

Article

Temporal Microbial Dynamics in Feces Discriminate by Nutrition, Fecal Color, Consistency and Sample Type in Suckling and Newly Weaned Piglets

Barbara U. Metzler-Zebeli ^{1,2,*}, Frederike Lerch ^{1,2}, Fitra Yosi ^{1,2,3}, Julia Vötterl ^{1,2}, Juliane Ehmig ^{1,2}, Simone Koger ^{2,4} and Doris Verhovsek ⁵

¹ Unit Nutritional Physiology, Department of Biomedical Sciences, University of Veterinary Medicine Vienna, 1210 Vienna, Austria

² Christian-Doppler Laboratory for Innovative Gut Health Concepts of Livestock, University of Veterinary Medicine Vienna, 1210 Vienna, Austria

³ Department of Animal Science, Faculty of Agriculture, University of Sriwijaya, Palembang 30662, Indonesia

⁴ Institute of Animal Nutrition and Functional Plant Compounds, Department for Farm Animals and Veterinary Public Health, University of Veterinary Medicine Vienna, 1210 Vienna, Austria

⁵ University Clinic for Swine, Department for Farm Animals and Veterinary Public Health, University of Veterinary Medicine Vienna, 1210 Vienna, Austria

* Correspondence: barbara.metzler@vetmeduni.ac.at

Supplementary Materials

Citation: Metzler-Zebeli, B.U.; Lerch, F.; Yosi, F.; Vötterl, J.; Ehmig, J.; Koger, S.; Verhovsek, D. Temporal Microbial Dynamics in Feces Discriminate by Nutrition, Fecal Color, Consistency and Sample Type in Suckling and Newly Weaned Piglets. *Animals* **2023**, *13*, 2251. <https://doi.org/10.3390/ani13142251>

Academic Editor: Kelsy J. Robinson

Received: 6 June 2023

Revised: 5 July 2023

Accepted: 7 July 2023

Published: 9 July 2023



Copyright: © 2023 by the authors. Submitted for possible open access publication under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).



Table S1. Analyzed nutrient composition of the piglets and sow diet.

Chemical Composition, % DM	Milk		
	Lactation Diet ¹	Replacer ²	Prestarter Diet ³
Dry matter, %	89.0	94.8	91.9
Crude ash	5.5	5.6	5.5
Crude protein	17.9	19.8	20.5
Crude fibre	5.8	0.4	5.2
Neutral-detergent fibre	17.3	3.0	15.2
Acid-detergent fibre	6.7	0.6	5.8
Acid-detergent lignin	1.8	0.3	1.5
Crude fat	5.2	7.8	7.5
Nitrogen-free extract	65.7	66.5	61.6
Starch	47.3	29.4	31.9
Sugar	5.5	26.8	14.2
Metabolizable energy, MJ/kg	14.7	16.9	15.3

¹ZuchtsauenKorn S Vital, Garant-Tiernahrung GmbH, Pöchlarn, Austria. Ingredient composition: corn, wheat, barley, soybean meal, sunflower meal, wheat bran, apple pomace, soybean oil, calcium carbonate, monocalcium phosphate, sodium chloride, magnesium phosphate, fish oil, L-cellulose, molasses. Vitamin and mineral composition per kg feed: 10,000 IU of vitamin A, 1,800 IU of vitamin D, 100 mg of Fe as iron(II) sulfate, 15 mg of Cu as copper(II) sulfate, 90 mg of Zn as zinc sulfate, 40 mg of Mn as manganese(II) oxide, 1.5 mg of I as calcium iodate, 0.4 mg of Se as sodium selenite. Technological additives: 500 FTU phytase, 2 mg of butylated hydroxyanisole, 10 mg of butylated hydroxytoluene, 2 mg of propyl gallate.

²Weanplus-4, Startix, Voorthuizen, The Netherlands. Ingredient composition: whey powder, starch, soy protein, plant protein, plant oil (coconut oil and palm oil). Vitamin and mineral composition per kg feed: 25,000 IU of vitamin A, 8,000 IU of vitamin D₃, 200 mg of vitamin E, 140 mg of Cu as chelate of glycine hydrate, 108 mg of Fe as chelate of glycine hydrate, 3 mg of I as calcium iodate, 115 mg of Zn as chelate of glycine hydrate, 35 mg of Mn as glycine chelate, 0.3 mg of Se as sodium selenite. Technological additives: 5 g of citric acid, 1 g of calcium formiate. Mixing ratio: 200 g of powder mixed into 1 L of 40°C warm water.

³Ferkelabsetzkorn OGT, Garant-Tiernahrung GmbH, Pöchlarn, Austria. Ingredient composition: oat flakes, barley, wheat, whey powder, soy protein concentrate, wheat bran, sucrose, soybean meal, soy oil, corn gluten, L-cellulose, monocalcium phosphate, fish oil, sodium chloride, magnesium phosphate, calcium carbonate and molasses. Vitamin and mineral composition per kg feed: 16,000 IU of vitamin A, 2,000 IU of vitamin D₃, 200 mg vitamin E, 120 mg Fe as iron(II) sulfate, 140 mg Cu as copper(II) sulfate, 120 mg Zn as zinc sulfate, 60 mg Mn as manganese(II) oxide, 1.5 mg I as calcium iodate, 0.5 mg Se as sodium selenite. Technological additives: 1,000 IU of phytase, 1,500 EPU of xylanase, 11 mg of beta hydroxy acid, 21 mg of butylated hydroxytoluene, 11 mg of propyl gallate.

Table S2. Oligonucleotide primers for quantification of total bacterial 16S rRNA, protozoal 18S rRNA, fungal 26S rRNA and archaeal 16S rRNA gene copies.

Group		Primer sequence (5' to 3') ¹	Amplicon size (bp)	PCR Efficiency	Reference
Total bacteria	F:	CCTACGGGAGGCAGCAG	193	95.3%	[1]
	R:	ATTACCGCGGCTGCTGG			
Total protozoa	F:	GCTTTCGWTGGTAGTGATT	233	99.6%	[2]
	R:	CTTGCCCTCYAATCGTWCT			
Total fungi and yeasts	F:	GCATATCAATAAGCGGAGGAAAAG	250	91.1%	[3]
	R:	ATTCCCAAACAACCTCGACTC			
Total archaea	F:	CCGGAGATGGAACCTGAGAC	160	99.6%	[4]
	R:	CGGTCTTGCCAGCTCTTATTC			

¹F, forward primer; R, reverse primer.

References

1. Muyzer, G., De Waal, E.C., Uitterlinden, A.G. Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. *Appl. Environ. Microbiol.* **1993**, *59*, 695–700.
2. Sylvester, J.T., Karnati, S. K. R., Yu, Z., Morrison, M., Firkins, J.L. Development of an assay to quantify rumen ciliate protozoal biomass in cows using real-time PCR. *J. Nutr.* **2004**, *134*, 3378–3384. doi:10.1093/jn/134.12.3378.
3. Urubschurov, V., Büsing, K., Janczyk, P., Souffrant, W.B., Zeyner, A. Development and evaluation of qPCR assay for quantitation of *Kazachstania slooffiae* and total yeasts occurring in the porcine gut. *Curr. Microbiol.* **2015**, *71*:373–381. doi:10.1007/s00284-015-0862-2.
4. Zhou, M., Hernandez-Sanabria, E., Guan, L.L. Assessment of the microbial ecology of ruminal methanogens in cattle with different feed efficiencies. *Appl. Environ. Microbiol.* **2009**, *75*, 6524–6533. doi:10.1128/AEM.02815-08.



Table S3. Descriptive statistics for average daily creep feed intake during the suckling period.*

Daily intake (g dry matter)	Mean	SE	Minimum	Maximum	Median
DoL 10-16	10	1.9	4	23	8
DoL 17-23	18	3.7	7	41	14
DoL 24-25	30	3.8	14	52	29
DoL 26-28	79	10.3	40	125	78

*Creep feed consumption was estimated at litter level. DoL, day of life; SE, standard error of the mean. Piglets in the creep-fed group were offered the milk replacer from DoL 10 to 23, transitioned from the milk replacer to the prestarter on DoL 24 and 25 and were offered the prestarter diet to 100% from DoL 26. Piglets in the sow milk only group received the prestarter from weaning on day 28 of life.

Table S4. Body weight development of piglets selected for collection of feces.*

Item	Sow milk	Creep feed	SEM	litter_birth	P-value	
					diet	sex × diet
Birth weight	1.5	-	0.07	0.017	0.010	0.956
Day 2	1.6	-	0.09	0.036	0.016	0.852
Day 6	2.1	-	0.16	0.059	0.001	0.682
Day 13	4.4	3.4	0.23	0.239	0.013	0.566
Day 20	6.4	5.4	0.36	0.474	0.083	0.735
Day 27	8.6	7.1	0.47	0.172	0.067	0.742
Day 30	8.8	7.2	0.45	0.165	0.044	0.837
Day 34	8.9	7.2	0.45	0.39	0.030	0.909

*Values are least squares means ± standard error of the mean (SEM). Piglets were weaned on day 28 of life.

9

10

11

12

13

Table S5. Age-related development of relative bacterial abundances (% of total reads) in feces from suckling and newly weaned piglets fed either only sow milk or additional creep feed from day 10 of life.*

14
15

Day of Life (DoL)	2	6	13		20		27		30		34					
	Sow	Sow	Sow	Creep	Sow	Creep	Sow	Creep	Sow	Creep	Sow	Creep	DoL ×			
Feeding (Feed)	Milk	Milk	Milk	feed	Milk	feed	Milk	feed	Milk	feed	Milk	feed	Pooled SEM	DoL	Feed	Feed
<i>Lactobacillus</i>	1.91	4.82	7.93	9.15	4.18	4.56	2.79	4.04	1.57	1.90	5.96	4.14	1.517	<0.001	0.326	0.292
<i>Escherichia Shigella</i>	38.11	24.91	22.52	27.49	9.64	12.99	6.34	6.01	7.40	4.99	2.12	2.52	3.299	<0.001	0.516	0.912
<i>Bacteroides</i>	11.39	20.09	11.88	13.73	7.73	6.21	5.83	8.93	3.95	5.26	1.46	0.55	2.159	<0.001	0.067	0.240
<i>Prevotella</i>	0.80	1.90	3.36	1.66	3.60	2.71	4.47	6.11	3.68	9.61	6.59	7.51	1.141	<0.001	0.387	0.012
<i>Actinobacillus</i>	3.99	1.67	0.44	0.66	0.55	0.12	0.18	1.44	0.16	0.58	0.08	0.04	0.833	<0.001	0.332	0.595
<i>Fusobacterium</i>	13.65	9.32	1.27	0.67	0.82	2.95	5.08	8.37	1.84	3.12	0.88	0.06	1.881	<0.001	0.809	0.374
<i>Alloprevotella</i>	0.28	0.92	0.65	0.40	1.12	1.32	1.82	3.65	2.09	5.88	3.00	4.08	0.699	<0.001	0.004	0.067
<i>Rikenellaceae_RC9_gut_group</i>	0.09	0.25	2.42	1.47	7.54	4.91	9.30	4.63	4.25	2.17	3.01	4.57	1.039	<0.001	0.026	0.072
<i>Clostridium_sensu_stricto_1</i>	13.47	3.10	1.55	2.11	1.69	1.43	2.52	1.33	2.94	1.73	1.30	1.47	1.635	<0.001	0.477	0.959
<i>Streptococcus</i>	2.97	2.26	1.95	0.88	0.77	0.45	1.47	1.75	2.48	1.22	0.20	0.08	0.676	<0.001	0.524	0.706
<i>Lachnospirillum</i>	0.79	6.61	6.11	5.21	4.76	3.78	5.28	4.17	2.60	2.93	0.68	0.52	1.099	<0.001	0.827	0.199
<i>Phascolarctobacterium</i>	0.07	0.31	1.44	0.64	2.42	2.02	2.28	3.08	2.73	3.75	2.89	3.75	0.424	<0.001	0.543	0.165
<i>Campylobacter</i>	0.94	0.81	1.45	1.39	0.80	1.36	0.99	1.49	3.20	2.91	4.00	2.02	0.763	0.006	0.667	0.432
<i>Megasphaera</i>	0.07	0.14	0.18	0.48	0.82	1.15	1.82	2.75	2.16	1.92	4.46	3.52	0.879	<0.001	0.954	0.971
<i>Christensenellaceae_R_7_group</i>	0.04	0.18	0.73	1.15	7.30	6.14	4.18	2.74	4.03	1.36	4.27	2.87	0.861	<0.001	0.044	0.560
<i>Prevotellaceae_NK3B31_group</i>	0.03	0.34	0.67	0.10	0.61	0.92	0.84	1.66	1.98	2.71	3.03	2.57	0.406	<0.001	0.705	0.463
<i>Oscillospiraceae_UCG_002</i>	0.03	0.89	2.10	2.59	5.29	2.05	2.37	1.75	2.74	2.14	2.95	3.13	0.540	<0.001	0.044	0.018
<i>Roseburia</i>	0.14	0.16	0.43	0.32	0.77	1.50	1.17	0.99	1.99	1.99	1.93	1.69	0.402	<0.001	0.870	0.927
<i>NK4A214_group</i>	0.02	0.21	1.33	1.19	2.46	1.57	1.45	0.82	2.09	1.51	2.27	2.50	0.312	<0.001	0.134	0.481
<i>Moraxella</i>	0.22	0.05	0.03	0.04	0.01	0.02	0	0	0.01	0.01	0	0	0.047	<0.001	0.056	0.002
<i>Veillonella</i>	1.09	1.00	0.22	0.46	0.17	0.21	0.16	0.24	0.04	0.09	0.06	0	0.149	<0.001	0.883	0.717
<i>Enterococcus</i>	0.68	2.33	3.67	3.18	0.73	1.66	1.03	0.78	0.07	0.05	0.08	0.12	0.585	<0.001	0.972	0.919

Day of Life (DoL)	2	6	13		20		27		30		34					
	Sow	Sow	Sow	Creep	Sow	Creep	Sow	Creep	Sow	Creep	Sow	Creep	DoL ×			
Feeding (Feed)	Milk	Milk	Milk	feed	Milk	feed	Milk	feed	Milk	feed	Milk	feed	Pooled SEM	DoL	Feed	Feed
Family_XIII_AD3011_group	0.01	0.04	0.44	0.06	1.29	0.93	1.31	0.85	1.46	1.59	1.70	1.85	0.253	<0.001	0.325	0.779
Desulfovibrio	0.08	0.63	0.83	0.62	0.97	0.77	1.26	1.03	0.80	0.83	0.66	0.63	0.149	<0.001	0.154	0.867
Lachnospiraceae_NK4A136_group	0	0.01	0.01	0.01	0.42	0.31	0.16	0.98	1.94	3.19	1.41	1.82	0.345	<0.001	0.072	0.344
Colidextribacter	0.06	0.41	0.34	0.65	0.68	0.69	0.80	0.58	0.65	0.66	0.59	0.81	0.137	<0.001	0.833	0.424
Ruminococcus	0.08	0.59	0.54	0.78	0.86	1.05	1.33	1.30	1.46	1.50	0.80	1.24	0.242	<0.001	0.567	0.858
Rothia	0.08	0.07	0.04	0.05	0.04	0.04	0.01	0.01	0.01	0	0	0	0.016	<0.001	0.205	0.128
Subdoligranulum	0.02	0.11	0.15	0.55	0.98	0.32	0.69	1.47	0.57	1.61	1.23	1.60	0.274	<0.001	0.078	0.045
Mitsuokella	0.06	0.02	0.02	0.01	0.23	0.14	0.64	0.63	0.51	0.67	3.74	1.63	0.579	<0.001	0.364	0.453
Oscillibacter	0.01	0.02	0.23	0.06	0.98	0.88	1.20	0.89	0.72	0.90	0.51	0.61	0.209	<0.001	0.749	0.915
Butyricimonas	0.04	0.48	1.85	0.79	0.91	0.41	0.71	0.61	0.35	0.21	0.05	0.02	0.221	<0.001	0.027	0.164
Coprococcus	0.05	0.08	0.07	0.30	0.80	0.32	1.19	0.39	1.40	1.10	1.46	3.03	0.323	<0.001	0.900	0.016
Parabacteroides	0.30	0.80	1.28	0.25	0.58	0.82	0.28	0.39	0.81	0.41	0.78	0.41	0.261	0.315	0.013	0.096
Helicobacter	0.03	0.10	0.15	0.24	0.27	2.90	0.39	0.63	1.32	1.49	0.61	0.38	0.524	0.006	0.200	0.086
Agathobacter	0	0.02	0.04	0.00	0	0	0	0.24	0.70	1.01	1.34	2.23	0.233	<0.001	0.221	0.333
Terrisporobacter	0.39	0.10	0.32	0.25	0.14	0.74	0.20	0.23	0.66	0.95	0.44	0.59	0.177	0.004	0.293	0.220
Prevotellaceae_UCG_001	0	0.01	0.64	0.14	0.28	0.88	0.49	0.74	0.61	0.47	0.36	0.59	0.323	0.157	0.796	0.655
Tuzzerella	0.08	0.21	0.23	0.15	0.37	1.27	0.46	0.57	0.32	0.56	0.83	0.89	0.259	0.007	0.308	0.468
Romboutsia	0.19	0.08	0.32	0.32	0.29	0.30	0.23	0.39	0.41	0.21	0.03	0.03	0.112	0.040	0.407	0.408
Blautia	0.01	0.08	0.05	0.05	0.31	0.21	0.29	0.61	0.76	1.18	1.87	2.54	0.255	<0.001	0.229	0.644
Dorea	0.04	0.08	0.24	0.34	1.10	0.60	0.43	0.63	0.62	0.66	0.68	0.94	0.157	<0.001	0.922	0.274
Porphyromonas	0.05	0.32	0.47	0.17	0	0.02	0.18	0.00	0.36	0.06	0.05	0.01	0.158	0.152	0.133	0.822
Alistipes	0.01	0.33	0.90	0.91	0.71	0.15	0.79	0.82	0.32	0.30	0.01	0.05	0.188	<0.001	0.472	0.633
Lachnospiraceae_AC2044_group	0	0.01	0.03	0.07	0.39	0.63	0.08	0.04	0.50	1.61	0.64	0.99	0.200	<0.001	0.033	0.054

*Values are least squares means ± pooled standard error of the mean (SEM). Piglets were weaned on day 28 of life. Proportional abundances are presented that represent >0.2% of all reads.

Table S6. Differences in relative bacterial abundances (% of total reads) in feces of different colors and consistencies obtained from suckling and newly weaned piglets during the suckling and early postweaning phase.*

Day of Life (DoL)	2	2	2	2	2	6	6	6	13	13	13	13	20	20	20	20	20	20	20	20
Color	brown	brown	yellow	yellow	yellow	brown	yellow	yellow	brown	brown	yellow	yellow	brown	brown	brown	grey	grey	yellow	yellow	yellow
Consistency	balls	meconium	balls	soft	soft	balls	balls	soft	balls	soft	balls	soft	balls	very soft	soft	balls	soft	balls	very soft	soft
<i>Lactobacillus</i>	0	0	2.94	3.29	3.46	0	5.86	5.10	11.47	0.58	7.99	0	4.92	0.25	0	5.14	0	4.83	5.70	2.44
<i>Escherichia_Shigella</i>	43.84	59.35	34.00	18.67	23.54	27.82	24.84	10.97	23.75	11.65	26.69	6.68	15.93	5.62	4.04	5.18	5.51	12.79	2.19	7.70
<i>Bacteroides</i>	11.91	8.40	11.41	5.72	21.10	14.60	20.73	26.50	16.56	0.80	11.95	6.49	2.54	3.65	14.33	2.59	2.86	7.45	13.70	6.74
<i>Prevotella</i>	0.33	0.46	1.14	0.24	0.17	3.88	1.54	2.39	1.58	26.89	1.80	7.64	8.14	0.45	1.12	5.89	2.03	1.73	0.75	8.01
<i>Actinobacillus</i>	1.58	1.08	4.33	9.25	8.77	0.85	1.80	2.91	0.31	0	0.70	0.71	0.77	0.97	0.33	0.72	0.68	0.20	0.39	0.06
<i>Fusobacterium</i>	9.62	7.22	15.30	7.42	26.81	9.40	8.96	21.15	1.49	0	0.97	0	0.25	0	0	0	0	0.87	18.89	0.70
<i>Alloprevotella</i>	0.43	0.26	0.30	0	0.19	2.14	0.70	0.65	0.42	4.29	0.38	1.99	0.92	7.92	0.38	5.33	0.72	0.88	0.55	2.03
<i>Rikenellaceae_RC9_gut_group</i>	0	0	0.61	2.02	0	0	0.50	0.87	1.56	6.44	1.35	17.78	7.40	1.09	12.55	11.37	0.99	5.74	2.22	11.43
<i>Clostridium_sensu_stricto_1</i>	23.32	3.61	12.41	47.72	5	9.49	2.05	0	2.43	0.64	1.67	0.87	3.02	1.29	3.22	1.13	1.26	1.43	0.42	0.57
<i>Streptococcus</i>	3.24	0.62	4.05	0.75	1.13	2.73	2.12	3.88	1.62	0	1.43	0.29	1.51	0.88	0.43	0.67	0.76	0.41	0.61	0.34
<i>Lachnospirillum</i>	0.16	0	1.04	0.80	1.79	4.74	6.90	5.92	5.31	4.30	5.89	4.68	3.73	0	5.01	2.21	1.00	4.88	2.83	5.02
<i>Phascolarctobacterium</i>	0	0	0.13	0.32	0	0.02	0.36	0.30	0.69	3.96	1.06	1.36	2.40	3.83	1.99	2.40	2.08	2.01	2.50	2.81
<i>Campylobacter</i>	0	0	1.71	0.29	0.25	0	0.98	0.64	1.42	0	1.41	3.41	0.74	0.51	0.87	0.23	0.0	1.24	1.54	0.89
<i>Megasphaera</i>	0.08	0.27	0.02	0	0.11	0.56	0.07	0	0.07	0.15	0.44	0.38	3.34	0.44	0.11	0.18	0.23	0.67	0.12	0.63
<i>Christensenellaceae_R_7_group</i>	0	0	0.29	0.58	0	0	0.21	0.55	0.88	0.22	1.03	0	3.10	11.77	10.43	12.48	25.37	7.25	2.21	3.18
<i>Prevotellaceae_NK3B31_group</i>	0.01	0	0.11	0.13	0	0.03	0.40	0.35	0.16	9.38	0.15	0.10	0.24	1.96	0	2.34	6.50	0.59	0	1.62
<i>UCG_002</i>	0	0	0.11	0.24	0	0.82	0.88	1.90	2.29	1.08	2.49	0.42	2.06	1.71	11.08	2.52	0.88	3.95	2.12	5.63
<i>Roseburia</i>	0.01	0	0.21	0	0.29	0.02	0.17	0.47	0.70	0.06	0.26	0.09	0.29	1.03	0	0.58	0.36	1.07	5.04	0.33
<i>NK4A214_group</i>	0	0	0.02	0	0.10	0.17	0.23	0	1.51	1.76	1.14	1.20	1.54	5.14	2.72	1.00	2.49	2.07	1.07	2.28
<i>Moraxella</i>	0.17	0.07	0.12	1.47	0.57	0	0.06	0.04	0.02	0	0.04	0	0.01	0	0	0	0	0.02	0	0
<i>Veillonella</i>	1.51	0.65	1.10	0.77	1.52	1.55	0.91	0.75	0.24	0.87	0.36	0.43	0.08	0.23	0.06	0.23	0.07	0.18	0.44	0.29

Day of Life (DoL)	2	2	2	2	2	6	6	6	13	13	13	13	20	20	20	20	20	20	20	20
Color	brown	brown	yellow	yellow	very yellow	brown	yellow	yellow	brown	brown	yellow	yellow	brown	brown	brown	grey	grey	yellow	yellow	yellow
Consistency	balls	meconium	balls	soft	soft	balls	balls	soft	balls	soft	balls	soft	balls	very soft	soft	balls	soft	balls	very soft	soft
Enterococcus	1.25	1.89	0.33	0	0.49	3.39	2.23	0	3.07	1.03	3.76	0.75	1.01	1.11	0.79	0.97	1.09	1.47	0.32	0.48
Family_XIII_AD3011_group	0	0.01	0.02	0	0	0.02	0.04	0.02	0.04	1.58	0.19	2.90	0.33	8.79	0.43	1.86	1.50	0.94	0.23	2.13
Desulfovibrio	0	0.0	0.16	0.08	0	0.83	0.62	0.07	0.79	1.46	0.62	2.10	0.41	0.95	2.39	0.90	0.67	0.73	1.60	1.77
Lachnospiraceae_NK4A136_group	0	0.0	0.06	0.15	0	0	0.03	0.13	0	0	0.04	0	0.06	3.21	0	1.45	0.83	0.32	0	0.39
Colidextribacter	0.02	0.02	0.10	0	0.02	0.46	0.37	1.51	0.59	1.49	0.43	0.08	0.28	0.42	0.28	1.26	0.87	0.72	1.15	0.71
Ruminococcus	0	0	0.16	0.15	0	0.45	0.55	3.04	0.39	0.34	0.79	0.30	0.71	0.58	2.52	1.41	1.01	1.01	0.39	0.99
Rothia	0.08	0.06	0.08	0.18	0.06	0.13	0.06	0.01	0.05	0.04	0.05	0	0.04	0.04	0.04	0.02	0.07	0.04	0.02	0.06
Subdoligranulum	0.03	0.04	0.01	0.01	0.02	0.12	0.12	0	0.28	0.17	0.34	1.37	0.19	0.13	5.17	0.46	0.81	0.71	0.09	0.41
Mitsuokella	0.13	0.25	0	0.08	0.04	0.09	0.01	0	0.04	0.06	0.02	0	0.35	0	0.05	0.17	0.11	0.19	0.02	0.19
Oscillibacter	0	0.08	0	0	0.01	0.09	0.02	0	0.10	1.46	0.08	1.02	0.12	0.78	0.20	1.83	5.54	0.68	0.16	3.79
Butyricimonas	0	0	0.10	0.11	0	1.25	0.34	0.55	0.77	1.13	1.20	10.74	0.11	0	2.49	0	0.13	0.81	0.27	0.96
Coprococcus	0	0	0.08	0.05	0	0	0.10	0.04	0.19	0	0.20	0	0.45	0.81	1.29	0	1.79	0.60	0.11	0.37
Parabacteroides	0.20	0.40	0.33	0	0.23	0.79	0.80	1.05	0.54	0.05	0.91	0.09	0.04	0.20	0.09	7.03	7.27	0.47	0.19	0.46
Helicobacter	0.04	0.05	0.04	0	0.07	0	0.13	0.03	0.06	0.14	0.20	1.54	0.04	0.46	0.03	0.13	0.30	2.41	0.22	1.22
Agathobacter	0	0.05	0.01	0.07	0.03	0	0.06	0.05	0.05	0	0.02	0	0.03	0	0.05	0.0	0.04	0.00	0.08	0
Terrisporobacter	0.23	0.17	0.35	2.28	0.18	0.21	0.09	0	0.19	0.13	0.33	0.13	1.35	0.39	0.12	0.15	0.68	0.31	0.11	0.06
Prevotellaceae_UCG_001	0.25	0.18	0	0.12	0	0.23	0	0.02	1.29	0	0.05	0.20	0.25	0.22	0.48	0.16	0.23	0.79	0.13	0.39
Tuzzerella	0	0	0.22	0.04	0	0.07	0.22	0.80	0.18	0.30	0.18	0.15	0.59	0.32	0	0.10	0.29	0.24	6.61	1.04
Romboutsia	0.10	1.01	0	0	0.04	0.07	0.09	0	0.32	0.11	0.34	0.10	0.55	0.35	0.30	0.19	0.70	0.24	0.08	0.32
Blautia	0.09	0.07	0	0	0.03	0.27	0.05	0	0.11	0.09	0.03	0.09	0.46	0.09	0.46	0.09	0.09	0.28	0.05	0.03
Dorea	0.0	0.0	0.09	0	0.02	0.02	0.10	0	0.21	0.59	0.30	0.84	0.43	0	0.69	0.02	0.97	0.98	0.37	1.70
Porphyromonas	0.08	0.06	0.05	0	0.11	0.07	0.41	0	0.10	0.10	0.42	0.06	0.02	0.12	0.06	0	0	0	0.07	0.06
Alistipes	0	0	0.09	0.28	0.06	0.37	0.32	0.46	0.80	0.23	1.00	0.25	0.23	0.13	1.01	0.0	0.58	0.46	0	1.26
Lachnospiraceae_AC2044_group	0	0.02	0.01	0.00	0.03	0.03	0.01	0	0	0.23	0.06	0.11	0.12	1.35	0.06	1.39	0.46	0.66	0	0.31

Day of Life (DoL)	27	27	27	27	27	27	27	30	30	30	30	30	34	34	34	34	34	
Color	brown	brown	brown	grey	yellow	yellow	yellow	brown	brown	brown	yellow	yellow	brown	brown	brown	yellow	yellow	Pooled
Consistency	balls	diarrhea	soft	soft	balls	diarrhea	soft	balls	diarrhea	soft	balls	soft	balls	diarrhea	soft	balls	soft	SEM
<i>Lactobacillus</i>	1.73	4.01	3.49	0.32	3.49	5.50	3.40	1.96	0.65	1.18	2.70	1.59	2.92	9.79	2.20	1.07	6.11	3.960
<i>Escherichia_Shigella</i>	8.48	4.11	1.90	8.38	6.58	2.81	8.10	4.55	9.68	0	8.78	5.51	0	3.63	7.19	3.59	13.66	8.029
<i>Bacteroides</i>	5.02	6.61	11.85	10.21	8.07	2.76	8.06	2.63	0.74	2.42	11.72	3.16	1.61	1.03	0.00	11.38	0	5.547
<i>Prevotella</i>	1.96	11.69	5.67	29.05	2.28	11.10	5.87	8.01	6.38	15.96	2.67	6.28	7.20	5.98	9.16	0.19	10.13	2.505
<i>Actinobacillus</i>	0.62	1.40	1.41	0.61	0.87	0.45	0.49	0.11	0.70	0.30	0.37	0.62	0.12	0	0.22	0.55	0	2.095
<i>Fusobacterium</i>	1.21	5.25	0.10	0	7.69	18.70	5.66	1.26	0.48	2.04	6.16	2.46	1.28	0.29	0.00	3.48	0	4.641
<i>Alloprevotella</i>	1.18	11.06	3.59	6.14	1.89	3.12	1.16	3.03	6.93	0.83	3.17	3.53	2.89	4.62	3.28	3.67	2.24	1.735
<i>Rikenellaceae_RC9_gut_group</i>	13.09	2.89	6.08	6.65	6.84	2.71	7.61	3.45	1.97	4.85	3.70	3.17	2.79	3.81	5.39	3.36	6.78	2.670
<i>Clostridium_sensu_stricto_1</i>	5.84	0.82	1.72	0.40	2.01	0.34	0.40	2.71	1.72	2.52	2.50	1.44	1.43	1.06	2.29	0.00	0.72	3.848
<i>Streptococcus</i>	0.83	0.51	0.63	0.47	2.90	0.50	0.36	1.77	1.64	0.50	2.66	0.38	0.19	0	0.42	0.18	0	1.747
<i>Lachnospiraceae</i>	4.38	0.99	1.48	2.10	4.15	1.28	12.97	1.92	1.52	1.14	5.49	3.19	0.92	0.47	0.12	0.58	0.78	2.767
<i>Phascolarctobacterium</i>	3.29	3.07	8.13	5.69	1.36	3.13	2.40	2.32	5.50	3.87	1.91	4.03	3.05	3.78	3.74	1.59	0.56	1.008
<i>Campylobacter</i>	1.25	1.54	0.72	0.61	1.65	0.40	0.76	5.34	1.35	0.69	2.72	0.58	2.71	1.86	1.05	37.59	0.34	1.543
<i>Megasphaera</i>	0.91	3.04	4.92	3.63	0.85	4.20	4.54	1.95	3.65	0.29	1.18	0.36	1.36	7.20	4.99	0	0.26	2.202
<i>Christensenellaceae_R_7_group</i>	5.73	0	3.90	0.00	4.33	1.28	2.76	2.87	1.00	3.37	3.73	5.42	4.07	3.43	3.16	2.16	0.27	2.144
<i>Prevotellaceae_NK3B31_group</i>	1.83	6.03	2.14	6.22	0.30	0.67	0.34	2.56	2.80	5.14	0.72	3.74	2.53	2.17	4.43	0.13	4.97	0.873
UCG_002	3.74	0.32	1.16	0.29	1.88	4.34	1.31	1.55	2.60	4.30	3.00	1.35	2.99	2.65	3.59	0.46	6.92	1.487
<i>Roseburia</i>	0.61	4.03	2.64	0.46	0.38	0.79	1.61	1.66	3.78	0.93	0.89	2.09	1.68	1.87	2.14	0.30	2.03	0.981
<i>NK4A214_group</i>	1.26	0.78	0.54	0.32	1.21	0.83	1.61	2.16	1.90	2.13	0.82	5.46	2.92	2.22	1.83	0.38	2.54	0.798
<i>Moraxella</i>	0.01	0	0.02	0	0.01	0	0	0	0	0.01	0.02	0.02	0.01	0.01	0	0.01	0	0.109
<i>Veillonella</i>	0.04	0.70	0.47	0.34	0.07	0.31	0.23	0.01	0.17	0.03	0.03	0.05	0	0.08	0.01	0.05	0.02	0.386
<i>Enterococcus</i>	0	1.03	0.41	1.11	1.62	0.0	0.49	0.19	1.04	0	0	0	0	0.12	1.06	0	1.03	1.519
<i>Family_XIII_AD3011_group</i>	1.58	2.00	0.63	0.34	0.94	1.35	0.78	1.43	1.72	0.77	1.42	4.12	2.16	1.73	0.67	4.88	1.82	0.563
<i>Desulfovibrio</i>	1.23	0.93	1.27	1.58	0.94	1.17	1.66	0.50	0.75	1.22	1.14	1.29	0.67	0.42	0.81	1.28	1.01	0.377
<i>Lachnospiraceae_NK4A136_group</i>	0.18	0.17	4.33	0	0.49	0.02	0	2.25	3.04	8.38	0.58	6.29	1.59	1.08	2.78	1.02	0.30	0.745

Day of Life (DoL)	27	27	27	27	27	27	27	30	30	30	30	30	34	34	34	34	34	
Color	brown	brown	brown	grey	yellow	yellow	yellow	brown	brown	brown	yellow	yellow	brown	brown	brown	yellow	yellow	Pooled
Consistency	balls	diarrhea	soft	soft	balls	diarrhea	soft	balls	diarrhea	soft	balls	soft	balls	diarrhea	soft	balls	soft	SEM
<i>Colidextribacter</i>	0.68	0.85	0.93	0.18	0.74	1.21	0.11	0.58	0.63	0.69	0.60	2.25	0.87	0.77	0.32	0.26	0.77	0.350
<i>Ruminococcus</i>	3.92	0.24	2.34	0.09	1.32	0.04	0.18	1.72	0.82	2.21	1.55	2.16	1.26	0.59	1.39	0	0.94	0.571
<i>Rothia</i>	0.01	0	0.02	0	0.02	0.00	0.01	0.01	0	0.01	0.02	0.01	0.01	0	0	0.02	0	0.042
<i>Subdoligranulum</i>	1.60	0.51	1.54	0.14	1.17	0.55	0.94	1.26	0.59	4.10	0.64	0.13	1.66	1.45	1.21	0.14	0.66	0.700
<i>Mitsuokella</i>	0.24	1.48	0.97	0.19	0.23	1.49	1.09	0.31	1.35	1.19	0.04	0.44	2.06	3.89	2.69	0	0.06	1.549
<i>Oscillibacter</i>	2.07	1.92	0.48	1.48	0.94	1.10	0.25	0.88	0.79	1.35	0.57	1.06	0.38	0.59	0.93	0.32	0.43	0.466
<i>Butyricimonas</i>	0.52	0.24	0.20	0.92	0.62	0.59	1.33	0.21	0	0.13	0.68	0.42	0.07	0.06	0	0.22	0.05	0.469
<i>Coprococcus</i>	1.08	0.07	0.54	0.12	1.20	0.25	0.26	1.51	0.96	2.30	0.75	3.14	4.34	0.92	0.74	0.50	0.18	0.773
<i>Parabacteroides</i>	0.42	1.16	0.89	0.25	0.13	0.57	0.03	0.52	0.72	0.13	0.61	1.97	0.51	0.55	0.72	1.33	0.18	0.636
<i>Helicobacter</i>	0.88	0.23	0.10	0.56	0.70	0.03	0.27	2.03	0.19	0.11	2.26	0.43	1.01	0.10	0.02	0.87	0.02	1.446
<i>Agathobacter</i>	0	0	0.67	0	0.16	0	0.07	0.71	1.94	0.67	0.07	0.07	1.89	1.85	2.00	0.07	0	0.590
<i>Terrisporobacter</i>	0.20	0.16	0.16	0.26	0.30	0.14	0.05	1.15	0.34	1.94	0.60	0	0.63	0.12	0.93	0.76	0.13	0.441
<i>Prevotellaceae_UCG_001</i>	0.35	0.46	0.31	0.28	0.22	0.54	2.36	0.68	0.73	0.51	0.26	0	0.49	0.39	0.60	0.72	0.32	0.805
<i>Tuzzerella</i>	0.38	0.69	1.50	0.01	0.32	1.27	0.23	0.29	0.86	0.32	0.17	1.15	1.09	1.05	0	1.60	1.71	0.568
<i>Romboutsia</i>	0.47	0.11	0.60	0.10	0.38	0.05	0.14	0.37	0.18	0.16	0.44	0	0	0	0.12	0.30	0.11	0.288
<i>Blautia</i>	1.00	0.12	0.18	0.20	0.59	0.12	0.13	1.53	0.42	1.82	0.63	0.23	3.92	1.42	0.64	0	0.42	0.589
<i>Dorea</i>	0.38	0.31	0.26	0.12	0.43	0.47	1.29	0.77	0.29	1.13	0.67	0.75	1.11	0.82	0.35	0	0.63	0.398
<i>Porphyromonas</i>	0	0.02	0.06	0.10	0.20	0.05	0.00	0.21	0.08	0.01	0.42	0.10	0.05	0	0.08	0.05	0.10	0.420
<i>Alistipes</i>	1.05	0	1.88	1.29	0.48	0.16	1.83	0.16	0.29	0.25	0.58	0	0.15	0	0	0	0	0.470
<i>Lachnospiraceae_AC2044_group</i>	0.13	0.09	0.03	0	0.06	0.11	0	0.77	1.59	3.56	0.22	0.83	0.71	0.75	1.19	0.82	0.66	0.505

	P-value						
	DoL	Color	DoL × Color	Consistency	DoL × Consistency	Color × Consistency	DoL × Color × Consistency
<i>Lactobacillus</i>	0.900	0.516	0.431	0.813	0.398	0.931	0.951
<i>Escherichia_Shigella</i>	0.0002	0.887	0.846	0.069	0.752	0.875	0.998
<i>Bacteroides</i>	0.036	0.826	0.274	0.267	0.473	0.477	0.915
<i>Prevotella</i>	<0.001	0.003	0.0002	0.072	<0.001	0.403	0.116
<i>Actinobacillus</i>	0.003	0.998	0.971	0.774	0.887	0.989	0.997
<i>Fusobacterium</i>	0.004	0.037	0.875	0.800	0.044	0.210	0.855
<i>Alloprevotella</i>	0.182	0.015	0.847	0.013	0.238	0.008	0.714
<i>Rikenellaceae_RC9_gut_group</i>	<0.001	0.926	0.462	0.179	0.007	0.110	0.645
<i>Clostridium_sensu_stricto_1</i>	<0.001	0.329	0.289	<0.001	<0.001	0.986	0.994
<i>Streptococcus</i>	0.608	0.995	0.992	0.568	0.986	0.975	0.941
<i>Lachnoclostridium</i>	0.177	0.164	0.976	0.440	0.938	0.827	0.242
<i>Phascolarctobacterium</i>	<0.001	0.273	0.211	0.110	0.080	0.740	0.136
<i>Campylobacter</i>	<0.001	0.070	<0.001	0.015	<0.001	<0.001	<0.001
<i>Megasphaera</i>	0.509	0.799	0.985	0.742	0.541	0.974	0.933
<i>Christensenellaceae_R_7_group</i>	<0.001	0.032	0.006	0.198	0.697	0.080	0.019
<i>Prevotellaceae_NK3B31_group</i>	0.021	<0.001	0.039	0.0001	<0.001	0.016	0.758
<i>UCG_002</i>	0.017	0.413	0.761	0.725	0.101	0.126	0.018
<i>Roseburia</i>	0.115	0.824	0.251	0.087	0.192	0.936	0.154
<i>NK4A214_group</i>	<0.001	0.612	0.469	0.818	0.351	0.039	0.028
<i>Moraxella</i>	<0.001	0.972	0.997	<0.001	<0.001	0.999	1.000
<i>Veillonella</i>	<0.001	0.837	0.531	0.147	0.986	0.989	0.985
<i>Enterococcus</i>	0.769	0.861	0.925	0.918	0.957	0.900	0.933
<i>Family_XIII_AD3011_group</i>	<0.001	0.172	0.103	0.014	<0.001	<0.001	<0.001
<i>Desulfovibrio</i>	<0.001	0.626	0.475	0.774	0.078	0.275	0.510

	P-value						
	DoL	Color	DoL × Color	Consistency	DoL × Consistency	Color × Consistency	DoL × Color × Consistency
<i>Lachnospiraceae_NK4A136_group</i>	<0.001	0.004	0.700	0.015	<0.001	0.106	0.014
<i>Colidextribacter</i>	0.003	0.193	0.362	0.188	0.303	0.352	0.078
<i>Ruminococcus</i>	0.004	0.417	0.010	0.043	0.001	0.339	0.238
<i>Rothia</i>	0.032	0.937	0.671	0.923	0.920	0.980	0.995
<i>Subdoligranulum</i>	0.602	0.019	0.591	0.032	0.090	0.043	0.027
<i>Mitsuokella</i>	0.912	0.812	0.990	0.916	1.000	1.000	1.000
<i>Oscillibacter</i>	0.002	0.004	0.027	0.083	0.0010	0.032	0.074
<i>Butyricimonas</i>	<0.001	0.602	0.068	0.002	<0.001	0.759	0.142
<i>Coprococcus</i>	0.043	0.718	0.436	0.476	0.271	0.686	0.394
<i>Parabacteroides</i>	0.037	<0.001	0.005	0.989	0.975	0.993	0.604
<i>Helicobacter</i>	0.969	0.967	0.993	0.823	0.998	0.942	0.970
<i>Agathobacter</i>	0.167	0.476	0.532	0.968	0.769	0.968	0.972
<i>Terrisporobacter</i>	0.212	0.247	0.357	0.934	0.104	0.536	0.381
<i>Prevotellaceae_UCG_001</i>	0.856	0.731	0.475	0.930	0.910	0.956	0.623
<i>Tuzzerella</i>	<0.001	<0.001	0.006	<0.001	<0.001	<0.001	0.002
<i>Romboutsia</i>	0.635	0.780	0.969	0.027	0.999	0.811	0.913
<i>Blautia</i>	0.195	0.225	0.106	0.281	0.915	0.599	0.211
<i>Dorea</i>	0.046	0.290	0.549	0.294	0.502	0.465	0.709
<i>Porphyromonas</i>	0.986	0.935	0.992	0.916	0.996	0.996	0.998
<i>Alistipes</i>	0.025	0.503	0.992	0.175	0.091	0.996	0.732
<i>Lachnospiraceae_AC2044_group</i>	0.022	0.072	0.267	0.840	0.487	0.193	0.291

*Values are least squares means ± pooled standard error of the mean (SEM). Piglets were weaned on day 28 of life. Proportional abundances are presented that represent >0.2% of all reads.

Table S7. Differences in relative bacterial abundances (% of total reads) in different fecal sample types obtained from suckling and newly weaned piglets during the suckling and early postweaning phase.*

22
23

Day of Life (DoL)	2				6			13			20			27			30			34			P-value			
											F +												Pooled		DoL ×	
Sample Type	F + S	F	M	S	F + S	F	S	F + S	F	S	S	F	S	F + S	F	S	F + S	F	S	F + S	F	S	SEM	DoL	Type	type
<i>Lactobacillus</i>	0.89	1.10	0.02	2.93	6.31	3.75	4.13	11.58	14.89	2.25	2.24	4.95	4.30	2.22	3.62	3.46	0.85	2.83	1.42	1.64	8.11	2.43	2.234	<0.001	0.239	0.004
<i>Escherichia_Shigella</i>	34.18	24.44	57.97	34.21	16.18	20.12	33.07	11.92	21.47	33.57	7.80	8.85	15.76	2.10	3.41	11.13	5.55	5.11	6.83	3.00	4.64	0	4.836	<0.001	0.0001	0.107
<i>Bacteroides</i>	15.67	6.33	9.64	10.47	28.47	20.92	13.22	16.04	12.47	11.63	9.47	6.55	6.69	4.37	7.68	7.77	0.63	4.17	5.64	0	0.71	1.54	3.263	<0.001	0.601	0.100
<i>Prevotella</i>	0.56	0	0.53	1.03	3.15	4.39	0.25	7.85	2.06	0.49	2.83	4.08	2.03	16.21	5.70	1.81	8.22	6.31	6.47	7.83	7.57	6.47	1.707	<0.001	0.002	0.005
<i>Actinobacillus</i>	4.13	18.33	1.11	4.20	0.96	1.02	2.45	0.54	0.90	0.28	0.73	0.48	0.02	0.26	0.46	1.46	0.99	0.21	0.32	0.19	0.11	0	1.258	<0.001	0.0006	0.145
<i>Fusobacterium</i>	18.48	9.07	7.26	13.90	6.21	16.20	9.44	0	1.23	1.44	4.34	1.88	1.07	1.78	5.86	9.25	2.23	0.32	3.53	0	0	1.58	2.887	<0.001	0.291	0.343
<i>Alloprevotella</i>	0.16	0.14	0.10	0.38	1.05	0.09	1.09	1.19	0.25	0.45	1.80	1.41	0.77	5.32	2.66	2.15	9.46	3.27	3.18	4.08	3.99	2.96	1.072	<0.001	0.055	0.149
<i>Rikenellaceae_RC9_gut_group</i>	0	0.89	0.0	0.58	0	0	0.91	4.48	1.77	0.95	2.75	8.99	3.70	9.29	9.07	3.40	3.35	3.73	2.94	7.01	4.51	2.49	1.586	<0.001	0.132	0.019
<i>Clostridium_sensu_stricto_1</i>	16.19	30.37	3.63	14.66	3.28	5.44	2.32	1.02	1.91	2.13	0.72	2.14	1.06	0.33	0.89	3.81	1.35	1.20	3.06	2.29	1.28	1.28	2.541	<0.001	0.0003	0.785
<i>Streptococcus</i>	2.18	1.07	0.69	4.05	2.94	2.73	1.64	0.31	1.64	1.74	0.21	0.31	1.14	0.30	0.25	3.87	1.07	1.42	2.20	0.21	0.15	0.11	1.028	0.098	0.056	0.188
<i>Lachnoclostridium</i>	0.75	0.03	0.17	1.02	7.34	5.61	6.23	6.92	5.71	5.07	2.96	5.20	3.48	3.39	5.02	4.66	1.60	3.67	2.60	0.34	0.57	0.73	1.716	0.0001	0.991	0.993
<i>Phascolarctobacterium</i>	0	0.16	0.08	0.14	0.55	0.03	0.20	1.40	1.90	0.20	3.67	2.38	1.52	3.94	3.34	1.42	4.00	5.69	1.95	3.63	3.62	2.97	0.619	<0.001	0.0004	0.007
<i>Campylobacter</i>	0	0.59	0	1.92	0.18	0.10	1.49	0.92	0.37	2.46	0.19	0.46	2.19	1.25	0.62	2.10	0.17	1.63	4.31	0.99	1.39	4.95	1.163	0.466	0.0007	0.956
<i>Megasphaera</i>	0.16	0	0.32	0	0.39	0.12	0	0.17	0.77	0.06	1.47	1.16	0.58	4.56	3.07	0.58	2.21	4.82	0.73	0.41	5.79	2.61	1.309	0.012	0.141	0.452
<i>Christensenellaceae_R_7_group</i>	0	0.38	0	0.27	0	0	0.40	1.06	1.24	0.65	8.27	7.09	5.72	1.64	4.45	2.55	1.66	1.33	3.54	5.09	3.41	3.39	1.370	<0.001	0.995	0.746
<i>Prevotellaceae_NK3B31_group</i>	0	0.30	0	0.22	0.36	0	0.45	1.26	0.09	0.22	1.75	0.57	0.70	2.39	1.57	0.50	4.16	2.09	2.08	3.85	3.18	2.18	0.622	<0.001	0.057	0.324
<i>UCG_002</i>	0.32	0	0.26	0	2.05	0.80	0.05	4.07	3.77	0.48	0.89	5.72	1.86	1.51	2.50	1.60	2.80	4.12	1.59	3.00	3.47	2.58	0.837	0.001	0.0014	0.008
<i>Roseburia</i>	0	0.15	0	0.32	0.01	0	0.33	0	0.88	0.19	2.06	1.01	0.99	4.05	0.82	0.65	2.42	2.98	1.44	2.17	1.82	1.73	0.605	<0.001	0.309	0.050
<i>NK4A214_group</i>	0.13	0	0.11	0	0.46	0.11	0.05	1.38	2.61	0.15	2.04	2.43	1.44	0.93	1.43	0.77	2.67	1.95	1.55	2.64	2.22	2.53	0.465	<0.001	0.061	0.035
<i>Moraxella</i>	0.50	2.87	0.08	0.03	0.05	0.06	0.04	0.01	0.02	0.05	0	0	0.02	0	0	0.01	0.02	0	0	0	0	0	0.042	<0.001	<0.001	<0.001
<i>Veillonella</i>	1.36	1.46	0.71	1.09	1.23	1.75	0.61	0.40	0.67	0.05	0.12	0.28	0.09	0.53	0.23	0.06	0.24	0.08	0.02	0.05	0.08	0	0.220	<0.001	0.012	0.294
<i>Enterococcus</i>	0.61	0	1.61	0.48	1.03	1.49	3.62	0.66	1.82	5.90	0.27	0.67	2.20	0.22	0.15	2.14	0.27	0.21	0	0.45	0.23	0	0.843	<0.001	0.005	0.002

Day of Life (DoL)		2				6			13			20			27			30			34			P-value			
												F +												Pooled		DoL ×	
Sample Type		F + S	F	M	S	F + S	F	S	F + S	F	S	S	F	S	F + S	F	S	F + S	F	S	F + S	F	S	SEM	DoL	Type	Type
Family_XIII_AD3011_group		0.02	0.01	0.03	0.01	0.07	0.01	0.01	0.60	0.32	0.05	2.39	0.92	0.94	0.69	1.49	0.60	1.50	1.32	1.62	1.78	1.42	2.15	0.389	<0.001	0.778	0.122
Desulfovibrio		0	0.02	0.02	0.12	0.93	0.77	0.38	1.36	0.70	0.46	0.88	0.97	0.74	1.29	1.50	0.62	1.00	0.79	0.79	0.86	0.61	0.64	0.229	0.006	0.052	0.082
Lachnospiraceae_NK4A136_group		0	0.16	0	0.09	0	0	0.14	0	0	0.10	0.76	0.28	0.34	0.36	0.80	0.32	3.96	3.43	1.88	1.56	1.68	1.55	0.534	<0.001	0.800	0.412
Colidextribacter		0.10	0.00	0.07	0.05	0.68	0.49	0.19	0.95	0.60	0.21	0.56	0.68	0.73	0.56	1.00	0.30	0.86	0.52	0.67	0.55	0.62	0.84	0.208	0.129	0.466	0.033
Ruminococcus		0	0.21	0	0.19	0.51	0.28	0.76	0.56	0.43	0.88	0.39	0.83	1.31	0.16	1.24	1.73	1.37	0.69	1.86	1.05	0.91	1.13	0.374	0.026	0.030	0.686
Rothia		0.14	0.26	0.07	0.06	0.08	0.15	0.04	0.03	0.09	0.02	0.02	0.05	0.04	0.02	0.01	0.01	0	0.01	0.01	0	0	0.01	0.024	<0.001	0.002	0.008
Subdoligranulum		0.15	0	0.12	0	0.22	0.17	0.02	0.67	0.37	0.19	2.08	0.54	0.33	0.62	1.38	0.78	1.16	0.85	1.19	1.92	1.27	1.53	0.435	0.0005	0.498	0.598
Mitsuokella		0.05	0.22	0.24	0	0.06	0.11	0	0.04	0.01	0.01	0.57	0.16	0.09	1.09	0.83	0.24	0.80	1.24	0.25	0.60	2.86	2.87	0.911	0.104	0.917	0.993
Oscillibacter		0.03	0	0.09	0	0.09	0.02	0	0.42	0.17	0	1.37	1.01	0.68	1.39	1.54	0.26	0.95	0.72	0.83	1.10	0.70	0.32	0.317	<0.001	0.073	0.260
Butyrivimonas		0.01	0	0.02	0.06	0.67	1.03	0.18	2.95	1.25	0.65	0.56	0.93	0.33	0.50	0.82	0.47	0.09	0.15	0.37	0.01	0.05	0.04	0.334	<0.001	0.186	0.002
Coprococcus		0.02	0	0.04	0.06	0.07	0.22	0.04	0.19	0.12	0.24	1.94	0.40	0.31	1.56	0.81	0.54	1.82	0.52	1.47	1.20	0.87	4.00	0.463	<0.001	0.147	<0.001
Parabacteroides		0.23	0	0.43	0.31	1.32	0.76	0.44	0.72	1.16	0.48	2.98	0.58	0.10	0.17	0.54	0.09	0.71	0.48	0.64	0.66	0.65	0.49	0.408	0.074	0.105	0.029
Helicobacter		0	0.11	0	0.07	0.08	0	0.17	0.16	0.06	0.30	0.10	0.27	3.83	0.35	0.18	1.02	0.17	0.01	2.30	0	0	1.09	0.826	0.358	0.028	0.194
Agathobacter		0	0.13	0	0.08	0	0	0.14	0	0.04	0.08	0	0	0.08	0	0.09	0.22	2.02	1.10	0.50	1.92	1.71	1.88	0.362	<0.001	0.986	0.502
Terrisporobacter		0.19	0.06	0.14	0.55	0.15	0.04	0.09	0.11	0.04	0.54	0.23	0.47	0.47	0.10	0.17	0.30	0.61	0.35	1.05	0.90	0.39	0.58	0.274	0.066	0.186	0.846
Prevotellaceae_UCG_001		0.05	0	0.04	0.0	0.05	0.02	0	0.18	1.00	0.01	0.16	1.11	0.01	1.38	0.87	0.06	0.57	0.63	0.50	0.54	0.40	0.56	0.499	0.551	0.458	0.784
Tuzzerella		0	0.07	0	0.17	0.20	0.18	0.18	0.15	0.33	0.09	0.89	1.24	0.23	0.32	0.69	0.32	0.71	0.68	0.27	0.17	0.79	1.08	0.411	0.290	0.762	0.812
Romboutsia		0.10	0	1.01	0	0.16	0.05	0.04	0.23	0.31	0.37	0.28	0.32	0.27	0.11	0.42	0.20	0.15	0.17	0.41	0.10	0.05	0	0.170	0.238	0.0003	0.898
Blautia		0.05	0	0.04	0	0.11	0.16	0.04	0.07	0.10	0	0.49	0.20	0.26	0.14	0.21	0.87	0.52	0.39	1.33	2.36	0.61	4.00	0.333	<0.001	0.002	<0.001
Dorea		0.02	0	0.02	0.06	0.12	0.06	0.06	0.42	0.47	0.10	0.45	0.93	0.88	0.30	0.66	0.41	0.32	0.56	0.74	0.80	0.63	1.03	0.243	0.0007	0.854	0.599
Porphyromonas		0.04	0	0.01	0.07	0.14	0.01	0.57	0.05	0	0.68	0.01	0.01	0.01	0.01	0.01	0.23	0.01	0.01	0.35	0.03	0.01	0.06	0.246	0.788	0.152	0.841
Alistipes		0	0.04	0	0.03	0.58	0.25	0.15	1.76	1.18	0.31	0.30	0.69	0.13	0.62	1.29	0.18	0.24	0.42	0.28	0	0.03	0.05	0.279	<0.001	0.048	0.016
Lachnospiraceae_AC2044_group		0	0.01	0	0.01	0	0	0.01	0.05	0.01	0.08	0.31	0.38	0.76	0.08	0.03	0.10	1.86	1.60	0.64	0.90	0.92	0.70	0.313	<0.001	0.910	0.262

*Values are least squares means ± pooled standard error of the mean (SEM). Piglets were weaned on day 28 of life. Sample type: F, feces; M, meconium; S, swab; F + S, combined feces + swab sample. Proportional abundances are presented that represent >0.2% of all reads.