

Healthy Dietary Pattern Cycling Affects Gut Microbiota and Cardiovascular Disease Risk Factors: Results from a Randomized Controlled Feeding Trial with Young, Healthy Adults

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Supplemental Table S1. Nutrients of study diets consumed during each HDP and habitual intakes at baseline and washouts.

	Pre-1 (N=12)	SD	Post-1 (N=17)	SD	Pre-2 (N=11)	SD	Post-2 (N=17)	SD	Pre-3 (N=7)	SD	Post-3 (N=12)	SD
Energy (kcal)	2216	388	2366	299	2306	521	2431	226	2252	383	2393	240
Total fat (g)	84.2	18.7	68.9	9.6	107.3	31.1	72.6	6.3	82.3	21.8	70.8	6.3
% Energy from Fat	33.5	5.3	25.4	2.0	40.7	6.6	26.2	2.4	32.3	7.2	26.0	2.6
Total carbohydrate (g)	275.0	54.0	356.1	42.9	240.2	61.3	356.9	41.5	288.9	56.7	354.2	45.3
% Energy from Carbohydrate	48.7	5.4	58.3	2.7	41.7	8.2	56.7	2.8	50.8	8.3	57.1	3.1
Total Protein (g)	96.4	26.6	103.1	18.4	93.0	38.5	109.6	12.7	93.9	30.6	107.1	13.4
% Energy from Protein	17.5	3.9	16.3	1.2	15.7	3.8	17.0	0.8	16.3	3.6	16.9	0.9
Cholesterol (mg)	375	135	216	47	375	219	239	31	280	196	231	33
Saturated Fatty Acids (g)	29.9	8.5	18.6	3.5	33.7	15.1	20.1	2.3	27.7	8.3	19.4	2.4
% Energy from SFA	11.8	2.4	6.9	0.8	12.7	4.3	7.3	0.9	10.8	2.5	7.2	1.0
Monounsaturated fatty acids (g)	30.2	7.2	26.0	4.0	40.5	15.2	27.7	2.8	28.0	9.1	26.9	2.8
% Energy from MUFA	12.1	2.5	9.6	1.0	15.1	3.7	10.0	1.2	11.0	3.2	9.9	1.2
Polyunsaturated fatty acids (g)	16.4	7.6	16.0	1.0	23.6	12.4	16.4	0.8	19.5	8.8	16.3	0.9
% Energy from PUFA	6.5	3.0	5.9	0.4	9.2	4.8	5.9	0.3	7.8	3.3	5.9	0.3
Total Dietary Fiber (g)	26.1	7.5	55.6	7.7	23.7	8.3	55.7	7.6	24.7	7.8	55.3	8.0
Iron (mg)	16.3	5.0	33.9	4.9	15.6	7.0	34.5	4.4	21.9	9.2	34.1	4.7
Sodium (mg)	3357	999	2826	448	3342	895	3250	641	3628	576	3276	667

Notes: HDP, healthy dietary pattern. Total nutrient contents are based on average consumption by participants and presented as means \pm standard deviations.

Supplemental Table S2. Daily food group servings from baseline, each HDP (averages of 4-day menus), and washouts, presented in cup or ounce-equivalents^[1].

	Pre-1	Post-1	Pre-2	Post-2	Pre-3	Post-3
Food group or Subgroup	N=12	N=17	N=11	N=17	N=7	N=12
Vegetables (serving/d) [2]	2.0 (1.1)	5.2 (0.7)	2.2 (1.2)	5.2 (0.7)	1.7 (0.9)	5.1 (0.8)
[Dark-Green Vegetables]	0.4 (0.5)	1.0 (0.2)	0.5 (0.7)	1.0 (0.2)	0.2 (0.3)	1.0 (0.2)
[Red and Orange Vegetables]	0.5 (0.4)	0.7 (0.1)	0.5 (0.4)	0.7 (0.1)	0.4 (0.2)	0.7 (0.1)
[Beans, Peas, Lentils (Legumes)]	0.2 (0.4)	1.5 (0.4)	0.1 (0.2)	1.5 (0.4)	0.2 (0.4)	1.5 (0.4)
[Starchy Vegetables]	0.3 (0.4)	0.7 (0.1)	0.4 (0.4)	0.7 (0.1)	0.4 (0.5)	0.7 (0.1)
[Other Vegetables]	0.7 (0.9)	1.3 (0.1)	0.8 (0.6)	1.3 (0.1)	0.5 (0.6)	1.2 (0.1)
Fruits (serving/d) [2]	1.7 (1.6)	2.1 (0.2)	0.6 (0.8)	2.1 (0.2)	0.8 (1.1)	2.1 (0.2)
Grains (serving/d) [3]	7.5 (3.0)	7.4 (0.7)	6.7 (2.5)	7.4 (0.6)	9.2 (3.5)	7.4 (0.7)
[Whole Grains]	2.4 (2.7)	3.5 (0.3)	1.8 (1.6)	3.5 (0.3)	1.8 (1.5)	3.5 (0.3)
[Refined Grains]	5.1 (4.0)	3.9 (0.4)	4.9 (2.5)	4.0 (0.4)	7.5 (4.0)	3.9 (0.5)
Dairy (serving/d) [4]	2.9 (1.4)	2.5 (0.2)	2.0 (1.7)	2.5 (0.2)	2.8 (0.9)	2.4 (0.3)
Protein Foods(serving/d) [5]	6.5 (2.8)	5.9 (1.8)	8.3 (4.9)	7.0 (1.2)	5.4 (2.0)	6.7 (1.4)
[Meats, Poultry, Eggs]	4.7 (2.3)	2.1 (1.6)	5.4 (4.6)	3.2 (1.2)	4.4 (2.1)	3.0 (1.3)
-Red meat	2.1 (1.8)	1.2 (1.4)	3.2 (3.9)	1.5 (1.2)	0.8 (0.6)	1.2 (1.1)
-Poultry	1.7 (2.4)	0	1.0 (1.0)	0	2.5 (1.4)	0
-Eggs	0.8 (0.8)	0.7 (0.1)	0.8 (0.9)	0.7 (0.1)	0.5 (0.8)	0.7 (0.1)
-Other [6]	0.2 (0.4)	0.2 (0.7)	0.4 (0.7)	1.0 (1.1)	0.6 (0.8)	1.0 (1.1)
[Seafood]	1.0 (1.4)	0	0.6 (1.6)	0	0.2 (0.4)	0
[Nuts, Seed, Soy Products]	0.8 (1.5)	3.8 (0.4)	2.3 (3.2)	3.8 (0.4)	0.9 (1.3)	3.7 (0.5)
Oils (serving/day) [7]	2.0 (0.9)	2.5 (0.3)	3.8 (2.2)	2.5 (0.3)	3.1 (2.8)	2.4 (0.3)
Calories for Other Uses	7.4 (3.3)	0.9 (0.1)	8.1 (3.7)	0.9 (0.1)	6.0 (2.7)	0.9 (0.1)
2015-HEI Score [8]	55.5 (13.1)	80.9 (2.1)	50.5 (9.2)	78.6 (3.0)	44.0 (15.6)	78.4 (3.1)

Notes:

HDP, healthy dietary pattern.

[1] Food group servings based on the 2015-2020 Dietary Guidelines for Americans presented for three study diets with averaged consumed amount across a 4-d menu cycle.

[2] 1 cup equivalent: 1 cup raw or cooked vegetable or fruit, 1 cup vegetable or fruit juice, 2 cups leafy salad greens, ½ cup dried fruit or vegetable.

[3] 1 ounce-equivalent: ½ cup cooked rice, pasta, or cereal; 1 ounce dry pasta or rice; 1 medium (1 ounce) slice bread; 1 ounce of ready-to-eat cereal (about 1 cup of flaked cereal).

[4] 1 cup-equivalent: 1 cup milk, yogurt, or fortified soymilk; 1½ ounces natural cheese such as cheddar cheese or 2 ounces of processed cheese.

[5] 1 ounce-equivalent is: 1 ounce lean meat, poultry, or seafood; 1 egg; ¼ cup cooked beans or tofu; 1 Tbsp peanut butter; ½ ounce nuts or seeds.

[6] "Other Meat" includes processed meat products such as cold cuts and sausages.

[7] 1 serving: 1 teaspoon for margarine, oil, shortening, butter, and other animal fats; 30 grams for poured salad dressing; and 15 grams for mayonnaise or mayonnaise type dressing.

[8] The 2015-HEI score for participants habitual diets was calculated for the first baseline (N=33) and presented as mean (standard deviation).

Supplemental Table S3. Alpha diversity assessments.

Diet	Time	N participants	N samples	Chao (m)	Chao (SD)	ACE (m)	ACE (SD)	Invsimpson (m)	Invsimpson (SD)	Shannon (m)	Shannon (SD)	p-values (fdr adjusted for wilcoxon test)	Chao	ACE	Invsimpson	Shannon
Adoption of HEP: pre versus post with three HDPs combined																
All	pre	17	87	207.97	49.53	225.49	55.18	20.78	8.07	3.60	0.36	post-pre pair-wise wilcoxon test	0.34	0.19	0.18	0.40
All	post	17	88	219.33	57.41	240.76	70.60	18.96	7.88	3.54	0.40					
Abandonment of HEP: post-previous-HDP versus pre-next-HDP with two washouts combined																
All	post-previous-HDP		65	228.62	58.61	250.53	72.12	19.33	7.87	3.59	0.35	post-pre pair-wise wilcoxon test	0.001	0.0004	0.61	0.05
All	pre-next-HDP		54	202.90	50.13	217.76	52.62	19.81	7.39	3.57	0.35					
1st Adoption of HEP																
HDP 1	pre-1		33	214.86	47.83	236.42	55.98	22.39	8.98	3.64	0.38	post-pre pair-wise wilcoxon test	0.55	0.50	0.12	0.31
HDP 1	post-1		34	224.48	44.18	245.98	53.33	19.55	8.23	3.59	0.33					
1st Abandonment of HEP																
Washout 1	pre-2		34	224.48	44.18	245.98	53.33	19.55	8.23	3.59	0.33	post-pre pair-wise wilcoxon test	0.52	0.46	0.49	0.44
Washout 1	post-1		32	214.67	51.99	232.76	55.11	20.81	7.46	3.65	0.33					
2nd Adoption of HEP																
HDP 2	pre-2		32	214.67	51.99	232.76	55.11	20.81	7.46	3.65	0.33	post-pre pair-wise wilcoxon test	0.42	0.52	0.35	0.64
HDP 2	post-2		31	233.16	71.70	255.51	88.99	19.09	7.58	3.59	0.37					
2nd Abandonment of HEP																
Washout 2	pre-3		31	233.16	71.70	255.51	88.99	19.09	7.58	3.59	0.37	post-pre pair-wise wilcoxon test	0.007	0.001	0.74	0.19
Washout 2	post-2		22	185.78	42.85	195.95	40.80	18.35	7.19	3.47	0.35					
3rd Adoption of HEP																
HDP 3	pre-3		22	185.78	42.85	195.95	40.80	18.35	7.19	3.47	0.35	post-pre pair-wise wilcoxon test	0.73	0.32	0.96	0.99
HDP 3	post-3		23	192.45	45.46	211.43	55.82	17.96	8.01	3.40	0.49					
among three HDPs at pre												Kruskall-wallis test among 3 diets-pre	0.07	0.01	0.14	0.12
Pair-wise comparisons at pre for ACE																
HDP 1 vs HDP 2	0.881	HDP 1 vs HDP 3	0.014	HDP 2 vs HDP 3	0.023											

Supplemental Table S3. continued

Diet	Time	N participants	N samples	Chao (m)	Chao (SD)	ACE (m)	ACE (SD)	Invsimpson (m)	Invsimpson (SD)	Shannon (m)	Shannon (SD)	p-values (fdr adjusted for wilcoxon test)	Chao	ACE	Invsimpson	Shannon
among three HDPs at post												Kruskall-wallis test among 3 diets-post	0.01	0.03	0.93	0.45
Pair-wise comparisons at post for Chao																
HDP 1 vs HDP 2	0.943	HDP 1 vs HDP 3	0.032	HDP 2 vs HDP 3	0.032											
Pair-wise comparisons at post for ACE																
HDP 1 vs HDP 2	0.984	HDP 1 vs HDP 3	0.014	HDP 2 vs HDP 3	0.014											
post-pre changes among three HDPs																
HDP 1	post-pre change	17		11.53	28.06	12.17	45.52	-0.05	0.28	-2.92	6.69	Kruskall-wallis test among 3 diets	0.94	0.73	0.71	0.43
HDP 2	post-pre change	16		15.49	44.43	18.79	59.38	-0.06	0.27	-1.72	6.50					
HDP 3	post-pre change	12		11.37	26.15	18.93	31.53	-0.02	0.39	0.55	7.15					
post-pre changes between two washouts																
Abandonment 1	post-pre change	17		-11.77	26.39	-15.11	36.75	0.05	0.26	1.30	6.92	pair-wise wilcoxon test	0.58	0.38	0.78	0.58
Abandonment 2	post-pre change	11		-29.12	54.33	-42.65	71.49	-0.01	0.18	1.01	3.35					
Other comparisons																
pre1 versus pre2 versus post1 versus post2 with three HDPs combined																
All	pre1	17	43	206.37	44.14	222.04	46.01	19.99	8.58	3.58	0.35	pre1-pre2 pair-wise wilcoxon test	0.98	0.92	0.17	0.44
All	pre2	17	44	209.54	54.75	228.87	63.24	21.56	7.56	3.62	0.37					
All	post1	17	44	220.88	60.69	245.39	76.36	19.33	8.85	3.55	0.41	post1-post2 pair-wise wilcoxon test	0.81	0.72	0.91	1.00
All	post2	17	44	217.79	54.60	236.13	64.88	18.60	6.85	3.53	0.39					

Supplemental Table S3. continued

Diet	Time	N participants	N samples	Chao (m)	Chao (SD)	ACE (m)	ACE (SD)	Invsimpson (m)	Invsimpson (SD)	Shannon (m)	Shannon (SD)	p-values adjusted for wilcoxon test	(fdr for	Chao	ACE	Invsimpson	Shannon
pre1 versus pre2 versus post1 versus post2 within each HDP																	
HDP 1	pre1		17	209.84	40.85	230.24	45.05	22.74	11.13	3.64	0.41	Kruskall-wallis test among 4 timepoints		0.93	0.88	0.23	0.54
HDP 1	pre2		16	220.19	55.15	242.98	66.57	22.02	6.32	3.63	0.37						
HDP 1	post1		17	222.90	44.41	245.75	61.44	18.56	10.37	3.52	0.38						
HDP 1	post2		17	226.07	45.26	246.21	45.72	20.53	5.49	3.66	0.26						
HDP 2	pre1		15	213.69	52.39	228.92	52.02	18.61	4.33	3.59	0.31	Kruskall-wallis test among 4 timepoints		0.78	0.69	0.16	0.36
HDP 2	pre2		17	215.53	53.22	236.14	59.08	22.75	9.11	3.70	0.35						
HDP 2	post1		16	242.84	78.08	269.83	95.38	21.21	8.04	3.66	0.40						
HDP 2	post2		15	222.84	65.28	240.24	82.09	16.82	6.58	3.51	0.34						
HDP 3	pre1		11	189.70	35.27	198.50	32.75	17.63	7.97	3.47	0.33	Kruskall-wallis test among 4 timepoints		0.77	0.64	0.93	1.00
HDP 3	pre2		11	181.87	50.77	193.40	49.07	19.07	6.63	3.47	0.39						
HDP 3	post1		11	184.62	38.13	204.37	44.68	17.81	7.67	3.41	0.44						
HDP 3	post2		12	199.63	51.90	217.90	65.74	18.11	8.65	3.39	0.56						

Note: HDP, healthy dietary pattern. Chao, Chao1 richness index; ACE, abundance-based coverage estimator richness index; Shannon, Shannon diversity index; Invsimpson, Inverse Simpson diversity index; m, mean; SD, standard deviation.

Supplemental Table S4. Beta diversity assessments

	pre vs post three HDPs combined			pre vs post two washouts combined					
pcoa axes	thetayc	jclass	braycurtis	thetayc	jclass	braycurtis			
rsq 1 axis	0.23	0.49	0.24	0.19	0.43	0.24			
rsq 2 axis	0.40	0.60	0.42	0.39	0.53	0.45			
rsq 3 axis	0.43	0.63	0.63	0.50	0.57	0.63			
	pre all samples			post all samples					
pcoa axes	thetayc	jclass	braycurtis	thetayc	jclass	braycurtis			
rsq 1 axis	0.23	0.49	0.32	0.26	0.47	0.17			
rsq 2 axis	0.40	0.57	0.49	0.44	0.59	0.39			
rsq 3 axis	0.45	0.58	0.55	0.56	0.63	0.63			
	pre vs post HDP 1			pre vs post HDP 2			pre vs post HDP 3		
pcoa axes	thetayc	jclass	braycurtis	thetayc	jclass	braycurtis	thetayc	jclass	braycurtis
rsq 1 axis	0.29	0.50	0.24	0.19	0.52	0.20	0.24	0.48	0.41
rsq 2 axis	0.43	0.64	0.45	0.35	0.62	0.36	0.52	0.58	0.60
rsq 3 axis	0.49	0.64	0.62	0.40	0.66	0.64	0.61	0.68	0.70
	pre vs post Washout 1			pre vs post Washout 2					
pcoa axes	thetayc	jclass	braycurtis	thetayc	jclass	braycurtis			
rsq 1 axis	0.23	0.52	0.32	0.18	0.46	0.24			
rsq 2 axis	0.38	0.62	0.49	0.39	0.55	0.45			
rsq 3 axis	0.45	0.66	0.56	0.48	0.58	0.64			

Supplemental Table S4. continued

	pre vs post three HDPs combined				pre vs post two washouts combined			
	post-pre	Among	Within	Total	post-pre	Among	Within	Total
	SS	0.55	53.48	54.03	SS	0.84	32.98	33.82
	df	1	173	174	df	1	104	105
	MS	0.55	0.31		MS	0.84	0.32	
	Fs:	1.78			Fs:	2.65		
amova-thetayc	p-value:	0.043*			p-value:	0.004*		
	post-pre	Among	Within	Total	post-pre	Among	Within	Total
	SS	0.27	44.59	44.85	SS	0.62	26.44	27.06
	df	1	173	174	df	1	104	105
	MS	0.27	0.26		MS	0.62	0.25	
	Fs:	1.04			Fs:	2.43		
amova-jclass	p-value:	0.37			p-value:	<0.001*		
	post-pre	Among	Within	Total	post-pre	Among	Within	Total
	SS	0.43	37.97	38.39	SS	0.74	23.41	24.15
	df	1	173	174	df	1	104	105
	MS	0.43	0.22		MS	0.74	0.23	
	Fs:	1.95			Fs:	3.29		
amova-braycurtis	p-value:	0.011*			p-value:	<0.001*		
	pre among HDP 1 vs HDP 2 vs HDP 3				post among HDP 1 vs HDP 2 vs HDP 3			
	preHDP1- preHDP2- preHDP3	Among	Within	Total	postHDP1- postHDP2- postHDP3	Among	Within	Total
	SS	0.28	25.41	25.69	SS	0.40	27.40	27.79
	df	2.00	84.00	86.00	df	2.00	85.00	87.00
	MS	0.14	0.30		MS	0.20	0.32	
	Fs:	0.46			Fs:	0.62		
amova-thetayc	p-value:	1.00			p-value:	0.94		

Supplemental Table S. 4.4 continued

	preHDP1- preHDP2- preHDP3	Among	Within	Total	postHDP1- postHDP2- postHDP3	Among	Within	Total				
	SS	0.41	21.48	21.89	SS	0.41	22.09	22.50				
	df	2	84	86	df	2	85	87				
	MS	0.20	0.26		MS	0.20	0.26					
	Fs:	0.80			Fs:	0.79						
	amova-jclass	p-value:	0.95		p-value:	0.95						
	post-pre	Among	Within	Total	postHDP1- postHDP2- postHDP3	Among	Within	Total				
	SS	0.24	17.92	18.16	SS	0.32	19.49	19.81				
	df	2.00	84.00	86.00	df	2.00	85.00	87.00				
	MS	0.12	0.21		MS	0.16	0.23					
	Fs:	0.56			Fs:	0.69						
	amova-braycurtis	p-value:	0.99		p-value:	0.91						
pre1-pre2-post1-post2 HDP 1				pre1-pre2-post1-post2 HDP 2				pre1-pre2-post1-post2 HDP 3				
	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total
	SS	0.42	19.82	20.24	SS	0.63	19.18	19.80	SS	0.43	13.17	13.60
	df	3.00	63.00	66.00	df	3.00	59.00	62.00	df	3.00	41.00	44.00
	MS	0.14	0.31		MS	0.21	0.33		MS	0.14	0.32	
	Fs:	0.45			Fs:	0.64			Fs:	0.45		
	amova-thetayc	p-value:	1.00		p-value:	0.98			p-value:	1.00		

Supplemental Table S4. continued

	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total
	SS	0.44	16.61	17.05	SS	0.46	15.63	16.09	SS	0.43	10.53	10.95
	df	3	63	66	df	3	59	62	df	3	41	44
	MS	0.15	0.26		MS	0.15	0.26		MS	0.14	0.26	
	Fs:	0.55			Fs:	0.58			Fs:	0.56		
amova-jclass	p-value: 1				p-value: 1				p-value: 1			
	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total
	SS	0.36	14.14	14.50	SS	0.44	13.58	14.02	SS	0.33	9.18	9.51
	df	3	63	66	df	3	59	62	df	3	41	44
	MS	0.12	0.22		MS	0.15	0.23		MS	0.11	0.22	
	Fs:	0.53			Fs:	0.64			Fs:	0.49		
amova-braycurtis	p-value:	1			p-value:	0.99			p-value:	1		
pre1-pre2-post1-post2 Washout 1				pre1-pre2-post1-post2 Washout 2								
	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total				
	SS	0.44	19.40	19.84	SS	0.73	16.18	16.91				
	df	3	62	65	df	3	49	52				
	MS	0.15	0.31		MS	0.24	0.33					
	Fs:	0.47			Fs:	0.74						
amova-thetayc	p-value:	1.00			p-value:	0.92						
	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total				
	SS	0.46	16.17	16.63	SS	0.60	12.90	13.50				
	df	3	62	65	df	3	49	52				
	MS	0.15	0.26		MS	0.20	0.26					
	Fs:	0.59			Fs:	0.76						
amova-jclass	p-value: 1				p-value:	1.00						

Supplemental Table S4. continued

	post1-post2- pre1-pre2	Among	Within	Total	post1-post2- pre1-pre2	Among	Within	Total
	SS	0.38	13.43	13.81	SS	0.58	11.49	12.08
	df	3	62	65	df	3	49	52
	MS	0.13	0.22		MS	0.19	0.23	
	Fs:	0.58			Fs:	0.83		
amova-braycurtis	p-value:	1.00			p-value:	0.83		
pre vs post among HDP 1 vs HDP 2 vs HDP 3								
homova-thetayc								
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values					
			postHDP1	postHDP 2	postHDP3	preHDP1	preHDP 2	preHDP 3
	0.13	0.71	0.31	0.34	0.32	0.30	0.30	0.31
homova-jclass								
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values					
			postHDP1	postHDP 2	postHDP3	preHDP1	preHDP 2	preHDP 3
	0.04	0.67	0.26	0.27	0.25	0.26	0.26	0.25
homova-braycurtis								
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values					
			postHDP1	postHDP 2	postHDP3	preHDP1	preHDP 2	preHDP 3
	0.25	0.40	0.22	0.24	0.23	0.22	0.21	0.21
pre vs post three HDPs combined					pre vs post two washouts combined			
homova-thetayc					homova-thetayc			
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values		HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values
			post	pre				postpre
	0.09	0.16	0.32	0.30		0.12	0.07	0.330.30

Supplemental Table S4. continued

homova-jclass				homova-jclass			
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values	HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values
			post pre				post pre
	0.01	0.53	0.26 0.26		0.07	0.015*	0.26 0.24
homova-braycurtis				homova-braycurtis			
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values	HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values
			post pre				post pre
	0.12	0.14	0.23 0.21		0.32	0.01*	0.24 0.20
pre1-pre2-post1-post2 HDP 1							
homova-thetayc							
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values				
			post1 post2 pre1 pre2				
	0.02	0.93	0.33 0.31 0.30 0.32				
homova-jclass							
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values				
			post1 post2 pre1 pre2				
post1-post2-pre1-pre2	0.01	0.80	0.26 0.26 0.26 0.27				
homova-braycurtis							
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values				
			post1 post2 pre1 pre2				
	0.07	0.73	0.23 0.22 0.21 0.24				
pre1-pre2-post1-post2 Washout 1							
homova-thetayc							
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values				
			post1 post2 pre1 pre2				
post1-post2-pre1-pre2	0.04	0.88	0.33 0.31 0.29 0.32				

Supplemental Table S4. continued

homova-jclass						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
post1-post2-pre1-pre2	0.003	0.96	0.26	0.26	0.26	0.26
homova-braycurtis						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
post1-post2-pre1-pre2	0.03	0.88	0.23	0.22	0.21	0.21
pre1-pre2-post1-post2 HDP 2						
homova-thetayc						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
post1-post2-pre1-pre2	0.13	0.40	0.33	0.36	0.30	0.32
homova-jclass						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
post1-post2-pre1-pre2	0.02	0.62	0.27	0.27	0.26	0.26
homova-braycurtis						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
post1-post2-pre1-pre2	0.21	0.24	0.24	0.26	0.21	0.21
pre1-pre2-post1-post2 Washout 2						
homova-thetayc						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
	0.11	0.45	0.33	0.36	0.33	0.29

Supplemental Table S4. continued

homova-jclass						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
	0.03	0.47	0.27	0.27	0.25	0.25
homova-braycurtis						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
	0.17	0.37	0.24	0.26	0.22	0.20
pre1-pre2-post1-post2 HDP 3						
homova-thetayc						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
	0.051	0.77	0.33	0.33	0.33	0.29
homova-jclass						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
	0.01	0.91	0.27	0.26	0.25	0.25
homova-braycurtis						
HOMOVA	BValue	P-value	SSwithin/(Ni-1)_values			
			post1	post2	pre1	pre2
	0.06	0.77	0.24	0.23	0.22	0.20

Notes: HDP, healthy dietary pattern.

Supplemental Table S5. Taxa that significantly differed between groups based on LEfSe analyses.

Group 1 vs Group 2	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LDA	Phylotype- OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative abundance (RA, %)	>=0.1% RA	
All HDPs, Pre vs Post	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	pre	3.7	OTU013	0.027945	0.000323	0.001926	0.01757	0.000286	0.001802	2.27278173	Yes	
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	genus	pre	3.7	OTU018	0.019352	0.000374	0.002073	0.009246	0.000129	0.001212	1.42702255	Yes	
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	genus	post	3.3	OTU021	0.010025	0.000112	0.001132	0.014385	0.000182	0.00144	1.22177549	Yes	
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	pre	3.5	OTU024	0.014693	0.000288	0.00182	0.00818	0.00013	0.001216	1.14177111	Yes	
	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	genus	post	3.3	OTU026	0.008302	0.000053	0.000778	0.012093	0.000106	0.001096	1.02085338	Yes	
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	genus	pre	3.5	OTU030	0.009972	0.000248	0.001687	0.004204	0.000035	0.000627	0.70716327	Yes	
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	genus	post	2.4	OTU038	0.00184	0.000031	0.000594	0.002025	0.000011	0.000356	0.1933062	Yes	
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	genus	pre	2.8	OTU054	0.002229	0.000072	0.000908	0.001012	0.00001	0.000336	0.16173215	Yes	
	Post, HDP 2 vs HDP 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes	genus	Post HDP1	3.8	OTU011	0.01785	0.000221	0.002668	0.030643	0.000743	0.004675	2.94548793	Yes
	Post, HDP 3 vs HDP 1	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	genus	Post HDP1	3.2	OTU016	0.003975	0.00003	0.001136	0.006409	0.000025	0.000862	0.59857727	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV	genus	Post HDP1	2.8	OTU049	0.0004	0	0.000107	0.001548	0.000014	0.000637	0.17888799	Yes	

Supplemental Table S5. continued

Group 1 vs Group 2	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LDA	Phylotype- OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative abundance (RA, %)	>=0.1% RA
Post, HDP 3 vs HDP 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	postHDP3	3.8	OTU013	0.026484	0.000709	0.005552	0.014053	0.000118	0.001955	2.27278173	Yes
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	genus	postHDP2	3.3	OTU016	0.003975	0.00003	0.001136	0.009112	0.000266	0.002929	0.59857727	Yes
	Bacteria	Bacteria _unclassified	Bacteria _unclassified	Bacteria _unclassified	Bacteria_unclassified	Bacteria _unclassified	genus	postHDP2	3.7	OTU020	0.003422	0.000036	0.001254	0.012616	0.000307	0.003149	0.68580683	Yes
Pre, HDP 2 vs HDP 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	genus	preHDP2	3.6	OTU014	0.017758	0.000331	0.003214	0.010443	0.000103	0.001767	1.50285885	Yes
Pre, HDP 3 vs HDP 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales _unclassified	genus	preHDP1	3.7	OTU009	0.00935	0.000171	0.002791	0.018953	0.000518	0.00396	1.52627814	Yes
	Bacteria	Bacteria _unclassified	Bacteria _unclassified	Bacteria _unclassified	Bacteria_unclassified	Bacteria _unclassified	genus	preHDP1	3.3	OTU020	0.002228	0.00002	0.000944	0.006265	0.000108	0.001809	0.68580683	Yes
Pre, HDP 3 vs HDP 2	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	genus	preHDP3	3.7	OTU023	0.017785	0.00147	0.008173	0.005924	0.00008	0.001585	0.84383763	Yes
HDP1, Pre vs Post	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	preHDP1	3.8	OTU013	0.027756	0.000336	0.003189	0.014746	0.000098	0.001695	2.27278173	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	genus	preHDP1	3.8	OTU018	0.019151	0.000243	0.002713	0.00751	0.00007	0.001438	1.42702255	Yes
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	preHDP1	3.6	OTU024	0.017478	0.000436	0.003633	0.009381	0.000263	0.002783	1.14177111	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	genus	preHDP1	3.7	OTU030	0.011777	0.000514	0.003948	0.003264	0.00002	0.000766	0.70716327	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	genus	preHDP1	2.7	OTU038	0.002554	0.00007	0.001452	0.002037	0.000009	0.000517	0.1933062	Yes
HDP2, Pre vs Post	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes	genus	preHDP2	3.8	OTU011	0.030977	0.000919	0.005358	0.01785	0.000221	0.002668	2.94548793	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	preHDP2	3.8	OTU013	0.026183	0.000236	0.002716	0.014053	0.000118	0.001955	2.27278173	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	genus	preHDP2	3.6	OTU018	0.016617	0.000185	0.002406	0.007421	0.000043	0.001174	1.42702255	Yes
	Bacteria	Actinobacteriac	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	preHDP2	3.7	OTU024	0.014546	0.000302	0.003074	0.007244	0.000041	0.001147	1.14177111	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	genus	preHDP2	3.3	OTU030	0.008262	0.000078	0.001565	0.004709	0.000055	0.001335	0.70716327	Yes
HDP3, Pre vs Post	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	preHDP3	3.2	OTU024	0.010729	0.000042	0.001374	0.007665	0.00006	0.001616	1.14177111	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	genus	postHDP3	2.4	OTU038	0.000907	0.000004	0.000427	0.00128	0.000003	0.000354	0.1933062	Yes
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	genus	preHDP3	2.8	OTU054	0.002219	0.000007	0.000557	0.000745	0.000002	0.000313	0.16173215	Yes

Supplemental Table S5. continued

Group 1 vs Group 2	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	L D A	Phylot ype- OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative abundance (RA, %)	>= 0.1 % RA
Washout 1, pre- HDP 2 vs post-HDP 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	preHDP2	3.8	OTU01 3	0.026183	0.000236	0.002716	0.014746	0.000098	0.001695	2.27278173	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	genus	preHDP2	3.7	OTU01 8	0.016617	0.000185	0.002406	0.00751	0.00007	0.001438	1.42702255	Yes
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	preHDP2	3.5	OTU02 4	0.014546	0.000302	0.003074	0.009381	0.000263	0.002783	1.14177111	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	genus	preHDP2	3.4	OTU03 0	0.008262	0.000078	0.001565	0.003264	0.00002	0.000766	0.70716327	Yes
Washout 2, pre- HDP 3 vs post-HDP 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	genus	preHDP3	4.5	OTU00 3	0.134056	0.00862	0.019794	0.082726	0.003272	0.010274	0.70716327	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales _unclassified	Clostridiales _unclassified	genus	postHDP2	3.7	OTU00 9	0.00935	0.000171	0.002791	0.018604	0.000405	0.003615	1.52627814	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	preHDP3	4.0	OTU01 3	0.030791	0.000449	0.004517	0.014053	0.000118	0.001955	2.27278173	Yes
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	genus	postHDP2	3.4	OTU01 6	0.003577	0.000047	0.001463	0.009112	0.000266	0.002929	0.59857727	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	genus	preHDP3	3.9	OTU01 8	0.023632	0.000857	0.006243	0.007421	0.000043	0.001174	1.42702255	Yes
	Bacteria	Bacteria _unclassified	Bacteria _unclassified	Bacteria _unclassified	Bacteria _unclassified	Bacteria _unclassified	genus	postHDP2	3.8	OTU02 0	0.002228	0.00002	0.000944	0.012616	0.000307	0.003149	0.68580683	Yes
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	genus	preHDP3	3.7	OTU02 3	0.017785	0.00147	0.008173	0.009235	0.000424	0.003697	0.84383763	Yes
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	preHDP3	3.2	OTU02 4	0.010729	0.000042	0.001374	0.007244	0.000041	0.001147	1.14177111	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	genus	preHDP3	3.3	OTU03 0	0.009751	0.000105	0.00218	0.004709	0.000055	0.001335	0.70716327	Yes
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Faecalibacillus	genus	preHDP3	3.6	OTU03 5	0.011849	0.000642	0.0054	0.003052	0.000018	0.000763	0.63864068	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	genus	postHDP2	3.0	OTU03 8	0.000907	0.000004	0.000427	0.002564	0.00002	0.000794	0.1933062	Yes
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	genus	preHDP3	3.0	OTU05 4	0.002219	0.000007	0.000557	0.000436	0.000001	0.000142	0.16173215	Yes
	Bacteria	Bacteroidetes	Bacteroidetes _unclassified	Bacteroidetes _unclassified	Bacteroidetes _unclassified	Bacteroidetes _unclassified	genus	postHDP2	3.0	OTU06 5	0.00184	0.000065	0.001719	0.003136	0.000094	0.00174	0.19673812	Yes
Washout, pre-HDPs 2&3 vs post-HDPs 1&2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	genus	pre	4.3	OTU00 3	0.119567	0.006124	0.010649	0.08421	0.002528	0.006236	0.70716327	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	genus	pre	3.8	OTU01 3	0.028061	0.000321	0.002438	0.014415	0.000106	0.001277	2.27278173	Yes
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	genus	post	3.4	OTU01 6	0.004097	0.000032	0.000775	0.007698	0.00014	0.001465	0.59857727	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	genus	pre	3.8	OTU01 8	0.019475	0.00046	0.002919	0.007468	0.000056	0.000931	1.42702255	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	genus	post	3.5	OTU02 1	0.009395	0.00012	0.001489	0.014872	0.000201	0.001758	1.22177549	Yes

Supplemental Table S5. continued

Group 1 vs Group 2	Doma in	Phylum	Class	Order	Family	Genus	Level	Higher	LD A	Phylotype-OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative abundance (RA, %)	>=0.1% RA
Washout, pre-HDPs 2&3 vs post-HDPs 1&2 (cont)	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	genus	pre	3.4	OTU024	0.012991	0.000197	0.00191	0.008362	0.000156	0.001549	1.14177111	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	genus	pre	3.4	OTU030	0.008869	0.000088	0.001275	0.003953	0.000037	0.000752	0.70716327	Yes
	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Akkermansiaceae	Akkermansia	genus	post	3.6	OTU032	0.013403	0.000983	0.004267	0.020282	0.001038	0.003996	1.70822572	Yes
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	genus	post	2.6	OTU038	0.001404	0.000007	0.000366	0.002288	0.000014	0.000463	0.1933062	Yes
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	genus	pre	2.5	OTU054	0.001664	0.000006	0.000323	0.001107	0.000013	0.000443	0.16173215	Yes
	Bacteria	Actinobacteria	Coriobacteriia	Eggerthellales	Eggerthellaceae	Adlercreutzia	genus	pre	2.4	OTU033	0.00093	0.000001	0.000129	0.000478	0.00000	0.000075	0.07028832	No
All HDPs, Pre vs Post	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	genus	pre	2.3	OTU061	0.001052	0.000002	0.000152	0.000722	0.000003	0.000169	0.08860291	No
	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Dysosmobacter	genus	post	2.2	OTU069	0.000315	0.00000	0.000058	0.000468	0.00000	0.000072	0.03918102	No
	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Pasteurella _unclassified	genus	pre	2.5	OTU097	0.000308	0.000008	0.00003	0.00003	0.00000	0.000012	0.01682465	No
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Massilimicrobiota	genus	pre	2.2	OTU125	0.000105	0.00000	0.000029	0.00002	0.00000	0.000006	0.0062296	No
	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Paraburkholderia	genus	pre	2.5	OTU131	0.000059	0.00000	0.000017	0.000008	0.00000	0.000003	0.00334624	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactacaseibacillus	genus	pre	2.3	OTU138	0.000343	0.000003	0.000177	0.000033	0.00000	0.000029	0.01870313	No
	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XI	Gemella	genus	pre	2.9	OTU139	0.000035	0.00000	0.000011	0.000006	0.00000	0.000002	0.00201855	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Latilactobacillus	genus	pre	2.8	OTU171	0.000018	0.00000	0.000007	0.000002	0.00000	0.000001	0.00098026	No
	Post, HDP 2 vs HDP 1	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales _unclassified	genus	Post HDP1	3.5	OTU153	0.000005	0.00000	0.000003	0.000023	0.00000	0.000007	0.00197116	No
	Post, HDP 3 vs HDP 1	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Odoribacteraceae	genus	Post HDP1	2.5	OTU042	0.000278	0.00000	0.000128	0.000943	0.000003	0.000287	0.07089194	No
		Bacteria	Firmicutes	Clostridia	Clostridia _unclassified	Clostridia _unclassified	genus	Post HDP1	2.3	OTU050	0.000224	0.00000	0.000068	0.000818	0.000003	0.000276	0.06304304	No
Post, HDP 3 vs HDP 2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Odoribacteraceae	Butyricimonas	genus	Post HDP2	2.2	OTU042	0.000278	0.00000	0.000128	0.000548	0.000001	0.000135	0.07089194	No
	Bacteria	Firmicutes	Clostridia	Clostridia _unclassified	Clostridia _unclassified	Clostridia _unclassified	genus	Post HDP2	2.6	OTU050	0.000224	0.00000	0.000068	0.000958	0.000004	0.000361	0.06304304	No
Pre, HDP 2 vs HDP 1	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Rothia	genus	Pre HDP2	3.2	OTU124	0.000016	0.00000	0.000006	0.000001	0.00000	0.000001	0.00093097	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactacaseibacillus	genus	Pre HDP1	2.3	OTU138	0.000066	0.00000	0.000059	0.000585	0.000006	0.000422	0.01870313	No
Pre, HDP 3 vs HDP 1	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	genus	Pre HDP1	2.8	OTU208	0.000207	0.00000	0.000125	0.001562	0.000079	0.001546	0.03708964	No
Pre, HDP 3 vs HDP 2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Odoribacteraceae	Butyricimonas	genus	Pre HDP2	2.4	OTU042	0.000301	0.00000	0.000123	0.000794	0.000001	0.000166	0.07089194	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactacaseibacillus	genus	Pre HDP3	2.1	OTU138	0.000382	0.000002	0.000288	0.000066	0.00000	0.000059	0.01870313	No

Supplemental Table S5. continued

Group 1 vs Group 2	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LD A	Phylotype-OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative abundance (RA, %)	>=0.1% RA
HDP1, Pre vs Post	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lacticaseibacillus	genus	preHD P1	2.3	OTU138	0.000585	0.000006	0.000422	0.000083	0	0.000076	0.01870313	No
	Bacteria	Actinobacteria	Coriobacteriia	Eggerthellales	Eggerthellaceae	Adlercreutzia	genus	preHD P2	3.1	OTU033	0.000836	0.000001	0.000213	0.000373	0.000001	0.000131	0.07028832	No
HDP2, Pre vs Post	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	genus	preHD P2	3.2	OTU061	0.001153	0.000003	0.000292	0.000615	0.000004	0.000362	0.08860291	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	genus	postH DP2	4.1	OTU089	0.000028		0.000008	0.000194		0.000007	0.021098	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lacticaseibacillus	genus	preHD P3	2.3	OTU138	0.000382	0.000002	0.000288	0.000002		0.000001	0.01870313	No
HDP3, Pre vs Post	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	Leptotrichiaceae_unclassified	genus	preHD P3	2.2	OTU203	0.000045		0.000003		0	0	0.0005791	No
	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	genus	preHD P3	2.0	OTU208	0.000207		0.000125	0.000005		0.000005	0.03708964	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	genus	postH DP1	3.1	OTU089	0.000028		0.000008	0.000143		0.000032	0.021098	No
Washout 1, pre-HDP 2 vs post-HDP 1	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Ligilactobacillus	genus	postH DP1	2.5	OTU110	0.000003		0.000002	0.000604	0.000005	0.000383	0.05015192	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	Lactobacillales_unclassified	genus	postH DP1	4.4	OTU153	0.000009		0.000005	0.000023		0.000007	0.00197116	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Latilactobacillus	genus	preHD P2	3.3	OTU171	0.000023		0.000017		0	0	0.00098026	No
	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	genus	postH DP1	2.5	OTU208	0.000041		0.000024	0.000166		0.000071	0.03708964	No
	Bacteria	Actinobacteria	Coriobacteriia	Eggerthellales	Eggerthellaceae	Adlercreutzia	genus	preHD P3	2.9	OTU033	0.001132	0.000002	0.000278	0.000373	0.000001	0.000131	0.07028832	No
Washout 2, pre-HDP 3 vs post-HDP 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter	genus	postH DP2	2.9	OTU056	0.000083		0.000034	0.000254		0.000066	0.01553742	No
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	genus	preHD P3	2.9	OTU061	0.001273	0.000003	0.000359	0.000615	0.000004	0.000362	0.08860291	No
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Barnesiellaceae	Coprobacter	genus	postH DP2	2.9	OTU092	0.000051		0.000031	0.000134		0.000049	0.01411601	No
	Bacteria	Lentisphaerae	Lentisphaeria	Victivallales	Victivallaceae	Victivallis	genus	postH DP2	3.4	OTU100	0.000013		0.000011	0.000089		0.000031	0.00617798	No
	Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Anaerofustis	genus	preHD P3	3.5	OTU115	0.000067		0.000032	0.000009		0.000004	0.00329076	No
	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Massilimicrobiota	genus	preHD P3	3.3	OTU125	0.000127		0.000073	0.000022		0.000012	0.0062296	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lacticaseibacillus	genus	preHD P3	2.9	OTU138	0.000382	0.000002	0.000288	0.000001		0.000001	0.01870313	No
	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XI	Gemella	genus	preHD P3	3.1	OTU139	0.000081		0.000004	0.000002		0.000002	0.00201855	No
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	Lactobacillales_unclassified	genus	preHD P3	3.4	OTU153	0.000006		0.000025	0.000005		0.000003	0.00197116	No
	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	Leptotrichiaceae_unclassified	genus	preHD P3	3.4	OTU203	0.000045		0.000003		0	0	0.0005791	No
	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	genus	preHD P3	2.8	OTU208	0.000207		0.000125	0.000056		0.000048	0.03708964	No

Group 1	vs																			
Group 2		Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LD A	Phylotype-OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative (RA, %)	abundance	>=0.1% RA
		Bacteria	Firmicutes						preHDP2	2.7										

Supplemental Table S5. continued

Group 1 vs Group 2																		
	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LDA	Phylotype-OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative abundance (RA, %)	>=0.1% RA
HDP1, Pre vs Post	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae			preHDP1	3.6									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales				preHDP1	3.6									
	Bacteria	Actinobacteria	Coriobacteriia					preHDP1	3.7									
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae			preHDP1	3.7									
HDP2, Pre vs Post	Bacteria	Firmicutes	Clostridia					preHDP2	4.7									
	Bacteria	Firmicutes	Clostridia	Clostridiales				preHDP2	4.7									
	Bacteria	Bacteroidetes						postHDP2	4.7									
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales				postHDP2	4.7									
	Bacteria	Bacteroidetes	Bacteroidia					postHDP2	4.7									
	Bacteria	Firmicutes						preHDP2	4.7									
	Bacteria	Actinobacteria	Coriobacteriia					preHDP2	3.7									
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae			preHDP2	3.4									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae			preHDP2	4.2									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales				preHDP2	4.2									
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			preHDP2	4.6									
	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae			preHDP2	4.1									
HDP3, Pre vs Post	Bacteria	Fusobacteria	Fusobacteriia					preHDP3	2.4									
	Bacteria	Fusobacteria						preHDP3	2.2									
	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales				preHDP3	2.3									
	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae			preHDP3	2.3									
	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales				preHDP3	2.3									
	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae			preHDP3	2.2									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae			preHDP3	3.2									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales				preHDP3	3.2									

Supplemental Table S5. continued

Group 1 vs Group 2	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LDA	Phylotyp e-OTU	Mea n 1	Var 1	SD 1	Mea n 2	Var 2	SD 2	Relative abundance (RA, %)	>=0.1 % RA
Washout 1, pre-HDP 2 vs post-HDP 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae			preHDP2	3.4									
	Bacteria	Bacteroidetes						postHDP1	4.7									
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales				postHDP1	4.7									
	Bacteria	Bacteroidetes	Bacteroidia					postHDP1	4.7									
	Bacteria	Firmicutes	Clostridia					preHDP2	4.7									
	Bacteria	Firmicutes	Clostridia	Clostridiales				preHDP2	4.7									
	Bacteria	Firmicutes						preHDP2	4.7									
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae			postHDP1	2.6									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae			preHDP2	3.5									
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales				preHDP2	3.5									
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclas sified			postHDP1	4.4									
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae			postHDP1	3.4									
	Bacteria	Actinobacteria	Coriobacteriia					preHDP2	3.5									
Washout 2, pre-HDP 3 vs post-HDP 2	Bacteria	Firmicutes	Bacilli	Bacillales				preHDP3	3.3									
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclas sified			preHDP3	3.4									
	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Se dis_XI			preHDP3	3.1									
	Bacteria	Firmicutes	Bacilli	Lactobacillales				preHDP3	3.7									
	Bacteria	Firmicutes	Bacilli					preHDP3	3.7									
	Bacteria	Firmicutes	Clostridia					preHDP3	4.8									
	Bacteria	Firmicutes	Clostridia	Clostridiales				preHDP3	4.8									
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae			postHDP2	3.4									
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			preHDP3	4.8									
	Bacteria	Bacteria_unclas sified						postHDP2	3.8									
	Bacteria	Bacteria_unclas sified	Bacteria_unclas sified	Bacteria_unclas sified	Bacteria_unclassified			postHDP2	3.8									
	Bacteria	Bacteria_unclas sified	Bacteria_unclas sified	Bacteria_unclas sified				postHDP2	3.8									
	Bacteria	Bacteria_unclas sified	Bacteria_unclas sified					postHDP2	3.8									
	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassif ied			postHDP2	3.7									
	Bacteria	Lentisphaerae	Lentisphaeria	Victivallales				postHDP2	3.5									

Supplemental Table S5. continued

Group 1 vs Group 2																			abundance >=0.1% RA
	Domain	Phylum	Class	Order	Family	Genu s	Lev el	Higher	LD A	Phylotype- OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative (RA, %)		
Washo ut 2, pre- HDP 3 vs post- HDP 2 (cont)	Bacteria	Lentisphaerae	Lentisphaeria					postHDP2	3.3										
	Bacteria	Lentisphaerae	Lentisphaeria	Victivallales	Victivallaceae			postHDP2	3.4										
	Bacteria	Lentisphaerae						postHDP2	3.3										
	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae			preHDP3	3.7										
	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae			preHDP3	3.4										
	Bacteria	Firmicutes						preHDP3	4.7										
	Bacteria	Bacteroidetes	Bacteroidetes_unclassified					postHDP2	3.0										
	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified				postHDP2	3.0										
	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified			postHDP2	3.0										
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae			preHDP3	3.2										
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales				preHDP3	3.2										
	Bacteria	Actinobacteria	Coriobacteriia					preHDP3	3.5										
	Bacteria	Fusobacteria	Fusobacteriia					preHDP3	3.4										
	Bacteria	Fusobacteria						preHDP3	3.3										
	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales				preHDP3	3.3										
	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae			preHDP3	3.2										
	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales				preHDP3	3.2										
	Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae			preHDP3	3.6										
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae			preHDP3	3.4										
	Bacteria	Actinobacteria	Coriobacteriia	Eggerthellales				preHDP3	3.1										
	Bacteria	Actinobacteria	Coriobacteriia	Eggerthellales	Eggerthellaceae			preHDP3	3.1										
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales				postHDP2	4.6										
	Bacteria	Bacteroidetes	Bacteroidia					postHDP2	4.6										

Supplemental Table S5. continued

Group 1 vs Group 2	Domain	Phylum	Class	Order	Family	Genus	Level	Higher	LD A	Phylotype-OTU	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	Relative (RA, %)	abundance	>=0.1% RA
Washout, pre-HDPs 2&3 vs post-HDPs 1&2	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XI			pre	3.9										
	Bacteria	Firmicutes	Clostridia					pre	4.7										
	Bacteria	Firmicutes	Clostridia	Clostridiales				pre	4.7										
	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae			pre	3.4										
	Bacteria	Bacteroidetes						post	4.7										
	Bacteria	Firmicutes						pre	4.7										
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales				post	4.7										
	Bacteria	Bacteroidetes	Bacteroidia					post	4.7										
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae			pre	3.4										
	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales				pre	3.4										
	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae			pre	4.7										
	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae			post	3.4										
	Bacteria	Actinobacteria	Coriobacteriia					pre	3.5										
	Bacteria	Firmicutes	Bacilli	Bacillales				pre	3.2										
	Bacteria	Lentisphaerae	Lentisphaeria	Victivallales				post	3.5										
	Bacteria	Lentisphaerae	Lentisphaeria					post	3.5										
	Bacteria	Lentisphaerae	Lentisphaeria	Victivallales	Victivallaceae			post	3.4										
	Bacteria	Lentisphaerae						post	3.5										
	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales				post	3.6										
	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Akkermansiaceae			post	3.6										
	Bacteria	Verrucomicrobia	Verrucomicrobiae					post	3.6										
	Bacteria	Verrucomicrobia						post	3.7										

Notes: HDP, healthy dietary pattern.

Supplemental Table S6. OTUs that significantly differed between groups based on LEfSe analyses.

Group 1 vs Group 2		OTU	Domain	Phylum	Class	Order	Family	Genus	Abundant in	LDA	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	RA, %	>=0.1 % RA
All_pre vs post		OTU0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	pre	3.67363	0.039833	0.001071	0.003509	0.030773	0.000722	0.002864	2.13473132	Yes
All_pre vs post		OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	pre	3.85471	0.024086	0.000272	0.00177	0.014685	0.00024	0.001652	1.171481	Yes
All_pre vs post		OTU0025	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	pre	3.45094	0.013265	0.000302	0.001862	0.008018	0.000129	0.001211	0.64304063	Yes
All_pre vs post		OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	pre	3.61994	0.013798	0.000247	0.001685	0.005585	0.000044	0.000709	0.58505898	Yes
All_pre vs post		OTU0032	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	pre	3.37702	0.007796	0.000093	0.001036	0.005237	0.000061	0.000836	0.39391874	Yes
All_pre vs post		OTU0034	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	post	3.24333	0.005057	0.000058	0.000818	0.008583	0.00014	0.001263	0.41331586	Yes
All_pre vs post		OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	pre	3.56989	0.010118	0.000249	0.001693	0.004421	0.000041	0.000686	0.43889908	Yes
All_pre vs post		OTU0037	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	pre	3.41508	0.008117	0.000108	0.001115	0.004896	0.000034	0.000619	0.3931848	Yes
All_pre vs post		OTU0043	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	post	2.69433	0.003597	0.000047	0.000736	0.006505	0.000091	0.001019	0.3061599	Yes
All_pre vs post		OTU0058	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	post	2.90775	0.00184	0.000024	0.000522	0.003611	0.000089	0.001005	0.16524246	Yes
All_pre vs post		OTU0061	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	post	2.64727	0.002691	0.000016	0.000426	0.003111	0.000016	0.000423	0.17562254	Yes
All_pre vs post		OTU0066	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	post	2.71227	0.001363	0.000006	0.000252	0.003291	0.000035	0.000631	0.14112713	Yes
All_pre vs post		OTU0076	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	post	2.77281	0.00192	0.000033	0.000616	0.002126	0.000013	0.000386	0.12246396	Yes
All_pre vs post		OTU0088	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcaceae_unclassified	pre	2.27594	0.002217	0.000016	0.000431	0.001595	0.000013	0.000381	0.11522936	Yes
post13, HDP 3 vs HDP 1		OTU0050	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Post HDP3	3.21715	0.007132	0.00027	0.003426	0.00264	0.000051	0.001229	0.19334207	Yes
post13, HDP 3 vs HDP 1		OTU0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	Post HDP3	3.32568	0.004377	0.000013	0.000739	0.002176	0.000003	0.000284	0.20529489	Yes
post13, HDP 3 vs HDP 1		OTU0063	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	Post HDP1	2.98586	0.001477	0.000015	0.000797	0.003451	0.000015	0.000672	0.18516383	Yes
post23, HDP 3 vs 2		OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	Post HDP3	3.75487	0.022609	0.000613	0.005163	0.010925	0.000077	0.001579	1.171481	Yes
post23, HDP 3 vs 2		OTU0034	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	Post HDP2	3.68898	0.004298	0.000023	0.000997	0.012011	0.000266	0.00293	0.41331586	Yes
post23, HDP 3 vs 2		OTU0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	Post HDP3	3.18505	0.004377	0.000013	0.000739	0.002778	0.000012	0.00063	0.20529489	Yes
post23, HDP 3 vs 2		OTU0063	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	Post HDP2	3.18813	0.001477	0.000015	0.000797	0.002983	0.000013	0.000642	0.18516383	Yes

Supplemental Table S6. continued

Group 1 vs Group 2	OTU	Domain	Phylum	Class	Order	Family	Genus	Abundant in	LDA	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	RA, %	>=0.1% RA
pre13, HDP 3 vs 1	OTU0023	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	preHDP3	2.0276	0.011178	0.000056	0.0016	0.009978	0.000185	0.00237	0.62899083	Yes
pre13, HDP 3 vs 1	OTU0050	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	preHDP3	3.2392	0.003707	0.000043	0.001391	0.001571	0.000023	0.000841	0.19334207	Yes
pre13, HDP 3 vs 1	OTU0073	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	preHDP3	2.86676	0.002784	0.000009	0.00065	0.001534	0.000006	0.000417	0.11984273	Yes
pre23, HDP 3 vs 2	OTU0012	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	preHDP2	3.60879	0.009937	0.000151	0.002616	0.016506	0.000207	0.002542	1.32969856	Yes
pre23, HDP 3 vs 2	OTU0078	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	preHDP2	3.18894	0.001034	0.000009	0.000642	0.001601	0.00001	0.000552	0.13242464	Yes
HDP1, pre vs post	OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	preHDP1	3.96612	0.023596	0.000265	0.002832	0.012753	0.000093	0.001658	1.171481	Yes
HDP1, pre vs post	OTU0025	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	preHDP1	3.44922	0.0163	0.000477	0.003801	0.008972	0.000253	0.002729	0.64304063	Yes
HDP1, pre vs post	OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP1	3.8019	0.012753	0.000131	0.001991	0.004789	0.00003	0.000947	0.58505898	Yes
HDP1, pre vs post	OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	preHDP1	3.33086	0.012064	0.000515	0.00395	0.003326	0.00002	0.000765	0.43889908	Yes
HDP1, pre vs post	OTU0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	preHDP1	3.1361	0.003905	0.000008	0.000493	0.002176	0.000003	0.000284	0.20529489	Yes
HDP1, pre vs post	OTU0066	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	postHDP1	3.20611	0.00124	0.000005	0.00037	0.004673	0.000064	0.001374	0.14112713	Yes
HDP1, pre vs post	OTU0071	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	postHDP1	2.67687	0.001498	0.000003	0.000316	0.002854	0.000014	0.000634	0.13567497	Yes
HDP1, pre vs post	OTU0076	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	preHDP1	3.14531	0.002609	0.000073	0.001491	0.00198	0.000007	0.000468	0.12246396	Yes
HDP2, pre vs post	OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	preHDP2	3.8101	0.022485	0.000201	0.002503	0.010925	0.000077	0.001579	1.171481	Yes
HDP2, pre vs post	OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP2	3.63697	0.012583	0.000161	0.002245	0.004519	0.000021	0.000818	0.58505898	Yes
HDP2, pre vs post	OTU0032	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP2	3.09912	0.00669	0.000025	0.000886	0.00403	0.000025	0.000901	0.39391874	Yes
HDP2, pre vs post	OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	preHDP2	2.99785	0.008319	0.000077	0.001549	0.005047	0.000073	0.001533	0.43889908	Yes
HDP3, pre vs post	OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP3	4.21471	0.017132	0.000558	0.005038	0.0082	0.000091	0.00199	0.58505898	Yes
W, pre vs post	OTU0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	pre	3.60741	0.041338	0.001173	0.00466	0.027271	0.000589	0.00301	2.13473132	Yes
W, pre vs post	OTU0008	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Fusicatenibacter	pre	3.59161	0.034381	0.000737	0.003693	0.023875	0.000292	0.00212	1.80068152	Yes
W, pre vs post	OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	pre	3.55308	0.024386	0.000282	0.002285	0.011881	0.000085	0.001145	1.171481	Yes
W, pre vs post	OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	pre	3.67415	0.014436	0.000321	0.002437	0.00466	0.000025	0.000626	0.58505898	Yes
W, pre vs post	OTU0032	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	pre	2.76317	0.008147	0.000112	0.001439	0.00417	0.000022	0.000576	0.39391874	Yes

Supplemental Table S6. continued

Group 1 vs Group 2	OTU	Domain	Phylum	Class	Order	Family	Genus	Abundant in	LDA	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	RA, %	>=0.1% RA
W, pre vs post	OTU0034	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	post	2.71581	0.005857	0.000083	0.001241	0.010099	0.000174	0.001636	0.41331586	Yes
W, pre vs post	OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	pre	3.44685	0.008928	0.00009	0.001291	0.004147	0.000045	0.000833	0.43889908	Yes
W, pre vs post	OTU0039	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes	post	3.24651	0.00356	0.00003	0.000741	0.00682	0.000093	0.001194	0.33709043	Yes
W, pre vs post	OTU0043	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	post	2.95713	0.00356	0.000057	0.001029	0.006293	0.00008	0.001109	0.3061599	Yes
W, pre vs post	OTU0056	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	pre	3.23707	0.004486	0.000053	0.000994	0.001997	0.000007	0.000334	0.19501966	Yes
W, pre vs post	OTU0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	pre	2.46311	0.003779	0.000011	0.000443	0.002463	0.000007	0.000335	0.20529489	Yes
W, pre vs post	OTU0058	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	post	3.01754	0.001325	0.000003	0.000239	0.004016	0.000113	0.001319	0.16524246	Yes
W, pre vs post	OTU0066	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	post	3.27179	0.001437	0.000006	0.000339	0.003508	0.000041	0.000798	0.14112713	Yes
W, pre vs post	OTU0076	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	post	2.84951	0.001499	0.000009	0.000402	0.002426	0.000016	0.000502	0.12246396	Yes
W, pre vs post	OTU0110	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	pre	2.77961	0.001668	0.000006	0.000319	0.00125	0.000015	0.000475	0.10076016	Yes
W1, pre vs post	OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	preHDP2	3.65353	0.022485	0.000201	0.002503	0.012753	0.000093	0.001658	1.171481	Yes
W1, pre vs post	OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP2	3.62676	0.012583	0.000161	0.002245	0.004789	0.00003	0.000947	0.58505898	Yes
W1, pre vs post	OTU0032	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP2	3.44031	0.00669	0.000025	0.000886	0.004299	0.000019	0.000747	0.39391874	Yes
W1, pre vs post	OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	preHDP2	3.52397	0.008319	0.000077	0.001549	0.003326	0.00002	0.000765	0.43889908	Yes
W1, pre vs post	OTU0056	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	preHDP2	3.4756	0.004122	0.000037	0.001082	0.001908	0.000008	0.00049	0.19501966	Yes
W1, pre vs post	OTU0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	preHDP2	3.19561	0.003648	0.00001	0.000561	0.002176	0.000003	0.000284	0.20529489	Yes
W2, pre vs post	OTU0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	preHDP3	4.09052	0.043787	0.000962	0.006613	0.028561	0.000847	0.005226	2.13473132	Yes
W2, pre vs post	OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	preHDP3	3.74755	0.027151	0.000402	0.004276	0.010925	0.000077	0.001579	1.171481	Yes
W2, pre vs post	OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	preHDP3	3.60534	0.017132	0.000558	0.005038	0.004519	0.000021	0.000818	0.58505898	Yes
W2, pre vs post	OTU0034	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	postHDP2	3.80422	0.002743	0.000014	0.000797	0.012011	0.000266	0.00293	0.41331586	Yes
W2, pre vs post	OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	preHDP3	2.58201	0.009813	0.000112	0.00226	0.005047	0.000073	0.001533	0.43889908	Yes
W2, pre vs post	OTU0038	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Faecalibacillus	preHDP3	3.42793	0.012583	0.00075	0.00584	0.003218	0.000024	0.000882	0.39454784	Yes
W2, pre vs post	OTU0044	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	postHDP2	3.54104	0.002853	0.000024	0.001038	0.008206	0.000137	0.002104	0.36498034	Yes

Supplemental Table S6. continued

Group 1 vs Group 2	OTU	Domain	Phylum	Class	Order	Family	Genus	Abundant in	LDA	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	RA, %	>=0.1 % RA
W2, pre vs post	OTU0058	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	postHDP2	3.12151	0.001089	0.000003	0.000366	0.005556	0.000225	0.002694	0.16524246	Yes
W2, pre vs post	OTU0076	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	postHDP2	2.99944	0.001006	0.000004	0.000444	0.002915	0.000026	0.000921	0.12246396	Yes
W2, pre vs post	OTU0110	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	preHDP3	3.05119	0.002122	0.000007	0.000552	0.000548	0.000001	0.0002	0.10076016	Yes
All_pre vs post	OTU0086	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	post	2.69485	0.000739	0.000004	0.000223	0.000193	0.000013	0.000385	0.08094364	No
All_pre vs post	OTU0125	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	pre	2.74647	0.001011	0.000002	0.000153	0.000737	0.000003	0.000175	0.05284404	No
All_pre vs post	OTU0138	Bacteria	Actinobacteria	Coriobacteriia	Eggerthellales	Eggerthellaceae	Adlercreutzia	pre	2.55024	0.000809	0.000002	0.000134	0.000448	0.000001	0.000084	0.03795544	No
All_pre vs post	OTU0180	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	post	2.62114	0.000289	0	0.000059	0.000479	0	0.000069	0.02327654	No
post13, HDP 3 vs HDP 1	OTU0145	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	postHDP1	3.03372	0.000224	0	0.000086	0.001106	0.000005	0.000383	0.03470511	No
pre12, HDP 2 vs 1	OTU0115	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	preHDP2	2.43174	0.001232	0.000002	0.000272	0.001057	0.000007	0.000444	0.06783748	No
pre12, HDP 2 vs 1	OTU0189	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	preHDP1	2.92913	0.000332	0	0.000115	0.000919	0.000007	0.000462	0.02495413	No
pre123	OTU0167	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	preHDP3	3.25409	NA	NA	NA	NA	NA	NA	0.0295675	No
pre13, HDP 3 vs 1	OTU0152	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Odoribacteraceae	Butyricimonas	preHDP1	2.58272	0.000289	0	0.00012	0.001002	0.000002	0.000259	0.04214941	No
pre13, HDP 3 vs 1	OTU0167	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	preHDP3	2.65083	0.001475	0.000012	0.000736	0.000248	0	0.000072	0.0295675	No
pre13, HDP 3 vs 1	OTU0189	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	preHDP1	2.42685	0.000221	0	0.00006	0.000919	0.000007	0.000462	0.02495413	No
pre23, HDP 3 vs 2	OTU0099	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	preHDP3	2.91277	0.002012	0.000003	0.000363	0.001251	0.000002	0.000263	0.0797903	No
pre23, HDP 3 vs 2	OTU0152	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Odoribacteraceae	Butyricimonas	preHDP2	3.08649	0.000289	0	0.00012	0.000749	0.000001	0.000162	0.04214941	No

Supplemental Table S6. continued

Group 1 vs Group 2	OTU	Domain	Phylum	Class	Order	Family	Genus	Abundant in	LDA	Mean 1	Var 1	SD 1	Mean 2	Var 2	SD 2	RA, %	>=0.1 % RA
HDP1, pre vs post	OTU014 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified	postHDP1	2.7926 1	0.00021 1		0.00008 1	0.00110 6	0.00000 5	0.00038 3	0.0347051 1	No
HDP1, pre vs post	OTU023 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Lawsonibacter	postHDP1	2.5597 7	0.00014 7		0.00004 8			0.00009 1	0.0161467 9	No
HDP2, pre vs post	OTU012 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	preHDP2	2.4880 5	0.00104 2	0.00000 2	0.00025 8	0.00060 6	0.00000 4	0.00036 3	0.0528440 4	No
W, pre vs post	OTU008 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified	post	2.3957 7	0.00058 4	0.00000 2	0.00018 8	0.00216 4	0.00001 6	0.00050 1	0.0809436 4	No
W, pre vs post	OTU009 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified	pre	2.7778 8	0.00156 1	0.00000 3	0.00021 9	0.00093 3	0.00000 1	0.00011 3	0.0797903 4	No
W, pre vs post	OTU012 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	pre	2.4586 6	0.00113 4	0.00000 3	0.00022 5	0.00069 5	0.00000 3	0.00021 8	0.0528440 4	No
W, pre vs post	OTU013 8	Bacteria	Actinobacteri a	Coriobacterii a	Eggerthellales	Eggerthellaceae	Adlercreutzia	pre	2.6399 4	0.00088 7	0.00000 2	0.00018 1	0.00035 9		0.00008 5	0.0379554 4	No
W, pre vs post	OTU014 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified	post	2.5768 2	0.00052 2	0.00000 2	0.00017 2	0.00092 4	0.00000 4	0.00024 1	0.0347051 1	No
W, pre vs post	OTU018 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Ruminococcaceae _unclassified	post	2.7279 3	0.00031 4		0.00008 0	0.00051 8		0.00008 3	0.0232765 4	No
W, pre vs post	OTU019 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Dysosmobacter	post	2.6652 8	0.00025 8		0.00007 9	0.00041 1		0.00008 0	0.0195019 7	No
W1, pre vs post	OTU014 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Intestinimonas	preHDP2	3.0728 5	0.00111 8	0.00000 2	0.00023 5	0.00042 8		0.00011 7	0.0473918 7	No
W2, pre vs post	OTU008 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified	postHDP2	3.0041 1	0.00045 5	0.00000 2	0.00028 2	0.00243 5	0.00002 1	0.00083 1	0.0809436 4	No
W2, pre vs post	OTU009 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified	preHDP3	2.9018 9	0.00201 2	0.00000 3	0.00036 3	0.00101 7	0.00000 1	0.00017 6	0.0797903 4	No
W2, pre vs post	OTU012 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	preHDP3	2.3997 2	0.00126 8	0.00000 4	0.00041 6	0.00060 4	0.00000 4	0.00036 3	0.0528440 4	No
W2, pre vs post	OTU013 8	Bacteria	Actinobacteri a	Coriobacterii a	Eggerthellales	Eggerthellaceae	Adlercreutzia	preHDP3	2.7917 1	0.00107 5	0.00000 2	0.00036 0.0003	0.00101 3	0.00000 0	0.00011 5	0.0379554 4	No
W2, pre vs post	OTU016 7	Bacteria	Firmicutes	Bacilli	Lactobacillale s	Streptococcaceae	Streptococcus	preHDP3	2.9893 7	0.00147 5	0.00001 2	0.00073 6	0.00044 1	0.00000 1	0.00015 1	0.0295675 4	No
W2, pre vs post	OTU018 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Ruminococcaceae _unclassified	postHDP2	2.3922 7	0.00024 8		0.00014 2	0.00046 9		0.00009 5	0.0232765 4	No
W2, pre vs post	OTU024 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Ruminococcaceae _unclassified	preHDP3	2.9272 7		0 0		0.00048 9	0.00000 3	0.00029 9	0.0222280 5	No
post12	None	#N/A						NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Notes: HDP, healthy dietary pattern.

Supplemental Table S7. Comparison of post/pre fold changes of selected taxa with at least 0.1% of relative abundance among HDPs 1-3 and between washouts 1-2.

Phylotype-OTU	Domain	Phylum	Class	Order	Family	Genus	Shapiro-Wilk test of post/pre p-value	p-value after log2 transformation	Levene's test for Homogeneity of Variance p-value	Anova p-value, HDP	Welch Two Sample t-test p-value, washout
OTU003	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	<0.001	0.81	NA	0.84	0.84
OTU009	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified	<0.001	0.33	NA	0.09	0.39
OTU011	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes	<0.001	0.52	NA	0.58	0.82
OTU013	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	<0.001	0.08	NA	0.99	0.84
OTU014	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	<0.001	0.52	NA	0.47	0.74
OTU016	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	<0.001	0.73	NA	0.58	0.69
OTU018	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	<0.001	0.19	NA	0.74	0.91
OTU020	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	<0.001	0.77	NA	0.20	0.31
OTU021	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	<0.001	0.29	NA	0.91	0.92
OTU023	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	<0.001	0.02	0.89	0.11	0.13
OTU024	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	<0.001	0.15	NA	0.81	0.74
OTU026	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	<0.001	0.15	NA	0.91	0.74
OTU030	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	<0.001	0.62	NA	0.79	0.85
OTU032	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Akkermansiaceae	Akkermansia	<0.001	0.01	0.72	0.32	0.98
OTU035	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Faecalibacillus	<0.001	0.21	NA	0.18	0.21
OTU038	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	<0.001	0.86	NA	0.61	0.20
OTU049	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV	<0.001	0.21	NA	0.55	0.76
OTU054	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	<0.001	<0.01	0.98	0.88	0.44
OTU065	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	<0.001	<0.01	0.81	0.28	0.65

Notes: HDP, healthy dietary pattern.

Supplemental Table S8. Comparison of post/pre fold changes of selected OTUs with at least 0.1% of relative abundance among HDPs 1-3 and between washouts 1-2.

OTU	Domain	Phylum	Class	Order	Family	Genus	Shapiro-Wilk test of post/pre p-value	p-value after log2 transformation	Levene's test for Homogeneity of Variance p-value	Anova p- value, HDP	Welch Two Sample t-test p-value, washout
OTU0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	<0.001	<0.01	0.66	0.24	0.51
OTU0008	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Fusicatenibacter	<0.001	0.15	NA	0.56	0.64
OTU0012	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	<0.001	0.23	NA	0.64	0.46
OTU0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	<0.001	0.34	NA	0.44	0.55
OTU0023	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	<0.001	0.45	NA	0.54	0.98
OTU0025	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	<0.001	0.36	NA	0.81	0.70
OTU0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	<0.001	0.65	NA	0.48	0.97
OTU0032	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Mediterraneibacter	<0.001	0.53	NA	0.31	0.78
OTU0034	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	<0.001	0.39	NA	0.84	0.06
OTU0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	<0.001	0.32	NA	0.80	0.79
OTU0037	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	<0.001	<0.01	0.96	0.29	0.43
OTU0038	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Faecalibacillus	<0.001	0.07	NA	0.44	0.16
OTU0039	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes	<0.001	0.61	NA	0.83	0.44
OTU0043	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	<0.001	<0.01	0.50	0.56	0.18
OTU0044	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	<0.001	0.40	NA	0.57	0.60
OTU0050	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	<0.001	<0.01	0.39	0.42	0.83
OTU0056	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	<0.001	0.76	NA	0.61	0.50
OTU0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	<0.001	0.03	0.98	0.08	0.92
OTU0058	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	<0.001	0.04	0.70	0.82	0.69
OTU0061	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	<0.001	0.60	NA	0.70	0.16
OTU0063	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	<0.001	0.20	NA	0.37	0.53
OTU0066	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	<0.001	0.61	NA	0.53	0.95
OTU0071	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	<0.001	0.03	0.76	0.11	0.41
OTU0073	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	<0.001	0.02	0.27	0.23	0.72
OTU0076	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	<0.001	0.66	NA	0.40	0.14
OTU0078	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	<0.001	<0.01	0.76	0.77	0.59

Notes: HDP, healthy dietary pattern.

Supplemental Table S9. Participant responses in cardiovascular risk factors from consuming study diets for 3 times (HDPs 1-3). Results are presented as LS means ± SEM.

	HDP 1									Washout 1			HDP 2									Washout 2			HDP 3									p-value	
Outcomes [1]	Pre	SE	N	Post	SE	N	Change	SE	N	Change	SE	N	Pre	SE	N	Post	SE	N	Change	SE	N	Change	SE	N	Pre	SE	N	Post	SE	N	Change	SE	N	time	time by HDP
WHC	0.87	0.01	17	0.86	0.01	17	-0.01	0.01	17	0.01	0.01	17	0.87	0.01	17	0.86	0.01	17	-0.01	0.01	17	0.0005	0.01	12	0.86	0.01	12	0.86	0.01	12	0.001	0.01	12	0.45	0.35
SAD [2]	18.9	0.3	17	18.9	0.3	17	0.03	0.2	17	0.3	0.3	17	19.3	0.3	17	18.8	0.3	17	-0.4	0.2	17	0.3	0.3	12	19.1	0.3	12	19.2	0.3	12	0.02	0.2	12	0.59	0.06
SysBP	108 ^{a,b}	1.2	17	109 ^{c,d}	1.2	17	0.9	1.4	17	-1.8	1.5	17	107 ^a	1.2	17	106 ^c	1.2	17	-1.0	1.4	17	4.2	1.6	12	110 ^b	1.3	12	110 ^d	1.4	12	-0.3	1.6	12	0.93	0.41
DiaBP	68 ^a	1.3	17	67 ^c	1.3	17	-0.8	1.4	17	0.5	1.5	17	68 ^a	1.3	17	67 ^c	1.3	17	-0.8	1.4	17	5.3*	1.6	12	72 ^b	1.4	12	70 ^d	1.4	12	-2.2	1.5	12	0.33	0.45
TC	163	5.3	17	146 ^a	5.1	17	-17.4*	5.0	17	19.8*	5.4	17	165	5.3	17	150 ^a	5.0	17	-15.7*	5.0	17	21.6*	5.7	12	171	5.6	12	158 ^b	5.2	12	-13.3*	5.2	12	0.01	0.49
TAG [2]	82.6	6.9	17	71.2	6.1	17	-11.4	6.8	17	10.9	7.5	17	82.2	6.9	17	65.5	6.0	17	-16.6*	6.8	17	13.1	8.0	12	78.7	7.4	12	70.9	6.4	12	-7.8	7.4	12	0.08	0.59
HDLC	53	1.9	17	50	2.0	17	-3.5	1.9	17	3.6	2.1	17	53	1.9	17	52	2.0	17	-1.3	1.9	17	2.1	2.3	12	54	2.1	12	52	2.1	12	-2.2	2.0	12	0.20	0.29
LDLC	93 ^a	4.6	17	82 ^c	3.7	17	-11.6*	4.2	17	13.9*	4.6	17	96 ^{a,b}	4.6	17	85 ^c	3.7	17	-11.0*	4.2	17	16.7*	4.8	12	101 ^b	4.8	12	91.7 ^d	3.9	12	-9.7*	4.5	12	0.02	0.82
CHOL/HDLC [2]	3.1	0.2	17	3.0	0.1	17	-0.1	0.1	17	0.2	0.2	17	3.2	0.2	17	3.0	0.1	17	-0.3	0.1	17	0.3	0.2	12	3.3	0.2	12	3.1	0.1	12	-0.2	0.2	12	0.18	0.51
Glucose	86.2	1.5	17	84.1	1.4	17	-2.1	1.8	17	1.2	1.9	17	85.2	1.5	17	86.5	1.3	17	1.2	1.8	17	1.6	2.1	12	88.1	1.8	12	88.2	1.6	12	0.1	2.1	12	0.85	0.29
BUN	12.9	0.5	17	12.8	0.5	17	-0.1	0.7	17	0.4	0.7	17	13.2	0.5	17	13.9	0.5	17	0.8	0.7	17	-0.5	0.8	12	13.4	0.6	12	13.5	0.6	12	0.1	0.7	12	0.67	0.38
Creatinine [2]	0.9	0.02	17	0.9	0.02	17	0.01	0.02	17	-0.04	0.02	17	0.8	0.02	17	0.9	0.02	17	0.01	0.02	17	0.01	0.02	12	0.9	0.02	12	0.9	0.02	12	0.01	0.02	12	0.54	0.84

[1] Data were analyzed using repeated-measures ANOVA adjusted for age, sex, and body mass index.
[2] Data were transformed before ANOVA analyses using Box Cox transformation with lambda of -1 for SAD, -0.5 for TAG and CHOL/HDLC ratio, and -1.25 for creatinine. Results are presented using untransformed LS means ± SEM.
Different superscripts denote significant difference among HDPs at pre (a and b) and at post (c and d); * significant change; Abbreviations: HDP, healthy dietary pattern; WHC, waist-to-hip circumference; SAD, sagittal abdominal diamter; SysBP, systolic blood pressure; DiaBP, diastolic blood pressure; TC, total cholesterol; TAG, triglycerides; HDLC, HDL-cholesterol; LDLC, LDL-cholesterol; BUN, blood urea nitrogen.

Supplemental Table S10. Raw (unadjusted) means and SD of participant responses in cardiovascular risk factors from consuming study diets for 3 times (HDPs 1-3).

	HDP 1									Washout 1			HDP 2									Washout 2			HDP 3								
Outcomes	Pre	SD	N	Post	SD	N	Change	SD	N	Change	SD	N	Pre	SD	N	Post	SD	N	Change	SD	N	Change	SD	N	Pre	SD	N	Post	SD	N	Change	SD	N
WHC	0.87	0.05	17	0.86	0.06	17	-0.01	0.03	17	0.01	0.02	17	0.87	0.05	17	0.86	0.06	17	-0.01	0.02	17	-0.003	0.03	12	0.87	0.06	12	0.87	0.06	12	-0.001	0.01	12
SAD (cm)	19.0	2.4	17	18.9	2.3	17	-0.1	0.7	17	0.5	0.7	17	19.4	2.6	17	18.8	2.3	17	-0.5	0.6	17	0.2	0.4	12	19.6	2.5	12	19.5	2.4	12	-0.01	0.5	12
SysBP (mm Hg)	109	9.8	17	110	9.6	17	0.8	4.4	17	-1.6	3.8	17	108	9.8	17	107	9.6	17	-1.1	3.6	17	4.2	3.6	12	112	9.7	12	111	10.3	12	-0.5	5.4	12
DiaBP (mm Hg)	68	5.6	17	67	6.0	17	-0.7	5.1	17	0.4	4.7	17	68	7.0	17	67	5.9	17	-0.8	3.2	17	4.7	2.6	12	72	5.2	12	70	4.0	12	-1.8	3.5	12
TC (mg/dL)	164	23.9	17	146	23.1	17	-17.5	13.6	17	19.9	16.3	17	166	26.5	17	150	23.7	17	-15.7	15.6	17	21.4	13.1	12	168	20.7	12	155	22.5	12	-12.7	9.7	12
TAG (mg/dL)	83	32.5	17	72	20.3	17	-11.1	24.5	17	10.6	22.4	17	83	35.0	17	66	19.9	17	-16.3	21.1	17	15.7	28.0	12	79	36.6	12	70	32.9	12	-9.3	15.3	12
HDLC (mg/dL)	53	9.2	17	49	9.7	17	-3.4	5.7	17	3.5	4.8	17	53	10.2	17	51	9.4	17	-1.2	4.3	17	2.3	6.5	12	52	8.5	12	49	8.6	12	-2.4	5.4	12
LDLC (mg/dL)	94	23.8	17	82.4	20.0	17	-11.90	9.6	17	14.3	13.8	17	96.7	23.6	17	85.4	20.4	17	-11.3	14.0	17	16.0	11.1	12	100.3	24.1	12	91.8	23.1	12	-8.5	10.1	12
TC/HDLC	3.2	0.7	17	3.1	0.7	17	-0.1	0.3	17	0.2	0.4	17	3.3	0.8	17	3.0	0.7	17	-0.3	0.3	17	-0.02	0.3	12	3.4	0.9	12	3.3	0.8	12	-0.1	0.4	12
Glucose (mg/dL)	86.2	5.6	17	84.0	4.9	17	-2.2	4.5	17	1.3	6.0	17	85.3	7.3	17	86.4	7.2	17	1.1	8.4	17	3.8	6.7	12	87.8	5.7	12	87.6	3.3	12	-0.1	5.9	12
BUN (mg/dL)	13.1	2.8	17	12.9	2.8	17	-0.2	2.1	17	0.5	2.2	17	13.4	2.7	17	14.0	2.3	17	0.7	2.7	17	-0.8	2.3	12	13.5	2.6	12	13.8	1.7	12	0.2	2.0	12
Creatinine (mg/dL)	0.9	0.1	17	0.9	0.1	17	0.01	0.06	17	-0.04	0.07	17	0.9	0.1	17	0.9	0.1	17	0.01	0.05	17	-0.003	0.06	12	0.9	0.1	12	0.9	0.1	12	0.02	0.06	12

Abbreviations: HDP, healthy dietary pattern; WHC, waist-to-hip circumference; SAD, sagittal abdominal diameter; SysBP, systolic blood pressure; DiaBP, diastolic blood pressure; TC, total cholesterol; TAG, triglycerides; HDLC, high-density lipoprotein-cholesterol; LDLC, low-density lipoprotein cholesterol; BUN, blood urea nitrogen.

Supplemental Table S11. Rho values of significant correlations between changes in blood lipids and bacterial taxa.

TC	HDPs	HDP 1	HDP 2	HDP 3	Washouts	Washout 1	Washout 2
OTU0039_Alistipes	n.s.	-0.624	-0.563	n.s.	n.s.	n.s.	n.s.
OTU0056_Roseburia	n.s.	n.s.	n.s.	n.s.	n.s.	0.505	n.s.
OTU0037_Lachnospiraceae_unclassified	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	-0.710
OTU0057_Dorea	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	-0.624
Romboutsia	n.s.	n.s.	n.s.	n.s.	n.s.	-0.498	n.s.
Bacteroidetes_unclassified	n.s.	n.s.	n.s.	n.s.	n.s.	-0.576	n.s.
Dorea	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	-0.638
Triglycerides	HDPs	HDP 1	HDP 2	HDP 3	Washouts	Washout 1	Washout 2
OTU0025_Collinsella	-0.540	n.s.	n.s.	n.s.	n.s.	-0.548	n.s.
OTU0037_Lachnospiraceae_unclassified	-0.580	-0.802	n.s.	n.s.	n.s.	n.s.	n.s.
OTU0066_Roseburia	-0.550	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
OTU0043_Ruminococcaceae_unclassified	n.s.	n.s.	n.s.	n.s.	-0.580	n.s.	n.s.
OTU0026_Mediterraneibacter	n.s.	-0.52	n.s.	n.s.	n.s.	n.s.	n.s.
OTU0017_Dorea	n.s.	n.s.	-0.608	n.s.	n.s.	n.s.	n.s.
OTU0032_Mediterraneibacter	n.s.	n.s.	-0.639	n.s.	n.s.	n.s.	n.s.
OTU0038_Faecalibacillus	n.s.	n.s.	-0.529	n.s.	n.s.	n.s.	n.s.
OTU0057_Dorea	n.s.	n.s.	-0.582	n.s.	n.s.	n.s.	n.s.
OTU0076_Lachnospira	n.s.	n.s.	0.659	n.s.	n.s.	n.s.	n.s.
OTU0071_Ruminococcaceae_unclassified	n.s.	n.s.	n.s.	n.s.	n.s.	-0.496	n.s.
Parabacteroides	n.s.	n.s.	n.s.	n.s.	0.490	n.s.	n.s.
Akkermansia	n.s.	n.s.	n.s.	n.s.	-0.490	n.s.	n.s.
Dorea	n.s.	n.s.	-0.503	n.s.	n.s.	n.s.	n.s.
Bacteroidetes_unclassified	n.s.	n.s.	-0.692	n.s.	n.s.	n.s.	n.s.

Supplemental Table S11. continued

TC/HDL-C Ratio	HDPs	HDP 1	HDP 2	HDP 3	Washouts	Washout 1	Washout 2
OTU0057_Dorea	-0.490	n.s.	n.s.	n.s.	-0.600	n.s.	-0.645
OTU0056_Roseburia	n.s.	0.493	n.s.	n.s.	n.s.	n.s.	n.s.
OTU0066_Roseburia	n.s.	-0.572	n.s.	n.s.	n.s.	n.s.	n.s.
OTU0017_Dorea	n.s.	n.s.	-0.624	n.s.	n.s.	n.s.	n.s.
OTU0038_Faecalibacillus	n.s.	n.s.	-0.563	n.s.	n.s.	n.s.	n.s.
OTU0076_Lachnospira	n.s.	n.s.	0.721	n.s.	n.s.	n.s.	n.s.
OTU0061_Lachnospiraceae_unclassified	n.s.	n.s.	n.s.	0.668	n.s.	n.s.	n.s.
OTU0025_Collinsella	n.s.	n.s.	n.s.	n.s.	n.s.	-0.529	n.s.
OTU0026_Mediterraneibacter	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	-0.755
Blautia	-0.580	n.s.	n.s.	n.s.	-0.650	n.s.	-0.709
Mediterraneibacter	-0.490	n.s.	n.s.	n.s.	-0.640	n.s.	-0.809
Collinsella	-0.540	n.s.	n.s.	n.s.	-0.730	-0.588	-0.745
Bacteroidetes_unclassified	-0.580	n.s.	-0.626	0.698	n.s.	n.s.	n.s.
Clostridiales_unclassified	n.s.	n.s.	n.s.	n.s.	-0.570	-0.556	n.s.
Dorea	n.s.	n.s.	n.s.	n.s.	-0.690	n.s.	-0.664
Akkermansia	n.s.	n.s.	n.s.	n.s.	-0.530	n.s.	n.s.
Turicibacter	n.s.	n.s.	n.s.	n.s.	-0.610	n.s.	-0.756
Ruminococcus	n.s.	n.s.	-0.648	n.s.	n.s.	n.s.	n.s.
Romboutsia	n.s.	n.s.	n.s.	n.s.	n.s.	-0.650	n.s.
Anaerostipes	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	-0.736

Notes: HDP, healthy dietary pattern; TC, total cholesterol; LDL-C, low-density lipoprotein cholesterol; HDL-C, high-density lipoprotein cholesterol; OTU, operational taxonomic unit; n.s., not significant.