**SUPPLEMENTARY**

****

**Figure S1. Effects of omega-3 status on inflammatory outcomes. (A)** There were no significant differences in plasma inflammatory cytokines (TNFα, IL-1β, IL-10, IL-6) between treatment groups. **(B)** There was no differences in jejenum levels of the antimicrobial peptide intestinal alkaline phosphatase (IAP) between treatment groups. Data shown as mean ± SEM. n= 9-10 per group.

**Table S1. Composition of diets**

|  |  |  |  |
| --- | --- | --- | --- |
| **Ingredients (g/kg)** | **CON** | **n3+** | **n3-** |
| **Casein** | 200.00 | 200.00 | 200.00 |
| **L‐Cystine** | 3.00 | 3.00 | 3.00 |
| **Sucrose** | 100.00 | 100.00 | 100.00 |
| **Dextrose, monohydrate** | 200.00 | 200.00 | 200.00 |
| **Corn Starch** | 150.00 | 150.00 | 150.00 |
| **Maltodextrin** | 131.18 | 129.3 | 131.18 |
| **Coconut Oil, hydrogenated** | 60.00 | 38.78 | 66.00 |
| **Safflower Oil** | 32.00 | 31.50 | 34.00 |
| **Flaxseed Oil** | 8.00 | 8.00 |  |
| **Life'sOmega 45 (DHA+EPA)** |  | 23.00 |  |
| **Cellulose** | 50.00 | 50.00 | 50.00 |
| **Mineral Mix, AIN‐93G‐MX (94046)** | 48.00 | 48.00 | 48.00 |
| **Ferric Citrate** | 0.30 | 0.30 | 0.30 |
| **Vitamin Mix, AIN‐93‐VX (94047)** | 15.00 | 15.00 | 15.00 |
| **Choline Bitartrate** | 2.50 | 2.50 | 2.50 |
| **TBHQ, antioxidant** | 0.02 | 0.02 | 0.02 |

**Table S2. Fatty acid profile of diets**

|  |  |  |  |
| --- | --- | --- | --- |
| **% Total fatty acids** | **CON** | **n3+** | **n3-** |
| *Saturated fatty acids (SFA)* |  |  |  |
| **8:0** | 3.4 | 2.2 | 3.6 |
| **10:0** | 3.1 | 2 | 3.3 |
| **12:0** | 27 | 16.9 | 29 |
| **14:0** | 11.1 | 7.25 | 12.3 |
| **16:0** | 9 | 10.9 | 8.5 |
| **18:0** | 7.9 | 5.9 | 8.7 |
| **Total SFA** | 59.8 | 44 | 64.4 |
| *Monounsaturated fatty acids (MUFA)* |  |  |  |
| **18:1** | 7.1 | 13.3 | 6.5 |
| **Total MUFA** | 7.3 | 13.3 | 6.7 |
| *Polyunsaturated fatty acids (PUFA)* |  |  |  |
| **18:2 n-6** | 25.7 | 25.4 | 22.4 |
| **18:3 n-3** | 4.2 | 4.1 | tr |
| **20:4 n-6** | 0 | 0.26 | 0 |
| **20:5 n-3** | 0 | 3.2 | 0 |
| **22:5 n-3** | 0 | 1 | 0 |
| **22:6 n-3** | 0 | 5.7 | 0 |
| **Total n-6** | 25.7 | 25.66 | 22.4 |
| **Total n-3** | 4.2 | 14 | 0 |
| **Total PUFA** | 29.9 | 39.66 | 22.4 |

tr, trace

**Table S3. Tissue fatty acid profile**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Epididymal fat** | | | | | | **Liver** | | | | | | **Red blood** c **ells** | | | | | |
|  | **CON** | | **n3+** | | **n3-** | | **CON** | | **n3+** | | **n3-** | | **CON** | | **n3+** | | **n3-** | |
|  | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** | **%** | **SEM** |
| *SFA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **14:0** | 6.3a | 0.1 | 5.1b | 0.1 | 6.5a | 0.1 | 1.2a | 0.2 | 0.8b | 0.1 | 1.3a | 0.0 | 2.0 | 0.2 | 2.0 | 0.2 | 1.7 | 0.1 |
| **16:0** | 20.7a | 0.3 | 24.8b | 0.2 | 21.0a | 0.4 | 24.6a | 0.5 | 25.2a | 0.4 | 22.4b | 0.2 | 35.3 | 1.0 | 36.3 | 1 | 35.1 | 0.6 |
| **18:0** | 2.7 | 0.1 | 2.7 | 0.1 | 2.8 | 0.1 | 11.9 | 0.4 | 12.7 | 0.5 | 11.3 | 0.2 | 19.1 | 1.1 | 17.5 | 1.2 | 20.0 | 0.9 |
| **20:0** | 0.1 | 0.0 | 0.1 | 0.0 | 0.1 | 0.0 | 0.4 | 0.0 | 0.3 | 0.1 | 0.2 | 0.0 | 0.3 | 0.1 | 0.3 | 0.0 | 0.3 | 0.0 |
| **Total SFA** | 29.8a | 0.4 | 32.7b | 0.3 | 30.4a | 0.6 | 38.1a | 0.7 | 39.0a | 0.8 | 35.2b | 0.2 | 56.6 | 1.9 | 56.1 | 2.1 | 57.1 | 1.4 |
| *MUFA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **16:1** | 8.8 | 0.3 | 8.0 | 0.3 | 8.3 | 0.3 | 3.5a | 0.2 | 2.1b | 0.2 | 3.7a | 0.1 | 2.2 | 0.3 | 2.3 | 0.4 | 1.5 | 0.2 |
| **18:1t n-9** | 0.1a | 0.0 | 0.1b | 0.0 | 0.1a | 0.0 | n.d. | - | n.d. | - | n.d. | - | 0.1 | 0.0 | n.d. | - | n.d. | - |
| **18:1c** **n-9** | 31.4a b | 0.3 | 25.2a | 2.9 | 33.6b | 0.4 | 16.1a | 0.5 | 12.4b | 0.9 | 18.7a | 0.5 | 13.6 | 1.2 | 15.2 | 1.5 | 11.5 | 0.7 |
| **18:1 t n-7** | 2.2 | 0.1 | 4.1 | 2.7 | 3.2 | 0.1 | 2.7a | 0.1 | 1.0b | 0.1 | 4.3c | 0.3 | 1.7a | 0.1 | 1.2b | 0.0 | 1.8a | 0.1a |
| **20:1** | 0.6a | 0.0 | 0.4b | 0.0 | 0.7c | 0.0 | 0.5a | 0.1 | 0.3a | 0.0 | 0.7b | 0.0 | 0.6 | 0.2 | 2.1 | 1 | 3.1 | 1.3 |
| **Total MUFA** | 43.1a | 0.6 | 37.4b | 0.6 | 46.0c | 0.8 | 22.8a | 0.7 | 15.8b | 1.1 | 27.4c | 0.7 | 18.1 | 1.6 | 20.8 | 1.8 | 17.9 | 1.3 |
| *PUFA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *n-6 PUFA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **18:2 n-6** | 24.7a | 0.3 | 24a b | 0.4 | 23.0b | 0.4 | 18a | 0.3 | 16.2b | 0.3 | 17.6a | 0.3 | 10.0 | 0.7 | 9.7 | 0.9 | 7.7 | 0.5 |
| **18:3 n-6** | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1a b | 0.0 | n.d.a | - | 0.2b | 0.1 | 0.1 | 0.0 | n.d. | - | n.d. | - |
| **20:3 n-6** | 0.1a | 0.0 | 0b | 0.0 | 0.2a | 0.0 | 1.2a | 0.2 | 0.6b | 0.1 | 1.3a | 0.0 | 0.8a | 0.1 | 0.3b | 0.0 | 0.8a | 0.1a |
| **20:4 n-6** | 0.2a | 0.0 | 0.1b | 0.0 | 0.4c | 0.0 | 10.1a | 0.2 | 4.7b | 0.2 | 14.1c | 0.2 | 9.4a | 0.6 | 3.6b | 0.3 | 12.0c | 0.5c |
| **22:4 n-6** | 0.0a | 0.0 | 0.0a | 0.0 | 0.0b | 0.0 | 0.1a b | 0.1 | n.d.a | - | 0.3b | 0.1 | 0.8a | 0.1 | n.d.b | - | 1.7c | 0.2c |
| **22:5 n-6** | 0.0a | 0.0 | 0.1b | 0.0 | 0.1c | 0.0 | 0.1a | 0.1 | n.d.a | - | 3.6b | 0.1 | n.d.a |  | n.d.a | - | 2.8b | 0.3b |
| **Total n-6 PUFA** | 25.1 | 0.2 | 24.4 | 0.4 | 23.6 | 0.5 | 29.6a | 0.4 | 21.5b | 0.3 | 37.1c | 0.5 | 21a | 0.6 | 13.6b | 0.7 | 25.0c | 1.3c |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *n-3 PUFA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **18:3 n-3** | 1.9a | 0.0 | 2.3b | 0.1 | 0.0c | 0.0 | 0.8a | 0.1 | 1.0a | 0.0 | n.d.b | - | 0.3a b | 0.1 | 0.3a | 0.1 | n.d.b | - |
| **20:5 n-3** | 0.0a | 0.0 | 0.4b | 0.0 | 0.0a | 0.0 | 0.5a | 0.1 | 4.1b | 0.2 | n.d.a | - | 0.1a | 0.0 | 2.1b | 0.2 | n.d.a | - |
| **22:5 n-3** | 0.0a | 0.0 | 0.4b | 0.0 | 0.0a | 0.0 | 0.2a | 0.1 | 1.4b | 0.2 | n.d.a | - | 0.2a b | 0.1 | 0.6a | 0.2 | n.d.b | - |
| **22:6 n-3** | 0.1a | 0.0 | 2.2b | 0.1 | 0.0a | 0.0 | 8.0a | 0.3 | 17.3b | 0.4 | 0.3c | 0.2 | 3.8a | 0.3 | 6.5b | 0.4 | n.d.c | - |
| **Total n-3 PUFA** | 2.1a | 0.0 | 5.4b | 0.2 | 0.0c | 0.0 | 9.5a | 0.2 | 23.7b | 0.6 | 0.3c | 0.2 | 4.3a | 0.3 | 9.5b | 0.6 | n.d.c | - |
| **Total PUFA** | 27.2a | 0.2 | 29.9b | 0.5 | 23.6c | 0.5 | 39.1a | 0.6 | 45.2b | 0.6 | 37.4a | 0.7 | 25.3 | 0.9 | 23.1 | 1 | 25 | 1.3 |
| **n6:n3** | 12.1 | 0.3 | 4.5 | 0.1 | n/a | n/a | 3.1 | 0.1 | 0.9 | 0 | n/a | n/a | 5 | 0.3 | 1.5 | 0.1 | n/a | n/a |

Values expressed as mean ± SEM g/100g total FAME. Different superscript letters between treatment groups represents statistically significant differences.

FAME, Fatty acid methyl esters; SFA, Saturated fatty acids; MUFA, Monounsaturated fatty acids, PUFA, Polyunsaturated fatty acid; n.d., Not detected

**Table S4. Relative abundance of genera from mothers microbiota**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Mothers** | | | | |
| **Genus** | **CON** | **n3+** | **n3-** | **P-value** | **FDR corrected** |
| *Lachnospiraceae uncultured* | 22 | 14 | 17 | **0.024** | 0.399 |
| *Ruminococcaceae uncultured* | 13 | 11 | 10 | 0.104 | 0.568 |
| *Bacteroidales S24-7 uncultured* | 9.7 | 16.3 | 8.7 | 0.083 | 0.568 |
| *Alistipes* | 9.6 | 11.1 | 10.6 | 0.607 | 0.917 |
| *Ruminococcaceae Incertae Sedis* | 7.8 | 6.7 | 8.8 | 0.188 | 0.577 |
| *Odoribacter* | 4.6 | 5.4 | 4.6 | 0.997 | 1 |
| *Mucispirillum uncultured* | 4.4 | 2.9 | 5.5 | 0.566 | 0.893 |
| *Anaerotruncus* | 3.1 | 2.6 | 2.6 | 0.26 | 0.577 |
| *Bilophila* | 2.8 | 2.9 | 4 | 0.248 | 0.577 |
| *Lactobacillus* | 2.7 | 1 | 3.8 | 0.15 | 0.577 |
| *Oscillibacter* | 2.5 | 1.5 | 2.7 | 0.089 | 0.568 |
| *Lachnospiraceae Incertae Sedis* | 2.3 | 1.4 | 2.2 | 0.116 | 0.577 |
| *Bacteroides* | 2.1 | 3.6 | 4.4 | 0.58 | 0.895 |
| *Rikenellaceae RC9 gut group* | 2 | 2.9 | 2.2 | 0.516 | 0.833 |
| *Rikenella* | 1.3 | 1.5 | 0.9 | 0.3 | 0.609 |
| *Desulfovibrio* | 1.3 | 0.6 | 0.5 | 0.206 | 0.577 |
| *Escherichia-Shigella* | 1.2 | 0.6 | 0.7 | 0.176 | 0.577 |
| *Coprococcus* | 1.1 | 0.7 | 1.5 | **0.006** | 0.399 |
| *Clostridiales uncultured bacterium* | 1 | 2.9 | 2 | **0.037** | 0.399 |
| *Allobaculum* | 0.73 | 0.42 | 0.64 | 0.401 | 0.722 |
| *Akkermansia* | 0.66 | 6.17 | 3.18 | 0.249 | 0.577 |
| *Anaeroplasma* | 0.46 | 0.06 | 0.25 | 0.363 | 0.716 |
| *Peptococcaceae uncultured* | 0.45 | 0.41 | 0.38 | 0.713 | 0.993 |
| *Parasutterella* | 0.35 | 1.71 | 1.04 | 0.224 | 0.577 |
| *Turicibacter* | 0.33 | 0.06 | 0.11 | 0.233 | 0.577 |
| *Roseburia* | 0.24 | 0.16 | 0.21 | 0.514 | 0.833 |
| *Bifidobacterium;* | 0.19 | 0.34 | 0.4 | 0.285 | 0.595 |
| *Parabacteroides* | 0.19 | 0.23 | 0.19 | 0.904 | 1 |
| *Anaerovorax* | 0.17 | 0.07 | 0.12 | 0.248 | 0.577 |
| *Ruminococcus* | 0.16 | 0.09 | 0.02 | **0.045** | 0.399 |
| *Peptococcus* | 0.14 | 0.11 | 0.08 | 0.174 | 0.577 |
| *Peptostreptococcaceae uncultured* | 0.14 | 0.33 | 0.13 | 0.867 | 1 |
| *Candidate division TM7 uncultured other* | 0.12 | 0.11 | 0.06 | 0.165 | 0.577 |
| *Clostridium* | 0.1 | 0.01 | 0 | 0.424 | 0.734 |
| *Christensenellaceae uncultured* | 0.1 | 0.15 | 0.09 | 0.373 | 0.716 |
| *Family XIII Incertae Sedis* | 0.079 | 0.093 | 0.054 | 0.269 | 0.579 |
| *Enterorhabdus* | 0.036 | 0.032 | 0.024 | 0.677 | 0.961 |
| *Christensenella* | 0.031 | 0.027 | 0.041 | 0.482 | 0.815 |
| *Lachnospiraceae uncultured bacterium* | 0.027 | 0.029 | 0.068 | 0.846 | 1.000 |
| *Thalassospira* | 0.026 | 0.183 | 0.047 | 0.096 | 0.568 |
| *Other* | 0.026 | 0.038 | 0.057 | **0.03** | 0.399 |
| *Family XIII incertae sedis uncultured* | 0.022 | 0.018 | 0.011 | 0.212 | 0.577 |
| *Aerococcus* | 0.011 | 0.005 | 0.01 | 0.824 | 1 |
| *Erysipelotrichaceae Incertae Sedis* | 0.009 | 0.004 | 0.009 | 0.256 | 0.577 |
| *Hydrogenoanaerobacterium* | 0.008 | 0.006 | 0.006 | 0.87 | 1 |
| *Mogibacterium* | 0.006 | 0.007 | 0.002 | 0.191 | 0.577 |
| *Ruminococcaceae uncultured bacterium* | 0.006 | 0.007 | 0.006 | 0.673 | 0.961 |
| *Mollicutes RF9 uncultured bacterium other* | 0.005 | 0.007 | 0 | **0.017** | 0.399 |
| *Erysipelotrichaceae uncultured* | 0.003 | 0.003 | 0 | 0.144 | 0.577 |
| *Gelria* | 0.002 | 0 | 0.013 | 0.122 | 0.577 |
| *Staphylococcus* | 0.001 | 0.002 | 0.017 | 0.839 | 1 |
| *Enterococcus* | 0.001 | 0.002 | 0.008 | 0.231 | 0.577 |
| *Pseudobutyrivibrio* | 0.001 | 0.002 | 0.006 | 0.089 | 0.568 |
| *Coriobacteria uncultured* | 0 | 0 | 0.017 | **0.043** | 0.399 |
| *Barnesiella* | 0 | 0.001 | 0.002 | 0.645 | 0.954 |
| *Prevotella* | 0 | 0 | 0 | 1 | 1 |
| *Prevotellaceae uncultured* | 0 | 0 | 0 | 1 | 1 |
| *Flavobacterium* | 0 | 0 | 0 | 1 | 1 |
| *Cyanobacteria 4C0d-2 uncultured bacterium* | 0 | 0 | 0 | 1 | 1 |
| *Cyanobacteria 4C0d-2 uncultured organism other* | 0 | 0 | 0.009 | **0.043** | 0.399 |
| *Lactococcus* | 0 | 0 | 0 | 1 | 1 |
| *Streptococcus* | 0 | 0 | 0 | 1 | 1 |
| *Candidatus Arthromitus* | 0 | 0 | 0 | 1 | 1 |
| *clostridiaeceae uncultured* | 0 | 0 | 0 | 1 | 1 |
| *Anaerostipes* | 0 | 0 | 0 | 1 | 1 |
| *Blautia* | 0 | 0 | 0 | 1 | 1 |
| *Marvinbryantia* | 0 | 0 | 0.001 | 0.407 | 0.722 |
| *Clostridiales uncultured rumen bacterium* | 0 | 0.001 | 0 | 0.407 | 0.722 |
| *alpha proteobacterium* | 0 | 0 | 0 | 1 | 1 |
| *Mollicutes RF9 uncultured bacterium other* | 0 | 0 | 0 | 1 | 1 |
| *Mollicutes RF9 uncultured rumen bacterium other* | 0 | 0 | 0 | 1 | 1 |

**Table S5. Relative abundance of genera from offspring microbiota**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Offspring** | | | | |
| **Genus** | **CON** | **n3+** | **n3-** | **P-value** | **FDR Corrected** |
| *Lachnospiraceae uncultured* | 17 | 16 | 15 | 0.195 | 0.433 |
| *Alistipes* | 12 | 11 | 12 | 0.653 | 0.861 |
| *Ruminococcaceae Incertae Sedis* | 9.7 | 8.6 | 9.6 | 0.545 | 0.774 |
| *Ruminococcaceae uncultured* | 9.7 | 9.2 | 8.5 | 0.514 | 0.745 |
| *Odoribacter* | 9.5 | 13.1 | 12.2 | 0.211 | 0.454 |
| *Bacteroidales S247 uncultured bacterium* | 6.9 | 6.2 | 5.2 | 0.184 | 0.433 |
| *Mucispirillum uncultured bacterium* | 3.6 | 6.2 | 6.9 | **0.032** | 0.162 |
| *Bacteroides* | 3.4 | 3.7 | 3.7 | 0.964 | 1 |
| *Rikenella* | 3 | 2.8 | 3 | 0.88 | 1 |
| *Oscillibacter* | 3 | 2 | 3 | 0.077 | 0.288 |
| *Rikenellaceae RC9 gut group* | 2.6 | 2.7 | 3.2 | 0.174 | 0.426 |
| *Lachnospiraceae Incertae Sedis* | 2.6 | 1.4 | 1.6 | **0.008** | 0.063 |
| *Clostridiales uncultured uncultured bacterium* | 2.6 | 3 | 3.1 | 0.772 | 0.962 |
| *Anaerotruncus* | 2.4 | 2.9 | 2.5 | 0.135 | 0.398 |
| *Akkermansia* | 2.1 | 2.5 | 1.9 | 0.449 | 0.664 |
| *Lactobacillus* | 1.2 | 0.5 | 0.8 | 0.973 | 1 |
| *Bilophila* | 1.1 | 1.1 | 1.2 | 0.99 | 1 |
| *Parasutterella* | 0.94 | 0.91 | 0.77 | 0.928 | 1 |
| *Allobaculum* | 0.74 | 0.79 | 0.4 | 0.246 | 0.499 |
| *Coprococcus* | 0.66 | 0.44 | 0.58 | 0.303 | 0.552 |
| *Parabacteroides* | 0.6 | 0.97 | 0.58 | 0.723 | 0.917 |
| *EscherichiaShigella* | 0.58 | 0.23 | 0.28 | **0.004** | **0.036** |
| *Desulfovibrio* | 0.51 | 1.12 | 0.57 | **0.023** | 0.148 |
| *Christensenellaceae uncultured* | 0.43 | 0.41 | 0.41 | 0.564 | 0.785 |
| *Bifidobacterium* | 0.38 | 0.3 | 0.19 | 0.271 | 0.534 |
| *Anaerovorax* | 0.3 | 0.26 | 0.41 | **0.031** | 0.162 |
| *Ruminococcus* | 0.26 | 0.47 | 0.48 | 0.655 | 0.861 |
| *Peptococcaceae uncultured* | 0.23 | 0.24 | 0.25 | 0.918 | 1 |
| *Anaeroplasma* | 0.21 | 0.05 | 0.51 | **0.001** | **0.014** |
| *Peptostreptococcaceae uncultured* | 0.2 | 0.1 | 0.19 | 0.169 | 0.426 |
| *Clostridiales uncultured rumen bacterium* | 0.16 | 0.2 | 0 | **<0.0001** | **0.002** |
| *TM7 uncultured bacterium Other* | 0.15 | 0.19 | 0.1 | 0.105 | 0.339 |
| *Family\_XIII\_Incertae\_Sedis\_\_Incertae\_Sedis* | 0.13 | 0.11 | 0.15 | 0.287 | 0.551 |
| *Roseburia* | 0.13 | 0.17 | 0.17 | 0.072 | 0.284 |
| *Pseudobutyrivibrio* | 0.11 | 0.07 | 0.08 | 0.828 | 0.985 |
| *Turicibacter* | 0.11 | 0.01 | 0.11 | 0.092 | 0.325 |
| *Peptococcus* | 0.1 | 0.12 | 0.11 | 0.894 | 1 |
| *Thalassospira* | 0.1 | 0.19 | 0.12 | 0.157 | 0.413 |
| *Enterorhabdus* | 0.04 | 0.02 | 0.03 | **0.038** | 0.180 |
| *Other* | 0.04 | 0.1 | 0.05 | 0.246 | 0.499 |
| *Erysipelotrichaceae Incertae Sedis* | 0.03 | 0.05 | 0.04 | 0.832 | 0.985 |
| *Lachnospiraceae uncultured bacterium* | 0.03 | 0.02 | 0.02 | 0.195 | 0.433 |
| *Clostridium* | 0.03 | 0.08 | 0 | **0.003** | **0.030** |
| *Family XIII Incertae Sedis uncultured* | 0.02 | 0.03 | 0.02 | 0.947 | 1 |
| *Christensenella* | 0.02 | 0.02 | 0.03 | 0.331 | 0.585 |
| *A 4C0d2 uncultured bacterium Other Other* | 0.008 | 0 | 0.208 | **0.003** | **0.030** |
| *Hydrogenoanaerobacterium* | 0.008 | 0.016 | 0.008 | **0.045** | 0.200 |
| *RF9 uncultured bacterium Other* | 0.007 | 0.036 | 0.007 | **0.072** | 0.284 |
| *A 4C0d2 uncultured organism Other Other* | 0.006 | 0 | 0.275 | **0.001** | **0.014** |
| *Mogibacterium* | 0.005 | 0.005 | 0.004 | 0.976 | 1.000 |
| *Ruminococcaceae uncultured bacterium* | 0.004 | 0.005 | 0.005 | 0.704 | 0.909 |
| *uncultured\_Mollicutes\_bacteriumOther* | 0.004 | 0 | 0 | **0.015** | 0.107 |
| *Prevotellaceae uncultured* | 0.003 | 0 | 0 | 0.14 | 0.398 |
| *Erysipelotrichaceae uncultured* | 0.003 | 0.001 | 0 | 0.136 | 0.398 |
| *Blautia* | 0.002 | 0 | 0 | 0.387 | 0.585 |
| *Prevotella* | 0.001 | 0 | 0 | 0.387 | 0.585 |
| *Coriobacteriaceae uncultured* | 0 | 0 | 0.038 | **<0.0001** | **0.002** |
| *Barnesiella* | 0 | 0.002 | 0.004 | **0.096** | 0.325 |
| *Flavobacterium* | 0 | 0 | 0 | 0.387 | 0.585 |
| *Staphylococcus* | 0 | 0.001 | 0 | 0.387 | 0.585 |
| *Aerococcus* | 0 | 0 | 0 | 1 | 1 |
| *Enterococcus* | 0 | 0 | 0.001 | 0.296 | 0.552 |
| *Lactococcus* | 0 | 0.006 | 0 | 0.387 | 0.585 |
| *Streptococcus* | 0 | 0 | 0 | 0.996 | 1 |
| *Clostridiaceae Candidatus Arthromitus* | 0 | 0.006 | 0 | 0.146 | 0.399 |
| *Clostridiaceae uncultured* | 0 | 0.001 | 0 | 0.786 | 0.962 |
| *Anaerostipes* | 0 | 0.158 | 0 | 0.341 | 0.585 |
| *Marvinbryantia* | 0 | 0 | 0 | 0.627 | 0.856 |
| *Gelria* | 0 | 0 | 0.177 | **<0.0001** | **0.002** |
| *wr0007 uncultured alpha proteobacterium* | 0 | 0 | 0 | 0.387 | 0.585 |
| *RF9 uncultured rumen bacteriumOther* | 0 | 0 | 0.003 | **0.028** | 0.162 |

**SUPPLEMENTARY METHODS**

**Plasma cytokine analysis**

Cytokine production in plasma was assessed using a chemoilluminescence V-PLEX Kit (Proinflammatory Panel 1 - mouse) (Meso Scale Discovery, Maryland, USA) for TNFα, IL-10, IL-1β and IL-6 according to manufacturer’s instructions. The plate was read using a MESO QuickPlex SQ 120, SECTOR Imager 2400, SECTOR Imager 6000, SECTOR S 600.

**IAP enzyme activity**

Jejenum intestinal alkaline phosphatase (IAP) enzyme activity was carried out using a commercial alkaline phosphatase assay kit (Abcam, Cambridge, UK) as per manufacturers instructions and results expressed as ug IAP/minute reaction time/mg protein. Protein concentration of jejenum tissue was assessed using Bradford reagent as per manufacturers instructions (Sigma Aldrich, Wicklow, Ireland).