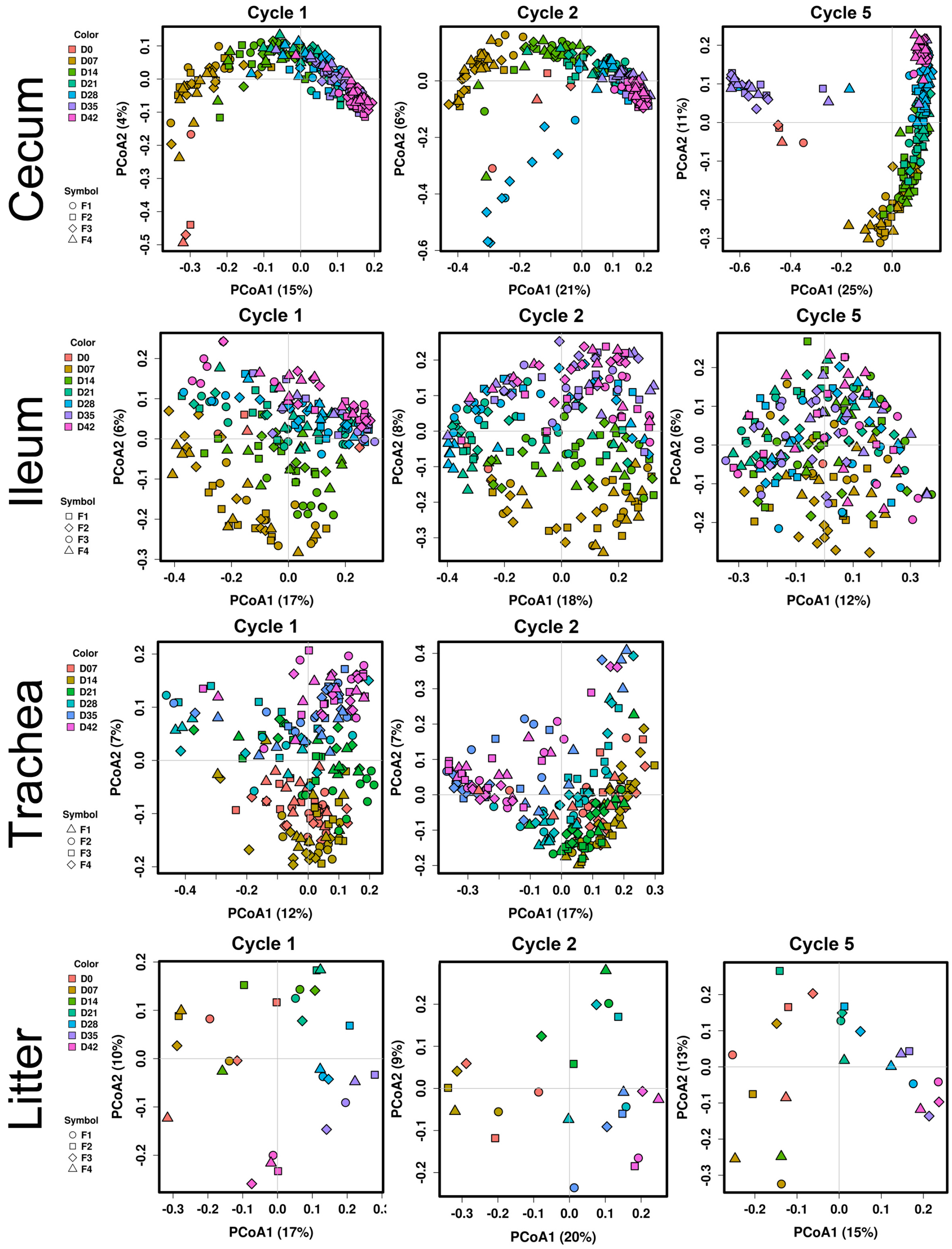
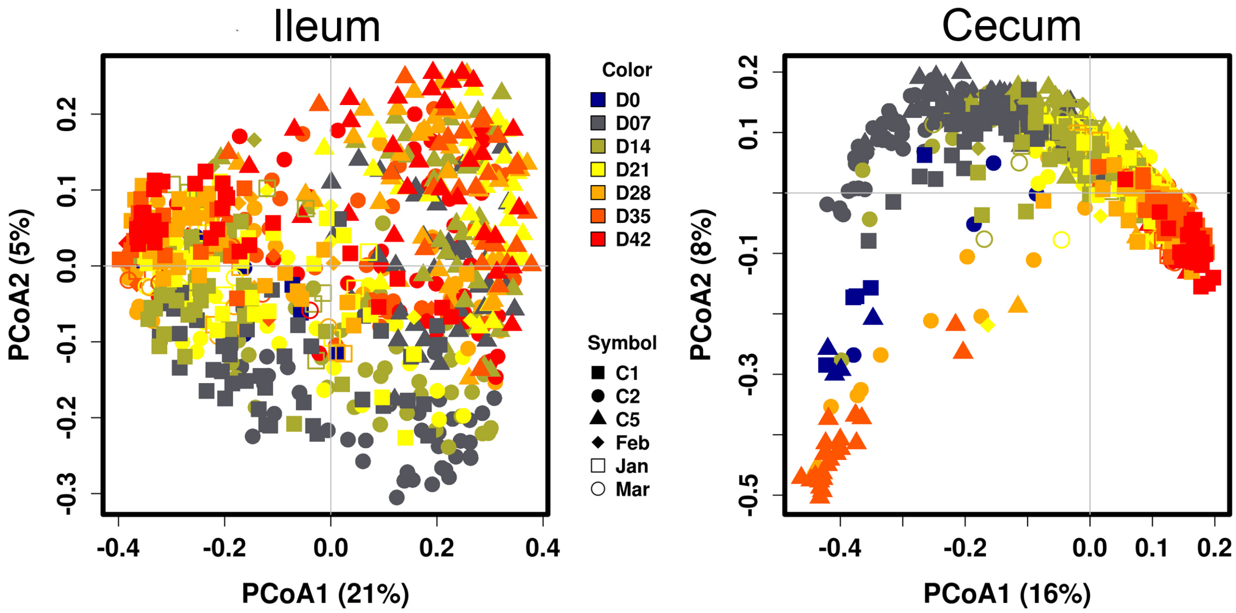
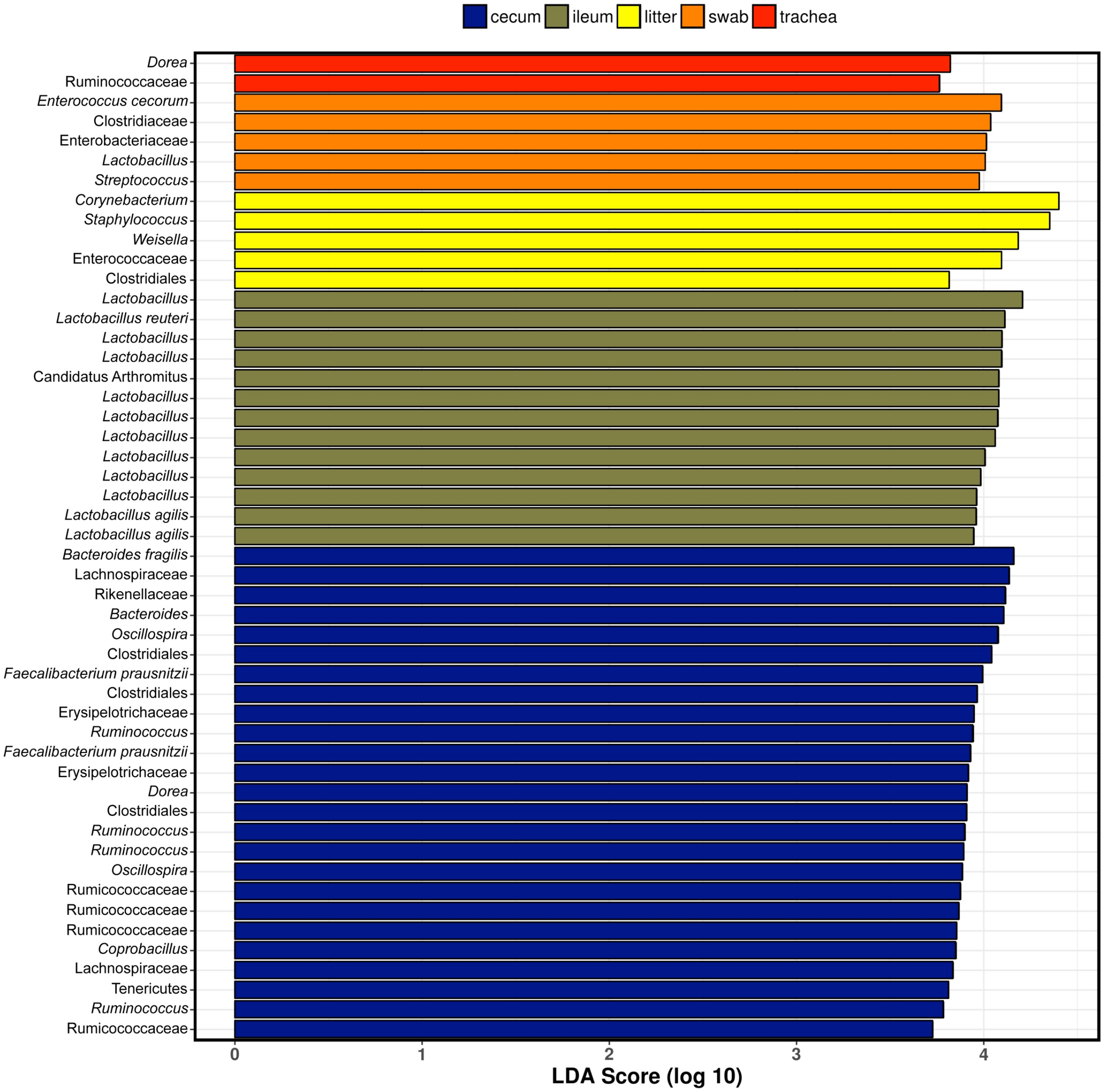
Supplementary Figure 1. Effects of age on the broiler microbiome. Unweighted UniFrac plotted using principal coordinate analysis. Samples are grouped by flock cycle and colored by bird age. Symbols represent flocks.



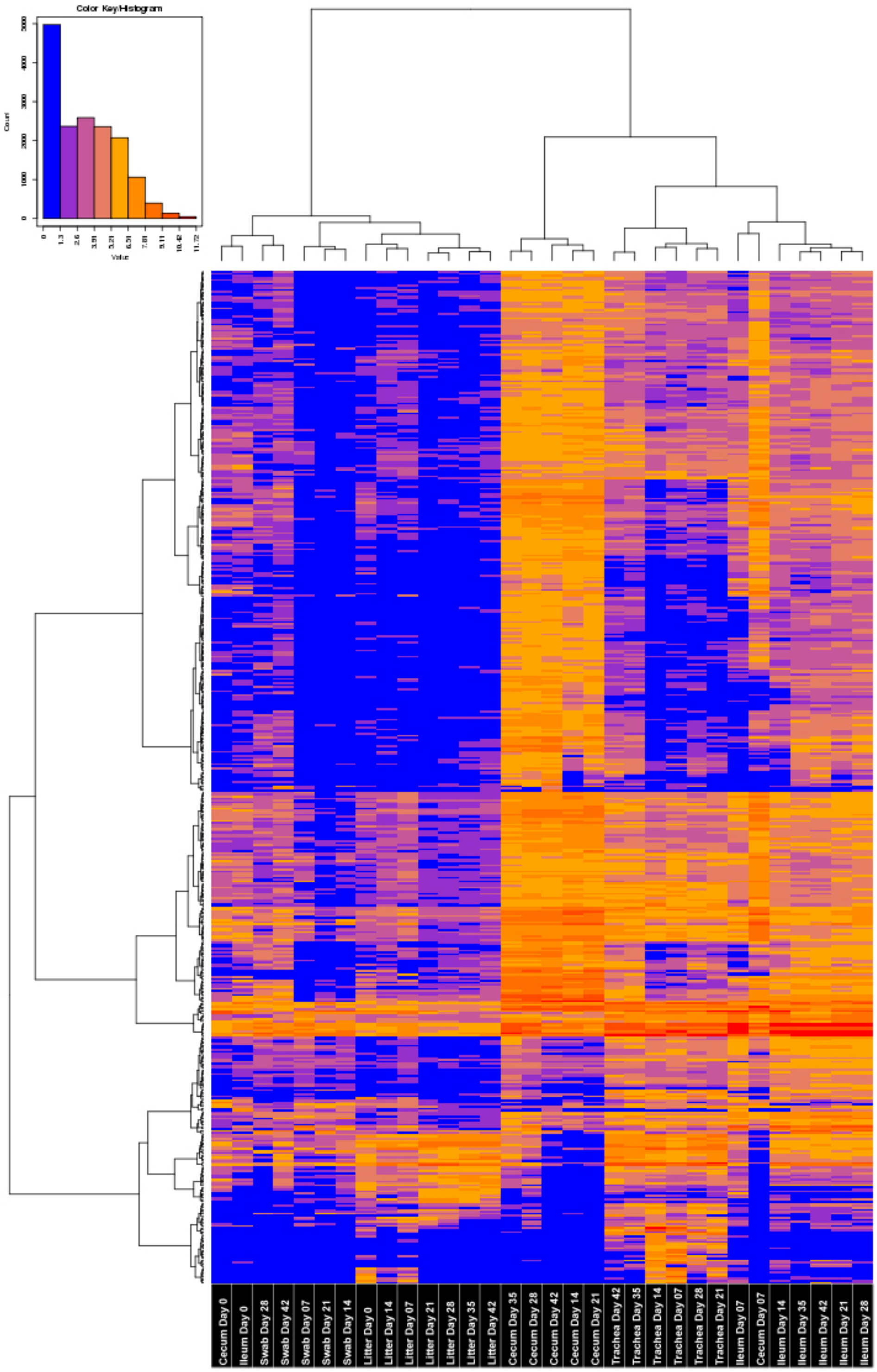
Supplementary Figure 2. Microbiome succession by age is highly consistent and predictable. Unweighted UniFrac of ileum and cecum samples from 37 different flocks plotted using principal coordinate analysis. Samples are colored by bird age, and shapes indicate collection from longitudinal or cross-sectional study.



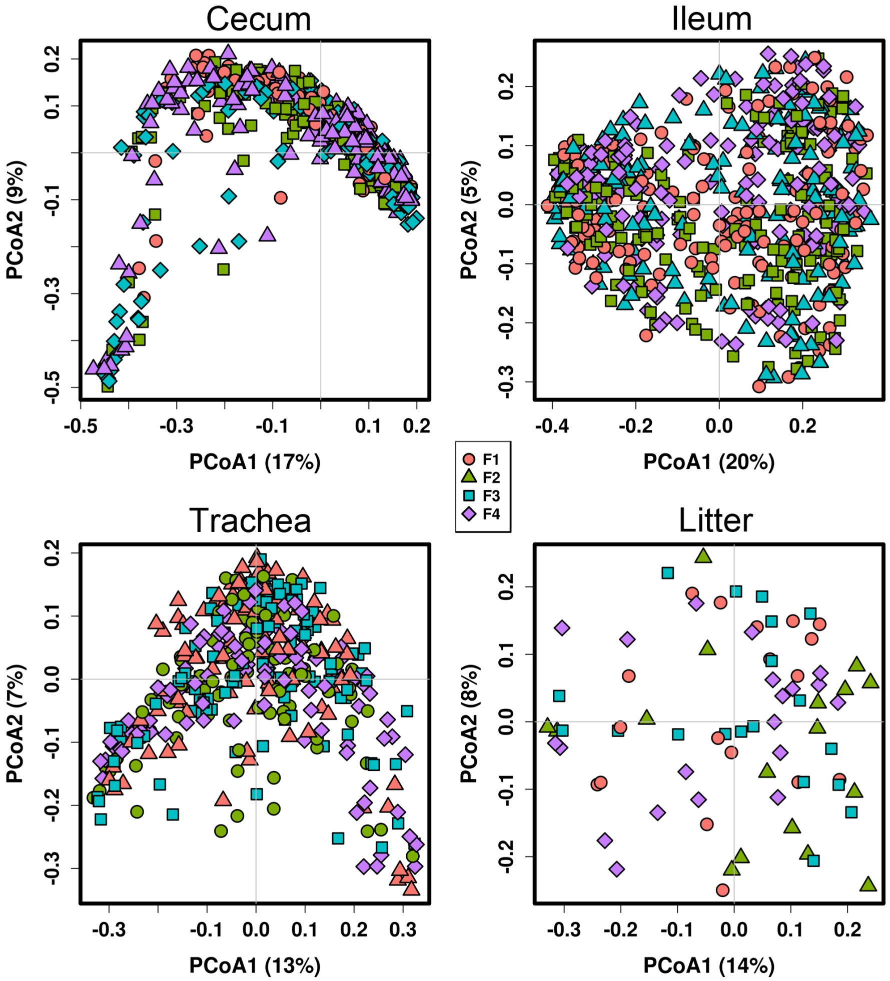
Supplementary Figure 3. Distinguishing OTUs of the broiler microbiome by sample type. LEfSe analysis was performed on the top 50 OTUs to identify distinguishing taxa.



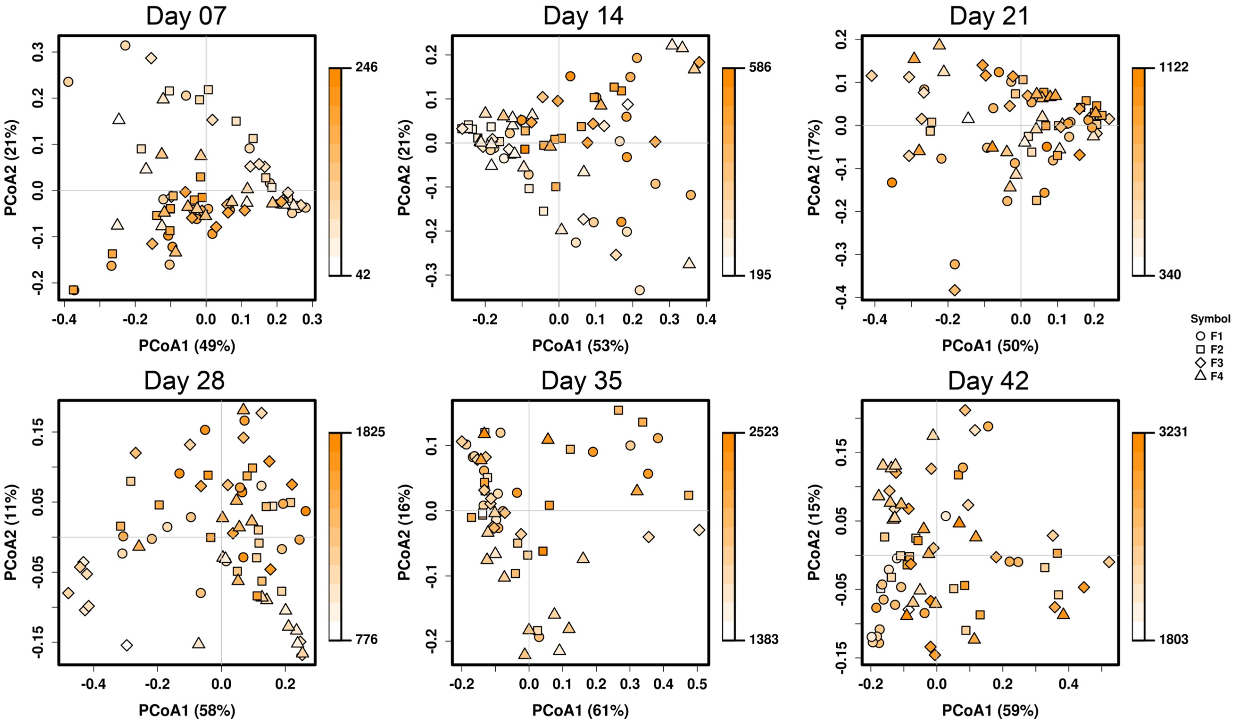
Supplementary Figure 4. Heat map depicting the relative abundance of the top 500 OTUs grouped by sample type and broiler age. Hierarchical clustering was performed to display similarities between samples. Normalized $\log_2$ values are depicted.



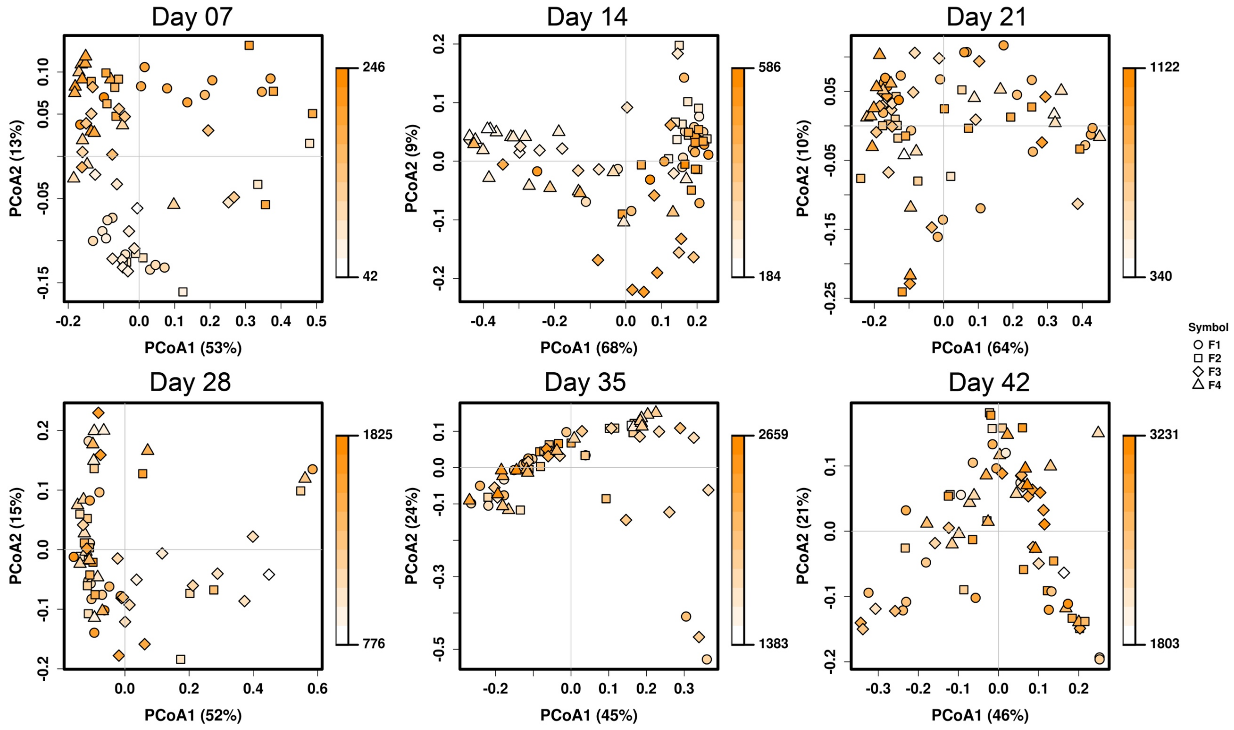
Supplementary Figure 5. Similarities in the broiler microbiome across flocks. Principal coordinate analysis of samples was performed using unweighted unifrac measures of beta diversity. Samples are colored by flock number.



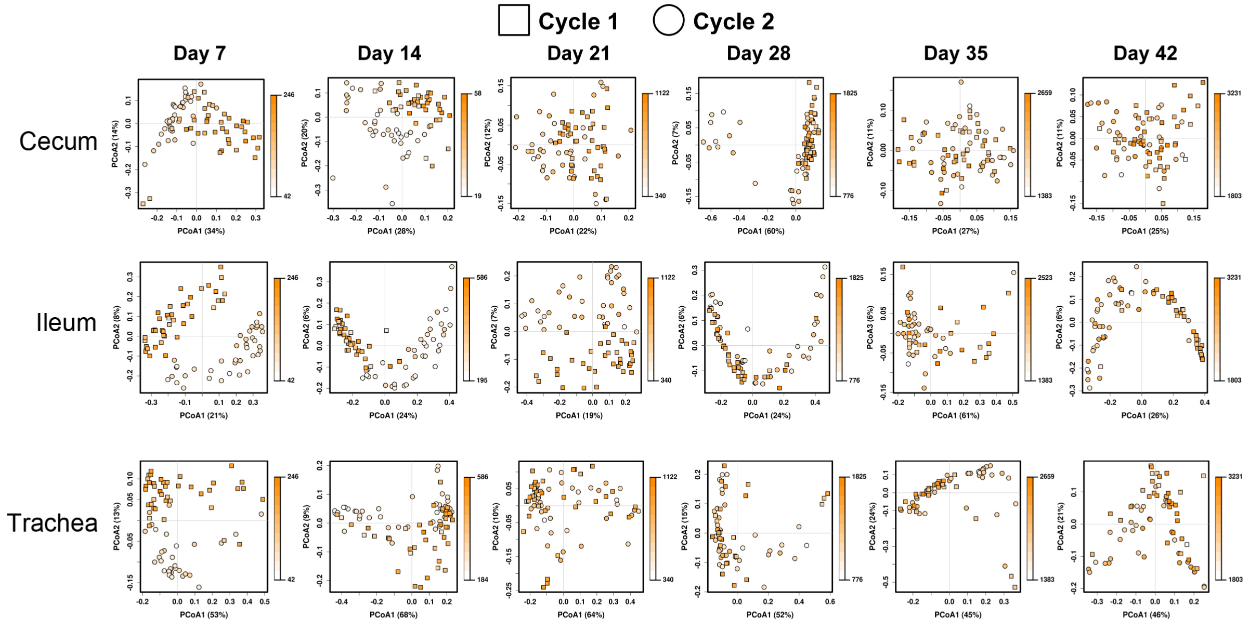
Supplementary Figure 6. Correlations between broiler weight and its ileal microbiome. Principal coordinate analysis of ileum samples was performed from flock cycles 1 and 2. Samples are colored by total body weight and scaled to minimum and maximum weights for each sampling age. Sample shapes represent the four different flocks sampled during each flock cycle.



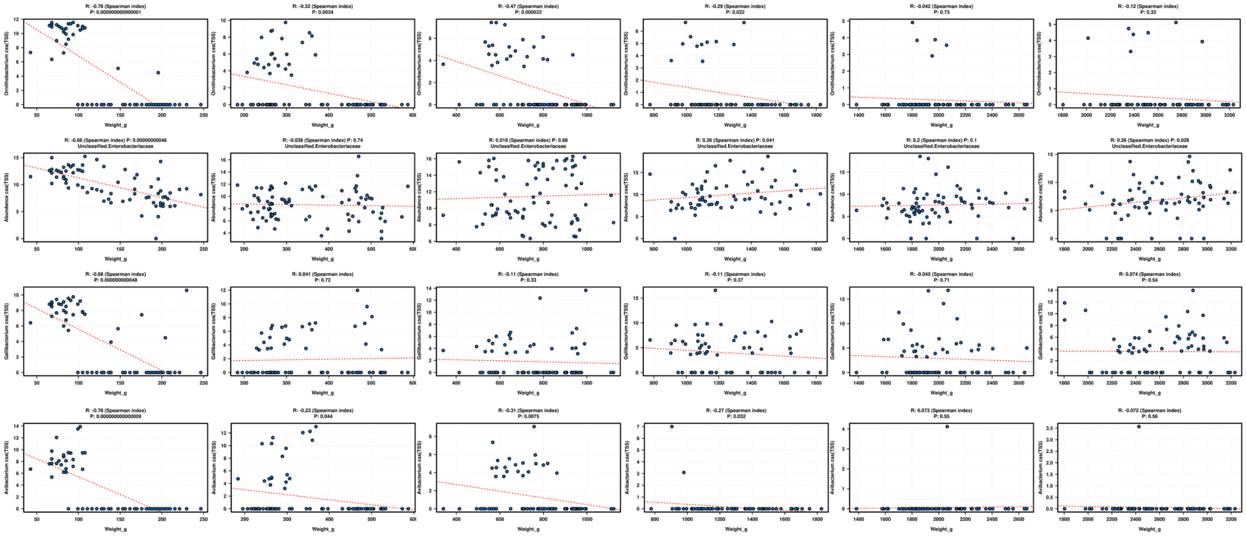
Supplementary Figure 7. Correlations between broiler weight and its tracheal microbiome. Principal coordinate analysis of trachea samples was performed from flock cycles 1 and 2. Samples are colored by total body weight and scaled to minimum and maximum weights for each sampling age. Sample shapes represent the four different flocks sampled during each flock cycle.



Supplementary Figure 8. Correlations between broiler weight stratified by flock cycle. Principal coordinate analysis of samples was performed from flock cycles 1 and 2. Samples are colored by total body weight and scaled to minimum and maximum weights for each sampling age. Sample shapes represent the different flock cycles.



Supplementary Figure 9. Correlations between broiler weight and potential bacterial pathogens (genus) in the trachea. For each bacterial taxa (top to bottom) samples are grouped according to increasing bird age (left to right).



Supplementary Figure 10. Correlations between broiler weight and potential commensal bacteria (genus) in the trachea. For each bacterial taxa (top to bottom) samples are grouped according to increasing bird age (left to right).