Supplemental Table S1 Bacterial counts (log cfu/g) in the crop, gizzard, ileum and ceca of broiler chickens fed with wheat based feed (WBF), maize based feed (MBF), maize feed with 15% crimped kernel maize silage (CKMS-15), and maize feed with 30% crimped kernel maize silage (CKMS-30) at different ages

	Diet					Day							P-value*	
Item	WBF	MBF	CKMS-15	CKMS-30	SE	8	15	22	25	29	36	SE	Diet	Day
Crop														
Coliform bacteria	5.2	5.0	5.1	5.0	0.32	5.4^{a}	5.0^{ab}	5.4^{a}	5.4^{a}	4.8^{b}	4.6^{b}	0.25	0.897	0.005
Lactose negative bacteria	4.2	4.0	4.3	4.1	0.16	4.7^{a}	4.1^{ab}	4.4^{ab}	4.3^{ab}	3.7^{b}	3.8^{b}	0.26	0.376	0.006
Lactic acid bacteria	9.0	8.9	9.0	8.8	0.09	8.9	9.0	8.9	8.9	8.9	8.8	0.11	0.228	0.795
Total anaerobic bacteria	8.8	8.7	8.8	8.7	0.10	8.8	8.8	8.8	8.7	8.7	8.6	0.12	0.467	0.554
Gizzard														
Coliform bacteria	4.0	3.6	3.8	3.6	0.24	3.9	3.4	3.7	3.8	3.7	3.7	0.27	0.355	0.641
Lactose negative bacteria	3.3	3.1	3.0	3.2	0.15	3.4	3.2	3.2	3.4	3.1	2.9	0.19	0.270	0.205
Lactic acid bacteria	7.5^{a}	7.0^{b}	7.2^{ab}	7.1^{b}	0.13	7.1	7.4	7.3	6.9	7.2	7.3	0.21	0.008	0.114
Total anaerobic bacteria	7.4^{a}	6.9^{b}	7.1^{b}	6.9^{b}	0.04	7.0	7.3	7.2	6.7	7.1	7.3	0.24	<0.001	0.164
Ileum														
Coliform bacteria	5.6	5.7	5.4	5.2	0.37	5.1	5.6	5.4	5.7	5.6	5.4	0.24	0.462	0.158
Lactose negative bacteria	5.1^{a}	4.8^{a}	4.6^{a}	4.4^{b}	0.18	4.5^{b}	5.4^{a}	4.7^{b}	4.6^{b}	4.7^{b}	4.2^{b}	0.22	0.014	<0.001
Clostridium perfringens	3.3	3.1	3.4	2.6	0.72	3.1	3.5	3.3	3.6	2.7	2.4	0.45	0.731	0.089
Lactic acid bacteria	8.6	8.5	8.6	8.5	0.08	8.6	8.6	8.6	8.5	8.6	8.5	0.11	0.505	0.840
Total anaerobic bacteria	8.4	8.4	8.3	8.3	0.11	8.5	8.3	8.5	8.2	8.5	8.4	0.12	0.442	0.063
Ceca														
Coliform bacteria	8.1	8.1	8.1	7.9	0.15	8.8^{a}	7.9^{bc}	7.8^{bc}	8.1^{b}	8.0^{b}	7.7^{c}	0.11	0.625	<0.001
Lactose negative bacteria	6.9^{a}	6.8^{ab}	6.8^{ab}	6.5^{b}	0.10	8.2^{a}	7.1^{b}	6.3^{c}	6.5^{c}	6.4^{c}	5.9^{d}	0.16	0.046	<0.001
Clostridium perfringens	3.4	3.2	3.8	2.9	0.59	3.5	3.5	3.6	3.7	2.9	2.8	0.47	0.542	0.301
Lactic acid bacteria	9.1	9.0	9.0	8.9	0.09	9.4^{a}	9.3^{a}	8.8^{b}	9.0^{b}	8.8^{b}	8.8^{b}	0.10	0.219	<0.001
Total anaerobic bacteria	9.8	10.0	9.7	9.9	0.15	10.1	9.9	9.6	9.8	9.9	9.7	0.18	0.333	0.183

$^{a-d}$ LSMeans within the same row with different superscripts differ significantly ($P \leq 0.05$)

*No significant interaction between day and diet was observed

Supplemental Table S2 pH, and concentrations (mmol/kg) of SCFA[1] and lactic acid in the contents of crop, gizzard, ileum and ceca of broilers fed with whole wheat based feed (WBF), maize based feed (MBF), maize feed with 15% crimped kernel maize silage (CKMS-15), and maize feed with 30% crimped kernel maize silage (CKMS-30) at different ages

	Diet					Day							P-value*	
Item	WBF	MBF	CKMS-15	CKMS-30	SE	8	15	22	25	29	36	SE	Diet	Day
Crop														
pH	5.0	5.2	5.0	4.9	0.08	5.1	4.9	5.0	5.1	5.1	4.9	0.11	0.080	0.136
Acetate	9.3^{ab}	7.9^{b}	10.4^{a}	11.1^{a}	1.14	9.9^{ab}	13.1^{a}	8.9^{b}	8.9^{b}	8.9^{b}	8.3^{b}	1.55	0.064	0.031
Propionate	0.2^{c}	0.3^{c}	0.8^{b}	1.7^{a}	0.15	ND	0.5	0.5	0.8	1.3	1.3	-	<0.001	-
Butyrate	0.1	0.1	0.3	0.1	0.11	ND	0.3	0.4	0.1	0.1	0.1	-	0.512	-
Isovalerate	0.2	0.3	0.3	0.2	0.11	0.7^{a}	0.3^{b}	0.1^{b}	0.2^{b}	0.1^{b}	0.1^{b}	0.13	0.714	<0.001
Lactate	48.8	36.1	45.7	49.6	6.01	46.3	45.0	47.3	44.4	42.2	45.1	8.01	0.171	0.995
Succinate	2.9	2.0	2.3	1.8	0.56	2.5^{ab}	3.6^{a}	1.9^{b}	1.2^{b}	1.8^{b}	2.5^{ab}	0.66	0.296	0.019
Gizzard														
pH	3.0	3.1	2.9	2.9	0.21	2.6^{b}	2.8^{ab}	2.9^{ab}	3.1^{ab}	3.2^{a}	3.2^{a}	0.19	0.758	0.009
Acetate	2.3	2.7	2.7	2.6	0.65	2.5	2.2	2.2	2.2	2.9	3.2	0.85	0.895	0.738
Propionate	0.2	0.4	0.3	0.4	0.19	0.1	ND	ND	0.1	0.6	1.1	-	0.637	-
Butyrate	0.10	0.40	0.33	0.66	0.27	0.3^{ab}	0.9^{a}	0.5^{ab}	0.5^{ab}	0.1^{b}	0.1^{b}	0.26	0.283	0.017
Lactic acid	7.1	4.1	5.6	6.9	1.62	4.7	6.6	8.2	4.6	6.4	5.1	2.12	0.271	0.488
Succinate	0.2	0.3	0.1	0.1	0.14	0.27	ND	ND	ND	0.1	0.7	-	0.806	-
Ileum														
pH	6.7	6.7	6.7	6.8	0.10	7.1^{a}	6.5^{b}	6.4^{b}	6.7^{b}	6.8^{ab}	6.8^{ab}	0.12	0.916	<0.001
Acetate	7.1^{b}	8.9^{a}	8.8^{a}	7.6^{ab}	0.69	7.2^{b}	5.9^{c}	7.5^{b}	7.9^{b}	9.3^{ab}	10.8^{a}	0.84	0.044	<0.001
Propionate	0.2	0.2	0.2	0.3	0.09	ND	ND	ND	ND	0.6^{a}	0.7^{b}	-	0.917	-
Butyrate	0.1	0.1	0.1	0.1	0.08	ND	0.1	0.1	0.0	ND	0.1	-	0.925	-
Lactate	29.7	26.6	32.9	29.7	5.14	24.5	26.1	33.9	28.9	32.3	32.5	5.81	0.688	0.530
Succinate	0.2	0.1	0.2	0.2	0.16	ND	ND	ND	ND	0.1^{b}	1.1^{a}	-	0.872	-

Ceca														
pH	6.1^{b}	6.4^{a}	6.5^{a}	6.3^{ab}	0.08	6.0^{b}	6.4^{a}	6.2^{ab}	6.3^{a}	6.4^{a}	6.3^{a}	0.10	<0.001	<0.001
Acetate	76.8	77.4	78.2	74.5	5.08	79.3	68.7	81.1	79.1	80.1	71.9^{b}	5.15	0.896	0.078
Propionate	4.9	5.2	5.3	4.6	0.36	0.9^{c}	3.2^{b}	6.0^{a}	6.3^{a}	7.3^{a}	6.3^{a}	0.72	0.305	<0.001
Butyrate	17.3	15.1	15.6	13.8	1.43	8.6^{c}	12.9^{b}	19.1^{a}	17.4^{ab}	18.1^{a}	16.4^{ab}	1.62	0.128	<0.001
Isovalerate	0.2	0.3	0.3	0.2	0.09	ND	0.1	0.3	0.3	0.3	0.3	0.01	0.691	-
Lactate	8.2	7.1	3.1	7.6	2.47	26.4^{a}	1.3^{b}	1.8^{b}	3.4^{b}	4.6^{b}	1.3^{b}	2.78	0.216	<0.001
Succinate	10.8	8.6	6.2	11.9	2.09	25.7^{a}	7.8^{b}	6.9^{b}	5.4^{b}	5.7^{b}	4.7^{b}	2.64	0.078	<0.001

[1] SCFA= short chain fatty acids

$^{a\text{-}c}$ LSMeans within the same row with different superscripts differ significantly ($P \leq 0.05$)

ND = Not detectable

*No significant interaction between day and diet was observed

Supplemental Table S3 Alpha diversity indices* (700 rarefaction depths) at day 8, 15, 22, 25, 29 and 36

	Day							
Indices	8	15	22	25	29	36	SE	P-value
PD whole tree	2.5^{c}	2.5^{c}	3.4^{a}	3.5^{a}	3.0^{b}	3.5^{a}	0.07	<0.001
Chao1	50.1^{b}	46.9^{b}	69.4^{a}	73.5^{a}	51.1^{b}	75.4^{a}	1.74	<0.001
Observed species	32.3^{b}	34.2^{b}	45.3^{a}	46.9^{a}	36.5^{b}	46.1^{a}	1.39	<0.001
Shannon	2.8^{c}	3.1^{b}	3.2^{a}	3.2^{a}	2.5^{d}	3.2^{a}	0.01	<0.001

$^{a\text{-}d}$ LSMeans within the same row with different superscripts differ significantly ($P \leq 0.05$)

*Pooled data of two treatments (MBF and CKMS-30) and four intestinal segments (crop, gizzard, ileum and ceca).

Supplemental Table S4 Relative abundance of bacteria in the upper digestive tract (crop and gizzard) of broilers at different ages

	Day							
Item	8	15	22	25	29	36	SE	P-value
Crop								
Firmicutes	97.4	97.8	98.3	98.3	98.4	97.4	0.91	0.751
Lactobacillaceae*	97.4	96.7	96.1	97.6	96.4	94.2	1.76	0.434
Lactobacillus	97.4	96.7	96.1	97.6	96.3	94.2	1.77	0.439
Planococcaceae	ND	1.0	2.2	0.6	1.8	1.7	0.80	-
Staphylococcaceae*								
Staphylococcus	ND	ND	0.1	0.02	0.1	1.1	0.36	-
Actinobacteria*								
Corynebacteriaceae								
Corynebacterium	ND	ND	0.03	0.02	0.2	0.9	0.25	-
Gizzard								
Firmicutes	88.9^{ab}	98.1^{a}	91.1^{ab}	90.0^{ab}	88.9^{ab}	86.9^{b}	3.31	0.031
Lactobacillaceae*								
Lactobacillus	64.2^{ab}	86.5^{a}	63.8^{ab}	62.3^{ab}	60.9^{b}	58.4^{b}	8.48	0.026
Lachnospiraceae	10.3^{a}	2.7^{b}	5.5^{ab}	4.8^{ab}	4.3^{ab}	2.3^{b}	2.57	0.047
Roseburia	6.3^{a}	1.2^{b}	2.1^{ab}	1.6^{b}	1.2^{b}	1.1^{b}	1.51	0.010
Blautia	1.7	0.2	0.6	0.6	0.1	0.2	0.62	0.132
Fusicatenibacter	1.1	0.4	1.1	0.8	1.3	0.3	0.45	0.164
Ruminococcaceae	9.3	3.8	6.2	8.8	8.7	4.7	2.77	0.238
Ruminococcus	7.4	2.8	4.0	4.6	4.9	2.1	2.00	0.153
Faecalibacterium	0.3^{b}	0.2^{b}	0.7^{b}	2.7^{a}	1.5^{ab}	1.7^{ab}	0.69	0.006
Enterococcaceae*								
Enterococcus	2.8	0.1	1.3	1.3	0.8	1.2	1.02	0.234
Clostridiaceae	0.6	1.3	1.3	1.4	2.5	3.3	0.97	0.115
Clostridium	0.4^{b}	1.3^{ab}	0.7^{ab}	0.9^{ab}	2.3^{ab}	3.2^{a}	0.97	0.044
Planococcaceae	0.01^{b}	3.4^{ab}	11.4^{a}	9.3^{ab}	9.5^{ab}	9.5^{ab}	3.65	0.025
Staphylococcaceae*								
Staphylococcus	ND	ND	0.2	0.4	0.8	4.8	-	-
Proteobacteria	10.6^{a}	1.4^{b}	5.7^{ab}	4.8^{ab}	3.4^{b}	2.4^{b}	2.16	0.002
Comamonadaceae	2.8^{a}	0.4^{b}	2.0^{ab}	0.9^{ab}	0.5^{ab}	0.6^{ab}	0.81	0.026
Moraxellaceae*								
Acenetobacter	1.9	0.2	0.9	1.4	1.0	5.0	0.57	0.068
Enterobacteriaceae	1.7	0.1	0.3	0.8	0.3	0.4	0.59	0.098
Escherichia	1.2	0.1	0.3	0.8	0.1	0.3	0.53	0.229
Sphingomonadaceae	1.6	0.1	1.6	1.0	0.5	0.4	0.59	0.064
Sphingomonas	0.9	0.1	1.2	0.4	0.2	0.1	0.47	0.119

Bacteroidetes	0.2^{b}	0.4^{ab}	1.3^{ab}	2.4^{ab}	3.2^{a}	0.8^{ab}	1.01	0.031
Rikenellaceae*								
Alistipes	0.1	0.2	1.2	2.2	2.8	0.4	0.99	0.061
Actinobacteria	0.2^{b}	0.1^{b}	1.4^{b}	1.3^{b}	2.9^{b}	9.5^{a}	1.95	<0.001
Corynebacteriaceae*								
Corynebacterium	ND	ND	0.6	0.8	0.5	3.7	-	-
Dermabacteraceae*								
Brachybacterium	ND	ND	0.6	0.3	1.8	2.5	-	-
Brevibacteriaceae*								
Brevibacterium	ND	ND	0.1	0.1	0.6	2.9	-	-
Tenericutes	0.1^{b}	0.1^{b}	0.4^{ab}	1.3^{a}	1.1^{ab}	0.3^{ab}	0.39	0.008

[1] Bacteria with a relative abundance of more than 1% in one the six sampling days are presented in the table

*99-100% sequences belong to their corresponding genus

$^{a-c}$LSMeans within the same row with different superscripts differ significantly ($P \leq 0.05$)

ND = not detectable

Supplemental Table S5 Relative abundance[1] of bacteria present in ileal content of broiler at different ages

	Day							
Item	8	15	22	25	29	36	SE	P-value
Firmicutes	97.7	93.8	97.4	97.1	96.4	97.2	2.58	0.675
Lactobacillaceae*								
Lactobacillus	61.3	65.9	72.6	73.3	67.3	67.7	10.54	0.874
Enterococcaceae*								
Enterococcus	25.3^a	0.6^b	2.2^b	2.4^b	1.8^b	0.9^b	4.04	<0.001
Lachnospiraceae	6.1	11.3	3.5	1.4	1.6	2.3	4.48	0.235
Roseburia	1.7	1.8	0.8	0.2	0.1	0.5	0.92	0.307
Clostridiaceae	4.7	16.7	11.7	12.0	18.4	19.3	6.03	0.171
Clostridium	1.5	11.6	7.9	10.8	15.5	18.1	5.54	0.074
Ruminococcaceae	2.0	3.1	1.7	1.3	2.4	1.3	1.37	0.753
Ruminococcus	1.5	1.8	0.9	0.5	1.2	0.5	0.80	0.501
Streptococcaceae*								
Streptococcus	1.2	0.1	0.7	1.7	2.5	4.7	1.82	0.176
Planococcaceae	0.0	1.5	6.2	5.1	3.2	1.5	2.13	0.063
Proteobacteria	2.2	5.4	0.6	1.0	1.0	0.6	2.23	0.251
Enterobacteriaceae*								
Escherichia	0.4	1.6	1.7	0.5	0.6	0.2	0.75	0.435
Actinobacteria	0.1	0.02	1.4	1.1	1.1	1.7	0.86	0.268
Corynebacteriaceae*								
Corynebacterium	ND	0.01	0.8	0.9	0.8	1.1	-	-

[1] Bacteria with a relative abundance of more than 1% in one the six sampling days are only presented in the table

*99-100% sequences belong to their corresponding genus

[a-c] LSMeans within the same row with different superscripts differ significantly ($P \leq 0.05$)

ND = not detectable

Supplemental Table S6 Relative abundance[1] of bacteria present in the ceca of broiler at different ages

	Day							
Item	8	15	22	25	29	36	SE	P-value
Firmicutes	93.4^{a}	96.3^{a}	71.6^{b}	70.1^{b}	57.5^{c}	75.4^{b}	5.14	<0.001
Lachnospiraceae	39.1^{a}	35.0^{ab}	27.3^{b}	20.1^{b}	19.5^{b}	22.7^{b}	3.03	<0.001
Roseburia	19.7^{a}	9.8^{b}	7.9^{bc}	5.7^{bc}	4.7^{c}	8.6^{bc}	1.76	<0.001
Blautia	9.8^{a}	3.9^{b}	2.4^{bc}	1.5^{bc}	1.0^{c}	1.6^{bc}	0.93	<0.001
Fusicatenibacter	4.8	8.1	8.7	5.34	4.8	4.1	1.93	0.108
Coprococcus	1.6^{a}	1.7^{a}	0.7^{ab}	0.6^{b}	0.56^{b}	1.0^{ab}	0.33	0.004
Ruminococcaceae	29.5^{ab}	43.9^{a}	32.5^{ab}	37.6^{ab}	28.4^{b}	36.1^{ab}	4.92	0.046
Ruminococcus	19.8	23.1	19.0	16.9	15.8	16.2	3.23	0.225
Oscillospira	5.9^{b}	9.9^{a}	4.5^{b}	5.5^{b}	4.4^{b}	5.9^{b}	1.19	<0.001
Butyricicoccus	2.0^{a}	1.6^{ab}	0.6^{b}	1.1^{ab}	0.5^{b}	1.1^{ab}	0.39	0.002
Faecalibacterium	0.4^{c}	4.2^{ab}	3.4^{b}	8.9^{a}	3.2^{b}	7.9^{ab}	1.81	<0.001
Ethanoligenes	0.7^{b}	2.3^{a}	1.3^{ab}	0.9^{b}	0.9^{b}	0.9^{b}	0.44	0.013
Lactobacillaceae[*]								
Lactobacillus	17.5^{a}	7.8^{b}	3.1^{bc}	3.1^{bc}	2.2^{c}	3.3^{bc}	1.79	<0.001
Streptococcaceae[*]								
Streptococcus	2.7^{a}	0.01^{b}	0.3^{b}	0.4^{b}	0.7^{b}	1.5^{ab}	0.64	0.003
Erysipelotrichaceae	2.01^{ab}	1.1^{b}	1.7^{b}	1.8^{ab}	1.5^{b}	3.2^{a}	0.49	0.005
Enterococcaceae[*]								
Enterococcus	1.7	0.1	0.1^{b}	0.04	ND	0.02	-	-
Clostridiaceae	0.7^{c}	5.7^{a}	4.3^{ab}	4.3^{ab}	3.1^{b}	4.8^{ab}	0.87	<0.001
Clostridium	0.7^{b}	4.7^{a}	3.4^{a}	3.3^{ab}	2.3^{b}	4.4^{a}	0.73	<0.001
Catabacteriaceae[*]								
Catabacter	ND	ND	0.4	0.6	0.4	1.2	-	-
Oscillospiraceae	ND	ND	0.8	0.4	0.2	1.0	-	-
Peptostreptococcaceae	ND	2.1	0.6	0.8	0.7	0.3	0.43	0.001
Proteobacteria	6.3^{a}	0.6^{b}	0.2^{b}	0.7^{b}	0.2^{b}	0.2^{b}	0.89	<0.001
Enterobacteriaceae	6.2^{a}	0.5^{b}	0.2^{b}	0.6^{b}	0.2^{b}	0.2^{b}	0.93	<0.001
Escherichia	4.9^{a}	0.5^{b}	0.2^{b}	0.6^{b}	0.2^{b}	0.2^{b}	0.81	<0.001
Bacteroidetes[*]								
Rikenellaceae								
Alistipes	0.1^{c}	1.8^{c}	23.6^{b}	21.2^{b}	35.7^{a}	20.2^{b}	5.04	<0.001
Tenericutes	0.1^{b}	1.1^{b}	4.3^{ab}	7.7^{a}	6.3^{a}	3.7^{ab}	1.8	0.002

[1] Bacteria with a relative abundance of more than 1% in one the six sampling days are presented in the table

[*] 99-100% sequences belong to their corresponding family and/or genus

$^{a-c}$LSMeans within the same row with different superscripts differ significantly ($P \leq 0.05$)

ND = not detectable