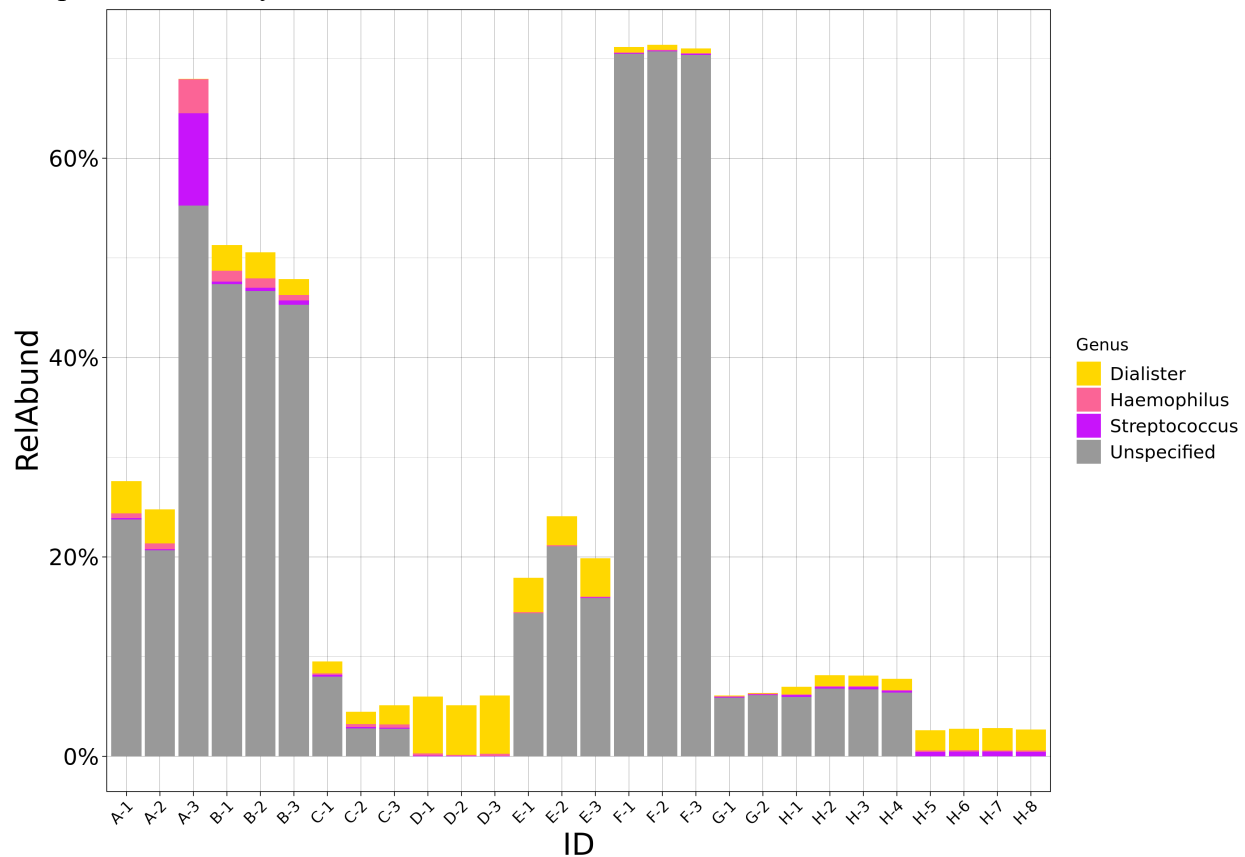


## Supplemental Material

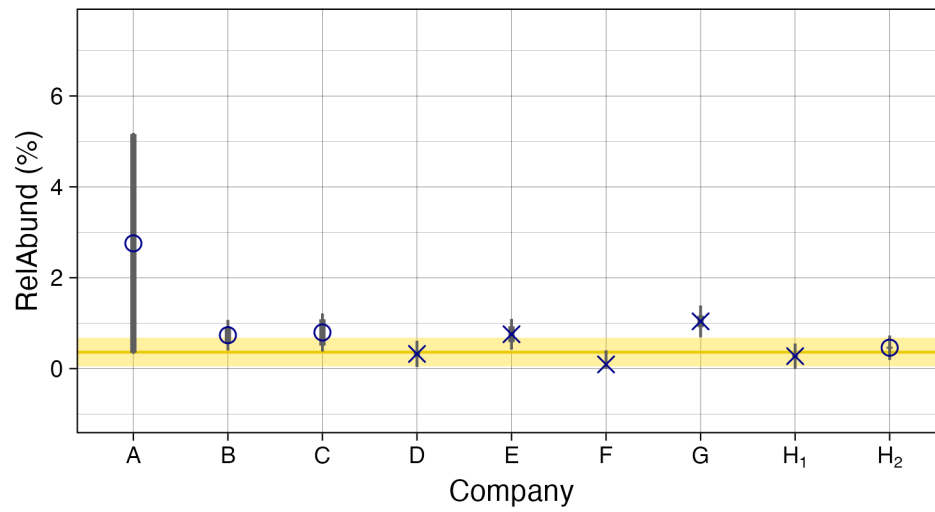
**Supplemental Figure 1. Common Genera across all Companies and Replicates** The relative abundance of genera that were identified in all tests conducted (present in all replicates from all companies); color coding is consistent with that of Fig 3; unspecified reads are included in both figures given that A-3 is absent from Fig 3. Each company is indicated by a letter, with replicate samples indicated by the number after the dash.



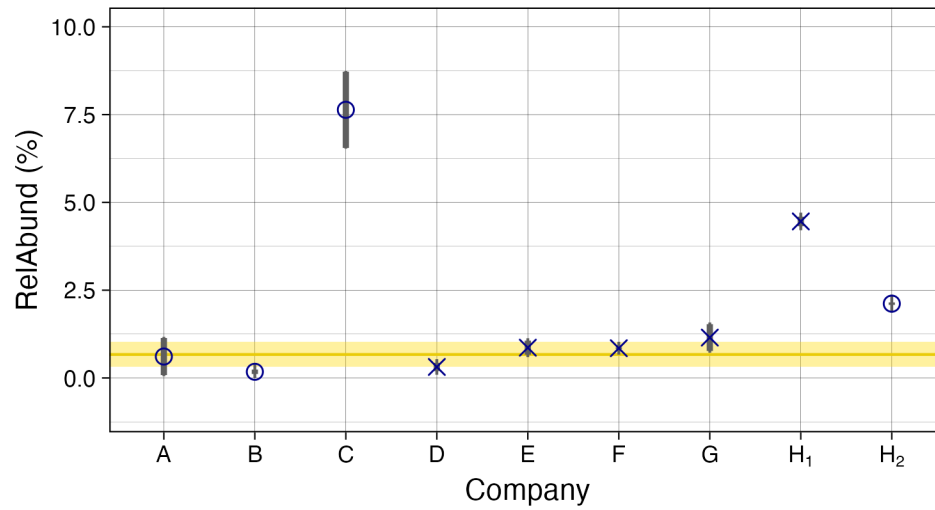
## Supplemental Figure 2. Consensus determination across 9 measurements.

Hierarchical Bayesian random effects model with a dark uncertainty was determined to compare individual company findings (A-G) and NIST findings (H<sub>1</sub>-WGS, H<sub>2</sub>-16S) to a consensus value (shown by yellow line), range (shown by yellow shaded region). The O's indicate the average value for each company using 16S analysis and the X's indicate the average value for companies using WMS. Thick grey lines represent the variability for each company, and the thin grey extensions capture additional variability attributed as dark uncertainty (further explained in the method section). This analysis was done for 18 genera that were found to be identified in at least 1 replicate from each company. Five genera are include in Fig 4, the remaining 13 are below.

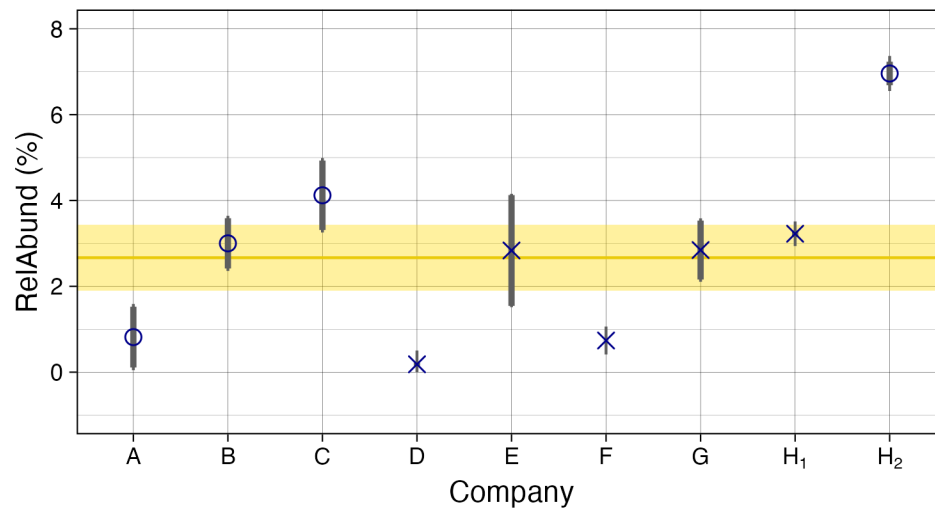
### Akkermansia



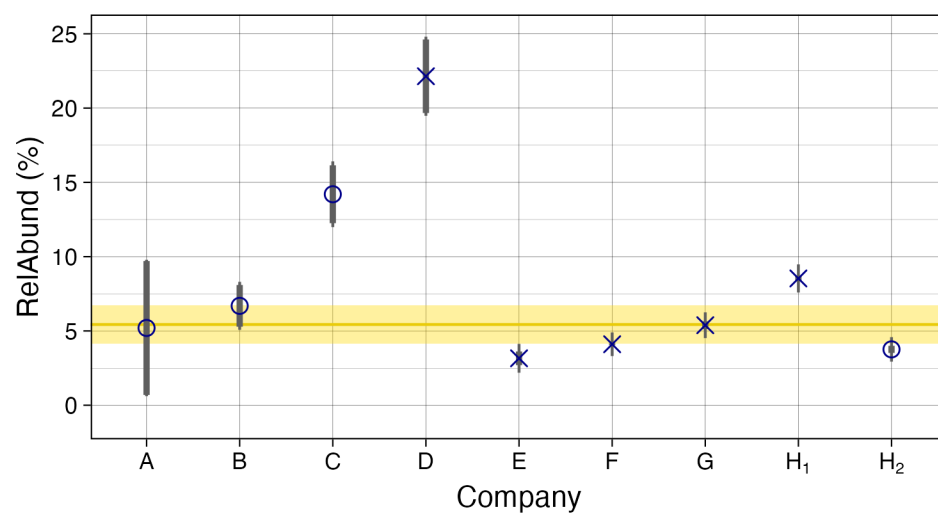
### Anaerostipes



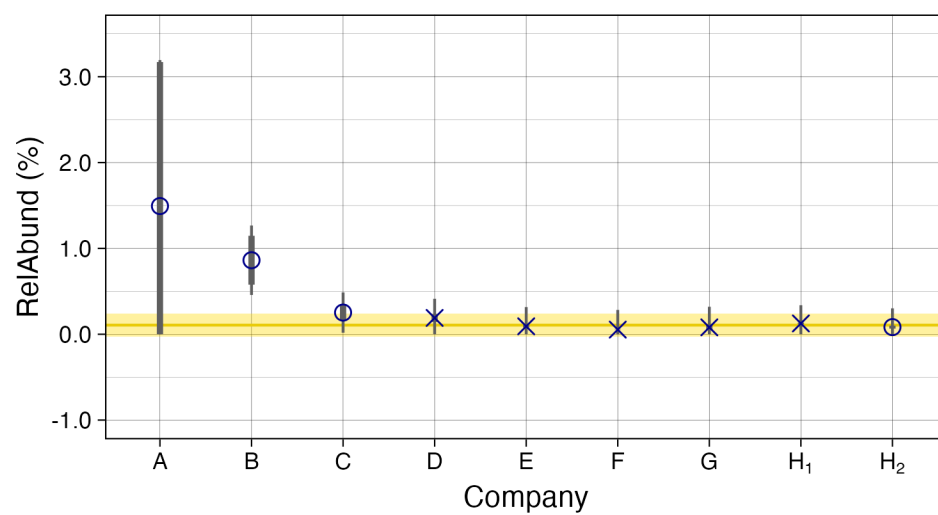
### Blautia



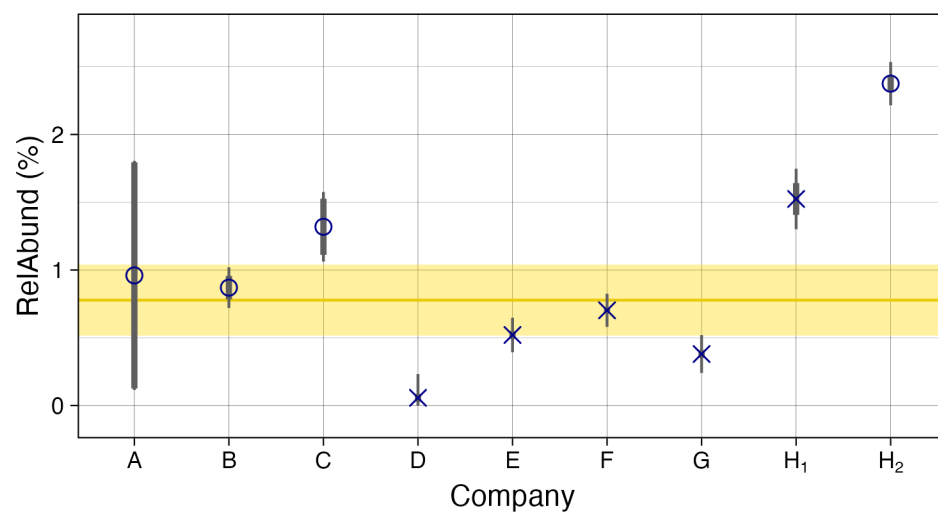
### Faecalibacterium

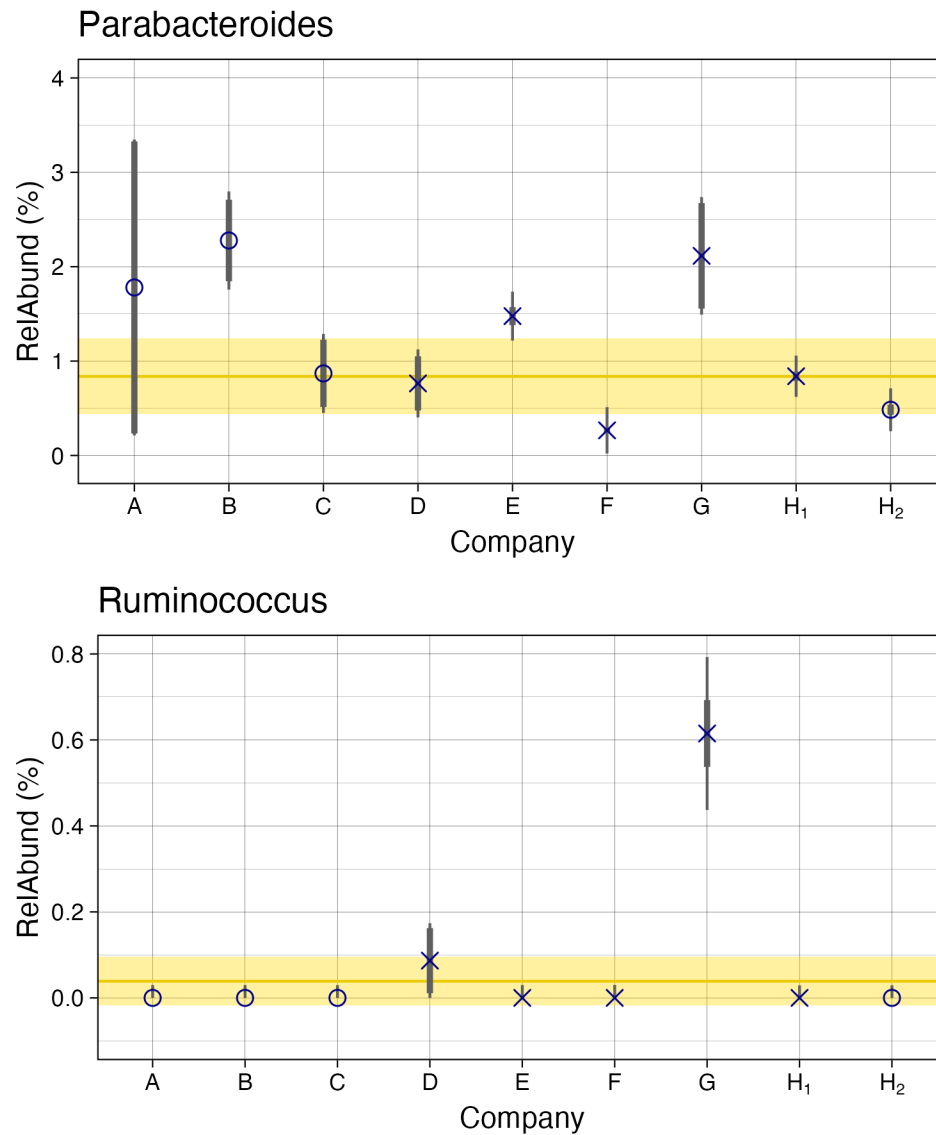


### Haemophilus



### Lachnospira





**Supplemental Table 1. Comparison of Consensus Values to Reported Comparator Values from Two DTC.**

|                         | reported range <sup>1</sup> | consensus range | reported avg <sup>2</sup> | consensus average |
|-------------------------|-----------------------------|-----------------|---------------------------|-------------------|
| <b>Bacteroides</b>      | 6.17-16.73                  | 5.94 – 16.95    | 29.09                     | 11.45             |
| <b>Bifidobacterium</b>  | 0.24-2.82                   | 3.41 – 15.35    | 1.13                      | 9.38              |
| <b>Clostridium</b>      | 0.06-0.28                   | 0.04 – 4.08     | 1.17                      | 2.06              |
| <b>Faecalibacterium</b> | 0.64-2.01                   | 4.26 – 11.90    | 8.73                      | 8.08              |
| <b>Roseburia</b>        | 0.73-3.49                   | 2.93 – 7.32     | 3.91                      | 5.13              |

<sup>1</sup>IQR used to define the healthy population as a comparator used by company E

<sup>2</sup>average from the American Gut Project reported by company G

