

Microbiome of Clothing Items Worn for a Single Day in a Non-Healthcare Setting

Kelly Whitehead, Jake Eppinger, Vanita Srinivasan, M. Khalid Ijaz, Raymond W. Nims, Julie McKinney

Microbial identification by sequencing. The results for identification of bacteria by sequencing for each control clothing item surveyed is displayed below in Figure S1 (abundance by genus) and Figure S2 (abundance by species). The most abundant bacterial genomic material recovered were for *Staphylobacteria*, *Corynebacteria*, and *Propionibacteria* (generally, human skin flora, which may have been derived from the washing machine used).

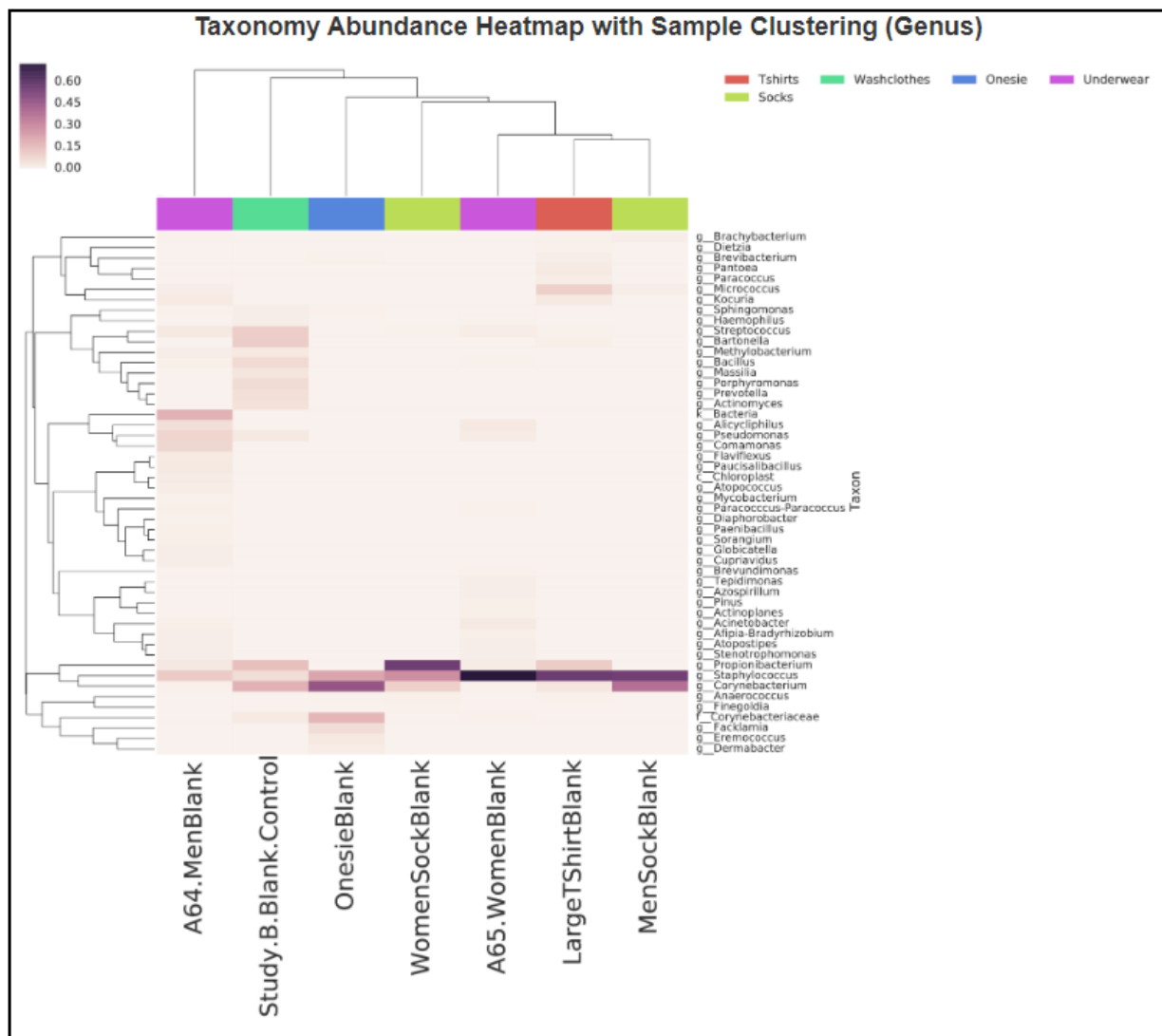


Figure S1. Sequence identification to the genus level of genomic material recovered from control (blank) clothing items.

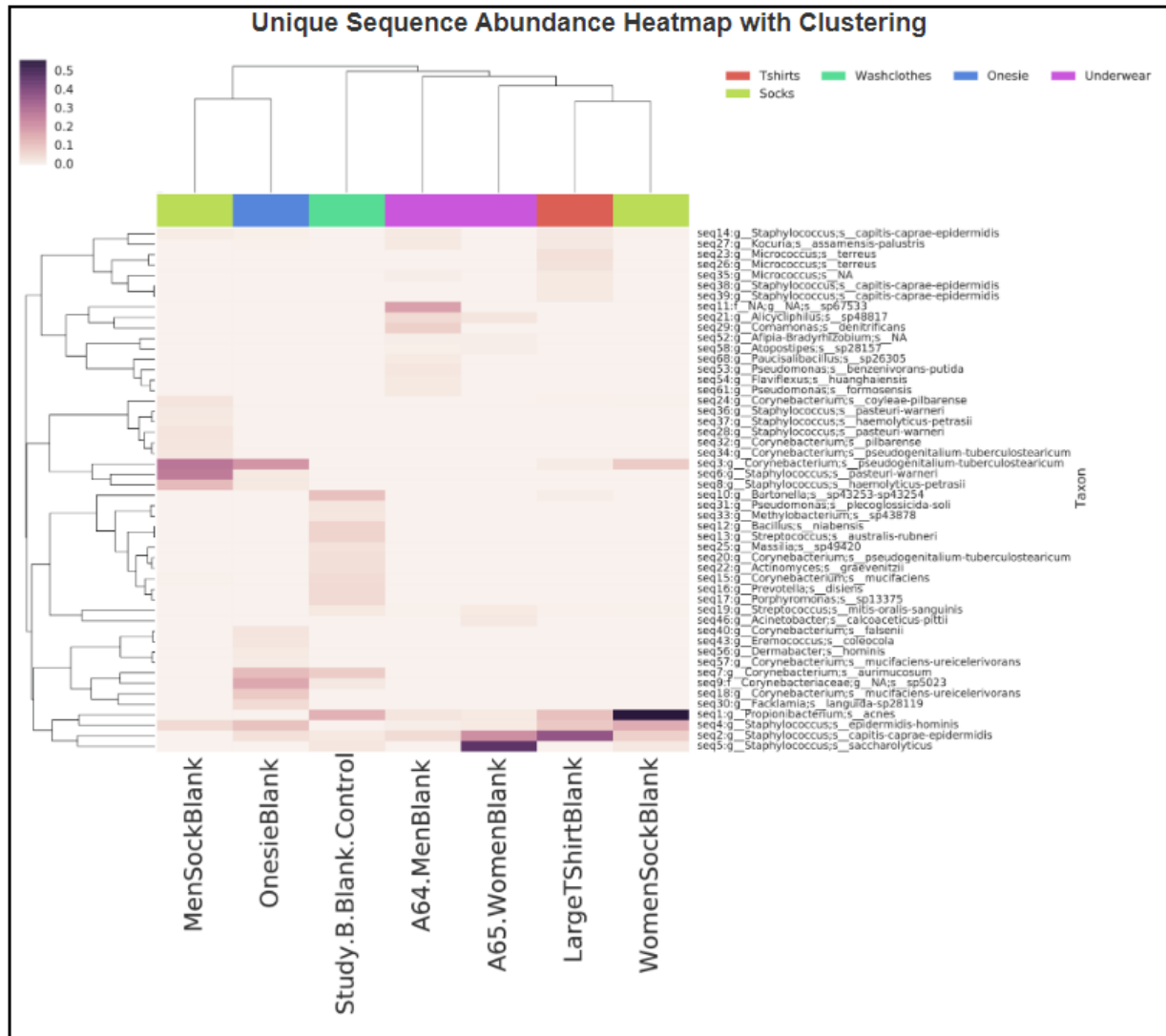


Figure S2. Sequence identification to the species level of genomic material recovered from control (blank) clothing items.