Supplementary Table 1. Effect of in-feed antimicrobials on the cecal bacteria composition

Taxonomy	Control	BMD	Tylosin	Virginiamycin	Monensin	Salinomycin	*P*_Value
Phylum							
Firmicutes	98.5	97.2	97.9	97.2	97.6	97.0	0.692
Proteobacteria	0.44	0.60	1.16	1.02	1.93	1.87	0.468
Bacteroidetes	0.61^{ab}	1.85^{a}	0.27^{b}	0.65^{ab}	0.23^{b}	0.87^{ab}	0.016
Actinobacteria	0.15^{a}	0.10^{ab}	0.08^{ab}	0.07^{b}	0.11^{ab}	0.13^{ab}	0.019
Others	0.24^{b}	0.20^{b}	0.54^{ab}	1.07^{a}	0.15^{b}	0.12^{b}	<0.001
Genus							
*Lachnospiraceae*_unclassified	53.91	56.11	50.17	54.06	58.89	48.56	0.135
*Ruminococcaceae*_unclassified	9.11^{bc}	10.63^{bc}	17.96^{a}	15.09^{ab}	7.00^{c}	11.17^{abc}	<0.001
Ruminococcus2	6.74	6.52	4.41	5.13	6.53	7.13	0.585
Butyricicoccus	3.15	3.10	3.53	3.46	3.77	4.14	0.101
Blautia	3.66	2.25	3.27	2.38	3.98	4.66	0.082
*Clostridiales*_unclassified	2.69^{b}	2.89^{b}	2.89^{b}	4.29^{a}	2.98^{ab}	3.19^{ab}	0.014
Anaerostipes	3.17	2.93	3.17	2.97	3.000	2.99	0.997
Romboutsia	3.25^{ac}	3.65^{c}	1.75^{ab}	0.65^{b}	2.44^{ac}	3.67^{c}	<0.001
*Clostridium*_XVIII	2.42	0.81	1.02	2.27	1.79	1.99	0.091
*Erysipelotrichaceae*_unclassified	1.80	1.99	1.40	1.05	1.49	1.58	0.294

Note: Mean relative abundance (%) of the bacterial phylum and top 10 genera are shown, with 12 samples per treatment. Statistical significance was determined using one-way ANOVA and *post hoc* Tukey's test. Columns not sharing a common superscript are considered significantly different ($p < 0.05$).

Supplementary Table 2. Differential regulation of the cecal bacterial composition by antibiotics and ionophores.

Taxonomy	Control	Antibiotics	Ionophores	*P*-Value
Phylum				
Firmicutes	98.54	97.45	97.29	0.346
Proteobacteria	0.44	0.92	1.9	0.119
Bacteroidetes	0.61	0.93	0.55	0.478
Actinobacteria	0.15[a]	0.09[b]	0.12[ab]	0.003
Others	0.24[a]	0.59[a]	0.13[b]	0.016
Genera				
*Lachnospiraceae*_unclassified	53.91	53.43	53.73	0.988
*Ruminococcaceae*_unclassified	9.11[a]	14.54[b]	9.10[a]	0.002
Ruminococcus2	6.74	5.36	6.83	0.350
Butyricicoccus	3.15	3.36	3.96	0.028
Blautia	3.66[ab]	2.64[a]	4.32[b]	0.019
*Clostridiales*_unclassified	2.69	3.33	3.09	0.267
Anaerostipes	3.17	3.03	2.99	0.938
Romboutsia	3.25[ab]	2.05[a]	3.06[b]	0.019
*Clostridium*_XVIII	2.42	1.34	1.89	0.125
*Erysipelotrichaceae*_unclassified	1.80	1.49	1.53	0.644

Note: Mean relative abundance (%) of the bacterial phylum and top 10 genera are shown, with 12 samples per treatment. Statistical significance was determined using one-way ANOVA and *post hoc* Tukey's test. Columns not sharing a common superscript are considered significantly different ($p < 0.05$).

Supplementary Table 3. Regulation of the cecal bacterial composition by antimicrobials

Taxonomy	Control	Antimicrobials	*P*-Value
Phylum			
Firmicutes	98.54^a	97.39^b	0.013
Proteobacteria	0.44^a	1.32^b	0.008
Bacteroidetes	0.61	0.78	0.581
Actinobacteria	0.15	0.10	0.088
Others	0.24	0.41	0.115
Genera			
*Lachnospiraceae*_unclassified	53.91	53.55	0.887
*Ruminococcaceae*_unclassified	9.11^a	12.32^b	0.009
Ruminococcus2	6.74	5.95	0.568
Butyricicoccus	3.15	3.60	0.268
Blautia	3.66	3.32	0.591
*Clostridiales*_unclassified	2.69^a	3.23^b	0.037
Anaerostipes	3.17	3.01	0.771
Romboutsia	3.25	2.46	0.189
*Clostridium*_XVIII	2.42	1.56	0.206
*Erysipelotrichaceae*_unclassified	1.80	1.51	0.319

Note: Mean relative abundance (%) of the bacterial phylum and top 10 genera are shown, with 12 samples per treatment. Statistical significance was determined using Student's t-test. Columns not sharing a common superscript are considered significantly different ($p < 0.05$).