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

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![Figure 2](image.png)

**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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