Supplemental Material.

TABLE S1 Primers used for quantification of total bacteria and target bacterial groups in gastrointestinal digesta of weaned pigs

Bacterial group	Primer (5`-3`)		A_T (°C)	Efficiency (*e*)	Amplicon size (bp)	Reference[c]
	Forward	Reverse				
Universal bacteria	CCTACGGGAGGCAGCAG	ATTACCGCGGCTGCTGG	61	2.01	189	1
Lactobacillus group[a]	AGCAGTAGGGAATCTTCCA	CACCGCTACACATGGAG	62	2.00	341	2,3
Enterococcus spp.	CCCTTATTGTTAGTTGCCATCATT	ACTCGTTGTACTTCCCATTGT	60	2.00	144	4
Streptococcus spp.	AGAGTTTGATCCTGGCTCAG	GTTAGCCGTCCCTTTCTGG	60	1.94	485	5,6
Clostridium cluster XIV	AAATGACGGTACCTGACTAA	CTTTGAGTTTCATTCTTGCGAA	60	1.94	438-441	7
Clostridium cluster IV	GCACAAGCAGTGGAGT	CTTCCTCCGTTTTGTCAA	60	2.00	130	8
Clostridium cluster I	ATGCAAGTCGAGCGAKG	TATGCGGTATTAATCTYCCTTT	60	2.00	120	4
Bifidobacterium spp.	TCGCGTCYGGTGTGAAAG	CCACATCCAGCRTCCAC	60	1.95	243	4
Bacteroides-Prevotella-Porphyromonas	GGTGTCGGCTTAAGTGCCAT	CGGAYGTAAGGGCCGTGC	60	2.01	140	4
Enterobacteriaceae family[b]	CATTGACGTTACCCGCAGAAGAAGC	CTCTACGAGACTCAAGCTTGC	63	1.97	195	9
Helicobacter spp.	CTATGACGGGTATCCGGC	ATTCCACCTACCTCTCCCA	60	1.96	376	10
Campylobacter spp.	GGATGACACTTTTCGGAG	AATTCCATCTGCCTCTCC	61	1.96	246	4
Fusobacterium spp.	CWAACGCGATAAGTAATC	TGGTAACATACGAWAAGG	55	1.95	273	4

F, forward; R, reverse; A_T, annealing temperature.

[a] Lactobacillus group includes the genera *Lactobacillus, Lactococcus, Leuconostoc, Pediococcus, Weisella*.

[b] *Enterobacteriaceae* family comprises the genera *Citrobacter*, *Cronobacter*, *Enterobacter*, *Erwinia*, *Escherichia*, *Pantoea*, *Pectobacterium* and *Shigella*.

[c] References:

1. **Muyzer G, de Waal EC, Uitterlinden AG.** 1993. Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. Appl. Environ. Microbiol.59:695-700.
2. **Walter J, Hertel C, Tannock GW, Lis CM, Munro K, Hammes WP.** 2001. Detection of *Lactobacillus*, *Pediococcus*, *Leuconostoc*, and *Weissella* species in human feces by using group-specific PCR primers and denaturing gradient gel electrophoresis. Appl. Environ. Microbiol. 67:2578-2585.
3. **Heilig HGHJ, Zoetendal EG, Vaughan EE, Marteau P, Akkermans ADL, de Vos WM.** 2002. Molecular diversity of *Lactobacillus* spp. and other lactic acid bacteria in the human intestine as determined by specific amplification of 16S ribosomal DNA. Appl. Environ. Microbiol. **68:**114-123.

4. **Rintillä T, Kassinen A, Malinen E, Krogius L, Palva A.** 2004. Development of an extensive set of 16S rDNA-targeted primers for quantification of pathogenic and indigenous bacteria in faecal samples by real-time PCR. J. Appl. Microbiol. **97**:1166-1177.
5. **Nübel U, Engelen B, Felske A, Snaidr J, Wieshuber A, Amann RI, Ludwig W, Backhaus HH.** 1996. Sequence heterogeneities of genes encoding 16S rRNAs in *Paenibacillus polymyxa* detected by temperature gradient gel electrophoresis. J. Bacteriol. **178:**5636–5643.
6. **Franks AH, Harmsen HJ, Raangs GC, Jansen GJ, Schut F, Welling GW.** 1998. Variations of bacterial populations in human feces measured by fluorescent *in situ* hybridization with group-specific 16S rRNA targeted oligonucleotide probes. Appl. Environ. Microbiol. **64:**3336–3345.
7. **Matsuki T, Watanabe K, Fujimoto J, Miyamoto Y, Takada T, Matsumoto K, Oyaizu H, Tanaka R.** 2002. Development of 16S rRNA-gene targeted group-specific primers for the detection and identification of predominant bacteria in human feces. Appl. Environ. Microbiol. **68:**5445–5451.
8. **Matsuki T, Watanabe K, Fujimoto J, Takada T, Tanaka R.** 2004. Use of 16S rRNA gene-targeted group-specific primers for real-time PCR analysis of predominant bacteria in human feces. Appl. Environ. Microbiol. **70:**7220–7228.
9. **Bartosch S, Fite A, Macfarlane GT, McMurdo MET.** 2004. Characterization of bacterial communities in feces from healthy elderly volunteers and hospitalized elderly patients by using real-time PCR and effects of antibiotic treatment on the fecal microbiota. Appl. Environ. Microbiol. **70**:3575-3581.
10. **Proietti PC, Bietta A, Brachelente C, Lepri E, Davidson I, Franciosini MP.** 2010 Detection of *Helicobacter* spp. in gastric, fecal and saliva samples from swine affected by gastric ulceration. J. Vet. Sci. **11**:221-225.

TABLE S2 Comparison of dry matter content, pH, lactate and SCFA found at different gut sites in weaned pigs[a]

Parameter	Stomach	Ileum	Colon	Feces	Pooled SEM	P-value
Dry matter (%)	26.7 b	14.2 d	20.6 c	29.5 a	1.07	<0.001
pH	3.6 c	6.1 ab	5.9 b	6.5 a	0.14	<0.001
µmol/g						
Total lactate	21.4 a	30.8 a	0.5 b	-	3.42	<0.001
D-lactate	13.0 a	5.8 b	0.3 c	-	1.84	<0.001
L-lactate	8.4 b	25.6 a	0.2 c	-	2.80	<0.001
Total SCFA				-		
Acetate	6.3 b	9.0 b	70.7 a	-	1.75	<0.001
Propionate	2.4 b	1.2 b	39.3 a	-	1.34	<0.001
Iso-butyrate	0.3 b	0.3 b	1.1 a	-	0.05	<0.001
Butyrate	1.1 b	0.7 b	18.7 a	-	0.58	<0.001
Iso-valerate	0.1 b	0.1 b	1.0 a	-	0.08	<0.001
Valerate	0.2 b	0.1 b	3.8 a	-	0.22	<0.001
Caproate	0.2 b	0.2 b	0.4 a	-	0.07	<0.001

Data are presented as least-square means ± SEM. Different letters within rows indicate significant difference ($P < 0.05$).

[a] Mean of $n = 31$ pigs for stomach, $n = 27$ pigs for ileum and $n = 31$ pigs for colon.