

Supplementary Tables

Supplementary Table S1: Demographics and markers of disease severity in cases, comparing those who fulfilled Rome III criteria for post-infectious irritable bowel syndrome (PI-IBS) and those who did not (Post-infectious bowel dysfunction; PI-BD)

	PI-IBS	PI-BD	p-value
Number of cases	10	12	
Age, median (IQR)	58 (45-69)	54 (42-63)	0.57
HADS-A, mean (SD)	8 (6)	6 (3)	0.36
HADS-D, median (IQR)	4 (3-9)	2 (1-8)	0.22
PHQ-12 SS, mean (SD)	5 (2)	4 (2)	0.82
Fever, <i>n</i> (%)	9 (90%)	9 (75%)	0.59
Blood in stool, <i>n</i> (%)	1 (10%)	3 (25%)	0.59
Vomiting, <i>n</i> (%)	3 (30%)	2 (17%)	0.62
Antibiotics taken, <i>n</i> (%)	3 (30%)	6 (50%)	0.41

HADS-A, Hospital Anxiety and Depression Scale – Anxiety subscale; HADS-D, Hospital Anxiety and Depression Scale – Depression subscale; PHQ-12 SS, Patient Health Questionnaire-12 Somatic Symptom Scale.

Supplementary Table S2: Markers of initial illness severity in cases and controls

	Cases (n=22)	Controls (n=77)	RR (95% CI)	p value
Fever, <i>n</i> (%)	18 (82%)	42 (55%)	2.9 (1.2, 7.9)	0.02
Blood in stool, <i>n</i> (%)	4 (18%)	21 (27%)	0.7 (0.2, 1.6)	0.58
Vomiting, <i>n</i> (%)	5 (23%)	16 (21%)	1.1 (0.4, 2.4)	>0.99
Antibiotics taken, <i>n</i> (%)	9 (41%)	25 (32%)	1.3 (0.6, 2.7)	0.46
>7 days unable to do normal activity, <i>n</i> (%)	10 (45%)	40 (52%)	0.8 (0.4, 1.7)	0.64
weight loss (kg), median (IQR)	3.2 (1.8-4.5)	3.2 (2.5-4.5)	-	0.48

Supplementary Table S3: Demographics and psychological scores of those who took antibiotics and those who did not, and the effect of consumption on disease recovery

	Antibiotics (n=34)	No antibiotics (n=65)	p-value	RR (95% CI)
Age, mean (SD)	59 (12)	58 (16)	0.84	-
Female, n(%)	18 (53%)	32 (49%)	0.83	1.1 (0.6, 1.9)
HADS-A, median (IQR)	6 (4-9)	5 (3-8)	0.36	-
HADS-D, median (IQR)	3 (2-6)	3 (1-6)	0.46	-
PHQ-12, median (IQR)	3 (1-5)	3 (1-5)	0.57	-
Fever, n (%)	23 (68%)	37 (57%)	0.39	1.4 (0.8, 2.5)
Blood in stool, n (%)	12 (35%)	13 (20%)	0.14	1.6 (0.9, 2.7)
Vomiting, n (%)	5 (15%)	16 (25%)	0.31	0.6 (0.3, 1.3)
>1 GP attendance for this illness, n (%)	17 (50%)	18 (28%)	0.05	1.8 (1.0, 3.1)
Attended hospital emergency rooms for this illness, n (%)	3 (12%)	14 (22%)	0.28	0.6 (0.2, 1.3)
Hospitalised for this illness, n (%)	3 (9%)	8 (12%)	0.74	0.8 (0.3, 1.7)
Weight loss (kg), median (IQR)	3.2 (2.3-3.8)	3.2 (2.6-4.5)	0.34	-
Days unable to do normal activity, median (IQR)	10 (4-16)	8 (3-13)	0.35	-

HADS-A, Hospital Anxiety and Depression Scale – Anxiety subscale; HADS-D, Hospital Anxiety and Depression Scale – Depression subscale; PHQ-12 SS, Patient Health Questionnaire-12 Somatic Symptom Scale.

Supplementary Table S4: Concomitant medication

	Cases (n=22)	Controls (n=77)
Atorvastatin/ simvastatin	2	3
Ramipril	1	3
Metformin	0	2
Lanzoprazole/ omeprazole	0	3
Amlodipine	0	2
Bisoprolol/ atenolol	0	3
Glicazide	0	1
Fluoxetine / Sertraline	0	2

Supplementary Table S5: Dietary and short chain fatty acid (SCFA) amounts per study group and time point. There were no statistical differences ($p>0.05$) between any of the groups or time points. Data are given as mean (SD).

	Visit 2		Visit 3	
	Case	Control	Case	Control
Energy (kcal/day)	2032.90 (772.75)	2103.54 (823.43)	1907.11 (596.5)	1690.56 (246.86)
Protein (g/day)	72.88 (20.73)	88.31 (37.26)	68.18 (25.3)	71.67 (16.97)
Fat (g/day)	83.83 (32.36)	87.13 (44)	72.769 (30.78)	66.25 (16.29)
CHOm (g/day)	229.54 (85.89)	234.8 (84.51)	226.13 (65.43)	198.36 (41.16)
NSP (g/day)	13.39 (4.93)	14.61 (6.27)	11.68 (3.67)	11.52 (2.89)
Fibre (g/day)	19.05 (6.77)	21.48 (8.31)	16.81 (5.13)	17.44 (4.58)
total SCFA ($\mu\text{mol/g}$)	44.59 (13.12)	43.27 (11.93)	41.53 (7.47)	41.46 (12.52)
Acetic ($\mu\text{mol/g}$)	28.01 (6.26)	25.87 (4.87)	25.43 (3.73)	24.77 (5.02)
Propanoic ($\mu\text{mol/g}$)	6.69 (4.20)	7.14 (3.47)	6.72 (3.20)	6.79 (5.10)
Isobutyric ($\mu\text{mol/g}$)	0.86 (0.36)	1.23 (0.59)	0.98 (0.31)	1.19 (0.44)
Butyric ($\mu\text{mol/g}$)	6.95 (4.39)	6.50 (4.22)	6.13 (2.84)	6.00 (2.84)
Isovaleric ($\mu\text{mol/g}$)	1.03 (0.53)	1.49 (0.81)	1.14 (0.46)	1.52 (0.63)
Valeric ($\mu\text{mol/g}$)	1.06 (1.17)	1.04 (0.61)	1.13 (0.77)	1.18 (0.75)

Supplemental Table S6: Comparison of demographics, psychological scores and markers of disease severity between cases in the clinical and mechanistic studies

	Clinical study cases	Mechanistic study cases	p value
Number of subjects	22	18	-
Age, median (IQR)	57 (41-64)	56 (39-62)	0.96
Female, <i>n</i> (%)	17 (77%)	14 (78%)	0.99
HADS-A, median (IQR)	5 (4-10)	8 (4-10)	0.78
HADS-D, median (IQR)	4 (1-6)	4 (1-7)	0.99
PHQ-12 SS, mean (SD)	5 (3-6)	5 (2-6)	0.85
Fever, <i>n</i> (%)	18 (82%)	17 (94%)	0.52
Blood in stool, <i>n</i> (%)	4 (18%)	4 (22%)	0.84
Vomiting, <i>n</i> (%)	5 (23%)	5 (28%)	0.78
Antibiotics taken, <i>n</i> (%)	9 (41%)	5 (28%)	0.70

Supplementary Table 7: Comparison of demographics, psychological scores and markers of disease severity between controls in the clinical and mechanistic studies

	Clinical study controls	Mechanistic study controls	p value
Number of subjects	77	48	-
Age, median (IQR)	62 (48-71)	63 (48-71)	0.69
Female, <i>n</i> (%)	33 (43%)	20 (42%)	0.91
HADS-A, median (IQR)	5 (3-7)	5 (3-7)	0.95
HADS-D, median (IQR)	3 (1-5)	3 (1-6)	0.67
PHQ-12 SS, mean (SD)	2 (1-4)	2 (1-4)	0.73
Fever, <i>n</i> (%)	42 (55%)	24 (50%)	0.67
Blood in stool, <i>n</i> (%)	21 (27%)	9 (19%)	0.42
Vomiting, <i>n</i> (%)	16 (21%)	12 (25%)	0.70
Antibiotics taken, <i>n</i> (%)	25 (32%)	14 (29%)	0.76

Supplementary Table S8: Significant microbiota differences between cases and controls in samples collected less than 40 days after infection. All samples effected by the antibiotic use were excluded from the analysis. The mean relative abundance of each taxa is shown along with the fold change in cases versus controls.

Phylum	Class	Order	Family	Genus	Case	Control	Fold change
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>		13.83 %	5.25 %	0.38
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Collinsella</i>	10.70 %	4.31 %	0.40
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Eggerthella</i>	1.82 %	0.18 %	0.10
Bacteroidetes	Bacteroidia	Bacteroidales	<i>Porphyromonadaceae</i>	<i>Butyricimonas</i>	0.01 %	0.13 %	11.85
Bacteroidetes	Bacteroidia	Bacteroidales	<i>Porphyromonadaceae</i>	<i>Porphyromonas</i>	0.00 %	0.24 %	62.19
Bacteroidetes	Bacteroidia	Bacteroidales	<i>Prevotellaceae</i>	<i>Paraprevotella</i>	0.06 %	0.41 %	7.48
Firmicutes	Bacilli	Lactobacillales	<i>Enterococcaceae</i>	<i>Enterococcus</i>	0.05 %	0.39 %	8.27
Firmicutes	Clostridia	Clostridiales	<i>Lachnospiraceae</i>	<i>Anaerosporebacter</i>	0.16 %	0.61 %	3.71
Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>		11.66 %	18.22 %	1.56
Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>	<i>Faecalibacterium</i>	6.06 %	8.45 %	1.39
Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Solobacterium</i>	0.00 %	0.11 %	34.95
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Phascolarctobacterium</i>	0.29 %	0.25 %	0.85
Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Megamonas</i>	0.00 %	0.69 %	579.67
Proteobacteria	Betaproteobacteria				0.48 %	1.97 %	4.12
Proteobacteria	Betaproteobacteria	Burkholderiales			0.45 %	1.80 %	4.03
Proteobacteria	Betaproteobacteria	Burkholderiales	<i>Alcaligenaceae</i>	<i>Sutterella</i>	0.40 %	1.77 %	4.41
Proteobacteria	Betaproteobacteria	Neisseriales	<i>Neisseriaceae</i>	<i>Neisseria</i>	0.03 %	0.13 %	4.12
Proteobacteria	Gammaproteobacteria	Enterobacteriales	<i>Enterobacteriaceae</i>	<i>Klebsiella</i>	0.00 %	0.26 %	146.38

Supplementary Table 8: Significant microbiota differences between cases and controls in samples collected between 40 to 80 days after infection. All samples effected by the antibiotic use are excluded from the analysis. The mean relative abundance of each taxa is shown along with the fold change in cases versus controls

Phylum	Class	Order	Family	Genus	Case	Control	Fold change
Actinobacteria	Actinobacteria	Micrococcales	<i>Micrococcaceae</i>		0.03 %	0.27 %	8.54
Actinobacteria	Actinobacteria	Micrococcales	<i>Micrococcaceae</i>	<i>Micrococcus</i>	0.00 %	0.01 %	26.96
Actinobacteria	Actinobacteria	Micrococcales	<i>Micrococcaceae</i>	<i>Rothia</i>	0.03 %	0.25 %	8.17
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Olsenella</i>	0.00 %	0.14 %	Inf
Bacteroidetes	Bacteroidia	Bacteroidales	<i>Porphyromonadaceae</i>	<i>Barnesiella</i>	0.18 %	0.58 %	3.13
Firmicutes	Clostridia	Clostridiales	<i>Peptostreptococcaceae</i>	<i>Peptostreptococcus</i>	0.00 %	0.00 %	1.98
Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Coprobacillus</i>	0.00 %	0.01 %	7.59
Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Erysipelothrix</i>	0.00 %	0.01 %	2.02
Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Solobacterium</i>	0.00 %	0.02 %	7.43
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>		0.40 %	0.94 %	2.36
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Phascolarctobacterium</i>	0.19 %	0.52 %	2.80
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Succiniclasticum</i>	0.00 %	0.08 %	38.37
Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Megamonas</i>	2.58 %	0.07 %	0.03
Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Megasphaera</i>	0.00 %	0.72 %	593.50
Fusobacteria	Fusobacteriia	Fusobacteriales	<i>Fusobacteriaceae</i>	<i>Fusobacterium</i>	2.24 %	0.02 %	0.01
Proteobacteria	Betaproteobacteria	Burkholderiales	<i>Burkholderiaceae</i>		0.03 %	0.00 %	0.06
Proteobacteria	Betaproteobacteria	Burkholderiales	<i>Burkholderiaceae</i>	<i>Burkholderia</i>	0.03 %	0.00 %	0.06
Proteobacteria	Epsilonproteobacteria	Campylobacteriales	<i>Campylobacteraceae</i>	<i>Campylobacter</i>	0.02 %	0.23 %	13.99
Proteobacteria	Gammaproteobacteria	Pasteurellales	<i>Pasteurellaceae</i>	<i>Haemophilus</i>	0.06 %	0.59 %	10.31

Supplementary Table 9: Significant microbiota differences between cases and controls in samples collected more than 80 days after infection. The mean relative abundance of each taxa is shown along with the fold change in cases versus controls

Phylum	Class	Order	Family	Genus	Case	Control	Fold change
Actinobacteria	Actinobacteria	Actinomycetales	<i>Actinomycetaceae</i>		0.11 %	0.05 %	0.45
Actinobacteria	Actinobacteria	Actinomycetales	<i>Actinomycetaceae</i>	<i>Actinomyces</i>	0.11 %	0.05 %	0.45
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>		13.56 %	8.71 %	0.64
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Eggerthella</i>	2.11 %	0.83 %	0.39
Firmicutes					56.67 %	66.47 %	1.17
Firmicutes	Bacilli	Lactobacillales	<i>Streptococcaceae</i>	<i>Lactococcus</i>	0.03 %	0.01 %	0.25
Firmicutes	Clostridia	Clostridiales			45.57 %	55.23 %	1.21
Firmicutes	Clostridia	Clostridiales	<i>FamilyXIIIncertaeSedis</i>	<i>IncertaeSedis</i>	0.08 %	0.15 %	1.87
Firmicutes	Clostridia	Clostridiales	<i>FamilyXIIIncertaeSedis</i>	<i>Peptoniphilus</i>	0.00 %	0.01 %	12.66
Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>	<i>Anaerofilum</i>	0.10 %	0.25 %	2.49
Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Solobacterium</i>	0.00 %	0.13 %	64.42
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Succiniclacticum</i>	0.08 %	0.25 %	3.31
Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Dialister</i>	1.97 %	1.25 %	0.64
Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Veillonella</i>	0.10 %	0.25 %	2.53
Fusobacteria	Fusobacteriia	Fusobacteriales	<i>Fusobacteriaceae</i>	<i>Fusobacterium</i>	0.12 %	0.01 %	0.08
Proteobacteria	Betaproteobacteria	Burkholderiales	<i>Burkholderiaceae</i>	<i>Burkholderia</i>	0.03 %	0.00 %	0.11
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	<i>Desulfovibrionaceae</i>	<i>Desulfovibrio</i>	0.02 %	0.14 %	8.67
Proteobacteria	Gammaproteobacteria	Pasteurellales	<i>Pasteurellaceae</i>		0.02 %	0.06 %	2.85
Proteobacteria	Gammaproteobacteria	Pasteurellales	<i>Pasteurellaceae</i>	<i>Haemophilus</i>	0.02 %	0.06 %	2.86

Supplementary Table S11: Significant associations between bacterial taxa and short chain fatty acids. The dietary information was collected from patients visits 2 and 3. Positive association indicated with + and orange, negative association indicated with – and blue.

Phylum	Class	Order	Family	Genus	Total SCFA	Isobutyric	Butyric	Propanoic	Acetic	Valeric	Isovaleric
Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Atopobium</i>					-		
Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Collinsella</i>							+
Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Gordonibacter</i>		+					+
Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae						+		
Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	<i>Paraprevotella</i>					+	+	
Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>	-				-		
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae		-		-	-			
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	<i>Enterococcus</i>	-		-	-			
Firmicutes	Clostridia				-			-	-		
Firmicutes	Clostridia	Clostridiales	Christensenellaceae							+	
Firmicutes	Clostridia	Clostridiales	Christensenellaceae	<i>Christensenella</i>						+	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae						-		
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>Clostridium</i>					-		
Firmicutes	Clostridia	Clostridiales	FamilyXIIIncertaeSedis		-				-		
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Anaerofilum</i>					-		
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Faecalibacterium</i>			+				
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Flavonifractor</i>				-			
Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Catenibacterium</i>		+					+
Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Solobacterium</i>					+		
Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	<i>Dialister</i>	+	+		+			
Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	<i>Mitsuokella</i>				-			
Proteobacteria	Epsilonproteobacteria								-		
Proteobacteria	Gammaproteobacteria				-		-	-			

Supplementary table S12: Significant associations between bacterial taxa and dietary components. The dietary information was collected from patients visits 2 and 3. Positive association indicated with + and orange, negative association indicated with – and blue.

Phylum	Class	Order	Family	Genus	CHO	Fat	Fibre	NPS	Starch
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Coriobacterium</i>	+				
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Olsenella</i>	+				
Actinobacteria	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Paraeggerthella</i>	-				+
Firmicutes	Bacilli	Lactobacillales	<i>Streptococcaceae</i>					-	-
Firmicutes	Bacilli	Lactobacillales	<i>Streptococcaceae</i>	<i>Streptococcus</i>				-	-
Firmicutes	Clostridia	Clostridiales	<i>FamilyXIIIIncertaeSedis</i>		-			-	
Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>	<i>Anaerofilum</i>	-				
Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>	<i>IncertaeSedis</i>		-			
Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>				-	-	
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>		-				
Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Succiniclasticum</i>	-	-			
Proteobacteria	Betaproteobacteria					-			
Proteobacteria	Gammaproteobacteria						-	-	-
Proteobacteria	Gammaproteobacteria	Enterobacteriales	<i>Enterobacteriaceae</i>					-	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	<i>Enterobacteriaceae</i>	<i>Klebsiella</i>			-		

