

Supplemental Material

Supplemental Results. Macro-Scale Spatial Variation in Minor Component Bacterial Families.

Pathogenic bacteria may negatively impact wound healing even if they are minor components in the polymicrobial community. In order to better evaluate low-abundance bacteria across the wounds, we re-analyzed the wound bacterial community after subtracting 16S RNA gene sequences from the three most prevalent bacterial families—Staphylococcaceae, Pseudomonadaceae, and Streptococcaceae. Relative abundance of the remaining bacterial families was calculated for each sample and used to generate a heat map display (Figure S3) and an nMDS plot (Figure S4). We observed that minor component bacterial families still demonstrated strong correlation among samples from the same wound (Figure S3, Figure S4). However, we also observed that removing the most prevalent bacterial families eliminated a masking effect in some samples that appeared to be dissimilar prior to subtraction, but similar afterwards (e.g., 22A and 22B; 39B and 39C). In addition, the post-subtraction heat map more effectively demonstrates the complexity of the wound microbiota, with many more bacterial families readily visible in each wound sample. The nMDS plot showed that the sequence subtraction did not significantly affect the macro-scale spatial variation. And when we used PerMANOVA to determine whether the subtraction procedure affected the difference between wounds (rather than among different sites in the same wound), we found that the wounds remain significantly different ($p < 0.001$).

Supplemental Figure Legends

Figure S1. Sampling strategy for evaluating macro-scale variation in wound microbiota.

A, leading edge; B, opposing, leading edge; C, wound center.

