

Supplementary Figures

Figure S1. Boxplots representing relative abundances of bacteriophages and eukaryotic viruses stratified by gestational age (left), delivery mode (middle) and BPD status (right). (Wilcoxon test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$)

Figure S2. Boxplots of virulent, temperate, and undetermined lifecycle phage abundances (VDR), stratified by delivery mode (left) and BPD status (right). (Wilcoxon test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$)

Figure S3. Relative abundances (top) and occurrences (bottom) of endotracheal bacterial genera identified via 16S rRNA-seq.

Figure S4. Abundance of transcriptionally active bacterial species ($\log_{10}$ bacterial decontaminated ratio) in endotracheal samples.

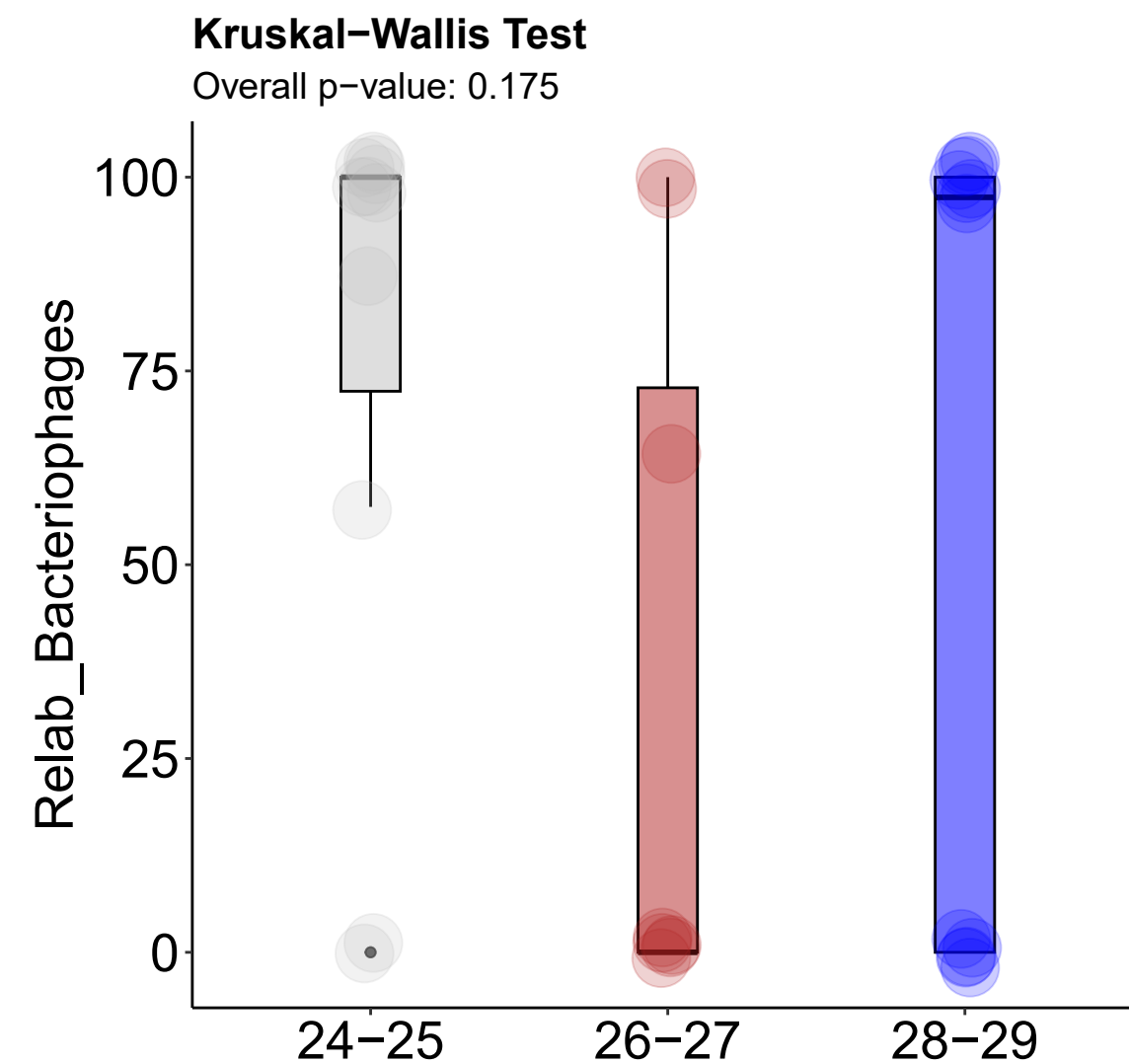
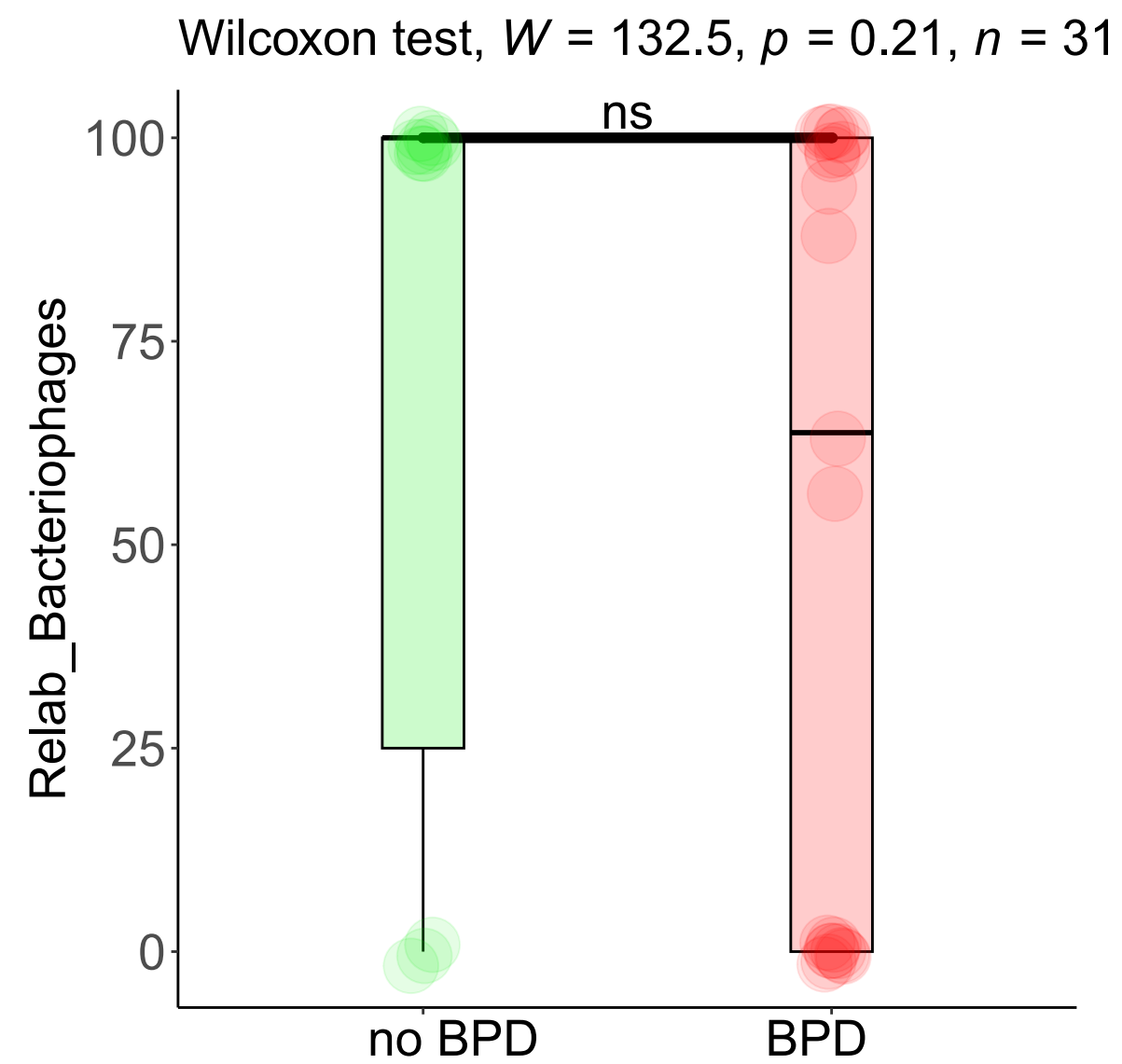
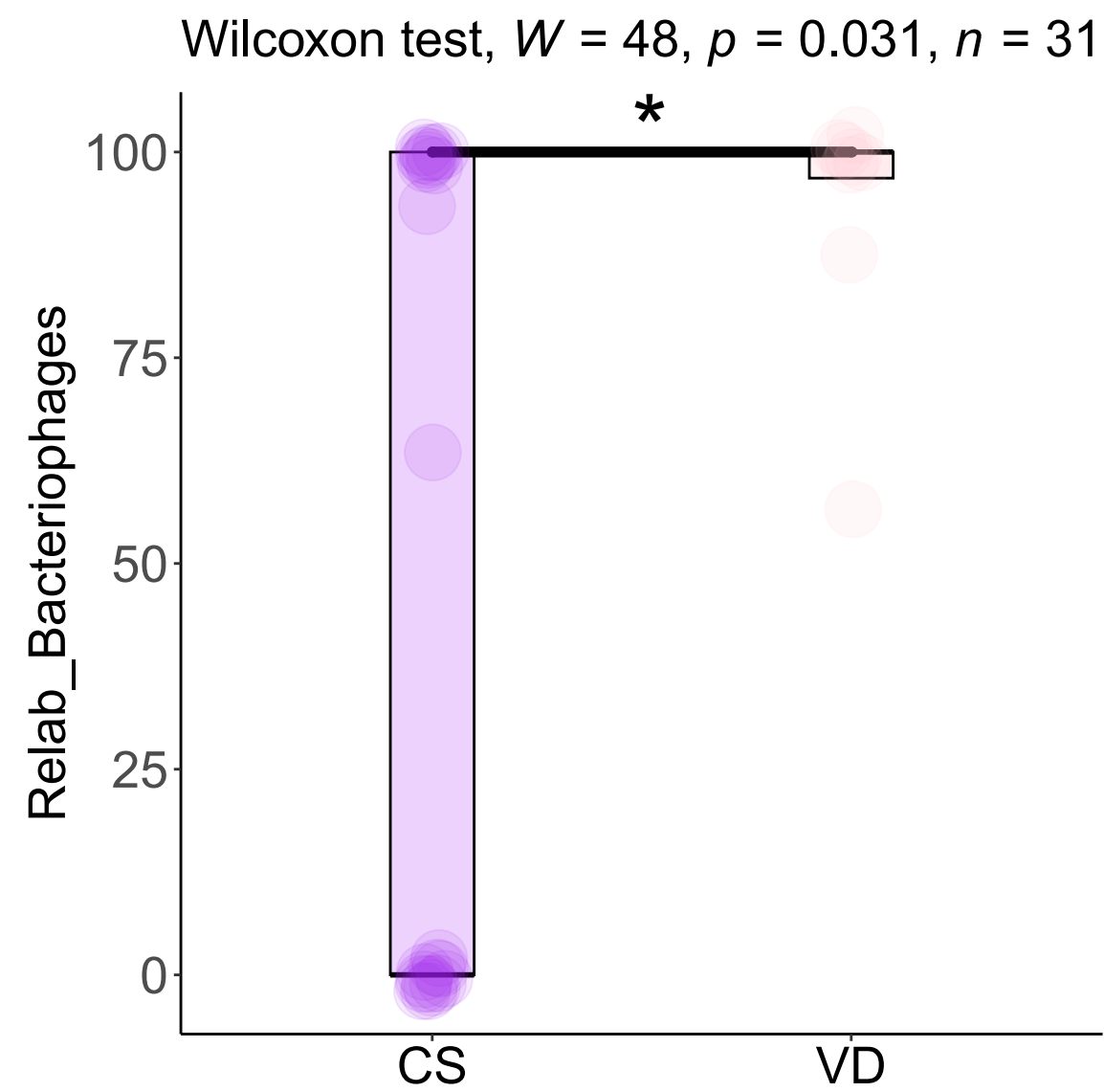
Figure S5. Boxplots of Shannon index and richness according to bacterial genera identified by 16S rRNA-seq (A-B) and RNA bacterial species identified by metaRNA-seq (C-D), and stratified by gestational age (left), delivery mode (middle) and BPD status (right). (Wilcoxon test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$)

Figure S6. Confusion matrix regarding aross-validation (10-fold), with random forest classification (caret R package)

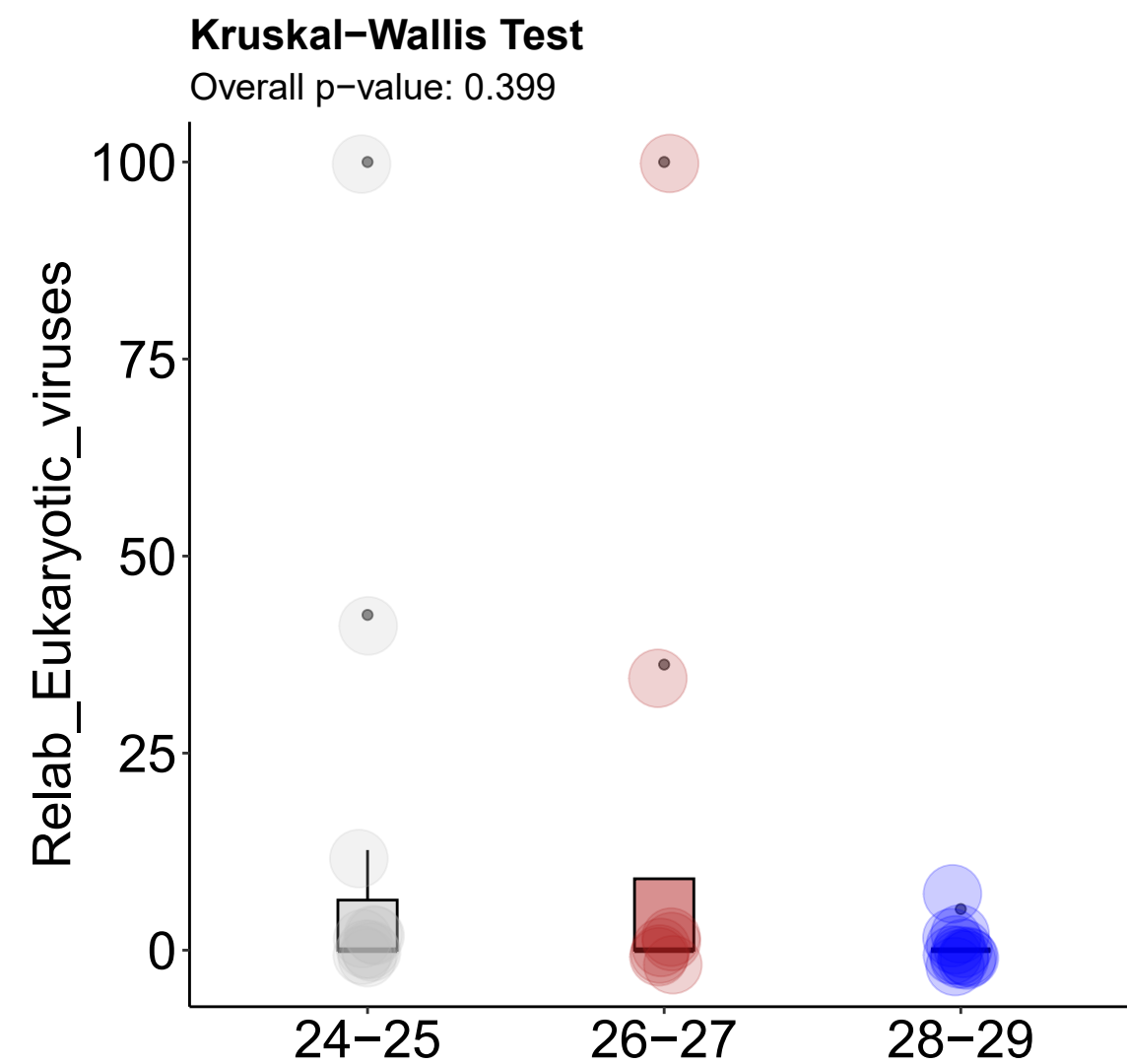
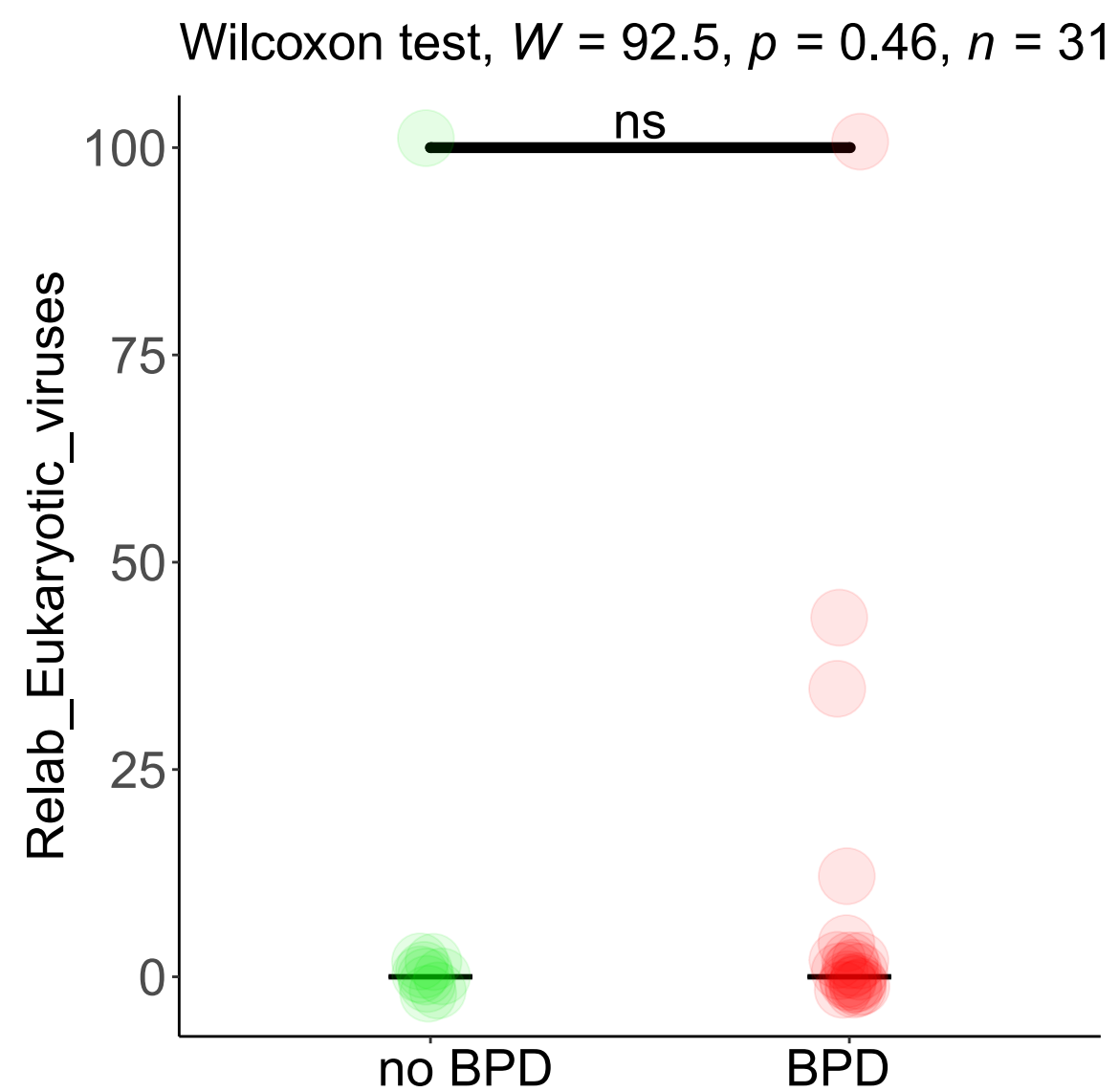
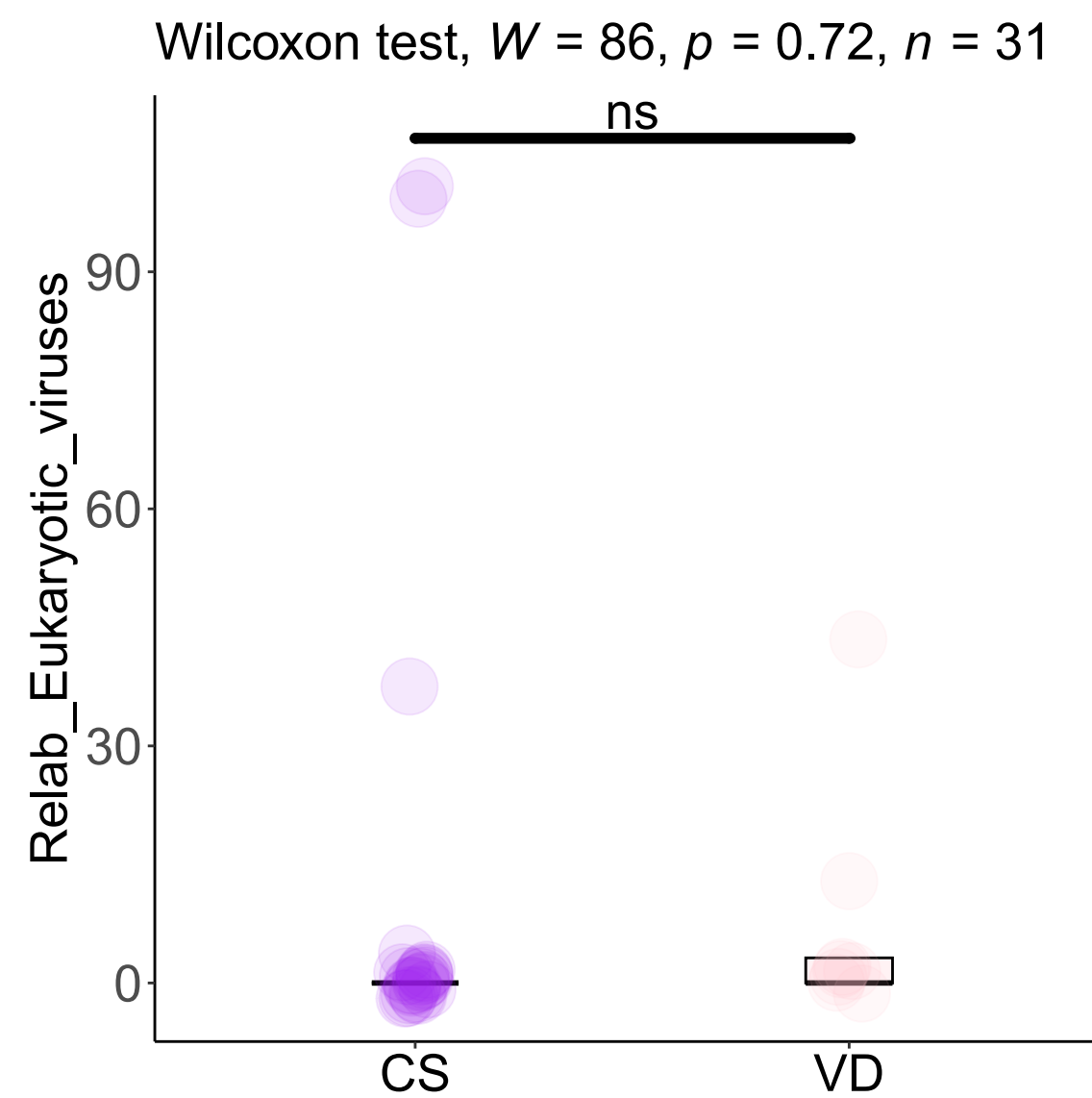
Supplementary Tables

Table S1. Summary of sequencing data characteristics.

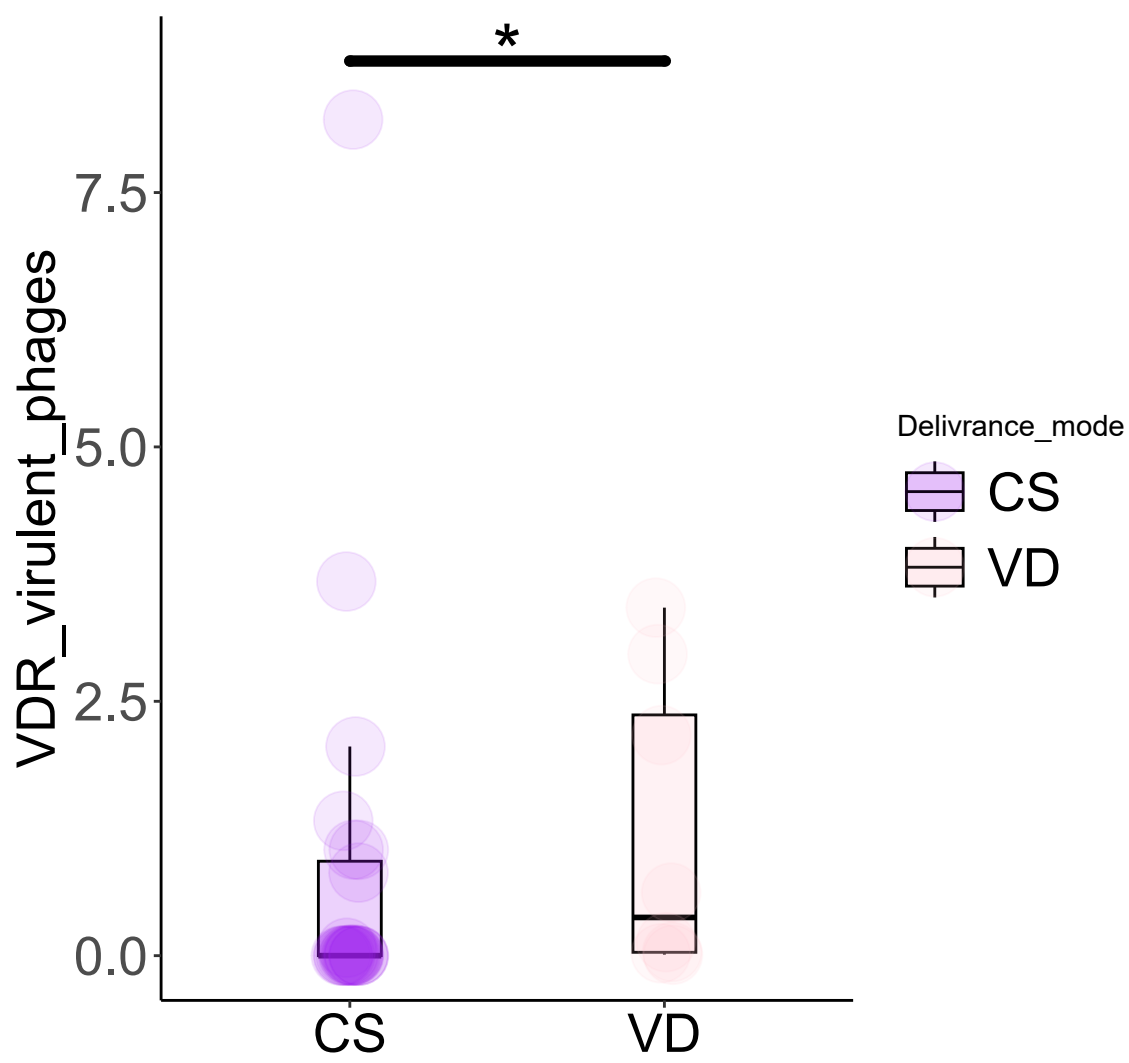
A



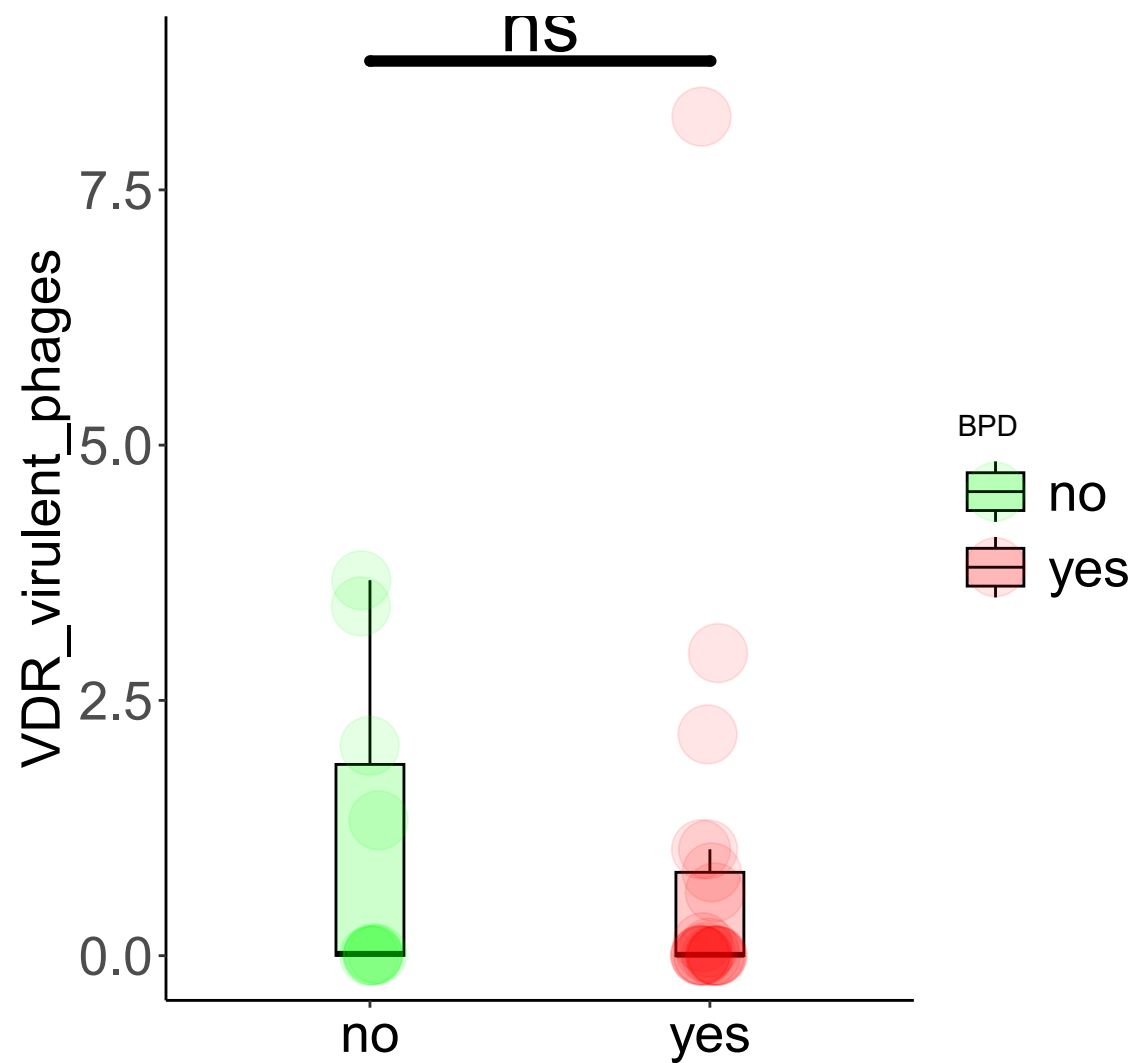
B



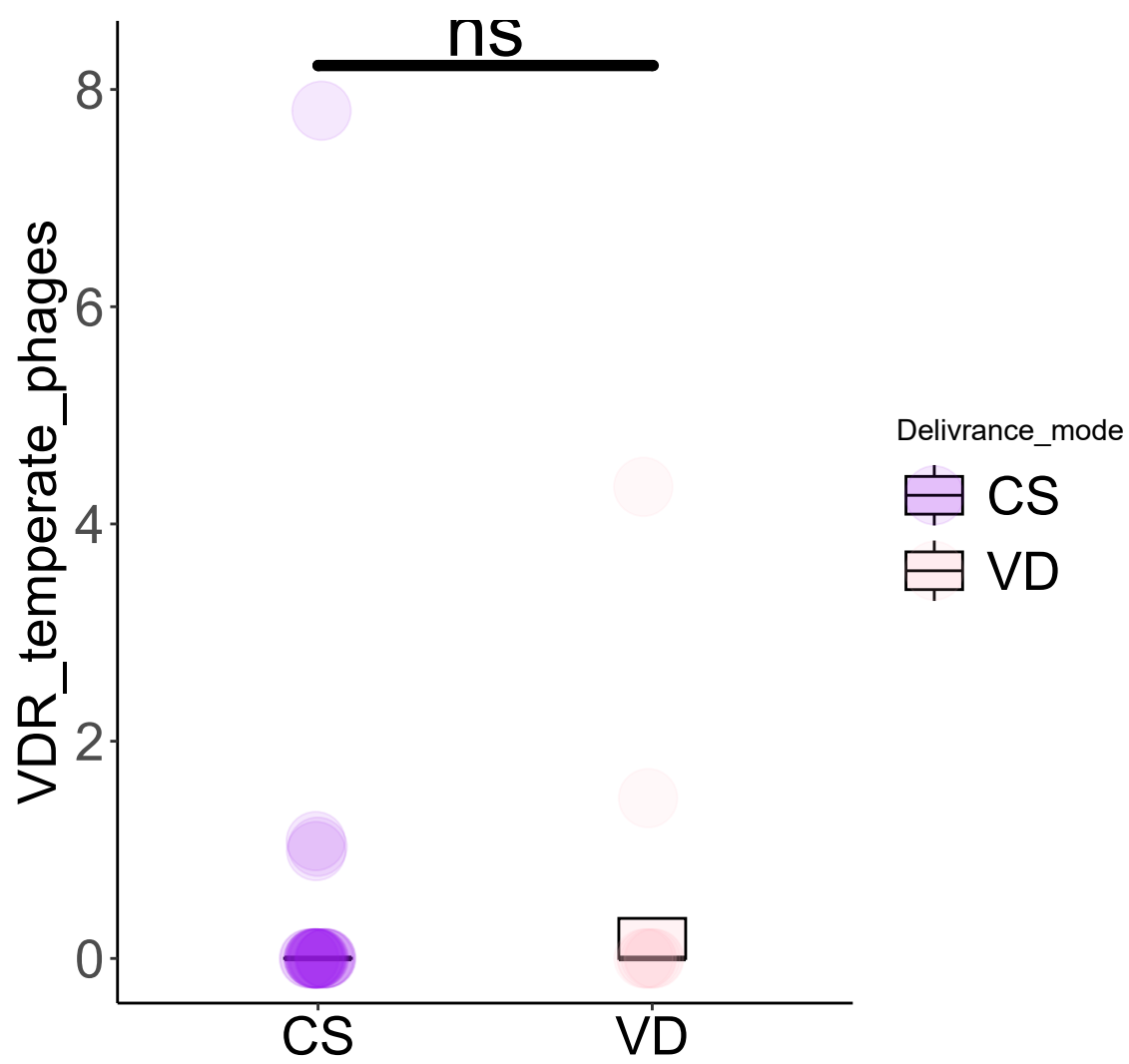
Wilcoxon test, $W = 45$, $p = 0.031$, $n = 31$



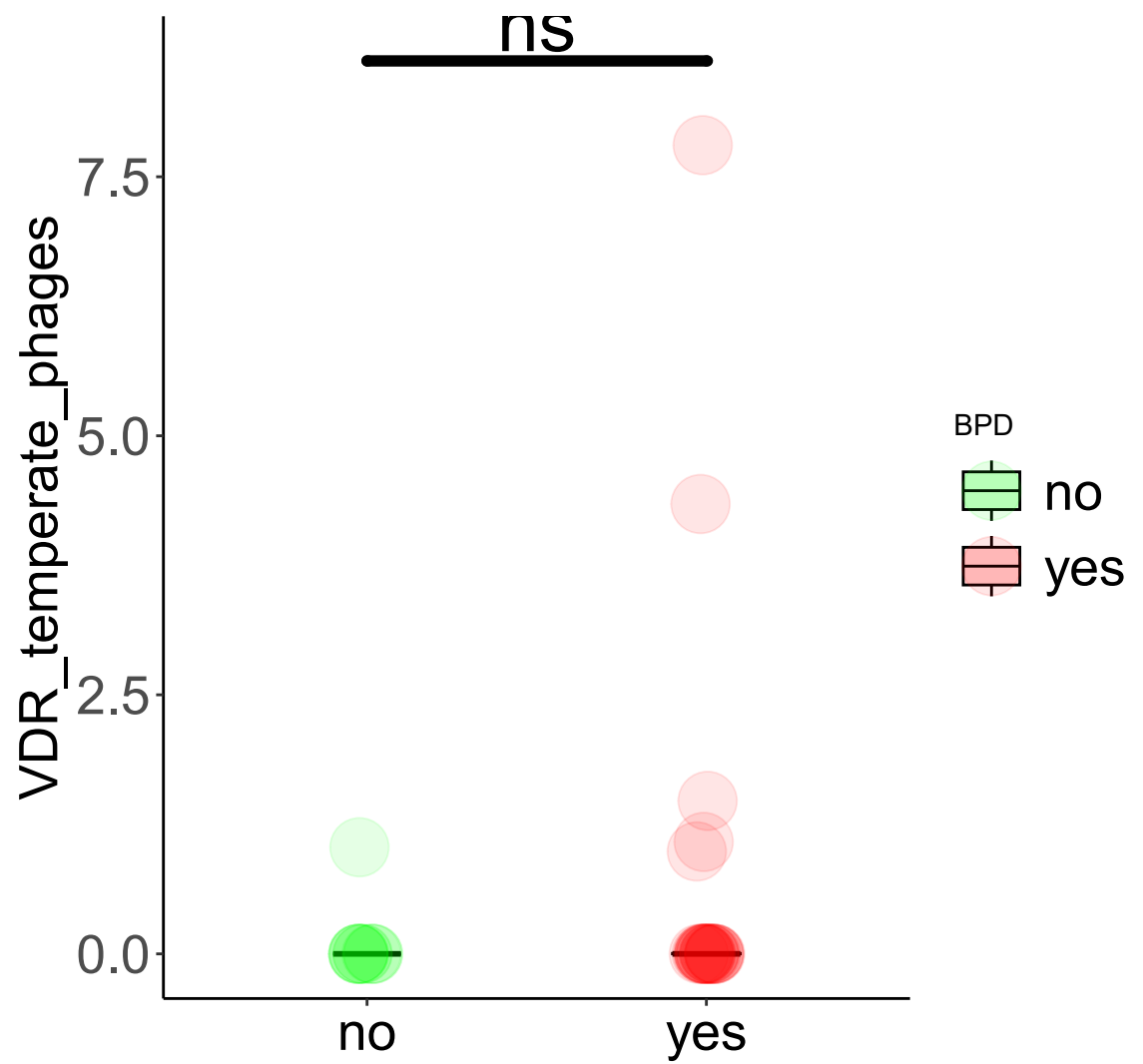
Wilcoxon test, $W = 122.5$, $p = 0.46$, $n = 31$



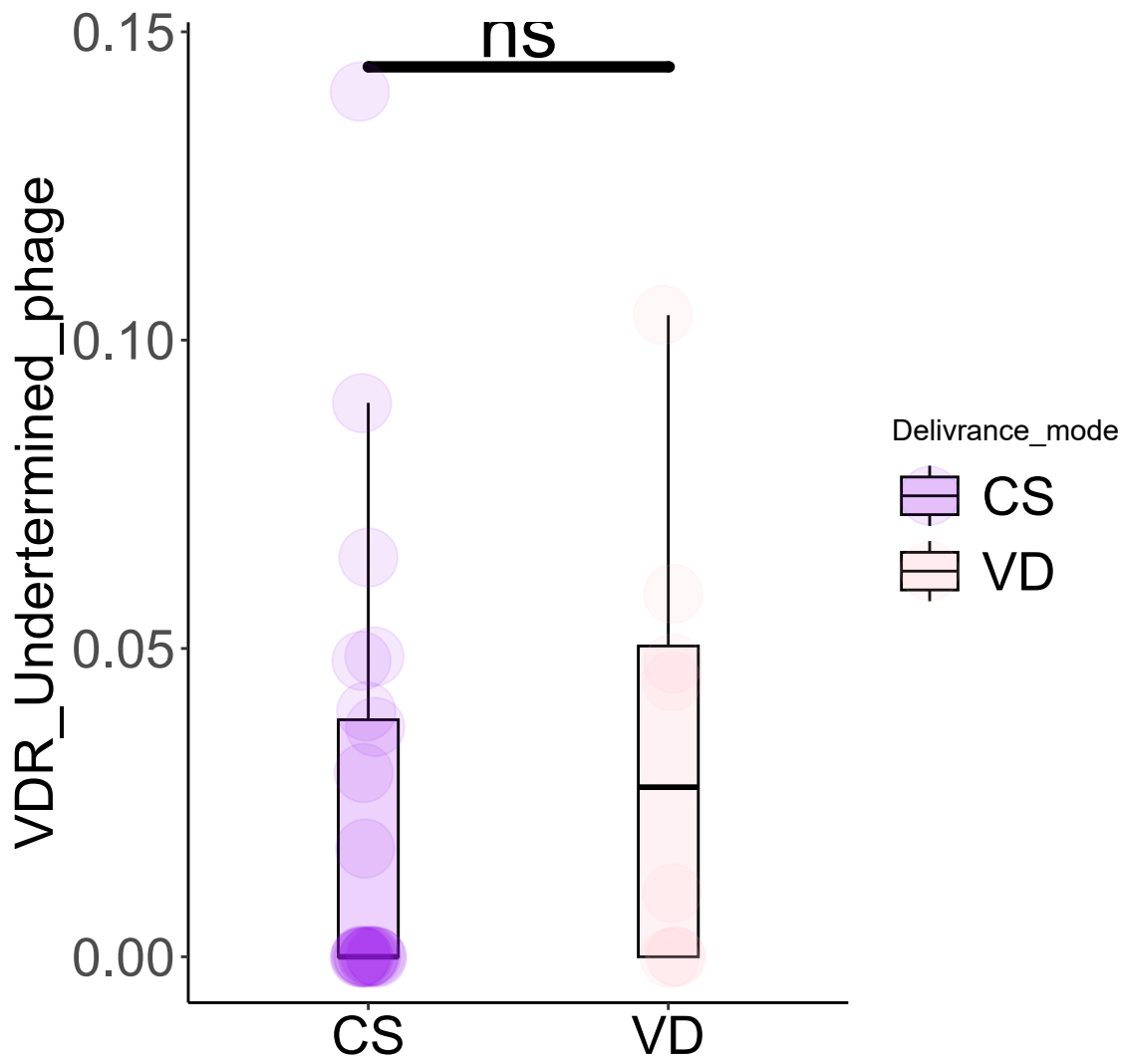
Wilcoxon test, $W = 89$, $p = 0.88$, $n = 31$



Wilcoxon test, $W = 80$, $p = 0.18$, $n = 31$



Wilcoxon test, $W = 71$, $p = 0.31$, $n = 31$



Wilcoxon test, $W = 83$, $p = 0.32$, $n = 31$

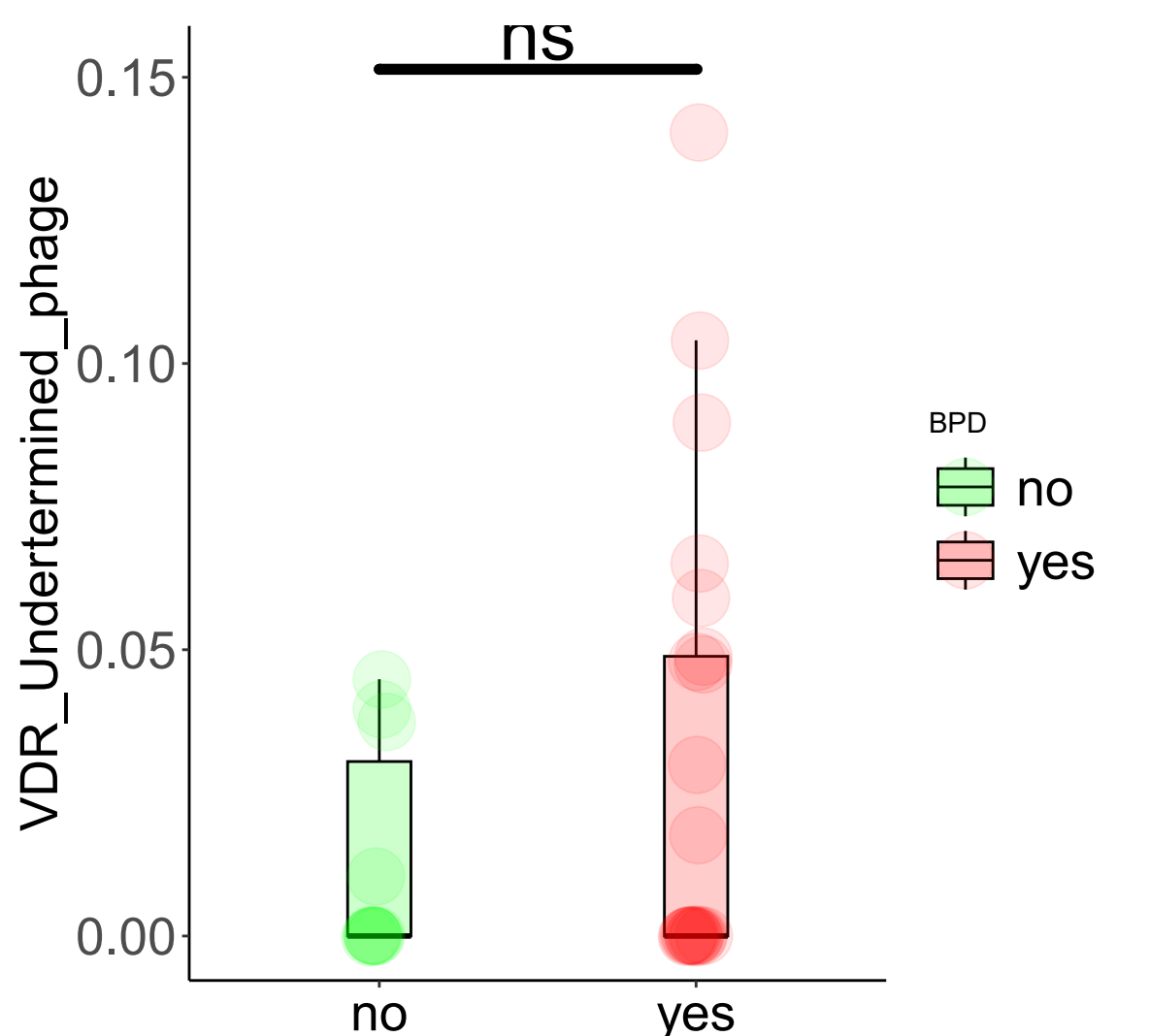
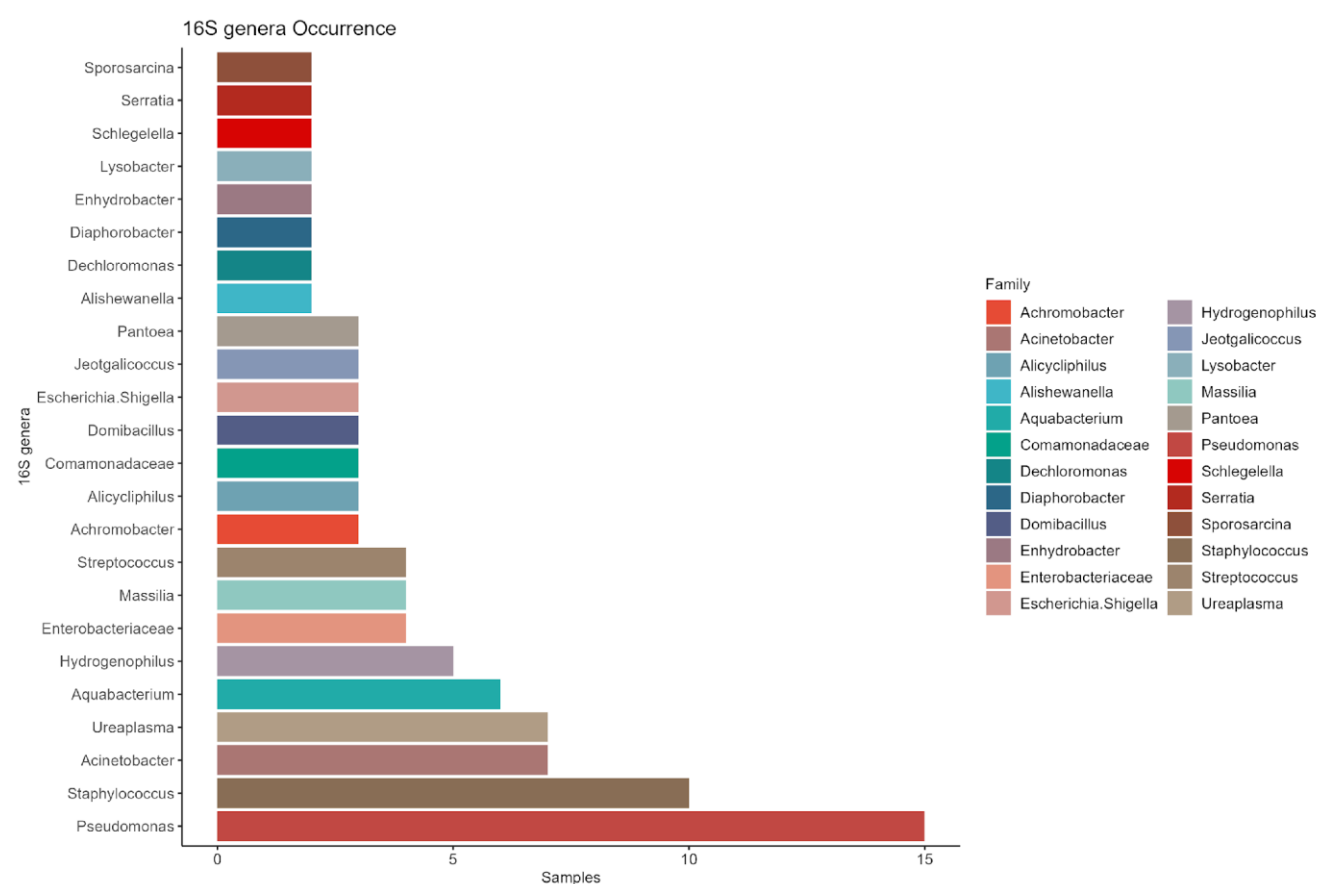
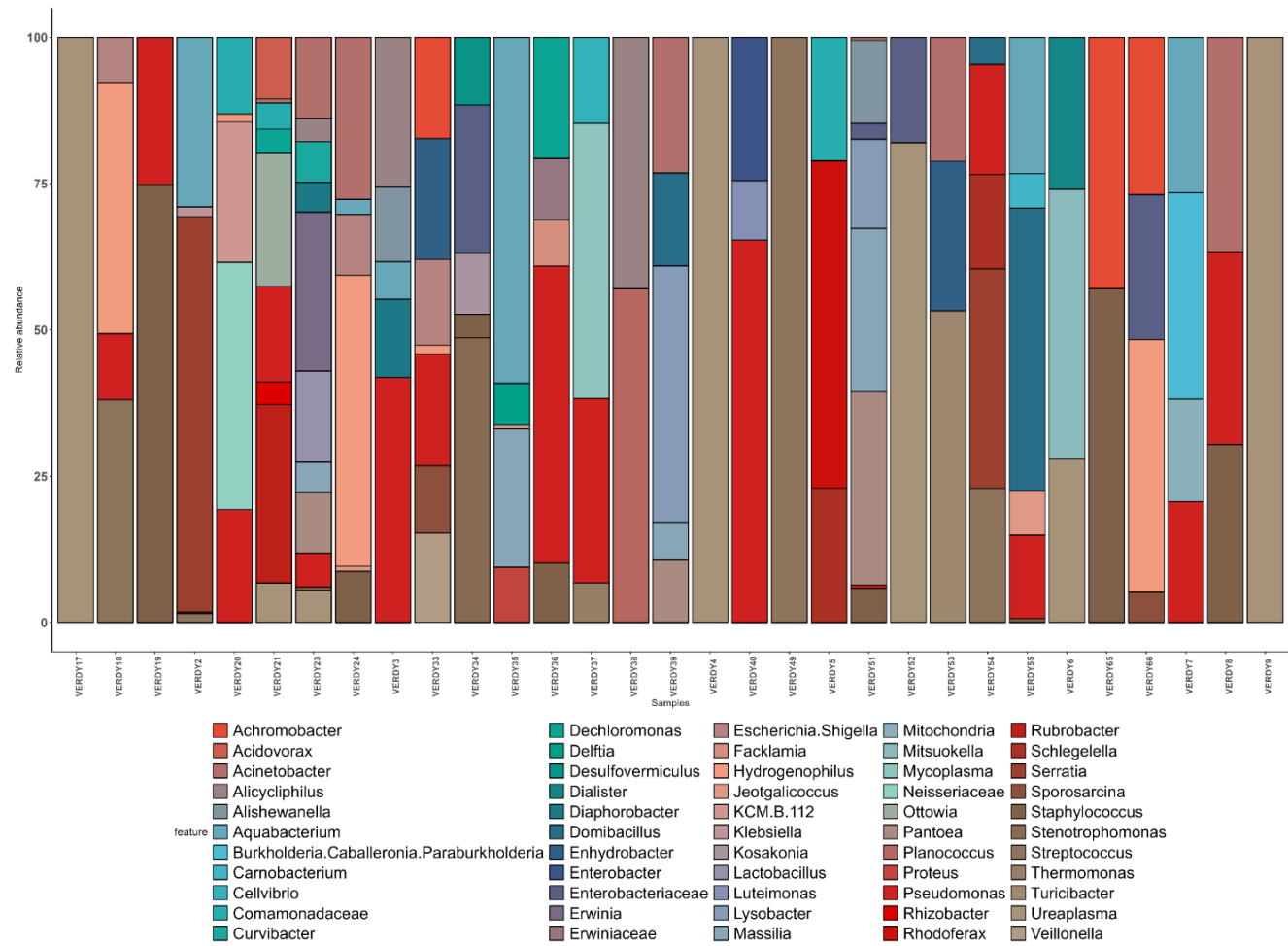
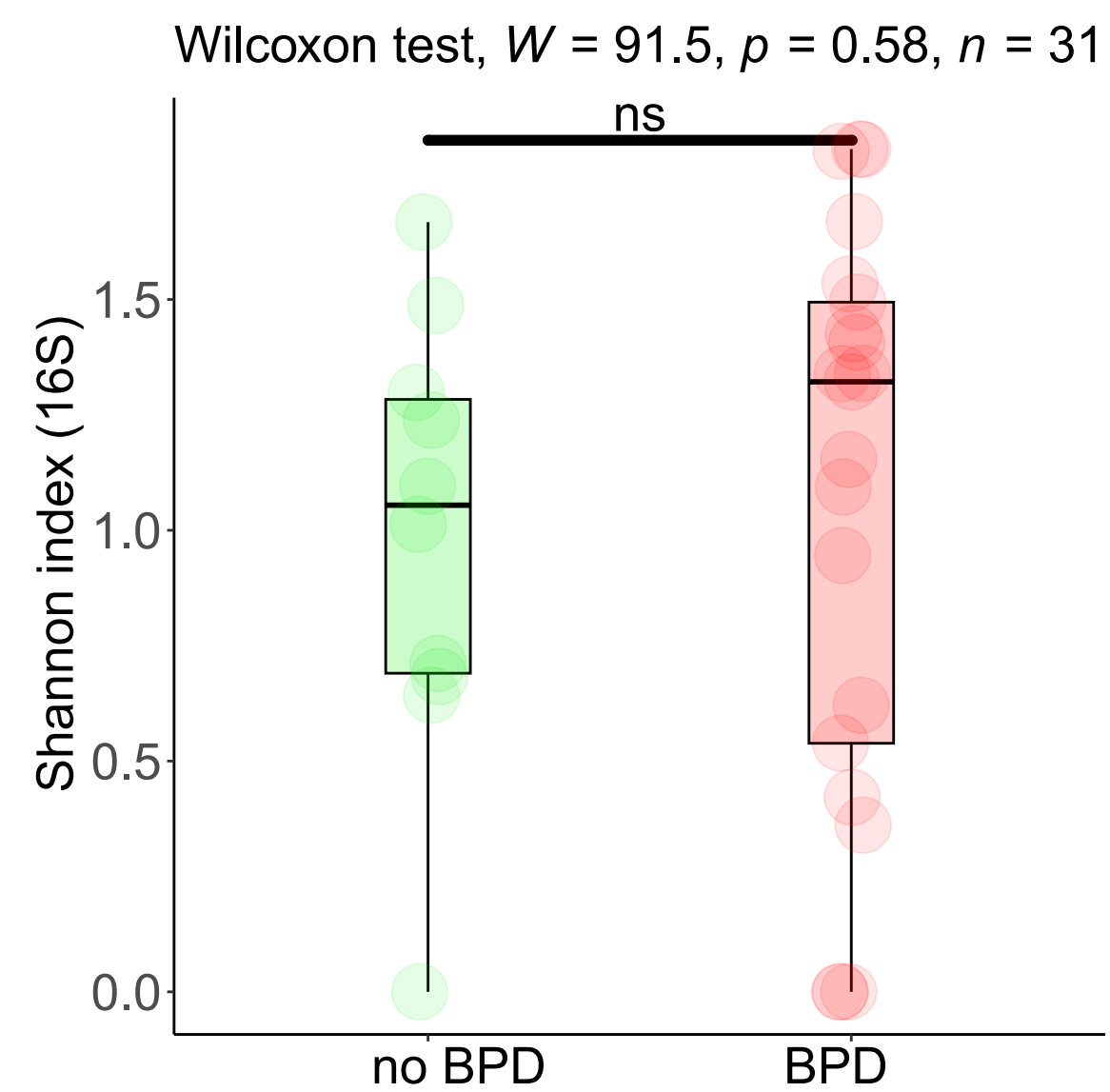
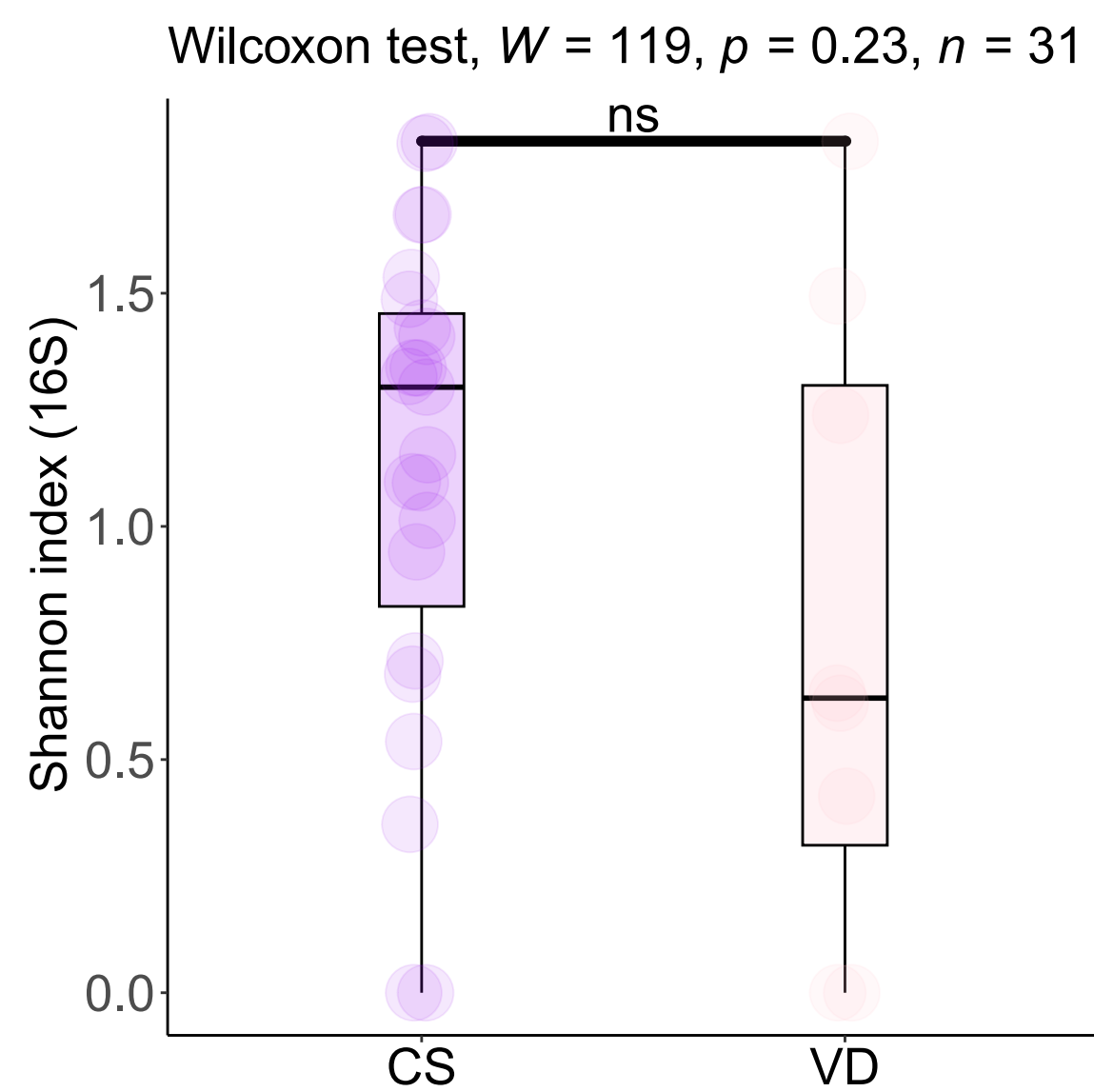
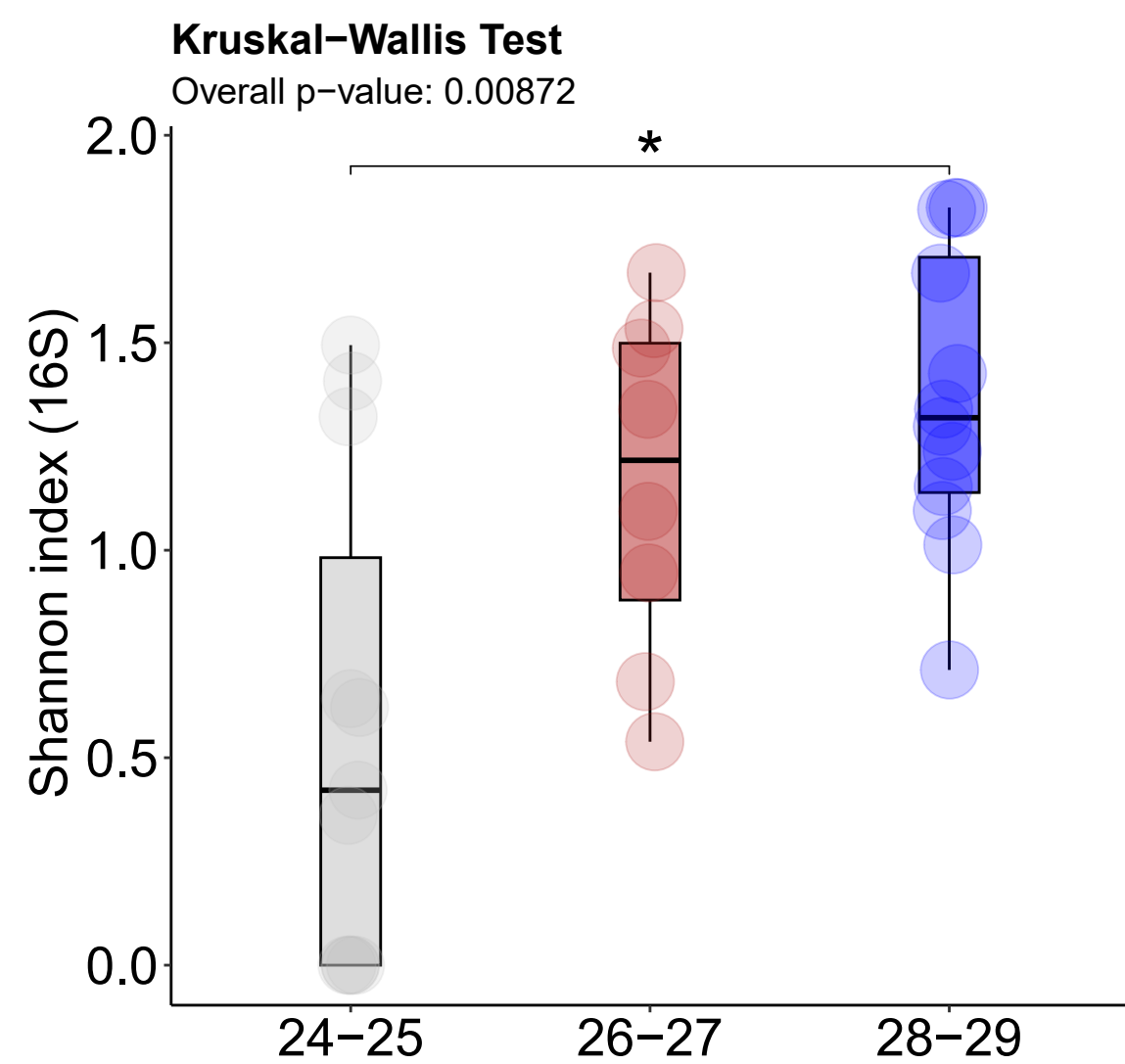


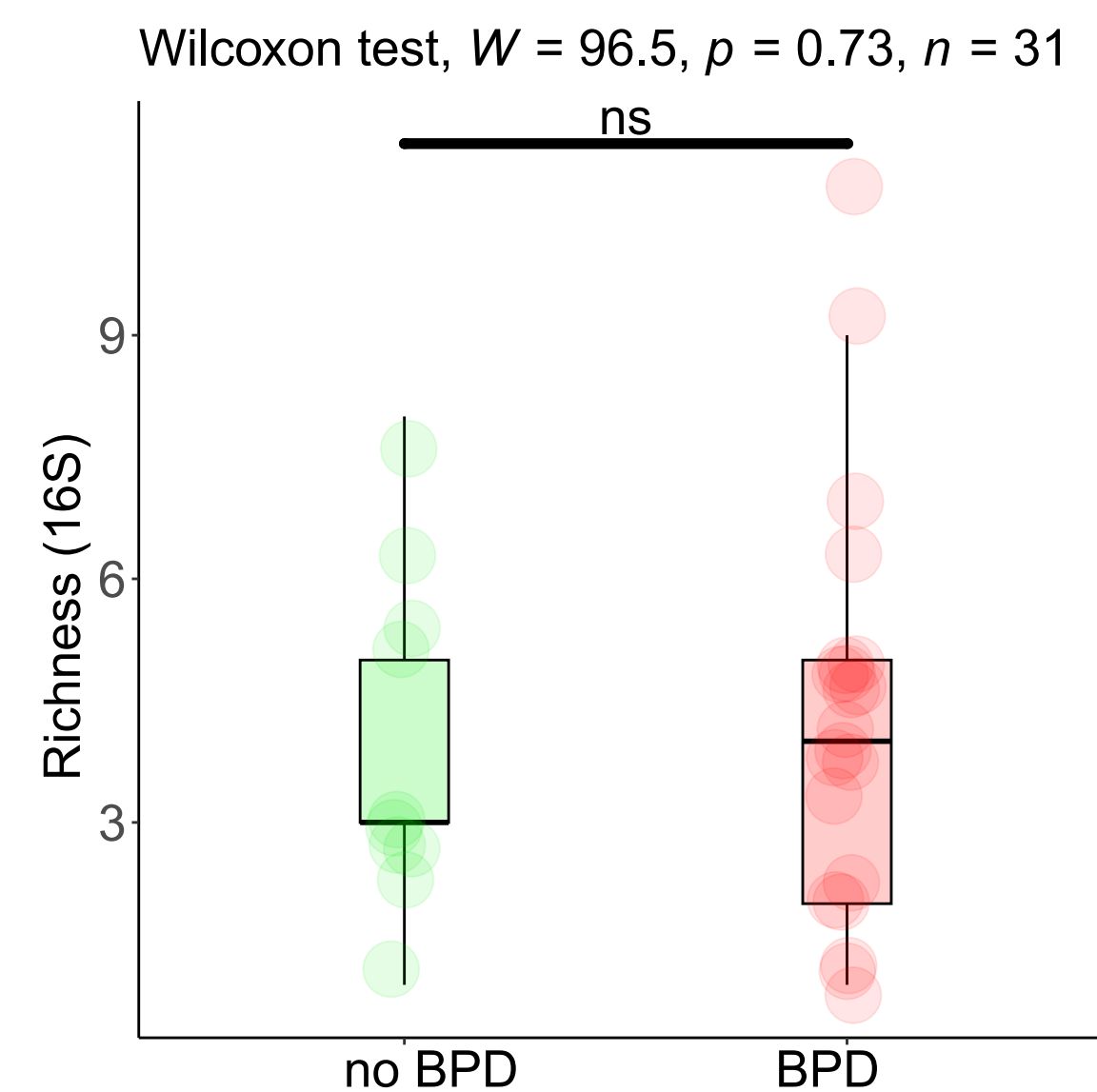
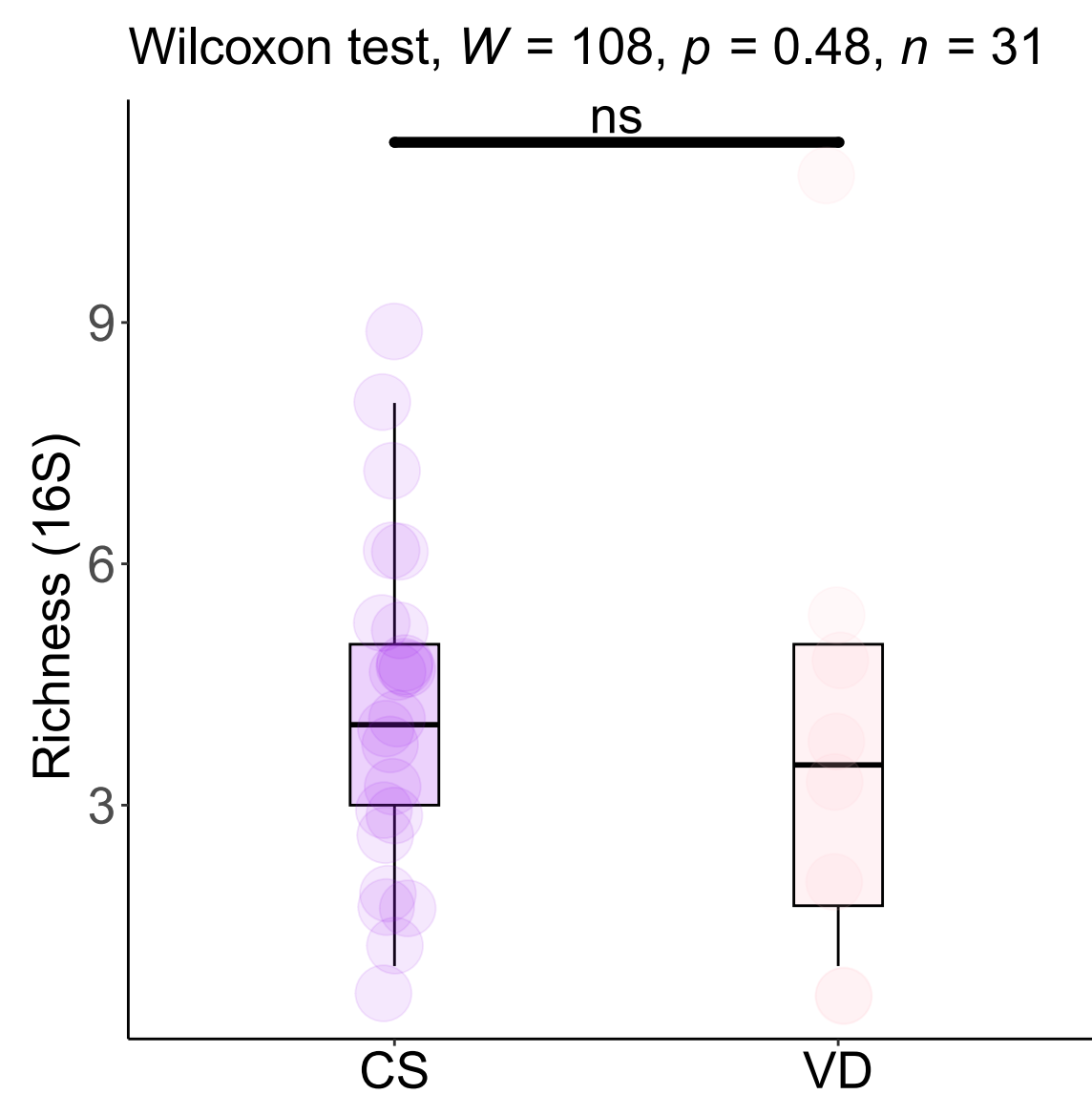
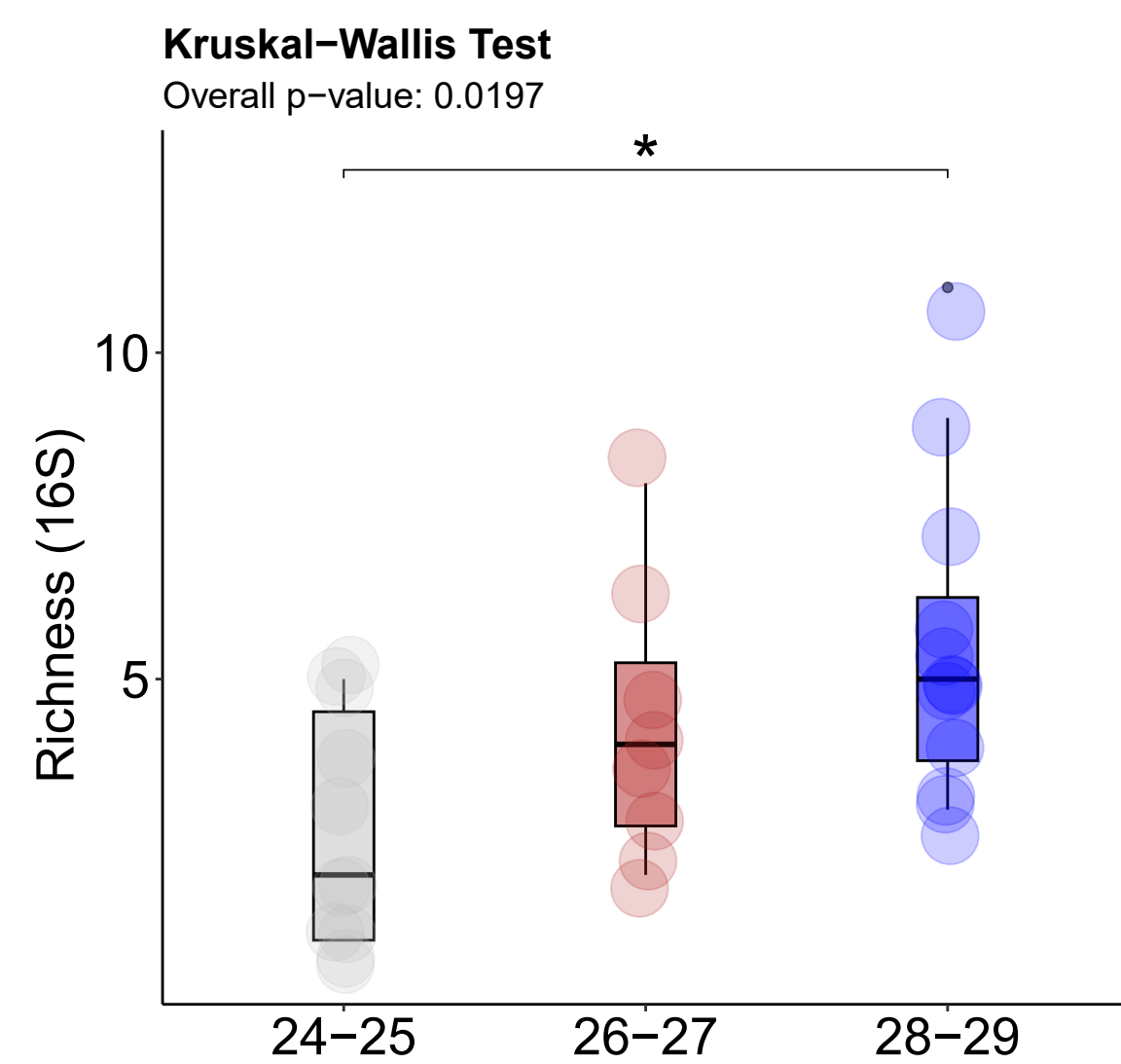
Fig S2.



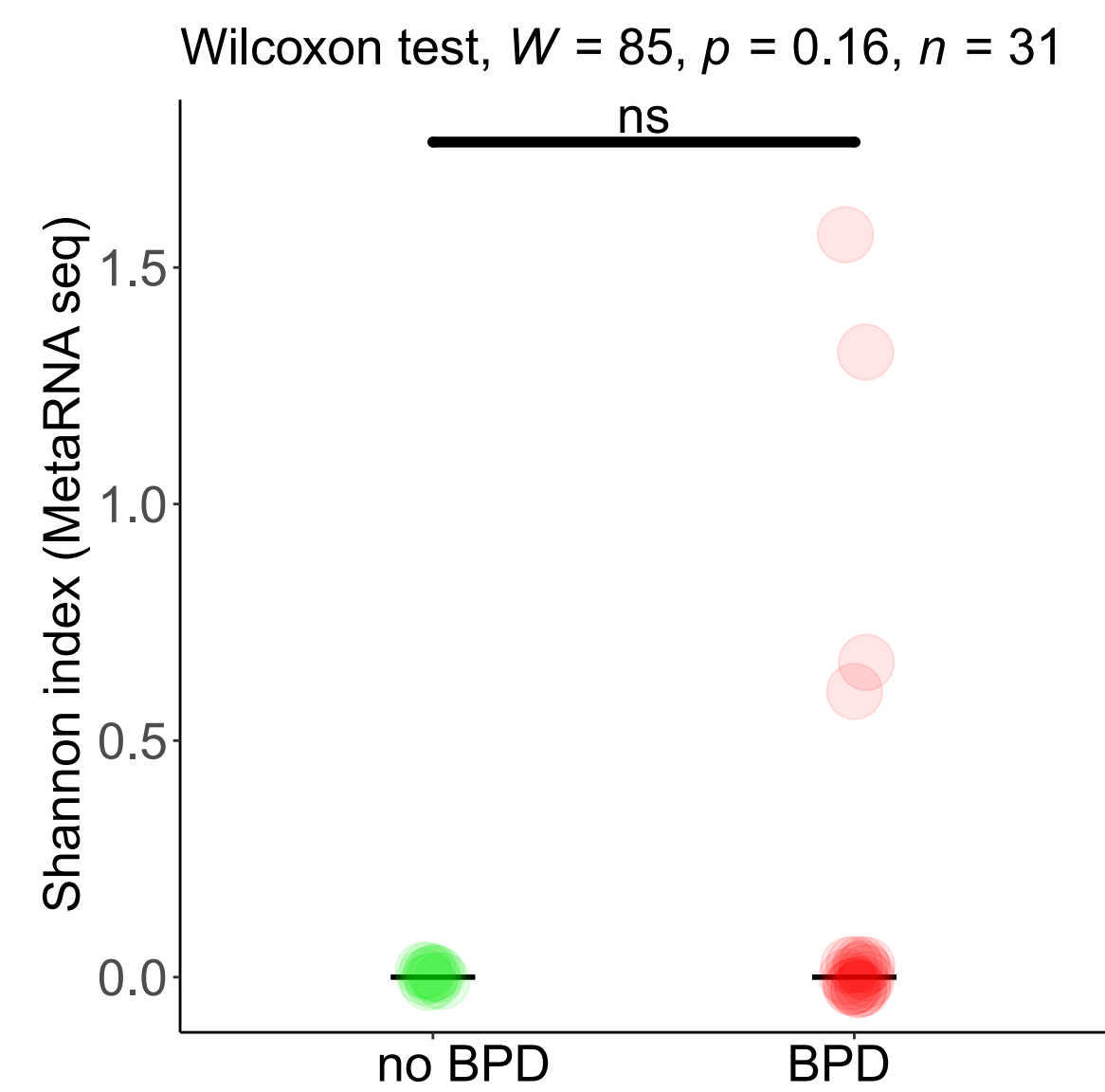
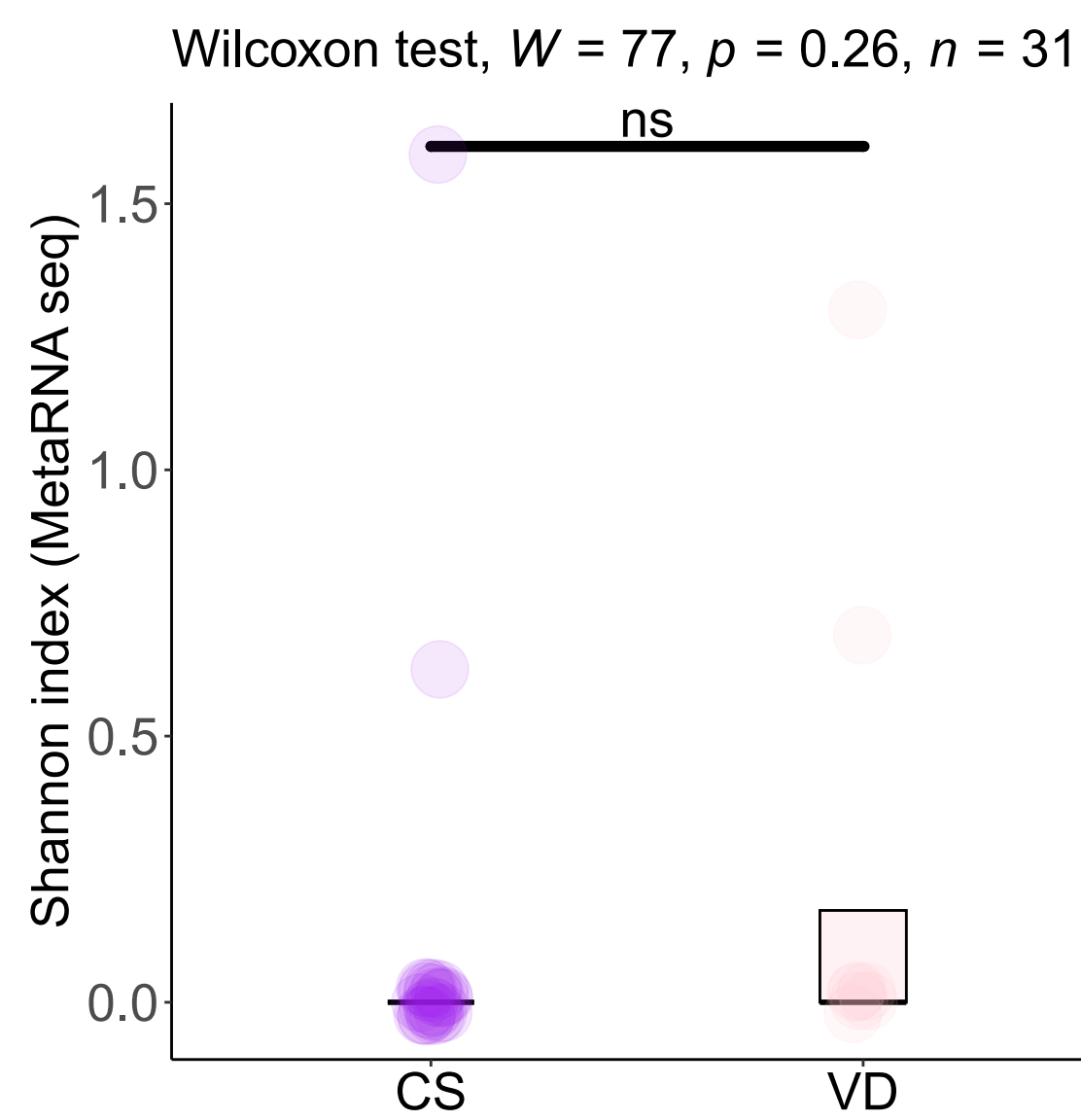
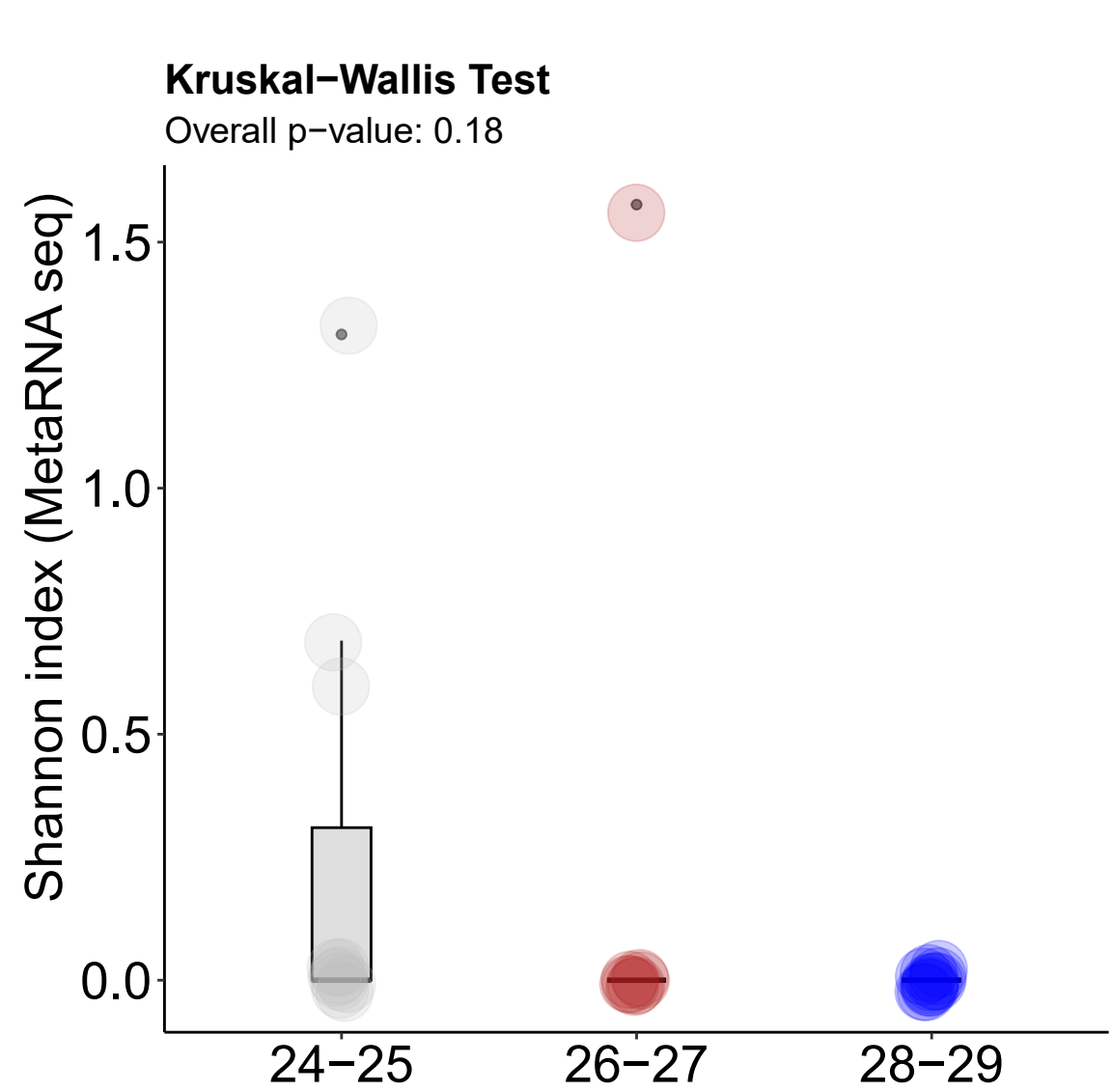
A



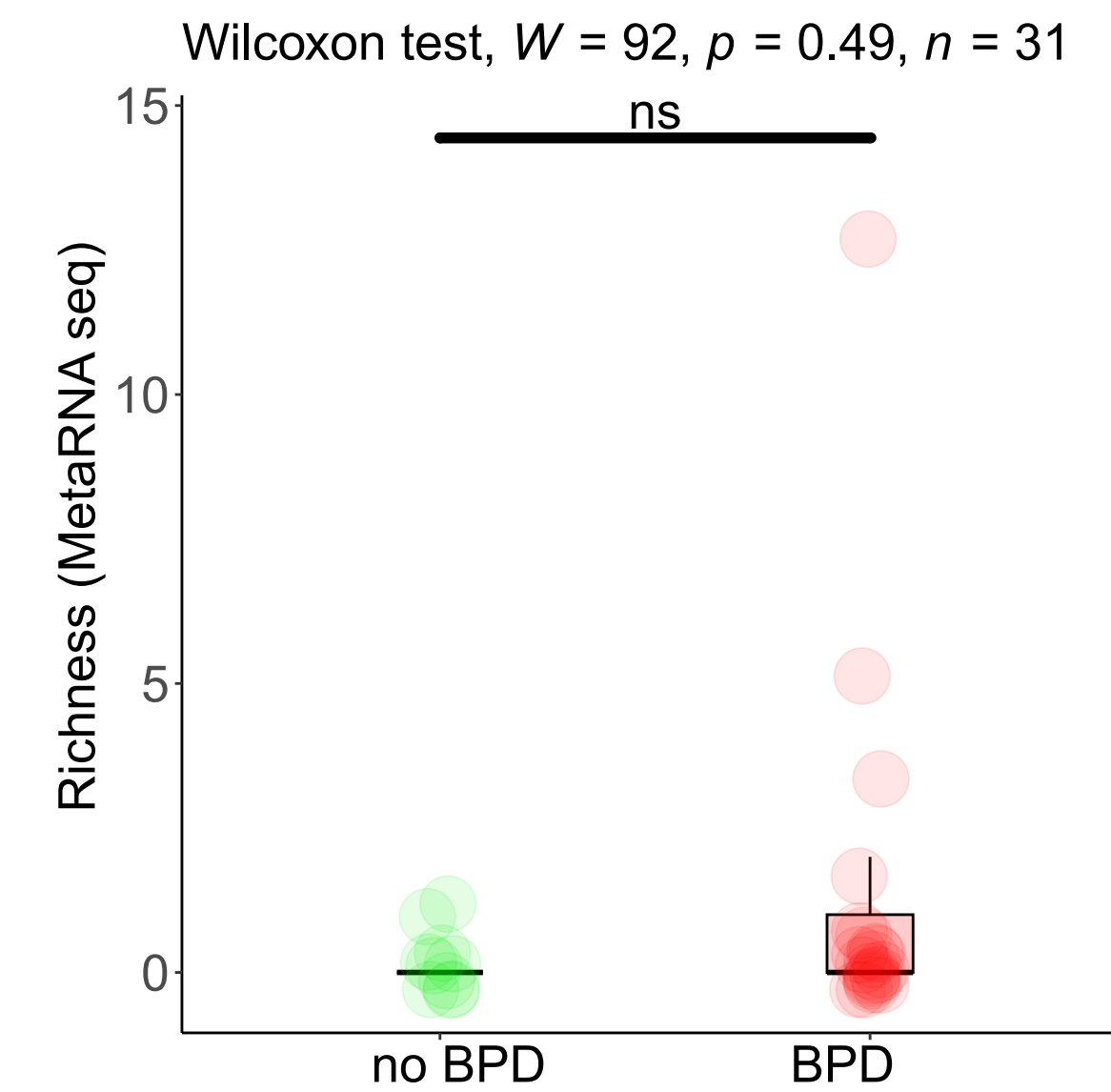
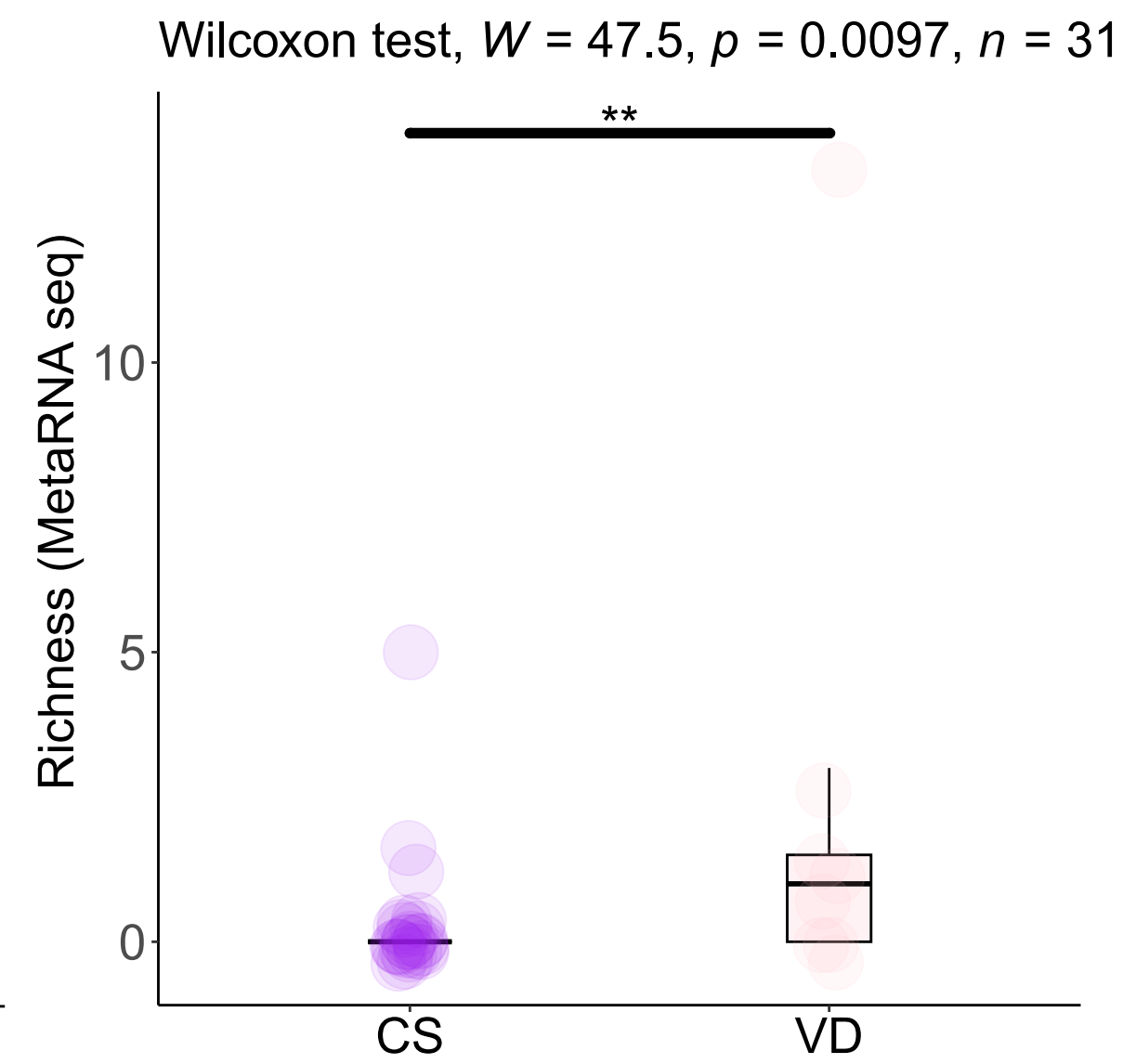
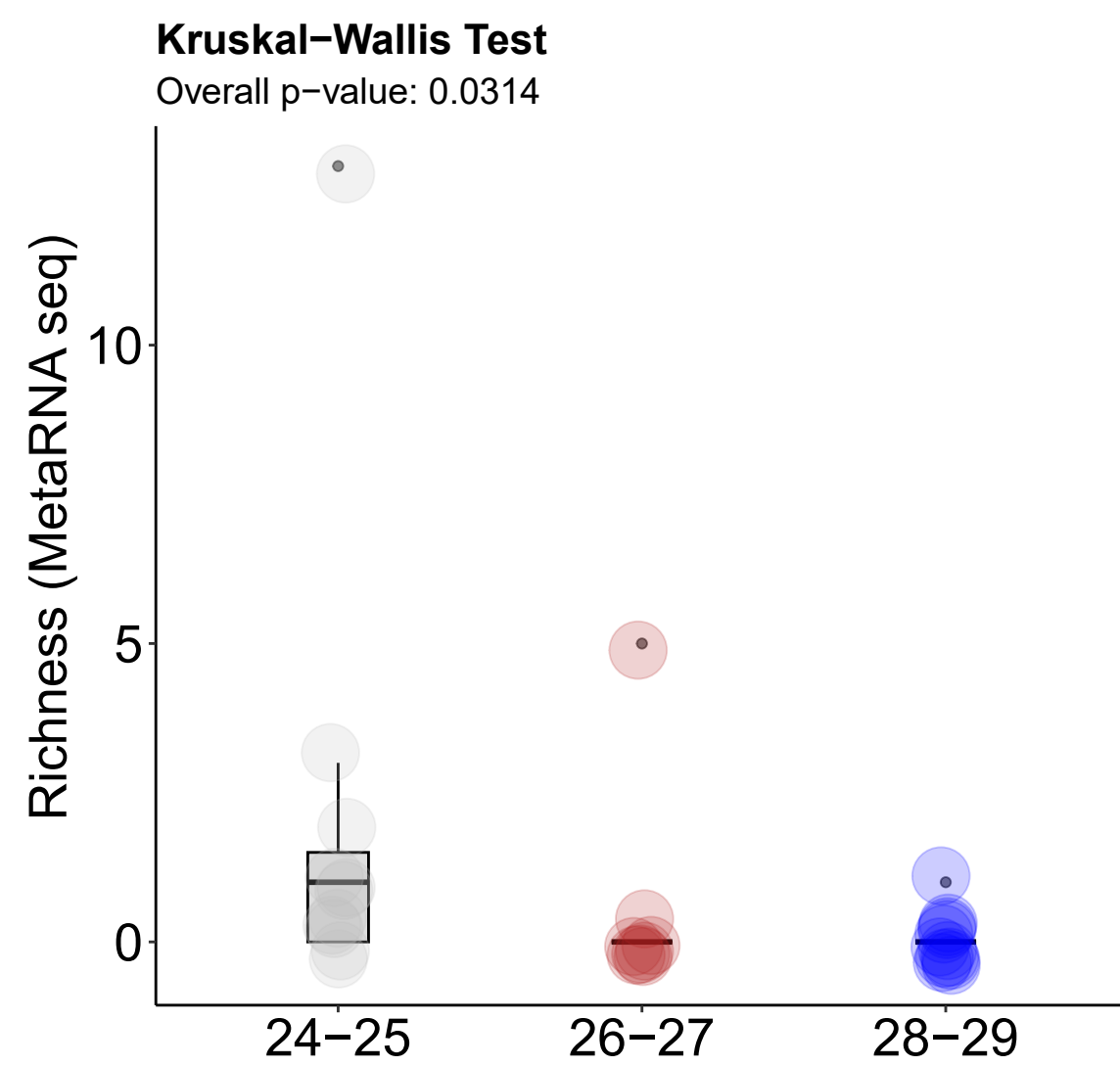
B



C



D



Reference Prediction	1	2	3	4
1	19.4	3.2	0.0	0.0
2	3.2	29.0	0.0	3.2
3	0.0	0.0	25.8	3.2
4	0.0	3.2	0.0	9.7

Accuracy (average) : 0.8387

Extended Data

As data on antibiotic exposure were missing for nearly half of the cohort (15/31), this variable was not included in the initial analyses. However, no obvious differences in endotype distribution related to antibiotic exposure were observed ($p > 0.05$). We also conducted supplementary analyses to specifically assess the impact of prenatal antibiotic therapy on the virome and bacterial composition. No significant differences were found in microbial load (Figure below), diversity, or the abundance of specific microorganisms using ANCOM-BC.

