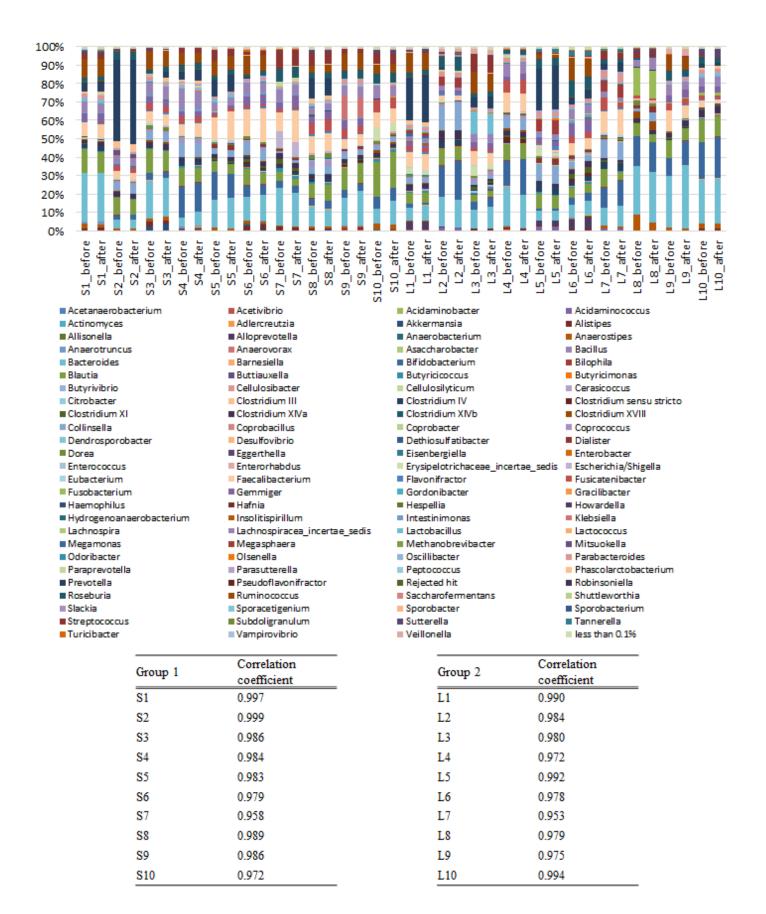


Supplementary Figure 1 The Shannon index of the gut microbiota stratified by VFA in each sex The data are presented as mean \pm standard error. The P-value was calculated using the Wilcoxon rank-sum test.



Supplementary Figure 2 Preservation stability of gut microbiota after storing for 1 year at 4°C

Pearson's correlation coefficient was used to evaluate the stability of the samples before and after preservation for 1 year. Group 1 and Group 2 were evaluated at different times. Gut microbiota with a relative abundance of less than 0.1% is described as < 0.1%.

Supplementary Table 1.	Characteristics of the subjects in t	the main study group	stratified by sex and VFA

Characteristics			Μ	Ien			P value	Women					P value	
	VFA<100		10)0 <u>≤</u> V	FA	r value	VFA<100		.00	100 <u><</u> VFA			P value	
Visceral fat area (cm²)	69.5	±	22.8	140.2	±	31.4		57.5	±	22.2	124.9	±	23.4	
Number		183			208				513			97		
Age (y) ^{*1}	49.1	±	14.8	53.1	±	13.3	0.009**	53.2	±	13.8	59.4	±	12.0	<0.001**
Height (cm) ^{*1}	169.2	±	6.8	169.0	±	6.5	0.966	155.9	±	6.0	154.2	±	6.6	0.015*
Body weight (kg) ^{*1}	62.2	±	7.0	72.9	±	10.8	<0.001**	52.0	±	6.8	65.1	±	9.1	<0.001**
Body mass index (kg/m ²) ^{*1}	21.7	±	2.0	25.5	±	3.0	<0.001**	21.4	±	2.7	27.4	±	3.5	<0.001**
Waist circumference (cm) ^{*1}	76.8	±	5.3	88.3	±	7.3	<0.001**	71.6	±	7.2	87.8	±	8.0	<0.001**
Serum Glucose (mg/dL) ^{*1}	4.4	±	0.6	4.9	±	1.2	<0.001**	4.4	±	0.7	4.8	±	0.7	<0.001**
HbA1c (%) ^{*1}	5.6	±	0.4	5.9	±	0.8	<0.001**	5.7	±	0.4	6.0	±	0.6	<0.001**
SBP (mmHg) ^{*1}	122.5	±	17.0	127.7	±	15.3	0.001**	117.8	±	17.2	129.7	±	17.5	<0.001**
DBP (mmHg) ^{*1}	76.3	±	12.2	80.3	±	10.7	<0.001**	72.1	±	11.1	78.2	±	11.0	<0.001**
Triglyceride (mg/dL) ^{*1}	1.1	±	0.7	1.7	±	1.5	<0.001**	0.9	±	0.4	1.2	±	0.6	<0.001**
Total cholesterol (mg/dL) ^{*1}	5.1	±	0.8	5.5	±	0.8	<0.001**	5.4	±	0.9	5.6	±	0.8	0.005**
HDL cholesterol (mg/dL) ^{*1}	1.7	±	0.4	1.5	±	0.4	<0.001**	1.9	±	0.4	1.6	±	0.4	<0.001**
LDL cholesterol (mg/dL) ^{*1}	109.6	±	27.2	123.1	±	26.8	<0.001**	116.4	±	29.4	129.0	±	26.9	<0.001**
Smoking habit (stick/d) ^{*1}	11.0	±	11.4	12.5	±	12.0	0.240	2.3	±	5.4	2.4	±	5.6	0.741
Sleep time (h/d) ^{*1}	7.1	±	1.3	7.2	±	1.2	0.328	6.8	±	1.0	7.0	±	1.0	0.039*
Walk speed (sec/10m) ^{*1}	3.6	±	0.8	3.6	±	0.7	0.866	4.0	±	0.7	4.5	±	1.0	0.001**
Habitual medicine use (% of Yes) ^{*2}	:	20.1%	6		36.79	%	<0.001**	1	27.3%	6		47.4%	6	<0.001**
Hypertension ^{*2}		14.1%	6	:	32.49	%	<0.001**	1	20.3%	6		38.1%	6	<0.001**
Hyperlipidaemia ^{*2}		4.9%			13.59	%	0.006**		11.3%	6		18.6%	6	0.069
Diabetes ^{*2}		2.7%			7.7%	ó	0.049*		1.8%			3.1%	0	0.637
Rheumatism ^{*2}		1.1%			0.5%	ó	0.918		1.8%			4.1%	0	0.272
Total energy intake (kcal/d) ^{*1}	8879.8	±	2597.8	8810.7	±	2266.7	0.782	6946.2	±	1920.5	7140.5	±	1802.1	0.402
Carbohydrate intake ^{*1}	0.60	±	0.08	0.59	±	0.07	0.119	0.57	±	0.07	0.58	±	0.07	0.042*
Fat intake ^{*1}	0.25	±	0.06	0.26	±	0.05	0.153	0.27	±	0.05	0.26	±	0.05	0.013*
Protein intake ^{*1}	0.15	±	0.03	0.15	±	0.03	0.100	0.16	±	0.03	0.16	±	0.03	0.426
Alcohol consumption (g/d) ^{*1}	19.0	±	21.9	23.9	±	24.6	0.041*	4.5	±	10.7	3.3	±	8.9	0.056
Total dietary fibre intake (g/d) ^{*1}	11.1	±	4.8	11.0	±	4.5	0.975	10.8	±	4.3	10.7	±	4.1	0.864

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

*1 Wilcoxon rank-sum test was used

*2 test for equality of proportions was used

Supplementary Table 2. Relation of the relative abundance of human gut microbial genera and VFA

	MEN			WOMEN								
	VFA <50	50≤ VFA <100	$100 \leq VFA \leq 150$	$150 \le VFA$	P for trend ^{*1}	Q value*2	VFA <50	$50 \le VFA \le 100$	$100 \leq VFA \leq 150$	$150 \le VFA$	P for trend ^{*1}	Q value ^{*2}
Number	38	145	140	68			197	311	88	14		
Genus												
Acidaminococcus	0.0009 ± 0.0022	0.0013 ± 0.0041	0.0018 ± 0.0043	0.0021 ± 0.0052	0.067 (I) 0.329	0.0012 ± 0.0037	0.0011 ± 0.0033	0.0012 ± 0.0037	0.0015 ± 0.0055	0.454 (D)	0.501
Akkermansia	0.0077 ± 0.0319	0.0088 ± 0.0357	0.0023 ± 0.0127	0.0020 ± 0.0065	0.226 (D	0.496	0.0063 ± 0.0172	0.0087 ± 0.0287	0.0039 ± 0.0105	0.0016 ± 0.0044	0.098 (D)	0.258
Alistipes	0.0147 ± 0.0221	0.0143 ± 0.0209	0.0124 ± 0.0193	0.0108 ± 0.0122	0.338 (I) 0.496	0.0282 ± 0.0322	0.0263 ± 0.0318	0.0236 ± 0.0289	0.0264 ± 0.0238	0.221 (D)	0.366
Alloprevotella	0.0032 ± 0.0104	0.0042 ± 0.0155	0.0065 ± 0.0208	0.0081 ± 0.0218	0.380 (I) 0.508	0.0022 ± 0.0113	0.0004 ± 0.0032	0.0023 ± 0.0121	0.0001 ± 0.0004	0.493 (D)	0.503
Anaerostipes	0.0470 ± 0.0574	0.0599 ± 0.0612	0.0588 ± 0.0635	0.0457 ± 0.0526	0.423 (D	0.508	0.0594 ± 0.0561	0.0499 ± 0.0497	0.0555 ± 0.0597	0.0242 ± 0.0188	0.067 (I)	0.238
Bacteroides	0.1171 ± 0.0913	0.1098 ± 0.0708	0.1166 ± 0.0771	0.0998 ± 0.0757	0.250 (D	0.496	0.1185 ± 0.0692	0.1120 ± 0.0686	0.1147 ± 0.0707	0.0915 ± 0.0628	0.088 (D)	0.257
Barnesiella	0.0011 ± 0.0022	0.0007 ± 0.0015	0.0009 ± 0.0022	0.0008 ± 0.0016	0.442 (D	0.508	0.0017 ± 0.0029	0.0015 ± 0.0033	0.0010 ± 0.0022	0.0013 ± 0.0015	0.091 (D)	0.257
Bifidobacterium	0.0696 ± 0.0903	0.0746 ± 0.0768	0.0655 ± 0.0815	0.0495 ± 0.0584	0.021* (D) 0.186*	0.0806 ± 0.0759	0.0712 ± 0.0752	0.0670 ± 0.0780	0.0355 ± 0.0337	0.002** (D)	0.033**
Bilophila	0.0009 ± 0.0013	0.0013 ± 0.0018	0.0020 ± 0.0030	0.0014 ± 0.0026	0.245 (I) 0.496	0.0018 ± 0.0026	0.0017 ± 0.0025	0.0015 ± 0.0020	0.0019 ± 0.0030	0.490 (D)	0.503
Blautia	0.0757 ± 0.0424		0.0657 ± 0.0344	0.0665 ± 0.0426	0.003** (D		0.0745 ± 0.0368				0.020* (D)	
Butyricicoccus	0.0060 ± 0.0062			0.0069 ± 0.0054	0.435 (D	* · · · · · · · · · · · · · · · · · · ·	0.0063 ± 0.0049				0.384 (I)	
Catenibacterium	0.0017 ± 0.0065		0.0054 ± 0.0147		0.161 (I	· · · · · · · · · · · · · · · · · · ·	0.0027 ± 0.0117		0.0027 ± 0.0095		0.362 (I)	
Clostridium.IV	0.0220 ± 0.0426			0.0198 ± 0.0308	0.256 (I		0.0212 ± 0.0251				0.270 (I)	
Clostridium.sensu.stricto	0.0021 ± 0.0060		0.0028 ± 0.0087	0.0024 ± 0.0065	0.154 (I		0.0014 ± 0.0053				<0.001** (I)	
Clostridium.XIVa	0.0050 ± 0.0048			0.0056 ± 0.0067	0.329 (I		0.0057 ± 0.0072		0.0052 ± 0.0039		0.216 (I)	
Clostridium.XIVb	0.0016 ± 0.0025		0.0027 ± 0.0036	0.0025 ± 0.0033	0.016* (I		0.0023 ± 0.0041				0.075 (D)	
Clostridium.XVIII	0.0070 ± 0.0023 0.0070 ± 0.0092		0.0027 ± 0.0050 0.0045 ± 0.0064	0.0023 ± 0.0033 0.0057 ± 0.0082	0.483 (I		0.0054 ± 0.0059		0.0010 ± 0.0030 0.0057 ± 0.0072		0.112 (D)	
Collinsella	0.0292 ± 0.0329			0.0508 ± 0.0543	0.063 (I		0.0392 ± 0.0432				0.409 (D)	
Coprococcus	0.0292 ± 0.0329 0.0069 ± 0.0109			0.0062 ± 0.0075	0.441 (D		0.00392 ± 0.00432 0.0065 ± 0.0094				0.040* (I)	
Dialister	0.0009 ± 0.0109 0.0016 ± 0.0034		0.0030 ± 0.0070 0.0020 ± 0.0041	0.0032 ± 0.0073 0.0034 ± 0.0053	0.042* (I	* · · · · · · · · · · · · · · · · · · ·	0.0005 ± 0.0094 0.0026 ± 0.0045				0.291 (I)	
Dorea	0.0018 ± 0.0034 0.0094 ± 0.0091		0.0020 ± 0.0041 0.0109 ± 0.0086	0.0034 ± 0.0033 0.0102 ± 0.0119	0.465 (D		0.0028 ± 0.0043 0.0075 ± 0.0070			0.0034 ± 0.0036 0.0113 ± 0.0084	0.291 (I) 0.025* (I)	
Eggerthella	0.0094 ± 0.0091 0.0017 ± 0.0031			0.0102 ± 0.0119 0.0018 ± 0.0041	0.485 (D 0.196 (D	· · · · · · · · · · · · · · · · · · ·	0.0073 ± 0.0070 0.0024 ± 0.0033				0.023* (I) 0.004 (D)	
						* · · · · · · · · · · · · · · · · · · ·						
Enterococcus	0.0006 ± 0.0015			0.0009 ± 0.0056	0.045* (D	·	0.0014 ± 0.0075				·····	
Erysipelotrichaceae_incertae_sedis	0.0056 ± 0.0157			0.0028 ± 0.0062	0.093 (D	·	0.0048 ± 0.0118		0.0020 ± 0.0046	010011 - 01002	0.003** (D)	
Escherichia/Shigella	0.0035 ± 0.0089			0.0073 ± 0.0231	0.489 (D	·	0.0023 ± 0.0106				0.396 (I)	
Faecalibacterium	0.0759 ± 0.0685				0.315 (D	·	0.0866 ± 0.0584				0.223 (I)	
Flavonifractor	0.0026 ± 0.0038		0.0021 ± 0.0024	0.0022 ± 0.0027	0.303 (D	·	0.0034 ± 0.0040			0.0015 ± 0.0017	<0.001** (D)	
Fusicatenibacter	0.0166 ± 0.0228				0.491 (I		0.0248 ± 0.0231				0.217 (I)	
Fusobacterium	0.0173 ± 0.0576			0.0072 ± 0.0251	0.566 (I		0.0048 ± 0.0227			0.0008 ± 0.0030	0.199 (D)	
Gemmiger	0.0292 ± 0.0250			0.0210 ± 0.0192	0.171 (D	·	0.0264 ± 0.0230		0.0267 ± 0.0214		0.072 (I)	
Holdemanella	0.0058 ± 0.0138			0.0053 ± 0.0105	0.397 (I		0.0056 ± 0.0135				0.101 (I)	
Intestinibacter	0.0014 ± 0.0022			0.0014 ± 0.0025	0.252 (D	· · · · · · · · · · · · · · · · · · ·	0.0030 ± 0.0046		0.0039 ± 0.0070		0.325 (I)	
Klebsiella	0.0003 ± 0.0008			0.0004 ± 0.0017	0.340 (D		0.0009 ± 0.0054		0.0007 ± 0.0037		0.448 (I)	
Lachnospiracea_incertae_sedis	0.0179 ± 0.0164				0.465 (I		0.0210 ± 0.0134				0.216 (I)	
Lactobacillus	0.0043 ± 0.0209			0.0024 ± 0.0098	0.391 (D		0.0018 ± 0.0070	010000 - 010101			0.111 (I)	
Megamonas	0.0129 ± 0.0327			0.0171 ± 0.0403	0.208 (I		0.0081 ± 0.0412				0.234 (I)	
Megasphaera	0.0044 ± 0.0102		0.0049 ± 0.0105	0.0065 ± 0.0133	0.227 (I		0.0021 ± 0.0086				0.041* (I)	
Mitsuokella	0.0004 ± 0.0014	0.0015 ± 0.0058	0.0017 ± 0.0068	0.0054 ± 0.0234	0.332 (I		0.0006 ± 0.0029	0.0004 ± 0.0022	0.0008 ± 0.0029	0.0000 ± 0.0000	0.268 (I)	0.404
Odoribacter	0.0008 ± 0.0011	0.0012 ± 0.0017	0.0008 ± 0.0011	0.0009 ± 0.0013	0.380 (D	* · · · · · · · · · · · · · · · · · · ·	0.0015 ± 0.0017	0.0015 ± 0.0022	0.0012 ± 0.0015	0.0023 ± 0.0018	0.170 (D)	0.366
Oscillibacter	0.0056 ± 0.0087	0.0035 ± 0.0038	0.0031 ± 0.0038	0.0046 ± 0.0067	0.499 (D	0.509	0.0055 ± 0.0061	0.0072 ± 0.0109	0.0052 ± 0.0084	0.0058 ± 0.0026	0.403 (I)	0.469
Parabacteroides	0.0160 ± 0.0305	0.0098 ± 0.0102	0.0084 ± 0.0085	0.0081 ± 0.0087	0.092 (D	0.387	0.0094 ± 0.0100	0.0103 ± 0.0153	0.0089 ± 0.0100	0.0053 ± 0.0046	0.994 (D)	0.994
Paraprevotella	0.0031 ± 0.0072	0.0024 ± 0.0054	0.0028 ± 0.0067	0.0026 ± 0.0088	0.479 (D	0.509	0.0017 ± 0.0043	0.0015 ± 0.0048	0.0028 ± 0.0051	0.0010 ± 0.0034	0.217 (I)	0.366
Parasutterella	0.0027 ± 0.0079	0.0042 ± 0.0096	0.0040 ± 0.0082	0.0040 ± 0.0083	0.221 (I) 0.496	0.0039 ± 0.0081	0.0045 ± 0.0092	0.0064 ± 0.0119	0.0042 ± 0.0064	0.018* (I)	0.104*
Phascolarctobacterium	0.0056 ± 0.0066	0.0065 ± 0.0075	0.0073 ± 0.0078	0.0069 ± 0.0085	0.193 (I) 0.496	0.0044 ± 0.0058	0.0041 ± 0.0064	0.0042 ± 0.0058	0.0026 ± 0.0035	0.349 (D)	0.459
Prevotella	0.0534 ± 0.0905	0.0671 ± 0.1194	0.0880 ± 0.1349	0.1131 ± 0.1416	0.003** (I) 0.052**	0.0330 ± 0.0789	0.0365 ± 0.0810	0.0373 ± 0.0799	$0.0305 \ \pm \ 0.0732$	0.482 (D)	0.503
Romboutsia	0.0018 ± 0.0034	$0.0050 \ \pm \ 0.0082$	$0.0035 \ \pm \ 0.0062$	0.0039 ± 0.0061	0.428 (I) 0.508	0.0037 ± 0.0064	0.0048 ± 0.0092	0.0057 ± 0.0106	$0.0048 \ \pm \ 0.0044$	0.021* (I)	0.104*
Roseburia	0.0426 ± 0.0448	0.0440 ± 0.0379	0.0357 ± 0.0319	0.0441 ± 0.0442	0.272 (D) 0.496	0.0372 ± 0.0342	0.0440 ± 0.0416	0.0443 ± 0.0356	0.0646 ± 0.0496	0.010** (I)	0.067**
Ruminococcus	0.0267 ± 0.0393	0.0241 ± 0.0356	0.0201 ± 0.0352	0.0280 ± 0.0383	0.338 (I) 0.496	0.0332 ± 0.0449	0.0399 ± 0.0460	0.0410 ± 0.0466	0.0623 ± 0.0560	0.006** (I)	0.055**
Senegalimassilia	0.0011 ± 0.0021	0.0011 ± 0.0026	0.0013 ± 0.0026	0.0008 ± 0.0019	0.279 (D		0.0007 ± 0.0018	0.0011 ± 0.0035	0.0008 ± 0.0019	0.0022 ± 0.0046	0.327 (I)	
Streptococcus	0.0262 ± 0.0513			0.0089 ± 0.0162		·	0.0180 ± 0.0341		0.0151 ± 0.0274		0.398 (D)	
Sutterella			0.0163 ± 0.0176		0.395 (I	· · · · · · · · · · · · · · · · · · ·	0.0095 ± 0.0152				0.008** (D)	
Turicibacter		0.0022 ± 0.0060		0.0024 ± 0.0074	0.308 (I	·	0.0019 ± 0.0041				0.464 (I)	
Veillonella		0.0022 ± 0.0000 0.0051 ± 0.0113			0.006** (D				0.0060 ± 0.0129		0.345 (D)	
P<0.05 and <0.01 are indicated by * and		0.0001 ± 0.0115	5.5652 ± 0.0125	0.0079	0.000 (D	, 0.007	5.0000 ± 0.0145	5.0004 ± 0.0140	0.0129	0.0071 ± 0.0079	5.575 (D)	0.437

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

Q<0.20 and <0.10 are indicated by * and **, respectively.

(D) indicates tendency to decrease, (I) indicates tendency to increase in relation to VFA

*1 Jonckheere test was used

*2 Q values were adjusted by false discovery rate (FDR)

Supplementary Table 3.	Relation of the relative	abundance of human gut	t microbial genera and VFA or BMI

	_	VFA				BMI					
	M Estimata			men P value		len Devolue		omen D velue			
enus	Estimate	1 value	Estimate	1 value	Estimate	1 value	Estimate	s i value			
Acidaminococcus	0.090	0.075	0.041	0.312	0.101	0.045*	0.060	0.139			
Akkermansia	-0.084	0.097	-0.054	0.186	-0.057	0.265	-0.061	0.133			
Alistipes	-0.009	0.861	-0.039	0.335	-0.012	0.814	-0.004	0.927			
Alloprevotella	0.037	0.466	0.010	0.797	0.008	0.868	-0.013	0.750			
Anaerostipes	-0.029	0.564	-0.098	0.015*	-0.016	0.750	-0.111	0.006**			
Bacteroides	-0.046	0.365	-0.062	0.128	-0.070	0.165	-0.090	0.027*			
Barnesiella	-0.001	0.989	-0.054	0.185	-0.003	0.951	-0.010	0.799			
Bifidobacterium	-0.135	0.008**		0.010**	-0.104	0.040*	-0.047	0.245			
Bilophila	0.018	0.715	0.015	0.707	0.034	0.500	-0.015	0.714			
Blautia	-0.154	0.002**		0.003**	-0.087	0.086	-0.117	0.004*			
Butyricicoccus	-0.035	0.493	0.010	0.814	-0.011	0.827	-0.027	0.513			
Catenibacterium	0.087	0.086	0.016	0.687	0.084	0.095	0.024	0.549			
Clostridium.IV	0.029	0.573	0.047	0.245	0.063	0.216	0.077	0.057			
Clostridium.sensu.stricto	0.027	0.599	0.144	< 0.001**		0.306	0.173	< 0.001			
Clostridium.XlVa	0.028	0.587	0.018	0.663	0.009	0.866	-0.017	0.668			
Clostridium.XIVb	0.090	0.076	-0.082	0.043*	0.093	0.066	-0.085	0.035			
Clostridium.XVIII	0.019	0.713	-0.056	0.168	0.013	0.793	-0.083	0.041			
Collinsella	0.057	0.259	0.015	0.718	0.015	0.761	0.021	0.612			
Coprococcus	-0.025	0.618	0.085	0.035*	0.037	0.464	0.062	0.124			
Dialister	0.093	0.067	0.044	0.283	0.070	0.167	0.072	0.074			
Dorea	0.005	0.919	0.087	0.032*	-0.013	0.793	0.090	0.026			
Eggerthella	-0.061	0.228	-0.129	0.001**	-0.013	0.054	-0.091	0.020			
Enterococcus	-0.069	0.170	0.042	0.297	-0.106	0.036*	0.068	0.024			
Erysipelotrichaceae incertae sedis	-0.055	0.170	-0.106	0.009**	-0.100	0.012*	-0.104	0.094			
Escherichia/Shigella	-0.055	0.274	0.038	0.352	-0.120	0.012*	0.040	0.324			
Faecalibacterium	-0.058	0.232	0.038	0.603	0.053	0.298	-0.004	0.924			
Flavonifractor	-0.033	0.290	-0.145	< 0.003		0.298	-0.115	0.920			
Fusicatenibacter	-0.028	0.767	0.047	0.243	0.019	0.706	0.058	0.004			
Fusicatembacter	0.011	0.833	-0.035	0.243	-0.045	0.378	-0.062	0.132			
Gemmiger	-0.073	0.833	0.059	0.394	-0.043	0.860	0.057	0.120			
Holdemanella	-0.073	0.148	0.039	0.148		0.030*	0.057				
Intestinibacter					0.110			0.185			
Klebsiella	-0.022	0.662	0.043	0.043*	-0.031	0.541	0.096				
	0.012	0.807	0.023	0.575	-0.012	0.821	0.063	0.123			
Lachnospiracea incertae sedis	-0.033	0.510	0.043	0.291	0.005	0.921	0.034	0.405			
Lactobacillus	0.010	0.849	0.086	0.034*	0.029	0.354	0.098	0.015			
Megamonas	0.083	0.100	0.049	0.222	0.034	0.503	0.030	0.467			
Megasphaera	0.036	0.480	0.114	0.005**	0.031	0.545	0.085	0.036			
Mitsuokella	0.036	0.473	0.068	0.095	0.059	0.242	0.046	0.262			
Odoribacter	-0.047	0.358	-0.037	0.365	-0.024	0.632	-0.026	0.518			
Oscillibacter	-0.012	0.813	0.001	0.988	0.011	0.834	0.025	0.538			
Parabacteroides	-0.067	0.184	-0.046	0.258	-0.072	0.158	-0.052	0.199			
Paraprevotella	0.007	0.888	0.046	0.259	0.013	0.796	0.046	0.258			
Parasutterella	0.050	0.323	0.099	0.015**	0.060	0.234	0.122	0.003*			
Phascolarctobacterium	0.065	0.199	-0.026	0.521	0.026	0.615	-0.017	0.684			
Prevotella	0.007	0.888	0.010	0.797	0.168	<0.001**		0.904			
Romboutsia	0.014	0.781	0.109	0.007**	0.066	0.195	0.154	< 0.001			
Roseburia	-0.024	0.638	0.104	0.010**	0.011	0.828	0.112	0.006*			
Ruminococcus	0.014	0.778	0.091	0.025*	0.053	0.297	0.097	0.017			
Senegalimassilia	-0.016	0.755	0.050	0.217	0.058	0.257	0.047	0.245			
Streptococcus	-0.002	0.960	-0.119	0.019**	-0.144	0.004**	0.007	0.871			
Sutterella	0.007	0.897	-0.119	0.003**	0.077	0.130	-0.106	0.009*			
Turicibacter	0.011	0.834	0.033	0.418	0.030	0.549	0.098	0.016			
Veillonella	-0.122	0.016*	-0.003	0.945	-0.147	0.004**	0.001	0.973			

Spearman's correlation coefficient was used.

Supplementary Table 4. Multiple regression analysis of association among Blautia and related factors

MEN			WOMEN		
	Estimate	P value ^{*1}		Estimate	P value ^{*1}
VFA	-1.09E-04	0.032*	VFA	-1.39E-04	0.015*
Age	-2.07E-02	0.175	Age	8.55E-05	0.528
			Smoking habit	6.08E-04	0.070
			Sleeptime	3.20E-03	0.074
			Walk speed	-4.28E-03	0.061

*P<0.05

*1 Step-wise method based on AIC criterion was used

Supplementary Table 5. Characteristics of the subjects in the confirmation group stratified by sex and VFA

Characteristics		Men		1	Nome	en e	P value
Visceral fat area (cm²)*1	95.4	±	47.6	63.6	±	34.4	<0.001**
Number		126			210		
Age (yr) ^{*1}	50.4	±	17.5	51.4	±	17.6	0.623
Height (cm) ^{*1}	168.7	±	6.8	156.0	±	6.7	<0.001**
Body weight (kg) ^{*1}	66.6	±	10.5	54.8	±	9.9	<0.001**
Body mass index (kg/m ²) ^{*1}	23.3	±	3.0	22.5	±	3.7	0.008**
Waist circumference (cm) ^{*1}	81.9	±	8.9	74.6	±	9.8	<0.001**
Serum Glucose (mg/dL) ^{*1}	5.15	±	0.91	5.13	±	1.73	0.030*
HbA1c (%) ^{*1}	5.8	±	0.5	5.9	±	0.9	0.580
SBP (mmHg) ^{*1}	127.0	±	16.0	122.7	±	20.5	0.012
DBP (mmHg) ^{*1}	78.2	±	11.8	72.7	±	11.8	<0.001**
Triglyceride (mg/dL) ^{*1}	1.3	±	0.8	1.0	±	0.8	< 0.001**
Total cholesterol (mg/dL) ^{*1}	5.0	±	0.9	5.3	±	1.1	0.054
HDL cholesterol (mg/dL) ^{*1}	1.5	±	0.4	1.7	±	0.4	<0.001**
LDL cholesterol (mg/dL) ^{*1}	2.9	±	0.7	3.0	±	0.9	0.478
Smoking habits (stick/d) ^{*1}	10.9	±	11.2	2.2	±	4.9	<0.001**
Sleep time (h/d) ^{*1}	7.1	±	1.3	6.9	±	1.2	0.138
Walk speed (sec/10m) ^{*1}	3.5	±	1.0	3.9	±	1.0	<0.001**
Habitual medicine use (% of Yes) ^{*2}		28.5%	Ď		29.0%	6	0.805
Hypertension ^{*2}		25.4%	þ		24.3%	ó	0.922
Hyperlipidaemia ^{*2}		11.1%	Ď		8.5%		0.565
Diabetes ^{*2}		7.1%			5.2%	•	0.634
Rheumatism ^{*2}		0.0%			0.5%	•	1.000
Total energy intake (kcal/d) ^{*1}	9004.1	±	2427.5	7027.9	±	2375.1	<0.001**
Carbohydrate intake ^{*1}	0.59	±	0.08	0.56	±	0.07	0.643
Fat intake ^{*1}	0.26	±	0.06	0.28	±	0.06	<0.001**
Protein intake ^{*1}	0.15	±	0.03	0.16	±	0.03	<0.001**
Alcohol consumption (g/d) ^{*1}	23.6	±	27.7	4.5	±	10.2	<0.001**
Total dietary fibre intake (g/d) ^{*1}	10.9	±	4.8	10.4	±	4.8	0.261
Diversity of intestinal microbiota ^{*1}	9.7	±	3.3	10.1	±	2.2	<0.001**

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

*1Wilcoxon rank-sum test was used

*2 test for equality of proportions was used