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In the above article, Figure 2B. has been updated as follows online:

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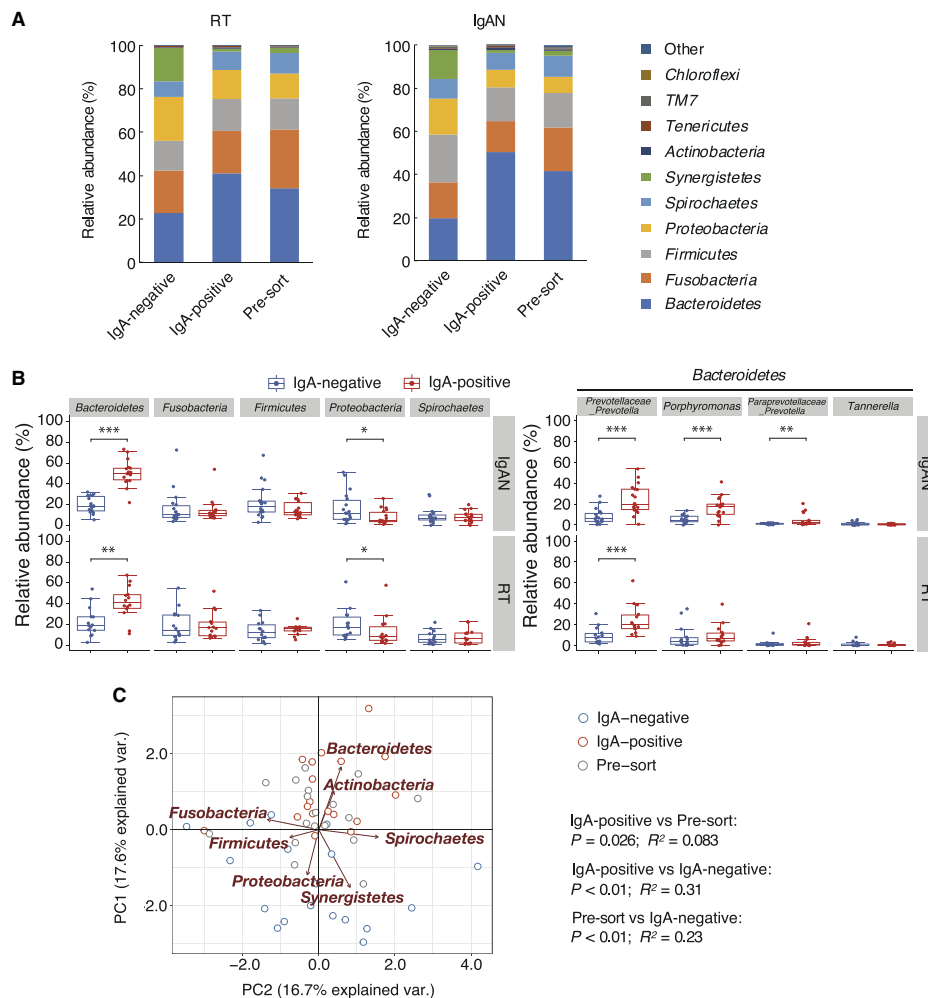


FIGURE 2: IgA-SEQ of tonsillar microbiota. (A) The mean relative abundance at the phylum level is shown for the IgA⁺ and IgA⁻ fractions and presort samples in the IgAN ($n = 18$) and RT ($n = 14$) groups. (B) Relative abundances of the top five phyla (top row) and genera of *Bacteroidetes* (bottom row) are shown for IgA⁺ (red) and IgA⁻ (blue) fractions. Data are presented as the median and IQR, and were statistically compared using the Mann-Whitney U test (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). (C) IgA-SEQ samples of IgAN were clustered using principal coordinate analysis with Bray-Curtis dissimilarities. The length of the black arrows represents taxon abundance. P-values and R^2 values calculated by permutational ANOVA (PERMANOVA) using 9999 permutations based on the Bray-Curtis dissimilarity index are indicated for the IgA⁺ fraction versus the presort sample, IgA⁺ versus IgA⁻ fraction and presort sample versus IgA⁻ fraction.

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