

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>FamilyXIIIIncertaeSedis</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>Succiniclasicum</i> | - | - | | | |
| Proteobacteria | Betaproteobacteria | | | | | - | | | |
| Proteobacteria | Gammaproteobacteria | | | | | | - | - | - |
| Proteobacteria | Gammaproteobacteria | Enterobacteriales | <i>Enterobacteriaceae</i> | | | | | - | |
| Proteobacteria | Gammaproteobacteria | Enterobacteriales | <i>Enterobacteriaceae</i> | <i>Klebsiella</i> | | | - | | |

