

Table S1. The ingredient composition of diets for the CON, HP, HF and HPHF groups.

Item	CON		HP		HF		HPHF	
	gm%	kcal%	gm%	kcal%	gm%	kcal%	gm%	kcal%
Protein	20	20	40	40	18	20	35	40
Carbohydrate	64	64	44	44	56	64	39	44
Fat	7	16	7	16	6	16	6	16
Total		100		100		100		100
kcal/gm	4.01		4.01		3.52		3.52	
Ingredient	gm	kcal	gm	kcal	gm	kcal	gm	kcal
Casein	122	488	246	984	121	484	245	980
L-Cystine	3	12	3	12	3	12	3	12
Soy isolate	80	320	160	640	80	320	160	640
Corn starch	412.5	1650	208.5	834	407.7	1630.8	203.7	814.8
Maltodextrin 10	132	528	132	528	132	528	132	528
Sucrose	100	400	100	400	100	400	100	400
Cellulose	50	0	50	0	50	0	50	0
Konjac powder	0	0	0	0	150	22.8	150	22.8
Soybean oil	73	657	73	657	73	657	73	657
Vitamin mix V10037	10	40	10	40	10	40	10	40
Mineral mix S10022G	35	0	35	0	35	0	35	0
Choline Bitartrate	2.5	0	2.5	0	2.5	0	2.5	0

Table S2. Paired primers for qPCR.

Gene	Primer sequence (5'-3')	
	Forward	Reverse
<i>Fasn</i>	CTGACTCGGCTACTGACACG	GGTGGTGGGAACCCTCAATGG
<i>Srebf1</i>	TTACCCCTCCACCCTCAGAC	CTGGGCTTTGACCTGGCTAT
<i>Ppar-γ</i>	GCTCCAAGAATACCAAAGTGCG	TTTATCCCCACAGACTCGGC
<i>Fxr (Nr1h4)</i>	AGATGGGGATGTTGGCTGAA	GCCGTGAGTTCCGTTTTCTC
<i>Shp (Nr0b2)</i>	GATGACTCCCCAAACCTCCAG	GGTCCTTCCACAAGCAACTAC
<i>Foxo1</i>	TCAACCTTCTCTCGTCCCA	TAGACTGGTGTGTTGGCGGTG
<i>Cox2</i>	CTCAACTTTACTGGGGTTTTTCC	GAGGTGGATTTTGGGATGGT
<i>Tnf-α</i>	CGTCGTAGCAAACCACCAAG	GAGAACCTGGGAGTAGACAAGG
<i>Tlr4</i>	CTCCAGTCGGTCAGCAAACG	AGAGGAAGTGAGAGTGCCAAC
<i>Gapdh</i>	TGTGTCCGTCGTGGATCTGA	TTGCTGTTGAAGTCGCAGGAG

FASN, fatty acid synthase; Srebf1, sterol regulatory element binding transcription factor 1; PPAR-γ, peroxisome proliferator activated receptor gamma; FXR, farnesoid X receptor; SHP, nuclear receptor subfamily 0, group B, member 2; FOXO1, forkhead box O1; COX2, cyclooxygenase-2; TNF-α, tumor necrosis factor-alpha; TLR4, toll-like receptor 4; GAPDH, glyceraldehyde 3-phosphate dehydrogenase.

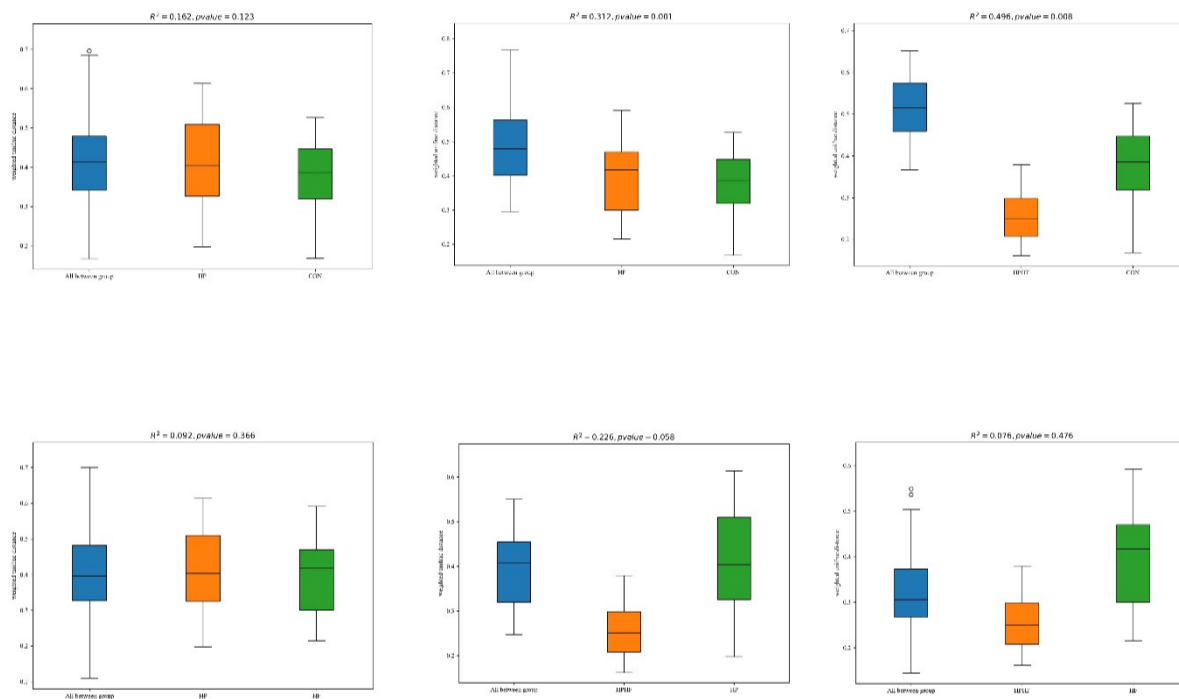


Figure S1. Beta diversity of colonic microbiota in mice. Weighted unifracc distance metrics based on PERMANOVA was used for analysing beta diversity of gut microbial communities in different groups. CON, control diet; HP, high protein diets; HF, high fiber diets; HPHF, high protein and high fiber diets. Data are presented as mean \pm SEM.

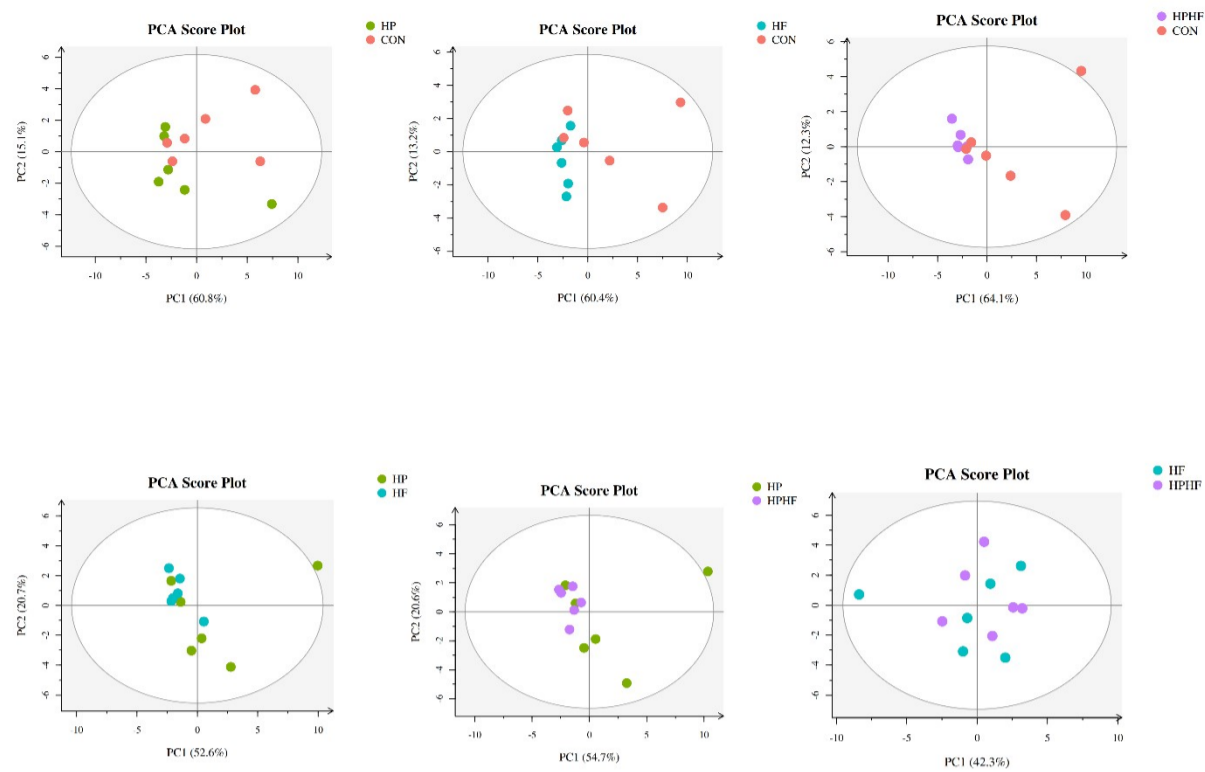


Figure S2. Principal component analysis (PCA) showed the clustering of colonic bile acids of mice. CON, control diet; HP, high protein diets; HF, high fiber diets; HPHF, high protein and high fiber diets.

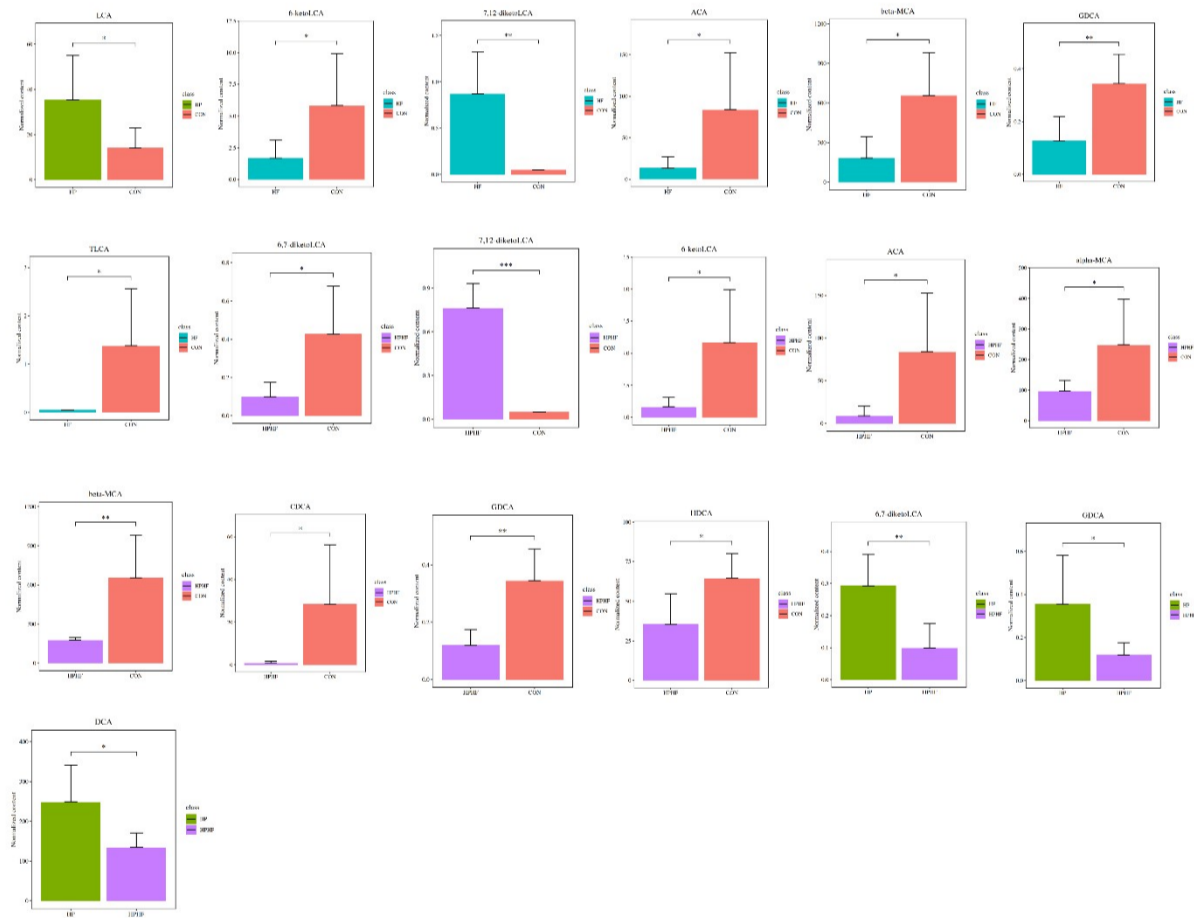


Figure S3. Significant changes in colonic bile acids between two dietary groups of mice. CON, control diet; HP, high protein diets; HF, high fiber diets; HPHF, high protein and high fiber diets. Data are presented as mean \pm SEM. Significant changes were marked by * $P < 0.05$, and ** $P < 0.01$.