# SUPPLEMENTARY INFORMATION

# Temporal variability in quantitative human gut microbiome profiles and implications for clinical research.

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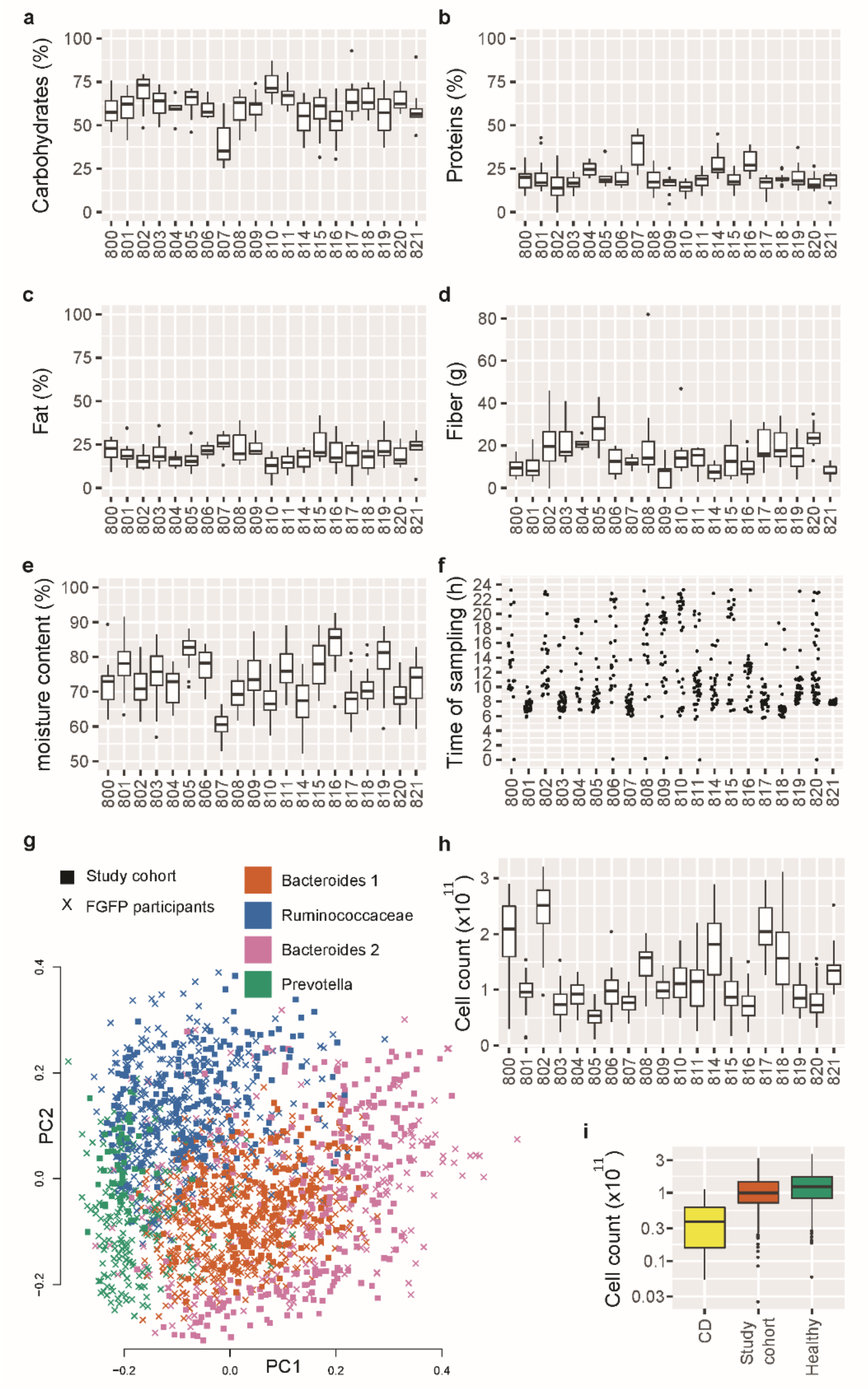
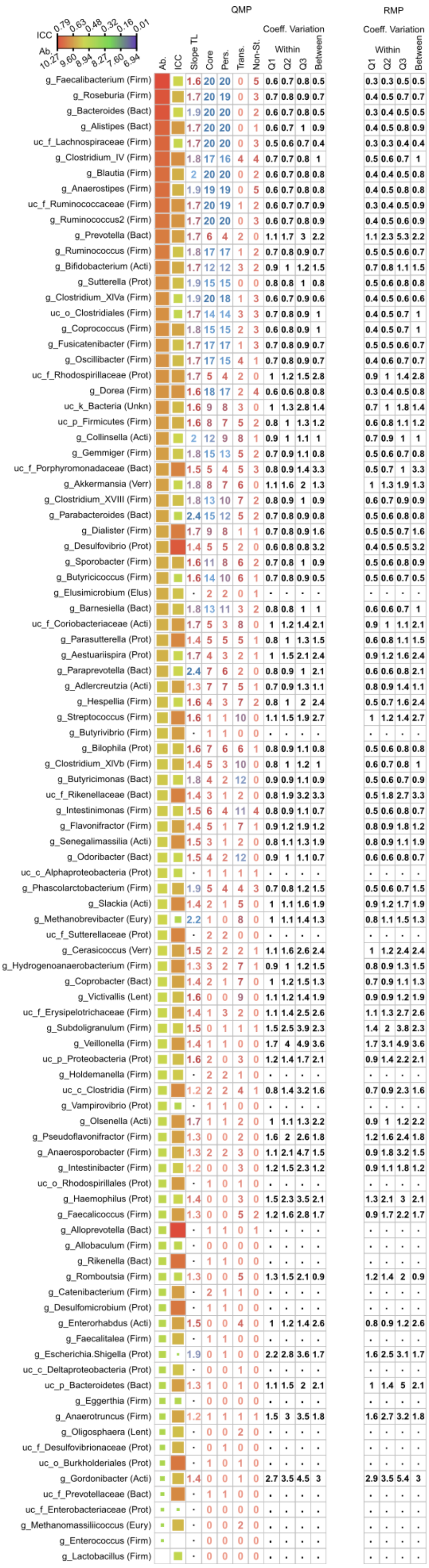
Content

# SUPPLEMENTARY FIGURES AND TABLES



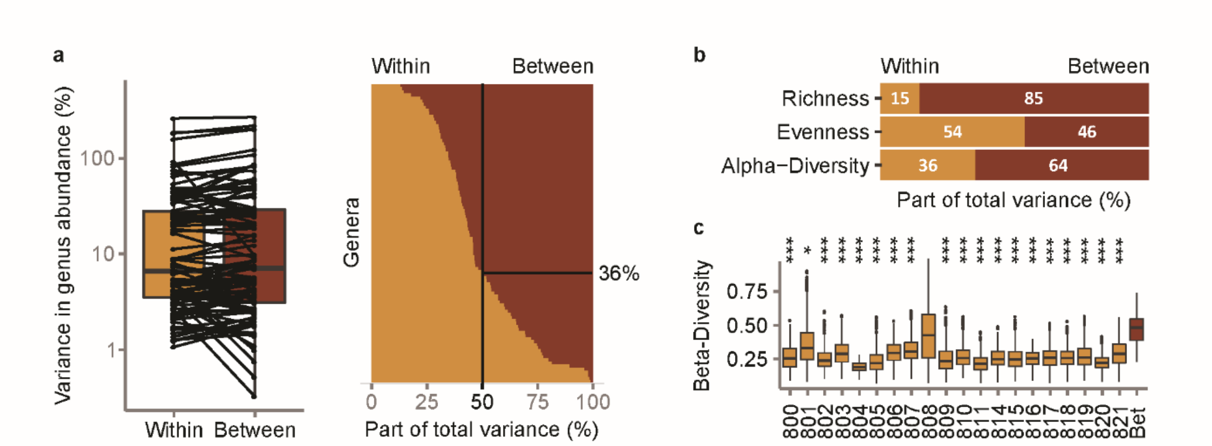
**Supplementary Figure 1**: **Overview of study cohort characteristics and variation in metadata.** Box plots of percentage of total weight of food products consumed per day for **a.** Carbohydrates (ICC: 0.21), **b.** Proteins (ICC: 0.40), and **c.** Fat (ICC: 0.21), for each participant. **d.** Total weight of fiber consumed per day (ICC: 0.32), for each participant. **e.** Box plots of stool moisture content (%) for each participant (ICC:0.51). **f.** Time of stool sampling according to a 24h-scale, for each participant. **g.** Principal Coordinate Analyses of RMPs of all study cohort samples (squares) and 1104 FGFP participants (crosses),

coloured according to enterotype, namely Ruminoccocaceae (R, blue), Bacteroides 1 (B1, orange), Bacteroides 2 (B2, Pink), Prevotella (P, green). **h.** Box plots of microbial load, in cell counts per gram of faeces, for each participant (ICC:0.61). **i.** Microbial load, in cell counts per gram of faeces, of all samples (Study Cohort) in comparison with previously sampled cohorts of Crohn's Disease patients (CD) and healthy volunteers (Healthy)[11].
The body of the box plots within these figures represents the first and third quartiles of the distribution, and the median line. The whiskers extend from the quartiles to the last data point within 1.5× IQR, with outliers beyond. Figures and summary measures are based on all data (N=20, n=713) (Supplementary Table S1 & S2).



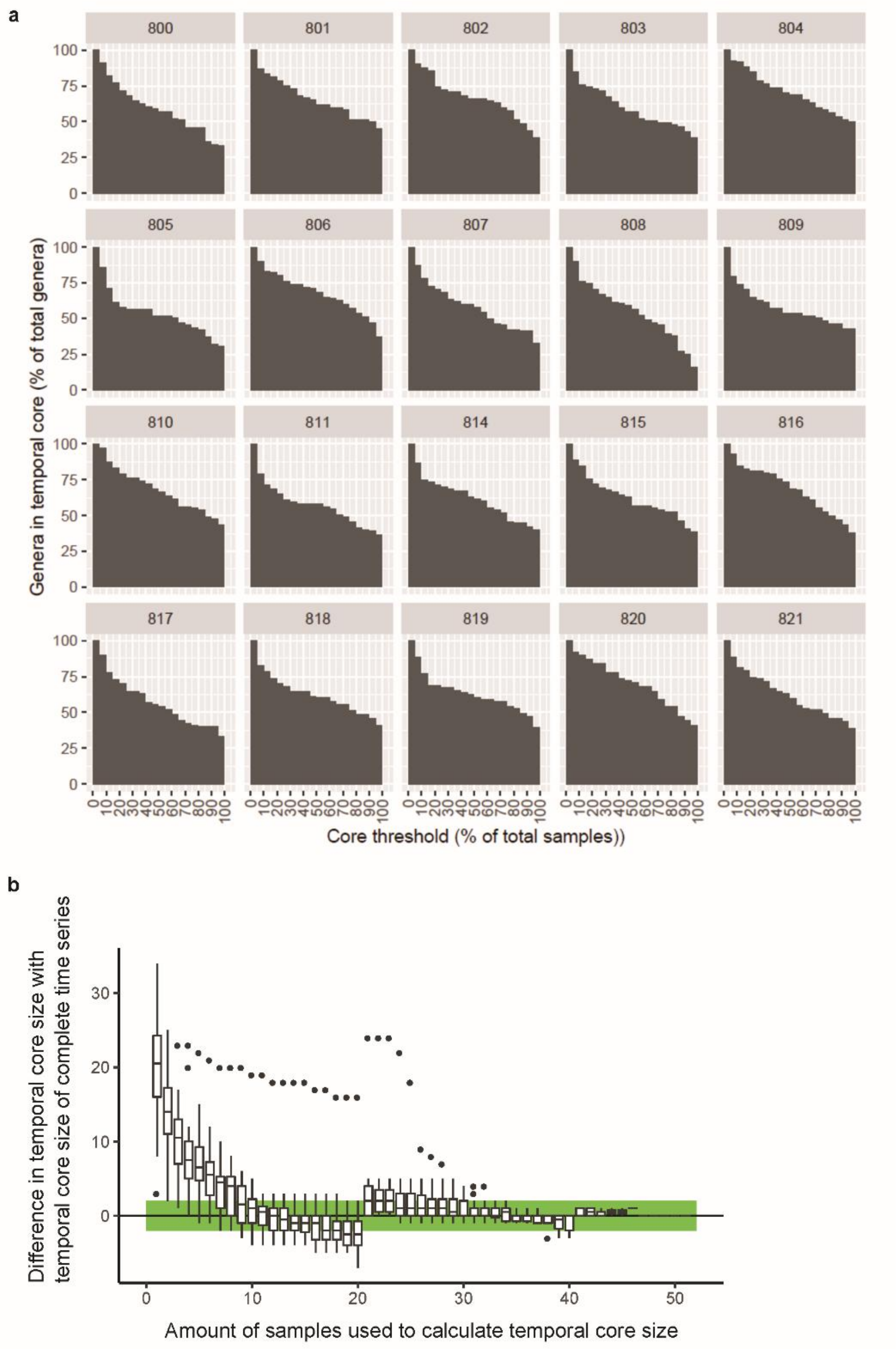
| | | | QMP | | | | | | | | | RMP | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | Coeff. Variation | | | | | Coeff. Variation | | | |
| | | | | | | | Within | | | | | Within | | | |
| | Ab. | ICC | Slope TL | Core | Pers. | Trans. | Non-St. | Q1 | Q2 | Q3 | Between | Q1 | Q2 | Q3 | Between |
| g_Faecalibacterium (Firm) | ■ | ■ | 1.6 | 20 | 20 | 0 | 5 | 0.6 | 0.7 | 0.8 | 0.5 | 0.3 | 0.3 | 0.5 | 0.5 |
| g_Roseburia (Firm) | ■ | ■ | 1.7 | 20 | 19 | 0 | 3 | 0.7 | 0.8 | 0.9 | 0.7 | 0.4 | 0.5 | 0.7 | 0.7 |
| g_Bacteroides (Bact) | ■ | ■ | 1.9 | 20 | 20 | 0 | 2 | 0.6 | 0.7 | 0.8 | 0.5 | 0.3 | 0.4 | 0.5 | 0.5 |
| g_Alistipes (Bact) | ■ | ■ | 1.7 | 20 | 20 | 0 | 1 | 0.6 | 0.7 | 1 | 0.9 | 0.4 | 0.5 | 0.8 | 0.9 |
| uc_f_Lachnospiraceae (Firm) | ■ | ■ | 1.7 | 20 | 20 | 0 | 3 | 0.5 | 0.6 | 0.7 | 0.4 | 0.3 | 0.3 | 0.4 | 0.4 |
| g_Clostridium_IV (Firm) | ■ | ■ | 1.8 | 17 | 16 | 4 | 4 | 0.7 | 0.7 | 0.8 | 1 | 0.5 | 0.6 | 0.7 | 1 |
| g_Blautia (Firm) | ■ | ■ | 2 | 20 | 20 | 0 | 2 | 0.6 | 0.7 | 0.8 | 0.8 | 0.4 | 0.4 | 0.5 | 0.8 |
| g_Anaerostipes (Firm) | ■ | ■ | 1.9 | 19 | 19 | 0 | 5 | 0.6 | 0.7 | 0.8 | 0.8 | 0.4 | 0.5 | 0.8 | 0.8 |
| uc_f_Ruminococcaceae (Firm) | ■ | ■ | 1.7 | 20 | 19 | 1 | 2 | 0.6 | 0.7 | 0.7 | 0.9 | 0.3 | 0.4 | 0.5 | 0.9 |
| g_Ruminococcus2 (Firm) | ■ | ■ | 1.7 | 20 | 20 | 0 | 3 | 0.6 | 0.7 | 0.8 | 0.9 | 0.4 | 0.5 | 0.6 | 0.9 |
| g_Prevotella (Bact) | ■ | ■ | 1.7 | 6 | 4 | 2 | 0 | 1.1 | 1.7 | 3 | 2.2 | 1.1 | 2.3 | 5.3 | 2.2 |
| g_Ruminococcus (Firm) | ■ | ■ | 1.8 | 17 | 17 | 1 | 2 | 0.7 | 0.8 | 0.9 | 0.7 | 0.5 | 0.5 | 0.6 | 0.7 |
| g_Bifidobacterium (Acti) | ■ | ■ | 1.7 | 12 | 12 | 3 | 2 | 0.9 | 1 | 1.2 | 1.5 | 0.7 | 0.8 | 1.1 | 1.5 |
| g_Sutterella (Prot) | ■ | ■ | 1.9 | 15 | 15 | 0 | 0 | 0.8 | 0.8 | 1 | 0.8 | 0.5 | 0.6 | 0.8 | 0.8 |
| g_Clostridium_XlVa (Firm) | ■ | ■ | 1.9 | 20 | 18 | 1 | 3 | 0.6 | 0.7 | 0.9 | 0.6 | 0.4 | 0.5 | 0.6 | 0.6 |
| uc_o_Clostridiales (Firm) | ■ | ■ | 1.7 | 14 | 14 | 3 | 3 | 0.7 | 0.8 | 0.9 | 1 | 0.4 | 0.5 | 0.7 | 1 |
| g_Coprococcus (Firm) | ■ | ■ | 1.8 | 15 | 15 | 2 | 3 | 0.6 | 0.8 | 0.9 | 1 | 0.4 | 0.5 | 0.7 | 1 |
| g_Fusicatenibacter (Firm) | ■ | ■ | 1.7 | 17 | 17 | 1 | 3 | 0.7 | 0.8 | 0.9 | 0.7 | 0.5 | 0.5 | 0.6 | 0.7 |
| g_Oscillibacter (Firm) | ■ | ■ | 1.7 | 17 | 15 | 4 | 1 | 0.7 | 0.8 | 0.9 | 0.7 | 0.4 | 0.6 | 0.7 | 0.7 |
| uc_f_Rhodospirillaceae (Prot) | ■ | ■ | 1.7 | 5 | 4 | 2 | 0 | 1 | 1.2 | 1.5 | 2.8 | 0.9 | 1 | 1.4 | 2.8 |
| g_Dorea (Firm) | ■ | ■ | 1.6 | 18 | 17 | 2 | 4 | 0.6 | 0.6 | 0.8 | 0.8 | 0.3 | 0.4 | 0.5 | 0.8 |
| uc_k_Bacteria (Unkn) | ■ | ■ | 1.6 | 9 | 8 | 3 | 0 | 1 | 1.3 | 2.8 | 1.4 | 0.7 | 1 | 1.8 | 1.4 |
| uc_p_Firmicutes (Firm) | ■ | ■ | 1.6 | 8 | 7 | 5 | 2 | 0.8 | 1 | 1.3 | 1.2 | 0.6 | 0.8 | 1.1 | 1.2 |
| g_Collinsella (Acti) | ■ | ■ | 2 | 12 | 9 | 8 | 1 | 0.9 | 1 | 1.1 | 1 | 0.7 | 0.9 | 1 | 1 |
| g_Gemmiger (Firm) | ■ | ■ | 1.8 | 15 | 13 | 5 | 2 | 0.7 | 0.9 | 1.1 | 0.8 | 0.5 | 0.6 | 0.7 | 0.8 |
| uc_f_Porphyromonadaceae (Bact) | ■ | ■ | 1.5 | 5 | 4 | 5 | 3 | 0.8 | 0.9 | 1.4 | 3.3 | 0.5 | 0.7 | 1 | 3.3 |
| g_Akkermansia (Verr) | ■ | ■ | 1.8 | 8 | 7 | 6 | 0 | 1.1 | 1.6 | 2 | 1.3 | 1 | 1.3 | 1.9 | 1.3 |
| g_Clostridium_XVIII (Firm) | ■ | ■ | 1.8 | 13 | 10 | 7 | 2 | 0.8 | 0.9 | 1 | 0.9 | 0.6 | 0.7 | 0.9 | 0.9 |
| g_Parabacteroides (Bact) | ■ | ■ | 2.4 | 15 | 12 | 5 | 2 | 0.7 | 0.8 | 0.9 | 0.8 | 0.5 | 0.6 | 0.8 | 0.8 |
| g_Dialister (Firm) | ■ | ■ | 1.7 | 9 | 8 | 1 | 1 | 0.7 | 0.8 | 0.9 | 1.6 | 0.5 | 0.5 | 0.7 | 1.6 |
| g_Desulfovibrio (Prot) | ■ | ■ | 1.4 | 5 | 5 | 2 | 0 | 0.6 | 0.8 | 0.8 | 3.2 | 0.4 | 0.5 | 0.5 | 3.2 |
| g_Sporobacter (Firm) | ■ | ■ | 1.6 | 11 | 8 | 6 | 2 | 0.7 | 0.8 | 1 | 0.9 | 0.5 | 0.6 | 0.8 | 0.9 |
| g_Butyricicoccus (Firm) | ■ | ■ | 1.6 | 14 | 10 | 6 | 1 | 0.7 | 0.8 | 0.9 | 0.5 | 0.5 | 0.6 | 0.7 | 0.5 |
| g_Elusimicrobium (Elus) | ■ | ■ | · | 2 | 2 | 0 | 1 | · | · | · | · | · | · | · | · |
| g_Barnesiella (Bact) | ■ | ■ | 1.8 | 13 | 11 | 3 | 2 | 0.8 | 0.8 | 1 | 1 | 0.6 | 0.6 | 0.7 | 1 |
| uc_f_Coriobacteriaceae (Acti) | ■ | ■ | 1.7 | 5 | 3 | 8 | 0 | 1 | 1.2 | 1.4 | 2.1 | 0.9 | 1 | 1.1 | 2.1 |
| g_Parasutterella (Prot) | ■ | ■ | 1.4 | 5 | 5 | 5 | 1 | 0.8 | 1 | 1.3 | 1.5 | 0.6 | 0.8 | 1.1 | 1.5 |
| g_Aestuariispira (Prot) | ■ | ■ | 1.7 | 4 | 3 | 2 | 1 | 1 | 1.5 | 2.1 | 2.4 | 0.9 | 1.2 | 1.6 | 2.4 |
| g_Paraprevotella (Bact) | ■ | ■ | 2.4 | 7 | 6 | 2 | 0 | 0.8 | 0.9 | 1 | 2.1 | 0.6 | 0.6 | 0.8 | 2.1 |
| g_Adlercreutzia (Acti) | ■ | ■ | 1.3 | 7 | 7 | 5 | 1 | 0.7 | 0.9 | 1.3 | 1.1 | 0.8 | 0.9 | 1.4 | 1.1 |
| g_Hespellia (Firm) | ■ | ■ | 1.6 | 4 | 3 | 7 | 2 | 0.8 | 1 | 2 | 2.4 | 0.5 | 0.7 | 1.6 | 2.4 |
| g_Streptococcus (Firm) | ■ | ■ | 1.6 | 1 | 1 | 10 | 0 | 1.1 | 1.5 | 1.9 | 2.7 | 1 | 1.2 | 1.4 | 2.7 |
| g_Butyrivibrio (Firm) | ■ | ■ | · | 1 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Bilophila (Prot) | ■ | ■ | 1.6 | 7 | 6 | 6 | 1 | 0.8 | 0.9 | 1.1 | 0.8 | 0.5 | 0.6 | 0.8 | 0.8 |
| g_Clostridium_XlVb (Firm) | ■ | ■ | 1.4 | 5 | 3 | 10 | 0 | 0.8 | 1 | 1.2 | 1 | 0.6 | 0.7 | 0.8 | 1 |
| g_Butyricimonas (Bact) | ■ | ■ | 1.8 | 4 | 2 | 12 | 0 | 0.9 | 0.9 | 1.1 | 0.9 | 0.5 | 0.6 | 0.7 | 0.9 |
| uc_f_Rikenellaceae (Bact) | ■ | ■ | 1.4 | 3 | 1 | 2 | 0 | 0.8 | 1.9 | 3.2 | 3.3 | 0.5 | 1.8 | 2.7 | 3.3 |
| g_Intestinimonas (Firm) | ■ | ■ | 1.5 | 6 | 4 | 11 | 4 | 0.8 | 0.9 | 1.1 | 0.7 | 0.5 | 0.6 | 0.8 | 0.7 |
| g_Flavonifractor (Firm) | ■ | ■ | 1.4 | 5 | 1 | 7 | 1 | 0.9 | 1.2 | 1.9 | 1.2 | 0.8 | 0.9 | 1.8 | 1.2 |
| g_Senegalimassilia (Acti) | ■ | ■ | 1.5 | 3 | 1 | 2 | 0 | 0.8 | 1.1 | 1.3 | 1.9 | 0.8 | 0.9 | 1.1 | 1.9 |
| g_Odoribacter (Bact) | ■ | ■ | 1.5 | 4 | 2 | 12 | 0 | 0.9 | 1 | 1.1 | 0.7 | 0.6 | 0.6 | 0.8 | 0.7 |
| uc_c_Alphaproteobacteria (Prot) | ■ | ■ | · | 1 | 1 | 1 | 1 | · | · | · | · | · | · | · | · |
| g_Phascolarctobacterium (Firm) | ■ | ■ | 1.9 | 5 | 4 | 4 | 3 | 0.7 | 0.8 | 1.2 | 1.5 | 0.5 | 0.6 | 0.7 | 1.5 |
| g_Slackia (Acti) | ■ | ■ | 1.4 | 2 | 1 | 5 | 0 | 1 | 1.1 | 1.6 | 1.9 | 0.9 | 1.2 | 1.7 | 1.9 |
| g_Methanobrevibacter (Eury) | ■ | ■ | 2.2 | 1 | 0 | 8 | 0 | 1 | 1.1 | 1.4 | 1.3 | 0.8 | 1.1 | 1.5 | 1.3 |
| uc_f_Sutterellaceae (Prot) | ■ | ■ | · | 2 | 2 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Cerasicoccus (Verr) | ■ | ■ | 1.5 | 2 | 2 | 2 | 1 | 1.1 | 1.6 | 2.6 | 2.4 | 1 | 1.2 | 2.4 | 2.4 |
| g_Hydrogenoanaerobacterium (Firm) | ■ | ■ | 1.3 | 3 | 2 | 7 | 1 | 0.9 | 1 | 1.2 | 1.5 | 0.8 | 0.9 | 1.3 | 1.5 |
| g_Coprobacter (Bact) | ■ | ■ | 1.4 | 2 | 1 | 7 | 0 | 1 | 1.2 | 1.5 | 1.3 | 0.7 | 0.9 | 1.1 | 1.3 |
| g_Victivallis (Lent) | ■ | ■ | 1.6 | 0 | 0 | 9 | 0 | 1.1 | 1.2 | 1.4 | 1.9 | 0.9 | 0.9 | 1.2 | 1.9 |
| uc_f_Erysipelotrichaceae (Firm) | ■ | ■ | 1.4 | 1 | 3 | 2 | 0 | 1.1 | 1.4 | 2.5 | 2.6 | 1.1 | 1.3 | 2.7 | 2.6 |
| g_Subdoligranulum (Firm) | ■ | ■ | 1.5 | 0 | 1 | 1 | 1 | 1.5 | 2.5 | 3.9 | 2.3 | 1.4 | 2 | 3.8 | 2.3 |
| g_Veillonella (Firm) | ■ | ■ | 1.4 | 1 | 1 | 0 | 0 | 1.7 | 4 | 4.9 | 3.6 | 1.7 | 3.1 | 4.9 | 3.6 |
| uc_p_Proteobacteria (Prot) | ■ | ■ | 1.6 | 2 | 0 | 3 | 0 | 1.2 | 1.4 | 1.7 | 2.1 | 0.9 | 1.4 | 2.2 | 2.1 |
| g_Holdemanella (Firm) | ■ | ■ | · | 2 | 2 | 1 | 0 | · | · | · | · | · | · | · | · |
| uc_c_Clostridia (Firm) | ■ | ■ | 1.2 | 2 | 2 | 4 | 1 | 0.8 | 1.4 | 3.2 | 1.6 | 0.7 | 0.9 | 2.3 | 1.6 |
| g_Vampirovibrio (Prot) | ■ | ■ | · | 1 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Olsenella (Acti) | ■ | ■ | 1.7 | 1 | 1 | 2 | 0 | 1 | 1.1 | 1.3 | 2.2 | 0.9 | 1 | 1.2 | 2.2 |
| g_Pseudoflavonifractor (Firm) | ■ | ■ | 1.3 | 0 | 0 | 2 | 0 | 1.6 | 2 | 2.6 | 1.8 | 1.2 | 1.6 | 2.4 | 1.8 |
| g_Anaerosporobacter (Firm) | ■ | ■ | 1.3 | 2 | 2 | 3 | 0 | 1.1 | 2.1 | 4.7 | 1.5 | 0.9 | 1.8 | 3.2 | 1.5 |
| g_Intestinibacter (Firm) | ■ | ■ | 1.2 | 0 | 0 | 3 | 0 | 1.2 | 1.5 | 2.3 | 1.2 | 0.9 | 1.1 | 1.8 | 1.2 |
| uc_o_Rhodospirillales (Prot) | ■ | ■ | · | 1 | 0 | 1 | 0 | · | · | · | · | · | · | · | · |
| g_Haemophilus (Prot) | ■ | ■ | 1.4 | 0 | 0 | 3 | 0 | 1.5 | 2.3 | 3.5 | 2.1 | 1.3 | 2.1 | 3 | 2.1 |
| g_Faecalicoccus (Firm) | ■ | ■ | 1.3 | 0 | 0 | 5 | 2 | 1.2 | 1.6 | 2.8 | 1.7 | 0.9 | 1.7 | 2.2 | 1.7 |
| g_Alloprevotella (Bact) | ■ | ■ | · | 1 | 1 | 0 | 1 | · | · | · | · | · | · | · | · |
| g_Allobaculum (Firm) | ■ | ■ | · | 0 | 0 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Rikenella (Bact) | ■ | ■ | · | 1 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Romboutsia (Firm) | ■ | ■ | 1.3 | 0 | 0 | 5 | 0 | 1.3 | 1.5 | 2.1 | 0.9 | 1.2 | 1.4 | 2 | 0.9 |
| g_Catenibacterium (Firm) | ■ | ■ | · | 2 | 1 | 1 | 0 | · | · | · | · | · | · | · | · |
| g_Desulfomicrobium (Prot) | ■ | ■ | · | 1 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Enterorhabdus (Acti) | ■ | ■ | 1.5 | 0 | 0 | 4 | 0 | 1 | 1.2 | 1.4 | 2.6 | 0.8 | 0.9 | 1.2 | 2.6 |
| g_Faecalitalea (Firm) | ■ | ■ | · | 1 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Escherichia.Shigella (Prot) | ■ | ■ | 1.9 | 0 | 1 | 0 | 0 | 2.2 | 2.8 | 3.6 | 1.7 | 1.6 | 2.5 | 3.1 | 1.7 |
| uc_c_Deltaproteobacteria (Prot) | ■ | ■ | · | 0 | 0 | 1 | 0 | · | · | · | · | · | · | · | · |
| uc_p_Bacteroidetes (Bact) | ■ | ■ | 1.3 | 1 | 0 | 1 | 0 | 1.1 | 1.5 | 2 | 2.1 | 1 | 1.4 | 5 | 2.1 |
| g_Eggerthia (Firm) | ■ | ■ | · | 0 | 0 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Anaerotruncus (Firm) | ■ | ■ | 1.2 | 1 | 1 | 1 | 1 | 1.5 | 3 | 3.5 | 1.8 | 1.6 | 2.7 | 3.2 | 1.8 |
| g_Oligosphaera (Lent) | ■ | ■ | · | 0 | 0 | 2 | 0 | · | · | · | · | · | · | · | · |
| uc_f_Desulfovibrionaceae (Prot) | ■ | ■ | · | 0 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| uc_o_Burkholderiales (Prot) | ■ | ■ | · | 1 | 0 | 1 | 0 | · | · | · | · | · | · | · | · |
| g_Gordonibacter (Acti) | ■ | ■ | 1.4 | 0 | 0 | 1 | 0 | 2.7 | 3.5 | 4.5 | 3 | 2.9 | 3.5 | 5.4 | 3 |
| uc_f_Prevotellaceae (Bact) | ■ | ■ | · | 1 | 1 | 0 | 0 | · | · | · | · | · | · | · | · |
| uc_f_Enterobacteriaceae (Prot) | ■ | ■ | · | 0 | 0 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Methanomassiliicoccus (Eury) | ■ | ■ | · | 0 | 0 | 2 | 0 | · | · | · | · | · | · | · | · |
| g_Enterococcus (Firm) | ■ | | · | 0 | 0 | 0 | 0 | · | · | · | · | · | · | · | · |
| g_Lactobacillus (Firm) | | ■ | · | 0 | 0 | 0 | 0 | · | · | · | · | · | · | · | · |

**Supplementary Figure 2. Variation and core measurements for all genera.**
For all genera above the abundance threshold: (Ab.) Log mean abundance of the genus over all samples in which it was present; (ICC) Intraclass correlation coefficient of the genus; (Slope TL) Slope of Taylor's law for the genus calculated over all individuals (1.6±0.25 [1.2-2.4]); (Core) The number of participants for which the genus belongs to the core, defined as present in more than 95% of the samples; (Pers.) The number of participants for which the genus can be considered persistent, defined as present in more than 20% of the samples with at least 90% of these observations being consecutive; (Trans.) The number of participants for which the genus can be considered transient, defined as present in more than 60% of the samples while less than 75% of these observations are consecutive; (Non-St.) The number of participants in which the genus shows non-stationary dynamics, defined as not satisfying a unit root process in which abundances vary around an equilibrium level (Augmented Dicky Fuller test, p>0.05). (Coef. Variation) Coefficient of variation in genus abundance within and between individuals. The coefficient of variation is defined as the ratio of the standard deviation to the mean and is a standardized measure of dispersion. Within-subject variation is summarized as the first, second and third quartile (Q1,Q2,Q3, respectively) of all values for the within-subject coefficient of variation, calculated for each time series (N=20). Data are based on either quantitative (QMP) or relative (RMP) microbiome profiling.



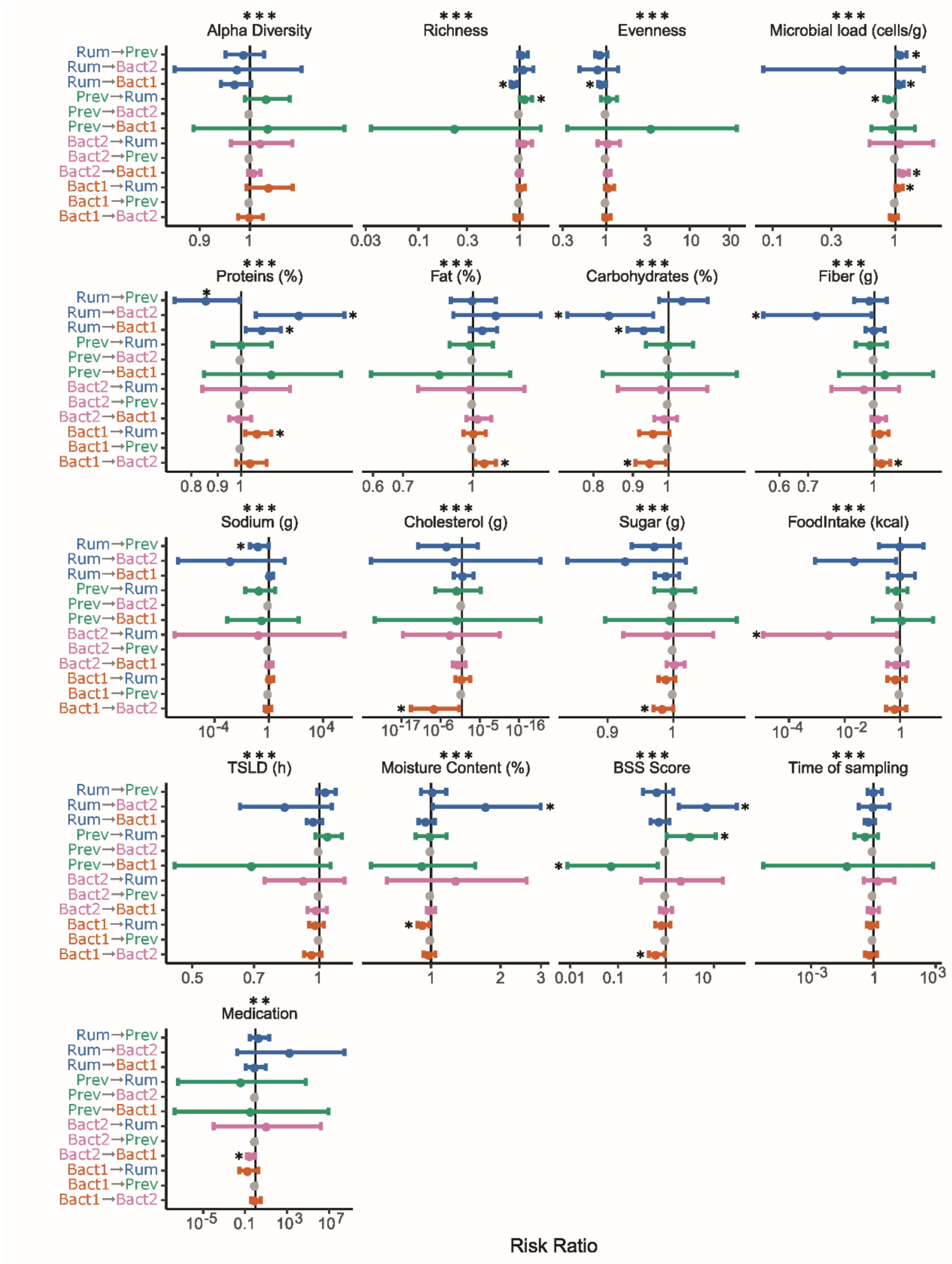
**Supplementary Figure 3. Within- compared to between-subject variance for relative abundance profiles. a.** Within- versus between-subject variance in relative genus abundance (Wilcoxon test, two-sided, n=98, P= 0.007154) (left) and within-subject and between-subject variance as part of the total variance in genus abundance (right) for all genera over the abundance threshold. **b.** Within- and between-subject variance as part of the total variance in alpha diversity measures, for observed richness, Pielou evenness, and Shannon diversity index based on RMPs. **c.** Beta-diversity, as assessed through Bray Curtis dissimilarity, between samples of the same individual (800-821), and between the first sample of each individual (Bet) based on RMPs (N=20, n=709),. Significance of the differences within and between individuals were tested through an ANOVA on multivariate homogeneity of group dispersions.

The body of the box plots represents the first and third quartiles of the distribution, and the median line. Whiskers extend from the quartiles to the last data point within 1.5×IQR, with outliers beyond. Significance levels: ***: 0.001, **: 0.01, *: 0.05.

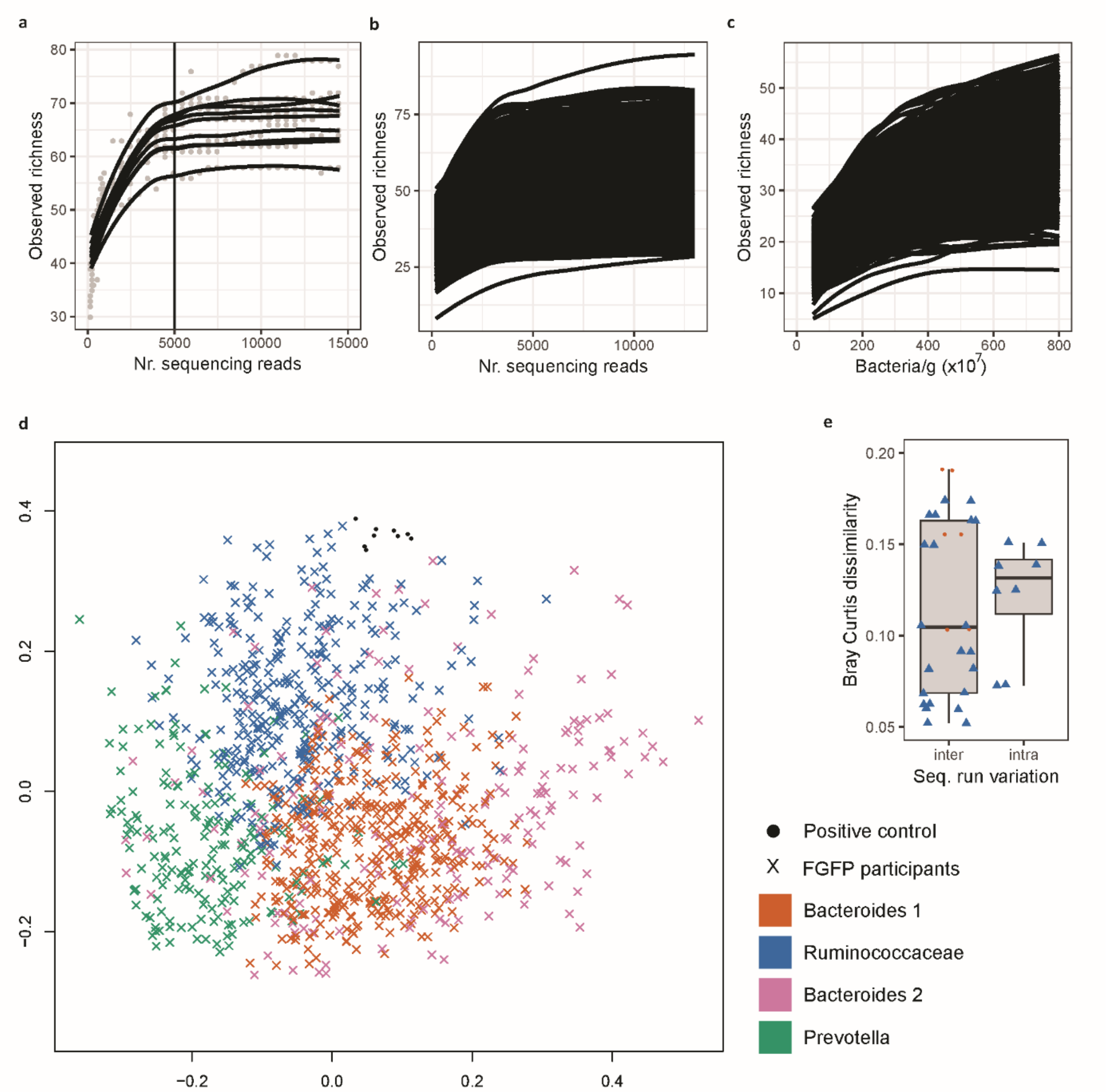


**Supplementary Figure 4. a. Percentage of genera belonging to the temporal core, according to different core thresholds, for each individual.** With a core threshold of 90%, about 44% [27-52%] of a person's genera are included. With less stringent temporal core thresholds more genera satisfy the conditions (e.g. about 73% [57-86%] of a person's genera are detected more than 20% of the time (the threshold for the persistent category), and about 58% [48-69%] of a person’s genera are detected more than 60% of the time (the threshold for the transient category). **b. Temporal core size falls within 90% of the all-samples estimate from 11 samples onwards for all non-perturbed time series.** For increasing lengths of time series (x-axis) we calculated the temporal core size (with a 95% threshold, which explains the stepwise increase after 20 and 40 samples, N=20, n=694) and compared it with the temporal core size obtained if all samples were to be included (y-axis). The time series of participant 808, which included an infection event, is responsible for the major outliers.

The body of the box plots represents the first and third quartiles of the distribution, and the median line. Whiskers extend from the quartiles to the last data point within 1.5×IQR, with outliers beyond. Significance levels: ***: 0.001, **: 0.01, *: 0.05.

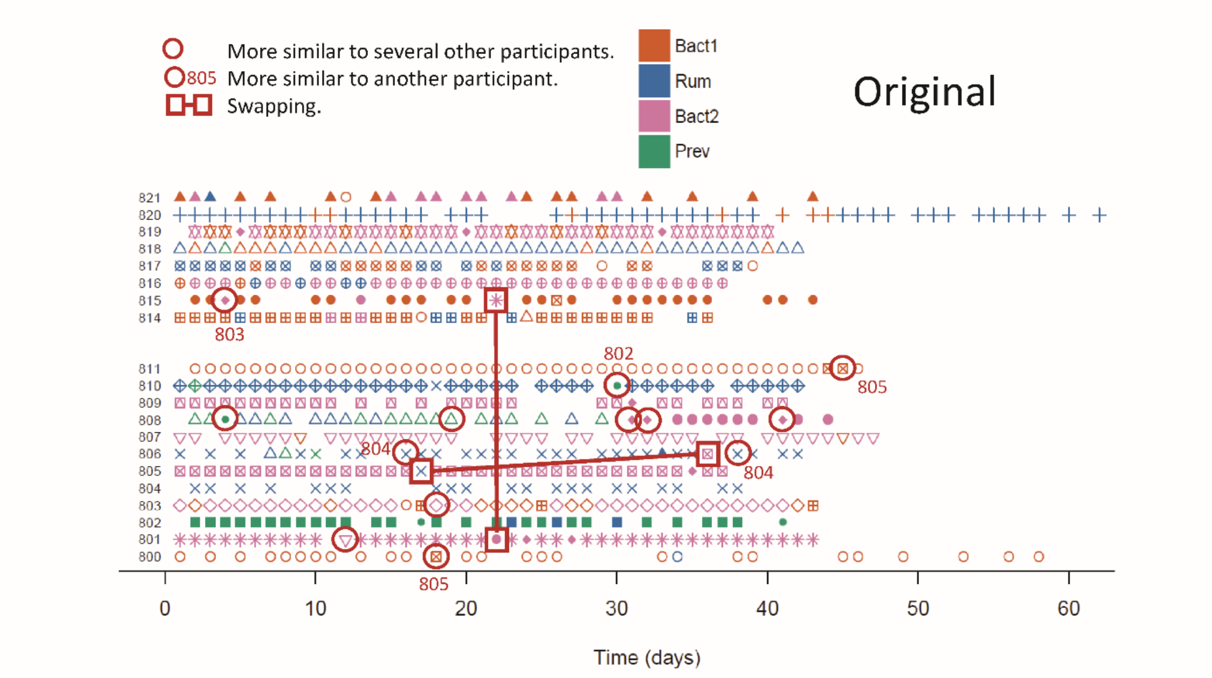


**Supplementary Figure 5. Enteroype switches are linked to several investigated parameters.** The relative risk of an enterotype switch with each unit increase in the parameter (risk ratio, x-axis), set out for each possible enterotype switch (y-axis). Switches are color coded according to data availability: no data (grey), and subsequently to direction of the switch: away from the Ruminoccocaceae (R, blue), Bacteroides 1 (B1, orange), Bacteroides 2 (B2, Pink), Prevotella (P, green) enterotype (N=20, n=709). Error bar dots indicate the median value with whiskers extending to the 95% confidence interval. Significance levels: ***: 0.001, **: 0.01, *: 0.05.

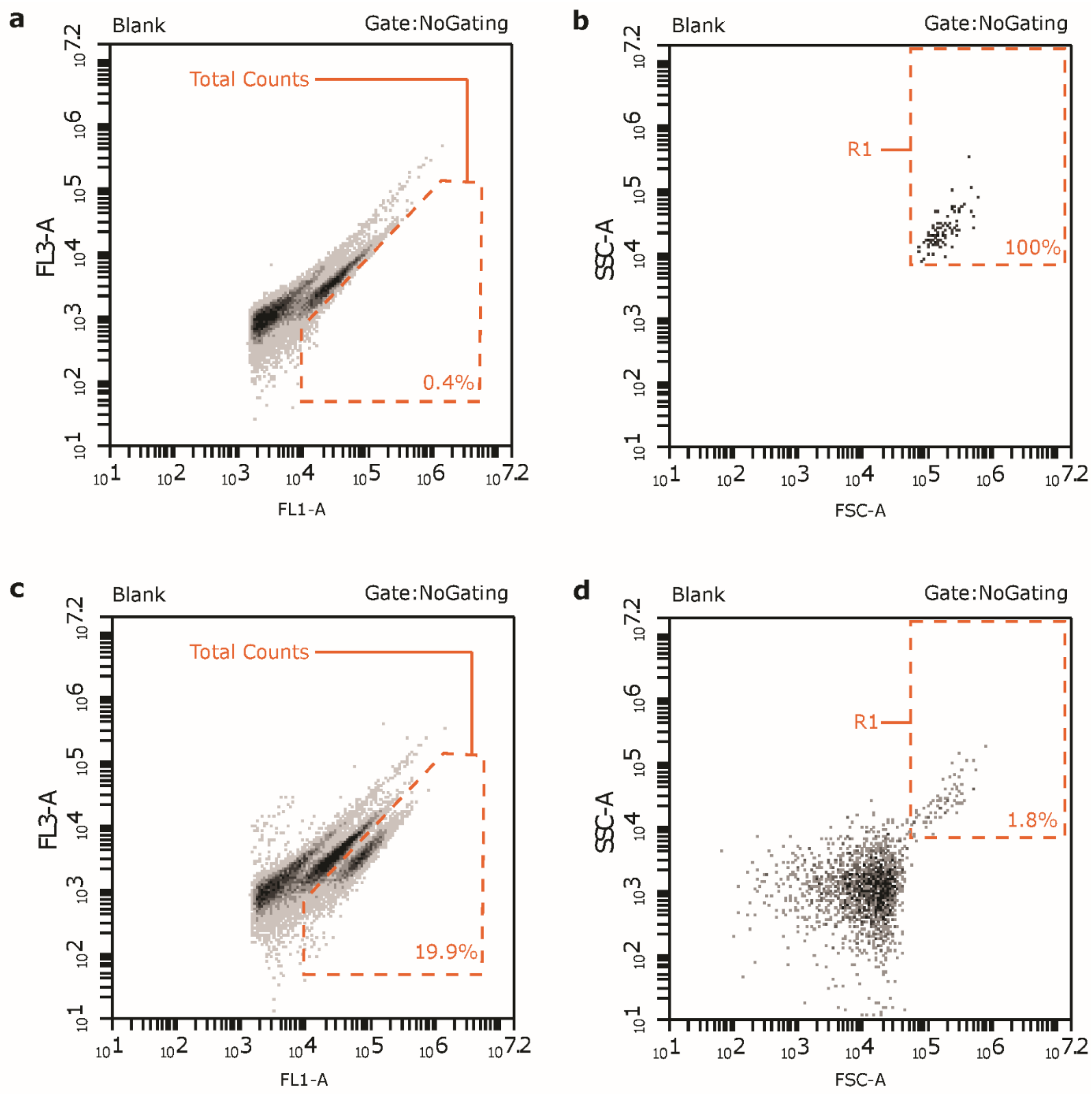


**Supplementary Figure 6. Quality control of sequencing data.** Richness could be considered stable in **a.** controls (n=9) and **b.** RMPs (N=20, n=709), from 5000 reads, and in **c.** QMPs (N=20, n=694), from 4x$10^9$ bacterial cells per gram of faeces, which is well below the applied subsampling thresholds. **d.** PCoA of the positive control samples (black points) together with the RMPs of 1103 FGFP participants (crosses), coloured according to enterotype, namely Ruminoccocaceae (R, blue), Bacteroides 1 (B1, orange), Bacteroides 2 (B2, Pink), Prevotella (P, green). **e.** Bray Curtis Dissimilarity between positive control samples, derived from 2 aliquots of DNA from the same high-richness stool sample (orange dots, blue triangles), between (inter) and within (intra) sequencing runs (n=9).

The body of the box plots represents the first and third quartiles of the distribution, and the median line. Whiskers extend from the quartiles to the last data point within 1.5×IQR, with outliers beyond. Significance levels: ***: 0.001, **: 0.01, *: 0.05.



**Supplementary Figure 7 Graphical presentation of the mislabelling analyses and corrections.** Two swapping events were identified based on comparisons between BC dissimilarities of a sample with those of same or different participants, and DMM-clustering. For each participant (800-821), samples are shown according to sampling moment with an indication of enterotype, namely, Ruminococcaceae (blue), Bacteroides 1 (orange), Bacteroides 2 (Pink), and Prevotella (green), and the assigned DMM sub-cluster (20 shapes). In our original data, 15 samples showed more similarity with samples from one (circles with participant number) or several other participants (circle). Swapping events (connected squares) were identified based on according mismatches in BC-dissimilarities, enterotyping, and DMM-clustering.



**Supplementary Figure 8: Gating Strategy Flow cytometry**

A fixed gating and staining approach was applied. Both blank and sample solutions were stained with SYBR Green I. **a**, The FL1-A/FL3-A acquisition plot of a blank sample (0.85% w/v physiological solution) with gate boundaries indicated. A threshold value of 2,000 was applied on the FL1 channel. **b**, Secondary gating was performed on the FSC-A/SSC-A channels to further discriminate between debris or background and microbial events. **c**, **d**, FL1-A/FL3-A count acquisition of a faecal sample (**c**) with secondary gating on FSC-A/SSC-A channels on the basis of blank analyses (**d**). Total counts were defined as events registered in the FL1-A/FL3-A gating area, excluding debris or background events observed in the FSC-A/SSC-A R1 gate. The flow rate was set at 14 µl per minute and the acquisition rate did not exceed 10,000 events per second. Each panel reflects events registered over the course of a 30-s acquisition period.

**Supplementary Table 1: Determination of lag-time.** Proposed lag time based on cross-correlation analysis between stool moisture and the P/C ratio of the previous day for each participant, slope and significance of the correlation, related information, and final lag time as used in the analyses.

| **Participant** | **Proposed lag time *** | **Associated slope** | **Significant?** | **Median stool moisture (%)** | **Median time since last defecation (h)** | **Time of sampling** | **Final lag time** |
|---|---|---|---|---|---|---|---|
| 800 | -4 | -0.263856122 | yes | 73.09 | 30 | Afternoon:12_Evening:6_Morning:10_Night:1 | -4 |
| 801 | -1 | -0.302007752 | yes | 78.07 | 24 | Morning:42 | -1 |
| 802 | -2 | -0.166510592 | no | 70.98 | 23.75 | Afternoon:11_Evening:5_Morning:14 | -1 |
| 803 | -3 | -0.067174532 | no | 75.9 | 14.5 | Afternoon:4_Morning:41 | -1 |
| 804 | -1 | -0.170934213 | no | 72.53 | 32.5 | Afternoon:5_Evening:5_Morning:11 | -1 |
| 805 | -2 | -0.408542242 | yes | 82.71 | 22.5 | Afternoon:3_Evening:1_Morning:35 | -2 |
| 806 | -2 | -0.189618863 | no | 77.07 | 22.5 | Afternoon:8_Evening:9_Morning:8_Night:1 | -1 |
| 807 | -1 | -0.195957759 | no | 60.23 | 17.5 | Afternoon:1_Morning:39 | -1 |
| 808 | -4 | -0.091100488 | no | 70.805 | 25 | Afternoon:11_Evening:11_Morning:10_Night:1 | -1 |
| 809 | -2 | -0.226582804 | no | 74.84 | 23.5 | Afternoon:10_Evening:13_Morning:7_Night:1 | -1 |
| 810 | -5 | -0.343098783 | yes | 67.01 | 22.5 | Afternoon:5_Evening:19_Morning:14 | -5 |
| 811 | -5 | -0.19020666 | no | 75.94 | 14 | Afternoon:7_Evening:5_Morning:31_Night:1 | -1 |
| 814 | -2 | -0.147461484 | no | 67.51 | 16 | Afternoon:5_Evening:2_Morning:22_Night:1 | -1 |
| 815 | 0 | -0.510107276 | yes | 77.98 | 25 | Afternoon:4_Evening:13_Morning:14 | 0 |
| 816 | -2 | -0.029807728 | no | 86.18 | 14 | Afternoon:22_Evening:1_Morning:14 | -1 |
| 817 | 0 | -0.183358611 | no | 67.94 | 24.5 | Afternoon:1_Morning:31 | -1 |
| 818 | -2 | -0.288589038 | no | 70.155 | 24 | Afternoon:1_Evening:3_Morning:37 | -1 |
| 819 | -3 | -0.207215476 | no | 81.18 | 23 | Afternoon:2_Evening:1_Morning:36 | -1 |
| 820 | -1 | -0.249295696 | yes | 68.57 | 14 | Afternoon:8_Evening:10_Morning:29_Night:1 | -1 |
| 821 | -2 | 0.037792959 | no | 74.12 | 12 | Morning:45 | -1 |

**Supplementary Table 2: Taylor law relationschips per genus.** For each genus, the linearity of the relationship between log(variance) and log(mean) over time was tested using function lm, calculating slopes, p-values and adjusted R$^2$.

| | **slope** | **pvalue** | **qvalue** | **adjR2** | **excluded** |
|---|---|---|---|---|---|
| g_Acetanaerobacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Acetitomaculum | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Acidaminococcus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Actinomyces | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Adlercreutzia | 1.318982 | 4.32E-10 | 8.53E-10 | 0.925856 | No |
| g_Aestuariispira | 1.719915 | 6.36E-08 | 8.59E-08 | 0.930594 | No |
| g_Akkermansia | 1.808826 | 4.02E-09 | 6.86E-09 | 0.915801 | No |
| g_Alistipes | 1.719098 | 1.67E-11 | 5.80E-11 | 0.919539 | No |
| g_Allisonella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Allobaculum | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Alloprevotella | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Anaerofilum | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Anaerofustis | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Anaerorhabdus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Anaerosporobacter | 1.272728 | 4.39E-12 | 1.89E-11 | 0.968111 | No |
| g_Anaerostipes | 1.926801 | 4.15E-09 | 6.89E-09 | 0.852016 | No |
| g_Anaerotruncus | 1.177491 | 0 | 0 | 0.988168 | No |
| g_Arcanobacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Bacteroides | 1.897164 | 3.68E-10 | 7.46E-10 | 0.886742 | No |
| g_Barnesiella | 1.773776 | 6.85E-09 | 1.02E-08 | 0.90917 | No |
| g_Bifidobacterium | 1.744071 | 8.44E-15 | 2.05E-13 | 0.977337 | No |
| g_Bilophila | 1.585377 | 2.79E-10 | 5.98E-10 | 0.930058 | No |
| g_Blautia | 2.006126 | 7.69E-11 | 2.21E-10 | 0.904727 | No |
| g_Butyricicoccus | 1.628223 | 4.58E-09 | 7.28E-09 | 0.850388 | No |
| g_Butyricimonas | 1.806271 | 6.80E-09 | 1.02E-08 | 0.893146 | No |
| g_Butyrivibrio | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Campylobacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Catabacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Catenibacterium | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Cerasicoccus | 1.470821 | 6.10E-07 | 7.68E-07 | 0.937922 | No |
| g_Christensenella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Citrobacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Cloacibacillus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Clostridium_III | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Clostridium_IV | 1.773913 | 7.11E-15 | 2.05E-13 | 0.96593 | No |
| g_Clostridium_sensu_stricto | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Clostridium_XlVa | 1.941787 | 4.17E-07 | 5.34E-07 | 0.754381 | No |
| g_Clostridium_XlVb | 1.440485 | 7.76E-13 | 4.72E-12 | 0.951729 | No |
| g_Clostridium_XVIII | 1.778503 | 1.15E-10 | 2.89E-10 | 0.900429 | No |
| g_Collinsella | 2.038511 | 7.35E-14 | 1.07E-12 | 0.963396 | No |
| g_Comamonas | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Coprobacillus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |

| | | | | | |
|---|---|---|---|---|---|
| g_Coprobacter | 1.408486 | 3.03E-09 | 5.40E-09 | 0.903993 | No |
| g_Coprococcus | 1.817 | 3.13E-12 | 1.43E-11 | 0.952627 | No |
| g_Corynebacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Defluviitalea | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Desulfomicrobium | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Desulfovibrio | 1.379804 | 3.69E-05 | 3.85E-05 | 0.943116 | No |
| g_Dialister | 1.740359 | 3.65E-05 | 3.85E-05 | 0.847092 | No |
| g_Dorea | 1.592714 | 4.34E-11 | 1.38E-10 | 0.910568 | No |
| g_Eggerthella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Eggerthia | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Eisenbergiella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Elusimicrobium | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Enterobacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Enterococcus | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Enterorhabdus | 1.529756 | 0.002209 | 0.002209 | 0.960201 | No |
| g_Escherichia.Shigella | 1.923327 | 4.32E-09 | 7.01E-09 | 0.867438 | No |
| g_Ethanoligenens | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Eubacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Ezakiella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Faecalibacterium | 1.586017 | 3.70E-08 | 5.10E-08 | 0.8117 | No |
| g_Faecalicoccus | 1.292338 | 3.65E-10 | 7.46E-10 | 0.952028 | No |
| g_Faecalitalea | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Flavonifractor | 1.374816 | 6.42E-10 | 1.20E-09 | 0.908063 | No |
| g_Frondihabitans | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Fusicatenibacter | 1.687615 | 1.57E-11 | 5.73E-11 | 0.920081 | No |
| g_Fusobacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Gemella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Gemmiger | 1.828643 | 6.36E-09 | 9.87E-09 | 0.861329 | No |
| g_Gordonibacter | 1.36327 | 1.46E-06 | 1.75E-06 | 0.980529 | No |
| g_Gracilibacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Guggenheimella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Haemophilus | 1.400717 | 2.44E-10 | 5.56E-10 | 0.918503 | No |
| g_Hafnia | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Hespellia | 1.604246 | 2.83E-08 | 3.98E-08 | 0.834914 | No |
| g_Holdemanella | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Holdemania | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Howardella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Hungatella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Hydrogenoanaerobacterium | 1.34709 | 7.88E-11 | 2.21E-10 | 0.971302 | No |
| g_Intestinibacter | 1.205145 | 9.25E-11 | 2.50E-10 | 0.915446 | No |
| g_Intestinimonas | 1.522959 | 7.51E-07 | 9.30E-07 | 0.77939 | No |
| g_Lactobacillus | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Lactococcus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Lactonifactor | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Lautropia | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Leuconostoc | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |

| | | | | | |
|---|---|---|---|---|---|
| g_Macellibacteroides | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Mannheimia | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Methanobrevibacter | 2.221264 | 9.70E-05 | 9.97E-05 | 0.810709 | No |
| g_Methanomassiliicoccus | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Methanosphaera | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Mitsuokella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Mogibacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Murdochiella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Neisseria | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Odoribacter | 1.526895 | 2.22E-06 | 2.57E-06 | 0.770637 | No |
| g_Oligosphaera | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Olsenella | 1.708358 | 0.000836 | 0.000847 | 0.941462 | No |
| g_Oscillibacter | 1.725078 | 1.93E-14 | 3.53E-13 | 0.961946 | No |
| g_Oxalobacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Papillibacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Parabacteroides | 2.365413 | 3.74E-11 | 1.24E-10 | 0.923954 | No |
| g_Paraprevotella | 2.391589 | 1.74E-05 | 1.92E-05 | 0.929521 | No |
| g_Parasutterella | 1.430587 | 4.76E-13 | 3.52E-12 | 0.976771 | No |
| g_Parvibacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Parvimonas | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Pelospora | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Peptococcus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Peptoniphilus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Phascolarctobacterium | 1.871308 | 1.51E-05 | 1.70E-05 | 0.903855 | No |
| g_Porphyromonas | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Prevotella | 1.668891 | 2.02E-10 | 4.92E-10 | 0.989488 | No |
| g_Proteus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Pseudobutyrivibrio | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Pseudoflavonifractor | 1.327879 | 5.36E-13 | 3.56E-12 | 0.953775 | No |
| g_Raoultella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Rikenella | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Romboutsia | 1.278416 | 1.11E-10 | 2.89E-10 | 0.913648 | No |
| g_Roseburia | 1.652482 | 5.24E-10 | 1.01E-09 | 0.882216 | No |
| g_Rothia | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Ruminococcus | 1.813903 | 5.84E-11 | 1.78E-10 | 0.919877 | No |
| g_Ruminococcus2 | 1.729004 | 1.46E-11 | 5.62E-11 | 0.920702 | No |
| g_Senegalimassilia | 1.523291 | 2.24E-08 | 3.27E-08 | 0.981002 | No |
| g_Slackia | 1.405686 | 4.04E-09 | 6.86E-09 | 0.969562 | No |
| g_Solobacterium | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Sporobacter | 1.576867 | 2.22E-10 | 5.24E-10 | 0.944212 | No |
| g_Staphylococcus | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Streptococcus | 1.635934 | 1.24E-11 | 5.04E-11 | 0.922133 | No |
| g_Subdoligranulum | 1.451881 | 1.82E-12 | 9.49E-12 | 0.946651 | No |
| g_Succinatimonas | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Succiniclasticum | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Sutterella | 1.920742 | 8.70E-08 | 1.15E-07 | 0.88912 | No |

| | | | | | |
|---|---|---|---|---|---|
| g_Terrisporobacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Turicibacter | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Ureaplasma | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Vampirovibrio | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| g_Varibaculum | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Veillonella | 1.426921 | 1.19E-12 | 6.71E-12 | 0.980074 | No |
| g_Victivallis | 1.580487 | 1.97E-06 | 2.32E-06 | 0.895632 | No |
| g_Weissella | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| g_Yersinia | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_c_Alphaproteobacteria | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_c_Clostridia | 1.227716 | 3.21E-13 | 2.96E-12 | 0.983721 | No |
| uc_c_Deltaproteobacteria | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_c_Gammaproteobacteria | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_c_Opitutae | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_f_Clostridiales_Incertae_Sedis_XIII | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_f_Coriobacteriaceae | 1.715084 | 4.82E-13 | 3.52E-12 | 0.962483 | No |
| uc_f_Cryomorphaceae | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_f_Desulfovibrionaceae | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_f_Enterobacteriaceae | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_f_Erysipelotrichaceae | 1.423754 | 2.60E-08 | 3.73E-08 | 0.940943 | No |
| uc_f_Lachnospiraceae | 1.743849 | 1.42E-07 | 1.86E-07 | 0.781691 | No |
| uc_f_Peptostreptococcaceae | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_f_Porphyromonadaceae | 1.488836 | 1.38E-06 | 1.68E-06 | 0.92567 | No |
| uc_f_Prevotellaceae | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_f_Rhodospirillaceae | 1.741228 | 6.81E-10 | 1.24E-09 | 0.986237 | No |
| uc_f_Rikenellaceae | 1.423355 | 2.42E-05 | 2.64E-05 | 0.973752 | No |
| uc_f_Ruminococcaceae | 1.747086 | 2.64E-13 | 2.96E-12 | 0.949162 | No |
| uc_f_Sutterellaceae | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_f_Synergistaceae | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_f_Veillonellaceae | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_k_Bacteria | 1.582117 | 3.24E-13 | 2.96E-12 | 0.964295 | No |
| uc_o_Bacillales | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_o_Bacteroidales | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_o_Burkholderiales | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_o_Clostridiales | 1.650315 | 2.64E-10 | 5.84E-10 | 0.904405 | No |
| uc_o_Desulfovibrionales | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_o_Lactobacillales | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_o_Rhodospirillales | NA | NA | NA | NA | Yes, present in < 5 ind with > 3 timepoints per timeseries |
| uc_p_Bacteroidetes | 1.306841 | 3.07E-05 | 3.30E-05 | 0.971147 | No |
| uc_p_Firmicutes | 1.581177 | 2.95E-12 | 1.43E-11 | 0.969873 | No |
| uc_p_Lentisphaerae | NA | NA | NA | NA | Yes, < abundance threshold 0.5% |
| uc_p_Proteobacteria | 1.58872 | 2.81E-06 | 3.21E-06 | 0.975789 | No |