Supplementary Information

Theabrownin remodels the circadian rhythm disorder of intestinal microbiota induced by high-fat diet to alleviate obesity in mice

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Table S1 45% fat energy supply ratio of formula mouse food

Energy-supplying substance	Quality ratio%	Kcal/Kg	Energy supply ratio%
protein	24	960	20.17
fat	24	2160	45.38
carbohydrate	41	1640	34.45

Table S2 Normal diet energy supply ratio of formula mouse food

Energy-supplying substance	Quality ratio%	Kcal/Kg	Energy supply ratio%
protein	18.6	672.3	20.6
fat	4.8	174	12.0
carbohydrate	61	2201	67.4

Table S3 Amplitude, acrophase and peak time of cecal contents microbiome at phylum level

Microbiota	Group	Amplitude	Acrophase	Peak time	SE(A)-A	*P* value
Firmicutes	Control	0.116	2.408	9.198	0.285	0.003
	HFD	NR	NR	NR	1.256	0.000
	TB	NR	NR	NR	0.343	0.959
Bacteroidota	Control	NR	NR	NR	6.457	0.523
	HFD	NR	NR	NR	0.808	0.006
	TB	0.08	4.797	18.325	0.169	0.029
Patescibacteria	Control	NR	NR	NR	0.794	0.614
	HFD	NR	NR	NR	0.263	0.075
	TB	0.016	4.296	16.41	0.204	0.002

Table S4 Amplitude, acrophase and peak time of cecal contents microbiome at genus level

Microbiota	Group	Amplitude	Acrophase	Peak time	SE(A)-A	*P* value
Lachnospiraceae_NK4A136_group	Control	0.088	2.076	7.930	0.273	0.000
	HFD	NR	NR	NR	2.516	0.000
	TB	0.064	1.281	4.894	0.288	0.043
Dubosiella	Control	0.026	4.537	17.33	0.259	0.000
	HFD	NR	NR	NR	0.531	0.000
	TB	0.043	4.02	15.356	0.273	0.000
Alloprevotella	Control	0.016	4.255	16.253	0.276	0.019
	HFD	NR	NR	NR	1.541	0.011
	TB	0.040	4.549	17.377	0.263	0.001
Alistipes	Control	0.017	5.74	21.925	0.211	0.022
	HFD	NR	NR	NR	1.461	0.109
	TB	0.012	5.79	22.114	0.116	0.042
Helicobacter	Control	0.009	0.35	1.336	0.271	0.025
	HFD	NR	NR	NR	0.45	0.119
	TB	NR	NR	NR	0.22	0.669
Prevotellaceae_UCG_001	Control	NR	NR	NR	1.318	0.45
	HFD	0.002	3.271	12.495	0.282	0.005
	TB	NR	NR	NR	0.552	0.018

Table S5 Amplitude, acrophase and peak time of colon microbiome at phylum level

Microbiota	Group	Amplitude	Acrophase	Peak time	SE(A)-A	*P*-value
Bacteroidota	Control	NR	NR	NR	1.386	0.486
	HFD	43923838	0.064	0.245	0.229	0.009
	TB	75451181	3.435	13.119	0.248	0.016
Proteobacteria	Control	47417509	4.641	17.726	0.193	0.049
	HFD	NR	NR	NR	0.015	0.192
	TB	38455342	2.237	8.546	0.263	0.011
Acidobacteriota	Control	13746787	4.786	18.282	0.164	0.019
	HFD	NR	NR	NR	0.370	0.332
	TB	NR	NR	NR	0.698	0.782
Actinobacteriota	Control	17594243	4.643	17.735	0.223	0.035
	HFD	NR	NR	NR	0.407	0.191
	TB	NR	NR	NR	1.064	0.821
Chloroflexi	Control	8031369	5.03	19.213	0.198	0.011
	HFD	11082425	0.28	1.069	0.261	0.041
	TB	9004030	1.779	6.796	0.291	0.037

Table S6 Amplitude, acrophase and peak time of colon microbiome at genus level

Microbiota	Group	Amplitude	Acrophase	Peak time	SE(A)-A	*P* value
	Control	NR	NR	NR	1.905	0.516
Lachnospiraceae_NK4A136_group	HFD	NR	NR	NR	1.043	0.004
	TB	29139838	3.027	11.562	1.258	0.553
	Control	NR	NR	NR	2.876	0.616
Bacteroides	HFD	17013962	0.003	0.013	0.13	0.048
	TB	NR	NR	NR	1.265	0.741
	Control	NR	NR	NR	2.455	0.25
Akkermansia	HFD	NR	NR	NR	0.508	0.092
	TB	6801548	2.99	11.422	0.259	0.049
	Control	NR	NR	NR	1.316	0.202
Blautia	HFD	2693111	0.023	0.088	0.246	0.039
	TB	NR	NR	NR	0.536	0.419
	Control	3430042	4.6	17.572	0.194	0.043
Subdoligranulum	HFD	NR	NR	NR	0.354	0.483
	TB	3360740	1.75	6.685	0.181	0.045
	Control	1936485	4.208	16.072	0.136	0.019
Leuconostoc	HFD	NR	NR	NR	0.896	0.185
	TB	NR	NR	NR	0.497	0.814
	Control	3133563	4.482	17.12	0.051	0.007
Stenotrophomonas	HFD	2733265	0.129	0.492	0.259	0.026
	TB	2041672	2.528	9.675	0.278	0.034
	Control	2281976	4.635	17.705	0.161	0.000
Sphingomonas	HFD	2094517	0.017	0.064	0.284	0.046
	TB	1672027	2.88	11.001	0.139	0.009
	Control	1526783	4.704	17.968	0.274	0.047
Nitrospira	HFD	2373579	0.169	0.644	0.25	0.014
	TB	1756420	2.312	8.833	0.282	0.014
	Control	1601483	4.253	16.247	0.103	0.034
Planktothrix_NIVA_CYA_15	HFD	NR	NR	NR	0.233	0.436
	TB	NR	NR	NR	0.716	0.583

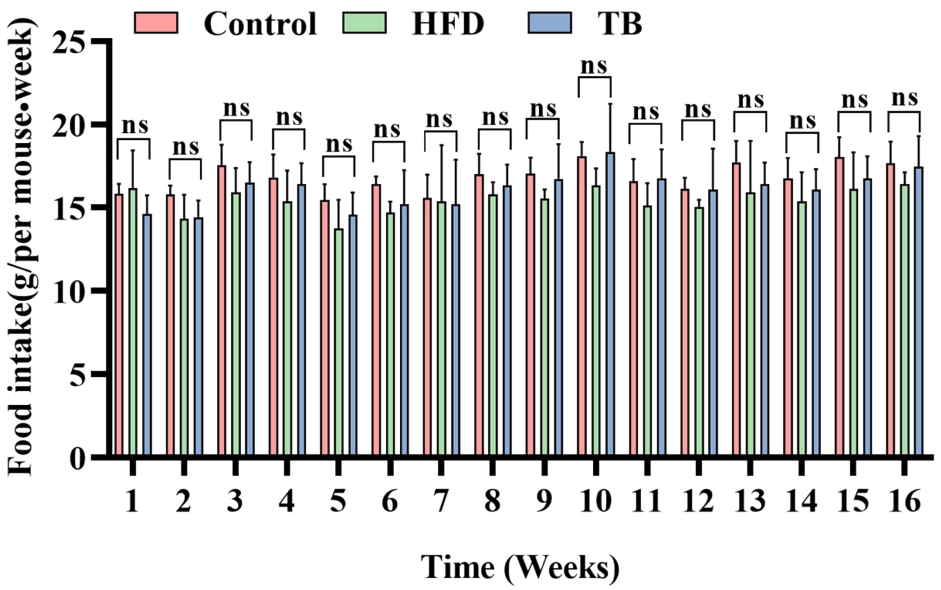
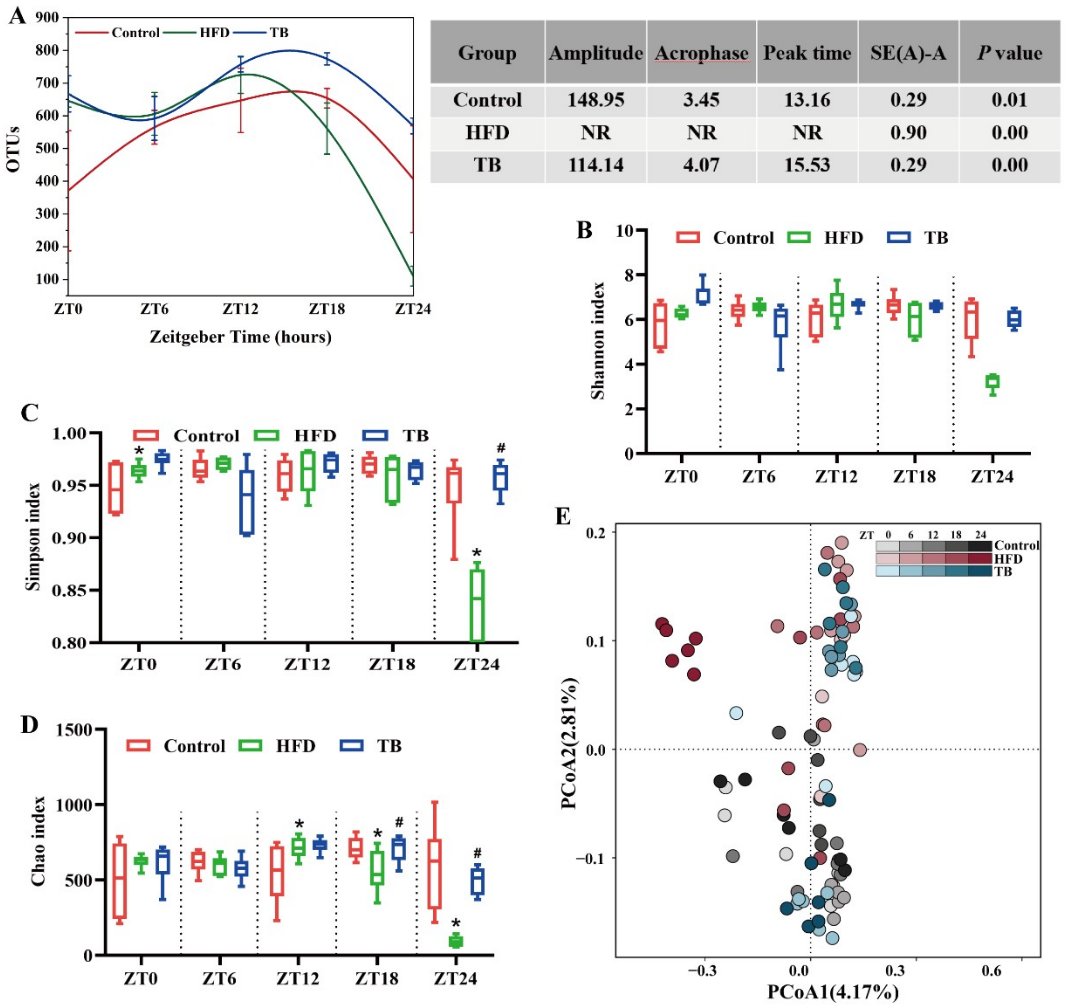


Figure S1 Mice food intake of per mouse of a week.



Group	Amplitude	Acrophase	Peak time	SE(A)-A	*P* value
Control	148.95	3.45	13.16	0.29	0.01
HFD	NR	NR	NR	0.90	0.00
TB	114.14	4.07	15.53	0.29	0.00

Figure S2. The impact of TB on the rhythmic expression of microbial OTUs in the cecal contents (A), daily variations in alpha diversity (B-D), and beta diversity (E). **P* < 0.05 versus the Control

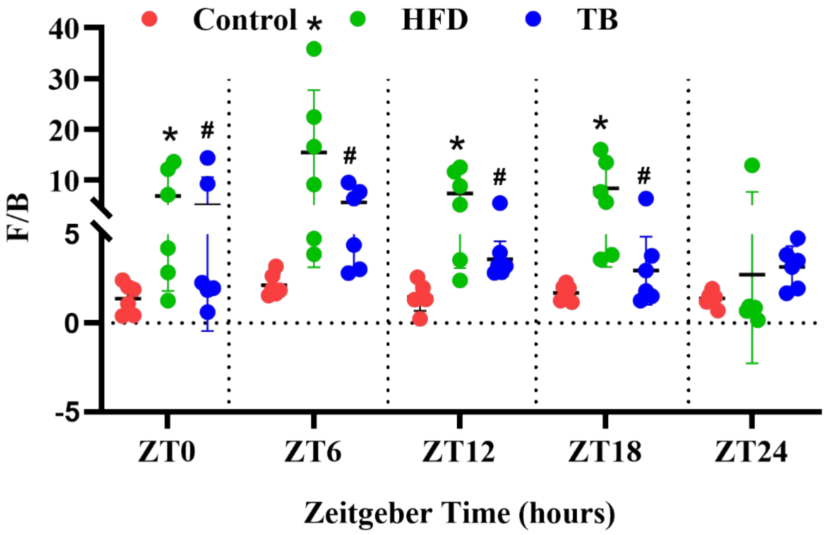


Figure S3. Ratio of Firmicutes to Bacteroidetes at different time points. *$P < 0.05$ versus the Control group, $^{\#}P < 0.05$ versus the HFD group.

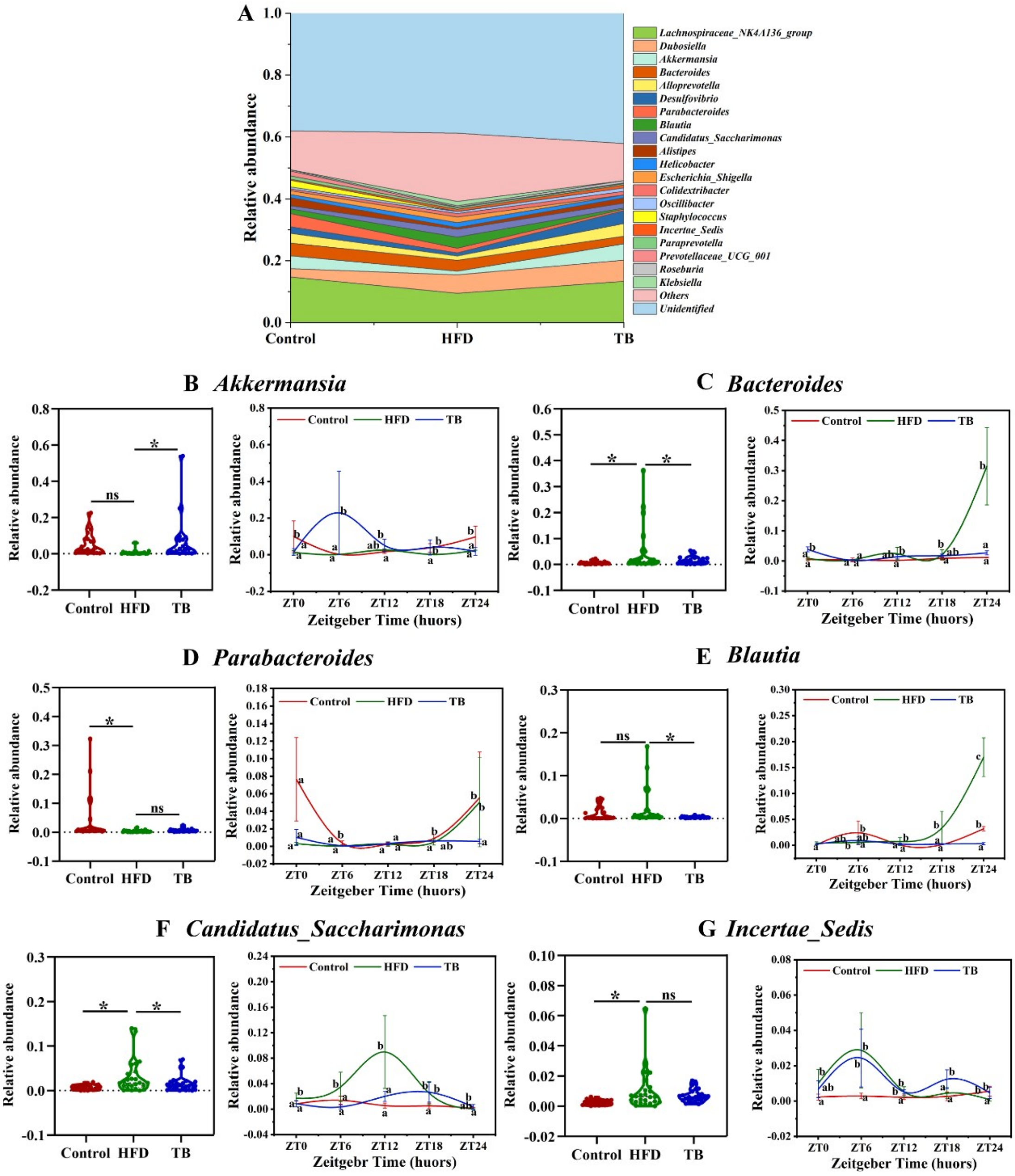


Figure S4. The microbial composition of cecal contents (A) and relative abundance of microorganisms without significant circadian rhythm showed 24 h diurnal fluctuation. (B-G) were at the genus level. Different lowercase letters (a, b, and c) were significantly different at the level of $P < 0.05$, $^*P < 0.05$ indicates a significant difference between the two groups.

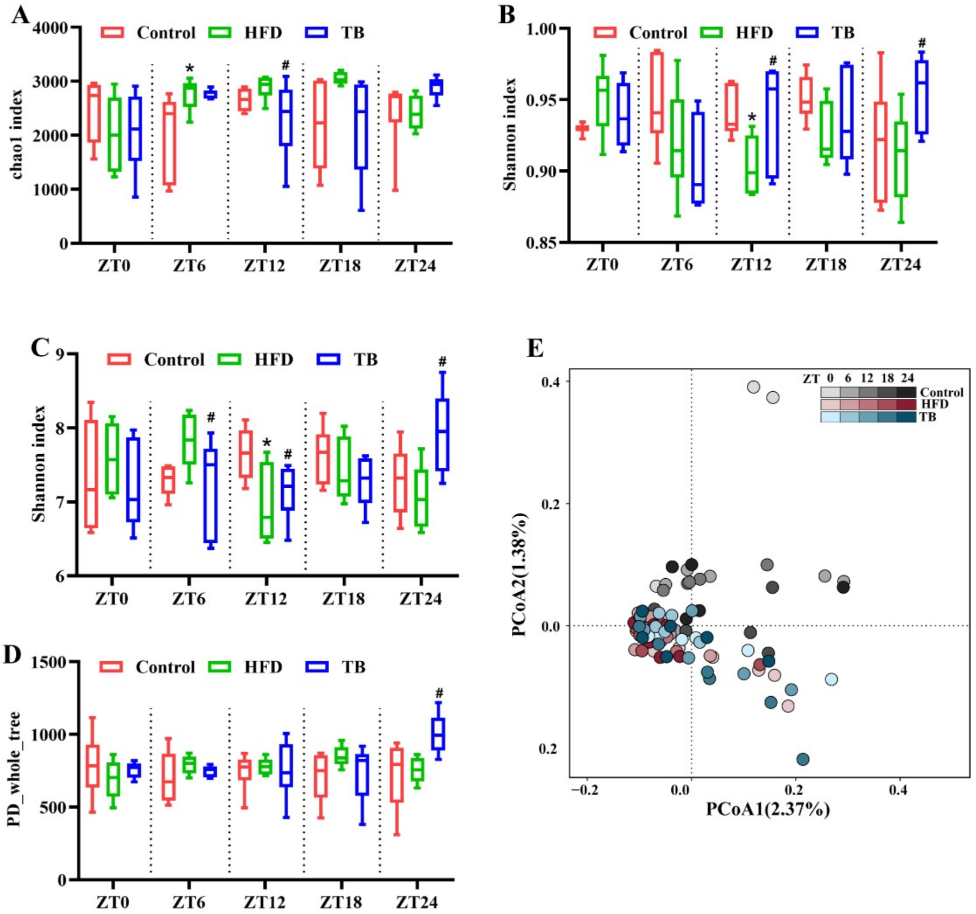


Figure S5. The impact of TB on the alpha diversity and beta diversity of colonic microbiota. * $P < 0.05$ versus the Control group, $^{\#}P < 0.05$ versus the HFD group.

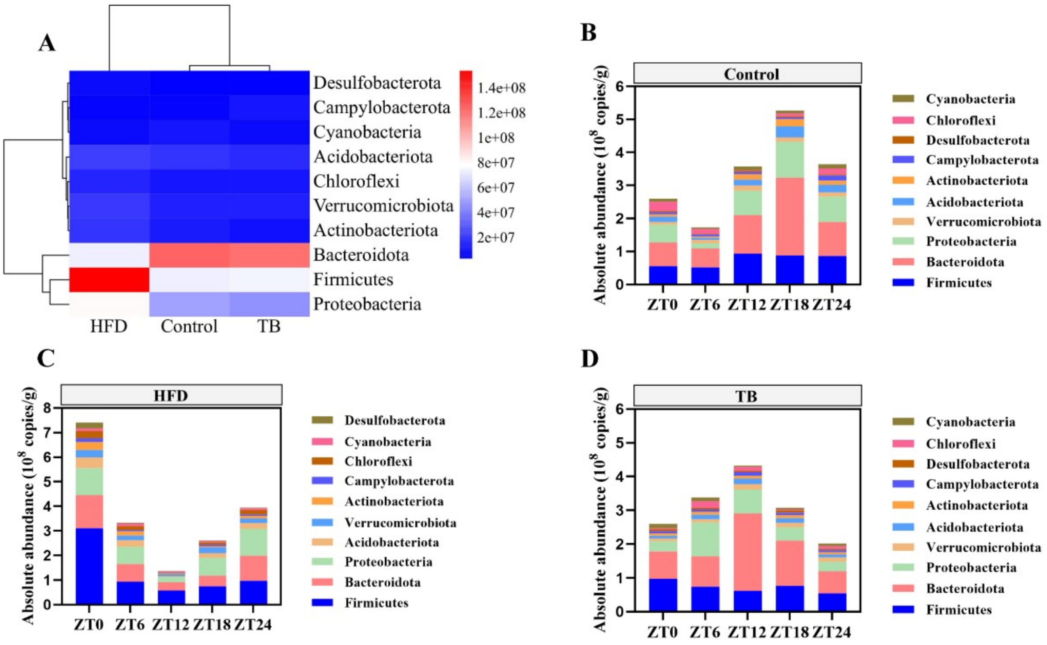


Figure S6. Colonic microbiota composition (A) Microbial absolute abundance stacked plot (B-D) at the phylum level.

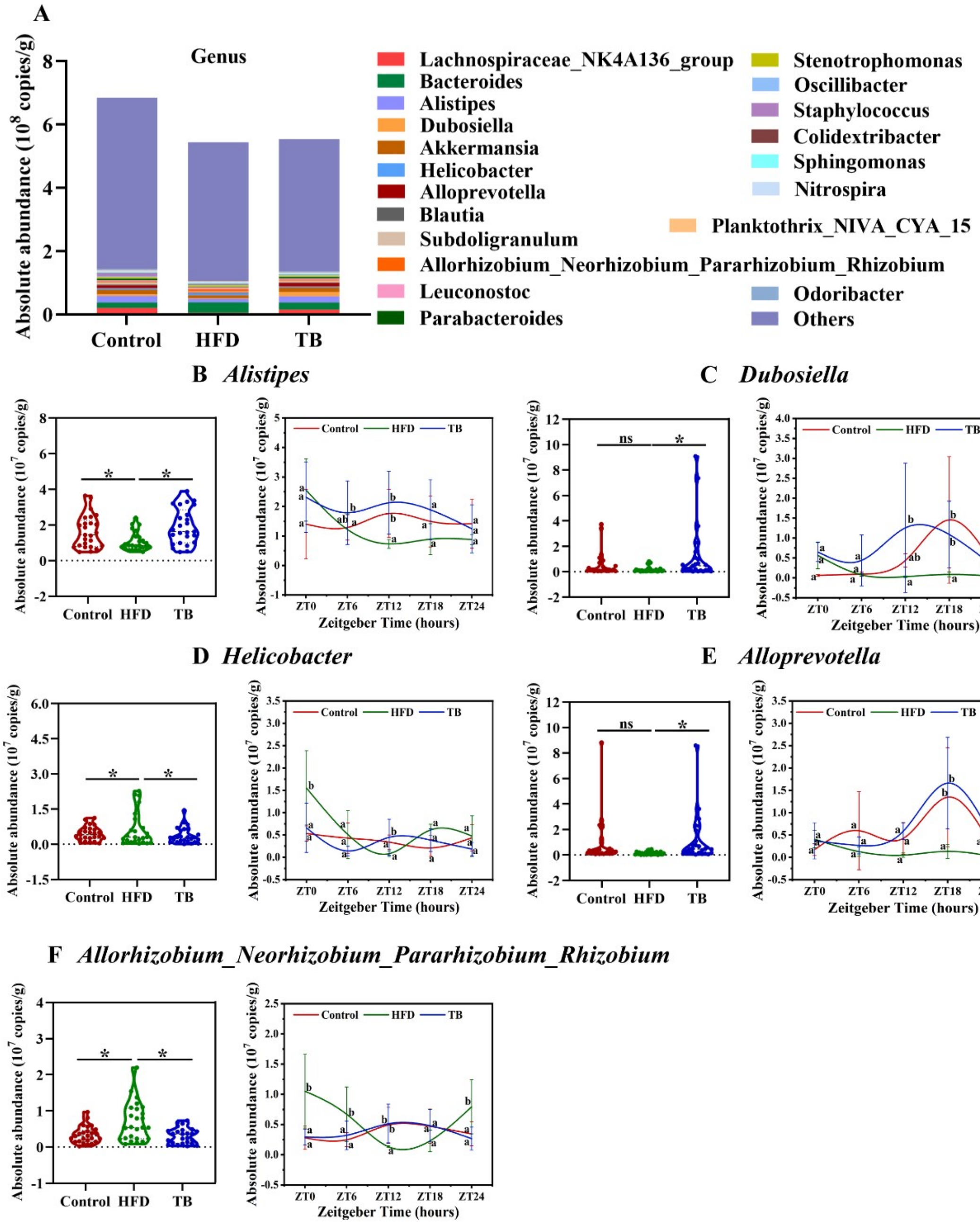


Figure S7. The composition of colonic microbial flora fluctuated at the genus level (A) and the absolute abundance of the flora fluctuated daily at 24 h (B-F). *$P < 0.05$ indicates a significant difference between the two groups.