

Supplementary table S1 Baseline data, number of specimens analysed, and health status in four groups

Group	Initial numbers	Final numbers	Health status (No. of specimens)	Sampled number
CD1	25	20	normal	15
CD2	25	24	normal	15
CD3	25	23	gallbladder disease (1)	15
HCD1	25	18	fatty liver (2)	15
HCD2	25	23	normal	15
HCD3	25	18	normal	15
HCB1	25	24	normal	15
HCB2	25	23	normal	15
HCB3	25	22	eye disease (1)	15
HC4B1	25	24	tail hyperaemia (1)	15
HC4B2	25	24	normal	15
HC4B3	25	25	normal	15

The four diet groups are: CD (control), HCD (high-carbohydrate), HCB (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks).

Supplementary table S2 Primers for liver qPCR

Target	Sequences	Fragment length (bp)
<i>fmo3</i>	F: TTCGGTAAAGCTGCCCACTC R: AGGTGGTGTGAATCGGGCTA	163
<i>cyp7a1</i>	F: TTGATCGTGCGTTCCTCTG R: AGCTGGCAGAGTATTCGCTT	242
<i>cyp27a1</i>	F: AGGGTGACAGAGTCCCAACA R: GCGGTCAGGTTTGAACCTTCG	239
<i>oapt1</i>	F: TCGGTCCAGTGTTTGGCTAC R: TCCTGGGGTGATGCTAATGC	98
<i>oapt4</i>	F: GGGCAGCTACATGAAAAGCTC R: ATCCAATCAGCGAGCTGGGAAT	71
<i>mrp2</i>	F: GTTCGATAACCGCCTGAGTT R: CCAGTTCGACCAACAATGCC	92
<i>bsep</i>	F: GGCCGTGAATCTACTAAGGTCA R: GGCTCCTGAGACACAATTCCA	68
<i>fxr</i>	F: CAAACATCGCATCCCTCAGGA R: TGGTGAAAACCTGGGCCGAA	230
<i>tgr5</i>	F: CCATCCTTTCCATTGCTGCG R: CGCATTTCCAGTCTCCGTCT	124

Supplementary table S3 Primers for microbial qPCR

Target	Primer names and sequences	Source
Labeled <i>16S rRNA</i>	27f: 6FAM-AGAGTTTGATCMTGGCTCAG 1492r: TACGGYTACCTTGTTACGACT	1
<i>16S rRNA</i>	F: GTGSTGCAYGGYTGTCGTCA R: ACGTCRTCCMCACCTTCCTC	2
<i>Lactobacillus</i> sp.	F: AGCAGTAGGGAATCTTCCA R: CACCGCTACACATGGAG	3
<i>Clostridium</i> sp.	F: GCGTAGGCGGATGTTTAAGTG R: CCTCACGGACTTCGGGTGT	4
<i>cutc</i>	F: TTYGCIGGITAYCARCCNTT R: TGNGGRTCIACYCAICCCAT	5
<i>cnta</i>	F: TAYCAYGCITGGRCITTYAARCT R: RCAGTGRTARCAYTCSAKRTAGTTRTCRAC	6
<i>grdh</i>	F: AYCARTTCTTTGGACAGRTAGG R: CCCATRAAGTTRTCWCCACATA	this study
<i>tora</i>	F: TTYGAYGAYTTYTGGAAYAA R: YTCRAACCACATIGGRTG	this study

Supplementary table S4 *P*-values for pairwise gene expression comparisons among the four groups

Parameter	Means ± standard deviation				<i>P</i> -value					
	CD	HCD	HCB	HC4B	CD vs HCD	CD vs HCB	CD vs HC4B	HCD vs HCB	HCD vs HC4B	HCB vs HC4B
<i>fmo3</i>	1.03±0.29	1.02±0.03	2.20±0.06***	2.41±0.27***	0.947	0.000	0.000	0.000	0.000	0.238
<i>cyp7a1</i>	1.00±0.06	1.51±0.14##	2.48±0.13***	2.73±0.10***	0.002	0.000	0.000	0.000	0.000	0.094
<i>cyp27a1</i>	1.00±0.04	1.21±0.00###	2.85±0.03***	1.51±0.06***	0.000	0.000	0.000	0.000	0.000	0.000
<i>oatp1</i>	1.00±0.03	8.53±1.30###	1.13±0.23***	2.95±0.33***	0.000	0.828	0.008	0.000	0.000	0.011
<i>oatp4</i>	1.00±0.04	1.37±0.01	2.23±0.65*	2.33±0.16**	0.211-	0.002	0.001	0.013	0.008	0.715
<i>mrp2</i>	1.00±0.00	0.55±0.04#	0.98±0.27*	0.70±0.02	0.015	0.996	0.097	0.020	0.558	0.134
<i>bsep</i>	1.00±0.10	1.03±0.06	1.27±0.05*	1.24±0.14*	0.776	0.008	0.014	0.012	0.021	0.713
<i>fxr</i>	1.00±0.06	2.02±0.24###	2.43±0.07	2.99±0.25***	0.001	0.000	0.000	0.087	0.001	0.020
<i>tgr5</i>	1.00±0.06	0.51±0.09###	1.89±0.04***	2.01±0.10***	0.000	0.000	0.000	0.000	0.000	0.109

The four groups are: CD (control), HCD (high-carbohydrate), HCB (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks). Values are presented as means of the entire group with standard deviation. #*p*<0.05, ##*p*<0.01 and ###*p*<0.001, compared to the CD group. **p*<0.05, ***p*<0.01 and ****p*<0.001, compared to the HCD group. “0.000” indicates *p*<0.001.

Supplementary table S5 *P*-values for pairwise metabolite concentration comparisons among the four groups

Parameter	CD vs HCD	CD vs HCB	CD vs HC4B	HCD vs HCB	HCD vs HC4B	HCB vs HC4B
Cholesterol	0.414	0.000	0.044	0.000	0.150	0.005
Choline	0.656	0.242	0.972	0.757	0.359	0.104
Betaine	0.028	0.620	0.086	0.083	0.439	0.240
TMA	0.000	0.000	0.000	0.005	0.004	0.876
TMAO	0.067	0.000	0.000	0.000	0.016	0.006

The four groups are: CD (control), HCD (high-carbohydrate), HCB (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks). “0.000” indicates $p < 0.001$.

Supplementary table S6 Microbial community indices: Shannon-Wiener (H'), Simpson (D') and Shannon evenness (E')

	<i>HaeIII</i>			<i>MspI</i>		
	H'	D'	E'	H'	D'	E'
CD	3.30±0.09	0.88±0.02	0.76±0.03	3.09±0.40	0.85±0.04	0.67±0.08
HCD	2.59±0.17 ^{##}	0.84±0.07	0.80±0.01	2.41±0.08 [#]	0.84±0.06	0.67±0.06
HCB	2.93±0.19	0.89±0.02	0.83±0.03	2.70±0.18	0.83±0.05	0.72±0.06
HC4B	2.98±0.19 [*]	0.91±0.03	0.84±0.03	2.42±0.09	0.80±0.06	0.69±0.07

H' and D' are measures of the diversity of a biological community; E' is the evenness (equitability of species relative abundances). Groups: CD (control), HCD (high-carbohydrate), HCB (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks). Values are presented as means of the entire group with standard deviation. [#] $p < 0.05$ and ^{##} $p < 0.01$, compared to the CD group. ^{*} $p < 0.05$, compared to the HCD group.

Supplementary table S7 *P*-values for pairwise microbial community indices comparisons among the four groups

Parameter		CD vs HCD	CD vs HCB	CD vs HC4B	HCD vs HCB	HCD vs HC4B	HCB vs HC4B
	H'	0.002	0.026	0.044	0.058	0.036	0.719
<i>HaeIII</i>	D'	0.287	0.764	0.378	0.185	0.072	0.551
	E'	0.203	0.025	0.011	0.289	0.141	0.586
	H'	0.039	0.155	0.042	0.275	0.950	0.298
<i>MspI</i>	D'	0.762	0.706	0.305	0.940	0.457	0.501
	E'	0.960	0.379	0.693	0.457	0.762	0.614

H': Shannon-Wiener, D': Simpson, E': Shannon evenness. The four groups are: CD (control), HCD (high-carbohydrate), HBD (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks).

Supplementary table S8 Range (%) of frequencies to the total peak height of some T-RF identified by T-RFLP from four groups, and their potential compatible bacteria.

Bacterial taxa (genus)	<i>HaeIII/MspI</i> (bp)	CD	HCD	HCB	HC4B
<i>Salicola</i> sp.	38/75	0.61-3.98	0.43-2.46	0.13-3.05	0.00-0.38
fenthion degrading bacterium sp.	38/80	0.00-3.98	0.76-2.46	0.12-3.05	0.00-0.38
<i>Pseudomonas/ Azotobacter/ Oceanobacillus/ Azotobacter/ Cronobacter/ Klebsiella/ Enterobacter</i> sp.	38/82	3.98-37.81	2.46-35.16	3.05-28.06	0.38-24.46
<i>Halomonas</i> sp.	38/126	1.80-3.98	0.00-2.46	0.18-3.05	0.38-1.42
<i>Methylosinus/ Bradyrhizobium/ Empedobacter</i> sp.	38/152	3.98-30.70	2.46-28.17	3.05-39.07	0.38-46.34
<i>Sphingobacterium</i> sp.	38/188	0.25-3.98	0.00-2.46	0.21-3.05	0.00-0.38
<i>Sphingomonas</i> sp.	63/152	0.71-30.70	1.93-28.17	2.70-39.07	1.92-46.34
<i>Lactobacillus</i> sp.	66/188	0.25-2.75	0.00-0.98	0.21-0.32	0.00-0.53
<i>Clostridium</i> sp.	115/188	0.00-0.25	0.00-0.9	0.21-0.93	0.00-1.22
<i>Kineococcus</i> sp.	224/33	0.39-1.62	1.51-2.60	0.42-2.58	2.08-3.26

<i>Streptomyces</i> sp.	224/33, 224/126	0.39-1.80	0.00-1.51	0.18-0.42	1.42-2.08
<i>Rhizobium</i> sp.	224/82, 224/126	1.62-1.80	0.00-1.51	0.18-0.42	1.42-3.26
<i>Mesorhizobium</i> sp.	224/126	1.62-1.80	0.00-1.51	0.18-0.42	1.42-3.26
<i>Arthrobacter/Paenibacillus</i> sp.	224/152	1.62-30.70	1.51-28.17	0.42-39.07	3.26-46.34
<i>Granulicatella</i> sp.	277/68	0.00-16.06	0.29-17.45	0.31-14.24	0.10-13.57
<i>Exiguobacterium</i> sp.	277/82	16.06-37.81	17.45-35.16	14.24-28.06	13.57-24.46

Four groups: CD (control), HCD (high-carbohydrate), HCB (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks). The values of line of *HaeIII/MspI* represent the T-RF lengths from the *HaeIII* and *MspI* restriction enzymes respectively. Bacterial taxa may be assigned to one or more T-RFs on the basis of a single restriction enzyme digestion result, and similarly, one T-RF length may be assigned to one or more bacteria taxa.

Supplementary table S9 *P*-values for pairwise abundance of microbes and gene expression comparisons among the four groups

Parameter	Means ± standard deviation				<i>P</i> -value					
	CD	HCD	HCB	HC4B	CD vs HCD	CD vs HCB	CD vs HC4B	HCD vs HCB	HCD vs HC4B	HCB vs HC4B
<i>Lactobacillus</i> sp.	1.00±0.05	696.80±139.67 ^{###}	3.70±1.52 ^{***}	9.36±1.53 ^{***}	0.000	0.963	0.887	0.000	0.000	0.923
<i>Clostridium</i> sp.	1.08±0.52	0.01±0.00 ^{###}	0.07±0.05	0.03±0.01	0.001	0.001	0.001	0.795	0.945	0.849
<i>cutc</i>	1.06±0.42	0.00±0.00 ^{###}	0.03±0.01	0.03±0.00	0.000	0.000	0.000	0.873	0.869	0.996
<i>cnta</i>	1.01±0.15	1.11±0.39	0.00±0.00 ^{***}	1.66±0.14	0.930	0.002	0.026	0.001	0.061	0.000
<i>grdh</i>	1.00±0.02	0.69±0.06	2.35±0.76 ^{***}	0.59±0.15	0.358	0.003	0.235	0.001	0.766	0.001

The four groups are: CD (control), HCD (high-carbohydrate), HCB (betaine supplementation for 16 weeks), HC4B (betaine supplementation for 4 weeks). Values are presented as means of the entire group with standard deviation. ^{###}*p*<0.001, compared to the CD group. ^{***}*p*<0.001, compared to the HCD group. “0.000” indicates *p*<0.001.

References

1. L. A. David, C. F. Maurice, R. N. Carmody, D. B. Gootenberg, J. E. Button, B. E. Wolfe, A. V. Ling, A. S. Devlin, Y. Varma, M. A. Fischbach, S. B. Biddinger, R. J. Dutton and P. J. Turnbaugh, Diet rapidly and reproducibly alters the human gut microbiome, *Nature*, 2013, **505**, 559-563.
2. H. Maeda, C. Fujimoto, Y. Haruki, T. Maeda, S. Koikeguchi, M. Petelin, H. Arai, I. Tanimoto, F. Nishimura and S. Takashiba, Quantitative real-time PCR using TaqMan and SYBR Green for *Actinobacillus actinomycetemcomitans*, *Porphyromonas gingivalis*, *Prevotella intermedia*, tetQ gene and total bacteria, *FEMS Immunology & Medical Microbiology*, 2003, **39**, 81-86.
3. T. Vanhoutte, P. V. De, B. E. De, K. Verbeke, J. Swings and G. Huys, Molecular monitoring of the fecal microbiota of healthy human subjects during administration of lactulose and *Saccharomyces boulardii*, *Applied & Environmental Microbiology*, 2006, **72**, 5990-5997.
4. T. Deltheil, B. P. Guiard, J. Cerdan, D. J. David, K. F. Tanaka, C. Repérant, J. P. Guilloux, F. Coudoré, R. Hen and A. M. Gardier, Behavioral and serotonergic consequences of decreasing or increasing hippocampus brain-derived neurotrophic factor protein levels in mice, *Neuropharmacology*, 2008, **55**, 1006-1014.
5. A. Martinez-del Campo, S. Bodea, H. A. Hamer, J. A. Marks, H. J. Haiser, P. J. Turnbaugh and E. P. Balskus, Characterization and detection of a widely distributed gene cluster that predicts anaerobic choline utilization by human gut bacteria, *mBio*, 2015, **6**.
6. S. Rath, B. Heidrich, D. H. Pieper and M. Vital, Uncovering the trimethylamine-producing bacteria of the human gut microbiota, *Microbiome*, 2017, **5**, 54.