

Supplemental Figures and Tables

Supplemental Tables

Table S1. Per-patient characteristics and summary

Table S2. Correlations between relative abundances calculated from 454 vs Sanger amplicon sequencing

Table S3. Summary of rarefaction analysis, subsampled

Table S4. Summary of patient treatments

Table S5. Shannon diversity indices and statistical testing on subsampled (n=100) data, by treatment effect

Table S6. Sample sizes for analysis

Table S7. Shannon diversity indices and statistical testing on subsampled (n=100) data

Table S8. Theta similarity indices and statistical testing for subsampled (n=100) values

Table S9. Genera significantly over/underrepresented (adjusted P -value < 0.1) between groups, all sites

Table S10. Staphylococcal species significantly over/underrepresented between groups, all sites

Table S11. Spearman correlation between taxonomic abundance (Af) and patient clinical metadata

Table S12. Fungal-based analysis of select individuals

Table S13. Order of subjects in relative abundance plots in Fig. 2, 6, S4, S7

Table S14. Random forests analysis of bacterial taxa.

Supplemental Figures

Figure S1. Partial Spearman correlation (ρ) between samples sequenced by Sanger vs. 454.

Colors indicate patient category; plots are separated by taxonomy. Most abundant taxonomies are shown. Table (bottom right) shows the partial correlation for each taxa, adjusting for patient, and associated *P*-value.

Figure S2. Rarefaction analysis for the skin and nares microbiota sampling at each site

(antecubital fossa (Af), retroauricular crease (Ra), nares (N), popliteal fossa (Pf), volar forearm (Vf)) calculated as operational taxonomic units (OTUs) at a cutoff of 97% similarity. Sanger samples are shown in (A); 454 samples are shown in (B). Each point represents mean $\pm$ SEM of all individuals at specified site and patient category.

Figure S3. The effect of treatment on community diversity. Treatments assessed were whether the patient (STAT3-HIES, DOCK8, or WAS; represented as different shapes) had taken antibiotics or steroids orally within the last month or topically within the last seven days (“recent treatment”, light blue) versus greater than one month or seven days, respectively (“no recent treatment”, dark blue). Each point represents the value for an individual patient timepoint, separated by site.

Figure S4. Additional bacterial taxonomic classifications for the (A) antecubital fossa, (B) nares, (C) retroauricular crease, and (D) volar forearm. Relative abundances of 14 major phyla-family taxonomies (top) are shown grouped by patient category. On the bottom are relative abundances

of species-level classification of staphylococcal and streptococcal species. Order of subjects follows the top; full subject information is shown in Table S13.

Figure S5. Barplots of mean proportions ($\pm$ SEM) of select significantly different major genera/species in the antecubital fossa by patient category, as represented by piecharts in Fig. 2 and Fig. 5.

Figure S6. Additional principal coordinates analysis (PCoA) plots of the Yue-Clayton theta coefficient showing taxonomies associated with variation within and between individuals. Description follows from Fig. 3. Biplot arrows indicate the most significant unique consensus taxonomies contributing to variation along axis 1; Spearman correlations (ρ) are with axis 1. Length of biplot arrows reflects the contribution of that taxa to the top three axes. Associated P -values $< 2.2 \times 10^{-16}$. % variation attributed to an axis is indicated. N nares; Vf volar forearm.

Figure S7. Heatmap of mean Theta similarity coefficients of pairwise comparisons of communities within or between different patient groups. Darker color indicates higher similarity: $\theta=0$ indicates that two samples have no species in common and $\theta=1$ indicates that two samples are identical. N.D. indicates no data available.

Figure S8. Additional fungal taxonomic classifications for the (A) antecubital fossa, (B) nares, (C) retroauricular crease, and (D) volar forearm, grouped by patient category. Description follows from Fig. 6B.

Figure S9. Correlations of relative abundances of fungal and bacterial taxa at each site.

Correlations were analyzed for fungal and bacterial genera, and when possible species, that occurred in >25% of either control or STAT3-HIES patient samples. Spearman correlations between relative abundances of fungal vs. bacterial phylotypes with mean abundance across samples > 0.25% were calculated for two-way unsupervised hierarchical clustering of the Spearman correlation coefficients. Reds indicate correlation; blues indicate anti-correlation. (A) Af, (B) N, (C) Ra, (D) Vf. Left, control heatmap; right, STAT3-HIES.

Figure S1.

Relative abundance, Sanger

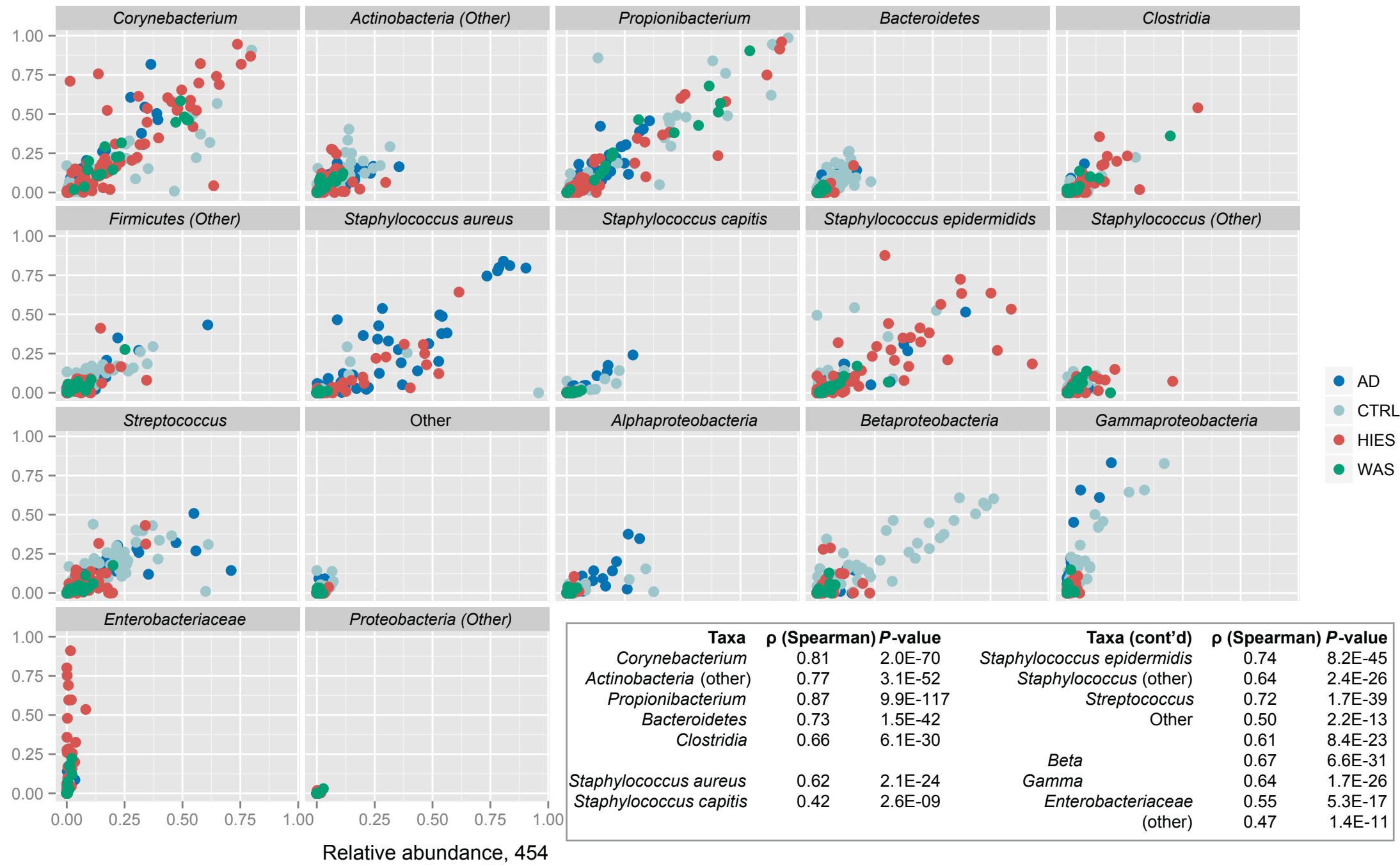
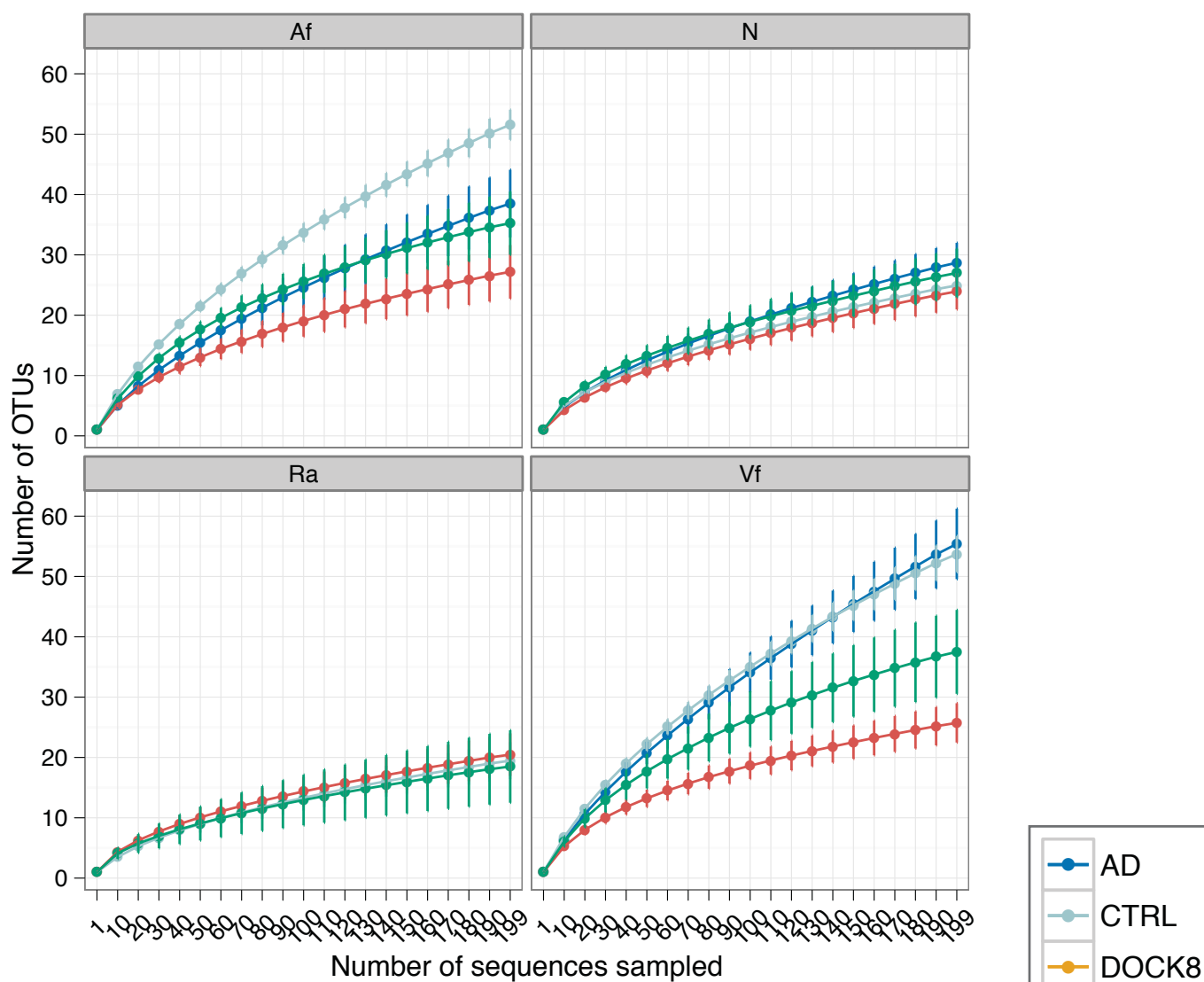


Figure S2.

A



B

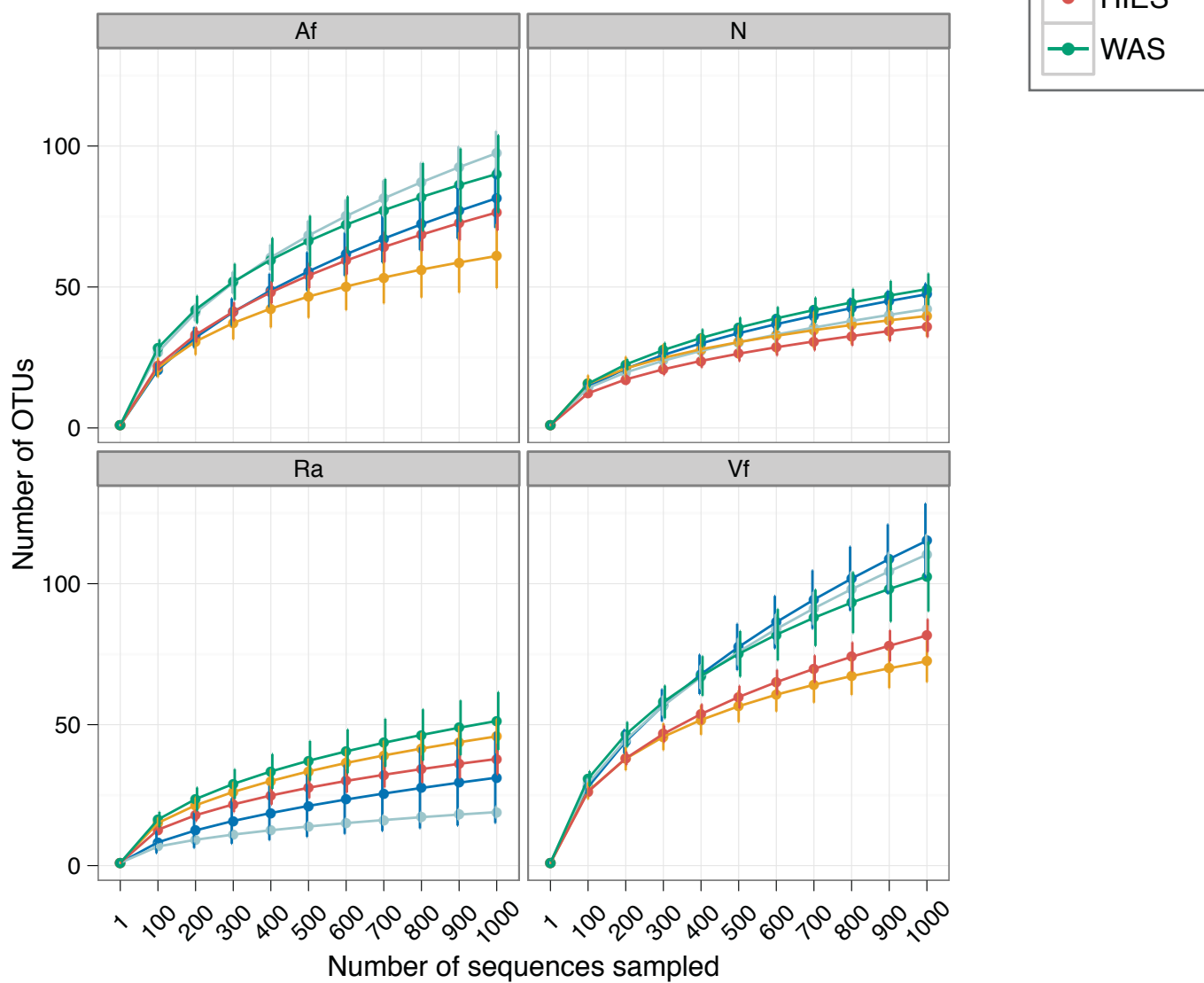


Figure S3.

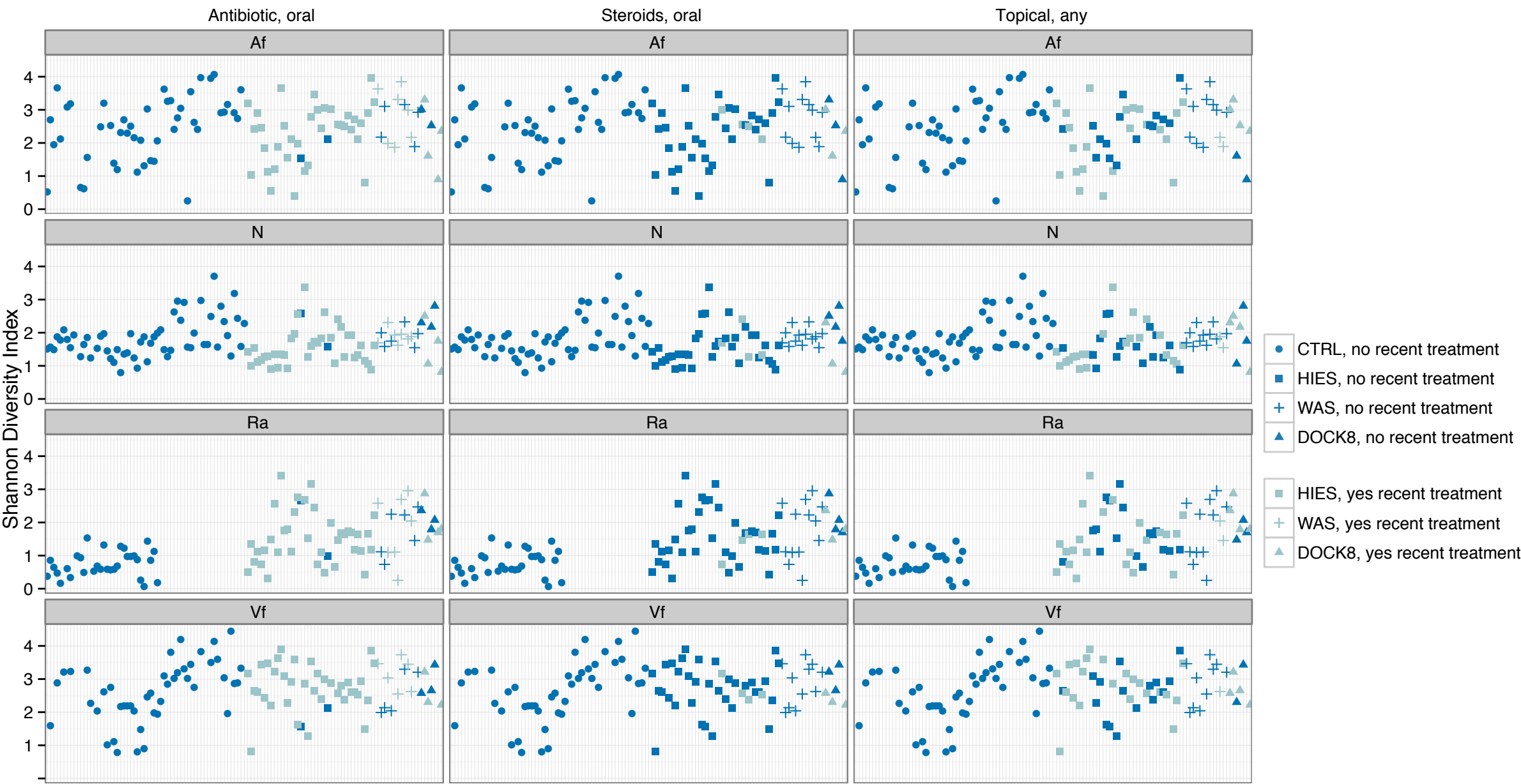


Figure S4A.

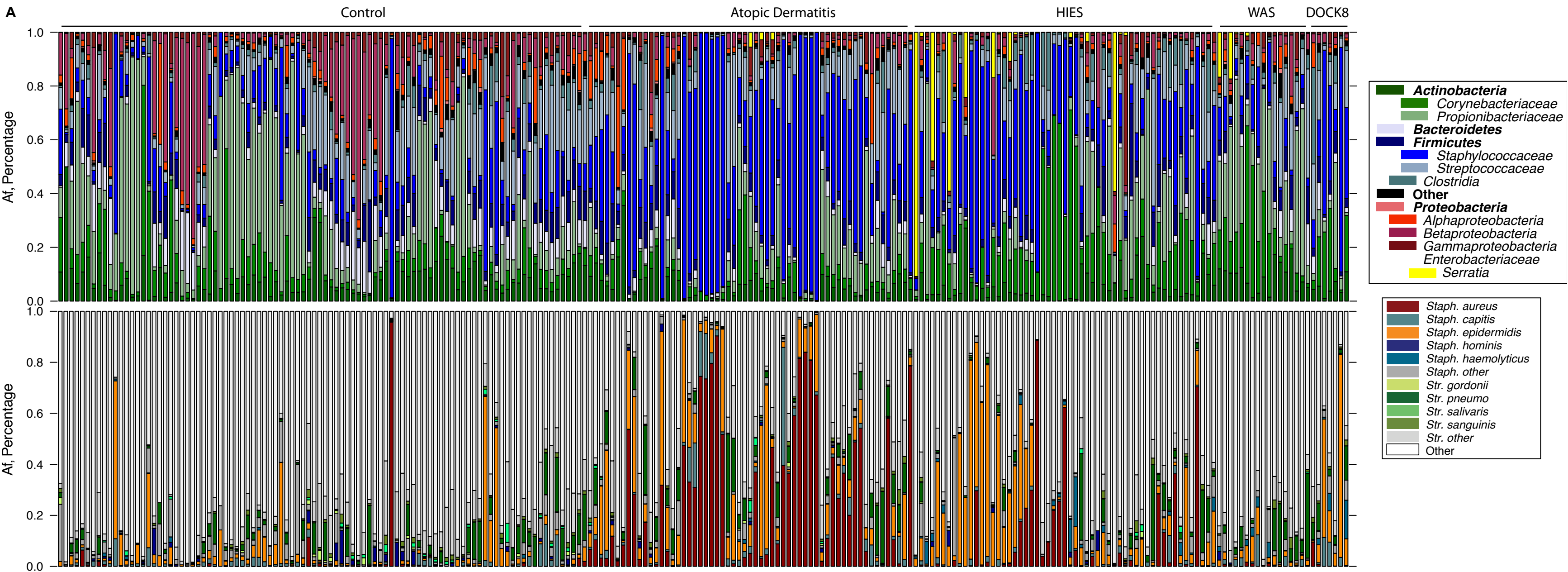


Figure S4B.

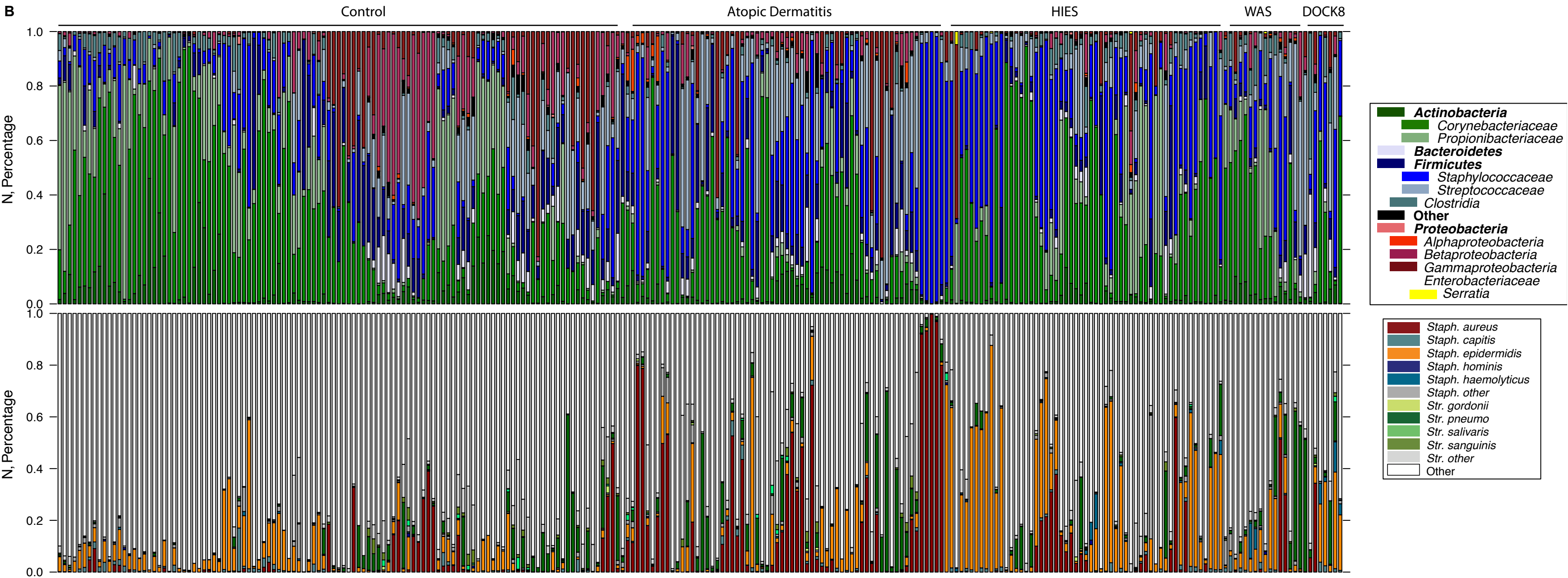


Figure S4C.

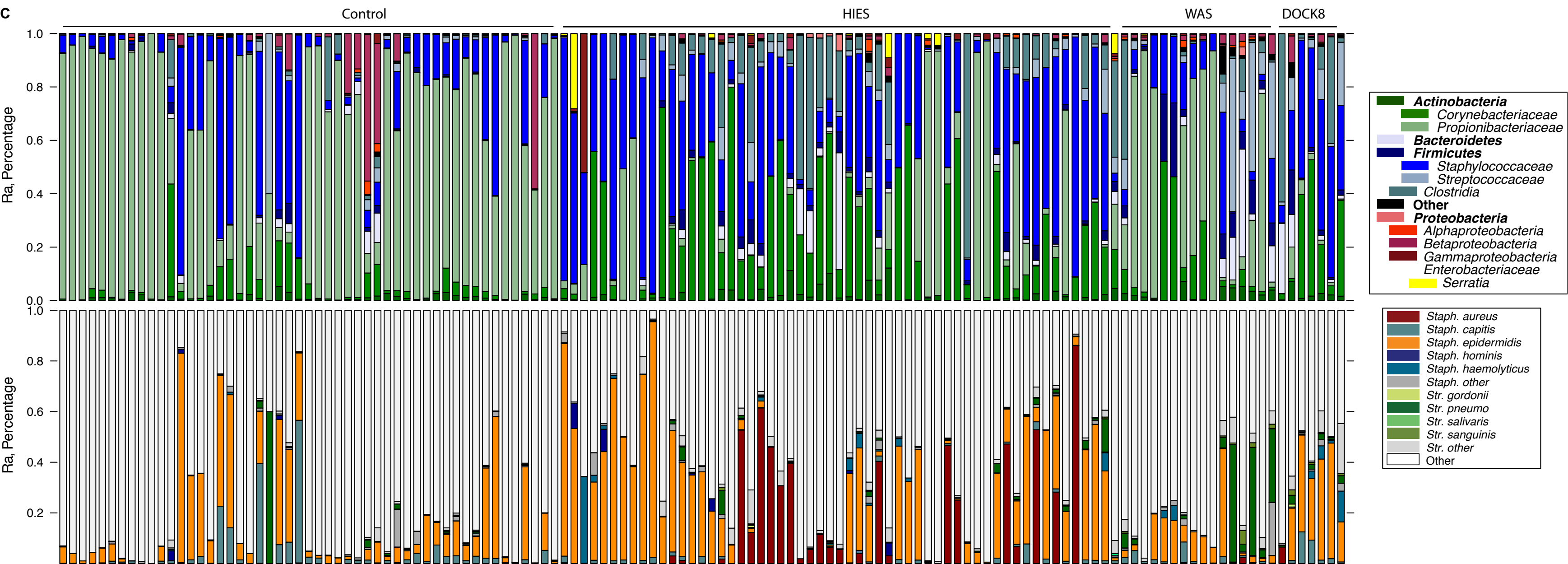


Figure S4D.

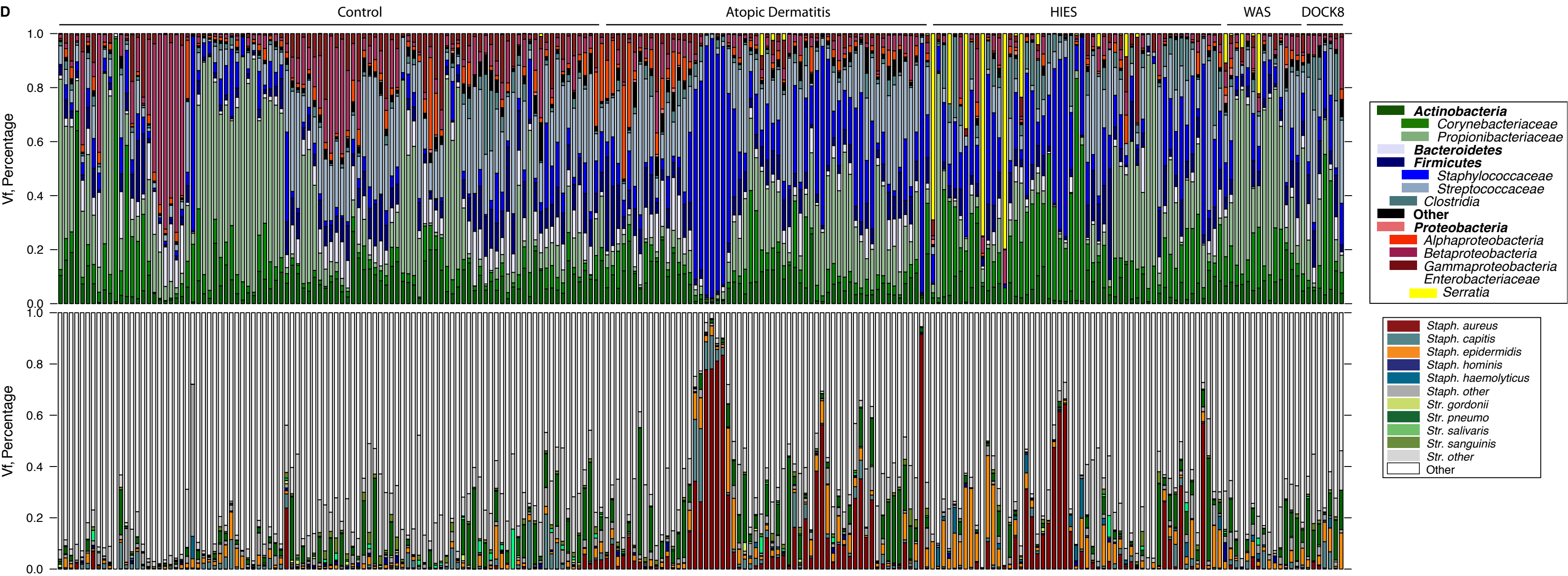


Figure S5.

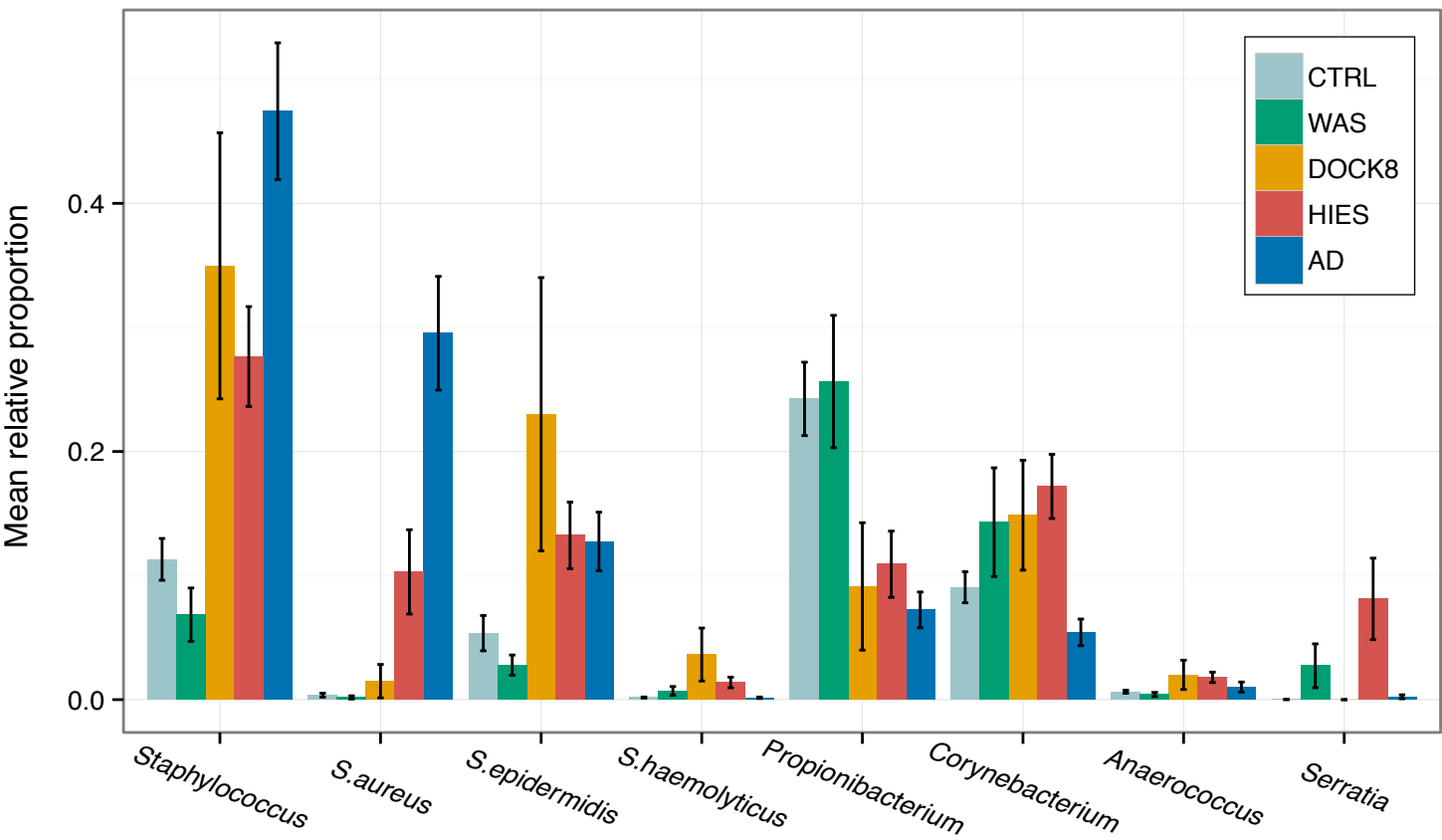


Figure S6.

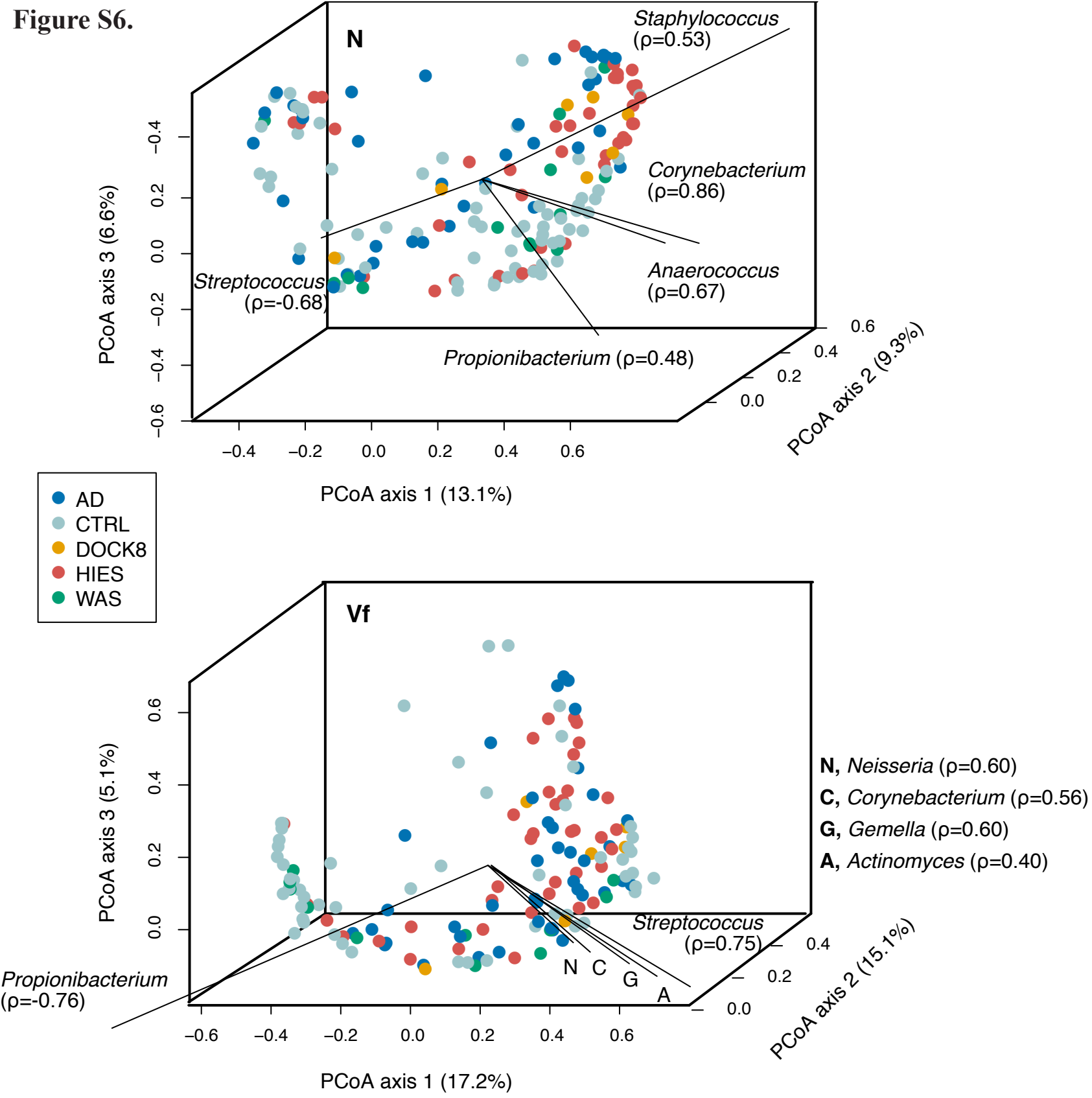


Figure S7.

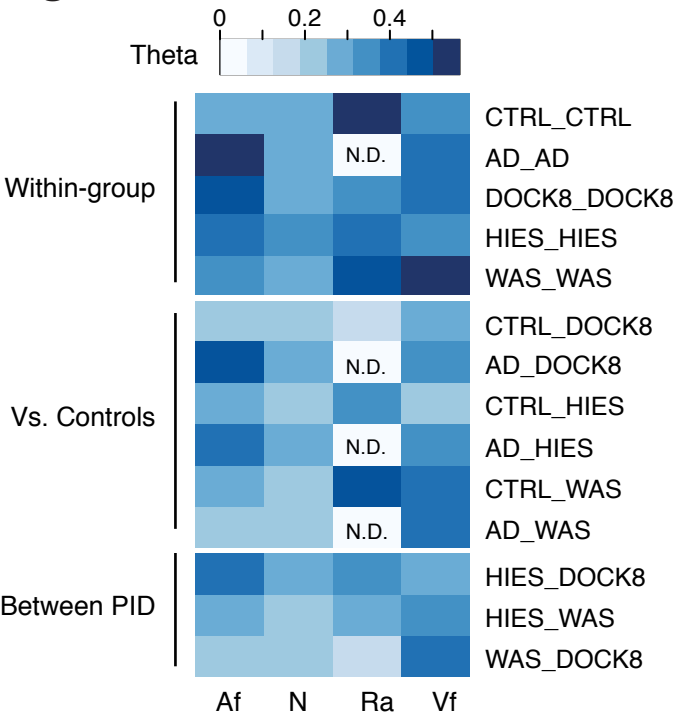


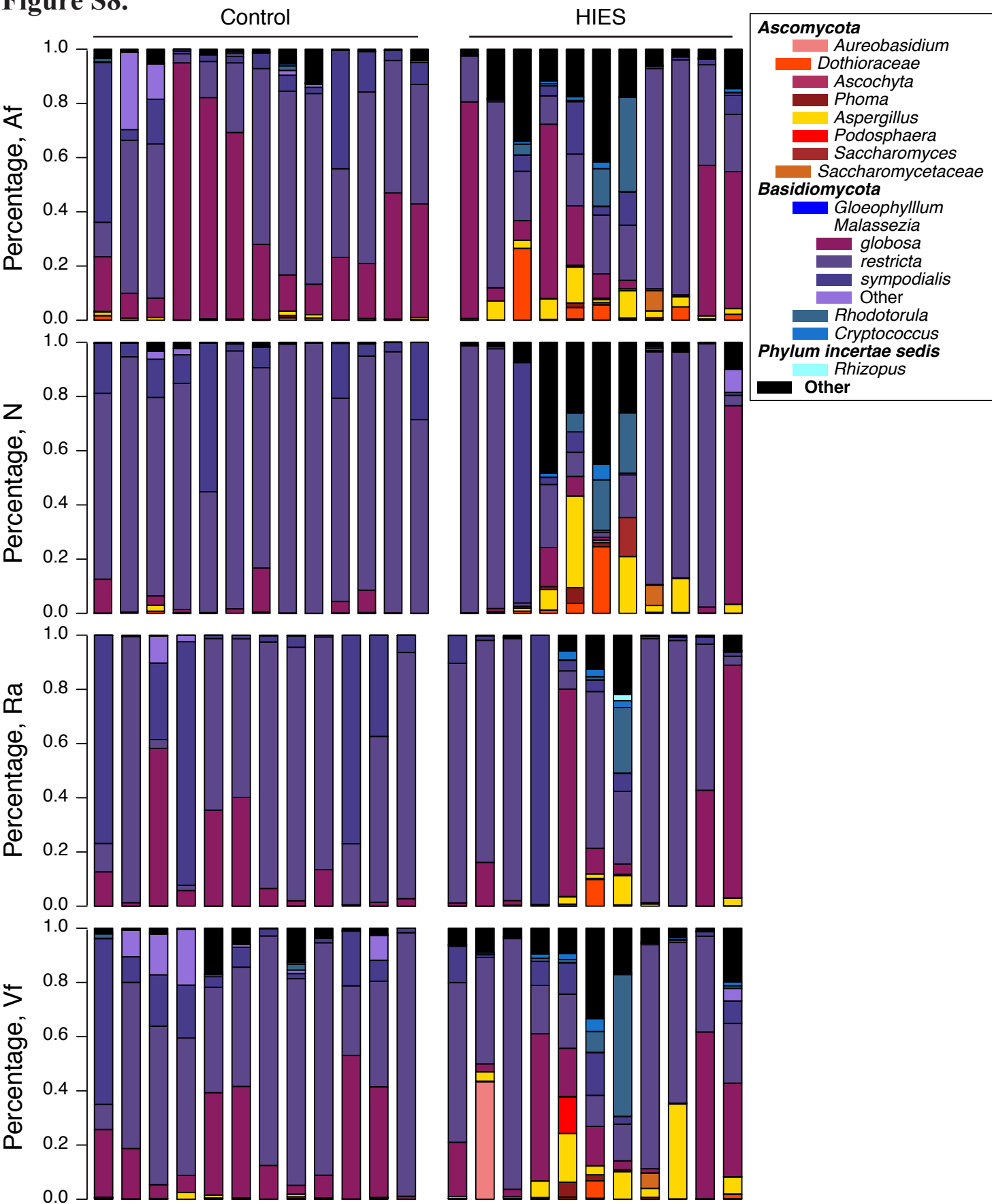
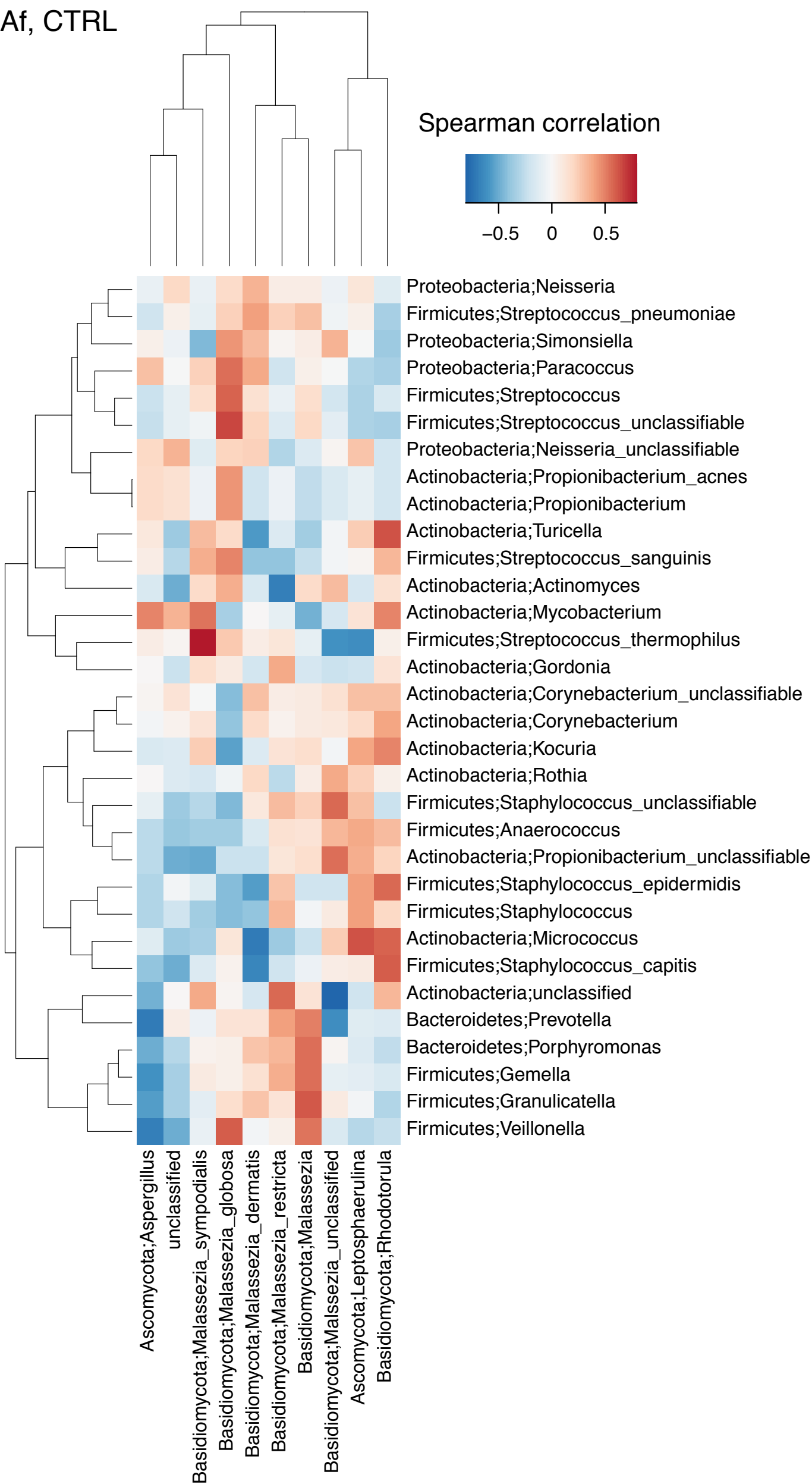
Figure S8.

Figure S9A.

Af, CTRL



Af, HIES

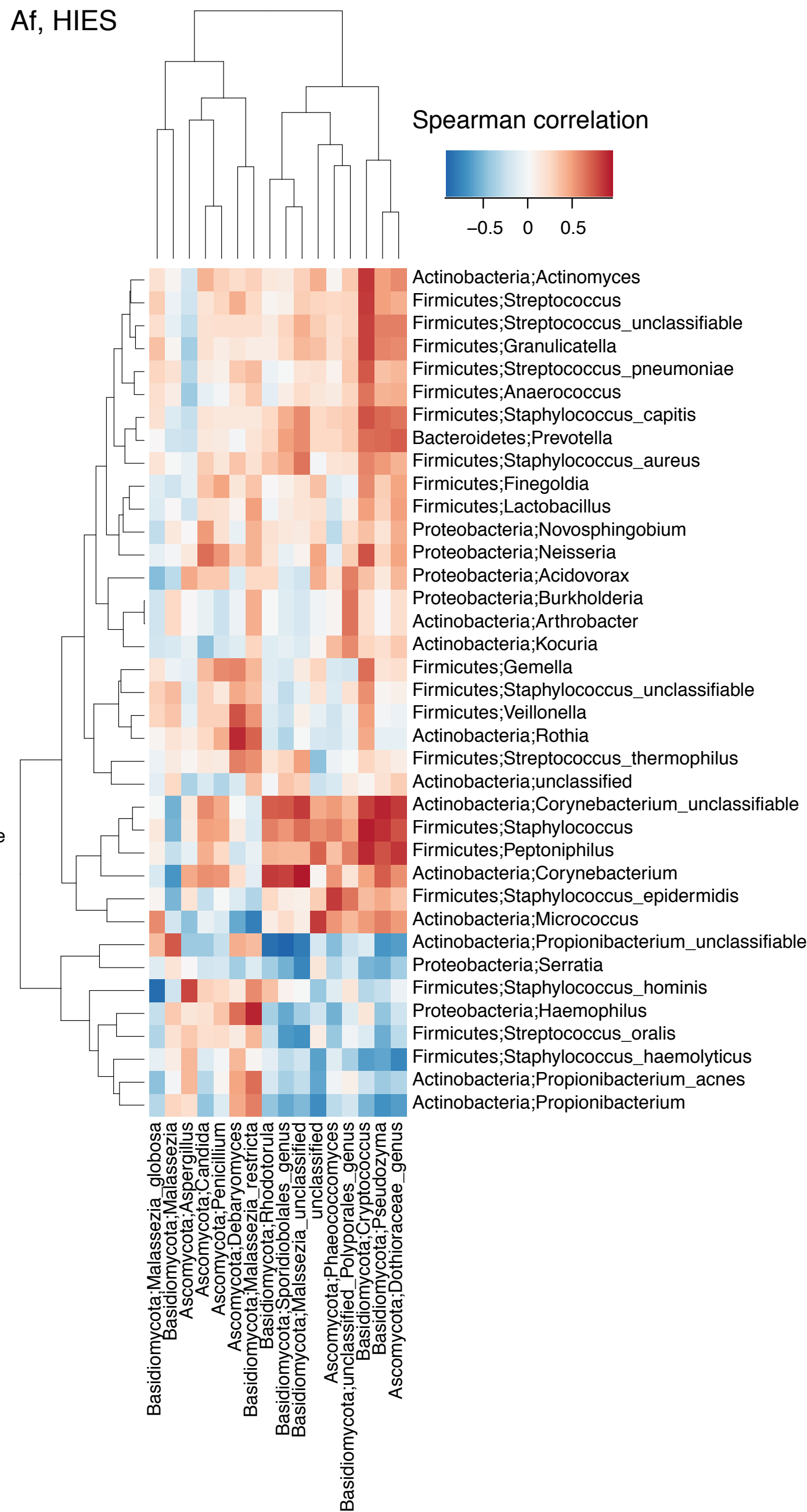
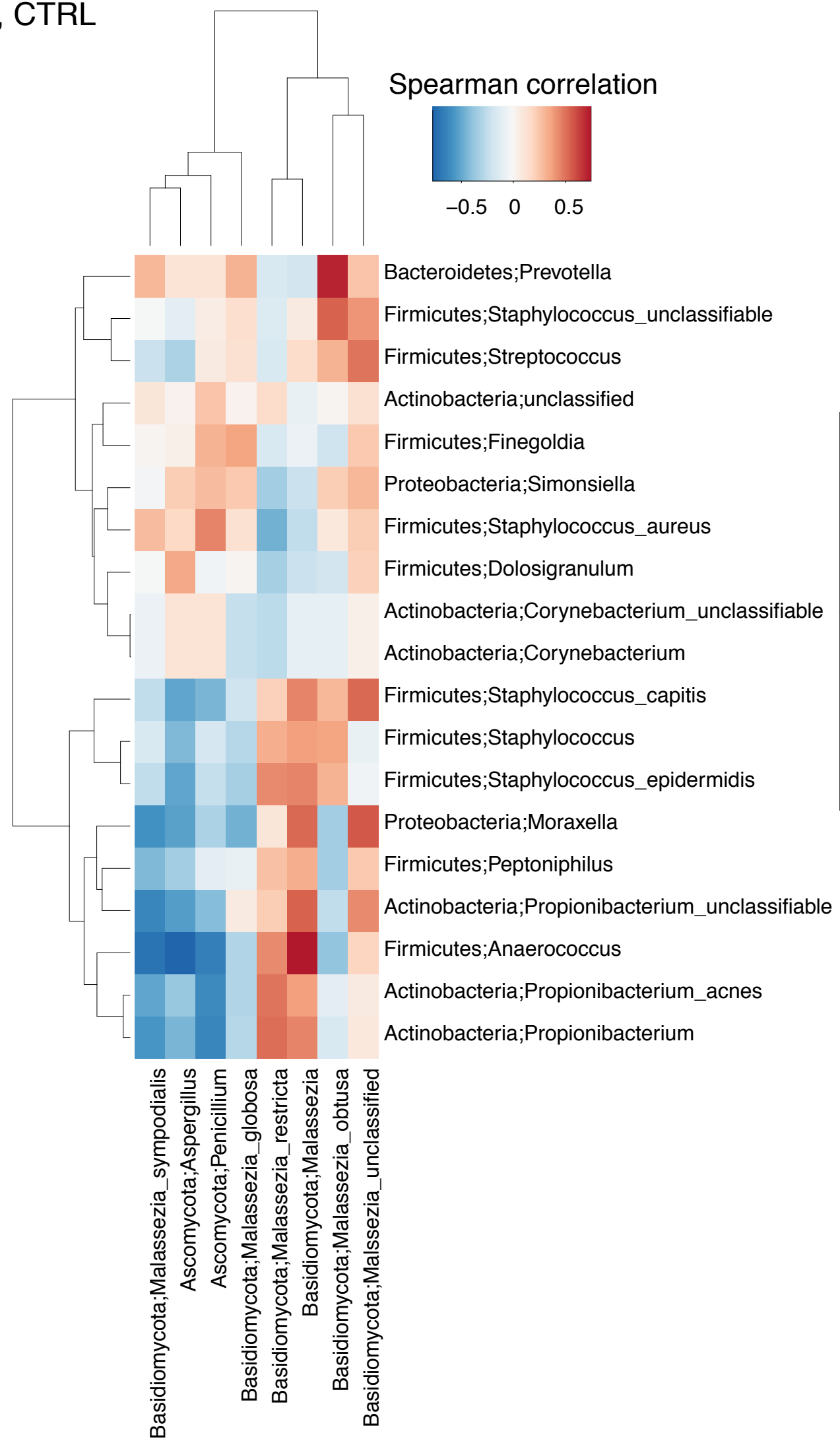


Figure S9B.

N, CTRL



N, HIES

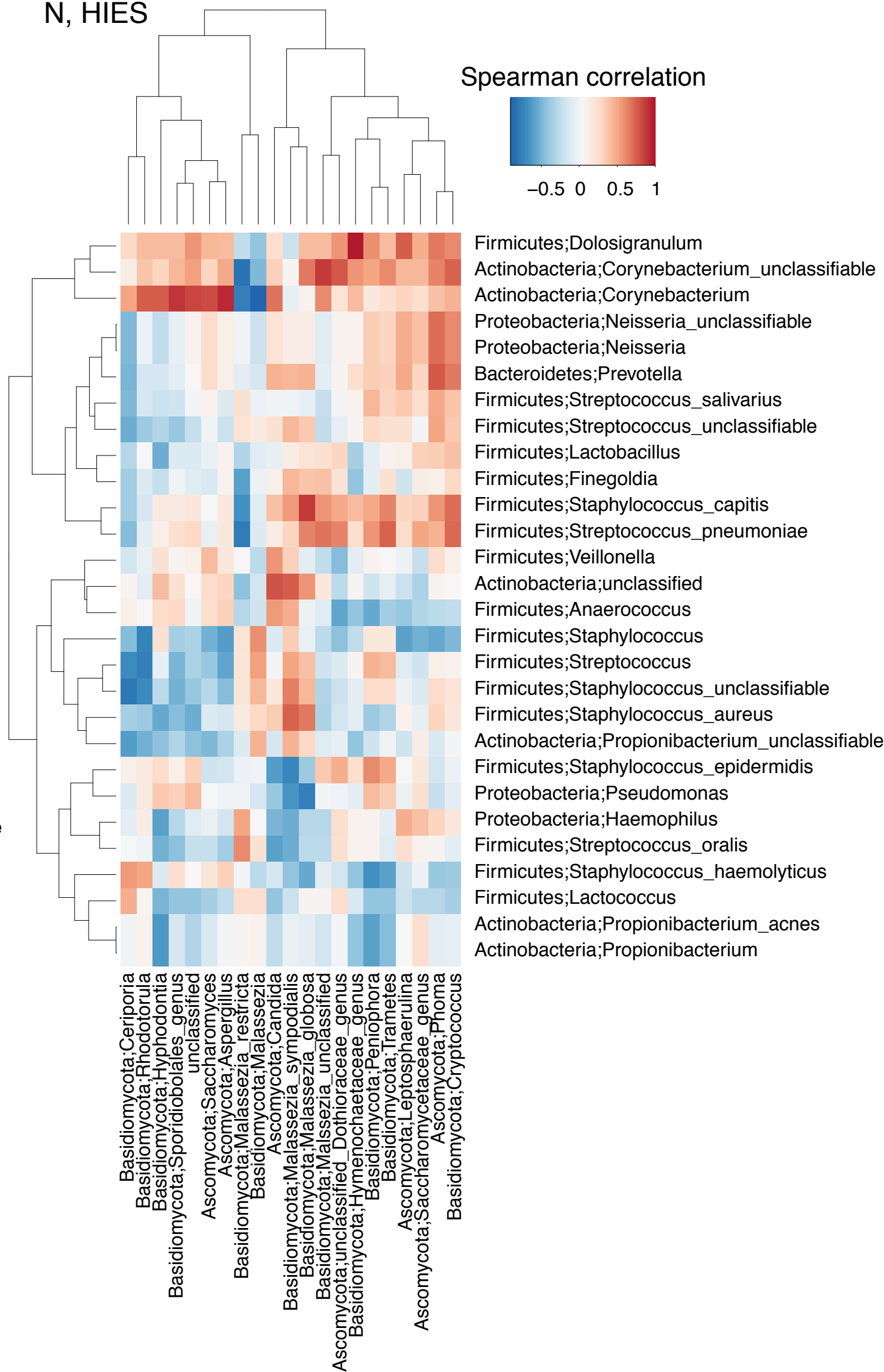
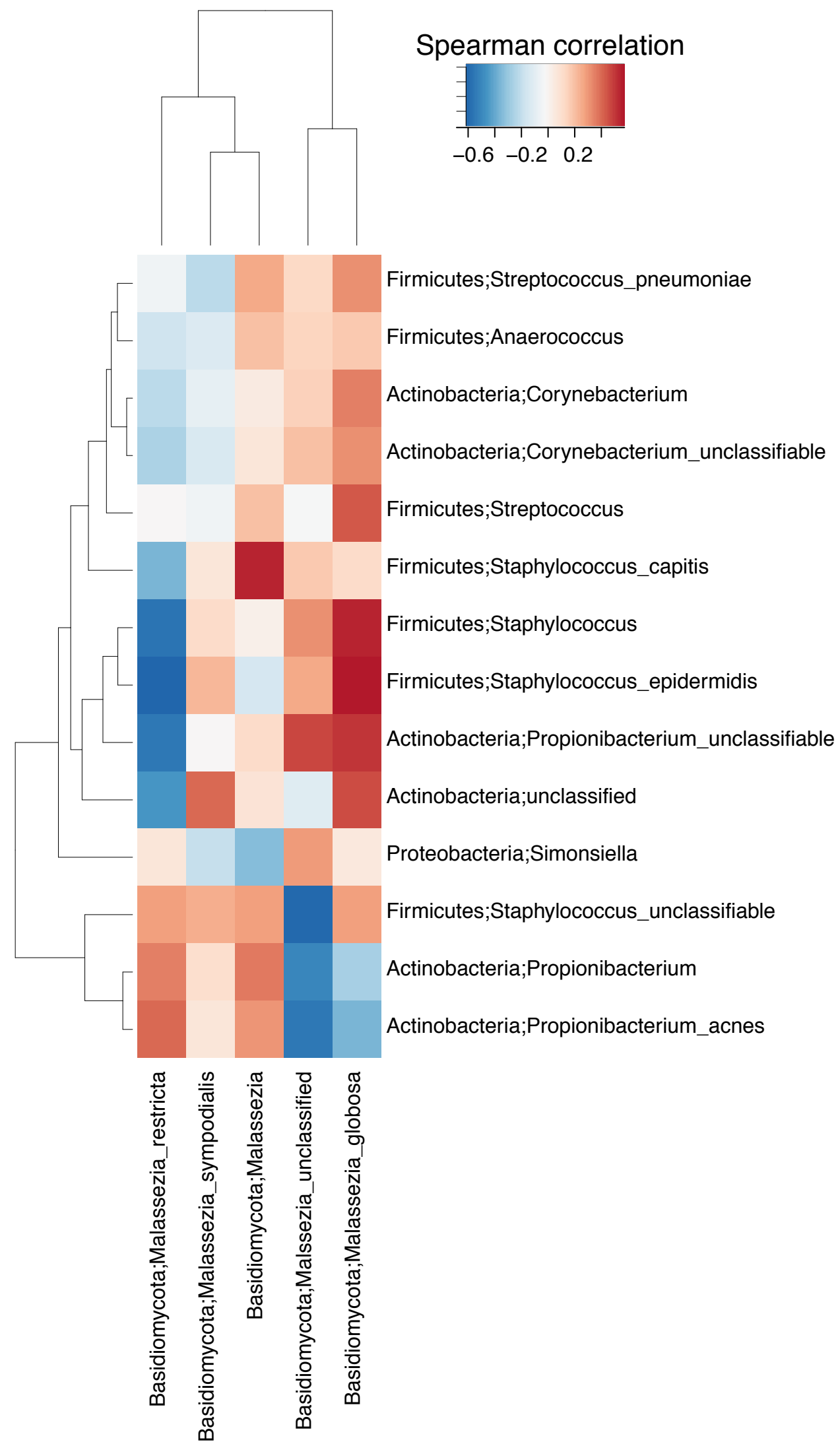


Figure S9C.

Ra, CTRL



Ra, HIES

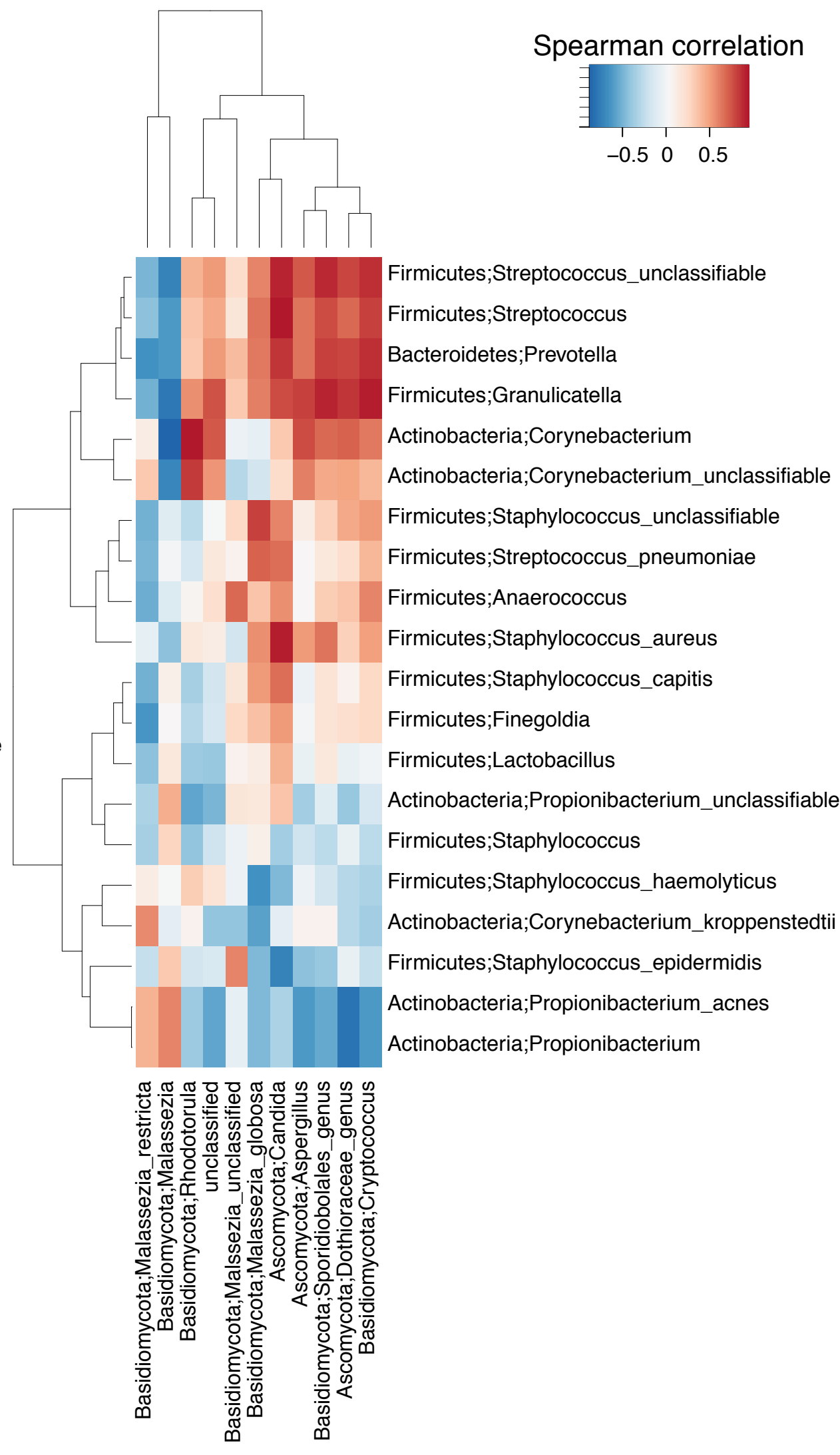
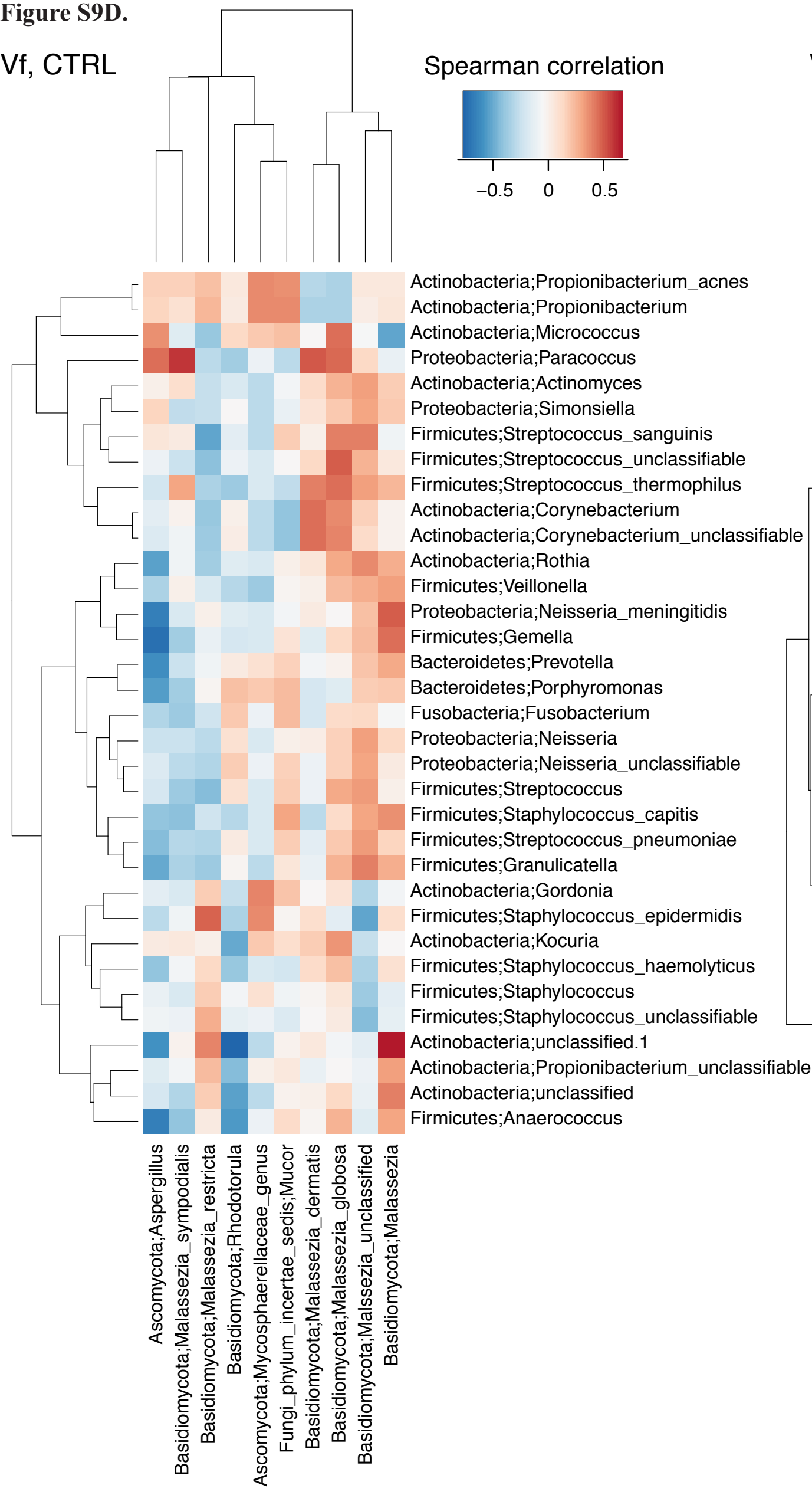


Figure S9D.

Vf, CTRL



Vf, HIES

