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Correction: Evaluation of the gastric microbiota based on body mass index using 16S rRNA gene sequencing

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KEYWORDS

body mass index, gastric microbiota, obesity, 16S rRNA sequencing, metabolic dysregulation

A Correction on

Evaluation of the gastric microbiota based on body mass index using 16S rRNA gene sequencing

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In the published article, **Figures 2A–D** and **Figures 3A–D** were mistakenly interchanged. The corrected arrangement is: **Figure 2A–D** should appear as **Figure 3A–D**, and **Figure 3A–D** should appear as **Figure 2A–D**.

The original article has been updated.

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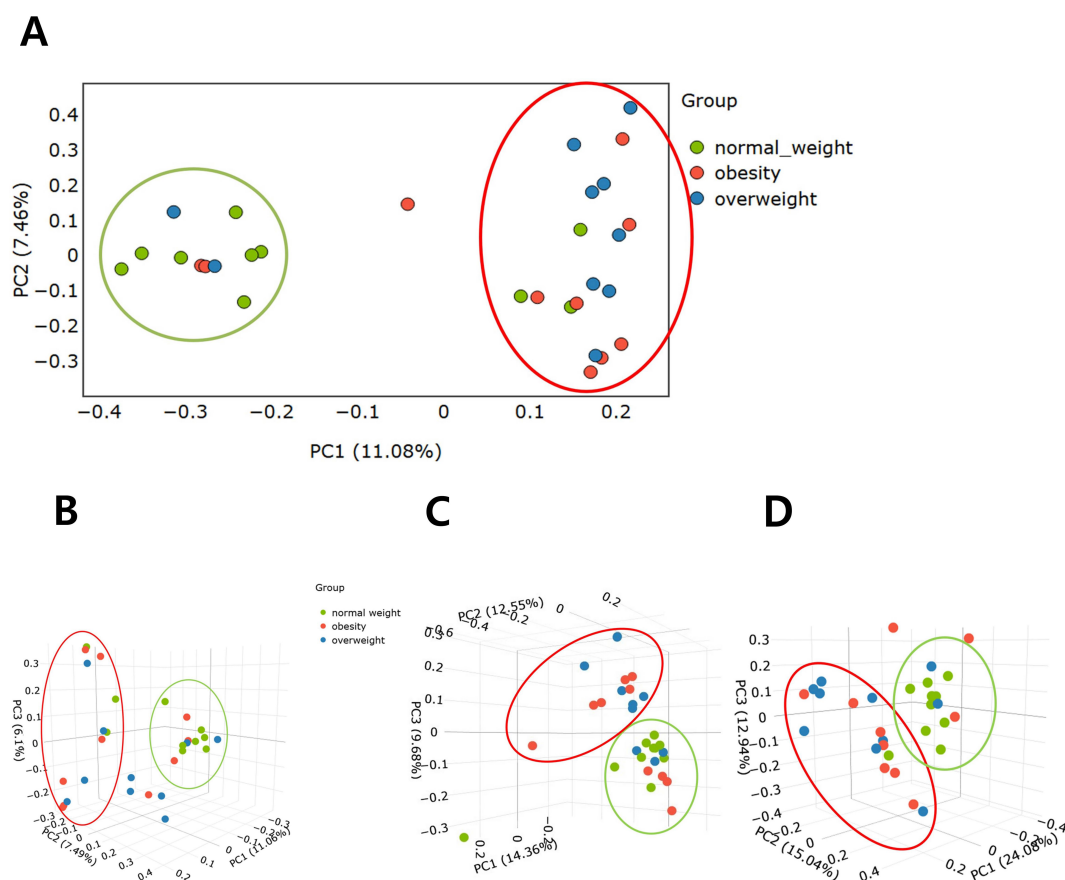


FIGURE 2

Comparison of beta diversity among the overweight, obese, and normal weight groups. (A) Bray-Curtis distance (2D). (B) Bray-Curtis distance (3D). (C) Unweighted UniFrac distance matrix. (D) Weighted UniFrac distance matrix..

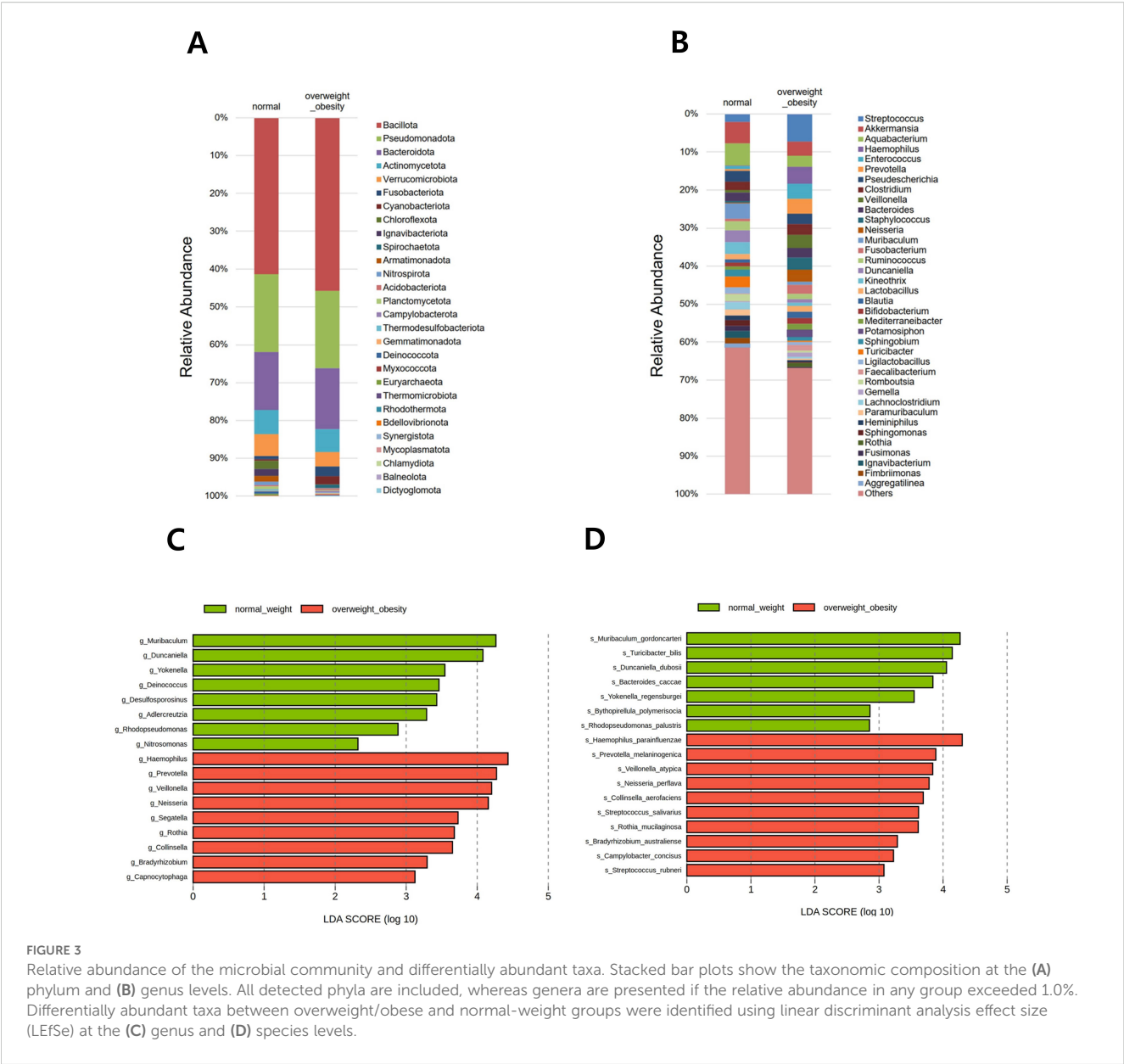


FIGURE 3 Relative abundance of the microbial community and differentially abundant taxa. Stacked bar plots show the taxonomic composition at the (A) phylum and (B) genus levels. All detected phyla are included, whereas genera are presented if the relative abundance in any group exceeded 1.0%. Differentially abundant taxa between overweight/obese and normal-weight groups were identified using linear discriminant analysis effect size (LEfSe) at the (C) genus and (D) species levels.