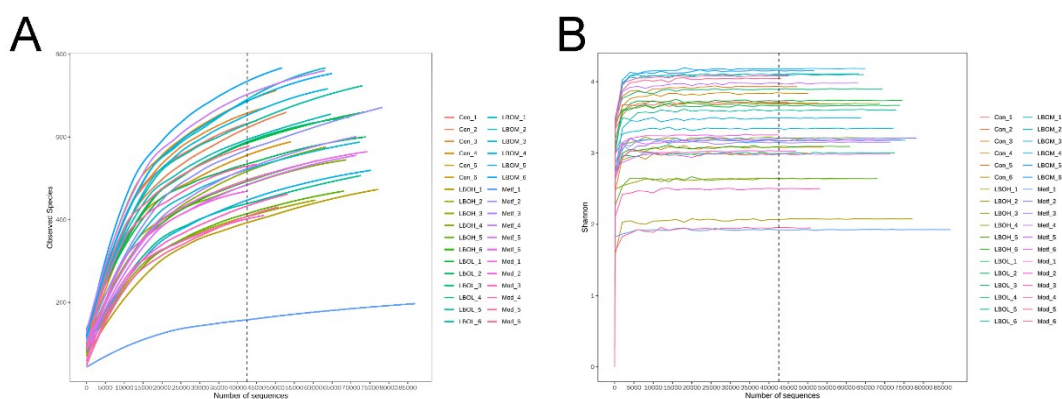
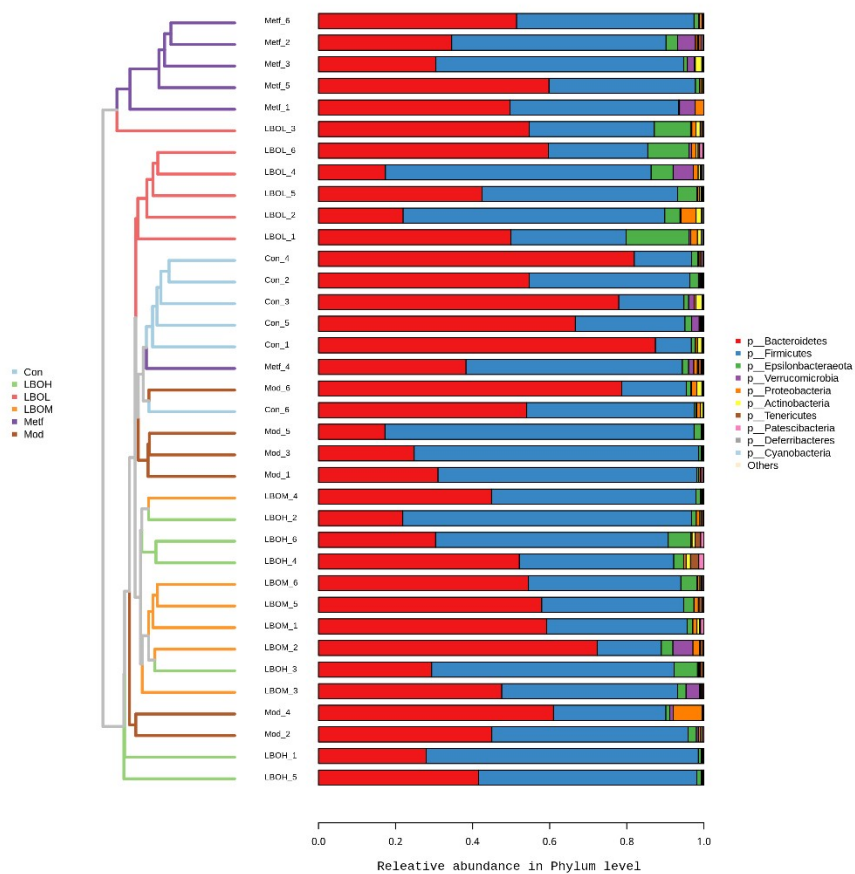


Supporting Information



5 **Figure S1. (A)** Rarefaction Curve. Abscissa: number of qualitatively sequence drawn
6 at random; ordinate: number of observed OTUs. The flatter the curve, the more
7 reasonable the amount of sequencing data, and more data volumes will only generate
8 a small number of new OTUs. **(B)** Shannon Curve. The flatter the curve, the larger
9 amount of sequencing data is enough to reflect the sample's vast majority of microbial
10 information.

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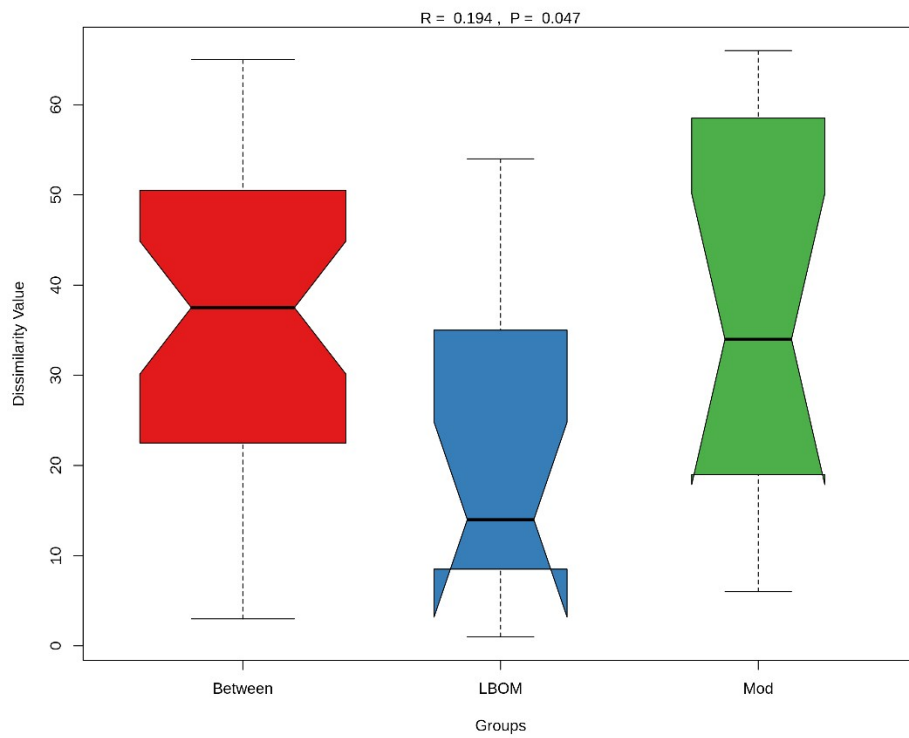


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13 **Figure S2.** UPGMA clustering tree based on unweighted unifrac distances and
 14 histograms of community structure at the phylum level.

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18 **Figure S3.** Boxplots represent the differences between and within the LBO-M and the
 19 Mod ($P < 0.05$).

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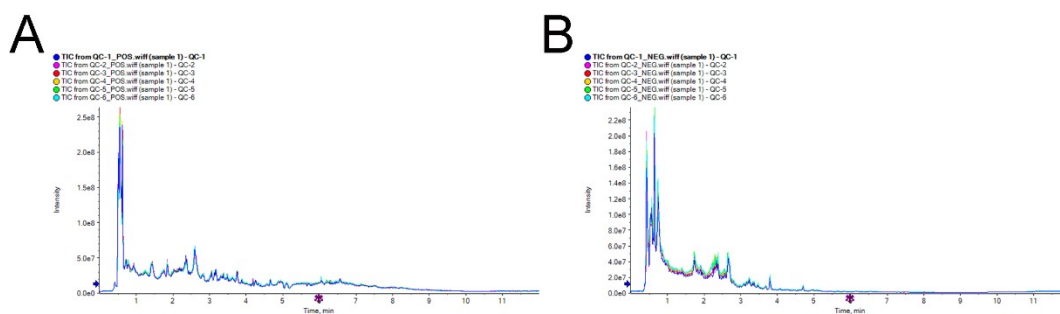
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28 **Figure S4.** Overlapping spectra of TIC diagrams of QC samples in **(A)** the positive
 29 and **(B)** the negative ion modes.

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