# **SUPPLEMENTARY MATERIAL**

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**Supplementary Figure 1:** Relative abundance of archaeal and bacterial phyla in ileal and caecal digesta of pigs fed a human-type diet (*n* 5).



**Supplementary Figure 2:** Relative abundance of archaeal and bacterial genera in ileal and caecal digesta of pigs fed a human-type diet (*n* 5).

**Supplementary Table 1:** Ingredient and determined nutrient composition of the experimental diet.

|  |  |  |
| --- | --- | --- |
|  |  | g DM/kg DM |
| Ingredient1 |
|  | Cooked carrot (minced) | 100 |
|  | Canned beans (minced) | 150 |
|  | Peeled hard-boiled egg (minced) | 120 |
|  | Cooked white rice (minced) | 550 |
|  | Raw apple (minced) | 48.5 |
|  | Premix of vitamins and minerals2 | 5.0 |
|  | Sodium chloride | 3.0 |
|  | Titanium dioxide | 3.0 |
|  | Calcium carbonate | 0.5 |
|  | Dicalcium phosphate | 20 |
|  |  |  |
| Nutrient | g/kg DM |
|  | Crude protein | 143 |
|  | Starch | 508 |
|  | Total lipid | 45 |
|  | Ash | 49 |
|  | Soluble fibre | 20 |
|  | Insoluble fibre | 96 |
|  | Total dietary fibre | 116 |
|  |  |  |
| Determined energy | MJ/kg DM |
|  | Gross energy | 18.1 |
| 1The chemical composition of the ingredients was obtained from the USDA National Nutrient Database (<https://ndb.nal.usda.gov/>; version 2.3.8).2Vitamin and mineral premixes were obtained from Vitec Nutrition Ltd (Auckland, New Zealand) and supplied (per kg of diet): Mn, 45 mg; Zn, 80 mg; Cu, 25 mg; Co, 0.5 mg; Se, 0.3 mg; Fe, 100 mg; Iodine, 1.0 mg; Choline, 100 mg; all-trans retinylacetate, 3.0 mg; cholecalciferol, 0.05 mg; α-tocopherol, 50 mg; menadione, 2.0 mg; thiamin, 1.0 mg; riboflavin, 3.0 mg; nicotinic acid, 15 mg; pantothenic acid, 20 mg; pyridoxine, 2.0 mg; cyanocobalamin, 0.01 mg; folic acid, 0.5 mg; biotin, 0.1 mg.DM, dry matter. |

**Supplementary Table 2:** Predicted metabolic activity (PICRUSt) (x106 relative activity/kg diet DM intake) for carbohydrate and protein metabolism, in ileal and caecal digesta of pigs fed a human-type diet (*n* 5).

|  |  |  |  |
| --- | --- | --- | --- |
|   |   | GIT location |   |
|   |   | Ileum | Caecum |  |
| KEGG reference pathway | Mean | SEM | Mean | *SEM* | *P* |
| Carbohydrate metabolism |  |  |  |  |   |
|  | Amino sugar and nucleotide sugar metabolism | 113 | 13.8 | 108 | 8.03 | 0.63 |
|  | Ascorbate and aldarate metabolism | 16.2 | 1.83 | 9.06 | 0.67 | 0.02 |
|  | Butanoate metabolism | 49.8 | 5.07 | 49.4 | 3.41 | 0.92 |
|  | C5-Branched dibasic acid metabolism | 17.1 | 2.76 | 25.3 | 2.16 | <0.01 |
|  | Citrate cycle (TCA cycle) | 30.6 | 2.48 | 43.8 | 3.62 | <0.01 |
|  | Fructose and mannose metabolism | 67.0 | 3.93 | 82.4 | 6.62 | 0.05 |
|  | Galactose metabolism | 73.9 | 8.55 | 61.6 | 4.51 | 0.17 |
|  | Glycolysis / Gluconeogenesis | 98.5 | 12.8 | 97.8 | 7.56 | 0.95 |
|  | Glyoxylate and dicarboxylate metabolism | 26.0 | 2.41 | 38.7 | 3.04 | <0.01 |
|  | Inositol phosphate metabolism | 7.07 | 0.79 | 6.71 | 0.54 | 0.23 |
|  | Pentose and glucuronate interconversions | 37.2 | 3.31 | 45.6 | 3.72 | 0.02 |
|  | Pentose phosphate pathway | 62.4 | 7.80 | 75.8 | 6.07 | 0.08 |
|  | Propanoate metabolism | 41.6 | 4.65 | 41.4 | 2.93 | 0.94 |
|  | Pyruvate metabolism | 76.0 | 9.28 | 90.3 | 6.66 | 0.02 |
|  | Starch and sucrose metabolism | 78.4 | 11.8 | 84.8 | 7.13 | 0.47 |
| Amino acid metabolism |  |  |  |  |  |
|  | Alanine, aspartate, and glutamate metabolism | 53.5 | 6.54 | 81.4 | 6.34 | <0.01 |
|  | Amino acid related enzymes | 89.0 | 11.1 | 117 | 8.77 | <0.01 |
|  | Arginine and proline metabolism | 60.4 | 6.63 | 96.2 | 7.53 | <0.01 |
|  | Cysteine and methionine metabolism | 55.9 | 6.94 | 75.3 | 5.45 | <0.01 |
|  | Glycine, serine, and threonine metabolism | 46.5 | 5.67 | 61.3 | 4.46 | <0.01 |
|  | Histidine metabolism | 27.6 | 3.62 | 50.3 | 3.82 | 0.02 |
|  | Lysine biosynthesis | 41.8 | 5.51 | 68.4 | 5.36 | <0.01 |
|  | Lysine degradation | 7.50 | 0.80 | 8.00 | 0.57 | 0.19 |
|  | Phenylalanine metabolism | 7.19 | 0.95 | 13.8 | 1.19 | <0.01 |
|  | Phenylalanine, tyrosine, and tryptophan biosynthesis | 33.3 | 4.87 | 68.4 | 5.83 | <0.01 |
|  | Tryptophan metabolism | 12.6 | 1.55 | 8.55 | 0.62 | 0.03 |
|  | Tyrosine metabolism | 30.9 | 3.63 | 28.3 | 2.03 | 0.39 |
|  | Valine, leucine, and isoleucine biosynthesis | 47.1 | 7.72 | 63.3 | 5.08 | <0.01 |
|  | Valine, leucine, and isoleucine degradation | 18.4 | 2.23 | 12.2 | 0.75 | 0.03 |
| Metabolism of other amino acids |  |  |  |  |  |
|  | Cyanoamino acid metabolism | 19.0 | 3.32 | 18.5 | 1.61 | 0.86 |
|  | D-Alanine metabolism | 11.6 | 1.66 | 8.76 | 0.60 | 0.09 |
|  | D-Arginine and D-ornithine metabolism | 0.11 | 0.05 | 0.14 | 0.02 | 0.56 |
|  | D-Glutamine and D-glutamate metabolism | 10.0 | 1.24 | 11.6 | 0.81 | 0.14 |
|  | Glutathione metabolism | 18.9 | 2.66 | 11.4 | 0.79 | 0.03 |
|  | Phosphonate and phosphinate metabolism | 5.38 | 0.58 | 5.71 | 0.76 | 0.69 |
|  | Selenocompound metabolism | 26.0 | 3.13 | 26.9 | 2.02 | 0.77 |
|  | Taurine and hypotaurine metabolism | 9.28 | 1.12 | 7.30 | 0.50 | 0.11 |
|   | β-Alanine metabolism | 6.29 | 0.53 | 10.5 | 1.00 | 0.02 |
|  | GIT, gastrointestinal tract; KEGG, Kyoto Encyclopedia of Genes and Genomes; PICRUSt, phylogenetic investigation of communities by reconstruction of unobserved states. |

**Supplementary Table 3:** SCFA production (mmol/kg substrate DM incubated) during *in vitro* ileal and hindgut fermentations of pigs fed a human-type diet (*n* 5).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|   |  | GIT location |  |  |
|   | Ileum | Hindgut |  |
|  | Mean | SEM | Mean | SEM | *P* |
| Acetate | 384 | 65.7 | 121 | 70.2 | 0.09 |
| Propionate | 11.5 | 2.19 | 97.6 | 19.2 | 0.02 |
| Butyrate | 6.90 | 4.60 | 113 | 13.0 | <0.01 |
| Iso-butyrate | 1.06 | 0.17 | 4.82 | 1.50 | 0.06 |
| Iso-valerate | 4.28 | 0.73 | 6.25 | 1.24 | 0.02 |
| Valerate | 1.71 | 1.00 | 14.7 | 1.40 | <0.01 |
| DM, dry matter; GIT, gastrointestinal tract. |

**Supplementary Table 4:** Nutrient composition and nutrient content (normalised) of terminal jejunum and terminal ileal digesta of pigs fed a human-type diet (*n* 5).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|   |  |   |  | GIT location |  |  |
|   |  |   | Terminal jejunum | Terminal ileum |  |
|  |  |  | Mean | SEM | Mean | *SEM* | *P* |
| Nutrient composition, g/kg DM |  |  |  |  |  |
|  | Organic matter | 891 | 76 | 834 | 9.49 | <0.01 |
|  |  | Crude protein | 236 | 8.68 | 188 | 9.13 | 0.01 |
|  |  | Lipid | 12.4 | 3.64 | 14.7 | 2.38 | 0.47 |
|  |  | Starch | 107 | 15.2 | 82.0 | 6.27 | 0.21 |
| Normalised nutrient content, g/kg diet DM intake |  |  |  |  |  |
|  | Organic matter | 246 | 21.8 | 141 | 10.3 | <0.01 |
|  |  | Crude protein | 65.4 | 6.69 | 32.0 | 2.90 | <0.01 |
|  |  | Lipid | 3.51 | 1.12 | 2.53 | 0.52 | 0.29 |
|  |  | Starch | 30.7 | 6.5 | 13.9 | 1.54 | 0.07 |
| Terminal jejunum and terminal ileal digesta were the substrate for ileal and hindgut fermentation, respectively. DM, dry matter; GIT, gastrointestinal tract. |