SUPPLEMENTARY MATERIAL

Oatmeal-based fiber diet outperforms resistant starch-based fiber diet in lowering serum uric acid via gut microbiota-metabolite interactions: A randomized controlled trial

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Supplementary Methods

Supplementary method 1. Campus nutrition window.

The "Healthy China Action 2019-2030" and "National Nutrition Plan 2017-2030," issued by the State Council of China, explicitly outline goals such as meeting the healthcare needs of the people, promoting balanced diets, and health education. Subsequently, the Ministry of Education, in collaboration with the National Health Commission and four other departments of China, released the "Guidelines for Nutrition and Health School Construction." In these guidelines, it is emphasized that the establishment of nutritionally balanced school cafeterias is necessary. In line with these documents, our project team, in collaboration with the catering group of Sun Yat-sen University, set up the "Campus Nutrition Window" on the ground floor of the Songtao Garden Cafeteria at Sun Yat-sen University in Guangzhou city, which was equipped with a team of skilled chefs and experienced nutritionists, and aimed at offering a balanced, quantitative, low-sodium, and low-oil healthy diet **(Fig. S1a)**.

The Campus Nutrition Window officially started its trial operation in October 2021, catering to all students in Sun Yat-Sen University **(Fig. S1b)**. Its distinctive features include: 1) Strict portion control of food items (specified quantities for each meal and clear information on total calorie and macronutrient content); 2) Scientific combination of ingredients with a wide variety (no less than 5 different types of food items daily and no less than 25 different types weekly); 3) Cooking method of reduced salt and oil (daily salt intake limited to less than 5g and oil usage ranging from 25-30g); 4) Offering various types of healthy meal packages to all students (including general health packages, muscle-building packages, and weight-loss packages, etc.).

Supplementary method 2. Nutritional design principles and content of daily meal packages for intervention groups

Firstly, we calculated the estimated ideal body weight by the empirical Devine formula, which takes into account the height of each individual. Based on the IBW, the daily Estimated Energy Requirement (EER) for each participant was calculated, defined as 25 kcal/kg (IBW)/day, which has been validated in the practice of improving metabolic parameter. Subsequently, the 25th percentile (1160kcal/day) and the 75th percentile (1630kcal/day) of the rang of the EERs were selected as two representative levels to categorize the EERs for participants in the OM and RS groups.

Based on the recommended macronutrient distribution ranges from the Chinese Dietary Guidelines, which suggest that carbohydrates should account for 50%-65% of total energy, protein for 10%-15%, and fat for 20%-30%, we set the macronutrient distribution in the meal packages as follows: carbohydrates 60%, fat 25%, and protein 15%. Using this distribution, we then calculated the target nutrient contents for two different energy levels of the meal packages. Specifically, for the group with a daily energy requirement of 1160 kcal, the target nutrient intake per meal package is: 32.2 g of fat, 174 g of carbohydrates, and 43.5 g of protein. For the group with a daily energy requirement of 1630 kcal, the target nutrient intake per meal package is: 45.3 g of fat, 244.5 g of carbohydrates, and 61.1 g of protein. For both energy levels, the daily fiber intake is uniformly set at 25 g. In designing the fiber-rich diet, we used the same type of ingredients in different amounts to create meal packages for the two energy levels, ensuring that the set energy requirements, macronutrient ratios, and dietary fiber intake levels are met.

Supplementary method 3. Preparation of the meal packages, and internet and on-site integrated dietary intervention.

Quantitative Fiber-rich meal packages were designed by project staff and nutritionists in alignment with The Dietary Guidelines for Chinese Residents (2016), the China Food Composition (2nd Edition), CHINESE DIETARY REFERENCE INTAKES (2013 Edition), and prepared by skilled chefs at the Campus Nutrition Window. A daily dietary plan regimen comprised breakfast, lunch, and dinner, and guaranteed a minimum of 25g/day of dietary fiber. Two sets of dietary menus were alternated twice per week (one menu from Mon-Wed and another from Thu-Fri) in order to reduce participants' aversion and fatigue, thus promoting adherence.

In order to design personalized dietary intervention plans, participants in the Oat meal (OM) and RS (resistant starch) groups were assigned to well-matched, diverse food sources, and quantified diet plans at different energy levels. The estimated ideal body weight (IBW) of each participant was calculated using the empirical Devine formula, which takes into account the height of each individual. Based on the IBW, the daily Estimated Energy Requirement (EER) for each participant was calculated, defined as 25 kcal/kg (IBW)/day, which has been validated in the practise of reducing body weight and improving metabolic parameter. Subsequently, the 25th percentile (1160kcal/day) and the 75th percentile (1630kcal/day) of the rang of the EERs were selected as two representative levels to categorize the EERs for undergraduates in the OM and RS groups, thus personalizing the energy provided with the three daily meal packages to the greatest extent. When designing the Fiber-rich diet, meal packages with different amounts of the same type of ingredients were paired to achieve these two different energy levels, ensuring the set energy needs, macronutrient ratios, and dietary 50fiber levels (25 g/day) were met. Given that RS comes in various types, we selected RS2 type, which is a form of RS with a granular structure, as the staple food for RS group. Finally, these meal packages were cooked, weighted quantitatively, packaged, and offered to participants at the Campus Nutrition Widow.

Those meal packages were distinguished based on packing boxes that were marked with various colours and features, allowing participants to select their corresponding

meals. During the 8-week intervention period, participants received three meal packages each day following the dietary plan from the Campus Nutrition Window, Monday through Friday.

To maintain quality control, participants were required to submit daily dietary intake records using an internet-based methodology. Before each meal, participants were tasked with photographing the meal boxes and upload them online as a check-in form to record package collection **(Fig. S10a)**. After dining, participants were instructed to indicate whether they fully consumed their meal packages. Furthermore, they were asked to document the type and amount of any food that were discarded after each meal and consumed between meals **(Fig. S10b)**. Every evening, the project team staff reviews these reports and provided reminders to participants who showed inconsistent compliance.

During weekends, participants in the intervention groups were given autonomy to choose their meals and dining venues. However, they were encouraged to adhere to a healthy diet and required to document their food consumption for the sake of consistency and assessment.

Supplementary method 4. Stool sampling, fecal microbial DNA extraction, amplification, and 16S rRNA gene sequencing.

Upon completion of the physical examination, all participants received a fecal sample collection kit, which included a fecal collection tube, a cotton swab, a label, and personal protective equipment. Within three days after the baseline and post-intervention examinations, all participants were required to collect a 3g sample of their own feces, which was to be delivered immediately to the refrigerator at -20 ℃. The samples were then stored in a refrigerator at -80°C in preparation for future gut microbiota testing.

Due to fund capacity, only the top 20 individuals with the highest BMI at baseline in each group were selected for gut microbiota analysis at baseline and 8-week. In accordance with the instructions provided by the DNA extraction kits, genomic DNA was extracted and then evaluated for integrity and purity through 1% agarose gel electrophoresis. The DNA concentration and purity were further determined using the NanoDropone system. PCR amplification was carried out using genomic DNA as the template, followed by product electrophoresis. Primer selection was informed by the desired sequencing regions and incorporated barcodes and PremixTag (TaKaRa). After comparing PCR product concentrations using GeneTools Analysis Software (Version 4.03.05.0, SynGene), the requisite volumes for each sample were calculated based on the principle of equimolarity. Subsequently, the PCR products were mixed in accordance with these calculations. The E.Z.N.A. Gel Extraction Kit was used to recover these mixed PCR products, with target DNA fragments eluted using TE buffer. Library construction adhered to the standard protocol of the NEBNext® Ultra™ DNA Library Prep Kit for Illumina. Sequencing was then executed on the HiSeq or MiSeq high-throughput platforms. Raw image data files obtained from the sequencing process were transformed into raw sequencing sequences (Raw Reads) via Base Calling analysis. The results were stored in the FASTQ file format, which encompasses both the sequencing sequence (Reads) information and the corresponding sequencing quality information.

In terms of 16s rRNA sequencing, raw paired-end FASTQ files generated from the DNA extraction, PCR amplification, library construction, and sequencing stages were initially filtered using FASTP (version 0.14.1). The sliding window for quality trimming was set at -W 4 -M 20. Primers were removed using CUTADAPT, which is based on the sequence information from both ends, yielding quality-controlled paired-end clean reads. The clean reads were subsequently assembled based on their overlap using the -fastq mergepairs function in USEARCH (version 10), with default settings requiring a minimum overlap length of 16bp and a maximum mismatch of 5bp in the overlapping area. Assembled sequences meeting these criteria were retained and underwent a second round of sliding window quality trimming with FASTP (-W 4 -M 20), providing effective clean assembled sequences. Following this, a feature table was generated using the DADA2 denoise procedure following the QIIME 2 (version 2020.11.0) pipeline. The table was aligned to the SILVA database (V.123) using the -sintax function in USEARCH for taxonomy annotation, with a confidence threshold of 0.8. Features annotated as chloroplasts or mitochondria, or those not annotated as bacteria at the kingdom level, were removed. The sequence feature table was rarefied to the minimum number of sequences within each sample to minimize the influence of sequencing depths on downstream analyses.

Supplementary method 5. Blood specimen collection, biochemical measurements, and serum metabolomics profiling.

All study participants were instructed to fast from 20:00 the evening before both the baseline and final examinations, with the allowance for minimal water intake. Examinations took place in the morning, during which trained clinical nurses collected a 5 ml fasting blood sample from each participant's antecubital vein. The collected blood samples were immediately stored in a refrigerator set at -20°C, followed by a centrifugal separation procedure (3000r/min, 10min). The separated serum samples were subsequently frozen and stored in a -80°C refrigerator, awaiting further biochemical analysis.

Stored venous blood samples from each participant, preserved at -80 °C, were subsequently analyzed for various health parameters. These included: 1) fasting plasma glucose (FPG), fasting insulin (FINS), homeostatic model assessment of insulin resistance (HOMA-IR), and homeostatic model assessment of β-cell function (HOMA-β); 2) serum lipid profiles, comprising triglyceride (TG), total cholesterol (TC), high-density lipoprotein cholesterol (HDL-C), and low-density lipoprotein cholesterol (LDL-C); and 3) uric acid (UA) and high-sensitivity C-reactive protein (hs-CRP). These assessments were conducted by a biomedical analysis company, KingMed Diagnostics Group Co., Ltd., located in Guangzhou, China.

For serum metabolomics profiling, only the top 10 individuals with the highest BMI at baseline in each group were selected for serum metabolomics analysis, due to budget constraints. For the participants examined, 100 μL of serum sample was transferred into an Eppendorf tube. We then added 400 μL of an extract solution (acetonitrile: methanol = 1: 1, including an isotopically-labelled internal standard mixture). The samples were vortexed for 30 seconds, sonicated for 10 minutes in an ice-water bath, and incubated at -40℃ for an hour to precipitate proteins. Post incubation, the samples were centrifuged at 12,000 rpm (RCF=13800(×g), R= 8.6cm) for 15 minutes at 4 ℃. The resulting supernatant was transferred to a fresh glass vial for subsequent analysis. Quality control (QC) samples were prepared by mixing equal aliquots of the supernatants from all samples. LC-MS/MS analyses were conducted

using an UHPLC system (Vanquish, Thermo Fisher Scientific) with a UPLC BEH Amide column (2.1 mm × 100 mm, 1.7 μm) coupled to an Orbitrap Exploris 120 mass spectrometer (Orbitrap MS, Thermo). The mobile phase consisted of 25 mmol/L ammonium acetate and 25 mmol/L ammonium hydroxide in water (pH = 9.75) (A), and acetonitrile (B). The auto-sampler temperature was set at 4 ℃, and the injection volume was 2 μL. The Orbitrap Exploris 120 mass spectrometer was utilized for its capacity to acquire MS/MS spectra on an information-dependent acquisition (IDA) mode under the control of the acquisition software (Xcalibur, Thermo). In this mode, the acquisition software continually evaluates the full scan MS spectrum. The ESI source conditions were set as follows: sheath gas flow rate at 50 Arb, Aux gas flow rate at 15 Arb, capillary temperature at 320 ℃, full MS resolution at 60000, MS/MS resolution at 15000, collision energy at 10/30/60 in NCE mode, and spray Voltage at 3.8 kV (positive) or -3.4 kV (negative). The raw data were transformed into the mzXML format using ProteoWizard and then processed with an in-house program developed in R, based on XCMS. This program facilitated peak detection, extraction, alignment, and integration. Following this, a metabolite annotation of each peak was carried out using an MS2 database, known as BiotreeDB. The threshold for annotation was set at 0.3.

Table S1 Comparison of baseline characteristics between microbiome and non-microbiome test groups

Characteristic	RS Group			OM group			CON group		
	Non-Microbiome Tested (n = 11)	Microbiome Tested (n = 20)	*P* value	Non-Microbiome Tested (n = 11)	Microbiome Tested (n = 20)	*P* value	Non-Microbiome Tested (n = 10)	Microbiome Tested (n = 20)	*P* value
Male n, %	2 (18.18)	11 (55.00)	0.066	5 (41.67%)	9 (45.00%)	1.000	5 (50.00%)	10 (50.00%)	1.000
Age, years	18.00 [18.00, 18.00]	18.00 [18.00, 18.00]	0.566	18.00 (18.00, 19.00)	18.00 (18.00, 18.00)	0.082	19.00 (18.25, 19.00)	19.50 (19.00, 20.00)	0.026
SUA, μ mol/L	397.00 (326.50, 470.00)	420.00 (361.75, 488.25)	0.730	437.00 (339.50, 523.00)	393.00 (358.75, 486.25)	0.985	362.50 (331.50, 446.25)	374.50 (348.00, 458.25)	0.628
Weight, Kg	70.60 (60.80, 74.25)	67.35 (63.23, 75.83)	0.869	71.40 (66.88, 79.23)	70.10 (63.00, 76.53)	0.893	77.25 (65.15, 87.78)	65.35 (61.80, 75.85)	0.153
WC, cm	85.40 (79.25, 88.35)	81.60 (76.42, 89.40)	0.741	78.90 (76.67, 92.30)	79.50 (74.42, 88.53)	0.984	83.50 (76.40, 94.90)	76.15 (72.98, 83.52)	0.155
BFM, kg	21.10 (18.65, 26.85)	19.15 (16.03, 22.60)	0.103	22.00 (18.02, 24.28)	20.70 (18.00, 22.85)	0.726	22.50 (18.52, 27.38)	18.15 (15.68, 20.45)	0.020
BFP, %	33.38 ± 5.90	27.43 ± 6.23	0.015	30.93 ± 7.52	29.61 ± 5.52	0.604	31.30 ± 6.29	26.88 ± 7.01	0.096
BMI, Kg/m2	25.20 (23.40, 26.10)	24.30 (22.48, 26.10)	0.471	24.65 (22.87, 28.43)	24.35 (23.20, 26.05)	0.953	25.20 (23.65, 29.28)	23.10 (22.78, 24.38)	0.009
TC, mmol/L	4.31 ± 0.73	4.11 ± 0.59	0.451	4.58 ± 0.51	4.19 ± 0.69	0.077	4.23 ± 0.92	4.47 ± 0.56	0.456
TG, mmol/L	0.90 (0.70, 0.95)	0.85 (0.68, 1.11)	0.901	0.78 (0.54, 1.13)	0.76 (0.68, 0.99)	0.640	1.02 (0.69, 1.77)	0.90 (0.74, 1.03)	0.333
HDL-C, mmol/L	1.48 (1.31, 1.62)	1.38 (1.26, 1.55)	0.635	1.40 (1.24, 1.54)	1.34 (1.23, 1.44)	0.830	1.21 (1.11, 1.33)	1.38 (1.24, 1.61)	0.153
LDL-C, mmol/L	2.48 ± 0.69	2.33 ± 0.52	0.536	2.75 ± 0.52	2.41 ± 0.53	0.098	2.50 ± 0.69	2.69 ± 0.50	0.446
GLU, μmol/L	4.28 ± 0.33	4.34 ± 0.30	0.594	4.47 ± 0.46	4.30 ± 0.51	0.361	4.47 ± 0.47	4.30 ± 0.47	0.373
FINs, μU/mL	12.27 ± 4.77	9.91 ± 4.67	0.198	9.91 ± 6.09	10.51 ± 6.69	0.798	12.97 ± 6.99	10.30 ± 6.12	0.320
hs-CRP, mg/L	1.07 (0.63, 1.81)	0.52 (0.45, 1.17)	0.433	0.79 (0.39, 0.99)	0.51 (0.33, 0.97)	0.402	0.42 (0.34, 2.56)	0.33 (0.25, 0.66)	0.179
Paternal educational level (%)			0.250			0.046			0.588
Junior high school and below	2 (18.18%)	6 (30.00%)		3 (27.27%)	4 (20.00%)		1 (10.00%)	4 (20.00%)	
High school to junior college	2 (18.18%)	8 (40.00%)		0 (0.00%)	8 (40.00%)		4 (40.00%)	10 (50.00%)	
Bachelor's degree and above	7 (63.64%)	6 (30.00%)		8 (72.73%)	8 (40.00%)		5 (50.00%)	6 (30.00%)	

Characteristic	RS Group			OM group			CON group		
	Non-Microbiome Tested (n = 11)	Microbiome Tested (n = 20)	*P* value	Non-Microbiome Tested (n = 11)	Microbiome Tested (n = 20)	*P* value	Non-Microbiome Tested (n = 10)	Microbiome Tested (n = 20)	*P* value
Maternal educational level (%)			0.450			0.320			0.611
Junior high school and below	3 (27.27%)	7 (35.00%)		2 (18.18%)	3 (15.00%)		1 (10.00%)	5 (25.00%)	
High school to junior college	4 (36.36%)	10 (50.00%)		3 (27.27%)	11 (55.00%)		3 (30.00%)	7 (35.00%)	
Bachelor's degree and above	4 (36.36%)	3 (15.00%)		6 (54.55%)	6 (30.00%)		6 (60.00%)	8 (40.00%)	
Monthly household income, RMB/person >5000 yuan (%)	6 (60.00%)	7 (38.89%)	0.433	4 (50.00%)	8 (44.44%)	1.000	2 (22.22%)	9 (52.94%)	0.217
Outdoor time h/d > 2h (%)	1 (9.09%)	2 (10.00%)	1.000	2 (18.18%)	1 (5.00%)	0.281	1 (10.00%)	1 (5.00%)	1.000
Dietary intake									
Energy, kcal/d	1335.00 (985.50, 1757.83)	1822.33 (1468.67, 2075.75)	0.215	1701.50 (1376.75, 2051.25)	1738.00 (1222.00, 2167.75)	0.924	1761.00 (1504.00, 1944.00)	1603.00 (1369.00, 1773.00)	0.434
Protein, g/d	55.20 (40.70, 78.13)	77.43 (59.32, 92.77)	0.129	63.10 (57.15, 81.45)	79.25 (56.70, 94.07)	0.580	57.70 (55.80, 80.80)	63.50 (50.80, 80.90)	0.936
Dietary fat, g/d	37.80 (35.57, 57.68)	59.00 (43.97, 67.50)	0.057	56.70 (43.45, 79.25)	68.20 (53.55, 78.00)	0.674	63.70 (60.80, 68.30)	63.60 (52.40, 71.60)	0.850
Carbohydrates, g/d	145.57 (120.50, 225.45)	251.30 (179.00, 300.57)	0.183	198.60 (176.80, 236.12)	247.70 (200.20, 287.47)	0.136	227.05 (178.78, 257.68)	189.10 (161.40, 239.70)	0.633
Dietary fiber, g/d	5.07 (3.90, 7.30)	7.20 (5.52, 8.48)	0.210	7.10 (5.55, 10.47)	11.15 (5.90, 14.35)	0.259	6.65 (4.48, 9.50)	6.70 (5.30, 12.30)	0.563

Data are presented as mean ± SD, median [IQR], or n (%), P-values among groups were determined by analysis of covariance, Kruskal-Wallis test, or chi-square test.

Abbreviations: BFM: Body fat mass; BMI: Body mass index; BFP: Body fat percentage; FINS: Fasting insulin; FPG: Fasting plasma glucose; HDL-C: High-density lipoprotein cholesterol; hs-CRP: High-sensitivity C-reactive protein; LDL-C: Low-density lipoprotein cholesterol; RS: resistant starch group; SUA: serum uric acid; TC: Total cholesterol; TG: Triglyceride; OM: oat meal group; WC: Waist circumference.

Table S2. Matching Table of Microbiome and Metabolomics Samples

Participant ID	Group	Microbiota sequencing	Metabolomics Profiling
1	resistant starch group	Completed	
6	resistant starch group	Completed	
10	oat meal group	Completed	
12	oat meal group	Completed	
13	resistant starch group	Completed	
17	resistant starch group	Completed	
18	oat meal group	Completed	
47	oat meal group	Completed	Completed
56	resistant starch group	Completed	
57	oat meal group	Completed	Completed
63	resistant starch group	Completed	
65	oat meal group	Completed	
68	resistant starch group	Completed	Completed
73	resistant starch group	Completed	Completed
76	oat meal group	Completed	Completed
87	oat meal group	Completed	Completed
88	resistant starch group	Completed	Completed
91	resistant starch group	Completed	Completed
95	oat meal group	Completed	Completed
96	resistant starch group	Completed	Completed
103	resistant starch group	Completed	
104	oat meal group	Completed	
106	oat meal group	Completed	
114	oat meal group	Completed	
118	oat meal group	Completed	Completed
121	resistant starch group	Completed	Completed
130	resistant starch group	Completed	Completed
133	resistant starch group	Completed	Completed
136	oat meal group	Completed	
138	resistant starch group	Completed	
142	oat meal group	Completed	
145	resistant starch group	Completed	
152	oat meal group	Completed	
154	resistant starch group	Completed	
187	oat meal group	Completed	Completed
193	resistant starch group	Completed	Completed
196	oat meal group	Completed	Completed
203	resistant starch group	Completed	Completed
207	oat meal group	Completed	Completed
208	control group	Completed	
216	oat meal group	Completed	Completed
602	control group	Completed	

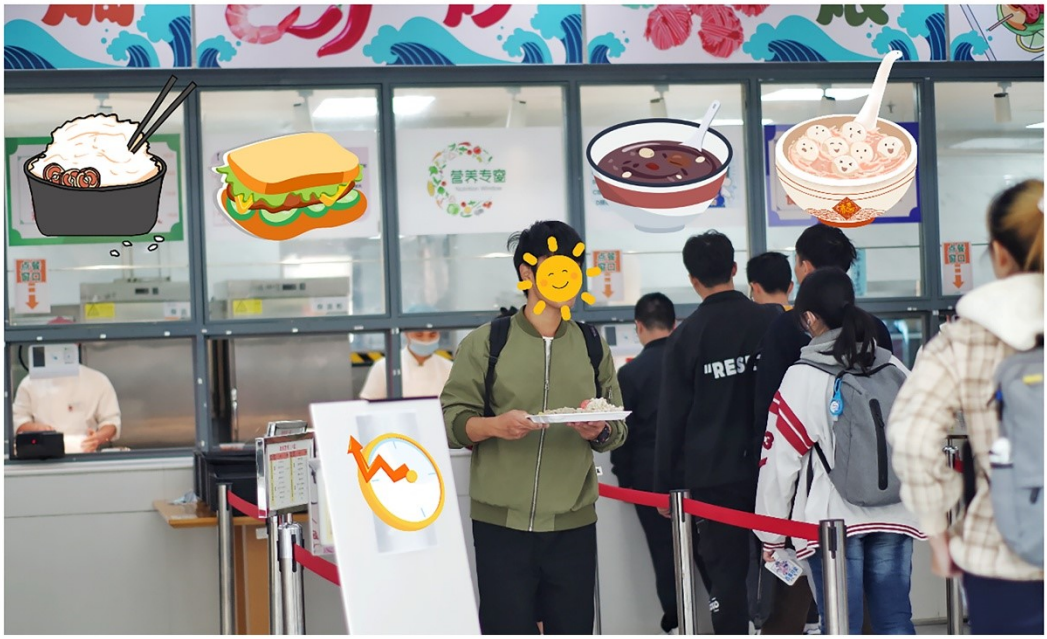
603	control group	Completed	Completed
606	control group	Completed	
607	control group	Completed	
608	control group	Completed	
609	control group	Completed	Completed
610	control group	Completed	Completed
612	control group	Completed	Completed
613	control group	Completed	Completed
614	control group	Completed	
615	control group	Completed	
619	control group	Completed	
620	control group	Completed	Completed
623	control group	Completed	Completed
625	control group	Completed	Completed
628	control group	Completed	
629	control group	Completed	
630	control group	Completed	Completed
631	control group	Completed	Completed

Supplementary Figures

Fig. S1 The Campus Nutrition Window

A

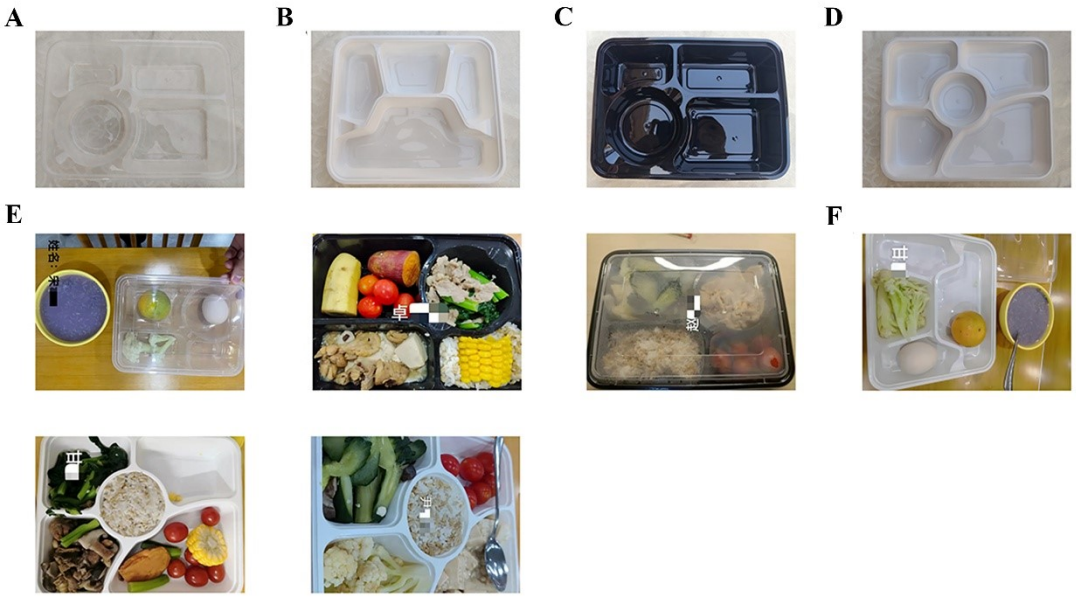
B



(A): Slogan of the Campus Nutrition Window.

(B): A scene of college students picking up meals at the Campus Nutrition Window

Fig. S2 Packing boxes and packed meals prepared for the participants.

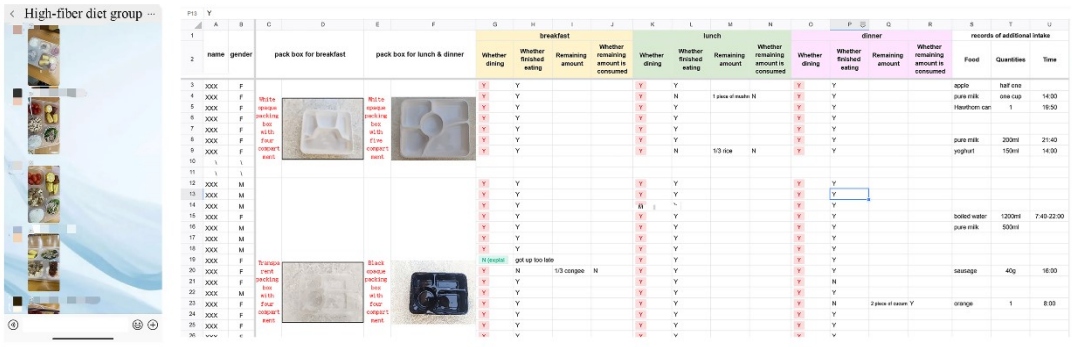


(A): Transparent four-compartment packing box: Used for packing breakfast for participants with an EER of 1630kcal/d. (B): White opaque four-compartment packing box: Used for packing breakfast for participants with an EER of 1160kcal/d. (C): Black opaque four-compartment packing box: Used for packing lunch and dinner for participants with an EER of 1630kcal/d. (D): White opaque five-compartment packing box: Used for packing lunch and dinner for participants with an EER of 1160kcal/d. (E): Example of breakfast, lunch, and dinner for participants with an EER of 1630kcal/d. (F): Example of breakfast, lunch, and dinner for participants with an EER of 1160kcal/d. Sample photos were taken by participants after retrieving their meals, with personal information redacted.

Abbreviation: EER: Estimated Energy Requirement.

Fig. S3 The follow-up of participants involved in dietary intervention groups.

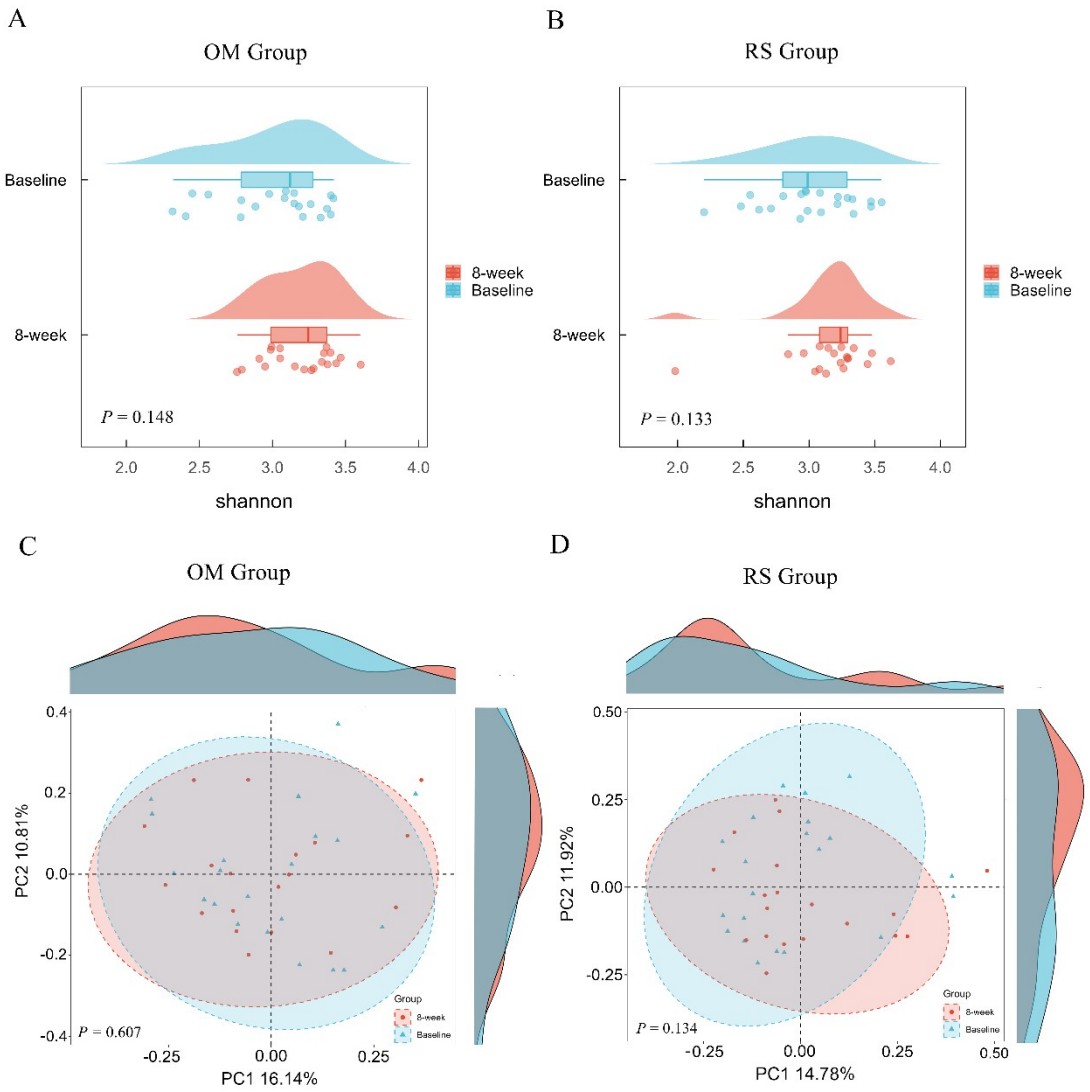
A **B**



(A): The meal-packages were taken by participants after retrieving their meals and sent to the online chat group as a check-in. Personal information was redacted.

(B): Daily dietary records for follow-up participants.

Fig. S4 Changes in gut microbiota diversity in OM and RS groups before and after an



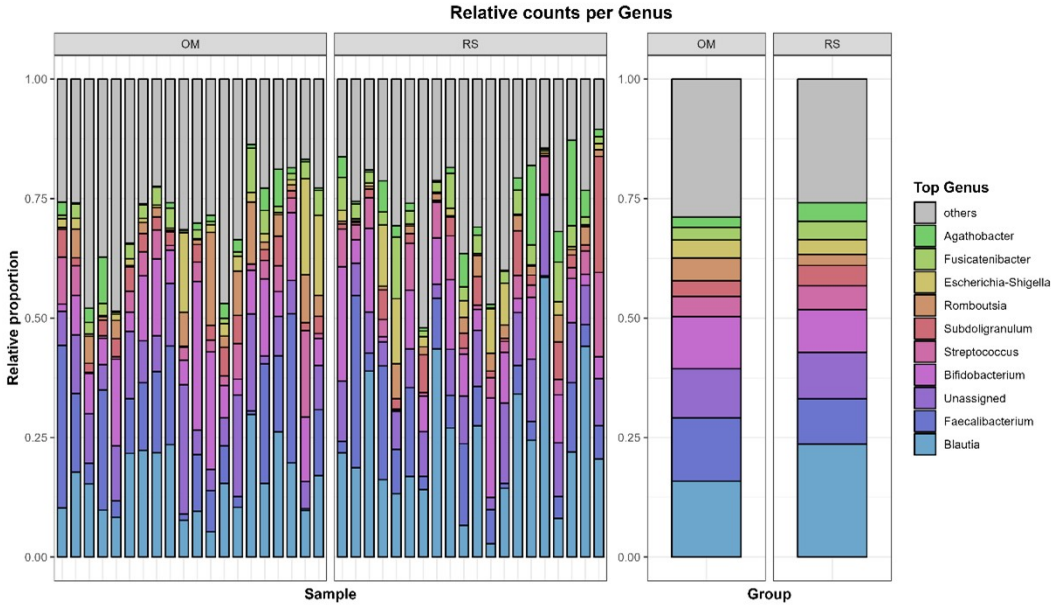
8-week intervention.

(A and B): alpha diversity of gut microbiota before and after interventions in OM (A) and RS (B) group participants.

(C and D): beta diversity of gut microbiota before and after interventions in OM (C) and RS (D) group participants.

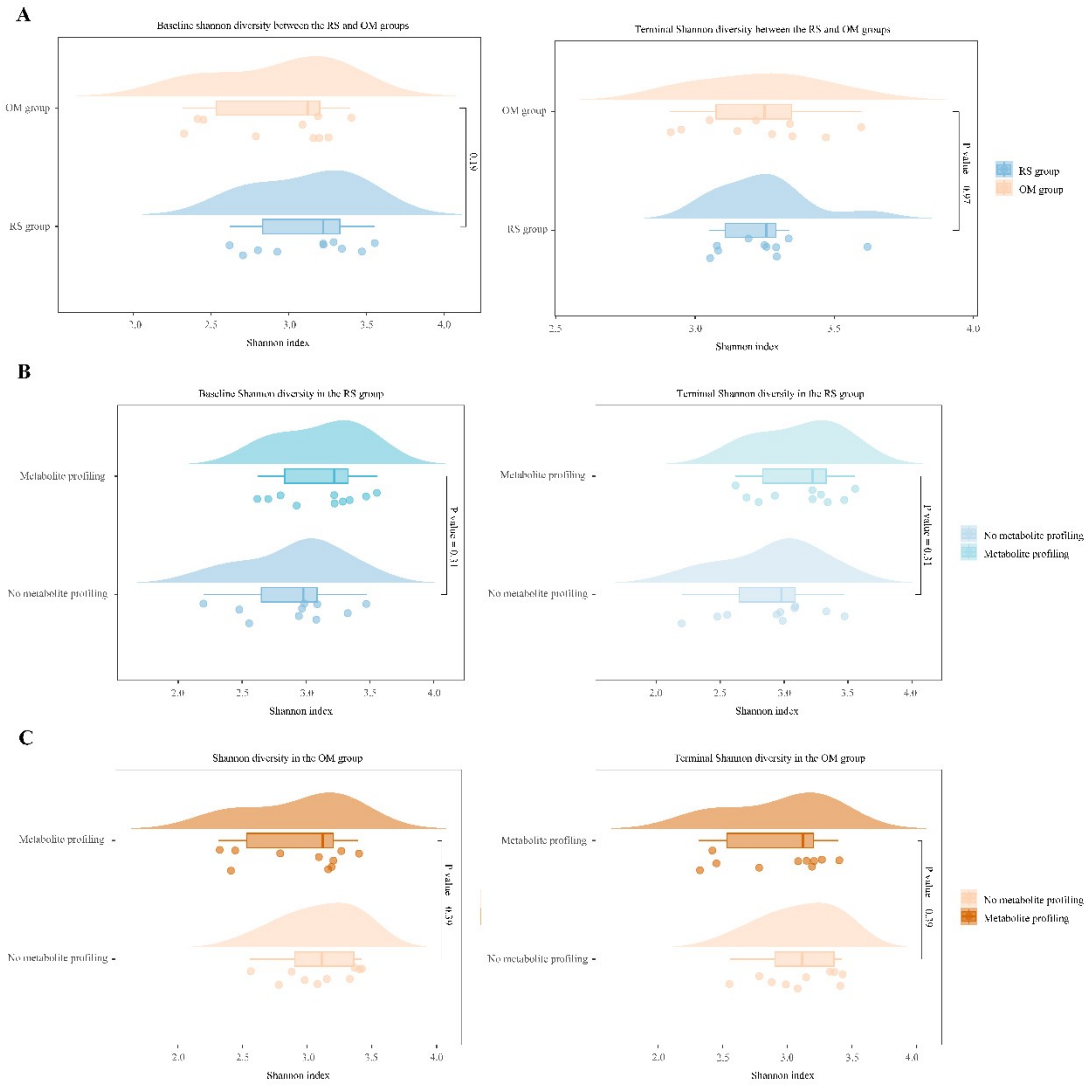
Abbreviation: OM: oat meal; RS: resistant starch.

Fig. S5 Stacked bar chart of the top 10 genera in the OM and RS groups following the intervention.



Abbreviation: OM: oat meal; RS: resistant starch.

Fig. S6 Gut microbiota alpha diversity analysis in the metabolomics-profiled subset and comparison with non-metabolomics participants



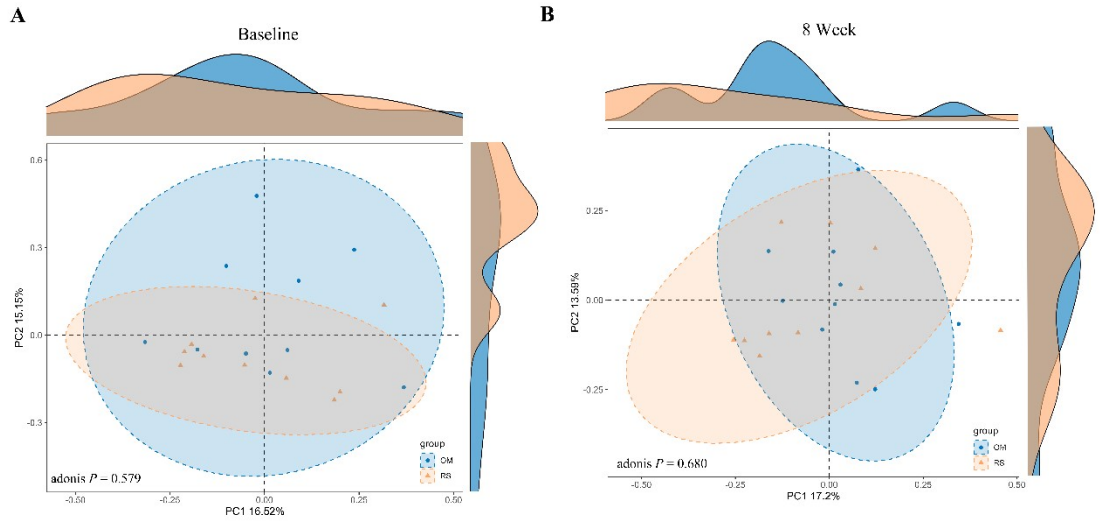
(A) Alpha diversity analysis of gut microbiota in the 20 participants who underwent metabolomics profiling, comparing the RS and OM groups at baseline and post-intervention.

(B) Comparison of alpha diversity between participants with and without metabolomics profiling within the RS group.

(C) Comparison of alpha diversity between participants with and without metabolomics profiling within the OM group.

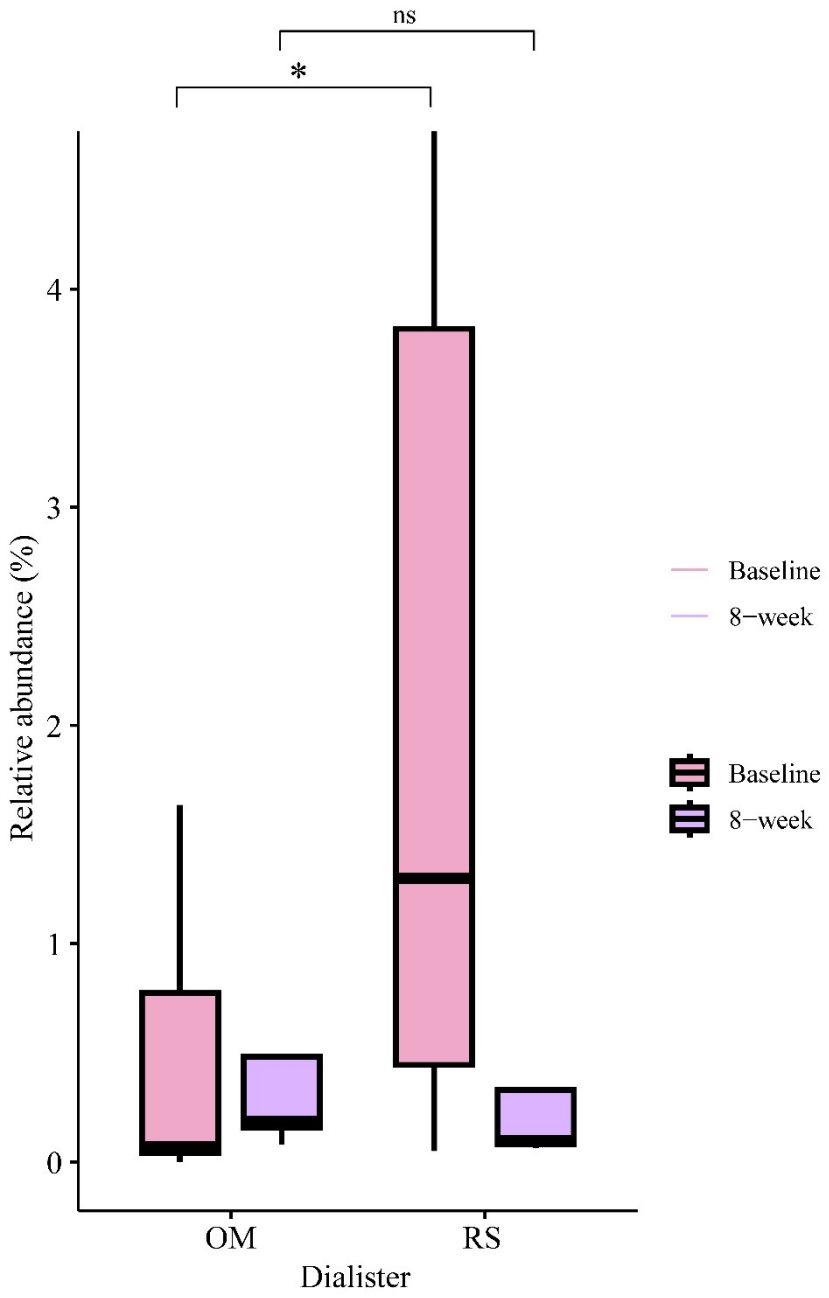
Abbreviation: OM: oat meal; RS: resistant starch.

Fig. S7 Comparable gut microbiota beta diversity in the subset of participants who underwent metabolomics profiling



Abbreviation: OM: oat meal; RS: resistant starch.

Fig. S8. Relative abundance of Dialister at baseline and after 8-week intervention in the subset of participants who underwent metabolomics profiling



Abbreviation: OM: oat meal; RS: resistant starch.

Fig. S9. Associations between differential genera and differential metabolites after the intervention