

Table S1. Morphometric measurements of the colon mucosa of 5 and 12 – day old suckling piglets splitted¹

Item	Age-group	Ala		Gln		SE	<i>p</i> values ²			
		LBW	NBW	LBW	NBW		Supp	BiW	Supp x BiW	Age
CD, μm	5	207 ^{ace}	220 ^{bde}	192 ^{aed}	220 ^{be}	1.421	0.005	0.000	0.003	0.000
	12	262 ^f	254 ^f	276 ^{bdf}	260 ^{af}	2.334	0.037	0.008	0.374	
CA, μm^2	5	9492 ^{ce}	9811 ^e	8679 ^{ade}	9573 ^e	88.15	0.002	0.000	0.097	0.000
	12	12267 ^{cdf}	12401 ^f	13418 ^{bdf}	12129 ^{af}	168.1	0.189	0.084	0.034	

¹Values are Means, the SE of all groups is shown; n = 12 / group (5, 12 d).

Colon samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and fixed in Formalin.

²ANOVA F test; Significant differences ($p < 0.05$) are marked in bold, trends ($p < 0.1$) are marked in italic and bold F-tests, none of the other fixed effects or their combination were significant ($p < 0.05$)

^{a, b}Labeled Means in a row within one BiW group and one age group without a common letter differ, $p < 0.05$ (Tukey-test).

^{c,d}Labeled Means in a row within one supplementation group and one age group without a common letter differ, $p < 0.05$ (Tukey-test).

^{e,f}Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.05$ (Tukey-test).

Ala = Alanine; BiW = birthweight, CA= crypt area; CD = crypt depth; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S2. Immunohistomorphometric measurements in the colon of 5 and 12-day old male suckling piglets splitted¹

Item	Age-group	Ala		Gln		SE	Supp	BiW	Suppl x BiW	Age	<i>p</i> values ²
		LBW	NBW	LBW	NBW						
CD3 ⁺ IEL	5	1.13 ^e	1.10 ^e	1.10 ^e	1.27 ^e	0.065	0.612	0.612	0.446		0.043
	12	2.03 ^{acf}	2.77 ^{bef}	2.82 ^{df}	2.84 ^f	0.094	0.020	0.040	0.054		
CD3 ⁺ lamina propria	5	5.13 ^e	5.93 ^e	6.03 ^e	6.48 ^e	0.166	0.028	0.058	0.595		0.603
	12	11.0 ^f	11.1 ^f	11.2 ^f	11.6 ^f	0.223	0.442	0.559	0.801		

¹Values are Means of CD3⁺ positive cells per 100 enterocytes and per 10 000 µm² lamina propria next to the crypts, the SE of all groups is shown; *n* = 12 / group (5, 12 d).

Colon samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and fixed in Formalin.

²ANOVA *F* test; Significant differences (*p* < 0.05) are marked in bold, trends (*p* < 0.1) are marked in italic and bold

F-tests, none of the fixed effects or their combination were significant (*p* < 0.05)

^{a, b}Labeled Means in a row within one BiW group and one age group without a common letter differ, *p* < 0.05 (Tukey-test).

^{c,d}Labeled Means in a row within one supplementation group and one age group without a common letter differ, *p* < 0.05 (Tukey-test).

^{e,f}Labeled Means in a column within one supplementation group and BiW group without a common letter differ, *p* < 0.05 (Tukey-test).

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S3. Goblet cells in colon of 5 and 12-day old male suckling piglets splitted¹

Item	Age-group	Ala		Gln		SE	<i>p</i> values ²
		LBW	NBW	LBW	NBW		
AB-PAS Staining							
Crypt	Acid	5	23.2	18.3	21.6	23.7	1.453
		12	22.1	24.0	24.0	29.3	1.549
	Neu	5	74.0	74.2	79.1	74.3	2.772
		12	71.1	49.1	59.4	63.8	4.266
	Mixed	5	93.5	94.9 ^e	102	95.7	2.593
		12	86.4	61.5 ^f	75.2	76.0	3.952
	Total	5	191	187	202	194	5.163
		12	179	134	159	169	8.552

¹Values are Means, the SE for all groups is shown; *n* = 12 / group (5, 12 d).

Colon samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and fixed in Formalin.

²ANOVA *F* test; Significant differences (*p* < 0.05) are marked in bold, trends (*p* < 0.1) are marked in italic and bold

F-tests, none of the other fixed effects or their combination were significant (*p* < 0.05)

^{e,f} Labeled Means in a column within one treatment group and BiW group without a common letter differ, *p* < 0.05 (Tukey-test).

Ala = Alanine; Acid = acidic mucins; Gln = Glutamine; LBW = low birth weight; NBW = normal body weight; Neu = neutral mucins.

Mixed = mixed neutral and acidic mucins; SE = standard error; Supp = supplementation; Total = total number of AB-PAS positive goblet cells

Table S4. IgA positive cells in the colon lamina propria of 12-day old male suckling piglets¹

Item	Age-group	Ala		Gln		SE
		LBW	NBW	LBW	NBW	
Lamina propria next to the crypt	12	8.25	9.17	7.83	8.5	0.541

¹Values are Means of IgA positive cells per 10000 µm² of Lamina propria, the SE for all groups is shown; *n* = 12 / group (5, 12 d). Colon samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and fixed in Formalin. ANOVA F test.

F-tests, none of the fixed effects or their combination were significant (*p* < 0,05)

Ala = Alanine; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error

Table S5. Concentrations of biogenic amines in the colon digesta of 5 and 12-d suckling piglets splitted¹

Item, $\mu\text{mol/g}$ wet weight	Age	Ala		Gln		SE	<i>p</i> values ²			
		LBW	NBW	LBW	NBW		Supp	BiW	Suppl x BiW	Age
Propylamine	5	0.12	0.10	0.02	0.03	0.03	0.215	0.998	0.863	0.196
	12	0.02	0.04	0.03	0.04	0.01	0.578	0.124	0.581	
Putrescine	5	0.79	0.98	0.31	0.71	0.13	0.200	0.298	0.689	0.020
	12	0.41	0.35	0.40	0.45	0.04	0.617	0.942	0.550	
Histamine	5	0.03	0.15	0.14	0.05	0.04	0.989	0.881	0.383	0.508
	12	0.03	0.07	0.08	0.09	0.01	0.242	0.310	0.582	
Cadaverine	5	0.03	0.04	0.03	0.82	0.14	0.051	0.048	0.053	0.388
	12	0.08	0.05	0.02	0.28	0.07	0.529	0.416	0.314	
Spermidine	5	0.43	0.39	0.60	0.37	0.04	0.329	0.100	0.211	0.002
	12	0.17	0.24	0.33	0.33	0.03	0.020	0.393	0.432	
Spermine	5	0.03	0.02	0.03	0.03	0.00	0.621	0.870	0.608	0.773
	12	0.01	0.04	0.04	0.03	0.00	0.284	0.431	0.038	
Tyramine	5	0.12	0.10	0.06	0.64	0.11	0.261	0.200	0.174	0.055
	12	0.01	0.04	0.04	0.05	0.01	0.426	0.580	0.828	
Total biogenic amine	5	1.55	1.79	1.18	2.65	0.23	0.393	0.029	0.076	0.002
	12	0.73	0.83	0.94	1.28	0.12	0.191	0.374	0.622	

¹Values are Means, the SE of all groups is shown; $n = 2$ / group (5 d), $n = 3$ / group (12 d).

Colonic digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and snap frozen in liquid nitrogen.

²ANOVA *F* test; Significant differences ($p < 0.05$) are marked in bold, trends ($p < 0.1$) are marked in italic and bold

F-tests, none of the other fixed effects or their combination were significant ($p < 0.05$)

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S6. SCFA concentrations in the colon digesta of 5 and 12-d old suckling piglets splitted¹

Item, mmol/L	Age	Ala		Gln		p values ²	
		LBW	NBW	LBW	NBW	SE	Suppl x BiW
Acetic acid	5	27.46	26.5	25.13	29.45	2.12	0.570
	12	29.13	21.5	25.33	28.85	1.86	0.156
Propionic acid	5	7.69	7.48	7.64	9.49	0.84	0.571
	12	10.25	6.36	7.19	13.63	1.44	0.084
i-butyric acid	5	1.39	1.40	1.26	1.52	0.16	0.708
	12	1.52	1.25	1.37	1.79	0.11	0.148
n-butyric acid	5	2.58	3.04	2.73	3.10	0.26	0.939
	12	4.16	2.21	2.64	5.92	0.73	0.084
i-valeric acid	5	1.14	1.34	1.05	1.41	0.14	0.793
	12	1.34	1.17	1.37	1.71	0.10	0.209
n-valeric acid	5	1.10	1.20	0.96	1.02	0.12	0.920
	12	1.34	0.86	1.12	1.65	0.12	0.040
Total SCFA	5	41.37	41.0	38.78	46.0	3.48	0.617
	12	47.7	33.3	39.0	53.6	3.46	0.039

¹Values are Means, the SE of all groups is shown; n = 5 / group (5, 12 d).

Colonic digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and snap frozen in liquid nitrogen.

²ANOVA F test; Significant differences ($p < 0.05$) are marked in bold, trends ($p < 0.1$) are marked in italic and bold

F-tests, none of the other fixed effects or their combination were significant ($p < 0.05$)

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S7. Relative abundance of bacterial order in colon digesta of male suckling piglets¹

Item, (%)	Supp		BiW		Age			p values ²						
	Gln	Ala	LBW	NBW	5d	12d	SEM	Supp	BiW	Age	Supp x BiW	Suppl x Age	BiW x Age	Suppl x BiW x Age
Clostridiales	35.2	30.0	30.2	35.2	29.6	35.8	1.83	0.455	0.684	0.767	0.474	0.808	0.967	0.692
Lactobacillales	31.7	35.2	32.4	34.4	34.0	32.8	2.05	0.253	0.116	0.063	0.262	0.137	0.100	0.258
Bacteroidales	22.1	21.9	23.6	20.4	23.8	20.2	1.40	0.301	0.423	0.052	0.412	0.175	0.180	0.420
Fusobacteriales	3.75	6.42	5.71	4.35	6.89	3.17	1.17	0.553	0.386	0.350	0.381	0.667	0.624	0.642
Pasteurellales	2.09	2.74	2.92	1.87	2.38	2.41	0.56	0.253	0.277	0.733	0.419	0.518	0.676	0.770
Erysipelotrichales	0.90	0.44	0.80	0.55	0.83	0.52	0.13	0.150	0.531	0.660	0.473	0.351	0.657	0.324
Selenomonadales	0.86	0.79	0.90	0.75	0.53	1.12	0.21	0.281	0.166	0.435	0.231	0.467	0.310	0.409
Enterobacteriales	0.44	0.63	0.68	0.38	0.66	0.40	0.13	0.322	0.767	0.956	0.253	0.712	0.970	0.702
unknown WPS-2	0.42	0.10	0.06	0.47	0.00	0.53	0.17	0.973	0.360	0.002	0.741	0.025	0.009	0.098
Bradymonadales	0.34	0.19	0.19	0.34	0.46	0.07	0.13	0.300	0.549	0.609	0.024	0.300	0.877	0.062
Spirochaetales	0.29	0.32	0.43	0.17	0.05	0.55	0.11	0.122	0.903	0.054	0.355	0.025	0.291	0.193
Pirellulales	0.27	0.17	0.26	0.18	0.07	0.38	0.06	0.187	0.435	0.297	0.440	0.413	0.606	0.618
Coriobacteriales	0.22	0.15	0.20	0.17	0.30	0.07	0.05	0.380	0.917	0.003	0.784	0.024	0.019	0.121
unknown Firmicutes	0.15	0.16	0.14	0.16	0.11	0.20	0.02	0.054	0.248	0.113	0.166	0.074	0.293	0.309
Desulfovibrionales	0.12	0.15	0.16	0.11	0.10	0.17	0.02	0.590	0.582	0.002	0.897	0.022	0.023	0.198
Mollicutes_RF39	0.12	0.03	0.10	0.06	0.00	0.15	0.05	0.850	0.911	0.058	0.982	0.299	0.039	0.195
Betaproteobacteriales	0.08	0.04	0.05	0.06	0.04	0.08	0.02	0.947	0.396	0.002	0.707	0.025	0.010	0.068
Micrococcales	0.07	0.06	0.07	0.06	0.04	0.09	0.01	0.965	0.974	0.092	0.875	0.372	0.365	0.493
Campylobacteriales	0.03	0.23	0.19	0.06	0.03	0.23	0.08	0.396	0.973	0.021	0.757	0.037	0.127	0.242
Corynebacteriales	0.02	0.03	0.02	0.03	0.00	0.05	0.01	0.622	0.300	0.005	0.691	0.037	0.022	0.178
WCHB1-41	0.02	0.11	0.06	0.07	0.00	0.12	0.03	0.834	0.402	0.880	0.096	0.889	0.863	0.408
Actinomycetales	0.02	0.01	0.02	0.01	0.02	0.01	0.00	0.701	0.062	0.468	0.120	0.876	0.139	0.292
Victivallales	0.01	0.03	0.02	0.02	0.03	0.01	0.01	0.482	0.635	0.037	0.574	0.077	0.127	0.246
Bacillales	0.00	0.01	0.01	0.01	0.00	0.01	0.00	0.172	0.341	0.155	0.355	0.259	0.376	0.542

Oligosphaerales	0.00	0.01	0.01	0.01	0.02	0.00	0.00	0.525	0.669	0.247	0.193	0.383	0.518	0.360
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¹Values are Means of relative abundance, the SE for all groups is shown; n = 22 / group.

Colon digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplementation and snap frozen in liquid nitrogen.

² Kruskal Wallis Test. asymptotic significance; Significant differences (*p* < 0.05) are marked in bold, trends (*p* < 0.1) are marked in italic and bold

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S8. Relative abundance of bacterial genera in colon digesta of male suckling piglets¹

Item, (%)	Supp		BiW		Age			p values ²						
	Gln	Ala	LBW	NBW	5d	12d	SEM	Supp	BiW	Age	Supp x BiW	Suppl x Age	BiW x Age	Suppl x BiW x Age
Lactobacillus	30.7	34.0	31.1	33.5	32.5	32.1	2.00	0.482	0.546	0.991	0.505	0.835	0.937	0.704
Clostridium_sensu_stric to_1	9.12	9.12	8.36	9.88	9.65	8.59	0.88	0.524	0.637	0.546	0.700	0.753	0.711	0.857
unknown	5.27	3.03	4.71	3.69	6.82	1.58	0.85	0.982	0.835	0.001	0.854	0.008	0.002	0.018
Muribaculaceae														
Bacteroides	4.38	2.18	3.69	2.97	4.49	2.16	0.72	0.141	0.869	0.150	0.528	0.232	0.263	0.487
Fusobacterium	3.71	6.37	5.65	4.32	6.83	3.14	1.16	0.301	0.435	0.052	0.410	0.175	0.181	0.415
unknown	3.41	2.94	2.53	3.84	2.44	3.93	0.43	0.429	0.177	0.223	0.379	0.546	0.142	0.224
Ruminococcaceae														
Prevotella_2	3.14	3.94	3.60	3.44	3.44	3.61	0.94	1.000	0.636	0.917	0.963	0.926	0.117	0.958
Rikenellaceae_RC9_gut_group	3.05	4.13	3.60	3.54	3.00	4.14	0.75	0.248	0.660	0.462	0.664	0.508	0.790	0.781
Romboutsia	2.84	2.46	2.69	2.62	1.93	3.38	0.33	0.886	0.660	0.010	0.299	0.082	0.056	0.142
unknown	2.70	2.15	1.68	3.19	3.79	1.08	0.55	0.660	0.287	0.013	0.562	0.042	0.048	0.157
Lachnospiraceae														
Actinobacillus	1.95	2.62	2.73	1.82	2.22	2.32	0.54	0.262	0.258	0.800	0.389	0.495	0.675	0.737
Ruminococcaceae_UCG-002	1.69	1.69	1.55	1.83	0.88	2.51	0.29	0.708	0.545	0.004	0.827	0.041	0.034	0.246
Ruminococcaceae_UCG-005	1.41	0.99	1.11	1.31	0.19	2.23	0.27	0.391	0.758	< 0.001	0.679	< 0.001	< 0.001	0.001
Alloprevotella	1.38	2.09	1.92	1.52	0.70	2.74	0.46	0.252	0.904	0.024	0.443	0.090	0.161	0.297
Christensenellaceae_R-7_group	1.23	0.95	0.95	1.25	0.24	1.96	0.21	0.930	0.742	< 0.001	0.940	< 0.001	< 0.001	0.002

Lachnoclostridium	1.17	1.04	1.03	1.18	1.42	0.79	0.17	0.248	0.742	0.022	0.597	0.083	0.149	0.359
unknown														
Clostridiales_vadinBB6	1.08	0.69	1.44	0.35	0.22	1.57	0.29	0.293	0.288	< 0.001	0.440	0.001	0.001	0.011
0_group														
Blautia	1.00	0.35	0.49	0.89	1.10	0.28	0.21	0.289	0.536	0.022	0.608	0.093	0.117	0.384
unknown F082	0.97	1.20	1.31	0.86	0.00	2.16	0.44	0.659	0.325	< 0.001	0.710	0.003	0.010	0.029
Ruminococcaceae_NK4														
A214_group	0.86	0.73	0.76	0.84	0.55	1.05	0.11	0.725	0.767	0.018	0.973	0.103	0.101	0.428
unknown p-2534-														
18B5_gut_group	0.85	0.48	0.53	0.82	0.03	1.32	0.26	0.703	0.341	< 0.001	0.575	< 0.001	0.008	0.006
Ruminococcus_2	0.84	0.35	0.66	0.55	0.69	0.52	0.13	0.167	0.648	0.041	0.545	0.059	0.216	0.335
Prevotellaceae_NK3B31														
_group	0.82	2.14	1.58	1.32	2.24	0.66	0.35	0.101	0.956	0.091	0.436	0.063	0.413	0.385
Streptococcus	0.78	0.95	1.11	0.62	1.28	0.44	0.17	0.843	0.435	0.006	0.430	0.054	0.038	0.133
Family_XIII_AD3011_gr														
oup	0.70	0.65	0.64	0.71	0.37	0.97	0.11	0.965	0.684	0.008	0.982	0.060	0.037	0.219
Prevotellaceae_UCG-														
003	0.67	0.34	0.71	0.30	0.53	0.49	0.15	0.827	0.330	0.053	0.407	0.251	0.161	0.385
Parabacteroides	0.63	1.48	1.04	1.04	1.63	0.44	0.35	0.965	0.307	< 0.001	0.598	0.010	0.004	0.054
Roseburia	0.60	0.33	0.55	0.40	0.13	0.81	0.25	0.374	0.354	0.009	0.637	0.045	0.042	0.148
Dorea	0.53	0.33	0.33	0.54	0.28	0.58	0.07	0.242	0.066	0.021	0.146	0.012	0.014	0.018
Terrisporobacter	0.52	0.30	0.37	0.45	0.30	0.53	0.08	0.266	0.676	0.166	0.213	0.241	0.539	0.394
Ruminiclostridium_9	0.48	0.28	0.37	0.40	0.24	0.53	0.06	0.257	0.590	0.170	0.660	0.074	0.471	0.373
Phascolarctobacterium	0.48	0.41	0.45	0.45	0.17	0.73	0.13	0.086	0.191	0.017	0.055	0.031	0.053	0.049
Escherichia/Shigella	0.44	0.62	0.67	0.38	0.65	0.40	0.13	0.150	0.531	0.660	0.473	0.351	0.657	0.324
unknown WPS-2	0.42	0.10	0.06	0.47	0.00	0.53	0.17	0.973	0.360	0.002	0.741	0.025	0.566	0.098
Turicibacter	0.41	0.24	0.41	0.24	0.43	0.22	0.10	0.689	0.172	0.226	0.255	0.564	0.360	0.577
Marvinbryantia	0.40	0.09	0.10	0.41	0.13	0.38	0.11	0.153	0.533	0.416	0.222	0.433	0.712	0.556
Intestinimonas	0.39	0.34	0.32	0.41	0.32	0.41	0.05	0.194	0.496	0.170	0.500	0.306	0.335	0.594
Ruminococcaceae_UCG														
-004	0.34	0.24	0.32	0.26	0.17	0.41	0.05	0.552	0.886	0.057	0.946	0.255	0.304	0.706
Subdoligranulum	0.34	0.10	0.11	0.33	0.09	0.35	0.13	0.605	0.834	0.547	0.950	0.887	0.216	0.990
unknown														
Bradyomonadales	0.34	0.19	0.19	0.34	0.46	0.07	0.13	0.300	0.549	0.609	0.024	0.300	0.008	0.062
Oscillospira	0.32	0.29	0.35	0.27	0.15	0.47	0.06	0.725	0.509	0.003	0.830	0.029	0.016	0.120

Tyzzerella	0.31	0.31	0.26	0.36	0.45	0.18	0.06	0.851	0.280	0.012	0.485	0.031	0.046	0.020
Peptostreptococcus	0.31	0.18	0.37	0.12	0.46	0.04	0.11	0.123	0.087	0.002	0.143	0.008	0.004	0.026
Clostridium_sensu_stric to_2	0.28	0.86	0.74	0.38	0.95	0.17	0.22	0.843	0.338	0.009	0.799	0.047	0.042	0.230
p-1088-a5_gut_group	0.27	0.17	0.26	0.18	0.07	0.38	0.06	0.590	0.582	0.002	0.897	0.022	0.902	0.198
Holdemanella	0.25	0.05	0.19	0.13	0.20	0.12	0.06	0.699	0.662	0.033	0.849	0.166	0.525	0.569
Veillonella	0.24	0.18	0.31	0.11	0.36	0.06	0.06	0.176	0.106	0.003	0.215	0.014	0.008	0.039
Butyricimonas	0.20	0.26	0.28	0.17	0.23	0.23	0.08	0.336	0.508	0.284	0.701	0.295	0.607	0.678
Ruminococcaceae_UCG -010	0.17	0.16	0.14	0.19	0.17	0.17	0.02	0.775	0.545	0.750	0.785	0.969	0.902	0.939
Eisenbergiella	0.17	0.17	0.19	0.15	0.30	0.04	0.05	0.584	0.657	< 0.001	0.891	< 0.001	< 0.001	0.001
Sphaerochaeta	0.17	0.24	0.33	0.08	0.05	0.35	0.09	0.392	0.991	0.015	0.746	0.081	0.607	0.230
unknown Clostridiaceae_1	0.16	0.28	0.19	0.24	0.29	0.14	0.04	0.091	0.501	0.085	0.342	0.089	0.242	0.233
unknown Lactobacillales	0.16	0.18	0.12	0.21	0.11	0.22	0.04	0.302	0.247	0.252	0.266	0.488	0.412	0.587
Collinsella	0.15	0.10	0.14	0.12	0.23	0.02	0.05	0.576	0.694	0.032	0.897	0.109	< 0.001	0.274
Prevotella	0.15	0.06	0.06	0.16	0.15	0.06	0.06	0.882	0.968	0.608	0.867	0.962	0.306	0.912
unknown Firmicutes	0.15	0.16	0.14	0.16	0.11	0.20	0.02	0.965	0.974	0.092	0.875	0.372	0.365	0.493
Epulopiscium	0.14	0.13	0.13	0.15	0.18	0.10	0.03	0.302	0.799	0.542	0.269	0.566	0.911	0.629
unknown Erysipelotrichaceae	0.13	0.08	0.08	0.13	0.13	0.08	0.04	0.911	0.527	0.973	0.183	0.854	0.090	0.117
unknown Pasteurellaceae	0.13	0.10	0.16	0.06	0.16	0.07	0.04	0.286	0.973	0.353	0.765	0.572	0.304	0.936
Treponema_2	0.12	0.08	0.10	0.09	0.00	0.20	0.04	0.291	0.644	< 0.001	0.689	0.002	0.454	0.038
unknown Mollicutes_RF39	0.12	0.03	0.10	0.06	0.00	0.15	0.05	0.947	0.396	0.002	0.707	0.025	0.014	0.068
unknown Prevotellaceae	0.11	0.09	0.07	0.13	0.09	0.11	0.03	0.694	0.063	0.510	0.049	0.332	0.046	0.106
Desulfovibrio	0.11	0.13	0.13	0.11	0.10	0.14	0.02	0.153	0.503	0.489	0.432	0.454	0.805	0.707
Lachnospiraceae_UCG- 004	0.10	0.07	0.09	0.09	0.04	0.14	0.02	0.548	0.686	< 0.001	0.897	0.003	0.014	0.031
Hungatella	0.10	0.10	0.10	0.10	0.15	0.06	0.04	0.764	0.690	0.003	0.941	0.008	0.019	0.083
unknown Clostridiales	0.09	0.08	0.06	0.10	0.05	0.12	0.01	0.947	0.134	0.011	0.217	0.074	0.019	0.066
Clostridium_sensu_stric to_4	0.09	0.07	0.08	0.08	0.03	0.12	0.02	0.573	0.445	0.010	0.219	0.040	0.413	0.068

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Prevotella_9	0.08	0.09	0.07	0.11	0.13	0.05	0.03	0.196	0.918	0.605	0.641	0.573	0.753	0.958	
Oscillibacter	0.08	0.11	0.06	0.13	0.10	0.09	0.03	0.434	0.434	0.308	0.567	0.317	0.525	0.169	
GCA-900066225	0.08	0.06	0.08	0.06	0.12	0.02	0.01	0.307	0.973	< 0.001	0.744	< 0.001	< 0.001	0.003	
Coprococcus_3	0.08	0.05	0.06	0.07	0.04	0.09	0.01	0.459	0.362	0.029	0.240	0.149	0.365	0.150	
Erysipelotrichaceae_UCG-004	0.07	0.04	0.08	0.03	0.03	0.08	0.03	0.411	0.185	0.377	0.209	0.630	0.041	0.574	
UBA1819	0.07	0.06	0.08	0.06	0.09	0.04	0.02	0.891	0.322	0.002	0.685	0.021	0.011	0.072	
Rothia	0.07	0.06	0.07	0.06	0.04	0.09	0.01	0.850	0.911	0.058	0.982	0.299	0.039	0.195	
Alistipes	0.06	0.07	0.12	0.01	0.08	0.06	0.03	0.368	0.043	0.680	0.030	0.764	0.004	0.205	
Intestinibacter	0.06	0.05	0.06	0.06	0.03	0.09	0.02	0.264	0.501	0.034	0.296	0.115	0.412	0.321	
Prevotellaceae_UCG-004	0.05	0.15	0.08	0.11	0.08	0.12	0.04	1.000	0.289	0.166	0.471	0.365	0.001	0.393	
Candidatus_Soleferrea	0.05	0.04	0.04	0.05	0.01	0.08	0.01	0.466	0.653	< 0.001	0.550	0.007	0.019	0.034	
unknown Family_XIII	0.05	0.05	0.05	0.05	0.09	0.01	0.02	0.389	0.734	< 0.001	0.835	0.006	0.090	0.082	
unknown Carnobacteriaceae	0.05	0.10	0.06	0.09	0.14	0.01	0.02	0.055	0.200	0.004	0.110	0.006	0.232	0.018	
Prevotellaceae_UCG-001	0.05	0.00	0.01	0.05	0.00	0.06	0.02	0.172	0.894	0.002	0.267	0.004	0.372	0.013	
dgA-11_gut_group	0.05	0.04	0.05	0.05	0.03	0.06	0.01	0.636	0.725	0.489	0.947	0.771	0.360	0.375	
GCA-900066575	0.05	0.01	0.04	0.01	0.01	0.05	0.02	0.200	1.000	0.051	0.340	0.096	0.508	0.236	
Sutterella	0.05	0.04	0.05	0.03	0.03	0.05	0.01	0.430	0.619	0.865	0.052	0.815	0.911	0.258	
Lachnospiraceae_UCG-010	0.04	0.05	0.04	0.06	0.03	0.07	0.01	0.509	0.585	0.092	0.862	0.270	0.994	0.638	
Hydrogenoanaerobacterium	0.04	0.04	0.05	0.04	0.07	0.02	0.01	0.973	0.928	0.001	0.970	0.013	0.008	0.037	
Mogibacterium	0.04	0.05	0.05	0.04	0.01	0.08	0.01	0.629	0.603	0.003	0.829	0.025	< 0.001	0.096	
Denitrobacterium	0.04	0.03	0.04	0.03	0.03	0.04	0.01	0.579	0.954	0.184	0.910	0.222	0.042	0.679	
Butyricicoccus	0.04	0.04	0.04	0.04	0.03	0.04	0.01	0.353	0.882	0.982	0.372	0.831	0.994	0.862	
unknown Paludibacteraceae	0.04	0.02	0.03	0.03	0.01	0.05	0.01	0.751	0.318	0.210	0.534	0.626	0.031	0.639	
Flavonifractor	0.04	0.03	0.03	0.04	0.07	0.00	0.01	0.703	0.751	< 0.001	0.435	< 0.001	0.242	< 0.001	
Negativibacillus	0.03	0.03	0.01	0.05	0.06	0.00	0.01	0.860	0.020	0.002	0.138	0.023	0.351	0.019	
unknown Fusobacteriaceae	0.03	0.05	0.05	0.03	0.06	0.02	0.01	0.257	0.597	0.009	0.635	0.036	0.712	0.242	
Faecalibacterium	0.03	0.01	0.01	0.04	0.03	0.02	0.01	0.522	0.039	0.887	0.197	0.777	0.082	0.439	

H1	0.03	0.02	0.04	0.01	0.00	0.05	0.01	0.654	0.611	0.019	0.873	0.118	< 0.001	0.490
Sarcina	0.03	0.02	0.01	0.05	0.05	0.00	0.01	0.725	0.187	0.165	0.581	0.533	0.059	0.495
Coprococcus_1	0.03	0.01	0.01	0.03	0.00	0.03	0.01	0.452	0.431	0.081	0.637	0.099	0.021	0.197
Howardella	0.03	0.05	0.05	0.03	0.07	0.02	0.01	0.129	0.777	0.002	0.157	0.009	0.019	0.011
Eubacterium	0.03	0.01	0.03	0.01	0.02	0.02	0.01	0.279	0.932	0.560	0.434	0.582	0.031	0.734
Lachnospiraceae_NC20_04_group	0.03	0.05	0.04	0.03	0.02	0.05	0.01	0.403	0.925	0.173	0.700	0.461	0.060	0.411
unknown Bacteroidales	0.03	0.03	0.02	0.04	0.04	0.02	0.01	0.918	0.289	0.155	0.769	0.563	0.175	0.679
Ruminococcaceae_UCG_-009	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.233	0.657	0.097	0.296	0.227	0.011	0.440
Campylobacter	0.02	0.20	0.18	0.03	0.00	0.22	0.08	0.772	0.176	0.022	0.484	0.150	0.495	0.384
Lachnospiraceae_FCS02_0_group	0.02	0.01	0.01	0.02	0.01	0.02	0.01	0.310	0.349	0.557	0.574	0.360	0.047	0.626
Corynebacterium_1	0.02	0.03	0.02	0.03	0.00	0.05	0.01	0.622	0.300	0.005	0.691	0.037	0.433	0.178
Ruminococcaceae_UCG_-013	0.02	0.02	0.02	0.02	0.01	0.03	0.00	0.568	0.865	0.054	0.939	0.198	0.008	0.595
unknown Peptostreptococcaceae	0.02	0.03	0.02	0.03	0.01	0.04	0.01	0.756	0.359	0.007	0.810	0.057	0.546	0.222
unknown WCHB1-41	0.02	0.11	0.06	0.07	0.00	0.12	0.03	0.396	0.973	0.021	0.757	0.037	0.063	0.242
Actinomyces	0.02	0.01	0.02	0.01	0.02	0.01	0.00	0.252	0.472	0.091	0.565	0.208	< 0.001	0.519
Ruminococcus_1	0.02	0.01	0.02	0.01	0.00	0.03	0.00	0.468	0.451	< 0.001	0.778	< 0.001	0.074	0.016
Pseudoflavonifractor	0.02	0.02	0.03	0.01	0.01	0.03	0.01	0.812	0.823	0.762	0.516	0.433	0.835	0.599
Peptococcus	0.02	0.00	0.01	0.01	0.00	0.02	0.00	0.081	0.318	0.962	0.237	0.181	0.090	0.444
Ruminococcaceae_UCG_-014	0.02	0.02	0.01	0.03	0.00	0.04	0.01	0.560	0.415	0.016	0.799	0.052	0.093	0.256
Enterococcus	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.232	0.738	0.792	0.397	0.653	0.564	0.815
Family_XIII_UCG-001	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.153	0.424	0.777	0.302	0.546	0.039	0.683
Mannheimia	0.01	0.02	0.03	0.00	0.01	0.03	0.01	0.499	0.075	0.925	0.302	0.334	< 0.001	0.358
Fournierella	0.01	0.01	0.01	0.01	0.02	0.00	0.00	0.611	0.763	0.001	0.842	0.010	0.969	0.105
Ruminiclostridium_5	0.01	0.00	0.01	0.01	0.02	0.00	0.00	0.428	0.988	< 0.001	0.887	0.004	0.054	0.058
Ruminococcaceae_UCG_-003	0.01	0.00	0.01	0.00	0.01	0.00	0.00	0.824	0.536	0.623	0.072	0.937	0.241	0.366
unknown Peptococcaceae	0.01	0.07	0.01	0.06	0.07	0.01	0.03	0.173	0.627	0.080	0.536	0.176	0.103	0.599
Clostridium_sensu_stricto_13	0.01	0.02	0.01	0.02	0.02	0.01	0.00	0.146	0.370	0.887	0.351	0.545	0.083	0.776

Asteroleplasma	0.01	0.00	0.01	0.00	0.00	0.01	0.00	0.699	0.635	0.765	0.885	0.922	0.854	0.989
Helicobacter	0.01	0.03	0.01	0.03	0.03	0.01	0.01	0.204	0.887	0.763	0.612	0.164	0.255	0.588
unknown vadinBE97	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.906	0.123	0.297	0.261	0.777	< 0.001	0.429
Anaerotruncus	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.985	0.409	0.431	0.324	0.891	0.009	0.630
Bilophila	0.01	0.02	0.02	0.00	0.00	0.02	0.01	0.360	0.103	0.002	0.250	0.012	0.012	0.025
unknown Atopobiaceae	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.751	0.646	0.623	0.934	0.911	0.029	0.994
unknown Desulfovibrionaceae	0.00	0.00	0.01	0.00	0.00	0.01	0.00	0.430	0.095	0.069	0.331	0.268	0.008	0.356
Victivallis	0.00	0.02	0.01	0.02	0.02	0.01	0.01	0.836	0.409	0.368	0.334	0.836	0.089	0.357
Pygmaiovacter	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.925	0.925	0.088	0.902	0.283	0.317	0.312
horsej-a03	0.00	0.01	0.01	0.01	0.02	0.00	0.00	0.482	0.635	0.037	0.574	0.077	0.299	0.246
Acetitomaculum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.860	0.212	0.586	0.644	0.934	0.074	0.874
Caproiciproducens	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.745	0.730	0.149	0.934	0.287	0.831	0.539
Defluviitaleaceae_UCG-011	0.00	0.02	0.01	0.00	0.01	0.01	0.00	0.251	0.868	0.135	0.099	0.228	0.295	0.248
Staphylococcus	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.276	0.329	0.955	0.028	0.262	0.001	0.058
unknown Streptococcaceae	0.00	0.02	0.01	0.00	0.01	0.00	0.00	0.053	0.348	0.095	0.053	0.058	0.013	0.068
CAG-873	0.00	0.01	0.01	0.00	0.01	0.00	0.00	0.113	0.138	0.019	0.015	0.015	0.488	< 0.001

¹Values are Means of relative abundance, the SE for all groups is shown; n = 22 / group.

Colon digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplementation and snap frozen in liquid nitrogen.

² Kruskal Wallis Test. asymptotic significance; Significant differences ($p < 0.05$) are marked in bold, trends ($p < 0.1$) are marked in italic and bold

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SEM = standard error of the Mean; Supp = supplementation group

Tabel S9. Diversity of bacterial abundance in the colon digesta of 5 and 12-d old suckling piglets splitted¹

Item	Age	Ala		Gln		SE
		LBW	NBW	LBW	NBW	
Richness	5	154	166	156	178	7.622
	12	183	163	193	186	7.869
Shannon.Index	5	3.73	3.58	3.50	3.84	0.070
	12	3.81	3.769	3.82	3.69	0.080
Evenness	5	0.74	0.70	0.69	0.74	0.108
	12	0.74	0.74	0.73	0.71	0.012

¹Values are Means, the SE of all groups is shown ; n = 5 / group (5 and 12 d).Kruskal – Wallis Test, none of the other fixed effects or their combination were significant ($p < 0.05$)

Ala = Alanine; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error

Table S10. Relative abundance of bacterial phyla in the colon digesta of male suckling piglets splitted¹

Item, %	Age	Ala		Gln			p values ²			Suppl x BiW	Age
		LBW	NBW	LBW	NBW	SE	Supp	BiW	Suppl x BiW		
Firmicutes	5	55.9 ^a	74.4 ^{bd}	67.0	63.5 ^c	2.52	0.854	0.110	0.027		
Firmicutes	12	67.0	78.0	68.3	68.0	2.57	0.356	0.085	0.215		
Bacteroidetes	5	30.6	19.3	20.2	24.4	2.21	1.000	0.580	0.332		
Bacteroidetes	12	21.2	17.1	21.8	20.7	1.69	0.424	0.356	0.645		0.362
Fusobacteria	5	7.50	3.12	9.20	8.31	1.85	0.498	0.667	0.766		
Fusobacteria	12	3.64	0.74	3.07	5.63	1.36	0.356	0.176	0.432		0.052
Proteobacteria	5	5.29	2.76	3.27	3.23	0.78	0.902	0.424	0.877		
Proteobacteria	12	2.78	1.46	4.59	3.94	0.84	0.268	0.460	0.632		0.307
Actinobacteria	5	0.54	0.29	0.25	0.36	0.10	1.000	0.389	0.615		
Actinobacteria	12	0.29	0.18	0.21	0.17	0.03	0.268	0.389	0.544		0.869

Spirochates	5	0.09	0.10	0.06 ^e	0.27	0.04	0.563	0.347	0.495	0.003
Spirochates	12	1.19	0.44	0.98 ^f	0.32	0.27	0.619	0.368	0.795	
Epsilonbacteraeota	5	0.01	0.00	0.04	0.24	0.07	0.031	0.381	0.129	0.113
Epsilonbacteraeota	12	0.16	0.95	0.10	0.37	0.332	0.445	0.406	0.745	
Plantomycetes	5	0.23	0.41	0.19	0.11	0.055	0.563	0.772	0.899	0.002
Plantomycetes	12	0.78	0.63	0.35	0.25	0.141	0.951	0.757	0.985	
Lentisphaerae	5	0.06	0.07	0.05	0.23	0.051	0.485	0.834	0.566	0.230
Lentisphaerae	12	0.03 ^a	0.00 ^b	0.08	0.00	0.020	0.426	0.009	0.036	
WPS-2	5	0.00	0.00 ^c	0.00	0.00	0.000	1.000	1.000	1.000	0.002
WPS-2	12	1.16	2.96 ^{+d}	0.12	0.96	0.887	0.942	0.193	0.594	
Verrucomicrobia	5	0.10	0.00	0.00	0.00	0.00	0.338	0.296	0.418	0.173
Verrucomicrobia	12	9.27	0.02	0.03	0.00	4.62	0.306	0.264	0.486	
Tenericutes	5	0.00	0.00	0.00	0.00 ^e	0.00	1.000	1.000	1.000	0.000
Tenericutes	12	1.10	0.30	0.04 ^{+f}	0.22 ^f	0.208	0.497	0.497	0.755	
Kritimatiellae	5	0.00	0.08	0.00	0.00	0.00	0.338	0.338	0.418	0.021
Kritimatiellae	12	0.22	0.17	0.37 ^{+f}	0.63	0.193	0.174	0.821	0.597	

¹Values are Means of relative abundance, the SE for all groups is shown; n = 5 / group (5, 12 d).

Colon digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and snap frozen in liquid nitrogen.

² Kruskal Wallis Test, asymptotic significance (significant differences are marked in bold, trends in bold and italics)

Asymptotic significance, none of the other fixed effects or their combination were significant ($p < 0.05$)

^{a, b}Labeled Means in a row within one BiW group and one age group without a common letter differ, $P < 0.05$ (Mann-Whitney-U-test).

^{c, d}Labeled Means in a row within one supplementation group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{e, f}Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

⁺Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.1$ (Mann-Whitney-U-test).

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low-birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S11. Relative abundance of bacterial order in the colon digesta of male suckling piglets splitted¹

Item, %	Age	Ala		Gln		SE	Supp	BiW	p values ²	
		LBW	NBW	LBW	NBW				Suppl X BiW	Age
Lactobacillales	5	26.5	38.8	41.2	30.9	3.05	0.902	0.712	0.262	
Lactobacillales	12	29.4	32.1	33.9	36.2	2.81	0.460	0.854	0.893	0.767
Clostridiales	5	27.0	34.4	24.9	31.4	2.23	0.902	0.850	0.383	
Clostridiales	12	35.2	44.2	32.8	29.9	2.81	0.157	0.460	0.368	0.063
Bacteroidales	5	30.6	19.3	20.2	24.4	2.20	1.000	0.580	0.332	
Bacteroidales	12	21.2	21.8	17.1	20.7	1.69	0.424	0.356	0.645	0.113
Fusobacteriales	5	7.50	3.12	9.20	8.13	1.85	0.498	0.667	0.766	
Fusobacteriales	12	3.64	0.74	3.07	5.63	1.36	0.356	0.176	0.432	0.052
Pasteurellales	5	4.51	1.34	1.38	2.14	3.71	0.806	0.295	0.700	
Pasteurellales	12	2.10	0.92	4.56	3.53	4.20	0.139	0.579	0.480	0.733
Erysipelotrichales	5	1.76	0.80	0.32	0.79	0.24	0.805	0.782	0.698	
Erysipelotrichales	12	0.91	0.55	0.42	0.14	0.14	0.157	0.056	0.111	0.435
Selenomodales	5	0.89	0.39	0.39	0.42	0.11	0.712	0.538	0.448	
Selenomodales	12	1.31	0.83	0.90	1.50	0.40	0.268	1.000	0.503	0.956
Enterobacteriales	5	0.74	0.23	1.01	1.08	0.25	0.156	0.951	0.375	
Enterobacteriales	12	0.83	0.24	0.46 ^b	0.15 ^a	0.14	0.667	0.097	0.154	0.660
Coriobacteriales	5	0.53	0.28	0.28	0.34 ⁺	0.12	0.902	0.902	0.955	
Coriobacteriales	12	0.11 ^c	0.11	0.07 ^d	0.05 ⁻	0.01	0.004	0.951	0.035	0.054
Pirellulales	5	0.23	0.41	0.19-	0.11	0.05	0.563	0.772	0.899	
Pirellulales	12	0.78	0.63	0.35 ⁺	0.23	0.14	0.951	0.757	0.985	0.002
Unknown Firmicutes	5	0.12 ^f	0.15 ⁻	0.22	0.09 ^f	0.02	0.665	0.665	0.435	
Unknown Firmicutes	12	0.21 ^E	0.26 ⁺	0.18	0.31 ^E	0.03	0.758	0.622	0.901	0.092
Desulfovibrionales	5	0.12	0.08	0.08	0.16	0.02	0.295	0.902	0.408	
Desulfovibrionales	12	0.16	0.14	0.28	0.08	0.04	0.460	0.424	0.683	0.297

Actinomycetales	5	0.10	0.04	0.03	0.02	0.01	0.219	0.563	0.480	
Actinomycetales	12	0.04	0.02	0.05	0.00	0.01	0.352	0.306	0.571	0.115
Betaproteobacteriales	5	0.10	0.04	0.04	0.07	0.02	0.653	0.653	0.597	
Betaproteobacteriales	12	0.20	0.33	0.05	0.08	0.06	0.507	0.528	0.199	0.880
Spirochaetales	5	0.09	0.06	0.10 ^E	0.27	0.04	0.563	0.347	0.495	
Spirochaetales	12	1.19	0.44	0.98 ^F	0.32	0.27	0.619	0.368	0.795	0.003
Victivallales	5	0.05	0.01	0.01	0.26	0.06	0.880	0.623	0.455	
Victivallales	12	0.03 [#]	0.00 [*]	0.08	0.00	0.02	0.701	0.019	0.114	0.468
Micrococcales	5	0.05	0.07	0.04 ^E	0.11	0.01	0.703	0.163	0.475	
Micrococcales	12	0.20	0.07	0.10 ^{F#}	0.09 [*]	0.02	1.000	0.095	0.362	0.058
Betaproteobacteriales	5	0.10	0.04	0.04	0.07	0.02	0.653	0.653	0.597	
Betaproteobacteriales	12	0.20	0.33	0.05	0.08	0.06	0.507	0.528	0.199	0.880
Oligosphaerales	5	0.01	0.06	0.10	0.06 ⁺	0.01	0.202	0.426	0.466	
Oligosphaerales	12	0.03	0.00	0.00	0.00 ⁻	0.00	0.338	0.338	0.418	0.037
Campylobacterales	5	0.01 ^z	0.00	0.04 ^x	0.24	0.07	0.031	0.381	0.129	
Campylobacterales	12	0.16	0.10	0.95	0.37	0.33	0.445	0.406	0.745	0.113
Bradymondales	5	0.00 [*]	2.23 ⁺⁺	1.30 ^{**}	0.05 ⁺⁺	0.67	0.743	0.763	0.084	
Bradymondales	12	0.08 ^b	0.23 ^{a-}	0.11 ⁺	0.03 ^{-*}	0.06	0.054	0.572	0.103	0.609
Mollicutes_RF39	5	0.00	0.00	0.00	0.00 ^F	0.00	1.000	1.000	1.000	
Mollicutes_RF39	12	1.09	0.30	0.03	0.22 ^E	0.25	1.000	0.247	0.477	0.002
Unknown WPS-2	5	0.00	0.00 ⁻	0.00	0.00	0.00	1.000	1.000	1.000	
Unknown WPS-2	12	1.16	2.96 ⁺	0.12	0.95	0.89	0.942	0.193	0.594	0.002
WCHB1-41	5	0.00	0.08	0.00 ⁻	0.00	0.00	0.338	0.338	0.418	
WCHB1-41	12	0.22	0.17	0.37 ⁺	0.63	0.19	0.174	0.821	0.597	0.021
Corynebacteriales	5	0.00	0.00	0.00 ⁻	0.00	0.00	1.000	1.000	1.000	
Corynebacteriales	12	0.09	0.35	0.06 ⁺	0.37	0.06	0.623	0.428	0.834	0.005

¹Values are Means of relative abundance, the largest SE is shown; n = 5 / group (5, 12 d).

Colon digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and snap frozen in liquid nitrogen.

² Kruskal Wallis Test, asymptotic significance (significant differences are marked in bold, trends in bold and italics)

Asymptotic significance, none of the other fixed effects or their combination were significant ($p < 0.05$)

^{a, b}Labeled Means in a row within one BiW group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{c,d}Labeled Means in a row within one supplementation group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{e,f}Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{xz}Labeled Means in a row within one BiW group and one age group without a different superscripts differ, $p < 0.1$ (Mann-Whitney-U-test).

^{*#}Labeled Means in a row within one supplementation group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{zr}Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.1$ (Mann-Whitney-U-test).

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight; SE = standard error; Supp = supplementation group

Table S12. Relative abundance of bacterial genera in the colon digesta of male suckling piglets splitted¹

Item, %	Age	Ala		Gln			p values ²			
		LBW	NBW	LBW	NBW	SE	Suppl	BiW	BiwxSupp	Age
Lactobacillus	5	24.9	37.6	38.7	29.6	0.032	1.000	0.538	0.245	0.991
Lactobacillus	12	28.8	31.4	33.0	35.7	2.761	0.424	0.758	0.859	0.991
unknown Muribaculaceae	5	11.1 ^E	7.33	6.13 ^E	2.61	0.052	0.176	0.140	0.238	0.001
unknown Muribaculaceae	12	0.58 ^F	2.09	1.28 ^F	2.53	0.368	0.356	0.056	0.118	0.001
Clostridium_sensu_stricto_1	5	7.82	10.7	8.91	11.0	0.078	0.389	0.268	0.569	0.546
Clostridium_sensu_stricto_1	12	7.55	10.3	9.23	6.94	1.284	1.000	0.622	0.738	0.546
Fusobacterium	5	7.43	3.06	9.10	8.09	0.051	0.498	0.712	0.757	0.052
Fusobacterium	12	3.62	0.74	3.03	5.59	1.351	0.356	0.176	0.432	0.052
Bacteroides	5	6.66	5.39	2.45	3.13	0.013	0.291	0.398	0.345	0.061
Bacteroides	12	3.29	2.17	2.15	0.82	0.620	0.356	0.429	0.624	0.061
Prevotella_2	5	3.83	0.83	3.34	5.74	0.054	0.423	0.291	0.476	0.703
Prevotella_2	12	5.81	2.07	1.38	5.47	1.491	0.475	0.886	0.854	0.703
Rikenellaceae_RC9_gut_group	5	3.58	2.80	1.41	3.93	0.496	0.725	0.944	0.398	0.805
Rikenellaceae_RC9_gut_group	12	1.75	4.09	7.30	3.29	1.259	0.157	0.498	0.437	0.805
Actinobacillus	5	4.10	1.30	1.28	2.05	0.004	0.768	0.533	0.896	0.548
Actinobacillus	12	1.68	0.73	3.60	3.45	0.814	0.221	0.462	0.515	0.548
unknown Ruminococcaceae	5	3.21	1.77	1.35	3.25	0.022	0.424	1.000	0.217	0.128
unknown Ruminococcaceae	12	2.88	5.78	2.51	4.70	0.724	0.279	0.158	0.405	0.128
unknown Lachnospiraceae	5	2.62	5.51	2.53	4.29	0.038	0.622	0.712	0.825	0.013
unknown Lachnospiraceae	12	1.08	1.57	0.64 ⁺	1.00	0.168	0.157	0.140	0.257	0.013
Roseburia	5	0.43	0.07	0.01	0.00	0.002	0.121	0.439	0.392	1.000
Roseburia	12	1.59	0.33	0.08	1.34	0.477	0.884	0.558	0.928	1.000
Prevotellaceae_UCG-003	5	1.44	0.19	0.16	0.25	0.005	0.327	0.606	0.630	0.686
Prevotellaceae_UCG-003	12	0.76	0.27	0.39	0.54	0.115	0.501	0.700	0.095	0.686
Romboutsia	5	1.84	2.94	1.55 ^F	1.35	0.006	0.667	0.196	0.440	0.001

Romboutsia	12	2.90	3.67	4.28 ^E	2.52	0.426	0.673	0.673	0.791	0.001
Streptococcus	5	1.47	0.84 ^F	1.98	0.95	0.026	0.673	0.360	0.732	0.003
Streptococcus	12	0.47	0.35 ^F	0.64	0.28	0.100	0.821	0.226	0.637	0.003
Prevotellaceae_NK3B31_group	5	1.07	0.75	4.05 ^E	3.41	0.244	0.016	1.000	0.107	0.004
Prevotellaceae_NK3B31_group	12	0.93	0.54	0.68 ^F	0.44	0.187	0.328	0.965	0.362	0.004
Alloprevotella	5	1.05	0.21 ⁻	0.27	1.18	0.003	0.845	0.248	0.289	0.097
Alloprevotella	12	3.08	1.17 ⁺	2.99	3.90	0.859	0.324	0.526	0.651	0.097
Lachnoclostridium	5	1.56	1.47	0.78	1.77	0.477	0.242	0.951	0.432	0.055
Lachnoclostridium	12	0.88	0.76	0.87	0.61	0.188	0.439	0.573	0.752	0.055
Peptostreptococcus	5	0.97	0.23 ^E	0.42	0.21	0.013	0.534	0.354	0.737	0.001
Peptostreptococcus	12	0.04	0.00 ^F	0.07	0.04	0.010	0.242	0.866	0.470	0.001
Turicibacter	5	0.89	0.30	0.16	0.33	0.014	0.906	1.000	0.870	0.470
Turicibacter	12	0.23	0.21	0.33	0.08	0.066	0.965	0.286	0.745	0.470
Blautia	5	0.90	2.47	0.59	0.37	0.085	0.131	0.470	0.238	unkonw
Blautia	12	0.20	0.44	0.29	0.16	0.075	0.059	0.958	0.071	0.065
Parabacteroides	5	1.06	0.71 ^E	1.66	3.09 ^E	0.013	0.902	0.712	0.781	0.013
Parabacteroides	12	0.65	0.10 ^F	0.87	0.09 ^F	0.221	0.534	0.038	0.193	0.013
Collinsella	5	0.34	0.20	0.16	0.22	0.022	0.749	0.808	0.930	0.673
Collinsella	12	0.05	0.03	0.00	0.01	0.012	0.480	1.000	0.670	0.673
Holdemanella	5	0.48	0.11	0.09	0.08	0.068	0.253	0.199	0.181	0.522
Holdemanella	12	0.12	0.29	0.03	0.00	0.078	0.083	1.000	0.284	0.522
Veillonella	5	0.74 ⁺	0.12	0.34 ^E	0.25 ^E	0.011	0.597	0.131	0.220	0.025
Veillonella	12	0.05 ⁻	0.04	0.10 ^{aF}	0.02 ^{bF}	0.017	0.796	0.071	0.193	0.025
Ruminococcus_2	5	0.81	0.85	0.51	0.55	0.035	1.000	0.398	0.669	0.351
Ruminococcus_2	12	1.01	0.68	0.27	0.04	0.184	0.131	0.100	0.146	0.351
unknown Pasteurellaceae	5	0.39	0.04	0.10	0.09	0.009	0.817	0.059	0.291	0.775
unknown Pasteurellaceae	12	0.05	0.03	0.11	0.08	0.020	0.006	0.201	0.034	0.775
Escherichia/Shigella	5	0.62	0.18	0.97	0.89	0.018	0.174	0.762	0.174	0.940
Escherichia/Shigella	12	0.70	0.25	0.46	0.15	0.132	0.922	0.033	0.113	0.940
Ruminococcaceae_UCG-002	5	0.60	1.27	0.63	0.97	0.007	0.929	0.270	0.715	0.059
Ruminococcaceae_UCG-002	12	2.26	2.63	2.54	2.60	0.480	1.000	0.622	0.961	0.059

Ruminococcaceae_NK4A214_group	5	0.54	0.53	0.41	0.69	0.000	0.974	0.510	0.891	0.029
Ruminococcaceae_NK4A214_group	12	1.15	1.21	0.88	0.93	0.166	0.460	0.806	0.871	0.029
Alistipes	5	0.20	0.03	0.09 ^a	0.00 ^b	0.010	0.221	0.121	0.127	0.145
Alistipes	12	0.00 ^x	0.02	0.18 ^z	0.00	0.038	0.086	0.796	0.251	0.145
Tyzzerella	5	0.56 ^E	0.22	0.22	0.75 ^E	0.014	0.673	0.439	0.229	0.048
Tyzzerella	12	0.16 ^F	0.31	0.10	0.14 ^F	0.042	0.102	0.043	0.117	0.048
Family_XIII_AD3011_group	5	0.55	0.21 ^F	0.35	0.38 ^F	0.025	0.498	0.806	0.775	0.003
Family_XIII_AD3011_group	12	0.68	1.36 ^E	0.92	0.93 ^E	0.179	0.792	0.065	0.332	0.003
Lachnospiraceae_UCG-004	5	0.08	0.04	0.00	0.04	0.825	0.643	0.143	0.213	0.484
Lachnospiraceae_UCG-004	12	0.16	0.14	0.11	0.14	0.025	0.050	1.000	0.250	0.484
Clostridium_sensu_stricto_2	5	0.43	0.51	2.27	0.79	0.070	0.758	0.712	0.957	0.429
Clostridium_sensu_stricto_2	12	0.11	0.08	0.39	0.08	0.079	0.409	0.327	0.568	0.429
Terrisporobacter	5	0.33	0.45	0.22	0.18	0.004	0.184	0.545	0.574	0.088
Terrisporobacter	12	0.43	0.85	0.50	0.28	0.140	0.597	0.762	0.946	0.088
Prevotella	5	0.06	0.41	0.01	0.09	0.001	0.827	1.000	0.986	0.606
Prevotella	12	0.12	0.01	0.04	0.10	0.026	1.000	0.881	0.761	0.606
unknown Lactobacillales	5	0.06	0.13	0.12	0.15	0.009	0.808	0.610	0.681	0.165
unknown Lactobacillales	12	0.07	0.38	0.23	0.19	0.064	0.565	0.338	0.327	0.165
Epulopiscium	5	0.17	0.27	0.17	0.09	0.014	0.630	0.172	0.580	0.344
Epulopiscium	12	0.05	0.08	0.13	0.14	0.023	0.248	0.630	0.674	0.344
unknown Clostridiaceae_1	5	0.17	0.27	0.46 ^E	0.30	0.003	1.000	0.753	0.692	0.374
unknown Clostridiaceae_1	12	0.07	0.14	0.11 ^F	0.27	0.039	0.045	0.144	0.130	0.374
Intestinimonas	5	0.29	0.31	0.11	0.54	0.028	1.000	0.105	0.364	0.353
Intestinimonas	12	0.51	0.47	0.35	0.31	0.064	0.295	0.758	0.740	0.353
Prevotella_9	5	0.05	0.16	0.11	0.18	0.003	0.643	0.050	0.232	0.005
Prevotella_9	12	0.09	0.04	0.03	0.03	0.023	0.670	0.754	0.862	0.005
Ruminococcaceae_UCG-005	5	0.24 ^F	0.19 ^F	0.17 ^F	0.14 ⁻	0.003	0.271	0.053	0.177	0.000
Ruminococcaceae_UCG-005	12	2.11 ^E	3.10 ^E	1.76 ^E	1.91 ⁺	0.441	0.178	0.622	0.579	0.000
unknown Family_XIII	5	0.14	0.06 [*]	0.04	0.12 ⁺	0.006	0.728	0.643	0.174	0.026
unknown Family_XIII	12	0.00	0.01 ⁻	0.01	0.01 ⁻	0.003	0.564	0.083	0.284	0.026
Dorea	5	0.09	0.39	0.22	0.43	0.057	0.560	0.234	0.634	0.150

Dorea	12	0.57	1.07 ^c	0.42	0.21 ^d	0.112	0.065	0.439	0.148	0.150
Christensenellaceae_R-7_group	5	0.22 ^f	0.20 ^f	0.30	0.25	0.081	0.360	0.570	0.747	0.000
Christensenellaceae_R-7_group	12	1.78 ^e	2.74 ^e	1.39	1.91	0.334	0.481	0.291	0.600	0.000
Eisenbergiella	5	0.25 ^e	0.40 ^e	0.40	0.16	0.109	0.776	0.118	0.249	0.054
Eisenbergiella	12	0.04 ^f	0.01 ^f	0.11	0.01	0.026	0.827	0.064	0.312	0.054
p-1088-a5_gut_group	5	0.08	0.07	0.08-	0.05	0.009	0.101	0.564	0.256	0.317
p-1088-a5_gut_group	12	0.52	0.42	0.35 ⁺	0.19	0.117	0.131	0.859	0.396	0.317
Ruminococcaceae_UCG-010	5	0.19	0.15	0.10	0.22	0.032	0.568	0.620	0.824	0.465
Ruminococcaceae_UCG-010	12	0.14	0.21	0.14	0.18	0.034	0.762	0.650	0.701	0.465
Butyrimonas	5	0.22	0.40 ^e	0.13	0.15	0.050	0.380	0.290	0.293	0.023
Butyrimonas	12	0.09	0.08 ^f	0.66	0.06	0.154	0.462	0.022	0.090	0.023
Negativibacillus	5	0.04	0.08	0.01	0.09	0.021	0.917	0.794	0.938	1.000
Negativibacillus	12	0.00	0.02	0.00	0.00	0.005	n.a	n.a	n.a	1.000
Ruminiclostridium_9	5	0.20	0.21	0.23	0.33	0.012	0.389	0.295	0.623	0.045
Ruminiclostridium_9	12	0.76	0.77	0.27	0.27	0.114	0.014	0.573	0.081	0.045
Phascolarctobacterium	5	0.16	0.27	0.05	0.17	0.023	0.131	0.305	0.102	0.072
Phascolarctobacterium	12	0.72	0.79	0.80	0.60	0.251	0.124	0.498	0.245	0.072
Oscillospira	5	0.15 ^f	0.20	0.06 ^f	0.16	0.011	0.965	0.859	0.997	0.017
Oscillospira	12	0.57 ^e	0.37	0.56 ^e	0.38	0.102	0.375	0.429	0.680	0.017
Ruminococcaceae_UCG-004	5	0.18	0.17	0.13	0.20	0.010	0.970	0.821	0.995	0.006
Ruminococcaceae_UCG-004	12	0.57	0.43	0.38	0.24	0.094	0.072	0.806	0.287	0.006
Eubacterium	5	0.05	0.01	0.00	0.01	0.013	0.480	1.000	0.741	0.685
Eubacterium	12	0.04	0.01	0.02	0.01	0.009	1.000	0.480	0.733	0.685
Hungatella	5	0.13	0.27	0.07	0.11	0.019	0.841	0.482	0.893	0.671
Hungatella	12	0.01	0.00	0.20	0.02	0.051	0.655	0.655	0.861	0.671
unknown Paludibacteraceae	5	0.02	0.00	0.02	0.00	0.007	0.221	n.a	0.221	0.197
unknown Paludibacteraceae	12	0.03	0.09	0.04	0.03	0.022	0.513	0.827	0.934	0.197
GCA-900066225	5	0.14 ⁺	0.12 ^e	0.15 ⁺	0.09 ⁺	0.031	0.700	0.650	0.949	0.051
GCA-900066225	12	0.02-	0.04 ^f	0.01-	0.00-	0.009	0.050	0.827	0.232	0.051
Marvinbryantia	5	0.09	0.22	0.14	0.06	0.113	0.346	1.000	0.809	0.610
Marvinbryantia	12	0.06	1.24	0.11	0.07	0.207	0.290	0.149	0.209	0.610

Sutterella	5	0.05	0.01	0.01	0.05	0.002	0.831	0.286	0.187	0.597
Sutterella	12	0.11	0.02 ^x	0.01 ^b	0.07 ^{az}	0.025	0.917	0.465	0.786	0.597
Fournierella	5	0.04	0.01	0.01	0.04	0.009	1.000	0.624	0.087	n.a
Fournierella	12	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Acetitomaculum	5	0.00	0.00	0.00	0.00	0.001	0.221	n.a	0.221	0.157
Acetitomaculum	12	0.00	0.01	0.00	0.00	0.002	1.000	0.121	0.392	0.157
Actinomyces	5	0.05	0.01	0.01	0.01	0.007	0.025	0.083	0.090	1.000
Actinomyces	12	0.01	0.00	0.01	0.00	0.003	1.000	0.221	0.368	1.000
Anaerotruncus	5	0.01	0.00	0.00	0.00	0.003	0.317	0.317	0.317	0.355
Anaerotruncus	12	0.00	0.01	0.00	0.01	0.003	0.121	0.655	0.259	0.355
Asteroleplasma	5	0.01	0.00	0.00	0.00	0.003	0.221	1.000	0.368	0.289
Asteroleplasma	12	0.01	0.00	0.00	0.00	0.004	0.121	1.000	0.392	0.289
Bilophila	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Bilophila	12	0.02	0.00	0.06	0.01	0.010	0.881	0.317	0.692	n.a
Butyricoccus	5	0.06	0.01	0.02	0.03	0.000	0.277	0.796	0.669	0.217
Butyricoccus	12	0.02	0.05	0.04	0.05	0.014	0.200	0.167	0.359	0.217
CAG-873	5	0.00	0.00	0.04	0.00	0.005	0.157	0.157	0.157	n.a
CAG-873	12	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Campylobacter	5	0.00	0.00	0.00	0.00	0.001	0.317	n.a	0.317	0.117
Campylobacter	12	0.07	0.02	0.63	0.13	0.163	0.386	0.881	0.614	0.117
Candidatus_Soleaferrea	5	0.01 ⁻	0.00 ⁻	0.00 ^f	0.03	0.000	1.000	1.000	1.000	0.050
Candidatus_Soleaferrea	12	0.08 ⁺	0.12 ⁺	0.07 ^e	0.06	0.021	0.083	0.643	0.184	0.050
Caproiciproducens	5	0.00	0.00	0.00	0.01	0.002	0.180	0.121	0.259	0.480
Caproiciproducens	12	0.00	0.00	0.00	0.00	0.001	n.a	n.a	n.a	0.480
Clostridium_sensu_stricto_13	5	0.00	0.02	0.02	0.04	0.027	1.000	0.355	0.565	0.423
Clostridium_sensu_stricto_13	12	0.00	0.01	0.01	0.02	0.004	0.643	0.275	0.463	0.423
Clostridium_sensu_stricto_4	5	0.03	0.08	0.02 ^f	0.00	0.163	0.739	0.456	0.373	0.061
Clostridium_sensu_stricto_4	12	0.08	0.16	0.16 ^{E#}	0.08 [*]	0.027	0.563	0.142	0.287	0.061
Coprococcus_1	5	0.00	0.00	0.00	0.01	0.002	n.a	n.a	n.a	0.770
Coprococcus_1	12	0.02	0.10	0.01	0.00	0.025	1.000	0.157	0.344	0.770
Coprococcus_3	5	0.02	0.07	0.06	0.01	0.005	0.302	0.624	0.416	0.428

Coprococcus_3	12	0.08	0.14	0.09	0.06	0.023	0.958	0.664	0.487	0.428
Corynebacterium_1	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Corynebacterium_1	12	0.03	0.06	0.03	0.07	0.022	0.724	0.053	0.258	n.a
Defluviitaleaceae_UCG-011	5	0.00	0.00	0.03	0.00	0.007	0.317	0.317	0.317	0.739
Defluviitaleaceae_UCG-011	12	0.00 ^x	0.00	0.02 ^z	0.01	0.004	0.064	0.513	0.117	0.739
Denitrobacterium	5	0.03	0.02	0.03	0.04	0.002	0.670	0.394	0.839	1.000
Denitrobacterium	12	0.05	0.06	0.03	0.02	0.009	0.157	0.908	0.418	1.000
Desulfovibrio	5	0.11	0.08	0.08	0.13	0.006	0.510	0.818	0.336	0.650
Desulfovibrio	12	0.13	0.13	0.21	0.07	0.033	0.295	0.498	0.582	0.650
dgA-11_gut_group	5	0.04	0.01	0.02	0.06	0.009	0.462	1.000	0.839	0.676
dgA-11_gut_group	12	0.05	0.10	0.07	0.02	0.018	0.045	0.257	0.219	0.676
Enterococcus	5	0.01	0.00	0.00	0.00	0.002	0.180	0.121	0.259	0.157
Enterococcus	12	0.01	0.03	0.00	0.01	0.009	0.221	1.000	0.368	0.157
Erysipelotrichaceae_UCG-004	5	0.01	0.00	0.00	0.10	0.027	0.439	0.180	0.407	0.201
Erysipelotrichaceae_UCG-004	12	0.29	0.00	0.01	0.02	0.054	0.064	0.355	0.180	0.201
Faecalibacterium	5	0.01	0.06	0.00*	0.05 [#]	0.015	0.827	0.770	0.953	0.423
Faecalibacterium	12	0.02	0.05	0.00	0.01	0.009	0.355	0.643	0.801	0.423
Family_XIII_UCG-001	5	0.02	0.01	0.00	0.01	0.022	0.796	0.142	0.261	1.000
Family_XIII_UCG-001	12	0.02	0.01	0.01	0.01	0.003	0.305	0.394	0.651	1.000
Flavonifractor	5	0.09	0.05	0.04	0.09	0.002	0.283	0.923	0.738	n.a
Flavonifractor	12	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
GCA-900066575	5	0.00	0.01	0.00	0.01	0.004	0.221	0.221	0.368	0.926
GCA-900066575	12	0.15 ^z	0.02	0.01 ^x	0.01	0.031	0.071	0.462	0.348	0.926
H1	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
H1	12	0.09	0.04	0.04	0.01	0.027	0.083	0.564	0.284	n.a
Helicobacter	5	0.00	0.00	0.02	0.08	0.019	n.a	1.000	1.000	0.624
Helicobacter	12	0.01	0.01	0.00	0.02	0.006	1.000	0.083	0.284	0.624
horsej-a03	5	0.00	0.01	0.02	0.03	0.006	0.165	1.000	0.300	0.317
horsej-a03	12	0.00	0.00	0.00	0.00	0.001	n.a	n.a	n.a	0.317
Howardella	5	0.04 ^c	0.06 ^E	0.14 ^{adE}	0.04 ^b	0.004	0.270	0.021	0.097	0.039
Howardella	12	0.01	0.01 ^F	0.02 ^F	0.02	0.005	0.569	0.754	0.753	0.039

Hydrogenoanaerobacterium	5	0.09 ^E	0.05*	0.06	0.07 ^E	0.056	0.722	0.135	0.386	0.013
Hydrogenoanaerobacterium	12	0.01 ^F	0.02-	0.03	0.00 ^F	0.005	0.465	0.732	0.619	0.013
Intestinibacter	5	0.03	0.06	0.02	0.00	0.001	0.480	0.564	0.497	0.752
Intestinibacter	12	0.08	0.08	0.10	0.09	0.028	0.685	0.685	0.444	0.752
Lachnospiraceae_FCS020_group	5	0.00	0.01	0.01	0.01	0.004	0.121	0.180	0.259	0.086
Lachnospiraceae_FCS020_group	12	0.04	0.04	0.00	0.01	0.011	0.157	0.564	0.368	0.086
Lachnospiraceae_NC2004_group	5	0.01	0.02	0.00*-	0.05 ^F	0.005	1.000	0.480	0.670	0.549
Lachnospiraceae_NC2004_group	12	0.06	0.02	0.10*	0.03	0.018	0.806	0.302	0.311	0.549
Lachnospiraceae_UCG-010	5	0.00	0.09	0.00	0.02	0.009	0.513	0.355	0.543	0.366
Lachnospiraceae_UCG-010	12	0.04	0.05	0.09	0.10	0.022	0.273	0.465	0.638	0.366
Mannheimia	5	0.03	0.00	0.00	0.00	0.006	n.a	1.000	1.000	0.275
Mannheimia	12	0.02	0.00	0.08	0.00	0.020	1.000	n.a	1.000	0.275
Mogibacterium	5	0.00 ^F	0.01	0.00-	0.03	0.004	1.000	n.a	1.000	0.089
Mogibacterium	12	0.08 ^E	0.08	0.12*	0.05	0.025	0.391	0.391	0.139	0.089
Oscillibacter	5	0.10	0.07	0.01	0.21	0.001	0.465	0.262	0.629	0.963
Oscillibacter	12	0.03	0.13	0.11	0.09	0.024	0.745	0.874	0.851	0.963
Peptococcus	5	0.00	0.00	0.00	0.01	0.002	0.248	0.480	0.223	0.014
Peptococcus	12	0.03	0.04	0.00	0.00	0.009	n.a	0.439	0.439	0.014
Prevotellaceae_UCG-001	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Prevotellaceae_UCG-001	12	0.02	0.18	0.00	0.02	0.045	0.739	0.248	0.472	n.a
Prevotellaceae_UCG-004	5	0.06	0.01	0.00	0.22	0.004	0.439	0.724	0.481	0.390
Prevotellaceae_UCG-004	12	0.06	0.09	0.21	0.12	0.052	0.584	0.571	0.696	0.390
Pseudoflavonifractor	5	0.01	0.03	0.01	0.00	0.001	0.245	0.480	0.508	1.000
Pseudoflavonifractor	12	0.03	0.01	0.05	0.01	0.013	0.881	0.881	0.590	1.000
Pygmaeobacter	5	0.00	0.01	0.01	0.01	0.004	1.000	0.248	0.301	0.770
Pygmaeobacter	12	0.00	0.00	0.00	0.00	0.001	n.a	n.a	n.a	0.770
Rothia	5	0.03	0.05	0.02 ^F	0.07	0.103	0.796	0.071	0.338	0.138
Rothia	12	0.13	0.06	0.10 ^{E#}	0.05*	0.021	0.691	0.076	0.227	0.138
Ruminiclostridium_5	5	0.02	0.02	0.01	0.01	0.005	0.088	0.917	0.320	n.a
Ruminiclostridium_5	12	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Ruminococcaceae_UCG-003	5	0.02	0.00	0.00	0.01	0.005	0.083	0.248	0.223	0.327

Ruminococcaceae_UCG-003	12	0.01	0.00	0.00	0.01	0.002	0.121	0.121	0.121	0.327
Ruminococcaceae_UCG-009	5	0.03	0.01	0.00	0.04	0.333	0.157	0.248	0.344	0.114
Ruminococcaceae_UCG-009	12	0.04	0.02	0.02	0.02	0.006	0.935	0.109	0.394	0.114
Ruminococcaceae_UCG-013	5	0.01	0.02	0.01	0.00	0.001	1.000	0.480	0.634	0.405
Ruminococcaceae_UCG-013	12	0.03	0.03	0.02	0.03	0.007	0.199	0.668	0.577	0.405
Ruminococcaceae_UCG-014	5	0.00	0.00	0.00	0.00	0.001	n.a	n.a	n.a	0.127
Ruminococcaceae_UCG-014	12	0.01	0.06	0.02	0.07	0.019	0.121	0.289	0.277	0.127
Ruminococcus_1	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
Ruminococcus_1	12	0.04	0.03	0.02	0.02	0.007	0.167	0.570	0.517	n.a
Sarcina	5	0.02	0.10	0.00	0.07	0.026	0.564	0.480	0.497	0.053
Sarcina	12	0.00	0.01	0.00	0.00	0.002	0.317	0.317	0.317	0.053
Sphaerochaeta	5	0.03	0.02	0.02	0.13	0.000	0.083	0.297	0.160	0.907
Sphaerochaeta	12	0.53	0.08	0.67	0.08	0.185	0.700	0.149	0.490	0.907
Staphylococcus	5	0.00	0.01	0.01	0.00	0.002	0.221	0.221	0.221	0.513
Staphylococcus	12	0.00	0.00	0.02	0.00	0.002	n.a	n.a	n.a	0.513
Subdoligranulum	5	0.03	0.28	0.01	0.02	0.045	0.327	0.462	0.523	0.288
Subdoligranulum	12	0.08	0.96	0.30	0.02	0.241	0.251	0.201	0.186	0.288
Treponema_2	5	0.00 ⁻	0.00 ⁻	0.00 ⁻	0.00 ⁻	0.003	n.a	0.317	0.317	0.027
Treponema_2	12	0.26 ⁺	0.21 ⁺	0.14 ⁺	0.17 ⁺	0.081	0.568	0.391	0.793	0.027
UBA1819	5	0.10	0.05	0.13	0.08	0.010	0.624	0.414	0.666	0.633
UBA1819	12	0.04	0.08	0.04	0.00	0.022	0.386	1.000	0.250	0.633
unknown Atopobiaceae	5	0.01	0.01	0.00	0.00	0.003	0.564	0.248	0.532	0.327
unknown Atopobiaceae	12	0.00	0.00	0.00	0.00	0.001	1.000	0.121	0.392	0.327
unknown Bacteroidales	5	0.03	0.04	0.02	0.06	0.002	0.917	0.569	0.936	0.329
unknown Bacteroidales	12	0.01	0.02	0.02	0.01	0.006	0.513	0.827	0.836	0.329
unknown Bradymonadales	5	0.00 ⁻	1.12	0.78	0.01	0.095	0.289	1.000	0.276	0.021
unknown Bradymonadales	12	0.04 ⁺	0.19	0.04	0.01	0.032	0.540	1.000	0.387	0.021
unknown Carnobacteriaceae	5	0.00	0.20 ⁺	0.26 ⁺	0.14	0.044	0.305	0.569	0.317	0.086
unknown Carnobacteriaceae	12	0.00	0.00 ⁻	0.01 ⁻	0.02	0.005	n.a	0.317	0.317	0.086
unknown Clostridiales	5	0.05	0.09 ⁻	0.04 ⁻	0.03 ⁻	0.008	0.203	0.814	0.625	0.004
unknown Clostridiales	12	0.06	0.17 ⁺	0.11 ⁺	0.13 ⁺	0.021	0.825	0.248	0.627	0.004

unknown										
Clostridiales_vadinBB60_group	5	0.01 ^F	0.11 ^F	0.66	0.19	0.054	0.088	0.465	0.197	0.083
unknown	12	3.51 ^E	0.70 ^E	1.47	0.40	0.544	1.000	0.049	0.212	0.083
Clostridiales_vadinBB60_group										
unknown Desulfovibrionaceae	5	0.00	0.00	0.00	0.00	0.001	n.a	n.a	n.a	0.143
unknown Desulfovibrionaceae	12	0.01	0.01	0.01	0.00	0.003	0.248	0.480	0.497	0.143
unknown Erysipelotrichaceae	5	0.03 ⁻	0.24	0.01 ^b	0.20 ^{a+}	0.020	0.462	0.004	0.020	0.719
unknown Erysipelotrichaceae	12	0.24 ^{a+}	0.02 ^b	0.04	0.03 ⁻	0.040	0.626	0.003	0.016	0.719
unknown F082	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
unknown F082	12	1.93	1.95	3.08	1.59	0.825	0.715	0.850	0.892	n.a
unknown Firmicutes	5	0.08 ⁻	0.12	0.17	0.08	0.040	0.825	0.214	0.196	0.048
unknown Firmicutes	12	0.17 ⁺	0.22	0.15	0.25	0.034	0.744	0.462	0.753	0.048
unknown Fusobacteriaceae	5	0.06	0.06	0.09	0.04	0.011	0.749	0.406	0.350	0.781
unknown Fusobacteriaceae	12	0.02	0.00	0.04	0.03	0.012	1.000	1.000	1.000	0.781
unknown Mollicutes_RF39	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
unknown Mollicutes_RF39	12	0.36	0.10	0.01	0.13	0.095	0.564	0.456	0.708	n.a
unknown p-2534-18B5_gut_group	5	0.00	0.00	0.16	0.00	0.003	n.a	n.a	n.a	0.540
unknown p-2534-18B5_gut_group	12	1.62	1.80	0.30	1.61	0.496	0.600	0.791	0.931	0.540
unknown Peptococcaceae	5	0.02	0.01	0.01	0.22	0.025	1.000	0.602	0.929	0.572
unknown Peptococcaceae	12	0.01	0.00	0.01	0.01	0.003	0.655	0.180	0.259	0.572
unknown Peptostreptococcaceae	5	0.00	0.01	0.01	0.01	0.020	1.000	0.221	0.368	0.186
unknown Peptostreptococcaceae	12	0.02	0.06	0.03	0.06	0.013	0.361	0.100	0.229	0.186
unknown Prevellaceae	5	0.04	0.05 ^d	0.06	0.22 ^{cE}	0.003	0.022	0.537	0.120	0.355
unknown Prevellaceae	12	0.17	0.20	0.01	0.04 ^F	0.050	0.055	0.465	0.223	0.355
unknown Streptococcaceae	5	0.00	0.00	0.04	0.01	0.006	0.157	0.564	0.344	0.380
unknown Streptococcaceae	12	0.00	0.00	0.01	0.00	0.003	n.a	n.a	n.a	0.380
unknown vadinBE97	5	0.01	0.00	0.00	0.02	0.005	0.157	0.480	0.180	0.850
unknown vadinBE97	12	0.01	0.00	0.00	0.00	0.002	0.121	n.a	0.121	0.850
unknown WCHB1-41	5	0.00	0.01	0.00	0.00	0.004	n.a	n.a	n.a	0.827
unknown WCHB1-41	12	0.04	0.03	0.19	0.25	0.068	0.699	0.724	0.895	0.827
unknown WPS-2	5	0.00	0.00	0.00	0.00	0.000	n.a	n.a	n.a	n.a
unknown WPS-2	12	0.19	1.48	0.04	0.38	0.333	0.386	0.180	0.423	n.a

Victivallis	5	0.02	0.00	0.00	0.06	0.014	1.000	1.000	1.000	0.643
Victivallis	12	0.00	0.00	0.02	0.00	0.005	0.317	n.a	0.317	0.643

¹Values are Means of relative abundance, the largest SE is shown; n = 5 / group (5, 12 d).

Colon digesta samples were obtained at 2 h after oral administration of milk replacer and Gln or Ala supplement and snap frozen in liquid nitrogen.

² Kruskal Wallis Test, asymptotic significance (significant differences are marked in bold, trends in bold and italics)

Asymptotic significance, none of the other fixed effects or their combination were significant ($p < 0.05$)

^{a,b}Labeled Means in a row within one BiW group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{c,d}Labeled Means in a row within one supplementation group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{e,f}Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

^{x,z}Labeled Means in a row within one BiW group and one age group without a different superscripts differ, $p < 0.1$ (Mann-Whitney-U-test).

^{*#}Labeled Means in a row within one supplementation group and one age group without a common letter differ, $p < 0.05$ (Mann-Whitney-U-test).

⁺Labeled Means in a column within one supplementation group and BiW group without a common letter differ, $p < 0.1$ (Mann-Whitney-U-test).

Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal bodyweight; n.a = not available; SE = standard error; Supp = supplementation group

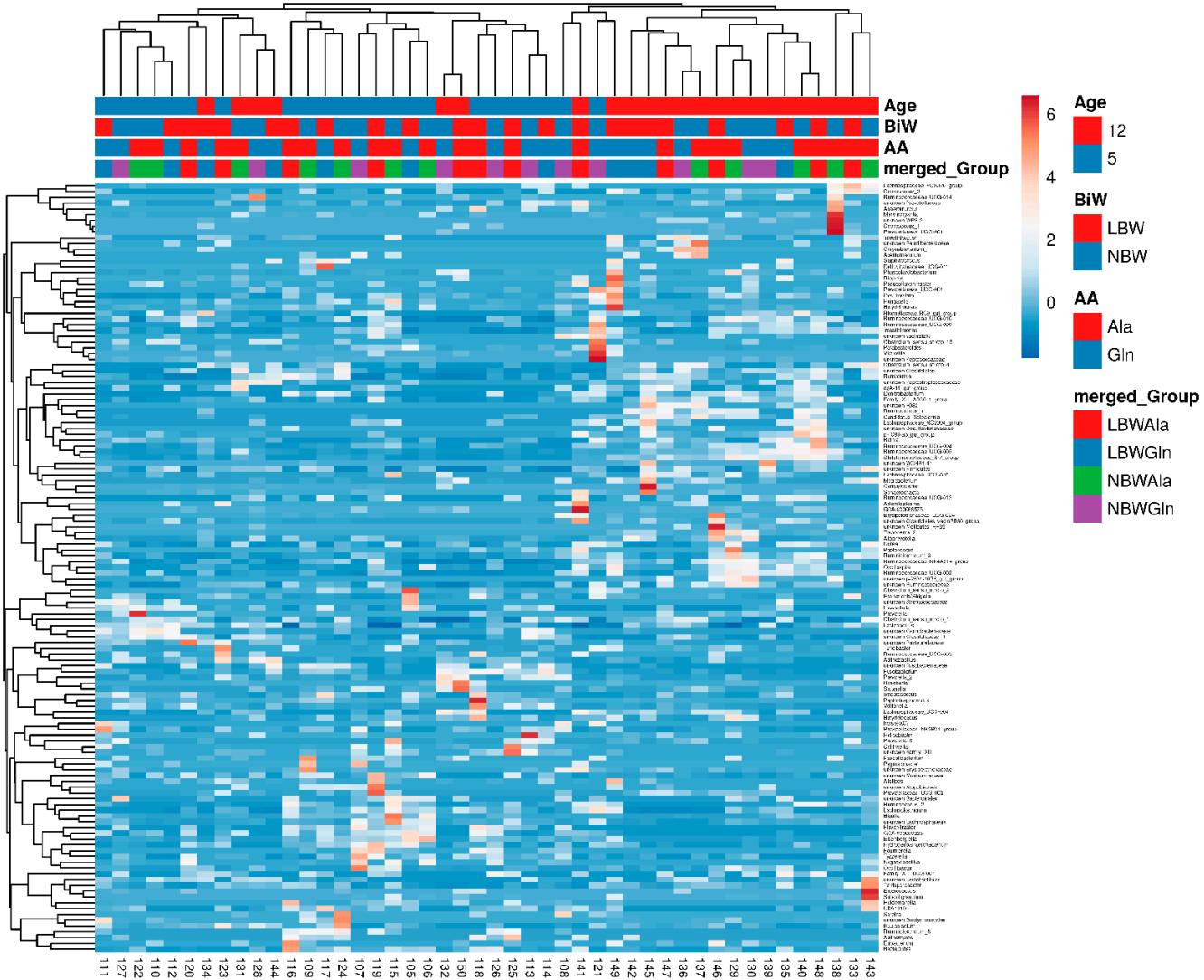


Figure S1. Hierarchical clustering of bacterial genera in colon of male suckling piglets

AA = amino acids; Ala = Alanine; BiW = birthweight; Gln = Glutamine; LBW = low birthweight; NBW = normal birthweight;