

Supplementary Information

Supplementary Table 1. Correlation Between BDI-II Score and Intestinal Microbiome and Dietary Intake

Correlation between BDI and intestinal microbiome				Correlation between BDI and dietary intake			
	Pearson's <i>r</i>	<i>p</i> -value	<i>q</i> -value		Pearson's <i>r</i>	<i>p</i> -value	<i>q</i> -value
Shannon α	-0.12	0.03 *	0.07 †	staple food	-0.14	0.01 *	0.03 *
Actinomyces	0.09	0.10	0.11	unrefined grain	-0.02	0.75	0.32
Bifidobacterium	-0.07	0.18	0.13	root vegetable	-0.07	0.23	0.16
Collinsella	-0.01	0.87	0.36	green and yellow vegetables	-0.08	0.15	0.13
Eggerthella	0.01	0.82	0.35	light colored vegetables	-0.07	0.18	0.13
Bacteroides	-0.07	0.18	0.13	fruits	-0.14	0.01 *	0.03 *
Odoribacter	-0.06	0.25	0.16	meat	-0.19	0.00 **	0.00
Alistipes	-0.10	0.07	0.10	fish and shellfish	-0.06	0.26	0.17
Parabacteroides	0.00	0.94	0.37	egg	-0.09	0.12	0.12
Erysipelatoclostridium	0.06	0.30	0.18	milk and cheese	-0.23	0.00 **	0.00 **
Turicibacter	-0.04	0.44	0.23	yogurt and lactic fermenting beverage	-0.13	0.02 *	0.05 †
Streptococcus	-0.10	0.07	0.10	soy product	-0.07	0.18	0.13
Intestinibacter	-0.01	0.90	0.36	natto	0.10	0.08	0.10
Romboutsia	-0.04	0.46	0.23	pickled vegetables	-0.02	0.65	0.29
Agathobacter	-0.01	0.89	0.36	seaweed	-0.11	0.05	0.09 †
Anaerostipes	-0.11	0.04 *	0.08 †	mushrooms	-0.10	0.08	0.10
Blautia	0.00	0.98	0.38	snacks	-0.11	0.05	0.09 †
Dorea	-0.05	0.38	0.21	sugary drinks	0.03	0.61	0.27
Fusicatenibacter	-0.08	0.15	0.13	Japanese Diet Index (JDI12)	-0.07	0.23	0.16
Lachnoclostridium	0.09	0.11	0.12				
Lachnospira	-0.18	0.00 **	0.00 **				
Roseburia	-0.08	0.14	0.13				
Sellimonas	-0.05	0.40	0.22				
Tuzzerella	-0.03	0.53	0.25				
UCG-004	-0.06	0.30	0.18				
Colidextribacter	-0.05	0.36	0.21				
Flavonifractor	-0.05	0.35	0.21				
Oscillibacter	-0.03	0.59	0.27				
Butyricicoccus	-0.12	0.02 *	0.05 †				
Faecalibacterium	-0.15	0.00 **	0.00 **				
Negativibacillus	-0.04	0.51	0.25				
Subdoligranulum	-0.15	0.01 *	0.03 *				
UBA1819	-0.08	0.14	0.13				
Monoglobus	-0.10	0.08	0.10				
Phascolarctobacterium	-0.09	0.09	0.11				
Veillonella	0.04	0.43	0.23				
Bilophila	-0.07	0.17	0.13				
Parasutterella	-0.03	0.54	0.25				
Sutterella	-0.04	0.46	0.23				
Escherichia-Shigella	0.06	0.25	0.16				

***p* or *q* < .01, **p* or *q* < .05, †*q* < .10.

Supplementary Table 2. Statistical Comparisons of Intestinal Microbiome Between the High-Risk and Healthy Groups

		All participants (N = 344)		Healthy Group (N = 296)		High Risk Group (N = 48)		Mann-Whitney <i>U</i> test (High risk vs Healthy)		
		<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>	<i>W</i>	<i>p</i> -value	<i>q</i> -value
	Shannonα	6.12	0.48	6.14	0.47	6.02	0.51	8027.00	0.15	0.26
	Actinomyces	-4.02	0.82	-4.03	0.82	-3.94	0.86	6704.00	0.52	0.40
	Bifidobacterium	-1.24	0.38	-1.22	0.30	-1.34	0.69	7197.00	0.88	0.46
	Collinsella	-2.76	1.60	-2.77	1.60	-2.69	1.61	6738.00	0.56	0.40
	Eggerthella	-2.94	0.78	-2.95	0.77	-2.91	0.80	6748.00	0.58	0.40
	Bacteroides	-0.56	0.15	-0.56	0.14	-0.57	0.20	6913.00	0.77	0.46
	Odoribacter	-3.13	1.16	-3.13	1.16	-3.17	1.17	7488.00	0.54	0.40
	Alistipes	-2.21	1.20	-2.19	1.18	-2.35	1.27	7644.00	0.40	0.40
	Parabacteroides	-1.88	1.09	-1.89	1.08	-1.81	1.14	6051.50	0.10	0.20
	Erysipelatoclostridium	-2.80	0.79	-2.81	0.81	-2.72	0.67	6930.00	0.79	0.46
	Turicibacter	-3.91	1.04	-3.89	1.04	-4.02	1.08	7562.00	0.45	0.40
	Streptococcus	-2.09	0.69	-2.08	0.66	-2.14	0.86	6957.00	0.82	0.46
	Intestinibacter	-3.43	1.04	-3.43	1.04	-3.45	1.08	7095.00	0.99	0.49
	Romboutsia	-3.71	1.13	-3.69	1.12	-3.85	1.21	7525.00	0.49	0.40
	Agathobacter	-3.04	1.54	-3.01	1.54	-3.19	1.56	7597.00	0.43	0.40
	Anaerostipes	-2.07	0.74	-2.04	0.70	-2.27	0.93	8019.00	0.15	0.26
	Blautia	-1.31	0.23	-1.32	0.23	-1.28	0.23	6404.00	0.27	0.35
	Dorea	-2.40	1.05	-2.38	1.04	-2.55	1.16	7658.00	0.39	0.40
	Fusicatenibacter	-2.45	1.30	-2.43	1.28	-2.62	1.43	7375.00	0.67	0.43
	Lachnoclostridium	-1.86	0.36	-1.88	0.36	-1.74	0.34	5536.00	0.01 *	0.04 *
	Lachnospira	-2.70	1.17	-2.63	1.12	-3.13	1.34	8672.50	0.01 *	0.04 *
	Roseburia	-3.20	1.23	-3.16	1.20	-3.43	1.40	7789.50	0.28	0.35
	Sellimonas	-2.99	1.11	-2.98	1.12	-3.06	1.11	7500.00	0.53	0.40
	Tuzzerella	-3.89	1.05	-3.86	1.05	-4.06	1.08	7721.00	0.31	0.36
	Lachnospiraceae_UCG-004	-3.59	1.20	-3.59	1.20	-3.58	1.25	7061.00	0.94	0.48
	Colidextribacter	-3.04	1.05	-3.04	1.06	-3.01	1.04	6972.50	0.84	0.46
	Flavonifractor	-2.96	0.75	-2.96	0.74	-2.94	0.81	6700.00	0.53	0.40
	Oscillibacter	-2.88	0.91	-2.88	0.91	-2.90	0.95	7207.00	0.87	0.46
	Butyrivibrio	-2.60	0.61	-2.59	0.60	-2.66	0.63	7286.00	0.78	0.46
	Faecalibacterium	-1.53	0.97	-1.47	0.88	-1.89	1.37	8442.50	0.04 *	0.08 †
	Negativibacillus	-3.94	1.04	-3.93	1.05	-4.02	1.02	7482.50	0.53	0.40
	Subdoligranulum	-3.07	1.37	-3.02	1.34	-3.36	1.47	7928.50	0.19	0.31
	UBA1819	-3.72	0.94	-3.71	0.92	-3.81	1.06	7422.50	0.61	0.41
	Monoglobus	-2.91	1.15	-2.88	1.14	-3.12	1.20	7846.00	0.24	0.35
	Phascolarctobacterium	-3.19	1.48	-3.17	1.46	-3.34	1.59	7179.00	0.90	0.46
	Veillonella	-3.25	1.51	-3.26	1.51	-3.16	1.58	6808.00	0.63	0.41
	Bilophila	-3.11	1.17	-3.10	1.16	-3.17	1.24	7014.00	0.89	0.46
	Parasutterella	-3.18	1.47	-3.14	1.46	-3.40	1.52	7750.00	0.30	0.36
	Sutterella	-3.03	1.64	-3.00	1.63	-3.21	1.69	7398.00	0.63	0.41
	Escherichia-Shigella	-3.52	1.33	-3.57	1.32	-3.26	1.39	6137.50	0.12	0.22

***p* or *q* < .01, **p* or *q* < .05, †*q* < .10.

Supplementary Table 3. Statistical Comparisons Between High and Low JDI12 Groups

		JDI low Group (N = 172)		JDI high Group (N = 172)		T test (JDI high vs low)		
		Mean	SD	Mean	SD	t	p-value	q-value
	age	34.08	5.04	35.19	4.46	-2.16	0.03 *	0.07 †
	Depression (BDI-II)	11.93	8.73	10.08	7.45	2.09	0.04 *	0.08 †
	MDPStotal	15.48	5.75	13.84	5.52	2.70	0.01 **	0.02 *
Psychological and physical indices	Physical activity index (MDPS_PAI)	3.27	1.58	2.89	1.45	2.35	0.02 *	0.05 †
	Somatic disorders index (MDPS_SDI)	1.04	1.24	0.91	1.21	0.97	0.33	0.49
	Hormone activity index (MDPS_HAI)	4.38	1.70	4.12	1.77	1.40	0.16	0.29
	Microvascular disorders index (MDPS_MDI)	3.88	2.06	3.38	1.91	2.34	0.02 *	0.05 †
	Meteoropathy related index (MDPS_MRI)	2.91	1.69	2.54	1.59	2.07	0.04 *	0.08 †
	sleeping time (hours)	6.77	1.11	6.76	1.07	0.06	0.95	0.78
	sleeping quality	1.89	0.62	1.93	0.58	-0.63	0.53	0.58
	staple food	4.39	0.98	4.62	0.84	-2.37	0.02 *	0.05 †
	unrefined grain	1.15	0.60	1.66	1.14	-5.29	0.00 **	0.00 **
	root vegetable	2.81	0.95	3.77	0.92	-9.53	0.00 **	0.00 **
	green and yellow vegetables	2.49	0.78	3.65	0.95	-12.30	0.00 **	0.00 **
	light colored vegetables	2.76	0.87	3.68	0.96	-9.36	0.00 **	0.00 **
	fruits	2.06	0.84	3.22	0.94	-12.11	0.00 **	0.00 **
	meat	3.24	0.97	3.77	0.89	-5.34	0.00 **	0.00 **
	fish and shellfish	2.22	0.69	3.00	0.83	-9.46	0.00 **	0.00 **
	egg	2.77	0.84	3.27	0.84	-5.51	0.00 **	0.00 **
Dietary intake	milk and cheese	2.66	1.16	3.27	1.12	-4.92	0.00 **	0.00 **
	yogurt and lactic fermenting beverage	1.93	0.88	2.68	1.13	-6.89	0.00 **	0.00 **
	soy product	2.10	0.62	3.11	0.92	-11.97	0.00 **	0.00 **
	natto	1.52	0.65	2.28	0.93	-8.81	0.00 **	0.00 **
	pickled vegetables	1.53	0.58	1.84	0.87	-3.86	0.00 **	0.00 **
	seaweed	1.75	0.58	2.45	0.77	-9.44	0.00 **	0.00 **
	mushrooms	2.11	0.63	3.04	0.81	-11.84	0.00 **	0.00 **
	snacks	3.34	1.05	3.56	0.96	-2.09	0.04 *	0.08 †
	sugary drinks	3.03	1.23	2.72	1.15	2.45	0.01 *	0.04 *
	Japanese Diet Index (JDI12)	13.70	1.93	20.49	3.19	-23.91	0.00 **	0.00 **
	Shannonα	6.08	0.50	6.16	0.46	-1.56	0.12	0.23
	Actinomyces	-4.00	0.83	-4.04	0.81	0.43	0.67	0.66
	Bifidobacterium	-1.24	0.43	-1.24	0.33	-0.11	0.91	0.76
	Collinsella	-2.75	1.63	-2.78	1.57	0.20	0.84	0.75
	Eggerthella	-2.96	0.80	-2.92	0.76	-0.42	0.68	0.66
	Bacteroides	-0.56	0.16	-0.56	0.15	0.20	0.84	0.75
	Odoribacter	-3.13	1.18	-3.13	1.15	0.02	0.98	0.79
	Alistipes	-2.25	1.19	-2.17	1.21	-0.67	0.50	0.58
	Parabacteroides	-1.95	1.19	-1.81	0.98	-1.13	0.26	0.40
	Erysipelatoclostridium	-2.77	0.78	-2.83	0.80	0.64	0.52	0.58
	Turicibacter	-3.88	1.05	-3.94	1.03	0.53	0.60	0.61
	Streptococcus	-2.11	0.75	-2.07	0.62	-0.58	0.56	0.60
	Intestinibacter	-3.45	1.05	-3.41	1.04	-0.36	0.72	0.68
	Romboutsia	-3.66	1.13	-3.77	1.14	0.90	0.37	0.53
	Agathobacter	-3.23	1.59	-2.85	1.47	-2.32	0.02 *	0.05 †
	Anaerostipes	-2.08	0.68	-2.07	0.80	-0.12	0.90	0.76
	Blautia	-1.31	0.22	-1.32	0.23	0.38	0.70	0.68
	Dorea	-2.47	1.11	-2.33	1.00	-1.18	0.24	0.38
	Fusicatenibacter	-2.49	1.31	-2.42	1.29	-0.54	0.59	0.61
Intestinal microbiome	Lachnoclostridium	-1.87	0.37	-1.85	0.35	-0.65	0.52	0.58
	Lachnospira	-2.77	1.17	-2.62	1.16	-1.19	0.23	0.38
	Roseburia	-3.21	1.29	-3.19	1.18	-0.13	0.90	0.76
	Sellimonas	-2.95	1.11	-3.03	1.12	0.64	0.52	0.58
	Tuzzerella	-3.97	1.06	-3.81	1.05	-1.38	0.17	0.29
	Lachnospiraceae_UCG-004	-3.64	1.22	-3.54	1.19	-0.74	0.46	0.57
	Colidextribacter	-3.03	1.04	-3.05	1.07	0.19	0.85	0.75
	Flavonifractor	-2.98	0.76	-2.93	0.73	-0.70	0.48	0.58
	Oscillibacter	-2.91	0.89	-2.85	0.94	-0.55	0.58	0.61
	Butyricicoccus	-2.63	0.68	-2.57	0.53	-0.98	0.33	0.49
	Faecalibacterium	-1.53	0.98	-1.52	0.97	-0.12	0.91	0.76
	Negativibacillus	-3.99	1.04	-3.90	1.05	-0.79	0.43	0.56
	Subdoligranulum	-3.26	1.42	-2.88	1.29	-2.55	0.01 *	0.04 *
	UBA1819	-3.76	0.93	-3.68	0.96	-0.74	0.46	0.57
	Monoglobus	-2.93	1.12	-2.90	1.17	-0.29	0.77	0.72
	Phascolarctobacterium	-3.26	1.49	-3.12	1.47	-0.88	0.38	0.53
	Veillonella	-3.18	1.52	-3.31	1.51	0.84	0.40	0.55
	Bilophila	-3.19	1.19	-3.03	1.15	-1.29	0.20	0.33
	Parasutterella	-3.25	1.49	-3.12	1.44	-0.82	0.41	0.55
	Sutterella	-3.03	1.65	-3.03	1.63	0.01	0.99	0.79
	Escherichia-Shigella	-3.42	1.32	-3.63	1.34	1.43	0.15	0.29

***p* or *q* <.01, **p* or *q* <.05, †*q* <.10.

Supplementary Table 4. This Study's Prevalent Microbiome

Prevalent microbiota_genus	Kingdom	Phylum	Class	Order	Family	Genus
Actinomyces	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Agathobacter	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Agathobacter
Alistipes	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Anaerostipes	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Bacteroides	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Bifidobacterium	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Bilophila	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
Blautia	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Butyricoccus	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricoccus
Colidextribacter	Bacteria	Firmicutes	Clostridia	Clostridiales	Oscillospiraceae	Colidextribacter
Collinsella	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella
Dorea	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Eggerthella	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Eggerthella
Erysipelatoclostridium	Bacteria	Firmicutes	Bacilli	Erysipelotrichales	Erysipelatoclostridiaceae	Erysipelatoclostridium
Escherichia-Shigella	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia-Shigella
Faecalibacterium	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Flavonifractor	Bacteria	Firmicutes	Clostridia	Clostridiales	Oscillospiraceae	Flavonifractor
Fusicatenibacter	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Fusicatenibacter
Intestinibacter	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Intestinibacter
Lachnoclostridium	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostridium
Lachnospira	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira
Lachnospiraceae_UCG-004	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	UCG-004
Monoglobus	Bacteria	Firmicutes	Clostridia	Monoglobales	Monoglobaceae	Monoglobus
Negativibacillus	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Negativibacillus
Odoribacter	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Marinifilaceae	Odoribacter
Oscillibacter	Bacteria	Firmicutes	Clostridia	Clostridiales	Oscillospiraceae	Oscillibacter
Parabacteroides	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Tannerellaceae	Parabacteroides
Parasutterella	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Sutterellaceae	Parasutterella
Phascolarctobacterium	Bacteria	Firmicutes	Negativicutes	Acidaminococcales	Acidaminococcaceae	Phascolarctobacterium
Romboutsia	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Romboutsia
Roseburia	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Sellimonas	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Sellimonas
Streptococcus	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Subdoligranulum	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
Sutterella	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Turicibacter	Bacteria	Firmicutes	Bacilli	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Tuzzerella	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Tuzzerella
UBA1819	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	UBA1819
Veillonella	Bacteria	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Veillonella