Supplemental Figures and Tables.

Supplemental Tables.

Table S1. Treatments used by AD patients prior to sampling

Table S2. Summary of full-length 16S rRNA sequence data for 16 AD patients and 11 controls

Table S3. Shannon diversity indices for 11 HCs and 12 AD patients

Table S4. Yue & Clayton theta and Jaccard similarity coefficients for 11 HC and 12 AD patients for the Ac and Pc

Table S5. Community shifts across timepoints, AD vs. HC

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Table S7. Proportion of *Staphylococcus spp.* averaged for Ac and Pc

Table S8. Shannon diversity index, SCORAD, and proportion of *S. aureus* for the AcPc

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Table S11. Genera significantly overrepresented in AcPc present in all timepoints

Table S12. Summary of rarefaction analysis

Table S13. Culture data, SCORAD, and proportion of *S. aureus* proportion for nares

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Supplemental Figures.

Figure S1. Comparisons of within-group and between-group bacterial community structure. Mean Theta (θ) similarity coefficients ± SEM of all pairwise comparisons of community structure between individuals within a control or AD disease group. $\theta=1$ indicates identical community structure; $\theta=0$ indicates dissimilar community structure. Pairwise comparisons are listed on the x-axis. See Fig. 2D for additional description. Values for Ac and Pc are averaged.

Figure S2. Bacterial taxonomic classifications of the skin microbiome over AD disease progression versus controls, by site. Each panel shows the mean relative abundance for 14 major bacterial phyla-order across the skin microbiomes for controls, AD B, F(no-treatment and intermittent-treatment), and PF, sorted from highest to lowest for relative *Staphylococcus* abundance, by site. For the ordering of subjects for each site, see Table S13.

Figure S3. Cross-site comparisons of abundant taxonomic classifications. In this correlation matrix, each point represents a taxonomic classification as in Figure S2. Site comparisons are indicated in the upper left with the partial correlations adjusting for disease state, which are colored as in the legend. Upper left quadrant of comparisons are between-site in AD patients; the bottom right quadrant of comparisons (in gray) are between-site comparisons of controls.

Figure S4. Alpha and beta diversity metrics for communities with *S. aureus* removed. *S. aureus* sequences were removed from the analysis and samples were normalized to have an equivalent number of sequences prior to calculating diversity statistics. To obtain an accurate representation of the community, sequences were subsampled 100X and diversity indices calculated were averaged. (A) Mean Shannon diversity ± SEM in controls and all AD disease states (Ac, Pc, volar forearm (Vf), nares (N)). (B) Heatmap of mean Theta similarity coefficients of pairwise comparisons of communities within or between individuals at each comparison indicated. 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. Site abbreviations are as in (A). (C) Relationship between objective SCORAD and Shannon diversity in the Ac (left) and Pc (right) of AD patients.

Figure S5. Rarefaction curves for the skin microbiota sampling at each site (Ac, Pc, Vf, and N) calculated as operational taxonomic units (OTUs) at a cutoff of 98% similarity. Each point represents mean ± SEM of all individuals at specified site and disease category.

Figure S6. *S. aureus* culture and genomic sequenced-based analyses in AD patients. Cultures were scored based on the following criteria: 0 colonies of *S. aureus* (negative for *S. aureus*), 1-10 colonies (light *S. aureus* bioburden), and >10 colonies per plate (moderate to heavy *S. aureus* bioburden). (*A*) Nose culture results for *S. aureus* compared to the sequenced-based relative abundance values of *S. aureus*. (*B*) Nose culture results for *S. aureus* compared to objective SCORAD disease severity scores. (*C*) Mean relative abundance for 14 major bacterial phyla-order across the skin microbiomes for controls, AD B, F(no-treatment (trt) and intermittent-trt), and PF, sorted from highest to lowest for relative *Staphylococcus* abundance. (*D*) Relative abundance of *S. aureus* genomic sequences for controls as compared to AD disease baseline, flare (no-trt and intermittent-trt), and post-flare.

Figure S1

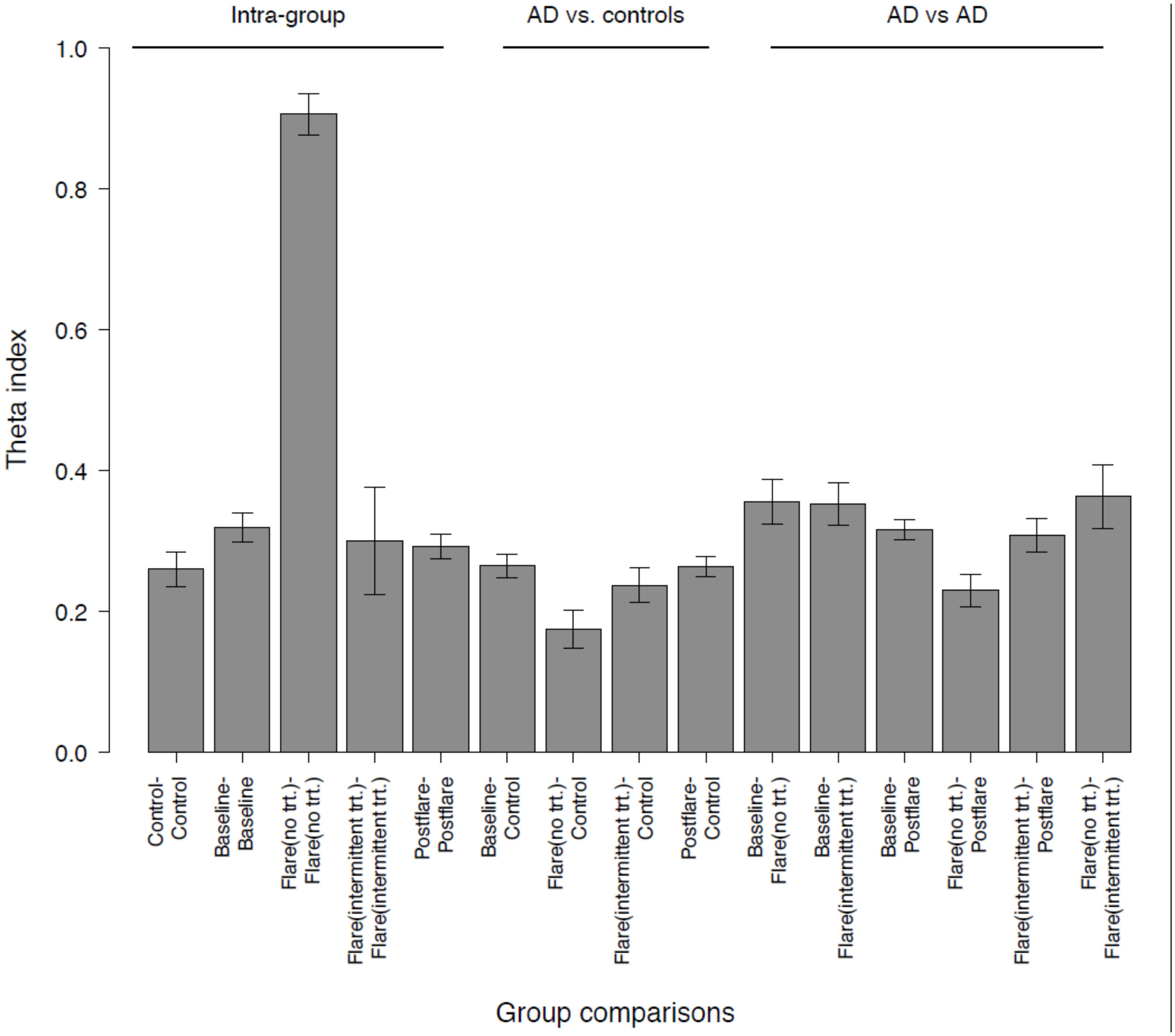

Intra-group
AD vs. controls
AD vs AD
Theta index
1.0
0.8
0.6
0.4
0.2
0.0
Control-Control
Baseline-Baseline
Flare(no trt.)-Flare(no trt.)
Flare(intermittent trt.)-Flare(intermittent trt.)
Postflare-Postflare
Baseline-Control
Flare(no trt.)-Control
Flare(intermittent trt.)-Control
Postflare-Control
Baseline-Flare(no trt.)
Baseline-Flare(intermittent trt.)
Baseline-Postflare
Flare(no trt.)-Postflare
Flare(intermittent trt.)-Postflare
Flare(no trt.)-Flare(intermittent trt.)
Group comparisons

Figure S2

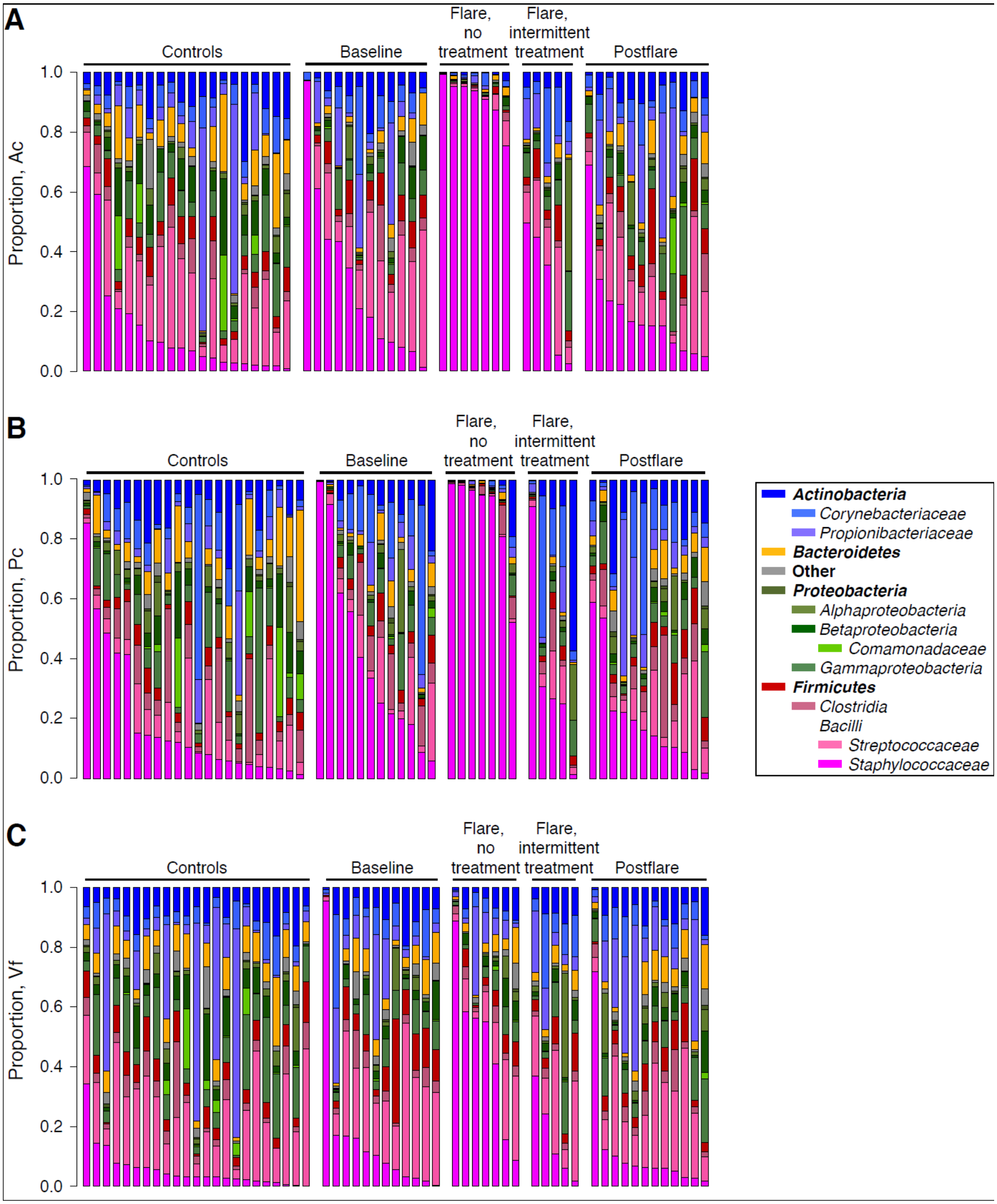

A
Controls
Baseline
Flare, no treatment
Flare, intermittent treatment
Postflare
Proportion, Ac
1.0
0.8
0.6
0.4
0.2
0.0
B
Controls
Baseline
Flare, no treatment
Flare, intermittent treatment
Postflare
Proportion, Pc
1.0
0.8
0.6
0.4
0.2
0.0
C
Controls
Baseline
Flare, no treatment
Flare, intermittent treatment
Postflare
Proportion, Vf
1.0
0.8
0.6
0.4
0.2
0.0
Actinobacteria
Corynebacteriaceae
Propionibacteriaceae
Bacteroidetes
Other
Proteobacteria
Alphaproteobacteria
Betaproteobacteria
Comamonadaceae
Gammaproteobacteria
Firmicutes
Clostridia
Bacilli
Streptococcaceae
Staphylococcaceae

Figure S3

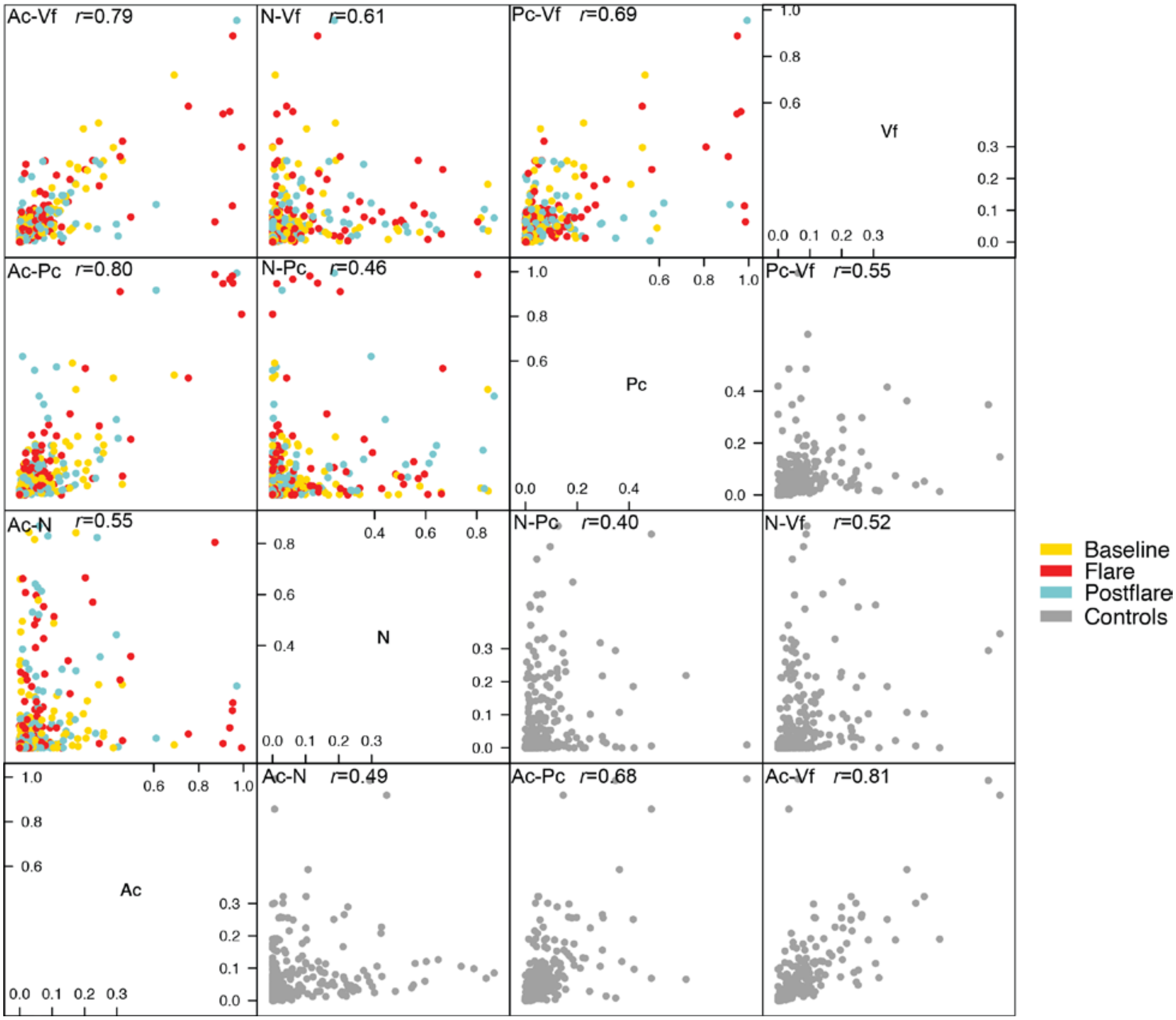

Ac-Vf r=0.79
N-Vf r=0.61
Pc-Vf r=0.69
Vf
1.0
0.8
0.6
0.3
0.2
0.1
0.0
0.0 0.1 0.2 0.3
Ac-Pc r=0.80
N-Pc r=0.46
Pc
1.0
0.8
0.6
0.6 0.8 1.0
0.4
0.2
0.0
0.0 0.2 0.4
Pc-Vf r=0.55
Ac-N r=0.55
N
0.8
0.6
0.4
0.4 0.6 0.8
0.3
0.2
0.1
0.0
0.0 0.1 0.2 0.3
N-Pc r=0.40
N-Vf r=0.52
Ac
1.0
0.8
0.6
0.6 0.8 1.0
0.3
0.2
0.1
0.0
0.0 0.1 0.2 0.3
Ac-N r=0.49
Ac-Pc r=0.68
Ac-Vf r=0.81
Baseline
Flare
Postflare
Controls

Figure S4

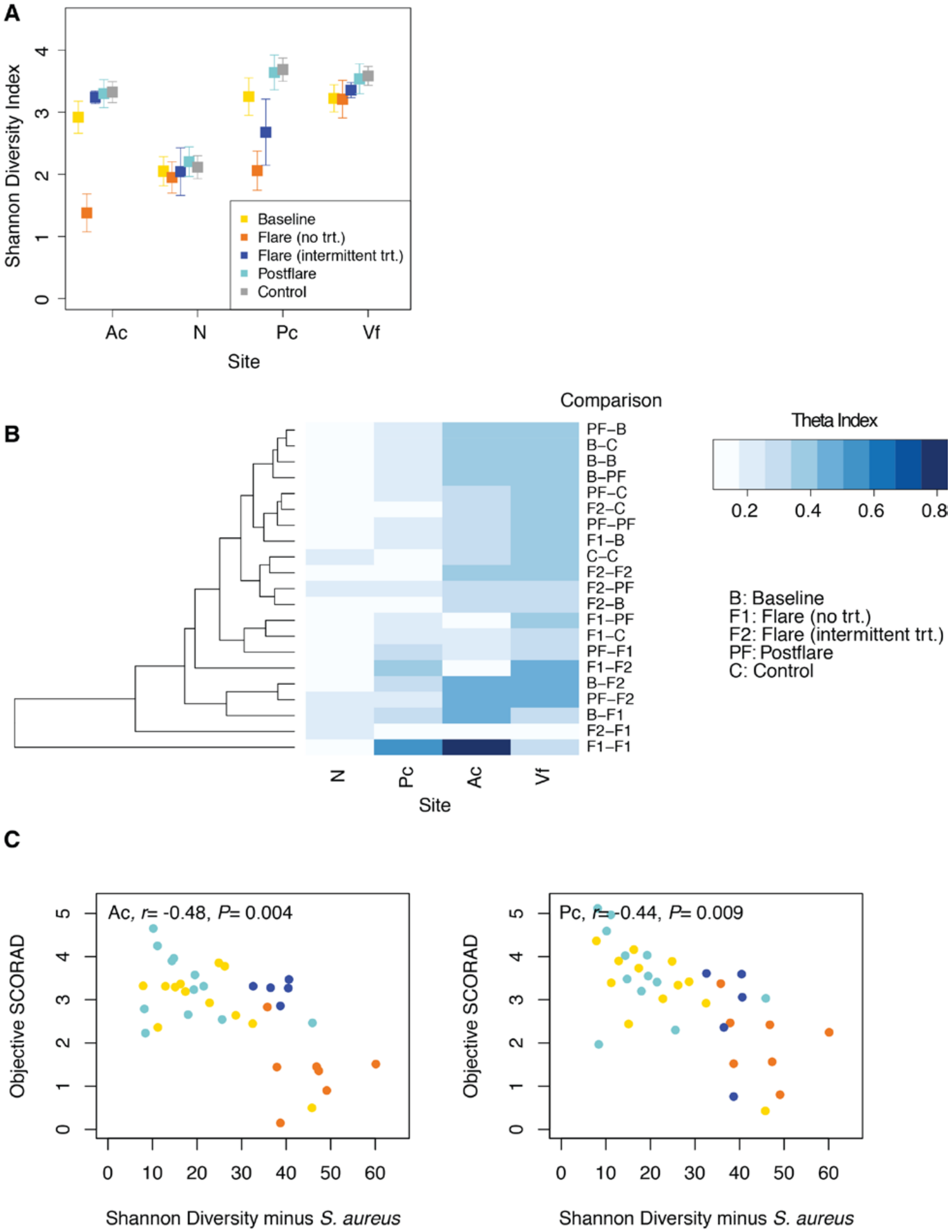

A
Shannon Diversity Index
0
1
2
3
4
Ac
N
Pc
Vf
Site
Baseline
Flare (no trt.)
Flare (intermittent trt.)
Postflare
Control
B
Comparison
PF–B
B–C
B–B
B–PF
PF–C
F2–C
PF–PF
F1–B
C–C
F2–F2
F2–PF
F2–B
F1–PF
F1–C
PF–F1
F1–F2
B–F2
PF–F2
B–F1
F2–F1
F1–F1
N
Pc
Ac
Vf
Site
Theta Index
0.2
0.4
0.6
0.8
B: Baseline
F1: Flare (no trt.)
F2: Flare (intermittent trt.)
PF: Postflare
C: Control
C
Ac, r= -0.48, P= 0.004
Pc, r= -0.44, P= 0.009
Objective SCORAD
0
1
2
3
4
5
0
10
20
30
40
50
60
Shannon Diversity minus S. aureus

Figure S5

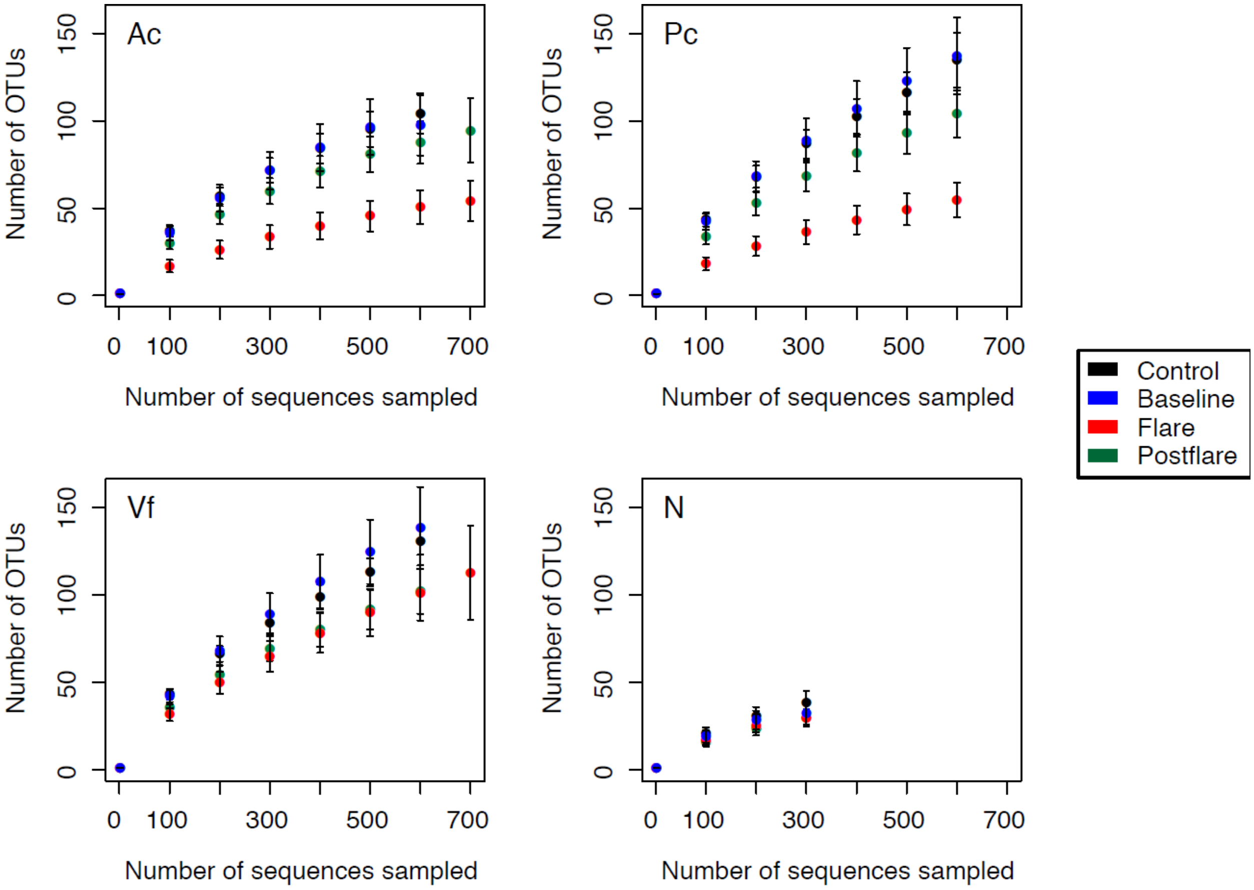
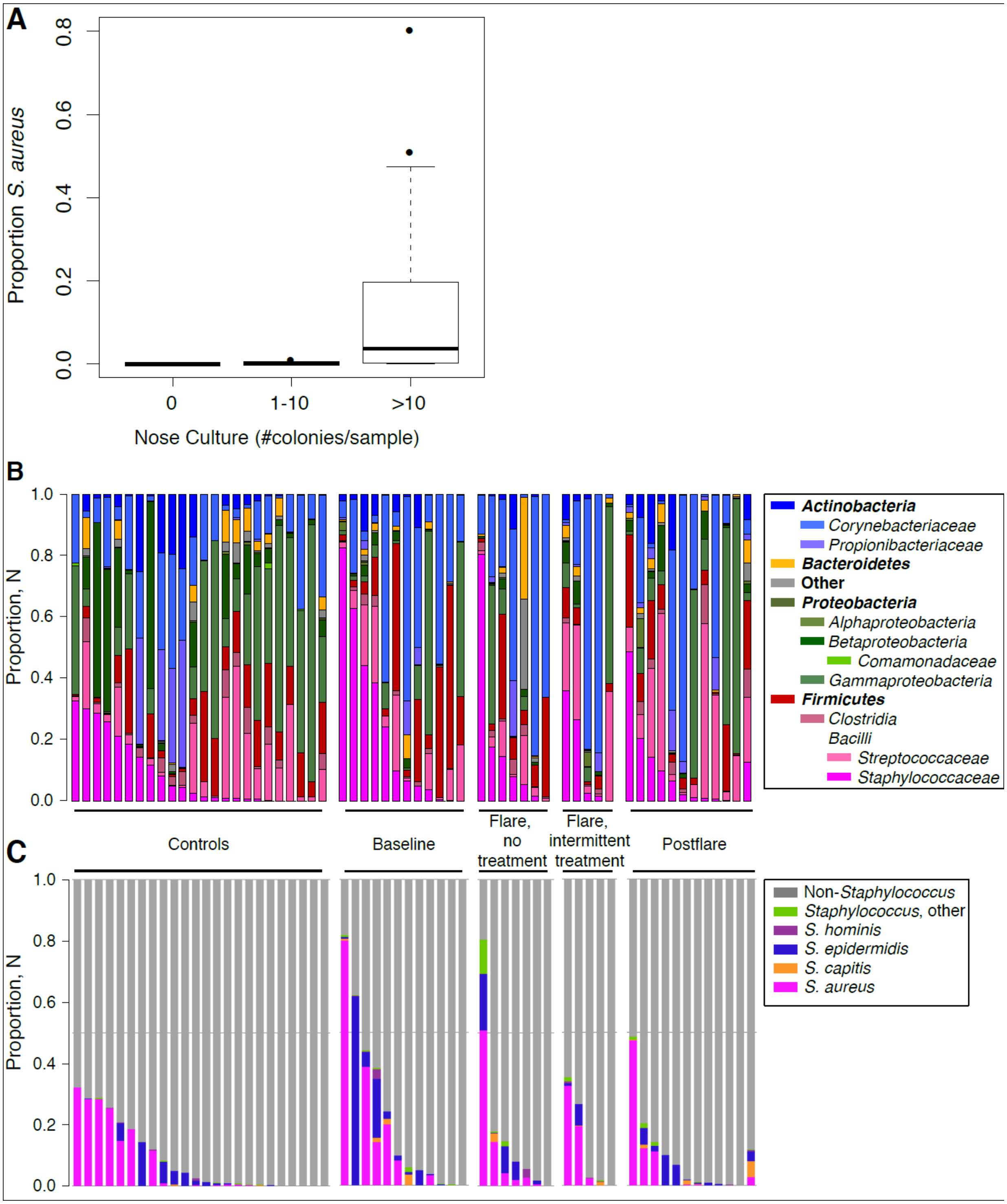

Ac
Pc
Vf
N
Number of OTUs
Number of sequences sampled
0
50
100
150
0
100
300
500
700
Control
Baseline
Flare
Postflare

Figure S6


A
Proportion S. aureus
0.0
0.2
0.4
0.6
0.8
0
1-10
>10
Nose Culture (#colonies/sample)
B
Proportion, N
0.0
0.2
0.4
0.6
0.8
1.0
Actinobacteria
Corynebacteriaceae
Propionibacteriaceae
Bacteroidetes
Other
Proteobacteria
Alphaproteobacteria
Betaproteobacteria
Comamonadaceae
Gammaproteobacteria
Firmicutes
Clostridia
Bacilli
Streptococcaceae
Staphylococcaceae
Controls
Baseline
Flare, no treatment
Flare, intermittent treatment
Postflare
C
Proportion, N
0.0
0.2
0.4
0.6
0.8
1.0
Non-Staphylococcus
Staphylococcus, other
S. hominis
S. epidermidis
S. capitis
S. aureus