Hiroki Yamaguchi, Shin Goto, Nao Takahashi, Masafumi Tsuchida, Hirofumi Watanabe, Suguru Yamamoto, Yoshikatsu Kaneko, Koichi Higashi, Hiroshi Mori, Yukio Nakamura, Arata Horii, Ken Kurokawa and Ichiei Narita

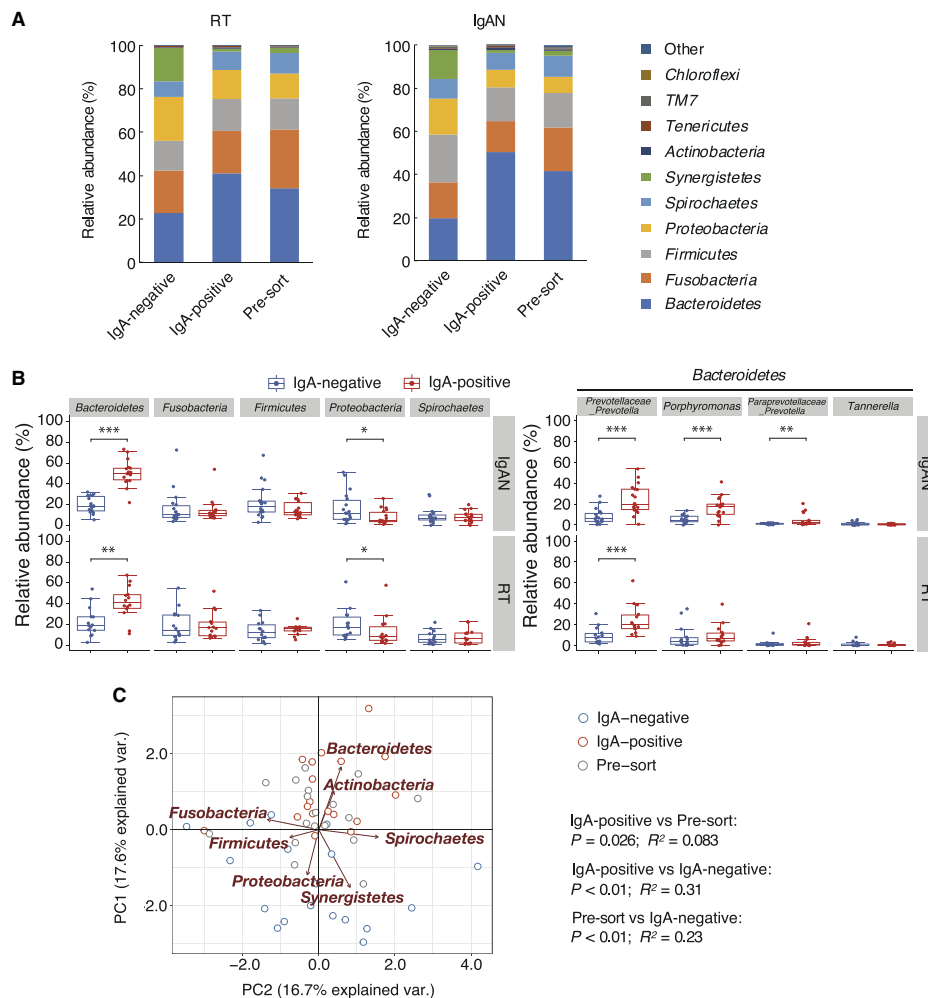In the above article, Figure 2B. has been updated as follows online:

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.