Chlortetracycline promotes differentiation of intestinal bacterial community in broiler chicken

Ruonan Zhao
South China Agricultural University
Siyuan Chen
South China Agricultural University
TianTian Xu
South China Agricultural University
Jie Hao
South China Agricultural University
Hongbin Si
South China Agricultural University
Zhenling Zeng
South China Agricultural University
wenguang xiong (xiongwg@scau.edu.cn)
South China Agricultural University https://orcid.org/0000-0002-8965-2915

Research

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Abstract

Background Chlortetracycline is widely used for disease treatment and prevention in animal production system. However, the impact of chlortetracycline on gastrointestinal tract microbial communities of growing chickens has not been fully explored.

Results Chickens received 5-day-course of chlortetracycline at actual therapeutic dose/low doses. By using 16S-rRNA sequencing-based approach, We found the predominant Firmicutes and Oscillospira significantly increased, while Shigella significantly decreased in the therapeutic-dose group. The main responders at phylum level to the chlortetracycline were Proteobacteria in the therapeutic-dose group and Firmicutes in the low-dose group. The therapeutic-dose of chlortetracycline significantly increased the α-diversity index including Shannon diversity index, Chao1 index and PD whole tree index. Both therapeutic and low dose increased the Weighted Unifrac distance.

Conclusions The significantly changed bacterial community diversity indicated chlortetracycline promoted differentiation of bacterial community in broiler chicken gut. We provided a comprehensive understanding on chlortetracycline-induced changes of gastrointestinal tract microbial communities of growing chickens to optimize the use of antibiotics in health management programs in broiler industry.

Full Text

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Figures

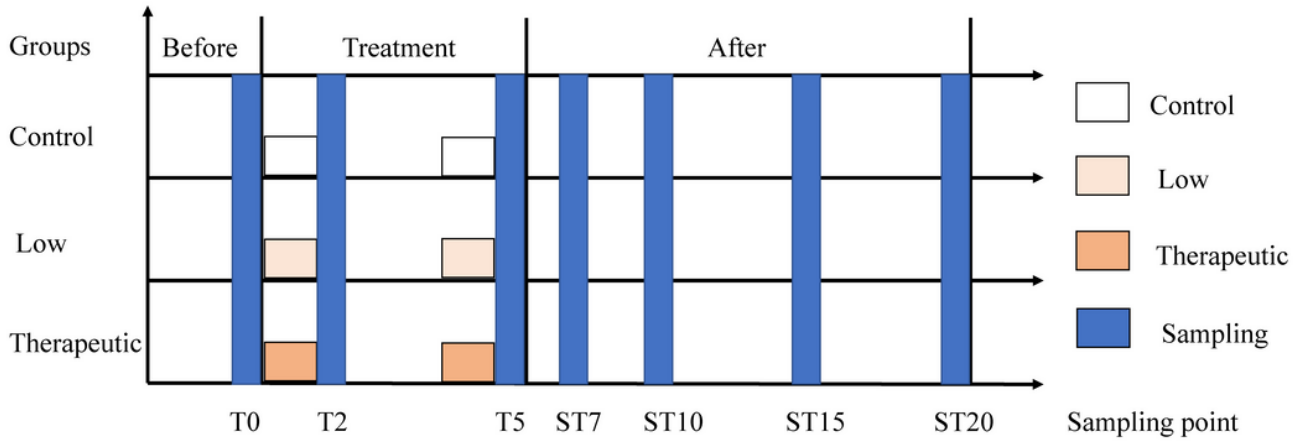
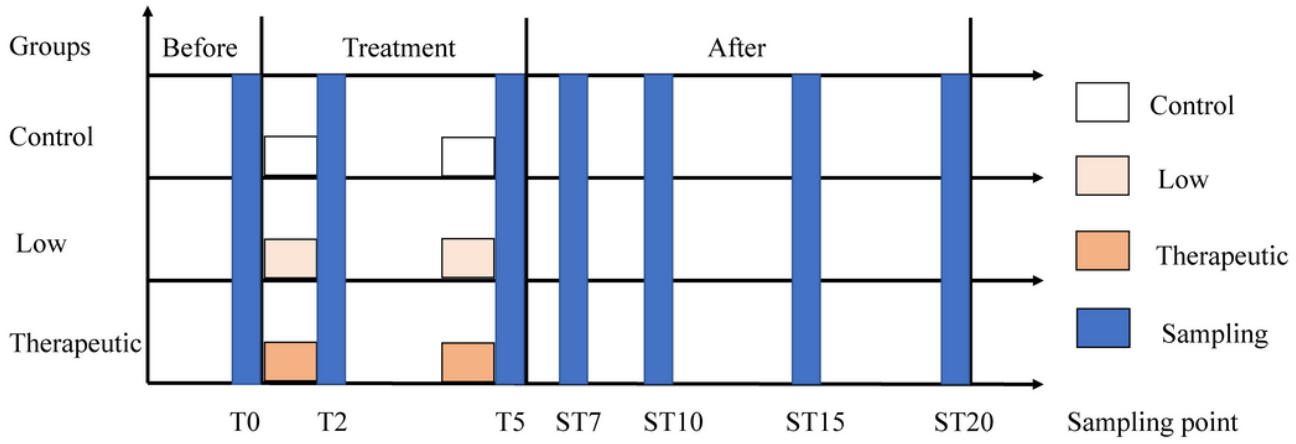


Figure 1

Animal groups with chlortetracycline administration and sampling time points. 560 The 54 chickens were divided into three groups. Each group had three replicates. each replicate had six chickens. A 5-day course of chlortetracycline was administered at 2 g/L (the therapeutic-dose group) and 0.2 g/L (the low-dose group) in the drinking water. Mixed fresh feces from six chickens in each cage were collected on seven time points: T0 (day 0, before treatment), T2 (day2, during treatment), T5 (day5, during treatment), ST7 (day7, during stopped treatment), ST10 (day10, during stopped treatment), ST15 (day15, during stopped treatment), ST20 (day20, during stopped treatment).



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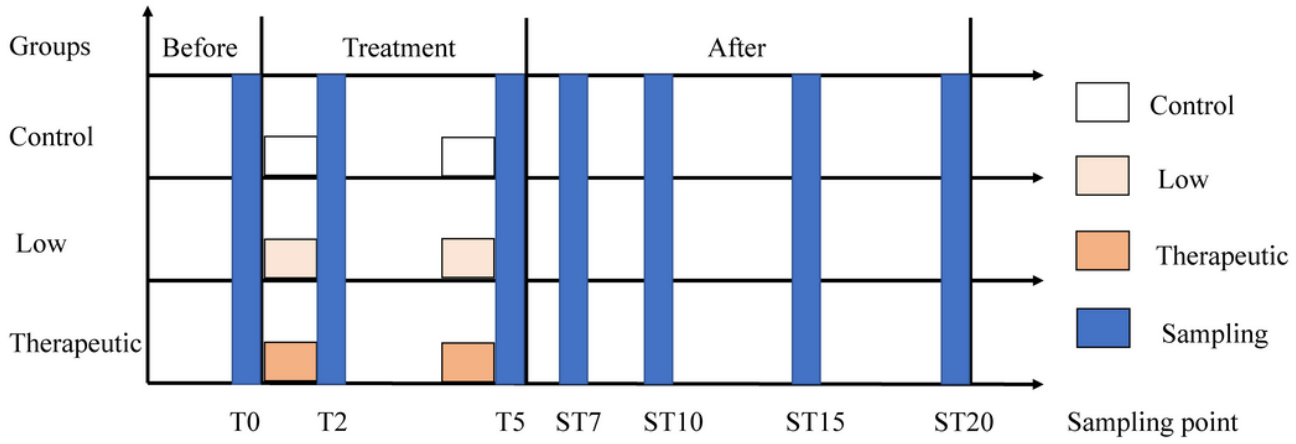

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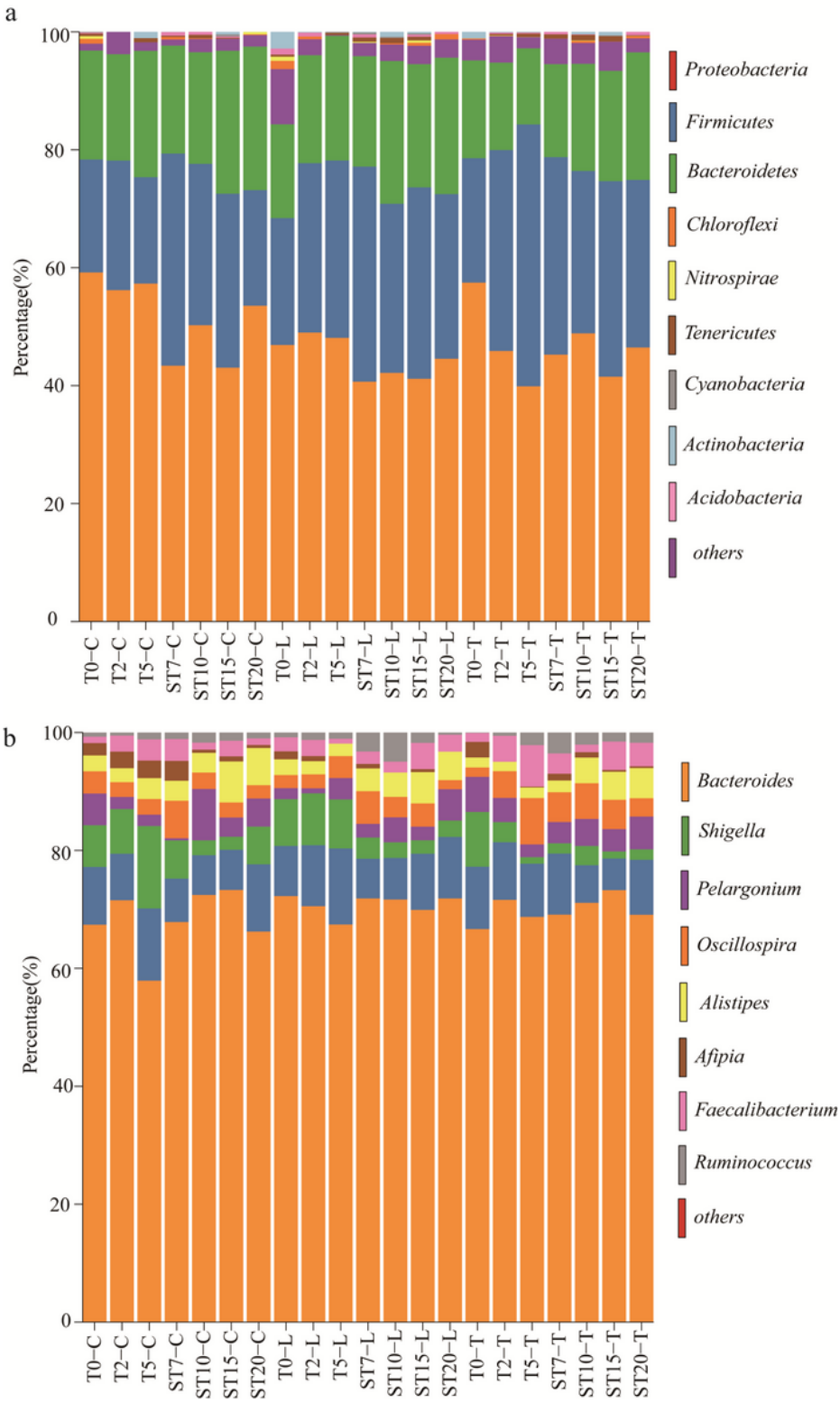

Figure 2

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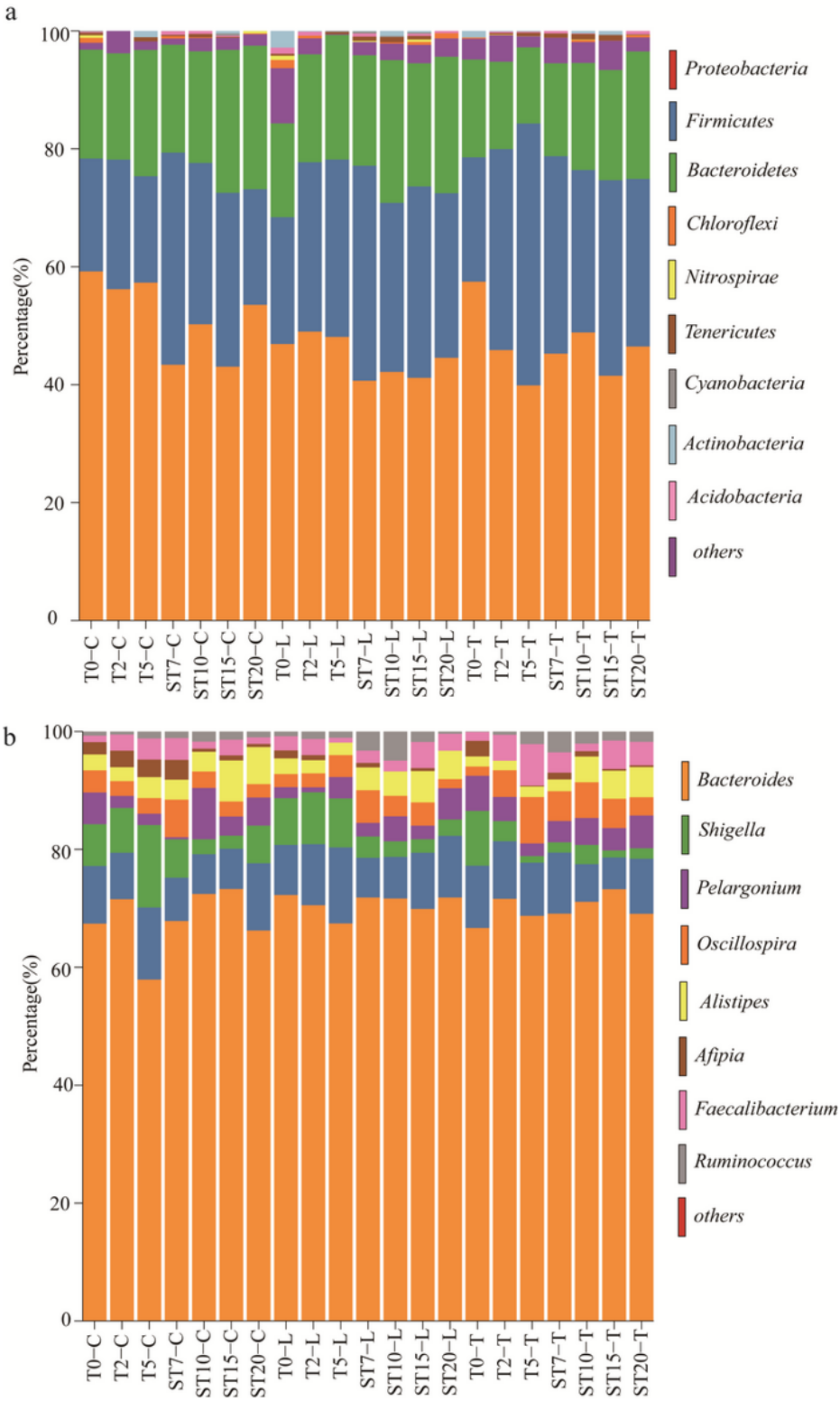

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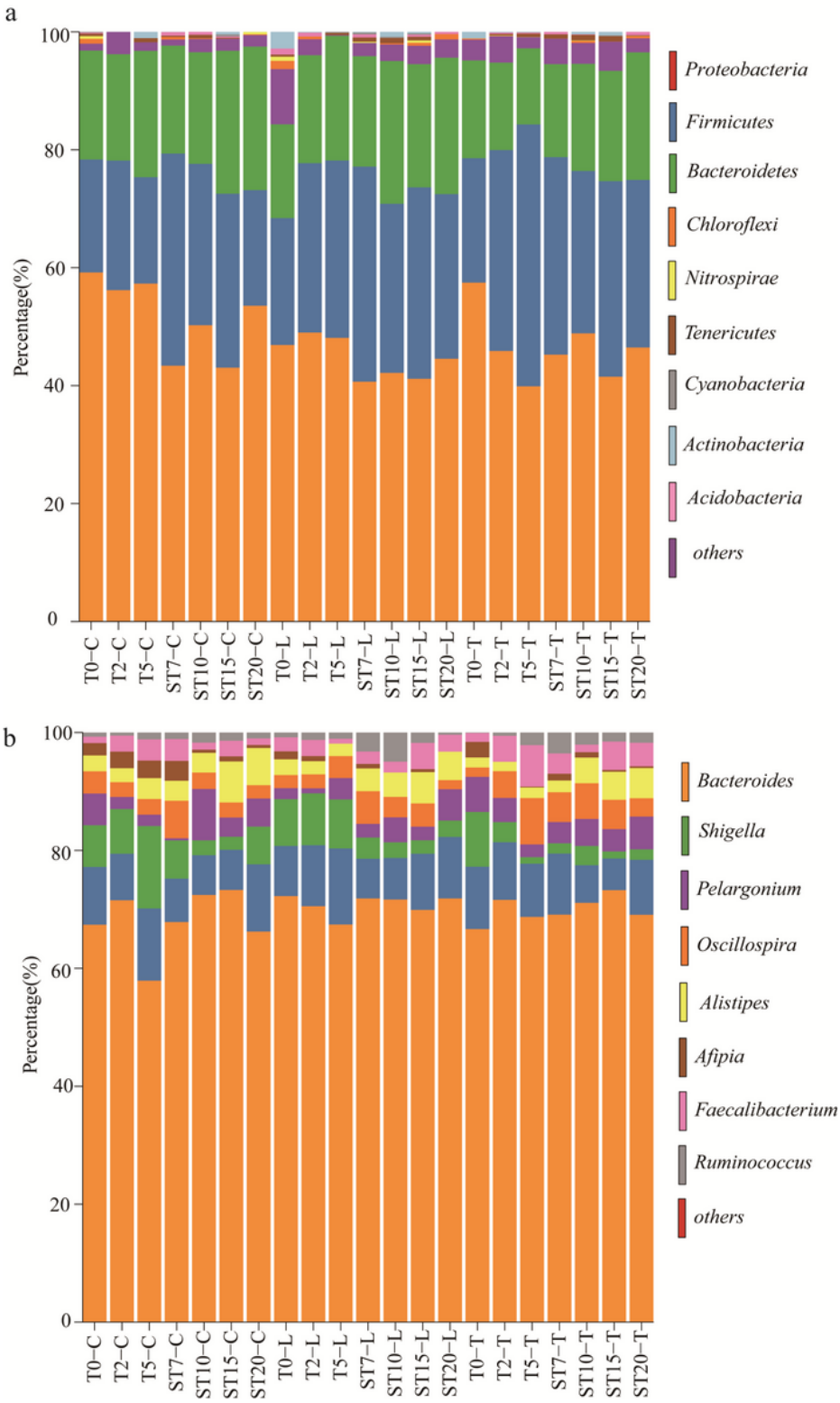

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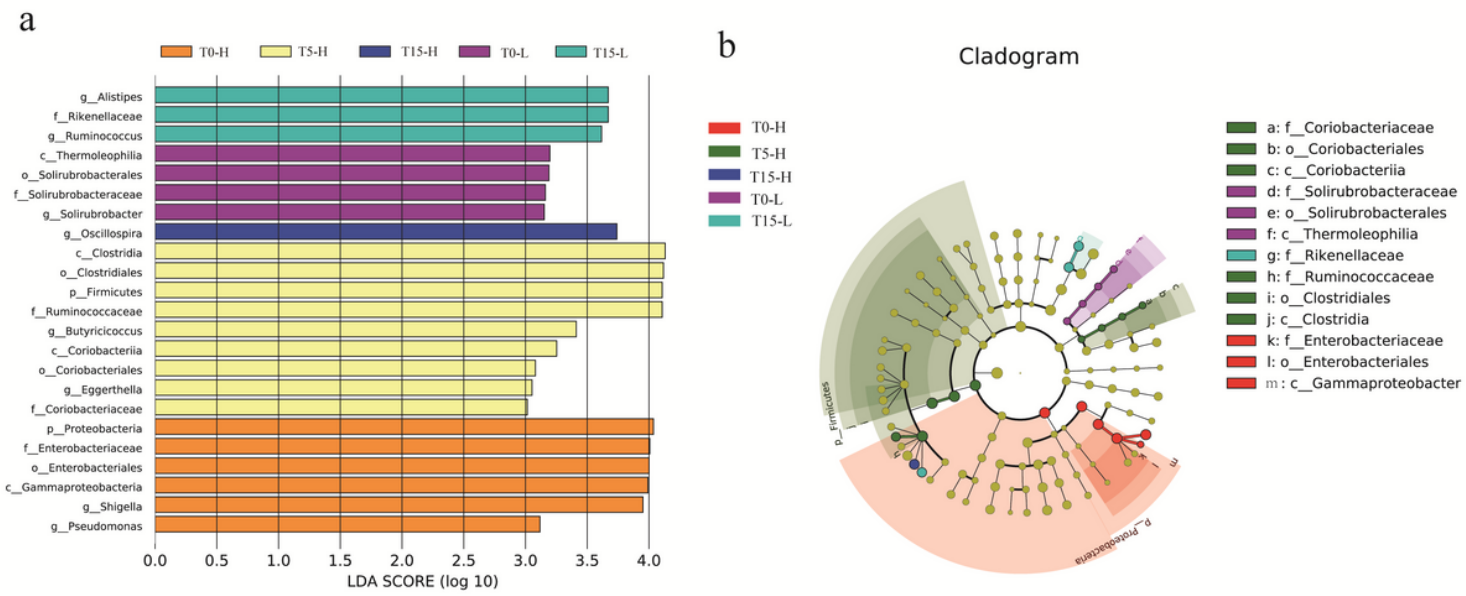

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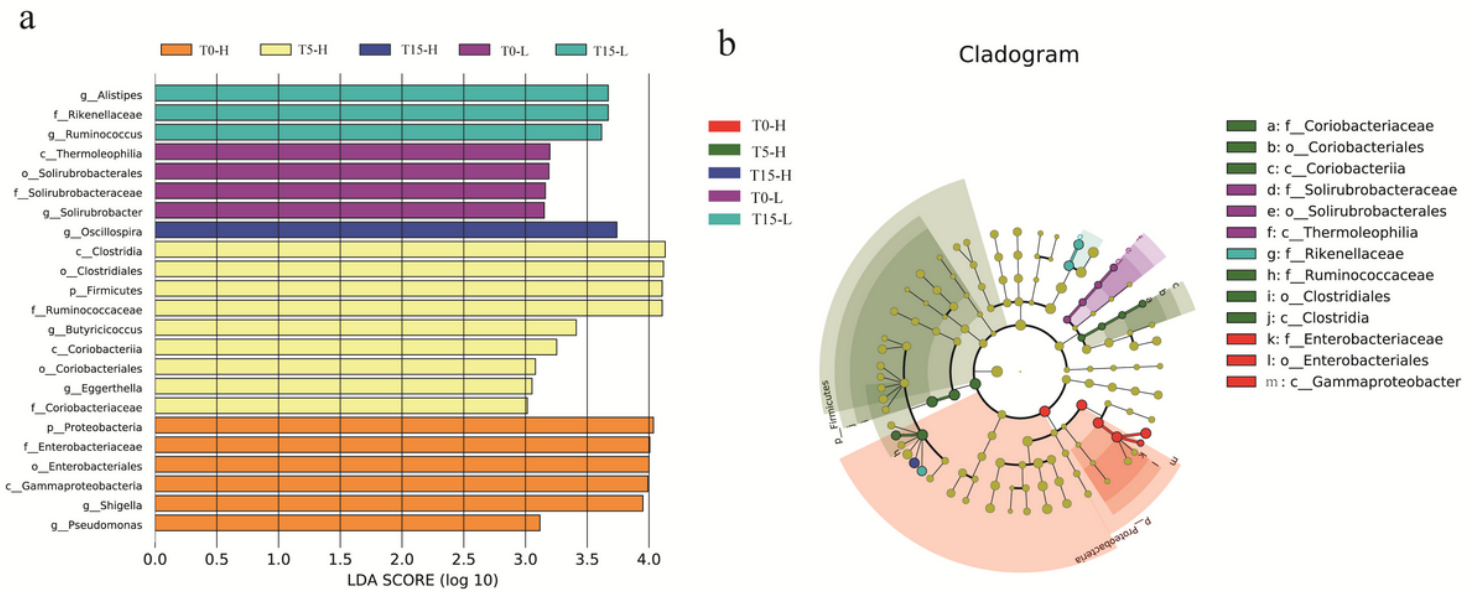
Main bacterial responders of the gut microbiome to chlortetracycline administration. a LDA score of the LEfSe analysis. b Cladogram representing the bacterial biomarkers associated to the groups. The cutoff value of linear discriminant analysis >3.5.



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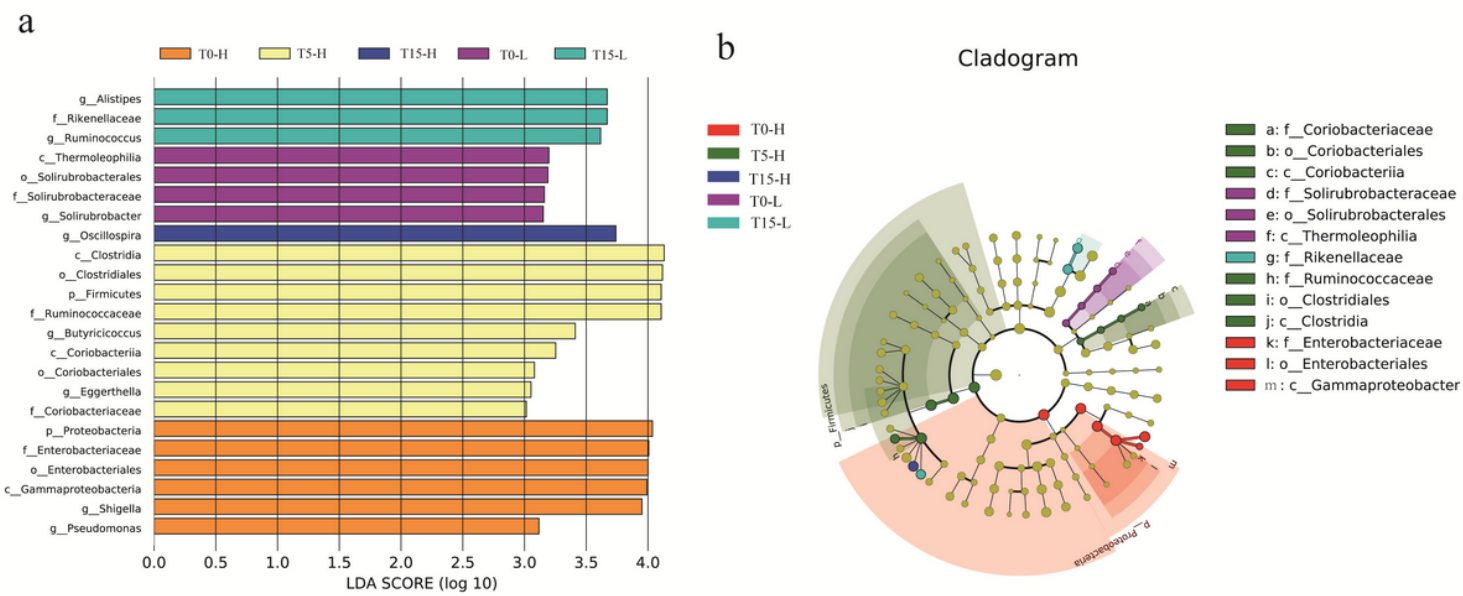

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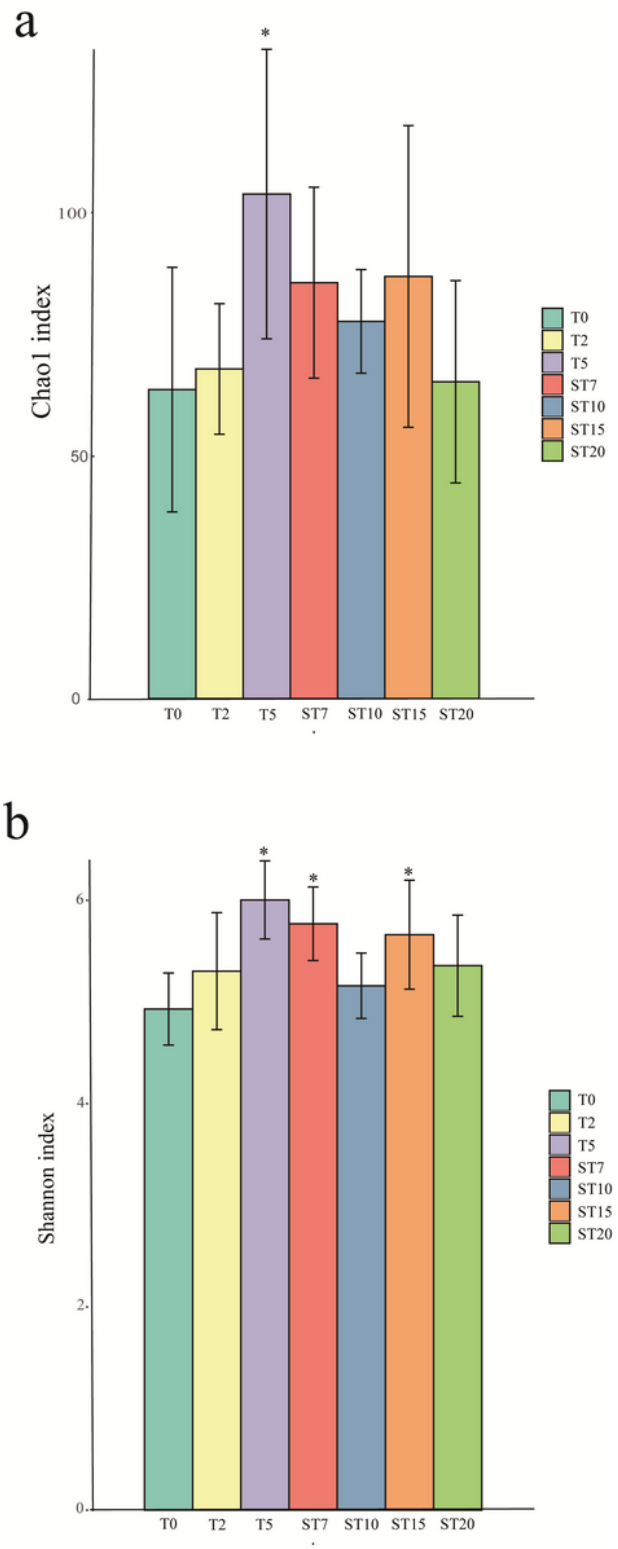

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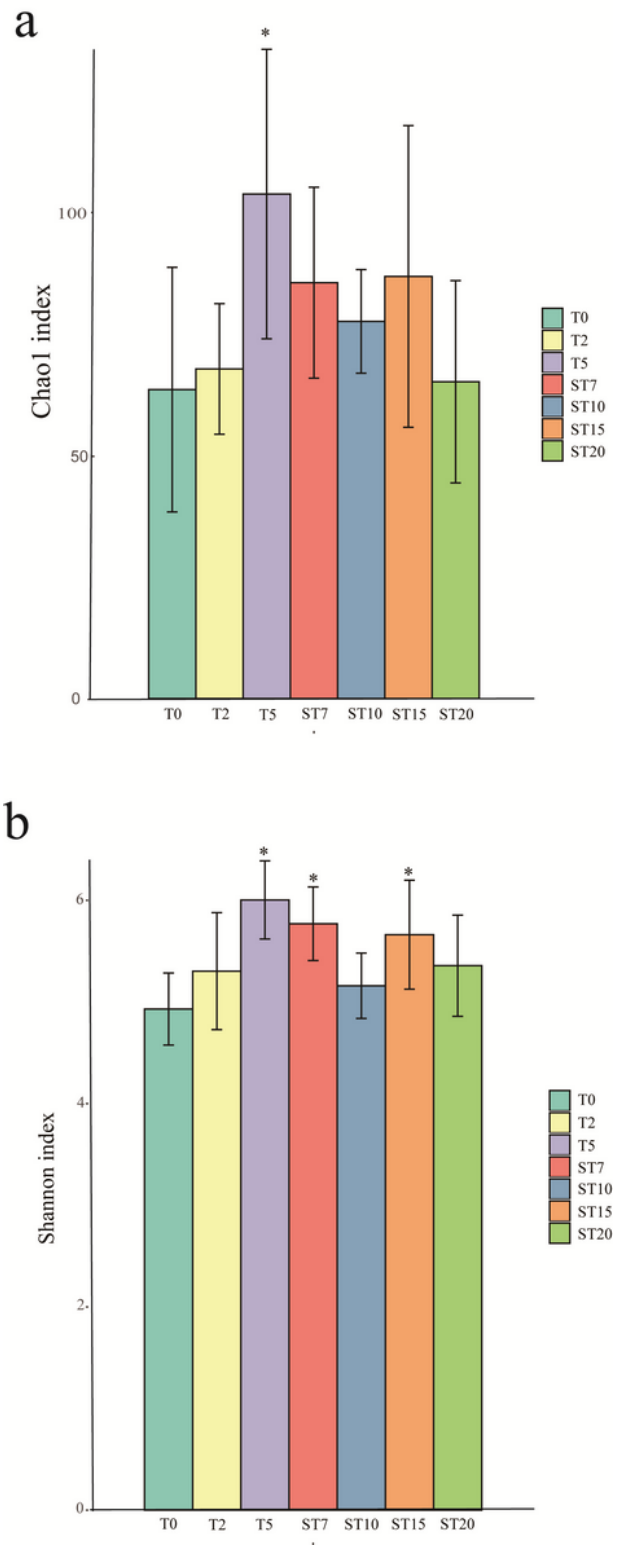
α-diversity index of the therapeutic-dose group over 576 time. a Chao1 index. b Shannon index. T0 (day 0, before treatment), T2 (day2, during treatment), T5 (day5, during treatment), ST7 (day7, during stopped treatment), ST10 (day10, during stopped treatment), ST15 (day15, during stopped treatment), ST20 (day20, during stopped treatment).



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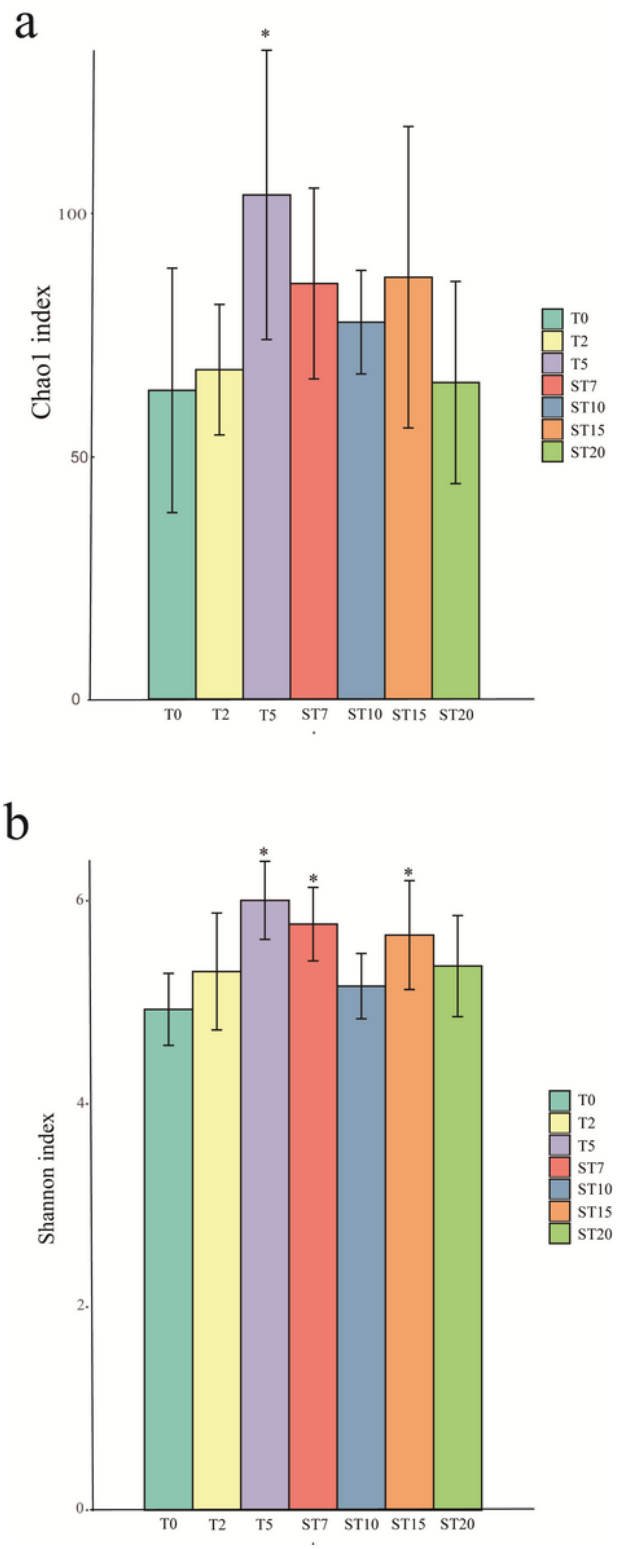

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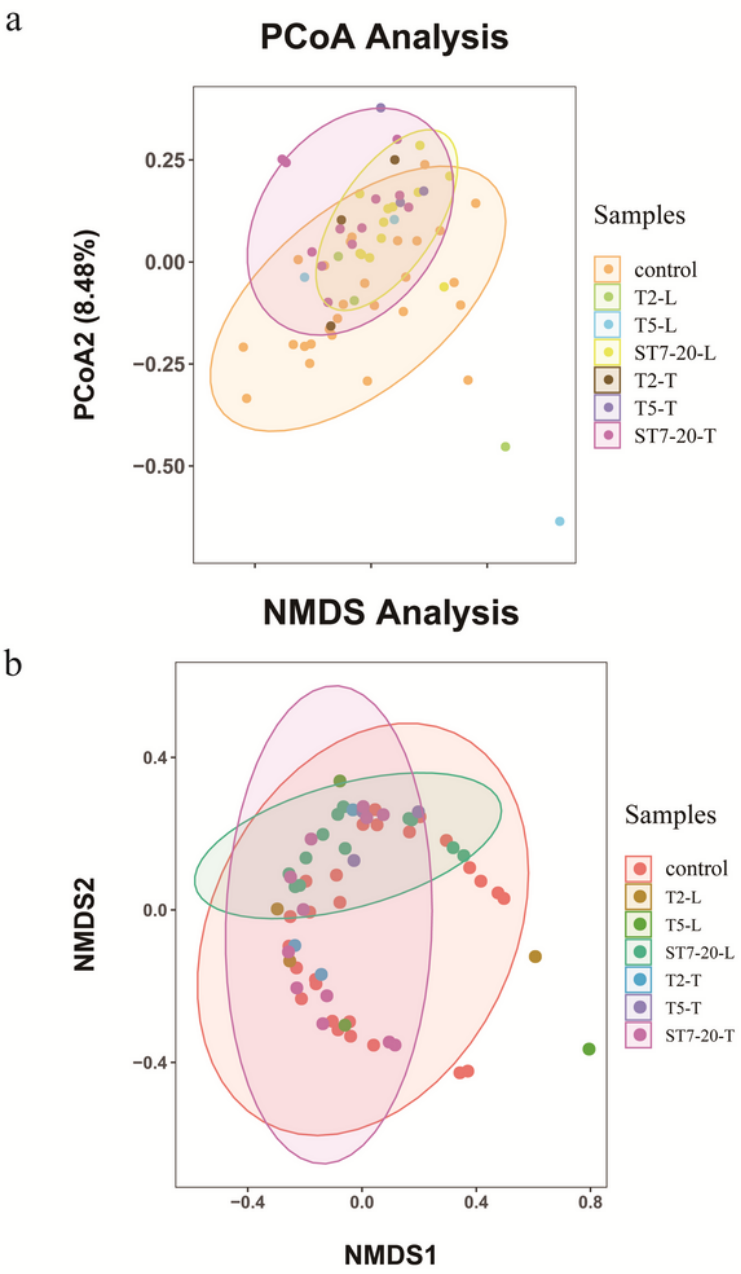

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Microbial diversity changes in the chicken fecal microbiome structure at different administrated stages. a Principal coordinate analysis (PCoA) plots based on the Weighted Unifrac distance showed distinct clusters in the test trial. b Non-metric multidimensional scaling (NMDS) performed based on the Weighted Unifrac distance showed difference between the groups. All the samples without chlortetracycline

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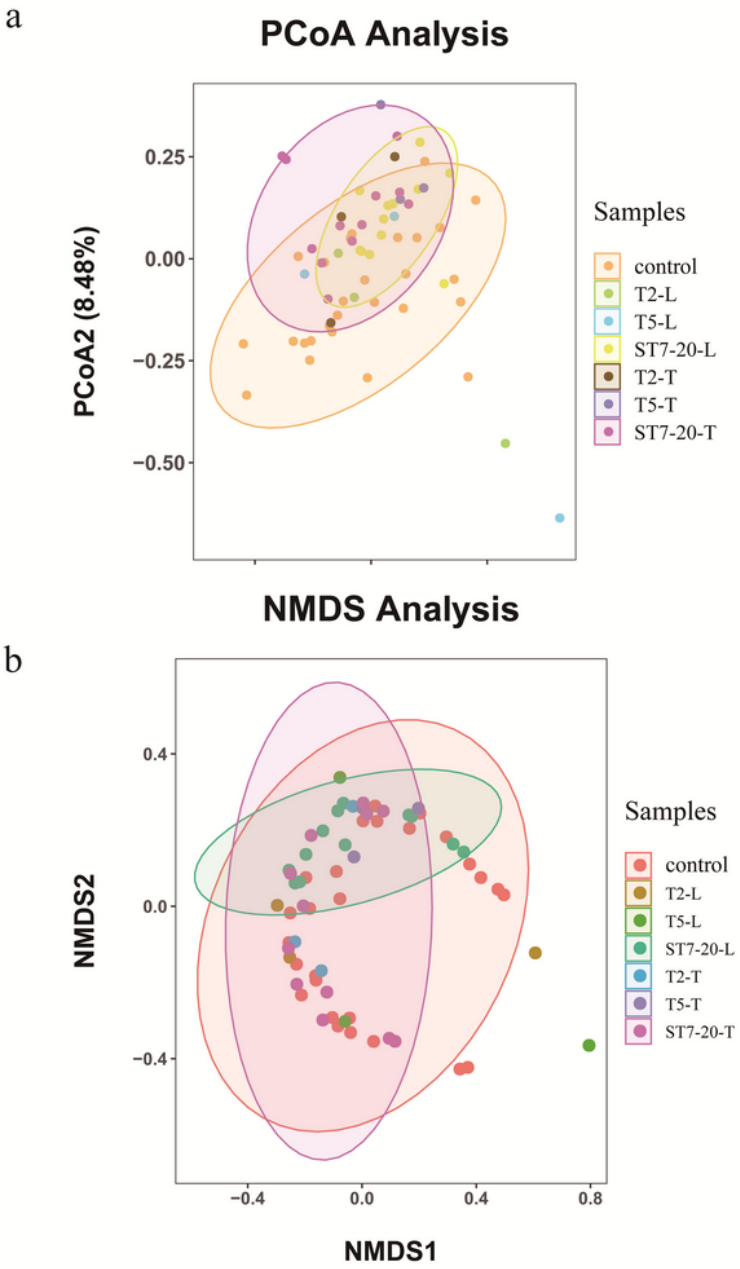

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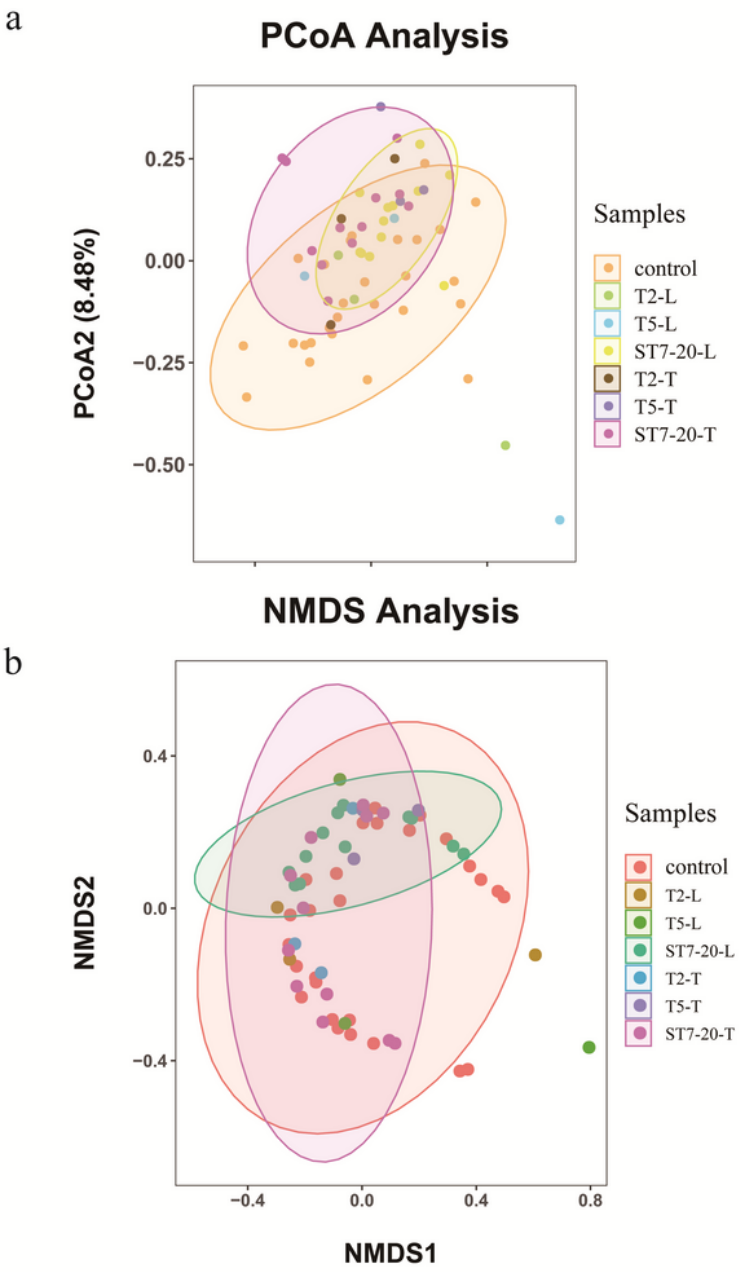

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