Supplementary Tables

Supplementary Table 1. The model parameters of OPLS-DA in different comparative groups

WTND vs. WTHFD	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.254	0.254	0.961	0.961	0.833	0.833
	o1	0.191	0.444	0.028	0.028	0.0483	0.0483
	sum		0.444		0.989		0.881
WTHFD vs. WTHFDH	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.339	0.339	0.967	0.967	0.878	0.878
	o1	0.195	0.534	0.022	0.022	0.0223	0.0223
	sum		0.534		0.989		0.9
AbND vs. AbHFD	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.31	0.31	0.915	0.915	0.836	0.836
	o1	0.371	0.682	0.0716	0.0716	0.109	0.109
	sum		0.682		0.987		0.944
AbHFD vs. AbHFDH	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.208	0.208	0.891	0.891	0.697	0.697
	o1	0.208	0.416	0.103	0.103	0.0813	0.0813
	sum		0.416		0.994		0.778
AbND vs. WTND	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.249	0.249	0.872	0.872	0.764	0.764
	o1	0.355	0.604	0.122	0.122	0.156	0.156
	sum		0.604		0.994		0.919
AbHFD vs. WTHFD	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.312	0.312	0.975	0.975	0.911	0.911
	o1	0.081	0.393	0.0242	0.0242	0.0281	0.0281
	sum		0.393		0.999		0.939
AbHFDH vs. WTHFDH	A	r2x	r2x(cum)	r2y	r2y(cum)	q2	q2(cum)
	p1	0.317	0.317	0.983	0.983	0.897	0.897
	o1	0.105	0.421	0.0157	0.0157	0.027	0.027
	sum		0.421		0.999		0.924

Supplementary Table 2. Relative abundance of OTUs showing differences between HFD and HFD+FBT groups in healthy mice

OUT ID	Relative abundance (%)			*P* value*			
	WTND	WTHFD	WTHFDH	ND vs. HFD	HFD vs. HFDH	HFDH vs. ND	sign
OTU12 // Parabacteroides_goldsteinii	7.53	1.66	1.97	0.0390	1.0000	0.0520	☆
OTU593 // uncultured_bacterium_g__norank_f__Bacteroidales_S24-7_group	21.77	0.35	0.38	0.0090	1.0000	0.0120	
OTU594 // uncultured_bacterium_g__norank_f__Bacteroidales_S24-7_group	0.84	0.01	0.01	0.0080	1.0000	0.0130	
OTU600 // Lactobacillus_johnsonii	0.83	0.41	1.55	/	/	/	
OTU420 // unclassified_f__Erysipelotrichaceae	0.59	0.10	0.49	/	/	/	
OTU276 // Bacteroides_thetaiotaomicron	4.90	12.88	13.01	0.0170	1.0000	0.0280	
OTU415 // uncultured_bacterium_g__Lachnospiraceae_UCG-006	0.18	0.79	0.40	0.0050	0.4790	0.2510	☆
OTU401 // unclassified_g__[Eubacterium]_nodatum_group	0.08	0.90	0.50	0.0110	1.0000	0.0450	
OTU435 // unclassified_g__Lactobacillus	0.04	0.60	0.12	0.0090	0.5550	0.2970	☆
OTU270 // [Clostridium]_leptum_g__Ruminococcaceae_UCG-009	0.43	1.94	1.20	0.0030	0.4790	0.1750	☆
OTU443 // uncultured_bacterium_g__Intestinimonas	0.18	0.98	0.56	0.0040	0.5830	0.1550	☆
OTU461 // uncultured_bacterium_g__norank_f__Lachnospiraceae	0.02	0.94	0.49	0.0020	0.7000	0.0910	
OTU307 // unclassified_f__Ruminococcaceae	0.12	0.61	0.46	0.0070	1.0000	0.0240	
OTU442 // unclassified_g__Oscillibacter	0.08	0.49	0.30	0.0020	0.9130	0.0600	
OTU249 // uncultured_bacterium_g__Intestinimonas	0.30	0.45	0.42	/	/	/	
OTU465 // uncultured_bacterium_g__Lachnospiraceae_FCS020_group	0.22	0.35	0.24	/	/	/	
OTU416 // unclassified_g__Ruminiclostridium_5	0.21	0.93	0.11	0.1200	0.0090	1.0000	☆
OTU494 // Anaerotruncus_sp._G3_2012_	0.22	0.72	0.15	0.1200	0.0090	1.0000	☆
OTU391 // unclassified_g__Blautia	0.35	3.59	0.64	/	/	/	
OTU366 // unclassified_g__Desulfovibrio	0.00	0.17	0.00	/	/	/	

OTU447 // uncultured_organism_g__Ruminococcaceae_UCG-010	0.08	0.23	0.34	/	/	/	
OTU438 // unclassified_f__Ruminococcaceae	0.09	0.07	0.21	/	/	/	
OTU121 // uncultured_bacterium_g__Lachnospiraceae_NK4A136_group	0.27	0.11	0.68	1.0000	0.0090	0.1190	☆
OTU578 // unclassified_g__Alistipes	0.15	0.06	0.32	1.0000	0.0360	0.3390	☆
OTU572 // uncultured_bacterium_g__norank_f__Lachnospiraceae	0.44	0.09	0.72	/	/	/	
OTU545 // uncultured_organism_g__[Eubacterium]_ventriosum_group	0.05	0.12	0.16	1.0000	0.0690	0.1540	
OTU454 // uncultured_bacterium_g__norank_f__Bacteroidales_S24-7_group	0.40	0.22	1.15	0.9130	0.0020	0.0600	☆
OTU323 // uncultured_Bacteroidales_bacterium_g__norank_f__Bacteroidales_S24-7_group	0.00	1.25	12.01	1.0000	0.0050	0.0100	
OTU389 // uncultured_bacterium_g__Clostridium_sensu_stricto_1	0.03	0.02	0.30	1.0000	0.0140	0.0270	☆
OTU369 // uncultured_bacterium_g__norank_f__Lachnospiraceae	0.10	0.59	0.88	0.0910	0.7020	0.0025	
OTU577 // unclassified_g__Lachnospiraceae_NK4A136_group	0.09	0.37	0.99	0.0980	1.0000	0.0110	
OTU529 // unclassified_f__Lachnospiraceae	0.28	1.61	1.95	0.0330	1.0000	0.0030	
OTU274 // unclassified_g__norank_f__Lachnospiraceae	0.11	1.18	0.65	0.1050	1.0000	0.0850	
OTU456 // unclassified_g__norank_f__Clostridiales_vadinBB60_group	0.02	0.11	0.14	0.2460	0.9440	0.0180	
OTU412 // unclassified_f__Lachnospiraceae	0.02	0.03	0.71	1.0000	0.0550	0.0050	
OTU557 // unclassified_g__norank_f__Lachnospiraceae	0.09	0.10	0.24	/	/	/	
OTU320 // uncultured_bacterium_g__Lachnospiraceae_NK4A136_group	0.01	0.01	2.57	1.0000	0.0270	0.0020	☆
OTU352 // unclassified_g__norank_f__Clostridiales_vadinBB60_group	0.04	0.06	0.27	/	/	/	

Note: The OTUs significantly increased in group WTHFDH compared to WTHFD or significantly decreased in group WTHFD compared to WTND are shown in red; On the contrary, the OTUs are shown in green; The OTUs significantly increased in group WTHFDH, in which significantly decreased in group WTHFD are shown signed with "★", while those insignificantly decreased in group WTHFD yet insignificantly changed in group WTHFDH compared to WTND are signed with "☆".On the contrary, the OTUs are shown in green with "★" or green with "☆". Other OTUs that had no significant changes are shown in grey. **P* values were calculated using Kruskal–Wallis test with Bonferroni's correction. Significant *P* values (<0.05) are shown in red, yellow,or green.

Supplementary Table 3. Relative abundance of matabolics showing differences between HFD and HFD+FBT groups in healthy mice

Metabolites	Relative abundance (%)			*P* value*				HFD vs. ND		HFDH vs. HFD	
	WTND	WTHFD	WTHFDH	HFD vs. ND	HFDH vs. HFD	HFDH vs. ND	Effect of FBT	Trend	Fold change	Trend	Fold change
LysoPC(P-16:0)	0.61	0.58	0.47	/	/	/		↓	0.96	↓	0.81
Bis(2-ethylhexyl) phthalate	0.46	0.35	0.19	0.703	0.281	0.012		↓	0.75	↓	0.55
10,11-dihydro-20-trihydroxy-leukotriene B4	3.61	1.46	0.46	0.351	0.175	0.002		↓	0.40	↓	0.32
Aliskiren	2.79	1.65	0.92	0.390	0.136	0.001		↓	0.59	↓	0.56
LysoPE(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/0:0)	7.30	7.25	5.44	1.000	0.092	0.080		↓	0.99	↓	0.75
LysoPC(22:5(4Z,7Z,10Z,13Z,16Z))	6.19	6.10	4.91	/	/	/		↓	0.98	↓	0.81
PE(18:0/0:0)	5.05	4.99	3.89	1.000	0.120	0.039		↓	0.99	↓	0.78
LysoPE(18:0/0:0)	3.54	6.05	5.41	/	/	/		↑	1.71	↓	0.89
Oleamide	0.52	0.60	0.14	1.000	0.011	0.017	☆	↑	1.15	↓ *	0.23
Janthitrem C	1.09	0.71	0.89	/	/	/		↓	0.65	↑	1.26
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/18:2(9Z,12Z))	0.63	0.39	0.58	0.013	0.027	0.787	★	↓ *	0.61	↑ *	1.49
PC(20:3(8Z,11Z,14Z)/16:0)	0.71	0.50	0.64	0.028	0.223	1.000	☆	↓ *	0.71	↑	1.27
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/20:4(5Z,8Z,11Z,14Z))	0.36	0.16	0.27	0.021	0.198	1.000	☆	↓ *	0.44	↑	1.68
LysoPC(22:5(7Z,10Z,13Z,16Z,19Z))	1.38	0.88	1.44	/	/	/		↓	0.64	↑	1.64
LysoPC(20:3(5Z,8Z,11Z))	13.22	10.06	13.41	0.092	0.052	1.000		↓	0.76	↑	1.33
Lactosylceramide (d18:1/12:0)	1.15	0.95	1.26	0.175	0.060	1.000		↓	0.83	↑	1.32
LysoPC(22:1(13Z))	0.30	0.08	0.07	0.024	1.000	0.004		↓ *	0.26	↓	0.93
LysoPE(20:1(11Z)/0:0)	3.15	1.58	1.60	/	/	/		↓	0.50	↑	1.01
LysoPC(18:1(11Z))	10.85	7.19	7.36	/	/	/		↓	0.66	↑	1.02
1-Heptadecanoylglycerophosphoethanolamine	0.67	0.34	0.38	0.015	0.838	0.251	☆	↓ *	0.51	↑	1.11

LysoPC(16:1(9Z))	14.85	4.82	4.92	0.006	1.000	0.017		↓ **	0.32	↑	1.02
PC(20:2(11Z,14Z)/14:1(9Z))	1.05	0.47	0.52	0.003	1.000	0.033		↓ **	0.45	↑	1.09
PC(20:4(5Z,8Z,11Z,14Z)/16:1(9Z))	0.81	0.36	0.42	0.002	0.768	0.069	☆	↓ **	0.44	↑	1.17
LysoPC(20:1(11Z))	1.07	0.40	0.43	0.002	0.991	0.045		↓ **	0.38	↑	1.07
6-(4-ethyl-3-hydroxyphenoxy)-3,4,5-trihydroxyoxane-2-carboxylic acid	0.28	0.06	0.13	0.000	0.136	0.198	☆	↓ ***	0.22	↑	2.09
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/16:1(9Z))	0.67	0.25	0.33	0.003	0.479	0.175	☆	↓ **	0.37	↑	1.33
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/18:1(9Z))	0.35	0.13	0.17	0.001	0.251	0.175	☆	↓ **	0.36	↑	1.33
LysoPC(20:4(5Z,8Z,11Z,14Z))	28.24	26.45	31.41	0.641	0.005	0.175	☆	↓	0.94	↑ **	1.19
LysoPC(20:4(8Z,11Z,14Z,17Z))	3.65	4.15	5.78	1.000	0.060	0.007		↑	1.14	↑	1.39
PE(18:1(9Z)/0:0)	3.54	6.05	5.41	0.006	1.000	0.069	☆	↑ **	1.71	↓	0.89
1-Linoleoylglycerophosphocholine	47.08	52.04	52.13	0.092	1.000	0.033		↑	1.11	↑	1.00
3a,7a-Dihydroxy-5b-cholestane	0.36	0.62	0.64	0.092	1.000	0.033		↑	1.73	↑	1.03
1-Hydroxy-2,12,15-heneicosatrien-4-one	0.07	0.09	0.18	0.991	0.314	0.028		↑	1.38	↑	1.98
Asn Lys Ala Val Gly	0.12	0.50	0.54	0.039	1.000	0.002		↑ *	4.14	↑	1.09
Cytochalasin Ppho	0.02	0.34	0.36	0.028	1.000	0.004		↑ ***	22.13	↑	1.08
3-Indolepropionic acid	0.03	0.02	0.04	0.390	0.002	0.198	☆	↓	0.69	↑ **	1.83

Note: Trend ↑, ↓ denote that the metabolite content increased and decreased, respectively. * denotes that the difference is significant ($p < 0.05$), **denotes that the difference is highly significant ($p < 0.01$), and *** denotes that the difference is highly significant ($p < 0.001$).The metabolites significantly increased in group WTHFDH or significantly decreased in group WTHFD,in which different changes of metabolites exist in WTHFDH and WTDN groups compared with group WTHFD,are shown in red; On the contrary, the metabolites are shown in green; The metabolites significantly increased in group WTHFDH while significantly decreased in group WTHFD are shown in red with "★".On the contrary, the metabolites are shown in green with "★". The metabolites shown in red or green towards or beyond the levels in group WTND are signed with "☆". Other metabolites that had no significant changes are shown in grey. **P* values were calculated using Kruskal–Wallis test with Bonferroni's correction. Significant *P* values (<0.05) are shown in red, yellow,or green.

Supplementary Table 4. Relative abundance of matabolics showing differences between HFD and HFD+FBTgroups in microbiota-depleted mice

metabolites	Relative abundance (%)			*P* value*`				AbHFD vs. AbND		AbHFDH vs. AbHFD	
	AbND	AbHFD	AbHFDH	HFD vs. ND	HFDH vs. HFD	HFDH vs. ND	Effect of FBT	Trend	Fold change	Trend	Fold change
LysoPC(16:1(9Z))	11.39	3.29	3.03	0.036	1.000	0.004		↓**	0.29	↓	0.92
1-Linoleoylglycerophosphocholine	41.26	50.42	51.24	0.026	1.000	0.019		↑*	1.22	↑	1.02
LysoPC(18:1(11Z))	8.41	6.13	6.22	/	/	/		↓	0.73	↑	1.02
PE(18:1(9Z)/0:0)	2.71	3.32	4.78	1.000	0.109	0.011		↑	1.23	↑	1.44
10,11-dihydro-20-trihydroxy-leukotriene B4	1.58	0.26	0.23	0.067	1.000	0.010		↓	0.16	↓	0.89
LysoPE(20:1(11Z)/0:0)	2.34	1.25	1.18	/	/	/		↓	0.53	↓	0.94
Aliskiren	1.53	1.06	0.64	/	/	/		↓	0.69	↓	0.60
LysoPC(20:1(11Z))	0.66	0.30	0.25	/	/	/		↓	0.46	↓	0.82
PC(20:2(11Z,14Z)/14:1(9Z))	0.89	0.31	0.28	/	/	/		↓**	0.34	↓	0.90
PC(20:4(5Z,8Z,11Z,14Z)/16:1(9Z))	0.72	0.24	0.23	0.049	1.000	0.015		↓*	0.34	↓	0.94
Asn Lys Ala Val Gly	0.08	0.29	0.28	0.005	1.000	0.035		↓***	3.67	↓	0.94
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/16:1(9Z))	0.77	0.26	0.16	1.000	0.059	0.007		↓	0.33	↓	0.64
Cytochalasin Ppho	0.01	0.18	0.16	0.006	1.000	0.029		↑***	25.13	↓	0.86
1-Heptadecanoylglycerophosphoethanolamine	0.54	0.26	0.25	/	/	/		↓	0.48	↓	0.96
6-(4-ethyl-3-hydroxyphenoxy)-3,4,5-trihydroxyoxane-2-carboxylic acid	0.18	0.18	0.25	/	/	/		↑	1.04	↑	1.39
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/18:1(9Z))	0.28	0.13	0.12	/	/	/		↓	0.47	↓	0.87
LysoPC(22:1(13Z))	0.18	0.05	0.04	/	/	/		↓*	0.31	↓	0.83
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/18:2(9Z,12Z))	0.67	0.40	0.29	/	/	/		↓	0.59	↓	0.73
3a,7a-Dihydroxy-5b-cholestane	0.27	0.97	0.96	0.013	1.000	0.023		↑*	3.57	↓	0.99

LysoPC(20:4(5Z,8Z,11Z,14Z))	27.63	31.12	29.08	/	/	/	↑	1.13	↓	0.93
LysoPC(20:3(5Z,8Z,11Z))	12.73	11.08	9.51	/	/	/	↓	0.87	↓	0.86
LysoPE(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/0:0)	4.61	6.12	5.23	/	/	/	↑	1.33	↓	0.85
LysoPC(20:4(8Z,11Z,14Z,17Z))	3.77	5.17	5.03	/	/	/	↑	1.37	↓	0.97
LysoPC(22:5(4Z,7Z,10Z,13Z,16Z))	4.11	4.42	4.64	/	/	/	↑	1.07	↑	1.05
LysoPE(18:0/0:0)	4.11	4.42	4.64	/	/	/	↑	1.07	↑	1.05
PE(18:0/0:0)	3.96	3.83	4.16	/	/	/	↓	0.97	↑	1.09
LysoPC(22:5(7Z,10Z,13Z,16Z,19Z))	1.66	1.46	1.19	/	/	/	↓	0.88	↓	0.81
Oleamide	2.48	1.61	2.26	/	/	/	↓	0.65	↑	1.40
Lactosylceramide (d18:1/12:0)	1.14	0.98	0.82	/	/	/	↓	0.87	↓	0.83
Janthitrem C	1.40	1.28	1.03	/	/	/	↓	0.92	↓	0.80
Bis(2-ethylhexyl) phthalate	1.28	0.49	0.46	0.026	1.000	0.019	↓*	0.38	↓*	0.95
PC(20:3(8Z,11Z,14Z)/16:0)	0.71	0.44	0.42	/	/	/	↓	0.63	↓	0.95
PC(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/20:4(5Z,8Z,11Z,14Z))	0.42	0.19	0.12	/	/	/	↓	0.45	↓	0.62
LysoPC(P-16:0)	0.37	0.41	0.42	/	/	/	↑	1.09	↑	1.03
1-Hydroxy-2,12,15-heneicosatrien-4-one	0.06	0.27	0.33	0.026	1.000	0.006	↑*	4.29	↑	1.21
3-Indolepropionic acid	0.00	0.00	0.00	1.000	0.021	0.062	↑	1.13	↑*	1.79

Note: Trend ↑, ↓ denote that the metabolite content increased and decreased, respectively. * denotes that the difference is significant ($p < 0.05$), **denotes that the difference is highly significant ($p < 0.01$), and *** denotes that the difference is highly significant ($p < 0.001$).The metabolites significantly increased in group WTHFDH or significantly decreased in group WTHFD,in which different changes of metabolites exist in WTHFDH and WTDN groups compared with group WTHFD,are shown in red; On the contrary, the metabolites are shown in green; The metabolites significantly increased in group WTHFDH while significantly decreased in group WTHFD are shown in red with "★".On the contrary, the metabolites are shown in green with "★". The metabolites shown in red or green towards or beyond the levels in group WTND are signed with "☆". Other metabolites that had no significant changes are shown in grey. **P* values were calculated using Kruskal–Wallis test with Bonferroni's correction. Significant *P* values (<0.05) are shown in red, yellow,or green.

	AbND	**AbHFD**	**AbHFDH**	**WTND**	**WTHFD**	**WTHFDH**	**lower(Ab vs. WT)**			
PC(20:2(11Z,14Z)/14:1(9Z))	0.89	0.31	0.28	1.05	0.47	0.52	0.15	0.35	0.46	0.32
LysoPC(20:1(11Z))	0.66	0.30	0.25	1.07	0.40	0.43	0.38	0.25	0.42	0.35

3-Indolepropionic acid	0.00	0.00	0.00	0.03	0.02	0.04	0.96	0.94	0.94	0.94
PC(20:4(5Z,8Z,11Z,14Z)/16:1(9Z))	0.72	0.24	0.23	0.81	0.36	0.42	0.11	0.32	0.46	0.30
LysoPE(20:1(11Z)/0:0)	2.34	1.25	1.18	3.15	1.58	1.60	0.26	0.21	0.26	0.24
LysoPC(16:1(9Z))	11.39	3.29	3.03	14.85	4.82	4.92	0.23	0.32	0.38	0.31
1-Heptadecanoylglycerophosphoethanolamine	0.54	0.26	0.25	0.67	0.34	0.38	0.20	0.26	0.35	0.27

Supplementary Table 5. Metabolites values involved in glycerophospholipid metabolism showing differences between HFD and HFD+FBT groups in healthy mice and microbiota-depleted mice

Metabolites	Average values			P value*		Average values			*P* value*	
	WTND	WTHFD	WTHFDH	WTHFD vs. WTND	WTHFDH vs. WTHFD	AbND	AbHFD	AbHFDH	AbHFD vs. AbND	AbHFDH vs. AbHFD
C04230 (1-Acyl-sn-glycero-3-phosphocholine)	80.52	72.35	85.67	0.3481	0.0804	77.94	81.91	74.83	0.9463	0.8403
C00157 (Phosphatidylcholine)	5.937	3.548	4.392	0.0009	0.2606	5.905	3.337	2.86	0.0916	0.9073
C00350 (Phosphatidylethanolamine)	4.507	4.686	4.481	0.8626	0.8233	3.975	3.882	3.893	0.9923	>0.9999

Note: *P values were calculated using Tukey's HSD test. Significant *P* values (<0.05) are shown in grey.

Supplementary Table 6. Primer sequences for qRT-PCR analysis, related to Figures 8

Genes	Forward Primer Sequence	Reverse Primer Sequence
AhR	ACCGGCTGAACACAGAGTTA	CCATTCAGCGCCATCAAAGA
Cyp1a1	CAGGCTGACTCTGAACTTGC	AGACCAAGAGCTGATGCAGT
Pemt	AGCAGAGAACTCGGAAGCTG	CCAGGAAGTAGGTGGTGTGG
Fasn	TCGGGTGTGGTGGGTTTGGT	GGCGTGAGATGTGTTGCTGAGG
β-actin	GCTGTCCCTGTATGCCTCTG	TGATGTCACGCACGATTTCC