

**Table S1.** Target sequence of materials utilized in the study.

Target	Primer (5'-3')	Product size (bp)	Annealing temp.	Reference
Phylum: <i>Firmicutes</i>	F: GGAGYATGTGGTTTAATTCGAAGCA R: AGCTGACGACAACCATGCAC	126	60	Anaerobe 14:224 (2008)
<i>C. leptum</i> group (IV)	F: GTTGACAAAACGGAGGAAGG R: GACGGGCGGTGTGTACAA	245	60	JCM 52:398 (2014)
<i>Faecalibacterium prausnitzii</i>	F: AGATGGCCTCGCGTCCGA R: CCGAAGACCTTCTTCCTCC	199	60	JCM 52:398 (2014)
Phylum: <i>Bacteroidetes</i>	F: GGARCATGTGGTTTAATTCGATGAT R: AGCTGACGACAACCATGCAG	126	60	Anaerobe 14:224 (2008)
<i>Bacteroides</i>	F: GTCAGTTGTGAAAGTTTGC R: CAATCGGGAGTTCTTCGTG	127	60	JCM 52:398 (2014)
Phylum: <i>Actinobacteria</i>				
<i>Bifidobacterium</i>	F: AGGGTTTCGATTCTGCTCAG R: CATCCGGCATTACCACCC	156	60	JCM 52:398 (2014)
Phylum: <i>Proteobacteria</i>				
<i>Escherichia coli</i>	F: CATGCCGCGTGTATGAAGAA R: CGGGTAACGTCAATGAGCAAA	96	60	PEDIATRICS118(2):511-21 (2006)
Phylum: <i>Verrucomicrobia</i>				
<i>Akkermansia muciniphila</i>	F: CAGCACGTGAAGGTGGGGAC R: CCTTGCGTTGGCTTCAGAT	327	60	Obesity 2257-2261 (2012)
Total bacteria	F: ACTCCTACGGGAGGCAGCAGT R: GTATTACCGCGGCTGCTGGCAC	200	60	JCM 52:398 (2014)

**Table S2.** The microbiome distribution of study participates stratified by different medication.

	Entire Cohort (n=154)	SU user (n=71)	Non-SU user (n=83)	Insulin user (n=29)	Non-Insulin user (n=125)	Metformin user (n=132)	Non- Metformin user (n=22)	DPP-4 inhibitor user (n=112)	Non-DPP-4 inhibitor user (n=42)
<i>Firmicutes</i> , copies*10 <sup>9</sup> /g	4.4(2.3,7.2)	4.4(2.2,6.9)	4.5(2.6,8.2)	<b>3.2(1.4,5.3)</b>	<b>4.8(2.7,8.1)</b>	4.5(2.5,7.8)	4.1(1.8,6.2)	4.7(2.6,7.0)	3.6(1.7,8.2)
<i>Bacteroidetes</i> , copies*10 <sup>9</sup> /g	8.9(3.8,17.2)	8.3(3.6,14.6)	9.9(4.3,18.3)	8.6(3.3,15.7)	9.1(3.9,17.5)	8.9(3.8,17.2)	8.1(3.6,17.1)	8.6(3.8,18.2)	10.1(3.7,14.8)
<i>Firmicutes/Bacteroidetes</i>	0.5(0.2,1.1)	0.5(0.3,1.3)	0.5(0.3,1.1)	0.5(0.2,1.0)	0.5(0.3,1.2)	0.5(0.3,1.2)	0.5(0.3,1.0)	0.5(0.3,1.2)	0.5(0.3,1.2)
<i>C. leptum</i> group, copies*10 <sup>8</sup> /g	5.9(2.2,11.6)	4.8(2.1,9.7)	7.8(2.3,12.2)	4.3(2.3,9.1)	6.4(2.2,12.0)	6.1(2.0,11.4)	5.5(3.5,13.2)	6.5(2.9,11.7)	4.4(0.9,10.8)
<i>F. prausnitzii</i> , copies*10 <sup>7</sup> /g	11.0(2.0,28.3)	<b>8.3(0.9,21.4)</b>	<b>15.1(3.3,43.8)</b>	<b>4.0(2.0,13.0)</b>	<b>12.8(2.3,30.6)</b>	9.6(1.9,28.5)	13.8(5.8,24.6)	11.4(2.4,27.0)	8.1(1.2,34.5)
<i>Bacteroides</i> , copies*10 <sup>9</sup> /g	1.6(0.8,3.6)	1.4(0.9,3.4)	1.7(0.8,3.9)	1.4(0.8,3.2)	1.6(0.9,3.6)	1.6(0.9,3.6)	1.5(0.8,3.8)	1.6(0.9,3.5)	1.8(0.5,3.8)
<i>Bifidobacterium</i> , copies*10 <sup>6</sup> /g	3.6(0.3,13.8)	2.6(0.2,9.2)	4.3(0.4,15.7)	<b>0.7(0.1,5.8)</b>	<b>4.4(0.4,14.8)</b>	3.9(0.3,14.1)	2.7(0.2,10.8)	3.4(0.2,11.7)	4.1(0.5,18.9)
<i>A. muciniphila</i> , copies*10 <sup>4</sup> /g	0.8(0.2, 410.0)	0.8(0.2,852.2)	0.8(0.2,368.4)	0.8(0.2,2078.0)	0.8(0.2,386.0)	<b>0.7(0.2,158.5)</b>	<b>86.0(0.4,7743.6)</b>	0.9(0.2,530.7)	0.9(0.4,89.8)
<i>E.coli</i> , copies*10 <sup>8</sup> /g	1.2(0.3,5.9)	<b>2.0(0.5,11.7)</b>	<b>1.0(0.2,4.5)</b>	3.3(0.3,17.2)	1.2(0.3,5.8)	1.4(0.3,6.0)	0.9(0.06,6.7)	<b>1.6(0.3,11.5)</b>	<b>0.9(0.3,3.3)</b>