



Erratum: Taxonomic Characterization and Short-Chain Fatty Acids Production of the Obese Microbiota

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An Erratum on

Taxonomic Characterization and Short-Chain Fatty Acids Production of the Obese Microbiota
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Due to a production error, there was a mistake in **Figures 5, 6, and 7** as published. **Figure 5** should contain parts A and B, rather than just part A. What was published as **Figure 6** should be **Figure 5B**. What was published as **Figure 7** should be **Figure 6**. **Figure 7** was subsequently left out of the article. The corrected **Figures 5, 6, and 7** appear below.

The publisher apologizes for this mistake.

The original version of this article has been updated.

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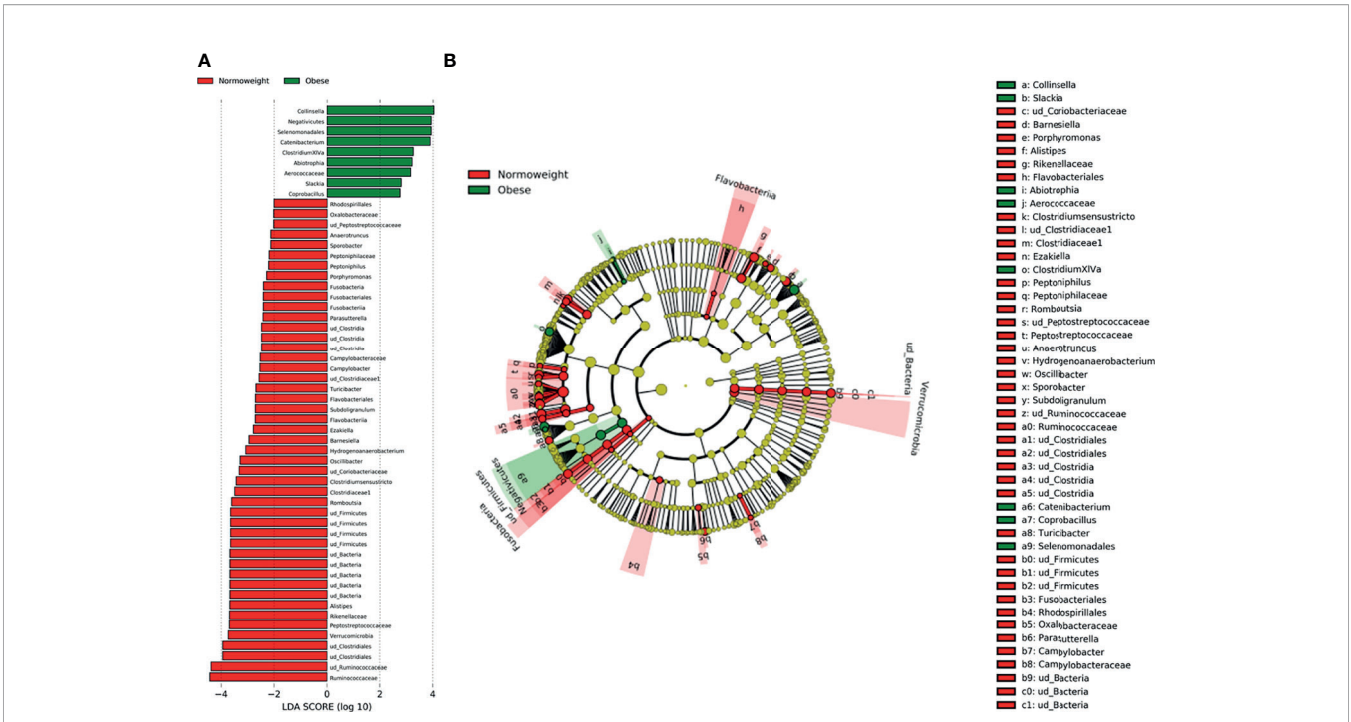


FIGURE 5 | Characterization of microbiomes by LEfSe analysis and LDA. **(A)** Histogram of the LDA scores (log10) computed for features with differential abundance in normal weight (N) and obese (O) subjects. **(B)** Cladograms showing the significant differences of gut microbiota composition in normoweight (N) and obese (O) subjects.

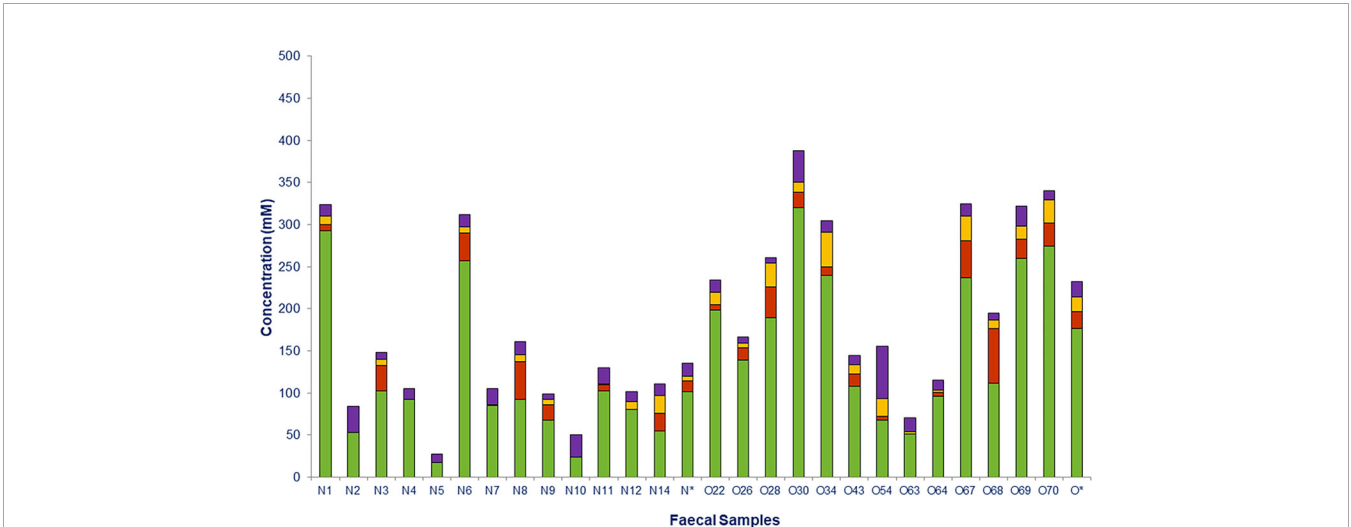


FIGURE 6 | Short chain fatty acids (SCFAs) and lactate measured in fecal samples from normoweight (N) and obese (O) individuals: acetate (green), propionate (red), butyrate (yellow), and lactate (purple). The column (*) represents the median value of each group.

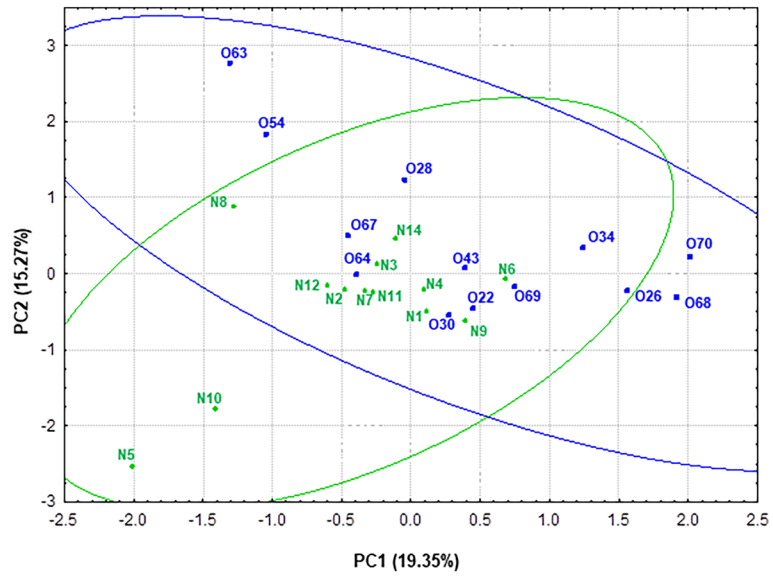


FIGURE 7 | Representation of the samples from normoweight (N) and obese (O) individuals in the plane defined by the two first components (PC1 and PC2) resulting from a PCA that takes into account both genera taxonomic groups and the metabolic activity-SCFAs and ammonium-data.