWAAYYTHGAY	F	AAR39435, BAF39637, AAF67801, AAN24611, CDB23390, BAQ98062, BAP83517, AAX86039	105
	RTTNARDCCDGCHATVCCWAVHCC	R		
3D	GAGGATGGACTAGGAATGGC	F	ABE00605, CDK34338	104
	TGGAATAAACTCGAACGGCG	R		

4 *Accession number of the reference *bsh* is from EMBL database (<http://www.ebi.ac.uk/>)

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7 **Supplemental Figure legend:**

8 **Figure S1:** Physiological and biochemical indexes (serum lipid: **A**; and liver lipid: **B**) were used to
9 evaluate the fat-reducing function of BSH strain in these five groups (ND: normal diet; HFD: high-fat
10 diet; HFD+NB5462: high-fat diet + empty plasmid control NB5462; HFD+YB334-H: high-fat diet +
11 recombinant YB334 with high BSH activity; and HFD+YB334-L: high-fat diet + recombinant YB334
12 with low BSH activity). TC: total cholesterol; TG: triacylglycerols; LDL-C: low-density lipoprotein
13 cholesterol; and HDL-C: high-density lipoprotein cholesterol. Values were expressed as mean \pm SD (n
14 = 8). * Represents a significant ($p < 0.01$) difference from HFD+NB5462 group. ** Represents a
15 significant ($p < 0.0001$) difference from HFD+NB5462 group. # $p < 0.01$, ## $p < 0.0001$.

16
17 **Figure S2:** Fecal bile acid levels were used to evaluate the pathway of BSH involved in bile acid
18 metabolism in these five groups (ND: normal diet; HFD: high-fat diet; HFD+NB5462: high-fat diet +
19 empty plasmid control NB5462; HFD+YB334-H: high-fat diet + recombinant YB334 with high BSH
20 activity; and HFD+YB334-L: high-fat diet + recombinant YB334 with low BSH activity). UDCA:
21 ursodeoxycholic acid; α - β - ω -MCA: α - β - ω -muricholic acid; CA: cholic acid; CDCA:
22 chenodeoxycholic acid; DCA: deoxycholic acid; LCA: lithocolic acid; TUDCA: tauroursodeoxycholic
23 acid; T α (β / ω)MCA: tauro- α (β / ω)-muricholic acid; TCA: taurocholic acid; TCDCA:
24 taurochenodeoxycholic acid; TDCA: taurodeoxycholic acid; TLCA: tauroolithocolic acid. Values were
25 expressed as mean \pm SD (n = 8). * ($p < 0.01$) and ** ($p < 0.0001$) represent a significant difference
26 from HFD+NB5462 group, respectively.

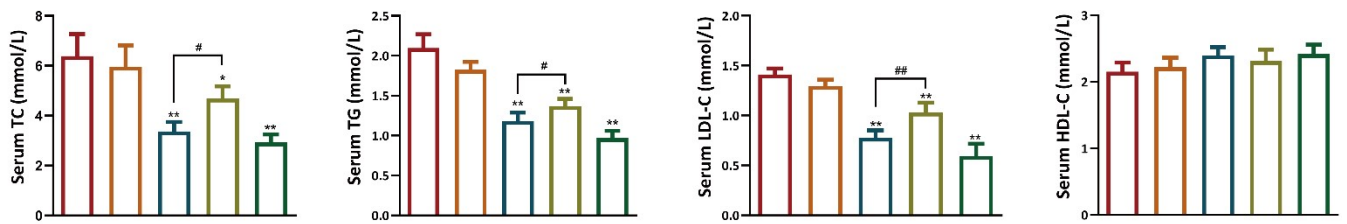
27
28 **Figure S3:** Alpha diversity (**A**), Bacteria composition (phylum level, **B**), and Heatmap clustering
29 analysis of biodiversity (**C**) of mouse gut microbiota in these four groups (HFD+NB5462: high-fat diet
30 + empty plasmid control NB5462; HFD: high-fat diet; HFD+YB334-H: high-fat diet + recombinant
31 YB334 with high BSH activity; ND: normal diet).

32
33 **Figure S4:** Cecum short-chain fatty acids (SCFAs) were detected to verify the relationship between
34 intestinal flora and fat metabolism. HFD+NB5462: high-fat diet + empty plasmid control NB5462;
35 HFD: high-fat diet; HFD+YB334-H: high-fat diet + recombinant YB334 with high BSH activity; ND:
36 normal diet. Values were expressed as mean \pm SD (n = 8). ** Represents a significant ($p < 0.0001$)
37 difference from HFD+NB5462 group.

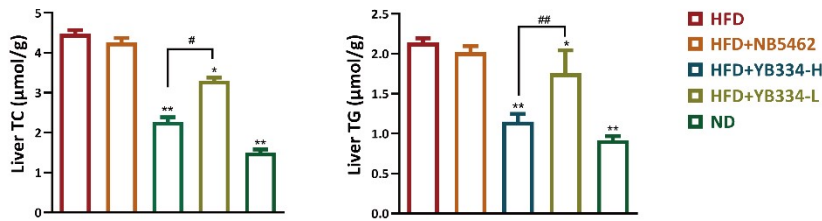
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A. Serum lipid



B. Liver lipid

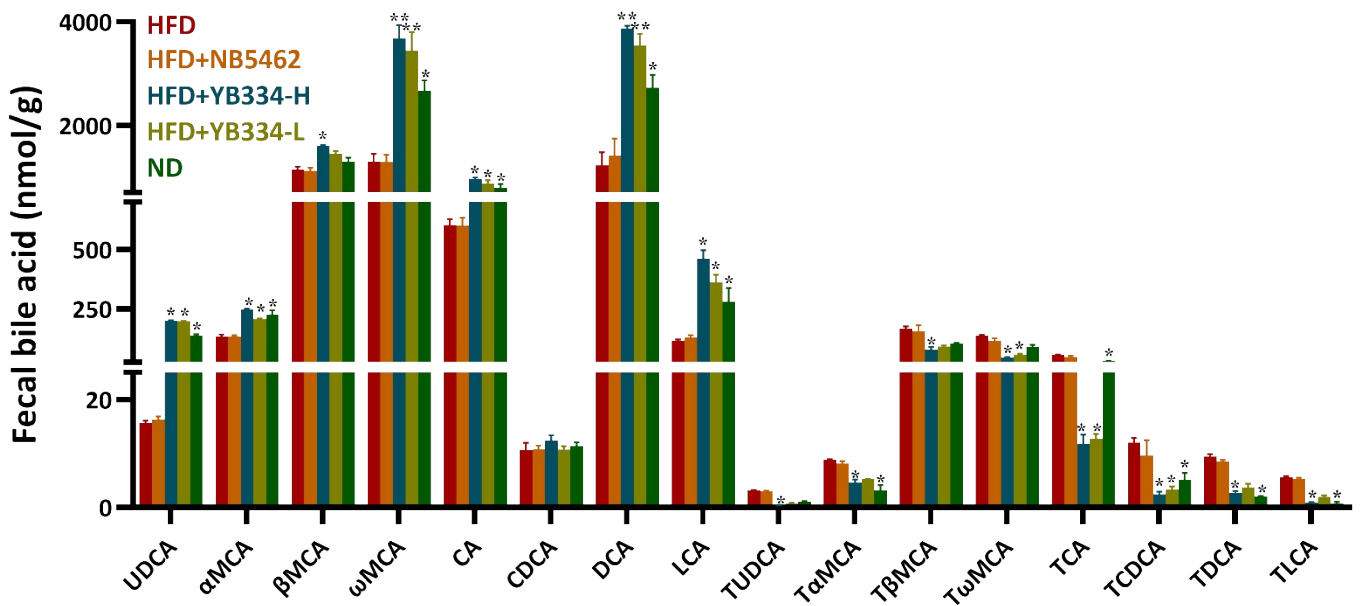


40

41 **Fig. S1:** Physiological and biochemical indexes (serum lipid: **A**; and liver lipid: **B**) were used to evaluate
 42 the fat-reducing function of BSH strain in these five groups (ND: normal diet; HFD: high-fat diet;
 43 HFD+NB5462: high-fat diet + empty plasmid control NB5462; HFD+YB334-H: high-fat diet +
 44 recombinant YB334 with high BSH activity; and HFD+YB334-L: high-fat diet + recombinant YB334 with
 45 low BSH activity). TC: total cholesterol; TG: triacylglycerols; LDL-C: low-density lipoprotein cholesterol;
 46 and HDL-C: high-density lipoprotein cholesterol. Values were expressed as mean \pm SD (n = 8). *
 47 Represents a significant ($p < 0.01$) difference from HFD+NB5462 group. ** Represents a significant (p
 48 < 0.0001) difference from HFD+NB5462 group. # $p < 0.01$, ## $p < 0.0001$.

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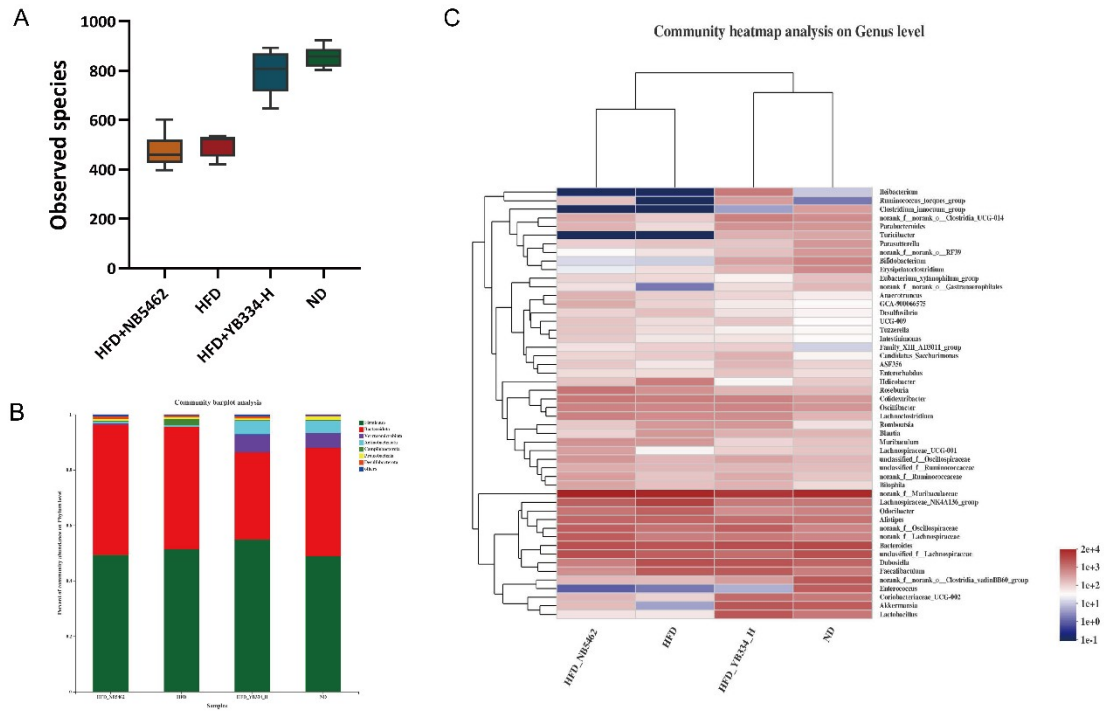


51

52 **Fig. S2:** Fecal bile acid levels were used to evaluate the pathway of BSH involved in bile acid metabolism
 53 in these five groups (ND: normal diet; HFD: high-fat diet; HFD+NB5462: high-fat diet + empty plasmid
 54 control NB5462; HFD+YB334-H: high-fat diet + recombinant YB334 with high BSH activity; and
 55 HFD+YB334-L: high-fat diet + recombinant YB334 with low BSH activity). UDCA: ursodeoxycholic acid;
 56 α -/ β -/ ω -MCA: α -/ β -/ ω -muricholic acid; CA: cholic acid; CDCA: chenodeoxycholic acid; DCA:
 57 deoxycholic acid; LCA: lithocolic acid; TUDCA: tauroursodeoxycholic acid; T α (β / ω)MCA: tauro- α (β / ω)-
 58 muricholic acid; TCA: taurocholic acid; TCDC: taurochenodeoxycholic acid; TDCA: taurodeoxycholic
 59 acid; TLCA: tauroolithocolic acid. Values were expressed as mean \pm SD (n = 8). * ($p < 0.01$) and ** ($p <$
 60 0.0001) represent a significant difference from HFD+NB5462 group, respectively.

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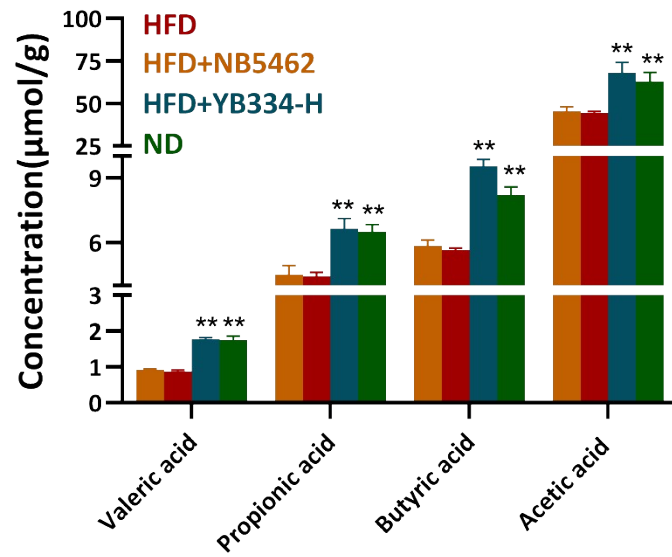


63

64 **Fig. S3:** Alpha diversity (A), Bacteria composition (phylum level, B), and Heatmap clustering analysis of
 65 biodiversity (C) of mouse gut microbiota in these four groups (HFD+NB5462: high-fat diet + empty
 66 plasmid control NB5462; HFD: high-fat diet; HFD+YB334-H: high-fat diet + recombinant YB334 with
 67 high BSH activity; ND: normal diet).

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71 **Fig. S4:** Cecum short-chain fatty acids (SCFAs) were detected to verify the relationship between
 72 intestinal flora and fat metabolism. HFD+NB5462: high-fat diet + empty plasmid control NB5462; HFD:
 73 high-fat diet; HFD+YB334-H: high-fat diet + recombinant YB334 with high BSH activity; ND: normal diet.
 74 Values were expressed as mean \pm SD (n = 8). ** Represents a significant ($p < 0.0001$) difference from
 75 HFD+NB5462 group.

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