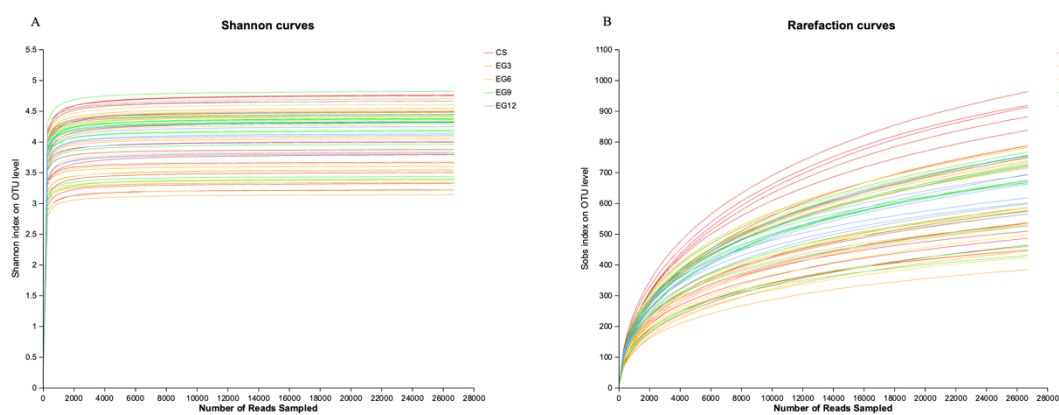
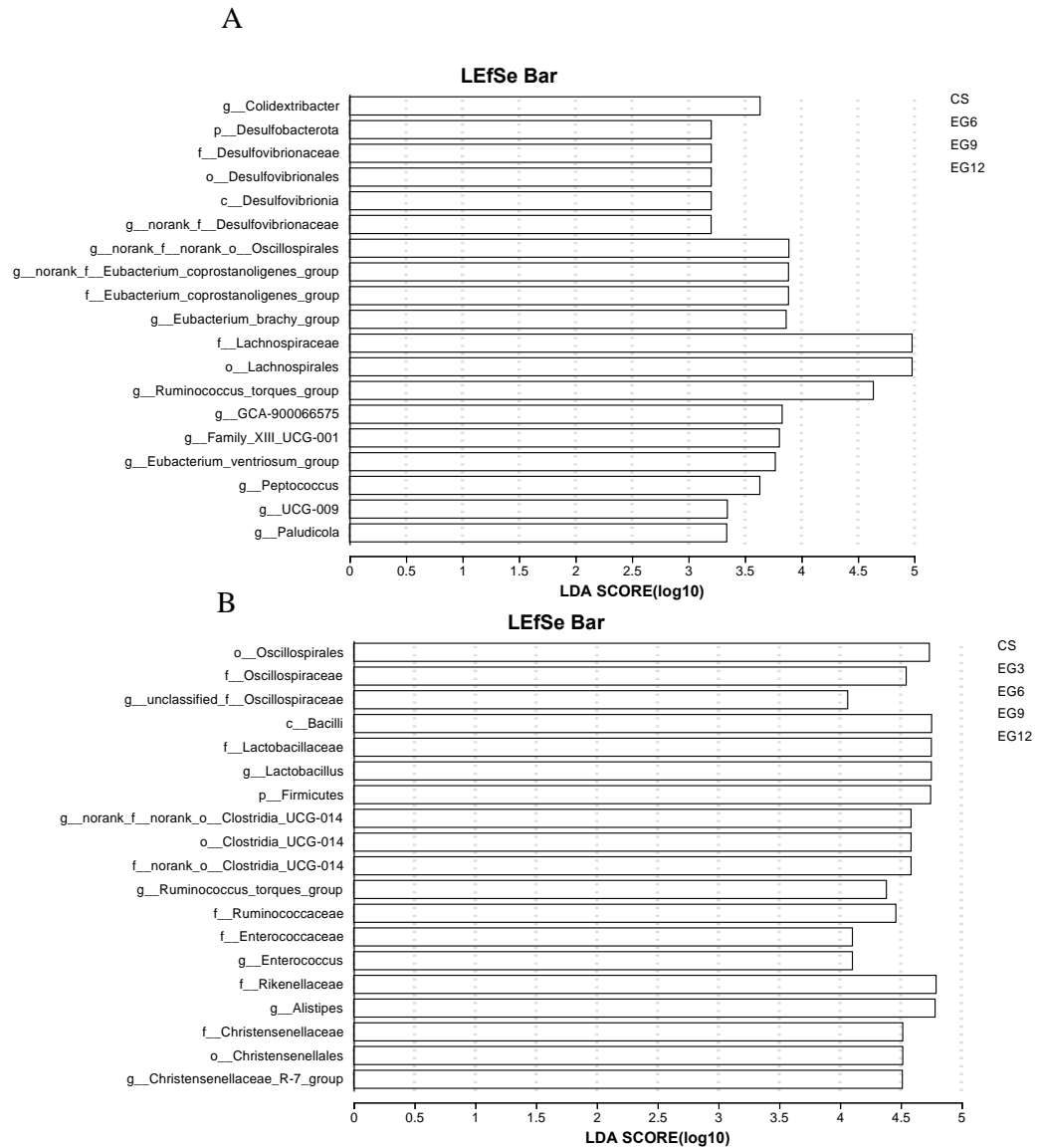


**Supplementary Figure S1:** Standard curves for SCFAs.(A,acetate; B, propionate; C, butyrate; D isobutyrate; E valerate; F isovalerate.)



**Supplementary Figure S2:** Dilution curves for sequencing of broiler cecum contents (with Shannon and Sobs indices).



**Supplementary Figure S3: LDA Discriminant Bar Chart of Cecal Microbiota in Broilers at 21 and 42 Days Old**

**Supplementary Table S1:** Amino acid Composition of Edible Grass( air-dried basis).

Items	Edible Grass	Soybean meal	Corn
Arg, %	1.26	3.19	0.38
His, %	0.90	1.09	0.23
Ile, %	1.24	1.80	0.26
Leu, %	2.19	3.26	1.03
Lys, %	0.93	2.66	0.26
Met, %	0.27	0.62	0.19
Cys, %	0.39	0.68	0.22
Phe, %	1.44	2.23	0.43
Tyr, %	0.87	1.57	0.34
Thr, %	1.19	1.92	0.31
Trp, %	/	0.64	0.08
Val, %	1.58	1.99	0.40

Note: The data on soybean meal and corn is sourced from the "Chicken Feeding Standard" (NY/T 33-2004) of the People's Republic of China.

**Supplementary Table S2:** Microbial  $\alpha$ -diversity in the cecum of 21- and 42-day-old broilers

Index type	CS	EG3	EG6	EG9	EG12	p-Value
21d-sobs	502.70±47.07	506.3±76.85	516.5±72.29	554.3±101.00	623.5±47.53	0.035
21d-shannon	3.59±0.31	3.49±0.34	3.69±0.40	3.938±0.44	4.16±0.33	0.054
21d-simpson	0.11±0.06	0.13±0.07	0.10±0.04	0.08±0.04	0.06±0.03	0.172
21d-ace	645±85.47	654.3±91.38	650±106.1	683.9±122	776.8±58.18	0.063
42d-sobs	883.2±63.03	711.3±90.83	742.5±26.88	719.8±38.96	722.3±38.24	0.007
42d-shannon	4.46±0.37	4.44±0.22	4.461±0.11	4.42±0.21	4.31±0.20	0.530
42d-simpson	0.05±0.03	0.04±0.01	0.03±0.01	0.04±0.01	0.05±0.02	0.371
42d-ace	1114±72.32	930.7±148.1	957.4±41.72	952.1±67.2	961.5±57.07	0.007

**Supplementary Table S3:** The composition and percentage of cecal microbiota at the phylum level in broilers at 21-days-old of age.

Phylum name	CS	EG3	EG6	EG9	EG12	p-Value	p-adjust
F_ <i>Firmicutes</i>	85.88±7.92	89.21±4.92	83.88±12.49	88.79±7.05	91.43±5.11	0.441	0.687
F_ <i>Bacteroidota</i>	12.57±6.66	8.47±3.68	7.68±4.92	9.84±7.09	12.47±6.66	0.384	0.687
F_ <i>Proteobacteria</i>	0.88±1.63	1.86±2.44	1.07±0.51	0.27±0.23	0.22±0.16	0.700	0.778

**Supplementary Table S4:** The composition and percentage of cecal microbiota at the phylum level in broilers at 42-days-old of age.

Phylum name	CS	EG3	EG6	EG9	EG12	p-Value	p-adjust
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F_Firmicutes	76.49±9.64	86.7±4.41	84.34±8.56	83.27±7.85	74.97±5.93	0.042	0.138
F_Bacteroidota	21.23±10.33	22.88±5.13	13.65±8.13	8.43±0.06	22.88±5.13	0.06	0.16
F_Desulfobacterota	1.26±0.63	0.24±1.18	0.94±1.03	1.03±0.70	0.77±0.14	0.456	0.495
F_Proteobacteria	0.25±0.03	0.43±0.36	0.18±0.14	1.53±1.23	0.94±0.43	0.179	0.332

**Supplementary Table S5:** Tests for multiple differences in cecum microbial diversity in 21-day-old broilers(Kruskal-Wallis H), Mean±Sd%

Genus name	CS	EG3	EG6	EG9	EG12	p-Value	p-adjust
<i>g_Ruminococcus_torques_group</i>	3.03±1.20	6.36±7.16	7.43±4.90	10.79±7.12	7.67±3.23	0.024	0.3215
<i>g_norank_f_Eubacterium_coprostanoligenes_group</i>	0.17±0.09	0.88±1.32	1.52±0.94	0.92±0.39	1.51±0.38	0.006	0.3027
<i>g_Colidextribacter</i>	1.43±0.69	0.67±0.33	0.56±0.23	1.20±0.40	0.95±0.57	0.025	0.3215
<i>g_GCA-900066575</i>	0.51±0.38	0.37±0.23	0.20±0.15	0.35±0.13	1.44±0.61	0.005	0.3027

**Supplementary Table S6:** Tests for multiple differences in cecum microbial diversity in 42-day-old broilers(Kruskal-Wallis H), Mean±Sd%

Genus name	CS	EG3	EG6	EG9	EG12	p-Value	p-adjust
<i>g_Alistipes</i>	16.41±10.95	8.19±3.58	9.54±4.27	11.94±7.98	20.53±5.97	0.036	0.2148
<i>g_norank_f_norank_o_Clostridia_UCG-014</i>	4.94±1.33	10.77±4.92	12.64±7.08	8.67±3.39	10.26±2.99	0.023	0.1750
<i>g_Christensenellaceae_R-7_group</i>	2.88±1.44	4.83±1.16	8.06±3.02	8.15±3.86	9.71±3.13	0.003	0.0802
<i>g_Lactobacillus</i>	7.00±8.81	13.09±8.85	6.92±4.30	2.13±2.15	3.52±2.75	0.024	0.1781
<i>g_Ruminococcus_torques_group</i>	4.98±0.98	4.45±2.19	7.42±2.17	5.16±2.56	2.64±1.20	0.012	0.1291
<i>g_unclassified_f_Oscillospiraceae</i>	3.81±3.79	3.81±3.79	3.08±1.086	1.26±1.52	1.42±0.85	0.021	0.1685
<i>g_Lachnoclostridium</i>	1.19±0.38	1.38±0.34	2.25±0.68	2.27±1.27	2.05±0.58	0.007	0.1291
<i>g_Shuttleworthia</i>	1.34±0.78	1.66±0.85	0.73±0.24	0.82±0.40	0.83±0.33	0.039	0.2195
<i>g_norank_f_Erysipelotrichaceae</i>							
<i>g_Enterococcus</i>	0.08±0.08	0.67±0.87	0.15±0.26	1.90±3.56	1.37±0.87	0.009	0.1291
<i>g_Parabacteroides</i>	0.89±0.55	0.83±1.55	1.55±2.87	0.09±0.07	0.33±0.26	0.011	0.1291
<i>g_Colidextribacter</i>	1.31±0.32	0.63±0.29	0.78±0.43	0.47±0.31	0.26±0.10	<0.001	0.053