

**Supplementary Table S1:** Demographic characteristics and self-reported health issues at enrollment

	<b>Peanut</b>		<b>P</b>
	<b>Control</b>	<b>intervention</b>	
	(N=43)	(N=35)	
	n (%) / Mean $\pm$ sd	n (%) / Mean $\pm$ sd	
Age (years old)	56.2 $\pm$ 9.0	54.9 $\pm$ 8.6	
Under 50 years old	14 (32.6)	10 (28.6)	0.171
50-59 years old	8 (18.6)	13 (37.1)	
60+ years old	21 (48.8)	12 (34.3)	
Gender			
Male	21 (48.8)	21 (60.0)	0.325
Female	22 (51.2)	14 (40.0)	
BMI (kg/m <sup>2</sup> )	23.9 $\pm$ 2.4	24.3 $\pm$ 2.5	
Normal weight (18.5 – 22.9)	16 (37.2)	12 (34.3)	0.427
Asian Overweight (23-24.9)	13 (30.2)	7 (20.0)	
Asian obese (25+)	14 (32.6)	16 (45.7)	
<b>Self-report during past 3 months</b>			
Diabetes	4 (9.3)	2 (5.7)	0.686
Hypertension	11 (25.6)	4 (11.4)	0.153
Hyperlipidemia	13 (30.2)	10 (28.6)	0.873
Infection requiring antibiotic treatment	1 (2.3)	2 (5.7)	0.585
Health issue changed diet habits	2 (4.7)	0 (0.0)	0.499
Health issue changed bowel movements	4 (9.3)	0 (0.0)	0.123
Food allergy	1 (2.3)	2 (5.7)	0.585
Constipation	2 (4.7)	0 (0.0)	0.499
Gain or loss of more than 2.5 kg of weight	0 (0.0)	0 (0.0)	1.000

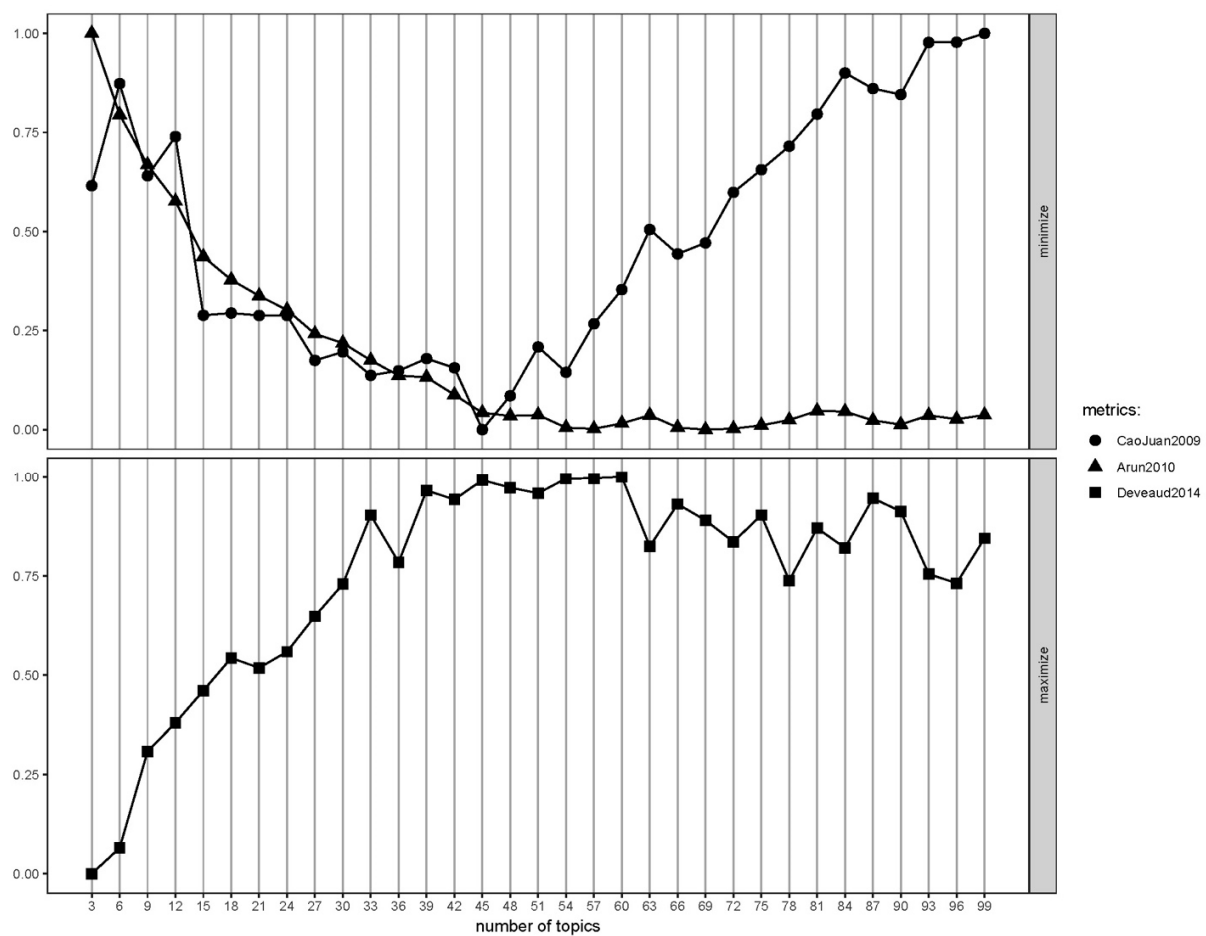
**Supplementary Table S2: Average daily intake of food groups**

Food groups	Control			Intervention			Control	Intervention	P
	Baseline	Weeks 16 Follow-up	P	Baseline	Weeks 16 Follow-up	P	Combined baseline & weeks 16 FU	Combined baseline & weeks 16 FU	
	N=43	N=43		N=35	N=35		N=43	N=35	
	Mean ± sd	Mean ± sd		Mean ± sd	Mean ± sd		Mean ± sd	Mean ± sd	
Grain (g/d)	299.0±91.7	283.1±94.5	0.279	295.4±94.2	286.2±105.9	0.461	291.1±80.1	209.8±93.4	0.989
Staple foods (g/d)	14.6±28.8	10.1±22.9	0.277	8.1±18.8	6.2±19.2	0.549	12.3±18.2	7.1±13.3	0.102
Fruit (g/d)	149.1±112.1	125.1±105.5	0.234	101.4±89.0	123.4±100.5	0.403	137.1±93.3	112.4±73.5	0.285
Vegetables (g/d)	96.7±66.6	111.5±84.8	0.391	96.2±73.2	75.2±65.5	0.065	104.1±53.6	85.7±52.9	0.069
Legumes (g/d)	7.2±19.0	7.2±21.1	0.613	5.2±15.0	4.1±11.7	0.715	7.5±14.2	4.6±8.9	0.661
Red meats (g/d)	78.0±51.6	87.6±66.5	0.491	90.6±94.9	78.5±57.7	0.812	82.8±44.2	84.6±65.3	0.648
Poultry (g/d)	37.7±51.5	72.1±74.0	0.023	53.8±60.4	57.3±65.9	0.773	54.9±47.5	55.5±47.9	0.844
Fish & Shrimp (g/d)	54.5±53.9	40.1±35.9	0.095	63.4±86.6	55.0±58.0	0.870	47.3±39.0	59.2±48.1	0.280
Eggs (g/d)	17.4±19.4	14.5±17.5	0.458	12.3±17.2	18.5±26.6	0.347	16.0±14.0	15.4±16.9	0.596
Dairy products (g/d)	25.6±58.5	18.0±49.5	0.220	28.6±47.2	23.7±64.5	0.251	21.8±47.9	26.2±47.2	0.686
Soybean products (g/d)	18.4±37.8	11.8±21.1	0.270	7.1±16.4	8.0±16.0	0.656	15.1±21.3	7.5±10.6	0.081
Another nut* (g/d)	0.4±2.5	0.5±2.6	0.573	0.3±1.7	0.0±0.0	0.317	0.4±1.8	0.1±0.8	0.408

<sup>1</sup> Comparing the mean of average daily nutrient intake between 24HDR at baseline and 24HDR at the 16-week follow-up: Paired T-tests were used for food groups with normal distribution; Wilcoxon signed-rank tests were used for food groups with no normal distribution.

<sup>2</sup> Comparing the mean of average daily nutrient intake combined 24HDR at baseline and post-16 weeks between control and intervention: T-tests were used for food groups with normal distribution; Wilcoxon rank-sum tests were used for food groups with no normal distribution.

\* Other nuts, including walnuts, lotus seeds, pumpkin seeds, etc. Legume: beans and Peas

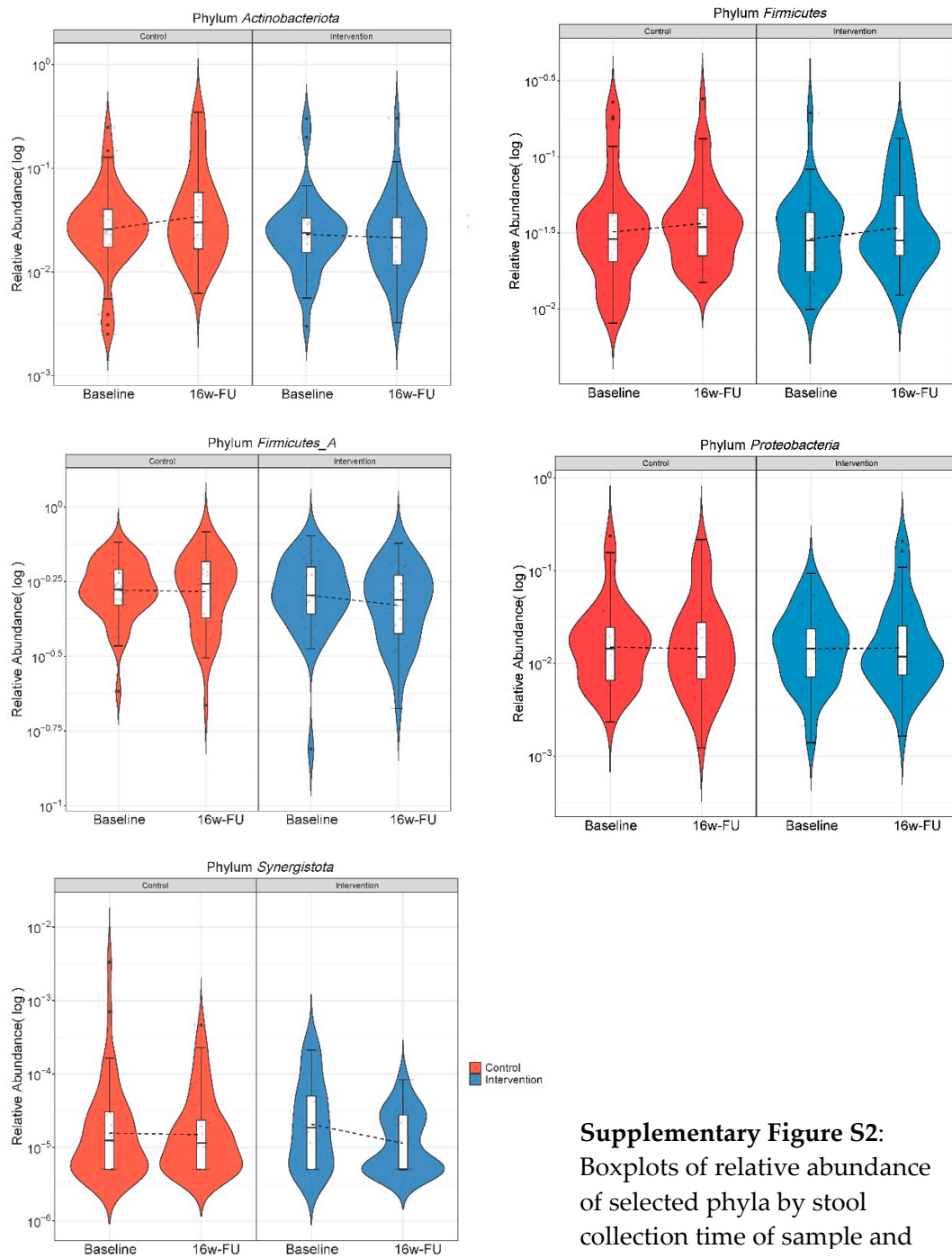


**Supplementary Figure S1:** Model fitness estimation of the number of species-level sub-communities using Latent Dirichlet Allocation

**Supplementary Table S3.** Change in relative abundance between weeks 16 follow-up and baseline in selected individual microbial taxa

Microbial taxa	Control		Intervention		Change between 16w-FU and baseline	
	Baseline	16w-FU	Baseline	16w-FU	Control	Intervention
	RA, median (%)	RA, median (%)	RA, median (%)	RA, median (%)	Absolute change, median (%)	Absolute change, median (%)
Phylum <i>Actinobacteriota</i>	2.6	3.0	2.4	2.1	0.2	-0.1
Class <i>Coriobacteriia</i>	1.9	2.1	1.8	1.5	0.2	-0.3
Order <i>Coriobacteriales</i>	1.9	2.1	1.8	1.5	0.2	-0.3
Phylum <i>Firmicutes</i>	2.9	3.5	2.8	2.8	0.5	0.2
Class <i>Bacilli</i>	2.9	3.5	2.8	2.8	0.5	0.2
Order <i>Erysipelotrichales</i>	1.7	1.7	1.4	1.8	0.0	0.2
Phylum <i>Firmicutes A</i>	53.0	55.4	50.6	48.9	2.4	-1.6
Class <i>Clostridia</i>	53.0	55.4	50.6	48.9	2.4	-1.6
Phylum <i>Proteobacteria</i>	1.4	1.2	1.4	1.2	0.2	0.0
Class <i>Gammaproteobacteria</i>	1.4	1.2	1.4	1.2	0.2	0.0
Phylum <i>Synergistota</i>	1.25x10 <sup>-3</sup>	1.15x10 <sup>-3</sup>	0.0	0.0	0.0	0.0
Class <i>Synergistia</i>	1.25x10 <sup>-3</sup>	1.15x10 <sup>-3</sup>	0.0	0.0	0.0	0.0

RA: Relative abundance



**Supplementary Figure S2:**  
Boxplots of relative abundance  
of selected phyla by stool  
collection time of sample and

**Supplementary Table S4:** Association of peanut intervention with 45 species levels subgroups

Subgroup and top 5 species	$\beta$ (SE)	P	FDR
<b>Subgroup 1</b> MGYG-HGUT-00200 (53.34%), <i>Faecalicatena faecis</i> (11.75%), <i>Anaerostipes hadrus</i> (2.94%), <i>Blautia A</i> sp900066165 (2.56%), MGYG-HGUT-02772 (1.62%)	-4.633 (1.415)	1.33x10 <sup>-3</sup>	0.020
<b>Subgroup 2</b> <i>Faecalibacterium prausnitzii</i> G (38.92%), <i>Faecalicatena faecis</i> (19.10%), <i>Bacteroides uniformis</i> (3.99%), <i>Bacteroides A plebeius</i> (2.96%), <i>Parabacteroides distasonis</i> (2.89%)	-1.824 (1.223)	0.138	0.398
<b>Subgroup 3</b> CAG-127 sp900319515 (24.86%), <i>Ruminococcus C callidus</i> (8.00%), <i>Lachnospira rogosae</i> (6.99%), <i>Acetatifactor</i> sp900066365 (4.34%), <i>Blautia A wexlerae</i> (4.15%)	-2.329 (1.836)	0.207	0.489
<b>Subgroup 4</b> <i>Prevotella copri A</i> (31.49%), MGYG-HGUT-02603 (10.89%), MGYG-HGUT-03347 (9.28%), MGYG-HGUT-02834 (4.48%), MGYG-HGUT-00644 (3.77%)	-0.082 (1.545)	0.958	0.991
<b>Subgroup 5</b> <i>Bacteroides eggerthii</i> (14.19%), <i>Bacteroides uniformis</i> (12.47%), <i>Bacteroides B dorei</i> (6.97%), <i>Blautia A wexlerae</i> (5.37%), <i>Bacteroides B massiliensis</i> (4.08%)	0.057 (1.672)	0.973	0.991
<b>Subgroup 6</b> <i>Megamonas funiformis</i> (32.72%), <i>Prevotella copri</i> (14.52%), <i>Prevotella</i> sp000436915 (4.72%), <i>Faecalibacterium prausnitzii C</i> (3.32%), <i>Blautia A massiliensis</i> (2.63%)	-4.629 (1.962)	0.020	0.110
<b>Subgroup 7</b> <i>Roseburia inulinivorans</i> (24.12%), <i>Bacteroides B dorei</i> (4.33%), <i>Faecalicatena torques</i> (3.93%), <i>Holdemanella</i> sp002299315 (3.71%), <i>Dorea longicatena B</i> (3.34%)	-6.125 (1.804)	8.85x10 <sup>-4</sup>	0.020
<b>Subgroup 8</b> <i>Faecalibacterium prausnitzii J</i> (14.12%), <i>Prevotella copri</i> (9.63%), <i>Bacteroides B dorei</i> (8.52%), MGYG-HGUT-03699 (3.75%), KLE1615 sp900066985 (3.43%)	0.9 (1.589)	0.572	0.786
<b>Subgroup 9</b> <i>Bacteroides B dorei</i> (30.17%), <i>Bacteroides stercoris</i> (21.64%), <i>Megamonas funiformis</i> (15.55%), <i>Faecalicatena gnavus</i> (4.91%), <i>Parabacteroides distasonis</i> (4.41%)	-1.359 (2.184)	0.535	0.786
<b>Subgroup 10</b> <i>Eubacterium R</i> sp000436835 (19.31%), <i>Agathobacter rectale</i> (9.93%), <i>Coprococcus B comes</i> (5.11%), <i>Dorea longicatena</i> (3.86%), <i>Faecalibacterium prausnitzii K</i> (3.69%)	-0.939 (1.793)	0.601	0.793
<b>Subgroup 11</b>	-3.111 (1.691)	0.068	0.304

Subgroup and top 5 species	$\beta$ (SE)	P	FDR
<i>Blautia A wexlerae</i> (20.95%), <i>Fusicatenibacter saccharivorans</i> (16.09%), <i>Anaerostipes hadrus</i> (5.05%), CAG-56 sp900066615 (3.31%), <i>Eubacterium</i> <i>E hallii</i> A (2.96%)			
<b>Subgroup 12</b>	-2.562 (1.489)	0.087	0.304
<i>Streptococcus salivarius</i> (32.07%), <i>Streptococcus vestibularis</i> (11.10%), <i>Streptococcus</i> sp001556435 (5.90%), CAG-56 sp900066615 (4.92%), <i>Dorea</i> <i>longicatena</i> B (4.75%)			
<b>Subgroup 13</b>	0.71 (1.417)	0.617	0.793
<i>Prevotella copri</i> A (7.95%), <i>Prevotella stercora</i> (6.36%), <i>Blautia A wexlerae</i> (4.17%), <i>Ruminococcus D bicirculans</i> (3.95%), <i>Acetatifactor</i> sp900066365 (3.44%)			
<b>Subgroup 14</b>	0.021 (1.922)	0.991	0.991
<i>Faecalibacterium prausnitzii</i> E (13.58%), <i>Blautia</i> sp000436935 (9.38%), <i>Lachnospira eligens</i> B (4.87%), KLE1615 sp900066985 (4.15%), TF01-11 sp003529475 (3.48%)			
<b>Subgroup 15</b>	-2.838 (1.085)	9.84x10 <sup>-3</sup>	0.074
<i>Bifidobacterium pseudocatenulatum</i> (66.15%), <i>Anaerostipes hadrus</i> (6.14%), <i>Fusicatenibacter saccharivorans</i> (3.62%), <i>Dorea longicatena</i> B (3.12%), <i>Faecalibacterium prausnitzii</i> D (1.80%)			
<b>Subgroup 16</b>	-0.313 (1.443)	0.829	0.91
<i>Faecalibacterium prausnitzii</i> C (12.00%), <i>Blautia A wexlerae</i> (6.24%), <i>Blautia A massiliensis</i> (4.26%), <i>Blautia A</i> sp900066165 (4.11%), <i>Fusicatenibacter saccharivorans</i> (3.61%)			
<b>Subgroup 17</b>	-1.888 (1.7)	0.269	0.576
<i>Faecalicatena faecis</i> (16.60%), <i>Prevotella copri</i> (8.99%), <i>Faecalibacterium</i> <i>prausnitzii</i> K (5.18%), <i>Faecalicatena lactaris</i> (3.71%), <i>Fusicatenibacter</i> <i>saccharivorans</i> (3.45%)			
<b>Subgroup 18</b>	-4.741 (1.98)	0.018	0.110
<i>Bacteroides B massiliensis</i> (34.24%), <i>Bacteroides B dorei</i> (14.05%), <i>Faecalicatena torques</i> (10.41%), <i>Bacteroides B sartorii</i> (3.12%), MGYG- HGUT-02610 (3.10%)			
<b>Subgroup 19</b>	-0.864 (1.544)	0.577	0.786
<i>Prevotella copri</i> (41.57%), <i>Megamonas funiformis</i> (10.59%), <i>Prevotella copri</i> A (6.36%), MGYG-HGUT-04456 (3.05%), <i>Alistipes putredinis</i> (2.39%)			
<b>Subgroup 20</b>	1.555 (1.777)	0.383	0.690
<i>Lachnospira eligens</i> B (18.31%), <i>Bacteroides B dorei</i> (16.96%), <i>Bacteroides</i> <i>caccae</i> (11.31%), <i>Lachnospira</i> sp003537285 (4.84%), MGYG-HGUT-03899 (2.67%)			
<b>Subgroup 21</b>	-4.664 (1.351)	7.23x10 <sup>-4</sup>	0.020
<i>Escherichia coli</i> D (63.50%), <i>Escherichia fergusonii</i> (6.90%), <i>Escherichia</i> sp000208585 (3.76%), <i>Bacteroides stercoris</i> (2.37%), <i>Lachnospira rogosae</i> (1.95%)			
<b>Subgroup 22</b>	2.89 (1.714)	0.094	0.304
<i>Prevotella copri</i> (19.60%), <i>Alistipes putredinis</i> (10.07%), <i>Blautia A obeum</i> (2.78%), <i>Blautia A</i> sp900066165 (2.62%), KLE1615 sp900066985 (2.34%)			
<b>Subgroup 23</b>	0.904 (1.574)	0.567	0.786

Subgroup and top 5 species	$\beta$ (SE)	P	FDR
<i>Prevotella</i> sp000434515 (30.04%), <i>Prevotella</i> copri (16.45%), MGYG-HGUT-04456 (3.67%), <i>Acetatifactor</i> sp900066365 (2.65%), MGYG-HGUT-00200 (2.00%)			
<b>Subgroup 24</b>	-4.91 (1.733)	5.26x10 <sup>-3</sup>	0.059
<i>Ruminococcus D bicirculans</i> (26.69%), <i>Faecalibacterium prausnitzii</i> D (11.07%), <i>Fusicatenibacter saccharivorans</i> (10.02%), <i>Blautia A</i> sp900066165 (4.28%), <i>Bacteroides stercoris</i> (3.45%)			
<b>Subgroup 25</b>	2.192 (1.554)	0.161	0.425
<i>Prevotella</i> sp000436035 (20.77%), <i>Prevotella</i> copri (9.93%), MGYG-HGUT-00644 (7.46%), <i>Prevotella</i> sp002265625 (4.02%), <i>Prevotellamassilia timonensis</i> (3.39%)			
<b>Subgroup 26</b>	-2.979 (1.699)	0.082	0.304
<i>Ruminococcus E bromii</i> B (54.20%), <i>Ruminococcus E bromii</i> (14.56%), <i>Bacteroides B dorei</i> (4.49%), <i>Bacteroides ovatus</i> (2.17%), <i>Blautia A obeum</i> (2.13%)			
<b>Subgroup 27</b>	0.416 (1.875)	0.825	0.910
<i>Bacteroides uniformis</i> (15.74%), <i>Bacteroides stercoris</i> (13.28%), MGYG-HGUT-00200 (7.66%), <i>Bacteroides B dorei</i> (5.22%), <i>Acetatifactor</i> sp900066565 (4.96%)			
<b>Subgroup 28</b>	-1.564 (1.56)	0.318	0.622
<i>Agathobacter rectale</i> (65.63%), MGYG-HGUT-02670 (10.16%), <i>Fusicatenibacter saccharivorans</i> (1.55%), <i>Blautia A massiliensis</i> (1.33%), MGYG-HGUT-01186 (1.05%)			
<b>Subgroup 29</b>	0.833 (1.887)	0.66	0.825
<i>Prevotella</i> copri (72.58%), MGYG-HGUT-04456 (3.73%), MGYG-HGUT-00644 (2.22%), <i>Prevotella</i> sp000434515 (1.61%), MGYG-HGUT-00553 (1.55%)			
<b>Subgroup 30</b>	1.065 (1.454)	0.465	0.776
<i>Megamonas funiformis</i> (9.87%), <i>Faecalicatena gnavus</i> (7.62%), <i>Blautia A wexlerae</i> (7.49%), <i>Prevotella</i> sp000436915 (6.87%), MGYG-HGUT-02303 (6.17%)			
<b>Subgroup 31</b>	-2.28 (1.542)	0.142	0.398
<i>Bacteroides A plebeius A</i> (68.78%), <i>Bacteroides A plebeius</i> (11.73%), <i>Faecalicatena faecis</i> (4.32%), <i>Bacteroides uniformis</i> (2.47%), <i>Anaerostipes hadrus</i> (1.17%)			
<b>Subgroup 32</b>	-0.854 (1.036)	0.411	0.712
<i>Prevotella</i> sp000434975 (47.92%), <i>Prevotella stercorea</i> (3.96%), <i>Blautia A wexlerae</i> (3.82%), <i>Faecalibacterium prausnitzii</i> E (3.48%), MGYG-HGUT-03899 (2.08%)			
<b>Subgroup 33</b>	-2.137 (1.77)	0.229	0.515
<i>Faecalicatena faecis</i> (13.99%), <i>Romboutsia timonensis</i> (9.64%), MGYG-HGUT-00839 (9.11%), CAG-56 sp900066615 (7.42%), <i>Dorea longicatena B</i> (4.45%)			
<b>Subgroup 34</b>	1.031 (1.531)	0.502	0.786



Subgroup and top 5 species	$\beta$ (SE)	P	FDR
<i>Prevotella</i> sp002265625 (27.80%), <i>Faecalicatena faecis</i> (5.84%), <i>Prevotellamassilia timonensis</i> (5.39%), <i>Prevotella copri</i> A (4.37%), <i>Roseburia inulinivorans</i> (3.55%)			
<b>Subgroup 35</b> <i>Holdemanella biformis</i> (30.75%), <i>Blautia A wexlerae</i> (8.45%), <i>Holdemanella</i> sp002299315 (3.05%), <i>Dorea formicigenerans</i> (2.76%), <i>Dorea longicatena</i> (2.51%)	-4.001 (1.450)	6.56x10 <sup>-3</sup>	0.059
<b>Subgroup 36</b> <i>Klebsiella pneumoniae</i> (47.50%), <i>Holdemanella</i> sp002299315 (3.64%), MGYG-HGUT-03899 (2.78%), MGYG-HGUT-00245 (2.37%), <i>Bacteroides</i> <i>B dorei</i> (2.31%)	-3.409 (1.562)	0.031	0.153
<b>Subgroup 37</b> <i>Acetatifactor</i> sp900066565 (21.38%), <i>Bacteroides B massiliensis</i> (10.99%), <i>Faecalibacterium</i> sp003449675 (6.03%), MGYG-HGUT-00245 (4.91%), <i>Species</i> KLE1615 sp900066985 (3.88%)	0.584 (1.593)	0.715	0.869
<b>Subgroup 38</b> <i>Bacteroides B sartorii</i> (23.86%), <i>Bacteroides thetaiotaomicron</i> (13.79%), <i>Bacteroides uniformis</i> (8.12%), <i>Parabacteroides merdae</i> (7.99%), <i>Faecalicatena gnavus</i> (7.26%)	-0.602 (1.827)	0.742	0.879
<b>Subgroup 39</b> <i>Faecalicatena gnavus</i> (40.99%), <i>Tyzzerella nexilis</i> (10.94%), <i>Blautia</i> <i>hansenii</i> (5.63%), <i>Dorea longicatena B</i> (4.36%), <i>Blautia A</i> sp900066165 (2.85%)	-2.002 (2.114)	0.345	0.647
<b>Subgroup 40</b> <i>Agathobacter faecis</i> (38.45%), <i>Roseburia intestinalis</i> (6.52%), MGYG- HGUT-03899 (6.06%), <i>Fusicatenibacter saccharivorans</i> (5.78%), <i>Faecalibacterium prausnitzii D</i> (5.33%)	0.046 (1.553)	0.976	0.991
<b>Subgroup 41</b> MGYG-HGUT-00644 (17.66%), <i>Prevotella</i> sp900313215 (6.97%), MGYG- HGUT-04456 (5.48%), <i>Prevotella copri</i> (4.05%), <i>Acetatifactor</i> sp900066565 (3.29%)	0.321 (1.471)	0.828	0.910
<b>Subgroup 42</b> <i>Bacteroides B dorei</i> (47.01%), <i>Blautia A wexlerae</i> (4.45%), <i>Bacteroides</i> <i>stercoris</i> (4.42%), <i>Bacteroides thetaiotaomicron</i> (4.05%), <i>Parabacteroides</i> <i>distasonis</i> (4.03%)	-2.391 (1.785)	0.183	0.456
<b>Subgroup 43</b> <i>Bacteroides A coprocola</i> (31.36%), MGYG-HGUT-02275 (7.77%), <i>Bacteroides B dorei</i> (7.33%), <i>Bacteroides B massiliensis</i> 6.94%), <i>Fusicatenibacter saccharivorans</i> (4.77%)	-3.14 (1.866)	0.095	0.304
<b>Subgroup 44</b> <i>Megamonas funiformis</i> (17.64%), <i>Bacteroides A plebeius</i> (15.08%), <i>Roseburia intestinalis</i> (7.78%), <i>Lachnospira rogosae</i> (6.37%), <i>Roseburia</i> <i>inulinivorans</i> (6.29%)	-2.042 (2.003)	0.31	0.622
<b>Subgroup 45</b>	-1.076 (1.68)	0.523	0.786

Subgroup and top 5 species	$\beta$ (SE)	P	FDR
<i>Coprococcus</i> sp900066115 (21.08%), <i>Ruminococcus C callidus</i> (5.52%), <i>Fusicatenibacter saccharivorans</i> (3.10%), <i>Dorea longicatena B</i> (2.88%), <i>Holdemanella_sp002299315</i> (2.74%)			

\*LinDA Linear Mixed-effect Models were conducted with adjustment for age, gender, BMI, and intake of poultry and legumes.

**Supplementary Table S5.** Change in relative abundance between weeks 16 follow-up and baseline in selected individual microbial metabolic pathways

Microbial metabolic pathways		Control		Intervention		Change between 16w-FU and baseline	
		Baseline	16w-FU	Baseline	16w-FU	Control	Intervention
		RA, median (%)	RA, median (%)	RA, median (%)	RA, median (%)	Absolute change, median (%)	Absolute change, median (%)
NAD-BIOSYNTHESIS-II	NAD salvage pathway III (to nicotinamide riboside)	0.014	0.013	0.011	0.010	0.002	0.003
P461-PWY	Hexitol fermentation to lactate, formate, ethanol and acetate	0.083	0.093	0.075	0.083	0.023	0.006
P4-PWY	Superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	0.060	0.062	0.055	0.059	0.003	0.008
PWY0-301	L-ascorbate degradation I (bacterial, anaerobic)	0.015	0.016	0.021	0.019	0.001	0.002
PWY0-781	Aspartate superpathway	0.064	0.065	0.058	0.062	0.004	0.008
PWY-5675	Nitrate reduction V (assimilatory)	0.011	0.011	0.016	0.016	0.002	0.006
PWY-5705	Allantoin degradation to glyoxylate III	0.002	0.001	0.002	0.002	0.000	0.000
PWY-5723	Rubisco shunt	0.026	0.021	0.026	0.026	-0.001	0.004
PWY-5837	2-carboxy-1,4-naphthoquinol biosynthesis	0.021	0.025	0.023	0.018	0.004	0.004
PWY-5838	Superpathway of menaquinol-8 biosynthesis I	0.059	0.060	0.066	0.048	0.001	-0.001
PWY-5840	Superpathway of menaquinol-7 biosynthesis	0.046	0.054	0.047	0.047	0.008	8.82x10 <sup>-5</sup>
PWY-5845	Superpathway of menaquinol-9 biosynthesis	0.044	0.043	0.052	0.040	-0.001	0.003
PWY-5861	Superpathway of demethylmenaquinol-8 biosynthesis I	0.041	0.041	0.046	0.033	0.001	-0.001
PWY-5862	Superpathway of demethylmenaquinol-9 biosynthesis	0.031	0.030	0.036	0.028	-0.001	0.002
PWY-5897	Superpathway of menaquinol-11 biosynthesis	0.054	0.062	0.061	0.046	0.002	-0.001
PWY-5898	Superpathway of menaquinol-12 biosynthesis	0.054	0.062	0.061	0.046	0.002	-0.001
PWY-5899	Superpathway of menaquinol-13 biosynthesis	0.054	0.062	0.061	0.046	0.002	-0.001
PWY-5913	Partial TCA cycle (obligate autotrophs)	0.066	0.090	0.061	0.060	0.018	0.003

PWY-5918	Superpathway of heme b biosynthesis from glutamate	0.025	0.024	0.031	0.027	0.001	-0.001
PWY-6285	Superpathway of fatty acids biosynthesis (E. coli)	0.064	0.056	0.072	0.076	2.42x10 <sup>-4</sup>	0.006
PWY-6531	Mannitol cycle	0.018	0.020	0.015	0.020	0.001	0.001
PWY66-389	Phytol degradation	0.005	0.009	0.007	0.007	0.004	-0.001
PWY-6961	L-ascorbate degradation II (bacterial, aerobic)	0.014	0.013	0.016	0.017	0.001	0.003
PWY-7385	1,3-propanediol biosynthesis (engineered)	0.011	0.005	0.007	0.014	0.000	0.007

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RA: Relative abundance