Corrigendum


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The authors regret an error in the original heat map for Figure 4. The heat map highlighted an abundance of \textit{Bifidobacterium} in the HIE treatment group which was incorrect. A new heat map has been generated which agrees with the results in the paper (see corrected Figure 4 below). There is no correction required in the main text of the manuscript, just a correction for the legend for Fig. 4, as written below.

The authors would like to apologise for any inconvenience caused.
Fig. 4 Hierarchically clustered heat map showing correlations between the relative microbial compositions in each group (control = C, HIE treatment group = HP). Clustering was performed with the hclust function in the R package ‘pheatmap’. The colour of each tile of the heat map indicates the strength of the correlation for a given genera (red = ~35-40%, orange = ~30-35%, yellow = ~20-30%, white = ~15-20%, light blue = ~10-15%, blue = 0-10%).