Supplementary Tables S17

**Reagents**

Phospholipid mixtures were obtained from Avanti Polar Lipids, Inc. (Alabaster, AL). Lipid mediator standards and deuterium-labeled compounds used as internal standards were obtained from Cayman Chemical (Ann Arbor, MI). Trace element standard solutions, special grade reagents of ammonium bicarbonate, sodium chloride, diethyl ether and chloroform, nitric acid and perchloric acid of toxic metal determination grade, hydrogen peroxide for atomic absorption spectrometry, and high-performance liquid chromatography grade solvents (methanol, isopropanol, and acetonitrile) were purchased from Wako Pure Chemical Co. and from Kanto Chemical Co. Inc. (for untargeted lipidomics). Deionized water was produced by a Millipore-Q water system (Millipore, Bedford, MA, USA).

**Measuring instruments and measurement parameters**

GC--2010 Plus (Shimadzu Co., Kyoto, Japan) and LCMS-8060 (Shimadzu Co.) for targeted lipidomics, ThermoScientific Orbitrap Fusion Lumos with ThermoScientific Vanquish DGP system (Thermo Fisher Scientific Inc, Waltham, MA) for untargeted lipidomics, ThermoScientific Orbitrap Fusion Lumos with ThermoScientific Ultimate3000RS (ThermoScientific) for untargeted metabolomics, and an inductively coupled plasma-mass spectrometer (ICP-MS; Agilent 7700/Mass Hunter, Agilent Technologies, Inc. Agilent Technologies, USA) were used.

For GC-FID analysis, a FAMEWAX capillary column (30 m x 0.25 mm I.D x 0.25 μm, (Resteck Corporation) was used. The flow rate of carrier gas (He) was set at 45 cm/sec linear velocity. The temperature of the injection unit and the detector were 240°C and 250°C, respectively. The temperature of column oven was initiated at 140°C, then raised to 200°C at a rate of 11°C/min, then increased to 225°C at a rate of 3°C/min, and finally increased to 240°C at a rate of 20°C/min and held at this temperature for 5min. The injection volume was 2 μL in the split injection mode. Fatty acid methyl esters were identified and quantified using a mixture of Supelco 37 component FAME Mix (Merck, Germany), C22:5(n-3)-FAME (Sigma), C22:5(n-6)-FAME (Nu-Chek Prep. Inc., USA), and C22:4(n-6)-FAME (Cayman, USA) for calibration.

For untargeted lipidomics, AcquityUPLC BEH C8 column (1.7 μm, 2.1 mm x 100 mm, Waters) was used for reversed-phase chromatography and column temperature was 47˚C. Injection volume was 5 μL. A gradient analysis was performed with 5 mM NH4HCO3/Acetonitrile/2-propanol as mobile phase at a flow rate of 0.35 mL/min for 55 min per analysis. Pump gradient time was as follows: 0 min (5 mM NH4HCO3/Acetonitrile/2-propanol: 75/20/5)–20 min (20/75/5)–40 min (20/5/75)–45 min (5/5/90)–50 min (5/5/90)–55 min (75/20/5). For targeted lipidomics for fatty acid-derived lipid mediators and their related metabolites using was performed as described previously with some modifications1. Kinetex C8 column (2.6 μm, 2.1 mm × 150 mm, Phenomenex, Torrance, CA) was used and 5 μL of the prepared sample was injected. Gradient analysis was performed with water 0.1 %formic acid in water /Acetonitrile as mobile phase at a flow rate of 0.4 mL/min as described previously for urine samples as a 27 min gradient program. And for plasma and feces samples, extra wash was performed with 2-propanol. The washing method is as follows; 27 min (0.1% fomic acid in water/Acetonitrile/2-propanol: 5/95/0) - 30 min (5/50/45) - 35 min (5/50/45) - 38 min (5/5/90) - 42 min (5/5/90) – 42.1 min (5/95/0) – 44 min (5/95/0) – 44.1 min (90/10/0) – 48 min (90/10/0).

The trace elements (magnesium (Mg), calcium (Ca), chromium (Cr), manganese (Mn), iron (Fe), cobalt (Co), copper (Cu), zinc (Zn), and selenium (Se)) in the solutions were identified and quantitated by inductively coupled plasma-mass spectrometry (ICP-MS; Agilent7700/Mass Hunter, Agilent Technologies, Santa Clara, CA). Standard curves were plotted by preparing 1,000 µg/ml (ppm) standard solutions of Mg, Ca, Cr, Mn, Fe, Co, Cu, Zn, and Se (Fujifilm Wako Pure Chemical Industries Ltd., Osaka, Japan) and diluting them in 5% (v/v) nitric acid to final metal concentrations of 0, 1, 2, 5, 10, 20, 50, 100, and 200 ng/ml (ppb). For quality control, 1 ng/ml (ppb) of a reference internal standard (indium; In) was measured along with the samples. The standard curves of each trace metal exhibited good linear regression (over r = 0.999) in the concentration range of 1-200 ng/ml (ppb). Additionally, all elements placed in the mass number table by Agilent were semi-quantified simultaneously according to the recommended analytical method by Agilent. Briefly, mass intensities of all elements were corrected and semi-quantified by those of ICP-MS tuning solution, including five standard elements such as lithium (Li), Co, yttrium (Y), cerium (Ce), and thallium (Tl) at each final concentration of 1 ng/mL (ppb).

**Sequencing data processing and analysis**

Demultiplexed sequencing reads were subjected to primer trimming using Cutadapt v3.2 2, with the following command line options: -g ^GTGYCAGCMGNNNNNNNNN -G ^GGACTACNVGNNNNNNNNNN --no-indels --error-rate 0.2 --discard-untrimmed --max-n 0 --minimum-length 200:200. Amplicon sequence variants (ASVs) were then inferred using DADA2 v1.16.0 3, following additional trimming and filtering of reads using DADA2’s filterAndTrim function, specifying options truncLen = c(180, 180) and maxEE = c(3, 3). Learning of error models for forward and reverse reads (function learnErrors), denoising of forward and reverse reads (function data), merging of reads (function mergePairs), and removal of bimeras (function removeBimeraDenovo) were performed with default settings, with the exception that a minimal number of 2 × 108 bases from randomly selected samples were used (option 2 × 108 (option nbases = 2e+08 and randomize = TRUE). Taxonomy of the inferred ASVs was assigned using RDP’s naïve Bayesian classifier v2.134 specifying option --format fixrank.

Subsequently, a filtered ASVs table was generated by discarding ASVs lacking domain- and/or phylum-level taxonomic assignment (a bootstrap confidence score of 80%) as well as ASVs with an aberrant length (that is, shorter than 250 or longer than 255 bp based on the expected length of 253 bp for the V4 hypervariable region of the 16S rRNA gene). The filtered ASV table was 10 times randomly subsampled to 60,000 total counts per sample using *vegan* v2.5 (https://CRAN.R-project.org/package=vegan) rarefy function, averaged across subsamples (arithmetic mean), and converted to relative abundances by total sum scaling. Further, duplicate measurements for each monkey were averaged prior to downstream analysis by taking the arithmetic mean of ASV-wise relative abundances.

To correlate ASV relative abundance with water content, we considered ASVs detected (that is, with non-zero count in the rarified ASV table) in at least half of the samples. Spearman correlation coefficients and *p-values* were calculated using R v4.0.2 stats’s cor.test function and adjusted *p-values* generated using R stats’s p.adjust function (method = "fdr"), with a cut-off of 0.1 for significant correlations. Graphics were generated using *ggplot2* v3.3.3 (https://ggplot2.tidyverse.org) and *dplyr* v1.0.3 (https://CRAN.R-project.org/package=dplyr) in R.

**Lipid Data analysis**

Lipid species in plasma, urine, and stool samples of 20 monkeys were identified by LipidSearch4.2 using raw data file from mass spectrometry, aligned among monkeys, and then Spearman's rank correlation coefficients by arrays of quantitation value from 20 monkeys with all combination of identified lipids were calculated for each sample. The search parameters of Lipid Search were set as follows: precursor ion m/z tolerance and product ion m/z tolerance were both set to 5 ppm, intensity threshold of product ion was set to 1% of the precursor ion. If peaks within 5 ppm were detected more than once within a retention time of 0.1 min, they were considered the same lipid. The m-score was set to 5 or higher, and the lipid was identified if the grade (lipid subtype and fatty acid chains (full or partial) were identified) was displayed by the Lipid Search criteria.

For data analysis, Labsolutions version 5.61(Shimadzu Co.), GCsolution version 2.44 (Shimadzu Co.,), Compound Discoverer 2.1 (Thermo Fisher Scientific Inc), LipidSearch version 4.2 (Thermo Fisher Scientific Inc.), Human Metabolome Database (HMDB)(https://hmdb.ca/), MetaboAnalyst (https://www.metaboanalyst.ca/), Excel 2016 (Microsoft) were used for the calculation of Spearman's rank correlation and *p*-values, and *p*-values for a correlation coefficient were calculated by Excel program (https://www.statology.org/p-value-correlation-excel/).

References

1. Yamada, M. *et al.* A comprehensive quantification method for eicosanoids and related compounds by using liquid chromatography/mass spectrometry with high speed continuous ionization polarity switching. *J. Chromatogr. B Anal. Technol. Biomed. Life Sci.* **995**–**996**, 74–84 (2015).

2. Tácito, L. H. B., Yamada, L. N., de Souza Pinhel, M. A., Yugar-Toledo, J. C. & Souza, D. R. S. Influence of Apolipoprotein E on the Lipid Profile and Postprandial Triglyceride Levels in Brazilian Postmenopausal Women With Artery Disease. *Clin. Med. Insights Cardiol.* **11**, (2017).

3. Callahan, B. J. *et al.* DADA2: High-resolution sample inference from Illumina amplicon data. *Nat. Methods* **13**, 581–583 (2016).

4. Wang, Q., Garrity, G. M., Tiedje, J. M. & Cole, J. R. Naïve Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Appl. Environ. Microbiol.* **73**, 5261–5267 (2007).