Item Name	**Quantity**	**Measure**	**Wgt (g)**	**Cals (kcal)**	**FatCals (kcal)**	**SatCals (kcal)**	**Prot (g)**	**Carb (g)**	**TotFib (g)**
1 Bag Totals			294.44	422	148	43.7	15.72	54.2	3.22
rice, basmati, white, cooked	65	Gram	65	83.9	1.64	0.45	1.74	18.2	0.26
cheese, parmesan	7	Gram	7	27.5	15.75	9	2.5	0	0
broccoli florets, steamed	12.5	Gram	12.5	4.28	0.46	0.08	0.29	0.88	0.4
carrots, cooked	12.5	Gram	12.5	4.37	0.2	0.03	0.09	1.03	0.38
corn, sweet, frozen, premium, organic	22.5	Gram	22.5	18.5	2.38	0	0.79	4.76	0.53
hot dog, chicken & pork, classic, bun size	12.5	Gram	12.5	30.7	23.4	8.49	1.18	0.47	0
oil, soybean	2.5	Gram	2.5	22.1	22.1	3.52	0	0	0
potato, red bliss, roasted	12.5	Gram	12.5	23.33	13.5	1.5	0.33	2	0.17
chicken breast, seasoned, rotisserie, skinless	23	Gram	23	31.51	5.78	1.6	6.44	0	0
almonds, dry roasted	2.5	Gram	2.5	15.0	11.8	0.92	0.52	0.53	0.27
bouillon, chicken	2.5	Gram	2.5	0.15	0.05	0	0.02	0.01	0
salt, table	0.5	Gram	0.5	0	0	0	0	0	0
stock, chicken	7.5	Gram	7.5	1.41	0.28	0	0.25	0.03	0.03
onion, sauteed, from fresh	27.5	Gram	27.5	12.1	0.47	0.08	0.37	2.78	0.39
juice, orange	2	Fluid ounce	59.1	27.6	0	0	0.39	6.71	0
cookie, chocolate chip, Chips Ahoy!, mini	4	Each	24.8	120	50.4	18	0.8	16.8	0.8
Total	216.5		588.88	845	296	87.34	31.43	108.9	6.45

Table S1, Related to Figure 1: Food composition of the homogenous diet intervention

Class	Time point 1 (0)	Time point 4 (1)	Class Error	type
0	11	6	0.35	Macronutrients
1	4	13	0.24	Macronutrients
0	10	7	0.41	ASVs
1	9	8	0.53	ASVs
0	11	6	0.35	Fecal-metabolome
1	5	12	0.29	Fecal-metabolome
0	12	5	0.29	Plasma-metabolome
1	3	14	0.18	Plasma-metabolome
0	9	8	0.47	Urine-metabolome
1	5	12	0.29	Urine-metabolome

Table S2, Related to Figure 3: Classification error for random forest models

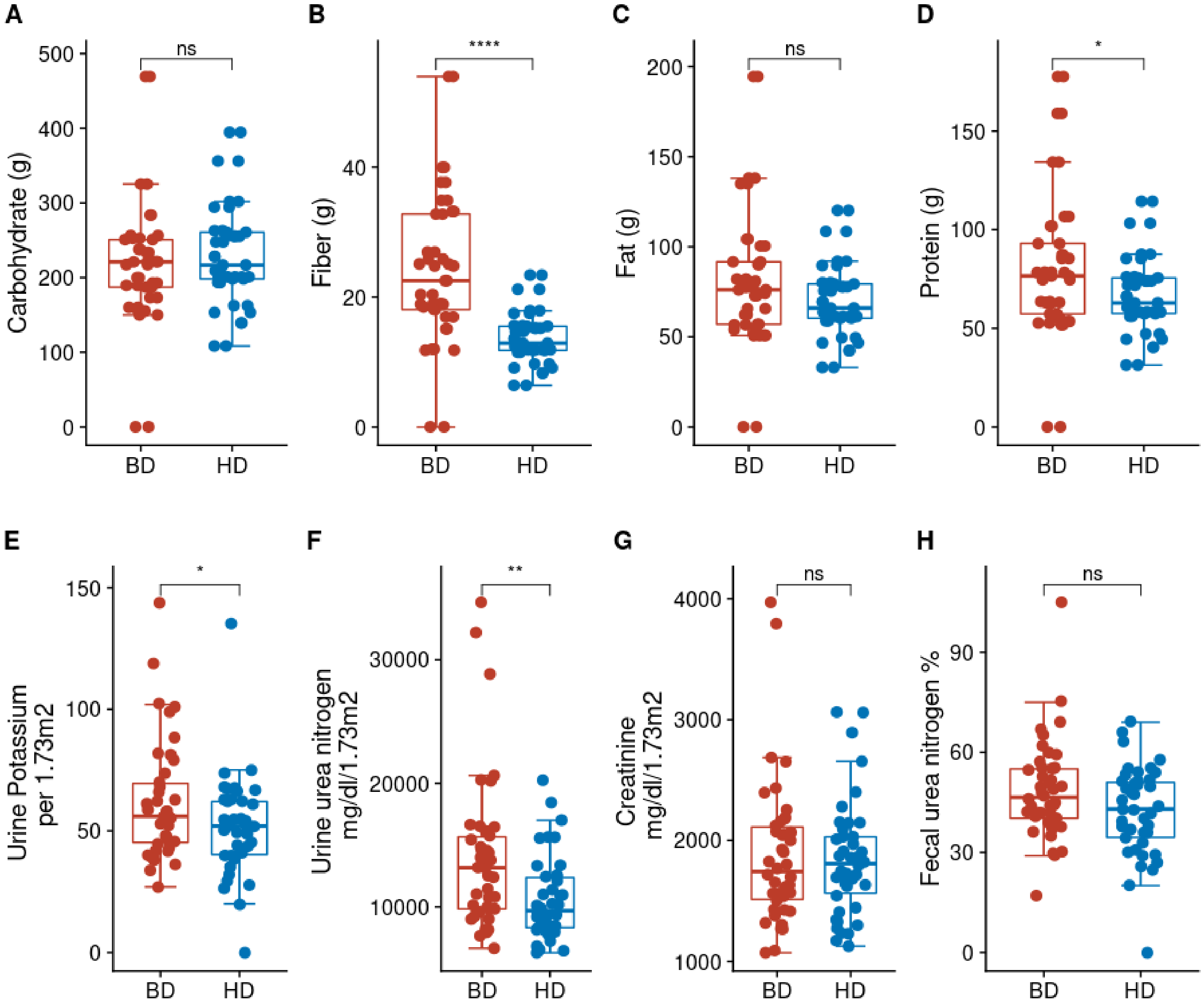

Figure S1, Related to Figure 1: Macronutrient and clinical parameters between BD and HD
Mean **(A)** carbohydrate, **(B)** fiber, **(C)** fat, and **(D)** protein intake during the BD and HD phases. Participants **(E)** urine potassium, **(F)** urine urea nitrogen, **(G)** creatinine, and **(H)** fecal urea nitrogen quantified at all study phases.

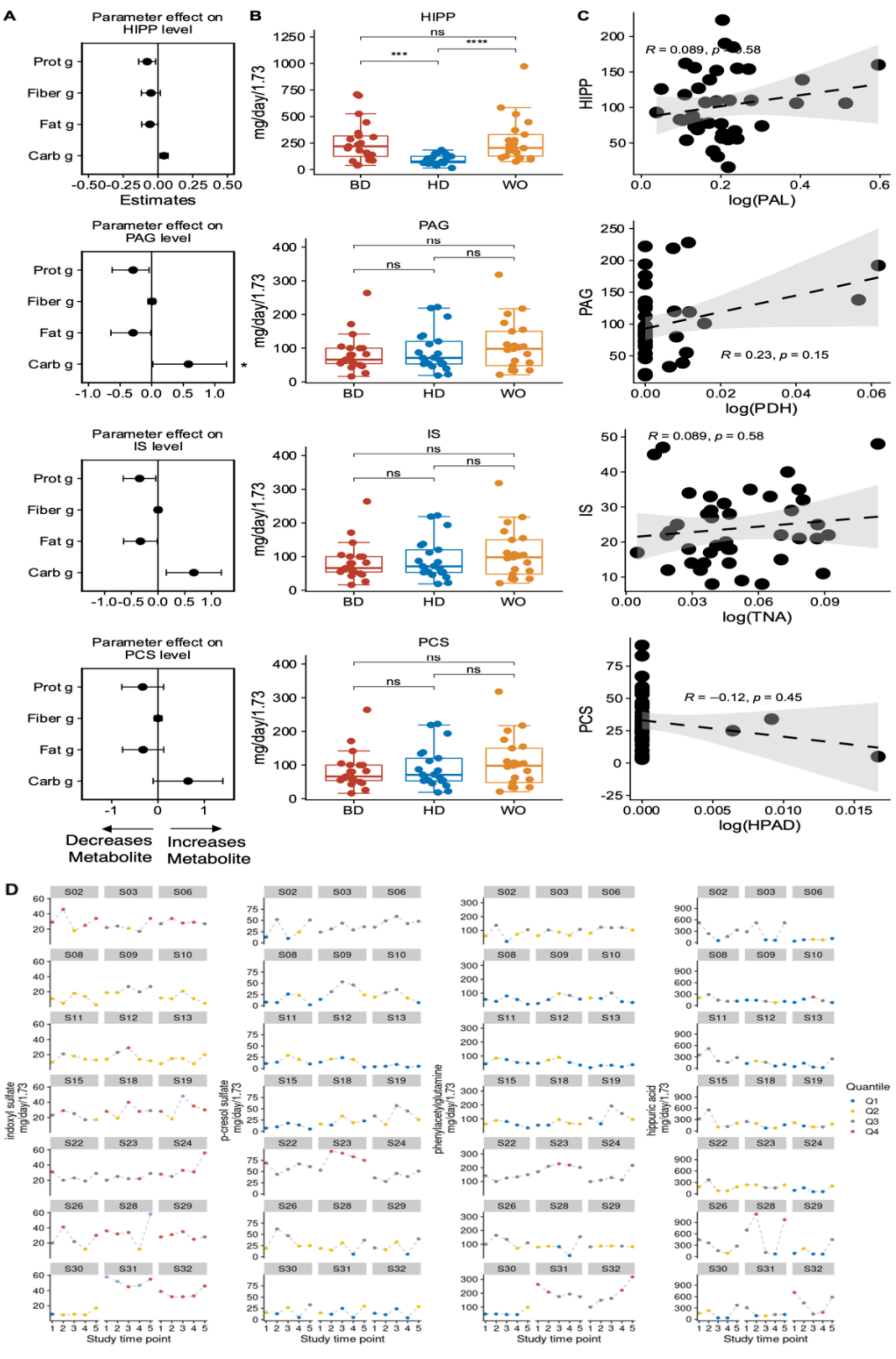

Figure S2, Related to Figure 2: Primary outcome uremic solute levels and correspondence with microbiome encoded metabolism

(A) Effect sizes of contribution of dietary macronutrients to hippuric acid (HIPP), phenylacetylglutamine (PAG), indoxyl sulfate (IS), and *p*-cresol sulfate (PCS) levels quantified by a mixed-effects model (bars represent a 95% CI). (B) Mean HIPP, PAG, IS, and PCS levels (mg/day/1.73) at the BD, HD, and WO phases.
(C) Correlation between urine IS, PAG, PCS levels with the relative abundances of the microbiome-encoded enzyme involved in their production.

(D) Uremic solute levels over the course of the MISO study by subject and colored by tertile.

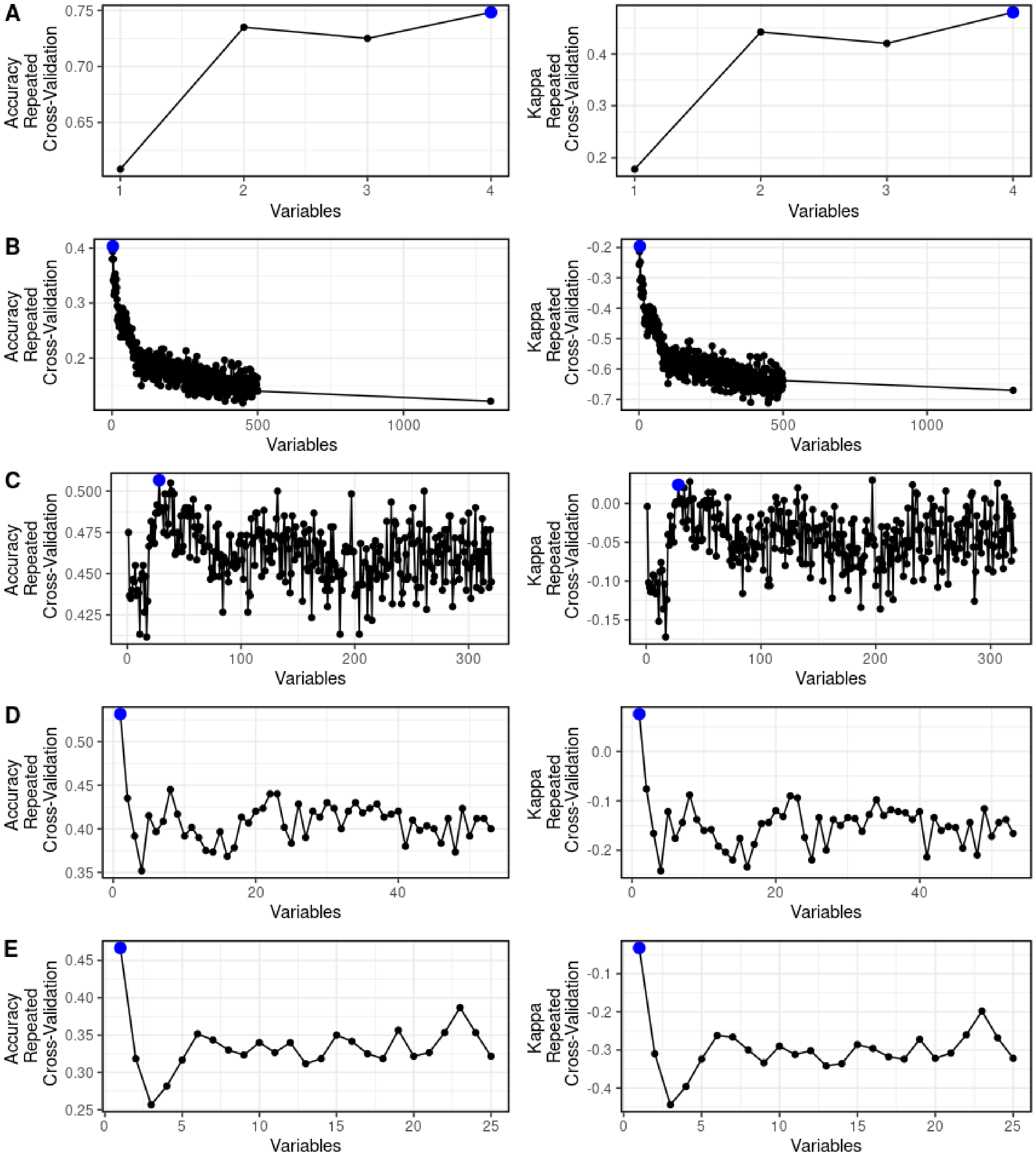

Figure S3, Related to Figure 3: Accuracy and Cohen's Kappa for each individual recursive random forest models for (A) Macronutrients, (B), ASVs, (C) fecal metabolome, (D) plasma metabolome, and (E) urine metabolome.

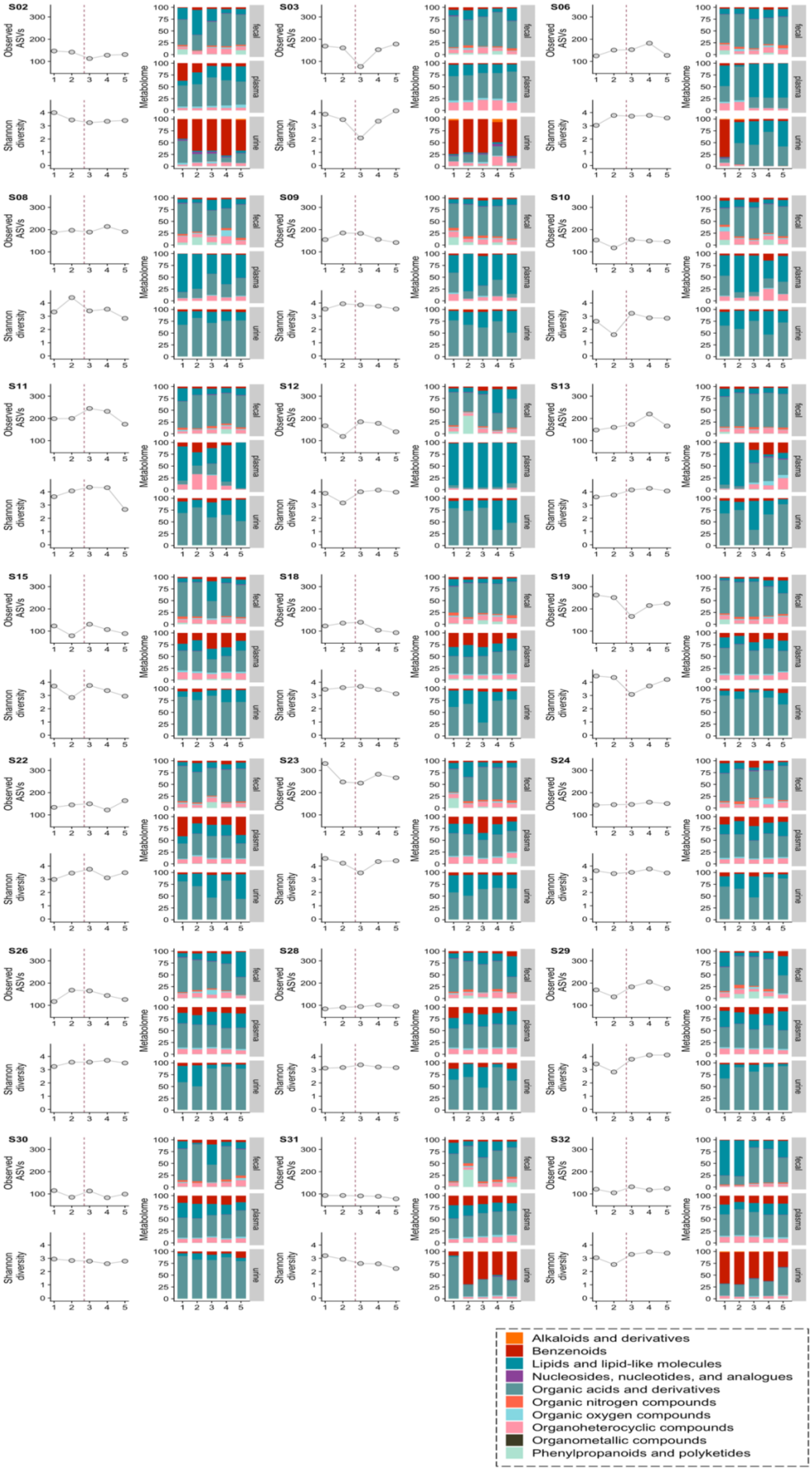
S02
S03
S06
S08
S09
S10
S11
S12
S13
S15
S18
S19
S22
S23
S24
S26
S28
S29
S30
S31
S32
Observed ASVs
Shannon diversity
Metabolome
fecal
plasma
urine
0
1
2
3
4
100
200
300
25
50
75
1
2
3
4
5
Alkaloids and derivatives
Benzenoids
Lipids and lipid-like molecules
Nucleosides, nucleotides, and analogues
Organic acids and derivatives
Organic nitrogen compounds
Organic oxygen compounds
Organoheterocyclic compounds
Organometallic compounds
Phenylpropanoids and polyketides

Figure S4, Related to Figure 4: MISO participants personalized temporal variation in observed ASVs, Shannon diversity, and metabolome profiles. Observed ASVs and Shannon diversity were determined using 16S amplicon sequencing of fecal samples.