



Figure S1. Changes in intestinal microflora composition in one year ($N = 767$). Four phyla, Firmicutes (A), Bacteroidetes (B), Actinobacteria (C), and Proteobacteria (D), account for the majority (~98%) of the human gut phyla. Spearman correlation was used to evaluate the association.

Table S1. Association between changes in intestinal microflora composition and changes in VFA and BMI.

Components	Explained variance [%]	Changes in VFA		Changes in BMI	
		P for trend	P for trend	P for trend	P for trend
PC1	13.5	0.026*	(I)	0.293	(I)
PC2	11.8	0.390	(D)	0.446	(D)
PC3	9.4	0.471	(I)	0.175	(I)
PC4	8.2	0.189	(I)	0.357	(D)
PC5	7.5	0.075	(D)	0.009**	(D)

P for trend was evaluated by Jonckheere test. (D) indicates a tendency to decrease, while (I) indicates a tendency to increase in relation to VFA.

P < 0.05 and <0.01 are indicated by * and **, respectively.

Table S2. Association between changes in intestinal microflora genera and changes in VFA and BMI.

Genus	Changes in VFA		Changes in BMI	
	R	P-values	R	P-values
<i>Alistipes</i>	-0.060	0.098	-0.059	0.102
<i>Anaerostipes</i>	-0.013	0.717	0.040	0.265
<i>Bacteroides</i>	-0.009	0.807	-0.003	0.925
<i>Bifidobacterium</i>	0.085	0.018*	0.049	0.176
<i>Blautia</i>	-0.047	0.198	-0.035	0.327
<i>Butyrivibrio</i>	-0.021	0.563	-0.032	0.370
<i>Clostridium.IV</i>	0.011	0.756	-0.002	0.946
<i>Clostridium.sensu.stricto</i>	-0.004	0.902	0.017	0.629
<i>Clostridium.XIVa</i>	0.000	0.990	-0.055	0.125
<i>Clostridium.XIVb</i>	-0.037	0.303	0.018	0.609
<i>Clostridium.XVIII</i>	0.013	0.712	-0.017	0.631
<i>Collinsella</i>	0.020	0.575	-0.025	0.490
<i>Dialister</i>	0.043	0.232	0.044	0.228
<i>Dorea</i>	0.036	0.314	0.063	0.081
<i>Eggerthella</i>	-0.019	0.601	-0.071	0.049*
<i>Erysipelotrichaceae incertae sedis</i>	-0.037	0.311	-0.030	0.401
<i>Escherichia/Shigella</i>	0.034	0.352	-0.006	0.859
<i>Faecalibacterium</i>	0.010	0.777	0.038	0.292
<i>Flavonifractor</i>	-0.098	0.007**	-0.077	0.033*
<i>Fusicatenibacter</i>	0.009	0.805	-0.002	0.964
<i>Gemmiger</i>	0.003	0.941	-0.045	0.209
<i>Intestinibacter</i>	0.001	0.985	0.023	0.527

<i>Lachnospiracea incertae sedis</i>	0.040	0.264	-0.016	0.665
<i>Lactobacillus</i>	0.026	0.474	-0.055	0.127
<i>Odoribacter</i>	-0.038	0.293	-0.037	0.302
<i>Oscillibacter</i>	-0.031	0.391	-0.072	0.045
<i>Parabacteroides</i>	-0.025	0.496	-0.008	0.820
<i>Phascolarctobacterium</i>	0.001	0.969	0.026	0.474
<i>Prevotella</i>	-0.031	0.391	-0.046	0.206
<i>Romboutsia</i>	0.058	0.108	0.036	0.321
<i>Roseburia</i>	0.010	0.787	0.051	0.158
<i>Ruminococcus</i>	-0.001	0.978	-0.048	0.188
<i>Streptococcus</i>	0.025	0.481	0.028	0.435
<i>Sutterella</i>	-0.009	0.811	0.027	0.454
<i>Turicibacter</i>	-0.010	0.775	-0.019	0.603
<i>Veillonella</i>	0.025	0.485	0.089	0.014

Spearman was used.

P < 0.05 and <0.01 are indicated by * and **, respectively.

Table S3. Adjusted association between changes in intestinal microflora 1 genera and changes in VFA and BMI.

Genus	Changes in VFA		Changes in BMI	
	β	P-values	β	P-values
<i>Alistipes</i>	-23.449	0.365	-4.171	0.038*
<i>Anaerostipes</i>	11.659	0.328	1.460	0.115
<i>Bacteroides</i>	-5.155	0.590	0.513	0.491
<i>Bifidobacterium</i>	11.402	0.153	0.053	0.932
<i>Blautia</i>	-36.189	0.015*	-0.520	0.656
<i>Butyrivibacter</i>	-128.407	0.295	-54.272	0.695
<i>Clostridium.IV</i>	18.660	0.281	-0.848	0.530
<i>Clostridium.sensu.stricto</i>	-78.195	0.261	-1.481	0.784
<i>Clostridium.XIVa</i>	-96.466	0.550	-16.368	0.193
<i>Clostridium.XIVb</i>	-173.652	0.300	-30.693	0.019*
<i>Clostridium.XVIII</i>	-63.564	0.359	-5.464	0.312
<i>Collinsella</i>	-6.200	0.686	1.004	0.401
<i>Dialister</i>	174.615	0.103	2.966	0.722
<i>Dorea</i>	79.906	0.406	12.565	0.092
<i>Eggerthella</i>	-201.284	0.444	-24.598	0.229
<i>Erysipelotrichaceae incertae sedis</i>	-16.244	0.856	-46.209	<0.001**
<i>Escherichia/Shigella</i>	38.438	0.272	3.550	0.188
<i>Faecalibacterium</i>	6.276	0.591	1.171	0.196
<i>Flavonifractor</i>	-486.139	0.016*	-18.445	0.239
<i>Fusicatenibacter</i>	41.656	0.137	0.401	0.854
<i>Gemmiger</i>	4.839	0.860	0.427	0.841
<i>Intestinibacter</i>	-64.557	0.587	2.755	0.766
<i>Lachnospiracea incertae sedis</i>	37.402	0.393	0.655	0.848
<i>Lactobacillus</i>	8.578	0.769	-5.574	0.014*
<i>Odoribacter</i>	-336.166	0.294	-26.357	0.291
<i>Oscillibacter</i>	-46.310	0.628	-26.357	0.291
<i>Parabacteroides</i>	-83.617	0.188	-4.903	0.322
<i>Phascolarctobacterium</i>	10.539	0.897	5.042	0.424
<i>Prevotella</i>	-5.816	0.405	0.080	0.883
<i>Romboutsia</i>	63.004	0.374	5.004	0.365
<i>Roseburia</i>	10.841	0.421	1.719	0.101
<i>Ruminococcus</i>	-12.835	0.379	-0.397	0.727
<i>Streptococcus</i>	12.859	0.343	1.968	0.687
<i>Sutterella</i>	56.780	0.365	1.968	0.687
<i>Turicibacter</i>	-104.343	0.120	-0.024	0.996
<i>Veillonella</i>	12.526	0.760	2.871	0.368

Multiple regression analysis was used with changes in VFA/BMI as an objective variable.

As for VFA, the following factors were used for the adjustment: age, sex, VFA, and the abundance ratio of each gut microbiota genus at baseline.

As for BMI, the following factors were used for the adjustment: age, sex, BMI, and the abundance ratio of each gut microbiota genus at baseline.

$P < 0.05$ and <0.01 are indicated by * and **, respectively.

Table S4. Multiple regression analysis of the association between change in VFA and changes in *Blautia* or *Flavonifractor*, including related factors.

	Changes in VFA	
	β	P-values
For <i>Blautia</i>		
Change in the abundance ratios of <i>Blautia</i>	-34.66	0.017*
Change in alcohol consumption	-0.04	0.311
Change in total fiber intake	0.08	0.576
Change in smoking habits	0.03	0.725
Change in BMI	3.36	<0.001**
Change in medicine use	-0.82	0.742
Abundance ratios of <i>Blautia</i> at the baseline	25.61	0.107
Age at the baseline	0.00	0.953
Sex at the baseline	-5.50	<0.001**
VFA at the baseline	-0.07	<0.001**
For <i>Flavonifractor</i>		
Change in the abundance ratios of <i>Flavonifractor</i>	-435.40	0.026*
Change in alcohol consumption	-0.05	0.272
Change in total fiber intake	0.09	0.506
Change in smoking habits	0.05	0.610
Change in BMI	3.29	<0.001**
Change in medicine use	-0.46	0.852
Abundance ratios of <i>Flavonifractor</i> at the baseline	-164.70	0.421
Age at the baseline	0.01	0.813
Sex at the baseline	-5.91	<0.001**
VFA at the baseline	-0.07	<0.001**

β = regression coefficient

P < 0.05 and <0.01 are indicated by * and **, respectively.