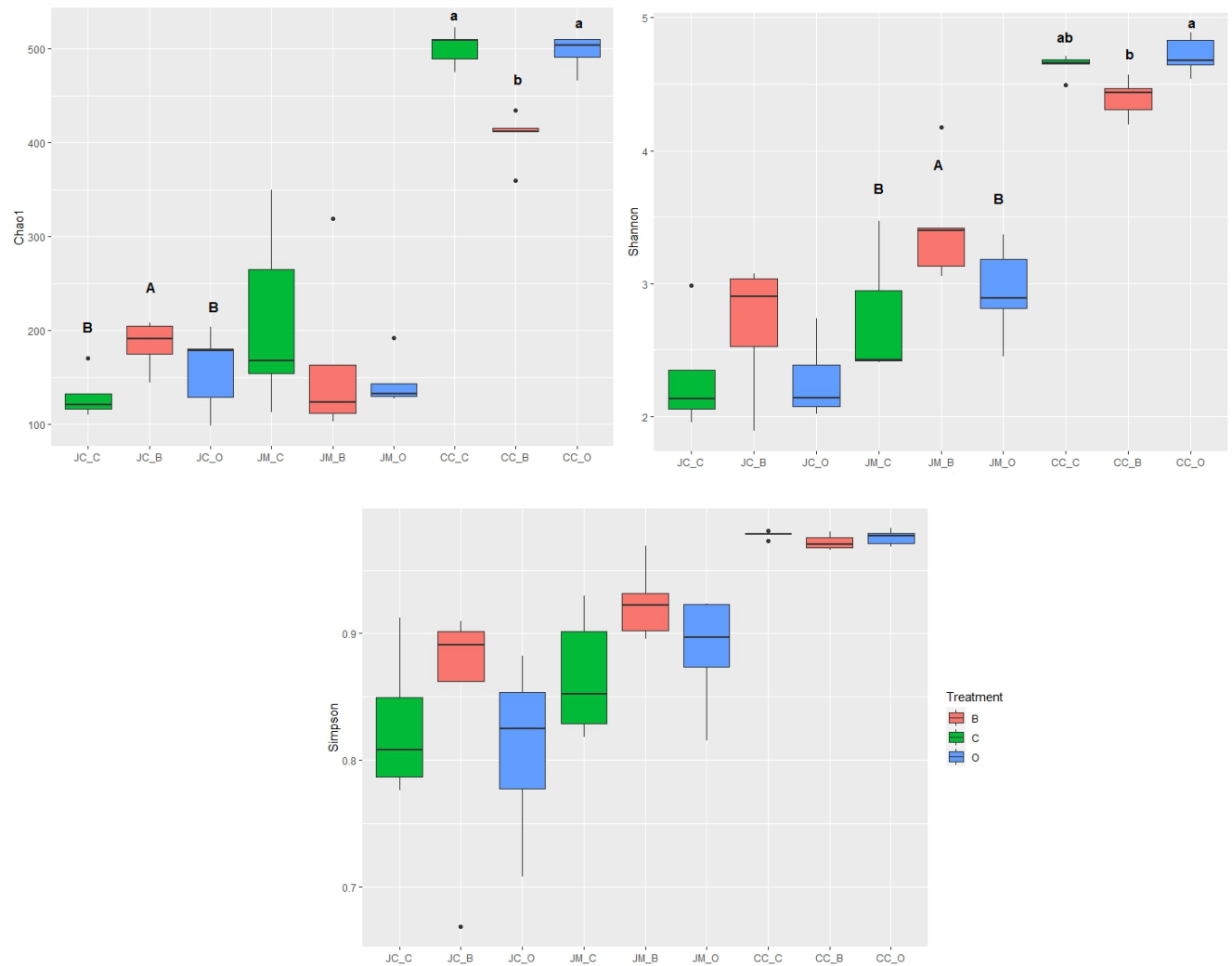# Supplementary Materials

Figure S1. Diversity indices of the intestinal microbiota of broiler chickens C—Control: maize—based diet; B: Barley—based diet; O: Oat—based diet. The values are the mean of relative abundances ± SD (standard deviation). Results of Kruskal—Wallis test (K—W) and the post hoc Dunn's multiple comparisons test with Bonferroni correction. a. b: values within the mean columns with different lowercase letters were significantly different ($p < 0.05$). A, B: p values between 0.05 and 0.1 were considered as a trend.
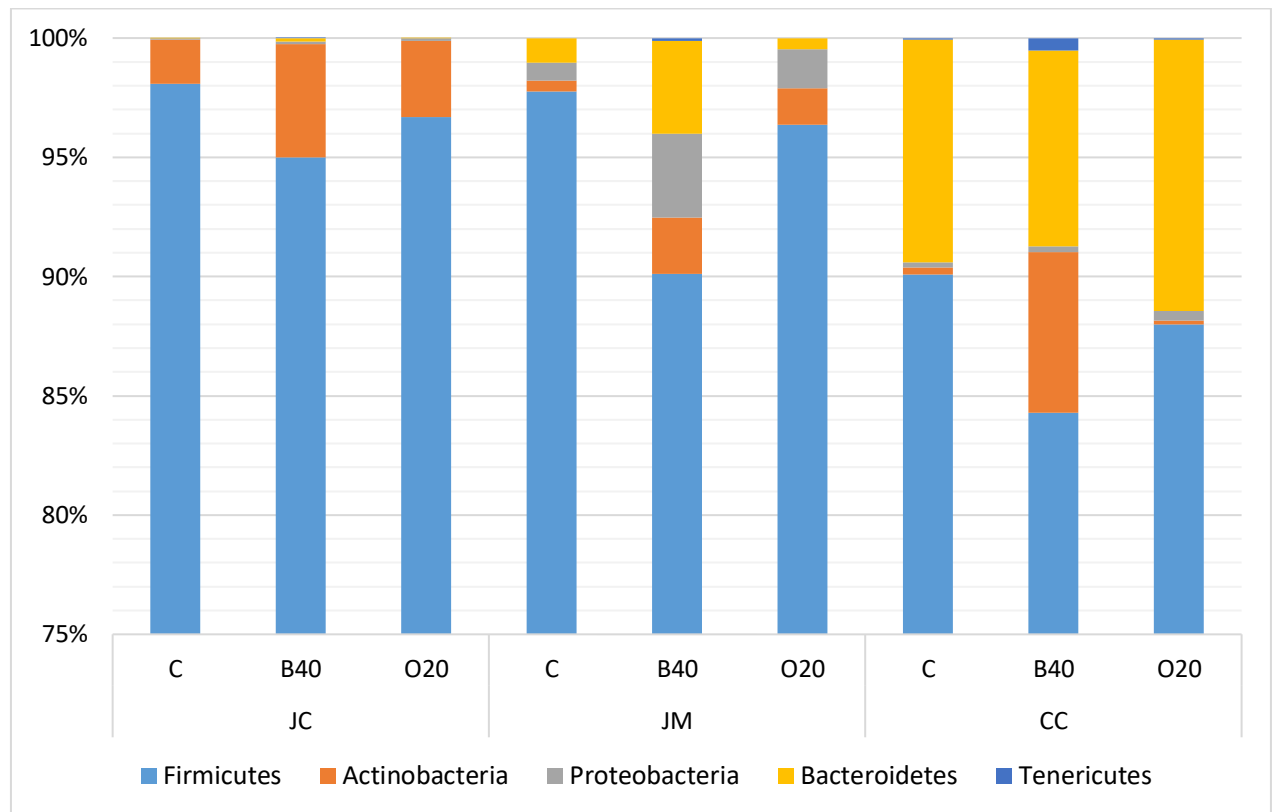
Figure S2. The most abundant phyla relative abundance of microbiota in the jejunum chymus (JC), jejunum mucosa (JM), and caecal chymus (CC) as affected by dietary treatments (C—Control, B—Barley, O—Oat feed supplementation).

Figure S3. Relative abundance of bacterial genera in the different sampling places of broiler chickens as affected by dietary treatments (%). Sampling places were marked jejunum chymus (JC), jejunum mucosa (JM), and caecal chymus (CC) as affected by dietary treatments (C—Control, B—Barley, O—Oat feed supplementation).
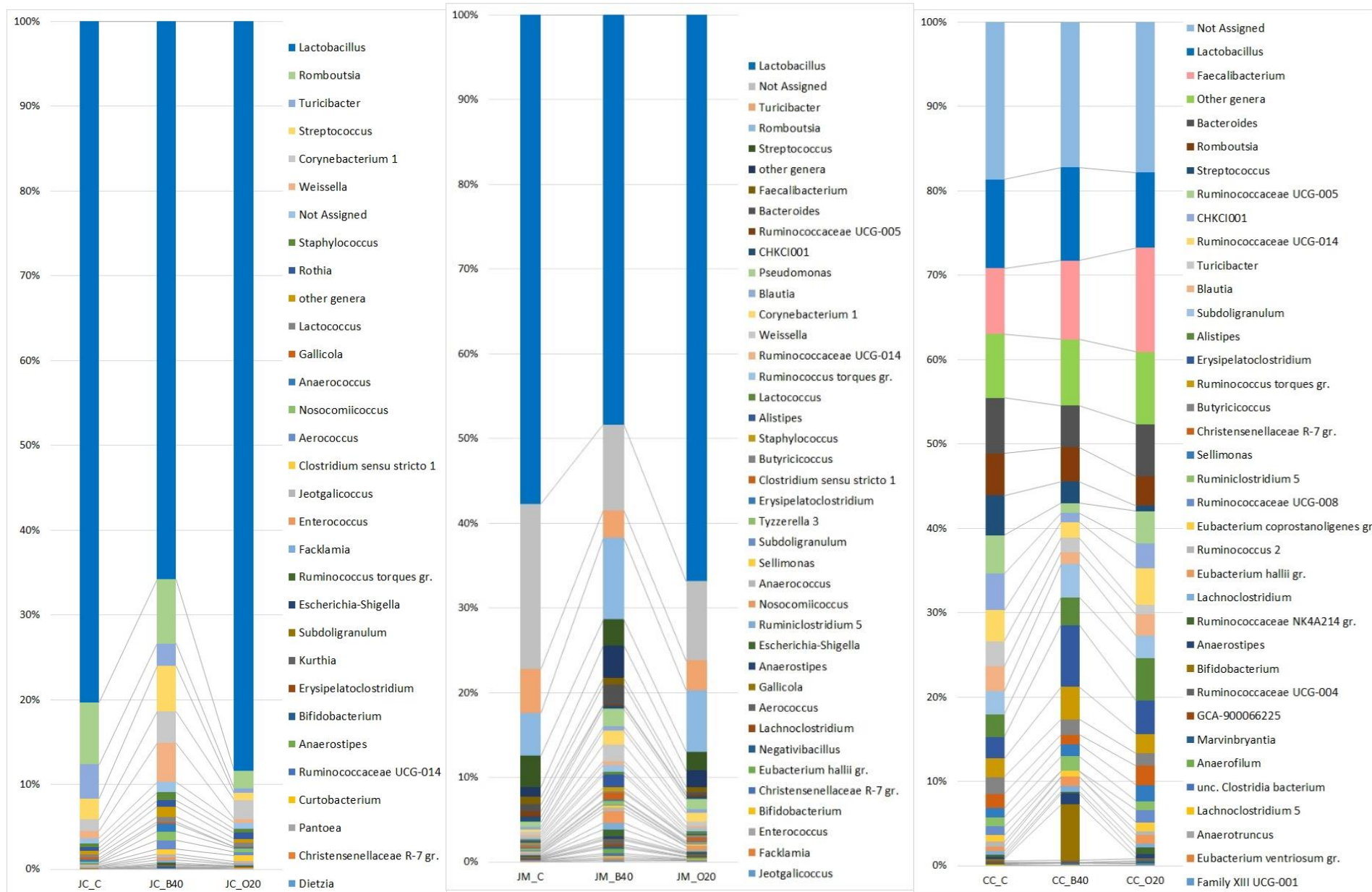
Table S1. Relative abundance of bacterial genera in jejunum chymus of broiler chickens as affected by dietary treatments (%).

Phylum Class Order	Family	Genus	C	B	O	Pooled SEM	Sig.
Actinobacteria Actinobacteria	Bifidobacteriaceae	Bifidobacterium	0.01 [b]	0.11 [a]	0.01 [b]	0.03	**0.019**
	Corynebacteriaceae	Corynebacterium 1	1.35	3.75	2.25	0.97	0.221
	Dietziaceae	Dietzia	0.00 [b]	0.01 [a]	0.00 [b]	0.00	**0.032**
	Microbacteriaceae	Curtobacterium	0.00 [b]	0.01 [ab]	0.13 [a]	0.03	**0.004**
	Micrococcaceae	Rothia	0.43	0.72	0.71	0.23	0.677
Firmicutes Bacilli Bacillales	Planococcaceae	Kurthia	0.01	0.14	0.07	0.08	0.951
	Staphylococcaceae	Jeotgalicoccus	0.12	0.34	0.26	0.13	0.611
		Nosocomiicoccus	0.16	1.04	0.43	0.41	0.269
		Staphylococcus	0.48	0.97	0.46	0.27	0.468
Bacilli Lactobacillales	Aerococcaceae	Aerococcus	0.16	1.01	0.42	0.22	0.194
		Facklamia	0.08	0.32	0.16	0.10	0.195
	Enterococcaceae	Enterococcus	0.09	0.32	0.09	0.08	0.257
	Lactobacillaceae	Lactobacillus	80.31	65.81	88.38	6.39	0.137
	Leuconostocaceae	Weissella	0.86	4.58	0.44	1.89	0.482
	Streptococcaceae	Lactococcus	0.39	0.63	0.41	0.18	0.949
		Streptococcus	2.48	5.35	0.85	1.85	0.141
Clostridia Clostridiales	Christensenellaceae	Christensenellaceae R-7 gr.	0.00 [b]	0.03 [a]	0.00 [b]	0.01	**0.031**
	Clostridiaceae 1	Clostridium sensu stricto 1	0.15	0.63	0.70	0.46	0.326
	Family XI	Anaerococcus	0.23	0.90	0.14	0.25	0.267
		Gallicola	0.26	0.22	0.07	0.16	0.566
	Lachnospiraceae	Anaerostipes	0.00	0.03	0.00	0.01	0.096
		Ruminococcus torques gr.	0.03 [b]	0.16 [a]	0.06 [ab]	0.05	**0.023**
	Peptostreptococcaceae	Romboutsia	7.31	7.59	2.08	3.40	0.543
	Ruminococcaceae	Ruminococcaceae UCG-014	0.00	0.03	0.00	0.01	0.066
		Subdoligranulum	0.02	0.06	0.02	0.01	0.092
Erysipelotrichia Erysipelotrichia	Erysipelotrichaceae	Erysipelatoclostridium	0.01 [b]	0.07 [a]	0.03 [ab]	0.01	**0.019**
		Turicibacter	4.03	2.63	0.54	1.25	0.193
Proteobacteria Gammaproteobacteria	Enterobacteriaceae	Escherichia-Shigella	0.02	0.10	0.02	0.02	0.061
		Pantoea	0.00	0.02	0.07	0.02	0.064
Not Assigned	Not Assigned	Not Assigned	0.59	1.20	0.71	0.38	0.650
		other genera	0.42	1.22	0.51	0.58	
			100.00	100.00	100.00		

C-Control: maize-based diet; B: Barley-based diet; O: Oat-based diet. The values are the mean of relative abundances ± SEM (standard error of the mean). Results of Kruskal-Wallis test and the post hoc Dunn's multiple comparisons test with Bonferroni correction. a, b: values within the mean rows with different lowercase letters were significantly different (p < 0.05). Results between 0.05 and 0.1 (0.05 < p < 0.10) were considered a trend (T).

Table S2. Relative abundance of bacterial genera in jejunum mucosa of broiler chickens as affected by dietary treatments (%).

Phylum / Class / Order	Family	Genus	C	B	O	Pooled SEM	Sig.
Actinobacteria Actinobacteria	Bifidobacteriaceae	Bifidobacterium	0.05	0.24	0.03	0.11	0.906
	Corynebacteriaceae	Corynebacterium 1	0.31	1.65	1.05	0.80	0.457
	Nocardiaceae	Rhodococcus	0.01	0.05	0.00	0.02	0.100
	Microbacteriaceae	Curtobacterium	0.01 [b]	0.06 [ab]	0.14 [a]	0.03	**0.031**
	Micrococcaceae	Rothia	0.03	0.24	0.13	0.10	0.362
	Propionibacteriaceae	Cutibacterium	0.01 [b]	0.03 [ab]	0.09 [a]	0.02	**0.039**
Bacteroidetes Bacteroidia Bacteroidales	Bacteroidaceae	Bacteroides	0.80	2.35	0.33	0.77	0.262
	Rikenellaceae	Alistipes	0.22	1.48	0.15	0.83	0.883
Firmicutes Bacilli Bacillales	Staphylococcaceae	Jeotgalicoccus	0.04	0.18	0.14	0.10	0.329
		Nosocomiicoccus	0.11	1.33	0.47	0.66	0.844
		Staphylococcus	0.21	0.46	0.11	0.17	0.784
Firmicutes Bacilli Lactobacillales	Aerococcaceae	Aerococcus	0.07	0.54	0.23	0.20	0.094
		Facklamia	0.05	0.15	0.12	0.09	0.547
		Globicatella	0.01	0.12	0.10	0.07	0.326
	Enterococcaceae	Enterococcus	0.05	0.16	0.04	0.04	0.694
	Lactobacillaceae	Lactobacillus	57.70	48.36	66.86	8.20	0.289
	Leuconostocaceae	Weissella	0.29	1.95	0.52	0.71	0.174
	Streptococcaceae	Lactococcus	0.24	0.34	0.36	0.14	0.961
		Streptococcus	3.76	3.10	2.21	1.10	0.691
Firmicutes Clostridia Clostridiales	Christensenellaceae	Christensenellaceae R-7 gr.	0.06	0.28	0.03	0.15	0.887
	Clostridiaceae 1	Candidatus Arthromitus	0.04	0.05	0.18	0.06	0.280
		Clostridium sensu stricto 1	0.17	0.80	0.45	0.37	0.378
	Clostridiales vadinBB60 gr.	uncultured bacterium	0.04	0.11	0.07	0.07	0.896
	Family XI	Anaerococcus	0.12	0.46	0.03	0.15	0.161
		Gallicola	0.08	0.15	0.07	0.07	0.670
	Lachnospiraceae	Anaerostipes	0.10	0.27	0.09	0.12	0.676
		Blautia	0.36	0.51	0.48	0.12	0.468
		CHKCI001	0.62	0.40	0.28	0.27	0.619
		Eubacterium hallii gr.	0.06	0.59	0.20	0.21	0.301
		GCA-900066575	0.02	0.19	0.01	0.09	0.624
		Lachnoclostridium	0.07	0.26	0.06	0.12	0.873
		Ruminococcus torques gr.	0.25	0.84	0.33	0.33	0.331
		Sellimonas	0.12	0.28	0.20	0.11	0.318
		Tyzzerella	0.03	0.13	0.02	0.05	0.846
		Tyzzerella 3	0.15	0.42	0.06	0.22	0.680
	Peptostreptococcaceae	Romboutsia	5.01	9.62	7.31	3.45	0.763
	Ruminococcaceae	Butyricicoccus	0.20	0.20	0.12	0.08	0.793
		DTU089	0.01	0.10	0.01	0.05	0.681
		Eubacterium coprostanoligenes gr.	0.04	0.18	0.03	0.07	0.531
		Faecalibacterium	0.89	0.78	0.64	0.47	0.756
		GCA-900066225	0.02 [a]	0.00 [b]	0.00 [b]	0.01	**0.032**
		Negativibacillus	0.06	0.20	0.07	0.07	0.934
		Oscillibacter	0.03	0.10	0.10	0.06	0.200
		Ruminiclostridium 5	0.10	0.79	0.19	0.41	0.789
		Ruminococcaceae UCG-004	0.00	0.07	0.00	0.02	0.076
		Ruminococcaceae UCG-005	0.65	0.12	0.18	0.26	0.537
		Ruminococcaceae UCG-014	0.26	0.43	0.27	0.18	0.954
		Ruminococcus 1	0.00	0.11	0.04	0.03	0.243
		Subdoligranulum	0.15	0.11	0.14	0.08	0.551
Firmicutes	Erysipelotrichaceae	Erysipelatoclostridium	0.16	0.14	0.12	0.07	0.884

			C	B	O	SEM	p-value
Erysipelotrichia Erysipelotrichales		Turicibacter	5.21	3.21	3.50	1.90	0.527
Proteobacteria Alphaproteobacteria	Beijerinckiaceae	Methylobacterium	0.00 [b]	0.02 [ab]	0.10 [a]	0.02	**0.044**
	Rhodobacteraceae	Paracoccus	0.00	0.09	0.01	0.02	0.063
	Sphingomonadaceae	Sphingomonas	0.02	0.11	0.14	0.07	0.083
Proteobacteria Gammaproteobacteria	Enterobacteriaceae	Escherichia-Shigella	0.10	0.83	0.15	0.28	0.522
	Moraxellaceae	Enhydrobacter	0.01	0.06	0.00	0.01	0.100
	Pseudomonadaceae	Pseudomonas	0.55 [b]	2.08 [a]	1.17 [ab]	0.38	**0.046**
Not Assigned			19.48	10.15	9.33	4.86	0.468
other genera			0.81	1.99	0.77	1.30	
			100.00	100.00	100.00		

C-Control: maize-based diet; B: Barley-based diet; O: Oat-based diet. The values are the mean of relative abundances ± SEM (standard error of the mean). Results of Kruskal-Wallis test and the post hoc Dunn's multiple comparisons test with Bonferroni correction. a, b: values within the mean rows with different lowercase letters were significantly different (p < 0.05). Results between 0.05 and 0.1 (0.05 < p < 0.10) were considered a trend (T).