



Figure S7. Comparison of *S. aureus* and *S. epidermidis* abundances between lesional and non-lesional skin. **A)** Differential abundance analysis based on *tuf* sequences, thus representing abundances within the staphylococcal community. Bars represent the estimated log fold change in species abundance between groups (effect size) and error bars the 95% confidence interval, which were estimated with an ANCOM-BC model, which uses the natural logarithm. Analyses were adjusted for multiple testing using the Benjamini-Hochberg method (fdr), with ** indicating adj. $p < 0.01$. **B and C)** Comparison of the estimated absolute abundance of *S. aureus* (B) and *S. epidermidis* (C) between lesional and non-lesional skin. The absolute abundance was estimated by combining the proportional species abundance within the bacterial community with the total bacterial abundance quantified by qPCR. Thus, the y-axis shows the estimated number of 16S rRNA gene copies within 1 μ l DNA eluate (\log_{10} transformed). Differences between lesional and non-lesional skin were tested with a paired Wilcoxon signed rank test, and p-values adjusted for multiple testing using fdr correction. Box plots represent the median and interquartile range (IQR) with whiskers extending to the minimum/maximum value, but no longer than 1.5xIQR. Abbreviations; AD: atopic dermatitis, LS: lesional skin, NLS: non-lesional skin; n.s.: not significant