

Supporting Information

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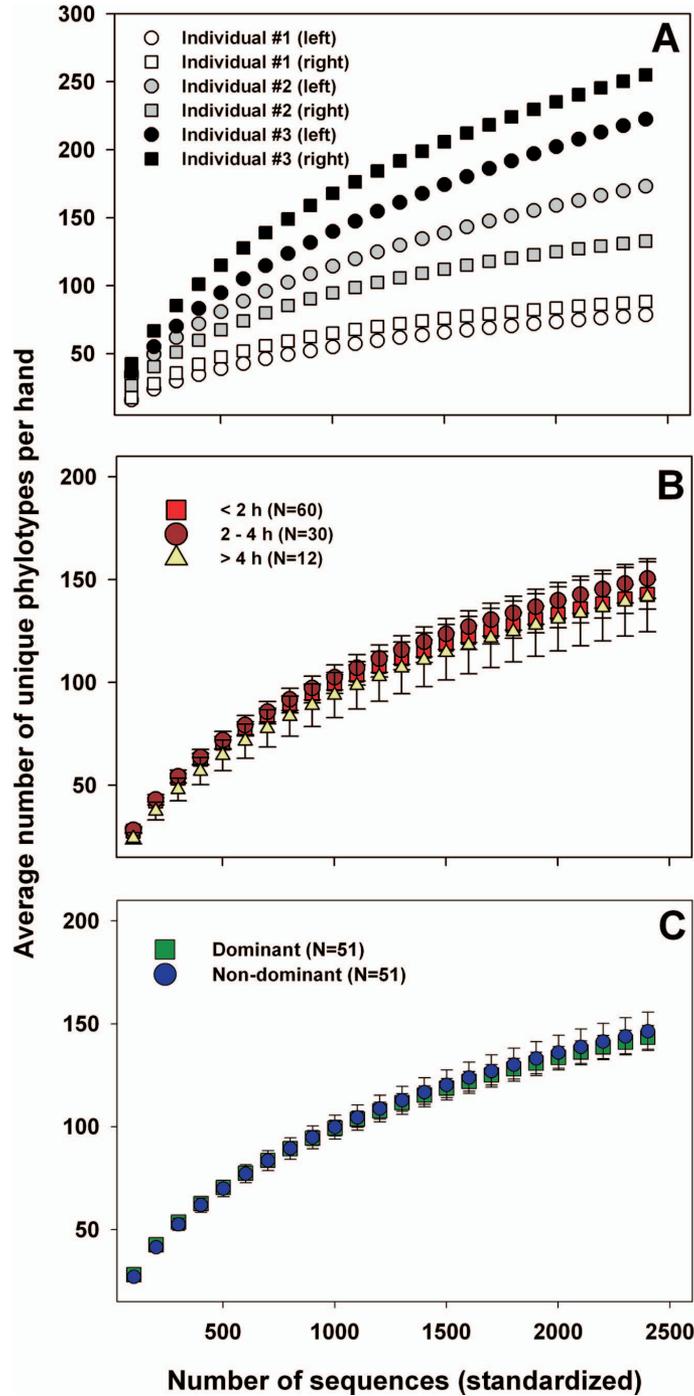


Fig. S1. (A) Rarefaction curves from three individual hand samples, selected to be representative of individual palms with low, average, and high levels of bacterial diversity. (B and C) Rarefaction curves for samples grouped into categories based on time since last hand washing (B) and the dominant versus nondominant hands (C). Curves were estimated by randomly selecting 2,400 sequences per hand sample so the average number of phylotypes per hand is lower than that estimated for the full dataset. The number of individual hand samples included in each category is indicated in the legend. Confidence intervals are shown at the 95% level.

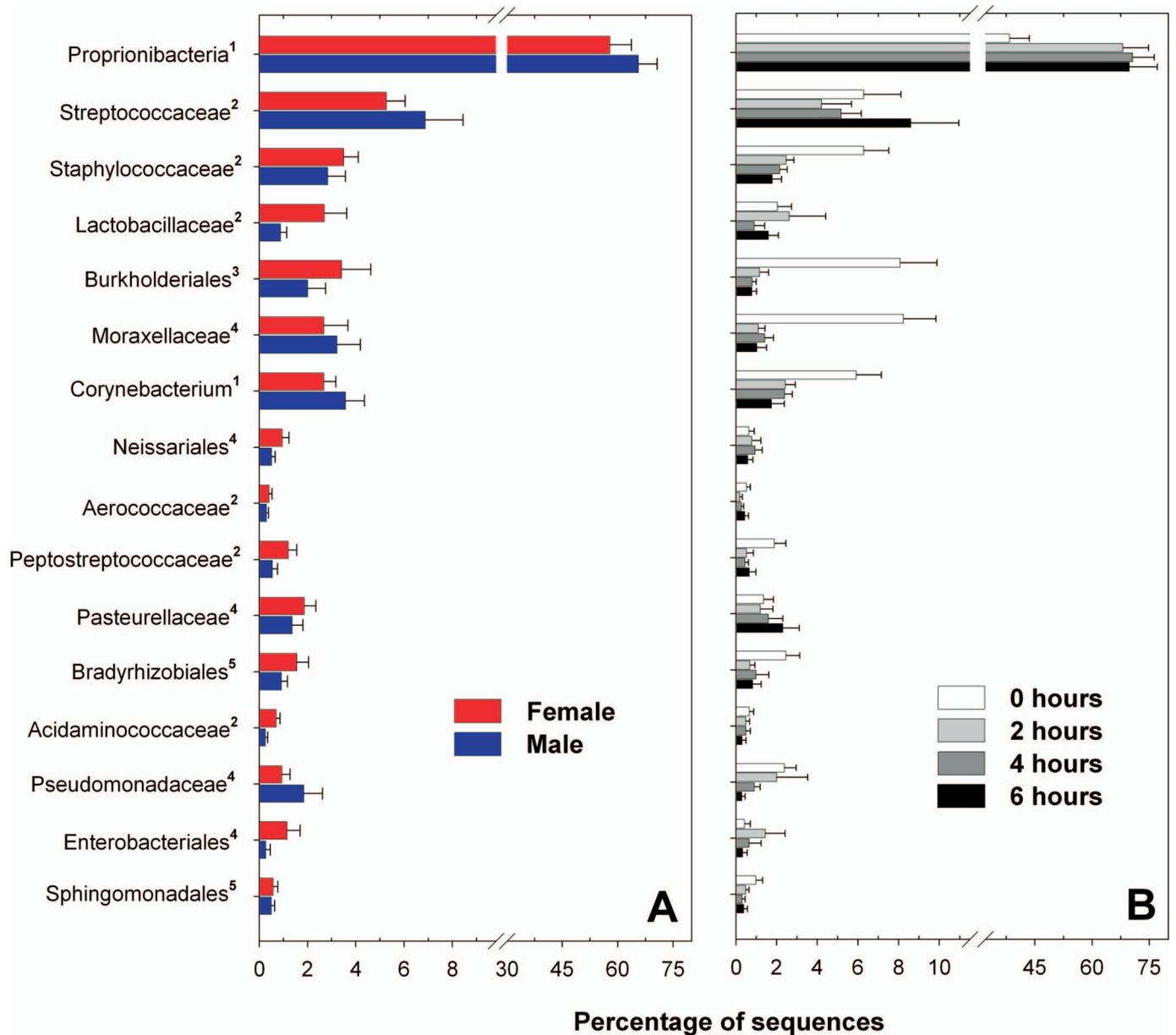


Fig. S2. Relative abundances of the most abundant bacterial groups on the hand surfaces sampled as part of the smaller scale study, with the hand samples divided into categories of sex (A) and time since last hand washing (B). Four men and 4 women were sampled every 2 h for a 6-h period after hands were thoroughly washed. Error bars are one standard error of the mean. For the number of sequences and number of samples included in each category and the full taxonomic description of the hand-surface bacterial communities see [Table S2](#). Superscripts on the taxon name indicate the phylum or subphylum: 1, Actinobacteria; 2, Firmicutes; 3, Betaproteobacteria; 4, Gammaproteobacteria; 5, Alphaproteobacteria.

