Table S1. Comparison of the composition and abundance of gut microbial communities in the top 20 phylum between rural and urban groups.

Top 20 phylum	Rural group	Urban group	*Z*	*P*
Firmicutes	57.843%	48.968%	-1.965	0.049
Proteobacteria	25.051%	33.047%	-1.890	0.059
Bacteroidetes	8.661%	9.317%	-0.378	0.705
Actinobacteria	6.288%	6.407%	-0.832	0.406
Tenericutes	0.776%	0.815%	-1.134	0.257
Cyanobacteria	0.288%	0.306%	-1.739	0.082
Spirochaetes	0.125%	0.128%	-0.113	0.910
Chloroflexi	0.154%	0.152%	-1.512	0.131
TM7	0.113%	0.134%	-2.495	0.013
[Thermi]	0.131%	0.150%	-0.605	0.545
Verrucomicrobia	0.128%	0.134%	-0.529	0.597
Acidobacteria	0.067%	0.070%	-0.529	0.597
OD1	0.086%	0.092%	-0.945	0.345
Planctomycetes	0.043%	0.045%	-1.209	0.226
Chlamydiae	0.054%	0.054%	-0.379	0.704
Armatimonadetes	0.043%	0.044%	-0.457	0.648
Deferribacteres	0.022%	0.023%	-0.077	0.939
Gemmatimonadetes	0.011%	0.011%	-1.268	0.205
Nitrospirae	0.011%	0.012%	-0.228	0.820
Fusobacteria	0.015%	0.017%	-0.383	0.702

Table S2. Comparison of the composition and abundance of gut microbial communities in the top 20 genera between rural and urban groups.

Top 20 genera	Rural group	Urban group	*Z*	*P*
Lactobacillus	9.898%	10.153%	-0.756	0.450
Enterococcaceae_Enterococcus	8.965%	3.774%	-2.343	0.019
Aquabacterium	3.987%	4.084%	-1.285	0.199
Pseudomonadaceae_Pseudomonas	0.179%	0.266%	-2.343	0.019
Methylobacterium	2.357%	2.374%	-0.907	0.364
Acidovorax	1.942%	1.994%	-0.076	0.940
Staphylococcaceae_Staphylococcus	0.702%	0.706%	-0.870	0.384
Agrobacterium	2.032%	2.057%	-0.832	0.406
Microbacterium	1.119%	1.142%	-0.454	0.650
Acinetobacter	1.560%	1.576%	-1.285	0.199
Sediminibacterium	1.291%	1.358%	-0.907	0.364
Ochrobactrum	1.191%	1.250%	-1.058	0.290
Oscillospira	0.763%	0.805%	-0.151	0.880
Bacteroidaceae_Bacteroides	1.069%	1.100%	-0.529	0.597
Campylobacter	1.717%	1.717%	-0.937	0.349
Streptococcus	0.585%	0.590%	-0.756	0.450
Curtobacterium	0.263%	0.278%	-1.136	0.256
Ruminococcus	0.557%	0.573%	-0.151	0.880
Prevotella	0.186%	0.249%	-1.739	0.082
Blautia	0.944%	0.980%	-1.436	0.151

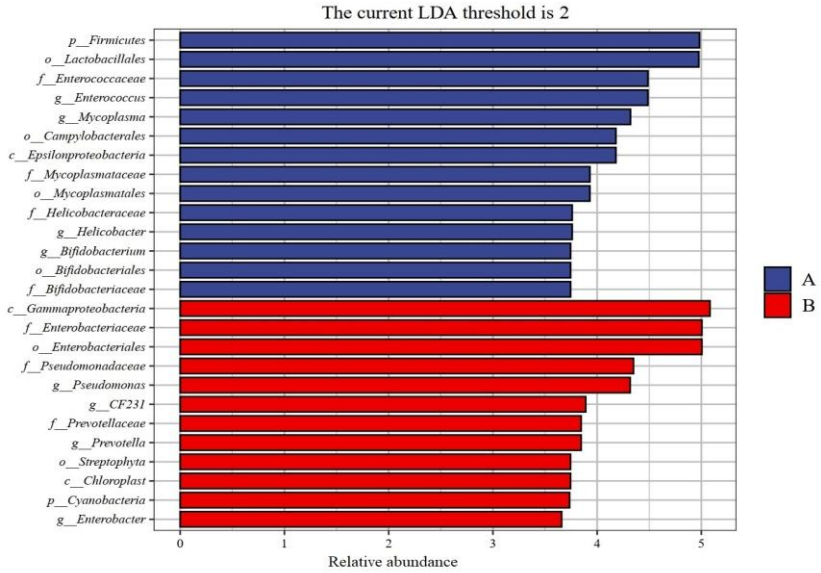


Figure S1. The bar chart displays bacteria (from phylum to genus) represented by red and blue bars, indicating significantly higher and lower levels respectively in the fecal samples of rural tree sparrows (group A) compared to urban tree sparrows (group B).