Supplementary Material

# Supplementary Figures and Tables

## Supplementary Figures

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**Supplementary Figure 1.** The class composition of colonic microbiomeamong three groups.

C:\Users\asus\Desktop\FMT-断奶应激\结果图\目.tif**Supplementary Figure 2.** The order composition of colonic microbiome in nursing and weaned piglets.

## Supplementary Tables

**SupplementaryTable1.** Ingredient composition and nutritional levels of basic diet

|  |  |  |  |
| --- | --- | --- | --- |
| Item |  | Nutritional level2 |  |
| Corn | 567 | Digestible Energy (MJ/kg) | 13.98 |
| Puffed soybean | 130 | Crude protein (g/Kg) | 191 |
| Soybean meal | 155 | Crude fat (g/Kg) | 65.7 |
| Sucrose | 10 | Ash (g/Kg) | 53.1 |
| Fish meal | 30 | Moisture (g/Kg) | 110.3 |
| Whey powde | 30 | Calcium (g/Kg) | 9.3 |
| Plasma protein powder | 10 | Phosphorus (g/Kg) | 6.5 |
| Soybean oil | 10 | Lysine (g/Kg) | 11.5 |
| Stone powder | 8 | Methionine (g/Kg) | 3.0 |
| Calcium dihydrogen phosphate | 10 |  |  |
| Vitamin premix1 | 40 |  |  |

1Provided per kilogram of diet: 16,000 IU vitamin A, 4000IU vitamin D3, 100 IU vitamin E, 0.5mg vitamin K3, 2mg vitamin B1, 4.5mg vitamin B2, 7mg vitamin B6, 0.03mg vitamin B12, 0.2mg biotin, 10mg folic acid, 30mg nicotinic acid, 22mg pantothenic acid; 85mg Fe(FeSO4), 100mg Cu(CuSO4),0.3mg Mn(MnSO4), 0.14 mg I(CaI2).

2The data regarding crude protein, crude fat, crude ash, moisture, calcium and total phosphorus are measured values, the others are calculated values.

**SupplementaryTable2.**Target genes detected in the study and their primers sequences

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Genbank accession | Primer sequence (5’- 3’) | Size(bp) | Annealing (℃) |
| IL-6 | NM\_214399.1 | GCCTTCAGTCCAGTCGCCTTCT | 101 | 60 |
| GTGGCATCACCTTTGGCATCTTC |
| IL-10 | NM\_214041.1 | GACCAGATGGGCGACTTGTTG | 160 | 60 |
| GGGAGTTCACGTGCTCCTTGAT |
| TNF-α | NM\_001143690.1 | CGCTCTTCTGCCTACTGCACTT | 156 | 60 |
| CGGCTTTGACATTGGCTACAA |

|  |  |  |  |
| --- | --- | --- | --- |
| tax\_name | S | W | FW |
| *Bacteroidetes* | 55.75 | 35.01 | 41.70 |
| *Firmicutes* | 35.09 | 50.24 | 40.03 |
| *Proteobacteria* | 3.28 | 9.31 | 10.85 |
| *Fusobacteria* | 4.37 | 4.30 | 0.03 |
| *Spirochaetes* | 0.79 | 0.06 | 2.98 |
| *Synergistetes* | 0.05 | 0.01 | 1.52 |
| *Euryarchaeota* | 0.16 | 0.01 | 1.02 |
| *Actinobacteria* | 0.07 | 0.53 | 0.15 |
| *Verrucomicrobia* | 0.00 | 0.00 | 0.35 |
| *Deferribacteres* | 0.00 | 0.00 | 0.27 |
| *Fibrobacteres* | 0.00 | 0.00 | 0.12 |
| *CandidatusSaccharibacteria* | 0.01 | 0.00 | 0.00 |
| *Elusimicrobia* | 0.00 | 0.00 | 0.01 |
| *Planctomycetes* | 0.00 | 0.00 | 0.00 |
| *Acidobacteria* | 0.00 | 0.00 | 0.00 |

**SupplementaryTable3.** The phyla composition of colonic microbiome among three groups

**SupplementaryTable4.** The class composition of colonic microbiome among three groups

|  |  |  |  |
| --- | --- | --- | --- |
| tax\_name | S | W | FW |
| *Bacteroidia* | 50.51 | 34.73 | 35.79 |
| *Clostridia* | 27.46 | 39.45 | 30.63 |
| *Epsilonproteobacteria* | 0.28 | 6.86 | 8.42 |
| *Bacilli* | 5.23 | 4.19 | 3.75 |
| *Negativicutes* | 0.95 | 6.48 | 5.05 |
| *Fusobacteriia* | 4.37 | 4.30 | 0.03 |
| *Spirochaetia* | 0.79 | 0.06 | 2.98 |
| *Gammaproteobacteria* | 1.29 | 0.99 | 0.65 |
| *Deltaproteobacteria* | 0.92 | 0.29 | 1.19 |
| *Synergistia* | 0.05 | 0.01 | 1.52 |
| *Betaproteobacteria* | 0.08 | 1.17 | 0.15 |
| *Methanobacteria* | 0.15 | 0.01 | 0.88 |
| *Actinobacteria* | 0.07 | 0.53 | 0.15 |
| *Deferribacteres* | 0.00 | 0.00 | 0.27 |
| *Verrucomicrobiae* | 0.00 | 0.00 | 0.24 |
| *Thermoplasmata* | 0.01 | 0.00 | 0.14 |
| *Erysipelotrichia* | 0.01 | 0.08 | 0.04 |
| *Fibrobacteria* | 0.00 | 0.00 | 0.12 |
| *Subdivision5* | 0.00 | 0.00 | 0.10 |
| *Alphaproteobacteria* | 0.01 | 0.00 | 0.03 |
| *Other* | 7.84 | 0.85 | 7.86 |

**SupplementaryTable5.** The order composition of colonic microbiome among three groups

|  |  |  |  |
| --- | --- | --- | --- |
| tax\_name | S | W | FW |
| *Bacteroidales* | 50.51 | 34.73 | 35.79 |
| *Clostridiales* | 27.38 | 39.45 | 30.44 |
| *Campylobacterales* | 0.28 | 6.86 | 8.42 |
| *Lactobacillales* | 5.23 | 4.19 | 3.75 |
| *Selenomonadales* | 0.95 | 6.48 | 5.05 |
| *Fusobacteriales* | 4.37 | 4.30 | 0.03 |
| *Spirochaetales* | 0.79 | 0.06 | 2.98 |
| *Desulfovibrionales* | 0.91 | 0.29 | 1.07 |
| *Synergistales* | 0.05 | 0.01 | 1.52 |
| *Pasteurellales* | 1.06 | 0.10 | 0.15 |
| *Burkholderiales* | 0.07 | 0.88 | 0.10 |
| *Methanobacteriales* | 0.15 | 0.01 | 0.88 |
| *Enterobacteriales* | 0.21 | 0.29 | 0.38 |
| *Coriobacteriales* | 0.05 | 0.52 | 0.15 |
| *Aeromonadales* | 0.01 | 0.59 | 0.12 |
| *Deferribacterales* | 0.00 | 0.00 | 0.27 |
| *Verrucomicrobiales* | 0.00 | 0.00 | 0.24 |
| *Methanomassiliicoccales* | 0.01 | 0.00 | 0.14 |
| *Erysipelotrichales* | 0.01 | 0.08 | 0.04 |
| *Fibrobacterales* | 0.00 | 0.00 | 0.12 |
| *Other* | 7.96 | 1.16 | 8.35 |

**SupplementaryTable6.** The family composition of colonic microbiome among three groups

|  |  |  |  |
| --- | --- | --- | --- |
| tax\_name | S | W | FW |
| *Prevotellaceae* | 32.94 | 20.42 | 18.58 |
| *Ruminococcaceae* | 16.93 | 18.95 | 15.16 |
| *Lachnospiraceae* | 6.45 | 19.52 | 10.09 |
| *Porphyromonadaceae* | 12.72 | 4.03 | 10.77 |
| *Bacteroidaceae* | 3.84 | 10.15 | 4.79 |
| *Campylobacteraceae* | 0.27 | 6.83 | 7.75 |
| *Lactobacillaceae* | 5.12 | 4.13 | 3.74 |
| *Fusobacteriaceae* | 4.37 | 4.30 | 0.03 |
| *Veillonellaceae* | 0.30 | 5.55 | 0.79 |
| *Acidaminococcaceae* | 0.65 | 0.94 | 4.26 |
| *Spirochaetaceae* | 0.79 | 0.06 | 2.98 |
| *Desulfovibrionaceae* | 0.91 | 0.29 | 1.05 |
| *Rikenellaceae* | 0.66 | 0.03 | 1.12 |
| *Synergistaceae* | 0.05 | 0.01 | 1.52 |
| *Pasteurellaceae* | 1.06 | 0.10 | 0.15 |
| *Methanobacteriaceae* | 0.15 | 0.01 | 0.88 |
| *Enterobacteriaceae* | 0.21 | 0.29 | 0.38 |
| *Sutterellaceae* | 0.04 | 0.76 | 0.05 |
| *Coriobacteriaceae* | 0.05 | 0.52 | 0.15 |
| *Succinivibrionaceae* | 0.01 | 0.59 | 0.12 |
| *Other* | 12.48 | 2.54 | 15.65 |

**SupplementaryTable7.** The genus composition of colonic microbiome among three groups

|  |  |  |  |
| --- | --- | --- | --- |
| tax\_name | S | W | FW |
| *Prevotella* | 19.63 | 16.61 | 7.04 |
| *Alloprevotella* | 7.88 | 1.39 | 9.78 |
| *Bacteroides* | 3.84 | 10.15 | 4.79 |
| *Campylobacter* | 0.27 | 6.83 | 7.75 |
| *Lactobacillus* | 5.12 | 4.13 | 3.74 |
| *Fusobacterium* | 4.28 | 4.30 | 0.03 |
| *Barnesiella* | 4.94 | 0.97 | 1.44 |
| *Roseburia* | 1.16 | 3.89 | 1.55 |
| *Faecalibacterium* | 0.04 | 6.23 | 0.24 |
| *Phascolarctobacterium* | 0.65 | 0.94 | 4.13 |
| *Oscillibacter* | 3.00 | 0.51 | 1.49 |
| *Clostridium XlVb* | 1.10 | 1.77 | 0.59 |
| *Parabacteroides* | 1.44 | 0.27 | 1.37 |
| *Megasphaera* | 0.04 | 2.64 | 0.31 |
| *Clostridium XlVa* | 0.47 | 1.62 | 0.84 |
| *Butyricicoccus* | 0.04 | 1.69 | 0.90 |
| *Treponema* | 0.58 | 0.02 | 1.95 |
| *Blautia* | 0.05 | 2.29 | 0.20 |
| *Flavonifractor* | 0.00 | 2.00 | 0.02 |
| *Gemmiger* | 0.33 | 1.48 | 0.18 |
| *Other* | 45.15 | 30.25 | 51.67 |