

Supplementary Material

TABLE S.1. Median (25th, 75th percentile) relative abundance of the seven most abundant bacterial families according to group

Family	Control	BLISS	Mean difference (95% CI) ^a	p-value
<i>Bifidobacteriaceae</i>				
7 mth	38 (9,45)	44 (38,55)	9.9 (-3.9,24)	0.156
12 mth	22 (12,32)	20 (8,30)	0.2 (-9.0,9.4)	0.966
<i>Enterobacteriaceae</i>				
7 mth	10 (3,20)	6 (4,20)	-3.0 (-12,5.9)	0.502
12 mth	1 (0,2)	0 (0,3)	-0.0 (-0.9,0.9)	0.948
<i>Veillonellaceae</i>				
7 mth	4 (1,6)	1 (0,4)	-0.9 (-0.3,1.4)	0.445
12 mth	1 (0,3)	1 (1,3)	0.2 (-1.1,1.5)	0.775
<i>Bacteroidaceae</i>				
7 mth	12 (0,24)	4 (0,19)	-3.8 (-16,8.6)	0.546
12 mth	8 (1,14)	8 (0,20)	-0.0 (-9.3,9.3)	0.999
<i>Erysipelotrichaceae</i>				
7 mth	1 (0,2)	1 (0,4)	0.5 (-1.0,1.9)	0.500
12 mth	2 (1,3)	2 (1,4)	0.6 (-0.6,1.7)	0.345
<i>Lachnospiraceae</i>				
7 mth	11 (1,26)	7 (1,25)	-0.1 (-12,12)	0.981
12 mth	35 (25,42)	29 (14,40)	-8.3 (-19,2.2)	0.119
<i>Ruminococcaceae</i>				
7 mth	0 (0,1)	0 (0,1)	-0.1 (-0.4,0.6)	0.786
12 mth	12 (4,21)	10 (1,16)	-4.9 (-13,3.4)	0.240

Abbreviations: BLISS, Baby-Led Introduction to Solids; mth, month.

^a Mean difference using quantile regression

TABLE S.2. Median (25th,75th percentile) relative abundance of the seven most abundant bacterial families at 7 and 12 months

Family	7 months (n=73)	12 months (n=68)	Mean difference (95% CI) ^a (n=141)	p-value
<i>Bifidobacteriaceae</i> ^b	42 (24,55)	21 (11,31)	-16 (-21,-10)	<0.001
<i>Enterobacteriaceae</i>	7.2 (2.9,20)	0.6 (0.2,2.5)	-8.9 (-12,-5.8)	<0.001
<i>Veillonellaceae</i>	2.2 (0.5,5.2)	1.1 (0.6,3.1)	-1.9 (-3.4,-0.3)	0.020
<i>Bacteroidaceae</i>	6.0 (0.0,22)	8.0 (1.0,19)	-2.5 (-6.9,1.9)	0.272
<i>Erysipelotrichaceae</i>	0.9 (0.1,3.2)	1.9 (1.1,3.3)	0.4 (-1.0,1.7)	0.586
<i>Lachnospiraceae</i>	9.0 (1.5,26)	32 (19,41)	16 (12,21)	<0.001
<i>Ruminococcaceae</i>	0.1 (0.0,0.9)	10 (1.6,19)	9.4 (7.3,12)	<0.001

^a Mean difference using mixed regression model with participant identification number as a random effect.

^b p-for-interaction between group and time was close to significance at p = 0.050, with the BLISS group having a greater mean decrease (95% CI) (-21 (-29,-13)) compared to the Control group (-11 (-18,-3.3)).

Table S.3: OTUs in which a difference of >=10 individuals (presence) was observed between dietary groups

Phylum	Class	Order	Family	Genus	Species	OTU ^a	BLISS 07M n=36			Control 07M n=37			BLISS 12M n=34			Control 12M n=34			Delta* 07M	Delta* 12M
							Prevalence	count > 0	Mean Abundance	Prevalence	count > 0	Mean Abundance	Prevalence	count > 0	Mean Abundance	Prevalence	count > 0	Mean Abundance		
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Ruminococcus	OTU_981117	22.22%	8	0.001%	24.32%	9	0.002%	52.94%	18	0.007%	85.29%	29	0.020%	-1	-11
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	uncultured bacterium	OTU_189986	2.78%	1	0.000%	0.00%	0	0.000%	8.82%	3	0.001%	41.18%	14	0.002%	1	-11
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Eubacterium	rectale	OTU_126593	5.56%	2	0.001%	21.62%	8	0.004%	38.24%	13	0.008%	67.65%	23	0.029%	-6	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Incertae Sedis	uncultured bacterium	OTU_184758	5.56%	2	0.004%	5.41%	2	0.001%	17.65%	6	0.000%	47.06%	16	0.003%	0	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	faecis	OTU_66323	13.89%	5	0.004%	18.92%	7	0.005%	47.06%	16	0.015%	76.47%	26	0.043%	-2	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	uncultured bacterium	OTU_73320	11.11%	4	0.002%	10.81%	4	0.001%	35.29%	12	0.010%	76.47%	26	0.024%	0	-14
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	uncultured organism	OTU_54	22.22%	8	0.016%	45.95%	17	0.007%	41.18%	14	0.298%	73.53%	25	0.651%	-9	-11
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia		OTU_4232	16.67%	6	0.001%	21.62%	8	0.000%	32.35%	11	0.008%	70.59%	24	0.152%	-2	-13
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia		OTU_98034	8.33%	3	0.001%	10.81%	4	0.005%	35.29%	12	0.020%	70.59%	24	0.023%	-1	-12
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia		OTU_252387	0.00%	0	0.000%	0.00%	0	0.000%	2.94%	1	0.000%	35.29%	12	0.002%	0	-11
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia		OTU_141281	5.56%	2	0.001%	5.41%	2	0.001%	20.59%	7	0.006%	50.00%	17	0.011%	0	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	uncultured	uncultured bacterium	OTU_221083	0.00%	0	0.000%	0.00%	0	0.000%	0.00%	0	0.000%	38.24%	13	0.001%	0	-13
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	uncultured	uncultured bacterium	OTU_44413	5.56%	2	0.000%	13.51%	5	0.005%	35.29%	12	0.011%	64.71%	22	0.035%	-3	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	uncultured	uncultured bacterium	OTU_222918	0.00%	0	0.000%	5.41%	2	0.000%	29.41%	10	0.008%	58.82%	20	0.016%	-2	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			OTU_278989	0.00%	0	0.000%	5.41%	2	0.000%	17.65%	6	0.001%	55.88%	19	0.006%	-2	-13
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			OTU_142101	2.78%	1	0.000%	5.41%	2	0.001%	26.47%	9	0.003%	61.76%	21	0.010%	-1	-12
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			OTU_81464	8.33%	3	0.001%	5.41%	2	0.003%	26.47%	9	0.002%	61.76%	21	0.007%	1	-12
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			OTU_131961	2.78%	1	0.000%	0.00%	0	0.000%	8.82%	3	0.001%	38.24%	13	0.002%	1	-10
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			OTU_204587	0.00%	0	0.000%	5.41%	2	0.000%	14.71%	5	0.000%	44.12%	15	0.002%	-2	-10
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	prausnitzii	OTU_182325	0.00%	0	0.000%	5.41%	2	0.000%	26.47%	9	0.006%	61.76%	21	0.010%	-2	-12
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	prausnitzii	OTU_302854	2.78%	1	0.000%	10.81%	4	0.001%	23.53%	8	0.003%	55.88%	19	0.006%	-3	-11
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	thetaiotaomicron	OTU_87946	22.22%	8	0.006%	48.65%	18	0.024%	35.29%	12	0.002%	38.24%	13	0.008%	-10	-1
Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella	parvula_denticariosi	OTU_288390	52.78%	19	0.118%	78.38%	29	0.144%	61.76%	21	0.050%	58.82%	20	0.034%	-10	1
Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera	micronuciformis	OTU_120	30.56%	11	0.107%	56.76%	21	0.039%	61.76%	21	0.126%	38.24%	13	0.112%	-10	8
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Ruminococcus_gnavus	OTU_127554	25.00%	9	0.003%	35.14%	13	0.005%	50.00%	17	0.006%	17.65%	6	0.010%	-4	11
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum		OTU_143101	11.11%	4	0.006%	16.22%	6	0.001%	41.18%	14	0.002%	8.82%	3	0.000%	-2	11

^a - OTU number was generated as part of VSEARCH sequence clustering

* - Delta = individuals with OTU present in BLISS group - individuals with OTU present in Control group

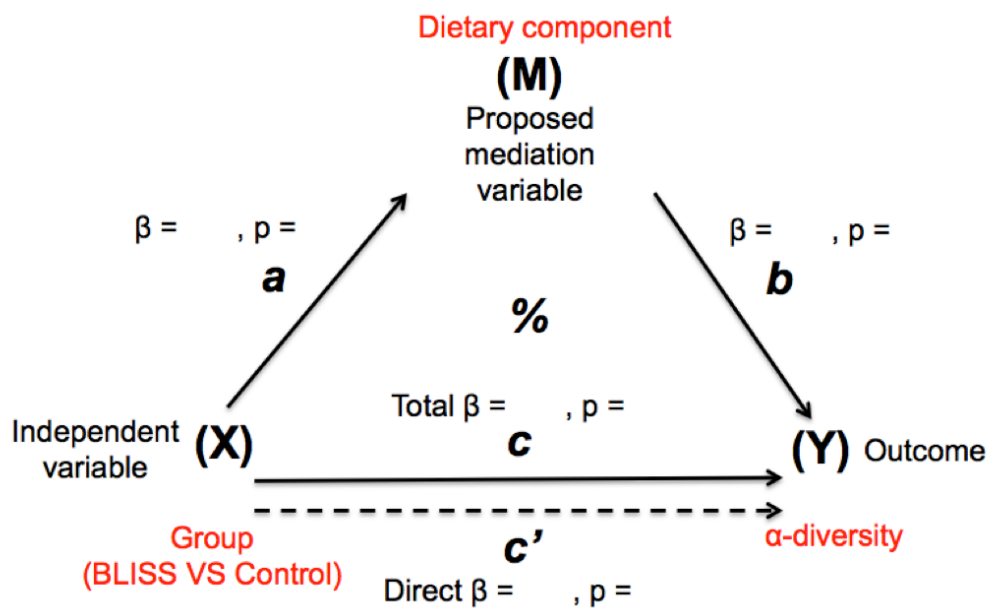


FIG S.1. Illustration of a single mediation model.

As adapted from Fairchild and McDaniel [1] and Fairchild and MacKinnon [2].

Note: X= the independent variable; Y= the dependent variable; and M= the mediating variable. $c=ab+c'$: The mediation model breaks down the total effect of X on Y (i.e. c), into two parts: the indirect effect of X on Y through M, quantified by ab (the product of a and b), and the direct effect of X on Y controlling for M, quantified by c' . %: Represents the proportion of the total effect that is mediated. β is the effect size and p is the p-value for the effect.

REFERENCES

1. Fairchild AJ, McDaniel HL. 2017. Best (but oft-forgotten) practices: mediation analysis. *Am J Clin Nutr* 105:1259-1271.
2. Fairchild AJ, MacKinnon DP. 2009. A General Model for Testing Mediation and Moderation Effects. *Prev Sci* 10:87-99.