**Supplementary Methods and Materials**

Sample collection protocol

Skin and rectal swabs were collected using BBL CultureSwab EZ (Becton Dickinson, Franklin Lakes, NJ) and were moistened prior to sample collection using a solution of 0.1% Tween 20 (Sigma Aldrich, St. Louis, MO) and 0.15 M NaCl (Fisher Scientific, Pittsburgh, PA). Skin swabs were rotated on the skin forcefully for 5 revolutions at the antecubital fossa and then the chest. Rectal swabs were inserted approximately 2 to 3 cm into the anus and rotated for 5 revolutions.

Oral cavity swabs were not moistened prior to collection. Swabs were inserted into the mouth and rotated for 5 revolutions on the tongue dorsum. Tracheal aspirates were collected by flushing the endotracheal suction catheter with 10 cc of sterile saline and subsequently collected in a specimen trap. Urine samples were taken directly from the foley catheter collection chamber. Ten milliliters were obtained.

DNA extraction

Extractions of stool samples were done using the MO BIO PowerSoil DNA Isolation kit. There were some changes to the manufacturer’s protocol. Fecal samples were added directly into bead tubes and incubated at 65°C for 10 minutes followed by 95°C for 10 minutes. After addition of 60 µL of Solution C1 the bead tubes were then shaken horizontally on a lab mixer for 10 min at maximum speed using a MO BIO vortex adaptor. All remaining steps followed the manufacturer’s protocol. For all swab samples, the swab head was cut off directly into bead tubes containing 60 µL of Solution C1 and then incubated at 65°C for 10 minutes. Tubes were then shaken horizontally on a lab mixer for 2 minutes at maximum speed using a MO BIO vortex adaptor. All remaining steps followed the manufacturer’s protocol.

Extractions of urine samples were done using the MO BIO UltraClean DNA Isolation kit. 10 ml of urine in 15 ml conical tubes were centrifuged for 20 minutes on 3400xg. Supernatant was aspirated and the pellet was resuspended in 500 μl of Bead Solution. This was then transferred into a dry 0.1 mm glass bead tube and incubated for 10 min at 65°C. The dry bead tubes were then placed on a horizontal vortex adaptor and was vortexed for 3 min at maximum speed. All remaining steps followed the manufacturer’s protocol.

Extractions of tracheal aspirates were also done using the MO BIO UltraClean DNA Isolation kit. Approximately 5 ml of tracheal aspirate in 15 ml conical tubes were cen centrifuged for 20 minutes on 3400xg. Supernatant was aspirated and the pellet was resuspended in 700 μl of TD1 Solution and transferred into a dry bead tube. Dry bead tubes were then incubated for 10 min at 65°C. The dry bead tubes were then placed on a horizontal vortex adaptor and was vortexed for 3 min at maximum speed. All remaining steps followed the manufacturer’s protocol.

Extractions of individual oral, skin, and stool swabs were performed using the MO BIO PowerSoil DNA Isolation kit. Individual swabs were cut into dry bead tube and 60 μl of C1 Solution was then added. Tubes were incubated for 10 min at 65°C and then vortexed on a horizontal vortex adaptor for 2 min at high speed. C2 and C3 Solution steps were combined using 200 μl of each. All remaining steps followed the manufacturer’s protocol.

High-throughput extractions of oral, skin, and stool swabs were performed using MO BIO PowerSoil 96-well kit.

16S amplicon PCR and sequencing

Primers utilized either the Illumina adaptor, primer pad and linker (forward primer) or Illumina adaptor, Golay barcode, primer pad and linker (reverse primer) followed by a sequence targeting a conserved region of the bacterial 16S rRNA gene as previously described (18). All individual PCR amplicons were purified, quantified, pooled in equimolar ratios, and the library pool was gel purified prior to submission for sequencing as described in (19) with the exception that 30 PCR cycles were done.

Sequence processing

Forward and reverse reads from both runs were merged into a single amplicon sequence using PEAR[1]. QIIME (v1.9) was then used to demultiplex the forward reads from both sequencing runs, and the QIIME demultiplexed fasta file was used as a guide to assign barcodes to the assembled read file.

Reads were then combined with V3-V5 reads from the Human Microbiome project (HMP) sampled from the tongue, skin and rectal sites. Reads were trimmed to a uniform length for clustering with UPARSE. UPARSE (v8.0) was then used to quality filter the reads, cluster the reads at a 0.97 operational taxonomic unit (OTU) threshold, and remove chimeric sequences. QIIME was used to assign taxonomy, using UCLUST and the green genes database (v13.8) as a reference. OTUs with unassigned taxonomy were stripped from the OTU table, and those matching members of the Streptophyta were removed as contaminants originating from pollen, or from plant material in the gut.

A second OTU table was generated, combining reads from the American gut project with those from this experiment. After trimming assembled reads to match the length of the American gut read amplicons, sortMeRNA 2.0 was run to identify reads matching the bloom.fasta file of predicted contaminants from the combined set of American gut project reads, and reads from this project. The results were outputted as a BLAST style tabular format, and matches greater or equal to 97% identity with greater than 97% match coverage were excluded using an in-house perl script. An OTU table with samples from this experiment, and those from the American Gut project was generated using the same method as used for the HMP dataset.