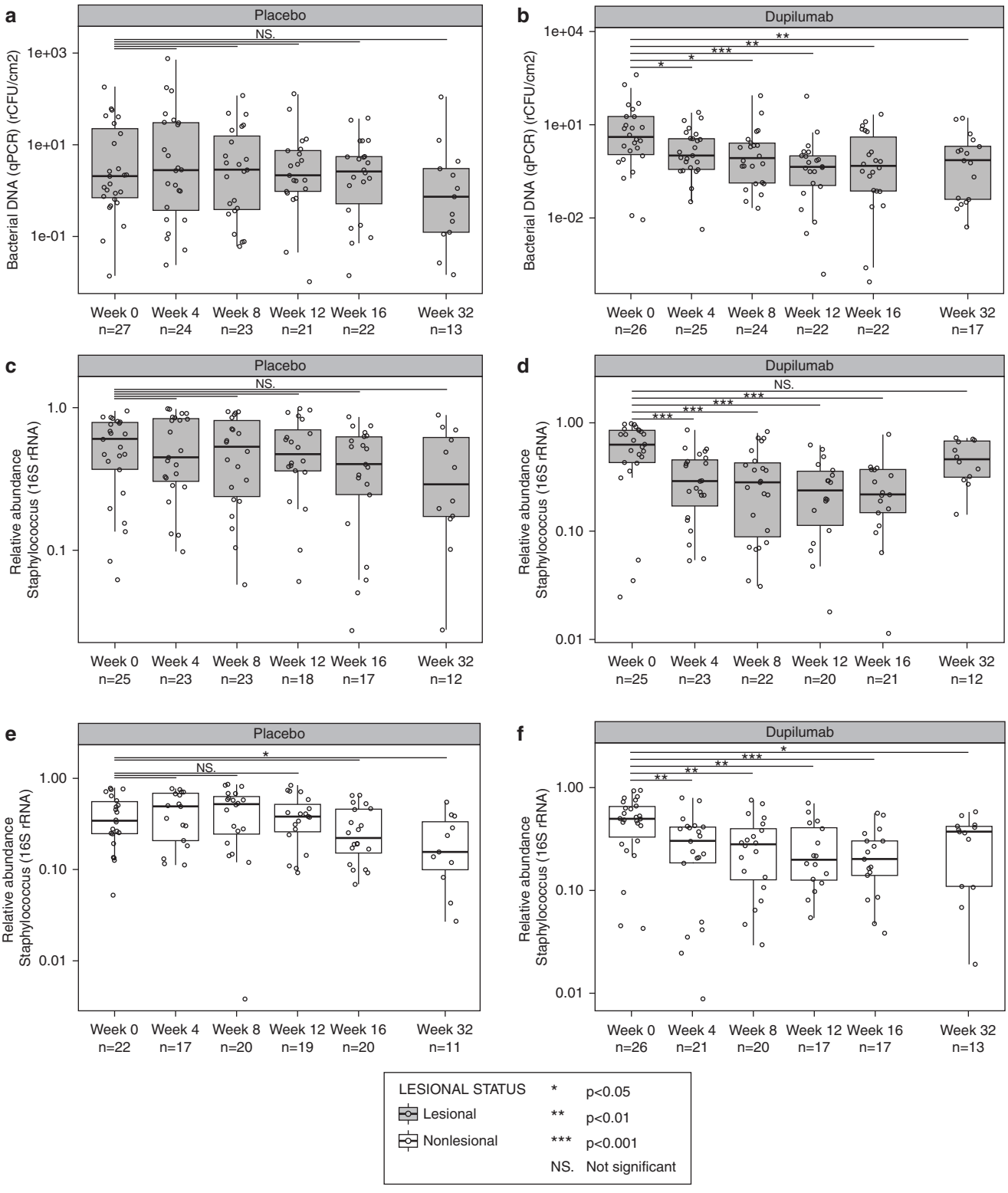
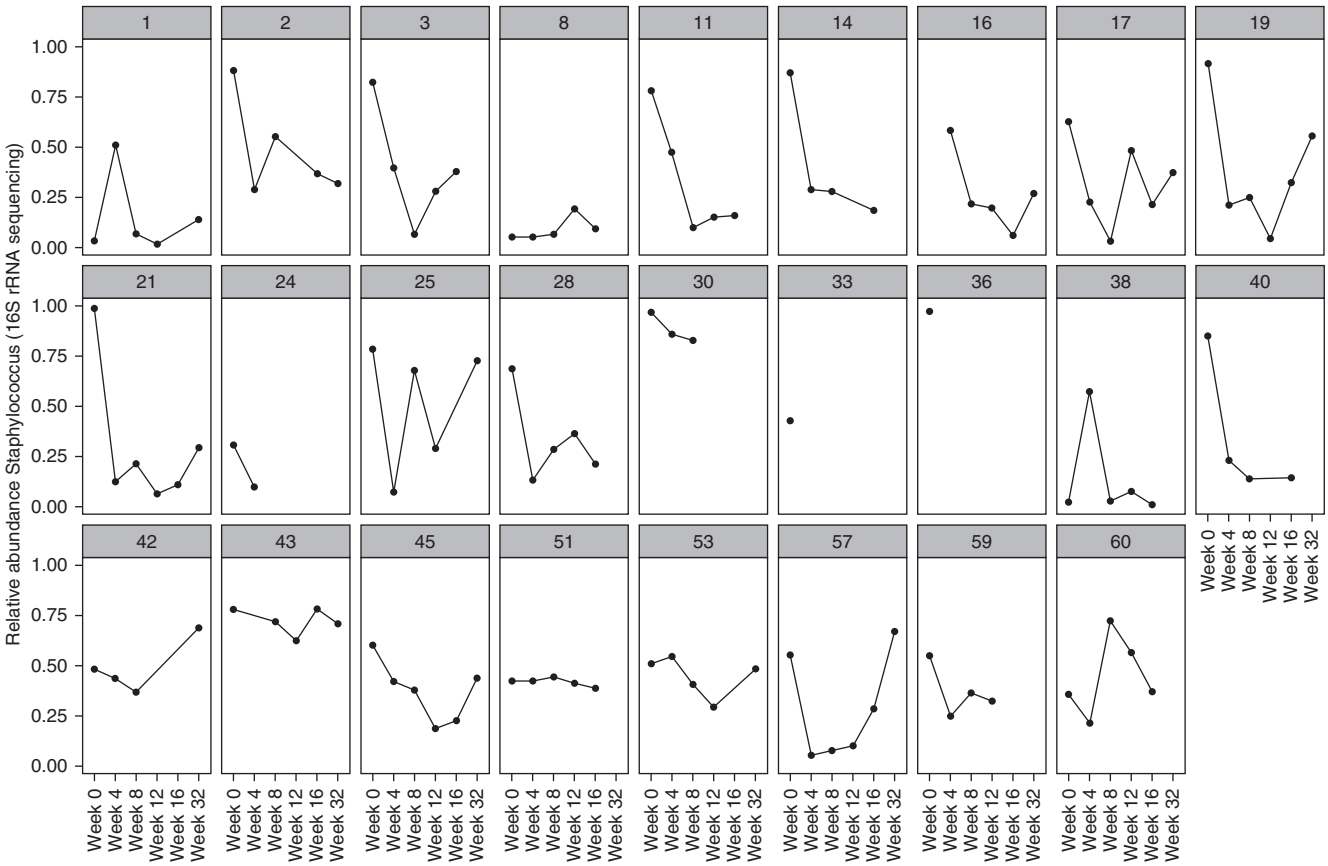
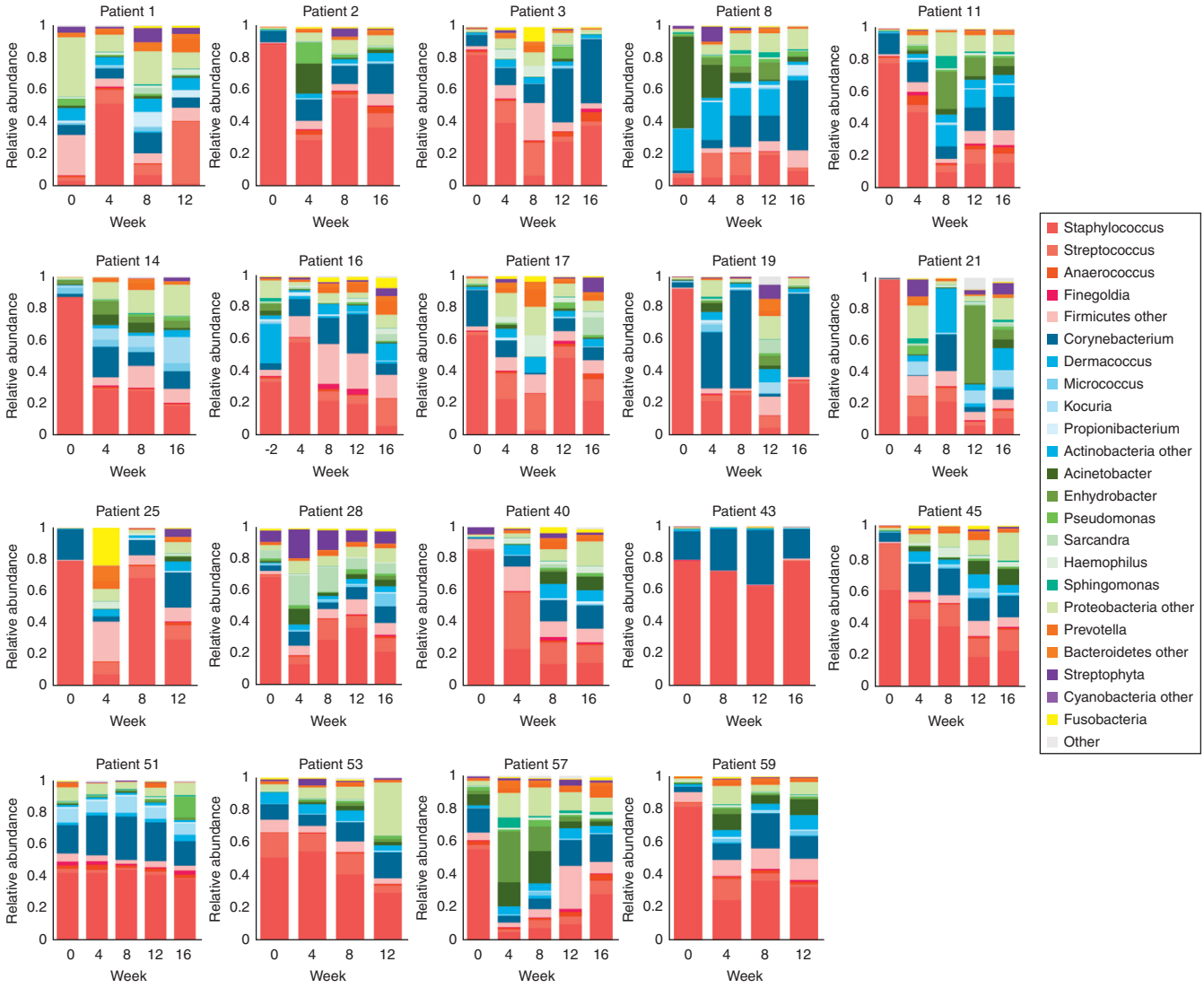


Supplementary Figure S1. Absolute abundance of total bacteria in lesional skin samples from the (**a**) placebo group and (**b**) dupilumab-treated group. Relative abundance of *Staphylococcus* over time in lesional skin samples in the (**c**) placebo group and (**d**) dupilumab-treated group. Relative abundance of *Staphylococcus* over time in nonlesional skin samples in the (**e**) placebo group and (**f**) dupilumab-treated group. Changes in abundance from baseline were assessed using the nonparametric Mann–Whitney U test, with Bonferroni correction for multiple comparison. qPCR, quantitative PCR; rCFU, relative colony-forming units; rRNA, ribosomal RNA.

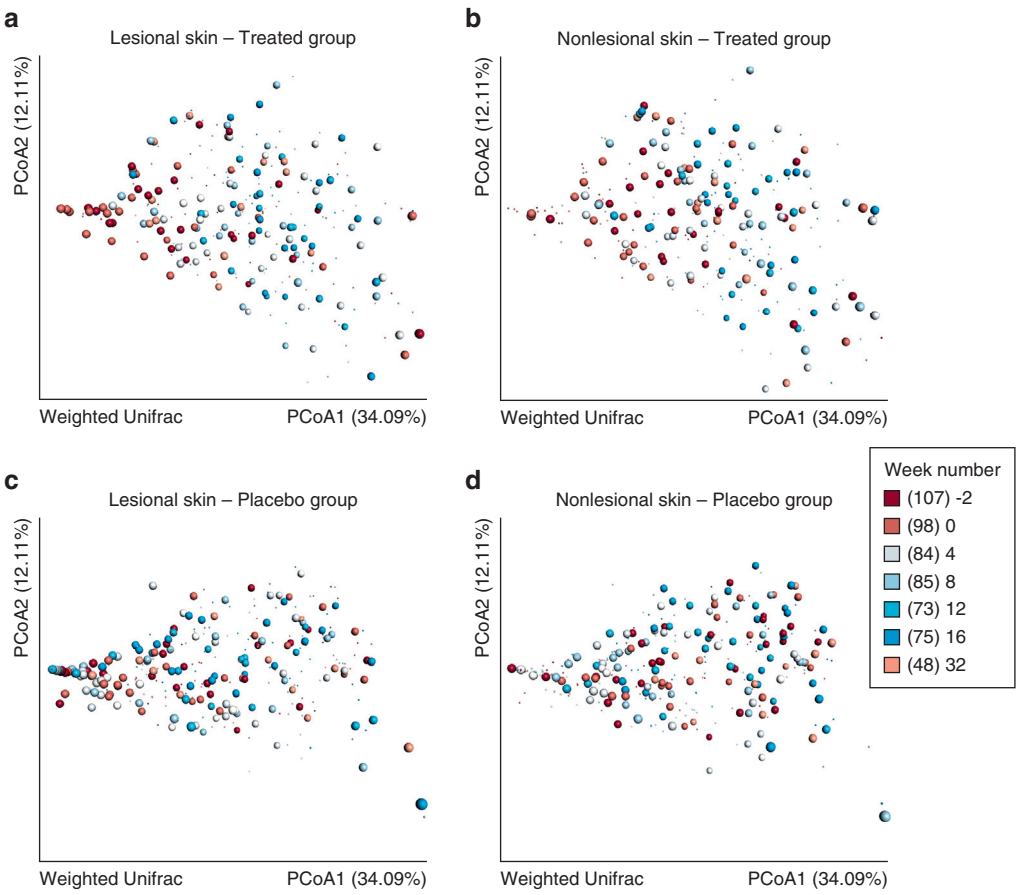


Supplementary Figure S2. Relative abundance of *Staphylococcus* in individual patients over time in lesional skin (dupilumab-treated group). Only patients receiving active treatment were included; some patient dropout is noted. rRNA, ribosomal RNA.

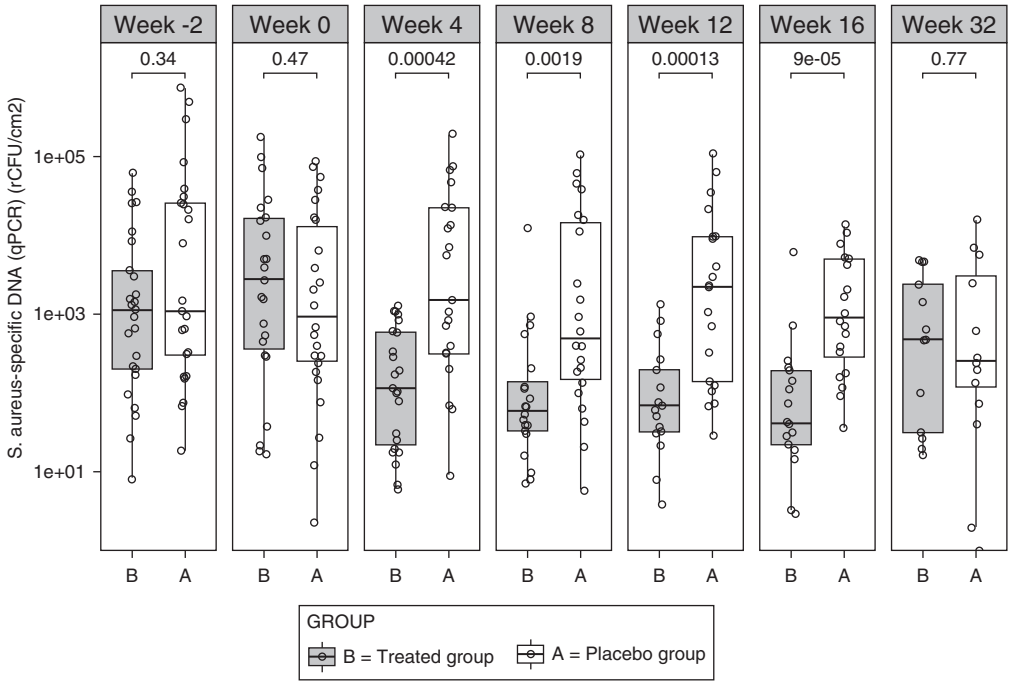


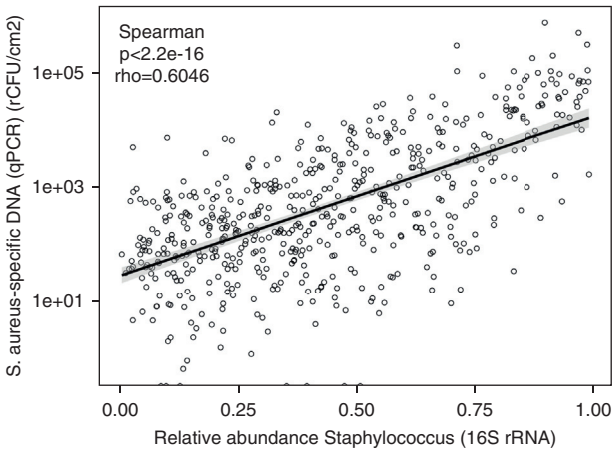
Supplementary Figure S3. Relative abundance of bacterial taxonomic distribution of individual patients over time in lesional skin (dupilumab-treated group). Only weeks 0, 4, 8, 12, and 16 are shown for simplicity.

Supplementary Figure S4. β-Diversity (PCoA) plot color-coded per week number of the (**a**) dupilumab-treated group of lesional skin (small dots represent nonlesional skin samples); (**b**) dupilumab-treated group of nonlesional skin (small dots represent lesional skin samples); (**c**) placebo group of lesional skin (small dots represent nonlesional skin samples); and (**d**) placebo group of nonlesional skin (small dots represent lesional skin samples). Each dot represents a different sample. PCoA, principal coordinates analysis.

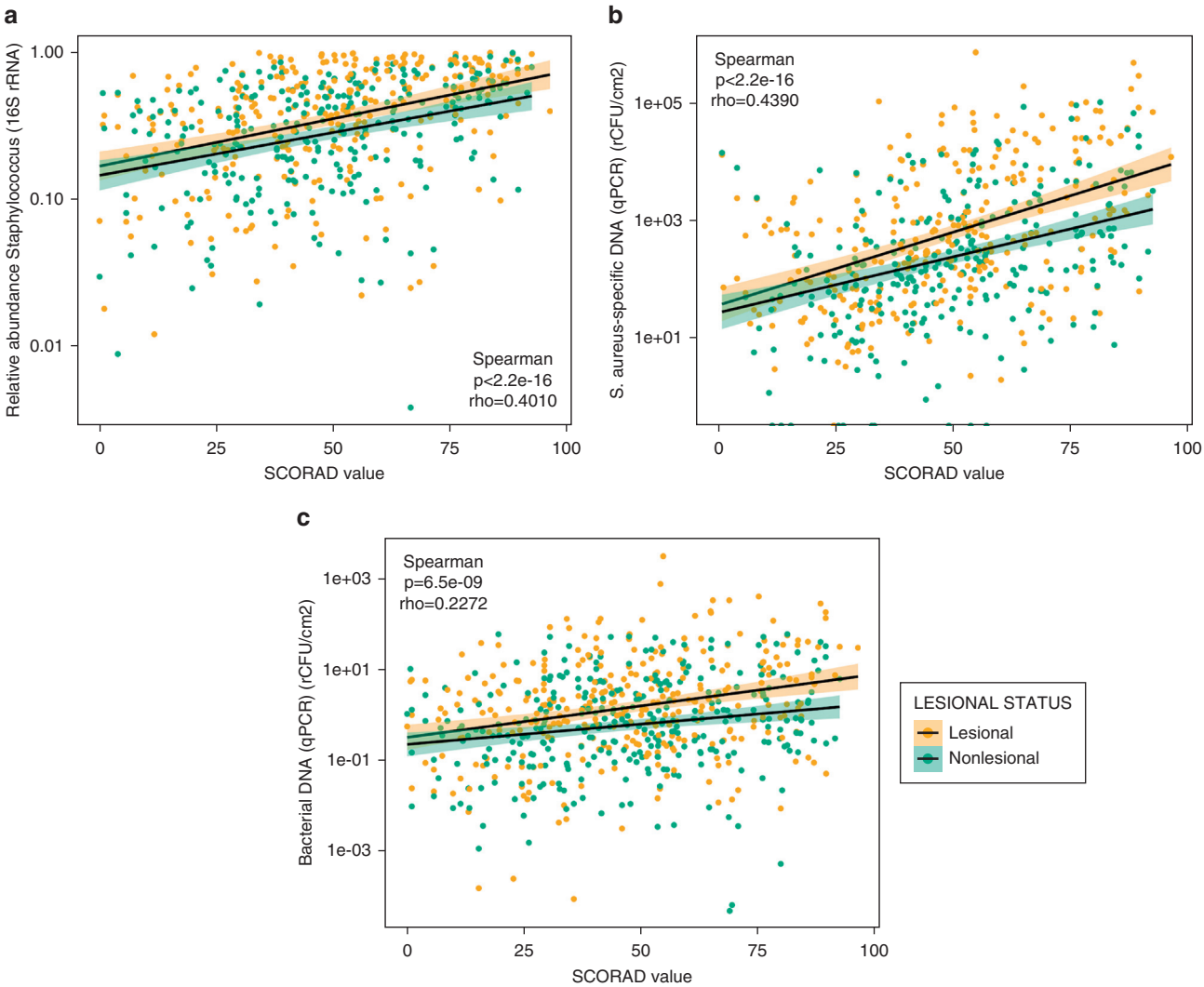


Supplementary Figure S5. Absolute abundance of *Staphylococcus aureus* per week in lesional skin samples in dupilumab-treated group (group B) and placebo group (group A). Statistical differences between treatment groups at each time point were assessed using the nonparametric Mann–Whitney U test, with Bonferroni correction for multiple comparison. qPCR, quantitative PCR; rCFU, relative colony-forming units.

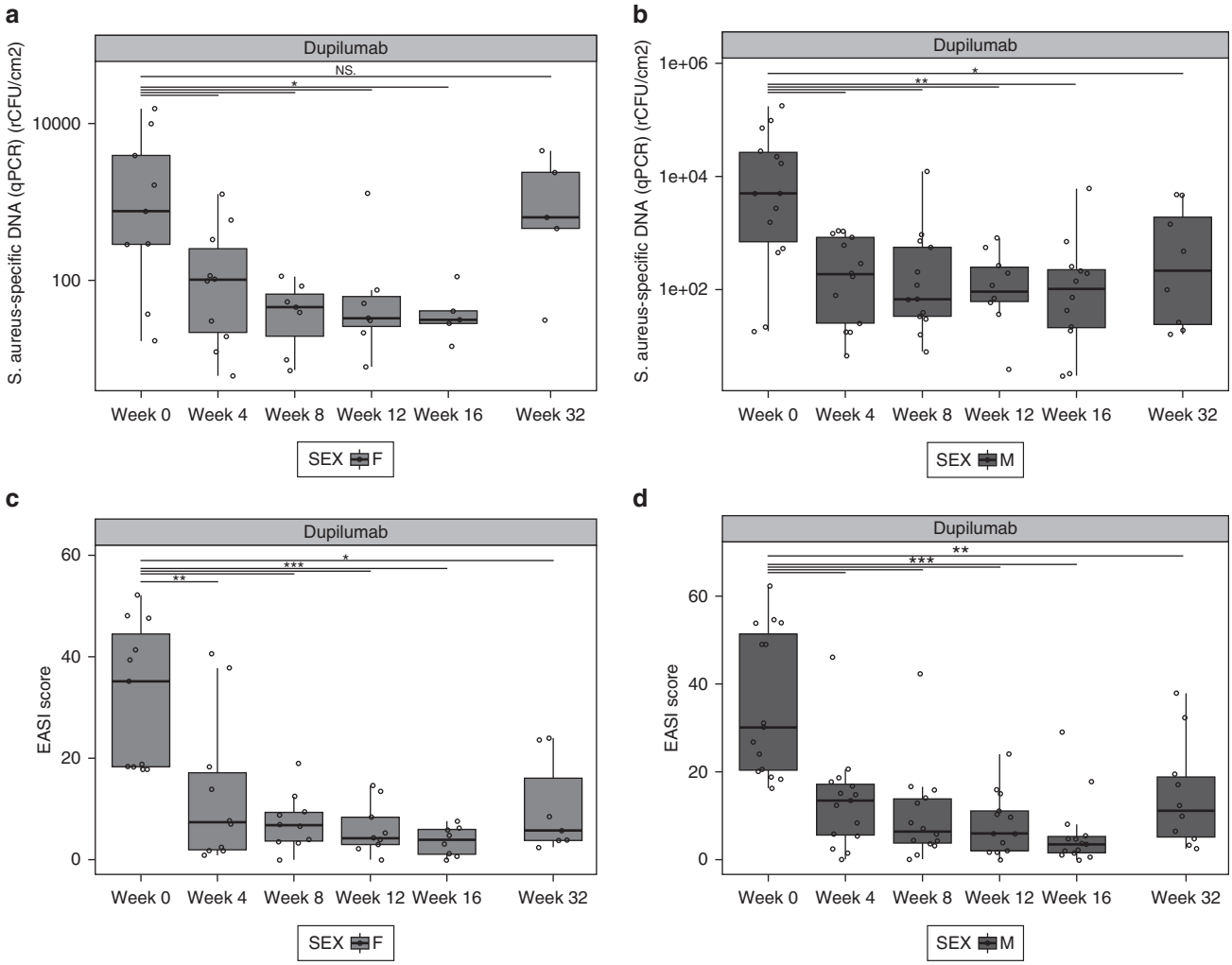




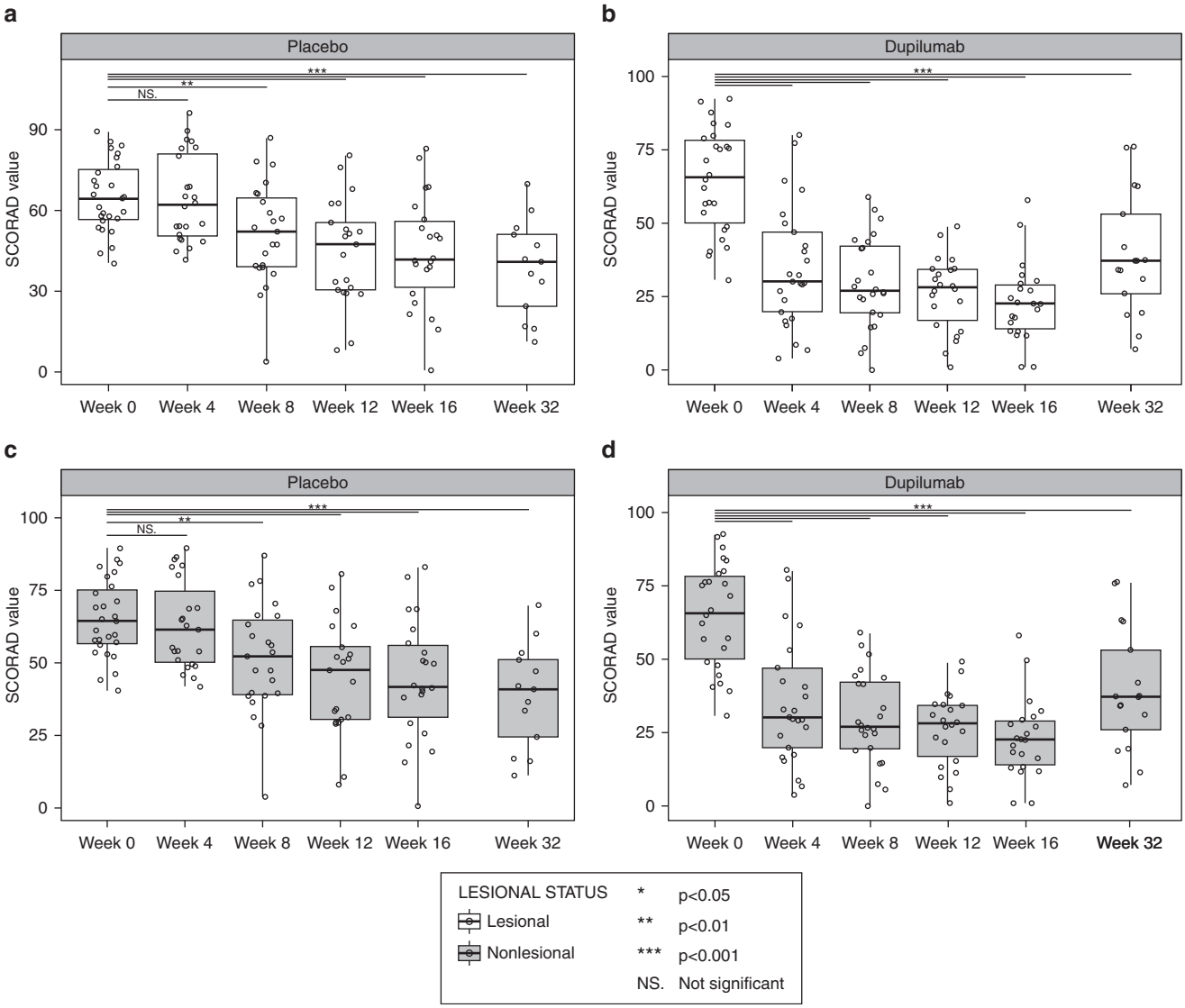
Supplementary Figure S6. Correlation between quantitative PCR (qPCR) detection of *Staphylococcus aureus* and relative abundance of *Staphylococcus* using 16S ribosomal RNA (rRNA) gene sequencing. qPCR, quantitative PCR; rCFU, relative colony-forming units; rRNA, ribosomal RNA.



Supplementary Figure S7. Correlation of baseline Scoring Atopic Dermatitis (SCORAD) score and (**a**) relative and (**b**) absolute abundance of *Staphylococcus aureus* and (**c**) absolute abundance of all bacteria. qPCR, quantitative PCR; rCFU, relative colony-forming units; rRNA, ribosomal RNA.



Supplementary Figure S8. Absolute abundance *Staphylococcus aureus* and EASI scores over time in lesional skin samples of dupilumab-treated group for (**a**, **c**) female and (**b**, **d**) male subsets. Statistical differences in *S. aureus* abundance and EASI scores versus baseline were assessed using the nonparametric Mann–Whitney U test, with Bonferroni correction for multiple comparison. $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.01$. EASI, Eczema Area and Severity Index; F, female; M, male; qPCR, quantitative PCR; rCFU, relative colony-forming units.



Supplementary Figure S9. SCORAD, score over time in (**a**) placebo-treated and (**b**) dupilumab-treated lesional skin, and (**c**) placebo-treated and (**d**) dupilumab-treated nonlesional skin. Statistical differences with week 0 (baseline) were assessed using the nonparametric Mann–Whitney U test, with Bonferroni correction for multiple comparison.SCORAD, Scoring Atopic Dermatitis.