Corrigendum: Altered composition of the oral microbiota in depression among cigarette smokers: A pilot study

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A corrigendum on
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In the published article, there was an error in Figure 3 and Figure 4 as published. In the published article, the edges between nodes were not visible (Figure 3) and the figure/text was blurry (Figures 3, 4). The corrected Figure 3 and Figure 4 and their caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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Differential network analysis between BADS avoidance and activation groups shows different correlations between genera. (A) Network analysis of the top 50 genera showing the highest variation between the two conditions and visualized the results (degree, betweenness centrality, closeness centrality; p > 0.05). Network specific hub nodes are shown in bold font. (B) The differential network shows the different correlations between genera (Fisher exact test, p-adj < 0.1 BH adjusted); if genus annotation was not available, phylum and family are shown.
Functional profiling analysis of oral microbiota based on BADS. Functional profiling between BADS avoidance and activation groups (A) alpha diversity (Shannon index) and (B) beta diversity (Aitchison distance). (C) Average functional profiles with an abundance > 1% are shown. (D) Lysine degradations different abundance between the two conditions (ANCOM-BC, q = 0.0092).