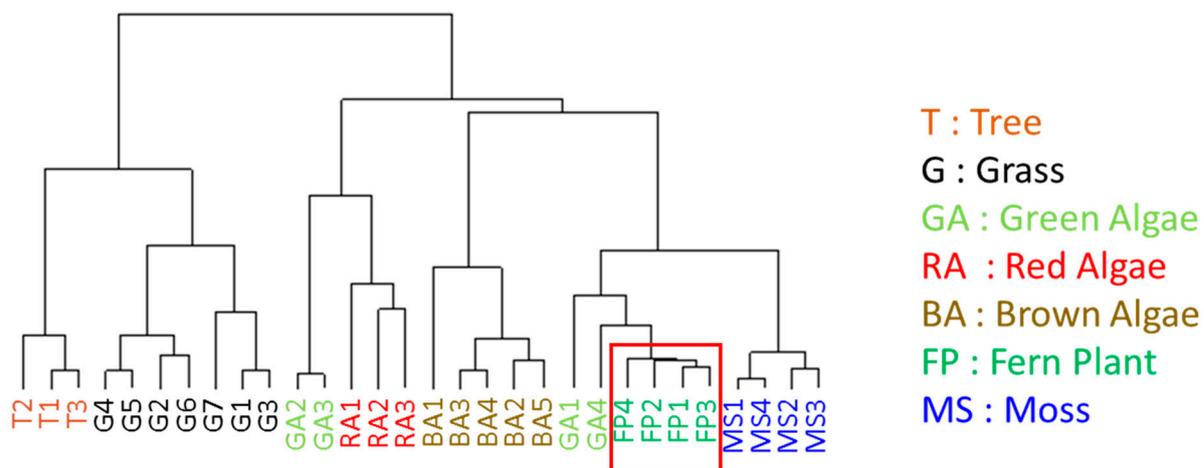
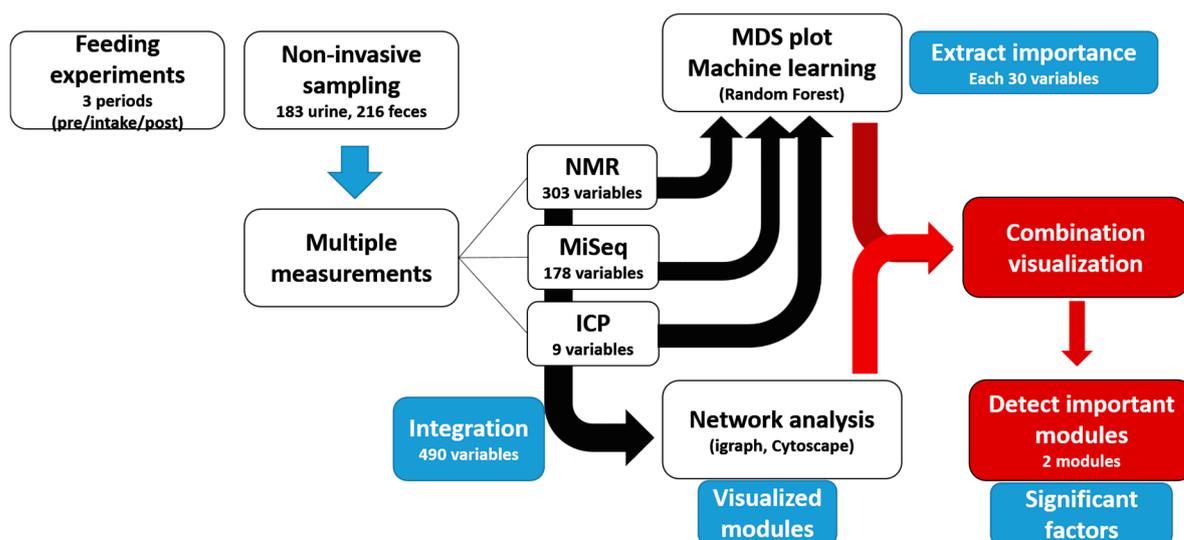


**Supplementary Materials:**


**Figure S1.** Tree diagram of plant components based on data set obtained by NMR measurement. This image is a modified version of a tree diagram. Raw or boiled edible parts of *Pteridium aquilinum* and *Matteuccia struthiopteris* classified at an intermediate point between moss and algae, not in higher plants, are surrounded by a red line. This image was partially revised from original presented in [31].



**Figure S2.** Flow chart of the analytical procedure in this study.

This flow chart indicates analytical steps. Arrows indicated experimental or analytical direction. Black arrows meant already exist methods or analysis steps. Text in the blue boxes show concept of the steps. Red arrows and box meant a novel approach developed in this study. This study shows that detection method of significant factor which respond to food intake at the final step.

**Table S1.** Information on primers used for performing microbiome analysis.

name	sequence
v4.SA501	AATGATACGGCGACCACCGAGATCTACACATCGTACGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA502	AATGATACGGCGACCACCGAGATCTACACACTATCTGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA503	AATGATACGGCGACCACCGAGATCTACACTAGCGAGTTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA504	AATGATACGGCGACCACCGAGATCTACACCTGCGTGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA505	AATGATACGGCGACCACCGAGATCTACACCTACTATATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA506	AATGATACGGCGACCACCGAGATCTACACCGTGAGTGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA507	AATGATACGGCGACCACCGAGATCTACACGGATATCTTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA508	AATGATACGGCGACCACCGAGATCTACACGACACCGTTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB501	AATGATACGGCGACCACCGAGATCTACACCTACTATATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB502	AATGATACGGCGACCACCGAGATCTACACCGTTACTATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB503	AATGATACGGCGACCACCGAGATCTACACAGAGTCACTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB504	AATGATACGGCGACCACCGAGATCTACACTACGAGACTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB505	AATGATACGGCGACCACCGAGATCTACACCTCGTCTCGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB506	AATGATACGGCGACCACCGAGATCTACACTCGACGAGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB507	AATGATACGGCGACCACCGAGATCTACACGATCGTGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB508	AATGATACGGCGACCACCGAGATCTACACGTCAGATATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SA701	CAAGCAGAAGACGGCATAACGAGATACTATGTCAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA702	CAAGCAGAAGACGGCATAACGAGATACTATGTCAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA703	CAAGCAGAAGACGGCATAACGAGATAGTAGCGTAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA704	CAAGCAGAAGACGGCATAACGAGATCAGTAGTGTAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA705	CAAGCAGAAGACGGCATAACGAGATCGTACTCAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA706	CAAGCAGAAGACGGCATAACGAGATCTACGACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA707	CAAGCAGAAGACGGCATAACGAGATGGAGACTAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA708	CAAGCAGAAGACGGCATAACGAGATGTCGCTCGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA709	CAAGCAGAAGACGGCATAACGAGATGTCGTCAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA710	CAAGCAGAAGACGGCATAACGAGATTACGACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA711	CAAGCAGAAGACGGCATAACGAGATTCATAGACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SA712	CAAGCAGAAGACGGCATAACGAGATTCGCTATAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB701	CAAGCAGAAGACGGCATAACGAGATAAGTCGAGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB702	CAAGCAGAAGACGGCATAACGAGATATACTTCGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB703	CAAGCAGAAGACGGCATAACGAGATAGCTGCTAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB704	CAAGCAGAAGACGGCATAACGAGATCATAGAGAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB705	CAAGCAGAAGACGGCATAACGAGATCGTAGATCAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB706	CAAGCAGAAGACGGCATAACGAGATCGTTACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB707	CAAGCAGAAGACGGCATAACGAGATGCGCACGTAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB708	CAAGCAGAAGACGGCATAACGAGATGGTACTATAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB709	CAAGCAGAAGACGGCATAACGAGATGTATACGACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB710	CAAGCAGAAGACGGCATAACGAGATTACGAGCAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB711	CAAGCAGAAGACGGCATAACGAGATTCAGCGTTAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB712	CAAGCAGAAGACGGCATAACGAGATTCGCTACGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB501	AATGATACGGCGACCACCGAGATCTACACCTACTATATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB502	AATGATACGGCGACCACCGAGATCTACACCTACTATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB503	AATGATACGGCGACCACCGAGATCTACACAGAGTCACTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB504	AATGATACGGCGACCACCGAGATCTACACTACGAGACTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB505	AATGATACGGCGACCACCGAGATCTACACACGTCCTCGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB506	AATGATACGGCGACCACCGAGATCTACACTCGACGAGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB507	AATGATACGGCGACCACCGAGATCTACACGATCGTGTATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB508	AATGATACGGCGACCACCGAGATCTACACGTCAGATATATGGTAATTGTGTGCCAGCMGCCGCGGTAA
v4.SB701	CAAGCAGAAGACGGCATAACGAGATAAGTCGAGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB702	CAAGCAGAAGACGGCATAACGAGATACTTCGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB703	CAAGCAGAAGACGGCATAACGAGATAGCTGCTAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB704	CAAGCAGAAGACGGCATAACGAGATCATAGAGAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB705	CAAGCAGAAGACGGCATAACGAGATCGTAGATCAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB706	CAAGCAGAAGACGGCATAACGAGATCCTCGTTACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB707	CAAGCAGAAGACGGCATAACGAGATGCGCACGTAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB708	CAAGCAGAAGACGGCATAACGAGATGGTACTATAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB709	CAAGCAGAAGACGGCATAACGAGATGTATACGACAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB710	CAAGCAGAAGACGGCATAACGAGATTACGAGCAAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB711	CAAGCAGAAGACGGCATAACGAGATTCAGCGTTAGTCAGTCAGCCGGACTACHVGGGTWCTAAT
v4.SB712	CAAGCAGAAGACGGCATAACGAGATTCGCTACGAGTCAGTCAGCCGGACTACHVGGGTWCTAAT

This primer information is referenced from a previous report [41].

**Table S2.** List of sequential numbers for bacterial detection by MiSeq analysis. Numbers in all Figures are equivalent to bacterial names in this list.

No.1	k__Bacteria;Other;Other;Other;Other;Other
No.2	k__Bacteria;p__Actinobacteria;Other;Other;Other;Other
No.3	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Brevibacteriaceae;g__Brevibacterium
No.4	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium
No.5	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;Other
No.6	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria
No.7	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Renibacterium
No.8	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae;g__Mycobacterium
No.9	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;Other
No.10	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;Other
No.11	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__
No.12	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Adlercreutzia
No.13	k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__AK1AB1_02E;g__
No.14	k__Bacteria;p__Bacteroidetes;Other;Other;Other;Other
No.15	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;Other;Other
No.16	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides
No.17	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;Other
No.18	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella
No.19	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;Other
No.20	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__
No.21	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__
No.22	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Barnesiellaceae];g__
No.23	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;Other;Other
No.24	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__;g__
No.25	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Cryomorphaceae;g__Cryomorpha
No.26	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;Other
No.27	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Ascidianibacter
No.28	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Polaribacter
No.29	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Sediminicola
No.30	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Chryseobacterium
No.31	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Cloacibacterium
No.32	k__Bacteria;p__Bacteroidetes;c__[Rhodothermi];o__[Rhodothermales];f__Rhodothermaceae;g__
No.33	k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Lacibacter
No.34	k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Sediminibacterium
No.35	k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Saprospiraceae;g__
No.36	k__Bacteria;p__Chlamydiae;c__Chlamydia;o__Chlamydiales;Other;Other
No.37	k__Bacteria;p__Chlamydiae;c__Chlamydia;o__Chlamydiales;f__;g__
No.38	k__Bacteria;p__Cyanobacteria;Other;Other;Other;Other
No.39	k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__YS2;f__;g__
No.40	k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Stramenopiles;f__;g__
No.41	k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Streptophyta;f__;g__
No.42	k__Bacteria;p__Cyanobacteria;c__Oscillatoriothycideae;Other;Other;Other
No.43	k__Bacteria;p__Cyanobacteria;c__Oscillatoriothycideae;o__Chroococcales;f__Xenococcaceae;g__
No.44	k__Bacteria;p__Deferribacteres;c__Deferribacteres;o__Deferribacterales;f__Deferribacteraceae;g__Mucispirillum
No.45	k__Bacteria;p__Firmicutes;Other;Other;Other;Other
No.46	k__Bacteria;p__Firmicutes;c__Bacilli;Other;Other;Other
No.47	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus
No.48	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus
No.49	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus
No.50	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus

Table S2. (Continued)

No.51	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;Other;Other
No.52	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g__
No.53	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;Other
No.54	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;Other
No.55	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus
No.56	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae;Other
No.57	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus
No.58	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus
No.59	k_Bacteria;p_Firmicutes;c_Bacilli;o_Turicibacterales;f_Turicibacteraceae;g_Turicibacter
No.60	k_Bacteria;p_Firmicutes;c_Clostridia;Other;Other;Other
No.61	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;Other;Other
No.62	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__g__
No.63	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;Other
No.64	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium
No.65	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium
No.66	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Anaerofustis
No.67	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;Other
No.68	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g__
No.69	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Anaerostipes
No.70	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blautia
No.71	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Clostridium
No.72	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus
No.73	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea
No.74	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Epulo piscium
No.75	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Roseburia
No.76	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_[Ruminococcus]
No.77	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g__
No.78	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;Other
No.79	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;Other
No.80	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g__
No.81	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerotruncus
No.82	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Butyricoccus
No.83	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Clostridium
No.84	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium
No.85	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira
No.86	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus
No.87	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Veillonella
No.88	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];Other
No.89	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g__
No.90	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Anaerococcus
No.91	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;Other
No.92	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g__
No.93	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum
No.94	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium
No.95	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Coprobacillus
No.96	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Erysipelothrix
No.97	k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Cetobacterium
No.98	k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;g_Leptotrichia
No.99	k_Bacteria;p_Lentisphaerae;c_[Lentisphaeria];o_Lentisphaerales;f_Lentisphaeraceae;g__
No.100	k_Bacteria;p_Planctomycetes;c_OM190;o_agg27;f_g

Table S2. (Continued)

No.101	k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_
No.102	k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_
No.103	k_Bacteria;p_Proteobacteria;Other;Other;Other;Other
No.104	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;Other;Other;Other
No.105	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;Other
No.106	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;Other;Other
No.107	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;Other
No.108	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Balneimonas
No.109	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Bradyrhizobium
No.110	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;Other
No.111	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_
No.112	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_Methylobacterium
No.113	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;Other
No.114	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Phyllobacterium
No.115	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;Other
No.116	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_
No.117	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;Other
No.118	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Loktanelia
No.119	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus
No.120	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Phaeobacter
No.121	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodobacter
No.122	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;Other
No.123	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseomonas
No.124	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;Other
No.125	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;Other
No.126	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;Other
No.127	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;Other
No.128	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas
No.129	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter
No.130	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;Other
No.131	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Comamonas
No.132	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Tepidimonas
No.133	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;Other
No.134	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;Other
No.135	k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_
No.136	k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio
No.137	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;Other;Other;Other
No.138	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;Other;Other
No.139	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Alteromonas
No.140	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_BD2-13
No.141	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Marinobacter
No.142	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Colwelliaceae;Other
No.143	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Colwelliaceae;g_
No.144	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Idiomarinaceae;g_Idiomarina
No.145	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_OM60;g_
No.146	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Shewanellaceae;g_Shewanella
No.147	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;Other
No.148	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Serratia
No.149	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_HTCC2188;f_HTCC2089;g_
No.150	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o Legionellales;f Legionellaceae;Other

Table S2. (Continued)

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No.151	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Legionellales;f	Legionellaceae;g	
No.152	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Oceanospirillales;f	Alcanivoracaceae;g	Alcanivorax
No.153	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Oceanospirillales;f	Halomonadaceae;g	Halomonas
No.154	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Oceanospirillales;f	Oceanospirillaceae;g	Oleibacter
No.155	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Oceanospirillales;f	Oceanospirillaceae;g	Oleispira
No.156	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Oceanospirillales;f	Oceanospirillaceae;g	Spongüspira
No.157	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	Acinetobacter
No.158	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	Enhydrobacter
No.159	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;Other	
No.160	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas
No.161	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Thiotrichales;f	Piscirickettsiaceae;g	
No.162	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Vibrionales;f	Pseudoalteromonadaceae;g	Pseudoalteromonas
No.163	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Vibrionales;f	Vibrionaceae;Other	
No.164	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Vibrionales;f	Vibrionaceae;g	Photobacterium
No.165	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Vibrionales;f	Vibrionaceae;g	Vibrio
No.166	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;Other	
No.167	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Stenotrophomonas
No.168	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Xanthomona s
No.169	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	[Marinicellales];f	[Marinicellaceae];g	
No.170	k	Bacteria;p	Proteobacteria;c	Gammaproteobacteria;o	[Marinicellales];f	[Marinicellaceae];g	Marinicella
No.171	k	Bacteria;p	SBR1093;c	EC214;o	;f	;g	
No.172	k	Bacteria;p	Tenericutes;c	Mollicutes;o	Mycoplasmatales;f	Mycoplasmataceae;g	
No.173	k	Bacteria;p	Tenericutes;c	Mollicutes;o	Mycoplasmatales;f	Mycoplasmataceae;g	Mycoplasma
No.174	k	Bacteria;p	Tenericutes;c	Mollicutes;o	RF39;f	;g	
No.175	k	Bacteria;p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae;g	
No.176	k	Bacteria;p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae;g	Akkemansia
No.177	k	Bacteria;p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae;g	Persicirhabdus
No.178	k	Bacteria;p	[Thermi];c	Deinococci;o	Deinococcales;f	Deinococcaceae;g	Deinococcus

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**Table S3.** List of annotated metabolites and unknown signals from NMR measurements.

Annotated metabolites detected by 1D and 2D NMR measurements (Figures S5, S6) (a). List of alternative names given to unknown <sup>1</sup>H chemical shifts from urinary analysis data (b) and from fecal analysis data (c).

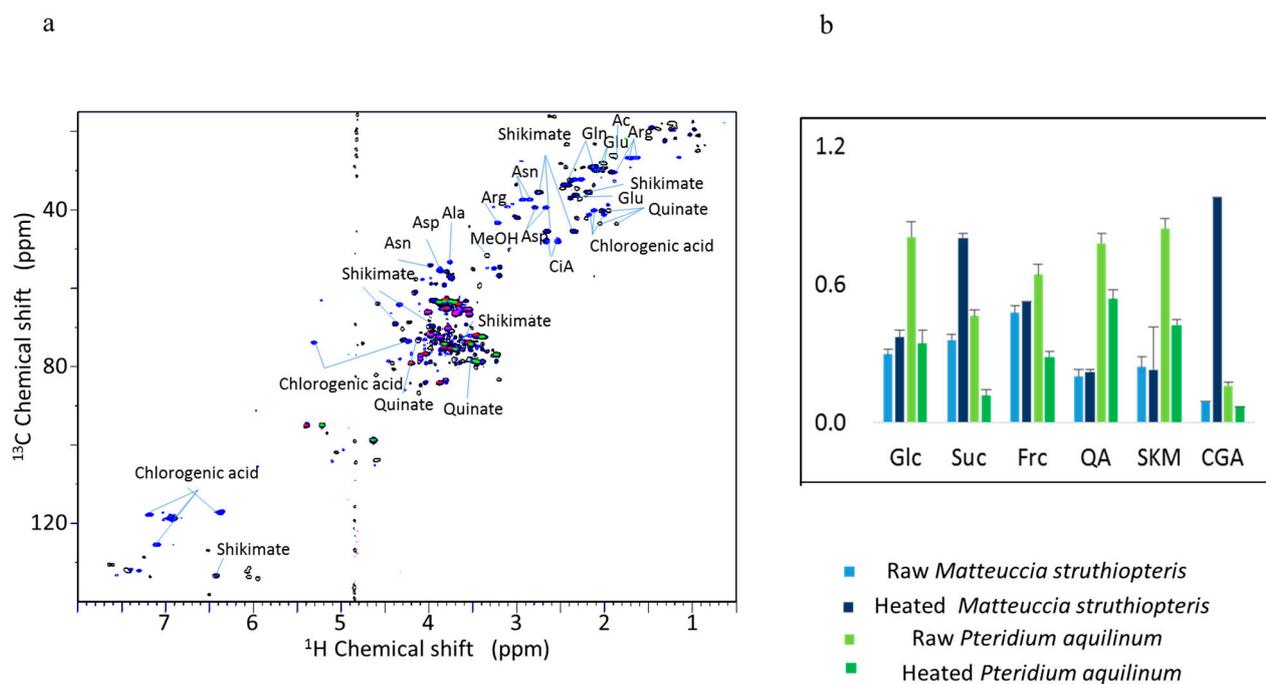
Metabolites		<sup>1</sup> H Chemical Shift (ppm) and multiplicity
Acetic acid	Ac	1.91 (s)
Acetylglycine	AcGly	2.02 (s), 3.74 (d)
Adenosine monophosphate	3'-AMP	3.89 (m), 4.43 (m), 6.11 (d), 8.25 (s), 8.37 (s)
α-Hydroxyisobutyrate	HydroxyisoBuA	1.34 (s)
Allantoin	Allantoin	5.37 (s)
Betaine	Betaine	3.25 (s), 3.89 (s)
Butanoic acid	BuA	0.88 (t), 1.55 (q), 2.15 (t)
Cholic acid	Cholate	0.71 (s), 2.22 (m)
Choline	Choline	3.20 (s), 3.50 (dd), 4.05 (m)
Cis-Aconitic acid	Aconi	3.11 (d), 6.58 (s)
Citric acid	CIa	2.54 (d), 2.68 (d)
Creatine	Creatine	3.02 (s), 3.92 (s)
Creatinine	Creatinine	3.03 (s), 4.05 (s)
Cytidine Monophosphate	3'-CMP	3.98 (dd), 4.04 (dd), 4.23 (d), 4.36 (m), 5.93 (d), 6.13 (d), 8.08 (d)
Deoxyadenosine	Deoxyadenosine	2.56 (d), 2.82 (dd), 3.79 (dd), 3.84 (dd), 4.18 (q), 4.65 (m), 8.18 (s), 8.29 (s)
D-Glucose	Glc	3.24 (dd), 3.39 (m), 3.46 (m), 3.53 (dd), 3.70 (m), 3.83 (m), 3.89 (dd), 4.64 (d), 5.23 (d)
Dimethylamine	DMA	2.71 (s)
Dimethylglycine	DMG	2.88 (s)
Ethanol	EtOH	1.17 (t), 3.65 (q)
Ethanolamine	EtNH	3.13 (d), 3.81 (d)
Formic acid	FoA	8.45 (s)
Fumaric acid	FuA	6.51 (s)
Galactaric acid	Galactarate	3.93 (s), 4.26 (s)
Gamma-Aminobutyric acid	GABA	1.89 (m), 2.29 (t), 3.00 (t)
Gluconic acid	Gluconate	3.66 (m), 3.76 (m), 3.82 (m), 4.12 (d)
Glucuronate	Glucuronate	3.28 (t), 3.57 (dd), 3.72 (m), 4.07 (d), 4.63 (d), 5.23 (d)
Glycine	Gly	3.55 (s)
Guanidinoacetic acid	GuanAc	3.78 (s)
Guanosine	Guanosine	3.82 (d), 3.87 (d), 4.22 (q), 4.41 (dd), 5.09 (d)
Hippuric acid	Hippurate	3.95 (d), 7.54 (m), 7.62 (t), 7.82 (dd)
Homovanillic acid	Homovanillate	3.44 (s), 3.86 (s), 6.77 (dd), 6.87 (d), 6.96 (d)
Hypotaurine	Hypotaurine	2.64 (t), 3.34 (t)
Inosine	Inosine	3.83 (dd), 3.90 (dd), 4.26 (dd), 6.06 (d), 8.19 (s)
Inosinemonophosphate	IMP	4.03 (m), 4.36 (dd), 4.50 (dd), 6.14 (d), 8.21 (s)
Isovalerylglycine	IsovalerylGly	0.93 (d), 2.16 (d), 3.75 (d)
Itaconic acid	Itaconate	3.40 (s), 5.85 (s)
L-Acetylcarnithine	AcCarni	2.12 (s), 2.48 (dd), 2.61 (dd), 3.18 (s), 3.61 (d), 3.82 (dd)
Lactic acid	Lactate	1.32 (d), 4.10 (q)
L-Alanine	Ala	1.47 (d), 3.76 (q)
L-Asparagine	Asn	2.85 (m), 2.94 (m), 4.00 (dd)
L-Aspartic acid	Asp	2.67 (dd), 2.80 (dd), 3.89 (dd)
L-Glutamic acid	Glu	2.05 (m), 2.11 (m), 2.34 (m), 3.74 (dd)
L-Glutamine	Gln	2.12 (m), 2.44 (m), 3.76 (t)
L-Isoleucine	Ile	0.93 (t), 1.00 (d), 1.25 (m), 1.45 (m), 1.96 (m), 3.66 (d)
L-Leucine	Leu	0.95 (t), 1.70 (m), 3.73 (m)
L-Lysine	Lys	1.46 (m), 1.72 (m), 1.89 (m), 3.01 (t), 3.74 (t)
L-Methionine	Met	2.15 (m), 2.63 (t), 3.85 (dd)
L-Phenylalanine	Phe	3.19 (m), 3.98 (dd), 7.32 (d), 7.36 (m), 7.42 (m)
L-Serine	Ser	3.83 (dd), 3.96 (s)
L-Threonine	Thr	1.31 (d), 3.58 (d), 4.25 (m)
L-Tyrosine	Tyr	3.02 (dd), 3.17 (dd), 3.92 (dd), 6.89 (d), 7.17 (m)
L-Valine	Val	0.98 (d), 1.03 (d), 2.27 (m), 3.60 (d)
Methanol	MtOH	3.34 (s)
Methylamine	Methylamine	2.59 (s)
N-Acetyl	N-Act	2.05 (s)
Propionic acid	PrA	1.05 (t), 2.17 (q)
Putrescine	Putrescine	1.76 (t), 3.04 (t)
Sarcosine	Sarcosine	2.74 (s), 3.60 (s)
Succinic acid	SuA	2.40 (s)
Taurine	Taurine	3.26 (t), 3.42 (t)
Trigonelline	Trigonelline	4.43 (s), 8.07 (m), 8.82 (m), 9.11 (s)
Trimethylamine	TMA	2.88 (s)
Uridine	Uridine	3.80 (dd), 3.90 (dd), 4.12 (m), 4.22 (dd), 4.34 (dd), 5.89 (d), 5.90 (d), 7.86 (d)
Urocanic acid	Urocanate	6.39 (d), 7.28 (d), 7.37 (s), 7.85 (s)
Xylobiose	Xyl	2.91 (m), 3.22 (dd), 3.25 (m), 3.30 (m), 3.37 (dd), 3.42 (t), 3.54 (t), 3.62 (m), 3.68 (dd), 3.77 (m), 3.92 (dd), 3.97 (dd), 4.05 (dd), 4.45 (d), 4.58 (d)
2-oxoglutarate	2Oxoglutarate	2.42 (t), 3.00 (t)
2-oxoisovaleric acid	2Oxoisovalerate	0.82 (s), 0.95 (d), 2.01 (m), 3.84 (d)
2-oxopentanoic acid	2Oxopentanoate	0.91 (t), 1.61 (m)
3-ureidopropionate	3-UrPrA	2.72 (t), 3.29 (t)
4-amino-hippurate	4aminoHippurate	3.89 (d), 6.85 (d), 7.66 (d)

b

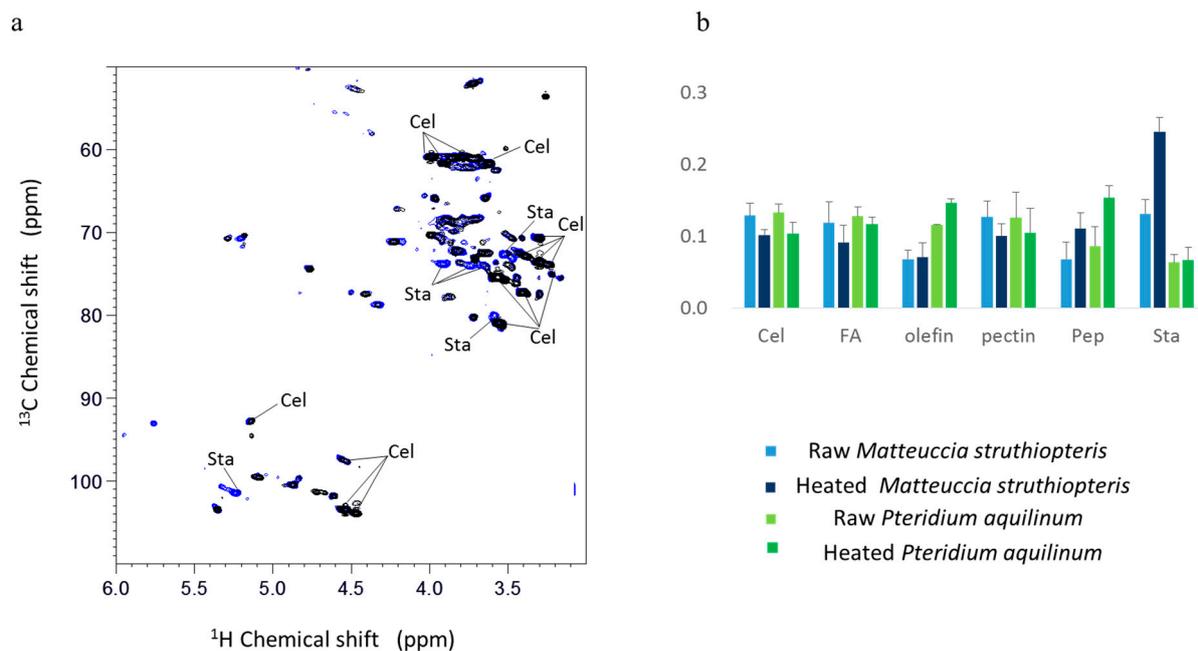
Unknown <sup>1</sup> H Chemical Shift (ppm)			
ROI.1	1.24	ROI.32	3.64
ROI.2	3.14	ROI.33	3.85
ROI.3	0.87	ROI.34	3.94
ROI.4	0.88	ROI.35	4.12
ROI.5	0.90	ROI.36	4.14
ROI.6	1.09	ROI.37	4.29
ROI.7	1.11	ROI.38	4.47
ROI.8	1.20	ROI.39	4.51
ROI.9	1.22	ROI.40	4.55
ROI.10	1.35	ROI.41	4.57
ROI.11	1.36	ROI.42	5.01
ROI.12	1.48	ROI.43	5.37
ROI.13	1.76	ROI.44	5.70
ROI.14	1.97	ROI.45	6.53
ROI.15	1.99	ROI.46	6.72
ROI.16	2.06	ROI.47	6.84
ROI.17	2.08	ROI.48	6.86
ROI.18	2.24	ROI.49	6.87
ROI.19	2.27	ROI.50	6.93
ROI.20	2.29	ROI.51	7.05
ROI.21	2.46	ROI.52	7.19
ROI.22	2.50	ROI.53	7.21
ROI.23	2.58	ROI.54	7.25
ROI.24	2.60	ROI.55	7.27
ROI.25	2.62	ROI.56	7.35
ROI.26	2.92	ROI.57	7.37
ROI.27	3.03	ROI.58	7.56
ROI.28	3.15	ROI.59	7.67
ROI.29	3.22	ROI.60	3.80
ROI.30	3.29	ROI.61	3.67
ROI.31	3.59	ROI.62	3.61

c

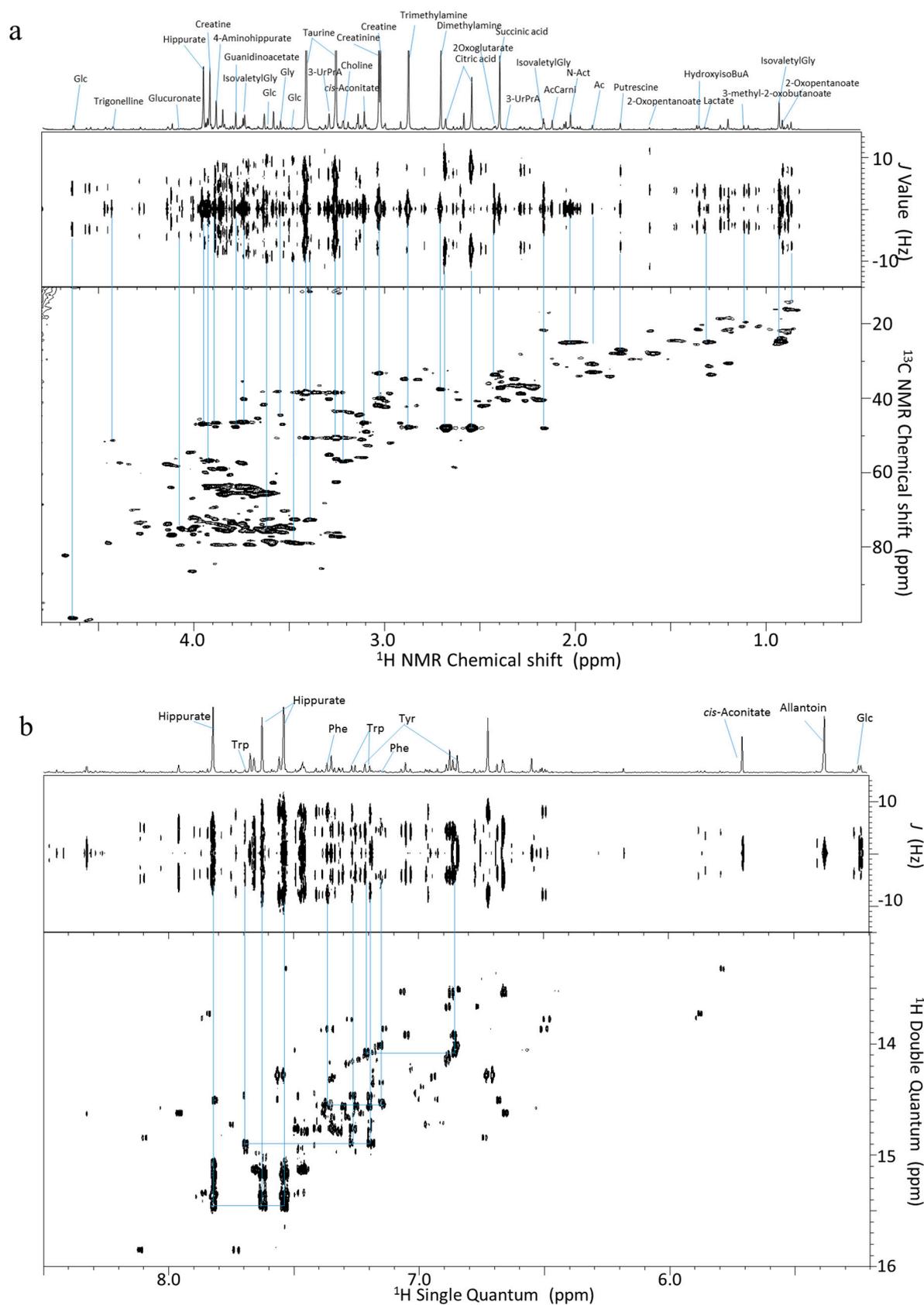
Unknown <sup>1</sup> H Chemical Shift (ppm)			
ROI.1	2.90	ROI.35	2.92
ROI.2	3.48	ROI.36	3.03
ROI.3	2.46	ROI.37	3.40
ROI.4	2.36	ROI.38	3.65
ROI.5	2.33	ROI.39	3.67
ROI.6	4.04	ROI.40	3.68
ROI.7	7.23	ROI.41	3.75
ROI.8	4.27	ROI.42	3.86
ROI.9	2.88	ROI.43	3.87
ROI.10	3.10	ROI.44	3.90
ROI.11	3.13	ROI.45	4.06
ROI.12	3.99	ROI.46	4.10
ROI.13	3.99	ROI.47	4.46
ROI.14	3.94	ROI.48	4.47
ROI.15	3.98	ROI.49	4.59
ROI.16	1.52	ROI.50	4.60
ROI.17	2.48	ROI.51	4.61
ROI.18	2.49	ROI.52	4.61
ROI.19	2.55	ROI.53	5.09
ROI.20	2.86	ROI.54	5.10
ROI.21	2.89	ROI.55	5.13
ROI.22	2.93	ROI.56	5.86
ROI.23	7.89	ROI.57	5.92
ROI.24	7.85	ROI.58	6.05
ROI.25	5.18	ROI.59	6.06
ROI.26	1.13	ROI.60	6.07
ROI.27	1.16	ROI.61	6.13
ROI.28	1.19	ROI.62	6.82
ROI.29	1.20	ROI.63	7.73
ROI.30	1.36	ROI.64	7.67
ROI.31	1.37	ROI.65	7.91
ROI.32	2.61	ROI.66	7.96
ROI.33	2.71	ROI.67	8.59
ROI.34	2.73		



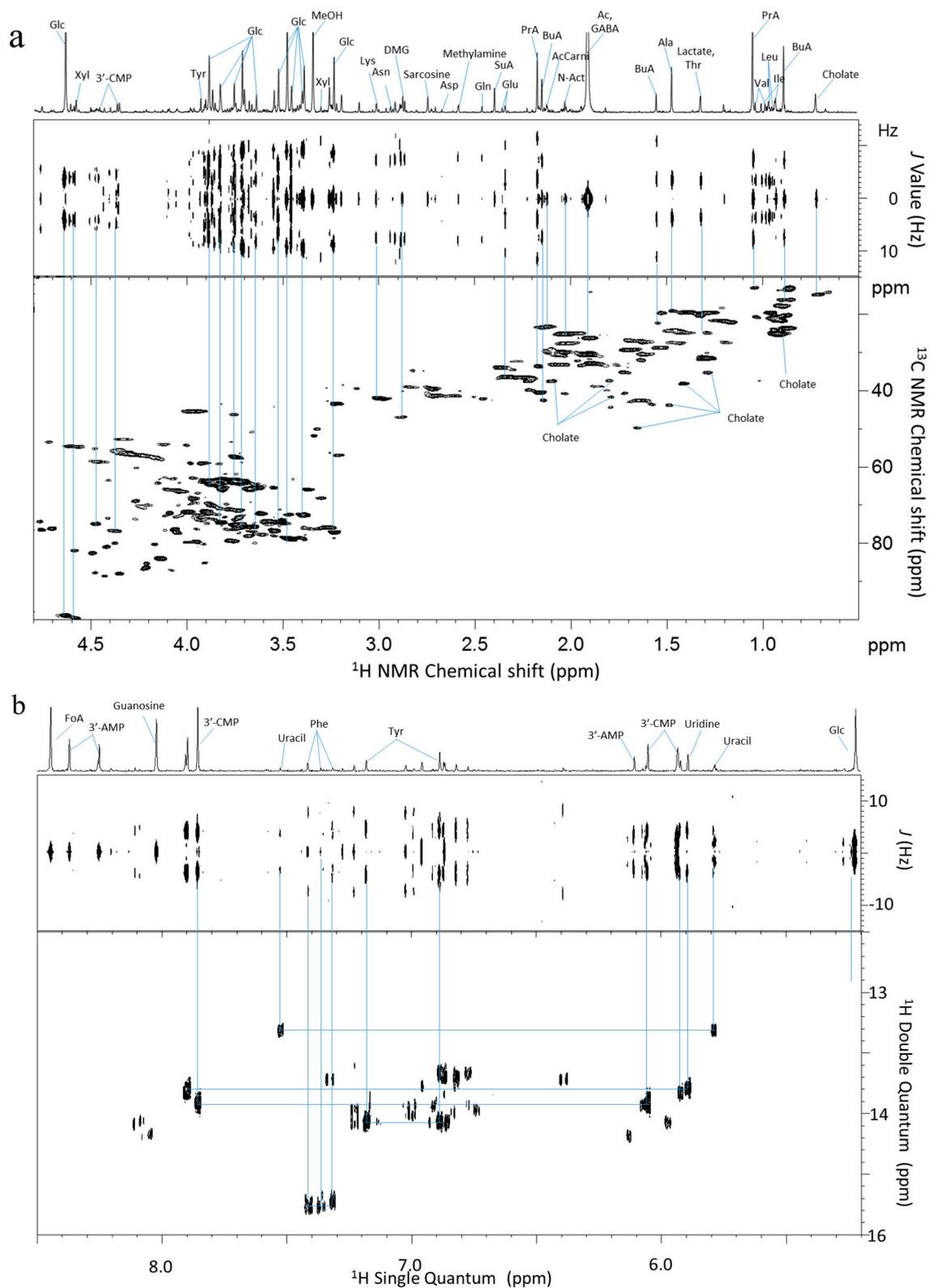
**Figure S3.**  $^1\text{H}$ - $^{13}\text{C}$  HSQC NMR spectra of *Pteridium aquilinum* and *Matteuccia struthiopteris* extracted by KPi/D<sub>2</sub>O solvent. (a) Black and blue line spectra are from *P. aquilinum* and *M. struthiopteris*, respectively. Green, red, and purple spectra are derived from glucose, sucrose, and fructose, respectively. Annotations for the referenced metabolites listed in Table S3. (b) Sugar group and organic acid compositions in raw or boiled *P. aquilinum* and *M. struthiopteris* are shown as a bar graph.



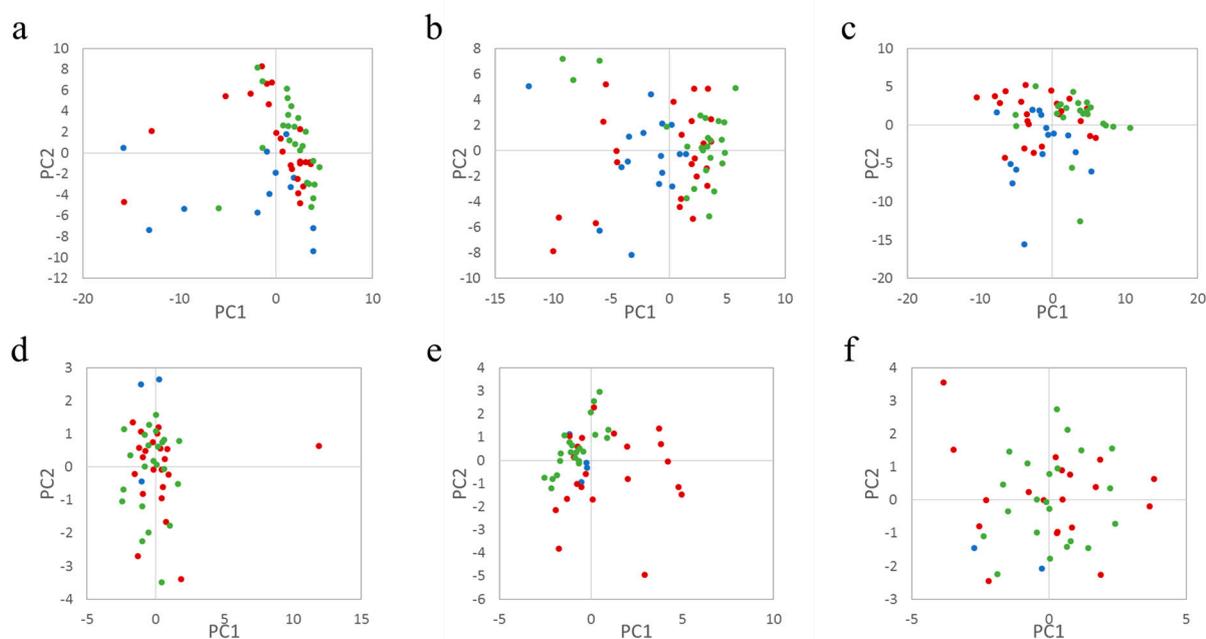
**Figure S4.**  $^1\text{H}$ - $^{13}\text{C}$  HSQC NMR spectra of *Pteridium aquilinum* and *Matteuccia struthiopteris* components extracted by DMSO-pyridine- $d_5$  (4:1) solvent. (a) Black and blue line spectra represent *Pteridium aquilinum* and *Matteuccia struthiopteris*, respectively. (b) Carbohydrate compositions in raw or boiled *P. aquilinum* and *M. struthiopteris* are shown as a bar graph.



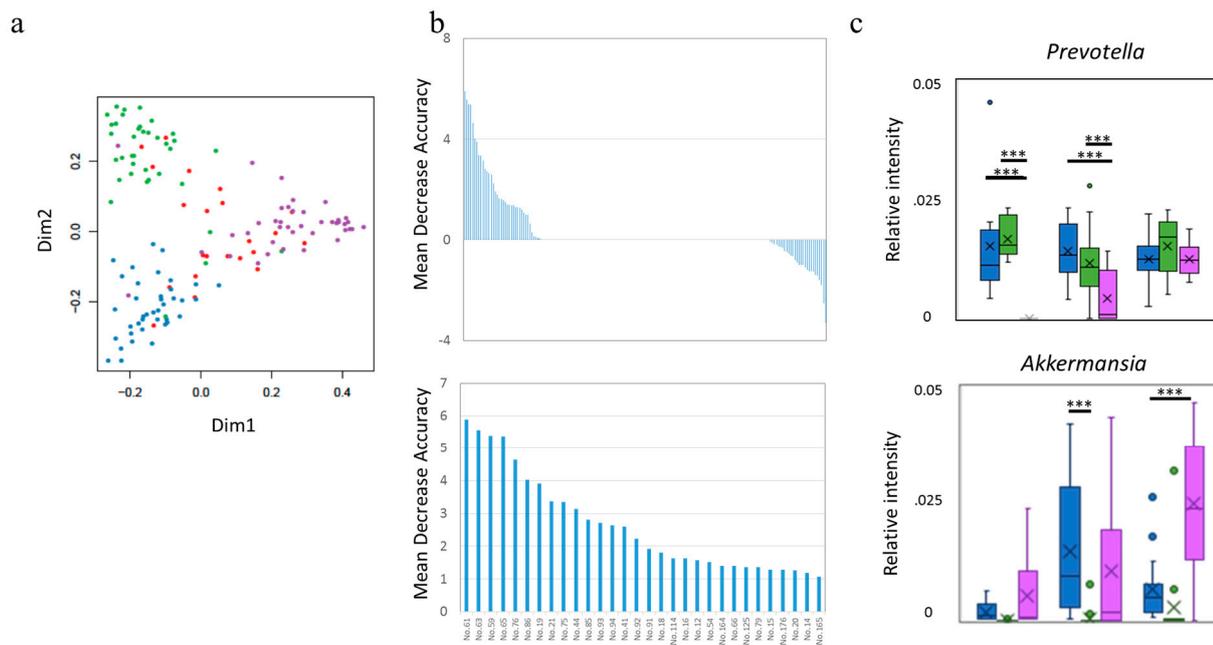
**Figure S5.** Annotation of metabolites in urine NMR spectra. Expanded version of  $^1\text{H}$  NMR spectra from treated mouse urine (top panel), 2D  $J$ -resolved NMR spectra (middle panel), and DQ-SQ NMR spectra (bottom panel) from 0.5 to 4.8 ppm (a), and 5.2 to 8.5 ppm (b). Annotations for the referenced metabolites listed in Table S3.



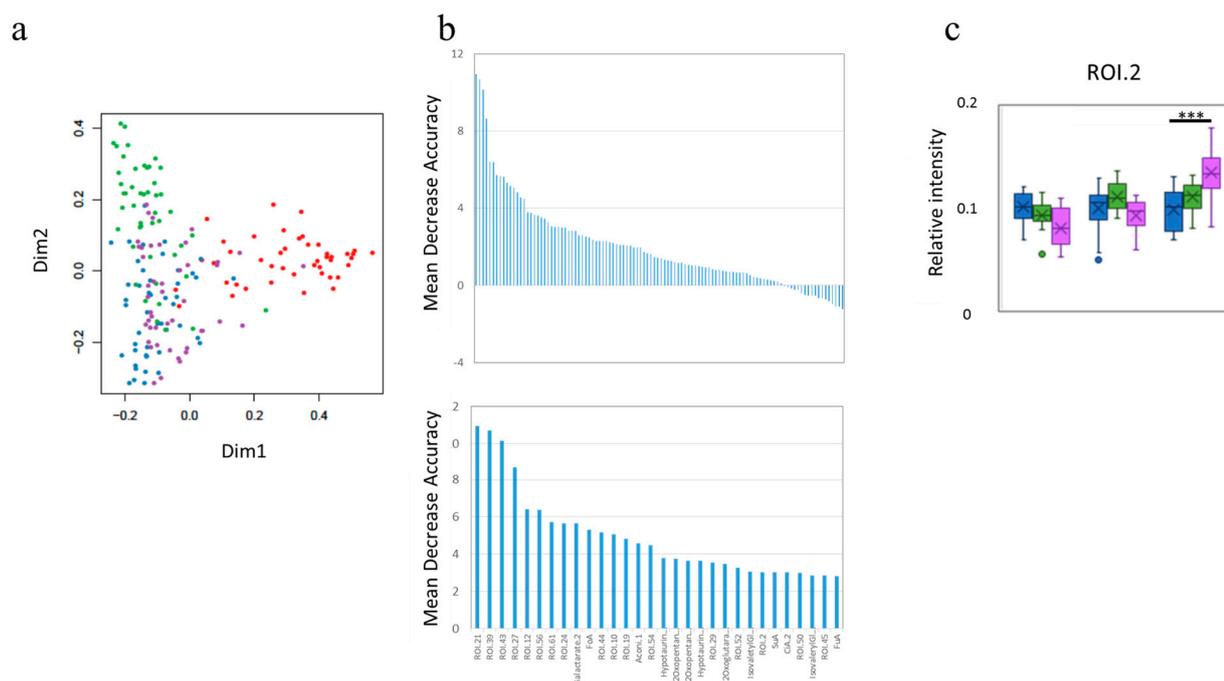
**Figure S6.** Annotation of metabolites in fecal NMR spectra. Expanded  $^1\text{H}$  NMR spectra from treated mouse feces (top panel), 2D  $J$ -resolved NMR spectra (middle panel), and DQ-SQ NMR spectra (bottom panel) from 0.5 to 4.8 ppm (a), and 5.2 to 8.5 ppm (b). Annotations for referenced metabolites listed in Table S3.



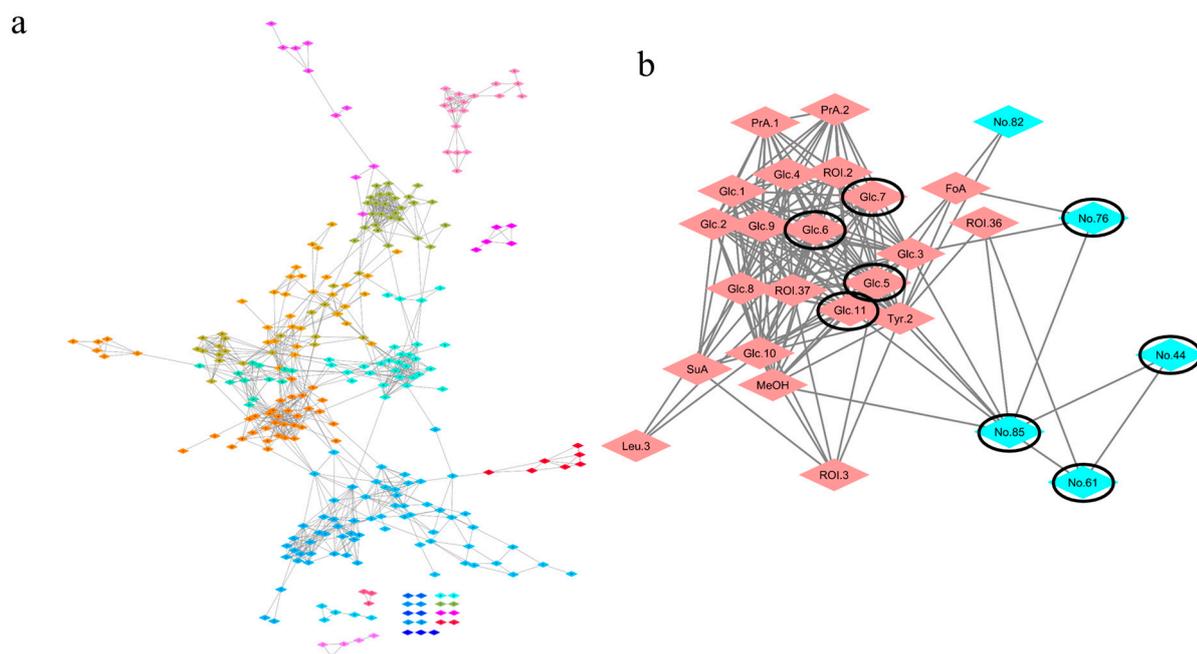
**Figure S7.** Principal component analysis of urinary metabolites and ions. Red, blue, and green spheres represent single data points from pretreatment, during treatment, and posttreatment, respectively. Upper panels indicate the results of urinary NMR measurement analyzed by PCA. The data based on experimentally treated mouse groups (a–c) administered cellulose, *Pteridium aquilinum*, and *Matteuccia struthiopteris*, respectively. (d–f) show PCA score plots for the ICP-OES data from each group. (d–f) represent ions of mice treated with cellulose, *Pteridium aquilinum*, and *M. struthiopteris* measured by ICP-OES, respectively. The data analysis was performed using the package “muma” in R [45].



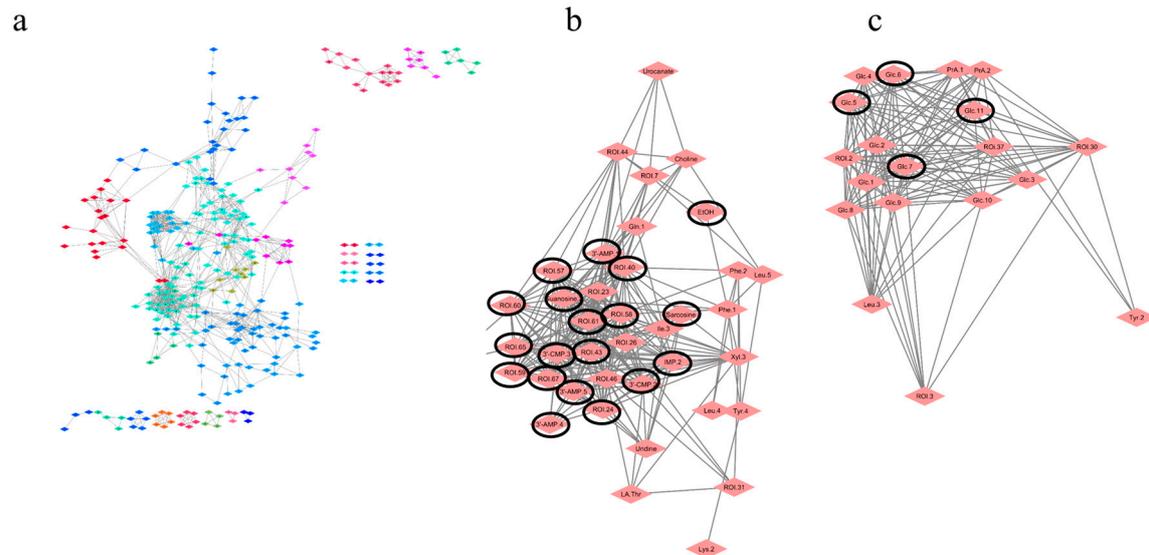
**Figure S8.** The results of Random Forest for the fecal microbiome. MDS plot (a) and factors important for separating the groups (b): upper panel indicates all important factors, while lower panel indicates the top 30 most important factors with annotation. In (a), red, blue, green, and purple spheres represent single data points from the pretreatment period of all groups, and cellulose-, *Pteridium aquilinum*-, and *Matteuccia struthiopteris*-treated groups, respectively. Boxplot of a representative important factor that can be applied on to network module (c). Upper panel and lower panel depict the genera *Prevotella* and *Akkermansia*, respectively. Blue, green, and purple boxes represent cellulose-, *P. aquilinum*-, and *M. struthiopteris*-treated groups, respectively. \*\*\*  $P < 0.001$  calculated by the Holm method.



**Figure S9.** The results of Random Forest for urinary metabolites. MDS plot (a) and factors important for separating the groups (b): upper panel indicates all important factors, while lower panel indicates the top 30 most important factors with annotation. In (a), red, blue, green, and purple spheres represent single data points from the pretreatment period of all groups, and cellulose-, *Pteridium aquilinum*-, and *Matteuccia struthiopteris*-treated groups, respectively. Boxplot of a representative important factor that can be applied onto network module, which depicts ROI.2 (c). Blue, green, and purple boxes represent cellulose-, *P. aquilinum*-, and *M. struthiopteris*-treated groups, respectively. \*\*\*  $P < 0.001$  calculated by the Holm method.



**Figure S10.** Network community correlation coefficients for *Matteuccia struthiopteris*-treated mice based on the combined data set. The network depiction is based on calculations by the igraph package with Cytoscape. All communities of *Matteuccia struthiopteris*-treated mice are depicted (a). The same color diamonds represent components belonging to the same community. The glucose community in *M. struthiopteris*-treated mice is depicted (b). Black-line-circled diamonds represent factors selected by Random Forest as being important for separating the groups (Table S3).



**Figure S11.** Network community correlation coefficients for *Pteridium aquilinum*-treated mice based on the combined data set. The network depiction is based on calculations by the igraph package with Cytoscape. All communities of *P. aquilinum*-treated mice are depicted (a). The same color diamonds represent components belonging to the same community. Purine/pyrimidine and glucose communities in *Matteuccia struthiopteris*-treated mice are indicated in (b) and (c), respectively. Black-line-circled diamonds represent factors selected by Random Forest as being important for separating the groups (TableS3).