

## Supplemental Tables

**Table S1. ICCs for phyla at each treatment phase and the relative abundance of the corresponding phyla.**

Treatment Phase	Phylum	ICC	Mean Proportion (SD)
Pre	Verrucomicrobia	0.711	0.049 (0.078)
	Bacteroidetes	0.692	0.388 (0.243)
	Actinobacteria	0.658	0.013 (0.029)
	Fusobacteria	0.616	0.003 (0.014)
	Proteobacteria	0.531	0.033 (0.044)
	Firmicutes	0.498	0.502 (0.211)
	Euryarchaeota	0.409	0.009 (0.035)
	Tenericutes	0.166	0.003 (0.017)
During	Verrucomicrobia	0.763	0.052 (0.090)
	Actinobacteria	0.563	0.015 (0.029)
	Bacteroidetes	0.536	0.409 (0.237)
	Tenericutes	0.488	0.001 (0.007)
	Firmicutes	0.430	0.489 (0.215)
	Proteobacteria	0.387	0.025 (0.034)
	Euryarchaeota	0.363	0.005 (0.025)
	Fusobacteria	0.278	0.003 (0.012)
Post	Verrucomicrobia	0.487	0.045 (0.082)
	Tenericutes	0.436	0.002 (0.009)
	Bacteroidetes	0.377	0.422 (0.240)
	Firmicutes	0.377	0.493 (0.222)
	Actinobacteria	0.197	0.012 (0.027)
	Euryarchaeota	0.168	0.003 (0.015)
	Proteobacteria	0.156	0.022 (0.025)
	Fusobacteria	0.131	0.001 (0.002)

**Table S2. Five largest ICCs for genera at each treatment phase and the relative abundance of the corresponding genera**

Treatment Phase	Genus	ICC	Mean Proportion (SD)
Pre	<i>Ruminococcaceae (Unc01f0v)</i>	0.936	3.64 E-2 (6.02 E-2)
	<i>Barnesiella</i>	0.929	7.82 E-4 (2.49 E-3)
	<i>Sellimonas</i>	0.919	2.90 E-4 (7.68 E-4)
	<i>Ruminococcaceae (UncB4473)</i>	0.906	4.08 E-4 (1.39 E-3)
	<i>Howardella</i>	0.901	1.65 E-4 (4.78 E-4)
During	<i>Catenibacterium</i>	0.909	2.52 E-3 (8.40 E-3)
	<i>Barnesiella</i>	0.866	1.01 E-3 (3.48 E-3)
	<i>Pseudobutyrvibrio</i>	0.845	6.15 E-4 (1.72 E-3)
	<i>Eubacterium</i>	0.829	1.46 E-4 (4.60 E-4)
	<i>Prevotellaceae (Unc019nc)</i>	0.822	6.18 E-2 (1.55 E-1)
Post	<i>Prevotellaceae (Unc00v6o)</i>	0.928	6.12 E-4 (1.56 E-3)
	<i>Barnesiella</i>	0.923	8.05 E-4 (2.16 E-3)
	<i>Prevotellaceae (Unc019nc)</i>	0.923	4.88 E-2 (1.49 E-1)
	<i>Pseudobutyrvibrio</i>	0.914	4.95 E-4 (1.46 E-3)
	<i>Lachnospiraceae (Unc04x9p)</i>	0.898	2.46 E-3 (7.10 E-3)

**Table S3. Five smallest ICCs of genera at each treatment phase and the relative abundance of the corresponding genera**

Treatment Phase	Genus	ICC	Mean Proportion (SD)
Pre	<i>Prevotella</i>	0.010	5.40 E-5 (2.51 E-4)
	<i>Candidatus_Soleaferrea</i>	0.038	3.47 E-5 (8.84 E-5)
	<i>Lactococcus</i>	0.059	7.79 E-5 (2.67 E-4)
	<i>Bacteroidales (Unc16803)</i>	0.063	2.93 E-5 (7.06 E-5)
	<i>Actinomyces</i>	0.078	1.75 E-4 (3.55 E-4)
During	<i>Ruminococcaceae (Unc52502)</i>	0.059	1.28 E-4 (2.28 E-4)
	<i>Lachnospiraceae (Unc05iug)</i>	0.061	2.45 E-5 (7.89 E-5)
	<i>Lactonifactor</i>	0.073	8.79 E-5 (2.34 E-4)
	<i>Enterobacter</i>	0.078	2.09 E-4 (5.98 E-4)
	<i>Clostridiales (Unc0317w)</i>	0.086	2.66 E-4 (8.79 E-4)
Post	<i>Erysipelotrichaceae (Unc02aea)</i>	0.009	2.47 E-3 (1.42 E-2)
	<i>Candidatus_Soleaferrea</i>	0.013	3.47 E-5 (8.84 E-5)
	<i>Christensenellaceae (Unc32212)</i>	0.016	4.45 E-5 (1.46 E-4)
	<i>Atopobium</i>	0.020	6.32 E-5 (1.55 E-4)
	<i>Anaerofustis</i>	0.029	7.35 E-5 (1.97 E-4)

## Supplemental Figure Legends

**Figure S1.** Dietary composition as assessed by the Block Food Frequency Questionnaire administered at baseline (Week 0) and at the end of each study phase (Weeks 8, 20, and 28).

**Figure S2.** Principal Coordinate Analysis (PCoA) with the weighted UniFrac distance for the microbiome samples. The top panel plot shows the two principal coordinates from the PCoA analysis with the weighted UniFrac distances for the microbiome samples for all participants. Different symbols indicate different participants, and different colors represent different treatment phases. The bottom panel shows the re-plots of the result of the PCoA analysis for each participant. The symbol \* indicates the sample at Week 28 (i.e., the last measurement).

**Figure S3.** Principal Component Analysis (PCA) for the log-transformed stool metabolome samples. The top panel plot shows the principal coordinates from the PCA analysis for the metabolome samples for all participants. The plots in the bottom panel are re-plots of the top panel plot for each participant. The symbol \* indicates the sample at Week 28.

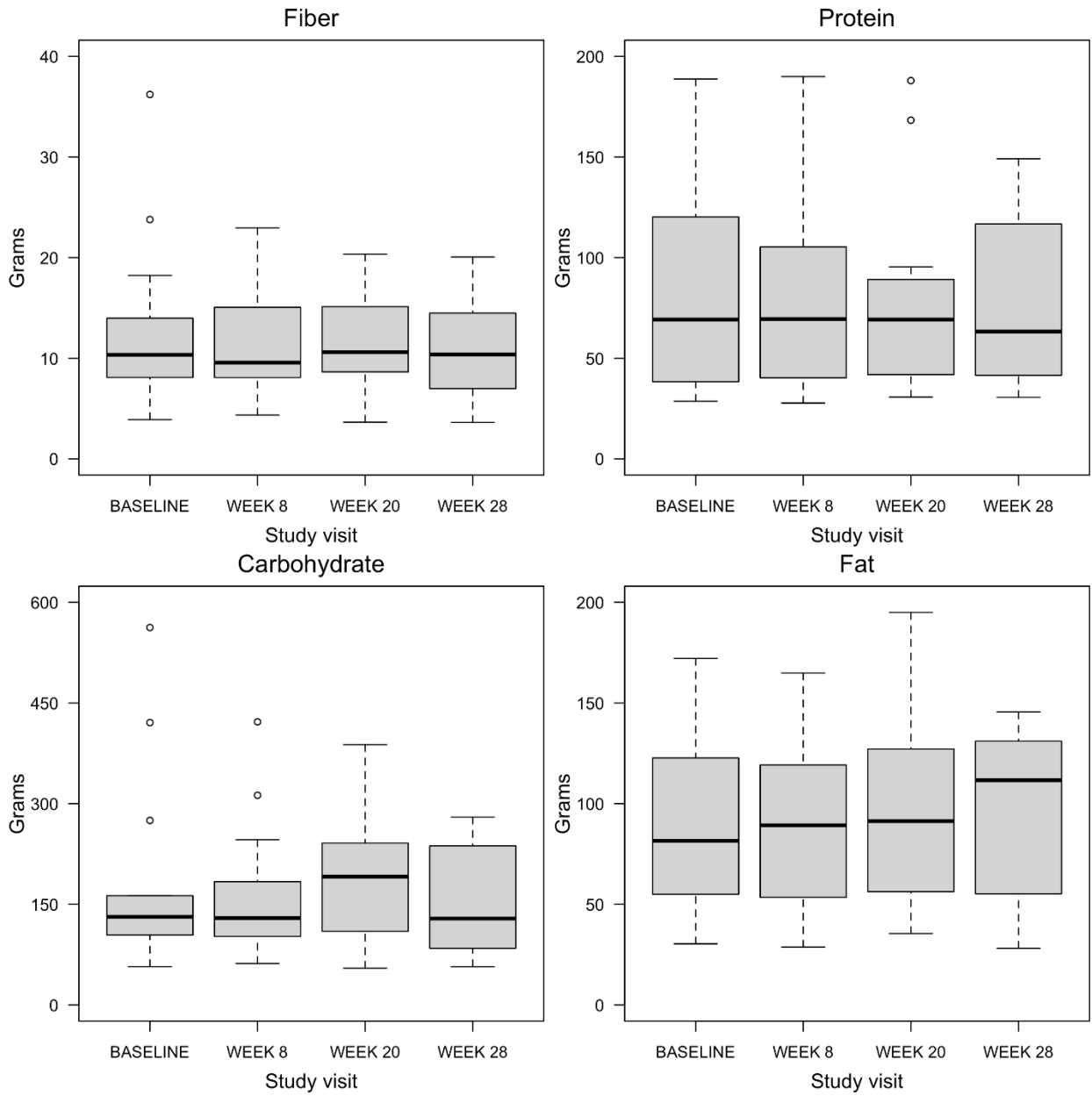
**Figure S4.** Principal Component Analysis (PCA) for the log-transformed plasma metabolome samples. The top panel plot shows the principal coordinates from the PCA analysis for the metabolome samples for all participants. The plots in the bottom panel are re-plots of the top panel plot for each participant. The symbol \* indicates the sample at Week 28.

**Figure S5.** Taxonomic composition of stool. Relative abundance of phyla are depicted across the treatment phases for each participant. The three bars for each participant represent the pre-treatment, p-inulin, and post treatment phases, respectively. The tick mark indicates the treatment phase for each participant

**Figure S6.** Heatmap plots of 20 most abundant (a) genera, (b) stool metabolites, and (c) plasma metabolites. The genera are in proportions, and the metabolites are in the log-transformed values. Each cell indicates a proportion, and white color represents zero. The columns within a participant represent proportions at the 14 different time points from Week 2 to Week 28.

**Figure S7.** (a) Differentially abundant genera across the treatment phases. The adjusted p-values for Ruminococcaceae Unc01f0v and Clostridiales Unc04shn across the treatment phases are 0.003 and 0.033, respectively. (b) Differentially abundant metabolites across the treatment phases. The adjusted p-values for uridine in plasma samples and stool samples are 0.003 and 0.001, respectively.

**Figure S8.** Abundance of targeted metabolites across the treatment phases.



**Figure S1**

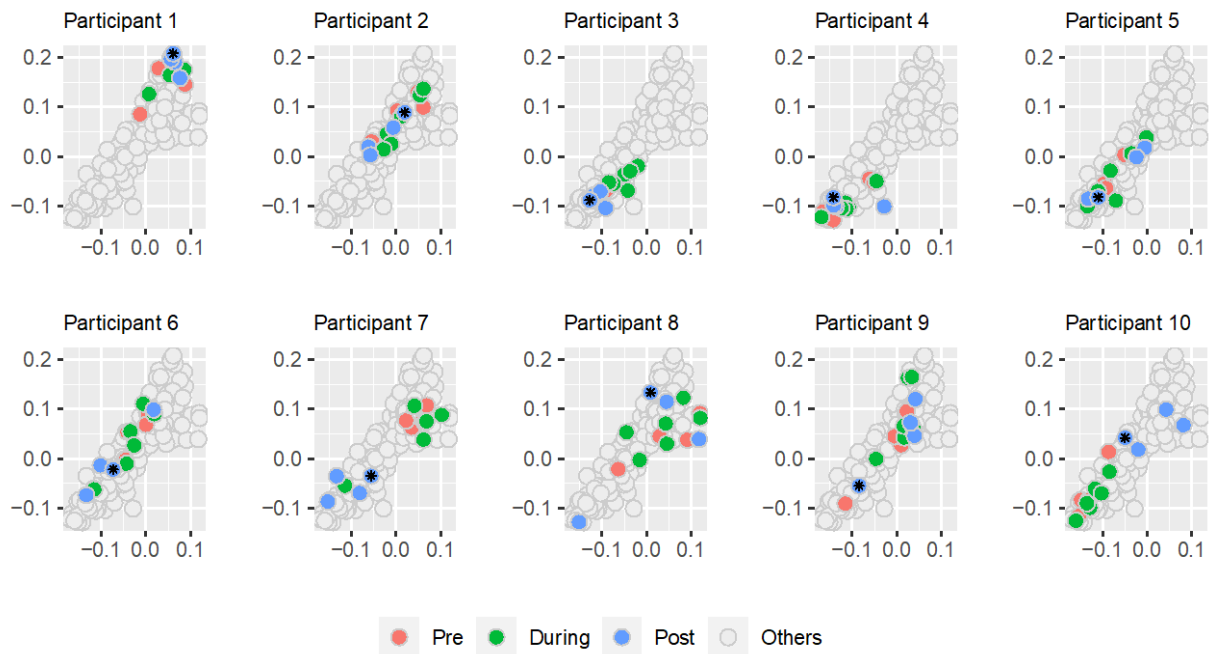
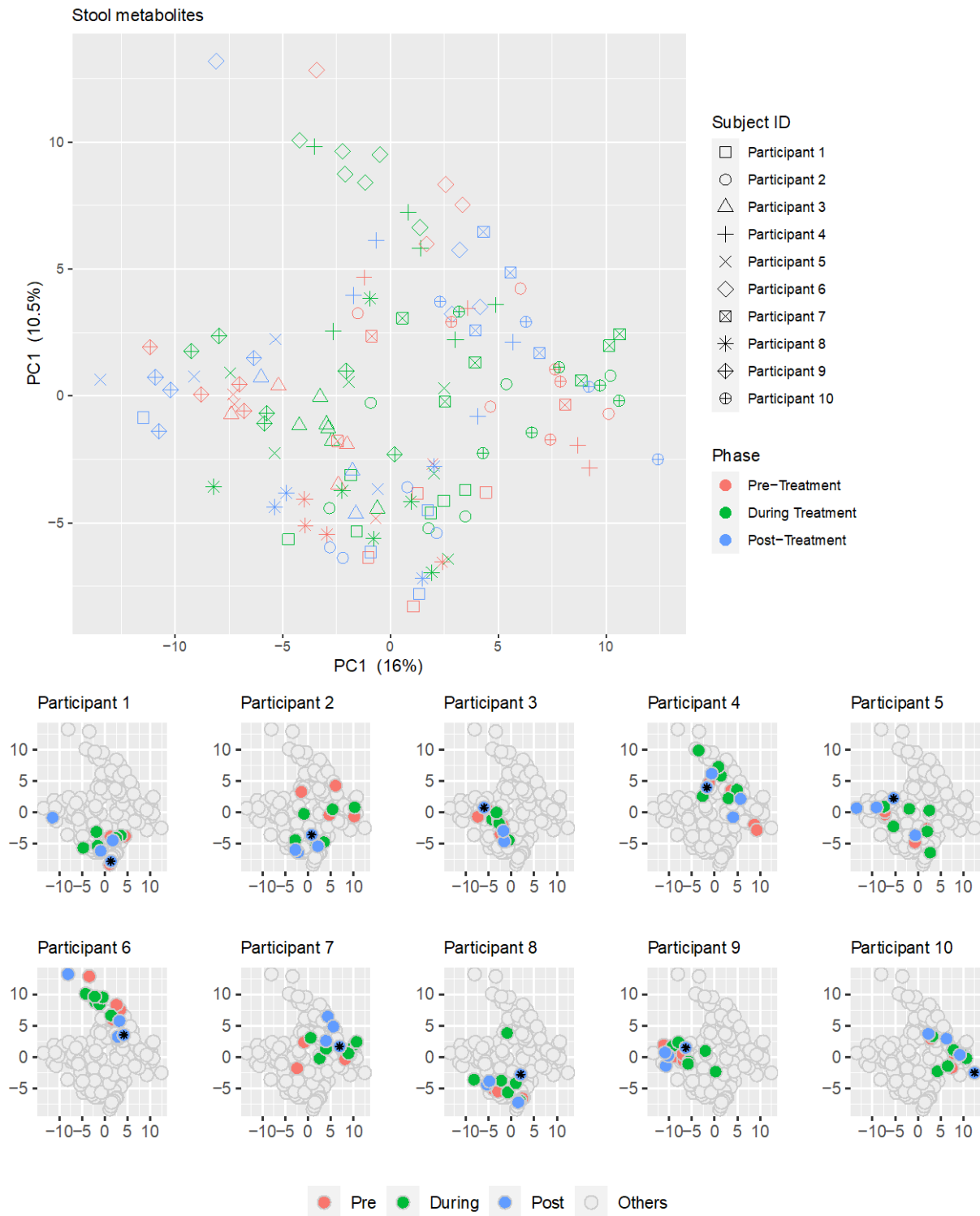
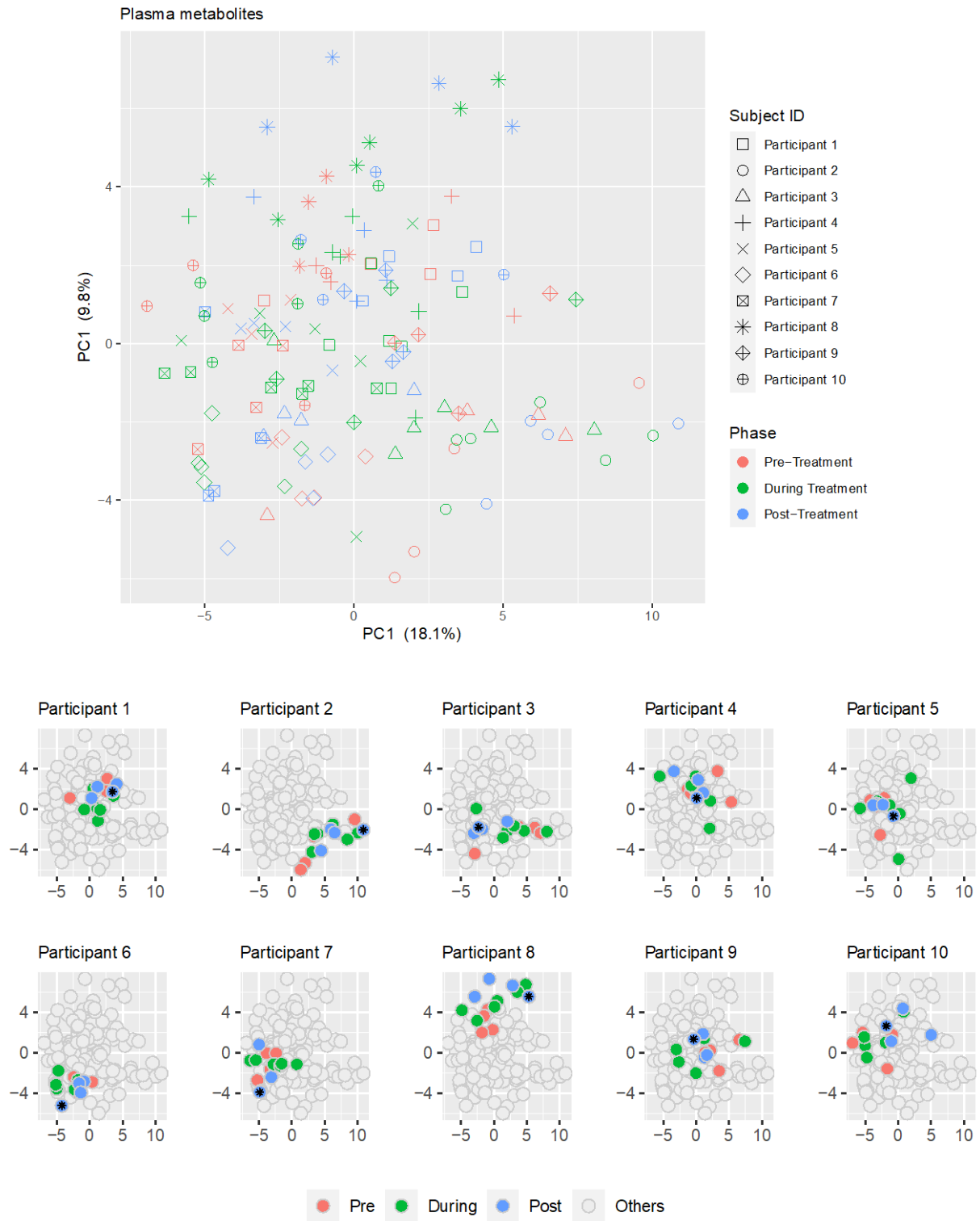


Figure S2

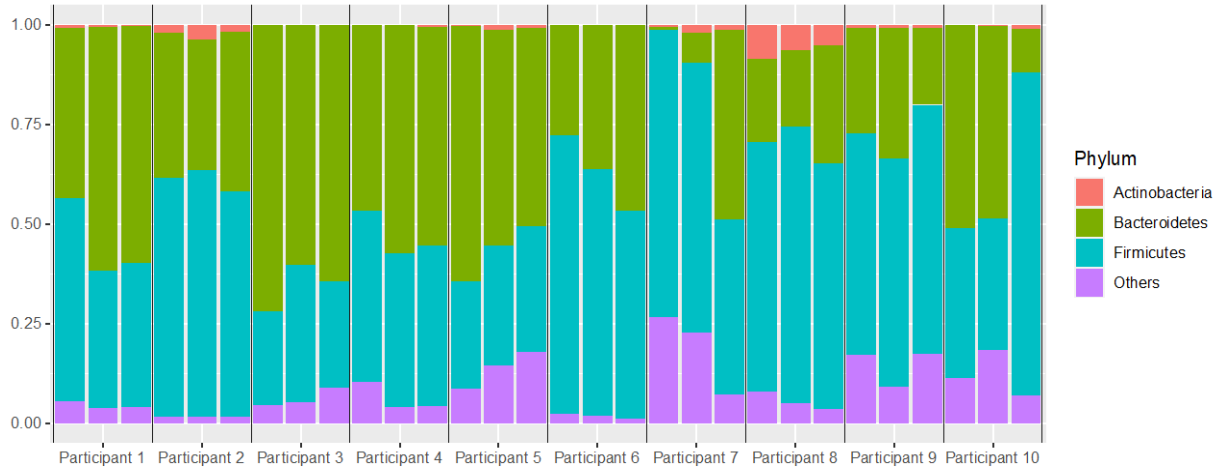


**Figure S3**



**Figure S4**





**Figure S5**

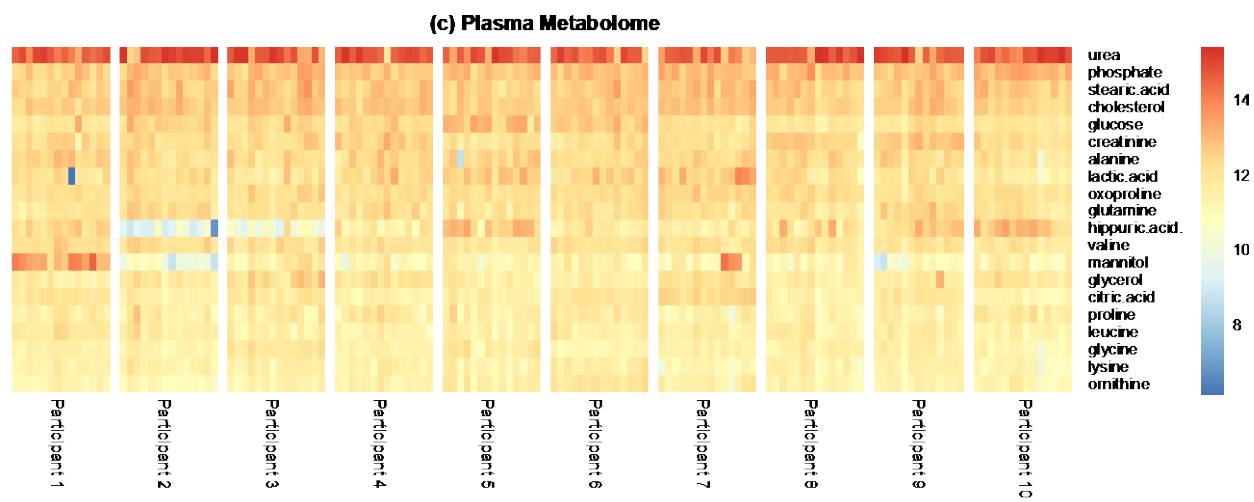
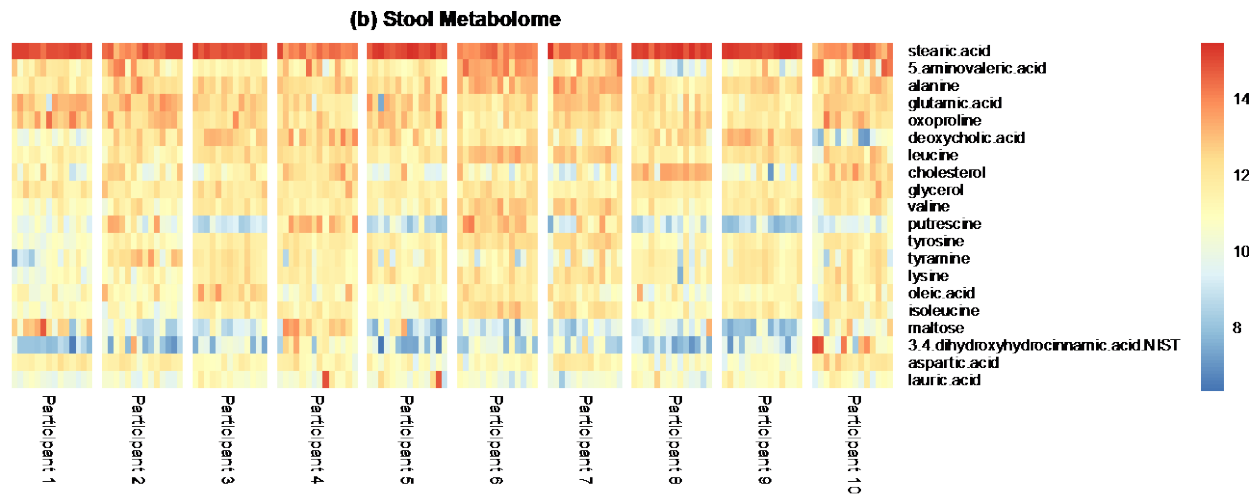
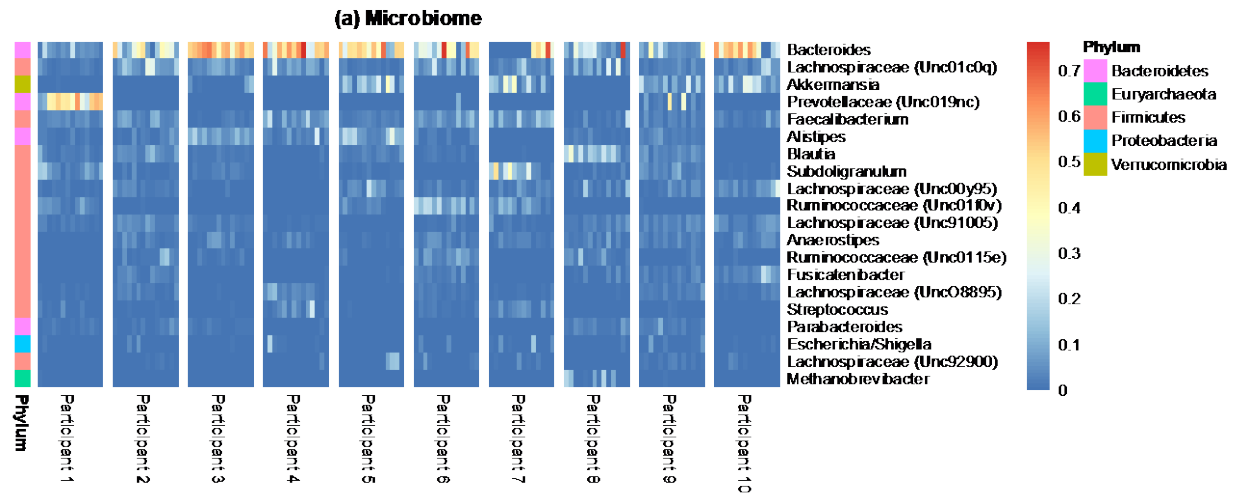
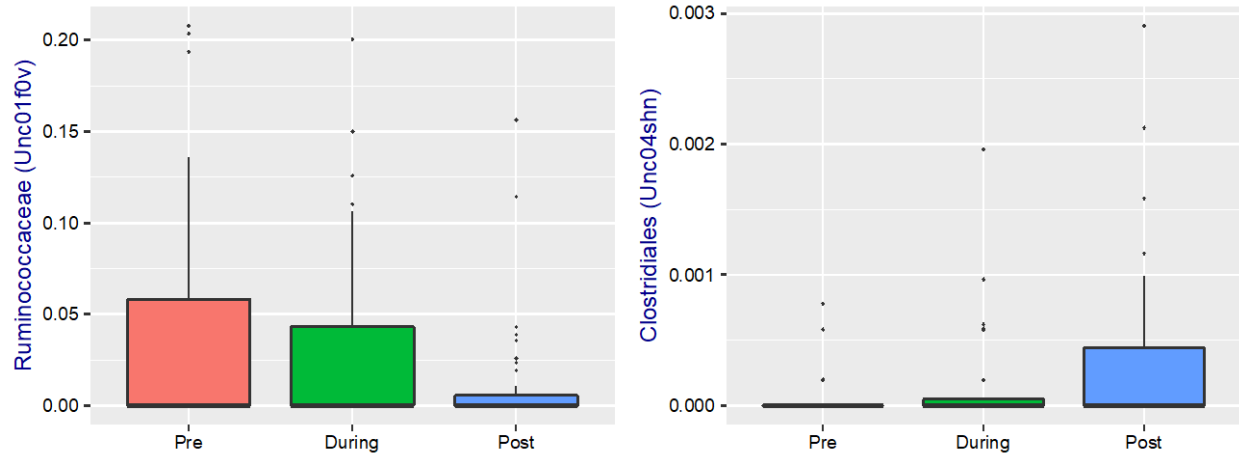
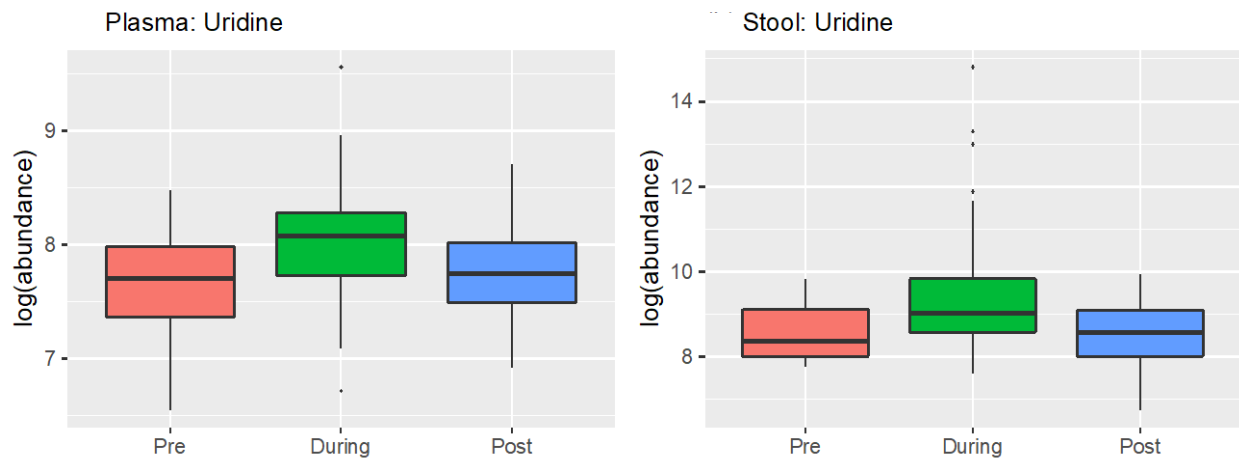


Figure S6

**a.**



**b.**



**Figure S7**

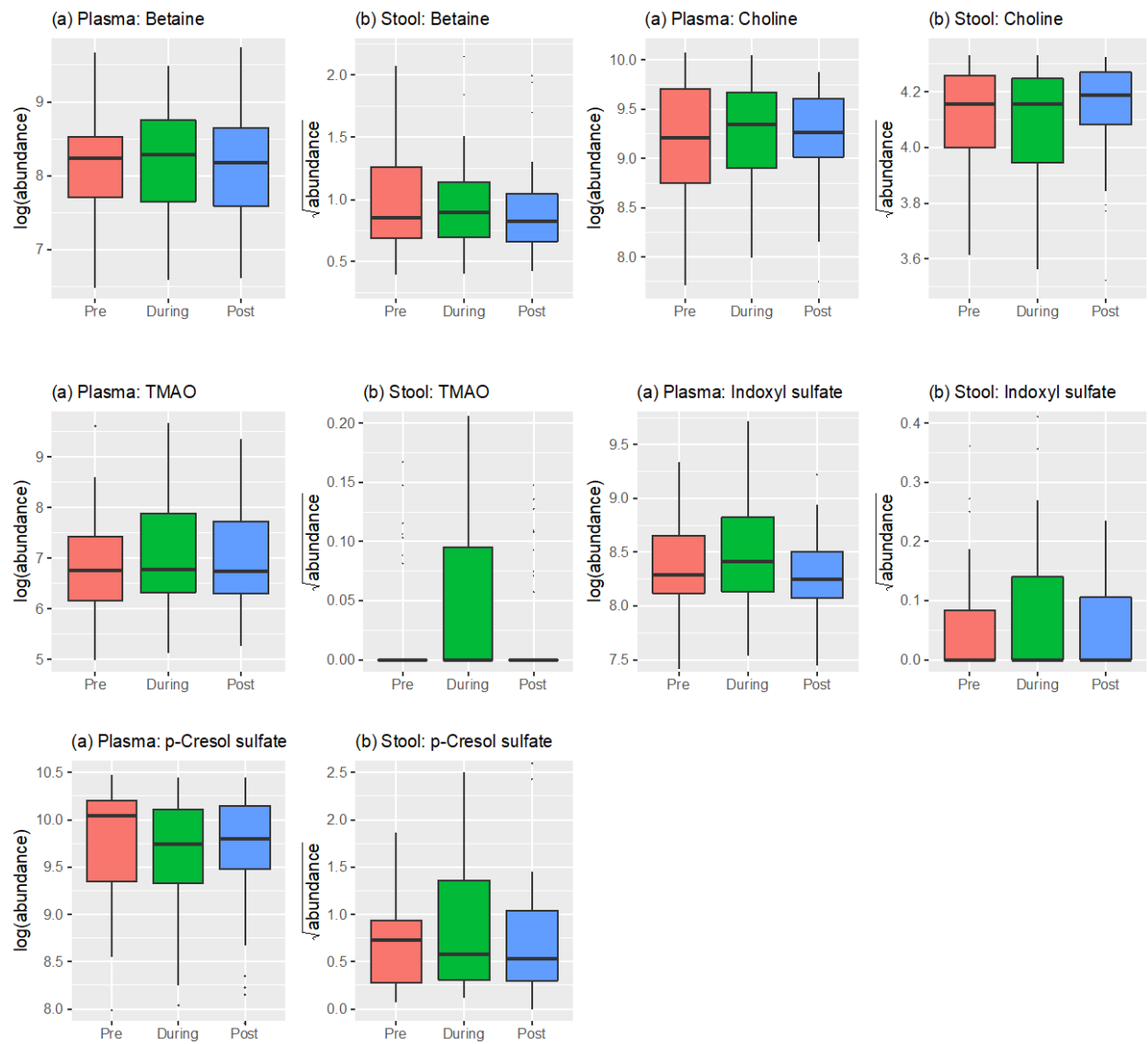


Figure S8