**Supplementary Table 1.** Determined taxonomic microbial composition of ileal and caecal digesta for pigs fed a high-fibre human-type diet and the corresponding selected bacterial strain for carbohydrate active enzymes (CAZy).

|  |  |
| --- | --- |
| Determined genus | CAZy |
| Actinomycetales\* | *Actinomyces sp.* 2129 |
| Bacteroidales\* | *Bacteroidales* bacterium CF |
| *Blautia* | *Blautia sp.* N6H1-15 KCTC 15426 |
| Christensenellaceae\* | *Christensenella minuta* DSM 22607 |
| Clostridiaceae\* | Clostridiaceaebacterium 14S0207 |
| Clostridiales\* | *Clostridiales* bacterium 70B-A |
| *Collinsella* | *Collinsella aerofaciens* C11 |
| *Coprococcus* | *Coprococcus sp.* ART55/1 |
| Coriobacteriaceae\* | Coriobacteriaceaebacterium 68-1-3 |
| *Dorea* | Lachnospiraceaebacterium oral taxon 500 W11650 |
| Enterobacteriaceae\* | Enterobacteriaceaebacterium bta3-1 |
| *Enterococcus* | *Enterococcus sp.* 7L76 |
| Erysipelotrichaceae\* | Erysipelotrichaceae bacterium I46 |
| *Lachnospira* | Lachnospiraceaebacterium oral taxon 500 W11650 |
| Lachnospiraceae\* | Lachnospiraceaebacterium oral taxon 500 W11650 |
| *Lactobacillus* | *Lactobacillus sp.* CBA3605 |
| *Leuconostoc* | *Leuconostoc sp.* C2 |
| *Methanosphaera* | - |
| Micrococcaceae\* | *Micrococcus luteus* SA211 |
| Mogibacteriaceae\* | *Mogibacterium diversum* CCUG 47132 |
| *Prevotella* | *Prevotella jejuni* CD3\_33 |
| *Roseburia* | *Roseburia intestinalis* M50/1 |
| Ruminococcaceae\* | Ruminococcaceaebacterium CPB6 |
| *Ruminococcus* | *Ruminococcus sp.* SR1/5 |
| *Streptococcus* | *Streptococcus sp.* A12 |
| TM7-3\_F16 | - |
| *Treponema* | *Treponema sp.* OMZ 838 |
| *Turicibacter* | *Turicibacter sp.* H121 |
| Unassigned | - |

\* Bacteria could only be classified only as class, order or family level.

**Supplementary Table 2.** Predicted number (x108) of sequences for each glycoside hydrolase family (GHF) in the ileal and caecal absolute number of bacterial 16S rRNA gene copies\* for pigs fed a high-fibre human-type diet.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GHF | Ileal | Caecal |  | GHF | Ileal | Caecal |
| 1 | 326 | 316 |  | 73 | 136 | 267 |
| 2 | 87.2 | 301 |  | 74 | 0.002 | 1.14 |
| 3 | 8.79 | 227 |  | 77 | 69.5 | 178 |
| 4 | 12.8 | 66.8 |  | 78 | 0.583 | 76.8 |
| 5 | 0.646 | 22.8 |  | 84 | 0.293 | 15.4 |
| 8 | 7.82 | 5.63 |  | 85 | 65.8 | 84.6 |
| 9 | 0.098 | 13.16 |  | 87 | 0.000 | 15.4 |
| 13 | 588 | 998 |  | 88 | 28.6 | 31.1 |
| 15 | 0.293 | 0.005 |  | 89 | 0.008 | 15.1 |
| 16 | 0.004 | 38.3 |  | 91 | 7.69 | 68.8 |
| 18 | 17.9 | 101 |  | 92 | 71.6 | 79.7 |
| 19 | 0.000 | 46.1 |  | 94 | 11.5 | 61.1 |
| 20 | 204 | 205 |  | 95 | 0.000 | 15.4 |
| 23 | 220 | 273 |  | 97 | 0.008 | 45.8 |
| 24 | 0.395 | 15.9 |  | 99 | 0.000 | 15.4 |
| 25 | 180 | 378 |  | 102 | 0.395 | 0.543 |
| 26 | 0.103 | 22.7 |  | 103 | 0.395 | 0.543 |
| 27 | 0.002 | 31.9 |  | 104 | 0.395 | 0.543 |
| 28 | 0.475 | 14.3 |  | 105 | 13.8 | 30.9 |
| 29 | 66.1 | 151 |  | 109 | 0.156 | 55.9 |
| 30 | 0.553 | 42.7 |  | 112 | 0.108 | 33.4 |
| 31 | 16.7 | 189 |  | 113 | 0.049 | 3.94 |
| 32 | 102 | 206 |  | 114 | 0.078 | 12.6 |
| 33 | 0.062 | 32.6 |  | 120 | 0.002 | 1.14 |
| 35 | 79.1 | 51.3 |  | 123 | 5.25 | 20.2 |
| 36 | 9.81 | 171 |  | 125 | 65.7 | 43.7 |
| 38 | 72.1 | 57.6 |  | 127 | 0.412 | 5.28 |
| 39 | 0.080 | 13.7 |  | 130 | 0.179 | 43.4 |
| 42 | 7.95 | 39.2 |  | 133 | 0.000 | 15.4 |
| 43 | 15.1 | 44.3 |  | 136 | 0.002 | 1.14 |
| 50 | 0.004 | 7.55 |  | 140 | 0.046 | 1.00 |
| 51 | 0.194 | 43.2 |  | 146 | 0.013 | 2.46 |
| 53 | 0.064 | 7.54 |  | 153 | 0.395 | 0.543 |
| 57 | 0.004 | 31.2 |  | 154 | 19.6 | 19.7 |
| 63 | 0.000 | 4.15 |  | 155 | 0.000 | 15.3 |
| 65 | 42.1 | 42.3 |  | NC | 5.45 | 70.2 |
| 66 | 0.000 | 15.4 |  |  |  |  |

\* The mean ileal and caecal absolute bacterial 16S rRNA gene copy number determined through qPCR total bacteria determination was 98.7 and 172 x108/g DM digesta respectively.



**Supplementary Figure 1.** Individual ileal and caecal relative abundances of bacteria at the genus level for five growing pigs fed a high-fibre human-type diet as determined by Illumina MiSeq 16S rRNA gene sequencing.



**Supplementary Figure 2.** Individual ileal and caecal relative abundances of bacteria at the phylum level for five growing pigs fed a high-fibre human-type diet.