

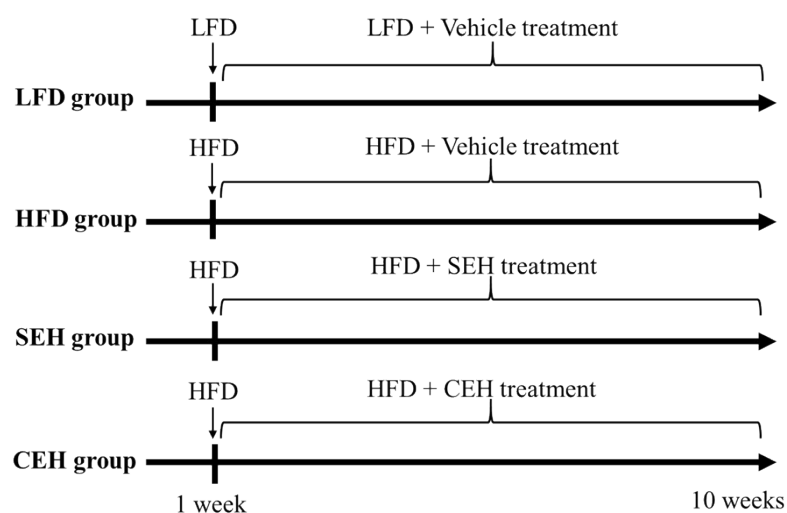


Fig. S1 Schematic of the animal experimental procedures.

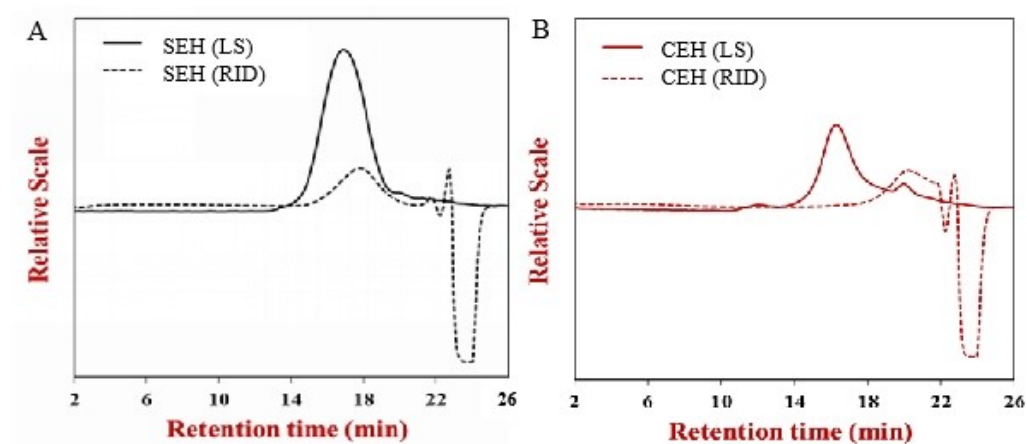


Fig. S2 Molecular weight of *Porphyra* enzymatic hydrolysates. (A) The HPSEC-MALLS-RI chromatograms of SEH. (B) The HPSEC-MALLS-RI chromatograms of CEH.

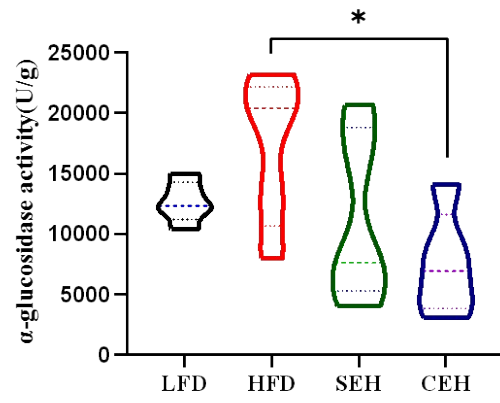


Fig. S3 CEH inhibited α -glucosidase activity in the small intestine of HFD-fed mice (n=8).

Table S1 PCR amplification primer sequences.

Gene	Forward (5'-3')	Reverse (5'-3')
G6Pase	TGGTTGGGATTCTGGATCGT	TGTAGATGCTCTGGATGTGG
	C	C
PEPCK	GGTTAGTTATGCCCAGGATC	GAACTCACTGCTTGGGAAGA
	AGC	AATG
GLUT4	AGCCAGCCTACGCCACCATA	AGCCAGCCTACGCCACCATA

Table S2 Effect of SEH and CEH on obesity-related indexes (n=8).

Group	Initial body weight (g)	Final body weight (g)	Food intake (g/day)	Food efficiency (%)
LFD	19.96 ± 0.30	27.60 ± 0.58***	3.08 ± 0.09	2.48 ± 0.20*
HFD	19.96 ± 0.31	32.54 ± 0.90	4.04 ± 0.15	3.12 ± 0.22
SEH	19.88 ± 0.23	31.57 ± 1.16	4.31 ± 0.17	2.71 ± 0.25
CEH	20.02 ± 0.16	29.86 ± 0.68*	5.29 ± 0.16	1.86 ± 0.15***

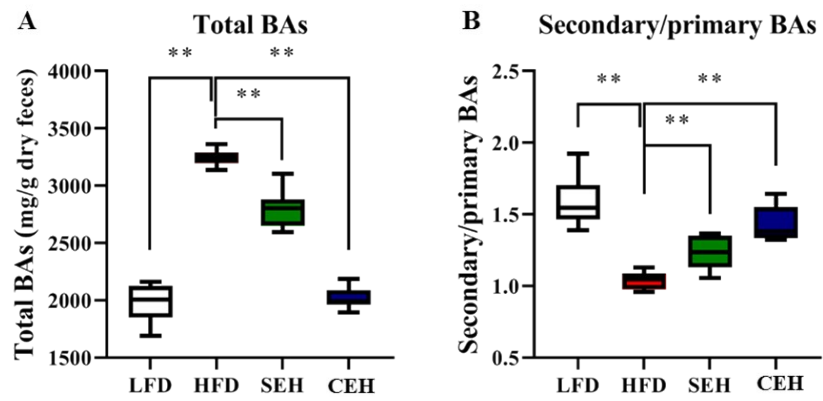


Fig. S4 CEH regulated BAs contents in HFD-fed mice (n=8). (A) Relative amount of total fecal bile acids. (B) The ratio of secondary to primary bile acid.

Table S3 Significantly different genera between HFD and SEH groups identified by ANCOM (n=8).

Taxa	P-values	Adjusted p-values	Relative abundance (%)	
			HFD	SEH
<i>Kocuria</i>	0.00	0.00	0.0013 ± 0.0009	0.0009±0.0000
<i>Collinsella</i>	0.00	0.00	0.0006 ± 0.0004	0.0004±0.0007
<i>vadinBB60</i>	0.00	0.00	0.0116 ± 0.0065	0.0044±0.0036
<i>Anaerostipes</i>	0.00	0.00	0.0008 ± 0.0004	0.0004±0.0004
<i>Frisingicoccus</i>	0.00	0.00	0.0016 ± 0.0011	0.0011±0.0014
<i>Fusicatenibacter</i>	0.00	0.00	0.0006 ± 0.0013	0.0004±0.0008
<i>Sellimonas</i>	0.00	0.00	0.0010 ± 0.0005	0.0000±0.0000
<i>Harryflintia</i>	0.00	0.00	0.0010 ± 0.0002	0.0006±0.0002
Unidentified	0.00	0.00	0.0017 ± 0.0012	0.0000±0.0000
Ruminococcaceae				
<i>Dialister</i>	0.00	0.00	0.0010 ± 0.0010	0.0005±0.0008
<i>Bosea</i>	0.00	0.00	0.0018 ± 0.0008	0.0002±0.0002
<i>Proteus</i>	0.00	0.00	0.0010 ± 0.0015	0.0008±0.0007
<i>Halomonas</i>	0.00	0.00	0.0004 ± 0.0012	0.0003±0.0005
Unclassified	0.00	0.00	0.0056 ± 0.0046	0.0031±0.0006
Erysipelotrichaceae				
Unclassified	0.00	0.00	0.0070 ± 0.0023	0.0055±0.0021
Ruminococcaceae				

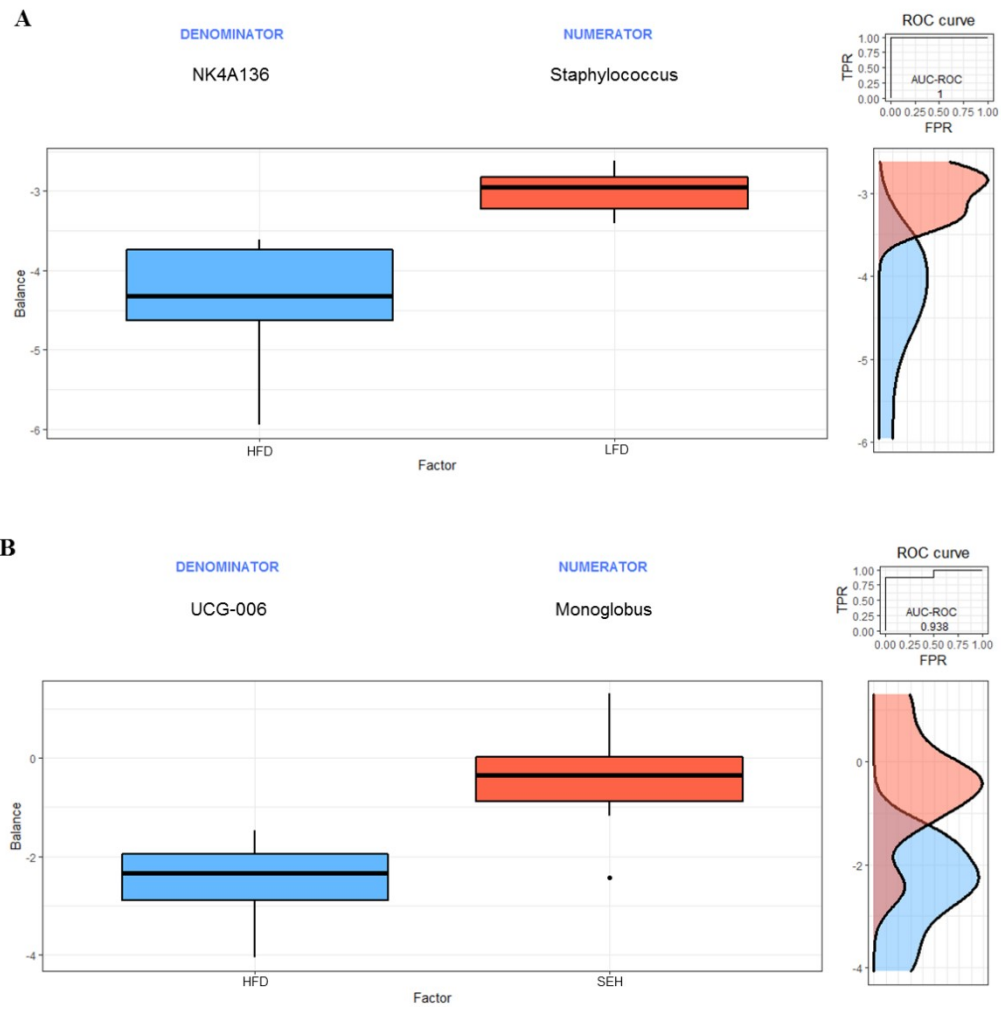


Fig. S5 The boxplot shows the distribution of the balance scores for (A) LFD and HFD groups and (B) HFD and SEH groups.

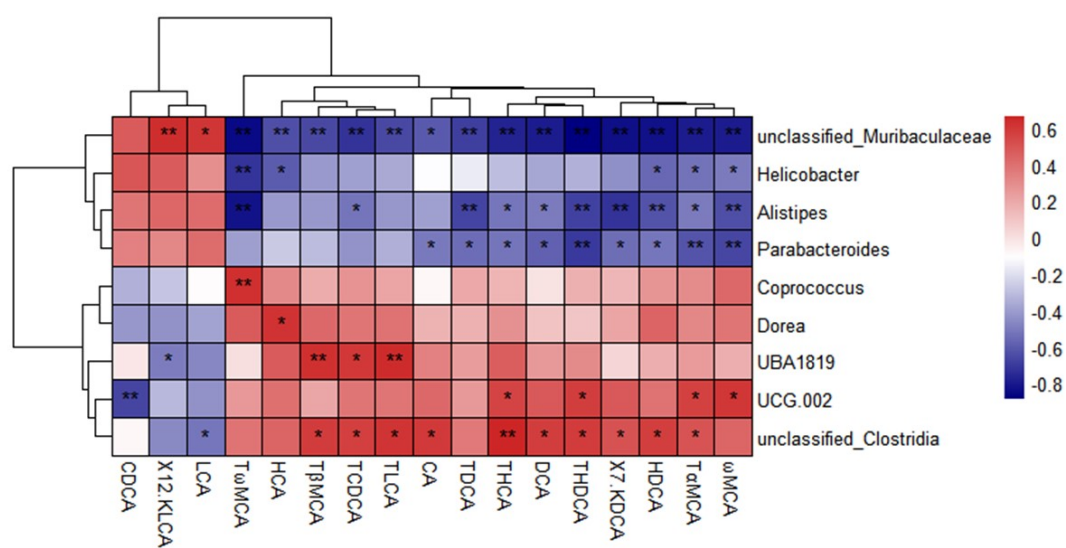


Fig. S6 Spearman correlation between fecal bile acids and differentially abundant bacteria. Correlation coefficient scale is represented on the right with the red square showing positive correlation and blue square negative correlation. Significance was accepted at * $P < 0.05$, ** $P < 0.01$.

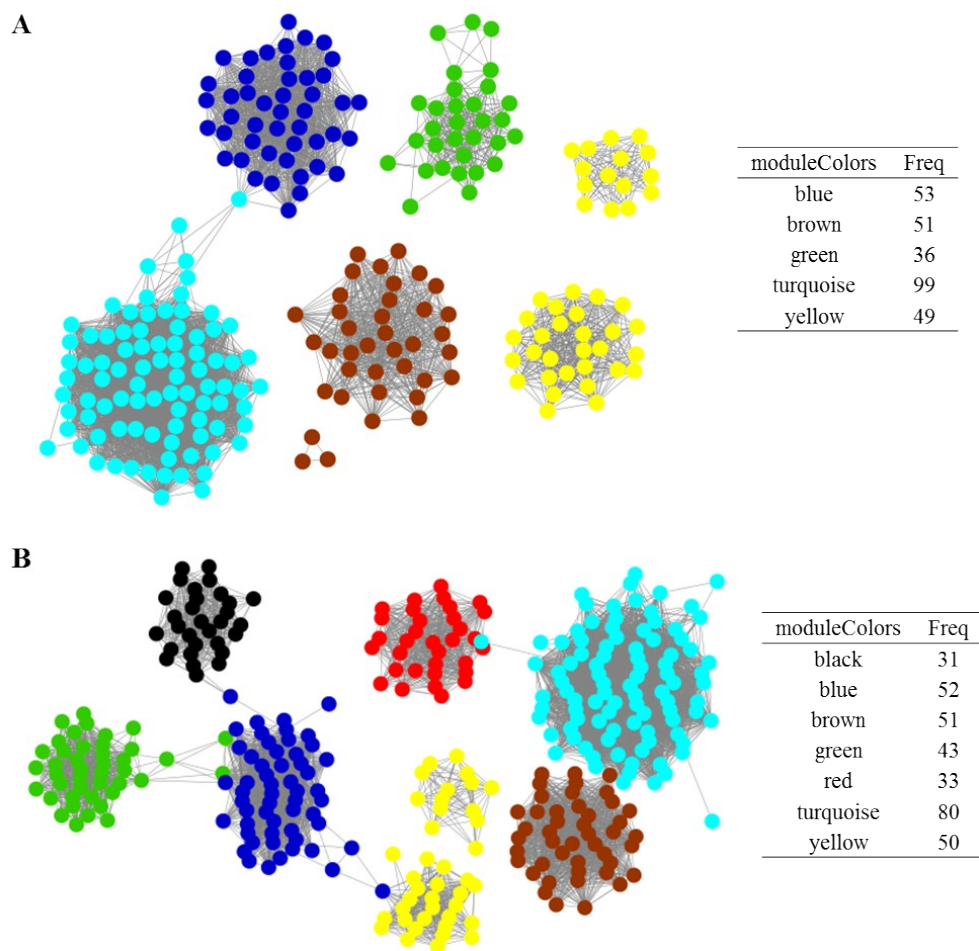


Fig. S7 Microbial co-occurrence network of (A) HFD group and (B) CEH group showing the associations between modules. The numbers of nodes in constructed modules were shown in tables on the right.

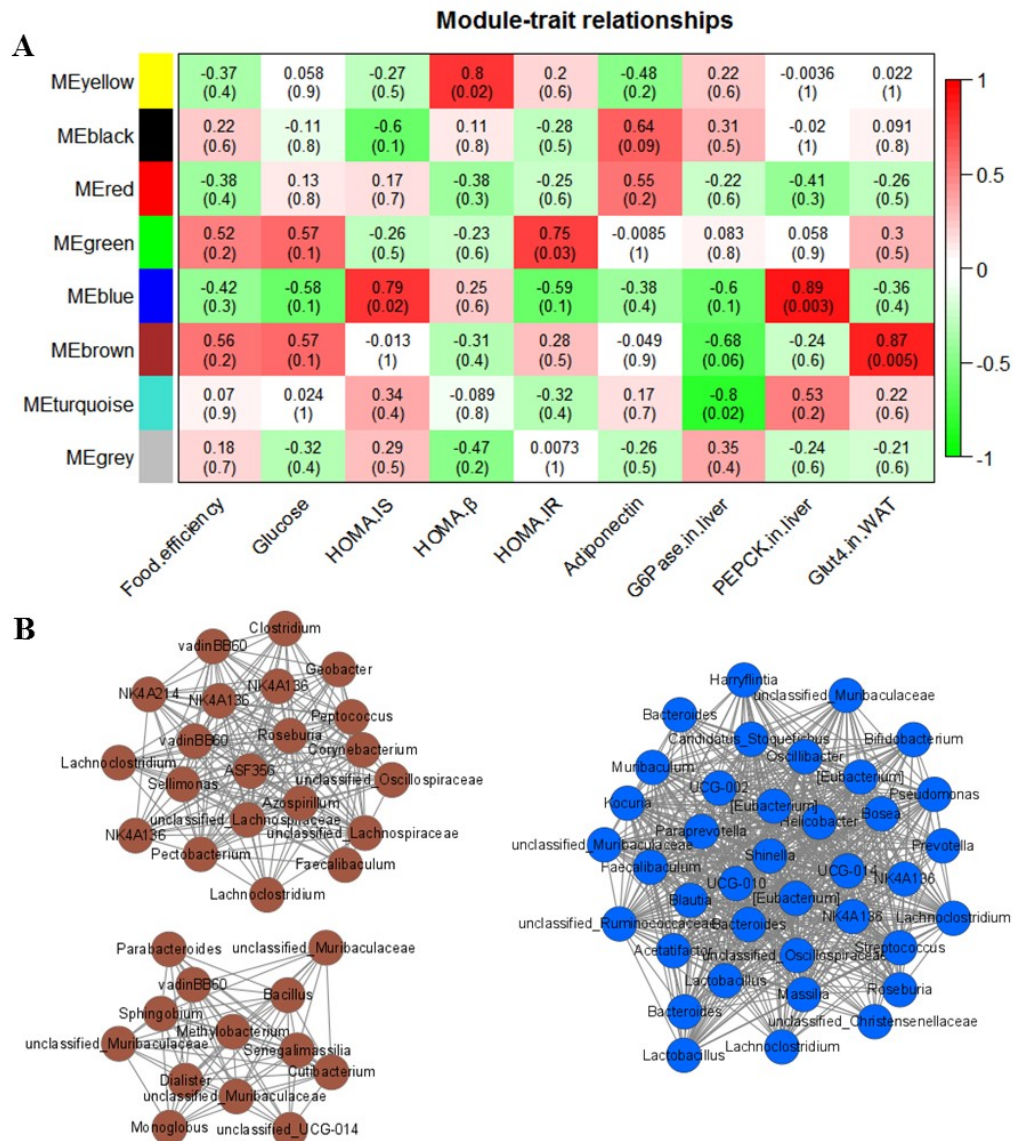


Fig. S8 Correlations between glucose metabolism indexes and modules in microbial network. (A) The heatmap illustrating module-trait relationships of CEH group. Each row represents different modules, and each column represents indicators related to glucose homeostasis. Each cell contains the corresponding correlation coefficients and p-value. (B) Co-association among the microbes in specific modules (MEbrown and MEblue).