[2] Data were available from 7 of 8 patients.

Figure Legend

Figure 1. Distribution of bacterial taxa across patients and anatomical subsites. Each stacked barchart summarizes the percent relative abundances (displayed on y-axes of plots) of bacterial taxa based on 16S rRNA sequencing. The top panels present average values across all 8 patients for phylum- and genus-level classifications. The bottom panels present genus-level data for each individual patient. To simplify data presentation, only taxa with relative abundances greater than 1% are shown; the remainder of low-abundance taxa are presented as "Other". In the lower panels, subjects with polyps are labeled CRSwNP and those without polyps are labeled CRSsNP.

Figure 2. Principal coordinates analysis (PCoA) of microbial communities was performed on genus-level microbiome data using the Morisita-Horn similarity score calculated on each pair of samples. These plots indicate that interpersonal variability outweighs the differences noted among the sampled subsites within a subject. The top two plots show all samples plotted by subject (top left) and by site (top right), and the lower panels show samples from each individual. Subjects with polyps are denoted by asterisks.

Figure 3. Heat map illustrating the Morisita-Horn beta diversity values by subject and site (1=identical, 0=complete dissimilarity).

Figure 4. Morisita-Horn comparison among sample sites demonstrates similarity of the middle meatus to other sites with a few outliers (1=identical, 0=complete dissimilarity). "Deeper sinuses" (maxillary, sphenoid, frontal) exhibit closest similarity, whereas the middle meatus demonstrates fairly good similarity to all sites.

Figure 5. *Corynebacterium spp.* are more abundant in the middle meatus and anterior nares (AN) samples, possibly owing to a contribution from the anterior nares as seen on the heatmap. The results of paired Wilcoxon Signed Rank tests comparing middle meatus to AN, Maxillary, Sphenoid, and Frontal sinus corynebacterial relative abundances are noted [**=$p<0.01$, *=$p<0.05$, •=$p<0.1$].

Supplementary Figure 1. Heatmap illustration of taxa identified in all samples (L:left, R:right, AN:anterior nares, NP:nasopharynx, MM:middle meatus, MAX:maxillary, SPH:sphenoid, FR:frontal).